Uncovering the molecular networks underlying organismal health and disease

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Dedicated to the man who "eradicated malaria" from Lebanon.

I miss you jeddo (grandpa)

Acknowledgment

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Abstract

Networks of diverse cells are required to sustain the life of multicellular organisms. These cells are in turn made up of distinctive genetic networks that define their identity, functions, and interactions. These levels of biological organization rely on each other and a single perturbation to a cell's gene network can have detrimental consequences on the whole system and lead to disease or death. Therefore, studying the genetic networks of a cell in various contexts of health and disease can give important insights into the molecular drivers of disease and identify effective points of intervention. Here, I present three projects that explore the relationship between intracellular gene networks and organismal health. In the first project, we show how the gene *adh-1*, which encodes an alcohol dehydrogenase, acts downstream of several well-known genetic pathways involved in nutrient sensing and is both required and sufficient to extend lifespan and healthspan in the model organism, *C. elegans*. We also find that *adh-1* is sufficient to extend lifespan in yeast and is induced in response to geroprotective interventions in mice and humans hinting at a conserved role for this gene in promoting longevity. This makes *adh-1* a promising longevity-promoting candidate. In the second and third projects, we take a different approach to unveiling the genetic networks underlying animal health and disease. First, we take advantage of recent technological advances and develop new tools to systemically identify, with single-cell resolution, the genetic networks that characterize the functioning of a healthy multicellular organism. In the third project, we use these tools to identify the changes that occur to these genetic networks in the context of disease, specifically diet-induced obesity. We identify common and cell-type specific transcriptional changes and use publicly available experimental data to begin elucidating the role of various genes and the specific tissues in which they are expressed in the development of obesity.

Chapter I: Introduction

The overarching goal of my PhD is to begin elucidating the molecular networks that drive health and disease, specifically aging and obesity, in a multicellular organism. Despite recent advances in our understanding of these diseases, the molecular drivers of both aging and obesity remain elusive. This is largely due to the complexity of both diseases with hundreds of genes, multiple tissues and environmental and social factors all playing important roles. In the projects described here, I use different approaches to identify some of the genetic factors involved in the functioning of a healthy multicellular organism and those that are involved in the development of aging and obesity. Although varying in scope and methodology, a common theme for all projects is the use of omics datasets. To identify drivers of aging, we use publicly available transcriptomic, proteomic, and ChIP-Seq data of a known mediator of longevity to identify downstream molecules involved in the regulation of lifespan. This led to the identification of a potent and potentially conserved longevity-promoting gene. Similarly, we generate single-cell transcriptomic data for animals undergoing diet-induced obesity to identify systemically and with single-cell resolution potential drivers of obesity. Another commonality between the projects described here is the use of *Caenorhabditis elegans* as a model organism. *C. elegans* provides several advantages for this kind of endeavor some of which are discussed below.

***Caenorhabditis elegans*: an optimal model for the study of the genetic basis of aging and obesity**

Since its introduction by Sydney Brenner, the nematode *C. elegans* has become a popular model organism in the field of biomedical research [1]. Studies in *C. elegans* have led to fundamental insights into various biological processes including the discovery of the molecular mechanisms of apoptosis [2] and gene silencing by small RNAs [3]. Another area where *C. elegans* has been a leading model organism, is the field of aging [4]. For centuries it was assumed that aging was an intractable process [5] caused by the accumulation of damage over time. However, the discovery that the mutation of a single gene can significantly extend the lifespan of *C. elegans* [6] revealed that genetics plays a critical role in the rate of aging and ultimately the lifespan of an organism. A practical implication of this discovery is that aging is more malleable than previously thought. Since then, studies in *C. elegans* and other model organisms revealed several interventions that slow down aging including caloric restriction [7], reduced insulin signaling [6], inactivation of the protein mTOR [8], and sterility [9]. *C. elegans* offers several advantages for the study of the genetic basis of aging. The most significant one is the fact that it has a relatively short lifespan. On average, these worms live roughly 15 days compared to 70 days for drosophila and 30 months for mice. Another significant advantage is its genetic malleability. Gene knockdown can be performed by simply feeding the worms bacteria carrying double-stranded RNA against the gene of interest which will cause RNA interference-mediated knockdown. Additionally, the advent of CRISPR-Cas9 technology has made the generation of mutant and transgenic *C. elegans* strains significantly simpler. Despite their simple anatomy, being made up of only 959 somatic cells, the *C. elegans* genome encodes roughly the same number of genes as humans of which the majority (>70%) is conserved [10]. Therefore, fundamental discoveries made in *C. elegans* are likely to translate to higher organisms. Finally, the fact that *C. elegans* exhibits complex behavior [11] including the ability to navigate through complicated environments, hunt prey, avoid predators and toxic chemicals, and train via associative learning gives it a significant advantage over simpler model organisms like yeast. For example, unlike yeast, *C. elegans* can be used to study more advanced age-associated diseases such as neurodegeneration[12]. These characteristics have made *C. elegans* the leading model for the study of aging.

The advantages presented here are also the reason why *C. elegans* is the optimal model to achieve the goals set out by the second project, identifying the tissue-specific genetic changes associated with diet-induced obesity (DIO). Specifically, its simple anatomy (959 somatic cells) and stereotypical cellular composition and distribution, makes the goal of performing single-cell RNA-Seq to identify the transcriptome of every cell type in a systemic manner attainable. Additionally, we had previously developed a *C. elegans* model of DIO which exhibits many of the characteristics of human DIO[13]. We had shown that feeding worms a fructose-rich diet results in fat accumulation, lifespan reduction and increased neurodegeneration which are all characteristics of human DIO[13]. Finally, as previously mentioned, *C. elegans* is genetically malleable, which would allow us to not only identify differentially expressed genes but also perform screens to determine the genes that link excess sugar consumption to fat accumulation and disease progression. All these advantages make *C. elegans* an excellent model for elucidating the genetic basis of disease.

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Chapter II: Increased alcohol dehydrogenase 1 activity promotes longevity

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Abstract

Several molecules can extend healthspan and lifespan across organisms. However, most are upstream signaling hubs or transcription factors orchestrating complex anti-aging programs. Therefore, these molecules point to but do not reveal the fundamental mechanisms driving longevity. Instead, downstream effectors that are necessary and sufficient to promote longevity across conditions or organisms may reveal the fundamental anti-aging drivers. Towards this goal, we searched for effectors acting downstream of the transcription factor EB (TFEB), known as HLH-30 in *C. elegans*, because TFEB/HLH-30 is necessary across anti-aging interventions and its overexpression is sufficient to extend *C. elegans* lifespan and reduce biomarkers of aging in mammals including humans. As a result, we present an *A*lcohol-dehydrogenase *M*ediated anti-*A*ging *R*esponse (AMAR) that is essential for *C. elegans* longevity driven by HLH-30 overexpression, caloric restriction, mTOR inhibition, and insulin-signaling deficiency. The sole overexpression of ADH-1 is sufficient to activate AMAR, which extends healthspan and lifespan by reducing the levels of glycerol – an age-associated and aging-promoting alcohol. *Adh1* overexpression is also sufficient to promote longevity in yeast, and *adh-1* orthologs are induced in calorically restricted mice and humans, hinting at ADH-1 acting as an anti-aging effector across phyla.

Introduction

Advances in the field of aging include the discovery of several genetic and biochemical pathways that shorten or extend lifespan. However, the molecules found to be necessary and sufficient to extend health and lifespan have mostly been upstream signaling hubs (*e.g.* mTOR) or intermediate transcription factors (*e.g.* FOXO/DAF-16). Therefore, it remains unclear whether there are downstream effectors that are necessary and sufficient for longevity. This is relevant, as downstream molecules with robust anti-aging effects may reveal the fundamental mechanisms that determine the rate of aging and may be safer and more effective geroprotective targets.

An attractive approach to the discovery of downstream effectors of longevity is the study of the transcription factors (TFs) responsible for activating anti-aging programs in multiple pro-longevity conditions. A prominent anti-aging TF in this class is the Transcription Factor EB (TFEB). Activation of TFEB, and its *C. elegans* ortholog HLH-30, is necessary to extend healthspan and lifespan across anti-aging interventions[1,2]. Furthermore, activating HLH-30/TFEB is sufficient to promote longevity and reduce biomarkers of aging across organisms[1,3–7]. As a master regulator of autophagy and lysosomal biogenesis[8], the current model states that HLH-30/TFEB extends health and lifespan through the activation of autophagy[1], a cell rejuvenating process that is also thought to be required across anti-aging interventions and organisms[9–13].

While investigating the potential role of autophagy in the *hlh-30* dependent longevity of the *mxl-3 C. elegans* mutant, we found that the current model has exceptions. Since *mxl-3*-driven longevity requires the activity of *hlh-30*, HLH-30/TFEB is the master regulator of autophagy, and autophagy is thought to be universally required for longevity, we hypothesized that *hlh-30* was promoting longevity in the *mxl-3* mutants through the activation of autophagy. However, contrary to expectation, we found that autophagy is not activated in the *mxl-3* mutant, and that neither autophagy nor lysosomal activity are required for the longevity phenotype observed in these mutant animals. Therefore, *mxl-3* longevity is *hlh-30*-dependent but autophagy-independent. Instead, we found the gene encoding the Alcohol DeHydrogenase ADH-1 induced in *mxl-3* and other *hlh-30*-dependent anti-aging interventions, including caloric restriction (*eat-2* mutants), insulin-signaling deficiency (*daf-2* deficient) and mTOR-inhibition. More importantly, *adh-1* is necessary for the longevity phenotype of all these anti-aging interventions, and ADH-1 overexpression is sufficient to extend *C. elegans* lifespan. We propose that ADH-1 extends lifespan through metabolizing the otherwise toxic alcohol glycerol, which accumulates with age. Finally, we present evidence suggesting that ADH-1's anti-aging capacity may be conserved across species. Altogether, we establish ADH-1 as an effector of longevity acting downstream of multiple anti-aging interventions and propose it as a druggable enzyme whose activation may suffice to promote healthspan and lifespan in organisms ranging from yeast to humans.

Results

Autophagy and lysosomal activity can be dispensable for hlh-30-dependent longevity

C. elegans mutants for the helix-loop-helix transcription factor *mxl-3* are long lived, and this longevity phenotype is suppressed by inactivation of the transcription factor HLH-30 (TFEB in mammals) ([2], Figure 1A & Data S1A). Given that it was *hlh-30*-dependent, we hypothesized that *mxl-3*'s longevity was also dependent on autophagic and lysosomal activity. However, the levels of autophagy in the long-lived *mxl-3* animals are normal at the transcriptional (Figure S1A), biochemical (Figure S1B) and cytological levels (Figure S1C). Most importantly, (i) post-developmental inactivation by RNAi of two autophagy genes *lgg-1* (a.k.a. Atg-8 or LC3) and *bec-*

1, which are lethal when mutated (Figure S1D and Data S1B), (ii) loss-of-function mutation of the non-lethal autophagy gene *atg-18* (Figure 1B and Data S1C), and (iii) chemical inhibition of all lysosomal enzymes with chloroquine do not suppress or rescue *mxl-3*'s longevity (Figure S1E and Data S1C). In fact, post-developmental RNAi against *atg-18*, *lgg-1* and *bec-1* and post-developmental administration of chloroquine further increased *mxl-3* lifespan (Figure S1D, Figure S1E and Data S1B and S1C), demonstrating that the treatments work but, more importantly, that autophagic and lysosomal activity are not always necessary for longevity.

***adh-1* mediates HLH-30-driven longevity**

To identify alternative effectors driving HLH-30-mediated longevity, we mined published *hlh-30* mutant transcriptomics[14], and HLH-30 overexpression (HLH-30^{OE}) transcriptomics[15], proteomics[15], and ChIP-Seq studies[16]. The top gene that met the following criteria: (i) mRNA and protein dysregulated in the *hlh-30* mutant and HLH-30^{OE} strains, respectively, and (ii) a hit in the HLH-30 ChIP-seq study, was K12G11.3, which encodes for the alcohol dehydrogenase ADH-1. We therefore used the *mxl-3* mutant model to investigate *adh-1*'s potential role in *hlh-30*-driven longevity. In line with ADH-1 playing a role in *hlh-30*-mediated longevity, *adh-1* was induced in the *mxl-3* mutant animals in an *hlh-30*-dependent manner (Figure 1C). More importantly, loss-of-function mutation of *adh-1* suppressed *mxl-3*'s longevity phenotype (Figure 1D & Data S1D). Therefore, unlike autophagy, the activity of the alcohol dehydrogenase ADH-1 is necessary for *hlh-30*-dependent *mxl-3* longevity.

We then investigated whether *adh-1* played a role in HLH-30-mediated longevity beyond the *mxl-3* model. In *C. elegans*, the sole overexpression of HLH-30 is sufficient to extend lifespan[1]. We confirmed this result, while also finding the pro-longevity effect of overexpressing HLH-30 to be more pronounced in the *C. elegans* line OP433^{17} than in the previously described MAH235 and MAH240 lines^{1} (Data S1D). This, in addition to OP433 being the *C. elegans* line used in the referred ChIP-Seq and proteomics analyses, persuaded us to use OP433 as the model for HLH-30 hyperactivation throughout this study (hereinafter referred to as HLH-30^{OE}; please refer to the Methods section "*C. elegans* lifespan assays" for experimental conditions). In line with ADH-1 being an anti-aging effector downstream of HLH-30, we found *adh-1* induced in HLH-30^{OE} animals (Figure 1E). More importantly, loss-of-function mutation of *adh-1* fully suppressed HLH-30^{OE} longevity (Figure 1F, Figure S2, Data S1D & Data S1E). This result indicates that *adh-1* plays a critical role in HLH-30-driven longevity in contexts beyond the loss of *mxl-3*.

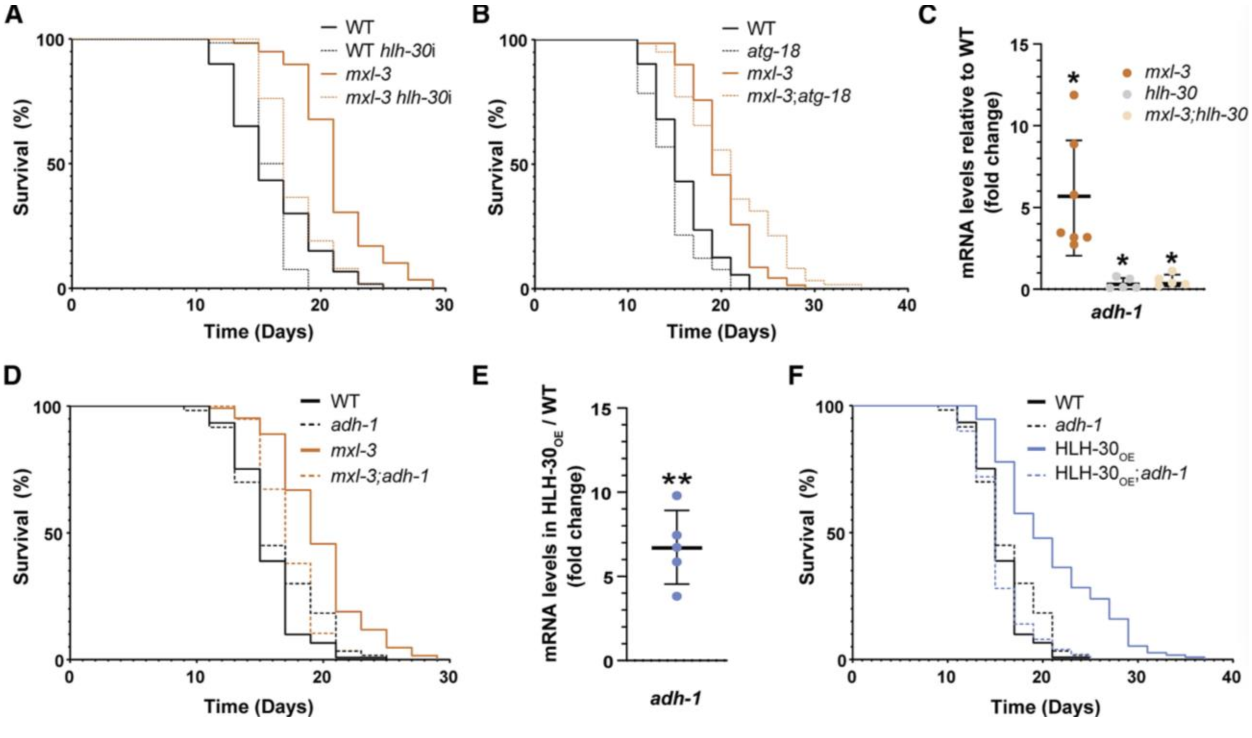

Figure 1. *adh-1* activation promotes HLH-30-mediated longevity. (A) The master regulator of autophagy and lysosomal biogenesis, TF *hlh-30/Tfeb,* is required for the longevity phenotype of the *mxl-3 C. elegans* mutant (representative of 3 biological replicates; see Data S1A). **(B)** Loss-of-function mutation of the non-lethal autophagy gene *atg-18* does not suppress *mxl-3* longevity (representative of 3 biological replicates; see Data S1C). In addition, autophagy levels are not elevated at the transcriptional (Figure S1A), biochemical (Figure S1B), or cellular (Figure S1C) levels in the *mxl-3* mutant, and RNAi against the lethal autophagy genes *bec-1* and *lgg-1* or full inhibition of lysosomal activity and autophagy with chloroquine do not suppress *mxl-3* longevity (Figure S1D-E). **(C)** As measured by RT-qPCR, *adh-1* transcript levels are elevated in the *mxl-3* mutant in an *hlh-30* dependent manner (n=5-7 biological replicates). See Table S1 for RT-qPCR primers. **(D)** The longevity of the *mxl-3* mutant is suppressed by loss-of-

function mutation of *adh-1* (representative of three biological replicates; see Data S1D). **(E)** *adh-1* transcript levels are elevated in the HLH-30^{OE} animals (n=5 biological replicates). **(F)** Loss-of-function mutation of *adh-1* fully suppresses the extended lifespan of the HLH-30^{OE} animals (representative of 3 biological replicates; see Data S1D and Figure S2). **(A-F)** Error bars denote SEM. ns= not significant, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001; *hlh-30*i = *hlh-30* RNAi. All experiments were performed using *E. coli* XU363 carrying L4440 (empty vector) or L4440 + the gene of interest.

ADH-1 is necessary and sufficient to promote longevity

Given that *hlh-30* is necessary for longevity across anti-aging interventions[1], we then tested whether *adh-1* similarly contributes to longevity across interventions, namely: (i) caloric restriction through the use of the eating-deficient mutant *eat-2*, (ii) mTOR inhibition through RNAi knockdown of its encoding gene *let-363*, and (iii) reduced insulin signaling through RNAi knockdown of the insulin receptor-encoding gene *daf-2*. Mining published microarray data suggested that *adh-1* is induced in the *eat-2*[18] and *daf-2*[18,19] models. We confirmed these observations in dedicated transcriptional analyses and, critically, we found that *hlh-30* is necessary for the induction of *adh-1* in all three longevity models (Figure 2A). More importantly, *adh-1* inactivation partially suppressed the extended lifespan of *C. elegans* subject to caloric restriction (Figure 2B & Data S1F) and mTOR deficiency (Figure 2C & Data S1G) and, most strikingly, fully suppressed the extremely long lifespan of the *daf-2*-deficient animals (Figure 2D & Data S1H), demonstrating that *adh-1* is a potent downstream effector of longevity across anti-aging interventions.

Having found that *adh-1* is necessary for lifespan extension across longevity models, we set out to test whether hyperactivating *adh-1* was sufficient to promote longevity. For this, we generated three independent ADH-1 overexpressing *C. elegans* strains (GMW20, GMW21, GMW22 referred to as ADH-1^{OE}). After backcrossing and confirming that all three strains had increased *adh-1* transcript levels (Figure S3A), we found all three to be long-lived relative to the wild-type strain (Figure 2E, Figure S3C, Data S1I & Data S1J). We also found that aged ADH-1^{OE} animals show improved locomotor endurance compared to the age-matched WT counterparts (Figure 2F), suggesting that hyperactivation of ADH-1 may also extend healthspan. Therefore, ADH-1 is not only necessary for longevity across anti-aging interventions, but it is also sufficient to extend lifespan and likely healthspan.

Next, we characterized the ADH-1^{OE} animals. We found no difference in the size (Figure S2D) or in the feeding rate (pharyngeal pumping) (Figure S2E) of ADH-1^{OE} animals compared to WT animals, suggesting that overexpressing ADH-1 does not cause caloric restriction in *C. elegans*. The defecation rate of ADH-1^{OE} animals was also normal (Figure S2F), suggesting normal passage of food through the digestive system. We also sought to determine whether there was a tradeoff between the extended lifespan and fertility in ADH-1^{OE} animals, as this tradeoff occurs in several longevity models[20,21]. Indeed, we found that the ADH-1^{OE} animals exhibit reduced brood size compared to their WT counterparts (Figure S2G and Figure S2H).

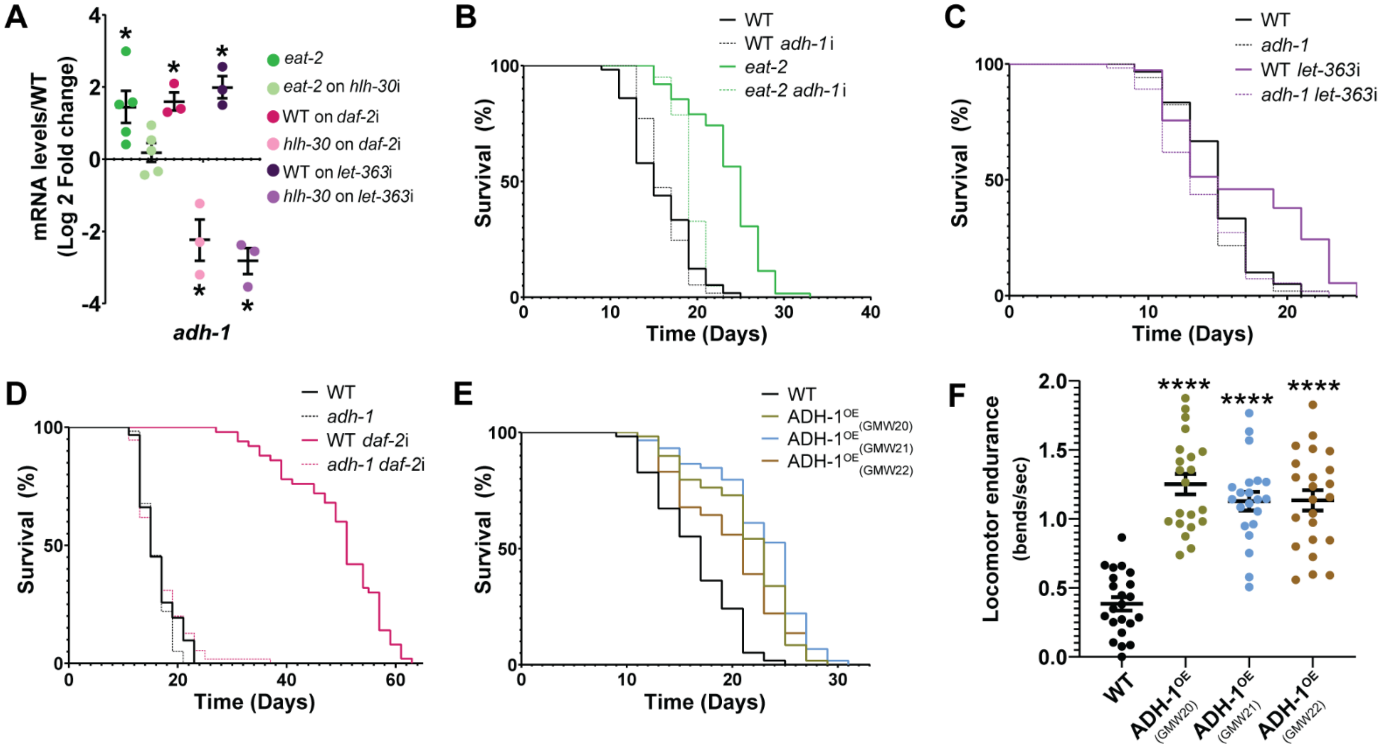

Figure 2. *adh-1* is necessary and sufficient to extend lifespan and healthspan. (A) *adh-1* is induced in an *hlh-30*-dependent manner in the longevity models caloric restriction (*eat-2*), insulin insensitivity (*daf-2*), and mTOR inhibition (*let-363* RNAi) (n=3 to 5 biological replicates). See Table S1 for RT-qPCR primers. **(B-D)** In *C. elegans*, *adh-1* is required for longevity driven by **(B)** caloric restriction, **(C)** mTOR inhibition, and **(D)** deficient insulin-signaling (representative of three biological replicates; see Data S1F-H). **(E)** Overexpressing ADH-1 (ADH-1^{OE}) is sufficient to promote longevity in *C. elegans*. Survival curves for three independent overexpression lines (GWM20-22) are presented (representative of three biological replicates; see Data S1I). **(F)** ADH-1 promotes locomotor endurance as measured by thrashing in liquid medium in 12-days old ADH-1^{OE} and wild-type *C. elegans* (representative of three biological replicates; repeats in Data S1N). Also see Figure S3 for further characterization of *C. elegans* overexpressing ADH-1. **(A-F)** Error bars denote SEM. ns= not significant, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001. **(A-D)** *daf-2*i = *daf-2* RNAi, *hlh-30*i = *hlh-30* RNAi, *adh-1*i = *adh-1* RNAi, *let-363*i = *let-363* RNAi. All experiments were performed using *E. coli* XU363 carrying L4440 (empty vector) or L4440 + the gene of interest.

ADH-1 promotes longevity by reducing glycerol toxicity

Alcohol dehydrogenases are among the most conserved and studied enzymes due to their biotechnological (*e.g.* wine production) and biomedical relevance (*e.g.* alcohol toxicity). To gain insight into the mechanism through which ADH-1 extends *C. elegans* lifespan, we tested the primary sequence prediction that ADH-1 can metabolize alcohols using a specific *in vivo* alcohol dehydrogenase (AD) assay validated in organisms ranging from yeast to humans[22–24]. In this assay, ADs convert allyl-alcohol (AA) into the lethal aldehyde acrolein; hence, higher AD activity leads to higher lethality[25]. ADH-1^{OE} *C. elegans* showed hypersensitivity to allyl-alcohol (Figure 3A), confirming these animals have increased capacity to metabolize alcohols.

Using scRNA-Seq[26] (Figure S4A), we found *adh-1* expressed in the distal tip cells of the gonad, in the marginal and muscle cells of the pharynx (pm3_pm4_pm5 & pm6_pm7), in all body wall muscle cells, and in the anterior intestinal cells. We then used CRISPR/Cas9 to knock-in wrmScarlet[27] in frame with the coding sequence of *adh-1* to generate a strain carrying *adh-1*P::ADH-1::wrmScarlet::*adh-1* 3'UTR in the *adh-1* locus. In congruence with the scRNA-Seq expression pattern, we found ADH-1::wrmScarlet expressed in the distal tip, pharynx, body-wall muscle, and the intestinal cells of adult *C. elegans* (Figure 3B, 3C and S4B). At the subcellular level, we noticed that ADH-1 was expressed in droplet-like structures in the intestine, which was intriguing because homologous alcohol dehydrogenases are mainly found in the cytoplasm or in the mitochondria[28,29]. Co-expression of *adh-1*P::ADH-1::wrmScarlet::*adh-1* 3'UTR with the intestinal lipid droplet (LD) reporter *daf-22*P::PLIN1::GFP[30] showed that ADH-1 colocalizes with LDs (Figure 3C).

Given that (i) ADH-1 is an alcohol dehydrogenase expressed in close proximity to LDs, (ii) the major molecular class present in LDs is triglycerides, which are composed of fatty acids and the alcohol glycerol, and (iii) glycerol had previously been shown to reduce lifespan[31], we hypothesized that ADH-1 extends *C. elegans* lifespan by reducing the levels of the aging-promoting alcohol glycerol. In support of this hypothesis, we found that wild-type *C. elegans* accumulate glycerol as they age (Figure 3D), and that ADH-1^{OE} animals show reduced glycerol levels relative to wild-type worms (Figure 3E) and are resistant to the pro-aging effect of glycerol (Figure 3F & Data S1K & S1L). We also performed a food choice assay to determine whether

ADH-1^{OE} animals show a differential attraction to glycerol. Wild-type *C. elegans* showed no preference for glycerol at the doses used in the lifespan assays (0.04% and 0.4%), and we observed no differences between the ADH-1^{OE} and WT genotypes (Figure S3I & S3J); therefore, ADH-1^{OE} animals are not living longer because they are avoiding the glycerol or the glycerol-embedded food. Altogether, the data support a model in which wild-type *C. elegans* accumulate glycerol as they age which results in reduced lifespan. However, when *adh-1* is induced, as in the HLH-30-dependent longevity models, glycerol levels are lower, and lifespan is extended (schematic model in Figure 4F). We name this lifespan-extending mechanism *A*lcohol dehydrogenase *M*ediated *A*nti-aging *R*esponse or AMAR, which in Sanskrit means immortal. A prediction of the AMAR model is that HLH-30^{OE} animals would have reduced glycerol levels relative to WT worms, and that this reduction would depend on the activity of ADH-1. Indeed, we find that HLH-30^{OE} animals have reduced glycerol levels compared to WT worms, and that this reduction is suppressed when *adh-1* is mutated (Figure 3G).

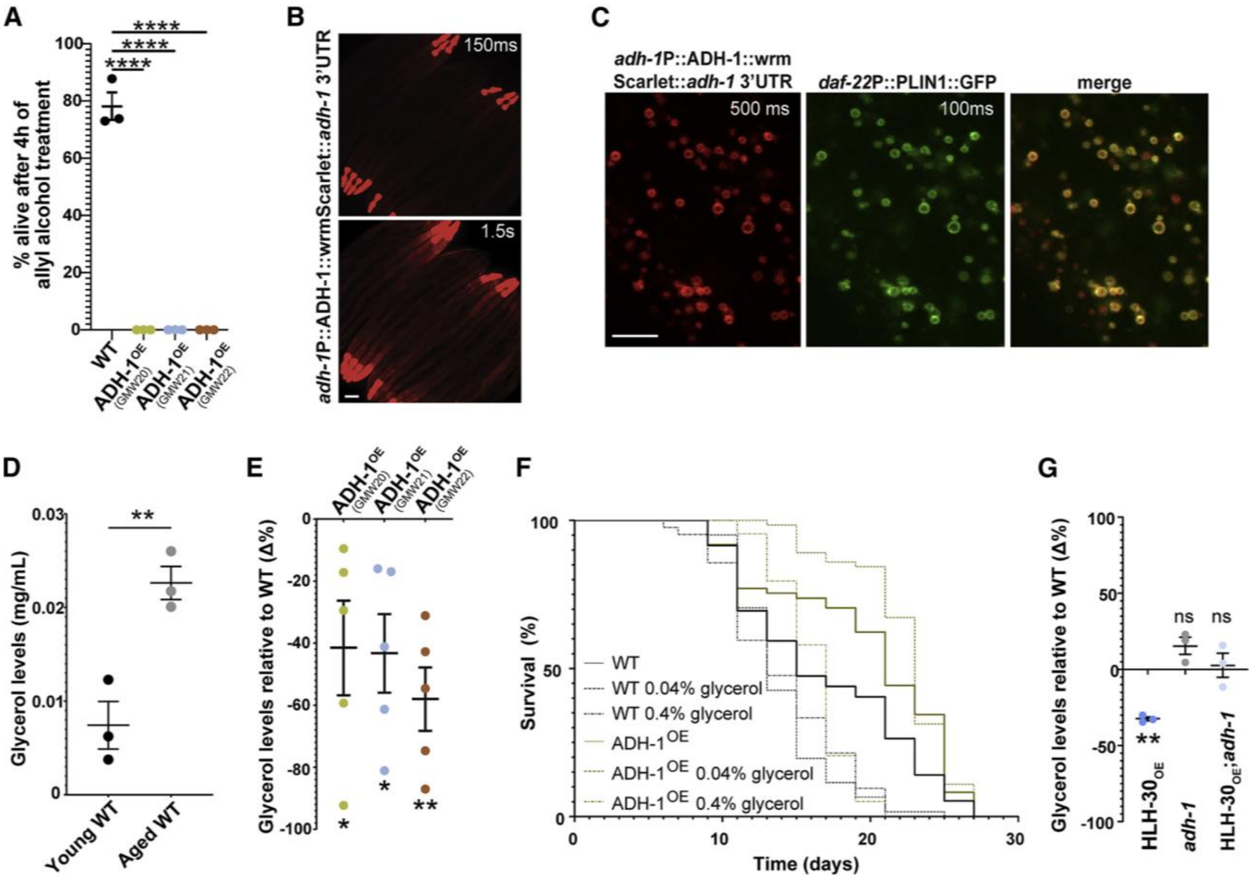

Figure 3. ***adh-1*** **extends lifespan by preventing the accumulation of the aging-promoting metabolite glycerol.** **(A)** ADH-1^{OE} strains are hypersensitive to allyl alcohol, indicating increased *in vivo* alcohol dehydrogenase activity (n=3 biological replicates). **(B)** Whole-body expression of the ADH-1 protein as observed in N2 *C. elegans* carrying wrmScarlet knocked-in in frame in the *adh-1* locus via CRISPR/Cas9 (scale bar = 100µm). Two exposure times of the same image are depicted. At the 1.5s exposure time, muscle and intestinal signals are visible. See also Figure S4A-B for additional information on the anatomical localization of ADH-1. **(C)** ADH-1 co-localizes with intestinally expressed *D. melanogaster* perilipin, a lipid droplet marker expressed from the integrated transgene P*daf-22*::PLIN1::GFP[30] (scale bar = 5µm). Exposure times are depicted. See Figure S4C for autofluorescence control. **(D)** Wild type worms accumulate glycerol as they age. Young corresponds to day-1 adult, and aged corresponds to day-8 adult, the latest day we can harvest live worms free of contaminating dead worms (n=3 biological replicates). **(E)** Three independent ADH-1^{OE} lines show decreased glycerol levels relative to wild type (n=5 biological replicates). **(F)** ADH-1^{OE} animals are resistant to the pro-aging effect of glycerol (representative of three biological replicates; see Data S1K & Data S1L). **(G)** Loss-of-function mutation of *adh-1* suppresses the otherwise low glycerol levels observed in HLH-30^{OE} animals. Statistical significance relative to wild-type controls (n=3 biological replicates). **(A-G)** Error bars denote SEM. ns= not significant, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001. All experiments (except the glycerol supplementation experiment) were performed using *E. coli* XU363 carrying L4440 (empty vector). The glycerol supplementation experiment was performed using *E. coli* OP50 bacteria.

ADH-1 mediated longevity requires ALH activity

Another prediction of the AMAR model is that increased glycerol metabolism by ADH-1 will lead to increased levels of another toxic and aging-promoting metabolite, glyceraldehyde[32]. We therefore hypothesized that *adh-1*-driven longevity would require aldehyde dehydrogenase (ALH) activity to convert glyceraldehyde into its non-toxic salt, glycerate. *C. elegans* has over 12 aldehyde dehydrogenase encoding genes. Therefore, to determine whether ALH activity is required for ADH-1 mediated longevity, we used the ALH-specific inhibitor cyanamide[33,34]. Treating ADH-1^{OE} worms with cyanamide fully rescued their longevity phenotypes (Figure 4A, Figure S3C & Data S1I and S1J). Furthermore, cyanamide suppressed the extended lifespan of the *hlh-30*-dependent longevity models *mxl-3* (Figure 4B & Data S1M), *eat-2* (Figure 4C & Data S1F), *daf-2* (Figure 4D & Data S1H), and, as predicted by the model, HLH-30^{OE} animals (Figure 4E, Figure S2B & Data S1E and S1M). Therefore, concerted alcohol- and aldehyde-dehydrogenase function is required for lifespan extension across anti-aging interventions.

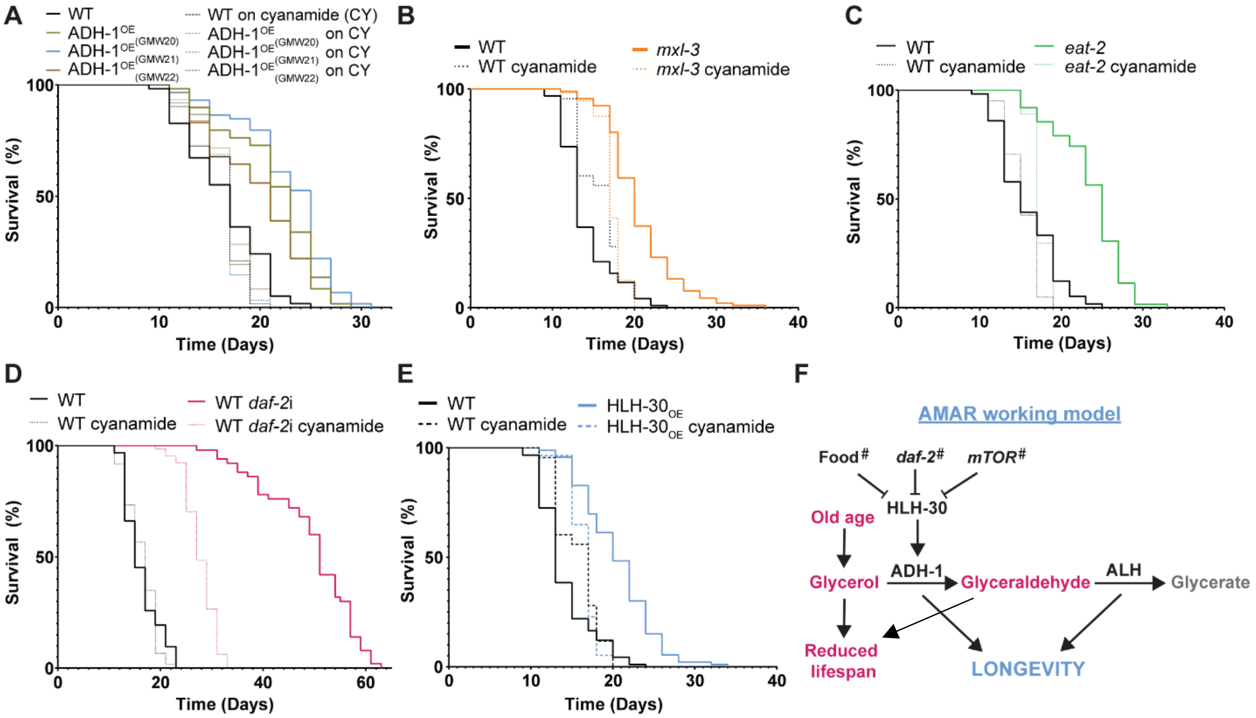

Figure 4. *adh-1* mediated lifespan requires aldehyde dehydrogenase activity. (A-E) Treatment with the aldehyde dehydrogenase inhibitor cyanamide rescues the extended lifespan driven by **(A)** ADH-1^{OE} (GWM20-22 are three independent ADH-1^{OE} lines), **(B)** *mxl-3* mutation, **(C)** Caloric restriction (*eat-2* mutation), **(D)** reduced insulin sensitivity (*daf-2* RNAi), and **(E)** HLH-30^{OE}. See also Data S1F, Data S1H, Data S1I, and Data S1M. **(F)** Working model of the Alcohol and aldehyde dehydrogenase-Mediated Anti-aging Response (AMAR= immortal in Sanskrit). # Indicates that it remains to be defined how the three

inhibitors of HLH-30 tested here (food, the insulin receptor DAF-2, and mTOR) interact among them (or not) to regulate HLH-30 activity. **(A-F)** Error bars denote SEM. ns = not significant, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001. All experiments were performed using *E. coli* XU363 carrying L4440 (empty vector) or L4440 + the gene of interest.

ADH-1 is a conserved anti-aging effector

Having found that *adh-1* is necessary and sufficient for longevity in *C. elegans*, we mined the literature in search for evidence of conservation. We found studies in yeast demonstrating that alcohol dehydrogenase (AD) activity decreases with age[35]. On the other hand, here we show that Adh1 protein levels increase in yeast subject to caloric restriction (Figure 5A) and, more importantly, using an estradiol-based system to increase Adh1 levels (Figure S5), we show that Adh1 promotes a dose-dependent increase in yeast chronological lifespan (Figure 5B). Adh1's necessity and sufficiency to extend lifespan in *C. elegans*, and sufficiency to extend yeast lifespan, suggest that this enzyme's anti-aging role might be conserved across species.

To test this notion, we mined the literature for transcriptomics analyses of mammals subject to two life-extending treatments: fasting or caloric restriction. Data S1S lists all the studies we found in which *Adh1*, or other close homologs of *C. elegans*' *adh-1* such as *Adh4*, *Adh5*, and *Sord*, were induced (see Data S1S). Briefly, we found 18 transcriptomic datasets where the mouse orthologs of *C. elegans adh-1* were induced in fasted or calorically restricted mice. Similarly, we found 6 transcriptomic datasets where the human orthologs of *C. elegans adh-1* are induced in calorically restricted humans. Altogether, the data demonstrate that ADH-1 is an anti-aging effector common to multiple anti-aging interventions and suggest that it may promote longevity across species.

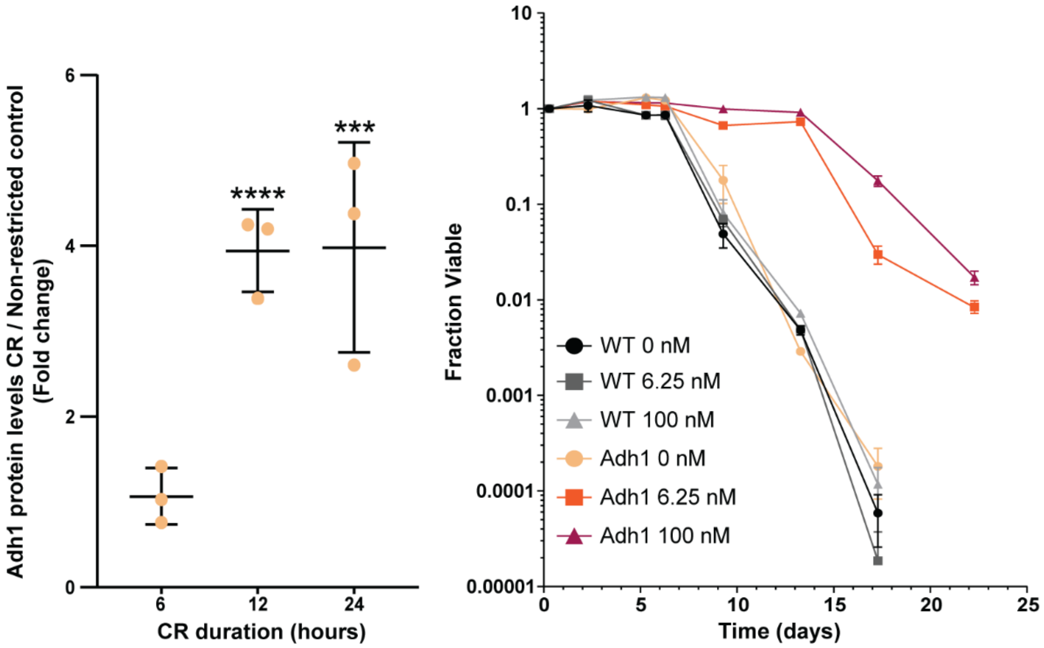

Figure 5. *Adh1* is induced upon caloric restriction and is sufficient to extend chronological lifespan in yeast. (A) Adh1 protein levels are increased in calorically restricted (CR) compared to non-restricted yeast as assessed by Western blot. CR duration indicates time since entering the diauxic shift (n=3 biological replicates). **(B)** Adh1 overexpression extends yeast chronological lifespan under non-restricted conditions (representative of n=3 biological replicates). Two different doses of estradiol were added to cultures to induce Adh1 expression. See also Figure S5. **(A-B)** Error bars denote SEM. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

Discussion

The transcription factor HLH-30, known as Mitf in flies and TFEB in mammals, has been the focus of intense study. At the molecular level, HLH-30/TFEB is known as the master regulator of lysosomal biogenesis and autophagy because *in vitro* in cellular models[36,37] and *in vivo* in animal models, HLH-30/TFEB is necessary and sufficient for the expansion of the lysosomal compartment and the activation of autophagy[2,8,38,39]. At the organismal level, HLH-30/TFEB promotes survival to acute stress[40–42] and reduces the incidence and severity of the symptoms of aging across model systems[5–7,43], and, in *C. elegans*, *hlh-30* is necessary for longevity[1,2]. Autophagy, a downstream output of HLH-30/TFEB activation is also thought to be indispensable for extended lifespan[11,12]. Therefore, it was reasonable to hypothesize that the broad requirement of HLH-30/TFEB to promote survival was due to its role in the activation of the cellular rejuvenating process of autophagy. However, work from the Antebi lab showed that the months-long survival of the germline in *C. elegans* undergoing starvation, a survival program known as adult reproductive diapause (ARD), depends on the activity of HLH-30 but not of autophagy[44]. This indicates that autophagy is not always necessary for HLH-30-driven survival to stress. Furthermore, enhanced autophagy may not be sufficient to promote long-term survival. For instance, *C. elegans* carrying a hypomorphic mutation in the gene encoding the insulin receptor *daf-2* are long lived, and loss-of-function mutation of the transcription factor *daf-16* (mammalian *Foxo*) fully suppresses this longevity phenotype. However, *daf-16* does not suppress the high levels of autophagy observed in the *daf-2* mutant worms[10]. Therefore, *daf-2*;*daf-16* double mutant worms have high-levels of autophagy but are not long-lived. Together, the ARD and *daf-2*;*daf-16* studies suggest that autophagy is neither universally required nor sufficient to promote long-term survival.

By contrast, HLH-30/TFEB seems necessary across anti-aging interventions and sufficient to reduce the burden of aging across species. Therefore, common downstream effectors of longevity could be discovered by investigating *hlh-30*'s mechanism of lifespan extension. To identify these effectors, we here characterized the *C. elegans* mutant *mxl-3*. On one side, we chose this anti-aging intervention because the *mxl-3*'s longevity phenotype is completely suppressed by loss of *hlh-30* function. On the other hand, distinct from other *hlh-30*-dependent anti-aging interventions (*e.g.*, mTOR or insulin receptor inactivation) that perturb upstream signaling hubs with broad cellular impacts, *mxl-3* encodes for a transcription factor with the same DNA-binding site as HLH-30[2]. Therefore, the study of the *mxl-3-hlh-30* longevity model was more likely to point us to critical anti-aging effectors acting downstream of HLH-30.

The initial characterization of the *mxl-3 C. elegans* mutant showed that its longevity phenotype does not require autophagy. It is worth noting here that, distinct from some previous studies, we used post-developmental RNAi and post-developmental chloroquine treatment to test the contribution of the autophagy and lysosomal machinery to *mxl-3*'s longevity. Post-developmental treatment was necessary because inactivation of autophagy during development leads to several developmental defects ranging from developmental arrest[45,46] to altered adult physiology (*e.g.*, reduced fat accumulation[47]). We found that post-developmental RNAi against *atg-18, lgg-1*, and *bec-1*, as well as complete inhibition of lysosomal activity with chloroquine, further increased the lifespan of the *mxl-3* mutant worms. Future studies may investigate whether this enhanced longevity is due to a hormetic effect by which reduced autophagy promotes the activation of alternative cellular homeostatic processes such as the heat-shock response, proteasomal function, or other compensatory responses to dysfunctional autophagy, as previously observed *in vitro*[48,49]. Furthermore, our observations are in line with previous studies showing that post-developmental inactivation of autophagy can extend *C. elegans* lifespan[50] and a study showing that chloroquine treatment can increase lifespan in rats, in part through the modulation of autophagy[51]. The results presented here indicate that longevity is possible in the absence of enhanced autophagy and that the master regulator of autophagy, HLH-30/TFEB, can promote longevity by mechanisms that are autophagy-independent.

Our search for alternative mechanisms of longevity orchestrated by HLH-30 pointed us to the alcohol dehydrogenase ADH-1. In the intestine of *C. elegans*, we found that ADH-1 localizes to the surface of lipid droplets (LDs). The main component of LDs are triglycerides, and triglycerides are composed of fatty acids and glycerol. Although most of the attention given to lipotoxicity focuses on the detrimental effects of free fatty acids, the alcohol glycerol can also be toxic. In fact, glycerol has been shown to shorten *C. elegans* lifespan[31], and we show here that it normally accumulates in aging worms. Therefore, ADH-1 is in the right place in the cell to access and metabolize glycerol and, therefore, reduce the pro-aging effects of this naturally occurring alcohol (working model in Figure 4F). In line with this model, ADH-1^{OE} worms have lower levels of glycerol compared to wild type worms and are resistant to the pro-aging effects of glycerol. It is worth noting that ADH-1 overexpression and *adh-1* loss of function mutation do not have opposite phenotypes in *C. elegans*, which is similar to *hlh-30* itself. Loss of *hlh-30* function does not reduce *C. elegans* lifespan[1,2] while *hlh-30* overexpression promotes longevity. Nevertheless, we here demonstrate that loss of *adh-1* leads to higher levels of glycerol in the HLH-30^{OE} background, which otherwise shows low levels of glycerol. Therefore, ADH-1 activity negatively correlates with the levels of glycerol, and glycerol levels negatively correlate with lifespan. We propose that ADH-1 extends lifespan, at least in part, through alleviating the toxic effects of glycerol likely derived from fat stores that normally increase with age.

Additionally, in line with *adh-1* being a critical downstream effector of HLH-30 longevity, loss of *adh-1* function suppresses the longevity phenotype of all the *hlh-30*-dependent longevity models tested (*eat-2, daf-2* and mTOR). Interestingly, although loss of *adh-1* function significantly suppresses the extreme longevity phenotype of *daf-2 C. elegans*, inhibition of the next step in the metabolism of glycerol (aldehyde dehydrogenase) only partially rescued *daf-2* longevity. There are at least two possible interpretations for this observation. From a technical perspective, it is possible that the dose of cyanamide was insufficient to fully inhibit all aldehyde dehydrogenase activity. From a biological perspective, it is possible that ADH-1 contributes to longevity through additional mechanisms.

Interestingly, the longevity models dependent on *adh-1* either mimic fasting conditions (*e.g.*, reduced insulin and mTOR signaling, and HLH-30 overexpression), or reduce food intake (*i.e.*, *eat-2*). Furthermore, the *hlh-30*-dependent but autophagy-independent ARD program of germline-survival is activated in response to fasting[44]. Fasting and caloric restriction are anti-aging interventions effective across species and because ADH-1 is a common mediator of fasting-like anti-aging interventions, we hypothesized that ADH-1 may promote lifespan extension across species. We here confirmed this hypothesis in *Saccharomyces cerevisiae*, where we observed that overexpressing *Adh1* is sufficient to extend chronological lifespan. We also found several studies showing that alcohol-dehydrogenase levels decrease in aging flies, rodents, and humans[52–56], and our mining of published transcriptomics studies of mammals subject to fasting or caloric restriction identified *adh-1* orthologs induced in 18 mouse and 6 human transcriptomic datasets. Furthermore, a meta-analysis of transcriptomic studies of calorically restricted mice, rats, pigs, and rhesus monkeys identified *ADH1* as the most induced gene[57]. A separate meta-analysis of mouse transcriptomic data identified *ADH1* as induced in response to several longevity-promoting interventions including caloric restriction, every-other-day feeding, and rapamycin treatment[58]. Additionally, comparing the mouse inbred lines C3H and C57BL/6J, showed that C57BL/6J has twice as much liver ADH1 activity[59] and correspondingly, on average, C57BL/6J mice outlive CH3 by more than 100 days[60]. Admittedly, these studies are correlative, however, coupled to our *C. elegans* and yeast causal tests they suggest that *Adh1* may be a universal anti-aging effector. Indeed, two causal studies in mice support this hypothesis. Tissue-specific overexpression of *Adh1* protects mice against neurodegeneration[61] and cardiac dysfunction[62]. In summary, the evidence points to the ***A***lcohol-dehydrogenase ***M***ediated anti-***A***ging ***R***esponse, or AMAR, as a convergent anti-aging effector acting across longevity programs and possibly across organisms including humans.

Materials and Methods

EXPERIMENTAL MODEL AND SUBJECT DETAILS

C. elegans strains and husbandry

C. elegans N2 (Bristol, UK), *adh-1 (ok2799), mxl-3 (ok1947), atg-18* (*gk378*), *eat-2* (*ad456*), OP433 *[hlh-30::TY1::EGFP::3xFLAG + unc-119(+)]*, MAH235 (sqIs19 [*hlh-30*p::*hlh-30*::GFP + rol-6(su1006)]) and MAH240 (sqIs17 [*hlh-30*p::*hlh-30*::GFP + rol-6(su1006)]) were obtained from the Caenorhabditis Genetics Center (CGC). The CRISPR-Cas9 *adh-1*KI strain (PHX2365) and the 3 independent ADH-1^{OE} strains (PHX2888, PHX2889, PHX2890) were generated for this study by SunyBiotech (China). After UV-driven integration, PHX2888, PHX2889, and PHX2890 were backcrossed ≥3 times; the respective backcrossed strains are referred to as GMW20, GMW21, GMW22. XD3971 strain (xdIs143[P*daf-22*::PLIN1::GFP; rol-6(su1006)]) was a generous gift from Dr. Monica Driscoll and Dr. Xun Huang. Genetic crosses were performed to generate *mxl-3;adh-1, mxl-3;atg-18*, HLH-30^{OE};*adh-1*, and pLIPIN::GFP;*adh-1*::wrmScarlet strains. For maintenance, *C. elegans* were grown at 20°C on NGM plates seeded with *E. coli* strain OP50. All experiments (except the glycerol supplementation aging experiments) including those not involving RNAi were performed using *E. coli* XU363[63] carrying L4440 (empty vector) or L4440 plus the gene of interest. We used *E. coli* XU363 to avoid changing the bacterial background.

Yeast strains and culture

The estradiol-inducible *ADH1* overexpression strain SY1144 is isogenic to diploid strain Y15090 (*MAT*a/α [*HAP1-NatMX-ACT1pr-Z3EV-ENO2term]/HAP1 ura3Δ0/URA3* [*can1Δ::STE2pr-SpHIS5]/CAN1 his3Δ1/his3Δ1 lyp1Δ/LYP1*)[64]. Estradiol supplementation of the media causes translocation of a constitutively expressed Z_3EV artificial transcriptional activator into the nucleus. Z_3EV activates the expression of the *ADH1* gene, which was engineered to contain six Z_3EV binding sites in the promoter[64]. Yeast strains were grown in Synthetic Complete (SC) media with 2% glucose for the chronological lifespan and western blotting assays. To induce *ADH1* expression, β-estradiol (dissolved in DMSO) was added to the liquid cultures at a final concentration of 6.25 or 100nM. All liquid cultures and agar plates were grown at 30°C.

METHOD DETAILS

C. elegans lifespan assays

Gravid worms of the strains of interest were bleached and the embryos rocked at 20ºC for 18 hours to synchronize the hatchlings. After estimating the concentration of hatchlings by counting the number of hatchlings in ≥5x 5µl drops, around 200 hatchlings were seeded on NGM + 1mM IPTG + 25µg/mL carbenicillin plates (RNAi plates) seeded with *E. coli* strain XU363 carrying an empty L4440 plasmid (control). To initiate the lifespan assays, 30-40 young-adult worms were picked onto 6cm RNAi plates supplemented with 100µg/mL FUdR (RPI, United States) and seeded with *E. coli* XU363 carrying the L4440 control plasmid (EV) or a dsRNA-producing plasmid. For RNAi against *lgg-1*, knockdown was confirmed by western blotting (Figure S1E). When stated, cyanamide (1mM) or chloroquine (1mM) were added to plates right before transferring the young adults.

Aging experiments in the absence of FUdR (Figures S2 and S3C) were performed as described above but omitting the FUdR. Once worms reached adulthood, they were moved every day to fresh NGM plates seeded with *E. coli* XU363 L4440 (empty plasmid) until progenies were no longer produced.

For lifespan assays on glycerol, glycerol was added to the molten agar at a final concentration of 0.04% or 0.4%. Hatchlings were seeded on NGM plates without glycerol. Once worms reached the L4 stage, they were moved to glycerol containing-NGM plates seeded with OP50 and 50µM FUdR as previously described[65]. Survival was scored daily or every other day. Worms were scored as dead if they did not respond to prodding with a platinum pick. Animals that escaped or died by bursting through the vulva were censored. Results were analyzed on SPSS using the Kaplan-Meier estimate with log rank test comparison across different strata. Figures were made using GraphPad Prism.

Yeast lifespan assays

For yeast chronological lifespan assays (CLS), 10 mL of Synthetic Complete (SC) media with 2% glucose was inoculated with 100 µl of overnight culture and incubated on a roller drum (TC-7, New Brunswick Scientific) in glass tubes with metal caps allowing for gas exchange. After 72 hours, the first measurement of colony forming units (CFUs) on YPD agar plates was made and this was treated as day 1 for the experiment (100% starting viability), to which all the other CFU data was normalized. Measurements were taken every 2 days as previously described[66,67]. Briefly, at each time point, 20 µl of the cell suspension were removed from each tube and 10-fold serially diluted three times with sterile water. Next, 2.5 µl aliquots of each dilution were spotted onto a YPD plate. After 16 hours, images of the spots were taken under a Nikon Eclipse

E400 brightfield microscope at 30x magnification. Microcolonies within the spots were automatically counted from the digital images using OrganoSeg[68], with the parameters adjusted for yeast colony counting[64]. After accounting for the dilution factor, colony numbers from each day were divided by the number of colonies from the first time point (day 1) to calculate the viability score. Mean lifespan (in days) and the 95% confidence intervals were calculated using OASIS 2[69].

RT-qPCR

Worms were grown and synchronized as described in "Lifespan assays". Approximately 1,500 synchronized L1 worms were seeded per 10cm RNAi plates containing control *E. coli* XU363. Once they reached the young adult stage, worms were transferred to RNAi plates containing 100µg/mL FUdR. At day 8 of adulthood, the animals were harvested using a mesh to remove the dead eggs, and worms were flash frozen in liquid nitrogen and preserved at -80ºC until processing.

RNA extraction was performed on frozen worms using TRI Reagent (MRC, United States) as described by the manufacturer. The purity and concentration of the RNA samples were determined using a NanoDrop. 3µg of RNA were then used to synthesize 20µL of complementary DNA (cDNA). Quantitative PCR was finally carried out by running a mixture of cDNA, SYBR green and primers for the genes of interest (Table S1) in a real time PCR thermal cycler (Biorad, United States). Fold changes were calculated using the Pfaffl method[70] and statistical significance compared to the WT control was calculated using an unpaired Student's t-test.

C. elegans western blotting

Worms were grown and synchronized as described in “Lifespan assays”. Approximately 2,000 synchronized L1 worms were seeded onto 10cm RNAi plates containing *E. coli* XU363 control. After growing the worms to day 1 adults, half the worms were transferred to RNAi plates containing 20mM chloroquine (Sigma, United States) while the other half of the worms (controls) were harvested, meshed to remove any laid eggs, and then flash frozen in liquid nitrogen. After 8 hours of treatment with chloroquine (CQ), CQ-treated animals were harvested, meshed, and flash frozen in liquid nitrogen.

RIPA buffer (Cold Spring Harbor protocols) was added to 100µL of packed worm pellets which were subsequently sonicated at 40% amplitude for 10 secs, a total of 5 times (keeping them on ice in between cycles). Protein content in the lysate was estimated using a Bradford assay (Thermo Scientific, United States), and lysates were then stored at -20ºC after adding protein loading buffer. From each lysate, 30µg of protein were loaded and resolved in a 4-12% Bis-Tris precast gel (Thermo Scientific, United States, Cat #: NP0322BOX) and then transferred to a nitrocellulose membrane. The membrane was blocked using Intercept (PBS) Blocking Buffer (Li-cor, United States) for 4 hours at room temperature, followed by an overnight incubation in 1:250 of our previously published anti-LGG-1[71] or in 1:5,000 anti-tubulin (DSHB, United States) primary antibodies. The next day, after washing, the membranes were incubated for an hour in the secondary antibody, Alexa Fluor® 800cw anti-rabbit (Li-cor, United States) or IRDye 800cw anti-mouse (Li-cor, United States). The proteins were visualized using a Li-cor Odyssey imaging system (Li-cor, United States) and the bands were quantified using densitometry analysis on ImageJ. Statistical significance compared to the WT and/or untreated control was calculated using an unpaired Student’s t-test.

Yeast western blotting

Western blots for yeast proteins were performed as previously described[72]. Cells were pelleted and stored at -80ºC. To extract protein, cells were thawed on ice and resuspended in 0.5mL 20% trichloroacetic acid (TCA) at 4ºC and then vortexed with glass beads 4 times for 30 seconds with 15 second rests on ice in between. Cell lysates were transferred to new microcentrifuge tubes. The beads were washed twice with 0.5mL 5% TCA at 4ºC and the washes combined with the lysates, then centrifuged at 3,000 rpm for 10 minutes. Supernatants were discarded and the crude protein pellets were resuspended in 200µL of sample buffer (50 mM Tris HCl, pH 6.8, 2% SDS, 10% glycerol, 0.1% bromophenol blue, 5% 2-mercaptoethanol). After resuspension, 50µL of 2M Tris base was added and proteins were boiled for 5 minutes at 100ºC. Samples (20 µl) were run on a 10% SDS polyacrylamide gel, then transferred onto PVDF membranes using a Biorad semi-dry transfer apparatus at 25 volts for 60 minutes. Membranes were blocked overnight with 5% non-fat milk in TBST at 4ºC. Membranes were then incubated with either anti-alcohol dehydrogenase antibody (Rockland Immunochemicals, 200-4143-0100) at 1:1,000 or anti-alpha-tubulin antibody (Invitrogen, MA1-80017) at 1:5,000 in blocking buffer for 1 hour at room temperature. Membranes were washed in TBST once for 10 minutes followed by 3 washes for 5 minutes each. Membranes were then incubated in a secondary antibody, either HRP-conjugated anti-rabbit IgG (Promega Corporation, W4018) or HRP-conjugated anti-rat IgG (Abcam, ab6734) for 1 hour at room temperature. The membrane was washed again and then soaked for 5 minutes in HRP peroxidase substrate (Millipore, WBKLS0500), followed by a 1-minute soak in luminol (Millipore, WBKLS0500). Proteins were visualized using an Amersham ImageQuant 800 (Cytiva Life Sciences, 29399481) and the resulting bands were quantified using densitometry analysis on ImageJ. Statistical significance comparing Adh1 levels in CR relative to the non-restricted (NR) condition was determined by two-way ANOVA. Significance of estradiol induced Adh1 overexpression was determined by one-way ANOVA.

For caloric restriction, yeast cells were grown in Synthetic Complete (SC) media with 0.5% glucose. For no restriction (NR), they were grown in SC media containing 2% glucose. For Adh1 overexpression, beta-estradiol dissolved in DMSO was added to the SC NR media at the time of inoculation of yeast cells in concentrations of 0nM, 6.25nM and 100nM.

Immunostaining

Whole-body immunostaining against LGG-1 was performed using an in-house protocol (Ghaddar *et al*., STAR Protocols, in press). Briefly, adult worms were treated with mock or chloroquine as described above and then fixed in 60% isopropanol. They were then immobilized on slides using a polyacrylamide gel where they were treated with **β**-mercaptoethanol and collagenase. Worms were then incubated in a blocking solution before being incubated in anti-LGG-1 antibody (1:250) overnight at 4ºC. Worms were then washed and incubated in a goat anti-rabbit antibody (1:500) (Invitrogen, United States) at room temperature for 2 hours. Images were taken using a Leica spinning disk confocal microscope (Leica, Germany) and analyzed using ImageJ.

Allyl alcohol survival assay

Worms were grown and synchronized as described in “Lifespan assays”. Fifty day-1 adults were transferred to RNAi plates supplemented with 0.3% Allyl Alcohol (Sigma, United States). Worms were scored 4 hours post-treatment; animals not responding to prodding with a platinum pick were scored as dead. Statistical significance relative to the appropriate control was calculated using an unpaired Student's t-test.

Fluorescent imaging

Worms were grown and synchronized as described in "Lifespan assays". On day 1 of adulthood, ~100 worms were harvested and immobilized with 100mg/mL levamisole. Worms were then mounted on agar pads and imaged using a Leica spinning disk confocal microscope (Leica, Germany) at 60x magnification (numerical aperture: 1.4). The *daf-22*P::PLIN1::GFP was excited and visualized with a CSU-488 laser (emission filter 540 nm) and the *adh-1*P::ADH-1::wrmScarlet::*adh-1*3'UTR was excited and visualized with a CSU-561 laser (emission filter 600 nm). We also imaged the PLIN1::GFP;*adh-1*::WrmScarlet strains in the blue channel (CSU-405 laser; emission filter 488 nm) to ensure that the signal observed in the other channels was not due to autofluorescence from the gut granules (Figure S4C). Images were analyzed using ImageJ. Statistical significance relative to the appropriate control was calculated using an unpaired Student's t-test.

Glycerol measurement

Glycerol quantification was performed as previously described with some modifications[73]. Worms were grown and synchronized as described in "Lifespan assays". On day 1 (young) or 8 (aged) of adulthood, ~2,000 worms were harvested, flash-frozen in liquid nitrogen and stored at -80ºC. Day 8 was picked because it is the last day that worms can be harvested without including a large number of dead animals in the samples. Additionally, by day 8, the worms already show significant signs of aging including damaged tissues, tubular lysosomes, atrophied intestine, and loss of self-fertility. To prepare worm lysates, 85µL of water were added to the frozen pellets of worms which were then sonicated for 10 seconds 5 times, keeping them for 2 minutes on ice between each sonication pulse. Samples were then centrifuged at 18,600g for 5 minutes at 4ºC. Part of the supernatant was kept for protein quantification using a BCA assay, while the rest was deproteinized using trichloroacetic acid (TCA) and then neutralized following the manufacturer's instructions (AAT Bioquest, United States). The neutralization solution (AAT Bioquest, United States) was added to the samples until the pH was between 6.7-7.5. Glycerol was then measured in the deproteinized samples using a commercial kit following the manufacturer's protocol (R-Biopharm, Germany, Cat #: NC9662370). The measured amount of glycerol was then normalized to the corresponding sample's amount of protein, and to a standard glycerol curve per manufacturer instructions. Statistical significance relative to the appropriate control was calculated using an unpaired Student's t-test.

For glycerol measurement of HLH-30^{OE} animals, the same protocol was followed except L1 worms were grown on *E. coli* XU363 carrying L4440 + GFP plasmids before being switched to *E. coli* XU363 carrying L4440 (empty plasmid) at the L4 stage for 24 hours. The worms were then harvested as described above. This approach allowed us to perform an acute overexpression of HLH-30.

Locomotor endurance assay

Approximately twenty-four 12-days old worms were picked into individual wells of 24-well RNAi plates. Worms were let to adapt to the wells for ~1h. Wells were then flushed one at a time with S-buffer and one-minute videos were taken using an Olympus SZX7 microscope fitted with an Olympus U-CMAD3 camera. Videos were then analyzed using the wrMTrck plugin on

ImageJ[74]. Statistical significance relative to the appropriate control was calculated using an unpaired Student's t-test.

Egg laying assay

As soon as the N2 and GMW20 (ADH-1^{OE}) worms reached the adult stage, single worms were picked into ten individual 6cc RNAi plates seeded with *E. coli* XU363 bacteria. Each of the ten worms was moved to fresh individual RNAi plates every 12h until reproduction ceased. The progenies laid during each 12h-period were allowed to develop until the L3-L4 stage at 20°C, and then counted. Statistical significance relative to the appropriate control was calculated using an unpaired Student's t-test.

Glycerol choice assay

Eight 10µL spots of *E. coli* XU363 were seeded on 10cc RNAi plates equidistant from the plate-center and from each other. Alternating between the spots, glycerol was added to 4 of the *E. coli* XU363 spots. In parallel 1-day old worms were harvested, washed with S-buffer, and the concentration of worms in the suspension was estimated by counting worms in five 5µl drops. Worms were concentrated to five worms per microliter by centrifugation. To start the assay, approximately 200 synchronized adult worms (40µl) were seeded in the center of the plate. Plates were incubated at 20ºC. After 3h, 6h, 12h and 24h, the number of worms on each spot was counted. Statistical significance was calculated using an unpaired Student's t-test.

QUANTIFICATION AND STATISTICAL ANALYSIS

Data were considered statistically significant when $p < 0.05$ by Kaplan-Meier estimator with log rank test comparison across different strata (for aging experiments), unpaired Student's t-test or one-way and two-way ANOVA (for non-aging experiments) as indicated in the Figure, Figure legends or experimental methods. Asterisks denote corresponding statistical significance: ns = not significant, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001. For aging experiments all p-values are reported in Data S1. Individual data points are presented where relevant, in addition to the mean and standard error of the mean (SEM) denoted by the error bars. The number of biological replicates for each experiment is stated in the legend of every figure or in the corresponding supplementary tables. In the figure legends or supplementary tables, N refers to the number of animals and n refers to the number of biological replicates. All statistical analyses were performed on SPSS (for aging experiments) or GraphPad Prism (for non-aging experiments).

Excel tables titles and legends **(Note this file is only available at doi:10.1016/j.cub.2023.01.059)**

Data S1. Data and statistical analysis of lifespan assays and physiological assessments in *C. elegans*, and results of mining mammalian transcriptomics data. Related to Figures 1, 2, 3, 4, S1, S2 and S3. **(A)** Knockdown of *hlh-30* suppresses *mxl-3* longevity. EV = empty vector. Blue delta lifespan (as %) and stats as compared to WT and red as compared to *mxl-3* mutants. (*) denotes repeat depicted in Figure 1A. **(B)** Knockdown of autophagy genes *atg-18*, *bec-1* and *lgg-1* further extends *mxl-3* lifespan. EV = empty vector. Blue delta lifespan (as %) and stats as compared to WT and red as compared to *mxl-3* mutants. (*) denotes repeats depicted in Figure S1D. **(C)** Impairing autophagy by mutating *atg-18* or lysosomal function and autophagy by treating worms with 1mM chloroquine does not suppress *mxl-3* longevity. EV = empty vector. Blue delta lifespan (as %) and stats as compared to WT and red as compared to *mxl-3* mutants. (*) denotes repeats depicted in Figures 1B and S1E. **(D)** *adh-1* mediates *mxl-3* and HLH-30^{OE} longevity. EV = empty vector. Blue delta lifespan (as %) and stats as compared to WT, red as compared to *mxl-3* mutants. and green as compared to HLH-30^{OE}. (*) denotes repeats depicted in Figures 1D & 1F. (**E)** Knockout of *adh-1* and treatment with the aldehyde dehydrogenase inhibitor cyanamide decreases HLH-30^{OE} lifespan in the absence of FUdR. Blue delta lifespan (as %) and stats as compared to WT and red as compared to HLH-30^{OE} worms. (*) denotes repeat depicted in Figure S2. (**F)** Knockdown of *adh-1* and treatment with the aldehyde dehydrogenase inhibitor cyanamide partially suppress *eat-2* longevity. Blue delta lifespan (as %) and stats as compared to WT and red as compared to *eat-2* mutants. (*) denotes repeats depicted in Figures 2B & 4C. **(G)** Knockdown of *adh-1* suppresses *let-363* RNAi lifespan extension. Blue delta lifespan (as %) and stats as compared to WT and red as compared to *let-363* RNAi. (*) denotes repeats depicted in Figure 2C (**H)** Mutation of *adh-1* and treatment with the aldehyde dehydrogenase inhibitor cyanamide suppress *daf-2* RNAi-mediated longevity. Blue delta lifespan (as %) and stats as compared to WT and red as compared to *daf-2* RNAi. (*) denotes repeats depicted in Figures 2D & 4D. **(I)** Overexpression of ADH-1 is sufficient to promote longevity. This extended lifespan is dependent on cyanamide. Blue delta lifespan (as %) and stats as compared to WT and red as compared to

ADH-1^{OE} (GMW20, GMW21 or GMW22). (*) denotes repeats depicted in Figures 2E & 4A. **(J)** ADH-1 overexpression prolongs lifespan in the absence of FUdR. This extended lifespan is dependent on cyanamide. Blue delta lifespan (as %) and stats as compared to WT and red as compared to ADH-1^{OE} (GMW20). (*) denotes repeats depicted in Figures S3C. **(K)** Overexpression of ADH-1 alleviates the pro-aging effect of glycerol (0.04%). Blue delta lifespan (as %) and stats as compared to WT and red as compared to ADH-1^{OE} (GMW20) untreated. (*) denotes repeats depicted in Figure 3F. **(L)** Overexpression of ADH-1 alleviates the pro-aging effect of glycerol (0.4%). Blue delta lifespan (as %) and stats as compared to WT and red as compared to ADH-1^{OE} (GMW20) untreated. (*) denotes repeats depicted in Figure 3F. **(M)** The aldehyde dehydrogenase inhibitor cyanamide suppresses *mxl-3* and HLH-30^{OE} longevity. EV = empty vector. Blue delta lifespan (as %) and stats as compared to WT, red as compared to *mxl-3* mutants, and green is compared to HLH-30^{OE}. (*) denotes repeat depicted in Figures 3B and 3E. **(N)** Raw data for locomotor endurance assay to compare 12-days old wild type to same age ADH-1^{OE} animals. (*) denotes repeat depicted in Figure 2F. **(O)** Raw data for size measurements of WT and ADH-1^{OE} animals. (*) denotes repeat depicted in Figure S3D. **(P)** Pharyngeal pumping assay to compare WT and ADH-1^{OE} animals. (*) denotes repeat depicted in Figure S3E. **(Q)** Defecation assay to compare WT and ADH-1^{OE}. (*) denotes repeat depicted in Figure S1F. **(R)** Fertility assay to compare WT and ADH-1^{OE}. (*) denotes repeat depicted in Figures S1G and S1H. **(S)** ADH1 encoding genes are induced upon calorie restriction across species. The result of literature mining is shown as brackets of levels of induction relative to the controls.

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Author contributions

The study was conceived and designed by AG and EJO. *C. elegans* experiments were performed by AG, VKM, SB, EH, AP, MKH and EJO and analyzed by AG, VKM and EJO. Yeast experiments were performed and analyzed by SM, JCJ, EEH and JSS. The manuscript was written by AG, VKM and EJO.

Supplemental material

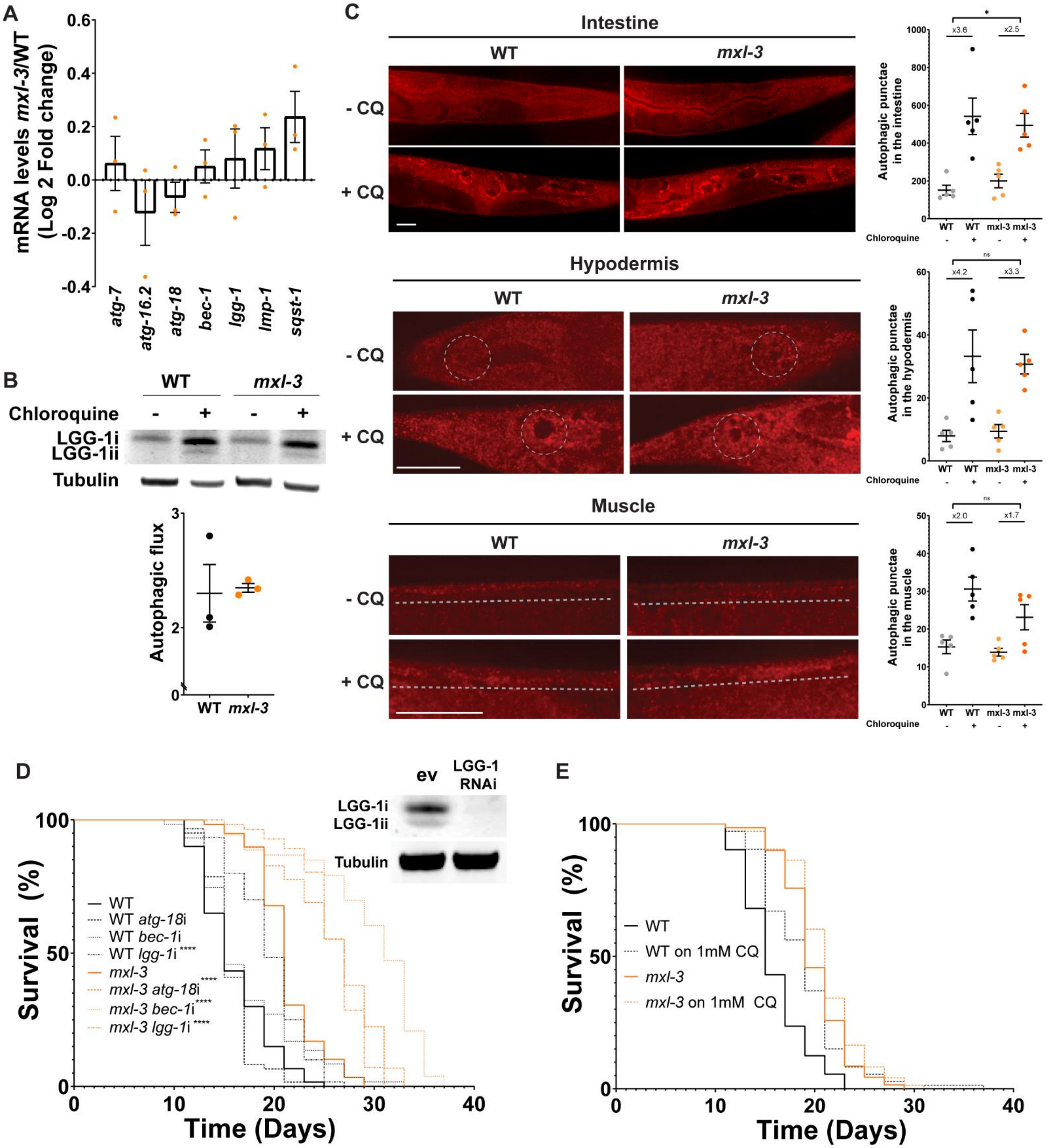


Figure S1. HLH-30 promotes autophagy-independent longevity in the *mxl-3 C. elegans* mutant, related to Figure 1. (A) Autophagy genes are not induced in the *mxl-3* mutant animals as measured by RT-qPCR relative to wild-type worms (n=3 biological replicates). See Table S1 for qRT-PCR primers. **(B)** There is no difference in autophagy flux as measured by western blotting against LGG-1 on wild-type and *mxl-3* mutant worms treated with mock or the lysosome/autophagy inhibitor chloroquine (n=3 biological replicates). **(C)** Similarly, immunostaining against LGG-1 reveals no increase in autophagy flux (+/- chloroquine) in the intestine, hypodermis (area within dotted circle) or muscle (area above dotted line) of *mxl-3* mutants relative to wild-type worms (n=5 biological replicates; scale bar = 25µm). **(D)** Knockdown of autophagy genes does not suppress the extended lifespan of the *mxl-3* mutant (representative of three 3 biological replicates, Data S1B). RNAi against *lgg-1* indeed results in a significant decrease in LGG-1 protein levels as measured by western blotting (inset). **(E)** Treatment with 20mM of the lysosomal, and hence autophagy, inhibitor chloroquine (CQ), does not suppress the extended lifespan of the *mxl-3* mutant (representative of 3 biological replicates, Data S1C). **(A-E)** EV = empty vector. Error bars denote SEM. ns= not significant, $*p<0.05$, $**p<0.01$, $***p<0.001$, $****p<0.0001$.

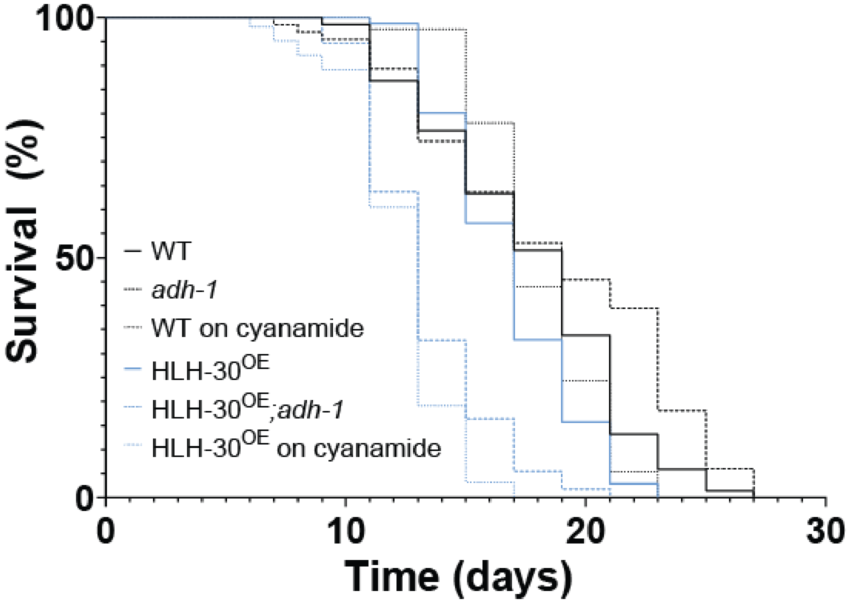


Figure S2. HLH-30^{OE} lifespan relative to WT in the absence of FUdR, related to Figure 1. HLH-30^{OE} animals show high rates of bagging (Figure S3B), which results in premature death due to matricide (rather than old age). Fluorodeoxyuridine (FUdR) prevents embryogenesis and, consequently, premature death from matricide in *C. elegans*[S1]. Therefore, to prevent matricide, we performed the aging analyses in the presence of FUdR (Fig. 1F). Importantly, even though HLH-30^{OE} animals are not long-lived relative to wild type worms in the absence of FUdR, loss-of-function mutation of *adh-1* and cyanamide treatment still reduce HLH-30^{OE} lifespan. These results imply that *adh-1* and aldehyde dehydrogenase activity promote lifespan extension in the HLH-30 overexpression context even when FUdR is absent (representative of two biological replicates).

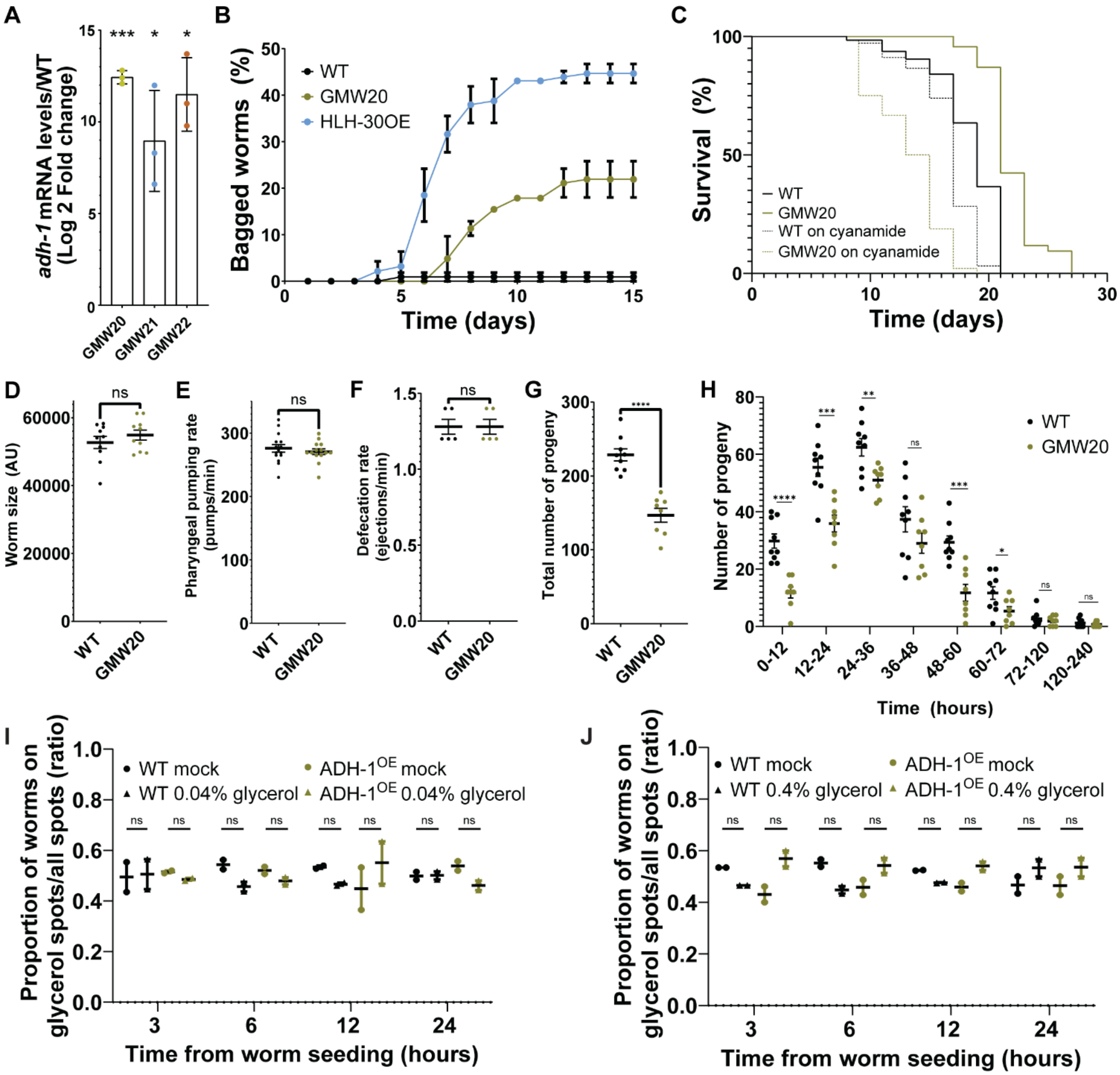


Figure S3. **Characterization of the ADH-1^{OE} worms, related to Figure 2. (A)** ADH-1^{OE} strains show increased *adh-1* transcript levels (n=3 biological replicates). **(B)** Percentage of bagging in the HLH-30^{OE} and ADH-1^{OE} compared to WT worms (N=60-70, two biological replicates). ADH-1^{OE} worms show a mild and HLH-30^{OE} worms a severe bagging phenotype. **(C)** Unlike HLH-30 overexpression, ADH-1 overexpression prolongs lifespan in the absence of FUdR (representative of four biological replicates), which is likely due to the less severe bagging phenotype of ADH-1OE worms. Cyanamide rescues ADH-1^{OE} longevity in the absence of FUdR. Therefore, AMAR-dependent longevity is not FUdR dependent. **(D-J)** WT and ADH-1^{OE} worms show indistinguishable: **D)** Body size (N=10, two biological replicates); **(E)** Feeding rate as measured through pharyngeal pumping (N=14-15, two biological replicates); and **(F)** Defecation rate (N=5, two biological replicates). However, ADH-1^{OE} worms show **(G)** Reduce total progeny output (N=10, two biological replicates) and **(H)** Less progeny per time unit than WT worms (N=10, two biological replicates). **(I-J)** Food choice assay shows that wild type and ADH-1^{OE} worms are neither attracted to nor repulsed by **(I)** 0.04% or **(J)** 0.4% glycerol (two biological replicates of each). *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

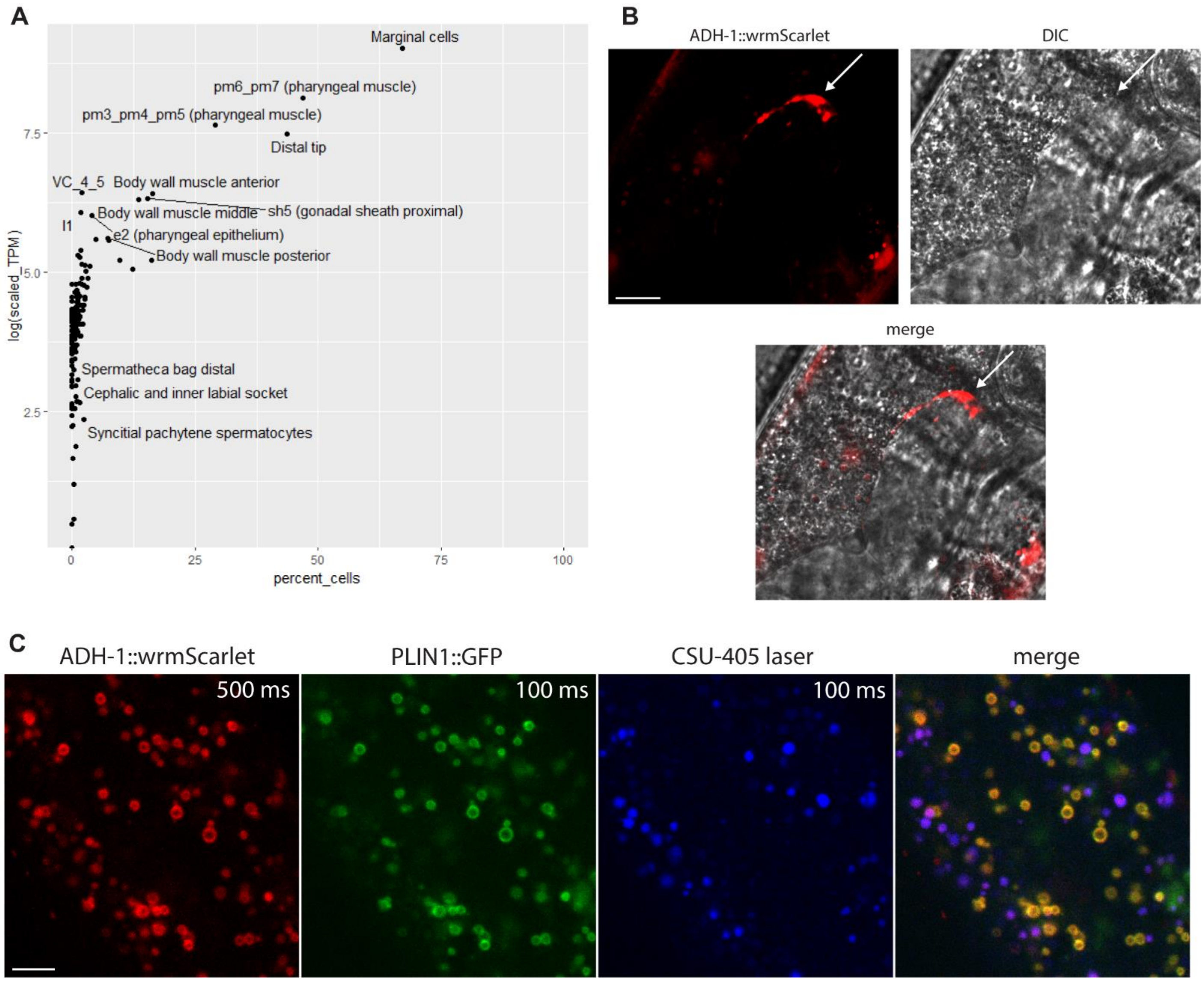
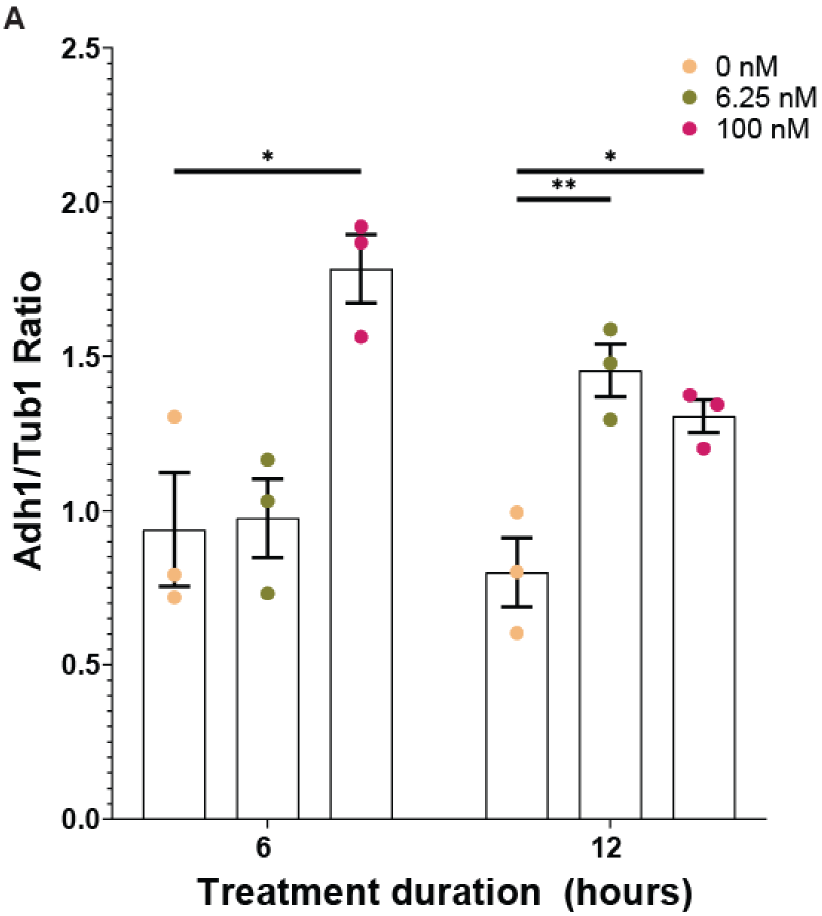


Figure S4. ADH-1 anatomical and subcellular expression of *adh-1*/ADH-1, related to Figure 3. (A) Cell-specific expression of *adh-1* as obtained from whole-body scRNA-Seq of a young adult (www.wormseq.org). Log(scaled_TPM) indicates levels of expression of *adh-1* in each cell type. Percent cells indicates the percentage of cells of each type that expresses *adh-1*. Obtained **(B)** Expression of *adh-1*P::ADH-1::wrmScarlet::*adh-1*3'UTR in the distal tip cell (arrow). **(C)** The droplets observed in the red (ADH-1::WrmScarlet) and green (PLIN::GFP) channels do not overlap with the autofluorescence droplets observed in the blue channel, indicating that the ADH-1::wrmScarlet signal does not overlap with the autofluorescent lysosome-related organelle. ns = not significant, *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.



B

Strain (estradiol concentration)	Average lifespan (days) ± standard error	95% C.I.
WT (0 nM)	9.34 ± 0.14	9.07 ~ 9.62
WT (6.25 nM)	8.98 ± 0.15	8.69 ~ 9.27
WT (100 nM)	10.15 ± 0.08	9.99 ~ 10.31
Adh1 (0 nM)	10.25 ± 0.13	9.99 ~ 10.51
Adh1 (6.25 nM)	14.91 ± 0.33	13.55 ~ 14.84
Adh1 (100 nM)	16.94 ± 0.31	16.33 ~ 17.54

Figure S5. Induction of Adh1 using an estradiol-based system extends yeast lifespan, related to Figure 5. **(A)** Estradiol treatment increases Adh1 protein levels (n=3 biological replicates) as measured by Western blot. Estradiol was added at the time of culture inoculation. Both concentrations increase expression during the diauxic shift (12 hours). **(B)** Adh1 overexpression extends yeast chronological lifespan under non-restricted conditions (n=3 biological replicates). Estradiol was added to cultures at indicated concentrations to induce Adh1 expression. Mean lifespans and 95% confidence intervals were calculated using OASIS 2. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

Target gene	**Forward primer**	**Reverse primer**
atg-18	AAATGGACATCGGCTCTTTG	TGATAGCATCGAACCATCCA
atg-7	AGCAGAAAAGATCTGGGA	GAGATGATAGTGGTGTGA
atg-16.2	CGCAAAGACTATTGAGTAC	AATACTACTGATATCCCAA
bec-1	TTTTGTTGAAAGAGCTCAAGGATC	CCATTGCACGAGTCCATCG
lgg-1	CCACAAACCATGACCACA	ACCTCTCCTCCATACACA
lmp-1	ATCCGCCACCGCTTCGCATT	TCGAGCTCCCACTCTTTGGCG
sqst-1	GATTATCGTCTCTACTACGGTG	GAGTTCGAGAGAATGTAGTG
adh-1	GGAAAGAATGTTACTGGATGGCA	ATTCGCAGTTGAGGCAGTTG

Table S1. qRT-PCR primers, related to Figures 1, 2 and S1.

Supplemental References

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Chapter III: Whole-body gene expression atlas of an adult metazoan

A version of this paper is currently under review in *Science Advances*

A version is currently available on Biorxiv (doi: 10.1101/2022.11.06.515345)

Abstract

Gene activity defines cell identity, intercellular communication, and underlies the functioning of multicellular organisms. Here we present the single-cell resolution atlas of gene activity of a fertile adult metazoan: *Caenorhabditis elegans*. This compendium comprises 180 distinct cell types and a total of 18,033 expressed genes. We predict 7,361 transcription factor–expression profile associations likely responsible for defining cellular identity. We also predict thousands of intercellular interactions across the *C. elegans* body and the ligand-receptor pairs that mediate them, some of which we experimentally validate. We identify 172 genes that show consistent expression across cell types, are involved in basic and essential functions, are conserved across phyla, and we therefore present as experimentally validated housekeeping genes. All data presented in this study are available in the user-friendly app *wormseq.org*. In addition to the new biology, we present genome-scale single-cell resolution testable hypotheses that we anticipate will advance our understanding of the molecular mechanisms underlying the functioning of a multicellular organism and the perturbations that lead to its malfunction.

Introduction

A wide range of different cell types sustains growth and reproduction in multicellular organisms. Even a simple animal like *Caenorhabditis elegans* develops according to a selected plan, discerns food-quality, finds mates, escapes predators, learns to associate environmental cues, and survives biotic and abiotic stressors. In *C. elegans*, these functions are carried out by around 20 broadly-defined cell types and more than 150 specific cell types(*1*–*3*). Underlying the morphological and functional differences between cells, are cell-type specific networks of active genes. Therefore, to unveil the molecular mechanisms underlying the functioning of multicellular organisms in physiological and pathological conditions we need a single-cell resolution catalog of gene expression and the ability to discern genes that are common and essential, from genes that define and sustain cell identity and function, and genes that enable local and distal intercellular communication. This information will enable future studies assess how perturbations (genetic, chemical, or environmental) alter gene expression at the cellular level and how these changes in turn result in phenotypes at higher levels of organization.

Recent advances in single-cell transcriptomics and *C. elegans* cell-dissociation protocols(*4*, *5*) have led to single-cell gene expression profiles of *C. elegans* embryos and larvae(*1*, *3*, *4*, *6*, *7*), and a recent preprint reports the transcriptional map of sterile, mutant, adult *C. elegans*(*8*). Here we present the expression profiles of 180 cell types identified in wild-type and fertile adult *C. elegans*. The single-cell resolution transcriptional map presented here adds several cell types that are absent in the embryonic, larval stages, and in the sterile adults. For instance, various germ cells and cells involved in reproduction and egg laying are presented here for the first time. Additionally, we sequenced >150,000 cells for a single experimental condition (in three biological replicates), giving unique robustness to this dataset.

We use this catalog of adult gene expression to explore the concepts of housekeeping gene, transcription factor (TF)-mediated cellular identity, and molecular drivers of cell-cell interaction. We identified 172 genes that meet the canonical definition of a housekeeping gene and, as such, are responsible for basic cellular maintenance across cell types and possibly kingdoms. On the other hand, with 7,361 predicted TF-cell type associations (some of which had been experimentally validated), we begin to elucidate, at a systems level, the relationship between transcriptional programs and the identity of cells. We also predict patterns of ligand-receptor pairs that promote molecular interactions between all the cell types identified in *C. elegans*. As a result, novel cell-type specific cell communication signatures are proposed, some of which we experimentally validate *in vivo*. Finally, we present a web interface to mine our dataset, *wormseq.org*, that together with the abundant literature and the genetic tools available to manipulate *C. elegans* will allow the community to experimentally test the hundreds of hypotheses and predictions presented in this study.

Results

Identification of over 180 distinct C. elegans cell types and subtypes

Wild-type hermaphrodite *C. elegans* were harvested as young adults (YA), defined by vulva morphology and the presence of ≤5 eggs (Fig. S1A). Worms were immediately dissociated into single cells and subjected to scRNA-Seq using the 10X Chromium platform (See Materials and Methods). Three independent biological replicates were collected and after the removal of low quality and damaged cells (see Materials and Methods), the dataset contained 154,251 cells that passed the quality filters. The cells were then processed following the Monocle3 pipeline (*9*) and visualized using UMAP. After Louvain clustering the cells separated into 170 distinct clusters ranging from 21 to 5841 cells (Fig. 1). Comparing replicates did not show batch-dependent differences in the average reads per cell (Fig. S1B) or median unique genes per cell (Fig. S1C). Batch-dependent differences in the proportion of cells of different types were small (Fig. S1D), suggesting high reproducibility between independent experiments in the dissociation and capture of cell types. Additionally, even prior to batch correction, cell type-specific gene expression profiles between biological replicates were highly correlated (Fig. S1E; Pearson correlation coefficient: 0.86-0.95), which suggests that although batch differences exist, well-controlled replicates accurately recapitulate average cell types and gene-expression profiles, and that the effect of cell type on the measured gene expression is stronger than the batch effect.

The clusters were annotated using a multi-pronged approach that took advantage of previously published scRNA-Seq data from *C. elegans* larvae (*1, 3*) and the rich literature on *C. elegans* tissue and cell-specific markers(*10*). First, we generated a list of marker genes expressed in each cluster using Monocle3's top_markers function (Data S1). We then searched for the broad cell types in which these marker genes were expressed in the CeNGEN app (*3*) because this dataset contains scRNA-Seq data from the L4 larval stage, which is the larval stage preceding the YA. This approach yielded broadly defined tissues. However, some clusters were still not confidently annotated using this approach alone because they lacked sufficient detail in the CeNGEN dataset (*e.g.*, pharyngeal gland cells g1A vs g1P vs g2), or because the clusters were not expected to be present in CeNGEN because they are exclusive to the adult (*e.g.*, cells involved in egg laying). We therefore used Wormbase to identify gene markers and manually annotate each unannotated cluster; the markers and rationale behind every annotation can be found in Data S1.

We identified all expected broad cell types in the adult hermaphrodite *C. elegans* (*2*) including intestine, pharyngeal cell types, hypodermis, non-striated and body wall muscle, neurons, glial cells, rectum and anus, seam, somatic gonad, vulva and uterus, excretory, coelomocytes, GLR cells, head mesodermal cells and XXX cells. More importantly, several major cell types could be further annotated into specific cell types. The data was sufficiently exhaustive that we were able to identify cell types represented by a few or even one cell in the *C. elegans* adult. For example, we were able to identify specific pharyngeal gland cells (g1A, g1P and g2), individual gonadal sheath cells (sh1, sh2, sh3_sh4, sh5), and vulval muscle cells (vm1 and vm2). Finally, we identified 112 out of the 118 distinct neuronal classes previously reported (*11*). This includes 9 GABAergic, 51 cholinergic, 35 glutamatergic, 3 dopaminergic, 1 octopaminergic, and 2 serotonergic neuron types. Classifying the neurons by function, we found 32 sensory neurons, 22 motor neurons, 11 pharyngeal neurons, 36 interneurons, and 14 polymodal neurons. The only neurons we were not able to identify in our dataset were the I3, I6, MC, ADA, AVG and ALN. Overall, we defined 180 specific cell types (Data S1 & Fig. 1).

A limitation of current single-cell RNA-Seq technologies is that they only sequence a sample of the transcriptome of each cell. Therefore, to build more accurate transcriptional profiles for each cell type, we sought to distinguish between actual gene expression and noise. We used bootstrap resampling to estimate the average and confidence interval for the expression level of each gene per cell type (available through *wormseq.org*). If the lower bound of the 95% bootstrap confidence interval of the calculated TPM was greater than 0, then we considered that gene to be robustly expressed in the analyzed cell type. Using this thresholding criterion, we estimated a median of 5,871 genes robustly expressed per cell type. However, a strong positive correlation between the number of genes and number of cells per cell type indicates that the number of genes detected per cell type depends on the number of cells sequenced in each cluster (Fig. S2B; Pearson correlation coefficient: 0.64). We therefore used a different metric, to estimate the percentage of the transcriptome covered for each cell type given the number of cells in the cluster. The modeling (see Materials and Methods) suggests that for 177 out of 180 cell types we identified at least half of the genes expressed in that cell type. Moreover, for the majority of these cell types (135/180), we identified at least 75% of the transcriptome (Data S2).

An unexpected consequence of our classification is the identification of transcriptionally distinct spermatheca subpopulations that had not been reported before. [Note: the rationale of all annotations can be found in Data S1]. Traditionally, the spermatheca is divided into three compartments: the spermatheca neck, the spermatheca bag, and the spermatheca-uterine junction. However, our spermatheca cells clustered into 5 distinct clusters. Our results suggest that the spermatheca neck can be further subdivided into at least two populations of cells that relative to the uterus we name: (i) spermatheca neck distal – this cluster expresses *apx-1* and *let-502* highly (*12*, *13*), and (ii) spermatheca neck proximal –this cluster does not prominently express *apx-1* and *let-502*. Similarly, the spermatheca bag can be subdivided into: (i) spermatheca bag distal –this cluster prominently expresses *ajm-1* and *par-3*(*14*), and (ii) spermatheca bag proximal, which does not express these markers as prominently. On the other hand, a single cluster corresponds to the spermatheca-uterine junction. Therefore, even in an organism with every cell anatomically mapped, potentially novel divisions of labor between cells can be uncovered using whole-body scRNA-Seq.

Another unexpected observation is the presence of cell types that are not typically found in adult hermaphrodite *C. elegans*. One of these clusters expressed seminal-vesicle gene markers, which are exclusively found in males. We suspect these reflect the presence of rare males (≤0.01%) in our cultures (*15, 16*). There were also cell clusters characteristic of the L4 stage (*e.g.*, spermatocytes and spermatids), and of early embryos. We postulate that these anachronic clusters came from younger (L4) and older adults which are expected to rarely occur in the three independent populations of 100,000 animals that we used to isolate the cells. Once we remove the cell types corresponding to L4s, males, and embryos, we end up with 175 adult hermaphrodite cell types. It is worth noting that the fact that the dataset included the transcriptome of scarce cell types emphasizes the power of droplet-based scRNA-Seq in capturing underrepresented cell populations or subtle perturbations.

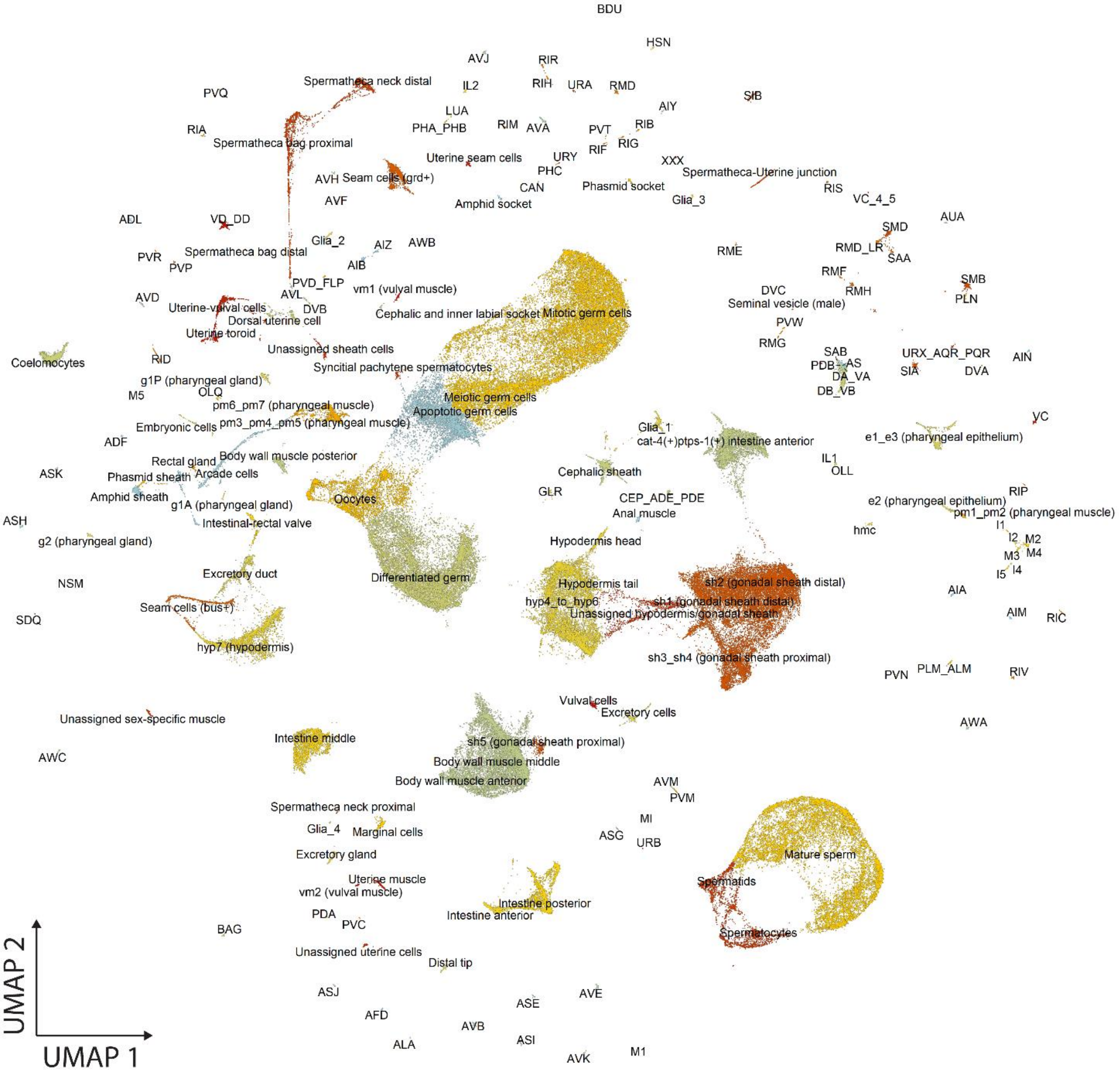

Figure 1. UMAP visualization of the 180 identified cell types. UMAP reduction of 154,251 cells. Each dot represents a cell. Colors indicate distinct cell types and are used to facilitate distinguishing close clusters.

Identification of housekeeping genes

Housekeeping genes can provide insight into intriguing biological questions such as which genes are under the strongest selective pressure or from a reductionist perspective, which genes are essential to cellular function in eukaryotes. Housekeeping genes also serve as references in various molecular and biochemical assays. However, it remains unclear whether commonly employed housekeeping genes, or any gene, meet the commonly used criteria to define housekeepingness, namely: consistent expression across cell types and conditions, essentiality, and conservation. To assess consistent expression, we employed two different criteria. We first applied a stringent criterion: abundant expression within each cell type and expression across cells. For this, we created a gene-by-cell-type matrix to define for each cell type how many cells expressed a given gene. We then used density plots to visualize the prevalence of every gene across cells within each cell type. A gene with a density plot skewed to the right (negative skewness score) is expressed in most cell types and in the majority of cells in each cell type (*e.g.*, *ctc-3* in Fig. 2A). By contrast, a gene with a density plot skewed to the left (positive skewness score) is expressed in a few cell types and, when expressed in a cell type, it is expressed in the minority of the cells (e.g., *sax-7* in Fig. 2A). Out of the 18,033 genes we detected, only 50 genes had negative skewness scores (Data S3A), indicating that, in our dataset, very few genes meet the criteria of being ubiquitously and abundantly expressed across cell types. Nevertheless, the 50 genes with negative skewness scores were enriched in "basal cellular" functions including protein translation and mitochondrial respiration (Fig. 2B), and in essential genes (identified as lethal in sub-genome (*17*) and full-genome RNAi screens (*18, 19*)) (Fig. 2C), two features in line with these genes being *bona fide* housekeeping genes.

It is important to acknowledge here that inherent limitations of current scRNA-Seq technology could have explained, at least in part, the small number of genes robustly expressed across all cell types; however, this is unlikely to be the sole or even the main explanation (see Discussion). A more likely explanation is that we are missing housekeeping genes when using the skewness score because housekeeping genes are not necessarily abundantly expressed. Instead, housekeeping genes are expected to be consistently expressed. To identify genes consistently but not necessarily abundantly expressed, we applied a metric of inequality called the Gini coefficient or Gc (*17*). Genes with lower Gc's are expressed more equally across cell types, and genes with higher Gc's are expressed in a more cell-type-specific manner. In our scRNA-Seq dataset, more than 90% of genes had Gc's indicative of inconsistent expression across cell types (Gc $\geq$0.4). By contrast, 367 genes had Gc's considered to represent good to perfect equality (<0.3) (Fig. 2D & Data S3B), which suggests they might play a role in common or core cellular functions. Indeed, GO term analysis showed that the genes with low Gc (<0.3) were enriched in "basal cellular" functions, including ribosomal activity and mitochondrial respiration (Fig. 2E).

Housekeeping genes are also expected to be similarly expressed across conditions. scRNA-Seq is not yet available for *C. elegans* subject to perturbations (genetic, chemical, or other); therefore, we used time, in the form of a different life stage, as an alternative condition. Specifically, we looked at the overlap between genes consistently expressed (Gc <0.3) in young adults and a list of putative housekeeping genes reported for the *C. elegans* L2 larvae (*17*). We found that all genes with high expression equality (Gc $\leq$0.2) and most genes (306/367) with good expression equality (Gc <0.3) in the young adults were also consistently expressed across cell types in the L2 larvae (Data S3C). Furthermore, 248 out of the 306 genes were experimentally shown to be essential (lethal) in partial (*17*) and full-genome RNAi screens (*18, 19*) (Fig. 2F-G; Data S3D).

Finally, based on the conservation criteria defined in Tabach *et al* (*20*), and as expected for essential genes, we found most of them (172/248) conserved across animals, plants, and fungi (Fig. 2G; Data S3E). Therefore, the 172-gene list meets several of the ascribed, but rarely tested, criteria that define housekeeping genes: (i) expressed consistently across cell types, (ii) expressed consistently across conditions (*e.g.*, developmental stages), (iii) involved in basic cellular functions, (iv) essential for life, and (v) conserved across species.

Next, we applied the Gini coefficient estimate to assess the “housekeeping-ness” of 26 genes broadly used as “housekeeping” genes for normalization of gene expression in *C. elegans* (*21, 22*). The majority of these genes (16/26) had Gc ≤0.3, indicating that these may be appropriate reference genes (Fig. 2H). Four out of the 16 genes had a negative skewness score in our dataset *–rpl-24.1, rpl-35, rps-26,* and *rps-23*, indicating that these 4 genes are not only consistently but also abundantly expressed across cell types (Fig. 2H). On the other hand, 6 commonly used “housekeeping genes” *–rbd-1, tba-1, pmp-3, act-1, arp-6,* and *csq-1*, had a Gc of more than 0.5. This severe expression gap indicates that these 6 genes are inadequate normalization factors (Fig. 2H); in fact, all 6 genes are expressed in a tissue-specific manner (Fig. S3A-F). We therefore recommend avoiding the use of *rbd-1, tba-1, pmp-3, act-1, arp-6,* and *csq-1*, especially in studies involving adult *C. elegans*. Additionally, we identified 172 housekeeping genes that, for the first time, are experimentally tested for the 4 criteria axiomatically ascribed to housekeeping genes. The consistent expression of these 172 genes across cell types, conditions, and species suggest that, in line with essential functions, they are under strong selective pressure.

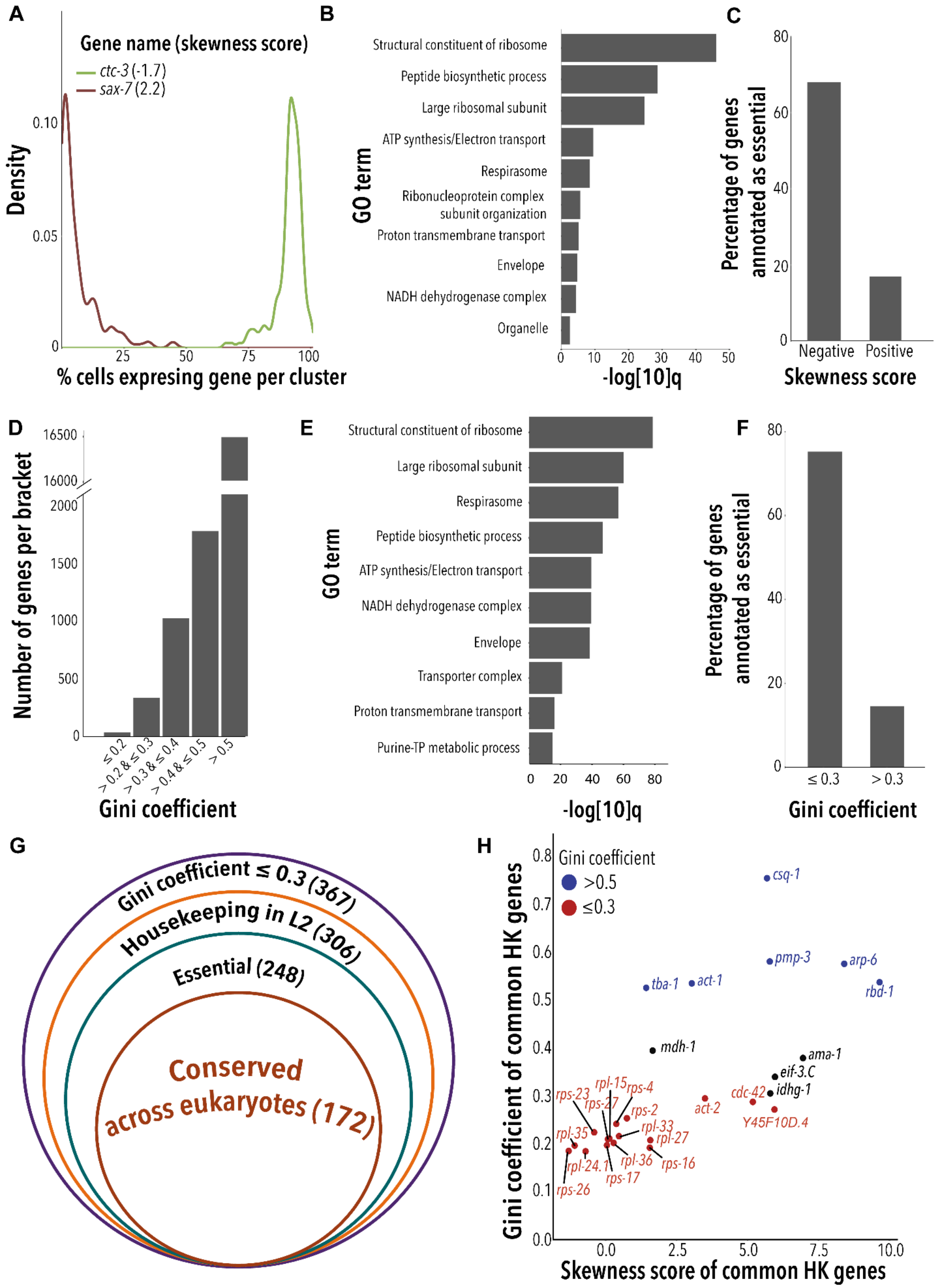
A
Gene name (skewness score)
ctc-3 (-1.7)
sax-7 (2.2)
Density
0.10
0.05
0
25
50
75
100
% cells expresing gene per cluster
B
GO term
Structural constituent of ribosome
Peptide biosynthetic process
Large ribosomal subunit
ATP synthesis/Electron transport
Respirasome
Ribonucleoprotein complex subunit organization
Proton transmembrane transport
Envelope
NADH dehydrogenase complex
Organelle
0
10
20
30
40
50
-log[10]q
C
Percentage of genes annotated as essential
80
60
40
20
0
Negative
Positive
Skewness score
D
Number of genes per bracket
16500
16000
2000
1500
1000
500
0
≤ 0.2
> 0.2 & ≤ 0.3
> 0.3 & ≤ 0.4
> 0.4 & ≤ 0.5
> 0.5
Gini coefficient
E
GO term
Structural constituent of ribosome
Large ribosomal subunit
Respirasome
Peptide biosynthetic process
ATP synthesis/Electron transport
NADH dehydrogenase complex
Envelope
Transporter complex
Proton transmembrane transport
Purine-TP metabolic process
0
20
40
60
80
-log[10]q
F
Percentage of genes annotated as essential
80
60
40
20
0
≤ 0.3
> 0.3
Gini coefficient
G
Gini coefficient ≤ 0.3 (367)
Housekeeping in L2 (306)
Essential (248)
Conserved across eukaryotes (172)
H
Gini coefficient of common HK genes
Gini coefficient
>0.5
≤0.3
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
csq-1
pmp-3
arp-6
tba-1
act-1
rbd-1
mdh-1
ama-1
eif-3.C
idhg-1
cdc-42
act-2
Y45F10D.4
rpl-15
rps-4
rps-23
rps-27
rps-2
rpl-33
rpl-27
rpl-35
rpl-24.1
rpl-36
rps-16
rps-17
rps-26
0.0
2.5
5.0
7.5
10.0
Skewness score of common HK genes

Figure 2. Identification of 172 experimentally validated *C. elegans* housekeeping genes. (A) The skewness score (in parenthesis) represents the relative abundance of mRNAs within and across cell types for a given gene. The depicted density plots illustrate 2 genes at the ends of the spectrum of skewness scores. **(B)** Gene Ontology (GO) enrichment analysis for genes with negative skewness scores (q-value threshold = 0.1). **(C)** Proportion of essential genes (defined as lethal when knocked down by RNAi) among the 50 genes with negative and positive skewness scores. Fisher's exact test for enrichment p-value <2.2e-16, which is the smallest p-value possible for this test. **(D)** Number of genes within each Gini coefficient (Gc) bracket: ≤ 0.2 perfect, >0.2 to ≤ 0.3 good, and >0.3 to ≤ 0.4 adequate expression equality. Gc >0.4 to ≤ 0.5 big and >0.5 severe expression gap. **(E)** GO enrichment analysis for genes with low Gini coefficient (<0.3) (q-value threshold = 0.1). **(F)** Proportion of essential genes among genes with low (≤0.3) and high (>0.3) Gini coefficients. Fisher's exact test for enrichment p-value <2.2e-16, which is the smallest p-value possible for this test. **(G)** Concentric diagram to represent: number of genes with low Gc (<0.3) in our scRNA-Seq dataset, number of genes previously classified as housekeeping genes in the L2 worm (*17*), number of genes experimentally shown to be essential, and number of genes conserved across species (see also Table S2). **(H)** Distribution of a set of commonly used housekeeping genes across Gini coefficients and skewness scores. Red font indicates genes with perfect or good expression equality (Gc ≤ 0.3) and blue indicates genes with a severe expression gap (Gc > 0.5). HK = housekeeping.

Inferring transcriptional regulators underlying cell identity

We then used an analysis successfully applied to the single-cell RNA-Seq data of the *C. elegans* L2 stage to gain insights into the regulatory programs that drive cell-specific gene expression (*6*). Briefly, the known binding patterns of transcription factors (TF), as defined through ChIP-Seq (*23–25*), are correlated with the cell-specific gene expression profiles defined through scRNA-Seq. To this end, we constructed regression models to predict the expression level of each gene in each of the 180 different cell types based on the strength of the ChIP-Seq peak(s) proximal to its promoter region. We then restricted correlations to TFs that were detectably expressed in our scRNA-Seq dataset. This analysis yielded 7,361 distinct TF-cell type associations that showed correlation coefficients larger than zero (Data S4 and *wormseq.org*). To assess the validity of these associations –which we refer to as "TF activity" associations, we tested whether the TF-cell type association scores inferred from the ChIP-Seq-scRNA-Seq analysis were able to predict cellular identity as defined by the expression of all 18,033 genes in our dataset. We clustered cell types using all-gene expression (Fig. 3A) and separately using "TF activity" scores alone (Fig. 3B). We then assessed the extent to which the 'TF activity dendrogram' correlated with the 'all expressed genes dendrogram'. We found that the two dendrograms were highly correlated

(Baker's gamma correlation coefficient: 0.70) demonstrating that TF activity as defined by our model largely drives cellular identity and, as such, it can predict cell-ontological relationships between cell populations. Interestingly, using only TF expression (Fig. 3C), rather than TF activity, yielded a much weaker correlation (Baker's gamma correlation coefficient: 0.21), suggesting that using TF activity is better at inferring the TF–cell type associations that drive cellular identity.

Importantly, the regression analysis was able to recapitulate known TF-cell type associations including *hlh-1* and *unc-120* with body wall muscle (*26*), *nhr-25* and *elt-3* with hypodermis (*27, 28*), *elt-1* with seam cells (*29*), *elt-2* and *pqm-1* with intestine (*30, 31*), and *pha-4 with* pharynx (*32*) (Fig. 3D). We also found that some TF–cell type associations were congruent with TFs reported to act as terminal regulators of neuronal identity (*33*) (summarized in Fig. S4). For instance, we found *ceh-14*, a terminal regulator of PVN identity, significantly associated with PVN neurons. Similarly, *egl-13* was associated with BAG, URX, AQR and PQR expression profiles. The regression analysis also suggested several previously unreported regulatory relationships (Fig. 3D-F). For instance, *nhr-25* appears to be specifically active in the hyp7 hypodermal cells, while *elt-3* is predicted to be active in hyp4_hyp6, head and tail hypodermal cells but not in hyp7. We also found that *unc-120* shows a high regression coefficient in several muscle cells including all sex-specific muscle cells as well as body wall muscle while *hlh-1* had a high regression coefficient in anal and uterine muscle cells in addition to body wall muscles. We were also able to identify common and distinctive TFs between closely related cell types. For example, our analysis predicts that the TFs *madf-5, ekl-4,* and *egl-18* are common to all three pharyngeal gland subtypes while *ztf-1* is specific to g1A, *daf-19* is specific to g2, and *ztf-19* is specific to g1P cells (Fig. 3F). Similarly, the TFs *hinf-1* and *pat-9* are common to all gonadal sheath cells (sh1, sh2, sh3_sh4 and sh5). By contrast, *lag-1* and ZK546.5 are specific to sh1 and sh2; *ztf-1* is specific to sh3_sh4; and *daf-12* and *sup-37* are specific to sh5 cells (Fig. 3G). While additional experiments will be needed to validate these inferred relationships, the results highlight the potential of combining expression data with TF binding data to advance our understanding of the transcriptional programs responsible for driving the identity of even closely related cells.

Finally, we investigated the relationship between the predicted TF activity–cell identity associations and cellular function. Specifically, we checked whether combining our scRNA-Seq data with published ChIP-Seq and *in vivo* experimental data accurately predicted the molecular targets through which a TF of interest maintains the functional identity of a cell. For instance, the TF activity score predict that the TF *dsc-1* is active in the anal muscle. In agreement with this association, RNAi against *dsc-1* causes constipation and shorter defecation cycles (*34*). Correspondingly, our scRNA-Seq dataset shows 1089 DSC-1 target genes expressed in the anal muscle. Among the 1089 genes, 29 are known to contribute to normal defecation in *C. elegans*, a significant enrichment as measured by a Fisher's exact test (p-value = 3.183e-09, Data S5A). From the remaining DSC-1 targets, at least 70 genes are known to be required for muscle activity(*10*), and hence, may similarly contribute to defecation (Data S5B). Together, our scRNA-Seq dataset, published ChIP-seq, and published genome-wide RNAi screens, allow us to postulate that DSC-1 acts cell autonomously in the anal muscle, where it controls the expression of at least 99 genes important for normal defecation (Data S5A-B). Like this example, our dataset enables the generation of hundreds of novel and testable hypotheses across fields of study.

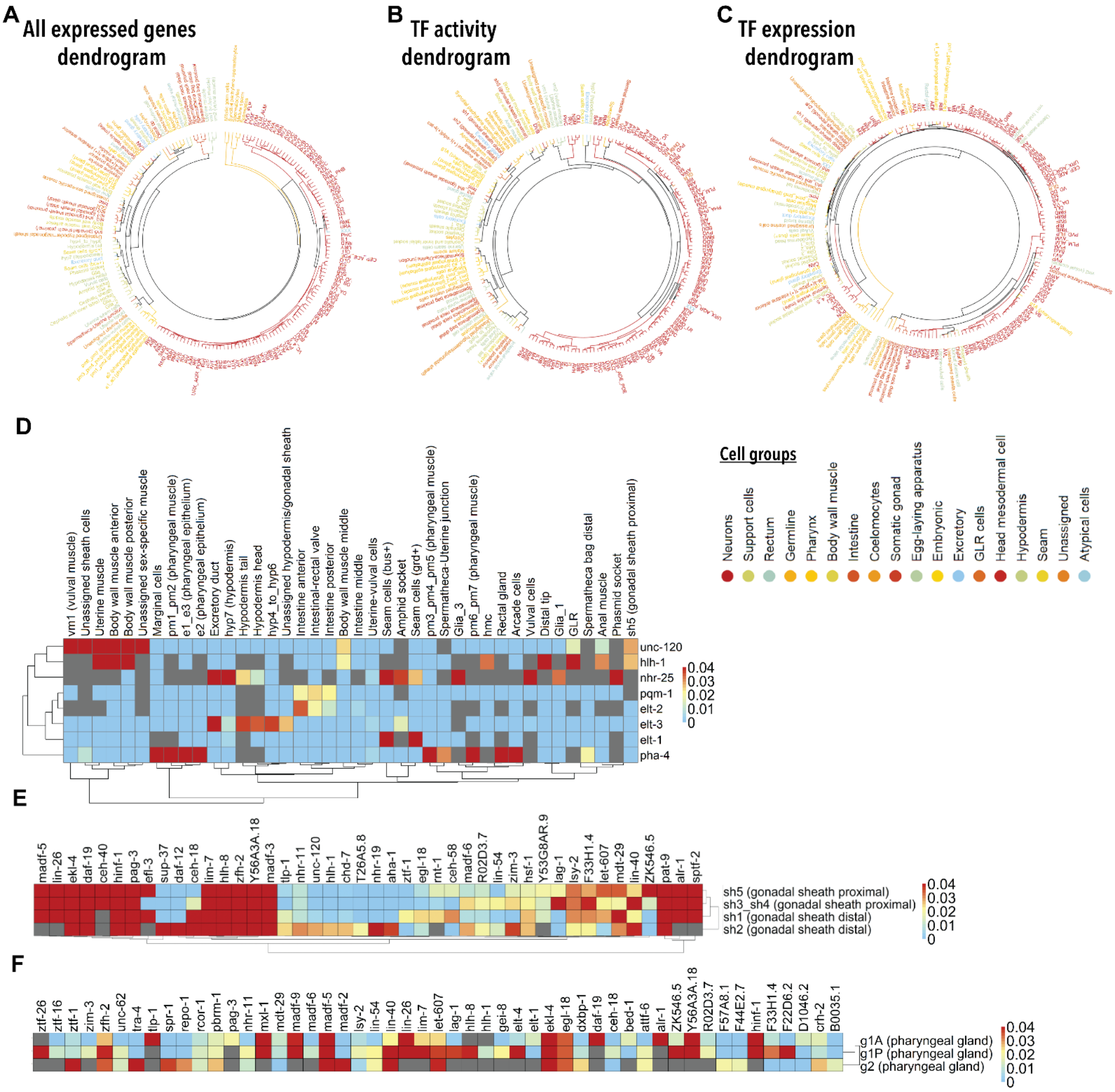

Figure 3. TF activity defines cell-type identity. (A-C) Circularized dendrograms depicting the relationship between cell types constructed using **(A)** all 18,033 genes expressed in our scRNA-Seq dataset **(B)** predicted TF activity. Hierarchical clustering was performed using the Ward.D2 method (*73*). Subtypes of cells are colored by broadly defined cell types as depicted in the inset. **(D)** Sub-heatmap showing that the TF activity analysis recapitulates previously known TF-cell type associations. **(E)** Sub-heatmap showing predicted TF activity for all gonadal sheath subtypes. Only transcription factors that positively correlate with at least one of the cell types are shown here. **(F)** Sub-heatmap showing predicted TF activity for all three pharyngeal gland subtypes. Only transcription factors that positively correlate with at least one of the cell types are shown here.

Whole-body reconstruction of cell-to-cell interactions

Cell-cell interactions (CCIs) are critical to the maintenance of the tissues and organ systems that sustain metazoan life. We previously developed the tool *cell2cell* to infer CCIs from the expression of ligand and receptor encoding genes across cells in single-cell transcriptomics datasets. In the original *cell2cell* study, we published a curated database of ligand-receptor (LR) pairs to study CCIs in the *C. elegans* L2 larvae (*35*). Here, we use this list together with *cell2cell*'s permutation analysis (*36*, *37*) to identify CCIs between all 180 cell types and subtypes across the whole-body of an adult *C. elegans* and to predict the likely molecular drivers of those interactions. A large matrix of putative interactions was obtained (see *wormseq.org* to browse these interactions), below we discuss a few illustrative examples.

Without any information on cell-cell interactions and using only LR pairs and cell-specific gene expression data, *cell2cell* was able to predict known CCIs. For example, *cell2cell* predicted that the distal tip cells interact with germ cells (*38*), and that a major driver of this CCI is the molecular interaction between the ligand *lag-2* and the receptor *glp-1*; a CCI dissected through several decades of experimental studies. Additionally, *cell2cell* predicted several unreported molecular interactions between cell types. For example, the LR pair *nlg-1*/*nrx-1* is the highest-scored driver of the interaction between AVA and various motor neurons. Although AVA neurons are involved in touch-induced locomotion (*39*) and *nlg-1* RNAi treated worms are resistant to touch-induced locomotion (*40*), it was not known which signaling molecules produced by AVA contributed to the touch response. However, the combination of the published data with the *cell2cell* results enables us to hypothesize that the interaction between the AVA-generated NLG-1 ligand and the NRX-1 receptor in motor neurons contributes to the touch response. Similarly, *cell2cell* predicts that *sax-7*/*pat-2* and *sax-7*/*pat-3* contribute to the interaction between DVB neurons and anal muscle cells. In support of these molecular interactions, DVB neurons innervate the anal muscle to regulate defecation, and *sax-7* mutant worms have reduced defecation rates relative to wild-type worms (*41*). However, it was not known the site of action of *sax-7* as it relates to the control of defecation, or which receptor would receive its signal in the anal muscle. Together, the *cell2cell* analysis and the published work enable us to hypothesize that the molecular interaction between DVB-generated SAX-7 and the PAT-2/3 receptor in the anal muscle contributes to normal defecation in *C. elegans*. In addition, *cell2cell* predicts that the pairs *sax-7/pat-2* and *sax-7/pat-3* mediate a functional interaction between VC4 and VC5 neurons and the sex-specific muscles. This prediction is supported by the fact that *sax-7* mutants are also egg-laying defective (*41*). Therefore, the results suggest that the expression of the *sax-7* ligand in VC4 and VC5 is necessary for normal egg laying. Altogether, these examples illustrate the power of *cell2cell* analyses in combination with *in vivo* genetic analysis to predict the molecular drivers of biologically relevant cell-cell interactions.

From the thousands of predictions made by *cell2cell*, we next sought to group LR pairs based on the cell-cell interactions they mediate with the goal of identifying molecular signatures that mediate the interaction between groups of cells. To do so, we used *Tensor-cell2cell*, an unsupervised machine-learning method that identifies patterns of cell-cell communication, and reports them as signatures that summarize the cell types and the operative LR pairs driving their interaction (*42*). Using only our whole-body scRNA-Seq data and our previously published LR pair list, *Tensor-cell2cell* identified 7 unique signatures, each capturing a combination of ligand-receptor pairs and groups of cell types carrying out a biological function (Fig. 4A-C, Data S6).

Validating the *Tensor-cell2cell* approach, some of the identified signatures were well-supported by previously published data. For instance, Signature 7 (Fig. 4A-C) predicts a functional interaction between several neurons and germ and intestinal cells mediated by the insulin-signaling pathway. On the ligand side, the analysis predicts that insulin-like peptides (ILPs) are mainly produced by neurons (Fig. 4A). In support of this *Tensor-cell2cell* prediction, multiple labs have shown that, with a few exceptions, insulin-like peptides (ILPs) are generated by neurons (*42–46*). However, our analysis goes beyond these data because it predicts the specific neuronal subtypes that produce the ILPs in the fed adult *C. elegans,* which include: ADF, AFD, AIA, AIN, ASE, ASI, ASJ, ASK, AWA, AWB, AWC, RIR, URB, and URX_AQR_PQR (Fig. 4A and Fig. S5D). Additionally, weaker ILP production is predicted to occur in ADL, ASG, ASH, BAG, M1 and RMH neurons. Furthermore, we can assign specific ILPs to specific neurons. For example, *ins-28* is prominently expressed in AIA, AIN, AWA and M1 neurons, while *ins-6* is more prominently expressed in ASI and ASJ neurons (Fig. S5D). On the receptor side, the most prominent receiver (receptor-producing) cells enriched in this interaction are intestinal and various germ cells (Fig. 4B). Correspondingly, several groups demonstrated the presence and functional relevance of the sole *C. elegans* insulin receptor, *daf-2*, in the germline (*47*) and intestinal cells (*48*). Additionally, we find several neurons enriched as insulin-signaling receiver cells (Fig. 4B), which is supported by published work showing that insulin-signaling also mediates interneuronal communication (*42*). For example, we recapitulated the insulin-signaling mediated interaction between AIA neurons and ASE neurons, which is required for salt chemotaxis learning (*49*). Specifically, in our dataset, AIA neurons prominently express *ins-1* and ASE neurons express *daf-2* (Fig. S4E & F), which are both required for salt chemotaxis learning as previously reported (*49*). The results also predict novel insulin-signaling mediated communication between other ILP-producing and receptor-producing neuronal subtypes including the *daf-2*/*daf-4* expressing neurons (Data S6).

Tensor-cell2cell was also able to predict novel cell communication signatures. For example, Signature 3 predicts that the ligands *adm-2*, *cle-1*, *emb-9*, *let-2*, *sax-7*, *sup-17*, and *unc-52* and their corresponding receptors *pat-2* and *pat-3*, mediate the interaction between motor neurons (senders) and muscle cells (receivers). Signature 3 specifically predicts that these ligand-receptor pairs mediate the interaction between the AS, DA, DB, DD, PDA, SIA, SIB, VC, and VD neurons and muscle cells from the body wall, anus, vulva, and uterus. Reassuringly, some of these predictions appear to be supported by published results. For example, CLE-1 is enriched in neuromuscular junctions (*50*), and *pat-2*, *pat-3*, *emb-9*, *let-2*, and *unc-52* contribute to muscle function (*51*, *52*). However, the site of expression and neuro-muscular function of the *adm-2*, *cle-1*, and *sup-17* ligands has not been reported. We, therefore, used a levamisole-sensitivity assay to test the *Tensor-cell2cell* prediction that inactivation of these three ligands may affect neuromuscular junction function. Levamisole is an acetylcholine receptor agonist that causes continued neuronal stimulation of the muscles, leading to paralysis (*53*, *54*). Resistance or hypersensitivity to levamisole is indicative of a neuromuscular junction dysfunction (*55*). We performed whole-body and tissue-specific RNAi knockdown of the ligand genes of interest starting at the young L4 stage. When the animals reached the young adult stage, we treated them with levamisole. As predicted by Signature 3, intestine- and hypodermis-specific ligand knockdown of *adm-2*, *cle-1*, or *sup-17* did not alter sensitivity to levamisole. By contrast, whole-body and neuron-specific knockdown of all three ligands resulted in levamisole hypersensitivity (Fig. 4D). Interestingly, the paralysis phenotype was more pronounced in the worm strain TU3401 (Fig. 4D), which is engineered to promote RNAi knockdown specifically in the neurons of *C. elegans* (*56*). Importantly, animals treated with RNAi against the ligands showed normal chemotaxis to sodium salts, which is another reported function of the neurons expressing these ligands (PDA,VC, VD DD, SIB) (data not shown), implying that knocking down the tested ligands does not cause pleiotropic dysfunction of the relevant neurons. Altogether, the match between the *Tensor-cell2cell* results and functional analyses suggests that this analysis can generate meaningful hypotheses about the molecules driving cell-to-cell communication and cell-to-cell-to-functional interactions in *C. elegans*.

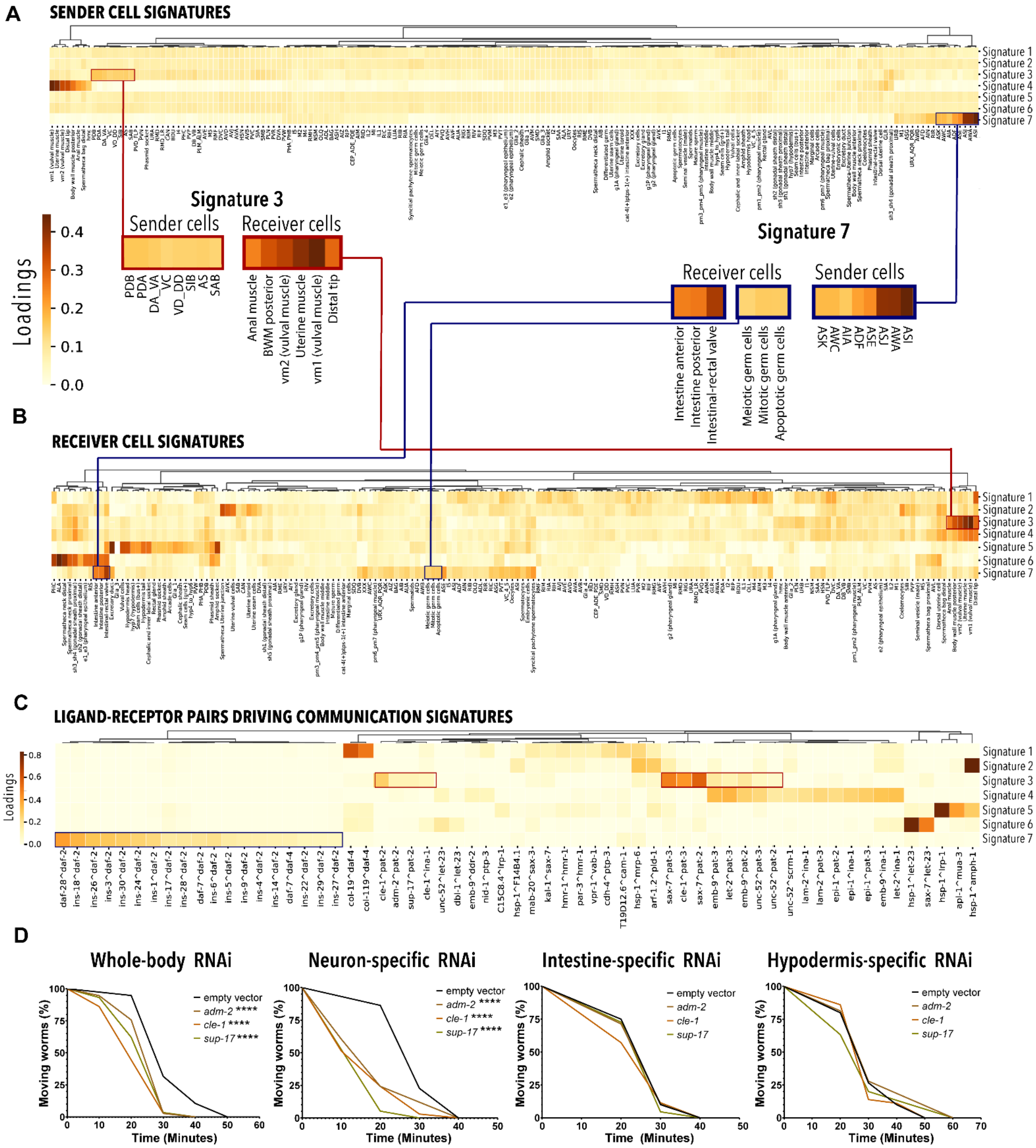

Figure 4. Identification of cell-type specific cell-cell interactions. (A) Heatmap depicts the cell types identified as the main senders across the seven communication signatures predicted by *cell2cell* in the adult *C. elegans*. Inset shows which cell types are driving the sender function in signatures 3 and 7. **(B)** Heatmap depicts cell types identified as the main receivers across the seven communication signatures predicted by *cell2cell* in the adult *C. elegans*. Inset shows which cell types are driving the receiver function in signatures 3 and 7. **(C)** Heatmap showing

the ligand-receptor pairs mediating each signature. Highlighted are the ligand-receptor pairs important for signatures 3 and 7. In panels **(A-C)**, Loadings represent the importance that *Tensor-cell2cell* assigned to each element (sender or receiver cell or ligand/receptor pair) within their respective signature. Panel **(C)** Only shows ligand-receptor pairs that are important (loading value > 0.1) in at least one signature. **(D)** Curves depict the time it takes for RNAi-treated or control-treated (empty vector) worms to become paralyzed upon levamisole treatment. **** p-value < 0.001

WormSeq app: Explore the whole-body transcriptional landscape of the adult C. elegans

To make the scRNA-Seq data accessible to non-coding users, we created an RShiny app we called WormSeq. This resource is available as a web application and can be accessed using the following link: *wormseq.org*. WormSeq has several features, including heatmap visualization of gene expression by count and by percentage of cells expressing a gene. Users can identify cell type specific gene markers by browsing gene marker tables or by using percentage gene expression per cell type. The interface also enables the identification of genes expressed in one cell type but not another one. Users interested in the abundance or consistency of gene expression can also browse genes by skewness score or Gini coefficient. The app also allows users to browse the regulatory program analysis data and identify transcription factors enriched in cell types of interest. Finally, users can also browse the *cell2cell* analysis and identify the list of interactors driving communication between two cell types of interest.

Discussion

We present here a comprehensive single-cell atlas of a wild-type adult *C. elegans*. Although single-cell transcriptional atlases have been generated for other metazoans, including mice and humans (*57*, *58*), this scRNA-Seq dataset is unique due to the following: (i) it derives from three independent populations each composed of ~100,000 animals, (ii) it was obtained from hermaphroditic, genetically homogeneous animals, which entails lower expression noise than what can be achieved in gonochoric species, and (iii) the soma, tissues, and organs of each and all adult *C. elegans* have the same cell types and number of cells (*e.g.*, 95 body muscle cells in total). Such redundancy yielded a high-resolution scRNA-Seq dataset that captures all cell transcriptomes including those underrepresented in the starting worm populations (*e.g.,* male cell types). Additionally, although current scRNA-seq protocols capture only a small fraction of the total RNA molecules per cell, our oversampling of *C. elegans* cells (total of 154,251 cells) and the aggregation of cells from the same cell type, enabled the reconstruction of a representative transcriptional profile for each cell type composed of a median number of 5,871 genes per cell type. This level of gene activity per cell type poses interesting questions for future investigation. Which of these genes are required to maintain cell identity and function? Which ones are part of transcript reservoirs ready to act upon stress or other contexts? Which ones reflect biological or experimental noise? A more general limitation of any RNA analysis is that mRNA expression may or may not reflect protein abundance. In fact, previous studies have shown that the correlation between mRNA levels and protein levels can be poor (*59–61*). Therefore, incorporating proteomic data, and in the future single-cell proteomic data, is anticipated to increase the accuracy of functional predictions.

Despite the technical limitations, the *C. elegans* transcriptional atlas reported here is composed of the gene expression profiles of 180 distinct cell types. In addition to identifying most known *C. elegans* cell types, our annotation revealed differences in expression profiles between cell types previously assumed to be the same due to morphological similarity. For example, *apx-1* and *let-502* being highly expressed in the *distal* but not in the *proximal spermatheca neck* together with the reports showing that whole-body RNAi against *apx-1* (*62*) and *let-502* (*63*) lead to dysregulated expansion of the germline, suggest that the *distal spermatheca neck* cells may contribute to tumorous processes in the germline. Therefore, the transcriptome-based annotation of *C. elegans* cells presented here opens doors to learn new cell-specific biology.

In this study, we also use the single cell data to begin to address three fundamental questions about the relationship between gene expression and cellular function: Which, if any, genes meet the definition of housekeeping gene? What transcriptional programs generate and maintain cellular identity in *C. elegans*? Which genes mediate the interactions between cells in this metazoan?

What genes are housekeeping?

Using scRNA-Seq we were able to directly test for a feature commonly attributed to housekeeping genes: consistent expression across cell types. We scored all genes in our dataset based on the abundance and consistency of expression across cell types using a skewness score, or only for consistency of expression using a Gini coefficient. Although skewness score and Gini coefficient positively correlate with each other (Pearson correlation coefficient = 0.66), the Gini coefficient is more likely to have fewer false negatives since housekeeping genes are not necessarily abundantly expressed. Supporting the use of the more permissive Gini coefficient to identify housekeeping genes, the resulting list of consistently expressed genes (Gini coefficient ≤ 0.3) is enriched in genes essential to *C. elegans* survival (276/367) to an extent similar to the most restrictive skewness set (34/50). Furthermore, 248 out of the 276 genes are consistently expressed in two very distinct ontogenetic stages, the L2 larvae and the adult *C. elegan*s, showing that the Gini coefficient analysis applied to one condition can capture genes consistently expressed across conditions.

Because our housekeeping genes analysis is limited to the N2 wild type *C. elegans* strain, and it compares only two developmental stages (L2 larvae and young adult), it may be too inclusive. Additional scRNA-Seq experiments in other genetic backgrounds, developmental stages, or in the presence of abiotic or biotic stressors may further narrow the number of housekeeping genes, or even challenge the concept of housekeeping gene altogether. On the other hand, scRNA-Seq limitations such as low depth of sequencing and the incomplete sampling of each cell could account for false negatives. Nonetheless, the 248 genes found in the Gini analysis represent a solid beginning. As expected, these 248 genes are enriched in basic cellular functions including mitochondrial function, protein synthesis (*e.g.*, ribosome and protein translation), and protein stability (*e.g.*, chaperones). Intriguingly, we did not find DNA synthesis/replication genes in this set, likely a reflection of the fact that apart from the germline, cells in the adult *C. elegans* are post-mitotic. We also did not find enrichment for RNA synthesis genes even though at least some of these genes are well represented across cell types (*e.g.*, the RNApol encoding gene *ama-1*). Nevertheless, of the 248 genes consistently expressed in *C. elegans*, we found that 172 are conserved (*20*) in organisms ranging from yeast to rice and humans (Data S3E), and as such, they could be part of the core of genes indispensable to build and maintain a eukaryotic cell.

What transcriptional programs generate and maintain cellular identity in C. elegans?

Our regression analysis of ChIP-Seq data with the cell type-specific gene expression profiles revealed 7,361 TF–cell type expression profile associations. Some of the TF-cell type associations were known and, consequently, they validate the approach. However, we also generated new predictions that, in line with the high resolution of our dataset, reveal TF-cell type associations that are distinct even between closely related cell subtypes such as pharyngeal gland g1A and g1P. In WormSeq, the web interface accompanying this study, users can search for all the TFs predicted to be active in each cell type, as well as all the cell types in which a given TF is predicted to be active. As the number of TFs with ChIP-seq data increases from the 362 TFs used here to encompass the 900 or so TFs predicted to exist in *C. elegans* (*64*), the association between TF binding patterns and cell-specific transcriptional profiles should become even more powerful in revealing regulatory relationships. Also, while we only evaluated the activating role of TFs, other advances may permit the investigation of negative regulators. Finally, unlike our transcriptomic data, the ChIP-Seq data we relied on were generated in bulk samples; this may lead to inaccurate results for TFs that are only active in a small set of cells. Therefore, as single-cell ChIP-Seq becomes more popular, we expect this kind of analysis to become more accurate for more sparsely expressed TFs.

By combining our scRNA-Seq with published ChIP-Seq and functional data, we proposed cell type-TF-targets triads that may mediate cellular function and morphology. For example, knockdown of the gene encoding the TF *dsc-1* and of several of its ChIP-seq targets can alter defecation cycles in the worm (*34*). Our analysis predicts that *dsc-1* is active in anal muscle and that 29 of its downstream targets involved in defecation are expressed in the anal muscle. Therefore, we hypothesize that DSC-1, its 29 downstream effectors, and likely another set of 70 target genes that yield more general muscle phenotypes but are expressed in the anal muscle, orchestrate a cell-autonomous transcriptional program critical for normal defecation in *C. elegans*. The results presented in this study promise to accelerate advances by reducing the number of candidate genes for functional studies and by placing molecular players in their anatomical sites of action.

Which genes mediate the interactions between cells in C. elegans?

We used the algorithm *cell2cell* and a curated list of ligand-receptor (LR) pairs to make thousands of predictions about the gene pairs mediating the interactions between the cells of the adult *C. elegans*. We also used a permutation analysis and *Tensor-cell2cell* (*65*) to identify cell-type specific communication signatures. Validating our approach, we detected known CCI-LR associations including insulin signaling mediated neurons–germline and neurons–intestine communication. Additionally, even for this well-characterized communication pathway, our analyses provided new testable hypotheses including the specific neurons that produce the insulin-like ligands in the adult worm.

Our predictions, however, are only based on the expression of LR pairs without accounting for spatial constraints. This omission may lead to predictions that do not match the biology, most notably membrane bound LR pairs predicted to mediate the interaction between physically distant cells. For this reason, in our web interface WormSeq, we included a feature that allows users to browse our CCI-LR predictions by LR class: (i) membrane-bound, (ii) ECM component, and/or (iii) secreted. Additionally, the analysis is limited to present LR interaction data. As more accurate and extensive LR interaction data become available, we expect this analysis to lead to a more comprehensive map of the molecules mediating the interactions between cells.

Overall, this study is a major step forward toward identifying the key molecular players whose function or dysfunction defines the functional status of the intra and inter-cellular gene networks that constitute an animal. Putting together: (i) genetic tractability, (ii) stereotypical number and physical interactions between cells dissected to the level of synapses, (iii) known lineage for every cell in the body, and (iv) existing scRNA-Seq datasets of the wild-type embryo, two larval stages, and now the adult, will enable the development of tools that track gene expression across space and time for a whole living animal, as well as predictive models of cellular, tissue, organ, and ultimately whole-animal function. These tools can help many fields in at least two ways: (i) they may tell us how much information and of which kind is necessary to develop *in silico* models that can accurately predict the effect of perturbations (biological, chemical, physical, or others), and (ii) the tools themselves may serve as the basis or guide the development of predictive tools for more complex organisms.

Materials and Methods

C. elegans strains and husbandry

C. elegans N2 (Bristol, UK), WM118 (rde-1(ne300);neIs9 [myo-3::HA::RDE-1 + rol-6(su1006)]), MGH171 (sid-1(qt9);alxIs9[vha-6p::sid-1::SL2::GFP]), JM43 (rde-1(ne219);xkIs99[wrt-2p::rde-1::unc-54 3'UTR]), TU3401 (sid-1(pk3321);uIs69 [pCFJ90 (myo-2p::mCherry) + unc-119p::sid-1] were obtained from the Caenorhabditis Genetics Center (CGC). All strains were typically grown at 20°C on NGM plates seeded with *E. coli* strain OP50. Bacterial strains used for RNAi were obtained from the Ahringer library (*66*).

Sample preparation and scRNA-Seq

A synchronous population of L1 worms was obtained by double bleaching gravid N2 *C. elegans* with hypochlorite followed by 4 washes in S-buffer. The released eggs were then allowed to hatch in the absence of food in S-buffer over a period of 18 hours. Approximately 100,000 synchronized L1 worms were then grown in NGM plates seeded with HT115 bacteria at 20°C for approximately 55h. 55h post-seeding, worms were staged under a microscope to ensure that the bulk of the population had reached the young adult stage. Young adult worms were then harvested in S-buffer and centrifuged at 1,300g for 1 min. The worm pellet was washed until the suspension was no longer turbid (2-3 times) and then transferred to a 1.5mL Eppendorf tube. The cuticle was then disrupted by incubating the worms in 200µL SDS-DTT (20mM HEPES pH8.0, 0.25% SDS 200 mM DTT, 3% sucrose) (*67*) for 4 minutes. Immediately after SDS-DTT treatment, 800 mL of egg buffer was added to the treated worms, the worms were centrifuged, the supernatant was aspirated and the worm pellet was washed 5 times in egg buffer (118 mM NaCl, 48 mM KCl, 2 mM CaCl2, 2 mM MgCl2, 25 mM HEPES, at osmolarity of 340 Osm). After the final wash, egg buffer was added to a final volume of 1mL and the worm solution was then transferred to a 15-mL conical tube. 500µL of 350 units/mL Pronase (EMD Millipore Corp) was added and the worms were then dissociated into single cells by passing them through a 21-gage needle about 20 times. The worm/cell lysate was centrifuged at 4°C for 1 min at 200g and then most of the supernatant, containing dissociated cells, was transferred to a new 15-mL conical tube leaving behind enough liquid for a second round of dissociation. After passing the worm lysate through the needle for a second time, the samples were centrifuged (4°C for 1 min at 200g) and then the supernatant was transferred to the same tube containing the cells from the first transfer. The cells were then centrifuged at 4°C for 5 min at 500g and the cell pellet was washed 3 times in egg buffer containing 1% BSA gently pipetting the cells with wide-end tips. Finally, to separate single cells from bigger chunks of tissue, the cell suspension was gently passed through a 10µm filter.

For single cell capture, approximately 15,000 *C. elegans* cells were mixed with the reverse transcriptase solution and then loaded onto each channel of the 10x Chromium Controller (we used a total of 10 channels for three biological replicates). The libraries were then built following the Chromium Next GEM Single Cell Kits v3.1 published protocols and then sequenced on an Illumina NextSeq 500 platform. It is important to note that with this methodology we are only capturing polyadenylated transcripts therefore excluding most non-coding RNA. Additionally, this method does not allow for capturing alternative splicing variants.

scRNA-Seq data processing

The scRNA-Seq data was first processed following the CellRanger pipeline. Reads were mapped to a modified version of the WormBase WS260 reference transcriptome that had transcript 3′ untranslated regions extended by 0 to 500 base pairs (*1*). To distinguish cells from empty droplets we used the knee plots reported by CellRanger to set a UMI threshold below which droplets were considered empty. The expression matrix generated by CellRanger was then decontaminated for ambient RNA using DecontX (*68*). We then followed the Monocle3 pipeline to perform dimensionality reduction and clustering (*9*). First, we combined all three biological replicates into a single cds object. We then used Monocle3's preprocess_cds function (method = "PCA", num_dim = 200) which normalizes the data by log factor and generates a lower dimensional space for downstream dimensionality reduction. Next, we used Monocle3's align_cds function to perform further background correction and remove unwanted batch effects which we noticed came mostly from the different samples. We then performed UMAP dimensionality reduction on the matrix using Monocle3's reduce_dimension function run with default parameters. Finally, we used Monocle3's cluster_cells function to define individual clusters of cells using the Louvain algorithm (k=50).

After clustering, we noticed that there were clusters containing mostly cells with a high mitochondrial fraction (mitochondrial-only umi/total umi > 0.2). These clusters were removed since high mitochondrial fraction is an indication of damaged cells (*69*). We then re-performed dimensionality reduction and clustering on the remaining cells as described above. We also noted that some cells labeled "Intestine middle" prominently expressed hypodermal gene markers and were therefore removed from the data since they were likely intestine-hypodermis doublets.

Cell type annotation

To annotate the different clusters of cells with their corresponding cell types we used Monocle3's top_markers function to identify for every cluster a list of 10 gene markers. We then used the CeNGEN app (*3*) to broadly define where these genes are typically expressed in the L4 worm. In addition to the L4 data, we used gene markers identified through scRNA-Seq of L2 worms (*1*). The annotation of the L2 worms was more detailed than the CeNGEN data and allowed us to annotate several clusters more carefully. We also used Wormbase to identify gene markers for cell types that were absent from the L2 and L4 data and those that could not be confidently annotated using the L2 and L4 data alone. Finally, we found that certain clusters contained several distinct cell types. We created subsets of these clusters on which we performed dimensionality reduction and clustering to differentiate these cell types. This allowed us to improve our annotation and distinguish between cell types which were previously bundled together. We must note however that even after sub-clustering, certain cell types could still not be distinguished (e.g. URX_AQR_PQR). A detailed rationale for the annotation can be found in Table S1.

Computing gene expression by cell type

The aggregate gene expression profile for a cell type was computed following the method described by Packer *et al* (*1*). We first used Monocle3's normalized_counts function to normalize the gene by cell expression matrix by size factor alone. For every cell type, we then: **(1)** subsetted the gene by cell matrix to include only those cells belonging to that cell type, **(2)** took the mean of each row (gene), **(3)** calculated the sum of the values obtained in (2), **(4)** divided each value in (2) by the sum calculated in (3) and finally, **(5)** multiplied all values by a million to obtain a scaled transcript per million (TPM).

We also performed the same calculations using bootstrap resampling to estimate a confidence interval for the expression of each gene by cell type (*1*). For every cell type with N number of cells, we randomly sampled with replacement, N cells from that cell type and calculated gene expression as described above. This was performed 1000 times for each cell type, and we then used the resulting distribution of scaled TPMs to compute confidence intervals (95% and 80%).

Estimating transcriptome coverage of every cell type

To estimate the fraction of the transcriptome covered for every cell type in our dataset we used the method described by Taylor *et al* (*3*). We performed 100 iterations of down-sampling for each cell type calculating scaled TPM as described above with each iteration. We then plotted the number of genes by the number of cells for every cell type (Fig. S2C). Based on the shape of the curves (Fig. S2C), we modeled the relationship between gene number and cell number using a three-parameter log-logistic function (*70*). Using that model, we calculated a predicted maximum number of genes per cell type (G_{MAX}) and a predicted number of cells that would allow us to identify half of G_{MAX} for every cell type (Data S2). This allowed us to generate an estimate of the fraction of the transcriptome covered by the number of cells we have in our scRNA-Seq dataset.

Identification and evaluation of housekeeping genes

To calculate the skewness score, we computed the percentage of cells within every cell type expressing each gene present in our scRNA-Seq data. We then used baseR’s skewness function to score the skewness of every gene with respect to their percent of cells expressed within each cell type: a negative value (left skew) indicating expression in the majority of cells and cell types and a positive value (right skew) indicating expression in the minority of cells and cell types. To compute the Gini coefficient for every gene across cell types, we used the ineq function from the ineq package on the scaled TPM gene by cell type matrix. To perform gene ontology enrichment analysis, we used Wormbase's gene set enrichment analysis tool with the default q-value threshold of 0.1. To measure the enrichment of essential genes in our various housekeeping genes list, we first downloaded the list of genes annotated as "embryonic lethal", "larval lethal" and "adult lethal" from Wormbase. We combined these lists into a final list of essential genes made up of 3275 genes. We then used Fisher's exact test to determine the extent of enrichment of essential genes in our housekeeping genes lists.

Inferring transcriptional regulators underlying cellular identity

To infer the potential role of TFs in mediating cell-type specific gene expression, we correlated transcription factor binding patterns obtained from ChIP-Seq analysis with the gene expression profile of each cell type. We first collected all the available ChIP-Seq data from the modENCODE/modERN projects (*23–25*). All ChIP-Seq data are currently available from the ENCODE Data Coordination Center (DCC). We included in the analysis ChIP-Seq data performed in any post-embryonic stage (276 TFs) and ChIP-Seq data at embryonic stages (87 TFs) if the TF had not been tested post-embryonically. The ChIP-Seq peaks were then clustered along the genome by sorting the peaks by the apex base position of the peak. The peaks were accumulated into clusters moving along the genome until a gap of 200 bases between peaks was encountered, at which point a new cluster was begun. This resulted in 56729 clusters, varying in size between 1 TF and hundreds of TFs. Clusters that contained more than 70 TFs were excluded from the analysis since these are considered HOT (high occupancy target) sites and are not likely to represent tissue specific binding events. Similarly, clusters containing a single TF were also excluded since they are likely enriched in spurious binding. The target genes of the peak clusters were assigned by proximity of the cluster to the transcription start site (TSS) of the nearby genes. If the average of the apex of the peaks in the cluster met two criteria, the cluster was assigned to the gene with the closest TSS. The first criterion was that the peak cluster must be within 2000 bases of the nearest gene TSS. The second criterion was that the distance to the next closest gene TSS must be at least 1.5 times the distance to the nearest gene TSS. The peaks in each experiment (TF/stage) were ranked by signal strength and normalized to a cumulative probability. We then used a matrix containing the normalized signal strength as values, the TF as columns and the target genes as rows as the predictor variable matrix input for a generalized linear model (glmnet in R). If the cluster had multiple peaks of a given TF or there were multiple clusters assigned to the same target with the same TF, the maximum signal strength for the TF was used in the predictor variable matrix. The response vector for the model was the aggregated gene by cell type matrix we generated from our scRNA-Seq data. We then ran a separate model for each cell type, generating a determined coefficient for each TF-cell type association. These coefficients were used to generate the heatmaps found in Fig. 3D, Fig. 3E, Fig. 3F (Data S4). Any negative coefficients were set to 0 in the heatmap. Finally, we performed a 20-fold cross validation to determine the mean square error for the cell type model. That number was appended to each cell type (Data S4) with a lower number indicating a higher confidence in the predictions of the model.

Inferring cell-cell communication from the gene expression of ligands and receptors in cells

To study CCIs, we used a list of 245 ligand-receptor interactions of *C. elegans* (*35*). We employed *cell2cell* by using the pipeline cell2cell.analysis.SingleCellExperiment found in the *cell2cell* python package, which allows running a permutation analysis for computing the significance of the inferred communication scores for each combination of LR interaction and sender-receiver cell pairs, as previously introduced (*36*). To run this analysis, the expression level of each gene was aggregated at the cell type level by computing the log1p(CPM) average expression within each cluster. Then, the communication score was computed as the geometric mean of the expression of the ligand in a sender cell type and the receptor in a receiver cell type.

To run *Tensor-cell2cell* to identify latent patterns of communication, only the communication scores with a P-value < 0.05 (indicating cell-type specific CCC) were used to build a 3D-communication tensor (Fig. S5A). This 3D tensor was decomposed by using *Tensor-cell2cell* into 7 factors, each factor representing a signature or module of CCC that summarizes a biological process involving specific cell types and ligand-receptor pairs.

Levamisole treatment

The levamisole assays were performed as previously described (*71*) with some modification. N2 and tissue-specific RNAi *C. elegans* strains were bleached and the embryos rocked at 20°C for 18 hours to synchronize the hatchlings. We then seeded around 200 hatchlings on NGM + 1mM IPTG + 25µg/mL carbenicillin plates (RNAi plates) seeded with *E. coli* strain HT115 carrying an empty L4440 plasmid (control). A day before the worms became L4s, HT115 carrying either an empty plasmid or an L4440 plasmid carrying the gene of interest were seeded on 24-well RNAi plates. Once the worms reached the L4 stage, we moved ~20-40 worms to each bacteria-seeded well. After 24h, the wells were flushed in a sequential manner with 1mL 0.4mM levamisole. Every 10 minutes, we counted the number of moving worms until all worms were paralyzed. Results were analyzed on SPSS using the Kaplan-Meier estimate with log rank test comparison across different strata. Figures were made using GraphPad Prism.

Statistical Analysis

All statistical analyses were performed in R except the levamisole analysis which was analyzed in SPSS. All statistical analyses are described in their appropriate section in the main text, figure legend and methods. We used Fisher's exact test to perform enrichment analyses (the lower limit of the p-value in R is 2.2e-16). Correlation analysis between different datasets was performed using Pearson correlation coefficient and correlation analysis between different dendrograms was performed using Baker's gamma correlation coefficient available through the dendextend R package (*72*). The levamisole data was analyzed using the Kaplan-Meier estimator with log rank test comparison across different strata. We considered p-values < 0.05 as statistically significant.

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Author contributions

The study was conceived by AG and EJO and its planning and execution was carried out by AG, NEL, RW, and EJO. CH performed the scRNA-Seq experiment and AG, CH, RW, and EJO analyzed the scRNA-Seq data. AG performed the housekeeping gene analysis and AG and EJO interpreted the housekeeping genes results. LG performed the transcription factor analysis and AG, LG, RW, and EJO interpreted the results. EA performed the CCI analysis and AG, EA, NEL, and EJO interpreted the results. AG performed the RNAi experiment for the CCI analysis and EJO the chemotaxis controls. AG and EJO wrote the original draft of the manuscript and all authors contributed to the final version of manuscript.

Supplementary materials

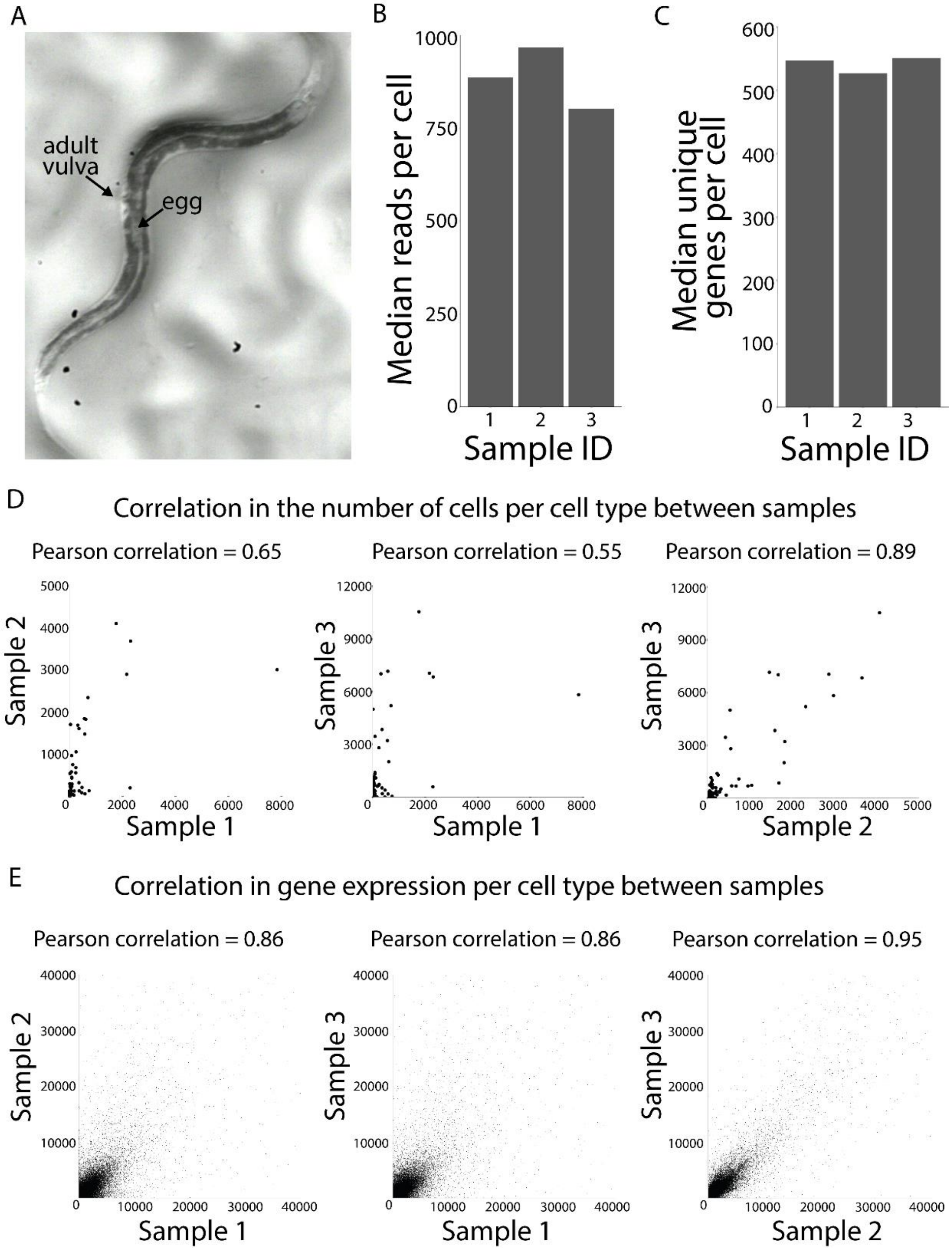


Fig. S1. scRNA-Seq of young adult *C. elegans* **(A)** Representative image of young adult *C. elegans*, which we identified by the characteristic shape of the vulva (arrow). **(B)** Average count per cell for each biological replicate. **(C)** Average gene per cell for each biological replicate. **(D)** Correlation in the number of cells per cell type between the three biological replicates. Each dot represents the number of cells in a particular cell type in two samples. **(E)** Correlation of the cell-type specific gene expression profiles between the three biological replicates. Each dot represents the levels of expression of a gene within a cell type (scaled TPM).

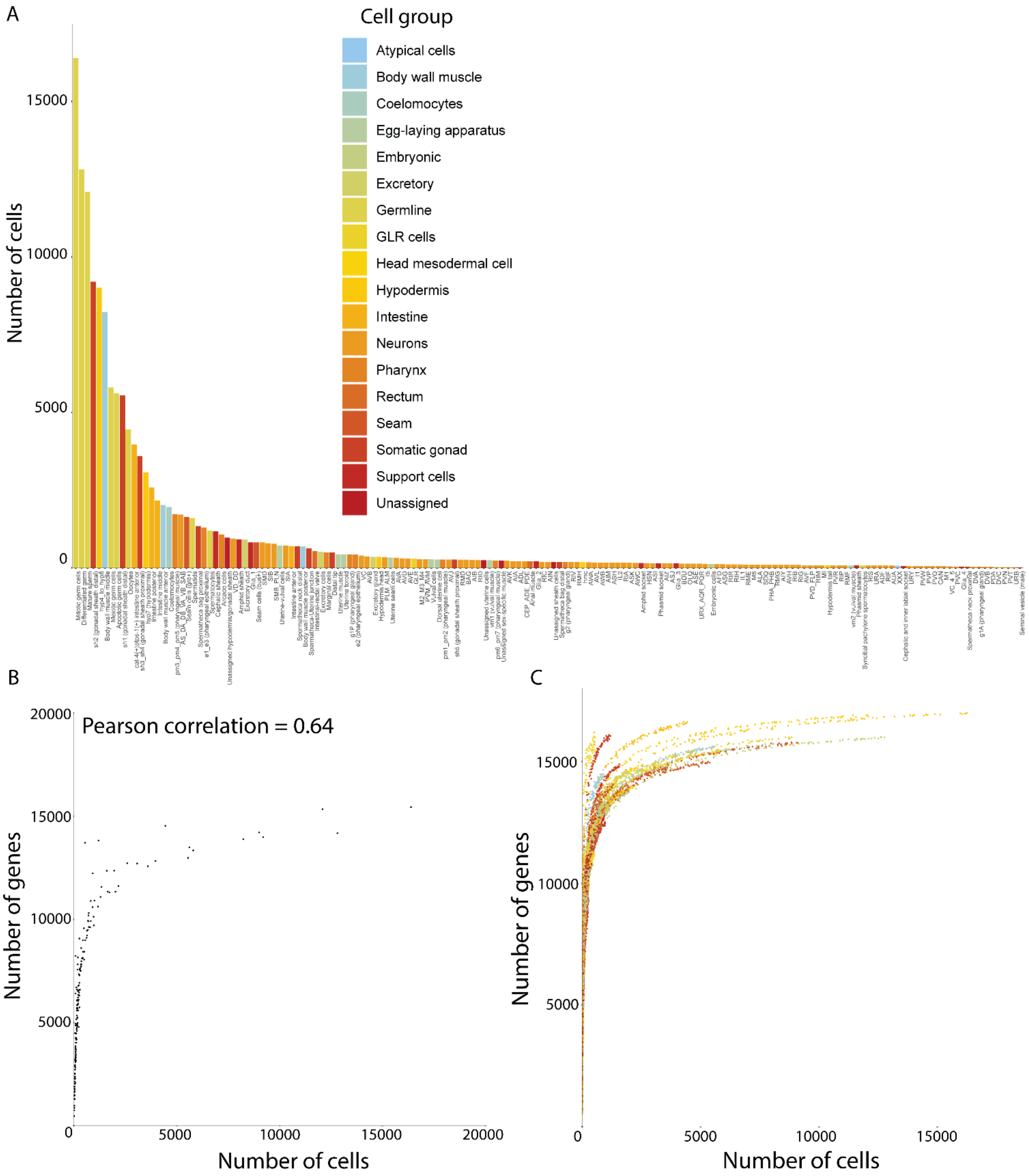


Fig. S2. Distribution of cell numbers per cell type and relationship between cell number and gene number. (A) Distribution of cell numbers per cell type. Subtypes of cells are colored by broadly defined cell types. **(B)** Number of genes detected for all cell types plotted against the number of cells. Pearson correlation coefficient = 0.64 shows a strong correlation between number of genes and number of cells. **(C)** Number of genes detected versus number of cells for all cell types after down sampling.

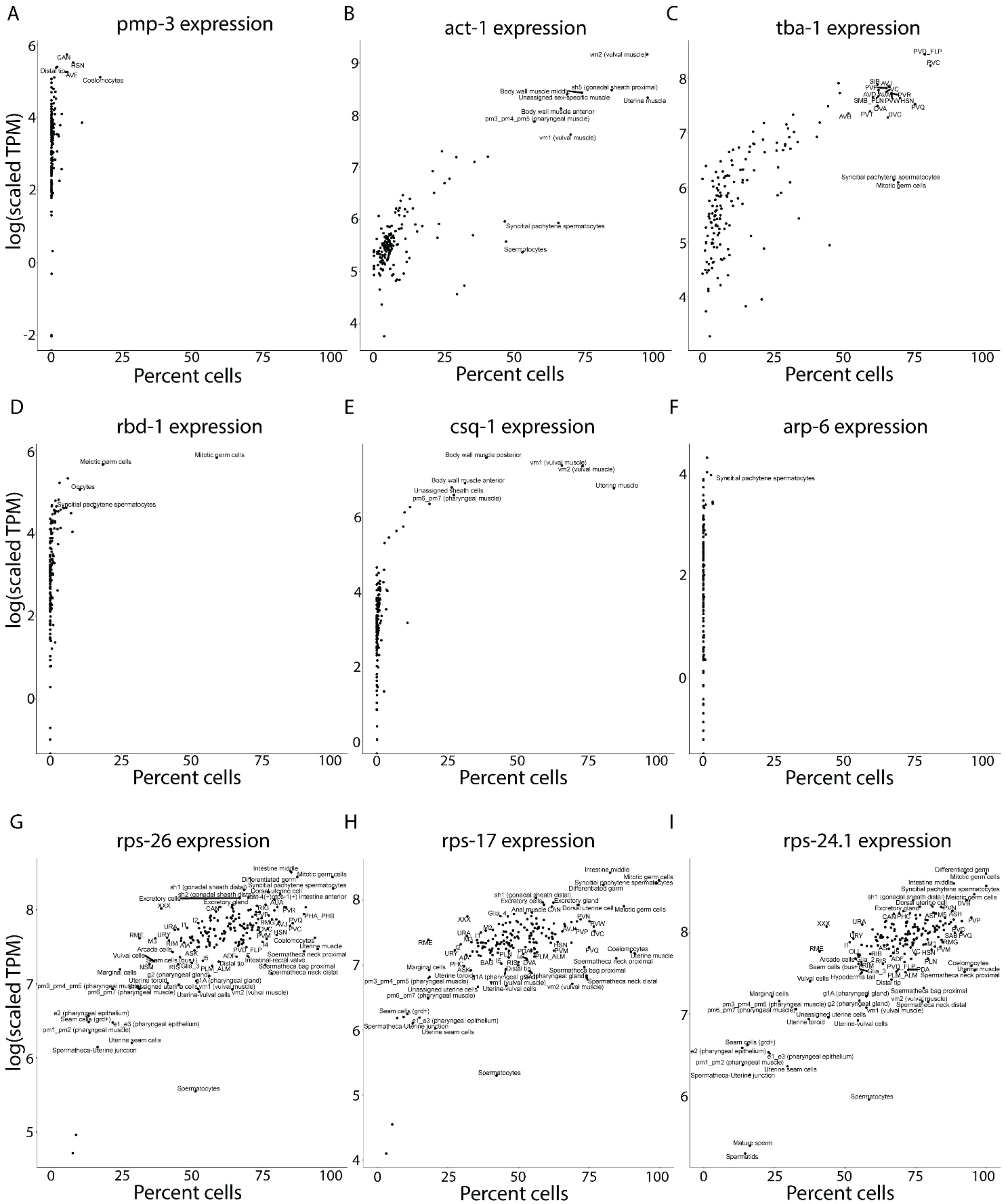


Fig. S3. Expression of commonly used housekeeping genes across cell types. (A-F) Gene expression of traditional housekeeping genes with high Gini coefficient (>0.5). Based on these results, these genes may not be appropriate housekeeping genes. **(G-I)** Gene expression of traditional housekeeping genes with low Gini coefficient (<0.3). These genes may be more appropriate housekeeping genes.

Transcription factor	**Cell type**
ceh-14	PVN
egl-13	BAG, URX, AQR, PQR
lim-6	DVB
lin-11	ADL, ASG, PVP
ttx-3	AIA
unc-3	SAB, DA, DB, VA, VB, AS, PDB, AVA, AVD, PDA
unc-42	ASH, AIB, AVA, AVD, AVE, AVK, SMD
unc-86	ALM, AQR, AVM, FLP, IL2, PLM, PQR, PVD, PVM, URA, URB, URX, AIM, AIZ, BDU, RIH, HSN

Fig. S4. List of TFs and the cell types in which they are known to mediate neuronal identity. These TF-cell type associations were confirmed by our TF analysis.

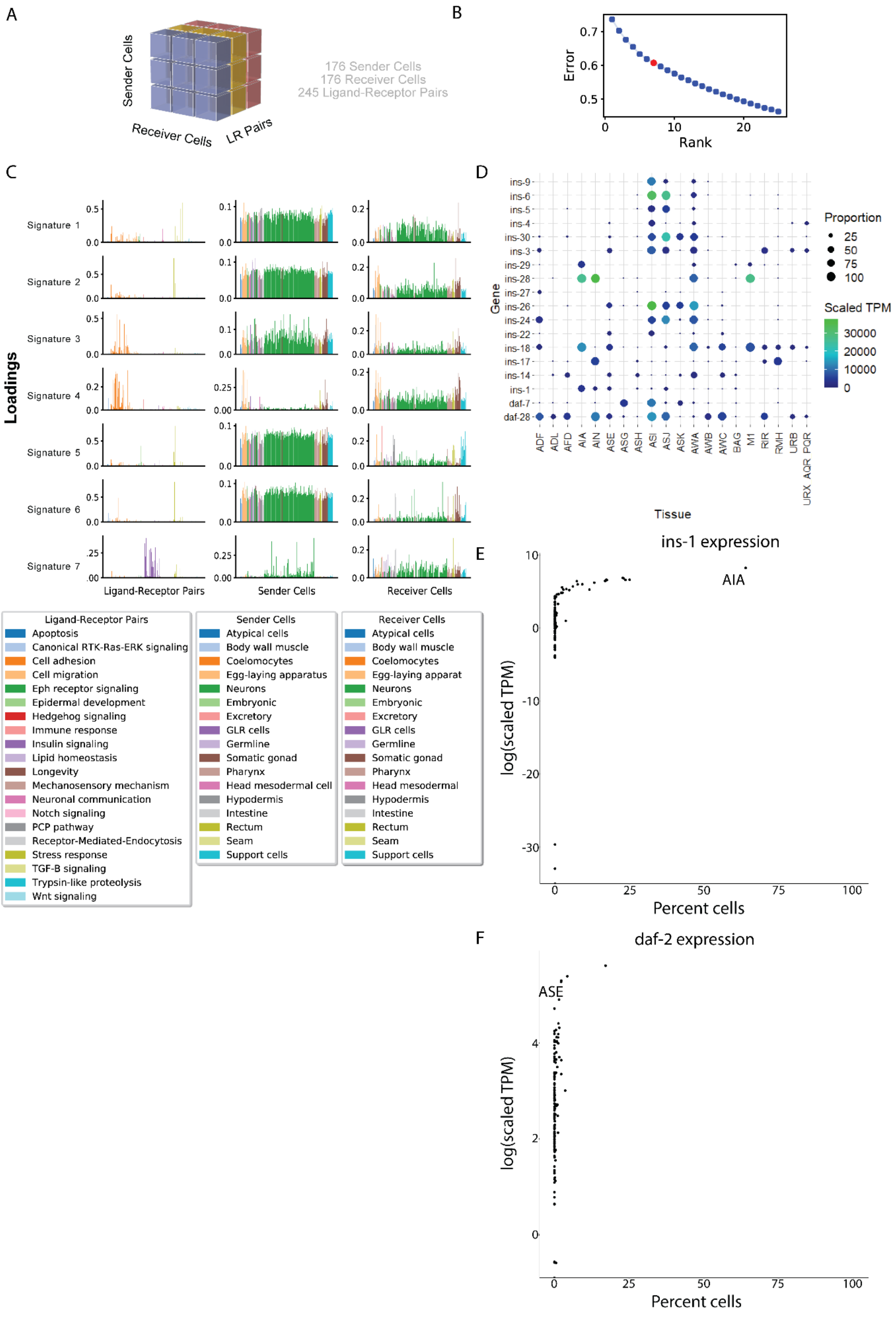

A
Sender Cells
Receiver Cells
LR Pairs
176 Sender Cells
176 Receiver Cells
245 Ligand-Receptor Pairs
B
Error
0.7
0.6
0.5
0
10
20
Rank
C
Loadings
Signature 1
Signature 2
Signature 3
Signature 4
Signature 5
Signature 6
Signature 7
Ligand-Receptor Pairs
Sender Cells
Receiver Cells
Ligand-Receptor Pairs
Apoptosis
Canonical RTK-Ras-ERK signaling
Cell adhesion
Cell migration
Eph receptor signaling
Epidermal development
Hedgehog signaling
Immune response
Insulin signaling
Lipid homeostasis
Longevity
Mechanosensory mechanism
Neuronal communication
Notch signaling
PCP pathway
Receptor-Mediated-Endocytosis
Stress response
TGF-B signaling
Trypsin-like proteolysis
Wnt signaling
Sender Cells
Atypical cells
Body wall muscle
Coelomocytes
Egg-laying apparatus
Neurons
Embryonic
Excretory
GLR cells
Germline
Somatic gonad
Pharynx
Head mesodermal cell
Hypodermis
Intestine
Rectum
Seam
Support cells
Receiver Cells
Atypical cells
Body wall muscle
Coelomocytes
Egg-laying apparat
Neurons
Embryonic
Excretory
GLR cells
Germline
Somatic gonad
Pharynx
Head mesodermal
Hypodermis
Intestine
Rectum
Seam
Support cells
D
Gene
ins-9
ins-6
ins-5
ins-4
ins-30
ins-3
ins-29
ins-28
ins-27
ins-26
ins-24
ins-22
ins-18
ins-17
ins-14
ins-1
daf-7
daf-28
ADF
ADL
AFD
AIA
AIN
ASE
ASG
ASH
ASI
ASJ
ASK
AWA
AWB
AWC
BAG
M1
RIR
RMH
URB
URX AQR PQR
Tissue
Proportion
25
50
75
100
Scaled TPM
30000
20000
10000
0
E
ins-1 expression
AIA
log(scaled TPM)
10
0
-10
-20
-30
Percent cells
0
25
50
75
100
F
daf-2 expression
ASE
log(scaled TPM)
4
2
0
Percent cells
0
25
50
75
100

Fig. S5. Identification of cell-type specific communication signatures using Tensor-cell2cell. **(A)** Graphical representation of Tensor analysis. **(B)** Elbow plot to determine the optimal number of factors/signatures. **(C)** Tensor-cell2cell analysis: The first column of graphs represents the importance of each ligand-receptor in each signature colored by ligand-receptor pair class, the second column of graphs represents the importance of each sender cell in each signature colored by tissue type, the third column of graphs represents the importance of each receiver cell in each signature colored by tissue type. Color legend of functional, sender-cell, and receiver-cell classes can be found below the graphs. **(D)** The distribution of insulin ligands important across the sender cells in signature 7. **(E)** Enrichment of *ins-1* expression in AIA neurons. **(F)** Enrichment of *daf-2* expression in ASE neurons.

Note these files will only be available with the published paper.

Data S1. (separate file)

This file includes the gene markers (output from Monocle3's find_markers function) and rationale used to annotate the various clusters as well as a list of the identified cell types. NOTE: some clusters contained several cell types. The cell types that could not be distinguished after sub-clustering are denoted by the "_". The cell types that could be distinguished after sub-clustering were annotated separately.

Data S2. (separate file)

This file includes the results of the analysis described in "Estimating transcriptome coverage for every cell type". Readers can find the actual number of cells identified and the actual number of genes identified per cell type in addition to the predicted maximum number of genes in every cell type (G_{MAX}) and the predicted number of cells required to identify half of G_{MAX}.

Data S3. (separate file)

This file contains several tables that pertain to the housekeeping genes analysis. **(A)** List of genes with negative skew. **(B)** List of genes with Gini < 0.3. **(C)** List of genes with Gini < 0.3 identified as housekeeping in L2. **(D)** List of genes with Gini < 0.3 identified as housekeeping in L2 and found to be essential in RNAi screens. **(E)** List of genes with Gini < 0.3 identified as housekeeping in L2, found to be essential in RNAi screens, and found to be conserved across species (Drosophila melanogaster, Danio rerio, Xenopus tropicalis, Gallus gallus, Homo sapiens, Mus musculus, Neurospora crassa, Saccharomyces cerevisiae, Arabidopsis thaliana).

Data S4. (separate file)

This file contains the results of the transcription factor analysis. The columns represent transcription factors, and the rows represent cell types. The values represent the correlation coefficient between the binding patterns of the transcription factors defined by ChIP-Seq and the gene expression profile of the cell types defined by scRNA-Seq. The numbers next to the cell types are the mean square error for the cell type model.

Data S5. (separate file)

This file includes the *dsc-1* targets expressed in the anal muscle that are known to play a role in **(A)** defecation/anal muscle function and, **(B)** muscle system morphology.

Data S6. (separate file)

This file includes the results of the Tensor-cell2cell analysis. **(A)** Loading values of ligand-receptor pairs per signature. **(B)** Loading values of sender cells per signature. **(C)** Loading values of receiver cells per signature.

Chapter IV: Single-cell deconstruction of the molecular networks underlying diet-induced obesity

Abstract

The obesity epidemic has become a major strain on societies worldwide. This complex disease is driven by multiple factors including diet and genetics. It is characterized by systemic changes at the molecular and physiological levels across the whole body of the organism. An additional layer of complexity is the role of multiple genes and tissues in the etiology of the disease with many molecules playing context-specific roles. To begin elucidating the molecular changes that drive diet-induced obesity, we here present a single-cell transcriptional atlas of *C. elegans* fed a regular diet and a fructose-rich diet which is associated with the most common form of obesity, diet-induced obesity. We identify common and cell-type specific changes to the expression of various genes in response to excess fructose consumption. We combine our scRNA-Seq data with publicly available ChIP-Seq data to infer changes in transcription factor activity across cell types in obesogenic conditions. We validate some of the predictions of these analyses using publicly available experimental data as well as using human disease databases. Finally, we present three examples of the molecular changes associated with excess fructose consumption that highlight the context-specific role of genetic networks in the development of obesity and associated metabolic syndrome.

Introduction

Obesity is a major risk factor for debilitating and deadly diseases including type 2 diabetes[1], Alzheimer's[2], cancer[3], and cardiovascular disease[4]. Therefore, the global rise in obesity rates has led to a major public health crisis[5] and a critical need for the development of safe and effective interventions to combat this epidemic. Obesity, however, is a complex disease with genetic and environmental factors such as diet, exercise and socioeconomic status contributing to its most common form, known as diet-induced obesity (DIO)[6]. Specifically, fructose overconsumption has been singled out as a major driver of DIO and its associated metabolic syndrome[7]. Despite recent advances in our understanding of obesity, the specific genes linking excessive sugar intake to fat accumulation and disease development remain largely elusive[8,9]. This gap in knowledge is largely due to the complex etiology of the disease and the metabolic pathways involved with several genes having tissue- and context-specific roles. Adding to the complexity of this disease, is the fact that excess sugar consumption has been linked to systemic physiological and behavioral changes including alterations to fertility[10], satiety[11] and food seeking[12]. Therefore, to begin elucidating the mechanisms underlying the development of DIO, it is critical to gain a systemic, single-cell resolution, understanding of the molecular changes that occur in response to excess fructose consumption.

Highlighting the need for a systemic understanding of the molecular changes underlying DIO is the role of several tissues in the development of the disease. Studies have shown that the nervous system[13,14], adipose tissue[15], skeletal muscles[16], liver[17], and the gastrointestinal tract along with its extensive microbiome[18] can all play a role in the development and progression of DIO and DIO-associated metabolic syndrome. Furthermore, the activity of certain genes can have distinct or even opposite phenotypic impact depending on the cell type in which they are activated or inhibited. For example, in mice, removing the insulin receptor in muscle cells results in the development of obesity and an associated decrease in lifespan[19], while removing the insulin receptor in adipocytes does not result in the development of obesity, and extends lifespan[20]. Similarly, a recent study has shown that while fructose metabolism in the liver drives metabolic dysfunction, fructose metabolism in the intestine protects the liver from excess lipid accumulation and insulin resistance[21]. These examples of the context-specific nature of gene function highlight the need to identify the molecular changes associated with obesity in a tissue- and cell-specific manner.

Towards this goal, we here report a whole-body, single-cell transcriptional atlas of *Caenorhabditis elegans* fed a regular diet and a fructose-rich diet. We had previously shown that *C. elegans* fed a fructose-rich diet is a model for DIO[22] recapitulating many of the known consequences of human DIO including fat accumulation, reduced lifespan, and increased neurodegeneration[22]. We use this compendium to identify genes that are differentially expressed in response to excess fructose consumption in 155 *C. elegans* cell types. We identify common and cell-type specific differentially expressed genes, a subset of which have been experimentally validated to play a role in fat accumulation. We also identify differentially expressed genes linked to human obesity and obesity-related diseases. We combine our single-cell resolution transcriptional atlas with available ChIP-Seq data to identify cell type-specific changes in transcriptional programs caused by excess fructose consumption. Finally, we describe three results that highlight the power of the newly generated data and tools. We show that excess fructose consumption may be causing widespread changes to basal cellular functions including protein translation and mitochondrial respiration. However, we find that these changes are not the same across cell types with some cells showing signs of increased protein translation and mitochondrial respiration and others showing the opposite. We also show that excess fructose consumption leads to changes in fertility associated with tissue-specific changes in the expression of vitellogenin genes. Finally, we find that excess fructose consumption is associated with changes in the transcriptional landscape and activity of pharyngeal cells and associated neurons which may point to fructose-driven changes in the feeding behavior of the worm. The presented single-cell transcriptional atlas of DIO animals will shed new light on the mechanisms linking excess sugar consumption to the disease. It will also help disentangle the role of different genes and the tissues in which they are active in the development of phenotypes associated with excess fructose consumption and obesity.

Results

scRNA-Seq of DIO C. elegans

To define the changes to the transcriptional profile of DIO *C. elegans* at single-cell resolution we performed scRNA-Seq, as previously described[23], in wild-type hermaphrodite *C. elegans* young adult fed a regular *E. coli*-only diet and *C. elegans* young adult fed an *E. coli* diet supplemented with 55mM fructose. Three independent biological replicates were collected and after the removal of low quality and damaged cells, the dataset contained 365,540 cells that passed quality filters. Cells from both worms fed a regular diet (155,631 cells) and a fructose rich diet (209,909 cells) were well represented in our dataset. The cells were visualized by UMAP, and after clustering them using the Louvain algorithm, they separated into 209 distinct clusters ranging in size from 35 to 7966 cells. The clusters were then annotated as previously described[23] and we were able to identify over 155 cell types (Fig. 1; summarized in Appendix Table S1). Similar to our previously reported scRNA-Seq of wild type healthy *C. elegans*[23], we identified all expected broadly defined cell types including intestine, pharyngeal cell types, hypodermis, non-striated and body wall muscle, neurons, glial cells, rectum and anus, seam, somatic gonad, vulva and uterus, excretory, coelomocytes, GLR cells, head mesodermal cells and XXX cells. We were also able to identify sub-populations of the broadly defined cell types (e.g., intestine anterior, middle, posterior or mc1, mc2_mc3 marginal cells).

We found that regular-fed worms and fructose-fed worms were well represented across clusters (Fig. 2A) and cell types (Appendix Table S1). Indeed, there was a strong positive correlation in the number of cells per cell type between conditions (Fig. 2B; Pearson correlation coefficient: 0.98) suggesting that we can perform cell type-specific comparisons of the transcriptomes of regular-fed worms and fructose-fed worms.

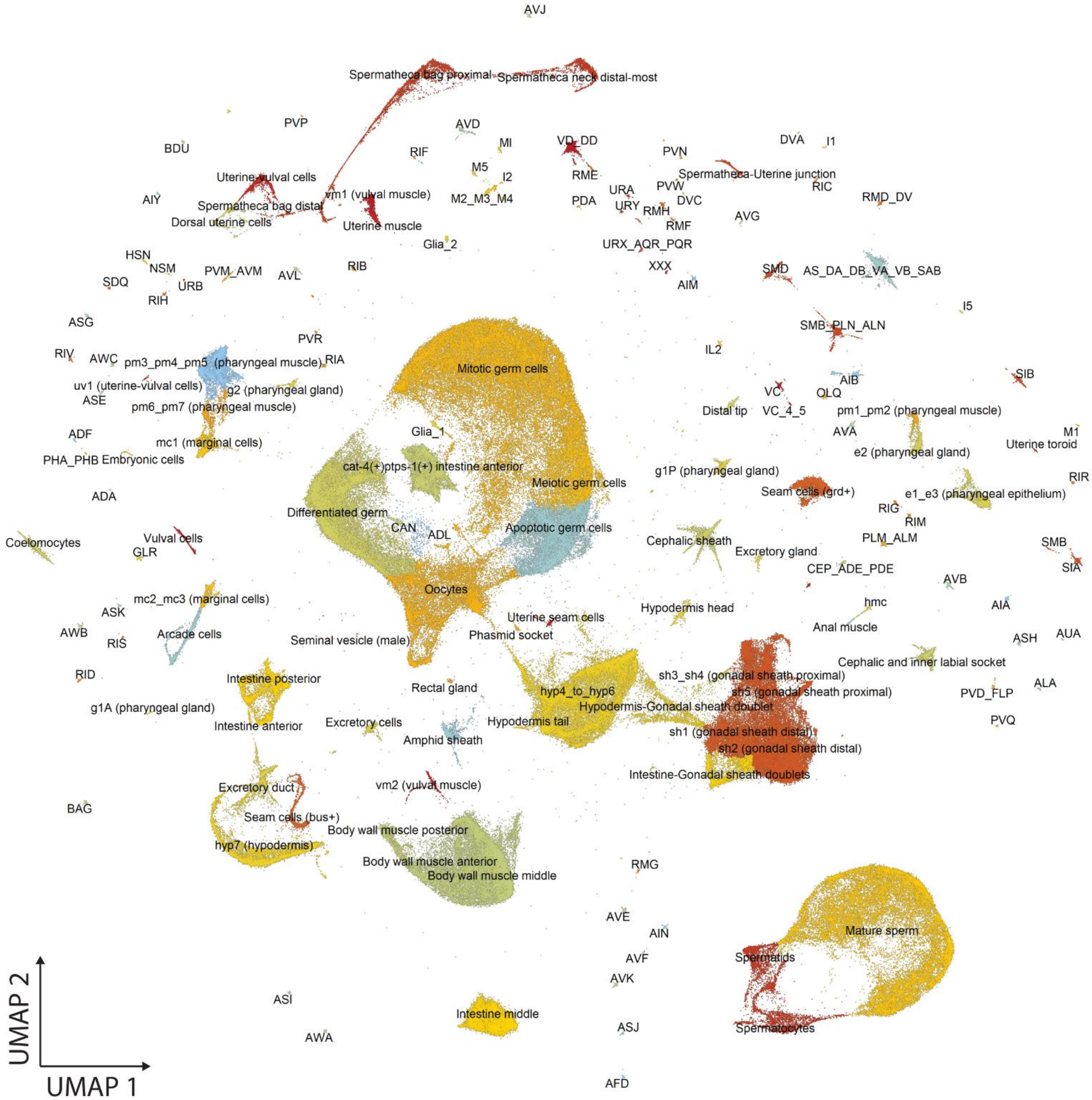


Figure 1. UMAP visualization of the 155 identified cell types. UMAP reduction of 365,540 cells. Each dot represents a cell. Colors indicate distinct cell types.

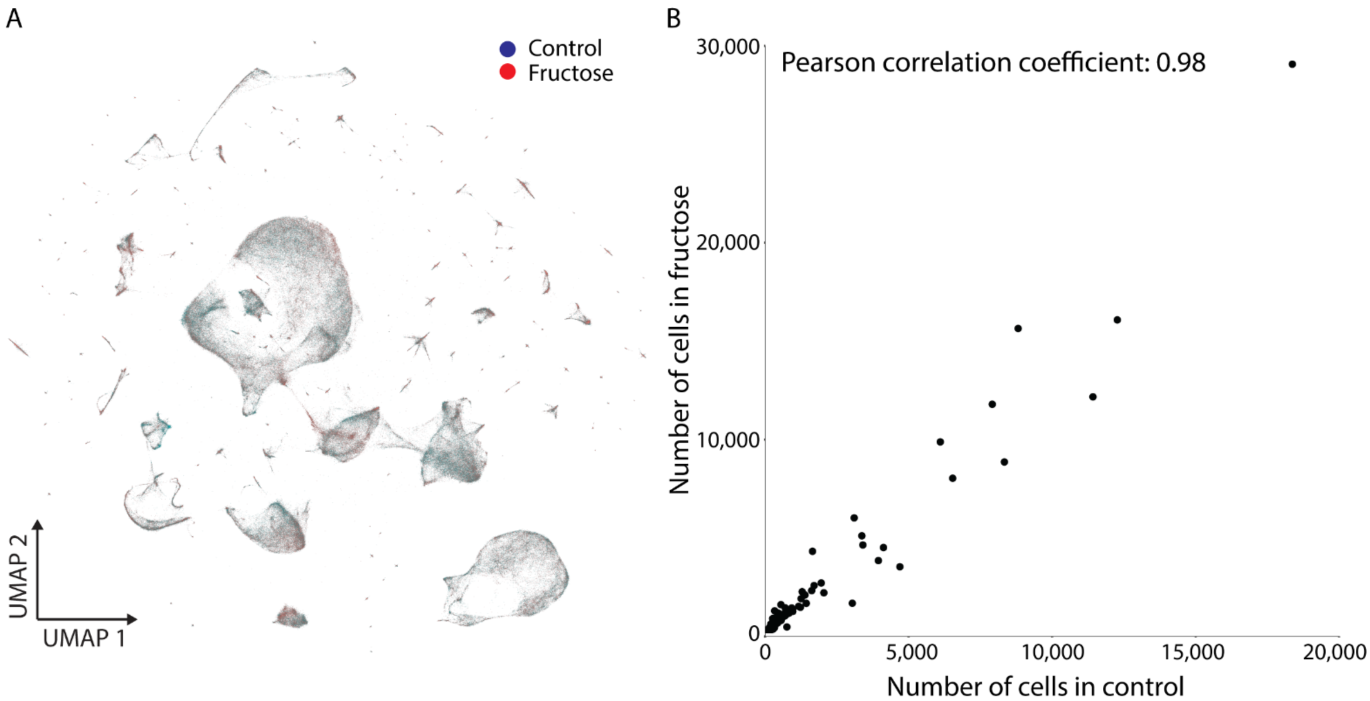


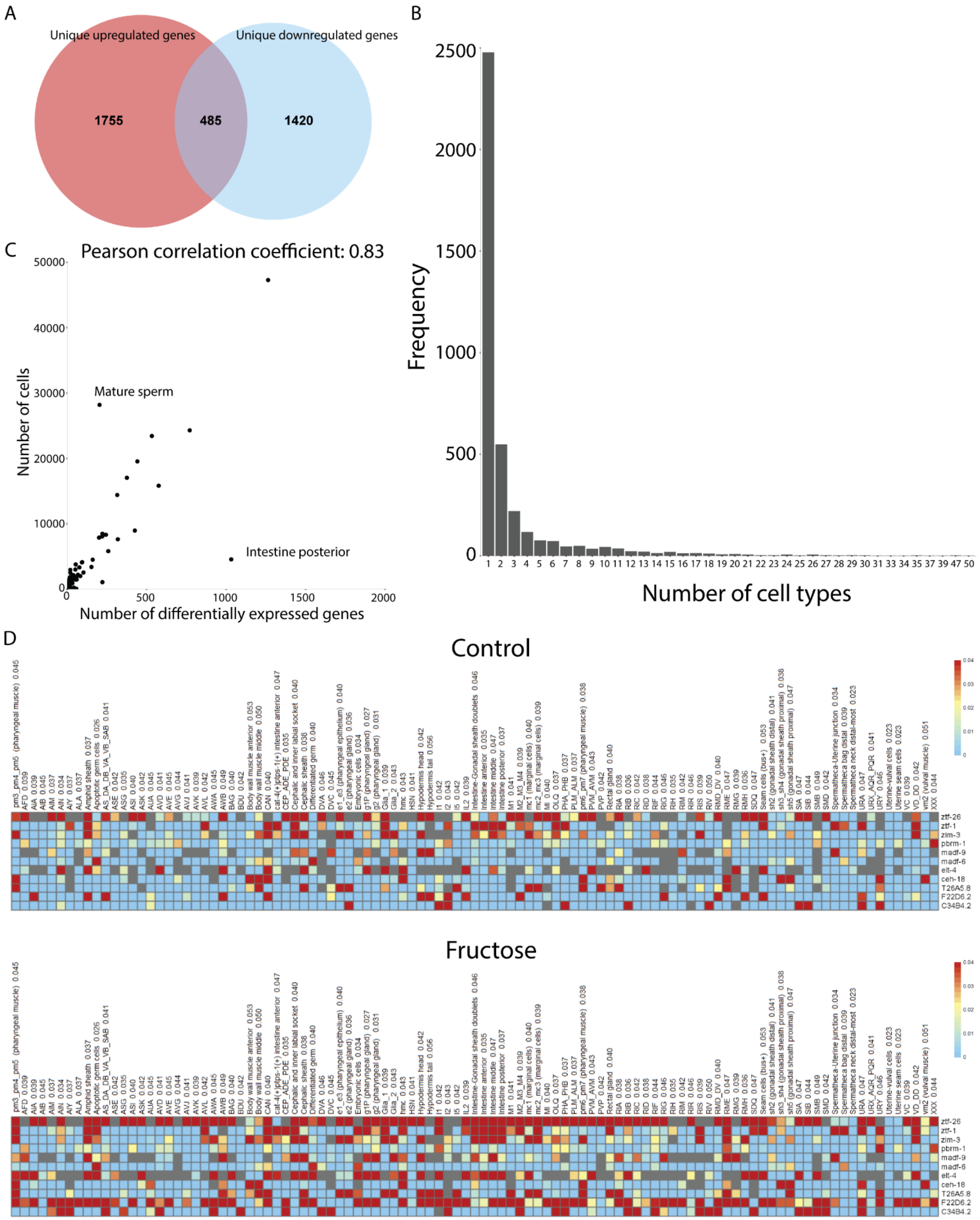
Figure 2. Comparison of control and fructose data. (A) UMAP reduction of 365,540 cells colored by condition indicates a good overlap between control and fructose data per cluster. **(B)** Strong correlation between the number of cells per cell type in control samples and fructose samples.

Identification of differentially expressed genes and transcriptional programs in DIO worms

We then used our scRNA-Seq compendium of normal-fed and fructose-fed worms to determine, in a tissue-specific manner, the changes that occur to the transcriptome in response to excess fructose consumption. We used Monocle3's fit_models function[24], which uses a general additive model, to identify differentially expressed genes in DIO worms. We identified 3,683 unique differentially expressed genes (Appendix Table S2). There were 2,240 upregulated genes and 1,905 downregulated genes (Fig. 3A). The fact that the total of unique upregulated and downregulated genes (4,145) was higher than the total number of unique differentially expressed genes (3,683) indicated that there were several genes that were upregulated in certain tissues and downregulated in others. Indeed, we found that 485 genes were differentially regulated in opposite directions in different tissues (Fig. 3A). We also found that the majority (2,368/3,683) of differentially expressed genes were specific to a single cell type (Fig 3B). It is important to note however, that there’s a strong correlation between the number of cells in a cell type and the number of differentially expressed genes per cell type (Fig. 3C; Pearson correlation coefficient: 0.83) suggesting that our ability to detect differentially expressed genes is limited by (partly depends on) the number of available cells. The potential consequences of this observation on our interpretation of the presented results are discussed below (Limitations section). Nonetheless, even when taking the previous limitation into account, the uniqueness of every tissue in responding to a common perturbation highlights the importance of examining transcriptional changes with a cellular resolution.

Next, we wanted to determine which of the differentially expressed genes had previously been shown to play a role in fat accumulation. First, we obtained a list of genes that have been shown to cause fat accumulation or fat reduction in an RNAi screen[25]. We then crossed our list of differentially expressed genes with the experimentally validated list of genes involved in the regulation of fat content. We identified 167 differentially expressed genes that are also known to play a role in fat reduction and 59 differentially expressed genes known to increase fat content. Out of the 167 genes, we found that 47 genes were differentially expressed in the expected direction; these genes are known to reduce fat content and they are downregulated in response to excess fructose consumption. Similarly, 46 genes out of the 59 differentially expressed genes known to increase fat content, are upregulated in response to excess fructose consumption. These genes, therefore, are more likely involved in increasing fat content in response to excess sugar consumption.

In addition to identifying changes in the expression of individual genes, we investigated whether cell-type specific transcriptional programs are also changing in response to excess fructose consumption. Specifically, we wanted to determine whether there were cell-type specific changes to the activity of certain transcription factors (TF) was different between regular-fed worms and fructose-fed worms. For this, we used previously published ChIP-Seq data to infer the activity of 362 transcription factors in each cell type in regular-fed worms and fructose-fed worms, as previously described[23]. We identified 6,457 TF-cell type associations in regular-fed worms and 6,606 TF-cell type associations in fructose-fed worms, defined as a correlation of more than 0 between TF binding patterns as defined by ChIP-Seq and cell-type specific gene expression profiles as defined by scRNA-Seq (Appendix Table S3). We found 550 TF-cell type associations that were specific to fructose-fed worms which involved 133 distinct TFs, and 714 associations that were specific to regular-fed worms which involved 161 distinct TFs. Several TFs were predicted to be commonly activated across several cell types in fructose-fed worms including F22D6.2 (58 cell types), C34B4.2 (20 cell types), *madf-9* (20 cell types), *zim-3* (15 cell types), and T26A5.8 (13 cell types) (Fig. 1D). Conversely, some of the transcription factors that were predicted to be commonly inactivated in fructose-fed worms included *lag-1* (27 cell types), ZK546.5 (25 cell types), *attf-6* (24 cell types), *ceh-18* (20 cell types), and *lin-13* (18 cell types). Additionally, there were several transcription factors that were predicted to be activated (49/133) or inactivated (48/161) in a single cell-type in fructose-fed worms. There were also several TFs known to play a role in fat accumulation, that are predicted to be differentially active in fructose-fed and regular-fed worms. For example, the TF *lin-26*, which promotes fat accumulation, is predicted to be active in fructose-fed pm3_pm4_pm5 and pm6_pm7 pharyngeal muscle cells, and spermatheca-uterine junction. Interestingly, at the same time, *lin-26* activity is predicted to be decreased in other cell types, including vm1 (vulval muscle) cells, suggesting a cell-type specific role for this transcription factor in fat accumulation. Another example is the TF *hsf-1*, which promotes leanness and is predicted to be more active in several cell types of regular-fed worms including: ADF, AIN, ALA, AVG, BAG, NSM, PVW, VC, VC_4_5, URX_AQR_PQR neurons, hyp7 and head hypodermal cells as well as several pharyngeal gland and epithelial cells. At the same time, *hsf-1* is predicted to be less active in anterior and posterior intestinal cells and several neurons. The results presented here suggest that excess fructose consumption can lead to the activation and inactivation of transcriptional programs, including common and cell-type specific transcriptional programs. The experimental validation of the role of some of the TFs in fat regulation suggests that these TFs may be involved in the development or maintenance of obesity in animals fed excess fructose.


A
Unique upregulated genes
Unique downregulated genes
1755
485
1420
B
Frequency
2500
2000
1500
1000
500
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 33 34 35 37 39 47 50
Number of cell types
C
Pearson correlation coefficient: 0.83
Number of cells
50000
40000
30000
20000
10000
0
Mature sperm
Intestine posterior
0
500
1000
1500
2000
Number of differentially expressed genes
D
Control
pm3_pm4_pm5 (pharyngeal muscle) 0.045
AFD 0.039
AIA 0.039
AIB 0.045
AIM 0.037
AIN 0.034
AIY 0.037
ALA 0.037
Amphid sheath 0.037
Apoptotic germ cells 0.026
AS_DA_DB_VA_VB_SAB 0.041
ASE 0.042
ASG 0.035
ASI 0.040
ASK 0.042
AUA 0.045
AVD 0.041
AVE 0.045
AVG 0.044
AVJ 0.041
AVK 0.039
AVL 0.042
AWA 0.045
AWB 0.049
BAG 0.040
BDU 0.042
Body wall muscle anterior 0.053
Body wall muscle middle 0.050
CAN 0.040
cat-4(+)ptps-1(+) intestine anterior 0.047
CEP_ADE_PDE 0.035
Cephalic and inner labial socket 0.040
Cephalic sheath 0.038
Differentiated germ 0.040
DVA 0.046
DVC 0.045
e1_e3 (pharyngeal epithelium) 0.040
e2 (pharyngeal gland) 0.036
Embryonic cells 0.034
g1P (pharyngeal gland) 0.027
g2 (pharyngeal gland) 0.031
Glia_1 0.039
Glia_2 0.043
hmc 0.043
HSN 0.041
Hypodermis head 0.042
Hypodermis tail 0.056
I1 0.042
I2 0.043
I5 0.042
IL2 0.039
Intestine-Gonadal sheath doublets 0.046
Intestine anterior 0.035
Intestine middle 0.047
Intestine posterior 0.037
M1 0.041
M2_M3_M4 0.039
mc1 (marginal cells) 0.040
mc2_mc3 (marginal cells) 0.039
MI 0.040
OLQ 0.037
PHA_PHB 0.037
PLM_ALM 0.037
pm6_pm7 (pharyngeal muscle) 0.038
PVM_AVM 0.043
PVP 0.042
Rectal gland 0.040
RIA 0.038
RIB 0.036
RIC 0.042
RID 0.038
RIF 0.044
RIG 0.046
RIH 0.035
RIM 0.042
RIR 0.046
RIS 0.039
RIV 0.050
RMD_DV 0.040
RME 0.047
RMG 0.039
RMH 0.036
SDQ 0.047
Seam cells (bus+) 0.053
sh2 (gonadal sheath distal) 0.041
sh3_sh4 (gonadal sheath proximal) 0.038
sh5 (gonadal sheath proximal) 0.047
SIA 0.047
SIB 0.044
SMB 0.049
SMD 0.042
Spermatheca-Uterine junction 0.034
Spermatheca bag distal 0.039
Spermatheca neck distal-most 0.023
URA 0.047
URX_AQR_PQR 0.041
URY 0.046
Uterine-vulval cells 0.023
Uterine seam cells 0.023
VC 0.039
VD_DD 0.042
vm2 (vulval muscle) 0.051
XXX 0.044
0.04
0.03
0.02
0.01
0
ztf-26
ztf-1
zim-3
pbrm-1
madf-9
madf-6
elt-4
ceh-18
T26A5.8
F22D6.2
C34B4.2
Fructose
pm3_pm4_pm5 (pharyngeal muscle) 0.045
AFD 0.039
AIA 0.039
AIB 0.045
AIM 0.037
AIN 0.034
AIY 0.037
ALA 0.037
Amphid sheath 0.037
Apoptotic germ cells 0.026
AS_DA_DB_VA_VB_SAB 0.041
ASE 0.042
ASG 0.035
ASI 0.040
ASK 0.042
AUA 0.045
AVD 0.041
AVE 0.045
AVG 0.044
AVJ 0.041
AVK 0.039
AVL 0.042
AWA 0.045
AWB 0.049
BAG 0.040
BDU 0.042
Body wall muscle anterior 0.053
Body wall muscle middle 0.050
CAN 0.040
cat-4(+)ptps-1(+) intestine anterior 0.047
CEP_ADE_PDE 0.035
Cephalic and inner labial socket 0.040
Cephalic sheath 0.038
Differentiated germ 0.040
DVA 0.046
DVC 0.045
e1_e3 (pharyngeal epithelium) 0.040
e2 (pharyngeal gland) 0.036
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Glia_1 0.039
Glia_2 0.043
hmc 0.043
HSN 0.041
Hypodermis head 0.042
Hypodermis tail 0.056
I1 0.042
I2 0.043
I5 0.042
IL2 0.039
Intestine-Gonadal sheath doublets 0.046
Intestine anterior 0.035
Intestine middle 0.047
Intestine posterior 0.037
M1 0.041
M2_M3_M4 0.039
mc1 (marginal cells) 0.040
mc2_mc3 (marginal cells) 0.039
MI 0.040
OLQ 0.037
PHA_PHB 0.037
PLM_ALM 0.037
pm6_pm7 (pharyngeal muscle) 0.038
PVM_AVM 0.043
PVP 0.042
Rectal gland 0.040
RIA 0.038
RIB 0.036
RIC 0.042
RID 0.038
RIF 0.044
RIG 0.046
RIH 0.035
RIM 0.042
RIR 0.046
RIS 0.039
RIV 0.050
RMD_DV 0.040
RME 0.047
RMG 0.039
RMH 0.036
SDQ 0.047
Seam cells (bus+) 0.053
sh2 (gonadal sheath distal) 0.041
sh3_sh4 (gonadal sheath proximal) 0.038
sh5 (gonadal sheath proximal) 0.047
SIA 0.047
SIB 0.044
SMB 0.049
SMD 0.042
Spermatheca-Uterine junction 0.034
Spermatheca bag distal 0.039
Spermatheca neck distal-most 0.023
URA 0.047
URX_AQR_PQR 0.041
URY 0.046
Uterine-vulval cells 0.023
Uterine seam cells 0.023
VC 0.039
VD_DD 0.042
vm2 (vulval muscle) 0.051
XXX 0.044
0.04
0.03
0.02
0.01
0
ztf-26
ztf-1
zim-3
pbrm-1
madf-9
madf-6
elt-4
ceh-18
T26A5.8
F22D6.2
C34B4.2

Figure 3. scRNA-Seq of DIO worms reveals common and cell-type specific changes to transcriptional programs. (A) Number of unique upregulated genes, downregulated genes and genes that show upregulation in one cell type and downregulation in another. **(B)** Frequency of the number of cell types in which differentially expressed genes are differentially expressed. **(C)** Strong correlation between the number of cells per cell type and the number of differentially expressed genes per cell type. **(D)** Heatmap of TF-cell type associations coefficients of a subset of TFs showing activation across several cell types in fructose-fed worms. Only cell types that show differential activation in DIO conditions for at least one transcription are shown. Hierarchical clustering of cell types and TFs was performed using the Ward.D2 method.

DIO results in changes to basal cellular functions

We then examined more closely the differentially expressed genes that were common among cell types. Surprisingly, we found only 3 genes that were commonly differentially expressed in at least 25% of identified cell types: the cytochrome c oxidase encoding gene *ctc-3*, the ribosomal protein encoding gene *rpl-41.2* and the collagen encoding gene *col-122* (Fig. 4A-C). The gene *ctc-3* was upregulated in 49 cell types, *col-122* was upregulated in 47 cell types and *rpl-41.2* was downregulated in 43 cell types (Fig. 4A-C). In line with a relatively common role for these classes of genes in the response to fructose overconsumption, we found that the list of genes differentially expressed in at least 10 cell types (193 genes) was enriched in GO terms associated with ribosomal function, cellular respiration, and cuticle formation (Fig. 4D). These results suggest that although most transcriptional changes are tissue-specific, many tissues experience changes to basal cellular functions, specifically protein translation and mitochondrial respiration, upon excess fructose consumption.

We next wanted to determine the extent to which DIO worms alter basal cellular functions and whether there were tissue-dependent differences in how these functions changed. We first examined changes to ribosomal function in response to excess fructose consumption. We found that at least 55 cell types exhibited transcriptional changes to at least one ribosomal gene. Additionally, we identified 110 ribosome-encoding genes that were differentially expressed in at least one cell type. However, we found that the response of ribosomal genes to DIO was tissue-and gene-dependent. The majority of tissues (40/55) exhibited downregulation of ribosomal genes. This included most non-pharyngeal muscle cells (uterine muscle, body wall muscle anterior, body wall muscle posterior, vm1 vulval muscle), some neurons, germ cells (mature sperm and oocytes), hypodermal cells (hypodermis head and hyp4-6) and intestine middle cells (Fig. 4E-F). On the other end of the spectrum, there were 6 cell types that exhibited upregulation of ribosomal genes including intestine posterior and anterior and most pharyngeal cells (pm3_pm4_pm5 and pm6_pm7 pharyngeal muscle, mc1 marginal cells and e2 pharyngeal cells) (Fig. 4G-H). Finally, some cell types showed gene-dependent upregulation or downregulation of ribosomal genes. These results indicate that there are tissue-dependent changes to ribosomal function, and by extension protein translation, in response to excess fructose consumption. At face value, they suggest that while most cell types may decrease protein translation in response to DIO, some pharyngeal and intestinal cells may increase it.

We then examined changes to mitochondrial respiration in response to excess fructose consumption. Specifically, we wanted to look at the expression of three classes of mitochondrial genes: NADH ubiquinone oxidoreductase (*nduo* and *ndfl*), cytochrome c oxidase (*ctc*), and ATP synthase (*atp* and *asb*). There were 10 cell types where all three gene classes were upregulated suggesting mitochondrial respiration being increased in these cell types. These include intestine (anterior, middle, posterior), germ cells (mitotic, meiotic, apoptotic, oocytes), coelomocytes, and hyp7 hypodermal cells (Fig. 4I-J). Intriguingly, the pm3_pm4_pm5 pharyngeal muscle cells showed upregulation of *nduo-1, nduo-2, nduo-5,* and *ctc-1, ctc-2, ctc-3* but downregulation of *atp-4, atp-5, and asb-2* (Fig. 4K). Finally, 19 cell types exhibited decreased *nduo*/*ndfl* expression and 13 out of these simultaneously exhibited increased *ctc* expression. Altogether, the results suggest that tissue-dependent changes in mitochondrial respiration occur in response to excess fructose consumption.

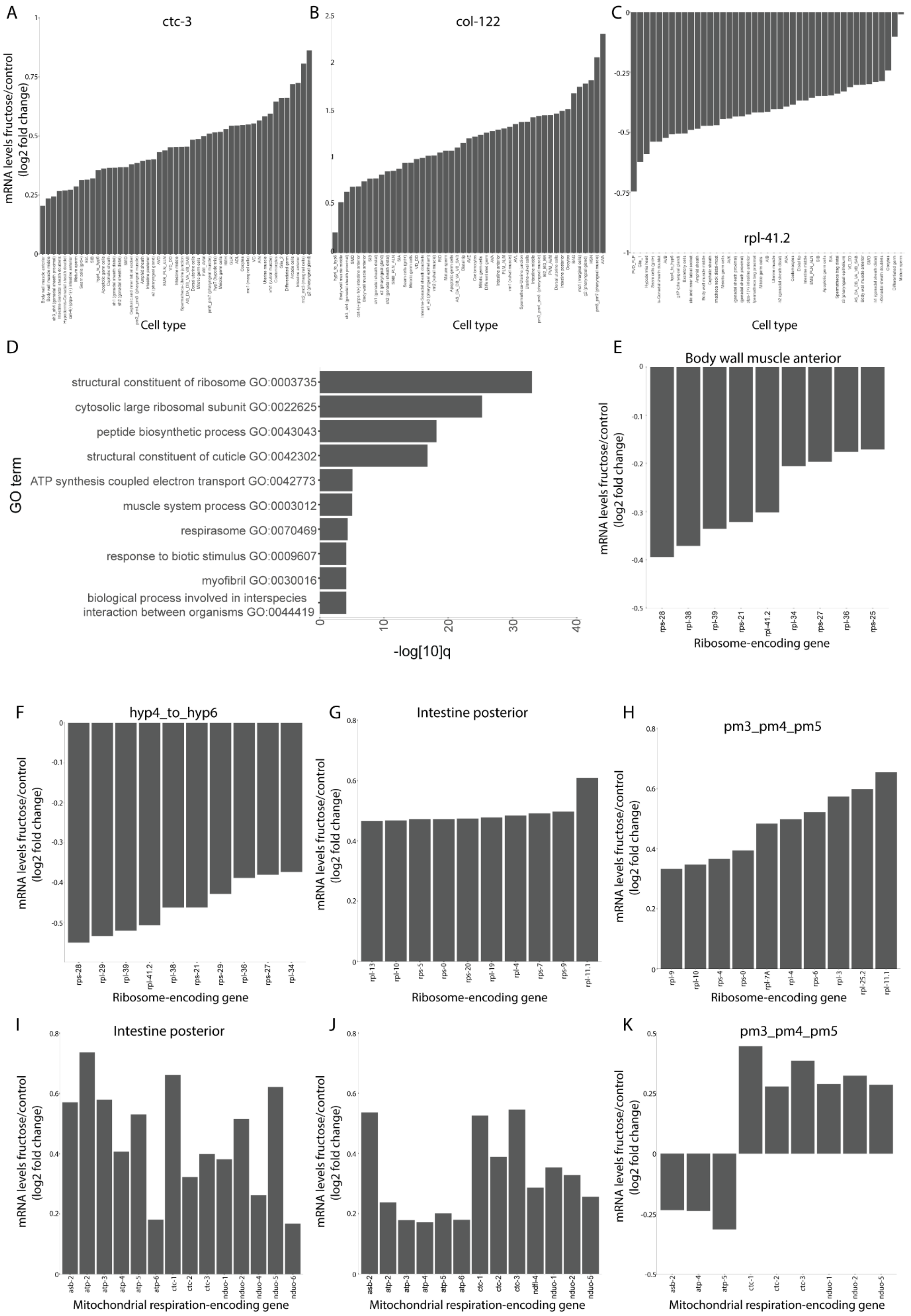
A
ctc-3
mRNA levels fructose/control (log2 fold change)
Cell type
B
col-122
Cell type
C
rpl-41.2
Cell type
D
GO term
structural constituent of ribosome GO:0003735
cytosolic large ribosomal subunit GO:0022625
peptide biosynthetic process GO:0043043
structural constituent of cuticle GO:0042302
ATP synthesis coupled electron transport GO:0042773
muscle system process GO:0003012
respirasome GO:0070469
response to biotic stimulus GO:0009607
myofibril GO:0030016
biological process involved in interspecies interaction between organisms GO:0044419
0
10
20
30
40
-log[10]q
E
Body wall muscle anterior
rps-28
rpl-38
rpl-39
rps-21
rpl-41.2
rpl-34
rps-27
rpl-36
rps-25
Ribosome-encoding gene
F
hyp4_to_hyp6
rps-28
rpl-29
rpl-39
rpl-41.2
rpl-38
rps-21
rps-29
rpl-36
rps-27
rpl-34
Ribosome-encoding gene
G
Intestine posterior
rpl-13
rpl-10
rps-5
rps-0
rps-20
rpl-19
rpl-4
rps-7
rps-9
rpl-11.1
Ribosome-encoding gene
H
pm3_pm4_pm5
rpl-9
rpl-10
rps-4
rps-0
rpl-7A
rpl-4
rps-6
rpl-3
rpl-25.2
rpl-11.1
Ribosome-encoding gene
I
Intestine posterior
asb-2
atp-2
atp-3
atp-4
atp-5
atp-6
ctc-1
ctc-2
ctc-3
nduo-1
nduo-2
nduo-4
nduo-5
nduo-6
Mitochondrial respiration-encoding gene
J
asb-2
atp-2
atp-3
atp-4
atp-5
atp-6
ctc-1
ctc-2
ctc-3
ndfl-4
nduo-1
nduo-2
nduo-5
Mitochondrial respiration-encoding gene
K
pm3_pm4_pm5
asb-2
atp-4
atp-5
ctc-1
ctc-2
ctc-3
nduo-1
nduo-2
nduo-5
Mitochondrial respiration-encoding gene

Figure 4. Tissue-specific changes in basal cellular function occur in fructose-fed worms. (A) ctc-3 is upregulated in 49 cell types. (B) col-122 is upregulated in 47 cell types. (C) rpl-41.2 is downregulated in 43 cell types. (D) GO term enrichment analysis reveals genes that are differentially expressed in at least 10 cell types are enriched in basal cellular functions. (E) Body wall muscle anterior shows downregulation of ribosome-encoding genes. (F) hyp4_to_hyp6 hypodermal cells show downregulation of ribosome-encoding genes. (G) Intestine posterior shows upregulation in ribosome-encoding genes. (H) pm3_pm4_pm5 pharyngeal muscle cells show upregulation of ribosome-encoding genes. (I) Genes involved in mitochondrial respiration (*atp, asb, ctc, nduo*) are upregulated in intestine posterior. (J) Genes involved in mitochondrial respiration (*atp, asb, ctc, nduo*) are upregulated in oocytes. (K) ATP synthase encoding genes are downregulated in pm3_pm4_pm5 pharyngeal muscle cells but cytochrome c oxidase and NADH ubiquinone oxidoreductase encoding genes are upregulated.

DIO worms show tissue-specific changes in vitellogenin production

Going through our list of differentially expressed genes, we found that among the most responsive group of genes were those encoding vitellogenins. The vitellogenins are a family of yolk proteins that the adult hermaphrodite uses to transport nutrients from the intestine to the oocytes and developing progeny[26]. In *C. elegans*, vits bound to lipids and other nutrients are secreted from intestinal cells and then taken up by oocytes through receptor mediated endocytosis[26]. We found all 6 vitellogenin-encoding genes (*vit-1* through *vit-6*) differentially expressed in fructose-fed worms. However, intriguingly, the *vit* response to excess fructose consumption seems to be tissue specific. In the anterior and posterior intestine, all 6 *vit* genes were downregulated (Fig. 5A). On the other hand, in the oocytes, all 6 *vit* genes were upregulated (Fig. 5B). Additionally, we found that the receptor of the vit genes, *rme-2*, was downregulated in the oocytes (Fig. 5C). Given the change in the expression of genes responsible for carrying nutrients to oocytes, we wanted to determine whether excess fructose consumption causes any changes to *C. elegans* fertility. Surprisingly, we found that worms fed excess fructose had increased progeny output relative to worms fed a regular diet indicating increased fertility (Fig. 5D-E). Additional experiments would be necessary to determine whether the change in the expression of vitellogenin-encoding genes is directly responsible for the change in fertility.

We then investigated whether any of the known regulators of *vit* gene expression were responsible for the observed changes in *vit* expression[26]. We found that several activators of *vit* gene expression were downregulated in intestinal cells including *unc-62, ceh-60, skn-1, sma-4, sma-6, sma-9,* and *sma-10.* These changes may contribute to the decrease in *vit* gene expression in the intestinal cells. On the other hand, we found no significant changes in the expression of these same activators in the oocytes. However, we did find that *unc-62* was significantly more active in the oocytes in the fructose-fed worms compared to the worms fed a regular diet in our TF analysis indicating that *unc-62* might be responsible for the upregulation of *vit* genes in the oocytes. This tissue-specific variability in the response of the same set of genes to the same perturbation highlights the importance of interrogating transcriptomic changes with single-cell resolution.

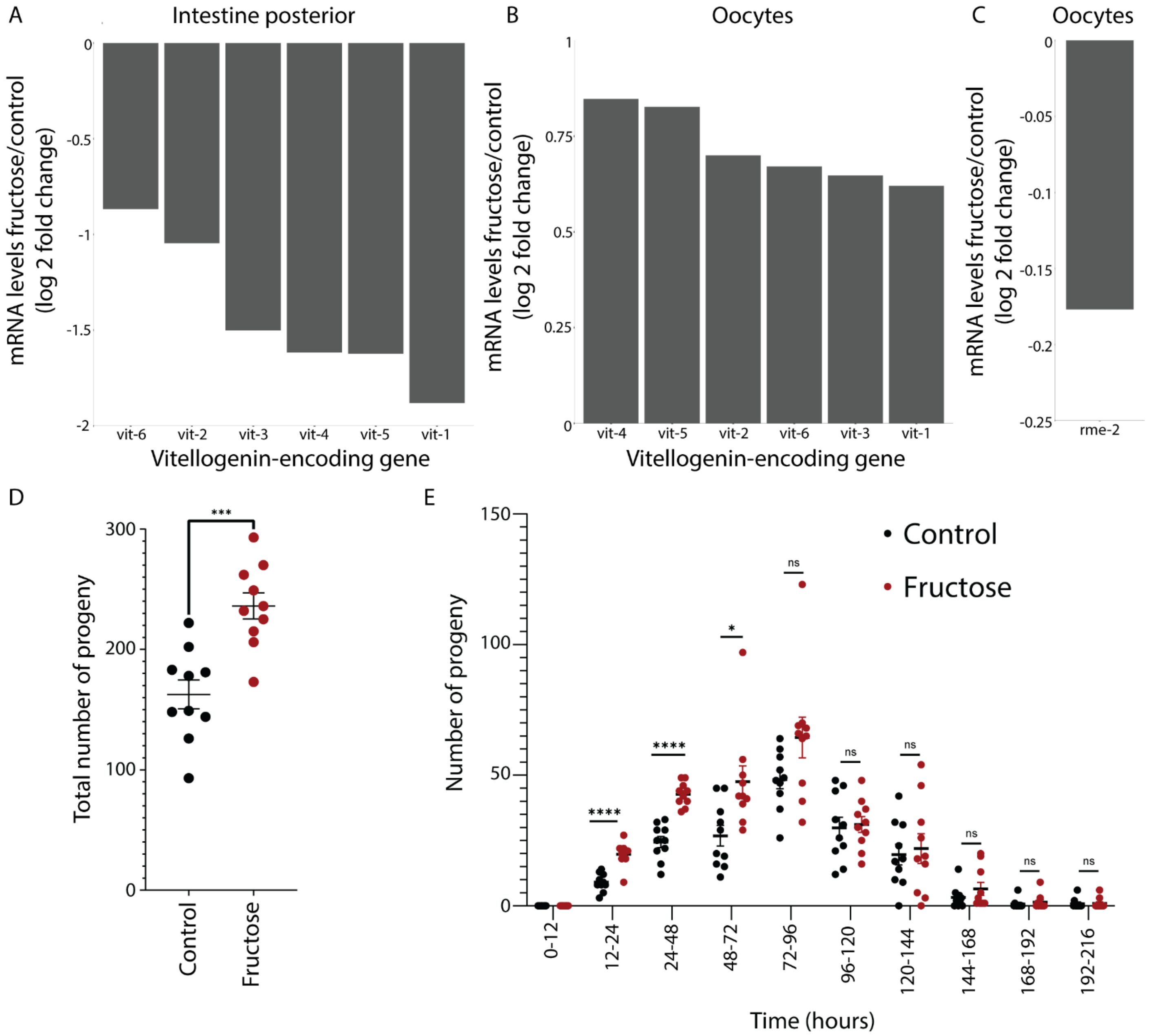

Figure 5. DIO results in tissue-specific changes in the production of vitellogenin-encoding genes. (A-B) Vitellogenin-encoding genes are **(A)** downregulated in intestine posterior and **(B)** upregulated in the oocytes. **(C)** The vitellogenin receptor, *rme-2*, is downregulated in oocytes. **(D-E)** Fructose-fed worms show **(D)** increased total progeny output (N=10) and **(E)** increased progeny per time unit compared to regular-fed worms (N=10).

C. elegans increases pumping rates in the presence of fructose

Ranking our list of cell types from the most responsive to the least responsive to excess fructose consumption using the machine learning-based tool Augur[27], we found that among the topmost responsive cell types were those that are associated with pharyngeal function (Fig. 6A; Appendix Table S4). Among the most responsive cell types were the pharyngeal muscle cells (pm3_pm4_pm5, pm6_pm7), several pharyngeal neurons (M1, M2_M3_M4, NSM, I1, I2, I5) and the mc1 marginal cells. It is worth noting that the second-most responsive cell type according to this analysis is NSM (Fig. 6A), a serotonergic neuron known to regulate feeding behavior, including glucose-induced reinforcement[28]. Together, these results suggest changes to feeding rates or behavior in response to excess fructose consumption.

We then looked through the list of differentially expressed genes to identify genes involved in pharyngeal function that were differentially regulated after excess fructose consumption. In the pm3_pm4_pm5 pharyngeal muscle cells we found several downregulated genes involved in pharyngeal pumping[29] including *cco-1, mlc-1, mlc-2, lev-11, tni-4, tnc-2* and *tnt-3* (Fig. 6B). Additionally, we found *flp-5*, a gene that encodes a neuropeptide known to increase pharyngeal pumping[30], downregulated in the pharyngeal I5 neurons. We also found that *flp-16*, a gene encoding a neurotransmitter that inhibits pharyngeal pumping[30], was induced 9-fold in the I5 neuron; however, this difference would need to be confirmed because the difference was not statistically significant. Together, the results point to pharyngeal pumping being decreased in worms fed a high-fructose diet. However, when we measured pumping rates in DIO worms, we were surprised to find that they were increased (Fig. 6C). This difference between the expected behavior based on molecular data and the observed behavior measured *in vivo* can have several explanations, some of which are discussed below. Nonetheless, these results suggest that *C. elegans* changes its feeding pattern in response to excess dietary fructose.

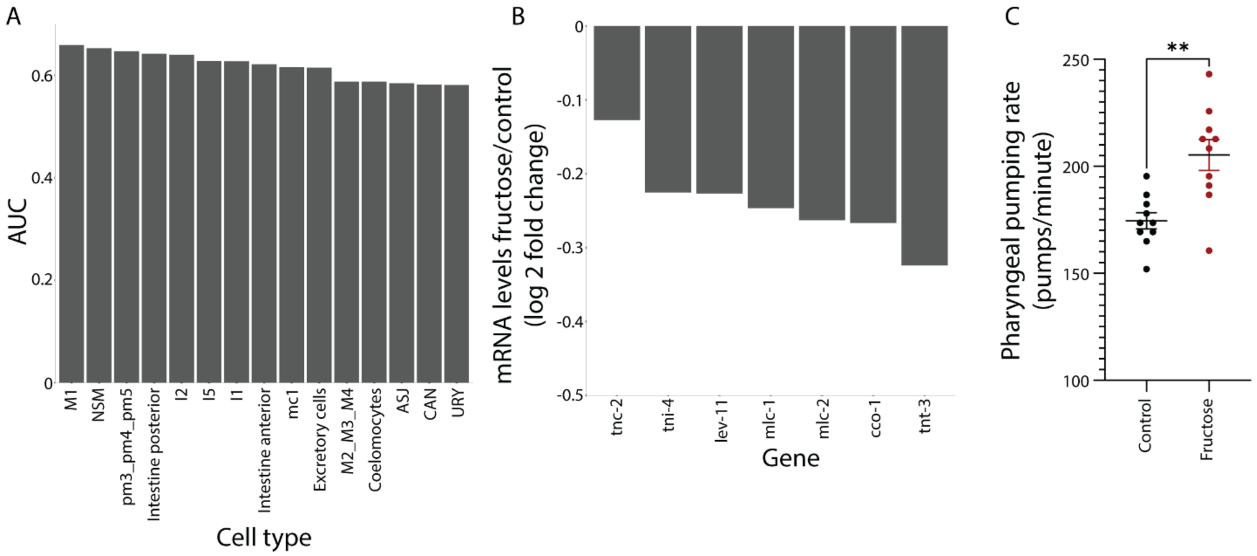

Figure 6. Excess fructose consumption results in changes to pharyngeal pumping in *C. elegans*. (A) Augur analysis reveals that cell types associated with pharyngeal function are among the most responsive to excess fructose consumption. **(B)** Several genes involved in the pharyngeal pumping are downregulated in pharyngeal muscle cells. **(C)** Pharyngeal pumping is increased in worms in fructose-fed worms.

Identifying differentially expressed genes associated with human disease

Finally, we wanted to determine whether any of the differentially expressed genes identified in DIO *C. elegans* scRNA-Seq data were associated with human disease. First, we used a previously published list of human genes found to be associated with obesity in GWAS studies[22]. We then identified *C. elegans* orthologs of these genes using Ortholist 2[31]. We found 70 unique genes associated with human obesity in GWAS studies differentially expressed in our DIO scRNA-Seq data. This subset of hits included genes differentially expressed across several cell types such as *cpn-4*/TAGLN (20 cell types), *pck-2*/PCK1 (20 cell types), *alh-1*/ALDH2 (18 cell types), and genes differentially expressed in a single cell type (48/70 genes). Out of the 70 genes associated with human obesity that are differentially expressed in the scRNA-Seq data, we also identified 11 genes that have been experimentally validated to play a role in fat accumulation in

C. elegans[22,25]. Out of the 11 genes, 7 genes were differentially expressed in the expected direction. We found that *gon-1*/ADAMTS9, *nhr-64*/HNF4G, and *mtch-1*/MTCH2, which are associated with human obesity and promote fat reduction in *C. elegans*, were downregulated in the posterior intestine. We also found *ard-1*/HSD17B downregulated in the coelomocytes, another gene that promotes leanness in *C. elegans*. On the other hand, *rpt-5*/PSMC3, *let-767*/HSD17B12, and *hsp-4*/HSPA1B, which promote fat accumulation, were upregulated in DIO worms. We found *rpt-5* upregulated in the mitotic germ cells, *let-767* in the oocytes and *hsp-4* in the coelomocytes, SIA neurons, and ASH neurons.

We also identified human orthologs of all our differentially expressed genes using Ortholist2 and then used DisGeNET[32] to identify those genes that were associated with human disease. We found over 334 unique differentially expressed genes that are associated with human disease in the DisGeNET database including 53 genes associated with human obesity. We also found 79 genes associated with Alzheimer's disease and 205 genes associated with cardiovascular disease, two diseases that show increased incidence in humans with obesity. Further investigation into the genes that are differentially expressed in response to excess dietary fructose in *C. elegans* and that are associated with human disease (e.g. Alzheimer's and cardiovascular disease) could reveal the molecular changes that link excess fructose consumption and/or diet induced obesity to obesity-associated diseases.

Discussion

Obesity in its most common form, diet-induced obesity (DIO), is a complex disease involving many genes and cell types and is associated with systemic changes across the whole body of the organism. To begin elucidating, with single-cell resolution, the molecular changes that link excess sugar consumption to fat accumulation and obesity, we here present the single-cell transcriptional atlas of regular-fed worms and worms fed excess fructose, which causes DIO. We identify thousands of common and tissue-specific differentially expressed genes and differentially activated transcriptional programs. We use publicly available databases to identify differentially expressed genes that have been experimentally validated to play a role in the regulation of fat content. These genes would be prioritized for future testing, to determine whether they play a role in linking excess fructose consumption to fat accumulation and disease. Additionally, in combination with tissue-specific genetic manipulation available in *C. elegans*, the scRNA-Seq data of DIO worms can provide information about the specific tissues in which these genes mediate the development of obesity. We also use human disease databases to identify differentially expressed genes associated with human disease. Follow-up studies will be necessary to discern the gene expression changes directly responsible for fat accumulation, from those that are caused by fat accumulation and those that are responsible for obesity-related diseases such as lifespan reduction and neurodegeneration. For example, whole-body and tissue-specific gene knockdown screens can be set-up to determine which genes are involved in fat accumulation using oil red o fat staining, lifespan reduction through aging assays and neurodegeneration through chemotaxis assays. Therefore, by combining our scRNA-Seq data, with *in vivo* experimental data, and human disease data, it could be possible to infer, tissue-specifically, the molecules linking excess fructose consumption to fat accumulation to disease development.

The limitations discussed below, including the correlation between cluster size and number of differentially expressed genes and rate of false positives in the identification of differentially expressed genes, should be considered in the interpretation of the DIO-related changes presented below. However, we don't anticipate that they will fundamentally change the conclusions presented here. That is because the conclusions are not solely based on the tissue-specific activation of a single gene. We show that groups of genes involved in protein translation, mitochondrial respiration, and vitellogenin-production are activated in response to excess fructose consumption. Additionally, we not only find tissue-specific activation of these processes, but we also find evidence that the same processes may be inactivated in other tissues. This suggests that there are tissue-specific changes in these processes in response to obesogenic condition. Nonetheless, it is important to recognize that follow-up studies are required to confirm these observations.

DIO may be causing widespread changes to protein translation

Protein translation and ribosomal biogenesis are both energy intensive processes [33]. It is therefore not surprising that protein translation is closely linked to the nutrient status of the cell [34,35] with nutrient-sensing proteins such as mTOR[36] and AMPK playing a major role[37]. Here we find that the excess availability of fructose is no exception. We find that worms fed a fructose-rich diet exhibit widespread changes to the expression of ribosomal genes across cell types. However, not all cells respond the same way. We find that in most cell types, ribosomal gene expression was decreased, while in the intestine and pharynx, ribosomal gene expression was increased. The results suggest that while in most cell types, protein translation is decreased in response to excess dietary fructose, in the intestinal and pharyngeal cells protein translation may be increased. Interestingly, the cell types that show increased protein translation are also among the cell types that are transcriptionally most responsive to excess fructose consumption (Fig. 6A).

Our observations that DIO likely affects ribosomal biogenesis and protein translation in a tissue-specific manner are supported by several mouse studies. For example, Sitnick *et al* and Hatanaka *et al.* have shown that mice fed a high fat diet have reduced protein translation in the muscle[38] and pancreatic islet cells[39], respectively. In accordance with reduced protein translation, we also see a decrease in ribosomal gene expression in the non-pharyngeal muscle cells of *C. elegans*. A leading hypothesis that could explain how a high fat diet can cause reduced protein translation is through ER stress[40,41]. Excess supply of lipids results in ER dysfunction due to excess demands on the organelle[41]. This leads to a buildup of improperly folded proteins which causes the cell to respond by altering regulatory pathways to inhibit protein synthesis [41]. This inhibition is largely driven by the phosphorylation of eukaryotic translation initiation factor 2α (EIF2α) which directly inhibits protein translation. It remains unclear whether the decrease in protein translation observed in the worms fed a high fructose diet is also driven by ER stress. This could be explored using transgenic reporters of ER stress which would allow us to determine the status of the ER in a cell type specific manner. Additionally, it is important to note that the mechanism of direct protein translation inhibition through EIF2α phosphorylation cannot fully explain the predicted decrease in translation observed in our worms since it doesn't explain the observed decrease in the expression of ribosomal genes. Therefore, there could be alternative mechanisms mediating decreased protein translation in response to excess fructose consumption. On the other hand, it is noteworthy that in some cell types including the intestine, the data suggests that protein translation is increased. This is supported by proteomic analysis of the small intestine mucosa of mice fed a high fat diet[42] which suggests that proteins involved in protein translation are increased. It would be interesting to explore the reasons for these tissue-specific differences. Are the intestinal and pharyngeal cells not as susceptible to high fat diet-induced ER stress? Or are they experiencing ER stress but their important role in the response to fructose overconsumption prevents a decrease in protein translation? Additionally, it is unclear what mechanism is mediating the fructose-dependent increase in protein translation in these tissues. One possibility is that the activation of protein translation in response to nutrient availability is mediated by the central nutrient-sensing protein, mTOR which is known to activate protein translation [36]. It is also unclear what role the tissue-specific changes to protein translation play in the development of DIO and associated diseases. This could be explored using broad inhibitors of protein translation and measuring DIO outcomes such as fat accumulation, lifespan determination and neurodegeneration.

DIO may be causing widespread changes to mitochondrial respiration

Mitochondrial dysfunction is a well-studied characteristic of obesity caused in part by the excess availability of nutrients[43]. Here we find that excess fructose consumption causes changes to the expression of various genes involved in mitochondrial respiration. However, similar to the changes in ribosomal expression, mitochondrial genes were also differentially expressed in a tissue-specific manner. In several tissues including intestinal cells and germ cells, we found that three classes of genes involved in mitochondrial respiration (*nduo*/*ndfl*, *ctc*, *atp/asb*) were upregulated suggesting that mitochondrial respiration is increased in these tissues. However, in most cell types we found gene-dependent changes in expression where some genes involved in mitochondrial respiration were increased or decreased and others were changing in the opposite direction or were unchanged. It is therefore unclear what the status of mitochondrial respiration is in those cell types. Previous studies had shown that high fructose diet can cause a decrease in the protein levels of several genes involved in mitochondrial respiration[44]. This is accompanied by impaired mitochondrial morphology, density, and respiration[44].

The potential tissue-specific role of mitochondrial function and dysfunction in the presence of excess fructose warrants further examination. In general, studies have focused on mitochondrial dysfunction in obesogenic conditions[43], however, the results presented here suggest that not all cell types are undergoing the same kind of changes to the mitochondria. Nonetheless, additional experiments are necessary to elucidate the status of the mitochondria in fructose-fed worms in a tissue-specific manner. The use of transgenic lines carrying mitochondrial markers will help determine, tissue-specifically, the changes in mitochondrial density and morphology in response to excess fructose consumption. Similarly, the use of probes such as MitoROS, MitoSOX and MitoTracker may help examine mitochondrial function and dysfunction in a tissue-specific manner.

DIO causes changes to C. elegans fertility

Nutrient availability plays an important role in the regulation of animal reproduction [45–47]. Starvation can cause severe reductions in germ cell production, while the presence of key nutrients, including fructose can increase germ cell proliferation [48]. On the other hand, studies have shown a clear relationship between obesity and reduced fertility in both men and women [10,49]. Here we show that in DIO worms, drastic changes to the expression of genes involved in nutrient transfer to the germ line occur. In wild type worms fed a regular diet, the vitellogenin proteins, a family of yolk proteins, are produced and secreted by the intestine where they recruit lipids and other nutrients [26]. These nutrient-loaded proteins are then taken up by the oocytes to provide nutrients for the developing embryos [26]. Here we report that in the fructose-fed worms, the expression of vitellogenin genes is downregulated across the board in intestinal cells and upregulated in the oocytes. At the same time, the oocytes are downregulating the expression of the receptor mediating the entry of the vitellogenin proteins, *rme-2*. This suggests that in obesogenic conditions, vitellogenin production in the intestine is halted or decreased while at the same time the uptake of vitellogenin proteins by oocytes is decreased. On the other hand, the production of vitellogenin proteins appears to be increased in the oocytes. The reason for this shift remains unclear. One hypothesis is that nutrient stores in the oocytes are tightly regulated. When they reach maximum capacity, the oocytes signal to the intestine to halt the release of nutrient-carrying proteins, decreases the uptake of these proteins and increases the production of nutrient-carrying proteins, potentially to release some of the excess nutrients to its surroundings. An observation that supports the idea that this shift in the production and release of vitellogenin proteins is not necessarily negative, is the fact that fertility rates in worms fed excess fructose appears to be higher than that of worms fed a regular diet. Another hypothesis is that obesogenic conditions cause dysregulations in the production and release of vitellogenin proteins. Nonetheless, additional experiments need to be carried out to determine the full effect of this shift on reproduction. An important role for the vitellogenin proteins is to not only provide nutrients for germ cell development, but also nutrients for the next generation of worms [26]. Specifically, in times of starvation, these stores of nutrients allow the progeny to survive for longer periods of time. It would therefore be interesting to look at the effect of the obesogenic diet of the adult hermaphrodite on the fat content of the progeny and their ability to survive starvation. This could be performed in wild type worms and worms carrying mutations in the vitellogenin genes or upstream regulators that are required for the production of vitellogenin proteins. On the other hand, the fact that the oocytes are producing and potentially releasing nutrient-loaded vitellogenin proteins to their surroundings could suggest an increase in ectopic fat, a known characteristic of DIO. It would therefore be interesting to assess the levels of ectopic fat or ectopic yolk proteins in worms grown in obesogenic conditions.

DIO causes changes to feeding behavior

An important contributor to the obesity epidemic is the addictive nature of sugar [50]. This is likely an adaptive feature that may have been critical for survival when nutrient availability was limited[50]. However, in the modern era, where food with high fat and high sugar content is readily available for most people combined with a sedentary lifestyle, this evolutionary feature has become a bane. Additionally, animal studies have shown that sugar addiction may not be exclusive to humans[12]. Here, we find evidence that sugar may influence the feeding behavior of worms. We find that *C. elegans* fed a fructose-rich diet increase pumping rates suggesting that the presence of fructose causes physiological changes that encourage the worm to eat more of it. Interestingly, the pharynx and the neurons involved in regulating its functions are among the most responsive cells to excess fructose consumption. However, the transcriptional evidence suggests that the presence of fructose reduces pumping rates with many genes involved in pharyngeal pumping downregulated. This discordance between the genetic and physiological evidence suggests that there’s some critical information missing in the link between excess sugar consumption and pharyngeal function. One possible explanation is that although mRNA levels of the genes involved in pumping are reduced, protein levels may be increased. In interpreting transcriptomics data, it is important to keep in mind that the correlation between mRNA and protein levels is not necessarily high [51–53]. A supporting piece of evidence for the hypothesis that protein levels of these genes are increased even though their transcripts are reduced is the observation that ribosomal-encoding genes are upregulated across the board in pharyngeal cells including pharyngeal muscle cells. To confirm this hypothesis, however, transgenic strains of the genes of interest would need to be generated and analyzed. Additionally, we find that neurotransmitters involved in increasing pumping rates downregulated in the pharyngeal neurons while neurotransmitters involved in decreasing pumping rates are upregulated in those neurons.

Given that we observe increased pumping in response to excess fructose consumption, the evidence suggests that while some pharyngeal neurons are attempting to signal to the pharynx to decrease pumping rates, the pharynx is not responding. One possibility is that the pharyngeal muscle cells are decreasing the expression or presentation of receptors involved in binding to these neurotransmitters and as a result are not responding to these signals. Another possible explanation is that the pharynx is receiving pro-pumping signals from other neurons. Single-neuron laser ablations may help determine the role of neurons in regulating the pumping rates of worms in the presence of fructose. One important neuron that could link excess fructose availability to changes in feeding behavior is the NSM. In the Augur analysis, NSM neurons are the second-most responsive cells to excess fructose consumption. These pharyngeal, serotonergic, neurons have been suggested to play an important role in signaling the presence of food to the rest of the body[28] and could be involved in linking fructose availability to physiological changes in *C. elegans*. Specifically, NSM neurons have been shown to play a role in glucose-induced reinforcement[28] and could mediate similar changes to the feeding behavior of the worm in response to excess fructose consumption.

Altogether, the results presented here demonstrate the large number of hypotheses that can be made from the datasets and tools generated by this study. We have made hundreds of predictions, some supported by human data, about the potential role of various genes and tissues in linking excess fructose consumption to obesity and obesity-related diseases such as Alzheimer’s and cardiovascular disease that are awaiting to be experimentally validated. We also show how this single-cell compendium can be used to understand the physiological and behavioral changes associated with DIO. We expect this single-cell transcriptional atlas, together with the abundant tools available to manipulate *C. elegans* in a single-gene, single-cell manner, to advance our understanding of the molecular changes that link obesogenic conditions to the development of the disease.

Limitations

An important limitation that should be considered when interpreting some of the results presented here is the strong positive correlation between the number of cells in a cell type and the number of differentially expressed genes identified (Fig. 3C). This is likely because the higher the number of cells, the more power there is to statistically identify differentially expressed genes. However, it is also noteworthy that there are cell types with relatively low number of cells that have an unusually large number of differentially expressed genes (e.g. intestine posterior) and cell types with high number of cells that have an unusually low number of differentially expressed genes (e.g. mature sperm) (Fig. 3C). Therefore, our observation, for example, that the intestine posterior is a highly metabolically active cell type in the DIO condition cannot simply be explained by the number of cells available. On the other hand, if a differentially expressed gene is only identified in a larger cell type, we cannot confidently claim that it's only differentially expressed in that cell type since this "specificity" could be driven by the large number of cells. A potential solution to this issue would be to simply look at the fold change in the expression of this gene to determine whether there's any evidence that it's differentially expressed in a smaller cell type. This would be an appropriate solution if the correlation between cell number and differentially expressed gene number is due to statistical power. It is also important to recognize that this is less of a problem for genes that are found to only be differentially expressed in smaller cell types. We must also note that the Augur analysis presented in Figure 6A (Appendix Table S4) accounts for cell number when calculating the "responsiveness score". Therefore, if the goal is to determine which cell types are most responsive to excess fructose consumption, instead of looking at the total number of differentially expressed genes per cell type, it may be more appropriate to use the results of that analysis.

Another potential limitation that should be considered is the method used to identify differentially expressed genes. Although several tools have been developed to analyze differential gene expression in scRNA-Seq data, there is still no consensus on the best approach[54]. Here we use Monocle3's fit_models function which uses a generalized additive model to identify differentially expressed genes. A study comparing various scRNA-Seq differential gene expression tools found that while Monocle's tool is the most sensitive in identifying true differentially expressed genes (sensitivity = 0.765 True Positives/1000 Gold Standard), it is also more prone to type 1 errors (false positive rate = 0.126 False Positives/False Positive + True Positive)[55]. The same study suggests that while their sensitivity in identifying differentially expressed genes is lower (e.g. DESeq2 sensitivity = 0.695 and edgeR sensitivity = 0.58), pseudobulk approaches are less prone to type 1 errors (e.g. DESeq2 false positive rate = 0.003 and edgeR false positive rate = 0). Similarly, a more recent study suggests that pseudobulk tools for the identification of differentially expressed genes are more suitable due to their low false positive rate[56]. Nonetheless, questions remain about their sensitivity and ability to identify true positives[57]. We ran differential gene expression analysis using both edgeR and DESeq2 using the Libra package[56]. We found a significantly lower number of differentially expressed genes using the pseudobulk tools. Using edgeR we were only able to identify 334 differentially expressed genes, of which 231 genes were unique, and using DESeq2 we were able to identify 31 differentially expressed genes, of which 15 genes were unique. Many genes that we found to be differentially expressed using Monocle3's tool and that are known to play a role in fat metabolism (e.g., the *fat* genes) were not identified as differentially expressed using the pseudobulk approaches. This suggests that the significant difference in the number of differentially expressed genes identified is not necessarily due to the lower number of false positives and it is more likely that we are missing many true positives using the pseudobulk methods. For this reason, we decided to proceed with the Monocle3 analysis. However, it is important to note that follow-up studies (smFISH, RNAScope…) are always needed to confirm the results of the differential gene expression analysis.

Materials and Methods

C. elegans strains and husbandry

C. elegans N2 (Bristol, UK) was obtained from the Caenorhabditis Genetics Center (CGC). Worms were maintained at 20°C on NGM plates seeded with *E. coli* strain OP50.

Sample preparation and scRNA-Seq

Samples were prepared as previously described (Chapter 3 Materials and Methods) with one modification: synchronized L1 worms were either grown on NGM plates seeded with HT115 (regular-fed worms) or NGM plates seeded with HT115 and filter-sterilized 55mM fructose (fructose-fed worms).

The scRNA-Seq data was processed as described in Chapter 3 (Materials and Methods).

Differential gene expression analysis

To identify differentially expressed genes in DIO worms, we used Monocle3's [24] fit_models function which identifies differentially expressed genes by fitting a regression model to test whether a particular gene changes its expression in response to a treatment:

$$\log(y_i) = \beta_0 + \beta_1 x_1$$

Where y_i is the expression level of the gene, x_1 is the condition (i.e. fed a normal diet or fed a fructose rich diet), and β_1 is the effect of the treatment on the expression. For every gene, the algorithm will generate a q-value that will indicate whether the effect size β_1 is statistically significant or not. We considered differentially expressed genes with a q-value of less than 0.05 as statistically significant.

We also performed differential gene expression analysis using edgeR-LRT and DESeq2-LRT which are both available from the Libra package.

Inferring differentially active transcriptional regulators

To identify, tissue-specifically, TFs that are differentially active in fructose fed worms we generated a gene by cell-type matrix for each condition and then performed correlation analysis, as previously described (Chapter 3 Materials and Methods), between TF binding patterns as defined by ChIP-Seq and single-cell gene expression profiles as defined by scRNA-Seq.

Gene ontology term enrichment analysis

GO term enrichment analysis was performed using Wormbase's [25] Gene Set Enrichment Analysis run with the default q-value threshold = 0.1.

Fertility assay

Fertility assay was performed as previously described in Chapter 2 Materials and Methods with one modification: synchronized L1 worms were either grown on NGM plates seeded with HT115 (regular-fed worms) or NGM plates seeded with HT115 and filter-sterilized 55mM fructose (fructose-fed worms).

Pharyngeal pumping assay

Synchronized L1 worms were either grown on NGM plates seeded with HT115 (regular-fed worms) or NGM plates seeded with HT115 and filter-sterilized 55mM fructose (fructose-fed worms). Once they've reached the L4 stage, one-minute videos of the worms were taken using an Olympus SZX7 microscope fitted with an Olympus U-CMAD3 camera.

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Chapter V: Conclusion

I here present three different projects with the goal of advancing our understanding of the molecular networks that drive organismal health and disease. In the first project, we examine the role of a single gene, encoding the alcohol dehydrogenase, *adh-1* in promoting longevity across interventions and potentially across organisms. In the second project, we use single-cell RNA-Seq in combination with various tools and datasets, to determine, with single-cell resolution, the molecular networks responsible for basal cellular function, maintaining cellular identity, and mediating intercellular communications. Finally, in the third project, we present the single-cell transcriptome of worms fed a regular diet and worms fed a fructose-rich diet. We use this single-cell compendium of gene expression in combination with publicly available experimental data and human disease data to begin elucidating the molecular networks that link excess sugar consumption to fat accumulation and obesity.

The role of alcohol dehydrogenase and fat metabolism in the development of aging and obesity

An unexpected discovery that came from these divergent projects is the seemingly important role that alcohol dehydrogenase plays in fat metabolism, specifically in the context of aging and obesity. As previously mentioned, we discovered that the alcohol dehydrogenase encoding gene, *adh-1*, plays a necessary and sufficient role in lifespan extension. However, an unexpected observation was the fact that *adh-1* may also be a potent mediator of fat metabolism. We found that not only is *adh-1* required for the reduced fat levels observed in other long-lived *C. elegans*, such as *mxl-3* mutants and HLH-30 overexpressing worms, ADH-1 overexpression is also sufficient in reducing fat levels. Additionally, we find that ADH-1 co-localizes with lipid droplets supporting the hypothesis that it plays an important role in lipid metabolism. ADH-1's role in regulating fat content may occur, at least in part, through the metabolism of the major triglyceride component, glycerol. This is an interesting finding since most of the studies linking fat metabolism and aging have focused on the buildup of fatty acid and the subsequent lipotoxicity. These studies have largely ignored the fact that glycerol may also be toxic at elevated levels as shown in this study. One potential hypothesis linking glycerol buildup to aging is by promoting the formation of methylglyoxal which is known to cause proteostasis dysfunction [1–4]. It has also been suggested that glycerol may reduce lifespan by downregulating the expression of the gene *aqp-1* that is thought to activate the pro-longevity transcription factor, *daf-16* [5]. Ultimately however, glycerol is a central metabolite that can readily enter core biochemical pathways [6], including gluconeogenesis, so its role in aging may be much more complex. Additionally, it remains unclear whether *adh-1* regulates fat content by modulating glycerol levels as speculated or whether there are additional mechanisms underlying *adh-1*'s role in fat metabolism.

Interestingly, our scRNA-Seq analysis of DIO worms similarly reveals a potential role for *adh-1* in regulating fat content. We find that *adh-1* is upregulated in 21 cell types in response to excess fructose consumption, one of the most responsive genes. This does not only support a role for *adh-1* in fat metabolism but may also point to a potential role for *adh-1* in DIO. It would therefore be interesting to test whether whole-body or tissue-specific *adh-1* knockout can break or exacerbate the link between excess sugar consumption and fat accumulation. Based on the results presented in the aging project, we would expect that the observed upregulation of *adh-1* is associated with the breakdown of fat. Therefore, mutation of *adh-1* should theoretically lead to increased fat content and obesity. Similarly, it may be worth testing whether ADH-1 overexpressing animals are less susceptible to fat accumulation after excess fructose consumption. The link between *adh-1*, fat metabolism, aging and potentially obesity warrants further dissection, especially given the known relationships between these different processes.

The conserved role of *adh-1* in longevity across interventions and in *C. elegans* and yeast suggest that it may play a role in lifespan determination across organisms including humans. However, this needs to be experimentally tested. The next step would be to confirm that *adh-1* orthologs can promote lifespan using cell line models of aging as well as mice models. Additionally, if it turns out that *adh-1* does play a role in *C. elegans* DIO, it would be interesting to test whether it similarly plays a role in mammalian obesity. Finally, to be able to translate these findings into potential interventions, it would be important to identify safe chemicals that can activate this gene at the transcriptional, translational, or post-translational level.

A systemic approach to elucidate the genetic networks driving aging and obesity

Traditionally, biologists have taken a reductionist approach to deal with the overwhelming complexity of biological systems [7]. This approach relies on taking the pieces of the system apart and studying them in isolation [7]. The underlying assumption of the reductionist approach is that simplifying the problem by studying the system in parts will provide us with insight on the functioning of the whole system. However, recent technological advances, particularly in the fields of omics and single-cell omics and the computational tools that came along with them have opened the door to a different approach to the study of systems. This approach, in theory, treats the system as an integrated network of genes, proteins and biochemical processes and provides a more holistic approach to the study of biological systems [8]. The reason a systemic approach is necessary to understand biological systems is because the role of molecules in generating phenotypes is often context dependent [8].

Although there are several examples in the literature, some of the results presented here reinforce this idea. We find that the same process (e.g. expression of ribosomal genes) in response to the same perturbation (e.g. excess fructose consumption) will respond differently depending on the cell type (e.g. increase in the intestine and decrease in the muscle). This highlights the importance of context in the function of molecules and emphasizes the importance of studying the system as an integrated network rather than isolating its different parts and studying them out of their appropriate context.

The projects presented here also highlight the ability of omics datasets in facilitating our ability to identify molecular drivers of disease. For example, we show how the integration of various omics datasets (ChIP-Seq, proteomic, transcriptomic) led us to the identification of a critical mediator of longevity that acts downstream of multiple pro-longevity interventions and is sufficient to promote lifespan extension. However, our study also highlights why follow-up experiments are necessary to take full advantage of these omics datasets.

Finally, we also show how single-cell transcriptomic analysis combined with computational tools and publicly available *in vivo* experiments can generate hundreds of hypotheses about the relationship between the regulatory and genetic networks of cells, and their functional and morphological identities, their intercellular communications, and the dysfunctions that can lead to their breakdown. Follow-up studies will be invaluable in investigating these hypotheses and in advancing our understanding of the molecular changes that drive disease.

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Appendix

Appendix Table S1. Number of cells per cell type for each condition.

cell_type	fructose	no_fructose
pm3_pm4_pm5 (pharyngeal muscle)	4168	1652
ADA	98	92
ADF	73	75
ADL	404	346
AFD	144	121
AIA	291	217
AIB	664	392
AIM	222	189
AIN	244	199
AIY	107	94
ALA	131	97
Amphid sheath	1007	790
Anal muscle	191	154
Apoptotic germ cells	7878	6536
Arcade cells	1297	699
AS_DA_DB_VA_VB_SAB	2429	1707
ASE	148	135
ASG	175	120
ASH	134	167
ASI	213	151
ASJ	132	144
ASK	167	160
AUA	98	72
AVA	528	320
AVB	516	367
AVD	487	355
AVE	372	297
AVF	73	88
AVG	104	58
AVJ	315	262
AVK	325	228
AVL	284	171
AWA	145	176
AWB	121	164
AWC	160	156
BAG	290	262
BDU	163	136

Body wall muscle anterior	2059	2046
Body wall muscle middle	11638	7915
Body wall muscle posterior	1069	806
CAN	176	214
cat-4(+)ptps-1(+) intestine anterior	3696	3947
CEP_ADE_PDE	210	214
Cephalic and inner labial socket	1023	829
Cephalic sheath	1764	1254
Coelomocytes	2560	1956
Differentiated germ	12014	11423
Distal tip	833	506
Dorsal uterine cells	658	559
DVA	48	33
DVC	43	26
e1_e3 (pharyngeal epithelium)	2116	1290
e2 (pharyngeal gland)	1047	426
Embryonic cells	91	106
Excretory cells	637	513
Excretory duct	1113	966
Excretory gland	290	327
g1A (pharyngeal gland)	76	34
g1P (pharyngeal gland)	1010	483
g2 (pharyngeal gland)	477	203
Glia_1	450	210
Glia_2	228	148
GLR	220	282
hmc	295	193
HSN	309	154
hyp4_to_hyp6	15487	8817
hyp7 (hypodermis)	4955	3371
Hypodermis-Gonadal sheath doublet	1288	927
Hypodermis head	534	441
Hypodermis tail	93	89
I1	107	59
I2	77	41
I5	123	87
IL2	216	167
Intestine-Gonadal sheath doublets	1325	1230
Intestine anterior	325	759
Intestine middle	5868	3104
Intestine posterior	1529	3038
M1	113	55

M2_M3_M4	411	272
M5	192	104
Mature sperm	15922	12272
mc1 (marginal cells)	1458	552
mc2_mc3 (marginal cells)	623	277
Meiotic germ cells	4492	3405
MI	188	91
Mitotic germ cells	28913	18370
NSM	24	20
OLQ	127	135
Oocytes	9725	6104
PDA	41	30
PHA_PHB	89	60
Phasmid socket	167	120
PLM_ALM	462	340
pm1_pm2 (pharyngeal muscle)	751	263
pm6_pm7 (pharyngeal muscle)	1146	333
PVD_FLP	143	101
PVM_AVM	388	270
PVN	39	25
PVP	81	57
PVQ	80	56
PVR	123	83
PVW	106	76
Rectal gland	129	74
RIA	231	166
RIB	266	207
RIC	286	199
RID	258	191
RIF	87	75
RIG	130	93
RIH	145	113
RIM	148	87
RIR	128	110
RIS	111	84
RIV	263	187
RMD_DV	350	266
RME	105	105
RMF	97	85
RMG	108	96
RMH	328	272
SDQ	112	78
Seam cells (bus+)	1058	704

Seam cells (grd+)	2170	1623
Seminal vesicle (male)	26	32
sh1 (gonadal sheath distal)	3383	4695
sh2 (gonadal sheath distal)	8707	8338
sh3_sh4 (gonadal sheath proximal)	4360	4125
sh5 (gonadal sheath proximal)	679	481
SIA	827	619
SIB	1145	779
SMB	84	16
SMB_PLN_ALN	1205	759
SMD	1040	819
Spermatheca-Uterine junction	899	594
Spermatheca bag distal	579	401
Spermatheca bag proximal	1950	1389
Spermatheca neck distal-most	989	741
Spermatids	1525	1435
Spermatocytes	1369	1168
URA	89	84
URB	39	23
URX_AQR_PQR	157	137
URY	51	52
Uterine-vulval cells	897	698
Uterine muscle	591	322
Uterine seam cells	527	336
Uterine toroid	146	139
uv1 (uterine-vulval cells)	111	67
VC	586	394
VC_4_5	109	49
VD_DD	1204	955
vm1 (vulval muscle)	763	346
vm2 (vulval muscle)	504	385
Vulval cells	596	352
XXX	83	73

Appendix Table S2. List of differentially expressed genes (q-value < 0.1) and the cell types in which they are differentially expressed. log2FC = log2 fold change(fructose/control)

column_label	gene_short_name	log2FC	q_value
ADF	flp-21	-1.220573649	0.056527626
ADL	R102.2	-0.76837344	5.36341E-06
ADL	ctc-1	0.557567042	5.53211E-05
ADL	ctc-3	0.544338574	0.00012434
ADL	flp-5	-0.98459882	0.000290691
ADL	col-119	1.006341995	0.038195894
ADL	col-20	0.705007747	0.065812069
AIA	ins-28	-0.472398445	2.91202E-07
AIA	F41E7.7	-0.860487957	0.005518532
AIA	msp-152	-0.120909616	0.082260275
AIB	msp-31	-0.431814844	1.30604E-06
AIB	rpl-41.2	-0.414808158	7.09895E-06
AIB	msp-40	-0.422146836	9.03429E-05
AIB	smgl-2	-1.765534746	0.000688457
AIB	T06E4.14	-1.765534746	0.000688457
AIB	hsp-110	0.573724047	0.004812933
AIB	msp-152	-0.390866943	0.009379273
AIB	rpl-39	-0.61937294	0.013396671
AIB	nspd-2	-0.107420266	0.031758472
AIB	hsp-16.41	0.627360019	0.034012146
AIB	Y43F8B.2	0.441785713	0.039862376
AIB	rpl-38	-0.417731543	0.058030945
AIB	msp-51	0	0.070428103
AIM	C05E7.2	4.196397213	1.77945E-36
AIN	ins-28	-0.524285957	8.47334E-10
AIN	C35C5.8	-2.807354921	5.13465E-05
AIN	ctc-3	0.565085083	0.036947544

AIN	msp-152	-0.579167872	0.092896412
AIN	rpl-41.2	-0.483478943	0.099574181
ALA	col-88	2.321928095	0.00017948
ASE	gcy-1	-2.966391607	2.92862E-05
ASH	R102.2	-0.71437501	1.39536E-09
ASH	ZK856.6	2.054309986	5.12718E-08
ASH	cyp-36A1	2.049135345	1.3436E-05
ASH	C27A7.8	1.66564136	0.000189174
ASH	F22B5.4	-0.92255025	0.000204994
ASH	C10C5.7	-0.574146495	0.000480872
ASH	lap-2	0.859895468	0.00097847
ASH	T02C12.5	-1.445098732	0.001005592
ASH	nlp-50	-0.839326774	0.005437222
ASH	sbt-1	-0.434730589	0.008643503
ASH	hsp-4	1.673904818	0.019742125
ASH	fkh-8	1.062035885	0.027053365
ASH	F38B7.3	1.382924942	0.052637138
ASH	F56C4.1	1.824421473	0.092743673
ASH	T05H10.8	1.287668193	0.093124035
ASI	R102.2	-0.466427818	0.002191595
ASI	daf-7	-0.508128607	0.080179941
ASK	C47D2.1	-0.778003481	0.00032769
ASK	F58H10.1	-1.496917641	0.001279249
ASK	F44E7.5	-3	0.001529892
ASK	snet-1	-0.560896086	0.004938364
ASK	flp-5	-0.525483404	0.017448384
AS_DA_DB_VA_VB_SAB	ctc-3	0.455157193	3.72242E-32
AS_DA_DB_VA_VB_SAB	col-122	1.117146224	2.18111E-26
AS_DA_DB_VA_VB_SAB	ctc-1	0.383065499	3.93709E-17
AS_DA_DB_VA_VB_SAB	col-184	0.939227912	3.30876E-16
AS_DA_DB_VA_VB_SAB	col-124	0.57888152	1.91947E-15
AS_DA_DB_VA_VB_SAB	col-119	0.781933436	3.76288E-15

AS_DA_DB_VA_VB_SAB	msp-31	-0.190951154	7.02787E-15
AS_DA_DB_VA_VB_SAB	col-181	0.838776463	1.53052E-14
AS_DA_DB_VA_VB_SAB	col-20	0.592260419	9.42296E-14
AS_DA_DB_VA_VB_SAB	nspd-2	-0.030013721	3.71494E-13
AS_DA_DB_VA_VB_SAB	F22B5.4	-0.586337557	4.34362E-13
AS_DA_DB_VA_VB_SAB	hsp-16.48	-0.513282083	1.24002E-12
AS_DA_DB_VA_VB_SAB	msp-40	-0.131589856	3.47972E-12
AS_DA_DB_VA_VB_SAB	rpl-41.2	-0.302338941	7.09934E-12
AS_DA_DB_VA_VB_SAB	col-140	0.537114683	7.28405E-12
AS_DA_DB_VA_VB_SAB	msp-57	-0.000283577	2.77651E-11
AS_DA_DB_VA_VB_SAB	Y119D3B.21	-0.706945129	6.24242E-11
AS_DA_DB_VA_VB_SAB	C14C6.5	-1.685285841	1.35066E-10
AS_DA_DB_VA_VB_SAB	col-160	1.020668141	5.20145E-10
AS_DA_DB_VA_VB_SAB	msp-45	-0.020723544	5.22077E-10
AS_DA_DB_VA_VB_SAB	col-8	0.973045467	1.64906E-09
AS_DA_DB_VA_VB_SAB	C54D10.3	0.708157782	1.08625E-08
AS_DA_DB_VA_VB_SAB	col-178	0.813734337	1.70041E-08
AS_DA_DB_VA_VB_SAB	rps-28	-0.547609783	1.71243E-08
AS_DA_DB_VA_VB_SAB	C17F3.1	-5.27792E-06	2.46534E-08
AS_DA_DB_VA_VB_SAB	rpl-39	-0.461766968	7.93772E-08
AS_DA_DB_VA_VB_SAB	rpl-38	-0.336258075	9.07703E-08
AS_DA_DB_VA_VB_SAB	dct-16	-0.48553345	2.01025E-07
AS_DA_DB_VA_VB_SAB	msp-3	-0.042570765	2.49103E-07
AS_DA_DB_VA_VB_SAB	col-98	0.905937634	3.15909E-07
AS_DA_DB_VA_VB_SAB	gpd-2	-0.305926354	3.90322E-07
AS_DA_DB_VA_VB_SAB	col-80	0.622641963	5.76362E-07
AS_DA_DB_VA_VB_SAB	rpl-36	-0.275431327	7.55059E-07
AS_DA_DB_VA_VB_SAB	ssp-9	0	9.65311E-07

AS_DA_DB_VA_VB_SAB	msp-78	-0.058971281	1.10618E-06
AS_DA_DB_VA_VB_SAB	msp-152	-0.024579803	1.33646E-06
AS_DA_DB_VA_VB_SAB	col-106	0.732736026	1.66445E-06
AS_DA_DB_VA_VB_SAB	rps-29	-0.394711908	2.19014E-06
AS_DA_DB_VA_VB_SAB	nspd-10	-0.002685389	2.57142E-06
AS_DA_DB_VA_VB_SAB	W01D2.1	-0.371059137	2.94408E-06
AS_DA_DB_VA_VB_SAB	col-19	0.461750453	3.6055E-06
AS_DA_DB_VA_VB_SAB	C05D11.5	0.86478543	9.7691E-06
AS_DA_DB_VA_VB_SAB	msp-33	-0.004407607	2.4592E-05
AS_DA_DB_VA_VB_SAB	spp-5	-0.881389974	2.55282E-05
AS_DA_DB_VA_VB_SAB	msp-51	-0.000136805	3.07382E-05
AS_DA_DB_VA_VB_SAB	rps-27	-0.255828793	3.08695E-05
AS_DA_DB_VA_VB_SAB	col-139	0.423930698	3.79748E-05
AS_DA_DB_VA_VB_SAB	F11E6.3	0.832782714	4.62995E-05
AS_DA_DB_VA_VB_SAB	gst-4	0.911879694	6.93526E-05
AS_DA_DB_VA_VB_SAB	nlp-21	-0.181164176	0.000131062
AS_DA_DB_VA_VB_SAB	R06C1.4	-0.294716143	0.0001468
AS_DA_DB_VA_VB_SAB	ctc-2	0.249678853	0.000152607
AS_DA_DB_VA_VB_SAB	nspd-1	-0.001193396	0.000162848
AS_DA_DB_VA_VB_SAB	T13F3.6	0.968460924	0.000170956
AS_DA_DB_VA_VB_SAB	col-81	0.469203482	0.000225372
AS_DA_DB_VA_VB_SAB	msp-64	-0.142041653	0.000331041
AS_DA_DB_VA_VB_SAB	msp-49	-0.013607858	0.000335476
AS_DA_DB_VA_VB_SAB	far-3	2.686971866	0.000342454
AS_DA_DB_VA_VB_SAB	spp-2	-1.760219513	0.000509207
AS_DA_DB_VA_VB_SAB	rpl-29	-0.564904941	0.000677471
AS_DA_DB_VA_VB_SAB	ssp-11	0	0.000693608
AS_DA_DB_VA_VB_SAB	nduo-1	0.217455581	0.000754741
AS_DA_DB_VA_VB_SAB	hsp-16.2	0.421388599	0.000818139

AS_DA_DB_VA_VB_SAB	rpl-43	-0.235559381	0.000956463
AS_DA_DB_VA_VB_SAB	iff-1	0.504559092	0.001147919
AS_DA_DB_VA_VB_SAB	C13A10.2	-0.521310061	0.001259352
AS_DA_DB_VA_VB_SAB	rps-25	-0.161211281	0.001485022
AS_DA_DB_VA_VB_SAB	rpl-11.1	0.361691812	0.001499551
AS_DA_DB_VA_VB_SAB	H36L18.2	0.295679979	0.001546734
AS_DA_DB_VA_VB_SAB	mig-6	1.746425922	0.001594329
AS_DA_DB_VA_VB_SAB	rpl-34	-0.249455149	0.002156652
AS_DA_DB_VA_VB_SAB	col-143	0.668930691	0.002197725
AS_DA_DB_VA_VB_SAB	aldo-1	-0.223321743	0.002202242
AS_DA_DB_VA_VB_SAB	F48D6.4	-0.814781516	0.002701727
AS_DA_DB_VA_VB_SAB	tni-3	0.357823375	0.002951182
AS_DA_DB_VA_VB_SAB	pud-3	-2.262865648	0.003046846
AS_DA_DB_VA_VB_SAB	gln-3	0.751431679	0.003155148
AS_DA_DB_VA_VB_SAB	F34D10.8	-6.90739E-06	0.003883403
AS_DA_DB_VA_VB_SAB	ZC116.1	2.32031731	0.005990546
AS_DA_DB_VA_VB_SAB	nspa-8	-0.000825863	0.007876573
AS_DA_DB_VA_VB_SAB	F21C10.9	1.369267997	0.008116645
AS_DA_DB_VA_VB_SAB	nduo-6	-0.140135233	0.013598101
AS_DA_DB_VA_VB_SAB	C37A2.7	-0.278731083	0.014177562
AS_DA_DB_VA_VB_SAB	msp-76	-0.121686669	0.017252577
AS_DA_DB_VA_VB_SAB	fip-2	0.440099629	0.018701226
AS_DA_DB_VA_VB_SAB	mdl-1	-0.597907013	0.0207928
AS_DA_DB_VA_VB_SAB	fipr-10	1.638548315	0.025145012
AS_DA_DB_VA_VB_SAB	clec-47	1.837919088	0.030291348
AS_DA_DB_VA_VB_SAB	ckr-2	-0.752467103	0.032865744
AS_DA_DB_VA_VB_SAB	col-129	0.402525884	0.033092496
AS_DA_DB_VA_VB_SAB	cblc-1	-0.735511882	0.033847281
AS_DA_DB_VA_VB_SAB	zig-8	-0.380798647	0.038647061
AS_DA_DB_VA_VB_SAB	hil-5	1.025468869	0.040592882

AS_DA_DB_VA_VB_SAB	sams-1	0.667931848	0.042466528
AS_DA_DB_VA_VB_SAB	F56H9.2	-0.495966056	0.045065304
AS_DA_DB_VA_VB_SAB	msp-56	-2.63068E-05	0.057531316
AS_DA_DB_VA_VB_SAB	ant-1.1	0.154707116	0.059792685
AS_DA_DB_VA_VB_SAB	Y73F4A.3	2.627360241	0.059937397
AS_DA_DB_VA_VB_SAB	enol-1	-0.170568161	0.073360965
AS_DA_DB_VA_VB_SAB	nspd-7	-6.02444E-06	0.083821975
AS_DA_DB_VA_VB_SAB	ZK652.8	0.508223711	0.087492132
AS_DA_DB_VA_VB_SAB	rpl-25.2	0.260437545	0.090359887
AS_DA_DB_VA_VB_SAB	pud-4	-1.807857819	0.092586884
AVA	nlp-57	-0.514280087	5.54281E-06
AVA	F41E7.7	-0.985131003	3.12078E-05
AVA	col-122	1.29269396	6.42627E-05
AVA	flp-18	-0.336434936	7.25382E-05
AVA	acs-2	1.448049408	0.00053559
AVA	acp-6	-0.534936826	0.004444245
AVA	rpl-41.2	-0.392964982	0.008203999
AVA	col-184	1.397250179	0.008518259
AVA	hsp-16.48	-0.450293908	0.009082471
AVA	msp-40	-0.126438873	0.024743729
AVB	hsp-16.48	-0.581764654	5.02181E-08
AVB	rpl-41.2	-0.522426571	2.03335E-07
AVB	K07D4.9	-0.304719782	0.000179803
AVB	rps-28	-0.752334976	0.005077358
AVB	msp-3	-0.413814409	0.009498464
AVB	fipr-2	3.619756993	0.024918718
AVD	rpl-38	-0.473554437	0.000305223

AVD	T23F2.3	-0.970194242	0.00080521
AVD	rps-27	-0.42088886	0.002690385
AVD	ctc-3	0.431437853	0.003800439
AVD	Y76B12C.8	-0.59521076	0.008316286
AVD	T02C12.5	-0.469054282	0.010896552
AVD	xbp-1	-0.508221442	0.012295234
AVD	rpl-39	-0.629127161	0.044317959
AVE	flp-5	-1.426539248	1.22448E-07
AVE	C18A11.2	-0.571929901	5.85219E-06
AVE	nlp-21	-0.295058452	0.00031341
AVE	msp-152	-0.120638979	0.000668874
AVE	col-122	1.213169456	0.002805214
AVE	grl-27	-2.152003093	0.002979188
AVE	nlp-57	-1.36507279	0.003415189
AVE	C44B11.4	-0.344311369	0.020659143
AVF	col-138	-3.94753258	2.88108E-11
AVF	F10E7.2	-2.5849625	0.004034551
AVF	rpl-41.2	-0.786118964	0.097322806
AVG	col-38	-1.736965594	0.0140925
AVG	col-162	1.584962501	0.014527216
AVJ	C39D10.2	-0.692485724	2.71166E-11
AVJ	F13E9.12	-0.751737111	4.13819E-10
AVJ	acp-6	-0.889015077	0.000322048
AVJ	col-65	-1.700439718	0.002760927
AVK	col-119	1.69845122	8.37418E-05
AVK	rpl-41.2	-0.442410773	0.012447567
AVK	col-98	1.930229566	0.021308391
AVK	col-184	1.410961188	0.026091259

AVK	dyf-11	-2.169925001	0.039445244
AVL	hcp-3	-2.289506617	5.42926E-07
AVL	col-122	1.36654554	0.039464801
AWA	T02C12.5	-1.419152857	2.41342E-13
AWA	M02D8.6	-0.988141795	1.28049E-07
AWA	col-91	-3.295455883	3.87274E-07
AWA	F26A10.1	-0.947864797	2.4094E-05
AWA	ins-28	-0.802450661	4.30253E-05
AWA	ins-18	-0.878470899	0.000547819
AWA	oig-8	-0.795640163	0.001259718
AWA	ZC334.13	-0.803171807	0.001791761
AWA	C44B11.4	-0.629275401	0.012663338
AWA	K07C5.9	-1.388164542	0.013951997
AWA	R06C1.4	-0.932616411	0.020399852
AWA	col-184	2.367547907	0.023974227
AWA	col-122	2.32391472	0.037690254
AWA	ins-26	-0.596928505	0.07611564
AWB	F02E11.2	-0.913765198	5.95708E-08
AWB	H17B01.5	-1.247653125	0.000194677
AWB	glb-1	-2.443847427	0.002439887
AWB	C44B11.4	-0.563828002	0.003233166
AWC	F13E9.12	-1.061245348	3.45697E-05
AWC	Y43F8C.11	-1.72447771	0.002015906
AWC	his-37	-0.850855389	0.008686003
Amphid sheath	gst-10	-1.171007769	8.2087E-18

Amphid sheath	K09C6.9	-1.731219027	2.23536E-17
Amphid sheath	F11C7.7	1.490022273	3.51472E-12
Amphid sheath	rpl-41.2	-0.484467291	7.26006E-12
Amphid sheath	C14C6.5	-2.883300257	6.14986E-11
Amphid sheath	T03F1.11	3.038689809	5.18163E-10
Amphid sheath	C12D5.9	-0.92180969	3.45756E-09
Amphid sheath	tnc-2	3.620570869	1.30836E-08
Amphid sheath	T02B11.4	0.737666585	8.88316E-08
Amphid sheath	K01A6.8	1.340527813	2.67025E-07
Amphid sheath	vha-16	0.841970128	6.00582E-07
Amphid sheath	rpl-36.A	-0.399905702	4.92441E-06
Amphid sheath	rps-25	-0.314256146	7.03388E-06
Amphid sheath	hsp-12.2	1.846344225	1.15482E-05
Amphid sheath	K02E11.5	-0.650633784	1.19209E-05
Amphid sheath	ctc-3	0.394651973	1.30529E-05
Amphid sheath	rpl-32	-0.323018372	1.73051E-05
Amphid sheath	rpl-38	-0.450929223	2.13052E-05
Amphid sheath	F41E6.15	2.926939915	3.58773E-05
Amphid sheath	cpn-4	3.048296911	0.00010422
Amphid sheath	C46F11.5	0.834402331	0.000149561
Amphid sheath	C47E12.9	-0.949747977	0.000192057
Amphid sheath	R11D1.3	0.604399542	0.000469411
Amphid sheath	W01D2.1	-0.485614037	0.000495873
Amphid sheath	rps-29	-0.532034659	0.000558304
Amphid sheath	C24A3.2	1.567151823	0.000751204
Amphid sheath	C08F11.1	0.683244223	0.000892143
Amphid sheath	hsp-16.2	1.264011127	0.001322129
Amphid sheath	Y87G2A.19	3.670680361	0.00140504
Amphid sheath	rpl-34	-0.376850244	0.001457944
Amphid sheath	rpl-39	-0.539701235	0.001488511
Amphid sheath	C53C9.2	2.487680183	0.001637956
Amphid sheath	vha-8	0.591641624	0.001661254

Amphid sheath	vha-9	0.593560239	0.001882125
Amphid sheath	F59A7.2	0.804021658	0.002485664
Amphid sheath	rpl-36	-0.331296005	0.002985628
Amphid sheath	gst-4	0.912466906	0.004926437
Amphid sheath	ctc-1	0.340436357	0.005121986
Amphid sheath	cyp-36A1	-0.970655163	0.007175369
Amphid sheath	col-143	0.916426941	0.008834195
Amphid sheath	R09B3.3	-0.374969397	0.011710682
Amphid sheath	rpl-43	-0.339494138	0.012434246
Amphid sheath	F59E11.2	1.338284915	0.016350396
Amphid sheath	Y55B1BL.1	1.169340691	0.020181136
Amphid sheath	F11C7.2	-0.539996987	0.020960251
Amphid sheath	fipr-1	2.998211623	0.026564247
Amphid sheath	gst-28	0.598635223	0.027236179
Amphid sheath	rps-27	-0.323503887	0.03742228
Amphid sheath	vha-11	0.626592666	0.04724673
Amphid sheath	rpl-30	-0.323293652	0.067511877
Amphid sheath	rps-26	-0.255970719	0.093911349
Amphid sheath	sodh-1	1.292397764	0.097204241
Anal muscle	rpl-41.2	-0.577723523	0.072104996
Apoptotic germ cells	col-122	1.083153096	5.6946E-122
Apoptotic germ cells	col-119	0.991241941	1.92138E-95
Apoptotic germ cells	ctc-3	0.362258714	1.16072E-81
Apoptotic germ cells	col-124	0.608658347	9.69816E-76
Apoptotic germ cells	rpl-41.2	-0.347284108	1.06833E-70
Apoptotic germ cells	col-181	0.875108739	6.23988E-70
Apoptotic germ cells	col-184	0.926658401	2.58457E-69
Apoptotic germ cells	col-20	0.651246431	5.48486E-68
Apoptotic germ cells	ctc-1	0.321840696	3.91243E-67
Apoptotic germ cells	col-140	0.618666224	8.71253E-67
Apoptotic germ cells	col-98	1.239833327	9.48255E-63
Apoptotic germ cells	T03F1.11	1.650579055	1.73968E-60
Apoptotic germ cells	col-8	1.23019113	5.86038E-60
Apoptotic germ cells	tnc-2	1.767310533	8.67328E-59
Apoptotic germ cells	col-143	1.061008966	8.12554E-47

Apoptotic germ cells	W01D2.1	-0.373053048	1.42852E-44
Apoptotic germ cells	C06A8.3	0.844461299	2.99065E-44
Apoptotic germ cells	col-103	1.213350483	3.11301E-44
Apoptotic germ cells	sodh-1	1.562506028	3.62658E-44
Apoptotic germ cells	col-19	0.531920384	7.18793E-42
Apoptotic germ cells	col-106	0.879413142	4.57865E-41
Apoptotic germ cells	ZC116.1	2.351537149	6.74544E-41
Apoptotic germ cells	col-80	0.69262049	1.35468E-40
Apoptotic germ cells	rps-25	-0.201424489	1.72245E-40
Apoptotic germ cells	mlc-3	0.482659272	3.2708E-39
Apoptotic germ cells	far-3	2.757730057	1.15899E-38
Apoptotic germ cells	C53C9.2	1.806257452	1.51641E-37
Apoptotic germ cells	C54D10.3	1.190206028	7.66156E-37
Apoptotic germ cells	fipr-1	2.00399624	1.44782E-36
Apoptotic germ cells	pqn-60	2.41163253	3.93451E-36
Apoptotic germ cells	cpn-4	1.503442471	7.31862E-36
Apoptotic germ cells	Y73F4A.2	2.696990238	6.64532E-34
Apoptotic germ cells	rpl-38	-0.30598938	4.7775E-33
Apoptotic germ cells	col-160	0.928009905	1.37917E-31
Apoptotic germ cells	C14C6.5	-1.490160803	3.94852E-31
Apoptotic germ cells	rps-28	-0.443201513	7.40408E-31
Apoptotic germ cells	F11E6.3	0.928473203	8.40979E-31
Apoptotic germ cells	R09B3.2	-0.272439652	9.61932E-31
Apoptotic germ cells	gst-4	0.742228079	4.74399E-30
Apoptotic germ cells	myo-2	2.548834534	2.01273E-29
Apoptotic germ cells	fip-2	1.210556567	1.09089E-28
Apoptotic germ cells	rpl-39	-0.344761602	2.87864E-28
Apoptotic germ cells	fipr-2	2.190681443	8.61934E-28
Apoptotic germ cells	C45G9.6	1.519098335	2.69702E-27
Apoptotic germ cells	col-178	0.747081088	2.95953E-25
Apoptotic germ cells	ctc-2	0.221678857	7.27063E-25
Apoptotic germ cells	rpl-36	-0.206001474	3.88899E-24
Apoptotic germ cells	rpl-36.A	-0.213263895	1.1808E-23
Apoptotic germ cells	T13F3.6	0.912871415	1.19058E-23
Apoptotic germ cells	F15A4.6	0.983119887	1.27862E-23
Apoptotic germ cells	col-101	0.804488869	1.0075E-22

Apoptotic germ cells	ctb-1	0.203667542	1.2851E-22
Apoptotic germ cells	nduo-1	0.204060751	4.80837E-22
Apoptotic germ cells	F41E6.15	1.024504771	1.57341E-21
Apoptotic germ cells	rps-21	-0.33521556	1.62941E-21
Apoptotic germ cells	T20G5.8	0.880130204	2.71113E-21
Apoptotic germ cells	myo-1	2.443100198	5.04011E-21
Apoptotic germ cells	C24A3.2	0.952313736	1.20896E-20
Apoptotic germ cells	his-60	-0.530818316	4.20661E-20
Apoptotic germ cells	vamp-8	1.781430598	2.79622E-19
Apoptotic germ cells	msra-1	1.431106571	9.63861E-19
Apoptotic germ cells	cpr-5	1.132325107	1.04367E-18
Apoptotic germ cells	pud-4	-2.074765368	2.44875E-18
Apoptotic germ cells	ttr-21	1.796573882	2.63663E-18
Apoptotic germ cells	rpl-43	-0.207315623	4.3753E-18
Apoptotic germ cells	pud-3	-1.961048097	7.36047E-18
Apoptotic germ cells	hsp-16.41	1.325131632	1.12691E-17
Apoptotic germ cells	C05D11.5	0.380625259	2.79696E-17
Apoptotic germ cells	fipr-7	2.061320028	2.86309E-17
Apoptotic germ cells	ttr-15	0.564613267	7.12692E-17
Apoptotic germ cells	rpl-34	-0.216098256	7.16452E-17
Apoptotic germ cells	col-81	0.392954428	1.12618E-16
Apoptotic germ cells	dod-6	0.879635771	1.17011E-16
Apoptotic germ cells	col-93	0.480872442	1.44222E-16
Apoptotic germ cells	clec-47	1.999128258	1.45571E-16
Apoptotic germ cells	mlc-2	0.417221199	1.67266E-16
Apoptotic germ cells	col-42	0.736528572	4.76951E-16
Apoptotic germ cells	fipr-5	1.671018019	8.29776E-16
Apoptotic germ cells	Y73F4A.3	2.242198979	1.27864E-15
Apoptotic germ cells	R09B3.3	-0.172754251	1.33054E-15
Apoptotic germ cells	C17F4.7	0.492406633	1.41722E-15
Apoptotic germ cells	asp-2	0.866887579	4.3574E-15
Apoptotic germ cells	fipr-11	2.605175018	7.01757E-15
Apoptotic germ cells	col-129	0.377854664	1.49858E-14
Apoptotic germ cells	hsp-16.2	1.032565848	3.7708E-14
Apoptotic germ cells	rps-12	-0.128698962	4.74896E-14
Apoptotic germ cells	col-139	0.319900825	6.0511E-14

Apoptotic germ cells	dct-16	-0.299981236	1.36273E-13
Apoptotic germ cells	pck-2	0.482438824	1.47455E-13
Apoptotic germ cells	F32A5.4	2.032663983	1.83682E-13
Apoptotic germ cells	K08D12.6	0.649566437	2.9107E-13
Apoptotic germ cells	col-142	0.661323312	2.99205E-13
Apoptotic germ cells	cbd-1	-0.216686812	2.99741E-13
Apoptotic germ cells	hsp-12.2	1.138690869	1.66769E-12
Apoptotic germ cells	F13C5.5	2.423482678	2.12553E-12
Apoptotic germ cells	W10C8.6	1.569522465	2.56969E-12
Apoptotic germ cells	far-2	0.308237315	3.32533E-12
Apoptotic germ cells	atp-6	0.128752243	4.47436E-12
Apoptotic germ cells	fipr-4	1.763023558	5.94424E-12
Apoptotic germ cells	rps-26	-0.149379645	7.79748E-12
Apoptotic germ cells	tni-4	0.961987227	1.57742E-11
Apoptotic germ cells	Y119D3B.21	-0.373323218	1.8403E-11
Apoptotic germ cells	pmt-2	0.413708715	2.5192E-11
Apoptotic germ cells	K03E5.2	0.652341517	2.66925E-11
Apoptotic germ cells	gst-10	-0.732690005	4.15745E-11
Apoptotic germ cells	rps-29	-0.220929261	6.92958E-11
Apoptotic germ cells	rpl-31	-0.147105042	3.1902E-10
Apoptotic germ cells	ttr-2	0.879996476	4.25333E-10
Apoptotic germ cells	ifa-1	1.682631418	4.28757E-10
Apoptotic germ cells	F21C10.9	1.121230283	7.50823E-10
Apoptotic germ cells	nspd-1	-0.406686329	8.83887E-10
Apoptotic germ cells	ttr-27	1.391256682	1.34152E-09
Apoptotic germ cells	rpl-29	-0.334797941	1.74231E-09
Apoptotic germ cells	K10D2.5	-0.264919926	2.04469E-09
Apoptotic germ cells	spp-18	-1.330798803	2.09809E-09
Apoptotic germ cells	gpx-5	0.957920049	2.12583E-09
Apoptotic germ cells	K07C5.4	-0.23501886	2.81224E-09
Apoptotic germ cells	rpl-32	-0.121543636	3.32083E-09
Apoptotic germ cells	anmt-2	1.058797917	3.81469E-09
Apoptotic germ cells	F53F4.13	0.532875024	5.78497E-09

Apoptotic germ cells	cgh-1	-0.228860861	6.06031E-09
Apoptotic germ cells	gln-3	0.550040146	6.38495E-09
Apoptotic germ cells	ttr-26	1.295812265	1.0732E-08
Apoptotic germ cells	rps-27	-0.146087452	1.08251E-08
Apoptotic germ cells	T24B8.5	-1.702714719	1.99567E-08
Apoptotic germ cells	fipr-3	1.732373454	2.36719E-08
Apoptotic germ cells	ZK593.3	1.202063318	2.91042E-08
Apoptotic germ cells	prg-1	-0.348888087	2.94891E-08
Apoptotic germ cells	pqn-94	1.641993171	3.41111E-08
Apoptotic germ cells	rla-2	-0.162960072	8.18808E-08
Apoptotic germ cells	Y82E9BR.3	0.136710039	9.15759E-08
Apoptotic germ cells	tnt-3	1.041540962	9.70541E-08
Apoptotic germ cells	cth-1	0.452762591	1.18033E-07
Apoptotic germ cells	fipr-6	1.964888589	1.54617E-07
Apoptotic germ cells	nspb-12	1.407419555	2.15619E-07
Apoptotic germ cells	sams-1	0.486711657	2.39192E-07
Apoptotic germ cells	lec-2	0.445898337	2.86289E-07
Apoptotic germ cells	F36F2.1	1.092997768	3.3605E-07
Apoptotic germ cells	sec-61	0.250904071	3.99688E-07
Apoptotic germ cells	cpl-1	0.661477749	4.4226E-07
Apoptotic germ cells	M163.8	0.543484765	4.46452E-07
Apoptotic germ cells	lev-11	0.274496934	5.23276E-07
Apoptotic germ cells	hpo-26	1.542019868	5.40287E-07
Apoptotic germ cells	dhc-1	-0.190164523	5.73219E-07
Apoptotic germ cells	fat-7	1.937637009	6.23233E-07
Apoptotic germ cells	Y111B2A.2	-0.308777521	6.37675E-07
Apoptotic germ cells	rpl-7A	-0.123017906	7.90783E-07
Apoptotic germ cells	spp-2	-1.106452177	8.72982E-07
Apoptotic germ cells	abf-5	1.234700352	1.03711E-06
Apoptotic germ cells	pgl-1	-0.203905678	1.40369E-06
Apoptotic germ cells	F46H5.3	0.26648088	1.85551E-06
Apoptotic germ cells	nduo-5	0.150382513	2.60556E-06
Apoptotic germ cells	nspd-10	-0.458916488	2.72506E-06

Apoptotic germ cells	C23H5.8	-0.590988962	2.98154E-06
Apoptotic germ cells	scl-6	0.906209603	3.12709E-06
Apoptotic germ cells	C53B7.3	1.691060978	3.13062E-06
Apoptotic germ cells	pab-1	-0.13102565	3.32515E-06
Apoptotic germ cells	argk-1	0.658505495	4.25745E-06
Apoptotic germ cells	C45E5.4	1.505416715	5.42803E-06
Apoptotic germ cells	acs-2	0.626599544	5.74752E-06
Apoptotic germ cells	eef-1G	-0.113903412	6.24155E-06
Apoptotic germ cells	ant-1.1	0.106274949	6.26083E-06
Apoptotic germ cells	unc-54	0.370114773	6.31032E-06
Apoptotic germ cells	ppw-2	-0.231123075	6.47601E-06
Apoptotic germ cells	lys-4	0.566817796	7.54988E-06
Apoptotic germ cells	let-711	-0.382292512	9.96876E-06
Apoptotic germ cells	imb-3	-0.205095774	1.02584E-05
Apoptotic germ cells	mpc-1	0.39349415	1.174E-05
Apoptotic germ cells	ZK863.8	1.091577417	1.52074E-05
Apoptotic germ cells	F23A7.8	-0.54845535	1.55068E-05
Apoptotic germ cells	ZK596.1	1.481988524	1.72165E-05
Apoptotic germ cells	rpl-14	-0.114113291	1.8678E-05
Apoptotic germ cells	cpg-1	0.27356347	2.09155E-05
Apoptotic germ cells	nspd-2	-0.350669122	2.33267E-05
Apoptotic germ cells	act-3	0.222728954	2.4069E-05
Apoptotic germ cells	mlc-1	0.316355623	2.88962E-05
Apoptotic germ cells	T08G11.1	-0.184892826	2.90694E-05
Apoptotic germ cells	ubl-1	-0.10959628	3.29073E-05
Apoptotic germ cells	msp-51	-0.259660767	3.44435E-05
Apoptotic germ cells	C28H8.3	-0.21471294	3.64607E-05
Apoptotic germ cells	marg-1	1.710979464	3.79303E-05
Apoptotic germ cells	pqn-31	1.789608422	4.42995E-05
Apoptotic germ cells	atp-5	0.212979468	4.7024E-05
Apoptotic germ cells	wago-1	-0.231537109	4.84796E-05
Apoptotic germ cells	asp-5	0.549077302	4.98225E-05
Apoptotic germ cells	tag-174	0.220669408	5.22504E-05
Apoptotic germ cells	fipr-21	0.426239261	5.38862E-05
Apoptotic germ cells	fipr-9	1.684701525	7.78507E-05

Apoptotic germ cells	rps-20	0.113269492	9.14775E-05
Apoptotic germ cells	R02C2.7	1.130160952	0.000110054
Apoptotic germ cells	abf-6	2.183623333	0.000118147
Apoptotic germ cells	msp-49	-0.380392537	0.000119964
Apoptotic germ cells	mat-2	-0.32800291	0.000120677
Apoptotic germ cells	ZC449.5	2.025241998	0.000122729
Apoptotic germ cells	C15H9.9	0.426081744	0.000123625
Apoptotic germ cells	msp-40	-0.308859823	0.000134191
Apoptotic germ cells	Y54F10AM.5	0.379442955	0.000158491
Apoptotic germ cells	F19F10.9	-0.213015919	0.00017298
Apoptotic germ cells	F23A7.4	-0.507941879	0.000184689
Apoptotic germ cells	Y69H2.3	-2.527496893	0.000185894
Apoptotic germ cells	C27B7.9	0.69553679	0.000186734
Apoptotic germ cells	D1054.18	-0.47049137	0.000207694
Apoptotic germ cells	T04F8.8	0.553910291	0.000209298
Apoptotic germ cells	ZC21.3	1.649915126	0.000249676
Apoptotic germ cells	msp-57	-0.30370376	0.00026919
Apoptotic germ cells	asp-4	0.729457602	0.000269943
Apoptotic germ cells	act-4	0.200833523	0.000304873
Apoptotic germ cells	C49G7.3	0.587658509	0.000305041
Apoptotic germ cells	nduo-2	0.138384268	0.000314411
Apoptotic germ cells	C30G12.2	0.95343772	0.000351744
Apoptotic germ cells	Y105C5B.5	0.290309255	0.000354347
Apoptotic germ cells	F35A5.2	0.558932654	0.000355836
Apoptotic germ cells	F08D12.2	2.401824517	0.000404048
Apoptotic germ cells	lys-7	-1.148202701	0.000541397
Apoptotic germ cells	nfx-1	-0.279086953	0.000547435
Apoptotic germ cells	crt-1	0.311846428	0.000564986
Apoptotic germ cells	F56H9.2	-0.362333507	0.000599403
Apoptotic germ cells	asp-13	0.736714303	0.000672895
Apoptotic germ cells	calu-1	0.497869302	0.000778477
Apoptotic germ cells	let-716	-0.191759421	0.000996542
Apoptotic germ cells	clec-1	0.528074369	0.001042469
Apoptotic germ cells	glh-1	-0.182440618	0.001064461
Apoptotic germ cells	nex-3	0.966451549	0.001065124

Apoptotic germ cells	lec-4	0.4734527	0.001130365
Apoptotic germ cells	Y47G6A.33	0.392563868	0.001149588
Apoptotic germ cells	act-2	-0.209252732	0.001152884
Apoptotic germ cells	F42A8.1	0.74734337	0.00116541
Apoptotic germ cells	ZK622.4	1.072181206	0.001235789
Apoptotic germ cells	ttr-22	2.267249267	0.001306644
Apoptotic germ cells	C18D11.3	-0.373413116	0.001525747
Apoptotic germ cells	F58A6.9	-0.198364474	0.001593958
Apoptotic germ cells	rps-24	-0.09889162	0.001679264
Apoptotic germ cells	C37C3.12	2.366097012	0.00180847
Apoptotic germ cells	F08B4.8	-0.606123337	0.001864408
Apoptotic germ cells	cco-2	0.178306634	0.001899366
Apoptotic germ cells	xpc-1	-0.359700457	0.002282612
Apoptotic germ cells	dod-19	-1.117407491	0.002397849
Apoptotic germ cells	rack-1	-0.100758658	0.002499393
Apoptotic germ cells	K01G5.5	-0.1632542	0.002786497
Apoptotic germ cells	gst-13	-0.649131082	0.002805323
Apoptotic germ cells	ncx-2	1.568580359	0.002872249
Apoptotic germ cells	nol-5	-0.176870486	0.002905282
Apoptotic germ cells	cpi-1	0.362869221	0.002970955
Apoptotic germ cells	eef-1B.1	-0.084924769	0.003083172
Apoptotic germ cells	nspd-7	-0.379712214	0.003094851
Apoptotic germ cells	oig-3	0.574395173	0.003172901
Apoptotic germ cells	nspb-6	1.287537145	0.003258264
Apoptotic germ cells	rpl-12	-0.060257474	0.00348449
Apoptotic germ cells	ZC477.3	-0.275224696	0.003632741
Apoptotic germ cells	ttr-18	0.661917483	0.003984061
Apoptotic germ cells	scl-3	0.645880319	0.004703865
Apoptotic germ cells	mai-2	0.21036597	0.005374584
Apoptotic germ cells	eef-2	-0.104615653	0.005395679
Apoptotic germ cells	ZK809.8	0.381742748	0.005476605

Apoptotic germ cells	F22F4.9	0.961315144	0.005607808
Apoptotic germ cells	F41G3.21	0.660852977	0.0056322
Apoptotic germ cells	grd-3	1.033747637	0.005658095
Apoptotic germ cells	gfat-2	-0.240790134	0.005870126
Apoptotic germ cells	F35B12.3	2.053141957	0.006046699
Apoptotic germ cells	F48D6.4	-0.466905042	0.006162782
Apoptotic germ cells	C30F2.3	1.981758813	0.006294342
Apoptotic germ cells	cpr-4	0.691434704	0.006862382
Apoptotic germ cells	alh-1	0.316606503	0.007504312
Apoptotic germ cells	msp-152	-0.359629628	0.007618792
Apoptotic germ cells	C53A3.2	0.215028911	0.007743179
Apoptotic germ cells	K09G1.1	0.462851989	0.00782465
Apoptotic germ cells	dhs-21	0.238074391	0.009006281
Apoptotic germ cells	set-5	-0.44405213	0.009118854
Apoptotic germ cells	drd-10	-1.597861397	0.009342355
Apoptotic germ cells	msp-31	-0.302726486	0.009597815
Apoptotic germ cells	Y87G2A.19	1.597653392	0.009694925
Apoptotic germ cells	fln-1	-0.185417284	0.01044457
Apoptotic germ cells	unc-52	1.063101788	0.010553146
Apoptotic germ cells	C39E9.8	0.644724356	0.011725577
Apoptotic germ cells	ahcy-1	0.179469971	0.011730621
Apoptotic germ cells	nuo-3	0.159032547	0.012065181
Apoptotic germ cells	elo-6	0.410614638	0.012234964
Apoptotic germ cells	zbp-1	-0.326086966	0.012667243
Apoptotic germ cells	M02H5.8	0.393495911	0.01297511
Apoptotic germ cells	F41G3.10	0.607842266	0.013225783
Apoptotic germ cells	nspb-8	1.135361196	0.015182672
Apoptotic germ cells	asb-2	0.304946127	0.015763311
Apoptotic germ cells	B0410.3	0.601363799	0.017423592
Apoptotic germ cells	F40A3.2	0.429383119	0.017933866
Apoptotic germ cells	tni-3	0.192612298	0.019023547
Apoptotic germ cells	F43D2.6	1.345259003	0.019749099
Apoptotic germ cells	fipr-13	1.272402957	0.020068286
Apoptotic germ cells	Y105E8A.25	-0.337658786	0.020221246
Apoptotic germ cells	pat-10	0.128916304	0.020409742
Apoptotic germ cells	cco-1	0.145861938	0.020645449

Apoptotic germ cells	lys-2	-0.685697295	0.021001439
Apoptotic germ cells	mes-6	-0.614087328	0.022057575
Apoptotic germ cells	glp-4	-0.24038151	0.022468288
Apoptotic germ cells	W09C5.8	0.206303732	0.025545366
Apoptotic germ cells	cpz-1	0.507035405	0.026041127
Apoptotic germ cells	F17A9.4	0.608637883	0.028996702
Apoptotic germ cells	atp-2	0.109759219	0.029262751
Apoptotic germ cells	ZK1067.2	-0.240477594	0.029350734
Apoptotic germ cells	ags-3	0.341953939	0.030918518
Apoptotic germ cells	hsp-70	0.891296767	0.032041071
Apoptotic germ cells	W03G9.8	-0.333000578	0.032883764
Apoptotic germ cells	rpl-21	-0.082779151	0.033244454
Apoptotic germ cells	tos-1	-0.157220685	0.037644266
Apoptotic germ cells	T28D6.3	0.49161481	0.037856138
Apoptotic germ cells	F10E9.5	-0.309693824	0.038770774
Apoptotic germ cells	pyk-2	0.53057249	0.040983859
Apoptotic germ cells	rpl-26	-0.087681498	0.041309044
Apoptotic germ cells	R53.4	0.121525665	0.041528538
Apoptotic germ cells	tag-290	0.761655879	0.04436472
Apoptotic germ cells	R74.10	2.305021189	0.045256434
Apoptotic germ cells	mup-2	0.188430795	0.045414007
Apoptotic germ cells	asg-2	0.256432506	0.045470111
Apoptotic germ cells	hacd-1	-0.530304578	0.045717223
Apoptotic germ cells	ubr-1	-0.270237548	0.048084001
Apoptotic germ cells	gst-5	0.444146865	0.048087169
Apoptotic germ cells	cdr-6	0.94238802	0.051923364
Apoptotic germ cells	mdt-22	-0.232077188	0.052384429
Apoptotic germ cells	F53A9.9	1.201765876	0.056033082
Apoptotic germ cells	F55H12.4	0.462138759	0.058606962
Apoptotic germ cells	lbp-3	-1.428876575	0.060171679
Apoptotic germ cells	F14F8.8	2.158140672	0.061443299
Apoptotic germ cells	lec-10	-0.343560464	0.063071304

Apoptotic germ cells	grd-5	0.633969934	0.064485671
Apoptotic germ cells	C37A2.8	-0.272348409	0.0674977
Apoptotic germ cells	anmt-3	0.720707452	0.071374763
Apoptotic germ cells	fipr-10	2.110168057	0.074735436
Apoptotic germ cells	msp-45	-0.34395154	0.075205362
Apoptotic germ cells	sca-1	0.21082675	0.07756464
Apoptotic germ cells	icl-1	0.520033236	0.078145347
Apoptotic germ cells	rps-3	-0.078176379	0.081627211
Apoptotic germ cells	C46C2.5	-1.527496911	0.086236925
Apoptotic germ cells	ttr-51	0.252279826	0.088663851
Apoptotic germ cells	atp-3	0.188266123	0.090576192
Apoptotic germ cells	dim-1	0.227321419	0.096419751
Apoptotic germ cells	acp-6	0.66329335	0.098374631
Arcade cells	F08B12.4	-0.928004314	3.76345E-09
Arcade cells	W08E12.4	-1.063517597	9.07491E-09
Arcade cells	Y102A11A.7	-0.762983335	1.06731E-08
Arcade cells	abu-14	-0.624073603	2.34717E-07
Arcade cells	pqn-54	-1.047323794	3.91947E-07
Arcade cells	C14C6.5	-1.412118937	4.50545E-07
Arcade cells	ctc-3	0.719017637	5.23399E-07
Arcade cells	ZK662.2	-0.626340838	5.52462E-07
Arcade cells	nas-1	-1.107941915	5.9691E-07
Arcade cells	mlp-1	-0.951030432	1.34277E-06
Arcade cells	abu-1	-0.933335314	1.80934E-06
Arcade cells	clec-50	-1.161490743	1.91583E-06
Arcade cells	abu-11	-0.998789951	2.06394E-06
Arcade cells	ndk-1	0.291097795	4.76469E-06
Arcade cells	W08E12.2	-0.670139227	1.4912E-05
Arcade cells	F59B10.3	-0.799843098	2.06739E-05

Arcade cells	asns-1	-0.831571476	4.56828E-05
Arcade cells	pud-3	-2.172321214	0.00013976
Arcade cells	W08E12.3	-0.868893242	0.000159169
Arcade cells	pud-4	-2.40666373	0.00032543
Arcade cells	lys-4	0.818634374	0.000336966
Arcade cells	F41E6.15	1.826464071	0.000459311
Arcade cells	lys-2	-1.269201668	0.000587965
Arcade cells	pqn-74	-0.66195574	0.000686274
Arcade cells	dod-19	-2.005617672	0.00076154
Arcade cells	far-3	2.088875628	0.001319418
Arcade cells	rcan-1	-0.819776563	0.002053913
Arcade cells	Y47D3B.6	-0.531248005	0.002563622
Arcade cells	tnt-4	-0.750305159	0.003810434
Arcade cells	atp-2	0.386863132	0.009628851
Arcade cells	pdi-6	0.75310884	0.010013272
Arcade cells	T23E7.2	-0.685275206	0.010099087
Arcade cells	F55G11.4	-2.094372262	0.01593858
Arcade cells	C25E10.8	-0.901722946	0.016042212
Arcade cells	T06E4.8	-0.691604515	0.017495229
Arcade cells	elo-6	0.94812362	0.018224373
Arcade cells	pqn-2	-0.839201108	0.021905657
Arcade cells	T06E4.12	-0.609540801	0.024108826
Arcade cells	R02F11.1	-0.434148927	0.027866295
Arcade cells	tag-273	-0.884453971	0.045317699
Arcade cells	col-119	0.904222043	0.048307555
Arcade cells	T06E4.9	-0.715122047	0.048665523
Arcade cells	sodh-1	1.768390767	0.0518564
Arcade cells	col-98	1.342631355	0.063756093

Arcade cells	D2096.6	-0.627606369	0.068759941
Arcade cells	F26F12.4	-0.588389351	0.085715045
Arcade cells	nduo-1	0.454049017	0.085806364
Arcade cells	rpl-9	0.381200002	0.086104484
Arcade cells	col-101	0.947176741	0.089159147
BAG	nlp-41	-1.324083319	2.34483E-13
BAG	C44B11.4	-1.386737177	8.01144E-08
BAG	col-122	1.69268941	2.58562E-05
BAG	flp-6	-0.61246226	3.70752E-05
BAG	spp-9	5.110051913	0.000253103
BAG	hsp-16.48	-0.846004445	0.001076643
BAG	msp-40	-0.267175556	0.002988861
BAG	sul-2	0.839381924	0.004717827
BAG	daf-7	2.437363522	0.00543531
BAG	col-124	0.890381137	0.008448789
BAG	col-160	2.175757727	0.008572101
BAG	nlp-8	0.711351885	0.038731277
BAG	flp-22	1.325883602	0.074926618
BAG	ist-1	0.873184414	0.094831628
BAG	Y57G7A.1	-1.184238749	0.096690079
BAG	col-119	1.101467106	0.098301769
BDU	B0464.6	-2.099535673	0.084482151
BDU	Y47D7A.13	-2.099535673	0.084482151
Body wall muscle anterior	Y71H2B.4	-0.652252814	5.64386E-43
Body wall muscle anterior	F56H9.2	-0.798793106	3.32507E-22
Body wall muscle anterior	sodh-1	0.936925704	2.34851E-21
Body wall muscle anterior	acs-2	2.551751112	3.448E-21
Body wall muscle anterior	icl-1	1.069634352	1.12178E-19
Body wall muscle anterior	spp-15	-0.581218371	8.56103E-17
Body wall muscle anterior	col-122	0.75726668	2.25412E-16
Body wall muscle anterior	act-3	0.357295275	1.28462E-15
Body wall muscle anterior	acer-1	0.775987499	1.58169E-15

Body wall muscle anterior	rpl-41.2	-0.301574956	1.62572E-13
Body wall muscle anterior	rpl-38	-0.371362865	1.33078E-12
Body wall muscle anterior	oig-2	-0.553010527	1.35925E-12
Body wall muscle anterior	perm-2	-0.610452841	1.80043E-12
Body wall muscle anterior	unc-54	0.722991034	1.83014E-12
Body wall muscle anterior	T03F1.11	1.166401462	3.25576E-12
Body wall muscle anterior	F53C11.9	-1.144818318	1.8896E-11
Body wall muscle anterior	col-119	0.620844036	8.90985E-11
Body wall muscle anterior	pat-10	-0.170187227	2.02438E-10
Body wall muscle anterior	col-8	0.996155107	2.28418E-09
Body wall muscle anterior	hsp-16.41	0.952650265	3.02491E-09
Body wall muscle anterior	cth-1	0.778092206	4.54752E-09
Body wall muscle anterior	dim-1	0.321019083	6.5565E-09
Body wall muscle anterior	tag-18	-0.25878663	3.14554E-08
Body wall muscle anterior	mdh-2	0.550457405	4.77814E-08
Body wall muscle anterior	alh-1	0.793319689	8.00565E-08
Body wall muscle anterior	gst-4	0.687775156	3.25523E-07
Body wall muscle anterior	far-3	2.164238971	5.60158E-07
Body wall muscle anterior	col-20	0.423364405	6.69207E-07
Body wall muscle anterior	ctc-1	0.266743158	1.43789E-06
Body wall muscle anterior	act-2	-0.422899473	1.60519E-06
Body wall muscle anterior	ant-1.1	0.145403928	1.6889E-06
Body wall muscle anterior	col-181	0.548964317	1.69326E-06
Body wall muscle anterior	tnc-2	1.378636069	1.80721E-06
Body wall muscle anterior	D1086.1	-1.264101524	1.8608E-06
Body wall muscle anterior	col-140	0.408276468	2.08057E-06
Body wall muscle anterior	Y82E9BR.3	0.15696247	5.72606E-06
Body wall muscle anterior	ttr-16	-0.242407362	6.16361E-06
Body wall muscle anterior	lys-4	1.031750634	7.13491E-06
Body wall muscle anterior	F25E2.2	-0.478912634	7.41007E-06
Body wall muscle anterior	rps-25	-0.170777398	8.26921E-06
Body wall muscle anterior	pyp-1	0.601079336	9.86478E-06
Body wall muscle anterior	F11E6.3	0.710932824	1.3374E-05
Body wall muscle anterior	C06A8.3	0.597510427	1.38369E-05

Body wall muscle anterior	isp-1	0.359111701	1.69438E-05
Body wall muscle anterior	ttr-6	-0.577057817	1.95281E-05
Body wall muscle anterior	rps-21	-0.321810683	3.55317E-05
Body wall muscle anterior	rps-28	-0.394502565	4.78861E-05
Body wall muscle anterior	pud-4	-2.084776159	7.27539E-05
Body wall muscle anterior	W01D2.1	-0.281820499	9.06649E-05
Body wall muscle anterior	col-124	0.34422678	9.79906E-05
Body wall muscle anterior	pud-3	-2.119123503	0.000126927
Body wall muscle anterior	W08A12.2	-0.516913099	0.000260196
Body wall muscle anterior	C17F4.7	0.56004335	0.000413493
Body wall muscle anterior	anmt-2	1.168391299	0.000422181
Body wall muscle anterior	col-184	0.508595627	0.000467536
Body wall muscle anterior	lbp-2	-0.416786281	0.000491143
Body wall muscle anterior	atp-2	0.259420818	0.000566662
Body wall muscle anterior	col-98	0.629160441	0.000577119
Body wall muscle anterior	R13H4.2	-0.299812393	0.000687751
Body wall muscle anterior	rpl-39	-0.335849019	0.000691073
Body wall muscle anterior	hsp-12.2	0.763296794	0.000737854
Body wall muscle anterior	gln-3	0.541157633	0.000765053
Body wall muscle anterior	F21C10.9	1.625892198	0.000914784
Body wall muscle anterior	F47B7.1	-0.343320799	0.001150489
Body wall muscle anterior	perm-4	-0.491125758	0.00127913
Body wall muscle anterior	rps-27	-0.196579932	0.001609496
Body wall muscle anterior	F21C10.7	1.053617167	0.001915391
Body wall muscle anterior	asb-2	0.310482638	0.002129676
Body wall muscle anterior	F01G4.6	0.290696032	0.002357266
Body wall muscle anterior	msp-33	-1.162948489	0.002754513
Body wall muscle anterior	hsp-16.2	0.639301272	0.003252104
Body wall muscle anterior	col-19	0.364205673	0.003306392
Body wall muscle anterior	pmt-2	0.490237799	0.003808238
Body wall muscle anterior	C18B2.3	0.366008417	0.005383003

Body wall muscle anterior	mup-2	0.190749113	0.005738737
Body wall muscle anterior	nuo-6	0.376097503	0.005866154
Body wall muscle anterior	col-106	0.538227596	0.009720294
Body wall muscle anterior	ctc-3	0.203871741	0.009764758
Body wall muscle anterior	cct-5	0.457670613	0.012238205
Body wall muscle anterior	Y51A2D.14	-0.574384024	0.012830782
Body wall muscle anterior	col-103	0.708928421	0.01316318
Body wall muscle anterior	rpl-34	-0.205772973	0.014701875
Body wall muscle anterior	F48D6.4	-0.621156358	0.015882341
Body wall muscle anterior	pqn-22	0.400695228	0.017659911
Body wall muscle anterior	F10G2.2	1.353484551	0.01879084
Body wall muscle anterior	ZC449.4	-0.908597472	0.024173845
Body wall muscle anterior	lev-11	0.144606657	0.029778772
Body wall muscle anterior	cpr-5	0.904050525	0.029837212
Body wall muscle anterior	Y69A2AR.18	0.230695041	0.038329919
Body wall muscle anterior	Y4C6B.7	-0.363029667	0.041079061
Body wall muscle anterior	gst-10	-0.809227117	0.044753165
Body wall muscle anterior	Y17D7B.4	-0.646996396	0.047435971
Body wall muscle anterior	rpl-36	-0.175509691	0.048063981
Body wall muscle anterior	myo-3	0.560007685	0.053460843
Body wall muscle anterior	rps-29	-0.253614096	0.060005934
Body wall muscle anterior	nuo-2	0.434916142	0.063423171
Body wall muscle anterior	rpl-35	-0.147702611	0.07199282
Body wall muscle anterior	M60.4	-0.558743514	0.083335343
Body wall muscle anterior	xbp-1	-0.539400875	0.085288379
Body wall muscle anterior	msra-1	0.998850925	0.08552658
Body wall muscle anterior	ttr-41	-0.34139867	0.087560958
Body wall muscle anterior	rpl-43	-0.176641435	0.096803549
Body wall muscle anterior	cco-2	0.194341978	0.097188462
Body wall muscle anterior	col-143	0.504304713	0.099473486
Body wall muscle anterior	T03G6.3	0.834883772	0.099578176

Body wall muscle middle	rpl-41.2	-0.472427443	2.2226E-166
Body wall muscle middle	acs-2	2.480588386	5.00331E-92
Body wall muscle middle	icl-1	0.992005692	6.13359E-87
Body wall muscle middle	rps-25	-0.260740207	7.97212E-80
Body wall muscle middle	sodh-1	0.753777288	3.77138E-77
Body wall muscle middle	acer-1	0.686005438	1.39258E-73
Body wall muscle middle	rpl-38	-0.423351631	1.49637E-72
Body wall muscle middle	act-2	-0.534148033	5.53814E-66
Body wall muscle middle	dct-16	-0.504607751	1.43248E-65
Body wall muscle middle	rpl-36.A	-0.331877933	1.58054E-62
Body wall muscle middle	Y82E9BR.3	0.190503186	1.40311E-61
Body wall muscle middle	C14C6.5	-1.598428945	9.51261E-57
Body wall muscle middle	W01D2.1	-0.417688893	1.33567E-55
Body wall muscle middle	rpl-43	-0.323172383	1.09776E-54
Body wall muscle middle	R53.4	0.248823112	3.67448E-54
Body wall muscle middle	mup-2	0.275987443	4.76029E-54
Body wall muscle middle	mlc-3	0.151684575	3.7095E-53
Body wall muscle middle	nduo-6	-0.250259288	7.38135E-52
Body wall muscle middle	dim-1	0.311124464	8.52174E-52
Body wall muscle middle	rps-27	-0.301800921	8.61372E-52
Body wall muscle middle	rpl-36	-0.30434224	1.27371E-50
Body wall muscle middle	mlp-1	0.561445557	2.35687E-50
Body wall muscle middle	far-2	0.394050475	1.46188E-49
Body wall muscle middle	tni-3	0.398921638	2.76167E-48
Body wall muscle middle	lev-11	0.19554516	6.3739E-46
Body wall muscle middle	ant-1.1	0.164110889	9.26873E-46
Body wall muscle middle	gst-10	-1.160094119	2.75463E-44
Body wall muscle middle	R09B3.3	-0.00849915	3.53815E-44
Body wall muscle middle	Y119D3B.21	-0.55809856	4.59862E-44
Body wall muscle middle	cpn-3	0.155349661	1.43586E-42
Body wall muscle middle	rps-28	-0.475923104	1.76859E-42
Body wall muscle middle	col-122	0.536041646	1.64186E-41

Body wall muscle middle	rpl-39	-0.415456588	2.1218E-41
Body wall muscle middle	mlc-2	0.160598933	3.05206E-41
Body wall muscle middle	ZK809.8	0.303535352	4.75788E-41
Body wall muscle middle	rps-29	-0.381472024	1.56625E-40
Body wall muscle middle	cco-2	0.254800088	1.59632E-40
Body wall muscle middle	clik-1	0.145810371	1.76743E-40
Body wall muscle middle	cyc-2.1	0.224008721	1.77312E-40
Body wall muscle middle	R04B3.3	0.954385968	3.87807E-40
Body wall muscle middle	eef-1A.1	-0.221365877	7.67787E-39
Body wall muscle middle	gst-4	0.780294721	1.1792E-38
Body wall muscle middle	rps-21	-0.395030915	1.66035E-38
Body wall muscle middle	zig-12	0.265241005	4.73978E-38
Body wall muscle middle	rpl-32	-0.214161376	1.75688E-36
Body wall muscle middle	F58F12.1	0.223016658	3.48172E-36
Body wall muscle middle	unc-54	0.464731507	4.1967E-36
Body wall muscle middle	rpl-27	-0.308657606	8.42716E-35
Body wall muscle middle	ndk-1	0.129722068	4.13814E-34
Body wall muscle middle	hsp-16.41	0.979489441	4.59117E-34
Body wall muscle middle	rpl-34	-0.283288448	4.79899E-34
Body wall muscle middle	col-8	0.791389205	2.91777E-33
Body wall muscle middle	atp-2	0.272165965	3.94437E-33
Body wall muscle middle	far-3	1.913958149	3.03871E-32
Body wall muscle middle	H36L18.2	0.255487971	8.23083E-32
Body wall muscle middle	F43C9.2	0.515972935	9.12907E-32
Body wall muscle middle	pud-4	-1.987164674	5.58475E-31
Body wall muscle middle	hsp-16.2	0.789165926	1.32507E-30
Body wall muscle middle	nuo-3	0.218361237	2.88676E-30
Body wall muscle middle	R04F11.2	0.17934218	3.6868E-30
Body wall muscle middle	rpl-14	-0.216908917	3.76028E-30
Body wall muscle middle	F56H9.2	-0.461527088	5.87636E-30
Body wall muscle middle	mdh-2	0.391312915	1.10133E-29
Body wall muscle middle	asg-2	0.254140413	1.58555E-29
Body wall muscle middle	F36A2.7	0.308904789	2.05953E-29
Body wall muscle middle	C24A3.2	0.483107132	2.39952E-29
Body wall muscle middle	anmt-2	0.872272598	8.13254E-29

Body wall muscle middle	ctc-3	0.235123594	2.74765E-28
Body wall muscle middle	ubq-2	-0.191889133	3.87951E-28
Body wall muscle middle	R31.2	0.429650868	4.79002E-28
Body wall muscle middle	pud-3	-1.821135429	4.88356E-28
Body wall muscle middle	pck-2	0.328745422	6.66066E-28
Body wall muscle middle	col-119	0.466295728	1.08113E-27
Body wall muscle middle	ril-1	0.236490677	8.07264E-27
Body wall muscle middle	Y69E1A.5	0.279528337	1.13224E-26
Body wall muscle middle	C05D11.5	0.485019862	2.52489E-26
Body wall muscle middle	asb-2	0.281998536	6.11082E-26
Body wall muscle middle	C46G7.2	0.29652062	2.71251E-25
Body wall muscle middle	rps-26	-0.177352995	4.73893E-25
Body wall muscle middle	T22B7.7	0.800294724	5.81144E-25
Body wall muscle middle	gyg-1	0.343802948	9.94971E-25
Body wall muscle middle	rps-19	-0.164160053	1.48177E-24
Body wall muscle middle	rpl-35	-0.176931057	4.10948E-24
Body wall muscle middle	eef-2	-0.260339296	6.14868E-24
Body wall muscle middle	alh-1	0.573840395	2.12297E-23
Body wall muscle middle	col-143	0.595904417	2.75605E-23
Body wall muscle middle	rpl-29	-0.451156439	3.87186E-23
Body wall muscle middle	rpl-30	-0.228429803	8.0842E-23
Body wall muscle middle	rps-15	-0.182330904	3.69876E-22
Body wall muscle middle	lec-10	-0.626153728	8.45684E-22
Body wall muscle middle	T02H6.11	0.180433871	1.25529E-21
Body wall muscle middle	R09B3.2	-0.000532623	1.39422E-21
Body wall muscle middle	nuo-6	0.3010793	1.88218E-21
Body wall muscle middle	F01G4.6	0.244882917	3.33532E-21
Body wall muscle middle	rpl-31	-0.196331092	7.80905E-21
Body wall muscle middle	pfn-3	0.284758741	8.01965E-21
Body wall muscle middle	atp-5	0.190940604	9.89861E-21
Body wall muscle middle	C49F5.7	-0.273855183	2.5159E-20
Body wall muscle middle	alp-1	0.338321203	4.94315E-20

Body wall muscle middle	col-98	0.648844407	6.70577E-20
Body wall muscle middle	rla-2	-0.210318886	2.45013E-19
Body wall muscle middle	rps-14	-0.137654761	6.75998E-19
Body wall muscle middle	cth-1	0.452205654	8.34846E-19
Body wall muscle middle	Y54F10AM.5	0.295880927	9.56688E-19
Body wall muscle middle	mlc-1	0.130347056	2.21758E-18
Body wall muscle middle	C37A2.7	-0.24157759	2.39009E-18
Body wall muscle middle	dlc-2	0.340302351	2.96119E-18
Body wall muscle middle	msra-1	0.952762499	9.68278E-18
Body wall muscle middle	ndfl-4	-0.209856699	1.05784E-17
Body wall muscle middle	T04G9.7	-0.500981884	1.14569E-17
Body wall muscle middle	F46H5.3	0.136136151	1.50222E-17
Body wall muscle middle	cco-1	0.156319891	2.22193E-17
Body wall muscle middle	atp-3	0.18696942	2.29664E-17
Body wall muscle middle	ZK1321.4	0.275305296	2.43618E-17
Body wall muscle middle	F11E6.3	0.576432454	5.10673E-17
Body wall muscle middle	atp-4	0.170090246	5.73397E-17
Body wall muscle middle	mev-1	0.288600316	9.51108E-17
Body wall muscle middle	spp-18	-1.238036429	1.05354E-16
Body wall muscle middle	col-181	0.358296225	1.74208E-16
Body wall muscle middle	rpl-22	-0.185532315	1.96305E-16
Body wall muscle middle	F42G8.10	0.31058046	2.1707E-16
Body wall muscle middle	pqn-22	0.340872314	3.06707E-16
Body wall muscle middle	gln-3	0.441945505	4.47363E-16
Body wall muscle middle	ags-3	1.004166317	6.02421E-16
Body wall muscle middle	lec-9	-0.43011938	7.73729E-16
Body wall muscle middle	rpl-25.2	-0.202063572	9.2339E-16
Body wall muscle middle	spp-5	-0.598785355	1.2705E-15
Body wall muscle middle	W09C5.8	0.213765818	1.42506E-15
Body wall muscle middle	clec-50	-0.707994474	1.46487E-15
Body wall muscle middle	cpn-4	1.059039411	1.58239E-15
Body wall muscle middle	F28H7.3	-0.791026748	2.28976E-15
Body wall muscle middle	rps-12	-0.141882165	3.83023E-15

Body wall muscle middle	C23H5.8	-0.698132481	4.30937E-15
Body wall muscle middle	C25H3.9	0.335949177	4.31325E-15
Body wall muscle middle	mpc-1	0.484033815	8.21717E-15
Body wall muscle middle	Y51H1A.3	0.225004574	8.87168E-15
Body wall muscle middle	ctc-1	0.18211549	8.93213E-15
Body wall muscle middle	cex-2	0.404026295	1.00753E-14
Body wall muscle middle	tag-174	0.189601602	1.75256E-14
Body wall muscle middle	oig-2	-0.239300549	2.69703E-14
Body wall muscle middle	col-106	0.446091673	3.1681E-14
Body wall muscle middle	col-184	0.3669637	6.4688E-14
Body wall muscle middle	gdh-1	-0.254444383	1.1251E-13
Body wall muscle middle	rps-2	-0.168024241	1.21522E-13
Body wall muscle middle	T24B8.5	-1.102637036	1.23288E-13
Body wall muscle middle	gst-27	-0.663102279	1.31701E-13
Body wall muscle middle	cisd-3.2	0.264276939	1.79762E-13
Body wall muscle middle	lpd-5	0.265119026	2.82934E-13
Body wall muscle middle	F10G2.1	0.487385106	2.89553E-13
Body wall muscle middle	tpi-1	0.312616521	2.90175E-13
Body wall muscle middle	F48D6.4	-0.553436441	3.02451E-13
Body wall muscle middle	far-1	0.284910395	3.41991E-13
Body wall muscle middle	C34B2.8	0.229478436	3.56842E-13
Body wall muscle middle	lys-4	0.701514535	3.96437E-13
Body wall muscle middle	F21C10.9	1.03263474	4.07123E-13
Body wall muscle middle	nuo-2	0.312261382	6.89825E-13
Body wall muscle middle	tnt-2	0.143663689	6.92073E-13
Body wall muscle middle	oxy-5	0.312223224	1.18666E-12
Body wall muscle middle	T03F1.11	0.978283911	1.51807E-12
Body wall muscle middle	iff-2	0.204596801	1.75428E-12
Body wall muscle middle	rps-16	-0.202463084	1.7865E-12
Body wall muscle middle	rpl-12	-0.095480666	1.83671E-12
Body wall muscle middle	acaa-2	0.442510527	1.99393E-12
Body wall muscle middle	K03E5.2	-0.446805709	2.76751E-12
Body wall muscle middle	F53F4.10	0.22997739	2.89065E-12
Body wall muscle middle	hsp-70	0.734249469	3.039E-12

Body wall muscle middle	rpl-26	-0.149473269	3.2887E-12
Body wall muscle middle	ZK637.2	0.401858394	3.29517E-12
Body wall muscle middle	cpr-5	0.770440595	3.65574E-12
Body wall muscle middle	rpl-21	-0.128957609	3.77982E-12
Body wall muscle middle	C06A8.3	0.378561391	4.7096E-12
Body wall muscle middle	F29C4.2	0.156749146	6.04216E-12
Body wall muscle middle	Y69A2AR.18	0.165621891	6.83908E-12
Body wall muscle middle	rpl-17	-0.121714724	8.35075E-12
Body wall muscle middle	isp-1	0.197112625	9.01914E-12
Body wall muscle middle	pccb-1	0.346738005	1.04113E-11
Body wall muscle middle	pyp-1	0.412960748	1.72462E-11
Body wall muscle middle	hsp-16.48	0.822396626	2.03225E-11
Body wall muscle middle	clec-47	1.600355415	2.40153E-11
Body wall muscle middle	nduo-3	-0.356994134	3.47897E-11
Body wall muscle middle	rpl-33	-0.158220272	3.48909E-11
Body wall muscle middle	rpl-23	-0.145460109	3.88093E-11
Body wall muscle middle	F39H12.3	0.625623299	5.20644E-11
Body wall muscle middle	rps-24	-0.144970532	6.13472E-11
Body wall muscle middle	Y111B2A.2	-4.27352E-05	6.77971E-11
Body wall muscle middle	col-140	0.238535757	6.804E-11
Body wall muscle middle	cts-1	0.248612543	7.08263E-11
Body wall muscle middle	lec-8	-0.517332567	9.36981E-11
Body wall muscle middle	F23C8.5	0.306620015	1.31962E-10
Body wall muscle middle	calu-1	0.472709743	1.48921E-10
Body wall muscle middle	rpl-24.1	-0.120185006	1.5818E-10
Body wall muscle middle	unc-87	0.125344143	1.61347E-10
Body wall muscle middle	F23A7.8	-0.194357734	1.73505E-10
Body wall muscle middle	Y71H2AM.5	0.155224512	1.79268E-10
Body wall muscle middle	spp-2	-0.970980056	3.20356E-10
Body wall muscle middle	D2030.4	0.218065702	3.40808E-10
Body wall muscle middle	mce-1	0.283546889	3.67451E-10
Body wall muscle middle	cysl-2	-0.276483983	4.99536E-10

Body wall muscle middle	lpd-9	0.270116414	5.44118E-10
Body wall muscle middle	spp-15	-0.329590024	5.68618E-10
Body wall muscle middle	cyn-1	0.304728872	6.19015E-10
Body wall muscle middle	col-124	0.219794136	6.75565E-10
Body wall muscle middle	col-20	0.23992177	7.46112E-10
Body wall muscle middle	rps-13	-0.137222716	8.5347E-10
Body wall muscle middle	F22H10.3	-0.474190501	1.41531E-09
Body wall muscle middle	R13H4.2	-0.17599509	1.7662E-09
Body wall muscle middle	Y87G2A.19	1.126497298	2.60397E-09
Body wall muscle middle	ZC116.5	1.69055582	2.67772E-09
Body wall muscle middle	hsp-12.2	0.677635302	2.74542E-09
Body wall muscle middle	rps-30	-0.132738921	3.1349E-09
Body wall muscle middle	rps-23	-0.116804312	3.75719E-09
Body wall muscle middle	Y37E3.8	-0.109737467	3.8866E-09
Body wall muscle middle	ZK809.3	0.253580197	4.33096E-09
Body wall muscle middle	unc-44	0.161403587	5.74222E-09
Body wall muscle middle	nduo-4	-0.157271506	6.13137E-09
Body wall muscle middle	H28O16.1	0.148414526	1.28355E-08
Body wall muscle middle	C53B7.3	2.006969849	1.40698E-08
Body wall muscle middle	col-103	0.488909811	1.74712E-08
Body wall muscle middle	rpl-10	-0.107138394	1.87117E-08
Body wall muscle middle	col-160	0.385415126	2.047E-08
Body wall muscle middle	phb-1	0.263010279	3.46211E-08
Body wall muscle middle	idha-1	0.253489755	4.14998E-08
Body wall muscle middle	rpl-7	-0.132275381	4.16161E-08
Body wall muscle middle	pdhb-1	0.290400891	5.77685E-08
Body wall muscle middle	rla-1	-0.15257232	5.902E-08
Body wall muscle middle	EGAP4.1	0.528974629	6.91632E-08
Body wall muscle middle	F53F4.13	0.351392176	8.16702E-08
Body wall muscle middle	D1054.18	-0.424588352	9.24599E-08
Body wall muscle middle	rpl-2	-0.120728853	9.46868E-08
Body wall muscle middle	cey-1	0.167154626	9.77133E-08
Body wall muscle middle	F45H10.3	0.202828325	1.1366E-07

Body wall muscle middle	spp-3	-0.575075208	1.20069E-07
Body wall muscle middle	cyc-1	0.293655367	1.68781E-07
Body wall muscle middle	cgh-1	-0.000454529	1.86809E-07
Body wall muscle middle	rpl-15	-0.125234288	2.15586E-07
Body wall muscle middle	lys-2	-0.774319093	2.38141E-07
Body wall muscle middle	rpl-7A	-0.14013431	2.95061E-07
Body wall muscle middle	dlat-1	0.32360972	3.0512E-07
Body wall muscle middle	rps-22	-0.131964376	4.31667E-07
Body wall muscle middle	mdh-1	0.194387587	6.51117E-07
Body wall muscle middle	F19B2.5	-0.694800632	6.78706E-07
Body wall muscle middle	aldo-1	0.2161063	8.09246E-07
Body wall muscle middle	vps-25	0.392944783	8.91354E-07
Body wall muscle middle	ssp-19	-0.883419685	1.03753E-06
Body wall muscle middle	nduf-7	0.180273913	1.05299E-06
Body wall muscle middle	farl-11	0.380831888	1.07258E-06
Body wall muscle middle	mmaa-1	0.42149434	1.16324E-06
Body wall muscle middle	rps-9	-0.083391411	1.17784E-06
Body wall muscle middle	ttr-24	0.413204571	1.31684E-06
Body wall muscle middle	C27B7.9	0.191659614	1.36489E-06
Body wall muscle middle	spn-4	-0.031491835	1.75062E-06
Body wall muscle middle	rps-3	-0.111188031	1.78495E-06
Body wall muscle middle	acbp-1	-0.338938277	2.66478E-06
Body wall muscle middle	cpg-9	0.177230277	2.9114E-06
Body wall muscle middle	ucr-2.1	0.306216036	3.05572E-06
Body wall muscle middle	test-1	0.379214403	4.27545E-06
Body wall muscle middle	lipl-5	-0.68595004	4.64485E-06
Body wall muscle middle	prdx-2	0.213370409	5.40586E-06
Body wall muscle middle	col-178	0.319135311	5.56587E-06
Body wall muscle middle	bca-2	0.322267386	5.72184E-06
Body wall muscle middle	mxl-3	0.388704113	5.96684E-06
Body wall muscle middle	T20H4.5	0.206815372	6.54659E-06
Body wall muscle middle	C18B2.3	0.212094343	6.85837E-06
Body wall muscle middle	F55G11.4	-1.866923527	6.9937E-06

Body wall muscle middle	rps-17	-0.113361086	8.85147E-06
Body wall muscle middle	Y76A2B.5	0.244413021	8.93335E-06
Body wall muscle middle	hsp-1	-0.208345788	1.21876E-05
Body wall muscle middle	C33A12.1	0.19886646	1.40714E-05
Body wall muscle middle	misc-1	0.405761371	1.4989E-05
Body wall muscle middle	C39D10.7	-0.102852559	1.66105E-05
Body wall muscle middle	clec-150	-0.71943155	1.73256E-05
Body wall muscle middle	lec-2	0.177838242	1.83569E-05
Body wall muscle middle	T28B8.1	0.459140946	1.9292E-05
Body wall muscle middle	F27D4.1	0.293133567	2.09325E-05
Body wall muscle middle	rnr-2	-0.047328178	2.29744E-05
Body wall muscle middle	tnc-2	0.783547144	2.29859E-05
Body wall muscle middle	K03H6.2	-0.774515601	2.93766E-05
Body wall muscle middle	unc-60	0.122191613	3.0854E-05
Body wall muscle middle	col-42	0.418942642	3.09148E-05
Body wall muscle middle	K07C5.4	-0.000156964	3.18893E-05
Body wall muscle middle	H10D18.5	-1.348763048	3.27754E-05
Body wall muscle middle	Y22D7AL.10	0.189905284	3.77909E-05
Body wall muscle middle	E01G4.3	-0.167751381	5.7832E-05
Body wall muscle middle	erm-1	-0.182351595	6.09591E-05
Body wall muscle middle	D1086.1	-0.614433904	6.1505E-05
Body wall muscle middle	rps-0	-0.120140175	6.57198E-05
Body wall muscle middle	T20G5.14	0.258531858	6.90499E-05
Body wall muscle middle	dcr-1	-0.000641031	7.0497E-05
Body wall muscle middle	Y71H2B.4	-0.157938168	7.28125E-05
Body wall muscle middle	rpl-19	-0.092205717	7.44923E-05
Body wall muscle middle	B0491.5	0.220020098	7.73458E-05
Body wall muscle middle	rps-5	-0.090456267	8.48711E-05
Body wall muscle middle	W08E12.4	2.049725349	0.000104867
Body wall muscle middle	nuo-4	0.27011421	0.000118299

Body wall muscle middle	msp-40	0.340428032	0.000135889
Body wall muscle middle	cyn-7	-0.139838019	0.000136409
Body wall muscle middle	cpz-1	0.404134065	0.000137462
Body wall muscle middle	snr-7	-0.243494711	0.000137484
Body wall muscle middle	C04G6.7	-2.027090191	0.000138938
Body wall muscle middle	zyx-1	0.264348075	0.00014683
Body wall muscle middle	dod-6	7.52473E-05	0.000149353
Body wall muscle middle	unc-27	0.123985278	0.000175493
Body wall muscle middle	R11A5.3	0.860478742	0.000183753
Body wall muscle middle	strl-1	0.463816695	0.000191628
Body wall muscle middle	sucl-2	0.25836961	0.000205428
Body wall muscle middle	hpo-15	-0.273509734	0.000214124
Body wall muscle middle	F46G10.1	-0.406028275	0.000215311
Body wall muscle middle	F40A3.2	0.224047675	0.000225735
Body wall muscle middle	upb-1	0.215558457	0.000261514
Body wall muscle middle	rps-10	-0.09195345	0.000281592
Body wall muscle middle	F41E6.15	0.648895083	0.000335525
Body wall muscle middle	pck-1	0.275540724	0.000347508
Body wall muscle middle	E02H9.3	-0.012005052	0.000358664
Body wall muscle middle	sams-1	0.253574191	0.000360231
Body wall muscle middle	asp-4	0.547135561	0.000362369
Body wall muscle middle	F47B7.1	0.150815456	0.000377697
Body wall muscle middle	T20G5.8	0.000140183	0.000385974
Body wall muscle middle	pos-1	-0.202350505	0.000413756
Body wall muscle middle	F23A7.4	-0.187100949	0.000471865
Body wall muscle middle	ZC449.5	-2.179093271	0.00050293
Body wall muscle middle	skpo-1	-0.075515576	0.00051992
Body wall muscle middle	clec-87	-0.002148359	0.000576438
Body wall muscle middle	D1086.12	0.312565398	0.000659227
Body wall muscle middle	ceh-34	0.531000402	0.000690958
Body wall muscle middle	rpl-5	-0.092573135	0.000697591
Body wall muscle middle	sod-1	0.22888992	0.000744104

Body wall muscle middle	rpl-1	-0.102322071	0.000792331
Body wall muscle middle	F32D1.5	0.143398075	0.000817283
Body wall muscle middle	cpr-4	0.629048253	0.000822699
Body wall muscle middle	R02C2.7	0.720206054	0.000885823
Body wall muscle middle	M02D8.6	0.3824545	0.000886806
Body wall muscle middle	col-80	0.215684682	0.000898424
Body wall muscle middle	F59A6.10	-2.857165076	0.000925752
Body wall muscle middle	mai-2	0.108944173	0.000931228
Body wall muscle middle	ran-4	0.251091868	0.000983068
Body wall muscle middle	rps-8	-0.084313707	0.001037
Body wall muscle middle	F01D5.3	-0.692894636	0.001249965
Body wall muscle middle	T07E3.3	0.316024056	0.00126823
Body wall muscle middle	tre-2	0.437597306	0.001277669
Body wall muscle middle	R09H10.3	-0.40315129	0.001396577
Body wall muscle middle	dif-1	0.461500168	0.001627619
Body wall muscle middle	ttr-45	0.665942079	0.001740536
Body wall muscle middle	clec-41	-1.014749752	0.001890542
Body wall muscle middle	heh-1	0.21014211	0.001924827
Body wall muscle middle	gst-13	-0.397245357	0.001981756
Body wall muscle middle	C50C3.2	-2.399733104	0.00223381
Body wall muscle middle	abf-5	1.208670135	0.002249167
Body wall muscle middle	F59C6.16	-0.214496337	0.002273519
Body wall muscle middle	act-3	0.091873134	0.002457816
Body wall muscle middle	drd-10	-1.204692286	0.002470369
Body wall muscle middle	haly-1	-0.018948969	0.002474184
Body wall muscle middle	C17F4.7	0.250700228	0.00249448
Body wall muscle middle	T04A6.1	0.244303312	0.002550324
Body wall muscle middle	Y71H2B.1	-0.075783284	0.002550845
Body wall muscle middle	F53C11.3	0.370648595	0.002662157
Body wall muscle middle	C30G12.2	0.52471264	0.002864909
Body wall muscle middle	hsp-12.1	0.283966647	0.002987402
Body wall muscle middle	aqp-7	0.3387638	0.003139641
Body wall muscle middle	cdr-6	0.925018281	0.003195362

Body wall muscle middle	swm-1	-0.434692442	0.003407341
Body wall muscle middle	rps-11	-0.074781786	0.003679146
Body wall muscle middle	mesp-1	-0.002619438	0.003712299
Body wall muscle middle	F57B9.1	0.291688721	0.00375286
Body wall muscle middle	lys-7	-0.790222841	0.003806389
Body wall muscle middle	C49A1.10	0.411994764	0.003871128
Body wall muscle middle	ife-3	-9.26309E-05	0.003905224
Body wall muscle middle	ZK512.7	-0.328639831	0.003907358
Body wall muscle middle	clec-84	-0.012359678	0.003941867
Body wall muscle middle	col-96	1.4372749	0.004120615
Body wall muscle middle	fib-1	-0.000177064	0.004314648
Body wall muscle middle	M28.5	-0.000497543	0.004381209
Body wall muscle middle	C25E10.8	-0.676313462	0.004792991
Body wall muscle middle	col-19	0.168063181	0.004884196
Body wall muscle middle	nspd-10	-0.521627477	0.00539993
Body wall muscle middle	F35E12.9	-0.257204877	0.005533129
Body wall muscle middle	glh-1	-0.000112507	0.005550061
Body wall muscle middle	ani-1	-0.000186627	0.005767417
Body wall muscle middle	nlp-25	1.235199188	0.005855447
Body wall muscle middle	ubl-1	-0.085430815	0.006000787
Body wall muscle middle	snr-6	-0.047066207	0.006615327
Body wall muscle middle	F53F1.2	0.204975276	0.006794563
Body wall muscle middle	pyk-2	0.41140511	0.006799015
Body wall muscle middle	dhs-25	0.211320936	0.007078777
Body wall muscle middle	F49C12.15	-1.310820226	0.007475448
Body wall muscle middle	timm-23	0.265507996	0.00816187
Body wall muscle middle	Y53C12B.2	-0.245505568	0.00851701

Body wall muscle middle	F22F7.8	-0.458737478	0.009237165
Body wall muscle middle	K02D10.1	0.216597547	0.010178431
Body wall muscle middle	K02F3.9	0.398022961	0.01120169
Body wall muscle middle	T01C3.3	-0.008572294	0.011337055
Body wall muscle middle	dct-18	-0.413140135	0.011450079
Body wall muscle middle	T13F3.6	0.209813015	0.01152691
Body wall muscle middle	sca-1	0.306284758	0.011572577
Body wall muscle middle	sss-1	-1.231457809	0.014234306
Body wall muscle middle	F30A10.13	-1.788649699	0.014468897
Body wall muscle middle	cdc-48.1	-0.200137753	0.014638352
Body wall muscle middle	F14H8.4	-0.719366526	0.014673577
Body wall muscle middle	chch-3	0.189172184	0.014948549
Body wall muscle middle	rpl-11.1	-0.000811371	0.015553495
Body wall muscle middle	hpo-18	-0.271896345	0.015972206
Body wall muscle middle	rsu-1	0.204321897	0.016773392
Body wall muscle middle	atn-1	0.248894395	0.016924528
Body wall muscle middle	F59C6.5	0.18292068	0.017308313
Body wall muscle middle	unc-98	0.226936644	0.017336729
Body wall muscle middle	B0001.2	-0.026590651	0.01757767
Body wall muscle middle	B0513.4	-0.165623805	0.018340123
Body wall muscle middle	enol-1	0.117041105	0.01882795
Body wall muscle middle	sdhd-1	0.157700665	0.018962183
Body wall muscle middle	ddo-2	0.537452206	0.019330929
Body wall muscle middle	gale-1	-0.111972956	0.020361819
Body wall muscle middle	W10C8.6	0.925327717	0.020366332
Body wall muscle middle	snr-5	-0.077768836	0.021327739
Body wall muscle middle	cyb-1	-0.001144206	0.023313486
Body wall muscle middle	nduf-6	0.163018263	0.025268243
Body wall muscle middle	gba-4	-0.978015707	0.026006288
Body wall muscle middle	rpl-3	-0.08251078	0.026307016

Body wall muscle middle	pud-1.2	-0.618727859	0.026932323
Body wall muscle middle	T28A11.2	1.105259878	0.0278548
Body wall muscle middle	R08E5.3	-0.400698861	0.032969062
Body wall muscle middle	Y51H7C.13	-1.063616096	0.033550952
Body wall muscle middle	hrde-1	-0.001583409	0.03399377
Body wall muscle middle	ZK622.4	0.863951224	0.035000729
Body wall muscle middle	dod-19	-0.989278814	0.037543545
Body wall muscle middle	F48C1.9	0.260642432	0.037885827
Body wall muscle middle	K07C11.3	2.063034073	0.037930828
Body wall muscle middle	mrpl-14	0.26755333	0.038083243
Body wall muscle middle	M05D6.6	0.25283817	0.038122472
Body wall muscle middle	F23D12.11	-0.18099793	0.038187233
Body wall muscle middle	nuo-1	0.1588678	0.038198488
Body wall muscle middle	F53A9.8	-0.855682606	0.038910146
Body wall muscle middle	ncs-4	0.368604428	0.039599993
Body wall muscle middle	ugt-44	-0.381303821	0.042354652
Body wall muscle middle	rpl-20	-0.087097242	0.042910354
Body wall muscle middle	thoc-7	-0.008236552	0.042982544
Body wall muscle middle	dlst-1	0.206509933	0.043244227
Body wall muscle middle	trap-4	0.338598456	0.043290924
Body wall muscle middle	mig-18	0.494480568	0.043725916
Body wall muscle middle	gfat-2	-0.015637161	0.043775501
Body wall muscle middle	sod-3	-0.748006308	0.046934012
Body wall muscle middle	Y51F10.2	-0.034260523	0.04862356
Body wall muscle middle	rpl-41.1	-0.184988412	0.048693197
Body wall muscle middle	atp-6	-0.07823734	0.048894948
Body wall muscle middle	mrpl-11	0.2709353	0.052007976
Body wall muscle middle	nas-6	2.312759746	0.052116505
Body wall muscle middle	ptr-3	2.312759746	0.052116505
Body wall muscle middle	best-14	0.341831634	0.052635042
Body wall muscle middle	K12H4.5	0.125615348	0.053884762
Body wall muscle middle	col-101	0.28023436	0.056500357

Body wall muscle middle	puf-5	-0.185915684	0.058562471
Body wall muscle middle	srr-4	-1.594130794	0.059236253
Body wall muscle middle	fzy-1	-6.29899E-05	0.063176224
Body wall muscle middle	scl-6	1.87254E-06	0.064749245
Body wall muscle middle	act-4	0.074412895	0.064760057
Body wall muscle middle	C15H9.9	0.242249763	0.06513417
Body wall muscle middle	mlc-4	-0.111056417	0.065908721
Body wall muscle middle	ZC395.5	-0.372113081	0.06666455
Body wall muscle middle	ceh-33	0.40121613	0.067076395
Body wall muscle middle	msp-81	0.384967296	0.068617455
Body wall muscle middle	rec-8	-0.000331648	0.069589868
Body wall muscle middle	fat-7	0.978819257	0.072985443
Body wall muscle middle	cmd-1	0.171648008	0.073376017
Body wall muscle middle	R13D11.4	0.795907897	0.078019751
Body wall muscle middle	C41G7.9	0.176036483	0.084827328
Body wall muscle middle	tbh-1	-0.019231015	0.087394791
Body wall muscle middle	C28H8.5	-1.857165173	0.088938616
Body wall muscle middle	rack-1	-0.093482109	0.089445766
Body wall muscle middle	Y53H1B.2	0.166722011	0.089600154
Body wall muscle middle	rpl-18	-0.079413294	0.091462035
Body wall muscle middle	cyn-9	-5.48758E-06	0.094965351
Body wall muscle middle	cyn-6	0.841786824	0.097261706
Body wall muscle posterior	acs-2	2.206757095	7.71112E-15
Body wall muscle posterior	icl-1	0.802017217	2.04388E-07
Body wall muscle posterior	C14C6.5	-1.431810295	2.19568E-06
Body wall muscle posterior	clec-50	-1.193693196	2.15212E-05
Body wall muscle posterior	cpna-2	0.419680013	0.000369091
Body wall muscle posterior	T03F1.11	1.83145241	0.000389628
Body wall muscle posterior	M60.4	-0.80787182	0.001362803
Body wall muscle posterior	Y71H2B.4	-0.548716796	0.00186247
Body wall muscle posterior	tnc-2	2.066903053	0.001993328

Body wall muscle posterior	F28H7.3	-1.382484078	0.002654897
Body wall muscle posterior	ctc-1	0.36378315	0.003000714
Body wall muscle posterior	F54D5.4	-1.525832556	0.003045683
Body wall muscle posterior	acer-1	0.593357772	0.009938388
Body wall muscle posterior	dct-16	-0.484292183	0.010780888
Body wall muscle posterior	pud-3	-2.296601703	0.010996557
Body wall muscle posterior	F56H9.2	-0.830388416	0.018117414
Body wall muscle posterior	rpl-36.A	-0.326476239	0.026286024
Body wall muscle posterior	F55G11.4	-2.003845152	0.043482622
Body wall muscle posterior	cpz-1	-0.609328246	0.046231831
Body wall muscle posterior	lec-9	-0.742369168	0.048970031
Body wall muscle posterior	ZK6.11	-1.201071115	0.054779323
Body wall muscle posterior	cpi-1	-0.677703912	0.06833811
Body wall muscle posterior	spp-5	-0.71098556	0.071561211
Body wall muscle posterior	T21H3.1	-0.766932139	0.073773902
Body wall muscle posterior	asp-1	-0.550397586	0.07540582
Body wall muscle posterior	sqrd-1	1.32661522	0.086063327
CEP_ADE_PDE	col-154	-3.139064034	0.0259665
Cephalic and inner labial socket	rpl-41.2	-0.489117975	2.14913E-15
Cephalic and inner labial socket	C14C6.5	-2.530375585	2.65451E-09
Cephalic and inner labial socket	W01D2.1	-0.595534737	6.37392E-09
Cephalic and inner labial socket	dct-16	-0.709400302	2.61046E-08
Cephalic and inner labial socket	Y119D3B.21	-0.814722834	5.52583E-07
Cephalic and inner labial socket	zipt-2.2	-0.704356579	1.09447E-06
Cephalic and inner labial socket	ctc-3	0.37975058	1.20082E-06
Cephalic and inner labial socket	rpl-38	-0.45647115	6.87657E-06

Cephalic and inner labial socket	nduo-6	-0.276523014	4.92986E-05
Cephalic and inner labial socket	gst-21	1.141665899	0.000647211
Cephalic and inner labial socket	gst-4	0.906338203	0.000675043
Cephalic and inner labial socket	rps-28	-0.547361649	0.005052157
Cephalic and inner labial socket	rpl-36	-0.325598873	0.005457262
Cephalic and inner labial socket	asp-6	-1.157210832	0.007255458
Cephalic and inner labial socket	rpl-36.A	-0.302932713	0.018155583
Cephalic and inner labial socket	gst-35	1.344930729	0.02084948
Cephalic and inner labial socket	C37A2.7	-0.409884135	0.021500634
Cephalic and inner labial socket	rps-27	-0.301419887	0.041458302
Cephalic and inner labial socket	rps-29	-0.412452087	0.052336929
Cephalic and inner labial socket	spp-2	-2.720756666	0.063268928
Cephalic sheath	rpl-41.2	-0.471816292	2.90039E-24
Cephalic sheath	ule-2	-3.222392418	1.37036E-18
Cephalic sheath	rps-25	-0.355648055	1.48506E-18
Cephalic sheath	ctc-3	0.365221397	4.00926E-12
Cephalic sheath	W01D2.1	-0.520566159	4.9942E-12
Cephalic sheath	C35C5.9	-0.72944088	8.79025E-12
Cephalic sheath	H24K24.3	0.849333965	1.23573E-11
Cephalic sheath	rps-29	-0.538505497	3.57198E-10
Cephalic sheath	gst-21	0.872746971	1.26234E-09
Cephalic sheath	rpl-39	-0.550308268	2.65979E-09
Cephalic sheath	rpl-36.A	-0.347210193	4.57217E-09
Cephalic sheath	dct-16	-0.583122417	8.84145E-09
Cephalic sheath	R09B3.3	-0.373732321	9.6137E-09
Cephalic sheath	F32A5.4	0.850223721	4.18506E-08
Cephalic sheath	C14C6.5	-1.642844824	4.24261E-08

Cephalic sheath	ctc-1	0.340476764	3.80309E-07
Cephalic sheath	fipr-2	2.286881996	4.23353E-07
Cephalic sheath	rpl-38	-0.373247357	8.91107E-07
Cephalic sheath	rpl-43	-0.333461881	1.98845E-06
Cephalic sheath	rps-28	-0.560810408	2.78131E-06
Cephalic sheath	R05D8.7	0.529762467	5.71284E-06
Cephalic sheath	rpl-36	-0.293131059	6.59475E-06
Cephalic sheath	C37A2.7	-0.395783845	8.0813E-06
Cephalic sheath	Y119D3B.21	-0.573098142	0.000107201
Cephalic sheath	lec-9	-0.709802777	0.000123201
Cephalic sheath	F53F4.13	0.807972009	0.000154682
Cephalic sheath	C54D10.3	1.216363726	0.000164396
Cephalic sheath	nduo-6	-0.201960037	0.000171272
Cephalic sheath	F48D6.4	-1.022211485	0.000174971
Cephalic sheath	fip-2	1.352678877	0.000187064
Cephalic sheath	rpl-27	-0.324530055	0.000447884
Cephalic sheath	Y37E3.8	-0.215134645	0.00087919
Cephalic sheath	gst-35	0.985269153	0.000992008
Cephalic sheath	C05D11.5	0.64786115	0.00119128
Cephalic sheath	pud-3	-2.03689171	0.001621626
Cephalic sheath	lys-2	-1.63593036	0.002251055
Cephalic sheath	rpl-26	-0.248605727	0.003352691
Cephalic sheath	gst-4	0.800873858	0.003748179
Cephalic sheath	sams-1	0.676739948	0.004291479
Cephalic sheath	W08E12.2	1.57568719	0.004727015
Cephalic sheath	acs-2	2.114652	0.005985118
Cephalic sheath	F28H7.3	-1.189051082	0.006712843
Cephalic sheath	col-98	0.76277523	0.009626415
Cephalic sheath	col-8	0.836667254	0.011330314
Cephalic sheath	snf-3	-0.421926766	0.012527023
Cephalic sheath	T02B11.6	1.829642329	0.012718335

Cephalic sheath	rpl-34	-0.271966595	0.019169141
Cephalic sheath	tni-4	1.31336713	0.021435344
Cephalic sheath	msra-1	1.281609628	0.023478637
Cephalic sheath	spp-5	-0.780812673	0.024787634
Cephalic sheath	F53F1.2	0.961244834	0.026220436
Cephalic sheath	asp-1	-0.600794136	0.039328348
Cephalic sheath	nex-3	0.717708591	0.05885457
Cephalic sheath	ndfl-4	-0.221384265	0.079470823
Cephalic sheath	acer-1	0.576704228	0.085913072
Cephalic sheath	rpl-35	-0.182835611	0.086270367
Cephalic sheath	rpl-32	-0.188664581	0.09179916
Cephalic sheath	col-103	0.814375121	0.094140468
Cephalic sheath	col-160	0.699154378	0.099934975
Coelomocytes	aman-1	-0.531666737	1.5312E-117
Coelomocytes	ttr-1	-0.336504843	2.8349E-104
Coelomocytes	hsp-16.41	1.00985216	1.92231E-84
Coelomocytes	hsp-16.2	0.966601216	3.55918E-71
Coelomocytes	F53C11.9	-0.56951868	1.64687E-68
Coelomocytes	nurf-1	0.895752451	1.51456E-65
Coelomocytes	Y73F4A.1	0.193986409	8.46861E-63
Coelomocytes	ttx-7	0.342551858	1.04415E-54
Coelomocytes	hsp-70	0.614535137	1.27856E-49
Coelomocytes	ctc-3	0.645171137	1.72139E-47
Coelomocytes	rpl-41.2	-0.384476036	5.67883E-44
Coelomocytes	fmo-5	2.94024027	1.42528E-39
Coelomocytes	rpl-38	-0.544688285	4.68669E-38
Coelomocytes	gst-1	0.956357376	2.86705E-37
Coelomocytes	gst-7	0.379664541	1.81371E-36
Coelomocytes	K07E3.4	-0.387014826	2.46782E-36
Coelomocytes	rps-25	-0.317306105	3.17469E-36
Coelomocytes	E01G4.3	0.364620551	9.64646E-36
Coelomocytes	R107.5	0.768484441	4.75812E-34

Coelomocytes	W01D2.1	-0.593293227	3.51059E-33
Coelomocytes	Y69H2.3	-0.350811256	1.68119E-31
Coelomocytes	T19C3.5	-0.240042636	2.07409E-31
Coelomocytes	rps-27	-0.374203273	1.50666E-30
Coelomocytes	rpl-36	-0.350311741	2.29143E-29
Coelomocytes	ctc-1	0.464972338	1.1167E-28
Coelomocytes	alh-1	1.195923247	5.60267E-24
Coelomocytes	rpl-43	-0.344555074	1.19416E-22
Coelomocytes	rps-21	-0.547103438	1.60158E-22
Coelomocytes	rpl-35	-0.243077946	3.84425E-22
Coelomocytes	Y39B6A.5	-0.26623362	1.77355E-21
Coelomocytes	rpl-36.A	-0.316161751	1.74895E-20
Coelomocytes	pqn-44	0.674377486	1.8505E-20
Coelomocytes	F17C11.4	0.824446576	2.39688E-19
Coelomocytes	rps-28	-0.782086163	1.0395E-18
Coelomocytes	W02D9.10	0.915832413	2.35051E-18
Coelomocytes	R06C1.4	-0.260017364	8.28171E-18
Coelomocytes	rps-29	-0.559373111	1.24412E-17
Coelomocytes	lgg-1	0.372894153	2.84265E-17
Coelomocytes	nduo-1	0.44703582	3.98398E-16
Coelomocytes	C55A6.7	-0.374017997	9.63563E-16
Coelomocytes	ndk-1	-0.146749961	1.04677E-15
Coelomocytes	pah-1	0.710367647	1.31949E-15
Coelomocytes	rpl-33	-0.256074732	3.93556E-15
Coelomocytes	F17C11.11	1.523293679	4.45073E-15
Coelomocytes	T22B7.7	0.574376652	5.88831E-15
Coelomocytes	ubq-2	-0.20832242	7.50406E-15
Coelomocytes	R09B3.3	-0.75048881	1.95759E-14
Coelomocytes	C37A2.7	-0.34280573	3.41632E-14
Coelomocytes	F53C11.3	0.709831793	1.74107E-13

Coelomocytes	rps-26	-0.206640059	2.06363E-13
Coelomocytes	calu-1	0.284983489	2.18757E-13
Coelomocytes	rpl-34	-0.277388492	2.29891E-13
Coelomocytes	dhs-19	2.196396665	6.51076E-13
Coelomocytes	ctb-1	0.392827082	1.08525E-12
Coelomocytes	rpl-30	-0.264013877	2.20985E-11
Coelomocytes	T28F4.5	0.500619849	2.59517E-11
Coelomocytes	rpl-32	-0.191501314	2.79075E-11
Coelomocytes	atp-6	0.283863518	2.80286E-11
Coelomocytes	hsp-110	0.492929625	3.36914E-11
Coelomocytes	F32E10.8	-0.156140987	4.38121E-11
Coelomocytes	hsp-1	0.32135984	6.38735E-11
Coelomocytes	rpl-17	-0.17229231	6.69015E-11
Coelomocytes	rpl-31	-0.215331249	7.52643E-11
Coelomocytes	sodh-1	1.097129822	8.82023E-11
Coelomocytes	pck-1	-0.970942884	1.22764E-10
Coelomocytes	rla-2	-0.254355089	2.80404E-10
Coelomocytes	rps-14	-0.161127485	3.62815E-10
Coelomocytes	ctc-2	0.360144635	6.55154E-10
Coelomocytes	T14A8.2	1.039054172	6.85734E-10
Coelomocytes	col-122	1.232562075	1.23468E-09
Coelomocytes	F26A3.4	0.442089485	2.00255E-09
Coelomocytes	col-20	0.872586831	2.0351E-09
Coelomocytes	wdr-23	1.064491701	3.50849E-09
Coelomocytes	ZC116.3	-0.254634411	3.7904E-09
Coelomocytes	K01A2.4	0.815584196	4.36573E-09
Coelomocytes	rpl-12	-0.128757085	4.99437E-09
Coelomocytes	rps-23	-0.163495933	6.25062E-09
Coelomocytes	F08B12.4	-0.132069918	1.27107E-08
Coelomocytes	F18C5.10	0.330990957	1.37797E-08
Coelomocytes	xbp-1	0.234377348	1.45091E-08

Coelomocytes	Y37E3.8	-0.155408473	2.52147E-08
Coelomocytes	ard-1	-0.715697714	2.5255E-08
Coelomocytes	eef-2	-0.149453074	6.64385E-08
Coelomocytes	rmd-2	0.260887038	8.31538E-08
Coelomocytes	hsp-4	0.887764732	8.38353E-08
Coelomocytes	rpl-22	-0.189588805	1.91363E-07
Coelomocytes	R09H10.7	1.831657133	2.41945E-07
Coelomocytes	lbp-9	0.579995779	2.6154E-07
Coelomocytes	aip-1	0.701281029	2.86662E-07
Coelomocytes	F23H11.5	-0.283289452	5.65354E-07
Coelomocytes	rps-10	-0.157105119	9.11126E-07
Coelomocytes	rpl-28	-0.224723914	9.82775E-07
Coelomocytes	col-140	0.791858643	9.91456E-07
Coelomocytes	rps-19	-0.138864274	1.50415E-06
Coelomocytes	rps-13	-0.171844607	1.51703E-06
Coelomocytes	aldo-2	-0.21757789	1.68775E-06
Coelomocytes	vha-2	0.258864078	2.09251E-06
Coelomocytes	rps-12	-0.156799242	2.25048E-06
Coelomocytes	scp-1	0.920340504	3.01133E-06
Coelomocytes	rpl-21	-0.145253309	5.50333E-06
Coelomocytes	C06G3.3	0.41051877	6.74579E-06
Coelomocytes	pck-2	0.210275992	6.80053E-06
Coelomocytes	col-124	0.654391733	7.8241E-06
Coelomocytes	ccg-1	-0.236054036	1.61606E-05
Coelomocytes	rpl-39	-0.410021854	2.1898E-05
Coelomocytes	C02F5.12	1.402376761	2.29749E-05
Coelomocytes	col-125	-3.411337328	2.74308E-05
Coelomocytes	rpl-29	-1.048172947	3.28616E-05
Coelomocytes	C25H3.10	-0.874286124	3.33426E-05
Coelomocytes	flp-10	0.328959	3.92661E-05

Coelomocytes	rps-15	-0.151604289	4.11575E-05
Coelomocytes	rpl-23	-0.155733223	5.19029E-05
Coelomocytes	rpl-26	-0.158398575	5.46833E-05
Coelomocytes	nhr-17	1.250265968	7.25665E-05
Coelomocytes	col-119	1.097664512	7.33825E-05
Coelomocytes	M05D6.6	1.393512066	8.22185E-05
Coelomocytes	rps-5	-0.127956096	8.48973E-05
Coelomocytes	dnj-13	0.58392564	9.56901E-05
Coelomocytes	ubq-1	0.332091622	0.000150791
Coelomocytes	rpl-2	-0.133615109	0.00016482
Coelomocytes	R09E12.9	4.354588086	0.000251927
Coelomocytes	rpl-24.1	-0.124950018	0.000262224
Coelomocytes	mak-1	0.343022611	0.000320331
Coelomocytes	C06A12.3	-0.105407115	0.000345588
Coelomocytes	mig-6	-0.117091256	0.000562444
Coelomocytes	F17H10.1	0.821418683	0.000642953
Coelomocytes	C14H10.3	0.35564036	0.000945175
Coelomocytes	M01H9.3	0.579318957	0.00102792
Coelomocytes	rpl-13	-0.117598649	0.001136205
Coelomocytes	rps-9	-0.103513678	0.001273963
Coelomocytes	col-19	0.740896381	0.001291615
Coelomocytes	ubl-1	-0.12981634	0.002120139
Coelomocytes	glb-1	0.772177226	0.002809778
Coelomocytes	rps-7	-0.112271373	0.00281876
Coelomocytes	C06B3.6	0.568444974	0.003094851
Coelomocytes	abhd-5.2	1.407509832	0.003687745
Coelomocytes	mlc-3	0.755796222	0.003919932
Coelomocytes	tos-1	0.153267874	0.004291707
Coelomocytes	gpc-2	-0.236438805	0.007316289
Coelomocytes	nmat-2	0.882996086	0.00808641
Coelomocytes	fat-1	0.372561157	0.008640331
Coelomocytes	mnk-1	0.428830968	0.008640331
Coelomocytes	C17F4.7	0.763955521	0.009070583

Coelomocytes	unc-122	-0.112112524	0.010230446
Coelomocytes	acer-1	0.629614354	0.010469762
Coelomocytes	col-181	0.991408198	0.011256059
Coelomocytes	anat-1	0.463850356	0.016414386
Coelomocytes	rpl-20	-0.116280702	0.016715874
Coelomocytes	nduo-4	0.247789752	0.01726988
Coelomocytes	inos-1	-0.080925805	0.019413678
Coelomocytes	rps-11	-0.101401532	0.019739556
Coelomocytes	hsp-16.11	0.848296928	0.022509351
Coelomocytes	C48B6.10	-0.187296522	0.023563174
Coelomocytes	rps-3	-0.109464462	0.024289408
Coelomocytes	syx-6	0.252063738	0.027909792
Coelomocytes	rps-22	-0.139604568	0.032357262
Coelomocytes	F28F5.6	0.681348289	0.039964731
Coelomocytes	Y71H2AM.5	-0.183938086	0.042839478
Coelomocytes	col-184	0.958873328	0.043402547
Coelomocytes	grd-14	-3.858796303	0.043890419
Coelomocytes	F29C4.2	-0.250638604	0.049823756
Coelomocytes	oga-1	0.820257952	0.055045016
Coelomocytes	hsp-6	0.80474854	0.055966986
Coelomocytes	rpl-14	-0.125589982	0.059467854
Coelomocytes	rpl-27	-0.162421952	0.06379818
Coelomocytes	atgp-2	0.044823675	0.07758494
Coelomocytes	rps-0	-0.136544337	0.079091399
Coelomocytes	Y60A3A.9	0.479919354	0.082432071
Coelomocytes	skn-1	0.751895735	0.088197836
Coelomocytes	pfn-2	0.452978149	0.090812262
DVA	Y47G6A.15	36.19496259	3.61794E-80
DVA	Y51H7C.13	36.19496259	3.61794E-80
DVA	slc-36.4	2.807354922	0.081162778
DVA	R166.3	2.807354922	0.081162778
DVC	hil-5	2.736965594	0.00350698

Differentiated germ	ctc-3	0.661161587	0
Differentiated germ	col-122	1.275335013	0
Differentiated germ	ctc-1	0.605884008	3.911E-291
Differentiated germ	T03F1.11	2.42184987	4.3394E-291
Differentiated germ	col-119	1.210122432	1.3955E-290
Differentiated germ	tnc-2	2.64671111	4.8585E-263
Differentiated germ	col-20	0.8305933	3.2893E-224
Differentiated germ	col-124	0.714199646	2.3791E-218
Differentiated germ	col-184	1.114319925	3.8318E-206
Differentiated germ	eef-2	-0.363905766	3.0329E-200
Differentiated germ	hsp-12.2	1.766180989	6.2805E-191
Differentiated germ	col-98	1.492016565	7.1892E-186
Differentiated germ	col-140	0.703723006	1.7149E-184
Differentiated germ	mlc-3	0.776391537	1.5423E-181
Differentiated germ	col-8	1.507733825	7.8121E-173
Differentiated germ	ctc-2	0.524557505	1.2077E-158
Differentiated germ	col-181	0.902154714	1.6433E-149
Differentiated germ	F41E6.15	1.821892326	1.3015E-147
Differentiated germ	fipr-2	3.141023262	9.9757E-140
Differentiated germ	nduo-1	0.451258515	2.8747E-135
Differentiated germ	col-143	1.270859139	1.1368E-133
Differentiated germ	cpn-4	2.441599666	5.1494E-133
Differentiated germ	C53C9.2	2.343229815	3.3472E-121
Differentiated germ	sodh-1	1.589504302	1.5036E-110
Differentiated germ	col-19	0.615894523	2.8998E-109
Differentiated germ	col-80	0.817340918	3.8179E-109
Differentiated germ	col-106	0.9910544	5.4241E-108
Differentiated germ	tni-4	1.724717897	8.396E-106
Differentiated germ	atp-6	0.296332947	2.1471E-105
Differentiated germ	col-103	1.367130853	2.0503E-104
Differentiated germ	C24A3.2	1.432403482	1.1505E-103
Differentiated germ	Y73F4A.2	3.154184498	2.6098E-99
Differentiated germ	fipr-1	2.604838911	7.3221E-99
Differentiated germ	ZC116.1	2.886828978	2.4345E-97
Differentiated germ	Y87G2A.19	2.426957697	2.70621E-93
Differentiated germ	hsp-16.2	1.694595579	4.65074E-91
Differentiated germ	C06A8.3	0.868882091	2.06675E-87
Differentiated germ	far-2	0.574043994	5.21071E-84
Differentiated germ	pqn-60	2.959352876	8.38421E-83
Differentiated germ	hsp-16.41	1.92402442	1.05657E-80
Differentiated germ	C45G9.6	2.165341417	1.08562E-78
Differentiated germ	col-101	1.029905015	1.08072E-77

Differentiated germ	ctb-1	0.350523426	1.24367E-77
Differentiated germ	C54D10.3	1.038917038	2.20358E-74
Differentiated germ	K03E5.2	1.083137765	4.062E-73
Differentiated germ	F15A4.6	1.139571299	6.77937E-73
Differentiated germ	col-160	1.004528314	1.25343E-72
Differentiated germ	fip-2	1.224153218	1.36555E-67
Differentiated germ	W01D2.1	-0.26640321	7.20384E-67
Differentiated germ	F11E6.3	0.987036479	7.51592E-66
Differentiated germ	C14C6.5	-1.450989383	3.68956E-65
Differentiated germ	far-3	2.176342434	1.79384E-63
Differentiated germ	mlc-2	0.54937531	6.44909E-62
Differentiated germ	ttr-21	2.700675615	1.36821E-60
Differentiated germ	rps-2	-0.181463884	2.46067E-59
Differentiated germ	gst-4	0.586970072	6.00578E-58
Differentiated germ	col-42	0.966038049	2.95905E-57
Differentiated germ	fipr-10	2.416040094	1.53483E-53
Differentiated germ	tnt-4	1.860483167	2.0898E-53
Differentiated germ	fipr-5	2.045803888	2.40728E-51
Differentiated germ	T13F3.6	0.802499354	3.13725E-51
Differentiated germ	T20G5.8	0.824986036	5.85225E-51
Differentiated germ	rpl-38	-0.215949994	1.13941E-49
Differentiated germ	myo-2	2.193042525	2.44766E-49
Differentiated germ	fipr-7	2.003129692	1.1419E-48
Differentiated germ	ndk-1	-0.141432425	3.19451E-48
Differentiated germ	act-4	0.414361336	1.06923E-47
Differentiated germ	rpl-12	-0.110653817	2.01786E-47
Differentiated germ	F35B12.3	2.480632534	2.2322E-47
Differentiated germ	R09B3.3	-0.139633949	4.16502E-46
Differentiated germ	pck-2	0.640271785	2.08526E-45
Differentiated germ	eef-1A.1	-0.129092503	5.41354E-43
Differentiated germ	ndfl-4	0.270784114	1.58351E-42
Differentiated germ	rpl-13	-0.114895268	1.81768E-42
Differentiated germ	ttr-2	1.258635738	1.89453E-42
Differentiated germ	ttr-26	1.802816865	3.91581E-42
Differentiated germ	C17F4.7	0.514975748	4.52915E-42

Differentiated germ	rpl-2	-0.126740612	2.18046E-41
Differentiated germ	ZC116.5	2.038748794	8.00947E-41
Differentiated germ	pab-1	-0.215411947	3.63243E-40
Differentiated germ	rps-3	-0.128242534	1.2233E-39
Differentiated germ	anmt-2	1.229320454	1.30691E-39
Differentiated germ	rpl-36	-0.153394683	3.0606E-38
Differentiated germ	Y73F4A.3	2.313622083	5.18964E-38
Differentiated germ	tnt-3	1.30806314	2.66859E-37
Differentiated germ	rack-1	-0.144537017	4.86348E-37
Differentiated germ	cpr-5	1.233297662	7.22793E-37
Differentiated germ	vamp-8	1.677090386	7.94603E-37
Differentiated germ	fipr-3	2.049572722	1.45403E-36
Differentiated germ	col-178	0.670987368	3.24662E-36
Differentiated germ	rpl-18	-0.124355317	5.24908E-36
Differentiated germ	ttr-15	0.554682087	6.03523E-36
Differentiated germ	rps-5	-0.108710304	2.3423E-35
Differentiated germ	rpl-32	-0.117710393	2.39631E-35
Differentiated germ	rps-0	-0.147742044	3.22179E-35
Differentiated germ	rps-28	-0.287484693	1.06995E-34
Differentiated germ	dod-6	0.80894137	1.49496E-34
Differentiated germ	hsp-70	1.508930305	1.54834E-34
Differentiated germ	rpl-21	-0.111563392	2.00933E-34
Differentiated germ	myo-1	2.050868263	2.5508E-34
Differentiated germ	nduo-6	0.164859885	7.19202E-34
Differentiated germ	rpl-34	-0.173714113	8.93751E-34
Differentiated germ	rps-21	-0.238922158	1.05079E-33
Differentiated germ	rpl-17	-0.108881969	2.3905E-33
Differentiated germ	lev-11	0.400281611	2.5161E-33
Differentiated germ	cyc-2.1	0.301706606	5.22398E-33
Differentiated germ	K08D12.6	0.677901577	5.1622E-32
Differentiated germ	abf-5	1.90815058	5.36682E-32

Differentiated germ	fipr-11	2.384743002	7.69959E-32
Differentiated germ	col-142	0.658146343	4.46739E-31
Differentiated germ	F36F2.1	1.251625778	6.80868E-31
Differentiated germ	nduo-2	0.309806579	3.34743E-30
Differentiated germ	R02C2.7	1.760021617	5.13118E-30
Differentiated germ	fipr-4	1.679850637	5.62451E-30
Differentiated germ	gpx-5	1.073728975	2.09237E-29
Differentiated germ	rps-25	-0.098794845	3.16526E-29
Differentiated germ	mlc-1	0.472839323	5.93352E-29
Differentiated germ	ttr-27	1.572122178	6.69036E-29
Differentiated germ	oig-3	0.915945871	1.88379E-28
Differentiated germ	W10C8.6	1.279909696	4.18929E-28
Differentiated germ	rps-9	-0.083454343	4.78402E-28
Differentiated germ	C05D11.5	0.327454924	1.59087E-27
Differentiated germ	rpl-7A	-0.125972842	1.82068E-27
Differentiated germ	col-93	0.447257575	2.14344E-27
Differentiated germ	C45E5.4	1.858694311	1.10173E-26
Differentiated germ	fib-1	-0.225676293	1.38382E-26
Differentiated germ	Y43F8B.1	0.812438873	5.29663E-26
Differentiated germ	nduo-5	0.259106635	9.2199E-26
Differentiated germ	pqn-94	1.820716981	9.89797E-26
Differentiated germ	rps-23	-0.100874213	1.04355E-25
Differentiated germ	F32A5.4	1.753082109	2.54147E-25
Differentiated germ	rpl-7	-0.118806178	4.76352E-25
Differentiated germ	pud-3	-1.721128338	6.22471E-25
Differentiated germ	F46H5.3	0.357115158	3.37401E-24
Differentiated germ	K07H8.10	-0.263276561	6.93805E-24
Differentiated germ	pud-4	-1.666069758	4.12559E-23
Differentiated germ	acp-6	0.671046045	9.44572E-23
Differentiated germ	K07C5.4	-0.260578388	1.23634E-22
Differentiated germ	C15H9.9	0.6236558	1.3355E-22
Differentiated germ	F13C5.5	2.078882632	1.59207E-22
Differentiated germ	asp-2	0.843295879	1.68048E-22
Differentiated germ	perm-2	0.400445276	2.11045E-22

Differentiated germ	rpl-15	-0.103451074	1.45284E-21
Differentiated germ	lec-2	0.49552247	1.56161E-21
Differentiated germ	F53F4.13	0.573110282	2.10965E-21
Differentiated germ	R04F11.2	0.19521384	4.34491E-21
Differentiated germ	rpl-5	-0.101932906	5.85136E-21
Differentiated germ	rps-29	-0.176602402	9.52087E-21
Differentiated germ	act-2	-0.250158524	1.13752E-20
Differentiated germ	hpo-26	1.721367008	4.0278E-20
Differentiated germ	ttr-45	1.130224579	5.28534E-20
Differentiated germ	M163.8	0.400753857	6.1396E-20
Differentiated germ	lys-4	0.701654164	1.075E-19
Differentiated germ	pmt-2	0.416026002	2.50149E-19
Differentiated germ	rps-13	-0.105196891	2.65175E-19
Differentiated germ	gst-10	-0.75096281	2.90287E-19
Differentiated germ	Y105C5B.5	0.348444466	3.40174E-19
Differentiated germ	nspb-6	1.659071592	4.60451E-19
Differentiated germ	col-139	0.261068519	4.60987E-19
Differentiated germ	pudl-1	1.468667795	5.30154E-19
Differentiated germ	ifa-1	1.122227721	5.89231E-19
Differentiated germ	ubl-1	-0.103557487	6.60744E-19
Differentiated germ	ZK622.4	1.066720787	7.33469E-19
Differentiated germ	col-129	0.320964768	1.08254E-18
Differentiated germ	marg-1	1.66415696	1.14675E-18
Differentiated germ	rpl-28	-0.130733401	2.29834E-18
Differentiated germ	fipr-6	1.790142398	2.97779E-18
Differentiated germ	nspb-8	1.516759704	4.13902E-18
Differentiated germ	flp-28	1.770227156	4.23225E-18
Differentiated germ	ZK863.8	0.944754798	1.36401E-17
Differentiated germ	rps-15	-0.091504239	1.49081E-17
Differentiated germ	gpx-3	1.738199355	1.79823E-17
Differentiated germ	Y47G6A.33	0.480807092	2.75218E-17
Differentiated germ	T19H12.6	0.876545866	3.5873E-17
Differentiated germ	rpl-3	-0.084143655	4.864E-17
Differentiated germ	rpl-33	-0.108677476	5.94332E-17

Differentiated germ	R09B3.2	-0.138609159	5.97835E-17
Differentiated germ	msp-36	0.288340213	6.54919E-17
Differentiated germ	C53B7.3	1.725368102	9.7659E-17
Differentiated germ	Y47G6A.15	1.546086398	1.24603E-16
Differentiated germ	rpl-29	-0.250780843	1.69546E-16
Differentiated germ	rps-6	-0.126690204	1.82954E-16
Differentiated germ	gln-3	0.531430394	2.39817E-16
Differentiated germ	T28D6.3	0.466485462	2.42153E-16
Differentiated germ	rpl-36.A	-0.103126565	3.30804E-16
Differentiated germ	eef-1G	-0.117588558	3.71773E-16
Differentiated germ	M02H5.8	0.519470288	3.88232E-16
Differentiated germ	rpl-16	-0.089206453	5.76971E-16
Differentiated germ	rpl-41.2	-0.101765178	8.74776E-16
Differentiated germ	rpl-20	-0.087685032	1.96787E-15
Differentiated germ	F35A5.2	0.530470604	2.39198E-15
Differentiated germ	W03F8.6	1.368936944	2.44785E-15
Differentiated germ	glh-1	-0.288155385	2.63279E-15
Differentiated germ	flp-22	1.680916902	3.93637E-15
Differentiated germ	rps-18	-0.074851096	4.40587E-15
Differentiated germ	C49G7.3	0.658291561	4.73538E-15
Differentiated germ	rpl-1	-0.08514577	5.06591E-15
Differentiated germ	ZK596.1	1.082515312	5.08028E-15
Differentiated germ	rpl-24.1	-0.07699265	6.17725E-15
Differentiated germ	K09G1.1	0.581750771	7.69882E-15
Differentiated germ	ZC21.3	1.749840027	8.60145E-15
Differentiated germ	nspb-12	1.20057857	1.01882E-14
Differentiated germ	spp-18	-1.153654966	1.85832E-14
Differentiated germ	rpl-4	-0.111452161	4.69596E-14
Differentiated germ	dct-16	-0.215821286	5.07208E-14
Differentiated germ	M03F4.6	0.628872777	5.08921E-14
Differentiated germ	rla-0	-0.077321625	5.80987E-14

Differentiated germ	cyn-7	-0.10285885	9.76653E-14
Differentiated germ	fipr-9	1.545833638	1.3482E-13
Differentiated germ	clec-47	1.251097128	1.56834E-13
Differentiated germ	col-81	0.264879396	1.90853E-13
Differentiated germ	elo-6	0.554315885	2.39642E-13
Differentiated germ	C44B11.6	0.743045771	2.72476E-13
Differentiated germ	F22F4.9	0.843732288	2.90447E-13
Differentiated germ	F22B5.4	1.127041039	3.66453E-13
Differentiated germ	scl-6	0.514084185	3.80231E-13
Differentiated germ	anmt-3	0.796054875	3.88207E-13
Differentiated germ	vig-1	-0.20567242	4.17591E-13
Differentiated germ	daf-21	-0.120469142	5.87907E-13
Differentiated germ	lbp-1	1.411452899	5.90246E-13
Differentiated germ	lec-10	-0.513403289	8.20323E-13
Differentiated germ	nduo-4	0.160243861	1.04194E-12
Differentiated germ	gst-5	0.499966786	1.28539E-12
Differentiated germ	msra-1	0.95969898	1.76223E-12
Differentiated germ	Y119D3B.21	-0.309931977	1.87248E-12
Differentiated germ	hsp-17	0.793247933	2.26603E-12
Differentiated germ	ttr-22	1.997742137	3.60851E-12
Differentiated germ	F08D12.2	2.071409739	3.63416E-12
Differentiated germ	rps-26	-0.082934274	3.97816E-12
Differentiated germ	C27B7.9	0.543947103	3.98053E-12
Differentiated germ	rps-10	-0.078894063	7.09874E-12
Differentiated germ	T04F8.8	0.541856035	7.49022E-12
Differentiated germ	rps-4	-0.081286948	7.64849E-12
Differentiated germ	Y37E3.8	-0.066921788	8.85802E-12
Differentiated germ	rpl-9	-0.084916536	9.10619E-12
Differentiated germ	C53A3.2	0.236837221	1.12112E-11
Differentiated germ	clec-50	-0.640807039	1.14908E-11
Differentiated germ	ZC449.5	1.671147169	1.70358E-11
Differentiated germ	icd-2	-0.116780671	3.3165E-11
Differentiated germ	T24B8.5	-1.235471846	4.74193E-11
Differentiated germ	unc-87	0.313779401	4.78647E-11

Differentiated germ	ncx-2	1.597886892	6.77398E-11
Differentiated germ	C10G8.4	0.780914866	7.14318E-11
Differentiated germ	hsp-16.48	0.51661198	1.15236E-10
Differentiated germ	F43D2.6	1.359710085	1.20778E-10
Differentiated germ	asp-4	0.825712818	1.2561E-10
Differentiated germ	tni-3	0.234982524	1.65082E-10
Differentiated germ	spp-2	-0.916287689	1.69004E-10
Differentiated germ	Y110A2AL.9	1.845497209	1.84855E-10
Differentiated germ	flp-5	1.496762112	2.24493E-10
Differentiated germ	F43C9.2	0.654436057	3.05602E-10
Differentiated germ	lys-7	-0.933181979	3.08341E-10
Differentiated germ	rpl-26	-0.081878752	7.83045E-10
Differentiated germ	fat-7	1.224825468	8.43264E-10
Differentiated germ	rpl-31	-0.090987163	1.30881E-09
Differentiated germ	rpl-27	-0.104034269	1.31353E-09
Differentiated germ	icd-1	-0.113798648	1.36517E-09
Differentiated germ	rps-1	-0.070813176	1.37138E-09
Differentiated germ	ttr-51	0.313742072	1.61965E-09
Differentiated germ	asg-2	0.320611314	1.65922E-09
Differentiated germ	F14F8.8	1.874194306	2.1533E-09
Differentiated germ	C23H5.8	-0.595117741	2.81119E-09
Differentiated germ	rpl-43	-0.095444053	2.82366E-09
Differentiated germ	tomm-20	0.316528012	3.00595E-09
Differentiated germ	Y82E9BR.3	0.095561222	3.53244E-09
Differentiated germ	C23H3.2	0.619995804	3.61985E-09
Differentiated germ	cgh-1	-0.202591477	3.92097E-09
Differentiated germ	snet-1	1.370564972	4.1262E-09
Differentiated germ	F55A4.7	1.279553492	4.14375E-09
Differentiated germ	F41G3.10	0.411003731	4.22668E-09
Differentiated germ	cpr-4	0.793788764	4.58184E-09
Differentiated germ	F53A9.9	1.021986043	4.76719E-09
Differentiated germ	Y106G6D.8	0.990873556	5.37296E-09
Differentiated germ	acs-2	0.494632264	6.42451E-09
Differentiated germ	C44B7.5	0.562803732	6.53626E-09
Differentiated germ	best-14	0.444517264	7.77162E-09

Differentiated germ	asb-2	0.365305091	7.91906E-09
Differentiated germ	pqn-31	1.519067934	1.32114E-08
Differentiated germ	C37C3.12	1.591959224	1.45492E-08
Differentiated germ	grd-3	0.859970754	1.86268E-08
Differentiated germ	sip-1	-0.184374774	1.87783E-08
Differentiated germ	tsp-16	1.41621443	1.95878E-08
Differentiated germ	ifg-1	-0.325900624	1.97013E-08
Differentiated germ	spat-2	-0.399030771	2.60223E-08
Differentiated germ	Y105C5A.8	0.49975413	2.91197E-08
Differentiated germ	ubq-2	-0.071971184	2.99406E-08
Differentiated germ	nog-1	-0.243073341	3.12701E-08
Differentiated germ	Y111B2A.2	-0.295707036	3.25203E-08
Differentiated germ	ttr-23	1.042050856	4.04282E-08
Differentiated germ	F48D6.4	-0.465265975	4.10711E-08
Differentiated germ	rpl-10	-0.052919331	4.29925E-08
Differentiated germ	sbt-1	1.193415203	4.37953E-08
Differentiated germ	F08D12.3	1.334997038	5.81167E-08
Differentiated germ	F40A3.2	0.319419789	6.36727E-08
Differentiated germ	myo-5	0.712356641	6.47781E-08
Differentiated germ	asp-13	0.720009122	6.8547E-08
Differentiated germ	ZK822.2	0.555778467	7.64936E-08
Differentiated germ	F21C10.9	0.730679296	7.7555E-08
Differentiated germ	rpl-39	-0.144345663	7.94364E-08
Differentiated germ	T21D12.12	0.933471695	8.38831E-08
Differentiated germ	F08B4.8	-0.48183763	9.16482E-08
Differentiated germ	rpl-6	-0.065684404	9.23472E-08
Differentiated germ	C06A8.8	1.276253155	9.5183E-08
Differentiated germ	cey-3	-0.142747898	1.0228E-07
Differentiated germ	emo-1	0.178457956	1.90333E-07
Differentiated germ	nlp-27	0.402044943	1.96489E-07
Differentiated germ	F22H10.3	-0.468628658	1.99262E-07
Differentiated germ	ben-1	0.78650886	2.2061E-07
Differentiated germ	cpl-1	0.531252385	2.38438E-07

Differentiated germ	K10H10.12	1.205403404	2.38882E-07
Differentiated germ	dod-19	-1.244067383	2.51971E-07
Differentiated germ	sqd-1	-0.304416726	2.6779E-07
Differentiated germ	sams-1	0.3329426	2.77958E-07
Differentiated germ	fipr-21	0.369381082	2.94431E-07
Differentiated germ	dim-1	0.277855545	3.81796E-07
Differentiated germ	F55C10.5	1.046691129	3.90143E-07
Differentiated germ	aqp-1	0.652463299	4.03458E-07
Differentiated germ	nap-1	-0.133124027	4.17558E-07
Differentiated germ	cpz-1	0.572778893	4.23292E-07
Differentiated germ	tag-290	0.528933002	4.5143E-07
Differentiated germ	F42A8.1	0.320438349	4.84581E-07
Differentiated germ	C44C10.9	0.816321791	6.37403E-07
Differentiated germ	aqp-7	0.441810081	7.75203E-07
Differentiated germ	flp-12	1.257405655	8.96149E-07
Differentiated germ	Y43B11AR.1	1.031870555	9.00104E-07
Differentiated germ	C46G7.2	0.174444026	1.10774E-06
Differentiated germ	T22B7.7	0.181737221	1.13752E-06
Differentiated germ	asp-5	0.492828725	1.17831E-06
Differentiated germ	hsp-25	0.3484981	1.33241E-06
Differentiated germ	lys-2	-0.738156001	1.3387E-06
Differentiated germ	cco-2	0.142014714	1.4964E-06
Differentiated germ	F41G3.21	0.38168317	1.53097E-06
Differentiated germ	F01D5.3	-0.789017403	1.53449E-06
Differentiated germ	flp-14	0.993556602	1.66526E-06
Differentiated germ	clec-1	0.411700452	1.96391E-06
Differentiated germ	lec-7	1.474175701	1.98505E-06
Differentiated germ	F48C1.9	1.137154408	1.98751E-06
Differentiated germ	nol-5	-0.180358079	2.05349E-06
Differentiated germ	Y75B7AR.1	1.202168096	2.12885E-06
Differentiated germ	col-179	0.441053086	2.16249E-06
Differentiated germ	nlp-6	1.594943525	2.59263E-06
Differentiated germ	calu-1	0.491150132	3.51903E-06
Differentiated germ	mpc-1	0.344551259	3.52602E-06
Differentiated germ	csq-1	0.555088685	3.97976E-06
Differentiated germ	scl-3	0.509650061	4.53302E-06
Differentiated germ	prmt-1	-0.137609877	4.59692E-06

Differentiated germ	exc-9	0.739962416	4.70182E-06
Differentiated germ	aldo-1	0.464437897	5.976E-06
Differentiated germ	F12A10.1	0.465017011	6.18677E-06
Differentiated germ	C37A2.7	-0.094917297	6.30361E-06
Differentiated germ	F26F2.8	0.943528246	8.01239E-06
Differentiated germ	rps-27	-0.076679244	8.96944E-06
Differentiated germ	fipr-13	0.818029807	9.27391E-06
Differentiated germ	ZK809.8	0.331333627	9.43746E-06
Differentiated germ	C30G12.2	0.588279516	9.57817E-06
Differentiated germ	F55G11.4	-1.53111475	9.66702E-06
Differentiated germ	acer-1	0.284099679	1.06503E-05
Differentiated germ	unc-15	0.326028844	1.12287E-05
Differentiated germ	C01G10.15	1.298394738	1.12331E-05
Differentiated germ	ttr-29	1.287251186	1.15157E-05
Differentiated germ	Y45F10D.2	1.097465084	1.15915E-05
Differentiated germ	F13H10.6	0.622610516	1.23113E-05
Differentiated germ	C30F2.3	1.25569307	1.35256E-05
Differentiated germ	T23E7.2	0.500621283	1.41512E-05
Differentiated germ	tag-18	-0.16772593	1.51796E-05
Differentiated germ	lec-4	0.371116236	1.61471E-05
Differentiated germ	C10B5.3	1.002291693	1.62555E-05
Differentiated germ	cct-2	-0.228561694	1.67863E-05
Differentiated germ	F55H12.4	0.400476354	1.86651E-05
Differentiated germ	atp-2	0.108601669	1.87482E-05
Differentiated germ	grd-5	0.535418928	1.99871E-05
Differentiated germ	F46F2.3	0.419959455	2.04469E-05
Differentiated germ	flp-9	1.088892317	2.12135E-05
Differentiated germ	F14H12.3	1.286540833	2.50121E-05
Differentiated germ	F28H7.3	-0.522874823	2.54412E-05
Differentiated germ	Y41C4A.11	1.021542152	3.14522E-05
Differentiated germ	rpl-23	-0.064459763	3.40633E-05
Differentiated germ	col-96	1.103260474	3.41271E-05
Differentiated germ	gst-13	-0.41331374	3.41349E-05
Differentiated germ	F09B12.7	1.127240587	3.44302E-05
Differentiated germ	col-77	-0.475235897	3.47648E-05
Differentiated germ	nas-20	-2.894454985	3.61525E-05
Differentiated germ	flp-24	0.910596593	4.41151E-05

Differentiated germ	prg-2	-0.432344329	4.83317E-05
Differentiated germ	abf-6	1.599440774	5.03492E-05
Differentiated germ	F23D12.11	0.203931895	5.32038E-05
Differentiated germ	eat-6	0.317662079	5.52761E-05
Differentiated germ	rpl-35	-0.055199201	5.69656E-05
Differentiated germ	T03D8.7	0.665394781	5.88527E-05
Differentiated germ	ttr-18	0.483413111	5.89116E-05
Differentiated germ	grd-10	0.401684134	6.05296E-05
Differentiated germ	ifet-1	-0.253808599	6.5348E-05
Differentiated germ	C48E7.1	0.347591563	6.54144E-05
Differentiated germ	F36F2.2	0.627699952	6.67603E-05
Differentiated germ	ifa-4	1.119877587	6.87801E-05
Differentiated germ	col-133	-0.372201085	7.28066E-05
Differentiated germ	T04C12.3	1.208137496	8.23561E-05
Differentiated germ	piit-1	1.273781066	8.88864E-05
Differentiated germ	nuo-3	0.126880299	9.6731E-05
Differentiated germ	grl-30	-4.194015049	9.86232E-05
Differentiated germ	nspa-8	-0.166540864	0.000105441
Differentiated germ	nlp-3	1.082695618	0.000105622
Differentiated germ	vit-5	0.372343805	0.00010629
Differentiated germ	F34D10.8	-0.121718807	0.000108865
Differentiated germ	nuo-4	0.266172219	0.00013092
Differentiated germ	his-37	0.336187899	0.000134765
Differentiated germ	pgp-14	1.275295379	0.000139104
Differentiated germ	F13H8.3	1.064625001	0.000179126
Differentiated germ	aqp-8	0.540864519	0.000185542
Differentiated germ	hsp-1	-0.100403414	0.000198651
Differentiated germ	F08B12.4	0.532048442	0.000232524
Differentiated germ	lec-8	-0.440545485	0.000247615
Differentiated germ	hmg-1.1	-0.16848242	0.000279386
Differentiated germ	nspd-2	-0.1926759	0.000287269
Differentiated germ	scl-5	0.512014134	0.000292417
Differentiated germ	cpg-9	0.20991027	0.000300517
Differentiated germ	ZK836.3	0.754773901	0.000337954
Differentiated germ	msrp-7	0.30417991	0.000386556

Differentiated germ	Y110A2AL.3	1.032371456	0.000416937
Differentiated germ	tmd-2	0.558661695	0.000426283
Differentiated germ	msp-40	0.19272097	0.000433441
Differentiated germ	fmo-2	0.804111282	0.000508342
Differentiated germ	rpl-14	-0.056519332	0.000521376
Differentiated germ	msp-57	-0.135407473	0.000537466
Differentiated germ	R09E12.9	0.801558391	0.000554972
Differentiated germ	T18D3.5	1.127378823	0.000585848
Differentiated germ	T23B3.2	0.801065469	0.000603564
Differentiated germ	R13D11.4	0.95266834	0.000666151
Differentiated germ	spp-5	-0.342145119	0.000684473
Differentiated germ	rps-22	-0.064615229	0.000792571
Differentiated germ	F23A7.4	-0.397761485	0.000843519
Differentiated germ	nex-3	0.558061443	0.000845031
Differentiated germ	eif-3.D	-0.227996284	0.000924228
Differentiated germ	nspb-10	1.045395803	0.001087663
Differentiated germ	Y116A8B.4	0.279026618	0.001274868
Differentiated germ	Y102A11A.5	2.014944945	0.001406023
Differentiated germ	F57F5.1	0.281988081	0.001458174
Differentiated germ	Y48E1B.8	0.392975306	0.001545213
Differentiated germ	rla-2	-0.075004287	0.001612907
Differentiated germ	lec-9	-0.251806937	0.001616846
Differentiated germ	ram-2	-0.409798539	0.001666105
Differentiated germ	C39E9.8	0.47195356	0.001722295
Differentiated germ	ugt-61	0.462786242	0.00173601
Differentiated germ	T27C4.1	1.154313151	0.001777691
Differentiated germ	nkb-3	0.598303738	0.001976187
Differentiated germ	gst-7	0.320110844	0.001998393
Differentiated germ	T02H6.11	0.118615805	0.00210175
Differentiated germ	nmy-2	-0.243388621	0.002120892
Differentiated germ	mix-1	-0.308431002	0.00246428
Differentiated germ	lgg-1	0.243752904	0.002515549
Differentiated germ	clu-1	-0.215959593	0.002589649

Differentiated germ	Y45F10C.4	-0.523543821	0.002729478
Differentiated germ	gpd-2	0.28628646	0.002745401
Differentiated germ	C15H9.11	0.701335276	0.003070692
Differentiated germ	cpb-3	-0.227278521	0.003207052
Differentiated germ	H36L18.2	0.203596614	0.003318516
Differentiated germ	cyn-6	0.754833208	0.003327237
Differentiated germ	nspd-7	-0.126282183	0.003375124
Differentiated germ	Y17D7B.4	-0.529553653	0.003474363
Differentiated germ	enol-1	0.222108808	0.003498833
Differentiated germ	D1054.18	-0.197926707	0.003662924
Differentiated germ	msa-1	0.80768306	0.00381204
Differentiated germ	cth-2	0.183412313	0.003928898
Differentiated germ	F55F10.1	-0.289337369	0.004001571
Differentiated germ	R06F6.14	0.227465836	0.004228938
Differentiated germ	C28C12.4	1.639861663	0.004475058
Differentiated germ	cpg-1	0.236073026	0.004575871
Differentiated germ	rps-8	-0.044428203	0.005117839
Differentiated germ	cab-1	0.88797439	0.005334763
Differentiated germ	fipr-8	0.984824067	0.005437888
Differentiated germ	nuo-6	0.188919005	0.005764027
Differentiated germ	K07A1.13	0.109943422	0.005788017
Differentiated germ	mai-2	0.131025273	0.006255255
Differentiated germ	tba-2	-0.12713732	0.00715965
Differentiated germ	B0410.3	0.472757179	0.007211141
Differentiated germ	F16B3.2	0.222900001	0.007441973
Differentiated germ	F42G8.10	0.198923869	0.007486566
Differentiated germ	W08E12.7	-0.138311523	0.007983513
Differentiated germ	rpl-19	-0.043489604	0.008482869
Differentiated germ	puf-12	-0.192631641	0.008858207
Differentiated germ	ugt-44	-0.487447094	0.009220404
Differentiated germ	vha-4	0.337594409	0.00983247
Differentiated germ	F53F1.2	0.356805718	0.010335217
Differentiated germ	cex-2	0.232766177	0.011140608
Differentiated germ	Y44A6D.2	0.935589245	0.011224643

Differentiated germ	ttr-59	0.418802701	0.011388254
Differentiated germ	R06C1.4	-0.184215471	0.012521842
Differentiated germ	rbd-1	-0.248749116	0.013011612
Differentiated germ	crf-1	0.953846768	0.013237039
Differentiated germ	col-147	0.238908378	0.014030659
Differentiated germ	D2030.4	0.190984333	0.014105268
Differentiated germ	cal-5	0.226498415	0.014402568
Differentiated germ	W10C8.4	0.865911449	0.014525304
Differentiated germ	pghm-1	1.008950259	0.015518921
Differentiated germ	W02D9.10	0.353524288	0.015725043
Differentiated germ	set-18	0.268899717	0.016050333
Differentiated germ	T22B11.4	0.636428351	0.016465127
Differentiated germ	Y71F9B.13	0.309241432	0.016491794
Differentiated germ	T02B11.4	0.19595361	0.016677648
Differentiated germ	pho-4	0.545291838	0.016834842
Differentiated germ	T23B12.11	1.13631512	0.017042759
Differentiated germ	cal-3	1.007808785	0.018173143
Differentiated germ	ifb-1	0.359116762	0.018209035
Differentiated germ	nop-1	-0.25102017	0.01845792
Differentiated germ	C54E4.4	0.900986861	0.019982067
Differentiated germ	F26B1.8	-0.560087014	0.020907138
Differentiated germ	dhs-20	0.328893314	0.021135159
Differentiated germ	egl-45	-0.196686479	0.021137511
Differentiated germ	inf-1	-0.12294685	0.021624839
Differentiated germ	F17A9.4	0.327180761	0.022888168
Differentiated germ	T16H12.9	0.721768123	0.027958261
Differentiated germ	K01G5.5	-0.122994249	0.029995956
Differentiated germ	C17F3.1	-0.038750239	0.032886842
Differentiated germ	F46G10.1	-0.345898121	0.033744163
Differentiated germ	cpi-1	0.249822061	0.034232266
Differentiated germ	F36H9.4	0.321750894	0.034275899
Differentiated germ	avr-15	0.984949175	0.034794869
Differentiated germ	nlp-13	1.079905503	0.036138222
Differentiated germ	fat-3	0.359180948	0.038721791
Differentiated germ	rpl-11.1	-0.044416457	0.039300755
Differentiated germ	phat-3	0.228111313	0.03953353

Differentiated germ	cdr-6	0.65173334	0.039756561
Differentiated germ	unc-44	0.258279148	0.039807957
Differentiated germ	vha-17	0.260503109	0.039808691
Differentiated germ	msd-4	0.119701091	0.040196562
Differentiated germ	rpoa-12	0.291386486	0.040880625
Differentiated germ	ears-1	-0.216389009	0.041113905
Differentiated germ	myo-6	0.711652622	0.043652175
Differentiated germ	C25H3.9	0.193796922	0.043772585
Differentiated germ	K07A12.8	0.487591546	0.045827937
Differentiated germ	W10C8.5	0.346632041	0.048321622
Differentiated germ	sdz-27	0.130962021	0.049103892
Differentiated germ	gas-1	0.38386737	0.049994106
Differentiated germ	perm-4	0.2258954	0.050460543
Differentiated germ	flp-26	0.907109123	0.051507131
Differentiated germ	K08D12.3	-0.105353354	0.052362188
Differentiated germ	pgp-5	-0.447885135	0.052875225
Differentiated germ	ugt-41	0.535841034	0.057360765
Differentiated germ	ucr-2.1	0.379825031	0.05747228
Differentiated germ	rps-7	-0.038886774	0.057951278
Differentiated germ	camt-1	0.449465913	0.062306063
Differentiated germ	apl-1	0.749913911	0.062662921
Differentiated germ	F47B8.2	1.055476993	0.064823556
Differentiated germ	R12E2.7	-0.463263407	0.065205971
Differentiated germ	top-2	-0.257018646	0.069862516
Differentiated germ	R07B1.11	0.900390132	0.069872772
Differentiated germ	gyg-1	0.213695097	0.073165746
Differentiated germ	elo-2	0.351572966	0.073580393
Differentiated germ	atp-3	0.118152659	0.074982229
Differentiated germ	ZK593.3	0.553542063	0.078856487
Differentiated germ	unc-52	0.720895399	0.079573718
Differentiated germ	asb-1	-0.138869273	0.082118251
Differentiated germ	nol-1	-0.219234312	0.082744811
Differentiated germ	mdt-26	-0.319933997	0.083327564
Differentiated germ	amt-1	0.396767351	0.085466238
Differentiated germ	egl-21	0.995605688	0.090764993

Differentiated germ	ncam-1	0.815829948	0.092582696
Differentiated germ	prp-8	-0.19920185	0.098365593
Distal tip	acs-2	3.042728103	4.41616E-12
Distal tip	sodh-1	0.796265836	8.66402E-10
Distal tip	Y4C6B.7	-0.946980586	1.28491E-05
Distal tip	hsp-16.2	1.000688832	4.07874E-05
Distal tip	D2092.4	-0.864831033	0.000129651
Distal tip	rpl-41.2	-0.367534314	0.000195289
Distal tip	gst-4	1.028593181	0.00081933
Distal tip	F40F8.5	-0.283925158	0.001060489
Distal tip	far-1	-0.293523395	0.001290123
Distal tip	alh-1	0.547257464	0.001581433
Distal tip	hsp-70	0.584234281	0.001671399
Distal tip	col-122	1.166186705	0.00361202
Distal tip	rpl-43	-0.439564452	0.004458709
Distal tip	C26F1.1	-2.838719087	0.013615178
Distal tip	hsp-16.41	0.873322631	0.015624974
Distal tip	rpl-38	-0.485219264	0.018005212
Distal tip	gpd-3	-0.842612579	0.019584448
Distal tip	col-124	0.787272551	0.019585102
Distal tip	rpl-36	-0.37259584	0.028216725
Distal tip	col-20	0.863064985	0.029743128
Distal tip	gst-7	0.546937292	0.030740288
Distal tip	hsp-110	0.686693935	0.050203523
Distal tip	C06A8.3	1.54501568	0.09310916
Dorsal uterine cells	col-119	1.328310967	2.58986E-08
Dorsal uterine cells	col-124	1.072723691	7.53599E-08
Dorsal uterine cells	col-20	1.162245071	1.67631E-07
Dorsal uterine cells	ule-4	-0.278986722	3.25503E-07
Dorsal uterine cells	F09E10.1	-1.170424409	1.71021E-06
Dorsal uterine cells	col-140	0.926769085	8.11737E-06
Dorsal uterine cells	Y22D7AR.10	-0.548080202	2.26508E-05

Dorsal uterine cells	mfap-1	-2.509013647	0.000220612
Dorsal uterine cells	col-98	1.455124662	0.000248591
Dorsal uterine cells	ctc-3	0.484131667	0.000266638
Dorsal uterine cells	gst-5	0.656359634	0.001047097
Dorsal uterine cells	ctc-1	0.493377147	0.001473897
Dorsal uterine cells	rpl-38	-0.571293684	0.002448197
Dorsal uterine cells	hmg-3	3.075948853	0.003633214
Dorsal uterine cells	col-122	1.477444787	0.007739194
Dorsal uterine cells	col-80	1.579950137	0.011259245
Dorsal uterine cells	F11E6.3	1.790154051	0.01509287
Dorsal uterine cells	col-143	1.337884207	0.057993422
Dorsal uterine cells	C08F11.12	-0.764565167	0.065671902
Dorsal uterine cells	col-8	2.434373087	0.075229325
Dorsal uterine cells	C25E10.8	-0.923301965	0.075953728
Dorsal uterine cells	rps-25	-0.271504828	0.07928507
Excretory cells	rpl-41.2	-0.503976866	1.11712E-08
Excretory cells	dsbn-1	1.155105255	3.8632E-06
Excretory cells	C53A3.2	1.462664414	0.000349115
Excretory cells	C14C6.5	-2.064940404	0.000643935
Excretory cells	mutd-1	0.945734052	0.001281983
Excretory cells	nduo-6	-0.310735667	0.001328576
Excretory cells	Y55B1BL.1	0.698659955	0.00165524
Excretory cells	W01D2.1	-0.510488293	0.001853922
Excretory cells	R09B3.2	-0.669208565	0.002374689
Excretory cells	blos-2	0.866455023	0.002528939
Excretory cells	R09H10.7	0.847199866	0.007499117
Excretory cells	ant-1.1	0.299415229	0.028986183
Excretory cells	ugt-36	1.779484775	0.030074373
Excretory cells	Y105C5B.5	0.520168509	0.041673204
Excretory cells	cysl-2	-2.109083695	0.096312996
Excretory duct	F15E6.3	1.185687379	1.56755E-16
Excretory duct	col-42	-1.310878865	2.60225E-16

Excretory duct	clec-50	-1.287742458	2.62162E-16
Excretory duct	C45B2.1	-0.901774719	4.03107E-16
Excretory duct	catp-3	0.662023975	1.56619E-15
Excretory duct	cpi-1	-0.972974425	3.90537E-14
Excretory duct	phy-2	1.275409237	1.17958E-11
Excretory duct	ZK970.7	-2.267817854	8.91001E-11
Excretory duct	F17C11.11	-0.810264745	5.66887E-10
Excretory duct	W01F3.2	-1.116217311	1.29963E-09
Excretory duct	C14C6.5	-1.314886942	1.67636E-09
Excretory duct	pud-3	-2.752239475	2.45833E-09
Excretory duct	nlp-29	-1.17661309	1.39261E-08
Excretory duct	C45B2.2	-1.369673111	1.51626E-08
Excretory duct	col-8	-0.884625579	4.4084E-08
Excretory duct	far-3	1.440514941	4.71965E-08
Excretory duct	F28H7.3	-1.566385286	9.61739E-08
Excretory duct	pud-4	-2.284843158	9.70674E-08
Excretory duct	acdh-1	-0.455394379	3.58167E-07
Excretory duct	col-81	-0.500116457	5.06136E-07
Excretory duct	K10H10.4	1.459339485	1.35967E-06
Excretory duct	F13D12.3	-1.932698675	2.00406E-06
Excretory duct	dod-19	-1.631252036	2.25132E-06
Excretory duct	nlp-24	0.525634761	6.12822E-06
Excretory duct	ZK6.11	-1.077330489	1.20962E-05
Excretory duct	F55G11.4	-1.817063768	1.43102E-05
Excretory duct	col-129	-0.438273735	1.50334E-05
Excretory duct	rhr-1	-1.346510389	1.73839E-05

Excretory duct	lys-2	-1.110073504	6.28947E-05
Excretory duct	col-139	-0.410118185	6.85504E-05
Excretory duct	bli-6	0.445934382	7.92256E-05
Excretory duct	nlp-25	0.684286221	0.000103351
Excretory duct	clec-47	1.903812741	0.000113838
Excretory duct	C10C5.3	1.207324843	0.000138815
Excretory duct	ddo-3	-0.079223834	0.000152638
Excretory duct	mthf-1	-0.69613993	0.000224423
Excretory duct	nlp-33	0.33674253	0.000248423
Excretory duct	lips-10	0.529411597	0.00045901
Excretory duct	F54D5.4	-1.107999384	0.000499378
Excretory duct	cdd-1	-1.053312981	0.000587851
Excretory duct	F12A10.1	0.822407471	0.001089694
Excretory duct	spp-18	-1.40770631	0.001345962
Excretory duct	F56H9.2	-0.92286354	0.001405301
Excretory duct	dct-16	-0.419777737	0.001530618
Excretory duct	lipl-5	-1.14330916	0.001869746
Excretory duct	Y69H2.3	-1.573790963	0.002048699
Excretory duct	cytb-5.1	0.69062724	0.002604027
Excretory duct	ndk-1	0.240166918	0.003324912
Excretory duct	ram-2	0.455517744	0.005410184
Excretory duct	col-133	0.376776537	0.005664627
Excretory duct	Y48G8AL.12	0.534481937	0.005690183
Excretory duct	asp-1	-0.402386298	0.007634692
Excretory duct	farl-11	-0.718212062	0.007861097
Excretory duct	atf-7	0.669482334	0.008025556
Excretory duct	brp-1	-0.59545315	0.010631159
Excretory duct	tnc-2	0.909134774	0.011315585
Excretory duct	C49F5.7	-0.678404295	0.011932204
Excretory duct	T04F3.1	0.452845056	0.013928438
Excretory duct	T27F6.8	0.737756406	0.016794738
Excretory duct	nhx-3	1.160772825	0.025455917
Excretory duct	drd-10	-1.099777247	0.026963133

Excretory duct	scl-2	-1.504483862	0.027716089
Excretory duct	ttr-15	-0.402272566	0.033831392
Excretory duct	asp-3	-0.489203773	0.034709149
Excretory duct	col-182	-1.454848602	0.041949881
Excretory duct	fat-1	0.680115712	0.045029508
Excretory duct	grsp-3	-1.061460057	0.04551398
Excretory duct	clec-150	-0.984552426	0.048066393
Excretory duct	K10D3.6	-1.801206378	0.049912167
Excretory duct	fmo-2	1.619627541	0.05707985
Excretory duct	T04G9.7	-0.97899831	0.077268522
Excretory duct	F53B2.8	-1.404201936	0.095183514
Excretory gland	nspc-15	0.982328616	0.000657526
Excretory gland	cut-2	1.610957709	0.004498577
Excretory gland	nspc-12	1.004867149	0.085016449
GLR	T28H10.3	-2.415037499	0.001506696
GLR	ctc-3	0.543668511	0.001557308
GLR	catp-3	-2.415037499	0.017240932
Glia_1	col-65	-3.610497592	2.25961E-14
Glia_1	kin-15	-1.194510323	3.18956E-11
Glia_1	vem-1	-0.846318124	1.8604E-06
Glia_1	rpl-41.2	-0.623059378	0.000313285
Glia_2	grl-27	0.582274193	0.000531549
Glia_2	ZK596.3	0.915817606	0.003348751
Glia_2	ctc-3	0.660613039	0.037477513
HSN	F41E7.7	-0.759097211	9.67205E-12
HSN	lys-7	-1.584962501	0.000119086
HSN	T04C12.3	-0.415290583	0.003633536
HSN	col-122	1.83145474	0.004524159
HSN	col-140	1.29679905	0.019551489

HSN	col-184	1.694726563	0.020863265
HSN	hsp-16.48	-0.611624546	0.031058987
HSN	col-181	1.618954849	0.065241859
Hypodermis head	far-3	2.341172452	1.65811E-31
Hypodermis head	pck-2	1.197749357	7.30872E-16
Hypodermis head	lips-10	1.297953422	1.35021E-11
Hypodermis head	far-4	1.449531811	1.28459E-10
Hypodermis head	Y102A11A.5	1.754887502	8.40064E-10
Hypodermis head	F25E5.8	3.191179143	5.86574E-08
Hypodermis head	F44E7.2	2.547996961	7.64277E-08
Hypodermis head	rpl-41.2	-0.590539301	3.81229E-07
Hypodermis head	cysl-2	-1.017641841	6.04666E-07
Hypodermis head	C17C3.1	1.794615609	7.08705E-06
Hypodermis head	col-95	-3.062700841	0.000122238
Hypodermis head	ttr-21	3.902585029	0.000176784
Hypodermis head	W01D2.1	-0.687071681	0.000898469
Hypodermis head	nduo-4	-0.477007434	0.001120704
Hypodermis head	fat-5	1.260790631	0.001188453
Hypodermis head	C05D11.5	1.424728556	0.00131576
Hypodermis head	gst-4	1.705730589	0.001525072
Hypodermis head	B0410.3	0.776425156	0.003294659
Hypodermis head	grl-27	1.365519054	0.004992667
Hypodermis head	cnc-10	-0.691439831	0.005797284
Hypodermis head	Y119D3B.21	-1.116544994	0.006278971
Hypodermis head	F23F12.12	-1.067306916	0.008604233
Hypodermis head	C53A3.2	1.76970036	0.008899677
Hypodermis head	F46C3.6	1.010820969	0.013377015
Hypodermis head	alh-3	-0.755709951	0.017893304
Hypodermis head	rpl-29	-1.133969994	0.018082492
Hypodermis head	F48D6.4	1.232511883	0.02118965
Hypodermis head	pgp-10	1.341023699	0.028614154
Hypodermis head	Y57G11A.4	-0.704138199	0.040439546

Hypodermis head	gst-28	-0.949293225	0.044157556
Hypodermis head	F08F3.4	-1.021155472	0.046058677
Hypodermis head	T25B9.1	-0.792785315	0.071881524
Hypodermis head	dpf-6	-1.717432817	0.073735659
Hypodermis head	R09B3.3	-0.502266302	0.079976772
Hypodermis tail	C49H3.4	-33.66637507	3.1175E-190
Hypodermis tail	F42A9.8	-33.66637507	3.1175E-190
Hypodermis tail	K11H3.8	-33.66637507	3.1175E-190
Hypodermis tail	T25B6.4	-33.66637507	3.1175E-190
Hypodermis tail	gpx-3	-33.66637507	3.1175E-190
Hypodermis tail	fpn-1.1	-33.66637507	3.1175E-190
Hypodermis tail	kpc-1	-33.66637507	3.1175E-190
Hypodermis tail	Y50D4C.6	-33.66637507	3.1175E-190
Hypodermis tail	R02F11.1	-33.66637507	3.1175E-190
Hypodermis tail	cut-2	-33.66637507	3.1175E-190
Hypodermis tail	T02B5.3	-33.66637507	3.1175E-190
Hypodermis tail	nspb-9	-33.66637507	3.1175E-190
Hypodermis tail	ncx-3	-32.81227866	1.5221E-186
Hypodermis tail	Y54E10BL.3	-32.81227866	1.5221E-186
Hypodermis tail	Y47G6A.7	-32.81227866	1.5221E-186
Hypodermis tail	Y45F10C.4	31.84048068	8.0843E-185
Hypodermis tail	R02E4.3	-2	1.40621E-29
Hypodermis tail	far-3	4.892400686	4.92433E-05
Hypodermis-Gonadal sheath doublet	unc-129	-29.70186416	0
Hypodermis-Gonadal sheath doublet	slo-2	-29.70186416	0

Hypodermis-Gonadal sheath doublet	npr-4	-29.70186416	0
Hypodermis-Gonadal sheath doublet	eva-1	-29.70186416	0
Hypodermis-Gonadal sheath doublet	mig-6	-28.68848744	0
Hypodermis-Gonadal sheath doublet	C13C4.7	-28.68848744	0
Hypodermis-Gonadal sheath doublet	F37H8.5	-28.68848744	0
Hypodermis-Gonadal sheath doublet	gst-10	-2.331603586	3.55389E-32
Hypodermis-Gonadal sheath doublet	rpl-41.2	-0.538407841	5.59233E-27
Hypodermis-Gonadal sheath doublet	nduo-6	-0.336993013	2.54913E-18
Hypodermis-Gonadal sheath doublet	sams-1	1.100494772	9.07663E-18
Hypodermis-Gonadal sheath doublet	C05D11.5	1.153536711	5.49358E-15
Hypodermis-Gonadal sheath doublet	cysl-2	-1.57117224	2.49609E-14
Hypodermis-Gonadal sheath doublet	F53F1.2	1.743675661	2.3767E-13
Hypodermis-Gonadal sheath doublet	ahcy-1	0.674468979	2.65734E-13
Hypodermis-Gonadal sheath doublet	dct-16	-0.590539676	1.90964E-11
Hypodermis-Gonadal sheath doublet	R09B3.3	-0.436813021	4.61695E-11
Hypodermis-Gonadal sheath doublet	gst-4	0.856473939	1.16834E-10
Hypodermis-Gonadal sheath doublet	W04A4.2	0.720836705	2.75566E-10
Hypodermis-Gonadal sheath doublet	ndfl-4	-0.414115384	6.35603E-10
Hypodermis-Gonadal sheath doublet	F21C10.9	1.751597351	7.33831E-10
Hypodermis-Gonadal sheath doublet	gln-3	0.731368189	2.90412E-09
Hypodermis-Gonadal sheath doublet	rpl-39	-0.64314282	4.88485E-09
Hypodermis-Gonadal sheath doublet	T01D1.4	0.610204279	7.21958E-09
Hypodermis-Gonadal sheath doublet	rps-25	-0.280596156	1.75434E-08

Hypodermis-Gonadal sheath doublet	tnc-2	1.352731732	3.98059E-08
Hypodermis-Gonadal sheath doublet	C53A3.2	0.865141412	1.48124E-07
Hypodermis-Gonadal sheath doublet	cpn-4	1.702035859	1.63749E-07
Hypodermis-Gonadal sheath doublet	drd-10	-3.274766515	1.71568E-07
Hypodermis-Gonadal sheath doublet	K07A1.13	0.621497978	1.84507E-07
Hypodermis-Gonadal sheath doublet	dhs-21	0.526910582	3.39766E-07
Hypodermis-Gonadal sheath doublet	pqn-60	3.316396971	1.92227E-06
Hypodermis-Gonadal sheath doublet	msra-1	1.409652745	2.32633E-06
Hypodermis-Gonadal sheath doublet	rpl-36.A	-0.344810373	4.42178E-06
Hypodermis-Gonadal sheath doublet	gst-20	-1.702777176	6.97073E-06
Hypodermis-Gonadal sheath doublet	T03F1.11	1.475131476	9.17278E-06
Hypodermis-Gonadal sheath doublet	ctc-3	0.269506343	9.24149E-06
Hypodermis-Gonadal sheath doublet	T04G9.7	-0.327422957	1.72507E-05
Hypodermis-Gonadal sheath doublet	rpl-36	-0.332446761	1.90368E-05
Hypodermis-Gonadal sheath doublet	iff-2	0.410386714	2.42846E-05
Hypodermis-Gonadal sheath doublet	acdh-1	0.496283939	6.08655E-05
Hypodermis-Gonadal sheath doublet	eef-1A.1	-0.25098388	0.000112543
Hypodermis-Gonadal sheath doublet	D1022.4	0.988625836	0.000139111
Hypodermis-Gonadal sheath doublet	ZC116.1	2.408999541	0.000140661
Hypodermis-Gonadal sheath doublet	F44E7.2	0.778092693	0.00020099
Hypodermis-Gonadal sheath doublet	gpdh-2	0.806607663	0.000246219
Hypodermis-Gonadal sheath doublet	sri-40	0.652148998	0.000314774
Hypodermis-Gonadal sheath doublet	rps-27	-0.315486087	0.000320005

Hypodermis-Gonadal sheath doublet	F18E3.12	0.727080675	0.000466512
Hypodermis-Gonadal sheath doublet	far-3	4.322157371	0.00060901
Hypodermis-Gonadal sheath doublet	C45B2.1	-0.501616743	0.000638349
Hypodermis-Gonadal sheath doublet	W01D2.1	-0.391132059	0.001134317
Hypodermis-Gonadal sheath doublet	pyk-2	0.814167859	0.00160462
Hypodermis-Gonadal sheath doublet	F59C6.16	-1.016207729	0.001701632
Hypodermis-Gonadal sheath doublet	rpl-38	-0.343729182	0.003240576
Hypodermis-Gonadal sheath doublet	msp-76	-1.092255228	0.003316491
Hypodermis-Gonadal sheath doublet	T27D12.6	-1.136353468	0.00391648
Hypodermis-Gonadal sheath doublet	gst-27	-0.849506897	0.004030003
Hypodermis-Gonadal sheath doublet	lips-10	1.097908997	0.008767571
Hypodermis-Gonadal sheath doublet	pmp-5	1.588032192	0.013042428
Hypodermis-Gonadal sheath doublet	unc-132	0.433574496	0.022181585
Hypodermis-Gonadal sheath doublet	C49F5.7	-0.367719739	0.02503783
Hypodermis-Gonadal sheath doublet	acs-2	1.259816811	0.025737705
Hypodermis-Gonadal sheath doublet	rpl-30	-0.295356814	0.029337053
Hypodermis-Gonadal sheath doublet	K07C5.2	0.486125312	0.02951176
Hypodermis-Gonadal sheath doublet	pck-2	0.356404688	0.030804812
Hypodermis-Gonadal sheath doublet	rps-28	-0.493746134	0.035232603
Hypodermis-Gonadal sheath doublet	C06A8.3	0.35021738	0.039461016
Hypodermis-Gonadal sheath doublet	ubq-2	-0.224074884	0.051320246
Hypodermis-Gonadal sheath doublet	rpl-7A	-0.278393546	0.052940704
Hypodermis-Gonadal sheath doublet	rla-2	-0.300139997	0.05331002

Hypodermis-Gonadal sheath doublet	R08E5.3	-0.900580788	0.05726658
Hypodermis-Gonadal sheath doublet	col-160	0.34375851	0.058504926
Hypodermis-Gonadal sheath doublet	spp-17	-0.815283082	0.067047276
Hypodermis-Gonadal sheath doublet	Y119D3B.21	-0.513624758	0.075944255
Hypodermis-Gonadal sheath doublet	B0410.3	0.606397731	0.080733037
Hypodermis-Gonadal sheath doublet	C14C6.5	-1.491385066	0.086193833
I2	F37C12.1	-2.162310303	2.21211E-05
I5	R74.10	-0.610988086	3.57631E-05
I5	lys-7	-5.154027842	0.000385192
I5	flp-5	-0.893541621	0.003344319
I5	K07C5.9	-0.594984113	0.070814568
IL2	col-65	-2.169925001	3.64884E-06
IL2	clec-194	-0.799632939	6.64981E-05
IL2	F02E11.2	-0.733948992	0.05642186
Intestine anterior	folt-2	-1.777866804	2.41448E-24
Intestine anterior	cbl-1	-1.634871243	1.09397E-16
Intestine anterior	zip-10	-1.818043075	3.30869E-16
Intestine anterior	vit-2	-1.540972152	4.73231E-16
Intestine anterior	fat-6	-1.032318196	9.35952E-16
Intestine anterior	vit-5	-2.019354522	1.32538E-15
Intestine anterior	C17F4.7	1.055269609	1.9257E-15
Intestine anterior	ugt-44	-2.22018156	2.83414E-15
Intestine anterior	C23H5.8	-0.944243561	9.74388E-15
Intestine anterior	vit-6	-1.28881914	1.59144E-14
Intestine anterior	tos-1	-0.744218392	2.16108E-14

Intestine anterior	ctc-1	0.856361232	4.2734E-14
Intestine anterior	col-184	1.450705687	2.34589E-12
Intestine anterior	spp-2	-1.567759178	3.99863E-12
Intestine anterior	tag-10	-1.452892633	7.28828E-12
Intestine anterior	C18H9.6	-1.323533775	7.51439E-12
Intestine anterior	T12D8.5	-1.5280254	1.60345E-11
Intestine anterior	ctb-1	0.802050928	2.41838E-11
Intestine anterior	rpl-2	0.660335513	5.87999E-11
Intestine anterior	col-8	1.857887126	8.88202E-11
Intestine anterior	vit-4	-2.284109745	2.05682E-10
Intestine anterior	F48D6.4	-1.4895183	3.01814E-10
Intestine anterior	rpl-5	0.663037184	4.92813E-10
Intestine anterior	rpl-25.2	0.824024063	5.4025E-10
Intestine anterior	rpl-10	0.601434803	7.36033E-10
Intestine anterior	ahcy-1	1.092144502	1.0526E-09
Intestine anterior	acs-19	-2.142188668	1.14553E-09
Intestine anterior	F31F7.1	-1.76780332	1.23115E-09
Intestine anterior	rpl-12	0.496944829	1.25368E-09
Intestine anterior	ctc-3	0.724260716	1.3556E-09
Intestine anterior	rme-1	-1.597083604	1.64074E-09
Intestine anterior	col-19	0.953382968	1.7182E-09
Intestine anterior	col-143	1.534802627	2.01428E-09
Intestine anterior	atp-2	0.841974541	2.16409E-09
Intestine anterior	col-124	0.989518868	2.47025E-09
Intestine anterior	col-122	1.306102323	2.94328E-09
Intestine anterior	col-20	1.014584496	2.99718E-09
Intestine anterior	rps-7	0.56773326	3.09391E-09
Intestine anterior	nduo-6	0.601189627	3.10614E-09
Intestine anterior	Y37E3.8	0.553706632	3.15311E-09
Intestine anterior	rpl-19	0.557765499	4.88223E-09
Intestine anterior	ifc-1	-1.964489454	6.23914E-09
Intestine anterior	col-106	1.376698014	8.61678E-09
Intestine anterior	rpl-24.1	0.53132113	1.09425E-08
Intestine anterior	rps-8	0.540756458	1.09431E-08
Intestine anterior	Y82E9BR.3	0.642400909	1.18508E-08
Intestine anterior	D1054.18	-3.89528578	1.54059E-08

Intestine anterior	fat-5	-1.678006857	1.61657E-08
Intestine anterior	F54C9.3	-1.345809549	2.54853E-08
Intestine anterior	F29C4.2	0.886943825	2.79346E-08
Intestine anterior	nduo-5	0.813186754	3.28153E-08
Intestine anterior	eps-8	-1.586762813	3.60157E-08
Intestine anterior	F53B2.8	-1.215947079	4.03159E-08
Intestine anterior	far-3	2.859326315	5.29658E-08
Intestine anterior	vit-3	-1.693366312	5.6E-08
Intestine anterior	rps-11	0.510160401	5.94832E-08
Intestine anterior	col-140	0.886852364	6.41132E-08
Intestine anterior	vit-1	-1.761922066	7.09631E-08
Intestine anterior	nduo-1	0.688211933	9.35126E-08
Intestine anterior	ant-1.1	0.587307355	1.13829E-07
Intestine anterior	K09F6.7	-1.125296666	1.15659E-07
Intestine anterior	rla-0	0.609429667	1.18755E-07
Intestine anterior	rps-9	0.4737748	1.26536E-07
Intestine anterior	col-119	1.148266948	1.36075E-07
Intestine anterior	T28F4.5	-0.75256463	1.50397E-07
Intestine anterior	ndk-1	0.514655361	1.56741E-07
Intestine anterior	ctsa-2	-1.586014347	1.57396E-07
Intestine anterior	rps-5	0.54753066	2.39886E-07
Intestine anterior	K08D12.6	1.625591148	2.73564E-07
Intestine anterior	msd-4	-2.0487591	3.27789E-07
Intestine anterior	max-2	-1.827022995	3.91729E-07
Intestine anterior	rps-26	0.529509914	4.59714E-07
Intestine anterior	eef-1A.1	0.720909135	4.64308E-07
Intestine anterior	zip-2	-1.306696136	5.01895E-07
Intestine anterior	rpl-6	0.577167407	5.08495E-07
Intestine anterior	rpl-18	0.551018294	6.69137E-07
Intestine anterior	rpl-7A	0.574067139	9.40556E-07
Intestine anterior	eef-1B.2	0.974774622	1.12828E-06
Intestine anterior	T05E12.3	-1.353072315	1.41397E-06
Intestine anterior	F17C11.11	-1.462937405	1.62367E-06

Intestine anterior	rpl-16	0.536459739	1.84308E-06
Intestine anterior	anc-1	-0.445080574	2.76948E-06
Intestine anterior	msp-40	-2.343525023	3.04478E-06
Intestine anterior	C31H5.6	-1.732130603	3.47263E-06
Intestine anterior	xbp-1	-1.501730526	3.72643E-06
Intestine anterior	rps-12	0.481038895	4.31862E-06
Intestine anterior	rps-18	0.485851137	5.83937E-06
Intestine anterior	C50F4.1	-1.564324619	6.91815E-06
Intestine anterior	F35E12.9	-1.290922087	7.11086E-06
Intestine anterior	col-181	1.068788639	1.06336E-05
Intestine anterior	W02F12.4	-1.448829481	1.31943E-05
Intestine anterior	lys-7	-0.970530987	1.44856E-05
Intestine anterior	pck-2	0.872359889	1.66119E-05
Intestine anterior	acd-5	-1.438185641	1.72759E-05
Intestine anterior	lec-8	-1.132871505	2.11372E-05
Intestine anterior	nhr-68	-0.866742828	2.2045E-05
Intestine anterior	rpl-4	0.693415772	2.27772E-05
Intestine anterior	rpl-13	0.464417655	2.34595E-05
Intestine anterior	math-18	-1.073959774	2.38504E-05
Intestine anterior	rpl-22	0.501151694	2.38932E-05
Intestine anterior	rps-4	0.512585233	2.56073E-05
Intestine anterior	F22H10.3	-1.092919666	2.62601E-05
Intestine anterior	dod-3	-2.068779626	2.95873E-05
Intestine anterior	rpl-17	0.432408593	3.43887E-05
Intestine anterior	ipla-1	-1.267155555	3.87689E-05
Intestine anterior	ule-4	-1.334976307	4.09535E-05
Intestine anterior	clec-84	-1.1901168	4.4253E-05
Intestine anterior	ssp-10	-1.58912301	4.59649E-05
Intestine anterior	rpl-23	0.468877602	5.72193E-05
Intestine anterior	pmt-2	0.908606599	5.82899E-05

Intestine anterior	F57F5.1	-0.784708531	6.05303E-05
Intestine anterior	R08E3.1	-0.695593122	6.08398E-05
Intestine anterior	tag-244	-1.690846669	6.22092E-05
Intestine anterior	E02H9.3	-0.974744267	6.85561E-05
Intestine anterior	Y6G8.2	-1.426423807	6.94612E-05
Intestine anterior	rps-3	0.487955424	8.77866E-05
Intestine anterior	rpl-7	0.525254618	0.000120343
Intestine anterior	atp-3	0.803334883	0.000121728
Intestine anterior	dhs-14	-0.991242231	0.000131789
Intestine anterior	cpn-4	2.071722323	0.000156278
Intestine anterior	C05D12.4	-1.382648294	0.000157705
Intestine anterior	hpo-34	-0.675519031	0.000159927
Intestine anterior	C06B3.6	-1.124938995	0.000161586
Intestine anterior	rpl-3	0.507540696	0.000166173
Intestine anterior	gst-1	-0.762821316	0.000200353
Intestine anterior	hrg-1	-2.088246748	0.000215929
Intestine anterior	F32D8.12	-0.934606745	0.000222755
Intestine anterior	cyn-7	0.685441225	0.000226243
Intestine anterior	T02H6.11	0.658316016	0.000239571
Intestine anterior	har-1	1.164994586	0.000246031
Intestine anterior	E01G4.3	-1.096845579	0.000259452
Intestine anterior	C08F11.13	-1.17629972	0.000274799
Intestine anterior	pkc-2	-2.0756983	0.000280435
Intestine anterior	clec-41	-1.223754145	0.000287865
Intestine anterior	asg-2	0.79696161	0.00031379
Intestine anterior	C49C3.4	-1.045404608	0.000315445
Intestine anterior	metr-1	0.895760632	0.000321155
Intestine anterior	ttr-49	-1.228303161	0.000332118
Intestine anterior	R04F11.2	0.602192882	0.000503387

Intestine anterior	C25F9.5	-0.997040255	0.000544828
Intestine anterior	C52B11.5	-1.216690069	0.000630934
Intestine anterior	F55H12.3	-0.985102732	0.000727454
Intestine anterior	F08B4.8	-3.356092319	0.000988682
Intestine anterior	R09F10.1	-1.431014796	0.001033539
Intestine anterior	fat-7	1.34204114	0.001100907
Intestine anterior	rps-2	0.551306676	0.001101746
Intestine anterior	ctc-2	0.565863472	0.001209361
Intestine anterior	rpl-21	0.404985343	0.001223484
Intestine anterior	rpl-15	0.464300974	0.0012773
Intestine anterior	C05D12.3	-0.909712521	0.001303086
Intestine anterior	col-101	1.320004661	0.001310751
Intestine anterior	rps-0	0.501689282	0.001403635
Intestine anterior	rps-19	0.379387712	0.001608012
Intestine anterior	atp-6	0.419578837	0.00163749
Intestine anterior	rps-23	0.405468188	0.001704981
Intestine anterior	Y82E9BR.5	-1.391855714	0.00190296
Intestine anterior	rps-20	0.467734605	0.002052174
Intestine anterior	sma-9	-0.904454051	0.002446962
Intestine anterior	rps-24	0.432572011	0.00251319
Intestine anterior	cpr-6	-0.827696406	0.002580703
Intestine anterior	R05F9.6	0.832172265	0.002898888
Intestine anterior	msp-36	-1.456919453	0.002986507
Intestine anterior	dod-6	1.324360848	0.003502539
Intestine anterior	H43E16.1	-1.28837762	0.003858188
Intestine anterior	spch-3	-2.346114574	0.003859404
Intestine anterior	ubq-2	0.434707129	0.003997771
Intestine anterior	ubl-1	0.4296582	0.004287867
Intestine anterior	cyp-35A2	-1.000915635	0.004304834
Intestine anterior	rack-1	0.519943406	0.00432409
Intestine anterior	zip-12	-0.713561163	0.004707412
Intestine anterior	asb-2	0.941888613	0.005072007

Intestine anterior	rps-14	0.368367509	0.005163526
Intestine anterior	F21D5.3	-0.963509228	0.005665002
Intestine anterior	col-42	1.482670572	0.00594834
Intestine anterior	Y105C5B.15	-1.701126632	0.006848523
Intestine anterior	W04D2.6	-0.882993619	0.006934314
Intestine anterior	emo-1	0.582278548	0.0069482
Intestine anterior	rpl-32	0.387467637	0.00715086
Intestine anterior	col-103	1.226840376	0.007460093
Intestine anterior	F43C1.5	-2.191098692	0.007756204
Intestine anterior	rps-1	0.438379656	0.008212175
Intestine anterior	T20H4.5	1.194341527	0.008642207
Intestine anterior	clec-50	-0.781067756	0.008690195
Intestine anterior	gcy-28	-1.191819005	0.008845756
Intestine anterior	E02H4.7	-2.389625446	0.008927537
Intestine anterior	rpl-11.1	0.769143805	0.009593327
Intestine anterior	nduo-2	0.647310486	0.009670095
Intestine anterior	itr-1	-0.907094856	0.009812453
Intestine anterior	F08H9.2	-1.498147524	0.010443995
Intestine anterior	rla-1	0.465733342	0.0117349
Intestine anterior	F58G6.9	-1.693444471	0.011959299
Intestine anterior	atf-7	-0.729806925	0.013178141
Intestine anterior	rps-10	0.403697369	0.014965045
Intestine anterior	acox-1.5	-0.924828857	0.015734562
Intestine anterior	rpl-31	0.418626355	0.015914448
Intestine anterior	ugt-22	-0.93762857	0.016219468
Intestine anterior	msp-45	-2.009069619	0.016712794
Intestine anterior	cco-2	0.591550245	0.018830868
Intestine anterior	F53C11.1	-1.156166523	0.019082392
Intestine anterior	tag-174	0.656751679	0.019353161
Intestine anterior	H06H21.8	-0.946144809	0.019640133

Intestine anterior	ugt-47	-0.689768148	0.020491404
Intestine anterior	prdx-2	0.757617527	0.022930438
Intestine anterior	orai-1	-1.225068313	0.023788255
Intestine anterior	lec-10	-0.631594552	0.024290897
Intestine anterior	msp-33	-2.044380903	0.024463664
Intestine anterior	clec-47	2.024264675	0.025012923
Intestine anterior	msp-31	-1.943848094	0.02559934
Intestine anterior	nspd-1	-1.920889473	0.026549243
Intestine anterior	T24B8.5	-2.405272316	0.026731371
Intestine anterior	Y69A2AR.18	0.725627326	0.028500403
Intestine anterior	msp-49	-2.33655571	0.028918397
Intestine anterior	pcyt-1	-1.58557459	0.032539678
Intestine anterior	msp-50	-2.142714404	0.034866352
Intestine anterior	H03A11.2	-0.684990657	0.035793873
Intestine anterior	dhs-3	-0.707128521	0.036604608
Intestine anterior	mth-1	-1.014831346	0.039750836
Intestine anterior	ZK1290.5	-1.29731678	0.04118311
Intestine anterior	clec-165	-2.886023688	0.043401521
Intestine anterior	atp-5	0.603070042	0.045561409
Intestine anterior	pgp-1	-1.447401829	0.048424798
Intestine anterior	lys-2	-1.332610087	0.048430617
Intestine anterior	rpl-36.A	0.376655101	0.054621838
Intestine anterior	F22B7.9	-1.736005291	0.054928358
Intestine anterior	iff-1	0.796328818	0.055019785
Intestine anterior	Y43C5B.3	-3.156579415	0.055419118
Intestine anterior	F22H10.2	-2.653096642	0.05569387
Intestine anterior	F28H7.3	-1.453353691	0.055886512
Intestine anterior	sdhd-1	1.122367014	0.057191696

Intestine anterior	nmy-1	-2.093060414	0.060852599
Intestine anterior	ilys-5	-0.4358133	0.065984363
Intestine anterior	rpl-1	0.401815339	0.068005364
Intestine anterior	rpl-9	0.431631279	0.069000696
Intestine anterior	mpk-2	-2.882956377	0.071175299
Intestine anterior	Y71H2AM.5	0.569743167	0.072466494
Intestine anterior	T03E6.8	-1.267769629	0.073954545
Intestine anterior	ifc-2	-1.064691949	0.079427761
Intestine anterior	rpl-20	0.397752284	0.080530905
Intestine anterior	nuo-3	0.732574655	0.083532846
Intestine anterior	nduo-4	0.491615013	0.083656877
Intestine anterior	lys-4	1.029002048	0.084813315
Intestine anterior	F22E5.8	-0.674638097	0.087200651
Intestine anterior	pas-1	1.009017382	0.099112544
Intestine middle	col-122	1.437016977	3.3648E-161
Intestine middle	col-119	1.603478205	2.2694E-145
Intestine middle	clec-47	1.886892497	1.0344E-143
Intestine middle	col-20	1.134812303	1.7132E-136
Intestine middle	col-184	1.280257846	3.3823E-115
Intestine middle	col-124	0.872850145	2.0082E-106
Intestine middle	col-140	0.883256761	6.8102E-101
Intestine middle	T03F1.11	2.410237146	7.7104E-101
Intestine middle	spp-5	-0.67140508	4.29504E-97
Intestine middle	col-181	1.131165364	7.33995E-92
Intestine middle	tnc-2	2.484621116	4.2792E-89
Intestine middle	col-98	1.790131503	3.99434E-88
Intestine middle	col-19	0.852438062	6.11169E-84
Intestine middle	msra-1	1.935183249	9.23025E-84
Intestine middle	ctc-3	0.452979602	5.12814E-80
Intestine middle	mlc-3	0.753200606	4.43332E-74
Intestine middle	col-8	1.569192024	3.46265E-72
Intestine middle	col-80	1.074982662	1.4661E-71
Intestine middle	hsp-12.2	1.873471343	9.8053E-71
Intestine middle	col-143	1.604643021	1.10044E-69
Intestine middle	cth-1	0.666155007	2.47496E-68
Intestine middle	ZK593.3	1.535829923	3.08355E-68
Intestine middle	B0035.13	-0.610009204	7.13874E-68
Intestine middle	ctc-1	0.43976555	7.07028E-67

Intestine middle	asp-1	-0.433450191	8.53559E-65
Intestine middle	rps-25	-0.258801383	1.37606E-61
Intestine middle	clec-50	-0.517860946	2.68742E-58
Intestine middle	rpl-41.2	-0.367283654	3.09478E-57
Intestine middle	C30G12.2	1.933711633	4.01391E-56
Intestine middle	col-106	1.126810725	1.3744E-54
Intestine middle	far-2	0.655720783	2.51198E-54
Intestine middle	col-103	1.622485772	6.52312E-53
Intestine middle	fipr-2	2.619308963	3.86733E-49
Intestine middle	lipl-2	-2.476291973	4.58424E-49
Intestine middle	col-160	1.245241185	9.72769E-48
Intestine middle	F53A9.8	-1.137693511	2.79562E-47
Intestine middle	col-101	1.421343904	1.58156E-46
Intestine middle	hsp-16.2	1.700596413	2.31203E-45
Intestine middle	F41E6.15	1.860622379	3.15281E-45
Intestine middle	F28H7.3	-0.665674551	4.41586E-43
Intestine middle	fip-2	1.665049064	2.86821E-42
Intestine middle	hsp-16.41	1.985857659	8.90434E-42
Intestine middle	cpz-1	0.876787198	2.46361E-41
Intestine middle	F11E6.3	1.237093693	1.99925E-40
Intestine middle	fipr-1	2.89180072	2.94132E-40
Intestine middle	rpl-12	-0.185812698	3.06507E-40
Intestine middle	gst-10	-0.856864475	3.64914E-40
Intestine middle	cpn-4	2.203385903	8.31903E-40
Intestine middle	T13F3.6	1.461479414	1.2844E-39
Intestine middle	cpl-1	0.943951414	2.37105E-39
Intestine middle	pud-4	-1.971217101	3.59562E-39
Intestine middle	C53C9.2	2.35489598	8.35703E-39
Intestine middle	C24A3.2	1.656787077	9.78875E-39
Intestine middle	rpl-38	-0.368150483	2.07104E-37
Intestine middle	rpl-32	-0.236776804	5.11605E-37
Intestine middle	C54D10.3	1.498087037	1.74408E-36
Intestine middle	pmt-2	0.392655827	5.85918E-36

Intestine middle	Y73F4A.2	3.191224577	1.97832E-35
Intestine middle	irg-5	-2.346420256	7.68788E-35
Intestine middle	C06A8.3	0.778656192	4.96558E-34
Intestine middle	ZC116.1	2.753353165	5.29859E-34
Intestine middle	Y87G2A.19	2.657386618	7.24377E-34
Intestine middle	dct-16	-0.223822804	2.85941E-33
Intestine middle	pud-3	-1.790899893	3.51907E-33
Intestine middle	F21C10.9	0.998851972	8.33776E-32
Intestine middle	sodh-1	1.544556342	2.40842E-31
Intestine middle	rps-27	-0.287819055	6.49527E-31
Intestine middle	lys-4	0.553915864	5.27539E-30
Intestine middle	pqn-60	2.72535923	2.7304E-29
Intestine middle	tni-4	1.583550573	2.89392E-29
Intestine middle	gst-7	-0.874414412	9.2317E-29
Intestine middle	rpl-30	-0.303091373	9.40703E-29
Intestine middle	asp-4	0.697609285	1.14769E-28
Intestine middle	W01D2.1	-0.35264665	3.96396E-28
Intestine middle	rpl-36.A	-0.250932903	5.51274E-28
Intestine middle	pck-2	0.653170374	1.51808E-27
Intestine middle	rps-17	-0.237776629	3.68887E-27
Intestine middle	K03E5.2	1.135513359	6.84406E-27
Intestine middle	rpl-34	-0.288756337	4.15227E-26
Intestine middle	fipr-21	0.884220667	1.07139E-25
Intestine middle	R06C1.4	-0.31440126	5.10133E-25
Intestine middle	far-3	2.212136717	5.1976E-25
Intestine middle	asp-14	-0.674605203	5.40464E-25
Intestine middle	rps-23	-0.203697638	6.76597E-25
Intestine middle	rps-9	-0.165915455	8.9635E-25
Intestine middle	rps-24	-0.233427304	1.64235E-24
Intestine middle	sams-1	0.807325476	2.80536E-24
Intestine middle	lbp-6	0.320002687	5.45345E-24
Intestine middle	col-178	0.81103695	7.96631E-24

Intestine middle	acdh-1	0.287416286	1.07928E-23
Intestine middle	nduo-1	0.286926621	1.41106E-23
Intestine middle	col-42	1.037853546	2.56857E-23
Intestine middle	rpl-36	-0.24065674	2.58106E-23
Intestine middle	rps-26	-0.21397381	3.06893E-23
Intestine middle	rps-13	-0.219269248	1.09567E-22
Intestine middle	gst-4	1.044688924	1.44322E-22
Intestine middle	cpr-5	1.19604344	1.73438E-22
Intestine middle	rps-10	-0.211683333	2.06166E-22
Intestine middle	mlc-2	0.527944897	2.16001E-22
Intestine middle	rps-19	-0.166377934	3.35592E-22
Intestine middle	rpl-27	-0.284535982	3.74512E-22
Intestine middle	eef-1B.1	-0.188068118	4.02097E-22
Intestine middle	lec-9	-0.25442284	4.33704E-22
Intestine middle	asp-13	0.58580819	9.68876E-22
Intestine middle	rpl-35	-0.196890686	1.8622E-21
Intestine middle	cpr-4	0.961448772	3.67155E-21
Intestine middle	col-142	0.991379297	5.36788E-21
Intestine middle	ldp-1	0.985384507	2.2019E-20
Intestine middle	clec-150	-0.599203304	3.2648E-20
Intestine middle	C14C6.5	-1.245065505	5.40266E-20
Intestine middle	rpl-21	-0.186081043	5.69271E-20
Intestine middle	tnt-4	2.276553906	6.01245E-20
Intestine middle	rpl-14	-0.204774834	6.74857E-20
Intestine middle	rpl-43	-0.23688356	6.91384E-20
Intestine middle	ahcy-1	0.485062114	9.1327E-20
Intestine middle	ttr-21	2.39302657	1.2978E-19
Intestine middle	rps-11	-0.16139335	1.43111E-19
Intestine middle	Y37E3.8	-0.17350731	2.99414E-19
Intestine middle	F15A4.6	1.039086981	3.67598E-19
Intestine middle	Y34F4.2	1.453108442	5.65198E-19
Intestine middle	rps-12	-0.182784005	7.32773E-19
Intestine middle	ctc-2	0.265480731	7.40955E-19

Intestine middle	rpl-22	-0.225135995	8.19889E-19
Intestine middle	K03H6.2	-1.35702137	1.78109E-18
Intestine middle	fipr-7	2.813672422	1.79195E-18
Intestine middle	myo-2	2.894307574	3.59935E-18
Intestine middle	rla-2	-0.244571204	9.87197E-18
Intestine middle	F48D6.4	-0.6046272	2.30433E-17
Intestine middle	rpl-33	-0.223692309	2.53826E-17
Intestine middle	spp-18	-1.001692564	3.16215E-17
Intestine middle	perm-2	0.563511925	3.96404E-17
Intestine middle	rpl-26	-0.198771841	4.07847E-17
Intestine middle	rps-5	-0.165316977	5.29985E-17
Intestine middle	fipr-10	2.455351655	8.25292E-17
Intestine middle	rpl-16	-0.198260363	2.33315E-16
Intestine middle	C45G9.6	2.331781042	3.55628E-16
Intestine middle	rps-30	-0.197469299	3.76866E-16
Intestine middle	rpl-31	-0.217691348	6.20007E-16
Intestine middle	vamp-8	2.372997103	6.21357E-16
Intestine middle	rps-22	-0.230337139	7.3768E-16
Intestine middle	crt-1	-0.408827676	1.58555E-15
Intestine middle	irg-7	-0.625223425	1.69033E-15
Intestine middle	fipr-5	2.240907199	2.15507E-15
Intestine middle	hsp-70	1.654453903	2.65213E-15
Intestine middle	rpl-17	-0.163159128	3.50709E-15
Intestine middle	lipl-5	-0.585914506	4.62655E-15
Intestine middle	F35B12.3	2.385292325	5.0402E-15
Intestine middle	fat-7	1.091314102	5.05608E-15
Intestine middle	rpl-19	-0.158992699	6.34965E-15
Intestine middle	drd-5	0.857869527	7.66518E-15
Intestine middle	col-129	0.419186939	8.33371E-15
Intestine middle	col-93	0.488536359	8.75677E-15

Intestine middle	rps-14	-0.139102708	1.61578E-14
Intestine middle	rps-28	-0.343811507	1.91621E-14
Intestine middle	act-4	0.373125799	2.04758E-14
Intestine middle	rps-16	-0.228954783	4.21718E-14
Intestine middle	dod-19	-0.805005666	7.68181E-14
Intestine middle	tnt-3	1.500925359	8.9293E-14
Intestine middle	ttr-15	0.517794397	1.2647E-13
Intestine middle	ctb-1	0.242620813	1.69059E-13
Intestine middle	rpl-24.1	-0.154014697	1.73475E-13
Intestine middle	lev-11	0.394696364	1.79006E-13
Intestine middle	rpl-11.2	-0.191953909	2.66355E-13
Intestine middle	asp-6	-0.32752817	3.17198E-13
Intestine middle	T20G5.8	0.916303299	4.5049E-13
Intestine middle	ttr-26	1.386814388	8.43608E-13
Intestine middle	rps-3	-0.159485278	1.12267E-12
Intestine middle	vit-5	0.515708278	1.19079E-12
Intestine middle	T26H5.14	-1.471864796	1.67616E-12
Intestine middle	Y73F4A.3	2.722319419	2.02693E-12
Intestine middle	rpl-15	-0.167201681	2.66575E-12
Intestine middle	Y17D7B.4	-0.61545067	3.14912E-12
Intestine middle	dct-18	-0.3210623	3.6418E-12
Intestine middle	ttr-27	1.719974077	3.67638E-12
Intestine middle	myo-1	2.7730012	5.22441E-12
Intestine middle	rpl-39	-0.310272709	5.85603E-12
Intestine middle	F33H12.7	-1.85646759	6.53335E-12
Intestine middle	fipr-3	2.244402848	7.10279E-12
Intestine middle	rpl-28	-0.215072822	7.35522E-12
Intestine middle	T22B7.7	0.949000258	1.02542E-11
Intestine middle	rpl-2	-0.166488673	1.10069E-11
Intestine middle	Y47G6A.33	0.718556705	1.1559E-11
Intestine middle	rpl-13	-0.14118884	1.61446E-11
Intestine middle	gst-20	-1.140017989	1.79241E-11

Intestine middle	Y119D3B.21	-0.214090719	2.08414E-11
Intestine middle	F46G10.1	-0.278748148	2.45376E-11
Intestine middle	K08D12.6	0.710321636	2.64267E-11
Intestine middle	R09B3.3	-0.206450405	2.78128E-11
Intestine middle	dod-24	-2.200677054	3.03491E-11
Intestine middle	ZC116.5	2.454996271	3.70513E-11
Intestine middle	ZK970.7	-2.623244631	3.93756E-11
Intestine middle	T15B7.1	0.517995034	4.29513E-11
Intestine middle	rps-7	-0.137326901	4.56034E-11
Intestine middle	acp-6	1.097785638	7.48235E-11
Intestine middle	nlp-27	0.861401243	1.70415E-10
Intestine middle	dod-6	0.771811524	2.38284E-10
Intestine middle	anmt-2	1.556747976	2.91239E-10
Intestine middle	ubl-1	-0.157985916	2.96677E-10
Intestine middle	rpl-20	-0.16322908	4.11188E-10
Intestine middle	ttr-2	1.063791591	4.3129E-10
Intestine middle	rps-18	-0.125609931	4.515E-10
Intestine middle	sec-61	0.409791336	4.73773E-10
Intestine middle	C45E5.4	2.948918463	4.99643E-10
Intestine middle	asp-2	0.269567411	5.67792E-10
Intestine middle	rpl-18	-0.159918847	8.33563E-10
Intestine middle	spp-2	-0.964425507	9.37623E-10
Intestine middle	argk-1	0.483231178	9.42917E-10
Intestine middle	C51E3.10	-1.067498395	1.22503E-09
Intestine middle	pacs-1	0.608896151	1.29344E-09
Intestine middle	F36F2.1	1.622915045	1.29581E-09
Intestine middle	F08D12.2	2.179107014	1.33077E-09
Intestine middle	hpo-26	2.302303703	1.34473E-09
Intestine middle	irg-4	-0.95853466	1.40984E-09
Intestine middle	T26H5.9	-1.283886924	2.31655E-09
Intestine middle	spp-3	-0.424136562	2.42018E-09
Intestine middle	F46F2.3	0.860107887	2.59206E-09

Intestine middle	fat-2	0.295990993	3.37655E-09
Intestine middle	F01D5.3	-1.643645337	3.52602E-09
Intestine middle	col-139	0.291971295	3.54215E-09
Intestine middle	rpl-9	-0.159175872	4.5208E-09
Intestine middle	fipr-11	2.755055345	9.70444E-09
Intestine middle	mpc-2	0.657517824	1.37982E-08
Intestine middle	rps-21	-0.263218682	1.65276E-08
Intestine middle	abf-5	2.032249126	1.88128E-08
Intestine middle	F23D12.11	0.421181952	1.89789E-08
Intestine middle	cpg-9	0.424137775	2.47992E-08
Intestine middle	fat-6	0.451701366	2.75075E-08
Intestine middle	C05D11.5	0.646261912	3.41176E-08
Intestine middle	C23H5.8	-0.376533558	4.17242E-08
Intestine middle	mpc-1	0.540629453	4.36007E-08
Intestine middle	rla-1	-0.179948554	4.80132E-08
Intestine middle	gst-27	-0.329346855	4.92708E-08
Intestine middle	gpx-5	0.955687209	5.15644E-08
Intestine middle	pqn-94	2.047745296	7.58555E-08
Intestine middle	F32A5.4	1.912972054	9.5314E-08
Intestine middle	ubq-2	-0.142352727	9.82603E-08
Intestine middle	W10C8.6	1.654460125	1.00314E-07
Intestine middle	vit-2	0.289940961	1.04298E-07
Intestine middle	gst-38	-1.229015467	1.08247E-07
Intestine middle	grd-3	1.538880058	1.21577E-07
Intestine middle	nspb-6	2.066836863	1.52011E-07
Intestine middle	M03F4.6	0.858373769	1.5448E-07
Intestine middle	ifa-1	1.95571568	1.83899E-07
Intestine middle	F35E12.9	-0.960241979	2.21207E-07
Intestine middle	oig-3	1.085982082	2.9592E-07
Intestine middle	eef-2	-0.199613746	2.96419E-07
Intestine middle	C49G7.12	-1.342096815	3.11611E-07
Intestine middle	rpl-23	-0.145178512	3.18379E-07
Intestine middle	F42G8.10	0.367273932	3.80353E-07

Intestine middle	W09C5.8	0.301416214	4.36449E-07
Intestine middle	ndk-1	-0.107725982	5.20154E-07
Intestine middle	rps-15	-0.139699321	5.22306E-07
Intestine middle	cth-2	0.508735888	5.78097E-07
Intestine middle	col-152	-1.965475823	7.75762E-07
Intestine middle	smd-1	0.700743542	8.24544E-07
Intestine middle	R09H10.3	-0.277366183	8.88722E-07
Intestine middle	sdz-24	-0.780252898	9.48809E-07
Intestine middle	lec-2	0.547274971	1.11697E-06
Intestine middle	C24B9.3	-0.773828956	1.30335E-06
Intestine middle	gst-13	-0.603649245	1.45098E-06
Intestine middle	Y105C5B.5	0.422433067	1.47916E-06
Intestine middle	farl-11	0.629241878	1.51355E-06
Intestine middle	cpr-6	0.382097832	1.85665E-06
Intestine middle	lec-10	-0.224263119	1.88717E-06
Intestine middle	ZC395.5	-0.685736738	2.28549E-06
Intestine middle	F21C10.11	-0.69530027	2.58703E-06
Intestine middle	dod-23	1.038549982	2.64903E-06
Intestine middle	F42A10.6	-0.406579932	2.85789E-06
Intestine middle	rps-29	-0.230345529	3.54078E-06
Intestine middle	T28H10.3	-0.73912488	4.65676E-06
Intestine middle	fat-1	0.364027636	4.68876E-06
Intestine middle	Y43F8B.1	0.901553874	4.77167E-06
Intestine middle	fipr-4	1.599702871	5.99889E-06
Intestine middle	scl-6	1.04717809	7.13731E-06
Intestine middle	lbp-1	1.361323803	8.57584E-06
Intestine middle	F13C5.5	2.888076772	9.04897E-06
Intestine middle	Y39G8B.9	-1.470233535	9.99135E-06
Intestine middle	rps-1	-0.123622853	1.34447E-05
Intestine middle	T24B8.5	-1.759582125	1.36754E-05
Intestine middle	fipr-6	2.291697735	1.47868E-05

Intestine middle	ZC204.12	-0.500317356	1.48986E-05
Intestine middle	scl-2	-0.508262031	1.51402E-05
Intestine middle	T04F8.8	0.66324215	1.66434E-05
Intestine middle	C49G7.3	0.793739707	1.68101E-05
Intestine middle	spp-1	-0.485682187	1.79963E-05
Intestine middle	col-147	0.460491693	1.98941E-05
Intestine middle	spp-4	-0.910190155	2.06417E-05
Intestine middle	elo-6	0.231995178	2.28637E-05
Intestine middle	tkt-1	0.528383485	2.4848E-05
Intestine middle	marg-1	2.146792737	2.68162E-05
Intestine middle	F53B2.8	-0.859630535	3.23827E-05
Intestine middle	lipl-1	-1.311513871	3.8426E-05
Intestine middle	M02H5.8	0.231294682	3.96498E-05
Intestine middle	R02C2.7	1.562179026	4.04288E-05
Intestine middle	lys-2	-0.411086308	4.46074E-05
Intestine middle	rpl-29	-0.331412124	6.9452E-05
Intestine middle	C33H5.13	-0.515432353	9.35744E-05
Intestine middle	fipr-9	2.129135956	9.66783E-05
Intestine middle	gpx-3	2.41184609	0.000107681
Intestine middle	F12A10.1	1.004095865	0.000112903
Intestine middle	rpl-7A	-0.139112786	0.000119009
Intestine middle	ZK863.8	1.31154874	0.0001203
Intestine middle	F35A5.2	0.667946306	0.000125887
Intestine middle	rack-1	-0.134833151	0.000140315
Intestine middle	F22H10.3	-0.312310995	0.000146924
Intestine middle	F55G11.4	-1.552884013	0.000151337
Intestine middle	R10H10.3	0.471115608	0.000153873
Intestine middle	C45B2.1	0.362505722	0.00019355
Intestine middle	pudl-1	1.534314044	0.000194056
Intestine middle	C27B7.9	0.942912105	0.000222139
Intestine middle	col-179	0.718104394	0.000224748
Intestine middle	C27A7.1	1.564074893	0.000228873

Intestine middle	F08B12.4	0.445101486	0.000230041
Intestine middle	gln-3	0.452321703	0.000232308
Intestine middle	mel-32	0.484235442	0.00025691
Intestine middle	K09G1.1	0.674261346	0.000259805
Intestine middle	C17H12.8	-0.425755653	0.000267479
Intestine middle	clec-1	0.740366587	0.000284237
Intestine middle	F53F4.13	0.546626422	0.000285386
Intestine middle	elo-5	0.214416858	0.000285838
Intestine middle	C41G7.9	0.555874524	0.000287551
Intestine middle	enol-1	0.362657516	0.000315726
Intestine middle	F23F12.12	0.508893242	0.000365004
Intestine middle	acs-1	0.611931788	0.000420805
Intestine middle	mdh-2	0.465999765	0.000442759
Intestine middle	Y110A2AL.9	2.0736487	0.000446516
Intestine middle	atp-6	0.098567432	0.000456403
Intestine middle	T28D6.3	0.616154668	0.000477993
Intestine middle	Y53C12B.2	-0.300664598	0.000485734
Intestine middle	rpl-1	-0.121416773	0.000555455
Intestine middle	ZC21.3	2.165583257	0.000576637
Intestine middle	mlc-1	0.352249025	0.000579942
Intestine middle	flp-12	1.300353539	0.00064545
Intestine middle	F57F4.4	-0.381705359	0.0006625
Intestine middle	T19H12.6	1.046229413	0.000883453
Intestine middle	hsp-16.48	0.811987483	0.000915102
Intestine middle	col-81	0.24954014	0.000991723
Intestine middle	Y79H2A.2	1.722580159	0.001033175
Intestine middle	ZK622.4	1.155628218	0.001039832
Intestine middle	C44B7.5	0.634907136	0.001041809
Intestine middle	F41G3.10	0.72219842	0.001212253
Intestine middle	flp-14	1.011274456	0.001438934
Intestine middle	nspb-12	1.160035356	0.001576883
Intestine middle	lys-6	1.144346604	0.001587019
Intestine middle	C53A3.2	0.813730869	0.001744047
Intestine middle	lec-4	0.581161827	0.001852857
Intestine middle	aqp-7	0.728895423	0.002211795
Intestine middle	ben-1	1.355442539	0.002250777
Intestine middle	ain-2	-1.014913918	0.002588828
Intestine middle	F22F4.9	1.164621836	0.002598607
Intestine middle	ugt-62	0.822480371	0.002737495

Intestine middle	anmt-3	1.031558522	0.002798023
Intestine middle	C39E9.8	0.807924046	0.002823798
Intestine middle	vit-4	0.599702567	0.002837592
Intestine middle	C01B10.3	1.076463104	0.002861147
Intestine middle	Y22D7AL.10	0.293144653	0.002866985
Intestine middle	F55G11.8	-0.866877235	0.003239579
Intestine middle	mai-2	0.232313982	0.003344081
Intestine middle	rpl-5	-0.106996073	0.00439156
Intestine middle	nduo-5	0.18303863	0.004582908
Intestine middle	rps-0	-0.122264754	0.004820245
Intestine middle	spp-16	-0.325302223	0.004975499
Intestine middle	B0205.13	1.136533041	0.00508697
Intestine middle	spp-14	-0.239234464	0.005805139
Intestine middle	ncx-2	2.544481287	0.006085003
Intestine middle	dhs-25	-0.389487074	0.007281595
Intestine middle	tald-1	0.45320034	0.007379443
Intestine middle	Y69H2.3	-2.277419804	0.007814616
Intestine middle	nspd-10	-0.343115076	0.00840901
Intestine middle	hsp-3	-0.390437084	0.008711401
Intestine middle	Y38F2AR.9	0.2489212	0.008731023
Intestine middle	nep-17	-0.851651766	0.009813999
Intestine middle	F43C9.2	0.86713229	0.009828817
Intestine middle	C17F3.1	-0.078001666	0.009883177
Intestine middle	rpl-7	-0.103858453	0.010164058
Intestine middle	ttr-22	2.168362211	0.010194803
Intestine middle	rps-2	-0.113614694	0.010675789
Intestine middle	asg-1	0.238645892	0.010810317
Intestine middle	acbp-1	-0.195479809	0.010880139
Intestine middle	C37A2.7	-0.156330018	0.011013702
Intestine middle	hsp-17	0.743835183	0.011500136

Intestine middle	trap-3	0.350464356	0.0119872
Intestine middle	T28F4.5	-0.438094875	0.012284414
Intestine middle	ZK809.8	0.429544931	0.01272615
Intestine middle	col-39	-0.477418431	0.012742968
Intestine middle	C53B7.3	1.518793959	0.01288184
Intestine middle	grd-10	1.271092433	0.013432778
Intestine middle	F58G6.9	0.756289603	0.013601289
Intestine middle	ret-1	0.321847025	0.014177483
Intestine middle	F27D4.1	0.443421121	0.014409386
Intestine middle	best-14	1.023006461	0.014754838
Intestine middle	C15H9.9	0.268423652	0.015970314
Intestine middle	F56H9.2	-0.29756116	0.016160611
Intestine middle	hpo-19	0.682380909	0.016546247
Intestine middle	F23C8.5	0.287808911	0.018392327
Intestine middle	aldo-1	0.731857866	0.018454065
Intestine middle	gpd-2	0.380833474	0.019392247
Intestine middle	W03F8.6	1.260892027	0.019412375
Intestine middle	nlp-26	0.9346868	0.021584405
Intestine middle	tag-290	0.980992635	0.023654991
Intestine middle	acer-1	0.458970062	0.024406922
Intestine middle	zip-2	-0.508750572	0.024652688
Intestine middle	acs-2	1.097510172	0.025142657
Intestine middle	C53A3.1	1.324766627	0.025589334
Intestine middle	Y22D7AL.15	-0.401067272	0.02560095
Intestine middle	C49G7.10	-0.998837921	0.026493034
Intestine middle	cts-1	0.266808313	0.032871757
Intestine middle	C18D4.12	-1.268401335	0.033996482
Intestine middle	nduo-2	0.185813247	0.034180754
Intestine middle	vha-9	0.274735603	0.03421504
Intestine middle	oac-57	-0.538155952	0.034396494
Intestine middle	elo-2	0.346824505	0.037173618
Intestine middle	arf-1.2	0.332548651	0.037177766
Intestine middle	sucl-2	0.46360535	0.037927769
Intestine middle	rps-6	-0.133498764	0.038386647
Intestine middle	M163.8	0.463100356	0.038637904
Intestine middle	D1022.4	0.436288505	0.039794349

Intestine middle	F42A8.1	0.990509311	0.040829051
Intestine middle	T20H4.5	0.34815765	0.0417619
Intestine middle	oatr-1	0.506537156	0.042050103
Intestine middle	F17A9.4	0.835787967	0.04284586
Intestine middle	cyc-2.1	0.136701603	0.043042308
Intestine middle	cab-1	1.278724859	0.046740222
Intestine middle	F36A2.7	0.218987343	0.048848791
Intestine middle	flp-22	1.365883349	0.049546795
Intestine middle	ZC449.5	1.896681934	0.049560809
Intestine middle	lec-6	0.256026653	0.051534532
Intestine middle	clec-84	-0.530655348	0.051666674
Intestine middle	T26H5.4	-2.648445511	0.058115132
Intestine middle	C25F9.11	-1.29294713	0.060313924
Intestine middle	T19B4.3	0.550003896	0.061057359
Intestine middle	C25F9.14	-0.587996202	0.06177879
Intestine middle	nspb-8	1.248950286	0.064249912
Intestine middle	Y48A6B.7	-0.817758626	0.069291721
Intestine middle	dod-3	-1.011890624	0.069552347
Intestine middle	sptl-1	0.505509726	0.069555673
Intestine middle	unc-15	0.373457138	0.072201434
Intestine middle	pdf-1	1.302223196	0.075944544
Intestine middle	T24C4.4	-0.934377024	0.077022879
Intestine middle	bckd-1B	0.499291047	0.082158768
Intestine middle	mct-3	0.949509044	0.083545444
Intestine middle	rpl-10	-0.084248728	0.086140651
Intestine middle	Y43F8B.2	1.040063056	0.089907929
Intestine middle	rpl-25.1	-0.191435206	0.091973031
Intestine middle	myo-5	0.979320704	0.095537531
Intestine middle	rps-8	-0.086698785	0.096954704
Intestine middle	col-76	-0.515848216	0.099846272
Intestine posterior	vit-5	-1.622888793	3.4958E-121
Intestine posterior	vit-2	-1.0452883	2.6943E-102
Intestine posterior	tos-1	-0.976534988	1.87148E-91

Intestine posterior	vit-1	-1.879992353	8.00469E-82
Intestine posterior	vit-6	-0.867109094	3.25297E-75
Intestine posterior	vit-3	-1.500663253	1.19639E-72
Intestine posterior	C23H5.8	-0.886613343	2.37584E-71
Intestine posterior	folt-2	-2.082573436	2.36058E-70
Intestine posterior	vit-4	-1.616416349	6.89227E-69
Intestine posterior	anc-1	-0.639922749	3.73042E-67
Intestine posterior	ugt-44	-1.869566606	2.50652E-66
Intestine posterior	F31F7.1	-1.640173349	9.82857E-64
Intestine posterior	col-124	1.09876145	1.0304E-61
Intestine posterior	col-20	1.17263291	1.51665E-59
Intestine posterior	acs-19	-1.773008694	9.85127E-58
Intestine posterior	lipl-5	-1.268826507	1.99961E-57
Intestine posterior	col-184	1.499466095	1.16317E-56
Intestine posterior	col-122	1.505627335	1.58868E-56
Intestine posterior	ttr-49	-1.440427532	1.28224E-55
Intestine posterior	ctc-1	0.661575069	3.2388E-55
Intestine posterior	rps-9	0.496530698	4.59713E-53
Intestine posterior	col-8	1.95260873	1.97512E-51
Intestine posterior	col-19	0.992907708	4.65669E-51
Intestine posterior	col-119	1.46123178	6.63483E-51
Intestine posterior	col-181	1.352787928	2.67565E-48
Intestine posterior	F48D6.4	-1.190173253	2.94195E-48
Intestine posterior	C05D12.4	-1.836832656	1.34279E-47
Intestine posterior	rme-1	-1.386460584	7.2486E-47
Intestine posterior	C05D12.3	-1.307744198	8.96396E-47
Intestine posterior	col-140	0.950950759	1.51857E-44
Intestine posterior	Y82E9BR.3	0.503496313	2.3629E-43
Intestine posterior	rps-7	0.490946644	3.69846E-43

Intestine posterior	C05C10.3	-1.605696149	1.52058E-42
Intestine posterior	ndk-1	0.53564449	2.37142E-42
Intestine posterior	D1054.18	-2.82190724	3.94791E-41
Intestine posterior	rps-11	0.44749093	3.82049E-40
Intestine posterior	rpl-19	0.477144599	9.29004E-40
Intestine posterior	K09F6.7	-1.004324868	1.56814E-39
Intestine posterior	rla-0	0.546395484	1.92702E-39
Intestine posterior	atp-2	0.735938676	2.64765E-39
Intestine posterior	rpl-17	0.435559461	1.55938E-38
Intestine posterior	rps-8	0.454087648	2.10175E-38
Intestine posterior	col-80	1.10494413	6.51412E-38
Intestine posterior	rps-5	0.471775743	2.33877E-37
Intestine posterior	rpl-13	0.465848477	4.34046E-37
Intestine posterior	rpl-12	0.408882625	5.80131E-37
Intestine posterior	F11E6.3	1.61036943	3.93768E-36
Intestine posterior	H06H21.8	-1.057399956	1.75149E-35
Intestine posterior	pud-4	-3.521868306	1.88894E-35
Intestine posterior	F35E12.9	-1.593067507	6.80849E-35
Intestine posterior	rpl-10	0.467201096	9.09599E-35
Intestine posterior	math-22	-0.803761619	4.29497E-34
Intestine posterior	W04B5.3	-0.936707638	1.54565E-33
Intestine posterior	eef-1A.1	0.613451602	1.58976E-33
Intestine posterior	zip-2	-1.352162077	1.80898E-33
Intestine posterior	xbp-1	-1.330224633	2.32636E-33
Intestine posterior	fat-6	-0.614390728	5.08574E-33
Intestine posterior	C52B11.5	-1.201969828	4.80835E-32
Intestine posterior	rps-19	0.404144004	6.95489E-32
Intestine posterior	ugt-29	-1.297667493	9.15364E-32
Intestine posterior	C06A8.3	1.402406429	2.40029E-31
Intestine posterior	rpl-2	0.464691562	4.59405E-31
Intestine posterior	rps-18	0.416114858	1.22741E-30
Intestine posterior	clec-47	2.455394017	1.52176E-30
Intestine posterior	nduo-5	0.62120571	2.01346E-30

Intestine posterior	rpl-16	0.457927941	2.28526E-30
Intestine posterior	F17C11.11	-1.74732541	3.33875E-30
Intestine posterior	msp-40	-1.804764517	4.04606E-30
Intestine posterior	rpl-6	0.455388111	6.96516E-30
Intestine posterior	ctb-1	0.535944281	7.90821E-30
Intestine posterior	C54D10.3	1.603731673	8.17377E-30
Intestine posterior	rpl-5	0.462671325	8.59346E-30
Intestine posterior	hacd-1	-1.589653985	9.18018E-30
Intestine posterior	rps-20	0.473497002	1.52894E-29
Intestine posterior	rpl-24.1	0.395443328	2.44995E-29
Intestine posterior	amx-3	-1.017360842	3.15954E-29
Intestine posterior	ssp-10	-1.47047022	4.05148E-29
Intestine posterior	col-106	1.202033784	6.56821E-29
Intestine posterior	rps-0	0.47178188	7.23512E-29
Intestine posterior	rpl-7A	0.465686942	7.78861E-29
Intestine posterior	C17F4.7	0.661874756	1.67213E-28
Intestine posterior	gba-4	-2.060554119	2.47732E-28
Intestine posterior	E02H9.3	-0.919190896	3.18371E-28
Intestine posterior	clec-50	-0.795191161	7.8896E-28
Intestine posterior	rps-1	0.444611262	1.29118E-27
Intestine posterior	Y82E9BR.5	-1.175329274	2.53979E-27
Intestine posterior	Y37E3.8	0.386452139	3.00025E-27
Intestine posterior	cyn-7	0.64963795	3.64723E-27
Intestine posterior	C50F4.1	-1.094372675	4.44744E-27
Intestine posterior	hrg-1	-1.809820968	8.40325E-27
Intestine posterior	K09F6.6	-0.768865671	9.39748E-27
Intestine posterior	R09F10.1	-1.096382403	1.28081E-26
Intestine posterior	rps-3	0.430002419	1.64761E-26
Intestine posterior	F32D8.12	-0.873781945	3.42242E-26
Intestine posterior	cpr-6	-0.784583955	4.29003E-26
Intestine posterior	pod-2	-1.003788079	7.28884E-26

Intestine posterior	rpl-1	0.455264268	1.46573E-25
Intestine posterior	hpo-34	-0.570521561	1.63583E-25
Intestine posterior	rpl-18	0.415464149	1.91752E-25
Intestine posterior	R04F11.2	0.530258476	2.00576E-25
Intestine posterior	fip-2	1.774534614	2.25667E-25
Intestine posterior	lys-4	0.884389626	6.66606E-25
Intestine posterior	rack-1	0.5172023	1.1025E-24
Intestine posterior	math-18	-0.950388729	1.20131E-24
Intestine posterior	rps-4	0.408069516	1.78196E-24
Intestine posterior	cco-2	0.622863756	2.83015E-24
Intestine posterior	col-139	0.783146417	5.08804E-24
Intestine posterior	msp-31	-1.726311299	9.78034E-24
Intestine posterior	gon-1	-1.144652451	1.52947E-23
Intestine posterior	ddo-2	-0.702543428	1.53054E-23
Intestine posterior	F57F5.1	-0.512284382	1.87723E-23
Intestine posterior	R193.2	-1.187840667	1.922E-23
Intestine posterior	ant-1.1	0.41619091	1.99511E-23
Intestine posterior	T28F4.5	-0.550708416	5.09419E-23
Intestine posterior	ppat-1	-1.920554201	6.11297E-23
Intestine posterior	zip-12	-0.648770283	7.17752E-23
Intestine posterior	gldc-1	-1.647746154	7.5811E-23
Intestine posterior	sur-5	-1.436354286	1.07639E-22
Intestine posterior	Y6G8.2	-1.138348534	1.23464E-22
Intestine posterior	E01G4.3	-0.961988737	1.34336E-22
Intestine posterior	F36A2.7	0.775867489	2.45892E-22
Intestine posterior	R53.4	0.514742456	4.38226E-22
Intestine posterior	rpl-3	0.41337885	5.1676E-22
Intestine posterior	rpl-20	0.395397654	5.47177E-22
Intestine posterior	hpo-15	-1.523109672	6.49584E-22
Intestine posterior	vrp-1	-1.026000315	1.14804E-21

Intestine posterior	cth-2	-1.116159097	1.3102E-21
Intestine posterior	rps-12	0.334322893	1.3518E-21
Intestine posterior	T01B11.2	-1.598173424	1.36636E-21
Intestine posterior	ets-4	-1.000995112	2.54029E-21
Intestine posterior	col-143	1.207001621	2.68051E-21
Intestine posterior	W02F12.4	-1.276483096	3.86936E-21
Intestine posterior	fat-7	1.432194742	6.12414E-21
Intestine posterior	msp-36	-1.287294159	6.97689E-21
Intestine posterior	clec-173	-1.586755397	7.31453E-21
Intestine posterior	spch-3	-2.089980865	9.19287E-21
Intestine posterior	far-3	2.832516326	9.96009E-21
Intestine posterior	lbp-6	0.485966368	1.15704E-20
Intestine posterior	R09H10.5	-0.880006028	1.55845E-20
Intestine posterior	pkg-2	-0.987975829	1.87063E-20
Intestine posterior	fbxa-26	-1.781504421	2.84257E-20
Intestine posterior	unc-70	-1.348766844	3.21478E-20
Intestine posterior	col-160	1.243773611	4.4262E-20
Intestine posterior	lipl-2	-2.573801226	4.79011E-20
Intestine posterior	msd-4	-1.187253378	4.8114E-20
Intestine posterior	ttr-15	1.144697021	6.60056E-20
Intestine posterior	pud-3	-2.8339666	7.94029E-20
Intestine posterior	ZK1240.2	-1.030810494	1.03672E-19
Intestine posterior	E02C12.8	-1.24903018	1.86127E-19
Intestine posterior	icd-2	0.619405785	1.94057E-19
Intestine posterior	rpl-22	0.379031782	2.17281E-19
Intestine posterior	fipr-21	0.968735559	3.06724E-19
Intestine posterior	ZK470.2	-1.294454219	3.93441E-19
Intestine posterior	ver-4	-1.278664367	5.49619E-19
Intestine posterior	lmp-2	-1.303164395	6.61596E-19

Intestine posterior	fat-5	-1.307093662	6.99602E-19
Intestine posterior	itr-1	-0.739014783	6.99876E-19
Intestine posterior	col-42	1.19899267	7.65871E-19
Intestine posterior	ilys-5	-0.38024709	7.84865E-19
Intestine posterior	rps-10	0.342438834	9.57549E-19
Intestine posterior	Y16B4A.2	-1.025573277	1.99662E-18
Intestine posterior	rfip-1	-1.003827234	2.13723E-18
Intestine posterior	dhs-14	-1.255539973	2.1797E-18
Intestine posterior	klo-2	-2.495051857	2.47117E-18
Intestine posterior	rpl-23	0.343821116	2.96859E-18
Intestine posterior	daf-21	0.554677606	3.34943E-18
Intestine posterior	F39C12.1	-0.671205474	5.09177E-18
Intestine posterior	gst-1	-0.795891933	6.75629E-18
Intestine posterior	spp-2	-1.257411813	7.7241E-18
Intestine posterior	atf-7	-0.881706768	9.51482E-18
Intestine posterior	fipr-2	3.527726951	3.12518E-17
Intestine posterior	slc-17.6	-0.867898113	3.63885E-17
Intestine posterior	K08D12.6	1.107284419	3.76067E-17
Intestine posterior	nduo-2	0.515038466	3.9354E-17
Intestine posterior	lys-2	-1.05645588	4.02927E-17
Intestine posterior	msp-50	-3.117898434	6.1086E-17
Intestine posterior	rpl-7	0.355858815	6.80472E-17
Intestine posterior	ftn-2	-0.560091365	8.70784E-17
Intestine posterior	ZK593.3	1.506886131	9.93136E-17
Intestine posterior	M02H5.8	0.694297558	1.0532E-16
Intestine posterior	eef-1B.1	0.370586085	1.1082E-16
Intestine posterior	atp-3	0.579118275	1.12525E-16
Intestine posterior	iff-1	0.758655354	1.59886E-16
Intestine posterior	ctc-3	0.398917591	1.69028E-16
Intestine posterior	vab-10	-0.609221132	2.28939E-16
Intestine posterior	col-98	1.185966357	2.85313E-16

Intestine posterior	prdx-2	0.694588984	3.04498E-16
Intestine posterior	lys-1	-0.69421993	3.08798E-16
Intestine posterior	msp-33	-2.041717237	3.37205E-16
Intestine posterior	C32D5.6	-1.829903558	3.82934E-16
Intestine posterior	T13F3.6	1.105036529	4.32278E-16
Intestine posterior	rps-23	0.322774757	4.87108E-16
Intestine posterior	F14D7.6	-0.70000858	5.38001E-16
Intestine posterior	T10B5.4	-1.558928223	5.62994E-16
Intestine posterior	rpl-4	0.484199581	5.9042E-16
Intestine posterior	nrf-6	-1.000653906	6.00901E-16
Intestine posterior	msp-49	-2.39963712	6.69756E-16
Intestine posterior	col-129	0.720348266	6.80618E-16
Intestine posterior	rpl-26	0.328234982	7.27366E-16
Intestine posterior	ssq-1	-1.760549644	8.35021E-16
Intestine posterior	fipr-1	2.016903589	8.53969E-16
Intestine posterior	T20G5.8	0.594163034	9.18849E-16
Intestine posterior	pcp-1	-0.687508039	1.20242E-15
Intestine posterior	T03E6.8	-0.928217815	1.78524E-15
Intestine posterior	eef-1G	0.458497284	1.89396E-15
Intestine posterior	C49C3.4	-0.749314155	1.9168E-15
Intestine posterior	ifc-2	-0.918522537	2.06792E-15
Intestine posterior	atp-5	0.530547833	2.06804E-15
Intestine posterior	F28H7.3	-1.213860948	2.16653E-15
Intestine posterior	C24B9.3	-1.731143318	2.18412E-15
Intestine posterior	F57F4.4	-0.643630644	2.43387E-15
Intestine posterior	msp-45	-2.23883985	2.63892E-15
Intestine posterior	T02H6.11	0.489195713	5.05075E-15
Intestine posterior	clec-84	-0.691368965	5.12639E-15
Intestine posterior	C44H9.6	-1.123548471	5.18886E-15
Intestine posterior	spch-1	-1.962382334	6.48343E-15

Intestine posterior	cco-1	0.470342359	7.54467E-15
Intestine posterior	zip-10	-1.237511814	8.47654E-15
Intestine posterior	F54C9.3	-0.978752252	8.54249E-15
Intestine posterior	K09F6.10	-0.643564338	8.96438E-15
Intestine posterior	T02C5.1	-0.651475559	1.04596E-14
Intestine posterior	T02B5.3	-0.98746217	1.05074E-14
Intestine posterior	rpl-9	0.363961525	1.10152E-14
Intestine posterior	ehbp-1	-0.708410884	1.36772E-14
Intestine posterior	tnc-2	1.770063963	1.39614E-14
Intestine posterior	C42D4.1	-0.797197103	1.45047E-14
Intestine posterior	pmt-2	0.525240711	1.46066E-14
Intestine posterior	asp-10	-1.577250874	2.07909E-14
Intestine posterior	catp-5	-1.92695738	2.24154E-14
Intestine posterior	Y37E11B.2	-1.56961122	2.34298E-14
Intestine posterior	rps-14	0.269561662	2.65997E-14
Intestine posterior	F49E2.5	-0.64746777	2.68949E-14
Intestine posterior	msp-3	-1.804116824	3.31287E-14
Intestine posterior	nspd-1	-1.856818481	3.37472E-14
Intestine posterior	scav-4	-1.571922383	3.46657E-14
Intestine posterior	hmit-1.3	-1.249181487	3.53285E-14
Intestine posterior	col-142	1.018968656	3.64421E-14
Intestine posterior	W04D2.6	-0.684214937	3.71293E-14
Intestine posterior	math-3	-0.387364579	3.72527E-14
Intestine posterior	nduo-1	0.381513205	4.18685E-14
Intestine posterior	rps-2	0.383613457	4.28884E-14
Intestine posterior	tag-174	0.546163193	4.30455E-14
Intestine posterior	col-178	0.939241861	5.01147E-14
Intestine posterior	msra-1	1.053730418	5.12153E-14
Intestine posterior	C08F11.13	-0.797028979	7.13401E-14
Intestine posterior	C25F9.5	-0.731700841	9.37588E-14

Intestine posterior	dod-3	-1.377811424	9.62985E-14
Intestine posterior	rps-13	0.295713947	1.05317E-13
Intestine posterior	dod-6	1.090721034	1.16459E-13
Intestine posterior	pcyt-1	-1.042055331	1.62436E-13
Intestine posterior	C06B3.6	-0.944658755	1.71652E-13
Intestine posterior	tag-244	-1.297803581	1.78426E-13
Intestine posterior	rps-26	0.290462017	1.8135E-13
Intestine posterior	rps-15	0.309859807	2.02173E-13
Intestine posterior	F27D4.6	-1.635497334	2.5071E-13
Intestine posterior	hsp-110	0.714210298	2.86882E-13
Intestine posterior	tni-4	1.40002622	3.21583E-13
Intestine posterior	F52G2.3	-1.252254025	3.3585E-13
Intestine posterior	dsc-4	-0.975701521	3.47461E-13
Intestine posterior	acox-1.5	-1.156930161	3.88481E-13
Intestine posterior	F53F4.13	1.116330769	4.11986E-13
Intestine posterior	Y71H2AM.5	0.483732602	4.47105E-13
Intestine posterior	nhr-101	-1.139440354	4.48424E-13
Intestine posterior	dhs-3	-0.617862626	4.80895E-13
Intestine posterior	cgt-3	-0.874919061	5.62849E-13
Intestine posterior	pqn-60	3.120096911	6.77243E-13
Intestine posterior	F10G7.9	-0.641944672	7.1215E-13
Intestine posterior	hif-1	-1.026548909	7.41463E-13
Intestine posterior	ubq-2	0.307913915	7.50913E-13
Intestine posterior	rpl-15	0.318946373	8.06124E-13
Intestine posterior	cgt-2	-0.889074019	9.7668E-13
Intestine posterior	gon-2	-0.689822291	1.10134E-12
Intestine posterior	col-93	0.737232297	1.40099E-12
Intestine posterior	mrp-3	-1.459484577	1.47175E-12
Intestine posterior	F01G4.6	0.553703775	1.5862E-12
Intestine posterior	F29C4.2	0.502590927	1.79035E-12

Intestine posterior	vha-11	-0.615602084	1.96249E-12
Intestine posterior	asg-2	0.512228565	2.30889E-12
Intestine posterior	F42G2.2	-1.367391011	2.43119E-12
Intestine posterior	W07G4.3	-0.710317515	2.73524E-12
Intestine posterior	col-81	0.69785765	2.97155E-12
Intestine posterior	K08D8.4	-1.886990866	3.33185E-12
Intestine posterior	col-103	1.175246177	3.68659E-12
Intestine posterior	rpl-25.2	0.401230935	3.79697E-12
Intestine posterior	F15E6.6	-0.933892452	3.80525E-12
Intestine posterior	C25F9.14	-0.765713107	4.25004E-12
Intestine posterior	sbp-1	-1.316889095	4.28887E-12
Intestine posterior	C08B6.11	-1.759250882	4.45217E-12
Intestine posterior	T05F1.11	-1.20643476	5.89925E-12
Intestine posterior	T21C9.6	-1.16317358	6.28076E-12
Intestine posterior	bre-2	-1.849466638	6.70073E-12
Intestine posterior	W09C5.8	0.623324199	6.7303E-12
Intestine posterior	rpl-11.1	0.60875145	7.28873E-12
Intestine posterior	F43C1.5	-1.456057994	9.84919E-12
Intestine posterior	tatn-1	-1.137991542	1.0258E-11
Intestine posterior	cbl-1	-1.065653122	1.06889E-11
Intestine posterior	fbxa-189	-1.305797417	1.10289E-11
Intestine posterior	math-40	-1.364324268	1.12517E-11
Intestine posterior	acdh-1	-0.311627027	1.42159E-11
Intestine posterior	pqn-52	-0.986567777	1.57823E-11
Intestine posterior	F58F12.1	0.462509533	1.96513E-11
Intestine posterior	T25C12.3	-0.604972016	2.18314E-11
Intestine posterior	T12D8.5	-0.658676479	2.21892E-11

Intestine posterior	pkc-2	-1.648423729	2.2366E-11
Intestine posterior	ipla-1	-0.873503434	2.51809E-11
Intestine posterior	ubl-1	0.272337739	2.81666E-11
Intestine posterior	R08E3.1	-0.573559537	3.15997E-11
Intestine posterior	spp-5	-0.49090688	3.4438E-11
Intestine posterior	msp-152	-1.686909202	3.72359E-11
Intestine posterior	Y39E4B.6	-1.702171803	4.12082E-11
Intestine posterior	tag-234	-0.897780346	4.15237E-11
Intestine posterior	sma-10	-0.939624059	4.30084E-11
Intestine posterior	icd-1	0.502575577	4.64003E-11
Intestine posterior	cah-5	-1.233264777	4.72813E-11
Intestine posterior	nhr-114	-0.611829602	4.89334E-11
Intestine posterior	vab-8	-1.253513096	5.91204E-11
Intestine posterior	tmem-135	-1.020758173	7.38933E-11
Intestine posterior	K03H1.5	-0.802458383	7.91117E-11
Intestine posterior	unc-16	-0.908705495	7.92985E-11
Intestine posterior	F11D5.7	-1.354843703	8.06168E-11
Intestine posterior	hsp-1	0.474017122	8.08652E-11
Intestine posterior	nspd-2	-1.503153957	8.98198E-11
Intestine posterior	fbxa-60	-1.300614507	9.31785E-11
Intestine posterior	Y75B8A.24	-0.894595532	1.22896E-10
Intestine posterior	tag-260	-1.204010907	1.27345E-10
Intestine posterior	C01B9.1	-1.281162656	1.42098E-10
Intestine posterior	F22F7.8	-1.086187455	1.42352E-10
Intestine posterior	ddo-1	-1.335260666	1.44725E-10

Intestine posterior	acs-2	2.025068714	1.64417E-10
Intestine posterior	rps-17	0.282316055	1.75517E-10
Intestine posterior	mtrr-1	0.902016177	1.93124E-10
Intestine posterior	rps-6	0.349673727	2.07198E-10
Intestine posterior	tre-2	-1.311619639	2.25976E-10
Intestine posterior	C49A9.9	-1.122680764	2.35249E-10
Intestine posterior	ZK228.4	-0.818333157	2.56896E-10
Intestine posterior	fshr-1	-0.784288264	2.92727E-10
Intestine posterior	T05E7.1	-1.241594165	3.01234E-10
Intestine posterior	dkf-2	-0.925658458	3.1316E-10
Intestine posterior	R10E8.1	-1.072182472	3.14914E-10
Intestine posterior	msp-76	-1.097138698	3.76913E-10
Intestine posterior	ssq-2	-1.696903932	4.68154E-10
Intestine posterior	sma-9	-0.620707952	5.14331E-10
Intestine posterior	cyp-13A2	-1.618471173	5.16704E-10
Intestine posterior	aagr-1	-1.407068491	5.3562E-10
Intestine posterior	ssp-35	-1.442588815	5.42731E-10
Intestine posterior	F55F10.1	-0.462471392	5.45496E-10
Intestine posterior	nep-17	-1.220779407	5.57354E-10
Intestine posterior	cutl-18	-1.538126796	5.97229E-10
Intestine posterior	Y57G11C.9	-0.688115607	6.53561E-10
Intestine posterior	fmo-5	0.875982407	6.65495E-10
Intestine posterior	C34D4.3	-2.190948235	7.01484E-10
Intestine posterior	T19D12.2	-0.791240961	7.15882E-10
Intestine posterior	F43C11.7	-1.146863521	7.33454E-10

Intestine posterior	lfe-2	-0.841964244	7.39105E-10
Intestine posterior	mrp-5	-1.025058784	7.41618E-10
Intestine posterior	F15A4.6	0.980052866	7.85705E-10
Intestine posterior	del-5	-1.32777005	8.57184E-10
Intestine posterior	dpy-22	-0.546683983	8.826E-10
Intestine posterior	math-45	-2.100232626	9.21761E-10
Intestine posterior	unc-43	-0.88518169	1.01837E-09
Intestine posterior	obr-1	-1.031114658	1.02856E-09
Intestine posterior	C55B7.3	-2.834377402	1.15749E-09
Intestine posterior	gfi-1	-1.369613046	1.32146E-09
Intestine posterior	clec-186	-1.2397181	1.34378E-09
Intestine posterior	M28.5	0.540978359	1.36472E-09
Intestine posterior	D2030.4	0.676561344	1.3904E-09
Intestine posterior	D1005.4	-1.734237442	1.40132E-09
Intestine posterior	ugt-53	-2.093118669	1.44827E-09
Intestine posterior	hpd-1	-1.005498315	1.48795E-09
Intestine posterior	C29F3.7	-1.180090403	1.57511E-09
Intestine posterior	gst-7	-0.563442228	1.70432E-09
Intestine posterior	mai-1	-1.085916162	1.7229E-09
Intestine posterior	F13H10.8	-0.642050253	1.74134E-09
Intestine posterior	spp-8	-1.029539521	1.84514E-09
Intestine posterior	C56E6.2	-0.878579658	1.97078E-09
Intestine posterior	orai-1	-0.945757073	2.02826E-09
Intestine posterior	metr-1	0.426109197	2.2405E-09
Intestine posterior	cyp-35A2	-0.693045779	2.34995E-09
Intestine posterior	asp-2	0.55222876	2.39628E-09
Intestine posterior	ads-1	-0.539640505	2.66263E-09

Intestine posterior	cpn-4	1.786479185	2.72074E-09
Intestine posterior	H41C03.3	-2.794023563	3.04006E-09
Intestine posterior	gipc-2	-2.502767338	3.30506E-09
Intestine posterior	pyk-2	-0.693970071	3.59859E-09
Intestine posterior	daf-2	-0.918361132	3.73471E-09
Intestine posterior	vgln-1	-0.557584541	3.98308E-09
Intestine posterior	F31F4.1	-1.01479073	4.03815E-09
Intestine posterior	rpl-28	0.314383813	4.32905E-09
Intestine posterior	B0252.1	-1.111914661	4.36194E-09
Intestine posterior	R102.4	-1.086506436	4.56369E-09
Intestine posterior	C05B5.5	-0.939055204	4.71153E-09
Intestine posterior	F28B4.3	-0.859169434	4.77127E-09
Intestine posterior	spp-1	-0.827227505	5.08624E-09
Intestine posterior	C31C9.7	-0.807748313	5.12544E-09
Intestine posterior	tba-2	0.70129432	5.71335E-09
Intestine posterior	msp-38	-1.624274164	5.73902E-09
Intestine posterior	C51E3.10	-2.086061297	5.77611E-09
Intestine posterior	atp-4	0.406463459	6.50775E-09
Intestine posterior	col-159	0.691553067	6.62204E-09
Intestine posterior	acly-1	-2.043144258	7.60089E-09
Intestine posterior	ZK550.2	-1.181614898	7.66725E-09
Intestine posterior	myo-2	2.528918526	8.69698E-09
Intestine posterior	K10C2.1	-0.66969715	1.05408E-08
Intestine posterior	T19D12.1	-0.792198777	1.05434E-08
Intestine posterior	ZC116.1	3.194418319	1.13673E-08
Intestine posterior	ctc-2	0.322133089	1.15508E-08
Intestine posterior	eps-8	-0.904523221	1.16073E-08
Intestine posterior	pnk-1	-0.875989767	1.26275E-08

Intestine posterior	asb-2	0.570574189	1.28961E-08
Intestine posterior	F35B12.3	2.563279365	1.4142E-08
Intestine posterior	E01G6.3	-1.317660502	1.44304E-08
Intestine posterior	F46H5.2	-1.030941493	1.46326E-08
Intestine posterior	ahcy-1	0.40688435	1.85504E-08
Intestine posterior	F13B12.3	-0.692933219	1.91689E-08
Intestine posterior	nuo-6	0.689188232	2.27409E-08
Intestine posterior	ifb-2	-0.713998274	2.43313E-08
Intestine posterior	tig-3	-1.588420263	2.90542E-08
Intestine posterior	dct-11	-0.704767289	3.17401E-08
Intestine posterior	ZK813.2	-3.239141327	3.20895E-08
Intestine posterior	ugt-47	-0.475548651	3.21131E-08
Intestine posterior	ZK1290.5	-0.838456004	3.24429E-08
Intestine posterior	gtl-1	-0.538103661	3.26815E-08
Intestine posterior	lact-4	0.635101002	3.30055E-08
Intestine posterior	pab-1	0.479527886	3.36966E-08
Intestine posterior	fipr-7	2.444162396	3.65574E-08
Intestine posterior	hum-8	-0.46692923	3.92648E-08
Intestine posterior	nmy-1	-2.791406131	3.96688E-08
Intestine posterior	rpl-35	0.235966138	4.32399E-08
Intestine posterior	cyc-2.1	0.344006453	4.48586E-08
Intestine posterior	par-5	0.464052235	4.58501E-08
Intestine posterior	fipr-10	2.289398599	4.64448E-08
Intestine posterior	F56C4.4	-4.176388088	5.1171E-08
Intestine posterior	msp-57	-2.154932955	5.76695E-08
Intestine posterior	F23F12.3	-1.636278601	5.83229E-08
Intestine posterior	rpl-21	0.231327498	5.86512E-08
Intestine posterior	trpp-12	-1.198205922	6.46579E-08
Intestine posterior	sup-37	-1.015765654	6.84425E-08

Intestine posterior	Y119C1B.10	-0.889009117	7.04461E-08
Intestine posterior	F21D5.3	-0.933747563	7.31428E-08
Intestine posterior	ugt-65	-2.065968645	7.57751E-08
Intestine posterior	rpa-4	-0.591943589	7.79702E-08
Intestine posterior	nhr-125	-1.356447825	8.20678E-08
Intestine posterior	C35A11.4	-1.554904665	8.51348E-08
Intestine posterior	papl-1	-0.973063089	9.2815E-08
Intestine posterior	nspd-10	-1.715408025	9.38463E-08
Intestine posterior	C49A9.2	-0.828214314	9.72206E-08
Intestine posterior	kbrl-1	-0.985737934	1.03124E-07
Intestine posterior	C53C9.2	2.078874821	1.09078E-07
Intestine posterior	pgp-1	-1.83566187	1.16267E-07
Intestine posterior	asg-1	0.562978345	1.18738E-07
Intestine posterior	F22H10.3	-0.547007464	1.26425E-07
Intestine posterior	C31H5.6	-1.272829332	1.29803E-07
Intestine posterior	ztf-18	-1.437624569	1.42397E-07
Intestine posterior	H28O16.1	0.396934451	1.43003E-07
Intestine posterior	F21C10.9	0.574107937	1.46655E-07
Intestine posterior	abt-2	-1.119060217	1.50781E-07
Intestine posterior	C05D11.5	0.547736122	1.58297E-07
Intestine posterior	F08H9.2	-0.807990726	1.71918E-07
Intestine posterior	eef-2	0.404510507	1.74178E-07
Intestine posterior	plc-3	-1.12446621	1.82361E-07
Intestine posterior	F52A8.1	0.780206849	1.91523E-07
Intestine posterior	msd-2	-1.887366194	2.12683E-07
Intestine posterior	lst-6	-0.662206243	2.19499E-07
Intestine posterior	F29B9.11	0.467796643	2.24275E-07
Intestine posterior	Y87G2A.19	1.528362306	2.31597E-07
Intestine posterior	nlp-33	0.939978186	2.39174E-07

Intestine posterior	saeg-1	-0.73173789	2.42727E-07
Intestine posterior	C49C3.9	-1.307315976	2.48978E-07
Intestine posterior	sptl-1	-0.732063708	2.49926E-07
Intestine posterior	dhs-25	-0.892142374	2.60493E-07
Intestine posterior	F59C6.5	0.665829315	2.79032E-07
Intestine posterior	klp-4	-1.208013123	3.16566E-07
Intestine posterior	rps-30	0.243179398	3.37124E-07
Intestine posterior	rpl-14	0.240550698	3.51339E-07
Intestine posterior	acs-7	-1.457360938	3.54849E-07
Intestine posterior	nhr-232	-1.123230818	3.84832E-07
Intestine posterior	ptr-24	-1.241295837	3.9322E-07
Intestine posterior	B0252.3	-1.582787519	4.28258E-07
Intestine posterior	mom-5	-1.305516093	4.2872E-07
Intestine posterior	F26B1.8	-3.151298352	4.35504E-07
Intestine posterior	F56H9.2	-0.620562052	4.47213E-07
Intestine posterior	Y51H1A.3	0.577041135	4.49414E-07
Intestine posterior	Y22D7AL.10	0.537450908	4.52776E-07
Intestine posterior	fkb-2	0.562972938	5.30475E-07
Intestine posterior	pals-24	-0.690839224	5.76756E-07
Intestine posterior	nhr-202	-0.661686949	6.15707E-07
Intestine posterior	D2023.4	-1.037205124	6.70834E-07
Intestine posterior	acl-7	-1.066140795	6.9993E-07
Intestine posterior	ZK550.6	-0.893674294	7.222E-07
Intestine posterior	ule-4	-1.06580445	7.44776E-07
Intestine posterior	T20H4.5	0.720914794	7.64332E-07
Intestine posterior	Y7A5A.1	-1.003092935	7.70577E-07
Intestine posterior	fipr-5	1.703268418	7.97895E-07
Intestine posterior	rpl-32	0.217928212	8.49105E-07

Intestine posterior	tank-1	-1.126291545	9.03345E-07
Intestine posterior	grk-1	-0.954842407	9.12687E-07
Intestine posterior	cpr-4	0.765276797	9.54609E-07
Intestine posterior	msp-81	-1.298450105	9.81515E-07
Intestine posterior	K02C4.5	-1.20064903	1.00569E-06
Intestine posterior	lpd-5	0.715557422	1.03073E-06
Intestine posterior	C01B10.6	-0.88107822	1.05844E-06
Intestine posterior	col-147	0.750807519	1.08676E-06
Intestine posterior	nhr-31	-0.826103068	1.10325E-06
Intestine posterior	egl-8	-0.570653708	1.18184E-06
Intestine posterior	dod-19	-1.063821771	1.25282E-06
Intestine posterior	F22H10.2	-1.409226584	1.29304E-06
Intestine posterior	T03F1.11	1.232261609	1.44588E-06
Intestine posterior	Y75B8A.32	-1.210660576	1.4883E-06
Intestine posterior	hrg-4	-1.839862787	1.50484E-06
Intestine posterior	ZK250.13	-0.955063952	1.52083E-06
Intestine posterior	B0281.3	-1.097021018	1.5222E-06
Intestine posterior	F58B4.5	-1.711207237	1.53796E-06
Intestine posterior	tbb-2	0.521519916	1.53798E-06
Intestine posterior	C10G8.8	-0.70700794	1.6024E-06
Intestine posterior	M02E1.1	-0.858374068	1.60453E-06
Intestine posterior	klo-1	-0.86873739	1.61011E-06
Intestine posterior	ttm-2	-1.284983572	1.67332E-06
Intestine posterior	gst-10	-0.771323697	1.68497E-06
Intestine posterior	glr-6	-0.996347765	2.06799E-06
Intestine posterior	C01B10.4	-1.098284217	2.14087E-06
Intestine posterior	ceh-60	-0.826056202	2.25274E-06

Intestine posterior	clec-49	-1.197031571	2.35787E-06
Intestine posterior	nap-1	0.520339925	2.44324E-06
Intestine posterior	T28C6.7	-0.484795657	2.48395E-06
Intestine posterior	F22B8.7	-0.938765057	2.6204E-06
Intestine posterior	F42G8.10	0.630959692	2.62103E-06
Intestine posterior	chat-1	-0.558197652	2.63612E-06
Intestine posterior	rege-1	-0.899823348	2.81543E-06
Intestine posterior	sesn-1	-1.068241526	2.83771E-06
Intestine posterior	F40F9.5	-1.241560865	2.86539E-06
Intestine posterior	gcy-28	-0.781020087	2.8934E-06
Intestine posterior	vha-6	-0.614663342	2.94897E-06
Intestine posterior	ceh-44	-0.67574858	3.0781E-06
Intestine posterior	F42G4.5	-2.869260448	3.24182E-06
Intestine posterior	ifc-1	-1.471618169	3.35706E-06
Intestine posterior	C25H3.9	0.662981226	3.58086E-06
Intestine posterior	K08D8.6	-1.838232057	3.64268E-06
Intestine posterior	C49A9.3	-0.86236598	3.65754E-06
Intestine posterior	col-101	0.781016562	3.7193E-06
Intestine posterior	pks-1	-0.919094011	3.88758E-06
Intestine posterior	rga-5	-1.287780565	3.95644E-06
Intestine posterior	ttr-21	2.698557609	4.26655E-06
Intestine posterior	hil-4	0.785373478	4.44417E-06
Intestine posterior	clec-41	-1.205533863	5.13877E-06
Intestine posterior	oac-20	-1.566100622	5.56014E-06
Intestine posterior	eat-16	-1.05882911	5.63093E-06
Intestine posterior	ZK185.3	-1.580593412	5.66713E-06
Intestine posterior	nuo-2	0.734098797	6.22376E-06
Intestine posterior	W09B6.4	-1.079138682	6.37072E-06

Intestine posterior	C24A3.2	0.894137399	6.55917E-06
Intestine posterior	Y46D2A.2	-1.95739529	6.72384E-06
Intestine posterior	lbp-9	0.57620102	6.89155E-06
Intestine posterior	F53C11.1	-1.365503587	6.99622E-06
Intestine posterior	daf-36	-1.243302882	7.19152E-06
Intestine posterior	ZC395.5	-0.926624878	7.27202E-06
Intestine posterior	nlp-26	1.32128205	7.52174E-06
Intestine posterior	irx-1	-1.793144568	7.89993E-06
Intestine posterior	C49G7.3	0.978949027	7.9981E-06
Intestine posterior	F45H10.3	0.578413596	8.26615E-06
Intestine posterior	kdp-1	0.582113455	8.48744E-06
Intestine posterior	dhs-7	-1.2467683	8.53054E-06
Intestine posterior	C52B9.8	-0.837464321	8.55058E-06
Intestine posterior	tax-6	-1.027928918	8.8895E-06
Intestine posterior	acl-8	-1.072284338	9.04005E-06
Intestine posterior	gsto-1	-1.267218735	9.52466E-06
Intestine posterior	ugt-22	-0.611341681	9.7023E-06
Intestine posterior	nhr-176	-0.856301717	9.77079E-06
Intestine posterior	Y105C5B.15	-1.244780268	1.00341E-05
Intestine posterior	F36F2.1	1.247861741	1.01375E-05
Intestine posterior	gcp-2.1	-1.069000369	1.05839E-05
Intestine posterior	Y53G8AR.7	-1.172004298	1.13861E-05
Intestine posterior	fbxa-54	-0.897588375	1.18593E-05
Intestine posterior	fard-1	-0.729251668	1.2063E-05
Intestine posterior	lin-10	-0.635564027	1.25202E-05
Intestine posterior	rde-12	-0.811039507	1.29055E-05
Intestine posterior	C46H11.2	-0.923984651	1.34673E-05

Intestine posterior	ZC266.1	-2.296494646	1.45247E-05
Intestine posterior	T19H5.4	-1.051689549	1.46106E-05
Intestine posterior	cpz-1	-0.384892308	1.58768E-05
Intestine posterior	anmt-2	1.454411888	1.65288E-05
Intestine posterior	Y48G9A.9	-1.011983785	1.66616E-05
Intestine posterior	T05E12.3	-1.387378031	1.68886E-05
Intestine posterior	nhr-64	-0.947442631	1.716E-05
Intestine posterior	pals-23	-0.584972736	1.72699E-05
Intestine posterior	Y47G6A.33	0.58236012	1.75704E-05
Intestine posterior	rla-1	0.252793433	1.84651E-05
Intestine posterior	ucr-1	0.697110435	2.07862E-05
Intestine posterior	C31C9.6	-1.238275941	2.39986E-05
Intestine posterior	R07E4.1	-1.408568432	2.44252E-05
Intestine posterior	fbxa-31	-0.873035507	2.60916E-05
Intestine posterior	nhr-68	-0.461495807	2.6905E-05
Intestine posterior	Y39B6A.5	-1.968464817	2.81552E-05
Intestine posterior	hpo-13	-0.845800139	2.86267E-05
Intestine posterior	ttr-26	1.677376599	2.88794E-05
Intestine posterior	jun-1	-0.718445851	2.90783E-05
Intestine posterior	F49C12.11	0.807026282	2.9222E-05
Intestine posterior	aex-1	-0.537777502	2.95368E-05
Intestine posterior	ssp-19	-2.154524168	3.01913E-05
Intestine posterior	ZC239.16	-1.1842393	3.02875E-05
Intestine posterior	atg-2	-0.450764032	3.23004E-05
Intestine posterior	Y106G6H.1	-0.884911054	3.26685E-05
Intestine posterior	amt-4	-1.530807407	3.5623E-05

Intestine posterior	ceeh-1	-1.054108045	3.56281E-05
Intestine posterior	pmp-5	0.458208711	3.61029E-05
Intestine posterior	fipr-3	2.147135303	3.74087E-05
Intestine posterior	R09E10.6	-2.528810011	3.84552E-05
Intestine posterior	C52E2.5	-1.41535082	3.88669E-05
Intestine posterior	Y20C6A.1	-1.150572978	4.08353E-05
Intestine posterior	fbxa-80	-1.265805333	4.15168E-05
Intestine posterior	gstk-1	-1.289591087	4.203E-05
Intestine posterior	W05H9.1	-0.403418848	4.33256E-05
Intestine posterior	T20D3.2	0.507814125	4.39151E-05
Intestine posterior	ril-1	0.339322827	4.56973E-05
Intestine posterior	ubq-1	0.416266651	4.62947E-05
Intestine posterior	aly-3	-0.462311556	4.69096E-05
Intestine posterior	E04F6.15	-0.977663875	5.04551E-05
Intestine posterior	alh-12	-0.818481066	5.06942E-05
Intestine posterior	mthf-1	-0.577257694	5.16845E-05
Intestine posterior	let-19	-0.355357286	5.30092E-05
Intestine posterior	pept-1	-0.454951607	5.626E-05
Intestine posterior	unc-44	-0.726356148	5.96605E-05
Intestine posterior	Y32F6A.4	-1.129378605	6.0649E-05
Intestine posterior	daf-3	-1.006279646	6.17356E-05
Intestine posterior	Y51F10.7	-0.416184019	6.27885E-05
Intestine posterior	sss-1	-2.55398111	6.401E-05
Intestine posterior	kin-4	-0.649348874	6.4238E-05
Intestine posterior	gei-17	-0.7201092	6.48154E-05
Intestine posterior	tcer-1	-0.464225586	6.5789E-05
Intestine posterior	gba-1	-0.918392516	6.70042E-05

Intestine posterior	bgal-2	-1.073516826	6.86275E-05
Intestine posterior	Y73F4A.2	2.92738177	6.99554E-05
Intestine posterior	W07G4.5	-0.734245942	7.05872E-05
Intestine posterior	mec-5	-1.315602299	7.11208E-05
Intestine posterior	F32D8.11	-0.794957162	7.60109E-05
Intestine posterior	ctsa-2	-1.342833667	7.748E-05
Intestine posterior	acdh-9	-1.065885713	7.81317E-05
Intestine posterior	F53A9.8	-1.068926828	7.8366E-05
Intestine posterior	F54D5.4	-0.593486937	7.92637E-05
Intestine posterior	egl-44	-1.276019537	7.98721E-05
Intestine posterior	fbxa-99	-1.932976034	8.1758E-05
Intestine posterior	Y54F10AM.5	0.601419015	8.20087E-05
Intestine posterior	ZC328.3	-0.782234897	8.22336E-05
Intestine posterior	nhr-22	-1.061320781	8.42129E-05
Intestine posterior	C01H6.4	-0.970341426	8.49341E-05
Intestine posterior	F53F4.10	0.610212577	8.57906E-05
Intestine posterior	mai-2	0.397989128	8.84807E-05
Intestine posterior	idh-1	-0.472548349	9.4204E-05
Intestine posterior	emo-1	0.285235296	9.70385E-05
Intestine posterior	Y17G9B.8	-0.815040253	9.86348E-05
Intestine posterior	rps-24	0.21012246	9.94074E-05
Intestine posterior	cey-2	0.582903843	0.000101644
Intestine posterior	nspd-5	-2.336711029	0.000103229
Intestine posterior	par-1	-0.634467539	0.000103652
Intestine posterior	R07H5.8	0.631387623	0.000107948
Intestine posterior	Y73B6BL.31	-0.834789823	0.000110205
Intestine posterior	ran-1	0.540411936	0.000113189
Intestine posterior	T04F8.8	0.865893512	0.000116055

Intestine posterior	D2021.4	-0.795980443	0.000118504
Intestine posterior	T19H12.2	0.752260243	0.000121426
Intestine posterior	rps-25	0.181096347	0.000122169
Intestine posterior	pho-13	-0.813855225	0.000124222
Intestine posterior	ZC376.3	-0.985749733	0.000126578
Intestine posterior	C52D10.3	-1.264747409	0.000128271
Intestine posterior	C28G1.6	-1.440338481	0.000131116
Intestine posterior	Y105E8A.25	-0.3424855	0.000132641
Intestine posterior	ttr-27	1.803745138	0.000133733
Intestine posterior	eif-1	0.581671483	0.000136389
Intestine posterior	Y49E10.18	-1.218669128	0.000139613
Intestine posterior	H20E11.3	-0.70466003	0.000140151
Intestine posterior	faah-2	-0.826492517	0.000141252
Intestine posterior	myo-1	2.00194057	0.000145941
Intestine posterior	B0041.5	-0.745673687	0.000149019
Intestine posterior	nduo-4	0.262156553	0.000163447
Intestine posterior	crh-1	-0.862038941	0.000164276
Intestine posterior	fbxa-105	-2.685701751	0.000164465
Intestine posterior	K02D7.1	-0.93519087	0.000167258
Intestine posterior	rop-1	-0.857355812	0.000168528
Intestine posterior	lec-10	-0.370480891	0.000172404
Intestine posterior	R107.5	0.498893161	0.00017651
Intestine posterior	F30A10.9	0.53035695	0.000183054
Intestine posterior	F09C8.1	-2.600330659	0.000187863
Intestine posterior	ceh-88	-1.422573778	0.00019497
Intestine posterior	vha-2	0.367645104	0.000201489
Intestine posterior	R03G8.3	-0.966616696	0.000202441
Intestine posterior	F17B5.8	-1.664753073	0.000202445
Intestine posterior	Y102A11A.3	-0.564294889	0.000203032

Intestine posterior	msrp-2	-3.335485061	0.000208542
Intestine posterior	C23G10.2	0.603863675	0.000211592
Intestine posterior	dhhc-14	-1.223829445	0.000218021
Intestine posterior	lipl-1	-2.471641992	0.000218638
Intestine posterior	acs-14	-0.876897965	0.00022083
Intestine posterior	F53F1.2	0.7352507	0.000226308
Intestine posterior	W09D10.4	-0.682627943	0.000228241
Intestine posterior	Y40C5A.4	-1.105863964	0.000234801
Intestine posterior	lec-2	0.592141201	0.00024349
Intestine posterior	ssl-1	-0.522502333	0.000248638
Intestine posterior	F43C9.1	-0.766189222	0.000248825
Intestine posterior	gei-6	-0.696159521	0.000248922
Intestine posterior	rbm-5	-0.562127281	0.000249275
Intestine posterior	sql-1	-0.495196258	0.00025222
Intestine posterior	frm-10	-0.645347692	0.000270425
Intestine posterior	Y48A6B.3	0.537556311	0.000279143
Intestine posterior	nhr-210	-0.623786516	0.000280541
Intestine posterior	nhr-121	-0.990594967	0.000295379
Intestine posterior	C17F3.1	-1.302588455	0.000310252
Intestine posterior	isp-1	0.478863443	0.000318984
Intestine posterior	F58A6.9	-2.064400243	0.000330207
Intestine posterior	C10G11.8	-2.528111026	0.000342431
Intestine posterior	daao-1	-0.913049134	0.000342914
Intestine posterior	oig-3	0.721947241	0.000345734
Intestine posterior	nhr-133	-1.486886484	0.000360958
Intestine posterior	F55H12.3	-0.408332933	0.000374104

Intestine posterior	glo-4	-1.660486793	0.000375325
Intestine posterior	R05F9.6	0.439259413	0.000375489
Intestine posterior	Y48A6B.7	-1.367739375	0.000380914
Intestine posterior	F10F2.2	-0.630183802	0.000396141
Intestine posterior	nrfl-1	-0.626294684	0.000410772
Intestine posterior	nhr-55	-1.381876382	0.000422835
Intestine posterior	crm-1	-1.166430183	0.000430698
Intestine posterior	acd-5	-0.834895445	0.000448965
Intestine posterior	W02B12.4	-0.887288208	0.000462874
Intestine posterior	lin-14	-1.153930421	0.000463687
Intestine posterior	slc-36.2	-0.888238766	0.000493237
Intestine posterior	C27B7.9	0.968364574	0.000500011
Intestine posterior	rpl-36.A	0.196602286	0.000512872
Intestine posterior	C42D4.2	-0.846599253	0.000517872
Intestine posterior	sod-1	0.5830562	0.000518499
Intestine posterior	ZK185.5	-1.609636751	0.000531531
Intestine posterior	nspd-7	-2.508042305	0.000540264
Intestine posterior	T10D4.6	-0.819305873	0.00054092
Intestine posterior	F54D5.12	-0.792901959	0.000554848
Intestine posterior	sym-4	-0.654479723	0.000564999
Intestine posterior	F11D5.5	-1.412899045	0.000570534
Intestine posterior	cccp-1	-0.994163983	0.000575975
Intestine posterior	seu-1	-0.566417562	0.000602912
Intestine posterior	ZC116.5	1.409280599	0.000624464
Intestine posterior	F32B5.6	-0.760023162	0.000626794

Intestine posterior	ZK1240.5	-1.347977109	0.000631021
Intestine posterior	C34B2.10	-0.710283594	0.000667427
Intestine posterior	M163.8	0.17098988	0.000667522
Intestine posterior	C45E5.4	2.385366222	0.000693234
Intestine posterior	clec-63	0.375316008	0.000716872
Intestine posterior	mth-1	-1.184743834	0.000730162
Intestine posterior	T16G1.6	-1.365038662	0.00073513
Intestine posterior	F10C1.9	-0.920264031	0.000739876
Intestine posterior	acl-4	-0.785708299	0.000754157
Intestine posterior	K04A8.1	-0.959498728	0.0007963
Intestine posterior	mpc-2	0.666778765	0.000801196
Intestine posterior	mans-2	-1.54357734	0.00080826
Intestine posterior	kqt-2	-1.113075794	0.000811
Intestine posterior	fbxa-14	-0.993257264	0.000825315
Intestine posterior	rme-4	-0.857459274	0.000843371
Intestine posterior	rskn-2	-0.804541138	0.000866138
Intestine posterior	nhr-79	-0.979857119	0.000877753
Intestine posterior	nhr-80	-0.798798197	0.000881422
Intestine posterior	ZK1240.9	-0.939381926	0.000900172
Intestine posterior	elo-6	-0.355876822	0.000904857
Intestine posterior	add-1	-0.670286017	0.000977359
Intestine posterior	C03A7.13	-0.620183715	0.000999136
Intestine posterior	gei-13	-0.964207351	0.001001868
Intestine posterior	Y57G11C.22	-1.139830005	0.001010524
Intestine posterior	C06C3.12	-0.687332609	0.001085155

Intestine posterior	tom-1	-0.888506163	0.001086662
Intestine posterior	srh-48	-0.985886381	0.001157274
Intestine posterior	tre-1	-0.553670683	0.001194731
Intestine posterior	svh-2	-0.871022493	0.001194859
Intestine posterior	K09G1.1	0.722834038	0.001198284
Intestine posterior	dpy-27	-0.684426985	0.001228727
Intestine posterior	abf-5	1.739771102	0.00122997
Intestine posterior	tag-10	-2.031147509	0.001232391
Intestine posterior	slo-2	-1.065572205	0.001232583
Intestine posterior	E02H9.2	-1.229788314	0.001250338
Intestine posterior	ttr-59	0.942790292	0.001256015
Intestine posterior	C14C6.5	-0.884472706	0.001277867
Intestine posterior	hipr-1	-0.784349384	0.001300746
Intestine posterior	ZC376.2	-0.677621818	0.00131177
Intestine posterior	gld-2	-0.545180177	0.001345268
Intestine posterior	msp-64	-1.25378924	0.001382358
Intestine posterior	F13B9.1	-0.7721631	0.001396278
Intestine posterior	islo-1	-1.678918774	0.001439161
Intestine posterior	cyp-33E1	-0.960347589	0.001444637
Intestine posterior	acox-1.2	-0.982961058	0.001449442
Intestine posterior	hsp-16.41	0.611835708	0.001504935
Intestine posterior	let-23	-0.61507127	0.00153416
Intestine posterior	eef-1B.2	0.372112846	0.001534296
Intestine posterior	slc-17.3	-0.853702977	0.001585777
Intestine posterior	ssp-16	-3.456079779	0.001587499
Intestine posterior	btb-9	-1.421554619	0.001625785
Intestine posterior	unc-54	0.587251193	0.001630943
Intestine posterior	Y119D3B.12	-0.72013326	0.00168944

Intestine posterior	unc-62	-0.654457016	0.001709722
Intestine posterior	hum-5	-0.72291341	0.001743945
Intestine posterior	egl-10	-1.390237418	0.001747786
Intestine posterior	B0393.9	-2.058192336	0.001769743
Intestine posterior	lfi-1	-0.383217742	0.001794915
Intestine posterior	vha-9	0.472743036	0.001859851
Intestine posterior	W07A12.8	-1.497989306	0.001915528
Intestine posterior	Y113G7B.12	-0.608290694	0.001917001
Intestine posterior	Y105C5A.8	0.673791608	0.001986491
Intestine posterior	ccar-1	-0.638388292	0.002001975
Intestine posterior	mtl-2	0.479619091	0.00200279
Intestine posterior	nhr-179	-0.803703268	0.002025485
Intestine posterior	F26E4.6	0.315511396	0.002049545
Intestine posterior	C49A9.6	-0.839692657	0.002069296
Intestine posterior	F35B12.10	-1.495067826	0.0021092
Intestine posterior	bcat-1	-0.604909705	0.002212168
Intestine posterior	mgl-2	-1.010933562	0.002232781
Intestine posterior	snf-6	-1.167375502	0.002242651
Intestine posterior	pcn-1	0.724993616	0.002402742
Intestine posterior	ifa-1	1.904150114	0.002422772
Intestine posterior	skn-1	-0.378351046	0.002454637
Intestine posterior	K09F6.9	-0.300864813	0.002461969
Intestine posterior	abt-4	-0.933580707	0.002464892
Intestine posterior	vamp-8	1.344834831	0.002480144
Intestine posterior	ttyh-1	-1.033923217	0.002508448
Intestine posterior	sid-3	-0.773171061	0.00252127
Intestine posterior	rpl-34	0.206279249	0.002592476
Intestine posterior	R09E12.9	1.549672868	0.002674902

Intestine posterior	F09F7.5	-0.830653471	0.002691956
Intestine posterior	Y18D10A.22	-1.181639011	0.002696356
Intestine posterior	C15H9.9	0.521705606	0.002698024
Intestine posterior	K08D12.3	0.519837316	0.002785909
Intestine posterior	Y69A2AR.18	0.354315642	0.002800264
Intestine posterior	hsp-12.2	0.89859569	0.002859195
Intestine posterior	K08C7.1	-1.04794081	0.002884357
Intestine posterior	C12D8.1	-0.711911655	0.00289105
Intestine posterior	lec-9	-0.322554678	0.002972799
Intestine posterior	ttr-45	-0.759768166	0.002973361
Intestine posterior	egl-30	-0.667351373	0.002976062
Intestine posterior	B0491.6	-0.874023645	0.002978272
Intestine posterior	acl-5	-1.11188172	0.002991947
Intestine posterior	C18B12.6	-1.125979629	0.003015962
Intestine posterior	K09F6.4	-0.486404805	0.003104277
Intestine posterior	gap-2	-1.366039106	0.003112572
Intestine posterior	ell-1	-0.422012724	0.003197135
Intestine posterior	Y22D7AR.2	-1.810610792	0.003235174
Intestine posterior	lpd-9	0.584131722	0.003256293
Intestine posterior	cisd-3.2	0.54721954	0.003302885
Intestine posterior	plc-2	-0.924284501	0.00331515
Intestine posterior	C08B6.3	-3.076304858	0.003341537
Intestine posterior	nspa-8	-1.987953253	0.0034668
Intestine posterior	T21G5.2	-1.368580102	0.00350301
Intestine posterior	nhr-109	-0.77130406	0.003627164
Intestine posterior	F19C6.4	-3.738746051	0.003672782
Intestine posterior	H20E11.1	-1.053061778	0.003675887

Intestine posterior	B0261.6	-2.095299073	0.003684901
Intestine posterior	F07A5.2	-1.905694754	0.003684901
Intestine posterior	F32A5.4	2.238344139	0.003694551
Intestine posterior	ZK596.1	0.952649814	0.00369896
Intestine posterior	sav-1	-1.352859254	0.003843925
Intestine posterior	col-179	0.820971139	0.003862484
Intestine posterior	F35D11.3	-1.460252501	0.003944379
Intestine posterior	let-70	0.492545518	0.0039585
Intestine posterior	C17H12.4	-0.89290501	0.00409231
Intestine posterior	W09G12.9	-1.32040433	0.00416918
Intestine posterior	C39E9.8	0.98426123	0.004186849
Intestine posterior	cytb-5.2	0.433016972	0.004232143
Intestine posterior	sdc-2	-0.53155315	0.004315514
Intestine posterior	nlp-24	0.751609941	0.004416398
Intestine posterior	haf-4	-0.699504005	0.00457638
Intestine posterior	skr-4	-1.394821862	0.004617069
Intestine posterior	fipr-11	2.104771356	0.004707744
Intestine posterior	ZK1240.3	-0.548395355	0.004804728
Intestine posterior	Y56A3A.19	0.578917201	0.004811566
Intestine posterior	nhr-183	-1.174370511	0.004826516
Intestine posterior	F01D5.1	-1.309947503	0.004846623
Intestine posterior	C44E4.4	0.655427471	0.005001928
Intestine posterior	W09B6.5	-1.686017091	0.005041342
Intestine posterior	K04C1.2	-1.988532631	0.005100971
Intestine posterior	chil-23	-1.497066588	0.005259416
Intestine posterior	mbl-1	-1.426114732	0.005267252
Intestine posterior	cnnm-3	-1.22823882	0.005320188
Intestine posterior	sma-1	-0.435051607	0.005384472
Intestine posterior	C05D2.8	-0.521988765	0.005437166
Intestine posterior	C16B8.3	-0.446960138	0.0055468

Intestine posterior	C29F7.1	-0.932573478	0.005588347
Intestine posterior	W01C8.5	-1.094327402	0.0056299
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Intestine posterior	D1053.3	-1.618940853	0.005743009
Intestine posterior	Y105C5A.24	-0.788722955	0.005775826
Intestine posterior	F34D10.8	-1.992562606	0.005844009
Intestine posterior	pqe-1	-0.505796505	0.005917615
Intestine posterior	ugt-43	-1.689868547	0.005960245
Intestine posterior	F44E2.3	-0.486940557	0.006060743
Intestine posterior	ostb-1	0.711748458	0.006229507
Intestine posterior	inst-1	-0.639992562	0.006403614
Intestine posterior	wdr-23	-0.505049367	0.006432936
Intestine posterior	F08B4.8	-3.504018656	0.006584954
Intestine posterior	Y53C12B.2	-0.42092602	0.006605273
Intestine posterior	aqp-7	0.553306141	0.006722296
Intestine posterior	W04B5.2	-1.587411284	0.006876638
Intestine posterior	T24B8.7	-0.60957218	0.00691147
Intestine posterior	nuo-4	0.579186856	0.007041364
Intestine posterior	R11E3.1	-2.152514401	0.007095107
Intestine posterior	F58G6.9	-0.701288309	0.007378649
Intestine posterior	F52H2.5	-0.679223771	0.007403895
Intestine posterior	F35A5.2	0.205944187	0.007548877
Intestine posterior	bre-1	-1.59126133	0.007570106
Intestine posterior	asp-1	0.258410883	0.007613747
Intestine posterior	clec-1	0.646388559	0.007658234
Intestine posterior	ugt-30	-1.082084703	0.007867377
Intestine posterior	K03H6.2	-1.457442393	0.008001244
Intestine posterior	Y102A11A.5	2.402013268	0.00804731

Intestine posterior	Y53C10A.5	-0.895013992	0.008155776
Intestine posterior	tct-1	0.258891821	0.008200688
Intestine posterior	F28F5.6	-1.018622873	0.008479308
Intestine posterior	nlp-25	1.740896335	0.008740228
Intestine posterior	hsp-16.2	0.467386387	0.008805877
Intestine posterior	dlc-1	0.414143587	0.009004671
Intestine posterior	nuo-3	0.345882069	0.009238706
Intestine posterior	mel-11	-0.738977476	0.009335893
Intestine posterior	elt-4	-0.938435892	0.009592352
Intestine posterior	nhr-35	-0.716087538	0.00964725
Intestine posterior	har-1	0.467922398	0.009652128
Intestine posterior	mtm-5	-0.815281879	0.009676464
Intestine posterior	C05C12.4	-0.50716254	0.009959207
Intestine posterior	F55H12.4	0.685920175	0.010166321
Intestine posterior	mrp-1	-0.562379561	0.010621729
Intestine posterior	ssq-4	-1.47272079	0.010901518
Intestine posterior	msp-51	-2.315973283	0.010933993
Intestine posterior	aakg-1	-0.616093619	0.0110651
Intestine posterior	T23G11.1	-2.249791028	0.011178897
Intestine posterior	R10E8.6	-1.135395839	0.011446163
Intestine posterior	lbp-7	-0.779492722	0.011564003
Intestine posterior	F53B2.8	-0.695980889	0.011935726
Intestine posterior	atp-6	0.181017642	0.011963652
Intestine posterior	egl-9	-0.997349524	0.012137456
Intestine posterior	marg-1	1.788925885	0.012210922
Intestine posterior	cln-3.1	-1.241271117	0.012398177
Intestine posterior	K07C5.2	0.59661318	0.012485601
Intestine posterior	R07B7.9	-1.563560794	0.012970523
Intestine posterior	rpl-11.2	0.211236424	0.013129236

Intestine posterior	fbxa-89	-1.032833329	0.013164157
Intestine posterior	C01B10.10	-0.942493141	0.013272406
Intestine posterior	mab-31	-0.914330644	0.013406154
Intestine posterior	C07H6.4	-0.879723169	0.013413675
Intestine posterior	act-3	0.498871968	0.013593797
Intestine posterior	F58G6.3	-0.783101754	0.014224852
Intestine posterior	sma-6	-0.927860449	0.014770868
Intestine posterior	pfkb-1.1	-0.802410155	0.015235706
Intestine posterior	asp-6	-0.308725781	0.015253673
Intestine posterior	ttr-18	0.838848709	0.015253673
Intestine posterior	tat-1	-0.693310352	0.015725273
Intestine posterior	Y44A6D.3	-1.07424706	0.015739839
Intestine posterior	cyc-2.2	-2.100159692	0.016148567
Intestine posterior	C40H1.8	-1.776872579	0.016184109
Intestine posterior	Y39H10B.2	-1.24040609	0.016363264
Intestine posterior	F31D4.8	-0.850653007	0.01664645
Intestine posterior	cpl-1	-0.281818019	0.016846453
Intestine posterior	nhr-4	-1.308180549	0.016950035
Intestine posterior	ajm-1	-0.44559411	0.016985409
Intestine posterior	T10B5.7	-0.82720238	0.017091248
Intestine posterior	ugt-24	-0.854318964	0.017739346
Intestine posterior	C48E7.1	0.85990385	0.017747272
Intestine posterior	gpa-17	-0.591015975	0.017836143
Intestine posterior	T01D3.6	-1.179989316	0.017960403
Intestine posterior	nspb-8	1.734547254	0.01804829
Intestine posterior	lec-11	-1.024917898	0.018074424
Intestine posterior	T10B11.5	-1.736069171	0.018769408

Intestine posterior	cyn-5	0.443672651	0.019196271
Intestine posterior	T05C3.6	-0.791135917	0.019874152
Intestine posterior	cdk-5	-0.743945047	0.020130935
Intestine posterior	D1007.15	-0.934792978	0.020220502
Intestine posterior	C45G9.6	1.998800656	0.020769319
Intestine posterior	C40H1.2	-1.245852384	0.021024915
Intestine posterior	C44H9.5	-1.066161741	0.021102235
Intestine posterior	sqst-5	-1.474522575	0.021147794
Intestine posterior	B0001.3	-1.00350268	0.022040212
Intestine posterior	mtch-1	-0.38712773	0.022276799
Intestine posterior	K06A9.1	-0.709916539	0.022507533
Intestine posterior	Y79H2A.3	-0.606217448	0.022518164
Intestine posterior	rbc-1	-0.640077079	0.0227322
Intestine posterior	ssp-34	-1.862281123	0.023451226
Intestine posterior	Y34B4A.2	-1.057252823	0.023466438
Intestine posterior	fipr-4	2.023553217	0.023543928
Intestine posterior	C45B2.6	-0.887560639	0.023640394
Intestine posterior	F54C8.4	-0.519987797	0.023790286
Intestine posterior	snr-1	0.571991734	0.023948632
Intestine posterior	tag-290	0.403520696	0.02401593
Intestine posterior	pdha-1	0.590150207	0.024479254
Intestine posterior	aat-6	-1.978381368	0.024525014
Intestine posterior	M05D6.5	0.670382568	0.024668478
Intestine posterior	pfd-6	0.550359048	0.024945477
Intestine posterior	ZC395.10	0.468278777	0.025606106
Intestine posterior	ugt-62	-0.640742524	0.026083285
Intestine posterior	rpm-1	-0.973125587	0.026608179
Intestine posterior	F47H4.2	-0.7641788	0.026759294
Intestine posterior	Y38H6C.21	1.140884906	0.026988705

Intestine posterior	C12D12.1	-0.802229878	0.027168746
Intestine posterior	epg-5	-1.003197308	0.027749243
Intestine posterior	fbxa-59	-0.573546311	0.027965923
Intestine posterior	lipl-4	1.92201918	0.028076527
Intestine posterior	vps-36	-0.651493216	0.028773702
Intestine posterior	F32D1.5	0.432299063	0.028930364
Intestine posterior	F07A11.5	-1.009008604	0.028959319
Intestine posterior	fbxa-61	-0.995263095	0.029577354
Intestine posterior	F44G4.2	0.502280104	0.030910788
Intestine posterior	kin-18	-0.633791435	0.031703181
Intestine posterior	Y18H1A.11	-2.385232688	0.032174463
Intestine posterior	F41C3.7	-1.438684158	0.0323797
Intestine posterior	F08D12.2	1.898095307	0.032859003
Intestine posterior	F21F8.5	-3.29497726	0.0333605
Intestine posterior	B0244.7	-1.32951689	0.034640333
Intestine posterior	ZK1290.13	-0.920574423	0.035220952
Intestine posterior	tnt-4	1.212609382	0.035544649
Intestine posterior	nas-39	-2.073292124	0.035564383
Intestine posterior	cup-5	-0.649945925	0.0356107
Intestine posterior	snr-6	0.554968751	0.035699022
Intestine posterior	bas-1	-1.190322396	0.035786423
Intestine posterior	C48D1.1	-1.794497317	0.035918321
Intestine posterior	nhr-110	-0.711732029	0.03835098
Intestine posterior	ufm-1	0.607112389	0.039167861
Intestine posterior	mlc-2	0.426280516	0.040737071
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Intestine posterior	F22F4.9	1.318764523	0.041617801
Intestine posterior	enol-1	0.428289126	0.041746649
Intestine posterior	F14H12.3	1.848989042	0.043930515

Intestine posterior	puf-9	-0.575441552	0.044134173
Intestine posterior	C49A9.5	-1.384871456	0.044718413
Intestine posterior	gbh-2	-0.558835076	0.044983128
Intestine posterior	F19C7.1	0.433468031	0.045430723
Intestine posterior	cpg-1	0.855171429	0.045509046
Intestine posterior	C36E6.1	-1.318788836	0.045671528
Intestine posterior	rnp-4	0.572901432	0.045901686
Intestine posterior	mau-2	-0.759416232	0.046314066
Intestine posterior	nduo-6	0.167812312	0.047118629
Intestine posterior	hip-1	0.891493584	0.047278112
Intestine posterior	ZK228.3	-1.050891769	0.04803979
Intestine posterior	K03E5.2	0.802796533	0.048109335
Intestine posterior	B0244.10	-0.667076298	0.048292515
Intestine posterior	Y22D7AR.7	-1.530635538	0.048822451
Intestine posterior	lbp-1	1.618141445	0.049177083
Intestine posterior	let-607	-0.513936517	0.050224104
Intestine posterior	ZK1127.6	-0.436725209	0.050678658
Intestine posterior	C34B2.8	0.40828114	0.050939234
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Intestine posterior	math-39	-0.824262643	0.051805517
Intestine posterior	T16G12.1	-0.460065247	0.051961072
Intestine posterior	rde-1	-0.598484475	0.052464801
Intestine posterior	rps-16	0.208392701	0.053586012
Intestine posterior	Y110A7A.21	-0.876963427	0.053738007
Intestine posterior	sphk-1	-0.81881417	0.053932584
Intestine posterior	ulp-4	-0.727923888	0.054177615
Intestine posterior	blmp-1	-0.984049143	0.054392451
Intestine posterior	try-10	-1.955268626	0.05502157

Intestine posterior	C52E2.4	-1.706838823	0.056214319
Intestine posterior	aat-4	-0.745141338	0.056946746
Intestine posterior	ugt-50	-0.613935038	0.057702437
Intestine posterior	T07E3.4	-0.697563868	0.057790216
Intestine posterior	epc-1	-0.326253142	0.058420259
Intestine posterior	C33A12.1	0.493329785	0.060150959
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Intestine posterior	C03B1.7	-0.699904634	0.061760186
Intestine posterior	C14H10.3	-1.353950898	0.062037419
Intestine posterior	fbxa-209	-0.779301372	0.062232265
Intestine posterior	atgp-2	-1.056705	0.063477133
Intestine posterior	fbxa-5	-1.302846776	0.063568391
Intestine posterior	let-383	-1.048642959	0.063893778
Intestine posterior	dapk-1	-0.608875984	0.065124393
Intestine posterior	F57B10.5	0.823067032	0.065882844
Intestine posterior	nhr-32	-1.082868315	0.06674977
Intestine posterior	F22F7.7	-1.83560617	0.068263793
Intestine posterior	daf-16	-0.411140017	0.069418113
Intestine posterior	F44E5.4	1.015670509	0.06945192
Intestine posterior	mpst-3	-0.922863069	0.070206605
Intestine posterior	nfi-1	-0.707229687	0.070295486
Intestine posterior	clec-10	-0.918348809	0.071142665
Intestine posterior	trpp-8	-0.611381637	0.073186489
Intestine posterior	nhr-193	-0.575475233	0.073984352
Intestine posterior	clec-150	-0.608492406	0.074482939
Intestine posterior	T28D9.1	0.53037921	0.074501816

Intestine posterior	nra-1	-0.895474993	0.076769323
Intestine posterior	K12H4.7	-0.40993839	0.07763884
Intestine posterior	mdl-1	-0.707602235	0.077643493
Intestine posterior	pkn-1	-0.759578918	0.07907042
Intestine posterior	C44C10.9	1.502916853	0.07910347
Intestine posterior	ears-2	-0.802475591	0.08120624
Intestine posterior	C14B4.2	-0.727535368	0.081368632
Intestine posterior	galt-1	-3.099667697	0.081616136
Intestine posterior	aco-2	0.612683272	0.085503389
Intestine posterior	nhr-17	0.592211251	0.086870374
Intestine posterior	mrpl-35	0.406128164	0.090324364
Intestine posterior	Y54G2A.50	-0.802649882	0.090905333
Intestine posterior	Y106G6H.13	-1.603229344	0.091100003
Intestine posterior	F58F9.4	-0.64979377	0.091415311
Intestine posterior	F22E5.8	-0.905298731	0.092227899
Intestine posterior	sur-7	-0.725780594	0.092640052
Intestine posterior	zipt-2.1	-0.727464045	0.093868494
Intestine posterior	tomm-20	0.684607994	0.095094829
Intestine posterior	C13A10.1	-0.974956237	0.09547865
Intestine posterior	sma-4	-0.576602431	0.096328755
Intestine posterior	agxt-1	-1.259915866	0.097576491
Intestine posterior	F25B3.5	-1.169354601	0.098046806
Intestine posterior	B0457.6	-1.024336036	0.098545424
Intestine posterior	T23B5.3	-0.96529968	0.099827077
Intestine-Gonadal sheath doublets	col-122	1.006789544	5.14072E-28
Intestine-Gonadal sheath doublets	T03F1.11	1.810716386	1.80671E-24
Intestine-Gonadal sheath doublets	tnc-2	1.905201318	2.89375E-23
Intestine-Gonadal sheath doublets	clec-47	2.268536268	1.31092E-21
Intestine-Gonadal sheath doublets	C17F4.7	0.593702396	2.27369E-20
Intestine-Gonadal sheath doublets	lys-4	1.05800355	1.73752E-16

Intestine-Gonadal sheath doublets	cth-1	0.736298528	6.8667E-16
Intestine-Gonadal sheath doublets	col-119	0.757449484	2.25736E-15
Intestine-Gonadal sheath doublets	col-20	0.568455368	1.20711E-13
Intestine-Gonadal sheath doublets	Y73F4A.2	3.133426429	3.31988E-12
Intestine-Gonadal sheath doublets	col-184	0.851056455	4.49007E-12
Intestine-Gonadal sheath doublets	col-124	0.458211629	5.3248E-12
Intestine-Gonadal sheath doublets	F21C10.9	1.757324825	5.61224E-12
Intestine-Gonadal sheath doublets	C54D10.3	1.328634845	3.75723E-11
Intestine-Gonadal sheath doublets	fipr-2	2.369928733	1.01754E-10
Intestine-Gonadal sheath doublets	fipr-1	2.11705449	2.73886E-10
Intestine-Gonadal sheath doublets	C14C6.5	-1.980559244	3.48046E-10
Intestine-Gonadal sheath doublets	cpr-5	1.281933117	4.23033E-10
Intestine-Gonadal sheath doublets	gst-10	-1.131214321	4.58051E-10
Intestine-Gonadal sheath doublets	hsp-16.41	2.064875988	4.99239E-10
Intestine-Gonadal sheath doublets	ZK593.3	1.578151373	5.24518E-10
Intestine-Gonadal sheath doublets	rpl-12	-0.185442529	1.51021E-09
Intestine-Gonadal sheath doublets	asp-13	1.156912903	1.68631E-09
Intestine-Gonadal sheath doublets	asp-2	0.825727025	1.71443E-09
Intestine-Gonadal sheath doublets	rpl-41.2	-0.286525017	2.28853E-09
Intestine-Gonadal sheath doublets	col-181	0.702741646	2.60241E-09
Intestine-Gonadal sheath doublets	C53C9.2	2.106604603	3.0073E-09
Intestine-Gonadal sheath doublets	nduo-6	-0.197886649	3.1355E-09
Intestine-Gonadal sheath doublets	col-140	0.462879484	3.25198E-09
Intestine-Gonadal sheath doublets	ctc-3	0.266516727	4.81141E-09
Intestine-Gonadal sheath doublets	ZC116.1	2.341516271	5.77458E-09
Intestine-Gonadal sheath doublets	C06A8.3	0.860249229	7.14781E-09
Intestine-Gonadal sheath doublets	W01D2.1	-0.380882733	2.99724E-08
Intestine-Gonadal sheath doublets	pmt-2	0.504094437	5.23215E-08
Intestine-Gonadal sheath doublets	col-8	1.070684996	6.92301E-08
Intestine-Gonadal sheath doublets	pqn-60	2.747929016	1.93158E-07
Intestine-Gonadal sheath doublets	hsp-16.2	1.4989869	4.658E-07
Intestine-Gonadal sheath doublets	ndfl-4	-0.284327526	7.82983E-07
Intestine-Gonadal sheath doublets	hsp-70	1.882990977	8.98088E-07
Intestine-Gonadal sheath doublets	rps-25	-0.18603269	1.39747E-06
Intestine-Gonadal sheath doublets	Y87G2A.19	2.172286001	1.52668E-06
Intestine-Gonadal sheath doublets	C45G9.6	2.327101993	1.53526E-06

Intestine-Gonadal sheath doublets	rpl-38	-0.332325071	1.56533E-06
Intestine-Gonadal sheath doublets	cpr-4	1.439061852	2.05262E-06
Intestine-Gonadal sheath doublets	acdh-1	0.470889476	2.79157E-06
Intestine-Gonadal sheath doublets	pud-4	-2.22687575	4.59839E-06
Intestine-Gonadal sheath doublets	R09B3.3	-0.300664745	5.79648E-06
Intestine-Gonadal sheath doublets	rpl-36	-0.264839771	8.81756E-06
Intestine-Gonadal sheath doublets	pud-3	-2.003100017	9.57349E-06
Intestine-Gonadal sheath doublets	T13F3.6	1.206498877	1.11062E-05
Intestine-Gonadal sheath doublets	far-3	2.750495366	1.55057E-05
Intestine-Gonadal sheath doublets	msra-1	1.552618126	1.94173E-05
Intestine-Gonadal sheath doublets	asp-4	0.921244706	3.75773E-05
Intestine-Gonadal sheath doublets	rpl-36.A	-0.246828426	4.2307E-05
Intestine-Gonadal sheath doublets	ttr-21	2.45968655	4.70428E-05
Intestine-Gonadal sheath doublets	cpn-4	1.212289664	7.47616E-05
Intestine-Gonadal sheath doublets	C30G12.2	1.276917944	8.75271E-05
Intestine-Gonadal sheath doublets	col-98	0.731171316	0.000115132
Intestine-Gonadal sheath doublets	cpz-1	0.717917931	0.000135438
Intestine-Gonadal sheath doublets	col-80	0.558192625	0.000151592
Intestine-Gonadal sheath doublets	hsp-12.2	0.662819204	0.000172314
Intestine-Gonadal sheath doublets	fipr-5	2.790784535	0.000275543
Intestine-Gonadal sheath doublets	rps-29	-0.35846902	0.000412993
Intestine-Gonadal sheath doublets	rps-27	-0.23709098	0.000447955
Intestine-Gonadal sheath doublets	fip-2	0.975543124	0.00050359
Intestine-Gonadal sheath doublets	C05D11.5	1.1879017	0.000513283
Intestine-Gonadal sheath doublets	cpl-1	0.887092963	0.000629408
Intestine-Gonadal sheath doublets	sodh-1	1.050319369	0.000658384
Intestine-Gonadal sheath doublets	F11E6.3	0.848804128	0.000770826
Intestine-Gonadal sheath doublets	F35B12.3	3.649874425	0.00097628
Intestine-Gonadal sheath doublets	T20D3.2	0.598372123	0.000998232
Intestine-Gonadal sheath doublets	rpl-30	-0.262258915	0.001054747
Intestine-Gonadal sheath doublets	alh-1	0.721788994	0.001307337
Intestine-Gonadal sheath doublets	ttr-15	0.841847245	0.002203198
Intestine-Gonadal sheath doublets	cht-3	-0.430212544	0.002833513
Intestine-Gonadal sheath doublets	rps-28	-0.39232531	0.003544909
Intestine-Gonadal sheath doublets	ctc-1	0.212647244	0.003640639
Intestine-Gonadal sheath doublets	dct-16	-0.215938606	0.003792651

Intestine-Gonadal sheath doublets	ttr-26	1.972790079	0.004136895
Intestine-Gonadal sheath doublets	Y34B4A.6	0.563017389	0.00492451
Intestine-Gonadal sheath doublets	fipr-7	3.176557995	0.005456175
Intestine-Gonadal sheath doublets	argk-1	0.737582333	0.006015696
Intestine-Gonadal sheath doublets	col-106	0.646954996	0.006385558
Intestine-Gonadal sheath doublets	F55H12.4	0.94085058	0.006532852
Intestine-Gonadal sheath doublets	col-160	0.778758248	0.006610268
Intestine-Gonadal sheath doublets	rpl-31	-0.218472084	0.007086655
Intestine-Gonadal sheath doublets	col-103	0.884744345	0.007360224
Intestine-Gonadal sheath doublets	F41E6.15	1.168656857	0.007797706
Intestine-Gonadal sheath doublets	fat-7	1.979024996	0.013153453
Intestine-Gonadal sheath doublets	rps-26	-0.180882491	0.019799153
Intestine-Gonadal sheath doublets	col-42	0.847160925	0.021564018
Intestine-Gonadal sheath doublets	col-143	0.641508994	0.022263973
Intestine-Gonadal sheath doublets	gln-3	0.57509347	0.023453434
Intestine-Gonadal sheath doublets	tnt-4	2.122719515	0.024464379
Intestine-Gonadal sheath doublets	rpl-32	-0.163695011	0.030512266
Intestine-Gonadal sheath doublets	smd-1	0.817607493	0.03267021
Intestine-Gonadal sheath doublets	col-178	0.668740514	0.033174122
Intestine-Gonadal sheath doublets	vamp-8	2.017813843	0.035925879
Intestine-Gonadal sheath doublets	col-101	0.717558846	0.03800715
Intestine-Gonadal sheath doublets	sams-1	0.695812203	0.039311744
Intestine-Gonadal sheath doublets	col-139	0.31629508	0.040751296
Intestine-Gonadal sheath doublets	spp-18	-0.993833406	0.041688298
Intestine-Gonadal sheath doublets	lbp-6	0.224319192	0.046824999
Intestine-Gonadal sheath doublets	F15A4.6	0.899654586	0.066073436
Intestine-Gonadal sheath doublets	pgp-2	0.864042431	0.066735025
Intestine-Gonadal sheath doublets	F08D12.2	3.21522657	0.068043465
Intestine-Gonadal sheath doublets	T04G9.7	-0.24363138	0.070494408
Intestine-Gonadal sheath doublets	Y119D3B.21	-0.275580253	0.072696117
M1	eri-5	33.72462171	1.0051E-172
M1	Y54G2A.11	33.72462171	1.0051E-172
M1	B0546.3	33.72462171	1.0051E-172
M1	tsg-101	33.72462171	1.0051E-172
M1	F13E9.15	33.72462171	1.0051E-172
M1	JC8.2	33.72462171	1.0051E-172
M1	paf-2	33.72462171	1.0051E-172
M1	scav-1	33.72462171	1.0051E-172
M1	C23H4.7	33.72462171	1.0051E-172

M1	snx-17	33.72462171	1.0051E-172
M1	C27C12.1	33.72462171	1.0051E-172
M1	F09B12.3	33.72462171	1.0051E-172
M1	Y87G2A.25	33.72462171	1.0051E-172
M1	C14C6.2	33.72462171	1.0051E-172
M1	R02F11.11	33.72462171	1.0051E-172
M1	hda-11	33.72462171	1.0051E-172
M1	dhs-24	33.72462171	1.0051E-172
M1	Y25C1A.8	33.72462171	1.0051E-172
M1	nlp-57	-1.09890653	0.051236972
M2_M3_M4	kbp-5	-2.276840205	0.000302485
M2_M3_M4	T03F1.11	1.58718315	0.002614443
M2_M3_M4	ser-7	-0.764882746	0.007763095
M2_M3_M4	col-20	0.816383562	0.013375536
M2_M3_M4	col-122	1.459764185	0.018839908
M2_M3_M4	col-124	0.743597875	0.042835839
M5	grl-4	-2.544320516	0.02542943
Mature sperm	sams-5	0.775282573	2.3691E-132
Mature sperm	msrp-6	-0.290749093	3.2148E-113
Mature sperm	F26B1.8	0.194963187	1.76107E-74
Mature sperm	dct-16	-0.531564937	4.67285E-71
Mature sperm	rpl-41.2	-0.008286423	1.2951E-68
Mature sperm	nduo-6	-0.233102603	3.44545E-64
Mature sperm	Y59E9AL.6	-0.174413586	1.81752E-62
Mature sperm	ctc-3	0.28585825	3.18596E-62
Mature sperm	T08B2.12	-0.285927427	4.65477E-62
Mature sperm	C32E8.4	-0.260774816	5.34104E-60
Mature sperm	col-122	1.083015084	3.73482E-57
Mature sperm	C33F10.11	0.231949147	2.1135E-53
Mature sperm	F58A6.9	-0.252314931	8.27922E-51
Mature sperm	msd-2	0.222099624	2.79954E-50
Mature sperm	col-124	0.415897168	5.59094E-47
Mature sperm	F34D10.8	-0.288034868	2.25036E-46

Mature sperm	nspd-1	-0.162273511	7.04037E-44
Mature sperm	C17F3.1	-0.249245308	1.28932E-43
Mature sperm	nspd-10	-0.22785187	3.68756E-42
Mature sperm	Y106G6A.4	0.224519984	2.51356E-41
Mature sperm	msp-77	0.288118701	2.9135E-32
Mature sperm	rps-25	-3.57512E-05	4.40878E-28
Mature sperm	col-140	0.315877567	1.0341E-26
Mature sperm	nlp-4	0.209506209	2.38107E-26
Mature sperm	F56D6.13	-0.181510393	4.10486E-26
Mature sperm	ZK512.10	-0.204614717	9.61204E-26
Mature sperm	mlc-3	0.108685583	1.00063E-24
Mature sperm	Y43F8C.9	-0.155716484	1.6737E-24
Mature sperm	col-20	0.305729509	3.77711E-24
Mature sperm	ssp-9	-0.366886863	5.22678E-24
Mature sperm	ssp-34	0.215066469	2.57708E-23
Mature sperm	nduo-3	-0.118855615	7.34943E-23
Mature sperm	C41G7.6	-0.150968402	9.82106E-22
Mature sperm	msp-64	0.185293255	1.928E-21
Mature sperm	F23A7.8	-0.455972402	2.50605E-21
Mature sperm	spch-3	0.104601109	5.83774E-21
Mature sperm	col-119	0.488315083	9.66766E-21
Mature sperm	ssp-11	-0.32017294	1.56909E-20
Mature sperm	C33F10.1	0.103696254	6.38715E-20
Mature sperm	C05D11.5	0.471990794	4.00103E-19
Mature sperm	C48E7.7	-0.197737811	7.54823E-19
Mature sperm	col-181	0.197071538	4.84834E-18
Mature sperm	spch-1	0.138377949	5.89608E-18
Mature sperm	nspd-2	-0.130350372	1.36965E-17
Mature sperm	ndk-1	0.242196705	1.51746E-17
Mature sperm	Y119D3B.21	-0.042952283	2.01445E-17
Mature sperm	sams-1	0	7.21114E-17
Mature sperm	col-81	0.010887696	2.97114E-16

Mature sperm	msd-4	0.116289618	6.73951E-16
Mature sperm	msp-53	0.196234136	1.29526E-15
Mature sperm	msp-81	0.165758027	1.45817E-15
Mature sperm	ndfl-4	-0.222555691	1.61029E-15
Mature sperm	cpn-3	0.077550256	2.33113E-15
Mature sperm	F08H9.2	0.135622354	4.97976E-15
Mature sperm	msrp-1	-0.096738722	5.46486E-15
Mature sperm	pat-10	0.167853882	1.05322E-14
Mature sperm	C17F4.7	0.460624824	2.10872E-14
Mature sperm	Y54G2A.15	0.135767818	3.50477E-14
Mature sperm	D1081.12	0.13631511	3.50571E-14
Mature sperm	msp-59	0.169411019	1.50799E-13
Mature sperm	C43G2.3	0.147648965	2.48667E-12
Mature sperm	msp-19	0.176487776	5.98874E-12
Mature sperm	ctc-1	0.16950995	1.57145E-11
Mature sperm	nspd-7	-0.127439956	4.21195E-11
Mature sperm	rmd-3	0.133051385	4.6017E-11
Mature sperm	Y69E1A.2	0.090956195	6.36016E-11
Mature sperm	ZK512.8	0.155134911	1.33091E-10
Mature sperm	F37C12.18	0.223743201	1.82459E-10
Mature sperm	act-2	-0.354542114	2.11035E-10
Mature sperm	R10E9.2	0.104178213	3.56739E-10
Mature sperm	col-184	0.335095894	5.17548E-10
Mature sperm	ZK1307.4	0.115871919	5.88168E-10
Mature sperm	Y59E9AR.7	-0.556697535	7.05367E-10
Mature sperm	col-139	0.027167736	7.24702E-10
Mature sperm	clik-1	0.010492551	1.26191E-09
Mature sperm	col-19	0.13846318	1.36082E-09
Mature sperm	nspa-8	-0.182248004	1.43885E-09
Mature sperm	let-754	0.178859048	2.27072E-09
Mature sperm	ZK354.3	-0.174022709	2.75547E-09
Mature sperm	gst-4	1.14713E-06	3.0108E-09
Mature sperm	msrp-2	-0.072221049	3.76149E-09
Mature sperm	rpl-10	-0.1526087	3.7933E-09
Mature sperm	Y57G11C.52	-0.263673156	5.85886E-09

Mature sperm	C34D4.3	0.078156414	6.95861E-09
Mature sperm	R09B3.3	-0.111169606	8.99918E-09
Mature sperm	Y75B8A.23	-0.195337145	2.14293E-08
Mature sperm	dhs-21	0	4.22053E-08
Mature sperm	nduo-4	-0.133067424	5.26374E-08
Mature sperm	ZK84.2	0.144331309	9.50113E-08
Mature sperm	E03H12.5	-0.07481103	1.15509E-07
Mature sperm	msp-76	0.091417626	1.26121E-07
Mature sperm	rmd-6	0.231422389	2.3745E-07
Mature sperm	spch-2	0.12892526	2.62697E-07
Mature sperm	msp-51	-0.113320484	2.81593E-07
Mature sperm	gpx-1	0.278410745	3.94245E-07
Mature sperm	Y43C5B.3	0.158089908	4.01245E-07
Mature sperm	rpl-39	-0.127725418	4.17498E-07
Mature sperm	F23A7.4	-0.301979065	4.91149E-07
Mature sperm	Y111B2A.2	-0.219645638	5.69495E-07
Mature sperm	Y59E9AL.2	-0.130782561	6.159E-07
Mature sperm	C02F5.5	0.086394021	6.4828E-07
Mature sperm	cyc-2.2	0.108293729	9.79832E-07
Mature sperm	rps-14	-0.000673442	1.05624E-06
Mature sperm	C05C12.5	0.125700175	1.07875E-06
Mature sperm	ins-37	-0.292873285	1.11368E-06
Mature sperm	ubc-7	0.235828906	1.41468E-06
Mature sperm	msp-36	0.078494854	1.44383E-06
Mature sperm	col-80	0.028829692	2.18083E-06
Mature sperm	pud-4	-0.370720852	2.23698E-06
Mature sperm	F27C1.1	0.090556865	2.41395E-06
Mature sperm	F07A5.2	0.09771153	2.59711E-06
Mature sperm	F36D1.4	-0.279880733	4.38702E-06
Mature sperm	ssq-4	0.100019094	5.53749E-06
Mature sperm	C15C6.2	-0.110822778	5.9032E-06
Mature sperm	C04F12.7	0.070738594	6.18736E-06

Mature sperm	ZK849.6	-0.222653481	6.68464E-06
Mature sperm	col-93	0.002378232	6.86312E-06
Mature sperm	cth-2	0.144124036	7.07154E-06
Mature sperm	F53B6.4	0.08730391	1.19908E-05
Mature sperm	msp-113	-0.320249308	1.24365E-05
Mature sperm	F17E9.5	-0.05014015	1.97815E-05
Mature sperm	C28C12.11	0.10837115	2.18164E-05
Mature sperm	M05B5.7	-0.22688534	2.51268E-05
Mature sperm	T27C10.8	0.295400904	3.47375E-05
Mature sperm	F52H3.6	-0.103557246	3.52543E-05
Mature sperm	W09C5.8	0.157273616	4.14194E-05
Mature sperm	F46H5.3	4.07523E-05	6.84468E-05
Mature sperm	crt-1	-0.420989387	7.50063E-05
Mature sperm	col-129	0.006999358	7.7564E-05
Mature sperm	ZC477.7	0.138531257	8.66514E-05
Mature sperm	K04H4.5	0.118380215	0.000124443
Mature sperm	hphd-1	-0.415980241	0.000127297
Mature sperm	rps-15	-0.040528136	0.000130186
Mature sperm	F56D6.19	-0.198470037	0.000132968
Mature sperm	C54D10.3	6.02193E-05	0.000133214
Mature sperm	C17F3.3	-0.146770152	0.000152194
Mature sperm	Y105C5B.18	0.104503906	0.000152492
Mature sperm	C39H7.1	0.084254805	0.000161416
Mature sperm	rps-26	-0.006725173	0.00017031
Mature sperm	B0025.5	-0.091209696	0.000189771
Mature sperm	cco-1	0.130478688	0.000195706
Mature sperm	F42A9.7	0.132632164	0.000198784
Mature sperm	H36L18.2	1.05116E-05	0.000242679
Mature sperm	C35E7.9	-0.168400868	0.000256885
Mature sperm	ZK550.5	0.125698906	0.000258083
Mature sperm	acdh-1	0.004107274	0.000291864
Mature sperm	B0273.1	0.14572055	0.00030432
Mature sperm	R08A2.1	-0.156830787	0.000342156

Mature sperm	Y59E9AL.3	-0.1187457	0.000356084
Mature sperm	rps-3	-0.183177434	0.000449447
Mature sperm	cco-2	0.138461136	0.000498985
Mature sperm	Y53F4A.2	-0.169121885	0.000536317
Mature sperm	F36H12.3	-0.140733098	0.000646786
Mature sperm	spe-15	0.150535601	0.000684505
Mature sperm	lys-4	0.000427474	0.000698926
Mature sperm	F46A9.1	0.134848765	0.000775108
Mature sperm	T23B3.5	-0.057329319	0.000869467
Mature sperm	W02B12.12	0.109828731	0.000994044
Mature sperm	gba-4	-0.417650075	0.001130391
Mature sperm	ssp-19	-0.104349065	0.001143112
Mature sperm	F47B3.4	-0.287875178	0.001177564
Mature sperm	Y106G6G.4	-0.091134514	0.001186139
Mature sperm	C24A11.1	0.139216723	0.001235168
Mature sperm	F54H12.7	0.183103156	0.002408195
Mature sperm	mlc-2	0.005005899	0.003000051
Mature sperm	F44G4.5	0.226804379	0.003034573
Mature sperm	mup-2	7.28918E-06	0.003053561
Mature sperm	sodh-1	7.15509E-05	0.003789422
Mature sperm	vit-5	-0.032570867	0.003927124
Mature sperm	Y106G6H.13	0.097104811	0.003982566
Mature sperm	T16G1.13	-0.25029936	0.004078223
Mature sperm	K04C2.8	0.243741187	0.004110766
Mature sperm	msp-142	0.12169252	0.004379032
Mature sperm	msp-38	0.078385397	0.005229223
Mature sperm	rps-9	-0.092557986	0.005339786
Mature sperm	lev-11	8.26164E-06	0.00541907
Mature sperm	col-178	7.34641E-05	0.006171672
Mature sperm	eef-1B.1	-0.355820664	0.006759566
Mature sperm	C54G6.8	-0.201033976	0.007414566
Mature sperm	F58E6.5	0.129639212	0.007591292
Mature sperm	tag-174	0.157788434	0.007840437

Mature sperm	lab-1	0.158753662	0.007951258
Mature sperm	ZK262.4	-0.231618245	0.009622513
Mature sperm	cope-1	0.230696457	0.009695424
Mature sperm	irld-3	0.126701949	0.012835049
Mature sperm	C45G9.9	-0.270979889	0.013628011
Mature sperm	rpl-36.A	-0.00024595	0.015593392
Mature sperm	Y38C1AA.7	-0.03967672	0.016958947
Mature sperm	msp-57	-0.074675618	0.018773399
Mature sperm	C07G1.6	0.225902844	0.01918801
Mature sperm	ZK858.8	0.140443833	0.022346783
Mature sperm	ssp-10	0.054809139	0.022762821
Mature sperm	F42C5.5	0.191919791	0.023934681
Mature sperm	ZK354.7	0.216111691	0.025009211
Mature sperm	C17C3.15	0.21766469	0.02527614
Mature sperm	msrp-3	-0.096174184	0.027002955
Mature sperm	C17H12.12	0.099892314	0.029809336
Mature sperm	T13F3.8	-0.208890958	0.031244281
Mature sperm	Y38F2AR.10	0.25477834	0.0316179
Mature sperm	col-160	0.000773467	0.032837407
Mature sperm	Y51B9A.5	0.309540489	0.037271137
Mature sperm	ZK858.2	0.116747082	0.038045586
Mature sperm	T03F6.6	0.08244097	0.048792435
Mature sperm	ZK970.8	0.385036121	0.049824917
Mature sperm	unc-15	0	0.051912086
Mature sperm	hsp-16.2	0.000793332	0.05512723
Mature sperm	C14A6.13	0.246306994	0.056112122
Mature sperm	sma-1	-0.378323674	0.059449177
Mature sperm	col-106	0.021119108	0.064792625
Mature sperm	clec-50	-0.002649521	0.067825214
Mature sperm	hacd-1	-0.267242999	0.071191829
Mature sperm	alh-8	-0.309565222	0.092777674
Mature sperm	vit-1	-0.042194411	0.097976336
Mature sperm	ssq-3	0.119449569	0.099244133
Meiotic germ cells	rpl-41.2	-0.444634536	5.45877E-94

Meiotic germ cells	ctc-3	0.517416436	1.92196E-93
Meiotic germ cells	W01D2.1	-0.454898102	4.9789E-78
Meiotic germ cells	ctc-1	0.417030522	2.73721E-73
Meiotic germ cells	rps-25	-0.260102677	3.42686E-70
Meiotic germ cells	R09B3.3	-0.307848199	9.83727E-61
Meiotic germ cells	rpl-36	-0.297828231	1.09266E-60
Meiotic germ cells	rpl-38	-0.395366348	7.70163E-60
Meiotic germ cells	R09B3.2	-0.347560757	7.63044E-58
Meiotic germ cells	rps-28	-0.528954711	5.91663E-54
Meiotic germ cells	rpl-39	-0.445682532	1.85623E-48
Meiotic germ cells	rpl-43	-0.312620953	5.48763E-47
Meiotic germ cells	rpl-34	-0.294392912	1.17341E-42
Meiotic germ cells	col-122	0.955842452	8.37918E-42
Meiotic germ cells	rps-21	-0.396311377	1.47191E-40
Meiotic germ cells	rps-29	-0.366688611	4.71153E-39
Meiotic germ cells	eef-2	-0.20259102	3.79274E-35
Meiotic germ cells	rpl-36.A	-0.239340529	7.56434E-34
Meiotic germ cells	atp-6	0.277773485	1.47863E-33
Meiotic germ cells	C54D10.3	1.292049935	1.89841E-33
Meiotic germ cells	ctc-2	0.340168161	1.55556E-30
Meiotic germ cells	nduo-1	0.321523009	6.97612E-30
Meiotic germ cells	rpl-29	-0.516922355	2.56804E-29
Meiotic germ cells	rps-27	-0.247806955	2.78345E-29
Meiotic germ cells	col-124	0.578840218	3.56331E-29
Meiotic germ cells	col-140	0.592531346	1.44129E-26
Meiotic germ cells	rpl-21	-0.172000486	1.2622E-25
Meiotic germ cells	col-119	0.781454734	1.84114E-25
Meiotic germ cells	C37A2.7	-0.262484129	2.34782E-25
Meiotic germ cells	col-181	0.773178583	2.81615E-23

Meiotic germ cells	col-184	0.803979841	6.7228E-22
Meiotic germ cells	ctb-1	0.260501936	1.4931E-20
Meiotic germ cells	rpl-32	-0.148464655	3.37261E-20
Meiotic germ cells	rla-2	-0.212699197	8.31583E-20
Meiotic germ cells	col-20	0.529152588	9.97197E-20
Meiotic germ cells	rps-26	-0.176631305	5.16732E-19
Meiotic germ cells	gst-4	0.642806489	1.93357E-17
Meiotic germ cells	rpl-31	-0.174667415	5.91841E-17
Meiotic germ cells	col-81	0.574493857	4.91897E-15
Meiotic germ cells	far-3	2.764754065	7.3958E-15
Meiotic germ cells	mlc-3	0.509261659	1.29739E-14
Meiotic germ cells	col-98	0.957871229	1.3352E-14
Meiotic germ cells	rps-12	-0.131518029	2.61863E-14
Meiotic germ cells	rpl-14	-0.138268249	3.91494E-14
Meiotic germ cells	col-19	0.508307862	4.99199E-14
Meiotic germ cells	fip-2	0.823633443	2.65283E-13
Meiotic germ cells	sams-1	0.691315314	5.18847E-13
Meiotic germ cells	col-139	0.434043213	1.32867E-12
Meiotic germ cells	col-106	0.800294903	1.95188E-12
Meiotic germ cells	rpl-28	-0.159153831	3.45776E-12
Meiotic germ cells	rla-1	-0.156425891	3.8738E-12
Meiotic germ cells	rps-15	-0.125060281	9.39956E-12
Meiotic germ cells	col-8	0.903399478	1.18454E-11
Meiotic germ cells	rpl-33	-0.144459125	1.18484E-11
Meiotic germ cells	dct-16	-0.431911883	1.90504E-11
Meiotic germ cells	col-160	0.916010323	2.69545E-11
Meiotic germ cells	col-103	1.046811483	3.3411E-11
Meiotic germ cells	F11E6.3	0.922840593	4.49513E-11
Meiotic germ cells	rpl-30	-0.151542615	9.12945E-11
Meiotic germ cells	T20G5.8	0.908250535	1.13706E-10
Meiotic germ cells	col-178	0.740461081	1.55323E-10
Meiotic germ cells	nduo-4	0.20042394	5.1585E-10
Meiotic germ cells	F15A4.6	1.091285487	5.44651E-10

Meiotic germ cells	T13F3.6	0.926777574	5.52392E-10
Meiotic germ cells	pgl-1	-0.208398079	5.83927E-10
Meiotic germ cells	col-80	0.546912083	6.08771E-10
Meiotic germ cells	rpl-26	-0.122163518	2.73604E-09
Meiotic germ cells	pck-2	0.61756878	3.33202E-09
Meiotic germ cells	pat-10	0.312198888	3.41235E-09
Meiotic germ cells	rpl-22	-0.125207571	4.98702E-09
Meiotic germ cells	nduo-5	0.225908918	5.45626E-09
Meiotic germ cells	pab-1	-0.120488425	7.05106E-09
Meiotic germ cells	fipr-2	2.206133723	7.71053E-09
Meiotic germ cells	Y119D3B.21	-0.536376814	9.24339E-09
Meiotic germ cells	dod-6	0.874091305	1.33152E-08
Meiotic germ cells	sodh-1	1.259743	1.75726E-08
Meiotic germ cells	cgh-1	-0.25005373	2.21858E-08
Meiotic germ cells	C05D11.5	0.242904206	4.63458E-08
Meiotic germ cells	C53C9.2	1.508188847	5.93836E-08
Meiotic germ cells	C06A8.3	1.106383743	7.99612E-08
Meiotic germ cells	ttr-15	0.752855683	1.08451E-07
Meiotic germ cells	F35B12.3	2.393635085	1.47194E-07
Meiotic germ cells	his-60	-0.409031712	1.49993E-07
Meiotic germ cells	tnc-2	1.118053457	2.26229E-07
Meiotic germ cells	Y111B2A.2	-0.361459283	2.42039E-07
Meiotic germ cells	F53F4.13	0.699608231	2.50771E-07
Meiotic germ cells	cpn-3	0.364841275	2.51269E-07
Meiotic germ cells	ZC116.1	2.067387916	3.02991E-07
Meiotic germ cells	F46H5.3	0.417947931	5.30708E-07
Meiotic germ cells	cpi-1	0.742630275	5.81766E-07
Meiotic germ cells	gln-3	0.812376585	1.26305E-06
Meiotic germ cells	rps-22	-0.12622611	1.28901E-06
Meiotic germ cells	col-143	0.69889664	1.3519E-06
Meiotic germ cells	tni-4	1.101218676	1.44716E-06
Meiotic germ cells	rps-24	-0.103012153	1.48586E-06
Meiotic germ cells	rack-1	-0.104165625	1.54394E-06
Meiotic germ cells	act-2	-0.235433384	1.64566E-06
Meiotic germ cells	nduo-2	0.214810561	2.58708E-06

Meiotic germ cells	T03F1.11	0.880644951	2.94908E-06
Meiotic germ cells	C24A3.2	0.948493912	3.20971E-06
Meiotic germ cells	dhs-21	0.268467832	4.61612E-06
Meiotic germ cells	K10D2.5	-0.2463926	4.75694E-06
Meiotic germ cells	rps-2	-0.096993602	5.21155E-06
Meiotic germ cells	gst-10	-0.942148119	6.53837E-06
Meiotic germ cells	cpn-4	1.200727035	9.16342E-06
Meiotic germ cells	hsp-16.2	0.971861187	1.21389E-05
Meiotic germ cells	gpx-5	1.379199681	1.37301E-05
Meiotic germ cells	F21C10.9	0.858643976	1.38411E-05
Meiotic germ cells	ttr-51	0.452655754	1.40059E-05
Meiotic germ cells	eef-1G	-0.100010783	1.61345E-05
Meiotic germ cells	H36L18.2	0.393239342	2.79935E-05
Meiotic germ cells	Y37E3.8	-0.083776563	2.94592E-05
Meiotic germ cells	atp-3	0.290353436	3.0891E-05
Meiotic germ cells	K08D12.6	0.631982184	3.18423E-05
Meiotic germ cells	C14C6.5	-1.518503072	3.78881E-05
Meiotic germ cells	rpl-4	0.200531354	4.05873E-05
Meiotic germ cells	myo-2	2.594924986	4.16214E-05
Meiotic germ cells	gst-5	0.965042803	4.57891E-05
Meiotic germ cells	pud-4	-2.381258881	9.0719E-05
Meiotic germ cells	col-147	0.497563384	9.14402E-05
Meiotic germ cells	iff-2	0.387432693	9.85089E-05
Meiotic germ cells	T04F8.8	0.773136402	0.000101404
Meiotic germ cells	rpl-27	-0.121400606	0.000111455
Meiotic germ cells	rpl-41.1	-0.388219207	0.000127856
Meiotic germ cells	far-2	0.341635701	0.000140296
Meiotic germ cells	C53A3.2	0.737870753	0.000170563
Meiotic germ cells	rpl-15	-0.081261403	0.000180229
Meiotic germ cells	rps-0	-0.087952606	0.000181083
Meiotic germ cells	col-129	0.378187923	0.000201214
Meiotic germ cells	rps-23	-0.084069152	0.000203867
Meiotic germ cells	unc-54	0.478751361	0.000215082
Meiotic germ cells	Y87G2A.19	1.309441956	0.000254141

Meiotic germ cells	clik-1	0.324164063	0.000300828
Meiotic germ cells	pmt-2	0.455344889	0.000314948
Meiotic germ cells	lys-4	0.934552172	0.000320282
Meiotic germ cells	T01D1.4	0.287306527	0.000364612
Meiotic germ cells	W04A4.2	0.039227176	0.000385024
Meiotic germ cells	pqn-60	3.024052063	0.000412906
Meiotic germ cells	F23A7.8	-0.621041765	0.000442994
Meiotic germ cells	cpr-5	1.172615769	0.000462618
Meiotic germ cells	rpl-35	-0.089192883	0.000526317
Meiotic germ cells	act-4	0.300214471	0.000546531
Meiotic germ cells	cct-5	0.21770191	0.000615963
Meiotic germ cells	tni-3	0.288483895	0.000624415
Meiotic germ cells	pud-3	-1.614180024	0.000700052
Meiotic germ cells	myo-1	2.707930039	0.000722896
Meiotic germ cells	lev-11	0.352075837	0.000787646
Meiotic germ cells	vamp-8	1.530070173	0.001022572
Meiotic germ cells	mlc-2	0.364485242	0.001065093
Meiotic germ cells	rps-14	-0.069951249	0.001260069
Meiotic germ cells	H28O16.1	-0.12021565	0.001440189
Meiotic germ cells	asb-2	0.518456795	0.001479537
Meiotic germ cells	M28.5	-0.107329582	0.00155034
Meiotic germ cells	col-42	0.701730621	0.001583229
Meiotic germ cells	hsp-12.2	0.745084525	0.001680982
Meiotic germ cells	col-93	0.428984785	0.001704739
Meiotic germ cells	C44E4.4	0.188694134	0.001835389
Meiotic germ cells	nspd-2	-0.476069872	0.001903113
Meiotic germ cells	eef-1A.1	-0.063322624	0.001968729
Meiotic germ cells	tnt-4	1.457927459	0.002031821
Meiotic germ cells	perm-2	0.441495662	0.002059373
Meiotic germ cells	C49G7.3	0.897411424	0.002326815
Meiotic germ cells	T19H12.2	0.216766483	0.002600951
Meiotic germ cells	Y73F4A.3	2.190385328	0.003318407
Meiotic germ cells	C30G12.2	1.207575633	0.003417049
Meiotic germ cells	col-142	0.572925612	0.003812066
Meiotic germ cells	cth-1	0.512943799	0.003980451
Meiotic germ cells	acdh-1	0.435328565	0.004369104
Meiotic germ cells	bath-42	0.429865714	0.004417166

Meiotic germ cells	lec-2	0.48652341	0.004812266
Meiotic germ cells	clec-47	1.672358826	0.005398575
Meiotic germ cells	ZK809.8	0.542686226	0.006361255
Meiotic germ cells	pmr-1	0.593533592	0.006494563
Meiotic germ cells	nspd-10	-0.437162389	0.007149488
Meiotic germ cells	Y73F4A.2	2.746057936	0.008396899
Meiotic germ cells	K07A1.13	0.06133835	0.008737847
Meiotic germ cells	ahcy-1	0.182832188	0.009345136
Meiotic germ cells	rps-16	-0.105267907	0.00981329
Meiotic germ cells	rpn-3	0.267484257	0.010161615
Meiotic germ cells	C34B2.8	0.268359774	0.010315381
Meiotic germ cells	C45G9.6	1.184120102	0.010506266
Meiotic germ cells	gdh-1	-0.1463431	0.011025731
Meiotic germ cells	hsp-60	0.210907315	0.01145446
Meiotic germ cells	msra-1	1.165502857	0.011925128
Meiotic germ cells	hsp-25	0.532892303	0.012327525
Meiotic germ cells	F35A5.2	0.652936733	0.015245438
Meiotic germ cells	acs-2	0.468577654	0.015271002
Meiotic germ cells	oxy-5	0.33129037	0.018786007
Meiotic germ cells	spp-5	-0.685619439	0.019630222
Meiotic germ cells	cco-2	0.168569498	0.021574738
Meiotic germ cells	glb-1	0.192791445	0.023415693
Meiotic germ cells	mrpl-49	0.353377147	0.028679024
Meiotic germ cells	marg-1	2.165862623	0.034104548
Meiotic germ cells	col-101	0.564418114	0.034302332
Meiotic germ cells	rpl-5	-0.069626298	0.034816577
Meiotic germ cells	C45E5.4	2.271044903	0.035865656
Meiotic germ cells	C27B7.9	0.703962735	0.036083513
Meiotic germ cells	rps-10	-0.075923793	0.036467848
Meiotic germ cells	spp-2	-1.374299244	0.039867414
Meiotic germ cells	alh-1	0.353182197	0.045064364
Meiotic germ cells	nol-5	-0.114936015	0.046679357
Meiotic germ cells	ubq-1	0.204851989	0.056527632
Meiotic germ cells	B0303.4	0.525397685	0.05759366
Meiotic germ cells	spp-18	-1.519428444	0.061124273
Meiotic germ cells	nuo-2	0.290548215	0.066070323

Meiotic germ cells	Y105C5B.5	0.331755324	0.071212905
Meiotic germ cells	rpl-23	-0.075237694	0.075526166
Meiotic germ cells	lec-4	0.597496463	0.077716712
Meiotic germ cells	nuo-6	0.247067874	0.07979257
Meiotic germ cells	lgg-1	0.335510958	0.081728753
Meiotic germ cells	vha-17	0.386728378	0.085302014
Meiotic germ cells	F23A7.4	-0.567517454	0.09879034
Mitotic germ cells	rps-28	-0.49499482	0
Mitotic germ cells	rps-25	-0.185228609	0
Mitotic germ cells	rpl-29	-0.525292956	0
Mitotic germ cells	rps-29	-0.402013208	0
Mitotic germ cells	rpl-36	-0.279551179	0
Mitotic germ cells	rps-21	-0.394983197	0
Mitotic germ cells	rpl-41.2	-0.416443534	0
Mitotic germ cells	eef-2	-0.156797545	0
Mitotic germ cells	R09B3.2	-0.251293357	0
Mitotic germ cells	R09B3.3	-0.280256693	0
Mitotic germ cells	rps-27	-0.267467276	0
Mitotic germ cells	rpl-39	-0.486813159	0
Mitotic germ cells	rpl-38	-0.396939443	0
Mitotic germ cells	rpl-36.A	-0.221340087	0
Mitotic germ cells	rpl-43	-0.303774891	0
Mitotic germ cells	W01D2.1	-0.426796532	0
Mitotic germ cells	rpl-34	-0.201893042	5.7135E-295
Mitotic germ cells	C37A2.7	-0.212800423	3.0758E-271
Mitotic germ cells	ctc-1	0.41267353	1.1806E-243

Mitotic germ cells	rpl-35	-0.127351545	1.2357E-235
Mitotic germ cells	rpl-32	-0.119784495	1.4971E-234
Mitotic germ cells	ctc-3	0.486500842	2.9189E-232
Mitotic germ cells	rpl-31	-0.141034185	6.4368E-209
Mitotic germ cells	ubq-2	-0.138166535	2.8163E-203
Mitotic germ cells	rpl-30	-0.151323983	1.4203E-200
Mitotic germ cells	rpl-33	-0.134717724	5.8911E-195
Mitotic germ cells	rla-2	-0.162818367	1.2837E-186
Mitotic germ cells	rpl-21	-0.096168254	3.3132E-175
Mitotic germ cells	rpl-14	-0.113269596	5.6728E-171
Mitotic germ cells	rpl-28	-0.133887571	3.131E-162
Mitotic germ cells	rpl-22	-0.120835506	3.9961E-161
Mitotic germ cells	rps-22	-0.122266274	4.7163E-152
Mitotic germ cells	Y37E3.8	-0.090207883	8.4385E-144
Mitotic germ cells	rpl-15	-0.093089515	1.4068E-141
Mitotic germ cells	rps-23	-0.082790007	9.831E-133
Mitotic germ cells	col-122	1.251604985	1.2271E-132
Mitotic germ cells	Y111B2A.2	-0.508600306	8.1057E-129
Mitotic germ cells	rps-26	-0.111661381	2.0132E-126
Mitotic germ cells	rps-15	-0.095513886	6.2614E-125
Mitotic germ cells	col-124	0.736546586	5.2933E-117
Mitotic germ cells	rps-13	-0.088445311	1.4344E-115
Mitotic germ cells	rps-10	-0.082959031	1.2595E-111
Mitotic germ cells	col-20	0.791737577	3.4178E-103
Mitotic germ cells	col-140	0.757785837	4.4654E-103

Mitotic germ cells	rpl-27	-0.111884607	4.34337E-96
Mitotic germ cells	rps-14	-0.065655576	6.37381E-91
Mitotic germ cells	rpl-26	-0.085789885	2.3951E-90
Mitotic germ cells	col-119	1.031508825	2.66552E-89
Mitotic germ cells	ctc-2	0.312753725	6.06549E-87
Mitotic germ cells	nduo-1	0.329632004	4.39458E-85
Mitotic germ cells	rps-30	-0.079518233	3.07936E-79
Mitotic germ cells	rps-24	-0.073013106	3.18034E-79
Mitotic germ cells	rps-2	-0.073434465	2.04256E-78
Mitotic germ cells	rpl-17	-0.07634769	2.5909E-77
Mitotic germ cells	sams-3	0.350091996	4.89111E-76
Mitotic germ cells	rps-12	-0.06805833	2.75953E-75
Mitotic germ cells	col-181	0.892731001	1.69828E-69
Mitotic germ cells	rpl-5	-0.067203024	3.55592E-68
Mitotic germ cells	mlc-3	0.777499206	6.89704E-68
Mitotic germ cells	hsp-110	0.309128635	3.39159E-67
Mitotic germ cells	rpl-24.1	-0.058580628	1.61023E-64
Mitotic germ cells	ctb-1	0.252926547	6.33728E-63
Mitotic germ cells	atp-6	0.219875087	5.75922E-59
Mitotic germ cells	act-2	-0.141888351	1.11239E-58
Mitotic germ cells	F29B9.11	-0.278927984	1.8014E-56
Mitotic germ cells	col-184	0.898801735	1.40376E-54
Mitotic germ cells	hil-5	0.105834487	4.89984E-54
Mitotic germ cells	his-60	-0.458467973	9.09413E-54
Mitotic germ cells	col-19	0.625420155	1.1882E-52
Mitotic germ cells	F23H11.5	-0.138793828	3.86569E-51
Mitotic germ cells	ubq-1	0.309413486	5.89622E-50
Mitotic germ cells	cpg-1	0.697059546	9.91104E-50
Mitotic germ cells	T19H12.2	0.151828319	3.79788E-49
Mitotic germ cells	col-139	0.49247907	3.99924E-49
Mitotic germ cells	rpl-18	-0.051346355	8.83746E-49

Mitotic germ cells	rla-1	-0.081435539	9.33729E-49
Mitotic germ cells	rpl-41.1	-0.410191718	3.47994E-48
Mitotic germ cells	K10D2.5	-0.233953954	1.45026E-44
Mitotic germ cells	rps-18	-0.044699709	1.1163E-43
Mitotic germ cells	col-81	0.54962622	2.67818E-42
Mitotic germ cells	C14B9.10	-0.235850865	5.57188E-41
Mitotic germ cells	rpl-2	-0.045328985	1.48441E-40
Mitotic germ cells	pat-10	0.47167569	4.34307E-39
Mitotic germ cells	F23A7.8	-0.637368393	6.29971E-39
Mitotic germ cells	rps-19	-0.04720504	9.01986E-39
Mitotic germ cells	attf-2	0.255884932	1.36553E-38
Mitotic germ cells	eif-3.L	0.293074678	5.25805E-38
Mitotic germ cells	col-80	0.595192379	2.35517E-36
Mitotic germ cells	ubl-1	-0.056634126	3.75427E-36
Mitotic germ cells	C17F4.7	0.703622989	3.5221E-35
Mitotic germ cells	pyp-1	0.273101192	2.08946E-34
Mitotic germ cells	anat-1	0.408774213	2.38112E-34
Mitotic germ cells	ubc-7	0.309583841	3.24719E-34
Mitotic germ cells	rbpl-1	0.459780875	1.26867E-33
Mitotic germ cells	ran-4	0.285366947	1.6653E-33
Mitotic germ cells	snr-1	0.131710197	2.38211E-33
Mitotic germ cells	cpn-3	0.462927224	7.394E-33
Mitotic germ cells	unc-60	0.262117475	1.27083E-32
Mitotic germ cells	rpb-6	0.23311576	1.35907E-32
Mitotic germ cells	erfa-3	0.3047088	1.64081E-32
Mitotic germ cells	rps-16	-0.070844636	8.37439E-32
Mitotic germ cells	snr-2	0.118654732	1.01824E-31
Mitotic germ cells	C49H3.3	-0.125938719	1.46919E-31
Mitotic germ cells	ahcy-1	0.110617198	5.14688E-31
Mitotic germ cells	lin-53	0.373199244	5.47466E-31
Mitotic germ cells	daf-21	0.059132251	6.03548E-31
Mitotic germ cells	col-178	0.498623558	1.11803E-30
Mitotic germ cells	idhg-1	0.256276446	1.71409E-30
Mitotic germ cells	clik-1	0.310838912	3.08706E-30
Mitotic germ cells	pabp-2	0.343093764	8.57164E-30

Mitotic germ cells	abcf-3	0.323075367	7.86828E-29
Mitotic germ cells	col-93	0.521160297	1.75115E-28
Mitotic germ cells	rpn-6.1	0.300335702	1.937E-28
Mitotic germ cells	nuo-3	0.090513958	4.48017E-28
Mitotic germ cells	cct-5	0.132860551	5.63078E-28
Mitotic germ cells	rpb-5	0.320929343	7.50586E-28
Mitotic germ cells	lev-11	0.422307313	1.25219E-27
Mitotic germ cells	snr-7	-0.203410099	2.12915E-27
Mitotic germ cells	rpn-3	0.283984423	4.18239E-27
Mitotic germ cells	rnp-4	0.196391868	4.63737E-27
Mitotic germ cells	sec-61	0.246497562	4.64421E-27
Mitotic germ cells	F22D6.2	0.361504542	6.81395E-27
Mitotic germ cells	snr-4	0.094215969	7.3002E-27
Mitotic germ cells	smn-1	0.292662998	1.29618E-26
Mitotic germ cells	col-129	0.457577122	1.84221E-26
Mitotic germ cells	rpn-5	0.380576115	2.06155E-26
Mitotic germ cells	txl-1	0.309986387	2.70928E-26
Mitotic germ cells	nduo-4	0.187775553	5.73492E-26
Mitotic germ cells	hrp-2	0.291041484	5.88442E-26
Mitotic germ cells	cey-2	0.136961562	6.98448E-26
Mitotic germ cells	col-160	0.685067379	7.49531E-26
Mitotic germ cells	fars-1	0.254115575	5.31524E-25
Mitotic germ cells	Y94H6A.5	0.3210555	1.12236E-24
Mitotic germ cells	rpt-2	0.309395634	2.77136E-24
Mitotic germ cells	C44E4.4	0.101773595	3.05065E-24
Mitotic germ cells	mdh-2	0.254140683	3.83228E-24
Mitotic germ cells	gst-4	0.097220091	4.20501E-24
Mitotic germ cells	rps-17	-0.044286394	5.66594E-24
Mitotic germ cells	T20G5.14	0.24686912	8.29605E-24
Mitotic germ cells	col-143	0.763551788	9.95274E-24
Mitotic germ cells	mrps-24	0.294888841	1.03831E-23
Mitotic germ cells	col-8	0.808492196	1.15976E-23
Mitotic germ cells	hsr-9	0.234236021	1.353E-23
Mitotic germ cells	R02F2.1	0.295117781	1.37842E-23
Mitotic germ cells	D2030.4	0.288481353	2.11657E-23
Mitotic germ cells	dct-16	-0.371296236	3.28834E-23
Mitotic germ cells	rpl-12	-0.03444113	4.99302E-23
Mitotic germ cells	inf-1	0.084980823	4.9976E-23
Mitotic germ cells	F46H5.3	0.404158828	7.72177E-23
Mitotic germ cells	T25G3.3	0.262852077	9.86945E-23

Mitotic germ cells	eif-3.J	0.280863072	1.811E-22
Mitotic germ cells	pck-2	0.389901577	3.13472E-22
Mitotic germ cells	air-1	0.281438453	4.06248E-22
Mitotic germ cells	col-106	0.651847953	4.45066E-22
Mitotic germ cells	nuo-4	0.248450926	5.42184E-22
Mitotic germ cells	eif-2A	0.218863157	6.1294E-22
Mitotic germ cells	rps-7	-0.038732248	1.09466E-21
Mitotic germ cells	rack-1	-0.040265356	1.39254E-21
Mitotic germ cells	Y71F9AL.9	0.306555494	1.48299E-21
Mitotic germ cells	pdhb-1	0.25062279	2.44288E-21
Mitotic germ cells	bud-31	0.3194632	3.24069E-21
Mitotic germ cells	ran-3	0.247649199	4.38711E-21
Mitotic germ cells	nuo-6	0.203662257	5.38292E-21
Mitotic germ cells	ZC395.10	0.071988281	7.94999E-21
Mitotic germ cells	rps-3	-0.038535003	1.38045E-20
Mitotic germ cells	sams-1	0.067186753	1.60575E-20
Mitotic germ cells	ran-1	0.064326232	1.69271E-20
Mitotic germ cells	ddx-17	0.133187151	1.85794E-20
Mitotic germ cells	rpn-7	0.204388097	3.52549E-20
Mitotic germ cells	hel-1	0.107827745	3.93238E-20
Mitotic germ cells	tiar-1	0.277066973	4.06359E-20
Mitotic germ cells	swd-2.2	0.277658124	6.1131E-20
Mitotic germ cells	pbs-2	0.198419896	6.22392E-20
Mitotic germ cells	F44B9.8	0.339803971	6.54169E-20
Mitotic germ cells	uba-1	0.28836848	6.83884E-20
Mitotic germ cells	mag-1	0.289730014	7.29E-20
Mitotic germ cells	hpo-18	-0.33884398	8.41263E-20
Mitotic germ cells	npp-2	0.30762533	9.62867E-20
Mitotic germ cells	let-70	0.103015287	1.00974E-19
Mitotic germ cells	alh-1	0.334078847	1.21085E-19
Mitotic germ cells	mlc-2	0.419918185	1.27361E-19
Mitotic germ cells	cpg-2	0.466417604	1.58399E-19
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Mitotic germ cells	dlc-1	0.075612364	1.903E-19
Mitotic germ cells	npp-10	0.297883746	2.19369E-19
Mitotic germ cells	dpy-30	0.219108329	5.45332E-19
Mitotic germ cells	sodh-1	0.706394134	5.61087E-19
Mitotic germ cells	C14C6.5	-1.482552596	7.37181E-19
Mitotic germ cells	nduf-7	0.224873425	7.56541E-19
Mitotic germ cells	tnc-2	1.218608466	8.19865E-19

Mitotic germ cells	C35D10.13	0.330184372	8.53285E-19
Mitotic germ cells	act-4	0.359002472	1.03777E-18
Mitotic germ cells	nxt-1	0.3289068	1.39771E-18
Mitotic germ cells	spt-16	0.21656083	2.01247E-18
Mitotic germ cells	rab-1	0.359217016	2.30114E-18
Mitotic germ cells	C54D10.3	0.346721124	2.53925E-18
Mitotic germ cells	wdr-12	0.227509242	2.58657E-18
Mitotic germ cells	uev-1	0.352088516	2.59833E-18
Mitotic germ cells	mlc-1	0.379569469	3.00473E-18
Mitotic germ cells	mrpl-17	0.330259921	3.13041E-18
Mitotic germ cells	rpt-4	0.260165603	4.18936E-18
Mitotic germ cells	let-754	0.240160947	6.63655E-18
Mitotic germ cells	smc-5	0.240408046	7.47068E-18
Mitotic germ cells	F10E7.5	0.208418464	8.15953E-18
Mitotic germ cells	ima-2	0.248389537	9.18786E-18
Mitotic germ cells	rpl-23	-0.037612728	1.10421E-17
Mitotic germ cells	idha-1	0.244885899	1.2222E-17
Mitotic germ cells	sftb-1	0.302570967	1.55878E-17
Mitotic germ cells	C36E8.1	0.219632788	1.64777E-17
Mitotic germ cells	C06A8.3	0.779106918	1.85924E-17
Mitotic germ cells	F55F8.2	0.293224778	2.36596E-17
Mitotic germ cells	rab-11.1	0.316589183	2.59138E-17
Mitotic germ cells	dlst-1	0.238579955	2.75562E-17
Mitotic germ cells	E02D9.1	0.254424543	3.31222E-17
Mitotic germ cells	cdc-5L	0.357182314	4.14156E-17
Mitotic germ cells	T20H4.5	0.263399296	5.57192E-17
Mitotic germ cells	F32D8.5	0.237450021	6.51664E-17
Mitotic germ cells	Y66D12A.9	0.248902074	7.60312E-17
Mitotic germ cells	prmt-1	0.063988565	7.65693E-17
Mitotic germ cells	lpd-6	0.270051559	8.09164E-17
Mitotic germ cells	pmt-2	0.470115	8.61087E-17
Mitotic germ cells	usp-48	0.375394865	1.03576E-16
Mitotic germ cells	nol-5	-0.065261777	1.14784E-16
Mitotic germ cells	nmt-1	0.220335379	1.15658E-16
Mitotic germ cells	bath-42	0.33354118	1.6669E-16
Mitotic germ cells	R53.4	0.064615888	2.08113E-16
Mitotic germ cells	lpd-5	0.287777998	2.95631E-16
Mitotic germ cells	ragc-1	0.281315533	5.05492E-16
Mitotic germ cells	F42A10.5	0.213280077	5.18278E-16
Mitotic germ cells	Y57G11C.3	0.287733654	5.5275E-16
Mitotic germ cells	rsp-3	0.115689559	5.83184E-16

Mitotic germ cells	rpl-13	-0.029124246	6.80519E-16
Mitotic germ cells	sucg-1	0.246122206	6.99893E-16
Mitotic germ cells	ubh-4	0.224072213	7.99098E-16
Mitotic germ cells	F13H8.2	0.234921237	9.83942E-16
Mitotic germ cells	nduo-2	0.230934384	1.07518E-15
Mitotic germ cells	snrp-200	0.261856768	1.2538E-15
Mitotic germ cells	rbx-1	0.295332755	1.84346E-15
Mitotic germ cells	ngp-1	0.203184069	2.16993E-15
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Mitotic germ cells	mtss-1	0.253771741	2.99851E-15
Mitotic germ cells	R74.7	0.20585393	3.05579E-15
Mitotic germ cells	acdh-1	0.558762455	4.16837E-15
Mitotic germ cells	cey-1	0.208626499	4.51451E-15
Mitotic germ cells	T03F1.11	1.058782367	4.60731E-15
Mitotic germ cells	hsb-1	0.266962167	5.68995E-15
Mitotic germ cells	tofu-2	0.25364721	6.28433E-15
Mitotic germ cells	oxy-5	0.241351982	6.43243E-15
Mitotic germ cells	mob-4	0.230668079	6.63437E-15
Mitotic germ cells	F23A7.4	-0.368112337	6.67858E-15
Mitotic germ cells	rpt-1	0.27377412	9.54685E-15
Mitotic germ cells	mrpl-9	0.221155477	9.63119E-15
Mitotic germ cells	rpt-5	0.291675837	9.88148E-15
Mitotic germ cells	C34C12.8	0.234461895	1.06425E-14
Mitotic germ cells	mup-2	0.110240535	1.08362E-14
Mitotic germ cells	rfc-4	0.313622854	1.47134E-14
Mitotic germ cells	ZK512.2	0.248652606	1.47699E-14
Mitotic germ cells	cdk-1	0.326413165	1.94919E-14
Mitotic germ cells	mrpl-34	0.265313764	2.04573E-14
Mitotic germ cells	nol-10	0.247816749	2.25388E-14
Mitotic germ cells	cyb-1	0.245208665	2.29912E-14
Mitotic germ cells	otub-1	0.227557383	2.94545E-14
Mitotic germ cells	dnj-19	0.359399285	3.28562E-14
Mitotic germ cells	exos-8	0.265096065	3.96854E-14
Mitotic germ cells	rpl-7A	-0.033304365	5.07671E-14
Mitotic germ cells	emb-4	0.231428327	5.10031E-14
Mitotic germ cells	C08B6.8	0.28207958	5.30755E-14
Mitotic germ cells	dis-3	0.218298727	5.99259E-14
Mitotic germ cells	sucl-2	0.210731398	6.04964E-14
Mitotic germ cells	col-98	0.830065387	6.14014E-14
Mitotic germ cells	F30A10.9	0.228062485	6.78117E-14

Mitotic germ cells	eif-3.B	0.25745311	6.965E-14
Mitotic germ cells	daf-31	0.332221686	7.4948E-14
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Mitotic germ cells	rpc-1	0.217839009	7.91794E-14
Mitotic germ cells	T27E9.2	-0.164043981	8.16171E-14
Mitotic germ cells	let-504	0.231423125	8.51322E-14
Mitotic germ cells	tni-3	0.091164495	9.8694E-14
Mitotic germ cells	F11E6.3	0.497257893	1.44148E-13
Mitotic germ cells	let-858	0.291254326	1.71576E-13
Mitotic germ cells	aos-1	0.188489012	1.92145E-13
Mitotic germ cells	F27C1.6	0.346629275	2.07144E-13
Mitotic germ cells	rpoa-2	0.185596413	2.2024E-13
Mitotic germ cells	nst-1	0.18755927	2.20826E-13
Mitotic germ cells	dnj-11	0.15959215	2.21014E-13
Mitotic germ cells	C34B2.8	0.182010506	2.46933E-13
Mitotic germ cells	C34E10.10	0.240757914	2.60525E-13
Mitotic germ cells	W08E12.7	0.069158908	2.87811E-13
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Mitotic germ cells	K07F5.15	0.223367882	3.30727E-13
Mitotic germ cells	T04A8.8	0.318694145	3.31349E-13
Mitotic germ cells	syf-1	0.295011935	3.59774E-13
Mitotic germ cells	ddx-15	0.239691522	3.68643E-13
Mitotic germ cells	icd-1	-0.041493693	3.71547E-13
Mitotic germ cells	baf-1	0.126598697	3.96281E-13
Mitotic germ cells	Y14H12B.1	0.292451663	4.78051E-13
Mitotic germ cells	sna-2	0.31483461	4.79859E-13
Mitotic germ cells	mma-1	0.206452529	5.06736E-13
Mitotic germ cells	rpn-9	0.341405179	5.58696E-13
Mitotic germ cells	ZC116.1	1.854554416	5.76149E-13
Mitotic germ cells	emr-1	0.285654585	6.03889E-13
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Mitotic germ cells	crn-3	0.303041598	6.36928E-13
Mitotic germ cells	rsr-1	0.201702018	6.80288E-13
Mitotic germ cells	cisd-3.1	0.226843857	7.02922E-13
Mitotic germ cells	mtr-4	0.243338076	7.2878E-13
Mitotic germ cells	cdl-1	0.264386017	7.37381E-13
Mitotic germ cells	car-1	0.110976512	7.38414E-13
Mitotic germ cells	chp-1	0.257533961	7.41283E-13
Mitotic germ cells	K12H4.3	0.229460815	8.44385E-13
Mitotic germ cells	sftb-2	0.280518365	9.03205E-13
Mitotic germ cells	emb-5	0.262182279	9.4334E-13

Mitotic germ cells	tag-262	0.282646144	1.01288E-12
Mitotic germ cells	nuo-1	0.174746656	1.46946E-12
Mitotic germ cells	mrps-34	0.181031295	1.64959E-12
Mitotic germ cells	mcm-2	0.23718241	1.67047E-12
Mitotic germ cells	K08D12.6	0.366635562	1.68133E-12
Mitotic germ cells	rpn-8	0.245467049	1.94572E-12
Mitotic germ cells	Y53C12B.1	0.177586286	1.95393E-12
Mitotic germ cells	rnr-2	0.244795448	2.00014E-12
Mitotic germ cells	unc-87	0.125163177	2.13233E-12
Mitotic germ cells	atad-3	0.190204361	2.1915E-12
Mitotic germ cells	pam-1	0.261162966	2.19403E-12
Mitotic germ cells	nduo-5	0.136769712	2.48703E-12
Mitotic germ cells	rpb-8	0.208668951	2.94932E-12
Mitotic germ cells	mrps-17	0.239467636	2.94932E-12
Mitotic germ cells	lsm-4	0.336949867	3.26774E-12
Mitotic germ cells	fipr-2	1.664831854	3.28741E-12
Mitotic germ cells	rpn-12	0.241222473	3.31574E-12
Mitotic germ cells	his-72	0.140653151	3.41124E-12
Mitotic germ cells	hmg-12	0.125643081	3.9686E-12
Mitotic germ cells	pas-4	0.196294296	3.9836E-12
Mitotic germ cells	far-2	0.328486644	3.98502E-12
Mitotic germ cells	mrps-18A	0.222633719	4.02052E-12
Mitotic germ cells	dpt-1	0.186528834	4.24748E-12
Mitotic germ cells	sars-1	0.202102794	4.65205E-12
Mitotic germ cells	gsp-1	0.219890149	4.72421E-12
Mitotic germ cells	dnj-5	0.305533233	5.04652E-12
Mitotic germ cells	tofu-6	0.226341381	5.14048E-12
Mitotic germ cells	patr-1	0.304158353	5.2285E-12
Mitotic germ cells	dnj-12	0.24083918	5.5613E-12
Mitotic germ cells	prp-6	0.218910149	5.71345E-12
Mitotic germ cells	mrpl-12	0.229581805	6.08534E-12
Mitotic germ cells	C35A5.8	0.261093247	6.12695E-12
Mitotic germ cells	Y22D7AL.10	0.062653631	6.13779E-12
Mitotic germ cells	Y45F10D.7	0.203905468	7.0103E-12
Mitotic germ cells	hint-1	0.224964281	7.59361E-12
Mitotic germ cells	hrpf-2	0.233479892	8.11122E-12
Mitotic germ cells	npp-23	0.165814648	8.34017E-12
Mitotic germ cells	Y54E5A.5	0.222956792	1.00449E-11
Mitotic germ cells	him-19	0.180072139	1.13763E-11
Mitotic germ cells	pfd-5	0.181827656	1.19485E-11
Mitotic germ cells	nuo-2	0.2296046	1.24621E-11
Mitotic germ cells	F10B5.8	0.27527118	1.32232E-11
Mitotic germ cells	K05C4.5	0.207393151	1.44855E-11

Mitotic germ cells	dim-1	0.050596514	1.67607E-11
Mitotic germ cells	ddx-19	0.218511565	1.74972E-11
Mitotic germ cells	byn-1	0.215192689	1.98803E-11
Mitotic germ cells	C24D10.6	0.327680417	1.99295E-11
Mitotic germ cells	him-3	0.236798285	2.11676E-11
Mitotic germ cells	ZK1127.5	0.156124646	2.12618E-11
Mitotic germ cells	F30F8.1	0.287372971	2.17155E-11
Mitotic germ cells	skr-1	0.224125244	2.21122E-11
Mitotic germ cells	H14A12.3	0.374329929	2.2322E-11
Mitotic germ cells	hrp-1	0.111248578	2.33965E-11
Mitotic germ cells	sod-1	0.162643046	2.40582E-11
Mitotic germ cells	F49E8.2	0.206496884	2.44109E-11
Mitotic germ cells	vha-9	0.247563036	2.44298E-11
Mitotic germ cells	rps-9	-0.023943871	2.83744E-11
Mitotic germ cells	tbp-1	0.147527812	3.20382E-11
Mitotic germ cells	top-1	0.266960476	3.26486E-11
Mitotic germ cells	cyk-7	0.27144059	3.33423E-11
Mitotic germ cells	col-103	0.6785892	3.35159E-11
Mitotic germ cells	F08B4.7	0.28869602	3.84147E-11
Mitotic germ cells	aly-3	0.175363444	4.10919E-11
Mitotic germ cells	F21D5.7	0.191624428	4.2225E-11
Mitotic germ cells	lars-1	0.188180477	4.24648E-11
Mitotic germ cells	nduf-2.2	0.190709003	4.34167E-11
Mitotic germ cells	F52C12.2	0.192598348	4.7905E-11
Mitotic germ cells	ZK637.2	0.263651368	4.89962E-11
Mitotic germ cells	T02H6.1	0.209001414	4.93244E-11
Mitotic germ cells	natb-1	0.168814133	4.96616E-11
Mitotic germ cells	utp-20	0.138741021	4.98399E-11
Mitotic germ cells	cth-1	0.246398925	4.99935E-11
Mitotic germ cells	B0464.6	0.218710748	5.6607E-11
Mitotic germ cells	map-2	0.212039741	6.09877E-11
Mitotic germ cells	rps-0	-0.030798957	8.45435E-11
Mitotic germ cells	B0285.4	0.210384085	9.50549E-11
Mitotic germ cells	exos-4.1	0.200084893	9.60864E-11
Mitotic germ cells	ttr-15	0.509169949	1.01247E-10
Mitotic germ cells	unc-132	0.185858353	1.0504E-10
Mitotic germ cells	C16C8.16	0.236620975	1.16494E-10
Mitotic germ cells	rbd-1	0.149944129	1.18174E-10
Mitotic germ cells	dcaf-1	0.258732419	1.21305E-10
Mitotic germ cells	cks-1	0.224736269	1.21401E-10
Mitotic germ cells	rnp-6	0.272076583	1.23349E-10

Mitotic germ cells	F59C6.5	0.214973248	1.25219E-10
Mitotic germ cells	ZK418.9	0.230302885	1.34568E-10
Mitotic germ cells	T07C4.3	0.295327151	1.57468E-10
Mitotic germ cells	Y18D10A.11	0.194081491	1.65263E-10
Mitotic germ cells	cct-7	0.135462274	1.68672E-10
Mitotic germ cells	acin-1	0.242285372	1.99911E-10
Mitotic germ cells	nath-10	0.240149038	2.08605E-10
Mitotic germ cells	Y37E11AL.3	0.282953164	2.30805E-10
Mitotic germ cells	rnp-2	0.250069868	2.32622E-10
Mitotic germ cells	C01F6.9	-0.228707436	2.34039E-10
Mitotic germ cells	dld-1	0.24582749	2.36434E-10
Mitotic germ cells	mfap-1	0.356272298	2.38104E-10
Mitotic germ cells	oaz-1	0.220397348	2.46728E-10
Mitotic germ cells	W04A4.2	0.003740402	2.59695E-10
Mitotic germ cells	ctr-9	0.212716647	2.9127E-10
Mitotic germ cells	daz-1	0.20103241	2.96661E-10
Mitotic germ cells	ubc-20	0.215221887	3.1118E-10
Mitotic germ cells	rps-5	-0.023152563	3.18947E-10
Mitotic germ cells	vps-37	0.265685201	3.20695E-10
Mitotic germ cells	T13F3.6	0.193349755	3.79445E-10
Mitotic germ cells	kin-3	0.153110651	3.82106E-10
Mitotic germ cells	JC8.2	0.225016929	4.01261E-10
Mitotic germ cells	K10C3.5	0.180820868	4.01884E-10
Mitotic germ cells	R07H5.8	0.231057117	4.88033E-10
Mitotic germ cells	rpa-1	0.236768546	5.01573E-10
Mitotic germ cells	B0024.11	0.209763542	5.09092E-10
Mitotic germ cells	pars-1	0.217287646	5.11529E-10
Mitotic germ cells	F44G4.1	0.140568833	6.09532E-10
Mitotic germ cells	riok-1	0.250669884	6.85019E-10
Mitotic germ cells	bath-5	0.13858514	6.94268E-10
Mitotic germ cells	cco-2	0.067214178	7.84814E-10
Mitotic germ cells	spt-5	0.241643248	7.85512E-10
Mitotic germ cells	prp-3	0.334884269	7.92012E-10
Mitotic germ cells	T26G10.1	0.231370102	8.13178E-10
Mitotic germ cells	mrps-15	0.221839129	8.45791E-10
Mitotic germ cells	Y119D3B.21	-0.358269281	8.80529E-10
Mitotic germ cells	ZK795.3	0.26413312	1.00553E-09
Mitotic germ cells	skr-18	0.299427785	1.13404E-09
Mitotic germ cells	prp-19	0.196893719	1.15322E-09
Mitotic germ cells	far-3	1.617276311	1.17283E-09

Mitotic germ cells	F19B6.1	0.19236065	1.23417E-09
Mitotic germ cells	lec-2	0.243961519	1.29934E-09
Mitotic germ cells	pbs-1	0.222242917	1.37585E-09
Mitotic germ cells	C41G7.9	0.22567093	1.43521E-09
Mitotic germ cells	mrpl-13	0.174591027	1.46585E-09
Mitotic germ cells	ndk-1	0.033348299	1.5276E-09
Mitotic germ cells	cyn-1	0.122677949	1.85389E-09
Mitotic germ cells	ncbp-1	0.234878176	1.87123E-09
Mitotic germ cells	mrpl-18	0.248347264	2.10624E-09
Mitotic germ cells	rad-50	0.239680588	2.28776E-09
Mitotic germ cells	dhfr-1	0.288552769	2.35416E-09
Mitotic germ cells	mrpl-51	0.204253068	2.56703E-09
Mitotic germ cells	hrpk-1	0.228267523	2.59246E-09
Mitotic germ cells	pas-1	0.227959715	2.62247E-09
Mitotic germ cells	C52E12.1	0.274153575	2.85392E-09
Mitotic germ cells	E02H1.1	0.166149564	2.90048E-09
Mitotic germ cells	mcm-7	0.252915891	3.07292E-09
Mitotic germ cells	Y61A9LA.10	0.182236613	3.08247E-09
Mitotic germ cells	R02F2.7	0.159230748	3.27514E-09
Mitotic germ cells	W05F2.6	0.279787534	3.42978E-09
Mitotic germ cells	cpsf-2	0.259354469	3.5006E-09
Mitotic germ cells	mev-1	0.219630242	3.90836E-09
Mitotic germ cells	plrg-1	0.247209379	4.12003E-09
Mitotic germ cells	K07C5.6	0.31635463	4.30049E-09
Mitotic germ cells	cpr-5	1.177949671	4.31594E-09
Mitotic germ cells	vha-2	0.313342051	4.40091E-09
Mitotic germ cells	cmd-1	0.254006675	4.73684E-09
Mitotic germ cells	syf-2	0.184961065	4.78554E-09
Mitotic germ cells	lgg-1	0.267374137	4.95909E-09
Mitotic germ cells	gen-1	0.198672347	5.13124E-09
Mitotic germ cells	B0238.11	0.251414491	5.33367E-09
Mitotic germ cells	tpi-1	0.195846368	5.49117E-09
Mitotic germ cells	T20D3.3	0.181505844	5.58196E-09
Mitotic germ cells	F55F8.3	0.201171983	6.11064E-09
Mitotic germ cells	gln-3	0.188400455	6.86431E-09
Mitotic germ cells	pqn-87	0.270493766	7.45724E-09
Mitotic germ cells	srpa-68	0.177323259	7.55354E-09
Mitotic germ cells	exos-3	0.15396959	8.19021E-09
Mitotic germ cells	C53C9.2	1.027869942	8.978E-09
Mitotic germ cells	fln-1	-0.240510529	9.05463E-09
Mitotic germ cells	tpp-2	0.184339201	9.14339E-09
Mitotic germ cells	clec-87	0.279968705	9.35417E-09

Mitotic germ cells	mrps-7	0.253831934	9.37622E-09
Mitotic germ cells	C06A5.3	0.297534573	9.68226E-09
Mitotic germ cells	toe-1	0.158667958	1.05625E-08
Mitotic germ cells	col-101	0.600070752	1.08626E-08
Mitotic germ cells	ZC434.4	0.222076861	1.09833E-08
Mitotic germ cells	sams-4	0.097118253	1.11494E-08
Mitotic germ cells	ZK632.4	0.228316088	1.14846E-08
Mitotic germ cells	rpoa-49	0.166141767	1.16446E-08
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Mitotic germ cells	rsp-5	0.176688241	1.3511E-08
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Mitotic germ cells	col-147	0.158240293	1.39903E-08
Mitotic germ cells	Y55F3AM.3	0.21802535	1.49062E-08
Mitotic germ cells	mog-2	0.180618544	1.49088E-08
Mitotic germ cells	acer-1	0.233252465	1.63523E-08
Mitotic germ cells	mex-3	0.317056108	1.65297E-08
Mitotic germ cells	let-611	0.170474869	1.78374E-08
Mitotic germ cells	Y46E12BL.2	0.209660959	1.80212E-08
Mitotic germ cells	ddx-23	0.292265905	1.85058E-08
Mitotic germ cells	mnat-1	0.230466168	1.92783E-08
Mitotic germ cells	fkb-6	0.172987237	2.14495E-08
Mitotic germ cells	C43E11.9	0.241087065	2.15174E-08
Mitotic germ cells	rpt-3	0.221078071	2.16663E-08
Mitotic germ cells	csn-3	0.189568654	2.19764E-08
Mitotic germ cells	isp-1	0.114161966	2.35377E-08
Mitotic germ cells	glp-4	0.173055971	2.51621E-08
Mitotic germ cells	cct-4	0.131639329	2.5856E-08
Mitotic germ cells	teg-4	0.18116835	2.59474E-08
Mitotic germ cells	sca-1	0.260538425	2.79156E-08
Mitotic germ cells	K07H8.10	0.044366971	2.90464E-08
Mitotic germ cells	gls-1	0.221362062	2.9945E-08
Mitotic germ cells	eif-3.H	0.197502206	3.07117E-08
Mitotic germ cells	ddx-27	0.232068021	3.57815E-08
Mitotic germ cells	rpl-10	-0.020558217	3.61828E-08
Mitotic germ cells	M03F8.3	0.259322354	3.62267E-08
Mitotic germ cells	Y54G2A.75	0.288879897	3.64435E-08
Mitotic germ cells	asb-2	0.246914335	3.82367E-08
Mitotic germ cells	ribo-1	0.254960084	3.98872E-08
Mitotic germ cells	hsp-60	0.122493911	4.09784E-08
Mitotic germ cells	ddb-1	0.18314427	4.45041E-08
Mitotic germ cells	ddi-1	0.210336094	4.50517E-08
Mitotic germ cells	C47E12.7	0.197588053	4.52512E-08

Mitotic germ cells	ify-1	0.192573746	4.73078E-08
Mitotic germ cells	atp-5	0.061752207	4.77431E-08
Mitotic germ cells	perm-3	0.241428762	4.9035E-08
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Mitotic germ cells	npp-11	0.17048541	5.17872E-08
Mitotic germ cells	unc-54	0.091402843	5.47848E-08
Mitotic germ cells	otub-3	0.224262675	5.73767E-08
Mitotic germ cells	mpc-1	0.208863928	5.75376E-08
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Mitotic germ cells	hars-1	0.182300283	7.39857E-08
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Mitotic germ cells	chch-3	0.217238522	7.85992E-08
Mitotic germ cells	timm-23	0.213085135	7.99891E-08
Mitotic germ cells	dnj-16	0.160962583	9.69982E-08
Mitotic germ cells	gars-1	0.168469534	9.86444E-08
Mitotic germ cells	chdp-1	0.215245294	9.97203E-08
Mitotic germ cells	dnj-13	0.251500599	1.01112E-07
Mitotic germ cells	xpo-3	0.154729856	1.01826E-07
Mitotic germ cells	cec-5	0.183382286	1.04893E-07
Mitotic germ cells	F56C9.6	0.266792296	1.05323E-07
Mitotic germ cells	rsp-2	0.303008381	1.0933E-07
Mitotic germ cells	unc-15	0.211973781	1.12968E-07
Mitotic germ cells	F26E4.4	0.240278689	1.13539E-07
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Mitotic germ cells	rpac-19	0.169492958	1.33099E-07
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Mitotic germ cells	Y53C10A.6	0.175621626	1.47035E-07
Mitotic germ cells	htp-3	0.269348763	1.48091E-07
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Mitotic germ cells	hmg-1.2	0.179694534	1.76148E-07
Mitotic germ cells	mog-5	0.235795342	1.79357E-07
Mitotic germ cells	pqn-51	0.257533979	1.93982E-07
Mitotic germ cells	pfd-4	0.142375535	2.09531E-07
Mitotic germ cells	fipp-1	0.280522625	2.11726E-07
Mitotic germ cells	prde-1	0.181496251	2.14451E-07
Mitotic germ cells	syx-5	0.217854689	2.15143E-07
Mitotic germ cells	C32F10.8	0.183482407	2.25189E-07
Mitotic germ cells	pfn-1	0.157195324	2.29114E-07

Mitotic germ cells	cyc-1	0.206168775	2.2921E-07
Mitotic germ cells	daf-16	0.19382033	2.41998E-07
Mitotic germ cells	rpb-7	0.17475797	2.49989E-07
Mitotic germ cells	rpl-37	0.171096114	2.6245E-07
Mitotic germ cells	B0041.8	0.160845384	2.68038E-07
Mitotic germ cells	tbg-1	0.170296135	2.7073E-07
Mitotic germ cells	mrpl-28	0.250095932	2.77587E-07
Mitotic germ cells	suf-1	0.14608083	2.94681E-07
Mitotic germ cells	ZK418.5	0.167882928	3.01578E-07
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Mitotic germ cells	xnp-1	0.250566222	4.00678E-07
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Mitotic germ cells	npp-16	0.179219305	5.367E-07
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Mitotic germ cells	let-630	0.198594881	5.65805E-07
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Mitotic germ cells	fib-1	-0.036530813	7.4101E-07
Mitotic germ cells	iff-1	0.024887699	7.47387E-07
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Mitotic germ cells	sam-4	0.210239033	8.0691E-07
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Mitotic germ cells	sas-6	0.289153096	8.62757E-07
Mitotic germ cells	K06A5.1	0.254552355	9.48482E-07

Mitotic germ cells	sti-1	0.253856719	1.05891E-06
Mitotic germ cells	F36A2.7	-0.073314334	1.07912E-06
Mitotic germ cells	E01A2.2	0.238301678	1.1145E-06
Mitotic germ cells	K04C2.2	0.12119626	1.20893E-06
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Mitotic germ cells	copz-1	0.197421716	1.27231E-06
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Mitotic germ cells	rpb-4	0.199363535	1.4126E-06
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Mitotic germ cells	vha-1	0.321045537	1.43994E-06
Mitotic germ cells	pfd-3	0.0899542	1.45506E-06
Mitotic germ cells	gop-3	0.124953866	1.46576E-06
Mitotic germ cells	smc-6	0.27677963	1.47953E-06
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Mitotic germ cells	lap-2	0.309064799	1.49374E-06
Mitotic germ cells	hpo-9	0.175513218	1.55108E-06
Mitotic germ cells	mrpl-19	0.195089809	1.59868E-06
Mitotic germ cells	skih-2	0.178204302	1.60399E-06
Mitotic germ cells	cpn-4	0.936379944	1.61709E-06
Mitotic germ cells	ubr-4	0.20476456	1.64351E-06
Mitotic germ cells	cri-3	0.075033434	1.67075E-06
Mitotic germ cells	rnp-5	0.27686821	1.69105E-06
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Mitotic germ cells	ensa-1	0.234706709	1.87221E-06
Mitotic germ cells	eif-2Balpha	0.196430676	1.91304E-06
Mitotic germ cells	trap-4	0.295113677	1.99345E-06
Mitotic germ cells	M01E5.4	0.164663407	2.03481E-06
Mitotic germ cells	C16A11.4	0.182695654	2.10732E-06
Mitotic germ cells	mrpl-11	0.199684172	2.14061E-06
Mitotic germ cells	pri-2	0.228750864	2.16525E-06
Mitotic germ cells	hoe-1	0.20418402	2.18356E-06
Mitotic germ cells	C17E4.4	0.207168489	2.20038E-06
Mitotic germ cells	F10B5.2	0.17855368	2.25027E-06
Mitotic germ cells	JC8.7	0.151369627	2.272E-06
Mitotic germ cells	hil-2	0.072662501	2.38355E-06
Mitotic germ cells	spn-4	0.228273976	2.45783E-06
Mitotic germ cells	fip-2	0.297840124	2.47743E-06
Mitotic germ cells	vrk-1	0.248323145	2.52618E-06
Mitotic germ cells	metr-1	0.232504901	2.5339E-06

Mitotic germ cells	C25A1.4	0.216145885	2.62858E-06
Mitotic germ cells	fkb-2	0.040134254	2.65384E-06
Mitotic germ cells	T10B5.3	0.173688982	2.73173E-06
Mitotic germ cells	C45G9.6	1.130467929	2.75924E-06
Mitotic germ cells	ufd-3	0.217827671	2.76944E-06
Mitotic germ cells	mcm-6	0.183242165	2.80352E-06
Mitotic germ cells	F54D5.9	0.189502869	2.88917E-06
Mitotic germ cells	dod-6	0.555379206	3.15432E-06
Mitotic germ cells	rsp-7	0.217677172	3.16758E-06
Mitotic germ cells	ran-5	0.225163972	3.17767E-06
Mitotic germ cells	pbs-3	0.18517276	3.21839E-06
Mitotic germ cells	C17G10.2	0.207959438	3.41316E-06
Mitotic germ cells	dlat-1	0.156764168	3.6226E-06
Mitotic germ cells	C05C10.7	0.193745233	3.65849E-06
Mitotic germ cells	mut-16	0.234879323	3.69871E-06
Mitotic germ cells	tnt-2	0.065239792	3.85866E-06
Mitotic germ cells	cyk-4	0.307018158	4.01483E-06
Mitotic germ cells	let-418	0.174640625	4.18722E-06
Mitotic germ cells	dars-1	0.171554207	4.26203E-06
Mitotic germ cells	T21B10.3	0.245510974	4.43189E-06
Mitotic germ cells	chaf-1	0.350245505	4.55324E-06
Mitotic germ cells	K02C4.3	0.174462996	4.68618E-06
Mitotic germ cells	rps-6	-0.031378851	4.71152E-06
Mitotic germ cells	F26E4.6	-0.096240965	4.75137E-06
Mitotic germ cells	mrg-1	0.18941292	4.76009E-06
Mitotic germ cells	clsp-1	0.263091691	4.82188E-06
Mitotic germ cells	algn-13	0.125541671	4.84245E-06
Mitotic germ cells	let-502	0.280632961	5.09978E-06
Mitotic germ cells	F58G11.3	0.184668996	5.19153E-06
Mitotic germ cells	prp-17	0.124551308	5.19195E-06
Mitotic germ cells	pas-5	0.159317684	5.29644E-06
Mitotic germ cells	smu-1	0.211508749	5.66751E-06
Mitotic germ cells	hpo-32	0.157730464	5.80045E-06
Mitotic germ cells	Y57A10A.13	0.159514162	5.87546E-06
Mitotic germ cells	pas-6	0.157047213	6.27708E-06
Mitotic germ cells	Y48B6A.1	0.194622713	6.37521E-06
Mitotic germ cells	cdd-2	0.2029455	6.76051E-06
Mitotic germ cells	pbs-7	0.135488111	7.2072E-06
Mitotic germ cells	rpb-2	0.170297797	7.40213E-06
Mitotic germ cells	atp-3	0.0647728	7.4441E-06
Mitotic germ cells	got-2.1	0.163296117	7.61883E-06

Mitotic germ cells	Y69E1A.5	0.009167095	7.90409E-06
Mitotic germ cells	cchl-1	0.207928138	8.0315E-06
Mitotic germ cells	M03C11.8	0.249288485	8.13221E-06
Mitotic germ cells	mcm-5	0.194633836	8.15929E-06
Mitotic germ cells	ZK809.8	0.163497308	8.17667E-06
Mitotic germ cells	rpl-16	-0.022329666	8.57778E-06
Mitotic germ cells	mrpl-37	0.109794553	9.02042E-06
Mitotic germ cells	F52B5.2	0.148518022	9.10056E-06
Mitotic germ cells	T07A9.8	0.141491056	9.48919E-06
Mitotic germ cells	C30H6.9	0.192274763	9.66817E-06
Mitotic germ cells	bir-2	0.191417357	9.84751E-06
Mitotic germ cells	kin-10	0.194662442	1.05179E-05
Mitotic germ cells	pdcd-2	0.198782024	1.11644E-05
Mitotic germ cells	M01E11.2	0.189952528	1.15167E-05
Mitotic germ cells	ZK792.5	0.178150235	1.18811E-05
Mitotic germ cells	C02B10.4	0.238639488	1.22435E-05
Mitotic germ cells	rpn-2	0.199553362	1.22726E-05
Mitotic germ cells	pas-2	0.146632997	1.2315E-05
Mitotic germ cells	eftu-2	0.182053348	1.35577E-05
Mitotic germ cells	Y66D12A.10	0.295023057	1.36898E-05
Mitotic germ cells	riok-3	0.115379669	1.38287E-05
Mitotic germ cells	F35B12.3	1.660665232	1.43397E-05
Mitotic germ cells	ostb-1	0.163456071	1.47644E-05
Mitotic germ cells	ZK430.7	0.223719548	1.48741E-05
Mitotic germ cells	hpo-40	0.187379357	1.499E-05
Mitotic germ cells	tni-4	0.717215243	1.52016E-05
Mitotic germ cells	C37C3.9	0.312566357	1.55011E-05
Mitotic germ cells	perm-5	0.092870014	1.56735E-05
Mitotic germ cells	F21C10.9	0.201460481	1.56976E-05
Mitotic germ cells	K07A1.13	0.015620719	1.5921E-05
Mitotic germ cells	prmt-5	0.138157363	1.61476E-05
Mitotic germ cells	T20G5.8	0.274177039	1.67967E-05
Mitotic germ cells	unc-27	0.076012349	1.68048E-05
Mitotic germ cells	col-159	0.223854204	1.68241E-05
Mitotic germ cells	syp-2	0.27537932	1.68273E-05
Mitotic germ cells	lsl-1	0.189106241	1.69011E-05
Mitotic germ cells	C47E12.2	0.183083829	1.73222E-05
Mitotic germ cells	aps-1	0.162785901	1.74178E-05
Mitotic germ cells	skp-1	0.195586446	1.84207E-05
Mitotic germ cells	F56A8.3	0.153827224	1.85106E-05
Mitotic germ cells	tag-72	0.111763574	1.85829E-05
Mitotic germ cells	guk-1	0.183764717	1.86064E-05

Mitotic germ cells	col-142	0.235060693	1.8626E-05
Mitotic germ cells	nbet-1	0.20597049	1.92081E-05
Mitotic germ cells	nos-3	0.198777108	1.99723E-05
Mitotic germ cells	C09G9.1	0.140863356	2.04776E-05
Mitotic germ cells	tag-124	0.206695359	2.05004E-05
Mitotic germ cells	W09C3.4	0.134853827	2.13126E-05
Mitotic germ cells	C12D8.1	0.251761753	2.18813E-05
Mitotic germ cells	cux-7	0.227294033	2.25663E-05
Mitotic germ cells	drh-3	0.190908401	2.26454E-05
Mitotic germ cells	mrpl-49	0.188565971	2.27854E-05
Mitotic germ cells	prx-19	0.157112822	2.30218E-05
Mitotic germ cells	usip-1	0.185797359	2.30781E-05
Mitotic germ cells	C05D11.9	0.172192004	2.38006E-05
Mitotic germ cells	pab-1	-0.028008972	2.42166E-05
Mitotic germ cells	R05H5.3	0.104213679	2.48023E-05
Mitotic germ cells	ola-1	0.118005419	2.50637E-05
Mitotic germ cells	rars-1	0.158485663	2.50751E-05
Mitotic germ cells	pro-1	0.171279305	2.54983E-05
Mitotic germ cells	B0393.3	0.224300068	2.5512E-05
Mitotic germ cells	cec-10	0.265607075	2.55567E-05
Mitotic germ cells	pdi-3	0.229998257	2.58132E-05
Mitotic germ cells	msh-6	0.185632817	2.67753E-05
Mitotic germ cells	K04G7.1	0.271047567	2.75368E-05
Mitotic germ cells	npp-3	0.17346935	2.76028E-05
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Mitotic germ cells	drp-1	0.172820524	2.88491E-05
Mitotic germ cells	aly-2	0.220659916	3.10033E-05
Mitotic germ cells	Y54G11A.3	0.221151764	3.12598E-05
Mitotic germ cells	copd-1	0.149340233	3.32835E-05
Mitotic germ cells	eif-1.A	0.098222899	3.43291E-05
Mitotic germ cells	sgt-1	0.189402631	3.54431E-05
Mitotic germ cells	zig-12	0.012367821	3.88202E-05
Mitotic germ cells	R07B7.2	0.191985508	4.00543E-05
Mitotic germ cells	cpf-1	0.17868582	4.03568E-05
Mitotic germ cells	H36L18.2	0.137301214	4.3143E-05
Mitotic germ cells	dnj-9	0.116898871	4.52479E-05
Mitotic germ cells	gad-1	0.237335267	4.66849E-05
Mitotic germ cells	F46F11.1	0.22165061	4.86449E-05
Mitotic germ cells	ima-3	0.208803337	4.92787E-05
Mitotic germ cells	eif-3.C	0.076143818	4.94757E-05
Mitotic germ cells	T22D1.5	0.329324428	4.95958E-05
Mitotic germ cells	pas-7	0.20608549	5.06836E-05

Mitotic germ cells	rpb-12	-0.156551423	5.09306E-05
Mitotic germ cells	sdha-2	0.181602933	5.14427E-05
Mitotic germ cells	F31C3.2	0.2217615	5.34538E-05
Mitotic germ cells	ZK686.2	0.136829288	5.37681E-05
Mitotic germ cells	C47B2.2	0.108643839	5.50077E-05
Mitotic germ cells	Y49F6B.2	0.204622269	5.54177E-05
Mitotic germ cells	pro-2	0.168479026	5.55656E-05
Mitotic germ cells	Y105C5B.5	0.120283446	5.60802E-05
Mitotic germ cells	mrps-22	0.152911166	5.70637E-05
Mitotic germ cells	B0464.9	0.189144856	5.84328E-05
Mitotic germ cells	let-355	0.094445849	5.90223E-05
Mitotic germ cells	prpf-4	0.291791924	6.02742E-05
Mitotic germ cells	T01B7.5	0.252025075	6.41914E-05
Mitotic germ cells	gcn-1	0.159479137	6.72298E-05
Mitotic germ cells	arx-7	0.222325289	6.78631E-05
Mitotic germ cells	pir-1	0.18903988	6.80144E-05
Mitotic germ cells	F49D11.10	0.105077334	6.86455E-05
Mitotic germ cells	prmt-7	0.106743338	7.21801E-05
Mitotic germ cells	gsr-1	0.219401695	7.52347E-05
Mitotic germ cells	mrpl-16	0.126802742	7.80305E-05
Mitotic germ cells	F25H2.4	0.235198482	8.03283E-05
Mitotic germ cells	Y37E11AM.3	0.04678875	8.07345E-05
Mitotic germ cells	ooc-5	0.128728844	8.3595E-05
Mitotic germ cells	K10D2.1	0.209464933	9.37471E-05
Mitotic germ cells	dap-3	0.1215239	9.44954E-05
Mitotic germ cells	rpb-3	0.171125954	9.51464E-05
Mitotic germ cells	ubc-13	0.190127746	9.67153E-05
Mitotic germ cells	asg-1	-0.047932334	9.69752E-05
Mitotic germ cells	plk-2	0.207621041	9.8014E-05
Mitotic germ cells	T01D1.4	0.015980494	9.81953E-05
Mitotic germ cells	F27D4.4	0.15660053	9.84433E-05
Mitotic germ cells	sart-3	0.161774888	0.000104582
Mitotic germ cells	rsa-1	0.22609585	0.000105317
Mitotic germ cells	C27F2.9	0.179133771	0.00010569
Mitotic germ cells	ccar-1	0.098877772	0.000106713
Mitotic germ cells	mrpl-20	0.295828837	0.000107259
Mitotic germ cells	F58A4.2	0.222136427	0.000117398
Mitotic germ cells	ubc-9	0.168728657	0.000119024
Mitotic germ cells	mrps-26	0.172037748	0.000119232
Mitotic germ cells	lys-4	0.66341468	0.000119763
Mitotic germ cells	hpo-29	0.207939699	0.000120504

Mitotic germ cells	Y14H12B.2	0.157524957	0.000122588
Mitotic germ cells	wdr-5.1	0.210016591	0.000124891
Mitotic germ cells	eif-3.F	0.160392067	0.00012597
Mitotic germ cells	T07A9.15	-0.183286967	0.000126839
Mitotic germ cells	cdc-48.2	0.217086696	0.000128307
Mitotic germ cells	pqn-60	1.75565132	0.000129427
Mitotic germ cells	mlc-5	0.253258592	0.000129721
Mitotic germ cells	ttr-21	2.515801082	0.00013258
Mitotic germ cells	K07F5.14	0.256167898	0.000134451
Mitotic germ cells	C11D2.4	0.144403662	0.000136537
Mitotic germ cells	C05C8.2	0.214215989	0.000141105
Mitotic germ cells	dnj-22	0.259310338	0.000142396
Mitotic germ cells	npp-14	0.268571293	0.000142783
Mitotic germ cells	Y73B6BL.23	0.153631652	0.000143084
Mitotic germ cells	nduf-5	0.17287716	0.000143401
Mitotic germ cells	dsb-1	0.209520254	0.000143987
Mitotic germ cells	pyk-1	0.184992508	0.00014878
Mitotic germ cells	evl-14	0.210709368	0.000149134
Mitotic germ cells	C16A3.6	0.181057812	0.000155659
Mitotic germ cells	dvc-1	0.23232212	0.000158986
Mitotic germ cells	mvk-1	0.122064367	0.000159649
Mitotic germ cells	aars-2	0.188665611	0.000167222
Mitotic germ cells	cyn-11	0.189200949	0.000181622
Mitotic germ cells	C38D4.4	0.159765675	0.000184826
Mitotic germ cells	asg-2	0.253368848	0.000184959
Mitotic germ cells	Y37H2A.12	0.080714463	0.000191453
Mitotic germ cells	dnc-2	0.181499261	0.000195794
Mitotic germ cells	nud-1	0.211070043	0.000198601
Mitotic germ cells	ntl-2	0.232683931	0.000201036
Mitotic germ cells	K03E5.2	0.486615612	0.000208106
Mitotic germ cells	fbxc-44	0.16007038	0.000215402
Mitotic germ cells	bub-3	0.217470058	0.000221211
Mitotic germ cells	R11A8.7	0.197970562	0.000221685
Mitotic germ cells	hsp-12.2	0.740235402	0.000223494
Mitotic germ cells	ptp-2	0.209664013	0.000223773
Mitotic germ cells	kin-18	0.292388445	0.000234536
Mitotic germ cells	cra-1	0.135684389	0.000236983
Mitotic germ cells	B0261.7	0.196671661	0.000237382
Mitotic germ cells	R144.10	0.102906437	0.000244497
Mitotic germ cells	Y38A10A.7	0.157398566	0.000247721
Mitotic germ cells	Y48G10A.1	0.066781016	0.000264331
Mitotic germ cells	mrps-6	0.165908409	0.000266754

Mitotic germ cells	asp-2	0.730291017	0.000268906
Mitotic germ cells	npp-1	0.138104907	0.000271069
Mitotic germ cells	ZK973.1	0.234079109	0.000302943
Mitotic germ cells	tads-1	0.18551922	0.000303857
Mitotic germ cells	sna-1	0.12324975	0.000315198
Mitotic germ cells	ssup-72	0.120746103	0.00032197
Mitotic germ cells	rpn-11	0.196334297	0.000329917
Mitotic germ cells	Y23H5B.6	0.209373253	0.000337835
Mitotic germ cells	egl-45	0.087468573	0.000341806
Mitotic germ cells	anmt-2	0.38248318	0.000343178
Mitotic germ cells	rpl-1	-0.019347184	0.000348806
Mitotic germ cells	lex-1	0.259778964	0.000352049
Mitotic germ cells	cyc-2.1	0.074764053	0.000356143
Mitotic germ cells	stl-1	0.158659063	0.000357092
Mitotic germ cells	myo-2	1.109155083	0.000358952
Mitotic germ cells	zfp-2	0.124727904	0.000380985
Mitotic germ cells	csn-2	0.175547382	0.000386441
Mitotic germ cells	emo-1	0.121073765	0.000401692
Mitotic germ cells	fbf-2	0.131640407	0.000404436
Mitotic germ cells	abhd-12	0.177477508	0.000407395
Mitotic germ cells	srp-7	0.12954328	0.000409486
Mitotic germ cells	usp-14	0.240602914	0.000414859
Mitotic germ cells	rsp-4	0.194454494	0.000415277
Mitotic germ cells	spch-1	0.052375942	0.000425482
Mitotic germ cells	arf-1.2	0.160413326	0.000443977
Mitotic germ cells	Y51H4A.15	0.228577267	0.000449248
Mitotic germ cells	ufd-2	0.159462504	0.000456776
Mitotic germ cells	T23B3.1	0.115414494	0.000457158
Mitotic germ cells	sur-6	0.181855499	0.000461636
Mitotic germ cells	snrp-27	0.228545638	0.000463785
Mitotic germ cells	icp-1	0.213691713	0.000464566
Mitotic germ cells	C56A3.5	0.147778897	0.000470151
Mitotic germ cells	atg-18	0.191860968	0.000470451
Mitotic germ cells	mdf-2	0.132834068	0.000471364
Mitotic germ cells	mdt-9	0.161546286	0.000482272
Mitotic germ cells	W04D2.4	0.17481873	0.000492775
Mitotic germ cells	rpac-40	0.141247376	0.000503047
Mitotic germ cells	pri-1	0.161432465	0.000504636
Mitotic germ cells	M28.5	-0.026329511	0.000504872
Mitotic germ cells	larp-1	-0.09950064	0.000512671
Mitotic germ cells	cpz-1	0.771155055	0.000514966

Mitotic germ cells	inx-14	0.176541338	0.000531439
Mitotic germ cells	fcp-1	0.190283957	0.000548654
Mitotic germ cells	wdr-4	0.16579887	0.000548932
Mitotic germ cells	nurf-1	0.179430342	0.00055401
Mitotic germ cells	F52A8.1	0.207865321	0.00056582
Mitotic germ cells	mrps-35	0.092331887	0.000577582
Mitotic germ cells	B0491.7	0.125269312	0.000588933
Mitotic germ cells	F11A10.7	0.182091111	0.000600122
Mitotic germ cells	tag-18	0.086359937	0.000612696
Mitotic germ cells	sco-1	0.18023999	0.000614457
Mitotic germ cells	F46F11.8	0.160466205	0.000630721
Mitotic germ cells	F44E2.8	0.238214747	0.000642029
Mitotic germ cells	nyn-1	0.161752781	0.000643487
Mitotic germ cells	lpd-2	0.210441406	0.00064985
Mitotic germ cells	T21C9.4	0.083144735	0.000651366
Mitotic germ cells	lea-1	-0.302791234	0.000673277
Mitotic germ cells	idh-1	0.209347374	0.00068317
Mitotic germ cells	F55F10.1	0.095493548	0.000683234
Mitotic germ cells	rab-6.1	0.270676176	0.000689624
Mitotic germ cells	plp-1	-0.066389861	0.000697601
Mitotic germ cells	ubxn-6	0.201261383	0.000722477
Mitotic germ cells	R08D7.1	0.291874693	0.00073016
Mitotic germ cells	F54D5.2	0.243207494	0.000740119
Mitotic germ cells	frm-1	0.153357982	0.000748392
Mitotic germ cells	ZK616.5	0.131981297	0.000752344
Mitotic germ cells	Y53C12B.2	0.174225826	0.000788591
Mitotic germ cells	dpf-3	0.177770059	0.000807916
Mitotic germ cells	T28A8.4	0.154261193	0.000825235
Mitotic germ cells	mrpl-15	0.154911205	0.000841095
Mitotic germ cells	F58A4.6	0.191525218	0.000855473
Mitotic germ cells	Y53F4B.9	0.154104827	0.00086231
Mitotic germ cells	pgl-3	0.274390387	0.000865056
Mitotic germ cells	Y23H5A.3	0.237769633	0.000891059
Mitotic germ cells	zyg-9	0.235488566	0.000897486
Mitotic germ cells	tgt-1	0.101440809	0.000904755
Mitotic germ cells	Y57A10A.27	0.100832064	0.000923473
Mitotic germ cells	rde-8	0.22324094	0.000933677
Mitotic germ cells	Y18D10A.9	0.115257447	0.00098618
Mitotic germ cells	tofu-5	0.190688073	0.001010421
Mitotic germ cells	T06D8.9	0.309860296	0.001032839
Mitotic germ cells	vpr-1	0.149483552	0.001051635

Mitotic germ cells	elpc-1	0.180721391	0.001068815
Mitotic germ cells	C01B10.8	0.105933506	0.001084533
Mitotic germ cells	npp-13	0.148470517	0.001086536
Mitotic germ cells	Y87G2A.19	0.869633439	0.00110027
Mitotic germ cells	glp-1	0.176776003	0.001115484
Mitotic germ cells	cpb-3	0.159638867	0.001120149
Mitotic germ cells	swsn-4	0.247583556	0.001120172
Mitotic germ cells	F23B12.7	0.136110917	0.001158607
Mitotic germ cells	F42G9.1	-0.143581031	0.001185149
Mitotic germ cells	rpl-6	-0.01898772	0.001196667
Mitotic germ cells	ZK1248.11	0.114600144	0.001255394
Mitotic germ cells	T22C1.1	0.15033888	0.001257798
Mitotic germ cells	rap-1	0.138919793	0.001272119
Mitotic germ cells	orc-1	0.19171508	0.00127442
Mitotic germ cells	R151.2	0.167316543	0.001274627
Mitotic germ cells	C23H5.8	-0.575132116	0.001284674
Mitotic germ cells	dcap-1	0.139807671	0.0012886
Mitotic germ cells	snr-3	0.067932453	0.001316521
Mitotic germ cells	nud-2	0.13896166	0.001332286
Mitotic germ cells	Y44F5A.1	0.103173079	0.001334245
Mitotic germ cells	him-17	0.189951969	0.001348624
Mitotic germ cells	disl-2	0.170964711	0.001351409
Mitotic germ cells	Y73E7A.1	0.248355449	0.001360272
Mitotic germ cells	F44E7.4	0.191636458	0.001366236
Mitotic germ cells	K01D12.6	0.156268274	0.001372918
Mitotic germ cells	C36A4.4	0.17601205	0.001373368
Mitotic germ cells	pola-1	0.205489318	0.001413229
Mitotic germ cells	cids-1	0.153334422	0.001438583
Mitotic germ cells	tomm-40	0.123034055	0.001489486
Mitotic germ cells	R04F11.5	0.139258458	0.001586166
Mitotic germ cells	C49G7.3	0.233023444	0.001593313
Mitotic germ cells	acs-4	0.18193095	0.001594497
Mitotic germ cells	ess-2	0.154628993	0.0016117
Mitotic germ cells	F44E7.5	0.242379325	0.001631786
Mitotic germ cells	smc-3	0.173024117	0.001635296
Mitotic germ cells	F10E9.7	0.230385869	0.001693279
Mitotic germ cells	deps-1	0.233703423	0.001708377
Mitotic germ cells	ubc-6	0.25637768	0.001763174
Mitotic germ cells	R148.4	0.148698802	0.00178847
Mitotic germ cells	eif-2D	0.145015206	0.001840397

Mitotic germ cells	spp-2	-0.804120219	0.001948977
Mitotic germ cells	F08H9.2	0.092714517	0.001962299
Mitotic germ cells	B0035.15	0.152454029	0.001995908
Mitotic germ cells	mrps-9	0.130569668	0.002002408
Mitotic germ cells	ska-3	0.230867251	0.002085595
Mitotic germ cells	lbp-4	0.138527856	0.00209322
Mitotic germ cells	W02D3.4	0.116281399	0.002094043
Mitotic germ cells	M02H5.8	0.327029441	0.002107331
Mitotic germ cells	gmps-1	0.156690433	0.002179989
Mitotic germ cells	ZK546.2	0.140065628	0.002183795
Mitotic germ cells	ril-2	0.156565357	0.002190875
Mitotic germ cells	capg-1	0.180969615	0.002251137
Mitotic germ cells	fipr-5	0.488946548	0.002285194
Mitotic germ cells	T06E6.1	0.22508877	0.002315447
Mitotic germ cells	rbm-28	0.188146897	0.002316596
Mitotic germ cells	R08D7.2	0.186872425	0.002504112
Mitotic germ cells	C18B2.3	0.002584145	0.00251446
Mitotic germ cells	lbp-6	0.212401412	0.002521056
Mitotic germ cells	bag-1	0.128826309	0.002541797
Mitotic germ cells	D2030.3	0.148009344	0.00254249
Mitotic germ cells	T10E9.14	0.136811096	0.002573753
Mitotic germ cells	ppm-1	0.235517052	0.002624388
Mitotic germ cells	F32A5.4	0.655142912	0.002641728
Mitotic germ cells	rpl-7	-0.019595443	0.002644884
Mitotic germ cells	R07E5.7	0.186116862	0.002661225
Mitotic germ cells	let-60	0.125214078	0.002692618
Mitotic germ cells	mcm-4	0.21337227	0.002744922
Mitotic germ cells	pges-2	0.188770247	0.002842775
Mitotic germ cells	rpc-2	0.112158306	0.002853326
Mitotic germ cells	pfkb-1.2	0.084554054	0.00292412
Mitotic germ cells	C14B1.9	0.23869451	0.002937737
Mitotic germ cells	B0280.9	0.137994698	0.003067143
Mitotic germ cells	csn-5	0.225304638	0.003078983
Mitotic germ cells	mbk-2	0.185227875	0.003124171
Mitotic germ cells	wdr-20	0.177453504	0.003139791
Mitotic germ cells	mars-1	0.11067307	0.003151596
Mitotic germ cells	gcsh-2	0.178387955	0.003164653
Mitotic germ cells	cyn-15	0.113011026	0.003198832
Mitotic germ cells	prp-31	0.223803837	0.003249736
Mitotic germ cells	npp-15	0.18734067	0.003317817
Mitotic germ cells	sin-3	0.210174387	0.003324993

Mitotic germ cells	eef-1A.1	-0.015761471	0.003328699
Mitotic germ cells	his-62	-0.395492954	0.003404261
Mitotic germ cells	F10E7.2	0.27870578	0.003433294
Mitotic germ cells	nfx-1	0.203908218	0.00344557
Mitotic germ cells	ZK1127.4	0.161978335	0.003604404
Mitotic germ cells	C35E7.8	0.061823155	0.003688707
Mitotic germ cells	hpo-12	0.161862372	0.003693389
Mitotic germ cells	F39H2.3	0.085319244	0.003723911
Mitotic germ cells	mppa-1	0.110711377	0.003767656
Mitotic germ cells	fbxa-101	0.117724893	0.003819589
Mitotic germ cells	Y52B11A.10	0.175095066	0.003985463
Mitotic germ cells	F15A4.6	0.539728624	0.004029102
Mitotic germ cells	snpc-1.1	0.244724417	0.004116349
Mitotic germ cells	gtbp-1	0.065743214	0.004211993
Mitotic germ cells	rtcb-1	0.145350742	0.00433956
Mitotic germ cells	C09G4.4	0.135141934	0.004356327
Mitotic germ cells	T20F5.7	0.106196215	0.004372902
Mitotic germ cells	isw-1	0.172626749	0.004384193
Mitotic germ cells	unc-44	0.177818258	0.00444663
Mitotic germ cells	F09E5.3	0.118579344	0.004461913
Mitotic germ cells	bath-41	0.136668458	0.004480015
Mitotic germ cells	F40F8.11	0.227132479	0.004488978
Mitotic germ cells	mdf-1	0.169161828	0.004547736
Mitotic germ cells	cope-1	0.099066093	0.004705036
Mitotic germ cells	R05D11.4	0.153744465	0.004773526
Mitotic germ cells	dcs-1	0.170295499	0.004847939
Mitotic germ cells	akir-1	0.212550941	0.004854308
Mitotic germ cells	C01G10.8	0.0782485	0.004982598
Mitotic germ cells	djr-1.1	0.227150158	0.005098183
Mitotic germ cells	qars-1	0.1535952	0.00517317
Mitotic germ cells	uaf-1	0.140469486	0.005211886
Mitotic germ cells	rnp-7	0.19492648	0.005256758
Mitotic germ cells	Y10G11A.1	0.101553115	0.005265172
Mitotic germ cells	nrd-1	0.173901968	0.005274805
Mitotic germ cells	rfp-1	0.174425006	0.005386846
Mitotic germ cells	gpdh-2	0.126359663	0.005402011
Mitotic germ cells	ego-1	0.148815481	0.005410486
Mitotic germ cells	rsp-1	0.097693807	0.005484253
Mitotic germ cells	hcf-1	0.187796837	0.005577409
Mitotic germ cells	K02F3.12	0.15485028	0.005582065
Mitotic germ cells	gld-3	0.201451747	0.005603706

Mitotic germ cells	T13H5.4	0.169404448	0.005624934
Mitotic germ cells	F25H8.1	0.191230557	0.005687626
Mitotic germ cells	natc-1	0.185728331	0.005746639
Mitotic germ cells	tag-267	0.167907804	0.006053569
Mitotic germ cells	pud-3	-0.528067909	0.006092718
Mitotic germ cells	vamp-8	0.971729278	0.006166018
Mitotic germ cells	W04D2.6	0.225796418	0.006248279
Mitotic germ cells	mbf-1	0.123101733	0.006318315
Mitotic germ cells	T24D1.2	0.150940012	0.006334927
Mitotic germ cells	dyci-1	0.120791392	0.006564285
Mitotic germ cells	tars-1	0.121228841	0.006909535
Mitotic germ cells	T24H10.1	0.188023267	0.007014886
Mitotic germ cells	ttll-12	0.12423111	0.007031891
Mitotic germ cells	rpoa-1	0.162764235	0.007181261
Mitotic germ cells	dhs-21	0.036484209	0.007206346
Mitotic germ cells	nas-22	-2.683198671	0.007533035
Mitotic germ cells	F48C1.6	0.101210945	0.00761201
Mitotic germ cells	ima-1	0.146589259	0.00771142
Mitotic germ cells	T26C12.1	0.134731292	0.007792466
Mitotic germ cells	ZK1127.6	0.153588098	0.008130085
Mitotic germ cells	mtx-1	0.221455802	0.008160108
Mitotic germ cells	perm-4	0.069262732	0.00823068
Mitotic germ cells	Y67D2.7	0.219344349	0.008409276
Mitotic germ cells	F10C5.2	0.22162689	0.008470824
Mitotic germ cells	tag-153	0.163473664	0.008484068
Mitotic germ cells	cid-1	0.146967648	0.008565579
Mitotic germ cells	mcm-3	0.189474759	0.008680008
Mitotic germ cells	F01F1.2	0.186010076	0.008683021
Mitotic germ cells	F53H1.4	0.204900063	0.008873445
Mitotic germ cells	W07E6.2	0.149814637	0.008875249
Mitotic germ cells	Y41E3.1	0.093475261	0.008969315
Mitotic germ cells	Y94H6A.8	0.205436778	0.009229414
Mitotic germ cells	F55A12.5	0.129678553	0.00932276
Mitotic germ cells	eat-6	0.145129988	0.00938271
Mitotic germ cells	ufc-1	0.131800942	0.009393468
Mitotic germ cells	lin-65	0.154269829	0.009393468
Mitotic germ cells	clec-1	0.169389175	0.009541978
Mitotic germ cells	mrpl-39	0.15159168	0.009690653
Mitotic germ cells	eef-1G	-0.021896332	0.009704099
Mitotic germ cells	B0207.6	0.062762371	0.009751197

Mitotic germ cells	klc-1	0.194344056	0.010041524
Mitotic germ cells	argk-1	0.15124821	0.010071728
Mitotic germ cells	F33H1.3	0.268953743	0.010157802
Mitotic germ cells	R107.5	0.274597887	0.010231307
Mitotic germ cells	fzy-1	0.134117371	0.010378935
Mitotic germ cells	F52B5.3	0.143205903	0.010437859
Mitotic germ cells	T13F2.2	0.083099865	0.010464477
Mitotic germ cells	F53F4.14	0.218683803	0.01049397
Mitotic germ cells	cir-1	0.239034621	0.010577405
Mitotic germ cells	nra-2	0.165338869	0.010764927
Mitotic germ cells	R04F11.2	0.036826515	0.010792673
Mitotic germ cells	W03F8.4	0.180117224	0.010872272
Mitotic germ cells	tag-349	0.229766393	0.010899978
Mitotic germ cells	wsp-1	0.217669299	0.010960483
Mitotic germ cells	B0035.6	0.166505282	0.011410813
Mitotic germ cells	ubr-1	0.18728927	0.011689506
Mitotic germ cells	F57F5.1	0.386901616	0.011711841
Mitotic germ cells	rps-11	-0.015953338	0.011876422
Mitotic germ cells	pbs-4	0.123483876	0.011909301
Mitotic germ cells	clic-1	0.241499708	0.012074942
Mitotic germ cells	cct-6	0.103172524	0.012113327
Mitotic germ cells	C09D4.4	0.069297276	0.012158373
Mitotic germ cells	cya-1	0.092154322	0.01216534
Mitotic germ cells	arp-11	0.121059845	0.01225467
Mitotic germ cells	mrps-2	0.121999762	0.012403507
Mitotic germ cells	CD4.8	0.093048202	0.012444376
Mitotic germ cells	arx-2	0.167306711	0.012474687
Mitotic germ cells	rae-1	0.133986659	0.012521556
Mitotic germ cells	sgo-1	0.196272251	0.012579701
Mitotic germ cells	scc-3	0.178894612	0.013427199
Mitotic germ cells	C17G10.1	0.143085565	0.013429639
Mitotic germ cells	tut-2	0.135405583	0.013529658
Mitotic germ cells	arl-8	0.218026857	0.013572572
Mitotic germ cells	mdh-1	0.235828509	0.013748213
Mitotic germ cells	mrps-28	0.213212641	0.013939537
Mitotic germ cells	T02H6.11	0.043663942	0.013978969
Mitotic germ cells	gst-5	0.098452873	0.014352331
Mitotic germ cells	T08G11.1	0.087196549	0.014572677
Mitotic germ cells	M110.3	0.195375785	0.014618397
Mitotic germ cells	mrps-16	0.155301355	0.014645222
Mitotic germ cells	C02F5.3	0.158007842	0.01475046
Mitotic germ cells	F53F1.2	0.079384866	0.015009261

Mitotic germ cells	mrpl-2	0.131035453	0.015148136
Mitotic germ cells	syx-4	0.215971731	0.015530987
Mitotic germ cells	nuo-5	0.136355432	0.015609202
Mitotic germ cells	hsp-25	0.096320413	0.015741424
Mitotic germ cells	F07E5.5	0.21538388	0.015820557
Mitotic germ cells	F45H10.3	0.119556347	0.01587229
Mitotic germ cells	erfa-1	0.114799731	0.016298477
Mitotic germ cells	T28D6.6	0.17145493	0.016421121
Mitotic germ cells	htp-2	0.20849973	0.016429698
Mitotic germ cells	T04F8.8	0.14055725	0.016622167
Mitotic germ cells	vps-25	0.103625835	0.016710906
Mitotic germ cells	F53C11.5	0.175614681	0.017173145
Mitotic germ cells	rad-23	0.142451606	0.017368209
Mitotic germ cells	pgl-2	0.102157516	0.017482927
Mitotic germ cells	hmg-4	0.265994323	0.01776596
Mitotic germ cells	ifet-1	0.126176116	0.017827819
Mitotic germ cells	ccf-1	0.197573195	0.017990767
Mitotic germ cells	unc-85	0.181368599	0.018226075
Mitotic germ cells	vha-18	0.174917894	0.018265686
Mitotic germ cells	prp-4	0.113249468	0.018492627
Mitotic germ cells	acdh-3	0.167238458	0.018667779
Mitotic germ cells	mrpl-10	0.142035307	0.018724525
Mitotic germ cells	ctf-4	0.184567161	0.018756699
Mitotic germ cells	mff-2	0.19318834	0.018820223
Mitotic germ cells	rnf-1	0.199993883	0.018859478
Mitotic germ cells	cpn-1	0.172039616	0.019166761
Mitotic germ cells	T25B9.9	0.170309355	0.019234143
Mitotic germ cells	smg-3	0.156335143	0.019421815
Mitotic germ cells	T22H9.1	0.207493594	0.019484032
Mitotic germ cells	F32A11.1	0.2183192	0.019599114
Mitotic germ cells	K09G1.1	0.111303081	0.019714833
Mitotic germ cells	C03H5.3	0.191484952	0.019734113
Mitotic germ cells	mrpl-35	0.159546835	0.019847087
Mitotic germ cells	pud-4	-0.472940975	0.019914082
Mitotic germ cells	spd-5	0.176040838	0.020317765
Mitotic germ cells	lis-1	0.123973478	0.020436949
Mitotic germ cells	spas-1	0.234107464	0.020469504
Mitotic germ cells	ztf-7	0.068506707	0.020525758
Mitotic germ cells	gei-14	0.15920192	0.020629825
Mitotic germ cells	C53A3.2	0.008466168	0.021156861
Mitotic germ cells	atf-7	0.193659461	0.021240612
Mitotic germ cells	Y43H11AL.1	0.17133328	0.022026528

Mitotic germ cells	Y73E7A.2	0.155531611	0.022176884
Mitotic germ cells	algn-11	0.151831745	0.022368827
Mitotic germ cells	sel-9	0.203296202	0.022616759
Mitotic germ cells	mut-14	0.100405962	0.022704567
Mitotic germ cells	K08E3.5	0.265158751	0.022932213
Mitotic germ cells	gpcp-2	0.160026551	0.023014462
Mitotic germ cells	efa-6	0.156805403	0.023179236
Mitotic germ cells	npp-22	0.145007769	0.023224119
Mitotic germ cells	aldo-2	0.242719972	0.023236298
Mitotic germ cells	dif-1	0.196367289	0.024075142
Mitotic germ cells	vps-28	0.170333533	0.024173314
Mitotic germ cells	hecd-1	0.157333156	0.024447025
Mitotic germ cells	lsm-1	0.190397449	0.024847209
Mitotic germ cells	hus-1	0.040933604	0.024851469
Mitotic germ cells	C16A11.3	0.044367103	0.025202512
Mitotic germ cells	cul-4	0.1267219	0.025574072
Mitotic germ cells	ral-1	0.044090185	0.027744285
Mitotic germ cells	Y32B12B.2	0.185406153	0.027945369
Mitotic germ cells	gpx-5	0.424065295	0.028421733
Mitotic germ cells	ncbp-2	0.150855276	0.02882491
Mitotic germ cells	C55B7.11	0.090497944	0.029556925
Mitotic germ cells	sao-1	0.115523832	0.029617982
Mitotic germ cells	pcn-1	0.081044958	0.029704046
Mitotic germ cells	rpn-10	0.175936315	0.029993703
Mitotic germ cells	msp-36	0.170822615	0.030226793
Mitotic germ cells	ulp-2	0.150955907	0.03045818
Mitotic germ cells	cal-5	0.072298543	0.030864925
Mitotic germ cells	Y56A3A.19	0.103940513	0.031193942
Mitotic germ cells	msh-2	0.129850841	0.03142933
Mitotic germ cells	madf-8	0.139549964	0.032001504
Mitotic germ cells	cdc-37	0.24394258	0.032001504
Mitotic germ cells	dtmk-1	0.164892457	0.032160042
Mitotic germ cells	Y53H1B.2	0.02487131	0.032282641
Mitotic germ cells	T22F3.3	0.285844912	0.032539435
Mitotic germ cells	smk-1	0.179818064	0.032881924
Mitotic germ cells	lin-13	0.170675771	0.033181886
Mitotic germ cells	F29C4.2	-0.099621396	0.034064651
Mitotic germ cells	hrpf-1	0.104581417	0.034373052
Mitotic germ cells	sap-49	0.17470766	0.035550807
Mitotic germ cells	Y41D4B.11	0.199297326	0.035747981
Mitotic germ cells	fnta-1	0.107101872	0.035889293
Mitotic germ cells	myo-1	1.082477633	0.03591998

Mitotic germ cells	slc-17.2	0.203244073	0.03600788
Mitotic germ cells	Y73F8A.27	0.251399359	0.036863998
Mitotic germ cells	pqe-1	0.230984126	0.036895607
Mitotic germ cells	pqn-68	0.048447475	0.037036221
Mitotic germ cells	coq-5	0.169948386	0.037050879
Mitotic germ cells	mans-1	0.165491147	0.037153331
Mitotic germ cells	F40F11.3	0.206329485	0.037237457
Mitotic germ cells	clec-47	0.407585154	0.037538402
Mitotic germ cells	icd-2	-0.023937917	0.037762624
Mitotic germ cells	M05D6.6	0.131529123	0.03886298
Mitotic germ cells	nhr-86	0.118070876	0.038940468
Mitotic germ cells	R02F2.9	0.203381575	0.039207388
Mitotic germ cells	R31.2	0.101030805	0.039510536
Mitotic germ cells	sir-2.1	0.11338483	0.039615649
Mitotic germ cells	adss-1	0.114688016	0.040093979
Mitotic germ cells	F02A9.4	0.123685728	0.040449036
Mitotic germ cells	T07E3.3	0.119536773	0.040572215
Mitotic germ cells	F41G3.21	0.183900928	0.040766635
Mitotic germ cells	use-1	0.15373283	0.042057884
Mitotic germ cells	akt-1	0.189997594	0.042495281
Mitotic germ cells	duo-3	0.158350826	0.042515888
Mitotic germ cells	Y48G1A.4	0.153537841	0.042852801
Mitotic germ cells	exos-7	0.117686838	0.043063148
Mitotic germ cells	puf-8	0.137268913	0.043442227
Mitotic germ cells	golg-2	0.187679829	0.045255769
Mitotic germ cells	ndc-80	0.278371829	0.04543732
Mitotic germ cells	F32B6.3	0.144487654	0.045770525
Mitotic germ cells	F45F2.11	0.195491551	0.046356365
Mitotic germ cells	mvb-12	0.101259202	0.046383442
Mitotic germ cells	F44E5.1	-0.150681629	0.04665347
Mitotic germ cells	nuaf-1	0.106065846	0.046821072
Mitotic germ cells	pld-1	0.159481191	0.046892954
Mitotic germ cells	cyn-10	0.178754946	0.047444578
Mitotic germ cells	C11D2.7	0.107706777	0.047970661
Mitotic germ cells	C13F10.7	0.195504581	0.048055746
Mitotic germ cells	C28C12.12	0.137250835	0.048280536
Mitotic germ cells	tag-174	0.048751118	0.048741265
Mitotic germ cells	msd-2	0.026972623	0.048905656
Mitotic germ cells	egl-27	0.219572573	0.049330605
Mitotic germ cells	oatr-1	0.125821454	0.049370683
Mitotic germ cells	snpc-1.2	0.202967426	0.049785233

Mitotic germ cells	gip-2	0.082381697	0.050607389
Mitotic germ cells	mrps-18C	0.185528825	0.051178434
Mitotic germ cells	CD4.3	0.098656283	0.052605681
Mitotic germ cells	mel-46	0.171659095	0.053167906
Mitotic germ cells	vps-24	0.230019941	0.05428869
Mitotic germ cells	vha-17	0.182716397	0.056159148
Mitotic germ cells	K08E4.6	0.151308653	0.056294393
Mitotic germ cells	fbxa-107	0.129663598	0.056365371
Mitotic germ cells	R74.8	0.187010232	0.056589289
Mitotic germ cells	ulp-1	0.165688683	0.056792209
Mitotic germ cells	T09B4.2	0.143051417	0.057849037
Mitotic germ cells	T28D9.4	0.129716448	0.057951141
Mitotic germ cells	klp-12	0.215660841	0.058805879
Mitotic germ cells	txdc-9	0.130201765	0.058934754
Mitotic germ cells	pch-2	0.151260794	0.05927037
Mitotic germ cells	zbp-1	0.181311559	0.059683057
Mitotic germ cells	F28H7.3	-0.370377535	0.059862653
Mitotic germ cells	hcp-3	0.253771888	0.060893194
Mitotic germ cells	Y75B12B.1	0.245468317	0.061833641
Mitotic germ cells	lin-9	0.111097891	0.062664819
Mitotic germ cells	K04F10.3	0.183230351	0.063097681
Mitotic germ cells	ddl-3	0.080636198	0.064103696
Mitotic germ cells	ztf-15	0.188366634	0.064547676
Mitotic germ cells	hmg-1.1	-0.040437121	0.065787418
Mitotic germ cells	wago-4	0.142698581	0.065791731
Mitotic germ cells	F09G2.2	0.157251609	0.066288017
Mitotic germ cells	fntb-1	0.196784482	0.066965901
Mitotic germ cells	F54D8.6	0.236531842	0.067245241
Mitotic germ cells	gld-1	0.100926791	0.06747638
Mitotic germ cells	mrps-30	0.135150905	0.06760856
Mitotic germ cells	hach-1	0.145129108	0.067871898
Mitotic germ cells	trd-1	0.112132614	0.06790122
Mitotic germ cells	ruvb-1	0.104447217	0.068117952
Mitotic germ cells	F21D5.6	0.162244984	0.068134341
Mitotic germ cells	cdc-73	0.192359705	0.068260124
Mitotic germ cells	oma-1	0.20034645	0.068643367
Mitotic germ cells	tnt-4	0.638738603	0.071105428
Mitotic germ cells	epc-1	-0.298005944	0.071154257
Mitotic germ cells	F32D8.14	0.182327332	0.071235754
Mitotic germ cells	ubr-5	0.147122652	0.071403053

Mitotic germ cells	sld-5	0.059937228	0.073545194
Mitotic germ cells	sac-1	0.214599115	0.075828085
Mitotic germ cells	btb-20	0.090177341	0.076137332
Mitotic germ cells	pnn-1	0.166313572	0.077227462
Mitotic germ cells	spch-3	0.016729122	0.077312339
Mitotic germ cells	hmg-3	0.125672095	0.077574436
Mitotic germ cells	ttll-5	0.137037668	0.078668696
Mitotic germ cells	imp-2	0.166299198	0.078698925
Mitotic germ cells	taco-1	0.088957436	0.080240362
Mitotic germ cells	T04H1.2	0.14029543	0.080895331
Mitotic germ cells	C01F1.1	0.212338223	0.081967727
Mitotic germ cells	sld-2	0.135652807	0.082718109
Mitotic germ cells	T09F3.2	0.139221191	0.083988409
Mitotic germ cells	fbf-1	0.087350214	0.084047917
Mitotic germ cells	npp-18	0.181787642	0.084796724
Mitotic germ cells	F42A9.6	0.116957554	0.084878494
Mitotic germ cells	rbg-3	0.143131069	0.084953696
Mitotic germ cells	knl-1	0.204524712	0.085619402
Mitotic germ cells	C33A12.1	0.130635336	0.085964986
Mitotic germ cells	ivd-1	0.192411896	0.086392706
Mitotic germ cells	csr-1	0.12220745	0.087998209
Mitotic germ cells	ada-2	0.185478443	0.090543387
Mitotic germ cells	skr-2	0.059234245	0.090830085
Mitotic germ cells	pat-3	0.114048885	0.093289831
Mitotic germ cells	B0410.3	0.117974089	0.093811944
Mitotic germ cells	cec-7	0.204398792	0.094081047
Mitotic germ cells	jhdm-1	0.190397648	0.094693732
Mitotic germ cells	T28D9.1	0.034824514	0.095056379
Mitotic germ cells	Y54E10A.10	0.120915591	0.098114666
Mitotic germ cells	glh-4	0.192569724	0.099074436
Mitotic germ cells	dsb-2	0.141568989	0.099074436
Mitotic germ cells	vig-1	-0.033713526	0.09996417
NSM	F42G9.1	35.68323934	7.83937E-45
NSM	moag-4	35.68323934	7.83937E-45
Oocytes	col-122	1.524575464	8.6213E-263
Oocytes	col-119	1.55295974	5.8476E-243
Oocytes	col-20	1.182555371	3.8097E-217
Oocytes	col-124	1.050149917	1.4654E-210
Oocytes	col-140	1.067317276	5.1241E-207
Oocytes	col-8	2.084936533	1.9699E-194
Oocytes	col-184	1.294469485	6.1512E-165
Oocytes	col-181	1.232108209	6.0218E-161

Oocytes	col-106	1.490519904	1.468E-148
Oocytes	col-143	1.628807308	3.7126E-126
Oocytes	col-80	1.133499576	8.7941E-123
Oocytes	T03F1.11	2.246034759	1.3169E-121
Oocytes	ctc-3	0.545505553	3.2529E-111
Oocytes	ctc-1	0.525833174	8.8837E-104
Oocytes	col-19	0.876576671	2.77945E-95
Oocytes	col-98	1.563437312	1.13391E-94
Oocytes	tnc-2	2.324851035	3.78331E-92
Oocytes	mlc-3	0.838352393	6.28003E-91
Oocytes	col-160	1.312226844	3.84881E-84
Oocytes	col-101	1.312924865	5.24665E-82
Oocytes	cpr-5	1.699727004	2.92302E-78
Oocytes	hsp-12.2	1.701068336	1.33987E-75
Oocytes	col-103	1.503529608	2.23892E-72
Oocytes	tni-4	1.795581112	4.38756E-68
Oocytes	sodh-1	1.914763847	4.58138E-62
Oocytes	col-42	1.263365172	8.65254E-61
Oocytes	sip-1	-0.43764373	2.56943E-59
Oocytes	ZC116.1	2.835041867	4.50498E-59
Oocytes	col-178	1.01986108	1.43029E-55
Oocytes	col-129	0.663563678	1.43356E-55
Oocytes	col-142	1.230422955	2.581E-54
Oocytes	cpn-4	2.160794801	2.58139E-53
Oocytes	F41E6.15	1.619252818	4.12178E-53
Oocytes	C54D10.3	1.557717944	6.06473E-53
Oocytes	Y46H3C.7	-1.739983616	4.67286E-51
Oocytes	fipr-1	2.632971349	9.77274E-51
Oocytes	col-139	0.54560591	8.6482E-50
Oocytes	ctc-2	0.388222702	1.07172E-49
Oocytes	F15A4.6	1.385134913	2.10077E-49
Oocytes	fipr-2	3.007923936	5.98379E-49
Oocytes	C53C9.2	2.189636864	2.56045E-48
Oocytes	fip-2	1.87627169	1.18881E-47
Oocytes	pmt-2	0.714988782	1.0452E-46
Oocytes	Y87G2A.19	2.289678962	8.13964E-46
Oocytes	mlc-2	0.655881267	1.56565E-45
Oocytes	C24A3.2	1.36712644	1.77989E-45
Oocytes	pck-2	0.659472841	1.78489E-45
Oocytes	col-93	0.689021063	4.06232E-44
Oocytes	act-4	0.495962587	3.0951E-42
Oocytes	nduo-1	0.352924045	2.40608E-41

Oocytes	K08D12.6	1.168424708	2.85893E-41
Oocytes	asp-2	1.032110721	3.19118E-41
Oocytes	vit-5	0.826357815	1.45354E-39
Oocytes	cpl-1	0.964425384	3.66329E-39
Oocytes	myo-2	2.615867415	4.41912E-38
Oocytes	elo-6	0.862561186	1.49117E-37
Oocytes	gst-4	0.938726268	2.40429E-37
Oocytes	pud-3	-2.132609193	2.45171E-37
Oocytes	vit-2	0.699980512	1.40053E-36
Oocytes	pud-4	-2.186765575	3.96881E-36
Oocytes	T13F3.6	1.121862657	8.10928E-36
Oocytes	C14C6.5	-1.130327633	1.12918E-35
Oocytes	K03E5.2	1.074955138	1.60563E-35
Oocytes	Y73F4A.2	3.411115318	2.74883E-35
Oocytes	C17F4.7	0.564218376	3.77707E-34
Oocytes	pqn-60	2.782384691	7.45576E-34
Oocytes	fipr-10	2.587662222	2.55767E-33
Oocytes	col-81	0.514958193	3.8535E-33
Oocytes	Y46H3C.5	-1.866665722	1.08606E-32
Oocytes	ctb-1	0.305224819	1.00385E-30
Oocytes	vit-6	0.670930001	2.23394E-30
Oocytes	myo-1	2.439359554	3.76723E-30
Oocytes	fipr-5	2.311556852	5.11742E-29
Oocytes	hsp-16.2	1.32493732	7.69542E-29
Oocytes	ttr-21	2.632365042	1.6243E-28
Oocytes	Y51H7C.15	-1.83301941	2.86917E-28
Oocytes	tnt-4	2.004484534	3.5607E-28
Oocytes	F35B12.3	2.679458744	1.2369E-27
Oocytes	hsp-16.41	1.50540823	1.81349E-27
Oocytes	rpl-41.2	-0.241779487	2.57118E-27
Oocytes	fipr-7	2.407087621	8.73197E-27
Oocytes	gln-3	0.839142139	8.58624E-26
Oocytes	ndfl-4	0.28617485	4.80862E-25
Oocytes	rpl-36	-0.226218185	8.53637E-25
Oocytes	anmt-2	1.749384408	2.06545E-24
Oocytes	clec-87	-0.311598686	3.41838E-24
Oocytes	cpz-1	0.843453902	3.62661E-24

Oocytes	F11E6.3	0.848417993	9.08755E-24
Oocytes	asp-13	1.205889041	2.51752E-23
Oocytes	cpg-3	-0.406655172	4.51183E-23
Oocytes	rpl-38	-0.278148371	8.66184E-23
Oocytes	ZC116.5	2.553634595	3.94837E-22
Oocytes	fipr-11	2.731395429	8.05875E-22
Oocytes	nduo-2	0.327723049	8.58641E-22
Oocytes	Y73F4A.3	2.518944547	1.24357E-21
Oocytes	asp-5	0.708593361	1.92945E-21
Oocytes	fipr-21	0.687344366	3.39853E-21
Oocytes	fat-7	2.035570799	3.58491E-21
Oocytes	W10C8.6	1.858410391	1.42077E-20
Oocytes	cyc-2.1	0.327775185	2.62342E-20
Oocytes	rmd-1	-0.31956082	3.4515E-20
Oocytes	F36F2.1	1.653246899	6.16029E-20
Oocytes	F57F5.1	0.514361449	8.48027E-20
Oocytes	atp-2	0.236815952	8.53316E-20
Oocytes	C45G9.6	1.569054862	8.68814E-20
Oocytes	C05C10.5	-0.34536265	9.68684E-20
Oocytes	abf-5	2.120663231	1.12316E-19
Oocytes	rps-25	-0.156530834	1.43571E-19
Oocytes	vit-4	0.847505744	2.48873E-19
Oocytes	W01D2.1	-0.275728033	2.53682E-19
Oocytes	M03F4.6	0.976565321	3.39245E-19
Oocytes	ahcy-1	0.339590117	3.49319E-19
Oocytes	fipr-3	2.219003506	5.23745E-19
Oocytes	Y47G6A.33	0.730884761	1.45978E-18
Oocytes	T20G5.8	0.797376927	1.65284E-18
Oocytes	lec-2	0.641457773	3.29952E-18
Oocytes	asb-2	0.535883241	3.39117E-18
Oocytes	nlp-27	0.886092622	5.60375E-18
Oocytes	hpo-26	2.211832314	8.28215E-18
Oocytes	H37A05.4	-1.694780636	1.03161E-17
Oocytes	pqn-94	2.020958892	1.09292E-17
Oocytes	F08D12.2	2.171567443	1.24929E-17
Oocytes	F53F4.13	0.907241833	1.61818E-17
Oocytes	C45E5.4	2.277065607	4.52151E-17
Oocytes	tnt-3	1.40191157	8.8182E-17
Oocytes	Y82E9BR.3	0.168920377	9.47769E-17

Oocytes	eef-2	-0.18914756	1.05912E-16
Oocytes	rpl-34	-0.218804042	1.30975E-16
Oocytes	ttr-2	1.041753398	1.60471E-16
Oocytes	ttr-15	0.603860081	6.21112E-16
Oocytes	ttr-27	1.840808134	8.43692E-16
Oocytes	ilys-5	0.368747562	1.05639E-15
Oocytes	acer-1	0.526915475	1.10058E-15
Oocytes	F13C5.5	2.45471152	1.26963E-15
Oocytes	asg-2	0.42746908	1.29734E-15
Oocytes	atp-6	0.179151466	5.02064E-15
Oocytes	clec-47	1.718791816	5.37637E-15
Oocytes	Y9D1A.1	-1.506358619	1.24295E-14
Oocytes	msra-1	1.034393112	1.60666E-14
Oocytes	col-179	0.973951389	1.92076E-14
Oocytes	vit-3	0.647353449	2.44475E-14
Oocytes	nduo-5	0.255902873	2.46646E-14
Oocytes	rps-12	-0.149858833	2.53098E-14
Oocytes	vit-1	0.620527025	3.97676E-14
Oocytes	fipr-4	1.712144391	5.01642E-14
Oocytes	Y32H12A.8	-0.739130752	5.12562E-14
Oocytes	lev-11	0.409024401	9.19839E-14
Oocytes	cpr-4	0.854637053	1.02903E-13
Oocytes	vamp-8	1.262822489	1.09336E-13
Oocytes	grd-3	1.591489776	1.16E-13
Oocytes	C05D11.5	0.558610103	1.73124E-13
Oocytes	tos-1	-0.382252051	2.0299E-13
Oocytes	gst-10	-0.722623692	2.69589E-13
Oocytes	R04F11.2	0.222024295	3.18152E-13
Oocytes	F46H5.3	0.323293137	6.15406E-13
Oocytes	asp-4	0.816209852	6.49358E-13
Oocytes	F55G11.4	-1.771844239	8.00512E-13
Oocytes	F32A5.4	1.569131063	8.23317E-13
Oocytes	ttr-45	0.995075512	2.45227E-12
Oocytes	rpl-18	-0.151874117	2.80547E-12
Oocytes	ZK622.4	1.480457326	4.91989E-12
Oocytes	pudl-1	1.625798421	6.56632E-12

Oocytes	lips-10	0.529712014	7.56582E-12
Oocytes	cco-2	0.238703661	8.21345E-12
Oocytes	fat-3	0.838462019	1.07832E-11
Oocytes	elo-2	0.743888298	1.40668E-11
Oocytes	try-1	-0.408571236	2.14581E-11
Oocytes	C15H9.9	0.570360112	2.29334E-11
Oocytes	gpx-5	0.887515612	2.77068E-11
Oocytes	oig-3	0.812431534	3.06107E-11
Oocytes	lab-1	-0.355882098	3.19924E-11
Oocytes	C50F4.6	-0.66695555	3.25282E-11
Oocytes	fat-2	0.473943832	3.66632E-11
Oocytes	R09B3.3	-0.16344854	3.89185E-11
Oocytes	R09B3.2	-0.205282747	4.27966E-11
Oocytes	lys-1	0.547086097	5.91114E-11
Oocytes	tag-290	0.935965015	8.05446E-11
Oocytes	rps-21	-0.257577933	8.88922E-11
Oocytes	K09G1.1	0.645263515	1.03398E-10
Oocytes	marg-1	1.870429125	1.48197E-10
Oocytes	hil-4	-0.217627432	1.73454E-10
Oocytes	F18A1.7	-0.317075763	1.85182E-10
Oocytes	EEED8.3	-0.278009945	2.76728E-10
Oocytes	otub-3	-0.359772965	2.98179E-10
Oocytes	F39C12.1	-0.780775953	3.01183E-10
Oocytes	B0041.11	-1.929949822	3.10572E-10
Oocytes	T19H12.6	1.273150428	3.18291E-10
Oocytes	cth-1	0.449000516	3.51616E-10
Oocytes	C23H5.8	-0.614204384	3.66942E-10
Oocytes	calu-1	0.555523305	3.73309E-10
Oocytes	ZK863.8	1.347428183	3.761E-10
Oocytes	rgs-11	-0.604209925	4.03344E-10
Oocytes	his-60	-0.570363908	4.08749E-10
Oocytes	T02H6.11	0.239545881	4.24919E-10

Oocytes	csq-1	0.90269058	5.73142E-10
Oocytes	Y43F8B.1	0.809238345	5.89774E-10
Oocytes	nspb-12	1.328515096	6.19085E-10
Oocytes	acdh-1	0.332797403	6.67858E-10
Oocytes	spp-18	-1.030158299	7.12044E-10
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Oocytes	fipr-6	1.783528916	8.52577E-10
Oocytes	nspb-8	1.512055502	9.13752E-10
Oocytes	gpx-3	1.959439013	9.9634E-10
Oocytes	T05F1.2	-0.273349049	1.00838E-09
Oocytes	fipr-9	1.848943858	1.2702E-09
Oocytes	T24B8.5	-1.834084463	1.5739E-09
Oocytes	F29C4.2	0.272059812	3.86498E-09
Oocytes	hsp-17	1.148675991	3.8967E-09
Oocytes	unc-15	0.554072307	4.85808E-09
Oocytes	lys-4	0.545017868	5.8833E-09
Oocytes	C30G12.2	1.110317581	6.00293E-09
Oocytes	sams-1	0.526514268	6.28145E-09
Oocytes	ncx-2	1.823902258	6.58919E-09
Oocytes	dod-6	0.761436243	9.47276E-09
Oocytes	W03F8.6	1.456176235	9.48798E-09
Oocytes	crt-1	-0.281525652	1.05707E-08
Oocytes	R09F10.8	-0.519046157	1.18076E-08
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Oocytes	cyp-35A2	1.105285785	1.89726E-08
Oocytes	far-2	0.361715589	2.12011E-08
Oocytes	nkb-3	1.082391223	2.27926E-08
Oocytes	gpd-2	0.471311686	2.37868E-08
Oocytes	Y110A2AL.9	2.003764938	2.82691E-08
Oocytes	C10B5.3	1.403115963	2.89445E-08
Oocytes	spat-3	-0.706213803	3.16867E-08
Oocytes	argk-1	0.594933304	3.23179E-08
Oocytes	rpl-43	-0.160530187	3.79304E-08
Oocytes	rpl-16	-0.132532292	3.96549E-08
Oocytes	msp-36	0.378876595	4.6088E-08
Oocytes	F21C10.9	0.965018062	4.7254E-08

Oocytes	R04E5.8	-0.938176259	4.88687E-08
Oocytes	rpl-32	-0.121043099	5.00633E-08
Oocytes	ZC21.3	2.058215018	8.00028E-08
Oocytes	rps-28	-0.267442203	8.54646E-08
Oocytes	klp-12	-0.472613564	8.83574E-08
Oocytes	sqv-4	-0.33573616	9.15569E-08
Oocytes	F18E3.13	0.560901391	9.48499E-08
Oocytes	hil-5	-0.209659365	1.07233E-07
Oocytes	T02G6.5	-0.758242135	1.08173E-07
Oocytes	R12C12.5	-0.650307691	1.19363E-07
Oocytes	rps-27	-0.153557557	1.66646E-07
Oocytes	far-3	1.836799724	1.7522E-07
Oocytes	lbp-6	0.276666323	2.0594E-07
Oocytes	enpl-1	-0.271484027	2.67338E-07
Oocytes	nspb-6	1.399716763	2.759E-07
Oocytes	Y48E1B.8	1.468042581	2.81909E-07
Oocytes	act-2	-0.219069079	3.92854E-07
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Oocytes	rgs-9	-0.601613414	4.21948E-07
Oocytes	dim-1	0.414557002	4.28081E-07
Oocytes	hsp-16.48	0.782978592	4.83201E-07
Oocytes	gpd-1	-0.309746489	4.9622E-07
Oocytes	clec-1	0.668302729	5.368E-07
Oocytes	fmo-5	1.013220846	5.53214E-07
Oocytes	C23H3.2	0.870583137	5.72357E-07
Oocytes	cpr-6	0.51858116	5.74766E-07
Oocytes	C49G7.3	0.760134874	5.80885E-07
Oocytes	rpl-36.A	-0.13558037	7.86496E-07
Oocytes	ifa-1	0.964491625	8.52828E-07
Oocytes	C35B1.4	-0.795625323	8.84806E-07
Oocytes	cpg-1	-0.187555937	1.08268E-06

Oocytes	pos-1	-0.179192027	1.23439E-06
Oocytes	hsp-70	1.038562569	1.59684E-06
Oocytes	gst-2	0.008217202	1.60334E-06
Oocytes	F35A5.2	0.653725876	1.61275E-06
Oocytes	T10C6.7	-0.421231097	1.75375E-06
Oocytes	rpl-12	-0.087421267	1.79293E-06
Oocytes	Y47G6A.15	1.217231322	1.84465E-06
Oocytes	R02C2.7	1.345333254	1.86007E-06
Oocytes	spsb-2	-0.278538398	1.96899E-06
Oocytes	sdc-2	-0.940470378	2.03926E-06
Oocytes	rps-29	-0.194363914	2.04931E-06
Oocytes	W05F2.3	-0.225948463	2.2959E-06
Oocytes	cpg-2	-0.173024089	2.47382E-06
Oocytes	best-14	1.033946415	2.48191E-06
Oocytes	R10H10.3	0.786656039	3.06861E-06
Oocytes	rpl-21	-0.111235692	3.29443E-06
Oocytes	C27B7.9	0.837696552	3.30392E-06
Oocytes	ldp-1	0.43377784	3.82954E-06
Oocytes	C30F2.3	2.026020525	3.88895E-06
Oocytes	M163.8	0.627119597	4.00302E-06
Oocytes	ndk-1	-0.099690391	4.17566E-06
Oocytes	pgp-14	1.769443393	4.1855E-06
Oocytes	ZK1307.8	-0.394638163	4.58649E-06
Oocytes	ZC449.5	2.203427101	4.60004E-06
Oocytes	atp-5	0.200917858	4.66303E-06
Oocytes	myo-5	0.944879844	5.08449E-06
Oocytes	mai-2	0.227724298	5.12612E-06
Oocytes	ril-1	0.210595534	5.51529E-06
Oocytes	aqp-7	0.524956659	6.1983E-06
Oocytes	F01D5.3	-1.143681457	6.55994E-06
Oocytes	F46F2.3	0.504516954	6.84236E-06
Oocytes	mesp-1	-0.187910503	7.01598E-06

Oocytes	aldo-1	0.687766323	7.49603E-06
Oocytes	T04C12.3	1.449398009	7.86095E-06
Oocytes	vab-10	-0.467488681	8.43322E-06
Oocytes	hmg-1.1	-0.209876819	8.49937E-06
Oocytes	dpy-22	-0.678432787	8.66122E-06
Oocytes	pqn-31	1.698411917	8.7401E-06
Oocytes	din-1	-0.773110216	9.40613E-06
Oocytes	F12A10.1	0.793146967	9.4285E-06
Oocytes	polk-1	-0.32674814	9.87491E-06
Oocytes	col-96	1.587540631	1.00639E-05
Oocytes	lys-7	-0.720293921	1.00977E-05
Oocytes	T23F2.5	-0.333449463	1.03395E-05
Oocytes	R05H5.3	-0.229439659	1.10241E-05
Oocytes	spp-17	0.348046925	1.11366E-05
Oocytes	anmt-3	0.871526214	1.17619E-05
Oocytes	ant-1.1	0.099821317	1.20071E-05
Oocytes	T16G12.8	-0.483665693	1.33185E-05
Oocytes	F23D12.11	0.309661163	1.38941E-05
Oocytes	rps-5	-0.100969077	1.44847E-05
Oocytes	let-767	0.463699497	1.48738E-05
Oocytes	asp-6	0.359035771	1.54055E-05
Oocytes	F53A9.9	1.305637931	1.59513E-05
Oocytes	F14H12.3	1.762809263	1.93887E-05
Oocytes	acly-2	-0.33379332	1.96308E-05
Oocytes	ugt-41	1.235481749	1.97614E-05
Oocytes	smo-1	-0.197888655	2.1182E-05
Oocytes	F43D2.6	1.250995306	2.32248E-05
Oocytes	mex-5	-0.234714277	2.38157E-05
Oocytes	F42A8.1	0.766315277	2.41476E-05
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Oocytes	sma-1	-0.472610448	2.51461E-05
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Oocytes	Y106G6D.8	0.851408537	2.55663E-05
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Oocytes	elo-5	0.404577626	3.92003E-05
Oocytes	pqn-65	-0.628015576	4.20549E-05
Oocytes	ttr-18	0.728200739	4.31167E-05
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Oocytes	rpl-27	-0.146968954	4.83822E-05
Oocytes	F49E8.2	-0.307929238	4.90366E-05
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Oocytes	unc-22	0.72102756	5.11883E-05
Oocytes	ZK593.3	0.98071286	6.04493E-05
Oocytes	pmp-5	0.790033569	6.14817E-05
Oocytes	rps-3	-0.101935763	7.38734E-05
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Oocytes	C44B11.6	0.646174777	7.92397E-05
Oocytes	dod-19	-0.85584838	8.99498E-05
Oocytes	upb-1	0.456769243	9.72287E-05
Oocytes	unc-87	0.336762975	0.000101275
Oocytes	sql-1	-0.687903906	0.000106684
Oocytes	Y105C5A.8	0.095759108	0.000113021
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Oocytes	fat-1	0.329991523	0.000123717
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Oocytes	aqp-8	0.848764704	0.000135736
Oocytes	cts-1	0.230732693	0.00013939
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Oocytes	pcm-1	-0.580926384	0.000164882
Oocytes	rps-10	-0.105843366	0.000165684

Oocytes	rps-17	-0.116675572	0.000170574
Oocytes	ttr-29	1.639318925	0.000179177
Oocytes	F19B10.2	-0.600230922	0.00017943
Oocytes	F26F4.8	-0.496826228	0.000184973
Oocytes	rpl-35	-0.103840693	0.000190307
Oocytes	rps-30	-0.115298806	0.000209782
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Oocytes	pyk-2	0.615633361	0.000242277
Oocytes	nspb-11	1.528271477	0.000246236
Oocytes	C07D8.6	-0.355900413	0.000255719
Oocytes	mdt-26	-0.302057053	0.000256267
Oocytes	clec-88	-0.221267047	0.000257661
Oocytes	nspb-10	1.625568116	0.000262893
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Oocytes	icl-1	0.647959326	0.000327893
Oocytes	cco-1	0.151295454	0.000332507
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Oocytes	C37C3.9	-0.239741694	0.000339321
Oocytes	unc-54	0.39666081	0.000343883
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Oocytes	lipl-2	-1.907390158	0.000381435
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Oocytes	spp-23	1.013891483	0.00039227
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Oocytes	nos-2	-0.263078504	0.000404939
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Oocytes	Y17D7B.4	-0.645708253	0.000408272
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Oocytes	F14F8.8	1.730469168	0.000442587
Oocytes	rps-23	-0.097594845	0.000468316
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Oocytes	rack-1	-0.107787102	0.000712388
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Oocytes	ZK809.8	0.405737542	0.000892502
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Oocytes	cyp-29A2	1.114782352	0.001162313
Oocytes	F26E4.6	0.214379744	0.001199327
Oocytes	alh-1	0.345954512	0.001279889
Oocytes	K10D2.5	-0.248665742	0.001386459
Oocytes	mdh-1	0.246144765	0.001430618
Oocytes	apy-1	0.684526425	0.001462751
Oocytes	rpl-15	-0.101558996	0.001496719
Oocytes	F17A9.4	0.523427471	0.001511466
Oocytes	rpl-7A	-0.108116135	0.001662698
Oocytes	gcc-1	-0.773146911	0.001683464
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Oocytes	ttr-59	0.633876995	0.001792083
Oocytes	piit-1	1.74669013	0.001892282
Oocytes	rpl-30	-0.124476901	0.001925272
Oocytes	knl-2	-0.267784174	0.001930614
Oocytes	gst-7	-0.225408546	0.002018789
Oocytes	F36A2.7	0.197287629	0.002122552
Oocytes	F55C10.5	1.124644312	0.002190458
Oocytes	C49H3.3	-0.240081599	0.002274612
Oocytes	rps-0	-0.107249315	0.002310674
Oocytes	ugt-12	0.083192823	0.002335377
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Oocytes	K04B12.2	-0.821083024	0.002383662
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Oocytes	F36F2.2	0.882076708	0.002487528
Oocytes	ssp-19	-0.160796771	0.002688157
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Oocytes	nuo-6	0.284191784	0.002900217
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Oocytes	nmy-2	-0.21464058	0.003174493
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Oocytes	pqn-41	-0.437505801	0.003450039
Oocytes	F58F12.1	0.160281991	0.003468359
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Oocytes	rpl-14	-0.101761312	0.003790452
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Oocytes	F49F1.5	-1.615812548	0.004062491
Oocytes	sma-9	-0.649256242	0.004169677
Oocytes	atp-3	0.178127178	0.004258814
Oocytes	nspa-8	-0.380310159	0.004419713
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Oocytes	W01B11.6	0.560831003	0.004499261
Oocytes	clec-50	-0.361173015	0.00455557
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Oocytes	col-147	0.348317458	0.004811911
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Oocytes	F19F10.9	-0.240545581	0.005198334
Oocytes	rmd-2	-0.22841046	0.005705879
Oocytes	wago-1	-0.18211841	0.00576367
Oocytes	ncbp-2	-0.307079433	0.005778678
Oocytes	rpl-22	-0.107251335	0.006147432
Oocytes	ugt-63	0.87114373	0.00656039
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Oocytes	fmo-2	1.226645872	0.006841605
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Oocytes	his-72	-0.198856775	0.007548726
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Oocytes	atp-4	0.171132385	0.007696092
Oocytes	F18A12.7	-0.725303855	0.007736832

Oocytes	afd-1	-0.400873204	0.008163355
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Oocytes	unc-52	0.818524308	0.008795706
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Oocytes	htz-1	-0.179844544	0.009101632
Oocytes	F53F1.2	0.413513566	0.009399291
Oocytes	rsa-1	-0.229876879	0.00966411
Oocytes	R13D11.4	1.337254206	0.00980741
Oocytes	Y119C1B.10	-0.752102746	0.010205873
Oocytes	C41G7.9	0.285794302	0.010322158
Oocytes	mei-2	-0.207698639	0.010427049
Oocytes	C25H3.9	0.239733472	0.010444183
Oocytes	T28C12.4	0.343278185	0.010464758
Oocytes	ucr-1	0.3036156	0.010556333
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Oocytes	clec-91	-0.173840906	0.010724622
Oocytes	rsp-6	-0.190504228	0.010851854
Oocytes	meg-1	-0.353232107	0.011357319
Oocytes	apc-10	-0.33967496	0.011358321
Oocytes	mpc-1	0.33556503	0.011719518
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Oocytes	clec-150	-0.551801272	0.011843206
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Oocytes	bet-2	-0.678420196	0.012272734
Oocytes	fat-6	0.339703423	0.012384954
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Oocytes	cnx-1	-0.301563276	0.012634908
Oocytes	lys-2	-0.52338624	0.012863331

Oocytes	duxl-1	-0.558897211	0.013230987
Oocytes	eef-1B.1	-0.08449057	0.013522156
Oocytes	let-19	-0.500896883	0.013682732
Oocytes	hip-1	-0.371465747	0.01394405
Oocytes	smc-3	-0.342692901	0.014215031
Oocytes	ugt-22	0.74881317	0.014482608
Oocytes	R04D3.2	-0.541902921	0.014883241
Oocytes	W02B8.2	-0.718510709	0.015661086
Oocytes	C52B9.8	-0.678290538	0.015766006
Oocytes	mdh-2	0.241797078	0.015882096
Oocytes	F41G3.10	0.588795566	0.01622973
Oocytes	rme-2	-0.176903566	0.016470704
Oocytes	F19H6.4	-0.545557274	0.016678472
Oocytes	rpl-17	-0.083386957	0.016768982
Oocytes	vha-5	0.197559119	0.017030779
Oocytes	cytb-5.1	0.312788451	0.017176345
Oocytes	F35E12.9	-0.666113132	0.017684146
Oocytes	cux-7	-0.41490464	0.017742129
Oocytes	msp-57	-0.194307912	0.01800765
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Oocytes	K07E3.2	-0.672765764	0.020717026
Oocytes	dad-1	-0.187570638	0.021375595
Oocytes	pan-1	-0.758090357	0.021425718
Oocytes	vha-20	0.475263517	0.021531025
Oocytes	rps-26	-0.092515911	0.021675275
Oocytes	K03H6.2	-0.844863359	0.022091585

Oocytes	fib-1	-0.143151717	0.022095572
Oocytes	M151.4	-0.946108313	0.023142688
Oocytes	mek-1	-0.413016767	0.023362912
Oocytes	taf-11.2	-0.371670364	0.023534617
Oocytes	skpt-1	-0.295834088	0.023549022
Oocytes	ZK1320.3	0.529923832	0.023971546
Oocytes	H28G03.2	-0.514857582	0.024011765
Oocytes	Y105C5B.5	0.411799882	0.024021895
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Oocytes	ben-1	0.747795747	0.027605645
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Oocytes	gex-2	-0.591438176	0.029150403
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Oocytes	ucr-2.2	0.56118844	0.03117651
Oocytes	spp-5	-0.29372445	0.031307283
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Oocytes	gst-24	0.807663142	0.043569214
Oocytes	aqp-1	0.819311395	0.045341114
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Oocytes	tsp-16	1.197739127	0.052059862
Oocytes	ifb-1	0.481326359	0.052245355
Oocytes	blos-8	-0.446182905	0.052618818
Oocytes	rpl-2	-0.084510711	0.05329776
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Oocytes	Y43C5A.2	0.858220961	0.056415851
Oocytes	grk-1	-0.606381556	0.056480343
Oocytes	egg-2	-0.247912329	0.056553862
Oocytes	dsh-1	-0.699096068	0.058149689
Oocytes	baz-2	-0.599841702	0.059971768
Oocytes	lsm-5	-0.326944737	0.061856056
Oocytes	rla-2	-0.111395772	0.062447634
Oocytes	K02F6.7	-0.550386526	0.063653837

Oocytes	Y105E8A.25	-0.419797917	0.064348607
Oocytes	F22F4.9	0.982833838	0.06473671
Oocytes	K08D12.3	-0.178919897	0.065625596
Oocytes	F56A11.5	-0.435633702	0.066543577
Oocytes	M4.1	-0.647871872	0.067200597
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Oocytes	cpr-1	0.419398187	0.068231131
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Oocytes	ftn-2	0.242130888	0.068493479
Oocytes	oma-2	-0.187594104	0.070477495
Oocytes	catp-3	0.346737239	0.071444812
Oocytes	pen-2	-0.301954135	0.071518361
Oocytes	ZK669.2	1.403913562	0.071801206
Oocytes	Y38F2AR.9	0.188478516	0.072820964
Oocytes	nasp-2	-0.155461464	0.075237423
Oocytes	flp-1	1.534378038	0.076809722
Oocytes	F26F2.8	1.072547206	0.076980889
Oocytes	D2030.4	0.248835329	0.077894033
Oocytes	cal-3	1.483394537	0.078586025
Oocytes	T08H10.1	0.542939854	0.078880598
Oocytes	Y110A2AR.1	-0.274429438	0.079676822
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Oocytes	D1054.18	-0.386234724	0.080186464
Oocytes	C46E10.9	-0.720054538	0.080809088
Oocytes	K10H10.12	1.383664379	0.083498386
Oocytes	rme-6	-0.683445188	0.083499785
Oocytes	aagr-2	0.685510713	0.083712237
Oocytes	Y79H2A.3	-0.49886653	0.083973658
Oocytes	ckc-1	0.768540251	0.087362734
Oocytes	C01G10.15	1.429302438	0.08800182

Oocytes	his-74	-0.198573763	0.088120939
Oocytes	C50D2.10	-0.628648137	0.08951027
Oocytes	nduf-6	0.303690108	0.089557983
Oocytes	dld-1	0.311529935	0.089894938
Oocytes	scpl-3	-0.668093776	0.091338631
Oocytes	ZK632.10	-0.217798417	0.093498942
Oocytes	C25A11.10	-0.718992796	0.094921303
Oocytes	F23C8.5	0.2854981	0.094961174
Oocytes	F42G8.10	0.233153256	0.095870577
Oocytes	his-68	-0.335544199	0.096773912
Oocytes	F52H2.1	-0.816836471	0.098927307
PDA	knl-1	-34.64229469	4.50947E-74
PLM_ALM	hsp-16.48	-0.799251326	5.38932E-12
PLM_ALM	lips-1	-0.764958523	8.97052E-07
PLM_ALM	flp-20	-0.346923634	3.91211E-06
PLM_ALM	col-122	1.318162752	6.17557E-05
PLM_ALM	T20B3.14	-0.625922663	0.000250303
PLM_ALM	pifk-1	-2.415319426	0.000262979
PLM_ALM	clec-62	-2.169925001	0.001878354
PLM_ALM	col-181	1.342151224	0.002566905
PLM_ALM	col-140	0.844315341	0.011338206
PLM_ALM	pqn-44	-0.432486991	0.028700907
PLM_ALM	T07D1.3	-0.471343764	0.029992575
PLM_ALM	col-124	0.751415771	0.034754667
PLM_ALM	C45E1.4	-0.717339521	0.035661498
PLM_ALM	col-184	1.168610317	0.039593523
PLM_ALM	C04F12.5	-0.532240572	0.067597453

PLM_ALM	nlp-55	-0.807908153	0.074746752
PLM_ALM	nlp-50	-0.311591282	0.080241334
PVD_FLP	hil-5	-3.292781749	2.61008E-07
PVD_FLP	hsp-16.48	-0.803462858	0.000140188
PVD_FLP	rpl-41.2	-0.74511777	0.020833602
PVD_FLP	F55G11.4	-2.485426827	0.038515237
PVD_FLP	C05B5.8	-2.80735492	0.077565265
PVM_AVM	col-122	1.461254833	0.004095437
PVM_AVM	ctc-3	0.499439995	0.015175098
PVM_AVM	rpl-41.2	-0.408056788	0.07778717
PVM_AVM	C02B8.3	-0.49781559	0.093487837
PVR	flp-12	-0.385691906	0.047819251
RIA	R12G8.1	-1.267088934	0.025931289
RIA	col-181	1.299741555	0.026530835
RIA	F41E7.7	-0.771075712	0.028334759
RIC	C54D2.2	-1.388810421	8.49113E-08
RIC	Y76B12C.8	-0.578892873	5.76814E-07
RIC	K01D12.9	-1.415037499	3.4711E-06
RIC	flp-32	-0.546903245	5.03988E-05
RIC	F28F9.3	-0.78764696	0.000162483
RIC	msp-51	0	0.002291144
RIC	M03D4.3	-0.469082082	0.040814345
RID	col-122	1.064357694	0.041356541
RIF	F55G11.4	-33.90807463	6.2933E-175
RIF	col-73	33.69736934	2.4314E-169
RIF	dod-19	-32.8655434	3.1324E-166
RIF	rig-4	33.01386412	6.3382E-164
RIF	C05E7.2	33.01386412	6.3382E-164
RIF	dpy-5	33.01386412	6.3382E-164
RIF	Y71A12B.12	33.01386412	6.3382E-164

RIF	gpdh-1	33.01386412	6.3382E-164
RIF	mlt-10	33.01386412	6.3382E-164
RIF	T09A5.5	33.01386412	6.3382E-164
RIF	F28C6.8	33.01386412	6.3382E-164
RIF	Y53C12A.11	33.01386412	6.3382E-164
RIF	col-33	-32.02787904	1.7934E-162
RIF	R08C7.4	-32.02787904	1.7934E-162
RIF	K08F4.3	-32.02787904	1.7934E-162
RIF	F10F2.2	-32.02787904	1.7934E-162
RIF	C27F2.7	-32.02787904	1.7934E-162
RIF	Y56A3A.33	-32.02787904	1.7934E-162
RIF	T05D4.2	-32.02787904	1.7934E-162
RIF	C43H6.4	-32.02787904	1.7934E-162
RIF	klp-13	-32.02787904	1.7934E-162
RIF	sto-1	-32.02787904	1.7934E-162
RIF	tbc-1	-32.02787904	1.7934E-162
RIF	ZK662.2	-32.02787904	1.7934E-162
RIF	C06G1.2	-32.02787904	1.7934E-162
RIF	ekl-7	-32.02787904	1.7934E-162
RIF	Y23H5A.3	-32.02787904	1.7934E-162
RIF	T12F5.2	-32.02787904	1.7934E-162
RIF	nhx-8	-32.02787904	1.7934E-162
RIF	F44A2.3	-32.02787904	1.7934E-162
RIF	F53A10.2	-32.02787904	1.7934E-162
RIF	C08F1.8	-32.02787904	1.7934E-162

RIF	C25H3.14	-32.02787904	1.7934E-162
RIF	pho-13	-32.02787904	1.7934E-162
RIF	E04D5.4	-32.02787904	1.7934E-162
RIF	clec-61	-32.02787904	1.7934E-162
RIF	B0334.13	-32.02787904	1.7934E-162
RIF	Y39G8B.9	-32.02787904	1.7934E-162
RIF	F01D5.5	-32.02787904	1.7934E-162
RIF	T11G6.2	32.14798533	1.4054E-160
RIG	nlp-50	-0.650694504	0.043711648
RIG	T22E5.1	-0.856596819	0.082859291
RIH	cpg-7	-2.584962501	1.16497E-18
RIH	col-125	-3	7.41186E-09
RIH	F55G11.4	-2	0.007586639
RIM	grl-21	-2.392317423	4.48451E-07
RIM	col-97	-1.807354922	0.001939472
RIR	col-156	34.3484907	1.7913E-259
RIR	col-109	34.21479065	2.0015E-257
RIR	lgc-21	33.72344431	4.7151E-253
RIR	R10D12.1	33.72344431	4.7151E-253
RIR	F33A8.6	33.72344431	4.7151E-253
RIR	F11E6.7	33.23472038	1.1171E-250
RIR	B0303.11	33.23472038	1.1171E-250
RIR	fmo-3	33.23472038	1.1171E-250
RIR	npax-2	33.23472038	1.1171E-250
RIR	asns-2	33.23472038	1.1171E-250
RIR	Y18H1A.8	33.23472038	1.1171E-250
RIR	lron-11	33.23472038	1.1171E-250
RIR	W03D8.11	33.23472038	1.1171E-250
RIR	F54C1.1	33.23472038	1.1171E-250
RIR	fitm-2	33.23472038	1.1171E-250
RIR	ZC434.7	33.23472038	1.1171E-250
RIR	T27F6.8	33.23472038	1.1171E-250
RIR	Y73C8B.5	33.23472038	1.1171E-250

RIR	C26F1.1	33.23472038	1.1171E-250
RIR	nhr-205	33.23472038	1.1171E-250
RIR	K01D12.9	33.23472038	1.1171E-250
RIR	clec-230	33.23472038	1.1171E-250
RIR	C17F4.12	33.23472038	1.1171E-250
RIR	F56D3.1	33.23472038	1.1171E-250
RIR	F13H8.5	33.23472038	1.1171E-250
RIR	F01D5.6	33.23472038	1.1171E-250
RIR	C13B4.1	33.23472038	1.1171E-250
RIR	tag-297	33.23472038	1.1171E-250
RIR	T09B4.5	32.28577414	1.7927E-247
RIR	nep-1	32.28577414	1.7927E-247
RIR	col-115	2.584962501	3.38894E-60
RIR	col-90	2	1.14969E-39
RIR	Y95B8A.2	2	1.14969E-39
RIR	suro-1	2	1.14969E-39
RIR	T19B10.2	2	1.14969E-39
RIR	cut-2	2	1.14969E-39
RIR	dct-5	2	1.14969E-39
RIR	M106.2	2	1.14969E-39
RIR	col-73	1.584962501	2.56262E-25
RIR	R12E2.15	1	2.41924E-08
RIR	col-161	-1.459431619	3.93715E-08
RIR	nlp-52	-0.667468057	0.030727183
RIR	R11D1.12	-1.955702143	0.043431199
RIS	cut-2	2.584962501	0.004233661
RIV	M02E1.2	-0.381617209	0.03838328
RMD_DV	tyr-2	-3	1.7135E-13
RMD_DV	col-154	-3	1.7135E-13
RMD_DV	col-88	-1.321928095	0.000491167
RMD_DV	tag-267	-2	0.005385668
RMD_DV	msp-31	-0.386805238	0.009616758
RME	W08E12.2	3.754887502	0.053475493
RME	col-65	2.432959407	0.064456619
RME	F41F3.3	-1.152003093	0.090004726
RMF	T19D12.4	2.754887502	2.3926E-05
RMF	lam-1	2.169925001	0.086649602

RMF	C42D4.3	2.169925001	0.086649602
RMG	F19G12.3	-33.94017953	1.1943E-217
RMH	cut-2	-2.485426827	4.48237E-06
RMH	ctc-3	0.529287272	0.000117032
RMH	msp-57	-0.00480891	0.001914685
RMH	msp-31	-0.270389056	0.002368854
RMH	ZK742.7	-0.704278185	0.002555819
RMH	nlp-50	-0.332253356	0.005710753
Rectal gland	grd-5	5.169925001	1.047E-13
Rectal gland	grd-3	5.837020249	4.74488E-06
Rectal gland	col-125	1.584962501	0.016998589
SDQ	F26G1.15	-0.552678681	0.000571706
SDQ	Y75B7AR.1	-2.070389328	0.021285937
SIA	hsp-70	0.877498417	3.70933E-07
SIA	col-122	0.893030888	1.9569E-06
SIA	Y43F8B.2	0.568254592	1.43974E-05
SIA	ZK971.1	-0.45156969	3.77726E-05
SIA	msp-31	-0.199529668	6.96341E-05
SIA	R107.5	0.457004399	9.02907E-05
SIA	nduo-6	-0.284663346	0.000110358
SIA	hsp-16.2	0.631939836	0.000125506
SIA	msp-40	-0.419349899	0.000209957
SIA	msp-45	-0.01972484	0.000228051
SIA	rpl-41.2	-0.346167044	0.000343039
SIA	K07D4.9	-0.276472841	0.00043147
SIA	col-119	0.867863263	0.00043446
SIA	msp-152	-0.041404544	0.000514171
SIA	mks-1	-0.523857582	0.000542795
SIA	msp-57	-0.001218578	0.000759131
SIA	rps-29	-0.57329014	0.000913206

SIA	C14C6.5	-1.903955655	0.001272665
SIA	msp-76	-0.253360342	0.001465856
SIA	ctc-3	0.314901669	0.001773533
SIA	flp-14	-0.329653455	0.002517916
SIA	msp-51	-0.000184114	0.003202
SIA	hsp-16.41	0.499341508	0.004266541
SIA	rpl-38	-0.406038633	0.006232144
SIA	T23B12.8	-0.360086541	0.009651239
SIA	hsp-4	1.018032684	0.009879529
SIA	C54D10.3	0.817601399	0.010484623
SIA	dod-6	2.393863429	0.016683734
SIA	Y119D3B.21	-0.741666732	0.017812084
SIA	col-184	0.737144717	0.020812296
SIA	rps-28	-0.628979087	0.024762387
SIA	gpd-3	-0.585098973	0.03021539
SIA	col-181	0.738508925	0.063333632
SIA	ndfl-4	-0.335805717	0.063480541
SIA	ctc-1	0.294901694	0.097975194
SIB	rpl-43	-0.435994734	9.88635E-10
SIB	rpl-38	-0.489310736	3.3645E-09
SIB	msp-40	-0.270389485	3.55488E-07
SIB	rpl-41.2	-0.34798773	4.20726E-07
SIB	col-122	0.785859835	1.77485E-06
SIB	ctc-3	0.320370685	2.49073E-06
SIB	ctc-1	0.328445864	8.19507E-06
SIB	flp-21	-0.797388137	2.2696E-05
SIB	nduo-6	-0.23833717	2.61339E-05
SIB	rps-25	-0.24892096	4.58455E-05
SIB	rps-28	-0.637373504	4.63973E-05
SIB	nspd-2	-0.056297131	8.42745E-05

SIB	W01D2.1	-0.446102427	0.000140206
SIB	hsp-16.48	-0.465687351	0.000199114
SIB	C06A8.3	0.915427898	0.000311598
SIB	col-160	1.216589882	0.00074021
SIB	C54D10.3	0.74803584	0.000914143
SIB	rps-27	-0.305308186	0.001339828
SIB	rpl-34	-0.33236096	0.001608147
SIB	pqn-60	3.086058508	0.002172279
SIB	zig-2	-0.355523553	0.002278566
SIB	msp-55	-0.001582662	0.002879232
SIB	Y41C4A.17	-0.688546961	0.002962921
SIB	col-184	0.697154054	0.003174675
SIB	rpl-36	-0.303495841	0.003208443
SIB	cysl-2	-1.78361758	0.004143664
SIB	rpl-39	-0.476036129	0.006263989
SIB	C17F3.1	-0.000653336	0.01565946
SIB	msp-78	-0.107272268	0.019598873
SIB	hsp-12.2	1.251760411	0.022724927
SIB	rpl-29	-0.677368343	0.025656295
SIB	fipr-2	1.539022665	0.046517601
SIB	col-181	0.583777007	0.050859992
SIB	twk-26	-0.529992553	0.057882205
SIB	rps-10	-0.231263612	0.071967245
SIB	rps-30	-0.248060517	0.083051756
SIB	msp-49	-0.016632518	0.086252504
SIB	msp-36	-0.342968838	0.089636331
SMB	stg-1	-33.17631532	3.0401E-108
SMB	nlp-41	-33.17631532	3.0401E-108

SMB_PLN_ALN	msp-31	-0.37973376	7.6055E-12
SMB_PLN_ALN	ctc-3	0.438786552	7.00965E-10
SMB_PLN_ALN	C04E6.13	-0.333621293	7.56987E-09
SMB_PLN_ALN	rpl-41.2	-0.355400012	3.78266E-08
SMB_PLN_ALN	ins-17	-0.198317177	8.0545E-07
SMB_PLN_ALN	C14C6.5	-2.049921141	6.76777E-06
SMB_PLN_ALN	msp-152	-0.322733359	6.8965E-06
SMB_PLN_ALN	Y43F8B.2	0.442117549	7.18821E-06
SMB_PLN_ALN	dct-16	-0.619583467	2.70836E-05
SMB_PLN_ALN	msp-45	-0.042167324	6.14128E-05
SMB_PLN_ALN	col-122	0.869163829	6.31407E-05
SMB_PLN_ALN	C06A8.3	1.038813434	6.63022E-05
SMB_PLN_ALN	ssp-9	0	0.000188208
SMB_PLN_ALN	dod-6	2.231301812	0.00060187
SMB_PLN_ALN	msp-3	-0.26444704	0.000962925
SMB_PLN_ALN	msp-57	-0.000205718	0.000977751
SMB_PLN_ALN	rpl-36	-0.311928454	0.001019723
SMB_PLN_ALN	fipr-2	1.59602228	0.002590899
SMB_PLN_ALN	rpl-38	-0.332431598	0.004670775
SMB_PLN_ALN	msp-78	-0.287687551	0.004887878
SMB_PLN_ALN	nspd-10	-0.047733482	0.005870699
SMB_PLN_ALN	col-124	0.518934393	0.005876774
SMB_PLN_ALN	C17F3.1	0	0.007034453
SMB_PLN_ALN	rps-27	-0.280952507	0.007646953
SMB_PLN_ALN	msp-40	-0.248466472	0.0137309
SMB_PLN_ALN	rpl-36.A	-0.288819464	0.013800076
SMB_PLN_ALN	ZC116.1	2.096587077	0.016804812
SMB_PLN_ALN	cab-1	-0.226150559	0.018427531
SMB_PLN_ALN	cyn-7	0.307621043	0.018865026

SMB_PLN_ALN	Y119D3B.21	-0.627426258	0.021183467
SMB_PLN_ALN	col-119	0.694548347	0.022730043
SMB_PLN_ALN	col-184	0.699869555	0.036742032
SMB_PLN_ALN	msp-81	-0.217012775	0.03970257
SMB_PLN_ALN	msp-33	-0.014369228	0.056403635
SMB_PLN_ALN	C32E8.4	-0.002726099	0.058099762
SMB_PLN_ALN	hsp-16.2	0.534727356	0.063239915
SMB_PLN_ALN	hsp-16.41	0.471694575	0.067744572
SMB_PLN_ALN	C05D11.5	1.124995725	0.068939736
SMB_PLN_ALN	nspd-2	-0.090901958	0.088394859
SMB_PLN_ALN	ctc-1	0.266099133	0.095886045
SMD	M02E1.2	-0.292156524	1.10707E-13
SMD	ctc-3	0.367578248	2.1035E-08
SMD	tnc-2	1.948350795	1.55687E-06
SMD	msp-45	-0.044295108	2.2297E-06
SMD	mdl-1	-0.857702152	0.000135166
SMD	rpl-41.2	-0.299074516	0.0001514
SMD	ZC116.1	2.896721137	0.000203474
SMD	gst-4	0.848792251	0.000266109
SMD	rpl-39	-0.532559894	0.000492935
SMD	rps-29	-0.460318437	0.001344101
SMD	C32E8.4	0	0.001670928
SMD	pgal-1	-0.316878146	0.001896745
SMD	ctc-1	0.299559091	0.002230528
SMD	rpl-38	-0.346802239	0.004727577
SMD	C18A11.2	-0.800389219	0.005450981
SMD	nduo-6	-0.218732958	0.007057832
SMD	nspd-2	-0.084911059	0.01347955
SMD	C54D10.3	0.752499083	0.015178216

SMD	msp-3	-0.060017327	0.017161274
SMD	nspd-5	0	0.021682035
SMD	msp-31	-0.294327083	0.021988647
SMD	C14C6.5	-1.986667436	0.024996935
SMD	F41E7.7	-1.035053234	0.029158658
SMD	col-122	0.699945464	0.031784974
SMD	pqn-60	3.134640043	0.033853214
SMD	rps-28	-0.525774513	0.038869894
SMD	msp-76	-0.227864092	0.047443533
SMD	msp-78	-0.433076116	0.049228307
SMD	msp-57	-0.000183456	0.0619778
SMD	T20G5.8	2.802186528	0.068473754
SMD	col-20	0.499011053	0.090253714
SMD	nspd-10	-0.045770222	0.09650654
Seam cells (bus+)	cnc-4	-0.749460114	2.30349E-07
Seam cells (bus+)	B0403.5	-0.77828805	4.31691E-07
Seam cells (bus+)	ahcy-1	0.707767119	1.78043E-05
Seam cells (bus+)	C14C6.5	-1.539393308	2.24319E-05
Seam cells (bus+)	clec-50	-1.313605973	4.89315E-05
Seam cells (bus+)	grl-27	-1.129662989	0.000107994
Seam cells (bus+)	ndk-1	0.414158237	0.00028913
Seam cells (bus+)	nspd-1	-0.032235725	0.00044167
Seam cells (bus+)	D1014.5	1.115945584	0.000586675
Seam cells (bus+)	col-110	1.313621052	0.001529004
Seam cells (bus+)	F55G11.4	-2.587742958	0.002703164
Seam cells (bus+)	grl-4	-0.765278706	0.004922257
Seam cells (bus+)	cpi-1	-0.903712687	0.016765504
Seam cells (bus+)	col-154	-0.406145067	0.023149147

Seam cells (bus+)	tag-297	-0.737368304	0.023164964
Seam cells (bus+)	bli-2	0.978715022	0.030058137
Seam cells (bus+)	bus-8	0.863240532	0.040297107
Seam cells (bus+)	col-77	-0.275231612	0.041707155
Seam cells (bus+)	C42D4.3	-0.929490107	0.045969965
Seam cells (bus+)	pud-3	-2.252160154	0.063048088
Seam cells (bus+)	Y38A10A.2	1.782113588	0.06390217
Seam cells (bus+)	col-79	0.947279301	0.083800959
Seam cells (bus+)	lys-4	0.682829486	0.090254618
Seam cells (bus+)	col-167	-0.536151256	0.09865741
Seam cells (grd+)	lips-10	1.794746832	5.12225E-45
Seam cells (grd+)	C39E9.8	1.029594786	1.82934E-24
Seam cells (grd+)	col-80	-0.251600852	1.21003E-17
Seam cells (grd+)	C05D11.5	1.42594768	1.78719E-17
Seam cells (grd+)	fipr-21	-0.482244715	2.07255E-17
Seam cells (grd+)	F18E3.13	1.03979536	1.06565E-16
Seam cells (grd+)	col-122	0.954128964	4.95085E-16
Seam cells (grd+)	far-3	3.771879885	9.74853E-12
Seam cells (grd+)	ndfl-4	-0.403226752	4.01099E-11
Seam cells (grd+)	T01D1.4	1.144262294	6.72881E-11
Seam cells (grd+)	col-19	-0.234482652	2.37656E-10
Seam cells (grd+)	col-184	0.799781865	3.28556E-10
Seam cells (grd+)	fat-5	1.748129875	3.54595E-10
Seam cells (grd+)	nduo-6	-0.26462301	9.00123E-10
Seam cells (grd+)	ctc-3	0.313724776	3.64367E-09
Seam cells (grd+)	glb-1	0.708808208	4.52913E-09
Seam cells (grd+)	nlp-28	-0.827506191	8.03456E-09
Seam cells (grd+)	B0410.3	1.291186609	1.15336E-08
Seam cells (grd+)	Y34F4.4	2.321928094	2.23693E-07
Seam cells (grd+)	alkb-8	2.321928094	2.23693E-07
Seam cells (grd+)	Y66D12A.7	2.321928094	2.23693E-07
Seam cells (grd+)	dct-16	-0.550764018	2.51772E-07
Seam cells (grd+)	cysl-2	-0.969462163	2.99654E-07

Seam cells (grd+)	rpl-41.2	-0.538421637	6.32448E-07
Seam cells (grd+)	cyp-13B1	1.203578359	1.13826E-06
Seam cells (grd+)	F56H9.2	-0.689286101	4.0581E-06
Seam cells (grd+)	col-181	0.664009278	9.27178E-06
Seam cells (grd+)	abu-11	1.906890595	1.47109E-05
Seam cells (grd+)	gst-4	0.922459966	4.7128E-05
Seam cells (grd+)	F25E5.8	1.737090208	5.20854E-05
Seam cells (grd+)	C14C6.5	-1.963363745	0.000112955
Seam cells (grd+)	pck-2	0.372066495	0.000116318
Seam cells (grd+)	nlp-27	-0.415139073	0.000243147
Seam cells (grd+)	C53A3.2	0.79927815	0.00052502
Seam cells (grd+)	alh-1	0.636303258	0.000608132
Seam cells (grd+)	T03F6.4	1.807164935	0.000917343
Seam cells (grd+)	F53F1.2	0.960254871	0.001389307
Seam cells (grd+)	ctc-1	0.25467217	0.001423338
Seam cells (grd+)	hsp-16.48	-0.345729081	0.001487433
Seam cells (grd+)	T03F6.10	0.671815861	0.001924951
Seam cells (grd+)	fip-5	-0.639113833	0.002581892
Seam cells (grd+)	msp-45	-0.581777262	0.003543238
Seam cells (grd+)	tni-3	0.537960688	0.003577606
Seam cells (grd+)	Y43C5A.3	0.936899353	0.004262867
Seam cells (grd+)	rhr-1	-0.303972913	0.007633713
Seam cells (grd+)	Y119D3B.21	-0.494828352	0.007643465
Seam cells (grd+)	F44E7.2	0.532109748	0.009415813
Seam cells (grd+)	col-92	0.318111114	0.014403925
Seam cells (grd+)	sodh-1	0.895948684	0.019378684
Seam cells (grd+)	col-106	0.619748852	0.02971085
Seam cells (grd+)	T25G12.3	0.271126473	0.030866527
Seam cells (grd+)	C23H5.15	0.53651624	0.032837633
Seam cells (grd+)	C49F5.7	-0.517131895	0.039722502
Seam cells (grd+)	col-143	0.278325714	0.040085466
Seam cells (grd+)	F34D10.8	-0.194867276	0.053719369
Seam cells (grd+)	C27A7.6	0.651267846	0.054729076

Seam cells (grd+)	Y22D7AL.11	-0.776798165	0.060088718
Seam cells (grd+)	lec-11	2.218046759	0.068505211
Seam cells (grd+)	clec-50	-0.887307842	0.092192061
Seam cells (grd+)	ahcy-1	0.319661842	0.099712446
Seminal vesicle (male)	Y48A6B.8	0	5.71186E-67
Seminal vesicle (male)	zip-11	0	9.87777E-65
Seminal vesicle (male)	C49A9.10	0	9.87777E-65
Seminal vesicle (male)	B0035.18	0	9.87777E-65
Seminal vesicle (male)	efa-6	0	9.87777E-65
Seminal vesicle (male)	ggtb-1	0	9.87777E-65
Seminal vesicle (male)	ZK686.2	0	9.87777E-65
Seminal vesicle (male)	M153.1	0	9.87777E-65
Seminal vesicle (male)	set-29	0	9.87777E-65
Seminal vesicle (male)	usp-5	0	9.87777E-65
Seminal vesicle (male)	eif-3.E	0	9.87777E-65
Seminal vesicle (male)	apx-1	0	9.87777E-65
Seminal vesicle (male)	gana-1	0	9.87777E-65
Seminal vesicle (male)	efl-1	0	9.87777E-65
Seminal vesicle (male)	ZK1240.3	0	9.87777E-65
Seminal vesicle (male)	sec-6	0	9.87777E-65
Seminal vesicle (male)	eif-2Bgamma	0	9.87777E-65
Seminal vesicle (male)	D2089.8	0	9.87777E-65
Seminal vesicle (male)	mif-4	0	5.31576E-63
Seminal vesicle (male)	fbxa-11	0	5.31576E-63
Seminal vesicle (male)	pals-26	0	5.31576E-63
Seminal vesicle (male)	pcca-1	0	5.31576E-63
Seminal vesicle (male)	gei-3	0	5.31576E-63
Seminal vesicle (male)	crh-2	0	5.31576E-63
Seminal vesicle (male)	ntl-11	0	6.04723E-06
Seminal vesicle (male)	set-3	0	6.04723E-06
Seminal vesicle (male)	gld-1	0	6.04723E-06
Spermatheca bag distal	rpl-38	-0.437768588	0.001231161
Spermatheca bag distal	rpl-41.2	-0.338786549	0.028295959
Spermatheca bag distal	Y43F8B.2	1.063476969	0.098693892
Spermatheca bag proximal	Y37D8A.19	-0.338562907	1.66889E-42
Spermatheca bag proximal	rpl-38	-0.665713868	3.17398E-27
Spermatheca bag proximal	F57C2.4	-0.323611813	4.17415E-26

Spermatheca bag proximal	rps-25	-0.300959769	4.29382E-23
Spermatheca bag proximal	rpl-41.2	-0.41689978	1.11639E-22
Spermatheca bag proximal	W01D2.1	-0.700365029	8.26143E-22
Spermatheca bag proximal	rpl-43	-0.449946811	6.51077E-20
Spermatheca bag proximal	hsp-16.41	0.680828384	8.8704E-20
Spermatheca bag proximal	rpl-36	-0.350668402	2.32773E-18
Spermatheca bag proximal	hsp-16.2	0.713979486	2.91346E-18
Spermatheca bag proximal	col-135	-1.663628483	1.08295E-17
Spermatheca bag proximal	rps-21	-0.793922239	2.60181E-17
Spermatheca bag proximal	rpl-33	-0.323878793	2.34739E-16
Spermatheca bag proximal	rps-27	-0.365717563	1.78365E-14
Spermatheca bag proximal	ahcy-1	0.641785054	8.79119E-14
Spermatheca bag proximal	rla-2	-0.351338951	9.40181E-12
Spermatheca bag proximal	rps-29	-0.742138056	1.54825E-11
Spermatheca bag proximal	hsp-70	0.648512295	2.33386E-11
Spermatheca bag proximal	Y69H2.3	-0.692227985	2.36632E-11
Spermatheca bag proximal	rpl-39	-0.750965952	2.49796E-10
Spermatheca bag proximal	rpl-32	-0.225575838	4.81315E-10
Spermatheca bag proximal	rpl-34	-0.312231032	5.62361E-10
Spermatheca bag proximal	rpl-36.A	-0.277336884	1.08439E-09
Spermatheca bag proximal	ttn-1	-2.321928094	3.44615E-09
Spermatheca bag proximal	C37A2.7	-0.365519475	3.89441E-09
Spermatheca bag proximal	rpl-35	-0.218952754	5.98448E-09
Spermatheca bag proximal	cpl-1	-2.447458976	2.15339E-08
Spermatheca bag proximal	hil-2	2.459431618	4.01688E-08
Spermatheca bag proximal	rpl-21	-0.191132844	1.73426E-07

Spermatheca bag proximal	F32A5.4	0.843436267	8.72459E-07
Spermatheca bag proximal	msa-1	-2.447458976	1.13285E-06
Spermatheca bag proximal	rps-28	-0.811919496	4.62269E-06
Spermatheca bag proximal	unc-54	-1.769387072	5.00833E-06
Spermatheca bag proximal	lbp-2	-2.18442457	8.10476E-06
Spermatheca bag proximal	cytb-5.1	-2.18442457	8.10476E-06
Spermatheca bag proximal	rpl-31	-0.211210455	9.66586E-06
Spermatheca bag proximal	rps-26	-0.192037862	1.14496E-05
Spermatheca bag proximal	rps-23	-0.172698352	1.15078E-05
Spermatheca bag proximal	rps-19	-0.176094262	1.34695E-05
Spermatheca bag proximal	mlp-1	0.285181758	1.69208E-05
Spermatheca bag proximal	Y51H7C.13	-2.055141554	1.72815E-05
Spermatheca bag proximal	F02D8.4	0.677987912	2.229E-05
Spermatheca bag proximal	hel-1	2.137503523	4.54179E-05
Spermatheca bag proximal	Y37E3.8	-0.170795416	4.66935E-05
Spermatheca bag proximal	rps-12	-0.196129277	4.97458E-05
Spermatheca bag proximal	rpl-20	-0.178802196	7.97066E-05
Spermatheca bag proximal	rpl-26	-0.186217422	8.74687E-05
Spermatheca bag proximal	lbp-5	2.011972641	0.000106569
Spermatheca bag proximal	rpl-7	-0.175623223	0.000134485
Spermatheca bag proximal	ost-1	-3.129283017	0.000173752
Spermatheca bag proximal	C14F11.4	0.210762977	0.000220124
Spermatheca bag proximal	rps-18	-0.1483256	0.000495738
Spermatheca bag proximal	rpl-30	-0.226874953	0.000540593
Spermatheca bag proximal	nlp-36	1.459431618	0.00080642
Spermatheca bag proximal	rps-14	-0.136089161	0.001516636
Spermatheca bag proximal	act-2	-1.737715423	0.001621125
Spermatheca bag proximal	nurf-1	0.755184141	0.001747

Spermatheca bag proximal	rps-13	-0.174330098	0.002245939
Spermatheca bag proximal	daf-21	0.33064422	0.002296676
Spermatheca bag proximal	rpl-24.1	-0.157786999	0.002629505
Spermatheca bag proximal	C24A3.2	0.372571567	0.00270859
Spermatheca bag proximal	inx-9	2.459431618	0.002798667
Spermatheca bag proximal	ubq-2	-0.168014759	0.002914713
Spermatheca bag proximal	fat-3	-2.18442457	0.003497455
Spermatheca bag proximal	bath-42	-1.862496475	0.003750478
Spermatheca bag proximal	F55B11.3	0.195544839	0.003989943
Spermatheca bag proximal	rpl-23	-0.17355302	0.003998199
Spermatheca bag proximal	ZC247.1	1.722466024	0.009565261
Spermatheca bag proximal	zyx-1	0.270783173	0.012677187
Spermatheca bag proximal	rpl-17	-0.140367734	0.014081905
Spermatheca bag proximal	inx-8	-1.669851397	0.016395837
Spermatheca bag proximal	rps-10	-0.14630424	0.020296057
Spermatheca bag proximal	efhd-1	2.722466024	0.022435086
Spermatheca bag proximal	cpn-4	0.296223384	0.023286664
Spermatheca bag proximal	col-49	2.459431618	0.037342283
Spermatheca bag proximal	ubl-1	-0.15189231	0.044287576
Spermatheca bag proximal	C04H5.7	-0.200216028	0.049093494
Spermatheca bag proximal	C10B5.3	0.506930476	0.056622277
Spermatheca bag proximal	C06A8.8	0.682614885	0.058051351
Spermatheca bag proximal	rla-1	-0.235081312	0.062059839
Spermatheca bag proximal	mdt-19	1.722466023	0.065121248
Spermatheca bag proximal	snr-5	1.722466023	0.065121248
Spermatheca bag proximal	Y47G6A.33	1.722466023	0.065121248
Spermatheca bag proximal	W09C3.7	-1.084888897	0.069136379
Spermatheca bag proximal	rps-15	-0.14346777	0.072155335
Spermatheca bag proximal	far-1	-1.331981759	0.084526004
Spermatheca bag proximal	rpl-27	-0.222396354	0.086396967
Spermatheca bag proximal	hsp-12.2	-2.18442457	0.093501472
Spermatheca neck distal-most	Y37D8A.19	-0.271965943	5.75078E-19

Spermatheca neck distal-most	rpl-41.2	-0.470031445	1.55461E-17
Spermatheca neck distal-most	F57C2.4	-0.284912326	2.85477E-13
Spermatheca neck distal-most	rpl-36	-0.387032494	6.39954E-12
Spermatheca neck distal-most	dig-1	3.17990909	6.85307E-12
Spermatheca neck distal-most	daf-21	0.707363209	4.19058E-10
Spermatheca neck distal-most	D1054.10	0.130715966	6.70987E-10
Spermatheca neck distal-most	rpl-38	-0.571357309	7.10651E-08
Spermatheca neck distal-most	rps-29	-0.750493818	7.76496E-08
Spermatheca neck distal-most	hsp-16.41	0.7028759	8.25427E-08
Spermatheca neck distal-most	nurf-1	1.314082321	3.69386E-07
Spermatheca neck distal-most	Y69H2.3	-0.28980235	7.03325E-07
Spermatheca neck distal-most	W01D2.1	-0.590449818	1.79969E-06
Spermatheca neck distal-most	hsp-70	0.534047047	2.40224E-06
Spermatheca neck distal-most	hsp-16.2	0.648337238	4.86016E-06
Spermatheca neck distal-most	rps-25	-0.237573443	7.6775E-06
Spermatheca neck distal-most	far-1	4.048580951	8.09731E-06
Spermatheca neck distal-most	rpl-43	-0.369646355	1.38782E-05
Spermatheca neck distal-most	ZC373.2	-0.150444066	3.83353E-05
Spermatheca neck distal-most	lec-6	0.545382983	3.90685E-05
Spermatheca neck distal-most	rps-27	-0.351634503	5.22866E-05
Spermatheca neck distal-most	test-1	0.369688237	0.000198612
Spermatheca neck distal-most	lbp-1	1.857980995	0.000228198
Spermatheca neck distal-most	F47B7.1	1.857980995	0.000228198
Spermatheca neck distal-most	sodh-1	1.857980995	0.000228198
Spermatheca neck distal-most	rpl-36.A	-0.268328444	0.000480275
Spermatheca neck distal-most	rpl-34	-0.32289641	0.001782952
Spermatheca neck distal-most	F25H5.8	-0.486867362	0.005421961
Spermatheca neck distal-most	gst-7	1.442943496	0.007565352
Spermatheca neck distal-most	ZK813.3	-0.381125564	0.031488482
Spermatheca neck distal-most	rps-21	-0.567266928	0.032403059

Spermatheca neck distal-most	rpl-35	-0.178237649	0.072999188
Spermatheca neck distal-most	rps-28	-0.74333901	0.093974748
Spermatheca-Uterine junction	K11D12.13	-0.650979233	1.40871E-07
Spermatheca-Uterine junction	ZK813.7	-3.465380883	5.08106E-05
Spermatheca-Uterine junction	ctc-3	0.454109849	0.000127714
Spermatheca-Uterine junction	W09C3.7	1.874469117	0.000178644
Spermatheca-Uterine junction	D1054.10	1.348400306	0.000455503
Spermatheca-Uterine junction	unc-60	-0.635366562	0.001421944
Spermatheca-Uterine junction	F56H9.2	-0.880933526	0.003031073
Spermatheca-Uterine junction	pfn-1	-0.5879891	0.013161736
Spermatheca-Uterine junction	col-98	1.521793225	0.0169923
Spermatheca-Uterine junction	col-124	0.695969095	0.017430105
Spermatheca-Uterine junction	ctc-1	0.443012906	0.019334344
Spermatheca-Uterine junction	W02D9.7	-2.102810805	0.022497056
Spermatheca-Uterine junction	col-140	0.662078325	0.025185663
Spermatheca-Uterine junction	F25H5.8	-0.272278302	0.036186779
Spermatheca-Uterine junction	col-122	1.387941482	0.048611738
Spermatheca-Uterine junction	C07A4.3	0.34389842	0.067915936
Spermatids	nduo-6	-0.316244206	2.99379E-14
Spermatids	msrp-6	-0.397987511	2.81767E-11
Spermatids	nspd-1	-0.233827405	0.000715982
Spermatids	larp-5	-1.756944925	0.000745315
Spermatids	W09C3.7	0.323347185	0.001176472
Spermatids	nspa-8	-0.570300234	0.00131841
Spermatids	ssp-16	-0.288327804	0.003728239
Spermatids	ctb-1	-0.288747046	0.004172406
Spermatids	nspd-7	-0.251880432	0.004737318
Spermatids	nduo-4	-0.258270507	0.005011058
Spermatids	F10C1.3	-0.519317763	0.005227147

Spermatids	R09E10.6	0.210932389	0.006907244
Spermatids	dct-16	-0.544647862	0.007345098
Spermatids	F17E9.5	0.172404741	0.008245928
Spermatids	C17F3.1	-0.415747379	0.009418003
Spermatids	C12D8.9	-0.541507846	0.014274508
Spermatids	tat-3	-0.436609384	0.017674088
Spermatids	ndfl-4	-0.255682133	0.030212241
Spermatids	nduo-3	-0.191343094	0.032235047
Spermatids	F40H6.1	0.285188581	0.043652371
Spermatids	T27A3.5	-0.349594104	0.057585034
Spermatids	Y67A10A.3	-0.53120593	0.060073682
Spermatids	atp-6	-0.183130472	0.098069138
Spermatocytes	nspd-1	-0.327598936	1.82996E-14
Spermatocytes	nspd-7	-0.421558537	3.18433E-13
Spermatocytes	msrp-6	-0.389018764	1.62236E-09
Spermatocytes	F58A6.9	-0.261993432	2.40251E-06
Spermatocytes	nspd-2	-0.25051532	4.31996E-06
Spermatocytes	msrp-2	-0.206315535	4.89668E-05
Spermatocytes	sams-5	0.425230597	0.00033496
Spermatocytes	nspd-5	-0.241656458	0.000645726
Spermatocytes	D1081.12	0.249049613	0.000981265
Spermatocytes	nspa-4	-0.70863986	0.00313844
Spermatocytes	B0393.4	0.713189601	0.003989838
Spermatocytes	F10C1.3	-0.31906032	0.006549028
Spermatocytes	ZK849.6	-0.477408971	0.006857418
Spermatocytes	nlp-4	0.362016996	0.007952927
Spermatocytes	Y45F10B.3	-0.305614965	0.008090898
Spermatocytes	F56D6.19	-0.5202133	0.010348848
Spermatocytes	ssp-11	-0.587933083	0.011552969

Spermatocytes	C28C12.11	0.281859374	0.013076612
Spermatocytes	ZK1248.5	0.271333702	0.025286404
Spermatocytes	nspa-8	-0.381482154	0.028595088
Spermatocytes	T22C1.9	0.234320407	0.068484829
Spermatocytes	C47A4.5	-0.558779828	0.090047374
Spermatocytes	ZK858.2	0.541905587	0.090722233
Spermatocytes	acdh-10	-0.282726679	0.090784775
URB	cpr-1	1	2.11E-255
URB	ZK54.3	-35.26173009	6.75297E-65
URB	ZC168.2	-34.89449757	7.70996E-64
URB	T05C7.7	-34.15039843	2.42498E-62
URB	egl-18	-34.15039843	2.42498E-62
URB	nhr-78	-34.15039843	2.42498E-62
URB	F42A9.9	-34.15039843	2.42498E-62
URB	nhr-34	-34.15039843	2.42498E-62
URB	F25H8.1	-34.15039843	2.42498E-62
URB	Y50D7A.8	-34.15039843	2.42498E-62
URB	pals-19	-34.15039843	2.42498E-62
URB	sms-3	-34.15039843	2.42498E-62
URB	Y71H2AM.4	-34.15039843	2.42498E-62
URB	nhr-6	-34.15039843	2.42498E-62
URB	cid-1	-34.15039843	2.42498E-62
URB	coq-2	-34.15039843	2.42498E-62
URB	henn-1	-34.15039843	2.42498E-62
URB	rsp-8	-34.15039843	2.42498E-62

URB	Y79H2A.3	-34.15039843	2.42498E-62
URB	ani-1	-34.15039843	2.42498E-62
URB	sax-1	-34.15039843	2.42498E-62
URB	sem-5	-34.15039843	2.42498E-62
URB	col-180	-34.15039843	2.42498E-62
URB	C34E7.3	-34.15039843	2.42498E-62
URB	F11C1.7	-34.15039843	2.42498E-62
URB	epn-1	-34.15039843	2.42498E-62
URB	dhs-30	-34.15039843	2.42498E-62
URB	npr-23	-34.15039843	2.42498E-62
URB	crtc-1	-34.15039843	2.42498E-62
URB	scpl-3	-34.15039843	2.42498E-62
URB	eaf-1	-34.15039843	2.42498E-62
URB	ugt-25	-34.15039843	2.42498E-62
URB	dpy-5	-34.15039843	2.42498E-62
URB	rpb-5	-34.15039843	2.42498E-62
URB	cup-2	-34.15039843	2.42498E-62
URB	C35E7.4	-34.15039843	2.42498E-62
URB	col-65	-34.15039843	2.42498E-62
URB	K11B4.1	-34.15039843	2.42498E-62
URB	cnc-4	-34.15039843	2.42498E-62
URB	Y45G5AM.7	-34.15039843	2.42498E-62
URB	C02E7.7	-34.15039843	2.42498E-62

URB	abu-15	-34.15039843	2.42498E-62
URB	F26F12.8	-34.15039843	2.42498E-62
URB	F07G11.1	-34.15039843	2.42498E-62
URB	rgef-1	-34.15039843	2.42498E-62
URB	F25B3.5	-34.15039843	2.42498E-62
URB	C35A5.11	-34.15039843	2.42498E-62
URB	col-154	-34.15039843	2.42498E-62
URB	R11H6.2	-34.15039843	2.42498E-62
URB	Y59A8B.24	-34.15039843	2.42498E-62
URB	aagr-2	-34.15039843	2.42498E-62
URB	srh-39	-34.15039843	2.42498E-62
URB	ZK669.3	-34.15039843	2.42498E-62
URB	taf-13	-34.15039843	2.42498E-62
URB	cyn-16	-34.15039843	2.42498E-62
URB	W01G7.4	-34.15039843	2.42498E-62
URB	Y53F4B.9	-34.15039843	2.42498E-62
URB	T27A10.2	-3.169925001	7.5093E-18
URX_AQR_PQR	nlp-3	-1.089364862	0.005833922
URX_AQR_PQR	fbp-1	-1.339016627	0.052692339
URY	col-161	-2.321928095	0.002566079
Uterine muscle	Y47G6A.15	-0.435703163	2.695E-18
Uterine muscle	act-1	-0.408562053	1.73664E-14
Uterine muscle	Y57G11C.40	0.471012771	1.17331E-12
Uterine muscle	F56H9.2	-0.46789955	5.40756E-11

Uterine muscle	rpl-43	-0.540627522	4.89612E-10
Uterine muscle	rpl-41.2	-0.403907846	5.66336E-08
Uterine muscle	R06C1.4	-0.455668388	9.90899E-07
Uterine muscle	M02D8.6	-0.621903058	1.69295E-06
Uterine muscle	W01D2.1	-0.684422569	8.16231E-06
Uterine muscle	rpl-36	-0.359197688	1.13689E-05
Uterine muscle	rpl-39	-0.984063682	2.33933E-05
Uterine muscle	rpl-38	-0.529081204	4.84844E-05
Uterine muscle	ctc-3	0.582866858	0.000148165
Uterine muscle	rps-25	-0.257902796	0.000173092
Uterine muscle	rpl-36.A	-0.353891194	0.000276201
Uterine muscle	unc-15	-0.212590991	0.000294492
Uterine muscle	ctc-1	0.483132659	0.00064659
Uterine muscle	rpl-35	-0.257464232	0.000649176
Uterine muscle	col-138	-1.540568381	0.002033774
Uterine muscle	W02B8.1	1.781359713	0.002099736
Uterine muscle	rpl-32	-0.251522252	0.003195995
Uterine muscle	C06G3.3	-0.324412928	0.003891815
Uterine muscle	rps-28	-1.26129558	0.003910909
Uterine muscle	rpl-34	-0.332254288	0.003953367
Uterine muscle	hsp-16.48	-0.393240541	0.004138433
Uterine muscle	hsp-70	0.333424774	0.004143197
Uterine muscle	C37A2.7	-0.478546961	0.00451784
Uterine muscle	rps-27	-0.326290013	0.004627722
Uterine muscle	act-4	-0.136971777	0.012360687

Uterine muscle	rpl-21	-0.223851895	0.015163009
Uterine muscle	hsp-16.2	0.526339558	0.017411686
Uterine muscle	ubq-2	-0.232782377	0.025543902
Uterine muscle	rpl-30	-0.316528788	0.046278393
Uterine muscle	tag-18	-0.152166227	0.05475118
Uterine muscle	cpn-3	0.104006921	0.079243797
Uterine seam cells	Y22D7AR.10	-0.569285141	6.12259E-12
Uterine seam cells	Y45F10C.4	-0.297257661	8.23229E-12
Uterine seam cells	T12B5.15	-0.323472222	5.80473E-06
Uterine seam cells	abf-2	-1.169001411	5.53181E-05
Uterine seam cells	C25E10.8	-1.514104917	0.00057711
Uterine seam cells	ZK669.3	0.829180085	0.000872216
Uterine seam cells	Y47D7A.13	-2.750771393	0.001569842
Uterine seam cells	C14F11.4	2.056583528	0.002474475
Uterine seam cells	col-119	1.618176632	0.002908619
Uterine seam cells	ZC373.2	-2.265344566	0.005529076
Uterine seam cells	col-98	2.374135872	0.009362251
Uterine seam cells	dhs-21	0.479593249	0.00939123
Uterine seam cells	srd-5	-1.528378972	0.023303868
Uterine toroid	ost-1	-32.35354468	0
Uterine toroid	rnp-5	-32.35354468	0
Uterine toroid	far-1	-32.35354468	0
Uterine toroid	T16G12.4	-32.35354468	0
Uterine toroid	C18B2.3	-32.35354468	0
Uterine toroid	R160.3	-32.35354468	0
Uterine toroid	K09E9.4	-32.35354468	0

Uterine toroid	ncbp-1	-32.35354468	0
Uterine toroid	pdpr-1	-32.35354468	0
Uterine toroid	T19B10.8	-32.35354468	0
Uterine toroid	T09E8.4	-32.35354468	0
Uterine toroid	T01C3.11	-32.35354468	0
Uterine toroid	fkb-6	-32.35354468	0
Uterine toroid	smu-2	-32.35354468	0
Uterine toroid	F59B10.4	-32.35354468	0
Uterine toroid	rsp-1	-32.35354468	0
Uterine toroid	gsy-1	-32.35354468	0
Uterine toroid	rps-25	-0.647052397	0.00039821
Uterine toroid	cpi-1	0.371684969	0.002821425
Uterine toroid	ttr-2	0.351187286	0.041148722
Uterine-vulval cells	ule-4	-0.210517864	5.99197E-15
Uterine-vulval cells	F30A10.13	-0.520449774	1.58709E-12
Uterine-vulval cells	Y69H2.3	-1.461426762	1.52512E-08
Uterine-vulval cells	col-124	1.139675432	2.22862E-08
Uterine-vulval cells	Y22D7AR.10	-0.372419237	5.80419E-08
Uterine-vulval cells	grd-14	3.043741463	2.59727E-07
Uterine-vulval cells	col-20	1.171533701	4.15288E-06
Uterine-vulval cells	tbc-7	-0.842949747	3.7425E-05
Uterine-vulval cells	col-122	1.390353599	8.44311E-05
Uterine-vulval cells	col-98	1.788628239	0.000116501
Uterine-vulval cells	B0001.2	-3.213646377	0.000129927
Uterine-vulval cells	W09C3.7	2.541241121	0.000143641
Uterine-vulval cells	Y105E8B.9	0.865145516	0.000208029
Uterine-vulval cells	ifa-4	0.498015217	0.000712485
Uterine-vulval cells	dhs-21	0.475869506	0.000833789

Uterine-vulval cells	C53B7.2	-2.851076297	0.000882947
Uterine-vulval cells	col-140	0.961092426	0.002508614
Uterine-vulval cells	ttr-2	0.204026996	0.003516682
Uterine-vulval cells	C10G8.4	-0.362896762	0.005126578
Uterine-vulval cells	F11E6.3	1.909610354	0.007732234
Uterine-vulval cells	col-42	1.991038342	0.010628076
Uterine-vulval cells	hsp-16.2	0.56519788	0.011778279
Uterine-vulval cells	C25E10.8	-0.896855142	0.014472741
Uterine-vulval cells	rpl-36	-0.386503124	0.014658564
Uterine-vulval cells	ifa-1	0.476983307	0.020724115
Uterine-vulval cells	col-139	1.197389782	0.022963017
Uterine-vulval cells	rpl-38	-0.528960851	0.02777247
Uterine-vulval cells	F30A10.14	-0.236056611	0.027802276
Uterine-vulval cells	col-119	1.113712107	0.034422992
Uterine-vulval cells	col-103	1.765571677	0.040121332
Uterine-vulval cells	F35E12.6	-0.863931932	0.046617098
Uterine-vulval cells	F09E10.1	-2.282490065	0.068167084
Uterine-vulval cells	col-184	1.436300001	0.0760078
Uterine-vulval cells	hsp-16.41	0.579446546	0.078487899
VC	flp-28	-0.212880002	1.20654E-07
VC	ctc-3	0.552574178	5.2143E-06
VC	B0252.8	-0.557284838	4.55122E-05
VC	col-98	1.65151735	0.000294446
VC	F33H1.6	-0.289923196	0.000350707
VC	nlp-6	-0.179611582	0.000770481
VC	col-20	0.747022773	0.008126477
VC	ctc-1	0.494142317	0.093613625
VC_4_5	Y43C5A.3	-2.584962501	2.7498E-06
VC_4_5	far-8	-2.584962501	2.7498E-06
VC_4_5	B0303.11	-2.584962501	2.7498E-06

VD_DD	T20B3.14	-0.5772213	5.15036E-21
VD_DD	hsp-16.48	-0.862291105	1.17332E-17
VD_DD	ctc-3	0.452226887	6.39671E-15
VD_DD	col-122	0.995486036	1.45526E-11
VD_DD	col-184	0.946331501	3.06309E-08
VD_DD	ctc-1	0.379023115	6.63261E-08
VD_DD	col-119	0.737061529	8.25553E-08
VD_DD	col-124	0.550898113	1.71455E-06
VD_DD	C16D2.2	-0.567052238	5.09987E-06
VD_DD	col-140	0.515751954	1.16195E-05
VD_DD	F53C11.9	-0.582666849	1.59846E-05
VD_DD	nspd-2	-0.013301084	1.8378E-05
VD_DD	rpl-41.2	-0.311683085	2.35997E-05
VD_DD	B0252.8	-0.367671844	9.65145E-05
VD_DD	msp-40	-0.211102299	0.000169103
VD_DD	C14C6.5	-1.742602767	0.000237127
VD_DD	col-98	0.972163718	0.000256748
VD_DD	F15A4.6	1.872080601	0.000307403
VD_DD	ahcy-1	0.733014072	0.0003745
VD_DD	rps-28	-0.590839753	0.000406192
VD_DD	F48D6.4	-1.246949391	0.000512681
VD_DD	msp-57	-0.000450022	0.00052245
VD_DD	rpl-38	-0.36595021	0.000587849
VD_DD	ssp-9	0	0.001259685
VD_DD	C04F12.5	-0.326930189	0.00218567
VD_DD	C54D10.3	0.782888095	0.002783226
VD_DD	msp-31	-0.173483131	0.004485756
VD_DD	C05D11.5	0.788040171	0.009896508
VD_DD	nspd-5	0	0.012378631
VD_DD	F58A6.9	0	0.012695646
VD_DD	msp-3	-0.084705828	0.015895345

VD_DD	msp-55	-6.20133E-05	0.02053854
VD_DD	tnc-2	1.640856604	0.02067336
VD_DD	msp-33	-0.053849344	0.021950921
VD_DD	F34D10.8	0	0.026396337
VD_DD	ilys-4	0.207852822	0.028112551
VD_DD	W01D2.1	-0.374914507	0.030703789
VD_DD	msp-78	-0.291998778	0.035035671
VD_DD	nspd-1	-0.011678594	0.047988844
VD_DD	col-181	0.560779593	0.058131145
VD_DD	T20G5.8	2.491706174	0.077644528
VD_DD	ssp-11	0	0.085346009
VD_DD	unc-76	-0.271011808	0.092764087
XXX	col-125	-3.115477217	9.48498E-12
XXX	dyc-1	-3.700439718	2.33584E-07
XXX	T22B7.3	-3.115477217	0.003946451
XXX	F46H5.2	-3.115477217	0.003946451
XXX	T24D5.1	-3.115477217	0.003946451
XXX	coh-4	-3.115477217	0.003946451
cat-4(+)ptps-1(+) intestine anterior	F21C10.9	1.856167855	1.7403E-173
cat-4(+)ptps-1(+) intestine anterior	cth-1	0.640838055	1.4595E-135
cat-4(+)ptps-1(+) intestine anterior	argk-1	0.843842526	1.5366E-131
cat-4(+)ptps-1(+) intestine anterior	acdh-1	0.733862293	7.0664E-111
cat-4(+)ptps-1(+) intestine anterior	gst-4	1.401162327	1.7839E-104
cat-4(+)ptps-1(+) intestine anterior	ahcy-1	0.740882583	5.78266E-81
cat-4(+)ptps-1(+) intestine anterior	gst-10	-0.698521992	7.44453E-74
cat-4(+)ptps-1(+) intestine anterior	F48D6.4	-0.781568985	2.50085E-64
cat-4(+)ptps-1(+) intestine anterior	gst-13	-0.800668294	1.49378E-63
cat-4(+)ptps-1(+) intestine anterior	C14C6.5	-0.96537733	4.47861E-63
cat-4(+)ptps-1(+) intestine anterior	rpl-41.2	-0.425607664	7.78487E-63
cat-4(+)ptps-1(+) intestine anterior	cpr-5	1.085484615	7.45546E-62

cat-4(+)ptps-1(+) intestine anterior	pud-4	-2.801795728	2.36581E-61
cat-4(+)ptps-1(+) intestine anterior	dct-16	-0.315581861	9.16788E-57
cat-4(+)ptps-1(+) intestine anterior	pud-3	-2.59616169	4.49286E-54
cat-4(+)ptps-1(+) intestine anterior	C18H9.6	1.565755959	3.98737E-50
cat-4(+)ptps-1(+) intestine anterior	spp-18	-1.784303656	3.37112E-48
cat-4(+)ptps-1(+) intestine anterior	T24B8.5	-3.446996042	9.38992E-47
cat-4(+)ptps-1(+) intestine anterior	tnc-2	2.122707088	2.50714E-42
cat-4(+)ptps-1(+) intestine anterior	T03F1.11	1.923558488	1.07235E-41
cat-4(+)ptps-1(+) intestine anterior	T22B7.7	1.012955565	1.26502E-39
cat-4(+)ptps-1(+) intestine anterior	cat-4	0.572638542	1.99173E-39
cat-4(+)ptps-1(+) intestine anterior	ZK742.3	0.93412219	4.32824E-37
cat-4(+)ptps-1(+) intestine anterior	C30G12.2	0.914011208	8.31867E-37
cat-4(+)ptps-1(+) intestine anterior	smd-1	0.979471421	9.80579E-36
cat-4(+)ptps-1(+) intestine anterior	F01D5.3	-1.327706353	2.20351E-35
cat-4(+)ptps-1(+) intestine anterior	lec-10	-0.379505705	2.82203E-34
cat-4(+)ptps-1(+) intestine anterior	bigr-1	1.532056761	8.19133E-32
cat-4(+)ptps-1(+) intestine anterior	R09B3.3	-0.423059963	9.82879E-31
cat-4(+)ptps-1(+) intestine anterior	spp-2	-1.148248055	6.96193E-30
cat-4(+)ptps-1(+) intestine anterior	lec-9	-0.311978361	2.77881E-29
cat-4(+)ptps-1(+) intestine anterior	fat-7	2.189203212	2.10861E-27
cat-4(+)ptps-1(+) intestine anterior	W01D2.1	-0.419437163	2.6198E-27
cat-4(+)ptps-1(+) intestine anterior	spp-5	-0.592514259	2.958E-27
cat-4(+)ptps-1(+) intestine anterior	nduo-6	-0.290784761	4.87554E-27
cat-4(+)ptps-1(+) intestine anterior	col-122	0.702822557	7.02751E-27
cat-4(+)ptps-1(+) intestine anterior	act-5	0.285558292	2.99787E-26
cat-4(+)ptps-1(+) intestine anterior	pud-1.2	-2.748832475	8.22347E-26
cat-4(+)ptps-1(+) intestine anterior	F22H10.3	-0.349394171	3.26442E-25
cat-4(+)ptps-1(+) intestine anterior	gln-3	0.503502565	3.36673E-25
cat-4(+)ptps-1(+) intestine anterior	F49F1.5	-2.212628204	4.46518E-25
cat-4(+)ptps-1(+) intestine anterior	acs-1	0.643209816	1.51083E-24

cat-4(+)ptps-1(+) intestine anterior	lys-2	-1.067039174	4.19912E-24
cat-4(+)ptps-1(+) intestine anterior	M02H5.8	0.441648947	2.36641E-23
cat-4(+)ptps-1(+) intestine anterior	Y73F4A.2	3.184810753	3.24935E-23
cat-4(+)ptps-1(+) intestine anterior	lec-8	-0.428108101	1.04281E-22
cat-4(+)ptps-1(+) intestine anterior	F28H7.3	-0.657772094	1.35853E-22
cat-4(+)ptps-1(+) intestine anterior	ZC395.5	-1.297365179	1.35368E-21
cat-4(+)ptps-1(+) intestine anterior	cpn-4	2.432029828	2.11147E-21
cat-4(+)ptps-1(+) intestine anterior	clec-50	-0.671944209	4.06286E-21
cat-4(+)ptps-1(+) intestine anterior	F53F1.2	1.255504599	6.09887E-21
cat-4(+)ptps-1(+) intestine anterior	far-3	2.63113993	7.26186E-21
cat-4(+)ptps-1(+) intestine anterior	pqn-60	3.385601168	9.02847E-21
cat-4(+)ptps-1(+) intestine anterior	pck-2	0.474051923	1.58156E-20
cat-4(+)ptps-1(+) intestine anterior	lec-6	-0.27367466	4.18071E-20
cat-4(+)ptps-1(+) intestine anterior	acs-2	1.916547227	4.20096E-20
cat-4(+)ptps-1(+) intestine anterior	iff-2	0.297831349	1.64829E-19
cat-4(+)ptps-1(+) intestine anterior	dod-3	-1.202988929	1.93847E-19
cat-4(+)ptps-1(+) intestine anterior	nhr-68	0.609557445	2.00678E-19
cat-4(+)ptps-1(+) intestine anterior	rpl-38	-0.323785816	3.03951E-19
cat-4(+)ptps-1(+) intestine anterior	ZC116.1	3.638758165	4.5395E-19
cat-4(+)ptps-1(+) intestine anterior	C06A8.3	0.78382788	1.95773E-18
cat-4(+)ptps-1(+) intestine anterior	C53A3.2	1.148274645	3.52274E-18
cat-4(+)ptps-1(+) intestine anterior	ret-1	0.668877218	4.26837E-18
cat-4(+)ptps-1(+) intestine anterior	F44E7.2	1.011394599	5.62063E-17
cat-4(+)ptps-1(+) intestine anterior	fipr-2	2.166058323	1.95274E-16
cat-4(+)ptps-1(+) intestine anterior	rpl-39	-0.423555433	2.04174E-16
cat-4(+)ptps-1(+) intestine anterior	C45G9.6	2.158781823	2.42584E-16
cat-4(+)ptps-1(+) intestine anterior	C54D10.3	0.96118162	3.8996E-16
cat-4(+)ptps-1(+) intestine anterior	ilys-5	-0.336756278	1.21217E-15
cat-4(+)ptps-1(+) intestine anterior	clec-41	-1.028678581	1.41738E-15
cat-4(+)ptps-1(+) intestine anterior	emo-1	0.218350599	1.66913E-15
cat-4(+)ptps-1(+) intestine anterior	cts-1	0.300132515	2.43812E-15
cat-4(+)ptps-1(+) intestine anterior	clec-150	-0.869664779	3.23726E-15
cat-4(+)ptps-1(+) intestine anterior	msra-1	1.075157384	4.10512E-15
cat-4(+)ptps-1(+) intestine anterior	C53C9.2	2.178377697	4.41051E-15

cat-4(+)ptps-1(+) intestine anterior	Y87G2A.19	2.254586915	4.429E-15
cat-4(+)ptps-1(+) intestine anterior	gdh-1	-0.363458358	9.14705E-15
cat-4(+)ptps-1(+) intestine anterior	rps-27	-0.23466719	1.00451E-14
cat-4(+)ptps-1(+) intestine anterior	col-119	0.53029516	2.30395E-14
cat-4(+)ptps-1(+) intestine anterior	ctc-3	0.272598587	2.32229E-14
cat-4(+)ptps-1(+) intestine anterior	R09B3.2	-0.510644623	4.21519E-14
cat-4(+)ptps-1(+) intestine anterior	K06A4.7	-0.744112072	7.73439E-14
cat-4(+)ptps-1(+) intestine anterior	rps-29	-0.348498821	9.4775E-14
cat-4(+)ptps-1(+) intestine anterior	C17F4.7	0.381934178	1.1013E-13
cat-4(+)ptps-1(+) intestine anterior	rps-28	-0.437533131	1.64635E-13
cat-4(+)ptps-1(+) intestine anterior	Y48A6B.7	-0.654868656	1.70735E-13
cat-4(+)ptps-1(+) intestine anterior	rpl-19	0.155873077	1.74727E-13
cat-4(+)ptps-1(+) intestine anterior	gpdh-2	0.896983036	1.83059E-13
cat-4(+)ptps-1(+) intestine anterior	col-124	0.374882633	1.84579E-13
cat-4(+)ptps-1(+) intestine anterior	F55G11.4	-1.555513791	2.45036E-13
cat-4(+)ptps-1(+) intestine anterior	ndk-1	0.130796764	3.75027E-13
cat-4(+)ptps-1(+) intestine anterior	rps-25	-0.162094294	6.93898E-13
cat-4(+)ptps-1(+) intestine anterior	hprt-1	0.309984613	8.02439E-13
cat-4(+)ptps-1(+) intestine anterior	col-184	0.568670453	8.51462E-13
cat-4(+)ptps-1(+) intestine anterior	gst-38	-1.034265474	9.07282E-13
cat-4(+)ptps-1(+) intestine anterior	F17A9.4	0.578888556	1.03186E-12
cat-4(+)ptps-1(+) intestine anterior	atf-5	0.494862296	1.25632E-12
cat-4(+)ptps-1(+) intestine anterior	col-98	0.719968769	1.47316E-12
cat-4(+)ptps-1(+) intestine anterior	gst-7	-0.442983407	1.56184E-12
cat-4(+)ptps-1(+) intestine anterior	F31F7.1	0.637088768	2.16396E-12
cat-4(+)ptps-1(+) intestine anterior	col-181	0.535861607	2.69285E-12
cat-4(+)ptps-1(+) intestine anterior	rpl-36.A	-0.222388313	2.74043E-12
cat-4(+)ptps-1(+) intestine anterior	lys-7	-0.762014435	2.81259E-12
cat-4(+)ptps-1(+) intestine anterior	col-20	0.391896623	3.85839E-12
cat-4(+)ptps-1(+) intestine anterior	dhs-26	1.098795445	7.51346E-12
cat-4(+)ptps-1(+) intestine anterior	pmt-2	0.32465415	7.77512E-12
cat-4(+)ptps-1(+) intestine anterior	sams-1	0.565391184	7.78093E-12
cat-4(+)ptps-1(+) intestine anterior	F41E6.15	1.277027311	7.78681E-12

cat-4(+)ptps-1(+) intestine anterior	D1054.18	-0.49429573	8.00255E-12
cat-4(+)ptps-1(+) intestine anterior	myo-2	2.630468054	9.51356E-12
cat-4(+)ptps-1(+) intestine anterior	clec-47	1.43712534	1.48107E-11
cat-4(+)ptps-1(+) intestine anterior	rpl-43	-0.2421126	1.51006E-11
cat-4(+)ptps-1(+) intestine anterior	C05D11.5	0.753854561	1.57336E-11
cat-4(+)ptps-1(+) intestine anterior	cpz-1	0.620167774	1.64616E-11
cat-4(+)ptps-1(+) intestine anterior	lipl-5	-0.878999248	1.70635E-11
cat-4(+)ptps-1(+) intestine anterior	sucl-2	0.463876815	3.12007E-11
cat-4(+)ptps-1(+) intestine anterior	D1054.8	0.392726441	3.89052E-11
cat-4(+)ptps-1(+) intestine anterior	F32D1.5	0.309583735	4.47579E-11
cat-4(+)ptps-1(+) intestine anterior	fipr-1	2.152929509	5.2121E-11
cat-4(+)ptps-1(+) intestine anterior	msp-31	-0.810435346	8.0828E-11
cat-4(+)ptps-1(+) intestine anterior	ttr-21	2.487606273	9.06155E-11
cat-4(+)ptps-1(+) intestine anterior	ech-7	-0.568149407	1.02497E-10
cat-4(+)ptps-1(+) intestine anterior	ZK593.3	1.422088562	1.19563E-10
cat-4(+)ptps-1(+) intestine anterior	F32D8.12	0.850220555	2.42126E-10
cat-4(+)ptps-1(+) intestine anterior	acbp-1	-0.266144646	2.77035E-10
cat-4(+)ptps-1(+) intestine anterior	rps-21	-0.321943595	3.21381E-10
cat-4(+)ptps-1(+) intestine anterior	E02H4.7	-1.652378255	3.43547E-10
cat-4(+)ptps-1(+) intestine anterior	fipr-10	2.927859739	3.8875E-10
cat-4(+)ptps-1(+) intestine anterior	ctc-1	0.257779402	5.93071E-10
cat-4(+)ptps-1(+) intestine anterior	C29F7.3	0.349055027	6.86548E-10
cat-4(+)ptps-1(+) intestine anterior	rpl-11.2	0.18308439	7.38346E-10
cat-4(+)ptps-1(+) intestine anterior	T28F4.5	-0.482249881	1.0402E-09
cat-4(+)ptps-1(+) intestine anterior	ndfl-4	-0.275766728	1.56752E-09
cat-4(+)ptps-1(+) intestine anterior	hsp-12.2	0.905350361	1.63641E-09
cat-4(+)ptps-1(+) intestine anterior	pes-9	-0.485403116	1.94947E-09
cat-4(+)ptps-1(+) intestine anterior	asp-6	-0.429645199	2.00658E-09
cat-4(+)ptps-1(+) intestine anterior	R53.4	0.184452156	2.01761E-09
cat-4(+)ptps-1(+) intestine anterior	farl-11	1.005043839	2.07901E-09
cat-4(+)ptps-1(+) intestine anterior	col-140	0.334209868	2.10769E-09
cat-4(+)ptps-1(+) intestine anterior	F35B12.3	2.983338085	2.3282E-09
cat-4(+)ptps-1(+) intestine anterior	Y119D3B.21	-0.202591256	2.53524E-09
cat-4(+)ptps-1(+) intestine anterior	gst-27	-0.33011333	3.48135E-09

cat-4(+)ptps-1(+) intestine anterior	tba-4	0.652134315	4.72087E-09
cat-4(+)ptps-1(+) intestine anterior	mlc-3	0.412716192	5.60315E-09
cat-4(+)ptps-1(+) intestine anterior	msp-40	-0.649836497	5.84733E-09
cat-4(+)ptps-1(+) intestine anterior	fip-2	0.93529772	7.70025E-09
cat-4(+)ptps-1(+) intestine anterior	ZK673.1	0.57657261	8.89615E-09
cat-4(+)ptps-1(+) intestine anterior	rpl-29	-0.488891849	9.48716E-09
cat-4(+)ptps-1(+) intestine anterior	gst-20	-1.0802161	1.0037E-08
cat-4(+)ptps-1(+) intestine anterior	F54D5.12	0.700212167	1.31107E-08
cat-4(+)ptps-1(+) intestine anterior	col-103	0.770333038	1.31619E-08
cat-4(+)ptps-1(+) intestine anterior	F56H9.2	-0.373251592	1.57259E-08
cat-4(+)ptps-1(+) intestine anterior	C24B9.3	-1.01856053	1.58503E-08
cat-4(+)ptps-1(+) intestine anterior	fat-1	0.392843319	1.62979E-08
cat-4(+)ptps-1(+) intestine anterior	fipr-7	2.610633911	1.71644E-08
cat-4(+)ptps-1(+) intestine anterior	C17H12.8	-0.704154623	2.26913E-08
cat-4(+)ptps-1(+) intestine anterior	rpl-36	-0.190498228	2.29596E-08
cat-4(+)ptps-1(+) intestine anterior	srh-237	1.064747609	3.58265E-08
cat-4(+)ptps-1(+) intestine anterior	F26D11.1	0.79581232	5.4505E-08
cat-4(+)ptps-1(+) intestine anterior	F33H12.7	-1.51145569	6.84279E-08
cat-4(+)ptps-1(+) intestine anterior	C45E5.1	0.633501678	8.08898E-08
cat-4(+)ptps-1(+) intestine anterior	asns-2	0.839787376	8.45422E-08
cat-4(+)ptps-1(+) intestine anterior	tnt-4	2.143214961	9.11484E-08
cat-4(+)ptps-1(+) intestine anterior	gstk-1	-0.640556802	9.86691E-08
cat-4(+)ptps-1(+) intestine anterior	fat-2	0.311801062	1.24052E-07
cat-4(+)ptps-1(+) intestine anterior	F35E12.9	-1.183421483	2.00771E-07
cat-4(+)ptps-1(+) intestine anterior	F01D5.1	-0.841591313	2.00967E-07
cat-4(+)ptps-1(+) intestine anterior	dod-19	-0.97167516	2.20072E-07
cat-4(+)ptps-1(+) intestine anterior	H36L18.2	0.251876754	2.59884E-07
cat-4(+)ptps-1(+) intestine anterior	spp-4	-0.649936049	2.97643E-07
cat-4(+)ptps-1(+) intestine anterior	fipr-5	2.181137352	3.05065E-07
cat-4(+)ptps-1(+) intestine anterior	acs-19	-0.387296038	3.07342E-07
cat-4(+)ptps-1(+) intestine anterior	F11E6.3	0.648029396	3.17303E-07
cat-4(+)ptps-1(+) intestine anterior	F46G10.1	-0.210980239	3.30837E-07
cat-4(+)ptps-1(+) intestine anterior	Y73F4A.3	2.540515202	3.39857E-07
cat-4(+)ptps-1(+) intestine anterior	vit-2	0.329626676	3.46365E-07

cat-4(+)ptps-1(+) intestine anterior	col-8	0.657313906	4.78953E-07
cat-4(+)ptps-1(+) intestine anterior	col-160	0.651051639	5.13313E-07
cat-4(+)ptps-1(+) intestine anterior	vit-6	0.406218371	5.40384E-07
cat-4(+)ptps-1(+) intestine anterior	tni-4	0.893666943	5.53456E-07
cat-4(+)ptps-1(+) intestine anterior	gst-29	0.661164464	5.84991E-07
cat-4(+)ptps-1(+) intestine anterior	fipr-3	2.666746571	6.27406E-07
cat-4(+)ptps-1(+) intestine anterior	ttr-26	1.811363603	6.61351E-07
cat-4(+)ptps-1(+) intestine anterior	F23C8.5	0.269894593	6.98614E-07
cat-4(+)ptps-1(+) intestine anterior	lips-10	1.467427659	7.05809E-07
cat-4(+)ptps-1(+) intestine anterior	C30G7.4	-2.245476025	7.29197E-07
cat-4(+)ptps-1(+) intestine anterior	gst-33	0.769547618	7.34698E-07
cat-4(+)ptps-1(+) intestine anterior	asp-4	0.763457332	9.49953E-07
cat-4(+)ptps-1(+) intestine anterior	cyp-35A2	1.238004502	1.65547E-06
cat-4(+)ptps-1(+) intestine anterior	ddo-2	0.892446795	2.26721E-06
cat-4(+)ptps-1(+) intestine anterior	pyk-2	0.325650539	2.36258E-06
cat-4(+)ptps-1(+) intestine anterior	myo-1	2.80007156	5.24105E-06
cat-4(+)ptps-1(+) intestine anterior	asah-1	-1.002276063	6.23757E-06
cat-4(+)ptps-1(+) intestine anterior	ttr-15	0.593207268	7.22834E-06
cat-4(+)ptps-1(+) intestine anterior	B0272.3	0.602243056	7.65357E-06
cat-4(+)ptps-1(+) intestine anterior	rpl-4	0.169602807	9.33173E-06
cat-4(+)ptps-1(+) intestine anterior	ech-6	0.207072316	1.33978E-05
cat-4(+)ptps-1(+) intestine anterior	ssp-10	-0.317028134	1.52758E-05
cat-4(+)ptps-1(+) intestine anterior	hsp-16.2	0.956366324	1.64011E-05
cat-4(+)ptps-1(+) intestine anterior	lys-4	0.527882149	2.13676E-05
cat-4(+)ptps-1(+) intestine anterior	col-80	0.402868455	2.16066E-05
cat-4(+)ptps-1(+) intestine anterior	max-2	-0.528752254	2.16355E-05
cat-4(+)ptps-1(+) intestine anterior	F07G6.10	1.924448964	2.20682E-05
cat-4(+)ptps-1(+) intestine anterior	crt-1	-0.437916203	2.6102E-05
cat-4(+)ptps-1(+) intestine anterior	scl-2	-1.153543831	2.84086E-05
cat-4(+)ptps-1(+) intestine anterior	vrp-1	0.196332037	2.967E-05
cat-4(+)ptps-1(+) intestine anterior	trap-1	0.504597866	3.16871E-05
cat-4(+)ptps-1(+) intestine anterior	F36G3.2	0.552398919	3.4573E-05
cat-4(+)ptps-1(+) intestine anterior	cpr-4	0.607747525	3.58756E-05
cat-4(+)ptps-1(+) intestine anterior	F35D11.4	-0.871061032	3.83941E-05
cat-4(+)ptps-1(+) intestine anterior	cpl-1	0.598647376	4.02274E-05
cat-4(+)ptps-1(+) intestine anterior	act-2	-0.507961763	4.90698E-05

cat-4(+)ptps-1(+) intestine anterior	asp-13	0.878847231	5.26888E-05
cat-4(+)ptps-1(+) intestine anterior	col-81	0.324140274	6.26347E-05
cat-4(+)ptps-1(+) intestine anterior	rps-4	0.127528175	6.54561E-05
cat-4(+)ptps-1(+) intestine anterior	col-178	0.498718903	9.64565E-05
cat-4(+)ptps-1(+) intestine anterior	F54C9.3	-0.29610621	0.000102117
cat-4(+)ptps-1(+) intestine anterior	dod-24	-1.554212321	0.000121967
cat-4(+)ptps-1(+) intestine anterior	R07H5.8	0.375541011	0.000126858
cat-4(+)ptps-1(+) intestine anterior	F21C10.10	0.718971655	0.000133595
cat-4(+)ptps-1(+) intestine anterior	cdd-1	0.459811016	0.000140271
cat-4(+)ptps-1(+) intestine anterior	Y71H2AM.11	0.465941233	0.000159257
cat-4(+)ptps-1(+) intestine anterior	T09A12.5	-0.67665547	0.000180684
cat-4(+)ptps-1(+) intestine anterior	vamp-8	1.672177201	0.000185447
cat-4(+)ptps-1(+) intestine anterior	B0024.4	-1.350394253	0.000213453
cat-4(+)ptps-1(+) intestine anterior	asp-2	0.489917362	0.000282361
cat-4(+)ptps-1(+) intestine anterior	Y34F4.2	2.492357632	0.000300223
cat-4(+)ptps-1(+) intestine anterior	hpo-18	-0.332324169	0.000301012
cat-4(+)ptps-1(+) intestine anterior	rps-1	0.113633659	0.000336678
cat-4(+)ptps-1(+) intestine anterior	mel-32	0.382555053	0.000344921
cat-4(+)ptps-1(+) intestine anterior	msp-152	-0.696439651	0.000369658
cat-4(+)ptps-1(+) intestine anterior	Y82E9BR.3	0.094219599	0.000396844
cat-4(+)ptps-1(+) intestine anterior	tatn-1	-0.813017703	0.000405002
cat-4(+)ptps-1(+) intestine anterior	C49G7.3	0.792398523	0.000454227
cat-4(+)ptps-1(+) intestine anterior	rpl-34	-0.165886631	0.000475537
cat-4(+)ptps-1(+) intestine anterior	F13C5.5	3.032544247	0.000525012
cat-4(+)ptps-1(+) intestine anterior	spp-8	-0.792251275	0.000535581
cat-4(+)ptps-1(+) intestine anterior	spp-3	-0.457741154	0.000554506
cat-4(+)ptps-1(+) intestine anterior	nspd-2	-0.520076887	0.000576585
cat-4(+)ptps-1(+) intestine anterior	K12H4.7	-0.38270598	0.000608553
cat-4(+)ptps-1(+) intestine anterior	nuo-6	0.254200643	0.000669594
cat-4(+)ptps-1(+) intestine anterior	nspd-1	-0.425972135	0.000717641
cat-4(+)ptps-1(+) intestine anterior	Y111B2A.2	-0.388327665	0.00072678
cat-4(+)ptps-1(+) intestine anterior	col-143	0.514235975	0.000731
cat-4(+)ptps-1(+) intestine anterior	fipr-11	3.975633488	0.000770709

cat-4(+)ptps-1(+) intestine anterior	gst-1	-0.381724818	0.000850305
cat-4(+)ptps-1(+) intestine anterior	dhs-25	-0.358978379	0.000906753
cat-4(+)ptps-1(+) intestine anterior	gpx-5	0.929834726	0.000908538
cat-4(+)ptps-1(+) intestine anterior	rps-18	0.099130214	0.000931292
cat-4(+)ptps-1(+) intestine anterior	mmaa-1	0.946693761	0.001013301
cat-4(+)ptps-1(+) intestine anterior	rpl-11.1	-0.247543734	0.001066115
cat-4(+)ptps-1(+) intestine anterior	tald-1	-0.330724325	0.001178013
cat-4(+)ptps-1(+) intestine anterior	strl-1	0.618844079	0.001335253
cat-4(+)ptps-1(+) intestine anterior	F17C11.11	-0.70668881	0.001445406
cat-4(+)ptps-1(+) intestine anterior	thn-2	0.835886532	0.001479823
cat-4(+)ptps-1(+) intestine anterior	rpl-32	-0.112761693	0.001530308
cat-4(+)ptps-1(+) intestine anterior	tnt-3	1.255745054	0.001684761
cat-4(+)ptps-1(+) intestine anterior	col-93	0.361025671	0.001795003
cat-4(+)ptps-1(+) intestine anterior	dif-1	0.473330494	0.001992362
cat-4(+)ptps-1(+) intestine anterior	cyc-2.1	0.142482707	0.002320976
cat-4(+)ptps-1(+) intestine anterior	asp-14	-0.784781104	0.002820972
cat-4(+)ptps-1(+) intestine anterior	hpo-26	2.877932008	0.002823242
cat-4(+)ptps-1(+) intestine anterior	F01G4.6	0.181456979	0.003032123
cat-4(+)ptps-1(+) intestine anterior	F53A9.8	-1.276442041	0.003187416
cat-4(+)ptps-1(+) intestine anterior	hacd-1	-0.262227014	0.003722065
cat-4(+)ptps-1(+) intestine anterior	C49G7.12	-0.891996942	0.003932997
cat-4(+)ptps-1(+) intestine anterior	Y47G6A.15	2.361814098	0.004092019
cat-4(+)ptps-1(+) intestine anterior	cco-2	0.143688675	0.004699535
cat-4(+)ptps-1(+) intestine anterior	nspd-10	-0.498096033	0.004963763
cat-4(+)ptps-1(+) intestine anterior	rpl-1	0.118018577	0.005059629
cat-4(+)ptps-1(+) intestine anterior	C49A9.9	0.446516829	0.006091438
cat-4(+)ptps-1(+) intestine anterior	F01D5.2	-0.65428595	0.006114445
cat-4(+)ptps-1(+) intestine anterior	B0303.3	0.453478685	0.006244166
cat-4(+)ptps-1(+) intestine anterior	C23H5.8	-0.327591976	0.006279341
cat-4(+)ptps-1(+) intestine anterior	fipr-6	3.087528651	0.006312115
cat-4(+)ptps-1(+) intestine anterior	acdh-7	0.76018338	0.00646328
cat-4(+)ptps-1(+) intestine anterior	asp-1	-0.226029027	0.006482516
cat-4(+)ptps-1(+) intestine anterior	mdh-1	0.264902228	0.00696941

cat-4(+)ptps-1(+) intestine anterior	C24A3.2	0.684006234	0.007234861
cat-4(+)ptps-1(+) intestine anterior	klo-2	-0.929565802	0.007720718
cat-4(+)ptps-1(+) intestine anterior	hpd-1	-0.479561239	0.007816599
cat-4(+)ptps-1(+) intestine anterior	pmp-5	1.004019646	0.008365299
cat-4(+)ptps-1(+) intestine anterior	sec-61	0.290303406	0.009696105
cat-4(+)ptps-1(+) intestine anterior	ZK6.11	-0.55289515	0.010437363
cat-4(+)ptps-1(+) intestine anterior	mxl-3	0.558222701	0.010614992
cat-4(+)ptps-1(+) intestine anterior	msd-4	-0.277213222	0.012154348
cat-4(+)ptps-1(+) intestine anterior	skr-5	0.502264716	0.0127378
cat-4(+)ptps-1(+) intestine anterior	cytb-5.1	0.167194947	0.013084165
cat-4(+)ptps-1(+) intestine anterior	T13F3.6	0.523932489	0.013254664
cat-4(+)ptps-1(+) intestine anterior	F52B11.2	-0.372262644	0.013356666
cat-4(+)ptps-1(+) intestine anterior	spp-1	-0.376950041	0.014631994
cat-4(+)ptps-1(+) intestine anterior	hsp-16.41	1.327980243	0.014943761
cat-4(+)ptps-1(+) intestine anterior	asb-2	0.183580657	0.015246599
cat-4(+)ptps-1(+) intestine anterior	F33H2.6	0.635506845	0.016247067
cat-4(+)ptps-1(+) intestine anterior	math-14	0.438559085	0.016516004
cat-4(+)ptps-1(+) intestine anterior	Y94H6A.10	-0.281889273	0.017057709
cat-4(+)ptps-1(+) intestine anterior	F58F12.1	0.128964337	0.017697453
cat-4(+)ptps-1(+) intestine anterior	pyp-1	0.210257328	0.017937942
cat-4(+)ptps-1(+) intestine anterior	pqn-94	1.785309568	0.018072832
cat-4(+)ptps-1(+) intestine anterior	cyn-1	0.295929598	0.018723869
cat-4(+)ptps-1(+) intestine anterior	C15B12.1	0.618792919	0.019563803
cat-4(+)ptps-1(+) intestine anterior	gpx-1	0.326825224	0.019952816
cat-4(+)ptps-1(+) intestine anterior	ttr-27	1.32470739	0.020115978
cat-4(+)ptps-1(+) intestine anterior	Y43F8C.13	0.387260884	0.020131859
cat-4(+)ptps-1(+) intestine anterior	col-19	0.246634196	0.020662141
cat-4(+)ptps-1(+) intestine anterior	C31C9.2	0.742726994	0.021553077
cat-4(+)ptps-1(+) intestine anterior	D1022.4	0.326567587	0.0228964
cat-4(+)ptps-1(+) intestine anterior	F10D2.8	1.451538925	0.023338562
cat-4(+)ptps-1(+) intestine anterior	lec-11	-0.42096324	0.023372212
cat-4(+)ptps-1(+) intestine anterior	tni-3	0.194217696	0.023796166
cat-4(+)ptps-1(+) intestine anterior	mdh-2	0.229969171	0.026329253
cat-4(+)ptps-1(+) intestine anterior	bckd-1B	0.318500055	0.027705269
cat-4(+)ptps-1(+) intestine anterior	Y39B6A.1	-0.565936032	0.031899512
cat-4(+)ptps-1(+) intestine anterior	rpl-3	0.093399739	0.035119414
cat-4(+)ptps-1(+) intestine anterior	C53B7.3	2.364401304	0.035750896

cat-4(+)ptps-1(+) intestine anterior	dod-22	-0.253205818	0.037825344
cat-4(+)ptps-1(+) intestine anterior	F32A5.4	1.405448974	0.045537209
cat-4(+)ptps-1(+) intestine anterior	valv-1	-0.817859991	0.046775647
cat-4(+)ptps-1(+) intestine anterior	str-7	0.620767384	0.054685816
cat-4(+)ptps-1(+) intestine anterior	rps-8	0.094243143	0.054820537
cat-4(+)ptps-1(+) intestine anterior	fat-3	0.471376745	0.059451014
cat-4(+)ptps-1(+) intestine anterior	ZK1307.1	-0.330253121	0.059747929
cat-4(+)ptps-1(+) intestine anterior	rps-9	0.072590542	0.06384287
cat-4(+)ptps-1(+) intestine anterior	try-10	-1.245476032	0.0647982
cat-4(+)ptps-1(+) intestine anterior	F08D12.2	2.619658572	0.065158831
cat-4(+)ptps-1(+) intestine anterior	rpl-9	0.113891643	0.065203941
cat-4(+)ptps-1(+) intestine anterior	fipr-9	2.126889632	0.065589838
cat-4(+)ptps-1(+) intestine anterior	rpl-30	-0.136463863	0.068405755
cat-4(+)ptps-1(+) intestine anterior	cysl-2	-0.698450385	0.069440813
cat-4(+)ptps-1(+) intestine anterior	his-41	0.215612332	0.074125384
cat-4(+)ptps-1(+) intestine anterior	C51E3.10	-0.674752999	0.074700512
cat-4(+)ptps-1(+) intestine anterior	ZC116.5	1.465454758	0.075396361
cat-4(+)ptps-1(+) intestine anterior	pes-23	-1.660513523	0.079996742
cat-4(+)ptps-1(+) intestine anterior	col-106	0.379242797	0.090801858
cat-4(+)ptps-1(+) intestine anterior	rps-7	0.086963586	0.095611697
cat-4(+)ptps-1(+) intestine anterior	abf-5	1.531935793	0.096822971
e1_e3 (pharyngeal epithelium)	ttr-29	-1.614519554	1.5099E-121
e1_e3 (pharyngeal epithelium)	ttr-28	-1.836287022	2.0721E-114
e1_e3 (pharyngeal epithelium)	ttr-21	0.668476454	1.23663E-74
e1_e3 (pharyngeal epithelium)	ttr-22	1.011522947	6.61803E-73
e1_e3 (pharyngeal epithelium)	ZC21.3	1.063983793	1.40694E-45
e1_e3 (pharyngeal epithelium)	F13E9.14	2.635480037	7.56712E-40
e1_e3 (pharyngeal epithelium)	ttr-27	-0.543472217	2.08267E-37
e1_e3 (pharyngeal epithelium)	otpl-7	-1.586902377	4.08092E-35
e1_e3 (pharyngeal epithelium)	mdh-1	0.833548453	2.29628E-34
e1_e3 (pharyngeal epithelium)	ndk-1	0.411219029	2.89886E-32
e1_e3 (pharyngeal epithelium)	fipr-2	-0.439876379	3.6438E-30

e1_e3 (pharyngeal epithelium)	nhr-10	2.022999785	2.69787E-28
e1_e3 (pharyngeal epithelium)	F17A9.4	1.695561985	3.00969E-28
e1_e3 (pharyngeal epithelium)	pnc-1	-0.357275855	1.82629E-26
e1_e3 (pharyngeal epithelium)	F14F8.8	1.322701331	9.24939E-26
e1_e3 (pharyngeal epithelium)	F13D12.9	1.256990137	2.23751E-25
e1_e3 (pharyngeal epithelium)	C53B7.3	-0.519430973	1.75868E-21
e1_e3 (pharyngeal epithelium)	R07B1.11	0.82952961	9.47245E-21
e1_e3 (pharyngeal epithelium)	hsp-16.48	-0.888416989	2.27774E-20
e1_e3 (pharyngeal epithelium)	F56D5.3	2.865271967	3.01777E-20
e1_e3 (pharyngeal epithelium)	nhr-3	1.173595959	3.19632E-19
e1_e3 (pharyngeal epithelium)	K06A4.7	-0.893498745	4.07781E-19
e1_e3 (pharyngeal epithelium)	cyp-33C8	-0.630509455	1.67656E-18
e1_e3 (pharyngeal epithelium)	fmo-2	6.664505985	2.54912E-18
e1_e3 (pharyngeal epithelium)	nduo-6	-0.414460746	5.91298E-18
e1_e3 (pharyngeal epithelium)	VF13D12L.3	1.222060265	1.97222E-17
e1_e3 (pharyngeal epithelium)	mxl-3	1.642554682	2.27153E-17
e1_e3 (pharyngeal epithelium)	lec-7	0.814939421	3.99718E-17
e1_e3 (pharyngeal epithelium)	col-122	1.029353615	2.04919E-16
e1_e3 (pharyngeal epithelium)	F46H5.3	-0.66941454	3.47735E-16
e1_e3 (pharyngeal epithelium)	C17C3.1	1.099628807	8.11212E-15
e1_e3 (pharyngeal epithelium)	F26A3.4	-0.565328282	1.39882E-14
e1_e3 (pharyngeal epithelium)	ZK262.3	0.528067358	1.76652E-14
e1_e3 (pharyngeal epithelium)	C17C3.15	0.631288107	1.84942E-13
e1_e3 (pharyngeal epithelium)	hex-5	-0.858152931	3.24635E-13
e1_e3 (pharyngeal epithelium)	col-184	1.108803437	4.37405E-13
e1_e3 (pharyngeal epithelium)	W02D9.10	0.654129449	1.63385E-12
e1_e3 (pharyngeal epithelium)	gpx-3	-0.745070937	5.62381E-12
e1_e3 (pharyngeal epithelium)	nhr-21	1.347583347	7.2034E-12
e1_e3 (pharyngeal epithelium)	B0238.12	-0.390782892	1.23799E-10
e1_e3 (pharyngeal epithelium)	col-8	1.343888762	7.80473E-10
e1_e3 (pharyngeal epithelium)	ZK262.2	0.338539617	1.37129E-09
e1_e3 (pharyngeal epithelium)	dct-16	-0.638272369	4.95454E-09
e1_e3 (pharyngeal epithelium)	T21D12.12	-0.4938487	7.26225E-09
e1_e3 (pharyngeal epithelium)	F25H2.6	0.51587892	1.20767E-08

e1_e3 (pharyngeal epithelium)	C14C6.5	-2.278196218	1.54244E-08
e1_e3 (pharyngeal epithelium)	ndfl-4	-0.41462321	1.69894E-08
e1_e3 (pharyngeal epithelium)	K07C5.2	1.046906071	1.71328E-08
e1_e3 (pharyngeal epithelium)	col-181	0.794388631	2.00835E-08
e1_e3 (pharyngeal epithelium)	clec-87	2.151453563	3.47275E-08
e1_e3 (pharyngeal epithelium)	F35A5.5	2.031026895	3.82568E-08
e1_e3 (pharyngeal epithelium)	mlt-8	2.031026895	3.82568E-08
e1_e3 (pharyngeal epithelium)	col-119	0.73567195	3.96205E-08
e1_e3 (pharyngeal epithelium)	srr-3	0.848909447	5.52955E-08
e1_e3 (pharyngeal epithelium)	W02F12.2	0.989201593	1.14516E-07
e1_e3 (pharyngeal epithelium)	acp-7	-0.392688332	1.57731E-07
e1_e3 (pharyngeal epithelium)	gon-2	-0.792633443	5.24731E-07
e1_e3 (pharyngeal epithelium)	pck-2	0.626702011	6.23646E-07
e1_e3 (pharyngeal epithelium)	pab-1	0.920899058	6.78933E-07
e1_e3 (pharyngeal epithelium)	Y69H2.3	-0.747880757	1.63263E-06
e1_e3 (pharyngeal epithelium)	gst-30	0.879569598	1.68199E-06
e1_e3 (pharyngeal epithelium)	R09B3.2	1.548521498	2.46999E-06
e1_e3 (pharyngeal epithelium)	ddo-2	0.66613423	2.65729E-06
e1_e3 (pharyngeal epithelium)	C02B8.12	-0.509452295	2.87043E-06
e1_e3 (pharyngeal epithelium)	cpn-1	0.505943301	3.73339E-06
e1_e3 (pharyngeal epithelium)	iff-1	1.296856145	4.64363E-06
e1_e3 (pharyngeal epithelium)	rps-6	1.05217315	5.81564E-06
e1_e3 (pharyngeal epithelium)	msp-76	-0.361431487	7.16563E-06
e1_e3 (pharyngeal epithelium)	fipr-7	-0.436594311	7.23399E-06
e1_e3 (pharyngeal epithelium)	nhr-271	0.645185783	1.14129E-05
e1_e3 (pharyngeal epithelium)	gst-7	0.363272126	2.28524E-05
e1_e3 (pharyngeal epithelium)	rpl-41.2	-0.329627325	3.21532E-05
e1_e3 (pharyngeal epithelium)	lpd-7	3.443959362	3.30119E-05
e1_e3 (pharyngeal epithelium)	best-1	-0.420642212	3.3331E-05
e1_e3 (pharyngeal epithelium)	F32A5.4	0.199027784	4.7031E-05
e1_e3 (pharyngeal epithelium)	Y119D3B.21	-0.68046098	5.05571E-05
e1_e3 (pharyngeal epithelium)	C23H5.8	-1.313316865	5.24351E-05
e1_e3 (pharyngeal epithelium)	R09B3.3	1.314839115	6.03661E-05
e1_e3 (pharyngeal epithelium)	R08F11.4	-0.592290459	8.81945E-05

e1_e3 (pharyngeal epithelium)	C04A2.15	-0.490989322	8.85269E-05
e1_e3 (pharyngeal epithelium)	let-721	1.032108526	9.48486E-05
e1_e3 (pharyngeal epithelium)	col-143	0.845222135	9.57561E-05
e1_e3 (pharyngeal epithelium)	spe-10	-0.26255785	0.000103756
e1_e3 (pharyngeal epithelium)	T22B7.7	0.834799111	0.000115449
e1_e3 (pharyngeal epithelium)	col-124	0.477895257	0.000217539
e1_e3 (pharyngeal epithelium)	eef-1G	0.768377688	0.000226603
e1_e3 (pharyngeal epithelium)	fib-1	1.279942248	0.000248823
e1_e3 (pharyngeal epithelium)	cah-4	-0.504495037	0.000296794
e1_e3 (pharyngeal epithelium)	ahcy-1	0.741519203	0.000313594
e1_e3 (pharyngeal epithelium)	fat-5	2.231289508	0.000384688
e1_e3 (pharyngeal epithelium)	gst-35	1.546567338	0.000400661
e1_e3 (pharyngeal epithelium)	far-7	-0.475955923	0.000457185
e1_e3 (pharyngeal epithelium)	col-106	0.780859677	0.000475747
e1_e3 (pharyngeal epithelium)	far-3	2.477747323	0.000523319
e1_e3 (pharyngeal epithelium)	gst-4	0.84120137	0.000560674
e1_e3 (pharyngeal epithelium)	F17C11.11	-0.426706652	0.000612955
e1_e3 (pharyngeal epithelium)	ran-1	1.262660639	0.000650914
e1_e3 (pharyngeal epithelium)	wago-1	3.302701192	0.000817056
e1_e3 (pharyngeal epithelium)	srr-4	0.626999318	0.000926566
e1_e3 (pharyngeal epithelium)	acer-1	0.57824754	0.000952577
e1_e3 (pharyngeal epithelium)	sipa-1	-0.633256525	0.0011146
e1_e3 (pharyngeal epithelium)	pqn-94	-0.257008258	0.001130059
e1_e3 (pharyngeal epithelium)	C45E5.4	0.291634841	0.001268266
e1_e3 (pharyngeal epithelium)	F48D6.4	-1.107330222	0.001380958
e1_e3 (pharyngeal epithelium)	mdl-1	-0.457541806	0.001402492
e1_e3 (pharyngeal epithelium)	eef-1A.1	0.363533533	0.001588044
e1_e3 (pharyngeal epithelium)	msp-152	-0.162911695	0.002382375
e1_e3 (pharyngeal epithelium)	ttr-26	0.3160682	0.002954913
e1_e3 (pharyngeal epithelium)	vap-2	-1.130493804	0.002956652
e1_e3 (pharyngeal epithelium)	sdz-8	0.871781476	0.003028596
e1_e3 (pharyngeal epithelium)	nspd-10	-0.056943284	0.003076058
e1_e3 (pharyngeal epithelium)	msp-40	-0.521462348	0.003373367

e1_e3 (pharyngeal epithelium)	lec-4	-0.311035375	0.003550656
e1_e3 (pharyngeal epithelium)	svop-1	0.723344018	0.004740812
e1_e3 (pharyngeal epithelium)	Y46H3A.4	-1.481733625	0.00543267
e1_e3 (pharyngeal epithelium)	T13F3.6	1.030659365	0.005504592
e1_e3 (pharyngeal epithelium)	msp-31	-0.48187736	0.005883878
e1_e3 (pharyngeal epithelium)	pcs-1	-0.878835581	0.006067522
e1_e3 (pharyngeal epithelium)	spp-2	-2.498740286	0.007941248
e1_e3 (pharyngeal epithelium)	aly-2	2.957017107	0.0081958
e1_e3 (pharyngeal epithelium)	rpl-7A	0.625849233	0.009538126
e1_e3 (pharyngeal epithelium)	pgp-14	0.254574492	0.010539873
e1_e3 (pharyngeal epithelium)	htz-1	1.937742746	0.010680325
e1_e3 (pharyngeal epithelium)	soc-1	-0.492827113	0.011234126
e1_e3 (pharyngeal epithelium)	rpl-25.2	0.751213827	0.0113293
e1_e3 (pharyngeal epithelium)	lec-9	-0.67965386	0.015022254
e1_e3 (pharyngeal epithelium)	pck-1	-0.322599699	0.015401673
e1_e3 (pharyngeal epithelium)	Y53C10A.5	0.925665655	0.015460006
e1_e3 (pharyngeal epithelium)	C02D5.4	0.591687449	0.015662183
e1_e3 (pharyngeal epithelium)	gln-1	-0.488423015	0.015830842
e1_e3 (pharyngeal epithelium)	ZK742.4	0.396663528	0.015989734
e1_e3 (pharyngeal epithelium)	ugt-7	-0.351265357	0.01705894
e1_e3 (pharyngeal epithelium)	rps-20	0.333829358	0.01717113
e1_e3 (pharyngeal epithelium)	C18D11.3	3.591546683	0.018831373
e1_e3 (pharyngeal epithelium)	hpo-26	-0.186215413	0.018964191
e1_e3 (pharyngeal epithelium)	col-20	0.414246136	0.019037279
e1_e3 (pharyngeal epithelium)	ttr-15	1.060975065	0.019512131
e1_e3 (pharyngeal epithelium)	cbd-1	1.807781873	0.020209926
e1_e3 (pharyngeal epithelium)	msp-36	-0.395973228	0.020274558
e1_e3 (pharyngeal epithelium)	rpl-3	0.432043084	0.020846974
e1_e3 (pharyngeal epithelium)	cyp-33C5	-0.874174803	0.021832216
e1_e3 (pharyngeal epithelium)	F48A9.1	0.556860673	0.021998046
e1_e3 (pharyngeal epithelium)	C17F3.1	-0.007923893	0.024993423
e1_e3 (pharyngeal epithelium)	gpd-2	-0.34472058	0.026260286
e1_e3 (pharyngeal epithelium)	K01G5.5	1.756790385	0.028162426

e1_e3 (pharyngeal epithelium)	C05D11.5	0.523998273	0.029004637
e1_e3 (pharyngeal epithelium)	hsp-16.41	-0.428655585	0.032477649
e1_e3 (pharyngeal epithelium)	F47B8.2	0.277210331	0.033624087
e1_e3 (pharyngeal epithelium)	nspd-1	-0.049037205	0.034331953
e1_e3 (pharyngeal epithelium)	inx-13	-0.340480337	0.03462623
e1_e3 (pharyngeal epithelium)	glb-1	0.283541614	0.036157822
e1_e3 (pharyngeal epithelium)	lec-6	-0.734526406	0.03671687
e1_e3 (pharyngeal epithelium)	rpl-11.1	1.002061024	0.041377571
e1_e3 (pharyngeal epithelium)	ZK1067.3	2.371192625	0.052376104
e1_e3 (pharyngeal epithelium)	fipr-3	-0.510877812	0.052889327
e1_e3 (pharyngeal epithelium)	col-140	0.391214122	0.057203378
e1_e3 (pharyngeal epithelium)	msp-51	-0.000278908	0.057580821
e1_e3 (pharyngeal epithelium)	lec-10	-0.848828504	0.060435153
e1_e3 (pharyngeal epithelium)	elo-6	0.3049387	0.062360254
e1_e3 (pharyngeal epithelium)	snr-4	1.347185788	0.07343504
e1_e3 (pharyngeal epithelium)	rpl-20	0.42794679	0.076290985
e1_e3 (pharyngeal epithelium)	rps-4	0.423727036	0.077382516
e1_e3 (pharyngeal epithelium)	sams-1	0.76692369	0.078345918
e1_e3 (pharyngeal epithelium)	col-101	1.046695434	0.081911723
e1_e3 (pharyngeal epithelium)	nhr-11	1.067452458	0.083359388
e1_e3 (pharyngeal epithelium)	hil-4	1.247972922	0.084554509
e1_e3 (pharyngeal epithelium)	T04A8.6	2.692587922	0.086583767
e1_e3 (pharyngeal epithelium)	msp-78	-0.32846521	0.08830562
e1_e3 (pharyngeal epithelium)	camt-1	0.627390574	0.092096197
e1_e3 (pharyngeal epithelium)	haf-7	-0.743399633	0.092474327
e1_e3 (pharyngeal epithelium)	hil-2	2.063940271	0.096188927
e1_e3 (pharyngeal epithelium)	ssp-19	-0.043544222	0.099836899
e2 (pharyngeal gland)	F22F4.9	-0.855716247	3.98998E-21
e2 (pharyngeal gland)	pnc-1	-0.602416708	1.5631E-14
e2 (pharyngeal gland)	F32A5.4	0.758083624	2.14915E-13
e2 (pharyngeal gland)	pqn-60	1.202028354	6.19231E-12
e2 (pharyngeal gland)	C45E5.4	0.692019168	8.9205E-12
e2 (pharyngeal gland)	ttr-21	0.47018759	1.57829E-11

e2 (pharyngeal gland)	hsp-16.48	-0.965244067	6.88155E-11
e2 (pharyngeal gland)	ttr-29	-1.637186029	1.55462E-09
e2 (pharyngeal gland)	F46H5.3	-0.466144803	5.6932E-09
e2 (pharyngeal gland)	adss-1	-0.629659177	7.25588E-09
e2 (pharyngeal gland)	F22B5.4	-1.124689153	3.32124E-08
e2 (pharyngeal gland)	nduo-6	-0.359589925	6.35969E-08
e2 (pharyngeal gland)	rpl-7A	1.684872561	1.23467E-07
e2 (pharyngeal gland)	eef-1G	1.512441229	2.95386E-07
e2 (pharyngeal gland)	rla-0	0.889945876	9.5912E-07
e2 (pharyngeal gland)	elo-6	1.206730789	2.44727E-06
e2 (pharyngeal gland)	ctc-3	0.400707346	9.45729E-05
e2 (pharyngeal gland)	ndk-1	0.315519664	0.000277046
e2 (pharyngeal gland)	rpl-25.2	1.505793226	0.000299093
e2 (pharyngeal gland)	col-119	0.879438194	0.000322422
e2 (pharyngeal gland)	gst-7	0.817802766	0.000430075
e2 (pharyngeal gland)	rpl-3	1.016658376	0.000443175
e2 (pharyngeal gland)	eef-1A.1	0.9557887	0.000633829
e2 (pharyngeal gland)	col-122	0.830205796	0.000638448
e2 (pharyngeal gland)	hil-4	2.476501727	0.000902473
e2 (pharyngeal gland)	R09B3.2	2.270698478	0.001074282
e2 (pharyngeal gland)	fmo-2	3.351116793	0.00138993
e2 (pharyngeal gland)	rps-4	1.013461987	0.001458582
e2 (pharyngeal gland)	col-170	1.362570079	0.002183197
e2 (pharyngeal gland)	srr-6	1.362570079	0.002183197
e2 (pharyngeal gland)	rps-1	0.838737909	0.002213138
e2 (pharyngeal gland)	rpl-10	0.529373271	0.002367
e2 (pharyngeal gland)	ttr-22	1.922082078	0.002378947
e2 (pharyngeal gland)	R09B3.3	1.656264097	0.003423865
e2 (pharyngeal gland)	T25B9.9	0.644460267	0.003430966
e2 (pharyngeal gland)	fipr-7	-0.698996533	0.003776627
e2 (pharyngeal gland)	F17A9.4	0.922809716	0.004562676
e2 (pharyngeal gland)	nhr-10	1.324877883	0.004804086
e2 (pharyngeal gland)	ZK1073.1	-0.889885709	0.006799339
e2 (pharyngeal gland)	cyn-7	0.87196873	0.011838419
e2 (pharyngeal gland)	srr-3	1.031376112	0.012155858
e2 (pharyngeal gland)	F13E9.14	1.981533571	0.012369069

e2 (pharyngeal gland)	M28.5	1.807537677	0.012768049
e2 (pharyngeal gland)	ttr-27	-0.526298679	0.014037783
e2 (pharyngeal gland)	C17F4.7	1.254373088	0.014653367
e2 (pharyngeal gland)	rpl-20	0.831554652	0.016923473
e2 (pharyngeal gland)	rpl-7	0.749391073	0.02016071
e2 (pharyngeal gland)	C14C6.5	-1.768147536	0.024077815
e2 (pharyngeal gland)	rps-9	0.394940804	0.030708975
e2 (pharyngeal gland)	rack-1	0.868137914	0.033245962
e2 (pharyngeal gland)	vamp-8	-0.325157217	0.0398019
e2 (pharyngeal gland)	F56D5.3	1.492314942	0.041951967
e2 (pharyngeal gland)	rps-6	1.14351193	0.063428968
e2 (pharyngeal gland)	rps-19	0.39988418	0.067522504
e2 (pharyngeal gland)	rps-3	0.5930024	0.089370341
e2 (pharyngeal gland)	rpl-4	1.610592285	0.096062617
g1P (pharyngeal gland)	ZK596.1	0.92500295	8.46796E-12
g1P (pharyngeal gland)	pqn-75	0.97376102	1.40274E-07
g1P (pharyngeal gland)	hsp-16.2	1.439513826	1.85222E-07
g1P (pharyngeal gland)	phat-3	0.53878356	8.04947E-05
g1P (pharyngeal gland)	C14C6.5	-2.283495427	8.62593E-05
g1P (pharyngeal gland)	rpl-41.2	-0.504093243	0.000108376
g1P (pharyngeal gland)	hsp-16.41	1.094007325	0.000753875
g1P (pharyngeal gland)	C43F9.5	0.560113717	0.001781417
g1P (pharyngeal gland)	rpl-39	-0.748838089	0.002914906
g1P (pharyngeal gland)	scl-6	0.436227875	0.010110001
g1P (pharyngeal gland)	rpl-36	-0.456530602	0.015081186
g1P (pharyngeal gland)	rpl-36.A	-0.463984112	0.019438628
g1P (pharyngeal gland)	col-111	1.563900885	0.019998531
g1P (pharyngeal gland)	Y39G8B.9	1.563900885	0.019998531
g1P (pharyngeal gland)	inpp-1	-3.131945537	0.050926592
g1P (pharyngeal gland)	C49G7.3	0.316566948	0.086940483
g2 (pharyngeal gland)	F55G11.4	-2.621488377	1.16269E-10
g2 (pharyngeal gland)	col-65	-2.621488376	1.63487E-06
g2 (pharyngeal gland)	col-122	1.795131467	0.000222163
g2 (pharyngeal gland)	col-20	1.272482171	0.000258974

g2 (pharyngeal gland)	ctc-3	0.861813698	0.000334734
g2 (pharyngeal gland)	ctc-1	0.966196978	0.000389773
g2 (pharyngeal gland)	col-140	1.209664768	0.000696111
g2 (pharyngeal gland)	col-119	1.672401719	0.000735554
g2 (pharyngeal gland)	atp-2	1.199040594	0.0011488
g2 (pharyngeal gland)	trx-3	-2.621488376	0.006358242
g2 (pharyngeal gland)	F08D12.2	-0.425641938	0.008909272
g2 (pharyngeal gland)	Y110A2AL.3	-0.721464202	0.010066728
g2 (pharyngeal gland)	cco-2	1.255003719	0.01110576
g2 (pharyngeal gland)	Y110A2AL.9	-0.610004118	0.033365497
g2 (pharyngeal gland)	col-124	1.135149025	0.034177348
g2 (pharyngeal gland)	col-8	2.1511446	0.042923875
g2 (pharyngeal gland)	fip-2	-0.392471848	0.052811544
g2 (pharyngeal gland)	crt-1	-0.794717543	0.093105536
hmc	lbp-2	-0.981304622	1.62119E-07
hmc	msp-33	0	0.000990537
hmc	msp-40	-0.026065753	0.042938785
hmc	col-8	2.187324574	0.052838981
hmc	nspd-1	0	0.055633097
hmc	T23B12.8	-0.54043804	0.057427171
hmc	Y59C2A.1	-1.139962907	0.093971587
hyp4_to_hyp6	gst-10	-2.352975544	0
hyp4_to_hyp6	C05D11.5	1.234241008	6.2032E-231
hyp4_to_hyp6	rpl-41.2	-0.507179405	6.8854E-195
hyp4_to_hyp6	gst-4	1.06511996	2.3321E-194
hyp4_to_hyp6	T03F1.11	2.220773578	4.6598E-191
hyp4_to_hyp6	tnc-2	2.427302179	1.5594E-181
hyp4_to_hyp6	cysl-2	-1.355016948	7.2203E-153
hyp4_to_hyp6	F53F1.2	1.271115279	2.6358E-137
hyp4_to_hyp6	F21C10.9	1.680659675	3.4945E-136
hyp4_to_hyp6	ahcy-1	0.561423276	3.0289E-123
hyp4_to_hyp6	sams-1	0.80682846	1.7017E-117

hyp4_to_hyp6	rps-25	-0.333472306	9.941E-114
hyp4_to_hyp6	cpn-4	2.555413561	4.3826E-112
hyp4_to_hyp6	fipr-2	3.198209072	3.4347E-107
hyp4_to_hyp6	W01D2.1	-0.558498526	1.3693E-103
hyp4_to_hyp6	drd-10	-3.368160249	7.6575E-101
hyp4_to_hyp6	B0410.3	0.723656956	2.1138E-99
hyp4_to_hyp6	C53A3.2	0.864564804	4.9238E-99
hyp4_to_hyp6	C14C6.5	-1.947566764	1.58552E-98
hyp4_to_hyp6	C53C9.2	2.456104954	2.48115E-97
hyp4_to_hyp6	pck-2	0.524875067	3.16124E-97
hyp4_to_hyp6	C45B2.1	-0.526759988	8.93352E-97
hyp4_to_hyp6	dct-16	-0.538132343	5.86441E-96
hyp4_to_hyp6	Y69H2.3	-2.31410859	9.09354E-94
hyp4_to_hyp6	fipr-1	2.725825691	7.60693E-93
hyp4_to_hyp6	gst-20	-2.220932405	1.87777E-88
hyp4_to_hyp6	ctc-3	0.355275153	2.5187E-87
hyp4_to_hyp6	rpl-38	-0.462857227	9.51399E-87
hyp4_to_hyp6	msra-1	1.609312306	6.14935E-85
hyp4_to_hyp6	hsp-12.2	1.308412479	2.09084E-84
hyp4_to_hyp6	rpl-36	-0.388679633	1.038E-83
hyp4_to_hyp6	F59C6.16	-0.901884683	2.96632E-82
hyp4_to_hyp6	R08E5.3	-1.287760885	2.76502E-81
hyp4_to_hyp6	R09B3.3	-0.399071489	4.72803E-81
hyp4_to_hyp6	pyk-2	0.911285597	1.81706E-80
hyp4_to_hyp6	gln-3	0.625203667	2.09658E-79
hyp4_to_hyp6	rpl-36.A	-0.366657066	6.87449E-78
hyp4_to_hyp6	rps-27	-0.380454874	8.94789E-78
hyp4_to_hyp6	ZC116.1	3.247615179	1.74487E-76
hyp4_to_hyp6	far-3	3.268460786	4.54459E-76
hyp4_to_hyp6	C06A8.3	0.430526401	5.48181E-76
hyp4_to_hyp6	pqn-60	3.120299528	1.34434E-74

hyp4_to_hyp6	Y87G2A.19	2.238710626	1.57164E-73
hyp4_to_hyp6	F41E6.15	1.505592247	1.66029E-69
hyp4_to_hyp6	C45B2.2	-0.793603314	1.24368E-68
hyp4_to_hyp6	rpl-39	-0.520771322	2.17592E-67
hyp4_to_hyp6	F48C1.9	3.11594581	2.93961E-66
hyp4_to_hyp6	lips-10	0.954231577	1.3797E-65
hyp4_to_hyp6	rpl-34	-0.37379092	3.39773E-63
hyp4_to_hyp6	myo-2	3.454055161	1.34155E-61
hyp4_to_hyp6	C24A3.2	1.347079129	8.04789E-60
hyp4_to_hyp6	C39E9.8	0.562566684	4.59116E-58
hyp4_to_hyp6	rpl-32	-0.271100633	1.00061E-57
hyp4_to_hyp6	rpl-35	-0.274710258	2.38437E-57
hyp4_to_hyp6	ctc-1	0.320502152	3.81053E-57
hyp4_to_hyp6	C45G9.6	2.253704174	1.0807E-56
hyp4_to_hyp6	rps-28	-0.550584471	1.35093E-56
hyp4_to_hyp6	Y119D3B.21	-0.570652707	7.48709E-56
hyp4_to_hyp6	hsp-16.41	1.386268772	1.0766E-55
hyp4_to_hyp6	F12A10.1	0.71491814	1.98312E-55
hyp4_to_hyp6	rps-21	-0.462483011	3.04913E-54
hyp4_to_hyp6	rpl-43	-0.327624667	8.62663E-53
hyp4_to_hyp6	acs-2	1.287503253	1.72121E-52
hyp4_to_hyp6	tnt-4	2.168810964	1.35166E-51
hyp4_to_hyp6	amt-1	2.370221057	3.942E-51
hyp4_to_hyp6	pud-4	-1.820982416	6.57486E-51
hyp4_to_hyp6	nduo-6	-0.221751108	1.39705E-50
hyp4_to_hyp6	rps-26	-0.265454575	3.01698E-50
hyp4_to_hyp6	asns-2	1.215487613	4.28454E-49
hyp4_to_hyp6	tni-4	1.24565494	9.25856E-49
hyp4_to_hyp6	rps-29	-0.428656116	9.98372E-49
hyp4_to_hyp6	D1086.3	-1.013361813	1.13705E-48
hyp4_to_hyp6	C49F5.7	-0.356809613	1.86709E-48

hyp4_to_hyp6	hsp-16.2	1.123372643	2.40354E-47
hyp4_to_hyp6	rpl-14	-0.272805992	4.97381E-47
hyp4_to_hyp6	fipr-7	2.793366035	5.16947E-47
hyp4_to_hyp6	col-160	0.282510032	2.85979E-45
hyp4_to_hyp6	F35B12.3	2.50499107	6.89507E-45
hyp4_to_hyp6	nlp-25	1.557289145	1.11983E-44
hyp4_to_hyp6	fipr-10	2.425057097	1.89113E-44
hyp4_to_hyp6	rpl-27	-0.336905299	5.82484E-44
hyp4_to_hyp6	atp-2	0.330094145	6.03096E-44
hyp4_to_hyp6	mpc-1	0.438806008	2.54954E-43
hyp4_to_hyp6	mlc-3	0.403132103	3.4249E-43
hyp4_to_hyp6	F18E3.12	0.527742074	4.22346E-43
hyp4_to_hyp6	ttr-26	1.86054313	5.539E-43
hyp4_to_hyp6	rla-2	-0.31014535	1.35629E-42
hyp4_to_hyp6	F17C11.11	-0.906474794	1.8812E-42
hyp4_to_hyp6	rps-12	-0.234902778	4.25383E-42
hyp4_to_hyp6	K07C5.2	0.756250618	6.77261E-42
hyp4_to_hyp6	C27B7.9	0.603529317	1.45376E-41
hyp4_to_hyp6	F32A5.4	2.132186295	9.75651E-41
hyp4_to_hyp6	ttr-21	2.429216885	1.53033E-40
hyp4_to_hyp6	myo-1	3.168830898	1.18778E-39
hyp4_to_hyp6	vamp-8	2.058176638	1.20942E-39
hyp4_to_hyp6	rpl-30	-0.296295889	9.29449E-39
hyp4_to_hyp6	F56H9.2	-0.469033524	1.86066E-38
hyp4_to_hyp6	rpl-21	-0.225880773	1.95073E-38
hyp4_to_hyp6	cpr-5	1.255829248	1.03777E-37
hyp4_to_hyp6	T01D1.4	0.605808262	1.30039E-37
hyp4_to_hyp6	rps-19	-0.203014678	3.78077E-37
hyp4_to_hyp6	fat-1	0.49624163	1.13795E-36
hyp4_to_hyp6	C25H3.10	-1.456802602	1.6053E-36
hyp4_to_hyp6	col-122	0.216365046	3.56203E-36
hyp4_to_hyp6	fipr-5	2.129886602	3.61689E-36
hyp4_to_hyp6	fipr-3	2.696765488	3.7392E-36
hyp4_to_hyp6	rps-23	-0.220472361	4.55606E-36
hyp4_to_hyp6	gpdh-2	0.701936333	5.09584E-36

hyp4_to_hyp6	W01B11.6	0.583555128	1.49107E-35
hyp4_to_hyp6	fip-2	1.554569002	2.3207E-35
hyp4_to_hyp6	C54D10.3	1.344406492	2.30652E-34
hyp4_to_hyp6	gst-27	-0.666516579	3.49866E-34
hyp4_to_hyp6	C45E5.4	2.786638903	4.15191E-34
hyp4_to_hyp6	F44E7.2	0.541301978	7.48568E-34
hyp4_to_hyp6	dhs-21	0.427178062	1.76478E-33
hyp4_to_hyp6	C23H5.8	-0.926890046	2.4027E-33
hyp4_to_hyp6	clec-1	0.392362905	2.51814E-33
hyp4_to_hyp6	ubq-2	-0.225390448	3.41169E-33
hyp4_to_hyp6	col-181	0.199639334	1.37107E-32
hyp4_to_hyp6	rps-15	-0.22634328	2.27675E-32
hyp4_to_hyp6	rpl-31	-0.260293176	3.31492E-32
hyp4_to_hyp6	col-95	-1.563541768	6.06578E-32
hyp4_to_hyp6	ttr-27	1.969831154	9.95399E-32
hyp4_to_hyp6	fipr-11	2.89502269	1.48138E-31
hyp4_to_hyp6	rpl-29	-0.534242526	2.05775E-31
hyp4_to_hyp6	rps-14	-0.181156131	6.57884E-31
hyp4_to_hyp6	rpl-15	-0.228143904	6.73835E-31
hyp4_to_hyp6	lec-10	-0.680533793	1.03925E-30
hyp4_to_hyp6	D1022.4	0.605384342	1.1653E-30
hyp4_to_hyp6	tnt-3	1.358863968	2.84806E-30
hyp4_to_hyp6	rpl-26	-0.22726116	3.74799E-30
hyp4_to_hyp6	T22B7.7	0.585065549	4.26418E-30
hyp4_to_hyp6	Y73F4A.2	3.541599947	4.83137E-30
hyp4_to_hyp6	nhr-68	0.685498044	6.35856E-30
hyp4_to_hyp6	rps-24	-0.230651992	7.96375E-30
hyp4_to_hyp6	rpl-22	-0.239048694	9.85376E-30
hyp4_to_hyp6	Y73F4A.3	4.016100425	2.27266E-29
hyp4_to_hyp6	R09B3.2	-0.376379718	2.41571E-29
hyp4_to_hyp6	C17C3.15	0.503413641	2.94427E-29
hyp4_to_hyp6	hsp-70	1.482246312	6.39243E-29
hyp4_to_hyp6	abf-5	2.420616244	7.42522E-29

hyp4_to_hyp6	fipr-4	2.881551311	8.41313E-29
hyp4_to_hyp6	rps-10	-0.206521731	2.61911E-28
hyp4_to_hyp6	col-139	0.167916532	3.70936E-28
hyp4_to_hyp6	pqn-94	2.315974793	7.29083E-28
hyp4_to_hyp6	spp-2	-1.457450265	1.71111E-27
hyp4_to_hyp6	asp-2	0.896946746	2.05249E-27
hyp4_to_hyp6	col-81	0.183162523	2.15145E-27
hyp4_to_hyp6	ZK512.7	-0.314135711	2.68945E-27
hyp4_to_hyp6	R07H5.8	0.381631751	5.79E-27
hyp4_to_hyp6	col-103	0.277038924	7.90133E-27
hyp4_to_hyp6	Y37E3.8	-0.179652042	8.07706E-27
hyp4_to_hyp6	W10C8.6	2.244351415	1.60429E-26
hyp4_to_hyp6	C37A2.7	-0.290492529	5.47944E-26
hyp4_to_hyp6	rps-13	-0.210329817	9.45964E-26
hyp4_to_hyp6	nit-1	-0.850178224	1.2771E-25
hyp4_to_hyp6	col-129	0.163165277	2.65103E-25
hyp4_to_hyp6	bli-6	-0.493827645	3.58541E-25
hyp4_to_hyp6	F16B4.4	-0.266538688	5.05732E-25
hyp4_to_hyp6	haly-1	-0.797876818	1.35737E-24
hyp4_to_hyp6	metr-1	0.708769863	2.08932E-24
hyp4_to_hyp6	act-4	0.319084776	2.28982E-24
hyp4_to_hyp6	rpl-12	-0.142126667	2.4814E-24
hyp4_to_hyp6	lec-9	-0.467778311	2.52725E-24
hyp4_to_hyp6	F08D12.2	3.179593472	3.4676E-24
hyp4_to_hyp6	nspd-1	-0.678544544	5.28797E-24
hyp4_to_hyp6	ttr-45	1.206892247	1.1287E-23
hyp4_to_hyp6	farl-11	0.688802019	1.21829E-23
hyp4_to_hyp6	col-140	0.145301135	2.17212E-23
hyp4_to_hyp6	rpl-17	-0.168071168	2.46725E-23
hyp4_to_hyp6	unc-15	0.619785262	2.49527E-23
hyp4_to_hyp6	icl-1	0.568786154	3.07245E-23

hyp4_to_hyp6	col-93	0.170732018	3.13843E-23
hyp4_to_hyp6	Y37A1B.5	0.573435743	4.85707E-23
hyp4_to_hyp6	csq-1	1.167591854	4.91437E-23
hyp4_to_hyp6	C33G8.2	-1.140399468	9.45196E-23
hyp4_to_hyp6	pud-3	-1.05892985	1.87892E-22
hyp4_to_hyp6	rpl-33	-0.216546194	5.53133E-22
hyp4_to_hyp6	rps-18	-0.164769039	5.99443E-22
hyp4_to_hyp6	ifa-1	1.915940061	7.63882E-22
hyp4_to_hyp6	mdh-1	0.318186952	7.66456E-22
hyp4_to_hyp6	nspd-2	-0.721932294	8.7784E-22
hyp4_to_hyp6	F22H10.3	-0.678817396	9.22462E-22
hyp4_to_hyp6	fipr-21	-0.223432697	1.30379E-21
hyp4_to_hyp6	F15A4.6	0.742690443	1.32348E-21
hyp4_to_hyp6	rpl-19	-0.169175943	2.09164E-21
hyp4_to_hyp6	clec-47	1.720983685	2.61829E-21
hyp4_to_hyp6	mthf-1	0.45947542	2.62995E-21
hyp4_to_hyp6	ugt-41	0.758453008	3.35381E-21
hyp4_to_hyp6	gpdh-1	0.305243912	3.42263E-21
hyp4_to_hyp6	far-4	2.275399624	5.83452E-21
hyp4_to_hyp6	rpl-23	-0.193424108	6.72568E-21
hyp4_to_hyp6	asp-4	1.046685212	7.07865E-21
hyp4_to_hyp6	col-143	0.241728371	7.98511E-21
hyp4_to_hyp6	F45D3.4	-0.629100203	8.81403E-21
hyp4_to_hyp6	K03E5.2	0.637505658	9.56955E-21
hyp4_to_hyp6	Y79H2A.2	2.592782002	9.89737E-21
hyp4_to_hyp6	col-20	0.15175126	1.39619E-20
hyp4_to_hyp6	rpl-13	-0.158387913	1.80365E-20
hyp4_to_hyp6	spp-5	-0.596426993	2.4812E-20
hyp4_to_hyp6	col-178	0.188099556	3.92619E-20
hyp4_to_hyp6	ZC250.4	0.754540172	4.70755E-20
hyp4_to_hyp6	col-124	0.134280937	5.15742E-20
hyp4_to_hyp6	rps-9	-0.136431121	5.95857E-20
hyp4_to_hyp6	col-98	0.22513351	6.4404E-20

hyp4_to_hyp6	spp-18	-1.276760042	1.00258E-19
hyp4_to_hyp6	F23F12.12	-0.261132818	1.11189E-19
hyp4_to_hyp6	ttr-2	0.625935165	1.17764E-19
hyp4_to_hyp6	rpl-2	-0.180532408	1.44085E-19
hyp4_to_hyp6	rps-22	-0.207324157	1.49162E-19
hyp4_to_hyp6	nspb-6	2.015557338	1.53022E-19
hyp4_to_hyp6	pmp-5	1.114612643	1.98535E-19
hyp4_to_hyp6	nlp-27	-0.253074578	2.76332E-19
hyp4_to_hyp6	T28F4.5	-0.403212494	3.8011E-19
hyp4_to_hyp6	unc-54	0.601619996	5.12955E-19
hyp4_to_hyp6	cpz-1	0.72706928	6.10977E-19
hyp4_to_hyp6	lys-2	-1.032024726	7.01318E-19
hyp4_to_hyp6	nspd-10	-0.851192044	8.61949E-19
hyp4_to_hyp6	C10C5.3	0.857162626	1.0402E-18
hyp4_to_hyp6	ttn-1	0.895034399	1.30001E-18
hyp4_to_hyp6	ZC395.5	-0.58007678	1.40189E-18
hyp4_to_hyp6	col-142	0.23282378	1.45649E-18
hyp4_to_hyp6	F11E6.3	0.218507715	1.71786E-18
hyp4_to_hyp6	anmt-2	1.316407557	2.22943E-18
hyp4_to_hyp6	T24B8.5	-2.196308376	2.43406E-18
hyp4_to_hyp6	sip-1	-0.521773662	2.66708E-18
hyp4_to_hyp6	C53B7.3	2.141840687	3.38076E-18
hyp4_to_hyp6	rps-11	-0.14465046	3.93846E-18
hyp4_to_hyp6	F25E5.8	0.508163106	7.4595E-18
hyp4_to_hyp6	K08D12.6	0.224026463	8.14324E-18
hyp4_to_hyp6	R06C1.4	-0.247632621	9.30661E-18
hyp4_to_hyp6	F13C5.5	2.671500438	1.31938E-17
hyp4_to_hyp6	rps-16	-0.231476114	1.49009E-17
hyp4_to_hyp6	hpo-26	2.144938817	1.4991E-17
hyp4_to_hyp6	ZC116.5	2.430673175	1.62378E-17
hyp4_to_hyp6	msp-31	-0.565615454	1.93782E-17
hyp4_to_hyp6	W03F8.6	1.830250118	2.22463E-17

hyp4_to_hyp6	acdh-1	0.238541783	2.7693E-17
hyp4_to_hyp6	rps-3	-0.168032074	3.21327E-17
hyp4_to_hyp6	F23D12.11	-0.23119495	3.31217E-17
hyp4_to_hyp6	rpl-24.1	-0.154074254	3.60046E-17
hyp4_to_hyp6	ncx-2	2.448156145	5.44882E-17
hyp4_to_hyp6	ZC21.3	3.348971079	6.06009E-17
hyp4_to_hyp6	fipr-9	2.540384159	6.15149E-17
hyp4_to_hyp6	nspb-12	1.514709178	6.7042E-17
hyp4_to_hyp6	fat-5	0.667026775	7.07665E-17
hyp4_to_hyp6	rps-2	-0.188821575	7.80743E-17
hyp4_to_hyp6	cpi-1	-0.27468383	8.61982E-17
hyp4_to_hyp6	rpl-11.1	-0.234734416	1.04561E-16
hyp4_to_hyp6	nspb-8	2.336704018	1.08253E-16
hyp4_to_hyp6	F36F2.1	1.35760534	1.41025E-16
hyp4_to_hyp6	R05F9.6	0.40241987	1.57168E-16
hyp4_to_hyp6	act-2	-0.372462289	1.84024E-16
hyp4_to_hyp6	Y105C5A.8	0.594684612	2.26725E-16
hyp4_to_hyp6	Y110A2AL.9	3.088353097	2.87775E-16
hyp4_to_hyp6	rps-5	-0.145794177	4.01214E-16
hyp4_to_hyp6	H32K16.2	0.354813462	5.47531E-16
hyp4_to_hyp6	gpx-5	0.471285588	6.30506E-16
hyp4_to_hyp6	rla-1	-0.207195768	8.58863E-16
hyp4_to_hyp6	C50F4.8	-0.594173272	9.48902E-16
hyp4_to_hyp6	Y106G6D.8	1.025009689	9.76478E-16
hyp4_to_hyp6	R02C2.7	1.767720776	1.00739E-15
hyp4_to_hyp6	mmaa-1	0.716064973	1.11073E-15
hyp4_to_hyp6	pmt-2	0.19911795	1.21862E-15
hyp4_to_hyp6	C24B5.4	0.483344475	1.40303E-15
hyp4_to_hyp6	rps-17	-0.170130562	1.45186E-15
hyp4_to_hyp6	ttr-22	3.393000648	1.56781E-15
hyp4_to_hyp6	C45E5.1	0.459754677	1.8296E-15
hyp4_to_hyp6	ugt-21	1.403328139	1.86935E-15
hyp4_to_hyp6	mel-32	0.43156493	2.07073E-15
hyp4_to_hyp6	rps-30	-0.171749586	2.27306E-15
hyp4_to_hyp6	F17A9.4	0.640175395	2.33228E-15

hyp4_to_hyp6	nstp-2	0.752997089	2.72891E-15
hyp4_to_hyp6	mpc-2	0.277312491	2.87363E-15
hyp4_to_hyp6	Y48E1B.8	0.73499835	3.18966E-15
hyp4_to_hyp6	rhr-1	-0.568367006	5.46677E-15
hyp4_to_hyp6	F28H7.3	-0.717755705	7.45723E-15
hyp4_to_hyp6	F26D11.1	0.40745963	7.47223E-15
hyp4_to_hyp6	ndfl-4	-0.168513055	7.81333E-15
hyp4_to_hyp6	ZK742.3	0.462863484	9.70362E-15
hyp4_to_hyp6	K09G1.1	0.293968145	1.04632E-14
hyp4_to_hyp6	R09E12.9	1.065152379	1.66823E-14
hyp4_to_hyp6	col-101	-0.227319156	1.69235E-14
hyp4_to_hyp6	alh-1	0.421440233	1.8467E-14
hyp4_to_hyp6	rpl-9	-0.175832066	2.44702E-14
hyp4_to_hyp6	acbp-1	-0.318164078	3.09007E-14
hyp4_to_hyp6	C17F3.1	-0.49991337	4.06459E-14
hyp4_to_hyp6	rps-7	-0.140748528	4.90336E-14
hyp4_to_hyp6	F19B2.5	-0.915381215	5.34239E-14
hyp4_to_hyp6	mtrr-1	0.674310338	5.39798E-14
hyp4_to_hyp6	F01D5.3	-1.201525501	5.56907E-14
hyp4_to_hyp6	aqp-8	0.488520035	6.49598E-14
hyp4_to_hyp6	acdh-2	-0.680122049	8.31098E-14
hyp4_to_hyp6	eat-6	0.39890268	9.42435E-14
hyp4_to_hyp6	rpl-16	-0.158606267	9.81162E-14
hyp4_to_hyp6	C17F4.7	0.372168718	1.15944E-13
hyp4_to_hyp6	iff-2	0.232018817	1.22501E-13
hyp4_to_hyp6	F02D8.5	1.787843509	1.25906E-13
hyp4_to_hyp6	abf-6	3.303426311	1.28544E-13
hyp4_to_hyp6	cah-4	-0.376280056	1.55948E-13
hyp4_to_hyp6	lec-8	-0.645678507	2.06919E-13
hyp4_to_hyp6	col-119	0.161055548	2.80703E-13
hyp4_to_hyp6	pudl-1	1.993142943	4.35429E-13
hyp4_to_hyp6	fipr-6	2.19882265	4.96675E-13

hyp4_to_hyp6	apy-1	0.683950259	5.31759E-13
hyp4_to_hyp6	pqn-31	2.220030624	6.26488E-13
hyp4_to_hyp6	vit-2	0.581621812	6.89717E-13
hyp4_to_hyp6	ZK1320.9	0.380715705	7.56622E-13
hyp4_to_hyp6	cnc-2	-1.65142697	8.53869E-13
hyp4_to_hyp6	F46G10.1	-0.517106975	1.11517E-12
hyp4_to_hyp6	rpl-28	-0.196470811	1.31596E-12
hyp4_to_hyp6	acer-1	0.346326582	1.56546E-12
hyp4_to_hyp6	fip-5	-0.573497148	1.64038E-12
hyp4_to_hyp6	F55G11.4	-2.156416984	2.00414E-12
hyp4_to_hyp6	Y43F8B.2	0.588445695	2.14186E-12
hyp4_to_hyp6	gst-28	-0.45218829	3.66262E-12
hyp4_to_hyp6	M03F4.6	0.621035639	4.32717E-12
hyp4_to_hyp6	comt-5	0.570035727	4.4476E-12
hyp4_to_hyp6	R02D1.2	0.498591687	4.71686E-12
hyp4_to_hyp6	gst-2	0.369567625	5.06806E-12
hyp4_to_hyp6	C10B5.3	1.735196194	6.351E-12
hyp4_to_hyp6	D1054.18	-0.420463942	7.58383E-12
hyp4_to_hyp6	ZK622.4	1.473215242	8.91299E-12
hyp4_to_hyp6	ZC449.5	2.628862846	1.33756E-11
hyp4_to_hyp6	C08E8.10	-0.618871963	1.50382E-11
hyp4_to_hyp6	Y46G5A.36	0.992429614	1.56248E-11
hyp4_to_hyp6	mlc-2	0.26260807	1.79911E-11
hyp4_to_hyp6	nlp-28	-0.329524814	1.85703E-11
hyp4_to_hyp6	rpl-7	-0.15259052	2.24441E-11
hyp4_to_hyp6	ctc-2	0.162770254	2.84095E-11
hyp4_to_hyp6	gst-26	-0.657618228	2.90867E-11
hyp4_to_hyp6	C15H9.9	0.412971279	2.98315E-11
hyp4_to_hyp6	T21D12.12	0.749482033	3.17322E-11
hyp4_to_hyp6	rpl-25.2	-0.184151578	3.22992E-11
hyp4_to_hyp6	clec-150	-0.824429907	3.85736E-11
hyp4_to_hyp6	ant-1.1	0.105272649	4.79931E-11
hyp4_to_hyp6	rpl-10	-0.120110696	5.951E-11
hyp4_to_hyp6	marg-1	2.254353503	7.25741E-11

hyp4_to_hyp6	F46F2.3	-0.282397665	8.25488E-11
hyp4_to_hyp6	F57H12.6	-0.993123261	9.91718E-11
hyp4_to_hyp6	rpl-20	-0.144934325	1.18574E-10
hyp4_to_hyp6	rpl-5	-0.1383653	1.33493E-10
hyp4_to_hyp6	F14F8.8	3.181905919	2.08699E-10
hyp4_to_hyp6	far-2	0.22896953	2.38555E-10
hyp4_to_hyp6	col-159	0.159843859	3.06381E-10
hyp4_to_hyp6	rps-8	-0.124371705	3.09063E-10
hyp4_to_hyp6	T04G9.7	-0.423690648	3.31786E-10
hyp4_to_hyp6	C29F7.3	0.293799653	5.77537E-10
hyp4_to_hyp6	DH11.2	0.38461524	6.30314E-10
hyp4_to_hyp6	C35C5.9	-0.316421378	6.57898E-10
hyp4_to_hyp6	mct-3	0.665893952	6.62763E-10
hyp4_to_hyp6	W01F3.2	-0.390619038	7.33685E-10
hyp4_to_hyp6	col-12	-0.395997408	7.38766E-10
hyp4_to_hyp6	gpx-3	2.215051894	7.49192E-10
hyp4_to_hyp6	piit-1	2.677507586	8.43344E-10
hyp4_to_hyp6	rps-0	-0.158255741	8.6055E-10
hyp4_to_hyp6	F46C5.10	0.270657825	9.84378E-10
hyp4_to_hyp6	eef-2	-0.169664805	1.38977E-09
hyp4_to_hyp6	ssp-10	-0.271175417	1.47484E-09
hyp4_to_hyp6	ubl-1	-0.131256433	1.82199E-09
hyp4_to_hyp6	F23A7.8	-0.626156645	1.83973E-09
hyp4_to_hyp6	col-147	0.213973313	2.07232E-09
hyp4_to_hyp6	col-8	0.166987621	2.26749E-09
hyp4_to_hyp6	fbxa-72	0.382091068	2.29452E-09
hyp4_to_hyp6	Y39B6A.1	-0.605728791	2.62208E-09
hyp4_to_hyp6	C30F2.3	2.827651946	2.84181E-09
hyp4_to_hyp6	ZK970.7	-1.931308527	3.04305E-09
hyp4_to_hyp6	F26E4.3	0.965112541	3.38329E-09

hyp4_to_hyp6	gdh-1	-0.205211254	3.66132E-09
hyp4_to_hyp6	clec-50	-0.498051495	3.90213E-09
hyp4_to_hyp6	F14H12.3	3.49263329	4.68348E-09
hyp4_to_hyp6	cth-2	0.220069648	5.04173E-09
hyp4_to_hyp6	C29G2.6	0.384280695	5.18628E-09
hyp4_to_hyp6	cyp-29A2	0.816133852	5.4607E-09
hyp4_to_hyp6	ZK863.8	1.274376672	5.48432E-09
hyp4_to_hyp6	lys-7	-1.056370217	5.50328E-09
hyp4_to_hyp6	M28.5	-0.222455094	5.68823E-09
hyp4_to_hyp6	Y71F9B.13	0.564313169	5.85741E-09
hyp4_to_hyp6	ccg-1	0.705224926	5.91402E-09
hyp4_to_hyp6	ttr-29	1.833333299	5.92253E-09
hyp4_to_hyp6	iff-1	-0.202892093	6.12722E-09
hyp4_to_hyp6	F43D2.6	0.951965832	6.84525E-09
hyp4_to_hyp6	eef-1B.1	-0.126457724	7.2663E-09
hyp4_to_hyp6	cey-2	-0.322600472	7.39304E-09
hyp4_to_hyp6	asp-13	0.77071605	7.64595E-09
hyp4_to_hyp6	fat-7	1.690997063	1.03234E-08
hyp4_to_hyp6	cgh-1	-0.367092909	1.03445E-08
hyp4_to_hyp6	C06A8.8	2.049947877	1.04684E-08
hyp4_to_hyp6	tsp-16	3.323033054	1.11296E-08
hyp4_to_hyp6	F55A4.7	2.347582498	1.12138E-08
hyp4_to_hyp6	F54C9.3	-0.778913435	1.4193E-08
hyp4_to_hyp6	alh-5	1.160648373	1.70159E-08
hyp4_to_hyp6	ugt-19	0.524712786	1.79431E-08
hyp4_to_hyp6	C44B11.6	0.626865602	1.8596E-08
hyp4_to_hyp6	rps-20	-0.133734221	1.86663E-08
hyp4_to_hyp6	C33A12.19	-0.436003345	2.03053E-08
hyp4_to_hyp6	H24K24.3	0.355874271	2.74861E-08
hyp4_to_hyp6	F08B12.4	0.764818337	2.88067E-08
hyp4_to_hyp6	F40A3.2	0.357399169	2.9842E-08
hyp4_to_hyp6	msp-57	-0.630388648	3.59794E-08

hyp4_to_hyp6	msp-152	-0.583654908	4.54238E-08
hyp4_to_hyp6	T19B10.2	0.675082348	5.80135E-08
hyp4_to_hyp6	dhs-5	1.329680271	5.80261E-08
hyp4_to_hyp6	ZK593.3	1.007193351	6.01382E-08
hyp4_to_hyp6	ras-2	0.295596215	6.22792E-08
hyp4_to_hyp6	pgp-14	1.903002726	6.74911E-08
hyp4_to_hyp6	H28O16.1	0.167100134	7.28539E-08
hyp4_to_hyp6	ipgm-1	0.400659622	8.8319E-08
hyp4_to_hyp6	F19C6.4	-3.28125738	9.78665E-08
hyp4_to_hyp6	nkb-3	0.796583292	1.03966E-07
hyp4_to_hyp6	T20G5.8	0.534854116	1.16313E-07
hyp4_to_hyp6	dod-3	-1.485532258	1.23902E-07
hyp4_to_hyp6	C48E7.1	0.340376752	1.27379E-07
hyp4_to_hyp6	cpl-1	0.503688188	1.30943E-07
hyp4_to_hyp6	F23A7.4	-0.639173138	1.3162E-07
hyp4_to_hyp6	F42A8.1	0.364130935	1.40601E-07
hyp4_to_hyp6	eef-1A.1	-0.113719414	1.69226E-07
hyp4_to_hyp6	rpl-6	-0.123397552	1.69777E-07
hyp4_to_hyp6	unc-89	0.660794717	1.74895E-07
hyp4_to_hyp6	ssp-35	-0.321376786	2.01261E-07
hyp4_to_hyp6	msp-76	-0.351133729	2.08068E-07
hyp4_to_hyp6	sod-3	-0.588662202	2.11011E-07
hyp4_to_hyp6	C35A5.3	0.604273065	2.15231E-07
hyp4_to_hyp6	C37C3.12	2.558085437	2.21782E-07
hyp4_to_hyp6	C23G10.6	1.043191237	2.26939E-07
hyp4_to_hyp6	cpna-2	0.650750774	2.57482E-07
hyp4_to_hyp6	F22B5.4	1.492479599	2.64414E-07
hyp4_to_hyp6	R08E5.1	-0.437706146	2.78187E-07
hyp4_to_hyp6	dod-6	0.548212483	2.80916E-07
hyp4_to_hyp6	ZK809.8	0.383401615	2.83616E-07
hyp4_to_hyp6	ttr-18	0.271802142	2.96537E-07
hyp4_to_hyp6	cysl-3	-0.938855087	3.26051E-07
hyp4_to_hyp6	apl-1	0.740721961	3.34988E-07
hyp4_to_hyp6	Y22D7AL.10	0.197140144	3.54234E-07
hyp4_to_hyp6	nspb-11	2.164963349	4.01183E-07

hyp4_to_hyp6	gst-8	0.468783351	4.66692E-07
hyp4_to_hyp6	gst-13	-0.30127282	5.11325E-07
hyp4_to_hyp6	dod-19	-1.1658886	5.21313E-07
hyp4_to_hyp6	col-19	0.108560557	5.61727E-07
hyp4_to_hyp6	C32D5.12	0.990216283	6.97743E-07
hyp4_to_hyp6	rpl-7A	-0.136382253	8.4414E-07
hyp4_to_hyp6	F08D12.3	3.32170037	8.65733E-07
hyp4_to_hyp6	flp-22	2.035598082	9.51817E-07
hyp4_to_hyp6	fat-2	0.286568037	9.56994E-07
hyp4_to_hyp6	ssp-19	-0.594293166	1.13723E-06
hyp4_to_hyp6	fip-6	-0.591520335	1.42343E-06
hyp4_to_hyp6	nhr-43	0.460568995	1.4855E-06
hyp4_to_hyp6	F53F4.13	0.410614346	1.51806E-06
hyp4_to_hyp6	F01D5.2	-1.250555296	1.64234E-06
hyp4_to_hyp6	M163.8	0.506895272	1.6983E-06
hyp4_to_hyp6	msp-49	-0.489993346	1.73228E-06
hyp4_to_hyp6	Y41C4A.11	3.106475915	1.7968E-06
hyp4_to_hyp6	rack-1	-0.133115557	1.80021E-06
hyp4_to_hyp6	nspd-3	-0.686761988	1.97341E-06
hyp4_to_hyp6	fmo-5	0.639895382	2.09492E-06
hyp4_to_hyp6	T25B9.1	-0.28387637	2.40386E-06
hyp4_to_hyp6	dhs-19	0.597316712	2.52078E-06
hyp4_to_hyp6	cpt-5	0.738251248	3.10753E-06
hyp4_to_hyp6	T04C12.3	1.706295096	3.55525E-06
hyp4_to_hyp6	F18E3.13	0.163084856	3.82042E-06
hyp4_to_hyp6	asb-2	0.213522202	3.85556E-06
hyp4_to_hyp6	msd-4	-0.240535701	4.19865E-06
hyp4_to_hyp6	K10H10.12	1.871028348	4.54226E-06
hyp4_to_hyp6	ssq-1	-0.056181226	5.17751E-06
hyp4_to_hyp6	F58F12.1	0.14242971	5.82833E-06
hyp4_to_hyp6	comt-3	0.379879329	7.18389E-06
hyp4_to_hyp6	lbp-1	0.359033784	7.27583E-06
hyp4_to_hyp6	Y43F8B.1	0.548968969	8.96833E-06
hyp4_to_hyp6	K07C5.4	-0.276896111	9.7044E-06

hyp4_to_hyp6	F49F1.5	-1.869046531	9.97293E-06
hyp4_to_hyp6	srp-2	-0.353192971	1.05722E-05
hyp4_to_hyp6	nlp-36	-0.408933599	1.06556E-05
hyp4_to_hyp6	msp-33	-0.511285698	1.08215E-05
hyp4_to_hyp6	F44E5.1	-0.243419707	1.10845E-05
hyp4_to_hyp6	sbt-1	1.140907472	1.16779E-05
hyp4_to_hyp6	tni-3	0.236274651	1.18897E-05
hyp4_to_hyp6	W02H5.8	0.668899928	1.32444E-05
hyp4_to_hyp6	spc-1	0.952350175	1.37051E-05
hyp4_to_hyp6	mdh-2	0.246561483	1.42387E-05
hyp4_to_hyp6	F48D6.4	0.238071601	1.45803E-05
hyp4_to_hyp6	unc-22	0.684258584	1.62203E-05
hyp4_to_hyp6	fmo-2	1.530818508	1.64338E-05
hyp4_to_hyp6	T18D3.5	2.611921271	1.74444E-05
hyp4_to_hyp6	F53C11.3	0.28985547	1.8109E-05
hyp4_to_hyp6	T23B12.11	1.017050126	2.09378E-05
hyp4_to_hyp6	F22F4.4	-0.403367081	2.2235E-05
hyp4_to_hyp6	alh-10	0.398373396	2.34945E-05
hyp4_to_hyp6	F26F2.8	3.084556874	2.4509E-05
hyp4_to_hyp6	Y71F9B.1	0.383780192	2.49283E-05
hyp4_to_hyp6	fipr-8	3.050223274	2.50249E-05
hyp4_to_hyp6	zip-2	-0.444361894	2.59309E-05
hyp4_to_hyp6	C53D6.7	0.35771498	2.66052E-05
hyp4_to_hyp6	K11H12.7	0.577744134	2.78792E-05
hyp4_to_hyp6	W06A7.4	0.422670543	2.9437E-05
hyp4_to_hyp6	oig-3	0.58989111	2.99018E-05
hyp4_to_hyp6	R53.4	0.124376525	3.20525E-05
hyp4_to_hyp6	F08B4.8	-1.331693201	3.21761E-05
hyp4_to_hyp6	K11H3.3	0.498896415	3.37778E-05
hyp4_to_hyp6	F46C3.6	0.375257978	3.44027E-05
hyp4_to_hyp6	col-13	-0.421440906	3.52297E-05
hyp4_to_hyp6	F36A2.3	0.369310123	4.02066E-05
hyp4_to_hyp6	rpl-11.2	-0.134693549	4.18435E-05
hyp4_to_hyp6	haao-1	0.263807695	4.22093E-05
hyp4_to_hyp6	cal-3	2.707968758	4.22257E-05

hyp4_to_hyp6	rpl-1	-0.110510285	4.72768E-05
hyp4_to_hyp6	pccb-1	0.277876069	4.77271E-05
hyp4_to_hyp6	Y53C12B.7	-0.421076063	4.91563E-05
hyp4_to_hyp6	nhr-10	0.627201684	5.19589E-05
hyp4_to_hyp6	C06A6.4	0.235658459	5.24179E-05
hyp4_to_hyp6	Y17D7B.4	-0.625963402	5.24789E-05
hyp4_to_hyp6	ben-1	1.43856097	5.26087E-05
hyp4_to_hyp6	cco-2	0.140824834	5.30792E-05
hyp4_to_hyp6	rpl-18	-0.107407525	5.77047E-05
hyp4_to_hyp6	gst-35	0.062490834	5.99031E-05
hyp4_to_hyp6	F22F4.9	1.109847269	6.50901E-05
hyp4_to_hyp6	sqrd-1	-0.479808847	6.78581E-05
hyp4_to_hyp6	spp-17	-0.284653474	6.79073E-05
hyp4_to_hyp6	cbl-1	-0.380494558	7.01903E-05
hyp4_to_hyp6	daf-22	0.488068585	7.34789E-05
hyp4_to_hyp6	ifa-4	0.972812781	7.39056E-05
hyp4_to_hyp6	dct-18	-0.420399911	7.7049E-05
hyp4_to_hyp6	C28C12.4	2.619175015	7.79675E-05
hyp4_to_hyp6	upb-1	0.171467465	8.33317E-05
hyp4_to_hyp6	F54D5.12	0.338413731	8.68834E-05
hyp4_to_hyp6	lipl-2	-1.66353614	8.71017E-05
hyp4_to_hyp6	poml-2	0.488944652	8.90485E-05
hyp4_to_hyp6	sucl-2	0.287136806	9.30241E-05
hyp4_to_hyp6	atp-5	0.14190054	9.37446E-05
hyp4_to_hyp6	F52A8.1	0.219961196	9.9279E-05
hyp4_to_hyp6	T19H12.6	1.06414663	0.000101882
hyp4_to_hyp6	nspa-8	-0.90349915	0.000103737
hyp4_to_hyp6	lec-7	2.357910106	0.000104921
hyp4_to_hyp6	rpl-25.1	-0.261040959	0.000105705
hyp4_to_hyp6	grd-5	1.072115737	0.000107504
hyp4_to_hyp6	nlp-42	3.974433809	0.000122051
hyp4_to_hyp6	ttr-59	0.190090141	0.000132454
hyp4_to_hyp6	vha-13	-0.203228194	0.000134084
hyp4_to_hyp6	T23B3.2	1.242908275	0.000143023

hyp4_to_hyp6	msp-45	-0.517647602	0.000146345
hyp4_to_hyp6	Y42H9AR.5	-0.684464069	0.000148791
hyp4_to_hyp6	flp-8	2.747912142	0.000149851
hyp4_to_hyp6	cnc-8	-0.198969165	0.000156343
hyp4_to_hyp6	spp-4	-0.892631439	0.000170905
hyp4_to_hyp6	fib-1	-0.220120291	0.000180394
hyp4_to_hyp6	tag-290	0.726508603	0.000199089
hyp4_to_hyp6	C50B8.1	0.315606808	0.000199203
hyp4_to_hyp6	Y95B8A.2	-1.052675499	0.000208518
hyp4_to_hyp6	F17C8.9	0.227208638	0.000222453
hyp4_to_hyp6	nlp-31	0.420054942	0.000230343
hyp4_to_hyp6	F36H9.4	0.305669708	0.000240685
hyp4_to_hyp6	F13H8.3	0.943277209	0.000241523
hyp4_to_hyp6	acox-1.1	0.504836423	0.000242416
hyp4_to_hyp6	lbp-9	-0.201052735	0.000245226
hyp4_to_hyp6	tct-1	-0.177738359	0.000314512
hyp4_to_hyp6	F45E1.4	-0.344564233	0.000317909
hyp4_to_hyp6	cyp-13B1	1.751026922	0.000323224
hyp4_to_hyp6	F35E12.9	-0.570139203	0.000331018
hyp4_to_hyp6	col-80	0.0886728	0.000345825
hyp4_to_hyp6	asah-1	-1.015294205	0.000353545
hyp4_to_hyp6	mua-3	-0.462421613	0.000360473
hyp4_to_hyp6	nduo-4	-0.106570213	0.000370169
hyp4_to_hyp6	msp-38	-0.483854045	0.000370277
hyp4_to_hyp6	R09E10.13	0.29965384	0.000375489
hyp4_to_hyp6	R09H10.3	-0.386351425	0.000382545
hyp4_to_hyp6	ugt-26	0.57928725	0.000401843
hyp4_to_hyp6	Y11D7A.10	-0.42542073	0.00040508
hyp4_to_hyp6	unc-87	0.241809291	0.00042125
hyp4_to_hyp6	Y44A6D.2	1.375612312	0.000431962

hyp4_to_hyp6	nhr-62	0.996704996	0.000487123
hyp4_to_hyp6	ech-1.2	0.441480065	0.00048824
hyp4_to_hyp6	dhrs-4	0.378932769	0.000494776
hyp4_to_hyp6	Y47G6A.19	0.439685828	0.000498584
hyp4_to_hyp6	nduo-1	0.103705849	0.000515573
hyp4_to_hyp6	C31C9.7	0.208112499	0.00052797
hyp4_to_hyp6	K03H6.2	-0.996799574	0.000557009
hyp4_to_hyp6	ugt-44	-0.522759825	0.000564373
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hyp4_to_hyp6	msp-50	-0.576612666	0.000595099
hyp4_to_hyp6	C25H3.9	0.227376873	0.000604127
hyp4_to_hyp6	B0238.12	1.659297054	0.000623377
hyp4_to_hyp6	vit-5	0.407166797	0.000631053
hyp4_to_hyp6	C44C1.1	0.375072321	0.000646621
hyp4_to_hyp6	unc-68	0.678543046	0.000655341
hyp4_to_hyp6	F55C10.5	1.467654738	0.000685739
hyp4_to_hyp6	sca-1	0.443876128	0.000688011
hyp4_to_hyp6	nlp-17	2.287762869	0.000723521
hyp4_to_hyp6	grd-10	1.281360599	0.000739862
hyp4_to_hyp6	cyp-25A3	1.090768114	0.000774115
hyp4_to_hyp6	ZC204.12	-0.745439368	0.000776533
hyp4_to_hyp6	myo-5	0.88912889	0.000811153
hyp4_to_hyp6	ZK836.3	1.740152121	0.000842435
hyp4_to_hyp6	best-14	0.313632959	0.000874848
hyp4_to_hyp6	K07C11.7	1.548726578	0.000887407
hyp4_to_hyp6	Y111B2A.2	-0.228339577	0.000904101
hyp4_to_hyp6	T05A7.1	0.486955603	0.000916418
hyp4_to_hyp6	trap-1	0.402852098	0.000937536
hyp4_to_hyp6	C48B6.10	-0.297478309	0.000938172
hyp4_to_hyp6	F18C5.10	1.087095918	0.000952459
hyp4_to_hyp6	B0303.3	0.388327682	0.000984077
hyp4_to_hyp6	Y54E10A.17	0.240367428	0.000987339
hyp4_to_hyp6	ifb-2	-0.618194611	0.0009934
hyp4_to_hyp6	H04D03.4	0.660461732	0.000997068
hyp4_to_hyp6	asg-2	0.15249301	0.001027964
hyp4_to_hyp6	avr-15	1.410121024	0.001140069

hyp4_to_hyp6	dhs-26	0.098003407	0.001167768
hyp4_to_hyp6	nspb-9	1.75418056	0.001222936
hyp4_to_hyp6	W07A12.8	2.454757734	0.001228279
hyp4_to_hyp6	lbp-6	-0.128521305	0.001248512
hyp4_to_hyp6	ssq-2	-0.234511426	0.001270375
hyp4_to_hyp6	gst-38	-0.981621394	0.001277156
hyp4_to_hyp6	M7.12	0.646125553	0.001364799
hyp4_to_hyp6	B0272.3	0.373348833	0.001371722
hyp4_to_hyp6	T12D8.5	-0.781450933	0.001383678
hyp4_to_hyp6	aqp-2	0.931501927	0.001457765
hyp4_to_hyp6	F40G12.2	2.373107356	0.001478863
hyp4_to_hyp6	Y50D4B.1	2.262606012	0.001485758
hyp4_to_hyp6	K06A4.7	-0.523395105	0.001589663
hyp4_to_hyp6	msp-40	-0.27951572	0.001624818
hyp4_to_hyp6	F41G3.10	0.532616644	0.001670237
hyp4_to_hyp6	K07C11.3	0.744866307	0.001758926
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hyp4_to_hyp6	got-2.2	-0.297605117	0.001813253
hyp4_to_hyp6	R08E3.1	-0.759563694	0.001895317
hyp4_to_hyp6	Y57G11C.31	0.516801403	0.001901982
hyp4_to_hyp6	E02H9.3	-0.725532717	0.001940925
hyp4_to_hyp6	F35A5.2	0.491866439	0.001949802
hyp4_to_hyp6	spp-1	-0.562397475	0.001956587
hyp4_to_hyp6	ketn-1	0.68112844	0.00197239
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hyp4_to_hyp6	lev-11	0.162038366	0.002091764
hyp4_to_hyp6	pud-1.2	-0.85397138	0.002097536
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hyp4_to_hyp6	C01G10.15	1.97348101	0.002493377
hyp4_to_hyp6	F44A6.5	0.723544348	0.002546995
hyp4_to_hyp6	cey-3	-0.275094423	0.002654792
hyp4_to_hyp6	dpyd-1	-0.331669175	0.002932755
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hyp4_to_hyp6	F09F9.1	3.796206356	0.003036584
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hyp4_to_hyp6	ZK822.2	0.525238562	0.003269095
hyp4_to_hyp6	acs-5	0.648483803	0.003323672
hyp4_to_hyp6	hsp-60	0.202204995	0.003347333
hyp4_to_hyp6	T13F3.6	0.140556511	0.00337086
hyp4_to_hyp6	ugt-25	0.540835792	0.003440082
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hyp4_to_hyp6	Y60A3A.21	1.202112815	0.003558815
hyp4_to_hyp6	gas-1	0.370854991	0.003658234
hyp4_to_hyp6	pgp-6	-0.665845904	0.003798151
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hyp4_to_hyp6	ugt-12	0.254646279	0.004129905
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hyp4_to_hyp6	F55G11.8	-1.43351905	0.005936892
hyp4_to_hyp6	pqn-44	0.64342792	0.006093639
hyp4_to_hyp6	Y26E6A.3	0.245149734	0.006196685

hyp4_to_hyp6	swt-3	-0.547467342	0.006578165
hyp4_to_hyp6	acox-1.5	-0.45689395	0.006650018
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hyp4_to_hyp6	ric-4	1.325529711	0.007148599
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hyp4_to_hyp6	T15B7.1	0.948932697	0.007630598
hyp4_to_hyp6	nhr-11	0.908886094	0.007844814
hyp4_to_hyp6	col-77	-0.678380271	0.00787863
hyp4_to_hyp6	rpl-4	-0.11957437	0.008097228
hyp4_to_hyp6	T22B11.4	1.86587431	0.008120613
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hyp4_to_hyp6	C06G3.5	0.529873931	0.008178661
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hyp4_to_hyp6	casy-1	2.089734152	0.009703039
hyp4_to_hyp6	swt-6	0.717450644	0.009714407
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hyp4_to_hyp6	vha-12	-0.209960115	0.010097393
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hyp4_to_hyp6	F22F7.8	-0.427788606	0.011435424
hyp4_to_hyp6	nuo-6	0.194612276	0.011547596
hyp4_to_hyp6	F23H11.5	-0.11823833	0.011623743
hyp4_to_hyp6	argk-1	0.391514961	0.011653668
hyp4_to_hyp6	col-96	1.25015458	0.012042091
hyp4_to_hyp6	hpo-18	-0.23578231	0.012308586
hyp4_to_hyp6	spp-3	-0.385691795	0.012610767
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hyp4_to_hyp6	col-71	-0.670832043	0.01498844
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hyp4_to_hyp6	inx-6	3.144000497	0.016731976
hyp4_to_hyp6	asp-5	0.341442285	0.017968711
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hyp4_to_hyp6	nhr-237	1.127321199	0.01828113
hyp4_to_hyp6	fipr-13	1.321360236	0.018431501
hyp4_to_hyp6	unc-13	2.802087976	0.018981786
hyp4_to_hyp6	vha-8	-0.15069418	0.019035989
hyp4_to_hyp6	T23E7.2	0.527593776	0.01954918
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hyp4_to_hyp6	F01G4.6	0.139973896	0.022100584

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hyp4_to_hyp6	R13D11.4	1.429571701	0.023619581
hyp4_to_hyp6	lpd-5	0.196352845	0.024729424
hyp4_to_hyp6	cyp-35A2	1.113127682	0.025249543
hyp4_to_hyp6	F35H10.3	0.436162081	0.025535403
hyp4_to_hyp6	mig-6	0.592782005	0.025900245
hyp4_to_hyp6	ril-1	0.128020544	0.025931649
hyp4_to_hyp6	T01D1.3	0.592122987	0.025985948
hyp4_to_hyp6	gly-8	0.488256914	0.026432236
hyp4_to_hyp6	calu-1	0.254115415	0.027296419
hyp4_to_hyp6	pcca-1	0.292683314	0.02970432
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hyp4_to_hyp6	mlc-1	0.197505722	0.030347425
hyp4_to_hyp6	cyp-34A9	0.857243736	0.030930799
hyp4_to_hyp6	msa-1	0.474948874	0.031642218
hyp4_to_hyp6	nspb-10	1.315671651	0.032216655
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hyp4_to_hyp6	Y54G2A.36	-0.891421283	0.033141893
hyp4_to_hyp6	dct-5	-1.101915448	0.033687965
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hyp4_to_hyp6	T07E3.4	0.385234512	0.040178115
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hyp4_to_hyp6	gpd-3	-0.151392085	0.042141777
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hyp4_to_hyp6	smo-1	-0.208493279	0.043647405

hyp4_to_hyp6	npa-1	-0.599521734	0.045629969
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hyp4_to_hyp6	idhb-1	0.385694579	0.051587047
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hyp4_to_hyp6	egl-9	1.201736697	0.054301202
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hyp4_to_hyp6	isp-1	0.153873575	0.057447276
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hyp4_to_hyp6	rpb-12	-0.213402871	0.058878355
hyp4_to_hyp6	nduo-3	-0.189881197	0.061430448
hyp4_to_hyp6	pmp-2	0.563947534	0.061762808
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hyp4_to_hyp6	F53A9.8	-0.813834126	0.062597883
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hyp4_to_hyp6	nlp-26	0.288200509	0.063964244
hyp4_to_hyp6	msp-78	-0.465302474	0.065073852
hyp4_to_hyp6	lam-1	1.094839678	0.065159614
hyp4_to_hyp6	nlp-15	1.579564459	0.066747984
hyp4_to_hyp6	grd-3	1.191980646	0.068445005
hyp4_to_hyp6	D1086.12	0.029477197	0.068710323
hyp4_to_hyp6	acs-19	-0.309801243	0.073181351
hyp4_to_hyp6	odc-1	-0.617099361	0.073610675
hyp4_to_hyp6	col-118	0.748817253	0.07366983
hyp4_to_hyp6	C52G5.2	0.29574065	0.076972124
hyp4_to_hyp6	F27D4.1	0.247225495	0.077287785
hyp4_to_hyp6	ttr-23	1.036186078	0.078656758
hyp4_to_hyp6	Y50E8A.5	2.394791196	0.079737319
hyp4_to_hyp6	paf-2	0.554317305	0.079761715
hyp4_to_hyp6	tbcb-1	-0.362559774	0.080101433
hyp4_to_hyp6	nex-3	0.97093417	0.082874005

hyp4_to_hyp6	nol-5	-0.211124022	0.084919882
hyp4_to_hyp6	flp-28	1.880822916	0.08595818
hyp4_to_hyp6	R05H5.3	-0.311734919	0.087889728
hyp4_to_hyp6	F33H12.7	-1.840213406	0.090698896
hyp4_to_hyp6	F09B12.7	1.451892087	0.091520604
hyp4_to_hyp6	K09A9.6	2.489336059	0.09481402
hyp4_to_hyp6	lec-6	-0.272277307	0.096439842
hyp4_to_hyp6	col-106	0.081026029	0.098372609
hyp4_to_hyp6	B0035.13	-0.448026406	0.098679939
hyp4_to_hyp6	col-162	-0.665728333	0.099857197
hyp7 (hypodermis)	far-3	1.5868646	5.88198E-77
hyp7 (hypodermis)	cpi-1	-0.769237986	9.04022E-47
hyp7 (hypodermis)	ctc-3	0.514787224	4.13921E-40
hyp7 (hypodermis)	C14C6.5	-1.300736521	1.35609E-38
hyp7 (hypodermis)	ant-1.1	0.336595255	7.18678E-35
hyp7 (hypodermis)	ndk-1	0.314106091	2.24308E-31
hyp7 (hypodermis)	R08E5.3	-1.357663971	3.10116E-31
hyp7 (hypodermis)	ctc-1	0.475683026	2.01844E-30
hyp7 (hypodermis)	pud-3	-2.508953982	6.59066E-30
hyp7 (hypodermis)	pud-4	-2.469201675	1.97678E-28
hyp7 (hypodermis)	T03F1.11	2.215516805	1.2808E-27
hyp7 (hypodermis)	clec-50	-0.913284361	1.00557E-26
hyp7 (hypodermis)	cyc-2.1	0.583632185	4.59118E-26
hyp7 (hypodermis)	col-154	-0.720425629	2.10368E-25
hyp7 (hypodermis)	col-150	-0.983444466	2.57984E-25
hyp7 (hypodermis)	F55G11.4	-2.135502874	3.95245E-25
hyp7 (hypodermis)	C45B2.1	-0.765418025	3.31559E-24
hyp7 (hypodermis)	dod-19	-1.52126934	1.81748E-21
hyp7 (hypodermis)	pck-2	0.617005376	2.44475E-20
hyp7 (hypodermis)	F23F1.2	-1.11718456	3.96619E-20

hyp7 (hypodermis)	Y82E9BR.3	0.28790975	6.43573E-20
hyp7 (hypodermis)	F41E6.15	2.035137227	5.71068E-19
hyp7 (hypodermis)	gst-4	1.091216944	6.03031E-19
hyp7 (hypodermis)	nlp-29	-0.88782872	2.98827E-18
hyp7 (hypodermis)	hsp-12.2	1.317691104	1.46526E-17
hyp7 (hypodermis)	clec-47	1.948804298	1.79011E-17
hyp7 (hypodermis)	orai-1	-1.182359817	4.51756E-17
hyp7 (hypodermis)	F13D12.3	-1.502092745	8.99821E-17
hyp7 (hypodermis)	lys-4	0.598578274	1.12844E-16
hyp7 (hypodermis)	cnc-4	-0.789416419	5.99085E-16
hyp7 (hypodermis)	nlp-31	-0.788085721	1.36843E-15
hyp7 (hypodermis)	R04F11.2	0.340673576	3.00975E-15
hyp7 (hypodermis)	sodh-1	1.299336064	3.13981E-15
hyp7 (hypodermis)	lys-7	-0.980817185	6.2467E-15
hyp7 (hypodermis)	tnc-2	2.146261852	6.65554E-15
hyp7 (hypodermis)	C05D11.5	1.099140369	1.07709E-14
hyp7 (hypodermis)	cpr-5	0.86024065	1.61235E-13
hyp7 (hypodermis)	asg-2	0.483857691	5.24515E-13
hyp7 (hypodermis)	tni-4	1.237924408	5.52268E-13
hyp7 (hypodermis)	Y87G2A.19	1.817468524	7.1985E-13
hyp7 (hypodermis)	col-145	-0.394186396	1.59365E-12
hyp7 (hypodermis)	R53.4	0.332561431	2.75636E-12
hyp7 (hypodermis)	ahcy-1	0.438060267	3.00729E-12
hyp7 (hypodermis)	fip-2	1.268140106	3.56027E-12
hyp7 (hypodermis)	col-143	0.846196464	4.85359E-12
hyp7 (hypodermis)	cpn-4	1.363684533	7.15253E-12
hyp7 (hypodermis)	K01D12.9	-0.594711792	7.65692E-12
hyp7 (hypodermis)	ZK970.7	-1.699877946	1.62069E-11
hyp7 (hypodermis)	Y73F4A.2	1.946757982	2.43479E-11
hyp7 (hypodermis)	W01F3.2	-0.949643613	5.16081E-11
hyp7 (hypodermis)	C04G6.2	-0.709147935	6.5357E-11
hyp7 (hypodermis)	cpg-7	-0.315735564	7.2725E-11
hyp7 (hypodermis)	col-65	-0.542026862	1.32398E-10

hyp7 (hypodermis)	nlp-30	-0.588287456	1.6258E-10
hyp7 (hypodermis)	C53C9.2	1.686130182	1.81738E-10
hyp7 (hypodermis)	icl-1	0.878031674	2.07268E-10
hyp7 (hypodermis)	ctc-2	0.315053372	2.08125E-10
hyp7 (hypodermis)	H32K16.2	0.719718562	2.48155E-10
hyp7 (hypodermis)	Y69A2AR.18	0.428870648	2.70274E-10
hyp7 (hypodermis)	Y69H2.3	-2.260943187	2.94895E-10
hyp7 (hypodermis)	pmt-2	0.358331792	4.70998E-10
hyp7 (hypodermis)	C24A3.2	1.035894448	5.35893E-10
hyp7 (hypodermis)	col-38	-0.322344479	5.60747E-10
hyp7 (hypodermis)	K01D12.8	-1.17475774	5.9E-10
hyp7 (hypodermis)	fipr-2	1.649738529	8.39658E-10
hyp7 (hypodermis)	nlp-34	-1.329652499	8.4933E-10
hyp7 (hypodermis)	F41D9.2	0.938166456	8.83961E-10
hyp7 (hypodermis)	mlc-3	0.608970952	9.78368E-10
hyp7 (hypodermis)	fipr-1	1.775690032	2.26163E-09
hyp7 (hypodermis)	gst-13	-0.910260683	2.83952E-09
hyp7 (hypodermis)	F12A10.1	1.108388894	3.13451E-09
hyp7 (hypodermis)	nlp-25	0.46128347	3.21664E-09
hyp7 (hypodermis)	H10E21.4	-0.402481014	4.43471E-09
hyp7 (hypodermis)	lys-8	-0.672656677	5.66609E-09
hyp7 (hypodermis)	fat-1	0.671895371	5.67472E-09
hyp7 (hypodermis)	lys-2	-0.809130743	6.60262E-09
hyp7 (hypodermis)	col-155	-0.503649186	7.8463E-09
hyp7 (hypodermis)	C35A5.3	1.154058252	8.06133E-09
hyp7 (hypodermis)	Y47D7A.13	-0.299056482	9.06914E-09
hyp7 (hypodermis)	T14A8.2	-0.930460317	1.072E-08
hyp7 (hypodermis)	msp-36	0.406162961	1.09354E-08
hyp7 (hypodermis)	nduo-1	0.275714553	1.44691E-08
hyp7 (hypodermis)	col-167	-0.437881098	1.75195E-08
hyp7 (hypodermis)	fat-7	1.715732655	2.90966E-08
hyp7 (hypodermis)	col-138	-0.300909435	3.61646E-08

hyp7 (hypodermis)	spp-2	-0.838117804	3.62616E-08
hyp7 (hypodermis)	F01D5.3	-1.649913846	4.26472E-08
hyp7 (hypodermis)	atp-5	0.359607606	4.6613E-08
hyp7 (hypodermis)	col-162	-0.245512651	4.95629E-08
hyp7 (hypodermis)	F58F12.1	0.317155603	7.06382E-08
hyp7 (hypodermis)	ZC116.1	1.605132694	1.22954E-07
hyp7 (hypodermis)	spp-18	-1.01193075	2.3188E-07
hyp7 (hypodermis)	ril-1	0.353738178	2.46063E-07
hyp7 (hypodermis)	B0024.4	-1.787492864	2.68406E-07
hyp7 (hypodermis)	col-157	-0.321457708	2.69245E-07
hyp7 (hypodermis)	H28O16.1	0.299687709	2.84279E-07
hyp7 (hypodermis)	col-119	0.455210501	2.935E-07
hyp7 (hypodermis)	tag-297	-0.56685032	2.97626E-07
hyp7 (hypodermis)	K03E5.2	0.861358649	3.06563E-07
hyp7 (hypodermis)	ZK909.3	-0.434407194	3.18645E-07
hyp7 (hypodermis)	cpr-1	0.555496114	3.22699E-07
hyp7 (hypodermis)	col-58	-0.406947654	3.29848E-07
hyp7 (hypodermis)	C45B2.8	-0.967354884	5.29681E-07
hyp7 (hypodermis)	tnt-4	1.444616241	6.91556E-07
hyp7 (hypodermis)	dpy-4	-0.277746631	8.95748E-07
hyp7 (hypodermis)	dpy-13	-0.260071539	1.09542E-06
hyp7 (hypodermis)	F41F3.3	-0.231938222	1.12112E-06
hyp7 (hypodermis)	lipl-5	-0.747969295	1.47961E-06
hyp7 (hypodermis)	col-49	-0.300698025	1.77975E-06
hyp7 (hypodermis)	R12E2.7	-0.345599454	2.13328E-06
hyp7 (hypodermis)	col-101	0.694380693	2.17191E-06
hyp7 (hypodermis)	grl-16	-0.291797549	2.26167E-06
hyp7 (hypodermis)	R06C1.4	0.299553487	2.44266E-06
hyp7 (hypodermis)	F35B3.4	-0.52219146	2.53933E-06
hyp7 (hypodermis)	F08F3.4	-0.504779034	2.8703E-06

hyp7 (hypodermis)	C54D10.3	0.785001939	3.11044E-06
hyp7 (hypodermis)	fat-2	0.574061993	3.11476E-06
hyp7 (hypodermis)	F26G1.5	-0.474606058	4.4227E-06
hyp7 (hypodermis)	col-77	-0.194126654	4.5927E-06
hyp7 (hypodermis)	bli-6	-0.167602845	5.16837E-06
hyp7 (hypodermis)	nuo-3	0.324695014	5.84049E-06
hyp7 (hypodermis)	F15E6.3	1.217419839	5.92536E-06
hyp7 (hypodermis)	ZK6.11	-0.603607937	6.24739E-06
hyp7 (hypodermis)	col-71	-0.256220706	6.38724E-06
hyp7 (hypodermis)	F53F1.4	-0.226419263	6.68641E-06
hyp7 (hypodermis)	C45G9.6	1.531226668	6.88572E-06
hyp7 (hypodermis)	atp-2	0.248669556	7.86948E-06
hyp7 (hypodermis)	col-130	-0.244040949	8.24658E-06
hyp7 (hypodermis)	C02E7.7	-0.311708365	9.32798E-06
hyp7 (hypodermis)	cnc-3	1.08017668	9.74822E-06
hyp7 (hypodermis)	prdx-2	0.324593799	9.94751E-06
hyp7 (hypodermis)	F15A4.6	0.712329157	1.01834E-05
hyp7 (hypodermis)	spp-17	0.453277288	1.08188E-05
hyp7 (hypodermis)	grd-6	-0.50788876	1.15544E-05
hyp7 (hypodermis)	hsp-16.41	0.743139914	1.42057E-05
hyp7 (hypodermis)	mpc-1	0.654393867	1.48121E-05
hyp7 (hypodermis)	F25E5.8	0.680588053	1.60569E-05
hyp7 (hypodermis)	acs-2	1.622778766	1.83235E-05
hyp7 (hypodermis)	gst-10	-0.836519212	2.02642E-05
hyp7 (hypodermis)	F54D5.4	-0.747995091	2.15849E-05
hyp7 (hypodermis)	W10C8.5	0.691717455	2.23312E-05
hyp7 (hypodermis)	K10H10.4	0.840597221	2.3135E-05
hyp7 (hypodermis)	F29C4.2	0.311263394	2.32434E-05
hyp7 (hypodermis)	T20G5.8	0.794183478	2.45373E-05
hyp7 (hypodermis)	pqn-60	1.188946471	2.71985E-05
hyp7 (hypodermis)	cco-1	0.252735926	3.00088E-05
hyp7 (hypodermis)	hsp-16.2	0.716405778	3.73906E-05
hyp7 (hypodermis)	F17C11.11	-0.5471139	5.28252E-05
hyp7 (hypodermis)	Y95B8A.2	-0.5098206	6.81252E-05
hyp7 (hypodermis)	cytb-5.1	0.469649604	6.85338E-05

hyp7 (hypodermis)	col-98	1.054514345	7.42019E-05
hyp7 (hypodermis)	T24B8.5	-2.158338208	8.06541E-05
hyp7 (hypodermis)	Y71H2AM.5	0.282073055	0.000105965
hyp7 (hypodermis)	C45B2.2	-0.582801432	0.000137272
hyp7 (hypodermis)	dct-7	1.934653138	0.000138482
hyp7 (hypodermis)	col-129	-0.227143529	0.000184113
hyp7 (hypodermis)	decr-1.1	0.848173962	0.000225891
hyp7 (hypodermis)	msp-40	0.288170615	0.000239535
hyp7 (hypodermis)	atp-4	0.288328883	0.000254358
hyp7 (hypodermis)	atp-6	0.168827563	0.000254767
hyp7 (hypodermis)	clec-1	0.443321538	0.000304908
hyp7 (hypodermis)	F28H7.3	-0.657042695	0.000311588
hyp7 (hypodermis)	C53A3.2	0.601460663	0.000323186
hyp7 (hypodermis)	cth-2	0.436805286	0.000374182
hyp7 (hypodermis)	gln-3	0.486327396	0.000387948
hyp7 (hypodermis)	F36A2.7	0.311215819	0.000406641
hyp7 (hypodermis)	col-103	0.972443303	0.000407545
hyp7 (hypodermis)	dpy-18	0.469666082	0.000414593
hyp7 (hypodermis)	col-73	-0.245360082	0.000440356
hyp7 (hypodermis)	F35B12.3	1.124102549	0.00044616
hyp7 (hypodermis)	Y36E3A.2	-1.309214021	0.000532525
hyp7 (hypodermis)	catp-3	0.584663902	0.000600903
hyp7 (hypodermis)	W10C8.6	1.029741499	0.000609587
hyp7 (hypodermis)	D2030.4	0.440242989	0.000664398
hyp7 (hypodermis)	asah-1	-1.375287002	0.000745389
hyp7 (hypodermis)	acdh-1	-0.215266024	0.000768894
hyp7 (hypodermis)	atp-3	0.289042367	0.000819997
hyp7 (hypodermis)	vamp-8	1.03743317	0.000820693
hyp7 (hypodermis)	col-170	-0.569818652	0.000927433
hyp7 (hypodermis)	nlp-33	-0.208704845	0.000963639
hyp7 (hypodermis)	comt-3	-0.749234513	0.001006176
hyp7 (hypodermis)	ttr-21	1.265123414	0.00103051
hyp7 (hypodermis)	R12E2.14	-0.332598916	0.001180091

hyp7 (hypodermis)	F45D3.3	0.517792444	0.001221155
hyp7 (hypodermis)	lec-10	-0.476332684	0.001495891
hyp7 (hypodermis)	Y102A11A.5	0.878812758	0.001623977
hyp7 (hypodermis)	fat-5	0.861985034	0.001743914
hyp7 (hypodermis)	Y38F2AR.9	0.351495127	0.001757942
hyp7 (hypodermis)	F48C1.9	1.437870693	0.001781614
hyp7 (hypodermis)	F15E6.4	0.75764849	0.001800855
hyp7 (hypodermis)	Y37A1B.5	-0.701317057	0.001995229
hyp7 (hypodermis)	Y41C4A.32	-1.092938167	0.002146244
hyp7 (hypodermis)	F01D5.1	-1.336853523	0.002178964
hyp7 (hypodermis)	R07E5.4	-0.487796104	0.002209133
hyp7 (hypodermis)	ins-20	-1.485674596	0.002225194
hyp7 (hypodermis)	col-93	-0.202805363	0.002287332
hyp7 (hypodermis)	C15H9.9	0.498547666	0.002431487
hyp7 (hypodermis)	F23D12.11	0.365209743	0.002574411
hyp7 (hypodermis)	act-5	-0.493029741	0.002891066
hyp7 (hypodermis)	C10C5.3	0.924240382	0.002897047
hyp7 (hypodermis)	T13F3.6	0.555757452	0.003088104
hyp7 (hypodermis)	mlt-10	0.763915775	0.003418897
hyp7 (hypodermis)	moag-4	0.554998687	0.003421793
hyp7 (hypodermis)	F45D3.4	0.495468675	0.003588701
hyp7 (hypodermis)	lys-6	1.705241211	0.003589831
hyp7 (hypodermis)	asg-1	0.367948194	0.003834527
hyp7 (hypodermis)	F38B7.2	-0.512326917	0.003996631
hyp7 (hypodermis)	cco-2	0.221713791	0.004389921
hyp7 (hypodermis)	F32A5.4	0.815139928	0.004872794
hyp7 (hypodermis)	F46C5.10	0.399259969	0.0048739
hyp7 (hypodermis)	hsp-25	0.472773669	0.005044248
hyp7 (hypodermis)	mdh-2	0.483263618	0.005649658
hyp7 (hypodermis)	T01D1.4	0.527489985	0.0057822
hyp7 (hypodermis)	C31C9.2	0.439544135	0.006028444
hyp7 (hypodermis)	F36F2.1	0.88966821	0.006043714
hyp7 (hypodermis)	phy-2	0.876107968	0.006505466
hyp7 (hypodermis)	col-125	-0.164042933	0.006643775
hyp7 (hypodermis)	F27D4.1	0.486755655	0.007893787

hyp7 (hypodermis)	mpc-2	0.550277094	0.008063598
hyp7 (hypodermis)	act-4	0.292706617	0.00841845
hyp7 (hypodermis)	nas-38	-0.61842888	0.011262789
hyp7 (hypodermis)	R02C2.7	0.994030414	0.011677269
hyp7 (hypodermis)	H36L18.2	0.31320827	0.012085224
hyp7 (hypodermis)	spp-5	-0.331379583	0.012373015
hyp7 (hypodermis)	cts-1	0.364241497	0.012634718
hyp7 (hypodermis)	gpd-2	0.46694382	0.014419181
hyp7 (hypodermis)	abf-5	1.162000412	0.0169485
hyp7 (hypodermis)	acer-1	0.503516671	0.017479056
hyp7 (hypodermis)	his-41	0.457535343	0.018664585
hyp7 (hypodermis)	col-175	-0.203257612	0.019707523
hyp7 (hypodermis)	pqn-94	0.986754831	0.021981481
hyp7 (hypodermis)	mlc-2	0.413108659	0.024680398
hyp7 (hypodermis)	dao-2	0.968721562	0.025900198
hyp7 (hypodermis)	mltn-1	1.630269988	0.02997824
hyp7 (hypodermis)	msp-64	0.295758446	0.030240896
hyp7 (hypodermis)	got-2.2	0.605724448	0.030994639
hyp7 (hypodermis)	C42D4.3	-0.40645154	0.031472089
hyp7 (hypodermis)	fipr-11	1.085141945	0.03158003
hyp7 (hypodermis)	fipr-10	1.063560519	0.031709016
hyp7 (hypodermis)	nduo-6	0.137774055	0.034632652
hyp7 (hypodermis)	enol-1	0.322826961	0.041657419
hyp7 (hypodermis)	grl-4	-0.404734092	0.042338097
hyp7 (hypodermis)	fmo-2	1.201819257	0.048843324
hyp7 (hypodermis)	fipr-5	1.17040317	0.049821071
hyp7 (hypodermis)	C30G12.2	0.880009504	0.052755668
hyp7 (hypodermis)	asp-3	-0.283039338	0.063772994
hyp7 (hypodermis)	lips-10	0.420485734	0.06597051
hyp7 (hypodermis)	B0410.3	0.26072326	0.067451372
hyp7 (hypodermis)	did-2	-0.509365214	0.067615854
hyp7 (hypodermis)	C11H1.9	0.644514326	0.069301824
hyp7 (hypodermis)	myo-2	0.936331388	0.074266032
hyp7 (hypodermis)	col-169	-0.491743478	0.081431283
hyp7 (hypodermis)	isp-1	0.299476514	0.083324383
hyp7 (hypodermis)	sdz-27	0.116229401	0.084136452
hyp7 (hypodermis)	F13C5.5	1.037658675	0.084873159
hyp7 (hypodermis)	cpr-4	0.40219107	0.085042876

hyp7 (hypodermis)	F18E3.12	0.287059891	0.090819723
hyp7 (hypodermis)	dod-6	0.656119492	0.099011432
mc1 (marginal cells)	col-122	1.76167817	3.45552E-24
mc1 (marginal cells)	col-119	1.722803243	8.36548E-23
mc1 (marginal cells)	aqp-1	1.141121135	1.131E-22
mc1 (marginal cells)	acer-1	1.003266212	9.25529E-19
mc1 (marginal cells)	col-20	1.212096776	3.39992E-18
mc1 (marginal cells)	ttr-26	-0.755393864	1.11392E-17
mc1 (marginal cells)	col-140	1.047220616	7.22876E-17
mc1 (marginal cells)	col-124	1.007497283	2.20773E-15
mc1 (marginal cells)	F41E6.15	-0.671589191	3.66126E-14
mc1 (marginal cells)	col-8	1.942597457	2.14002E-13
mc1 (marginal cells)	gst-20	-1.110138508	2.4325E-13
mc1 (marginal cells)	col-143	1.817748819	5.19061E-13
mc1 (marginal cells)	pck-2	0.666217382	6.36244E-13
mc1 (marginal cells)	col-181	1.290948996	6.44226E-13
mc1 (marginal cells)	col-19	1.065332394	1.60371E-12
mc1 (marginal cells)	icl-1	1.55019679	2.82529E-12
mc1 (marginal cells)	adss-1	-0.833405282	3.26404E-12
mc1 (marginal cells)	col-184	1.256136264	6.93487E-12
mc1 (marginal cells)	Y38H6C.23	-1.340404043	7.24744E-12
mc1 (marginal cells)	ctc-1	0.601070534	3.86377E-11
mc1 (marginal cells)	col-106	1.476358123	4.29801E-11
mc1 (marginal cells)	col-98	1.654786045	7.49366E-11
mc1 (marginal cells)	C55A1.6	3.640244936	1.38678E-10
mc1 (marginal cells)	ctc-3	0.548313679	3.03046E-10
mc1 (marginal cells)	col-80	1.078934708	3.46571E-09
mc1 (marginal cells)	act-1	-0.802143792	5.46708E-09
mc1 (marginal cells)	F17A9.4	2.059423412	5.95776E-09
mc1 (marginal cells)	gdh-1	-0.5963638	1.84008E-08
mc1 (marginal cells)	alh-1	0.747424753	1.00476E-07
mc1 (marginal cells)	col-103	2.001836541	1.51843E-07
mc1 (marginal cells)	sodh-1	0.495535557	3.8414E-07
mc1 (marginal cells)	K03E5.2	-0.725653667	1.46746E-06
mc1 (marginal cells)	vamp-8	-0.507270806	3.77998E-06
mc1 (marginal cells)	cdr-4	0.747584864	4.20137E-06

mc1 (marginal cells)	ugt-61	0.721854893	5.04112E-06
mc1 (marginal cells)	C32F10.8	-0.723585827	5.14469E-06
mc1 (marginal cells)	F14H12.3	-0.941328077	7.26582E-06
mc1 (marginal cells)	nspb-6	-1.405631074	1.05643E-05
mc1 (marginal cells)	lec-4	-0.511576148	1.34314E-05
mc1 (marginal cells)	ctc-2	0.472550202	2.23597E-05
mc1 (marginal cells)	col-101	1.309022552	3.57399E-05
mc1 (marginal cells)	F17C11.11	-0.893696139	4.35049E-05
mc1 (marginal cells)	cpr-5	2.338369082	5.10894E-05
mc1 (marginal cells)	C54D10.3	1.105534259	6.65699E-05
mc1 (marginal cells)	mutd-1	-0.64811669	7.67211E-05
mc1 (marginal cells)	F11E6.3	1.293761293	8.17375E-05
mc1 (marginal cells)	col-160	1.340859313	0.000154007
mc1 (marginal cells)	rpl-3	0.633300474	0.000168986
mc1 (marginal cells)	ZC116.1	0.470432659	0.000174524
mc1 (marginal cells)	iff-1	0.964253513	0.000293119
mc1 (marginal cells)	hsp-12.2	1.051893447	0.000331366
mc1 (marginal cells)	ZC21.3	0.538999363	0.000523324
mc1 (marginal cells)	F35B12.3	0.395029714	0.000706617
mc1 (marginal cells)	col-139	0.656932446	0.000917328
mc1 (marginal cells)	F23H11.5	-0.356810813	0.00093406
mc1 (marginal cells)	Y73B6A.3	-1.039171301	0.001189392
mc1 (marginal cells)	col-93	0.855805204	0.001342657
mc1 (marginal cells)	col-42	1.260022732	0.001503512
mc1 (marginal cells)	nduo-1	0.385952766	0.002015277
mc1 (marginal cells)	W03F8.6	-0.862295677	0.002760031
mc1 (marginal cells)	Y53F4B.14	-1.165324411	0.003073517
mc1 (marginal cells)	col-178	1.067007311	0.004440292
mc1 (marginal cells)	pudl-2	-1.197492295	0.004467122
mc1 (marginal cells)	C17F4.7	0.790518388	0.004690421
mc1 (marginal cells)	F53A9.9	-0.623942643	0.004771111
mc1 (marginal cells)	Y48G9A.9	-1.881074937	0.004794836

mc1 (marginal cells)	ifb-1	-0.419206486	0.005458832
mc1 (marginal cells)	asp-2	1.333621477	0.006096764
mc1 (marginal cells)	cyp-33C8	-1.053902446	0.007646122
mc1 (marginal cells)	fipr-21	1.212766599	0.007942095
mc1 (marginal cells)	skr-3	-0.82322423	0.010479574
mc1 (marginal cells)	K07C5.2	1.435167694	0.011204996
mc1 (marginal cells)	ctb-1	0.376347641	0.011943696
mc1 (marginal cells)	col-129	0.674972547	0.012281865
mc1 (marginal cells)	ivd-1	-0.746203683	0.012320486
mc1 (marginal cells)	ttr-27	-0.785282331	0.019883678
mc1 (marginal cells)	pfn-2	-0.531933023	0.022057495
mc1 (marginal cells)	C25E10.8	-1.078554085	0.023674752
mc1 (marginal cells)	gst-24	-0.82212038	0.026046472
mc1 (marginal cells)	stl-1	0.969918501	0.026138055
mc1 (marginal cells)	acs-2	0.899836286	0.038240766
mc1 (marginal cells)	C15C7.5	-0.576001061	0.047099506
mc1 (marginal cells)	col-142	0.997873283	0.048680674
mc1 (marginal cells)	fip-2	0.784809462	0.051956216
mc1 (marginal cells)	tnc-2	0.848389224	0.058385123
mc1 (marginal cells)	tag-290	0.355659268	0.061718098
mc1 (marginal cells)	mpc-1	0.733176976	0.062403664
mc1 (marginal cells)	H24K24.3	1.101854598	0.067898135
mc1 (marginal cells)	hsp-25	-0.379138247	0.069032702
mc1 (marginal cells)	eef-1G	0.542170414	0.075712557
mc1 (marginal cells)	pud-3	-2.090950555	0.090405128
mc1 (marginal cells)	ZC434.8	1.246062706	0.093839279
mc1 (marginal cells)	R09B3.3	0.641173219	0.097748808
mc2_mc3 (marginal cells)	fipr-6	-0.762356263	3.36122E-16
mc2_mc3 (marginal cells)	fipr-3	-0.688813607	3.53701E-08
mc2_mc3 (marginal cells)	fipr-4	-0.901663987	5.54596E-08
mc2_mc3 (marginal cells)	nspb-1	-0.584936487	1.41843E-05

mc2_mc3 (marginal cells)	nspb-6	-0.541440408	0.00012847
mc2_mc3 (marginal cells)	ctc-3	0.806218205	0.000251526
mc2_mc3 (marginal cells)	fipr-10	-0.483979139	0.000746956
mc2_mc3 (marginal cells)	nspb-12	-0.606113289	0.001321987
mc2_mc3 (marginal cells)	nspb-2	-0.520584397	0.00162495
mc2_mc3 (marginal cells)	nduo-1	0.657993536	0.006109948
mc2_mc3 (marginal cells)	nspb-11	-0.472405041	0.006757653
mc2_mc3 (marginal cells)	fipr-2	-0.550985962	0.008145282
mc2_mc3 (marginal cells)	ctc-2	0.697175439	0.010384554
mc2_mc3 (marginal cells)	fipr-8	-0.501674444	0.011355168
mc2_mc3 (marginal cells)	fipr-7	-0.738043868	0.011517693
mc2_mc3 (marginal cells)	ctc-1	0.640407179	0.061536943
mc2_mc3 (marginal cells)	col-106	1.437505362	0.078151389
pm1_pm2 (pharyngeal muscle)	pnc-1	-0.835584395	5.83976E-13
pm1_pm2 (pharyngeal muscle)	K07A12.8	-0.969413313	1.41757E-06
pm1_pm2 (pharyngeal muscle)	nduo-6	-0.385599679	2.03888E-06
pm1_pm2 (pharyngeal muscle)	cyp-33C8	-1.047806895	2.49817E-06
pm1_pm2 (pharyngeal muscle)	Y73F4A.2	0.450432314	1.20404E-05
pm1_pm2 (pharyngeal muscle)	acer-1	1.030467599	1.32395E-05
pm1_pm2 (pharyngeal muscle)	F46H5.3	-0.498247038	1.58403E-05
pm1_pm2 (pharyngeal muscle)	daf-37	-1.008871572	3.26339E-05
pm1_pm2 (pharyngeal muscle)	pgp-13	-1.331808085	9.34786E-05
pm1_pm2 (pharyngeal muscle)	ZK792.4	-1.666527866	0.000128628
pm1_pm2 (pharyngeal muscle)	abf-6	-0.613294415	0.000192241
pm1_pm2 (pharyngeal muscle)	F32A5.4	0.328474208	0.005040662
pm1_pm2 (pharyngeal muscle)	F22F4.9	-0.675894203	0.005851193
pm1_pm2 (pharyngeal muscle)	ndfl-4	-0.473508103	0.008896244

pm1_pm2 (pharyngeal muscle)	C14C6.5	-2.417539858	0.017000254
pm1_pm2 (pharyngeal muscle)	ttr-21	0.691487174	0.019548348
pm1_pm2 (pharyngeal muscle)	T06E6.1	-2.739097731	0.019831929
pm1_pm2 (pharyngeal muscle)	C14B9.10	-0.538236878	0.023703246
pm1_pm2 (pharyngeal muscle)	C45E5.4	1.168528726	0.025589378
pm1_pm2 (pharyngeal muscle)	F28H7.3	-2.277751292	0.028526801
pm1_pm2 (pharyngeal muscle)	F17A9.4	1.133633376	0.029138523
pm1_pm2 (pharyngeal muscle)	C54D2.1	-1.269166741	0.032806208
pm1_pm2 (pharyngeal muscle)	Y116A8B.4	-0.771034763	0.035067045
pm1_pm2 (pharyngeal muscle)	gst-7	1.116005801	0.03810674
pm1_pm2 (pharyngeal muscle)	cpn-4	0.37325507	0.046933788
pm1_pm2 (pharyngeal muscle)	gdh-1	-0.504831192	0.076176915
pm3_pm4_pm5 (pharyngeal muscle)	sodh-1	1.856423596	7.4996E-141
pm3_pm4_pm5 (pharyngeal muscle)	col-122	1.452857811	1.01833E-54
pm3_pm4_pm5 (pharyngeal muscle)	T03F1.11	-0.457526972	4.47934E-53
pm3_pm4_pm5 (pharyngeal muscle)	hsp-12.2	-0.386045684	7.89977E-52
pm3_pm4_pm5 (pharyngeal muscle)	acer-1	1.006305151	1.52801E-50
pm3_pm4_pm5 (pharyngeal muscle)	F41E6.15	-0.656067955	8.38996E-47
pm3_pm4_pm5 (pharyngeal muscle)	alh-1	1.256833261	2.934E-40
pm3_pm4_pm5 (pharyngeal muscle)	col-184	1.341639844	3.32238E-39
pm3_pm4_pm5 (pharyngeal muscle)	col-20	0.973962168	6.08164E-37
pm3_pm4_pm5 (pharyngeal muscle)	ant-1.1	-0.276388928	1.77004E-36
pm3_pm4_pm5 (pharyngeal muscle)	act-4	-0.382091646	4.52272E-36
pm3_pm4_pm5 (pharyngeal muscle)	R02C2.7	-0.934653187	5.8053E-36
pm3_pm4_pm5 (pharyngeal muscle)	col-8	1.597890571	9.51565E-34

pm3_pm4_pm5 (pharyngeal muscle)	Y82E9BR.3	-0.258370446	4.78271E-33
pm3_pm4_pm5 (pharyngeal muscle)	col-119	1.087758886	5.71104E-33
pm3_pm4_pm5 (pharyngeal muscle)	col-124	0.820231147	6.59485E-33
pm3_pm4_pm5 (pharyngeal muscle)	col-140	0.832228777	1.59072E-32
pm3_pm4_pm5 (pharyngeal muscle)	col-106	1.312012024	1.0875E-29
pm3_pm4_pm5 (pharyngeal muscle)	pck-2	0.968861014	1.44642E-29
pm3_pm4_pm5 (pharyngeal muscle)	col-181	1.09662582	1.63067E-29
pm3_pm4_pm5 (pharyngeal muscle)	K03E5.2	-0.361958139	2.71654E-28
pm3_pm4_pm5 (pharyngeal muscle)	F23H11.5	-0.351102647	8.81934E-27
pm3_pm4_pm5 (pharyngeal muscle)	tnt-4	-0.535520585	1.20883E-26
pm3_pm4_pm5 (pharyngeal muscle)	col-19	0.762909299	3.35888E-23
pm3_pm4_pm5 (pharyngeal muscle)	col-80	0.932277769	5.04736E-23
pm3_pm4_pm5 (pharyngeal muscle)	Y69A2AR.18	-0.370647142	2.53871E-21
pm3_pm4_pm5 (pharyngeal muscle)	asp-2	2.17212877	4.65313E-21
pm3_pm4_pm5 (pharyngeal muscle)	ctc-1	0.445653013	8.99268E-21
pm3_pm4_pm5 (pharyngeal muscle)	C17F4.7	1.070034702	1.38937E-20
pm3_pm4_pm5 (pharyngeal muscle)	col-139	0.746484219	3.70799E-20
pm3_pm4_pm5 (pharyngeal muscle)	ctc-3	0.385651761	3.80969E-20
pm3_pm4_pm5 (pharyngeal muscle)	C41G7.9	-0.460051477	4.09638E-19
pm3_pm4_pm5 (pharyngeal muscle)	col-81	0.831259491	6.15365E-19
pm3_pm4_pm5 (pharyngeal muscle)	cco-1	-0.266505544	1.23295E-18
pm3_pm4_pm5 (pharyngeal muscle)	atp-5	-0.314148327	3.24019E-18
pm3_pm4_pm5 (pharyngeal muscle)	cyc-2.1	-0.25205214	3.97441E-18

pm3_pm4_pm5 (pharyngeal muscle)	mlc-3	-0.221017013	3.99874E-18
pm3_pm4_pm5 (pharyngeal muscle)	F11E6.3	1.360436894	2.46232E-17
pm3_pm4_pm5 (pharyngeal muscle)	rpl-3	0.572694263	4.3936E-17
pm3_pm4_pm5 (pharyngeal muscle)	mlc-2	-0.262808723	1.03864E-16
pm3_pm4_pm5 (pharyngeal muscle)	gst-1	-0.570950921	9.06594E-16
pm3_pm4_pm5 (pharyngeal muscle)	T02H6.11	-0.27257237	2.62383E-15
pm3_pm4_pm5 (pharyngeal muscle)	mlc-1	-0.246452265	5.25626E-15
pm3_pm4_pm5 (pharyngeal muscle)	Y54F10AM.5	-0.433140604	1.40932E-14
pm3_pm4_pm5 (pharyngeal muscle)	lev-11	-0.226761846	2.07392E-14
pm3_pm4_pm5 (pharyngeal muscle)	cpr-5	2.068627633	2.0912E-14
pm3_pm4_pm5 (pharyngeal muscle)	R09B3.3	0.658029407	2.26782E-14
pm3_pm4_pm5 (pharyngeal muscle)	tag-290	0.826631491	4.92171E-14
pm3_pm4_pm5 (pharyngeal muscle)	col-143	0.941280217	2.29324E-13
pm3_pm4_pm5 (pharyngeal muscle)	F57F5.1	1.047099541	4.03893E-13
pm3_pm4_pm5 (pharyngeal muscle)	F58F12.1	-0.253725723	4.29478E-13
pm3_pm4_pm5 (pharyngeal muscle)	tni-4	-0.225313325	4.54138E-13
pm3_pm4_pm5 (pharyngeal muscle)	col-160	1.112641961	7.47268E-13
pm3_pm4_pm5 (pharyngeal muscle)	cpz-1	1.620400327	9.60699E-13
pm3_pm4_pm5 (pharyngeal muscle)	eef-1A.1	0.533048252	9.96006E-13
pm3_pm4_pm5 (pharyngeal muscle)	mai-2	-0.303037872	1.85588E-12
pm3_pm4_pm5 (pharyngeal muscle)	nuo-3	-0.246624279	1.92387E-12
pm3_pm4_pm5 (pharyngeal muscle)	pud-4	-2.458678249	2.30401E-12
pm3_pm4_pm5 (pharyngeal muscle)	iff-1	0.793755891	2.37988E-12

pm3_pm4_pm5 (pharyngeal muscle)	M28.5	0.947260429	2.8143E-12
pm3_pm4_pm5 (pharyngeal muscle)	pud-3	-2.338473609	3.38794E-12
pm3_pm4_pm5 (pharyngeal muscle)	R04F11.2	-0.208483447	5.44681E-12
pm3_pm4_pm5 (pharyngeal muscle)	ctb-1	0.363672722	6.60159E-12
pm3_pm4_pm5 (pharyngeal muscle)	F32A5.4	0.648868389	7.23959E-12
pm3_pm4_pm5 (pharyngeal muscle)	col-129	0.682183983	1.45838E-11
pm3_pm4_pm5 (pharyngeal muscle)	C44B11.6	-0.460366766	1.49514E-11
pm3_pm4_pm5 (pharyngeal muscle)	Y71H2AM.5	-0.272941213	1.58955E-11
pm3_pm4_pm5 (pharyngeal muscle)	Y87G2A.19	-0.264530106	2.65695E-11
pm3_pm4_pm5 (pharyngeal muscle)	isp-1	-0.340789529	6.66667E-11
pm3_pm4_pm5 (pharyngeal muscle)	atp-4	-0.237256641	1.07241E-10
pm3_pm4_pm5 (pharyngeal muscle)	F54B8.4	0.652343701	1.28042E-10
pm3_pm4_pm5 (pharyngeal muscle)	F21C10.10	0.970615952	2.42419E-10
pm3_pm4_pm5 (pharyngeal muscle)	adss-1	-0.605892999	2.44818E-10
pm3_pm4_pm5 (pharyngeal muscle)	hsp-16.41	0.473914154	2.73996E-10
pm3_pm4_pm5 (pharyngeal muscle)	rpl-25.2	0.597957664	3.08699E-10
pm3_pm4_pm5 (pharyngeal muscle)	asp-5	1.324229165	3.63065E-10
pm3_pm4_pm5 (pharyngeal muscle)	lys-4	1.360287381	4.10276E-10
pm3_pm4_pm5 (pharyngeal muscle)	F29C4.2	-0.252158979	6.32435E-10
pm3_pm4_pm5 (pharyngeal muscle)	asp-1	0.791681789	7.25671E-10
pm3_pm4_pm5 (pharyngeal muscle)	R06C1.4	-0.434822436	9.95963E-10
pm3_pm4_pm5 (pharyngeal muscle)	pqn-60	0.815078976	1.28269E-09
pm3_pm4_pm5 (pharyngeal muscle)	ahcy-1	0.793038953	1.65409E-09

pm3_pm4_pm5 (pharyngeal muscle)	C18E9.4	-0.336464703	1.98951E-09
pm3_pm4_pm5 (pharyngeal muscle)	ttr-15	0.828477645	2.14521E-09
pm3_pm4_pm5 (pharyngeal muscle)	gdh-1	-0.335032815	2.29469E-09
pm3_pm4_pm5 (pharyngeal muscle)	col-142	0.989354576	3.3833E-09
pm3_pm4_pm5 (pharyngeal muscle)	rpl-11.1	0.654468536	3.56274E-09
pm3_pm4_pm5 (pharyngeal muscle)	R09B3.2	0.810107199	5.11367E-09
pm3_pm4_pm5 (pharyngeal muscle)	hsp-16.2	0.447859536	5.62238E-09
pm3_pm4_pm5 (pharyngeal muscle)	icl-1	1.080905816	1.07662E-08
pm3_pm4_pm5 (pharyngeal muscle)	col-98	0.822835268	1.28568E-08
pm3_pm4_pm5 (pharyngeal muscle)	rpl-7A	0.482801057	1.43645E-08
pm3_pm4_pm5 (pharyngeal muscle)	cpl-1	1.289500701	1.5652E-08
pm3_pm4_pm5 (pharyngeal muscle)	rpl-10	0.346755825	1.84346E-08
pm3_pm4_pm5 (pharyngeal muscle)	W03F8.6	-0.573886904	2.12473E-08
pm3_pm4_pm5 (pharyngeal muscle)	C53C9.2	-0.194124868	3.03615E-08
pm3_pm4_pm5 (pharyngeal muscle)	zip-2	-0.934644467	3.65751E-08
pm3_pm4_pm5 (pharyngeal muscle)	nduo-1	0.288917768	4.00933E-08
pm3_pm4_pm5 (pharyngeal muscle)	eat-6	0.54712272	4.08326E-08
pm3_pm4_pm5 (pharyngeal muscle)	clec-63	1.115312016	5.62705E-08
pm3_pm4_pm5 (pharyngeal muscle)	cth-1	0.752993825	6.35825E-08
pm3_pm4_pm5 (pharyngeal muscle)	pmt-2	0.612072374	6.44943E-08
pm3_pm4_pm5 (pharyngeal muscle)	ilys-5	0.633548238	7.90069E-08
pm3_pm4_pm5 (pharyngeal muscle)	K08D12.6	0.989620689	1.06781E-07
pm3_pm4_pm5 (pharyngeal muscle)	rpl-19	0.309987088	2.02864E-07

pm3_pm4_pm5 (pharyngeal muscle)	ddo-2	0.441489858	2.13735E-07
pm3_pm4_pm5 (pharyngeal muscle)	mpc-1	0.546242183	2.76079E-07
pm3_pm4_pm5 (pharyngeal muscle)	ugt-26	0.223713298	2.92886E-07
pm3_pm4_pm5 (pharyngeal muscle)	ZK809.8	-0.306507898	3.27182E-07
pm3_pm4_pm5 (pharyngeal muscle)	F29B9.11	-0.27918542	3.3983E-07
pm3_pm4_pm5 (pharyngeal muscle)	F15A4.6	1.096940861	3.55007E-07
pm3_pm4_pm5 (pharyngeal muscle)	rla-0	0.354379937	3.98295E-07
pm3_pm4_pm5 (pharyngeal muscle)	ctc-2	0.279177773	4.71504E-07
pm3_pm4_pm5 (pharyngeal muscle)	col-178	0.758681387	5.43461E-07
pm3_pm4_pm5 (pharyngeal muscle)	asp-13	1.776758851	1.1458E-06
pm3_pm4_pm5 (pharyngeal muscle)	col-93	0.622819808	1.61848E-06
pm3_pm4_pm5 (pharyngeal muscle)	R102.2	-0.889491223	1.88044E-06
pm3_pm4_pm5 (pharyngeal muscle)	rps-6	0.520657399	2.29073E-06
pm3_pm4_pm5 (pharyngeal muscle)	csq-1	0.477035901	2.35059E-06
pm3_pm4_pm5 (pharyngeal muscle)	Y39B6A.5	-0.553426775	2.71875E-06
pm3_pm4_pm5 (pharyngeal muscle)	clec-87	0.880750654	2.92862E-06
pm3_pm4_pm5 (pharyngeal muscle)	Y47G6A.33	0.917930855	4.40408E-06
pm3_pm4_pm5 (pharyngeal muscle)	rps-7	0.316119625	4.43041E-06
pm3_pm4_pm5 (pharyngeal muscle)	F46H5.3	-0.201819906	4.62928E-06
pm3_pm4_pm5 (pharyngeal muscle)	Y63D3A.7	-0.416111882	5.3959E-06
pm3_pm4_pm5 (pharyngeal muscle)	sec-61	1.150944773	6.95515E-06
pm3_pm4_pm5 (pharyngeal muscle)	T27E9.2	-0.269033754	8.24922E-06
pm3_pm4_pm5 (pharyngeal muscle)	asp-6	0.900792341	9.94261E-06

pm3_pm4_pm5 (pharyngeal muscle)	asp-4	1.451439605	1.03513E-05
pm3_pm4_pm5 (pharyngeal muscle)	T21H3.1	1.101843224	1.09972E-05
pm3_pm4_pm5 (pharyngeal muscle)	cpr-4	1.85190958	1.15878E-05
pm3_pm4_pm5 (pharyngeal muscle)	rpl-4	0.497990101	1.16303E-05
pm3_pm4_pm5 (pharyngeal muscle)	vamp-8	-0.369969815	1.25518E-05
pm3_pm4_pm5 (pharyngeal muscle)	far-3	2.219982381	1.4112E-05
pm3_pm4_pm5 (pharyngeal muscle)	xbp-1	-0.725255153	1.76653E-05
pm3_pm4_pm5 (pharyngeal muscle)	Y51H1A.3	-0.257422677	1.94759E-05
pm3_pm4_pm5 (pharyngeal muscle)	F13H10.6	-0.625909037	2.12245E-05
pm3_pm4_pm5 (pharyngeal muscle)	elo-6	0.772944709	2.38423E-05
pm3_pm4_pm5 (pharyngeal muscle)	rack-1	0.407527324	2.57131E-05
pm3_pm4_pm5 (pharyngeal muscle)	gst-4	0.933822615	2.96398E-05
pm3_pm4_pm5 (pharyngeal muscle)	T13F3.6	0.989565075	3.5461E-05
pm3_pm4_pm5 (pharyngeal muscle)	Y43F8B.1	-0.25962918	4.13438E-05
pm3_pm4_pm5 (pharyngeal muscle)	F53F4.10	-0.300814998	4.45939E-05
pm3_pm4_pm5 (pharyngeal muscle)	R53.4	-0.172814815	4.85554E-05
pm3_pm4_pm5 (pharyngeal muscle)	K07C5.2	1.02705026	5.91386E-05
pm3_pm4_pm5 (pharyngeal muscle)	lgg-1	-0.334945305	6.30966E-05
pm3_pm4_pm5 (pharyngeal muscle)	rps-0	0.393952905	6.83029E-05
pm3_pm4_pm5 (pharyngeal muscle)	ssp-9	0	6.87643E-05
pm3_pm4_pm5 (pharyngeal muscle)	gst-10	-0.827692487	7.31987E-05
pm3_pm4_pm5 (pharyngeal muscle)	hpo-26	-0.701741484	7.6778E-05
pm3_pm4_pm5 (pharyngeal muscle)	asg-2	-0.207831402	8.232E-05

pm3_pm4_pm5 (pharyngeal muscle)	F38B2.4	-0.408824841	9.47094E-05
pm3_pm4_pm5 (pharyngeal muscle)	fkb-2	0.605475035	9.97545E-05
pm3_pm4_pm5 (pharyngeal muscle)	Y17D7B.4	-1.013348435	0.000113771
pm3_pm4_pm5 (pharyngeal muscle)	K12H4.5	-0.26012755	0.000136301
pm3_pm4_pm5 (pharyngeal muscle)	rps-4	0.365505499	0.000147005
pm3_pm4_pm5 (pharyngeal muscle)	asb-2	-0.23427627	0.000152282
pm3_pm4_pm5 (pharyngeal muscle)	ril-1	-0.186820719	0.000170509
pm3_pm4_pm5 (pharyngeal muscle)	anmt-3	-0.326205331	0.000183253
pm3_pm4_pm5 (pharyngeal muscle)	fmo-2	4.06459125	0.000185497
pm3_pm4_pm5 (pharyngeal muscle)	fipr-7	0.475782774	0.000218116
pm3_pm4_pm5 (pharyngeal muscle)	C54D10.3	0.672475926	0.000218528
pm3_pm4_pm5 (pharyngeal muscle)	lys-1	0.932257401	0.000229895
pm3_pm4_pm5 (pharyngeal muscle)	gst-20	-0.487127556	0.000248257
pm3_pm4_pm5 (pharyngeal muscle)	sip-1	0.811166651	0.000259566
pm3_pm4_pm5 (pharyngeal muscle)	rpl-5	0.3239548	0.000265563
pm3_pm4_pm5 (pharyngeal muscle)	trap-1	1.000622928	0.000306395
pm3_pm4_pm5 (pharyngeal muscle)	nduo-2	0.323577482	0.000307036
pm3_pm4_pm5 (pharyngeal muscle)	far-2	0.354170762	0.000314816
pm3_pm4_pm5 (pharyngeal muscle)	rps-8	0.272627036	0.000328544
pm3_pm4_pm5 (pharyngeal muscle)	F53C11.9	-0.180846116	0.000347875
pm3_pm4_pm5 (pharyngeal muscle)	C49G7.3	1.101249126	0.000393495
pm3_pm4_pm5 (pharyngeal muscle)	col-103	0.806257977	0.000399109
pm3_pm4_pm5 (pharyngeal muscle)	mel-32	1.311313455	0.000404189

pm3_pm4_pm5 (pharyngeal muscle)	col-147	0.730305229	0.000441984
pm3_pm4_pm5 (pharyngeal muscle)	R07E4.3	-0.424241145	0.000453803
pm3_pm4_pm5 (pharyngeal muscle)	spp-14	1.047926394	0.000605446
pm3_pm4_pm5 (pharyngeal muscle)	cey-2	0.741705539	0.000624628
pm3_pm4_pm5 (pharyngeal muscle)	ZC434.8	0.842707455	0.000643921
pm3_pm4_pm5 (pharyngeal muscle)	cex-2	-0.81840284	0.0006852
pm3_pm4_pm5 (pharyngeal muscle)	rps-3	0.29096879	0.000690922
pm3_pm4_pm5 (pharyngeal muscle)	T04F8.8	1.152262132	0.00070224
pm3_pm4_pm5 (pharyngeal muscle)	C14C6.5	-1.002307831	0.000759522
pm3_pm4_pm5 (pharyngeal muscle)	tag-174	-0.189441353	0.000791398
pm3_pm4_pm5 (pharyngeal muscle)	lbp-6	0.430937741	0.000814588
pm3_pm4_pm5 (pharyngeal muscle)	lec-4	-0.412005632	0.000819168
pm3_pm4_pm5 (pharyngeal muscle)	rpl-16	0.319039701	0.000824211
pm3_pm4_pm5 (pharyngeal muscle)	rpl-7	0.313803962	0.000880073
pm3_pm4_pm5 (pharyngeal muscle)	F22H10.2	-0.941013356	0.001061234
pm3_pm4_pm5 (pharyngeal muscle)	rpl-9	0.332550844	0.001103767
pm3_pm4_pm5 (pharyngeal muscle)	C06A8.3	0.356165595	0.001313792
pm3_pm4_pm5 (pharyngeal muscle)	gpd-3	-0.359350983	0.001315868
pm3_pm4_pm5 (pharyngeal muscle)	vha-2	0.490019321	0.001492722
pm3_pm4_pm5 (pharyngeal muscle)	clec-47	1.984259524	0.001865471
pm3_pm4_pm5 (pharyngeal muscle)	rps-26	0.269465105	0.001938232
pm3_pm4_pm5 (pharyngeal muscle)	rpl-23	0.290925892	0.001941637
pm3_pm4_pm5 (pharyngeal muscle)	hil-4	0.90160132	0.002095434

pm3_pm4_pm5 (pharyngeal muscle)	rpl-1	0.326634105	0.002165915
pm3_pm4_pm5 (pharyngeal muscle)	fip-2	0.54402979	0.002246356
pm3_pm4_pm5 (pharyngeal muscle)	F44E5.1	-0.265264643	0.002303315
pm3_pm4_pm5 (pharyngeal muscle)	tnc-2	-0.127247635	0.002453519
pm3_pm4_pm5 (pharyngeal muscle)	oig-3	-0.241973206	0.002514938
pm3_pm4_pm5 (pharyngeal muscle)	T20G5.8	0.967888064	0.002745299
pm3_pm4_pm5 (pharyngeal muscle)	T24B8.5	-2.158368996	0.002769664
pm3_pm4_pm5 (pharyngeal muscle)	Y37E3.8	0.259460889	0.003014441
pm3_pm4_pm5 (pharyngeal muscle)	asp-3	0.781021561	0.003274078
pm3_pm4_pm5 (pharyngeal muscle)	F22B5.4	-0.47910458	0.003274261
pm3_pm4_pm5 (pharyngeal muscle)	col-42	0.675311265	0.003406631
pm3_pm4_pm5 (pharyngeal muscle)	nap-1	0.750643379	0.003632473
pm3_pm4_pm5 (pharyngeal muscle)	scl-6	1.519613395	0.003761518
pm3_pm4_pm5 (pharyngeal muscle)	tnt-3	-0.324134304	0.003833795
pm3_pm4_pm5 (pharyngeal muscle)	ttr-23	-0.759520884	0.004093191
pm3_pm4_pm5 (pharyngeal muscle)	C23H5.8	-0.704599088	0.004246383
pm3_pm4_pm5 (pharyngeal muscle)	unc-54	0.62586379	0.004539306
pm3_pm4_pm5 (pharyngeal muscle)	ldp-1	1.154748452	0.004795805
pm3_pm4_pm5 (pharyngeal muscle)	nduo-5	0.286236637	0.00526051
pm3_pm4_pm5 (pharyngeal muscle)	nspd-10	-0.025146126	0.005356782
pm3_pm4_pm5 (pharyngeal muscle)	F26E4.6	-0.187250536	0.00606529
pm3_pm4_pm5 (pharyngeal muscle)	aldo-2	-0.238452554	0.008370648
pm3_pm4_pm5 (pharyngeal muscle)	eef-1G	0.332983888	0.010348866

pm3_pm4_pm5 (pharyngeal muscle)	F22F4.9	-0.433543788	0.011936421
pm3_pm4_pm5 (pharyngeal muscle)	F54D5.4	1.304209697	0.011987855
pm3_pm4_pm5 (pharyngeal muscle)	ftn-2	0.52504772	0.012225381
pm3_pm4_pm5 (pharyngeal muscle)	nlp-27	0.813999024	0.012637224
pm3_pm4_pm5 (pharyngeal muscle)	rpl-22	0.292272509	0.013523247
pm3_pm4_pm5 (pharyngeal muscle)	col-101	0.569280777	0.013568933
pm3_pm4_pm5 (pharyngeal muscle)	unc-43	-0.479068616	0.013595009
pm3_pm4_pm5 (pharyngeal muscle)	F21C10.9	1.729354724	0.013931056
pm3_pm4_pm5 (pharyngeal muscle)	T21D12.12	0.614300887	0.014674462
pm3_pm4_pm5 (pharyngeal muscle)	rpl-20	0.303709618	0.014950353
pm3_pm4_pm5 (pharyngeal muscle)	tag-196	0.817921247	0.015574905
pm3_pm4_pm5 (pharyngeal muscle)	rps-2	0.323272886	0.016942559
pm3_pm4_pm5 (pharyngeal muscle)	gpx-5	0.555312127	0.01803428
pm3_pm4_pm5 (pharyngeal muscle)	hsp-70	0.45740254	0.018820547
pm3_pm4_pm5 (pharyngeal muscle)	Y53F4B.14	0.674205545	0.019043556
pm3_pm4_pm5 (pharyngeal muscle)	cyn-7	0.269719168	0.020234995
pm3_pm4_pm5 (pharyngeal muscle)	F54D5.3	1.228621378	0.021652867
pm3_pm4_pm5 (pharyngeal muscle)	ttr-22	0.781056558	0.021672479
pm3_pm4_pm5 (pharyngeal muscle)	hsp-1	0.367574433	0.022785628
pm3_pm4_pm5 (pharyngeal muscle)	F55H12.4	1.072691178	0.024211877
pm3_pm4_pm5 (pharyngeal muscle)	K07A12.8	-0.368275144	0.026433101
pm3_pm4_pm5 (pharyngeal muscle)	act-1	-0.185039747	0.027399644
pm3_pm4_pm5 (pharyngeal muscle)	anmt-2	-0.225521758	0.027728922

pm3_pm4_pm5 (pharyngeal muscle)	cpr-6	0.871508525	0.028044482
pm3_pm4_pm5 (pharyngeal muscle)	rpl-13	0.23307938	0.029804809
pm3_pm4_pm5 (pharyngeal muscle)	cisd-3.2	-0.248685222	0.030398173
pm3_pm4_pm5 (pharyngeal muscle)	smo-1	0.711709927	0.0304322
pm3_pm4_pm5 (pharyngeal muscle)	fat-5	0.348826282	0.03054255
pm3_pm4_pm5 (pharyngeal muscle)	rps-20	0.280778715	0.03264019
pm3_pm4_pm5 (pharyngeal muscle)	rps-1	0.2647057	0.036230055
pm3_pm4_pm5 (pharyngeal muscle)	eef-1B.2	0.511456215	0.040396816
pm3_pm4_pm5 (pharyngeal muscle)	rpl-2	0.266727359	0.040799582
pm3_pm4_pm5 (pharyngeal muscle)	C18A11.1	-0.799675728	0.042064474
pm3_pm4_pm5 (pharyngeal muscle)	argk-1	1.049256273	0.042570789
pm3_pm4_pm5 (pharyngeal muscle)	C01G10.15	-0.446973271	0.043082191
pm3_pm4_pm5 (pharyngeal muscle)	R09E12.9	1.569982727	0.046421388
pm3_pm4_pm5 (pharyngeal muscle)	Y73F4A.3	1.343562403	0.048284482
pm3_pm4_pm5 (pharyngeal muscle)	F47B7.1	-0.338027926	0.048884218
pm3_pm4_pm5 (pharyngeal muscle)	aqp-1	1.094380969	0.049073293
pm3_pm4_pm5 (pharyngeal muscle)	ttr-21	0.395740835	0.052882773
pm3_pm4_pm5 (pharyngeal muscle)	F15G9.6	-0.563298994	0.054591997
pm3_pm4_pm5 (pharyngeal muscle)	C14B9.10	-0.187913122	0.061571913
pm3_pm4_pm5 (pharyngeal muscle)	fipr-21	0.587533036	0.062721641
pm3_pm4_pm5 (pharyngeal muscle)	Y51B9A.5	0	0.063180299
pm3_pm4_pm5 (pharyngeal muscle)	lpd-5	-0.238764764	0.063558146
pm3_pm4_pm5 (pharyngeal muscle)	Y116A8B.4	-0.759373004	0.064760542

pm3_pm4_pm5 (pharyngeal muscle)	C45E5.1	0.845277986	0.065742377
pm3_pm4_pm5 (pharyngeal muscle)	F17A9.4	0.807931529	0.065756109
pm3_pm4_pm5 (pharyngeal muscle)	rpl-6	0.260255409	0.067787563
pm3_pm4_pm5 (pharyngeal muscle)	msp-113	0	0.068098094
pm3_pm4_pm5 (pharyngeal muscle)	nspd-1	-0.014862085	0.070065526
pm3_pm4_pm5 (pharyngeal muscle)	C17F3.1	-0.000768477	0.070472867
pm3_pm4_pm5 (pharyngeal muscle)	F55C10.5	-0.657095162	0.070721248
pm3_pm4_pm5 (pharyngeal muscle)	C05D11.5	0.675429666	0.075379706
pm3_pm4_pm5 (pharyngeal muscle)	lec-1	-0.280451325	0.076453501
pm3_pm4_pm5 (pharyngeal muscle)	rps-30	0.259388549	0.080915344
pm3_pm4_pm5 (pharyngeal muscle)	rla-1	0.297919194	0.08585389
pm3_pm4_pm5 (pharyngeal muscle)	ZK1320.3	1.134366792	0.091877049
pm3_pm4_pm5 (pharyngeal muscle)	T19H12.6	1.185165446	0.09575028
pm3_pm4_pm5 (pharyngeal muscle)	ddp-1	-0.480645924	0.096085306
pm6_pm7 (pharyngeal muscle)	sodh-1	1.364547035	4.20458E-29
pm6_pm7 (pharyngeal muscle)	ttr-26	-0.987142375	1.1826E-16
pm6_pm7 (pharyngeal muscle)	col-122	2.075561695	1.88954E-15
pm6_pm7 (pharyngeal muscle)	acer-1	1.077259285	1.00907E-12
pm6_pm7 (pharyngeal muscle)	alh-1	1.410728268	1.02059E-11
pm6_pm7 (pharyngeal muscle)	col-140	1.3919886	1.02651E-11
pm6_pm7 (pharyngeal muscle)	col-124	1.318566009	2.01283E-11
pm6_pm7 (pharyngeal muscle)	col-20	1.371130518	3.42739E-11
pm6_pm7 (pharyngeal muscle)	col-184	2.038174195	4.3623E-11
pm6_pm7 (pharyngeal muscle)	col-119	1.970305249	5.64727E-11
pm6_pm7 (pharyngeal muscle)	col-181	1.702552577	1.37633E-09
pm6_pm7 (pharyngeal muscle)	F49E2.5	-1.302502289	1.49109E-07
pm6_pm7 (pharyngeal muscle)	R09B3.3	1.304861446	3.19485E-07
pm6_pm7 (pharyngeal muscle)	zip-2	-1.366395031	5.91803E-07

pm6_pm7 (pharyngeal muscle)	Y39B6A.5	-0.884641805	1.27466E-06
pm6_pm7 (pharyngeal muscle)	cpi-1	-0.654195526	3.40961E-06
pm6_pm7 (pharyngeal muscle)	col-19	1.133771314	3.5777E-06
pm6_pm7 (pharyngeal muscle)	col-80	1.564587498	3.65345E-06
pm6_pm7 (pharyngeal muscle)	col-98	2.409523734	5.38826E-06
pm6_pm7 (pharyngeal muscle)	pqn-36	-1.699966266	1.18877E-05
pm6_pm7 (pharyngeal muscle)	F17C11.11	-1.540977243	1.21624E-05
pm6_pm7 (pharyngeal muscle)	F14H12.3	-0.73370057	1.41518E-05
pm6_pm7 (pharyngeal muscle)	rpl-25.2	1.388360273	2.05154E-05
pm6_pm7 (pharyngeal muscle)	C25E10.8	-1.916515886	5.98752E-05
pm6_pm7 (pharyngeal muscle)	eef-1A.1	0.85798269	6.15569E-05
pm6_pm7 (pharyngeal muscle)	col-8	1.836519225	9.22643E-05
pm6_pm7 (pharyngeal muscle)	col-143	1.862669243	0.000158784
pm6_pm7 (pharyngeal muscle)	K03E5.2	-0.388585698	0.000203212
pm6_pm7 (pharyngeal muscle)	col-106	1.524956561	0.000241255
pm6_pm7 (pharyngeal muscle)	cex-2	-0.571403419	0.000537246
pm6_pm7 (pharyngeal muscle)	rps-7	0.702593521	0.000618363
pm6_pm7 (pharyngeal muscle)	eat-16	-1.42722002	0.000715769
pm6_pm7 (pharyngeal muscle)	iff-1	1.184423785	0.000716501
pm6_pm7 (pharyngeal muscle)	fipr-5	-0.458271081	0.000800445
pm6_pm7 (pharyngeal muscle)	rpl-11.1	1.13078469	0.000885465
pm6_pm7 (pharyngeal muscle)	F08B12.4	-0.637704516	0.001519116
pm6_pm7 (pharyngeal muscle)	fipr-1	-0.392840275	0.002693256
pm6_pm7 (pharyngeal muscle)	fipr-9	-0.438477003	0.003221339
pm6_pm7 (pharyngeal muscle)	rpl-7A	0.900045975	0.00410973
pm6_pm7 (pharyngeal muscle)	R09B3.2	1.422073821	0.004926784
pm6_pm7 (pharyngeal muscle)	Y55D5A.4	-1.3921256	0.006195988
pm6_pm7 (pharyngeal muscle)	rla-0	0.582544967	0.006979592
pm6_pm7 (pharyngeal muscle)	col-103	2.156735652	0.00956576
pm6_pm7 (pharyngeal muscle)	ssp-11	0	0.011777751
pm6_pm7 (pharyngeal muscle)	rps-0	0.789017366	0.012400927
pm6_pm7 (pharyngeal muscle)	rpl-3	0.69767836	0.012451232
pm6_pm7 (pharyngeal muscle)	rpl-2	0.694631099	0.014357495
pm6_pm7 (pharyngeal muscle)	ctc-3	0.510673764	0.015259779

pm6_pm7 (pharyngeal muscle)	col-160	1.556668229	0.016073417
pm6_pm7 (pharyngeal muscle)	rps-2	0.792068083	0.018927586
pm6_pm7 (pharyngeal muscle)	lec-6	-0.64830444	0.019547218
pm6_pm7 (pharyngeal muscle)	rps-22	0.773901285	0.023207261
pm6_pm7 (pharyngeal muscle)	C17F4.7	1.13575494	0.02576223
pm6_pm7 (pharyngeal muscle)	rps-1	0.67560003	0.026272659
pm6_pm7 (pharyngeal muscle)	F41E6.15	-0.397584708	0.030761684
pm6_pm7 (pharyngeal muscle)	rpl-10	0.555080427	0.031107161
pm6_pm7 (pharyngeal muscle)	pqn-31	-0.598487814	0.033975791
pm6_pm7 (pharyngeal muscle)	cyp-13A5	-1.995086601	0.035647645
pm6_pm7 (pharyngeal muscle)	cts-1	0.430049492	0.037693541
pm6_pm7 (pharyngeal muscle)	Y37E3.8	0.567960536	0.041347467
pm6_pm7 (pharyngeal muscle)	rpl-9	0.703087508	0.08434524
pm6_pm7 (pharyngeal muscle)	eef-1B.1	0.48892786	0.08883219
pm6_pm7 (pharyngeal muscle)	rpl-5	0.611486123	0.089072205
sh1 (gonadal sheath distal)	T03F1.11	1.894192743	8.53088E-79
sh1 (gonadal sheath distal)	tnc-2	2.179501151	1.69411E-72
sh1 (gonadal sheath distal)	dct-16	-0.674871798	1.11729E-67
sh1 (gonadal sheath distal)	fipr-2	3.215699965	1.36952E-67
sh1 (gonadal sheath distal)	ctc-3	0.365517614	8.34734E-57
sh1 (gonadal sheath distal)	Y73F4A.2	3.476328393	5.18704E-54
sh1 (gonadal sheath distal)	col-122	0.789242335	2.21093E-53
sh1 (gonadal sheath distal)	C53C9.2	2.635571864	5.14607E-47
sh1 (gonadal sheath distal)	ZC116.1	3.350330344	7.81271E-45
sh1 (gonadal sheath distal)	ctc-1	0.368673064	1.41551E-43
sh1 (gonadal sheath distal)	cpn-4	2.156234443	7.84775E-43
sh1 (gonadal sheath distal)	fipr-1	2.827265014	1.86268E-40
sh1 (gonadal sheath distal)	pqn-60	3.021553406	5.86607E-35
sh1 (gonadal sheath distal)	C54D10.3	1.159875734	1.41145E-31
sh1 (gonadal sheath distal)	col-184	0.706152601	7.56158E-31
sh1 (gonadal sheath distal)	rpl-41.2	-0.290198893	3.40683E-30
sh1 (gonadal sheath distal)	tnt-4	3.0242312	5.39892E-28
sh1 (gonadal sheath distal)	C45G9.6	1.914562213	5.81806E-28
sh1 (gonadal sheath distal)	C06A8.3	0.839278485	1.52897E-27
sh1 (gonadal sheath distal)	col-181	0.617002203	9.47873E-27
sh1 (gonadal sheath distal)	far-3	3.15815311	2.65992E-26
sh1 (gonadal sheath distal)	fip-2	1.110500067	5.50478E-26
sh1 (gonadal sheath distal)	Y87G2A.19	1.932013708	8.49997E-26
sh1 (gonadal sheath distal)	ttr-21	2.630992122	6.2644E-25

sh1 (gonadal sheath distal)	R09B3.3	-0.313143705	4.18429E-24
sh1 (gonadal sheath distal)	sodh-1	1.20903284	2.30632E-23
sh1 (gonadal sheath distal)	ttr-26	2.107066022	9.41105E-23
sh1 (gonadal sheath distal)	gst-4	0.82753321	1.25929E-22
sh1 (gonadal sheath distal)	fipr-10	3.094195266	1.5366E-22
sh1 (gonadal sheath distal)	col-124	0.399722266	3.14818E-22
sh1 (gonadal sheath distal)	gln-3	0.780527835	4.24908E-22
sh1 (gonadal sheath distal)	rps-28	-0.545374893	2.50984E-21
sh1 (gonadal sheath distal)	F35B12.3	2.747097608	3.31366E-21
sh1 (gonadal sheath distal)	Y119D3B.21	-0.53986981	4.50596E-20
sh1 (gonadal sheath distal)	col-8	0.830407109	1.60565E-19
sh1 (gonadal sheath distal)	col-140	0.404335866	1.11769E-18
sh1 (gonadal sheath distal)	mlc-3	0.345091614	1.69742E-18
sh1 (gonadal sheath distal)	hsp-16.41	1.719014153	4.68674E-18
sh1 (gonadal sheath distal)	C14C6.5	-1.800567473	6.36778E-18
sh1 (gonadal sheath distal)	W01D2.1	-0.357465707	1.81859E-17
sh1 (gonadal sheath distal)	fipr-5	3.854038292	1.73547E-16
sh1 (gonadal sheath distal)	ttr-27	2.470095505	1.21893E-15
sh1 (gonadal sheath distal)	col-119	0.480124142	3.04847E-15
sh1 (gonadal sheath distal)	unc-132	0.454119983	4.51363E-15
sh1 (gonadal sheath distal)	Y73F4A.3	2.82252705	4.94199E-15
sh1 (gonadal sheath distal)	fipr-7	3.294604971	7.7406E-15
sh1 (gonadal sheath distal)	K07A1.13	0.478507562	7.76264E-15
sh1 (gonadal sheath distal)	hsp-12.2	0.606436962	1.94176E-14
sh1 (gonadal sheath distal)	eef-1A.1	-0.229213111	3.37684E-14
sh1 (gonadal sheath distal)	F11E6.3	0.749589858	1.06074E-13
sh1 (gonadal sheath distal)	C23H5.8	-1.321870189	1.2091E-13
sh1 (gonadal sheath distal)	fipr-11	3.505028021	1.48984E-13
sh1 (gonadal sheath distal)	sams-1	0.701373909	1.8799E-13
sh1 (gonadal sheath distal)	rpl-36.A	-0.231580853	1.98171E-13
sh1 (gonadal sheath distal)	col-106	0.583790277	2.11007E-13
sh1 (gonadal sheath distal)	fipr-3	2.577763977	2.34275E-13
sh1 (gonadal sheath distal)	rps-25	-0.168112594	3.38291E-13
sh1 (gonadal sheath distal)	sri-40	0.528967648	5.71678E-13
sh1 (gonadal sheath distal)	vamp-8	2.255059895	6.39626E-13
sh1 (gonadal sheath distal)	myo-2	2.1424205	9.52822E-13

sh1 (gonadal sheath distal)	col-160	0.694654678	2.11763E-12
sh1 (gonadal sheath distal)	rps-29	-0.346400378	3.64601E-12
sh1 (gonadal sheath distal)	W04A4.2	0.512414634	3.95758E-12
sh1 (gonadal sheath distal)	hpo-26	2.911939028	5.54309E-12
sh1 (gonadal sheath distal)	sams-4	0.579530202	5.82405E-12
sh1 (gonadal sheath distal)	ilys-5	-0.529005726	1.02547E-11
sh1 (gonadal sheath distal)	rpl-39	-0.35673615	1.27281E-11
sh1 (gonadal sheath distal)	nduo-6	-0.138928912	1.31097E-11
sh1 (gonadal sheath distal)	F08D12.2	3.712146831	1.47024E-11
sh1 (gonadal sheath distal)	col-81	0.373118146	4.0925E-11
sh1 (gonadal sheath distal)	hsp-16.2	1.442546103	5.36182E-11
sh1 (gonadal sheath distal)	pqn-94	3.7222549	6.4656E-11
sh1 (gonadal sheath distal)	gpx-5	1.179206504	1.31391E-10
sh1 (gonadal sheath distal)	col-20	0.340873177	1.57083E-10
sh1 (gonadal sheath distal)	col-103	0.771160042	1.89318E-10
sh1 (gonadal sheath distal)	rpl-38	-0.25474324	2.28278E-10
sh1 (gonadal sheath distal)	gpx-3	3.340383361	2.29532E-10
sh1 (gonadal sheath distal)	F21C10.9	1.058128355	4.8949E-10
sh1 (gonadal sheath distal)	F41E6.15	0.84781213	6.7103E-10
sh1 (gonadal sheath distal)	lec-9	-0.573000932	7.75601E-10
sh1 (gonadal sheath distal)	tnt-3	1.627116852	1.1159E-09
sh1 (gonadal sheath distal)	C05D11.5	0.718830989	1.31054E-09
sh1 (gonadal sheath distal)	C24A3.2	0.761386679	1.58224E-09
sh1 (gonadal sheath distal)	msp-31	-0.73918996	1.72494E-09
sh1 (gonadal sheath distal)	nspb-8	2.393111385	1.78496E-09
sh1 (gonadal sheath distal)	nspb-6	2.648414867	2.34426E-09
sh1 (gonadal sheath distal)	F53F4.13	0.614301853	2.54767E-09
sh1 (gonadal sheath distal)	col-139	0.289090672	4.63449E-09
sh1 (gonadal sheath distal)	nspb-12	2.187719698	5.28896E-09
sh1 (gonadal sheath distal)	col-143	0.563181774	5.91991E-09
sh1 (gonadal sheath distal)	fipr-4	2.825716175	8.78448E-09
sh1 (gonadal sheath distal)	skpo-1	-0.351747607	9.52278E-09
sh1 (gonadal sheath distal)	iff-2	0.335580196	1.37449E-08
sh1 (gonadal sheath distal)	gst-10	-0.843144533	1.48344E-08
sh1 (gonadal sheath distal)	rpl-30	-0.224488469	1.72851E-08
sh1 (gonadal sheath distal)	W03F8.6	2.171754463	1.92915E-08
sh1 (gonadal sheath distal)	col-98	0.863630802	2.97416E-08

sh1 (gonadal sheath distal)	rpl-32	-0.164850454	3.27664E-08
sh1 (gonadal sheath distal)	perm-2	0.194867674	4.61036E-08
sh1 (gonadal sheath distal)	alh-1	0.557335938	6.25372E-08
sh1 (gonadal sheath distal)	myo-1	3.065472497	7.06823E-08
sh1 (gonadal sheath distal)	spp-2	-1.831256134	7.47089E-08
sh1 (gonadal sheath distal)	T20G5.8	0.656924153	7.47825E-08
sh1 (gonadal sheath distal)	hsp-70	1.440363104	7.63341E-08
sh1 (gonadal sheath distal)	B0545.4	0.5212188	8.699E-08
sh1 (gonadal sheath distal)	clec-50	-1.111034638	9.54809E-08
sh1 (gonadal sheath distal)	F28H7.3	-1.203124093	1.05789E-07
sh1 (gonadal sheath distal)	col-129	0.330999129	1.1401E-07
sh1 (gonadal sheath distal)	dhs-21	0.36724152	1.59025E-07
sh1 (gonadal sheath distal)	pgp-2	0.814145731	3.01241E-07
sh1 (gonadal sheath distal)	rpl-43	-0.201176709	8.63388E-07
sh1 (gonadal sheath distal)	dhs-25	-0.929752001	1.14464E-06
sh1 (gonadal sheath distal)	rps-2	-0.196511487	1.18085E-06
sh1 (gonadal sheath distal)	F13C5.5	2.343891422	1.28482E-06
sh1 (gonadal sheath distal)	Y47G6A.15	1.148632713	1.33048E-06
sh1 (gonadal sheath distal)	abf-6	2.80069947	1.9173E-06
sh1 (gonadal sheath distal)	rps-27	-0.184245663	2.32996E-06
sh1 (gonadal sheath distal)	abf-5	2.161794036	2.33359E-06
sh1 (gonadal sheath distal)	eef-2	-0.220334748	2.39404E-06
sh1 (gonadal sheath distal)	msp-40	-0.615589174	2.54532E-06
sh1 (gonadal sheath distal)	ttr-45	0.981993935	2.68187E-06
sh1 (gonadal sheath distal)	col-178	0.482610592	2.70657E-06
sh1 (gonadal sheath distal)	pat-10	0.172467595	3.64026E-06
sh1 (gonadal sheath distal)	clec-47	1.493856561	3.78417E-06
sh1 (gonadal sheath distal)	col-19	0.261462071	3.82157E-06
sh1 (gonadal sheath distal)	pud-4	-2.065847444	4.27063E-06
sh1 (gonadal sheath distal)	flp-5	2.115503384	4.4406E-06
sh1 (gonadal sheath distal)	clik-1	0.1456023	5.25613E-06
sh1 (gonadal sheath distal)	acs-2	0.958251879	5.68926E-06
sh1 (gonadal sheath distal)	rpl-36	-0.173656431	7.43646E-06

sh1 (gonadal sheath distal)	ifa-1	2.031878511	7.98179E-06
sh1 (gonadal sheath distal)	msra-1	0.981724905	9.90674E-06
sh1 (gonadal sheath distal)	W10C8.6	2.035747444	1.45606E-05
sh1 (gonadal sheath distal)	C45E5.4	1.882768726	1.47266E-05
sh1 (gonadal sheath distal)	pud-3	-1.816575544	1.62619E-05
sh1 (gonadal sheath distal)	nduo-1	0.148615059	1.67257E-05
sh1 (gonadal sheath distal)	T22B7.7	0.631749275	2.3535E-05
sh1 (gonadal sheath distal)	K08D12.6	0.543122662	2.56628E-05
sh1 (gonadal sheath distal)	F47B7.1	0.343271224	2.63234E-05
sh1 (gonadal sheath distal)	ctb-1	0.157927556	4.114E-05
sh1 (gonadal sheath distal)	ahcy-1	0.3380225	4.17402E-05
sh1 (gonadal sheath distal)	spp-18	-1.809243969	4.41769E-05
sh1 (gonadal sheath distal)	rla-2	-0.196672981	4.59417E-05
sh1 (gonadal sheath distal)	T04G9.7	-0.194287424	5.23654E-05
sh1 (gonadal sheath distal)	rpl-11.1	-0.208819038	6.09654E-05
sh1 (gonadal sheath distal)	pudl-1	1.469568814	6.37184E-05
sh1 (gonadal sheath distal)	tni-3	0.293747616	7.64141E-05
sh1 (gonadal sheath distal)	col-133	0.699418341	8.85573E-05
sh1 (gonadal sheath distal)	elo-5	-0.659832446	9.01195E-05
sh1 (gonadal sheath distal)	gdh-1	-0.359165548	9.99681E-05
sh1 (gonadal sheath distal)	rpl-12	-0.100699095	0.00010488
sh1 (gonadal sheath distal)	ndfl-4	-0.148950491	0.000116146
sh1 (gonadal sheath distal)	cpi-1	0.476709177	0.000134529
sh1 (gonadal sheath distal)	Y110A2AL.9	3.358790442	0.000144091
sh1 (gonadal sheath distal)	C27B7.9	1.099259268	0.000161808
sh1 (gonadal sheath distal)	cgh-1	-0.471910766	0.000183633
sh1 (gonadal sheath distal)	cht-3	-0.274234998	0.000187506
sh1 (gonadal sheath distal)	lec-2	0.410284329	0.000208993
sh1 (gonadal sheath distal)	F48D6.4	-0.692253447	0.000234462
sh1 (gonadal sheath distal)	C53B7.3	2.257556949	0.000235109
sh1 (gonadal sheath distal)	ZC21.3	2.694983622	0.000251904
sh1 (gonadal sheath distal)	ncx-2	2.451215156	0.000253647
sh1 (gonadal sheath distal)	pck-2	0.370618176	0.00025501

sh1 (gonadal sheath distal)	rps-0	-0.176804947	0.000292745
sh1 (gonadal sheath distal)	col-93	0.331552242	0.000340009
sh1 (gonadal sheath distal)	Y44A6D.2	2.484923944	0.000360244
sh1 (gonadal sheath distal)	F22B5.4	2.33214324	0.000372051
sh1 (gonadal sheath distal)	rla-1	-0.187851509	0.000379285
sh1 (gonadal sheath distal)	ttr-15	0.551958716	0.000385157
sh1 (gonadal sheath distal)	fipr-6	5.683528418	0.000490122
sh1 (gonadal sheath distal)	anmt-2	1.165032947	0.00058556
sh1 (gonadal sheath distal)	cpn-3	0.154525152	0.000609718
sh1 (gonadal sheath distal)	msp-76	-0.479080392	0.000684596
sh1 (gonadal sheath distal)	Y106G6D.8	1.206168234	0.000695268
sh1 (gonadal sheath distal)	rpl-29	-0.369179645	0.00069663
sh1 (gonadal sheath distal)	eef-1B.1	-0.136984854	0.000744442
sh1 (gonadal sheath distal)	nspd-2	-0.444456972	0.000760338
sh1 (gonadal sheath distal)	flp-12	1.744867706	0.000984727
sh1 (gonadal sheath distal)	C17F3.1	-0.383188887	0.00113816
sh1 (gonadal sheath distal)	act-2	-0.403891125	0.001144112
sh1 (gonadal sheath distal)	T04C12.3	2.420148812	0.001314459
sh1 (gonadal sheath distal)	ZC116.5	1.351867809	0.00131934
sh1 (gonadal sheath distal)	F43D2.6	2.586890666	0.001588722
sh1 (gonadal sheath distal)	T13F3.6	0.559465615	0.001729996
sh1 (gonadal sheath distal)	gst-27	-0.635214486	0.001744179
sh1 (gonadal sheath distal)	H36L18.2	0.246271998	0.001932792
sh1 (gonadal sheath distal)	Y43B11AR.1	2.276569977	0.00206349
sh1 (gonadal sheath distal)	rpl-34	-0.171314579	0.002311773
sh1 (gonadal sheath distal)	msp-152	-0.865628356	0.002685828
sh1 (gonadal sheath distal)	C10B5.3	1.493416037	0.003207713
sh1 (gonadal sheath distal)	msp-57	-0.255439393	0.003793618
sh1 (gonadal sheath distal)	cysl-2	-0.851698238	0.003818709
sh1 (gonadal sheath distal)	F15A4.6	0.567960804	0.004015927
sh1 (gonadal sheath distal)	F53F1.2	0.653146751	0.004704379
sh1 (gonadal sheath distal)	perm-4	0.172985454	0.004884088

sh1 (gonadal sheath distal)	T01C8.2	0.460399005	0.005309546
sh1 (gonadal sheath distal)	ttr-29	2.908485029	0.005547893
sh1 (gonadal sheath distal)	ssp-10	-0.268235264	0.007231668
sh1 (gonadal sheath distal)	lipl-5	-1.170461354	0.009350244
sh1 (gonadal sheath distal)	rps-19	-0.103753338	0.009685407
sh1 (gonadal sheath distal)	F14F8.8	4.047372312	0.009759709
sh1 (gonadal sheath distal)	ZK1193.2	0.463939105	0.010689155
sh1 (gonadal sheath distal)	ZC449.5	3.313304883	0.011029504
sh1 (gonadal sheath distal)	F55C10.5	1.886476593	0.011856477
sh1 (gonadal sheath distal)	acer-1	0.408896605	0.012375999
sh1 (gonadal sheath distal)	pyr-1	0.41944813	0.013014009
sh1 (gonadal sheath distal)	col-80	0.287732241	0.013105615
sh1 (gonadal sheath distal)	col-42	0.575243517	0.013680441
sh1 (gonadal sheath distal)	vit-1	-0.729537095	0.021960234
sh1 (gonadal sheath distal)	clec-150	-1.094580165	0.022170887
sh1 (gonadal sheath distal)	C49G7.3	0.554861622	0.024283244
sh1 (gonadal sheath distal)	F44E7.2	0.555482774	0.025148477
sh1 (gonadal sheath distal)	pqn-31	1.752172345	0.026220296
sh1 (gonadal sheath distal)	lec-10	-0.464307036	0.028380986
sh1 (gonadal sheath distal)	F56H9.2	-0.414735947	0.028579058
sh1 (gonadal sheath distal)	rps-24	-0.131116036	0.030125911
sh1 (gonadal sheath distal)	casy-1	2.241519549	0.031573144
sh1 (gonadal sheath distal)	F32A5.4	1.057625876	0.033170114
sh1 (gonadal sheath distal)	F23A7.8	-0.710217404	0.034640171
sh1 (gonadal sheath distal)	fipr-8	3.788349145	0.048791396
sh1 (gonadal sheath distal)	C53D6.7	0.217664419	0.049415616
sh1 (gonadal sheath distal)	C30F2.3	3.816445329	0.050308199
sh1 (gonadal sheath distal)	ctc-2	0.126385049	0.050541128
sh1 (gonadal sheath distal)	ZK622.4	1.127391665	0.05529857
sh1 (gonadal sheath distal)	F22H10.3	-0.478062075	0.057487997
sh1 (gonadal sheath distal)	lys-4	0.652479141	0.059314194
sh1 (gonadal sheath distal)	fasn-1	0.285303807	0.059511147
sh1 (gonadal sheath distal)	T24B8.5	-2.378664066	0.063978634

sh1 (gonadal sheath distal)	msp-3	-0.683067014	0.068219178
sh1 (gonadal sheath distal)	F08D12.3	2.997317771	0.068627799
sh1 (gonadal sheath distal)	gpdh-1	0.275231149	0.071113059
sh1 (gonadal sheath distal)	T04F8.8	0.542938493	0.071618586
sh1 (gonadal sheath distal)	apl-1	1.387914137	0.083355533
sh1 (gonadal sheath distal)	M28.5	-0.218800408	0.088327574
sh1 (gonadal sheath distal)	tsp-16	4.441277941	0.08876142
sh1 (gonadal sheath distal)	ZK856.7	0.552771894	0.092757524
sh2 (gonadal sheath distal)	Y69H2.3	-2.888004545	4.5352E-157
sh2 (gonadal sheath distal)	rpl-41.2	-0.402303059	1.9048E-133
sh2 (gonadal sheath distal)	col-122	0.863953289	8.1025E-127
sh2 (gonadal sheath distal)	ctc-3	0.367152011	2.1409E-118
sh2 (gonadal sheath distal)	gln-3	0.81103236	5.038E-98
sh2 (gonadal sheath distal)	nduo-6	-0.236444264	3.51634E-92
sh2 (gonadal sheath distal)	cht-3	-0.489181927	9.88353E-88
sh2 (gonadal sheath distal)	skpo-1	-0.487030985	3.21881E-80
sh2 (gonadal sheath distal)	dct-16	-0.580778406	7.28517E-80
sh2 (gonadal sheath distal)	sodh-1	1.354147732	5.81847E-75
sh2 (gonadal sheath distal)	ddo-3	-0.411128834	1.67637E-74
sh2 (gonadal sheath distal)	col-119	0.656892264	9.09779E-68
sh2 (gonadal sheath distal)	far-2	-0.239047234	2.26165E-67
sh2 (gonadal sheath distal)	fip-2	1.589579546	1.48929E-65
sh2 (gonadal sheath distal)	C54D10.3	1.480144423	6.99698E-65
sh2 (gonadal sheath distal)	alh-1	0.816147972	1.79507E-64
sh2 (gonadal sheath distal)	ctc-1	0.282889462	1.56648E-63
sh2 (gonadal sheath distal)	B0513.4	-0.262547024	6.88698E-63
sh2 (gonadal sheath distal)	W04A4.2	0.461799634	3.29708E-61
sh2 (gonadal sheath distal)	T03F1.11	1.633373024	1.66766E-60
sh2 (gonadal sheath distal)	col-8	1.095439353	1.56761E-59
sh2 (gonadal sheath distal)	Y119D3B.21	-0.616131723	2.34615E-59
sh2 (gonadal sheath distal)	col-184	0.677654471	1.72383E-56
sh2 (gonadal sheath distal)	col-140	0.467280407	8.2644E-56

sh2 (gonadal sheath distal)	W01D2.1	-0.396242976	9.52704E-56
sh2 (gonadal sheath distal)	tnc-2	1.676428355	2.73733E-54
sh2 (gonadal sheath distal)	C39D10.7	-0.32618127	2.95466E-54
sh2 (gonadal sheath distal)	C06A8.3	0.765040578	5.17637E-54
sh2 (gonadal sheath distal)	col-98	0.958919091	9.83178E-54
sh2 (gonadal sheath distal)	col-124	0.399528322	7.37524E-53
sh2 (gonadal sheath distal)	fipr-2	2.638208032	2.60735E-52
sh2 (gonadal sheath distal)	rps-25	-0.200737124	1.72235E-51
sh2 (gonadal sheath distal)	T04G9.7	-0.272510991	2.00991E-50
sh2 (gonadal sheath distal)	col-181	0.599099247	4.75936E-50
sh2 (gonadal sheath distal)	unc-132	0.323490782	7.14487E-50
sh2 (gonadal sheath distal)	far-3	2.495368876	1.05716E-47
sh2 (gonadal sheath distal)	R09B3.3	-0.295812969	5.94703E-46
sh2 (gonadal sheath distal)	rpl-38	-0.325392168	4.19447E-44
sh2 (gonadal sheath distal)	rps-27	-0.261291873	1.03937E-41
sh2 (gonadal sheath distal)	Y73F4A.2	2.880808852	7.97545E-41
sh2 (gonadal sheath distal)	col-20	0.400247125	1.41264E-40
sh2 (gonadal sheath distal)	rpl-36.A	-0.247467326	2.40188E-40
sh2 (gonadal sheath distal)	sri-40	0.413893526	4.58769E-38
sh2 (gonadal sheath distal)	pgp-2	0.759514293	1.00371E-37
sh2 (gonadal sheath distal)	pqn-60	3.01259324	3.22018E-36
sh2 (gonadal sheath distal)	rpl-43	-0.269718111	4.37379E-36
sh2 (gonadal sheath distal)	rpl-39	-0.39252905	3.80111E-35
sh2 (gonadal sheath distal)	fipr-1	2.194715136	7.782E-35
sh2 (gonadal sheath distal)	rps-28	-0.438367777	1.72305E-34
sh2 (gonadal sheath distal)	dod-23	-0.678432434	1.42659E-33
sh2 (gonadal sheath distal)	rps-29	-0.343150212	5.61892E-31
sh2 (gonadal sheath distal)	C14C6.5	-1.334703724	4.94967E-30
sh2 (gonadal sheath distal)	tbh-1	-0.371752772	9.10815E-30
sh2 (gonadal sheath distal)	Y87G2A.19	1.692543085	1.17246E-29
sh2 (gonadal sheath distal)	ule-3	-1.357426776	1.80776E-29

sh2 (gonadal sheath distal)	ZC116.1	1.985904193	1.93397E-29
sh2 (gonadal sheath distal)	rpl-36	-0.215582731	3.31859E-29
sh2 (gonadal sheath distal)	C05D11.5	0.642038859	8.02442E-28
sh2 (gonadal sheath distal)	C45G9.6	1.908559935	1.29591E-27
sh2 (gonadal sheath distal)	ttr-21	2.415537646	8.07699E-27
sh2 (gonadal sheath distal)	K07A1.13	0.276818736	1.21882E-26
sh2 (gonadal sheath distal)	F56H9.2	-0.589017889	1.56575E-25
sh2 (gonadal sheath distal)	C53C9.2	1.803675379	1.58681E-25
sh2 (gonadal sheath distal)	ZK813.1	-1.420410055	5.02638E-25
sh2 (gonadal sheath distal)	F41E6.15	1.222703975	6.35294E-25
sh2 (gonadal sheath distal)	F35B12.3	2.547263841	7.11354E-25
sh2 (gonadal sheath distal)	myo-2	2.883302549	1.18623E-24
sh2 (gonadal sheath distal)	col-19	0.339930514	2.51429E-24
sh2 (gonadal sheath distal)	F11E6.3	0.723329763	1.35333E-23
sh2 (gonadal sheath distal)	K11D12.13	0.844562154	6.8604E-23
sh2 (gonadal sheath distal)	fipr-10	2.577707251	3.46745E-22
sh2 (gonadal sheath distal)	F21C10.9	0.595457903	4.16014E-22
sh2 (gonadal sheath distal)	col-160	0.684601208	4.91172E-22
sh2 (gonadal sheath distal)	B0545.4	0.344415313	1.32979E-21
sh2 (gonadal sheath distal)	cpn-4	0.91236136	2.19403E-21
sh2 (gonadal sheath distal)	rps-21	-0.295524344	2.40729E-21
sh2 (gonadal sheath distal)	F14H12.6	-0.450334735	1.34352E-20
sh2 (gonadal sheath distal)	col-178	0.574012031	1.87452E-20
sh2 (gonadal sheath distal)	col-106	0.533730603	1.99805E-20
sh2 (gonadal sheath distal)	ttr-26	1.957109314	2.22036E-20
sh2 (gonadal sheath distal)	rpl-34	-0.211623172	3.83354E-20
sh2 (gonadal sheath distal)	col-81	0.33703335	6.76706E-20
sh2 (gonadal sheath distal)	fipr-7	2.296703206	9.10875E-20
sh2 (gonadal sheath distal)	gst-10	-0.738244481	2.63894E-19
sh2 (gonadal sheath distal)	col-143	0.592918054	3.69908E-19
sh2 (gonadal sheath distal)	F44E7.2	0.48869784	6.43084E-19
sh2 (gonadal sheath distal)	mlc-3	0.244598338	7.38387E-19
sh2 (gonadal sheath distal)	acer-1	0.497364846	1.75511E-18
sh2 (gonadal sheath distal)	lec-9	-0.483893745	2.75486E-18
sh2 (gonadal sheath distal)	gst-4	0.452411778	4.58021E-18
sh2 (gonadal sheath distal)	C24A3.2	0.540284777	4.7091E-18

sh2 (gonadal sheath distal)	pyr-1	0.38916119	7.61391E-18
sh2 (gonadal sheath distal)	T05E11.2	-2.034342208	1.0172E-17
sh2 (gonadal sheath distal)	dod-6	0.691345643	2.0321E-17
sh2 (gonadal sheath distal)	hsp-16.41	0.896790637	2.42313E-17
sh2 (gonadal sheath distal)	R09B3.2	-0.316740993	7.6738E-17
sh2 (gonadal sheath distal)	pud-3	-1.305456085	8.06351E-17
sh2 (gonadal sheath distal)	ndfl-4	-0.18159156	1.02756E-16
sh2 (gonadal sheath distal)	hsp-16.2	0.936105325	1.07627E-16
sh2 (gonadal sheath distal)	dhs-21	0.263986793	2.379E-16
sh2 (gonadal sheath distal)	gst-27	-0.550550706	2.55644E-16
sh2 (gonadal sheath distal)	hsp-12.2	0.429399073	5.30745E-16
sh2 (gonadal sheath distal)	spp-10	-0.262471454	6.04147E-16
sh2 (gonadal sheath distal)	myo-1	2.463471657	8.59517E-16
sh2 (gonadal sheath distal)	iff-2	0.214294073	1.39117E-15
sh2 (gonadal sheath distal)	F48E3.4	-0.179929019	1.73988E-15
sh2 (gonadal sheath distal)	fipr-5	1.850820679	1.91071E-15
sh2 (gonadal sheath distal)	acs-2	0.31431344	2.88021E-15
sh2 (gonadal sheath distal)	F15A4.6	0.667765292	3.07238E-15
sh2 (gonadal sheath distal)	T20G5.8	0.569721756	3.60838E-15
sh2 (gonadal sheath distal)	C37A2.7	-0.208424043	4.02378E-15
sh2 (gonadal sheath distal)	F22H10.3	-0.489249633	5.54004E-15
sh2 (gonadal sheath distal)	F32A5.4	1.108466036	6.65069E-15
sh2 (gonadal sheath distal)	Y37D8A.19	-0.97920955	1.39165E-14
sh2 (gonadal sheath distal)	anmt-2	1.432463924	2.25846E-14
sh2 (gonadal sheath distal)	ahcy-1	0.349341984	2.78168E-14
sh2 (gonadal sheath distal)	C53A3.2	0.455776116	3.97669E-14
sh2 (gonadal sheath distal)	cysl-2	-0.358859225	5.62262E-14
sh2 (gonadal sheath distal)	col-103	0.724480603	6.24304E-14
sh2 (gonadal sheath distal)	fipr-3	2.142813036	1.53092E-13
sh2 (gonadal sheath distal)	fipr-4	2.550940658	1.60591E-13
sh2 (gonadal sheath distal)	Y55B1AL.1	-0.940176458	1.94642E-13
sh2 (gonadal sheath distal)	col-42	0.599789263	4.68447E-13
sh2 (gonadal sheath distal)	cpr-5	0.970480197	5.79387E-13
sh2 (gonadal sheath distal)	lys-4	0.779296782	5.9418E-13
sh2 (gonadal sheath distal)	C23H5.8	-0.69493073	3.97445E-12

sh2 (gonadal sheath distal)	F18E3.13	0.392881863	4.35959E-12
sh2 (gonadal sheath distal)	hphd-1	-0.476712311	4.47698E-12
sh2 (gonadal sheath distal)	C49G7.3	0.500829206	6.93676E-12
sh2 (gonadal sheath distal)	pyp-1	0.282113994	1.02604E-11
sh2 (gonadal sheath distal)	col-93	0.350760552	1.05016E-11
sh2 (gonadal sheath distal)	F13C5.5	2.440213417	1.64939E-11
sh2 (gonadal sheath distal)	F53F4.13	0.451531883	3.55903E-11
sh2 (gonadal sheath distal)	C25E10.8	-0.769874834	3.79621E-11
sh2 (gonadal sheath distal)	gst-20	-0.692434932	4.37738E-11
sh2 (gonadal sheath distal)	col-80	0.326200723	7.92781E-11
sh2 (gonadal sheath distal)	spp-5	-0.637589656	8.03446E-11
sh2 (gonadal sheath distal)	T27D12.6	-0.604858882	1.46611E-10
sh2 (gonadal sheath distal)	M05B5.4	-0.474806781	1.62626E-10
sh2 (gonadal sheath distal)	ZK1193.2	0.311704038	2.29634E-10
sh2 (gonadal sheath distal)	rpl-32	-0.111731226	3.7968E-10
sh2 (gonadal sheath distal)	rps-26	-0.118119364	4.38733E-10
sh2 (gonadal sheath distal)	T13F3.6	0.509664471	4.50402E-10
sh2 (gonadal sheath distal)	pud-4	-1.421398237	7.25378E-10
sh2 (gonadal sheath distal)	tnt-4	1.44111165	8.36781E-10
sh2 (gonadal sheath distal)	pat-10	0.206207118	8.38559E-10
sh2 (gonadal sheath distal)	ZC116.5	2.219306691	9.4796E-10
sh2 (gonadal sheath distal)	grd-5	1.628538693	9.61539E-10
sh2 (gonadal sheath distal)	F41C3.5	-0.136268511	1.00247E-09
sh2 (gonadal sheath distal)	rpl-29	-0.33994601	1.01253E-09
sh2 (gonadal sheath distal)	C46C2.5	-2.556444674	1.09566E-09
sh2 (gonadal sheath distal)	msp-31	-0.414006886	1.09999E-09
sh2 (gonadal sheath distal)	Y62H9A.5	-0.811949791	1.1113E-09
sh2 (gonadal sheath distal)	F08D12.2	2.042281341	1.24537E-09
sh2 (gonadal sheath distal)	cco-2	0.176432129	1.37782E-09
sh2 (gonadal sheath distal)	T01D1.4	0.157887802	1.44781E-09
sh2 (gonadal sheath distal)	W10C8.6	1.655865888	1.51683E-09
sh2 (gonadal sheath distal)	sams-1	0.394010981	2.28841E-09

sh2 (gonadal sheath distal)	tni-3	0.41673241	2.32066E-09
sh2 (gonadal sheath distal)	gmps-1	0.405707701	3.39494E-09
sh2 (gonadal sheath distal)	R09H10.3	-0.427781927	3.51361E-09
sh2 (gonadal sheath distal)	M163.8	0.465614201	4.05391E-09
sh2 (gonadal sheath distal)	col-142	0.464469481	5.46189E-09
sh2 (gonadal sheath distal)	F48D6.4	-0.515560321	6.68305E-09
sh2 (gonadal sheath distal)	clec-47	1.098645544	7.1694E-09
sh2 (gonadal sheath distal)	C45E5.4	2.373634792	7.32062E-09
sh2 (gonadal sheath distal)	F36F2.1	1.244938056	7.32497E-09
sh2 (gonadal sheath distal)	abf-5	1.60666654	9.34965E-09
sh2 (gonadal sheath distal)	gpx-5	0.841407951	1.12227E-08
sh2 (gonadal sheath distal)	C27A7.5	-0.416756195	1.12563E-08
sh2 (gonadal sheath distal)	C17F4.7	0.38777738	1.18288E-08
sh2 (gonadal sheath distal)	msp-152	-0.262215361	1.30664E-08
sh2 (gonadal sheath distal)	C10B5.3	0.986525277	1.78047E-08
sh2 (gonadal sheath distal)	col-101	0.464968049	1.9055E-08
sh2 (gonadal sheath distal)	F46H5.3	0.171586016	2.1832E-08
sh2 (gonadal sheath distal)	odc-1	0.585451241	2.27302E-08
sh2 (gonadal sheath distal)	col-118	1.585137331	2.91919E-08
sh2 (gonadal sheath distal)	glb-1	0.27972554	3.06573E-08
sh2 (gonadal sheath distal)	rpl-27	-0.159664493	3.46113E-08
sh2 (gonadal sheath distal)	lec-10	-0.442601992	3.70243E-08
sh2 (gonadal sheath distal)	spp-18	-1.034831583	6.34432E-08
sh2 (gonadal sheath distal)	sams-4	0.249329473	7.24479E-08
sh2 (gonadal sheath distal)	cpn-3	0.160748935	8.90416E-08
sh2 (gonadal sheath distal)	F16C3.2	-1.213847361	1.38564E-07
sh2 (gonadal sheath distal)	R06C1.4	-0.143156993	1.45531E-07
sh2 (gonadal sheath distal)	nduo-1	0.115406233	2.33867E-07
sh2 (gonadal sheath distal)	col-139	0.189690965	2.38052E-07
sh2 (gonadal sheath distal)	C10G8.4	-1.515268012	2.42832E-07
sh2 (gonadal sheath distal)	H36L18.2	0.165719354	2.43782E-07
sh2 (gonadal sheath distal)	msp-40	-0.499833533	3.30073E-07
sh2 (gonadal sheath distal)	swm-1	-0.717260104	3.51868E-07

sh2 (gonadal sheath distal)	T22D1.3	0.221606185	3.7982E-07
sh2 (gonadal sheath distal)	tnt-3	1.093096214	3.81352E-07
sh2 (gonadal sheath distal)	asp-4	1.09034713	4.11017E-07
sh2 (gonadal sheath distal)	H17B01.2	-3.89347963	4.46207E-07
sh2 (gonadal sheath distal)	asp-2	0.712274025	4.59538E-07
sh2 (gonadal sheath distal)	fipr-11	2.215575554	5.16271E-07
sh2 (gonadal sheath distal)	mlc-2	0.224039579	5.90099E-07
sh2 (gonadal sheath distal)	fmo-4	-0.226635185	7.60781E-07
sh2 (gonadal sheath distal)	K07A1.6	-1.182986293	7.67776E-07
sh2 (gonadal sheath distal)	Y32F6A.5	-0.275828732	8.42503E-07
sh2 (gonadal sheath distal)	scl-6	0.537334178	8.62153E-07
sh2 (gonadal sheath distal)	msra-1	0.476131912	8.98272E-07
sh2 (gonadal sheath distal)	fgt-1	-0.486883086	9.20391E-07
sh2 (gonadal sheath distal)	aagr-2	0.578841321	1.04429E-06
sh2 (gonadal sheath distal)	C27B7.9	0.702877456	1.18131E-06
sh2 (gonadal sheath distal)	nspb-6	1.785214562	1.56552E-06
sh2 (gonadal sheath distal)	F58F12.1	0.156199051	1.78369E-06
sh2 (gonadal sheath distal)	B0393.9	-0.788645863	1.90128E-06
sh2 (gonadal sheath distal)	nuo-6	0.266536514	2.16426E-06
sh2 (gonadal sheath distal)	ZC373.2	-0.378621414	2.3919E-06
sh2 (gonadal sheath distal)	marg-1	2.086949969	2.50448E-06
sh2 (gonadal sheath distal)	rpl-30	-0.128797655	2.88531E-06
sh2 (gonadal sheath distal)	hpo-26	1.733966437	3.11913E-06
sh2 (gonadal sheath distal)	D1054.18	-0.395093517	3.42807E-06
sh2 (gonadal sheath distal)	exc-6	-3.008956844	3.46302E-06
sh2 (gonadal sheath distal)	Y73F4A.3	1.942013054	4.04798E-06
sh2 (gonadal sheath distal)	pqn-48	-0.346291019	4.51965E-06
sh2 (gonadal sheath distal)	pqn-94	1.476803801	4.52833E-06
sh2 (gonadal sheath distal)	rmd-2	-0.1924719	4.74108E-06
sh2 (gonadal sheath distal)	C06A12.3	-0.916199751	4.92084E-06
sh2 (gonadal sheath distal)	F28H7.3	-0.616211812	4.94644E-06
sh2 (gonadal sheath distal)	ifa-1	1.249721441	4.95605E-06
sh2 (gonadal sheath distal)	F38B2.6	0.810423897	5.2479E-06

sh2 (gonadal sheath distal)	fipr-6	1.969596068	5.89817E-06
sh2 (gonadal sheath distal)	cpz-1	0.434870569	6.3394E-06
sh2 (gonadal sheath distal)	C17G1.2	-0.186094759	7.23892E-06
sh2 (gonadal sheath distal)	Y94H6A.10	0.256061149	7.57734E-06
sh2 (gonadal sheath distal)	ZC21.3	2.188162147	7.87974E-06
sh2 (gonadal sheath distal)	Y65B4BL.6	0.124888435	9.97354E-06
sh2 (gonadal sheath distal)	hprt-1	0.192617539	1.35064E-05
sh2 (gonadal sheath distal)	ubq-2	-0.094686895	1.3688E-05
sh2 (gonadal sheath distal)	T24B8.5	-0.738508079	1.61543E-05
sh2 (gonadal sheath distal)	ssp-10	-0.190783027	2.01287E-05
sh2 (gonadal sheath distal)	spp-2	-0.809506356	2.06762E-05
sh2 (gonadal sheath distal)	nspd-2	-0.136383204	2.80565E-05
sh2 (gonadal sheath distal)	mlck-1	-0.918134918	2.91499E-05
sh2 (gonadal sheath distal)	F22B5.6	-1.403674407	2.9827E-05
sh2 (gonadal sheath distal)	rege-1	0.614844366	3.01436E-05
sh2 (gonadal sheath distal)	spp-17	-0.363342698	3.29974E-05
sh2 (gonadal sheath distal)	cpr-4	1.127303184	3.57924E-05
sh2 (gonadal sheath distal)	C05C10.3	-0.468683184	3.87208E-05
sh2 (gonadal sheath distal)	ttr-27	1.098977143	4.54877E-05
sh2 (gonadal sheath distal)	atp-2	0.115281716	5.22286E-05
sh2 (gonadal sheath distal)	F53H4.2	-0.893479676	5.44006E-05
sh2 (gonadal sheath distal)	gbh-1	0.723549827	5.98885E-05
sh2 (gonadal sheath distal)	comt-3	0.275360519	6.32376E-05
sh2 (gonadal sheath distal)	ZK622.4	0.813334598	6.52987E-05
sh2 (gonadal sheath distal)	pqn-31	2.701245186	7.14992E-05
sh2 (gonadal sheath distal)	C49F5.7	-0.224230403	7.77055E-05
sh2 (gonadal sheath distal)	F41G3.10	0.355067372	8.64445E-05
sh2 (gonadal sheath distal)	K08D12.6	0.365879939	0.000103366
sh2 (gonadal sheath distal)	F01D5.3	-0.752309771	0.00011605
sh2 (gonadal sheath distal)	nspb-12	1.435433694	0.000117825
sh2 (gonadal sheath distal)	mctp-1	1.498837742	0.000119176
sh2 (gonadal sheath distal)	F42A8.1	0.632762746	0.000122159

sh2 (gonadal sheath distal)	F23H12.3	-3.247116611	0.000124145
sh2 (gonadal sheath distal)	vamp-8	1.044834455	0.000127091
sh2 (gonadal sheath distal)	D1054.10	-0.399569156	0.000143969
sh2 (gonadal sheath distal)	ndk-1	0.067320626	0.000154081
sh2 (gonadal sheath distal)	F35C12.3	1.054052901	0.00018329
sh2 (gonadal sheath distal)	gst-13	-0.443950221	0.00019492
sh2 (gonadal sheath distal)	hpo-18	-0.291574473	0.000200654
sh2 (gonadal sheath distal)	ctc-2	0.110431496	0.000202388
sh2 (gonadal sheath distal)	pck-2	0.210792709	0.000206789
sh2 (gonadal sheath distal)	msp-3	-0.438942265	0.000217392
sh2 (gonadal sheath distal)	F02D8.4	-1.165738994	0.000244529
sh2 (gonadal sheath distal)	rla-2	-0.1194737	0.000248652
sh2 (gonadal sheath distal)	F25H5.8	-0.859209774	0.000272036
sh2 (gonadal sheath distal)	F53F1.2	0.474535263	0.000318072
sh2 (gonadal sheath distal)	rps-1	0.09248801	0.000325501
sh2 (gonadal sheath distal)	K03E5.2	0.251760797	0.000329564
sh2 (gonadal sheath distal)	ule-5	-0.681176072	0.000337703
sh2 (gonadal sheath distal)	abf-6	2.573271612	0.000379238
sh2 (gonadal sheath distal)	ncx-2	1.567638995	0.00038796
sh2 (gonadal sheath distal)	Y22D7AL.10	0.197883432	0.000391589
sh2 (gonadal sheath distal)	nmat-1	0.204800792	0.000429491
sh2 (gonadal sheath distal)	fasn-1	0.179565837	0.000439448
sh2 (gonadal sheath distal)	acbp-1	-0.332588835	0.000450884
sh2 (gonadal sheath distal)	pfn-1	0.207920569	0.000460605
sh2 (gonadal sheath distal)	C18D4.12	-1.220450862	0.000480778
sh2 (gonadal sheath distal)	ZK809.8	0.308521116	0.000512871
sh2 (gonadal sheath distal)	col-129	0.195693542	0.000514927
sh2 (gonadal sheath distal)	rla-0	0.078962942	0.000549902
sh2 (gonadal sheath distal)	D1086.7	-1.226055013	0.00055949
sh2 (gonadal sheath distal)	clik-1	0.194706954	0.000611923
sh2 (gonadal sheath distal)	Y111B2A.2	-0.181126411	0.000763379
sh2 (gonadal sheath distal)	W02D9.7	1.964501315	0.000778436
sh2 (gonadal sheath distal)	F35A5.2	0.309229677	0.000843273

sh2 (gonadal sheath distal)	gpx-3	1.768340027	0.000933366
sh2 (gonadal sheath distal)	C30F2.3	2.538840734	0.00112545
sh2 (gonadal sheath distal)	lipl-5	-0.704253206	0.001292802
sh2 (gonadal sheath distal)	T09A12.5	-0.478538663	0.001314871
sh2 (gonadal sheath distal)	T07F10.1	0.900936188	0.001438201
sh2 (gonadal sheath distal)	act-2	-0.278989042	0.001505855
sh2 (gonadal sheath distal)	rpl-14	-0.088015736	0.001524899
sh2 (gonadal sheath distal)	hacd-1	-0.447712252	0.001677981
sh2 (gonadal sheath distal)	ZK596.1	0.90271315	0.001905891
sh2 (gonadal sheath distal)	fipr-9	2.29537666	0.001907228
sh2 (gonadal sheath distal)	rpl-31	-0.098201142	0.0021318
sh2 (gonadal sheath distal)	Y38E10A.24	-0.388497713	0.002305804
sh2 (gonadal sheath distal)	W03F8.6	1.144154397	0.002369576
sh2 (gonadal sheath distal)	F41G3.21	0.340316287	0.002374071
sh2 (gonadal sheath distal)	klp-4	1.022491177	0.00239647
sh2 (gonadal sheath distal)	elo-5	-0.41411134	0.002452237
sh2 (gonadal sheath distal)	gdh-1	-0.202700896	0.002542678
sh2 (gonadal sheath distal)	F43D2.6	1.291119135	0.002662489
sh2 (gonadal sheath distal)	fmo-2	2.026281464	0.002787952
sh2 (gonadal sheath distal)	idha-1	0.242151813	0.002847519
sh2 (gonadal sheath distal)	F29B9.11	-0.161119111	0.003118658
sh2 (gonadal sheath distal)	ZK1037.6	-2.893479624	0.00325453
sh2 (gonadal sheath distal)	nduo-3	-0.230440621	0.003295896
sh2 (gonadal sheath distal)	lips-10	0.509905109	0.003420084
sh2 (gonadal sheath distal)	F55B11.3	-0.939283365	0.003420312
sh2 (gonadal sheath distal)	lim-8	0.876623201	0.003920852
sh2 (gonadal sheath distal)	lea-1	0.196410738	0.003924116
sh2 (gonadal sheath distal)	cup-16	-1.364921369	0.004504795
sh2 (gonadal sheath distal)	T04C12.3	1.861637533	0.004718196
sh2 (gonadal sheath distal)	chdp-1	0.165535038	0.00515275
sh2 (gonadal sheath distal)	C31H2.14	0.510162698	0.005439785
sh2 (gonadal sheath distal)	ril-1	0.13708709	0.005951612

sh2 (gonadal sheath distal)	msp-45	-0.20630082	0.006706928
sh2 (gonadal sheath distal)	F14H12.3	2.707568794	0.006971266
sh2 (gonadal sheath distal)	ZK863.8	1.047711804	0.007093488
sh2 (gonadal sheath distal)	cth-1	0.25283816	0.007719134
sh2 (gonadal sheath distal)	eef-2	-0.103096959	0.008192085
sh2 (gonadal sheath distal)	F35E12.9	-0.418426182	0.00904671
sh2 (gonadal sheath distal)	F19B2.5	-0.621641107	0.009147769
sh2 (gonadal sheath distal)	gst-5	0.528257434	0.009561469
sh2 (gonadal sheath distal)	T12D8.5	-0.423426436	0.009571039
sh2 (gonadal sheath distal)	C52G5.2	0.42485142	0.009779927
sh2 (gonadal sheath distal)	unc-60	0.210660455	0.010055503
sh2 (gonadal sheath distal)	ctb-1	0.090781255	0.01023082
sh2 (gonadal sheath distal)	F14F8.8	2.440529852	0.010765514
sh2 (gonadal sheath distal)	grd-10	1.443444914	0.011637632
sh2 (gonadal sheath distal)	C05D12.3	-0.606872061	0.012210031
sh2 (gonadal sheath distal)	cco-1	0.107366509	0.012718748
sh2 (gonadal sheath distal)	cpt-2	0.379504599	0.012798451
sh2 (gonadal sheath distal)	H29C22.1	-0.478442177	0.013553648
sh2 (gonadal sheath distal)	F16B3.2	0.13113929	0.014710392
sh2 (gonadal sheath distal)	F18E3.12	0.321437994	0.016277012
sh2 (gonadal sheath distal)	cbs-1	-0.4635743	0.017113414
sh2 (gonadal sheath distal)	dhs-25	-0.398685749	0.017917996
sh2 (gonadal sheath distal)	ZK813.7	-0.697559466	0.018208385
sh2 (gonadal sheath distal)	lbp-3	-0.426861025	0.01885366
sh2 (gonadal sheath distal)	K01A2.5	-0.41090563	0.019036445
sh2 (gonadal sheath distal)	ucr-11	-0.335584471	0.01941095
sh2 (gonadal sheath distal)	act-1	-0.164584664	0.021319692
sh2 (gonadal sheath distal)	ZC449.5	1.857259365	0.022651142
sh2 (gonadal sheath distal)	nuo-3	0.142835819	0.023999156
sh2 (gonadal sheath distal)	F55H12.4	0.254965273	0.024989993
sh2 (gonadal sheath distal)	spp-3	-0.468265325	0.025725018
sh2 (gonadal sheath distal)	tsp-16	1.885093147	0.02657245

sh2 (gonadal sheath distal)	lec-5	-0.200079241	0.026665798
sh2 (gonadal sheath distal)	Y51H1A.3	0.164406367	0.026970139
sh2 (gonadal sheath distal)	ant-1.1	0.056796992	0.027062727
sh2 (gonadal sheath distal)	nspd-1	-0.071726554	0.027437184
sh2 (gonadal sheath distal)	icl-1	0.340890005	0.028087851
sh2 (gonadal sheath distal)	pmp-5	0.518689868	0.029094224
sh2 (gonadal sheath distal)	skr-1	0.220591119	0.029456802
sh2 (gonadal sheath distal)	C39E9.8	0.450806186	0.029935518
sh2 (gonadal sheath distal)	ttr-29	1.603857903	0.030990148
sh2 (gonadal sheath distal)	nlp-25	0.584547234	0.031994625
sh2 (gonadal sheath distal)	puf-5	-0.48442816	0.032154302
sh2 (gonadal sheath distal)	atp-5	0.125069073	0.034308175
sh2 (gonadal sheath distal)	R31.2	0.33341267	0.035397736
sh2 (gonadal sheath distal)	lys-2	-0.590964781	0.037038676
sh2 (gonadal sheath distal)	rpl-22	-0.084012392	0.038078824
sh2 (gonadal sheath distal)	rpl-35	-0.06749028	0.04488095
sh2 (gonadal sheath distal)	R04F11.2	0.088498033	0.046880611
sh2 (gonadal sheath distal)	best-20	-0.26782524	0.047038168
sh2 (gonadal sheath distal)	set-18	0.533563895	0.04811186
sh2 (gonadal sheath distal)	C50B8.6	-1.890583888	0.048265058
sh2 (gonadal sheath distal)	fat-7	1.038296735	0.048666226
sh2 (gonadal sheath distal)	heh-1	-0.219360686	0.04899918
sh2 (gonadal sheath distal)	F53A9.9	1.401733529	0.049092704
sh2 (gonadal sheath distal)	clec-178	2.013410869	0.051959624
sh2 (gonadal sheath distal)	C41G7.9	0.201687122	0.052390381
sh2 (gonadal sheath distal)	cts-1	0.17204525	0.054756306
sh2 (gonadal sheath distal)	B0410.3	0.266361512	0.060513798
sh2 (gonadal sheath distal)	K10H10.12	1.789888113	0.062557739
sh2 (gonadal sheath distal)	clec-150	-0.597790171	0.067126017
sh2 (gonadal sheath distal)	ZK669.3	0.255699559	0.068735674
sh2 (gonadal sheath distal)	dod-3	-0.779157155	0.072386452
sh2 (gonadal sheath distal)	cex-1	0.379101292	0.0760447
sh2 (gonadal sheath distal)	ugt-44	-0.208220836	0.087601329
sh2 (gonadal sheath distal)	ZK593.3	0.519290274	0.090880157
sh2 (gonadal sheath distal)	asp-13	0.547330917	0.092890882

sh2 (gonadal sheath distal)	mlc-1	0.204224903	0.097282293
sh3_sh4 (gonadal sheath proximal)	nduo-6	-0.326550424	1.78485E-66
sh3_sh4 (gonadal sheath proximal)	rpl-41.2	-0.433918172	2.51142E-65
sh3_sh4 (gonadal sheath proximal)	tbh-1	-0.71537268	3.55238E-65
sh3_sh4 (gonadal sheath proximal)	C39D10.7	-0.430920428	1.83554E-39
sh3_sh4 (gonadal sheath proximal)	mig-6	1.059680206	1.36548E-34
sh3_sh4 (gonadal sheath proximal)	Y119D3B.21	-0.729230293	4.36319E-34
sh3_sh4 (gonadal sheath proximal)	skpo-1	-0.413821564	7.24479E-34
sh3_sh4 (gonadal sheath proximal)	dct-16	-0.603836385	1.43156E-32
sh3_sh4 (gonadal sheath proximal)	col-122	0.647654199	5.3787E-28
sh3_sh4 (gonadal sheath proximal)	ndfl-4	-0.352911416	9.40629E-28
sh3_sh4 (gonadal sheath proximal)	pat-10	0.33662384	1.93071E-27
sh3_sh4 (gonadal sheath proximal)	rpl-38	-0.387980222	6.08802E-27
sh3_sh4 (gonadal sheath proximal)	R09B3.3	-0.359979569	8.09436E-26
sh3_sh4 (gonadal sheath proximal)	W01D2.1	-0.3954207	3.71366E-25
sh3_sh4 (gonadal sheath proximal)	Y94H6A.10	0.613707291	5.89504E-23
sh3_sh4 (gonadal sheath proximal)	W04A4.2	0.518035752	2.83133E-22
sh3_sh4 (gonadal sheath proximal)	far-2	-0.248246494	1.03324E-20
sh3_sh4 (gonadal sheath proximal)	rps-27	-0.277374759	1.33842E-20
sh3_sh4 (gonadal sheath proximal)	ctc-3	0.24364284	6.58399E-20
sh3_sh4 (gonadal sheath proximal)	C14C6.5	-1.629350372	3.41471E-19
sh3_sh4 (gonadal sheath proximal)	Y73F4A.2	3.003949501	4.15092E-19
sh3_sh4 (gonadal sheath proximal)	rpl-43	-0.2982132	5.95499E-19
sh3_sh4 (gonadal sheath proximal)	T03F1.11	1.497384367	6.61357E-18
sh3_sh4 (gonadal sheath proximal)	Y69H2.3	-1.213121976	1.56977E-17
sh3_sh4 (gonadal sheath proximal)	fipr-2	2.305434597	1.95219E-17
sh3_sh4 (gonadal sheath proximal)	rps-25	-0.194593601	2.50997E-17
sh3_sh4 (gonadal sheath proximal)	C06A8.3	0.67882896	5.36826E-17
sh3_sh4 (gonadal sheath proximal)	rpl-36.A	-0.252122705	7.95726E-17
sh3_sh4 (gonadal sheath proximal)	rpl-36	-0.243760957	1.42353E-16

sh3_sh4 (gonadal sheath proximal)	C54D10.3	1.206026684	1.90205E-16
sh3_sh4 (gonadal sheath proximal)	far-3	2.337548605	3.34905E-16
sh3_sh4 (gonadal sheath proximal)	clik-1	0.338839941	4.92574E-16
sh3_sh4 (gonadal sheath proximal)	rpl-39	-0.401417352	8.00729E-16
sh3_sh4 (gonadal sheath proximal)	hsp-16.2	1.10407828	8.48945E-16
sh3_sh4 (gonadal sheath proximal)	fip-2	1.225934136	1.0606E-15
sh3_sh4 (gonadal sheath proximal)	B0513.4	-0.256908408	1.08173E-15
sh3_sh4 (gonadal sheath proximal)	mlc-7	-0.530353284	1.8457E-15
sh3_sh4 (gonadal sheath proximal)	sri-40	0.662446629	3.64106E-15
sh3_sh4 (gonadal sheath proximal)	rps-28	-0.431843737	3.70366E-15
sh3_sh4 (gonadal sheath proximal)	pyp-1	0.422225669	1.42689E-14
sh3_sh4 (gonadal sheath proximal)	sodh-1	1.137433678	1.82402E-14
sh3_sh4 (gonadal sheath proximal)	mlc-3	0.263121053	4.02074E-14
sh3_sh4 (gonadal sheath proximal)	ctc-1	0.21886507	4.52095E-14
sh3_sh4 (gonadal sheath proximal)	odc-1	0.610246858	4.72433E-14
sh3_sh4 (gonadal sheath proximal)	pqn-60	2.888319352	1.62831E-13
sh3_sh4 (gonadal sheath proximal)	nduo-3	-0.479291646	4.91112E-13
sh3_sh4 (gonadal sheath proximal)	iff-2	0.321064379	6.61387E-13
sh3_sh4 (gonadal sheath proximal)	col-184	0.541092438	6.92784E-13
sh3_sh4 (gonadal sheath proximal)	cpn-4	0.853298665	1.84407E-12
sh3_sh4 (gonadal sheath proximal)	hsp-70	0.755312676	2.80743E-12
sh3_sh4 (gonadal sheath proximal)	col-98	0.736524947	3.57873E-12
sh3_sh4 (gonadal sheath proximal)	unc-132	0.416166287	6.82405E-12
sh3_sh4 (gonadal sheath proximal)	tnc-2	1.451589485	9.58351E-12
sh3_sh4 (gonadal sheath proximal)	T01D1.4	0.318838229	1.2507E-11
sh3_sh4 (gonadal sheath proximal)	msp-31	-0.316391522	1.9553E-11
sh3_sh4 (gonadal sheath proximal)	fgt-1	-0.509576052	2.86675E-11
sh3_sh4 (gonadal sheath proximal)	gst-10	-0.843036867	3.01329E-11
sh3_sh4 (gonadal sheath proximal)	C05D11.5	0.824779067	3.13041E-11
sh3_sh4 (gonadal sheath proximal)	Y73F4A.1	3.312231032	6.92925E-11
sh3_sh4 (gonadal sheath proximal)	col-8	0.77206943	1.49533E-10
sh3_sh4 (gonadal sheath proximal)	ZC116.1	1.97535046	1.52563E-10
sh3_sh4 (gonadal sheath proximal)	rps-29	-0.310048289	3.01849E-10
sh3_sh4 (gonadal sheath proximal)	gst-4	0.650527164	3.68369E-10
sh3_sh4 (gonadal sheath proximal)	C25E10.8	-0.501636315	5.04815E-10

sh3_sh4 (gonadal sheath proximal)	R09B3.2	-0.366861492	6.48543E-10
sh3_sh4 (gonadal sheath proximal)	F54F7.2	-1.143509723	1.48846E-09
sh3_sh4 (gonadal sheath proximal)	col-181	0.436723119	1.78903E-09
sh3_sh4 (gonadal sheath proximal)	F35B12.3	3.041353239	3.8831E-09
sh3_sh4 (gonadal sheath proximal)	F56H9.2	-0.537437239	5.7009E-09
sh3_sh4 (gonadal sheath proximal)	pud-3	-1.572391365	5.75465E-09
sh3_sh4 (gonadal sheath proximal)	hsp-16.41	0.812107241	7.60153E-09
sh3_sh4 (gonadal sheath proximal)	myo-2	2.942538947	8.65E-09
sh3_sh4 (gonadal sheath proximal)	mup-2	0.260653072	1.05815E-08
sh3_sh4 (gonadal sheath proximal)	T04G9.7	-0.198893022	5.96289E-08
sh3_sh4 (gonadal sheath proximal)	chdp-1	0.375139551	6.98413E-08
sh3_sh4 (gonadal sheath proximal)	ddo-3	-0.24271653	1.01893E-07
sh3_sh4 (gonadal sheath proximal)	acer-1	0.570711045	1.13129E-07
sh3_sh4 (gonadal sheath proximal)	Y106G6D.8	-1.592972428	1.64526E-07
sh3_sh4 (gonadal sheath proximal)	Y47G6A.15	-0.564693518	2.15607E-07
sh3_sh4 (gonadal sheath proximal)	C53C9.2	1.484622687	2.90089E-07
sh3_sh4 (gonadal sheath proximal)	act-3	0.271550464	3.12636E-07
sh3_sh4 (gonadal sheath proximal)	hpo-15	-0.579719652	3.98218E-07
sh3_sh4 (gonadal sheath proximal)	col-124	0.272319176	4.0225E-07
sh3_sh4 (gonadal sheath proximal)	Y37D8A.19	-1.138763746	4.95182E-07
sh3_sh4 (gonadal sheath proximal)	F55B11.2	-0.893504042	5.22667E-07
sh3_sh4 (gonadal sheath proximal)	lec-9	-0.506671829	7.2209E-07
sh3_sh4 (gonadal sheath proximal)	atp-2	0.201536413	1.12726E-06
sh3_sh4 (gonadal sheath proximal)	K11D12.13	1.280866864	1.20458E-06
sh3_sh4 (gonadal sheath proximal)	msd-4	-0.238845877	1.24009E-06
sh3_sh4 (gonadal sheath proximal)	lbp-3	-0.556219405	1.33316E-06
sh3_sh4 (gonadal sheath proximal)	gbh-1	1.172037496	1.71816E-06
sh3_sh4 (gonadal sheath proximal)	Y116A8C.3	2.280866854	1.77041E-06
sh3_sh4 (gonadal sheath proximal)	lea-1	0.379307663	1.87958E-06
sh3_sh4 (gonadal sheath proximal)	gst-27	-0.580735234	1.9475E-06
sh3_sh4 (gonadal sheath proximal)	col-119	0.368616812	2.14543E-06

sh3_sh4 (gonadal sheath proximal)	clec-178	3.750352103	2.26677E-06
sh3_sh4 (gonadal sheath proximal)	col-20	0.294675631	2.28391E-06
sh3_sh4 (gonadal sheath proximal)	ant-1.1	0.128730056	2.29863E-06
sh3_sh4 (gonadal sheath proximal)	mlc-2	0.22622857	2.58694E-06
sh3_sh4 (gonadal sheath proximal)	alh-1	0.547443101	3.23549E-06
sh3_sh4 (gonadal sheath proximal)	clec-47	1.396108281	3.6738E-06
sh3_sh4 (gonadal sheath proximal)	rla-2	-0.197133839	4.18081E-06
sh3_sh4 (gonadal sheath proximal)	pud-4	-1.707690422	4.40805E-06
sh3_sh4 (gonadal sheath proximal)	rpl-32	-0.139225441	5.13389E-06
sh3_sh4 (gonadal sheath proximal)	fipr-1	1.768766449	6.48482E-06
sh3_sh4 (gonadal sheath proximal)	cht-3	-0.407342037	1.04937E-05
sh3_sh4 (gonadal sheath proximal)	B0545.4	0.360581339	1.125E-05
sh3_sh4 (gonadal sheath proximal)	lbp-6	0.250746744	1.25049E-05
sh3_sh4 (gonadal sheath proximal)	W02D9.7	1.972744565	1.25983E-05
sh3_sh4 (gonadal sheath proximal)	ttr-1	2.091389055	1.31391E-05
sh3_sh4 (gonadal sheath proximal)	F48D6.4	-0.675581821	1.3241E-05
sh3_sh4 (gonadal sheath proximal)	ctg-1	0.241966064	1.54351E-05
sh3_sh4 (gonadal sheath proximal)	F15A4.6	0.680373777	1.58661E-05
sh3_sh4 (gonadal sheath proximal)	spp-18	-1.20120582	1.67402E-05
sh3_sh4 (gonadal sheath proximal)	col-160	0.563266591	1.98635E-05
sh3_sh4 (gonadal sheath proximal)	Y87G2A.19	1.532225434	3.0534E-05
sh3_sh4 (gonadal sheath proximal)	hsp-110	0.445405352	3.27123E-05
sh3_sh4 (gonadal sheath proximal)	ZK813.1	-1.219274203	3.4852E-05
sh3_sh4 (gonadal sheath proximal)	try-6	1.165389645	5.66524E-05
sh3_sh4 (gonadal sheath proximal)	ncx-2	3.484925658	6.0911E-05
sh3_sh4 (gonadal sheath proximal)	aman-1	3.165389632	6.12181E-05
sh3_sh4 (gonadal sheath proximal)	swm-1	-0.820204922	7.14146E-05
sh3_sh4 (gonadal sheath proximal)	rps-21	-0.246785086	7.74375E-05
sh3_sh4 (gonadal sheath proximal)	F21C10.9	0.610256782	7.79409E-05
sh3_sh4 (gonadal sheath proximal)	tnt-4	1.648939504	9.00566E-05
sh3_sh4 (gonadal sheath proximal)	ttr-21	1.81957515	0.000101452
sh3_sh4 (gonadal sheath proximal)	lec-10	-0.538001542	0.000102302
sh3_sh4 (gonadal sheath proximal)	rpl-29	-0.37257502	0.000118094
sh3_sh4 (gonadal sheath proximal)	rps-20	0.142553963	0.000140021
sh3_sh4 (gonadal sheath proximal)	nspd-2	-0.106560545	0.000152274

sh3_sh4 (gonadal sheath proximal)	ssp-10	-0.154254396	0.000152537
sh3_sh4 (gonadal sheath proximal)	ZK1193.2	0.46107711	0.000165888
sh3_sh4 (gonadal sheath proximal)	F23A7.8	-0.52176879	0.000168599
sh3_sh4 (gonadal sheath proximal)	fipr-10	1.965934797	0.000186541
sh3_sh4 (gonadal sheath proximal)	F28H7.3	-0.800624335	0.000187672
sh3_sh4 (gonadal sheath proximal)	sams-4	0.380177867	0.000191305
sh3_sh4 (gonadal sheath proximal)	F11E6.3	0.546879598	0.00020743
sh3_sh4 (gonadal sheath proximal)	R53.4	0.178145458	0.000217381
sh3_sh4 (gonadal sheath proximal)	unc-60	0.275226628	0.000238937
sh3_sh4 (gonadal sheath proximal)	nspb-6	2.521357531	0.000294693
sh3_sh4 (gonadal sheath proximal)	Y62H9A.5	0.859286519	0.00031635
sh3_sh4 (gonadal sheath proximal)	gln-3	0.476710122	0.000350577
sh3_sh4 (gonadal sheath proximal)	lbp-9	0.210314929	0.000359862
sh3_sh4 (gonadal sheath proximal)	spp-5	-0.649041767	0.000400469
sh3_sh4 (gonadal sheath proximal)	C24A3.2	0.476008476	0.000400886
sh3_sh4 (gonadal sheath proximal)	cex-1	0.315253781	0.000493165
sh3_sh4 (gonadal sheath proximal)	fipr-7	1.878040192	0.000509819
sh3_sh4 (gonadal sheath proximal)	msp-40	-0.521045944	0.000632654
sh3_sh4 (gonadal sheath proximal)	cpt-2	0.555408159	0.000812582
sh3_sh4 (gonadal sheath proximal)	ndk-1	0.103737517	0.000840299
sh3_sh4 (gonadal sheath proximal)	H36L18.2	0.222552101	0.000900365
sh3_sh4 (gonadal sheath proximal)	msp-36	-0.454550531	0.000901989
sh3_sh4 (gonadal sheath proximal)	pfn-1	0.216754195	0.000922535
sh3_sh4 (gonadal sheath proximal)	daf-21	0.203464794	0.000954737
sh3_sh4 (gonadal sheath proximal)	pfd-3	0.411965529	0.001028306
sh3_sh4 (gonadal sheath proximal)	nspd-1	-0.140183261	0.001088641
sh3_sh4 (gonadal sheath proximal)	sams-1	0.386289841	0.001132634
sh3_sh4 (gonadal sheath proximal)	acs-2	0.172164015	0.001212627
sh3_sh4 (gonadal sheath proximal)	fkh-6	-1.641965268	0.001223271
sh3_sh4 (gonadal sheath proximal)	C36E6.8	-0.964950367	0.001587246
sh3_sh4 (gonadal sheath proximal)	col-143	0.493190054	0.001664651
sh3_sh4 (gonadal sheath proximal)	acbp-1	-0.44581116	0.001948867
sh3_sh4 (gonadal sheath proximal)	cysl-2	-0.173733771	0.002010618
sh3_sh4 (gonadal sheath proximal)	H28O16.1	0.186323472	0.00236034
sh3_sh4 (gonadal sheath proximal)	ZK813.3	1.432176187	0.002483761

sh3_sh4 (gonadal sheath proximal)	pes-8	2.302893161	0.002541432
sh3_sh4 (gonadal sheath proximal)	col-103	0.582909248	0.002754867
sh3_sh4 (gonadal sheath proximal)	F35E12.10	-0.20733535	0.003053314
sh3_sh4 (gonadal sheath proximal)	cyc-2.1	0.19189804	0.003365874
sh3_sh4 (gonadal sheath proximal)	lev-11	0.17760093	0.004013845
sh3_sh4 (gonadal sheath proximal)	efhd-1	0.253609132	0.004332883
sh3_sh4 (gonadal sheath proximal)	idha-1	0.377347682	0.004363927
sh3_sh4 (gonadal sheath proximal)	rla-0	0.111492745	0.004566938
sh3_sh4 (gonadal sheath proximal)	F58F12.1	0.194752334	0.004662365
sh3_sh4 (gonadal sheath proximal)	gdh-1	-0.250669228	0.005099027
sh3_sh4 (gonadal sheath proximal)	msp-76	-0.407759626	0.00522241
sh3_sh4 (gonadal sheath proximal)	unc-54	0.214059821	0.006501418
sh3_sh4 (gonadal sheath proximal)	tni-4	0.238635823	0.006932372
sh3_sh4 (gonadal sheath proximal)	asd-2	0.564936893	0.006941943
sh3_sh4 (gonadal sheath proximal)	F22B7.1	1.52795972	0.007443657
sh3_sh4 (gonadal sheath proximal)	ZK593.3	1.123462665	0.00748874
sh3_sh4 (gonadal sheath proximal)	spp-17	-0.459178403	0.007566577
sh3_sh4 (gonadal sheath proximal)	dim-1	0.379717879	0.007695959
sh3_sh4 (gonadal sheath proximal)	cco-2	0.182021507	0.007810367
sh3_sh4 (gonadal sheath proximal)	C23H5.8	-0.609671966	0.008308146
sh3_sh4 (gonadal sheath proximal)	ZK970.7	-1.813444043	0.008473425
sh3_sh4 (gonadal sheath proximal)	zfh-2	1.497530814	0.009029435
sh3_sh4 (gonadal sheath proximal)	hpo-26	2.050303569	0.00924351
sh3_sh4 (gonadal sheath proximal)	F30H5.5	0.649407024	0.009438441
sh3_sh4 (gonadal sheath proximal)	dlc-5	0.438200427	0.009473783
sh3_sh4 (gonadal sheath proximal)	lam-2	1.57360955	0.010096196
sh3_sh4 (gonadal sheath proximal)	W06H8.6	0.669636477	0.010248112
sh3_sh4 (gonadal sheath proximal)	spp-2	-0.9532344	0.011219506
sh3_sh4 (gonadal sheath proximal)	T13C2.6	-0.378362372	0.01169612
sh3_sh4 (gonadal sheath proximal)	msp-152	-0.281004395	0.011747607
sh3_sh4 (gonadal sheath proximal)	hprt-1	0.304083865	0.012389816
sh3_sh4 (gonadal sheath proximal)	D1054.18	-0.282242069	0.012655573
sh3_sh4 (gonadal sheath proximal)	msp-33	-0.254230527	0.013420777
sh3_sh4 (gonadal sheath proximal)	C18D4.12	-2.815857647	0.013812925
sh3_sh4 (gonadal sheath proximal)	fipr-11	2.701094873	0.015305273

sh3_sh4 (gonadal sheath proximal)	Y73F4A.3	1.824618063	0.016885525
sh3_sh4 (gonadal sheath proximal)	lips-10	0.312071929	0.017649736
sh3_sh4 (gonadal sheath proximal)	F13C5.5	2.107619687	0.019410639
sh3_sh4 (gonadal sheath proximal)	mlc-1	0.252209797	0.019410639
sh3_sh4 (gonadal sheath proximal)	B0393.9	-0.809395323	0.019669743
sh3_sh4 (gonadal sheath proximal)	rps-1	0.118893615	0.019865301
sh3_sh4 (gonadal sheath proximal)	unc-23	0.664196703	0.020325301
sh3_sh4 (gonadal sheath proximal)	ttm-5	2.679966142	0.020830066
sh3_sh4 (gonadal sheath proximal)	C45G9.6	1.430582213	0.021742935
sh3_sh4 (gonadal sheath proximal)	T19C3.5	2.487317711	0.022967612
sh3_sh4 (gonadal sheath proximal)	rpl-11.2	0.137532289	0.023501548
sh3_sh4 (gonadal sheath proximal)	oct-2	0.8886307	0.027094185
sh3_sh4 (gonadal sheath proximal)	atp-5	0.190927008	0.027455106
sh3_sh4 (gonadal sheath proximal)	fipr-6	2.720187244	0.028711361
sh3_sh4 (gonadal sheath proximal)	sod-5	3.165389632	0.028852763
sh3_sh4 (gonadal sheath proximal)	M28.5	-0.22958658	0.028958619
sh3_sh4 (gonadal sheath proximal)	F48E3.4	-0.128328994	0.031622767
sh3_sh4 (gonadal sheath proximal)	rps-26	-0.11436404	0.031743691
sh3_sh4 (gonadal sheath proximal)	F52D10.2	0.713585844	0.032568635
sh3_sh4 (gonadal sheath proximal)	Y69E1A.5	0.352631003	0.032809738
sh3_sh4 (gonadal sheath proximal)	gem-4	-3.004535298	0.034987818
sh3_sh4 (gonadal sheath proximal)	ahcy-1	0.285743068	0.046035997
sh3_sh4 (gonadal sheath proximal)	ule-2	-1.214091304	0.057351081
sh3_sh4 (gonadal sheath proximal)	vit-3	-0.68697085	0.05973394
sh3_sh4 (gonadal sheath proximal)	rpl-30	-0.139291416	0.065286227
sh3_sh4 (gonadal sheath proximal)	T24B8.5	-0.459914738	0.06768172
sh3_sh4 (gonadal sheath proximal)	lsm-5	-0.495429788	0.071643299
sh3_sh4 (gonadal sheath proximal)	T20G5.8	0.378690853	0.080245664
sh3_sh4 (gonadal sheath proximal)	sca-1	0.217883751	0.0877135
sh3_sh4 (gonadal sheath proximal)	ttr-27	1.347622209	0.094273453
sh3_sh4 (gonadal sheath proximal)	Y106G6D.4	2.227954069	0.096754386
sh3_sh4 (gonadal sheath proximal)	C49F5.7	-0.19523833	0.098376758
sh3_sh4 (gonadal sheath proximal)	fipr-4	2.050201035	0.099556401
sh5 (gonadal sheath proximal)	M02D8.2	-2.440572591	6.19344E-13
sh5 (gonadal sheath proximal)	T19A6.4	-2.440572591	6.19344E-13

sh5 (gonadal sheath proximal)	dct-16	-0.914689007	4.88267E-12
sh5 (gonadal sheath proximal)	rpl-41.2	-0.433361384	6.34872E-08
sh5 (gonadal sheath proximal)	mlc-7	-1.118644496	9.10753E-08
sh5 (gonadal sheath proximal)	nmy-1	1.72935241	6.25779E-06
sh5 (gonadal sheath proximal)	F56H9.2	-0.931918877	1.52328E-05
sh5 (gonadal sheath proximal)	acs-2	1.326014996	3.46063E-05
sh5 (gonadal sheath proximal)	nduo-6	-0.28434815	4.68369E-05
sh5 (gonadal sheath proximal)	W01D2.1	-0.514503256	0.001173753
sh5 (gonadal sheath proximal)	icl-1	1.003184096	0.001348284
sh5 (gonadal sheath proximal)	rpl-38	-0.462089573	0.002737837
sh5 (gonadal sheath proximal)	alh-1	0.942552064	0.008283769
sh5 (gonadal sheath proximal)	ilys-5	-1.033136933	0.013701632
sh5 (gonadal sheath proximal)	F22B7.1	-1.440572591	0.021860383
sh5 (gonadal sheath proximal)	flp-28	-1.440572591	0.021860383
sh5 (gonadal sheath proximal)	hsp-16.2	1.52194437	0.025156396
sh5 (gonadal sheath proximal)	lec-9	-0.874569363	0.027722381
sh5 (gonadal sheath proximal)	W04A4.2	0.727485808	0.038562846
sh5 (gonadal sheath proximal)	K11D12.13	1.259867127	0.045529546
sh5 (gonadal sheath proximal)	rpl-36.A	-0.337696172	0.075668532
sh5 (gonadal sheath proximal)	act-2	-0.576365416	0.077304938
sh5 (gonadal sheath proximal)	ZK1073.2	-2.559621377	0.084670055
uv1 (uterine-vulval cells)	Y22D7AR.10	-0.399063935	0.084059924
vm1 (vulval muscle)	Y47G6A.15	-0.595322637	2.00941E-14
vm1 (vulval muscle)	R10H10.3	3.182864055	3.22438E-06
vm1 (vulval muscle)	ctc-3	0.594395708	9.98002E-05
vm1 (vulval muscle)	tpxl-1	2.919829649	0.00032851
vm1 (vulval muscle)	slx-1	2.919829651	0.00032851
vm1 (vulval muscle)	R12E2.15	2.057333175	0.000456697
vm1 (vulval muscle)	rmd-1	2.182864057	0.000459
vm1 (vulval muscle)	C33H5.13	2.182864056	0.000612921

vm1 (vulval muscle)	sws-1	3.405256477	0.001119738
vm1 (vulval muscle)	hsr-9	2.405256478	0.001271681
vm1 (vulval muscle)	col-122	1.33597363	0.001731689
vm1 (vulval muscle)	C17H12.8	-2.308989038	0.001890079
vm1 (vulval muscle)	ifet-1	2.282682914	0.003236023
vm1 (vulval muscle)	sams-3	2.597901554	0.005044696
vm1 (vulval muscle)	parp-1	2.597901554	0.005044696
vm1 (vulval muscle)	col-48	2.597901554	0.005044696
vm1 (vulval muscle)	rpl-35	-0.397609398	0.005192111
vm1 (vulval muscle)	C53B7.2	-0.382363443	0.005426177
vm1 (vulval muscle)	col-106	2.387052277	0.006172454
vm1 (vulval muscle)	F49E8.2	2.919829649	0.008873713
vm1 (vulval muscle)	far-3	1.445898463	0.010652547
vm1 (vulval muscle)	W01D2.1	-0.685115816	0.012294929
vm1 (vulval muscle)	ulp-2	3.182864056	0.016685543
vm1 (vulval muscle)	col-178	2.278708977	0.029959948
vm1 (vulval muscle)	col-119	1.688737694	0.030483098
vm1 (vulval muscle)	col-184	1.347872548	0.03496579
vm1 (vulval muscle)	hsp-16.2	0.628661453	0.035200911
vm1 (vulval muscle)	C05C12.4	2.597901554	0.038095765
vm1 (vulval muscle)	psf-1	2.597901554	0.038095765
vm1 (vulval muscle)	cpg-1	2.182864056	0.038624601
vm1 (vulval muscle)	rps-27	-0.457443873	0.050367517
vm1 (vulval muscle)	hsp-16.41	0.584991392	0.051797715
vm1 (vulval muscle)	rol-8	2.405256478	0.051892641
vm1 (vulval muscle)	klp-16	2.919829649	0.081003462
vm1 (vulval muscle)	spd-5	2.182864056	0.086904097
vm1 (vulval muscle)	air-1	2.182864056	0.086904097
vm2 (vulval muscle)	pat-10	-0.268423688	6.18362E-08
vm2 (vulval muscle)	nduo-5	1.175857809	4.57846E-07
vm2 (vulval muscle)	ctc-1	0.572449711	0.000423512
vm2 (vulval muscle)	K03E5.2	-0.657200954	0.000490382
vm2 (vulval muscle)	ctb-1	0.688320895	0.00059154
vm2 (vulval muscle)	asp-4	1.713827435	0.000798402
vm2 (vulval muscle)	lys-4	1.411348455	0.000939803
vm2 (vulval muscle)	tag-18	-0.380977473	0.00101531

vm2 (vulval muscle)	nduo-2	0.895375788	0.003761271
vm2 (vulval muscle)	cpr-1	1.796915115	0.007829687
vm2 (vulval muscle)	nduo-1	0.61398138	0.029054726
vm2 (vulval muscle)	col-122	1.03197302	0.047014903
vm2 (vulval muscle)	ctc-3	0.523648624	0.053879
vm2 (vulval muscle)	sodh-1	2.757534614	0.083486395

Appendix Table S3. Correlation between TF binding patterns and cell types in control worms and fructose-fed worms. The number next to the cell type is the mean square error for the cell type model with a lower number indicating a higher confidence in the predictions of the model. Only TF-cell type associations that have a positive correlation in at least one of the conditions are shown.

cell_types	tf	correlation_fruc	correlation_ctrl
ADA 0.047	aha-1	0.124120259405898	NA
ADA 0.047	alr-1	0.16848485053905	NA
ADA 0.047	atf-7	0.00129438182185769	0.00339928456207201
ADA 0.047	attf-6	0.00698698610324993	0.0110489440623237
ADA 0.047	C34B4.2	0.712784178235853	0.275136872565412
ADA 0.047	ceh-14	0.0094717395218079	0
ADA 0.047	crh-2	0.0422868923720255	0.0538780537549972
ADA 0.047	ctbp-1	0.144627171935294	0.129256145160833
ADA 0.047	daf-19	0.119815181743411	0.109970630519069
ADA 0.047	egl-18	NA	0.0711337237377839
ADA 0.047	egl-27	0.00479124336035587	0
ADA 0.047	ekl-4	0.0612882105913002	0.0701508109308543
ADA 0.047	elt-4	0.0870492118021833	NA
ADA 0.047	F22D6.2	0.0695792243639504	0.00210163431462426
ADA 0.047	F44E2.7	0	0.0277955734037925
ADA 0.047	F57A8.1	0	0.0209584882679606
ADA 0.047	hif-1	0.0209647006275931	0.0477814854863611
ADA 0.047	hinf-1	0.114707130399898	NA
ADA 0.047	hsf-1	NA	0.0267402107907071
ADA 0.047	lag-1	NA	0.0540644935516179
ADA 0.047	lim-7	NA	0.0491115032553823
ADA 0.047	lin-11	0.225344296753558	0.272505609448776
ADA 0.047	lin-14	0.0197127966901836	0.0168797998219137
ADA 0.047	lin-26	0.106610421386952	0.100966808420177
ADA 0.047	lin-39	NA	0.00841982660324864
ADA 0.047	lin-40	0.119933392726284	0.0481087469257389
ADA 0.047	lsy-2	0.0192527002007134	0.0147885302280965
ADA 0.047	madf-5	NA	0.065820912959659
ADA 0.047	madf-9	NA	0.0187090809285335
ADA 0.047	mdt-29	0.0230494677270811	0.0203360928226549
ADA 0.047	mef-2	0.056167292079069	0.0307967094110013
ADA 0.047	nfya-2	0.0163645618669261	0.0467657875542099
ADA 0.047	nhr-47	0	0.00369027631940334
ADA 0.047	nhr-71	0	0.00363639468659906
ADA 0.047	pag-3	0.058541128724419	0.0510715806625935
ADA 0.047	pat-9	NA	0.171255682524822

ADA 0.047	pbrm-1	0.00961999859992108	0.0199074285985265
ADA 0.047	sem-4	NA	0.0345484784837346
ADA 0.047	sox-4	0.0949769358494689	NA
ADA 0.047	unc-86	0.161094910521996	0.158904955775074
ADA 0.047	Y53G8AR.9	0.0146413189310853	0.0356894657214092
ADA 0.047	Y56A3A.18	NA	0.0399140687065436
ADA 0.047	zfh-2	0.0531324957162908	NA
ADA 0.047	zim-3	0.0131045031801387	0.00081898149553152
ADA 0.047	ZK546.5	NA	0.025712018026903
ADF 0.027	aha-1	0.0758963273801726	0.115424599981456
ADF 0.027	attf-6	0	0.0193733672189518
ADF 0.027	B0035.1	0	0.0090811839774772
ADF 0.027	C34B4.2	0.21155037133759	0.327312551376238
ADF 0.027	chd-7	0.00234887358097024	0.0216998572539519
ADF 0.027	crh-2	0.0226939274430038	0.020748536839224
ADF 0.027	ctbp-1	0.060020740029625	0.0598144231944379
ADF 0.027	daf-19	0.114463976835666	0.104765120429913
ADF 0.027	egl-18	0.0773087031186266	0.0673570303346334
ADF 0.027	ekl-4	0.0330028789884515	0.0641508167286204
ADF 0.027	elt-4	0.0188846458934281	NA
ADF 0.027	fkh-8	0.12922052270243	0.12686015166668
ADF 0.027	hif-1	0.0108214348127574	0.0111408438969101
ADF 0.027	hsf-1	0.00676659165137037	0.0187998831475476
ADF 0.027	lag-1	0.0136437699869427	0.0382719017137002
ADF 0.027	lim-7	0.0187741248463733	0.0603974793689739
ADF 0.027	lin-11	0.298423574797225	0.301156209419935
ADF 0.027	lin-26	0.0819956304088395	NA
ADF 0.027	lin-40	0.0413533810207056	0.0468737770697087
ADF 0.027	lsy-2	0.00206411111211359	0
ADF 0.027	madf-3	0.0562945076044289	NA
ADF 0.027	madf-5	0.0738166325642424	NA
ADF 0.027	madf-9	0	0.0382265379121681
ADF 0.027	mdt-29	0.0478619391337175	NA
ADF 0.027	mml-1	0.0284875181458043	0.0408071458189455
ADF 0.027	nfyb-1	0	0.00682871205582855
ADF 0.027	nhr-11	0.10063952430812	0.108812731000441
ADF 0.027	nhr-237	0.0291890241189661	0.00811185335345231
ADF 0.027	nhr-71	1.27149797430347e-06	0.00168244925605665
ADF 0.027	nhr-84	0.198160816505064	0.114662002683945
ADF 0.027	pbrm-1	0.00361782844281453	0.0190602919597358
ADF 0.027	R02D3.7	0	0.00978121921681991
ADF 0.027	saeg-2	0	0.00635668396386751
ADF 0.027	sox-4	0.0725623024163327	0.060998133464239

ADF 0.027	sptf-2	NA	0.321081152027004
ADF 0.027	Y53G8AR.9	0.00646768973775929	NA
ADF 0.027	Y56A3A.18	0.0377372544892094	NA
ADF 0.027	zfh-2	0.03063921262927	0.0324335869863732
ADF 0.027	zim-3	0.0153191367273911	0.0148375139011987
ADF 0.027	ZK546.5	0.00918963624076188	NA
ADF 0.027	ztf-1	0.0375574287288345	0.0255286244045696
ADF 0.027	ztf-26	0.0675872049395746	0.0749597831147743
ADL 0.033	aha-1	0.196349319422567	0.221659827348119
ADL 0.033	alr-1	NA	0.26011663568319
ADL 0.033	attf-6	0	0.00636796824424731
ADL 0.033	cebp-1	0.0042358171248548	0.00428360659010666
ADL 0.033	crh-2	0.0184428569737657	0.0243196314979643
ADL 0.033	ctbp-1	0.0141251067770318	0.0246718720780543
ADL 0.033	daf-19	0.084953976657489	0.0910713839900637
ADL 0.033	dxbp-1	0.0039308834170213	0.00515966241382322
ADL 0.033	egl-18	0.0342951238666869	NA
ADL 0.033	ekl-4	0.0768565328967515	0.0802518580806885
ADL 0.033	F22D6.2	0.0227981680706955	0.00192194042653066
ADL 0.033	F33H1.4	0.0328133056200644	0.0345675253158521
ADL 0.033	F44E2.7	0.00838182542049639	0.021207993904799
ADL 0.033	fkh-8	0.0439764770451366	0.055247645381722
ADL 0.033	hif-1	0.00510779300699064	0.00674321025070222
ADL 0.033	hinf-1	0.144971915265722	0.155060406751408
ADL 0.033	hlh-4	0.10001201424028	0.118784520456307
ADL 0.033	hlh-8	0.0317587865995674	0.0283709007409097
ADL 0.033	hsf-1	0.0207528893770259	0.0175855013544208
ADL 0.033	lag-1	0	0.0279048094011979
ADL 0.033	lim-7	0.0423785230010507	0.049243737349262
ADL 0.033	lin-11	0.223889513826304	0.253351528247258
ADL 0.033	lin-13	0	0.000646031367500534
ADL 0.033	lin-26	0.102447826482097	0.0963777704728211
ADL 0.033	lin-40	0.10424789671923	0.0800779907194469
ADL 0.033	lin-54	0.0148533229537427	0.0116043992982999
ADL 0.033	lsy-2	0.029647915941198	0.0224432699502165
ADL 0.033	madf-3	0.0726464435014279	0.0724778336504272
ADL 0.033	madf-5	0.0899002587452857	0.0780449751466739
ADL 0.033	madf-6	0.0259845449873663	0.0287280727785931
ADL 0.033	mdt-29	0.00733558699205298	0.0163593667162199
ADL 0.033	nhr-11	0.0632738820022057	0.0635595865759131
ADL 0.033	nhr-129	0.00238095068492022	0.000318805269377125
ADL 0.033	nhr-237	0.0140860422705232	0.0446705534644597
ADL 0.033	nhr-6	0	0.0012809937781757

ADL 0.033	pat-9	0.243830383688038	0.192714849718514
ADL 0.033	pbrm-1	0.000864421597190966	9.96440089537251e-05
ADL 0.033	R02D3.7	0.00717480501355572	0.00167877001776958
ADL 0.033	skn-1	0.00940028485039239	0.00909155197626871
ADL 0.033	sox-4	0.060244227706424	0.0642472086607964
ADL 0.033	sptf-2	0.444019738938919	0.428882296208937
ADL 0.033	Y53G8AR.9	0.0230477842389668	0.0242447781984853
ADL 0.033	Y56A3A.18	0.0440342372065839	0.053306537707853
ADL 0.033	zfh-2	0.0446982729972682	0.040167976589677
ADL 0.033	zim-3	0.012925718046364	0.00556041753134504
ADL 0.033	ZK546.5	0	0.00574354971040275
ADL 0.033	ztf-26	0.0434268219360583	0.00681650260263325
AFD 0.039	aha-1	0.170589178318515	0.136686017954021
AFD 0.039	akir-1	0.0091468442044193	0
AFD 0.039	alr-1	0.15549335647534	0.158979676646718
AFD 0.039	attf-6	0.00894337124402095	0
AFD 0.039	cebp-1	0.00391086858237721	0
AFD 0.039	ceh-27	0.113538707171892	0.104751194828223
AFD 0.039	crh-2	0.0571313978142489	0.0435865275170195
AFD 0.039	ctbp-1	NA	0.0583651246373013
AFD 0.039	D1046.2	0.0125742617884568	0
AFD 0.039	daf-19	0.0759189868295987	0.0691717987858844
AFD 0.039	dsc-1	0.0894804037589001	0.0730400212316167
AFD 0.039	dxbp-1	0.009647184673779	0.00772698834834514
AFD 0.039	egl-13	0.220714825483911	0.167480491355609
AFD 0.039	egl-27	0.00954396230075868	0.00170162513496925
AFD 0.039	ekl-4	0.0462458947228254	0.0415079410383231
AFD 0.039	elt-4	0.0467557543748999	0.0102157526402453
AFD 0.039	F22D6.2	0.0339558684287049	0
AFD 0.039	F44E2.7	0.00849009646487499	0.0164722092645157
AFD 0.039	F57A8.1	0.0807926310663537	0.0384118336524201
AFD 0.039	fkh-8	0.0358328288570044	0.0225308999072235
AFD 0.039	gei-8	0.0421554688523251	NA
AFD 0.039	hinf-1	0.105711160110963	0.110906293152364
AFD 0.039	hsf-1	0.0356377766549418	0.0214680503290059
AFD 0.039	klu-1	0.00826897138331839	0
AFD 0.039	lag-1	0	0.0127897241719261
AFD 0.039	lim-7	0.0405630335330574	0.0467591478722326
AFD 0.039	lin-11	0.150904225670198	0.136686831214622
AFD 0.039	lin-14	0.0104255968017508	0
AFD 0.039	lin-26	0.100380211027613	0.0834813859957753
AFD 0.039	lin-40	0.0737356134754771	0.0114810818326985
AFD 0.039	lsy-2	NA	0.0099543652964602

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AFD 0.039	madf-6	0.00485920554943195	0.000348768030943246
AFD 0.039	madf-9	0.036038568297281	NA
AFD 0.039	mdt-29	0.0272630970701427	0.0195531470025948
AFD 0.039	mep-1	0.00383470948921799	0.000496184869590066
AFD 0.039	mml-1	0.0196642709758054	0.0126219263302188
AFD 0.039	nhr-11	0.0526016011518277	0.0564226753767952
AFD 0.039	nhr-6	0.00181938052750624	0
AFD 0.039	nhr-84	0.159678589919543	0.147419747816406
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AFD 0.039	pbrm-1	0.0280270297474882	0.0242227645831417
AFD 0.039	R02D3.7	0.0236907753688597	0.0223104962909677
AFD 0.039	sem-4	0.0265410199843645	NA
AFD 0.039	somi-1	0.00756382036349115	NA
AFD 0.039	sox-4	NA	0.0326041500318827
AFD 0.039	unc-42	0.000697815867276923	NA
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AFD 0.039	Y56A3A.18	0.0177235009213062	0.0188055356441103
AFD 0.039	zfh-2	0.0420097435663925	0.0453287837503158
AFD 0.039	zim-3	0.000771004239420725	0
AFD 0.039	ZK546.5	NA	0.146064555503723
AFD 0.039	ztf-26	NA	0.0970756139322528
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AIA 0.039	atf-7	0.0103090239806643	0.0229216271133312
AIA 0.039	attf-6	0.000271823953939421	0.0106545638193097
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AIA 0.039	ceh-27	0.0114923445459501	0.035509454125667
AIA 0.039	ceh-63	0.02461254443041	NA
AIA 0.039	ces-1	0.00147579335960341	NA
AIA 0.039	crh-2	0.0369061855160584	0.0489717268991881
AIA 0.039	ctbp-1	0.155093437590525	0.164065978204075
AIA 0.039	daf-19	0.0712367851943652	0.0820165893236967
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AIA 0.039	egl-18	0.0764928381675445	0.110957652959126
AIA 0.039	egl-27	0.00986158026477854	0.0210472494081388
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AIA 0.039	elt-4	0.0414258455473826	NA
AIA 0.039	ets-5	0.0524562354105226	0.0622760382689617
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AIA 0.039	F57A8.1	0.0709891872712229	0.0434432290846482
AIA 0.039	hif-1	0.0201968116412396	0.030556497099779
AIA 0.039	hinf-1	0.093608217925137	0.105289279955928

AIA 0.039	hsf-1	0.032952142014961	0.0369671651049282
AIA 0.039	isw-1	0.0305176003099505	0.0331042930721893
AIA 0.039	lag-1	0.0158180208812114	0.0514088400359929
AIA 0.039	lim-6	0	0.0309687321737169
AIA 0.039	lim-7	0.0293111248919171	0.0499650205829819
AIA 0.039	lin-11	0.197465141126746	0.234807512737
AIA 0.039	lin-14	0.0173136047831322	0.0191124597676744
AIA 0.039	lin-26	0.0758371706845104	0.0753265009564458
AIA 0.039	lin-39	0.00138214500969605	NA
AIA 0.039	lin-40	0.0772865654211691	0.0591639393064736
AIA 0.039	lsy-2	0.00435102165729274	NA
AIA 0.039	madf-5	0.0952572472450302	0.066361913857689
AIA 0.039	mdt-29	0.0595535078273424	0.0666221117204038
AIA 0.039	mef-2	0.0220271228291769	0.0349456867374338
AIA 0.039	nfya-2	0.0164749099394728	0.0309244106233604
AIA 0.039	nhr-11	0.0368779972841784	0.0313544945059983
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AIA 0.039	nhr-6	0	0.00791666121146878
AIA 0.039	pag-3	NA	0.0556941899103736
AIA 0.039	pat-9	0.193890013282075	0.154313527272472
AIA 0.039	pax-3	0.0188789268296468	NA
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AIA 0.039	sup-37	0	0.0137584723743221
AIA 0.039	ttx-3	0	0.088765035157589
AIA 0.039	unc-86	0.0277730046546065	0.0312906940096329
AIA 0.039	Y53G8AR.9	0.0136582502111727	0.0105346940202287
AIA 0.039	Y56A3A.18	0.00841600304351735	0.0259568722871503
AIA 0.039	zag-1	0	0.00913089207913706
AIA 0.039	zfh-2	0.0437444781895325	0.0397724229363464
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AIA 0.039	ztf-26	0.107881555994471	NA
AIB 0.045	aha-1	0.222221577917804	0.200350832797135
AIB 0.045	alr-1	NA	0.122062388837708
AIB 0.045	atf-7	0.062672731241049	0.0610842760798659
AIB 0.045	attf-6	0.0157463028438062	0.0200307694710574
AIB 0.045	ceh-18	0.00164245051697448	0
AIB 0.045	ceh-27	0.0278415228709245	NA
AIB 0.045	ceh-40	0.0685347922261457	NA
AIB 0.045	ceh-8	NA	0.0475659065622267
AIB 0.045	ces-1	0.0573132398728545	NA
AIB 0.045	crh-2	0.0519157446865047	0.0524161403717105

AIB 0.045	ctbp-1	0.23857432594724	0.24813183962495
AIB 0.045	daf-19	0.0602595189079562	0.0697666409451515
AIB 0.045	egl-13	0.0560818034469847	0.0493308999492661
AIB 0.045	egl-18	0.0894204149745529	0.088544574841254
AIB 0.045	egl-27	0.0454921378485837	0.0477090767789731
AIB 0.045	ekl-4	0.0264186182392273	0.0357518068927662
AIB 0.045	elt-4	0.00863843934972882	NA
AIB 0.045	ets-5	NA	0.0487610137965279
AIB 0.045	F57A8.1	0.050034711284342	0.0537539063021226
AIB 0.045	hif-1	0.0253128652698297	0.0280531320655232
AIB 0.045	hinf-1	0.0628019771716354	0.0821935841099451
AIB 0.045	hsf-1	0.0381427617800032	0.0456880900394478
AIB 0.045	K09A11.1	0.0554565373844938	NA
AIB 0.045	lag-1	0.0331133414901605	0.0675648046427246
AIB 0.045	lim-7	0.0131327292856651	0.0285297298695698
AIB 0.045	lin-11	0.203782378694971	0.200805528645814
AIB 0.045	lin-14	0.0256371626016238	0.0254349877401724
AIB 0.045	lin-26	0.0740227848376959	0.0750135531069833
AIB 0.045	lin-40	0.0679363460809649	0.0602497640999937
AIB 0.045	lsy-2	0.0131027234335594	0.0126900218463987
AIB 0.045	madf-3	0.0294284893047825	NA
AIB 0.045	madf-5	0.0778650727569509	0.0672817327450216
AIB 0.045	mdt-29	0.0172460292159381	0.0215551975548514
AIB 0.045	mec-3	0.0311925509680634	NA
AIB 0.045	mef-2	0.106824558404171	0.110432042124074
AIB 0.045	nfya-2	0	0.00296751116950705
AIB 0.045	nhr-11	0.027699832374123	0.020304891797278
AIB 0.045	pat-9	0.194597694906167	0.1351497663039
AIB 0.045	sea-2	0.0341155782511683	0.0217964047520766
AIB 0.045	sem-4	0.0060033382988392	0.014149469015312
AIB 0.045	sox-4	0.0605818900814636	0.0576384207397241
AIB 0.045	sptf-2	0.257498497021357	0.274343243732217
AIB 0.045	sup-37	0.0471834626377454	0.011177235199733
AIB 0.045	unc-42	0	0.00831738442978028
AIB 0.045	unc-86	0.188378149840565	0.191144318335842
AIB 0.045	Y53G8AR.9	0.0339388910005741	0.0377933960570862
AIB 0.045	Y56A3A.18	0.00148643843379121	0.0162394777179774
AIB 0.045	zfh-2	0.045079791020759	0.0402687365977872
AIB 0.045	zim-3	0	0.000373136789070299
AIB 0.045	ZK546.5	0.0144251608671818	0.0379860981426696
AIB 0.045	ztf-26	0.0503350387093211	NA
AIM 0.037	aha-1	0.0695281020908517	0.108553899714684
AIM 0.037	alr-1	0.158400551413015	NA

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AIM 0.037	attf-6	0.00089252487015987	0.00456802292058579
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AIM 0.037	crh-2	0.0462072761095517	0.0492457307637212
AIM 0.037	ctbp-1	0.107266793700771	0.097728931771051
AIM 0.037	D1046.2	0.00367338125776197	0.00350875312832949
AIM 0.037	daf-19	0.0812991870979602	0.0891455688033403
AIM 0.037	dxbp-1	0	0.00133529406136091
AIM 0.037	egl-18	0.092881816632813	0.110098951401313
AIM 0.037	egl-27	0.0295410166425913	0.0325371435089115
AIM 0.037	ekl-4	0.037860212869835	0.0455488627717581
AIM 0.037	elt-4	0.0251303824619185	0
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AIM 0.037	lag-1	0.0270034220364947	0.0535062817141778
AIM 0.037	lim-6	0.0368498757766935	0.0236370644331212
AIM 0.037	lim-7	0.00741092861938773	0.0218456866188268
AIM 0.037	lin-11	0.177715128581193	NA
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AIM 0.037	lin-14	0.0231754451622059	0.0236604636507178
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AIM 0.037	lsy-2	0.0170973463468188	0.0175774552009961
AIM 0.037	madf-3	0.0472233433449361	0.0478618901856797
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AIM 0.037	nhr-11	0.0371623547490628	0.042086374968286
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AIM 0.037	row-1	0.00653992161519774	0.0304243268513351
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AIM 0.037	sem-4	0.0112057935067908	0.0144813070686295

AIM 0.037	sptf-2	0.291671200232888	0.362574491280312
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AIM 0.037	unc-86	0.240756352222355	0.246447455096314
AIM 0.037	Y53G8AR.9	0.0158270826462038	0.0190746615133502
AIM 0.037	Y56A3A.18	0.0342888751406657	0.0406364970850054
AIM 0.037	zfh-2	0.0373852143914243	0.0398909083070061
AIM 0.037	zim-3	0	0.00486009112014053
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AIN 0.034	alr-1	0.146422988620865	0.163339212324441
AIN 0.034	atf-7	0	0.000285549035771433
AIN 0.034	attf-6	0.0141674675600741	0.0172797198529734
AIN 0.034	bed-1	0	0.013344700712704
AIN 0.034	C34B4.2	0.205965084545549	0.015191668604256
AIN 0.034	ceh-18	0	0.0110684179506691
AIN 0.034	ceh-27	0.0424029307311259	0.065945276304265
AIN 0.034	ceh-63	0.0626148619466751	NA
AIN 0.034	crh-2	0.0514023889974963	0.0607986267115053
AIN 0.034	ctbp-1	0.159397837066251	0.177519344526213
AIN 0.034	daf-19	0.0553018870628935	0.0719176166787182
AIN 0.034	egl-13	0.0595254306559995	0.117594328157319
AIN 0.034	egl-18	0.113210778899749	0.0928983334799524
AIN 0.034	egl-27	0.0452592040320904	0.0544930186687274
AIN 0.034	ekl-4	0.0566380672296221	0.0726491554997335
AIN 0.034	elt-4	NA	0.0418328253733468
AIN 0.034	ets-5	NA	0.0588622598894585
AIN 0.034	F22D6.2	0.0662880782201314	0
AIN 0.034	fkh-10	0.037311422309922	NA
AIN 0.034	fkh-8	NA	0.0392284871762471
AIN 0.034	hif-1	0.0228292667564162	0.0201592344857361
AIN 0.034	hinf-1	0.073756970725139	0.0999413315186678
AIN 0.034	hlh-8	NA	0.0153842037663902
AIN 0.034	hsf-1	0.00892796338111535	0.0207243198813309
AIN 0.034	isw-1	0	0.0471786422049202
AIN 0.034	lag-1	0.0432209549137259	0.0760033908716258
AIN 0.034	lim-7	0.0132796234320582	0.0457155041027406
AIN 0.034	lin-11	0.189951803558003	NA
AIN 0.034	lin-13	0.000637992082147524	0.00786674570493295
AIN 0.034	lin-14	0.0300050884191739	0.0456379857188879
AIN 0.034	lin-26	0.0911813878676633	0.0875654828882781

AIN 0.034	lin-39	0	0.00494434859937331
AIN 0.034	lin-40	0.0441024541539263	0
AIN 0.034	lin-54	0.000185605128156119	0.0144704085103537
AIN 0.034	lsy-2	0.0191910674946036	0.0217382691769216
AIN 0.034	madf-3	0.0585478922602586	NA
AIN 0.034	madf-5	0.107708383972978	0.0632977489194879
AIN 0.034	madf-6	0.00227155209676012	0.0102034506279351
AIN 0.034	mdt-29	0.0548089216559363	0.0635841108908352
AIN 0.034	mec-3	NA	0.00535730314416516
AIN 0.034	mml-1	0.00551314933860171	0
AIN 0.034	nfya-2	0.00117990687509141	0.00622001620006175
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AIN 0.034	nhr-6	0	0.00697448645344566
AIN 0.034	pat-9	0.184446699395639	NA
AIN 0.034	pbrm-1	0.0100475067796473	0.0153295965103238
AIN 0.034	R02D3.7	0.00623747196972197	0.00282026944371549
AIN 0.034	row-1	0	0.077930085463808
AIN 0.034	sem-4	0	0.00270371120157397
AIN 0.034	sptf-2	0.30708093732762	NA
AIN 0.034	ttx-3	0.00741699661194087	0.0904460329379237
AIN 0.034	unc-42	0	0.00198021672418534
AIN 0.034	unc-86	0.133836985456245	NA
AIN 0.034	Y53G8AR.9	0.0154651341130302	NA
AIN 0.034	Y56A3A.18	0.0274589252962287	0.0357896967741014
AIN 0.034	zag-1	0	0.00678967542072133
AIN 0.034	zfh-2	0.0397294382341791	NA
AIN 0.034	zim-3	0.0285499051621658	0.015543121933341
AIN 0.034	ZK185.1	0.0067320013057728	NA
AIN 0.034	ZK546.5	0.0624841539058351	0.0659230529024768
AIN 0.034	ztf-1	0.0266443948411321	0.00860735120190007
AIN 0.034	ztf-26	0.131174275636332	0.0713854853342506
AIY 0.037	aha-1	0.348618514914094	0.343838240424709
AIY 0.037	alr-1	0.135855501648164	0.151204253631316
AIY 0.037	atf-7	0.00844701771514454	0.00458974847029565
AIY 0.037	attf-6	0	0.00453534396263255
AIY 0.037	C34B4.2	0.081399758891626	0
AIY 0.037	ceh-27	NA	0.0382865446267382
AIY 0.037	chd-7	0	0.000192674388044623
AIY 0.037	crh-2	0.0505260023147107	0.0500645224838321
AIY 0.037	ctbp-1	0.149462065308191	0.157030780202655
AIY 0.037	daf-19	0.0980944360939758	0.118268915322126
AIY 0.037	egl-13	0.129273850067047	0.140057540188369
AIY 0.037	egl-18	0.0682046443822358	0.0760149095924748

AIY 0.037	egl-27	0.00224424033986381	0.0038935474792964
AIY 0.037	ekl-4	0.0378554786376638	0.0372253741389345
AIY 0.037	F22D6.2	0.0691722317486871	0
AIY 0.037	F57A8.1	0.00050064396079949	0.103272937531314
AIY 0.037	hif-1	0.0335595222632551	0.0376710602649967
AIY 0.037	hinf-1	0.100506581326306	0.102736106665665
AIY 0.037	hsf-1	0.0180106372799639	0.0253472573890975
AIY 0.037	isw-1	0.0549303426280042	0.0864213328187762
AIY 0.037	K09A11.1	0.0609488870849908	0
AIY 0.037	K12H6.12	0.0847083816162657	NA
AIY 0.037	lag-1	0.00738859109751298	0.030476599933026
AIY 0.037	lin-14	0.0207337887579427	0.0178591812220822
AIY 0.037	lin-26	0.0778029411320461	0.0801436939116307
AIY 0.037	lin-39	0.00845448748642912	0.00972156756246597
AIY 0.037	lin-40	0.10263561569811	0.067117482682374
AIY 0.037	lsy-2	0.0142921751715179	NA
AIY 0.037	madf-5	0.0814325228930386	NA
AIY 0.037	mdt-29	0.0401479027170549	0.0475397895929446
AIY 0.037	mef-2	0.00231942550868837	0.0186437227702945
AIY 0.037	nfya-2	NA	0.0339603659686871
AIY 0.037	nhr-11	0.0436765870205465	0.0371390777633262
AIY 0.037	nhr-71	NA	0.00560627370559422
AIY 0.037	pat-9	NA	0.139009683758089
AIY 0.037	row-1	0.0455870016472632	0.0545878632065986
AIY 0.037	sem-4	NA	0.040137716786858
AIY 0.037	sptf-2	0.307176345218199	NA
AIY 0.037	T26A5.8	0.0190333725797593	NA
AIY 0.037	unc-120	0.00148855784614295	0
AIY 0.037	unc-55	NA	0.00144410125829935
AIY 0.037	Y53G8AR.9	0.0102402481362207	0.0162957127134486
AIY 0.037	Y56A3A.18	0.0331165456271581	0.0413160397468722
AIY 0.037	zfh-2	0.0570277116227593	0.0532957222619128
AIY 0.037	ztf-1	0.0093282976834987	0.0365594624552842
ALA 0.037	aha-1	0.0532012328064235	0.0554928683251991
ALA 0.037	akir-1	0	0.00186450269836373
ALA 0.037	atf-7	0.0301922757297138	0.0291166870550982
ALA 0.037	attf-6	0.00493462772639551	0.00630992129143742
ALA 0.037	cebp-1	0.00212064251294941	0.000361874672047825
ALA 0.037	ceh-27	0.103156311973618	NA
ALA 0.037	ceh-48	0.0127375522894193	0.00970862145038078
ALA 0.037	chd-7	0.0137608730839007	0.00997167241864943
ALA 0.037	crh-2	0.0461891769728105	0.0505368978618717
ALA 0.037	ctbp-1	NA	0.112595265406266

ALA 0.037	D1046.2	0.00700201849710425	0
ALA 0.037	daf-19	0.0949756951606368	0.0703797334983239
ALA 0.037	egl-13	NA	0.0747954759746671
ALA 0.037	egl-18	0.0949025377594359	0.0867793575246917
ALA 0.037	ekl-4	0.051829173781111	0.0546646400090542
ALA 0.037	ets-5	NA	0.0365712964271488
ALA 0.037	F22D6.2	0.0530186932144565	0
ALA 0.037	F44E2.7	0.0232571206762098	0.00849588334536882
ALA 0.037	gei-8	0.0155964142221848	0
ALA 0.037	hif-1	0.00833128683410314	0.0084306982129284
ALA 0.037	hinf-1	0.109158235787809	0.119295295059655
ALA 0.037	hsf-1	0.00643894080893753	0.0160114236495809
ALA 0.037	isw-1	0.0568405928109354	0.0286612406531106
ALA 0.037	lag-1	0.011282917079107	0.0853236023822905
ALA 0.037	lim-6	NA	0.0760622403276925
ALA 0.037	lim-7	0.037574513811311	0.0166240912971434
ALA 0.037	lin-13	0	0.00839966308783865
ALA 0.037	lin-14	0.0387720508705261	0.0349031130550664
ALA 0.037	lin-26	NA	0.0692348687266564
ALA 0.037	lin-40	0.101847967973413	0.0571963948309618
ALA 0.037	lsy-2	0.0290798970375289	0.0244411175586555
ALA 0.037	madf-3	0.0519388550114784	NA
ALA 0.037	madf-5	NA	0.0456572443008764
ALA 0.037	mbf-1	0.0350794499515924	0.0223734522703641
ALA 0.037	mdt-29	0	0.00171288278213044
ALA 0.037	nfya-1	NA	0.00898297046434003
ALA 0.037	nfya-2	0.00373995532909516	NA
ALA 0.037	nfyb-1	0.00809152988380164	0
ALA 0.037	nhr-11	NA	0.0400643391086785
ALA 0.037	nhr-6	0.0181656632654874	0.0244469575786344
ALA 0.037	nhr-71	0.00728603778330998	0
ALA 0.037	pbrm-1	0.013651590324522	0.010422922072492
ALA 0.037	R02D3.7	NA	0.00582490036734492
ALA 0.037	row-1	0.156009922551392	0.0814764763405462
ALA 0.037	sem-4	0.0666265136208696	0.0707517204320892
ALA 0.037	somi-1	0	0.00451236134427106
ALA 0.037	sptf-2	0.315871737008546	0.315032459062179
ALA 0.037	unc-86	NA	0.0569410239005657
ALA 0.037	Y53G8AR.9	NA	0.0127030421807596
ALA 0.037	Y56A3A.18	0.0394918818510251	0.0370169618034027
ALA 0.037	zag-1	0.175807426743529	0.110689056331228
ALA 0.037	zfh-2	0.0472445059231707	0.0387309996491657
ALA 0.037	zim-3	0.00163548546469292	0.00284298470251836

ALA 0.037	ZK185.1	NA	0.0137898177938117
ALA 0.037	ZK546.5	0.133169655307809	0.19487215193754
ASE 0.042	aha-1	0.304784471823287	NA
ASE 0.042	alr-1	0.124767627738354	0.148200585046235
ASE 0.042	cebp-1	0.00696294934910455	0
ASE 0.042	ceh-13	NA	0.000372779956688875
ASE 0.042	ceh-27	0.0606342435088458	NA
ASE 0.042	chd-7	0	0.000116762783018139
ASE 0.042	crh-2	0.0470460847236522	0.0460987030389593
ASE 0.042	ctbp-1	0.127996869285956	NA
ASE 0.042	D1046.2	0	1.55978903004112e-05
ASE 0.042	daf-19	0.0995973583288395	0.0881656742118394
ASE 0.042	dsc-1	0.0973038379582521	0.096242050269077
ASE 0.042	egl-18	0.0614094609811953	NA
ASE 0.042	ekl-4	0.0298049932894748	0.0492236540128197
ASE 0.042	elt-4	0.0303953591392222	NA
ASE 0.042	ets-5	NA	0.0538802532864933
ASE 0.042	F22D6.2	0.0369932096680443	0
ASE 0.042	F57A8.1	0.163707095645117	0.195837864300684
ASE 0.042	fkh-8	0.099946473116838	0.0895496927881277
ASE 0.042	hif-1	0.00673337938713856	0.0540771619833436
ASE 0.042	hinf-1	0.0861891377872561	0.106998035122271
ASE 0.042	hsf-1	0.0430627784127479	0.0477264969309939
ASE 0.042	lag-1	0	0.00807342123606363
ASE 0.042	lim-7	NA	0.0546188695290605
ASE 0.042	lin-11	NA	0.326662473139066
ASE 0.042	lin-26	0.0843366418739659	0.0655559983892299
ASE 0.042	lin-40	0.111645244248146	0.0832737028211911
ASE 0.042	lsy-2	0.00123311558014272	0
ASE 0.042	mdt-29	0.080215343967728	0.101177907701091
ASE 0.042	nhr-11	0.0654694924694828	0.0452588014526639
ASE 0.042	nhr-237	0.0318394837337332	0.0227777280935183
ASE 0.042	nhr-6	0.00612464763274059	0
ASE 0.042	nhr-84	0.11101365767857	0
ASE 0.042	R02D3.7	0.0101799600894931	NA
ASE 0.042	sem-4	NA	0.0375535834245065
ASE 0.042	sox-4	0.111085567989823	0.101601959074586
ASE 0.042	T26A5.8	0	0.0019141446864308
ASE 0.042	Y53G8AR.9	0.0308282330856472	NA
ASE 0.042	Y56A3A.18	0.00745255236360732	0.0290283129305328
ASE 0.042	zfh-2	0.0443901125578114	0.0375802417863975
ASE 0.042	zip-4	0.0366467599194752	0
ASE 0.042	ZK546.5	NA	0.15143701876402

ASE 0.042	ztf-26	NA	0.0258099384366065
ASG 0.035	aha-1	0.0807810330508295	0.15663675207887
ASG 0.035	attf-6	0.00640373472924593	0.00728166694378496
ASG 0.035	C34B4.2	0.0368053740578934	0
ASG 0.035	ceh-18	0	0.00884083412194006
ASG 0.035	chd-7	0	0.0138291624173717
ASG 0.035	crh-2	0.028039020551265	0.036628109345639
ASG 0.035	ctbp-1	0.109625087222608	0.0959977097456665
ASG 0.035	daf-19	NA	0.0474010436029466
ASG 0.035	egl-18	0.0942316241211388	0.103374579753964
ASG 0.035	ekl-4	0.0357214668802667	0.0395452290815684
ASG 0.035	elt-4	NA	0.0163011070932122
ASG 0.035	ets-5	0.0892833791660642	0.088315435581213
ASG 0.035	fkh-10	NA	0.00485484369094249
ASG 0.035	fkh-8	0.101018644875468	0.11252143900066
ASG 0.035	hif-1	0	0.00265691799651894
ASG 0.035	hinf-1	NA	0.12328332509856
ASG 0.035	hsf-1	0.0185635122684442	0.00315106584808311
ASG 0.035	lag-1	0	0.0313684285593832
ASG 0.035	lim-7	0.0237594983214155	0.0349435526387001
ASG 0.035	lin-11	0.301162591415111	0.33830487362436
ASG 0.035	lin-14	0.00298863730640908	0.0021812349380867
ASG 0.035	lin-26	0.0910307949377203	0.0793339707777913
ASG 0.035	lin-40	0.0826714884896386	0.0631079669332407
ASG 0.035	lsy-2	0.000333327181810599	0.0105785894467905
ASG 0.035	madf-3	NA	0.0668749548792618
ASG 0.035	madf-5	0.0824029051924266	0.0726456964759177
ASG 0.035	mdt-29	0.0260390834634267	0.0203940644041387
ASG 0.035	nhr-11	0.0725195702828809	0.0712524815590696
ASG 0.035	nhr-129	0.00640827908540341	NA
ASG 0.035	nhr-237	NA	0.147467394481558
ASG 0.035	nhr-71	0	0.00164822345118316
ASG 0.035	sox-4	0.0181444691640597	NA
ASG 0.035	sptf-2	NA	0.351332483051991
ASG 0.035	T26A5.8	0.014410690267622	0
ASG 0.035	unc-120	0	0.0133677711470001
ASG 0.035	Y53G8AR.9	0.0196503711829949	0.00786644256814921
ASG 0.035	Y56A3A.18	0.0311461710058899	NA
ASG 0.035	zfh-2	0.0381055901296281	0.0363524311559121
ASG 0.035	zim-3	0	0.0157530389199971
ASG 0.035	ZK546.5	0	0.0617373858289753
ASG 0.035	ztf-26	0.0482092122079003	NA
ASH 0.037	aha-1	0.243382927434881	0.275726673309091

ASH 0.037	alr-1	NA	0.172650185701873
ASH 0.037	attf-6	0.0196651100829732	0.0189009024515358
ASH 0.037	cebp-1	0.0030057606213656	0.00174692764654664
ASH 0.037	ceh-27	NA	0.0267829431737653
ASH 0.037	crh-2	0.0212283673469888	0.0217926093862784
ASH 0.037	ctbp-1	0.0812985834452729	0.0559248840957225
ASH 0.037	daf-19	0.0734725855434756	0.0763750265808103
ASH 0.037	dmd-9	0.0173797800151685	0.0478949875365915
ASH 0.037	dxbp-1	0.00283817611702113	0.00787029171836135
ASH 0.037	ekl-4	0.0377052305039739	0.0549951970716773
ASH 0.037	fkh-8	0.148938595068777	0.128850534090979
ASH 0.037	gei-8	0.0761299002595808	0.0999308942807402
ASH 0.037	hif-1	0	0.00448743215943715
ASH 0.037	hinf-1	0.114752602244627	0.134596556018137
ASH 0.037	hsf-1	0.0108505606569404	0.00984577875261875
ASH 0.037	lag-1	0.0204757487869913	0.0385100749490458
ASH 0.037	lim-7	0.10050666637671	0.10134220152908
ASH 0.037	lin-11	0.399636115584721	0.426226671650162
ASH 0.037	lin-26	0.083619794087093	0.086828075692723
ASH 0.037	lin-40	0.0737835354863482	0.0505575827327845
ASH 0.037	lin-54	0	0.00771992013158605
ASH 0.037	madf-5	0.0911588127999655	NA
ASH 0.037	madf-6	0	9.72530604737853e-06
ASH 0.037	mdt-29	0.0161653336095109	0.0193109968660236
ASH 0.037	mec-3	0.01778950068556	0
ASH 0.037	nhr-102	0	0.00162286753501696
ASH 0.037	nhr-11	0.0973838132276747	0.0795552480929065
ASH 0.037	nhr-237	0.0154418699226436	0.0268528260031853
ASH 0.037	nhr-47	0.0486538385286669	0.0467183114960639
ASH 0.037	nhr-71	0.0245339979921738	0.0184908889526962
ASH 0.037	pat-9	0.118778990527722	NA
ASH 0.037	sem-4	0.0160157884258415	0.0112745016766861
ASH 0.037	sox-4	0.0772126397452449	0.0755739561378837
ASH 0.037	spr-3	NA	0.178487935017523
ASH 0.037	sptf-2	NA	0.38301975317043
ASH 0.037	T26A5.8	0	0.00880227814223952
ASH 0.037	unc-42	0.00128402204061846	0.00340908001311227
ASH 0.037	Y53G8AR.9	0.0227452134196468	0.0296243157412086
ASH 0.037	Y56A3A.18	0.0396744158181223	0.0506869212642505
ASH 0.037	zfh-2	0.0289607479410963	0.0312568476809671
ASH 0.037	ZK546.5	0	0.0694146758695182
ASH 0.037	ztf-26	0.0684419353104118	NA
ASI 0.040	aha-1	0.0947506725058738	0.0652447121688404

ASI 0.040	atf-7	0	0.00235483575081642
ASI 0.040	attf-6	0.00262198225054288	0.000988810258192956
ASI 0.040	cebp-1	0.00199946522854965	0.000610824288399796
ASI 0.040	ceh-27	0.0154142587575998	NA
ASI 0.040	ceh-8	0.117381166565908	0.120991995243985
ASI 0.040	crh-2	0.0300909673995037	0.0278587190590667
ASI 0.040	ctbp-1	NA	0.0492499964948282
ASI 0.040	D1046.2	0.00928900958544396	0.00912027892173169
ASI 0.040	daf-19	0.112175779940275	0.0950778064058403
ASI 0.040	egl-18	NA	0.0461525545959849
ASI 0.040	egrh-3	0	0.00265204421022179
ASI 0.040	ekl-4	0.0515258318914432	0.0569722515609382
ASI 0.040	F22D6.2	0.0732820611779075	0
ASI 0.040	fkh-8	0.124683639839146	0.120735243448192
ASI 0.040	hif-1	0.0101551127862243	0.00563889297408649
ASI 0.040	hinf-1	0.109385796956231	0.116912529980549
ASI 0.040	hsf-1	0.0258824515150634	0.0146731800339765
ASI 0.040	lag-1	0	0.0311449175820086
ASI 0.040	lim-7	0.0366683057548889	0.034704806002674
ASI 0.040	lin-11	0.292919019352251	0.289387794320712
ASI 0.040	lin-26	0.0773641784414675	0.0787297734359226
ASI 0.040	lin-40	0.0884051883578108	0.050197415655571
ASI 0.040	madf-3	0.0590228313845881	0.0659920241104248
ASI 0.040	madf-5	NA	0.0702885239375545
ASI 0.040	madf-9	NA	0.00140051870488925
ASI 0.040	mdt-29	0.044454286818927	0.028860878630786
ASI 0.040	nfyb-1	0.00225248149407521	0.00198999845632055
ASI 0.040	nhr-11	0.0799786372799927	0.0736275448827268
ASI 0.040	nhr-232	NA	0.0358905441075448
ASI 0.040	nhr-71	0.0316258396970629	0.0197495853659204
ASI 0.040	nhr-84	0.124191686144104	0
ASI 0.040	pag-3	NA	0.0335463193281288
ASI 0.040	pat-9	0.206026643293726	NA
ASI 0.040	pbrm-1	0.0217671744977055	0.0117396928437386
ASI 0.040	row-1	0.0162305666492113	0
ASI 0.040	skn-1	0.0153001512988664	0.00925614089876558
ASI 0.040	sptf-2	NA	0.402946570752733
ASI 0.040	syd-9	0.00462098138582993	0.00435401831361037
ASI 0.040	Y53G8AR.9	0.0175275074660323	0.0148635328855976
ASI 0.040	Y55F3AM.14	0.0148983158330729	NA
ASI 0.040	Y56A3A.18	0.0452200375994934	0.0533008658582825
ASI 0.040	zfh-2	0.0378464007741388	NA
ASI 0.040	ZK546.5	0.0219663631183696	0.0747151946755007

ASI 0.040	ztf-1	0	0.00696106299647517
ASI 0.040	ztf-26	0.0618245291683883	0.0439878010693678
ASJ 0.037	aha-1	0.120153763813589	0.108216212358922
ASJ 0.037	attf-6	0.00493982521073806	0.0105894243985538
ASJ 0.037	ceh-27	0.0369039823024571	NA
ASJ 0.037	crh-2	0.0352556477323257	0.0270296286192995
ASJ 0.037	ctbp-1	0.0506691418110111	0.0777723154379611
ASJ 0.037	D1046.2	0	0.00840454585065795
ASJ 0.037	daf-19	0.0836290210362699	0.0953842354005615
ASJ 0.037	egl-18	0.0398169457336978	0.0454234649487551
ASJ 0.037	ekl-4	0.036212834133935	0.0569529186898927
ASJ 0.037	F22D6.2	0.129438773356648	0.0170025649723016
ASJ 0.037	F33H1.4	0.00133032255757371	0
ASJ 0.037	fkh-8	0.121901394209066	0.12094875407947
ASJ 0.037	hif-1	0.00365062381105024	0.000551982705306187
ASJ 0.037	hinf-1	0.110811087973049	0.11952921223745
ASJ 0.037	hsf-1	0.0358235434010055	0.044663922918118
ASJ 0.037	lim-7	0.0377880898243318	NA
ASJ 0.037	lin-11	0.275101480758988	0.286180372927412
ASJ 0.037	lin-26	0.0830230685299543	NA
ASJ 0.037	lin-40	0.0931937167758743	0.0668987252092324
ASJ 0.037	lin-54	0.000387387860836457	NA
ASJ 0.037	madf-3	0.0444331417062015	NA
ASJ 0.037	madf-5	0.101355486504123	NA
ASJ 0.037	madf-9	0.0128732653944675	NA
ASJ 0.037	mdt-29	0.0484257850223239	0.058006903222533
ASJ 0.037	mec-3	NA	0.0136229263495728
ASJ 0.037	mml-1	0.0167706220730817	0
ASJ 0.037	nhr-11	0.0839049419056135	0.0735069024551018
ASJ 0.037	nhr-71	0.0195705461143535	0.00767156203834315
ASJ 0.037	pag-3	0.0471053624813631	NA
ASJ 0.037	pbrm-1	0.0211439087412187	0.00850612245585033
ASJ 0.037	sox-4	0.000481858723453849	0.00738356809160949
ASJ 0.037	sup-37	0.00133305997555402	0
ASJ 0.037	tlp-1	0.0131434253401226	NA
ASJ 0.037	Y53G8AR.9	0.0174385349793514	0.0267180980269087
ASJ 0.037	Y56A3A.18	0.0417235227112683	0.0384488813703565
ASJ 0.037	zfh-2	0.0398984700189261	0.0367056619730293
ASJ 0.037	zim-3	0.00954099698510401	NA
ASJ 0.037	ZK546.5	0.0615221570906243	0.0679380137956233
ASJ 0.037	ztf-26	0.060117576924134	0.0361296293094075
ASK 0.042	aha-1	0.275529188587498	0.258205857379182
ASK 0.042	atf-7	0.0352720302812401	0.0291541657134629

ASK 0.042	attf-6	0	0.0144644730896622
ASK 0.042	B0035.1	0	0.000693872553459322
ASK 0.042	cebp-1	0.00768862613464578	0.0064955796979828
ASK 0.042	ceh-18	0.014852364633244	0
ASK 0.042	ceh-40	NA	0.06835041655366
ASK 0.042	chd-7	0	0.00848064701613484
ASK 0.042	crh-2	0.0251125807300404	0.0285923152992905
ASK 0.042	ctbp-1	0.122593835365248	NA
ASK 0.042	D1046.2	0.00154235456287956	0
ASK 0.042	daf-19	0.120434069677904	0.104696494840491
ASK 0.042	dmd-8	0	0.0141547445186461
ASK 0.042	egl-18	0.0653136085004418	NA
ASK 0.042	egrh-3	0.0204274983098809	0
ASK 0.042	ekl-4	0.0204579253806568	0.0244468002229755
ASK 0.042	elt-4	0.0411234985376419	0.00224052105981494
ASK 0.042	F10B5.3	0.191575056679471	0.215319107082483
ASK 0.042	F44E2.7	0.000676069714085627	0.00714395997068633
ASK 0.042	fkh-8	0.13272579033568	0.129145071548091
ASK 0.042	hif-1	0.00131076398333597	0.0056249161115919
ASK 0.042	hinf-1	0.106840240606916	0.123093922138407
ASK 0.042	hlh-8	0.00464235709272688	NA
ASK 0.042	hsf-1	0.0401033338277106	0.046228005890998
ASK 0.042	K12H6.12	NA	0.0509064037892585
ASK 0.042	lag-1	0.00378377449304994	0.0191731221978458
ASK 0.042	lim-6	0	0.000489698646387492
ASK 0.042	lim-7	0.0329853730978204	0.0535774664645394
ASK 0.042	lin-11	0.22648110390619	0.238662299074533
ASK 0.042	lin-13	0	0.000401114105793693
ASK 0.042	lin-26	0.0879895780160672	NA
ASK 0.042	lin-40	0.122286315776419	0.112517894797806
ASK 0.042	madf-3	0.0370559778307727	NA
ASK 0.042	madf-5	NA	0.113967674977883
ASK 0.042	mdt-29	0.0352734389080288	0.0310704729245691
ASK 0.042	mef-2	0.0223139113499146	0.0374699767645574
ASK 0.042	nhr-11	0.0786340839367437	0.0732482262352192
ASK 0.042	nhr-129	0.0100717466396003	0.0113574725123007
ASK 0.042	nhr-71	0.0274621550049342	0.025394329397978
ASK 0.042	nhr-84	0.0822734215208261	0.136923087977413
ASK 0.042	pax-3	0.0249197530675981	0.0268742815804694
ASK 0.042	sem-4	0	0.00569591633578994
ASK 0.042	sox-4	0.295253096201618	0.327684552547168
ASK 0.042	sptf-2	0.298003181939521	0.309560310297086
ASK 0.042	sup-37	0.10295339975077	0

ASK 0.042	unc-120	0.00415293326178623	0
ASK 0.042	unc-62	NA	0.00246463460296258
ASK 0.042	unc-86	5.77695658075449e-05	0.011562217331448
ASK 0.042	Y53G8AR.9	0.0153464260824423	0.0209317780426406
ASK 0.042	Y55F3AM.14	NA	0.0204865050834478
ASK 0.042	Y56A3A.18	0.00718191494204745	0.00954522037742295
ASK 0.042	zfh-2	NA	0.0350358056905455
ASK 0.042	zip-4	0	0.00672629722599354
ASK 0.042	ZK546.5	0.00498653749924409	0.128114167203645
ASK 0.042	ztf-26	0.040202456173616	0.0494768694705914
AS_DA_DB_VA_VB_SAB 0.041	aha-1	0.242058822406285	0.299362452434908
AS_DA_DB_VA_VB_SAB 0.041	ahr-1	0	0.0276207975726337
AS_DA_DB_VA_VB_SAB 0.041	alr-1	0.126890419551931	0.132695026809682
AS_DA_DB_VA_VB_SAB 0.041	atf-7	0	0.00216640372226158
AS_DA_DB_VA_VB_SAB 0.041	attf-6	0	0.00114497094815432
AS_DA_DB_VA_VB_SAB 0.041	C34B4.2	0.0693796677147268	0
AS_DA_DB_VA_VB_SAB 0.041	cebp-1	0.00694052057304538	0.0124581248496945
AS_DA_DB_VA_VB_SAB 0.041	ceh-20	0.038814772604322	0.0508028183956057
AS_DA_DB_VA_VB_SAB 0.041	ceh-40	NA	0.100014651469074
AS_DA_DB_VA_VB_SAB 0.041	ceh-63	0.105957862650363	NA
AS_DA_DB_VA_VB_SAB 0.041	ceh-82	NA	0.00938961361364712
AS_DA_DB_VA_VB_SAB 0.041	ces-1	0.0309487370419679	0.0385025052359325
AS_DA_DB_VA_VB_SAB 0.041	crh-2	0.0388849300278674	0.0423832475976645
AS_DA_DB_VA_VB_SAB 0.041	ctbp-1	0.124236103990296	0.117062387728627
AS_DA_DB_VA_VB_SAB 0.041	daf-19	0.0615939346493201	0.050465811959301
AS_DA_DB_VA_VB_SAB 0.041	dsc-1	NA	0.00487252610707248
AS_DA_DB_VA_VB_SAB 0.041	egl-13	0.0051414681573233	0.0146027700245037
AS_DA_DB_VA_VB_SAB 0.041	egl-18	0.074584472042884	0.0753092763700077
AS_DA_DB_VA_VB_SAB 0.041	ekl-4	0.0327902477317803	0.0373332094075803
AS_DA_DB_VA_VB_SAB 0.041	elt-1	0.00824304096741659	0
AS_DA_DB_VA_VB_SAB 0.041	elt-4	0.0101831114225583	0
AS_DA_DB_VA_VB_SAB 0.041	ets-5	0.0986710527524015	0.119089212619909
AS_DA_DB_VA_VB_SAB 0.041	F22D6.2	0.125045998786941	0.0705779737970511
AS_DA_DB_VA_VB_SAB 0.041	fkh-10	0.0103766214983	0.0113304903461268
AS_DA_DB_VA_VB_SAB 0.041	hif-1	0.00259588471786516	0.00882199994181171
AS_DA_DB_VA_VB_SAB 0.041	hinf-1	0.107066656273451	0.10650120222805
AS_DA_DB_VA_VB_SAB 0.041	hlh-8	0.011439775201205	0.00353298208106093
AS_DA_DB_VA_VB_SAB 0.041	hmg-1.1	0.0101009662307323	0.00858489073069096
AS_DA_DB_VA_VB_SAB 0.041	hsf-1	0.0133733512014371	0.0123136217966973
AS_DA_DB_VA_VB_SAB 0.041	isw-1	0.0342525065945164	0.0369720685127261
AS_DA_DB_VA_VB_SAB 0.041	K12H6.12	0.000701231432466385	NA
AS_DA_DB_VA_VB_SAB 0.041	lag-1	0.0337099345419063	0.0776758384086826
AS_DA_DB_VA_VB_SAB 0.041	lin-11	0.0779370497524747	0.0941763508905595

AS_DA_DB_VA_VB_SAB 0.041	lin-14	0.0898803340708217	0.090554313454828
AS_DA_DB_VA_VB_SAB 0.041	lin-26	0.0762039635954321	0.0656939612407881
AS_DA_DB_VA_VB_SAB 0.041	lin-39	0.0584712803038027	0.0683554899707671
AS_DA_DB_VA_VB_SAB 0.041	lin-40	0.100130121469501	0.0580758804229229
AS_DA_DB_VA_VB_SAB 0.041	lsy-2	0.0204427908198478	0.0205477462294977
AS_DA_DB_VA_VB_SAB 0.041	mab-5	0.00328587220601991	0
AS_DA_DB_VA_VB_SAB 0.041	madf-3	0.048313221716715	0.0503489761427551
AS_DA_DB_VA_VB_SAB 0.041	madf-5	0.103996821904788	0.0693948599820032
AS_DA_DB_VA_VB_SAB 0.041	madf-9	0.0287739634813247	0.0149372757893236
AS_DA_DB_VA_VB_SAB 0.041	mbf-1	0.0929311348533238	0.12095962901737
AS_DA_DB_VA_VB_SAB 0.041	mdt-29	0.0404804314581576	0.0516224632693828
AS_DA_DB_VA_VB_SAB 0.041	nfya-2	0.0310808420446966	0.0368966369288757
AS_DA_DB_VA_VB_SAB 0.041	nfyb-1	0.00555420733852299	0.0132397052132335
AS_DA_DB_VA_VB_SAB 0.041	nhr-11	0.00381746788048803	0.00467945806773687
AS_DA_DB_VA_VB_SAB 0.041	nhr-232	0.0661749710313123	0.0910848800842719
AS_DA_DB_VA_VB_SAB 0.041	pag-3	0.0666848888620631	0.0610691273062944
AS_DA_DB_VA_VB_SAB 0.041	pat-9	0.251461892225539	0.226987820662231
AS_DA_DB_VA_VB_SAB 0.041	pbrm-1	0.0107660614654767	0.00831163233479294
AS_DA_DB_VA_VB_SAB 0.041	sem-4	0.0361473251469055	0.0449344746749503
AS_DA_DB_VA_VB_SAB 0.041	sox-4	0.0377547316288363	0.0421476547160441
AS_DA_DB_VA_VB_SAB 0.041	sptf-2	0.271357617666296	0.27274308161799
AS_DA_DB_VA_VB_SAB 0.041	unc-3	0.170714689958707	0.196335893685076
AS_DA_DB_VA_VB_SAB 0.041	unc-42	0.0402528882099455	0.0506635104814709
AS_DA_DB_VA_VB_SAB 0.041	unc-55	0.0293904809501988	0.0332325020975868
AS_DA_DB_VA_VB_SAB 0.041	unc-62	0.00646708267352058	0.0100558587869481
AS_DA_DB_VA_VB_SAB 0.041	vab-7	0.0157410472713364	0.0349080671144612
AS_DA_DB_VA_VB_SAB 0.041	Y53G8AR.9	0.00849912385477012	0.0054557832202877
AS_DA_DB_VA_VB_SAB 0.041	Y55F3AM.14	0.0420057035027931	0.051086278877235
AS_DA_DB_VA_VB_SAB 0.041	Y56A3A.18	0.0464470106936727	0.0467215789259979
AS_DA_DB_VA_VB_SAB 0.041	zag-1	0.102886713105732	0.109194140609513
AS_DA_DB_VA_VB_SAB 0.041	zfh-2	0.0466857407319485	0.0426187704758813
AS_DA_DB_VA_VB_SAB 0.041	zim-3	0.00509487614795382	0.00303094962332524
AS_DA_DB_VA_VB_SAB 0.041	ZK546.5	0.0309347407407381	0.0917406444273105
AS_DA_DB_VA_VB_SAB 0.041	ztf-26	0.0814748412507246	0.0384417955110677
AUA 0.045	aha-1	0.19937368306992	0.2504847200008
AUA 0.045	alr-1	NA	0.20423290494335
AUA 0.045	atf-7	0	0.000818289380015169
AUA 0.045	attf-6	0	0.0115451744888188
AUA 0.045	C34B4.2	0.0154131267478025	0.0182907144550703
AUA 0.045	ceh-18	0.0340676400045031	0
AUA 0.045	ceh-27	NA	0.026623615154991
AUA 0.045	ceh-48	0.00202094482004129	0
AUA 0.045	crh-2	0.0373898411494923	0.0537943811214506

AUA 0.045	ctbp-1	0.122418217630678	0.114634461459837
AUA 0.045	daf-19	0.130327548815982	NA
AUA 0.045	egl-13	0.080295783289693	0.0734890850435772
AUA 0.045	egl-18	0.0449807741837293	0.0911344214422572
AUA 0.045	egl-27	0.0217788342674638	0
AUA 0.045	ekl-4	0.0488785277020859	0.0698133923190986
AUA 0.045	ets-5	0.0189416937377405	NA
AUA 0.045	F22D6.2	0.0791970582007507	0.0173983158270964
AUA 0.045	F57A8.1	0.00284290233354982	0.0759388528767079
AUA 0.045	fkh-10	0.0474498523761867	0.0572800030997999
AUA 0.045	fkh-8	0.0556403974787525	NA
AUA 0.045	hif-1	0.0299007291809469	0.0244892538023662
AUA 0.045	hinf-1	0.142673467422958	0.205720781561627
AUA 0.045	hmg-1.1	0	0.00879549794252934
AUA 0.045	hsf-1	0.012869006912668	0.0187985616273954
AUA 0.045	isw-1	0.0763202721554056	0.0235373405077594
AUA 0.045	lag-1	NA	0.0678302141922505
AUA 0.045	lim-7	0.0744556128304733	0.104944760249848
AUA 0.045	lin-11	NA	0.274892555081339
AUA 0.045	lin-14	0.019940154928381	0.0243152851402897
AUA 0.045	lin-26	0.100019854471022	NA
AUA 0.045	lin-39	0.0234859895928656	NA
AUA 0.045	lin-40	0.0847173218148052	0.0185170354225139
AUA 0.045	lsy-2	0.0259140963029715	NA
AUA 0.045	madf-9	NA	0.000944659768622308
AUA 0.045	mdt-29	0	0.00182699755543485
AUA 0.045	nhr-47	0	0.021424945263018
AUA 0.045	nhr-6	0.000489190196342385	0
AUA 0.045	pat-9	0.1610873508808	NA
AUA 0.045	pbrm-1	0.00346678005318234	0.0101687433490235
AUA 0.045	row-1	0.0533605606616707	0
AUA 0.045	sea-2	0.0727447571294197	0.0370230556016153
AUA 0.045	T26A5.8	0.0125956874694476	0
AUA 0.045	Y53G8AR.9	0.014456895089859	0.0260254149548072
AUA 0.045	Y56A3A.18	0.0297393381245172	0.0486381734833856
AUA 0.045	zfh-2	NA	0.0321920208417824
AUA 0.045	zim-3	0.0048869890523326	0.00575595795122064
AUA 0.045	ZK546.5	0	0.0669162422833766
AUA 0.045	ztf-4	0	0.00345590576922757
AVA 0.048	aha-1	0.252601542936306	0.269056624571222
AVA 0.048	alr-1	0.148022929470366	0.170109710507289
AVA 0.048	atf-7	0.0211224872371802	0.0260832012352882
AVA 0.048	attf-6	0.00596568796093723	0.0134678382625854

AVA 0.048	cebp-1	0.0190708866571147	0.0275389175574695
AVA 0.048	ceh-27	0.00642249946535573	0.0232092899639144
AVA 0.048	ceh-8	NA	0.0332625098811806
AVA 0.048	chd-7	0.00106744461767072	0.0165945640904007
AVA 0.048	crh-2	0.0462520930032253	0.0612573147738056
AVA 0.048	ctbp-1	0.20676073317443	0.197195589488699
AVA 0.048	daf-19	0.0833173819916433	0.0901566869685442
AVA 0.048	dxbp-1	0	0.00558762034352189
AVA 0.048	egl-13	0.0242333026997685	0.010629180859148
AVA 0.048	egl-18	0.102989957493024	0.116266566395224
AVA 0.048	egl-27	0.0202717225424116	0.0316834546380793
AVA 0.048	ekl-4	0.024227497262596	0.0303099984618215
AVA 0.048	ets-5	0	0.0145317260609984
AVA 0.048	F57A8.1	0	0.0367429712456215
AVA 0.048	fkh-10	0.0094878755835201	0.0085701354541705
AVA 0.048	gei-8	0.0195959037581012	0.0445406757043773
AVA 0.048	hif-1	0.0162651256927629	0.0227414939887653
AVA 0.048	hinf-1	0.0952677214729434	0.120609465900581
AVA 0.048	hlh-8	0.0152456504006139	0.0166901102973946
AVA 0.048	hmg-1.1	0	0.00922665282781601
AVA 0.048	hsf-1	0.00967031467804503	0.0137261866960349
AVA 0.048	isw-1	0.0052335106738307	0.0298939231607045
AVA 0.048	K12H6.12	0.00995025661894518	0.0170307158997238
AVA 0.048	klu-1	0	0.0223398552723268
AVA 0.048	lag-1	0.0753348491636549	0.118547121675181
AVA 0.048	lim-7	0	0.0237517456169378
AVA 0.048	lin-11	0.206976871335533	0.231690804548714
AVA 0.048	lin-14	0.0722873260114345	0.0829355283537916
AVA 0.048	lin-26	0.09663988305572	0.0968094300582809
AVA 0.048	lin-39	0.0160708977653124	NA
AVA 0.048	lin-40	0.114903696935181	0.0812465671067925
AVA 0.048	lsy-2	0.0217941058718911	0.034808046633816
AVA 0.048	madf-3	0.057161509931088	0.0695896177630203
AVA 0.048	madf-5	0.0409809458756732	0.0271756069797725
AVA 0.048	madf-6	0	0.00523685912678668
AVA 0.048	mbf-1	0.112074037714756	0.128569393366817
AVA 0.048	mdt-29	0.0163571780024396	0.0303665587527866
AVA 0.048	mef-2	0.0169773002969593	0.00660028822529996
AVA 0.048	nfya-2	0	0.0044043852316545
AVA 0.048	nfyb-1	0.0137174876247769	0.0202030568720352
AVA 0.048	nhr-11	0.0422326702026525	0.03036928177555
AVA 0.048	nhr-232	0.257679715312027	0.261492562211195
AVA 0.048	nhr-237	NA	0.0735748045780963

AVA 0.048	pag-3	0.0626597344504616	0.0653098505189229
AVA 0.048	pat-9	0.126959806200619	0.104033831829268
AVA 0.048	pbrm-1	0	0.0108975786086832
AVA 0.048	R02D3.7	0.00168472283604076	0.0193528356072793
AVA 0.048	saeg-2	0	0.00889167789790597
AVA 0.048	sem-4	0.0666998475853436	0.0933306131168789
AVA 0.048	sox-4	NA	0.0708882172379871
AVA 0.048	sptf-2	0.259333627138472	NA
AVA 0.048	syd-9	0	0.0144478877674874
AVA 0.048	tlp-1	0	0.00606190348374073
AVA 0.048	unc-3	0.077709003809048	0.100656016791236
AVA 0.048	unc-30	0.119277135461456	NA
AVA 0.048	unc-42	0.065773985850975	0.0677750734238264
AVA 0.048	unc-55	0.017913608329954	NA
AVA 0.048	unc-86	0.0587586977033551	0.0619774732554145
AVA 0.048	Y53G8AR.9	0.00690384197900493	0.00515236165918147
AVA 0.048	Y56A3A.18	0.0298632149454741	0.0419267398727397
AVA 0.048	zag-1	0.104911111463118	0.099004361832111
AVA 0.048	zfh-2	0.0474330145259893	0.0514129018182148
AVA 0.048	ZK185.1	0.00910796980962854	NA
AVA 0.048	ZK546.5	0.102268729114546	0.199557694339809
AVA 0.048	ztf-26	0.0542790133937515	0.0186331381794253
AVB 0.045	aha-1	0.124614836395052	0.146352255393117
AVB 0.045	alr-1	0.152630349975705	NA
AVB 0.045	atf-7	0.0211635502480243	0.01515270069677
AVB 0.045	attf-6	0.00038218416535043	0.00505043533443741
AVB 0.045	cebp-1	0.0111317541187112	0.0126939385228416
AVB 0.045	ceh-40	0.0687378166034594	NA
AVB 0.045	crh-2	0.0346464196981759	0.0329069473289294
AVB 0.045	ctbp-1	0.129360431321126	0.118358488181474
AVB 0.045	D1046.2	0.0185380196024766	0.0191812753313478
AVB 0.045	daf-19	0.0908394792962827	0.0997139098508396
AVB 0.045	egl-13	0.027237858771569	0.0330901203216963
AVB 0.045	egl-18	0.0620323616016785	0.0672485278384501
AVB 0.045	ekl-4	0.0325839063149047	0.0403426151926404
AVB 0.045	elt-4	0.116760711862425	NA
AVB 0.045	fkh-10	NA	0.0152743453451157
AVB 0.045	hif-1	0.0135685958806635	0.0147085900313645
AVB 0.045	hinf-1	0.0867021874529637	0.107339726591158
AVB 0.045	hsf-1	0.0184985856436359	0.025661874541304
AVB 0.045	isw-1	0.0116066437511198	0
AVB 0.045	K12H6.12	0.0357036239669974	0.0299861252394043
AVB 0.045	lag-1	0.0315885878399739	0.0461489549089346

AVB 0.045	lim-7	0.00361358112533553	0.00112213562475328
AVB 0.045	lin-11	0.13730538799428	0.143073784591434
AVB 0.045	lin-14	0.0555064648125497	0.0556276847679607
AVB 0.045	lin-26	0.0850665096608162	0.0798330152569385
AVB 0.045	lin-39	0.00792027440969815	0.00710358611857658
AVB 0.045	lin-40	0.101930652138417	0.0792783961225723
AVB 0.045	lsy-2	0.0233380476048886	0.0234425687536858
AVB 0.045	madf-3	0.0465779216925146	0.0511132538845272
AVB 0.045	madf-5	0.0476892338541971	0.0257592886585651
AVB 0.045	mbf-1	0.0606219318876983	0.0819525015585893
AVB 0.045	mdt-29	0.0283808959402096	0.0327594500709226
AVB 0.045	mef-2	0.013258765119773	0.0377367985805304
AVB 0.045	nfyb-1	0.00215096603640353	0.00329828468278318
AVB 0.045	nhr-11	0.0149395647847915	NA
AVB 0.045	nhr-232	0.243657303114809	0.124980351702362
AVB 0.045	pag-3	0.0555007095416298	NA
AVB 0.045	pat-9	NA	0.134461513262305
AVB 0.045	R02D3.7	0.0124062421445303	0.0135597256454378
AVB 0.045	saeg-2	0	0.00423383762946662
AVB 0.045	sem-4	0.0645708121364345	0.0728411835739429
AVB 0.045	somi-1	0	0.00123336704433407
AVB 0.045	sptf-2	NA	0.297807509332748
AVB 0.045	syd-9	0.0180802149125335	0.0400525470899247
AVB 0.045	unc-42	0.0519266247255329	0.0424683720018609
AVB 0.045	unc-55	0.0173563687656609	0.0165941308041638
AVB 0.045	Y53G8AR.9	0.00792443817241469	0
AVB 0.045	Y56A3A.18	0.0288397908245801	0.0383342461939974
AVB 0.045	zag-1	0.138621287368439	0.128639637701287
AVB 0.045	zfh-2	0.0423821464056163	0.0475822174167734
AVB 0.045	ZK546.5	0.124796313532896	0.201885733513328
AVB 0.045	ztf-26	0.046955659519966	0.0335411880788373
AVD 0.041	aha-1	0.028253182209352	0.0556948477808371
AVD 0.041	ahr-1	0.113696917948839	NA
AVD 0.041	alr-1	0.154372057649112	NA
AVD 0.041	atf-7	0	0.00332594843218786
AVD 0.041	attf-6	0.0191315405836324	0.0187733384483523
AVD 0.041	C34B4.2	0.204516900787188	0
AVD 0.041	cebp-1	0.00985088043297257	0.0160734674103075
AVD 0.041	ceh-19	NA	0.0329840774045096
AVD 0.041	ceh-27	0.0182839261425803	NA
AVD 0.041	ceh-48	0	0.00230548584816692
AVD 0.041	crh-2	0.0324066177578776	0.0354941734684371
AVD 0.041	ctbp-1	0.132349887098741	0.132930483533991

AVD 0.041	D1046.2	0.0212873608533196	0.0212498594081012
AVD 0.041	daf-19	0.0855370773909366	0.0883020938393927
AVD 0.041	dsc-1	0.0144314167159588	NA
AVD 0.041	egl-13	0.017249902573065	0.0269553341163169
AVD 0.041	egl-18	0.108013648316884	0.0991407862820182
AVD 0.041	ekl-4	0.051948217907929	0.0562123746363734
AVD 0.041	elt-4	NA	0.13331461639828
AVD 0.041	F22D6.2	0.0307570883369261	0
AVD 0.041	fkh-8	0	0.00365294798677652
AVD 0.041	hif-1	0	0.00283731788574863
AVD 0.041	hinf-1	0.115654012951664	0.118135279426695
AVD 0.041	hlh-8	0.0048291416076429	0
AVD 0.041	isw-1	0.00288649457960511	0.0131510775222267
AVD 0.041	lag-1	0.0741681206800051	0.115338736256619
AVD 0.041	lim-7	0.0216795450765858	0.0181271399702484
AVD 0.041	lin-11	0.146737028471372	0.162230297117438
AVD 0.041	lin-13	0	0.00140048339202135
AVD 0.041	lin-14	0.0603192921059731	0.0592293770196665
AVD 0.041	lin-26	0.0689589447590535	0.0615809453782861
AVD 0.041	lin-40	0.0844026546994776	0.0478532661494806
AVD 0.041	lsy-2	0.0254416579058493	0.0261281524649794
AVD 0.041	madf-3	0.0470111160470293	0.0474938356417788
AVD 0.041	madf-5	0.0581889406634106	0.0213541042577546
AVD 0.041	madf-6	0.00428822248737639	0
AVD 0.041	madf-9	0.00518597401930272	0
AVD 0.041	mbf-1	0.116435970508131	0
AVD 0.041	mdt-29	0	0.00634919922901056
AVD 0.041	nfyb-1	0.00719649317503793	0.00744687705026928
AVD 0.041	nhr-11	0.0191156936553839	0.0174894912875805
AVD 0.041	nhr-232	NA	0.256423995531273
AVD 0.041	pag-3	0.0349515556011259	0.0234441718230985
AVD 0.041	pat-9	0.20785667741384	0.105822093971137
AVD 0.041	pbrm-1	0.0135860204380364	0.010874707367827
AVD 0.041	R02D3.7	0.0154846202940702	0.00973608969044387
AVD 0.041	saeg-2	0.0248708658138451	0.0370234752055847
AVD 0.041	sem-4	0.0143613093940917	0.0154969602765181
AVD 0.041	sox-4	NA	0.0019566928826702
AVD 0.041	sptf-2	0.289153655768626	0.317179013622552
AVD 0.041	tlp-1	NA	0.00179429006337539
AVD 0.041	unc-3	0.00317562964546074	0.022398110780366
AVD 0.041	unc-42	0.0640064213284639	0.0717106152363537
AVD 0.041	unc-55	0.0271164613697084	NA
AVD 0.041	unc-86	0.0188382651129425	0.0155529190121627

AVD 0.041	Y53G8AR.9	0.00699699220399221	0.00367834580229246
AVD 0.041	Y55F3AM.14	0.0290594000784716	0.0354620717403181
AVD 0.041	Y56A3A.18	0.0422794425509207	0.0427057185275736
AVD 0.041	zag-1	0.132890725825976	0.144841779657322
AVD 0.041	zfh-2	0.0531767432836381	0.0418917865166682
AVD 0.041	zim-3	0.00060386040206837	0
AVD 0.041	ZK185.1	NA	0.00037580628520147
AVD 0.041	ZK546.5	0.0719955974208114	0.113823915829097
AVD 0.041	ztf-26	0.0629228511209549	0.0122400456267752
AVE 0.045	aha-1	0.158284120411301	0.187685446759478
AVE 0.045	attf-6	0.0146521839204278	0.024171853353199
AVE 0.045	cebp-1	0	0.00212270584063426
AVE 0.045	ceh-19	0.00403420304229126	0
AVE 0.045	ceh-82	0.0045916389845873	NA
AVE 0.045	chd-7	0	0.00381053967958661
AVE 0.045	crh-2	0.0496879041300165	0.0482604658929318
AVE 0.045	ctbp-1	0.180739530171287	0.168070252209129
AVE 0.045	daf-19	0.0716148606000175	0.0719758367191018
AVE 0.045	egl-18	0.0962132484813725	0.0938736258400701
AVE 0.045	egl-27	0.0464006905305932	0.038602154139051
AVE 0.045	ekl-4	0.0526101944787975	0.0574247935402756
AVE 0.045	elt-4	NA	0.00397097421674512
AVE 0.045	ets-5	0.0201335042163144	NA
AVE 0.045	F22D6.2	0.0512388168528838	0.00131984930250769
AVE 0.045	F57A8.1	0	0.0137597628251924
AVE 0.045	fkh-10	0.0788293843191235	0.0901116344494695
AVE 0.045	hif-1	0.0322397100827095	0.0339171917290266
AVE 0.045	hinf-1	0.094131709943862	0.0963916664512155
AVE 0.045	hlh-8	0.00322645576562084	0
AVE 0.045	hsf-1	0.0104469726774368	0.00842507642459424
AVE 0.045	isw-1	0.0242221094240242	0.00804123903855818
AVE 0.045	lag-1	0.0641874381426045	0.0996755950157217
AVE 0.045	lim-7	0.00286064111998943	0.0150379803315817
AVE 0.045	lin-11	0.190054031091706	0.190819305792771
AVE 0.045	lin-14	0.0607960820671227	0.0614441172818971
AVE 0.045	lin-26	0.0945919235555005	0.0863273870145722
AVE 0.045	lin-40	0.110975017918424	0.0557135610009881
AVE 0.045	lin-54	2.78615656074046e-05	0.00834447898305031
AVE 0.045	lsy-2	0.0256925976515474	0.025000949036098
AVE 0.045	madf-3	0.0454593395294838	0.0488316406058144
AVE 0.045	madf-5	0.0956325202556433	0.0523020410323166
AVE 0.045	madf-9	0.00760030474109702	0
AVE 0.045	mbf-1	0.119885668559112	0.0762071985296428

AVE 0.045	mdt-29	0.0348327014153275	0.0393805694907959
AVE 0.045	nfya-2	0.00419656219043259	NA
AVE 0.045	nfyb-1	0.0102871710497208	0.0151544482041873
AVE 0.045	nhr-11	0.0159387637433172	NA
AVE 0.045	pag-3	0.0639060720187019	0.0625571478104753
AVE 0.045	pat-9	0.183634372997135	0.166240790441539
AVE 0.045	pbrm-1	0.0129503356203627	0.0142186068858634
AVE 0.045	R02D3.7	0.00940034878132737	0.01079825059585
AVE 0.045	sem-4	0.0600590397513682	0.0575718106338363
AVE 0.045	sptf-2	0.304603549473581	NA
AVE 0.045	sup-37	0.0700975176993999	0.00870603294614394
AVE 0.045	tra-1	0	0.00279988622471685
AVE 0.045	unc-42	0.0619919150300652	0.071972911955736
AVE 0.045	unc-86	0.0557917071653915	0.0591237289109904
AVE 0.045	Y53G8AR.9	0.0167567103198638	0.0144126696684134
AVE 0.045	Y56A3A.18	0.0379319064120183	0.032053918624742
AVE 0.045	zag-1	0.0340149586484066	0.0207234763808396
AVE 0.045	zfh-2	0.0507045543964162	0.0462114154862835
AVE 0.045	zim-3	0.0218633882899337	0.0136731837234845
AVE 0.045	ZK185.1	NA	0.0153293141070958
AVE 0.045	ZK546.5	0.0709727638657877	0.0753141762225593
AVE 0.045	ztf-26	0.068781315307612	0.0288851731721607
AVF 0.044	aha-1	0.240418225241544	0.213244883319852
AVF 0.044	atf-7	0.00981183292196301	0.0053811590529845
AVF 0.044	attf-6	0.0258198814181959	0.0189230854791598
AVF 0.044	B0035.1	0.0237672670288188	0
AVF 0.044	ceh-27	NA	0.0401327803046618
AVF 0.044	ceh-48	0.00561191253730013	0
AVF 0.044	ceh-6	0	0.00246723620585891
AVF 0.044	crh-2	0.0576875256557295	0.0697171496320257
AVF 0.044	ctbp-1	NA	0.118015904938986
AVF 0.044	daf-19	0.067775363378575	0.0908477034233414
AVF 0.044	drap-1	0	0.021935975418966
AVF 0.044	dxbp-1	0	0.00395459542674456
AVF 0.044	egl-13	0.0987170928824158	NA
AVF 0.044	ekl-4	NA	0.0638205005515757
AVF 0.044	F22D6.2	0.0120109082593243	0.0522419172501229
AVF 0.044	F57A8.1	0	0.0538943054682293
AVF 0.044	fkh-8	0.0108447497506924	NA
AVF 0.044	hif-1	0.0441659213215856	0.0405664951809088
AVF 0.044	hinf-1	0.12271575151865	NA
AVF 0.044	hsf-1	0.029902321374287	0.025009692865695
AVF 0.044	isw-1	0.0324184217001422	0.0568220935030517

AVF 0.044	lag-1	0.0688120915172268	0.100817692667584
AVF 0.044	lim-7	0.0103888890452543	0.042875618644366
AVF 0.044	lin-11	0.250623131224056	0.245855678054881
AVF 0.044	lin-13	0.00187182685869754	0
AVF 0.044	lin-14	0.0483816157286201	0.0491255780316138
AVF 0.044	lin-26	0.0685106114168427	0.077269420392447
AVF 0.044	lin-40	0.083245079782436	0.0542608943191848
AVF 0.044	lin-54	0.0125892216355491	NA
AVF 0.044	lsy-2	NA	0.0356077796371208
AVF 0.044	madf-5	0.0623835480530985	0.0718947520140805
AVF 0.044	madf-9	0.00867404081466099	NA
AVF 0.044	mbf-1	0.180641635953312	0.247575832016845
AVF 0.044	mdt-29	0.058381834257222	NA
AVF 0.044	mef-2	0.0339891346952524	0.0269389036581617
AVF 0.044	nfya-2	NA	0.0426218623317938
AVF 0.044	nfyb-1	0.0169595611974847	0.00906700149723471
AVF 0.044	nhr-232	0.320143465208415	NA
AVF 0.044	nhr-71	0.012120408040773	0.00475688998211661
AVF 0.044	pag-3	0.0508886881166695	0.0329910126805543
AVF 0.044	pbrm-1	0.00645581992376875	0.0306921704519978
AVF 0.044	R02D3.7	0.00552251855197638	NA
AVF 0.044	row-1	NA	0.106824908445259
AVF 0.044	sem-4	0.114948073937175	0.133054912895423
AVF 0.044	sptf-2	0.374042764612083	NA
AVF 0.044	T26A5.8	0.0640905454100918	0.0357337345341585
AVF 0.044	Y53G8AR.9	0.0275919088921871	NA
AVF 0.044	Y55F3AM.14	0.0220985337440025	0.0288312976720055
AVF 0.044	Y56A3A.18	0.0355706364319271	0.068572498411509
AVF 0.044	zag-1	0.125602817216505	NA
AVF 0.044	zfh-2	0.0447288405928935	0.0512517689724192
AVF 0.044	ZK185.1	NA	0.00813874844642494
AVF 0.044	ZK546.5	NA	0.057690667698677
AVF 0.044	ztf-26	NA	0.0456824141534371
AVG 0.044	aha-1	0.305747182504187	0.429736378364481
AVG 0.044	attf-6	0	0.00653728383039826
AVG 0.044	cebp-1	0.0192356095552531	0.0312904121662649
AVG 0.044	ceh-18	0	0.0168036360212492
AVG 0.044	chd-7	0	0.0341888167555934
AVG 0.044	crh-2	0.0289107469520495	0.0390910478602254
AVG 0.044	ctbp-1	0.188264083208637	0.19057618183435
AVG 0.044	daf-19	0.0944291378188251	0.111885242308928
AVG 0.044	egl-18	0.0461825680187051	NA
AVG 0.044	egrh-3	0.0194499747011327	0.00839641005658039

AVG 0.044	ekl-4	0.0384813433991864	0.0533976680496492
AVG 0.044	F22D6.2	0.00362747144125435	0
AVG 0.044	F57A8.1	0.0774504820442442	0.0769850831608518
AVG 0.044	gei-8	0	0.00770429667453716
AVG 0.044	hif-1	0.00702782116190339	0.0226885153377698
AVG 0.044	hinf-1	0.0819897833790362	0.11005198336046
AVG 0.044	hmg-1.1	0.0123845630899036	0.0244885678937847
AVG 0.044	hsf-1	0.019477979462343	0.0394308026474101
AVG 0.044	isw-1	0	0.000447061585040347
AVG 0.044	lag-1	0.0364123749899728	NA
AVG 0.044	lin-11	0.173698222618648	0.231687096012139
AVG 0.044	lin-26	0.0931407697046464	0.0874579593983624
AVG 0.044	lin-40	0.140560929706263	0.053509427264983
AVG 0.044	lsy-2	0.0400067573813501	0.0529007361906233
AVG 0.044	madf-3	0.0402552378081108	NA
AVG 0.044	madf-5	0.0470323439192034	NA
AVG 0.044	mdt-29	0.0359251659114984	0.0409302888407383
AVG 0.044	mef-2	0.0268637260486661	0.0505289770426968
AVG 0.044	nfya-2	0.000424354993736079	0.033167950006611
AVG 0.044	nfyb-1	0.0150173035242933	0.0297762175644952
AVG 0.044	nhr-11	0.0689991862937064	NA
AVG 0.044	nhr-232	0.0995426683635158	NA
AVG 0.044	nhr-71	0.00343914506064424	0.0245811284365417
AVG 0.044	pat-9	0.0967846630707752	NA
AVG 0.044	pbrm-1	0.00399516838139895	0.026497964021202
AVG 0.044	sem-4	0.000867574413430699	0
AVG 0.044	syd-9	0.0493337230847291	0.126050236180853
AVG 0.044	unc-120	0.0148682409938651	NA
AVG 0.044	unc-62	0	0.00475306934392143
AVG 0.044	Y53G8AR.9	NA	0.0151560205102672
AVG 0.044	Y56A3A.18	0.0103647100884454	0.0288348254362075
AVG 0.044	zag-1	0.18384581773908	0.189510754489131
AVG 0.044	zim-3	0	0.00112285145770096
AVG 0.044	ZK546.5	0.0366816189851739	0.0636862729353653
AVJ 0.041	aha-1	0.0824606277280758	0.107453288896612
AVJ 0.041	ahr-1	NA	0.160780615119171
AVJ 0.041	alr-1	NA	0.205293219882758
AVJ 0.041	atf-7	0.0105078498138066	0.00299874429809199
AVJ 0.041	attf-6	0.00394109904626765	0.00582745338614697
AVJ 0.041	cebp-1	0.0169000298794992	0.0194990139897514
AVJ 0.041	ceh-19	NA	0.0815121518172309
AVJ 0.041	crh-2	0.0372919779312391	0.0399106629886148
AVJ 0.041	ctbp-1	0.106060265318151	0.0885566617542533

AVJ 0.041	daf-19	0.10584124755311	0.108013557461268
AVJ 0.041	dxbp-1	0.0107122056116768	0.0141739262331927
AVJ 0.041	egl-13	0.00620597065964605	0.0220111398021894
AVJ 0.041	egl-18	0.120875130350581	0.110873057480545
AVJ 0.041	ekl-4	0.0568468369216649	0.0557358600587621
AVJ 0.041	F22D6.2	0.0323508434898676	0.0122256719697734
AVJ 0.041	hif-1	0.0167092130681286	0.0224389116637631
AVJ 0.041	hinf-1	0.120985649332821	0.135685732947342
AVJ 0.041	hlh-8	0.0246156993869365	NA
AVJ 0.041	isw-1	0	0.00195361518228189
AVJ 0.041	klu-1	0.0122902873620349	0
AVJ 0.041	lag-1	0.0584755673944382	0.0885092055272781
AVJ 0.041	lim-7	0.06119429459424	0.0694481904858803
AVJ 0.041	lin-11	0.136701352490564	0.145090023533431
AVJ 0.041	lin-14	0.0546012759024098	0.0555377380855686
AVJ 0.041	lin-26	0.0808997335650502	0.073193753243242
AVJ 0.041	lin-39	0.013094371567312	0.0139039450906652
AVJ 0.041	lin-40	0.0758319594399238	0.0508026770713986
AVJ 0.041	lsy-2	0.018858069782017	0.016384977405184
AVJ 0.041	madf-3	0.0554779809802298	0.0541763899627297
AVJ 0.041	madf-5	NA	0.0842338850150339
AVJ 0.041	madf-6	0.000371740566539823	0
AVJ 0.041	mbf-1	0.0607995806590335	0.0233446725876105
AVJ 0.041	mdt-29	0.00935742581078716	0.0127616115969159
AVJ 0.041	nfya-2	0.00385436611314416	0.00487617323742867
AVJ 0.041	nfyb-1	0.0114049353304311	0.00810634348469207
AVJ 0.041	nhr-11	0.0249701228997069	0.0220129157150716
AVJ 0.041	nhr-232	0.647275854145576	0.566487044336457
AVJ 0.041	pag-3	0.0347821839193636	0.0238410585022673
AVJ 0.041	pat-9	NA	0.121647654616619
AVJ 0.041	pbrm-1	0.000401146250471302	0.00621120881554976
AVJ 0.041	sem-4	0.0316212638871125	0.0409515929790497
AVJ 0.041	sptf-2	0.387104243603975	NA
AVJ 0.041	syd-9	0.0691798373400324	0.0277446357139261
AVJ 0.041	T26A5.8	0.0134102780614059	0
AVJ 0.041	unc-120	0.00564782439656015	NA
AVJ 0.041	unc-30	0.242299585096727	0.245750701238909
AVJ 0.041	unc-42	0.0594252733290481	0.0594789413502831
AVJ 0.041	unc-55	0.02607526687543	0.0360805047035627
AVJ 0.041	unc-86	0.0463595339371094	NA
AVJ 0.041	Y53G8AR.9	0.0140886529792995	0.0167903959536878
AVJ 0.041	Y56A3A.18	0.0354955637053883	0.0361396841865087
AVJ 0.041	zag-1	0.119741743200531	0.123932365446567

AVJ 0.041	zfh-2	0.0467369141770722	0.0430987554384991
AVJ 0.041	ZK546.5	0.113587589802034	0.157861982223387
AVJ 0.041	ztf-26	0.0472896086631156	0.0087756777748941
AVK 0.039	aha-1	0.0691018486606453	0.0634520386721372
AVK 0.039	atf-7	0.0296828709182932	0.0302739477073937
AVK 0.039	attf-6	0.0115191671897655	0.0174572096314843
AVK 0.039	ceh-27	NA	0.0999355754529295
AVK 0.039	ceh-63	0.151256690109864	NA
AVK 0.039	crh-2	0.047485496329331	0.0548685930795489
AVK 0.039	ctbp-1	0.0944297272227153	0.10371006259988
AVK 0.039	daf-19	0.0813612482823253	NA
AVK 0.039	dxbp-1	0	0.00367756026378631
AVK 0.039	egl-13	0.111633827886484	0.144596071899487
AVK 0.039	egl-18	0.0946970058129074	0.114896892921959
AVK 0.039	egl-27	0.00359261856038744	0.0155712784792369
AVK 0.039	ekl-4	0.0386986302047795	0.0455670544568602
AVK 0.039	elt-4	0.00636767307568304	0
AVK 0.039	F22D6.2	0.00107934771014984	0
AVK 0.039	F33H1.4	0	0.00108999890870279
AVK 0.039	F57A8.1	0	0.16642125023334
AVK 0.039	hif-1	0.00436087390860903	0.0125050378339994
AVK 0.039	hinf-1	0.117655632462708	0.136042424536334
AVK 0.039	hlh-8	NA	0.0246930878275617
AVK 0.039	hsf-1	0.0217452017837817	0.0271035361470649
AVK 0.039	isw-1	0.0419029534059547	0.0771866380702804
AVK 0.039	lag-1	0.0513760891310322	0.0844110244003098
AVK 0.039	lim-6	0.0572313132972595	0.0660854186041568
AVK 0.039	lim-7	0.0351511994906267	0.0588331914464111
AVK 0.039	lin-11	0.184872082598491	NA
AVK 0.039	lin-13	0.000559319871021544	0.0132655909187295
AVK 0.039	lin-14	0.022945313318318	0.0273650089142245
AVK 0.039	lin-26	0.0638687395700564	0.0629367880921309
AVK 0.039	lin-40	0.0741982731748179	0.0397910808614723
AVK 0.039	lsy-2	0.0194901497196137	NA
AVK 0.039	madf-3	0.043594420389661	0.0558610691477594
AVK 0.039	madf-5	0.0723603657076875	0.046265846890099
AVK 0.039	madf-6	0	2.18530883891999e-05
AVK 0.039	mbf-1	0.108349176202844	0.0603197536521457
AVK 0.039	mdt-29	0.0203492595882248	0.0356548098629404
AVK 0.039	mef-2	0.0875226731115371	0.117461422816422
AVK 0.039	mxl-1	0	0.00288129073620419
AVK 0.039	nfya-2	0	0.0017929818782646
AVK 0.039	nfyb-1	0.00244078252462356	0.00875076191608897

AVK 0.039	nhr-11	0.0354602446568787	NA
AVK 0.039	nhr-129	0	0.0011065213648195
AVK 0.039	nhr-232	0.0447591514388478	NA
AVK 0.039	nhr-6	0.00527336828984274	0.0151379872839974
AVK 0.039	nhr-71	0	0.000934315663548768
AVK 0.039	pat-9	NA	0.188832943219174
AVK 0.039	pbrm-1	0	0.00199694910270505
AVK 0.039	R02D3.7	0.00570484381688067	0.0251064660524406
AVK 0.039	row-1	0.00438310592347273	0.0898471244289237
AVK 0.039	sem-4	NA	0.0317225305429859
AVK 0.039	sptf-2	0.376457684550973	NA
AVK 0.039	unc-120	0.00236014384895281	0
AVK 0.039	unc-42	0.0175289401086781	0.0205011208594974
AVK 0.039	unc-55	0.00113498560585011	NA
AVK 0.039	unc-86	0.00289160837740898	0.013216580485719
AVK 0.039	Y53G8AR.9	0.0132711046159365	0.0103618617444693
AVK 0.039	Y55F3AM.14	0.00597426662934106	NA
AVK 0.039	Y56A3A.18	0.0450539112348537	0.0432418328962793
AVK 0.039	zag-1	0.119789566526908	0.132559228960612
AVK 0.039	zfh-2	0.0526721362896723	0.0505811658418926
AVK 0.039	ZK546.5	0.0509583595834422	0.120788284272434
AVK 0.039	ztf-26	0.0422011798058559	0.00857643762975478
AVL 0.042	alr-1	0.191583954858624	0.179089162083887
AVL 0.042	atf-7	0.0287789939860916	0.0312891948161336
AVL 0.042	attf-6	0.0133960605397621	0.0183797666111172
AVL 0.042	ceh-27	0.13673735699747	0.132802167928976
AVL 0.042	ceh-48	0.00803625995386268	0.00709812760732648
AVL 0.042	ceh-63	NA	0.345113613935454
AVL 0.042	crh-2	0.043050078043418	0.0452040826294041
AVL 0.042	ctbp-1	0.102632594273562	0.110777070230289
AVL 0.042	daf-19	0.178121579088823	0.172769211281659
AVL 0.042	egl-18	0.0880823255944971	0.0994514074904303
AVL 0.042	egl-27	0.00647755033610515	0
AVL 0.042	egrh-3	0.0209110996455799	NA
AVL 0.042	ekl-4	0.0317452525101289	0.0484401845453442
AVL 0.042	F22D6.2	0.0802723466013186	0
AVL 0.042	fkh-10	0.0437914494971102	NA
AVL 0.042	hinf-1	0.111143646077289	0.115986013030285
AVL 0.042	hsf-1	0.0101419954706769	0.0192291232230611
AVL 0.042	lag-1	0.0292107007015903	0.0574561797085656
AVL 0.042	lim-6	0.140761029375475	0.111860315920028
AVL 0.042	lim-7	0.0324177222912254	0.0348250244424874
AVL 0.042	lin-11	0.183527540493322	0.192582525027573

AVL 0.042	lin-13	0.0058641063594704	0.00647025872795619
AVL 0.042	lin-14	0.0215972785636327	0.0274750456105169
AVL 0.042	lin-26	0.0820531202040408	0.0607466624545201
AVL 0.042	lin-40	0.0538927162125654	0.0120850210277013
AVL 0.042	lsy-2	0.0286895942061909	0.0270115848891154
AVL 0.042	madf-3	0.0507666050572232	NA
AVL 0.042	madf-5	0.0896955764185614	0.0547446110481106
AVL 0.042	mdt-29	0.0183207083883995	0.0210325352481324
AVL 0.042	nfya-1	NA	0.00507858689423551
AVL 0.042	nhr-11	0.0269209032551138	NA
AVL 0.042	nhr-232	0.0663214837264586	NA
AVL 0.042	pag-3	NA	0.043912330316657
AVL 0.042	pat-9	0.215971040629207	NA
AVL 0.042	R02D3.7	0.00702315189984373	0.00778486614482346
AVL 0.042	row-1	0.0532135649703761	0.0601942319952944
AVL 0.042	sem-4	0.0129159472295038	0.00783931515419464
AVL 0.042	sptf-2	NA	0.348509056744762
AVL 0.042	unc-86	0.041244542871289	0.0500491381404441
AVL 0.042	Y53G8AR.9	0.0238153438933218	0.0196691779591451
AVL 0.042	Y55F3AM.14	0.0409834620851291	NA
AVL 0.042	Y56A3A.18	0.0317068569916029	0.0335359051220208
AVL 0.042	zag-1	0.085025735833078	0.116037517640692
AVL 0.042	zim-3	0.0351222033268328	0.0246623062944228
AVL 0.042	ZK546.5	0.0513027749771303	0.102608351764045
AVL 0.042	ztf-1	0.0439761669676716	0.058896746650206
AVL 0.042	ztf-26	0.0841365083656001	0.0102124357022535
AWA 0.045	aha-1	0.2499889083361	0.257677125419434
AWA 0.045	alr-1	0.20790444229511	0.203157678629621
AWA 0.045	attf-6	0.0122188763879325	0.00983334990858987
AWA 0.045	C34B4.2	0.117343664379394	0
AWA 0.045	crh-2	0.0351898477813564	0.0325770316771453
AWA 0.045	ctbp-1	NA	0.104774452795813
AWA 0.045	D1046.2	0.0282151724469635	0.000471612489725118
AWA 0.045	daf-19	0.109422256908685	0.11684647681901
AWA 0.045	dxbp-1	0.0111149178120497	0.00734840933592534
AWA 0.045	egl-13	NA	0.0261958993523314
AWA 0.045	egl-18	0.107172368152318	NA
AWA 0.045	ekl-4	0.0494586529218649	0.0525336668754631
AWA 0.045	elt-4	0.065185356139285	NA
AWA 0.045	F22D6.2	0.103404298291963	0
AWA 0.045	F44E2.7	0.00501200780784071	0
AWA 0.045	fkh-8	0.129976890829218	0.145298741560769
AWA 0.045	hif-1	0.0128923887522276	0.014749129994517

AWA 0.045	hinf-1	0.120986191216479	0.124676200605831
AWA 0.045	hmg-1.1	0.00106784610107481	0
AWA 0.045	hsf-1	0.0437210322170004	0.0264181652006268
AWA 0.045	K12H6.12	0.097078466545421	0.0833559976061127
AWA 0.045	lag-1	0.0222636157946527	0.0555050760275601
AWA 0.045	lim-7	NA	0.0230338740014666
AWA 0.045	lin-11	0.148829741300904	0.13550628702142
AWA 0.045	lin-26	0.142561732632787	0.105374186711278
AWA 0.045	lin-39	0.000702133731101328	0
AWA 0.045	lin-40	0.160076231808131	0.0342376539229877
AWA 0.045	lsy-2	0.0175106771485736	0.0100160917566706
AWA 0.045	madf-3	NA	0.065047219099169
AWA 0.045	madf-6	4.49256752928685e-05	0
AWA 0.045	mdt-29	0.0435991512442419	0.0523971330531212
AWA 0.045	mml-1	NA	0.0868438987058047
AWA 0.045	nhr-11	0.0886159538374504	0.0798651935964271
AWA 0.045	nhr-71	0.0185062859551031	0.00808563235966779
AWA 0.045	pbrm-1	0.0115738382441262	0
AWA 0.045	R02D3.7	0.00717440674260744	0.0125771347978534
AWA 0.045	row-1	0.00716691686118954	0
AWA 0.045	sem-4	0.0235186821799028	NA
AWA 0.045	sox-4	0.113545449860593	0.100892494148995
AWA 0.045	unc-42	0.00394425302503536	0
AWA 0.045	Y53G8AR.9	0.019605730551655	0.0143549894147576
AWA 0.045	Y56A3A.18	0.047624444281344	0.0387212800312747
AWA 0.045	zfh-2	0.0503723434279173	0.0326018600005905
AWA 0.045	zim-3	0.0399105230115138	NA
AWA 0.045	ZK546.5	0	0.177379379928174
AWA 0.045	ztf-26	0.0743829817525511	0
AWB 0.049	aha-1	0.284033760016303	0.296440699023802
AWB 0.049	arid-1	NA	0.00566495286629582
AWB 0.049	attf-6	0.0129258911443914	0.0173252965554439
AWB 0.049	ceh-18	0.0297478314240902	0
AWB 0.049	crh-2	0.0386562624578745	0.0355047939163593
AWB 0.049	D1046.2	0.0285097890252531	0.0259280633674543
AWB 0.049	daf-19	0.0907860347057739	0.0953248209856912
AWB 0.049	dxbp-1	0.00223675701769615	0.00222347771431277
AWB 0.049	egl-13	0.0283054076778948	0.0341450836213598
AWB 0.049	egl-27	0.00508095002128142	0.00573068693272049
AWB 0.049	ekl-4	0.0606670085029996	0.0599140785487884
AWB 0.049	elt-4	NA	0.0703098371151183
AWB 0.049	F22D6.2	0.128280209620385	0.0530850746593773
AWB 0.049	F57A8.1	0.156832826480955	0.194584876115863

AWB 0.049	fkh-8	0.103273516385995	0.115482988185592
AWB 0.049	hif-1	0.0431965570726591	0.0375728328107552
AWB 0.049	hinf-1	0.112086304247837	0.124163137397024
AWB 0.049	hsf-1	0.00190931432843103	0.000914773297727161
AWB 0.049	isw-1	0.0199654231630784	0.0087547456697949
AWB 0.049	K12H6.12	NA	0.0133477365980094
AWB 0.049	lag-1	0.0255307561222697	0.0429442779563263
AWB 0.049	lim-6	0.0019102036453688	0
AWB 0.049	lim-7	0.0473261050808156	0.0746785965570054
AWB 0.049	lin-11	0.271687552662127	0.292851576140325
AWB 0.049	lin-14	0.01530743310217	0.00582166506562005
AWB 0.049	lin-26	0.118860264968248	NA
AWB 0.049	lin-40	0.111880031568425	0.0676269413235079
AWB 0.049	lsy-2	0.00532323770093489	0.00279189116203134
AWB 0.049	madf-3	NA	0.0747367766365287
AWB 0.049	madf-6	0	0.000205546696858517
AWB 0.049	madf-9	0.0421801966321879	0.0145258009765207
AWB 0.049	mdt-29	0.0303617191873451	0.0438006013087722
AWB 0.049	nfya-2	0.0288615528702788	0.00995287084272776
AWB 0.049	nfyb-1	0	0.00307308292340425
AWB 0.049	nhr-11	0.0333282685994001	0.0213301629227115
AWB 0.049	nhr-129	0.00586092072915731	0
AWB 0.049	nhr-71	0.0172843334859986	0.00350237498112173
AWB 0.049	pag-3	NA	0.0468239674786754
AWB 0.049	pat-9	NA	0.0997967831042796
AWB 0.049	pbrm-1	0.0273462905211621	0.0206025727196539
AWB 0.049	sem-4	0.0278939379809856	NA
AWB 0.049	sox-4	0.319608300991304	0.288982468252604
AWB 0.049	syd-9	0.0542339623983012	0.0269171226307277
AWB 0.049	T26A5.8	0.0392932218526012	0
AWB 0.049	unc-42	NA	0.00949531352044648
AWB 0.049	unc-86	0.0160055213418414	NA
AWB 0.049	Y53G8AR.9	0.0226560494576373	0.0195461675734091
AWB 0.049	Y56A3A.18	0.0389965426846453	0.0317434326013703
AWB 0.049	zfh-2	0.052737171296228	0.044851067769467
AWB 0.049	zim-3	0.02417206646945	0.0101791697905228
AWB 0.049	ZK546.5	0.0230483682364759	0.105439944310471
AWB 0.049	ztf-26	0.103419460088482	0.0700825654903904
AWB 0.049	ztf-4	0.0103920316209582	0.0254713124827018
AWC 0.045	aha-1	0.326875454175487	0.317465522047919
AWC 0.045	alr-1	NA	0.135868375362769
AWC 0.045	attf-6	0	0.00983806739283829
AWC 0.045	ceh-13	NA	0.00452614774315151

AWC 0.045	ceh-27	0.0663190691782332	NA
AWC 0.045	chd-7	0	0.0136062567055739
AWC 0.045	crh-2	0.0424722695746049	0.0556128459220028
AWC 0.045	ctbp-1	0.111224394150899	NA
AWC 0.045	D1046.2	0.00364878472114714	0.0261265402665785
AWC 0.045	daf-19	0.0540592858351238	0.105696089006604
AWC 0.045	dsc-1	0.141304224862965	0.139728382752794
AWC 0.045	dxbp-1	0	0.00554290119870558
AWC 0.045	egl-18	0.0550957113831146	NA
AWC 0.045	ekl-4	0.0276712798666811	0.0597095560097985
AWC 0.045	elt-4	NA	0.0364060585243127
AWC 0.045	F57A8.1	0.115545529934142	0.0618602538541834
AWC 0.045	fkh-8	0.0609798187324354	0.0926810532780668
AWC 0.045	hif-1	0.00686150095795207	0.0229897198231057
AWC 0.045	hinf-1	0.10325650981232	NA
AWC 0.045	hmg-1.1	0	0.00562738282491609
AWC 0.045	hsf-1	0.0403343106669085	0.044796740995792
AWC 0.045	K12H6.12	0.0778876393334995	0.145480580267202
AWC 0.045	lag-1	0	0.0271835980593573
AWC 0.045	lim-7	0.0226928230024001	0.0519385071628069
AWC 0.045	lin-11	0.189246343259157	NA
AWC 0.045	lin-26	0.0815369462935319	0.083403921719624
AWC 0.045	lin-40	0.107485990723841	0.0753705854178065
AWC 0.045	lsy-2	0.00913648491944859	NA
AWC 0.045	madf-5	0.0685699328193965	NA
AWC 0.045	madf-6	0	0.00740209701320919
AWC 0.045	mdt-29	0.100752149455406	NA
AWC 0.045	nfya-2	0.00485796710652675	0.0099639876161637
AWC 0.045	nhr-11	0.069206232658059	0.0718632822584706
AWC 0.045	pag-3	NA	0.0163420142808922
AWC 0.045	pbrm-1	0	0.00804332420870891
AWC 0.045	saeg-2	0	0.0201309958508614
AWC 0.045	sem-4	0.0193159754030626	0.0349716131679407
AWC 0.045	sox-4	0.299148130023512	0.272570933895493
AWC 0.045	sptf-2	NA	0.332583560817454
AWC 0.045	T26A5.8	0	0.0132500710753548
AWC 0.045	Y53G8AR.9	0.0198131977353182	0.0375014159695168
AWC 0.045	Y56A3A.18	0.00540086595354938	0.0353270704983997
AWC 0.045	zfh-2	0.0380149395807208	0.0381140666541697
AWC 0.045	ZK546.5	0.0730754894105805	0.147730527612504
AWC 0.045	ztf-4	0	0.00433087919733667
Amphid sheath 0.037	alr-1	0.21841580816579	0.240161826820638
Amphid sheath 0.037	attf-6	0.0162248356779698	0.0181267996742867

Amphid sheath 0.037	blmp-1	0.000902185867789757	0
Amphid sheath 0.037	C16A3.4	0	1.25322760218686e-05
Amphid sheath 0.037	ceh-18	0.00140356149177942	0
Amphid sheath 0.037	ceh-40	0.0877303187727012	NA
Amphid sheath 0.037	crh-2	0.00504094453421254	0.00932877530117813
Amphid sheath 0.037	ctbp-1	0.00159656780573322	0.00574286431667809
Amphid sheath 0.037	daf-19	0.0669719633451806	0.0982238885324027
Amphid sheath 0.037	dxbp-1	0.0011364733955478	0.0088145499218223
Amphid sheath 0.037	egl-18	0	0.00871926570187728
Amphid sheath 0.037	egrh-3	0.00330010749813595	0.00192029720203623
Amphid sheath 0.037	ekl-4	0.088174110463894	0.0974721497409361
Amphid sheath 0.037	elt-4	0.10968187279558	0.0864388320238927
Amphid sheath 0.037	F22D6.2	0.119602755233525	0.055152613240419
Amphid sheath 0.037	F33H1.4	0.017288863716638	0.0263707807441798
Amphid sheath 0.037	hinf-1	0.131811980980469	0.151807148634326
Amphid sheath 0.037	hlh-8	0.0411748222165327	0.0330979735666511
Amphid sheath 0.037	hsf-1	0	0.00475815244192421
Amphid sheath 0.037	lag-1	0.0060391519117195	0.0409338259410727
Amphid sheath 0.037	let-607	0.0110433958935406	0.0145877772500154
Amphid sheath 0.037	lim-7	0.0068899326096766	0.0200331745401785
Amphid sheath 0.037	lin-26	0.115426285960308	0.115018832783997
Amphid sheath 0.037	lin-40	0.164191410150626	0.121057386712561
Amphid sheath 0.037	lin-54	0.00773369656060276	0.0126481018389086
Amphid sheath 0.037	lsy-2	0.0163874788202884	0.020177711056835
Amphid sheath 0.037	madf-3	0.0415410694982115	0.0523695580522296
Amphid sheath 0.037	madf-5	0.218163103361367	0.207667288954899
Amphid sheath 0.037	madf-6	0.000277619662334983	0.0061476988399631
Amphid sheath 0.037	madf-9	0.0515379650571759	0.0278739822314883
Amphid sheath 0.037	mdt-29	0.0298384802309872	0.038153342559227
Amphid sheath 0.037	nhr-102	0	0.00311997296480037
Amphid sheath 0.037	nhr-11	0.0324288932706822	0.0257586166790029
Amphid sheath 0.037	nhr-179	0.159677882457891	0.106159010855357
Amphid sheath 0.037	pag-3	0.0895338348989211	0.0773508574816913
Amphid sheath 0.037	pat-9	0.277600752369377	0.241859876705412
Amphid sheath 0.037	pbrm-1	0.017068362287543	0.0181741921466877
Amphid sheath 0.037	R02D3.7	0.0181727538738741	0.0188949722021644
Amphid sheath 0.037	skn-1	0.000784811966220936	0
Amphid sheath 0.037	sptf-2	0.368822182998932	0.444993826448635
Amphid sheath 0.037	sup-37	0.00788492572664762	0
Amphid sheath 0.037	tlp-1	0.00577301258325431	0.0155699582573967
Amphid sheath 0.037	Y53G8AR.9	0.0178535775805288	0.0115284616357765
Amphid sheath 0.037	Y56A3A.18	0.050935252081691	0.0672224159179867
Amphid sheath 0.037	zfh-2	0.0482804947472911	0.0474782892717983

Amphid sheath 0.037	zim-3	0.104536572481921	0.105808180821669
Amphid sheath 0.037	ZK546.5	0.0138444204852833	0.0472913118119643
Amphid sheath 0.037	ztf-1	0.0460603205089098	0.0714761578018837
Amphid sheath 0.037	ztf-26	0.134798233362945	0.0996411760137732
Anal muscle 0.050	alr-1	0.29397698640604	0.281261340869925
Anal muscle 0.050	attf-6	0.0171137706389385	0.0217136808919982
Anal muscle 0.050	C16A3.4	0.0133026634387347	0.00674901279003721
Anal muscle 0.050	cebp-1	0.00101055928609583	0.0021452984595002
Anal muscle 0.050	ceh-18	0.223455740318218	0.201669346105664
Anal muscle 0.050	ceh-40	NA	0.137653447147029
Anal muscle 0.050	chd-7	0.0187995033889106	0.0242221181515786
Anal muscle 0.050	daf-16	0.0129593024396791	0.00925164574518892
Anal muscle 0.050	daf-19	0.109746330174956	0.0981604822950156
Anal muscle 0.050	dsc-1	0.113183595121184	0.110295852058085
Anal muscle 0.050	dxbp-1	0.0150015378173915	0.00786868029381382
Anal muscle 0.050	egl-18	0.0603554266445051	0.0735797834288347
Anal muscle 0.050	ekl-4	0.0925692030215867	0.112322970690135
Anal muscle 0.050	elt-4	NA	0.0176024408059159
Anal muscle 0.050	F22D6.2	0.0819758339134504	0.0409972083265221
Anal muscle 0.050	F33H1.4	0.047720280062142	0.0427638094630261
Anal muscle 0.050	hinf-1	0.165423558124959	0.150373996811397
Anal muscle 0.050	hlh-1	NA	0.0313855984242513
Anal muscle 0.050	hlh-8	0.181639207178021	0.154669118236112
Anal muscle 0.050	hsf-1	0.0306929442615721	0.0348367360747662
Anal muscle 0.050	let-607	0.00346966367879552	0.00371257245591452
Anal muscle 0.050	lim-7	NA	0.0500219491384795
Anal muscle 0.050	lin-26	0.118935890570933	0.106675341545378
Anal muscle 0.050	lin-40	0.0628554380740116	0.0682957596523494
Anal muscle 0.050	lin-54	0.0267450024770388	NA
Anal muscle 0.050	lsy-2	0.0444262333279802	0.0363978795033772
Anal muscle 0.050	madf-5	0.161418874826139	NA
Anal muscle 0.050	madf-6	0.0426642545741392	0.0430565004459159
Anal muscle 0.050	nfya-2	NA	0.00106730368801838
Anal muscle 0.050	nhr-11	0.0174935276844923	0.0170556564007462
Anal muscle 0.050	nhr-179	NA	0.0599697353337268
Anal muscle 0.050	nhr-19	0.0187062891694591	0.0207313114804309
Anal muscle 0.050	nhr-71	0.0234777332488019	NA
Anal muscle 0.050	pat-9	0.676742987765571	0.600625483818868
Anal muscle 0.050	pbrm-1	0.0128700521275906	0.00568352056277749
Anal muscle 0.050	R02D3.7	0.0294970172207294	0.0328827283065861
Anal muscle 0.050	skn-1	0.00472937495913896	0.00560187526280029
Anal muscle 0.050	somi-1	0.012301806358875	0.0357319470854428
Anal muscle 0.050	sptf-2	NA	0.492361703936843

Anal muscle 0.050	sup-37	0.178859917366774	0.13639080441203
Anal muscle 0.050	syd-9	0.0186865666165032	0.0236990830736169
Anal muscle 0.050	unc-120	0.0488835455878201	0.030828545551678
Anal muscle 0.050	Y53G8AR.9	0.0159000887178422	0.0219136059720098
Anal muscle 0.050	Y56A3A.18	0.0508807132505984	0.0552367325685687
Anal muscle 0.050	zfh-2	0.0547943582961943	0.0571850933694494
Anal muscle 0.050	zim-3	0.0185434939233273	NA
Anal muscle 0.050	zip-11	0.00663209914878895	NA
Anal muscle 0.050	ztf-26	0.0400797596611817	NA
Apoptotic germ cells 0.026	alr-1	0.273153166194542	0.275624614080334
Apoptotic germ cells 0.026	C06A6.2	0	0.000731760381642472
Apoptotic germ cells 0.026	C16A3.4	0.0313641585455788	0.031982877875683
Apoptotic germ cells 0.026	cebp-1	0.00372536422377731	0.0074130849745948
Apoptotic germ cells 0.026	ceh-40	0.0907187083187589	0.0938031181167756
Apoptotic germ cells 0.026	daf-19	0.0583240928220261	0.0585933380729996
Apoptotic germ cells 0.026	dpl-1	0.03603388253762	0.0384234803234523
Apoptotic germ cells 0.026	dxbp-1	0.00309846753295968	0.00380989018227221
Apoptotic germ cells 0.026	efl-1	0.01902117581178	0.0205556756217083
Apoptotic germ cells 0.026	ekl-4	0.081764684584074	0.0838162591721122
Apoptotic germ cells 0.026	elt-4	0.0549541753732241	0.0237661371662382
Apoptotic germ cells 0.026	F22D6.2	0.0770690624733319	0.00219825564120663
Apoptotic germ cells 0.026	F23B12.7	0.00543115708540196	2.08479210366905e-05
Apoptotic germ cells 0.026	F33H1.4	0.0939184084705821	0.0959436286824446
Apoptotic germ cells 0.026	F44E2.7	0.0119954617897284	0.0126685585286481
Apoptotic germ cells 0.026	hinf-1	0.121547347711757	0.12202791255176
Apoptotic germ cells 0.026	hlh-8	0.0113040441811919	0.00166236277171076
Apoptotic germ cells 0.026	hsf-1	0.0189528027479706	0.0228081166987803
Apoptotic germ cells 0.026	lag-1	0.00259019315707989	0.0310143488452279
Apoptotic germ cells 0.026	let-607	0.0184954991680029	0.0173502781855966
Apoptotic germ cells 0.026	lim-7	0.0214107279023329	0.0257650122777798
Apoptotic germ cells 0.026	lin-26	0.115014808917818	0.108684587510937
Apoptotic germ cells 0.026	lin-38	0.00819305690023799	0.00878077496416287
Apoptotic germ cells 0.026	lin-40	0.0532037017573175	0.0150236316389363
Apoptotic germ cells 0.026	lin-54	0.0200243033129567	0.0209814073598799
Apoptotic germ cells 0.026	lsy-2	0.0406950008349045	0.0395721584912672
Apoptotic germ cells 0.026	madf-3	0.0834283288486293	0.0887050109641195
Apoptotic germ cells 0.026	madf-5	0.11843967542332	0.0881358332024312
Apoptotic germ cells 0.026	madf-6	0.0539040324829451	0.0583476647731507
Apoptotic germ cells 0.026	madf-9	0.0198841141365131	0
Apoptotic germ cells 0.026	nhr-179	0.0139446520590773	0
Apoptotic germ cells 0.026	nhr-232	0.013148226590114	0.0251594090092686
Apoptotic germ cells 0.026	pag-3	0.0283682912372218	0.0170198916089205
Apoptotic germ cells 0.026	pat-9	0.17608281560185	0.151745111488244

Apoptotic germ cells 0.026	R02D3.7	0.0210606470738846	0.01945769175957
Apoptotic germ cells 0.026	sptf-2	0.372351946570825	0.393287316445186
Apoptotic germ cells 0.026	T20F7.1	0.00572397350539865	0.00548017916079132
Apoptotic germ cells 0.026	tlp-1	0.00437214932296681	0
Apoptotic germ cells 0.026	Y48G9A.11	0.00853332674735448	0.00839982723270996
Apoptotic germ cells 0.026	Y53G8AR.9	0.0086569475265593	0.00472854641948525
Apoptotic germ cells 0.026	Y56A3A.18	0.052922504649392	0.0543120002944308
Apoptotic germ cells 0.026	zfh-2	0.0388544290476907	0.0342466968153534
Apoptotic germ cells 0.026	zim-3	0.0316887331482358	0.0257829553827277
Apoptotic germ cells 0.026	zip-5	0.0135000223157893	0.0242514218909024
Apoptotic germ cells 0.026	ztf-1	0.0485815138396077	0.0248813029398781
Apoptotic germ cells 0.026	ztf-26	0.0446728564566104	0.00425221248580359
Arcade cells 0.044	akir-1	0.0613607213907034	0
Arcade cells 0.044	alr-1	0.227087054006192	0.208074029916773
Arcade cells 0.044	attf-6	0.00925089355780113	0.00572491426579437
Arcade cells 0.044	bcl-11	0.0155446910823117	0.0299717891810554
Arcade cells 0.044	ceh-22	0.351175699910361	0.438086859420021
Arcade cells 0.044	ceh-40	0.0697204030473691	NA
Arcade cells 0.044	ceh-6	0.254729766162953	0.317660525600871
Arcade cells 0.044	cey-2	0.0431340546075111	0.0331835083691794
Arcade cells 0.044	chd-7	0.0460035082892848	0.0547393992995178
Arcade cells 0.044	crh-2	0.0172055825340488	0.015807094883281
Arcade cells 0.044	daf-19	0.0681834406515341	0.0628446916248747
Arcade cells 0.044	dxbp-1	0.0138601150412553	0.0199125607113648
Arcade cells 0.044	egl-18	0.0860393933302618	0.0904154749316621
Arcade cells 0.044	egl-43	0.0181396894041903	0.0398111206917901
Arcade cells 0.044	egl-5	0.00344291053441742	NA
Arcade cells 0.044	egrh-3	0.0128773631996145	0.0205167917165816
Arcade cells 0.044	ekl-4	0.0665338862449895	0.0658265445107118
Arcade cells 0.044	elt-4	0.0269249958898364	0.031247141306689
Arcade cells 0.044	eyg-1	0.320032504937762	0.420727486836405
Arcade cells 0.044	F22D6.2	0.023221234995868	0.0256590266732412
Arcade cells 0.044	F33H1.4	0.0226220156776899	0.0223369117191778
Arcade cells 0.044	F44E2.7	0.013417663964013	0
Arcade cells 0.044	hinf-1	0.118740279915268	0.112707857196263
Arcade cells 0.044	hlh-8	0.0292060823240471	0.0461774795605067
Arcade cells 0.044	hsf-1	0.0206207087405091	0.0355503419453749
Arcade cells 0.044	isw-1	0.000889776932360551	0
Arcade cells 0.044	lag-1	0	0.006379781222369
Arcade cells 0.044	let-607	0.0289892528442935	0.0283277771064354
Arcade cells 0.044	lim-7	0.0437360972797165	0.0411863450255894
Arcade cells 0.044	lin-13	0.00167485208887544	0.000477998149253461
Arcade cells 0.044	lin-26	0.0892098074837233	0.0788619629259795

Arcade cells 0.044	lin-40	0.0602096063510136	0.0521178056589378
Arcade cells 0.044	lin-54	0.0184858631598872	0.0236719466316939
Arcade cells 0.044	lsy-2	0.0102645353659909	0.00492721901675129
Arcade cells 0.044	madf-2	0.300836421370117	0.465805823224407
Arcade cells 0.044	madf-3	0.064424261916735	NA
Arcade cells 0.044	madf-5	0.153449743237737	0.154533941729503
Arcade cells 0.044	madf-6	0.0190886532698303	0.0186805982078566
Arcade cells 0.044	madf-9	0.0507077503106553	0.0332659052912338
Arcade cells 0.044	mdt-29	0.0406569217817538	0.0462103383244495
Arcade cells 0.044	mec-3	0.143356201081812	NA
Arcade cells 0.044	mxl-1	0	0.0225745550410049
Arcade cells 0.044	nhr-102	0.0460519081028713	0.0385854694179706
Arcade cells 0.044	nhr-11	0.0493525499991318	0.0498162908844847
Arcade cells 0.044	nhr-129	0.00687285209685651	NA
Arcade cells 0.044	nhr-179	0.22011654059022	0.184493447930552
Arcade cells 0.044	nhr-237	0.0411966039461061	0.0135968187374003
Arcade cells 0.044	pag-3	0.0249770471026129	0.0336755754884352
Arcade cells 0.044	pat-9	0.236254288340703	0.254982180941521
Arcade cells 0.044	pbrm-1	0.0141767964481064	0.0169324760285593
Arcade cells 0.044	pha-2	0.0986936604442792	0.0670729563485816
Arcade cells 0.044	pha-4	0.0351126508911773	0.0374082616910223
Arcade cells 0.044	R02D3.7	0.0263049087988109	0.0211268900868756
Arcade cells 0.044	saeg-2	0.0124834057724974	0.0119319344845033
Arcade cells 0.044	skn-1	0.00967585233998204	0.0134620156337057
Arcade cells 0.044	spr-3	4.19685932949881e-05	0
Arcade cells 0.044	sptf-2	0.346854282037875	NA
Arcade cells 0.044	T26A5.8	0.019972375777605	0.0211543648668826
Arcade cells 0.044	tlp-1	0.0326003368761459	0.0410682746210423
Arcade cells 0.044	tra-4	0.262623791362157	0.415346931972098
Arcade cells 0.044	unc-62	0.00171283201803974	0
Arcade cells 0.044	Y53G8AR.9	0.00766198414376592	0.011932228939735
Arcade cells 0.044	Y56A3A.18	0.073657596055771	0.0644908452434301
Arcade cells 0.044	zfh-2	0.0952566493700738	0.0966196790087849
Arcade cells 0.044	zim-3	0.0157447944017222	0.0126065122581106
Arcade cells 0.044	ZK546.5	0.121125611933498	0.0850574732412209
Arcade cells 0.044	ztf-1	0.186305580022464	0.175872144565006
Arcade cells 0.044	ztf-26	0.0711765642713138	0.0531364439622114
BAG 0.040	aha-1	0.216494218198813	0.230901718863532
BAG 0.040	alr-1	0.107877126537499	0.115842153124079
BAG 0.040	atf-7	0.00256152031135784	0.00319108706965947
BAG 0.040	ceh-18	0.000908613186782952	0
BAG 0.040	ceh-27	0.0182973330647167	0.0138122997030599
BAG 0.040	ceh-40	0.0711743073238109	NA

BAG 0.040	ces-1	NA	0.0277334808844052
BAG 0.040	crh-2	0.0311920942731232	0.0276829693048054
BAG 0.040	daf-19	0.0403862273924442	0.0627738903753435
BAG 0.040	egl-13	0.221195936243234	0.200817190146294
BAG 0.040	egl-18	0.0165012779995226	0.0348714350834601
BAG 0.040	egl-27	0	0.007687738313375
BAG 0.040	ekl-4	0.0222575232950927	0.0355975254116237
BAG 0.040	elt-4	0.0483432286929521	0.00444940725698923
BAG 0.040	ets-5	0.0723821260988667	0.0908293304477102
BAG 0.040	F22D6.2	0.0412805655154367	0
BAG 0.040	F57A8.1	0	0.0341517975153724
BAG 0.040	fkh-10	0.00378602888895648	NA
BAG 0.040	fkh-8	0.0694741719104776	0.0528349406044177
BAG 0.040	gei-8	0.0236344027797316	0.0395944944297176
BAG 0.040	hif-1	0.0407956427611925	0.040335786394334
BAG 0.040	hinf-1	0.078233621140354	0.0999868291004661
BAG 0.040	hlh-8	0.00602137829154116	0
BAG 0.040	hsf-1	0	0.00910712065011744
BAG 0.040	isw-1	0.0214797768009018	0.0251053877045191
BAG 0.040	K12H6.12	0.0286891129748941	0.0429325144970756
BAG 0.040	lag-1	0	0.00190491199793327
BAG 0.040	lim-7	0.0122139000249555	0.0312722431933164
BAG 0.040	lin-11	0.19085820686892	0.199382364852392
BAG 0.040	lin-14	0.0238882123704248	0.00900265290900412
BAG 0.040	lin-26	0.0811107550387728	0.0747635186802613
BAG 0.040	lin-40	0.0618817493674461	0.0110425214538104
BAG 0.040	madf-3	0.0495836825871638	NA
BAG 0.040	madf-5	0.126491102414278	0.0900577074285624
BAG 0.040	mdt-29	0.0126225409726147	0.025368122077563
BAG 0.040	nfya-2	0.0357856512020779	0.0323434052047681
BAG 0.040	nfyb-1	0.00222995033818921	0.00607183566381972
BAG 0.040	nhr-11	0.0414345677948086	0.0108393959432382
BAG 0.040	nhr-129	NA	0.0134599559459524
BAG 0.040	nhr-47	0.00906302178603674	0.000473403830176056
BAG 0.040	nhr-6	0	0.00108708436108695
BAG 0.040	pag-3	NA	0.0443141097627566
BAG 0.040	pat-9	0.188006994875263	0.0930126233294689
BAG 0.040	sem-4	0.0151097931910879	0.0108969282326444
BAG 0.040	sox-4	NA	0.167481731036858
BAG 0.040	sptf-2	0.253513472857788	NA
BAG 0.040	T26A5.8	0.0294122954643895	0.0122482904613564
BAG 0.040	Y53G8AR.9	0.0112566578058836	0.0185310563866654
BAG 0.040	Y55F3AM.14	NA	0.0142331243674452

BAG 0.040	Y56A3A.18	0.0176203909314985	0.0189079609125911
BAG 0.040	zag-1	0.015023363716407	NA
BAG 0.040	zfh-2	0.0378306617754337	0.0325450786458228
BAG 0.040	ZK185.1	0.0149971997342102	NA
BAG 0.040	ZK546.5	0	0.035866750878218
BAG 0.040	ztf-26	0.0509461871700493	0
BDU 0.042	aha-1	0.0434256080570057	0.057257397215674
BDU 0.042	atf-7	0.00797885320048627	0.0051629706124192
BDU 0.042	attf-6	0.0100838393937808	0.0060236436128397
BDU 0.042	C34B4.2	0.364922246858708	0
BDU 0.042	ceh-27	NA	0.0262175455135967
BDU 0.042	ceh-40	NA	0.0818604982644674
BDU 0.042	ceh-63	0.158179434999128	NA
BDU 0.042	chd-7	0.000677018659239082	0
BDU 0.042	crh-2	0.0441386289537352	0.0435356806981171
BDU 0.042	ctbp-1	0.104538591536938	0.11262459864401
BDU 0.042	daf-19	0.0926813533036276	0.0749560329000292
BDU 0.042	egl-18	0.089437953681038	0.0501089731902011
BDU 0.042	ekl-4	0.0567125723963288	0.0475795859716755
BDU 0.042	ets-5	0.0274041923894138	0.0242947871723662
BDU 0.042	fkh-8	0.00525301391407919	NA
BDU 0.042	hif-1	0.0150251536482248	0.0192583734442808
BDU 0.042	hinf-1	0.119943784372153	0.110629343613758
BDU 0.042	hsf-1	0.0136047193164595	0.00926935616737714
BDU 0.042	K12H6.12	0.00411454588361769	NA
BDU 0.042	lag-1	0.0224925805583008	0.014517901788865
BDU 0.042	lim-7	0.0250810637940344	0.0201694702616152
BDU 0.042	lin-11	0.147602410829142	NA
BDU 0.042	lin-13	0.000591469406431854	0.00134160925186043
BDU 0.042	lin-14	0.0253890523631022	0.0303617348397979
BDU 0.042	lin-26	0.0664692049859475	0.0611225595262288
BDU 0.042	lin-40	0.0704260691718339	0.0416804628780982
BDU 0.042	lsy-2	0.0185060739623032	0.00846952089809863
BDU 0.042	madf-5	0.0502911859696426	0.0442673180687029
BDU 0.042	mdt-29	0.00908764697915279	0.00531746253859444
BDU 0.042	nhr-11	0.0147382730099333	0.0253191569809106
BDU 0.042	pag-3	0.0292876366902055	0.0174904872852558
BDU 0.042	pat-9	0.176338950433268	0.132503494758363
BDU 0.042	sem-4	0.0340501288791253	0.0417636213048673
BDU 0.042	sox-4	0.0720219538539116	0.0561397062224358
BDU 0.042	sptf-2	0.317501864557532	NA
BDU 0.042	tlp-1	NA	0.00263378909492444
BDU 0.042	unc-42	0.021737243531608	NA

BDU 0.042	unc-86	0.0770596715313192	0.100157027910904
BDU 0.042	Y53G8AR.9	0.00845598227915516	NA
BDU 0.042	Y56A3A.18	0.038995263434385	0.0210306879841724
BDU 0.042	zag-1	0.0923764156480126	0.109283256227493
BDU 0.042	zfh-2	0.0351584614983022	0.0315811709449816
BDU 0.042	ZK546.5	0.0222542404747377	0.0804127294403858
Body wall muscle anterior 0.053	aha-1	0.044202973683941	0.0357363239032194
Body wall muscle anterior 0.053	alr-1	0.201372071929275	0.205512733704001
Body wall muscle anterior 0.053	attf-6	0	0.00189531843811414
Body wall muscle anterior 0.053	ceh-18	0.269434523519535	0.173745095079227
Body wall muscle anterior 0.053	chd-7	0.0120256704294285	0.00477755897228929
Body wall muscle anterior 0.053	daf-12	0.219318374227055	0.28144791408663
Body wall muscle anterior 0.053	daf-16	0.0235417725291001	0.0198744688433434
Body wall muscle anterior 0.053	daf-19	0.0733729265788718	0.0827722797141845
Body wall muscle anterior 0.053	egl-5	0.0155745954587757	0.016784410500108
Body wall muscle anterior 0.053	ekl-4	0.0768888288842553	0.0849712730779037
Body wall muscle anterior 0.053	F33H1.4	0	0.00420808832862249
Body wall muscle anterior 0.053	hinf-1	0.119824716354683	0.133990336540419
Body wall muscle anterior 0.053	hlh-1	0.0600290856266926	0.0470838448533157
Body wall muscle anterior 0.053	hlh-11	0.00396878887542427	0
Body wall muscle anterior 0.053	hlh-8	0.160646398342672	0.151199154849714
Body wall muscle anterior 0.053	hsf-1	0.016941098683493	0.0165223789429262
Body wall muscle anterior 0.053	let-607	0.00297193051334598	0.00163091473107305
Body wall muscle anterior 0.053	lim-7	0.0533179860442344	0.0676052005624982
Body wall muscle anterior 0.053	lin-26	0.0933952877135787	0.0975864648385164
Body wall muscle anterior 0.053	lin-40	0.039048782130399	0.00516805578195042
Body wall muscle anterior 0.053	lin-54	0	1.10780200465517e-05
Body wall muscle anterior 0.053	lsy-2	0.00870003174367693	0.00883214104652592
Body wall muscle anterior 0.053	madf-3	0.0545937951105762	0.0610724803380328
Body wall muscle anterior 0.053	madf-5	0.118484589187219	0.100505278325938
Body wall muscle anterior 0.053	madf-6	0.00626864296820452	0.0113737903212083
Body wall muscle anterior 0.053	mdt-29	0.0386307461390904	0.0354765271856379
Body wall muscle anterior 0.053	nhr-11	0.0542670977352563	0.0396931601364254
Body wall muscle anterior 0.053	nhr-19	0.0381371891630914	0.0293086448817309
Body wall muscle anterior 0.053	nhr-71	0.0130319236586746	0.00224097386295572
Body wall muscle anterior 0.053	pag-3	NA	0.294202957258432
Body wall muscle anterior 0.053	pat-9	1.08723147490441	0.980398157090674
Body wall muscle anterior 0.053	R02D3.7	0.0156038974971056	0.00849248163739171
Body wall muscle anterior 0.053	rnt-1	0.0906576065199952	0.0722387897543919
Body wall muscle anterior 0.053	sptf-2	0.401481796382206	0.450074245021848
Body wall muscle anterior 0.053	sup-37	0.191925605329916	0.203494948521425
Body wall muscle anterior 0.053	syd-9	0.103999822447414	0.0302953954623956
Body wall muscle anterior 0.053	T26A5.8	0.0281870286295471	0.0238919490492147

Body wall muscle anterior 0.053	tlp-1	0.0282423857155047	0.0225205354773145
Body wall muscle anterior 0.053	unc-120	0.0547301470665943	0.030652797534891
Body wall muscle anterior 0.053	Y53G8AR.9	0.0211489685614529	0.021320081213944
Body wall muscle anterior 0.053	Y56A3A.18	0.0654485105914262	0.070445304971903
Body wall muscle anterior 0.053	zfh-2	0.0613024023296095	0.0581593614960177
Body wall muscle anterior 0.053	zim-3	0.0420528736672286	0.0172954721067466
Body wall muscle anterior 0.053	ZK546.5	0.0358309844950751	0.0319208097840269
Body wall muscle anterior 0.053	ztf-1	0.0171954850162834	0
Body wall muscle anterior 0.053	ztf-26	0.0106232061399542	0
Body wall muscle middle 0.050	aha-1	0.085898047352711	0.0624899452583823
Body wall muscle middle 0.050	alr-1	0.179593614071177	0.211046323160873
Body wall muscle middle 0.050	ceh-18	0.241536958794057	0.221532012510206
Body wall muscle middle 0.050	ceh-22	0.0323723351834848	0.0193486954257592
Body wall muscle middle 0.050	ceh-34	0.0124409118652454	0.00895463022963778
Body wall muscle middle 0.050	ceh-40	0.0990345572983273	0.113483249890721
Body wall muscle middle 0.050	chd-7	0.00424413836422041	0.0109937735609981
Body wall muscle middle 0.050	ctbp-1	0	0.00196876613677529
Body wall muscle middle 0.050	daf-12	0.0437064119369651	0.0625250459941036
Body wall muscle middle 0.050	daf-16	0.0116030037961645	0.0114403199236057
Body wall muscle middle 0.050	daf-19	0.0466073595241474	0.0617244311393091
Body wall muscle middle 0.050	egl-5	0.0125775561889166	0.012393338515252
Body wall muscle middle 0.050	ekl-4	0.0602228178409761	0.0737107478079784
Body wall muscle middle 0.050	eor-1	0.00424092782239572	0
Body wall muscle middle 0.050	F22D6.2	0.0242222228045788	0
Body wall muscle middle 0.050	F33H1.4	0.00240242313970493	0.0143458955448335
Body wall muscle middle 0.050	fkh-4	0.01578756717793	NA
Body wall muscle middle 0.050	hif-1	0.000320643883150199	0.00151107391492454
Body wall muscle middle 0.050	hinf-1	0.0940009257723253	0.119679438639335
Body wall muscle middle 0.050	hlh-1	0.0266373177180421	0.0205353700686552
Body wall muscle middle 0.050	hlh-11	0	0.00276289904226511
Body wall muscle middle 0.050	hlh-8	0.165427406891789	0.161329628751311
Body wall muscle middle 0.050	hsf-1	0.0105150362129978	0.015017837200648
Body wall muscle middle 0.050	let-607	0	0.00295971787667611
Body wall muscle middle 0.050	lim-7	0.0428181776649093	0.0556583252850979
Body wall muscle middle 0.050	lin-26	0.0903960346990455	0.100246435447538
Body wall muscle middle 0.050	lin-40	0.0495573943773226	0.0424328046410341
Body wall muscle middle 0.050	lin-54	0	0.00786765167653376
Body wall muscle middle 0.050	lsy-2	0.011632385197991	0.0161258182540739
Body wall muscle middle 0.050	madf-3	0.0544397741606863	0.0647422085797138
Body wall muscle middle 0.050	madf-5	0.13212220360179	0.134924389319782
Body wall muscle middle 0.050	madf-6	0.0156539597217469	0.023527909162332
Body wall muscle middle 0.050	mdt-29	0.0331033983673801	0.0310645176676409
Body wall muscle middle 0.050	nhr-11	0.0384831034141434	0.0355397225899967

Body wall muscle middle 0.050	nhr-19	0.0352574847044763	0.0298757587187938
Body wall muscle middle 0.050	nhr-71	0.00725043063369516	0.00594680964671022
Body wall muscle middle 0.050	pag-3	0.321709958240943	0.293762041369412
Body wall muscle middle 0.050	pat-9	0.963926487710546	0.927924944304933
Body wall muscle middle 0.050	pbrm-1	0	0.000963739787079006
Body wall muscle middle 0.050	R02D3.7	0.0233840135718015	0.0234202222063432
Body wall muscle middle 0.050	rnt-1	0.0426474752788595	0.0399677484946732
Body wall muscle middle 0.050	skn-1	0.000100322734480223	0.00188399139504909
Body wall muscle middle 0.050	sptf-2	0.320553422005963	0.390090125924361
Body wall muscle middle 0.050	sup-37	0.394704892342356	0.388925643488071
Body wall muscle middle 0.050	syd-9	0.0543154271340243	0.0419693477820964
Body wall muscle middle 0.050	T26A5.8	0.0614635565688064	0.0451293613929382
Body wall muscle middle 0.050	tlp-1	0.0251164208831314	0.0255466485203579
Body wall muscle middle 0.050	unc-120	0.0322218069928481	0.0260108636425536
Body wall muscle middle 0.050	Y53G8AR.9	0.0243249034642196	0.0207015553542587
Body wall muscle middle 0.050	Y56A3A.18	0.0433200627933143	0.0506110903080835
Body wall muscle middle 0.050	zfh-2	0.0597175667716912	0.0592638530150059
Body wall muscle middle 0.050	zim-3	0.0336115901719029	0.0351222249581078
Body wall muscle middle 0.050	ZK546.5	0.0282981446055058	0.0383900049105003
Body wall muscle middle 0.050	ztf-26	0.0278552692737263	0.0176638050605251
Body wall muscle posterior 0.043	aha-1	0	0.001102996452749
Body wall muscle posterior 0.043	alr-1	0.22230345512408	0.220249484591284
Body wall muscle posterior 0.043	attf-6	0.00964544024794482	0.0147015508267819
Body wall muscle posterior 0.043	ceh-18	0.103453938715938	0.0772202948723725
Body wall muscle posterior 0.043	ceh-22	NA	0.0211894435812283
Body wall muscle posterior 0.043	ceh-34	0.00290599369581168	0
Body wall muscle posterior 0.043	ceh-40	0.116769642735046	NA
Body wall muscle posterior 0.043	chd-7	0.0314428776484371	0.0391301521237692
Body wall muscle posterior 0.043	crh-2	0.0030481564897074	0.0174289517232778
Body wall muscle posterior 0.043	ctbp-1	0.000532299964035296	0.0254108305699807
Body wall muscle posterior 0.043	daf-12	0.314979498592304	0.253990936917803
Body wall muscle posterior 0.043	daf-16	0.0285830470656236	0.0307991144098835
Body wall muscle posterior 0.043	daf-19	0.0576750927113035	0.0886075662616879
Body wall muscle posterior 0.043	dmd-9	0	0.00430906482449292
Body wall muscle posterior 0.043	dsc-1	0.0193507199179982	0.0202561278216184
Body wall muscle posterior 0.043	dxbp-1	0	0.0109710592574411
Body wall muscle posterior 0.043	egl-18	0.209317497566718	0.26493287069919
Body wall muscle posterior 0.043	egl-5	0.014937966745531	0.0130273288561192
Body wall muscle posterior 0.043	egrh-3	0	0.016610517645549
Body wall muscle posterior 0.043	ekl-4	0.0730509951094073	0.0761391768283865
Body wall muscle posterior 0.043	elt-4	0.0770638804293128	0.0956945473551069
Body wall muscle posterior 0.043	F22D6.2	0.109816860182341	0.0748993925071149
Body wall muscle posterior 0.043	F33H1.4	0.0262812697211328	0.0288738546289978

Body wall muscle posterior 0.043	F44E2.7	0.0163511683936205	0.0429084757789695
Body wall muscle posterior 0.043	hinf-1	0.0993455382092598	0.103769653203554
Body wall muscle posterior 0.043	hlh-1	0.0584592511584167	0.0525679432887459
Body wall muscle posterior 0.043	hlh-11	0.00616872509281592	0.0165527401855908
Body wall muscle posterior 0.043	hlh-8	0.117123127333895	0.128813193180996
Body wall muscle posterior 0.043	hsf-1	0.0184453785158119	0.0183458861760432
Body wall muscle posterior 0.043	isw-1	0	0.00808215308259941
Body wall muscle posterior 0.043	let-607	0.0130159265777185	0.0148822150685287
Body wall muscle posterior 0.043	lim-7	0.0421821170411488	0.0724202747283114
Body wall muscle posterior 0.043	lin-13	0	0.00128100689613541
Body wall muscle posterior 0.043	lin-26	0.106073859276733	0.108630324689085
Body wall muscle posterior 0.043	lin-40	0.0712617502860515	0.0727650588218494
Body wall muscle posterior 0.043	lin-54	0.0120487538693391	0.0211649399662361
Body wall muscle posterior 0.043	lsy-2	0.0189366752469895	0.0171905520799718
Body wall muscle posterior 0.043	madf-2	0.251553275415895	0.333302244241216
Body wall muscle posterior 0.043	madf-3	0.0511099600376868	0.0595520544965934
Body wall muscle posterior 0.043	madf-5	0.218073190458879	NA
Body wall muscle posterior 0.043	madf-6	0.0172230390852351	0.0175410014010045
Body wall muscle posterior 0.043	madf-9	0	0.00520438567890618
Body wall muscle posterior 0.043	mdt-29	0.0519757133009824	0.0642393525243529
Body wall muscle posterior 0.043	mec-3	0	0.0405725931973421
Body wall muscle posterior 0.043	mxl-3	0	0.00129539087168636
Body wall muscle posterior 0.043	nhr-10	0.00871887628753986	0.0285169736391507
Body wall muscle posterior 0.043	nhr-102	0.000964966979849209	0.000432711612959557
Body wall muscle posterior 0.043	nhr-11	0.059036337272964	0.0617822503927119
Body wall muscle posterior 0.043	nhr-129	0.0049360513581891	0.00988303487475708
Body wall muscle posterior 0.043	nhr-179	0.148157789626036	0.463686472676306
Body wall muscle posterior 0.043	nhr-19	0.0367364373326684	0.0236296621849691
Body wall muscle posterior 0.043	nhr-48	0	0.00480305767407312
Body wall muscle posterior 0.043	nhr-71	0.026142378205713	0.0202541619133249
Body wall muscle posterior 0.043	pag-3	0.274113802396318	0.257120193008807
Body wall muscle posterior 0.043	pat-9	0.655735608878182	0.606042314061749
Body wall muscle posterior 0.043	pbrm-1	0.0101292778730401	0.0211901488699925
Body wall muscle posterior 0.043	R02D3.7	0.00737178531168708	0.0117830885330635
Body wall muscle posterior 0.043	rnt-1	0.0907679636456133	0.0985026323769107
Body wall muscle posterior 0.043	saeg-2	0.00875880398920077	0.0371959159209835
Body wall muscle posterior 0.043	spr-1	0	0.0228551415032461
Body wall muscle posterior 0.043	sptf-2	0.39358650418303	0.396886191943981
Body wall muscle posterior 0.043	sup-37	0.0260626387021338	0.0170812567870622
Body wall muscle posterior 0.043	syd-9	0.167650739873354	0.152469167921731
Body wall muscle posterior 0.043	tlp-1	0.0459025893484718	0.0860031067129528
Body wall muscle posterior 0.043	unc-120	0.0716770853273809	0.0715155182028589
Body wall muscle posterior 0.043	unc-62	0	0.00683469794602163

Body wall muscle posterior 0.043	unc-98	0.062230648830483	0.0766530513236889
Body wall muscle posterior 0.043	Y53G8AR.9	0.00974144367793282	0.0135456777134147
Body wall muscle posterior 0.043	Y56A3A.18	0.0641901035263921	0.0930406092189892
Body wall muscle posterior 0.043	zfh-2	0.0708127862138503	0.0691529607087506
Body wall muscle posterior 0.043	zim-3	0.0441152038747105	0.0583343359973045
Body wall muscle posterior 0.043	ztf-1	0.150018402737603	0.211333288558159
Body wall muscle posterior 0.043	ztf-26	0.0878899564916391	0.104689063908161
CAN 0.040	alr-1	0.315697603588343	0.324107702015162
CAN 0.040	attf-6	0.00926515912205252	0.00156779811619981
CAN 0.040	C16A3.4	0.00958227710860594	0.0161818124314008
CAN 0.040	ceh-18	0	0.0456622844814
CAN 0.040	ceh-40	NA	0.16269084671703
CAN 0.040	crh-2	0.0227452854087507	0.0148316122894184
CAN 0.040	die-1	0.0753260253758273	0.0366676313408751
CAN 0.040	dxbp-1	0.034664504325953	0.0250426131608431
CAN 0.040	efl-1	0.0113379169653507	0.00325030431958332
CAN 0.040	egl-18	0.0929565121493569	0.0107928417599521
CAN 0.040	egrh-3	0.0302710160893831	NA
CAN 0.040	ekl-4	0.104726523548899	0.0947520935935324
CAN 0.040	elt-4	0.123215378301856	0.0840494550749469
CAN 0.040	F22D6.2	0.205743163791281	0.110311840636043
CAN 0.040	F33H1.4	0.0462447705480181	0.0431843168276082
CAN 0.040	F44E2.7	0.0284532777963848	0
CAN 0.040	gei-8	0	0.0159477864408427
CAN 0.040	hinf-1	0.146703021962195	0.136966040850551
CAN 0.040	hlh-8	NA	0.0481158594985213
CAN 0.040	hsf-1	0.0288893313964837	0.0183811278940044
CAN 0.040	isw-1	0.0132519478057713	0
CAN 0.040	lag-1	0.00970060497626003	0.0701580761652067
CAN 0.040	let-607	0.0218945741126115	0.0281457201078016
CAN 0.040	lim-7	0.0709948901629494	0.0405299543923469
CAN 0.040	lin-13	0.0162351442792674	0.00828163553708266
CAN 0.040	lin-26	0.148096828287074	0.153625033301331
CAN 0.040	lin-40	0.128540040876705	0.104684198741686
CAN 0.040	lin-54	0.0293281917682818	0.0194192464583587
CAN 0.040	lsy-2	0.0292649171047322	NA
CAN 0.040	madf-3	NA	0.0602542309178265
CAN 0.040	madf-5	NA	0.191073063577041
CAN 0.040	madf-6	0.0245141538161956	0.0252324679601978
CAN 0.040	mdt-29	0.0449173391453405	0.0523220658451077
CAN 0.040	nhr-11	0.013445730087871	NA
CAN 0.040	nhr-179	NA	0.122799088878431
CAN 0.040	pag-3	0.0587005352708028	NA

CAN 0.040	pat-9	0.139414649499055	0.233022212060319
CAN 0.040	pbrm-1	0.0229659096152343	0.00609899222165839
CAN 0.040	R02D3.7	0.0304304726071384	0.0307800160634842
CAN 0.040	saeg-2	0.0053211397442728	NA
CAN 0.040	skn-1	0.00435716392120559	0.00570386196482455
CAN 0.040	T26A5.8	0.0853785749894669	0
CAN 0.040	unc-62	0.00974003036026927	NA
CAN 0.040	Y53G8AR.9	0.0387338728778982	0.0245755975726764
CAN 0.040	Y56A3A.18	0.0735719723203167	0.0639593118922167
CAN 0.040	zfh-2	0.0547023148525574	0.0499614927177427
CAN 0.040	zim-3	0.0748578702609632	0.0615765027603998
CAN 0.040	ZK546.5	0.0523125295247406	0.114556005488968
CAN 0.040	ztf-1	0.198756704747609	0.0976355123966451
CAN 0.040	ztf-16	0.0533511830508721	0
CAN 0.040	ztf-22	0.0106962959235559	NA
CAN 0.040	ztf-26	0.125473132985107	NA
CEP_ADE_PDE 0.035	aha-1	0.0881588567245145	0.11115150554959
CEP_ADE_PDE 0.035	alr-1	0.165629195054059	0.189410318102637
CEP_ADE_PDE 0.035	attf-6	0	0.00170698649898146
CEP_ADE_PDE 0.035	C34B4.2	0.316980928798793	0
CEP_ADE_PDE 0.035	cebp-1	0.0101470543680058	0.00805089875286019
CEP_ADE_PDE 0.035	crh-2	0.0341704922683188	0.0316972541293852
CEP_ADE_PDE 0.035	ctbp-1	0.0930844536649191	0.101154324200596
CEP_ADE_PDE 0.035	daf-19	0.127213739428114	0.141550572156866
CEP_ADE_PDE 0.035	egl-18	0.0994259363798521	0.0824381266685783
CEP_ADE_PDE 0.035	ekl-4	0.0401500820563622	0.0464854912832787
CEP_ADE_PDE 0.035	ets-5	0.00872630256927145	NA
CEP_ADE_PDE 0.035	F22D6.2	0.0572761528745839	0.00176081202837467
CEP_ADE_PDE 0.035	fkh-10	0.0212103872683077	0.0249784238063344
CEP_ADE_PDE 0.035	fkh-8	0.0389090392085861	0.0372126950342189
CEP_ADE_PDE 0.035	hif-1	0	0.00295105436892411
CEP_ADE_PDE 0.035	hinf-1	0.117439434607737	0.125320467311592
CEP_ADE_PDE 0.035	hlh-8	0.0114740959272916	0.00932159422620799
CEP_ADE_PDE 0.035	hmg-1.1	3.56152859520724e-05	0
CEP_ADE_PDE 0.035	isw-1	0	0.000766592878397967
CEP_ADE_PDE 0.035	lag-1	0.0263900219962551	0.0420991725875275
CEP_ADE_PDE 0.035	lim-7	NA	0.0177762685420684
CEP_ADE_PDE 0.035	lin-11	0.20913398079822	0.217295404679989
CEP_ADE_PDE 0.035	lin-14	0.0482638692920053	0.0475945272871085
CEP_ADE_PDE 0.035	lin-26	0.0876715287980969	0.0888378291310968
CEP_ADE_PDE 0.035	lin-39	0.00381651858723499	0.00449978923202081
CEP_ADE_PDE 0.035	lin-40	0.106495897453636	0.0484695846302493
CEP_ADE_PDE 0.035	lsy-2	0.0178787415775441	0.0153536601780445

CEP_ADE_PDE 0.035	madf-3	0.0511421124107727	0.0579595480821971
CEP_ADE_PDE 0.035	madf-5	0.0922325146479193	0.0555508447122754
CEP_ADE_PDE 0.035	madf-9	0.0280896394377341	0.00551678977085822
CEP_ADE_PDE 0.035	mbf-1	0.0785158548420765	0.109666153678791
CEP_ADE_PDE 0.035	mdt-29	0.0266830482690099	0.018286492292704
CEP_ADE_PDE 0.035	nfya-2	0.00157040078497425	0.0177373696873187
CEP_ADE_PDE 0.035	nfyb-1	0	0.000474932947969677
CEP_ADE_PDE 0.035	nhr-11	NA	0.0136640672456388
CEP_ADE_PDE 0.035	nhr-237	NA	0.00575502593801497
CEP_ADE_PDE 0.035	pat-9	0.238535109371738	NA
CEP_ADE_PDE 0.035	pbrm-1	0.00925667198561544	0
CEP_ADE_PDE 0.035	sem-4	0.0420484477352456	0.0379138256335227
CEP_ADE_PDE 0.035	sox-4	NA	0.00080167379383044
CEP_ADE_PDE 0.035	sptf-2	0.301844648719193	NA
CEP_ADE_PDE 0.035	unc-42	0	0.000995954881245504
CEP_ADE_PDE 0.035	unc-55	0.0116967059289873	NA
CEP_ADE_PDE 0.035	unc-62	0.00233092154460842	0.000707088129438115
CEP_ADE_PDE 0.035	unc-86	0.0285617395880268	0.0222292864617106
CEP_ADE_PDE 0.035	Y53G8AR.9	0.0149533992264757	0.00906850700927987
CEP_ADE_PDE 0.035	Y55F3AM.14	0.0217487533390653	NA
CEP_ADE_PDE 0.035	Y56A3A.18	0.0488339666899884	0.0480736824920714
CEP_ADE_PDE 0.035	zag-1	NA	0.0451580855984201
CEP_ADE_PDE 0.035	zfh-2	0.0556321870496942	0.0518766891593255
CEP_ADE_PDE 0.035	zim-3	0.0215615096463225	0
CEP_ADE_PDE 0.035	ZK546.5	0.128438052519981	0.0650285306160511
CEP_ADE_PDE 0.035	ztf-1	0.0925475181871449	0
CEP_ADE_PDE 0.035	ztf-26	NA	0.0646017219563319
Cephalic and inner labial socket 0.040	alr-1	0.20760087455675	0.230395660201385
Cephalic and inner labial socket 0.040	B0035.1	0.0348284201726307	0.0443573778183835
Cephalic and inner labial socket 0.040	blmp-1	0.0304469445929323	0.0277425896863736
Cephalic and inner labial socket 0.040	ceh-27	0.0164192171648494	0.0115547896442385
Cephalic and inner labial socket 0.040	D1046.2	0.00218895359672326	0
Cephalic and inner labial socket 0.040	daf-19	0.0661753032430867	0.0744925103088822
Cephalic and inner labial socket 0.040	dxbp-1	0	0.00229851084170561
Cephalic and inner labial socket 0.040	egrh-3	0.00575328255079752	0.00737522077967933
Cephalic and inner labial socket 0.040	ekl-4	0.0777485170238724	0.0858916184992803
Cephalic and inner labial socket 0.040	elt-4	0.186474965288743	NA
Cephalic and inner labial socket 0.040	F22D6.2	0.00396248615023291	0
Cephalic and inner labial socket 0.040	F33H1.4	0.0209920423856064	0.0293712186927915
Cephalic and inner labial socket 0.040	F44E2.7	0	0.0021278901711569 3
Cephalic and inner labial socket 0.040	gei-8	0.088628590817757	0.10930022236655
Cephalic and inner labial socket 0.040	grh-1	0.026916743700011	0.0321115591200658
Cephalic and inner labial socket 0.040	hinf-1	0.141355687189273	0.16189952406843

Cephalic and inner labial socket 0.040	hlh-8	0.0279843394320968	0.0309984226683885
Cephalic and inner labial socket 0.040	hsf-1	0.00421118851096073	0.00771889834549686
Cephalic and inner labial socket 0.040	lag-1	0	0.0469643236302902
Cephalic and inner labial socket 0.040	let-607	0	0.00516634483522842
Cephalic and inner labial socket 0.040	lim-7	0.0309407601806124	0.0400057049417345
Cephalic and inner labial socket 0.040	lin-14	0.00137845705356174	0
Cephalic and inner labial socket 0.040	lin-26	0.131833672654055	0.134742890400427
Cephalic and inner labial socket 0.040	lin-40	0.132491943983196	0.10114752452773
Cephalic and inner labial socket 0.040	lin-54	0.00237779374645029	0.0078656169726031
Cephalic and inner labial socket 0.040	lsy-2	0.0218718039201896	0.0209720692641479
Cephalic and inner labial socket 0.040	madf-3	0.0662454417373234	0.0689562260112358
Cephalic and inner labial socket 0.040	madf-5	0.18367140617542	0.168086348974411
Cephalic and inner labial socket 0.040	madf-6	8.86397206209093e-05	0.00653890449926743
Cephalic and inner labial socket 0.040	madf-9	0.0431003215062989	0.0351998406875868
Cephalic and inner labial socket 0.040	mdt-29	0.00834657766090419	0.0272309608043518
Cephalic and inner labial socket 0.040	mec-3	0	0.00115995455568502
Cephalic and inner labial socket 0.040	mep-1	0.00935814393645877	0.0111740760428439
Cephalic and inner labial socket 0.040	nhr-11	0.0388600844662139	0.0350945040684736
Cephalic and inner labial socket 0.040	nhr-179	0.0368337782345582	0
Cephalic and inner labial socket 0.040	nhr-237	0.0376719009113088	0.0103392976481317
Cephalic and inner labial socket 0.040	nhr-25	0.0270939101693733	0.0304470805807906
Cephalic and inner labial socket 0.040	nhr-85	0	1.37343759773009e-05
Cephalic and inner labial socket 0.040	pag-3	0.0720400513126817	0.0592977441638775
Cephalic and inner labial socket 0.040	pat-9	0.261618622832702	0.231404457796551
Cephalic and inner labial socket 0.040	R02D3.7	0.0205610633264509	0.0206814190202717
Cephalic and inner labial socket 0.040	saeg-2	0	0.0107251437958964
Cephalic and inner labial socket 0.040	skn-1	0.00433015423111375	0.00327024270849489
Cephalic and inner labial socket 0.040	snu-23	0.00103002204327949	0.0020681526514016
Cephalic and inner labial socket 0.040	spr-3	0.0189750486310214	0
Cephalic and inner labial socket 0.040	sptf-2	0.366348369951434	0.450478157688608
Cephalic and inner labial socket 0.040	tlp-1	0.007450214020801	0.00502181290382076
Cephalic and inner labial socket 0.040	Y53G8AR.9	0.0132730982185148	0.00869519992942757
Cephalic and inner labial socket 0.040	Y56A3A.18	0.0272009643286876	0.0394058654888266
Cephalic and inner labial socket 0.040	zfh-2	0.0494623351949082	0.0542363172352004
Cephalic and inner labial socket 0.040	zim-3	0.046488316048566	0.0499926907587285
Cephalic and inner labial socket 0.040	ztf-1	0.0556684473653086	0.0480323991901997
Cephalic and inner labial socket 0.040	ztf-26	0.0850377556737461	0.0492777572816223
Cephalic sheath 0.038	alr-1	0.215941039656691	0.241591039945918
Cephalic sheath 0.038	B0035.1	0.0314980059856304	0.0418966912601257
Cephalic sheath 0.038	blmp-1	0.00760409609383434	0.00451000932616397
Cephalic sheath 0.038	ceh-18	0.00780557477547309	0
Cephalic sheath 0.038	crh-2	0.00625971812939134	0.0126283307118336
Cephalic sheath 0.038	daf-19	0.0694725687187793	0.083174986238167

Cephalic sheath 0.038	egl-18	0	0.00124086136326076
Cephalic sheath 0.038	egl-5	0.00742478360677456	0.00626557859625511
Cephalic sheath 0.038	ekl-4	0.072418946591332	0.0850636898804174
Cephalic sheath 0.038	elt-3	0.013061624101452	0.0107504184754356
Cephalic sheath 0.038	elt-4	0.0987891545808339	0.0775475823308703
Cephalic sheath 0.038	F22D6.2	0.0574640500751898	0
Cephalic sheath 0.038	F33H1.4	0.017290085362681	0.0233959234262983
Cephalic sheath 0.038	hinf-1	0.134927884815425	0.145545648303894
Cephalic sheath 0.038	hlh-8	0.0436659033232822	0.0378822835088556
Cephalic sheath 0.038	hsf-1	0.00534882605619938	0.00728437455922115
Cephalic sheath 0.038	lag-1	0.0101081359042993	0.0583335909059148
Cephalic sheath 0.038	let-607	0.00177326198949191	0.00994741118176456
Cephalic sheath 0.038	lim-7	0.0116838135929408	0.020064832230905
Cephalic sheath 0.038	lin-26	0.123995648912747	0.122503462452376
Cephalic sheath 0.038	lin-40	0.131923484567112	0.0991951005517715
Cephalic sheath 0.038	lin-54	0	0.00894773170793978
Cephalic sheath 0.038	lsy-2	0.0178157340161354	0.0186516962283203
Cephalic sheath 0.038	madf-3	0.0668835253166759	0.0707415460925049
Cephalic sheath 0.038	madf-5	0.178817352662262	0.149435469595485
Cephalic sheath 0.038	madf-6	0.000449338552955803	0.00742749709535761
Cephalic sheath 0.038	madf-9	0.0475897804650389	0.0317128730669737
Cephalic sheath 0.038	mdt-29	0.0375650053470824	0.0510184946848809
Cephalic sheath 0.038	nhr-11	0.0327652280321412	0.0281857110993689
Cephalic sheath 0.038	nhr-179	0.00508199057129759	0
Cephalic sheath 0.038	nhr-237	0.040555771896294	0.0253161472854632
Cephalic sheath 0.038	pag-3	0.116866723357109	0.0915022462254428
Cephalic sheath 0.038	pat-9	0.252500773783609	0.215306434097834
Cephalic sheath 0.038	pbrm-1	0.00195977553177457	0.000819173969808738
Cephalic sheath 0.038	R02D3.7	0.0148987792182734	0.0174283230229613
Cephalic sheath 0.038	saeg-2	0	0.0134439037345549
Cephalic sheath 0.038	skn-1	0.00627149389851915	0.00706548798090487
Cephalic sheath 0.038	snu-23	0.0241137999980562	0.0247795184843002
Cephalic sheath 0.038	sptf-2	0.377925741983939	0.440738819649825
Cephalic sheath 0.038	T26A5.8	0.100545472332892	0.0686106549528636
Cephalic sheath 0.038	Y53G8AR.9	0.0153064402804334	0.017201047431943
Cephalic sheath 0.038	Y56A3A.18	0.0376498132986838	0.0449919722649167
Cephalic sheath 0.038	zfh-2	0.0466296664190381	0.0445271065212143
Cephalic sheath 0.038	zim-3	0.0896466408688866	0.0794193876275175
Cephalic sheath 0.038	ztf-1	0.013130560858412	0.00782054787369734
Cephalic sheath 0.038	ztf-26	0.0988760545363296	0.0726312055305877
Coelomocytes 0.044	alr-1	0.208512320293401	0.22552834200723
Coelomocytes 0.044	aptf-3	0.00972128437125113	0.0141980407466623
Coelomocytes 0.044	arid-1	0.0057539898933016	0.0128251393322447

Coelomocytes 0.044	attf-6	0.0212283834452671	0.0329872537897696
Coelomocytes 0.044	ceh-40	0.0932021389516293	0.110450298122915
Coelomocytes 0.044	cey-2	0.0246889325715219	0.0144336294011839
Coelomocytes 0.044	crh-2	0.0225458320142773	0.0200989340019543
Coelomocytes 0.044	D1046.2	0.0192128461747694	0.0170178903625725
Coelomocytes 0.044	daf-16	0.00427550896486695	0.00343161663458237
Coelomocytes 0.044	daf-19	0.0642720508997545	0.0726734198259018
Coelomocytes 0.044	dmd-9	0	0.000629062323807299
Coelomocytes 0.044	dxbp-1	0.0108454172296288	0.0149591521811256
Coelomocytes 0.044	egl-5	NA	0.0699876268466528
Coelomocytes 0.044	ekl-4	0.0283043825507474	0.0366785499206988
Coelomocytes 0.044	ets-5	0.0450271956775252	0.0655481923908604
Coelomocytes 0.044	F33H1.4	0	3.70570812746374e-05
Coelomocytes 0.044	F44E2.7	0.0214365333419175	0.032783348295835
Coelomocytes 0.044	fkh-2	0	0.0151703994426479
Coelomocytes 0.044	hif-1	0.0257484101442803	0.0266094028515926
Coelomocytes 0.044	hinf-1	0.05432108614981	0.0662739327400619
Coelomocytes 0.044	hlh-1	0.00776481146034829	0.00473008125823355
Coelomocytes 0.044	hlh-11	0.0205911025186666	0.0187291747617357
Coelomocytes 0.044	hlh-8	0.136682775343367	0.137192170373475
Coelomocytes 0.044	hmg-1.1	0.0154728763249021	0.014615070880994
Coelomocytes 0.044	hsf-1	0.027291413915892	0.0252001829880033
Coelomocytes 0.044	jun-1	0.00805281504503393	0.0139553511130926
Coelomocytes 0.044	K12H6.12	0.0242286944539807	0.0101058205135928
Coelomocytes 0.044	klf-2	0.0111921127487503	NA
Coelomocytes 0.044	let-607	0.0183902958477199	0.0232108989292836
Coelomocytes 0.044	lim-7	0.0135758214670729	0.0198807172137346
Coelomocytes 0.044	lin-11	0.00175986147710791	0.0154483256750172
Coelomocytes 0.044	lin-26	0.0452210636833667	0.0479270547640735
Coelomocytes 0.044	lsy-2	0.0224106862752419	0.0231054785599477
Coelomocytes 0.044	madf-3	0.0441906631815051	0.0494896190801315
Coelomocytes 0.044	madf-6	0.00790462972538107	0.0102813985132966
Coelomocytes 0.044	mdt-29	0.0106829702890985	0.00346169108955153
Coelomocytes 0.044	mml-1	0.118361701775918	0.0989728991725122
Coelomocytes 0.044	nfyb-1	0.00317417780762818	0.00511515119502823
Coelomocytes 0.044	nhr-11	0.0341204853575462	0.0264191483915963
Coelomocytes 0.044	nhr-237	0.0379328014476438	0.0324690625084913
Coelomocytes 0.044	nhr-48	0.00277199238657803	0.00384378463302398
Coelomocytes 0.044	pha-4	0.00801612954548071	0.00642122924045118
Coelomocytes 0.044	R02D3.7	0.00662798366334433	0.0137864496254482
Coelomocytes 0.044	rnt-1	0.00162727889330994	0
Coelomocytes 0.044	skn-1	0.0144854251444132	0.0106651412839238
Coelomocytes 0.044	sma-3	0	0.00530105330352824

Coelomocytes 0.044	spr-3	0.00106160629264909	0
Coelomocytes 0.044	sptf-2	0.236658111210238	0.2729763570092
Coelomocytes 0.044	tbx-37	NA	0.000298697291275025
Coelomocytes 0.044	unc-120	0	0.00136710455191338
Coelomocytes 0.044	xbp-1	0.00907554260231534	0.0108618364886355
Coelomocytes 0.044	Y53G8AR.9	0.00295083956612607	0.00391186939003531
Coelomocytes 0.044	Y56A3A.18	0.0622474123957743	0.0741942441186522
Coelomocytes 0.044	zfh-2	0.0124231312396523	0.0166324453348978
Coelomocytes 0.044	ZK546.5	0.209852375322111	0.291818982628606
Coelomocytes 0.044	ztf-23	0.0107857997689083	0.0128908879728668
Coelomocytes 0.044	ztf-7	0.00150186057669396	0
DVA 0.046	alr-1	0.154614153441148	NA
DVA 0.046	atf-7	0.0349183934504512	0.0370209041859725
DVA 0.046	attf-6	0.0229346675211029	0.0226705658806184
DVA 0.046	C34B4.2	0.106929527156922	0
DVA 0.046	cebp-1	0.00826094156441265	0.00625801481212856
DVA 0.046	ceh-18	0	0.00525091895509186
DVA 0.046	crh-2	0.059327969818908	0.0696001918432938
DVA 0.046	ctbp-1	0.201937078665632	0.206084350482211
DVA 0.046	daf-19	0.108217609614721	NA
DVA 0.046	die-1	NA	0.00143174751856297
DVA 0.046	dxbp-1	0	0.00638564448322405
DVA 0.046	egl-13	0.0623169420508941	0.106206166148521
DVA 0.046	egl-18	NA	0.133380346562033
DVA 0.046	egl-27	0.0214797465168212	0.0182247345529615
DVA 0.046	ekl-4	0.0827529968623642	0.0831516987089604
DVA 0.046	ets-5	0.0311950711139235	NA
DVA 0.046	F33H1.4	0.0129990257327358	0.00944458128796111
DVA 0.046	F57A8.1	0.0696716272578198	0.102304578189695
DVA 0.046	hif-1	0.0310412198400914	0.0375707104606492
DVA 0.046	hinf-1	NA	0.114942634839221
DVA 0.046	hsf-1	0.0246166298586863	0.0248315237240207
DVA 0.046	isw-1	0.00819457475548097	0.0760032731206067
DVA 0.046	K12H6.12	0.116839909767158	NA
DVA 0.046	lag-1	0.059489297850356	0.0825557586193643
DVA 0.046	lim-6	0.0807996717481223	NA
DVA 0.046	lin-11	0.192572797263616	0.188451653929468
DVA 0.046	lin-13	0	0.0154982335198124
DVA 0.046	lin-39	0.0458864687920369	NA
DVA 0.046	lin-40	0.0663947436034586	0.0393240282998912
DVA 0.046	lsy-2	NA	0.0284878746718867
DVA 0.046	madf-6	0.015243270763944	NA
DVA 0.046	mbf-1	0.159228051811653	0.177377975609418

DVA 0.046	mdt-29	0.014589903545424	NA
DVA 0.046	mef-2	0.0750134979203013	0.0708978949867426
DVA 0.046	nfya-2	0.0179416982802689	0
DVA 0.046	nfyb-1	0.00236979191057412	NA
DVA 0.046	nhr-6	0.00324568468390938	0.0121667346483794
DVA 0.046	nhr-71	0.0198683032143508	0.0163510903727399
DVA 0.046	pbrm-1	0	0.00553700781752737
DVA 0.046	sem-4	0.0390565505145497	0.0456949831379167
DVA 0.046	somi-1	0	0.00160375044475143
DVA 0.046	unc-86	0.0215860973790344	NA
DVA 0.046	Y53G8AR.9	0.00745801051566057	NA
DVA 0.046	Y56A3A.18	0.112399692443851	NA
DVA 0.046	zag-1	0.121644333557812	0.12384245526424
DVA 0.046	zfh-2	0.0404016890305645	0.0391397545034187
DVA 0.046	ZK546.5	0.0891034291600341	NA
DVA 0.046	ztf-1	0	0.0294516814257728
DVA 0.046	ztf-26	0.0644859708962221	0.0475760159931869
DVC 0.045	aha-1	0.295922749890555	NA
DVC 0.045	atf-7	0.015010576038099	0.0183432735618539
DVC 0.045	attf-6	0.00791169711688567	0.0320854701269103
DVC 0.045	C34B4.2	0.229748977849925	0
DVC 0.045	cebp-1	0.00692198457199562	0.0115924678785834
DVC 0.045	ceh-48	0.00501307814558464	0.0211637240225558
DVC 0.045	ceh-63	0.773095867174358	0.772514584773459
DVC 0.045	chd-7	0	0.0191480605687883
DVC 0.045	crh-2	0.0593435103771724	0.071331629156739
DVC 0.045	daf-19	0.125577882704007	0.142162325378656
DVC 0.045	egl-18	0.0802201633345364	0.0947017387065172
DVC 0.045	egl-27	0.0332991769088195	0.033972171767708
DVC 0.045	ekl-4	0.0609001697196009	0.0590816347723416
DVC 0.045	F22D6.2	0	0.0227555194037687
DVC 0.045	F57A8.1	0.0092289454339801	0.128052246345147
DVC 0.045	gei-8	0.00686138124547782	NA
DVC 0.045	hif-1	0.0243333439279073	0.075066174669877
DVC 0.045	hinf-1	0.127011458515253	0.137449637248577
DVC 0.045	hmg-1.1	0.0180365839816928	0.00937067343502221
DVC 0.045	hsf-1	0.0230919745390042	0.0285842051288327
DVC 0.045	isw-1	0.0838885171495176	0.118802893381271
DVC 0.045	K09A11.1	NA	0.0145962185992903
DVC 0.045	lag-1	0.000737729079148335	NA
DVC 0.045	lin-13	0.0085066572027163	0.00525787388397636
DVC 0.045	lin-14	0.064832334602644	0.0571349584567886
DVC 0.045	lin-26	0.0820011706198345	0.0760062922703584

DVC 0.045	lin-40	0.0327188877616065	0.0522072184315937
DVC 0.045	lsy-2	NA	0.0485394751024438
DVC 0.045	madf-5	NA	0.0223766933888496
DVC 0.045	madf-6	0	0.0020770153862887
DVC 0.045	madf-9	0.0069246635374463	0.0361065167319117
DVC 0.045	mbf-1	0.0816054111166756	0.211022629045599
DVC 0.045	mdt-29	0.0127975720063692	0.039953479137663
DVC 0.045	mef-2	0.0363208186313864	0.0845695553165324
DVC 0.045	mml-1	NA	0.0472654644782417
DVC 0.045	nfya-2	0	0.00190070806073887
DVC 0.045	nfyb-1	0.00600568323039314	0.0123311634369482
DVC 0.045	nhr-237	0.00530360604080842	NA
DVC 0.045	nhr-47	0.000186519639093593	0
DVC 0.045	nhr-6	0.00733100863397531	0.00449231201811703
DVC 0.045	pag-3	0.0216143496890729	0.0223517097728909
DVC 0.045	pat-9	0.129884489264943	0.0710717160858764
DVC 0.045	pbrm-1	0.00469953342188169	NA
DVC 0.045	R02D3.7	0.0175556288514375	0
DVC 0.045	row-1	0.0917417843754226	0.0801454709362655
DVC 0.045	sea-2	0.0601899378913869	0.04901407733806
DVC 0.045	sem-4	0.082329478707468	0.0836355889841047
DVC 0.045	somi-1	0	0.000436140160035602
DVC 0.045	T26A5.8	0	0.0183092623658354
DVC 0.045	Y53G8AR.9	0	0.0189581625856481
DVC 0.045	Y56A3A.18	0.0490144754558788	NA
DVC 0.045	zag-1	0.20042314721992	0.197836487749569
DVC 0.045	zfh-2	0.0426364120193746	0.04333682070409
DVC 0.045	ZK546.5	0.0592794763079399	NA
Differentiated germ 0.040	akir-1	0.0238697988285121	0.0287943316199438
Differentiated germ 0.040	alr-1	0.377701797310489	0.385585653918572
Differentiated germ 0.040	attf-6	0.0100729393973325	0.00877943460993313
Differentiated germ 0.040	C16A3.4	0.0265411434414436	0.0310153315476524
Differentiated germ 0.040	cebp-1	0	0.0008366820402161
Differentiated germ 0.040	ceh-40	0.157079335710353	0.170479571567135
Differentiated germ 0.040	daf-19	0.104080578211944	0.106480816774664
Differentiated germ 0.040	dpl-1	0.00298837886193785	0.00193912968423606
Differentiated germ 0.040	dxbp-1	0.00547510433129722	0.007192018280283
Differentiated germ 0.040	efl-1	0.0177605025725131	0.018717255011246
Differentiated germ 0.040	egl-18	0.028734254092079	0.0309862626289346
Differentiated germ 0.040	ekl-4	0.121473194003373	0.124821480224037
Differentiated germ 0.040	elt-4	0.0447825343953742	0.010886083302122
Differentiated germ 0.040	F13C5.2	0.00987149686706975	0.00683177898629657
Differentiated germ 0.040	F22D6.2	0.0488290947350968	0

Differentiated germ 0.040	F23B12.7	0.0052612199888074	0.00406229031103021
Differentiated germ 0.040	F33H1.4	0.0751926979005366	0.0788568772980699
Differentiated germ 0.040	F44E2.7	0.0139882061135651	0.0142735512168838
Differentiated germ 0.040	hinf-1	0.229463704179574	0.227057678261246
Differentiated germ 0.040	hlh-8	0.00174856915398354	0.00209368849771635
Differentiated germ 0.040	hsf-1	0.0147020618185683	0.0204487318230224
Differentiated germ 0.040	lag-1	0.0286842340038281	0.0575024469559356
Differentiated germ 0.040	lim-7	0.0577537460837326	0.0678597136007464
Differentiated germ 0.040	lin-26	0.148439958803323	0.14436702219753
Differentiated germ 0.040	lin-40	0.0568027428427968	0.0186289874391231
Differentiated germ 0.040	lin-54	0.0291917231847516	0.0307350185110662
Differentiated germ 0.040	lsy-2	0.0324488275701142	0.0326918559631626
Differentiated germ 0.040	madf-3	0.0995969603297572	0.10114368732122
Differentiated germ 0.040	madf-5	0.130057921457791	0.109272761099289
Differentiated germ 0.040	madf-6	0.0395614850030552	0.0434196664312733
Differentiated germ 0.040	madf-9	0.00906150141248481	0
Differentiated germ 0.040	pag-3	0.0185754392809931	0.0187781848673694
Differentiated germ 0.040	pat-9	0.155465882874406	0.156222812801594
Differentiated germ 0.040	pbrm-1	0.00270105323495037	0
Differentiated germ 0.040	R02D3.7	0.0192683996202438	0.0164858528561251
Differentiated germ 0.040	skn-1	0.00397859303980087	0.00480432297876045
Differentiated germ 0.040	sptf-2	0.576321358521578	0.585300353779126
Differentiated germ 0.040	Y48G9A.11	0.00827783178334332	0.0102944686201599
Differentiated germ 0.040	Y53G8AR.9	0.00976476622779342	0.00742185189121507
Differentiated germ 0.040	Y56A3A.18	0.072232943677331	0.0752247646941442
Differentiated germ 0.040	zfh-2	0.0506403740618949	0.0483853017487566
Differentiated germ 0.040	zim-3	0.0124560094389968	0.00416958351582027
Differentiated germ 0.040	ztf-26	0.0339396089748844	0
Distal tip 0.041	akir-1	0.0407045366668485	0.12648482132451
Distal tip 0.041	alr-1	0.161009143277592	0.175682997291911
Distal tip 0.041	arid-1	0	0.00828686790991509
Distal tip 0.041	attf-6	0	0.00324426351122789
Distal tip 0.041	cebp-1	0.0180688250507358	0.02594730446126
Distal tip 0.041	ceh-27	0.00804431587301294	0.0181661945097015
Distal tip 0.041	chd-7	0	0.00409518350617917
Distal tip 0.041	cnd-1	0.00822885096288146	NA
Distal tip 0.041	crh-2	0.000983746590778408	0.0068553427932056
Distal tip 0.041	ctbp-1	0.0362564345806803	0.034888465200789
Distal tip 0.041	D1046.2	0.00577972718357374	0.0155609833280156
Distal tip 0.041	daf-16	0	0.000187205643167232
Distal tip 0.041	daf-19	0.0680884923563247	0.0715105528718622
Distal tip 0.041	daf-8	0.0937071615938737	0.122688657994055
Distal tip 0.041	dxbp-1	0	0.00628231869428282

Distal tip 0.041	egl-18	0.00016836751824356	0.0227378493481751
Distal tip 0.041	ekl-4	0.0565092145592634	0.0682211620585029
Distal tip 0.041	F33H1.4	0	0.00852451639891051
Distal tip 0.041	fkh-2	NA	0.935072095522172
Distal tip 0.041	hif-1	0.00473236573549507	0.00600002250747229
Distal tip 0.041	hinf-1	0.0520736421130565	0.0616672894548928
Distal tip 0.041	hlh-1	0.118954115907634	0.123696171660567
Distal tip 0.041	hlh-11	0.0100746242758831	0.0157706503660362
Distal tip 0.041	hlh-30	0	0.00272691694309604
Distal tip 0.041	hlh-8	0.39521047003878	0.401344037994777
Distal tip 0.041	hmg-11	0.0101407925553182	0.0172464205982352
Distal tip 0.041	hnd-1	NA	0.0191855938074616
Distal tip 0.041	hsf-1	0.0263590151627594	0.0257988918246707
Distal tip 0.041	let-607	0.030348827715262	0.0376215207037558
Distal tip 0.041	lim-7	0.00308731653889498	0.0181808066871134
Distal tip 0.041	lin-11	0.0186045779867959	0.0646240414155644
Distal tip 0.041	lin-14	0.0186029589338861	0.026446253833018
Distal tip 0.041	lin-26	0.0468853462981014	0.0435219555112866
Distal tip 0.041	lin-32	0.0293065799234901	0.0433352823613933
Distal tip 0.041	lin-39	0.0392304917873562	0.0381311444244489
Distal tip 0.041	lin-40	0.0380943597540295	0.0170039717419386
Distal tip 0.041	lsy-2	0.0227443528930346	0.0246797166401816
Distal tip 0.041	madf-2	0.199224635961393	0.286832872613684
Distal tip 0.041	madf-3	0.0451421322851616	0.0478609797464078
Distal tip 0.041	madf-5	0.0745445698466231	0.0511859091708071
Distal tip 0.041	madf-6	0.0036968075886377	0.0127642297519413
Distal tip 0.041	madf-9	0.0171870811842912	0.0255297788263648
Distal tip 0.041	mdt-29	0.012742969407146	0.0185130848231428
Distal tip 0.041	mep-1	0.0242815936490695	0.0276677699859826
Distal tip 0.041	mml-1	0.0509410104026116	0.0449719044300192
Distal tip 0.041	nfyb-1	0.0238201202408108	0.0295532605766765
Distal tip 0.041	nhr-11	0	0.000454673472545599
Distal tip 0.041	nhr-129	0.0429774451760476	0.0441673801519507
Distal tip 0.041	nhr-19	0.0193553951197468	0.0267745381367791
Distal tip 0.041	pag-3	0.033329728870166	NA
Distal tip 0.041	pat-9	0.377752959251497	0.377029362390705
Distal tip 0.041	R02D3.7	0	0.00010603900509433
Distal tip 0.041	saeg-2	0.048132851543218	0.068477812688053
Distal tip 0.041	sox-4	0.0454866701982765	NA
Distal tip 0.041	sptf-2	0.228288074958371	0.267711647646817
Distal tip 0.041	T26A5.8	0.0264303546612006	0.0180363149491952
Distal tip 0.041	unc-62	0.00567525086125399	0.0137429734937254
Distal tip 0.041	Y56A3A.18	0.033523463515529	0.0465855186247252

Distal tip 0.041	zfh-2	0.040252377753675	0.0450420931154874
Distal tip 0.041	zim-3	0.00568562912812559	0.0224160301018921
Distal tip 0.041	zip-11	0.0245739061962849	0.115587416660035
Distal tip 0.041	ZK546.5	0	0.00102399600903453
Distal tip 0.041	ztf-23	0.0483256598117537	0.058339444526249
Distal tip 0.041	ztf-26	0.0410669091651747	0.0187287759894929
Dorsal uterine cells 0.029	alr-1	0.0962024186494904	0.120915000702697
Dorsal uterine cells 0.029	attf-6	0	0.00513815404192589
Dorsal uterine cells 0.029	B0035.1	0.45284129983799	0.546576774918888
Dorsal uterine cells 0.029	blmp-1	0.00704819937822014	0.00536079691752601
Dorsal uterine cells 0.029	cebp-1	0.0254011221456152	0.02913006093164
Dorsal uterine cells 0.029	ceh-40	0.0657708565110904	NA
Dorsal uterine cells 0.029	crh-2	0.00303994247963217	0.012884944975942
Dorsal uterine cells 0.029	daf-19	0.0120619637168205	0.046182279673893
Dorsal uterine cells 0.029	dve-1	0.0101953316063849	0.0172500463178464
Dorsal uterine cells 0.029	ekl-4	0.0288496712758284	0.0511675817047967
Dorsal uterine cells 0.029	elt-3	0.000724275377609136	0.00419047262556894
Dorsal uterine cells 0.029	F10B5.3	0	9.21042230938528e-05
Dorsal uterine cells 0.029	gmeb-2	NA	0.155019292139823
Dorsal uterine cells 0.029	hinf-1	0.0168737768046102	0.045034347361423
Dorsal uterine cells 0.029	hlh-11	0	0.000151462128740322
Dorsal uterine cells 0.029	hlh-8	0.0156340382670224	NA
Dorsal uterine cells 0.029	isw-1	0	0.0248268372704802
Dorsal uterine cells 0.029	jun-1	0	0.0103030745405221
Dorsal uterine cells 0.029	lag-1	0	0.00290898299695911
Dorsal uterine cells 0.029	let-607	0.00333401241461528	0.00811047138805569
Dorsal uterine cells 0.029	lim-7	0	0.0103148887362494
Dorsal uterine cells 0.029	lin-14	0.0237866417807955	0.0225081860174367
Dorsal uterine cells 0.029	lin-26	0.0324001448240281	0.0405559636071493
Dorsal uterine cells 0.029	lin-40	0.0844497106235121	0.0679330223771569
Dorsal uterine cells 0.029	lsy-2	0	0.00225275021427149
Dorsal uterine cells 0.029	madf-3	0.010496234331367	0.0215591866949204
Dorsal uterine cells 0.029	madf-5	0.0281902957216315	0.027367821912023
Dorsal uterine cells 0.029	mdt-29	0.0264508694082546	0.0350528418239434
Dorsal uterine cells 0.029	nfya-2	0	0.00826567234557095
Dorsal uterine cells 0.029	nhr-11	0.0202933023645662	0.0240908934581821
Dorsal uterine cells 0.029	nhr-129	0.012479890208661	0.0141750882587942
Dorsal uterine cells 0.029	nhr-237	0.143937836214514	0.126103934513029
Dorsal uterine cells 0.029	nhr-6	0.0307189894318677	NA
Dorsal uterine cells 0.029	pag-3	NA	0.0520502287761739
Dorsal uterine cells 0.029	pat-9	0.0465845885482656	NA
Dorsal uterine cells 0.029	pha-4	0.00263481061489116	0.00722969296152382
Dorsal uterine cells 0.029	R02D3.7	0.00296588147573756	0.0146202018836491

Dorsal uterine cells 0.029	sma-3	0.00528782373288728	0.0246355261964366
Dorsal uterine cells 0.029	spr-3	0.321242534403123	0.35307698265442
Dorsal uterine cells 0.029	sptf-2	0.0998613227822901	0.172959112058691
Dorsal uterine cells 0.029	tbx-9	0.36966202780816	NA
Dorsal uterine cells 0.029	Y53G8AR.9	0.0130401180144993	0.019968160104557
Dorsal uterine cells 0.029	Y56A3A.18	0.0230504619423558	0.0452846507333564
Dorsal uterine cells 0.029	zfh-2	0.0214848826452815	0.0260108402764293
Dorsal uterine cells 0.029	ZK546.5	0.185626539305135	0.300928838183899
Embryonic cells 0.034	akir-1	0.104992627851862	0
Embryonic cells 0.034	alr-1	NA	0.33079497419471
Embryonic cells 0.034	aptf-2	0.0192850731678747	0.0157880851909956
Embryonic cells 0.034	baz-2	0.05630666588973	0.0684697878562014
Embryonic cells 0.034	bed-1	0.0946987494534277	0.0878193023004249
Embryonic cells 0.034	C16A3.4	0	0.017451066708388
Embryonic cells 0.034	ceh-16	0.0194662790364059	0.00951926584698882
Embryonic cells 0.034	ceh-39	0.214925259389717	0.258134734371009
Embryonic cells 0.034	ceh-40	0.0384476113307704	0
Embryonic cells 0.034	cey-2	0.0224842229157254	0
Embryonic cells 0.034	chd-7	0.0256571223836864	0.0145575775763932
Embryonic cells 0.034	cnd-1	0.089834713308372	0.09754434755403
Embryonic cells 0.034	crh-2	0.00919735209658802	0
Embryonic cells 0.034	D1046.2	0.00826298053569514	0.00690366613369522
Embryonic cells 0.034	daf-19	NA	0.0483395189856583
Embryonic cells 0.034	dpl-1	0.023084922299805	0.0240708943047695
Embryonic cells 0.034	efl-1	0.0247524307439038	0.016823523533003
Embryonic cells 0.034	ekl-4	0.0296070349868391	0.0340720667262653
Embryonic cells 0.034	elt-4	0.0888191242556576	0.0100368438575731
Embryonic cells 0.034	ets-5	0.0201004425892391	NA
Embryonic cells 0.034	F13C5.2	0.0126211506219077	0
Embryonic cells 0.034	F22D6.2	0.206308216403487	0
Embryonic cells 0.034	F33H1.4	0.0176925486359887	0
Embryonic cells 0.034	hinf-1	0.274623478758686	0.294085239723263
Embryonic cells 0.034	hlh-26	0.626966149764799	0.442175529716312
Embryonic cells 0.034	hmg-1.1	0.0009506796585745	0
Embryonic cells 0.034	hsf-1	0.00103363802984738	0.00610560525159002
Embryonic cells 0.034	K09A11.1	0.0937157757656951	0.0518420280450265
Embryonic cells 0.034	let-607	0.0282025868623608	0.0209220476227056
Embryonic cells 0.034	lim-7	0.0287824629183888	0.0177529687013698
Embryonic cells 0.034	lin-26	0.100610976067748	0.0724512965732173
Embryonic cells 0.034	lin-40	0.110937281911862	0
Embryonic cells 0.034	lsy-2	0.0239228825294667	0.0175386840316863
Embryonic cells 0.034	madf-3	0.0974503971919834	0.102745638448297
Embryonic cells 0.034	madf-5	0.155367370788552	0.0679855773873893

Embryonic cells 0.034	madf-6	0.0375846097975241	0.0278210732615694
Embryonic cells 0.034	mdt-29	0.0487720775554344	0.0401518301131409
Embryonic cells 0.034	mep-1	0.0186138213421034	0.016610883479064
Embryonic cells 0.034	mxl-1	0.00513307003440098	0
Embryonic cells 0.034	nfya-2	0.0188693231234006	0
Embryonic cells 0.034	nhr-102	NA	0.0197374389295621
Embryonic cells 0.034	nhr-11	0.0276617539050705	0.0139135559214216
Embryonic cells 0.034	nhr-129	0.013404315704574	0.000676487726640807
Embryonic cells 0.034	nhr-179	0.0979066051304474	0
Embryonic cells 0.034	nhr-2	0.017432812451924	0.0210106216494039
Embryonic cells 0.034	nhr-232	0.0526076630579064	0
Embryonic cells 0.034	pat-9	NA	0.244173118139128
Embryonic cells 0.034	pbrm-1	0.00517073947131257	0
Embryonic cells 0.034	pes-1	0.0401352218850802	0.0378900511731901
Embryonic cells 0.034	R02D3.7	0.00762086468335075	0.00629272785850806
Embryonic cells 0.034	repo-1	0.00343285936467988	0
Embryonic cells 0.034	rnt-1	NA	0.012656189032478
Embryonic cells 0.034	sea-1	0.0241315563705356	0.034498291936971
Embryonic cells 0.034	skn-1	0.00276031366897665	0.000138501440788429
Embryonic cells 0.034	sox-2	0.156834105680558	0.155625976814558
Embryonic cells 0.034	spr-3	0.0558200924425961	0
Embryonic cells 0.034	sptf-2	NA	0.205660307943219
Embryonic cells 0.034	T20F7.1	0.00425918911236889	0.00593169027533238
Embryonic cells 0.034	T26A5.8	0.034399209397435	0
Embryonic cells 0.034	tlp-1	0.027728700533318	0
Embryonic cells 0.034	tra-4	0.100955650247901	0.0341452591071531
Embryonic cells 0.034	unc-120	0.000628951198419316	0
Embryonic cells 0.034	xbp-1	0.00410127165430293	0.000525403334627488
Embryonic cells 0.034	Y53G8AR.9	0.0190257967500849	0
Embryonic cells 0.034	Y56A3A.18	0.0158142438716648	0.00390176653225008
Embryonic cells 0.034	zfh-2	0.0541285926481397	0.0453287775027991
Embryonic cells 0.034	zim-3	0.0275896283184622	0
Embryonic cells 0.034	zip-8	0.00659309984959939	0
Embryonic cells 0.034	ztf-1	0.0773382533562689	0.00696022639493796
Embryonic cells 0.034	ztf-11	0.0623042044615571	0.0448797900972774
Excretory cells 0.041	akir-1	0.112349936790244	0.109299609245667
Excretory cells 0.041	alr-1	0.238866800326226	0.251347514516212
Excretory cells 0.041	ceh-18	0.0448459275379923	0.0111886998338658
Excretory cells 0.041	ceh-79	0.0183905391866051	0
Excretory cells 0.041	crh-2	0.0175344835396083	0.0185301509216464
Excretory cells 0.041	daf-19	0.0672099724592328	0.0916737468126717
Excretory cells 0.041	daf-8	0.128366283653114	0.127612026845675
Excretory cells 0.041	dxbp-1	0.000378526817639223	0.00855455647441671

Excretory cells 0.041	egl-18	NA	0.0250769495348518
Excretory cells 0.041	egrh-3	0	0.00392513976103497
Excretory cells 0.041	ekl-4	0.0775966012942005	0.0877970806486188
Excretory cells 0.041	elt-4	0.0819563227169049	0.0832548264794356
Excretory cells 0.041	F22D6.2	0.0262404033781004	0.00974690278944743
Excretory cells 0.041	F33H1.4	0.0184714761966177	0.0328575762491627
Excretory cells 0.041	hinf-1	0.11454757634953	0.133144791911586
Excretory cells 0.041	hlh-8	0.0645769703098578	NA
Excretory cells 0.041	hsf-1	0	0.00716363181069435
Excretory cells 0.041	lag-1	0.0735184419779008	0.0952023312298674
Excretory cells 0.041	let-607	0.00766478383806795	0.00842089313347715
Excretory cells 0.041	lim-7	0.00295748116067302	0.0229700689180471
Excretory cells 0.041	lin-26	0.12893515657666	0.135583356172482
Excretory cells 0.041	lin-40	0.163297235908777	0.133162009576938
Excretory cells 0.041	lin-54	0.00487689355435173	0.0216478803546671
Excretory cells 0.041	lsy-2	0.022392718090176	0.0251178198992648
Excretory cells 0.041	madf-2	0	0.0352073845238332
Excretory cells 0.041	madf-3	0.0669678099594433	0.0751431929760961
Excretory cells 0.041	madf-5	0.196226852893692	0.19574415001967
Excretory cells 0.041	madf-6	0	0.00886205394256516
Excretory cells 0.041	madf-9	0.0370113502339427	NA
Excretory cells 0.041	mdt-29	0.0328965135642594	0.0427363708076743
Excretory cells 0.041	nhr-11	0.0324431571686651	0.0208445715161937
Excretory cells 0.041	nhr-179	0.0387985147781909	0.0803803092928578
Excretory cells 0.041	pag-3	NA	0.0852084949632337
Excretory cells 0.041	pbrm-1	0.0133817532629179	0.012886675982877
Excretory cells 0.041	R02D3.7	0.021516670740003	0.0147777056546483
Excretory cells 0.041	skn-1	0	0.00516920376604044
Excretory cells 0.041	snu-23	0.0182821681729957	0.0115327373988907
Excretory cells 0.041	spr-3	0.0138278981839041	0.0361291389775352
Excretory cells 0.041	sptf-2	0.404362557640256	0.479234235601556
Excretory cells 0.041	sup-37	0.0341183936155267	0
Excretory cells 0.041	T26A5.8	0.185667260417931	0.16084441924659
Excretory cells 0.041	tlp-1	0	0.000503386312232166
Excretory cells 0.041	unc-120	0.0119741678817172	0.00382848596136766
Excretory cells 0.041	Y53G8AR.9	0.0328061638228056	0.0251186313315856
Excretory cells 0.041	Y56A3A.18	0.033005078699375	0.0532788218990273
Excretory cells 0.041	zfh-2	0.0572446044151931	0.0538940288392507
Excretory cells 0.041	zim-3	0.130692194351394	0.128334709584728
Excretory cells 0.041	ZK546.5	0.0461537848245707	0.0778021939148886
Excretory cells 0.041	ztf-1	0.0423409901191412	0.0650608915090369
Excretory cells 0.041	ztf-26	0.0901883690602773	0.0663293715785515
Excretory duct 0.045	alr-1	NA	0.184056416745728

Excretory duct 0.045	blmp-1	0.0252467406172853	0.0223036451076934
Excretory duct 0.045	ceh-40	NA	0.0220557982414938
Excretory duct 0.045	ceh-79	0.0909920506692978	0.108879118340579
Excretory duct 0.045	cey-2	0.0487134176111004	0.0825204242455515
Excretory duct 0.045	crh-2	0.0111624120521597	0.0197069333797354
Excretory duct 0.045	ctbp-1	0.0444427081019987	0.0587932200815259
Excretory duct 0.045	daf-19	0.0522717231620389	0.042641821308165
Excretory duct 0.045	dxbp-1	0.00502034610451355	0.0108605351029497
Excretory duct 0.045	egl-18	0.0213504097056063	0.0214294303062109
Excretory duct 0.045	egrh-3	0.143659073431519	0.144695176154017
Excretory duct 0.045	ekl-4	0.0407379055010788	0.0342544048078088
Excretory duct 0.045	elt-3	0.0492101692381511	0.051447245490393
Excretory duct 0.045	elt-4	0.20974688296968	0.229856263924779
Excretory duct 0.045	F22D6.2	0.178372590618211	0.200735920023158
Excretory duct 0.045	F33H1.4	0.00387879683362103	0.00492045680219524
Excretory duct 0.045	hif-1	0.0106906723608707	0.00455211913155097
Excretory duct 0.045	hinf-1	0.0895735586569245	0.07616789077294
Excretory duct 0.045	hlh-11	0.0168006892013408	0.0183251002275462
Excretory duct 0.045	hsf-1	0.00909267551355272	0.0100321375204085
Excretory duct 0.045	isw-1	0	0.00161430291285021
Excretory duct 0.045	lim-7	0.0124515962843822	0.00406755738950061
Excretory duct 0.045	lin-26	0.138487965354862	0.143441102068205
Excretory duct 0.045	lin-40	0.160627271050064	0.190576681429932
Excretory duct 0.045	lin-54	0.00640937959523191	0.0037904985157851
Excretory duct 0.045	madf-2	0.586421069922285	0.55204371651989
Excretory duct 0.045	madf-3	0.0530932527379926	0.0440622305044829
Excretory duct 0.045	madf-5	0.489243922286111	0.482420138127034
Excretory duct 0.045	madf-9	0.004236758095152	0.0204081498724898
Excretory duct 0.045	mdt-29	0.0577026211853657	0.0787321551125998
Excretory duct 0.045	mec-3	0.282362816857374	0.267539231693484
Excretory duct 0.045	mxl-2	0.0102482154556236	0.00329221995326329
Excretory duct 0.045	mxl-3	0	0.00840932894693793
Excretory duct 0.045	nhr-11	0.0558029824028877	0.0556713086293026
Excretory duct 0.045	nhr-179	0.875976861006455	0.959189783307033
Excretory duct 0.045	nhr-232	0.0218064655667584	0.0673978492930607
Excretory duct 0.045	nhr-25	0.0564871440940805	0.0529641092356898
Excretory duct 0.045	nhr-270	0.0302351449655645	0.056953976707865
Excretory duct 0.045	nhr-43	0.0668134284913845	0.0481165211480135
Excretory duct 0.045	nhr-48	0.0753597206936953	0.0585194219005341
Excretory duct 0.045	pag-3	NA	0.00293894943834619
Excretory duct 0.045	pat-9	0.0224306416050018	0.0149521379996639
Excretory duct 0.045	R02D3.7	0.00882564967136303	0.0100922941366705
Excretory duct 0.045	skn-1	0.00123304651446799	0.00739624421169237

Excretory duct 0.045	spr-1	0.174799550457267	0.152830359309557
Excretory duct 0.045	spr-3	0.0380609656020254	0.0882278514530751
Excretory duct 0.045	sptf-2	0.362782118657916	0.322007550701814
Excretory duct 0.045	T23F11.4	0.135421627063023	0.126028450211838
Excretory duct 0.045	tlp-1	0.043236539455932	0.0571337328071118
Excretory duct 0.045	Y53G8AR.9	0.0124306679088149	0.0209904406330361
Excretory duct 0.045	Y56A3A.18	0.0366606620690944	0.046873369469945
Excretory duct 0.045	zfh-2	0.0225064287330563	0.0213479430679994
Excretory duct 0.045	zim-3	0.0277219460961196	0.0647179501770841
Excretory duct 0.045	ztf-1	0.331453117505945	0.304732937235976
Excretory duct 0.045	ztf-16	0.0996707455882339	0.0918585605236459
Excretory duct 0.045	ztf-26	0.421039603997612	0.439304130164251
Excretory gland 0.030	alr-1	0.341920036488903	0.32424292373323
Excretory gland 0.030	attf-6	0.0189371522084695	0.00713012170026095
Excretory gland 0.030	C16A3.4	0.0147700640019904	0.00394466461642454
Excretory gland 0.030	ceh-18	0.0347818332463742	0.0364628886901599
Excretory gland 0.030	crh-2	0.015741273820277	0.0100664405247194
Excretory gland 0.030	daf-19	0.117698131486364	0.109565707766743
Excretory gland 0.030	dxbp-1	0.00754822397932896	0.00474645523437476
Excretory gland 0.030	egl-18	0.0469322918295452	NA
Excretory gland 0.030	ekl-4	0.100507570626103	0.0886942002683362
Excretory gland 0.030	elt-4	0.0564445054259494	NA
Excretory gland 0.030	F22D6.2	0.0883438779193563	0.0396655160373127
Excretory gland 0.030	F33H1.4	0.0492327935177871	0.0455191029317432
Excretory gland 0.030	F44E2.7	0.00872091131294504	0.0102467718559368
Excretory gland 0.030	hif-1	0.000169576971225121	0
Excretory gland 0.030	hinf-1	0.143878443905747	0.14093410516492
Excretory gland 0.030	hlh-8	0.048501147646512	0.0444896393889339
Excretory gland 0.030	hsf-1	0.0214470184853105	0.0153039974720698
Excretory gland 0.030	lag-1	0.0372287438594309	0.0574831750857768
Excretory gland 0.030	let-607	0.0290795254309111	0.0277169207646988
Excretory gland 0.030	lim-7	0.0467932097479959	0.050709902800055
Excretory gland 0.030	lin-11	0.00814150844056738	0
Excretory gland 0.030	lin-26	0.125844469399106	0.132848971102602
Excretory gland 0.030	lin-40	0.0901958526080912	0.10028964708267
Excretory gland 0.030	lin-54	0.0280746914586299	0.0195635628702561
Excretory gland 0.030	lsy-2	0.0346580154294281	0.0260195044747963
Excretory gland 0.030	madf-3	NA	0.0687497020889934
Excretory gland 0.030	madf-5	0.164836689802442	NA
Excretory gland 0.030	madf-6	0.0216335257360066	0.0211483739992615
Excretory gland 0.030	madf-9	0.0572386999659579	NA
Excretory gland 0.030	mdt-29	0.0169850016811515	0.029201193897848
Excretory gland 0.030	nhr-11	0.0263879548030498	0.0194286072668957

Excretory gland 0.030	nhr-129	0.00588696441988743	0
Excretory gland 0.030	pat-9	0.315604307387023	0.288285346315854
Excretory gland 0.030	pbrm-1	0.0192440285193562	0.0104089635632677
Excretory gland 0.030	R02D3.7	0.0285630423253925	0.0257168030498457
Excretory gland 0.030	rnt-1	0.00471878826526906	0.00505429162242953
Excretory gland 0.030	saeg-2	0	0.00715303531076647
Excretory gland 0.030	sptf-2	0.487036557810972	0.464017812017064
Excretory gland 0.030	sup-37	0.0298125447109686	0.00607847255450625
Excretory gland 0.030	T26A5.8	0.0102921982284539	0.0172588527836268
Excretory gland 0.030	tlp-1	0.0155986231105615	0.00249804096976244
Excretory gland 0.030	unc-120	0	0.000606708534090568
Excretory gland 0.030	Y53G8AR.9	0.0258875193948962	0.0121415306355445
Excretory gland 0.030	Y56A3A.18	0.0686032769737163	0.0674318391782021
Excretory gland 0.030	zfh-2	0.0514222516541924	0.0531861765069912
Excretory gland 0.030	zim-3	0.0570303128935313	0.0483616403338593
Excretory gland 0.030	ztf-1	0.0523989127730602	0.0525683903062967
Excretory gland 0.030	ztf-26	0.0928748740349374	NA
GLR 0.041	aha-1	0.151634538927637	0.232171965251578
GLR 0.041	alr-1	0.244005392439848	NA
GLR 0.041	attf-6	0.0173334447421035	0.00812214623242215
GLR 0.041	bed-1	0.00819487093998813	0
GLR 0.041	ceh-18	0.0133297798180587	0.0328489766679569
GLR 0.041	ceh-27	0.0148369382672261	0.0147735571874317
GLR 0.041	ceh-88	0.0169086530891836	0.00886799146172217
GLR 0.041	crh-2	0.0291732201012323	0.0221761200424052
GLR 0.041	daf-16	0.0035816940566256	0.00627035166790475
GLR 0.041	daf-19	0.0962917308507586	0.0921704735596142
GLR 0.041	daf-8	0	0.0352279007513207
GLR 0.041	dxbp-1	0.0139137409450498	0.00722562665190922
GLR 0.041	egl-18	0.0752536129225304	0.0355208483171643
GLR 0.041	ekl-4	0.0785581766638286	0.0663643400978595
GLR 0.041	F22D6.2	0.158495966888023	0.0518064027539168
GLR 0.041	F33H1.4	0.012836816581663	0
GLR 0.041	F44E2.7	0.00954259978513504	0.00746526745801457
GLR 0.041	fkh-2	0.40634385158332	0.443541211424666
GLR 0.041	hinf-1	0.144984840523942	0.131847995087382
GLR 0.041	hlh-1	0.0475548458259266	0.057136728249969
GLR 0.041	hlh-8	0.123773728115276	0.131575403242789
GLR 0.041	hmg-1.1	0.0134117618274731	0.0144662862609009
GLR 0.041	hsf-1	0.0110606463545087	0.00268050471648672
GLR 0.041	lag-1	0.00291865518966807	0.0342849763704886
GLR 0.041	let-607	0.00585910439410764	0.0103659924392026
GLR 0.041	lim-7	0.0278473200980818	0.00651382964783647

GLR 0.041	lin-14	0.0235636978528851	0.0198721903131941
GLR 0.041	lin-26	0.0946811048680582	0.0718929698084623
GLR 0.041	lin-39	0.0424895994625746	NA
GLR 0.041	lin-40	0.106064158021466	0.0557208639985268
GLR 0.041	lin-54	0.0101954825197421	0.00230515442298573
GLR 0.041	lsy-2	0.0287847826168551	0.0267488148307315
GLR 0.041	madf-3	NA	0.0620625329442058
GLR 0.041	madf-5	NA	0.0813645737578023
GLR 0.041	madf-6	0.0173991158605723	0.00767435253693774
GLR 0.041	madf-9	0.0657512529821643	0.0160178061344732
GLR 0.041	mdt-29	0.0393683521588968	0.0440227397482936
GLR 0.041	nfya-2	0.0213860643382076	NA
GLR 0.041	nhr-129	0.00583038930052766	0
GLR 0.041	nhr-179	0.0364259915888963	NA
GLR 0.041	nhr-71	0.00604781353228687	0.00452413643819435
GLR 0.041	pag-3	NA	0.0548836313483991
GLR 0.041	pat-9	0.415823511215819	NA
GLR 0.041	pbrm-1	0.0169975564942673	0.00958623703331073
GLR 0.041	R02D3.7	0.0274116148919049	0.0252355991219871
GLR 0.041	sptf-2	NA	0.396185801836677
GLR 0.041	syd-9	0.0406178131965231	0.0640442318824183
GLR 0.041	T26A5.8	0.023450690725885	0.0295210225283225
GLR 0.041	unc-120	0.00383130647279436	0.0157381024732975
GLR 0.041	unc-42	NA	0.0249784506014184
GLR 0.041	Y53G8AR.9	0.0170479710721307	0.00838712783135623
GLR 0.041	Y56A3A.18	0.0625751546152044	0.05406645243425
GLR 0.041	zag-1	0.0377466375533683	0.0482387405035534
GLR 0.041	zfh-2	0.0603307276990196	0.0501549343780634
GLR 0.041	zim-3	0.0485718500080309	0.0100881288510117
GLR 0.041	zip-11	0.0173885518246088	0
GLR 0.041	ZK546.5	0.127479471070007	0.197957193039028
GLR 0.041	ztf-1	0.0293637454990037	3.51435483039238e-05
Glia_1 0.039	alr-1	0.146917776479732	NA
Glia_1 0.039	B0035.1	0.155682462961169	0.124787420234145
Glia_1 0.039	blmp-1	0.0338300844526832	0.0470723167202978
Glia_1 0.039	ceh-18	0	0.0059223861532199
Glia_1 0.039	ceh-27	0.102015484496064	0.113392116473227
Glia_1 0.039	daf-19	0.0400250303170449	0.0420031984403869
Glia_1 0.039	egrh-3	0.0233475168929877	0.019707108470097
Glia_1 0.039	ekl-4	0.045794864185046	0.0549205869483734
Glia_1 0.039	elt-4	NA	0.0831239929550271
Glia_1 0.039	F33H1.4	0.0159824519537913	0.0187981371952342
Glia_1 0.039	gei-8	0.175762210712273	0.174778985339815

Glia_1 0.039	grh-1	0.0750135598386573	0.0897285651179839
Glia_1 0.039	hif-1	0.00263636727772856	0.00246133297451459
Glia_1 0.039	hinf-1	0.0839996727741273	0.0987721142228453
Glia_1 0.039	hlh-8	0.0143824524611178	0.0175177103910501
Glia_1 0.039	hsf-1	0.00350910095882929	0.00755043287272834
Glia_1 0.039	lag-1	0	0.00743289776662984
Glia_1 0.039	let-607	0.00625130393427268	0.00411332361486625
Glia_1 0.039	lim-7	0.0168338241041201	0.0315145333762396
Glia_1 0.039	lin-14	0	0.00155538503466136
Glia_1 0.039	lin-26	0.0997640537906643	0.106674799532076
Glia_1 0.039	lin-40	0.0974916252400237	0.0912561864563409
Glia_1 0.039	lin-54	9.13527023615612e-05	0.0102433248384845
Glia_1 0.039	lsy-2	0.00832841661283163	0.00942266856360268
Glia_1 0.039	madf-3	0.0549112538326178	0.0593856516011622
Glia_1 0.039	madf-5	0.139886063305364	0.143636286470313
Glia_1 0.039	madf-9	0.000353178075662209	0
Glia_1 0.039	mdt-29	0.00121839537870325	0
Glia_1 0.039	mxl-2	0.0036908428176203	0
Glia_1 0.039	nhr-11	0.0440794536383732	0.0453294950966398
Glia_1 0.039	nhr-129	0.00340243527069384	NA
Glia_1 0.039	nhr-25	0.0789490861060988	NA
Glia_1 0.039	nhr-85	0.0514542971703129	0.0877638968167349
Glia_1 0.039	pag-3	0.0409024252654049	NA
Glia_1 0.039	pat-9	0.188112567191566	NA
Glia_1 0.039	R02D3.7	0.0189948582294985	0.0165216277063267
Glia_1 0.039	skn-1	0.00324818500328684	0.000931628295802119
Glia_1 0.039	snu-23	0	0.0134028153651642
Glia_1 0.039	spr-3	0.0440186903873961	NA
Glia_1 0.039	sptf-2	0.272741292356875	0.331858640120769
Glia_1 0.039	T26A5.8	0.0661902608547548	0.0293629600550773
Glia_1 0.039	tlp-1	0.00936204350232001	NA
Glia_1 0.039	Y48G9A.11	0.00150968944188112	0.00332878072654988
Glia_1 0.039	Y56A3A.18	0.0309532906626242	0.0329163494209841
Glia_1 0.039	zfh-2	0.0352995232667211	0.0350339805386651
Glia_1 0.039	zim-3	0.0764599795651242	0.0822861213523157
Glia_1 0.039	ztf-1	0.105075518415196	0.0833698570197409
Glia_1 0.039	ztf-26	0.079388611401785	0.0601849779353978
Glia_2 0.043	alr-1	NA	0.198904481420223
Glia_2 0.043	attf-6	0.00188017813218206	0.00783181526299423
Glia_2 0.043	B0035.1	0.13440750852085	0.150875411396656
Glia_2 0.043	blmp-1	0.036768552510473	0.035900730740395
Glia_2 0.043	ceh-18	0	0.00641718378024926
Glia_2 0.043	ceh-27	0.0977080866495314	0.117582146207018

Glia_2 0.043	ceh-88	0.0157118497015375	0.0198617364010611
Glia_2 0.043	daf-19	0.0690690294711257	0.0670141571663311
Glia_2 0.043	egl-18	0.0148349772671342	0.0370780446657486
Glia_2 0.043	egrh-3	0.0136311474561327	NA
Glia_2 0.043	ekl-4	0.0545653535394712	0.0502779066070615
Glia_2 0.043	elt-4	0.0340801516566439	NA
Glia_2 0.043	F33H1.4	0.0222122508578496	0.0289617812206638
Glia_2 0.043	gei-8	0.105415534975298	0.147925778204377
Glia_2 0.043	grh-1	0.0539132535921332	0.0556434977732075
Glia_2 0.043	hif-1	0.0228183681489149	0.0248880971756066
Glia_2 0.043	hinf-1	0.08122009011949	0.101810382529431
Glia_2 0.043	hlh-8	0.0184499743334648	NA
Glia_2 0.043	hsf-1	0.00581572691530861	0.00293781204408535
Glia_2 0.043	klu-1	NA	0.0150628130515541
Glia_2 0.043	lag-1	0.00382648161987043	0.0412499548265711
Glia_2 0.043	let-607	0.00146433588802777	0.00377198970672241
Glia_2 0.043	lim-7	0.017790846293491	0.0378047905356286
Glia_2 0.043	lin-13	0	0.00251903659709625
Glia_2 0.043	lin-14	0.0197333275439842	0.0170153853635152
Glia_2 0.043	lin-26	0.138381208764752	0.148002439801862
Glia_2 0.043	lin-40	0.154325956729322	0.150589229404307
Glia_2 0.043	lin-54	0.0120103963201629	0.0110521282451529
Glia_2 0.043	lsy-2	0.0127458584981776	0.0143154902321658
Glia_2 0.043	madf-2	0	0.0188462144428088
Glia_2 0.043	madf-3	NA	0.06835379809006
Glia_2 0.043	madf-6	9.74627576642304e-05	0
Glia_2 0.043	madf-9	0.0508669990861293	0.0302266711184934
Glia_2 0.043	mdt-29	0.0299610151256957	0.046095297438082
Glia_2 0.043	mep-1	0.00699341216317437	0.00622733752311866
Glia_2 0.043	mxl-2	0.0325898885139638	0.0114966308908376
Glia_2 0.043	nfyb-1	0	0.00140556104188512
Glia_2 0.043	nhr-10	0.0259003228252513	0.0354569491174963
Glia_2 0.043	nhr-11	0.0654592779662336	0.0578439016188859
Glia_2 0.043	nhr-120	0.0193024546481758	0.0146503943017707
Glia_2 0.043	nhr-25	0.059978754422685	0.0688690998153461
Glia_2 0.043	nhr-85	0.091873846362296	0.0987521094539714
Glia_2 0.043	pat-9	0.201144950920836	NA
Glia_2 0.043	pbrm-1	0.011624283810334	0.0136858268935826
Glia_2 0.043	R02D3.7	0.0320324939949248	0.0258670451405806
Glia_2 0.043	skn-1	0.0266425030716643	0.0281917743364247
Glia_2 0.043	snu-23	0.0244224606768426	0.0348744828409665
Glia_2 0.043	sptf-2	0.31320344058427	NA
Glia_2 0.043	sup-37	0.0729797898375013	0.0778248490172671

Glia_2 0.043	T26A5.8	0.041396489143971	0
Glia_2 0.043	unc-62	0.000197019874133127	0
Glia_2 0.043	unc-98	0	0.00984761219122237
Glia_2 0.043	Y48G9A.11	NA	0.000159668840393109
Glia_2 0.043	Y53G8AR.9	0.028283256380758	0.0171043849113474
Glia_2 0.043	Y56A3A.18	0.0429602611741475	0.0507754260031573
Glia_2 0.043	zfh-2	0.0426785899758071	0.0503327493894435
Glia_2 0.043	zim-3	0.155299872451325	0.170884649700528
Glia_2 0.043	ztf-26	0.161243406733424	NA
HSN 0.041	aha-1	0.0767165149623114	0.0852876112051798
HSN 0.041	alr-1	0.136761744552773	NA
HSN 0.041	atf-7	0.0181037727708581	0.0108832161755705
HSN 0.041	attf-6	0.00865433931671766	0.0106717814583464
HSN 0.041	cebp-1	0	8.71205485770353e-05
HSN 0.041	ceh-48	0.0249841040932382	0.0328980458192423
HSN 0.041	crh-2	0.0317387081579602	0.0278669837424302
HSN 0.041	ctbp-1	0.159438402948759	0.149404655245844
HSN 0.041	daf-19	0.136935859901748	0.160238883243126
HSN 0.041	egl-13	0.038402634573051	NA
HSN 0.041	egl-18	0.102719843265993	0.101327721696593
HSN 0.041	egl-5	0.0272181428919733	0.0258573299088671
HSN 0.041	ekl-4	0.031818004501055	0.0445204151143328
HSN 0.041	elt-4	0.00315729787532461	0
HSN 0.041	F22D6.2	0.00730741158973628	0
HSN 0.041	F57A8.1	0	9.74766654479673e-05
HSN 0.041	fkh-10	NA	0.0215251385767673
HSN 0.041	fkh-8	0	0.00544572071489031
HSN 0.041	gei-8	0.00498075098166159	0.0254127008916398
HSN 0.041	hif-1	0	0.00258948364576663
HSN 0.041	hinf-1	0.0975467600884392	0.107520909465844
HSN 0.041	hlh-8	0.045059121833372	NA
HSN 0.041	hsf-1	0.0051847980753443	0.00517951941998015
HSN 0.041	isw-1	0	0.000818327133134652
HSN 0.041	K12H6.12	0.0432959844486562	0.0676798246708698
HSN 0.041	lag-1	0.0575201935806341	0.0862139123951231
HSN 0.041	lim-7	0	0.00263518679209693
HSN 0.041	lin-11	0.177838463499793	NA
HSN 0.041	lin-14	0.0365204331864807	0.0295949619291004
HSN 0.041	lin-26	0.0671285768009272	0.0652764546227028
HSN 0.041	lin-39	0.000486853008173951	NA
HSN 0.041	lin-40	0.0817398251069581	0.0239735321628606
HSN 0.041	lsy-2	0.0304421572211618	0.0269203176617944
HSN 0.041	madf-3	0.0408255182950265	0.049514868997777

HSN 0.041	madf-5	0.0359498465049713	0
HSN 0.041	mbf-1	0.175819433094223	0.138391710985559
HSN 0.041	mdt-29	0.00511375284968662	0
HSN 0.041	nfya-1	0.0107499785887975	0.0188825766070983
HSN 0.041	nfya-2	0	1.59123253469745e-05
HSN 0.041	nfyb-1	0.00120129542574792	0
HSN 0.041	nhr-11	0.0145697121330955	NA
HSN 0.041	nhr-232	0.179653980352857	NA
HSN 0.041	pag-3	NA	0.0219204163398004
HSN 0.041	sem-4	0.0553905068627076	0.0600714536110286
HSN 0.041	somi-1	0	0.0110387999082642
HSN 0.041	sptf-2	0.289523272862904	NA
HSN 0.041	unc-120	0.0033191110803043	NA
HSN 0.041	unc-42	0.0206681847298784	0.0178119611828352
HSN 0.041	unc-62	0.00154020092918886	0
HSN 0.041	unc-86	0.0997017389811205	0.11787711921168
HSN 0.041	Y53G8AR.9	0.0177258580018318	0.016411162732344
HSN 0.041	Y56A3A.18	0.0240360339455344	0.0266505334861322
HSN 0.041	zag-1	0.0662652504506414	0.0882457457313277
HSN 0.041	zfh-2	0.0377258500973177	0.0304090052295721
HSN 0.041	ZK546.5	0.0697516729934143	0.12220120607569
HSN 0.041	ztf-26	0.0750505402490382	NA
Hypodermis head 0.042	alr-1	0.342639821295865	0.362271175185362
Hypodermis head 0.042	blmp-1	0.0256478159578955	0.0275724015415827
Hypodermis head 0.042	ceh-45	0.138090967471471	0.154147938561306
Hypodermis head 0.042	ceh-79	0.0535580417726423	0.0487476156233438
Hypodermis head 0.042	cey-2	0.011994630315073	0.00327088442486827
Hypodermis head 0.042	daf-19	0.0404681129349479	0.0303584485735877
Hypodermis head 0.042	egrh-3	0.0140141138783594	0.0196349587849189
Hypodermis head 0.042	ekl-4	0.0366396363662392	0.0594753288825561
Hypodermis head 0.042	elt-3	0.036419633505081	0.0353513839473919
Hypodermis head 0.042	elt-4	0.155560798365984	NA
Hypodermis head 0.042	F22D6.2	0.166003550151958	0.148544269120752
Hypodermis head 0.042	F33H1.4	0.00529776564190042	0.0142259096841377
Hypodermis head 0.042	gei-8	0.0608519955562686	0.0426899659267343
Hypodermis head 0.042	grh-1	0.0200445221559788	0.0240025913869868
Hypodermis head 0.042	hinf-1	0.0770696387504417	0.106556960241895
Hypodermis head 0.042	hlh-8	0.0221914811547032	NA
Hypodermis head 0.042	hsf-1	0	0.015203503361714
Hypodermis head 0.042	lag-1	0	0.0619359198274094
Hypodermis head 0.042	lin-14	0.00878913169778094	0.00617218435704777
Hypodermis head 0.042	lin-26	0.153093061441198	0.16718565649359
Hypodermis head 0.042	lin-40	0.263074007139696	0.268536403713239

Hypodermis head 0.042	lin-54	0	0.00187875297160364
Hypodermis head 0.042	lsy-2	0.000371680179653479	0.00317070153165806
Hypodermis head 0.042	madf-3	0.0493279621168582	NA
Hypodermis head 0.042	madf-5	0.224081129172225	0.236418041542801
Hypodermis head 0.042	madf-9	0.0674581733659738	0.0741723976090863
Hypodermis head 0.042	mdt-29	0.00288020562968797	0
Hypodermis head 0.042	mxl-2	0.00606249605251326	0
Hypodermis head 0.042	nhr-11	0.0451816115625327	0.0324719542110171
Hypodermis head 0.042	nhr-120	0.0140895949765896	0.010356442987791
Hypodermis head 0.042	nhr-129	0.00134047303327809	0.00059464714486322
Hypodermis head 0.042	nhr-179	0.262915228443236	NA
Hypodermis head 0.042	nhr-20	0.00263111875570662	0.0025993638326025
Hypodermis head 0.042	nhr-25	0.00259988702539904	0.00350234259560655
Hypodermis head 0.042	nhr-270	0.0252782117386705	0.0320885342448535
Hypodermis head 0.042	nhr-85	0.0322259916012083	NA
Hypodermis head 0.042	pag-3	0.0945126967571438	0.0865688912898655
Hypodermis head 0.042	pat-9	0.203166934447928	0.183200678997303
Hypodermis head 0.042	pbrm-1	0.00399065203129406	0
Hypodermis head 0.042	R02D3.7	0.0125562363638261	0.0109363019241723
Hypodermis head 0.042	repo-1	0.016461468454546	0
Hypodermis head 0.042	skn-1	0.0125789697567578	0.0123250820902081
Hypodermis head 0.042	sma-3	0.0106240621152374	0.0101996136711312
Hypodermis head 0.042	snu-23	0	0.00608316830041214
Hypodermis head 0.042	sptf-2	NA	0.406388696337244
Hypodermis head 0.042	T26A5.8	0.0427277549879395	0.0195541689304174
Hypodermis head 0.042	Y48G9A.11	0	0.00460015080002473
Hypodermis head 0.042	Y53G8AR.9	0.0168693963985659	0.0216717124777941
Hypodermis head 0.042	Y56A3A.18	0.0220542658041483	0.0362658025410395
Hypodermis head 0.042	zfh-2	0.053327304311447	0.0558771118019483
Hypodermis head 0.042	zim-3	0.133830468620735	0.123969414417964
Hypodermis head 0.042	ztf-1	0.000977398742023302	0.00777365306357222
Hypodermis head 0.042	ztf-26	0.292047677968807	0.31632809558215
Hypodermis tail 0.056	B0035.1	0.0598176532246815	0.00800094361800495
Hypodermis tail 0.056	blmp-1	0.0376876124617532	0.0358081444044369
Hypodermis tail 0.056	ceh-79	NA	0.115358095774728
Hypodermis tail 0.056	cey-2	0.171809051509082	0.0992038730137244
Hypodermis tail 0.056	dxbp-1	0.0121148490331713	0.00701429573208224
Hypodermis tail 0.056	elt-3	0.0485596842842882	0.0350812765681924
Hypodermis tail 0.056	F22D6.2	0.430278556034911	0.22267749673489
Hypodermis tail 0.056	F37B4.10	0.00579492102544216	NA
Hypodermis tail 0.056	gei-8	NA	0.115262380896772
Hypodermis tail 0.056	hinf-1	0.0444307798057936	0.090975944031067
Hypodermis tail 0.056	lin-14	0.00760028057824077	0.00664525536368074

Hypodermis tail 0.056	lin-26	0.231157521784523	0.189322540424814
Hypodermis tail 0.056	lin-40	0.671919827934066	0.487334800069669
Hypodermis tail 0.056	madf-5	NA	0.481382293682712
Hypodermis tail 0.056	madf-9	NA	0.174227920680397
Hypodermis tail 0.056	mdt-29	0.0110429733691791	0
Hypodermis tail 0.056	mxl-1	0	0.0169340362357551
Hypodermis tail 0.056	mxl-2	0.0413214433672764	0
Hypodermis tail 0.056	nhr-11	0.0544705845235199	0.0394740281634644
Hypodermis tail 0.056	nhr-120	0.0615918690235249	0.0151064846809272
Hypodermis tail 0.056	nhr-179	NA	0.463700812045528
Hypodermis tail 0.056	nhr-20	0.0139484909923977	NA
Hypodermis tail 0.056	nhr-25	0.0505946743553784	0.0184032017345567
Hypodermis tail 0.056	nhr-85	0.129065458282658	0.105890089166476
Hypodermis tail 0.056	pbrm-1	0.0124787887982678	0.0032038796722675
Hypodermis tail 0.056	R02D3.7	NA	0.0176883237880954
Hypodermis tail 0.056	rcor-1	0.00834632115818534	0.037159914039825
Hypodermis tail 0.056	repo-1	0.0569922447030132	0
Hypodermis tail 0.056	sma-3	0.0149977938089133	NA
Hypodermis tail 0.056	snu-23	0.00457652835170783	0.027638687536642
Hypodermis tail 0.056	sptf-2	0.291219029542814	NA
Hypodermis tail 0.056	T26A5.8	0.0876003603501358	0
Hypodermis tail 0.056	tbx-9	NA	0.0578062304737946
Hypodermis tail 0.056	unc-120	0.00358397806182004	0
Hypodermis tail 0.056	unc-98	0.0114540088859952	0
Hypodermis tail 0.056	Y48G9A.11	0.00344407033606612	0
Hypodermis tail 0.056	Y53G8AR.9	NA	0.0312052089015757
Hypodermis tail 0.056	Y56A3A.18	0.0338991294248931	0.0325010553574675
Hypodermis tail 0.056	zfh-2	0.0899145165419187	0.0740506344351562
Hypodermis tail 0.056	ztf-26	NA	0.487795053426104
Hypodermis-Gonadal sheath doublet 0.046	alr-1	0.226446894525503	0.246406885942021
Hypodermis-Gonadal sheath doublet 0.046	ceh-40	NA	0.12196542446066
Hypodermis-Gonadal sheath doublet 0.046	ceh-79	0.00792052891658448	0.00617802565713046
Hypodermis-Gonadal sheath doublet 0.046	cey-2	0.0114360005274885	7.50294784103609e-05
Hypodermis-Gonadal sheath doublet 0.046	ctbp-1	0.0147868131286778	0.015741755795775
Hypodermis-Gonadal sheath doublet 0.046	daf-19	0.081223269574103	0.0691279077705972
Hypodermis-Gonadal sheath doublet 0.046	egrh-3	0.0207132792279076	0.0128962102910119

Hypodermis-Gonadal sheath doublet 0.046	ekl-4	0.0487152817035697	0.0555320924667006
Hypodermis-Gonadal sheath doublet 0.046	elt-3	0.0339430946540075	0.0241064699066447
Hypodermis-Gonadal sheath doublet 0.046	elt-4	0.170760778836134	0.160797030731598
Hypodermis-Gonadal sheath doublet 0.046	F22D6.2	0.281151579838474	0.242503392982125
Hypodermis-Gonadal sheath doublet 0.046	F33H1.4	0.0117185078557239	0.0184151890104663
Hypodermis-Gonadal sheath doublet 0.046	hinf-1	0.0917804602178868	0.104988195185816
Hypodermis-Gonadal sheath doublet 0.046	hlh-8	0.0429481130313174	0.0295514198477837
Hypodermis-Gonadal sheath doublet 0.046	hsf-1	0.00873153654006095	0.0108929397014197
Hypodermis-Gonadal sheath doublet 0.046	let-607	0	0.00254481089649177
Hypodermis-Gonadal sheath doublet 0.046	lin-26	0.171160651765856	0.175056602859929
Hypodermis-Gonadal sheath doublet 0.046	lin-40	0.324741595601779	0.302787224829012
Hypodermis-Gonadal sheath doublet 0.046	lin-54	0	0.0017869470781322
Hypodermis-Gonadal sheath doublet 0.046	lsy-2	0.0219963619501782	0.0219428251677619
Hypodermis-Gonadal sheath doublet 0.046	madf-3	0.0438919041657449	0.049671095047502
Hypodermis-Gonadal sheath doublet 0.046	madf-5	0.321738353396687	0.301044278098327
Hypodermis-Gonadal sheath doublet 0.046	madf-9	0.119838347724179	0.103665761782703
Hypodermis-Gonadal sheath doublet 0.046	mdt-29	0.00935427560883934	0.00945451260131065
Hypodermis-Gonadal sheath doublet 0.046	nhr-11	0.0334441499648635	0.0211685342951404
Hypodermis-Gonadal sheath doublet 0.046	nhr-179	0.29768113078011	0.35494247711067
Hypodermis-Gonadal sheath doublet 0.046	nhr-71	0.00629990164233113	0
Hypodermis-Gonadal sheath doublet 0.046	pag-3	0.105837333738945	0.0970844350204244
Hypodermis-Gonadal sheath doublet 0.046	pat-9	0.210552931028272	0.180524144720909
Hypodermis-Gonadal sheath doublet 0.046	pbrm-1	0.00458590024853941	0.0038011968563947

Hypodermis-Gonadal sheath doublet 0.046	R02D3.7	0.0316973042306813	0.0328995653172416
Hypodermis-Gonadal sheath doublet 0.046	skn-1	0.00111532087313047	0
Hypodermis-Gonadal sheath doublet 0.046	sptf-2	0.414499691825066	0.437244204609708
Hypodermis-Gonadal sheath doublet 0.046	T26A5.8	0.0607853383464956	0.0322638778144016
Hypodermis-Gonadal sheath doublet 0.046	tlp-1	0.00140740452724292	0
Hypodermis-Gonadal sheath doublet 0.046	Y53G8AR.9	0.0231873532069176	0.0183506105371025
Hypodermis-Gonadal sheath doublet 0.046	Y56A3A.18	0.0323460990300356	0.0373610895055049
Hypodermis-Gonadal sheath doublet 0.046	zfh-2	0.0599974096028582	0.0613863018648332
Hypodermis-Gonadal sheath doublet 0.046	zim-3	0.124318321874454	0.127434650314318
Hypodermis-Gonadal sheath doublet 0.046	ztf-26	0.322971187642599	0.289557394289065
I1 0.042	aha-1	NA	0.135653030373496
I1 0.042	alr-1	0.218329655820779	0.179181470881863
I1 0.042	attf-6	0.0157071195595192	0.0183318357359028
I1 0.042	bcl-11	0	0.00810268177713604
I1 0.042	C34B4.2	NA	0.20070472172954
I1 0.042	cebp-1	0.00144823526886374	NA
I1 0.042	ceh-18	0	0.0185111977901656
I1 0.042	ceh-34	0.0595557687413029	0.0828579802974835
I1 0.042	crh-2	0.0371401423725485	0.037567694117361
I1 0.042	ctbp-1	0.107757509474583	0.176953044900813
I1 0.042	daf-19	NA	0.102908586355981
I1 0.042	dxbp-1	0.0188716470430486	0.00932964589523886
I1 0.042	egl-18	0.123532588963963	0.124957243780333
I1 0.042	egl-27	0.0321713984734085	0.0400164523490988
I1 0.042	ekl-4	0.0676177370361933	0.0809032058984851
I1 0.042	elt-4	0.0484196679798088	NA
I1 0.042	F22D6.2	0.0907912971333343	0.0170852726320896
I1 0.042	F33H1.4	0.00707004952318018	0
I1 0.042	gei-8	0.011551724025644	0.0409988663754288
I1 0.042	hif-1	0.0260394219875308	0.0326166268014117
I1 0.042	hinf-1	NA	0.130893305502965
I1 0.042	hlh-30	0	0.0122690204832804
I1 0.042	hmg-1.1	0	0.0393032108824001
I1 0.042	hmg-11	0.00232163266345211	0.0195810072025724
I1 0.042	hsf-1	NA	0.00295055259296907

I1 0.042	isw-1	0.028289516490576	0
I1 0.042	lag-1	0.0447494231430305	0.0826053646825002
I1 0.042	let-607	0.00728226456538993	0
I1 0.042	lim-7	0.0612614687966798	NA
I1 0.042	lin-13	0.0225735364715755	0.0104184345959082
I1 0.042	lin-14	0.0579584230258801	NA
I1 0.042	lin-40	0.0873258088279409	0.0480741728675704
I1 0.042	lin-54	NA	0.00348444953903738
I1 0.042	lsy-2	0.0405726892673714	0.0617140483309642
I1 0.042	madf-3	0.0594409776718822	NA
I1 0.042	madf-5	0.126979676656821	0.0515386453169977
I1 0.042	madf-6	0.00150453809211683	0
I1 0.042	madf-9	NA	0.0067366385326861
I1 0.042	mbf-1	0.0555755158055616	0.0401457804241568
I1 0.042	mdt-29	0.0555039872910393	0.0356332009073604
I1 0.042	nfyb-1	0.00830663675156312	0.0123470448984646
I1 0.042	nhr-6	NA	0.0192319723087302
I1 0.042	pag-3	0.0467000431499312	0.0708176987551968
I1 0.042	pbrm-1	0.0357296534341535	0.0175122467359811
I1 0.042	R02D3.7	0.00800796831110411	0
I1 0.042	rcor-1	0	0.0108258022375744
I1 0.042	row-1	0.0910961547781192	0.0994859079257827
I1 0.042	T26A5.8	0.0991928807776045	0.00949292620450306
I1 0.042	tlp-1	0.000271510945836788	NA
I1 0.042	unc-42	0.0286057222650394	NA
I1 0.042	unc-62	NA	0.0146463224881455
I1 0.042	unc-86	0.097738090058701	0.156110288304701
I1 0.042	Y53G8AR.9	0.0187108822260685	0.0246027338797164
I1 0.042	Y56A3A.18	0.0727988459120947	0.0455332483529898
I1 0.042	zfh-2	0.0546030285393592	NA
I1 0.042	ZK546.5	0.14842390479995	0.159725524851211
I1 0.042	ztf-1	0.0823815585877716	0
I1 0.042	ztf-26	0.130550332501571	NA
I1 0.042	ztf-4	0	0.000543894785095931
I2 0.043	aha-1	0.138702185479881	NA
I2 0.043	alr-1	0.18611084647334	0.163201063608392
I2 0.043	attf-6	0	0.00213423526563429
I2 0.043	C34B4.2	0.562498005435642	0.211639757480976
I2 0.043	cebp-1	0.00530492870589661	0.00871958178551476
I2 0.043	ceh-18	NA	0.000699174354356578
I2 0.043	ceh-32	0.234948128885384	0.43403034779179
I2 0.043	ceh-34	0.0268321876929246	0.0293672513379911
I2 0.043	ceh-48	0	0.00568099673460977

I2 0.043	chd-7	0.0611309249341125	0.0640808813514297
I2 0.043	crh-2	0.029167439476289	0.0419265994962381
I2 0.043	ctbp-1	NA	0.110432500426333
I2 0.043	daf-19	0.0687650954374052	0.0964070056027034
I2 0.043	egl-18	0.0845179427424354	NA
I2 0.043	egl-27	0	0.000114632931915623
I2 0.043	ekl-4	0.0681638381971877	0.0766271061585547
I2 0.043	F22D6.2	0.125759877707809	0.0875378069009469
I2 0.043	hif-1	0.00504002401718899	0.0139642548551515
I2 0.043	hinf-1	0.0783584418334025	NA
I2 0.043	hmg-1.1	0.0284942754654339	0.0192882275150095
I2 0.043	hmg-11	0.0133969233947737	0.0114828271381873
I2 0.043	hsf-1	0.0122119495054091	0.0194375364217642
I2 0.043	isw-1	0.0663137844228749	0.0312053192385942
I2 0.043	K12H6.12	NA	0.00854114181636212
I2 0.043	lag-1	0.0624784100221059	0.139782568825937
I2 0.043	lim-7	0.00781379176158277	0.0524342935285118
I2 0.043	lin-11	NA	0.164640258287394
I2 0.043	lin-14	0.0376239019751814	0.0460676736078789
I2 0.043	lin-26	0.107672550937837	NA
I2 0.043	lin-40	0.0946967344934749	0.00987082943137494
I2 0.043	lsy-2	0.0132015307332138	0.0233810613856639
I2 0.043	madf-3	0.0437286531300257	NA
I2 0.043	madf-5	0.102206823613242	0.0488904650978639
I2 0.043	madf-9	0.01179702990199	0
I2 0.043	mbf-1	0.193025538200395	0.231068952906095
I2 0.043	nfya-2	0.0130150747851387	0.0597326062471625
I2 0.043	nfyb-1	0.0224318025641431	0.0275277696450832
I2 0.043	nhr-11	0.029391536937414	NA
I2 0.043	nhr-129	0.0199124299855441	NA
I2 0.043	pag-3	0.0450564844149326	0.0480413556250662
I2 0.043	pbrm-1	0.0153250931485759	0.0313004237538388
I2 0.043	R02D3.7	0.00931846466110722	NA
I2 0.043	row-1	0.0788051134717585	NA
I2 0.043	saeg-2	0.041305015538452	0.0511603254603235
I2 0.043	sem-4	0.00122467538981957	NA
I2 0.043	skn-1	0.0019167778815546	0
I2 0.043	T07F8.4	0.0242552096205151	0.0493053000973705
I2 0.043	unc-42	0.0345960267800088	NA
I2 0.043	unc-86	0.0451774424769485	0.0503165791071094
I2 0.043	unc-98	0	0.0112268983877167
I2 0.043	Y53G8AR.9	NA	0.035410786658666
I2 0.043	Y56A3A.18	0.0511176604489796	0.0669216274582294

I2 0.043	zim-3	0.0250395123437582	NA
I2 0.043	ztf-1	NA	0.0371582250585512
I5 0.042	aha-1	0.0285028573853419	0.0716197818746042
I5 0.042	alr-1	NA	0.132355587176142
I5 0.042	atf-7	0.00221605513456813	0.00896332752047302
I5 0.042	attf-6	0	0.0117036233757789
I5 0.042	ceh-18	0	0.00829669582769765
I5 0.042	ceh-48	0.00144506485472178	0.00996332854066087
I5 0.042	ceh-9	NA	0.276294526482615
I5 0.042	crh-2	0.0484430613170434	0.0547523862449849
I5 0.042	ctbp-1	0.166882531100647	0.172408946961812
I5 0.042	daf-19	NA	0.0401030177867519
I5 0.042	egl-18	NA	0.094792836799474
I5 0.042	egl-27	0.0224008913261577	0.0572336818970394
I5 0.042	egrh-3	0	0.00254661271470937
I5 0.042	ekl-4	0.0435294329683535	NA
I5 0.042	ets-5	NA	0.105925461901054
I5 0.042	F22D6.2	0.0839298035185243	0
I5 0.042	F44E2.7	0.0117081569484136	0.0350548132693062
I5 0.042	hif-1	0.00379598592113112	0.0157520627953886
I5 0.042	hinf-1	0.111513788320371	0.0984109191503164
I5 0.042	hsf-1	0.0309122517660773	0.0368632252781408
I5 0.042	isw-1	0.0011955397349261	0.0320308135268552
I5 0.042	lag-1	0.0292322126220362	NA
I5 0.042	lim-7	0.0243731934244187	0.0332585485428544
I5 0.042	lin-11	0.227878816082205	0.28703490536004
I5 0.042	lin-13	0	0.0110187828826742
I5 0.042	lin-14	0.0122853324015888	0.0226283885542955
I5 0.042	lin-26	0.100379993970732	0.0507998676488462
I5 0.042	lin-40	0.093710023751122	0
I5 0.042	lsy-2	0.0196770110525745	0.0210079721605652
I5 0.042	madf-5	NA	0.0378157941860532
I5 0.042	mdt-29	0.0141936482080115	0.0182796019378858
I5 0.042	mef-2	0.0275765185185352	0.020975369376524
I5 0.042	nhr-11	0.041408345447288	NA
I5 0.042	nhr-6	0.000123872488225435	0.015694879362205
I5 0.042	nhr-84	0.0302627054805403	0
I5 0.042	pag-3	0.0491524293085225	NA
I5 0.042	R02D3.7	0.00728523425411095	0.00308085431448663
I5 0.042	row-1	0.0504622826996317	NA
I5 0.042	sem-4	0	0.0214343270544572
I5 0.042	sptf-2	NA	0.289720026675384
I5 0.042	T26A5.8	0.0471209655214943	0.0435506861643102

I5 0.042	Y53G8AR.9	NA	0.0184885674320415
I5 0.042	Y56A3A.18	0.0455409434211238	0.0373629217283555
I5 0.042	zag-1	0.0300778977472579	0.064644070227269
I5 0.042	zfh-2	0.0514136914109337	NA
I5 0.042	zim-3	0.0118417273350801	0
I5 0.042	ztf-26	NA	0.0158869726870566
IL2 0.039	aha-1	0.093508495033824	0.0922106616819598
IL2 0.039	alr-1	0.183118808148562	NA
IL2 0.039	atf-7	0.0020270284796773	0.00541792875026225
IL2 0.039	attf-6	0.0224504299777772	0.0304319445864419
IL2 0.039	bed-1	0	0.00518237172307121
IL2 0.039	cebp-1	0.0162885251787365	0.0049944283214471
IL2 0.039	ceh-27	0.0221172354110148	0.0290942932987723
IL2 0.039	crh-2	0.0406733410573978	0.0370651775614916
IL2 0.039	ctbp-1	0.0616132658653808	0.0721373541900945
IL2 0.039	D1046.2	0.0181860223136005	0.0198868780913222
IL2 0.039	daf-19	0.0842236088577892	0.0785172796530619
IL2 0.039	egl-18	0.074912524407916	0.0669295466867782
IL2 0.039	egl-27	0.00369405302720763	0.0128536641932742
IL2 0.039	ekl-4	0.0407892709242854	0.0538413514722182
IL2 0.039	elt-4	0.120346431926565	0.106273248409682
IL2 0.039	ets-5	0.0387100467318951	NA
IL2 0.039	F22D6.2	0.0454948174306904	0.0389867797965738
IL2 0.039	F33H1.4	0	0.000564729916445883
IL2 0.039	fkh-10	0.0268628092260588	0.0358883087242278
IL2 0.039	fkh-8	0.02451253788043	0.023509314341119
IL2 0.039	hinf-1	0.108341291668278	0.133180482235041
IL2 0.039	lag-1	0.00317946422403828	0.0385238216157876
IL2 0.039	let-607	0.0103225927576477	0.0154582269330948
IL2 0.039	lim-7	0.00999143816718059	0.00997032394706522
IL2 0.039	lin-11	0.284167074754024	0.297623687485215
IL2 0.039	lin-13	0.000109415934416071	0.00452632517111442
IL2 0.039	lin-14	0.026176034395026	0.0312621938097168
IL2 0.039	lin-26	0.0812957142859141	0.0763055326223819
IL2 0.039	lin-40	0.0831351787515787	0.0650955884866492
IL2 0.039	lsy-2	0.0108224750118754	0.0104198836735089
IL2 0.039	madf-3	0.0433468619342283	NA
IL2 0.039	madf-5	0.136686839824944	0.0950544619901774
IL2 0.039	madf-9	0.0114392000114704	0
IL2 0.039	mef-2	0	0.015065117908507
IL2 0.039	nfya-2	0.0569656574291103	0.0664414072045622
IL2 0.039	nfyb-1	0.0196307795882306	0.021873517250455
IL2 0.039	nhr-11	0.0303902936578434	0.0276186193422929

IL2 0.039	nhr-129	0.0022604577855106	0
IL2 0.039	nhr-237	0.0574121915845863	0.0365840941271401
IL2 0.039	pag-3	0.0278570811081347	NA
IL2 0.039	pat-9	0.202772872521961	0.171333196461071
IL2 0.039	saeg-2	0.00483673209443581	0.000427092749165104
IL2 0.039	sem-4	0.0285772144444911	NA
IL2 0.039	sox-4	0.0217598046747778	NA
IL2 0.039	sptf-2	0.291174289833597	NA
IL2 0.039	T26A5.8	0	0.00758022262684604
IL2 0.039	unc-3	0.00763689613712668	NA
IL2 0.039	unc-55	0.0245383365521311	0.0283021166207635
IL2 0.039	unc-62	0.00473117173202278	0.00639131884375996
IL2 0.039	unc-86	0.0476658775120109	0.0352397774143032
IL2 0.039	Y53G8AR.9	0.00950494898607201	0.0194258295273163
IL2 0.039	Y55F3AM.14	0.028693787807222	NA
IL2 0.039	Y56A3A.18	0.0236682400969516	0.0309556287618898
IL2 0.039	zag-1	0.00433094587827201	0.0360754093884672
IL2 0.039	zfh-2	0.0386770003733947	0.0362528451706257
IL2 0.039	ZK546.5	0	0.0462258180276894
IL2 0.039	ztf-1	0.0363855821743745	0
IL2 0.039	ztf-26	0.0786098394581564	0.0444796512968482
Intestine anterior 0.035	alr-1	0.243841343818427	0.211645315153287
Intestine anterior 0.035	atf-7	0	0.0244763725335644
Intestine anterior 0.035	cebp-1	0.00432907540839985	0.00331772992363523
Intestine anterior 0.035	ceh-79	0.0228496778667067	0
Intestine anterior 0.035	chd-7	0.0206393453321811	0.0367307559665993
Intestine anterior 0.035	crh-2	0.0376145293199158	0.0252560507303797
Intestine anterior 0.035	daf-16	0.0171500428140149	0.019916869340049
Intestine anterior 0.035	daf-19	0.061490091582305	0.0557768166810446
Intestine anterior 0.035	daf-8	0.101498941171529	0.369458138421614
Intestine anterior 0.035	dmd-6	0.0191448803940573	0.038872520515302
Intestine anterior 0.035	dpff-1	0	0.0109881330825467
Intestine anterior 0.035	dve-1	0.00184900106396824	0
Intestine anterior 0.035	dxbp-1	0.00236706090513675	0
Intestine anterior 0.035	efl-3	0	0.0107877596494951
Intestine anterior 0.035	egl-18	0.123981618205378	0.0677548798775607
Intestine anterior 0.035	egrh-3	0.00962212767199939	0
Intestine anterior 0.035	ekl-4	0.0511705743734723	0.0454673803071857
Intestine anterior 0.035	elt-2	0.0269519427064655	0.0336394886839329
Intestine anterior 0.035	elt-4	0.0459065523369768	0.00390723028390457
Intestine anterior 0.035	ets-4	0.0211180571192376	0.0128786797367752
Intestine anterior 0.035	ets-5	0.00663683507892403	0.0575781901312497
Intestine anterior 0.035	F13C5.2	0.0289036715928964	0.0179426652029005

Intestine anterior 0.035	F22D6.2	0.0188448396239213	0
Intestine anterior 0.035	F33H1.4	0.0172273373451688	0
Intestine anterior 0.035	hinf-1	0.0849007450574543	0.0455343172331822
Intestine anterior 0.035	hlh-11	0.00915436776764303	0
Intestine anterior 0.035	hlh-8	0.00829660289015834	0.00519531576338821
Intestine anterior 0.035	hsf-1	0.0134141363350677	0
Intestine anterior 0.035	lag-1	0.072859748253063	0.135195007005968
Intestine anterior 0.035	let-526	0	0.00557091102509612
Intestine anterior 0.035	let-607	0.00852522662025966	0.0139857354800873
Intestine anterior 0.035	lim-7	0.0356791976684016	0.0116060875382004
Intestine anterior 0.035	lin-13	0.0108946006535894	0.00844166979788109
Intestine anterior 0.035	lin-26	0.09959397569851	0.0752157728674152
Intestine anterior 0.035	lin-40	0.0474604671035861	0
Intestine anterior 0.035	lin-54	0.018722545545922	0.0104317558496279
Intestine anterior 0.035	lsy-2	0.0113526889450514	0.00486271074566725
Intestine anterior 0.035	madf-10	0	0.00250288157976804
Intestine anterior 0.035	madf-2	0.593038993936141	0.489225300835086
Intestine anterior 0.035	madf-3	0.0606604906501549	0.0518347461026261
Intestine anterior 0.035	madf-5	0.194765178286162	0.108878407272355
Intestine anterior 0.035	madf-6	0.00884698818950449	0
Intestine anterior 0.035	madf-9	0.0187183815979676	0.00222794335875586
Intestine anterior 0.035	mdt-29	0.156117239757466	0.210720188206465
Intestine anterior 0.035	mec-3	0.0712964626057018	0.0197129224471816
Intestine anterior 0.035	mep-1	0.0152715540080081	0.0132455110790495
Intestine anterior 0.035	mxl-2	0	0.019901631873449
Intestine anterior 0.035	nhr-10	0.0214726424654069	0.0175148431725723
Intestine anterior 0.035	nhr-11	0.0356861947876324	0.0144608464091739
Intestine anterior 0.035	nhr-179	0.393154107682289	0.564250142181335
Intestine anterior 0.035	nhr-80	0.0165088072611764	0.0518644923718708
Intestine anterior 0.035	pat-9	0.193888601384767	0.166009513275699
Intestine anterior 0.035	pqm-1	0.0120689309261222	0.0191684706132047
Intestine anterior 0.035	R02D3.7	0.012629219190902	0.00163510101835088
Intestine anterior 0.035	saeg-2	0.129067346491773	0.142310458817767
Intestine anterior 0.035	skn-1	0.0136600561619643	0.0133744335576018
Intestine anterior 0.035	sptf-2	0.413986001172175	0.417469149144916
Intestine anterior 0.035	tbx-9	0.0103200692197926	0
Intestine anterior 0.035	unc-62	0.0180236911924683	0.0174885527200078
Intestine anterior 0.035	Y53G8AR.9	0.0396359355995699	0.0490453182776189
Intestine anterior 0.035	Y56A3A.18	0.0673495614918574	0.0680739544317455
Intestine anterior 0.035	Y5F2A.4	0	0.0431538649085732
Intestine anterior 0.035	Y75B8A.6	0	0.00358814168600477
Intestine anterior 0.035	zfh-2	0.0386276106776271	0.024921683071653
Intestine anterior 0.035	zim-3	0.0457474606369112	0.0229717273458371

Intestine anterior 0.035	zip-11	0.0746895371379799	0.0542133685285181
Intestine anterior 0.035	ZK546.5	0.0500706792695954	0.036065377309133
Intestine anterior 0.035	ztf-1	0.162372317784048	0.0523058481072926
Intestine anterior 0.035	ztf-22	0	0.0368562140253638
Intestine anterior 0.035	ztf-26	0.081043260959399	0
Intestine anterior 0.035	ztf-7	0	0.00416955705466784
Intestine middle 0.047	alr-1	0.280482668770109	0.296888757179722
Intestine middle 0.047	attf-6	0	0.000162029855231203
Intestine middle 0.047	ceh-40	0.102676975574605	0.116902532132408
Intestine middle 0.047	crh-2	0.0584550972372837	0.0594116338061187
Intestine middle 0.047	daf-19	0.11476929787237	0.115293074214212
Intestine middle 0.047	dmd-6	0.00998270975352487	0.00503491938176192
Intestine middle 0.047	dve-1	0.013334855079488	0.0104765693500147
Intestine middle 0.047	dxbp-1	0.0335368137020265	0.0370255831522263
Intestine middle 0.047	ekl-4	0.0947127241402287	0.105922381323579
Intestine middle 0.047	elt-2	0	0.00292615356312521
Intestine middle 0.047	elt-4	0.0922710675737629	0.035091892586455
Intestine middle 0.047	ets-5	0.0289597986066782	0.0268009770519535
Intestine middle 0.047	F10B5.3	0.0356980126464651	NA
Intestine middle 0.047	F22D6.2	0.0581010983162548	0
Intestine middle 0.047	F33H1.4	0.0229932455161128	0.0205058452291981
Intestine middle 0.047	F44E2.7	0.0293344085084452	0.0336597818909317
Intestine middle 0.047	hinf-1	0.138433388975256	0.158444520761217
Intestine middle 0.047	hlh-11	0.0105962076563404	0.0122927619530052
Intestine middle 0.047	hlh-8	0.00578072204247648	0
Intestine middle 0.047	isw-1	0.00871865336728486	9.38674665678642e-05
Intestine middle 0.047	lag-1	0.126005531510418	0.150447060924117
Intestine middle 0.047	let-607	0.0611427502658667	0.0572614270818621
Intestine middle 0.047	lim-7	0.0248776097237722	0.0311767806447879
Intestine middle 0.047	lin-13	0.00110271373760583	0.00426023232749534
Intestine middle 0.047	lin-26	0.138334560260585	0.122235170777832
Intestine middle 0.047	lin-40	0.0849041720880295	0.0105145448277402
Intestine middle 0.047	lin-54	0.0153826250593047	0.0183955927177308
Intestine middle 0.047	lsy-2	0.0125857188266583	0.00732550898433602
Intestine middle 0.047	madf-3	0.0553006414348385	0.0605263697663472
Intestine middle 0.047	madf-5	0.20507812766542	0.162556716304594
Intestine middle 0.047	madf-9	0.0406015101401872	0
Intestine middle 0.047	mdt-29	0.117560909184687	0.114061960793814
Intestine middle 0.047	mec-3	0.00138740488849079	0
Intestine middle 0.047	mxl-3	0.00137345599875721	0
Intestine middle 0.047	nhr-10	0.0353316783809303	0.0382876673576393
Intestine middle 0.047	nhr-102	0.00586675128845452	0.000642409636158786
Intestine middle 0.047	nhr-11	0.0173586468525574	0.00233506715053269

Intestine middle 0.047	nhr-179	0.530703241774282	0.185498455362678
Intestine middle 0.047	nhr-80	0	0.00132285284224155
Intestine middle 0.047	pag-3	0.0314348994749571	0.0240349549034855
Intestine middle 0.047	pat-9	0.166470118577079	0.144356632396624
Intestine middle 0.047	pbrm-1	0.0138746113955135	0.00397985413628368
Intestine middle 0.047	php-3	0.0158819433526676	0.0234776468222901
Intestine middle 0.047	R02D3.7	0.0322796821923855	0.0282660622447758
Intestine middle 0.047	saeg-2	0.0134169256732654	0.0141497635273107
Intestine middle 0.047	sptf-2	0.503994056591963	0.535095281484932
Intestine middle 0.047	tlp-1	0.0804605670759436	0.0675242161122002
Intestine middle 0.047	unc-62	0.0345736259305306	0.0262004941693634
Intestine middle 0.047	Y53G8AR.9	0.0466907088888756	0.0375155028717924
Intestine middle 0.047	Y56A3A.18	0.103433141621853	0.104660587158903
Intestine middle 0.047	zfh-2	0.0539031923201123	0.0456236437586563
Intestine middle 0.047	zim-3	0.0591031452765215	0.0392490861389696
Intestine middle 0.047	ZK546.5	0.24535010481463	0.30344481967818
Intestine middle 0.047	ztf-1	0.373224261746498	0.372086041585134
Intestine middle 0.047	ztf-22	0.00714677118317838	0
Intestine middle 0.047	ztf-26	0.119798375033055	0.0332865203171991
Intestine posterior 0.037	alr-1	0.247506720033232	0.231192700325358
Intestine posterior 0.037	bed-1	0	0.0206774508042772
Intestine posterior 0.037	C16A3.4	0.000303649503054631	0.000978540226896566
Intestine posterior 0.037	ceh-40	NA	0.0866062462649105
Intestine posterior 0.037	chd-7	0.00547006896688673	0.0410498813621486
Intestine posterior 0.037	crh-2	0.0425627653325277	0.0423439673013284
Intestine posterior 0.037	daf-16	0.0146612073839472	0.0178658487606804
Intestine posterior 0.037	daf-19	0.0601313451629473	0.0398669303623795
Intestine posterior 0.037	daf-8	0.177750637883537	0.384407469821082
Intestine posterior 0.037	dmd-6	0.0253822252465629	0.0505571831927465
Intestine posterior 0.037	dpff-1	0	0.0201379049434169
Intestine posterior 0.037	dve-1	0.00961182716606269	0.00154080875675814
Intestine posterior 0.037	dxbp-1	0.00498222409195593	0
Intestine posterior 0.037	efl-3	0	0.0101048497102852
Intestine posterior 0.037	egl-18	0.0705860299302634	0.0479128082387822
Intestine posterior 0.037	ekl-4	0.0591621598657466	0.0574507918629768
Intestine posterior 0.037	elt-2	0.00868917307920655	0.0125743622117334
Intestine posterior 0.037	elt-4	0.0624167209138912	0.00922562073188948
Intestine posterior 0.037	ets-4	0.0332735133334749	0.0581376646870605
Intestine posterior 0.037	ets-5	0.0400066757302106	0.0888831603730096
Intestine posterior 0.037	F13C5.2	0.0142808173390418	0.0326819009823304
Intestine posterior 0.037	F22D6.2	0.0467066027600563	0
Intestine posterior 0.037	F33H1.4	0.0142839776519288	0.0104321909048255
Intestine posterior 0.037	hinf-1	0.0870014183823804	0.0662794717491003

Intestine posterior 0.037	hlh-11	0.00302747181512377	0
Intestine posterior 0.037	hlh-8	0	0.00404639202149347
Intestine posterior 0.037	hsf-1	0.00386805702217693	0
Intestine posterior 0.037	lag-1	0.0695131085460516	0.122946922657618
Intestine posterior 0.037	let-526	0.0185230914666394	0.0849800671993483
Intestine posterior 0.037	let-607	0.0414379159818999	0.0564433132699532
Intestine posterior 0.037	lim-7	0.0397264917482588	0.0312715332411444
Intestine posterior 0.037	lin-13	0.000966800486027352	0.0082186510215945
Intestine posterior 0.037	lin-26	0.108678874461446	0.0872289009273566
Intestine posterior 0.037	lin-40	0.0339352974332134	0
Intestine posterior 0.037	lin-54	0.0170773446361916	0.0187948936110089
Intestine posterior 0.037	lsy-2	0.0156702152565163	0.0110613875026821
Intestine posterior 0.037	madf-2	0.449751065728355	0.48359300423521
Intestine posterior 0.037	madf-3	0.0666116641015171	0.0639648587295476
Intestine posterior 0.037	madf-5	0.17752677965407	0.108496548704128
Intestine posterior 0.037	madf-6	0.00441364153327663	0.004744899259535
Intestine posterior 0.037	madf-9	0.017260745897395	0.00428085187061085
Intestine posterior 0.037	mdt-29	0.150866594332172	0.198813670549282
Intestine posterior 0.037	mec-3	0.00898719518907217	0
Intestine posterior 0.037	mep-1	0.000881060692433971	0.00615382857185841
Intestine posterior 0.037	mxl-2	0	0.00467717952985652
Intestine posterior 0.037	nhr-10	0	0.00215102000371971
Intestine posterior 0.037	nhr-11	0.00807944850415664	0.0119166225916843
Intestine posterior 0.037	nhr-179	0.639110517372558	0.765909055102058
Intestine posterior 0.037	nhr-80	0.0219323374093605	0.0533662239389241
Intestine posterior 0.037	pag-3	0.023588209967115	0.0263603127050282
Intestine posterior 0.037	pat-9	0.118091331915071	0.145284634389508
Intestine posterior 0.037	pbrm-1	0.00232789411333007	0.00612535125798402
Intestine posterior 0.037	php-3	0.00187456639924433	0.00315185516526786
Intestine posterior 0.037	pqm-1	0.0136465455952656	0.0231846143770338
Intestine posterior 0.037	R02D3.7	0.00606966838729087	0.00671114250078246
Intestine posterior 0.037	saeg-2	0.0830647820792313	0.10575975612071
Intestine posterior 0.037	sptf-2	0.404906029746506	0.372868969898955
Intestine posterior 0.037	unc-62	0.0247621052621004	0.0334006219346085
Intestine posterior 0.037	Y53G8AR.9	0.0466649907383271	0.0459130661433852
Intestine posterior 0.037	Y56A3A.18	0.0973928714064004	0.11844231224264
Intestine posterior 0.037	Y75B8A.6	0	0.00362476698476104
Intestine posterior 0.037	zfh-2	0.0406030578809075	0.0276657800353446
Intestine posterior 0.037	zim-3	0.0437512839763796	0.0331465804109384
Intestine posterior 0.037	zip-11	0.0231857085109457	0.0260718785216358
Intestine posterior 0.037	ZK546.5	0.0408979449161232	0.115803297909952
Intestine posterior 0.037	ztf-1	0.144350974082323	0.104848812690469
Intestine posterior 0.037	ztf-22	0	0.0511443244109118

Intestine posterior 0.037	ztf-26	0.0757853511991412	0.00552598946265409
Intestine-Gonadal sheath doublets 0.046	alr-1	0.270498193624069	0.289476907249347
Intestine-Gonadal sheath doublets 0.046	attf-6	0.00857551512709986	0.00923481703055557
Intestine-Gonadal sheath doublets 0.046	ceh-18	0.0246459287438482	0
Intestine-Gonadal sheath doublets 0.046	chd-7	0.0133748684792532	0
Intestine-Gonadal sheath doublets 0.046	crh-2	0.0378982875401163	0.0346276892383193
Intestine-Gonadal sheath doublets 0.046	daf-16	0.00415436504530961	0.00366799688792279
Intestine-Gonadal sheath doublets 0.046	daf-19	0.130352080640083	0.135777107905871
Intestine-Gonadal sheath doublets 0.046	dxbp-1	0.019126108446125	0.0195149528980922
Intestine-Gonadal sheath doublets 0.046	egl-18	0.0239732090540504	0.0179771540396603
Intestine-Gonadal sheath doublets 0.046	ekl-4	0.103698668714695	0.104663749488239
Intestine-Gonadal sheath doublets 0.046	elt-4	0.0356053703073518	0
Intestine-Gonadal sheath doublets 0.046	ets-5	0.0126986278843424	0.00933756132394453
Intestine-Gonadal sheath doublets 0.046	F22D6.2	0.0123071730904052	0
Intestine-Gonadal sheath doublets 0.046	F33H1.4	0.0331536746797642	0.037256310863352
Intestine-Gonadal sheath doublets 0.046	F44E2.7	0.0367883721265637	0.0253153284966469
Intestine-Gonadal sheath doublets 0.046	hinf-1	0.139467237373798	0.157551495241067
Intestine-Gonadal sheath doublets 0.046	hlh-11	0.0157250270737811	0.00495821644484596
Intestine-Gonadal sheath doublets 0.046	hlh-8	0.0527058886463201	0.0333742485360703
Intestine-Gonadal sheath doublets 0.046	hsf-1	0.00360494313897317	0.0112507315980324
Intestine-Gonadal sheath doublets 0.046	lag-1	0.0842314152048177	0.110878006312481
Intestine-Gonadal sheath doublets 0.046	let-607	0.0533108332477618	0.0447540414588895
Intestine-Gonadal sheath doublets 0.046	lim-7	0.0556927017095372	0.0697996630490906
Intestine-Gonadal sheath doublets 0.046	lin-26	0.120486047043715	0.118392210873871
Intestine-Gonadal sheath doublets 0.046	lin-40	0.0600642944345423	0.0151292742498808
Intestine-Gonadal sheath doublets 0.046	lin-54	0.00934348733541732	0.0169089082334859
Intestine-Gonadal sheath doublets 0.046	lsy-2	0.0235665447148881	0.0238945944289541
Intestine-Gonadal sheath doublets 0.046	madf-3	0.0580991091621115	0.0630365626345374
Intestine-Gonadal sheath doublets 0.046	madf-5	0.144548531725935	0.114186625723141
Intestine-Gonadal sheath doublets 0.046	madf-6	0.00284333892216329	0.00955448639251617
Intestine-Gonadal sheath doublets 0.046	madf-9	0.0366555550447783	0.00423429719563966
Intestine-Gonadal sheath doublets 0.046	mdt-29	0.103943224473071	0.0907754173040634
Intestine-Gonadal sheath doublets 0.046	nhr-10	0.0136557635551797	0.020513967876581
Intestine-Gonadal sheath doublets 0.046	nhr-102	0.0114699021726623	0.00847598550327931
Intestine-Gonadal sheath doublets 0.046	nhr-11	0.0138822500956541	0.00622660989482305
Intestine-Gonadal sheath doublets 0.046	nhr-179	0.123681598114061	0
Intestine-Gonadal sheath doublets 0.046	nhr-232	0.0303941618859007	0
Intestine-Gonadal sheath doublets 0.046	pag-3	NA	0.0670336111534287
Intestine-Gonadal sheath doublets 0.046	pat-9	NA	0.183660753240616
Intestine-Gonadal sheath doublets 0.046	pbrm-1	0.0141665308423911	0.00881445232868307
Intestine-Gonadal sheath doublets 0.046	R02D3.7	0.0266237687221006	0.0212218896496943
Intestine-Gonadal sheath doublets 0.046	rnt-1	0.00746282184736159	NA
Intestine-Gonadal sheath doublets 0.046	saeg-2	0.00418347665678232	0

Intestine-Gonadal sheath doublets 0.046	sptf-2	0.515535495147722	0.552550428421745
Intestine-Gonadal sheath doublets 0.046	T26A5.8	0.0100040634863075	0
Intestine-Gonadal sheath doublets 0.046	tlp-1	0.0651648539596018	NA
Intestine-Gonadal sheath doublets 0.046	unc-120	0.00677961190984279	0
Intestine-Gonadal sheath doublets 0.046	unc-62	0.0252772833185171	0.017703373426506
Intestine-Gonadal sheath doublets 0.046	Y53G8AR.9	0.0407903142573166	0.0307511417587418
Intestine-Gonadal sheath doublets 0.046	Y56A3A.18	0.0906471507818207	0.0863891277387566
Intestine-Gonadal sheath doublets 0.046	zfh-2	0.0612415185921635	0.054265835903137
Intestine-Gonadal sheath doublets 0.046	zim-3	0.0640525895156074	0.034248462505045
Intestine-Gonadal sheath doublets 0.046	ZK546.5	0.217577468590377	0.18729568904288
Intestine-Gonadal sheath doublets 0.046	ztf-1	0.234166657852318	0.179662888061123
Intestine-Gonadal sheath doublets 0.046	ztf-26	0.0769425956865891	0.0178365720003931
M1 0.041	aha-1	0.0143127345779456	0
M1 0.041	attf-6	0.0011547110170244	0.00767871689029081
M1 0.041	ceh-32	0.170760591593716	0.364146694768386
M1 0.041	ceh-34	0	0.00603787332124796
M1 0.041	ceh-48	0.011168714715106	0.0144828085391429
M1 0.041	crh-2	0.0421670133577877	0.0524019973649659
M1 0.041	ctbp-1	0.121916271082511	0.115557835862496
M1 0.041	daf-19	NA	0.154165934788731
M1 0.041	dxbp-1	NA	0.000757796517942956
M1 0.041	egl-18	NA	0.107304035321747
M1 0.041	egl-27	0.00216270304226633	0.00438601269728538
M1 0.041	ekl-4	0.0444144289892523	0.0486018135374751
M1 0.041	F22D6.2	0.0548923574083562	0
M1 0.041	hif-1	0.00264072132553936	0.00890475342412309
M1 0.041	hinf-1	0.135036067458394	NA
M1 0.041	hmg-11	0.00107196851841905	0
M1 0.041	hsf-1	0.0188209377277343	NA
M1 0.041	isw-1	0.0703426354351296	0.0456889099613283
M1 0.041	K12H6.12	0.0187625206434132	0.02976976933391
M1 0.041	lag-1	0.0277893164861748	0.0697437509544373
M1 0.041	lim-6	0.0886478530281651	NA
M1 0.041	lim-7	0.0648216085393489	0.0737067578701763
M1 0.041	lin-13	0.0130502534512514	0.00575618408820226
M1 0.041	lin-14	0.0276047507973588	NA
M1 0.041	lin-26	0.087170984322818	NA
M1 0.041	lin-39	NA	0.0290903235243282
M1 0.041	lin-40	0.032193597763146	0
M1 0.041	lsy-2	0.0150709032524563	0.0169323519184621
M1 0.041	madf-3	NA	0.0422679125831357
M1 0.041	madf-5	0.0951244327285292	NA
M1 0.041	mdt-29	0.0183210600364516	NA

M1 0.041	nhr-11	0.0318456054432371	NA
M1 0.041	nhr-179	0.0100072352972683	NA
M1 0.041	nhr-6	0.0168688574790912	NA
M1 0.041	pat-9	0.262268402033969	NA
M1 0.041	pbrm-1	0	0.0093312319516481
M1 0.041	R02D3.7	0.0253244257218645	NA
M1 0.041	row-1	0.0969176804579695	0.0449201864773943
M1 0.041	saeg-2	0.081257874087185	0.11068801294466
M1 0.041	sea-2	0.0277162910643681	0.0224920319277656
M1 0.041	sem-4	0.0338657866306836	0.0467097915383234
M1 0.041	sox-4	NA	0.00844676784940597
M1 0.041	sup-37	0.0141055958337319	0
M1 0.041	T26A5.8	0.0421568577879173	NA
M1 0.041	unc-120	0.00010039355563063	NA
M1 0.041	unc-42	NA	0.0258710080691896
M1 0.041	unc-86	NA	0.0685395089195892
M1 0.041	Y53G8AR.9	0.0379752548660222	0.0226150497696793
M1 0.041	Y56A3A.18	NA	0.0706340557915674
M1 0.041	zag-1	0.0885697774246038	0.0832586129545862
M1 0.041	zim-3	0.00782216466729667	0.000455502982870816
M1 0.041	ZK546.5	0	0.0636431595274904
M1 0.041	ztf-1	0.0299680580221463	0.0109228397026768
M1 0.041	ztf-26	0.143728342413675	0.10864409853041
M2_M3_M4 0.039	aha-1	0	0.0597916570403741
M2_M3_M4 0.039	alr-1	0.182201345272894	0.18536539189373
M2_M3_M4 0.039	C34B4.2	0.0509841152719418	0
M2_M3_M4 0.039	ceh-34	0.020631450575212	0.0115240037093198
M2_M3_M4 0.039	ceh-48	0	0.00955847096482023
M2_M3_M4 0.039	ceh-9	0.00177987030735654	0
M2_M3_M4 0.039	crh-2	0.0414059359644695	0.0480816695862988
M2_M3_M4 0.039	ctbp-1	0.124783930341447	0.143690808997679
M2_M3_M4 0.039	daf-19	0.0676497912036519	0.0885494475198824
M2_M3_M4 0.039	egl-13	0.000233851223051882	NA
M2_M3_M4 0.039	egl-18	0.106571289279827	0.114597254996426
M2_M3_M4 0.039	egl-27	0	0.0161859289145627
M2_M3_M4 0.039	egl-5	0.00341136873807713	NA
M2_M3_M4 0.039	ekl-4	0.0560323229049214	0.0589497971642545
M2_M3_M4 0.039	elt-4	0.0252484941149395	NA
M2_M3_M4 0.039	ets-5	NA	0.0226045928705654
M2_M3_M4 0.039	F22D6.2	0.07731602210354	0.0484627427587359
M2_M3_M4 0.039	hif-1	0	0.00789584935557467
M2_M3_M4 0.039	hinf-1	0.130449432304907	0.128302765170033
M2_M3_M4 0.039	hlh-8	NA	0.0070811320996772

M2_M3_M4 0.039	hmg-11	0	0.0132853137392135
M2_M3_M4 0.039	isw-1	0.0152659658520769	0.0412815922574417
M2_M3_M4 0.039	K09A11.1	0	0.00581943233978792
M2_M3_M4 0.039	lag-1	0.0516946111599858	0.0950323874753908
M2_M3_M4 0.039	lim-7	0.0577216143131922	0.0737364904771904
M2_M3_M4 0.039	lin-11	0.143617719697023	NA
M2_M3_M4 0.039	lin-13	0	0.00546984665404497
M2_M3_M4 0.039	lin-14	0.0377954672101644	0.0511206599557236
M2_M3_M4 0.039	lin-26	0.0818444521223299	0.0763506735076321
M2_M3_M4 0.039	lin-39	0.00240819723813917	0.0170304354217126
M2_M3_M4 0.039	lin-40	0.050679282202962	0.016894285880865
M2_M3_M4 0.039	lsy-2	0.025948224952965	0.0224016560055793
M2_M3_M4 0.039	madf-3	0.0518692650396291	0.0606351973207796
M2_M3_M4 0.039	madf-5	0.0797930802164492	0.0388372702112593
M2_M3_M4 0.039	madf-9	0.00439619425042453	0
M2_M3_M4 0.039	mbf-1	0.0218761060396492	0.043527130874672
M2_M3_M4 0.039	mdt-29	0.0430125948749351	0.056792517092868
M2_M3_M4 0.039	nfya-2	0	0.00569604870337462
M2_M3_M4 0.039	nfyb-1	0	0.00676364344237862
M2_M3_M4 0.039	nhr-11	0.0269315640880466	0.0302805676874915
M2_M3_M4 0.039	nhr-6	0	0.00615999763811029
M2_M3_M4 0.039	pag-3	0.0322846169538264	0.0259390444044007
M2_M3_M4 0.039	pat-9	NA	0.11233142618803
M2_M3_M4 0.039	R02D3.7	0.016632810634504	0.0148215353417021
M2_M3_M4 0.039	row-1	0.029457448067391	0.0996224838095473
M2_M3_M4 0.039	saeg-2	0	0.00797452498488228
M2_M3_M4 0.039	sem-4	0.0260270184611065	0.0355878005891725
M2_M3_M4 0.039	sptf-2	0.342214683774663	NA
M2_M3_M4 0.039	T26A5.8	0.00438838107464308	0
M2_M3_M4 0.039	unc-42	NA	0.0251473238356842
M2_M3_M4 0.039	unc-62	0	0.00103036066335256
M2_M3_M4 0.039	unc-86	0.0459430785346019	0.0657313732939871
M2_M3_M4 0.039	Y53G8AR.9	0.0189255841550962	0.0148351012978014
M2_M3_M4 0.039	Y55F3AM.14	0.0189262450540239	0.0473604689174805
M2_M3_M4 0.039	Y56A3A.18	0.0522933501820036	0.0476856562088192
M2_M3_M4 0.039	zag-1	0.0710917445117972	0.0729009368606569
M2_M3_M4 0.039	zfh-2	0.0523647996740429	0.0447519189119793
M2_M3_M4 0.039	zim-3	0.0126799718101367	0
M2_M3_M4 0.039	ZK546.5	0.0308621374599214	0.120790864245135
M2_M3_M4 0.039	ztf-1	0.07290871088868	0.0353620901740687
M2_M3_M4 0.039	ztf-26	0.0947220441738098	0.05146626484528
M5 0.040	aha-1	0.0725115110697117	0.0564146592139692
M5 0.040	alr-1	0.172770003871199	0.196051594089834

M5 0.040	atf-7	0.00428106860577495	0.00871121844173938
M5 0.040	attf-6	0.0097007931901889	0.017872473160378
M5 0.040	ceh-27	0	0.0172301650004947
M5 0.040	ceh-34	0.0169192479843019	0.0190980263660219
M5 0.040	ceh-48	0.00547854968183093	0.00989444434407769
M5 0.040	ceh-9	NA	0.339511066483078
M5 0.040	crh-2	0.0426500804053507	0.0498887024870372
M5 0.040	ctbp-1	0.134653671469206	0.157163790587581
M5 0.040	daf-19	0.121665659838855	0.15602595226525
M5 0.040	egl-13	0.0388500319780827	NA
M5 0.040	egl-18	0.0758481461872995	0.106675983161686
M5 0.040	egl-27	0.00575633685672274	0.0206200813097228
M5 0.040	egrh-3	0	0.00788098568583587
M5 0.040	ekl-4	0.0577853448835637	0.0584190356418276
M5 0.040	elt-4	0.00390038931624012	NA
M5 0.040	ets-5	0	0.0228236453883357
M5 0.040	F22D6.2	0.0647851664100536	0.03160136221266
M5 0.040	gei-8	0.000721335738233816	0.0138564344486953
M5 0.040	hif-1	0.00423132613890768	0.0161602022434358
M5 0.040	hinf-1	0.121720763338005	0.158839224168503
M5 0.040	hlh-8	0.00576937878554567	NA
M5 0.040	hmg-1.1	0	0.00372552357335514
M5 0.040	hmg-11	0.0101771117180708	0.0245757549631981
M5 0.040	hsf-1	0.00786308442553432	0.00338312528694837
M5 0.040	isw-1	0.0443611721287199	0.0815470663795643
M5 0.040	K09A11.1	0.0405096289186223	0.0151497106571143
M5 0.040	lag-1	0.110035996832705	0.134853651924673
M5 0.040	lim-7	0.0263950172163755	0.0731138030611125
M5 0.040	lin-11	0.183991854283029	NA
M5 0.040	lin-13	0.00664467255860236	0.0179924502504965
M5 0.040	lin-14	0.0389142793855598	0.0443349021326663
M5 0.040	lin-26	0.0736795431979898	NA
M5 0.040	lin-39	0.0113533574483068	NA
M5 0.040	lin-40	0.0522656774423442	0.0109463566171607
M5 0.040	lsy-2	0.0251163910788923	0.0206055928816657
M5 0.040	madf-3	0.0435989923535897	0.054243696386662
M5 0.040	madf-5	0.0633158779475454	0.0474564153148024
M5 0.040	mbf-1	0.116875544625264	0.0876695517155379
M5 0.040	mdt-29	0.0172015469892616	0.00415114254811172
M5 0.040	nfya-2	0	0.00491278116240334
M5 0.040	nfyb-1	0	0.00332449057817193
M5 0.040	nhr-11	0.0172222336449523	NA
M5 0.040	nhr-6	0	0.00788718246754391

M5 0.040	pag-3	NA	0.0141446502753224
M5 0.040	pat-9	NA	0.0968061903986581
M5 0.040	pbrm-1	0	0.00685920911496162
M5 0.040	R02D3.7	0.0189730974840444	0.00468553558627851
M5 0.040	rbr-2	0	0.0287554792843351
M5 0.040	row-1	0.042830493338796	0.122509502010532
M5 0.040	saeg-2	0.00356734458260192	NA
M5 0.040	sea-2	0.00727400064548037	0.0047692728845272
M5 0.040	sem-4	NA	0.00796800651581473
M5 0.040	sptf-2	0.311043404878821	NA
M5 0.040	unc-42	0.0201756425769086	0.0165753493995211
M5 0.040	unc-86	0.006386633821895	NA
M5 0.040	Y53G8AR.9	0.018620732877786	0.0218350400263745
M5 0.040	Y55F3AM.14	0.0462175088559392	NA
M5 0.040	Y56A3A.18	0.0462030983238098	0.0436718839660202
M5 0.040	zag-1	0.0937455365981559	0.149367220538039
M5 0.040	zfh-2	0.0473315364329096	NA
M5 0.040	zim-3	0.021264750140017	0.0155756648110029
M5 0.040	ZK546.5	0.0528787860392802	0.14379833579814
M5 0.040	ztf-1	0	0.0408816511420083
M5 0.040	ztf-26	0.0548785219173222	0.0466409237513046
MI 0.040	alr-1	0.158264656998756	0.16243028281151
MI 0.040	atf-7	0	0.00965207520047953
MI 0.040	attf-6	0	0.0159938119552852
MI 0.040	ceh-18	0.00732682078499884	0
MI 0.040	ceh-22	0	0.0210710117679361
MI 0.040	ceh-34	0.0221501563727554	0.0384302969522275
MI 0.040	ceh-48	0.00631493364499484	0.0235893039149788
MI 0.040	ceh-9	0.325280790625733	0.363958836951021
MI 0.040	chd-7	0.0222162174931542	0.0283134324546417
MI 0.040	crh-2	0.0398963297275154	0.0418105153661785
MI 0.040	ctbp-1	0.10891110310721	0.10029513275303
MI 0.040	daf-19	0.0526247002099183	0.0646307534901742
MI 0.040	dsc-1	0.00543652818399736	NA
MI 0.040	egl-13	0.0483691950661752	0.0564085235843128
MI 0.040	egl-18	0.0938524958587067	0.129630338510356
MI 0.040	egl-27	0.0201045102135553	0.0378853674571718
MI 0.040	egl-43	0	0.00942798982973813
MI 0.040	ekl-4	0.0629436020166066	0.0740158642457503
MI 0.040	ets-5	0.0346607464123092	NA
MI 0.040	F22D6.2	0.0583946937066168	0.00653290896698166
MI 0.040	fkh-8	0	0.00921002166069151
MI 0.040	gei-8	0	0.0160860771480682

MI 0.040	hif-1	0	0.0165143262704908
MI 0.040	hinf-1	0.104343888721894	0.129166397055236
MI 0.040	hlh-8	0.00111253299930269	NA
MI 0.040	hmg-11	0	0.00088903143814156
MI 0.040	hsf-1	0.0164920889175758	0.02700973592115
MI 0.040	isw-1	0.0796985406962959	0.115766115441497
MI 0.040	K09A11.1	0	0.029720275680593
MI 0.040	lag-1	0.00572096435971686	0.0391614482976287
MI 0.040	lim-6	0.0197943347888509	NA
MI 0.040	lim-7	0.0147457364833836	0.0336248929996882
MI 0.040	lin-11	0.181656562896245	NA
MI 0.040	lin-14	0.0355125893662828	0.0349798605183598
MI 0.040	lin-26	0.0895398314990946	0.0800394798145842
MI 0.040	lin-39	0.0111849778793779	NA
MI 0.040	lin-40	0.0440938849188747	0.00304149115499374
MI 0.040	lsy-2	0.0140529867338276	0.0227968765542299
MI 0.040	madf-3	0.0379964201578394	NA
MI 0.040	madf-5	0.0810799143705897	0.0626832361659365
MI 0.040	mdt-29	0.00210444193156805	0.00351756321652953
MI 0.040	nfya-2	0	0.0132144912794949
MI 0.040	nfyb-1	0.000945126177462647	0.00426094750595438
MI 0.040	nhr-11	0.0191448200193941	NA
MI 0.040	nhr-129	1.51565243314377e-05	NA
MI 0.040	pag-3	NA	0.0326352084032571
MI 0.040	pbrm-1	0	0.0137646589148259
MI 0.040	R02D3.7	0.004973753172666	0.0188242817850413
MI 0.040	row-1	0	0.0279656527631358
MI 0.040	unc-42	0.0033649971851674	NA
MI 0.040	unc-62	0.00224660832197952	0.000132579067631483
MI 0.040	Y53G8AR.9	0.0156974921792734	0.0233262427209436
MI 0.040	Y56A3A.18	0.0325085024851016	0.0346948057137912
MI 0.040	zag-1	NA	0.0896687745277785
MI 0.040	zfh-2	0.056795507268486	0.051997836079483
MI 0.040	zim-3	0.0234667968339996	0.0186962672936964
MI 0.040	ZK546.5	0.000730260335427486	0.10138430752336
MI 0.040	ztf-26	0.0714860859648162	0.044525784667355
Meiotic germ cells 0.033	akir-1	0.0274046494062479	0.0782748213064539
Meiotic germ cells 0.033	alr-1	0.341364328698739	0.357356602302723
Meiotic germ cells 0.033	attf-6	0.00225801669319431	0.0119760215892538
Meiotic germ cells 0.033	C16A3.4	0.0418771104611353	0.0426807094008592
Meiotic germ cells 0.033	cebp-1	0.0104747136306788	0.0152272389047897
Meiotic germ cells 0.033	daf-19	0.114465167829216	0.125475903384203
Meiotic germ cells 0.033	dpl-1	0.0233371514355785	0.0247423681939386

Meiotic germ cells 0.033	dxbp-1	0.00378888961993747	0.0080961837386802
Meiotic germ cells 0.033	efl-1	0.0220491919961799	0.0242615059745911
Meiotic germ cells 0.033	egl-18	0.032961398212655	0.0496017278265082
Meiotic germ cells 0.033	ekl-4	0.107922835133146	0.113947188561535
Meiotic germ cells 0.033	F13C5.2	0.00622841968451848	0.0153530769810205
Meiotic germ cells 0.033	F23B12.7	0.00830193084117323	0.0104234783666112
Meiotic germ cells 0.033	F33H1.4	0.0998172541299064	0.110538029764288
Meiotic germ cells 0.033	F44E2.7	0.0233366929780917	0.0356021928154868
Meiotic germ cells 0.033	hinf-1	0.168281908168501	0.18219857109926
Meiotic germ cells 0.033	hsf-1	0.0244074646334226	0.029176694672058
Meiotic germ cells 0.033	lag-1	0	0.0394984580768976
Meiotic germ cells 0.033	lim-7	0.0463604322643342	0.0581556043497924
Meiotic germ cells 0.033	lin-26	0.115488431525047	0.114756256289247
Meiotic germ cells 0.033	lin-38	0.0102293410286834	0.00986185029487479
Meiotic germ cells 0.033	lin-54	0.0226759034226587	0.0258872352934356
Meiotic germ cells 0.033	lsy-2	0.0380782453115563	0.0390224090662762
Meiotic germ cells 0.033	madf-3	0.0998193239796932	0.107103954319426
Meiotic germ cells 0.033	madf-5	0.070640653358318	0.0548286270252185
Meiotic germ cells 0.033	madf-6	0.0573789811937061	0.0640587506832125
Meiotic germ cells 0.033	pag-3	0.00902160243423045	0.00193149892543977
Meiotic germ cells 0.033	pat-9	0.123338807785095	0.105055585061493
Meiotic germ cells 0.033	R02D3.7	0.0136261404751378	0.0138919217008979
Meiotic germ cells 0.033	sptf-2	0.485639253116672	0.537686029928586
Meiotic germ cells 0.033	T20F7.1	0.00359697748315179	0.00113151022754531
Meiotic germ cells 0.033	Y48G9A.11	0.00643131016230403	0.0128998944153678
Meiotic germ cells 0.033	Y53G8AR.9	0.00339072349517841	0.00566590791130021
Meiotic germ cells 0.033	Y56A3A.18	0.0681908549050023	0.0838867843212111
Meiotic germ cells 0.033	zfh-2	0.0363101287927705	0.0336118462441289
Meiotic germ cells 0.033	zim-3	0.00954701914411304	0.016819377546529
Meiotic germ cells 0.033	zip-5	0.0112961431811849	NA
Mitotic germ cells 0.041	akir-1	0.164241259507808	0.168780970533495
Mitotic germ cells 0.041	alr-1	0.408199614675215	0.413100887553245
Mitotic germ cells 0.041	attf-6	0.00675431102164068	0.0120134904792653
Mitotic germ cells 0.041	C16A3.4	0.0402465517702709	0.0416368914910663
Mitotic germ cells 0.041	cebp-1	0.0113032931442003	0.0119569254198282
Mitotic germ cells 0.041	ceh-40	0.165579114257905	0.169628839709888
Mitotic germ cells 0.041	daf-19	0.10732827456435	0.110550855291683
Mitotic germ cells 0.041	dpl-1	0.0225274934817925	0.0190376682075853
Mitotic germ cells 0.041	efl-1	0.0203737546734977	0.0204942059218745
Mitotic germ cells 0.041	egl-18	0.0428057468430052	0.0449571578024016
Mitotic germ cells 0.041	ekl-4	0.119642197508968	0.123562829618855
Mitotic germ cells 0.041	F13C5.2	0.0237235213191199	0.0218400824479238
Mitotic germ cells 0.041	F23B12.7	0.0174079139989219	0.0117944069978654

Mitotic germ cells 0.041	F33H1.4	0.106261904043912	0.105556196112074
Mitotic germ cells 0.041	F44E2.7	0.0149990782718619	0.015314924685896
Mitotic germ cells 0.041	hinf-1	0.267618915666851	0.274373383062705
Mitotic germ cells 0.041	hsf-1	0.0156017459834966	0.017305536319017
Mitotic germ cells 0.041	isw-1	0.00412395602108484	0.0058883562716934
Mitotic germ cells 0.041	lag-1	0.00772253982869905	0.0382570418295655
Mitotic germ cells 0.041	lim-7	0.0771479969038758	0.0845388282109295
Mitotic germ cells 0.041	lin-26	0.127663149919086	0.125520956667355
Mitotic germ cells 0.041	lin-38	0.00443494715976024	0.00314334214287665
Mitotic germ cells 0.041	lin-54	0.0291896898715503	0.0338307225350569
Mitotic germ cells 0.041	lsy-2	0.0353873161834365	0.0336828999560858
Mitotic germ cells 0.041	madf-3	0.111827940130159	0.114811012876177
Mitotic germ cells 0.041	madf-5	0.034270793008935	0.0216269859865583
Mitotic germ cells 0.041	madf-6	0.0575707422370528	0.0586062981707431
Mitotic germ cells 0.041	pat-9	0.0591290387860593	0.0177213805002163
Mitotic germ cells 0.041	R02D3.7	0.013878581510853	0.012780195075833
Mitotic germ cells 0.041	skn-1	0.00112421926017184	0.000158367839117851
Mitotic germ cells 0.041	sptf-2	0.546721417341344	0.587180882711853
Mitotic germ cells 0.041	Y48G9A.11	0.0132987999932497	0.0141686664761895
Mitotic germ cells 0.041	Y56A3A.18	0.0663542655999074	0.0750593256694031
Mitotic germ cells 0.041	zfh-2	0.0413085676061254	0.0387328107380844
Mitotic germ cells 0.041	zip-5	0.0141543082305255	0.0140890182029261
NSM 0.043	aha-1	0.0983918327561589	NA
NSM 0.043	atf-7	0	0.00284122931299027
NSM 0.043	B0035.1	0	0.0823878558496694
NSM 0.043	cebp-1	NA	0.0228368214655794
NSM 0.043	ceh-34	0.019888984403731	0.0288893035855949
NSM 0.043	ceh-48	0	0.0423226213186964
NSM 0.043	ceh-79	0.000947700690858546	NA
NSM 0.043	ctbp-1	NA	0.219163931205619
NSM 0.043	daf-19	NA	0.1360821290024
NSM 0.043	drap-1	0.0106419690384213	0.0242600597052492
NSM 0.043	dxbp-1	0.00421606602820439	NA
NSM 0.043	egl-27	NA	0.0722811518283321
NSM 0.043	egl-43	0.0230510552887704	0
NSM 0.043	ekl-4	0.0709383363779597	NA
NSM 0.043	elt-4	0.110562141451691	NA
NSM 0.043	F22D6.2	0.176010879099491	0.105773327515796
NSM 0.043	F57A8.1	NA	0.0630127277516924
NSM 0.043	gei-8	0	0.00771697205303238
NSM 0.043	hif-1	0	0.0462145205903869
NSM 0.043	hinf-1	0.145809008301591	NA
NSM 0.043	hmg-1.1	0.0409576976046977	0.0322520695196358

NSM 0.043	hmg-11	0.0225347987399963	0.0252454154741444
NSM 0.043	hsf-1	4.2498524820579e-05	0.0463508893377226
NSM 0.043	lag-1	0	0.048580445551276
NSM 0.043	let-607	0	0.00814389871765354
NSM 0.043	lim-7	0.0600446052054701	NA
NSM 0.043	lin-13	0.0241160058210626	0.0358579249257804
NSM 0.043	lin-14	0.047697342095534	0.0499365684617385
NSM 0.043	lin-40	0.127191239080593	NA
NSM 0.043	mbf-1	0	0.151548037597575
NSM 0.043	mdt-29	0.05118094476711	NA
NSM 0.043	mep-1	0	0.0220834473842704
NSM 0.043	nfyb-1	0.0152821562819279	0.0297187775986419
NSM 0.043	nhr-11	0.0648116458532224	NA
NSM 0.043	pbrm-1	0.0136107276835908	0.0552282851207932
NSM 0.043	rbr-2	0.0101397212713849	0.00570955728157953
NSM 0.043	row-1	0.103356709159404	NA
NSM 0.043	sea-2	0.0563168050118553	0
NSM 0.043	skn-1	0.0121686353830143	NA
NSM 0.043	unc-86	0.103611414980179	0.106394980657237
NSM 0.043	unc-98	NA	0.108418893686902
NSM 0.043	Y56A3A.18	0.0911138983237204	NA
NSM 0.043	zfh-2	NA	0.054653915379826
OLQ 0.037	aha-1	0.188609246377873	0.234828662036397
OLQ 0.037	alr-1	0.165604331596639	NA
OLQ 0.037	attf-6	0.0196948216821188	0.0206333130729665
OLQ 0.037	C34B4.2	0.232247635182501	0
OLQ 0.037	cebp-1	0.018929820494944	0.0259913041690366
OLQ 0.037	ceh-18	0	0.00420492285151694
OLQ 0.037	ceh-27	0.0418305875558944	0.0335648719246049
OLQ 0.037	ceh-34	0.0324801748150591	NA
OLQ 0.037	crh-2	0.0292320603336184	0.0375564367910428
OLQ 0.037	ctbp-1	0.0936889869941912	0.0961938570594014
OLQ 0.037	daf-19	0.0911381178764695	0.105785931627418
OLQ 0.037	dxbp-1	0.00656082731257445	0.00369326844833505
OLQ 0.037	egl-13	0.0110289950178377	NA
OLQ 0.037	egl-18	0.103955880897881	0.0881770927760629
OLQ 0.037	ekl-4	0.0384851672383057	0.0434645422550778
OLQ 0.037	elt-4	NA	0.019400069806905
OLQ 0.037	ets-5	0.0529396976714905	0.0513707318416295
OLQ 0.037	F22D6.2	0.0918668059585286	0
OLQ 0.037	F33H1.4	0.00773452244204485	0.00104622670736884
OLQ 0.037	F57A8.1	0.0180150785967111	0
OLQ 0.037	fkh-10	0	0.00719487009779946

OLQ 0.037	fkh-8	0.0446894068049889	0.0424945737817858
OLQ 0.037	hinf-1	0.128509544412654	0.132928661185629
OLQ 0.037	hlh-8	NA	0.014943759910618
OLQ 0.037	hmg-1.1	0.0196903986280083	0.0333209775012243
OLQ 0.037	isw-1	0.0269372044851593	0
OLQ 0.037	lag-1	0.0569105358102997	0.0329159328503253
OLQ 0.037	let-607	0	0.000703609519333332
OLQ 0.037	lim-7	0.0317665498759129	0.0289911735926244
OLQ 0.037	lin-11	0.18892092934622	0.214929435077217
OLQ 0.037	lin-14	0.0545353836612538	0.0455778604657345
OLQ 0.037	lin-26	0.0743840072900311	0.0699416762696334
OLQ 0.037	lin-40	0.0716226454634073	0.030181768157645
OLQ 0.037	lsy-2	0.0346804910881124	0.024236384971539
OLQ 0.037	mab-5	0.00798178971661408	NA
OLQ 0.037	madf-3	0.0662118649528964	0.0685564643665862
OLQ 0.037	madf-5	0.0784354578895354	0.0498713318256237
OLQ 0.037	madf-9	0.0291453575232326	0.00391048575149665
OLQ 0.037	mbf-1	0.212226846844018	0.141946527694924
OLQ 0.037	mdt-29	0.0193498153754133	0.0245951216568089
OLQ 0.037	nfya-2	0.029064996921516	0.0145053524462524
OLQ 0.037	nfyb-1	0.0050035651133932	0.00576203431876164
OLQ 0.037	nhr-11	0.0317461424547869	0.0263625339837609
OLQ 0.037	pag-3	0.0748444265127957	NA
OLQ 0.037	pbrm-1	0.0211575434757378	0.015962233508332
OLQ 0.037	row-1	0.00247389163713883	0
OLQ 0.037	saeg-2	NA	0.000998183262308282
OLQ 0.037	sem-4	0.0473668502590447	0.0432151174035984
OLQ 0.037	T26A5.8	0.00702846562196268	0
OLQ 0.037	unc-42	0.0243950009598293	0.0238334792034876
OLQ 0.037	unc-62	0.00931944492357514	0.00402625667952398
OLQ 0.037	Y53G8AR.9	0.00397306521555712	0.00756922249090543
OLQ 0.037	Y56A3A.18	0.0461709203402094	0.0334378267198263
OLQ 0.037	zag-1	0.0861907558338277	NA
OLQ 0.037	zfh-2	0.0517355545268945	0.0472516284692817
OLQ 0.037	zim-3	0.0356595363380393	0.0364102324302043
OLQ 0.037	ZK546.5	0.0464612993550948	0.0636445756302319
OLQ 0.037	ztf-1	0.0208040140502279	0.0819450926322557
OLQ 0.037	ztf-26	0.117811432641947	0.0616909559720834
Oocytes 0.029	alr-1	0.280084573570327	0.294819962571612
Oocytes 0.029	C16A3.4	0.0100066048664802	0.0120435630242116
Oocytes 0.029	C17E4.6	0.00950455012279719	0.00830716724301168
Oocytes 0.029	ceh-40	0.0646119978147003	0.0734167276360925
Oocytes 0.029	cey-2	0.0121974641297161	0

Oocytes 0.029	crh-2	0.00674080481181058	0.00828246413716593
Oocytes 0.029	daf-19	0.0472304266769116	0.0481510566165784
Oocytes 0.029	dpl-1	0.0432001254723367	0.048016140872556
Oocytes 0.029	dxbp-1	0.0121869375439185	0.0157506214325006
Oocytes 0.029	efl-1	0.0419261719198759	0.0495665679704734
Oocytes 0.029	egl-18	0.0103656600112806	0.0127138668218239
Oocytes 0.029	ekl-4	0.0913104809718401	0.0977389057433336
Oocytes 0.029	elt-4	0.093697513480702	0.0322678387534757
Oocytes 0.029	F13C5.2	0.00184631318152162	0.00103250469520091
Oocytes 0.029	F22D6.2	0.172437611661117	0.0486014047255498
Oocytes 0.029	F23B12.7	0.0144420591287892	0.0169766181381735
Oocytes 0.029	F33H1.4	0.0391109088858131	0.0357240164737457
Oocytes 0.029	F44E2.7	0.0101932174356158	0.00674162111333167
Oocytes 0.029	hif-1	0	2.49858298811803e-05
Oocytes 0.029	hinf-1	0.105496245084466	0.117350372924531
Oocytes 0.029	hlh-26	0.899005731699318	0.775843881112931
Oocytes 0.029	hlh-8	0.0124639815766259	0.00753758033878332
Oocytes 0.029	hsf-1	0.0255472188056447	0.0332774307318378
Oocytes 0.029	lag-1	0.011050798814951	0.0521679139031246
Oocytes 0.029	let-607	0.0300566227753153	0.0289104101316603
Oocytes 0.029	lim-7	0.0160169970519225	0.0259631961407659
Oocytes 0.029	lin-26	0.117604543494079	0.10062591700567
Oocytes 0.029	lin-40	0.110748519048364	0.0399480590367866
Oocytes 0.029	lir-1	0	0.00599277457285272
Oocytes 0.029	lsy-2	0.014411787792518	0.0125418387850374
Oocytes 0.029	madf-3	0.0940150892883595	0.102409949226761
Oocytes 0.029	madf-5	0.162825233534788	0.115626895942302
Oocytes 0.029	madf-6	0.0456390739360114	0.0582835190917303
Oocytes 0.029	madf-9	0.0451833223648875	0.00309430245250998
Oocytes 0.029	mdt-29	0.010915946293221	0.00435114409421094
Oocytes 0.029	nhr-11	0.0229296092249131	0.0148139724555128
Oocytes 0.029	nhr-179	0.360660661738623	0.102401162558435
Oocytes 0.029	nhr-270	0.0202649527195424	0
Oocytes 0.029	pag-3	0.0308097616073564	0.0192289818083452
Oocytes 0.029	pat-9	0.17262214817105	0.159507033973414
Oocytes 0.029	pbrm-1	0.0151575102016408	0.00840482631136136
Oocytes 0.029	R02D3.7	0.0206196242059075	0.0203641999394662
Oocytes 0.029	saeg-2	0	0.000473096825006521
Oocytes 0.029	skn-1	0	0.00155480598376593
Oocytes 0.029	spr-3	0.038278449784364	0.00104027827777824
Oocytes 0.029	sptf-2	0.351844854505363	0.368622168474205
Oocytes 0.029	T20F7.1	0	0.00104519323238771
Oocytes 0.029	tlp-1	0.0261797898400014	0.0173046454241775

Oocytes 0.029	unc-62	0.0115680702263691	0.00563521806866897
Oocytes 0.029	Y53G8AR.9	0.0194503094029378	0.00745509071778788
Oocytes 0.029	Y56A3A.18	0.0518681528943549	0.0457530738870378
Oocytes 0.029	zfh-2	0.0508302183770954	0.0427097918716165
Oocytes 0.029	zim-3	0.0434301977332564	0.0292868717557854
Oocytes 0.029	zip-5	0.00169209545236478	0.0109618349103004
Oocytes 0.029	ztf-1	0.0899689067392491	0.0859485147957094
Oocytes 0.029	ztf-26	0.114896594767819	0.0347962584060372
PDA 0.047	aha-1	0.118843395539426	0.148444083379166
PDA 0.047	akir-1	0	0.0444888589914156
PDA 0.047	atf-7	0.00856187779043586	0.0124207451461887
PDA 0.047	attf-6	0.00117693153511757	0.0158025286833603
PDA 0.047	cebp-1	0.00104213889552754	0.0117924011820916
PDA 0.047	ceh-20	0.0224901998008571	0.0308667161617908
PDA 0.047	ces-1	NA	0.00133296923290826
PDA 0.047	crh-2	0.0521555421317491	0.0768746946501793
PDA 0.047	ctbp-1	0.170649887401476	NA
PDA 0.047	daf-19	0.0544423811942708	0.0911679567439398
PDA 0.047	drap-1	0	0.00450491930269539
PDA 0.047	egl-18	NA	0.139857198013735
PDA 0.047	egl-27	0.0197173300692759	0.0552125887165792
PDA 0.047	ekl-4	0.0306338211356179	0.049193112025412
PDA 0.047	elt-4	0.0346403700516628	NA
PDA 0.047	F22D6.2	0.102198198707301	0.180371168940262
PDA 0.047	F44E2.7	0	0.00272425996086466
PDA 0.047	fkh-10	0.0245084200108864	NA
PDA 0.047	flh-1	0	0.0192579139496506
PDA 0.047	hif-1	0.00236853621359512	0.00514859128341923
PDA 0.047	hinf-1	0.146498252219098	NA
PDA 0.047	hmg-1.1	0.0269948233683121	0.0354780908485906
PDA 0.047	hmg-11	0	0.0241142269534956
PDA 0.047	hsf-1	0.0319093065894882	0.0396055010188167
PDA 0.047	isw-1	0.0584579145062407	0.0722543822090219
PDA 0.047	lag-1	0.0873784226574702	0.175761566115968
PDA 0.047	lin-11	NA	0.243330613005093
PDA 0.047	lin-13	0	0.00239094931091007
PDA 0.047	lin-14	0.0906835047703378	0.0956631609145962
PDA 0.047	lin-26	0.0521727811101844	0.0641429630483388
PDA 0.047	lin-39	NA	0.0410468353031363
PDA 0.047	lin-40	0.0725012102467674	0.0801050670001623
PDA 0.047	lin-54	0	0.0137753119120515
PDA 0.047	lsy-2	0.0170763120576116	NA
PDA 0.047	madf-5	0.068774682393365	0.052682278347077

PDA 0.047	madf-6	0	0.0100736401466555
PDA 0.047	mbf-1	0.0115256695030366	0.261504612998255
PDA 0.047	mdt-29	0.0357288378119631	NA
PDA 0.047	mep-1	0	0.00407905042286128
PDA 0.047	nfya-1	0.013608726754924	NA
PDA 0.047	nfya-2	0.00652169367428875	NA
PDA 0.047	pat-9	0.189840628158158	NA
PDA 0.047	pbrm-1	0.0136379836114691	0.0269345015149808
PDA 0.047	R02D3.7	0	0.0140911896982066
PDA 0.047	row-1	0.0559683240961629	0.053377687175767
PDA 0.047	sox-4	0.0602986562454289	NA
PDA 0.047	sptf-2	0.280204632768169	0.296826875283654
PDA 0.047	unc-3	0.0312836224706675	0.0154518153260693
PDA 0.047	unc-42	NA	0.0494843074180951
PDA 0.047	unc-55	0.0688362145456926	NA
PDA 0.047	unc-62	0	0.00103967212477667
PDA 0.047	Y53G8AR.9	NA	0.0201981151855249
PDA 0.047	Y56A3A.18	0.0200162924248485	0.0380304597195744
PDA 0.047	zag-1	0.198748468561215	0.21227447405073
PDA 0.047	zfh-2	0.0392648812465642	0.0421583931321639
PDA 0.047	zim-3	NA	0.0258296391365417
PDA 0.047	ZK546.5	0.0229425227504308	NA
PDA 0.047	ztf-1	0	0.0724887662719006
PDA 0.047	ztf-26	0.0336255330393708	0.0563008453640947
PDA 0.047	ztf-4	0	0.0159900557995755
PHA_PHB 0.037	aha-1	0.0500785473635437	0.0354405760471962
PHA_PHB 0.037	alr-1	0.220878440250026	NA
PHA_PHB 0.037	atf-7	0.000307556244149026	0
PHA_PHB 0.037	attf-6	0.038632683842802	0.0141866268749499
PHA_PHB 0.037	bed-1	0.000197762813197524	0
PHA_PHB 0.037	C34B4.2	0.775228692109983	0.158471162374131
PHA_PHB 0.037	cebp-1	0.0127535699325726	0.00858303298965335
PHA_PHB 0.037	ceh-63	NA	0.0611564957447901
PHA_PHB 0.037	ceh-9	0.201434430742904	0.221305767986595
PHA_PHB 0.037	crh-2	0.0404991010372092	0.0342974737246939
PHA_PHB 0.037	ctbp-1	0.102326917815662	0.0940067563939345
PHA_PHB 0.037	D1046.2	0.0115548801635294	0
PHA_PHB 0.037	daf-19	0.121958101052313	0.107574926447176
PHA_PHB 0.037	dxbp-1	0.0118682907762169	0.011484278478187
PHA_PHB 0.037	egl-18	0.138208225084613	NA
PHA_PHB 0.037	ekl-4	0.0725205162750502	0.0552256980293303
PHA_PHB 0.037	F22D6.2	0.081154327326782	0
PHA_PHB 0.037	F44E2.7	0.000389910782168326	0

PHA_PHB 0.037	fkh-8	0.130290610469974	0.135648530618856
PHA_PHB 0.037	hif-1	0.00483330126632225	0
PHA_PHB 0.037	hinf-1	0.134172587390784	0.130770275484665
PHA_PHB 0.037	hlh-8	0.00232509482045499	0
PHA_PHB 0.037	hsf-1	0.011349476376932	0.00257606117212465
PHA_PHB 0.037	lag-1	0.0704686555019734	NA
PHA_PHB 0.037	lim-6	0.0365826857350297	NA
PHA_PHB 0.037	lim-7	0.0945606373870067	0.0529738474820475
PHA_PHB 0.037	lin-11	0.345375484763008	0.323772455851624
PHA_PHB 0.037	lin-14	0.0131814357423016	0.0102961619490693
PHA_PHB 0.037	lin-26	NA	0.0855857864691721
PHA_PHB 0.037	lin-40	0.0883524319548879	0.0628694957887204
PHA_PHB 0.037	lin-54	0.0121303967277483	0
PHA_PHB 0.037	lsy-2	0.0226117491251144	0.0109136642071994
PHA_PHB 0.037	madf-2	NA	0.0107028743188478
PHA_PHB 0.037	madf-3	NA	0.0508884097883499
PHA_PHB 0.037	madf-5	0.0766465781617952	NA
PHA_PHB 0.037	madf-6	0.0126000540729024	NA
PHA_PHB 0.037	mbf-1	0.0518006284677588	0
PHA_PHB 0.037	mdt-29	0.0136761075178125	0.0126093816979459
PHA_PHB 0.037	mxl-1	0.0107592010041597	NA
PHA_PHB 0.037	nfya-2	0.013171926776336	NA
PHA_PHB 0.037	nhr-11	0.0762642255041894	0.0834006433319996
PHA_PHB 0.037	nhr-237	0.00263287554093552	0.0261860274344242
PHA_PHB 0.037	nhr-71	0.002353300200886	0
PHA_PHB 0.037	pag-3	0.0224782169892274	NA
PHA_PHB 0.037	pbrm-1	0.0220919772607198	0.00804675922779938
PHA_PHB 0.037	rcor-1	0.0101788874278123	0.000384183454502482
PHA_PHB 0.037	sem-4	0.0350310939322224	0.00644080822831423
PHA_PHB 0.037	sox-4	0.0145018333088445	0
PHA_PHB 0.037	unc-62	0.000446246197034236	NA
PHA_PHB 0.037	unc-86	0.0192404942673617	0
PHA_PHB 0.037	Y53G8AR.9	0.0349501418614351	0.0222221557012888
PHA_PHB 0.037	Y56A3A.18	0.0398020167730892	0.0433636242646721
PHA_PHB 0.037	zfh-2	0.0373109944470918	0.0309229520567099
PHA_PHB 0.037	zim-3	0.0280549676715887	0.0228020510643829
PHA_PHB 0.037	ZK546.5	0.0248498912639457	0.112024205657011
PHA_PHB 0.037	ztf-1	0.0185010290489329	0.0422073275470007
PHA_PHB 0.037	ztf-26	0.0738379440192919	0.013981237686767
PLM_ALM 0.037	aha-1	0.139969442131136	0.156300812521178
PLM_ALM 0.037	alr-1	0.149970447233026	0.142454866352646
PLM_ALM 0.037	atf-7	0	9.32880024410091e-05
PLM_ALM 0.037	cebp-1	0.00181387310328427	0.00752872956788385

PLM_ALM 0.037	ceh-19	0.202076853011861	0.2169175604957
PLM_ALM 0.037	ceh-34	0.0302055340852485	0.0244748813699369
PLM_ALM 0.037	ceh-9	0.0205665919913855	0.0390683329137325
PLM_ALM 0.037	crh-2	0.0222041704112452	0.0252659148150586
PLM_ALM 0.037	ctbp-1	0.0928341487893114	0.0777478964144145
PLM_ALM 0.037	daf-19	0.0567198252610212	0.0578247333060075
PLM_ALM 0.037	egl-18	0	9.23288534116784e-05
PLM_ALM 0.037	ekl-4	0.0256813252768804	0.0313219888924556
PLM_ALM 0.037	elt-4	0.0245482566631287	NA
PLM_ALM 0.037	F22D6.2	0.0489931180518796	0
PLM_ALM 0.037	F44E2.7	0.0181990370107053	0.0265949873696119
PLM_ALM 0.037	hinf-1	0.0928829587959192	0.102061705430316
PLM_ALM 0.037	hlh-1	0.00140560340143483	NA
PLM_ALM 0.037	hlh-8	NA	0.0432765623153083
PLM_ALM 0.037	hsf-1	0.00829515720789031	0.0129591523227892
PLM_ALM 0.037	lag-1	0.00940022072861446	0.0437941122722148
PLM_ALM 0.037	lim-7	0.0218033612808732	0.0315745916959818
PLM_ALM 0.037	lin-11	0.0539707216226176	0.0685022739980992
PLM_ALM 0.037	lin-14	0.0242895733484806	0.0236854199369476
PLM_ALM 0.037	lin-26	0.0575040598505766	0.0462835114605938
PLM_ALM 0.037	lin-39	0	0.00236494461764603
PLM_ALM 0.037	lin-40	0.0653453059564335	0.0356771956996761
PLM_ALM 0.037	lsy-2	0.00946505018626463	0.00696419823154418
PLM_ALM 0.037	madf-3	0.0446045577019954	0.0439758772737799
PLM_ALM 0.037	madf-5	0.072454551854855	0.0352633196146246
PLM_ALM 0.037	mbf-1	0.0129053520615424	0
PLM_ALM 0.037	mdt-29	0.0041007866553134	0.00941621319103439
PLM_ALM 0.037	nfya-2	0.0210329300086923	0.0254531954843143
PLM_ALM 0.037	nhr-11	0.0166316115366154	NA
PLM_ALM 0.037	nhr-48	0.00492983798109995	0.00505956198913452
PLM_ALM 0.037	pag-3	0.0690834017508781	0.0497739872865462
PLM_ALM 0.037	pbrm-1	0.00991991019438233	0
PLM_ALM 0.037	sem-4	0.0258892536555576	0.0321379526915369
PLM_ALM 0.037	sptf-2	NA	0.251796843594176
PLM_ALM 0.037	unc-42	0.00400526944036988	0.00352057937174455
PLM_ALM 0.037	unc-55	0.0361015614726423	0.0392008759557872
PLM_ALM 0.037	unc-62	0.000125152203367409	9.56926712254818e-05
PLM_ALM 0.037	unc-86	0.213894182089936	0.214710708052394
PLM_ALM 0.037	Y53G8AR.9	0.0288239030610606	0.0278539608277942
PLM_ALM 0.037	Y56A3A.18	0.0149751764437473	0.0133578863193928
PLM_ALM 0.037	zag-1	0.0819977363486492	0.0875890876776146
PLM_ALM 0.037	zfh-2	0.0372449837557927	0.0307775565860371
PLM_ALM 0.037	ZK546.5	0.017186623847528	0.0596920382627766

PLM_ALM 0.037	ztf-26	0.0587313467588184	0.0210727315087886
PVD_FLP 0.045	aha-1	0.133302963316445	0.148480573041288
PVD_FLP 0.045	cebp-1	0.0327661912004569	0.0347768416374041
PVD_FLP 0.045	ceh-22	0.00415815018678194	NA
PVD_FLP 0.045	crh-2	0.0109411060455537	0.0150047287507328
PVD_FLP 0.045	ctbp-1	0.110775169261317	0.108469420014718
PVD_FLP 0.045	D1046.2	0.0089661350553798	0
PVD_FLP 0.045	daf-19	0.0669476508770327	0.0690050179635526
PVD_FLP 0.045	egl-18	0.100190107224797	0.0809467761483442
PVD_FLP 0.045	ekl-4	0.024551266260698	0.032467171341059
PVD_FLP 0.045	elt-4	NA	0.0537939368048669
PVD_FLP 0.045	F22D6.2	0.0910540211774911	0.0109319976323141
PVD_FLP 0.045	fkh-8	0.0187321873636117	0.0162886711627931
PVD_FLP 0.045	hinf-1	0.0737146535325297	NA
PVD_FLP 0.045	hsf-1	0.00729457683776272	0.00211734005828738
PVD_FLP 0.045	K12H6.12	NA	0.0459889295565187
PVD_FLP 0.045	lag-1	0	0.0514185970958422
PVD_FLP 0.045	lim-7	0.0135584166400882	0.000713832048967942
PVD_FLP 0.045	lin-14	0.052524640437081	0.0532339898402386
PVD_FLP 0.045	lin-26	0.0820354378243551	0.0833962490353731
PVD_FLP 0.045	lin-39	0.0664537654050494	0.0719187106209995
PVD_FLP 0.045	lin-40	0.12933003778579	0.0726867458137055
PVD_FLP 0.045	lsy-2	0.0127361190171732	0.00999951102325968
PVD_FLP 0.045	madf-3	NA	0.0478563503116782
PVD_FLP 0.045	madf-5	0.0505575879643552	0.00970872291186139
PVD_FLP 0.045	mdt-29	0.000482879439050849	0.0128697551766009
PVD_FLP 0.045	nfyb-1	0.00821521383865964	0.00615076933172455
PVD_FLP 0.045	nhr-11	NA	0.0176089252850169
PVD_FLP 0.045	pag-3	0.0647301988403731	NA
PVD_FLP 0.045	pat-9	0.122018545030668	NA
PVD_FLP 0.045	pbrm-1	0.0206723813875178	0.0115425388288812
PVD_FLP 0.045	saeg-2	0	0.00664357188841174
PVD_FLP 0.045	sem-4	0.0226171543181443	NA
PVD_FLP 0.045	somi-1	0.0169679542204032	0.0307247781794274
PVD_FLP 0.045	syd-9	0.16433919981557	0.149440076164054
PVD_FLP 0.045	tlp-1	0.0193502273182624	0.00361807106474898
PVD_FLP 0.045	unc-3	0.0274062346232506	0.0259325758343627
PVD_FLP 0.045	unc-42	NA	0.0459897332501865
PVD_FLP 0.045	unc-86	0.0900816031024607	0.118009165904769
PVD_FLP 0.045	Y53G8AR.9	0.00224347293175282	0
PVD_FLP 0.045	Y56A3A.18	NA	0.0217031216440421
PVD_FLP 0.045	zag-1	0.0911040959696487	NA
PVD_FLP 0.045	zfh-2	0.0396638406600395	0.0303246684631113

PVD_FLP 0.045	ZK546.5	0.0583608610522608	0.0660260722497758
PVD_FLP 0.045	ztf-11	0.0201955306667707	0
PVM_AVM 0.043	aha-1	0.154731792283125	0.197945439113457
PVM_AVM 0.043	alr-1	0.140569854544479	0.14680757417779
PVM_AVM 0.043	attf-6	0	0.00479070867413046
PVM_AVM 0.043	C34B4.2	0.0138455487821417	0
PVM_AVM 0.043	cebp-1	0.000201165990382298	0.00699924512983476
PVM_AVM 0.043	ceh-19	0.0864381853848545	0.102735237690866
PVM_AVM 0.043	ceh-34	0.0125487346351228	0.0112422467439887
PVM_AVM 0.043	crh-2	0.0255149870481486	0.0332768251864995
PVM_AVM 0.043	ctbp-1	0.12098577975535	0.107537362184226
PVM_AVM 0.043	D1046.2	0.0022616600079393	0.0104041523212042
PVM_AVM 0.043	daf-19	0.0970032695857618	0.102145722114615
PVM_AVM 0.043	egl-18	0.0296526886038154	0.0417978120059349
PVM_AVM 0.043	ekl-4	0.0318097785748148	0.0433394395142453
PVM_AVM 0.043	elt-4	0.121372194163214	0.0896921095924994
PVM_AVM 0.043	F22D6.2	0.0196615575957686	0
PVM_AVM 0.043	F44E2.7	0	0.00406295542071552
PVM_AVM 0.043	hif-1	0	0.00286795662613308
PVM_AVM 0.043	hinf-1	0.102757004823511	0.114956728307773
PVM_AVM 0.043	hlh-8	0.0381957035946724	NA
PVM_AVM 0.043	hsf-1	0.00328218282249192	0.00322954855479202
PVM_AVM 0.043	lag-1	0	0.0148982163032484
PVM_AVM 0.043	lim-7	0.0471020241014211	0.0668441770114376
PVM_AVM 0.043	lin-11	0.105679432969666	0.136787775770329
PVM_AVM 0.043	lin-14	0.0177437906566484	0.0189981387462794
PVM_AVM 0.043	lin-26	0.063752199340814	0.052818212375391
PVM_AVM 0.043	lin-39	0	0.00980931355713421
PVM_AVM 0.043	lin-40	0.0795953326422593	0.0389802567673389
PVM_AVM 0.043	lsy-2	0.0118638896590121	0.0130964798231854
PVM_AVM 0.043	madf-3	0.0395505805132557	0.0452255643857599
PVM_AVM 0.043	madf-5	0.0579963610786983	0.0293653417894254
PVM_AVM 0.043	madf-9	0	0.000970524585654751
PVM_AVM 0.043	mdt-29	0.0206823958794149	0.0250126533413106
PVM_AVM 0.043	nfya-2	0	0.0103867872739163
PVM_AVM 0.043	nhr-11	0.0173380095874189	NA
PVM_AVM 0.043	pag-3	0.0633181955992801	0.0463008381407865
PVM_AVM 0.043	pat-9	NA	0.149334315120225
PVM_AVM 0.043	pbrm-1	0	0.00680383080603375
PVM_AVM 0.043	saeg-2	0	0.00512877483696072
PVM_AVM 0.043	sem-4	0.0549460115138409	0.0797242222242466
PVM_AVM 0.043	tlp-1	0.00139485689253342	NA
PVM_AVM 0.043	unc-62	0	0.00257200182504692

PVM_AVM 0.043	unc-86	0.175841926094083	0.17478136542982
PVM_AVM 0.043	Y53G8AR.9	0.0149385526580448	0.0107896780482786
PVM_AVM 0.043	Y56A3A.18	0.0178041551257411	0.0285113809946735
PVM_AVM 0.043	zag-1	0.10699673076286	0.120253961161446
PVM_AVM 0.043	zfh-2	0.0503199110823257	0.0462412158233444
PVM_AVM 0.043	ZK546.5	0	0.000497071405511625
PVM_AVM 0.043	ztf-26	0.0846377923085416	0.0441038162945721
PVN 0.046	aha-1	0.163558566373762	0.221889818654784
PVN 0.046	atf-7	0.0184113570016818	0
PVN 0.046	attf-6	0.0114001664376154	0.0385065137932188
PVN 0.046	C34B4.2	0.0934874293394828	NA
PVN 0.046	cebp-1	NA	0.0116832387350789
PVN 0.046	ceh-14	0.018003711413781	0.00497845536379949
PVN 0.046	ceh-31	0.0269167606418158	NA
PVN 0.046	ceh-48	0.0140557631238401	0.0156674387160499
PVN 0.046	chd-7	0.00614498654685891	0.000964399155618998
PVN 0.046	crh-2	0.0445597352131668	0.0336389885802543
PVN 0.046	ctbp-1	0.185868250592756	NA
PVN 0.046	daf-19	NA	0.142686145784918
PVN 0.046	dxbp-1	0.00913689321700071	0.00269347300013264
PVN 0.046	ekl-4	0.108642551909758	NA
PVN 0.046	F22D6.2	0.0349793926923053	0.0528747016473064
PVN 0.046	F33H1.4	0	0.0163322954891071
PVN 0.046	hif-1	0.000695681007979773	0.0122055058326656
PVN 0.046	hmg-1.1	0.00387849803655092	0.040545214763205
PVN 0.046	hmg-11	0.00854640709284989	0.016541828569313
PVN 0.046	hsf-1	0.0236034620545997	0.0365208949390597
PVN 0.046	isw-1	0.12846284254102	0.0894638133287342
PVN 0.046	lim-7	0.0487932478889753	0.110871140091925
PVN 0.046	lin-13	0.00607635603569011	0
PVN 0.046	lin-14	0.086966013055865	NA
PVN 0.046	lin-26	0.0744126946913076	NA
PVN 0.046	lin-39	0.0518963451140282	NA
PVN 0.046	lin-40	0.0676493517441883	0.046428713843681
PVN 0.046	lsy-2	0.0454186472739556	0.0401618404226174
PVN 0.046	madf-5	0.0333396754028186	NA
PVN 0.046	madf-9	0.0024428547849325	NA
PVN 0.046	mbf-1	0.306953946676437	0.0450121909575553
PVN 0.046	mdt-29	0.0498484898650696	0.053937388693496
PVN 0.046	mml-1	NA	0.0182226580122883
PVN 0.046	nfyb-1	0.00458677769779055	NA
PVN 0.046	nhr-47	0.0236957593938912	0
PVN 0.046	nhr-71	NA	0.0557212076015277

PVN 0.046	pat-9	NA	0.171408704199459
PVN 0.046	pbrm-1	0.0334354438926946	0.0541230811334548
PVN 0.046	rbr-2	0	0.00603171122932003
PVN 0.046	rcor-1	0	0.0383677187369623
PVN 0.046	row-1	0.0558772778091998	0.0550866629502942
PVN 0.046	saeg-2	0.027036721641056	0.0194566332749126
PVN 0.046	sem-4	0.0993715226375339	0.145866848058464
PVN 0.046	somi-1	0	0.0505879595711678
PVN 0.046	sptf-2	0.401643582988212	NA
PVN 0.046	syd-9	0.15127692796994	0.10114363487832
PVN 0.046	unc-3	0.0491954050157806	0
PVN 0.046	unc-62	NA	0.0132881517869542
PVN 0.046	Y53G8AR.9	0.0426769780636572	0.0459431199561912
PVN 0.046	Y56A3A.18	0.0635451052759522	0.109038190239022
PVN 0.046	zag-1	NA	0.237642664259566
PVN 0.046	zfh-2	0.0470895815485172	0.0400411692149138
PVN 0.046	zim-3	0.00547281277971347	NA
PVN 0.046	ZK546.5	NA	0.103381590677676
PVN 0.046	ztf-26	0.071687068456319	NA
PVP 0.042	aha-1	0.0290401866003967	0.087650049415119
PVP 0.042	attf-6	0.0131747221832103	0.0166894731529866
PVP 0.042	cebp-1	0.00517099516080376	0.0159019048892734
PVP 0.042	ceh-18	0	0.00413703048327356
PVP 0.042	ceh-34	NA	0.00296881409212772
PVP 0.042	ceh-48	4.46097938920897e-05	0.00985716728720181
PVP 0.042	ceh-63	0.245138607066482	NA
PVP 0.042	crh-2	0.0514635209850535	0.0630520924338544
PVP 0.042	ctbp-1	0.179571920171498	NA
PVP 0.042	daf-19	0.128465220658439	NA
PVP 0.042	drap-1	0	0.00233805761466902
PVP 0.042	egl-13	NA	0.0778834737482511
PVP 0.042	egl-18	0.116880749442399	NA
PVP 0.042	egl-27	0	0.0181770067198537
PVP 0.042	egrh-3	0.00611229476685108	NA
PVP 0.042	ekl-4	0.0449768858315962	0.0910440737891347
PVP 0.042	ets-5	0.020276757010095	NA
PVP 0.042	F22D6.2	0.00253929082505712	0
PVP 0.042	hif-1	0.00349130249751405	0.000939122431059579
PVP 0.042	hinf-1	0.136866802838371	NA
PVP 0.042	hmg-1.1	0	0.0384830442846354
PVP 0.042	hsf-1	0.0397869166080366	0.0323529285526231
PVP 0.042	isw-1	0.0317124450959949	0.0375059856310135
PVP 0.042	K12H6.12	NA	0.143632017919746

PVP 0.042	lag-1	0.0391377642506818	0.0855645545640049
PVP 0.042	lim-7	0.0868202061085441	0.0871295449729152
PVP 0.042	lin-11	0.176446899053967	0.207287913593622
PVP 0.042	lin-14	0.0510639525480843	NA
PVP 0.042	lin-40	0.0644803512580137	0.0481803327414429
PVP 0.042	lsy-2	0.0273372299392072	0.0456046186424688
PVP 0.042	madf-3	0.0487673708336016	0.0523674490191524
PVP 0.042	madf-5	NA	0.0808585699388114
PVP 0.042	madf-6	NA	0.00035492446018733
PVP 0.042	mbf-1	0.116377630290906	0.0757060186788057
PVP 0.042	mdt-29	0.0284646015919609	0.029033324222982
PVP 0.042	mml-1	0.0308237617027276	0.0637460151550492
PVP 0.042	nfya-2	NA	0.0383315174889835
PVP 0.042	nfyb-1	0	0.0134379555063117
PVP 0.042	nhr-71	0	0.0239667778753694
PVP 0.042	pbrm-1	0.00539852171865661	0.0157567103386539
PVP 0.042	rbr-2	0	0.00119979147394794
PVP 0.042	row-1	0	0.0719592674475542
PVP 0.042	sea-2	0	0.000397381146912487
PVP 0.042	sem-4	0.00787212713006061	0.0515593034591664
PVP 0.042	sox-4	0.0548484896588357	NA
PVP 0.042	sptf-2	NA	0.436065362565129
PVP 0.042	syd-9	0.0432560703441526	0.0855443273471239
PVP 0.042	T26A5.8	0	0.047773199159414
PVP 0.042	Y53G8AR.9	NA	0.00383026638093104
PVP 0.042	Y56A3A.18	0.0381973153557347	0.0652025518042008
PVP 0.042	zag-1	0.119455579104697	NA
PVP 0.042	ZK546.5	0.00561644703552483	0.0723433940271694
PVP 0.042	ztf-26	0.0533819153419385	NA
PVQ 0.034	aha-1	0.0141069245668473	NA
PVQ 0.034	ahr-1	NA	0.0145737633345047
PVQ 0.034	atf-7	0.00674792407003364	0.00722988542022114
PVQ 0.034	attf-6	0.00581868809915058	0.0245097801041393
PVQ 0.034	C34B4.2	0.196075584875714	NA
PVQ 0.034	cebp-1	0.000882055166258552	0.00907317896534056
PVQ 0.034	ceh-63	0.0813222462242389	0.101078854429172
PVQ 0.034	crh-2	0.0331780911344314	0.0469601535553966
PVQ 0.034	ctbp-1	0.126296518515777	0.115802068299515
PVQ 0.034	daf-19	0.0701751964538635	0.103877927902691
PVQ 0.034	egl-18	0.104152888242031	0.141352224543626
PVQ 0.034	egl-27	0	0.00659734087042011
PVQ 0.034	egrh-3	NA	0.00330498180383674
PVQ 0.034	ekl-4	0.0337267079198129	NA

PVQ 0.034	ets-5	NA	0.00995313673182839
PVQ 0.034	F22D6.2	0	0.0113577038405586
PVQ 0.034	hif-1	0.00852635659469303	0.0251718850659149
PVQ 0.034	hinf-1	0.0978708453825146	0.112072518457425
PVQ 0.034	hlh-8	0.00484482519043828	NA
PVQ 0.034	hsf-1	0.0266888346370492	0.0290187757252403
PVQ 0.034	isw-1	0.0223532902346638	0.0426580372761195
PVQ 0.034	lag-1	0.0210516477831166	NA
PVQ 0.034	lim-6	0.00406456147212661	NA
PVQ 0.034	lim-7	0.0230802219849992	0.0539560935371411
PVQ 0.034	lin-11	0.188076272778768	0.176590902624902
PVQ 0.034	lin-13	0	0.0158597306212582
PVQ 0.034	lin-14	0.0180206187910542	0.0169661588076974
PVQ 0.034	lin-26	0.0779115839386429	0.0847539468466598
PVQ 0.034	lin-40	0.0957359138262845	0.0816933509765433
PVQ 0.034	lin-54	0	0.00721550086794005
PVQ 0.034	lsy-2	0.017217304561325	NA
PVQ 0.034	madf-3	0.0381166940093568	0.0505421437464244
PVQ 0.034	madf-5	0.0593326828123522	NA
PVQ 0.034	madf-6	0	0.00976527083517877
PVQ 0.034	mbf-1	0.0902030402840924	0.0985934825878168
PVQ 0.034	nhr-6	0	0.00664437115076937
PVQ 0.034	nhr-71	0	0.00324953603510333
PVQ 0.034	pag-3	0.0383688632368691	0.0234721048148688
PVQ 0.034	pat-9	NA	0.172629620201248
PVQ 0.034	pbrm-1	0	0.0027998400333362
PVQ 0.034	row-1	0	0.00365624378023357
PVQ 0.034	sea-2	0.0548265540044025	0.0322493987580108
PVQ 0.034	sem-4	0.0545378827317111	0.0605782849095123
PVQ 0.034	sptf-2	0.29396424691881	NA
PVQ 0.034	syd-9	0.0233984636440102	0.0229693358800902
PVQ 0.034	unc-42	0.000539792475384271	0.00181450608733089
PVQ 0.034	unc-55	0.0129965823794785	NA
PVQ 0.034	unc-86	0.0558968083375274	0.0639335115593463
PVQ 0.034	Y53G8AR.9	NA	0.00897301147926691
PVQ 0.034	Y55F3AM.14	NA	0.00620947530495893
PVQ 0.034	Y56A3A.18	0.0440339749744912	0.0515109159824282
PVQ 0.034	zag-1	0.0877598101207638	0.0871757196742148
PVQ 0.034	ZK546.5	0.0054551050954398	0.0369670720274846
PVR 0.042	aha-1	0.0448053949979302	0.0649139291536509
PVR 0.042	attf-6	0.000221074670481516	NA
PVR 0.042	bed-1	0	0.0023450214761196
PVR 0.042	ceh-82	NA	0.0206748354615345

PVR 0.042	crh-2	0.0199616239551425	0.0229786302680924
PVR 0.042	ctbp-1	0.143638075552356	0.146977884261689
PVR 0.042	daf-19	0.0973653741015313	NA
PVR 0.042	egl-13	0.0130884936683183	NA
PVR 0.042	egl-18	0.0564309714429696	0.0673311080536978
PVR 0.042	egrh-3	0.00364563160933598	0
PVR 0.042	ekl-4	0.0574534389240562	0.06758892748364
PVR 0.042	hinf-1	NA	0.0979878751143933
PVR 0.042	hsf-1	0.0122719681307815	0.0111636065277559
PVR 0.042	isw-1	0.0173154598429175	0.0138184722029493
PVR 0.042	lag-1	0.00862531274690331	0.0220789342305414
PVR 0.042	lim-7	0.0106769335867326	0.0144252367276909
PVR 0.042	lin-11	0.145594031797798	0.164815466131194
PVR 0.042	lin-14	0.0313106866592135	0.0368836925018848
PVR 0.042	lin-26	0.109870319767459	0.0973552640628818
PVR 0.042	lin-39	0.0188926155782238	0.0185583263958927
PVR 0.042	lin-40	0.0701341335338077	0.0122859993608635
PVR 0.042	lsy-2	0.00992012457795738	0.0100654627383656
PVR 0.042	madf-3	0.0321210465857649	0.0321843282339607
PVR 0.042	madf-5	0.0742596757724277	NA
PVR 0.042	mdt-29	0.00166749655814377	0.00542137524959264
PVR 0.042	nfya-1	0.00289323070911873	NA
PVR 0.042	nfya-2	0.0076641113908641	NA
PVR 0.042	nfyb-1	0.0102777255417188	0.0116771490231091
PVR 0.042	nhr-232	0.23044158019009	NA
PVR 0.042	pag-3	0.0625868598363976	NA
PVR 0.042	sem-4	0.0452825838193562	0.0606552263969707
PVR 0.042	somi-1	0	0.0236198348726213
PVR 0.042	unc-42	0.026141453648919	NA
PVR 0.042	unc-55	0.00251744519114544	NA
PVR 0.042	unc-86	0.0146588470140071	NA
PVR 0.042	Y53G8AR.9	0.0247199949588308	0.0263070912445547
PVR 0.042	Y56A3A.18	0.00536235629508731	NA
PVR 0.042	zag-1	0.142462399039361	0.139924578580985
PVW 0.039	aha-1	0.0489413876400697	0.0757385404188098
PVW 0.039	alr-1	0.153237861298358	NA
PVW 0.039	atf-7	0.000988232091264885	0.00603530808613026
PVW 0.039	attf-6	0	0.00271536782610075
PVW 0.039	C34B4.2	0.447671313262955	0.205410902605899
PVW 0.039	cebp-1	0.00753966466126238	0.00113050944778971
PVW 0.039	ceh-48	0.00122948791828915	0.000243748526254717
PVW 0.039	ceh-63	0.448598759549609	0.41124158452388
PVW 0.039	crh-2	0.0404273615073784	0.0380205321331267

PVW 0.039	ctbp-1	0.164160774339844	0.147350177075974
PVW 0.039	daf-19	0.0889876071683261	0.106493916024042
PVW 0.039	dsc-1	NA	0.0261710164477451
PVW 0.039	egl-13	0.00963640278473983	0
PVW 0.039	egl-5	0.0156194294376053	0.0222806947140061
PVW 0.039	ekl-4	0.043769636960514	0.0487914836867159
PVW 0.039	hif-1	0.00607330382305054	0.00204300186905755
PVW 0.039	hinf-1	0.100646694298146	NA
PVW 0.039	hlh-8	NA	0.0184145835601204
PVW 0.039	hsf-1	0.00465984923506481	0.0179167404849624
PVW 0.039	lag-1	0.00583668459858933	0.0364929562012713
PVW 0.039	lim-7	0.0255528796794126	0.0183962720172952
PVW 0.039	lin-11	0.140263354632844	0.135864883329082
PVW 0.039	lin-26	0.0758315934621003	0.0770548112217895
PVW 0.039	lin-40	0.0750438379571517	0.0680414115614398
PVW 0.039	lsy-2	0.0384039808169778	0.0322111058031675
PVW 0.039	madf-3	0.0589828432419436	NA
PVW 0.039	madf-5	0.0500188196939597	0.0459441980434638
PVW 0.039	mbf-1	0.200627349319125	0.0963545591191343
PVW 0.039	mdt-29	0.0127759569732197	0.00442112530277496
PVW 0.039	mml-1	0	0.0175377060098963
PVW 0.039	nfya-2	NA	0.0413676362101332
PVW 0.039	nfyb-1	0	0.000664364178766992
PVW 0.039	nhr-232	0.280012984718263	0.137322931562305
PVW 0.039	nhr-71	0.0162323979811524	0.00897912066218595
PVW 0.039	pag-3	0.0458404934586699	0.0349049541347439
PVW 0.039	pbrm-1	0.0105154405176508	0.0103356401901537
PVW 0.039	sem-4	0.0641590407576684	0.0487814566534251
PVW 0.039	unc-86	0.064667226032997	0.0631748475086651
PVW 0.039	Y53G8AR.9	NA	0.0211683517289538
PVW 0.039	Y55F3AM.14	0.0152456780947547	NA
PVW 0.039	Y56A3A.18	0.0555201973931236	0.0507396606264183
PVW 0.039	zag-1	0.178844837458303	0.170620714423861
PVW 0.039	zfh-2	0.0464881479028595	0.0498481354173535
PVW 0.039	ZK546.5	0.0562662955390301	0.143157904378353
Phasmid socket 0.040	alr-1	0.202972099069697	0.218930837029962
Phasmid socket 0.040	attf-6	0.00193550916221479	0.0183453020216745
Phasmid socket 0.040	blmp-1	0.0389513027731415	0.0335778915178884
Phasmid socket 0.040	ceh-18	0	0.00709743212088717
Phasmid socket 0.040	ceh-27	0.0231917441929024	NA
Phasmid socket 0.040	ceh-58	0	0.0110464774549366
Phasmid socket 0.040	cey-2	0.0585576547257315	0.0579100939892466
Phasmid socket 0.040	daf-19	NA	0.123886428100466

Phasmid socket 0.040	die-1	0	0.00268702421000465
Phasmid socket 0.040	dxbp-1	0	0.00814241350451192
Phasmid socket 0.040	egl-18	0.0207533263990509	0.0378116107742887
Phasmid socket 0.040	ekl-4	0.0795923304310593	0.0928562861829592
Phasmid socket 0.040	F10B5.3	0.0825623834195984	NA
Phasmid socket 0.040	F22D6.2	0.07906817829264	0.00398515284744126
Phasmid socket 0.040	F33H1.4	0.0273540832498441	0.0260056413199728
Phasmid socket 0.040	gei-8	0.102322383002965	0.117828080307307
Phasmid socket 0.040	grh-1	0.0625860954292976	0.0651775354269196
Phasmid socket 0.040	hinf-1	NA	0.115501424424066
Phasmid socket 0.040	hlh-8	0.0368662848959617	0.041684455843793
Phasmid socket 0.040	hsf-1	0	0.00741866474548056
Phasmid socket 0.040	lag-1	0.00159171081572336	0
Phasmid socket 0.040	let-607	0	0.00014459406186822
Phasmid socket 0.040	lim-7	0.0198661331716818	0.0441714808097892
Phasmid socket 0.040	lin-13	0.0126140478416117	0.0162290659863365
Phasmid socket 0.040	lin-26	0.128352015658856	0.120009380306878
Phasmid socket 0.040	lin-40	0.150964832483337	0.0769687284911306
Phasmid socket 0.040	lin-54	0.0080836393613664	NA
Phasmid socket 0.040	lsy-2	0.0122872925310355	0.0167108551955951
Phasmid socket 0.040	madf-3	0.0664928261513204	NA
Phasmid socket 0.040	madf-5	0.168339047375691	NA
Phasmid socket 0.040	madf-6	0.0112360683887562	0.00818135088863891
Phasmid socket 0.040	mdt-29	0.0306031640624119	0.0354794591544807
Phasmid socket 0.040	mep-1	0.00370655090975574	0.000869781428577745
Phasmid socket 0.040	mxl-2	0.0335400539832975	0.0182511166136502
Phasmid socket 0.040	nhr-11	0.0611084478418226	0.0579482975469189
Phasmid socket 0.040	nhr-129	0.0171539627437058	NA
Phasmid socket 0.040	nhr-179	0.0165009488665047	NA
Phasmid socket 0.040	nhr-25	0.0438619228976361	0.0564273749046035
Phasmid socket 0.040	nhr-85	0.0372072372821368	0.0344421428531649
Phasmid socket 0.040	pat-9	0.224083331627939	NA
Phasmid socket 0.040	pbrm-1	0.00650814724764096	0.0139893770719703
Phasmid socket 0.040	R02D3.7	0.0255444894014493	0.0222484531986607
Phasmid socket 0.040	rcor-1	0	0.00160696002009342
Phasmid socket 0.040	saeg-2	0	0.0191629572873814
Phasmid socket 0.040	skn-1	0.0134464287608995	0.0109663287867938
Phasmid socket 0.040	snu-23	0.000315253828275614	0.00245377050872955
Phasmid socket 0.040	sptf-2	0.356757248473906	NA
Phasmid socket 0.040	sup-37	0.0891313535183832	0.0642094818739235
Phasmid socket 0.040	T26A5.8	NA	0.00266257412582578
Phasmid socket 0.040	Y48G9A.11	0.00309080561983937	0.00481356258855345
Phasmid socket 0.040	Y53G8AR.9	0.0178367084785808	0.01565637134951

Phasmid socket 0.040	Y56A3A.18	0.0527692448869807	0.054081026484795
Phasmid socket 0.040	zfh-2	0.0479691932702221	0.0454776843546201
Phasmid socket 0.040	zim-3	0.072407250517291	0.0717615168816405
Phasmid socket 0.040	ztf-1	0.00449326924145827	0.0257144832360404
RIA 0.038	aha-1	0.303695569747709	0.330935578347326
RIA 0.038	cebp-1	0	0.00841312105573858
RIA 0.038	ceh-18	0.0111285996875407	0.0124662833647284
RIA 0.038	ceh-32	1.13832803218203	1.36671951058018
RIA 0.038	ceh-8	0.0676663892136425	0.0866536039665079
RIA 0.038	ceh-88	0.00426808014949136	0.0330394452644475
RIA 0.038	crh-2	0.0424065780281545	0.0465787854090042
RIA 0.038	ctbp-1	0.173397477493148	0.188323067144536
RIA 0.038	daf-19	0.0482567341087033	0.0435079244231579
RIA 0.038	drap-1	0	0.0179182397389236
RIA 0.038	egl-13	0.0449616530377415	0.0391729289511944
RIA 0.038	egl-18	0.0591691424490413	0.105899207239825
RIA 0.038	ekl-4	0.0161189103465579	0.0369310837582634
RIA 0.038	elt-4	0.0243868052808999	NA
RIA 0.038	ets-5	0	0.0177345825167061
RIA 0.038	F22D6.2	0.0546975848653677	0
RIA 0.038	F57A8.1	0	0.0318525749923833
RIA 0.038	fkh-10	0.0377218306546616	0.0334304195447062
RIA 0.038	hif-1	0.0156995349436083	0.0149507885969696
RIA 0.038	hinf-1	0.0823378667505236	0.0985991347439398
RIA 0.038	hlh-8	NA	0.0136872381598684
RIA 0.038	hmg-1.1	0.0164493126021297	0.0105943867730882
RIA 0.038	hsf-1	0.0140865646369241	0.0233644941783082
RIA 0.038	K12H6.12	NA	0.0227630955550232
RIA 0.038	lag-1	0.0320750191559577	0.109717274585512
RIA 0.038	lim-7	0.0246532222634481	0.0470468588398556
RIA 0.038	lin-11	NA	0.247352269967585
RIA 0.038	lin-13	0.020035377005713	0.00925505586326299
RIA 0.038	lin-14	0.0572974986213528	0.060940993370137
RIA 0.038	lin-26	0.0719555804324157	0.061570812257035
RIA 0.038	lin-39	0.0207055662475579	NA
RIA 0.038	lin-40	0.05251725419236	0.0177623950350945
RIA 0.038	lsy-2	0.0171882443833846	0.0158753099925073
RIA 0.038	madf-3	0.0554199574362045	NA
RIA 0.038	madf-5	0.0810674207207764	0.0379987179246508
RIA 0.038	madf-9	0.0361915306889588	0.0197399266619467
RIA 0.038	mbf-1	0	0.00805064383087051
RIA 0.038	mdt-29	0.0275926136011218	0.0398902993369633
RIA 0.038	mec-3	NA	0.025593781933566

RIA 0.038	nfya-2	0.00478911615368723	0.016272407540548
RIA 0.038	nfyb-1	0.00135118139507537	0.00435235325009963
RIA 0.038	nhr-11	0.00791823858320363	0
RIA 0.038	nhr-129	NA	0.00233662212331987
RIA 0.038	pat-9	0.155755034953356	0.129824804621634
RIA 0.038	R02D3.7	0	0.000832008334219255
RIA 0.038	row-1	0.0178639382764576	0
RIA 0.038	sem-4	0.0194687630494287	0.0381139038038787
RIA 0.038	sox-4	NA	0.000907188865794635
RIA 0.038	T26A5.8	0.0622515938586578	0.0829358561884922
RIA 0.038	unc-120	0.00630836239216913	0.00506657582025288
RIA 0.038	unc-3	NA	0.0608532365384206
RIA 0.038	unc-42	0.0230070159186525	0.0402205593445659
RIA 0.038	unc-55	NA	0.022507347556372
RIA 0.038	unc-62	0	0.00110069187954565
RIA 0.038	unc-86	0.0364202003406352	NA
RIA 0.038	Y53G8AR.9	0.0165155345091309	0.0312907067149255
RIA 0.038	Y55F3AM.14	0.0492542215658161	0.066144202963667
RIA 0.038	Y56A3A.18	0.0500897615121285	0.0582431808543322
RIA 0.038	zag-1	0.075338732759935	0.0301730507502285
RIA 0.038	zfh-2	0.048740071504998	0.0436837359920047
RIA 0.038	zim-3	0.00821213085851858	0.00301119758290219
RIA 0.038	ZK185.1	0.0020467768320719	0.0269204282996088
RIA 0.038	ZK546.5	0.0440604103568159	0.0614917015607464
RIA 0.038	ztf-26	0.114315274480216	0.0746072402285998
RIB 0.036	aha-1	0.31031217276536	0.315875223260971
RIB 0.036	alr-1	0.14223273534773	0.157658059094388
RIB 0.036	attf-6	0.000470883088406878	0.00449443011992536
RIB 0.036	C34B4.2	0.299891512096724	0.0572095320786611
RIB 0.036	ceh-18	0.00339686654781939	0.00228660224801776
RIB 0.036	ceh-27	0.0119027430513439	0.0403401833232297
RIB 0.036	ceh-32	0.408404620546877	0.397302101781673
RIB 0.036	ceh-63	NA	0.0124205422419722
RIB 0.036	crh-2	0.0394226571003628	0.0502688718517465
RIB 0.036	ctbp-1	0.133714243167013	0.171716153007121
RIB 0.036	D1046.2	0.00163658154728747	0.00173904930903178
RIB 0.036	daf-19	0.0888627962232339	0.0868056810827196
RIB 0.036	egl-13	0.044537478691547	0.0370404366549713
RIB 0.036	egl-18	0.096841695808273	0.108228781224479
RIB 0.036	egl-5	0.00685799581067912	0
RIB 0.036	ekl-4	0.0338049039388499	0.0342518560691702
RIB 0.036	elt-4	0.051482769426594	0.0153055123893768
RIB 0.036	ets-5	0.0294978066036237	0.0629845308935486

RIB 0.036	F22D6.2	0.0501639092060657	0
RIB 0.036	F57A8.1	0	0.00787518548348755
RIB 0.036	fkh-10	0.0489822321338938	NA
RIB 0.036	fkh-8	0.0127193647164868	0.0215899124280273
RIB 0.036	hif-1	0.0159924123348071	0.0235978127630105
RIB 0.036	hinf-1	0.0998250920263156	0.121884291240328
RIB 0.036	hlh-8	0.0237449728727963	NA
RIB 0.036	hsf-1	0.00211946720293534	0.00221427076649652
RIB 0.036	isw-1	0	0.00410684254191831
RIB 0.036	K09A11.1	0.00629382804761525	0
RIB 0.036	K12H6.12	0.0321958625731064	NA
RIB 0.036	lag-1	0.0382198901573168	0.0750726434268446
RIB 0.036	lim-7	0.0155344206831145	0.0233776719273179
RIB 0.036	lin-11	0.204588834203105	0.215607960990832
RIB 0.036	lin-13	0	0.00413432943059912
RIB 0.036	lin-14	0.0452034062615158	0.0605428220064848
RIB 0.036	lin-26	0.0728830768363375	0.0727741481565041
RIB 0.036	lin-39	0.00522528020191229	0.0234946503379753
RIB 0.036	lin-40	0.0763926962156583	0.0681004085544263
RIB 0.036	lsy-2	0.0126830172572023	0.0163438644374322
RIB 0.036	madf-3	0.0608660648606323	0.0686063792009493
RIB 0.036	madf-5	0.0759649640399834	0.0411102382379594
RIB 0.036	madf-9	0.0102125839319819	0
RIB 0.036	mbf-1	0	0.00590509207156077
RIB 0.036	mdt-29	0.018065945530598	0.0347115423320025
RIB 0.036	mef-2	0.0186759416238003	0.0355412089226912
RIB 0.036	nfya-1	0	0.00590919600588917
RIB 0.036	nfya-2	0.00579876003925844	0.0159027389364991
RIB 0.036	nfyb-1	0.000848368862011022	0.00829479532280878
RIB 0.036	nhr-11	0.0339685125725643	0.0199662355440907
RIB 0.036	pag-3	0.0595828034082197	NA
RIB 0.036	row-1	0.0318697799567323	0.0931804736570849
RIB 0.036	sem-4	0.0179492274830994	0.0404667526502654
RIB 0.036	sox-4	0.00285875364222338	0.00547256693588723
RIB 0.036	unc-42	0.00807425282621062	NA
RIB 0.036	unc-55	0.0160217814379725	NA
RIB 0.036	unc-86	0.0436803375561767	0.072324650456193
RIB 0.036	Y53G8AR.9	0.0118699832938192	0.00973615887886542
RIB 0.036	Y55F3AM.14	0.0753317499604896	NA
RIB 0.036	Y56A3A.18	0.0410767153570424	0.0458346058823388
RIB 0.036	zag-1	0.03954519971377	NA
RIB 0.036	zfh-2	0.0484145209405349	0.0409505247740883
RIB 0.036	zim-3	0.0178424852017157	0.0169091523626419

RIB 0.036	ZK546.5	0	0.0465388651136772
RIB 0.036	ztf-1	0.0281356588924912	0.0122467545966084
RIB 0.036	ztf-26	0.0751795039019674	NA
RIC 0.042	aha-1	0.18205954592993	0.205212191303683
RIC 0.042	alr-1	0.14704727581789	0.167036959955237
RIC 0.042	atf-7	0.00186861727798297	0.00361702028884775
RIC 0.042	attf-6	0.0112116525551942	0.0130191037358208
RIC 0.042	C34B4.2	0.305509485128845	0
RIC 0.042	ceh-27	0.0172256874832295	0.00733408679842759
RIC 0.042	ceh-40	NA	0.135950232569622
RIC 0.042	crh-2	0.0498283324255285	0.046704481173243
RIC 0.042	ctbp-1	0.125874458372311	0.134049744124655
RIC 0.042	daf-19	0.0624039341085837	0.0442992879256364
RIC 0.042	egl-13	0.0502694668027674	NA
RIC 0.042	egl-18	0.177682944079528	NA
RIC 0.042	egl-27	0.00128419263698657	0
RIC 0.042	ekl-4	0.0408028015897935	0.039120176372982
RIC 0.042	elt-4	0.0205508462683803	NA
RIC 0.042	ets-5	0.0255727548078268	0.0391687419847817
RIC 0.042	F22D6.2	0.0173334685712623	0
RIC 0.042	fkh-10	NA	0.0713002377066701
RIC 0.042	fkh-8	0.011837257020642	0.0176083909207071
RIC 0.042	hif-1	0.0183148262992463	0.0133889195849999
RIC 0.042	hinf-1	0.106563932984508	0.103759094589272
RIC 0.042	hlh-8	0.0388118888994044	0.0193175247465229
RIC 0.042	hsf-1	0.0257511809500087	0.0274943731406306
RIC 0.042	isw-1	0.00753226594100094	0.00901104541050324
RIC 0.042	K09A11.1	0.0109052942189203	NA
RIC 0.042	lag-1	0.0124870444236766	0.0356441343975757
RIC 0.042	lim-7	0.0422681768586191	0.0297054840918424
RIC 0.042	lin-11	0.222362308386133	0.234457930942559
RIC 0.042	lin-14	0.0450680446595217	0.0416884500808848
RIC 0.042	lin-26	0.0782283010688872	0.0669247103907696
RIC 0.042	lin-39	0.00802511477566388	0.0169440791186757
RIC 0.042	lin-40	0.0469734175354149	0.0130101958671078
RIC 0.042	lsy-2	0.0128502488620114	0.0116664536000036
RIC 0.042	madf-3	0.043289608652991	NA
RIC 0.042	madf-9	0.0317259363371609	NA
RIC 0.042	mdt-29	0.0438946116657421	0.0349552428308047
RIC 0.042	mef-2	0	0.0341581148904271
RIC 0.042	nfya-2	0.00833300149650587	0.0190695718878189
RIC 0.042	nfyb-1	0.000238321130427464	0.00033840093723415
RIC 0.042	nhr-11	0.0149212274031931	0

RIC 0.042	nhr-179	0.0818547762263667	0.0497836839937171
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RIC 0.042	pax-3	NA	0.0870928604726604
RIC 0.042	sem-4	0.0201187532159709	0.0240809187338544
RIC 0.042	sox-4	0.0449897695913116	NA
RIC 0.042	sptf-2	0.302681813490004	NA
RIC 0.042	sup-37	NA	0.0352519731241478
RIC 0.042	T26A5.8	0.0166937774142718	0
RIC 0.042	unc-42	0.0294329503004099	NA
RIC 0.042	unc-62	0.00811396942851007	0
RIC 0.042	unc-86	0.0882828737188874	NA
RIC 0.042	Y53G8AR.9	4.24845581761792e-05	0.0107514306955516
RIC 0.042	Y55F3AM.14	0.0686950433861553	NA
RIC 0.042	Y56A3A.18	0.0353710173951504	0.0255249821823558
RIC 0.042	zag-1	NA	0.0398093021006562
RIC 0.042	zfh-2	0.0399367930688731	0.0323779282001654
RIC 0.042	zim-3	0	0.00211961238371862
RIC 0.042	ZK185.1	0.0133399295445325	0
RIC 0.042	ztf-26	0.0642322859806159	0.0286746216575948
RID 0.038	aha-1	0	0.0123825290307779
RID 0.038	alr-1	0.167998493745638	NA
RID 0.038	atf-7	0.0225969974518238	0.0134394299500679
RID 0.038	attf-6	0.0191640909584442	0.0147579340744595
RID 0.038	ceh-63	0.124661457169253	NA
RID 0.038	crh-2	0.0455644816492466	0.0311302709615616
RID 0.038	ctbp-1	0.110399103034715	0.110895229643483
RID 0.038	D1046.2	0.0220301298732273	0.00896338991434232
RID 0.038	daf-19	0.0952773804828188	0.104551073459428
RID 0.038	egl-13	0.056245826660159	NA
RID 0.038	ekl-4	0.0456218560609221	0.048487366336638
RID 0.038	elt-4	NA	0.146634980256325
RID 0.038	F22D6.2	0.0270408063701551	0
RID 0.038	hif-1	0	0.00299122925877801
RID 0.038	hinf-1	0.107264322510696	0.107055244489338
RID 0.038	hlh-8	NA	0.00739014166904487
RID 0.038	hsf-1	0.0226188405825471	0.0221418985937848
RID 0.038	isw-1	0.0205104579321875	0.031485132853544
RID 0.038	K12H6.12	NA	0.0769849897584992
RID 0.038	lag-1	0.0316705939535937	0.0446090029928146
RID 0.038	lim-7	0.0338979325955855	0.0257221870847471
RID 0.038	lin-11	0.164108654608637	NA
RID 0.038	lin-14	0.020927137386688	0.020418604347638
RID 0.038	lin-26	0.0902291808250343	0.0748518061235083

RID 0.038	lin-40	0.0914336722958976	0.057738740880023
RID 0.038	lsy-2	0.0289850313480232	0.024891799460432
RID 0.038	madf-3	0.0398559294339253	0.0453112307805345
RID 0.038	madf-5	0.0863637836816779	0.0513136364766149
RID 0.038	madf-9	0.00740563269468539	NA
RID 0.038	mbf-1	0.102805230322939	0
RID 0.038	mdt-29	0.0311371175722199	0.0245147656648945
RID 0.038	mef-2	0.0176347969280302	0.0176619212978868
RID 0.038	nfyb-1	0.000403546965102517	0
RID 0.038	nhr-11	0.0220581100768787	NA
RID 0.038	nhr-232	NA	0.103328293448489
RID 0.038	pag-3	0.0329789281390768	0.0501440301163607
RID 0.038	pat-9	0.182236615016153	NA
RID 0.038	pbrm-1	0.00788993200693859	0
RID 0.038	R02D3.7	0.012726224472513	0
RID 0.038	row-1	0.000117882966441506	0.038314711347963
RID 0.038	saeg-2	0.015671064621537	0.0317463322799733
RID 0.038	sem-4	0.0594334075836629	0.0440235203475271
RID 0.038	unc-42	NA	0.00893827253500297
RID 0.038	unc-86	0.00989810702003983	0.0414784972249616
RID 0.038	Y53G8AR.9	0.0144501611550745	0.0148950598045217
RID 0.038	Y56A3A.18	0.0438907382256583	0.0399316581804156
RID 0.038	zag-1	0.109130476850503	0.115992232767737
RID 0.038	zfh-2	0.0548803176096657	0.0429737751544773
RID 0.038	zim-3	0.00204982632327965	0
RID 0.038	ZK546.5	0.0128053452666887	0.0822060547140028
RID 0.038	ztf-1	0.00453586845355791	0
RID 0.038	ztf-26	0.0589132354458198	0.00555392479198909
RIF 0.044	aha-1	0.292891721995214	0.303525713876141
RIF 0.044	atf-7	0.0620321665664963	0.0508335362505182
RIF 0.044	attf-6	0.0317857396907512	0.0272131563770442
RIF 0.044	bed-1	0.0139097502451369	0.00123536786916993
RIF 0.044	C34B4.2	0.266445184293291	0
RIF 0.044	ceh-18	0	0.00214617966327922
RIF 0.044	ceh-40	NA	0.105536376297293
RIF 0.044	ceh-9	0.247276671177832	NA
RIF 0.044	crh-2	0.0557847082601661	0.0506925714914653
RIF 0.044	ctbp-1	0.18015885177813	0.202442769750884
RIF 0.044	daf-19	0.108760110963558	0.0955970426862074
RIF 0.044	egl-13	0.100721575992219	NA
RIF 0.044	egl-18	0.100735136910443	0.100727851971377
RIF 0.044	egl-27	0.0664256695921759	0.0421039272518818
RIF 0.044	ekl-4	0.0449303956947727	0.0333225373419357

RIF 0.044	ets-5	NA	0.0618964378112103
RIF 0.044	F22D6.2	0.0382860057123345	0
RIF 0.044	F44E2.7	0.0211618112212849	0.00488791093821174
RIF 0.044	F57A8.1	0.0795730426357335	0.0839079549559799
RIF 0.044	fkh-10	0.0620525368455289	0.0786516998127555
RIF 0.044	hif-1	0.0308193201549709	0.0314208668416442
RIF 0.044	hinf-1	0.0690483470339161	0.0782390041139536
RIF 0.044	hlh-11	0.0162548238850888	0
RIF 0.044	hsf-1	NA	0.0345168373092832
RIF 0.044	isw-1	0.0857819846802079	0.0847750849589951
RIF 0.044	K09A11.1	NA	0.197539762671789
RIF 0.044	lag-1	0.0947344647563595	0.0700565725939963
RIF 0.044	lim-6	0.0531237112504358	0.00103849195607528
RIF 0.044	lin-11	0.22151126283289	0.240856013162267
RIF 0.044	lin-14	0.0558271681355761	0.0481923485850943
RIF 0.044	lin-26	0.103642954377902	0.100613400185405
RIF 0.044	lin-40	0.0481293764623379	0.0386607387260124
RIF 0.044	lin-54	0.0218627806641394	0.0195296116699124
RIF 0.044	lsy-2	0.027729628319148	0.024286213807026
RIF 0.044	madf-3	0.0554673419099938	NA
RIF 0.044	madf-5	0.094390608127711	NA
RIF 0.044	madf-6	0.0117013240973755	0
RIF 0.044	madf-9	0.00272284224902898	NA
RIF 0.044	mdt-29	NA	0.0696158907519658
RIF 0.044	mef-2	0	0.0880668314896276
RIF 0.044	mml-1	0.0317818617452844	0
RIF 0.044	nfya-2	NA	0.0224266092717616
RIF 0.044	nhr-11	0.0471363941552665	NA
RIF 0.044	nhr-6	0.00774372479690559	NA
RIF 0.044	pag-3	0.0809873825206608	NA
RIF 0.044	pat-9	0.268091672070511	NA
RIF 0.044	pbrm-1	0.0186180421613747	0.0169989647417045
RIF 0.044	R02D3.7	0	0.00259615385301235
RIF 0.044	row-1	0.0295542685408939	0.0161556298283263
RIF 0.044	sem-4	0.0464528904800649	0.04618589463077
RIF 0.044	unc-55	0.00366571961259132	NA
RIF 0.044	unc-62	0.00083555758735951	0
RIF 0.044	unc-86	0.0555468791966993	NA
RIF 0.044	Y53G8AR.9	0.0442447478635062	0.0418565003983748
RIF 0.044	Y56A3A.18	0.00863290670772605	0.0105121677080423
RIF 0.044	zfh-2	0.0429741490828404	0.0455827211219422
RIF 0.044	zim-3	0.0226437977391225	0.0298507205444644
RIF 0.044	ZK546.5	NA	0.0666883122419385

RIF 0.044	ztf-1	0.0115982020278244	0
RIF 0.044	ztf-26	0.0974057167493172	NA
RIG 0.046	aha-1	0.170823688919321	0.241293426604607
RIG 0.046	alr-1	0.192947158193516	NA
RIG 0.046	attf-6	0.0214792944526335	0.0237195237085358
RIG 0.046	C34B4.2	0.0251486214619201	0
RIG 0.046	ceh-27	0.0270877294668683	NA
RIG 0.046	crh-2	0.0463497675696721	0.0599306999505652
RIG 0.046	ctbp-1	0.160101585976938	0.168791206586436
RIG 0.046	daf-19	0.104515764857303	0.127144228065304
RIG 0.046	dxbp-1	0.000242964484643691	0.0117341356122906
RIG 0.046	egl-13	0.132838464254377	0.130202196142911
RIG 0.046	egl-18	0.117636630038093	0.0847204913981075
RIG 0.046	egl-27	0.0412181229079447	0.0484575049965941
RIG 0.046	egl-44	0	0.00158008325128376
RIG 0.046	ekl-4	0.0612314029104333	0.0737459688373445
RIG 0.046	ets-5	NA	0.0387584858841717
RIG 0.046	F22D6.2	0.105634329965568	0.0788768644371434
RIG 0.046	F57A8.1	0	0.0600359138363433
RIG 0.046	fkh-10	0.0486964774194474	NA
RIG 0.046	hif-1	0.0270998472174977	0.0314478812475251
RIG 0.046	hinf-1	0.128436306712616	0.147476282424516
RIG 0.046	hsf-1	0.0236558445795818	0.0110072178479565
RIG 0.046	isw-1	0.0446469009674207	0.0587642071630992
RIG 0.046	lag-1	0.0786657042130055	0.0913421156316798
RIG 0.046	lim-6	0.108010865567859	0.0840455407587104
RIG 0.046	lim-7	0.0393572982240091	0.0817956102745011
RIG 0.046	lin-11	0.2466362047577	NA
RIG 0.046	lin-14	0.0406662720126119	0.0424777644856192
RIG 0.046	lin-26	0.0963690977240938	NA
RIG 0.046	lin-40	0.0813087871078293	0.0543102201348992
RIG 0.046	lsy-2	0.0347657211416402	0.0335652923931791
RIG 0.046	madf-5	0.0780963969496377	0.0401455966647691
RIG 0.046	madf-9	0.0385481324513366	NA
RIG 0.046	mbf-1	0.11874198878035	0
RIG 0.046	nfya-2	0.0257585315533344	NA
RIG 0.046	nfyb-1	0	0.0037239129028773
RIG 0.046	nhr-11	0.0421911603513436	0.0417794100543792
RIG 0.046	nhr-6	0.00612713764862474	NA
RIG 0.046	nhr-71	0	0.00601230439311614
RIG 0.046	pag-3	0.0664444530047085	0.054738459766085
RIG 0.046	pbrm-1	0.00545941709767097	0.0144359639505916
RIG 0.046	R02D3.7	0.0129222837192228	0.0132465320876718

RIG 0.046	row-1	0.00685175137165115	0.0952567993199203
RIG 0.046	sea-2	0.080989443604923	0.0764234944779544
RIG 0.046	sem-4	0.059093511386302	0.0481854848110832
RIG 0.046	sox-4	0.000647360716688996	0
RIG 0.046	sup-37	0.0246652302903494	0
RIG 0.046	unc-42	0.0149538393151977	0.0263482026926571
RIG 0.046	unc-55	0.00409579343199399	NA
RIG 0.046	unc-62	0.00632153565013929	0
RIG 0.046	unc-86	NA	0.0643408848851627
RIG 0.046	Y53G8AR.9	0.00980752429948409	NA
RIG 0.046	Y55F3AM.14	0.0260132265797659	NA
RIG 0.046	Y56A3A.18	0.0705550748641608	0.0696644731401379
RIG 0.046	zag-1	0.00129573796689817	0.0452297021506538
RIG 0.046	zfh-2	0.0449621907193694	0.0406193924753553
RIG 0.046	zim-3	0.00868484650978653	NA
RIG 0.046	ZK546.5	0.0265413628851173	0.100453933625282
RIG 0.046	ztf-1	0.0068855324217523	0.0151118491860794
RIG 0.046	ztf-26	0.0482999456933297	NA
RIH 0.035	aha-1	0.252661616440316	0.262754564180988
RIH 0.035	attf-6	0	0.00780777610464426
RIH 0.035	ceh-18	0.000734734557496566	0.00411091177636941
RIH 0.035	ceh-27	NA	0.00472196084546412
RIH 0.035	crh-2	0.0347428826800052	0.0433108030274535
RIH 0.035	ctbp-1	0.182730628368349	0.188978999507002
RIH 0.035	D1046.2	0.00297574976884151	0
RIH 0.035	daf-19	0.0969253517335832	0.0994164616742116
RIH 0.035	egl-13	0.0479733589545252	0.0376503716986002
RIH 0.035	egl-18	0.0630490186317414	0.0209567176764091
RIH 0.035	egl-27	0.0407492728894461	0.0404725029491794
RIH 0.035	egrh-3	0.0128835792085533	0
RIH 0.035	ekl-4	0.0388719402155627	0.0526623603968617
RIH 0.035	F22D6.2	0.0779378681075703	0.0055855978228481
RIH 0.035	F57A8.1	0.0453141365765986	0.0424865878299551
RIH 0.035	fkh-8	NA	0.0236828759596942
RIH 0.035	hif-1	0.0226894046675834	0.0278327277808052
RIH 0.035	hinf-1	0.0933702041005508	0.124902527010642
RIH 0.035	hlh-8	0.0195221347179494	NA
RIH 0.035	isw-1	0.0173302661297782	0.00100674463299816
RIH 0.035	K09A11.1	NA	0.0378551358016594
RIH 0.035	lag-1	0.029001367921512	0.0276851000576544
RIH 0.035	lim-7	0.0211633952542446	NA
RIH 0.035	lin-14	0.025555058282954	0.0324676974828986
RIH 0.035	lin-26	0.10238964632898	NA

RIH 0.035	lin-40	0.0590144329151931	0.0247887725287436
RIH 0.035	lsy-2	0.0241449049799872	NA
RIH 0.035	madf-3	0.0728968266110105	0.075251918035462
RIH 0.035	madf-5	NA	0.0427020302275394
RIH 0.035	mbf-1	0.0537882972600762	0.0778869633362154
RIH 0.035	mdt-29	0.0110319693588652	0.0294406407417956
RIH 0.035	nfya-2	0.0180527523999585	NA
RIH 0.035	nhr-11	0.0440144891321055	NA
RIH 0.035	nhr-129	0	0.00676510614589178
RIH 0.035	row-1	0.0921270785835863	0.0629409559511076
RIH 0.035	sem-4	0	0.0032143258642949
RIH 0.035	unc-42	NA	0.00154661463553726
RIH 0.035	unc-86	0.118961005882961	0.128631797186132
RIH 0.035	Y53G8AR.9	0.014798419849335	NA
RIH 0.035	Y56A3A.18	0.0548996056745173	0.048904468392072
RIH 0.035	zag-1	0.00608325459751452	NA
RIH 0.035	zfh-2	NA	0.0457013952438389
RIH 0.035	zim-3	NA	0.00136820096545694
RIH 0.035	ZK546.5	0.0204797694703159	0.0833156641320609
RIH 0.035	ztf-1	0.0247303349378049	0
RIM 0.042	aha-1	0.46035256622573	0.507535538968531
RIM 0.042	atf-7	0.035564696230218	0.0306125325799577
RIM 0.042	attf-6	0.00534487085881365	0.00698566930363289
RIM 0.042	ceh-18	0.0135185502317553	0.00846242769384386
RIM 0.042	ceh-27	0.00250158236091878	0.00852688005148532
RIM 0.042	ceh-32	0.312922778220537	0.219551377063561
RIM 0.042	ceh-8	NA	0.0222751450130318
RIM 0.042	crh-2	0.0512694080732986	0.0513926505224439
RIM 0.042	ctbp-1	0.252708841108999	0.223794711598483
RIM 0.042	daf-19	0.0869373308490505	0.0916326960173388
RIM 0.042	egl-13	0.0587934517053411	0.0166092139266846
RIM 0.042	egl-27	0	0.0223251703186517
RIM 0.042	ekl-4	0.0079747116564217	NA
RIM 0.042	F22D6.2	0.074786290400474	0
RIM 0.042	fkh-8	NA	0.00348147209013652
RIM 0.042	hif-1	0.0207641182691963	0.0267639334676889
RIM 0.042	hinf-1	NA	0.080221560905602
RIM 0.042	hsf-1	0.0213605627042371	0.0281802471906363
RIM 0.042	K09A11.1	NA	0.0407868277152677
RIM 0.042	lag-1	0.0171287686841684	0.0969229368355323
RIM 0.042	lim-7	0.0331025777303695	0.0255228410445491
RIM 0.042	lin-11	0.254519360945329	0.254084861485927
RIM 0.042	lin-14	0.0597055430426007	0.0483088512319905

RIM 0.042	lin-26	0.0691769186067982	0.0624752977688519
RIM 0.042	lin-40	0.0873168154015525	0.0476796725219739
RIM 0.042	lsy-2	0.0125849813416724	0.0188991826247487
RIM 0.042	madf-3	0.0475045437820069	NA
RIM 0.042	madf-5	0.0650174756142658	NA
RIM 0.042	madf-9	NA	0.0358306434705314
RIM 0.042	mbf-1	0.0117628332021579	0.0369390068322039
RIM 0.042	mdt-29	0.0234263721176646	0.0262081839171055
RIM 0.042	mef-2	0.109121861083261	0.0766119016575383
RIM 0.042	nfya-2	0.0448163928801405	0.0530157136363938
RIM 0.042	nhr-11	0.0410129437639245	0.0259473226906617
RIM 0.042	nhr-129	0.00395685884809441	NA
RIM 0.042	nhr-71	0.00315541975937762	0
RIM 0.042	pat-9	0.180487402139582	NA
RIM 0.042	sea-2	0.00269835179591705	0
RIM 0.042	syd-9	0.00861128368073641	0
RIM 0.042	unc-42	NA	0.0406620481045006
RIM 0.042	unc-86	NA	0.0806114615120887
RIM 0.042	Y53G8AR.9	0.0311579506066767	0.0274419524656828
RIM 0.042	Y55F3AM.14	NA	0.0324266473460095
RIM 0.042	Y56A3A.18	0.0414702610412673	0.0557951104066045
RIM 0.042	zfh-2	0.043052771252273	0.0437393204328868
RIM 0.042	ZK546.5	0.0278028434902757	0.000766625638814657
RIM 0.042	ztf-26	NA	0.00557093411559843
RIM 0.042	ztf-4	0	0.0062363999585863
RIR 0.046	aha-1	0.239877375812449	0.283471799684932
RIR 0.046	attf-6	0.00376412310150025	0.00569351895138826
RIR 0.046	C34B4.2	0.0108926356128226	NA
RIR 0.046	ceh-27	0.0320448842117716	0.0525115028387048
RIR 0.046	ceh-40	0.121526227796687	NA
RIR 0.046	crh-2	0.046870933598282	0.0603599145093587
RIR 0.046	ctbp-1	0.142580248331429	0.148421077547273
RIR 0.046	daf-19	0.121351861484957	0.132914217110445
RIR 0.046	egl-13	0.0700527124195358	0.0919648490773202
RIR 0.046	egl-18	0.0896287279496932	0.107254089564391
RIR 0.046	egl-27	0.00746907310836481	0.0162905940945023
RIR 0.046	ekl-4	0.0713238204286386	0.0622775747516009
RIR 0.046	elt-4	0.0211467349681376	NA
RIR 0.046	eor-1	0	0.00496555281456256
RIR 0.046	F22D6.2	0.00861993065510119	0
RIR 0.046	F57A8.1	0.0610910701979184	0.212119784240046
RIR 0.046	hif-1	0.026096883962412	0.0546326318835908
RIR 0.046	hinf-1	0.124370969508409	0.116189743021773

RIR 0.046	hmg-1.1	0	0.0173325643602322
RIR 0.046	hsf-1	0.0102855384004833	0.00381789133214933
RIR 0.046	isw-1	0	0.0195666924286893
RIR 0.046	lag-1	0.0416902085234725	0.0697706860032124
RIR 0.046	lim-7	0.0356849187809845	0.0323546287623357
RIR 0.046	lin-11	0.231284111452341	NA
RIR 0.046	lin-14	0.024689967136708	0.0247545062820022
RIR 0.046	lin-26	0.101154995083728	0.103990257423858
RIR 0.046	lin-40	0.0375094441209499	0.0079847166316465
RIR 0.046	lsy-2	0.0248134020529669	0.0225057531152074
RIR 0.046	madf-3	NA	0.0788879872939809
RIR 0.046	madf-5	0.071803398338143	NA
RIR 0.046	mdt-29	0.0298142391806008	0.0486828444162449
RIR 0.046	nfyb-1	0.00230203655656402	0.0068731578082337
RIR 0.046	nhr-11	0.0265562465947819	0.0492126766987598
RIR 0.046	nhr-47	0	0.0149134459891527
RIR 0.046	nhr-6	0.00440644994204245	NA
RIR 0.046	pat-9	0.167267014767129	NA
RIR 0.046	R02D3.7	0	0.00183423917439462
RIR 0.046	row-1	0	0.0207792839690705
RIR 0.046	saeg-2	NA	0.0120743083636634
RIR 0.046	sem-4	NA	0.0273898691583491
RIR 0.046	sox-4	0.063480845696607	NA
RIR 0.046	sptf-2	0.367413651637739	NA
RIR 0.046	sup-37	0	0.0111242042691949
RIR 0.046	T26A5.8	0	0.000241253471057155
RIR 0.046	unc-120	0	0.00525737030218874
RIR 0.046	unc-55	0.00480331630113804	NA
RIR 0.046	unc-86	0.127023814864729	0.152825414178193
RIR 0.046	Y53G8AR.9	0.0143689709740144	NA
RIR 0.046	Y56A3A.18	0.031055249397092	0.0420103584474668
RIR 0.046	zfh-2	0.0421432730617998	0.0331487632607329
RIR 0.046	zim-3	0.00504572340834832	0.00369243514868765
RIR 0.046	ZK546.5	NA	0.0842827909077439
RIR 0.046	ztf-26	0.0574855399116418	NA
RIS 0.039	aha-1	0.200390723914397	0.210768590047927
RIS 0.039	alr-1	0.122468647951333	0.112117044515812
RIS 0.039	atf-7	0.00105853375675305	0
RIS 0.039	attf-6	0.0051569998879538	0.00349977114919297
RIS 0.039	C34B4.2	0.0943912960196196	0.000256007114568899
RIS 0.039	ceh-18	NA	9.48662906717058e-05
RIS 0.039	chd-7	0.0132916635027837	0.0258652696002536
RIS 0.039	crh-2	0.059112488096786	0.0488257922641975

RIS 0.039	ctbp-1	0.182899602411877	NA
RIS 0.039	D1046.2	0.00516238262764536	NA
RIS 0.039	daf-19	0.092279352743671	0.104669823969292
RIS 0.039	egl-13	0.119843296575266	0.128657428251311
RIS 0.039	egl-18	0.0910660284839749	0.0969669676885518
RIS 0.039	egl-27	0.0401079672686	0.0628025920368376
RIS 0.039	egrh-3	NA	0.0173838159833963
RIS 0.039	ekl-4	0.0253274263387306	0.03140889618832
RIS 0.039	ets-5	NA	0.04972301018527
RIS 0.039	F22D6.2	0.0790973541251634	0
RIS 0.039	F57A8.1	0.0936393448388502	0.0804030447207148
RIS 0.039	hif-1	0.0274144638129637	0.034127446842182
RIS 0.039	hinf-1	0.0800610357189582	0.0733355697456762
RIS 0.039	hsf-1	0.0142576044184887	0.00253106972104986
RIS 0.039	isw-1	0.0245857144672646	0.0672442767034946
RIS 0.039	lag-1	0.0587184023737039	0.0608012426258534
RIS 0.039	lim-6	0.122017478198904	0.0985437424709052
RIS 0.039	lim-7	0.0220622968262709	0.0184137873674087
RIS 0.039	lin-11	0.246954138385831	NA
RIS 0.039	lin-13	0.0018245119815084	0
RIS 0.039	lin-14	0.0298650229362161	0.036129055964546
RIS 0.039	lin-26	0.0854236133526791	0.05986207061919
RIS 0.039	lin-39	0.0139963528049788	NA
RIS 0.039	lin-40	0.0823707194706187	0.00897273473275702
RIS 0.039	lsy-2	NA	0.0223054947046029
RIS 0.039	madf-3	NA	0.0604870505376005
RIS 0.039	mbf-1	0.0339490398611154	0
RIS 0.039	mdt-29	0.063800688468929	0.0394578045392061
RIS 0.039	mef-2	0	0.00985167059013114
RIS 0.039	nfyb-1	0.0233483359803957	0.0238675482244017
RIS 0.039	nhr-11	0.0322206631444025	NA
RIS 0.039	nhr-129	0.00643129179133595	0.00982638732309819
RIS 0.039	nhr-6	0.000942406995114646	0.00374555085558096
RIS 0.039	R02D3.7	0.00322620949367453	NA
RIS 0.039	rbr-2	0	0.0319787605192253
RIS 0.039	row-1	0.0467978550508224	NA
RIS 0.039	sem-4	0.0257195513560332	0.0212935130417266
RIS 0.039	sup-37	0	0.0676137887153059
RIS 0.039	T26A5.8	0	0.0218306441662389
RIS 0.039	unc-86	NA	0.107709742169534
RIS 0.039	Y53G8AR.9	0.00287586830928825	0
RIS 0.039	Y56A3A.18	0.0386549210126821	0.0277332220302415
RIS 0.039	zag-1	0.0304331817635485	0.100315064606675

RIS 0.039	zim-3	0.0453861187436186	0.0484397173322405
RIS 0.039	ZK546.5	0	0.0625422408027435
RIS 0.039	ztf-1	0.0454073939844997	0.00360094730847828
RIS 0.039	ztf-26	NA	0.0363592933719191
RIV 0.050	aha-1	0.0313677063785503	0.0501082058098758
RIV 0.050	alr-1	0.12131379490176	NA
RIV 0.050	atf-7	0.012668578051865	0.0145979317675959
RIV 0.050	attf-6	0	0.00428076989249431
RIV 0.050	C34B4.2	0.654315043499848	0.553250699655011
RIV 0.050	ceh-32	0.129608010067106	0.261670166923312
RIV 0.050	crh-2	0.0421741345115924	0.0496259747509267
RIV 0.050	ctbp-1	0.201016558191357	0.232370794185084
RIV 0.050	daf-19	0.0946303338381136	0.107355202729915
RIV 0.050	egl-13	0.0269150931301862	0.0539520649067519
RIV 0.050	egl-18	0.040559643919628	NA
RIV 0.050	egl-27	0.00301075667885959	0.0259742858991359
RIV 0.050	ekl-4	0.0165095071588936	0.0218569827515281
RIV 0.050	elt-4	0.0150038974118382	NA
RIV 0.050	fkh-10	0.123241537367255	NA
RIV 0.050	hif-1	0.000464741415510604	0
RIV 0.050	hinf-1	0.0945601401805526	0.103870691916798
RIV 0.050	hsf-1	0.0296628388242822	0.0228117445477772
RIV 0.050	K12H6.12	0.0179831131518788	0
RIV 0.050	lag-1	0	0.0361919353411347
RIV 0.050	lim-7	0.0180653887565939	0.0321166529882053
RIV 0.050	lin-11	NA	0.141888932294846
RIV 0.050	lin-14	NA	0.0470034590702811
RIV 0.050	lin-26	0.076809187523484	0.0655690591162299
RIV 0.050	lin-40	0.10230925392886	0.0503724935420682
RIV 0.050	lsy-2	0.00562883104162096	0.00493276791789016
RIV 0.050	madf-3	NA	0.0455065121114328
RIV 0.050	madf-5	0.0778680229994138	0.0540000029974892
RIV 0.050	mdt-29	0.0117028205550335	0.0162287426520665
RIV 0.050	mef-2	0.065279503445343	0.0871078648916093
RIV 0.050	nhr-11	0.0146805960690402	NA
RIV 0.050	nhr-71	0.000140674564482248	NA
RIV 0.050	pag-3	0.0446164702530076	NA
RIV 0.050	pat-9	0.16822640634602	NA
RIV 0.050	sem-4	0.00609852036886867	0.0172659220231483
RIV 0.050	sptf-2	0.255246162262593	0.281879272110501
RIV 0.050	T26A5.8	0.00881028459407685	0
RIV 0.050	tbx-9	NA	0.127077330339956
RIV 0.050	unc-42	0.000396653628634866	0.0271156233601699

RIV 0.050	unc-86	0.0846763413259293	0.091217344472235
RIV 0.050	Y53G8AR.9	0.0152920873396411	0.00423677906710054
RIV 0.050	Y56A3A.18	0.0162465837474983	0.0244412759636269
RIV 0.050	zfh-2	0.0444016451052776	0.0413978953370791
RIV 0.050	ZK546.5	0	0.0390961888429208
RIV 0.050	ztf-26	NA	0.00971467914499035
RMD_DV 0.040	aha-1	0.360441874063673	0.422155366294933
RMD_DV 0.040	alr-1	0.138469759812882	0.126664678761692
RMD_DV 0.040	C34B4.2	0.207852010054497	0
RMD_DV 0.040	cebp-1	0	0.00406041364663252
RMD_DV 0.040	ceh-18	0	0.000733479854964369
RMD_DV 0.040	ceh-32	1.52451363655257	1.37940404458088
RMD_DV 0.040	ceh-88	0	0.0151032158886071
RMD_DV 0.040	crh-2	0.0399865106212607	0.0427765700738794
RMD_DV 0.040	ctbp-1	0.222805631531232	0.185763067550724
RMD_DV 0.040	daf-19	0.0445123324944939	0.0419241446367325
RMD_DV 0.040	drap-1	0.023765476625003	0.0532446718653592
RMD_DV 0.040	egl-18	0.0436644084749915	0.024690862898491
RMD_DV 0.040	egl-27	0.000536039442035669	0
RMD_DV 0.040	ekl-4	0.0265377491746432	0.0321927471977451
RMD_DV 0.040	ets-5	0.00203744319018907	NA
RMD_DV 0.040	F22D6.2	0.122508759809149	0.122222532629144
RMD_DV 0.040	fkh-10	NA	0.134190418338566
RMD_DV 0.040	hif-1	0.0194750992373962	0.0292598574908747
RMD_DV 0.040	hinf-1	0.0999812598606092	0.106243110775528
RMD_DV 0.040	hmg-1.1	0.00414859645735864	0.0101334572886906
RMD_DV 0.040	hmg-11	0	0.00221344464807517
RMD_DV 0.040	hsf-1	0.0042528200526272	0.00173498404616258
RMD_DV 0.040	lag-1	0.0622844326536426	0.101057017339567
RMD_DV 0.040	lim-7	0.0153034953742901	0.0221549951207629
RMD_DV 0.040	lin-11	0.21623323687301	NA
RMD_DV 0.040	lin-14	0.0721395704372402	0.0615167253463709
RMD_DV 0.040	lin-26	0.075854141021921	0.0670464177016823
RMD_DV 0.040	lin-39	0.00249997908119636	NA
RMD_DV 0.040	lin-40	0.0558917097895219	0.0175727394711602
RMD_DV 0.040	lsy-2	0.0205795847134504	0.0232456942515656
RMD_DV 0.040	madf-3	0.0540500641299514	0.0630719803970621
RMD_DV 0.040	madf-5	0.0566904562588145	0.0295475359203024
RMD_DV 0.040	madf-9	0.0163886191544461	0.0100065384859058
RMD_DV 0.040	mbf-1	0.20187248445471	0.186674554111465
RMD_DV 0.040	mdt-29	0.0283490318083486	0.0397467503326139
RMD_DV 0.040	nfya-1	0.00623331363269479	0.0115073057038424
RMD_DV 0.040	nfya-2	0.0253582348923536	0.0277600229146605

RMD_DV 0.040	nfyb-1	0	0.00255292333708174
RMD_DV 0.040	pat-9	0.164374309670542	NA
RMD_DV 0.040	R02D3.7	0.011355785770473	0.0123713096494614
RMD_DV 0.040	row-1	0	0.0217775052744583
RMD_DV 0.040	sea-2	0.012586927254953	0
RMD_DV 0.040	sem-4	0	0.00231728590819579
RMD_DV 0.040	sox-4	0.00222233487476685	NA
RMD_DV 0.040	sptf-2	0.230723900739487	0.23704794284131
RMD_DV 0.040	syd-9	0	0.0112117600318936
RMD_DV 0.040	T26A5.8	0.0243129075525772	0.0226755832168126
RMD_DV 0.040	unc-42	0.0890175529733175	0.0637634069994174
RMD_DV 0.040	unc-55	0.00610541981003567	0.0166454566498576
RMD_DV 0.040	Y53G8AR.9	0.0119943638811395	0.0115158123526231
RMD_DV 0.040	Y56A3A.18	0.0350216116531816	0.045143268645636
RMD_DV 0.040	zag-1	0.0772107932300667	0.0786226605086163
RMD_DV 0.040	zfh-2	0.0551451780826163	0.0499563151415971
RMD_DV 0.040	zim-3	0.00605969993914452	0
RMD_DV 0.040	ZK546.5	0.0825722414082744	0.120652189956019
RMD_DV 0.040	ztf-26	0.0824963850966032	0.0464059598127024
RME 0.047	aha-1	0.250975196802105	0.293311688696604
RME 0.047	alr-1	0.172429145179526	0.144289844990117
RME 0.047	arid-1	0.013659203551576	NA
RME 0.047	atf-7	0.0353784400712243	0.0259708026923042
RME 0.047	attf-6	0.0387173606590222	0.0225229047929644
RME 0.047	cebp-1	NA	0.00917509883635025
RME 0.047	ceh-18	0.0281744096111873	0.0711986937102029
RME 0.047	ceh-27	0.174801600668994	0.212280450446148
RME 0.047	ceh-32	0.407627977887476	0.574539540766873
RME 0.047	ceh-88	0.0214068753222654	0
RME 0.047	chd-7	0.0354471546965584	0.0299669492543007
RME 0.047	crh-2	0.0603837859370026	0.0618039322372027
RME 0.047	ctbp-1	NA	0.152069075135345
RME 0.047	daf-19	0.0820161468628788	0.099552224792672
RME 0.047	egl-18	NA	0.0848134396280781
RME 0.047	ekl-4	NA	0.0521524987127765
RME 0.047	F22D6.2	0.0970032768963892	0
RME 0.047	F57A8.1	0.0721649708801353	0.0274573933572675
RME 0.047	fkh-10	0.099205435742477	0.112940848893173
RME 0.047	fkh-8	NA	0.0103105552848741
RME 0.047	hif-1	0.00251737959508705	0.0110661752434288
RME 0.047	hinf-1	0.139675321225813	0.115805013273512
RME 0.047	hsf-1	NA	0.0172872170687241
RME 0.047	lag-1	0.042475205373493	NA

RME 0.047	lim-7	0.040926711785734	0.0407604679519792
RME 0.047	lin-11	0.176224575072069	NA
RME 0.047	lin-14	0.0479883918884334	NA
RME 0.047	lin-26	0.0827233685425764	0.0772450085832952
RME 0.047	lin-40	0.0732762279133326	0.0974344820122329
RME 0.047	lin-54	0.00385127270025182	0
RME 0.047	lsy-2	0.0327046866946561	NA
RME 0.047	madf-9	0.0627844571281631	0.0284489461842333
RME 0.047	mbf-1	0.221536106484185	0.106723486228997
RME 0.047	mdt-29	0.0749411167011046	0.0678060465519966
RME 0.047	mef-2	0.0161496558127861	0.0812587003686512
RME 0.047	nfya-1	NA	0.0264406775624704
RME 0.047	nfya-2	0.0339089296941985	0.0572242479451786
RME 0.047	nfyb-1	0.0303004156463332	0.022686861314956
RME 0.047	nhr-11	0.0367967415193654	NA
RME 0.047	pax-3	0.00721586795167774	NA
RME 0.047	pbrm-1	0.03457767990559	0.022580373287907
RME 0.047	R02D3.7	0.00846297562273471	NA
RME 0.047	sptf-2	NA	0.263720129995166
RME 0.047	T26A5.8	0.0498246277805064	0.0540975130322664
RME 0.047	unc-120	0.000445743532925536	NA
RME 0.047	unc-62	0.00747726263590569	0
RME 0.047	unc-86	0.025283924085403	NA
RME 0.047	Y56A3A.18	0.0741609858003061	NA
RME 0.047	zag-1	0.168652096031176	0.232159072785933
RME 0.047	zfh-2	0.0646764800729075	NA
RME 0.047	zim-3	0.0841598888693406	NA
RME 0.047	ZK546.5	0.105310471066262	0.14499299330434
RME 0.047	ztf-1	0.281149809161534	NA
RME 0.047	ztf-26	0.0770502368286921	NA
RMF 0.043	aha-1	0.228774877462213	0.233827131476708
RMF 0.043	alr-1	0.195733423389599	NA
RMF 0.043	attf-6	0.00659952797056162	0.0214748958515115
RMF 0.043	ceh-27	0.0978653198008279	0.115760209727823
RMF 0.043	ceh-48	0	0.00264464407990379
RMF 0.043	crh-2	0.0556758619980044	0.0464856050912449
RMF 0.043	ctbp-1	0.216261921410214	0.229728211729508
RMF 0.043	daf-19	NA	0.107894589971124
RMF 0.043	egl-18	NA	0.09790444450191
RMF 0.043	egl-27	0.0231349755261127	0.0277528202844731
RMF 0.043	ekl-4	0.0709696905898882	0.0874845238529337
RMF 0.043	elt-4	0.017220515015758	0.0112701977605788
RMF 0.043	ets-5	NA	0.0265332372731878

RMF 0.043	F22D6.2	0.061530396630541	0.0367875382409581
RMF 0.043	F57A8.1	0.052824801070251	0
RMF 0.043	fkh-8	0.00751493921634796	NA
RMF 0.043	hif-1	0.0122021314249509	0.0293399470870018
RMF 0.043	hinf-1	0.107062749068913	NA
RMF 0.043	hmg-1.1	0	0.000920431610375516
RMF 0.043	hsf-1	0.0278161691105393	NA
RMF 0.043	isw-1	0.0419608485211551	0.0367214002946678
RMF 0.043	K09A11.1	0	0.0059731994970607
RMF 0.043	lag-1	0.0777670438254559	0.111281711110346
RMF 0.043	lin-14	0.0607619953821086	NA
RMF 0.043	lin-26	0.106894073309449	0.0924398187295824
RMF 0.043	lin-40	0.0837474289133984	0.0708440918725875
RMF 0.043	lin-54	0.0002081034798916	0.0251998028451938
RMF 0.043	lsy-2	0.0231128874289915	0.0268359266189245
RMF 0.043	madf-5	0.0890265088238902	NA
RMF 0.043	mbf-1	0.0628973537608677	0.0458090692993032
RMF 0.043	mdt-29	0.0529769949709379	0.0452333659166172
RMF 0.043	nfya-2	0.0301641159678365	NA
RMF 0.043	nhr-11	0.00495707559462036	NA
RMF 0.043	nhr-71	0	0.017835833642832
RMF 0.043	pbrm-1	0.0171204240594445	0.0178439767967475
RMF 0.043	R02D3.7	0.00690628159372276	0
RMF 0.043	rcor-1	0	0.0265614204643771
RMF 0.043	row-1	0.0718067003592387	0.0432716825268272
RMF 0.043	sea-2	0.0441825920640856	0.0537696384335611
RMF 0.043	somi-1	0	0.00330018102444166
RMF 0.043	unc-120	0	0.0126231093814209
RMF 0.043	unc-30	0.295812626437118	NA
RMF 0.043	unc-42	0.080349366390497	0.105120917888259
RMF 0.043	unc-55	0.0175905709055761	0.0382646095775374
RMF 0.043	Y53G8AR.9	0.0141442584271831	0.0367457588127369
RMF 0.043	Y56A3A.18	0.0691918667812083	0.066217655784446
RMF 0.043	zag-1	0.0215541409344835	0.0564293217662468
RMF 0.043	zfh-2	0.0459013182354764	0.0481055757527092
RMF 0.043	zim-3	0.0105475217307174	NA
RMF 0.043	ZK546.5	0	0.0886779346411049
RMF 0.043	ztf-4	0	0.00161497622672433
RMG 0.039	aha-1	0.089478789081224	0.0822854927561533
RMG 0.039	alr-1	0.184420258058298	NA
RMG 0.039	attf-6	0.0128651306793117	0.0125727577197449
RMG 0.039	ceh-27	0.0402820865932387	0.0498279820573181
RMG 0.039	chd-7	0	0.00298178564753252

RMG 0.039	crh-2	0.0372545024818819	0.0376509775607714
RMG 0.039	ctbp-1	NA	0.0969370047713895
RMG 0.039	D1046.2	0.0408428484731074	0.0243572357860902
RMG 0.039	daf-19	0.0717789868102406	0.0910952096312173
RMG 0.039	egl-13	0.0167690530045514	0.0293582504973666
RMG 0.039	egl-18	0.0907005307062891	0.0211787574554694
RMG 0.039	egl-27	0.00653740323811921	0.014832648585163
RMG 0.039	egrh-3	NA	0.00727191002322376
RMG 0.039	ekl-4	0.0545805715507764	0.0529281808229727
RMG 0.039	elt-4	NA	0.207349092512232
RMG 0.039	ets-5	0.00206862434515949	0.0126213010124642
RMG 0.039	F22D6.2	0.128676508475009	0
RMG 0.039	fkh-10	0.0166953290290244	NA
RMG 0.039	hif-1	0.0133440100815376	0.0198012095624256
RMG 0.039	hinf-1	0.12297121758611	0.114899574636301
RMG 0.039	hsf-1	0.0070850935156557	0
RMG 0.039	isw-1	0.0269040824940909	0.0360487083232131
RMG 0.039	lag-1	0.025018386210614	0.053390231677638
RMG 0.039	lim-7	0.0298447116548148	0.0294387764800507
RMG 0.039	lin-11	0.183292680196008	NA
RMG 0.039	lin-13	0	0.003119224848172
RMG 0.039	lin-14	0.00455088509212013	0
RMG 0.039	lin-26	0.094258983818529	0.0766284212920891
RMG 0.039	lin-39	0	0.00697509092635942
RMG 0.039	lin-40	0.105170461591663	0.0199511463317127
RMG 0.039	lsy-2	0.0180848027137785	0.0154737668640956
RMG 0.039	madf-3	0.0464303622313549	0.0523791738632799
RMG 0.039	madf-9	0.0458090651066147	0
RMG 0.039	mdt-29	0.022329607058918	0.00624821696535921
RMG 0.039	nhr-11	0.0193969257170372	NA
RMG 0.039	nhr-129	NA	0.00675809698356743
RMG 0.039	pag-3	0.0446201173791612	0.0303312594398116
RMG 0.039	pat-9	0.182593993594798	0.123491794152679
RMG 0.039	pbrm-1	0.00721480235189124	0
RMG 0.039	R02D3.7	0.0231772083067985	0.00108153868998396
RMG 0.039	row-1	0	0.0362938514597597
RMG 0.039	saeg-2	NA	0.03356598108402
RMG 0.039	sea-2	0	0.0124816603694182
RMG 0.039	sem-4	0.0354606596079113	0.0286456072218876
RMG 0.039	T26A5.8	0.0239099186594339	NA
RMG 0.039	unc-86	0.0571520506256373	0.0784688786773525
RMG 0.039	Y53G8AR.9	0.00674259755223557	0.00721832338750206
RMG 0.039	Y56A3A.18	0.0439954547441523	0.0386021436604468

RMG 0.039	zag-1	0.0444395027538769	0.0600431851203911
RMG 0.039	zfh-2	0.0577200090576169	NA
RMG 0.039	zim-3	0.018519905274438	0
RMG 0.039	ZK546.5	0.000941210539144731	0
RMH 0.036	aha-1	0.157973502316851	0.155737871416573
RMH 0.036	alr-1	0.168753415802414	0.163175314515268
RMH 0.036	attf-6	0.0135170685354686	0.0164595535519718
RMH 0.036	ceh-18	0	0.00384917018374729
RMH 0.036	ceh-27	0.054597495820104	0.0513874880427618
RMH 0.036	ceh-32	0.0389019980223329	0.130927999221254
RMH 0.036	crh-2	0.05152135161835	0.0500352382382901
RMH 0.036	ctbp-1	0.119633412338792	0.11743433788813
RMH 0.036	daf-19	0.0871355431520366	0.0850575476925539
RMH 0.036	egl-18	0.0812998491384278	0.0860927560825825
RMH 0.036	egl-27	0.027241473653871	0.0218567088181985
RMH 0.036	ekl-4	0.0519556288244233	0.0525268504831437
RMH 0.036	elt-4	0.0465683832438963	0.00781237861489506
RMH 0.036	ets-5	0.02155595900008	NA
RMH 0.036	F22D6.2	0.0877784490347835	0.0380600859135148
RMH 0.036	fkh-10	0.0781852021937981	0.0875050228476642
RMH 0.036	hif-1	0.0242079123833087	0.0263933940025914
RMH 0.036	hinf-1	0.0864209349083266	0.09207509589723
RMH 0.036	hlh-1	0	0.00185606506941377
RMH 0.036	hlh-8	0.038066883243626	NA
RMH 0.036	hsf-1	0.00699707548166677	0.00991660736425363
RMH 0.036	lag-1	0.0570106792921354	0.0861386018593661
RMH 0.036	lim-7	0.0155004382054252	0.021203197488133
RMH 0.036	lin-11	0.163089651321025	0.17292772524691
RMH 0.036	lin-14	0.0313637410396745	0.0325231306371793
RMH 0.036	lin-26	0.0866986693100536	0.0754237936100045
RMH 0.036	lin-39	0.0138733914064605	0.0192484474279334
RMH 0.036	lin-40	0.0593775481099015	0.0173506849691185
RMH 0.036	lsy-2	0.0217607252963566	0.0199770620054637
RMH 0.036	madf-2	0.0159024506310351	0
RMH 0.036	madf-3	0.0482941069263767	0.0440481468767691
RMH 0.036	madf-5	0.0878649248893381	0.0559713672043037
RMH 0.036	madf-9	NA	0.000159539735815477
RMH 0.036	mdt-29	0.0341460388057209	0.0353959880199498
RMH 0.036	nfya-2	0.00428622588528713	0.0191715811017907
RMH 0.036	nhr-11	0.0196990454052187	NA
RMH 0.036	nhr-6	0.000353940270756963	0.00635792372658378
RMH 0.036	pag-3	0.0550228685851771	NA
RMH 0.036	pbrm-1	0.0190597378695747	0.0146398152444842

RMH 0.036	R02D3.7	0.00122279437826655	0
RMH 0.036	sem-4	0.00992375730899409	0.015275915935713
RMH 0.036	sox-4	0.0784598041841752	0.0950958612645674
RMH 0.036	unc-30	0.340717591710301	0.249209680783049
RMH 0.036	unc-42	0.024213324296794	0.026238868242567
RMH 0.036	unc-55	0.00643112033864104	0.00220067413790539
RMH 0.036	unc-62	0.00351607784646915	0
RMH 0.036	unc-86	0.156494037270797	0.162507205500171
RMH 0.036	Y53G8AR.9	0.0195060848755279	0.0110899454516785
RMH 0.036	Y56A3A.18	0.0393914892094467	0.0415590538837145
RMH 0.036	zfh-2	0.0388614005047807	0.0354160254445929
RMH 0.036	zim-3	0.0419923034300592	0.0238174308349748
RMH 0.036	ZK546.5	0.0145193036627516	0.0811252676400278
RMH 0.036	ztf-1	0.000265830027022237	0
RMH 0.036	ztf-26	0.0953198998110326	0.0610733354290389
Rectal gland 0.040	akir-1	0	0.0543928368620165
Rectal gland 0.040	alr-1	0.23126666799516	0.250105028099958
Rectal gland 0.040	attf-6	0	0.00797463743270536
Rectal gland 0.040	bcl-11	0.0298754516076962	0.0335374038437664
Rectal gland 0.040	cebp-1	0	2.35499209196324e-05
Rectal gland 0.040	ceh-18	0	0.0266261028651995
Rectal gland 0.040	cey-2	0.00580450932926824	0
Rectal gland 0.040	crh-2	0	0.0187806325390515
Rectal gland 0.040	daf-19	0.0654601377296969	0.0829776123088479
Rectal gland 0.040	dxbp-1	0	0.0124287785915567
Rectal gland 0.040	ekl-4	0.0691577642635494	0.104250204636828
Rectal gland 0.040	F22D6.2	0.0182850338637091	0
Rectal gland 0.040	F23B12.7	0.010549702992208	0.035341799929487
Rectal gland 0.040	F33H1.4	0.0218525273558873	0.0276342995842426
Rectal gland 0.040	F44E2.7	0	0.00997683924138743
Rectal gland 0.040	fos-1	0	0.00518613725518505
Rectal gland 0.040	hinf-1	0.119538730483577	0.117512905491333
Rectal gland 0.040	hlh-8	NA	0.0737628839600718
Rectal gland 0.040	hsf-1	0.00973360368759723	NA
Rectal gland 0.040	jun-1	0	0.00722275249684614
Rectal gland 0.040	lag-1	0	0.0341421468932721
Rectal gland 0.040	let-607	0.0249540167652462	0.0331806032236286
Rectal gland 0.040	lim-7	0.0167229843419557	0.0329556866403028
Rectal gland 0.040	lin-26	0.100421177040214	0.0743732185928715
Rectal gland 0.040	lin-40	0.0895881396954178	0.00281063958499698
Rectal gland 0.040	lin-54	0.000753361826547227	NA
Rectal gland 0.040	lsy-2	0.00121705207455993	0.00853031898220179
Rectal gland 0.040	madf-3	0.0742456651199491	0.0842317184416341

Rectal gland 0.040	madf-5	0.162738283121303	0.110906922510951
Rectal gland 0.040	madf-6	0.0107573538082947	0.0212781552802151
Rectal gland 0.040	madf-9	0.0192284952805487	0
Rectal gland 0.040	mdt-29	0.0195706741008733	0.039507889353123
Rectal gland 0.040	mml-1	0	0.0117817718380831
Rectal gland 0.040	nfyb-1	0.00150419027118025	0.00403636486601865
Rectal gland 0.040	nhr-11	NA	0.0324793943366882
Rectal gland 0.040	nhr-129	0.00531339586031959	0.0054567143406726
Rectal gland 0.040	nhr-232	0.108314213554068	0.0596248704427965
Rectal gland 0.040	nhr-237	NA	0.00183391967890334
Rectal gland 0.040	pag-3	0.0445629715882123	NA
Rectal gland 0.040	pbrm-1	0	0.00524364216447153
Rectal gland 0.040	pha-4	0.0618163359753145	0.0504993588547871
Rectal gland 0.040	R02D3.7	0.00170665211996964	0.00234360899362946
Rectal gland 0.040	skn-1	0.0301949942569601	0.0292336647280695
Rectal gland 0.040	spr-3	0.0654613144170954	NA
Rectal gland 0.040	sup-37	0	0.116292162383746
Rectal gland 0.040	T20F7.1	0.00121311962232046	0
Rectal gland 0.040	T26A5.8	0.0458579711552423	0.0278871173416321
Rectal gland 0.040	unc-120	0	0.00345196143833861
Rectal gland 0.040	unc-62	0.0281607232743261	0.0251008654427011
Rectal gland 0.040	Y53G8AR.9	0.00921577148674259	0.0194389817187049
Rectal gland 0.040	Y56A3A.18	0.0321064582028922	0.0539246418833097
Rectal gland 0.040	zfh-2	0.0377825327968057	0.0422265021752969
Rectal gland 0.040	zim-3	0.0192671561355925	0.017959812139983
Rectal gland 0.040	ZK185.1	NA	0.0645216589451592
Rectal gland 0.040	ztf-1	0.259007324474161	NA
Rectal gland 0.040	ztf-26	0.105632664963755	0.0279706117615064
SDQ 0.047	aha-1	0.0864025169095427	0.105687538639761
SDQ 0.047	alr-1	NA	0.146732555188092
SDQ 0.047	atf-7	0.00943863131645584	0.00496955843709936
SDQ 0.047	C34B4.2	0.361352941886045	0
SDQ 0.047	crh-2	0.0343027311871885	0.0361160178905104
SDQ 0.047	ctbp-1	0.142837007628655	0.137472276499307
SDQ 0.047	egl-13	0.0852947757385873	NA
SDQ 0.047	egl-18	NA	0.0133671777085334
SDQ 0.047	egl-27	0	0.0028670355725116
SDQ 0.047	egrh-3	0.0104981311405984	0
SDQ 0.047	ekl-4	0.047357430367599	0.0637451430359867
SDQ 0.047	elt-4	0.0460122241510692	NA
SDQ 0.047	fkh-8	NA	0.0301480173194917
SDQ 0.047	hif-1	0.00496653145374495	0.00492390720397561
SDQ 0.047	hinf-1	0.102221396282915	0.126898534458256

SDQ 0.047	hmg-1.1	0.000799614375681118	0.00131583129611192
SDQ 0.047	hsf-1	0.00787639302492456	0.0100604009771285
SDQ 0.047	isw-1	0.0766886542679495	0.0636119167186808
SDQ 0.047	lag-1	0.0202799987892813	0.0587561363844193
SDQ 0.047	lim-7	0.0175594309230843	0.0183722464288501
SDQ 0.047	lin-14	0.0183752597883868	0.0176662792367686
SDQ 0.047	lin-26	0.089685799375389	0.0695849947552155
SDQ 0.047	lin-39	0.0217143072012078	0.0240234681749238
SDQ 0.047	lin-40	0.0724902345990241	0
SDQ 0.047	madf-5	0.111697246897118	0.025595319991504
SDQ 0.047	mdt-29	0.0475266901874111	0.0489214068083698
SDQ 0.047	mef-2	0.0542899092547385	0.0597233849192041
SDQ 0.047	nfyb-1	0.00247724722527442	0.00119928270396342
SDQ 0.047	nhr-11	0.0343076773782705	0.0176148028952865
SDQ 0.047	nhr-232	NA	0.0514754511853047
SDQ 0.047	nhr-6	0.000279385608254858	0.006612707477468
SDQ 0.047	row-1	NA	0.0719075048769559
SDQ 0.047	sem-4	0.0237219029027148	0.0372586936348995
SDQ 0.047	sptf-2	0.366107056168263	0.351304593786363
SDQ 0.047	Y53G8AR.9	0.016990685698907	0.00655596320910918
SDQ 0.047	Y56A3A.18	0.0257022646866567	0.018858887816434
SDQ 0.047	zag-1	0.123444721336131	0.120536506850107
SDQ 0.047	zfh-2	NA	0.0432373856046509
SDQ 0.047	ZK546.5	0	0.00384393494063782
SDQ 0.047	ztf-1	0.0385847305604457	0
SDQ 0.047	ztf-26	0.105893523918269	0.0404410858425193
SIA 0.047	aha-1	0.115437789351837	0.123900215485632
SIA 0.047	alr-1	0.111870267028632	NA
SIA 0.047	atf-7	0.0124124276046761	0.00756733454272158
SIA 0.047	attf-6	0.00289954926302162	0.00493131885675089
SIA 0.047	C34B4.2	0.709187099243747	0.4072309539972
SIA 0.047	cebp-1	0.0273624284953157	0.0287935214761432
SIA 0.047	ceh-20	0.0133347960091716	0.0161918096979548
SIA 0.047	ceh-32	0.0512677526469506	0.125125445310542
SIA 0.047	ceh-9	0.608013882584791	0.704572562439176
SIA 0.047	crh-2	0.0273009712319194	0.0269833817802984
SIA 0.047	ctbp-1	0.188480436308296	0.173361478881755
SIA 0.047	D1046.2	0.00303536444358739	0.00734176915769373
SIA 0.047	daf-19	0.0608944140644483	0.0699734044324302
SIA 0.047	drap-1	0	0.0203616249227468
SIA 0.047	dsc-1	NA	0.010748254908079
SIA 0.047	egl-13	0.0193606842533885	0.00997795482315884
SIA 0.047	egl-18	0.0517559532526415	0.0532990632374498

SIA 0.047	ekl-4	0.0243335966561135	0.0367214831395979
SIA 0.047	elt-4	0.080669418281444	NA
SIA 0.047	ets-5	NA	0.0482283395582135
SIA 0.047	F22D6.2	0.0213833877063773	0
SIA 0.047	hif-1	0.0170103286566126	0.0255168073748313
SIA 0.047	hinf-1	0.081390285787312	0.0923236440141278
SIA 0.047	hlh-8	0	6.60386362500061e-05
SIA 0.047	hsf-1	0.0160568239242149	0.0104294130131238
SIA 0.047	isw-1	0.015378629792405	0.0217852129883369
SIA 0.047	K09A11.1	0	0.0018016851203212
SIA 0.047	K12H6.12	0.0638627586921664	0.0630014080181572
SIA 0.047	lag-1	0.0163809931230055	0.0602383087079073
SIA 0.047	lim-7	0.00527465185965896	0.00762932197960572
SIA 0.047	lin-11	0.076707981671708	0.0905266798601968
SIA 0.047	lin-14	0.0772012817533497	0.0714378541213821
SIA 0.047	lin-26	0.0666289643492074	0.0602970373645675
SIA 0.047	lin-39	0.0108639180285938	0.0132509433225826
SIA 0.047	lin-40	0.114408333523769	0.0758310015844411
SIA 0.047	lsy-2	0.0146554012572271	0.0141819844965903
SIA 0.047	mab-5	0.0116088453786483	NA
SIA 0.047	madf-3	0.0452355805988342	0.0505330888281595
SIA 0.047	madf-5	0.0514786018150419	0.0250023385608857
SIA 0.047	mbf-1	0.0421337976383071	0.178801960200894
SIA 0.047	mdt-29	0.0167160392706862	0.0264065983251237
SIA 0.047	mef-2	0.0278914891513752	0.0264425580981184
SIA 0.047	mml-1	0.0764131597201724	0.103412906080167
SIA 0.047	nfyb-1	0.0153801528011729	0.0220138385341025
SIA 0.047	nhr-11	0.0170124137171279	0.0117948822395375
SIA 0.047	pag-3	NA	0.0541802760453494
SIA 0.047	pat-9	0.160294385255837	NA
SIA 0.047	R02D3.7	0.00690918266275057	0.00959265372738742
SIA 0.047	saeg-2	0	0.00781544012731334
SIA 0.047	sem-4	0.127531003993264	0.130554139834355
SIA 0.047	sptf-2	0.260056101650923	0.320658251111192
SIA 0.047	syd-9	0	0.00698076924231902
SIA 0.047	unc-42	0.0638866324998455	0.0720653176637047
SIA 0.047	unc-55	NA	0.00577627410516189
SIA 0.047	unc-62	0.000250910607316557	0.00500981503651235
SIA 0.047	Y53G8AR.9	0.00641969314021217	0.00893720907245634
SIA 0.047	Y56A3A.18	0.018251215058345	0.0296397713635009
SIA 0.047	zag-1	0.102995401299809	0.102881324615835
SIA 0.047	zfh-2	0.0420920451746714	0.044411652617304
SIA 0.047	ZK546.5	0.0635178752416803	0.145981037045427

SIA 0.047	ztf-26	0.0707280908540856	0.0512046366972602
SIB 0.044	aha-1	0.124991285139313	0.138801622007595
SIB 0.044	alr-1	0.133772793580708	0.141648792659113
SIB 0.044	atf-7	0.0185882476622947	0.0200181367994414
SIB 0.044	attf-6	0.00381213963692572	0.000700472231047834
SIB 0.044	C34B4.2	0.324241758594255	0.139808859561363
SIB 0.044	cebp-1	0.0314103982864037	0.0347185615806538
SIB 0.044	ceh-20	0	0.00169079722048232
SIB 0.044	ceh-9	1.27729042770199	1.41184890495061
SIB 0.044	ces-1	0.129609019061598	NA
SIB 0.044	crh-2	0.0328885622911122	0.0302574752893291
SIB 0.044	ctbp-1	0.13216242232767	0.142885042534494
SIB 0.044	daf-19	0.0746532668117617	0.0693634985476722
SIB 0.044	dsc-1	0.00243396353331753	NA
SIB 0.044	egl-13	0.0383257847920944	0.0399026986558383
SIB 0.044	egl-18	0.11005704299697	0.108286471074673
SIB 0.044	ekl-4	0.0325019268899557	0.03951712798639
SIB 0.044	ets-5	0.0245060520458974	0.0186923723031476
SIB 0.044	F22D6.2	0.0159503619936251	0
SIB 0.044	fkh-10	0	0.0234814879771561
SIB 0.044	hif-1	0.0223330816963816	0.0263455270050298
SIB 0.044	hinf-1	0.0996864811403536	0.103346242224234
SIB 0.044	hsf-1	0.0104408368353331	0.00742099786689282
SIB 0.044	isw-1	0.0276130365114572	0.0171801819160769
SIB 0.044	K12H6.12	0.0215924112863767	0.015032024782921
SIB 0.044	lag-1	0.0320017624250302	0.0617221966505794
SIB 0.044	lim-7	0.00344319833482156	0.000347260590180789
SIB 0.044	lin-11	0.117246206114407	0.11783372180605
SIB 0.044	lin-14	0.0706773568490718	0.0783434801491649
SIB 0.044	lin-26	0.0965159180204591	0.0935949665166629
SIB 0.044	lin-39	0.010389188026112	0.00401874833305157
SIB 0.044	lin-40	0.123887165659254	0.108100950017526
SIB 0.044	lsy-2	0.0103410087636062	0.00861656633728305
SIB 0.044	madf-3	0.0480162432085724	0.0533618598258422
SIB 0.044	madf-5	0.0471164312965502	0.0237495804198029
SIB 0.044	mbf-1	0.0514708523225616	0.0625021424237664
SIB 0.044	mdt-29	0.00334349179253981	0.00127825793971233
SIB 0.044	nfya-1	0.0138949542038267	0.0167020370158099
SIB 0.044	nfyb-1	0.0210667498092385	0.021618882600018
SIB 0.044	nhr-11	0.00525533005755098	0
SIB 0.044	pag-3	0.0695933264813832	0.0673411587322916
SIB 0.044	pat-9	0.15193344852629	0.127464346466149
SIB 0.044	R02D3.7	0.00516874890386426	0.00230547530070931

SIB 0.044	sem-4	0.0875832193047477	0.109495711255302
SIB 0.044	somi-1	0	0.00329078953081016
SIB 0.044	sox-4	0	0.000289730111987656
SIB 0.044	sptf-2	0.259413414571174	0.280911713331057
SIB 0.044	sup-37	0.085259394021811	0.0373304045555026
SIB 0.044	unc-42	0.057371186283429	0.0850373464238159
SIB 0.044	unc-55	0.00508974033517595	0
SIB 0.044	Y56A3A.18	0.0266170180800446	0.0267974729708614
SIB 0.044	zag-1	0.077745214240292	0.093582229463698
SIB 0.044	zfh-2	0.0425657081750632	0.0395378186273035
SIB 0.044	zim-3	0.00155248112584789	0
SIB 0.044	ZK546.5	0.0655803713693934	0.107869903877956
SIB 0.044	ztf-26	0.0813962112475529	0.0534553220081171
SIB 0.044	ztf-4	0	0.0038833687159326
SMB 0.049	aha-1	0.129250525424241	0.157072713044423
SMB 0.049	arid-1	0	0.0260433400961955
SMB 0.049	atf-7	0.0246595098104124	0.0387144331194057
SMB 0.049	attf-6	0.0222622085223358	0.035341593705559
SMB 0.049	bed-1	0	0.0309546560992876
SMB 0.049	C34B4.2	0.619184757594492	0
SMB 0.049	cebp-1	0.0305510332304723	0.0384478868159305
SMB 0.049	ceh-18	0	0.0130759972452544
SMB 0.049	ceh-88	0	0.00377245288929513
SMB 0.049	ceh-9	0.490868748821207	NA
SMB 0.049	chd-7	0	0.00856395155347599
SMB 0.049	crh-2	0.0354218948394156	0.0223514959262182
SMB 0.049	ctbp-1	0.17743497883583	NA
SMB 0.049	daf-19	0.0751757487648735	0.145151812157057
SMB 0.049	drap-1	0	0.0116053178583685
SMB 0.049	egl-13	0.0351815339067699	NA
SMB 0.049	egl-18	0.104426784987751	NA
SMB 0.049	ekl-4	0.0340494764320568	NA
SMB 0.049	elt-4	0.0545735339949363	NA
SMB 0.049	ets-5	NA	0.131418495635247
SMB 0.049	F22D6.2	0.0785796941338622	0
SMB 0.049	F57A8.1	0.0613659022128733	0.0820667561738461
SMB 0.049	fkh-10	NA	0.0315779665302228
SMB 0.049	hif-1	0.0219433981187977	0.0218556285854992
SMB 0.049	hinf-1	0.0893013654149048	NA
SMB 0.049	hmg-1.1	0	0.011097859580777
SMB 0.049	hsf-1	0.0380998225060526	0.0450138711304603
SMB 0.049	isw-1	0.0641874759645247	0.120221157907841
SMB 0.049	klu-1	0	0.000835133915975233

SMB 0.049	lag-1	0.0351153011686735	0.0814476241426353
SMB 0.049	lim-7	0.0285083071186404	NA
SMB 0.049	lin-11	0.138342181231743	NA
SMB 0.049	lin-14	0.0818976918934862	0.0855004681560061
SMB 0.049	lin-26	0.0737417593380948	NA
SMB 0.049	lin-40	0.0999116171627718	0.00709392888646761
SMB 0.049	lin-54	0.00289415018602155	NA
SMB 0.049	lsy-2	0.0201984640767033	0.0262771846785956
SMB 0.049	madf-5	0.0471267466322777	NA
SMB 0.049	mbf-1	0.0936018791824935	0.00621428908637855
SMB 0.049	mdt-29	0.0351063154715666	0.01676463712847
SMB 0.049	mef-2	0.0769037548614935	0.0730824449103152
SMB 0.049	mml-1	0.053174053896431	0.0671474514893729
SMB 0.049	nfyb-1	0.0243540773526888	0.0273799229414178
SMB 0.049	nhr-11	0.0346796353291561	NA
SMB 0.049	nhr-47	0	0.0014327756206167
SMB 0.049	pat-9	0.202344225910272	NA
SMB 0.049	pbrm-1	0	0.0254434306241171
SMB 0.049	rcor-1	0	0.0272915135964818
SMB 0.049	row-1	0.00198983282609125	NA
SMB 0.049	sem-4	0.117662555523206	0.104392519444294
SMB 0.049	somi-1	0	0.0793851005398857
SMB 0.049	sup-37	0	0.130789145963576
SMB 0.049	syd-9	0	0.0548576938903263
SMB 0.049	unc-3	0.00942930879047374	NA
SMB 0.049	unc-42	0.0599621747913317	0.0848922326647823
SMB 0.049	unc-55	0.0221526485033019	NA
SMB 0.049	unc-62	0.00955146548730862	NA
SMB 0.049	Y53G8AR.9	0.0207989568203537	0.0529397416025838
SMB 0.049	Y55F3AM.14	NA	0.0197223785842674
SMB 0.049	Y56A3A.18	0.000769396530208056	NA
SMB 0.049	zag-1	0.10495541355996	0.193291683166967
SMB 0.049	zfh-2	0.0538766935182226	0.048236357345117
SMB 0.049	zim-3	0.0154007628409276	0.021601175510573
SMB 0.049	zip-4	0.0169951389853277	0
SMB 0.049	ZK546.5	0.0501628857854736	0.167594020909301
SMB 0.049	ztf-26	0.0777516524287645	NA
SMB 0.049	ztf-4	0.00182982827466212	NA
SMB_PLN_ALN 0.039	aha-1	0.10699352015563	0.135495450248743
SMB_PLN_ALN 0.039	alr-1	0.12623546263378	0.120441520128515
SMB_PLN_ALN 0.039	atf-7	0.0246429026545963	0.0228344018312095
SMB_PLN_ALN 0.039	attf-6	0.0202230509141032	0.0231998479109406
SMB_PLN_ALN 0.039	cebp-1	0.0173758937616939	0.0205996189484034

SMB_PLN_ALN 0.039	ceh-20	0.0126245954914022	0.0102458461166005
SMB_PLN_ALN 0.039	ceh-63	NA	0.124389003786401
SMB_PLN_ALN 0.039	ceh-82	0.0440802368701173	NA
SMB_PLN_ALN 0.039	ceh-9	0.34462439994938	0.334816563581089
SMB_PLN_ALN 0.039	crh-2	0.0306878430383955	0.0327725433430537
SMB_PLN_ALN 0.039	ctbp-1	0.146116529808978	0.138924684258112
SMB_PLN_ALN 0.039	daf-19	0.0899708071946747	0.0914967647249732
SMB_PLN_ALN 0.039	egl-13	0.00316250149177105	0.0124490240316312
SMB_PLN_ALN 0.039	egl-18	0.0954868894755138	0.0902795998995553
SMB_PLN_ALN 0.039	ekl-4	0.0531498472837904	0.0573713747008866
SMB_PLN_ALN 0.039	ets-5	0.129241677782176	0.13015544544126
SMB_PLN_ALN 0.039	F22D6.2	0.0461874567033944	0.00242324423537879
SMB_PLN_ALN 0.039	fkh-10	3.2561906634216e-05	0.00290789215487968
SMB_PLN_ALN 0.039	hif-1	0.0181029967125026	0.0196649363575848
SMB_PLN_ALN 0.039	hinf-1	0.0882773114410489	0.093922332696746
SMB_PLN_ALN 0.039	hlh-8	0.0209609772795373	0.00458425767602752
SMB_PLN_ALN 0.039	hsf-1	0.0185468059577756	0.0183421599264817
SMB_PLN_ALN 0.039	isw-1	0.061945931351018	0.0797910545087278
SMB_PLN_ALN 0.039	lag-1	0.0307333916314283	0.0517406804746696
SMB_PLN_ALN 0.039	lim-7	0.0178606889799667	0.0179540946519089
SMB_PLN_ALN 0.039	lin-11	0.108715514772488	0.12642912832917
SMB_PLN_ALN 0.039	lin-14	0.0595537361006148	0.0633322473824977
SMB_PLN_ALN 0.039	lin-26	0.0822545481313187	0.0773691880588561
SMB_PLN_ALN 0.039	lin-39	0.00774990207422988	0.0110691280001556
SMB_PLN_ALN 0.039	lin-40	0.0837134412506701	0.0475529200971873
SMB_PLN_ALN 0.039	lsy-2	0.0196127379035142	0.0188751726555402
SMB_PLN_ALN 0.039	madf-3	0.033448679361672	0.0335177275370073
SMB_PLN_ALN 0.039	madf-5	0.0652326269883972	0.0432135512443959
SMB_PLN_ALN 0.039	madf-9	0.0171588932548292	0.000190559093525449
SMB_PLN_ALN 0.039	mbf-1	0.0153218214549006	0
SMB_PLN_ALN 0.039	mdt-29	0.0114922410138611	0.0196197117692868
SMB_PLN_ALN 0.039	mef-2	0.0285608572516342	0.0242031330340768
SMB_PLN_ALN 0.039	nfyb-1	0.00983406716307333	0.0108647298137284
SMB_PLN_ALN 0.039	nhr-11	0.0264610299682736	0.0239366779856175
SMB_PLN_ALN 0.039	nhr-232	0.0850467692828599	0
SMB_PLN_ALN 0.039	pag-3	0.0697993670373703	NA
SMB_PLN_ALN 0.039	pat-9	NA	0.16421878978633
SMB_PLN_ALN 0.039	sem-4	0.0461868228632096	0.0570437646756377
SMB_PLN_ALN 0.039	somi-1	0	0.00307989837529512
SMB_PLN_ALN 0.039	sox-4	0.0341461907036947	NA
SMB_PLN_ALN 0.039	sptf-2	0.272152541937301	0.28604530467321
SMB_PLN_ALN 0.039	unc-3	0	0.0130094714475708
SMB_PLN_ALN 0.039	unc-42	0.0371920255371122	0.0361047144290723

SMB_PLN_ALN 0.039	unc-55	0.00904875075423095	0.0165757155150014
SMB_PLN_ALN 0.039	unc-86	0.0147440222575832	0.00768433727666384
SMB_PLN_ALN 0.039	Y53G8AR.9	0.0229718683272748	0.0207623994515766
SMB_PLN_ALN 0.039	Y56A3A.18	0.00786919740949587	0.0150031095816774
SMB_PLN_ALN 0.039	zag-1	0.103673072084069	0.102621627687618
SMB_PLN_ALN 0.039	zfh-2	0.0466911052599343	0.0415234586469936
SMB_PLN_ALN 0.039	zim-3	0.0239837917609957	0.0219877580607079
SMB_PLN_ALN 0.039	zip-4	0.00644462860770617	0.0100452836161719
SMB_PLN_ALN 0.039	ZK546.5	0.0359103819735572	0.0744323572190625
SMB_PLN_ALN 0.039	ztf-26	0.0872646556139178	0.0574418213453006
SMD 0.042	aha-1	0.32026166936031	0.360726982341078
SMD 0.042	alr-1	0.127536416790011	0.127920719731998
SMD 0.042	atf-7	0	0.00287362997937722
SMD 0.042	C34B4.2	0.16391795976004	0
SMD 0.042	crh-2	0.0393675963639166	0.0426779314003374
SMD 0.042	ctbp-1	0.175335173130023	0.170299374036655
SMD 0.042	daf-19	0.0770058792107745	0.0858706445734699
SMD 0.042	egl-18	0.0672264944313958	0.0774812439923818
SMD 0.042	egl-27	0.00939568305898069	0.0121174910798638
SMD 0.042	ekl-4	0.0214792677231591	0.0295404687837412
SMD 0.042	ets-5	0.0164443644587555	0.0291900390709518
SMD 0.042	F22D6.2	0.0407469094909724	0
SMD 0.042	fkh-10	0.204223947609717	0.218459367888518
SMD 0.042	hif-1	0.0139039590145314	0.0237075034888172
SMD 0.042	hinf-1	0.0990537014114037	0.106651140227293
SMD 0.042	hlh-8	0.0152723561867806	0.00432265095206184
SMD 0.042	hsf-1	0.00973526251616891	0.0120093559323587
SMD 0.042	lag-1	0.0292081868836762	0.0594176102243849
SMD 0.042	lim-7	0.0198345373218656	0.0218352347045035
SMD 0.042	lin-11	0.159187214053659	0.177133272255126
SMD 0.042	lin-14	0.0465370739788645	0.0436834152664531
SMD 0.042	lin-26	0.0764143185414688	0.0617542637968082
SMD 0.042	lin-39	0.00703932631218291	0.00793025845792482
SMD 0.042	lin-40	0.0971833767638018	0.0455376152933854
SMD 0.042	lsy-2	0.0126977262621805	0.0116780848650507
SMD 0.042	madf-3	0.0525374756897245	0.0533061391750901
SMD 0.042	madf-5	0.0732100859027701	0.04051416824527
SMD 0.042	madf-9	0.0104013106957682	0
SMD 0.042	mdt-29	0.0294038616879273	0.0338644628131609
SMD 0.042	nfya-2	0	0.00382698133100992
SMD 0.042	nhr-11	0.00193611498805822	0.00186771429480966
SMD 0.042	pag-3	0.0682834635168364	0.0547864777162785
SMD 0.042	pat-9	NA	0.164897674851313

SMD 0.042	R02D3.7	0.000796614452201161	0.00234631296499097
SMD 0.042	sem-4	0.0511128176640047	0.0682747800468244
SMD 0.042	sptf-2	0.241697627892086	0.260615381232285
SMD 0.042	T26A5.8	0.0112161269125379	0.0103349500878959
SMD 0.042	unc-30	0.185738370877147	0.138742084148835
SMD 0.042	unc-42	0.031790293197894	0.0386690571131013
SMD 0.042	Y53G8AR.9	0.00803208098780494	0.00640208719777103
SMD 0.042	Y56A3A.18	0.035127717327415	0.0353898594505335
SMD 0.042	zfh-2	0.0467279658231773	0.0410245918425929
SMD 0.042	zim-3	0.0010723011753558	0
SMD 0.042	ZK546.5	0.00401374704068368	0.061862528291288
SMD 0.042	ztf-26	NA	0.0497330439400962
Seam cells (bus+) 0.053	alr-1	0.156901686308118	NA
Seam cells (bus+) 0.053	B0035.1	0.0733762560156229	0.0649788772264577
Seam cells (bus+) 0.053	bed-3	0.458316256936613	0.535073143562332
Seam cells (bus+) 0.053	blmp-1	0.0354123418183927	0.0330295664169703
Seam cells (bus+) 0.053	ceh-79	0.00744652102444761	0.0278818413074179
Seam cells (bus+) 0.053	ceh-8	0.024973861569155	NA
Seam cells (bus+) 0.053	cey-2	0	0.00176876965944151
Seam cells (bus+) 0.053	crh-2	0.0128814890803532	0.0121372524428008
Seam cells (bus+) 0.053	ctbp-1	0.0448930197911538	0.062473924932101
Seam cells (bus+) 0.053	daf-19	0.0237952941157987	0.0144319929685805
Seam cells (bus+) 0.053	dxbp-1	0.0283894651331175	0.0310969859774912
Seam cells (bus+) 0.053	egrh-3	0.190594728259765	0.214100290435281
Seam cells (bus+) 0.053	ekl-4	0.0355917450591347	0.0329390418122592
Seam cells (bus+) 0.053	elt-1	0.0922906064725526	0.0819851934076802
Seam cells (bus+) 0.053	elt-4	0.283417539708046	0.292127371246165
Seam cells (bus+) 0.053	F22D6.2	0.222075162146774	0.203547020094896
Seam cells (bus+) 0.053	hinf-1	0.07402912132618	0.0608991482933963
Seam cells (bus+) 0.053	hlh-8	0.0014676664637872	0
Seam cells (bus+) 0.053	hsf-1	0.00860353168527446	0.00381238831304966
Seam cells (bus+) 0.053	isw-1	0.0405752734892912	0.0402061330769763
Seam cells (bus+) 0.053	let-607	0.0146079425286736	0.00764238053944558
Seam cells (bus+) 0.053	lin-11	0.00198104932438262	0
Seam cells (bus+) 0.053	lin-26	0.094166207485911	0.0849196889194504
Seam cells (bus+) 0.053	lin-29	0.164035580674663	0.163576674932799
Seam cells (bus+) 0.053	lin-40	0.227640430287452	0.239617912866589
Seam cells (bus+) 0.053	madf-2	0.6449093610652	0.732857066708175
Seam cells (bus+) 0.053	madf-3	0.0357707602720733	0.0312420494136617
Seam cells (bus+) 0.053	madf-5	0.750395230913725	0.787556993926566
Seam cells (bus+) 0.053	mec-3	NA	0.309905710243287
Seam cells (bus+) 0.053	nhr-10	0.0425394810756928	0.0506422531960336
Seam cells (bus+) 0.053	nhr-11	0.0175286354929206	0.0173088886347248

Seam cells (bus+) 0.053	nhr-179	0.187858255349462	0.29943182186371
Seam cells (bus+) 0.053	nhr-25	0.135556280596445	0.150532329409226
Seam cells (bus+) 0.053	nhr-43	0.0692062080925174	0.0510736334652093
Seam cells (bus+) 0.053	nhr-48	0.0150116706353624	0.0193876926588508
Seam cells (bus+) 0.053	nhr-84	0.321287730334784	0.185315260700814
Seam cells (bus+) 0.053	pag-3	0.0136371760903166	NA
Seam cells (bus+) 0.053	pat-9	0.0944868773189845	0.0476086781968193
Seam cells (bus+) 0.053	pbrm-1	0.00563660814640574	0
Seam cells (bus+) 0.053	R02D3.7	0.0340759946339385	0.0198242607947931
Seam cells (bus+) 0.053	saeg-2	0.00285099575734245	0.0043021542696261
Seam cells (bus+) 0.053	spr-1	0.439595453376441	0.423242590970375
Seam cells (bus+) 0.053	sptf-2	0.213351913832415	0.195931390179711
Seam cells (bus+) 0.053	T23F11.4	0.286757166683259	NA
Seam cells (bus+) 0.053	tbx-9	0.0510824560455699	NA
Seam cells (bus+) 0.053	tlp-1	0.0450375148985926	0.0529050634454409
Seam cells (bus+) 0.053	Y56A3A.18	0.0283708872666411	0.024387826845395
Seam cells (bus+) 0.053	zfh-2	0.0200501807656687	0.0059291756603107
Seam cells (bus+) 0.053	zip-8	NA	0.0061344695337445
Seam cells (bus+) 0.053	ztf-1	0.396693342649203	0.366489990632997
Seam cells (bus+) 0.053	ztf-16	0.738463476196527	0.802029378802478
Seam cells (bus+) 0.053	ztf-22	0.00396432008171347	0.00330718595550686
Seam cells (bus+) 0.053	ztf-26	0.179833453397114	0.18924661014933
Seam cells (grd+) 0.057	alr-1	0.0352591485002862	0.0414030190184324
Seam cells (grd+) 0.057	B0035.1	0.262098616195706	0.245257845060642
Seam cells (grd+) 0.057	blmp-1	0.0151750594302767	0.0137897067114807
Seam cells (grd+) 0.057	ceh-16	0.0892118660541619	0.109787938424609
Seam cells (grd+) 0.057	cey-2	0.027476975610849	0
Seam cells (grd+) 0.057	ctbp-1	0.0569645832637528	0.0645553375752507
Seam cells (grd+) 0.057	egrh-3	0.13443726208406	0.1331195260638
Seam cells (grd+) 0.057	elt-1	0.0987912946047937	0.095829316769453
Seam cells (grd+) 0.057	elt-4	0.207751750371139	0.201945108622288
Seam cells (grd+) 0.057	F22D6.2	0.290533646031595	0.240244778333989
Seam cells (grd+) 0.057	gei-8	0.0896495086485214	0.0778792134737125
Seam cells (grd+) 0.057	hlh-8	0.0103320389903251	0.00581572340758593
Seam cells (grd+) 0.057	lin-14	0.0245138887907271	0.0249911074776109
Seam cells (grd+) 0.057	lin-26	0.179065056383891	0.183353537107176
Seam cells (grd+) 0.057	lin-40	0.59484316994799	0.603620004045719
Seam cells (grd+) 0.057	madf-5	0.57285086361697	0.572970217922526
Seam cells (grd+) 0.057	madf-9	0.15190908636595	0.148980774076227
Seam cells (grd+) 0.057	mec-3	0.169299468495734	0.179030299334637
Seam cells (grd+) 0.057	nhr-11	0.0201630739595576	0.0169639334317929
Seam cells (grd+) 0.057	nhr-23	0.000304681179175336	0.00023626045534308
Seam cells (grd+) 0.057	nhr-232	0.145496627308173	0.17122878599062

Seam cells (grd+) 0.057	nhr-25	0.0321854917132106	0.0260651422930624
Seam cells (grd+) 0.057	nhr-270	0.29470286001066	0.306721711463432
Seam cells (grd+) 0.057	nhr-85	0.183290256038045	0.178419770145134
Seam cells (grd+) 0.057	pag-3	0.0963667314910514	0.0920305394822209
Seam cells (grd+) 0.057	pat-9	0.0833212111351512	0.0520551420990417
Seam cells (grd+) 0.057	R02D3.7	0.0118241224436443	0.0122598991044608
Seam cells (grd+) 0.057	snu-23	0.0116068477687954	0.0106158882863792
Seam cells (grd+) 0.057	spr-3	0.107711095365136	0.108242922071449
Seam cells (grd+) 0.057	sptf-2	0	0.0045691721422216
Seam cells (grd+) 0.057	tbx-9	0.167315458759023	0.14968706881672
Seam cells (grd+) 0.057	zfh-2	0.00353475989323243	0.00211400152902274
Seam cells (grd+) 0.057	zim-3	0.118138478673079	0.128686800026699
Seam cells (grd+) 0.057	ztf-26	0.304984766116667	0.288908050579981
Seminal vesicle (male) 0.037	akir-1	0.299532008630337	NA
Seminal vesicle (male) 0.037	alr-1	NA	0.30828052916287
Seminal vesicle (male) 0.037	attf-6	0.014988690775926	0.0149592702299829
Seminal vesicle (male) 0.037	C16A3.4	0.00314406091407075	0.0134855719487899
Seminal vesicle (male) 0.037	ceh-18	0.0525224415757443	NA
Seminal vesicle (male) 0.037	cey-2	0	0.00240084704336732
Seminal vesicle (male) 0.037	crh-2	0.0250997443804083	0.0173385482926061
Seminal vesicle (male) 0.037	dxbp-1	NA	0.0250314349758875
Seminal vesicle (male) 0.037	efl-1	0.00854323735562151	0.00806554961436816
Seminal vesicle (male) 0.037	egrh-3	0.0378398057037757	0.00234539331859264
Seminal vesicle (male) 0.037	ekl-4	0.120520406751786	0.106644377266919
Seminal vesicle (male) 0.037	eyg-1	0.0305793170130942	NA
Seminal vesicle (male) 0.037	F13C5.2	NA	0.00932263615564395
Seminal vesicle (male) 0.037	F22D6.2	0.132081648226051	0.0710005926355894
Seminal vesicle (male) 0.037	F23B12.7	0	0.00301259540581053
Seminal vesicle (male) 0.037	F33H1.4	NA	0.0423961551785036
Seminal vesicle (male) 0.037	F44E2.7	0.0118438555438054	0.00965929812200066
Seminal vesicle (male) 0.037	hif-1	0.00232608470643357	0
Seminal vesicle (male) 0.037	hinf-1	0.149720741158267	0.148861761920656
Seminal vesicle (male) 0.037	lag-1	0.0419636967676941	0.00557342586346466
Seminal vesicle (male) 0.037	let-607	0.0580334127226166	0.0271642570796983
Seminal vesicle (male) 0.037	lin-13	0.0243290053571777	0.0151820699490083
Seminal vesicle (male) 0.037	lin-26	0.14042165359494	0.121328862041498
Seminal vesicle (male) 0.037	lin-40	0.09342626689992	0.0786708536064201
Seminal vesicle (male) 0.037	lin-54	0.0288380711242927	0.0353326673407157
Seminal vesicle (male) 0.037	madf-5	0.174669579476274	NA
Seminal vesicle (male) 0.037	madf-6	NA	0.0209225782179126
Seminal vesicle (male) 0.037	mdt-29	0.0226274264856122	0.0375328656162345
Seminal vesicle (male) 0.037	mep-1	0.0123597425203386	0.0166819131911385
Seminal vesicle (male) 0.037	mxl-1	NA	0.0383645686570274

Seminal vesicle (male) 0.037	nhr-11	NA	0.0365158003487288
Seminal vesicle (male) 0.037	nhr-232	0.067128072625239	NA
Seminal vesicle (male) 0.037	nhr-84	NA	0.291186675604346
Seminal vesicle (male) 0.037	pbrm-1	0.0334515661892014	0.0151519730531823
Seminal vesicle (male) 0.037	pha-4	0.000123120678080937	NA
Seminal vesicle (male) 0.037	R02D3.7	NA	0.0344197439520443
Seminal vesicle (male) 0.037	rcor-1	0.00042255818893249	0
Seminal vesicle (male) 0.037	snu-23	0.00999600231115285	0
Seminal vesicle (male) 0.037	spr-1	NA	0.0552352202901611
Seminal vesicle (male) 0.037	spr-3	NA	0.0305511494216751
Seminal vesicle (male) 0.037	sup-37	NA	0.0390984842483927
Seminal vesicle (male) 0.037	T23F11.4	NA	0.0313612800540521
Seminal vesicle (male) 0.037	xbp-1	0.0355944191484321	0.0354299752508577
Seminal vesicle (male) 0.037	Y53G8AR.9	NA	0.0231695872804882
Seminal vesicle (male) 0.037	Y56A3A.18	0.0831750226978522	0.0528533736846498
Seminal vesicle (male) 0.037	zfh-2	NA	0.0643352603730341
Seminal vesicle (male) 0.037	zim-3	NA	0.018887224744662
Seminal vesicle (male) 0.037	ZK546.5	0.342276658847122	0.193839653941951
Seminal vesicle (male) 0.037	ztf-1	NA	0.0554622909168441
Seminal vesicle (male) 0.037	ztf-26	0.113758302448395	NA
Spermatheca bag distal 0.039	alr-1	0.35459131857974	0.330564840298863
Spermatheca bag distal 0.039	attf-6	0.0356450409858176	0.036122315062257
Spermatheca bag distal 0.039	B0035.1	0.366997851448242	0.371796633613052
Spermatheca bag distal 0.039	bed-1	0.0120725112351577	0.0113744854404316
Spermatheca bag distal 0.039	blmp-1	0.00240124588154428	0.00358149061786134
Spermatheca bag distal 0.039	C16A3.4	0.0109435476337739	0.00949830340482435
Spermatheca bag distal 0.039	cebp-1	0.0253899734100658	0.0241951511973149
Spermatheca bag distal 0.039	ceh-22	0.0108996957646617	0
Spermatheca bag distal 0.039	ceh-63	0.00730778618752443	0
Spermatheca bag distal 0.039	daf-19	0.172546102208574	0.152830639516037
Spermatheca bag distal 0.039	dxbp-1	0.0304170379485319	0.0343362186176216
Spermatheca bag distal 0.039	egl-18	0.0960997120405304	0.0810530799011174
Spermatheca bag distal 0.039	egl-5	0.0131866531788755	0.00907111569185018
Spermatheca bag distal 0.039	ekl-4	0.0968238900681455	0.0995827114390199
Spermatheca bag distal 0.039	ets-5	0.0809888456614367	0.0887614998758563
Spermatheca bag distal 0.039	F10B5.3	0.0708057413975007	0.0786213026118885
Spermatheca bag distal 0.039	F33H1.4	0.0350402294672155	0.0314303977837637
Spermatheca bag distal 0.039	F44E2.7	0.0172744223755053	0.0135212542328326
Spermatheca bag distal 0.039	hinf-1	0.154498934897532	0.141863671007505
Spermatheca bag distal 0.039	hlh-1	0.0214151872066792	0.0237908485491005
Spermatheca bag distal 0.039	hlh-8	0.078026396142934	0.0576505975834157
Spermatheca bag distal 0.039	hsf-1	0.00697209645365879	0.00445504919098152
Spermatheca bag distal 0.039	isw-1	0.00291702666063851	0

Spermatheca bag distal 0.039	let-607	0.0343287481700536	0.0349344848958893
Spermatheca bag distal 0.039	lim-7	0.0674561418628538	0.0679738545203333
Spermatheca bag distal 0.039	lin-11	0.00978429515643629	0.0066191957713607
Spermatheca bag distal 0.039	lin-14	0.00028299434834989	0.00384850878239827
Spermatheca bag distal 0.039	lin-26	0.104732445233454	0.0911592635608742
Spermatheca bag distal 0.039	lin-40	0.0241002202381573	0.0133099050627909
Spermatheca bag distal 0.039	lin-54	0.0096069986759467	0.0077061075456457
Spermatheca bag distal 0.039	lsy-2	0.0365049687506284	0.0327577060163815
Spermatheca bag distal 0.039	madf-2	0.106002888556293	0.119509070031686
Spermatheca bag distal 0.039	madf-3	0.0768675244175284	0.0722557880397939
Spermatheca bag distal 0.039	madf-5	0.0368925220780951	NA
Spermatheca bag distal 0.039	madf-6	0.0302446601433111	0.0238477602555584
Spermatheca bag distal 0.039	mep-1	0.0160201920094539	0.0142152551815077
Spermatheca bag distal 0.039	nfya-2	0	0.00346253059356454
Spermatheca bag distal 0.039	nhr-11	0.0118448813906538	0.0161465091900324
Spermatheca bag distal 0.039	nhr-129	0.00931949273980073	0.0104243172299725
Spermatheca bag distal 0.039	nhr-237	0.068000756062573	NA
Spermatheca bag distal 0.039	nhr-6	0.0218602892131025	0.0263647792847983
Spermatheca bag distal 0.039	pag-3	0.0470383415531835	NA
Spermatheca bag distal 0.039	pat-9	0.269815048777802	0.170557942973497
Spermatheca bag distal 0.039	pha-4	0.00995346652204745	0.0111506729444116
Spermatheca bag distal 0.039	R02D3.7	0.0309984197952476	0.027751423152007
Spermatheca bag distal 0.039	spr-3	0.015980733033561	0.00934709750283804
Spermatheca bag distal 0.039	sptf-2	0.494647718403669	0.489708553487021
Spermatheca bag distal 0.039	tbx-9	NA	0.371708890519752
Spermatheca bag distal 0.039	xbp-1	0.0227349068973613	0.0214183192617408
Spermatheca bag distal 0.039	Y56A3A.18	0.132769926081857	0.138553382927505
Spermatheca bag distal 0.039	zfh-2	0.0517330633443453	0.0487809142607929
Spermatheca bag distal 0.039	ZK546.5	0.215803512295275	0.224179123207399
Spermatheca bag distal 0.039	ztf-1	0.0544965908428756	0.0352070015173563
Spermatheca bag distal 0.039	ztf-26	0.00653788785109408	0
Spermatheca bag proximal 0.026	aha-1	0.0105043965563235	0.00176099187930658
Spermatheca bag proximal 0.026	alr-1	0.148234407246112	0.155165523274454
Spermatheca bag proximal 0.026	attf-6	0.0127337184874657	0.0121852011230717
Spermatheca bag proximal 0.026	B0035.1	0.49782394390076	0.471405448007745
Spermatheca bag proximal 0.026	blmp-1	0.000542270018177267	0
Spermatheca bag proximal 0.026	cebp-1	0.0149963001094478	0.0138221588248181
Spermatheca bag proximal 0.026	ceh-16	0.00241411357042011	NA
Spermatheca bag proximal 0.026	ceh-22	0.0582003441380327	0.0418136443679707
Spermatheca bag proximal 0.026	ceh-40	NA	0.0823756741882822
Spermatheca bag proximal 0.026	daf-19	0.0497327504880377	0.0402460280266445
Spermatheca bag proximal 0.026	dxbp-1	0.0136589417847339	0.0111312823913781
Spermatheca bag proximal 0.026	ekl-4	0.0400040619537619	0.0392850657169788

Spermatheca bag proximal 0.026	ets-5	0.0641424434324859	0.0593720650096754
Spermatheca bag proximal 0.026	F10B5.3	0	0.000203040145850187
Spermatheca bag proximal 0.026	hinf-1	0.0501606758749701	0.0506300011047066
Spermatheca bag proximal 0.026	hlh-1	0.0243753655980599	0.0224970265178088
Spermatheca bag proximal 0.026	hlh-6	0.0194992650416367	NA
Spermatheca bag proximal 0.026	hmg-4	4.23251731748758e-05	0
Spermatheca bag proximal 0.026	let-607	0.025108919383357	0.0221058063220739
Spermatheca bag proximal 0.026	lim-7	0.0160031262590463	0.0103452192027953
Spermatheca bag proximal 0.026	lin-14	0.00644842531967459	0.00479990909989682
Spermatheca bag proximal 0.026	lin-26	0.0222077816164988	0.0254267503949342
Spermatheca bag proximal 0.026	lin-39	0.0055215237627708	0.00222724440948126
Spermatheca bag proximal 0.026	lin-40	0.000222590693780131	0
Spermatheca bag proximal 0.026	lsy-2	0.00826203094593468	0.00763641539294322
Spermatheca bag proximal 0.026	madf-2	0.0518389345595884	0.0327139009008478
Spermatheca bag proximal 0.026	madf-3	0.0305254410274531	0.0312379600051118
Spermatheca bag proximal 0.026	nhr-237	0.0462780184950801	NA
Spermatheca bag proximal 0.026	pag-3	0.0248595055168874	0.0216651374610822
Spermatheca bag proximal 0.026	pha-4	0.00289239509623845	0.000428284281861128
Spermatheca bag proximal 0.026	R02D3.7	0.0113155792571446	0.00944652653675199
Spermatheca bag proximal 0.026	sptf-2	0.200622686489022	0.216324055144034
Spermatheca bag proximal 0.026	T20F7.1	3.49992383641478e-05	0
Spermatheca bag proximal 0.026	tbx-9	0.486587764056692	0.456277503062206
Spermatheca bag proximal 0.026	xbp-1	0.0282181531671311	0.0224828432366918
Spermatheca bag proximal 0.026	Y55F3AM.14	0.0226657616963903	0.0175388403456772
Spermatheca bag proximal 0.026	Y56A3A.18	0.0950471016510493	0.0902712571625313
Spermatheca bag proximal 0.026	zfh-2	0.0162871343123084	0.0172238284839559
Spermatheca bag proximal 0.026	ZK546.5	0.198092035697323	0.222100014082954
Spermatheca bag proximal 0.026	ztf-26	0.0156102095451276	0.00397555845801012
Spermatheca bag proximal 0.026	ztf-4	0.00772787700637487	0.00519705360439746
Spermatheca neck distal-most 0.023	aha-1	0.0175930657484988	0.0214435497897218
Spermatheca neck distal-most 0.023	alr-1	0.146677656924327	NA
Spermatheca neck distal-most 0.023	attf-6	0.0111871688207744	0.0134253303007768
Spermatheca neck distal-most 0.023	B0035.1	0.0988969952441458	0.128836905327425
Spermatheca neck distal-most 0.023	cebp-1	0.0137793022471821	0.0144950774005395
Spermatheca neck distal-most 0.023	ceh-22	0.0327097827522357	NA
Spermatheca neck distal-most 0.023	ceh-40	0.114356848162714	NA
Spermatheca neck distal-most 0.023	ceh-58	0	0.00303088623650434
Spermatheca neck distal-most 0.023	daf-19	0.0352670501599825	0.0582415935394981
Spermatheca neck distal-most 0.023	dxbp-1	0.0265195610528299	0.0307201530052889
Spermatheca neck distal-most 0.023	ekl-4	0.0470334125215091	0.0496944013235837
Spermatheca neck distal-most 0.023	elt-4	0.00307978744205886	0.0101015094350766
Spermatheca neck distal-most 0.023	ets-5	0.0709930106718128	0.0754392688503836
Spermatheca neck distal-most 0.023	F10B5.3	0.0183636276986428	NA

Spermatheca neck distal-most 0.023	hinf-1	0.0436940426856421	0.0600259119961232
Spermatheca neck distal-most 0.023	hlh-1	0.0200061425830213	NA
Spermatheca neck distal-most 0.023	hlh-6	0.0333233581299302	0.0315568413520309
Spermatheca neck distal-most 0.023	hlh-8	0	0.00239620989099828
Spermatheca neck distal-most 0.023	hmg-4	0.0129029468450103	0.0169590069625731
Spermatheca neck distal-most 0.023	let-607	0.0110800522940769	0.0102899346584202
Spermatheca neck distal-most 0.023	lim-7	0.0120509629193927	0.0182318262232793
Spermatheca neck distal-most 0.023	lin-13	0.00010961322904914	0.000687049817475316
Spermatheca neck distal-most 0.023	lin-14	0.00426315988469214	0.00820935876607193
Spermatheca neck distal-most 0.023	lin-26	0.0240784227920629	0.0273366744355819
Spermatheca neck distal-most 0.023	lin-39	0.00476282913294927	0.00701439891151056
Spermatheca neck distal-most 0.023	lsy-2	0.00977941204686095	0.0103931823292239
Spermatheca neck distal-most 0.023	madf-2	0.0951260389820363	0.0760819737582566
Spermatheca neck distal-most 0.023	madf-3	0.0283767582924963	0.0360307216546841
Spermatheca neck distal-most 0.023	madf-6	0.000778543872248928	0.00130945561047019
Spermatheca neck distal-most 0.023	mep-1	0.00295182063638234	0
Spermatheca neck distal-most 0.023	nhr-237	0.0428028182043319	0.0389827971417966
Spermatheca neck distal-most 0.023	pag-3	0.0225304377905379	NA
Spermatheca neck distal-most 0.023	pha-4	0.00640678124129011	0.00441372339070059
Spermatheca neck distal-most 0.023	R02D3.7	0.00915597812261462	0.0103620573929472
Spermatheca neck distal-most 0.023	sptf-2	0.186638125234928	0.253141662993203
Spermatheca neck distal-most 0.023	tbx-9	0.163909039355138	0.171177002124954
Spermatheca neck distal-most 0.023	unc-120	0	0.00419867988192512
Spermatheca neck distal-most 0.023	xbp-1	0.0187729635756088	0.0218451619852408
Spermatheca neck distal-most 0.023	Y48G9A.11	0	0.00311485128478217
Spermatheca neck distal-most 0.023	Y56A3A.18	0.0788372129201655	0.0882032225862529
Spermatheca neck distal-most 0.023	zfh-2	0.0169525098978956	0.0179054043779473
Spermatheca neck distal-most 0.023	ZK546.5	0.207667491331395	0.247343300168414
Spermatheca neck distal-most 0.023	ztf-26	0.000113208118357504	0
Spermatheca neck distal-most 0.023	ztf-4	0.0229883973026201	0.0270599480865453
Spermatheca-Uterine junction 0.034	akir-1	0	0.00195101950772791
Spermatheca-Uterine junction 0.034	alr-1	0.0823375585188881	0.0701257297847409
Spermatheca-Uterine junction 0.034	attf-6	0	0.00406526355484775
Spermatheca-Uterine junction 0.034	blmp-1	0.0222040084464585	0.0243710780210097
Spermatheca-Uterine junction 0.034	cebp-1	0.0526415686016795	0.0609662562904755
Spermatheca-Uterine junction 0.034	ceh-63	0.0351731839838763	0.0667849047967075
Spermatheca-Uterine junction 0.034	ceh-88	0.0301304274081508	0.0218274539613006
Spermatheca-Uterine junction 0.034	chd-7	0.0050664348877289	0.0262591086967822
Spermatheca-Uterine junction 0.034	crh-2	0.0130341329484998	0.0129180881073779
Spermatheca-Uterine junction 0.034	D1046.2	0.0154425477472784	0.0188245471082792
Spermatheca-Uterine junction 0.034	daf-19	0.055662384992264	0.0572836215285273
Spermatheca-Uterine junction 0.034	dve-1	0.0132883902775112	0.0202445213658771
Spermatheca-Uterine junction 0.034	dxbp-1	0	0.00291075319596457

Spermatheca-Uterine junction 0.034	ekl-4	0.0282186797779413	0.0281850628021514
Spermatheca-Uterine junction 0.034	ets-4	0.00155553847875543	0.00754993265253588
Spermatheca-Uterine junction 0.034	ets-5	0.0383278480404558	0.0512141259212305
Spermatheca-Uterine junction 0.034	F22D6.2	0.0317744014205785	0
Spermatheca-Uterine junction 0.034	fkh-10	0	9.7869876220094e-05
Spermatheca-Uterine junction 0.034	fos-1	0.00808609745994656	0.0143299677324048
Spermatheca-Uterine junction 0.034	hinf-1	0.00695301053703552	0.00395100248570565
Spermatheca-Uterine junction 0.034	hlh-8	0.0858381658694196	0.0942099742578226
Spermatheca-Uterine junction 0.034	hmg-11	0.0076556606194458	0.00784125565448137
Spermatheca-Uterine junction 0.034	jun-1	0.0157790228901723	0.0239000198167771
Spermatheca-Uterine junction 0.034	K11D2.4	0	0.00174459542239065
Spermatheca-Uterine junction 0.034	K12H6.12	0.10451680614377	0.124585533907124
Spermatheca-Uterine junction 0.034	let-607	0.00666236486992594	0.0113082261502991
Spermatheca-Uterine junction 0.034	lim-6	0.0273825802512865	0.0654689713446042
Spermatheca-Uterine junction 0.034	lin-14	0.0271217792299782	0.032054499715326
Spermatheca-Uterine junction 0.034	lin-26	0.0158374870496041	0.00560280939704596
Spermatheca-Uterine junction 0.034	lin-40	0.154026447587393	0.133946563744415
Spermatheca-Uterine junction 0.034	lsy-12	0	0.00788304561737733
Spermatheca-Uterine junction 0.034	lsy-27	0.0533332865672425	0.0853129981692127
Spermatheca-Uterine junction 0.034	madf-3	0.0213762146250688	0.0240242914269285
Spermatheca-Uterine junction 0.034	madf-5	0.0497964385444692	0.0298702341967919
Spermatheca-Uterine junction 0.034	madf-9	0.0528436986550428	0.0474446243946559
Spermatheca-Uterine junction 0.034	mdt-29	0.0106966695337212	0.0171805474231833
Spermatheca-Uterine junction 0.034	nfya-2	0.00504349538592464	0.00529181637440951
Spermatheca-Uterine junction 0.034	nfyb-1	0.0252705371509237	0.0340917053263124
Spermatheca-Uterine junction 0.034	nhr-11	0.0482034433457564	0.0558518958205996
Spermatheca-Uterine junction 0.034	nhr-129	0.00145826545822149	0.00404188010118299
Spermatheca-Uterine junction 0.034	nhr-237	0.0524714085971861	NA
Spermatheca-Uterine junction 0.034	nhr-6	0.0555937612510277	0.0676321619563805
Spermatheca-Uterine junction 0.034	pag-3	0.0387364348748288	NA
Spermatheca-Uterine junction 0.034	pat-9	0.19861445081999	0.21275658359974
Spermatheca-Uterine junction 0.034	pha-4	0.0276130594896247	0.0301928228935995
Spermatheca-Uterine junction 0.034	sma-3	0	0.000910601507837003
Spermatheca-Uterine junction 0.034	somi-1	0	0.00438095562904546
Spermatheca-Uterine junction 0.034	spr-3	0.0539182447600801	NA
Spermatheca-Uterine junction 0.034	sptf-2	0.0232564833304032	NA
Spermatheca-Uterine junction 0.034	Y56A3A.18	0.0321493866807175	0.0309541190880836
Spermatheca-Uterine junction 0.034	zfh-2	0.0249629109061891	0.0279353360579242
Spermatheca-Uterine junction 0.034	ZK546.5	0.0487247239107813	0.0725636045899014
Spermatheca-Uterine junction 0.034	ztf-1	0.0550258995478633	0.0607297352738188
Spermatheca-Uterine junction 0.034	ztf-26	0.0100377345716748	0
Spermatids 0.029	akir-1	0.341382580852565	0.332075201871346
Spermatids 0.029	ceh-24	2.38594681236725	1.91613988066111

Spermatids 0.029	ceh-38	0.042773582717801	0.0159405568394393
Spermatids 0.029	egrh-3	0.0245961331253433	0.0178120148185223
Spermatids 0.029	F26F4.8	0.0424503647908123	0.0353271567087772
Spermatids 0.029	sptf-1	0.172335997335706	0.108722935297657
Spermatids 0.029	T22C8.4	NA	0.0394572068075692
Spermatocytes 0.031	akir-1	0.942323591960482	0.991030934906089
Spermatocytes 0.031	alr-1	0.0293102962411218	0.038240664721098
Spermatocytes 0.031	attf-6	0.0179944119969602	0.017969310990413
Spermatocytes 0.031	ceh-24	0.462682848846038	0.488177885410554
Spermatocytes 0.031	ceh-38	0.0263683974403532	0.0277536459400384
Spermatocytes 0.031	dmd-4	0.319515260509778	0.357758737710169
Spermatocytes 0.031	egrh-3	0.0486352400811165	0.0510420507701131
Spermatocytes 0.031	ekl-4	0.0223035436863659	0.0235754794336911
Spermatocytes 0.031	F26F4.8	0.0723805937302636	0.086616919123253
Spermatocytes 0.031	F44E2.7	0	0.00035296808817375
Spermatocytes 0.031	hlh-26	0.14155976203786	0.185231224557202
Spermatocytes 0.031	nhr-120	0.00791408588066315	0.0124921252357815
Spermatocytes 0.031	nhr-19	0	0.000307651802093933
Spermatocytes 0.031	pbrm-1	0.00769337897399165	0.0141017828265507
Spermatocytes 0.031	sptf-1	0.232417242118974	0.248942188344219
Spermatocytes 0.031	T22C8.4	0.0300445318479103	0.0304703154380253
Spermatocytes 0.031	unc-30	0.647090429530589	0.748697521042512
Spermatocytes 0.031	zfh-2	0.00153675618381935	0.00151138966548211
URA 0.047	aha-1	0.133687998263969	0.121891181111014
URA 0.047	alr-1	0.192882715211238	NA
URA 0.047	C34B4.2	0.294068340864583	0.135468184153975
URA 0.047	ceh-18	0.0399798281751543	0.00350539448651584
URA 0.047	ceh-27	NA	0.0608219653201488
URA 0.047	ceh-31	0.0112037546866035	0.0216041066626639
URA 0.047	ceh-48	0	0.0156091851244941
URA 0.047	crh-2	0.0517444118648256	0.0632031352875234
URA 0.047	ctbp-1	0.210601087079637	0.221318927570832
URA 0.047	daf-19	0.075974815819841	0.0965301037328177
URA 0.047	dxbp-1	0.00509999880784716	0.00149074763992067
URA 0.047	egl-18	0.0952894842230371	0.0673857164554949
URA 0.047	egl-27	0.0371087388419859	0.0466570892937351
URA 0.047	egrh-3	0.0172720061215755	NA
URA 0.047	ekl-4	0.0693263590113581	0.0691979763518944
URA 0.047	F22D6.2	0.132597831419003	0.0365189846910254
URA 0.047	F57A8.1	0.00429862248341448	0
URA 0.047	gei-8	0	0.00323651010166588
URA 0.047	hif-1	0.00111595601375645	0
URA 0.047	hlh-8	0.0091549770910846	0.0169139700845359

URA 0.047	hmg-1.1	0.00670697227338719	0.00717735682972832
URA 0.047	hmg-11	0	0.00330191585869083
URA 0.047	hsf-1	0.00478023708669943	NA
URA 0.047	lag-1	0.0655880922889142	0.101011664362028
URA 0.047	lim-7	0.0463844768431294	0.0305684341232502
URA 0.047	lin-14	0.0625960852894842	0.0820032299813334
URA 0.047	lin-26	0.0928782606479112	0.0806512283198268
URA 0.047	lin-39	0.0263701028685764	NA
URA 0.047	lin-40	0.057661650426126	0.0289463621812836
URA 0.047	lsy-2	NA	0.0322400132564025
URA 0.047	madf-3	NA	0.0705658108301167
URA 0.047	madf-9	0.00634734991885943	0.0241698580855255
URA 0.047	mbf-1	0	0.124813967061731
URA 0.047	mdt-29	0.0334509394696819	0.0565994491788549
URA 0.047	nfyb-1	0.00440892851804591	0.00384002916977051
URA 0.047	pbrm-1	0.0197486768102482	0.0164339074928136
URA 0.047	row-1	0.0643269088002469	NA
URA 0.047	sea-2	0.00919144901272077	0.0293142877659316
URA 0.047	sox-2	0	0.0186554702276383
URA 0.047	syd-9	0.0373434408686166	0
URA 0.047	T26A5.8	0.0170654095431623	0
URA 0.047	unc-120	0.00474224496107447	NA
URA 0.047	unc-42	0.0391063673586103	NA
URA 0.047	unc-86	0.21992573364714	0.219506831785228
URA 0.047	Y53G8AR.9	0.0355980092510912	0.0215006679578714
URA 0.047	Y55F3AM.14	0.0821456429115807	NA
URA 0.047	Y56A3A.18	0.0508804276275283	0.0459867533433055
URA 0.047	zfh-2	NA	0.0414232196853048
URA 0.047	zim-3	0.0084658354514713	0
URA 0.047	ZK546.5	0.113363497386604	0.162197569475235
URA 0.047	ztf-1	0.0616808872829934	0.0706536665512692
URA 0.047	ztf-26	0.108034660387894	NA
URB 0.042	aha-1	0.0392595420317417	0.117744791341423
URB 0.042	atf-7	0	0.0229956275710725
URB 0.042	C34B4.2	0.0665641728026487	NA
URB 0.042	cebp-1	NA	0.00617006634421795
URB 0.042	ceh-18	0.0235341567214653	NA
URB 0.042	ceh-58	NA	0.0224130440908927
URB 0.042	chd-7	0.0331218368343683	NA
URB 0.042	crh-2	0.0389829775313091	NA
URB 0.042	ctbp-1	0.179366369447047	0.211711811640266
URB 0.042	egl-18	NA	0.0970055096623477
URB 0.042	egl-27	0.0298328855345913	0.0515863078084362

URB 0.042	egl-44	0.00489568057226685	0
URB 0.042	ekl-4	NA	0.119422363668025
URB 0.042	F22D6.2	0.0957303763941529	0.00383038213770478
URB 0.042	F57A8.1	0.113462890082581	0.21545951528387
URB 0.042	hif-1	0.0176032451118456	0.0293471085096393
URB 0.042	hmg-1.1	0	0.00688798760907489
URB 0.042	hsf-1	0.0463713336312539	0.028873656042997
URB 0.042	isw-1	NA	0.00946552308213566
URB 0.042	lin-13	0.0132946964661045	0.0358511400634646
URB 0.042	lin-14	0.0243525351094399	0.034674386378927
URB 0.042	lin-39	0.00310533264847392	NA
URB 0.042	lin-40	0.121544605419967	0.0561256153704957
URB 0.042	lin-54	0.0270937956546734	NA
URB 0.042	lsy-2	0.0158104046839349	NA
URB 0.042	madf-5	0.144638626497533	NA
URB 0.042	madf-6	NA	0.0150370812120183
URB 0.042	mbf-1	0	0.0076807325235352
URB 0.042	mdt-29	NA	0.0662213975205091
URB 0.042	nfyb-1	0.0129399691550455	NA
URB 0.042	nhr-6	NA	0.00916105453425161
URB 0.042	nhr-71	0.000385018980615687	0.0212470325385687
URB 0.042	pbrm-1	0.056514397498801	0.0211067138228955
URB 0.042	R02D3.7	0.0146443585047036	0.00660563363854119
URB 0.042	row-1	0.0230016782005521	NA
URB 0.042	saeg-2	0	0.0109939843489129
URB 0.042	sea-2	0.0442727158914748	NA
URB 0.042	somi-1	0	0.000192912052194892
URB 0.042	syd-9	0.00561710366401504	0.000540782868585208
URB 0.042	T26A5.8	0.127115165497846	0.0500062793696091
URB 0.042	unc-62	NA	0.00770386783089943
URB 0.042	unc-86	0.124039437717053	0.210531096662655
URB 0.042	Y55F3AM.14	0.0541486555094214	NA
URB 0.042	Y56A3A.18	NA	0.0657871469245642
URB 0.042	zag-1	0.0272525625783429	NA
URB 0.042	ZK546.5	0.0497666168414856	0.0786780176538536
URB 0.042	ztf-1	0.00211138198490312	0.0675523265120005
URX_AQR_PQR 0.041	aha-1	0.157137026585386	0.197441810786196
URX_AQR_PQR 0.041	alr-1	0.166381652507158	0.165449011509144
URX_AQR_PQR 0.041	cebp-1	0.0034553929055685	0.0128595309403875
URX_AQR_PQR 0.041	crh-2	0.0230972529753578	0.0150644444124456
URX_AQR_PQR 0.041	ctbp-1	0.139575891676675	0.11144121292764
URX_AQR_PQR 0.041	daf-19	0.0804321782173922	0.0943977739833068
URX_AQR_PQR 0.041	egl-13	0.0921188055699697	0.0693086863471077

URX_AQR_PQR 0.041	egl-18	0.0128617898086857	NA
URX_AQR_PQR 0.041	ekl-4	0.0533633945438358	0.054963096450444
URX_AQR_PQR 0.041	F22D6.2	0.00827424230566481	0
URX_AQR_PQR 0.041	fkh-10	NA	0.0288860445485515
URX_AQR_PQR 0.041	fkh-8	0.0393527693736002	0.0465317281348191
URX_AQR_PQR 0.041	hif-1	0.00312665989866098	0.0104067714332627
URX_AQR_PQR 0.041	hinf-1	0.117404854425402	0.0981542806238449
URX_AQR_PQR 0.041	hsf-1	0.00366772905938039	0.0125513364920909
URX_AQR_PQR 0.041	lag-1	0	0.00672754184549861
URX_AQR_PQR 0.041	lim-7	0.0501835396537882	0.0601028315919538
URX_AQR_PQR 0.041	lin-11	0.198125698456165	0.230606475934817
URX_AQR_PQR 0.041	lin-14	0.0192307037461672	0.0135920337763112
URX_AQR_PQR 0.041	lin-26	0.0749467775545801	0.0668291577360144
URX_AQR_PQR 0.041	lin-40	0.0931240501932864	0.049663264290733
URX_AQR_PQR 0.041	lsy-2	0.0110211526052726	0.00636454192237353
URX_AQR_PQR 0.041	madf-5	0.0878248262930669	0.0633149321244611
URX_AQR_PQR 0.041	mdt-29	0.0100132808849418	0.0119490944798191
URX_AQR_PQR 0.041	nhr-11	0.0303693648514917	0.0356676489166937
URX_AQR_PQR 0.041	pag-3	0.0339874825543796	0.0335892595684637
URX_AQR_PQR 0.041	pat-9	0.0808859618830041	0.0635922389589386
URX_AQR_PQR 0.041	sox-4	0.0105963976497264	NA
URX_AQR_PQR 0.041	sptf-2	0.313805787465315	NA
URX_AQR_PQR 0.041	unc-55	NA	0.00150882968180439
URX_AQR_PQR 0.041	unc-86	0.0466541124378758	0.056832759868341
URX_AQR_PQR 0.041	Y53G8AR.9	0.0129027217381791	0.00386979653142855
URX_AQR_PQR 0.041	Y56A3A.18	0.0322340065188873	0.0375392695324425
URX_AQR_PQR 0.041	zfh-2	0.0425616489506885	0.0371858407231589
URX_AQR_PQR 0.041	zip-4	0	0.00515227068207078
URX_AQR_PQR 0.041	ztf-26	0.0548492615836275	0.0119550555013826
URY 0.046	aha-1	NA	0.195440511907826
URY 0.046	atf-7	0.0160522124644699	0.0132636324128312
URY 0.046	attf-6	NA	0.00146132463342656
URY 0.046	C34B4.2	NA	0.21173221962776
URY 0.046	cebp-1	0.00867547434050476	NA
URY 0.046	ceh-18	NA	0.0508753720860461
URY 0.046	ceh-27	NA	0.0560989218176598
URY 0.046	ceh-32	0.434291386837066	0.457257047234768
URY 0.046	cey-2	0.0101501597216489	0
URY 0.046	crh-2	0.0481234666774585	0.0406776088936861
URY 0.046	ctbp-1	0.13211442348933	0.169672621347072
URY 0.046	daf-19	0.0886771043542308	0.0695057166600806
URY 0.046	egl-18	0.155354938811601	0.0981242283585171
URY 0.046	egl-27	0.0230101835415679	0

URY 0.046	ekl-4	0.0655489181713701	0.0802308984571469
URY 0.046	F22D6.2	0.179373759392854	0.020786842516546
URY 0.046	F33H1.4	0.0122519487688109	NA
URY 0.046	F57A8.1	0.0697524350527316	0
URY 0.046	fkh-8	NA	0.0166098443050273
URY 0.046	gei-8	0.0240463240684035	0
URY 0.046	hif-1	0.0310884321673292	0
URY 0.046	hlh-8	0.00847739063925711	NA
URY 0.046	hmg-1.1	0.0251800593097525	0.0189412792125765
URY 0.046	hmg-11	0.00401132379237981	0
URY 0.046	hsf-1	0.0146609860882885	0.0113334364227116
URY 0.046	lag-1	0.0979890303074771	0.121667536460276
URY 0.046	lim-7	0.0486327923765744	0
URY 0.046	lin-11	0.169704192097046	NA
URY 0.046	lin-14	0.0647714104039049	NA
URY 0.046	lin-26	NA	0.0658258448274685
URY 0.046	lin-40	0.121741486368762	0
URY 0.046	lin-54	0.0113054219172212	NA
URY 0.046	lsy-2	NA	0.0295614924298861
URY 0.046	madf-5	0.0947302707023078	NA
URY 0.046	madf-6	0.00773862537072456	NA
URY 0.046	mbf-1	0.228682259853308	0
URY 0.046	mdt-29	0.0505236424516431	0.0324043590552509
URY 0.046	nfya-1	NA	0.0249526642337028
URY 0.046	nhr-6	0.00463200045667665	0
URY 0.046	pag-3	0.057549435316711	0.0660675782233426
URY 0.046	pbrm-1	0.0578567947477016	0.0147776104744071
URY 0.046	rcor-1	0.00712899875541228	0
URY 0.046	row-1	0	0.0318442036744218
URY 0.046	sem-4	0.0318778670598711	NA
URY 0.046	sup-37	0.0511997810092943	NA
URY 0.046	T26A5.8	0.0744533868823971	0.0320917099063887
URY 0.046	unc-42	0.0530768806433212	NA
URY 0.046	unc-86	0.153454532982861	0.168512753881615
URY 0.046	Y53G8AR.9	0.0615112206644169	NA
URY 0.046	Y55F3AM.14	0.0522473207508124	NA
URY 0.046	Y56A3A.18	0.0634774625892608	0.0518130846780776
URY 0.046	zfh-2	0.0603935848960206	0.0362074856780437
URY 0.046	zim-3	0.0289122166375553	0
URY 0.046	ZK546.5	NA	0.04370017802126
URY 0.046	ztf-1	0.0754416216801855	NA
Uterine muscle 0.058	alr-1	NA	0.126356851210585
Uterine muscle 0.058	baz-2	0.00726008536057137	0.00885786200949214

Uterine muscle 0.058	ceh-18	0.355879690544925	0.360504544208369
Uterine muscle 0.058	ceh-22	0.0601776630887459	0.0661380241707793
Uterine muscle 0.058	ceh-58	0.0216740150059516	0.0202500004570392
Uterine muscle 0.058	chd-7	0.0282828921833732	0.016233482532117
Uterine muscle 0.058	daf-16	0.0359627350592365	0.0312789694859603
Uterine muscle 0.058	daf-19	0.0688714146772288	0.0660902792518617
Uterine muscle 0.058	daf-8	0.0461776758774564	NA
Uterine muscle 0.058	egl-18	0.0953408100735123	0.0790032052338354
Uterine muscle 0.058	egl-5	NA	0.0150129043906964
Uterine muscle 0.058	ekl-4	0.0514735814372162	0.0579168733905011
Uterine muscle 0.058	eor-1	0.00155570997566372	0
Uterine muscle 0.058	ets-5	NA	0.00814767924732266
Uterine muscle 0.058	hinf-1	0.0657756102128327	0.0793530490066706
Uterine muscle 0.058	hlh-1	0.0777434134029785	0.0751357970434018
Uterine muscle 0.058	hlh-11	0.0104793255489451	0.00574641485586736
Uterine muscle 0.058	hlh-8	0.443172753915572	0.442433471407611
Uterine muscle 0.058	hsf-1	0.0300242862008834	0.0304427273997333
Uterine muscle 0.058	lim-7	0.0331232423674727	0.0425436240731464
Uterine muscle 0.058	lin-14	0.0267678940053072	0.0262378712933143
Uterine muscle 0.058	lin-26	0.0220042376232038	0.021514959235428
Uterine muscle 0.058	lsy-2	0.00471529259561621	0.0041135633703421
Uterine muscle 0.058	M03D4.4	0.0288894957693306	0.0383065283697573
Uterine muscle 0.058	madf-3	0.0150547095721507	0.0186450822704086
Uterine muscle 0.058	madf-5	0.0462086444267361	0.037725248291009
Uterine muscle 0.058	nhr-129	0.0310785787509003	0.0306823049486329
Uterine muscle 0.058	nhr-19	0.0224024123170311	0.0241008002119121
Uterine muscle 0.058	nhr-71	0.0411130271077893	0.0399111490622465
Uterine muscle 0.058	pat-9	1.50830785821233	1.53078505519193
Uterine muscle 0.058	R02D3.7	0	0.00195727480212384
Uterine muscle 0.058	somi-1	0.0219169146114665	0.0265414257151918
Uterine muscle 0.058	sptf-2	0.310104973825259	0.309730503334645
Uterine muscle 0.058	syd-9	0.349145254978947	0.383660286710652
Uterine muscle 0.058	unc-120	0.0870464087151835	0.0825219715752454
Uterine muscle 0.058	Y56A3A.18	0.0171608892818442	0.0310754775684714
Uterine muscle 0.058	zfh-2	0.0709165944270594	0.0718601635523845
Uterine muscle 0.058	ZK546.5	0.0283352205401642	0.068185751398364
Uterine muscle 0.058	ztf-7	0.0371047494183853	0.0297678990111557
Uterine seam cells 0.023	alr-1	0.169911691859745	NA
Uterine seam cells 0.023	attf-6	0.00863758889402154	0.00999547337273179
Uterine seam cells 0.023	blmp-1	0.00796612188109935	0.00434010106327303
Uterine seam cells 0.023	cebp-1	0.00886894522564632	0.00446891958459396
Uterine seam cells 0.023	crh-2	0.00126228765078066	0.00126471936371352
Uterine seam cells 0.023	D1046.2	0.00551948984233705	3.17781326698295e-05

Uterine seam cells 0.023	daf-19	0.0145729317627075	0.0131058859839961
Uterine seam cells 0.023	dve-1	0.000864153126420834	0.00143128994910809
Uterine seam cells 0.023	egl-43	0.0135887825192123	0.0169014428423319
Uterine seam cells 0.023	ekl-4	0.0167967381933322	0.0140388787121642
Uterine seam cells 0.023	ets-5	0.0713281854181834	NA
Uterine seam cells 0.023	F22D6.2	0.0685558953647722	0
Uterine seam cells 0.023	hinf-1	0.0251886120999877	0.0286844624826161
Uterine seam cells 0.023	hlh-8	0.0167282848996482	NA
Uterine seam cells 0.023	lag-1	0	0.00213659206173421
Uterine seam cells 0.023	let-607	0.0102389363737518	0.00850322508800746
Uterine seam cells 0.023	lin-14	0.0109851038090657	0.00145862332009043
Uterine seam cells 0.023	lin-26	0.0283272035831903	0.0240655821854703
Uterine seam cells 0.023	lin-40	0.0650321580074087	0.038733102150559
Uterine seam cells 0.023	madf-2	0.0405573487204509	0
Uterine seam cells 0.023	madf-3	0.0174108566588887	NA
Uterine seam cells 0.023	madf-5	0.0451846886339865	0.0360888792035034
Uterine seam cells 0.023	nhr-129	NA	0.0130218111861842
Uterine seam cells 0.023	nhr-237	0.0138444208914014	NA
Uterine seam cells 0.023	nhr-6	0.0400503581948606	NA
Uterine seam cells 0.023	pat-9	0.11294407538106	0.0747641240771347
Uterine seam cells 0.023	pbrm-1	0.0169368665329564	0.0162494984898852
Uterine seam cells 0.023	pha-4	0.0181568601030478	0.01748095147599
Uterine seam cells 0.023	saeg-2	0.0251250345481434	0.0268231230976948
Uterine seam cells 0.023	sma-3	0.0328708190480102	0.0280178090283398
Uterine seam cells 0.023	spr-1	0.142115547305632	0.156716825180315
Uterine seam cells 0.023	spr-3	0.734580872166087	0.708759099713732
Uterine seam cells 0.023	sptf-2	0.0983269476033074	NA
Uterine seam cells 0.023	T26A5.8	0.000781037059678225	0.00409715051632616
Uterine seam cells 0.023	xbp-1	0.040971126200152	0.0266975770480155
Uterine seam cells 0.023	Y56A3A.18	0.0116352100087778	0.00763093669216674
Uterine seam cells 0.023	zfh-2	0.0057050115238326	0.00268266303643455
Uterine seam cells 0.023	ZK546.5	0.00852895962509097	0.00271681047158559
Uterine seam cells 0.023	ztf-26	0.00215685030756227	0
Uterine seam cells 0.023	ztf-7	0.0117468216760745	0.0049322192050085
Uterine toroid 0.030	attf-6	0.0152783473343727	0.0160742823706724
Uterine toroid 0.030	B0035.1	0.217192286293973	0.301777348608663
Uterine toroid 0.030	blmp-1	NA	0.00335880394282157
Uterine toroid 0.030	cebp-1	0.00537421845915326	0.00788172301239733
Uterine toroid 0.030	crh-2	0.0104154051009631	0.0153674130201839
Uterine toroid 0.030	daf-19	0.0444071512633425	0.0596357237327474
Uterine toroid 0.030	dve-1	0.013306781498309	0.0106089432260959
Uterine toroid 0.030	ekl-4	0.0113246454109959	0.0307670812617757
Uterine toroid 0.030	elt-3	0.0208014387720102	0.0158736669585704

Uterine toroid 0.030	hinf-1	0.050241265783333	NA
Uterine toroid 0.030	let-607	0.0177001791365399	0.00959467975712527
Uterine toroid 0.030	lin-14	NA	0.0159496093127335
Uterine toroid 0.030	lin-26	0.0257991090878087	0.0320836596995859
Uterine toroid 0.030	lin-40	0.091486446377967	0.0867515508300243
Uterine toroid 0.030	lsy-2	0.00470748819043808	0.00856152302469045
Uterine toroid 0.030	mdt-29	0.0154320027887084	0.0274366790336978
Uterine toroid 0.030	nhr-11	0.0238372297438142	NA
Uterine toroid 0.030	nhr-129	0.0166682575380129	NA
Uterine toroid 0.030	pat-9	NA	0.0688787075342585
Uterine toroid 0.030	pha-4	0.00535665075571834	0.00166855128952096
Uterine toroid 0.030	R02D3.7	0.00859331712000127	0.0159317415676224
Uterine toroid 0.030	sma-3	0.0432038370537424	NA
Uterine toroid 0.030	spr-1	0.0765185445742032	0.0696551585271795
Uterine toroid 0.030	spr-3	0.605431265846144	0.595414942141056
Uterine toroid 0.030	Y53G8AR.9	0.00897965200811769	0.00956084519260436
Uterine toroid 0.030	Y56A3A.18	0.0275143339084137	0.0425043772546368
Uterine toroid 0.030	zfh-2	0.000129773084454133	0.000960494406788286
Uterine toroid 0.030	ZK546.5	0.240514166320604	0.356873351232521
Uterine-vulval cells 0.023	alr-1	0.145997752223225	0.138552853723467
Uterine-vulval cells 0.023	attf-6	0.00474557160502754	0.00213489987738014
Uterine-vulval cells 0.023	B0035.1	0.316670702059951	0.245806454002538
Uterine-vulval cells 0.023	blmp-1	0.0106469236715611	0.00684371091714548
Uterine-vulval cells 0.023	cebp-1	0.0145156070501992	0.00996528466259675
Uterine-vulval cells 0.023	ceh-40	0.0465760541027236	NA
Uterine-vulval cells 0.023	crh-2	0.0138703053721604	0.00938907957743226
Uterine-vulval cells 0.023	daf-19	0.0449671064231255	0.0442525215554542
Uterine-vulval cells 0.023	dve-1	0.0164450016763604	0.00764682796123069
Uterine-vulval cells 0.023	ekl-4	0.0331508946237567	0.0293516275384404
Uterine-vulval cells 0.023	elt-3	0.0112053043821429	0.00670195186050413
Uterine-vulval cells 0.023	hinf-1	0.0351273220516924	0.0403186677959508
Uterine-vulval cells 0.023	hlh-8	0.00865197368297576	0.00157757713412592
Uterine-vulval cells 0.023	hmg-1.1	0.00111128056710794	0
Uterine-vulval cells 0.023	jun-1	0.00674007513065803	0
Uterine-vulval cells 0.023	K12H6.12	0.016627952113548	NA
Uterine-vulval cells 0.023	let-607	0.0205069464696955	0.0152903102371695
Uterine-vulval cells 0.023	lim-7	0.00834112235659024	0.0091837950688122
Uterine-vulval cells 0.023	lin-14	0.0182171682151212	0.0116672886385361
Uterine-vulval cells 0.023	lin-26	0.0475439842634863	0.0376520274772715
Uterine-vulval cells 0.023	lin-40	0.0845996761762205	0.0515858216972215
Uterine-vulval cells 0.023	lsy-2	0.00322037935763402	0
Uterine-vulval cells 0.023	madf-3	0.0241396640276766	0.0264766935026157
Uterine-vulval cells 0.023	madf-5	0.06565593938429	0.0372258846202822

Uterine-vulval cells 0.023	mdt-29	0.0452021704308132	0.0360949004616983
Uterine-vulval cells 0.023	nhr-11	0.0359983313055713	0.0284835914835875
Uterine-vulval cells 0.023	nhr-129	0.00713827746521958	0.00517582257687715
Uterine-vulval cells 0.023	nhr-237	0.0832318423463209	NA
Uterine-vulval cells 0.023	nhr-25	NA	0.00653131739568354
Uterine-vulval cells 0.023	nhr-6	0.0424077045133398	0.0348872803097568
Uterine-vulval cells 0.023	pag-3	0.0285507063549772	0.0194722524844035
Uterine-vulval cells 0.023	pat-9	0.0732388450811408	0.0655074947457873
Uterine-vulval cells 0.023	pbrm-1	0.000533356892418258	0
Uterine-vulval cells 0.023	pha-2	NA	0.00818429926541585
Uterine-vulval cells 0.023	pha-4	0.00814784326603002	0.00662902478777585
Uterine-vulval cells 0.023	R02D3.7	0.0147079592087565	0.00706259153366513
Uterine-vulval cells 0.023	saeg-2	0.020762837798941	0.00701819167415381
Uterine-vulval cells 0.023	sma-3	0.0207308410622682	0.00998172737162406
Uterine-vulval cells 0.023	spr-1	0.0119576115552138	0.00405507763828246
Uterine-vulval cells 0.023	spr-3	0.361731656890426	0.321333454695729
Uterine-vulval cells 0.023	sptf-2	0.138762436476187	NA
Uterine-vulval cells 0.023	tbx-9	NA	0.192122119674036
Uterine-vulval cells 0.023	xbp-1	0.00669580076597132	0
Uterine-vulval cells 0.023	Y53G8AR.9	0.0221790459006181	0.01948664262103
Uterine-vulval cells 0.023	Y56A3A.18	0.0351219493242742	0.0314546282823903
Uterine-vulval cells 0.023	zfh-2	0.00802163745199206	0.00399966304899921
Uterine-vulval cells 0.023	ZK546.5	0.271357105868872	0.282449665664686
VC 0.039	aha-1	0.0195398395493758	0.0335543780375644
VC 0.039	alr-1	NA	0.138150351118758
VC 0.039	attf-6	0.00262243993084561	0.00786359200687162
VC 0.039	cebp-1	0	0.00224184339358187
VC 0.039	ceh-27	0.00654591156584563	0.0202103327776188
VC 0.039	ceh-48	0.0140745114917468	0.0255440134259912
VC 0.039	ceh-63	0.175868866864512	0.15609526475043
VC 0.039	chd-7	0	0.00715555404797979
VC 0.039	crh-2	0.0322464370765535	0.0423369029998067
VC 0.039	ctbp-1	0.128116727023351	0.125991327415213
VC 0.039	daf-19	0.160780956251349	0.156086657466873
VC 0.039	egl-13	0.0529693500821608	0.0649348523720772
VC 0.039	egl-18	0.150788166864775	0.176231773615458
VC 0.039	egl-27	0	0.0125267817524572
VC 0.039	ekl-4	0.032920362719719	0.0364793649212408
VC 0.039	elt-4	0.0162492259615469	0
VC 0.039	ets-5	0.064851374469658	0.0755161238351634
VC 0.039	F22D6.2	0.0539670351425675	0.00770734505448831
VC 0.039	fkh-10	0.0153655840541008	NA
VC 0.039	hinf-1	0.107742171093032	0.121389840140983

VC 0.039	hlh-8	NA	0.0248900185999587
VC 0.039	hsf-1	0	0.000539653588771758
VC 0.039	isw-1	0.0194524564427809	0.0250357615237063
VC 0.039	K09A11.1	0	0.0160484878802448
VC 0.039	lag-1	0	0.0331942299374319
VC 0.039	lim-7	0.0264299174437166	0.0372531889315487
VC 0.039	lin-11	0.151982701003903	0.163544395281762
VC 0.039	lin-14	0.0311075073196	0.0412640259083607
VC 0.039	lin-26	0.0718047547869991	0.0637341758526936
VC 0.039	lin-39	0.0289569884933375	0.0359449154991166
VC 0.039	lin-40	0.0570971097507188	0.0543563312318017
VC 0.039	lsy-2	0.0177015613526131	0.0252231878859135
VC 0.039	mab-5	NA	0.00533019013285215
VC 0.039	madf-3	0.0529047150308427	0.0557277832593211
VC 0.039	madf-5	0.0434290511228774	0.0204334448202554
VC 0.039	mbf-1	0.103893908113443	0.133020796956482
VC 0.039	mdt-29	0.00067980614932718	0.0115162360412968
VC 0.039	nfya-1	0.00569271177437138	0.0113960105719376
VC 0.039	nfyb-1	0	0.00538816363904979
VC 0.039	nhr-11	0.019201248621984	0.0158354234989143
VC 0.039	pag-3	0.0320848958235414	NA
VC 0.039	pbrm-1	0	9.63931927227248e-05
VC 0.039	row-1	0.0287148202011109	0.0606725612648763
VC 0.039	sem-4	0	0.00578141607624621
VC 0.039	somi-1	0	0.000899843547220403
VC 0.039	sox-4	NA	0.00591751855036691
VC 0.039	syd-9	0.0285352325232558	0.0374321649176394
VC 0.039	tlp-1	0.0119595089575674	0.00493597523942954
VC 0.039	unc-42	0.00936110872718992	0.0169947729154922
VC 0.039	unc-55	0.0226744715723378	NA
VC 0.039	unc-62	0.00674774191344605	0.00828617521966118
VC 0.039	unc-86	0.00181296194348946	0.0107698293409041
VC 0.039	Y53G8AR.9	0.0128220862443043	0.0126039388795663
VC 0.039	Y55F3AM.14	0.0158574412557669	0.0364344803549746
VC 0.039	Y56A3A.18	0.0372213401524471	0.0389072208923982
VC 0.039	zag-1	0.123523763502354	0.127489553729228
VC 0.039	zfh-2	0.0416905448634456	0.0374615239576447
VC 0.039	ZK546.5	0	0.0619337320642001
VC 0.039	ztf-1	0.00884598586719575	0
VC 0.039	ztf-26	0.0618661159975747	NA
VC_4_5 0.037	atf-7	0	0.00986902648064864
VC_4_5 0.037	attf-6	0	0.00474095286114392
VC_4_5 0.037	cebp-1	0.00140672483720301	0.00966608129348445

VC_4_5 0.037	ceh-48	0.00827037732907791	0.0231610055480947
VC_4_5 0.037	chd-7	0.0103887922762274	0.0376654342383965
VC_4_5 0.037	crh-2	0.0379713405526528	0.0380206691139064
VC_4_5 0.037	ctbp-1	0.133381746291153	0.149692080912316
VC_4_5 0.037	dxbp-1	0	0.000704828521320985
VC_4_5 0.037	egl-18	0.119641848418799	NA
VC_4_5 0.037	egl-27	0.0120925101864719	0.0164225020867919
VC_4_5 0.037	ekl-4	0.0412129826399163	0.050142536203252
VC_4_5 0.037	ets-5	0.0616527242785882	NA
VC_4_5 0.037	F22D6.2	0.0894174328774367	0.0266787312630836
VC_4_5 0.037	F44E2.7	0	0.00181872394419636
VC_4_5 0.037	hif-1	0.00129465083805409	0.00647692119117618
VC_4_5 0.037	hinf-1	0.125633673837854	NA
VC_4_5 0.037	hlh-8	0.0346835932176074	NA
VC_4_5 0.037	hmg-1.1	0	0.00501864969938572
VC_4_5 0.037	hsf-1	0	0.016850485520844
VC_4_5 0.037	isw-1	0.00430339658395139	0.0415265589046984
VC_4_5 0.037	lag-1	0	0.0831676689006707
VC_4_5 0.037	lim-7	0.00498002387223583	NA
VC_4_5 0.037	lin-11	0.149993743393366	0.174917045592857
VC_4_5 0.037	lin-13	0	0.00701788963283619
VC_4_5 0.037	lin-14	0.0343213244837648	NA
VC_4_5 0.037	lin-26	0.0827059722196792	0.0849447289186337
VC_4_5 0.037	lin-39	0.0222703859989773	0.0513913820458281
VC_4_5 0.037	lin-40	0.111717913333185	0.0450128170755798
VC_4_5 0.037	lin-54	0	0.00389505559588647
VC_4_5 0.037	lsy-2	0.0268624208344266	0.0342690085166652
VC_4_5 0.037	mab-5	0	0.00639504559316648
VC_4_5 0.037	madf-3	0.0484542892229152	NA
VC_4_5 0.037	madf-5	0.0852984702711386	0.0413612524004343
VC_4_5 0.037	madf-9	NA	0.0422024478952283
VC_4_5 0.037	mbf-1	0.13244141395888	0.122095197544518
VC_4_5 0.037	mdt-29	0.015931618090837	0.0110147701565152
VC_4_5 0.037	nfyb-1	0	0.00229074544735284
VC_4_5 0.037	pag-3	0.0217637156012785	NA
VC_4_5 0.037	pbrm-1	0	0.0290490766246853
VC_4_5 0.037	R02D3.7	0.002022759628139	0.0105112401230085
VC_4_5 0.037	rcor-1	0	0.000440960368826855
VC_4_5 0.037	row-1	5.89713567540734e-05	0.0184508189735792
VC_4_5 0.037	somi-1	0	0.0107895089688801
VC_4_5 0.037	unc-42	0.0136387481684446	0.0230919707408934
VC_4_5 0.037	unc-62	0.00597988899568602	0.0238409337332834
VC_4_5 0.037	unc-86	0.0690134299434223	NA

VC_4_5 0.037	unc-98	0	0.0268791782814326
VC_4_5 0.037	Y53G8AR.9	NA	0.0350596966875234
VC_4_5 0.037	Y56A3A.18	0.0469345492573306	NA
VC_4_5 0.037	zag-1	0.12499651681367	0.172252747604179
VC_4_5 0.037	zfh-2	0.0444002929807445	NA
VC_4_5 0.037	zim-3	0.00103603814730747	0.000763113861080507
VC_4_5 0.037	ZK546.5	0.0328133326505553	NA
VC_4_5 0.037	ztf-1	0.0218531704355404	NA
VD_DD 0.042	aha-1	0.172980609185311	0.192958888156996
VD_DD 0.042	alr-1	0.144033861438091	0.140306405391989
VD_DD 0.042	attf-6	0.0060372310768643	0.00300364673290413
VD_DD 0.042	ceh-20	0.0154817189291811	0.0231723522421546
VD_DD 0.042	ceh-27	0.120704521540193	0.121710211200627
VD_DD 0.042	ceh-40	NA	0.0762997230441072
VD_DD 0.042	ceh-63	NA	0.0692230128353045
VD_DD 0.042	crh-2	0.0334789052421196	0.0272634091042808
VD_DD 0.042	ctbp-1	0.0894276074933137	0.0844294446958095
VD_DD 0.042	daf-19	0.0561142703807422	0.0490909487194312
VD_DD 0.042	drap-1	0.0300080858426774	0.0163548625282143
VD_DD 0.042	egl-18	0.0961886661868218	0.0766095757723708
VD_DD 0.042	ekl-4	0.0350363593999278	0.0332297738456033
VD_DD 0.042	elt-4	0.0442915691031802	0.00767984757811139
VD_DD 0.042	F22D6.2	0.103038858318417	0.0170287779017439
VD_DD 0.042	fkh-10	0.0331995088010614	0.0394691271792821
VD_DD 0.042	hif-1	0.00615379409526224	0.00614009858615628
VD_DD 0.042	hinf-1	0.122543335777589	0.119583785246099
VD_DD 0.042	hsf-1	0.00450799468864169	9.4660556822048e-05
VD_DD 0.042	K12H6.12	NA	0.0358758801341204
VD_DD 0.042	lag-1	0.0763749906816005	0.0847408797716595
VD_DD 0.042	lim-7	0.0162065631621542	0.0149814523310186
VD_DD 0.042	lin-11	0.0646684901615443	0.0704909439972703
VD_DD 0.042	lin-14	0.0405235939671348	0.0397771797284473
VD_DD 0.042	lin-26	0.0693600039348159	0.0590629843524599
VD_DD 0.042	lin-39	0.067031715801339	0.0762731143712149
VD_DD 0.042	lin-40	0.0641418456103009	0.0355266353555439
VD_DD 0.042	lsy-2	0.00152908159256349	0
VD_DD 0.042	mab-5	0.114010690313635	0.116402634486767
VD_DD 0.042	madf-3	0.0490990073712363	0.0487697368401791
VD_DD 0.042	madf-5	0.0618752135768517	0.0261677212252209
VD_DD 0.042	madf-9	0.028451678372489	0
VD_DD 0.042	mbf-1	0.136670610004668	0.0562240618738621
VD_DD 0.042	mdt-29	0.0439263763181426	0.0512824018586271
VD_DD 0.042	nfya-2	0.0171213283813158	0.0265099405019216

VD_DD 0.042	nfyb-1	0.0264556325995416	0.0305335482128
VD_DD 0.042	nhr-11	0.0124878939894243	0.00220712839570787
VD_DD 0.042	nhr-232	0.00570058651329349	NA
VD_DD 0.042	pag-3	0.056898952397947	0.0459408733671698
VD_DD 0.042	pat-9	0.208342756922465	0.145907283262158
VD_DD 0.042	sem-4	0.00445135843070032	0.00569133751348547
VD_DD 0.042	sptf-2	0.293990602530359	0.295863342589106
VD_DD 0.042	sup-37	0.00673861639721154	0
VD_DD 0.042	unc-30	0.830534346663858	0.772349325697629
VD_DD 0.042	unc-42	0.0130627210192561	0.0154769371000402
VD_DD 0.042	unc-55	0.0861108586742563	0.0870929297196951
VD_DD 0.042	Y53G8AR.9	0.00492667162237772	0.0011819981059131
VD_DD 0.042	Y55F3AM.14	0.154230441017548	NA
VD_DD 0.042	Y56A3A.18	0.0429663994111891	0.037512006143142
VD_DD 0.042	zag-1	0.0802927372224218	0.0763683349813417
VD_DD 0.042	zfh-2	0.0429592523061897	0.0391414831555848
VD_DD 0.042	zim-3	0.0603123180398516	0.0641162443165605
VD_DD 0.042	ztf-1	0.127999381479245	0.10662510667408
VD_DD 0.042	ztf-26	0.0679333184915571	0.0340353249687218
Vulval cells 0.051	alr-1	0.120333878867311	0.136647991375519
Vulval cells 0.051	blmp-1	0.0666605531646571	0.0654220599746514
Vulval cells 0.051	ctbp-1	0.031054590543813	0.0163482516959922
Vulval cells 0.051	daf-19	0.0180408199267298	0.0135180000094937
Vulval cells 0.051	egl-27	0.0353859874541173	0.0218557760359199
Vulval cells 0.051	egrh-3	0.152528594906073	0.149256487728786
Vulval cells 0.051	ekl-4	0.0138884965538039	0.0241821229368282
Vulval cells 0.051	elt-4	0.0574110965379541	0.0554093922093563
Vulval cells 0.051	F22D6.2	0.331541438663625	0.292398762677771
Vulval cells 0.051	gei-8	0.0264903091013215	0.0282101044756999
Vulval cells 0.051	grh-1	0.00136200998305357	0.00551820289874559
Vulval cells 0.051	hinf-1	0.0581967246983609	0.072641133546821
Vulval cells 0.051	let-607	0.00428762436541442	0.00675863857207274
Vulval cells 0.051	lin-14	0.0146760257131337	0.0080970683146339
Vulval cells 0.051	lin-26	0.140267348424185	0.13988397951689
Vulval cells 0.051	lin-40	0.318951288861832	0.304973270578678
Vulval cells 0.051	madf-2	0.193841996959619	0.166918426610453
Vulval cells 0.051	madf-3	0.0400776874005093	0.0464982021180022
Vulval cells 0.051	madf-5	0.472896562522876	0.441940526102545
Vulval cells 0.051	mdt-29	0.0193233793789065	0.0324861361369819
Vulval cells 0.051	mec-3	0.346863225728323	0.349600533734591
Vulval cells 0.051	nhr-11	0.0552713326847132	0.0597127214885352
Vulval cells 0.051	nhr-232	0	0.0294210039860834
Vulval cells 0.051	nhr-25	0.077436514722703	0.0769404021296514

Vulval cells 0.051	nhr-76	0.0724036651419998	0.0484691316270297
Vulval cells 0.051	nhr-84	0.248957939762509	0.0444705109580578
Vulval cells 0.051	nhr-85	0.0929491973221147	0.0912075435190978
Vulval cells 0.051	pag-3	0.0744966021353857	NA
Vulval cells 0.051	pat-9	0.0739388496137103	0.0672815256687895
Vulval cells 0.051	pbrm-1	0.00865968002770687	0.00479279283509223
Vulval cells 0.051	R02D3.7	0.00753971734321124	0
Vulval cells 0.051	snu-23	0	0.00285443880726898
Vulval cells 0.051	spr-3	0.230092602592742	0.219691308478522
Vulval cells 0.051	sptf-2	0.224388613815214	0.230192683003072
Vulval cells 0.051	T26A5.8	0.149323282579916	0.149342332391069
Vulval cells 0.051	tlp-1	0.0380397277566616	0.0325935537348338
Vulval cells 0.051	Y56A3A.18	0.0155593322565859	0.0146333720439395
Vulval cells 0.051	zfh-2	0.0279628002008676	0.0334418220163504
Vulval cells 0.051	zim-3	0.187332784067251	0.21105085567845
Vulval cells 0.051	ztf-1	0.0249762801738725	0.05999311687417
Vulval cells 0.051	ztf-16	0.0780469899016	0.0856517411963014
Vulval cells 0.051	ztf-26	0.236869818110646	0.222435805088701
XXX 0.044	aha-1	0.0447233826800091	NA
XXX 0.044	attf-6	0.0104312311068292	0.0100798473668326
XXX 0.044	cebp-1	NA	0.00152118678739134
XXX 0.044	ceh-18	0	0.00384401479172452
XXX 0.044	ceh-48	0	0.00394005460532743
XXX 0.044	crh-2	0.0365694607838988	NA
XXX 0.044	ctbp-1	NA	0.108407984148848
XXX 0.044	daf-19	0.139673427328044	0.110783409004759
XXX 0.044	egl-18	0.111783293536417	0.124779655220915
XXX 0.044	egl-27	0.0149731030541355	0.00485112228194809
XXX 0.044	ekl-4	0.091600271194636	0.104160621994548
XXX 0.044	F22D6.2	0.0508533223967482	0
XXX 0.044	hif-1	0.0156189096213928	0.0372528662196661
XXX 0.044	hmg-1.1	0.0221697676776741	0.00503132477365952
XXX 0.044	hsf-1	0.0305962026132656	NA
XXX 0.044	isw-1	0.00233559435110613	0.002429623241528
XXX 0.044	K12H6.12	NA	0.0239902748240987
XXX 0.044	lag-1	0.0149655246884812	0.042468624899284
XXX 0.044	lim-7	0.0534914869065669	0.0492253482537445
XXX 0.044	lin-11	0.243100866042624	0.264493530390218
XXX 0.044	lin-14	0.016748154707154	0.0209008522743777
XXX 0.044	lin-26	0.122768485544668	0.126682946521719
XXX 0.044	lin-40	0.0865158288742172	0.0841595571820755
XXX 0.044	lsy-2	0.0370335542185654	0.0441871594307338
XXX 0.044	madf-5	0.114978561385042	NA

XXX 0.044	madf-6	0.000200718412711511	0
XXX 0.044	madf-9	0.0149487175543131	NA
XXX 0.044	mdt-29	0.0103103202810035	0.0526814927663956
XXX 0.044	nfya-2	0.123352879130996	NA
XXX 0.044	nfyb-1	0.00692788687125753	0.0141526361425063
XXX 0.044	nhr-11	0.027418233474006	NA
XXX 0.044	nhr-232	0.187714728892077	0.119641625645537
XXX 0.044	pag-3	0.0472429069110588	NA
XXX 0.044	pbrm-1	0.0363317364406674	0.0489104807635847
XXX 0.044	row-1	0.0508856473499634	NA
XXX 0.044	T26A5.8	0.0160681516142807	0.00399985335815859
XXX 0.044	unc-120	0.00562983968556415	NA
XXX 0.044	unc-42	0.010202584769701	0.0036834574995295
XXX 0.044	unc-62	0	0.0021008978422621
XXX 0.044	Y53G8AR.9	0.0141262194373077	0.018971717096219
XXX 0.044	Y55F3AM.14	NA	0.0129088566744361
XXX 0.044	Y56A3A.18	0.0664150374273079	0.0672019028417893
XXX 0.044	zfh-2	0.0564032387179061	0.0529884691130992
XXX 0.044	zim-3	0.004109868437712	0.0270476823811183
XXX 0.044	ZK546.5	0.00543828269196513	0.0877380187113671
XXX 0.044	ztf-26	0.0550199000036854	NA
cat-4(+)ptps-1(+) intestine anterior 0.047	akir-1	0.0705695658499789	0.026361106879809
cat-4(+)ptps-1(+) intestine anterior 0.047	alr-1	0.257948766273435	0.264187311881645
cat-4(+)ptps-1(+) intestine anterior 0.047	ceh-40	NA	0.10815703569091
cat-4(+)ptps-1(+) intestine anterior 0.047	ceh-6	NA	0.0325041338816934
cat-4(+)ptps-1(+) intestine anterior 0.047	chd-7	0.0126698503358708	0.0145544590717775
cat-4(+)ptps-1(+) intestine anterior 0.047	crh-2	0.0661048339470261	0.0684778120191752
cat-4(+)ptps-1(+) intestine anterior 0.047	daf-16	0.013666807379455	0.0125848937830234
cat-4(+)ptps-1(+) intestine anterior 0.047	daf-19	0.166878756157105	0.147331668500784
cat-4(+)ptps-1(+) intestine anterior 0.047	dmd-6	0.0218918001773766	0.0174791939573362
cat-4(+)ptps-1(+) intestine anterior 0.047	dve-1	0.000554466821278859	0
cat-4(+)ptps-1(+) intestine anterior 0.047	dxbp-1	0.0133411800770556	0.0123330672036281
cat-4(+)ptps-1(+) intestine anterior 0.047	ekl-4	0.0937188317993554	0.0958161943092233
cat-4(+)ptps-1(+) intestine anterior 0.047	elt-2	0.00798453705347472	0.00698113766739272
cat-4(+)ptps-1(+) intestine anterior 0.047	elt-4	0.038711116038948	0.0131855057136902
cat-4(+)ptps-1(+) intestine anterior 0.047	F33H1.4	0.0124447058490022	0.0140998220917389
cat-4(+)ptps-1(+) intestine anterior 0.047	F44E2.7	0.0321907449811207	0.0198009216611094
cat-4(+)ptps-1(+) intestine anterior 0.047	hinf-1	0.0934948026963587	0.099665166081301
cat-4(+)ptps-1(+) intestine anterior 0.047	hlh-11	0.0121342681118297	0.0116438844349086
cat-4(+)ptps-1(+) intestine anterior 0.047	hlh-8	0.0186729545454338	0.0190294297294749
cat-4(+)ptps-1(+) intestine anterior 0.047	lag-1	0.118494228939258	0.157790081770152
cat-4(+)ptps-1(+) intestine anterior 0.047	let-607	0.0847694625947802	0.0826388065280262
cat-4(+)ptps-1(+) intestine anterior 0.047	lim-7	0.0196473472691538	0.0222748811472096

cat-4(+)ptps-1(+) intestine anterior 0.047	lin-13	0.0271215251634734	0.0286532524576231
cat-4(+)ptps-1(+) intestine anterior 0.047	lin-26	0.110708484125822	0.105686341584015
cat-4(+)ptps-1(+) intestine anterior 0.047	lin-40	0.0243287165104435	0
cat-4(+)ptps-1(+) intestine anterior 0.047	lin-54	0.000477558584196658	0.00541689551238878
cat-4(+)ptps-1(+) intestine anterior 0.047	lsy-2	0.0158743694246481	0.0137011104706393
cat-4(+)ptps-1(+) intestine anterior 0.047	madf-3	0.05662201267043	0.0585226956544762
cat-4(+)ptps-1(+) intestine anterior 0.047	madf-5	0.121528406353338	0.101035599837718
cat-4(+)ptps-1(+) intestine anterior 0.047	madf-6	0.00219135733632143	0.0077636594358551
cat-4(+)ptps-1(+) intestine anterior 0.047	madf-9	0.000226177540263315	0
cat-4(+)ptps-1(+) intestine anterior 0.047	mdt-29	0.156049794599727	0.155549471802312
cat-4(+)ptps-1(+) intestine anterior 0.047	mml-1	0.0100219271156318	0
cat-4(+)ptps-1(+) intestine anterior 0.047	nfyb-1	0	0.00066895876393713
cat-4(+)ptps-1(+) intestine anterior 0.047	nhr-10	0.116225548309516	0.112323394586358
cat-4(+)ptps-1(+) intestine anterior 0.047	nhr-102	0.04140701723112	0.037992126058654
cat-4(+)ptps-1(+) intestine anterior 0.047	nhr-11	0.0143222274191064	0.00570552120403847
cat-4(+)ptps-1(+) intestine anterior 0.047	nhr-80	0	0.00252905750444502
cat-4(+)ptps-1(+) intestine anterior 0.047	pag-3	0.0323771761629079	0.0331792324071001
cat-4(+)ptps-1(+) intestine anterior 0.047	pat-9	0.176466935575171	0.158561503948121
cat-4(+)ptps-1(+) intestine anterior 0.047	R02D3.7	0.0379521350640582	0.0376052293352389
cat-4(+)ptps-1(+) intestine anterior 0.047	saeg-2	0.0822838881639831	0.0858114346270961
cat-4(+)ptps-1(+) intestine anterior 0.047	sem-2	0.139789044347	0.136617183079083
cat-4(+)ptps-1(+) intestine anterior 0.047	skn-1	0.00596815344509357	0.00815898742500486
cat-4(+)ptps-1(+) intestine anterior 0.047	spr-3	0.0935686187430113	0.0705968321937063
cat-4(+)ptps-1(+) intestine anterior 0.047	sptf-2	0.442156375438503	0.443663681300252
cat-4(+)ptps-1(+) intestine anterior 0.047	unc-62	0.0277891596933426	0.0256433398048766
cat-4(+)ptps-1(+) intestine anterior 0.047	Y53G8AR.9	0.0634442426452436	0.0546729462487194
cat-4(+)ptps-1(+) intestine anterior 0.047	Y56A3A.18	0.0749781194656632	0.0662046106456672
cat-4(+)ptps-1(+) intestine anterior 0.047	zfh-2	0.0501839649065333	0.0469813947373187
cat-4(+)ptps-1(+) intestine anterior 0.047	zim-3	0.0301855413573398	0.0266980444501318
cat-4(+)ptps-1(+) intestine anterior 0.047	ZK185.1	0.0120867644448598	0
cat-4(+)ptps-1(+) intestine anterior 0.047	ZK546.5	0.280870126574877	0.277229467902572
cat-4(+)ptps-1(+) intestine anterior 0.047	ztf-1	0.245811896794564	0.219089173901468
cat-4(+)ptps-1(+) intestine anterior 0.047	ztf-26	1.54278733059256e-05	0
e1_e3 (pharyngeal epithelium) 0.040	aha-1	0.123393122017285	0.157613387125324
e1_e3 (pharyngeal epithelium) 0.040	alr-1	0.0696538103002377	0.0719042754365649
e1_e3 (pharyngeal epithelium) 0.040	bcl-11	0.0769410051448973	0.0958301587286228
e1_e3 (pharyngeal epithelium) 0.040	blmp-1	0.00146824436141641	0.00248516875159964
e1_e3 (pharyngeal epithelium) 0.040	cebp-1	0.0118155581385302	0.0162232588486584
e1_e3 (pharyngeal epithelium) 0.040	ceh-19	0	0.0120518017623183
e1_e3 (pharyngeal epithelium) 0.040	ceh-27	0	0.00959545426945398
e1_e3 (pharyngeal epithelium) 0.040	ekl-4	0.00946994475594893	0.0122482598485882
e1_e3 (pharyngeal epithelium) 0.040	elt-4	0.0104519708543986	0
e1_e3 (pharyngeal epithelium) 0.040	gei-8	0.0262764034882667	0.0394421187807311

e1_e3 (pharyngeal epithelium) 0.040	grh-1	0	0.00594014588625653
e1_e3 (pharyngeal epithelium) 0.040	hinf-1	0.0262897740380476	0.0377619430282997
e1_e3 (pharyngeal epithelium) 0.040	hlh-8	0.0268992405984489	0.045038787219582
e1_e3 (pharyngeal epithelium) 0.040	hsf-1	0	0.0033745483894652
e1_e3 (pharyngeal epithelium) 0.040	K11D2.4	0.00346821789811655	0.00788837018894269
e1_e3 (pharyngeal epithelium) 0.040	lim-7	0.0104598958434068	0.020833673729306
e1_e3 (pharyngeal epithelium) 0.040	lin-11	0.00375346473370514	0.0204896353497645
e1_e3 (pharyngeal epithelium) 0.040	lin-14	0.0122622155624597	0.0141454428739838
e1_e3 (pharyngeal epithelium) 0.040	lin-26	0.0368083627426358	0.0302324334093344
e1_e3 (pharyngeal epithelium) 0.040	lin-40	0.0781859829701409	0.05387128115982
e1_e3 (pharyngeal epithelium) 0.040	madf-3	0.0392840924646288	0.0456468264558598
e1_e3 (pharyngeal epithelium) 0.040	madf-5	0.112998059341915	0.0919517336785114
e1_e3 (pharyngeal epithelium) 0.040	mdt-29	0	0.0184095605080289
e1_e3 (pharyngeal epithelium) 0.040	mml-1	0.0546885006624974	0.0340606511351621
e1_e3 (pharyngeal epithelium) 0.040	mxl-1	0.109151806443729	0.104992458392842
e1_e3 (pharyngeal epithelium) 0.040	mxl-3	0.00219800180320048	0.00101153106009244
e1_e3 (pharyngeal epithelium) 0.040	nfyb-1	0.000107444298665399	0.00207727224745274
e1_e3 (pharyngeal epithelium) 0.040	nhr-102	0	0.00648626395199098
e1_e3 (pharyngeal epithelium) 0.040	nhr-11	0.0454300703216194	0.0406064464857029
e1_e3 (pharyngeal epithelium) 0.040	nhr-129	0.0271983786038558	0.0356638823349257
e1_e3 (pharyngeal epithelium) 0.040	nhr-237	0.454830941633904	0.469762565292433
e1_e3 (pharyngeal epithelium) 0.040	pag-3	0.0437646198948573	0.0510229164152678
e1_e3 (pharyngeal epithelium) 0.040	pat-9	0.153570747386323	0.151599077390355
e1_e3 (pharyngeal epithelium) 0.040	pha-4	0.140794908796632	0.144798312675686
e1_e3 (pharyngeal epithelium) 0.040	skn-1	0.0140797695202728	0.00544765910673555
e1_e3 (pharyngeal epithelium) 0.040	spr-3	0.0474047531184763	0.0376896995079332
e1_e3 (pharyngeal epithelium) 0.040	sptf-2	0.0416954303420354	0.055945671970671
e1_e3 (pharyngeal epithelium) 0.040	T26A5.8	0.0795738921927638	0.0781946396064723
e1_e3 (pharyngeal epithelium) 0.040	unc-3	0	0.00933119310520088
e1_e3 (pharyngeal epithelium) 0.040	Y56A3A.18	0.0287807695226887	0.0311955759610003
e1_e3 (pharyngeal epithelium) 0.040	zfh-2	0.0174899625486055	0.0159561015546781
e1_e3 (pharyngeal epithelium) 0.040	zim-3	0.0470359406012464	0.0406981608185351
e1_e3 (pharyngeal epithelium) 0.040	zip-4	0.0334153821491761	0.0388988618470849
e1_e3 (pharyngeal epithelium) 0.040	ztf-1	0	0.0114243492687835
e1_e3 (pharyngeal epithelium) 0.040	ztf-26	0.0669631042273227	0.0452559312948944
e2 (pharyngeal gland) 0.036	aha-1	0.130602115288741	0.207695138267802
e2 (pharyngeal gland) 0.036	alr-1	0.0849739691976945	NA
e2 (pharyngeal gland) 0.036	bcl-11	0.0711105890624806	0.0806252720300775
e2 (pharyngeal gland) 0.036	C34B4.2	0	0.125422955762625
e2 (pharyngeal gland) 0.036	cebp-1	0.0044896472282591	0.0100629811669081
e2 (pharyngeal gland) 0.036	ceh-18	0	0.000539988406206582
e2 (pharyngeal gland) 0.036	ceh-22	0.0170859979605942	0
e2 (pharyngeal gland) 0.036	ceh-34	0.010695901870403	0.0289075492426275

e2 (pharyngeal gland) 0.036	ceh-40	0.0027233416637543	NA
e2 (pharyngeal gland) 0.036	D1046.2	0.008543777988864	0.0121316920439654
e2 (pharyngeal gland) 0.036	ekl-4	0.0234833146340377	0.0131939374231804
e2 (pharyngeal gland) 0.036	elt-4	0.010499084780729	0
e2 (pharyngeal gland) 0.036	gei-8	0	0.0208145236918803
e2 (pharyngeal gland) 0.036	hinf-1	0.0532850557042478	0.0446788713799777
e2 (pharyngeal gland) 0.036	hlh-8	0.0608551626912432	0.070951584294222
e2 (pharyngeal gland) 0.036	hsf-1	0.0135616923257237	0.00976129519737221
e2 (pharyngeal gland) 0.036	lim-7	0.0224796288239554	0.0133042409459701
e2 (pharyngeal gland) 0.036	lin-14	0.00872379063891377	0.0137540654900573
e2 (pharyngeal gland) 0.036	lin-26	0.0410253115100598	0.0245536755634234
e2 (pharyngeal gland) 0.036	lin-40	0.0692864783396606	0.0660275807218461
e2 (pharyngeal gland) 0.036	madf-2	0.129173413429668	0.16869735048499
e2 (pharyngeal gland) 0.036	madf-3	0.0495738399989892	0.0519502097270265
e2 (pharyngeal gland) 0.036	madf-5	0.123880069941917	0.093902977522938
e2 (pharyngeal gland) 0.036	madf-6	0.00265153638038438	0
e2 (pharyngeal gland) 0.036	madf-9	0.00969261284794795	0
e2 (pharyngeal gland) 0.036	mdt-29	0.0455516391425347	0.053081586494487
e2 (pharyngeal gland) 0.036	mml-1	0	0.0214987775861997
e2 (pharyngeal gland) 0.036	nfyb-1	0.00556248876963892	0.003935814264147
e2 (pharyngeal gland) 0.036	nhr-11	0.0404677534910108	0.0436657070561317
e2 (pharyngeal gland) 0.036	nhr-129	0.0316411557641562	0.0371057603272566
e2 (pharyngeal gland) 0.036	nhr-237	0.310470523914225	0.30876008688007
e2 (pharyngeal gland) 0.036	pag-3	0.0602420916462319	0.0634829326047405
e2 (pharyngeal gland) 0.036	pat-9	0.18189936690516	0.140673569247683
e2 (pharyngeal gland) 0.036	pha-4	0.138425236646138	0.15535270494708
e2 (pharyngeal gland) 0.036	skn-1	0.00805431592582227	0
e2 (pharyngeal gland) 0.036	spr-3	0.0144067493393365	0.0167094193281828
e2 (pharyngeal gland) 0.036	sptf-2	0.101500292972893	0.0563363225296973
e2 (pharyngeal gland) 0.036	T26A5.8	0.0696864741300832	0.0771751430309898
e2 (pharyngeal gland) 0.036	Y53G8AR.9	0.00502742116504903	0.00379537983463318
e2 (pharyngeal gland) 0.036	Y56A3A.18	0.0176653334296806	0.00225940083366328
e2 (pharyngeal gland) 0.036	zfh-2	0.0272278413213623	0.0190782996928105
e2 (pharyngeal gland) 0.036	zim-3	0.0410181789669403	0.0464395913646715
e2 (pharyngeal gland) 0.036	ztf-26	0.0871083552414863	NA
g1A (pharyngeal gland) 0.029	attf-6	0.0197253751211598	0.0309073363053871
g1A (pharyngeal gland) 0.029	B0035.1	0	0.00563533944636245
g1A (pharyngeal gland) 0.029	bed-1	0.0693662364420166	NA
g1A (pharyngeal gland) 0.029	C16A3.4	0	0.00319162288266012
g1A (pharyngeal gland) 0.029	crh-2	0.0289955028539328	0.0275165275516401
g1A (pharyngeal gland) 0.029	D1046.2	0.0167084082030006	0.00830180709776141
g1A (pharyngeal gland) 0.029	daf-16	0.00507236520522862	0.00224758481268952
g1A (pharyngeal gland) 0.029	dxbp-1	0.025406889953883	0.0257099656141993

g1A (pharyngeal gland) 0.029	egl-18	0.0176362147948015	0.0377610731330641
g1A (pharyngeal gland) 0.029	ekl-4	0.0749209781622137	0.0679083072317399
g1A (pharyngeal gland) 0.029	F33H1.4	0.000147215539762123	0.00565479744839827
g1A (pharyngeal gland) 0.029	F44E2.7	0.0045387886490803	0.019748418378198
g1A (pharyngeal gland) 0.029	F57A8.1	0	0.00252747008898494
g1A (pharyngeal gland) 0.029	hlh-8	0.00387816391524088	NA
g1A (pharyngeal gland) 0.029	hsf-1	0.000500582111372451	0.00810316103631348
g1A (pharyngeal gland) 0.029	jun-1	0	0.00401666182871778
g1A (pharyngeal gland) 0.029	let-607	0.0391267164282454	0.0327927631103656
g1A (pharyngeal gland) 0.029	lin-13	0	0.0012152422924713
g1A (pharyngeal gland) 0.029	lin-40	0.0207862868781372	0.0408881856149403
g1A (pharyngeal gland) 0.029	lin-54	0.00917692540009224	0.0199086611422821
g1A (pharyngeal gland) 0.029	lsy-2	0.00620974524249393	0.0103357110045391
g1A (pharyngeal gland) 0.029	madf-2	0	0.0558927631286591
g1A (pharyngeal gland) 0.029	madf-5	0.100067714035965	0.112538612029411
g1A (pharyngeal gland) 0.029	madf-6	0.0219832950572234	0.0292530863460901
g1A (pharyngeal gland) 0.029	madf-9	0.0499406018342711	NA
g1A (pharyngeal gland) 0.029	mxl-1	0.0893064260956993	0.135963788420721
g1A (pharyngeal gland) 0.029	mxl-3	0.000602463613263017	NA
g1A (pharyngeal gland) 0.029	nfya-2	0	0.00816295160724697
g1A (pharyngeal gland) 0.029	nhr-11	NA	0.0124452835843827
g1A (pharyngeal gland) 0.029	nhr-129	0.00214539022334063	0.00365858900982488
g1A (pharyngeal gland) 0.029	pat-9	0.0734974249894309	NA
g1A (pharyngeal gland) 0.029	pbrm-1	0.0259034596938171	0.0267915557206256
g1A (pharyngeal gland) 0.029	pha-4	0.00471672678447335	0.00734316742822141
g1A (pharyngeal gland) 0.029	R02D3.7	0.0246617408936882	NA
g1A (pharyngeal gland) 0.029	rcor-1	0.00738239962938619	0.0138877722749688
g1A (pharyngeal gland) 0.029	repo-1	0.00318675169493337	0.0227326508712867
g1A (pharyngeal gland) 0.029	saeg-2	0.010692531333916	NA
g1A (pharyngeal gland) 0.029	sptf-2	0.297680964864187	NA
g1A (pharyngeal gland) 0.029	tra-4	0	0.0136520182699382
g1A (pharyngeal gland) 0.029	unc-62	0.0123089101394706	0.0147648614756731
g1A (pharyngeal gland) 0.029	Y53G8AR.9	0.0119286111336013	NA
g1A (pharyngeal gland) 0.029	Y56A3A.18	0.0643860328654756	0.0654427551446938
g1A (pharyngeal gland) 0.029	zfh-2	NA	0.0382560283050839
g1A (pharyngeal gland) 0.029	ztf-1	0.124119374927545	0.114734079822292
g1A (pharyngeal gland) 0.029	ztf-26	0.031559731703896	NA
g1A (pharyngeal gland) 0.029	ztf-28	0.0151544906564627	NA
g1P (pharyngeal gland) 0.027	alr-1	0.184092937517584	0.226235924400673
g1P (pharyngeal gland) 0.027	attf-6	0.000714926913915879	0.0112398382183572
g1P (pharyngeal gland) 0.027	C16A3.4	0	0.00642146233389802
g1P (pharyngeal gland) 0.027	ceh-18	0	0.00068170221394027
g1P (pharyngeal gland) 0.027	ceh-39	0.00349631410189419	NA

g1P (pharyngeal gland) 0.027	ceh-43	0.0875511075936727	0.0790450811135003
g1P (pharyngeal gland) 0.027	crh-2	0.000620687866247085	0.00176645492165927
g1P (pharyngeal gland) 0.027	daf-16	0	0.000902873681663153
g1P (pharyngeal gland) 0.027	daf-19	0.0495555461322149	0.060402592350412
g1P (pharyngeal gland) 0.027	dve-1	0.00042777079624756	0
g1P (pharyngeal gland) 0.027	dxbp-1	0	0.00587894280568761
g1P (pharyngeal gland) 0.027	egl-18	0	0.0145324755975117
g1P (pharyngeal gland) 0.027	ekl-4	0.0677270183942184	0.0893325054666522
g1P (pharyngeal gland) 0.027	elt-4	0.0813169164128122	0.075095100739643
g1P (pharyngeal gland) 0.027	F22D6.2	0.0505835067228134	0
g1P (pharyngeal gland) 0.027	F33H1.4	0.0159541392628711	0.0268715690029997
g1P (pharyngeal gland) 0.027	gei-8	0.00904327712711633	0.0206276851714984
g1P (pharyngeal gland) 0.027	hinf-1	0.0988453755974206	0.118715252428205
g1P (pharyngeal gland) 0.027	hlh-1	0.00288023942631728	0.00567602004526597
g1P (pharyngeal gland) 0.027	hlh-8	0.0258023786651952	0.0223228010139443
g1P (pharyngeal gland) 0.027	hsf-1	0	0.00443587844580642
g1P (pharyngeal gland) 0.027	lag-1	0	0.0189850176474604
g1P (pharyngeal gland) 0.027	let-607	0.0314467580256912	0.0350273441105165
g1P (pharyngeal gland) 0.027	lim-7	0.029141623628954	0.0415308386799236
g1P (pharyngeal gland) 0.027	lin-26	0.0894226459877475	0.0931687478929654
g1P (pharyngeal gland) 0.027	lin-32	0.00488168676122577	NA
g1P (pharyngeal gland) 0.027	lin-40	0.0761507549287187	0.0894931766472917
g1P (pharyngeal gland) 0.027	lin-54	0.00970330395720006	0.0163520852569943
g1P (pharyngeal gland) 0.027	lsy-2	0.00873456588782327	0.0149168461414961
g1P (pharyngeal gland) 0.027	madf-3	0.0406130529885946	NA
g1P (pharyngeal gland) 0.027	madf-5	0.12640613893047	0.121746642289671
g1P (pharyngeal gland) 0.027	madf-6	0	0.00613137858277856
g1P (pharyngeal gland) 0.027	madf-9	0.0390275680199125	0.0320042504072453
g1P (pharyngeal gland) 0.027	mdt-29	0.0140059844893041	0.00684830793278636
g1P (pharyngeal gland) 0.027	mxl-1	0.0380564922796943	0.05621403481979
g1P (pharyngeal gland) 0.027	nhr-11	0.0177311632103156	0.019328101959695
g1P (pharyngeal gland) 0.027	pag-3	0.0598706145220528	NA
g1P (pharyngeal gland) 0.027	pat-9	0.192898514912065	0.18682869208977
g1P (pharyngeal gland) 0.027	pbrm-1	0.00548058452706559	0.005580090984124
g1P (pharyngeal gland) 0.027	pha-4	0.00562425440350318	0
g1P (pharyngeal gland) 0.027	R02D3.7	0.0147801267039249	0.01933650068998
g1P (pharyngeal gland) 0.027	saeg-2	0	0.0169657080610289
g1P (pharyngeal gland) 0.027	sptf-2	0.292782668916461	0.383697224253014
g1P (pharyngeal gland) 0.027	sup-37	0.00771468428892845	0
g1P (pharyngeal gland) 0.027	tlp-1	0.00561528422633591	0
g1P (pharyngeal gland) 0.027	unc-62	0.00963386252897012	0.007982572666567
g1P (pharyngeal gland) 0.027	Y53G8AR.9	0.00510979906551504	0.0128506123173002
g1P (pharyngeal gland) 0.027	Y56A3A.18	0.0481881523077971	0.0594138653328908

g1P (pharyngeal gland) 0.027	zfh-2	0.0328665856561265	0.0369043431125416
g1P (pharyngeal gland) 0.027	zim-3	0.0200759135888877	0.0253450852172545
g1P (pharyngeal gland) 0.027	ZK546.5	0	0.0359538234245813
g1P (pharyngeal gland) 0.027	ztf-1	0.0505643653523724	0.00536794780607039
g1P (pharyngeal gland) 0.027	ztf-26	0.0775095225255855	0.0810745240856803
g2 (pharyngeal gland) 0.031	akir-1	0.00869071412175649	0
g2 (pharyngeal gland) 0.031	alr-1	0.198431356408964	0.185799402311982
g2 (pharyngeal gland) 0.031	attf-6	0	0.000914475937646303
g2 (pharyngeal gland) 0.031	bcl-11	0.00837314194715968	0
g2 (pharyngeal gland) 0.031	bed-1	0.00440390739935607	0.0102475618669924
g2 (pharyngeal gland) 0.031	ceh-18	0.00199746401187223	0
g2 (pharyngeal gland) 0.031	ceh-22	0.0432911773228894	NA
g2 (pharyngeal gland) 0.031	crh-2	0.012119984593754	0.0199409972811318
g2 (pharyngeal gland) 0.031	D1046.2	0.0118359199554656	0.0181415073997357
g2 (pharyngeal gland) 0.031	daf-19	0.130821676587448	0.133241942123194
g2 (pharyngeal gland) 0.031	dxbp-1	0.00256329911216628	0.000885948979131667
g2 (pharyngeal gland) 0.031	egl-18	0.0181001090391405	0.0195088838255469
g2 (pharyngeal gland) 0.031	egl-5	NA	0.00269742189369905
g2 (pharyngeal gland) 0.031	ekl-4	0.0540889762330021	0.0499564639054305
g2 (pharyngeal gland) 0.031	elt-1	0.00666622528545184	0.01525742651051
g2 (pharyngeal gland) 0.031	elt-4	0.0510590332345697	NA
g2 (pharyngeal gland) 0.031	F22D6.2	0.105818104381704	0
g2 (pharyngeal gland) 0.031	F33H1.4	0.0184142881529725	0.0105860070106396
g2 (pharyngeal gland) 0.031	hinf-1	0.0952461465532988	0.0760779603060187
g2 (pharyngeal gland) 0.031	lag-1	0	0.00202648260803878
g2 (pharyngeal gland) 0.031	let-607	0.0208518524580448	0.0249147736862192
g2 (pharyngeal gland) 0.031	lim-7	0.0305738962052634	0.0235124773405999
g2 (pharyngeal gland) 0.031	lin-13	0	0.000219012715706264
g2 (pharyngeal gland) 0.031	lin-26	0.0828626800529157	0.0534614552615792
g2 (pharyngeal gland) 0.031	lin-40	0.0565457444659816	0.0128763750136234
g2 (pharyngeal gland) 0.031	lin-54	0.00445742328044175	0.00286819906896699
g2 (pharyngeal gland) 0.031	lsy-2	0.0127240853193607	0.00557099433719747
g2 (pharyngeal gland) 0.031	madf-3	0.0450540176347418	0.0371726077083851
g2 (pharyngeal gland) 0.031	madf-5	0.114574351079623	0.0746919960317406
g2 (pharyngeal gland) 0.031	madf-9	0.0554357145670128	NA
g2 (pharyngeal gland) 0.031	mdt-29	0.0157737151101056	0.0215247961081543
g2 (pharyngeal gland) 0.031	mxl-1	0.136453688391294	0.14926845006679
g2 (pharyngeal gland) 0.031	nhr-11	0.0198425264313625	0.00127432216621537
g2 (pharyngeal gland) 0.031	nhr-129	0.00306452643687387	0
g2 (pharyngeal gland) 0.031	nhr-179	0.00760426830916025	NA
g2 (pharyngeal gland) 0.031	pag-3	0.0434219632985343	0.0127867743481217
g2 (pharyngeal gland) 0.031	pat-9	NA	0.134282950930328
g2 (pharyngeal gland) 0.031	pbrm-1	0.020772541673408	0.0154919017898433

g2 (pharyngeal gland) 0.031	pha-4	0.0102909235157424	0.00516466992696196
g2 (pharyngeal gland) 0.031	R02D3.7	0.0111098936997365	0.00596345399465963
g2 (pharyngeal gland) 0.031	rcor-1	0	0.00785758749378819
g2 (pharyngeal gland) 0.031	saeg-2	0	0.0126972102026022
g2 (pharyngeal gland) 0.031	skn-1	0.00183181781678449	0
g2 (pharyngeal gland) 0.031	sup-37	0.00846827906674798	0
g2 (pharyngeal gland) 0.031	tlp-1	0.0747680424459501	0.0637850361301072
g2 (pharyngeal gland) 0.031	unc-120	0.0028006187537205	0
g2 (pharyngeal gland) 0.031	Y53G8AR.9	0.00294394688551919	0
g2 (pharyngeal gland) 0.031	Y56A3A.18	0.0565199694665178	0.0438995040132504
g2 (pharyngeal gland) 0.031	zfh-2	0.0400264136174615	0.0299426003863213
g2 (pharyngeal gland) 0.031	zim-3	0.0145572252234421	0
g2 (pharyngeal gland) 0.031	ZK546.5	0.000180301428832078	0.0459719066415913
g2 (pharyngeal gland) 0.031	ztf-1	0.0278904391769904	0.0127564782570315
g2 (pharyngeal gland) 0.031	ztf-26	0.0759985632858788	0.0242107485606126
hmc 0.043	akir-1	0.0681598283385222	0
hmc 0.043	attf-6	0.0191707325972539	0.0229937859589102
hmc 0.043	ceh-18	0.0580752325949632	0.043404402207907
hmc 0.043	ceh-22	0.00467002933651204	0
hmc 0.043	chd-7	0	0.0171611408532414
hmc 0.043	crh-2	0.0241608657898336	0.0216697994532566
hmc 0.043	ctbp-1	0.00477313237086209	0.00794444109736345
hmc 0.043	daf-16	0.0103411743562909	0.0208373170136396
hmc 0.043	daf-19	0.0813908300933624	0.105462649566905
hmc 0.043	dxbp-1	0.0158236273223924	0.0162707692823963
hmc 0.043	egl-18	0.00630655332699003	0.0469089018751081
hmc 0.043	ekl-4	0.076095333243423	0.0812373138190412
hmc 0.043	elt-4	0.0523215297612912	0.0454550381272681
hmc 0.043	F22D6.2	0.102222849771598	0.0132996672781345
hmc 0.043	F33H1.4	0.00672692026272968	0.00363237201612106
hmc 0.043	fkh-2	0	0.145936661838554
hmc 0.043	gei-8	0.0024695830725825	0.0494440175637095
hmc 0.043	hinf-1	0.127253232133339	0.129335613365023
hmc 0.043	hlh-1	0.0251536083000709	0.032423560214975
hmc 0.043	hlh-8	0.19890770140307	0.242363951720233
hmc 0.043	hmg-1.1	0	0.00273088886309532
hmc 0.043	hsf-1	0.0162507286092514	0.020617370464058
hmc 0.043	lag-1	0	0.0285096174840899
hmc 0.043	let-607	0.0139669587305757	0.0142294467820058
hmc 0.043	lim-7	0.00360885520280057	0.0252809283487414
hmc 0.043	lin-11	0	0.0130467828738301
hmc 0.043	lin-14	0.00463375046073812	0
hmc 0.043	lin-26	0.107046841182964	0.101592733720283

hmc 0.043	lin-40	0.103806640932572	0.0875531777101136
hmc 0.043	lin-54	0.00861554520977228	0.0123938355220014
hmc 0.043	lsy-2	0.0309513193470513	0.0327858864795086
hmc 0.043	madf-3	0.0569605728345549	0.0602037940344812
hmc 0.043	madf-5	0.208682379312859	NA
hmc 0.043	madf-6	0.0127222186629881	0.0154814197398163
hmc 0.043	madf-9	0.0345011515543747	NA
hmc 0.043	mdt-29	0.0117098005128803	0.0283184625245719
hmc 0.043	mml-1	0.00649557384031388	0.0443932077752323
hmc 0.043	nfya-2	0	0.000226222371026771
hmc 0.043	nhr-11	0.0487990463398541	NA
hmc 0.043	nhr-129	0.00177307261858712	0.00335890146247408
hmc 0.043	nhr-71	0.00269796374687609	0.00863199786746418
hmc 0.043	pag-3	NA	0.100997786830863
hmc 0.043	pat-9	0.290317916633736	0.31111700152487
hmc 0.043	pbrm-1	0	0.00176115803732964
hmc 0.043	R02D3.7	0.0140373897866541	0.015827190805116
hmc 0.043	spr-3	NA	0.00397327009443181
hmc 0.043	tlp-1	0.00181753318478266	NA
hmc 0.043	Y53G8AR.9	0.0106386331737948	0.00464459448224414
hmc 0.043	Y56A3A.18	0.047122388292688	0.0650521026300203
hmc 0.043	zfh-2	0.0591682221376968	0.0610312884365264
hmc 0.043	zim-3	0.0132157551039993	0
hmc 0.043	ZK546.5	0.142426788957989	0.18483111263914
hmc 0.043	ztf-1	0.0388971945494017	0.0250319548899181
hmc 0.043	ztf-26	0.0826685515274432	NA
hyp4_to_hyp6 0.049	alr-1	0.223329148341848	0.244425213069982
hyp4_to_hyp6 0.049	blmp-1	0.00933149175265626	0.0054568469577628
hyp4_to_hyp6 0.049	ceh-40	0.067297902194664	0.0885358172246923
hyp4_to_hyp6 0.049	ceh-79	0.0653282525610739	0.0412648418890253
hyp4_to_hyp6 0.049	cey-2	0.0440355147206628	0.0248931401544976
hyp4_to_hyp6 0.049	ctbp-1	0.0290744239743048	0.026645115574458
hyp4_to_hyp6 0.049	daf-19	0.0337059937513774	0.0437442645713424
hyp4_to_hyp6 0.049	egrh-3	0.0665131329940594	0.0603257029996378
hyp4_to_hyp6 0.049	ekl-4	0.0217489125359502	0.037137811732594
hyp4_to_hyp6 0.049	elt-3	0.0456434249925408	0.0400233181160781
hyp4_to_hyp6 0.049	elt-4	0.240694643503444	0.224448887157184
hyp4_to_hyp6 0.049	F22D6.2	0.347209376779213	0.299891263429351
hyp4_to_hyp6 0.049	F33H1.4	0.00350015808741133	0.00499312393541435
hyp4_to_hyp6 0.049	gei-8	0.0173040583898991	0
hyp4_to_hyp6 0.049	hinf-1	0.0647319485173138	0.0921047077258557
hyp4_to_hyp6 0.049	hlh-8	0.00837963208235788	0.00637370285082992
hyp4_to_hyp6 0.049	lin-26	0.186498882234914	0.195328226543913

hyp4_to_hyp6 0.049	lin-40	0.455387035493279	0.422688855971893
hyp4_to_hyp6 0.049	lin-54	0	0.00411218840473714
hyp4_to_hyp6 0.049	lsy-2	0.00405438880137877	0.00570531893180707
hyp4_to_hyp6 0.049	madf-3	0.0365812742073681	0.0441084637474039
hyp4_to_hyp6 0.049	madf-5	0.406320631946408	0.38638476161173
hyp4_to_hyp6 0.049	madf-9	0.135461308667457	0.119126477616751
hyp4_to_hyp6 0.049	mdt-29	0.000445608792477397	0
hyp4_to_hyp6 0.049	mec-3	0.0073733195520113	0
hyp4_to_hyp6 0.049	nhr-11	0.0353166257585537	0.0225351059904073
hyp4_to_hyp6 0.049	nhr-120	0.0289594791465391	0.00867011129097475
hyp4_to_hyp6 0.049	nhr-179	0.714773159021413	0.635550974255638
hyp4_to_hyp6 0.049	nhr-270	0.241002170617942	0.214513581262967
hyp4_to_hyp6 0.049	pag-3	0.0811204947996263	0.0725069513082713
hyp4_to_hyp6 0.049	pat-9	0.160517364646056	0.140778470910173
hyp4_to_hyp6 0.049	pbrm-1	0.00485235651402966	0.00258489285521786
hyp4_to_hyp6 0.049	R02D3.7	0.0342819203857008	0.0336320077336134
hyp4_to_hyp6 0.049	spr-3	0.0093740443832804	0
hyp4_to_hyp6 0.049	sptf-2	0.329432237110291	0.401441783907403
hyp4_to_hyp6 0.049	Y53G8AR.9	0.0230542263707	0.0160835941866368
hyp4_to_hyp6 0.049	Y56A3A.18	0.0266385607435817	0.0285747244483784
hyp4_to_hyp6 0.049	zfh-2	0.039915552012862	0.041008838003466
hyp4_to_hyp6 0.049	zim-3	0.150147978256222	0.155801689628975
hyp4_to_hyp6 0.049	ztf-26	0.454853021920565	0.41792897690119
hyp7 (hypodermis) 0.051	alr-1	0.194617587781827	0.191408722188031
hyp7 (hypodermis) 0.051	bed-3	0.23734473949418	0.290875212626203
hyp7 (hypodermis) 0.051	blmp-1	0.0352726367099789	0.0339649276415997
hyp7 (hypodermis) 0.051	ceh-40	0.0155647902981708	0.0200098223242141
hyp7 (hypodermis) 0.051	ceh-79	0.127467544626532	0.155187432740761
hyp7 (hypodermis) 0.051	cey-2	0.0209278175024878	0.0329568865473963
hyp7 (hypodermis) 0.051	crh-2	0.00138902009716887	0.0113891444768623
hyp7 (hypodermis) 0.051	ctbp-1	0.0479391645663249	0.0662178837241147
hyp7 (hypodermis) 0.051	daf-19	0.0424577086271653	0.0458218843542808
hyp7 (hypodermis) 0.051	dxbp-1	0.0213999951003488	0.0301032403423324
hyp7 (hypodermis) 0.051	egrh-3	0.189803830791185	0.20722206418241
hyp7 (hypodermis) 0.051	ekl-4	0.0599330701133443	0.0609817188045607
hyp7 (hypodermis) 0.051	elt-1	0.01031257726073	0.0105052280521943
hyp7 (hypodermis) 0.051	elt-3	0.0116935965608599	0.0115284046366577
hyp7 (hypodermis) 0.051	elt-4	0.281784850153559	0.294289208842009
hyp7 (hypodermis) 0.051	F10B5.3	0.000613022760878998	0.0199215986791702
hyp7 (hypodermis) 0.051	F22D6.2	0.146463620554746	0.186160558950375
hyp7 (hypodermis) 0.051	F44E2.7	0	0.00401813361193136
hyp7 (hypodermis) 0.051	gei-8	0.0249627890302637	0.0215485132679251
hyp7 (hypodermis) 0.051	hinf-1	0.0970220384123216	0.0955597867255599

hyp7 (hypodermis) 0.051	hlh-6	NA	0.0360504494253008
hyp7 (hypodermis) 0.051	hsf-1	0	0.00300553387197454
hyp7 (hypodermis) 0.051	isw-1	0.0082481820303165	0.0312544025340348
hyp7 (hypodermis) 0.051	let-607	0.00262332256818942	0.00213625046273861
hyp7 (hypodermis) 0.051	lim-7	0.0039224986452237	0.0055087504581033
hyp7 (hypodermis) 0.051	lin-13	0	0.010757644740185
hyp7 (hypodermis) 0.051	lin-26	0.0931126762582272	0.0881775505436774
hyp7 (hypodermis) 0.051	lin-29	0	0.0358698704087364
hyp7 (hypodermis) 0.051	lin-40	0.16647211758393	0.159798523303894
hyp7 (hypodermis) 0.051	lin-54	0	0.00307129617167864
hyp7 (hypodermis) 0.051	madf-2	0.439107553926655	0.561983149885434
hyp7 (hypodermis) 0.051	madf-3	0.0438609120627078	0.0408534371429472
hyp7 (hypodermis) 0.051	madf-5	0.57100234963054	0.606568028184085
hyp7 (hypodermis) 0.051	mec-3	0.385866684281839	0.413932540910227
hyp7 (hypodermis) 0.051	mxl-3	0.00761678421672803	0.0156236969402479
hyp7 (hypodermis) 0.051	nhr-10	0.0195342838872382	0.0417256020198336
hyp7 (hypodermis) 0.051	nhr-102	0.00555959170547205	0.00603716032424211
hyp7 (hypodermis) 0.051	nhr-11	0.0241526782821496	0.026800386141003
hyp7 (hypodermis) 0.051	nhr-179	1.10817255664115	1.30224519790748
hyp7 (hypodermis) 0.051	nhr-25	0.0652986038092553	0.086508290315309
hyp7 (hypodermis) 0.051	nhr-43	0.06574177673404	0.0722345909402752
hyp7 (hypodermis) 0.051	nhr-48	0.0187428975027391	0.0276907549866146
hyp7 (hypodermis) 0.051	nhr-84	0.199086211731514	0.20397973995456
hyp7 (hypodermis) 0.051	pag-3	0.0236582208411561	0.0205209024164563
hyp7 (hypodermis) 0.051	pat-9	0.0895334875123156	0.0742614262002787
hyp7 (hypodermis) 0.051	R02D3.7	0.0287379394503301	0.0276158266436482
hyp7 (hypodermis) 0.051	spr-1	0.434439738225631	0.490097990356715
hyp7 (hypodermis) 0.051	sptf-2	0.337297061126629	0.342659605075425
hyp7 (hypodermis) 0.051	T23F11.4	0.430351954381143	0.456847352102636
hyp7 (hypodermis) 0.051	tlp-1	0.0657029163505958	0.0921191868160786
hyp7 (hypodermis) 0.051	Y56A3A.18	0.0423086004530985	0.0461554748406494
hyp7 (hypodermis) 0.051	zfh-2	0.0279446957297643	0.0209422138170575
hyp7 (hypodermis) 0.051	zim-3	0.00694254454085548	0.0111054618940757
hyp7 (hypodermis) 0.051	ztf-1	0.444680528990754	0.470405152038577
hyp7 (hypodermis) 0.051	ztf-16	0.284522144953755	0.357840980147257
hyp7 (hypodermis) 0.051	ztf-26	0.256893726261636	0.268417831296657
mc1 (marginal cells) 0.040	aha-1	0.0319115850462208	0.106051927743927
mc1 (marginal cells) 0.040	alr-1	NA	0.117992284321518
mc1 (marginal cells) 0.040	attf-6	0.0028235276504312	0.00831081572813776
mc1 (marginal cells) 0.040	bcl-11	0.0487734976938867	0.0757199575569153
mc1 (marginal cells) 0.040	cebp-1	0	0.00581620785243194
mc1 (marginal cells) 0.040	ceh-40	0.0199425626568662	0.030851964266368
mc1 (marginal cells) 0.040	D1046.2	0	0.0140505044102778

mc1 (marginal cells) 0.040	daf-19	0.00958813945757181	0.0013793099957717
mc1 (marginal cells) 0.040	ekl-4	0.0507680526774758	0.0494082848032156
mc1 (marginal cells) 0.040	elt-4	0.0501781568780013	0.0156674229430391
mc1 (marginal cells) 0.040	F22D6.2	0.0177951444995209	0
mc1 (marginal cells) 0.040	F44E2.7	0.00623328393046459	0.0309903795921824
mc1 (marginal cells) 0.040	gei-8	0	0.0458746213317889
mc1 (marginal cells) 0.040	hinf-1	0.0677343086859818	0.0656122201169094
mc1 (marginal cells) 0.040	hlh-8	0.034791019529382	0.0556644926451634
mc1 (marginal cells) 0.040	hsf-1	0.0049521464431215	0.004493289294476
mc1 (marginal cells) 0.040	lag-1	0	0.0269085409860842
mc1 (marginal cells) 0.040	let-607	0.00114351473015832	0.00434181724605901
mc1 (marginal cells) 0.040	lim-7	0.0027626967880285	0.0270013479131229
mc1 (marginal cells) 0.040	lin-11	0	0.011487152023041
mc1 (marginal cells) 0.040	lin-26	0.0800611839695149	0.0628078278962706
mc1 (marginal cells) 0.040	lin-40	0.120515922220839	0.0759045449213094
mc1 (marginal cells) 0.040	lin-54	0	0.0013922530680499
mc1 (marginal cells) 0.040	madf-3	0.0532249427387968	0.0583675925407704
mc1 (marginal cells) 0.040	madf-5	0.153594264152944	0.118048765903075
mc1 (marginal cells) 0.040	madf-9	0.0183998142975885	0
mc1 (marginal cells) 0.040	mdt-29	0.0763688204475959	0.0928023066261293
mc1 (marginal cells) 0.040	mml-1	0.147140796971601	0.219804340959445
mc1 (marginal cells) 0.040	nfyb-1	0	0.0144253956277193
mc1 (marginal cells) 0.040	nhr-102	0.00612401170815536	0.0226421990259883
mc1 (marginal cells) 0.040	nhr-11	0.0387190414803212	0.040422493640359
mc1 (marginal cells) 0.040	nhr-129	0.0212603076169986	0.0229269288255977
mc1 (marginal cells) 0.040	nhr-179	0.0414916255490727	0
mc1 (marginal cells) 0.040	nhr-237	0	0.0813088868910027
mc1 (marginal cells) 0.040	pag-3	0.0591953470369519	0.068827148635627
mc1 (marginal cells) 0.040	pha-4	0.0758379576806019	0.101236688705521
mc1 (marginal cells) 0.040	R02D3.7	0.00591517913759801	0
mc1 (marginal cells) 0.040	skn-1	0	0.00515840630015997
mc1 (marginal cells) 0.040	spr-3	0.0487874685765377	NA
mc1 (marginal cells) 0.040	sptf-2	0.246299237928766	NA
mc1 (marginal cells) 0.040	T26A5.8	0.0851905623742472	0.119882236940116
mc1 (marginal cells) 0.040	Y53G8AR.9	0.00718349430982444	0.00299620358390067
mc1 (marginal cells) 0.040	Y56A3A.18	0.0244583321543117	0.0188656583378931
mc1 (marginal cells) 0.040	zfh-2	0.0415789894109174	NA
mc1 (marginal cells) 0.040	zim-3	0.072144058515707	0.0596849265657372
mc1 (marginal cells) 0.040	ZK546.5	0	0.0378082911631316
mc1 (marginal cells) 0.040	ztf-1	0.0137513917344315	0.0330321746514067
mc1 (marginal cells) 0.040	ztf-26	0.107625476270978	NA
mc2_mc3 (marginal cells) 0.039	alr-1	0.113003684829795	0.0907077729770411
mc2_mc3 (marginal cells) 0.039	bcl-11	0.139390468946217	0.156419983879357

mc2_mc3 (marginal cells) 0.039	ceh-22	0.337156033458907	0.379930171002987
mc2_mc3 (marginal cells) 0.039	chd-7	0.0254549633033642	0.0286490351869102
mc2_mc3 (marginal cells) 0.039	daf-19	0.00760760992646684	0.00426905197136555
mc2_mc3 (marginal cells) 0.039	egl-18	0.0641089497707428	NA
mc2_mc3 (marginal cells) 0.039	egl-43	0	0.0037903911717912
mc2_mc3 (marginal cells) 0.039	ekl-4	0.0445057968029212	0.0404273044331305
mc2_mc3 (marginal cells) 0.039	elt-4	0.00587675495796293	0
mc2_mc3 (marginal cells) 0.039	eyg-1	0.0538654155112498	0.0914084726703887
mc2_mc3 (marginal cells) 0.039	F22D6.2	0.0170080947811406	0
mc2_mc3 (marginal cells) 0.039	hinf-1	0.0812391077533881	0.0720205391596847
mc2_mc3 (marginal cells) 0.039	hlh-8	0.0454564428057666	0.0434308488990866
mc2_mc3 (marginal cells) 0.039	let-607	0.00269591971824127	0
mc2_mc3 (marginal cells) 0.039	lim-7	0.0320031204642525	0.044619702443124
mc2_mc3 (marginal cells) 0.039	lin-26	0.066369085800222	0.0450566065612711
mc2_mc3 (marginal cells) 0.039	lin-40	0.059136876219965	0.0189070581412629
mc2_mc3 (marginal cells) 0.039	lin-54	0.014522949814505	0.0149535578548486
mc2_mc3 (marginal cells) 0.039	madf-3	0.0438682971879327	0.0418076247594795
mc2_mc3 (marginal cells) 0.039	madf-5	0.130220568414517	0.0901284550230386
mc2_mc3 (marginal cells) 0.039	madf-9	0.00649947540062658	0
mc2_mc3 (marginal cells) 0.039	mdt-29	0.0505666831568229	0.041779931760098
mc2_mc3 (marginal cells) 0.039	mec-3	NA	0.0258931039405908
mc2_mc3 (marginal cells) 0.039	nhr-11	0.0255115590510328	0.0181837287782826
mc2_mc3 (marginal cells) 0.039	nhr-179	0.0119786185301292	0
mc2_mc3 (marginal cells) 0.039	nhr-237	0.0703356703196393	0.068978413423919
mc2_mc3 (marginal cells) 0.039	pag-3	0.0635297293849684	0.0536443031222876
mc2_mc3 (marginal cells) 0.039	pat-9	0.365342167412636	0.361513064829565
mc2_mc3 (marginal cells) 0.039	pbrm-1	0.00178776620458983	0
mc2_mc3 (marginal cells) 0.039	pha-4	0.0895713841168507	0.102086494989157
mc2_mc3 (marginal cells) 0.039	R02D3.7	0.00057885032732528	0.000520299219416011
mc2_mc3 (marginal cells) 0.039	spr-3	0.0201062281761002	0
mc2_mc3 (marginal cells) 0.039	sptf-2	0.212175992605978	NA
mc2_mc3 (marginal cells) 0.039	sup-37	0.0942807808378895	0.0545460517092711
mc2_mc3 (marginal cells) 0.039	T26A5.8	0.0524999531627278	0.0576833742669193
mc2_mc3 (marginal cells) 0.039	tra-4	0.0744658832155449	0.128353424119764
mc2_mc3 (marginal cells) 0.039	unc-3	0.0127528063645698	NA
mc2_mc3 (marginal cells) 0.039	Y53G8AR.9	0.00280976427517248	0
mc2_mc3 (marginal cells) 0.039	Y56A3A.18	0.0364613218424749	0.0197013279936546
mc2_mc3 (marginal cells) 0.039	zfh-2	0.0588917899471255	0.0512173045743469
mc2_mc3 (marginal cells) 0.039	zim-3	0.0416170162718754	0.0305369055177076
mc2_mc3 (marginal cells) 0.039	ZK546.5	0	0.00154720897036353
mc2_mc3 (marginal cells) 0.039	ztf-1	0.0555594604220192	0.00556310092333491
mc2_mc3 (marginal cells) 0.039	ztf-26	0.117263892236144	0.0891521472083861
mc2_mc3 (marginal cells) 0.039	ztf-4	0	0.00819890173903274

pm1_pm2 (pharyngeal muscle) 0.038	aha-1	0.0469503793049428	0.0843714600174559
pm1_pm2 (pharyngeal muscle) 0.038	alr-1	0.0678063428278872	0.043402595538517
pm1_pm2 (pharyngeal muscle) 0.038	bcl-11	0.0657883785746346	0.0718986592209005
pm1_pm2 (pharyngeal muscle) 0.038	C34B4.2	0	0.0826970071451836
pm1_pm2 (pharyngeal muscle) 0.038	cebp-1	0.00208902990271414	0.00571190549247773
pm1_pm2 (pharyngeal muscle) 0.038	ceh-18	0.0491726872575213	0.0460202182998293
pm1_pm2 (pharyngeal muscle) 0.038	ceh-22	0.388620201577767	0.428188449201602
pm1_pm2 (pharyngeal muscle) 0.038	ceh-34	0.0724907489502011	0.095101016898206
pm1_pm2 (pharyngeal muscle) 0.038	D1046.2	0.0166975441697763	0.0192680911644414
pm1_pm2 (pharyngeal muscle) 0.038	ekl-4	0.0163425991644181	0.0081827321380033
pm1_pm2 (pharyngeal muscle) 0.038	eyg-1	0.0151933425420515	0.0138726750170248
pm1_pm2 (pharyngeal muscle) 0.038	gei-8	0.0184174294816951	0.0463718739530986
pm1_pm2 (pharyngeal muscle) 0.038	hinf-1	0.0612118181775049	0.0569750450506111
pm1_pm2 (pharyngeal muscle) 0.038	hlh-8	0.0524040594416079	0.0517937288960024
pm1_pm2 (pharyngeal muscle) 0.038	hsf-1	0.00299046893612744	1.3253599125415e-05
pm1_pm2 (pharyngeal muscle) 0.038	lim-7	0.0509362331954958	0.0483800659624403
pm1_pm2 (pharyngeal muscle) 0.038	lin-14	0.0138236455880238	0.0184040538667542
pm1_pm2 (pharyngeal muscle) 0.038	lin-26	0.0281888421919944	0.0141387124079502
pm1_pm2 (pharyngeal muscle) 0.038	lin-40	0.0453252548704471	0.0344650976525356
pm1_pm2 (pharyngeal muscle) 0.038	madf-3	0.0513965042079889	0.0525225526366233
pm1_pm2 (pharyngeal muscle) 0.038	madf-5	0.0783550824417511	0.0508820167305354
pm1_pm2 (pharyngeal muscle) 0.038	mdt-29	0.0273712983091191	0.0411314061296927
pm1_pm2 (pharyngeal muscle) 0.038	nfyb-1	0.00481022686325656	0.00714295809722757
pm1_pm2 (pharyngeal muscle) 0.038	nhr-11	0.029546716398254	0.0281310245504008
pm1_pm2 (pharyngeal muscle) 0.038	nhr-129	0.0399147515012189	0.04465411935152
pm1_pm2 (pharyngeal muscle) 0.038	nhr-237	0.234382004943404	0.221045212023176
pm1_pm2 (pharyngeal muscle) 0.038	pag-3	0.0734552399317834	0.070201136670909
pm1_pm2 (pharyngeal muscle) 0.038	pat-9	0.298840444104769	0.278507440066061
pm1_pm2 (pharyngeal muscle) 0.038	pha-4	0.128473711256674	0.128697265415044
pm1_pm2 (pharyngeal muscle) 0.038	sptf-2	0.0735678117753059	NA
pm1_pm2 (pharyngeal muscle) 0.038	sup-37	0.231149123658017	0.24462467025359
pm1_pm2 (pharyngeal muscle) 0.038	syd-9	0.00194536291048676	0
pm1_pm2 (pharyngeal muscle) 0.038	T26A5.8	0.0487698217006053	0.0399748324598622
pm1_pm2 (pharyngeal muscle) 0.038	tbx-2	0	0.00680546415568721
pm1_pm2 (pharyngeal muscle) 0.038	Y53G8AR.9	0.0106207674700803	0.0115521243234245
pm1_pm2 (pharyngeal muscle) 0.038	Y56A3A.18	0.00542343141081335	0.00389698091574145
pm1_pm2 (pharyngeal muscle) 0.038	zfh-2	0.0322860111123023	0.0289307416388479
pm1_pm2 (pharyngeal muscle) 0.038	zim-3	0.032593922065756	0.0122974776997264
pm1_pm2 (pharyngeal muscle) 0.038	ztf-26	0.0904557406069515	NA
pm3_pm4_pm5 (pharyngeal muscle) 0.045	aha-1	0.0313706996276684	0.0807580017866473
pm3_pm4_pm5 (pharyngeal muscle) 0.045	alr-1	0.153271056804057	0.0998279636249771

pm3_pm4_pm5 (pharyngeal muscle) 0.045	bcl-11	0.040291260246833	0.0548567833086205
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ceh-18	0.0890937514431164	0.122595751430893
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ceh-22	0.601881558376184	0.691665648679306
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ceh-40	NA	0.0049128739188978
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ceh-88	0.0172201946185931	0.00272560966973915
pm3_pm4_pm5 (pharyngeal muscle) 0.045	crh-2	0.00927598264966828	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	D1046.2	0.0277789177726736	0.0273073548136596
pm3_pm4_pm5 (pharyngeal muscle) 0.045	daf-19	0.015151683615789	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	egl-5	0.0065711787091166	NA
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ekl-4	0.0518799617675388	0.0385753675550168
pm3_pm4_pm5 (pharyngeal muscle) 0.045	elt-4	0.0390451934828998	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	eyg-1	0.283150581148122	0.212682118139384
pm3_pm4_pm5 (pharyngeal muscle) 0.045	F22D6.2	0.0953756435711279	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	F33H1.4	0.0126934712824902	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	gei-8	0.0192267375777936	0.0151494170272644
pm3_pm4_pm5 (pharyngeal muscle) 0.045	hinf-1	0.109155138336241	0.0912029288637298
pm3_pm4_pm5 (pharyngeal muscle) 0.045	hlh-8	0.120039553081269	0.128674386653256
pm3_pm4_pm5 (pharyngeal muscle) 0.045	let-607	0.0105232904758171	0.00546009893403454
pm3_pm4_pm5 (pharyngeal muscle) 0.045	lim-7	0.0825854332720412	0.0780382032130953
pm3_pm4_pm5 (pharyngeal muscle) 0.045	lin-26	0.0763079233630119	0.0375412516642782
pm3_pm4_pm5 (pharyngeal muscle) 0.045	lin-40	0.109317061456817	0.0354166153738105
pm3_pm4_pm5 (pharyngeal muscle) 0.045	lin-54	0.00558087718148543	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	lsy-2	0.0085616192426358	0

pm3_pm4_pm5 (pharyngeal muscle) 0.045	M03D4.4	0.028843406210487	0.0190188275561557
pm3_pm4_pm5 (pharyngeal muscle) 0.045	madf-3	0.0531793288218385	0.0483341265808867
pm3_pm4_pm5 (pharyngeal muscle) 0.045	madf-5	0.180488381395891	0.110052921510592
pm3_pm4_pm5 (pharyngeal muscle) 0.045	madf-6	0.00703640072571718	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	madf-9	0.0281365713702573	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	mdt-29	0.0901451523571259	0.086684766267174
pm3_pm4_pm5 (pharyngeal muscle) 0.045	nhr-11	0.0242136169115993	0.0161840116625169
pm3_pm4_pm5 (pharyngeal muscle) 0.045	nhr-129	0.0192876131667305	NA
pm3_pm4_pm5 (pharyngeal muscle) 0.045	nhr-179	0.129047075052761	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	nhr-19	0.0070231261272764	0.00800539809782931
pm3_pm4_pm5 (pharyngeal muscle) 0.045	nhr-237	0.0164699333511824	0.0389519799955421
pm3_pm4_pm5 (pharyngeal muscle) 0.045	nhr-71	0.0111710606143818	0.0115048247154375
pm3_pm4_pm5 (pharyngeal muscle) 0.045	pag-3	0.104677122292107	0.116520188730268
pm3_pm4_pm5 (pharyngeal muscle) 0.045	pat-9	0.46157328203725	0.505891185924254
pm3_pm4_pm5 (pharyngeal muscle) 0.045	pbrm-1	0.00335605130789201	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	pha-4	0.0430402116014841	0.0540277103975854
pm3_pm4_pm5 (pharyngeal muscle) 0.045	R02D3.7	0.0250546444824829	0.0180154583491444
pm3_pm4_pm5 (pharyngeal muscle) 0.045	rnt-1	NA	0.00825199400332892
pm3_pm4_pm5 (pharyngeal muscle) 0.045	spr-3	0.0207325256572356	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	sptf-2	0.260501284066564	0.154750266894865
pm3_pm4_pm5 (pharyngeal muscle) 0.045	sup-37	0.220574338484204	0.269380016797789
pm3_pm4_pm5 (pharyngeal muscle) 0.045	T26A5.8	0.190259802824827	0.18406796685376
pm3_pm4_pm5 (pharyngeal muscle) 0.045	tbx-2	0.00269990285468335	5.36418658445221e-06

pm3_pm4_pm5 (pharyngeal muscle) 0.045	tlp-1	0.0444104692022077	0.00969820000281102
pm3_pm4_pm5 (pharyngeal muscle) 0.045	unc-62	0.00433458201568037	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	Y53G8AR.9	0.0298501509525842	0.0259114747257377
pm3_pm4_pm5 (pharyngeal muscle) 0.045	Y56A3A.18	0.0426560428135773	0.0193286356905091
pm3_pm4_pm5 (pharyngeal muscle) 0.045	zfh-2	0.0692416407301558	0.0566049438540174
pm3_pm4_pm5 (pharyngeal muscle) 0.045	zim-3	0.0932378736375477	0.0595607516835366
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ZK546.5	0	0.0113179731811316
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ztf-1	0.0501197902527555	0
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ztf-26	0.121459306635264	0.0359480961170494
pm3_pm4_pm5 (pharyngeal muscle) 0.045	ztf-28	0.0193041314535879	0.00236998778020537
pm6_pm7 (pharyngeal muscle) 0.038	aha-1	0.0103263714301863	0.0474777404139927
pm6_pm7 (pharyngeal muscle) 0.038	alr-1	0.112416314168933	0.0774796720493624
pm6_pm7 (pharyngeal muscle) 0.038	bcl-11	0.0740681753468851	0.0942836953933952
pm6_pm7 (pharyngeal muscle) 0.038	ceh-18	0.0836262878889794	0.0954760356516173
pm6_pm7 (pharyngeal muscle) 0.038	ceh-22	0.352530965412678	0.312243821831545
pm6_pm7 (pharyngeal muscle) 0.038	ceh-40	0.0142054679792813	NA
pm6_pm7 (pharyngeal muscle) 0.038	D1046.2	0.0025378595002486	0
pm6_pm7 (pharyngeal muscle) 0.038	egl-18	0.0307263800240997	0.0397942380731018
pm6_pm7 (pharyngeal muscle) 0.038	ekl-4	0.0383964999126787	0.0350552983938809
pm6_pm7 (pharyngeal muscle) 0.038	elt-4	0.0222130093325168	0
pm6_pm7 (pharyngeal muscle) 0.038	eyg-1	0.167127941489542	0.143545032949546
pm6_pm7 (pharyngeal muscle) 0.038	F22D6.2	0.0478987908689455	0
pm6_pm7 (pharyngeal muscle) 0.038	gei-8	0.0152639989864226	0.00653650193252789
pm6_pm7 (pharyngeal muscle) 0.038	hinf-1	0.084027717027331	0.0704730007032431
pm6_pm7 (pharyngeal muscle) 0.038	hlh-8	0.0924788980050656	NA
pm6_pm7 (pharyngeal muscle) 0.038	let-607	0.00370435873198222	0
pm6_pm7 (pharyngeal muscle) 0.038	lim-7	0.0531867987179643	0.0668576043933039
pm6_pm7 (pharyngeal muscle) 0.038	lin-26	0.0541146997545026	0.0205430883901046
pm6_pm7 (pharyngeal muscle) 0.038	lin-40	0.0841561037063605	0.00772161852579336
pm6_pm7 (pharyngeal muscle) 0.038	lin-54	0.00130446134581948	0.00300599523772017
pm6_pm7 (pharyngeal muscle) 0.038	lsy-2	0.00158347667883196	0
pm6_pm7 (pharyngeal muscle) 0.038	madf-2	0	0.0298002586407151
pm6_pm7 (pharyngeal muscle) 0.038	madf-3	0.05104787337117	0.0454463264664541
pm6_pm7 (pharyngeal muscle) 0.038	madf-5	0.142667778877962	0.0983955053583701
pm6_pm7 (pharyngeal muscle) 0.038	mdt-29	0.0705911370916518	0.0699297483055387

pm6_pm7 (pharyngeal muscle) 0.038	nhr-11	0.0438211927174062	0.0302932785900611
pm6_pm7 (pharyngeal muscle) 0.038	nhr-129	0.0179685685909527	0.0213218141637189
pm6_pm7 (pharyngeal muscle) 0.038	nhr-179	0.0445174518331034	0
pm6_pm7 (pharyngeal muscle) 0.038	nhr-237	0.0290537341354477	0.0396068700655879
pm6_pm7 (pharyngeal muscle) 0.038	pag-3	0.101289597695036	0.0992762816230597
pm6_pm7 (pharyngeal muscle) 0.038	pat-9	0.310108793630983	0.329545745447784
pm6_pm7 (pharyngeal muscle) 0.038	pbrm-1	0.0101270228603558	0.00210798547941182
pm6_pm7 (pharyngeal muscle) 0.038	pha-4	0.0773344142150418	0.0896172948741725
pm6_pm7 (pharyngeal muscle) 0.038	R02D3.7	0.010759256092911	0.00152897927765444
pm6_pm7 (pharyngeal muscle) 0.038	rnt-1	NA	0.000204627582337447
pm6_pm7 (pharyngeal muscle) 0.038	spr-3	0.0250594035268572	0
pm6_pm7 (pharyngeal muscle) 0.038	sptf-2	0.18070897927363	0.124808545128748
pm6_pm7 (pharyngeal muscle) 0.038	sup-37	0.162274763335321	0.207444719720667
pm6_pm7 (pharyngeal muscle) 0.038	T26A5.8	0.0938314034151193	0.0772846581364887
pm6_pm7 (pharyngeal muscle) 0.038	tlp-1	0.0227883144185581	0.00988339551320355
pm6_pm7 (pharyngeal muscle) 0.038	Y53G8AR.9	0.00990851869578824	0.00768930686712038
pm6_pm7 (pharyngeal muscle) 0.038	Y56A3A.18	0.0234909145905126	0.0151464601489594
pm6_pm7 (pharyngeal muscle) 0.038	zfh-2	0.055645696767353	0.0483172733003606
pm6_pm7 (pharyngeal muscle) 0.038	zim-3	0.0628227621884045	0.0321953497597546
pm6_pm7 (pharyngeal muscle) 0.038	ZK185.1	0	0.000508338112899575
pm6_pm7 (pharyngeal muscle) 0.038	ztf-1	0.00826769231305302	0.00253869672520972
pm6_pm7 (pharyngeal muscle) 0.038	ztf-26	0.111787386475937	0.0532709166193105
sh1 (gonadal sheath distal) 0.037	alr-1	0.266950208169266	0.291354326015772
sh1 (gonadal sheath distal) 0.037	attf-6	0.00884652626207773	0.0109120745328627
sh1 (gonadal sheath distal) 0.037	C16A3.4	0	0.00604030822539581
sh1 (gonadal sheath distal) 0.037	ceh-40	NA	0.13973956112109
sh1 (gonadal sheath distal) 0.037	chd-7	0	0.00282662388868624
sh1 (gonadal sheath distal) 0.037	crh-2	0	0.00096362717445696
sh1 (gonadal sheath distal) 0.037	daf-19	0.107428881227643	0.105829201120241
sh1 (gonadal sheath distal) 0.037	dxbp-1	0	0.00376335816283238
sh1 (gonadal sheath distal) 0.037	efl-3	0.0188582165977182	0.019718341825343
sh1 (gonadal sheath distal) 0.037	egl-18	0.0211361402013268	0.0232795271971101
sh1 (gonadal sheath distal) 0.037	ekl-4	0.0906029953433244	0.097910655112191
sh1 (gonadal sheath distal) 0.037	elt-4	0.0561893017626974	0.0290758999337565
sh1 (gonadal sheath distal) 0.037	F22D6.2	0.111615003231142	0.0337740129110081
sh1 (gonadal sheath distal) 0.037	F33H1.4	0.03961598065554	0.0490641602019606
sh1 (gonadal sheath distal) 0.037	F44E2.7	0.000159093098322926	0.00466287837521603
sh1 (gonadal sheath distal) 0.037	hinf-1	0.147583748811246	0.151078669148744
sh1 (gonadal sheath distal) 0.037	hlh-8	0.042474559266206	0.0391748529498566
sh1 (gonadal sheath distal) 0.037	hsf-1	0.0182250838683597	0.0213092924602777
sh1 (gonadal sheath distal) 0.037	lag-1	0.00784475577485754	0.0641382085286715
sh1 (gonadal sheath distal) 0.037	let-607	0.0165844557915287	0.025423353175548
sh1 (gonadal sheath distal) 0.037	lim-7	0.0588661692001059	0.0675651891847829

sh1 (gonadal sheath distal)	0.037	lin-26	0.135029550816104	0.133210895408741
sh1 (gonadal sheath distal)	0.037	lin-40	0.105207785594167	0.072628914760201
sh1 (gonadal sheath distal)	0.037	lin-54	0.0153222640167254	0.0223084568254464
sh1 (gonadal sheath distal)	0.037	lsy-2	0.0335488398498469	0.0350187787792527
sh1 (gonadal sheath distal)	0.037	madf-3	0.0649177257178696	0.0696403305052724
sh1 (gonadal sheath distal)	0.037	madf-5	0.169839287968386	0.146261199372177
sh1 (gonadal sheath distal)	0.037	madf-6	0.0161532878215585	0.0256464297583035
sh1 (gonadal sheath distal)	0.037	madf-9	0.0425976847099344	0.0237537085164726
sh1 (gonadal sheath distal)	0.037	mdt-29	0.012773932246141	0.0233710936290372
sh1 (gonadal sheath distal)	0.037	nhr-11	0.0183869232210388	0.0123915773198136
sh1 (gonadal sheath distal)	0.037	nhr-179	0.0206731922427043	0
sh1 (gonadal sheath distal)	0.037	pag-3	0.0896911800151932	0.08485733169819
sh1 (gonadal sheath distal)	0.037	pat-9	0.231172023832232	0.229635126879573
sh1 (gonadal sheath distal)	0.037	pbrm-1	0.00346302371426092	0.00231955870003705
sh1 (gonadal sheath distal)	0.037	R02D3.7	0.0203708437139978	0.0210710475399718
sh1 (gonadal sheath distal)	0.037	rnt-1	NA	0.00490237300267799
sh1 (gonadal sheath distal)	0.037	skn-1	2.26849268018585e-07	0.00277873758395767
sh1 (gonadal sheath distal)	0.037	sptf-2	0.495829342094677	0.513060801467184
sh1 (gonadal sheath distal)	0.037	tlp-1	0.00685689364995885	0.00705248313232862
sh1 (gonadal sheath distal)	0.037	Y53G8AR.9	0.0195691484968525	0.0156139011273192
sh1 (gonadal sheath distal)	0.037	Y56A3A.18	0.0626223151482149	0.0658974257107192
sh1 (gonadal sheath distal)	0.037	zfh-2	0.0635462210767798	0.0604379097231568
sh1 (gonadal sheath distal)	0.037	zim-3	0.0438558689637087	0.0382915849307729
sh1 (gonadal sheath distal)	0.037	ZK546.5	0	0.0381262079107133
sh1 (gonadal sheath distal)	0.037	ztf-26	0.0929900367331973	0.0462610940843728
sh2 (gonadal sheath distal)	0.041	alr-1	0.253433270548168	0.255524363363826
sh2 (gonadal sheath distal)	0.041	attf-6	0.0206804747708907	0.0166906267994521
sh2 (gonadal sheath distal)	0.041	cebp-1	0.00472601041524468	0.0052034281297575
sh2 (gonadal sheath distal)	0.041	ceh-40	0.124666364221286	0.129293188933856
sh2 (gonadal sheath distal)	0.041	ceh-58	0.010247712810521	0.0179244021321169
sh2 (gonadal sheath distal)	0.041	chd-7	0.00628268912356343	0.0100585266075979
sh2 (gonadal sheath distal)	0.041	crh-2	0	0.000908277250860192
sh2 (gonadal sheath distal)	0.041	daf-16	0.00180300432202177	0.00202457376894023
sh2 (gonadal sheath distal)	0.041	daf-19	0.104171293026258	0.102117483723244
sh2 (gonadal sheath distal)	0.041	dsc-1	0.00332346881768483	0.00172425609175938
sh2 (gonadal sheath distal)	0.041	efl-3	0.185496059808733	0.145781282332523
sh2 (gonadal sheath distal)	0.041	egl-18	0.0165794788651402	0.0140519137118767
sh2 (gonadal sheath distal)	0.041	ekl-4	0.0871258767527734	0.0894046878699815
sh2 (gonadal sheath distal)	0.041	ets-5	0.0179212676500659	0.0195948985222787
sh2 (gonadal sheath distal)	0.041	F22D6.2	0.0544740985845364	0
sh2 (gonadal sheath distal)	0.041	F33H1.4	0.0331720571031372	0.0329883941311011
sh2 (gonadal sheath distal)	0.041	F44E2.7	0.00700918381774819	0
sh2 (gonadal sheath distal)	0.041	hinf-1	0.1118526860003	0.121693623583392

sh2 (gonadal sheath distal) 0.041	hlh-1	0.00423483739844736	0.0023724750779477
sh2 (gonadal sheath distal) 0.041	hlh-8	0.0719527110656457	0.0591878022275715
sh2 (gonadal sheath distal) 0.041	hsf-1	0.0155516085684774	0.0181900173799744
sh2 (gonadal sheath distal) 0.041	lag-1	0	0.0244024955250326
sh2 (gonadal sheath distal) 0.041	let-607	0.0320215039425784	0.0349572691833789
sh2 (gonadal sheath distal) 0.041	lim-7	0.0759133852335637	0.0794884176736015
sh2 (gonadal sheath distal) 0.041	lin-11	0.0189091187145595	0.00956385851004166
sh2 (gonadal sheath distal) 0.041	lin-26	0.108772859460285	0.105145448748881
sh2 (gonadal sheath distal) 0.041	lin-40	0.0463366254675414	0.0248438116128234
sh2 (gonadal sheath distal) 0.041	lin-54	0	0.000719179319733283
sh2 (gonadal sheath distal) 0.041	lsy-2	0.0357026004230527	0.0337669019512249
sh2 (gonadal sheath distal) 0.041	madf-3	0.0547159259834459	0.0582735455368744
sh2 (gonadal sheath distal) 0.041	madf-5	0.117832550375452	0.0975086882485914
sh2 (gonadal sheath distal) 0.041	madf-6	0.0115165565801201	0.0125008224657545
sh2 (gonadal sheath distal) 0.041	madf-9	0.023290311455203	0
sh2 (gonadal sheath distal) 0.041	mdt-29	0.0269069746823949	0.0317618601718253
sh2 (gonadal sheath distal) 0.041	mep-1	0.00670941588310884	0.00108363623773741
sh2 (gonadal sheath distal) 0.041	nfyb-1	0.0129264212152216	0.0145132063655378
sh2 (gonadal sheath distal) 0.041	nhr-11	0.0140522798503692	0.0129067210609165
sh2 (gonadal sheath distal) 0.041	nhr-129	0.00524859607194869	0
sh2 (gonadal sheath distal) 0.041	nhr-232	0.0212349009043001	0
sh2 (gonadal sheath distal) 0.041	nhr-71	0.000906794312758276	0
sh2 (gonadal sheath distal) 0.041	pag-3	0.108778802539904	0.101367681669541
sh2 (gonadal sheath distal) 0.041	pat-9	0.227335753842322	0.201401759639448
sh2 (gonadal sheath distal) 0.041	R02D3.7	0.0169333707779902	0.013018640379577
sh2 (gonadal sheath distal) 0.041	rnt-1	0.0165685365298602	0.0178277388571605
sh2 (gonadal sheath distal) 0.041	sptf-2	0.414695033137056	0.439472037340653
sh2 (gonadal sheath distal) 0.041	tbx-8	NA	0.0367665096572681
sh2 (gonadal sheath distal) 0.041	tlp-1	0.0158640157839936	0.00521244755195448
sh2 (gonadal sheath distal) 0.041	Y53G8AR.9	0.0214554667561104	0.0193421415784498
sh2 (gonadal sheath distal) 0.041	Y56A3A.18	0.0481593095858158	0.0528146325626339
sh2 (gonadal sheath distal) 0.041	zfh-2	0.0651850154020929	0.0610283133275887
sh2 (gonadal sheath distal) 0.041	zim-3	0.0290527260680079	0.0190765799793106
sh2 (gonadal sheath distal) 0.041	ZK546.5	0.112923769029397	0.119889906759156
sh2 (gonadal sheath distal) 0.041	ztf-1	0.00166826339928271	0
sh2 (gonadal sheath distal) 0.041	ztf-26	0.037022416932617	0.00477109307501877
sh3_sh4 (gonadal sheath proximal) 0.038	alr-1	0.239383206980195	0.234837479712277
sh3_sh4 (gonadal sheath proximal) 0.038	attf-6	0.00697501683071334	0.00429726858897572
sh3_sh4 (gonadal sheath proximal) 0.038	cebp-1	0.0126884272253238	0.0101010086242962
sh3_sh4 (gonadal sheath proximal) 0.038	ceh-18	0.0562731269366079	0.0474472393542658
sh3_sh4 (gonadal sheath proximal) 0.038	ceh-40	0.105407762121777	NA
sh3_sh4 (gonadal sheath proximal) 0.038	ceh-58	0.0101421647549551	0.028152189571581
sh3_sh4 (gonadal sheath proximal) 0.038	ceh-63	0.00447241036052416	0

sh3_sh4 (gonadal sheath proximal) 0.038	chd-7	0.00696947775565603	0
sh3_sh4 (gonadal sheath proximal) 0.038	daf-16	0.000123995671919481	0
sh3_sh4 (gonadal sheath proximal) 0.038	daf-19	0.111424502723865	0.112894905612326
sh3_sh4 (gonadal sheath proximal) 0.038	dsc-1	0.00794224012677634	NA
sh3_sh4 (gonadal sheath proximal) 0.038	efl-3	0.318616156170779	0.273127695192502
sh3_sh4 (gonadal sheath proximal) 0.038	egl-18	0.0201279267938599	0.0212252525379688
sh3_sh4 (gonadal sheath proximal) 0.038	ekl-4	0.0855046282130549	0.0880029287091619
sh3_sh4 (gonadal sheath proximal) 0.038	ets-5	0.012769307466183	0.0115034861906087
sh3_sh4 (gonadal sheath proximal) 0.038	F22D6.2	0.0344924672222596	0
sh3_sh4 (gonadal sheath proximal) 0.038	F33H1.4	0.0294258426548258	0.0256018807662027
sh3_sh4 (gonadal sheath proximal) 0.038	hinf-1	0.0993591288378412	0.116622006622511
sh3_sh4 (gonadal sheath proximal) 0.038	hlh-1	0.00486541874952226	0.00356641840030456
sh3_sh4 (gonadal sheath proximal) 0.038	hlh-8	0.0904872593863904	0.0774940305195504
sh3_sh4 (gonadal sheath proximal) 0.038	hsf-1	0.0268848585069987	0.0290275135519579
sh3_sh4 (gonadal sheath proximal) 0.038	let-607	0.0246295586572046	0.0259731475189466
sh3_sh4 (gonadal sheath proximal) 0.038	lim-7	0.0805286159073335	0.0740143246700794
sh3_sh4 (gonadal sheath proximal) 0.038	lin-11	0.0152356161908833	0.00169523087143894
sh3_sh4 (gonadal sheath proximal) 0.038	lin-26	0.0950513515866016	0.0892412490866813
sh3_sh4 (gonadal sheath proximal) 0.038	lin-40	0.0341652482395545	0.014555251738212
sh3_sh4 (gonadal sheath proximal) 0.038	lin-54	0.000218153733631057	0.00286914531552422
sh3_sh4 (gonadal sheath proximal) 0.038	lsy-2	0.0371708953643024	0.031637695297736
sh3_sh4 (gonadal sheath proximal) 0.038	madf-2	0.0295500458685041	0
sh3_sh4 (gonadal sheath proximal) 0.038	madf-3	0.0498534864218407	0.0544532678320993
sh3_sh4 (gonadal sheath proximal) 0.038	madf-5	0.112834915807766	0.0909836989299953
sh3_sh4 (gonadal sheath proximal) 0.038	madf-6	0.00902799579133185	0.00630142734843806
sh3_sh4 (gonadal sheath proximal) 0.038	mdt-29	0.0421136785458159	0.0473389302423022
sh3_sh4 (gonadal sheath proximal) 0.038	nfyb-1	0.00280422865952515	0
sh3_sh4 (gonadal sheath proximal) 0.038	nhr-11	0.0115132375231446	0.00699808560465921
sh3_sh4 (gonadal sheath proximal) 0.038	nhr-129	0.000334186306490808	0
sh3_sh4 (gonadal sheath proximal) 0.038	pag-3	0.154653285772283	0.14333436495347
sh3_sh4 (gonadal sheath proximal) 0.038	pat-9	0.474795312854067	0.44329835049048
sh3_sh4 (gonadal sheath proximal) 0.038	R02D3.7	0.0111229266469559	0.00649909118312221
sh3_sh4 (gonadal sheath proximal) 0.038	rnt-1	0.020943750409153	0.0212551866566392
sh3_sh4 (gonadal sheath proximal) 0.038	skn-1	0.000981335681532478	0
sh3_sh4 (gonadal sheath proximal) 0.038	sptf-2	0.380837793803387	0.412533828899805
sh3_sh4 (gonadal sheath proximal) 0.038	sup-37	0.0156606829831908	0
sh3_sh4 (gonadal sheath proximal) 0.038	syd-9	0.0198124184423905	0
sh3_sh4 (gonadal sheath proximal) 0.038	tlp-1	0.0183184815763033	0.00824852320145817
sh3_sh4 (gonadal sheath proximal) 0.038	unc-120	0.0069936898852362	0.00620375319058963
sh3_sh4 (gonadal sheath proximal) 0.038	Y53G8AR.9	0.0133324379897924	0.0114680204420907
sh3_sh4 (gonadal sheath proximal) 0.038	Y56A3A.18	0.0443742835096414	0.0520967281301175
sh3_sh4 (gonadal sheath proximal) 0.038	zfh-2	0.0611340935964064	0.0539241299002421
sh3_sh4 (gonadal sheath proximal) 0.038	ztf-1	0.0261434000575958	0.0125981812752811

sh3_sh4 (gonadal sheath proximal) 0.038	ztf-26	0.0279928346311635	0.00357539329462699
sh5 (gonadal sheath proximal) 0.047	aha-1	0	0.0135893241376096
sh5 (gonadal sheath proximal) 0.047	alr-1	0.212912511968921	NA
sh5 (gonadal sheath proximal) 0.047	attf-6	0.00168148470386697	0
sh5 (gonadal sheath proximal) 0.047	ceh-18	0.199505676909786	0.251866572815375
sh5 (gonadal sheath proximal) 0.047	ceh-34	2.22981706543729e-05	0
sh5 (gonadal sheath proximal) 0.047	ceh-58	0	0.000621965798903575
sh5 (gonadal sheath proximal) 0.047	chd-7	0.0230793096243243	0.0198250164777172
sh5 (gonadal sheath proximal) 0.047	daf-12	0.0620052137206289	0.0259949053833811
sh5 (gonadal sheath proximal) 0.047	daf-16	0.0139279032563476	0.0157948596818443
sh5 (gonadal sheath proximal) 0.047	daf-19	0.0842757792768585	0.0992526062211734
sh5 (gonadal sheath proximal) 0.047	egl-18	0.00397925611841749	0.00816186713612696
sh5 (gonadal sheath proximal) 0.047	egl-5	0.0142106395482585	0.00163605626731982
sh5 (gonadal sheath proximal) 0.047	ekl-4	0.0746496322342142	0.0786929753555516
sh5 (gonadal sheath proximal) 0.047	F22D6.2	0.0350844416246103	0
sh5 (gonadal sheath proximal) 0.047	F33H1.4	0.0260060748786506	0.0198247582049162
sh5 (gonadal sheath proximal) 0.047	hif-1	0.00903805946035451	0
sh5 (gonadal sheath proximal) 0.047	hinf-1	0.114264329171124	0.127105037977445
sh5 (gonadal sheath proximal) 0.047	hlh-1	0.0267602068380813	0.0328073531079025
sh5 (gonadal sheath proximal) 0.047	hlh-8	0.14684993186244	NA
sh5 (gonadal sheath proximal) 0.047	hsf-1	0.0239484247758342	0.0264025649333508
sh5 (gonadal sheath proximal) 0.047	let-607	0.0065577140447669	0.0104694744306232
sh5 (gonadal sheath proximal) 0.047	lim-7	0.077507412392451	0.076698475482314
sh5 (gonadal sheath proximal) 0.047	lin-26	0.0986916989535925	0.0941327313494976
sh5 (gonadal sheath proximal) 0.047	lin-40	0.0397037368594462	0.0485019116067938
sh5 (gonadal sheath proximal) 0.047	lin-54	0.00886118045254569	0.00550524629828009
sh5 (gonadal sheath proximal) 0.047	lsy-2	0.0291808649115836	0.0236892313196343
sh5 (gonadal sheath proximal) 0.047	madf-3	0.0599046822975022	0.0618751146998556
sh5 (gonadal sheath proximal) 0.047	madf-5	0.126409274238971	NA
sh5 (gonadal sheath proximal) 0.047	madf-6	0.0244456449805063	0.0200091139475119
sh5 (gonadal sheath proximal) 0.047	mdt-29	0.0171402742251205	0.0248045220103442
sh5 (gonadal sheath proximal) 0.047	nhr-11	0.0311490599936709	0.0285509415970779
sh5 (gonadal sheath proximal) 0.047	nhr-19	0.0372196531205783	0.0265492981141766
sh5 (gonadal sheath proximal) 0.047	nhr-71	0.0132167479596457	0.0122063683413038
sh5 (gonadal sheath proximal) 0.047	pag-3	0.278340416448075	NA
sh5 (gonadal sheath proximal) 0.047	pat-9	0.756063253848344	0.795954027102197
sh5 (gonadal sheath proximal) 0.047	pbrm-1	0.000509045154067661	0
sh5 (gonadal sheath proximal) 0.047	R02D3.7	0.0239087149589124	0.018784046741217
sh5 (gonadal sheath proximal) 0.047	rnt-1	NA	0.0558248948953474
sh5 (gonadal sheath proximal) 0.047	skn-1	0.0086549037252085	0.00169572431378169
sh5 (gonadal sheath proximal) 0.047	sptf-2	0.398492681116078	0.432153637873983
sh5 (gonadal sheath proximal) 0.047	sup-37	0.390733650339925	0.336798467980164
sh5 (gonadal sheath proximal) 0.047	syd-9	0.00905076319284347	0.033325857481917

sh5 (gonadal sheath proximal) 0.047	T26A5.8	0.047461486223743	0.0187458810960211
sh5 (gonadal sheath proximal) 0.047	tlp-1	0.0184121236732709	0.0134002903384923
sh5 (gonadal sheath proximal) 0.047	unc-120	0.0253330861272577	0.0453564930140449
sh5 (gonadal sheath proximal) 0.047	Y53G8AR.9	0.0246852810284958	0.0189480836172044
sh5 (gonadal sheath proximal) 0.047	Y56A3A.18	0.0480329221477756	0.0504065621001021
sh5 (gonadal sheath proximal) 0.047	zfh-2	0.0617432356916686	0.0619365937529319
sh5 (gonadal sheath proximal) 0.047	zim-3	0.0299472122692971	0.0291528605057211
sh5 (gonadal sheath proximal) 0.047	ztf-26	0.0132842395241079	0.0130683838408538
uv1 (uterine-vulval cells) 0.040	attf-6	0.0107258154709735	0.00699410931116721
uv1 (uterine-vulval cells) 0.040	C34B4.2	0.0830491721269485	0.148922378121301
uv1 (uterine-vulval cells) 0.040	cebp-1	0.00653884551656282	0.00831582472905492
uv1 (uterine-vulval cells) 0.040	crh-2	0.0299751119353195	0.0283425134359805
uv1 (uterine-vulval cells) 0.040	ctbp-1	NA	0.0594568176766889
uv1 (uterine-vulval cells) 0.040	daf-19	0.124105657591772	0.117834291073849
uv1 (uterine-vulval cells) 0.040	egl-27	0	0.00576760834661114
uv1 (uterine-vulval cells) 0.040	ekl-4	0.0362873709705725	0.0251635239856891
uv1 (uterine-vulval cells) 0.040	elt-4	0.00390388798220908	NA
uv1 (uterine-vulval cells) 0.040	F22D6.2	0.0692515246377815	0.025546767975249
uv1 (uterine-vulval cells) 0.040	fkh-8	NA	0.000958737217824059
uv1 (uterine-vulval cells) 0.040	hinf-1	0.0684331321149395	0.0515466601865256
uv1 (uterine-vulval cells) 0.040	hsf-1	0.000474465836559329	0
uv1 (uterine-vulval cells) 0.040	isw-1	0.00383602049071935	0.0004299353388621
uv1 (uterine-vulval cells) 0.040	let-607	4.70376401410247e-05	0
uv1 (uterine-vulval cells) 0.040	lim-7	NA	0.00843900078543045
uv1 (uterine-vulval cells) 0.040	lin-11	0.094528885191758	0.108897146903045
uv1 (uterine-vulval cells) 0.040	lin-14	0.0307706532889538	0.0342994615430054
uv1 (uterine-vulval cells) 0.040	lin-26	0.0566000712500798	0.048852695365244
uv1 (uterine-vulval cells) 0.040	lin-40	0.0961806546492949	0.0704306111155204
uv1 (uterine-vulval cells) 0.040	lsy-2	0.00794696042110025	0.00371699643127388
uv1 (uterine-vulval cells) 0.040	madf-3	0.0468469287619936	0.0422669927686553
uv1 (uterine-vulval cells) 0.040	madf-5	0.0815528812946648	NA
uv1 (uterine-vulval cells) 0.040	mdt-29	0.0174560365878863	0.0516262179135063
uv1 (uterine-vulval cells) 0.040	mep-1	0	0.00476549791964146
uv1 (uterine-vulval cells) 0.040	nfya-1	0.00115792766558011	NA
uv1 (uterine-vulval cells) 0.040	nhr-11	0.00788109711652043	NA
uv1 (uterine-vulval cells) 0.040	nhr-129	0.0170463630706136	NA
uv1 (uterine-vulval cells) 0.040	pag-3	0.00952956209009189	NA
uv1 (uterine-vulval cells) 0.040	pat-9	0.148112759158278	NA
uv1 (uterine-vulval cells) 0.040	pbrm-1	0.000253887451532678	0.0102815144648772
uv1 (uterine-vulval cells) 0.040	sem-4	0.0152056423241569	NA
uv1 (uterine-vulval cells) 0.040	sox-4	0.0490867724944086	0.045772266405346
uv1 (uterine-vulval cells) 0.040	sptf-2	0.213727485482662	NA
uv1 (uterine-vulval cells) 0.040	Y53G8AR.9	NA	0.00399072863411432

uv1 (uterine-vulval cells) 0.040	Y55F3AM.14	0.0177277860518707	NA
uv1 (uterine-vulval cells) 0.040	Y56A3A.18	0.0190308843400956	0.0201599619927965
uv1 (uterine-vulval cells) 0.040	zfh-2	0.0280826560228275	0.0274068585690394
uv1 (uterine-vulval cells) 0.040	ZK546.5	0	0.0406444675918797
uv1 (uterine-vulval cells) 0.040	ztf-1	0.000179752045760599	0.00471838341368248
uv1 (uterine-vulval cells) 0.040	ztf-26	NA	0.0140529632306229
vm1 (vulval muscle) 0.056	alr-1	0.0879426657212938	NA
vm1 (vulval muscle) 0.056	baz-2	0.00877779003923469	0.0247595562797151
vm1 (vulval muscle) 0.056	C04F5.9	0	0.0182860129398652
vm1 (vulval muscle) 0.056	ceh-18	0.165980362324005	0.296399669552624
vm1 (vulval muscle) 0.056	ceh-22	NA	0.0924067403675516
vm1 (vulval muscle) 0.056	ceh-58	0.00316992907215897	0.00589288408476927
vm1 (vulval muscle) 0.056	chd-7	0.0140482675455993	0.050351245237982
vm1 (vulval muscle) 0.056	crh-2	0.00227236575378503	0.0196263802089793
vm1 (vulval muscle) 0.056	D1046.2	0	0.000480054854441517
vm1 (vulval muscle) 0.056	daf-16	0.0208094856256543	0.036254514294924
vm1 (vulval muscle) 0.056	daf-19	0.0426100804718336	0.0815904100601423
vm1 (vulval muscle) 0.056	daf-8	0.048169870347285	NA
vm1 (vulval muscle) 0.056	egl-18	0.0928494351813956	0.147059876346599
vm1 (vulval muscle) 0.056	ekl-4	0.0322158065116406	0.0599498804085625
vm1 (vulval muscle) 0.056	eor-1	0	0.0152357893301517
vm1 (vulval muscle) 0.056	ets-5	0.0265867407491821	0.0520656649369555
vm1 (vulval muscle) 0.056	hinf-1	0.0371139130634845	0.0635262126512158
vm1 (vulval muscle) 0.056	hlh-1	0.074934741735168	NA
vm1 (vulval muscle) 0.056	hlh-11	0	0.0233944049832159
vm1 (vulval muscle) 0.056	hlh-8	0.485581389135326	0.526707563343873
vm1 (vulval muscle) 0.056	hsf-1	0.0248594569270942	0.0298272133690947
vm1 (vulval muscle) 0.056	let-607	0	0.0132594184639194
vm1 (vulval muscle) 0.056	lim-7	0.00879087553830879	0.0403516471765817
vm1 (vulval muscle) 0.056	lin-14	0.00031899208079839	0.0291717806157902
vm1 (vulval muscle) 0.056	lin-26	0.0197778367840963	0.039763712979733
vm1 (vulval muscle) 0.056	lin-40	0	0.000174989152184116
vm1 (vulval muscle) 0.056	lin-54	0	0.0100975542729797
vm1 (vulval muscle) 0.056	lsy-2	0	0.00946605686100535
vm1 (vulval muscle) 0.056	M03D4.4	0	0.0515972499840178
vm1 (vulval muscle) 0.056	madf-3	0.00672812610472099	NA
vm1 (vulval muscle) 0.056	madf-5	0.0630027783141091	0.103945802600823
vm1 (vulval muscle) 0.056	madf-6	0	0.00267612979711951
vm1 (vulval muscle) 0.056	mdt-29	0.0082345837002971	0.0249708692171301
vm1 (vulval muscle) 0.056	nhr-102	0.0081643511354917	0.0200977690151015
vm1 (vulval muscle) 0.056	nhr-129	0.00921422511422862	0.0579666191836996
vm1 (vulval muscle) 0.056	nhr-19	0	0.0233992244048279
vm1 (vulval muscle) 0.056	nhr-71	0	0.0516107201715162

vm1 (vulval muscle) 0.056	pag-3	0.386564764933555	NA
vm1 (vulval muscle) 0.056	pat-9	1.17147745855825	1.27615535136118
vm1 (vulval muscle) 0.056	pbrm-1	0	0.0114008469841217
vm1 (vulval muscle) 0.056	R02D3.7	0	0.00513389924602804
vm1 (vulval muscle) 0.056	rnt-1	0.138704981415782	NA
vm1 (vulval muscle) 0.056	somi-1	0	0.047908807207592
vm1 (vulval muscle) 0.056	sptf-2	0.301718446693855	0.414972804096297
vm1 (vulval muscle) 0.056	syd-9	0.361333266316301	0.355162788493718
vm1 (vulval muscle) 0.056	tlp-1	0	0.0225484559857274
vm1 (vulval muscle) 0.056	unc-120	0.0707522952540586	0.155846401534559
vm1 (vulval muscle) 0.056	unc-62	0	0.00501918683700613
vm1 (vulval muscle) 0.056	Y56A3A.18	0.0138866528938659	0.0320577491407064
vm1 (vulval muscle) 0.056	zfh-2	0.0546684966339063	0.0748329660438646
vm1 (vulval muscle) 0.056	ZK546.5	0	0.112091153366717
vm1 (vulval muscle) 0.056	ztf-1	0	0.110441076363233
vm1 (vulval muscle) 0.056	ztf-7	0.0434599119381006	0.0273816803380037
vm2 (vulval muscle) 0.051	aha-1	0.0186243604102416	0.00975162287898997
vm2 (vulval muscle) 0.051	alr-1	0.100689102289885	0.129651832668188
vm2 (vulval muscle) 0.051	ceh-18	0.409795582436689	0.293882137286947
vm2 (vulval muscle) 0.051	ceh-22	0.14029697404506	NA
vm2 (vulval muscle) 0.051	ceh-34	0.020087083897098	0.0105549631943718
vm2 (vulval muscle) 0.051	chd-7	0.0470191552038296	0.0203884743039243
vm2 (vulval muscle) 0.051	crh-2	0.00417422462360431	0.000969412607906582
vm2 (vulval muscle) 0.051	ctbp-1	0.0111611434002115	NA
vm2 (vulval muscle) 0.051	daf-16	0.0301065571194709	0.0191909426417461
vm2 (vulval muscle) 0.051	daf-19	0.0599594171170746	0.0740557816463411
vm2 (vulval muscle) 0.051	daf-8	0.00942907093176139	0.00353076757651251
vm2 (vulval muscle) 0.051	dsc-1	0.113150241208915	0.114472771468361
vm2 (vulval muscle) 0.051	egl-18	0.0453420484105961	0.0622093405201847
vm2 (vulval muscle) 0.051	egl-5	0.0275544885195521	0.0194396354207458
vm2 (vulval muscle) 0.051	ekl-4	0.0479931622766857	0.0532123894734613
vm2 (vulval muscle) 0.051	F22D6.2	0.0256929030071783	0.00186651909815717
vm2 (vulval muscle) 0.051	hinf-1	0.0714570170703568	0.080284204236172
vm2 (vulval muscle) 0.051	hlh-1	NA	0.0330141882693446
vm2 (vulval muscle) 0.051	hlh-11	0.0273753097163882	0.00933813017239594
vm2 (vulval muscle) 0.051	hlh-8	0.316244168177045	0.279756345672407
vm2 (vulval muscle) 0.051	hsf-1	0.0180220827330815	0.0128341216739707
vm2 (vulval muscle) 0.051	lim-7	0.0325113928943394	0.0471064781109414
vm2 (vulval muscle) 0.051	lin-14	0.0195450409043386	0
vm2 (vulval muscle) 0.051	lin-26	0.0472297413388238	0.0559231930270594
vm2 (vulval muscle) 0.051	lin-40	0.0481856281060745	0.00710175059610131
vm2 (vulval muscle) 0.051	lin-54	0.000848011467065453	0
vm2 (vulval muscle) 0.051	lsy-2	0.0106139499032332	0.00801337889156522

vm2 (vulval muscle) 0.051	M03D4.4	0.0924353591339484	NA
vm2 (vulval muscle) 0.051	madf-3	0.0277078118530256	0.0399610086786586
vm2 (vulval muscle) 0.051	madf-5	0.122571181695211	0.102815767546974
vm2 (vulval muscle) 0.051	madf-6	0.000494934902317757	0
vm2 (vulval muscle) 0.051	mdt-29	0.0379015021512663	0.0400071212008464
vm2 (vulval muscle) 0.051	nhr-102	0.000946681120942034	0.00683590667028445
vm2 (vulval muscle) 0.051	nhr-11	0.0212957021205148	0.0197694683019712
vm2 (vulval muscle) 0.051	nhr-129	0.0208921259688492	NA
vm2 (vulval muscle) 0.051	nhr-19	0.0289132640022067	0.0220789131994017
vm2 (vulval muscle) 0.051	nhr-237	0	0.020628900060082
vm2 (vulval muscle) 0.051	nhr-71	0.0303587437734481	0.0192210445485647
vm2 (vulval muscle) 0.051	pag-3	NA	0.384279305899264
vm2 (vulval muscle) 0.051	pat-9	1.37702294806244	1.25115475115709
vm2 (vulval muscle) 0.051	pbrm-1	0.00556207502726898	0.0112058139931312
vm2 (vulval muscle) 0.051	R02D3.7	0.0124855117894491	0.00954117420748552
vm2 (vulval muscle) 0.051	sptf-2	0.252419937983763	NA
vm2 (vulval muscle) 0.051	sup-37	0.0792511748552352	0.140757638759187
vm2 (vulval muscle) 0.051	syd-9	0.280141361804041	0.149537859609526
vm2 (vulval muscle) 0.051	tlp-1	0.0260357736541727	0.0350608277936985
vm2 (vulval muscle) 0.051	unc-120	0.0847615962711575	0.0300223346874377
vm2 (vulval muscle) 0.051	Y53G8AR.9	0.00271045005398702	0.0101182324228085
vm2 (vulval muscle) 0.051	Y56A3A.18	0.0281941964682719	0.0337726827801527
vm2 (vulval muscle) 0.051	zfh-2	0.075408047703942	0.0699034829509439
vm2 (vulval muscle) 0.051	ZK546.5	0.124008939752975	0.135578205311597
vm2 (vulval muscle) 0.051	ztf-1	0.0169954446478025	0.000991300707185245
vm2 (vulval muscle) 0.051	ztf-26	0.0192509906465055	0

Appendix Table S4. August analysis results. AUC = Area Under the Curve. A higher AUC indicates higher responsiveness to excess fructose consumption.

cell_type	auc
M1	0.659002268
NSM	0.652639834
pm3_pm4_pm5 (pharyngeal muscle)	0.646585412
Intestine posterior	0.641738473
I2	0.639882842
I5	0.627993197
I1	0.627473545
Intestine anterior	0.621341648
mc1 (marginal cells)	0.615515873
Embryonic cells	0.61494898
M2_M3_M4	0.587437642
Coelomocytes	0.587324263
ASJ	0.584217687
CAN	0.581662887
URY	0.580941043
AVL	0.573639456
Dorsal uterine cells	0.572722978
pm6_pm7 (pharyngeal muscle)	0.571407785
RIF	0.5713322
hmc	0.566517385
ASH	0.56622449
SDQ	0.565232426
M5	0.564247921
vm2 (vulval muscle)	0.563172714
Spermatheca neck distal-most	0.562794785
RIH	0.560190854
AIN	0.559956538
e2 (pharyngeal gland)	0.559650416
RIR	0.557664399
ADA	0.556303855
AWA	0.556281179
RME	0.556241497
e1_e3 (pharyngeal epithelium)	0.555786092
Cephalic sheath	0.555714286
Glia_2	0.554761905
URX_AQR_PQR	0.553711262
sh1 (gonadal sheath distal)	0.55351096
g2 (pharyngeal gland)	0.553100907

URB	0.552987528
AUA	0.552964853
RIA	0.55191421
ALA	0.551780045
Glia_1	0.551243386
CEP_ADE_PDE	0.550965608
ASG	0.550712396
Intestine middle	0.549930083
HSN	0.549667423
Hypodermis tail	0.548150038
RIG	0.54792328
AIA	0.547513228
Intestine-Gonadal sheath doublets	0.547484883
Seminal vesicle (male)	0.546392668
pm1_pm2 (pharyngeal muscle)	0.545816327
g1P (pharyngeal gland)	0.545200302
AWB	0.545090703
Uterine-vulval cells	0.54404006
Hypodermis head	0.544021164
Hypodermis-Gonadal sheath doublet	0.543979592
Excretory duct	0.5424452
mc2_mc3 (marginal cells)	0.542190098
Mitotic germ cells	0.542069161
Arcade cells	0.541708239
VC	0.541388889
ADF	0.540765306
PVM_AVM	0.539501134
Meiotic germ cells	0.538501512
VD_DD	0.537331822
Uterine muscle	0.537210884
AVD	0.537044596
hyp4_to_hyp6	0.536972789
RIV	0.536851852
RIM	0.536662887
PVW	0.536315193
Body wall muscle middle	0.536241497
AVG	0.536039305
RMH	0.535842782
XXX	0.535508314
RIB	0.534722222
MI	0.534518141
OLQ	0.533798186

RIS	0.533590325
Vulval cells	0.533478836
AS_DA_DB_VA_VB_SAB	0.533306878
DVA	0.533229403
Oocytes	0.532830688
sh2 (gonadal sheath distal)	0.532730537
cat-4(+)ptps-1(+) intestine anterior	0.532312925
AWC	0.531562736
AVK	0.531386999
GLR	0.53084845
DVC	0.530806878
sh3_sh4 (gonadal sheath proximal)	0.530527211
RMD_DV	0.530483749
ASE	0.530366591
AIB	0.529790249
BAG	0.529417989
Body wall muscle anterior	0.528941799
RID	0.528665911
g1A (pharyngeal gland)	0.527981859
Spermatheca-Uterine junction	0.52766062
ASI	0.527176871
PVN	0.526099773
Excretory cells	0.525935374
PVD_FLP	0.525651927
PVR	0.525540438
Spermatids	0.525236206
Seam cells (grd+)	0.524905518
Differentiated germ	0.524584278
Body wall muscle posterior	0.524495465
AVJ	0.524142101
RIC	0.523741497
VC_4_5	0.523359788
AVF	0.522380952
hyp7 (hypodermis)	0.521730915
SMD	0.521326531
uv1 (uterine-vulval cells)	0.521067649
ASK	0.521007181
Excretory gland	0.520546107
Amphid sheath	0.520279667
Uterine toroid	0.520136054
Spermatheca bag distal	0.518745276
AIM	0.518628118
Uterine seam cells	0.518539305

Seam cells (bus+)	0.518412698
RMG	0.517654951
SIB	0.517573696
SMB_PLN_ALN	0.517229781
AVA	0.517150416
Phasmid socket	0.516286848
Spermatheca bag proximal	0.515753968
RMF	0.515394936
PVQ	0.512562358
AIY	0.511927438
SIA	0.511271731
sh5 (gonadal sheath proximal)	0.509765684
PVP	0.508556311
Cephalic and inner labial socket	0.508473167
AVE	0.508312547
ADL	0.508006425
IL2	0.507938398
Rectal gland	0.507613379
Spermatocytes	0.505672714
Anal muscle	0.502662509
BDU	0.502579365
URA	0.502137188
Apoptotic germ cells	0.501742252
Mature sperm	0.501738473
AFD	0.49792517
Distal tip	0.495325019
PHA_PHB	0.494289494
AVB	0.494087302
PLM_ALM	0.492815571
vm1 (vulval muscle)	0.491729025
PDA	0.484984883