An omics analysis of genetic sleep loss in *C. elegans*

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Affidavit

I herewith declare that this thesis was produced entirely by myself and that I have only used sources and materials cited. The thesis has not been submitted to any other examination board for any other academic award.

Anastasios Koutsoumparis

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"Ένα το χελιδόνι κι η Άνοιξη ακριβή,
για να γυρίσει ο ήλιος, θέλει δουλειά πολλή..."

Abbreviations

EEG	Electroencephalogram
REM	Rapid eye movement
VLPO	Ventrolateral preoptic nucleus
GABA	Gamma-amino butyric acid
SCN	Suprachiasmatic nucleus
EGF	Endothelial growth factor
FDR	False discovery rate
TGF-β	Transforming growth factor beta
FOXO	Forkhead box (transcription factor) O
ROS	Reactive oxygen species
DAG	Diacylglycerol
AMP	Adenosine monophosphate
ATP	Adenosine triphosphate
TCA	Tricarboxylic acid (cycle)
UPR	Unfolded protein response
gf	Gain of function

Abstract

Sleep is a state of consciousness that has persisted through evolution and has become a necessity for animal welfare. In humans sleep loss has been shown to be inextricably intertwined with poor health. The prevalence of sleep defects in elderly people not only associates sleep quality with aging, but also draws attention to an underrated problem that will continue to affect the life quality of the increasingly aging population of the western world.

Sleep regulates energy metabolism and higher brain functions. Little is known about the precise molecular mechanisms that control and are controlled by sleep, even though it has been extensively studied, due to its complex nature. In this thesis, I used the nematode *C. elegans,* which is a simple, yet complex enough model organism in order to discover the downstream processes that are regulated by sleep.

Although sleep is connected to development in *C. elegans*, I used sleep loss in L1 arrested worms, as a model that couples sleep, metabolism and aging phenotypes. This is more relevant to mammal physiology than developmental sleep. By genetically ablating the sleep-active neuron RIS and recruiting powerful omics techniques, I was able to identify those components of *C. elegans* physiology that are affected by sleep loss. I complemented the omics experiments with extensive genetic screening for sleep alterations in animals with defects in metabolic pathways, lifespan, egg-laying and other assays.

I was able to discover that sleep loss causes tissue-specific changes, reduces body size and increases the basal metabolic rate. Furthermore, I discovered that sleep loss upregulates the unfolded protein response in the endoplasmic reticulum by upregulating relevant transcription factors. Finally, I discovered that sleep loss causes oxidative stress and I characterized components of the life-prolonging antioxidant pathways that are directly regulated by the sleep-active neuron RIS.

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1. Introduction

1.1. The physiological state of sleep

Sleep is a state of consciousness that has persisted through evolution and has become a necessity for animal welfare. In humans (*Homo sapiens*) sleep loss has been shown to be inextricably intertwined with poor health. Insomnia and low sleep quality in general have been associated with susceptibility to infectious diseases and the untimely activation of proinflammatory immune responses that lead to the development of cardiovascular and metabolic diseases (e.g. type 2 diabetes) [1]. Furthermore, the comorbidity of insomnia and psychiatric disorders, such as depression and anxiety, has been well documented in the literature. Finally, the prevalence of sleep defects in elderly people not only associates sleep quality with aging, but also draws attention to an underrated problem that will continue to affect the life quality of the increasingly aging population of the western world [2].

Sleep studies in humans are based on electroencephalogram (EEG) readings, which show the existence of two phases with distinct characteristics: an "active" phase accompanied by rapid eye movements (REM) and a "quiet" phase (non-REM), which alternate periodically to result, on average, in 8 hours of sleep for a healthy adult [3]. Moreover, several behavioral criteria have been implemented to define the physiological state of sleep:

1. Elevated arousal threshold in response to sensory stimulation, which differentiates sleep from tranquility during wakefulness.

2. Reversibility, in the sense that the individual can easily recover its motor functions, unlike being paralyzed or in a coma.

3. Specific posture, indicative of muscle relaxation.

4. Homeostatic regulation, which compensates for sleep loss by increasing the duration of the subsequent sleep interval.

These criteria extend the notion of the sleep state to animals, in which EEG recordings are not possible [4].

So far, sleep states have been identified in all animals that possess a nervous system, the simplest ones being the jellyfish of the phylum *Cnidaria* [5]. The daily sleep fraction varies across species and depends on their environment, but a lower limit of 10% seems to exist (Figure 1) [6].

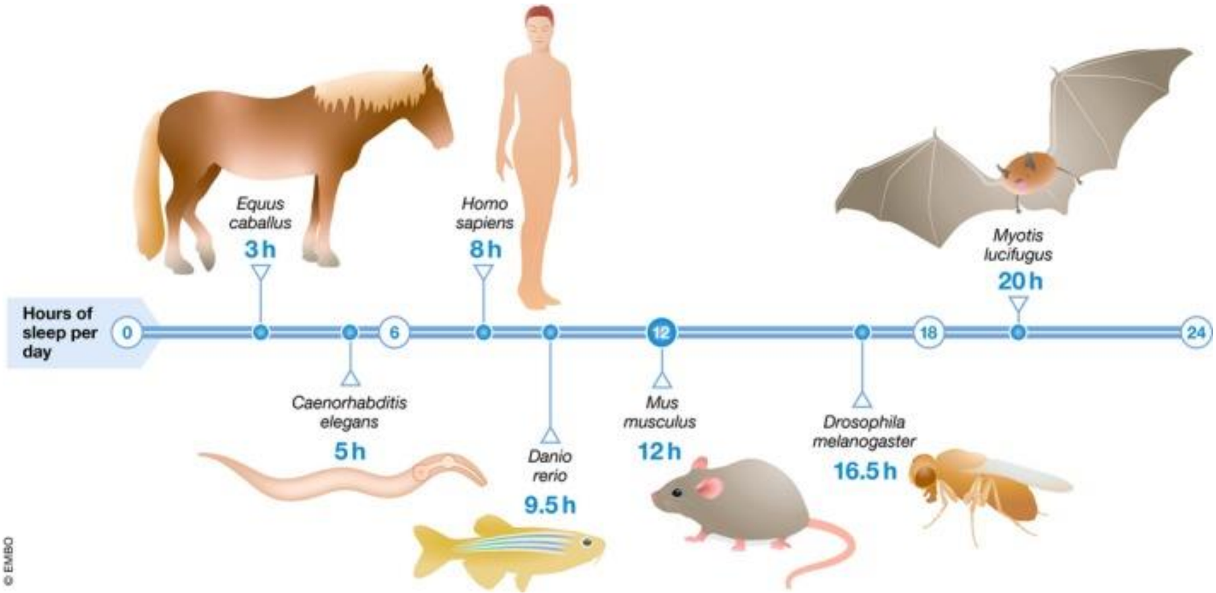

Figure 1. Daily sleep fraction variance among species
Figure adapted from Bringmann H. (2019) [6].

1.2. Sleep regulation in humans and other mammals

In humans, the wake state is controlled by the ascending arousal system. Cholinergic signals that originate in the pedunculopontine and laterodorsal tegmental nuclei of the brainstem, activate the thalamic relay neurons which activate the cerebral cortex. Complementarily, monoaminergic signals from the brainstem activate the neurons at the lateral hypothalamus, the basal forebrain and the cerebral cortex in order to promote wakefulness. On the other hand, the sleep state is controlled by the ventrolateral preoptic nucleus (VLPO). As a cluster of sleep-active neurons, the VLPO sends inhibitory signals (e.g. GABA) to the aforementioned centers of arousal. The wake-active neuronal network can in turn inhibit the VLPO, creating a flip-flop circuit, which permits fast transitions between the two states (Figure 2) [7,8]. The sleep-controlling center, VLPO, is also present in other mammals. In elderly populations, degeneration of the VLPO has been associated with poor sleep quality [9]. Additionally, other brain areas that have sleep-active neurons have been characterized in rats, such as the basal forebrain, the lateral hypothalamus and the brainstem [10].

Moreover, in studies done with mice, it was found that the appetite-promoting neuropeptide hormone orexin promotes wakefulness, establishing a link between nutritional status and sleep [11]. Human patients suffering from narcolepsy, reportedly have low levels of orexin in their cerebrospinal fluid [12].

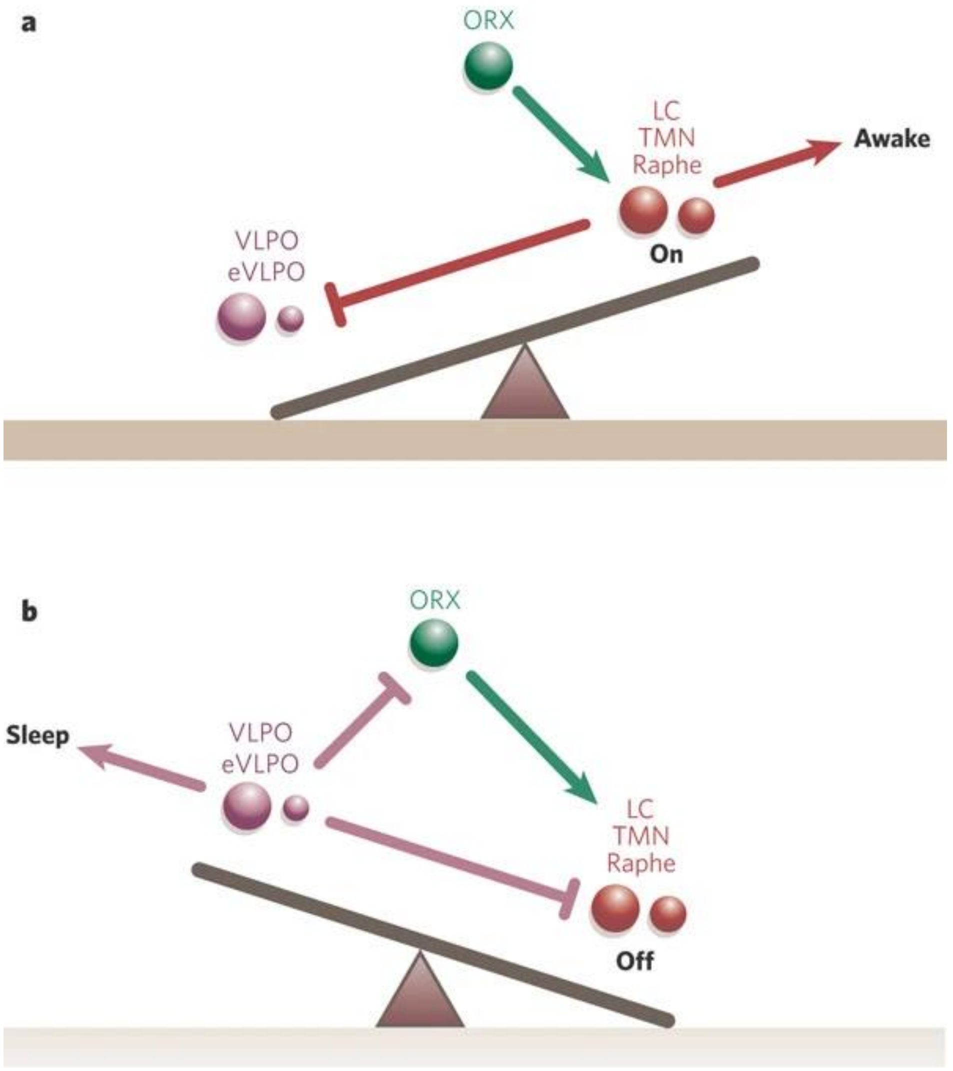

Figure 2. A flip-flop switch regulates sleep in mammals
(**A**) Wakefulness is established by cholinergic and monoaminergic nuclei (red) that inhibit the ventrolateral preoptic nucleus - VLPO (purple). This lifts the inhibition of the wake-promoting brainstem regions as well as that of the orexinergic neurons (green).
(**B**) Sleep is established by the activation of the sleep-promoting VLPO region (purple), which sends inhibitory signals to inactivate the centers of arousal (red) and orexinergic neurons (green). Crosstalk of these regions forms the sleep-regulating flip-flop switch.
ORX: orexinergic neurons, LC: locus coeruleus, TMN: tuberomammillary nucleus
Figure adapted from Saper et al. (2005) [7].

Finally, the sleep-wake cycle is controlled by the circadian clock. Humans are diurnal, as the majority of their activity happens throughout the day while rodents are nocturnal. The suprachiasmatic nucleus (SCN) is the center for circadian rhythm control and thus sleep behavior [13]. Melatonin, a sleep-promoting hormone that is secreted by the pineal gland in a circadian manner, acts on receptors at the SCN to regulate sleep by inhibiting orexinergic neurons [14,15].

1.3. Functions of sleep

Sleep is an ancient and conserved physiological process, despite the obvious disadvantage of leaving the organism open to attack by predators. It has been preserved through evolutionary pressure, indicating its importance and thus there are several hypotheses that address its purpose [16].

The most straightforward function of sleep seems to be energy conservation. However, this hypothesis has been challenged by the fact that REM sleep is a condition of increased brain energy metabolism and that, overall, the relative amount of energy saved is little compared to wakefulness. This has led to the “energy allocation” hypothesis, in which biological functions are differently regulated in a, wake- or sleep-, state-dependent manner. This allows the segregation of competing metabolic processes e.g. catabolism during wake and anabolism during sleep [17].

Apart from metabolic regulation, sleep has been shown to play a role in higher brain functions. During sleep, synapses undergo remodeling in order to achieve optimal transmission of information by removing or de-phosphorylating glutamate receptors [18]. Sleep also introduces quantitative and qualitative effects on memory representations, aiding memory consolidation [19]. Finally, chronic sleep deprivation results in accumulation of amyloid-β peptides in the brain, indicating a link to Alzheimer’s disease [20].

1.4. *C. elegans* as a model organism for sleep research

The sleep state is driven by the de-polarization of “sleep active” neurons that release inhibitory neurotransmitters [21]. However, this process is intricate and not well understood at the molecular level. Therefore, there was a necessity for a simple, yet complex enough model organism to be used in sleep research.

Caenorhabditis elegans (*C. elegans*) is a non-parasitic nematode that was introduced as a eukaryotic model organism by Sydney Brenner in 1974. It offers distinct advantages in biological research [22]:

1. All adult individuals have an exact number of 959 somatic cells, whose lineage has been traced since the start of embryogenesis. 302 of these cells constitute a simple nervous system with its wiring already characterized in a functional connectome.

2. Its genome has been sequenced and a wide selection of mutant and transgenic strains exist or can easily be created, making it a valuable tool in genetic analysis. The animals are mostly hermaphrodite (two X chromosomes), thus they have the capability to self-fertilize, although they can also cross-breed with males (one X chromosome). Furthermore, *C. elegans* is transparent, which allows for easy assessment of fluorescent transgene expression.

3. Moreover, *C. elegans* is easy to work with in the lab, since adult worms have an approximate size of 1 mm and can be observed using a simple stereo microscope. It grows on agar plates feeding on non-pathogenic *E. coli* and has a short generation time of 3 days at 20 ^{o}C. A single worm lays around 300 eggs and has an average lifespan of 18 days.

In addition to the aforementioned advantages, several quiescence states have been described in *C. elegans* that fulfill all the criteria that define the physiological state of sleep.

Sleep in *C. elegans* is most notably associated with development, through the 4 larval stages until adulthood (Figure 3). At the end of each larval stage there is a period of quiescence, characterized by reduced movement and cessation of feeding called lethargus [23]. When eggs hatch and there is no available food source, development comes to a halt and the worm repeatedly goes in and out of sleep bouts, a state termed L1 arrest quiescence [24]. Furthermore, in the presence of cellular stress e.g. in the form of heat-shock, worms enter a protective state that is also characterized by behavioral quiescence [25]. Finally, in adult individuals the fraction of sleep is dictated by the amount and the quality of the available food [24].

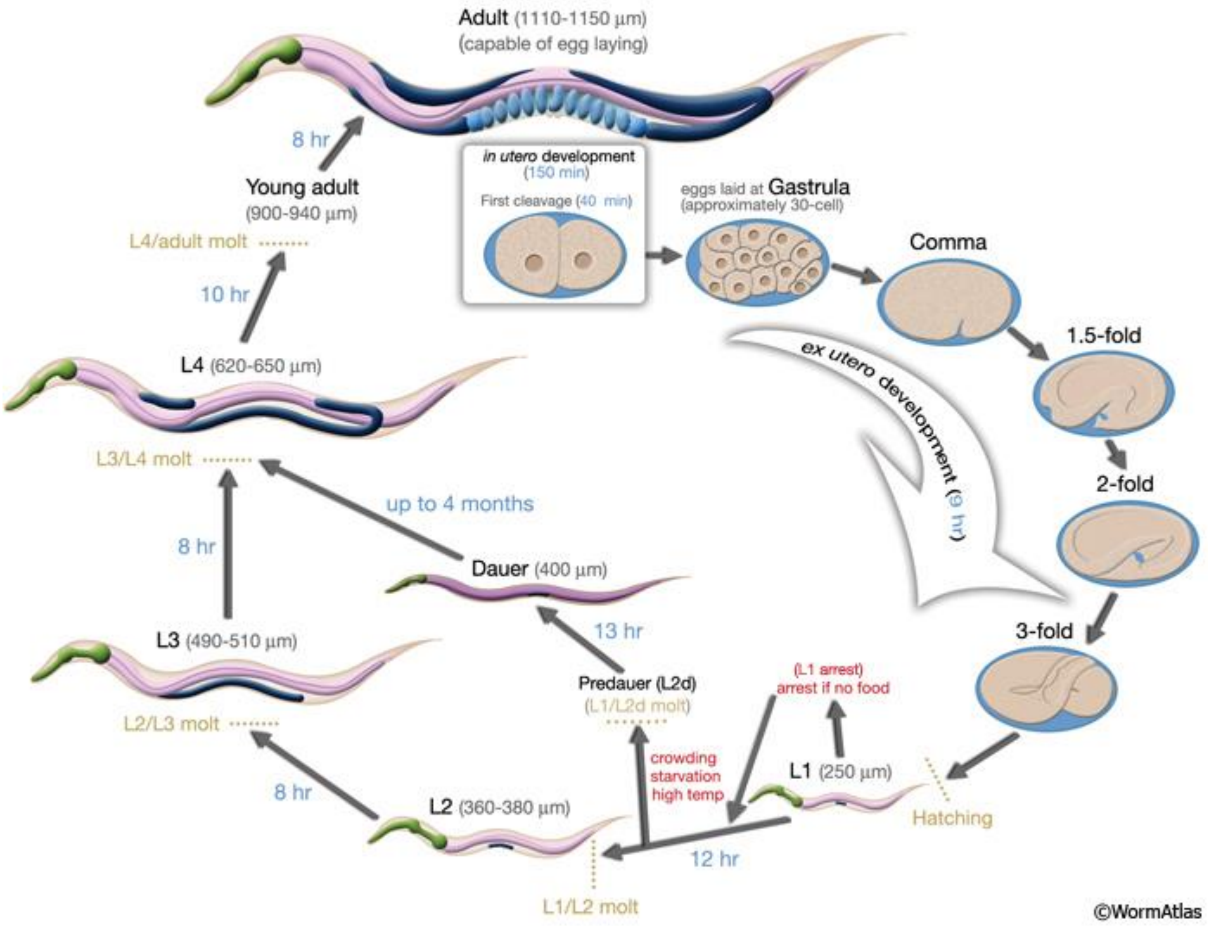

Figure 3. *C. elegans* life cycle
The molt of every larval stage is preceded by a quiescence interval (lethargus).
Starvation at the L1 stage induces sleep-bouts.
Figure adapted from Wormatlas.org

Sleep and its functions in *C. elegans* are under tight neuronal regulation. The protective response that follows a noxious stimulus, is carried out by the drowsiness-inducing neuron ALA which is activated by the EGF receptor. Genetic ablation of ALA (*ceh-14* loss of function) leads to reduced quiescence [26].

The neuron that governs all aspects of sleep behavior in *C. elegans* is the GABAergic and peptidergic head interneuron RIS. Sleep is induced by FLP-11, an RIS-specific, secreted neuropeptide. Gene expression in RIS is controlled by the AP2 transcription factor *aptf-1*, which is homologous to the human TFAP2 that has been linked to insomnia (Figure 4).

Genetic ablation of RIS either by *aptf-1* or *flp-11* loss of function leads to significant loss of sleep [27]. In turn, RIS activity is regulated by the upstream neurons PVC (cholinergic) and RIM (glutamatergic and tyraminergic) that are part of the locomotion circuit [28].

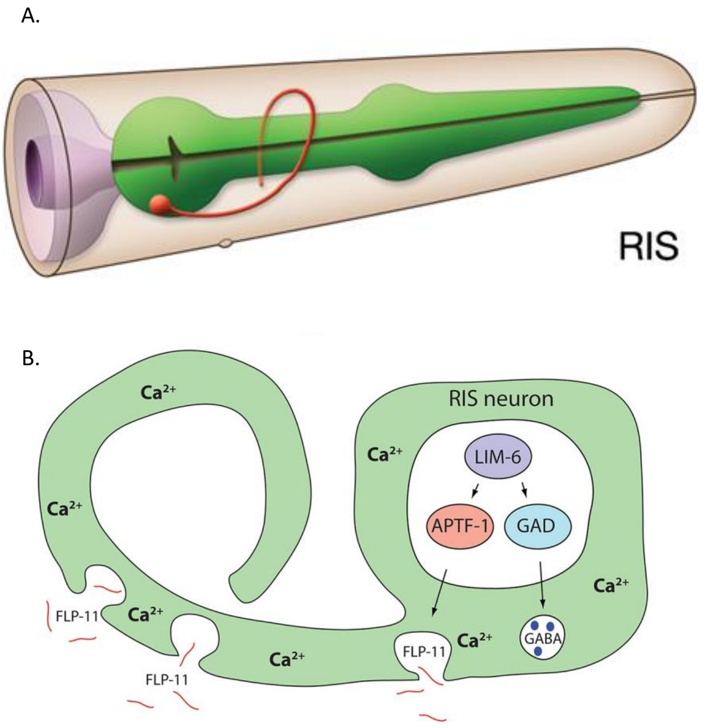

Figure 4. The sleep-active neuron RIS
(**A**) Anatomical position of the sleep-active RIS neuron in the head of *C. elegans*.
Figure adapted from Wormatlas.org
(**B**) The AP2 transcription factor *aptf-1*, regulates the expression of the sleep-inducing neuropeptide FLP-11 in RIS.
Figure adapted from Turek et al. (2016) [27].

1.5. Sleep during starvation and the L1 arrest state

Nutrient availability is a substantial concern for every living organism and for this reason they have developed protective mechanisms to survive, for as long as possible, the adversities of starvation. Sleep is one such mechanism, as it has been shown that in humans, starvation decreases the amount of active REM sleep while it increases the deep sleep phase (stage 3) of the quiet non-REM sleep [29]. Although there is an obvious trade-off during starvation between staying awake to search for food and sleeping to save energy, increased sleep during starvation is associated with greater lifespan in *Drosophila melanogaster* [30].

In *C. elegans*, post-embryonic development is completely dependent on food intake. When the worms hatch and there is no readily accessible source of sustenance, they enter a state of developmental arrest, during the first larval stage, called L1 arrest. This is a manifestation of the starvation response, regulated by the energy-sensing enzyme AMP-dependent protein kinase (AMPK). Survival during L1 arrest is ensured by cessation of cell divisions, as all available energy resources (coming from yolk components and autophagy) are directed towards maintenance of fundamental functions via differential regulation of gene expression. Furthermore, the worm becomes more resistant to heat-shock and oxidative stress [31].

The L1 arrest state is ultimately regulated by the FOXO transcription factor *daf-16*, downstream of the insulin signaling pathway [32]. *daf-16* was also shown to be responsible for RIS de-polarization during L1 arrest, which initiates sleep behavior. Should sleep be ablated in this case (e.g. by *aptf-1* loss of function), not only survival is halved but upon reintroduction to food worms fail to recover and continue their development [24]. Finally, worms accumulate aging-related cellular changes during L1 arrest, that can be reversed by feeding, provided that the unfolded protein response in the endoplasmic reticulum is not compromised [33].

2. Thesis aims

The complexity and inaccessibility of the human brain, gives rise to technical and ethical limitations in our quest to understand sleep on the molecular level. Efforts have been made to overcome this problem by using -omics techniques on blood samples (e.g. after sleep deprivation), which produced very general results that do not point specifically in one signaling pathway [34,35,36].

On the other hand, by using *C. elegans* we can genetically ablate sleep without resulting in lethality, which allows us to complement classic sleep deprivation protocols (e.g. mechanical stimulation), in order to get a tissue-wide image of sleep-related changes. Even though sleep is coupled to larval development in growing *C. elegans* (lethargus), results from nematode research have already been translated in mammals [37]. However, the recently-characterized starvation-induced sleep state (L1 arrest) [24] offers a more promising model, in which evolutionarily-conserved sleep-regulating pathways can be discovered.

Therefore, I have used the L1-arrested *C. elegans* to:

Aim 1 – Discover how sleep affects metabolism and vice versa

By using multiple -omics approaches (transcriptomics, proteomics and metabolomics), I wanted to determine how sleep loss affects metabolism globally (starvation response). I complemented these experiments with various other assays such as lifespan, isothermal microcalorimetry, egg-laying, size-measurement and aldicarb sensitivity assays. Also, in order to discover whether changes in metabolism alter sleep levels, I performed an extensive quiescence screening of metabolic deficient worms.

Aim 2 – Discover specific components regulated by sleep

Building on the results obtained in the experiments mentioned above, I used fluorescence quantification to measure how sleep loss affects the expression of FOXO homolog *daf-16* and its downstream target HSP-12.6. Finally, I used mechanical stimulation and optogenetics to further strengthen the link of FOXO regulation and the sleep neuron RIS.

3. Materials and methods

3.1. Worm maintenance and strain generation

3.1.1. Growth conditions, freezing and recovery

C. elegans strains were maintained on Nematode Growth Medium (NGM) seeded with OP50 *E. coli* bacteria, in medium-sized (60 x 15 mm) Petri dishes and incubated at 20°C (unless otherwise specified) [38].

Long-term storage of *C. elegans* can be achieved as follows:
L1-L2 stage worms can be collected from freshly starved and clean plates using 1 ml of freezing buffer in 2 ml cryovials. Then, they are put in a box made of expanded polystyrene at - 80°C overnight. The gradual freezing ensures that some worms survive the procedure. Older worms do not survive the freezing. It is imperative that new strains are frozen as soon as they are obtained, since they tend to accumulate random background mutations over a short period of time.

Recovery of frozen worms is achieved by transferring the cryovial at room temperature. When the content is thawed, it is pipetted on a fresh NGM plate.

A complete list of all strains used in this study can be found in section 6.1.

3.1.2. Crosses

Generation of male worms was achieved by transferring 10 L4 worms on a fresh plate, sealing it with Parafilm M and incubating it at 32°C for 4 hours. This process only works for strains that can survive the heat-shock and retain their fertility. Creating male worms with the “Roller” phenotype is not advised, because they do not mate effectively [39].

Mating took place on small-sized (35 x 10 mm) Petri dishes, optimally by picking 10 male and 5 hermaphrodite worms and then genotyping the offspring.

Deletion mutations and transgenic knock-ins were genotyped by Duplex PCR of single worms [40]. Single nucleotide changes were genotyped by tetra-primer ARMS-PCR [41]. A complete list of primers used in this study, can be found in section 6.2.

Isolation of genomic DNA for genotyping was done by digesting a single worm in 5 μl of Proteinase K (New England BioLabs®) solution:

Reagent	Concentration	Volume (μl)
Proteinase K Buffer	2 x	99
Proteinase K	20 mg/ml	1

Digestion was done in the thermal cycler at 65°C for 1 hour, then 95°C for 15 minutes and finally 15°C for indefinite storage. The resulting lysate can be stored at - 20°C, 4°C or be used immediately for PCR by adding PCR mix.

The PCR mix for 10 samples was prepared with reagents from New England BioLabs®:

Reagent	Concentration	Volume (μl)
Taq Buffer	10 x	10
dNTPs	10 mM	2
Primer mix	20 μM	3
Taq polymerase	5000 units/ml	1
Sterile H_2O	-	84

10 μl of PCR mix was mixed with 0,5 - 5 μl of worm lysate per sample.

PCR protocols were set up as follows:

Step	Temperature (°C)	Time
1. Initialization	94	2 min
2. Denaturation	94	30 sec
3. Annealing	T_a	30 sec
4. Elongation	68	25 sec
5. Final elongation	68	5 min
6. Final hold	15	indefinite

34 x

Samples were then mixed with 5 μl of Orange G dye (60% Glycerol) for electrophoresis or stored at 4°C overnight.

Gel preparation for electrophoresis was done by dissolving 0,3 g of UltraPure® Agarose (Thermo-Fisher Scientific) in 30 ml of TBE buffer (1 x) for a final concentration of 1 % and, after cooling down, adding 2,5 µl of SYBR Safe DNA Gel Stain (Thermo-Fisher Scientific). The agarose mix was poured in a custom-made plastic mold (10 x 7 cm) and was left for 30 - 45 min to solidify. 3 µl of DNA Ladder 100 bp (Thermo-Fisher Scientific) were added, to identify the sizes of the PCR products. The gels were run at 120 V for 30 min.

3.1.3. CRISPR-based gene editing

The strains PHX1364 (*hsp-12.6* (syb1364) knock-in allele) and PHX1652 (*cutl-17* (syb1652) deletion allele) were designed by Prof. Henrik Bringmann and created by Suny Biotech using CRISPR/Cas9. Briefly, PHX1364 contains an mKate2 sequence in the endogenous locus of *hsp-12.6* on chromosome IV, while PHX1652 contains a 3900 bp deletion in the promoter of *hsp-12.6* (syb1364) on chromosome IV.

>PHX1364: ***hsp-12.6* (coding sequence - exon 2)** - Linker - mKate2 - ***hsp-12.6* (end codon)**

CTAGAAGCCCATAACTTCCTCCCAAAAGAGATTGAAGTCAAGAACATTGGAG
AACTTCTTGAAATCCATATGGAGCACAATGTAAAGAAGGATTCATTTGGAGA
TGTCTCTCGTAACATTACTCGTTGTTACAAACTTCCAAAGAATGTTGATATGA
AGACAATCAAGAGCAACCTCGATTCACATGGAATTCTTCACATTGAAGCAAG
AAAAATGCATGGATCCGGATCCGGAATGTCCGAGCTCATCAAGGAGAACATGCA
CATGAAGCTCTACATGGAGGGAACCGTCAACAACCACCACTTCAAGTGCACCTCC
GAGGGAGAGGGAAAGCCATACGAGGGAACCCAAACCATGCGTATCAAGgtaagtttaa
acatatatatactaactaaccctgattatttaaattttcagGCCGTCGAGGGAGGACCACTCCCATTCGCCTT
CGACATCCTCGCCACCTCCTTCATGTACGGATCCAAGACCTTCATCAACCACACC
CAAGGAATCCCAGACTTCTTCAAGCAATCCTTCCCAGAGGGATTCACCTGGGAGC
GTGTCACCACCTACGAGGACGGAGGAGTCCTCACCGCCACCCAAGACACCTCCCT
CCAAGACGGATGCCTCATCTACAACGTCAAGATCCGTGGAGTCAACTTCCCATCC
AACGGACCAGTCATGCAAAAGAAGACCCTCGGATGGGAGGCCTCCACCGAGACC
CTCTACCCAGCCGACGGAGGACTCGAGGGACGTGCCGACATGGCCCTCAAGCTC
GTCGGAGGAGGACACCTCATCTGCAACCTCAAGgtaagtttaaacatgattttactaactaactaatctgat
ttaaattttcagACCACCTACCGTTCCAAGAAGCCAGCCAAGAACCTCAAGATGCCAGGA
GTCTACTACGTCGACCGTCGTCTCGAGCGTATCAAGGAGGCCGACAAGGAGACCT

ACGTCGAGCAACACGAGGTCGCCGTCGCCCGTTACTGCGACCTCCCATCCAAGCTCGGACACCGT**TAA**

>PHX1652: *hsp-12.6* (promoter) - Deletion - *hsp-12.6* (promoter) - ***hsp-12.6* (start codon)**

tgatgaacataatgaaattctccaacagtagtgattccggcattaatcatttctttgaaagttgataagcagtactgaaataatattttctttgaaacagcacaattattgaaattttcaaattctacgtttttctgaatttcctcattaacttgaattgagaagataataaaatttgaagttcaatttcacagtaggcacaaggatgttgaaggtaggcatgcaggcatcttaatgctcatttacctgataaatcttttccttcgtaacttcagcaaccaatccatacatattatctctccatttccaaaacgtatcagccgcagattttccaatttctgattttcctctcaaatgtcgatgaaatgcatgagaatgagtatttataaatcctggcagaagaacatggttgctcaaatgaacattctcatcgaatattttcttattaattccaacaatttttcccgtttcatcaactgatattgatacgttctcttctatttttccatcaatccaagcatatttgacatgaatggttttcccgcgaatgttcatctgaaattctattttttgagaacaaaaaataaaaaaaataattgttttaaaaacagtaaataacgtaattttccagttccaaactgccgatttatgtaaggttaaaacttgaatggacgttgcaaaaaaagctttcaaaaaatcatgattgacctaacagtcaaaaatgtcatattttcagGTGATTTGTGATGATTTGGAAATTCGAAATGTGGACAGTTTTGGCAGGAAAAAACGAAATTCAAATGTAGAAAAATGGTTGAAAGCTGGAgtaagtcttgaaattattatcactaacgatatgaaaagtgaactaatttggaagaatgtccctttctaaacttcaaaagttggaatccaaaagtaaaaataaataaattttggtttcaaccagaaataaataggttgaacattcttaaaatttaaagaagagaacatattcttcgaaatatgcacttttcggggcgacgtcacatttctgtgacaagtgcatcaaaatgtagaatttcaatttgatgtgtctcatccatcctcataaattttgaaaatatttattcgtatattgcagAACAAAAAAGAGACAAGAAAACGTCGTATGGTGACAGGAACACTTACAATAACCGATGAAGAAGAAACGAATACAACGGTCAAACCTCGTCCAGgtatctatttctgttgatttctgcgtctcttcatttcttcattatctcttttcaacttaattacacggtttcacagaaagtgttgtgttttatggctttgttgttcaggttgatgcaagttgagaaaccatgtaatttacacttgcataaaacaaccgttgcaaagtgtttcgaaatttgaaattgggcgttgaaatccctctgttagttgataagttatctccaatgggtaatatattaaaaacaattgttatggtgctaaaaatttttaaatatcatagtaaagcttttcaatattttttatgtttgagtataccaaaaattattgaagtgttttattattataattcatcatgttagcttaacaatactccacagtttaaaaatatctaacaactagcaaatcagaaatatttgaaacaaaacattatcacaaagaattatgataactgacttactagttaggcaaggctatgtaggttttaactatcaaactagtccaacaatcgttcaacagccatcccattaatttctaaaatttttttgacggcttttaaatgaaaaatgcatataaaaaagaagaagaattgaaaatttattgcacatccaaaagctgtgggaaagtgttgacaagtggaagtttgggtgagagggttaggaattatgaatgtcccactggaatttctgccaccaaaaacgtttttttcaaatattcaaaactcaactttttcgtttcacatcactcatcacttcagAGTTTTCAACATCCTCTTCTTCATCTTCTCAACAACAATATTGTGTTCAAAAGGATCGAATTGAATTTTTAATTGTGATTGTTGTACTTCTGATTCTACTTCAAATCGGATTGGCATTATTCTTCTATAGAAAATGTGTCAGCCGATCATCAATGGAAACATCAAGTGTTTATTCGGAAGGTAGTTCGAGATGCTCTGCCACGTCATCGGCCTATAATACATGTAATCGACAAATGGAACCACCTGTCTTACCGGTCAGACCTGCAAGGTTTTCAGATGGAGTTCAACCTCCATTCACGGAAAATCCATACAATCGATTACATCATTTCACATAAttggaacttttaaatttgtttatgtaaatgcgttttagtgtgaattttaactttttttgaaaaccattttaaattaata

tattggaaacatttatgagacacgacaaatattttcaacttttagtttcgcagtgaactcacatgaaacgtattaactccttgataaaatatttat
cattagagatccgtcaaggatttttgctcactactttccacactttttaatgtacatatcttgccgtttgaaatatttatttaatattttatttaattcc
tttctatattattttgtattttggctttccaattcctctaatactgtgcctttgaacaataattgtgtgtgtctttttaaaatctctagtgatctatgtca
ttttataaatctttttacttattctaattttgtatttatattttatattttgagtaattttacgaataataatcaatttttcacttactttcaaatgtgaatca
gacttgaacctaccggaataaatctgctcccgaaagaacacaaaacgagatacctcaatttccattacaactgaaaaaggttaaaacatt
gtttacaaattattataataacaattgatttttttctcttttaaatataaaaattgtttaaattcaaatcaaaaggtttttatttggtttcatttttatgttt
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agatttagtaggtcaacatgtttacgtggtttctggtttattacggcttcaggttatttcctaggtttctagaatttttcgaaaatatatcttcaga
gcacgtgcgaagattgaacagaaatcgtttttttcttaactttgttgtaatgttttcttttgttattaccttccgatgtctgctacttggggaaatct
gaaaatagcttggtttttgaaaaatccgtgttttcagcaaagaaaaaagaacaagttattaaaattgaaatgatattacgattgatttcaaata
tagaaattcaattccaaagtcactatggcatgtattgacatgaattcagaaaatgcaaaaaaaatttaaaagacaagaaagccgatggga
tcatgcttgacactttttttttgccaaaaatacgttttaacaaaactgtgaaaatttgtttctgatttaatattttaaaagtgaaaaattttttttaaaatt
aatttaaaaattataagacttccattgaaatatgggcatttgaaactataattttacattttctgtatacaaattaacatttcgaatattagtcgaat
ttggtcatttttcagatagaaaaattagacttcgggctatttcctatcaggaaaaaatttcgcgagatcagaatccgagtcgcctgaaaactt
ctttgtcagagttaaaacgtataacagtgtcaaaaaaaaaattttggaagcattttaaaatttcaaaagctctggaaaaggctgtttcacaattt
tctgataattaaaaaacacagtcttccccaaaaaaaagtacagattctgaaagcccaagatgacaatggacatgtttaaattttttaaaaca
actttctagtgagatgatgatttatataaatttataaggtttttttttctgtttcagaacatttttttttttaacttggtgtgatttattaaattatcttatgc
atcttctttcaagaagttatcaaaattgattagccatatcaactttccataaaatagagaaaaattctacagatattaaatttaatatatataattt
aaatcatttttttacagaaatttttataactaacagaattttcaaaatctcatgatttccagcatctaatatactggtttactgattgttttctgatttg
aagactgttttcatgaaatcgacgtgacttctacaagatatcaaagcttgacctttttgtttgcacctgaaatgctcccaattatcttttctgtttt
tcctctccagacacgtgtcccatgctttttctatcttcgaagctttcccatatcacacatatccacatacacatctgttcttttatttttatttttgtg
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agagagagaatgagaagaaaaaaaataaaatttgtaattttagaactcttaaaattcgatcccattgaaaacatcacatgtatctggttttct
ctggaaaaatatgttctcaagtatgaaatttctctgttttctctaagtcttattaactctcatttttcaactatttgtttattcttcaggacaatatgg
gcggagtctggatatgaaaaacaagtctgctagctgaaaatatgtgggcggagtcagtaactgtcatgcgacgaaagacatgaatctgt
gcgcgaagtaacaatataaaaagggtgagcattctgtgaatggacaacaatttcctctctttctaatactaacttctgaaaatttcagaaaa
aatcccaaaaacttttgccaag**ATG**

3.1.4. Synchronization

Synchronization of *C. elegans* at the L1 stage is based on the fact that adult worms are sensitive to treatment with alkaline hypochlorite (bleaching), while their eggshell protects the embryos from it [42]. The following steps were performed:

1. Alkaline hypochlorite solution was prepared fresh and heated to 36°C. The solution loses its potency over time, even though it can be stored at 4°C up to a week. Hypochlorite solution is more effective when it is warm. However, heating hypochlorite solutions at high temperatures for prolonged periods of time produces toxic phosgene gas. Handle with care, since hypochlorite is a whitening agent and will bleach fabrics. The solution was made by mixing 6 ml NaOCl (15% w/v), 12.5 ml NaOH (1 M) and 31.5 ml sterile H_2O for a final volume of 50 ml.
2. Worms were grown on NGM plates until they became gravid adults. Then they were washed off with M9 buffer and transferred to an Eppendorf or Falcon tube, depending on the volume of buffer used.
3. Afterwards, the tube was put in ice for 2-3 min which allowed all the adult worms to sink to the bottom, while younger larval-stage worms were suspended in the supernatant. *C. elegans* larvae are particularly resistant to bleaching and their presence will cause over-exposure of the eggs to the bleach solution, killing them in the process. The supernatant was then discarded.
4. 500 μl of hypochlorite solution was added per 100 μl of adult worm pellet as well as an equal amount of M9. The tube was shaken vigorously for 1 min and then centrifuged at 4200 x g for 30 sec. This killed the worms without dissolving them and a compact pellet was formed. The supernatant was then discarded.
5. 1000 μl of hypochlorite solution was added per 100 μl of adult worm pellet. The tube was shaken vigorously for 1 min. Under the stereomicroscope it was observed that the cuticles had started to dissolve and the eggs were released. Then it was centrifuged at 4200 x g for 30 sec. The pellet should have a yellow color. The supernatant was then discarded.
6. 1000 μl of M9 was added per 100 μl of adult worm pellet, the pellet was resuspended and centrifuged at 4200 x g for 30 sec. The pellet should be white and nearly all of the adult cuticles should be dissolved. The supernatant was then discarded.

7. 2 more rounds of washing with M9 (Step 6 above) were performed. The pellet was suspended in an appropriate amount of M9 (usually 1 ml M9 in a 2 ml Eppendorf tube), which allowed enough oxygen for worm development. The final suspension should not have the characteristic hypochlorite smell.
8. The worms were let to hatch overnight while rotating (20 rpm) at 20ºC. The next day, a healthy population L1 arrested worms should be swimming in the tube.

3.1.5. Bacterial culture for feeding

Bacteria were scraped off the surface of the frozen (- 80ºC) glycerol stock with a sterile pipette tip in a laminar flow hood. Then, the tip was discarded in an Erlenmeyer flask filled with 200 ml LB medium. The flask was incubated at 36ºC overnight, rotating at 60 rpm. If the bacteria were alive after thawing, the LB medium should turn opaque after incubation. The next day NGM plates were seeded with 200 µl (60 x 15 mm plates) or 500 µl (100 x 20 mm plates) of bacteria.

The following strains of bacteria were used in this study:

1. OP50: *E. coli* (Uracil auxotroph, standard *C. elegans* food source).
2. Na22: *E. coli* (Prototroph, grows in thick layers, abundant *C. elegans* food source).
3. HT115: *E. coli* (RNase III deficient, resistant to Tetracycline)
4. DL41: *E. coli* (Methionine auxotroph)

3.2. Microscopy and imaging

3.2.1. Long-term imaging using agarose hydrogel microchambers

Long-term imaging of L1 arrested worms was performed in agarose hydrogel microchambers as previously described [43]. Briefly, a poly-dimethyl-siloxane (PDMS) mold, activated by air plasma exposure for 30 sec, was used to create microcompartments from 1 ml of 3% (quiescence assessment and calcium imaging) or 5% (fluorescent imaging) high gelling temperature agarose (Sigma-Aldrich) dissolved in M9 buffer. The chamber size was 110 x 110 x 10 µm. The chambers were filled with 3-fold stage eggs without food, sealed with a glass coverslip and glued with double-sided adhesive tape into a square (2 x 2 cm) opening, milled in a 35 x 10 mm plate. The plate was filled with 2 ml of agarose, which would act as a moisture reservoir, and sealed with Parafilm M (Sigma-Aldrich) to prevent moisture loss. Chambers were incubated at 20°C until use.

3.2.2. DIC imaging for quiescence assessment in L1 arrest (48 hours)

Strains were assessed for quiescence in L1 arrest via continuous differential interference contrast (DIC) imaging. An “Eclipse Ti” microscope (Nikon) with an automated XY stage (Nikon), a digital DS-Qi2 camera (SLR, FX-format CMOS sensor, Nikon) and a 10x/0.45 Plan Apo λ objective lens (Nikon) were used. A red-light filter (BrightLine HC 785/62, 45 mm diameter, Semrock) was used in order to minimize behavioral changes due to illumination. A custom-made heating lid was used to keep the temperature constant at 25.5°C to avoid condensation (sample temperature was measured at 23.5°C). The software used for image acquisition and microscope control was “NIS elements” (Nikon). The length of the movies was 4 hours and the frame rate 0.2 FPS (1 frame / 5 sec). Exposure time was set to 50 ms and resolution was 14-bit 808 x 808.

Mean pixel intensity values (that correspond to the magnitude of the displacement) were extracted for individual worms via image subtraction [44], smoothed at 1% of total points (robust LOESS) and divided by the time interval to obtain speed values. Quiescence bouts were detected by applying a threshold of “speed < 40% of maximum speed continuously for a duration of time > 2 minutes”, with the custom-written MATLAB script found in section 6.3. This threshold was selected as it most accurately describes the wild-type worn quiescence in the 110 x 110 x 10 μm chamber that was used. Then, the fraction of quiescence was calculated for each worm. Eggs that did not hatch or worms that died before or during the measurement were excluded from the analysis. Each strain was imaged in at least 2 chambers (biological replicates). A median number of 15 animals was screened per strain (minimum = 7). The Effect Size (Cohen’s *d*), as well as 95% confidence intervals, were calculated by comparing each mutant strain to the wild-type. Precision was calculated as the reciprocal of the Standard Error of the Mean. Statistical significance was assessed by the 2-tailed Welch’s *t*-test (assuming unequal variances) and the resulting p-values were corrected for false discovery rate by the Benjamini-Hochberg method.

For a hit to be considered significant in this study, it has to satisfy the following criteria:
a. |Cohen’s *d* | > 1.2 “Very large” [45]
b. |95% Confidence Interval of mutant| > |95% Confidence Interval of wild-type|

The above criteria are stricter than the regular FDR < 0.05 threshold, but are justified by the extent of the study and the magnitude of the biological effect observed.

In the special cases of determination of the impact of 1. Maternal growth conditions and 2. Amino-acid supplementation (Figure 32) in L1 arrest quiescence of wild-type worms, only a threshold of FDR < 0.05 was applied because the expected biological effects are very small.

3.2.3. Fluorescence and calcium imaging in L1 arrest

Fluorescence-tagged transgene expression was quantified by fluorescence microscopy, and neuronal activity with calcium imaging. The same setup was used as above, with the following modifications: a 40x/0.75 Plan Fluor Oil objective lens was used combined with an additional built-in 1.5x lens for a total magnification of 60x. For GFP and mKate2 excitation, an LED system (CoolLED) provided light at 490 nm and 565 nm, respectively. Exposure time was set to 100 ms and EM Gain to 1.0x. Light intensity was measured to be 1.75 mW/mm^2 for 490 nm and 0.517 mW/mm^2 for 565 nm illumination, using an optical power meter (PM100A, Thorlabs). A standard set of GFP and Texas Red filters were used for light filtering.

Reporter transgene expression was measured either continuously for 3 days (1 frame every 15 or 30 min) or once every 24 hours for up to 12 days. Average worm fluorescence intensity was quantified per worm after background subtraction, assuming that the size of the worm is 10% of the total image size.

For the continuous 3-day imaging experiments, frames were extracted from the movies and aligned to the point of hatching. Frames before the hatching point were excluded from downstream analysis. At least 8 animals were imaged per strain in at least 2 chambers (biological replicates).

For the daily measurement experiments, chambers were made in the evening of the day prior to the start of the experiment (Day 0). That gave the eggs a time interval of 10-12 hours to complete embryogenesis and hatch but not yet starve. At least 20 animals were imaged per strain in 1 to 3 chambers (biological replicates). The chambers were kept at the 20 °C incubator when not being imaged.

In both cases, worms that died before or during the measurement period were omitted from downstream analysis. Single worms with transgene intensities > Q3 + 1.5 * IQR or transgene intensities < Q1 + 1.5 * IQR for every time point of the analysis, were scored as outliers and omitted from further analysis (Q1 = 25th percentile, Q3 = 75th percentile, IQR = Interquartile range). Significance was assessed at every time point by the 2-tailed Welch's *t*-test (assuming unequal variances), the resulting p-values were corrected for false discovery rate by the Benjamini-Hochberg method and FDR < 0.05 was selected as the significance threshold. In every case, error bars denote the standard error of the mean.

Neuronal activity was quantified by expressing the calcium-sensitive probe GCaMP 3.35 (codon-optimized for use in *C. elegans*) under a specific promoter and selecting only the neuron of interest (RIS neuron) or by average total fluorescence intensity (mechanosensory, dopaminergic and tyraminergic neurons). Specifically, for RIS, it was automatically detected by identifying the maximum intensity value of the image, selecting a 12 x 12 pixels region around it (size of RIS), subtracting the lowest pixel intensity as background and averaging the remaining intensities, with the custom-written MATLAB script found in section 6.4. (Figure 5).

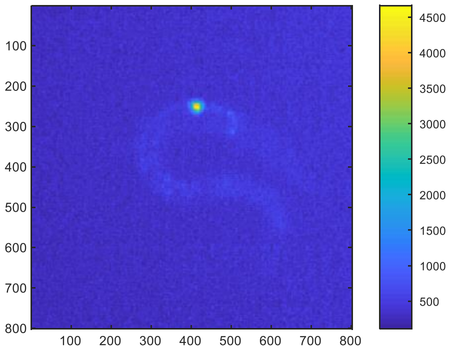


Figure 5. RIS detection by an automated MATLAB script
The absence of a background signal and the high fluorescence intensity of the *flp*-11::GCaMP transgene allows for easy automated tracking of RIS. These conditions ensure, that in all cases the maximum intensity value will be part of RIS. Averaging the intensities in the 12 x 12 pixels window centered at the maximum value gives a robust estimation of RIS intensity. Here, a representative worm of the wild-type HBR1361 strain is shown in L1 arrest (48 hours).

Images were taken once every 5 seconds for RIS neuron measurements or 10 seconds for the other neurons, for a total duration of 4 hours. In either case the intensity of GCaMP was normalized to the co-expressed mKate2 signal, which is not affected by the changes in calcium levels. For RIS at least 12 worms were imaged in 3 chambers (biological replicates), while for the other neurons at least 8 animals were imaged in 2 chambers. Significance was assessed at every time point by the 2-tailed Welch's *t*-test (assuming unequal variances), the resulting p-values were corrected for false discovery rate by the Benjamini-Hochberg method and FDR < 0.05 was selected as the significance threshold.

3.3. Transcriptional profiling by RNA-sequencing

Bulk sequencing of 3 *C. elegans* strains (N2, HBR227 and HBR1777) was performed by growing the worms on Nystatin-supplemented plates (NEP), seeded with Na22 bacteria, at 20°C until they reach adulthood. The population was then synchronized as described in section 3.1.4. and L1 arrested worms were harvested after 48 hours ("Starved"), at a final concentration of 20.000 worms/sample. The "Fed" samples were treated as described above, but were supplemented with OP50 for 4 hours after hatching. Then they were washed 3 times with M9 to remove the bacteria. In either case, the supernatant was aspirated from every sample and the pellet was either flash frozen in liquid N_2 or suspended in 1 ml RNA-later ICE (Thermo-Fisher Scientific) as requested. Then samples were stored at -80°C overnight and shipped on dry ice for downstream processing.

In the first case (CeGaT transcriptome) the project was outsourced to the company CeGaT. RNA extraction, library preparation and quality control were performed and the samples were sequenced with an Illumina HiSeq 2500 platform at 30 M reads/sample, single-end (1x50bp). An Excel file with genes and the corresponding counts was received.

In the second case (MPI-MG transcriptome) the project was outsourced to the Max Planck Institute for Molecular Genetics. The same processes as above were carried out and the samples were sequenced with an Illumina HiSeq 4000 platform at 50 M reads/sample, paired-end (2x50bp). FASTQ files were received and they were annotated by Jik Nijssen (Ph.D.). An Excel file with genes and the corresponding counts was received.

In both cases, the differential expression analysis was carried out through the custom-written MATLAB script found in 6.5. Briefly, principal component analysis was performed to detect any outlier samples, which were omitted from downstream analysis. Then, raw counts were normalized to a pseudo-reference sample and lowly expressed genes ($CPM < 0.5$) as well as genes with highly variant counts among replicates ($CV > 97.5^{th}$ percentile) were removed. The rest of the genes were fitted in a negative binomial model (mean-variance link was determined by local regression), assessed for statistical significance and the p-values were corrected for false discovery rate by the Benjamini-Hochberg method. Significance thresholds were set as follows: $|\log_2(FC)| > 1$ and $FDR < 0.05$. This was implemented in order to account for biological significance. However, genes with smaller fold changes were also considered for downstream Gene Set Enrichment analysis, performed with the online tool “g:Profiler”, using the default settings and the Bonferonni correction to get the adjusted p-values (p_{adj}) [46].

3.4. Agglomerative hierarchical clustering analysis of RNA-seq data

Normalized counts of the RNA-seq data (from MPI-MG) were analyzed with the “clustergram” MATLAB function which produces a dendrogram and the associated heatmap. Each row of the heatmap corresponds to one gene and each column to one sample.

The following algorithm was implemented:

1. Data were transformed to their base 2 logarithm values and standardization (Z-score calculation) was done by row, to account for changes in gene expression.
2. Pairwise observation distance was calculated both in rows and columns with the Euclidean metric.
3. The linkage criterion to determine the distance between sets of observations was Ward’s minimum variance method.
4. Data were clustered first among columns and then among rows and then optimal leaf ordering was applied to maximize the sum of similarities between adjacent leaves.

After that, enrichment analysis of selected pathways was carried out. The number of significantly regulated genes (either Up- or Down-) in a specific pathway, was statistically compared to the total number of significantly regulated genes in the whole transcriptome by using the right-sided Fisher’s exact test, corrected with the Bonferroni method. The significance threshold was set to $p_{adj} < 0.05$.

3.5. Proteomic characterization of *C. elegans*

C. elegans cultures of strains N2, HBR227 and HBR1777 were grown for proteome analysis as described in section 3.3. at a final concentration of 50.000 worms/sample. They were flash frozen in liquid N_2 and shipped to different facilities for downstream processing.

Proteome analysis by TMT quantification was carried out by the laboratory of Prof. Henning Urlaub (MPI-BPC). The samples were ground in liquid N_2 and soluble proteins were extracted. Proteins were labeled with TMTsixplex Isobaric Label Reagent (Thermo-Fisher Scientific) for quantitative analysis via mass spectrometry.

Proteome analysis by Label-Free Quantification (LFQ) was carried out by the laboratory of Dr. David Meierhofer (MPI-MG). Samples were digested, the soluble fraction was extracted and run through the mass spectrometer. The relative amount of proteins in each sample was then quantified and peptide intensities were corrected to remove systematic artefacts [47].

In both cases, the differential expression analysis was carried out through the custom-written MATLAB script found in section 6.6. Briefly, principal component analysis was performed to detect any outlier samples, which were omitted from downstream analysis. Peptides not detected (intensity = 0) in at least one sample were removed. Intensities were then quantile normalized and peptides with highly variant intensities among replicates (CV > 97.5th percentile) were removed. The remaining peptides were assessed for statistical significance using the 2-tailed Welch's *t*-test (assuming unequal variances) and the p-values were corrected for false discovery rate by the Benjamini-Hochberg method. Significance thresholds were set to $|\log_2(FC)| > 1$ and $FDR < 0.05$, to account for biological significance.

3.6. Metabolome analysis in L1 arrest

C. elegans cultures of strains N2, HBR227 and HBR1777 were grown for metabolome analysis as described in section 3.3. at a final concentration of 100.000 worms/sample.

Metabolome analysis by LC-MS was performed by the laboratory of Dr. David Meierhofer (MPI-MG) as previously described [48].

Differential expression analysis was carried out by the custom-written MATLAB script found in section 6.6. Briefly, principal component analysis was performed to detect any outlier samples, which were omitted from downstream analysis.

Metabolites not detected (intensity = 0) in at least one sample were removed. Intensities were then quantile normalized and peptides with highly variant intensities among replicates (CV > 97.5th percentile) were removed. The remaining peptides were assessed for statistical significance using the 2-tailed Welch's *t*-test (assuming unequal variances) and the p-values were corrected for false discovery rate by the Benjamini-Hochberg method. Significance thresholds were set as follows: $|\log_2(FC)| > 0.5$ and $FDR < 0.1$. This was implemented because metabolite levels are fluctuating fast and the changes in quantity are usually subtle (personal communication with Dr. Meierhofer).

3.7. Survival and behavioral assays

3.7.1. Lifespan of L1 arrested animals

Three different assays were used to evaluate survival in L1 arrest:

<u>Chamber assay</u>: 3-fold stage eggs were picked on 110 x 110 x 10 μm microchambers without food, made of 3% high gelling temperature agarose (Sigma-Aldrich) dissolved in M9 buffer. The chambers were stored in the 20°C incubator. Animals were scored as "dead", if they failed to move after exposure to blue light for 2 minutes. Measurements took place every day. Survival was estimated by using the Kaplan-Meier method, significance assessment was done by using the log-rank test and the significance threshold was set to $p < 0.05$.

<u>96-well plate assay</u>: 100 μl of 3% high gelling temperature agarose (Sigma-Aldrich) dissolved in M9 buffer were pipetted at the bottom of each well. Worms were synchronized as described in section 3.1.4. and transferred to the 96-well plate in 100 μl of M9. Approximately 10 worms were transferred in each well, so that it is possible to keep track of individual worms.
The plates were stored in the 20°C incubator. Animals were scored as "dead", if they failed to start swimming after exposure to blue light for 2 minutes. Measurements took place every day. Survival was estimated by using the Kaplan-Meier method, significance assessment was done by using the log-rank test and the significance threshold was set to $p < 0.05$.

Rotator assay: Worms were synchronized as described in section 3.1.4. and transferred to 2 ml Eppendorf tubes, at a concentration of 10.000 worms in 1 ml of M9 buffer. The tubes were strapped on a rotating device (20 rpm) and put in the 20°C incubator. Then, 10 μl of worm suspension was pipetted on NGM plates seeded with OP50 and the total number of worms was counted. One day later, worms were scored as "dead" if they have not shown any sign of movement (traces on the bacterial lawn) and were dried out. Measurements took place every day. Survival was estimated by using the Kaplan-Meier method, significance assessment was done by using Fisher's exact test for every time point, p-values were corrected for false discovery rate by the Benjamini-Hochberg method and the significance threshold was set to $FDR < 0.05$. Finally, the point of 50% survival was determined by fitting a 6th degree polynomial to the survival curve.

3.7.2. Sleep deprivation by optogenetic stimulation

Optogenetic stimulation of the worms was done in 110 x 110 x 10 μm microchambers without food, made of 5% high gelling temperature agarose (Sigma-Aldrich) dissolved in M9 buffer. The chambers were supplemented with 10 μl of 10 mM Retinal in 100% ethanol every 3 days (+) or 10 μl of 100% Ethanol (EtOH) or 10 μl of water (-). Long-term optogenetic experiments were carried out with the OptoGenBox, designed by Inka Busack [49]. Temperature was set to 20°C and orange light intensity to 10 mW. The "light" interval was set to 10 minutes and the "dark" interval was set to 20 minutes, alternating for 6 days until the end of the experiment. This setup was selected to avoid habituation. The samples were removed at the "dark" interval for daily transgene imaging and were promptly returned to the OptoGenBox.

3.7.3. Sleep deprivation by mechanical stimulation

Mechanical stimulation of the worms was done in 110 x 110 x 10 μm microchambers without food, made of 5% high gelling temperature agarose (Sigma-Aldrich) dissolved in M9 buffer. A piston (2.5 mm in diameter) was driven into the chamber at the xy-plane, by the use of an electromagnet and the whole setup was fitted in a custom-made aluminum holder [50]. To avoid habituation, a set of 5 taps were delivered every 5 minutes and the time interval between taps was 1 second. This was achieved by the use of an Arbitrary Waveform Generator (Hewlett Packard, 33120A), which created square waves with amplitude 5 V and frequency 5.000 mHz. This signal was further amplified at 24 V, by a TTL signal amplifier. A heating lid, set to 22°C, was fit on the chamber to keep it from drying out (sample temperature: 20°C). The chambers were imaged daily to assess transgene expression, as described above, and were then returned to the tapping device, taking care that a different spot will be tapped, since prolonged tapping at the same spot will destroy the plastic plate (Figure 6).

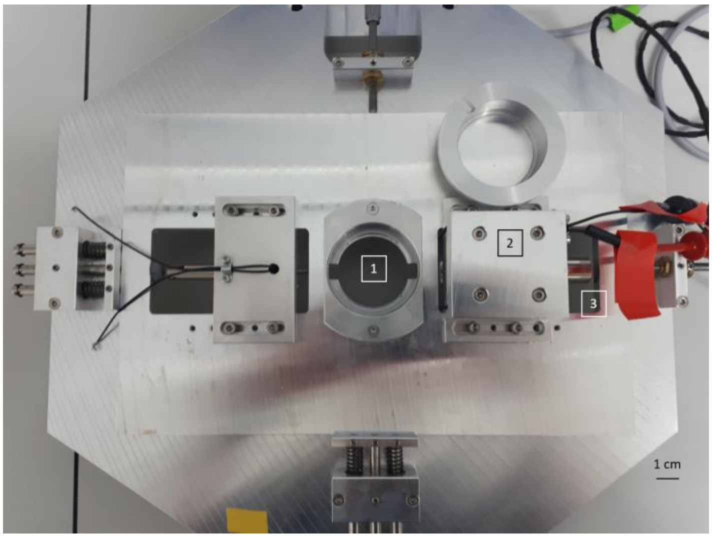


Figure 6. Tapping device for mechanical stimulation
The custom-made tapping device consists of a hexagonal aluminum frame which can also be mounted on a microscope and used as a stage. The chamber with the worms is fitted in the aluminum holder (1). An electrical current that passes through a coil, creates an electromagnet (2) which drives the tip of the piston (3) into the sample.

3.7.4. Heat production in L1 arrest (48 hours)

The rate of heat production of the strains N2, HBR227 and HBR1777 was assessed at the laboratory of Prof. Bart Braeckman (University of Ghent). Worms were synchronized as described in section 3.1.4. and the worm suspension in M9 was transferred in cylindrical, sterile glass containers. Isothermal microcalorimetry was performed using two 2277 Thermal Activity Monitors and Digitam software (Thermometric AB, Jarfalla, Sweden). The temperature was set to 24°C. A blank sample containing only M9 buffer was used to determine background heat production. Measurements were taken every 1 second for 4 hours (4 biological replicates). Only the last 5 minutes of measurements (equilibrium point) were used in the analysis, because at the start of the measurement there is increased heat production due to friction. Results were normalized to the total amount of worms per sample. Quantile normalization was used to remove technical variance, since the measurements are close to the detection limit. Statistical significance was assessed using the 2-tailed Welch’s *t*-test (assuming unequal variances) and the p-values were corrected for false discovery rate by the Benjamini-Hochberg method. The significance threshold was set to FDR < 0.05.

3.7.5. Egg-laying assay

For the egg-laying assay, L4 worms were picked on individual NGM plates with (OP50) and without food. Every day worms were transferred on fresh plates and the number of eggs was counted. Worms that died before the end of the experiment or escaped were removed from downstream analysis. Starved animals could not be assessed for more than 2 days, since they escaped the plate in search for food. Statistical significance was assessed using the 2-tailed Welch's *t*-test (assuming unequal variances) and the p-values were corrected for false discovery rate by the Benjamini-Hochberg method. The significance threshold was set to FDR < 0.05. Although the number of eggs laid is always an integer and the corresponding distribution discrete, the variables considered here (genetic mutations) are independent and therefore the Central Limit Theorem applies, which permits the use of the *t*-test for statistical significance.

3.7.6. Worm length in L1 arrest

Worm strains N2, HBR227 and HBR1777 were synchronized as described in section 3.1.4. The L1 arrested worms were put on NGM plates and fed with OP50. After reaching adulthood, 3-fold stage eggs were picked and put on 190 x 190 x 15 μm microchambers (without food) made of 3% high gelling temperature agarose (Sigma-Aldrich) dissolved in M9 buffer. The eggs were filmed continuously using the DIC setup described in section 3.2.2., taking 1 image every 1 minute, to determine the exact time of hatching (Day 0). The worms were imaged again exactly 48 hours after hatching (Day 2). Worm length was determined using a custom MATLAB script. Statistical significance was assessed using the 2-tailed Welch's *t*-test (assuming unequal variances) and the p-values were corrected for false discovery rate by the Benjamini-Hochberg method. The significance threshold was set to FDR < 0.05.

3.7.7. Aldicarb sensitivity assay

Small-sized (35 x 10 mm) Petri dishes were filled with 250 μl of 3% high gelling temperature agarose (Sigma-Aldrich) dissolved in M9 buffer, supplemented with 1 mM aqueous solution of Aldicarb (Sigma-Aldrich). Worm strains N2 and HBR227 were synchronized as described in section 3.1.4. Approximately 100 worms were pipetted on each plate and they were scored every 10 minutes for total lack of movement. Percentage of moving animals was estimated by using the Kaplan-Meier method, significance assessment was done by using the log-rank test and the significance threshold was set to $p < 0.05$.

3.7.8. tRNA U_{34} thiolation assay in L1 arrest (48 hours)

Worm strains N2 and HBR227 were synchronized as described in section 3.1.4. Hatched L1 worms were left to starve for 48 hours in M9 buffer at a concentration of $5 * 10^9$ worms/sample. 3 biological replicates were made for each strain. The samples were flash frozen in liquid N_2 and shipped to the laboratory of Prof. Sebastian Leidel (University of Bern). There, total RNA was isolated and Northern blots of APM ([(N-Acroyl-amino) phenyl] mercuric chloride – a molecule that reacts with thiolated biomolecules) gels, were quantified for Glutamine (UUG) and Lysine (UUU) tRNAs. Significance assessment was done by the 2-tailed Welch’s *t*-test (assuming unequal variances). The significance threshold was set to $p < 0.05$.

3.8. EMS mutagenesis data analysis

An EMS mutagenesis screening was performed by Dr. Elisabeth Maluck, in order to isolate mutations that suppress the *aptf-1* (-) phenotype. This resulted in 2 candidates that showed increased sleep fraction during lethargus in the *aptf-1* (-) background. Those candidates were subsequently sequenced and a dataset containing NGS data for those candidates was received. Dr. Maluck had already confirmed that the mutation is homozygous, it does not lie on the X chromosome, it is different in each candidate and it is not the insertion in the *rod-1* gene (personal communication with Dr. Elisabeth Maluck).

The following algorithm was implemented, to isolate the mutations of interest:

1. Discard all mutations common in both candidates.
2. Discard all heterozygous mutations (GENOTYPE: 1/1 is homozygous for the mutant).
3. Discard all mutations with do not PASS the NGS generated filter.
4. Create a list of Mutations of Interest (MOI) resulting from the filtering steps above.
5. Separate the chromosomes in intervals, accounting for different chromosome sizes (10% of total chromosome length was selected).

6. Calculate total mutations per interval for each chromosome. Identify hotspots (intervals with an increased number of mutations) on each chromosome, by using the right-sided Fisher's exact test on the mutations per interval. Correct the resulting p-values using the conservative Bonferroni method. The significance threshold was set to $p_{adj.} < 0.001$.
7. Create a list of MOI that lie in these hotspots.
8. Automatically map the list via WormBase to get a specific list of genes, introns and upstream/downstream loci that are altered by each MOI.
9. Calculate total mutations per interval around each GOI in the new list (density).
10. Employ biological criteria (EMS typical mutations (G → A, C → T), mutation density, position on the genome, effect on resulting protein etc.) to identify the most likely candidate.

3.9. RHEB-1 depletion via Auxin-inducible degradation

A deletion in the TOR regulator gene *rheb-1*, is lethal for C. elegans. For this reason, an Auxin-inducible protein degradation system was implemented, that eventually depletes the RHEB-1 protein from the organism. This is a reversible process that permits survival [51,52]. Briefly, a strain was obtained in which expression of the Auxin receptor of *Arabidopsis thaliana* TIR1 was driven under the ubiquitously expressed promoter *eft-3*. Then, a construct containing an Auxin Inducible Degron (AID) as well as an mKate2 fused to the endogenous *rheb-1* was also crossed into the aforementioned strain. Addition of Auxin (3-Indoleatic acid, Sigma-Aldrich), causes polyubiquitination and rapid proteasomal degradation of the AID-fused protein, which here can be assessed by complete loss of the mKate2 signal. For the lifespan experiment, 2 µl of a 100 mM solution (in DMSO) was added every 4 days, while for the HSP-12.6 expression experiment 10 µl of a 200 µM solution (in DMSO) was added every day on the chamber. Controls for these experiments were treated with the same volumes of DMSO.

4. Results

4.1. Sleep loss affects metabolism by regulating the starvation response in L1 arrested worms

In order to further our understanding of the relationship between sleep and starvation, I performed transcriptomic and proteomic analyses on two *C. elegans* strains that show reduced quiescence in the L1 arrested state, the *aptf-1*(gk794) loss of function mutant and the RIS-ablated *flp-11*::EGL-1 transgenic strain, which was created to induce apoptosis selectively in RIS (Figure 7).

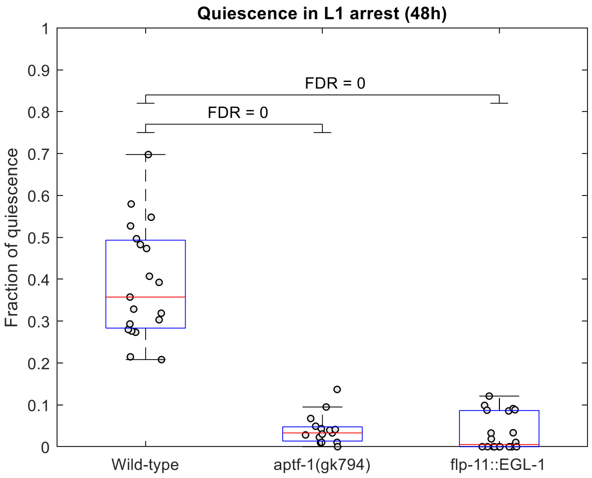


Figure 7. *aptf-1* loss of function and RIS-ablation reduce quiescence in L1 arrest
Boxplot showing almost complete reduction in the quiescence fraction of *aptf-1*(gk794) and *flp-11*::EGL-1 worms, calculated at 48 hours of starvation. Average quiescence values are: wild-type = 0.3924, *aptf-1*(gk794) = 0.0411 (10,47% of wild-type) and *flp-11*::EGL-1 = 0.0333 (8.49% of the wild-type) and the number of animals tested per condition is: 18, 14 and 19 respectively. Red horizontal line denotes the median value.

For the transcriptomic and proteomic analyses, I compared the “Starved” condition (48 hours in L1 arrest) with the “Fed” condition (4 hours in L1 development). In total, the expression of 12256 genes and 4066 proteins was quantified. The RNA-seq data (CeGaT) comes from 2 biological replicates, while the proteome data comes from 1 biological replicate processed with the TMT method. Although the low number of biological replicates in this experiment prohibits the identification of new regulatory genes/proteins, as well as downstream pathway enrichment analysis, it is nevertheless adequate to get a general overview of the changes induced by sleep loss and starvation. This is indeed the case both for *aptf-1* loss of function and RIS-ablation. In fact, in *aptf-1* loss of function we can observe the expected downregulation of *flp-11* since it is a downstream target of *aptf-1* (FLP-11 was not detected in the proteome) [27]. Also, there is greater differential regulation of genes and proteins in starvation than in development, which points to a different and perhaps more significant role of sleep in the L1 arrested state (Figure 8 and sections 6.7 - 6.10).

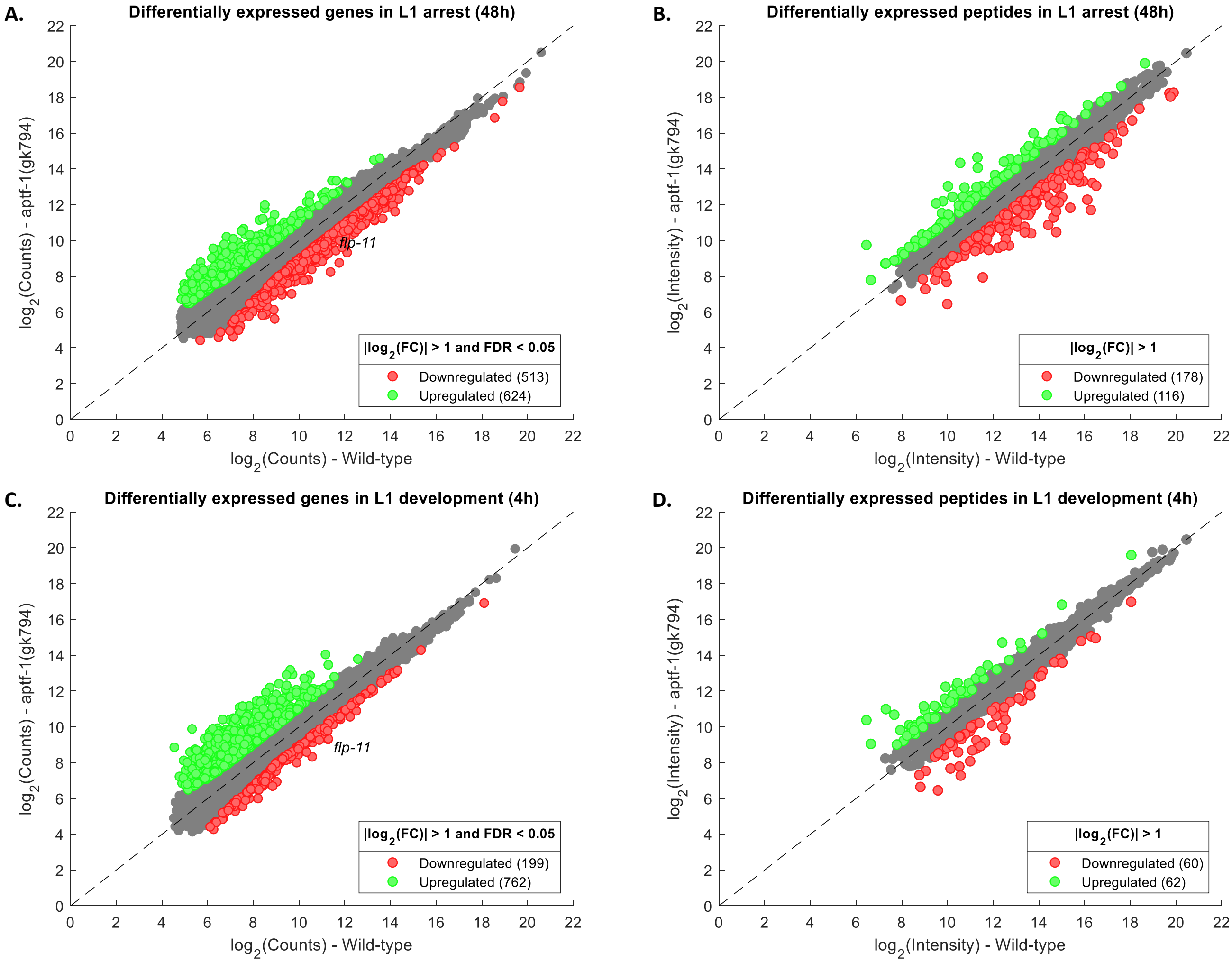


Figure 8. *aptf-1* loss of function leads to transcriptomic and proteomic changes
Scatter plot overview of gene and protein expression.
Not significant entities according to the selected thresholds, are marked in grey.
(**A-B**) In L1 arrest 10.77% of the transcriptome and 7.23% of the proteome changes.
(**C-D**) In L1 development 7.84% of the transcriptome and 3% of the proteome changes.

In the RIS-ablated strain, *flp-11* is, surprisingly, upregulated! This is was not expected from a strain that shows reduced quiescence, since FLP-11 is the major sleep-inducing neuropeptide [27]. With regard to *egl-1*, it is one of the most upregulated genes in the RIS-ablated condition. However, since there is no evidence of extensive apoptosis in this strain, it is logical to speculate that the differential regulation comes from constant expression of the transgene within RIS. Also, while differential regulation of protein levels remains similar to the *aptf-1* condition when comparing starvation and development, there is a reversal on the gene level which suggests that the role of RIS ablation is more important in L1 development (Figure 9 and sections 6.11 - 6.14).

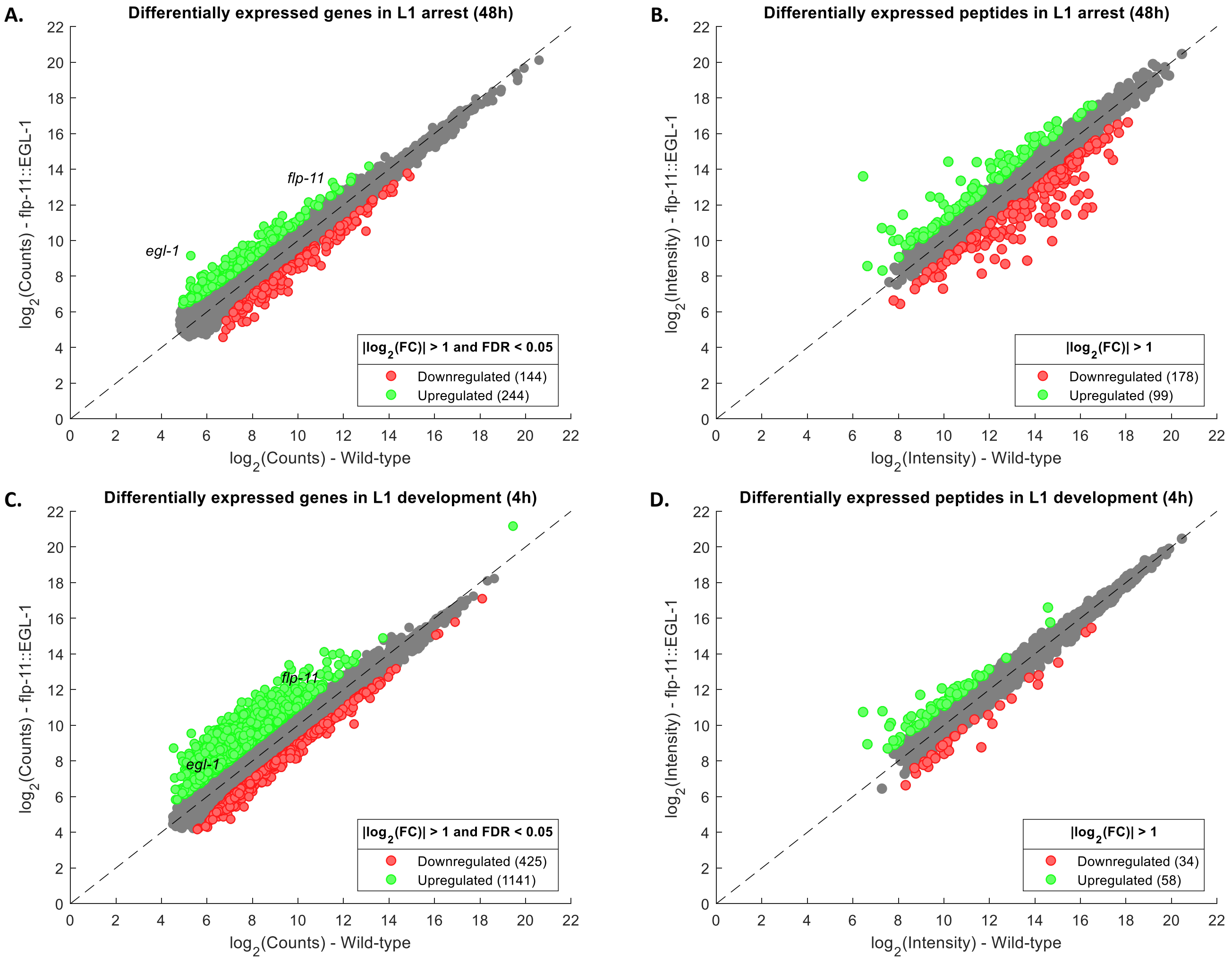


Figure 9. RIS ablation leads to transcriptomic and proteomic changes
Scatter plot overview of gene and protein expression.
Not significant entities according to the selected thresholds, are marked in grey.
(**A-B**) In L1 arrest 3.17% of the transcriptome and 6.81% of the proteome changes.
(**C-D**) In L1 development 12.78% of the transcriptome and 2.26% of the proteome changes.

Having analyzed the impact of sleep loss in different nutritional conditions, I followed up with the complementary analysis, investigating the starvation response in animals with different capacities for sleep. In all conditions, *hsp-12.6*, a gene coding for a small heat-shock protein that is induced by fasting and plays a role in lifespan extension during caloric restriction in the adult worm [53], was greatly upregulated (HSP-12.6 was not detected in the proteome) (Figure 10 and sections 6.15 - 6.20).

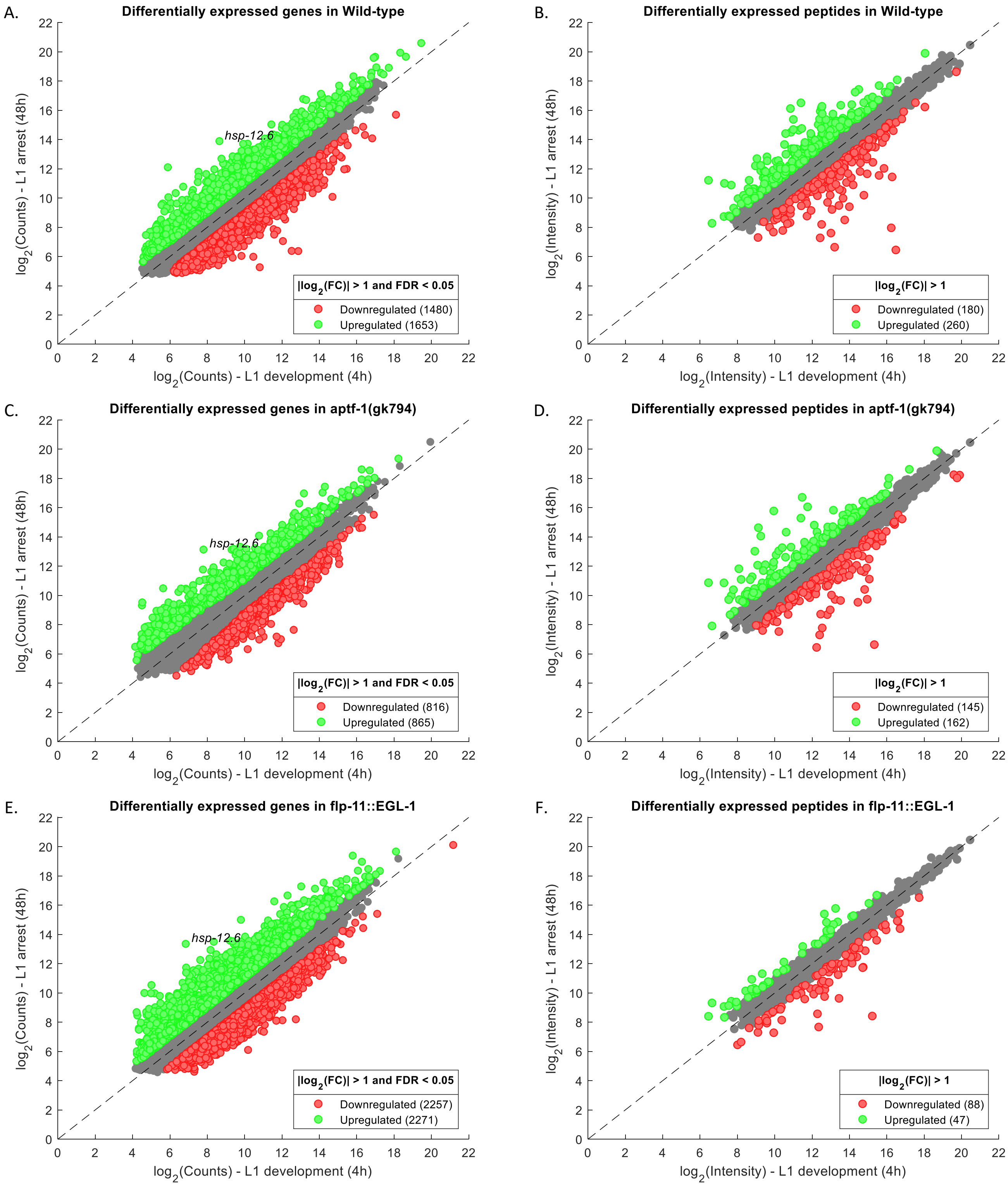


Figure 10. Starvation leads to transcriptomic and proteomic changes
Scatter plot overview of gene and protein expression.
Not significant entities according to the selected thresholds, are marked in grey.
(**A-B**) Starvation response in the wild-type, with $\log_2$(FC) = 5.24 for *hsp-12.6*.
(**C-D**) Starvation response in the *aptf-1*(gk794), with $\log_2$(FC) = 5.34 for *hsp-12.6*.
(**E-F**) Starvation response in the *flp-11*::EGL-1, with $\log_2$(FC) = 6.51 for *hsp-12.6*.

RIS function and consequently sleep, affect both the quantity and the quality of the starvation response. *aptf-1* loss of function reduces the number of genes and proteins that get differentially expressed in starvation compared to those in the wild-type, while RIS-ablation increases the number of genes but decreases the number of proteins (Figure 11 A, B). This is the first indication that RIS might play a role in protein synthesis, which will be further investigated below. With regard to qualitative changes in the starvation response, gene and protein regulation in both sleep loss conditions negatively correlate with their regulation during wild-type starvation (Figure 11 C-F).

To sum up, I have looked at the transcriptomic and proteomic profiles of two *C. elegans* strains which show reduced starvation-induced quiescence in the arrested L1 stage. The difference in the expression of the sleep-inducing neuropeptide FLP-11 and in the number of differentially expressed genes during starvation, signify that these strains are not equivalent in all of their aspects. However, in both sleepless strains, genes and proteins that should be upregulated to manifest a proper starvation response are downregulated and vice versa. This anti-correlation, provides direct evidence that sleep and RIS control one of the major metabolic processes, the starvation response.

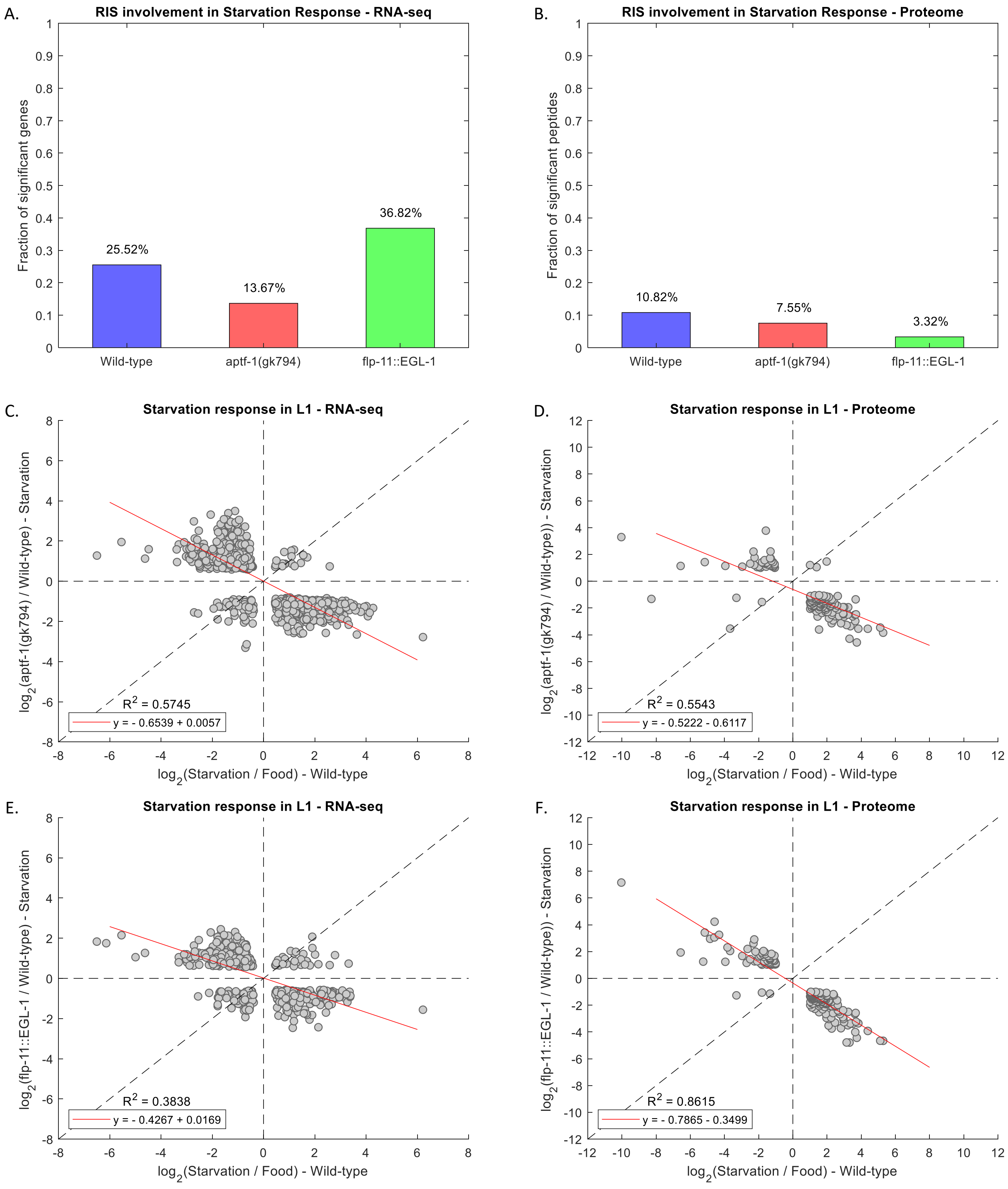


Figure 11. Starvation response depends on RIS function
(**A-B**) Bar plot showing the fraction of genes and proteins that globally change in starvation.
(**C-D**) Scatter plot showing the quality of the starvation response in *aptf-1*(gk794).
(**E-F**) Scatter plot showing the quality of the starvation response in *flp-11*::EGL-1.
Linear fits for each case were produced by regression analysis using the least-squares method.

4.2. Sleep loss in L1 arrest alters the physiology of *C. elegans*

In order to capitalize on the results produced by the initial transcriptomic and proteomic approaches, I repeated the analysis with more samples and increased sequencing depth. However, this time the "Fed" condition was omitted, because I had established the link between sleep and the starvation response previously. In total, 13849 genes and 1690 proteins were quantified. The RNA-seq data (MPI-MG) comes from 4 biological replicates for the wild-type and the *flp-11*::EGL-1 strains and 3 biological replicates for the *aptf-1*(gk794) strain, while the proteome data comes from 6 biological replicates processed with the LFQ method. This new analysis allows the detection of individual components that play a role in starvation-induced sleep, as well as downstream pathway enrichment analysis.

Although fewer genes and proteins were found to be differentially expressed in this new analysis, the "internal control" gene expression is reproducible with *flp-11* being downregulated in the *aptf-1* loss of function condition and upregulated in the *flp-11*::EGL-1 condition ($\log_2(FC) = 0.6377$ and $FDR = 7 \times 10^{-20}$). *aptf-1* is now detected and downregulated in both strains ($\log_2(FC) = -0.62$ and $FDR = 5.8 \times 10^{-5}$ in the *flp-11*::EGL-1 strain). Such disagreement in the expression of *flp-11* and its regulator *aptf-1*, has not been observed before. *egl-1* is still the most upregulated gene in the *flp-11*::EGL-1 condition, while the most downregulated hit is *dmsr-2*, a predicted G-protein coupled neuropeptide receptor. This receptor is activated by the neuropeptide NLP-13 (personal communication with Prof. Isabel Beets, KU Leuven), which is one of the characteristic RIS neuropeptides according to the transcriptome published by Cao et al. (Enrichment in RIS vs all other neurons: $\log_2(FC) = 2.22$ and $FDR = 5.7 \times 10^{-6}$) [54]. *nlp-13* is not differentially expressed in any of the sleep loss conditions examined here. Finally, one of the few proteins detected in this analysis was the starvation-induced protein HSP-12.6, which was downregulated in both sleep loss conditions. The corresponding gene was found to be downregulated in the *aptf-1* loss of function condition, but was upregulated in the *flp-11*::EGL-1 condition ($\log_2(FC) = 0.47$ and $FDR = 8.6 \times 10^{-11}$) (Figure 12 and sections 6.21 - 6.24).

The low number of differentially expressed proteins and the absence of significant results in downstream pathway enrichment analysis, has rendered the proteome of limited use. Of the detected proteins, only the role of HSP-12.6 will be extensively investigated, since it is the one component consistently detected and differentially expressed across all conditions and analyses.

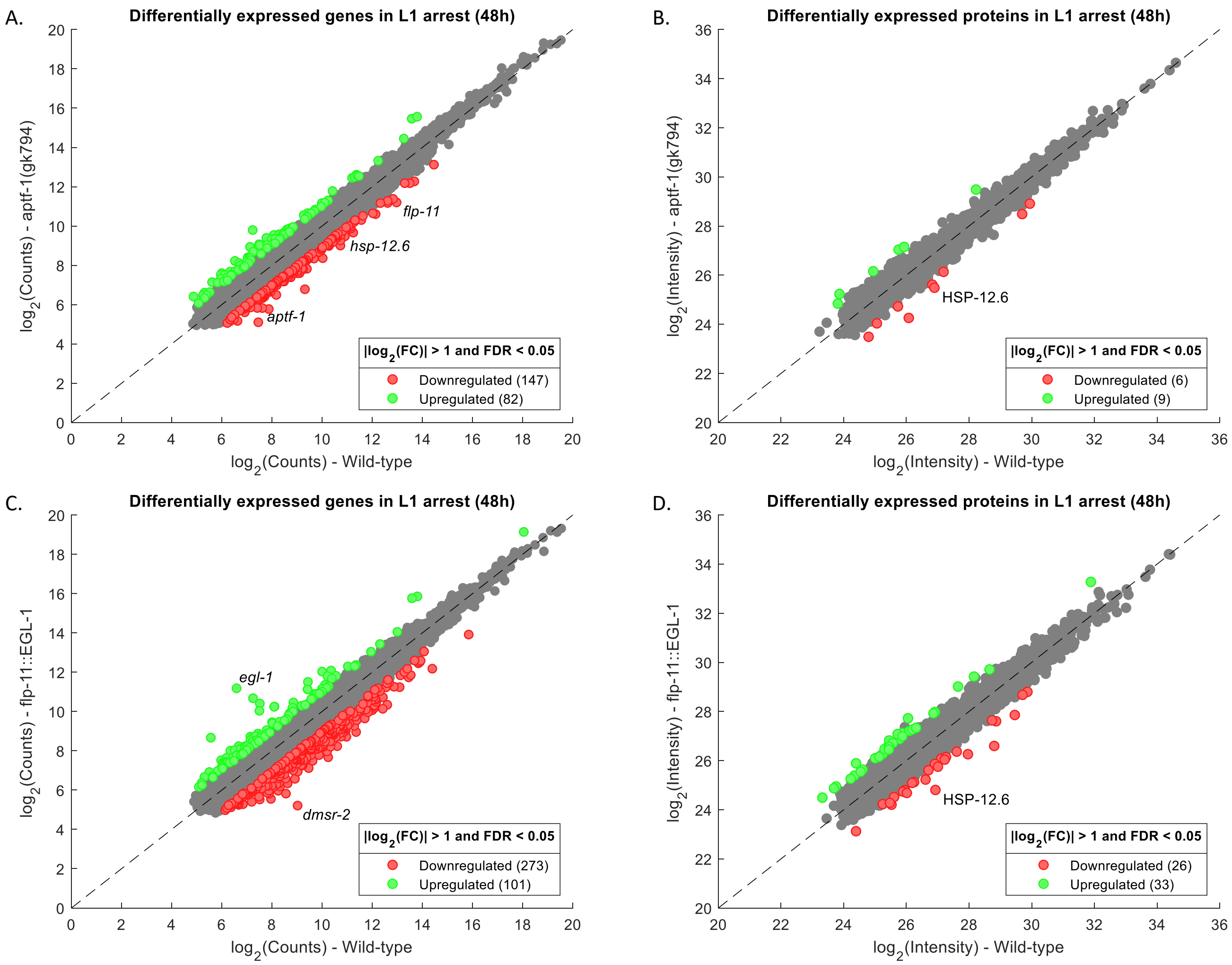


Figure 12. Sleep loss in L1 arrest leads to transcriptomic and proteomic changes
Scatter plot overview of gene and protein expression.
Not significant entities according to the selected thresholds, are marked in grey.
(**A**-**B**) In *aptf-1*(gk794), 1.65% of the transcriptome and 0.89% of the proteome changes.
(**C**-**D**) In *flp-11*::EGL-1, 2.7% of the transcriptome and 3.4% of the proteome changes.

To ensure the validity of the transcriptome and its reliability for downstream analysis, I selected individual genes, for which fluorescent transgenic lines already existed, crossed them into the *aptf-1* loss of function background and imaged them continuously from hatching to a time point greater than 48 hours in L1 arrest (the flp-11::EGL-1 strain was not used in this type of analysis, since it requires further characterization due to its unexpected transcriptomic and proteomic profile). This approach would not only verify the differential expression at 48 hours of starvation, but would also reveal the expression pattern of each gene.

However, this is not the case, as 6 out of 8 total transgenic lines, failed to reproduce the transcriptomic expression of the corresponding gene at the 48-hour time point (Figure 13).

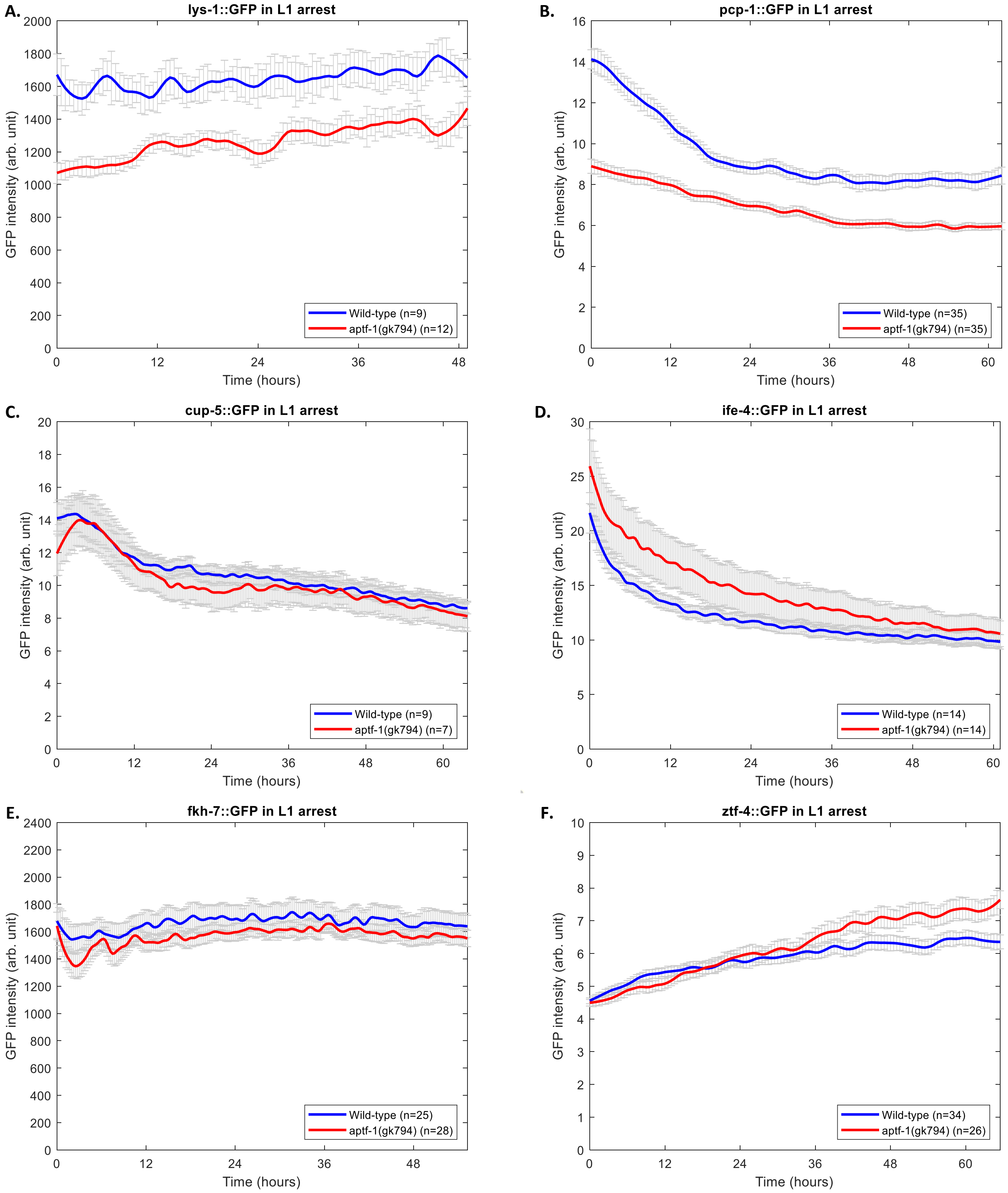


Figure 13. Transgene expression fails to verify the transcriptional changes
(**A-B**) The lysozyme homolog *lys-1* (RNA-seq: $\log_2(FC) = 0.69$) and the lysosomal prolyl-carboxy-peptidase *pcp-1* (RNA-seq: $\log_2(FC) = 0.01$), are downregulated (FDR < 0.05 for every time point) contrary to the transcriptome predictions.
(**C-F**) The mucolipin homolog *cup-5*, the translation initiation factor *ife-4*, and the transcription factors *fkh-7* and *ztf-4* (RNA-seq: $\log_2(FC) = 0.20$, $\log_2(FC) = -0.39$, $\log_2(FC) = 0.29$ and $\log_2(FC) = 0.15$ respectively), are not significantly changed.

On the other hand, for 2 transgenic lines (*hil-1*::GFP and *hsp-12.6*::GFP) the transcriptomic expression can accurately be reproduced at the 48-hour time point (Figure 14 A, B). With regard to *hsp-12.6*, sleepless worms can also induce its expression but in a less efficient way, once again verifying the role of sleep in the starvation response. A shorter promoter region in the *hsp-12.6*::GFP transgene, leads to loss of this phenotype (Figure 14 C).

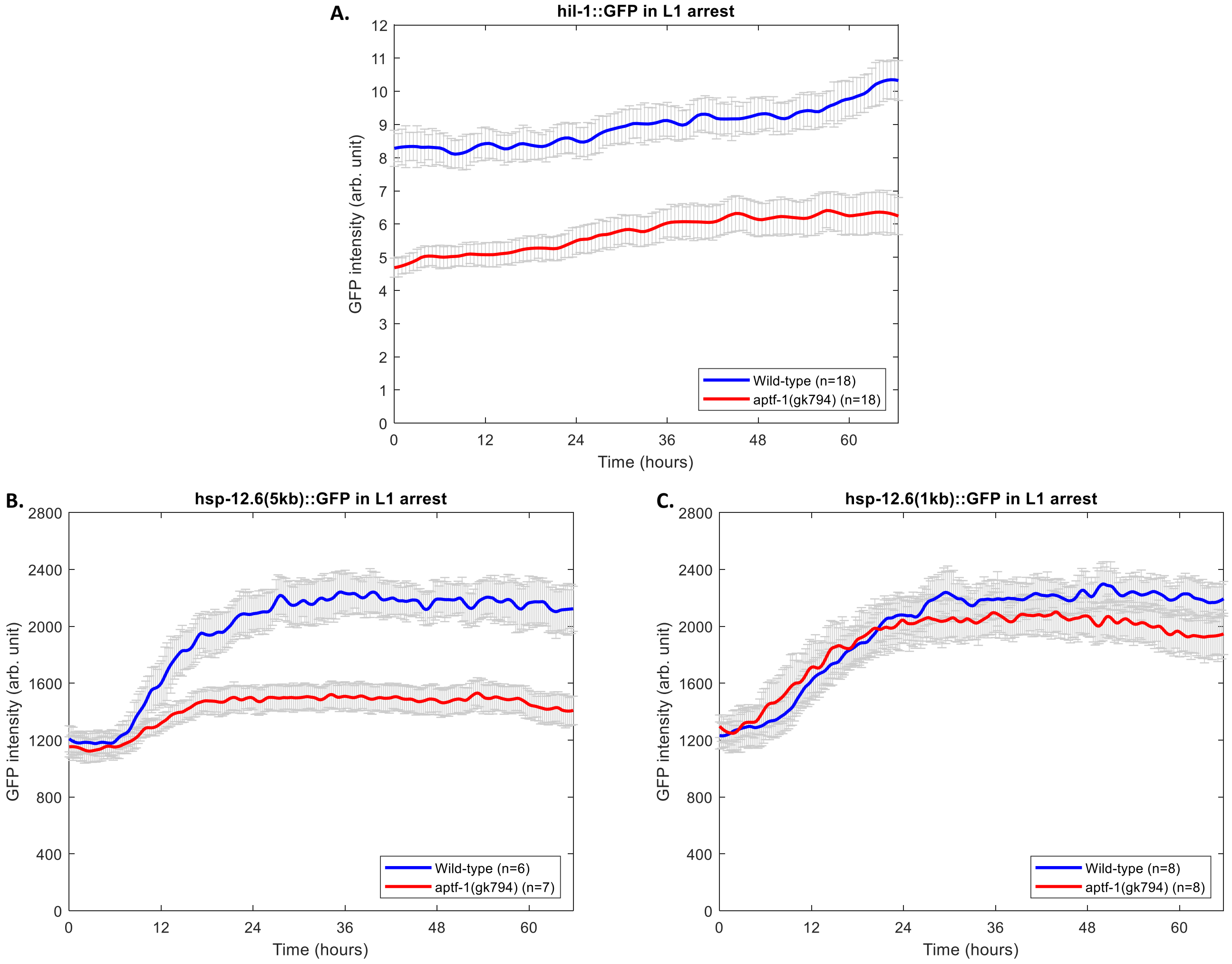


Figure 14. Transgene expression is in accordance to the transcriptional changes
(**A**) The histone *hil-1*, is significantly downregulated (FDR < 0.05 for every time point) as expected from the transcriptome (RNA-seq: $\log_2$(FC) = -0.15).
(**B-C**) The small heat-shock protein *hsp-12.6* is significantly downregulated (FDR < 0.05 for every time point), as expected (RNA-seq: $\log_2$(FC) = -1.43). Expression of the transgene from a shorter promoter region (1 kb vs 5kb), abolishes the differential expression.

The limited success of the transgene screening can be attributed to a variety of factors related to the transgenic lines, their creation and GFP expression or to the quality of the transcriptome. The former is difficult to detect and not relevant for this project while the latter needs to be addressed. For this reason, I performed hierarchical clustering analysis on the

RNA-seq samples, which showed that the samples of the same background cluster well together, ensuring the good quality of the dataset. It also showed that both RIS-manipulated strains are quite divergent in their gene expression patterns. This finding, taken together with the high expression levels of *egl-1* in the *flp-11*::EGL-1 strain, support the notion of a strain in which RIS is constantly active. (Figure 15).

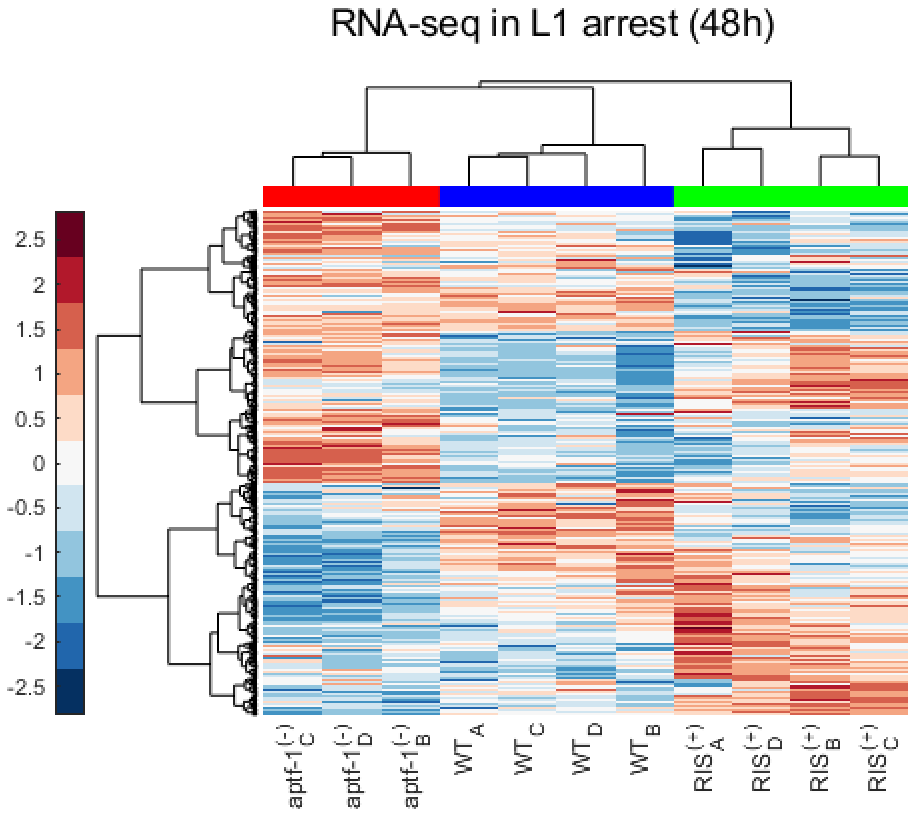


Figure 15. Hierarchical clustering analysis ensures the quality of the transcriptome
Dendrogram and heatmap representation of gene expression in sleep loss conditions. Every line of the heatmap corresponds to a single gene and every column to a single sample. Row Z-scores are color coded on the bar on the left side. aptf-1$^{(-)}$, WT and RIS$^{(+)}$ denote the different replicates of *aptf-1*(gk794), wild-type and *flp-11*::EGL-1 strains respectively.

After having ensured the quality of the transcriptome data, I performed Gene Ontology enrichment analysis. In the *aptf-1* loss of function background on the one hand, there are 4 major pathways that are downregulated: 1. Mitochondrial function, which directly affects energy availability and metabolism, 2. Translation, which affects protein turnover and homeostasis, 3. Splicing, which affects the flow of genetic information and 4. Kinetochore and Centromere, which affect the progression of cell division. On the other hand, 3 major pathways are upregulated: 1. Neuropeptide signaling, which regulates the function of all tissues and affects many of the animal's behaviors (e.g. sleep, egg-laying, defecation etc.) [55], 2. Defense response, which determines the ability to fight pathogens and 3. Unfolded protein response, which affects protein homeostasis and cellular stress levels (Figure 16 A). The picture is very different in the *flp-11*::EGL-1 background, where the pathways downregulated are 1. Muscle tissue components, 2. Glutathione, which homeostatically regulates the cellular redox status and 3. Unfolded protein response. However, only 2 major pathways are upregulated: 1. Proteasome, which degrades damaged or unnecessary proteins and 2. Organism development (Figure 16 B).

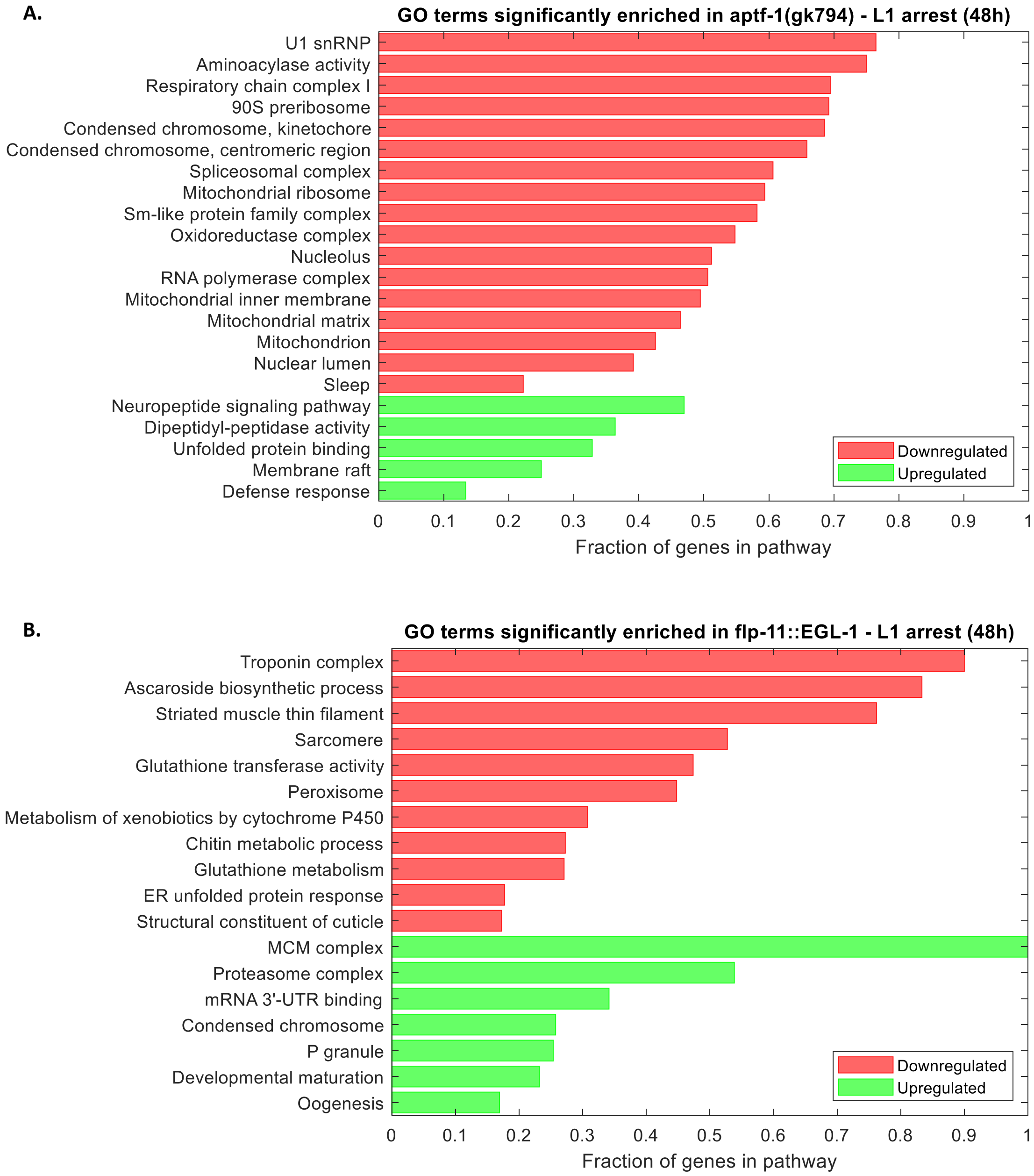


Figure 16. GO term enrichment analysis of the RNA-seq dataset
Horizontal bar chart representation of the GO terms that are affected by loss of sleep, at the transcript level. All of the shown pathways are significantly enriched with $p_{adj} < 0.05$.
(**A**) Wild-type vs *aptf-1*(gk794)
(**B**) Wild-type vs *flp-11*::EGL-1

The above results indicate that sleep loss induces organism-wide changes, in several major pathways necessary for life. I have now established that characterization of the *flp-11*::EGL-1 strain is incomplete. For this reason, it will be excluded from most downstream assays, which will focus on the well-characterized *aptf-1* loss of function strain. I have also showed that commercially available transgenic strains, might not be the optimal tool to assess gene expression with. In order to better understand and discover the origin of these sleep induced molecular changes, I performed tissue-specific enrichment analysis on the transcriptome data.

4.2.1. Sleep loss upregulates hypodermis-specific gene expression and reduces body size

The hypodermis is part of the epithelial system of *C. elegans*. It directs the development of the worm (molting), regulates cell fate and gives the worm its shape and its size [56]. I mined hypodermis-unique genes from the published dataset of Kaletsky et al. [57] and calculated the significance of enrichment in my sleep loss dataset. I found significant upregulation of hypodermis-unique genes in both sleep loss conditions. This led me to analyze the components of the TGF-β pathway (GO:0007179), which are mainly expressed in the hypodermis and control, among others, the body size of the worm [58]. Although there is significant upregulation of the pathway in the *aptf-1* loss of function background, there is no significant difference in the *flp-11*::EGL-1 strain (Figure 17 A, B). After that, I calculated the worm size at 2 time points in L1 arrest, immediately after hatching and at 48 hours of starvation. In the *aptf-1* loss of function strain there is approximately 5% reduction in body size compared to the wild-type, which is not the case in the flp-11::EGL-1 strain. Also, in all cases, body size remains constant in the first 2 days of starvation, regardless of sleep capacity (Figure 17 C, D).

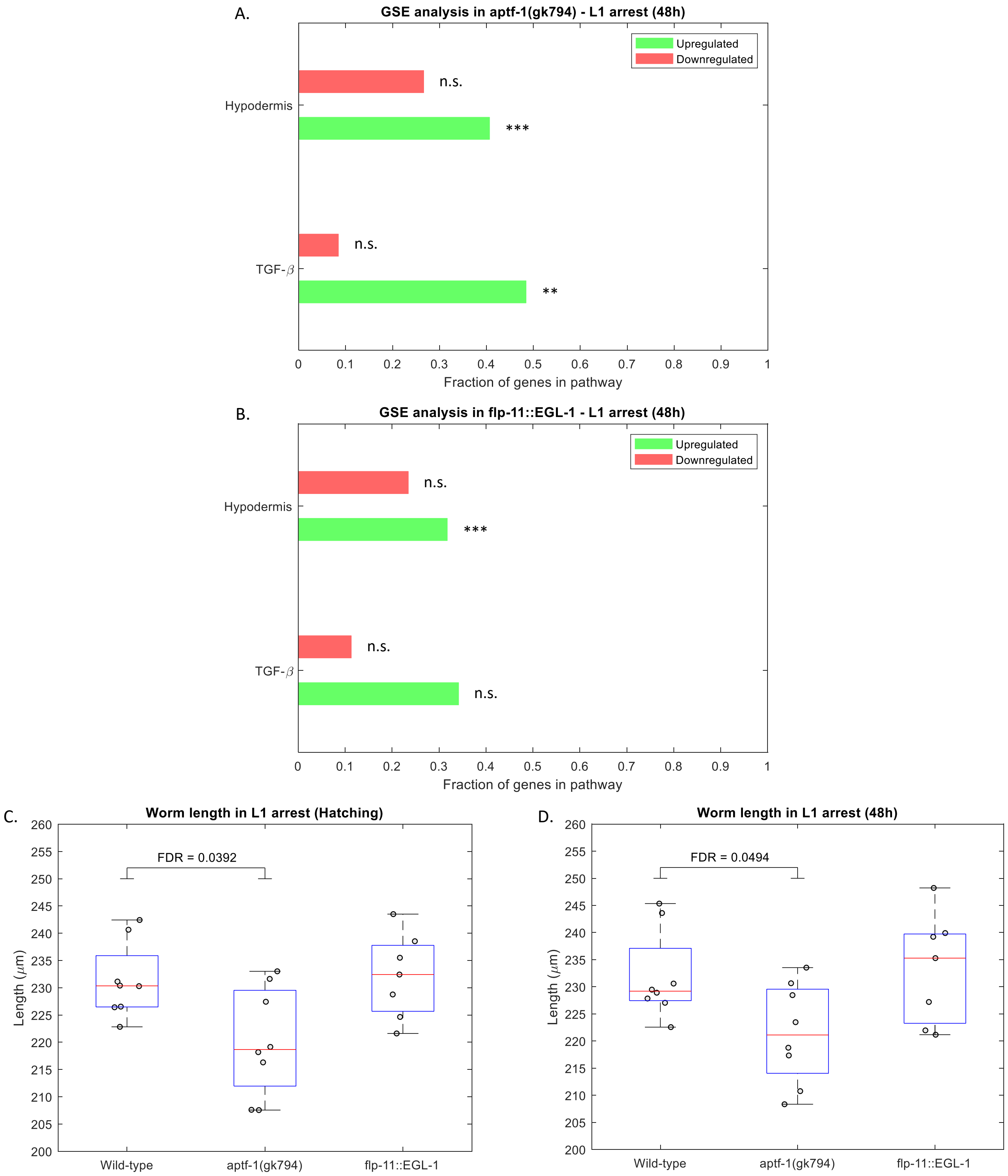


Figure 17. Sleep loss affects hypodermis-specific gene expression and body size
(**A-B**) Horizontal bar chart representation of hypodermis-related pathways that are affected by loss of sleep (***: $p_{adj} < 0.001$, **: $p_{adj} < 0.01$, *: $p_{adj} < 0.05$, n.s.: not significant).
(**C-D**) Boxplots indicating the worm length at hatching and at 2 days of starvation (n=8 for wild-type and *aptf-1*(gk794) and n=7 for *flp-11*::EGL-1).

4.2.2. Sleep loss conditionally changes muscle-specific and mitochondrial gene expression

In C. elegans, muscle tissue can be found in the body wall to control movement, in the pharynx to regulate the feeding behavior, in the vulva and uterus to facilitate reproduction and in the anus to regulate the defecation cycle [59]. I mined muscle-unique genes from the published dataset of Kaletsky et al. [57] and calculated the significance of enrichment in my sleep loss dataset. I found significant downregulation of muscle-specific genes only in the *flp-11*::EGL-1 condition. Since mitochondrial fragmentation in muscles is a consequence of sleep loss in the *aptf-1* loss of function background as shown by Wu et al. [24], I wanted to assess the enrichment of genes belonging to the Electron Transport Chain (GO:0022900) and the Mitochondrial Localization (GO:0070585) pathways. Both of these pathways are severely downregulated in the *aptf-1* loss of function strain. This is not the case in the *flp-11*::EGL-1 strain (Figure 18).

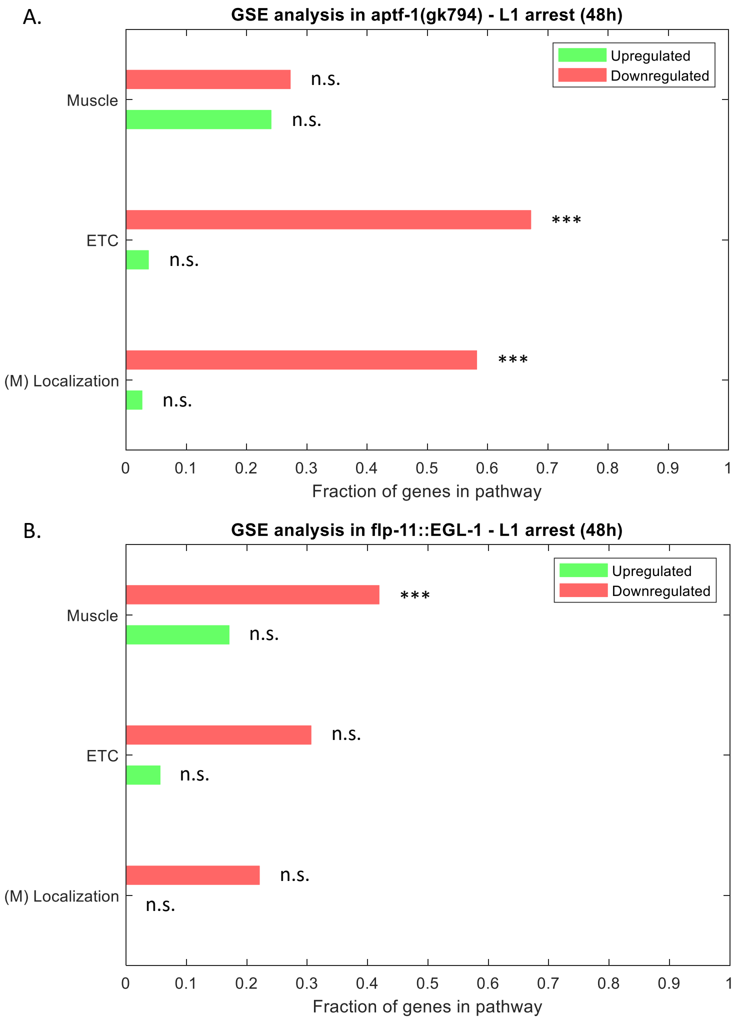


Figure 18. Sleep loss affects muscle-specific gene expression and mitochondrial function (**A-B**) Horizontal bar chart representation of muscle-related pathways that are affected by loss of sleep (***: $p_{adj} < 0.001$, **: $p_{adj} < 0.01$, *: $p_{adj} < 0.05$, n.s.: not significant).

4.2.3. Sleep loss affects intestine-specific and FOXO gene expression

The intestine is a multi-functional tissue in C. elegans, that not only controls food digestion and nutrient absorption, but also macromolecule synthesis and storage, as well as the initiation of the immune response [60]. I mined muscle-unique genes from the published dataset of Kaletsky et al. [57] and calculated the significance of enrichment in my sleep loss dataset. I found significant downregulation of intestine-specific genes in both sleep loss conditions and upregulation only in the *aptf-1* loss of function. The insulin signaling pathway and the FOXO homolog *daf-16* function in the intestinal cells non-autonomously to regulate the L1 arrested state [61]. For this reason, I mined the dataset of Murphy et. al [62] that splits the FOXO-regulated genes in 2 categories: Class I - genes that are downregulated and Class II - genes that are upregulated in absence of *daf-16* and calculated their enrichment (Figure 19).

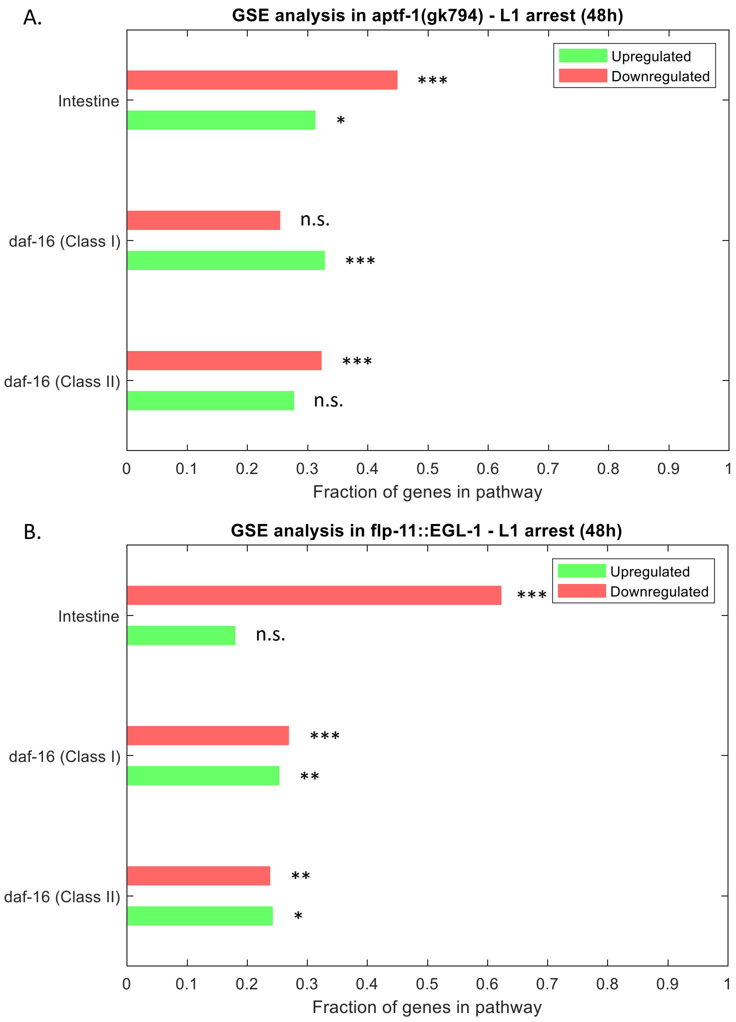


Figure 19. Sleep loss affects intestine-specific and FOXO target gene expression
(**A-B**) Horizontal bar chart representation of intestine-related pathways that are affected by loss of sleep (***: $p_{adj} < 0.001$, **: $p_{adj} < 0.01$, *: $p_{adj} < 0.05$, n.s.: not significant).

Genes that are downregulated by loss of *daf-16* (Class I) show a significantly enriched upregulated fraction in the *aptf-1* loss of function background, while genes that are upregulated by loss of *daf-16* (Class II) show a significantly enriched downregulated fraction. This antipodal regulation of the insulin signaling pathway targets, may determine the reduced survival phenotype of the *aptf-1*(gk794) mutant shown by Wu et al. [24]. As for the *flp-11*::EGL-1 background, there is significant enrichment both in Class I and Class II genes, once again showing that although both the strains studied here show reduced quiescence, the underlying biochemical mechanisms are, at least in part, distinct.

To further address the role of *daf-16*, I measured its expression using a transgenic line. In accordance with the transcriptome, DAF-16 expression is significantly upregulated in the *aptf-1* loss of function background at 48 hours (RNA-seq: $\log_2(FC) = 0.55$ and $FDR = 4 \times 10^{-24}$) (Figure 20 A). However, this goes against the downregulation of *hsp-12.6* (Class I) that was presented in the transgenic line screening above, as well as the downregulation of *sod-3* (Class I) (RNA-seq: $\log_2(FC) = -0.58$ and $FDR = 0.0009$) which encodes a superoxide dismutase, in the *aptf-1* loss of function background (Figure 20 B). DAF-16 is a transcription factor stationed in the cytoplasm and is subject to tight regulation via phosphorylation, which depending on the phosphorylated residue can permit or deny entry in the nucleus [63]. One possible explanation for the seemingly contradictory results (increased DAF-16 but decreased *hsp-12.6* and *sod-3*) would be that nuclear localization of DAF-16 is affected in the sleep loss state. For this reason, I assessed the localization of DAF-16 in the intestinal nuclei of the *aptf-1* loss of function mutant and of the low-quiescence, long-lived, RIS-hyperactive strain *flp-11*::UNC-58gf (characterized by my colleague Inka Busack). Although, DAF-16 is equally probable to be found in the nucleus of the L1 arrested worms in the first 2 days of starvation, the probability of nuclear localization drops dramatically for the non-sleeping strains at after the 3rd day. This consists definitive evidence that sleep controls the starvation response, through DAF-16 (Figure 20 C-E).

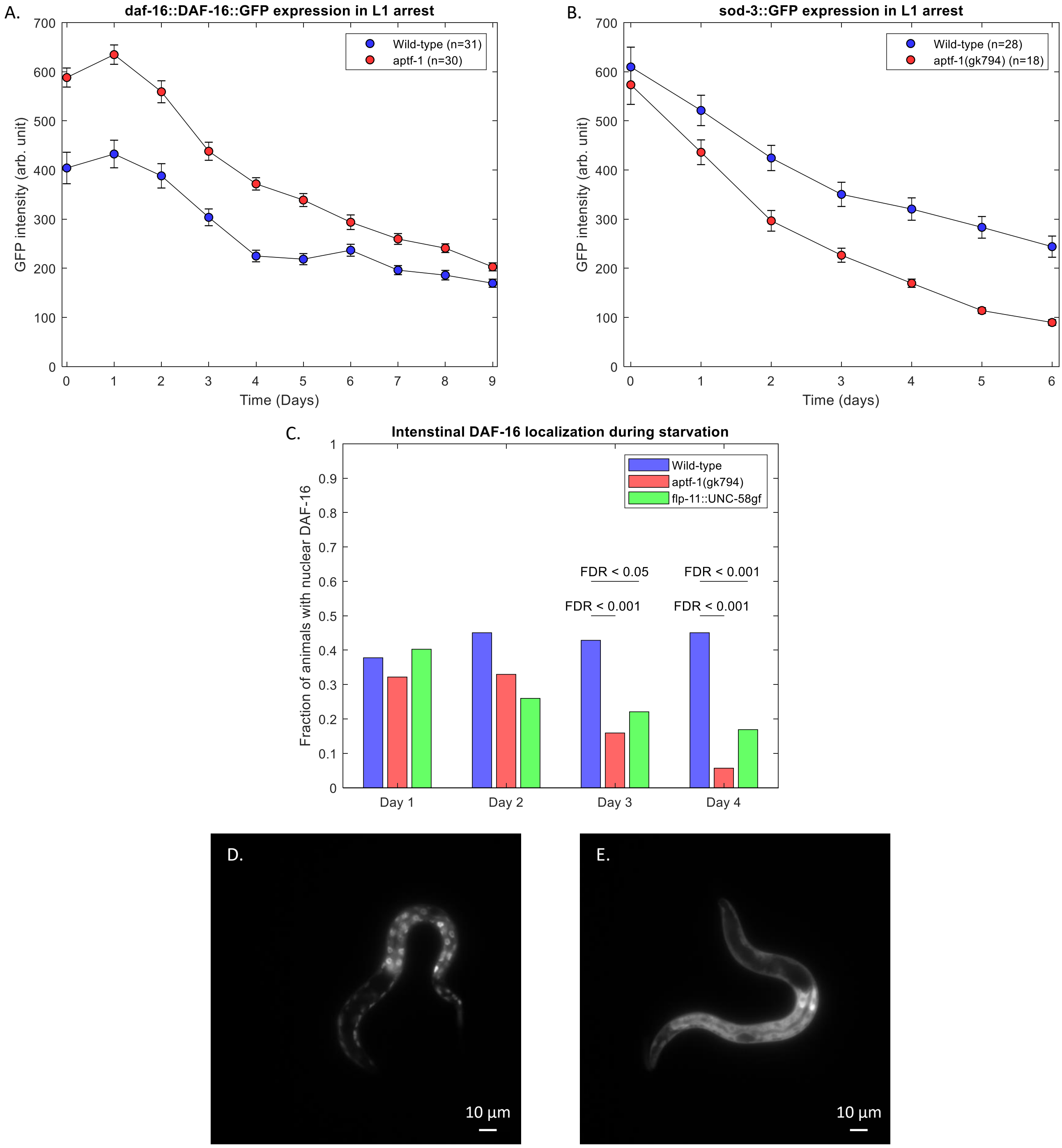


Figure 20. Sleep loss affects intestinal DAF-16 localization during L1 arrest
(**A**) DAF-16 is significantly upregulated in *aptf-1*(gk794) (FDR < 0.05 for all time points).
(**B**) *sod-3* is significantly downregulated in *aptf-1*(gk794) (FDR < 0.05 for Time > 1 days).
(**C**) Bar plot showing the fraction of animals with nuclear DAF-16 localization.
Results for days 1 and 2 are not significant (FDR > 0.05 for all comparisons).
Statistical significance was assessed with Fisher's exact test and the p-values were corrected for false discovery rate by the Benjamini-Hochberg method.
Wild-type: n=91, *aptf-1*(gk794): n=88 and flp-11::UNC-58gf: n = 77
(**D-E**) During nuclear localization GFP tagged DAF-16 shows a spherical distribution pattern, while during cytoplasmic localization the distribution pattern is diffuse.

4.2.4. Sleep loss conditionally affects components of germline-specific gene expression

The germline consists of 2 cells in the newly hatched L1 larvae, namely Z2 and Z3. These cells arrest during L1 starvation through the action of the PTEN homolog *daf-18*, which negatively regulates the insulin signaling pathway. However, *daf-16* action is not required for germline arrest, unlike for somatic cell arrest [64]. I mined germline-unique genes from the published dataset of Han et al. [65] and calculated the significance of enrichment in my sleep loss dataset. I found significant downregulation of germline-specific genes in the *aptf-1* loss of function background, contrary to the flp-11::EGL-1 which shows significant upregulation. In the light of these results, I decided to investigate if sleep loss leads to a difference in the proliferation potential of germline cells. The major pathway controlling germline proliferation during development and maintenance during adulthood, is the Notch signaling pathway via its receptor *glp-1* [66]. Then, I mined the *glp-1* regulated genes from the published dataset of Greer et al. [67], and calculated the significance of enrichment in my sleep loss dataset. I found significant downregulation of *glp-1* target genes in the *aptf-1* loss of function background, while in the *flp-11*::EGL-1 strain there is significant upregulation (Figure 21 A, B). Also, *glp-1* gain of function, significantly increased the lifespan of L1 arrested worms in the microchamber assay in an *aptf-1* dependent manner (Figure 21 C). During the early stages of embryogenesis, germline blastomeres use 2 unique regulatory systems to determine their fate: 1. Transcriptional silencing by *pie-1* and 2. control of RNA metabolism by RNA-rich granules, called P granules [68]. For this reason I assessed the enrichment of genes belonging to the P granules (GO:0043186) and I found significant upregulation only in the *flp-11*::EGL-1 strain. Additionally, I quantified the expression of the transcription regulator *pie-1* using a transgenic reporter line, which showed no difference between the wild-type and *aptf-1* loss of function as predicted by the transcriptome (RNA-seq: $\log_2(FC) = 0.12$ and $FDR = 0.27$) (Figure 21 D).

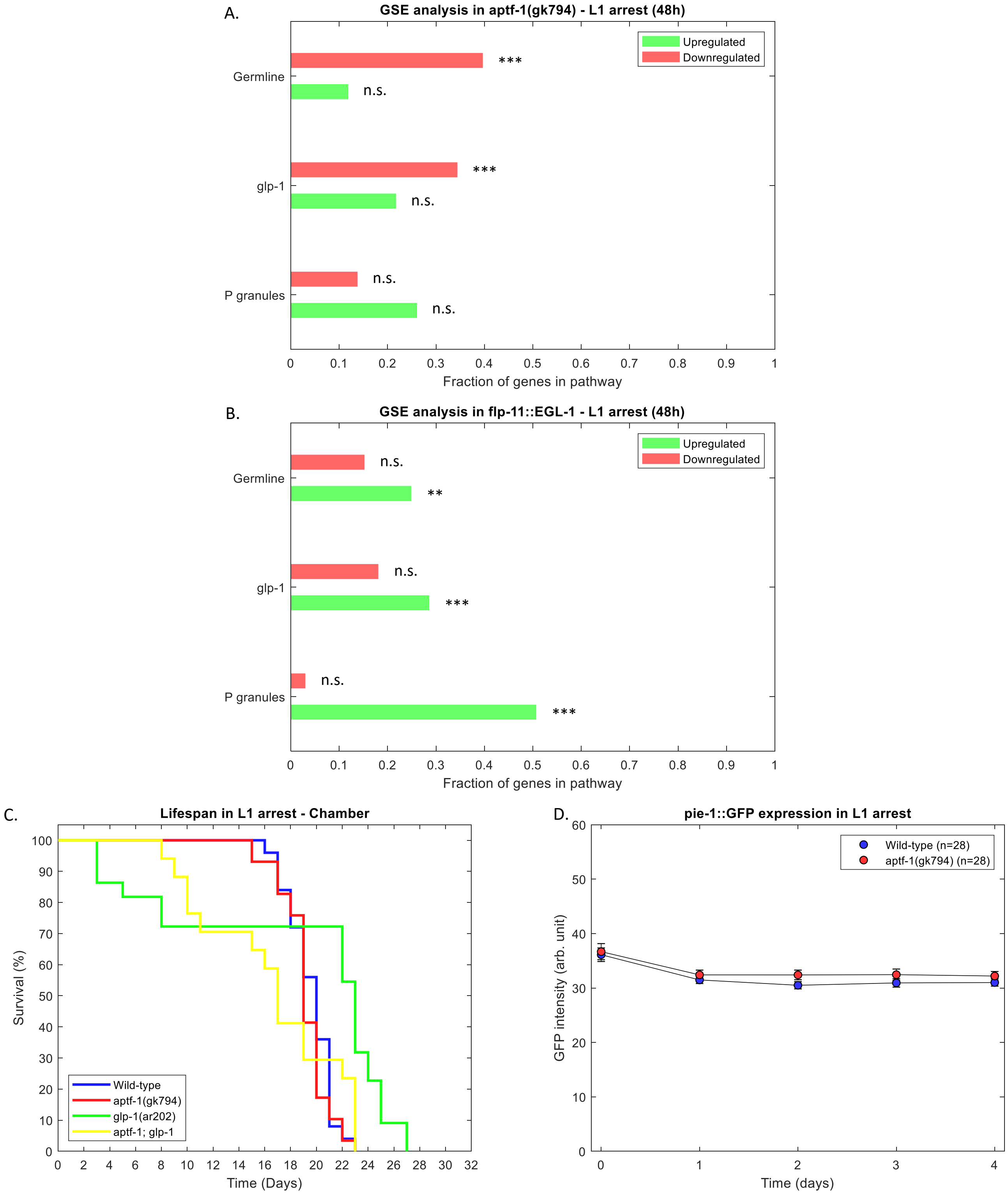


Figure 21. Sleep loss affects germline-specific gene expression and Notch signaling
(**A**-**B**) Horizontal bar chart representation of intestine-related pathways that are affected by loss of sleep (***: $p_{adj} < 0.001$, **: $p_{adj} < 0.01$, *: $p_{adj} < 0.05$, n.s.: not significant).
(**C**) *glp-1* gain of function significantly increases survival during L1 arrest in the wild type background, but not in the *aptf-1* loss of function (wild-type vs *glp-1*(ar202): p = 0.0015 and *aptf-1*(gk794) vs *aptf-1*; *glp-1*: p = 0.9481).
(**D**) *pie-1* expression is not changed in *aptf-1*(gk794) (FDR > 0.05 for all time points).

4.2.5. Sleep loss affects neuronal gene expression and neurotransmission

The nervous system is the most complex tissue in *C. elegans*. Specialized functions are carried out by distinct types of neurons, such as motor neurons for locomotion, sensory neurons for environment perception and interneurons for information processing among others [69]. I mined neuron-unique genes from the published dataset of Kaletsky et al. [57] and RIS, ALA and GABAergic neuron-unique genes ($\log_2(FC) > 2$ and $FDR < 0.05$) from the published dataset of Cao et al. [54] and calculated the significance of enrichment in my sleep loss dataset. In the aptf-1 loss of function condition, neuron as well as RIS, ALA and GABAergic neuron specific genes are upregulated. On the other hand, neuron and GABAergic neuron specific genes are downregulated in the flp-11::EGL-1 strain (Figure 22).

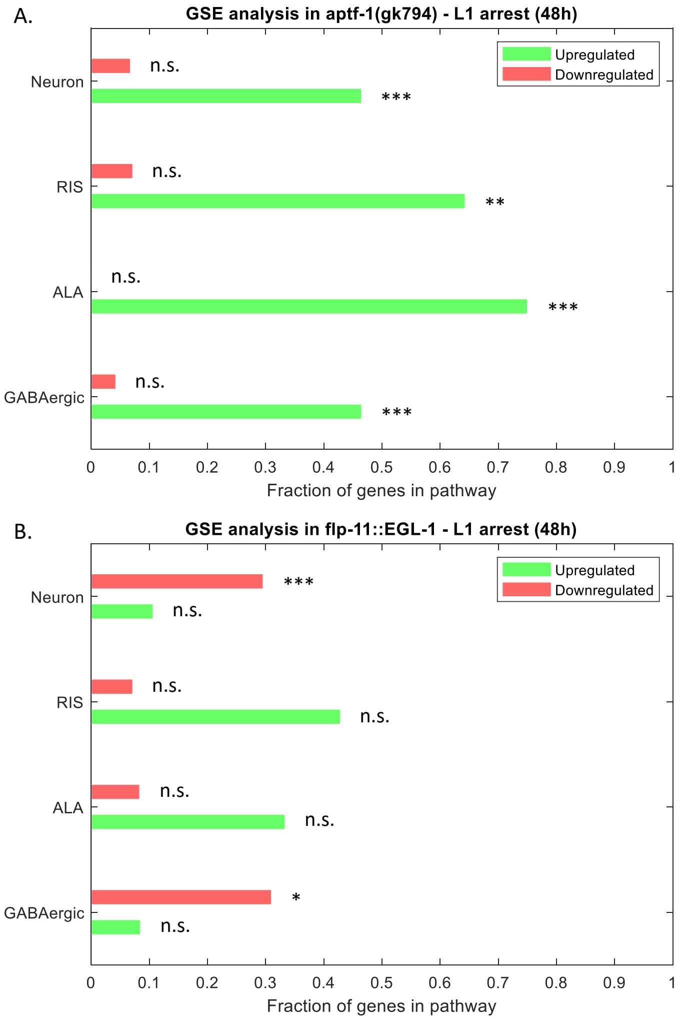


Figure 22. Sleep loss affects neuron-specific gene expression
(**A-B**) Horizontal bar chart representation of neuron-related pathways that are affected by loss of sleep (***: $p_{adj} < 0.001$, **: $p_{adj} < 0.01$, *: $p_{adj} < 0.05$, n.s.: not significant).

Apart from neuropeptides like FLP-11, neurotransmission in *C. elegans* employs several “classic” neurotransmitters. Glutamate, GABA, Acetylcholine and the biogenic amines Serotonin, Dopamine, Tyramine and Octopamine work in concert to modulate behavior, by binding to specific ionotropic or G-protein coupled receptors. Depending on their effect on the target cell, they can be inhibitory or excitatory [70]. In order to further investigate the impact of sleep loss in the nervous system functions, I compiled a list of all currently identified neurotransmitter receptor genes as they appear in WormBase (Version: WS277). These receptors receive neuronal input and their expression spans multiple tissues. Most of the neurotransmitter receptor classes follow the general transcriptome trend and are not significantly enriched. However, GABA receptors stand out because of their upregulation in the *aptf-1* loss of function background and their downregulation in the *flp-11*::EGL-1, in which also glutamate receptors are downregulated (Figure 23).

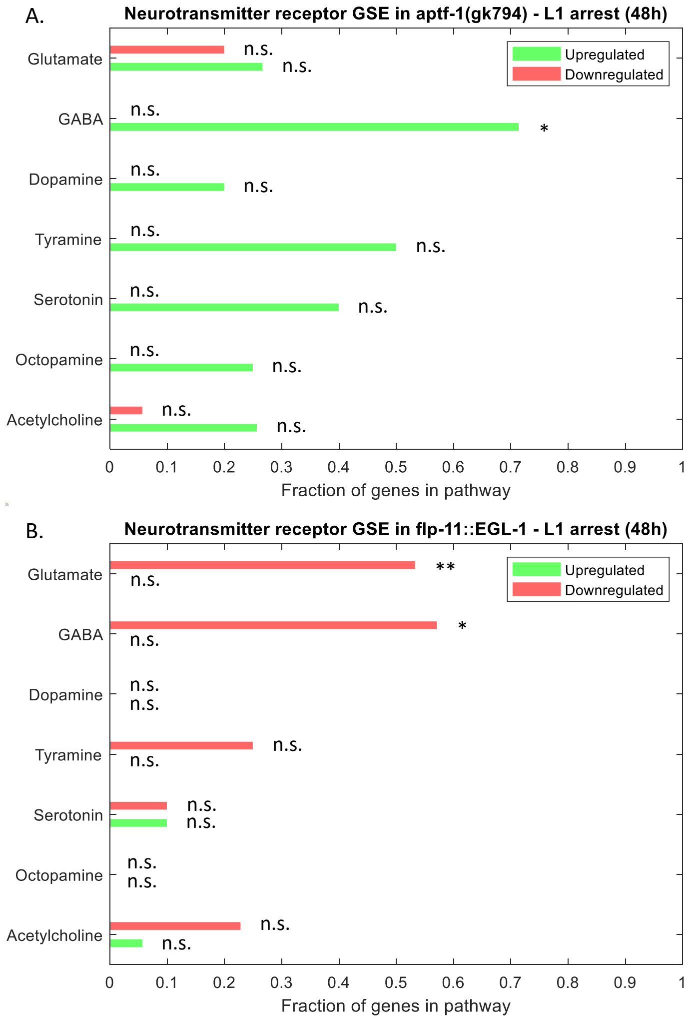


Figure 23. Sleep loss affects GABA and Glutamate receptor gene expression
(**A-B**) Horizontal bar chart representation of neurotransmitter receptor related pathways that are affected by loss of sleep (***: $p_{adj} < 0.001$, **: $p_{adj} < 0.01$, *: $p_{adj} < 0.05$, n.s.: not significant).

Of the GABA receptor genes identified above, the ones that stand out are *gbb-1*, *gbb-2* and *unc-49*, because they are regulated in opposite directions in the sleep loss conditions examined here. *unc-49* is a GABA$_A$ gated chloride channel expressed in the muscles and its expression has been shown to be upregulated in lethargus [71]. *gbb-1* and *gbb-2* form a heterodimeric, inhibitory, G-protein coupled GABA$_B$ receptor that is expressed in cholinergic motor neurons. Loss of function of that GABA$_B$ receptor has been associated with hypersensitivity to aldicarb, an acetylcholinesterase inhibitor that causes accumulation of acetylcholine in the neuro-muscular junction and subsequent paralysis [72]. For this reason, I tested the response of the *aptf-1* loss of function mutant to aldicarb. The response varies from resistance to hypersensitivity, depending on the time point of starvation (Figure 24).

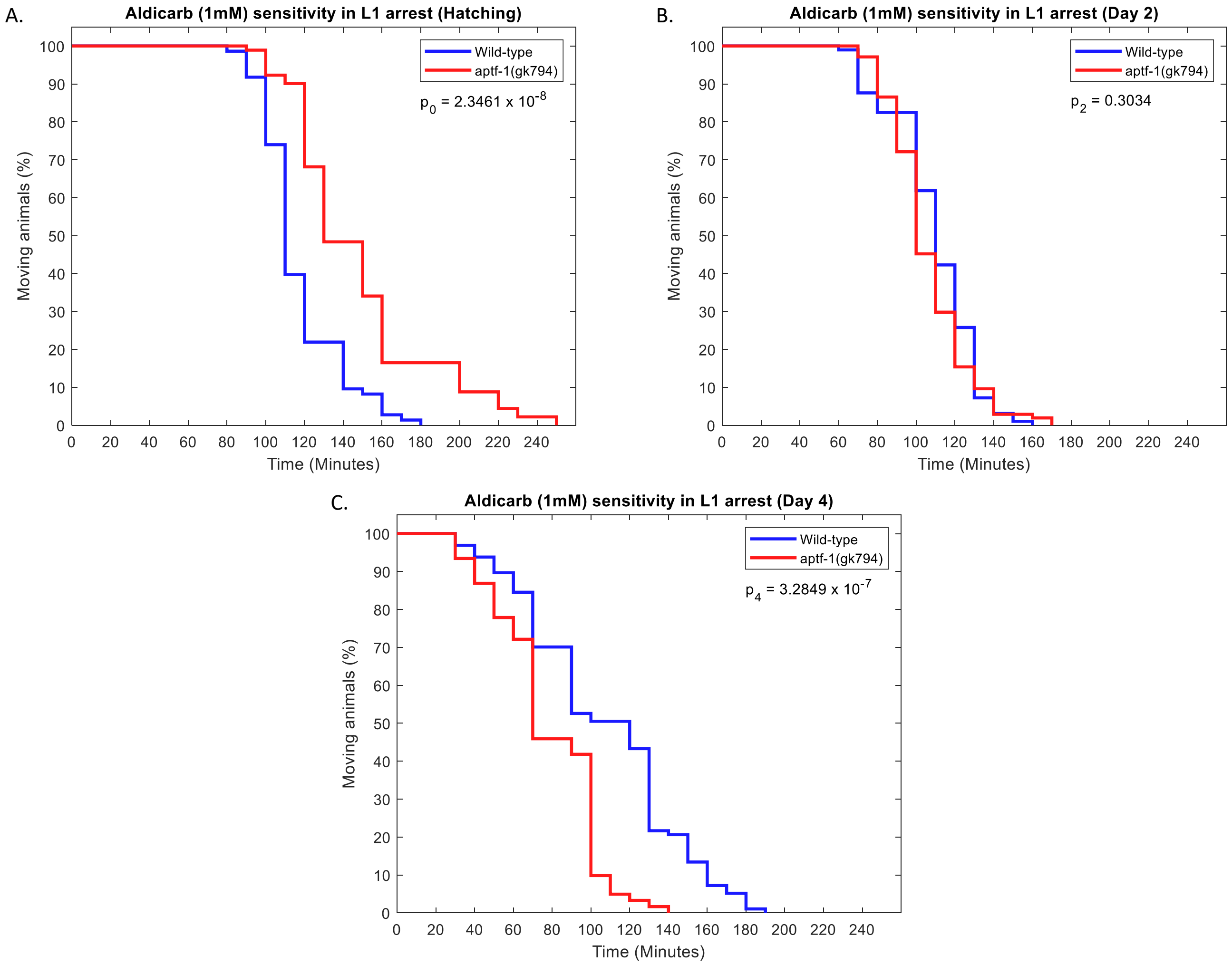


Figure 24. Sleep loss alters the sensitivity to aldicarb of C. elegans
(**A-C**) At hatching, *aptf-1* loss of function results in resistance to aldicarb, which is lost by the 2nd day of starvation. At day 4, the sleepless animals are hypersensitive to aldicarb.
Wild-type: n = 73, 97 and 97 for days 0, 2 and 4 respectively.
aptf-1(gk794): n = 91, 104 and 122 for days 0, 2 and 4 respectively.

As an interneuron, RIS processes signals from a variety of other neurons. While the GABA-related results point to the motor neurons and the muscles to be at the receiving end of the consequences of sleeplessness, it is also important to address the function of the neurons that function upstream of RIS. These neurons are part of the locomotion circuit that also controls sleep behavior and can be mechanosensory (ASH), dopaminergic (CEP) and tyraminergic (RIM) among others [28]. While no difference in baseline activity was observed in mechanosensory and dopaminergic neurons, the tyraminergic RIM neurons show significantly increased activity in the aptf-1 loss of function background (Figure 25).

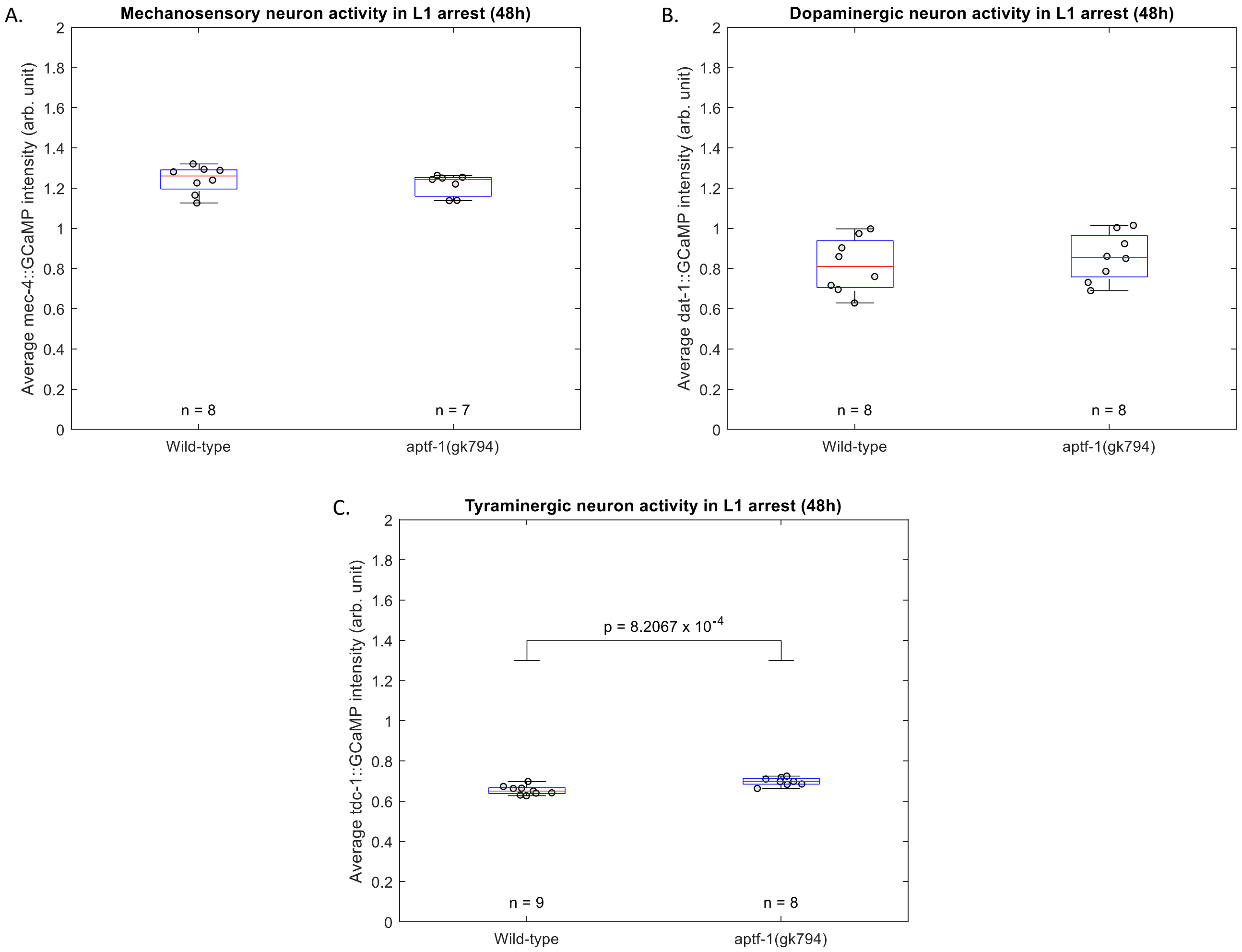


Figure 25. Sleep loss increases RIM neuron activity in L1 arrest
(**A-C**) Boxplots showing average GCaMP intensity under promoters specific for different neuron subgroups. Mechanosensory and dopaminergic neurons show no significant difference in the *aptf-1*(gk794) background (p = 0.4047 and p = 0.5365 respectively). In tyraminergic neurons average baseline intensity increases by 6,6% in the *aptf-1*(gk794) background. Red horizontal line denotes the median value.

4.2.6. Sleep controls protein synthesis via U_{34} thiolation in L1 arrest

I have shown above that sleep introduces imbalances to protein processing mechanisms, such as steps of the translation process and the unfolded protein response. In order to understand how gene expression translates to protein expression in sleep loss conditions, I performed a meta-analysis on the datasets by correlating gene and protein expression, keeping in mind that only approximately 10% of the genes had their corresponding proteins detected. There is almost zero correlation between the proteome and the transcriptome (Figure 26).

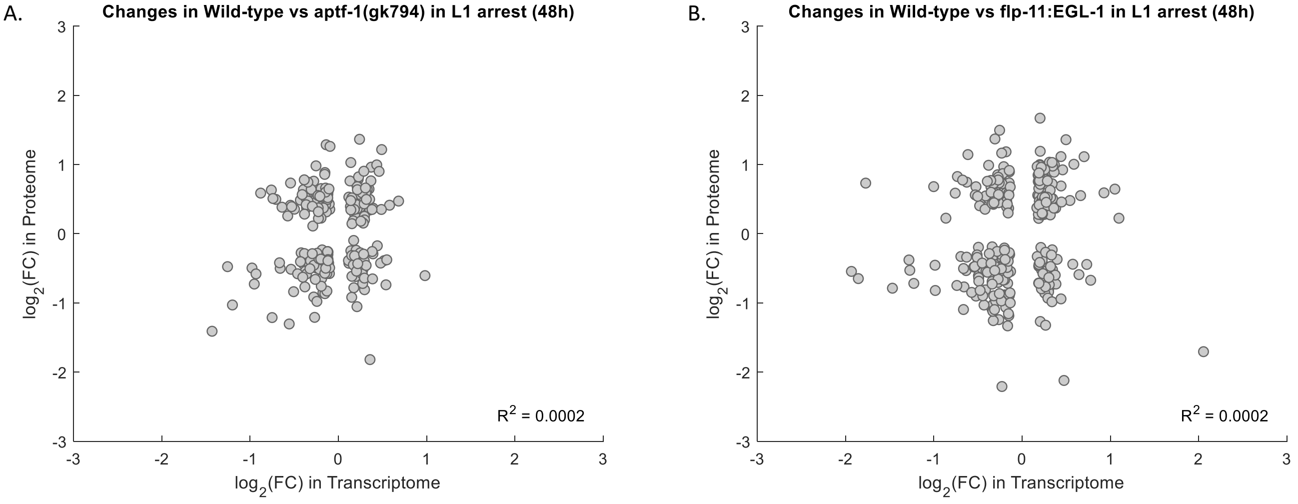


Figure 26. No correlation is found between gene and protein expression in L1 arrest
(**A-B**) Scatter plot representation of transcriptomic and proteomic changes. The four groups that are formed (one in each quadrant) have approximately equal elements.

Protein homeostasis is regulated by a plethora of pathways, to ensure proper development and a healthy lifespan. A gene that stands out is *tut-1* (RNA-seq: $\log_2(FC) = 0.22$ and $FDR = 5.48 \times 10^{-5}$ in the *aptf-1*(gk794) background), which is responsible for the 2-thiolation of wobble uridine (U_{34}) in the tRNAs of Lysine, Glutamine and Glutamate. Changes in thiolation can affect the rate of mRNA translation and the equilibrium between protein synthesis and folding, thus creating proteotoxic stress [73]. Although Lysine-tRNA U_{34} thiolation is not changed in the *aptf-1* loss of function background, Glutamine-tRNA U_{34} thiolation is significantly increased, in symphony with *tut-1* transcriptional expression. This is a significant finding, since changes in thiolation are very rare between different conditions (personal communication with Prof. Sebastian Leidel, University of Bern) (Figure 27 A, B). Also, loss of function of *tut-1* reduces the lifespan of L1 arrested worms and *aptf-1* loss of function is able to rescue this phenotype (Figure 27 C, D). Loss of function of another gene in the same pathway, *elpc-1*, reduces lifespan as well but the phenotype cannot be rescued by *aptf-1* loss of function (Figure 27 E, F).

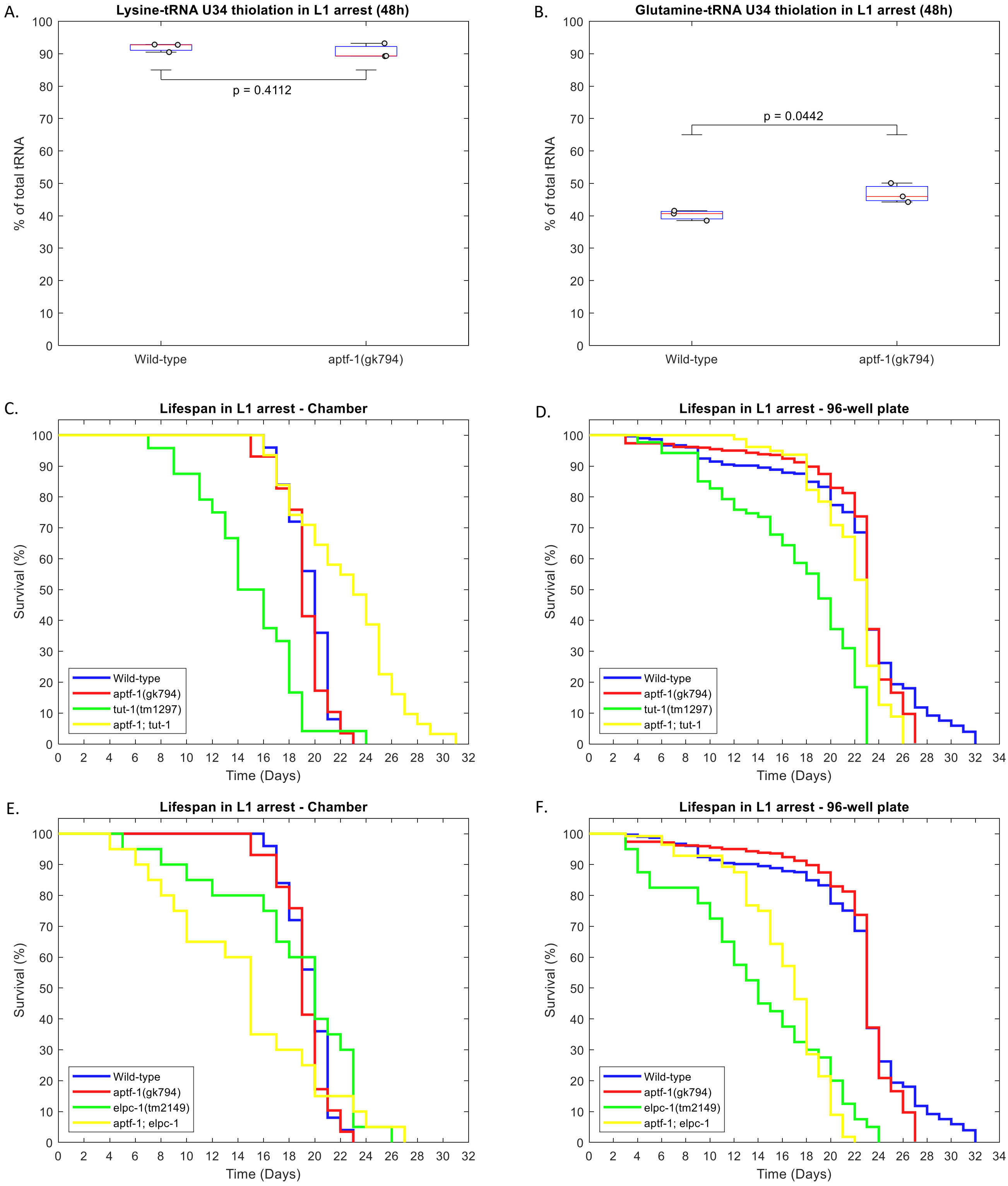


Figure 27. Sleep loss increases U_{34} thiolation in L1 arrest

(A-B) Glutamate tRNA shows increased thiolation in the *aptf-1*(gk794) background, while Lysine tRNA does not (3 samples were used per condition).

(C-D) *tut-1* loss of function shows significantly reduced lifespan compared to the wild-type in both the chamber and the 96-well plate assay ($p = 9.7 \times 10^{-4}$ and $p = 0$ respectively), that can be rescued by *aptf-1* loss of function ($p = 7 \times 10^{-4}$ and $p = 0.002$ respectively).

(E-F) *elpc-1* loss of function produces inconsistent results between assays, both in the wild-type and in the *aptf-1*(gk794) background.

4.2.7. Sleep loss alters lysosomal function in L1 arrest

Organisms degrade cytoplasmic components, by delivering them to lysosomes in a process known as autophagy. Macro-autophagy, is the most well studied autophagy pathway in *C. elegans*, and involves compartmentalization of cytoplasmic material in vesicles, subsequent fusion with lysosomes and degradation by hydrolases [74]. In the *aptf-1* loss of function background, macro-autophagy and lysosomal gene expression is upregulated (Figure 28 A). However, the number of autophagic vesicles does not change, neither in the intestine nor in the nerve ring (Figure 28 B). Genes coding for the H^+ pump v-ATPase, which acidifies the lumen of lysosomes, are downregulated, which might in turn affect the quality of autophagy.

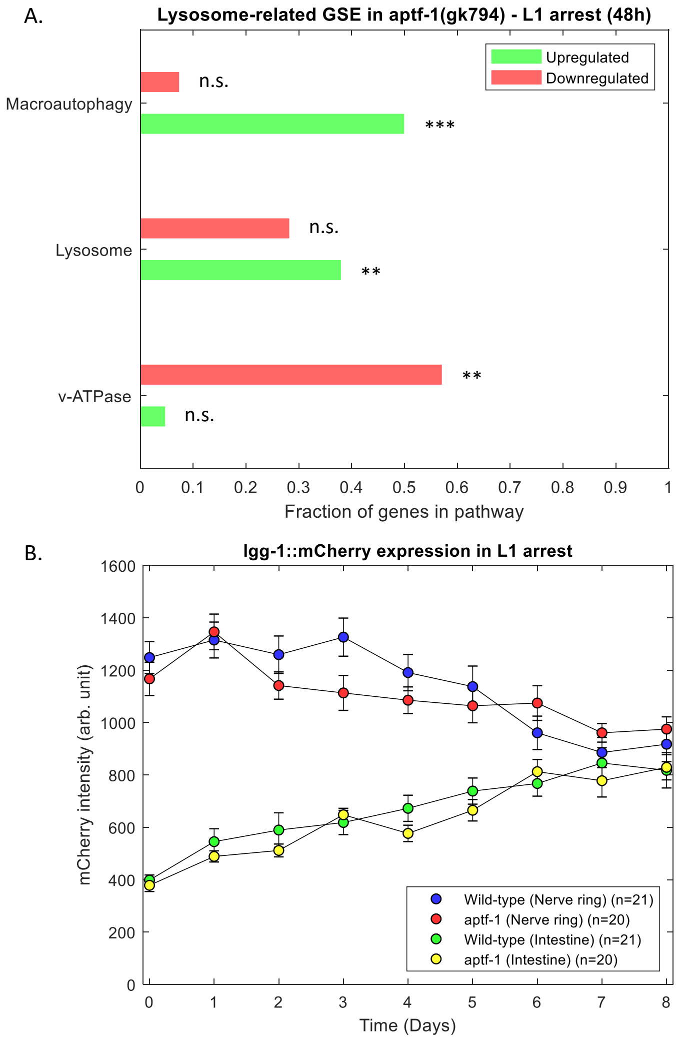


Figure 28. Sleep loss affects lysosomal gene expression in L1 arrest
(A) Horizontal bar chart representation of lysosomal related pathways that are affected by loss of sleep (***: $p_{adj} < 0.001$, **: $p_{adj} < 0.01$, *: $p_{adj} < 0.05$, n.s.: not significant).
(B) The number of autophagic vesicles in the nerve ring and the intestine does not change in the *aptf-1*(gk794) background (FDR > 0.05 for all time points).

To sum up, in this chapter I have shown that sleep loss in L1 arrest induces several changes in important pathways that end up altering the physiology of *C. elegans*.

More specifically in the *aptf-1* loss of function background:

Loss of sleep, decreases the expression of the starvation induced gene, *hsp-12.6*. Hypodermis and TGF-β gene expression is upregulated, resulting in reduction of size. Although muscle gene expression seems to follow the global transcriptome trend, this is not the case for the mitochondrial electron transport chain genes and the genes coding for mitochondrial localization proteins, which are downregulated. Intestine-specific gene expression is generally downregulated and expression of many targets of the insulin signaling pathway is affected by sleep loss because FOXO homolog nuclear localization is compromised. Notch signaling and germline gene expression is downregulated and *glp-1* gain of function lifespan increase is *aptf-1* dependent. Neuronal and GABA receptor gene expression is upregulated, indicating the significance of this neurotransmitter in sleep loss. Acetylcholine signaling changes, as indicated by the aldicarb sensitivity assays. Also, tyraminergic (RIM) neuron activity levels are increased. Finally, sleep controls protein homeostasis via tRNA wobble U_{34} thiolation and by affecting aspects of macro-autophagy.

With regard to the *flp-11*::EGL-1 strain:

This seems to be a strain in which RIS is constantly active. Its gene expression patterns are generally very different from the ones in the *aptf-1* loss of function strain. Neuropeptide receptor *dmsr-2* expression, is greatly downregulated. Insulin signaling targets are affected as well, probably because of low FOXO nuclear localization. Finally, neuronal, GABA receptor and glutamate receptor gene expression is downregulated, contrary to the *aptf-1* loss of function background.

4.3. Sleep loss induces specific metabolic changes in L1 arrest and vice versa

The transcriptomic and proteomic data collected so far, are an invaluable asset for identifying many components affected by sleep loss that were previously unknown. In order to get the complete image of the sleep loss condition, I performed 2 complementary metabolomic analyses at 48 hours and at 6 days of starvation. In total, 3 biological replicates per condition were measured, which led to the identification of 120 metabolites for the 48-hour time point and 141 metabolites for the 6-day time point.

At 48 hours of starvation, *aptf-1* loss of function, upregulates metabolites related to oxidative stress, such as Allantoin and Glutathione (Figure 29 A). Allantoin is the last component of the nucleic acid degradation pathway and since *C. elegans* lacks the enzyme responsible for converting uric acid to allantoin, its presence can be attributed to non-enzymatic oxidation of uric acid by ROS [75]. Succinic acid, an intermediate of the TCA cycle and Complex II of the electron transport chain, is also upregulated, as well as Tryptophan, which is known to be upregulated during sleep deprivation in humans [36]. A big group of downregulated metabolites are Sphingomyelins, lipids that take part in the composition of the cell membrane and can act as signaling molecules. The most downregulated hit, both in *aptf-1* loss of function and *flp-11*::EGL-1 is the amino-acid Methionine. Surprisingly, in the *flp-11*::EGL-1 strain there is no differential expression of any other metabolite (Figure 29 A, B and sections 6.25 – 6.26). At 6 days of starvation the metabolite profile looks different, with no oxidative stress metabolites differentially expressed. The only one that stands out is Kynurenic acid, a neuroactive molecule and endogenous antagonist to the glutamate NMDA receptors, that is regulated by insulin signaling and its production in the RIM neuron has been linked to ageing phenotypes [76]. Kynurenic acid is upregulated in *aptf-1* loss of function and downregulated in the *flp-11*::EGL-1 background (Figure 29 C, D and sections 6.27 – 6.28). In addition to the metabolomic analyses, I performed isothermal microcalorimetry analysis to measure the heat output of sleepless worms as a readout of their metabolic status. Indeed, heat production is increased more than 100% in the sleepless strains. The largest part of this increase can be attributed to the difference in movement capacity between the wild-type and the non-sleeping worms. However, there is still a 20% extra heat production that can only be explained by a difference in metabolic rates (calculations by Prof. Bart Braeckman, University of Ghent, personal communication) (Figure 29 E). Finally, changes in the metabolic rate, introduced by incubation at 25 °C did not alter the difference in lifespans between wild-type and sleepless worms (Figure 29 F).

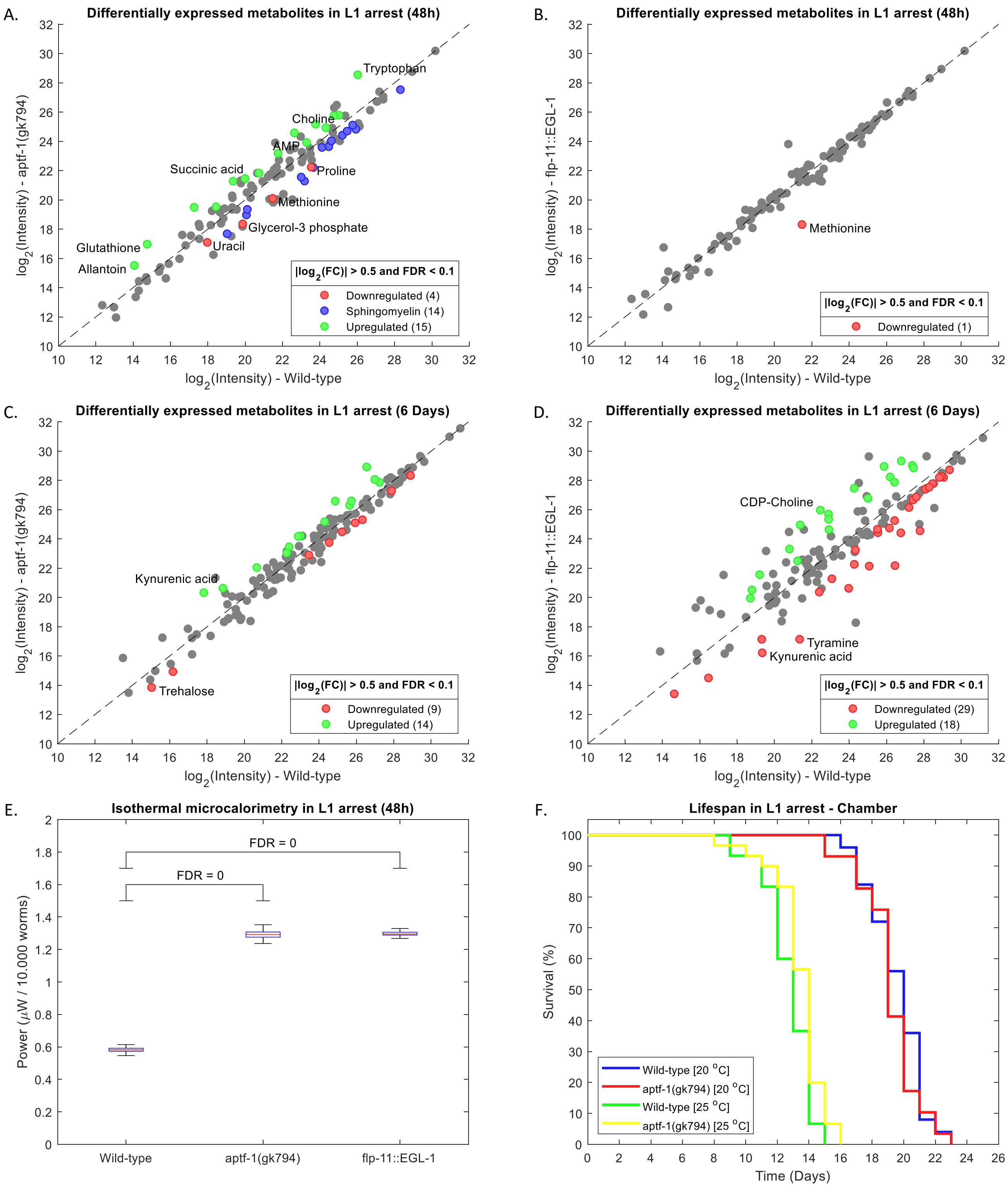


Figure 29. Sleep loss introduces metabolic changes in L1 arrest

(A-D) Scatter plot overview of metabolite expression at 48 hours and at 6 days of starvation. Not significant metabolites according to the selected thresholds, are marked in grey.

(E) Boxplot showing the increased power output of sleepless worms.

(F) Incubation at higher temperatures reduces the lifespan of C. elegans. This change is not affected by sleep loss since the difference in wild-type vs *aptf-1*(gk794) is not significant in either case (p = 0.5294 and p = 0.1121 at 20 ºC and 25 ºC respectively).

Another aspect of the metabolic profile, is the creation of offspring. Reduced developmental quiescence has been associated with defects in egg-laying in the past [50]. In order to assess the ability of the worm to convert energy and nutrients into organized and functional tissue, I counted the number of eggs laid by the adult worm in well-fed and starved conditions. Fed worms lay the same number of eggs regardless of their sleep status. However, starved and sleepless worms lay 2 times more eggs than the wild-type ones (Figure 30).

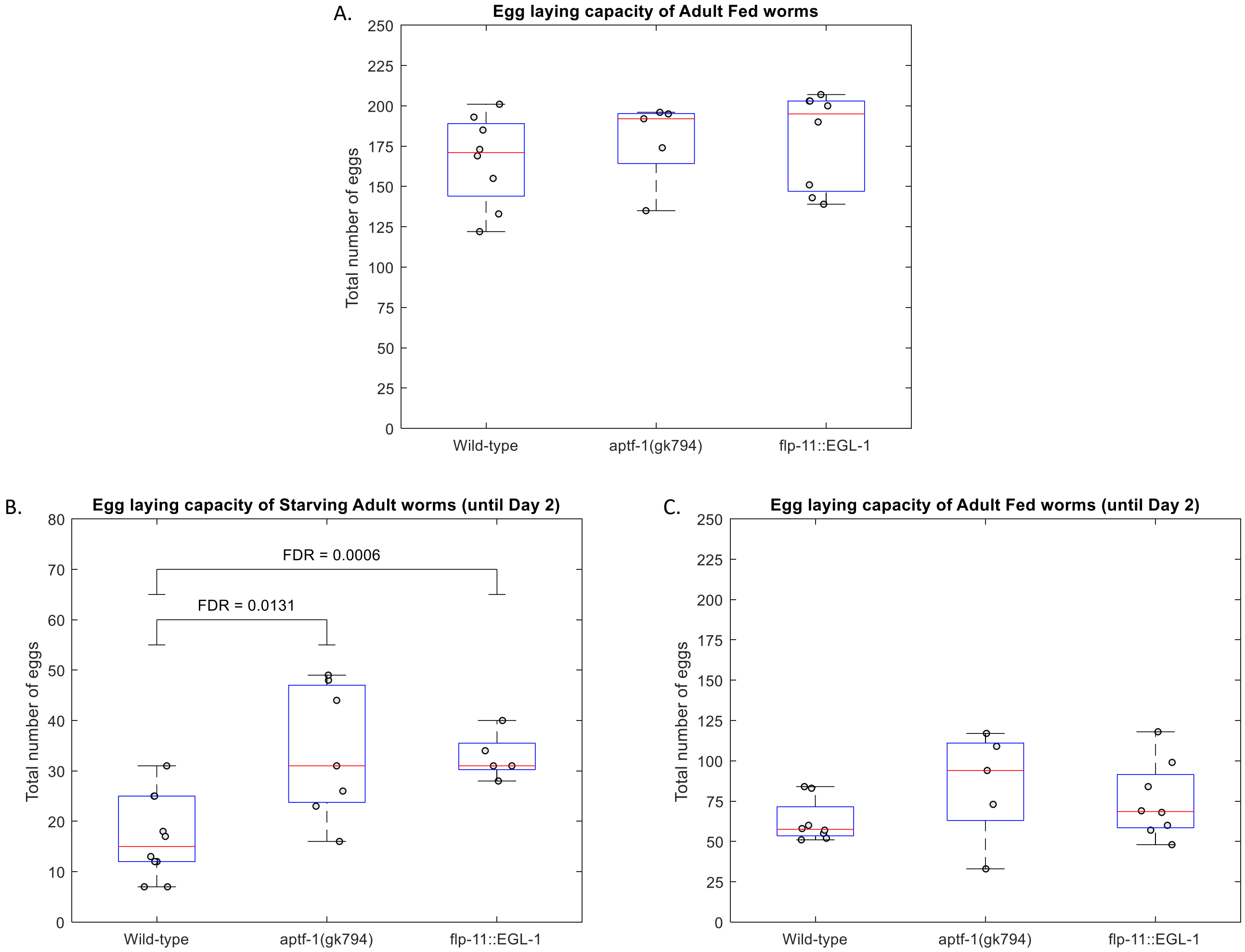


Figure 30. Sleep loss increases egg laying during adult starvation
(A) Sleep-deprived worms do not show egg laying defects (FDR > 0.05 for all comparisons).
(**B-C**) Starved and sleepless worms lay significantly more eggs. For the same time interval fed worms do not show differences in egg-laying (FDR > 0.05).
Fed – Wild-type: n = 8, *aptf-1*(gk794): n = 5, *flp-11*::EGL-1: n = 8
Starved – Wild-type: n = 10, *aptf-1*(gk794): n = 7, *flp-11*::EGL-1: n = 5
Red horizontal line denotes the median value.

The discovery of these sleeplessness-induced metabolic changes, has prompted the question whether this is a 2-way phenomenon, that is whether genetic defects in metabolism induce changes in sleep. To answer this question, I performed an extensive genetic screening of every non-lethal metabolic mutant that is publicly available and assessed their sleep amount at 48 hours of L1 arrest. In total 546 strains were screened, 121 strains showed reduced quiescence and 8 strains showed increased quiescence (Figure 31 A and section 6.29).

With regard to the increased quiescence strains, the only one that stands out is the insulin receptor *daf-2* loss of function mutant, with an increase of 59.72% in quiescence compared to the wild-type (Figure 31 A, B). The other strains should be considered with caution, since many of them show movement defects that can wrongly be considered as sleep.

As for the low quiescence strains, one in particular stands out, the mammalian diacyl-glycerol kinase theta (DKGθ) homolog *dgk-1* loss of function, with a decrease of 93.56% in quiescence compared to the wild-type (Figure 31 A, B). This mutation also resulted in a reduced lifespan phenotype in L1 arrest (Figure 31 D, E). The strain that showed the lowest quiescence is the *tdc-1*;*aptf-1* loss of function double mutant (Figure 31 C). This is important for 2 reasons: 1. it significantly reduced the quiescence of the *aptf-1* mutant, which is already low while *tdc-1* loss of function did not show any difference from the wild-type and 2. tdc-1 codes for tyrosine decarboxylase, the enzyme responsible for the production of tyramine in RIM neurons. In the rest of the low quiescence strains there is an enrichment ($p_{adj} = 10^{-6}$) in sphingolipid metabolism genes (*hyl-1*, *hyl-2*, *F33D4.4*, *sms-3*, *hpo-13*, *sptl-3*, *gba-1*, *lagr-1*). This is interesting not only because of the connection to the metabolome, where sleep loss is shown to reduce sphingomyelins but also because the second messenger DAG, a product of sphingomyelin catabolism is phosphorylated by *dgk-1* to transduce neuronal signals [77]. FOXO homolog *daf-16*, hypoxia response *hif-1*, *vhl-1* and *egl-9* and apoptosis regulator *ced-3* loss of function, all result in low quiescence phenotypes. These genes should be considered for downstream screening and have their role in sleep regulation clarified. Representative mobility traces of wild-type, aptf-1(gk794), dgk-1(ok1462) and daf-2(e1370) can be found in section 6.30.

Overall, the screening shows that metabolic manipulations are more likely to result in low quiescence and that mostly neurotransmission-related mutations produce the strongest phenotypes.

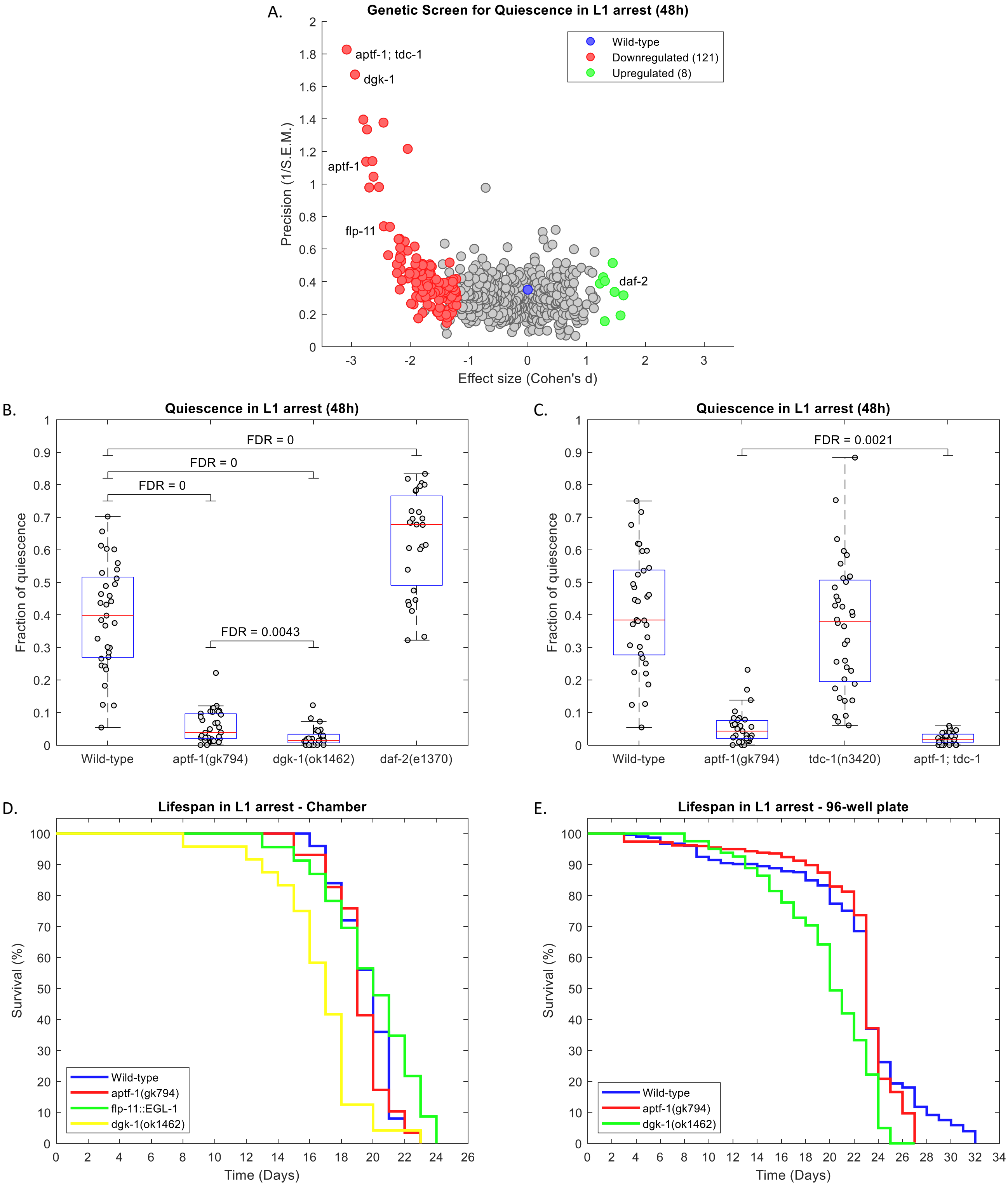


Figure 31. Metabolic defects cause changes in sleep and lifespan
(**A**) Genetic screening for quiescence assessment in L1 arrest.
(**B-C**) Boxplot representation of the fraction of quiescence of the most significant hits of the genetic screen. Wild-type: n = 33, *aptf-1*(gk794): n = 31, *dgk-1*(ok1462): n = 25, *daf-2*(e1370): n = 27, *tdc-1*(n3420): n = 36, *tdc-1*;*aptf-1*: n = 34. Red horizontal line denotes the median value.
(**D-E**) Loss of function of *dgk-1* reduces the lifespan in L1 arrest (Wild-type vs *dgk-1*(ok1642): p = 0.003 and p = 5.2 x 10^{-8} respectively).

In order to address the significant downregulation of methionine in the metabolome, I started another screening in the wild-type background. Initially I supplemented microchamber assays with various concentrations of methionine (0.01 - 25 mM) and followed up with glycine and glutamate, to assess any changes in L1 arrest quiescence behavior. Indeed, there is a significant sleep fraction reduction after supplementation with 10 mM of methionine, glycine and glutamate. Only methionine produces an effect large enough to be compared to the effects discovered in the genetic screening. However, 1 mM of methionine produce the opposite result, a small increase in quiescence. Such contradicting results, did not favor an expansion of the screening to the *aptf-1* loss of function mutant (Figure 32 A and section 6.31). Furthermore, in order to address the impact of maternal growth conditions in the arrested L1, I cultured the worms for 4 months on regular OP50 food source and various temperatures or at a constant temperature of 20 °C and different food sources. High incubation temperatures (25 °C) and rich food sources (Na22) reduce quiescence, while low incubation temperatures (15 °C) and poor food sources (DL42) increase quiescence in L1 arrest (Figure 32 B and section 6.32).

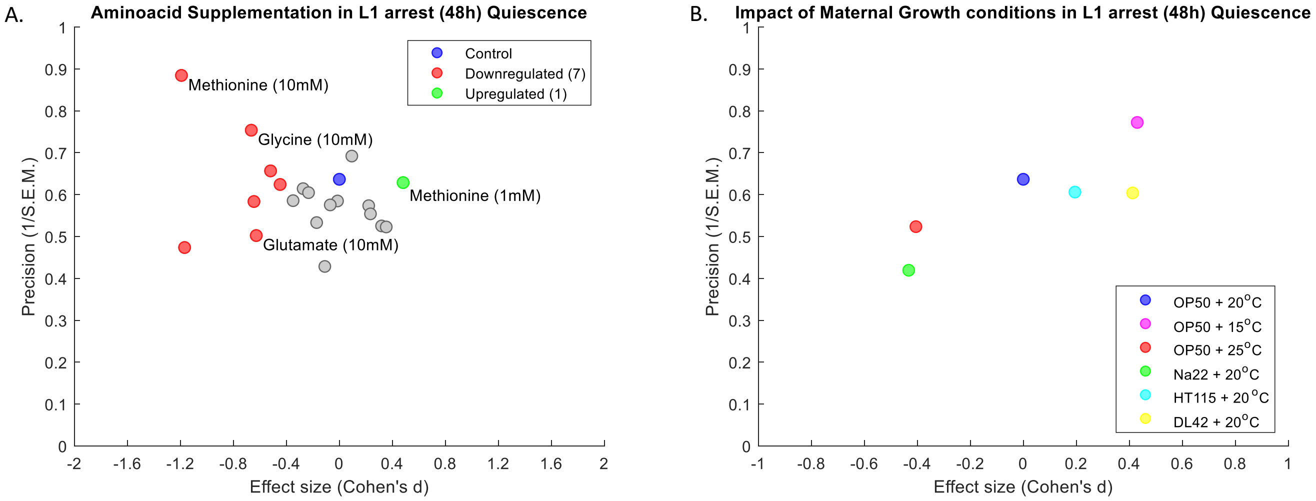


Figure 32. Maternal growth conditions and amino-acid supplementation affect sleep
(**A**) Methionine, Glycine and Glutamate supplementation at 10 mM decreases quiescence, while 1 mM of Methionine increases quiescence of wild-type animals.
(**B**) Growth temperature and nutritional status of the parent worm, affects offspring quiescence.

To sum up, sleep loss increases the metabolic rate of the worms. The key regulatory elements of L1 arrest quiescence are methionine metabolism, insulin signaling via *daf-2* and *daf-16*, neuronal signaling mediated by RIM and the action of *dgk-1* downstream of a G-protein coupled receptor probably regulated by sphingolipid metabolism. Maternal growth conditions play only a minor role in offspring quiescence.

4.4. *dgk-1* loss of function results in sleep loss by changing RIS physiology

In order to further investigate the *dgk-1* loss of function that produces the low quiescence phenotype in the genetic screen, I decided to assess the behavior of RIS in that background. In addition to the wild type, I have included two more control strains that were designed (by Prof. Henrik Bringmann) to keep RIS constantly de-polarized (flp-11::UNC-58(gf)) or hyper-polarized (flp-11::TWK-18). Surprisingly, both these strains show reduced quiescence in L1 arrest as was shown by my colleague Inka Busack. Diacylglycerol (DAG) is a second messenger that is responsible for neurotransmission by regulating synaptic vesicle release. *dgk-1* acts by phosphorylating DAG into phosphatidic acid, an action that reduces the amount of available DAG, inhibiting neurotransmitter release. *unc-13* (a homolog of mUNC13), is the target of DAG that promotes neurotransmitter release. Both these genes act downstream of G-protein coupled receptors to regulate quiescence [78]. Average activity of the RIS neuron as measured by GCaMP shows no differences in the *dgk-1* or *unc-13* loss of function backgrounds, although the characteristic RIS peaks are absent (representative traces can be found at section 6.33). As expected the engineered de-polarized and hyper-polarized strains show, respectively, increased and decreased average RIS activity (Figure 33 A). In all cases, the drop of speed that is observed by RIS activation in the wild-type is abolished. That, in turn, means that the inverse correlation of RIS activity and speed is lost (Figure 33 B). Finally, I investigated the signal complexity of RIS for each strain. Signal complexity of the electroencephalogram has been used as a predictive marker of brain health in neurodegenerative diseases, trauma, anesthesia and sleep-wakefulness studies [79]. Signal complexity, quantified here by fractal dimension, is higher in the *dgk-1* loss of function background as well as the RIS de-polarized strain. On the other hand, *unc-13* shows lower signal complexity and the RIS hyper-polarized strain shows no difference from the wild-type (Figure 33 C).

With this set of experiments, it is now evident that neurotransmission for sleep induction is not only dependent on RIS peaks, but also on the overall complexity of the neuronal signal. *dgk-1* loss of function seems to ablate sleep in a way different than simply de- or hyper- polarizing RIS.

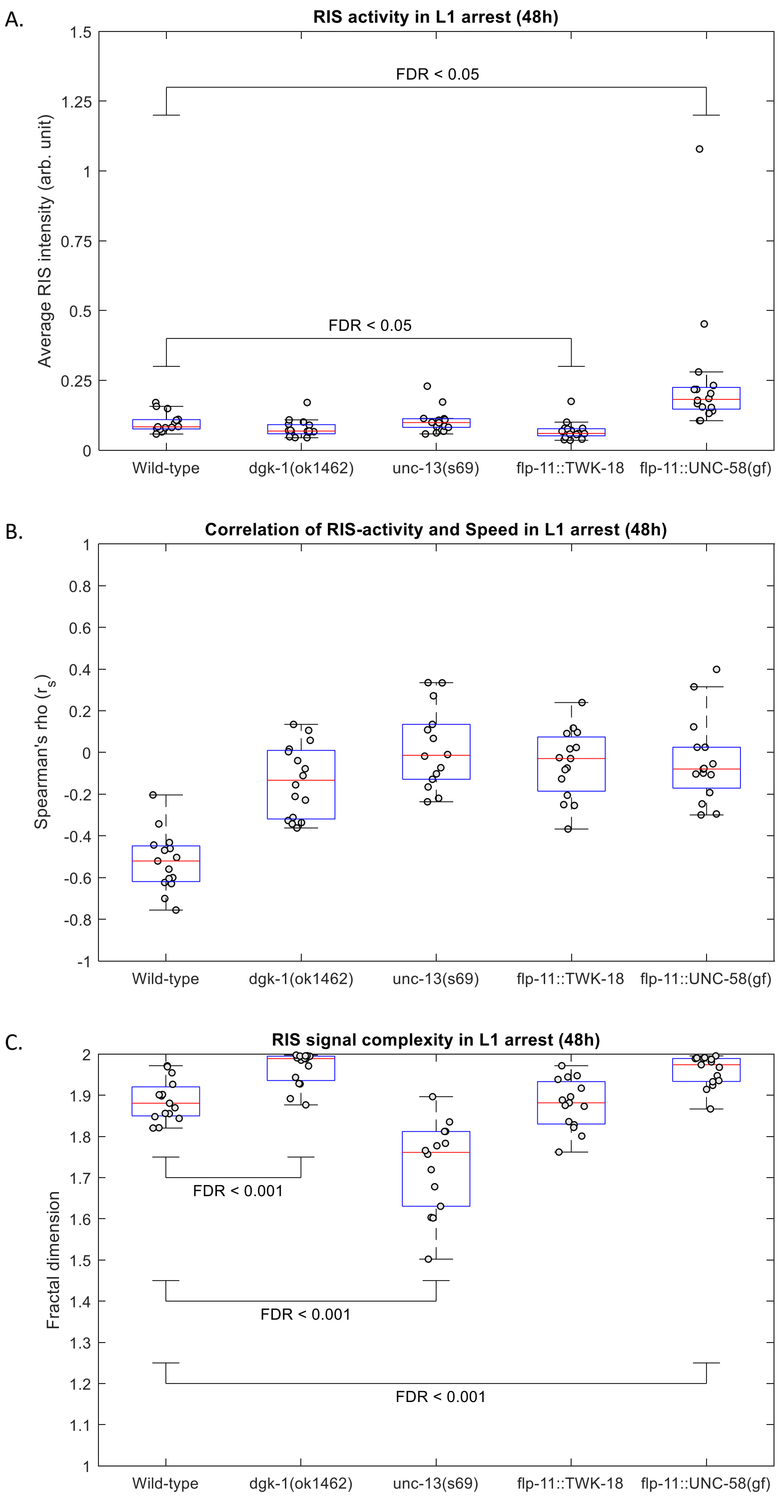


Figure 33. *dgk-1* loss of function mutants abolish sleep by altering RIS function
(**A**) RIS average GCaMP activity levels are not changed by *dgk-1* or *unc-13* loss of function.
(**B**) All of the tested manipulations result in decoupling of RIS activity levels and speed (FDR < 0.05 for all strains vs wild-type).
(**C**) RIS signal complexity is significantly higher in dgk-1(ok1462) and flp-11::UNC-58(gf) than the in the wild-type. Fractal dimension was calculated with Higuchi's algorithm (k = 100). Wild-type: n = 15, *dgk-1*(ok1462): n = 16, *unc-13*(s69): n = 14, *flp-11*::TWK-18: n = 15, *flp-11*::UNC-58(gf): n = 15

4.5. The transcription factor XBP-1 regulates aspects of L1 arrest quiescence

In order to identify genes that could reverse the loss of developmental quiescence induced by the *aptf-1* loss of function, an EMS mutagenesis assay was performed by Dr. Elisabeth Maluck (these results are documented in her Ph.D. thesis titled “Characterization of RIS presynaptic circuits for sleep regulation in *Caenorhabditis elegans*”). She was able to isolate 2 candidates, *aptf-1* loss of function, strains that showed almost wild-type developmental quiescence (code-named: Candidate 1 and Candidate 9). After she performed genetic sequencing on the 2 candidates, we collaborated for downstream analysis. I implemented an algorithm to find regions of high mutation density (hotspots) and eventually identify the bZIP transcription factor *xbp-1* (Candidate 1) and the zinc-finger transcription factor *ztf-20* (Candidate 9) as the genes with the highest probability of being responsible for the quiescence rescue (Figure 34 A, B). The most cost-effective strategy was to obtain commercially available strains that carry mutations in these genes and screen them for quiescence. Dr. Maluck assessed quiescence in L1 lethargus and I assessed quiescence in L1 arrest.

Neither Dr. Maluck nor I could replicate the phenotype of Candidate 9 with the *ztf-20* mutant in any condition. This might be due to the fact that the strain used did not exactly replicate the mutation identified in Candidate 9, but it was just a missense mutation (gk263563) with unknown effects on protein function.

However, *xbp-1* loss of function was able to partially rescue the quiescence of the *aptf-1* loss of function mutant both in L1 lethargus (personal communication with Dr. Maluck) and in L1 arrest (Figure 34 C). It has to be noted here that the strain used did not exactly replicate the original mutation of Candidate 1, but it contains a single nucleotide change that leads to a premature stop codon (zc12).

XBP-1 is the transcription factor responsible for the transcription of genes that take part in the unfolded protein response in the endoplasmic reticulum. Sleep deprivation is known to induce the unfolded protein response in young adult worms [80]. These findings taken together with my transcriptome analysis gene set enrichment analysis, show for the first time the interconnection of sleep loss in L1 arrest and the unfolded protein response in *C. elegans*.

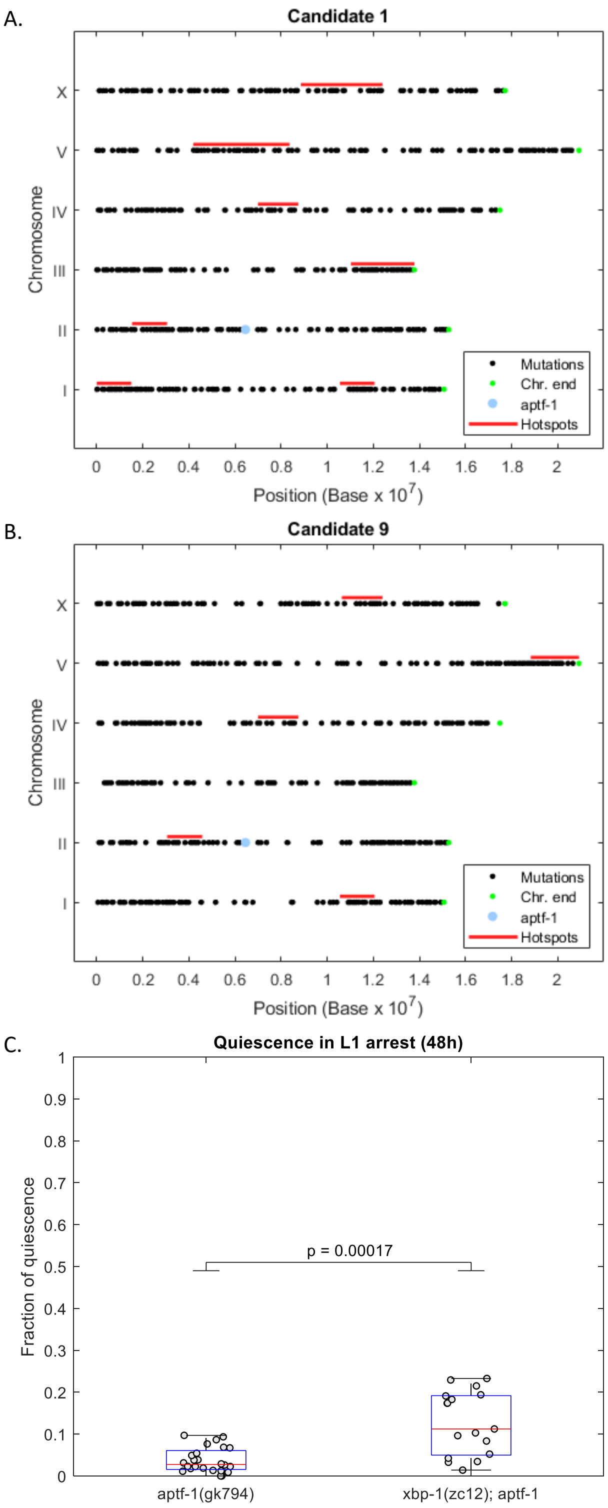


Figure 34. *xbp-1* loss of function partially rescues the *aptf-1*(gk794) loss of quiescence
(A-B) Hotspot regions as they were identified on the chromosomes of each candidate.
(C) *xbp-1* loss of function results in a 2.1-times increase in quiescence of the *aptf-1* loss of function mutant. *aptf-1*(gk794): n = 24, *xbp-1*(zc12): n = 17

4.6. Sleep loss affects FOXO-dependent transcription in muscles

As I have shown above, FOXO-dependent gene expression is greatly affected by sleep loss. I also presented the example of reduction in nuclear translocation of DAF-16 in intestinal cells. This is also the case for muscle cells in which decreased nuclear translocation of DAF-16 can be observed from day 2 of starvation (Figure 35 A). For this reason, downstream class I targets of FOXO that get expressed in the muscle, such as *hsp-12.6*, are downregulated (Figure 35 C, D). The case of HSP-12.6 is a particular one, since it stands at the crossroads of starvation, sleep and aging, with its loss reducing the lifespan of L1 arrested worms (Figure 35 B).

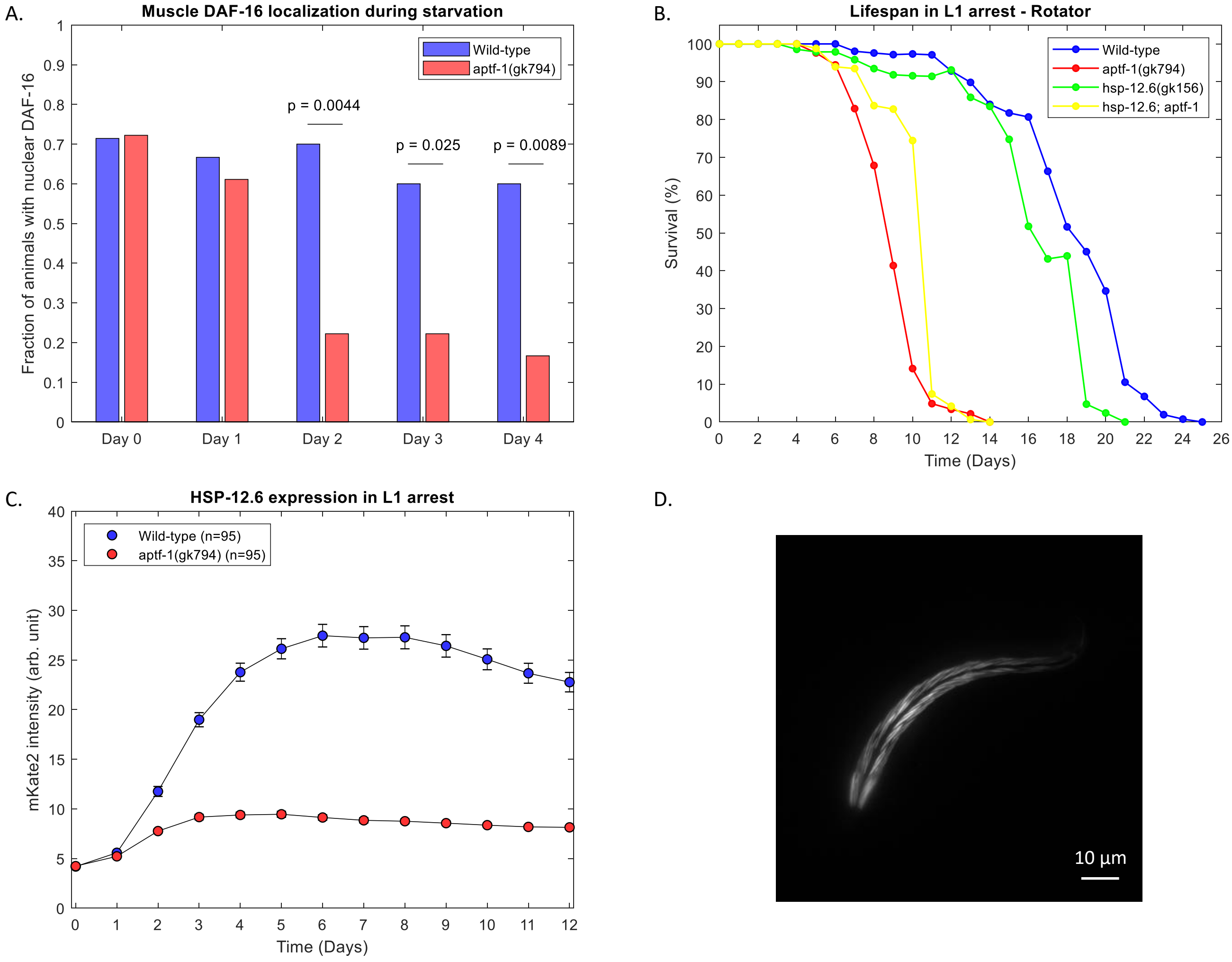


Figure 35. *aptf-1* loss of function reduces FOXO nuclear localization and HSP-12.6

(A) Bar plot showing the fraction of animals with nuclear DAF-16 localization. Statistical significance was determined with Fisher's exact test. Wild-type: n=20 and *aptf-1*(gk794): n=18

(B) *hsp-12.6* loss of function reduces the lifespan in the wild-type background (FDR = 3.7 x 10^{-11} at day 19) while it does not affect the lifespan of *aptf-1*(gk794) (FDR = 1 at day 12).

(C) HSP-12.6 expression is not induced as efficiently in the *aptf-1*(gk794) background during L1 starvation (FDR < 0.001 for all time points, except day 0 and day 1).

(D) HSP-12.6 expression driven by the endogenous promoter is localized in body wall muscles.

4.7. RIS and the nervous system control HSP-12.6 expression in muscles

In order to identify the rest of the pathway components that connect *aptf-1* to *hsp-12.6*, I performed a screen of HSP-12.6 expression in 70 different conditions during the first 12 days of L1 arrest (Figure 36 A). Although the FOXO transcription factor (*daf-16*) and the factors that control FOXO activity (*daf-2*, *jnk-1*, *aak-1* and *aak-2*, *rheb-1* and *fkh-9* [63,81]) all affect the expression of HSP-12.6, they do it parallel to *aptf-1* (Figure 36 B-E).

In order to address this issue, I hypothesized that HSP-12.6 expression is regulated by *aptf-1* via a non-canonical pathway. For this reason, I tested the expression of HSP-12.6 in worms that were engineered to have de- or hyper- polarized RIS. RIS de-polarization leads to increased expression of HSP-12.6, while RIS hyper-polarization leads to decreased expression (Figure 37 A). Loss of function of other RIS-specific components, such as the neuropeptide FLP-11 or the serotonin receptor SER-4 [54], increase or decrease the expression respectively (Figure 37 B). After having established the role of RIS, I assessed the effect of neurotransmission. Increased neurotransmission resulting from *dgk-1* loss of function, decreased the levels of HSP-12.6, while decreased neurotransmission resulting from *unc-13* loss of function did not significantly alter the expression (Figure 37 C). With regard to cholinergic signaling, reducing acetylcholine by loss of function of choline O-acetyltransferase (*cha-1*) as well as increasing acetylcholine by adding 100 μM of the acetylcholinesterase inhibitor Aldicarb, decreased HSP-12.6 levels (Figure 37 D, E). However, addition of 100 μM of the nicotinic receptor agonist Levamisole did not result in any change of the levels of HSP-12.6 (Figure 37 F).

By continuing the search for relevant neurotransmitters, I discovered that both supplementation of 10 μM of octopamine and loss of function of tyramine β-hydroxylase (*tbh-1*) responsible for octopamine synthesis from tyramine, increase the expression of HSP-12.6 in the wild type while inducing only a marginal increase in *aptf-1* loss of function background (Figure 38 A, B). Supplementation of 10 μM of tyramine and loss of function of tyrosine decarboxylase (*tdc-1*) responsible for tyramine synthesis, decrease the expression of HSP-12.6 (Figure 38 C, D). Finally, while reduction of glutamate signaling does not change the levels of HSP-12.6 in the wild-type background, increase of inhibitory glutamate signaling by the addition of 1 μg/ml Ivermectin (glutamate-gated chloride channel agonist) decreases HSP-12.6 expression in the wild type but increases it in the *aptf-1* loss of function background (Figure 38 E, F). Plots for the rest of the screened conditions can be found in section 6.34.

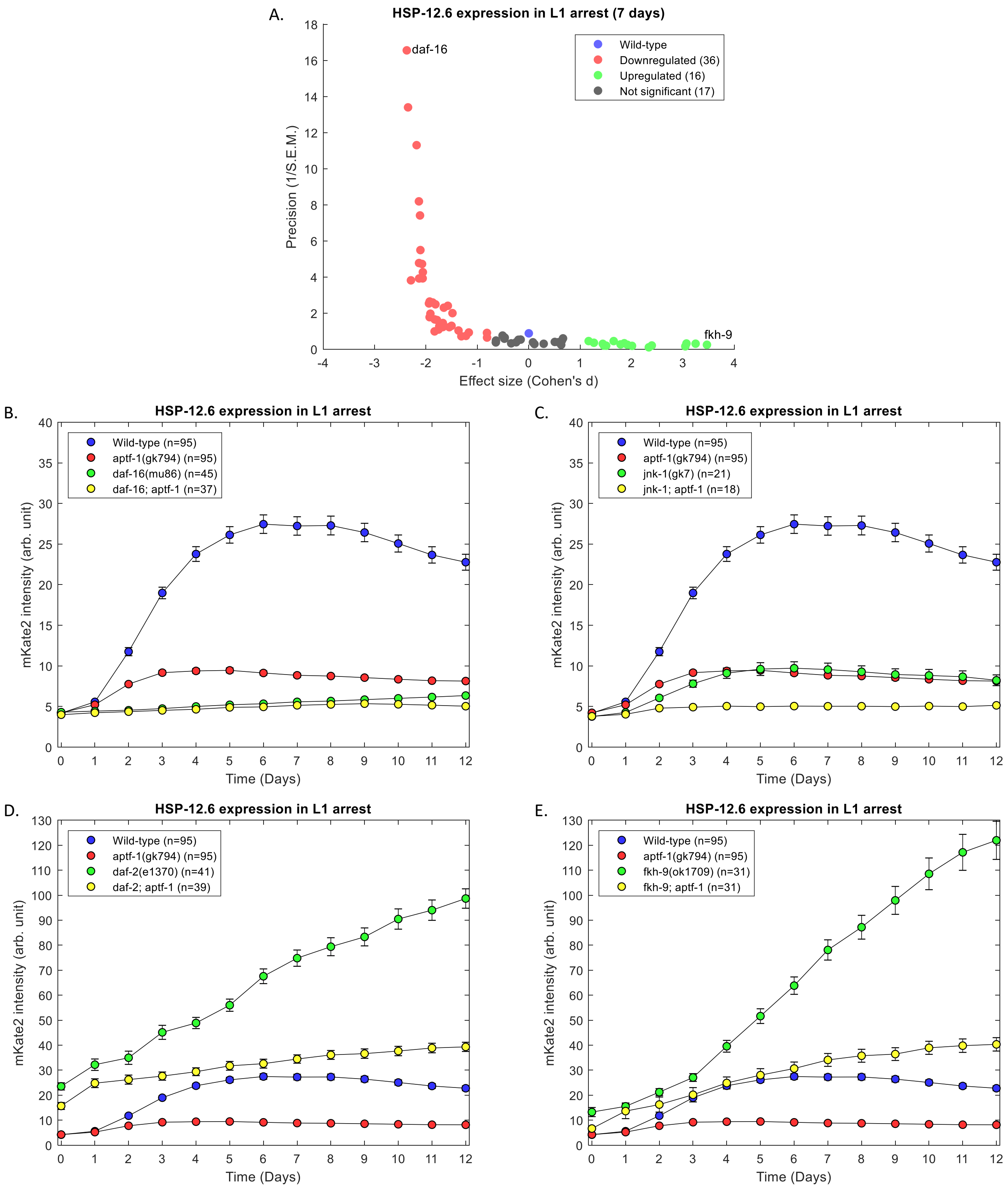


Figure 36. Regulation of HSP-12.6 by *aptf-1* depends on FOXO homolog *daf-16*
(A) HSP-12.6 expression levels, when induced by starvation, plateau at the 7-day time point in the wild-type worm. This time point was selected as representative of the total expression.
(B-E) HSP-12.6 expression over time depends on *daf-16* and the JNK pathway. It also depends on insulin signaling via *daf-2* as well as *fkh-9*, which both rescue the aptf-1 phenotype. In every case, FDR < 0.05 for all time points except day 0 and 1.

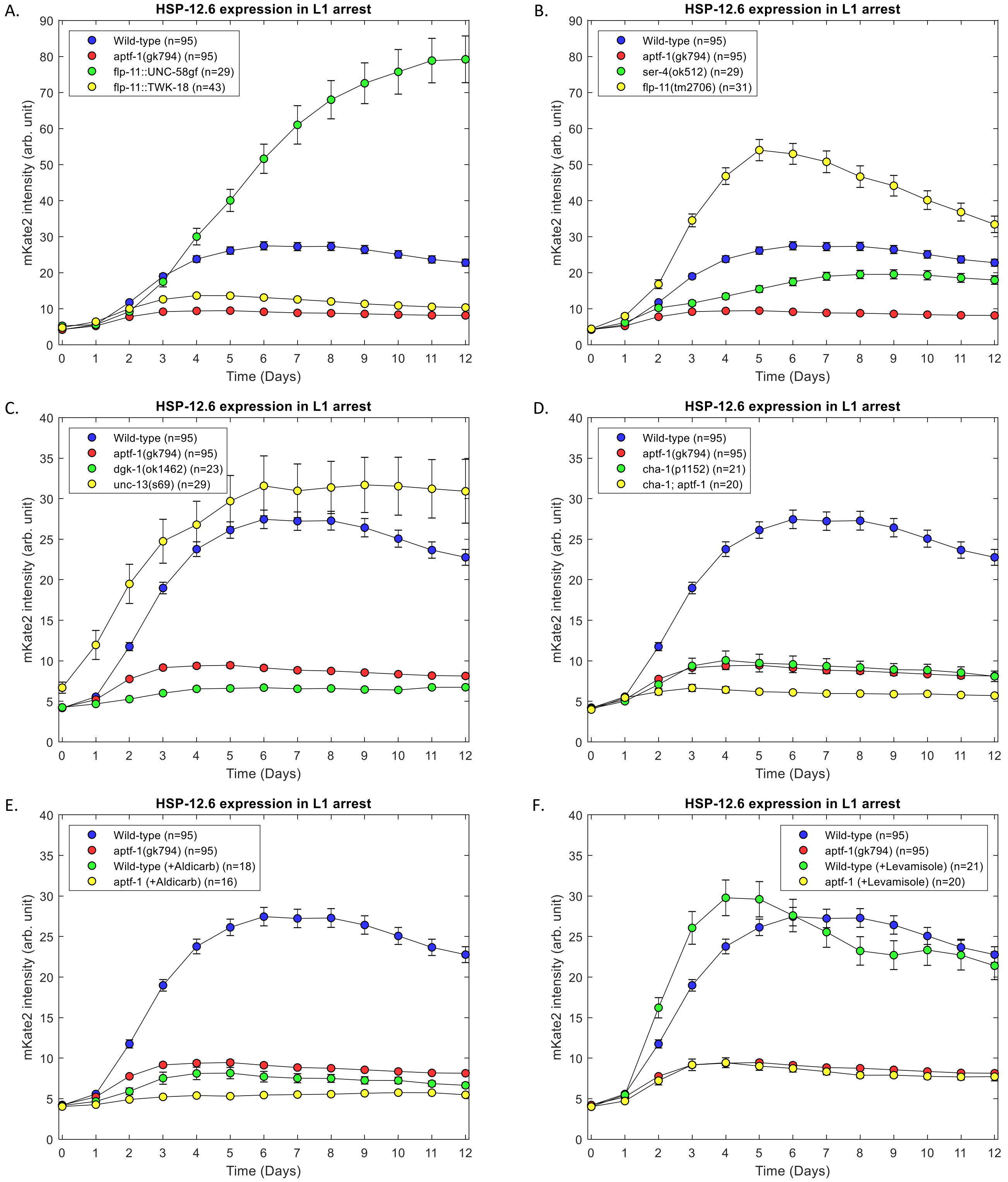


Figure 37. RIS and other neurons regulate HSP-12.6 expression in the muscle

(**A**) Constant RIS de- and hyper- polarization, increase and decrease HSP-12.6 levels respectively.

(**B**) Loss of function of *flp-11* increases HSP-12.6 expression, while loss of function of *ser-4* leads to decrease.

(**C**) Increase in synaptic transmission via *dgk-1* loss of function decreases HSP-12.6 expression.

(**D-F**) Decrease and increase in cholinergic signaling both lead to reduced HSP-12.6 levels. Treatment with Levamisole does not change the expression.

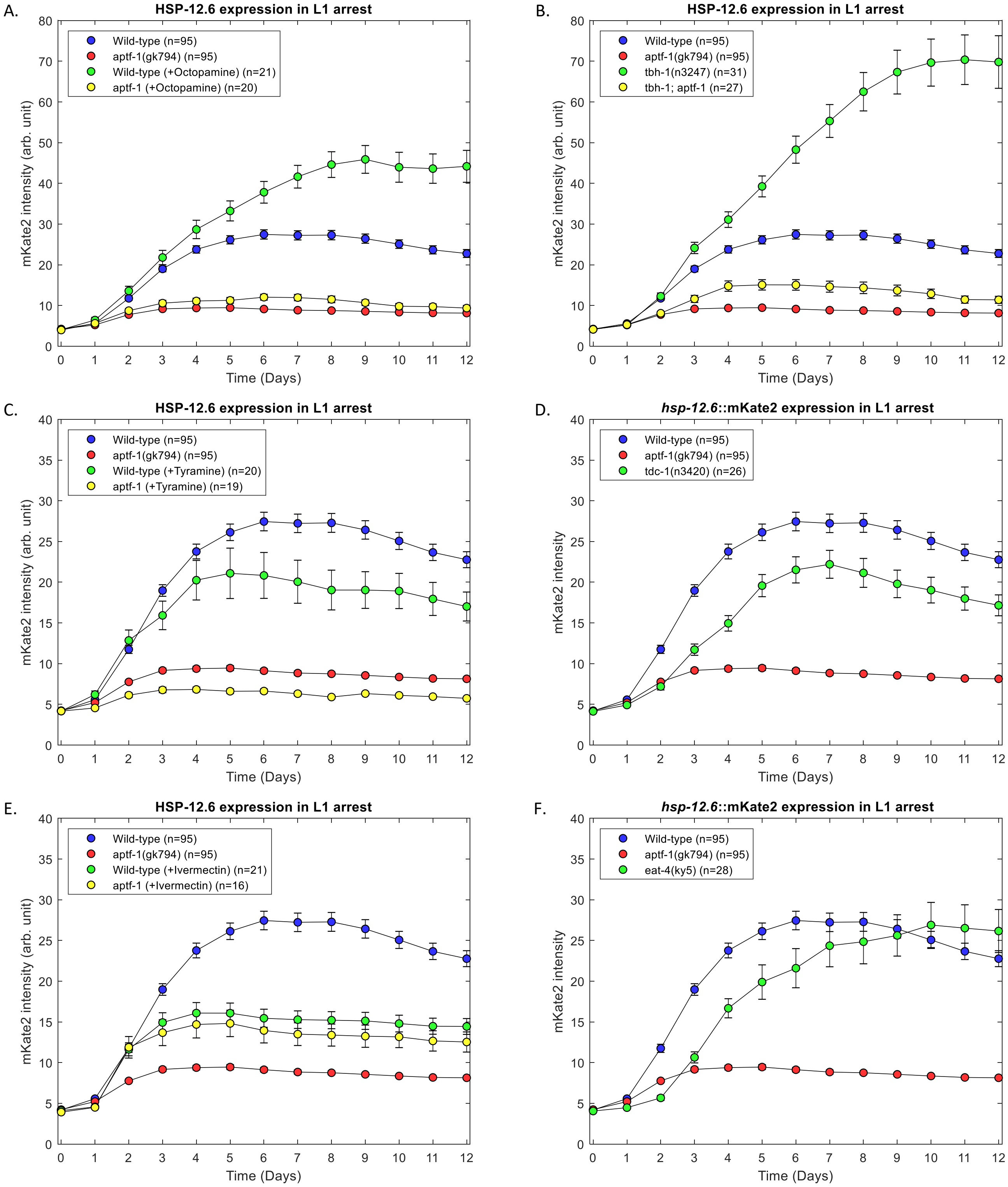


Figure 38. Octopamine, Tyramine and Glutamate affect HSP-12.6 expression
(A-B) Both loss and supplementation of Octopamine, increase the expression of HSP-12.6
(C-D) Both loss and supplementation of Tyramine decrease the expression of HSP-12.6
(E-F) Loss of glutamate vesicle transporter eat-4 does not change the expression of HSP-12.6 in the wild-type background. Glutamate receptor activation by Ivermectin results in reduced HSP-12.6 expression in the wild-type, but increased expression in *aptf-1*(gk794).

4.8. The endoplasmic reticulum unfolded protein response and the hypoxia response regulate HSP-12.6 expression in L1 arrest via *aptf-1*

The connection of the transcription factor XBP-1 and sleep in L1 arrest that I established above, can be further extended by assessing HSP-12.6 expression in the *xbp-1* loss of function condition. Indeed, the expression is decreased in the wild-type, while there is no difference in the *aptf-1* loss of function background. This suggests that *xbp-1* acts in the same pathway as *aptf-1*. However, there is no rescue of the aptf-1 phenotype, as was the case for the quiescence assessment (Figure 39 A). Loss of function of *egl-9* which codes for a negative regulator of the hypoxia-inducible factor HIF-1 [82], greatly increases HSP-12.6 expression in the wild-type but in the *aptf-1* loss of function mutant there is only a small increase of ambiguous biological relevance. This suggests that EGL-9 and APTF-1 act on the same pathway. *egl-9* expression in enriched in RIS compared to all other neurons ($\log_2(FC) = 1.28$ and $FDR = 0.0061$), as well as when compared to all other cells ($\log_2(FC) = 2.66$ and $FDR = 2.27 \times 10^{-12}$) according to the dataset published by Cao et al. [54]. These results taken together with the low-quiescence phenotype of the *egl-9* loss of function mutant that I discovered in the genetic screening discussed above, outline the interconnection of the hypoxia response and the starvation-induced quiescence in L1 arrest (Figure 39 B).

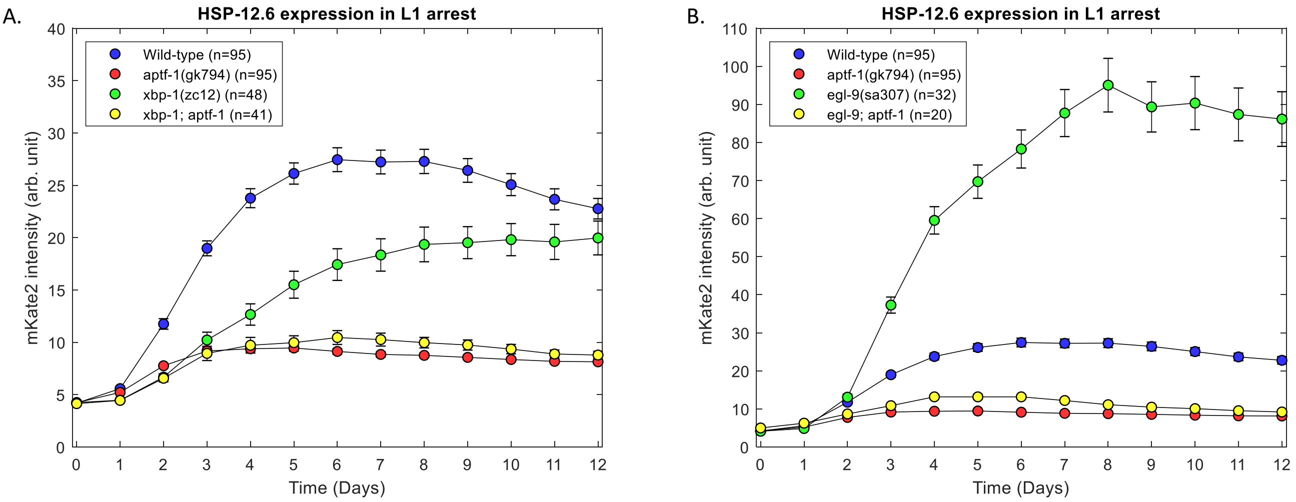


Figure 39. *xbp-1* and *egl-9* regulate HSP-12.6 expression via *aptf-1*
(A) *xbp-1*(zc12) reduces the expression of HSP-12.6 in the wild-type (FDR < 0.001 for all time points except days 0 and 1) but not in the *aptf-1*(gk794) (FDR > 0.05 for all time points).
(B) *egl-9*(sa307) greatly increases HSP-12.6 expression in the wild type and to a much lesser extent in the *aptf-1*(gk794) (FDR < 0.05 for all time points except days 0 and 1).

4.9. Heat-shock induces the expression of HSP-12.6 regardless of *aptf-1*

HSP-12.6 belongs to the family of small heat-shock proteins. Heat-shock has been shown to induce quiescence in a RIS-dependent manner, but it is the ALA neuron that conveys the protective – longevity-increasing effect. This “protective sleep” effect comes from the activation of EGF receptors that are present in both neurons [26]. Exposing L1 arrested worms to continuous heat-shock (32 °C), I discovered that the expression does not depend on *aptf-1*. The fact that even in the *aptf-1* loss of function background, expression can be induced normally is indicative of the different nature of the heat-shock and the L1 starvation responses. However, ALA ablation by loss of function of *ceh-14* does not affect the expression of HSP-12.6 during starvation in L1 arrest. This might indicate that the “protective role” that is played by ALA during heat stress of the adult worm, is played by RIS in the L1 arrest condition. Finally, gain of function of the EGF receptor homolog (*let-23*) increases HSP-12.6 expression only after 7 days of starvation (Figure 40).

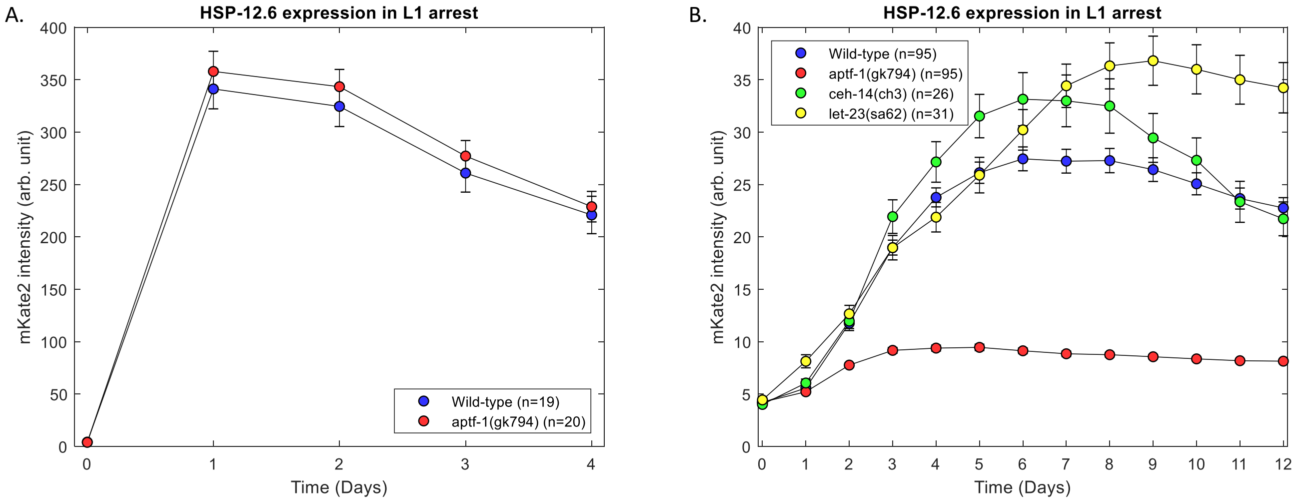


Figure 40. *aptf-1* loss of function does not affect HSP-12.6 expression during heat-shock
(**A**) Baseline measurements were taken right after hatching at 20 °C. The worms were then incubated at 32 °C for 4 days. At day 3 animals started dying. By day 5 (not shown here) every animal was dead. There is no significant difference in expression between wild type and *aptf-1*(gk794) (FDR > 0.05 for every time point).
(**B**) Genetic ablation of ALA (*ceh-14*(ch3)), does not change HSP-12.6 expression in L1 arrest (FDR > 0.05 for all time points). Gain of function of EGF receptor (*let-23*(sa62)) induces a belated increase of HSP-12.6 after 7 days (FDR < 0.01 from days 7 to 12).

4.10. *xbp-1* partially rescues the survival of *aptf-1* loss of function in L1 arrest

In this study, I have used 3 different types of lifespan assays: agarose microchambers, 96-well plates with agarose and M9 and rotating Eppendorf tubes with M9. There is an assay-related variance in the results, where new phenotypes may emerge. This is the case for the *aptf-1* loss of function mutant, which reproducibly shows no difference in longevity from the wild-type in the microchamber and 96-well plate assays, but shows a great reduction in the rotator assay. This is why I tried to find a condition, a genetic mutation, that rescues this phenotype. Plotting the time point of 50% survival in wild-type and aptf-1 backgrounds, has led to some potential candidates (Figure 41 A).

The obvious candidate was the *daf-2* loss of function mutant, which has been shown to increase longevity [63]. Indeed, this mutation was able to rescue the *aptf-1* loss of function phenotype, but the difference between the wild-type and *aptf-1*(gk794) was the same in the control and the *daf-2*(e1370) background. In this case the rescue comes from a pathway parallel to *aptf-1* (Figure 41 B). With regard to *daf-16* and *jkk-1* loss of function, there seems to be an epistatic relationship with *aptf-1* loss of function that leads to an even greater decrease in lifespan (Figure 41 C, D). Other candidates tested such as *hsf-1*, *nprl-3*, *crh-1* and *rheb-1* loss of function, did not significantly change the lifespan. However, *jmjd-3.1* loss of function did show a small rescue of the aptf-1 loss of function phenotype (Figure 41 F). *jmjd-3.1* is a conserved histone demethylase that regulates lifespan by activating the mitochondrial unfolded protein response [83]. My colleague, Dr. Yin Wu, found that loss of function in genes of the mitochondrial respiratory chain (*isp-1* and *nuo-6*) also rescue the *aptf-1* loss of function phenotype (these results are documented in her Ph.D. thesis titled “Mechanisms underlying the functions of sleep in aging during starvation in *Caenorhabditis elegans*”). These findings taken together show that disruption of important mitochondrial processes, such as the mitochondrial unfolded protein response and the respiratory chain, partially rescue the reduction in longevity of *aptf-1* loss of function. Finally, *xbp-1* loss of function is able to rescue the phenotype as well, although *xbp-1* in the wild-type background shows even more reduced lifespan than the *aptf-1* loss of function (Figure 41 E).

Survival plots for the rest of the conditions screened, can be found in section 6.35.

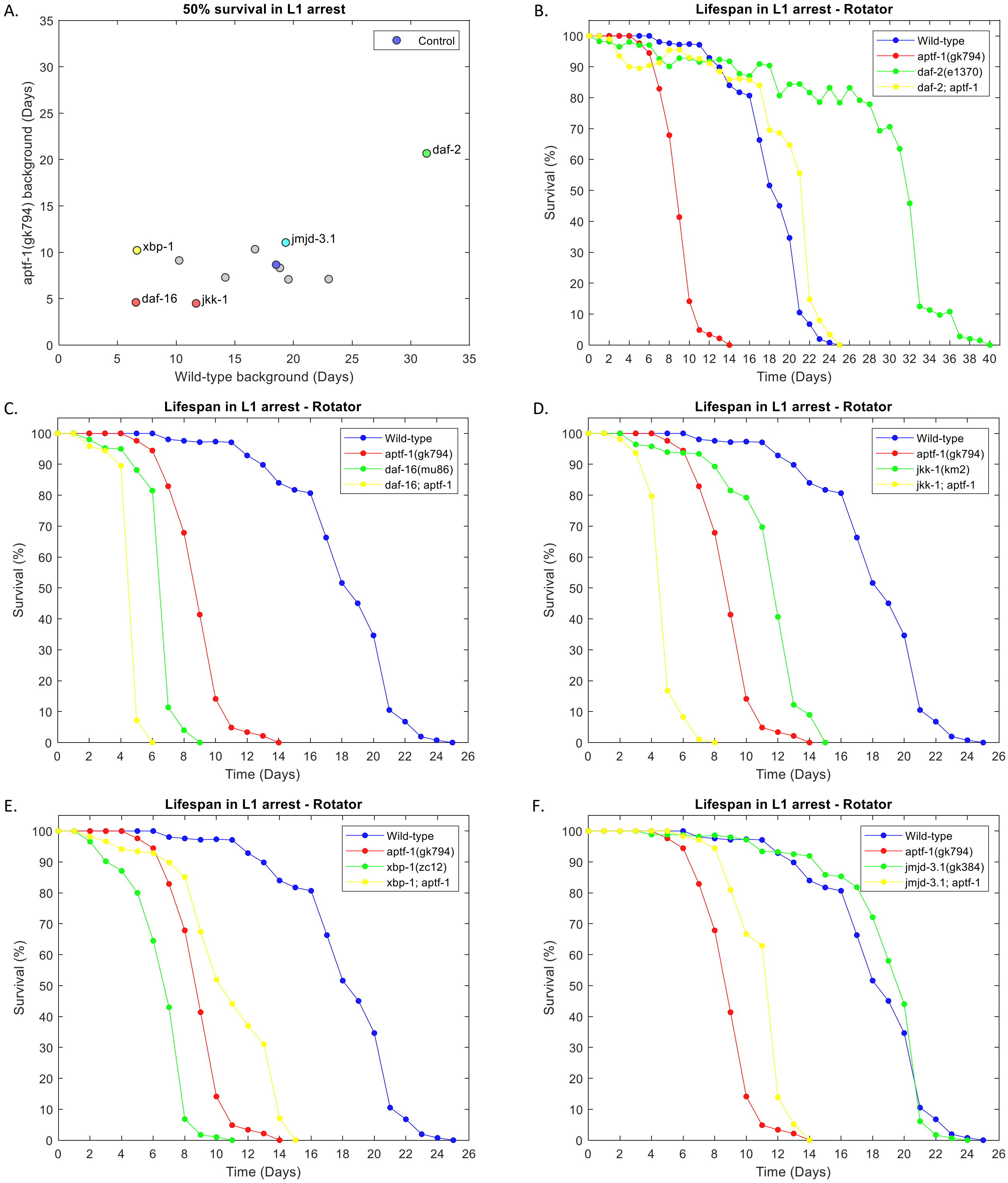


Figure 41. *xbp-1* and *jmjd-3.1* loss of function, partially rescue the reduced lifespan of aptf-1 loss of function during L1 arrest

(**A**) L1 arrest survival represented by the day that half the population has died. Conditions with at least 25% deviation from the control, were considered biologically significant.

(**B-F**) For the loss of function of *daf-16*, *jkk-1*, *daf-2* and *xbp-1*, the differences in survival depicted are statistically significant, both in the wild-type and the *aptf-1*(gk794) mutant (FDR < 0.05 for all days with Survival < 90%). For *jmjd-3.1* loss of function there is a significant difference only in the aptf-1(gk794) condition from day 7 to day 12 (FDR < 0.05).

4.11. RIS de-polarization via mechanical stimulation increases HSP-12.6 expression and lifespan, contrary to optogenetic hyper-polarization of RIS

In order to strengthen my argument that RIS controls HSP-12.6 expression, I induced sleep-loss by using the OptoGenBox for long-term optogenetic manipulation of RIS [49]. At first, I optogenetically inactivated RIS by expressing an Archaerhodopsin (ArchT) with the RIS-specific *flp-11* promoter. This resulted in decreased HSP-12.6 expression on days 2 and 3 of L1 arrest (Figure 42 A). Then, I selectively activated the nociceptive sensory neuron ASH, by expressing a red-shifted Channelrhodopsin (ReaChR) with the *sra-6* promoter, which has been shown to inactivate RIS via RIM [28]. In this case HSP-12.6 expression was also reduced on days 2 and 3 of L1 arrest (Figure 42 B). Finally, I activated the mechanosensory neurons by expressing ReaChR with the *mec-4* promoter which is expressed in the body wall touch receptor neurons ALM, AVM, PLM and PVM, as well as the nose tip FLP neurons [84]. Their activation has been shown to cause RIS inactivation, probably via engagement of the PVC neuron [24]. However, this resulted in increase of HSP-12.6 expression on days 2, 3 and 4 of L1 arrest (Figure 42 C). Although ASH and the rest of the mechanosensory neurons are glutamatergic, the difference in the results may come from the fact that they engage different neurons pre-synaptic to RIS.

To complement these experiments, I sleep-deprived the worms by applying a noxious mechanical stimulus continuously over their lifetime. In this case, sleep-deprivation has been shown to be a result of RIS de-polarization via PVC activation [28]. This led to an increase in the expression of HSP-12.6 only in the wild-type background, while there was no difference in the *aptf-1* loss of function (Figure 43 A). Similarly, lifespan was extended only in the wild-type background after mechanical stimulation (Figure 43 B). This is indicative of the importance of a functioning RIS neuron for protein expression and lifespan in L1 arrest. However, I was not able to get similar phenotypes from the unfolded protein response markers (*hsp-4* downstream of *xbp-1* in the endoplasmic reticulum and *hsp-6* downstream of *jmjd-3.1* in the mitochondria). This might be because these 2 genes are heat-inducible genes that are not directly controlled by sleep (Figure 43 C, D).

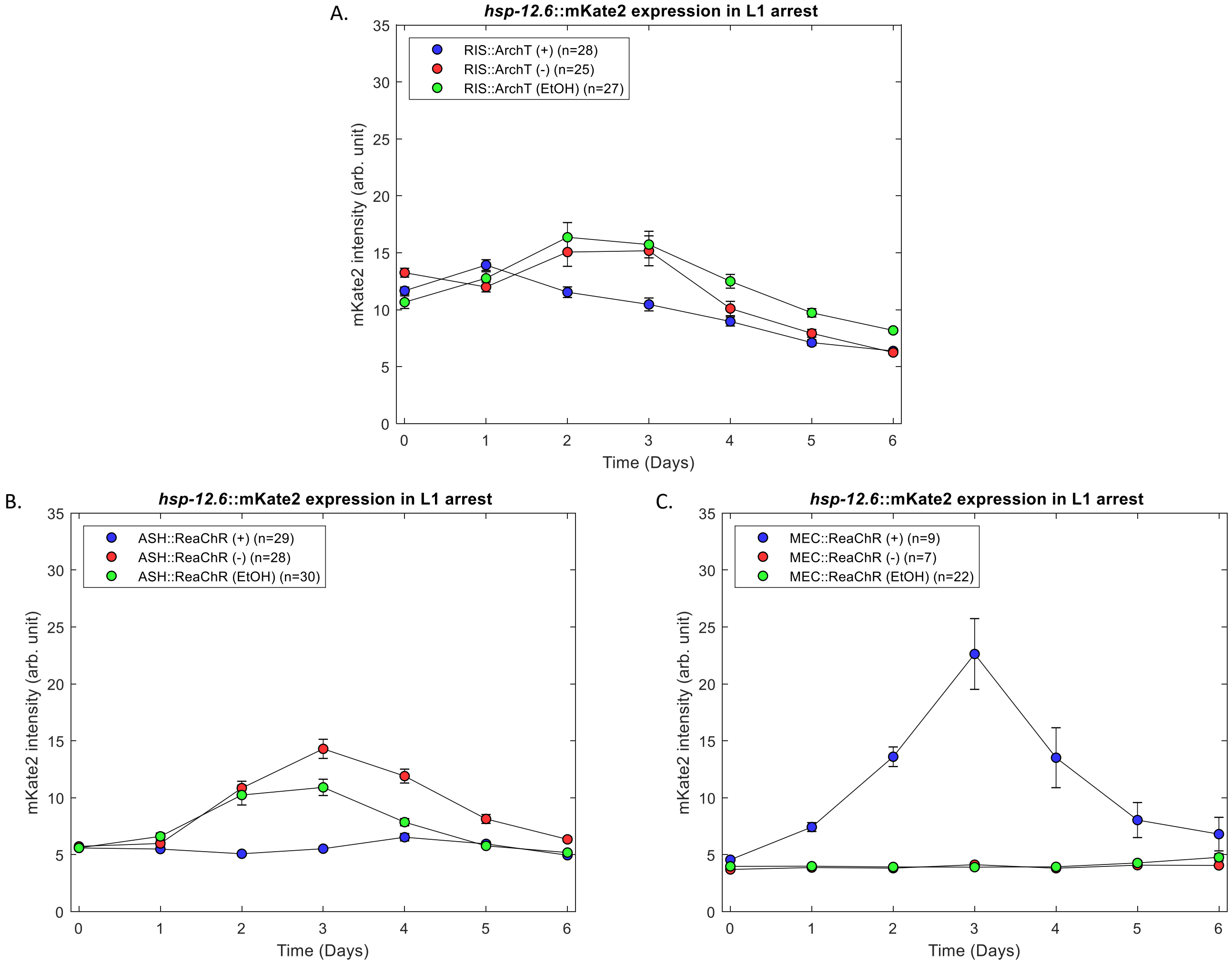


Figure 42. Optogenetic inactivation of RIS reduces HSP-12.6 expression

(**A**) Continuous RIS hyper-polarization of RIS results in reduced HSP-12.6 expression on days 2 and 3 (FDR < 0.05).

(**B**) Continuous ASH de-polarization results in reduced HSP-12.6 expression on days 2 and 3 (FDR < 0.05).

(**C**) Continuous mechanosensory neuron de-polarization results in increased HSP-12.6 expression on days 2,3 and 4 (FDR < 0.05).

In all cases samples have been treated as follows: (+) = Retinal, (-) = Water, (EtOH) = Ethanol

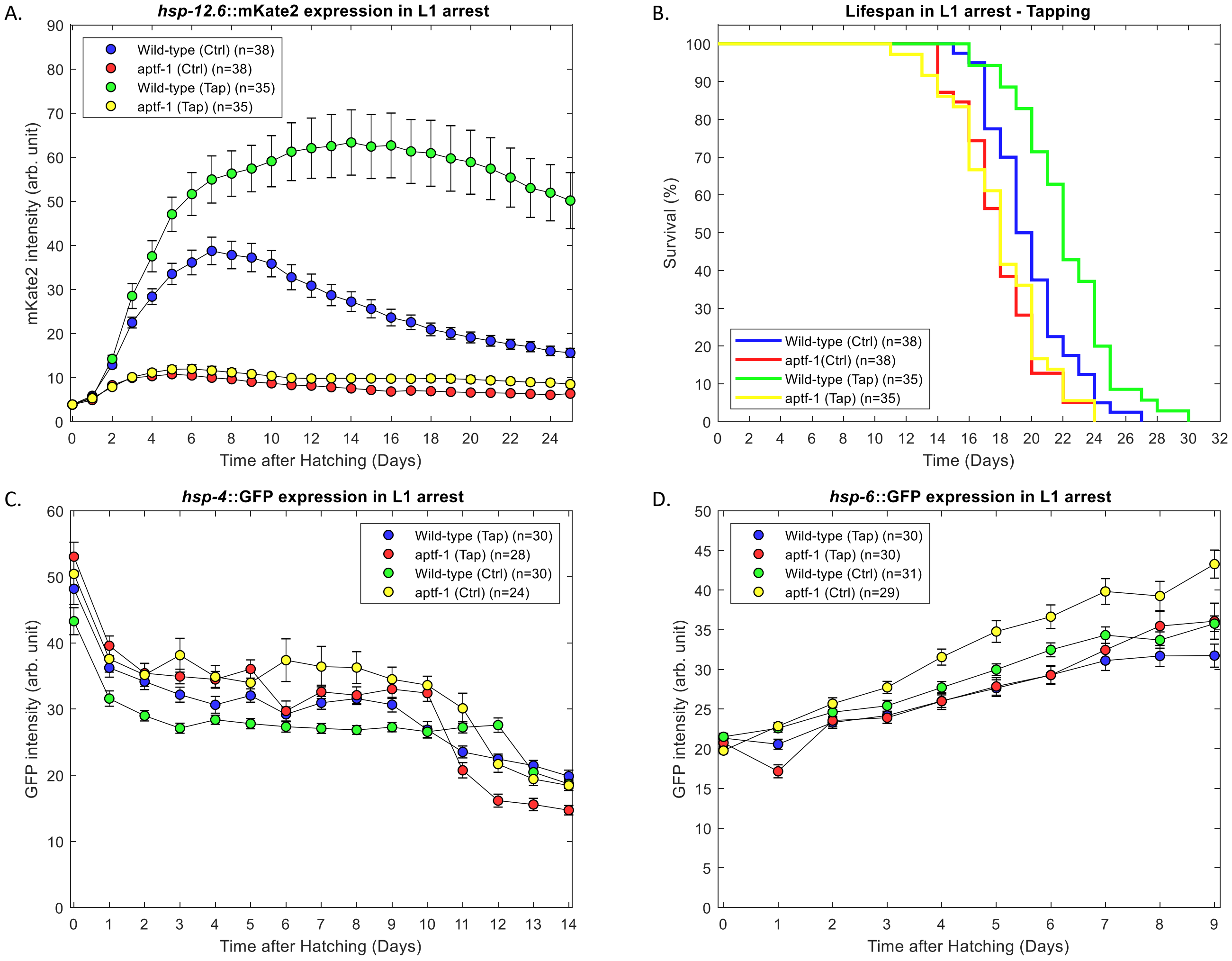


Figure 43. Mechanical stimulation increases HSP-12.6 expression and lifespan in an RIS-dependent way

(**A**) Sleep deprivation by mechanical stimulation increases HSP-12.6 expression in the wild-type (FDR < 0.01 from day 4 to day 24) but not in the *aptf-1*(gk794) background. The small increase in the expression of aptf-1(gk794) when it is mechanically stimulated does not correspond to HSP-12.6 expression, but rather comes from stress-induced intestinal vesicles.

(**B**) The lifespan of mechanically stimulated wild-type worms is significantly increased (FDR = 0.0028), in the *aptf-1*(gk794) background it is unchanged (FDR = 0.8151).

(**C**) *hsp-4* expression is upregulated in *aptf-1*(gk794) (FDR < 0.05 from day 2 to day 10). Mechanical stimulation eliminates that difference by upregulating the wild-type condition.

(**D**) hsp-6 expression is upregulated in the aptf-1(gk794) (FDR < 0.05 from day 4 to day 9). Mechanical stimulation does not affect the wild-type (FDR > 0.05 for every time point) but rather decreases the expression of *aptf-1*(gk794) to wild-type levels.

5. Discussion and perspectives

Sleep in *C. elegans* is traditionally connected to development [23]. Studying sleep in the L1 arrested state, uncouples it from worm development and provides the ground for discovery of those components that found their way to higher organisms through evolution. However, when this project started in late 2016, L1 arrest was only characterized as a state of developmental arrest in which quiescent behavior could be observed [31,85]. In 2018, Wu et al. showed that this quiescent behavior did in fact fulfill all the criteria to be characterized as sleep. This sleep state is controlled by the sleep-active neuron RIS, in a manner that involves the energy sensor AMPK and the FOXO homolog *daf-16*. Loss of sleep in L1 arrest results in shorter lifespan [24]. The work presented here aims to build on these observations and expand our understanding of sleep by utilizing omics approaches and other complementary assays.

5.1. Sleep loss induces global metabolic changes in *C. elegans*

5.1.1. Dysregulation of the starvation response

Sleep has been associated with metabolism in various instances. Changes in animal dietary habits, be it fasting or an eating disorder, impact the quality of sleep by affecting sleep architecture and melatonin levels [86,87,88,89]. When *C. elegans* hatches in the presence of food, L1 wild-type animals execute a developmental program that allows them to grow to adulthood, as long as there is an available nutrient source. If they hatch in a food-deprived environment, they enter L1 arrest and employ a series of metabolic changes to survive the fasting conditions. These manifest as changes (up- and down- regulation) in gene and protein expression and constitute the starvation response. In this thesis, I present evidence that lack of sleep hinders the proper execution of the starvation response. I have used the *aptf-1* loss of function and the RIS-ablated *flp-11*::EGL-1 strains that show significantly reduced sleep fraction in L1 arrest to get a transcriptomic and proteomic profile of the starvation response. In both cases, the starvation response is compromised. In fact, a reversal of gene and protein expression takes place. Components that are normally upregulated in the wild type are downregulated in the sleepless animals and vice versa. This is the first piece of evidence towards my aim to understand how sleep affects metabolism.

5.1.2. Increase of the basal metabolic rate

In any biological system, heat production is a measure of energy metabolism [90]. Sleep is characterized by an estimated 15% reduction in metabolic rate [91]. In order to discover differences in metabolism among the wild type and the 2 sleepless strains, I assessed their heat production over time by isothermal microcalorimetry. Indeed, sleeping worms produced less heat than the sleepless ones. After correcting for the amount of heat produced from movement during swimming (active metabolic rate) [92], there is a 20% heat production that corresponds to the increased basal metabolic rate of sleepless animals. This calculation is consistent with the 15% reported in the literature.

5.1.3. Increase in egg laying during adult starvation

Sleep loss during pregnancy, has been shown to affect both the mother and the offspring, causing structural and metabolic changes [93,94,95]. Although in adult *C. elegans* the amount of sleep depends on food intake [24], genetic ablation of sleep might interfere with offspring production. In well-fed animals the number of eggs laid, is invariant to sleep status. However, in starved adults the egg-laying capacity increases in sleep-deprived worms. The role of sleep loss during adult starvation, can be interpreted either as misallocation of continuously diminishing resources or as the last resort of a desperate animal to pass on its genes. Further experiments in this direction should assess egg viability as well as the percentage of hatched larvae that become fertile adults.

5.1.4. Decrease in body size

In the animal kingdom, poor sleep habits correlate negatively with development [96]. C. elegans size is regulated by the TGF-β pathway in the hypodermis [58]. Considering the limited resources available to an L1-arrested worm, it was logical to ask whether there would be a developmental defect in sleepless animals. This was actually the case for the *aptf-1* loss of function strain, which shows a 5% reduction in body size compared to the wild type, starting from the time point of hatching. Since APTF-1 expression is highest during late embryogenesis [27], reduction of body size could be a developmental and not a sleep-related defect. Maternal defects in resource allocation in the *aptf-1* loss of function strain, could lead to the creation of egg yolks with lower nutritional value, that in turn impact size. Finally, it could also be the result of embryonic sleep ablation, although this would be very difficult to assess with mobility criteria.

5.1.5. Increase in sleep-inducing metabolites

In order to acquire an overview of the metabolic status of the sleepless worms, I performed a metabolome analysis at 48 hours and 6 days of starvation. In the *aptf-1* loss of function strain, Tryptophan is upregulated at 48 hours, in accordance with the sleep deprivation literature for humans [36]. Tryptophan is an essential amino acid that can be metabolized to Serotonin, which in turn can be metabolized to Melatonin. All of these components have known roles in sleep induction and maintenance [97]. However, Serotonin was unchanged, and Melatonin was not detected in the metabolome analysis. Tryptophan can instead be converted into the neuroactive metabolite Kynurenic acid, which antagonizes the excitatory glutamatergic neurotransmission in the central nervous system. Sleep deprivation has been shown to increase the levels of Kynurenic acid in the hypothalamus and hippocampus of rat brains [98]. In *C. elegans,* Kynurenic acid is produced in the RIM neuron and is regulated by insulin signaling to control aspects of aging [76]. After 6 days of starvation, levels of Kynurenic acid increase. Taken together, these results show that the sleepless *aptf-1* loss of function strain tries to induce sleep by upregulating somnogenic components and reducing excitatory neurotransmission. Ultimately this fails, probably because the sleep-inducing signal eventually has to go through RIS, which is not functional due to the *aptf-1* loss of function.

5.1.6. Increase of oxidative stress and decrease of life-prolonging antioxidant factors

Recent research has shown that sleep deprivation in rats and *Drosophila*, causes accumulation of ROS in the gut, which kills the organism prematurely and is reversed by administration of antioxidants [99]. Metabolomic analysis of the *aptf-1* loss of function strain, shows that there is upregulation of Allantoin and Glutathione (but not Oxidized glutathione which remains unchanged) at the 48-hour time point. Allantoin can only be produced as a result of oxidative stress in *C. elegans* [75]. Glutathione is a free radical scavenger and the ratio of Glutathione/Oxidized glutathione is under strict homeostatic control [100]. This suggests that sleepless worms are under severe oxidative stress. Also, AMP is upregulated, which increases the AMP/ATP ratio. This puts the whole organism in an energy deficit state and in turn activates the AMPK, which engages the catabolism of fatty acids via beta oxidation to produce more energy [101]. This process happens in the mitochondria and results in production of ROS [102]. However, transcription of antioxidant genes such as *sod-3* is downregulated. This might explain the significantly reduced lifespan of the *aptf-1* loss of function strain in L1 arrest. Moreover, transcriptome analysis indicates that mitochondria are not functioning properly, because of extreme downregulation of the associated genes, especially those that are involved in energy production by oxidative phosphorylation. The link between fatty acid beta oxidation and oxidative phosphorylation is the TCA cycle, which is allosterically regulated by its metabolites. Upregulation of Succinic acid, which lies on the interface of the TCA cycle and complex III of the electron transport chain, may indicate the critical point of imbalance between energy and ROS production. Considering that AMPK activation can activate RIS [24], we end up with a strong link of energy status, sleep and longevity.

5.1.7. Increase of the unfolded protein response and dysregulation of proteostasis

Sleep can be separated in two distinct components. The first one is the circadian component, in which light availability regulates the levels of melatonin to induce sleep and wakefulness [14,15]. In C. elegans, there is no circadian regulation of sleep in the same way it is for other animals, but it has been shown that lethargus intervals correlate with expression of PERIOD homolog *lin-42* [103]. The second is the homeostatic component, in which cellular needs dictate molecule anabolism and catabolism. Protein metabolism is dynamically regulated at the levels of translation, folding, modification, localization and degradation, a process termed proteostasis. At the heart of proteostasis lies the unfolded protein response (UPR). UPR activation upregulates the expression of chaperone proteins e.g. BiP (homologous to *C. elegans hsp-4*), downregulates translation and increases the degradation of misfolded proteins. Sleep deprivation activates the UPR, while it has been shown that, in *Drosophila*, recovery sleep reduces BiP levels [104].

My results indicate that in the *aptf-1* loss of function strain, there is downregulation of ribosomal components at the transcript level, while in the meantime the essential amino acid and translation initiation component Methionine is also downregulated. Additionally, thiolation of Glutamine-tRNA wobble U_{34} is increased, decreasing the rate of translation of glutamine-rich proteins [73]. These findings consent to protein regulation at the level of translation, consistent with downregulation due to activated UPR.

Moreover, I observed increased expression of the BiP homolog *hsp-4* at the transcript level in the RNA-seq and in the transgenic assay experiments in the *aptf-1* loss of function strain. Mechanical stimulation of the worm leads to activation of RIS [28], which upregulates BiP in the wild type, but not in the *aptf-1* loss of function. This result not only agrees with the Drosophila literature [104], but indicates that RIS activity rather than sleep is responsible for the proper execution of the UPR. Furthermore, loss of function of the UPR-regulating transcription factor XBP1 (C. elegans homolog *xbp-1*), partially rescues the behavioral quiescence and survival of the *aptf-1* loss of function strain. Perhaps in this case, the downregulation of UPR offers temporary relief to the sleepless strain, mimicking the UPR downregulation of recovery sleep, which results in short-term survival rescue that cannot be maintained due to prolonged starvation.

In order to acquire a complete image of proteostasis, protein modifications, translocation and degradation need to be investigated further. Although glutathionylation is a well-known modification and the increased Glutathione observed in the *aptf-1* loss of function strain could affect protein homeostasis, it is not enough by itself to make safe conclusions.

5.2. Changes in metabolism result in changes in sleep

There is a two-way relationship between sleep and metabolism [86,87,88,89] and I have already shown that impaired sleep alters the starvation response. In order to establish this connection in *C. elegans,* I performed an extensive genetic screening of strains with metabolic defects. Knock-down of components of the sphingolipid metabolism pathway lead to reduced sleep in L1 arrest. Sphingolipids are a class of metabolites that are massively downregulated in the *aptf-1* loss of function strain. Since sphingolipids can have both structural and signaling biological roles, further experiments need to be made in that direction. Ceramide, which is at the center of sphingolipid metabolism, plays a role apoptosis [105]. Loss of function of *ced-3,* a homolog of mammalian caspases, results in decreased sleep. Its role needs to be addressed in the context of RIS activation. Furthermore, I showed that loss of function of the C. elegans homolog of DKGθ, *dgk-1,* results in almost complete loss of sleep and changes RIS physiology. DGKθ is a neuronal diacylglycerol kinase that is part of sphingolipid metabolism and synaptic vesicle trafficking by regulating DAG phosphorylation [78,106]. Finally, apart from the role of sphingolipids, the hypoxia response should be addressed in the context of sleep and RIS function since, loss of function of components in this pathway leads to reduced quiescence.

5.3. Sleep loss induces RIS-dependent tissue-wide changes

The case of the sleepless *flp-11*::EGL-1 strain is a peculiar one. This strain was originally created to induce apoptosis specifically in RIS. In the beginning it has been behaving as expected with decreased quiescence and lifespan. After it has been through some generations, the strain lost its survival phenotype. RIS was still visible and calcium imaging could not produce results. Since apoptosis is a process that involves calcium influx, we hypothesized that this strain is instead RIS-hyperactive and potentially upregulates the secretion of a neurotransmitter that is beneficial for survival, uncoupling it from sleep (personal communication with Prof. Henrik Bringmann). My datasets advocate for this hypothesis, since its body size is wild-type and its gene expression profile is very distinct both from the wild type and the *aptf-1* loss of function strains. Our interest in studying the benefits of sleep separate from sleep behavior, led to the creation of the *flp-11*::UNC-58(gf) strain which was engineered to have a constantly active RIS neuron.

With regard to specific tissues both *aptf-1* loss of function and *flp-11*::EGL-1 upregulate hypodermis-specific genes and downregulate intestine-specific genes. Muscle-specific genes are downregulated only in the RIS-hyperactive strain. Germline-specific genes and Notch signaling are downregulated in the *aptf-1* loss of function strain, while they are upregulated in *flp-11*::EGL-1. Contrary to that, neuronal-specific gene expression is upregulated in the *aptf-1* loss of function strain and downregulated in the RIS-hyperactive strain. While this is a very useful summary of RIS-dependent tissue-wide changes, research needs to focus on individual pathways. One such pathway involves the $GABA_A$ (UNC-49) and $GABA_B$ (GBB-1, GBB-2) receptors which are upregulated in the *aptf-1* loss of function strain and downregulated in the RIS-hyperactive strain. This result taken together with the downregulation of glutamate receptors and Kynurenic acid in the RIS-hyperactive strain show an impact of RIS activity on excitatory glutamatergic signaling. One interesting perspective would be to research whether RIS activity controls the GABA shunt, which connects the GABAergic and glutamatergic signaling with the TCA cycle [107]. Finally, the relevance of the tyraminergic, peptidergic and glutamatergic neuron RIM [28] should be further assessed since its activity levels are higher and tyrosine decarboxylase, *tdc-1*, loss of function enhances the reduction of the sleep phenotype in the *aptf-1* loss of function strain. Kynurenic acid production in RIM has been shown to affect lifespan [76] and RIM can both inhibit and activate RIS [28].

5.4. RIS controls the nuclear localization of FOXO homolog *daf-16*

The most important finding of this thesis is the regulation of the FOXO transcription factor homolog *daf-16* by RIS. Although RNA-seq data and reporter transgene expression experiments show that *daf-16* is upregulated in the *aptf-1* loss of function strain, this did not correlate well with the downregulation of the classic DAF-16 targets *hsp-12.6* and *sod-3*. These genes are categorized as Class I because they were found to be downregulated in *daf-16* loss of function conditions [62]. Therefore, since *daf-16* is upregulated in the *aptf-1* loss of function background, the downstream targets should also be upregulated which is not the case. For this reason, I checked DAF-16 nuclear localization and found that it was decreased in the intestine and muscles of the *aptf-1* loss of function strain. However, it is also decreased in the intestine of the RIS-hyperactive *flp-11*::UNC-58(gf) strain, which indicates that either the intestine is not the target tissue of RIS or that a normally functioning RIS is needed for proper nuclear DAF-16 translocation. This needs to be addressed further as well as the localization of DAF-16 in neurons, also because of the fact that *daf-16* loss of function and insulin receptor homolog *daf-2* loss of function produce strongly reduced and increased sleep phenotypes respectively.

Since the results of the DAF-16 localization assay are probabilistic in nature and can be subject to researcher bias, I used a fluorescent reporter fused to the endogenous locus of *hsp-12.6*, to track HSP-12.6 expression. This was used as an indirect, but more trustworthy measure of DAF-16 activity. RIS ablation (*aptf-1* loss of function and *flp-11*::TWK-18) downregulates the expression of HSP-12.6 while RIS hyperactivation upregulates its expression. Furthermore, mechanical stimulation, which was shown to activate RIS [28], increased the expression of HSP-12.6 and the lifespan in the wild type but not the *aptf-1* background, proving that RIS hyperactivation can convey benefits to the animal regardless of sleep status. The regulation of HSP-12.6 is very complicated, since I showed that it is also regulated by cholinergic, tyraminergic, octopaminergic and glutamatergic stimuli. In my ordeal to find the regulatory pathway of RIS-controlled DAF-16 nuclear localization, I discovered that all the classical pathways described in the literature [63,81], function upstream or in parallel to RIS. This means that there is a non-classical or not-identified pathway that controls DAF-16 localization downstream of RIS. As far as the current literature goes, there are only two promising candidate pathways: 1. GABA receptor signaling regulated by PKD [108] and 2. Calmodulin/CAMKII signaling [109]. These pathways might eventually converge.

6. Appendix

6.1. Strain list

Strain	Description	Strain	Description
N2	Wild-type	DA472	pha-2(ad472) X
CB1189	unc-51(e1189) V	DA521	egl-4(ad450) IV
CB189	unc-32(e189) III	DA609	npr-1(ad609) X
CB369	unc-51(e369) V	DG1867	glp-1(tn777) III.
EU552	glp-1(or178) III	DG2389	glp-1(bn18) III
FX02586	ptr-10(tm2586)	DR432	ama-1(m118) IV
FX04545	tatn-1(tm4545)	EG9631	unc-13(s69) I
FX06853	B0303.3(tm6853)	EW15	bar-1(ga80) X
FX07117	rpia-1(tm7117)	FX00841	cka-2(tm841)
GG60	glp-1(g60) III	FX00903	dat-1(tm903)
RB1950	F38A6.3(ok2564) V	FX01035	F47A4.5(tm1035)
RB2071	ced-3(ok2734) IV	FX01045	acl-10(tm1045)
RB2602	F01G10.1(ok3624) IV	FX01097	F20B4.6(tm1097)
RB789	tre-2(ok575) IV	FX01420	C34B2.7(tm1420)
VC2428	sams-1(ok2946) X	FX01472	asg-2(tm1472)
VC2520	aagr-2(ok3193) II	FX01584	ipla-3(tm1584)
VC410	elo-5(gk208) IV	FX01655	C54G7.2(tm1655)
EC106	eeEx106[hil-1::GFP + rol-6(su1006)]	FX01774	C31C9.2(tm1774)
AX1410	flp-18(db99) X	FX01778	acl-14(tm1778)
BC119	blmp-1(s71) I	FX01847	acl-13(tm1847)
BX106	fat-6(tm331) IV	FX01929	Y51H7C.9(tm1929)
BX107	fat-5(tm420) V	FX01936	cdo-1(tm1936)
BX14	elo-1(wa7) IV	FX01989	F18E3.7(tm1989)
BX153	fat-7(wa36) V	FX02028	F20H11.5(tm2028)
BX17	fat-4(wa14) IV	FX02178	T27F6.6(tm2178)
BX24	fat-1(wa9) IV	FX02311	T01C8.4(tm2311)
BX26	fat-2(wa17) IV	FX02369	C46C11.1(tm2369)
BX30	fat-3(wa22) IV	FX02390	fce-1(tm2390)
CB1111	cat-1(e1111) X	FX02598	fce-2(tm2598)
CB1112	cat-2(e1112)II	FX02680	Y46G5A.24(tm2680)
CB1370	daf-2(e1370)III	FX02689	acdh-2(tm2689)
CB156	unc-25(e156) III	FX02898	prdx-6(tm2898)
CB4876	clk-1(e2519) III	FX03142	acl-2(tm3142)
CB5602	vhl-1(ok161) X	FX03289	acl-1(tm3289)
CB6037	bus-18(e2795) V	FX03314	Y4C6B.6(tm3314)

Strain	Description	Strain	Description
CB6088	egl-9(sa307) hif-1(ia4) V	FX03340	acl-2(tm3340)
CB6090	hif-1(ia4) V; vhl-1(ok161) X	FX03349	Y4C6B.6(tm3349)
CE1255	cep-1(ep347) I	FX03396	acl-6(tm3396)
CE541	sbp-1(ep79) III	FX03424	C14E2.2(tm3424)
CE833	sbp-1(ep176) III	FX03557	mboa-4(tm3557)
CF1038	daf-16(mu86) I	FX03673	Y69A2AR.5(tm3673)
CF2218	ncl-1(e1942) III	FX03788	pyc-1(tm3788)
CF376	bar-1(mu63) X	FX03816	C33C12.3(tm3816)
CU2945	scrm-1(tm805) I	FX04172	F14B4.2(tm4172)
CW152	gas-1(fc21) X	FX04174	F14B4.2(tm4174)
CZ3391	vab-3(ju468) X	FX04284	prdx-6(tm4284)
FX04387	H12D21.7(tm4387)	HBR02118	F53H8.4(tm2613)
FX04853	acs-19(tm4853)	HBR02120	maoc-1(tm5257)
FX05123	B0365.1(tm5123)	HBR02122	dgk-1(sy428) X
FX05127	W02H5.8(tm5127)	HBR02214	metr-1(ok521) II
FX05430	R11F4.1(tm5430)	HBR02233	aptf-1(gk794); tut-1 (tm1297)
FX05491	K07B1.4(tm5491)	HBR02121	mes-2(tm5007)
FX05954	cpin-1(tm5954)	HBR02237	vha-2(ok619) III
FX06151	dhs-3(tm6151)	HBR02242	elpc-1(tm2149); aptf-1(gk794) II
FX06393	C27A7.3(tm6393)	HBR02269	flp-11(tm2706) X; tdc-1(n3420) II
FX06496	glna-1(tm6496)	HBR00227	aptf-1(gk794) II
FX06644	set-23(tm6644)	HBR02280	sms-2 (gk608906) X
FX06710	pho-5(tm6710)	HBR02286	ser-2(pk1357) X; aptf-1 (gk794) II
FX06805	set-23(tm6805)	HBR02298	sms-2(tm2757) X
FX06830	pho-5(tm6830)	HBR02312	glp-1(ar202); aptf-1 (gk794) II
FX06850	rpia-1(tm6850)	HBR02315	aptf-1(gk794) II; tdc-1(n3420) II
FX06913	C01B4.6(tm6913)	HBR02317	nlp-8(syb762) IV
FX06977	aldo-1(tm6977)	HBR02372	aptf-1(gk794) II; xbp-1(zc12) III
FX06984	C01G10.9(tm6984)	HBR02374	ztf-20(gk263563) V; aptf-1(gk794) II
FX627	lgc-11(tm627) X	SJ17	xbp-1(zc12) III; zcIs4[hsp-4::GFP] V
GC833	glp-1(ar202) III	HBR00507	flp-11(tm2706) X
GE68	glp-1(e2144) III	HS184	psa-4(os13) IV
GG14	emb-14(g14)I	HY520	pod-2(ye60) II
GG202	ace-2(g72)I	IK589	ttx-7(nj50) I
GG43	fasn-1(g43) I	JIN1375	hlh-30(tm1978) IV

Strain	Description	Strain	Description
GR1307	daf-16(mgDf50) I	JK289	glp-1(e2142) III
HBR01010	nas-38(ok3407) X	JN1071	snet-1(pe1063) X
HBR00012	goa-1(sa734) I	JT10800	ncr-2(nr2023) III; ncr-1(nr2022) X
HBR01403	daf-2(e1370); aptf-1(gk794) II	JT307	egl-9(sa307) V
HBR01493	flp-18(gk3063) X	KG2730	clu-1(ok2)
HBR01777	goeIs384 [pflp-11::egl-1::SL2-mkate2-flp-11-3'utr, unc-119(+)]	KJ550	aco-1(jh131) X
HBR2044	C23H3.4(ok1693) II	KP1097	dgk-1(nu62) X
HBR2045	F13B12.4(ok3489) IV	KP2048	ric-7(nu447) V
HBR2046	set-4(ok1481) II	KU12	dlk-1(km12) I
HBR2050	dgk-1(ok1462) X	KU2	jkk-1(km2) X
HBR2051	ckb-2(ok1922) III	LC143	pcbd-1(tm5924) I
HBR2057	R09B5.6(ok2776) V	LC144	agmo-1(e3016) III
HBR2059	ucr-2.3(ok3073) III.	LC33	bas-1(tm351) III
HBR2060	Y46G5A.19(ok3421) II	LC73	pah-1(tm520) II
HBR2076	set-4(n4600) II	LC74	pah-1(ok687) II
HBR02112	hpd-1(ok1955)	LS505	dyb-1(cx36) I
HBR02116	D1005.1(tm5122)	MH1090	cog-3(ku212) IV
HBR02117	agxt-1(tm6307)	RB1003	aco-1(ok924) X
MH1955	nhr-25(ku217) X	RB1005	R02D3.1(ok926) IV
MH5197	nprl-3(ku540) IV	RB1025	set-2(ok952) III
MQ1333	nuo-6(qm200) I	RB1029	hdl-1(ok956) IV
MQ1766	sod-2(ok1030) I; sod-5 (tm1146) sod-1(tm783) II; sod-4(gk101) III; sod-3(tm760) X	RB1031	fat-4(ok958) IV
MQ770	tpk-1(qm162) III	RB1036	hyl-1(ok976) IV
MQ989	isp-1(qm150) IV; ctb-1(qm189)	RB1046	elo-9(ok993) II
MT10549	tdc-1(n3421) II	RB1053	R05F9.10(ok1000) II
MT10661	tdc-1(n3420) II	RB1073	dgk-4(ok1031) IV
MT1083	egl-8(n488) V	RB1075	pes-9(ok1037) V
MT1216	egl-9(n586) V	RB1083	F27C8.5(ok1050) IV
MT13113	tdc-1(n3419) II	RB1118	ZK370.4(ok1107) III
MT13293	met-2(n4256) III	RB1123	Y105E8A.10(ok1130) I
MT14401	set-12(n4442) X	RB1134	Y105E8A.10(ok1157) I
MT1443	egl-10(n692) V	RB1160	ckb-4(ok1195) V
MT14480	set-11(n4488) II	RB1170	C04B4.2(ok1212) X
MT14851	set-2(n4589) III	RB1173	plc-4(ok1215) IV
MT1522	ced-3(n717) IV	RB1188	F23B12.6(ok1232) V
MT16973	met-1(n4337) I	RB1190	amx-2(ok1235) I

Strain	Description	Strain	Description
MT2257	lin-42(n1089) II	RB1203	T10B11.2(ok1252) I
MT7988	bas-1(ad446) III	RB1206	sks-1(ok1255) III
MT8347	ced-3(n2452) IV	RB1248	ckb-1(ok1312) III
MT8943	bas-1(ad446) III; cat-4(e1141) V	RB1264	elo-4(ok1346) III
MT9455	tbh-1(n3247) X	RB1274	F31C3.6(ok1365) I
NL1832	ucr-2.3(pk732) III	RB1304	wdr-5.1(ok1417) III
NM1568	ehs-1(ok146) II	RB1326	unc-129(ok1443) IV
OH149	ceh-23(ms23) III	RB1370	rabn-5(ok1555) III
OH313	ser-2(pk1357) X	RB1373	gpdh-1(ok1558) I
PD4588	ceh-24(cc539) V	RB1400	tre-3(ok394) V
PD4605	hlh-1(cc561) II	RB1404	lec-1(ok1597) II
PR1152	cha-1(p1152) IV	RB1434	mmcm-1(ok1637) III
PS1839	let-23(sa62) II	RB1482	gpdh-2 edit K11H3.1(ok1733) III
PS3551	hsf-1(sy441) I	RB1483	ifa-4(ok1734) X
PS3653	ipp-5(sy605) X	RB1484	ath-1(ok1735) I
QC122	paqr-2(tm3410) III; pcyt-1(et9) X	RB1487	asm-3(ok1744) IV
QC134	nduf-7(et19) I	RB1498	hyl-2(ok1766) X
VC1625	dylt-2(gk762) X	RB1525	E02H9.5(ok1830) III
VC1666	met-1(ok2172) I	RB1527	pnk-4(ok1832) X
VC1667	F55G7.2(ok2176) X	RB1548	F53C3.13(ok1861) II
VC1701	mif-1(gk1027) III	RB1549	klo-2(ok1862) III
VC1737	F43C11.2(gk3131) II; F13A2.3(gk3132) V; W07E11.1(gk3133)	RB1579	sptl-3(ok1927) V
VC1876	C39D10.3(ok2179) X	RB1588	mxl-3(ok1947) X
VC1896	ckb-3(ok2310) III	RB1618	hda-3(ok1991) I
VC1897	C32F10.8(tm2997) I	RB1633	mif-1(ok2009) III
VC199	sir-2.1(ok434) IV	RB1688	W05G11.6(ok2098) III
VC20014	gk246355	RB1690	ser-2(ok2103) X
VC20058	gk103693	RB1704	acp-2(ok2129) II
VC20143	gk115222	RB1710	Y39G10AR.18(ok2154) I
VC20191	gk237279	RB1715	aqp-2(ok2159) II
VC20279	gk245731	RB1721	Y71G12B.4(ok2189) I
VC20300	gk233890; gk947363	RB1737	pld-1(ok2222) II
VC20317	gk173266	RB1764	trxr-2(ok2267) III
VC20339	gk152785	RB1789	met-2(ok2307) III
VC20346	gk209511; gk246353	RB1790	D2096.3(ok2317) IV
VC20392	gk322672	RB1793	Y24D9A.2(ok2320) IV
VC20400	gk944084	RB1794	F53A2.7(ok2322) III
VC20403	gk324463	RB1795	fat-1(ok2323) IV

Strain	Description	Strain	Description
VC20453	gk161469	RB1796	set-21(ok2327) IV
VC20461	gk284720	RB1810	cpr-5(ok2344) V
VC20478	gk169410	RB1826	T26A5.5(ok2364) III
VC20488	gk133451	RB1828	dgk-5(ok2366) II
VC20504	gk329791	RB1843	lin-42(ok2385) II
VC20536	gk255075	RB1854	sms-1(ok2399) IV
VC20540	gk173675	RB1899	acs-2(ok2457) V
VC20545	gk293929	RB1919	W07E6.3(ok2498) II
VC20552	gk278589	RB1930	spr-3(ok2525) X
VC20560	gk267976	RB1932	ZK418.8(ok2535) III
VC20570	gk109644	RB1942	ace-2(ok2545) I
VC20602	gk350360	RB1954	csp-1(ok2570) II
VC20603	gk350699	RB1974	smd-1(ok2602) I
VC20624	gk360120	RB1997	mtr-4(ok2642) IV
VC20646	gk368637	RB2028	set-12(ok2686) X
VC20659	gk941707	RB2039	set-13(ok2697) II
VC20681	gk371738	RB2055	ugt-1(ok2718) V
VC20721	gk382986	RB2061	ora-1(ok2724) IV
VC20740	gk963053	RB2063	gst-5(ok2726) II
VC20773	gk398679	RB2067	flp-9(ok2730) IV
VC20777	gk399608	RB2070	Y110A7A.6(ok2733) I
VC20785	gk963087	RB2086	C29E4.10(ok2752) III
VC2142	gpd-3(ok2870) X	RB2105	T07D10.2(ok2780) I
VC2156	F59D12.1(gk1000) X	RB2114	sodh-1(ok2799) V
VC2171	tkr-1(ok2886) III	RB2120	Y6B3B.5(ok2805) I
VC2175	klo-1(ok2925) IV	RB2128	idh-1(ok2832) IV
VC218	dgk-3(gk110) III	RB2135	F33D4.4(ok2843) IV
VC2210	C12C8.2(ok2954) I	RB2165	sams-3(ok2932) IV
VC222	raga-1(ok386) II	RB2206	T25D3.3(ok2986) II
VC225	tps-1(ok373) X	RB2208	H22K11.2(ok2990) X
VC2285	F59D12.1(gk1122) X	RB2240	sams-1(ok3033) X
VC2294	W06D11.4(ok2831) X	RB2251	cpg-8 edit K03B4.7(ok3045) V
VC2309	ZK669.4(ok3001) II	RB2263	Y23B4A.2(ok3065) X
VC2346	hsp-12.3(ok3095) IV	RB2277	ser-5 edit (ok3087) I
VC2358	sptl-2(ok2753) V	RB2285	M02D8.4(ok3108) X
VC239	sams-5(gk147) IV	RB2301	F32E10.2(ok3124) IV
VC242	tag-38(ok490) V	RB2347	idh-2(ok3183) X
VC2490	W07E11.1&flp-2(gk1039) X	RB2348	idh-2(ok3184) X
VC2524	gpd-2(ok3243) X	RB2377	gana-1(ok3230) V
VC2569	cth-1(ok3319) V	RB2420	sams-4(ok3315) IV
VC26	pgp-12(gk19) X	RB2434	asg-2(ok3344) X

Strain	Description	Strain	Description
VC2612	cec-3(ok3432) III	RB2436	cysl-4 edit F59A7.9(ok3359) V
VC2683	set-6(ok2195) X	RB2535	K10H10.2(ok3516) II
VC281	hsp-12.6(gk156) IV	RB2549	sms-3(ok3540) III
VC30063	gk407477	RB2550	ugt-23(ok3541) X
VC30099	gk949270	RB2566	T02G5.7(ok3574) II
VC30165	gk428189	RB2588	efk-1(ok3609) III
VC30177	gk960608	RB2625	F40F12.7(ok3684) III
VC30220	gk440213	RB512	mce-1(ok243) I
VC30237	gk963405	RB608	tag-96(ok336) IV
VC40026	gk146187	RB681	cat-1(ok411) X
VC40041	gk122498	RB728	tre-1(ok327) I
VC40042	gk153470	RB737	snt-4(ok503) I
VC40057	gk298765	RB748	gta-1(ok517) IV
VC40071	gk452553	RB757	nhr-111(ok519) V
VC40107	gk465651	RB760	tps-2(ok526) II
VC40163	gk492147	RB766	gei-7(ok531) V
VC40209	gk514674	RB775	T28D9.3(ok555) II
VC40221	gk520889	RB782	F27E5.1(ok564) II
VC40235	gk527451	RB806	tre-5(ok612) II
VC40239	gk529935	RB810	R07E5.3(ok622) III
VC40249	gk535232	RB839	F54A3.4(ok666) II
VC40251	gk536170	RB865	C05D2.3(ok703) III
VC40283	gk553614	RB899	C17G1.7(ok762) X
VC40287	gk555057	RB910	elo-3(ok777) IV
VC40298	gk560755	RB927	T11G6.8(ok801) IV
VC40302	gk563241	RB938	vha-12(ok821) X
VC40328	gk576881	RB969	fat-2(ok873) IV
VC40336	NA	RB976	rhgf-1(ok880) X
VC40341	gk584646	RB993	tdc-1(ok914) II
VC40365	gk597083	RM2702	dat-1(ok157) III
VC40390	NA	SCL1	mcp-1(tm2679) V
VC40394	gk616761	SS579	pgl-1(bn101) IV
VC40396	gk961143; gk961144	SS580	pgl-1(bn102) IV
VC40402	gk620458	TG34	gld-1(op236) I
VC40428	gk633662	TJ1	cep-1(gk138) I
VC40434	gk635549	TK22	mev-1(kn1) III
VC40482	gk658979	TQ233	trpa-1(ok999) IV
VC40485	gk660351	TU228	mec-18(u228) X
VC40486	gk660920	TU55	mec-14(u55) III
VC40492	gk962314	VB1336	nnt-1(tm358) X

Strain	Description	Strain	Description
VC40512	gk672635	VB1876	tut-1(tm1297)
VC40546	gk687053	VB1890	elpc-1(tm2149)
VC40549	gk688401	VB674	nnt-1(sv34) X
VC40551	gk689405	VC1072	F29G6.2(gk455) X
VC40585	gk961365	VC107	tts-1(gk105) X
VC40638	gk737178	VC1163	T27A1.4(gk532) II
VC40640	gk738376	VC1184	T24H10.7(gk551) II
VC40643	gk961438	VC1198	Y39G8B.1(ok1682) II
VC40650	gk744178	VC1307	F52E4.1(ok1686) X
VC40670	gk942942	VC1339	Y49A10A.1(ok1856) X
VC40679	gk759089	VC138	elo-1(gk48) IV
VC40790	gk813443	VC1383	dgk-5 (gk631) II
VC40807	gk823783	VC142	dgk-2(gk124) X
VC40823	gk832037	VC1432	srh-159(ok1928) V
VC40861	gk852615	VC1471	nhr-186(gk732) V
VC40884	gk864611	VC1555	F13C5.2(gk716) X
VC40887	gk865337	VC32	haf-9(gk23) I
VC40898	gk872273	VC333	tap-1(gk202) X
VC40899	gk961751	VC334	hyl-1(gk203) IV
VC40901	gk873395	VC335	gly-2(gk204) I
VC40905	gk875298	VC343	glod-4(gk189) III
VC40912	gk961769	VC345	sgk-1(ok538) X
VC40929	gk886810	VC377	elo-5(gk182) IV
VC40937	gk889966	VC393	nduf-2.2(ok437) III
VC40946	gk948633; gk893848	VC425	elo-6(gk233) IV
VC40964	gk903134	VC426	hil-1(gk229) V
VC40973	gk907367	VC430	rhgf-1(gk217) X
VC40979	gk910077	VC505	ace-1(ok663) X
VC40983	gk912202	VC545	elo-3(gk236) IV
VC41008	gk925915	VC549	tdp-1(ok781) II
VC41013	gk927391	VC566	tag-174(gk274) III
VC3028	T03G6.3(ok3710) X	VC654	lim-8(ok941) III
VC3039	col-184(ok3742) X	VC657	gar-3(gk305) V
VC3058	thn-1(ok3735) IV	VC670	gar-3(gk337) V
VC3135	gba-3(gk3287) IV	VC693	cgt-1(ok1045) V
VC788	fat-3(ok1126) IV	VC736	gfl-1(gk321) IV
VC912	tag-279(gk387) X	VC747	lagr-1(gk327) I
VC916	sphk-1(ok1097) II	VC765	lagr-1(gk331) I
VC967	set-32(ok1457) I	VC784	ola-1(gk335)
VF2	pcs-1(tm1748) II	HBR02497	sqIs11 [lgg-1p::mCherry::GFP::lgg-1 + rol-6]

Strain	Description	Strain	Description
VL1176	alh-8(ww48) II	HBR02498	sqIs11 [lgg-1p::mCherry::GFP::lgg-1 + rol-6]; aptf-1(gk794) II
VM487	nmr-1(ak4) II	HBR02332	zIs356[daf-16::GFP]
VS18	maoc-1(hj13) II	HBR02482	flp-11(syb1445)X[flp-11-SL2-unc-58(L428F)-linker-mKate2]; zIs356[daf-16::GFP] IV
VS19	maoc-1(hj14) II	HBR02333	aptf-1(gk794); zIs356 [daf-16::GFP]
VS24	kat-1(tm1037) II	HBR02503	muIs126 [myo-3p::GFP::daf-16 + rol-6(su1006)]
VT1343	flh-1(bc374) IV	HBR02504	muIs126 [myo-3p::GFP::daf-16 + rol-6(su1006)]; aptf-1(gk794) II
WM99	cdk-1(ne2257) III	SJ4100	hsp-6::GFP(zcIs13)
WU970	haly-1(am132) X	HBR01810	aptf-1(gk794) II; zcIs13[hsp-6::GFP]V.
XA3101	paf-1(tj11) I	HBR01370	goeIs309[pdat-1::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'UTR, unc-119(+)].
XR3	lagr-1(gk327) I; hyl-1(ok976) IV	HBR01417	aptf-1(gk794) II, goeIs309[pdat-1::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'UTR, unc-119(+)].
YH461	ifta-2(tm1724) IV	HBR00560	goeIs120[ptdc-1::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'utr,unc119(+)].
YM19	cpb-3(bt17) I	HBR01118	aptf-1(gk794) II, goeIs120[ptdc-1::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'utr,unc119(+)].
YT17	crh-1(tz2) III	HBR00205	goeIs22[pmec-4::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'utr, unc-119(+)].

Strain	Description	Strain	Description
ZG31	hif-1(ia4) V	HBR00236	aptf-1(gk794) II; goeIs22[pmec-4::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'utr, unc-119(+)].
ZR2	jmjd-3.1 (gk384) X	HBR02201	goeIs304[pflp-11::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'UTR, unc-119(+)], dgk-1(ok1462) X.
ZZ12	lev-11(x12) I	HBR02356	goeIs304[pflp-11::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'UTR, unc-119(+)]; unc-13 (s69) I
BC12952	dpy-5(e907) I; sIs12952 [rCes ZK112.1::GFP + pCeh361]	PHX2193	flp-11(syb2193) [flp-11b-SL2(gpd-2)-mKate2-linker-twk-18(e1913)] X.
HBR02191	dpy-5(e907) I; sIs12952 [rCes ZK112.1::GFP + pCeh361], aptf-1(gk794) II	HBR02370	goeIs304[pflp-11::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'UTR, unc-119(+)], flp-11(syb2193)[flp-11b-SL2(gpd-2)-mKate2-linker-twk-18(e1913)]
HBR02212	eeEx106[hil-1::GFP + rol-6(su1006)]; aptf-1(gk794)	HBR02340	flp-11(syb1445)X[flp-11-SL2-unc-58(L428F)-linker-mKate2]
OP322	wgIs322 [ztf-4::TY1::EGFP:: 3xFLAG(92C12); unc-119(+)]	HBR02371	goeIs304[pflp-11::SL1-GCaMP3.35-SL2::mKate2-unc-54-3'UTR, unc-119(+)], "flp-11(syb1445)X[flp-11-SL2-unc-58(L428F)-linker-mKate2]"
SAL129	pha-1(e2123) III; denEx14. [lys-1::GFP; pha-1(+)]	HBR02266	hsp-12.6 (gk196) IV; aptf-1 (gk794) II
HBR02213	pha-1(e2123) III; denEx14 [lys-1::GFP + pha-1(+)]; aptf-1(gk794)	HBR02270	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II
OP711	unc-119(tm4063) III; wgIs711 [fkh-7::TY1::EGFP::3xFLAG + unc-119(+)]	HBR02283	cutl-17(syb1652); hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II

Strain	Description	Strain	Description
HBR02240	wgIs711 [fkh-7::TY1::EGFP::3xFLAG + unc-119(+)]; aptf-1(gk794)	PHX1364	hsp-12.6::mKate2 (syb1364)
HBR02327	sEx15051 [rCes C05D9.5::GFP + pCeh361]	PHX1652	cutl-17(syb1652); hsp-12.6::mKate2 (syb1364)
HBR02285	sEx15051[rCes C05D9.5::GFP + pCeh361]; aptf-1(gk794) II	HBR02319	hsp-12.6::mKate2 (syb1364); daf-16 (mu86) I
HBR02297	sEx10182[rCes R13A5.1a ::GFP + pCeh361]	HBR02320	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; daf-16 (mu86) I
HBR02241	sEx10182 [rCes R13A5.1a::GFP + pCeh361]; aptf-1(gk794)	HBR02325	hsp-12.6::mKate2 (syb1364); hsf-1(sy441) I
NIS1012	kytEx1012[hsp-12.6p(1kb):: hsp-12.6::GFP + rol-6(su1006)]	HBR02343	hsp-12.6::mKate2 (syb1364); elt-3 (gk121) X
HBR02235	kytEx1012 [hsp-12.6p(1kb): :hsp-12.6::GFP + rol-6(su1006)]; aptf-1(gk794)	HBR02344	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; elt-3 (gk121) X
NIS1013	kytEx1013hsp-12.6p(5kb):: hsp-12.6::GFP + rol-6(su1006)]	HBR02345	hsp-12.6::mKate2 (syb1364); daf-2 (e1370) III
HBR02234	kytEx1013 [hsp-12.6p(5kb):: hsp-12.6::GFP + rol-6(su1006)]; aptf-1(gk794)	HBR02346	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; daf-2 (e1370) III
CF1553	muIs84 [(pAD76) sod-3p::GFP + rol-6(su1006)];	HBR02346	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; daf-2 (e1370) III
HBR02397	muIs84 [(pAD76) sod-3p::GFP + rol-6(su1006)]; aptf-1(gk794) II.	HBR02347	hsp-12.6::mKate2 (syb1364); blmp-1 (s71) I
SS747	bnIs1[pie-1::GFP::pgl-1 + unc-119(+)]	HBR02348	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; blmp-1 (s71) I
HBR02102	aptf-1(gk794) II; bnIs1[pie-1::GFP::pgl-1 + unc-119(+)]	HBR02349	hsp-12.6::mKate2 (syb1364); glp-1 (q224) III
SJ4005	zcIs4[hsp-4::GFP] V.	HBR02350	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; glp-1 (q224) III

Strain	Description	Strain	Description
HBR01809	aptf-1(gk794) II; zcIs4 [hsp-4::GFP] V.	HBR02351	hsp-12.6::mKate2 (syb1364); glp-1(tn777) III
HBR02384	unc-119(ed3) III;goeIs251[mec-4::ReaChr::mKate2-unc-54-3'utr,unc-119(+)]; hsp-12.6::mKate2 (syb1364)	HBR02352	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; glp-1(tn777) III
HBR02410	hsp-12.6::mKate2 (syb1364); jmjd-3.1 (gk384) X	HBR02353	hsp-12.6::mKate2 (syb1364); glp-1(ar202) III
HBR02411	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; jmjd-3.1 (gk384) X	HBR02354	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; glp-1(ar202) III
HBR02412	hsp-12.6::mKate2 (syb1364); crh-1 (tz2) III	HBR02326	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; hsf-1(sy441) I
HBR02413	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; crh-1 (tz2) III	HBR02378	flp-11(syb2193) [flp-11b-SL2(gpd-2)-mKate2-linker-twk-18(e1913)]; hsp-12.6::mKate2 (syb1364)
HBR02414	hsp-12.6::mKate2 (syb1364); xbp-1 (zc12) III	HBR02379	flp-11(syb1445)X[flp-11-SL2-unc-58(L428F)-linker-mKate2]; hsp-12.6::mKate2 (syb1364)
HBR02415	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; xbp-1 (zc12) III	HBR02380	goeIs307[flp-11 prom::ArchT::SL2mKate-2-unc-54-3'utr,unc-119(+)]; hsp-12.6::mKate2 (syb1364)
HBR02416	hsp-12.6::mKate2 (syb1364); efl-1 (se1) V	HBR02381	goeIs232[psra-6::ReaChr::mKate2-unc-54-3'utr, unc-119(+)]; hsp-12.6::mKate2 (syb1364)
HBR02417	hsp-12.6::mKate2 (syb1364); aptf-1 (gk794) II; efl-1 (se1) V	HBR02382	eft-3p::TIR1::SEC; hsp-12.6::mKate2 (syb1364)
HBR02418	hsp-12.6::mKate2 (syb1364); flp-11 (tm2706) X	HBR02383	eft-3p::TIR1::SEC; hsp-12.6::mKate2 (syb1364); aptf-1(gk794) II
HBR02419	nprl-3 (ku540); aptf-1 (gk794)	HBR02456	hsp-12.6::mKate2 (syb1364) IV; unc-13(s69) I

Strain	Description	Strain	Description
HBR02432	hsp-12.6::mKate2 (syb1364) IV; tdc-1 (n3420) II	HBR02457	hsp-12.6::mKate2 (syb1364) IV; ceh-14(ch3) X
HBR02433	hsp-12.6::mKate2 (syb1364) IV; tbh-1 (n3247) X	HBR02458	hsp-12.6::mKate2 (syb1364) IV; cha-1(p1152) IV
HBR02434	hsp-12.6::mKate2 (syb1364) IV; cat-2 (n4547) II	HBR02459	hsp-12.6::mKate2 (syb1364) IV; ceh-23(ms23) II
HBR02435	hsp-12.6::mKate2 (syb1364) IV; tph-1 (mg280) II	HBR02460	hsp-12.6::mKate2 (syb1364) IV; ser-4(ok512)III
HBR02436	hsp-12.6::mKate2 (syb1364) IV; unc-25 (e156) III	HBR02461	hsp-12.6::mKate2 (syb1364) IV; fkh-9(ok1709) X
HBR02437	hsp-12.6::mKate2 (syb1364) IV; dgk-1 (ok1462) X	HBR02462	hsp-12.6::mKate2 (syb1364) IV; fkh-9(ok1709) X; aptf-1(gk794)II
HBR02438	hsp-12.6::mKate2 (syb1364) IV; eat-4 (ky5) III	HBR02463	hsp-12.6::mKate2 (syb1364) IV; let-23(sa62) II
HBR02439	hsp-12.6::mKate2 (syb1364) IV; egl-3 (ok979) V	HBR02464	hsp-12.6::mKate2 (syb1364) IV; aak-2 (ok524) X; aak-1(tm1944) III
HBR02454	hsp-12.6::mKate2 (syb1364) IV; jkk-1(km2) X	HBR02473	hsp-12.6::mKate2(syb1364) IV; aptf-1(gk794) II; egl-9(sa307) V
HBR02455	hsp-12.6::mKate2 (syb1364) IV; tbh-1 (n3247) X; aptf-1 (gk794)II	HBR02474	hsp-12.6::mKate2(syb1364) IV; aptf-1(gk794) II; jkk-1(km2) X
HBR02440	eft-3p::TIR1::SEC; hsp-12.6::mKate2 (syb1364) IV; rheb-1(re64 re285[AID::mKate2::3xFlag::rheb-1]) III	HBR02465	hsp-12.6::mKate2 (syb1364) IV; aptf-1 (gk794) II; aak-2 (ok524) X; aak-1(tm1944) III
HBR02441	eft-3p::TIR1::SEC; hsp-12.6::mKate2 (syb1364) IV; aptf-1(gk794) II; rheb-1(re64 re285[AID::mKate2::3xFlag::rheb-1]) III	HBR02466	hsp-12.6::mKate2 (syb1364) IV; egl-9(sa307) V

Strain	Description	Strain	Description
HBR02475	hsp-12.6::mKate2(syb1364) IV; asm-3(ok1744) IV	HBR02494	flp-11(syb2193)[flp-11b-SL2(gpd-2)-mKate2-linker-twk-18(e1913)] X; hsp-12.6::mKate2 (syb1364) IV; tph-1(tph-1 (mg280) II)
HBR02476	hsp-12.6::mKate2(syb1364) IV; aptf-1(gk794) II; asm-3(ok1744) IV	HBR02499	hsp-12.6::mKate2(syb1364) IV; lpIs1 [jnk-1(+) + rol-6(su1006)]
HBR02477	hsp-12.6::mKate2(syb1364) IV; jnk-1(gk7) IV	HBR02500	hsp-12.6::mKate2(syb1364) IV; lpIs1 [jnk-1(+) + rol-6(su1006)]; aptf-1(gk794) II
HBR02478	hsp-12.6::mKate2(syb1364) IV; aptf-1(gk794) II; jnk-1(gk7) IV	HBR02501	hsp-12.6::mKate2(syb1364) IV; lpIs2 [jnk-1(+) + rol-6(su1006)]
HBR02479	hsp-12.6::mKate2(syb1364) IV; nkat-1(ok566) X	HBR02502	hsp-12.6::mKate2(syb1364) IV; lpIs2 [jnk-1(+) + rol-6(su1006)]; aptf-1(gk794) II
HBR02480	hsp-12.6::mKate2(syb1364) IV; aptf-1(gk794) II; nkat-1(ok566) X	HBR02491	hsp-12.6::mKate2(syb1364) IV; alg-1(gk214) X
HBR02481	hsp-12.6::mKate2(syb1364) IV; nsy-1(ag3) II	HBR02492	hsp-12.6::mKate2 (syb1364) IV; cha-1(p1152) IV; aptf-1(gk794) II
HBR02485	hsp-12.6::mKate2(syb1364) IV; set-2(ok952) III.	HBR02493	hsp-12.6::mKate2(syb1364) IV; jnk-1(gk7) IV; aptf-1(gk794) II
HBR02486	aptf-1(gk794) II; set-2(ok952) III, hsp-12.6::mKate2(syb1364) IV		

6.2. Primer list

Target gene	Forward Outer	Forward Inner	Reverse Outer	Reverse Inner	Wild-type size	Mutant size	Annealing temperature
aak-1(tm1944)	AAGAAGATTTTCGGGCTTCT	-	TATGAAAACCAGGGCAGAAT	ATCGTGGAAGAATGAAAGGA	575	346	58
aak-2(ok524)	TCACTGGATGTCGTTGGAAA	-	GTTGGGAATACGCCAGCTAA	AGTAGTCAACGCCGGAAATG	229	530	60
alg-1 (gk214)	GATTTCCGATTCGTCGTGTC	ACAGCGCTCCAAAATGATCT	CGCTAAATGTTTGTGGCTGA	-	169	438	62
aptf-1 (gk794)	CGTTCGTGGATCTCAATGTG	AGTTTTGGGGAATGGGGTAG	CGGATCGATTGCTAGAGAGG	-	272	459	62
asm-3 (ok1744)	GACCCGGAGATTAGTAGGATTTT	CATGGCCTTGTAGAGCCAAT	ATTCGCTCGTATTTCCCAAA	-	177	371	60
blmp-1 (s71)	AGATGATGCGAGATCAAATTGGATGAAA	TCTGCATCAACTGCAATTGCGAGCTT	TGGATAACATTAGGCCGTGTGACTTCTG	TAATCAATTGCCACAATTGTTTCTGTTC	198	297	56
cat-2(n4547)	ATCGTGAAAGCGTCGAATTT	GTCGCAAGGAACGTCTCAAT	TACTTTGGTGGCGATGACTG	-	220	350	60
ceh-14(ch3)	AGCAGTTTATGGGGAGGACG	CGTTTCTACCAAACCCACCC	GCCAGAGTGTTGCGGTTTTA	-	642	861	53
ceh-23 (ms23)	AGCTGCAGAAATCGAGAAGG	TCATACGTGCCGAATTGAAA	CAAGGCGTTGAGCAAGATTT	-	207	381	62
crh-1 (tz2)	CTACAGAATTCGGCACAACG	GGAATGTGATTTTCCGTCGT	TGTTTTTGGAAGGAGGAGGA	-	247	339	62
daf-16 (mu86)	CTTCACTCGCCTTCATCATC	GAACTCGATCCGTCACAATC	TGAGTCGAAAAAGCTGAGAAA	-	272	397	58
daf-2 (e1370)	TTCTGAATCGTCAAGGATCA	TCATTACTCAAACCAATATAGGG	TGACTATTATAAGCCATCGGG	TTACACTCGGTGCTCCGT	169	263	54
dgk-1 (ok1462)	TCGCGTCTCTCTGAAAATCA	CCCATCCAATTGTTCCATCT	GCCAAATGTTCAACCACAGA	-	236	445	60
eat-4 (ky5)	GGGGCGTTTCCTTTTCTTTA	ACAGATCCATACGGAAAAGTTC	AAAATGCTCCGACTCCGATT	-	250	350	60
efl-1 (se1)	AAAGGTCTAAAGCTGCTCCTACT	GCTATAATGCTTACAAGAGCGTT	TTTATGCTAAAAGGCGGCTA	AGAAAAGAGTTATTCTGGTTACGG	~ 320	~ 400	52
elpc-1 (tm2149)	GGAAAAGCATCGAGTTGTCCAC	CGATGACACCCTTGATCACCA	TTGTGTCGGAGAGTTGTGCC	-	151	495	58
elt-3 (gk121)	TGACACTCCCCTTCCACTTC	TCAGTCAAGTACACTGTTCAC	AGGACGTCGGTTTCTCTTCA	-	400	580	54
fkh-9 (ok1709)	ACAACGGTCCAGAAGTGTCC	CGAAAAGCAAACAGGAGGTT	TCAAATATTATGGCACCACAGC	-	178	411	62
flp-11 (tm2706)	ATGATGAATTCGCCTCAGGA	TCTTCCAAATCGAACCAAGG	TAGCCGCTCGTCTCACTTTT	-	219	394	62
glp-1 (ar202)	CATTTCAGTGTCATTCGTGATCTATGCGA	ATTTTGATGGAGGTGATTGCTCAGGCGA	TTGCTTCTGTTCCGTTATTGCAATCTCC	TATTGACATTTGGAGAATGGTCTTTTCC	152	283	68
glp-1 (e2142)	GTGTTCTTTTTTTTCGCTTAACC	GTGCTTGCTCCGTCACTG	GTCACGGTTCATGAGAAAGC	CAGTTTTCCATTATAGCATTTGCT	124	248	56
glp-1 (q224)	GATGAGAATACTGCTCTGATGCT	TGCTAGTAGCACGTGAACTAGG	TGAAGAGCTGTTCGTCCTTT	CCATCTCCACTTGATGTTGTT	164	268	54

Target gene	Forward Outer	Forward Inner	Reverse Outer	Reverse Inner	Wild-type size	Mutant size	Annealing temperature
glp-1 (tn777)	CGATGTGAATGCAAGAGATT	GACCGGAATGGTATGAATG	TGGAATCTTTTCTAGCAGCA	ACGTGCTACTAGCATCAAGGT	131	262	54
hsf-1 (sy411)	ATAACAATTTTTCAGACATTTTTCGA	ACGGTACATTATTCCCAAAATCATACT	TCATCAAAATCTATATTCTCCAACTCTC	TTCAGAGATTTAGTCAGTAATCATAAGTG	249	165	58
hsp-12.6 (gk156)	TGGAGAACCGTCTGTGTTTT	CGAGGACCTGGAATCAAGTA	ATGATGAGCGTTCCAGTGAT	-	252	344	58
hsp-12.6 (syb1364)	CCCATAACTTCCTCCCAAAA	-	TTCCGGAAATAATCGAATTAAAAA	GATACGCATGGTTTGGGTTC	281	356	58
jkk-1 (km2)	AAATGTGTGCCTGGAGAACG	CGCGATATAAAACCCTCGAA	CGGCACATTTTTGTTCACAG	-	193	354	62
jmjd-3.1 (gk384)	CAGTTTGTTCCCCAGCATTT	AGTGTCGGAAGTTCGATTGG	CATGAAGGAGCGGAAGAGTC	-	233	392	62
jnk-1 (gk7)	CGCATCCTCCTCGATATCAT	GTTGCGAAAAATCGGAACAT	CGAACGACAATGTTTGATGG	-	239	397	60
let-23 (sa62)	AAAATGGAAATCATTGTGTGAAAGAATG	TACAAAAGATGTTAGAGAGTGTGAAAACTG	CCAAGTTTTTAAGTGTCTCGTTTGTCAG	TACTTTTTGGACAGCTGGAACTTCGGT	189	220	70
metr-1 (ok521)	CTGTTTTCGATTCAGCCAAC	ATTGGCGGAGCTACAACTTC	GTAATGTTCTTGGCGCACCT	-	244	359	54
nkat-1 (ok566)	TGACAAAAGAGCTTGCGTTG	GAAGGCTTGCTGAAAGGTTG	AGCGCTTCTCAATTCACGAT	-	280	478	60
nprl-3 (ku540)	TTTTGTGGAACTTGGATTTTGTGATGAAG	ATGTGTGGCCAACTCCAGATGCAACTT	GAATAGCACGTGTCCATTGCAGTAAGTG	CAATGACTGAGAAGTTTAGCAACAATAGG	240	160	66
nsy-1 (ag3)	TTTTGTTAATTTTCCATTTTCCACCTCA	CTGCTGGATTCTCTCATGTTCACATTT	ACTCAATTGGAATCCAGGATGAGACATA	AGTTGACAATGCATTCGATACAGTGTG	281	186	62
rheb-1 (re64)	AACAAGAAAACACTTCAGAGGAA	ATCCGTACATGAAGGAGGTGG	ATTCAGACTCTGACGATTTGATTG	-	600	1000	62
ser-4 (ok512)	CCCACCACGAAATGGTTACT	TGGCATGTTGCGAAACTAGA	ATGGAACGGAGCATTATTCG	-	267	498	60
sms-2 (gk608906)	AGTTCGAATCAAGCTTTTCAGTTCTCCCAA	GAATGTGCGGCGGAGCACACTT	TCTGTGCATATATGATAAACCACGGCCAA	ATCTTCCTTCACCATCAGCGGGGG	252	126	64
sms-2 (tm2757)	CCAATTTGGTCAGTTTACATAGC	AAACATCAGATCACCGCACA	TGACCAAACATCATGATTAAACG	-	212	360	56
tbh-1(n3247)	AAGCCGCCAAAGTCAAAGTC	-	TCTTGCCATGTTTTCCCAGC	-	> 1200	None	56
tdc-1(n3420)	GAGGATCCACGCCAGAATGA	-	CATGTGAATCCGCCCAGAAG	-	< 1000	> 1200	56
tph-1(mg280)	CATCATCCGAACGGAAAACT	TTTGCGCATAATAAAACAATCAA	ACGGAATCCAGTTTTTGCTG	-	280	380	60
tut-1 (tm1297)	ATTTTCAACGTCGGCATTTC	TTCAACCGAAATGTCCAAGT	AGCTGTGTGGACCCTGTTTC	-	225	403	58
xbp-1 (zc12)	AGCATATACCCTCACTTTCCTC	GTGCACTTCCAACAGCAC	GATCCATTTTCTCCTCCTGA	AGAAGTTGTGCGACAACGTA	115	230	58
ztf-20 (gk263563)	GCTTTTCGATTAGGAAAACTCC	TTTCCGATTGTTAAATGCATATC	GTCACCTGGAGCCGTCTAC	GAATTGTACTGTTTTACGTGGGA	147	294	58
flp-11 (syb1445)	ACGAGGAAGACTTTGCTCCA	-	GACACCAATCAAATTCTAGACAGC	AAACTCGCAAAAACGAGGAA	350	448	62

6.3. Quiescence bout detection script

```
clc;
close all;
clear;

% Read position data (image subtracion values)
a = readtable('FILE NAME','Sheet',1);
speed = table2array(a(:,1));
% If each worm has a different number of frames, matlab fills in NaN
speed = speed(~isnan(speed));
% Time interval between images (seconds)
dt1 = 5;
% Duration of the movie in frames
movie_frames = size(speed,1);
t1 = movie_frames * dt1;
% Set time axis
time = (dt1:dt1:t1)';
% Smooth imsub values according to frame density
if 1/t1 <= 10^-4
    s_speed = smooth(speed,0.01,'rloess');
else
    s_speed = speed;
end
% Calculate speed
s_speed = s_speed/dt1;
% Normalize speed at the 0.5th quantile
n_speed = zeros(length(s_speed),1);
for j=1:size(s_speed,1)
        n_speed(j,1) = (s_speed(j,1) -
quantile(s_speed,0.005))/(quantile(s_speed,0.995)-quantile(s_speed,0.005));
end
% Create list of indexes where normalized speed is under a threshold
index = zeros(size(n_speed,1),1);
threshold = 0.4;
for k=1:size(n_speed,1)
    if n_speed(k) <= threshold
        index(k) = k;
    else
        index(k) = 0;
    end
end
% Get the time points that correspond to the indexes
time_points = zeros(size(index,1),1);
for l=1:size(index,1)
    if index(l) ~= 0
        time_points(l) = time(l);
    end
end
% Specify quiescence bout time period of at least 120 sec
quiet_frames = 120/dt1;
quiescence_bouts = zeros(size(time_points,1)-quiet_frames,1);
for m=1:size(time_points,1)-quiet_frames
    if sum(time_points(m:(m+quiet_frames))) ==
sum(time(m:(m+quiet_frames))) % Continuity condition
        quiescence_bouts(m:(m+quiet_frames)) =
time_points(m:(m+quiet_frames));
    end
end
% Add extra 0 at the end of the interval to allow for limit calculations
```

```
quiescence_bouts = [quiescence_bouts;0];
% Find the limits of quiescence bout intervals
limits = zeros(size(quiescence_bouts,1),1);
% In case there is a quiescence bout in the beginning
if quiescence_bouts(1) > 0
    limits(1) = quiescence_bouts(1);
end
for n=2:size(quiescence_bouts,1)
    if quiescence_bouts(n) > 0 && quiescence_bouts(n-1) == 0
        limits(n) = quiescence_bouts(n);
    elseif quiescence_bouts(n) > 0 && quiescence_bouts(n+1) == 0
        limits(n) = quiescence_bouts(n);
    end
end
% Select for non-zero values - put help column at end
limits_elements = nonzeros(limits);
% Reshape into matrix (Row 1 = Beginning of bout, Row 2 = End of bout,
Columns = Different bouts)
limits_elements = reshape(limits_elements, [2,length(limits_elements)/2]);
% Add extra 0 column at the end to allow plotting
limits_elements = [limits_elements zeros(2,1)];
% Total quiescence time (minutes)
quiet_time = zeros(size(limits_elements,2)-1,1);
if size(limits_elements,2) > 1
    for q=1:size(limits_elements,2)-1
        quiet_time(q) = (limits_elements(2,q) - limits_elements(1,q))/60;
    end
else quiet_time = 0;
end
% Total wake time (minutes)
wake_time = zeros(size(limits_elements,2)-2,1);
if size(limits_elements,2) > 2
    for z=1:size(limits_elements,2)-2
        wake_time(z) = (limits_elements(1,z+1) - limits_elements(2,z))/60;
    end
else wake_time = NaN;
end
if mean(mean(limits_elements)) == 0 % In case there are no quiescence bouts
    wake_time = t1/60;
elseif max(time)-limits_elements(2,end-1) == 0 % In case movie ends in a
quiescence bout
   wake_time = [(limits_elements(1,1)-min(time))/60;wake_time];
else
    wake_time = [(limits_elements(1,1)-min(time))/60;wake_time;(max(time)-
limits_elements(2,end-1))/60];
end
% Quiescence fraction
Fraction_sleep = (sum(quiet_time)/(t1/60)) * 100;
```

6.4. RIS neuron automated detection script

```
clc;
close all;
clear;
% Import images from folder
imagefiles = dir('*.tif');
% Put all images into one variable "images"
for i=1:size(imagefiles,1)
   currentfilename = imagefiles(i).name;
   currentimage = imread(currentfilename);
   a{i,1} = currentimage;
end
% Find the maximum value and the index
for i=1:size(a,1)
    [maxval(i),idx(i)]= max(a{i}(:));
end
% Convert the index into x-y coordinates
for i=1:size(idx,2)
    [row,col]= ind2sub(size(a{i}), idx);
end
% Take the 12x12 (RIS size) values around the maximum
for i=1:size(row,2)
    x(i) = (col(i)-5);
    y(i) = (row(i)-5);
    s{i} = [x(i) y(i) 11 11];
end
% Isolate the signal
for i=1:size(a,1)
    I{i} = imcrop(a{i},s{i});
end
% Background is the pixel with the least intensity
for i=1:size(I,2)
    minval{i} = min(min(I{i}));
end
% Subtract background
for i=1:size(I,2)
    ImSub{i} = I{i} - minval{i};
end
% Average RIS intensity
for i=1:size(ImSub,2)
    m(i) = mean2(ImSub{i});
end
% Calculate speed for 5 second time interval
for i=2:size(row,2)
    speed(i) = (sqrt(((row(i) - row(i-1)).^2)+((col(i)-col(i-1)).^2)))./5;
end
```

6.5. RNA-seq differential expression analysis script

```
clc;
close all;
clear;
% Read raw counts
a = readtable('FILE NAME');
% Adjust indexes per dataset (here 2 conditions with 3 samples each)
Genes = table2array(a(:,1));
raw_counts = table2array(a(:,2:7));
% Normalize counts to sequencing depth and length of transcript
% Create a pseudo-reference sample by taking the geometric mean of all
samples
pseudo_ref_sample = geomean(raw_counts,2);
% Take only the non-zero values
nz = pseudo_ref_sample > 0;
% Compare the samples to the pseudo-reference
ratios = raw_counts(nz,:)./pseudo_ref_sample(nz,:);
% Calculate a size factor to correct the values for each sample
size_factors = median(ratios,1);
% Normalized counts
norm_counts = raw_counts./size_factors;
% Remove lowly expressed genes (CPM < 0.5)
% Calculate library sizes
count_sum = sum(raw_counts);
% Calculate counts per million (CPM)
cpm = count_sum./10^6;
% Filter out shot noise
c = raw_counts > ceil(cpm*0.5); % Artificial threshold of 0.5 CPM
% Select genes that are above threshold in all accepted samples
s = sum(c,2);
s1 = find(s == 6);
accepted_counts = norm_counts(s1,:);
accepted_genes = Genes(s1,:);
% Calculate statistical parameters
% Calculate mean
mean_WT = mean(accepted_counts(:,1:3),2);
mean_Mutant = mean(accepted_counts(:,4:6),2);
% Fold-change
FC = mean_Mutant ./ mean_WT;
log2FC_1 = log2(FC);
% Fit negative binomial model
tLocal =
nbintest(accepted_counts(:,1:3),accepted_counts(:,4:6),'VarianceLink','Loca
lRegression');
% Significance assessment
p_value= tLocal.pValue;
% False discovery rate
FDR = mafdr(p_value,'BHFDR',true);
```

6.6. Proteomics and metabolomics differential expression analysis script

```
clc;
close all;
clear;
% Read in data
% Adjust indexes according to the number of samples
a = readtable('FILE NAME');
Intensity = table2array(a(:,3:14));
Proteins = table2array(a(:,1:2));
% Quantile normalization
n_Int = quantilenorm(Intensity,'Median','true');
% Remove high variance peptides
% Calculate coefficient of vaiation
cv1 = std(log2(n_Int(:,1:6)),[],2)./mean(log2(n_Int(:,1:6)),2);
cv2 = std(log2(n_Int(:,7:12)),[],2)./mean(log2(n_Int(:,7:12)),2);
% Accept CVs < 97.5% of max
accepted_Int = n_Int(cv1<quantile(cv1,0.975)&cv2<quantile(cv2,0.975),:);
accepted_proteins =
Proteins(cv1<quantile(cv1,0.975)&cv2<quantile(cv2,0.975),:);
% Calculate statistical parameters
% Calculate the mean value
m_wt = mean(accepted_Int(:,1:6),2);
m_m = mean(accepted_Int(:,7:12),2);
% Fold-change
log2FC = log2(m_m./m_wt);
% Significance assessment
for i=1:size(accepted_Int,1)
    [h(i),p_value(i)] =
ttest2(accepted_Int(i,1:6),accepted_Int(i,7:12),'tail','both','vartype','un
equal');
end
p_value = p_value';
% False discovery rate
FDR = mafdr(p_value,'BHFDR',true);
```

6.7. RNA-seq (CeGaT) - N2 (wild-type) vs HBR227 (*aptf-1*) - 48h Starved

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
gsto-1	-3.31	col-80	-2	W04E12.7	-1.76	ctl-2	-1.6
txt-4	-3.14	asm-2	-1.99	nnt-1	-1.76	Y73B6A.3	-1.6
asp-13	-3.01	F45E1.5	-1.98	Y9C9A.8	-1.75	C08F11.3	-1.59
dpy-5	-2.78	gst-6	-1.96	arrd-11	-1.74	lys-7	-1.59
dod-24	-2.76	F47B8.4	-1.95	sqst-2	-1.74	Y70C5A.3	-1.59
sru-40	-2.68	pals-34	-1.95	pals-14	-1.74	hsp-16.41	-1.58
col-50	-2.66	F22B7.9	-1.95	C17H12.8	-1.74	C36B1.13	-1.58
dhs-20	-2.61	hsp-12.3	-1.94	cyp-29A2	-1.73	clec-52	-1.58
asp-14	-2.59	grd-3	-1.93	F10A3.4	-1.72	F58B4.5	-1.58
cest-9.1	-2.58	T05F1.11	-1.92	asp-1	-1.71	fbxa-185	-1.58
F42C5.3	-2.57	fbxa-182	-1.92	pgap-3	-1.71	B0410.3	-1.57
fbxa-172	-2.49	gldc-1	-1.92	col-159	-1.71	pck-2	-1.57
asm-3	-2.48	F40H3.2	-1.92	C08F11.13	-1.7	W10G11.1	-1.57
F55G11.8	-2.48	lmd-4	-1.91	gst-38	-1.69	F10G2.1	-1.56
F12A10.1	-2.45	cest-13	-1.9	prmt-6	-1.69	F37C4.6	-1.56
asp-2	-2.43	sdz-24	-1.9	C33E10.8	-1.69	R09E10.13	-1.56
linc-61	-2.36	T20D3.2	-1.9	fbxa-1	-1.69	E02H4.4	-1.55
C55A6.4	-2.27	B0403.6	-1.89	gst-41	-1.69	T05E7.1	-1.55
ugt-6	-2.27	col-93	-1.89	ZC196.2	-1.68	pho-11	-1.55
scav-1	-2.26	F42C5.5	-1.89	cdr-2	-1.68	pals-33	-1.55
col-101	-2.22	C06G3.3	-1.88	F08H9.3	-1.68	clec-55	-1.55
ctl-1	-2.21	F54H5.2	-1.88	afmd-1	-1.66	cyp-32B1	-1.53
dao-6	-2.19	nhr-17	-1.88	clec-60	-1.66	C39H7.4	-1.53
F18E3.11	-2.18	C24B5.4	-1.88	K08D12.6	-1.66	T25C12.3	-1.52
haf-9	-2.17	col-160	-1.87	ddn-1	-1.66	pcp-1	-1.52
T06C12.14	-2.17	fbxa-6	-1.86	clec-17	-1.65	T08E11.1	-1.52
C55A6.7	-2.14	C52E2.5	-1.85	klo-1	-1.65	Y47G6A.7	-1.51
C24B9.3	-2.14	CC8.2	-1.84	hrg-1	-1.64	ZK593.3	-1.51
ifc-1	-2.12	mul-1	-1.83	F19C7.1	-1.64	col-147	-1.51
pmp-5	-2.1	gst-14	-1.83	Y34B4A.9	-1.63	zig-9	-1.5
LLC1.2	-2.07	Y51H4A.24	-1.82	cyp-34A10	-1.63	F40G12.5	-1.5
far-5	-2.06	C31C9.7	-1.82	F13H8.11	-1.63	Y51B9A.9	-1.5
gfi-1	-2.05	gpx-7	-1.81	hpo-8	-1.61	mtl-2	-1.5
vha-6	-2.05	slc-17.9	-1.8	T28C6.8	-1.61	F56F10.1	-1.5
col-98	-2.04	F35F10.1	-1.8	ZK1240.1	-1.61	F17B5.1	-1.49
hpo-34	-2.03	R05F9.6	-1.78	Y37D8A.4	-1.61	Y105C5A.24	-1.49
clec-53	-2.03	Y34B4A.6	-1.78	F57F4.4	-1.61	T05C3.6	-1.49
ZK993.5	-2.02	mtl-1	-1.77	R13H4.2	-1.6	nep-17	-1.48
swt-3	-2.02	Y51F10.7	-1.77	F44A6.5	-1.6	cpin-1	-1.48
gpx-6	-2	haf-4	-1.77	F28A12.3	-1.6	paic-1	-1.47
fmo-2	-2	col-176	-1.77	catp-3	-1.6	ZC250.4	-1.47

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ugt-23	-1.37	F18E3.13	-1.3	T25B9.1	-1.24	tnt-2	-1.19
R07E3.4	-1.37	zmp-4	-1.3	vha-8	-1.24	vha-13	-1.19
aakg-4	-1.37	hlh-13	-1.29	asah-1	-1.24	R05A10.1	-1.19
C54F6.6	-1.36	mdl-1	-1.28	F41E7.2	-1.24	clec-5	-1.19
col-103	-1.36	hum-5	-1.28	F56C9.7	-1.24	C44E12.1	-1.19
clec-72	-1.36	cpr-5	-1.28	C10A4.3	-1.24	F49C12.6	-1.19
EGAP4.1	-1.36	Y7A5A.1	-1.28	dhs-21	-1.24	dhs-24	-1.19
dhs-7	-1.36	cyp-37B1	-1.28	F09C8.1	-1.23	K12C11.6	-1.19
aat-1	-1.36	F21C10.11	-1.27	xtr-1	-1.23	C46G7.2	-1.18
mca-1	-1.36	F35E12.6	-1.27	clec-76	-1.23	T21H3.1	-1.18
F14F3.5	-1.36	vha-5	-1.27	T10C6.6	-1.23	C06E4.3	-1.18
cbl-1	-1.35	Y119D3B.14	-1.27	hpo-15	-1.23	sqd-1	-1.18
F09B12.3	-1.35	B0334.3	-1.27	ndx-3	-1.23	irg-7	-1.18
fbxa-54	-1.35	F10E9.12	-1.27	M01E5.2	-1.23	C39D10.11	-1.17
col-91	-1.34	gst-16	-1.27	irg-3	-1.23	T04A8.7	-1.17
pcbd-1	-1.34	F46G10.1	-1.27	F47H4.2	-1.23	iars-2	-1.17
gta-1	-1.34	ZC196.5	-1.26	gst-33	-1.23	T15B7.1	-1.17
C49C3.4	-1.34	T19D12.1	-1.26	F29B9.1	-1.23	aakg-5	-1.17
F21H7.12	-1.33	F48D6.4	-1.26	cyp-25A3	-1.22	C49A9.3	-1.17
C18B2.5	-1.33	F46H5.7	-1.26	gpa-17	-1.22	nft-1	-1.16
ugt-2	-1.33	fat-4	-1.26	eol-1	-1.22	ucr-1	-1.16
ech-7	-1.33	F10G8.9	-1.26	ctps-1	-1.22	Y65B4BL.7	-1.16
Y67H2A.7	-1.33	idhg-2	-1.26	C32H11.4	-1.22	F32D8.12	-1.16
col-107	-1.33	T10C6.15	-1.26	F40A3.2	-1.22	pha-1	-1.16
vha-15	-1.33	gcst-1	-1.26	flp-11	-1.22	T25C12.12	-1.16
C50F4.1	-1.33	cars-1	-1.26	frm-4	-1.22	clec-84	-1.16
lys-8	-1.33	E04F6.9	-1.26	asg-2	-1.22	clec-82	-1.16
clec-85	-1.32	bath-46	-1.25	nstp-1	-1.21	Y43F8B.24	-1.16
fbxa-162	-1.32	alh-1	-1.25	ZK550.6	-1.21	F41C3.2	-1.16
ttr-24	-1.32	VF13D12L.3	-1.25	B0393.9	-1.21	gba-4	-1.16
Y34B4A.5	-1.31	F58F12.1	-1.25	Y43C5A.2	-1.21	lgc-25	-1.15
F52E1.5	-1.31	twk-18	-1.25	wars-1	-1.21	ctsa-3.1	-1.15
ncx-1	-1.31	nmur-2	-1.25	spp-1	-1.2	gst-10	-1.15
hda-5	-1.31	nhr-106	-1.25	prdx-6	-1.2	C28H8.14	-1.15
cyp-34A9	-1.31	aagr-2	-1.25	cpg-9	-1.2	ceeh-2	-1.15
exc-15	-1.31	mct-3	-1.25	drd-5	-1.2	pho-5	-1.15
kcc-1	-1.31	Y45F3A.9	-1.25	T28F3.8	-1.2	ZC373.5	-1.15
vgln-1	-1.3	maoc-1	-1.24	clu-1	-1.19	ucr-2.1	-1.15
C01G10.9	-1.3	Y69A2AR.18	-1.24	chil-16	-1.19	C44E4.5	-1.15
F52E1.14	-1.3	ril-2	-1.24	M28.10	-1.19	tkt-1	-1.14
T19H12.3	-1.3	vha-16	-1.24	dct-11	-1.19	F07H5.5	-1.14

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ril-1	-1.14	asp-6	-1.1	cdr-4	-1.06	F32A5.8	-1.02
T01D3.6	-1.14	C33A12.19	-1.1	D1022.4	-1.06	fig-1	-1.02
gcp-2.1	-1.14	F26D11.12	-1.1	cyp-33E1	-1.06	dig-1	-1.02
C49G7.3	-1.14	trxr-2	-1.1	acp-6	-1.06	Y37E11B.5	-1.02
col-142	-1.14	fbxa-105	-1.1	cpn-3	-1.06	adt-2	-1.02
gfm-1	-1.14	sek-1	-1.1	R10E8.6	-1.06	F25B5.5	-1.01
B0035.13	-1.14	serp-1.2	-1.1	tsn-1	-1.05	sqrd-1	-1.01
prx-6	-1.14	lmp-2	-1.1	C49A9.6	-1.05	let-611	-1.01
cyc-1	-1.14	vps-33.1	-1.1	cgr-1	-1.05	pals-24	-1.01
T01G1.4	-1.14	F14F9.8	-1.09	cox-15	-1.05	R10H10.3	-1.01
aex-5	-1.13	best-14	-1.09	H18N23.2	-1.05	mboa-7	-1.01
sur-5	-1.13	M01F1.3	-1.09	gly-6	-1.05	nas-11	-1.01
nuo-5	-1.13	gst-3	-1.09	dct-18	-1.05	F46C5.10	-1.01
K02E11.7	-1.13	vars-1	-1.09	dhs-9	-1.05	tsp-10	-1.01
F54D5.4	-1.13	gst-15	-1.09	vha-11	-1.05	pqn-25	-1.01
coa-7	-1.13	pin-2	-1.09	skr-19	-1.04	prx-5	-1.01
C14C6.5	-1.13	cal-5	-1.09	T08B1.1	-1.04	akt-2	-1
F23B12.4	-1.13	tag-18	-1.09	clec-66	-1.04	myo-3	-1
nstp-4	-1.13	acs-7	-1.09	hrpa-2	-1.04	ins-27	-1
gst-27	-1.13	rom-2	-1.09	apm-1	-1.04	mps-2	-1
F31A3.3	-1.13	F43D2.7	-1.09	M01B2.13	-1.04	Y102A11A.3	-1
egl-20	-1.13	ztf-17	-1.09	R07E3.1	-1.04	dsh-2	1
F08D12.3	-1.13	C01B10.6	-1.09	aqp-10	-1.04	col-121	1
C53A5.17	-1.12	T06A1.5	-1.08	abce-1	-1.04	spp-22	1.01
dct-6	-1.12	cav-2	-1.08	dlc-3	-1.04	otub-3	1.01
clec-37	-1.12	des-2	-1.08	R03H10.1	-1.04	rnr-1	1.01
asb-2	-1.12	R05D3.12	-1.08	ctsa-1.1	-1.03	ZK973.9	1.01
faah-3	-1.12	pals-18	-1.08	C05D2.11	-1.03	nlp-64	1.01
gst-4	-1.12	mboa-2	-1.08	tric-1B.1	-1.03	F59A2.5	1.01
sek-4	-1.11	elo-1	-1.08	cyp-32A1	-1.03	K05C4.7	1.01
ZK185.3	-1.11	gst-13	-1.07	ola-1	-1.03	Y37A1B.7	1.01
T24C12.3	-1.11	C38H2.2	-1.07	K12C11.1	-1.03	ceh-45	1.01
ZK1320.3	-1.11	Y6E2A.4	-1.07	F09E5.3	-1.03	dpy-3	1.01
Y54G11A.7	-1.11	dod-3	-1.07	pgrn-1	-1.03	F13A7.11	1.01
clp-1	-1.11	mus-81	-1.07	zyg-11	-1.03	wdr-48	1.01
spp-3	-1.11	fat-1	-1.07	Y39A1A.14	-1.03	bus-8	1.01
snet-1	-1.11	ttr-1	-1.06	T11B7.5	-1.02	nduo-3	1.01
C07D8.6	-1.11	F01D5.1	-1.06	gst-36	-1.02	igeg-1	1.02
pyr-1	-1.11	prmt-5	-1.06	mig-6	-1.02	rsp-4	1.02
alh-12	-1.1	gas-1	-1.06	T19D12.2	-1.02	suds-3	1.02
F58H1.3	-1.1	lipl-2	-1.06	spp-10	-1.02	R07E3.2	1.02

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
dhs-27	1.02	dscc-1	1.07	Y7A9D.1	1.12	grl-21	1.18
F58G11.3	1.02	snrp-27	1.07	F53B3.3	1.12	lrr-1	1.18
noah-2	1.02	T16G12.8	1.07	cpr-4	1.12	T11B7.2	1.19
tcab-1	1.02	swp-1	1.07	bath-41	1.12	F25H9.6	1.19
ugt-28	1.02	T22B7.3	1.07	his-74	1.12	abf-5	1.19
knl-2	1.02	cng-1	1.07	K08E4.2	1.13	K08B4.2	1.19
cdt-1	1.02	F59A6.5	1.08	F54D5.5	1.13	pph-4.2	1.19
ugt-29	1.02	nlp-16	1.08	uri-1	1.13	B0513.4	1.19
F16B4.4	1.03	puf-8	1.08	ins-28	1.13	mei-1	1.19
lsd-1	1.03	F14B4.1	1.08	pgl-2	1.13	bub-1	1.19
tre-5	1.03	lem-3	1.08	C47E8.11	1.14	F52B5.2	1.19
thoc-7	1.03	F59E12.15	1.08	Y17D7C.3	1.14	adal-1	1.19
blos-4	1.03	mlt-11	1.09	F22E5.9	1.14	C02F5.13	1.19
R02F11.2	1.03	C27B7.5	1.09	R08F11.7	1.14	dnsn-1	1.2
rad-50	1.03	fbxa-44	1.09	Y46G5A.7	1.14	pole-1	1.2
Y54G11A.3	1.03	B0511.7	1.09	rnh-2	1.14	bath-10	1.2
W10C8.4	1.03	C44C10.9	1.09	F46E10.2	1.14	ceh-86	1.2
rbmx-2	1.03	let-49	1.09	ego-1	1.14	F28F5.4	1.2
marg-1	1.04	aly-2	1.09	T09F5.12	1.14	ccch-3	1.2
C16C8.16	1.04	Y87G2A.19	1.09	K09F6.13	1.14	hmg-4	1.2
C08H9.16	1.04	K07C10.3	1.09	F56D2.2	1.15	him-5	1.2
nasp-1	1.04	nlp-79	1.09	F15D4.5	1.15	snpc-1.2	1.21
F42A9.6	1.05	pri-1	1.09	T09B9.1	1.15	ung-1	1.21
gln-5	1.05	ZK1053.4	1.1	oma-2	1.15	taf-8	1.21
pafo-1	1.05	tim-1	1.1	igeg-2	1.15	pgp-8	1.21
F27E5.7	1.05	K02B7.3	1.1	mcm-3	1.16	apc-10	1.21
daf-18	1.05	C49G7.12	1.1	erh-2	1.16	K09D9.1	1.21
F09G2.8	1.05	Y65A5A.1	1.1	Y68A4A.13	1.17	C09B8.5	1.21
C07A9.9	1.05	K08E4.3	1.1	F44E2.10	1.17	tnt-4	1.21
cup-15	1.06	fbxc-36	1.1	T14G8.4	1.17	C14B1.12	1.22
Y69A2AR.21	1.06	tsp-2	1.11	M28.5	1.17	Y54E10BR.2	1.22
F37H8.2	1.06	T07F12.4	1.11	ZK669.3	1.17	F56F11.4	1.22
F45F2.11	1.06	E01A2.2	1.11	ceh-2	1.17	gly-11	1.22
dsl-3	1.06	T12G3.4	1.11	ptr-13	1.18	ech-1.1	1.22
cdk-4	1.06	Y53F4B.9	1.11	clec-196	1.18	B0024.4	1.22
tni-4	1.06	F54E2.1	1.11	C44C1.6	1.18	F43C1.7	1.22
mcm-5	1.06	pqn-75	1.11	K09F6.6	1.18	dnj-20	1.22
lpr-7	1.06	wrt-10	1.11	lips-3	1.18	D2005.4	1.22
C25G6.4	1.07	F01D4.5	1.12	F47B10.8	1.18	W04E12.9	1.23
pgp-4	1.07	C06H2.7	1.12	skpt-1	1.18	alg-5	1.23
mre-11	1.07	F55A11.4	1.12	cht-1	1.18	nlp-31	1.23

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
lgc-11	1.23	C30F2.4	1.28	knl-3	1.32	F55C5.2	1.4
pgph-2	1.23	hcp-6	1.28	capg-2	1.32	F39F10.4	1.41
Y47D3A.1	1.23	B0001.7	1.28	mdf-2	1.32	pri-2	1.41
him-8	1.23	F31C3.6	1.28	klp-19	1.33	Y14H12B.2	1.41
F27C1.4	1.24	F13A7.14	1.28	skr-17	1.33	Y75B8A.18	1.41
sas-5	1.24	T04C12.7	1.28	Y47H9C.1	1.33	cbd-1	1.41
C31H1.8	1.24	K08H2.4	1.29	asns-2	1.33	wago-1	1.41
T05B9.1	1.24	dnj-11	1.29	mesp-1	1.33	cpg-1	1.41
Y46H3A.5	1.24	K06H7.7	1.29	pcn-1	1.33	rmd-1	1.41
hcp-1	1.24	B0348.2	1.29	fbxb-104	1.34	C35E7.5	1.42
ZK1037.6	1.24	C30G12.6	1.3	irg-5	1.34	W02B8.2	1.43
fbxa-206	1.25	ndfl-4	1.3	Y41D4B.26	1.34	C40A11.2	1.43
cep-1	1.25	C08F1.10	1.3	pch-2	1.34	F14F9.4	1.44
gla-3	1.25	hecw-1	1.3	tbb-6	1.34	ndc-80	1.44
zig-4	1.25	F25G6.1	1.3	fbxb-95	1.35	F26A1.9	1.44
nop-1	1.25	gpr-1	1.3	C33F10.4	1.35	col-78	1.45
orc-4	1.25	Y106G6H.6	1.3	B0285.3	1.35	fbxc-44	1.45
pcmd-1	1.25	col-111	1.3	csc-1	1.36	K09F6.10	1.45
rab-11.2	1.26	F52B5.7	1.3	W01D2.6	1.36	C03D6.9	1.45
inx-2	1.26	Y39A3A.4	1.3	T16G12.4	1.36	klp-18	1.45
hasp-1	1.26	tost-1	1.3	Y17G9B.2	1.37	nxf-2	1.46
sdz-28	1.26	cutl-2	1.3	Y49E10.4	1.37	ttr-29	1.46
Y51F10.2	1.26	ssna-1	1.3	C25F9.2	1.37	K10H10.10	1.46
hil-5	1.26	pqn-60	1.31	R13A5.7	1.37	C14B1.9	1.46
C34C12.7	1.26	pgl-3	1.31	dlc-5	1.37	Y58A7A.3	1.46
crn-4	1.26	B0261.7	1.31	clec-266	1.38	C50F4.6	1.46
C24H12.1	1.26	C42C1.12	1.31	B0393.3	1.38	C35E7.3	1.46
lpr-3	1.27	C25H3.1	1.31	chaf-2	1.38	exo-3	1.46
F17C11.11	1.27	C18H7.11	1.31	ify-1	1.38	T10B11.8	1.46
rsp-5	1.27	hrde-1	1.31	flh-3	1.39	T01C3.2	1.46
cmt-1	1.27	abf-6	1.31	ima-2	1.39	T11B7.1	1.46
rde-4	1.27	zeel-1	1.31	cdc-7	1.39	oef-1	1.47
icp-1	1.27	ncr-2	1.31	ptr-22	1.39	C41D11.9	1.47
9/1/2020	1.27	fbxb-75	1.31	col-169	1.39	iff-1	1.47
F10D2.10	1.27	F36A2.10	1.32	cec-4	1.39	kbp-3	1.47
acox-1.2	1.27	dnj-22	1.32	F41E6.7	1.39	gcna-1	1.47
pitr-3	1.27	pid-3	1.32	Y73F4A.3	1.39	F56A12.2	1.48
T02C1.1	1.28	M01D1.12	1.32	W04A8.1	1.39	aptf-2	1.48
T22F3.11	1.28	K09F6.9	1.32	scc-1	1.39	T25B6.5	1.48
cyp-33C6	1.28	hch-1	1.32	gpdh-1	1.4	fbxc-18	1.48
F48E3.6	1.28	C47D2.1	1.32	Y4C6B.1	1.4	sym-1	1.49

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T04C12.32	1.49	R144.10	1.57	air-2	1.65	rbm-3.1	1.76
cdk-1	1.49	msh-2	1.57	syp-1	1.66	fbxb-54	1.76
C05D9.4	1.49	col-181	1.57	R05H5.3	1.66	C38D4.4	1.76
K10H10.4	1.49	Y45F10D.2	1.57	T05D4.2	1.66	F40F11.3	1.77
nhr-2	1.5	ttr-27	1.57	Y39A3A.3	1.66	kbp-2	1.78
polh-1	1.5	mcm-4	1.57	cec-8	1.67	Y39G10AL.1	1.78
C08E3.1	1.5	W04A8.5	1.58	Y37H2A.14	1.67	T04D3.1	1.78
egg-3	1.5	ctf-4	1.58	pole-4	1.67	kbp-4	1.78
him-10	1.5	clx-1	1.58	fbxa-50	1.67	pash-1	1.78
C06E2.5	1.5	D2005.7	1.58	K04G2.10	1.67	spp-20	1.8
htp-1	1.5	F13A7.12	1.58	rsa-1	1.67	Y45G5AM.5	1.81
klc-1	1.5	F22B5.4	1.58	ZK829.9	1.68	T05A7.1	1.82
K07D4.4	1.51	Y17D7B.3	1.59	F59C12.4	1.69	T03G11.3	1.82
lron-1	1.52	Y52E8A.2	1.59	fbxb-3	1.69	vet-2	1.82
kbp-1	1.52	C23G10.11	1.59	san-1	1.69	F08F8.4	1.82
mei-2	1.52	chaf-1	1.59	ttr-28	1.69	F15A4.2	1.83
puf-3	1.52	C55B7.11	1.6	W03C9.2	1.7	clec-172	1.83
F32A7.8	1.52	Y38E10A.14	1.6	such-1	1.7	cah-4	1.83
set-31	1.52	ZK1127.13	1.6	kbp-5	1.7	psf-1	1.83
Y106G6D.2	1.53	fbxc-25	1.6	F08F3.4	1.71	hil-4	1.83
fbxb-15	1.53	set-9	1.6	F13E9.14	1.72	vet-1	1.83
C09B8.4	1.53	syp-6	1.6	pot-2	1.72	mbtr-1	1.84
ins-11	1.53	nhr-161	1.6	C48B4.9	1.72	T05H10.4	1.84
ZK622.4	1.53	ttr-38	1.6	F11E6.7	1.72	Y58A7A.4	1.85
nlp-67	1.53	K03H1.7	1.61	gna-2	1.73	skr-10	1.85
ttr-50	1.54	C50F7.5	1.61	hpr-17	1.73	dut-1	1.86
C13A10.2	1.54	ced-8	1.62	mcm-7	1.73	hcp-2	1.86
crn-1	1.54	cey-3	1.62	sdz-4	1.73	Y106G6D.1	1.86
col-145	1.54	valv-1	1.62	hal-2	1.73	skr-13	1.86
hal-3	1.54	immt-2	1.62	F54F7.6	1.73	R11.4	1.86
fbxb-84	1.54	memi-2	1.62	C24H10.1	1.73	T28A8.3	1.87
fbxc-40	1.54	psf-2	1.63	K08E5.1	1.74	spo-11	1.87
C08F1.6	1.55	aptf-4	1.63	Y59A8B.12	1.74	mis-12	1.87
mom-2	1.55	neg-1	1.63	C37C3.9	1.74	Y43B11AL.1	1.87
F09C6.3	1.55	psf-3	1.63	F23A7.4	1.74	K04H4.5	1.88
axl-1	1.55	T25E12.6	1.64	ogr-2	1.74	mcm-10	1.89
F15B9.6	1.55	C05D12.4	1.64	fbxa-155	1.74	F14B6.3	1.9
rnr-2	1.55	toca-2	1.65	btb-11	1.75	oig-3	1.9
ptr-2	1.55	atz-1	1.65	gld-1	1.75	skr-7	1.92
fzy-1	1.56	ndnf-1	1.65	fbxc-32	1.76	C29A12.1	1.92
hcp-4	1.56	C01B12.8	1.65	cyb-1	1.76	T28A8.4	1.92

Gene	log2FC	Gene	log2FC	Gene	log2FC
ZC434.8	1.92	gyg-2	2.17	ceh-83	2.49
fbxb-72	1.93	orc-3	2.17	ZC308.4	2.5
vet-6	1.94	F09C6.1	2.19	cdc-25.3	2.5
K02B12.2	1.94	ins-20	2.2	F09E10.15	2.51
R09F10.8	1.94	pie-1	2.2	cyb-3	2.52
F22H10.2	1.94	mct-5	2.21	F32D1.7	2.55
gpd-4	1.94	him-3	2.21	C08E8.3	2.59
F19B10.10	1.95	sun-1	2.22	cyb-2.2	2.6
gln-6	1.95	mans-4	2.22	gpd-1	2.64
T07D3.9	1.95	tipn-1	2.22	mex-1	2.67
sld-2	1.96	puf-5	2.23	Y39B6A.10	2.72
skr-9	1.97	F56F4.8	2.24	EEED8.3	2.72
flh-1	1.97	puf-11	2.25	3/3/2020	2.79
linc-6	1.97	T19H12.2	2.25	nasp-2	2.81
gei-14	1.97	syp-5	2.25	lsy-27	2.85
Y42H9B.3	1.98	set-22	2.26	F08F3.6	2.85
skr-8	1.98	htp-2	2.26	pos-1	2.88
F53F8.3	1.99	T05F1.2	2.26	ceh-49	2.93
mut-2	2.01	szy-4	2.27	C42C1.8	2.96
C17E4.2	2.01	mex-5	2.29	clec-91	2.97
Y111B2A.2	2.02	C09F12.2	2.29	nspe-1	2.98
skr-14	2.03	T21C9.13	2.3	C05C10.5	3.02
btb-6	2.04	W06B4.1	2.31	F23A7.8	3.05
sdz-30	2.05	Y54G9A.5	2.32	T12G3.6	3.07
DY3.8	2.05	glp-1	2.32	clec-88	3.09
ZC155.4	2.06	C08F8.3	2.33	F14D7.2	3.1
sip-1	2.06	R04D3.2	2.35	ins-3	3.28
F54H12.5	2.06	skr-15	2.36	era-1	3.31
Y60C6A.2	2.07	sdz-14	2.36	F14H3.6	3.39
gld-3	2.07	Y71A12B.11	2.39	clec-87	3.49
inx-14	2.07	str-112	2.42		
trt-1	2.08	cey-2	2.42		
C01G6.3	2.08	F56C9.6	2.42		
B0281.5	2.1	ctf-8	2.42		
hmg-3	2.1	taf-11.2	2.43		
htp-3	2.1	W05F2.3	2.44		
C44B9.3	2.11	fbxa-215	2.44		
C04A2.15	2.11	Y110A2AR.1	2.46		
dsl-2	2.12	trcs-1	2.46		
nspe-7	2.13	F18A1.7	2.47		
orc-1	2.16	spn-4	2.47		

6.8. RNA-seq (CeGaT) - N2 (wild-type) vs HBR227 (*aptf-1*) - 4h Fed

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
gst-33	-2.25	clec-230	-1.48	phat-3	-1.3	F09F7.6	-1.17
nspc-16	-2.2	F15E6.10	-1.47	irg-3	-1.3	clec-166	-1.16
F11C7.7	-2.15	asm-3	-1.47	C07H4.1	-1.29	T02B11.4	-1.16
cyp-13A6	-2.09	C06E4.3	-1.47	clec-199	-1.29	ins-29	-1.16
cyp-33C2	-1.98	T10H4.13	-1.46	grd-6	-1.29	F45E10.2	-1.16
gba-2	-1.97	W03D2.6	-1.46	gst-19	-1.28	F25E5.8	-1.16
cpr-2	-1.97	F19C6.4	-1.46	gst-12	-1.27	F55H12.2	-1.16
flp-11	-1.94	fbxa-203	-1.45	F42A8.1	-1.27	ZC395.5	-1.15
F16B4.5	-1.91	F14F3.5	-1.45	scl-5	-1.27	R08F11.4	-1.14
Y65B4BR.1	-1.89	F40E3.5	-1.45	dct-16	-1.26	F32H5.3	-1.14
fipr-7	-1.83	T05A10.6	-1.45	K02E11.6	-1.26	papl-1	-1.14
cyp-33D1	-1.81	T05E12.6	-1.44	T05E7.1	-1.26	nduo-3	-1.14
clec-55	-1.8	F09C8.1	-1.43	Y73F4A.1	-1.25	D2023.1	-1.14
F57H12.6	-1.75	B0478.3	-1.43	T19H12.3	-1.25	ftn-1	-1.14
rpr-1	-1.75	gst-8	-1.42	F22B7.9	-1.24	glt-5	-1.13
gst-38	-1.74	M01B2.13	-1.42	C06B8.2	-1.24	grd-14	-1.13
C08F11.1	-1.73	ent-4	-1.41	F17B5.1	-1.24	H11E01.2	-1.13
srb-16	-1.72	pud-4	-1.41	cdr-2	-1.24	ugt-61	-1.13
gst-14	-1.71	lips-17	-1.41	col-153	-1.24	rncs-1	-1.13
C40H1.7	-1.69	fbxa-38	-1.4	pho-6	-1.23	F53F4.13	-1.12
Y34F4.2	-1.69	B0334.13	-1.4	ZK593.2	-1.23	msrp-7	-1.12
clec-61	-1.68	C35A11.4	-1.4	F18E3.13	-1.23	ZK822.6	-1.11
ora-1	-1.68	mtl-2	-1.39	T11G6.3	-1.22	ndfl-4	-1.11
F46C5.10	-1.67	F44G4.6	-1.39	fipr-26	-1.22	C50F4.8	-1.11
pgp-12	-1.67	W02D7.11	-1.38	Y46G5A.36	-1.22	F41G3.10	-1.1
srg-34	-1.66	C27B7.9	-1.38	spp-18	-1.21	W10C8.6	-1.1
C24A11.1	-1.64	Y73B6A.3	-1.37	C06B3.6	-1.21	ZK593.3	-1.1
cyp-25A2	-1.64	F22D6.15	-1.37	R06F6.14	-1.21	nlp-18	-1.1
nspc-14	-1.64	W07G4.8	-1.37	F08H9.3	-1.2	cyp-13A10	-1.1
F18E3.11	-1.62	nspc-18	-1.36	bca-1	-1.2	ZK353.10	-1.09
Y55F3BR.10	-1.61	srsx-34	-1.35	vap-1	-1.2	folt-2	-1.09
snet-1	-1.61	B0410.3	-1.35	H32K16.2	-1.2	sulp-5	-1.09
col-184	-1.6	cyp-13A7	-1.35	nspc-20	-1.19	cdr-4	-1.09
ZK384.7	-1.57	T11B7.5	-1.34	F11C7.2	-1.19	K07A1.3	-1.09
pudl-2	-1.56	F57A8.4	-1.34	F25D1.5	-1.19	fip-2	-1.09
F12E12.11	-1.56	R13D7.2	-1.32	sodh-1	-1.19	C06G3.3	-1.09
C06E8.5	-1.54	Y39B6A.29	-1.32	ilys-5	-1.18	txt-4	-1.09
K01D12.9	-1.53	F32D8.11	-1.32	gpx-7	-1.18	R05D8.7	-1.08
T25G12.6	-1.52	txt-3	-1.31	Y69A2AR.22	-1.18	F56D6.17	-1.08
T07G12.5	-1.51	Y54G2A.41	-1.31	col-58	-1.18	T12B3.3	-1.08
C03A3.3	-1.51	fipr-6	-1.31	F21C10.10	-1.17	fmo-2	-1.08

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ZK1320.9	-1.07	apc-11	1.01	cdk-4	1.04	spd-5	1.1
CC8.2	-1.07	ergo-1	1.01	him-6	1.04	R17.3	1.1
ZK822.4	-1.07	clec-266	1.01	klp-19	1.04	lpr-4	1.1
C10C5.7	-1.06	F22E5.9	1.01	ZK688.9	1.04	hyl-1	1.1
T22C8.6	-1.06	mett-10	1.01	pafo-1	1.05	dpy-2	1.1
Y51F10.7	-1.06	dpy-7	1.01	ent-1	1.05	atf-8	1.1
ddo-2	-1.06	R11H6.4	1.01	cdc-25.2	1.05	T22C1.5	1.11
asp-14	-1.06	com-1	1.02	F33E2.5	1.05	ZC449.1	1.11
spp-2	-1.06	Y82E9BR.17	1.02	Y105C5B.19	1.05	drsh-1	1.11
cest-26	-1.06	C50D2.8	1.02	tbp-1	1.05	C16C8.16	1.11
F23F12.12	-1.05	F54H12.5	1.02	unc-59	1.06	ska-3	1.11
acs-2	-1.05	suds-3	1.02	ntp-1	1.06	B0205.9	1.11
Y49E10.18	-1.05	fbxa-101	1.02	C27H6.9	1.06	C48B4.11	1.11
T16G1.4	-1.04	arle-14	1.02	B0511.7	1.06	R07B7.10	1.12
F29C6.1	-1.04	snpc-3.4	1.02	F35D2.3	1.06	F36F12.1	1.12
T10C6.15	-1.04	F48E3.6	1.02	fkb-7	1.06	phf-10	1.12
C38C3.10	-1.04	rnp-5	1.03	drh-3	1.06	tag-342	1.12
gstk-1	-1.04	Y65A5A.1	1.03	fnci-1	1.06	trpl-2	1.12
F59A7.5	-1.03	F32H2.10	1.03	mdt-6	1.07	cec-6	1.12
frpr-19	-1.03	mom-5	1.03	K02B12.2	1.07	hcf-1	1.12
F19F10.3	-1.03	F33H1.3	1.03	ZK1127.13	1.07	dsl-6	1.12
Y41C4A.17	-1.03	lin-42	1.03	T20F5.4	1.07	F52D2.7	1.12
nlp-20	-1.02	F41G3.6	1.03	F13A7.14	1.07	slx-1	1.12
ZK1307.1	-1.02	wrt-1	1.03	F01F1.11	1.07	vang-1	1.13
col-77	-1.02	Y69A2AR.28	1.03	ego-1	1.08	chl-1	1.13
fig-1	-1.02	C15A11.4	1.03	hrpk-2	1.08	nspe-7	1.13
fip-6	-1.02	C25F6.7	1.03	egl-46	1.08	isw-1	1.13
nlp-69	-1.01	mes-6	1.03	ZK973.1	1.08	T24D1.2	1.13
fipr-1	-1.01	C09F9.2	1.03	rsp-4	1.08	cep-1	1.13
C31C9.7	-1.01	hhat-1	1.03	lin-37	1.09	EEED8.14	1.13
nduo-6	-1.01	F09E10.6	1.03	T25B6.5	1.09	Y69H2.7	1.13
C49A9.3	-1.01	Y48B6A.13	1.03	F39F10.4	1.09	algn-6	1.13
dod-3	-1	H03E18.1	1.04	Y105E8A.14	1.09	dpy-3	1.13
C33G8.4	-1	dnj-11	1.04	pes-5	1.09	F52C6.2	1.13
tag-209	-1	Y46G5A.7	1.04	ari-1.4	1.09	C27F2.10	1.14
F10E9.3	1	K10D3.4	1.04	inx-3	1.09	F44B9.8	1.14
C56C10.9	1	rsp-6	1.04	spdl-1	1.1	lpr-5	1.14
ssna-1	1	Y41D4B.14	1.04	Y37A1B.7	1.1	D1081.6	1.14
C08F1.10	1.01	T09B9.1	1.04	F01G4.4	1.1	ppm-1.G	1.14
R05D11.9	1.01	B0432.8	1.04	erh-1	1.1	fbxc-18	1.14
D1007.8	1.01	nfyc-1	1.04	mrt-1	1.1	R05H10.3	1.14

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T26C12.3	1.15	rfc-2	1.2	Y52B11A.8	1.25	cdc-6	1.31
Y73F8A.13	1.15	unc-85	1.2	tyms-1	1.26	trt-1	1.31
zipt-1	1.15	pig-1	1.2	pssy-2	1.26	C48B4.10	1.31
C45G3.3	1.15	hcp-3	1.2	ttr-50	1.26	evl-18	1.31
ced-4	1.15	wrt-10	1.2	sdz-38	1.26	lin-54	1.31
rsp-5	1.15	ZK829.9	1.2	zyg-1	1.26	fbxc-25	1.31
ztf-1	1.15	F42A9.6	1.21	cec-4	1.26	C40A11.2	1.31
C14F11.6	1.15	swd-2.1	1.21	dna-2	1.27	Y39G10AL.1	1.32
Y38A10A.7	1.15	pigk-1	1.21	lst-1	1.27	F23A7.4	1.32
npp-18	1.15	sdha-2	1.21	him-8	1.27	C16C8.11	1.32
lsl-1	1.15	C02F5.13	1.21	let-49	1.27	czw-1	1.32
W04A8.6	1.15	Y46G5A.8	1.21	hmbx-1	1.27	F09G2.8	1.32
K05C4.7	1.15	nasp-1	1.21	lpr-6	1.27	top-2	1.33
C06E7.88	1.16	btb-11	1.21	Y53G8AR.6	1.27	eme-1	1.33
such-1	1.16	htz-1	1.21	B0001.2	1.28	brc-1	1.33
ndc-80	1.16	T03F6.3	1.22	E_BE45912.2	1.28	Y106G6D.2	1.33
F26F4.5	1.16	F59A6.5	1.22	K08E4.2	1.28	noah-2	1.33
ostb-1	1.16	hmg-20	1.22	fbxb-104	1.28	Y49E10.4	1.33
aos-1	1.16	npp-2	1.22	F55A11.8	1.28	F27C1.4	1.33
cpf-1	1.16	tim-1	1.22	tdc-1	1.28	dsh-2	1.33
parp-2	1.16	C13F10.7	1.22	C48B6.9	1.28	C03D6.9	1.33
gras-1	1.16	C49F5.6	1.22	C04A11.2	1.28	cec-3	1.34
hcp-4	1.16	Y34D9A.7	1.22	kbp-3	1.28	D1046.2	1.34
C46A5.6	1.17	damt-1	1.22	sid-1	1.28	dnsn-1	1.34
ect-2	1.17	spr-3	1.23	F54D5.9	1.29	ZK616.5	1.34
rad-54.B	1.17	ZK813.6	1.23	ptr-2	1.29	pgl-2	1.35
skr-9	1.17	bub-3	1.23	nduf-2.2	1.29	bmk-1	1.35
dsl-3	1.17	mrg-1	1.23	imp-1	1.29	mut-7	1.35
F46E10.2	1.18	inx-2	1.23	ugt-63	1.29	eaf-1	1.35
T04D3.5	1.18	gbas-1	1.23	C13G5.2	1.29	R13A5.7	1.35
ZK1053.4	1.18	ceh-86	1.23	wago-4	1.29	R07E4.5	1.36
ceh-40	1.19	wrt-2	1.23	cpar-1	1.3	C35E7.5	1.36
div-1	1.19	sna-2	1.23	apc-2	1.3	T26A5.8	1.36
mig-32	1.19	kca-1	1.24	mlt-11	1.3	metl-9	1.36
F44F1.6	1.19	cye-1	1.24	coh-4	1.3	knl-3	1.37
Y48G10A.2	1.19	C17G10.1	1.25	ssup-72	1.3	Y53F4B.9	1.37
lin-53	1.19	set-9	1.25	skr-8	1.3	ani-1	1.37
simr-1	1.19	B0035.18	1.25	T08G5.3	1.3	asb-1	1.38
ZK643.2	1.19	sex-1	1.25	JC8.7	1.3	R57.2	1.38
nhr-23	1.2	pid-2	1.25	npp-23	1.31	F59G1.8	1.39
unc-71	1.2	fbxb-66	1.25	noah-1	1.31	Y75B8A.16	1.39

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
inft-2	1.4	F44E2.10	1.47	psf-3	1.56	chaf-2	1.68
icp-1	1.4	mcm-10	1.47	fubl-4	1.56	F01D4.5	1.68
tofu-1	1.4	rod-1	1.47	chaf-1	1.56	chk-1	1.68
Y51H7C.3	1.4	mis-12	1.48	Y66D12A.16	1.57	daf-18	1.68
Y41D4B.26	1.4	sas-1	1.48	fncm-1	1.57	hcp-1	1.7
lem-3	1.41	F35C11.5	1.48	erh-2	1.57	fbxb-53	1.7
C47F8.1	1.41	C44F1.1	1.48	mre-11	1.57	F15B10.3	1.7
orc-4	1.41	fbxb-35	1.48	mlh-1	1.57	hrde-2	1.7
Y95D11A.3	1.41	rpa-1	1.49	msh-6	1.57	ctf-8	1.7
tipn-1	1.42	fbxb-15	1.49	C41D11.9	1.58	C40A11.4	1.7
W02B8.2	1.42	pola-1	1.49	skr-10	1.58	sas-6	1.71
T13F2.6	1.42	aspm-1	1.49	hlh-3	1.58	Y106G6H.6	1.71
crn-1	1.42	W04A8.5	1.49	hcp-6	1.58	mans-4	1.71
F54D10.5	1.43	unc-61	1.5	ekl-5	1.58	dvc-1	1.71
cdt-1	1.43	mei-1	1.5	pal-1	1.58	Y49F6B.9	1.72
F56D2.2	1.43	F08F8.4	1.51	wrt-4	1.59	W05F2.6	1.72
F48A11.4	1.43	T05D4.2	1.51	F15A4.2	1.59	pid-3	1.72
D2030.8	1.43	npp-22	1.51	C36B1.11	1.6	Y71F9AL.6	1.72
C39E9.12	1.44	C56A3.8	1.52	cec-7	1.6	hcp-2	1.73
tag-63	1.44	cyk-4	1.52	bub-1	1.6	sygl-1	1.73
hmg-12	1.44	hal-3	1.52	fbxb-54	1.61	skr-2	1.73
him-10	1.44	lpr-3	1.52	F07H5.10	1.61	K04G2.10	1.74
tcab-1	1.44	fbn-1	1.53	dpl-1	1.61	neg-1	1.74
thk-1	1.44	xpo-2	1.53	C48B4.9	1.61	snrp-40.2	1.75
Y71F9AL.7	1.44	aly-2	1.53	B0041.8	1.61	glh-3	1.75
fbxa-107	1.44	pph-4.2	1.53	Y43B11AL.1	1.62	zipt-7.1	1.75
wdr-48	1.44	cutl-16	1.53	Y37E11AL.3	1.62	Y48G1A.2	1.76
pri-1	1.44	brd-1	1.53	cutl-2	1.62	dsl-2	1.76
ifa-3	1.45	Y39B6A.42	1.54	pole-1	1.63	ced-8	1.76
cdc-25.1	1.45	T07C4.3	1.54	prg-1	1.63	F12F6.7	1.76
adal-1	1.45	iff-1	1.54	efl-1	1.64	sld-2	1.77
mcm-6	1.46	gpr-2	1.54	F52B5.2	1.65	scc-1	1.77
got-2.1	1.46	T16G12.4	1.54	F21D5.1	1.65	lsd-1	1.78
Y17G9B.2	1.46	zhp-3	1.54	fbxa-83	1.65	klp-18	1.78
rmh-1	1.46	R11.4	1.54	C28C12.12	1.66	taf-11.2	1.78
bath-15	1.46	zwl-1	1.55	rnp-8	1.66	plk-1	1.78
Y75B8A.18	1.47	rfc-4	1.55	mes-4	1.67	F54F7.6	1.79
rnh-2	1.47	F45F2.11	1.55	T26A5.2	1.67	irg-5	1.79
cup-15	1.47	rfc-3	1.55	fbxc-29	1.67	K07A1.1	1.79
otub-3	1.47	sgo-1	1.56	gpaa-1	1.67	syp-1	1.8
cks-1	1.47	vet-2	1.56	cdl-1	1.67	sdz-30	1.8

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
fbxc-44	1.8	gcna-1	1.91	rnr-1	2.05	plk-2	2.21
B0281.5	1.8	D1081.7	1.91	sep-1	2.05	apc-10	2.21
F31B9.3	1.81	pif-1	1.92	C01G6.3	2.06	ogr-2	2.21
C17E4.2	1.81	Y4C6B.1	1.92	mcm-4	2.06	syp-2	2.21
tdpt-1	1.81	deps-1	1.92	tofu-6	2.07	mcm-2	2.21
knl-1	1.82	T04D3.1	1.92	ung-1	2.07	cyp-31A3	2.22
let-99	1.82	T05H10.4	1.92	kbp-5	2.07	him-3	2.23
dhs-11	1.82	T28A8.4	1.92	exo-1	2.08	C06E2.5	2.23
skr-17	1.83	F58G11.3	1.92	orc-3	2.08	F14B6.3	2.23
fbxc-32	1.83	hal-2	1.92	fbxa-206	2.08	skr-15	2.24
F40F11.3	1.83	dscc-1	1.92	tpxl-1	2.08	Y51F10.2	2.25
T25E12.6	1.83	gln-5	1.92	edg-1	2.08	set-31	2.25
kbp-4	1.83	F11E6.7	1.93	gmn-1	2.08	C27B7.5	2.25
gpr-1	1.83	K07A1.17	1.93	pcmd-1	2.1	set-32	2.25
M03B6.4	1.83	ceh-83	1.94	aptf-2	2.1	fog-2	2.25
K03H1.7	1.84	fem-3	1.94	prom-1	2.11	pcn-1	2.25
Y97E10AR.4	1.84	gei-14	1.94	F56F4.8	2.12	F59A3.12	2.25
ced-3	1.84	meg-3	1.96	C01B12.8	2.12	alg-5	2.26
kbp-1	1.84	F19B10.10	1.96	btb-19	2.13	nxf-2	2.26
dsb-2	1.85	cmt-1	1.97	mdf-2	2.13	ima-2	2.26
pash-1	1.85	rmd-1	1.97	W04A8.1	2.14	hrde-1	2.27
flh-1	1.85	fbxb-95	1.97	C50C3.1	2.14	htp-2	2.27
nemp-1	1.85	H04M03.3	1.98	air-1	2.14	rbm-3.1	2.28
aptf-4	1.85	skr-13	1.99	sdz-28	2.15	fbxa-210	2.28
cdk-1	1.85	sas-5	1.99	T16G12.8	2.15	cyk-7	2.29
polh-1	1.86	kbp-2	2	spo-11	2.15	syp-5	2.29
F10E9.7	1.86	B0001.7	2	bath-41	2.16	mcm-3	2.3
skr-7	1.86	C37C3.9	2	egg-6	2.17	pch-2	2.3
zim-3	1.86	gla-3	2.01	nop-1	2.18	eri-5	2.3
Y111B2A.3	1.86	rad-51	2.01	ctf-4	2.18	hpo-40	2.32
W06D11.1	1.86	D2030.7	2.01	F13D12.5	2.18	F54D5.2	2.32
vet-1	1.86	pri-2	2.02	ucr-2.3	2.18	klc-1	2.33
wdr-5.3	1.87	rsa-2	2.03	tost-1	2.18	D2005.4	2.33
air-2	1.87	btb-6	2.03	zen-4	2.19	T10B11.8	2.33
mcm-5	1.89	F54D5.5	2.03	W03C9.2	2.19	lrr-1	2.34
capg-2	1.89	csc-1	2.03	rnr-2	2.19	nhr-2	2.34
msh-2	1.89	skr-14	2.03	toe-2	2.19	C48B4.7	2.34
tofu-7	1.9	cpg-4	2.04	orc-5	2.19	ani-2	2.35
Y73B3A.1	1.9	san-1	2.04	mcm-7	2.2	mbtr-1	2.35
bir-2	1.9	F30F8.1	2.05	psf-1	2.2	pigv-1	2.36
flh-3	1.9	cdc-7	2.05	gpd-4	2.21	htp-3	2.37

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
cdc-25.3	2.37	orc-1	2.56	sip-1	2.89	DY3.8	3.36
fzy-1	2.37	F23A7.8	2.57	lsy-27	2.89	memi-2	3.37
mut-2	2.37	cyn-9	2.58	gld-1	2.9	spn-4	3.37
C14B1.9	2.38	mom-2	2.59	Y110A7A.15	2.91	szy-4	3.39
psf-2	2.38	T28A8.3	2.59	R04D3.2	2.92	cpg-1	3.45
set-22	2.38	wee-1.3	2.59	zif-1	2.94	nasp-2	3.45
T05B9.1	2.39	pid-4	2.61	inx-14	2.94	cbd-1	3.45
cyb-3	2.39	F33E11.2	2.62	C01G8.1	2.95	mei-2	3.48
B0304.2	2.4	T22D1.5	2.62	gln-6	2.95	cey-2	3.48
vet-6	2.41	C29A12.1	2.64	mex-5	2.96	puf-3	3.5
exo-3	2.41	syx-4	2.65	ify-1	2.96	clec-87	3.57
Y71A12B.11	2.41	T28A8.5	2.65	gyg-2	2.98	F14D7.2	3.6
C38D4.4	2.42	F18A1.7	2.65	gpd-1	2.99	trcs-1	3.62
snpc-1.2	2.42	hpr-17	2.66	wago-1	3.02	puf-11	3.67
cyb-1	2.43	sdz-14	2.67	C08F8.3	3.02	cey-3	3.7
rsa-1	2.44	egg-3	2.67	T05F1.2	3.03	oma-2	3.76
immt-2	2.45	B0393.3	2.68	daz-1	3.04	C31H1.8	4.31
K07F5.12	2.45	pgl-1	2.69	glp-1	3.05	puf-5	4.57
oef-1	2.46	ZC308.4	2.7	pie-1	3.05		
cpg-3	2.46	Y54G11A.3	2.71	F53F8.3	3.06		
Y42H9B.3	2.47	dut-1	2.71	mar-3	3.06		
F56F11.4	2.48	C42C1.8	2.71	fbxa-215	3.07		
his-74	2.48	R09F10.8	2.74	era-1	3.08		
nos-1	2.48	Y14H12B.2	2.74	W06B4.1	3.09		
ZC434.8	2.48	mct-5	2.78	T12G3.6	3.09		
Y111B2A.2	2.48	Y39B6A.10	2.78	EEED8.3	3.13		
R05H5.3	2.48	T21C9.13	2.79	cyb-2.2	3.14		
pgl-3	2.48	ceh-49	2.8	F14H3.6	3.15		
mesp-1	2.48	zim-1	2.81	Y110A2AR.1	3.15		
htp-1	2.49	Y54G9A.5	2.81	D2005.7	3.17		
R144.10	2.5	hil-5	2.81	Y73B6BL.23	3.18		
F08F3.6	2.51	hil-4	2.82	sun-1	3.18		
F56C9.3	2.51	gna-2	2.82	pos-1	3.22		
Y59A8B.12	2.51	hmg-3	2.84	W05F2.3	3.24		
skpt-1	2.51	B0261.7	2.85	clec-88	3.29		
C55B7.11	2.52	toca-2	2.86	F56C9.6	3.29		
puf-8	2.53	T19H12.2	2.86	Y52E8A.2	3.3		
syp-6	2.53	pot-2	2.87	clec-91	3.32		
H04D03.2	2.55	F32D1.7	2.88	mex-1	3.35		
spsb-2	2.56	xnd-1	2.88	C05C10.5	3.35		
C44B9.3	2.56	ZC155.4	2.88	gld-3	3.35		

6.9. Proteome (TMT) - N2 (wild-type) vs HBR227 (*aptf-1*) - 48h Starved

Protein	log2FC	Protein	log2FC	Protein	log2FC	Protein	log2FC
perm-4	-4.57	asp-5	-1.94	vit-2	-1.49	dao-2	-1.22
ilys-5	-4.29	vit-3	-1.94	F35C8.5	-1.49	set-18	-1.22
Y59E9AR.1	-3.84	dct-16	-1.93	dod-19	-1.48	gln-6	-1.21
madd-3	-3.61	fmo-5	-1.9	pmp-5	-1.48	pid-3	-1.21
folt-2	-3.55	F56C9.7	-1.9	glh-2	-1.48	F55G1.9	-1.21
K12H4.7	-3.55	ctsa-1.2	-1.89	vit-1	-1.48	ifp-1	-1.21
dpy-10	-3.54	hpo-40	-1.87	gfat-1	-1.47	asp-14	-1.19
ule-5	-3.46	nuc-1	-1.85	pcp-4	-1.45	gldc-1	-1.19
glh-1	-3.36	nrf-6	-1.83	ifc-1	-1.45	Y7A5A.1	-1.19
Y62H9A.5	-3.27	asp-13	-1.83	lec-8	-1.43	ugt-62	-1.18
D1054.10	-3.14	ost-1	-1.82	LLC1.2	-1.43	nhl-1	-1.17
ZK813.3	-3.14	W05F2.3	-1.81	pgp-3	-1.42	hpo-34	-1.16
cbd-1	-2.98	T21H3.1	-1.8	asp-2	-1.41	R74.8	-1.16
Y51F10.7	-2.92	T05H10.3	-1.78	C23H5.8	-1.39	him-17	-1.16
pgp-1	-2.76	hach-1	-1.77	rnr-1	-1.39	T16G12.1	-1.15
csr-1	-2.73	spp-5	-1.75	M02H5.8	-1.39	R10F2.4	-1.15
T28F3.8	-2.64	chat-1	-1.75	gfi-1	-1.38	Y54E2A.4	-1.15
C17G1.2	-2.64	vit-6	-1.72	far-2	-1.35	asp-3	-1.15
cey-2	-2.63	R10H10.3	-1.72	tba-4	-1.35	clec-87	-1.15
hrg-7	-2.61	F19C7.1	-1.7	dhs-25	-1.34	aagr-2	-1.14
lys-4	-2.6	anp-1	-1.69	skpo-3	-1.34	timm-23	-1.13
asp-1	-2.51	ima-2	-1.69	dnc-3	-1.34	afd-1	-1.13
F54E2.1	-2.5	lron-8	-1.67	W04B5.3	-1.33	rars-2	-1.13
perm-2	-2.49	clec-63	-1.67	lron-7	-1.33	mec-1	-1.12
ule-1	-2.48	egg-1	-1.66	B0379.6	-1.32	sptl-1	-1.11
F17E9.5	-2.46	vit-4	-1.64	grl-7	-1.32	bigr-1	-1.11
acdh-1	-2.41	C34H4.2	-1.63	R193.2	-1.31	sur-5	-1.11
asp-6	-2.37	F52E1.14	-1.63	F58B4.5	-1.31	sago-2	-1.11
F17E9.4	-2.34	F28B4.3	-1.63	F55G11.8	-1.3	Y69E1A.5	-1.1
col-92	-2.29	H20J04.1	-1.61	irg-7	-1.3	C35A5.11	-1.1
asns-2	-2.29	dot-1.1	-1.6	Y34B4A.6	-1.29	hcp-1	-1.09
spp-3	-2.29	spp-2	-1.59	T25C12.3	-1.29	Y41E3.1	-1.09
rme-2	-2.25	ugt-26	-1.59	cdr-4	-1.28	mct-2	-1.09
F21C10.9	-2.12	glh-4	-1.59	rnp-1	-1.27	czw-1	-1.08
F09C8.1	-2.1	hphd-1	-1.58	ech-6	-1.27	aagr-1	-1.08
ZK6.11	-2.1	dnj-11	-1.58	argk-1	-1.27	sip-1	-1.07
F57F5.1	-2.06	dut-1	-1.56	oxy-4	-1.27	ddx-17	-1.06
cyp-13A5	-2.03	leo-1	-1.55	C29F3.7	-1.26	gst-35	-1.05
clec-50	-1.99	pod-2	-1.55	gcst-1	-1.26	cdk-1	-1.05
cpr-4	-1.97	vit-5	-1.55	C05C10.3	-1.25	hsp-6	-1.04
C14F11.4	-1.97	F53F8.4	-1.53	spp-14	-1.24	pgp-6	-1.04
cey-3	-1.94	Y34B4A.9	-1.51	spin-1	-1.24	K08D8.6	-1.04

Protein	log2FC	Protein	log2FC	Protein	log2FC
R102.4	-1.04	hsp-16.2	1.09	lfi-1	1.26
Y48A6B.7	-1.04	F59F3.6	1.09	tni-3	1.27
ints-13	-1.03	gpx-5	1.09	ttr-23	1.28
M18.3	-1.03	Y53F4B.23	1.1	hmg-3	1.31
repo-1	-1.03	C02B10.3	1.1	ZK863.8	1.31
ipla-1	-1.02	C32D5.8	1.12	T10B10.3	1.35
wago-1	-1.02	ZC434.4	1.12	T03F1.11	1.37
mctp-1	-1.02	pdl-1	1.12	sod-3	1.37
vbh-1	-1.01	F47B8.2	1.13	nlp-24	1.38
mcm-4	-1.01	sgn-1	1.13	pqn-94	1.4
Y65B4A.2	1	srap-1	1.13	rpi-2	1.42
viro-2	1	pghm-1	1.14	F26G1.2	1.42
exp-2	1.01	nol-16	1.14	F07C3.2	1.43
F54E4.3	1.01	scl-3	1.14	col-39	1.43
sod-4	1.02	E02C12.9	1.14	tnt-2	1.43
F59B10.3	1.02	exc-13	1.14	cnnm-1	1.44
unc-27	1.02	hil-3	1.14	droe-4	1.44
ttr-16	1.02	F55F8.3	1.14	F58H1.7	1.46
his-24	1.02	F17H10.2	1.14	pud-1.1	1.47
gstk-2	1.02	W03G11.3	1.15	ttr-5	1.53
F39H12.3	1.02	ptl-1	1.15	best-14	1.54
C55A6.6	1.02	C24A3.2	1.15	ensa-1	1.57
H14N18.4	1.03	T03D8.6	1.15	F53B3.6	1.64
F45D11.15	1.04	F52E4.5	1.16	F43C9.2	1.71
dig-1	1.05	che-10	1.16	K02F3.9	1.72
F40A3.2	1.05	W05H12.1	1.17	ftn-1	1.76
rnp-5	1.05	T27C4.1	1.17	sod-5	1.76
gana-1	1.05	spp-13	1.17	grd-3	1.77
pud-2.1	1.05	R10H10.4	1.17	E04F6.9	1.83
ric-4	1.05	zmp-3	1.18	C18H7.1	1.83
C15C7.7	1.06	C53D6.7	1.18	msa-1	1.92
T28B11.1	1.06	slc-36.5	1.18	M01H9.3	1.93
F45E1.1	1.06	Y52E8A.3	1.18	C53B7.3	2.21
cat-1	1.06	rab-3	1.19	hil-1	2.22
tni-4	1.06	R07B1.9	1.2	F36H9.7	2.22
fkh-7	1.07	F41D9.2	1.21	Y53C10A.6	2.39
gst-20	1.07	Y39B6A.5	1.22	Y54G2A.57	2.57
ttr-46	1.07	plpr-1	1.22	cut-1	2.74
lron-2	1.07	mec-5	1.24	asp-9	3.01
sng-1	1.07	Y44A6D.2	1.25	H39E23.3	3.29
F54C8.6	1.08	sup-1	1.25	scl-11	3.33
hsp-16.48	1.08	dpf-1	1.25	scl-12	3.78

6.10. Proteome (TMT) - N2 (wild-type) vs HBR227 (*aptf-1*) - 4h Fed

Protein	log2FC	Protein	log2FC	Protein	log2FC
K12H4.7	-3.3	let-805	-1.15	vps-18	1.27
col-158	-3.26	F13D12.5	-1.13	lact-3	1.28
perm-4	-3.15	T21B6.3	-1.13	F25B4.7	1.28
cey-3	-3.13	unc-7	-1.12	F53F4.16	1.29
folt-2	-2.92	F23H11.5	-1.11	F39H11.1	1.3
Y62H9A.5	-2.74	endu-1	-1.1	eif-2Balpha	1.3
ilys-5	-2.53	F17E9.5	-1.07	F41D9.2	1.34
scl-11	-2.53	kdp-1	-1.07	C49H3.6	1.35
glh-1	-2.49	srp-1	-1.06	M02H5.8	1.41
pqn-94	-2.46	cyp-34A9	-1.06	B0432.7	1.41
grl-23	-2.46	grl-16	-1.06	comt-4	1.45
C14F11.4	-2.4	gst-19	-1.06	unc-85	1.46
hex-2	-2.17	unc-52	-1.06	sft-1	1.48
perm-2	-2.14	hpo-32	-1.06	nol-10	1.5
cut-1	-2.01	R02C2.7	-1.04	vit-1	1.5
tftc-3	-1.89	ZK185.5	-1.01	cka-2	1.51
lec-8	-1.89	spr-4	-1.01	trpp-8	1.52
pud-2.1	-1.87	Y51F10.7	-1.01	vit-4	1.54
pud-1.1	-1.8	syd-9	1	csn-5	1.55
col-39	-1.72	fdps-1	1.01	trpa-2	1.58
D1054.10	-1.6	Y54E5A.5	1.02	T10G3.3	1.6
cey-2	-1.57	egg-1	1.03	rbm-3.2	1.66
H39E23.3	-1.53	dpy-30	1.03	Y69E1A.5	1.68
scl-12	-1.53	F09F7.6	1.04	ger-1	1.69
ZK6.11	-1.52	C45G9.5	1.05	T26G10.1	1.74
cbd-1	-1.51	Y104H12D.2	1.05	C09G9.1	1.78
chat-1	-1.47	rps-10	1.07	vit-5	1.82
imp-1	-1.44	F09G2.8	1.08	C39D10.8	1.88
sec-11	-1.44	Y59A8B.12	1.11	ceh-20	1.89
dpy-10	-1.42	cdf-1	1.12	ikb-1	1.91
ZK813.3	-1.4	mrpl-13	1.12	Y53C10A.6	2.02
T12D8.5	-1.34	cdk-5	1.13	fip-5	2.19
asp-9	-1.29	grl-21	1.14	vit-3	2.31
pfs-2	-1.29	ZK970.7	1.14	vps-36	2.32
F58B4.5	-1.29	mbk-1	1.14	asps-1	2.41
F10D11.6	-1.25	vti-1	1.18	rpc-25	3.01
hmt-1	-1.24	atg-16.2	1.23	Y39H10A.6	3.69
dpy-14	-1.22	nola-3	1.24	C01H6.8	3.92
ule-5	-1.19	mig-2	1.24		
dpy-17	-1.18	nemp-1	1.24		
C17G1.2	-1.18	aps-2	1.25		
R05H10.1	-1.17	ttr-35	1.26		

6.11. RNA-seq (CeGaT) - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 48h Starved

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
cdr-4	-2.46	F23D12.11	-1.5	C45B11.7	-1.21	dhs-20	-1.07
gst-37	-2.43	F18E3.12	-1.48	C12D12.1	-1.2	mdl-1	-1.07
F18E3.11	-2.42	F55G11.8	-1.48	F41C3.2	-1.2	T05F1.11	-1.06
linc-72	-2.38	C36B1.13	-1.47	gst-41	-1.19	pals-37	-1.06
gba-2	-2.29	F22B7.9	-1.46	R13A1.10	-1.19	C40H1.7	-1.06
sru-40	-2.14	F12E12.11	-1.46	hsp-12.3	-1.18	col-98	-1.05
Y2H9A.6	-2.13	clec-1	-1.45	F47B8.4	-1.18	cyp-29A2	-1.05
gsto-2	-2.13	F14F3.5	-1.43	C55A6.7	-1.17	gba-4	-1.04
col-101	-2.05	B0507.8	-1.43	linc-96	-1.17	F31E3.6	-1.04
gst-33	-2.03	eol-1	-1.43	Y71H2AM.14	-1.17	R09H10.5	-1.04
catp-3	-1.93	C06E4.3	-1.42	gst-14	-1.17	gldc-1	-1.04
gsto-1	-1.93	B0507.6	-1.41	R05D8.7	-1.17	cdr-2	-1.04
gst-12	-1.86	R08F11.4	-1.4	irg-7	-1.17	F08H9.3	-1.03
gst-8	-1.84	cyp-13A10	-1.38	C17H12.8	-1.16	cpn-3	-1.03
swt-3	-1.82	F09C8.1	-1.38	asm-3	-1.16	twk-18	-1.03
ZK742.4	-1.82	C46G7.2	-1.37	R07E3.4	-1.16	C24B5.4	-1.03
pals-2	-1.81	sod-3	-1.37	nhr-17	-1.15	hpo-34	-1.03
cest-9.1	-1.81	aat-1	-1.35	R13H4.2	-1.15	Y42G9A.3	-1.02
ddn-1	-1.75	Y9C9A.8	-1.34	ctl-1	-1.14	fbxa-54	-1.02
fbxa-182	-1.74	C53D6.11	-1.33	Y34B4A.6	-1.14	gst-16	-1.01
C55A6.4	-1.74	fat-3	-1.33	T08E11.1	-1.13	B0310.1	-1.01
gst-39	-1.71	gst-5	-1.33	ctsa-3.1	-1.13	T16G1.9	-1.01
F42C5.3	-1.7	gpx-6	-1.32	pmp-5	-1.13	C24B9.3	-1
F54H5.2	-1.67	haf-9	-1.32	C17C3.15	-1.13	cyp-33E2	-1
scav-1	-1.66	sdz-24	-1.3	sdz-8	-1.12	csc-1	1
cdr-1	-1.62	oac-14	-1.29	ugt-16	-1.11	Y46H3A.5	1
clec-143	-1.61	C33E10.8	-1.29	T05E7.1	-1.11	kbp-2	1
txt-4	-1.6	gst-30	-1.28	T07E3.4	-1.11	Y38E10A.14	1
gfi-1	-1.6	F13H8.11	-1.28	D2023.1	-1.11	phat-3	1.01
Y37A1A.2	-1.6	pgap-3	-1.28	col-176	-1.11	cpg-8	1.01
F18E3.13	-1.57	col-93	-1.27	asp-13	-1.11	nduo-6	1.01
slc-17.9	-1.56	F20G2.1	-1.27	gpx-7	-1.1	mlt-9	1.01
dpy-5	-1.56	hsp-16.2	-1.26	F19C7.1	-1.1	his-74	1.01
hsp-16.41	-1.55	ugt-31	-1.26	F44A6.5	-1.1	skr-8	1.01
T19D12.1	-1.55	pals-39	-1.26	fbxa-59	-1.1	mdf-2	1.03
cyp-25A3	-1.55	D1022.3	-1.26	F40H3.2	-1.1	col-74	1.03
gst-31	-1.54	K08D12.6	-1.24	F38E11.9	-1.09	K09F6.6	1.03
T25C12.3	-1.54	Y46G5A.20	-1.23	fbxa-61	-1.08	T05H10.3	1.03
gst-7	-1.5	T20D3.2	-1.23	K02E11.7	-1.08	K02B12.2	1.04
col-159	-1.5	pals-14	-1.23	zyg-11	-1.07	aptf-2	1.04

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
bus-8	1.04	C31H2.3	1.11	hal-3	1.2	Y14H12B.2	1.29
pri-2	1.04	dpy-7	1.11	valv-1	1.2	unc-119	1.29
col-48	1.04	T26G10.5	1.11	F22H10.2	1.2	htp-3	1.29
C25G6.4	1.04	clec-196	1.12	gld-1	1.2	Y111B2A.2	1.29
mlt-8	1.04	hcp-2	1.12	K03B4.4	1.2	T25E12.6	1.31
Y69A2AR.28	1.05	ptr-22	1.12	Y65B4BL.6	1.2	taf-11.2	1.32
F41F3.3	1.05	C08F1.10	1.12	T21C9.9	1.2	sym-1	1.32
dpy-17	1.05	kbp-5	1.12	F32H5.1	1.21	F56C9.6	1.32
him-10	1.05	col-169	1.12	T20B3.14	1.21	ins-34	1.32
cah-4	1.05	klp-18	1.13	C44B9.3	1.21	btb-6	1.32
clec-266	1.05	fzy-1	1.13	hecw-1	1.21	B0563.5	1.32
F41B4.2	1.05	cec-4	1.13	C44C1.6	1.21	lpr-3	1.32
R02C2.7	1.06	kbp-4	1.14	skr-10	1.21	C50C3.1	1.32
nspc-19	1.06	sas-5	1.14	F53F8.3	1.22	hmg-3	1.32
T11B7.2	1.06	nlp-67	1.14	ZK669.3	1.22	nspe-7	1.34
C26B9.7	1.07	cec-8	1.14	cyb-1	1.22	H42K12.3	1.34
hcp-4	1.07	F15E6.3	1.14	ced-8	1.23	wrt-10	1.36
grl-5	1.07	oma-2	1.15	F46E10.2	1.23	cutl-2	1.36
zig-4	1.07	ZC308.4	1.15	Y41D4B.26	1.23	ndfl-4	1.36
K02B7.3	1.07	B0261.7	1.15	W06B4.1	1.23	nspc-20	1.36
ZK1053.4	1.08	flh-1	1.15	ZK813.6	1.23	R144.10	1.37
wrt-2	1.08	psf-1	1.15	mcm-7	1.24	fbxc-25	1.38
F39F10.4	1.08	scl-3	1.16	F23A7.4	1.24	F18A1.7	1.38
C02E7.6	1.08	lips-15	1.16	ZK829.9	1.25	F08F3.4	1.38
ptr-16	1.08	F48G7.4	1.16	F36A2.10	1.25	DY3.8	1.39
K10H10.4	1.08	hil-5	1.16	lpr-7	1.25	F23A7.8	1.39
col-121	1.08	immt-2	1.17	col-181	1.25	ceh-83	1.39
tost-1	1.09	R05H5.3	1.17	nlp-64	1.25	air-2	1.39
F14B6.3	1.09	dlc-5	1.17	skr-15	1.26	skr-7	1.4
gnrr-3	1.09	ung-1	1.18	syp-1	1.26	gpd-4	1.4
lips-3	1.09	K08E7.5	1.18	hch-1	1.26	B0281.5	1.4
mis-12	1.1	rbm-3.1	1.18	C17E4.2	1.26	skr-14	1.4
F01D5.6	1.1	T05D4.2	1.18	ctf-8	1.27	R11.4	1.41
col-111	1.1	skr-13	1.18	cpr-4	1.27	mex-5	1.42
F35C11.5	1.1	T05F1.2	1.18	cut-2	1.27	puf-5	1.43
rmd-1	1.1	C05D9.9	1.18	orc-1	1.28	T05H10.4	1.44
col-145	1.1	C04A2.15	1.19	cdc-25.3	1.28	gld-3	1.44
grl-7	1.1	rsa-1	1.19	Y65A5A.1	1.28	C09F12.2	1.44
dsl-2	1.1	ndnf-1	1.19	C30F2.4	1.28	cey-3	1.46
F22H10.10	1.11	daf-28	1.19	C13A10.2	1.29	scl-24	1.46

Gene	log2FC	Gene	log2FC
F32D1.7	1.46	pie-1	1.78
szy-4	1.48	C08F8.3	1.79
F09C6.1	1.48	linc-6	1.8
gyg-2	1.49	T05A7.1	1.8
ins-28	1.5	capa-1	1.82
orc-3	1.5	nspc-16	1.83
htp-2	1.5	T22F3.11	1.83
him-3	1.5	spn-4	1.89
nspc-17	1.51	C05C10.5	1.91
3/3/2020	1.51	F09E10.15	1.91
gln-6	1.51	cey-2	1.91
inx-14	1.51	W05F2.3	1.91
pud-4	1.51	nasp-2	1.93
T21C9.13	1.53	nspc-18	1.96
T19H12.2	1.54	pos-1	2.06
trcs-1	1.54	C08E8.3	2.06
R09F10.8	1.55	nspc-14	2.07
C42C1.8	1.56	clec-91	2.08
ceh-49	1.57	F14H3.6	2.12
tipn-1	1.58	T07D3.9	2.15
F15D4.5	1.58	clec-88	2.16
F08F3.6	1.59	W09C3.7	2.17
sun-1	1.6	ins-20	2.21
puf-11	1.6	mex-1	2.26
fbxa-215	1.61	era-1	2.29
Y39B6A.10	1.61	clec-87	2.31
Y54G9A.5	1.62	lsy-27	2.44
nspe-1	1.63	egl-1	3.86
EEED8.3	1.67		
sip-1	1.69		
F14D7.2	1.71		
gpd-1	1.71		
cyb-2.2	1.73		
flp-11	1.73		
hil-4	1.73		
cyb-3	1.74		
Y110A2AR.1	1.74		
Y39B6A.1	1.75		
C01G6.3	1.76		
T12G3.6	1.77		

6.12. RNA-seq (CeGaT) - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 4h Fed

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
fmo-2	-2.4	Y51H7BR.4	-1.54	F14H8.4	-1.38	C49A9.3	-1.28
Y40B10B.1	-2.31	C07G1.15	-1.54	C18H9.5	-1.37	gst-33	-1.28
ugt-37	-2.2	C28H8.2	-1.51	C09D4.2	-1.37	lipl-2	-1.28
clec-143	-1.94	drh-2	-1.51	gcy-15	-1.37	W03D2.6	-1.28
txt-3	-1.85	ckr-1	-1.49	B0432.14	-1.37	T19D12.9	-1.27
cyp-35B1	-1.85	egl-47	-1.49	nduo-2	-1.36	ace-2	-1.27
F53A2.9	-1.85	T16G1.6	-1.49	ugt-18	-1.36	nduo-6	-1.27
gst-2	-1.84	F47B8.4	-1.49	T10H4.13	-1.35	Y20C6A.1	-1.27
cyp-34A9	-1.82	F25E5.4	-1.48	Y51B9A.9	-1.35	T16G1.7	-1.27
hsp-12.6	-1.81	amt-2	-1.48	dlhd-1	-1.35	W04E12.7	-1.27
Y65B4BR.1	-1.77	ntr-2	-1.48	aagr-1	-1.35	Y70G10A.3	-1.27
F11C7.7	-1.75	dop-2	-1.48	nca-2	-1.35	tyra-3	-1.26
cpr-2	-1.74	gst-8	-1.47	pgp-1	-1.34	ugt-34	-1.26
C15B12.2	-1.73	frpr-15	-1.46	F32H5.3	-1.34	K09C8.8	-1.26
mgl-2	-1.73	cyp-13A6	-1.46	C07G3.15	-1.34	asm-2	-1.26
F16B4.5	-1.71	C08F11.1	-1.45	H37A05.2	-1.33	kvs-1	-1.26
T04C12.7	-1.69	mod-1	-1.45	F44A2.3	-1.33	cyp-35A2	-1.26
C50B6.7	-1.68	mltn-1	-1.44	gst-14	-1.33	C13C4.6	-1.26
lgc-49	-1.67	exc-13	-1.44	rncs-1	-1.33	C47E12.9	-1.26
F23F12.12	-1.66	D1086.2	-1.44	F40A3.7	-1.32	fbxa-80	-1.25
str-112	-1.66	clec-186	-1.44	cyp-37B1	-1.32	unc-31	-1.25
nmr-2	-1.65	F46C5.10	-1.43	clec-198	-1.32	clec-166	-1.25
col-142	-1.64	ndfl-4	-1.43	mtl-2	-1.32	C13A10.1	-1.25
gba-2	-1.64	glt-4	-1.43	F08A7.1	-1.32	T22F3.7	-1.25
C45E5.4	-1.63	F28H7.2	-1.42	gap-1	-1.31	cest-9.1	-1.25
nlp-20	-1.63	lurp-4	-1.42	F56A12.2	-1.31	F55G11.2	-1.25
C35E7.6	-1.63	clec-41	-1.41	mps-1	-1.31	C40H1.7	-1.25
F43C11.7	-1.63	H23N18.6	-1.41	nduo-3	-1.31	Y42G9A.3	-1.25
clec-76	-1.62	F38C2.4	-1.41	Y110A2AL.9	-1.3	F58B4.5	-1.25
cyp-25A2	-1.62	C32H11.3	-1.41	Y41D4B.24	-1.3	F17B5.8	-1.25
hizr-1	-1.62	B0379.7	-1.41	clh-2	-1.3	scl-14	-1.25
del-9	-1.61	F25B3.2	-1.41	anr-27	-1.3	F41E7.20	-1.25
T16G1.4	-1.6	sprr-3	-1.41	asm-3	-1.3	glb-20	-1.24
F56H9.9	-1.59	C08F11.3	-1.4	T23B3.6	-1.29	tsp-10	-1.24
nhr-144	-1.58	frpr-4	-1.4	twk-5	-1.29	str-176	-1.24
acr-18	-1.57	fil-1	-1.39	T05A10.6	-1.29	npr-27	-1.24
cyp-32B1	-1.57	gab-1	-1.38	ZK1307.7	-1.29	C30B5.7	-1.24
spp-8	-1.55	F23D12.11	-1.38	dhs-20	-1.29	T10C6.15	-1.24
chil-22	-1.55	ttll-11	-1.38	best-5	-1.29	clec-57	-1.24
sulp-5	-1.54	fbxa-190	-1.38	fbxc-7	-1.29	irld-34	-1.24

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
Y40H7A.10	-1.24	gst-6	-1.18	Y42A5A.1	-1.14	sad-1	-1.11
C18H7.6	-1.24	dod-24	-1.18	Y62H9A.15	-1.14	K06A9.1	-1.1
ugt-55	-1.23	glt-5	-1.18	C03B1.5	-1.14	scl-5	-1.1
clec-55	-1.23	asah-2	-1.18	asah-1	-1.14	Y110A2AL.3	-1.1
C17C3.15	-1.23	F59E12.6	-1.18	xbx-5	-1.14	pcp-4	-1.1
flp-20	-1.23	mxl-3	-1.18	F25E5.8	-1.14	ZK930.2	-1.1
ptr-3	-1.23	C39D10.11	-1.18	H04M03.12	-1.14	R05A10.4	-1.1
slc-36.3	-1.23	F14D2.19	-1.18	F18E3.11	-1.14	pbo-5	-1.1
C05D12.2	-1.23	F31F7.1	-1.18	F42A10.7	-1.14	klp-13	-1.1
F20G2.5	-1.22	F22B7.9	-1.18	F47G3.1	-1.14	T19D12.1	-1.1
srv-5	-1.22	linc-72	-1.17	nlp-80	-1.14	Y6G8.2	-1.1
C31C9.6	-1.22	col-181	-1.17	ceh-79	-1.13	sulp-2	-1.1
K05F6.10	-1.22	npr-35	-1.17	spp-18	-1.13	C16D9.9	-1.1
ent-4	-1.22	F42A10.6	-1.17	F27D4.6	-1.13	F15E6.6	-1.1
T03F6.9	-1.22	pgp-11	-1.17	acr-5	-1.13	B0035.13	-1.1
C34D1.4	-1.22	F40E3.5	-1.17	lact-3	-1.13	F18E3.13	-1.1
lgc-37	-1.22	ttr-39	-1.17	F37C12.10	-1.13	mfb-1	-1.1
acr-17	-1.22	endu-2	-1.17	nhr-36	-1.13	rbf-1	-1.1
des-2	-1.22	irg-3	-1.17	glc-3	-1.13	bgal-2	-1.09
F18E3.12	-1.21	poml-3	-1.16	acr-16	-1.13	C01B9.1	-1.09
ggr-3	-1.21	ptr-13	-1.16	T15B7.1	-1.13	tsp-6	-1.09
C08F11.13	-1.21	W02H5.2	-1.16	parg-2	-1.12	T02B11.4	-1.09
gst-41	-1.21	C32D5.6	-1.16	mec-14	-1.12	cnnm-2	-1.09
far-6	-1.21	lgc-1	-1.16	ZC395.5	-1.12	osm-9	-1.09
twk-25	-1.21	C54D10.3	-1.16	nspc-18	-1.12	lite-1	-1.09
nhr-107	-1.21	pho-4	-1.16	tts-1	-1.12	C32H11.4	-1.09
mdl-1	-1.21	slc-17.3	-1.16	Y55F3BR.10	-1.12	cest-13	-1.09
daf-37	-1.21	W07A12.4	-1.16	ZK250.13	-1.12	sqst-2	-1.09
T09F5.12	-1.2	glna-1	-1.16	asp-14	-1.12	Y49E10.18	-1.09
ndnf-1	-1.2	W02D7.11	-1.16	nlp-59	-1.11	F14H3.12	-1.09
ZC239.17	-1.2	pho-6	-1.16	F22F1.3	-1.11	Y8A9A.2	-1.08
D1044.7	-1.2	dgk-5	-1.15	H06H21.8	-1.11	aex-2	-1.08
math-35	-1.2	col-151	-1.15	C47E8.3	-1.11	C54D10.5	-1.08
F09C8.1	-1.2	gba-1	-1.15	chil-13	-1.11	daf-2	-1.08
C50F4.8	-1.19	smp-2	-1.15	F59B2.13	-1.11	T03D8.7	-1.08
nhr-19	-1.19	F22D6.15	-1.15	del-5	-1.11	egl-20	-1.08
F23F12.3	-1.19	mec-1	-1.15	F52H2.3	-1.11	F25B3.4	-1.08
Y82E9BR.5	-1.19	lys-4	-1.15	T05E7.1	-1.11	nhr-21	-1.08
W06H8.6	-1.18	fozi-1	-1.15	kvs-4	-1.11	K04D7.6	-1.08
ZK1240.2	-1.18	T05C12.11	-1.14	hpo-11	-1.11	Y43F8A.1	-1.08

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T23F2.2	-1.08	clec-65	-1.04	C05C12.6	-1.01	cpar-1	1.02
C17H12.8	-1.08	B0410.3	-1.04	ceeh-2	-1.01	ceh-93	1.02
K09H9.5	-1.08	spp-6	-1.04	pcp-2	-1.01	bcl-7	1.02
ZK593.2	-1.08	daao-1	-1.04	Y69A2AR.22	-1.01	ulp-2	1.02
gtl-2	-1.08	smg-2	-1.04	ugt-16	-1.01	C25A11.2	1.02
nlp-40	-1.08	cng-1	-1.04	dop-5	-1.01	K02E10.4	1.02
ZK353.10	-1.07	lbp-2	-1.04	unc-13	-1.01	dnj-22	1.03
egl-2	-1.07	lin-14	-1.04	F45E10.2	-1.01	T19C3.2	1.03
ggr-2	-1.07	C09E7.6	-1.04	txt-8	-1.01	R07E3.6	1.03
fbxa-173	-1.07	gst-19	-1.04	R10H10.3	-1.01	F26F4.5	1.03
cdr-1	-1.07	F17C11.13	-1.04	clec-61	-1.01	hst-1	1.03
clec-52	-1.07	unc-2	-1.04	clec-54	-1.01	B0035.3	1.03
Y105C5A.17	-1.07	F35B12.10	-1.04	nhr-5	-1.01	che-14	1.03
acox-1.2	-1.07	ZK822.6	-1.04	twk-1	-1.01	unc-37	1.03
daf-12	-1.07	H11E01.2	-1.04	F13E9.8	-1.01	ent-1	1.03
F43H9.4	-1.07	mec-9	-1.03	egl-10	-1.01	C05C10.2	1.03
dop-1	-1.06	ges-1	-1.03	nhr-88	-1.01	aipl-1	1.03
C13C4.7	-1.06	srsx-34	-1.03	F23C8.14	-1.01	grl-7	1.03
F17B5.1	-1.06	C15C7.4	-1.03	C29F7.2	-1.01	pign-1	1.03
ZK822.4	-1.06	rhgf-1	-1.03	fbxa-33	-1	C44C1.1	1.03
cyp-37A1	-1.06	glb-24	-1.03	ZK673.1	-1	ZK1127.3	1.03
tom-1	-1.06	npr-8	-1.03	spp-14	-1	sys-1	1.03
H20E11.1	-1.06	R10E8.3	-1.03	clec-74	-1	tbp-1	1.03
Y38C1AA.6	-1.06	del-6	-1.03	sodh-1	-1	spcs-2	1.03
C36A4.11	-1.06	faah-3	-1.03	T16H12.9	-1	hot-6	1.03
clec-84	-1.06	F55H12.2	-1.03	F23F1.10	1	Y94H6A.3	1.04
C05E11.6	-1.06	B0361.9	-1.03	gfi-3	1	spt-4	1.04
frpr-16	-1.06	Y45F10D.2	-1.03	eri-1	1	K06H7.7	1.04
F56H9.2	-1.06	nspc-16	-1.02	C14B1.8	1.01	F25H2.4	1.04
C09B9.1	-1.05	ist-1	-1.02	wht-2	1.01	rde-8	1.04
F32D8.11	-1.05	math-34	-1.02	spd-2	1.01	mdf-1	1.04
B0524.6	-1.05	F45D3.4	-1.02	Y71G12B.25	1.01	C56E6.2	1.04
tag-89	-1.05	npr-29	-1.02	C47E8.9	1.01	mls-2	1.04
C50A2.3	-1.05	clec-53	-1.02	B0310.6	1.01	isw-1	1.04
T09B4.6	-1.05	cnnm-3	-1.02	B0336.13	1.02	sptf-1	1.04
nhr-83	-1.05	Y69H2.10	-1.02	spp-7	1.02	taf-6.1	1.04
npr-4	-1.05	C36B1.13	-1.02	fbxb-85	1.02	B0205.9	1.04
T07E3.4	-1.05	R07C12.2	-1.02	C06H2.7	1.02	aly-3	1.04
asp-3	-1.04	cest-19	-1.02	hst-2	1.02	pigk-1	1.04
gcy-28	-1.04	flp-16	-1.02	R11H6.5	1.02	tab-1	1.05

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
snr-2	1.05	F36D3.1	1.08	npp-15	1.11	F52B5.7	1.14
C55A6.1	1.05	C53A5.2	1.08	F33D4.6	1.11	mat-2	1.14
col-131	1.05	pcaf-1	1.08	lsl-1	1.11	C27C12.1	1.14
lido-12	1.05	rad-54.B	1.08	sdha-2	1.11	col-105	1.14
cec-6	1.05	fkh-2	1.08	dnj-11	1.11	Y44E3A.1	1.14
B0432.8	1.05	lig-1	1.08	E_BE45912.2	1.11	Y105C5B.19	1.14
eri-7	1.05	K05C4.7	1.08	T27A1.2	1.11	fbxa-137	1.14
C29A12.6	1.05	T13F2.6	1.08	kle-2	1.11	cyp-23A1	1.14
hrpf-1	1.05	dhhc-3	1.08	lido-1	1.11	ostb-1	1.15
erg-28	1.05	F33A8.7	1.08	zipt-1	1.11	chmp-7	1.15
gras-1	1.06	F13A7.12	1.08	osm-8	1.11	wrt-6	1.15
T05H10.3	1.06	dpy-7	1.08	C38C6.3	1.11	F55G1.6	1.15
Y17D7C.4	1.06	mbd-2	1.08	Y37E11B.6	1.11	ZK675.4	1.15
H03E18.1	1.06	F37B4.10	1.09	csn-1	1.12	phf-30	1.15
hut-1	1.06	pot-3	1.09	C30G12.4	1.12	cya-1	1.16
bkip-1	1.06	F35C11.5	1.09	ent-6	1.12	gip-2	1.16
C48B4.6	1.06	F25H9.6	1.09	alh-13	1.12	Y69H2.7	1.16
B0205.1	1.06	K10D2.5	1.09	hcf-1	1.12	K02E7.6	1.16
tag-96	1.06	gtf-2H3	1.09	F44E7.5	1.12	pigu-1	1.16
C17E4.20	1.06	prp-38	1.09	fbxa-101	1.12	swsn-6	1.16
ooc-5	1.06	C16C8.14	1.09	ifa-3	1.12	T03F1.12	1.16
F22E5.9	1.07	mans-1	1.1	F32H2.10	1.12	set-1	1.16
lin-35	1.07	rde-2	1.1	apc-11	1.12	mek-5	1.16
nspb-11	1.07	fkb-3	1.1	F32E10.5	1.12	bath-5	1.16
C09G4.4	1.07	smut-1	1.1	W09D6.1	1.13	snpc-3.4	1.16
txdc-12.2	1.07	K08E4.2	1.1	mdt-11	1.13	pgl-2	1.16
T13H5.8	1.07	R03E9.2	1.1	E01A2.2	1.13	dpy-14	1.17
cnc-6	1.07	B0285.3	1.1	chl-1	1.13	unc-59	1.17
T14B4.3	1.07	dmd-5	1.1	F33H2.3	1.13	F57B1.6	1.17
pst-2	1.07	R10H10.6	1.1	ufd-3	1.13	ccch-3	1.17
pup-3	1.07	K08B12.1	1.1	arp-6	1.13	cbn-1	1.17
tag-273	1.07	his-3	1.1	cutl-18	1.13	F55A11.4	1.17
C16C10.4	1.07	let-268	1.1	K02E7.5	1.13	hira-1	1.17
npp-5	1.07	swt-4	1.1	T01D1.8	1.13	hrpk-2	1.17
mdt-18	1.07	T12G3.4	1.1	dhfr-1	1.13	atg-10	1.17
slx-1	1.07	T04A8.8	1.1	set-5	1.13	T10E9.2	1.17
dhs-27	1.07	suds-3	1.11	cdc-6	1.13	Y54F10AM.6	1.18
emb-27	1.07	spd-5	1.11	C27F2.7	1.13	hhat-2	1.18
C25A1.1	1.08	pqn-98	1.11	C08B6.4	1.14	mett-10	1.18
rba-1	1.08	F26A1.1	1.11	parp-2	1.14	D1007.8	1.18

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
mlt-11	1.18	F49E12.12	1.21	pssy-2	1.25	ZC434.3	1.32
hex-4	1.18	mdt-6	1.21	such-1	1.25	tpk-1	1.32
Y69A2AR.28	1.18	cyn-6	1.22	taf-8	1.25	F21D9.6	1.32
rnp-5	1.18	Y51H7C.7	1.22	JC8.7	1.25	gana-1	1.32
R07B1.13	1.18	K07B1.4	1.22	rnp-2	1.25	C48B4.11	1.32
cpt-6	1.18	ZK1248.13	1.22	blos-4	1.25	npp-23	1.32
strm-1	1.18	nduf-2.2	1.22	Y105E8B.9	1.25	swd-2.1	1.32
ZK829.9	1.18	drsh-1	1.22	Y51H7C.3	1.25	R13A5.7	1.32
F13B9.2	1.19	unc-119	1.22	zwl-1	1.25	spr-3	1.33
C05D9.7	1.19	C16C8.5	1.22	pid-2	1.26	Y47G6A.14	1.33
F41G3.6	1.19	emb-1	1.22	M01D1.12	1.26	F52B5.3	1.33
Y43F4B.10	1.19	C49F5.6	1.22	npp-1	1.26	unc-85	1.33
polk-1	1.19	pcp-5	1.22	com-1	1.26	acp-2	1.33
F33H1.3	1.19	C02E7.6	1.22	C17G10.1	1.26	rsp-5	1.33
ZK973.1	1.19	Y55F3C.9	1.22	B0393.5	1.26	phf-10	1.33
K08F4.3	1.19	rsp-4	1.22	C10C5.4	1.26	C54G4.9	1.33
mrg-1	1.19	cec-3	1.22	oac-51	1.26	F52C6.2	1.34
F56A8.4	1.2	F28B3.5	1.22	C33F10.4	1.27	R05H10.3	1.34
swip-10	1.2	smo-1	1.23	drh-3	1.27	ppt-1	1.34
par-2	1.2	sucl-2	1.23	gadr-5	1.27	grl-15	1.34
hse-5	1.2	rpb-4	1.23	cpf-1	1.27	C01H6.8	1.34
B0304.4	1.2	nasp-1	1.23	cyp-31A3	1.28	K08E7.5	1.34
col-121	1.2	ppm-1.G	1.23	pafo-1	1.28	smc-5	1.34
zip-8	1.2	ari-1.4	1.23	B0310.2	1.29	inx-3	1.34
henn-1	1.2	mom-5	1.23	lst-1	1.29	sna-2	1.34
Y66D12A.16	1.2	T01C3.2	1.23	hlh-32	1.29	C11H1.7	1.34
cec-8	1.2	npp-2	1.23	aman-1	1.29	dna-2	1.34
ptr-2	1.2	R08B4.3	1.23	cutl-16	1.3	F43C11.6	1.34
abu-13	1.21	Y11D7A.9	1.23	mut-7	1.3	C27F2.10	1.35
evl-18	1.21	isy-1	1.23	cht-2	1.3	C16C8.4	1.35
rsp-6	1.21	cyn-10	1.24	R05D11.9	1.31	C56A3.8	1.35
srv-7	1.21	R12E2.8	1.24	R07E4.5	1.31	F59B2.9	1.35
C06E1.1	1.21	gbas-1	1.24	ZK688.9	1.31	K01D12.8	1.35
hlh-2	1.21	unc-39	1.24	B0511.7	1.31	galt-1	1.35
Y75B8A.31	1.21	row-1	1.24	EEED8.14	1.31	F58A4.2	1.36
Y34D9A.7	1.21	him-8	1.24	cutl-28	1.31	wrt-4	1.36
acs-3	1.21	lin-42	1.24	F09E10.6	1.31	tofu-5	1.36
cdk-4	1.21	ztf-11	1.24	ZC449.2	1.31	hil-2	1.36
nfyc-1	1.21	unc-71	1.24	ptr-16	1.31	F44B9.8	1.36
cep-1	1.21	his-60	1.25	C27H6.9	1.32	F09F9.2	1.36

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
B0001.2	1.36	ego-1	1.4	F21H7.3	1.45	W05F2.6	1.51
fbxb-72	1.36	mlh-1	1.4	wrt-10	1.46	tyms-1	1.52
fbxc-51	1.36	pes-5	1.4	rnh-2	1.46	npp-22	1.52
div-1	1.37	vang-1	1.41	mre-11	1.46	C45G3.3	1.52
noah-1	1.37	Y41D4A.3	1.41	C10B5.1	1.46	Y52B11A.8	1.52
F33E2.5	1.37	lem-3	1.41	mam-5	1.46	C50F4.6	1.52
tag-63	1.37	mom-1	1.41	F21D5.1	1.47	pph-4.2	1.52
his-61	1.37	rfc-2	1.41	osr-1	1.47	cdc-25.1	1.52
F11E6.4	1.37	Y69A2AR.21	1.41	B0511.11	1.47	pole-4	1.52
F54D5.9	1.37	T28C6.10	1.41	C09B8.5	1.47	Y65A5A.1	1.53
mrt-1	1.37	cye-1	1.41	M03B6.3	1.47	Y39B6A.42	1.53
bub-3	1.37	pen-2	1.41	pig-1	1.48	knl-2	1.53
fbxb-7	1.37	W04A8.6	1.41	C33E10.3	1.48	T09F5.1	1.54
bath-1	1.37	Y73E7A.8	1.42	ZK1127.13	1.48	F09G2.8	1.54
lin-53	1.38	C50F4.12	1.42	C28C12.12	1.48	C44H9.7	1.54
mltn-9	1.38	czw-1	1.42	damt-1	1.48	F54D10.5	1.55
npp-18	1.38	asb-1	1.43	F55A11.8	1.49	Y53F4B.9	1.55
C16C8.16	1.38	R07B7.10	1.43	C13G5.2	1.49	C16C8.11	1.55
ani-1	1.38	ceh-36	1.43	set-10	1.49	T03F6.3	1.55
C02F4.4	1.38	zyg-1	1.43	C36B1.14	1.49	hasp-1	1.55
xpo-2	1.39	C56G2.15	1.43	kca-1	1.49	cuti-1	1.55
R04B3.2	1.39	T26A5.8	1.43	hmg-12	1.49	F47B8.5	1.55
inft-2	1.39	dpy-10	1.43	B0035.18	1.49	cyk-4	1.55
eme-1	1.39	coh-4	1.43	mcm-6	1.49	fbxb-88	1.55
mig-32	1.39	let-49	1.43	prg-1	1.49	Y38A10A.7	1.56
mam-3	1.39	Y106G6D.1	1.43	hcp-4	1.49	hcp-3	1.56
hmg-20	1.39	C13F10.7	1.44	zipt-7.1	1.49	T22C8.4	1.56
fkb-7	1.39	dtmk-1	1.44	Y38A10A.2	1.49	gei-14	1.56
C02F5.13	1.39	ssna-1	1.44	nstp-3	1.5	F12F6.7	1.56
grl-5	1.39	F25E5.2	1.44	lin-54	1.5	C32D5.12	1.57
W04H10.2	1.39	Y41D4B.6	1.44	rbbp-5	1.5	ZK616.5	1.57
F46F11.7	1.39	ska-3	1.44	metl-9	1.5	pola-1	1.57
C48B6.9	1.39	clec-266	1.44	ekl-5	1.5	F54H12.5	1.57
set-9	1.39	ect-2	1.44	tmem-17	1.5	msh-6	1.57
tofu-1	1.39	K11H12.5	1.45	erh-1	1.5	tim-1	1.57
wago-4	1.4	zeel-1	1.45	apc-2	1.5	F36H9.5	1.58
C14A4.9	1.4	imp-1	1.45	got-2.1	1.51	bmk-1	1.58
htz-1	1.4	ZK1098.3	1.45	F39F10.4	1.51	Y95D11A.3	1.58
B0212.3	1.4	dpy-2	1.45	D1046.2	1.51	F39G3.2	1.58
F59B2.8	1.4	spdl-1	1.45	T07C4.3	1.51	Y106G6H.16	1.58

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
hrde-2	1.58	grl-11	1.64	Y111B2A.3	1.71	unc-61	1.79
tag-342	1.58	K11H12.11	1.64	ZK829.3	1.71	tipn-1	1.79
fbxa-107	1.58	cpg-3	1.64	dao-2	1.71	C17E7.13	1.8
D2030.8	1.59	C39E9.12	1.64	F07H5.10	1.71	knl-3	1.8
C36B1.11	1.59	Y37E11AL.3	1.64	cut-6	1.71	deps-1	1.8
C42D4.13	1.59	top-2	1.65	W01C9.1	1.71	gla-3	1.8
rnp-8	1.59	Y54G2A.76	1.66	wrt-1	1.72	bath-15	1.8
cutl-9	1.59	F48A11.4	1.66	rrn-3.1	1.72	rod-1	1.8
F59G1.8	1.59	glh-3	1.66	C35A5.11	1.72	flp-11	1.81
rpa-1	1.59	Y49E10.4	1.66	thk-1	1.72	T22H2.4	1.81
F18C5.9	1.59	cec-7	1.66	K07A1.1	1.72	pri-1	1.81
cec-4	1.59	rmh-1	1.66	sgo-1	1.72	ceh-40	1.81
fubl-4	1.6	C07E3.10	1.66	ced-3	1.72	zim-3	1.81
lam-3	1.6	F52G3.5	1.66	C40A11.3	1.72	cks-1	1.81
cav-1	1.6	F15H10.8	1.67	brc-1	1.72	9/1/2020	1.82
F01F1.11	1.6	crn-1	1.67	fbxb-78	1.73	Y49F6B.9	1.82
T04D3.5	1.6	otub-3	1.67	hrde-1	1.73	bub-1	1.82
his-59	1.61	cutl-17	1.67	ZK287.4	1.73	B0365.9	1.82
mei-1	1.61	adal-1	1.67	erh-2	1.73	lips-15	1.82
dpl-1	1.61	wdr-48	1.67	B0041.8	1.73	orc-4	1.82
his-32	1.61	sygl-1	1.68	R11G1.7	1.74	sex-1	1.82
pal-1	1.61	tdpt-1	1.68	ntp-1	1.74	ces-2	1.83
dpy-3	1.61	gln-5	1.68	Y48G1A.2	1.74	brd-1	1.83
cpg-4	1.61	F13A7.14	1.68	hal-3	1.74	ugt-57	1.83
B0205.4	1.61	atf-8	1.68	Y73F8A.13	1.75	cdc-25.2	1.84
Y53G8AR.6	1.62	aly-2	1.68	Y75B8A.16	1.75	nemp-1	1.84
cdt-1	1.62	icp-1	1.69	plk-2	1.75	R57.2	1.84
tcab-1	1.62	rfc-3	1.69	C04A11.2	1.75	wdr-5.3	1.84
C48B4.9	1.62	ndc-80	1.69	F30A10.2	1.76	Y45G5AM.5	1.84
D1044.1	1.62	fbxb-77	1.69	taf-11.2	1.76	dnsn-1	1.85
bus-12	1.62	daf-18	1.69	fkb-5	1.76	skr-17	1.85
ssup-72	1.63	ZK813.6	1.69	Y37A1B.7	1.77	plk-1	1.85
kbp-3	1.63	pid-3	1.7	pgph-3	1.77	chk-1	1.85
dvc-1	1.63	mes-4	1.7	F44E2.10	1.77	T28A8.4	1.85
rrn-3.56	1.63	T03G6.1	1.7	gmn-1	1.78	hcp-1	1.86
C39B5.2	1.63	Y58A7A.2	1.7	nos-1	1.78	gpaa-1	1.86
trt-1	1.63	gpr-2	1.7	clec-196	1.78	C05D12.4	1.86
eaf-1	1.63	F23A7.4	1.7	dhs-11	1.78	F59A6.5	1.86
F36F12.1	1.63	T26C12.3	1.7	neg-1	1.79	hsp-12.1	1.86
F45F2.11	1.64	D1081.6	1.7	fncm-1	1.79	sas-6	1.87

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
dsh-2	1.87	aspm-1	1.94	hal-2	2.04	Y23H5B.8	2.15
K01D12.1	1.87	msh-2	1.94	cdk-1	2.04	let-99	2.15
T28C6.3	1.87	scc-1	1.94	atz-1	2.04	fbxa-206	2.15
C40A11.4	1.88	prom-1	1.94	F46F3.3	2.04	fbxb-45	2.15
inx-2	1.88	C26B9.7	1.94	Y17G9B.2	2.05	T05C1.3	2.15
chaf-2	1.88	lsd-1	1.94	Y68A4B.3	2.05	elo-4	2.15
Y97E10AR.4	1.88	iff-1	1.94	him-3	2.05	Y11D7A.5	2.16
D1014.5	1.88	F13D12.5	1.95	Y64H9A.2	2.05	hhat-1	2.16
txdc-12.1	1.89	T04D3.1	1.95	Y106G6H.6	2.06	sld-2	2.16
mis-12	1.89	edg-1	1.95	F58G11.3	2.06	F07H5.13	2.17
EEED8.15	1.89	ZC449.1	1.95	syp-1	2.06	kbp-5	2.17
F52B5.2	1.89	Y41D4B.14	1.96	dsl-3	2.07	cyk-7	2.17
C14F11.6	1.89	chaf-1	1.96	nxf-2	2.07	meg-3	2.17
F54D5.2	1.89	cdl-1	1.96	mcm-5	2.08	rnr-1	2.17
F37A4.3	1.89	psf-3	1.96	B0034.7	2.08	K03H1.7	2.17
T02C1.1	1.89	rmd-1	1.97	set-31	2.08	tpxl-1	2.17
pole-1	1.9	K05F6.4	1.97	W02B8.2	2.08	D2030.7	2.17
F27C1.4	1.9	mcm-10	1.97	W03C9.2	2.08	skr-9	2.18
jmjd-3.2	1.9	R12C12.10	1.97	F40F11.3	2.09	exo-1	2.18
F58H1.2	1.9	bgnt-1.2	1.98	ceh-86	2.09	tofu-7	2.18
D1081.7	1.9	him-10	1.98	egg-6	2.1	srpr-2.2	2.18
T26A5.2	1.91	fbxb-24	1.98	fbxb-75	2.1	T26C5.2	2.18
F01D4.5	1.91	K07A1.17	1.99	knl-1	2.1	Y4C6B.1	2.18
zhp-3	1.91	sul-1	1.99	F46E10.2	2.1	T11B7.1	2.18
F44F1.6	1.91	air-2	1.99	K08B4.2	2.1	nhr-127	2.18
btb-19	1.91	F30F8.1	1.99	klc-1	2.1	fbxb-53	2.18
glf-1	1.91	pash-1	2	cup-15	2.11	rad-51	2.19
pgl-3	1.91	mans-4	2	snrp-40.2	2.11	C01G6.9	2.19
hcp-6	1.92	F08F8.4	2.01	C41D11.9	2.11	fbxc-44	2.19
F59A3.12	1.92	fbxb-84	2.01	fem-3	2.12	rrn-2.1	2.19
efl-1	1.92	lpr-1	2.01	C24H12.1	2.12	set-32	2.19
Y46G5A.8	1.92	ZK643.2	2.02	C35E7.3	2.12	dscc-1	2.19
fbn-1	1.92	polh-1	2.02	B0001.7	2.13	C06E7.88	2.19
syp-2	1.92	ins-34	2.03	ctf-8	2.13	fbxc-32	2.2
ima-2	1.92	hcp-2	2.03	klp-18	2.13	F36H5.4	2.2
Y73B3A.1	1.92	hmbx-1	2.03	C08F1.10	2.13	egl-1	2.2
sdz-38	1.92	C35E7.5	2.03	bath-10	2.13	pcmd-1	2.21
Y47G6A.31	1.93	rsa-2	2.03	C50C3.1	2.13	T10E9.8	2.21
K08H2.4	1.93	dsb-2	2.04	rfc-4	2.13	Y47D3A.1	2.21
pif-1	1.93	skr-2	2.04	F49D11.6	2.13	Y71F9AL.7	2.21

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ani-2	2.22	swah-1	2.3	tost-1	2.43	spsb-2	2.56
cmt-1	2.22	spp-13	2.31	T08G5.3	2.43	mcm-7	2.57
sas-5	2.22	T06A1.1	2.31	ctf-4	2.44	fbxa-210	2.57
Y82E9BR.17	2.22	hpo-40	2.31	Y75B8A.18	2.44	sdz-30	2.58
W07G4.1	2.22	F19B10.10	2.31	flh-1	2.44	Y102A11A.5	2.58
T16G12.4	2.23	Y106G6D.2	2.32	kbp-1	2.44	wee-1.3	2.58
gcna-1	2.23	fbxa-83	2.33	zen-4	2.45	mct-5	2.59
bir-2	2.23	F11E6.7	2.33	T28A8.5	2.45	btb-11	2.59
psf-1	2.24	dsl-6	2.33	K07F5.12	2.45	cutl-2	2.59
T05B9.1	2.24	C55B7.11	2.34	oef-1	2.45	cyn-9	2.59
cdc-7	2.24	air-1	2.34	fbxc-18	2.46	his-74	2.59
Y46G5A.7	2.25	H04M03.3	2.34	fbxb-65	2.47	orc-1	2.6
gpd-4	2.25	mcm-3	2.35	C27B7.5	2.47	F56F4.8	2.61
Y41D4B.26	2.25	tofu-6	2.35	san-1	2.48	orc-3	2.62
alg-5	2.25	csc-1	2.36	F54F7.6	2.48	F08F3.6	2.62
pgl-1	2.25	F10E9.7	2.36	orc-5	2.48	Y54G11A.3	2.63
C14B1.9	2.25	snpc-1.2	2.37	sdz-4	2.48	C29A12.1	2.63
H23N18.5	2.26	bath-41	2.37	pcn-1	2.48	ZC434.8	2.63
K02B12.2	2.26	fbxc-25	2.37	F54D5.5	2.49	rsa-1	2.64
puf-8	2.26	exo-3	2.38	syx-4	2.49	aptf-4	2.64
mcm-4	2.26	F56C9.3	2.38	F48E3.6	2.49	srpr-2.1	2.64
C37C3.9	2.27	C38D4.4	2.38	H04D03.2	2.5	C17E4.2	2.64
F33E11.2	2.27	ucr-2.3	2.39	Y39G10AL.1	2.5	C48B4.7	2.65
lrr-1	2.27	htp-1	2.39	pigv-1	2.51	F15B10.3	2.65
htp-2	2.27	fbxb-100	2.39	R144.10	2.51	egg-3	2.66
W04A8.1	2.27	W06D11.1	2.4	R05H5.3	2.51	fbxc-29	2.66
T10B11.8	2.27	skr-8	2.4	rbm-3.1	2.51	pch-2	2.66
spo-11	2.27	mut-2	2.4	mdf-2	2.51	T16G12.8	2.66
pri-2	2.28	flh-3	2.4	T22D1.5	2.52	M03B6.4	2.67
capg-2	2.28	C47F8.1	2.4	ogr-2	2.52	dut-1	2.67
F56D2.2	2.28	fbxb-3	2.4	R11.4	2.53	eri-5	2.68
rnr-2	2.28	vet-2	2.4	ung-1	2.53	fog-2	2.68
linc-13	2.28	nop-1	2.4	T05H10.4	2.53	F56F11.4	2.68
kbp-4	2.28	C24H10.3	2.41	F46G11.6	2.53	ceh-83	2.68
gpr-1	2.29	apc-10	2.41	skpt-1	2.53	aptf-2	2.69
Y51F10.2	2.29	kbp-2	2.41	syp-5	2.54	Y14H12B.2	2.69
mcm-2	2.29	D2005.4	2.42	C01G8.1	2.54	cyb-3	2.7
htp-3	2.29	ttr-50	2.42	dsl-2	2.56	fbxb-54	2.7
hlh-3	2.29	toe-2	2.43	mom-2	2.56	fbxb-104	2.71
ZK1053.4	2.3	B0304.2	2.43	mbtr-1	2.56	mesp-1	2.71

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
immt-2	2.72	C44B9.3	2.88	F14B6.3	3.11	oma-2	3.61
C01G6.3	2.73	T25E12.6	2.89	cyb-2.2	3.12	F14D7.2	3.63
skr-10	2.74	K04G2.10	2.89	sdz-28	3.12	trcs-1	3.77
C08F1.6	2.74	T05D4.2	2.89	era-1	3.14	clec-87	3.78
T28A8.3	2.74	fbxb-35	2.89	nhr-2	3.14	C31H1.8	4.19
Y42H9B.3	2.75	Y71F9AL.6	2.91	C08F8.3	3.16	puf-5	4.23
cdc-25.3	2.75	hpr-17	2.92	Y110A2AR.1	3.17		
W04A8.5	2.75	syp-6	2.92	fbxa-215	3.17		
pid-4	2.77	hil-5	2.93	pie-1	3.18		
cyb-1	2.77	B0393.3	2.94	glp-1	3.18		
zim-1	2.77	cpg-1	2.94	T19H12.2	3.19		
F23A7.8	2.77	gpd-1	2.94	R04D3.2	3.2		
C06E2.5	2.78	B0281.5	2.95	F14H3.6	3.2		
xnd-1	2.78	ify-1	2.96	pot-2	3.21		
fbxb-15	2.78	F32D1.7	2.96	gld-3	3.22		
C42C1.8	2.78	sip-1	2.97	F56C9.6	3.23		
fzy-1	2.78	3/3/2020	2.98	szy-4	3.25		
Y43B11AL.1	2.79	ZC308.4	2.98	W05F2.3	3.25		
F15A4.2	2.79	gln-6	2.99	Y39B6A.10	3.27		
C01B12.8	2.8	inx-14	3	sdz-14	3.27		
hil-4	2.8	daz-1	3.01	F53F8.3	3.28		
skr-7	2.8	cbd-1	3.02	D2005.7	3.29		
gna-2	2.81	cey-2	3.02	sun-1	3.29		
fbxb-66	2.81	ced-8	3.03	puf-11	3.3		
vet-1	2.82	skr-15	3.03	EEED8.3	3.31		
Y110A7A.15	2.82	btb-6	3.03	vet-6	3.32		
Y54G9A.5	2.82	Y73B6BL.23	3.04	nasp-2	3.33		
psf-2	2.82	T12G3.6	3.04	cey-3	3.34		
gyg-2	2.83	C40A11.2	3.05	mei-2	3.36		
C03D6.9	2.83	T05F1.2	3.05	clec-88	3.36		
hmg-3	2.84	puf-3	3.05	ceh-49	3.39		
Y111B2A.2	2.84	mex-5	3.06	fbxb-95	3.4		
toca-2	2.84	R09F10.8	3.06	mex-1	3.41		
set-22	2.86	T21C9.13	3.07	pos-1	3.41		
gld-1	2.86	zif-1	3.07	spn-4	3.46		
skr-13	2.86	memi-2	3.07	C05C10.5	3.48		
wago-1	2.86	skr-14	3.09	DY3.8	3.48		
F18A1.7	2.86	W06B4.1	3.09	lsy-27	3.52		
Y59A8B.12	2.87	ZC155.4	3.1	Y52E8A.2	3.54		
B0261.7	2.88	Y71A12B.11	3.1	clec-91	3.59		

6.13. Proteome (TMT) - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 48h Starved

Protein	log2FC	Protein	log2FC	Protein	log2FC	Protein	log2FC
ilys-5	-4.79	tba-4	-2.07	F28B4.3	-1.53	spin-1	-1.27
Y62H9A.5	-4.79	F09C8.1	-2.06	mct-2	-1.52	F13D12.5	-1.27
Y59E9AR.1	-4.66	anp-1	-2.03	ifc-1	-1.52	C39D10.8	-1.26
ule-5	-4.66	F57F5.1	-2	pud-2.1	-1.51	W10C8.5	-1.26
perm-4	-4.44	bigr-1	-1.98	T01D1.4	-1.5	C23H3.2	-1.26
cbd-1	-4.01	nrf-6	-1.96	dod-19	-1.5	rnp-1	-1.24
folt-2	-3.92	R193.2	-1.94	Y37H2A.14	-1.49	phy-2	-1.23
ZK813.3	-3.75	F21C10.9	-1.92	T25C12.3	-1.49	AC3.5	-1.23
D1054.10	-3.72	F58B4.5	-1.89	ldp-1	-1.48	F25B4.7	-1.21
R10H10.3	-3.52	D1086.3	-1.89	sptl-3	-1.48	txdc-12.2	-1.21
perm-2	-3.5	argk-1	-1.89	gst-27	-1.46	fpn-1.1	-1.19
cey-2	-3.39	elo-1	-1.88	hpo-40	-1.46	T10G3.3	-1.19
glh-1	-3.37	fmo-5	-1.88	gfi-1	-1.46	C23H5.8	-1.18
K12H4.7	-3.36	spp-3	-1.85	ugt-16	-1.45	pgp-6	-1.17
hrg-7	-3.3	F35C8.5	-1.84	Y67D2.7	-1.45	ZK185.5	-1.17
T28F3.8	-3.27	poml-3	-1.83	Y58A7A.1	-1.44	ost-1	-1.16
ule-1	-3.23	rhr-1	-1.79	ugt-22	-1.44	F47B8.2	-1.15
pgp-1	-3.03	Y7A5A.1	-1.79	Y54F10AM.8	-1.44	imp-1	-1.15
F17E9.5	-3.03	asp-13	-1.76	hach-1	-1.43	acp-6	-1.15
C14F11.4	-2.96	aagr-2	-1.76	gldc-1	-1.41	Y16B4A.2	-1.14
lec-8	-2.94	pgp-3	-1.75	F55G11.8	-1.39	mlt-7	-1.14
dct-16	-2.9	sur-5	-1.75	pod-2	-1.39	gfat-1	-1.14
grl-23	-2.67	asp-1	-1.74	asns-2	-1.38	ifp-1	-1.14
col-92	-2.66	C17G1.2	-1.72	lron-7	-1.36	ech-6	-1.13
F54E2.1	-2.66	ugt-62	-1.72	coq-1	-1.35	K12B6.9	-1.13
Y51F10.7	-2.59	F19C7.1	-1.72	irg-7	-1.35	R09H10.5	-1.13
far-2	-2.58	lec-10	-1.66	spp-2	-1.34	hpo-34	-1.13
madd-3	-2.52	Y75B8A.14	-1.65	pud-1.1	-1.33	T21H3.1	-1.12
cey-3	-2.5	hphd-1	-1.64	cdr-4	-1.33	pept-1	-1.11
lys-4	-2.48	W05F2.3	-1.64	R10F2.4	-1.33	T07D3.9	-1.1
ZK6.11	-2.39	immp-1	-1.63	Y34B4A.6	-1.32	Y23H5B.6	-1.1
acdh-1	-2.38	Y34B4A.9	-1.62	Y14H12B.1	-1.29	sago-2	-1.1
ctsa-1.2	-2.31	C34H4.2	-1.6	oxy-4	-1.29	pmt-2	-1.1
ugt-26	-2.28	pcp-4	-1.58	C53D5.5	-1.29	acdh-9	-1.09
csr-1	-2.24	LLC1.2	-1.57	aqp-7	-1.29	wago-1	-1.09
cpr-4	-2.17	asp-6	-1.56	T16G12.1	-1.29	mpc-1	-1.09
cyp-13A5	-2.14	nuc-1	-1.55	spp-5	-1.29	zipt-15	-1.08
clec-50	-2.1	let-767	-1.55	glh-2	-1.29	timm-23	-1.08
F17E9.4	-2.08	W04B5.3	-1.54	clec-63	-1.28	C05C10.3	-1.08
F56C9.7	-2.08	dhs-25	-1.54	pmp-5	-1.27	sptl-1	-1.07

Protein	log2FC	Protein	log2FC	Protein	log2FC
Y54E2A.4	-1.07	col-121	1.1	ZK863.8	1.43
asp-5	-1.06	Y55D9A.2	1.1	F13D11.3	1.45
leo-1	-1.06	dpy-30	1.12	nlp-24	1.47
cpn-1	-1.06	Y52E8A.3	1.12	fbn-1	1.47
ifc-2	-1.06	hil-2	1.13	F36H9.7	1.48
rop-1	-1.05	lron-2	1.13	K02F3.9	1.54
fmo-3	-1.05	hsp-16.11	1.13	cht-1	1.61
let-716	-1.05	grd-13	1.14	Y53F4B.23	1.64
iff-2	-1.04	vps-60	1.15	F43C9.2	1.67
soap-1	-1.03	E04F6.9	1.15	hsp-16.2	1.67
nog-1	-1.02	F10D11.6	1.15	scl-3	1.67
C15A11.7	-1.02	F17H10.2	1.16	Y44A6D.2	1.68
col-159	-1.02	msa-1	1.16	slc-36.5	1.7
dpy-18	-1.02	rgs-3	1.16	cut-3	1.71
F09B12.3	-1.01	C33A12.4	1.17	C18H7.1	1.73
C35A5.11	-1.01	nlp-31	1.18	T03F1.11	1.79
alh-8	-1.01	his-35	1.21	hmg-3	1.81
nas-11	-1	clec-266	1.21	ttr-5	1.83
F56C9.8	1.02	nep-1	1.22	hsp-16.48	1.93
rpi-2	1.02	hil-3	1.23	E02C12.9	1.93
pdl-1	1.02	F55F8.3	1.24	ensa-1	1.97
C25F9.11	1.02	lpr-3	1.24	C01G6.3	1.99
F53E10.1	1.03	ipla-2	1.25	hil-1	2.01
clec-13	1.04	plpr-1	1.25	dpy-10	2.04
F59B10.3	1.04	sod-4	1.27	T10B10.3	2.04
exc-13	1.04	sod-5	1.27	F14B4.1	2.2
rnr-2	1.04	C15C7.7	1.28	grl-16	2.31
C06A5.3	1.04	F58H1.7	1.28	M01H9.3	2.36
tni-4	1.05	dsl-3	1.29	Y53C10A.6	2.6
oig-3	1.05	ttr-23	1.31	C53B7.3	2.61
hmg-1.1	1.05	T10H9.8	1.32	Y39B6A.5	2.91
nlt-1	1.05	cwc-15	1.33	dpy-14	2.95
C03G6.17	1.05	nhr-48	1.35	dpy-17	3.06
W10C8.4	1.06	cnnm-1	1.38	col-158	3.25
fkh-7	1.07	T11B7.5	1.38	col-39	3.42
ttr-33	1.08	F07C3.2	1.38	fipr-22	4.23
F26G1.2	1.08	T04C9.1	1.39	H39E23.3	7.15
snu-23	1.1	D2063.1	1.39		
F29B9.5	1.1	far-7	1.4		
ttr-16	1.1	gst-34	1.41		

6.14. Proteome (TMT) - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 4h Fed

Protein	log2FC	Protein	log2FC	Protein	log2FC
scl-11	-2.88	col-92	1.07	far-3	2.03
scl-12	-2.05	B0001.8	1.07	vps-36	2.16
smr-1	-1.85	F53F4.16	1.08	asps-1	2.3
mec-9	-1.68	fkb-5	1.09	Y67D2.7	2.34
asp-9	-1.65	Y104H12D.2	1.12	rpc-25	2.46
exp-2	-1.64	nhl-1	1.12	fip-5	2.74
madd-3	-1.61	syd-9	1.14	Y39H10A.6	3.49
sec-11	-1.51	vps-18	1.15	C01H6.8	4.3
hmg-3	-1.48	Y45F10B.13	1.16		
T04F8.7	-1.48	grd-13	1.16		
tag-65	-1.47	Y48C3A.20	1.17		
gst-19	-1.37	F53B1.8	1.17		
R02C2.7	-1.37	comt-4	1.17		
lars-2	-1.36	bigr-1	1.18		
pqbp-1.1	-1.34	cdk-5	1.19		
rpi-2	-1.32	F39H11.1	1.19		
clh-2	-1.29	nemp-1	1.2		
pqn-94	-1.21	C39D10.8	1.21		
sir-2.4	-1.21	ceh-20	1.22		
F55G1.9	-1.18	F20G2.1	1.25		
rfc-2	-1.17	F44G4.1	1.25		
bli-4	-1.16	mbk-1	1.26		
F13D12.5	-1.12	Y10G11A.1	1.27		
wrb-1	-1.1	lact-3	1.29		
zipt-15	-1.1	ger-1	1.3		
cubn-1	-1.09	Y48A6C.4	1.32		
ipla-2	-1.08	nol-10	1.33		
T04C9.1	-1.08	F41D9.2	1.36		
F52H2.1	-1.07	atg-16.2	1.36		
R151.6	-1.07	rbm-3.2	1.38		
H39E23.3	-1.03	csn-5	1.41		
ZK863.8	-1.02	eif-2Balpha	1.42		
bcs-1	-1.02	F09F7.6	1.46		
B0379.6	-1.02	T10B10.3	1.49		
C49H3.6	1.01	aps-2	1.58		
chd-3	1.02	trpp-8	1.59		
W01B11.6	1.03	C09G9.1	1.6		
nola-3	1.04	Y53C10A.6	1.62		
Y15E3A.4	1.04	T26G10.1	1.63		
C23H3.2	1.05	ikb-1	1.63		
M02H5.8	1.06	trpa-2	1.92		
cogc-2	1.07	B0432.7	1.93		

6.15. RNA-seq (CeGaT) - 4h Fed vs 48h Starved - N2 (wild-type)

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T22F3.11	-6.5	K02B7.3	-2.88	col-14	-2.61	clec-80	-2.42
Y39B6A.1	-6.14	E01G6.1	-2.87	idh-1	-2.6	misc-1	-2.41
T07D3.9	-5.54	ugt-41	-2.86	clec-180	-2.6	clx-1	-2.41
R02C2.7	-4.99	bca-1	-2.85	pgp-14	-2.59	sodh-1	-2.41
cpr-4	-4.62	mua-6	-2.84	Y60C6A.2	-2.59	B0403.5	-2.41
C23G10.11	-4.48	col-33	-2.84	T04F8.8	-2.58	daao-1	-2.4
W10C8.5	-4.08	col-145	-2.83	C49H3.16	-2.58	Y105C5B.5	-2.4
F46F2.3	-3.97	col-109	-2.82	phg-1	-2.57	alh-5	-2.4
nlp-30	-3.79	zig-4	-2.81	F57F4.4	-2.55	tyr-2	-2.39
gst-26	-3.68	Y37H2A.14	-2.81	F55H12.4	-2.54	ZK829.9	-2.39
F46C5.1	-3.64	Y47H9C.1	-2.81	pqn-74	-2.54	abu-12	-2.39
mdh-2	-3.47	K02G10.15	-2.8	Y37D8A.3	-2.53	C18H7.11	-2.38
irg-4	-3.43	nas-38	-2.79	cut-2	-2.53	R03C1.1	-2.37
F35B3.4	-3.41	acn-1	-2.79	F09E10.15	-2.53	F13D12.9	-2.37
F22B5.4	-3.39	asns-2	-2.77	aqp-7	-2.53	F09E10.1	-2.36
acs-2	-3.37	fbp-1	-2.77	Y22D7AL.10	-2.52	F07H5.8	-2.35
C35C5.8	-3.35	nlp-34	-2.77	M02G9.1	-2.51	C31H2.4	-2.35
hphd-1	-3.34	C23H5.8	-2.76	F53F1.4	-2.51	cnc-4	-2.35
T19B10.2	-3.31	ugt-34	-2.75	math-45	-2.5	tag-10	-2.35
cah-4	-3.31	icl-1	-2.75	gst-28	-2.48	kat-1	-2.34
folt-2	-3.24	clec-48	-2.75	M03F8.1	-2.48	mec-7	-2.34
lon-1	-3.22	col-97	-2.73	F20B10.3	-2.48	W08E12.3	-2.34
F17A9.5	-3.19	col-166	-2.73	lec-8	-2.48	T06A4.1	-2.34
ilys-5	-3.13	F41E6.5	-2.73	F21C10.9	-2.47	ptr-2	-2.33
F22H10.2	-3.09	nspe-1	-2.72	ldh-1	-2.47	F38B2.4	-2.33
ZK1320.9	-3.07	C09B8.4	-2.72	ttr-2	-2.47	Y106G6D.1	-2.33
col-113	-3.06	kreg-1	-2.71	R09E12.9	-2.47	T10E10.4	-2.33
C45B2.2	-3.05	pho-11	-2.71	grl-21	-2.47	skpo-2	-2.33
C42D4.3	-3.05	nlp-77	-2.71	C01G10.15	-2.46	K01A6.4	-2.33
best-1	-3.04	fmo-3	-2.7	T06D8.10	-2.46	col-144	-2.32
pqn-26	-3.04	nspe-7	-2.68	F15D3.6	-2.46	ddo-2	-2.32
nlp-31	-3.02	ZK1037.6	-2.68	T20B6.3	-2.45	acdh-1	-2.32
col-48	-3.02	hacd-1	-2.68	ech-9	-2.44	F56D2.3	-2.32
F32D8.11	-3.02	F15B9.6	-2.68	srg-31	-2.44	pqn-22	-2.3
F40E10.5	-3.01	dod-19	-2.67	ptr-22	-2.44	F16H11.1	-2.3
F49C12.7	-3.01	K10H10.4	-2.66	F10D11.6	-2.44	col-111	-2.3
valv-1	-3	F59A7.2	-2.66	daf-36	-2.43	C54D2.1	-2.29
spp-20	-2.98	E04F6.6	-2.66	ttr-31	-2.42	ndnf-1	-2.29
dct-16	-2.93	ZK6.11	-2.65	pqn-63	-2.42	K08D8.3	-2.29
B0024.4	-2.91	lbp-6	-2.61	D1054.9	-2.42	F44E5.4	-2.28
C50F7.5	-2.89	F13E9.14	-2.61	act-5	-2.42	C08F11.1	-2.28

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F13D12.3	-2.28	T22F3.10	-2.16	dex-1	-2.09	lgx-1	-2
lys-3	-2.28	nhr-137	-2.16	F20G2.2	-2.09	T02G5.7	-2
pqn-60	-2.28	cpr-3	-2.16	Y65B4BL.1	-2.09	nas-30	-2
hsp-17	-2.28	ptr-1	-2.16	ugt-19	-2.08	lgc-33	-2
lec-6	-2.27	cyn-17	-2.16	ttr-15	-2.08	rde-4	-2
T24C12.4	-2.26	ugt-33	-2.16	srh-2	-2.08	nspe-5	-2
anmt-3	-2.26	hpo-6	-2.15	cdh-5	-2.08	irg-5	-1.99
grl-4	-2.26	nduo-6	-2.15	col-182	-2.07	C55A6.12	-1.99
F41E6.11	-2.26	ifd-2	-2.15	dpy-1	-2.07	grl-6	-1.99
T26C5.4	-2.26	Y57G11C.42	-2.15	grd-14	-2.07	smd-1	-1.99
lbp-5	-2.25	pqn-32	-2.15	lron-2	-2.06	ttr-38	-1.98
col-169	-2.25	let-754	-2.14	era-1	-2.06	col-54	-1.98
R193.2	-2.25	hsp-60	-2.14	K01A6.7	-2.06	ugt-40	-1.98
bus-8	-2.25	ugt-45	-2.13	haao-1	-2.06	B0035.15	-1.98
hch-1	-2.24	Y49F6B.12	-2.13	F38A6.4	-2.06	F15D4.5	-1.98
rab-11.2	-2.23	nas-10	-2.13	tag-297	-2.05	col-3	-1.97
abu-14	-2.23	acer-1	-2.13	Y16B4A.2	-2.05	lron-1	-1.97
F13H8.5	-2.23	col-167	-2.13	T06G6.12	-2.05	acox-1.2	-1.97
C46A5.4	-2.23	F42A8.1	-2.13	ZC513.7	-2.05	cutl-23	-1.97
col-115	-2.23	C35A5.3	-2.13	F54E2.1	-2.05	mtp-18	-1.97
T06A4.3	-2.23	nspb-12	-2.13	cest-33	-2.05	Y49E10.18	-1.97
ZK662.2	-2.22	aqp-1	-2.13	T27E9.2	-2.05	F45E4.5	-1.96
R09E10.5	-2.21	Y7A9A.79	-2.12	C01B10.11	-2.04	R04B5.5	-1.96
ZK180.5	-2.21	plpr-1	-2.12	T11B7.2	-2.04	cutl-8	-1.96
cpr-1	-2.21	F28B4.3	-2.12	lips-10	-2.04	C34C12.8	-1.96
T17H7.7	-2.21	spp-2	-2.12	mtd-1	-2.03	ZK622.4	-1.96
C35B1.5	-2.21	apy-1	-2.12	act-3	-2.03	ram-5	-1.95
C35A5.10	-2.2	F46C3.6	-2.11	F46C8.8	-2.03	cnc-10	-1.95
Y43F8B.3	-2.2	acdh-6	-2.11	T05H4.7	-2.03	K09D9.1	-1.95
R02F11.1	-2.2	Y39A1A.21	-2.11	cysl-2	-2.02	nduo-3	-1.95
pho-14	-2.2	ttr-18	-2.11	F26A1.9	-2.02	Y37A1B.5	-1.95
M03E7.4	-2.2	pqn-71	-2.1	col-146	-2.02	EGAP4.1	-1.95
twk-11	-2.18	mlt-9	-2.1	ttr-45	-2.02	gsnl-1	-1.95
F01F1.3	-2.18	F59A6.10	-2.1	R12A1.3	-2.02	M153.1	-1.94
F44E5.5	-2.18	col-104	-2.1	F27D9.2	-2.02	lbp-3	-1.94
C54G4.4	-2.18	lpr-3	-2.1	acs-11	-2.02	gst-21	-1.94
nstp-2	-2.18	ndfl-4	-2.09	axl-1	-2.02	F59D6.1	-1.93
R07E5.4	-2.18	F08B12.4	-2.09	K08D12.4	-2.02	ins-26	-1.93
F59B10.3	-2.17	pqn-29	-2.09	cnc-8	-2.02	Y57G11A.4	-1.93
F32D8.7	-2.17	C50D2.1	-2.09	ttr-32	-2.01	ZK1290.10	-1.93
C18E9.7	-2.17	K06A9.3	-2.09	sym-1	-2.01	hpo-36	-1.92

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
K11G9.5	-1.92	C06G1.1	-1.85	K04H4.2	-1.79	C34E7.4	-1.74
abu-8	-1.91	lpr-6	-1.85	pho-1	-1.79	C03B1.14	-1.74
F11A5.9	-1.91	F27E5.9	-1.85	R07E3.2	-1.79	C49F8.3	-1.74
C34C12.7	-1.91	K08D12.8	-1.85	sdz-24	-1.79	M03F4.6	-1.74
mdh-1	-1.91	F53H4.3	-1.84	F09C8.1	-1.79	idhg-2	-1.74
papl-1	-1.91	ttr-7	-1.84	F13E9.13	-1.79	C52G5.2	-1.74
col-155	-1.91	H02F09.3	-1.84	pfn-1	-1.79	ugt-13	-1.74
lgc-27	-1.9	dpy-18	-1.84	col-65	-1.79	ZK180.6	-1.74
col-61	-1.9	lpr-7	-1.84	chs-2	-1.79	pges-2	-1.74
ZC513.14	-1.9	bca-2	-1.84	col-78	-1.78	Y47H10A.5	-1.74
T20B3.1	-1.9	ugt-9	-1.84	ztf-26	-1.78	M04C3.2	-1.73
T14G8.4	-1.9	gst-19	-1.84	ctg-2	-1.78	metr-1	-1.73
Y57G7A.1	-1.9	nas-13	-1.84	asns-1	-1.78	pho-8	-1.73
pqn-67	-1.9	col-177	-1.84	col-130	-1.78	ech-4	-1.73
ZK84.1	-1.89	grl-16	-1.84	ech-6	-1.78	grd-16	-1.73
ttr-30	-1.89	ugt-63	-1.83	tsp-1	-1.77	tts-2	-1.73
R07B1.8	-1.89	abu-10	-1.83	Y41G9A.5	-1.77	R74.2	-1.73
aagr-4	-1.89	R186.8	-1.83	D1005.2	-1.77	C30B5.6	-1.73
M7.12	-1.89	linc-6	-1.83	W05F2.3	-1.77	F29B9.5	-1.72
fbxc-40	-1.89	mlt-8	-1.83	cyp-33D1	-1.77	cht-1	-1.72
clec-78	-1.89	pgk-1	-1.83	Y38E10A.28	-1.77	clec-172	-1.72
slc-36.4	-1.89	cnc-3	-1.82	lgc-21	-1.77	lips-17	-1.72
ZC123.1	-1.89	cut-5	-1.82	T16G1.2	-1.77	C30G12.6	-1.72
C05C10.3	-1.88	ZK809.8	-1.82	K09B3.1	-1.77	ora-1	-1.72
T16G12.1	-1.88	nol-56	-1.82	npax-2	-1.77	dhs-8	-1.72
cutl-10	-1.88	T06E4.14	-1.81	F41F3.3	-1.77	hog-1	-1.72
F01D5.6	-1.87	F44E2.4	-1.81	T24F1.7	-1.77	pqn-36	-1.72
fipr-7	-1.87	linc-17	-1.81	twk-22	-1.76	K08D9.4	-1.72
linc-1	-1.87	D2092.8	-1.81	lagr-1	-1.76	Y47D3B.6	-1.72
ZK970.7	-1.87	F13C5.5	-1.81	C25F9.4	-1.76	Y68A4A.13	-1.72
hil-3	-1.87	cyp-35C1	-1.81	C25E10.5	-1.76	jud-4	-1.71
T19C4.1	-1.87	dod-3	-1.81	Y32G9B.1	-1.76	D2096.6	-1.71
Y57G11C.39	-1.86	T05A7.1	-1.8	F09F7.6	-1.76	mpst-3	-1.7
wrt-9	-1.86	H42K12.3	-1.8	F15E6.3	-1.76	B0205.13	-1.7
abu-11	-1.86	nex-1	-1.8	C18D11.3	-1.76	F55A11.7	-1.7
ptr-18	-1.86	ttr-28	-1.8	W02F12.8	-1.76	grd-13	-1.7
F53B3.3	-1.85	C08E8.3	-1.8	slc-25A10	-1.75	nhr-202	-1.7
Y48G1BR.1	-1.85	C35D10.5	-1.8	argk-1	-1.75	hsp-12.2	-1.7
C31C9.2	-1.85	tth-1	-1.79	F35A5.4	-1.75	Y43F8C.13	-1.7
pqn-73	-1.85	C34E11.2	-1.79	F52H2.3	-1.75	ttr-33	-1.7
col-74	-1.85	noah-2	-1.79	dlc-2	-1.74	Y37A1A.4	-1.7

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
Y59H11AR.4	-1.69	cec-8	-1.64	C24D10.6	-1.6	cblc-1	-1.55
R12E2.7	-1.69	F10C1.9	-1.64	R04B3.3	-1.59	C34B4.2	-1.55
K02D3.2	-1.69	C15F1.1	-1.64	H10E21.4	-1.59	F15G9.6	-1.55
lips-3	-1.69	lrx-1	-1.64	clec-42	-1.59	clec-88	-1.55
col-125	-1.69	col-165	-1.64	Y62E10A.19	-1.59	C08H9.15	-1.55
T10G3.3	-1.69	elo-6	-1.64	ndx-2	-1.59	W08E12.2	-1.54
arrd-16	-1.69	C48B4.13	-1.64	nep-22	-1.59	C05E7.2	-1.54
R11A5.3	-1.69	C06C3.4	-1.64	T05H10.3	-1.59	Y87G2A.19	-1.54
F30H5.3	-1.69	daf-6	-1.63	ztf-30	-1.59	pcs-1	-1.54
T25E4.1	-1.68	ptr-4	-1.63	C46C2.7	-1.58	ctf-8	-1.54
fip-5	-1.68	Y53F4B.27	-1.63	F57H12.6	-1.58	fbxb-72	-1.54
clec-266	-1.68	asp-8	-1.63	pcp-2	-1.58	hil-7	-1.54
F43D9.1	-1.68	F56B3.2	-1.63	C04G6.10	-1.58	ZK822.1	-1.54
C45E5.1	-1.68	atf-2	-1.63	Y82E9BR.6	-1.58	T01B7.8	-1.54
tipn-1	-1.68	gst-9	-1.63	ins-11	-1.58	phat-2	-1.53
C16D9.1	-1.68	lys-1	-1.63	Y17D7C.4	-1.58	nhr-12	-1.53
T07F10.6	-1.68	H37A05.2	-1.63	mec-12	-1.58	dhrs-4	-1.53
R13D11.4	-1.68	F02C12.1	-1.63	such-1	-1.58	F27D9.7	-1.53
F46G11.2	-1.67	R03H10.2	-1.62	F36H1.11	-1.58	Y62E10A.13	-1.53
col-168	-1.67	lips-7	-1.62	F54E7.6	-1.57	taf-11.2	-1.53
F17C11.11	-1.67	Y65B4BL.6	-1.62	C48B4.9	-1.57	col-58	-1.53
gcsh-1	-1.67	R08E5.3	-1.62	T23F2.3	-1.56	T19D12.4	-1.53
W03D2.9	-1.67	fip-6	-1.62	mtx-1	-1.56	R03G8.3	-1.53
nlp-16	-1.67	C29F3.7	-1.62	F48G7.5	-1.56	D2005.6	-1.53
lsy-27	-1.67	tsp-2	-1.62	ZK596.1	-1.56	F47D12.3	-1.53
C06C3.10	-1.67	col-186	-1.62	clec-173	-1.56	acs-19	-1.53
ugt-47	-1.67	cpt-4	-1.62	F10C1.8	-1.56	F14H12.3	-1.53
H01G02.1	-1.67	B0034.1	-1.62	cyb-2.2	-1.56	D1053.4	-1.53
F32A7.8	-1.66	cdc-50.B	-1.62	F55F8.8	-1.56	hsp-25	-1.53
ZC416.2	-1.66	F21C10.10	-1.61	C15B12.8	-1.56	abhd-11.2	-1.52
grl-1	-1.66	ifp-1	-1.61	C07A4.2	-1.56	dhcr-24	-1.52
Y69A2AR.28	-1.66	ttr-6	-1.61	phat-4	-1.56	F13B6.1	-1.52
M02H5.8	-1.66	R12E2.14	-1.61	ttr-26	-1.56	Y58A7A.3	-1.52
ZK154.1	-1.66	prx-19	-1.61	F53F4.2	-1.56	F52E4.5	-1.52
far-3	-1.65	K02D3.1	-1.61	cyb-3	-1.56	gpd-4	-1.52
mex-1	-1.65	T23F2.5	-1.61	T19C3.3	-1.56	fib-1	-1.52
C05D12.1	-1.65	nlp-29	-1.61	F45D3.3	-1.56	K08D8.6	-1.52
C18D11.6	-1.65	vglu-2	-1.6	set-20	-1.55	acaa-2	-1.52
mlc-6	-1.65	hxk-1	-1.6	F13E9.15	-1.55	lgc-34	-1.52
anmt-2	-1.65	C06E7.4	-1.6	ptps-1	-1.55	W04A8.4	-1.51
cpr-5	-1.65	B0294.1	-1.6	Y80D3A.9	-1.55	ppgn-1	-1.51

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
R13D7.2	-1.51	daf-22	-1.47	T21D12.14	-1.44	nlp-27	-1.42
agmo-1	-1.51	str-112	-1.47	K07D4.4	-1.44	C03A3.3	-1.42
Y68A4B.3	-1.51	C13A10.2	-1.47	T08B1.1	-1.44	Y41G9A.10	-1.42
F56C11.3	-1.51	T09B9.1	-1.47	K03A1.4	-1.44	cyp-13B1	-1.41
F14D7.12	-1.51	C15A11.4	-1.47	F57F5.1	-1.44	T14E8.4	-1.41
Y38E10A.14	-1.51	T23F6.1	-1.47	ZK742.6	-1.44	C17C3.1	-1.41
sqt-3	-1.51	C01G6.3	-1.47	F40H3.3	-1.44	F32D8.12	-1.41
T10H10.2	-1.5	dnj-11	-1.47	R05D3.9	-1.44	col-174	-1.41
F15B9.8	-1.5	lact-4	-1.47	F26G1.5	-1.44	moc-1	-1.41
sptl-2	-1.5	cpg-7	-1.47	B0334.13	-1.44	rocf-1	-1.41
ugt-29	-1.5	K10H10.12	-1.47	F08F1.3	-1.44	T05C1.1	-1.41
F53B1.4	-1.5	linc-4	-1.47	T20B3.14	-1.44	ZK1010.4	-1.4
F01D5.10	-1.5	F13A7.11	-1.47	R07B1.9	-1.44	gly-11	-1.4
BE0003N10.1	-1.5	F18E9.4	-1.47	C16B8.2	-1.44	F44E7.5	-1.4
sdhd-1	-1.5	F39D8.3	-1.46	T12B3.2	-1.44	air-2	-1.4
C28C12.4	-1.5	rdy-2	-1.46	K06G5.1	-1.44	sod-5	-1.4
mis-12	-1.5	T23F2.4	-1.46	T01H8.2	-1.44	F44G4.3	-1.4
K01D12.5	-1.5	C03F11.2	-1.46	mppa-1	-1.44	Y40B10B.1	-1.4
T05E12.6	-1.49	R11H6.4	-1.46	F55G1.1	-1.43	W03F9.4	-1.4
F56A12.2	-1.49	cpn-4	-1.46	tni-3	-1.43	C15H9.11	-1.39
T07A9.14	-1.49	pqn-37	-1.46	F22F7.7	-1.43	T05A7.7	-1.39
src-2	-1.49	clec-41	-1.46	Y105C5A.1268	-1.43	cisd-3.1	-1.39
VF13D12L.3	-1.49	ttr-51	-1.46	best-13	-1.43	H20E11.1	-1.39
F10D7.2	-1.49	act-1	-1.46	T20G5.8	-1.43	dhs-23	-1.39
F29G6.1	-1.49	C06E1.1	-1.46	phy-2	-1.43	cpi-1	-1.39
F48E3.2	-1.49	Y39A3CL.3	-1.45	cdk-5	-1.43	Y63D3A.7	-1.39
D2023.4	-1.48	Y17D7B.3	-1.45	ubc-12	-1.43	ric-7	-1.39
C55A1.6	-1.48	C34H4.2	-1.45	nhr-161	-1.43	cysl-1	-1.39
mrps-28	-1.48	clec-187	-1.45	fipr-6	-1.43	F26E4.3	-1.38
T26C5.5	-1.48	grl-7	-1.45	R13H4.8	-1.43	hach-1	-1.38
Y46G5A.36	-1.48	hic-1	-1.45	Y47D7A.13	-1.42	pgph-2	-1.38
Y56A3A.19	-1.48	cest-35.2	-1.45	Y55D5A.4	-1.42	Y45G12B.3	-1.38
wrt-2	-1.48	pos-1	-1.45	spn-4	-1.42	F58G1.7	-1.38
col-180	-1.48	R05G9R.1	-1.45	lact-7	-1.42	C05D2.8	-1.38
Y53F4B.23	-1.48	T12G3.6	-1.45	C25E10.10	-1.42	gpd-1	-1.38
pqn-13	-1.48	nhr-65	-1.45	eppl-1	-1.42	zipt-7.1	-1.38
col-117	-1.48	dpy-17	-1.45	T14B4.5	-1.42	F35C12.3	-1.38
pgp-8	-1.48	C36B7.5	-1.45	trx-3	-1.42	C14C6.5	-1.38
Y40A1A.3	-1.48	vab-2	-1.45	hpr-9	-1.42	srr-1	-1.38
ifb-1	-1.47	R12E2.15	-1.44	nep-16	-1.42	C05C10.5	-1.38
cts-1	-1.47	F58E6.13	-1.44	acs-1	-1.42	F13D11.3	-1.38

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F20G2.5	-1.38	tomm-40	-1.34	unc-59	-1.32	cyp-23A1	-1.29
doxa-1	-1.38	C54E4.4	-1.34	W06F12.2	-1.32	gmeb-2	-1.29
cest-12	-1.38	ZK909.3	-1.34	klp-19	-1.32	T12B3.3	-1.29
F16B4.4	-1.38	mex-5	-1.34	K03B4.4	-1.31	lgc-37	-1.29
C06G1.2	-1.38	ect-2	-1.34	ugt-48	-1.31	F49E12.8	-1.28
F14H3.6	-1.38	F49B2.6	-1.34	grl-10	-1.31	aco-2	-1.28
Y39F10A.1	-1.38	F21A3.3	-1.34	tyr-6	-1.31	nhr-21	-1.28
pash-1	-1.37	M28.5	-1.34	dhs-19	-1.31	M05D6.5	-1.28
ZK822.5	-1.37	C23H4.8	-1.34	dhs-30	-1.31	F45D3.4	-1.28
F25B3.2	-1.37	C13C12.2	-1.34	vha-12	-1.31	lec-1	-1.28
scrm-4	-1.37	nhr-105	-1.34	C07E3.3	-1.31	C01G10.7	-1.28
ptr-17	-1.37	col-172	-1.34	gst-36	-1.31	cdh-8	-1.28
pfn-3	-1.37	got-2.2	-1.34	C29F9.6	-1.31	mlp-1	-1.28
rcs-1	-1.37	grd-10	-1.33	Y47D3A.20	-1.31	W03C9.2	-1.28
F54H12.5	-1.37	cpn-2	-1.33	col-75	-1.31	tag-293	-1.28
inx-3	-1.37	F01G10.6	-1.33	K02E10.4	-1.31	R102.2	-1.27
Y71H2AM.6	-1.37	nlp-33	-1.33	F31D4.5	-1.3	C18B10.6	-1.27
fmo-2	-1.37	M04C9.3	-1.33	pck-1	-1.3	srr-6	-1.27
acox-1.1	-1.37	dnj-27	-1.33	E04D5.4	-1.3	C42C1.8	-1.27
mcm-7	-1.37	C45B2.8	-1.33	F13B6.2	-1.3	T01C8.2	-1.27
lgc-22	-1.36	tnt-4	-1.33	T02H6.11	-1.3	F56D3.1	-1.27
T13C2.2	-1.36	cpg-9	-1.33	T02C12.5	-1.3	F44D12.2	-1.27
col-121	-1.36	dhs-27	-1.33	his-24	-1.3	oig-5	-1.27
ttr-59	-1.36	lir-3	-1.33	C09F9.2	-1.3	F53A9.3	-1.27
C08E3.1	-1.36	cnc-6	-1.33	set-19	-1.3	mlt-11	-1.27
pie-1	-1.36	rsp-5	-1.33	F59E11.5	-1.3	cnp-2	-1.27
Y18H1A.9	-1.36	inf-1	-1.33	T24H10.4	-1.3	F59E12.15	-1.27
F53A9.7	-1.36	M60.6	-1.33	lec-7	-1.3	ztf-9	-1.27
natc-2	-1.36	F47E1.1	-1.33	F23H12.5	-1.3	gln-3	-1.27
3/3/2020	-1.36	Y51H4A.5	-1.33	T28C12.6	-1.3	R13A5.10	-1.27
romo-1	-1.36	ZK742.3	-1.33	trh-1	-1.3	pgp-15	-1.26
K11D2.1	-1.36	C14C11.7	-1.33	hcp-2	-1.29	cut-3	-1.26
R02E4.3	-1.36	H11E01.2	-1.32	mup-4	-1.29	F41E6.12	-1.26
mev-1	-1.35	Y58A7A.4	-1.32	spp-17	-1.29	amt-4	-1.26
cutl-12	-1.35	hcp-4	-1.32	C34C12.6	-1.29	R02F2.8	-1.26
acly-2	-1.35	ttc-36	-1.32	C29A12.6	-1.29	ceh-74	-1.26
phat-1	-1.35	flh-1	-1.32	C56C10.4	-1.29	exc-6	-1.26
ifa-3	-1.35	F59C12.4	-1.32	piit-1	-1.29	nhr-22	-1.26
Y71F9B.1	-1.35	dod-18	-1.32	him-3	-1.29	glrx-10	-1.26
dpy-7	-1.35	F36G3.1	-1.32	lpr-4	-1.29	slc-17.8	-1.26
F02E9.1	-1.35	zig-12	-1.32	M02D8.6	-1.29	K08E3.5	-1.26

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
mxl-3	-1.26	W02B12.13	-1.23	F28H7.3	-1.21	W01C8.5	-1.18
EGAP5.1	-1.26	T03F6.10	-1.23	T03D8.6	-1.21	Y57G11C.44	-1.18
C02B8.3	-1.25	nhr-237	-1.23	eat-5	-1.21	T06E4.9	-1.18
F35E12.6	-1.25	F38B6.4	-1.23	cec-4	-1.21	T06E4.8	-1.18
C15C7.5	-1.25	ZC443.1	-1.23	Y73B3A.1	-1.21	orai-1	-1.18
T09A5.15	-1.25	W08E12.6	-1.23	enol-1	-1.2	M163.8	-1.18
dif-1	-1.25	K08E4.3	-1.23	col-68	-1.2	cri-3	-1.18
mai-2	-1.25	T21G5.2	-1.23	F26F12.4	-1.2	gpn-1	-1.17
Y73F4A.1	-1.25	F59B1.10	-1.23	oig-2	-1.2	T19B10.5	-1.17
best-24	-1.25	atad-3	-1.23	F21D5.3	-1.2	lec-10	-1.17
F31E9.6	-1.25	C06B8.2	-1.23	cdh-9	-1.2	F33G12.7	-1.17
C09F12.2	-1.25	Y46H3A.4	-1.23	mth-1	-1.2	Y71G12B.10	-1.17
R11.4	-1.25	F01G10.10	-1.23	dpy-14	-1.2	mrps-6	-1.17
F46C5.10	-1.25	gba-1	-1.23	R09F10.5	-1.2	sdha-2	-1.17
F28H7.8	-1.25	F33H2.3	-1.22	pcyt-1	-1.2	F35H10.2	-1.17
lys-4	-1.25	wrt-10	-1.22	acbp-3	-1.2	F10D2.10	-1.17
bra-2	-1.25	F21E9.2	-1.22	W09G12.10	-1.2	C15H9.9	-1.17
F32D8.5	-1.25	Y39A3CL.4	-1.22	ugt-22	-1.2	mxt-1	-1.17
bag-1	-1.25	C38H2.3	-1.22	ZC455.1	-1.2	cdr-6	-1.17
poml-2	-1.25	gtr-1	-1.22	col-89	-1.2	cutl-14	-1.17
ppw-1	-1.25	T19A5.3	-1.22	lev-8	-1.19	irg-2	-1.17
ZK512.1	-1.24	cpn-1	-1.22	C16D9.4	-1.19	Y71G12B.17	-1.17
pyp-1	-1.24	puf-11	-1.22	K02E7.5	-1.19	Y52E8A.3	-1.17
bcmo-1	-1.24	elf-1	-1.22	ZK1307.8	-1.19	F56D6.17	-1.17
C30F2.4	-1.24	F14B4.1	-1.22	C08F8.9	-1.19	rpb-11	-1.17
lron-10	-1.24	clec-166	-1.22	Y92H12BL.5	-1.19	rad-8	-1.17
Y119D3B.12	-1.24	ech-1.1	-1.22	F25A2.1	-1.19	dnj-9	-1.17
rsp-4	-1.24	nmy-1	-1.22	Y60A3A.21	-1.19	slc-25A42	-1.16
cpt-5	-1.24	dim-1	-1.22	ugt-17	-1.18	K01A2.5	-1.16
cyp-14A5	-1.24	Y69A2AR.3	-1.21	crn-1	-1.18	F14F9.4	-1.16
col-154	-1.24	C26B2.7	-1.21	sod-2	-1.18	T19C3.2	-1.16
Y73C8B.1	-1.24	sod-1	-1.21	Y73C8B.2	-1.18	Y38C1AA.9	-1.16
set-9	-1.24	Y71H2AM.11	-1.21	Y87G2A.16	-1.18	ndx-8	-1.16
R03A10.5	-1.24	F33H2.6	-1.21	zip-10	-1.18	T05H10.4	-1.16
bigr-1	-1.23	M199.2	-1.21	efn-4	-1.18	C36C9.5	-1.16
enu-3.5	-1.23	Y73C8B.3	-1.21	crn-6	-1.18	W02F12.2	-1.16
Y75B7AR.1	-1.23	W04B5.3	-1.21	Y54G2A.45	-1.18	Y113G7A.14	-1.16
ttr-20	-1.23	fkb-4	-1.21	parg-2	-1.18	pole-4	-1.15
T09B4.5	-1.23	K02E10.6	-1.21	cat-1	-1.18	amx-2	-1.15
Y54G11A.4	-1.23	C49F5.6	-1.21	unc-52	-1.18	tba-6	-1.15
del-10	-1.23	col-131	-1.21	C07G3.15	-1.18	F22H10.3	-1.15

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F21D5.4	-1.15	col-10	-1.14	chw-1	-1.12	spg-7	-1.1
ugt-53	-1.15	C46H11.7	-1.14	dlhd-1	-1.12	T01D1.4	-1.1
C05D12.3	-1.15	uri-1	-1.13	mom-2	-1.12	F41G3.21	-1.1
ZK682.7	-1.15	Y6D1A.2	-1.13	clec-83	-1.12	alx-1	-1.1
Y56A3A.7	-1.15	Y97E10C.1	-1.13	far-8	-1.11	ZC21.3	-1.1
mpst-1	-1.15	ZC449.5	-1.13	C45G9.2	-1.11	tdc-1	-1.09
F19C6.4	-1.15	ost-1	-1.13	tag-307	-1.11	ech-8	-1.09
cng-1	-1.15	C40H1.7	-1.13	gly-8	-1.11	T22E5.1	-1.09
F38B2.2	-1.15	F14F9.3	-1.13	glt-1	-1.11	nas-33	-1.09
glb-13	-1.15	vdac-1	-1.13	K07C5.9	-1.11	ceh-49	-1.09
T05E7.1	-1.15	gei-14	-1.13	clec-87	-1.11	acs-7	-1.09
kdp-1	-1.15	F18C5.5	-1.13	cfim-1	-1.11	clik-1	-1.09
arx-5	-1.15	acds-10	-1.13	Y39A3A.4	-1.11	nas-7	-1.09
C26B2.8	-1.15	nduf-6	-1.13	T05F1.2	-1.11	F13D12.8	-1.09
nex-3	-1.15	skat-1	-1.13	K12G11.6	-1.11	lpr-5	-1.09
nadk-2	-1.15	Y113G7B.11	-1.13	mrpl-19	-1.11	tfg-1	-1.09
dmd-9	-1.15	eat-20	-1.13	vem-1	-1.11	hrg-7	-1.09
F33H12.7	-1.14	Y48A6B.7	-1.13	pat-12	-1.11	T11F8.12	-1.09
rig-5	-1.14	F10A3.4	-1.13	taco-1	-1.11	R10H10.4	-1.09
Y67A10A.9	-1.14	swip-10	-1.13	tbc-19	-1.11	C54E4.12	-1.09
gpx-5	-1.14	igcm-1	-1.13	ucr-11	-1.11	F25D1.5	-1.09
T12G3.4	-1.14	C13B4.1	-1.13	C08B6.4	-1.11	lin-24	-1.09
sco-1	-1.14	C25D7.5	-1.13	F09C3.2	-1.11	his-72	-1.09
sun-1	-1.14	Y58A7A.5	-1.13	glt-5	-1.1	lpd-5	-1.09
fkb-1	-1.14	gst-35	-1.12	M04B2.4	-1.1	kca-1	-1.09
K08B5.2	-1.14	nspe-4	-1.12	pyc-1	-1.1	ZK675.4	-1.09
hal-3	-1.14	Y10G11A.1	-1.12	C47E8.4	-1.1	rig-3	-1.09
T03G11.9	-1.14	ZC477.3	-1.12	mam-8	-1.1	inx-2	-1.09
ckc-1	-1.14	K02E10.1	-1.12	Y105E8A.36	-1.1	R05H10.1	-1.09
B0205.12	-1.14	tir-1	-1.12	htz-1	-1.1	B0205.14	-1.09
T05G5.1	-1.14	nhr-28	-1.12	clec-56	-1.1	inx-13	-1.09
let-383	-1.14	coq-5	-1.12	nlp-66	-1.1	bus-2	-1.09
F53A9.9	-1.14	Y71G12B.6	-1.12	phb-1	-1.1	T28A8.4	-1.09
F18E9.1	-1.14	C44B7.7	-1.12	ugt-21	-1.1	Y48G10A.1	-1.09
Y92H12BR.2	-1.14	K08E7.6	-1.12	eat-2	-1.1	ifa-1	-1.09
ZK1307.7	-1.14	igeg-2	-1.12	cdd-2	-1.1	rnp-8	-1.08
C33B4.4	-1.14	E01A2.2	-1.12	F18A11.2	-1.1	coq-8	-1.08
mif-1	-1.14	pfkb-1.2	-1.12	fat-5	-1.1	Y4C6B.1	-1.08
C44C1.1	-1.14	tpi-1	-1.12	lips-9	-1.1	F37H8.2	-1.08
C07G3.10	-1.14	C05D12.4	-1.12	abu-13	-1.1	daf-28	-1.08
C25F9.9	-1.14	gst-27	-1.12	Y102A11A.7	-1.1	T20F5.4	-1.08

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
lon-8	-1.08	ZK1053.4	-1.06	bus-4	-1.04	F35D11.4	-1.02
Y105C5B.19	-1.08	ptr-16	-1.06	nhr-158	-1.04	ugt-16	-1.02
ZC262.2	-1.08	T02D1.8	-1.06	pfk-1.1	-1.04	nlp-79	-1.02
W02B8.1	-1.08	pole-1	-1.06	nasp-2	-1.04	W05B10.4	-1.02
T08G2.2	-1.08	oat-1	-1.06	ceh-2	-1.04	col-12	-1.02
haf-1	-1.08	ina-1	-1.06	T21C9.9	-1.04	C04F12.5	-1.02
acp-6	-1.08	F35H10.10	-1.05	C56G2.4	-1.03	B0507.1	-1.02
dhs-3	-1.08	arrd-25	-1.05	dhs-25	-1.03	F09E10.7	-1.02
F23C8.14	-1.08	cyp-33C5	-1.05	F08F3.6	-1.03	dma-1	-1.02
enu-3.3	-1.08	snr-2	-1.05	F56H11.2	-1.03	ztf-4	-1.01
cisd-3.2	-1.08	dhs-29	-1.05	T13H5.6	-1.03	F36H9.2	-1.01
alh-10	-1.08	C53A5.2	-1.05	F33C8.4	-1.03	hsp-4	-1.01
ucp-4	-1.08	T26E3.10	-1.05	F31F7.1	-1.03	Y55F3C.17	-1.01
sups-1	-1.08	adt-1	-1.05	lat-2	-1.03	C49G7.10	-1.01
C25H3.14	-1.08	C01A2.4	-1.05	clec-4	-1.03	W01A11.1	-1.01
ttr-8	-1.08	C38C6.3	-1.05	aqp-11	-1.03	B0284.3	-1.01
T27F6.8	-1.07	F53F1.6	-1.05	F58A6.1	-1.03	grl-5	-1.01
dog-1	-1.07	C53H9.3	-1.05	nmgp-1	-1.03	cox-6C	-1.01
dhs-5	-1.07	R04A9.9	-1.05	elo-9	-1.03	B0238.12	-1.01
F58H1.5	-1.07	upp-1	-1.05	ZK1055.6	-1.03	plst-1	-1.01
nlp-24	-1.07	Y38H6C.20	-1.05	ceh-91	-1.03	zipt-13	-1.01
tbb-6	-1.07	F20D1.3	-1.05	C45G7.4	-1.03	F15G9.1	-1.01
cah-5	-1.07	brd-1	-1.05	gfl-1	-1.03	R06C1.4	-1.01
ZK973.9	-1.07	C44B9.3	-1.05	clec-91	-1.02	dhhc-1	-1.01
sel-7	-1.07	K11H12.7	-1.05	Y48G1A.1	-1.02	sdz-4	-1.01
nduo-2	-1.07	phat-5	-1.05	ZK228.4	-1.02	dsl-2	-1.01
swt-5	-1.07	pqn-31	-1.05	pgp-6	-1.02	F18A1.7	-1.01
C18H9.6	-1.07	Y53G8B.2	-1.05	DC2.5	-1.02	K10C9.1	-1.01
F13A7.12	-1.07	cdc-25.3	-1.05	Y7A9A.1	-1.02	F01D5.5	-1.01
cht-2	-1.07	Y25C1A.8	-1.04	zig-8	-1.02	asic-2	-1
cutl-25	-1.07	sdha-1	-1.04	mcm-3	-1.02	F57C2.5	-1
F23A7.4	-1.07	cox-17	-1.04	F36H9.7	-1.02	gbh-1	-1
T11G6.3	-1.06	cpd-2	-1.04	Y94H6A.16	-1.02	tyr-4	-1
ddl-3	-1.06	dpy-31	-1.04	Y87G2A.2	-1.02	math-22	-1
tps-2	-1.06	pqm-1	-1.04	swt-6	-1.02	B0495.8	-1
tyms-1	-1.06	suds-3	-1.04	F59F4.3	-1.02	F10D7.1	-1
C02F4.4	-1.06	B0272.4	-1.04	ero-1	-1.02	calu-1	-1
lin-42	-1.06	lron-8	-1.04	thoc-5	-1.02	W01B11.6	-1
R07E3.6	-1.06	hex-1	-1.04	Y39G10AR.32	-1.02	mrps-34	-1
icp-1	-1.06	B0272.3	-1.04	K12H4.5	-1.02	Y42H9AR.5	-1
C02E7.7	-1.06	F13A7.14	-1.04	svh-1	-1.02	mlt-4	-1

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
C01B10.3	-1	T22D1.3	1.02	Y104H12D.2	1.03	srpa-72	1.05
ddp-1	-1	cyl-1	1.02	F02A9.7	1.03	F55A3.2	1.05
gpc-2	-1	twk-8	1.02	ZK1240.3	1.03	glct-6	1.06
syp-1	-1	F21D9.4	1.02	npr-5	1.03	smg-1	1.06
mecr-1	1	catp-5	1.02	tads-1	1.03	nspc-20	1.06
mrpl-2	1	Y55D9A.2	1.02	Y71H2AM.3	1.04	C01C4.3	1.06
C49C3.10	1	K08D10.14	1.02	R07E3.4	1.04	F52E10.4	1.06
F52B11.5	1	fbxc-23	1.02	xbx-5	1.04	C17H11.6	1.06
pes-4	1	trpl-1	1.02	ttll-4	1.04	nhr-190	1.06
gtsf-1	1	tdpo-1	1.02	gtf-2A2	1.04	smu-2	1.06
arrd-13	1	cyk-3	1.02	T09F3.2	1.04	far-7	1.06
cdc-14	1	dhhc-9	1.02	nxf-1	1.04	gck-3	1.06
ubc-3	1	dgk-4	1.02	rom-2	1.04	nhr-5	1.06
egl-20	1	Y39G10AR.9	1.02	C25A11.2	1.04	C03B1.13	1.06
srw-85	1	let-526	1.02	F13B12.1	1.04	col-129	1.06
daf-15	1.01	bgal-2	1.02	spp-1	1.04	R12E2.13	1.06
ced-2	1.01	F54C8.4	1.02	ints-2	1.04	set-6	1.06
H05C05.1	1.01	hpk-1	1.02	nas-39	1.04	ZK1307.1	1.06
F26F4.12	1.01	F53A2.9	1.02	prmt-6	1.04	Y102A11A.5	1.06
figo-1	1.01	M04B2.2	1.03	Y20C6A.1	1.04	W09D10.5	1.06
C05D11.8	1.01	oaz-1	1.03	atg-13	1.04	mbk-2	1.06
rle-1	1.01	CD4.1	1.03	egl-5	1.04	hda-6	1.07
epn-1	1.01	T16H12.3	1.03	kel-1	1.04	F52H2.1	1.07
taf-12	1.01	tag-30	1.03	asp-12	1.04	trip-4	1.07
T12D8.10	1.01	ZK1127.12	1.03	nhr-274	1.04	srpa-68	1.07
daf-8	1.01	Y48G10A.3	1.03	tbc-9	1.04	ZK1128.7	1.07
F49E2.2	1.01	T21B4.15	1.03	aakg-1	1.05	nhr-184	1.07
pgph-3	1.01	ceh-38	1.03	unc-2	1.05	gcy-11	1.07
zif-1	1.01	dolk-1	1.03	mul-1	1.05	F40G9.5	1.07
kcc-1	1.01	Y55F3BR.2	1.03	nhr-126	1.05	W02D7.6	1.07
R06F6.12	1.01	F40G9.17	1.03	cdk-2	1.05	sur-6	1.07
tat-4	1.01	F58G11.4	1.03	mrp-5	1.05	D1022.3	1.07
rpl-9	1.01	tbg-1	1.03	Y75B8A.14	1.05	dsh-1	1.08
C16D9.9	1.01	T01B10.5	1.03	sop-2	1.05	crtc-1	1.08
tre-2	1.01	rpl-3	1.03	ZC196.5	1.05	F15D4.2	1.08
dhs-21	1.01	gap-1	1.03	D2023.1	1.05	lsl-1	1.08
edc-4	1.01	ubr-5	1.03	F47H4.2	1.05	T09B4.8	1.08
Y41D4B.1	1.02	ant-1.1	1.03	M116.2	1.05	nipa-1	1.08
rcq-5	1.02	linc-91	1.03	B0507.6	1.05	F45F2.9	1.08
rrn-2.1	1.02	pals-24	1.03	R02F2.7	1.05	ncl-1	1.08
rbm-28	1.02	Y53F4B.21	1.03	ccdc-55	1.05	mei-2	1.08

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
cbp-3	1.08	gbas-1	1.1	pab-2	1.11	cdc-25.1	1.13
try-10	1.08	Y48E1C.1	1.1	nrps-1	1.11	pqn-85	1.13
cil-1	1.08	stau-1	1.1	rpl-4	1.11	T06A1.5	1.13
xrn-1	1.08	F45E10.2	1.1	athp-2	1.11	sma-9	1.13
R11G1.2	1.08	fut-1	1.1	snf-6	1.11	ncx-7	1.14
rfth-1	1.08	ikb-1	1.1	acox-1.6	1.11	ZK131.11	1.14
mrps-5	1.08	cat-4	1.1	trx-2	1.12	zmp-4	1.14
F35H8.2	1.08	rbpl-1	1.1	Y95D11A.3	1.12	pro-2	1.14
T25C12.11	1.08	rskn-2	1.1	gpd-3	1.12	pir-1	1.14
F14B6.6	1.08	tam-1	1.1	F49E12.12	1.12	efsc-1	1.14
F57C12.6	1.08	par-4	1.1	snx-13	1.12	rde-2	1.14
cec-2	1.08	nlp-7	1.1	nuaf-1	1.12	rrn-3.1	1.14
rab-14	1.08	ptc-1	1.1	prdx-6	1.12	npr-28	1.14
nol-2	1.09	Y51F10.3	1.1	C34C12.9	1.12	lipl-7	1.14
F01D5.1	1.09	mca-2	1.1	kynu-1	1.12	rnf-1	1.14
C18B2.5	1.09	T03E6.8	1.1	H23N18.6	1.12	eif-3.D	1.14
syp-2	1.09	F46B6.12	1.1	F58G6.7	1.12	cdap-2	1.14
B0035.13	1.09	T19C3.6	1.1	uev-1	1.12	cdr-4	1.14
M03A1.8	1.09	B0495.9	1.11	fbxa-101	1.12	C18F10.7	1.14
F35C11.4	1.09	kqt-2	1.11	let-70	1.12	dct-6	1.14
rnh-1.0	1.09	sri-30	1.11	imp-2	1.12	gld-2	1.15
W01G7.4	1.09	acs-22	1.11	Y39B6A.34	1.13	F27C1.2	1.15
C04G6.4	1.09	fbxa-59	1.11	ftn-1	1.13	clec-178	1.15
Y56A3A.16	1.09	spk-1	1.11	ctsa-4.1	1.13	F36H2.3	1.15
T05F1.11	1.09	T26C12.1	1.11	Y55F3BL.4	1.13	rpc-11	1.15
saeg-1	1.09	F33D4.4	1.11	mtm-5	1.13	rsr-2	1.15
F21D5.5	1.09	Y22D7AL.4	1.11	rpi-2	1.13	F58B4.5	1.15
W08A12.2	1.09	C35D10.6	1.11	elt-7	1.13	lmtr-5	1.15
C06G3.6	1.09	egl-10	1.11	eri-12	1.13	T19D7.6	1.15
C31H1.8	1.09	C49A9.9	1.11	M01H9.3	1.13	fahd-1	1.15
nmur-2	1.09	bcl-11	1.11	spp-5	1.13	cdh-3	1.15
C08G9.1	1.09	T26A8.1	1.11	Y39H10B.2	1.13	zer-1	1.15
Y43F4B.9	1.09	wht-2	1.11	E01A2.5	1.13	eef-1G	1.15
T07D1.3	1.1	pstk-1	1.11	dop-6	1.13	lrp-2	1.15
apb-3	1.1	C32E8.6	1.11	R12B2.2	1.13	clec-146	1.15
ddx-52	1.1	Y110A7A.21	1.11	pqn-48	1.13	ZC250.4	1.15
taf-5	1.1	fic-1	1.11	ttr-1	1.13	crm-1	1.15
dhs-13	1.1	tag-294	1.11	ZK993.5	1.13	srpr-2.1	1.15
aatf-1	1.1	K09F5.6	1.11	sars-1	1.13	M176.4	1.15
Y46G5A.15	1.1	C45G7.13	1.11	F58G6.8	1.13	F10E9.12	1.15
ets-6	1.1	ZK1058.3	1.11	egl-43	1.13	T20D3.5	1.15

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
Y2H9A.4	1.15	pxmp-4	1.17	Y105E8A.1	1.19	ZK1127.5	1.21
Y75B8A.7	1.15	frpr-8	1.17	F58D5.5	1.19	M01F1.9	1.21
nhr-110	1.15	del-9	1.17	F09G2.1	1.19	clp-1	1.21
C03H12.1	1.15	chd-7	1.17	F13C5.1	1.19	zipt-9	1.21
C56A3.4	1.15	mrp-7	1.17	Y50D7A.1	1.19	Y59A8B.21	1.21
F46H5.7	1.16	vps-22	1.17	txt-18	1.19	Y40H7A.11	1.21
Y47A7.2	1.16	Y71F9AL.8	1.17	lpd-8	1.19	Y92H12A.2	1.21
F17B5.1	1.16	slcf-1	1.17	Y49A3A.3	1.19	C25G4.2	1.21
hecd-1	1.16	Y73B3A.3	1.17	gstk-2	1.19	F55G11.8	1.21
rps-16	1.16	C37H5.5	1.17	mps-1	1.19	K02D10.4	1.21
C24G6.8	1.16	cest-9.1	1.17	frm-7	1.19	fpn-1.1	1.21
pus-1	1.16	clec-76	1.18	vps-26	1.19	F46A8.13	1.21
aexr-1	1.16	T22C1.6	1.18	hda-4	1.19	T25C12.12	1.21
rps-23	1.16	mdt-15	1.18	C09E7.6	1.2	eas-1	1.21
tsp-11	1.16	W03D8.8	1.18	F11E6.6	1.2	F13H8.1	1.21
W05H9.3	1.16	Y34B4A.5	1.18	F07H5.5	1.2	mfn-1	1.21
gei-4	1.16	srh-210	1.18	linc-35	1.2	C29G2.6	1.21
gly-6	1.16	rpoa-49	1.18	tct-1	1.2	ain-2	1.21
C27H5.2	1.16	F57B10.8	1.18	gur-3	1.2	Y6B3B.9	1.21
pals-31	1.16	Y39B6A.3	1.18	ubc-21	1.2	pinn-4	1.21
R13A1.10	1.16	egl-8	1.18	dct-1	1.2	mes-6	1.21
gfi-3	1.16	nhr-227	1.18	gap-3	1.2	C15C8.7	1.22
Y40B1A.3	1.16	drd-1	1.18	R06A10.1	1.2	piki-1	1.22
M03F8.3	1.16	C13F10.5	1.18	F59C6.11	1.2	pqn-21	1.22
Y22D7AR.2	1.16	ttll-5	1.18	R02E4.2	1.2	mys-4	1.22
faah-4	1.16	C10B5.3	1.18	C48B6.3	1.2	aka-1	1.22
snap-29	1.16	F56C4.4	1.18	C30F12.3	1.2	daf-16	1.22
F33D11.16	1.17	prcc-1	1.18	fog-2	1.2	mct-3	1.22
F35E12.4	1.17	M176.11	1.18	rps-2	1.2	M02E1.3	1.22
hpo-31	1.17	Y57G11C.1135	1.18	lin-15A	1.2	atg-9	1.22
tftc-1	1.17	W02B12.1	1.18	zipt-7.2	1.2	ncs-3	1.22
ima-3	1.17	unc-31	1.19	dct-11	1.2	Y50D7A.8	1.22
rpl-2	1.17	col-181	1.19	spat-2	1.2	T10H4.13	1.22
C05C8.5	1.17	nhr-101	1.19	lrp-1	1.2	mig-18	1.22
ptl-1	1.17	col-95	1.19	kgb-2	1.2	K12D12.4	1.22
B0244.10	1.17	gsto-2	1.19	acp-2	1.2	tat-6	1.23
Y45G5AL.1	1.17	klo-1	1.19	memo-1	1.2	acl-2	1.23
C14C10.2	1.17	B0462.5	1.19	Y9C2UA.1	1.2	ubc-8	1.23
pdcd-2	1.17	clh-6	1.19	K12H4.7	1.2	H35N09.2	1.23
anr-36	1.17	F01G4.6	1.19	nrde-4	1.21	tub-2	1.23
fbxa-53	1.17	T08E11.1	1.19	F26H9.5	1.21	ZK757.1	1.23

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
supr-1	1.23	Y73B6BL.31	1.26	qars-1	1.29	gta-1	1.31
C28H8.2	1.23	Y38C1AA.12	1.26	Y54F10BM.12	1.29	F47H4.12	1.31
rpl-16	1.23	plk-2	1.26	ugt-23	1.29	atg-16.2	1.31
C07B5.3	1.23	ubh-3	1.26	rpia-1	1.29	cpna-1	1.31
mrp-3	1.23	asp-1	1.26	smk-1	1.29	glb-30	1.32
puf-9	1.23	K10B3.5	1.26	Y52B11A.12	1.29	fbxb-53	1.32
let-711	1.23	K05C4.2	1.26	cyn-5	1.29	F10G2.1	1.32
fbxa-189	1.23	C43H6.4	1.26	rev-1	1.29	gcs-1	1.32
btb-4	1.24	hrg-1	1.26	sms-1	1.29	K04F10.7	1.32
pgp-11	1.24	adpr-1	1.27	nhr-90	1.29	W09D6.1	1.32
Y43C5A.2	1.24	rabx-5	1.27	Y49F6B.2	1.29	M142.8	1.32
Y18H1A.11	1.24	nuc-1	1.27	gtbp-1	1.29	lis-1	1.32
C27D8.4	1.24	nlp-17	1.27	T24B8.7	1.29	C01G6.4	1.32
lgg-2	1.24	faah-6	1.27	W09C5.1	1.3	Y55F3C.9	1.32
kin-4	1.24	nlp-2	1.27	F42C5.4	1.3	Y73E7A.1	1.32
rps-20	1.24	slc-25A26	1.27	F22B7.1	1.3	C28D4.10	1.32
catp-7	1.24	nhr-10	1.27	trxr-1	1.3	elt-4	1.32
scl-2	1.24	F49H6.5	1.27	pde-4	1.3	Y53F4B.13	1.32
Y53G8AM.7	1.24	glb-26	1.27	T20F7.5	1.3	clec-37	1.32
ZK250.13	1.24	mdt-26	1.27	ZK971.1	1.3	pef-1	1.32
zhit-2	1.24	Y38F1A.1	1.27	R03H10.1	1.3	moe-3	1.32
F11C7.2	1.24	Y41E3.22	1.27	spr-3	1.3	cpd-1	1.33
alg-1	1.24	T25D10.1	1.27	hgo-1	1.3	F21H7.2	1.33
Y39A1A.14	1.24	B0507.2	1.27	lpr-2	1.3	ife-1	1.33
igdb-2	1.24	dhps-1	1.27	snx-6	1.3	ace-2	1.33
lin-49	1.25	Y42A5A.1	1.28	swan-2	1.3	pals-38	1.33
W02D3.4	1.25	dhs-15	1.28	F59C6.5	1.31	Y56A3A.18	1.33
F42A9.9	1.25	Y71F9AL.10	1.28	C45E5.3	1.31	brp-1	1.33
deg-3	1.25	ahr-1	1.28	Y67H2A.7	1.31	F35B12.10	1.33
ppfr-1	1.25	wdfy-3	1.28	ZK1320.3	1.31	cest-31	1.33
C01C10.2	1.25	K09H9.8	1.28	sdc-3	1.31	C25F9.5	1.33
ubc-7	1.25	mtl-1	1.28	D1014.2	1.31	R102.4	1.33
sax-1	1.25	R144.3	1.28	cif-1	1.31	C17G1.5	1.33
F22D6.14	1.25	T26H5.8	1.28	C32H11.3	1.31	tfbm-1	1.33
F09E5.10	1.25	prx-5	1.28	atg-16.1	1.31	zzz-1	1.33
B0563.5	1.26	F22D6.2	1.28	C32D5.11	1.31	larp-5	1.33
M04D8.7	1.26	btb-9	1.28	cyp-34A9	1.31	flp-20	1.33
dhp-1	1.26	Y53F4B.1	1.28	C06E1.9	1.31	Y55F3AM.13	1.34
henn-1	1.26	twk-12	1.28	cest-35.1	1.31	Y51H4A.7	1.34
ZK993.2	1.26	mrpl-9	1.28	F13D11.4	1.31	rpac-40	1.34
C36B1.13	1.26	fbxc-6	1.28	K07E3.1	1.31	cept-2	1.34

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ugt-56	1.34	twk-10	1.36	fbxb-65	1.38	F59C6.16	1.41
cyp-34A10	1.34	C45G3.3	1.36	eme-1	1.39	T26H5.14	1.41
gpa-16	1.34	cof-2	1.36	pry-1	1.39	F12A10.1	1.41
amx-3	1.34	irg-3	1.36	F40F12.9	1.39	cyp-13A3	1.41
klp-4	1.34	T21H3.1	1.37	ZK858.5	1.39	F53C11.9	1.41
T05G5.5	1.34	endu-2	1.37	K02E11.9	1.39	pdpr-1	1.41
drap-1	1.34	cct-2	1.37	ctl-1	1.39	T24C4.8	1.41
rpb-9	1.34	lite-1	1.37	R01H2.7	1.39	nubp-1	1.42
ptr-24	1.34	pgp-9	1.37	ZK822.4	1.39	arrd-20	1.42
scav-1	1.34	tgt-2	1.37	trpp-9	1.39	C28H8.14	1.42
txt-3	1.34	Y71H2B.2	1.37	sgk-1	1.39	pha-1	1.42
C18A11.1	1.34	C15H9.2	1.37	ears-1	1.39	mtl-2	1.42
yars-2	1.34	ZK632.14	1.37	F17C11.4	1.4	pfd-5	1.42
C38H2.2	1.34	iars-2	1.37	afmd-1	1.4	dcp-66	1.43
F40F4.7	1.34	Y66H1A.5	1.37	tag-280	1.4	C45B11.7	1.43
T02G5.14	1.34	pgap-1	1.37	Y92H12BL.1	1.4	spp-10	1.43
eol-1	1.35	K11E4.1	1.37	sinh-1	1.4	F16B4.5	1.43
emc-3	1.35	lgc-23	1.37	scav-6	1.4	F46G10.1	1.43
mrpl-1	1.35	Y43F8C.6	1.37	nhr-119	1.4	des-2	1.43
Y95B8A.6	1.35	pals-19	1.37	C28C12.11	1.4	K07F5.15	1.43
T08B1.4	1.35	E04F6.8	1.37	hsp-6	1.4	pap-1	1.43
F52E1.5	1.35	R10H1.1	1.37	Y71H2B.11	1.4	Y48C3A.3	1.43
byn-1	1.35	ctf-18	1.37	pup-2	1.4	W08F4.5	1.43
haf-4	1.35	AH9.4	1.37	C17G10.7	1.4	asm-3	1.43
pqbp-1.1	1.35	F49C12.10	1.38	icd-2	1.4	T26G10.1	1.43
F20B6.4	1.35	akt-2	1.38	rbm-34	1.4	pab-1	1.43
pigs-1	1.35	akap-1	1.38	zyg-11	1.4	rrp-1	1.44
C05E11.6	1.35	pcf-11	1.38	C54D10.10	1.4	Y22D7AR.6	1.44
E04F6.9	1.35	ctns-1	1.38	eif-2alpha	1.41	R13H4.2	1.44
gba-3	1.35	mxl-1	1.38	ncx-2	1.41	atg-10	1.44
eif-3.F	1.35	T19D12.3	1.38	plpp-1.1	1.41	Y71H2AM.2	1.44
nhr-219	1.36	cap-2	1.38	K10G6.9	1.41	cest-25	1.44
C17H12.8	1.36	mig-1	1.38	rmh-2	1.41	pmt-2	1.44
Y48C3A.12	1.36	E02H4.4	1.38	pals-16	1.41	T16G1.9	1.44
enpl-1	1.36	ZK813.4	1.38	Y50D4A.1	1.41	C39D10.8	1.44
eif-2gamma	1.36	lips-1	1.38	C34F6.5	1.41	F44A6.5	1.44
F13H8.11	1.36	asp-4	1.38	ekl-5	1.41	pho-4	1.44
fnip-2	1.36	abhd-14	1.38	cct-1	1.41	B0228.7	1.44
col-107	1.36	rpap-2	1.38	noca-1	1.41	mrps-11	1.44
nhr-64	1.36	gcst-1	1.38	C29F5.3	1.41	Y18D10A.23	1.44
T05A12.3	1.36	swsn-9	1.38	sir-2.4	1.41	epg-4	1.44

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F08F8.9	1.44	egl-45	1.48	lars-1	1.52	lin-28	1.55
fkh-7	1.44	Y94H6A.5	1.48	C49F5.7	1.52	Y71G12B.31	1.56
C44H9.5	1.45	hex-3	1.48	nlp-59	1.52	ascc-1	1.56
C25E10.16	1.45	dao-5	1.48	ZC443.2	1.53	ins-35	1.56
dhs-20	1.45	H04M03.3	1.48	alkb-8	1.53	F36H5.10	1.56
T07D4.2	1.45	F42F12.3	1.49	epg-6	1.53	nac-2	1.56
aex-5	1.45	F29C6.1	1.49	abce-1	1.53	cnx-1	1.56
rsd-6	1.45	exc-14	1.49	pigw-1	1.53	wdr-5.2	1.56
sma-2	1.45	coa-7	1.49	Y59C2A.1	1.53	mca-1	1.56
C33D9.3	1.45	pno-1	1.49	K04F10.1	1.53	ercc-1	1.56
Y54G2A.41	1.46	unk-1	1.49	Y92H12A.5	1.53	Y43F8C.3	1.56
C45E5.4	1.46	C04F5.8	1.49	adr-1	1.53	F58H1.3	1.56
Y41D4A.6	1.46	Y71H2AM.12	1.49	ddb-1	1.53	adss-1	1.56
ZK285.2	1.46	mboa-2	1.49	F08G12.11	1.53	T10H9.8	1.56
pinn-1	1.46	nmad-1	1.49	mtcu-1	1.53	eif-3.I	1.57
btb-19	1.46	his-60	1.5	nca-2	1.54	hil-1	1.57
F14H3.12	1.46	C14A11.2	1.5	tag-89	1.54	clec-63	1.57
R02F2.1	1.46	F53H4.4	1.5	M01E5.2	1.54	lido-13	1.57
nhl-1	1.46	fat-2	1.5	asp-14	1.54	C09D4.4	1.57
mfb-1	1.46	math-27	1.5	slcr-46.1	1.54	T05H4.10	1.57
R05A10.1	1.46	Y106G6G.2	1.5	abcf-3	1.54	fbxa-182	1.57
ttr-24	1.46	R06C1.6	1.5	F58A3.4	1.54	Y6E2A.4	1.57
ZK180.8	1.46	ints-1	1.5	Y54E5A.8	1.54	C47B2.2	1.57
R186.1	1.47	tpra-1	1.5	pals-5	1.54	plc-3	1.57
mdt-27	1.47	nhr-48	1.51	ifb-2	1.54	F54E7.9	1.57
unc-54	1.47	Y32F6A.4	1.51	trm-2A	1.54	C10B5.1	1.57
egl-27	1.47	F19B6.1	1.51	C07D8.6	1.54	B0454.5	1.57
Y18D10A.9	1.47	Y41C4A.8	1.51	atf-6	1.54	ampd-1	1.57
car-1	1.47	F42C5.6	1.51	ncr-2	1.54	D2045.8	1.57
rog-1	1.47	asna-1	1.51	frm-5.1	1.55	F08A7.1	1.58
clh-4	1.47	fbxa-74	1.51	rla-0	1.55	acl-7	1.58
C54C8.8	1.47	F36F2.2	1.51	mff-2	1.55	F59A7.8	1.58
ZK1098.11	1.47	cyp-13A1	1.51	fbxa-48	1.55	zgpa-1	1.58
sru-7	1.47	mop-25.1	1.51	ZC443.4	1.55	T06E6.1	1.58
K03H1.11	1.47	C44E12.1	1.52	K02E7.11	1.55	pals-18	1.58
trxr-2	1.47	zip-12	1.52	cnnm-2	1.55	C06G3.3	1.58
T27A10.6	1.47	M03C11.6	1.52	smp-2	1.55	pigk-1	1.58
C36B1.6	1.47	F55A4.7	1.52	hecw-1	1.55	nhr-152	1.58
irld-2	1.47	mrpl-37	1.52	D1054.18	1.55	F07E5.5	1.58
xdh-1	1.48	znfx-1	1.52	pcbd-1	1.55	B0563.7	1.58
nrde-1	1.48	F32E10.5	1.52	him-4	1.55	cpz-2	1.58

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F54F2.7	1.58	clec-186	1.63	R03D7.5	1.67	ril-2	1.72
Y71F9AL.12	1.58	fkh-9	1.63	F26A3.1	1.67	sorf-2	1.72
R05D3.12	1.59	adt-3	1.63	srap-1	1.67	F16C3.1	1.72
Y61A9LA.10	1.59	C03H5.3	1.63	nhl-2	1.68	sqst-2	1.72
ZC443.3	1.59	K02D10.8	1.63	adk-1	1.68	timm-23	1.72
C33H5.13	1.59	Y43C5A.3	1.63	dhs-11	1.68	fbxa-10	1.72
mak-2	1.59	ccdc-47	1.64	B0403.6	1.68	exos-8	1.72
F53F4.14	1.59	F37A8.5	1.64	nhr-106	1.68	ensa-1	1.73
col-42	1.6	coel-1	1.64	F55F8.2	1.68	T23D8.3	1.73
T01D3.6	1.6	F28B12.6	1.64	gldc-1	1.68	fbxa-138	1.73
cct-7	1.6	F28B4.4	1.64	F56D5.6	1.68	nst-1	1.73
F26F12.3	1.6	cpg-3	1.64	srh-48	1.68	apm-1	1.73
F46B6.5	1.6	gsa-1	1.64	Y51H4A.24	1.68	fbxa-163	1.73
F29B9.1	1.6	Y82E9BR.22	1.64	hpo-11	1.69	K12C11.6	1.73
slc-28.1	1.6	ric-19	1.64	nhr-210	1.69	F31A3.3	1.73
C56A3.5	1.6	hars-1	1.64	B0303.4	1.69	T10B11.5	1.74
ptp-1	1.6	nsy-1	1.64	pals-2	1.69	flp-10	1.74
efk-1	1.6	T21F4.1	1.65	daz-1	1.69	R151.1	1.74
eif-3.G	1.6	sca-1	1.65	fbxa-175	1.69	lipl-5	1.74
pfas-1	1.6	nhr-8	1.65	tric-1B.1	1.7	M01H9.4	1.74
lin-41	1.6	cps-6	1.65	mom-1	1.7	linc-39	1.74
F54D11.4	1.6	F09B12.3	1.65	plc-2	1.7	R12E2.8	1.74
pudl-2	1.61	hpo-34	1.65	C13B9.2	1.7	C42D8.1	1.74
sydn-1	1.61	ddn-1	1.65	R07C12.2	1.7	chil-23	1.75
F57C12.2	1.61	pro-3	1.65	odr-10	1.7	C25H3.18	1.75
C34F6.11	1.61	cct-5	1.65	rab-21	1.7	T28C6.8	1.75
eef-1A.1	1.61	T10G3.1	1.65	nhr-80	1.7	Y49E10.16	1.75
F37B12.3	1.61	K03B4.1	1.66	F32D8.13	1.7	aakb-2	1.75
gst-6	1.61	mtq-2	1.66	B0513.4	1.7	rpac-19	1.75
W05F2.6	1.61	mekk-3	1.66	B0393.9	1.71	C35B8.3	1.75
slc-17.9	1.61	M163.1	1.66	ttr-40	1.71	ufc-1	1.75
kin-10	1.61	Y6B3B.4	1.66	C06C3.11	1.71	F46B6.4	1.75
hsp-90	1.61	uev-3	1.66	eri-5	1.71	Y56A3A.31	1.75
F18C5.10	1.61	xpg-1	1.66	dph-3	1.71	M18.3	1.75
K10G4.3	1.61	nstp-4	1.66	pot-3	1.71	crn-3	1.75
Y39B6A.37	1.62	D2030.3	1.66	col-147	1.71	polg-1	1.75
nstp-1	1.62	C16A3.6	1.67	csr-1	1.71	C27A7.5	1.76
F41G3.18	1.62	cfim-2	1.67	C08F11.3	1.71	F31B12.3	1.76
fbxa-32	1.62	C05D11.1	1.67	lin-14	1.71	C47E12.12	1.76
pde-6	1.62	frm-4	1.67	yap-1	1.71	aldo-2	1.76
Y92H12BL.4	1.63	ccdc-149	1.67	noa-1	1.71	C16C10.2	1.76

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
sul-3	1.76	acs-16	1.81	crt-1	1.88	K02E11.7	1.93
got-2.1	1.76	M01F1.3	1.81	Y41C4A.9	1.88	F37C12.21	1.93
rrbs-1	1.77	col-93	1.81	vbh-1	1.88	frk-1	1.93
col-91	1.77	ugt-6	1.82	T10B5.3	1.88	T12D8.5	1.93
F20D6.5	1.77	gtl-1	1.82	F13G3.6	1.88	cgr-1	1.93
mus-81	1.77	nft-1	1.83	Y48C3A.20	1.88	M4.1	1.93
C44E4.5	1.77	F10E7.5	1.83	ugt-1	1.89	nhr-170	1.93
fshr-1	1.77	K09H9.5	1.83	ztf-7	1.89	Y70C5A.3	1.94
T01C8.3	1.78	hlh-11	1.83	eef-2	1.89	dohh-1	1.94
nape-2	1.78	abcf-2	1.83	ctn-1	1.89	C40H1.9	1.94
F35F10.1	1.78	moc-2	1.83	Y51B9A.9	1.89	T28F3.8	1.94
clec-75	1.78	ubc-26	1.83	swt-3	1.89	glb-17	1.95
klp-15	1.78	C47D12.5	1.83	gfat-1	1.9	smi-1	1.95
klp-16	1.78	F26G1.10	1.84	gpa-8	1.9	F21A3.11	1.95
K07G5.5	1.78	T20D3.6	1.84	T10C6.6	1.9	lact-2	1.95
pkn-1	1.78	let-611	1.84	fat-6	1.9	nape-1	1.95
T24H7.2	1.79	asah-1	1.84	tag-243	1.9	pals-34	1.95
siah-1	1.79	W08G11.3	1.85	K02A11.4	1.9	ztf-1	1.96
F58A3.3	1.79	mrps-17	1.85	fbxa-115	1.9	xpo-1	1.96
C11D2.3	1.79	C04H5.1	1.85	nspc-14	1.9	F23B2.10	1.96
cpz-1	1.79	C27A7.3	1.85	pud-4	1.9	prmt-1	1.96
nlp-69	1.79	B0564.2	1.85	F35D11.3	1.9	fars-3	1.96
alh-8	1.79	hlh-13	1.85	tag-151	1.91	clec-17	1.96
fem-2	1.79	R01H10.4	1.85	nhr-133	1.91	scrm-2	1.97
duxl-1	1.79	fbxa-185	1.86	H20E11.3	1.91	gpa-17	1.97
Y54G2A.10	1.79	ZC239.16	1.86	F41G4.7	1.91	ipla-7	1.97
dhs-7	1.79	H35B03.1	1.86	clec-82	1.91	C04F12.16	1.97
col-101	1.8	Y51H4A.15	1.86	H06H21.8	1.91	csp-2	1.98
C10E2.2	1.8	pyr-1	1.87	ZK792.5	1.91	H34I24.2	1.98
eng-1	1.8	nhr-35	1.87	cest-13	1.91	ZK550.2	1.98
nhr-55	1.8	peb-1	1.87	C23H3.5	1.92	dhs-1	1.98
mtx-2	1.8	copz-1	1.87	tax-6	1.92	T28A11.2	1.98
ugt-2	1.8	exos-9	1.87	F41E7.2	1.92	Y106G6E.4	1.98
T22C8.4	1.8	asp-3	1.87	tag-229	1.92	C02F5.3	1.99
F53H4.6	1.8	F16B3.2	1.87	T28C6.10	1.92	skr-19	1.99
Y54F10AR.2	1.81	nhr-108	1.87	C15B12.4	1.92	aakg-5	1.99
iff-2	1.81	nhr-221	1.87	M01E5.3	1.92	fubl-1	1.99
drd-5	1.81	Y45G5AM.7	1.88	F13B12.2	1.92	cct-4	1.99
M60.7	1.81	E02H9.2	1.88	paqr-1	1.92	clec-60	2
R09B5.11	1.81	C16C10.8	1.88	lep-5	1.93	bath-43	2
F31E3.6	1.81	mlst-8	1.88	Y32H12A.8	1.93	cdc-48.3	2

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
btb-17	2	C17G10.6	2.08	W07E6.2	2.18	wars-1	2.28
F44G4.1	2	F40F8.5	2.08	W06E11.1	2.18	cct-3	2.28
E02H1.1	2	Y32B12C.5	2.08	cars-1	2.19	Y46G5A.34	2.28
C05D9.9	2.01	C28H8.3	2.08	bath-47	2.19	unc-83	2.29
R11D1.13	2.01	tpk-1	2.08	AH9.7	2.2	R09F10.1	2.29
nhr-103	2.01	F35H8.1	2.09	ZK512.2	2.2	C53H9.2	2.29
nog-1	2.01	ptr-21	2.09	Y6G8.2	2.21	gst-3	2.29
F09G2.2	2.01	riok-2	2.09	obr-2	2.21	fbxa-173	2.29
ads-1	2.01	D2096.7	2.09	pgap-3	2.21	sek-4	2.29
ugt-54	2.01	twk-7	2.1	gpx-6	2.22	riok-3	2.3
T25B9.1	2.01	dhs-24	2.1	aakg-4	2.22	C09D4.2	2.3
hsp-12.3	2.02	ddx-17	2.11	nhr-129	2.22	R119.2	2.3
F41G4.8	2.02	JC8.2	2.11	rab-8	2.22	exos-7	2.3
smg-3	2.02	rev-3	2.11	K09C8.7	2.22	kin-14	2.3
rars-1	2.02	Y113G7A.13	2.12	lec-2	2.23	F45E1.5	2.3
ubc-1	2.02	psa-3	2.12	nhr-88	2.23	W06H8.6	2.31
asp-5	2.02	Y53C12B.7	2.12	D1054.3	2.23	C27F2.4	2.31
aat-8	2.02	alh-12	2.13	T09B4.6	2.23	Y18D10A.3	2.31
C54F6.6	2.02	C15C7.4	2.13	memb-2	2.23	Y97E10AL.1	2.31
F10G8.9	2.02	C03G6.17	2.13	Y37H9A.5	2.24	fbxc-7	2.32
clec-61	2.03	lpd-7	2.14	nhr-92	2.24	C45E1.4	2.32
mrpl-55	2.03	linc-43	2.14	W07G4.5	2.24	C52E2.4	2.32
Y67D2.5	2.03	Y119D3B.14	2.14	T22F3.2	2.24	far-5	2.32
daf-2	2.03	gst-37	2.14	clec-62	2.24	fil-1	2.32
ZC8.6	2.03	smf-3	2.14	K08F9.1	2.24	Y71H2AM.1	2.32
aak-1	2.03	ulp-3	2.14	D1022.4	2.25	wrb-1	2.32
elpc-4	2.03	imb-3	2.14	eif-3.E	2.25	srp-2	2.33
sel-8	2.03	clec-8	2.15	twk-5	2.25	ZC239.17	2.33
linc-96	2.04	kin-3	2.15	F30A10.9	2.25	ZK1290.13	2.33
ccm-2	2.05	F08H9.3	2.15	Y71G10AR.4	2.25	B0379.7	2.33
Y34F4.5	2.06	ZK430.7	2.16	lmd-4	2.26	B0524.6	2.34
upb-1	2.06	pho-6	2.16	B0511.6	2.26	pho-5	2.34
Y54F10AM.8	2.06	C50F4.1	2.17	clec-65	2.26	nhr-146	2.34
F53F10.1	2.07	F53F4.11	2.17	Y61A9LA.1	2.26	F32A5.8	2.34
nhr-85	2.07	Y57G11B.2	2.17	K11D12.12	2.26	ubc-15	2.34
gst-23	2.07	rsd-3	2.17	C36E8.1	2.26	F49C12.6	2.34
C24H12.4	2.07	nsun-2	2.17	F23F12.3	2.26	cpr-6	2.35
C53C11.2	2.07	afmd-2	2.17	Y45F3A.9	2.27	nlp-52	2.35
T19D12.2	2.07	rpom-1	2.18	T01B7.5	2.27	lgc-25	2.35
rars-2	2.07	W02D7.11	2.18	nap-1	2.28	C39H7.4	2.35
T08G11.4	2.08	C25H3.11	2.18	F26D11.12	2.28	spp-6	2.35

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ZK355.8	2.36	F31E9.3	2.54	W04E12.7	2.66	F40G12.5	2.98
epg-5	2.36	C33E10.3	2.54	Y7A5A.6	2.67	F36A2.2	2.99
T26H5.4	2.37	Y9C9A.8	2.54	asah-2	2.67	hpo-15	2.99
gst-22	2.38	lido-10	2.54	asp-6	2.67	ZK593.2	3.01
math-37	2.39	zig-9	2.54	F54F12.1	2.67	cest-1.2	3.02
T26C11.9	2.39	Y47G6A.7	2.55	Y43B11AR.3	2.67	T01G1.4	3.02
B0507.3	2.4	mboa-7	2.56	tts-1	2.68	F56H9.2	3.04
arch-1	2.4	nhr-18	2.56	R10E8.6	2.68	metl-18	3.05
C49C8.8	2.41	col-160	2.56	C28G1.6	2.69	fbxa-6	3.06
eif-3.B	2.41	linc-103	2.56	pin-2	2.69	F56A8.5	3.07
metl-2	2.42	F18G5.6	2.57	clec-85	2.71	acp-5	3.07
T10B5.7	2.42	col-92	2.57	ech-7	2.72	col-39	3.07
btb-16	2.42	R09E10.13	2.57	C39D10.11	2.72	fbxa-162	3.07
vps-33.1	2.42	F08F8.7	2.57	chil-13	2.73	F10G7.5	3.12
lgc-28	2.42	T25G3.3	2.57	Y54H5A.1	2.73	cup-16	3.13
F42C5.3	2.43	rrp-8	2.57	Y52B11A.10	2.73	faah-3	3.13
ttr-34	2.44	nhr-94	2.58	Y47G6A.5	2.75	C08F11.13	3.14
K02C4.5	2.45	Y39B6A.33	2.58	nas-9	2.76	clec-84	3.15
acl-9	2.45	T08A9.13	2.58	T08B6.2	2.76	cyp-37B1	3.15
pals-14	2.46	F48E8.3	2.58	C52E2.5	2.76	T28H10.1	3.16
fbxa-80	2.46	C29G2.2	2.59	ZK688.11	2.77	ZK470.14	3.16
F16A11.5	2.46	Y47H10A.3	2.59	C18H9.5	2.79	C53A5.17	3.18
nhr-232	2.47	F42A9.18	2.6	R07E3.1	2.8	C25F9.12	3.18
nhr-109	2.47	mnk-1	2.6	W03D8.2	2.8	ctps-1	3.2
col-118	2.47	R10E8.1	2.6	Y42G9A.1	2.81	B0546.3	3.21
Y56A3A.33	2.47	gsp-2	2.6	pqn-62	2.82	hrg-2	3.22
lnp-1	2.48	Y54H5A.2	2.61	cpr-2	2.82	F52E1.14	3.23
Y37E11B.5	2.48	fbxa-69	2.62	T13F2.6	2.82	chil-16	3.25
Y47D3A.32	2.49	nnt-1	2.62	riok-1	2.82	F47B8.8	3.26
Y54E10BR.4	2.5	pmt-1	2.63	sek-1	2.82	F47B8.4	3.27
gdh-1	2.5	F53F1.14	2.63	pqn-59	2.83	F35C8.5	3.28
M01B2.13	2.5	puf-12	2.63	pbo-6	2.86	srv-4	3.32
elpc-3	2.51	C32H11.4	2.63	dao-6	2.86	T06C12.14	3.32
F40E3.5	2.51	Y22D7AL.15	2.63	clec-264	2.87	exc-13	3.35
T22H9.1	2.51	T18D3.6	2.64	Y48G8AL.13	2.88	F43D2.7	3.39
C16A3.4	2.51	ulp-4	2.64	D1086.2	2.89	fard-1	3.39
ngp-1	2.52	gst-20	2.64	C34E11.4	2.89	C32F10.4	3.42
F54D5.3	2.52	asm-2	2.65	Y15E3A.4	2.94	T10C6.15	3.49
ZK1240.2	2.52	adah-1	2.65	Y40C5A.4	2.95	K05F6.10	3.52
C23F12.4	2.52	dph-1	2.65	W03D2.6	2.95	Y65B4BL.7	3.52
C49A9.6	2.53	C33E10.8	2.65	tut-1	2.96	T26E3.4	3.56

Gene	log2FC
ttr-49	3.59
W08E12.8	3.6
F43C11.7	3.6
spp-8	3.64
col-50	3.64
hda-5	3.71
cyp-32B1	3.79
F21C10.11	3.93
ZK185.5	3.93
F56F11.1	3.97
C10A4.3	4.01
T28A11.16	4.04
arrd-11	4.07
W10G11.1	4.14
F21H7.12	4.27
hsp-12.6	5.24
dpy-5	6.22

6.16. RNA-seq (CeGaT) - 4h Fed vs 48h Starved – HBR227 (*aptf-1*)

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F46F2.3	-5.06	R12A1.3	-2.65	dod-19	-2.41	F30H5.3	-2.26
T22F3.11	-4.98	R193.2	-2.65	asp-13	-2.41	clec-78	-2.26
Y39B6A.1	-4.93	C42D4.3	-2.64	clec-180	-2.41	pqn-71	-2.26
R02C2.7	-4.52	puf-11	-2.64	acdh-1	-2.4	ZK662.2	-2.25
irg-4	-3.83	col-109	-2.62	nlp-77	-2.39	T10E10.4	-2.25
gst-26	-3.83	kreg-1	-2.62	Y53F4B.23	-2.38	nlp-34	-2.24
W10C8.5	-3.8	col-14	-2.62	tag-10	-2.38	cut-2	-2.23
F57F4.4	-3.7	cpr-5	-2.61	tyr-2	-2.37	grl-21	-2.22
gsto-1	-3.53	grl-4	-2.58	F46C8.8	-2.37	lpr-6	-2.21
pho-11	-3.38	abu-10	-2.58	gfi-1	-2.37	Y16B4A.2	-2.21
F49C12.7	-3.36	W05F2.3	-2.57	F56D2.3	-2.37	C35C5.8	-2.21
T07D3.9	-3.17	EGAP4.1	-2.57	F44E2.4	-2.36	fmo-3	-2.21
col-166	-3.16	R02F11.1	-2.56	lpr-3	-2.35	pie-1	-2.21
C45B2.2	-3.02	cey-3	-2.56	F28B4.3	-2.34	F53F1.4	-2.2
dod-24	-2.97	cbd-1	-2.56	mex-1	-2.33	grd-3	-2.2
col-48	-2.96	ZK180.6	-2.55	act-3	-2.32	phat-1	-2.2
col-97	-2.95	idh-1	-2.55	spn-4	-2.32	ZK6.11	-2.2
C15A11.4	-2.94	act-5	-2.55	ttr-31	-2.32	F56C9.3	-2.19
mdh-2	-2.91	F35B3.4	-2.54	C09F9.2	-2.32	cutl-8	-2.19
C23H5.8	-2.9	K08D8.3	-2.52	gst-28	-2.32	F38B6.4	-2.18
alh-5	-2.9	hrg-7	-2.52	K02B7.3	-2.31	ldh-1	-2.18
puf-3	-2.89	M02G9.1	-2.51	smd-1	-2.31	pqn-22	-2.17
ugt-63	-2.82	F10D11.6	-2.49	ech-9	-2.31	acox-1.5	-2.17
col-113	-2.81	Y57G11C.42	-2.48	col-33	-2.3	E01G6.1	-2.17
C23G10.11	-2.81	F40E10.5	-2.48	R11H6.4	-2.3	ZK180.5	-2.17
lbp-6	-2.81	abu-12	-2.46	B0403.5	-2.3	nas-13	-2.17
hphd-1	-2.79	T08B1.1	-2.46	acn-1	-2.3	Y14H12B.2	-2.16
clec-48	-2.78	F46C5.1	-2.46	gsnl-1	-2.29	lgx-1	-2.16
Y65B4BL.1	-2.77	oma-2	-2.46	fmo-2	-2.29	lon-1	-2.16
T19B10.2	-2.77	F13D12.3	-2.45	grd-10	-2.29	mcm-3	-2.16
C01G10.15	-2.77	F35E12.6	-2.45	hpo-6	-2.29	ifa-3	-2.16
R09E10.5	-2.75	irg-5	-2.44	nas-30	-2.28	abu-8	-2.16
sdz-24	-2.74	dct-16	-2.44	lpr-5	-2.27	F09E10.1	-2.16
ilys-5	-2.73	ugt-33	-2.43	Y22D7AL.10	-2.27	mom-2	-2.16
cpr-4	-2.72	nas-38	-2.43	idhg-2	-2.27	skpo-2	-2.16
txt-4	-2.71	mua-6	-2.42	C01G8.1	-2.27	nas-10	-2.15
folt-2	-2.7	T24C12.4	-2.42	C06C3.10	-2.27	plpr-1	-2.14
pqn-26	-2.69	F59A6.10	-2.42	F38B2.4	-2.27	pqn-32	-2.14
nspb-12	-2.68	cnc-4	-2.42	gld-3	-2.26	nlp-30	-2.14
Y7A9A.79	-2.68	abu-14	-2.41	F20B10.3	-2.26	C25F6.7	-2.14
C48B4.13	-2.67	F41E6.5	-2.41	F13H8.5	-2.26	phg-1	-2.13

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
slc-17.8	-2.13	lbp-5	-2.04	F41E6.11	-1.97	kat-1	-1.88
Y73B3A.1	-2.13	C54G4.4	-2.04	C50F7.5	-1.96	K02G10.15	-1.88
C06G1.1	-2.13	ZK970.7	-2.03	C49H3.16	-1.96	T05F1.2	-1.88
grd-13	-2.13	Y34B4A.6	-2.02	zipt-7.1	-1.96	E04F6.6	-1.88
pgp-14	-2.13	cyn-17	-2.02	F39D8.3	-1.96	D1054.9	-1.88
F48G7.5	-2.13	phat-4	-2.02	cey-2	-1.96	vha-12	-1.88
F10A3.4	-2.12	hacd-1	-2.02	C29F3.7	-1.96	daao-1	-1.87
egg-6	-2.12	tts-2	-2.02	air-1	-1.96	dod-3	-1.87
B0024.4	-2.11	asns-2	-2.02	gst-21	-1.95	Y43F8B.3	-1.87
C35A5.10	-2.11	hsp-60	-2.02	ttr-15	-1.95	T06A4.1	-1.87
srg-31	-2.11	pqn-73	-2.02	T20B6.3	-1.95	K08D12.4	-1.87
pqn-74	-2.11	ptr-18	-2.01	mec-7	-1.95	gld-1	-1.86
C30B5.6	-2.11	K04H4.2	-2.01	wrt-2	-1.94	F16H11.1	-1.86
sun-1	-2.11	ZK84.1	-2.01	C50D2.1	-1.94	col-182	-1.85
T06A4.3	-2.11	Y73B6BL.23	-2.01	C52G5.2	-1.94	cpg-9	-1.85
cyb-2.2	-2.1	W03D2.9	-2.01	lys-1	-1.93	sod-1	-1.85
asp-8	-2.1	dex-1	-2.01	Y47H9C.1	-1.93	grl-16	-1.84
acp-6	-2.1	mex-5	-2.01	cpg-1	-1.93	R09E12.9	-1.84
noah-2	-2.1	F55A11.7	-2	valv-1	-1.93	abu-11	-1.84
cut-5	-2.1	F54D5.2	-2	F17A9.5	-1.93	ttr-45	-1.84
gcsh-1	-2.09	C34H4.2	-2	col-167	-1.92	T05B9.1	-1.84
cutl-23	-2.09	T19A5.3	-2	pqn-13	-1.92	puf-5	-1.84
ptr-1	-2.09	col-144	-2	tth-1	-1.92	F56D3.1	-1.84
Y110A7A.15	-2.09	twk-11	-2	dpy-1	-1.92	ugt-22	-1.83
VF13D12L.3	-2.08	F01D5.6	-1.99	Y47D3B.6	-1.92	mcm-7	-1.83
nos-1	-2.07	act-1	-1.99	lpr-4	-1.91	rnr-1	-1.83
tpxl-1	-2.07	mcm-2	-1.99	bus-8	-1.91	zig-4	-1.83
F32D8.7	-2.07	pcp-2	-1.99	ttr-2	-1.91	wee-1.3	-1.83
ptr-2	-2.07	C18E9.7	-1.98	C55A6.4	-1.91	jud-4	-1.83
phat-2	-2.07	clec-51	-1.98	W08E12.3	-1.91	haf-9	-1.83
lec-8	-2.07	C31H1.8	-1.98	C14C6.5	-1.91	col-80	-1.83
C46A5.4	-2.06	ugt-41	-1.98	ZK829.9	-1.91	F21C10.9	-1.83
col-98	-2.06	ugt-40	-1.98	F32D8.3	-1.91	era-1	-1.83
sqt-3	-2.06	ptr-4	-1.98	cpr-1	-1.91	szy-4	-1.83
lec-6	-2.06	pqn-63	-1.98	Y51F10.2	-1.91	ech-6	-1.83
mlt-8	-2.06	otpl-8	-1.97	rad-51	-1.91	ZC513.14	-1.83
hpo-36	-2.05	R05F9.6	-1.97	col-159	-1.9	nstp-2	-1.82
F23H12.5	-2.05	cdh-5	-1.97	col-3	-1.9	W04A8.4	-1.82
mlt-9	-2.05	ani-2	-1.97	hch-1	-1.89	col-145	-1.82
set-19	-2.04	lys-3	-1.97	F14H12.3	-1.89	gst-41	-1.82
F20G2.2	-2.04	fbp-1	-1.97	F43D9.1	-1.89	H42K12.3	-1.82

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
let-754	-1.81	F07H5.8	-1.75	clec-41	-1.69	atp-1	-1.65
D2005.6	-1.81	pho-14	-1.75	fip-5	-1.69	cutl-10	-1.65
D2096.6	-1.81	ugt-34	-1.75	H01G02.1	-1.69	C01B10.11	-1.65
F59F5.7	-1.8	T04F8.8	-1.75	M03F8.1	-1.69	sdhd-1	-1.65
clec-49	-1.8	lgc-22	-1.75	nspe-7	-1.69	Y111B2A.3	-1.65
cest-33	-1.8	clec-88	-1.75	pcn-1	-1.68	C12D12.1	-1.65
hil-4	-1.79	C50C3.1	-1.74	his-74	-1.68	T17H7.7	-1.65
F35H10.10	-1.79	T20F5.4	-1.74	nasp-2	-1.68	lron-2	-1.64
apy-1	-1.79	col-117	-1.74	snpc-1.2	-1.68	tag-297	-1.64
Y75B7AR.1	-1.79	chs-2	-1.74	ZK1320.9	-1.68	R09F10.8	-1.64
pos-1	-1.79	cdl-1	-1.74	mdh-1	-1.68	gst-19	-1.64
K11G9.5	-1.79	chtl-1	-1.73	puf-8	-1.68	toca-2	-1.63
nspe-5	-1.79	F30F8.1	-1.73	ttr-7	-1.68	dhcr-24	-1.63
gpd-4	-1.79	daf-6	-1.73	F08F1.3	-1.68	K10D3.4	-1.63
col-115	-1.79	gpd-1	-1.73	T06D8.10	-1.68	pals-26	-1.63
clik-1	-1.79	K01A6.4	-1.73	zwl-1	-1.68	brd-1	-1.63
trcs-1	-1.78	tost-1	-1.73	F58G1.7	-1.68	wrt-9	-1.63
grl-6	-1.78	R144.10	-1.72	F13D12.9	-1.68	ify-1	-1.63
hil-5	-1.78	Y48G1BR.1	-1.72	C14B1.9	-1.68	ZK154.1	-1.63
Y48G1A.2	-1.78	T16G1.2	-1.72	lgc-34	-1.67	eat-20	-1.62
ifd-2	-1.78	C04G6.10	-1.72	F40H3.3	-1.67	3/3/2020	-1.62
T23F6.1	-1.78	ttr-18	-1.72	C14B9.3	-1.67	R04B5.5	-1.62
Y69A2AR.28	-1.78	F01D5.10	-1.72	R12E2.7	-1.67	acly-2	-1.62
clec-53	-1.78	C49F5.6	-1.72	cnc-8	-1.67	air-2	-1.62
col-10	-1.78	lsy-27	-1.72	ced-3	-1.67	R07E5.4	-1.62
pgk-1	-1.78	mes-4	-1.72	col-104	-1.67	clec-72	-1.61
F12A10.1	-1.78	T27E9.2	-1.72	col-155	-1.67	egl-46	-1.61
R13H4.8	-1.77	F54E7.6	-1.71	Y41G9A.10	-1.66	C29A12.6	-1.61
M03E7.2	-1.77	W06B4.1	-1.71	aagr-4	-1.66	B0304.2	-1.61
lec-10	-1.77	M03F4.6	-1.7	C05D12.1	-1.66	tag-18	-1.61
srp-1	-1.77	F54D5.4	-1.7	zif-1	-1.66	F08D12.2	-1.61
deps-1	-1.77	Y37A1B.5	-1.7	lgc-27	-1.66	sas-6	-1.61
W03C9.2	-1.77	C05C10.5	-1.7	prom-1	-1.66	zen-4	-1.61
gyg-2	-1.77	atf-2	-1.7	ifp-1	-1.66	Y4C6B.1	-1.6
clec-10	-1.76	F08B12.4	-1.7	pfn-1	-1.66	K01A6.7	-1.6
pgl-3	-1.76	F18E9.4	-1.7	spp-17	-1.66	nlp-31	-1.6
R03C1.1	-1.76	F20G2.5	-1.7	T09B4.5	-1.66	F27E5.9	-1.6
wrt-4	-1.76	R05H5.3	-1.69	lys-8	-1.66	haao-1	-1.6
T28C12.6	-1.76	F13B6.2	-1.69	T19D12.1	-1.65	Y53F4B.39	-1.6
F45E1.4	-1.76	D2092.8	-1.69	F59A7.2	-1.65	dpy-17	-1.6
lys-4	-1.76	pmp-5	-1.69	F10C1.9	-1.65	F32D8.12	-1.59

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T25E4.1	-1.59	C35B1.5	-1.55	cld-9	-1.51	T06E4.14	-1.47
ect-2	-1.59	T02G5.7	-1.55	aqp-2	-1.51	sym-1	-1.47
F09C8.1	-1.59	anmt-2	-1.55	R07B1.9	-1.51	col-177	-1.47
hsp-25	-1.59	alg-5	-1.55	acs-11	-1.51	T12G3.6	-1.47
ZK105.13	-1.59	R03H10.2	-1.54	gst-27	-1.51	Y32G9B.1	-1.47
acaa-2	-1.59	ugt-13	-1.54	W09G12.10	-1.51	ctf-4	-1.46
C56G2.4	-1.59	lgc-21	-1.54	C29G2.3	-1.5	kdp-1	-1.46
ZK1290.10	-1.59	col-34	-1.54	M02H5.8	-1.5	syp-6	-1.46
ugt-45	-1.59	B0001.7	-1.54	C44B9.3	-1.5	tyms-1	-1.45
cyb-1	-1.59	dim-1	-1.54	col-154	-1.5	plk-1	-1.45
knl-1	-1.59	F57F5.1	-1.54	nol-56	-1.5	T22D1.5	-1.45
unc-59	-1.58	toe-2	-1.54	lec-1	-1.5	dhs-8	-1.45
rnp-8	-1.58	K08D8.6	-1.53	lgc-33	-1.5	div-1	-1.45
F53B1.4	-1.58	icl-1	-1.53	spsb-2	-1.5	daf-22	-1.45
F20G2.1	-1.58	M02D8.6	-1.53	B0261.7	-1.5	tdpt-1	-1.45
C08F8.3	-1.58	T10H10.2	-1.53	gst-4	-1.49	C01G6.3	-1.45
cdh-8	-1.58	fbxa-215	-1.53	hsp-17	-1.49	Y54G11A.3	-1.44
inx-3	-1.58	Y58A7A.1	-1.53	K08D12.6	-1.49	T02H6.11	-1.44
C06C3.4	-1.58	dpy-18	-1.53	F56C9.7	-1.49	R74.2	-1.44
mam-1	-1.58	gln-6	-1.53	grl-1	-1.49	R02E4.3	-1.44
col-186	-1.58	pfk-1.1	-1.53	pole-1	-1.49	C34C12.8	-1.44
cyk-7	-1.58	F42A10.9	-1.53	skpt-1	-1.49	mpst-1	-1.44
C15C6.1	-1.58	ech-4	-1.53	C15F1.1	-1.49	T03F6.3	-1.44
Y110A2AR.1	-1.58	col-169	-1.53	W01A11.1	-1.49	rocf-1	-1.44
F38A6.4	-1.58	noah-1	-1.53	K10H10.4	-1.49	hcp-1	-1.44
DY3.8	-1.58	C55A6.12	-1.53	R08E5.3	-1.49	ost-1	-1.43
ttr-59	-1.57	sptl-2	-1.53	clec-42	-1.49	C45B2.8	-1.43
best-1	-1.57	tnt-2	-1.53	C54D2.1	-1.49	C49F8.3	-1.43
unc-52	-1.57	dpl-1	-1.52	ctl-2	-1.49	oac-14	-1.43
F22B5.4	-1.57	zim-1	-1.52	ZK1037.6	-1.49	F26F12.4	-1.43
tdc-1	-1.57	F35D2.3	-1.52	Y51F10.7	-1.48	K08E3.5	-1.43
nmy-1	-1.57	sip-1	-1.52	bath-26	-1.48	ung-1	-1.43
pho-1	-1.56	F19C7.1	-1.52	mlt-11	-1.48	cyb-3	-1.43
cyp-35C1	-1.56	F56C9.6	-1.52	F41G3.21	-1.48	F33D4.6	-1.43
argk-1	-1.56	F15B9.8	-1.52	papl-1	-1.48	cyk-4	-1.42
dpy-7	-1.56	T19C4.1	-1.52	ZC443.1	-1.48	ZK675.4	-1.42
zig-12	-1.55	phat-5	-1.52	Y37H2A.14	-1.48	lec-9	-1.42
ZC123.1	-1.55	sdha-2	-1.52	slc-25A10	-1.48	edg-1	-1.42
M04C9.1	-1.55	pqn-60	-1.51	mcm-6	-1.48	F15D3.6	-1.42
ttr-33	-1.55	inx-14	-1.51	ifc-1	-1.47	spp-2	-1.41
mup-4	-1.55	sdz-28	-1.51	T21C9.13	-1.47	T23F2.5	-1.41

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
fzy-1	-1.41	acs-7	-1.35	F54D5.5	-1.3	mthf-1	-1.24
pqn-36	-1.41	gna-2	-1.35	dpy-14	-1.29	chaf-2	-1.24
cpr-3	-1.41	asns-1	-1.35	F31D4.5	-1.29	ttr-30	-1.24
hrde-1	-1.41	F11E6.3	-1.35	T21B6.3	-1.29	T05H10.4	-1.24
dhs-30	-1.41	Y41G9A.5	-1.35	rsa-1	-1.29	F39B2.3	-1.24
F22B7.9	-1.41	hmg-3	-1.34	col-111	-1.29	capg-2	-1.24
pri-2	-1.4	F33H2.3	-1.34	misc-1	-1.29	cyp-13B1	-1.24
C36B1.11	-1.4	cks-1	-1.34	hsp-16.41	-1.29	tsp-1	-1.24
aqp-7	-1.4	fat-1	-1.34	F21D5.1	-1.29	aly-2	-1.24
pdp-1	-1.4	lys-7	-1.34	mai-2	-1.29	cts-1	-1.23
F26G1.5	-1.4	ril-1	-1.34	ifo-1	-1.29	bca-2	-1.22
mec-12	-1.4	htz-1	-1.34	bca-1	-1.29	ttr-20	-1.22
agmo-1	-1.4	F44B9.2	-1.34	prg-1	-1.29	cdk-1	-1.22
sodh-1	-1.39	T25B9.9	-1.34	pigv-1	-1.28	acbp-3	-1.22
ucr-2.2	-1.39	pch-2	-1.34	F40A3.6	-1.28	pfn-3	-1.22
gst-36	-1.39	lst-1	-1.34	T19D12.4	-1.28	mab-20	-1.22
dut-1	-1.39	enol-1	-1.33	metr-1	-1.28	dnj-11	-1.22
ppm-1.G	-1.39	pam-1	-1.33	F11A5.9	-1.28	gsy-1	-1.22
nlp-29	-1.38	T04F3.1	-1.33	orc-1	-1.28	lagr-1	-1.21
LLC1.2	-1.38	tfg-1	-1.32	aco-2	-1.28	rsp-5	-1.21
rmd-1	-1.38	dpy-2	-1.32	tag-307	-1.27	tsfm-1	-1.21
Y60C6A.2	-1.38	pges-2	-1.32	F20D6.11	-1.27	flh-1	-1.21
ZK809.8	-1.38	wago-1	-1.32	H10E21.4	-1.27	col-130	-1.2
acs-2	-1.37	F42A8.1	-1.32	F59B10.3	-1.27	smc-3	-1.2
far-2	-1.37	mev-1	-1.32	sdha-1	-1.27	let-2	-1.2
swt-6	-1.37	bub-1	-1.32	B0272.3	-1.27	F58E6.13	-1.19
nxf-2	-1.37	Y71G12B.6	-1.32	cysl-1	-1.27	atp-5	-1.19
C15C7.5	-1.37	clec-266	-1.32	rsa-2	-1.27	ech-8	-1.19
clec-91	-1.37	grl-7	-1.32	Y67A10A.9	-1.27	F58A6.1	-1.19
top-2	-1.37	vha-11	-1.32	C17C3.1	-1.27	dnj-27	-1.19
cri-3	-1.36	K06G5.1	-1.31	vha-8	-1.27	perm-5	-1.17
cnc-10	-1.36	tbb-1	-1.31	ZC513.7	-1.27	Y63D3A.7	-1.17
vha-13	-1.36	clec-5	-1.31	T19H12.2	-1.26	pck-1	-1.12
mdf-2	-1.36	mcm-4	-1.31	pqn-52	-1.26	vdac-1	-1.12
cpn-1	-1.36	wrt-10	-1.31	col-125	-1.25	acer-1	-1.11
ttr-6	-1.36	taco-1	-1.31	ZK1058.9	-1.25	R04F11.2	-1.1
Y57G11A.4	-1.36	tni-3	-1.31	Y52B11A.8	-1.25	act-4	-1.01
nex-1	-1.36	xpo-2	-1.3	W02F12.2	-1.25	rpl-16	1
kbp-5	-1.35	rsp-4	-1.3	Y71G12B.10	-1.25	tatn-1	1.01
col-74	-1.35	unc-95	-1.3	cee-1	-1.25	egl-21	1.01
pgl-1	-1.35	Y56A3A.19	-1.3	T20D3.2	-1.24	eri-12	1.01

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F27C1.2	1.02	pho-4	1.13	F08F8.9	1.22	akap-1	1.27
osm-11	1.03	lact-2	1.14	Y47G6A.7	1.22	C16C10.2	1.27
pdcd-2	1.03	pah-1	1.14	R06F6.14	1.22	Y59C2A.1	1.28
xpo-1	1.04	R03H10.6	1.14	ZC395.5	1.22	ZK1127.5	1.28
aldo-2	1.04	flp-16	1.14	nlp-11	1.22	cct-3	1.28
pqn-48	1.05	nlp-8	1.14	klf-1	1.23	msrp-7	1.28
F58D5.5	1.05	F52G3.6	1.15	pfd-5	1.23	Y39E4B.6	1.28
hsp-90	1.07	tag-209	1.15	F26H9.5	1.23	mrps-11	1.28
cct-7	1.07	exc-14	1.15	T07F12.1	1.23	M01E5.3	1.29
cct-5	1.07	lgg-2	1.15	mtx-2	1.23	C01C10.2	1.29
byn-1	1.08	nhr-10	1.16	bath-43	1.23	F13G3.6	1.29
K12B6.9	1.08	hlh-11	1.16	Y66D12A.8	1.23	F56F10.2	1.29
egl-3	1.08	nhr-87	1.16	K07D4.9	1.23	Y54F10AR.2	1.29
flp-15	1.08	abhd-14	1.17	F41E7.7	1.23	F15D4.2	1.29
flp-14	1.08	smg-3	1.17	dct-1	1.24	Y22D7AR.6	1.29
hgo-1	1.08	cdr-4	1.17	ace-2	1.24	F22D6.2	1.29
T05H4.10	1.08	nxf-1	1.17	T28F3.8	1.24	gstk-2	1.29
ascc-1	1.09	rpia-1	1.17	fat-2	1.24	C03H5.3	1.29
kin-10	1.09	skr-19	1.18	unc-80	1.24	F17H10.2	1.29
Y54E5A.5	1.09	nlp-17	1.18	efk-1	1.24	rpl-24.2	1.29
Y45G5AM.7	1.1	F22F4.4	1.18	spp-18	1.25	C38C3.4	1.3
hars-1	1.1	nhr-138	1.18	fbxl-1	1.25	B0432.14	1.3
adk-1	1.1	T21F4.1	1.18	Y49F6B.2	1.25	cct-4	1.3
eef-2	1.1	gpx-3	1.19	Y37E11B.5	1.25	K03B4.1	1.3
ubc-3	1.1	ptr-24	1.19	nhr-55	1.25	sca-1	1.3
T28B11.1	1.1	F02E11.2	1.19	C35C5.9	1.26	dao-6	1.3
rpb-9	1.11	rab-21	1.19	sma-10	1.26	bath-38	1.3
lpin-1	1.11	nnt-1	1.19	W07E6.2	1.26	Y73E7A.1	1.31
rla-0	1.11	nhr-90	1.19	F18C5.10	1.26	Y105E8B.7	1.31
ncx-2	1.12	T26H5.9	1.19	M03D4.3	1.26	E02A10.3	1.31
ptl-1	1.12	F54D11.4	1.19	ist-1	1.26	nhl-2	1.31
asna-1	1.12	R119.5	1.19	ads-1	1.26	ikb-1	1.31
eef-1A.1	1.13	gst-12	1.2	Y50D4A.1	1.26	W02D3.12	1.31
ptp-1	1.13	nhr-101	1.2	ZK792.5	1.26	mtl-2	1.32
ril-2	1.13	T23G7.3	1.2	Y43F8C.3	1.27	ZK1098.11	1.32
F59C6.5	1.13	lite-1	1.21	Y47A7.2	1.27	Y39B6A.37	1.32
mfn-1	1.13	ipla-7	1.21	F13D11.4	1.27	C01C4.3	1.32
F43G6.8	1.13	slc-25A29	1.21	nlp-53	1.27	Y39B6A.3	1.32
Y54F10AM.8	1.13	Y42A5A.1	1.21	nlp-43	1.27	drh-2	1.32
sma-9	1.13	icd-2	1.21	nhr-100	1.27	F54E7.9	1.32
ida-1	1.13	ddx-52	1.22	ZC8.6	1.27	mlc-2	1.32

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
C50F4.1	1.32	K02E11.5	1.38	iff-2	1.43	ZK1240.9	1.48
F43C9.2	1.33	frm-7	1.38	cyn-2	1.43	T09E11.11	1.48
mboa-1	1.33	kin-14	1.38	R02E4.2	1.43	H34I24.2	1.48
F17C11.4	1.33	C35B8.3	1.38	alh-12	1.43	R11G10.3	1.49
M176.11	1.34	ccdc-149	1.38	C28H8.2	1.43	del-5	1.49
F58H1.7	1.34	K07G5.5	1.38	F59B2.13	1.43	asm-2	1.49
Y40B1B.7	1.34	ddx-17	1.39	irg-3	1.44	K01A2.10	1.49
fkh-9	1.34	duxl-1	1.39	T08B1.4	1.44	T26H5.8	1.49
ttr-27	1.34	lipl-5	1.39	F35B12.10	1.44	F23A7.3	1.5
ZK858.5	1.34	F13H8.1	1.39	endu-2	1.44	his-60	1.5
vps-33.1	1.34	F36H5.10	1.4	cgr-1	1.44	nrf-5	1.5
droe-4	1.34	F35D11.3	1.4	btb-4	1.44	C33H5.13	1.5
pde-4	1.34	C08G9.1	1.4	pin-2	1.44	F35B12.3	1.5
rrp-1	1.35	C49F5.7	1.4	F09C6.3	1.44	marg-1	1.5
Y66H1A.5	1.35	mop-25.1	1.4	eif-3.E	1.44	clec-8	1.5
zig-6	1.35	MTCE.33	1.4	VC5.2	1.44	F41E7.2	1.5
ubc-8	1.35	Y71H2B.11	1.41	C17G1.5	1.45	C25G4.2	1.5
D2023.1	1.35	F44A2.3	1.41	nhr-210	1.45	B0507.3	1.5
lin-28	1.35	Y67D2.5	1.41	ZK131.11	1.45	M01F1.3	1.51
twk-8	1.35	CD4.1	1.41	asah-1	1.45	nhr-110	1.51
asp-5	1.35	ZK1128.7	1.41	daf-2	1.46	cdd-1	1.51
T08G11.4	1.35	Y41E3.22	1.41	flp-9	1.46	Y49E10.16	1.51
M176.4	1.35	Y34F4.5	1.41	C07H4.1	1.46	imb-3	1.51
F43C1.7	1.35	haly-1	1.41	crt-1	1.46	ZC47.8	1.51
R10H1.1	1.36	C30G4.4	1.42	zig-9	1.46	fbxa-138	1.51
T25B9.1	1.36	K04F10.1	1.42	hil-1	1.46	Y51H4A.7	1.51
T07D4.2	1.36	lido-13	1.42	prmt-1	1.46	nhr-85	1.51
nlp-15	1.36	lin-14	1.42	nuaf-1	1.46	F26F12.3	1.52
eif-3.G	1.36	gst-22	1.42	ctn-1	1.46	riok-3	1.52
C06H5.8	1.36	far-6	1.42	fubl-1	1.47	C54F6.6	1.52
gei-3	1.36	mig-18	1.42	F09G2.2	1.47	C02F5.3	1.52
far-7	1.37	H10D18.1	1.42	C10E2.2	1.47	F07E5.5	1.53
tax-6	1.37	clec-75	1.42	mak-2	1.47	him-4	1.53
K09E2.2	1.37	T13F2.6	1.42	pho-5	1.47	T26H5.14	1.53
Y61A9LA.10	1.37	Y73F4A.3	1.42	timm-23	1.47	pgp-9	1.53
cdc-48.3	1.37	eif-3.I	1.43	W09C5.1	1.47	elpc-4	1.53
pno-1	1.37	aatf-1	1.43	C28H8.3	1.47	tag-151	1.53
srw-85	1.37	C25G6.4	1.43	Y73B3A.18	1.48	ZC443.3	1.53
M01H9.4	1.37	uev-3	1.43	C33G8.4	1.48	Y106G6E.4	1.54
cpz-2	1.37	ztf-7	1.43	psa-3	1.48	adt-3	1.54
K11E4.1	1.37	nhr-35	1.43	exos-9	1.48	ins-20	1.54

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
C03H5.7	1.54	ncx-7	1.58	M163.1	1.63	nhl-1	1.68
nhr-146	1.54	R06C1.6	1.58	moc-2	1.63	Y71H2AM.1	1.69
K07F5.15	1.54	fbxa-44	1.58	scl-24	1.63	F32H5.1	1.69
oig-3	1.54	ZC404.1	1.58	R07C12.2	1.63	nhr-219	1.69
scl-2	1.54	W06E11.1	1.58	pals-38	1.63	chil-23	1.69
F53F4.14	1.54	C49A9.6	1.58	Y71G12B.31	1.64	dohh-1	1.69
F33D11.16	1.54	M116.2	1.59	col-184	1.64	D1022.4	1.69
nape-1	1.55	gpa-6	1.59	pbo-6	1.64	C33D9.3	1.69
gtl-1	1.55	T23D8.3	1.59	gcy-11	1.64	gdh-1	1.69
F22D6.14	1.55	F14D2.19	1.59	Y57G11B.2	1.64	tpra-1	1.69
F45E10.2	1.55	F26D11.12	1.59	brp-1	1.64	sek-1	1.69
bath-47	1.55	F26A3.1	1.59	del-9	1.65	dph-1	1.7
coel-1	1.55	rsd-3	1.59	fnip-2	1.65	tos-1	1.7
fbxc-57	1.55	nhr-119	1.59	C05C10.7	1.65	srb-16	1.7
C10B5.3	1.56	nhr-232	1.59	abf-5	1.65	F40F12.9	1.7
col-156	1.56	gst-3	1.59	fbxa-140	1.65	F31E3.6	1.7
C54D10.10	1.56	lnp-1	1.6	fbxa-115	1.65	R11D1.13	1.7
F56C4.4	1.56	riok-2	1.6	rars-1	1.65	Y32H12A.8	1.7
adss-1	1.56	cyp-33C3	1.6	zip-12	1.65	Y39B6A.29	1.7
mtq-2	1.56	nhr-5	1.6	K10G4.3	1.65	F40G12.5	1.7
F19C6.12	1.56	D2096.7	1.6	F20D6.5	1.66	ttr-40	1.7
Y6G8.2	1.56	F58G6.7	1.6	dhp-1	1.66	fbxa-50	1.7
kin-3	1.56	K02A11.4	1.6	cat-4	1.66	nmad-1	1.7
scl-5	1.56	F59A7.5	1.61	slcf-2	1.66	M04D8.7	1.71
B0310.3	1.56	sir-2.4	1.61	Y43C5A.3	1.66	T20F7.5	1.71
fbxa-203	1.56	C04A2.15	1.61	mrps-17	1.66	T01C8.3	1.71
ttr-34	1.57	R09F10.1	1.61	fbxa-10	1.66	F55H12.7	1.72
math-27	1.57	hpo-11	1.61	asp-3	1.67	Y56A3A.18	1.72
ccm-2	1.57	F36F2.2	1.61	Y95B8A.6	1.67	T04C12.7	1.72
F27D4.3	1.57	rrp-8	1.61	rrbs-1	1.67	ins-35	1.73
T06E6.1	1.57	Y51H4A.15	1.61	lpr-2	1.67	ZK512.2	1.73
Y116A8A.10	1.57	R02F2.1	1.61	T09F5.12	1.68	C18H7.1	1.73
nst-1	1.57	fbxc-41	1.61	alh-8	1.68	F10E7.5	1.73
C18A11.1	1.57	srbc-20	1.61	unc-83	1.68	mltn-1	1.73
F46A8.13	1.57	H35B03.1	1.61	C36E8.1	1.68	catp-7	1.74
Y7A9C.1	1.57	aakb-2	1.61	nhr-133	1.68	T20D3.6	1.74
D1054.3	1.57	Y113G7A.13	1.62	C47E8.11	1.68	T10G3.1	1.74
ZK180.8	1.57	D2045.8	1.62	Y92H12BL.1	1.68	K02D10.8	1.74
capa-1	1.58	btb-17	1.63	cyp-33C2	1.68	F53A2.9	1.74
clec-62	1.58	F11E6.11	1.63	C25H3.11	1.68	rnt-1	1.74
R12E2.13	1.58	F02A9.7	1.63	F08H9.3	1.68	nspc-18	1.74

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
K09C8.7	1.75	nlp-47	1.82	gsp-2	1.94	C16D9.9	2.04
T01G1.4	1.75	aak-1	1.83	fbxa-6	1.94	Y82E9BR.22	2.04
C52E2.4	1.75	F55A4.4	1.83	F49C12.6	1.94	T01B7.5	2.05
ubc-1	1.75	R09E10.13	1.83	gst-23	1.94	C27F2.4	2.05
nspc-19	1.75	nlp-7	1.84	ZK1307.1	1.94	T22H9.1	2.05
pstk-1	1.75	Y105C5A.17	1.85	frk-1	1.94	nhr-109	2.06
smf-3	1.75	cps-6	1.85	C29F5.3	1.94	nspc-20	2.06
F41G4.8	1.76	C47D12.5	1.85	srh-210	1.94	C53C11.2	2.06
cpz-1	1.76	F48B9.1	1.85	paqr-1	1.95	ZC443.4	2.06
C49C8.8	1.76	ech-7	1.86	F49H6.5	1.95	W07G4.5	2.06
Y42G9A.1	1.77	C16A3.6	1.86	ZK430.7	1.95	C14A11.2	2.06
Y75B7AL.2	1.77	asp-6	1.86	nlp-59	1.96	lep-5	2.06
ptr-13	1.77	twk-7	1.86	lec-2	1.96	ZK1240.2	2.07
W03D8.8	1.78	gpcp-1	1.86	gpa-8	1.97	mrpl-55	2.07
T10B5.3	1.78	nhr-221	1.87	rpr-1	1.97	fbxa-163	2.07
memb-2	1.78	ZC239.16	1.87	E02H9.2	1.98	ins-29	2.07
B0478.3	1.79	C47D2.1	1.87	R01H10.4	1.98	nhr-103	2.07
exos-7	1.79	F53F4.11	1.88	F44G4.1	1.99	tre-5	2.08
srg-34	1.79	flp-20	1.88	pals-31	1.99	Y53C12B.7	2.08
nap-1	1.79	F21H7.2	1.88	C08F11.13	1.99	T12D8.5	2.08
wrb-1	1.79	C15B12.4	1.88	clec-65	1.99	ulp-4	2.09
yap-1	1.79	F02C12.3	1.88	btb-16	1.99	lgc-28	2.09
rncs-1	1.8	K02E7.11	1.89	F43D2.7	2	math-37	2.09
C38D4.7	1.8	nog-1	1.89	B0511.6	2	riok-1	2.09
K09E4.4	1.8	ulp-3	1.9	upb-1	2	obr-2	2.1
C25H3.18	1.8	T28A11.2	1.9	JC8.2	2	C28G1.6	2.1
nape-2	1.8	eif-3.B	1.9	F30A10.9	2	C40H1.9	2.1
F11C7.2	1.81	nhr-94	1.91	ZK355.8	2	adah-1	2.11
gcy-15	1.81	C23F12.4	1.91	ZK971.1	2	W02D7.11	2.11
C27B7.9	1.81	moe-3	1.91	C03G6.17	2.01	puf-12	2.11
peb-1	1.81	R10E8.6	1.91	fbxa-162	2.02	K09H9.5	2.11
elpc-3	1.81	F37A8.5	1.91	F55C5.2	2.02	B0563.5	2.11
fbxa-3	1.81	acl-9	1.91	C24H12.4	2.02	Y54H5A.1	2.11
T19C3.6	1.81	gst-20	1.92	nhr-80	2.02	E02H1.1	2.11
F40F8.5	1.81	K02C4.5	1.92	siah-1	2.02	mfb-1	2.12
K09F6.10	1.81	K02A2.5	1.92	ZK1290.13	2.02	odr-10	2.13
ZK822.4	1.82	clec-186	1.92	hpo-15	2.02	C53H9.2	2.14
Y47G6A.5	1.82	B0564.2	1.93	nas-9	2.03	H06H21.8	2.14
R02F11.2	1.82	rab-8	1.93	cpr-6	2.03	C34E11.4	2.14
fbxa-155	1.82	clec-146	1.93	lpd-7	2.03	F21A3.11	2.14
C39D10.11	1.82	linc-39	1.94	sma-2	2.04	linc-96	2.14

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
C10A4.3	2.15	Y34F4.2	2.27	B0524.6	2.4	ZC239.17	2.61
R09B5.11	2.15	W06H8.6	2.27	F54D5.3	2.4	AH9.7	2.61
T22F3.2	2.16	F10G7.5	2.28	nhr-129	2.4	Y32B12C.5	2.61
F57C12.6	2.16	lido-10	2.28	tag-243	2.4	chil-16	2.65
clec-85	2.16	Y54G2A.41	2.28	Y65B4BL.7	2.4	Y37H9A.5	2.65
ZK550.2	2.16	T25G3.3	2.29	T28H10.1	2.41	Y52B11A.10	2.66
T18D3.6	2.17	ZK688.11	2.29	srp-2	2.41	F47H4.12	2.66
fbxa-69	2.17	D1054.18	2.29	gst-37	2.42	flp-10	2.67
F36A2.2	2.17	ftn-1	2.29	ttr-49	2.42	Y56A3A.33	2.68
arch-1	2.17	dph-3	2.29	C05E11.6	2.42	cup-16	2.69
acp-5	2.17	F08F3.4	2.29	Y39B6A.33	2.44	lips-1	2.72
fbxa-80	2.17	F09C6.1	2.29	Y54G2A.10	2.45	F41G4.7	2.73
pudl-1	2.18	T02G5.14	2.29	ttr-29	2.45	pud-4	2.75
F48E8.3	2.18	C16C10.8	2.3	clec-84	2.45	T04C12.32	2.76
Y57G11C.1135	2.19	Y7A5A.6	2.3	F08F8.7	2.46	tut-1	2.79
nhr-18	2.19	K11D12.12	2.3	ctps-1	2.46	C25F9.12	2.81
Y40C5A.4	2.2	F47B8.4	2.3	nhr-88	2.47	col-95	2.82
C15C7.4	2.2	C45E5.4	2.31	F26G1.10	2.47	Y15E3A.4	2.82
T08B6.2	2.21	W03D8.2	2.31	M60.7	2.47	pudl-2	2.83
Y71G10AR.4	2.21	linc-43	2.32	metl-18	2.47	pqn-59	2.86
F29C6.1	2.22	B0546.3	2.33	F52E1.14	2.48	F18G5.6	2.87
C32H11.4	2.22	mnk-1	2.34	Y97E10AL.1	2.48	cyp-13A3	2.87
Y54H5A.2	2.22	C25F9.2	2.34	T26C11.9	2.49	chil-13	2.87
F08G12.11	2.23	T06C12.14	2.34	col-118	2.5	M01B2.13	2.88
Y47D3A.32	2.23	srap-1	2.35	faah-3	2.5	twk-5	2.88
C53A5.17	2.23	C11D2.3	2.35	linc-103	2.5	spp-8	2.9
metl-2	2.23	F58A3.3	2.35	tag-89	2.51	spp-6	2.91
fil-1	2.24	col-39	2.35	Y22D7AL.15	2.51	F54F12.1	2.91
R03D7.5	2.24	asah-2	2.36	F56A8.5	2.52	nlp-69	2.93
fbxa-173	2.24	tts-1	2.36	col-50	2.53	clec-61	2.94
F53F1.14	2.24	ngp-1	2.36	C09D4.2	2.54	Y48G8AL.13	2.96
T10H9.8	2.25	cyp-33C6	2.36	T03G11.3	2.54	nspc-16	2.96
txt-3	2.25	fat-6	2.37	Y54E10BR.4	2.54	arrd-11	2.97
F53F10.1	2.25	F31E9.3	2.37	nlp-2	2.54	ZK470.14	2.98
Y47H10A.3	2.25	C16A3.4	2.38	fard-1	2.55	nlp-52	3
cyp-37B1	2.26	pqn-62	2.38	T09B4.6	2.56	cyp-32B1	3
T22B7.3	2.26	T10H4.13	2.38	C29G2.2	2.58	W03D2.6	3.02
F21C10.11	2.26	F55A4.7	2.38	C24A11.1	2.58	T26H5.4	3.03
Y43B11AR.3	2.27	R10E8.1	2.39	Y46G5A.34	2.59	C17G10.6	3.06
R07E3.1	2.27	F59A7.8	2.39	exc-13	2.6	F35H8.1	3.07
F31B12.3	2.27	pho-6	2.4	T10B5.7	2.61	hda-5	3.08

Gene	log2FC
T26E3.4	3.1
D1086.2	3.11
pmt-1	3.15
cest-1.2	3.16
F16A11.5	3.17
F35C8.5	3.17
F36A2.10	3.17
F16B4.5	3.19
F23F12.3	3.19
K05F6.10	3.19
hecw-1	3.23
nspc-14	3.24
C05D9.9	3.26
T10C6.15	3.28
hrg-2	3.31
F43C11.7	3.32
C32F10.4	3.37
clec-264	3.39
C45E1.4	3.41
C18H9.5	3.42
W10G11.1	3.42
T08A9.13	3.43
col-181	3.47
ncr-2	3.48
ZK593.2	3.48
F42A9.18	3.5
F40E3.5	3.59
ZK185.5	3.6
B0379.7	3.61
F21H7.12	3.62
F56F11.1	3.68
B0513.4	3.79
F47B8.8	3.79
F56H9.2	3.81
cpr-2	3.84
W08E12.8	3.89
ins-3	4.01
dpy-5	4.82
T28A11.16	4.86
srv-4	5.01
hsp-12.6	5.35

6.17. RNA-seq (CeGaT) - 4h Fed vs 48h Starved - HBR1777 (*flp-11*::EGL-1)

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T22F3.11	-4.54	skr-15	-2.76	set-22	-2.56	mbtr-1	-2.41
C23G10.11	-4.08	gld-3	-2.75	sdz-30	-2.56	act-5	-2.41
Y39B6A.1	-3.89	grl-21	-2.75	hacd-1	-2.56	col-145	-2.41
W10C8.5	-3.69	kreg-1	-2.74	nspb-12	-2.55	F44E7.5	-2.41
R02C2.7	-3.59	lsy-27	-2.74	asns-1	-2.55	R04B5.5	-2.4
F46F2.3	-3.59	Y7A9A.79	-2.74	ora-1	-2.54	ctf-8	-2.4
T07D3.9	-3.5	F57F4.4	-2.74	clec-91	-2.54	pcn-1	-2.4
gst-26	-3.25	clec-88	-2.74	Y47D3B.6	-2.53	W03C9.2	-2.39
W05F2.3	-3.11	lbp-6	-2.74	idh-1	-2.53	Y73B3A.1	-2.39
C35C5.8	-3.08	T12G3.6	-2.72	lon-1	-2.53	tyr-2	-2.39
C09B8.4	-3.04	vet-2	-2.72	T21C9.13	-2.52	Y73F8A.13	-2.39
mdh-2	-3.01	C44B9.3	-2.71	nhr-2	-2.52	C14B1.9	-2.39
spn-4	-3	Y71A12B.11	-2.71	cyb-3	-2.51	best-1	-2.38
mex-5	-2.99	pqn-22	-2.7	cdc-25.3	-2.51	cbd-1	-2.38
aptf-4	-2.98	mcm-7	-2.69	Y68A4B.3	-2.5	ZK1290.10	-2.38
T05F1.2	-2.98	Y39G10AL.1	-2.69	fbxb-104	-2.5	ZC155.4	-2.38
C45B2.2	-2.98	srh-237	-2.69	F35B3.4	-2.49	Y42H9B.3	-2.38
cyb-2.2	-2.95	mom-2	-2.68	F18A1.7	-2.49	abu-8	-2.38
C05C10.5	-2.95	F22B5.4	-2.68	C42C1.8	-2.49	B0393.3	-2.38
sdz-28	-2.95	abu-10	-2.67	T04D3.1	-2.48	gld-1	-2.37
R09E12.9	-2.93	glp-1	-2.67	szy-4	-2.48	mcm-2	-2.37
puf-11	-2.92	Y43B11AL.1	-2.66	dct-16	-2.48	T06E4.14	-2.37
ceh-49	-2.92	ZC308.4	-2.65	cnc-6	-2.48	jmjd-3.2	-2.37
era-1	-2.91	C42D4.3	-2.65	F54F7.6	-2.48	gcna-1	-2.37
vet-6	-2.86	F14H12.3	-2.65	gna-2	-2.48	R04D3.2	-2.37
trcs-1	-2.85	F54H12.5	-2.65	fbxa-215	-2.47	gpd-4	-2.37
hphd-1	-2.85	sdz-4	-2.65	pho-11	-2.47	ctf-4	-2.36
F17A9.5	-2.85	col-166	-2.64	cyb-1	-2.47	tpxl-1	-2.36
sun-1	-2.84	C35E7.3	-2.64	pqn-26	-2.47	cey-3	-2.36
puf-3	-2.83	col-113	-2.62	C31H1.8	-2.46	cah-4	-2.36
folt-2	-2.82	flh-1	-2.62	Y106G6D.2	-2.45	F38B2.4	-2.36
mar-3	-2.82	F09E10.1	-2.61	dsl-2	-2.45	EEED8.3	-2.36
fbxb-35	-2.8	gpd-1	-2.61	phat-4	-2.45	gsnl-1	-2.36
pos-1	-2.8	mcm-3	-2.61	T19B10.2	-2.45	R11.4	-2.36
mex-1	-2.8	acdh-1	-2.6	F14H3.6	-2.45	Y110A7A.15	-2.36
F46C5.1	-2.79	clec-87	-2.58	col-33	-2.45	F28B4.3	-2.36
W06B4.1	-2.79	Y106G6D.1	-2.58	nasp-2	-2.44	DY3.8	-2.36
vet-1	-2.79	ZK1037.6	-2.58	syp-6	-2.44	C23H5.8	-2.35
pqn-63	-2.78	mct-5	-2.57	C01G6.3	-2.43	M195.2	-2.35
F41E6.11	-2.78	pqn-74	-2.56	C29A12.1	-2.42	Y4C6B.1	-2.35
pie-1	-2.76	ptr-2	-2.56	flh-3	-2.42	fmo-3	-2.35
cpr-4	-2.76	F56C9.6	-2.56	W04A8.5	-2.41	K11G9.5	-2.35

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
R09F10.8	-2.35	grl-4	-2.26	rnr-1	-2.2	scc-1	-2.14
pqn-71	-2.35	pch-2	-2.26	knl-1	-2.2	T05B9.1	-2.14
ZK662.2	-2.34	F13E9.14	-2.26	hcp-2	-2.2	inx-14	-2.14
F23A7.8	-2.34	fbxb-3	-2.26	col-48	-2.2	C06E2.5	-2.14
asns-2	-2.34	fbxb-95	-2.26	mut-2	-2.2	Y54G9A.5	-2.13
T11B7.1	-2.33	nlp-30	-2.26	orc-1	-2.2	sld-2	-2.13
T05D4.2	-2.33	Y22D7AL.10	-2.25	pole-1	-2.2	T14B4.5	-2.13
ZK829.9	-2.33	col-97	-2.25	zen-4	-2.19	D2096.6	-2.13
pash-1	-2.33	Y38E10A.28	-2.25	ify-1	-2.19	C55B7.11	-2.13
F22H10.2	-2.33	K01A6.4	-2.25	tost-1	-2.19	W08E12.3	-2.13
toca-2	-2.32	T04F8.8	-2.25	K07A1.17	-2.19	W08E12.6	-2.13
C50F7.5	-2.32	sdz-14	-2.25	sdz-24	-2.19	T25E12.6	-2.12
F14D7.2	-2.32	T05H10.4	-2.25	Y47H9C.1	-2.19	btb-11	-2.12
nlp-34	-2.32	fzy-1	-2.25	chaf-2	-2.19	Y47D3A.1	-2.12
egg-3	-2.32	K03H1.7	-2.24	F11E6.7	-2.19	abu-14	-2.12
Y39B6A.10	-2.32	dod-19	-2.24	R11A5.3	-2.19	acs-2	-2.11
K04G2.10	-2.32	Y14H12B.2	-2.24	lec-6	-2.18	F56F4.8	-2.11
egg-6	-2.32	C23H4.8	-2.24	C01G8.1	-2.18	hmg-3	-2.11
oma-2	-2.31	hlh-3	-2.23	skr-7	-2.17	F32D1.7	-2.11
puf-5	-2.31	T20B6.3	-2.23	fbp-1	-2.17	mcm-4	-2.11
sas-6	-2.31	skr-14	-2.23	act-3	-2.17	C27A2.5	-2.11
T19H12.2	-2.3	W03F9.4	-2.23	F08F8.4	-2.17	pqn-60	-2.1
Y110A2AR.1	-2.3	F19B10.10	-2.23	cnc-4	-2.17	ZK1320.9	-2.1
F59A7.2	-2.3	fbxc-18	-2.23	T16G12.8	-2.17	F16H11.1	-2.1
cdc-7	-2.3	tofu-7	-2.23	C31H2.4	-2.17	hpo-6	-2.1
capg-2	-2.3	ect-2	-2.22	F13A7.14	-2.16	Y49F6B.12	-2.09
wee-1.3	-2.3	F56C9.3	-2.22	F58G6.3	-2.16	col-109	-2.09
nlp-31	-2.29	fbxb-72	-2.22	EGAP4.1	-2.16	F54D5.2	-2.09
gyg-2	-2.29	Y51F10.2	-2.22	air-1	-2.15	pgph-2	-2.09
grd-13	-2.29	brd-1	-2.22	C48B4.9	-2.15	cdk-1	-2.09
T03F6.3	-2.29	pid-4	-2.22	ZK896.4	-2.15	inx-2	-2.09
mis-12	-2.28	ttr-31	-2.22	ttr-7	-2.15	irg-4	-2.09
R12A1.3	-2.28	ZK6.11	-2.22	T10B11.8	-2.15	T09F5.1	-2.08
F53F8.3	-2.28	R05H5.3	-2.21	nlp-77	-2.15	F21C10.9	-2.08
B0024.4	-2.28	F20B10.3	-2.21	C08F1.6	-2.15	col-14	-2.08
btb-6	-2.28	rad-51	-2.21	M03E7.4	-2.15	clec-266	-2.07
ZK1053.4	-2.27	T28A8.3	-2.21	F48E3.6	-2.15	zipt-7.1	-2.07
W04A8.1	-2.27	valv-1	-2.21	Y43F8B.3	-2.14	grl-6	-2.07
alg-5	-2.27	C38D4.4	-2.21	ceh-83	-2.14	bus-17	-2.07
C08F8.3	-2.27	B0281.5	-2.21	idhg-2	-2.14	D2005.7	-2.07
T24C12.4	-2.27	dut-1	-2.21	T01B7.8	-2.14	F08F3.6	-2.06
ugt-19	-2.27	ZK970.7	-2.2	ldh-1	-2.14	mltn-9	-2.06

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
Y37H2A.14	-2.06	tyms-1	-2.02	cdl-1	-1.98	clx-1	-1.94
pig-1	-2.06	ttr-2	-2.02	col-146	-1.98	cks-1	-1.94
dhcr-24	-2.06	R03C1.1	-2.02	nas-38	-1.97	adal-1	-1.94
syp-5	-2.06	skr-17	-2.01	D1054.9	-1.97	Y60C6A.2	-1.93
col-144	-2.06	smd-1	-2.01	plk-1	-1.97	anmt-2	-1.93
B0001.7	-2.06	cey-2	-2.01	C49F5.6	-1.97	grd-10	-1.93
hsp-16.41	-2.06	pole-4	-2.01	clec-78	-1.97	hmbx-1	-1.93
mua-6	-2.06	Y38H6A.3	-2.01	B0403.5	-1.97	cpt-4	-1.93
K05F6.4	-2.06	F53F1.4	-2.01	orc-3	-1.97	noah-2	-1.93
skr-10	-2.06	phg-1	-2	F09C8.1	-1.97	R144.10	-1.93
C54D2.1	-2.05	dod-18	-2	psf-2	-1.97	fip-5	-1.93
K02B7.3	-2.05	gln-6	-2	kbp-3	-1.97	pqn-29	-1.93
mcm-6	-2.05	fbxb-66	-2	ptr-1	-1.97	cmt-1	-1.93
F13H8.5	-2.05	ZC434.8	-2	mcm-5	-1.96	Y45G5AM.5	-1.93
toe-2	-2.05	F56F11.4	-2	such-1	-1.96	zim-1	-1.93
abu-11	-2.05	hil-5	-2	lbp-5	-1.96	C01B12.8	-1.93
T16G12.4	-2.05	air-2	-2	F55H12.4	-1.96	F58G11.3	-1.93
ZK742.3	-2.05	acdh-6	-2	B0034.7	-1.96	W02B8.2	-1.92
hpo-36	-2.05	T10E10.4	-2	mre-11	-1.96	dhs-27	-1.92
clec-48	-2.04	phat-1	-2	sip-1	-1.96	cnc-8	-1.92
W03D2.9	-2.04	snpc-1.2	-1.99	aqp-7	-1.96	mlc-7	-1.92
T06D8.10	-2.04	inx-3	-1.99	R12C12.10	-1.96	cup-15	-1.92
mdf-2	-2.04	lys-3	-1.99	nhr-12	-1.96	pri-1	-1.92
C36B7.5	-2.04	fbxc-32	-1.99	acox-1.4	-1.96	Y41D4B.15	-1.92
fbxb-54	-2.04	F44E2.4	-1.99	M03B6.4	-1.96	cpg-1	-1.92
F54D10.5	-2.04	C05D12.4	-1.99	C35E7.5	-1.96	C03D6.9	-1.92
T25E4.1	-2.03	R74.2	-1.99	acn-1	-1.96	F13D12.3	-1.92
clec-180	-2.03	T27A1.2	-1.99	F41E6.5	-1.96	dpl-1	-1.92
T05E12.6	-2.03	ilys-5	-1.99	EEED8.15	-1.96	C40A11.2	-1.92
abu-12	-2.03	nspe-5	-1.99	crn-1	-1.95	brc-1	-1.92
rod-1	-2.03	cdt-1	-1.98	hpo-40	-1.95	ung-1	-1.92
skr-13	-2.03	spp-20	-1.98	K08D8.3	-1.95	skr-8	-1.92
M153.3	-2.03	taf-11.2	-1.98	prom-1	-1.95	wago-1	-1.91
Y59A8B.12	-2.03	F20G2.2	-1.98	fbxb-15	-1.95	bub-1	-1.91
cest-33	-2.03	F07H5.13	-1.98	Y82E9BR.17	-1.95	noah-1	-1.91
pri-2	-2.03	ZK84.1	-1.98	C49H3.16	-1.95	bath-10	-1.91
skr-9	-2.03	srg-31	-1.98	Y46G5A.7	-1.95	his-74	-1.91
kbp-5	-2.02	rsa-1	-1.98	D2030.7	-1.94	icl-1	-1.91
fbxb-24	-2.02	srpr-2.1	-1.98	F54D5.5	-1.94	mcm-10	-1.91
fbxb-75	-2.02	kbp-2	-1.98	cht-2	-1.94	C06G1.1	-1.91
zif-1	-2.02	lec-8	-1.98	F49C12.7	-1.94	inft-2	-1.91
nspe-7	-2.02	F07H5.8	-1.98	F15A4.2	-1.94	C08F1.10	-1.91

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T28A8.4	-1.91	F54E7.6	-1.87	K10H10.4	-1.83	Y111B2A.2	-1.79
cyn-9	-1.9	Y52E8A.2	-1.87	aptf-2	-1.83	C35B1.5	-1.79
aly-2	-1.9	F15G9.6	-1.87	dpy-1	-1.83	Y69A2AR.28	-1.79
R05H10.3	-1.9	elo-6	-1.87	lem-3	-1.83	C36B1.11	-1.79
pgl-3	-1.9	C26B2.8	-1.86	cutl-23	-1.83	Y58A7A.2	-1.79
T06E4.8	-1.9	C24H12.1	-1.86	Y73B6BL.23	-1.83	msh-2	-1.79
F55A11.7	-1.9	cyp-23A1	-1.86	T23F2.5	-1.83	sdz-38	-1.79
Y46G5A.8	-1.9	acs-11	-1.86	mesp-1	-1.83	C55A1.6	-1.78
F11E6.4	-1.9	neg-1	-1.86	grl-1	-1.83	D1081.6	-1.78
immt-2	-1.89	T09B9.1	-1.86	skpt-1	-1.83	T12G3.4	-1.78
F49D11.6	-1.89	C55A6.12	-1.86	htp-3	-1.83	F59B10.3	-1.78
hcp-1	-1.89	san-1	-1.86	memi-2	-1.82	fncm-1	-1.78
hcp-6	-1.89	cyp-35C1	-1.86	elo-4	-1.82	htp-1	-1.78
tipn-1	-1.89	dscc-1	-1.86	dnsn-1	-1.82	klp-18	-1.78
skpo-2	-1.89	rsp-5	-1.86	misc-1	-1.82	F58G1.7	-1.78
orc-5	-1.89	klc-1	-1.86	nas-13	-1.82	dnj-11	-1.78
nstp-2	-1.89	Y57G11C.42	-1.86	nos-1	-1.81	vang-1	-1.78
F39D8.3	-1.89	C28C12.4	-1.85	lam-3	-1.81	gla-3	-1.78
K02B12.2	-1.89	T05H4.7	-1.85	ttr-50	-1.81	C45B2.8	-1.78
hsp-60	-1.89	ndc-80	-1.85	R07B1.9	-1.81	Y111B2A.3	-1.78
hsp-16.2	-1.89	C56C10.4	-1.85	trt-1	-1.81	pcmd-1	-1.78
rrn-2.1	-1.89	T06A4.3	-1.85	ced-3	-1.81	fem-3	-1.78
top-2	-1.89	Y52B11A.8	-1.85	K08D12.4	-1.81	ech-6	-1.78
gst-28	-1.88	cnc-3	-1.85	fbxc-44	-1.81	Y71F9AL.6	-1.77
math-45	-1.88	glh-3	-1.85	ttr-45	-1.81	kbp-1	-1.77
him-10	-1.88	tag-63	-1.85	ifa-3	-1.8	cdd-2	-1.77
aagr-4	-1.88	M03F8.1	-1.85	syp-1	-1.8	Y37A1B.5	-1.77
ttr-15	-1.88	bca-1	-1.85	lbp-3	-1.8	F32D8.11	-1.77
F53H4.3	-1.88	hpr-17	-1.84	col-182	-1.8	grl-16	-1.77
xnd-1	-1.88	C37C3.9	-1.84	F32D8.7	-1.8	oac-31	-1.77
T08B1.1	-1.88	act-1	-1.84	fib-1	-1.8	dsh-2	-1.77
F40E10.5	-1.88	F10D11.6	-1.84	F54E2.1	-1.8	C24H10.3	-1.77
mes-4	-1.87	Y75B8A.18	-1.84	C46C2.7	-1.8	C06E1.1	-1.77
B0310.6	-1.87	him-3	-1.84	lys-1	-1.8	K07F5.12	-1.77
spo-11	-1.87	atz-1	-1.84	mdh-1	-1.8	ech-4	-1.77
linc-13	-1.87	lron-2	-1.84	lips-7	-1.8	C35A5.10	-1.77
icp-1	-1.87	hsp-17	-1.84	csc-1	-1.8	Y105C5B.19	-1.77
K10D11.7	-1.87	F10D2.8	-1.84	col-186	-1.8	fkb-7	-1.77
fbxb-78	-1.87	let-754	-1.84	rnr-2	-1.8	cpg-9	-1.77
pqn-32	-1.87	C17E4.2	-1.84	R09E10.5	-1.8	C06C3.4	-1.77
hil-4	-1.87	rbm-3.1	-1.84	ZK180.5	-1.8	unc-59	-1.77
F31D4.8	-1.87	fbxa-83	-1.83	hasp-1	-1.79	F44E2.10	-1.76

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
C09B8.5	-1.76	Y42A5A.5	-1.73	F30F8.1	-1.7	hal-3	-1.69
D2005.4	-1.76	F01D4.5	-1.73	K08B4.2	-1.7	hch-1	-1.68
ceh-86	-1.76	Y32G9B.1	-1.73	Y106G6H.6	-1.7	M199.2	-1.68
fbxc-29	-1.76	cutl-10	-1.73	cutl-9	-1.7	ins-26	-1.68
nxf-2	-1.76	C48B4.13	-1.73	C27B7.5	-1.7	apy-1	-1.68
aspm-1	-1.76	mlt-11	-1.72	div-1	-1.7	ZK829.3	-1.68
H01G02.1	-1.76	pqn-36	-1.72	lpr-1	-1.7	Y57G11C.39	-1.68
oef-1	-1.76	mam-1	-1.72	R186.8	-1.7	dhs-8	-1.68
F33H2.3	-1.76	Y97E10AR.4	-1.72	C56E6.2	-1.7	dhs-23	-1.68
K04C2.5	-1.76	K01D12.8	-1.72	F55F8.8	-1.7	che-14	-1.68
cut-2	-1.76	K08D12.8	-1.72	col-115	-1.7	erh-2	-1.68
T04D3.5	-1.76	hal-2	-1.72	col-174	-1.7	kin-15	-1.68
E01G6.1	-1.75	tofu-6	-1.72	ram-5	-1.7	cyk-4	-1.68
par-2	-1.75	R04B3.3	-1.72	rmd-1	-1.7	nop-1	-1.68
C53A5.2	-1.75	gsto-1	-1.72	F53A2.3	-1.7	fbxb-84	-1.68
C15C6.1	-1.75	nhr-137	-1.72	F46G11.6	-1.7	htz-1	-1.68
C56G2.15	-1.75	T26C12.3	-1.72	bmk-1	-1.7	mans-4	-1.68
Y53F4B.27	-1.75	F32D8.12	-1.72	F58E6.13	-1.7	col-104	-1.68
argk-1	-1.75	T16G12.1	-1.72	Y71G12B.6	-1.7	cutl-17	-1.68
D2030.8	-1.75	set-31	-1.72	lgc-34	-1.69	F30H5.3	-1.68
F42A8.1	-1.75	fbxb-85	-1.72	F02C12.1	-1.69	C48B6.9	-1.68
F14B6.3	-1.75	Y11D7A.9	-1.72	Y68A4A.13	-1.69	fbn-1	-1.68
T19C4.1	-1.75	F59A6.5	-1.72	ZK512.1	-1.69	B0261.7	-1.68
K08H2.4	-1.75	pgp-14	-1.72	W08E12.2	-1.69	nol-56	-1.67
gbh-1	-1.75	T02G5.7	-1.72	chtl-1	-1.69	R02F11.1	-1.67
nhr-127	-1.75	R11H6.4	-1.72	glf-1	-1.69	C39B5.2	-1.67
papl-1	-1.75	pho-14	-1.71	F14D7.12	-1.69	K01D12.1	-1.67
cdk-4	-1.75	Y48G1A.2	-1.71	col-131	-1.69	prg-1	-1.67
hcp-4	-1.75	F13E9.13	-1.71	F46C8.8	-1.69	B0205.13	-1.67
M153.1	-1.74	W04H10.2	-1.71	F46C3.6	-1.69	cec-4	-1.67
kbp-4	-1.74	D2092.8	-1.71	C44C1.1	-1.69	ZK596.3	-1.67
pfn-1	-1.74	C46A5.4	-1.71	C34C12.7	-1.69	eat-5	-1.67
psf-3	-1.74	grl-11	-1.71	sodh-1	-1.69	C54G4.4	-1.67
txdc-12.1	-1.74	srpr-2.2	-1.71	C34C12.8	-1.69	F10E9.7	-1.67
htp-2	-1.74	sptl-2	-1.71	tsp-1	-1.69	sdha-2	-1.67
VF13D12L.3	-1.74	slc-25A10	-1.71	C17C3.1	-1.69	C18E9.7	-1.67
let-99	-1.74	bir-2	-1.71	Y39D8A.1	-1.69	fkb-4	-1.67
gst-39	-1.73	C09F9.2	-1.71	F44F1.6	-1.69	mlt-9	-1.66
hrde-1	-1.73	cht-1	-1.71	rmh-1	-1.69	ZK643.2	-1.66
psf-1	-1.73	cec-8	-1.71	rnp-8	-1.69	fbxc-40	-1.66
E04F6.6	-1.73	alh-5	-1.7	atf-8	-1.69	cuti-1	-1.66
C16D9.1	-1.73	dex-1	-1.7	rfc-4	-1.69	lin-53	-1.66

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
acaa-2	-1.66	hsp-12.1	-1.63	ifd-2	-1.6	F36H5.4	-1.58
ptr-18	-1.66	C40A11.3	-1.63	orc-4	-1.6	col-58	-1.58
smc-5	-1.66	C32D5.12	-1.63	cutl-8	-1.6	nstp-3	-1.58
kat-1	-1.66	F46F3.3	-1.63	C02F4.4	-1.6	F53A9.3	-1.58
fip-6	-1.66	mei-1	-1.63	gcsh-1	-1.6	fbxb-45	-1.58
chs-2	-1.66	set-9	-1.63	rde-4	-1.6	F32A7.8	-1.58
wdr-5.3	-1.65	ska-3	-1.63	F46G11.2	-1.6	knl-3	-1.58
F31D4.5	-1.65	pid-3	-1.63	F27C1.4	-1.6	slc-17.8	-1.58
bath-41	-1.65	oac-14	-1.63	K08B4.7	-1.6	C08B6.4	-1.58
hog-1	-1.65	bus-12	-1.62	ima-2	-1.59	T16G1.2	-1.58
R12E2.7	-1.65	ugt-29	-1.62	C29F3.7	-1.59	paqr-3	-1.58
nhr-205	-1.65	wrt-4	-1.62	F41C3.11	-1.59	Y47G6A.31	-1.58
col-54	-1.65	F59A6.10	-1.62	C49G7.7	-1.59	sdhd-1	-1.58
C48B4.11	-1.65	cpr-5	-1.62	R13H4.8	-1.59	T28C12.6	-1.58
zeel-1	-1.65	lst-1	-1.62	nex-1	-1.59	F44E5.4	-1.58
tag-307	-1.65	agmo-1	-1.62	fbxc-51	-1.59	F33H2.6	-1.58
chw-1	-1.65	C26B9.7	-1.62	cutl-28	-1.59	ugt-57	-1.58
Y65B4BL.1	-1.64	C14A4.9	-1.62	F40F11.3	-1.59	F07H5.10	-1.57
lrr-1	-1.64	algn-6	-1.62	smo-1	-1.59	gei-14	-1.57
F20G2.1	-1.64	cutl-18	-1.62	T26C5.2	-1.59	spd-5	-1.57
F59B2.8	-1.64	T27E9.2	-1.62	dpy-18	-1.59	pola-1	-1.57
cpr-1	-1.64	col-154	-1.62	F26A1.9	-1.59	F43D9.1	-1.57
ztf-11	-1.64	ttr-30	-1.62	Y49E10.4	-1.59	K06A9.3	-1.57
Y16B4A.2	-1.64	bgnt-1.2	-1.62	fbxc-25	-1.59	klp-19	-1.57
fog-2	-1.64	fbxa-210	-1.62	ogr-2	-1.59	R08A2.5	-1.57
metr-1	-1.64	mec-7	-1.62	F56D2.3	-1.59	R08F11.4	-1.57
cut-3	-1.64	F36F12.1	-1.61	B0393.5	-1.59	E01A2.2	-1.57
phat-2	-1.64	F44E5.5	-1.61	ZK675.4	-1.59	tts-2	-1.57
rsp-4	-1.64	pal-1	-1.61	ced-8	-1.59	lpr-5	-1.57
daf-6	-1.64	F30A10.2	-1.61	cest-10	-1.59	pck-1	-1.57
nas-30	-1.64	W06D11.1	-1.61	F15B10.3	-1.59	gfi-1	-1.57
Y39A1A.21	-1.64	ptr-15	-1.61	pgk-1	-1.59	nspe-1	-1.57
C41D11.9	-1.64	M03F4.6	-1.61	ckb-2	-1.59	F08B12.4	-1.57
C18D11.6	-1.64	C46H11.7	-1.61	T06G6.12	-1.59	ZK180.6	-1.56
F15H10.8	-1.64	ech-1.1	-1.61	mtp-18	-1.59	ZK742.4	-1.56
Y23H5B.8	-1.64	spdl-1	-1.61	Y71F9AL.7	-1.58	tag-297	-1.56
exo-1	-1.64	T05H10.3	-1.61	M04C9.3	-1.58	cpna-3	-1.56
T17H7.7	-1.64	cyn-10	-1.61	lips-3	-1.58	sys-1	-1.56
nep-16	-1.63	fipr-7	-1.61	Y75B7AR.1	-1.58	chaf-1	-1.56
swip-10	-1.63	F29G6.1	-1.6	plpr-1	-1.58	clec-196	-1.56
K02E10.4	-1.63	snr-2	-1.6	C30B5.6	-1.58	ani-2	-1.56
F35H10.10	-1.63	pho-1	-1.6	hmg-20	-1.58	cnc-11	-1.56

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
pigv-1	-1.56	F52B5.2	-1.54	F18E3.12	-1.52	daf-18	-1.49
nas-10	-1.56	ceh-30	-1.54	edg-1	-1.52	H10E21.4	-1.49
dod-3	-1.56	T07F10.6	-1.54	dhs-30	-1.52	Y63D3A.7	-1.49
T02C1.1	-1.56	ins-34	-1.54	eppl-1	-1.52	gpdh-2	-1.49
ugt-63	-1.56	tth-1	-1.54	D1081.7	-1.51	Y57G11A.4	-1.49
F26G1.5	-1.56	ndx-2	-1.54	lron-8	-1.51	ZK1098.3	-1.49
C50C3.1	-1.55	C01H6.8	-1.53	rocf-1	-1.51	C45G9.2	-1.49
swah-1	-1.55	F18A11.2	-1.53	lpr-6	-1.51	rfc-2	-1.49
tcab-1	-1.55	ttr-18	-1.53	sqt-3	-1.51	lin-54	-1.49
F56D2.2	-1.55	ZC449.1	-1.53	sid-1	-1.51	jud-4	-1.49
dnj-27	-1.55	Y39B6A.42	-1.53	M28.5	-1.51	VH15N14R.1	-1.49
ces-2	-1.55	coq-5	-1.53	F54D5.9	-1.51	knl-2	-1.49
rsa-2	-1.55	alh-13	-1.53	F08G12.5	-1.51	dsl-6	-1.49
H03E18.1	-1.55	C45E5.1	-1.53	dhs-19	-1.51	F35A5.4	-1.49
cutl-2	-1.55	tag-10	-1.53	T26A5.2	-1.51	Y37A1B.7	-1.49
D1005.2	-1.55	pcp-2	-1.53	C50D2.1	-1.51	col-74	-1.48
T14G8.4	-1.55	vap-2	-1.53	T19C3.2	-1.5	F09F9.2	-1.48
ugt-34	-1.55	linc-1	-1.53	npp-22	-1.5	let-268	-1.48
clik-1	-1.55	syx-4	-1.53	gpaa-1	-1.5	hira-1	-1.48
fan-1	-1.55	dnj-2	-1.53	cutl-16	-1.5	fbxa-206	-1.48
inf-1	-1.55	ctg-2	-1.53	C05C10.3	-1.5	daf-36	-1.48
ssna-1	-1.55	suds-3	-1.53	lpr-3	-1.5	aman-1	-1.48
dif-1	-1.55	F23A7.4	-1.53	F58H1.2	-1.5	F18C5.9	-1.48
F33H12.7	-1.55	tdpt-1	-1.53	lron-1	-1.5	Y73F8A.26	-1.48
C05E7.2	-1.55	zwl-1	-1.53	irg-5	-1.5	pot-2	-1.48
ZC123.1	-1.55	ttr-33	-1.53	unc-61	-1.5	grd-12	-1.48
ppm-1.G	-1.54	gpr-1	-1.53	T06E4.9	-1.5	F41G3.21	-1.48
F15D3.6	-1.54	exo-3	-1.53	Y17D7C.4	-1.5	C31C9.2	-1.48
col-75	-1.54	twk-11	-1.53	lact-4	-1.5	C44B7.7	-1.48
F21H7.3	-1.54	M02G9.1	-1.52	C05D11.5	-1.5	C04A11.2	-1.48
W04A8.6	-1.54	cutl-5	-1.52	F38A6.4	-1.5	fat-5	-1.48
Y73F4A.1	-1.54	col-111	-1.52	col-130	-1.5	C35A5.11	-1.48
pqn-73	-1.54	F01D5.6	-1.52	rba-1	-1.5	K01D12.5	-1.48
scl-6	-1.54	C01B10.11	-1.52	cutl-25	-1.49	dpy-2	-1.48
W01C9.1	-1.54	cut-5	-1.52	T10E9.8	-1.49	Y47D7A.13	-1.48
bus-8	-1.54	dna-2	-1.52	vha-12	-1.49	C27H6.9	-1.48
dsl-3	-1.54	cpg-4	-1.52	sas-5	-1.49	abu-13	-1.48
ifp-1	-1.54	spsb-2	-1.52	col-169	-1.49	sgo-1	-1.48
Y11D7A.5	-1.54	ttr-26	-1.52	lgc-27	-1.49	Y41G9A.5	-1.48
col-167	-1.54	cnc-10	-1.52	dyf-7	-1.49	F29B9.5	-1.48
ugt-33	-1.54	C06C3.10	-1.52	C25F9.4	-1.49	anmt-3	-1.48
C15A11.4	-1.54	F15B9.8	-1.52	B0432.8	-1.49	col-121	-1.48

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
tim-1	-1.48	mlt-8	-1.45	col-177	-1.42	ntp-1	-1.4
Y37A1A.4	-1.47	B0272.3	-1.45	dtmk-1	-1.42	ttr-20	-1.4
lgc-21	-1.47	F52G3.5	-1.45	F44G4.3	-1.42	F56C11.5	-1.4
T03G6.1	-1.47	tdc-1	-1.45	Y53F4B.23	-1.42	ZK154.1	-1.4
F53B1.4	-1.47	fkb-5	-1.45	ptps-1	-1.42	Y54G11A.3	-1.4
lgc-33	-1.47	msh-6	-1.45	F31E3.12	-1.42	pges-2	-1.4
F59A3.12	-1.47	B0205.4	-1.45	cblc-1	-1.42	F10C1.9	-1.4
clec-4	-1.47	R08D7.7	-1.45	npp-15	-1.42	ZK228.4	-1.4
C39E9.12	-1.47	cee-1	-1.45	deps-1	-1.42	B0334.13	-1.4
dhhc-1	-1.47	K11H12.5	-1.45	wdr-48	-1.42	cpt-6	-1.39
grl-15	-1.47	R05H11.2	-1.45	C01G6.9	-1.42	ttr-32	-1.39
puf-8	-1.47	cest-35.2	-1.44	hsp-25	-1.42	unc-71	-1.39
tag-342	-1.47	bub-3	-1.44	acdh-12	-1.42	erd-2.2	-1.39
T22D1.5	-1.47	rbbp-5	-1.44	C34H4.2	-1.42	ZK1307.8	-1.39
pqn-67	-1.47	B0041.8	-1.44	ZK287.4	-1.42	F14F9.3	-1.39
efl-1	-1.47	fcd-2	-1.44	rfc-3	-1.41	K02D3.2	-1.39
emb-27	-1.47	cutl-12	-1.44	T09B4.5	-1.41	F44B9.2	-1.39
grd-15	-1.47	npax-2	-1.44	sex-1	-1.41	meg-3	-1.39
Y62E10A.13	-1.46	bca-2	-1.44	swt-5	-1.41	set-32	-1.39
C52G5.2	-1.46	F55G1.6	-1.44	col-105	-1.41	pph-4.2	-1.39
dpy-10	-1.46	R02E4.3	-1.44	R10H10.6	-1.41	ZK596.1	-1.39
ugt-22	-1.46	bath-15	-1.44	dpy-14	-1.41	pot-1	-1.39
F12F6.7	-1.46	acer-1	-1.44	C28C12.12	-1.41	dhfr-1	-1.39
polh-1	-1.46	nas-7	-1.44	ttr-53	-1.41	lir-3	-1.39
swt-6	-1.46	hhat-2	-1.44	ucr-2.3	-1.41	F46E10.2	-1.39
T11G6.4	-1.46	F56D3.1	-1.44	ugt-45	-1.41	lec-10	-1.39
K09D9.1	-1.46	M02H5.8	-1.44	lgx-1	-1.41	cyn-17	-1.39
col-155	-1.46	F33D4.6	-1.44	pqn-13	-1.41	F42A10.7	-1.39
T24H10.4	-1.46	cpr-3	-1.44	otub-3	-1.4	smc-3	-1.39
C15F1.1	-1.46	Y69H2.7	-1.43	sod-1	-1.4	pam-1	-1.39
Y53G8AR.6	-1.46	M01D1.12	-1.43	iff-1	-1.4	dpy-17	-1.39
txt-4	-1.46	T06E4.10	-1.43	haao-1	-1.4	zim-3	-1.39
pfkb-1.2	-1.46	R07E5.4	-1.43	ceh-39	-1.4	F52B5.7	-1.39
dsb-2	-1.46	ZK816.4	-1.43	cutl-11	-1.4	blos-4	-1.38
Y66C5A.1	-1.46	B0035.15	-1.43	gsto-2	-1.4	F43C11.6	-1.38
oac-51	-1.45	F26F12.4	-1.43	T23F6.1	-1.4	W02F12.8	-1.38
Y62E10A.19	-1.45	atf-2	-1.43	ZK1127.13	-1.4	C14C6.5	-1.38
fbxb-77	-1.45	Y55F3C.17	-1.43	F45F2.11	-1.4	ZK973.1	-1.38
wrt-1	-1.45	cri-3	-1.43	chk-1	-1.4	set-10	-1.38
phy-2	-1.45	lec-7	-1.42	sym-1	-1.4	C50F4.6	-1.38
C48B4.7	-1.45	Y69A2AR.21	-1.42	spd-1	-1.4	ugt-9	-1.38
hhat-1	-1.45	Y18H1A.9	-1.42	ZC449.2	-1.4	F40A3.6	-1.38

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
C35A5.3	-1.38	dao-2	-1.35	txl-1	-1.33	gst-31	-1.31
dim-1	-1.38	nlp-33	-1.35	eri-7	-1.33	C35D10.5	-1.31
hmg-4	-1.38	hcp-3	-1.35	C49F8.3	-1.33	lsm-1	-1.31
ppw-1	-1.38	C18H7.11	-1.35	dpy-3	-1.33	efl-3	-1.31
K02G10.15	-1.38	F40H3.3	-1.35	Y41D4B.26	-1.33	swt-4	-1.31
C24D10.6	-1.38	col-180	-1.35	cye-1	-1.33	lbp-4	-1.31
grl-7	-1.38	Y38E10A.14	-1.35	mth-1	-1.33	F59B1.8	-1.31
C34E11.2	-1.38	ZK1010.4	-1.35	pgp-15	-1.33	slc-25A46	-1.31
hrpk-2	-1.38	F35D2.3	-1.35	tofu-1	-1.33	rad-8	-1.31
T06A1.1	-1.37	K06H7.7	-1.35	osr-1	-1.33	aly-3	-1.31
B0511.7	-1.37	cdc-25.2	-1.35	unc-85	-1.33	ssup-72	-1.31
swt-7	-1.37	B0464.6	-1.35	perm-5	-1.33	F25E5.2	-1.31
grd-14	-1.37	acbp-3	-1.35	K01A6.7	-1.33	cav-1	-1.31
crn-6	-1.37	pcs-1	-1.35	C47E8.4	-1.33	mlc-6	-1.31
ttr-6	-1.37	uri-1	-1.35	nemp-1	-1.33	kca-1	-1.31
bcmo-1	-1.37	col-125	-1.34	R08E5.3	-1.33	F13B9.2	-1.31
Y69A2AR.3	-1.37	ugt-41	-1.34	phat-5	-1.33	H04D03.2	-1.31
F01G10.10	-1.37	C15C7.5	-1.34	nasp-1	-1.33	imp-1	-1.31
npp-1	-1.37	mup-4	-1.34	F01F1.11	-1.33	nhr-237	-1.31
osm-8	-1.37	T24F1.7	-1.34	zip-8	-1.33	cup-5	-1.31
taco-1	-1.37	ttr-59	-1.34	B0310.1	-1.33	K08B12.1	-1.31
rsp-6	-1.37	C11D2.4	-1.34	grl-5	-1.33	C26B2.7	-1.31
T26C5.4	-1.37	C09G4.4	-1.34	ego-1	-1.33	F10C1.8	-1.31
sep-1	-1.36	fbxb-100	-1.34	ubc-12	-1.32	far-3	-1.3
rnp-5	-1.36	thk-1	-1.34	ppgn-1	-1.32	T01D1.8	-1.3
cut-6	-1.36	C07E3.10	-1.34	mev-1	-1.32	F09E10.6	-1.3
col-165	-1.36	col-68	-1.34	wrt-10	-1.32	dhs-4	-1.3
F25A2.1	-1.36	sups-1	-1.34	gly-8	-1.32	pif-1	-1.3
mtx-1	-1.36	M03E7.2	-1.34	R09H10.5	-1.32	K08D8.4	-1.3
zig-12	-1.36	slc-30A5	-1.34	gst-12	-1.32	F45E4.5	-1.3
gst-21	-1.36	bus-4	-1.34	dpy-7	-1.32	Y6D1A.2	-1.3
glrx-10	-1.36	hsp-70	-1.34	C15B12.8	-1.32	mppa-1	-1.3
gst-9	-1.36	eat-20	-1.34	F36H1.11	-1.32	gad-1	-1.3
D1014.5	-1.36	C34E7.4	-1.34	col-3	-1.32	F25D1.5	-1.3
ztf-30	-1.36	B0205.1	-1.34	ZK822.1	-1.32	dog-1	-1.3
Y17G9B.2	-1.36	txdc-12.2	-1.34	cfim-1	-1.32	trul-1	-1.3
F46F11.7	-1.36	tbb-1	-1.33	F41F3.3	-1.32	fbxb-88	-1.3
elo-9	-1.36	lips-10	-1.33	mrg-1	-1.32	R05D3.9	-1.3
mut-7	-1.35	sul-1	-1.33	lgc-22	-1.32	memb-1	-1.3
C11H1.7	-1.35	BE0003N10.1	-1.33	F17C11.13	-1.31	H21P03.2	-1.3
ttr-38	-1.35	C35D10.10	-1.33	gst-36	-1.31	H04M03.3	-1.3
R04A9.9	-1.35	F44B9.8	-1.33	gpr-2	-1.31	C48B6.10	-1.3

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
R03H10.2	-1.3	T28A8.5	-1.28	C29A12.6	-1.26	let-49	-1.24
xpo-2	-1.29	ZC434.3	-1.28	hsp-4	-1.26	pmp-5	-1.24
cyp-13B1	-1.29	exc-6	-1.28	F01D5.10	-1.26	Y43F4B.10	-1.24
F39B2.3	-1.29	pnn-1	-1.28	Y56A3A.19	-1.26	aff-1	-1.24
his-3	-1.29	Y55D5A.4	-1.28	F16B4.4	-1.26	F57C2.5	-1.24
K11D2.1	-1.29	nlp-29	-1.27	cyp-13A7	-1.26	K05C4.7	-1.24
E01G4.5	-1.29	bra-2	-1.27	C05D12.1	-1.26	M88.4	-1.24
T19D12.4	-1.29	F57B1.6	-1.27	Y44E3A.1	-1.26	ceh-74	-1.24
spp-7	-1.29	spl-2	-1.27	col-117	-1.25	C42C1.12	-1.24
Y75B8A.16	-1.29	F21D5.3	-1.27	srr-6	-1.25	Y106G6D.8	-1.24
B0024.13	-1.29	lido-1	-1.27	lpr-7	-1.25	hach-1	-1.24
Y62F5A.9	-1.29	strm-1	-1.27	ostb-1	-1.25	rnh-2	-1.23
col-65	-1.29	apc-2	-1.27	pcyt-1	-1.25	lagr-1	-1.23
sdha-1	-1.29	C06H2.7	-1.27	C29G2.3	-1.25	eif-2D	-1.23
F10A3.4	-1.29	R02D5.8	-1.27	fipr-6	-1.25	F38B6.4	-1.23
ani-1	-1.29	F55A11.4	-1.27	C25E10.5	-1.25	F53F4.2	-1.23
mei-2	-1.29	zipt-17	-1.27	gtr-1	-1.25	rpn-12	-1.23
F25H9.6	-1.29	H42K12.3	-1.27	pup-3	-1.25	F13D12.5	-1.23
K02G10.5	-1.29	hxk-1	-1.27	F21C10.10	-1.25	usp-39	-1.23
erh-1	-1.29	F13C5.5	-1.27	T11B7.2	-1.25	ccch-3	-1.23
T20G5.8	-1.29	H23N18.5	-1.27	F01G10.9	-1.25	tfg-1	-1.23
ptr-16	-1.29	C34C12.6	-1.27	ZC513.7	-1.25	row-1	-1.23
pdp-1	-1.28	ran-4	-1.27	C18D11.3	-1.25	C14F11.6	-1.23
C08H9.15	-1.28	lec-1	-1.27	W02F12.2	-1.25	K08F8.7	-1.23
F26E4.3	-1.28	C05E7.1	-1.27	rsp-1	-1.25	Y82E9BR.6	-1.23
grl-12	-1.28	his-24	-1.27	spp-13	-1.25	M02D8.6	-1.23
Y57G7A.1	-1.28	csn-1	-1.27	ZK809.8	-1.25	mdt-6	-1.23
C16C10.4	-1.28	JC8.7	-1.27	F27E5.9	-1.25	enol-1	-1.23
T06A4.1	-1.28	acly-2	-1.27	grl-10	-1.25	ger-1	-1.23
Y105C5B.5	-1.28	cyp-14A5	-1.27	K12G11.6	-1.25	eya-1	-1.23
D1007.10	-1.28	tab-1	-1.27	dad-1	-1.25	Y71H2AM.11	-1.23
F55G1.1	-1.28	D1046.2	-1.27	C02E7.7	-1.25	F25H2.4	-1.23
C08H9.16	-1.28	sod-2	-1.27	ddo-2	-1.25	M106.8	-1.23
ugt-53	-1.28	thoc-5	-1.27	R12E2.14	-1.25	got-2.2	-1.23
ooc-5	-1.28	gale-1	-1.27	C52D10.3	-1.25	mrps-28	-1.23
tag-18	-1.28	pqn-37	-1.26	T10G3.3	-1.25	F52A8.1	-1.23
hmg-12	-1.28	tag-72	-1.26	dnj-23	-1.24	mpst-1	-1.23
Y38A10A.7	-1.28	lpr-4	-1.26	kdp-1	-1.24	F13A7.11	-1.22
grd-6	-1.28	F33E11.2	-1.26	pfk-1.1	-1.24	C38C6.3	-1.22
nfyc-1	-1.28	T13C2.2	-1.26	T02H6.11	-1.24	K09A11.1	-1.22
pgl-1	-1.28	W04A8.4	-1.26	D2063.1	-1.24	lin-42	-1.22
B0304.2	-1.28	cpi-1	-1.26	E02H9.3	-1.24	nlp-27	-1.22

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
svh-1	-1.22	Y106G6H.16	-1.2	T03D8.6	-1.18	lsm-4	-1.16
C55A6.1	-1.22	ubl-5	-1.2	F36G3.1	-1.18	E04D5.4	-1.16
grd-16	-1.22	C54D10.13	-1.2	ZK1058.9	-1.18	M28.8	-1.16
skr-2	-1.22	nprl-2	-1.2	C06G1.2	-1.18	Y54G2A.45	-1.16
set-20	-1.22	nlp-24	-1.2	gna-1	-1.18	daao-1	-1.16
F33A8.7	-1.22	tag-275	-1.2	C10F3.7	-1.18	F25H5.10	-1.16
ZK353.2	-1.22	nsun-4	-1.2	dhs-29	-1.18	B0035.3	-1.16
mig-17	-1.22	cld-9	-1.2	Y108G3AL.2	-1.18	C03F11.2	-1.16
F59F5.7	-1.22	Y34B4A.6	-1.2	plpp-1.3	-1.18	B0205.9	-1.16
cysl-2	-1.22	gst-7	-1.2	T01C3.2	-1.18	ubc-23	-1.16
rsp-2	-1.22	T25B9.9	-1.2	T01H8.2	-1.18	fkb-3	-1.16
F44D12.2	-1.22	ost-1	-1.2	C27F2.10	-1.18	F18E3.11	-1.15
mek-5	-1.22	K07B1.4	-1.2	F09G2.8	-1.18	Y40A1A.3	-1.15
W09G12.10	-1.22	doxa-1	-1.2	gras-1	-1.18	ZK813.6	-1.15
acs-19	-1.22	T21C12.8	-1.2	zip-10	-1.18	Y65B4BL.6	-1.15
hil-3	-1.21	F25B4.4	-1.2	T26A5.8	-1.18	lips-9	-1.15
pyp-1	-1.21	R07E3.2	-1.2	F10E9.3	-1.17	H14E04.2	-1.15
H02F09.3	-1.21	F23H12.5	-1.2	R08D7.1	-1.17	rsp-3	-1.15
Y73E7A.8	-1.21	pals-37	-1.19	R11H6.5	-1.17	mib-1	-1.15
C44H9.7	-1.21	C01G10.7	-1.19	hil-2	-1.17	wapl-1	-1.15
unc-52	-1.21	tba-6	-1.19	sgcb-1	-1.17	F10D2.10	-1.15
cpn-4	-1.21	Y92H12BR.2	-1.19	let-721	-1.17	aco-2	-1.15
mus-101	-1.21	wago-4	-1.19	C14B1.8	-1.17	T19D12.1	-1.15
Y46H3A.4	-1.21	linc-17	-1.19	K02E7.5	-1.17	rpb-11	-1.15
lin-35	-1.21	T01D1.4	-1.19	T05B11.1	-1.17	ttr-8	-1.15
F37A4.3	-1.21	lrx-1	-1.19	B0507.1	-1.17	exc-12	-1.15
jmjc-1	-1.21	R57.2	-1.19	tnt-2	-1.17	R07G3.7	-1.15
mlp-1	-1.21	K07C5.6	-1.19	hrde-2	-1.17	Y119D3B.12	-1.15
lin-32	-1.21	mam-3	-1.19	atad-3	-1.17	aipl-1	-1.15
ZK930.6	-1.21	K08D8.6	-1.19	srh-2	-1.17	set-19	-1.15
C13C12.2	-1.21	F55A11.8	-1.19	sec-61.B	-1.17	hsp-12.2	-1.15
tyr-4	-1.21	Y51H7C.3	-1.19	mttu-1	-1.16	T05E7.1	-1.15
T23F2.4	-1.21	F10D7.2	-1.19	arv-1	-1.16	F23C8.5	-1.15
C06E7.88	-1.21	D1053.4	-1.19	alkb-7	-1.16	anmt-1	-1.15
Y54G2A.76	-1.2	Y41D4B.6	-1.19	ptr-4	-1.16	pgp-6	-1.15
F52E4.5	-1.2	fbxa-137	-1.19	hst-1	-1.16	rpa-1	-1.15
T07C4.3	-1.2	C14C11.7	-1.19	ttr-51	-1.16	C07D10.5	-1.15
tag-293	-1.2	T21D12.7	-1.19	C34B4.2	-1.16	unc-95	-1.15
srr-1	-1.2	npp-5	-1.19	F28H7.8	-1.16	ubc-18	-1.15
K06G5.1	-1.2	T19B10.5	-1.18	lin-9	-1.16	hut-1	-1.15
smut-1	-1.2	zig-4	-1.18	Y53F4B.9	-1.16	rrn-3.56	-1.15
daf-22	-1.2	tpi-1	-1.18	F08D12.2	-1.16	gst-19	-1.15

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T05G5.1	-1.15	nhr-123	-1.13	F37C12.3	-1.12	F58G6.9	-1.1
igcm-1	-1.15	D2005.6	-1.13	Y39G10AR.32	-1.12	mbf-1	-1.1
Y73C8B.1	-1.14	R07E3.6	-1.13	linc-42	-1.12	csn-3	-1.1
F45E1.4	-1.14	pde-12	-1.13	hcf-1	-1.12	F56B3.2	-1.09
let-653	-1.14	dlat-1	-1.13	C46G7.2	-1.12	Y39A1A.20	-1.09
poml-2	-1.14	best-13	-1.13	C07D10.1	-1.12	F01G4.4	-1.09
atn-1	-1.14	ZK688.9	-1.13	nud-1	-1.12	ubc-9	-1.09
T28A8.6	-1.14	F20D1.3	-1.13	F21C10.7	-1.12	dvc-1	-1.09
drsh-1	-1.14	Y38H6C.16	-1.13	nep-22	-1.12	K08E7.5	-1.09
nmy-1	-1.14	pafo-1	-1.13	rnp-2	-1.12	ZC416.2	-1.09
wrt-6	-1.14	R02F2.8	-1.13	W06H8.2	-1.11	T20F5.4	-1.09
Y57E12AL.6	-1.14	pgp-8	-1.13	zhp-3	-1.11	R07B1.8	-1.09
T08G5.3	-1.14	taf-8	-1.13	F48E3.2	-1.11	frg-1	-1.09
hic-1	-1.14	rpt-2	-1.13	clec-80	-1.11	gst-4	-1.09
him-8	-1.14	F42A10.9	-1.13	npp-2	-1.11	szy-5	-1.09
snrp-27	-1.14	eaf-1	-1.13	mls-2	-1.11	K08E4.2	-1.09
sna-2	-1.14	pho-8	-1.13	F33E2.5	-1.11	fkh-2	-1.09
F39H2.3	-1.14	col-12	-1.13	linc-4	-1.11	mat-2	-1.09
cpn-1	-1.14	his-32	-1.13	npp-3	-1.11	set-5	-1.09
coh-4	-1.14	ZC374.2	-1.13	W01A11.1	-1.11	F37C4.5	-1.09
lsd-1	-1.14	gip-2	-1.13	B0001.2	-1.11	C36A4.4	-1.09
F36H9.5	-1.14	F58E6.11	-1.12	ubxn-4	-1.11	T04F3.1	-1.09
chmp-7	-1.14	cysl-1	-1.12	F45H11.8	-1.11	ugt-21	-1.09
lon-8	-1.14	sucl-2	-1.12	F21D9.6	-1.11	F21D5.1	-1.09
dlc-2	-1.14	T07D4.5	-1.12	drh-1	-1.11	F09F7.6	-1.09
B0495.8	-1.14	hse-5	-1.12	F14B4.1	-1.11	col-89	-1.09
F26A1.1	-1.14	prx-19	-1.12	cpsf-4	-1.11	ugt-13	-1.09
Y48G10A.2	-1.14	tomm-40	-1.12	hrpf-1	-1.11	eif-2Bbeta	-1.09
B0280.7	-1.14	rap-3	-1.12	nhr-145	-1.11	ina-1	-1.09
F56C9.7	-1.14	pfn-2	-1.12	cpt-5	-1.1	snr-5	-1.09
dgat-2	-1.13	Y37E3.30	-1.12	F39H11.1	-1.1	dhs-9	-1.09
rpn-9	-1.13	wrt-9	-1.12	Y69E1A.5	-1.1	C15H9.11	-1.09
B0365.9	-1.13	F54D5.12	-1.12	Y54G11A.4	-1.1	bag-1	-1.09
sod-5	-1.13	Y73C8B.2	-1.12	fust-1	-1.1	col-172	-1.08
ent-1	-1.13	usp-14	-1.12	nstp-10	-1.1	B0212.3	-1.08
C02E7.6	-1.13	cutl-13	-1.12	nhr-23	-1.1	F45D3.3	-1.08
algn-8	-1.13	W01C8.5	-1.12	F47B8.5	-1.1	C33D9.13	-1.08
C05D2.8	-1.13	ugt-16	-1.12	his-59	-1.1	F15B9.6	-1.08
F56D6.16	-1.13	isw-1	-1.12	K08E4.3	-1.1	nduf-6	-1.08
acox-1.1	-1.13	cts-1	-1.12	F53B3.3	-1.1	F42A9.6	-1.08
K08E3.5	-1.13	ZK1055.6	-1.12	atp-1	-1.1	M01F1.4	-1.08
F18C5.5	-1.13	viln-1	-1.12	sqv-3	-1.1	algn-10	-1.08

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
wdr-5.1	-1.08	Y66D12A.16	-1.07	mpdu-1	-1.06	clc-1	-1.04
mam-5	-1.08	psr-1	-1.07	oac-7	-1.06	T13C2.3	-1.04
T05C1.3	-1.08	C06E4.3	-1.07	pen-2	-1.06	eif-2Bgamma	-1.04
exos-2	-1.08	tmed-13	-1.07	cdh-8	-1.06	stl-1	-1.04
efn-4	-1.08	mdt-10	-1.07	rpb-4	-1.06	Y97E10AR.2	-1.04
T09A5.15	-1.08	F48A11.4	-1.07	Y53C10A.6	-1.05	drh-3	-1.04
C06E7.4	-1.08	F13B12.4	-1.07	R05D11.9	-1.05	ceh-91	-1.04
T28C6.3	-1.08	gpx-5	-1.07	tag-296	-1.05	arx-4	-1.04
Y54G2A.18	-1.08	ced-11	-1.07	cyk-7	-1.05	F58F9.4	-1.04
pcp-5	-1.08	VW02B12L.2	-1.07	lec-9	-1.05	C47E12.2	-1.04
tmem-17	-1.08	Y66D12A.7	-1.07	rcs-1	-1.05	cutl-14	-1.04
F01F1.3	-1.08	acp-6	-1.07	rrn-3.1	-1.05	cox-18	-1.04
pfn-3	-1.08	Y34D9A.7	-1.07	col-61	-1.05	B0272.4	-1.04
vps-28	-1.08	F13E9.15	-1.07	inx-13	-1.05	F13H10.5	-1.04
enu-3.2	-1.08	zipt-1	-1.07	phf-30	-1.05	W02D7.5	-1.04
damt-1	-1.08	tsp-7	-1.07	F22E12.3	-1.05	W04B5.3	-1.04
rec-1	-1.08	D1007.5	-1.07	W04D2.4	-1.05	rig-4	-1.04
F13D12.9	-1.08	Y46G5A.20	-1.07	F58A6.1	-1.05	Y92H12BL.5	-1.04
F53F8.7	-1.08	spe-10	-1.06	rbm-7	-1.05	F13A7.12	-1.04
ztf-4	-1.08	cpn-2	-1.06	C30F12.2	-1.05	Y25C1A.13	-1.04
F11A5.9	-1.07	T10H10.2	-1.06	C33F10.4	-1.05	F18E3.13	-1.04
spcs-2	-1.07	cisd-3.2	-1.06	K08D12.6	-1.05	acox-1.5	-1.04
C47F8.1	-1.07	Y64H9A.2	-1.06	C42D4.13	-1.05	snrp-40.2	-1.04
acds-10	-1.07	B0303.3	-1.06	wip-1	-1.05	ccm-3	-1.03
gsy-1	-1.07	bed-3	-1.06	B0238.12	-1.05	cep-1	-1.03
gasr-8	-1.07	hpo-26	-1.06	M7.12	-1.05	npp-13	-1.03
bigr-1	-1.07	F32D8.5	-1.06	czw-1	-1.05	cpg-7	-1.03
C01A2.2	-1.07	nlp-63	-1.06	F01F1.15	-1.05	act-2	-1.03
dnj-22	-1.07	ska-1	-1.06	clec-194	-1.05	alx-1	-1.03
ran-1	-1.07	eri-5	-1.06	rab-11.2	-1.05	F49C12.9	-1.03
nspe-4	-1.07	dlc-1	-1.06	Y75B8A.31	-1.05	gln-5	-1.03
popl-7	-1.07	romo-1	-1.06	nbet-1	-1.05	vdac-1	-1.03
bud-31	-1.07	C16C8.16	-1.06	T10E9.2	-1.05	smr-1	-1.03
fbxa-50	-1.07	sdz-27	-1.06	F53C3.3	-1.05	gst-37	-1.03
F39H12.1	-1.07	srf-3	-1.06	Y37E11AL.3	-1.05	dnj-18	-1.03
C18B2.3	-1.07	hpo-18	-1.06	Y48G1BR.1	-1.05	hpr-9	-1.03
T07F10.3	-1.07	cuc-1	-1.06	nhr-63	-1.04	bcl-7	-1.03
mbd-2	-1.07	lsm-8	-1.06	hsb-1	-1.04	epi-1	-1.03
ZK177.8	-1.07	col-10	-1.06	rdy-2	-1.04	zyg-1	-1.03
egl-46	-1.07	cec-7	-1.06	mrps-15	-1.04	K01D12.9	-1.03
T19C9.8	-1.07	F20D6.11	-1.06	trpl-2	-1.04	mig-32	-1.03
F32H2.10	-1.07	nep-12	-1.06	C02F5.13	-1.04	cdh-5	-1.03

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ctsa-3.1	-1.03	B0035.18	-1.01	epn-1	1	car-1	1.02
F58D5.2	-1.03	trpa-1	-1.01	eif-3.D	1	Y6B3B.9	1.02
emc-5	-1.03	spr-3	-1.01	gck-3	1	C18F10.7	1.02
madf-8	-1.03	mrt-2	-1.01	pus-1	1	pqn-41	1.02
mtd-1	-1.03	algn-13	-1.01	btb-14	1.01	pll-1	1.02
lin-3	-1.03	vha-11	-1.01	K10G6.9	1.01	clec-7	1.02
letm-1	-1.03	Y62F5A.12	-1.01	lgc-50	1.01	Y18H1A.11	1.02
K03H1.13	-1.03	wrt-2	-1.01	C07H4.1	1.01	dhs-31	1.02
ins-11	-1.02	mrpl-19	-1.01	gopc-1	1.01	magi-1	1.02
linc-72	-1.02	T12B3.2	-1.01	Y37A1A.3	1.01	T07D1.2	1.02
tsfm-1	-1.02	nol-58	-1.01	M04B2.7	1.01	F53H2.1	1.02
M110.10	-1.02	emc-1	-1.01	glc-1	1.01	abf-5	1.02
R12E2.15	-1.02	nex-3	-1.01	fbxa-55	1.01	kvs-5	1.03
gtf-2H3	-1.02	ZK1248.19	-1.01	rpl-6	1.01	pcrg-1	1.03
Y39A3CL.4	-1.02	F22F7.7	-1.01	F25B3.4	1.01	arrd-22	1.03
nas-33	-1.02	C18H9.6	-1.01	nhr-54	1.01	fpn-1.1	1.03
K11H12.11	-1.02	mlc-1	-1.01	cla-1	1.01	B0222.11	1.03
gst-27	-1.02	fecl-1	-1.01	Y34D9A.8	1.01	ubq-2	1.03
trap-3	-1.02	F15G9.1	-1.01	gos-28	1.01	reps-1	1.03
Y48G10A.1	-1.02	nars-1	-1.01	gur-4	1.01	kvs-4	1.03
F22E5.6	-1.02	B0310.2	-1.01	K06A9.2	1.01	trpp-12	1.03
M04C9.1	-1.02	T05C1.1	-1	ilcr-1	1.01	pek-1	1.03
eri-1	-1.02	polk-1	-1	unc-16	1.01	F57B9.3	1.03
ZK909.3	-1.02	Y38A10A.2	-1	T25B2.2	1.01	D2005.3	1.03
pccb-1	-1.02	Y43F8C.13	-1	clh-6	1.01	T05A8.5	1.03
mex-3	-1.02	metl-9	-1	tag-180	1.01	Y71H2B.4	1.03
F59B2.9	-1.02	pes-5	-1	iars-2	1.01	F52H2.1	1.03
grd-5	-1.02	cpar-1	-1	kynu-1	1.01	srd-35	1.03
mdt-11	-1.02	nhx-9	-1	Y39E4B.10	1.01	Y41E3.6	1.03
C16C8.4	-1.02	Y37A1A.2	-1	C16A11.3	1.01	rpm-1	1.03
lsy-13	-1.02	T23F2.3	-1	F46F11.1	1.02	fbxa-146	1.03
hsp-110	-1.02	rps-8	1	cept-1	1.02	rps-23	1.03
K08F4.3	-1.02	qars-1	1	spat-2	1.02	F21D5.5	1.03
K08D9.4	-1.02	trpp-9	1	pigw-1	1.02	F23B12.4	1.03
slc-17.2	-1.02	unc-96	1	nlp-40	1.02	K12C11.3	1.03
T20H4.5	-1.02	supr-1	1	C25G6.3	1.02	ZC116.1	1.03
ufd-3	-1.02	linc-91	1	unc-10	1.02	F19C7.2	1.03
nra-2	-1.02	col-153	1	Y56A3A.2	1.02	fln-2	1.03
natc-2	-1.02	fbxa-156	1	Y43C5A.7	1.02	unc-75	1.03
acr-8	-1.02	snt-7	1	gld-4	1.02	F15G9.5	1.03
F49E11.2	-1.02	clec-205	1	aat-6	1.02	Y56A3A.30	1.03
blos-1	-1.02	fbxa-157	1	Y71H10B.1	1.02	cct-1	1.03

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ssl-1	1.03	F49C12.10	1.05	linc-109	1.07	obr-1	1.08
dop-2	1.03	cdo-1	1.05	F28H6.6	1.07	acs-22	1.08
pik-1	1.03	T07D3.4	1.05	T05G5.5	1.07	aka-1	1.08
ZK287.9	1.04	Y50D4C.5	1.05	R10F2.6	1.07	dlk-1	1.08
vps-26	1.04	R08F11.7	1.05	ckr-2	1.07	Y67D8A.2	1.08
klp-16	1.04	sulp-4	1.05	F10D7.5	1.07	abts-3	1.08
Y71A12B.18	1.04	math-28	1.05	itr-1	1.07	C01B10.6	1.08
sre-23	1.04	T22D1.3	1.05	rme-4	1.07	unc-104	1.08
nhr-79	1.04	elt-3	1.05	wnk-1	1.07	C28D4.10	1.08
K10D3.10	1.04	sulp-7	1.05	F13H8.11	1.07	R10E9.3	1.08
slc-25A26	1.04	C44H4.6	1.05	Y40B10A.5	1.07	lev-9	1.08
C05D12.7	1.04	col-107	1.05	ppfr-1	1.07	stau-1	1.08
C47E12.12	1.04	ZK1058.3	1.05	T26G10.5	1.07	apt-9	1.08
flp-7	1.04	tmbi-4	1.05	F40F9.10	1.07	rpl-3	1.08
F53A9.8	1.04	lrp-1	1.05	crh-2	1.07	akt-2	1.08
Y41D4A.6	1.04	K02E2.6	1.05	K01A11.1	1.07	flp-28	1.08
Y110A7A.21	1.04	F43H9.4	1.05	nlp-1	1.07	F45F2.9	1.08
spe-48	1.04	ctsa-4.2	1.05	fbxa-199	1.07	nrps-1	1.09
B0310.3	1.04	best-5	1.05	T28D6.7	1.07	seb-3	1.09
bet-1	1.04	lin-7	1.05	F13B12.3	1.07	btbd-10	1.09
ins-18	1.04	kcc-1	1.05	F53B2.8	1.07	fem-2	1.09
pha-1	1.04	rpl-5	1.05	K11D12.8	1.07	cdk-2	1.09
F32B4.4	1.04	dhcr-7	1.06	mdl-1	1.07	srw-85	1.09
rpl-4	1.04	rrf-2	1.06	F28B12.6	1.07	ZK836.3	1.09
H06I04.6	1.04	Y105E8A.25	1.06	vamp-7	1.07	K10D11.6	1.09
nhr-41	1.04	clec-178	1.06	K07C11.7	1.08	T19D7.6	1.09
scav-6	1.04	rimb-1	1.06	dbl-1	1.08	arrd-21	1.09
mecr-1	1.04	F26H9.5	1.06	mlc-3	1.08	F49D11.2	1.09
tdo-2	1.04	kin-19	1.06	glc-3	1.08	Y119D3B.13	1.09
K07E1.1	1.05	pde-2	1.06	srg-34	1.08	C39F7.5	1.09
drn-1	1.05	C55A6.10	1.06	F01E11.18	1.08	F57A8.1	1.09
abf-2	1.05	C30H6.12	1.06	mig-18	1.08	cdc-14	1.09
glr-4	1.05	Y67H2A.7	1.06	larp-5	1.08	F07F6.7	1.09
nhr-14	1.05	nhr-36	1.06	Y53H1B.2	1.08	del-6	1.09
ltah-1.2	1.05	somi-1	1.06	sta-1	1.08	F57C7.4	1.09
fip-2	1.05	unc-7	1.06	nmur-1	1.08	ccpp-6	1.09
F20G2.7	1.05	F58D5.5	1.06	sprr-3	1.08	svh-2	1.09
dpf-6	1.05	nfki-1	1.06	fig-1	1.08	F19G12.3	1.09
pup-2	1.05	F31E3.2	1.06	B0546.4	1.08	lrp-2	1.09
ncl-1	1.05	rpl-7	1.06	F27C1.11	1.08	ncs-2	1.09
F11C7.7	1.05	F41B4.2	1.06	T12B3.1	1.08	snx-6	1.09
gnrr-5	1.05	ptc-1	1.07	pkc-2	1.08	odr-3	1.09

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
lgc-26	1.09	cfi-1	1.11	glna-1	1.12	ttr-23	1.14
tub-1	1.09	F52C6.12	1.11	C38H2.2	1.12	B0462.5	1.14
C49A1.10	1.09	C49A9.9	1.11	clip-1	1.12	R11G1.6	1.14
mab-31	1.09	F25E5.4	1.11	F08D12.7	1.13	F58H1.3	1.14
sfxn-1.5	1.09	C04F12.8	1.11	Y92H12BR.7	1.13	Y23H5B.6	1.14
C18B2.5	1.09	ercc-1	1.11	cgt-2	1.13	hlh-13	1.14
Y37H2C.1	1.09	nhr-32	1.11	zer-1	1.13	ZC204.12	1.14
F52D1.2	1.1	C25F9.5	1.11	hpk-1	1.13	rpac-19	1.15
pals-25	1.1	Y40H7A.10	1.11	ahr-1	1.13	C05C12.6	1.15
crh-1	1.1	pab-2	1.11	flp-21	1.13	T01E8.1	1.15
ocr-2	1.1	F28F9.2	1.11	C47B2.2	1.13	R04E5.8	1.15
T19C3.7	1.1	T28B8.3	1.11	asp-1	1.13	sbp-1	1.15
pmk-2	1.1	faah-1	1.11	T28C6.8	1.13	marg-1	1.15
F47H4.2	1.1	flp-34	1.11	ogdh-1	1.13	R05A10.4	1.15
rps-6	1.1	Y23B4A.1	1.11	M01G12.9	1.13	efsc-1	1.15
ZK1127.5	1.1	T12A7.6	1.11	twk-46	1.13	tcer-1	1.15
col-156	1.1	rpl-9	1.11	lgc-46	1.13	Y41E3.22	1.15
ttll-5	1.1	spp-3	1.12	ZC196.5	1.13	C09D4.1	1.15
mctp-1	1.1	fbxa-219	1.12	nas-32	1.14	tatn-1	1.15
F07H5.5	1.1	T09B9.3	1.12	eef-1G	1.14	T26C12.1	1.15
ZC123.4	1.1	nhr-110	1.12	F38C2.4	1.14	F40F4.7	1.15
F42C5.6	1.1	C09G5.13	1.12	nmr-2	1.14	pes-4	1.15
B0302.5	1.1	rpb-9	1.12	K11D2.4	1.14	nlp-13	1.15
C04G6.4	1.1	T02H6.1	1.12	spk-1	1.14	mrpl-41	1.15
npr-26	1.1	gmeb-1	1.12	pqn-18	1.14	aex-4	1.15
Y55D5A.1	1.1	frpr-19	1.12	R06F6.14	1.14	olrn-1	1.15
C34F6.5	1.1	txt-18	1.12	T02D1.4	1.14	pdf-1	1.15
frpr-16	1.1	wdr-5.2	1.12	Y43F8C.11	1.14	cyp-33E1	1.16
mlk-1	1.1	madf-10	1.12	nhr-42	1.14	daf-15	1.16
tsct-1	1.1	C08F1.8	1.12	C30B5.7	1.14	nhl-3	1.16
cyk-3	1.1	nhr-95	1.12	nhr-195	1.14	daf-7	1.16
lin-1	1.1	nlt-1	1.12	pde-3	1.14	slc-36.3	1.16
scpl-1	1.1	linc-84	1.12	C50A2.3	1.14	suco-1	1.16
F42C5.4	1.1	fahd-1	1.12	clec-224	1.14	snt-2	1.16
tba-7	1.11	nipa-1	1.12	ent-2	1.14	Y44A6D.3	1.16
pdf-2	1.11	T01B4.3	1.12	ncr-1	1.14	dgk-3	1.16
H10E21.1	1.11	C17E4.10	1.12	Y55F3BR.10	1.14	sut-2	1.16
C01G5.25	1.11	C11G10.1	1.12	H05C05.1	1.14	mboa-2	1.16
mef-2	1.11	slc-25A29	1.12	serp-1.1	1.14	Y43F8B.11	1.16
F23F12.13	1.11	ccdc-55	1.12	C01G6.4	1.14	Y71H2B.8	1.16
R11G10.3	1.11	sro-1	1.12	col-147	1.14	osm-7	1.16
F13D12.10	1.11	rcq-5	1.12	F25B3.5	1.14	cyl-1	1.16

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F54F7.2	1.16	mbl-1	1.18	unc-77	1.2	Y77E11A.14	1.22
C07G1.15	1.16	F23H11.7	1.18	C44C1.6	1.2	nhr-206	1.22
eif-3.F	1.16	rskn-1	1.18	C44E4.5	1.2	nlp-21	1.22
clec-55	1.16	osm-11	1.18	twk-31	1.2	cca-1	1.22
Y38C1AA.6	1.16	F35E12.4	1.18	ZC443.2	1.2	rskn-2	1.22
C25E10.13	1.16	elt-7	1.18	Y39A1A.22	1.2	pxmp-4	1.22
Y39G8B.9	1.17	W04C9.8	1.18	fbxa-4	1.2	C14C11.4	1.22
cof-2	1.17	grk-2	1.18	C25F9.14	1.2	cdap-2	1.22
tct-1	1.17	dop-3	1.18	F54G2.1	1.2	tftc-1	1.22
C30F12.3	1.17	emc-3	1.18	rog-1	1.2	B0222.1	1.22
MTCE.33	1.17	ZK809.9	1.18	rps-16	1.2	M01E5.2	1.22
hex-3	1.17	hrg-1	1.18	srh-271	1.2	serp-1.2	1.22
glb-11	1.17	Y71F9AL.10	1.18	twk-42	1.2	Y11D7A.8	1.22
ghi-1	1.17	F21D12.3	1.18	sup-9	1.2	H04M03.12	1.22
Y62H9A.13	1.17	C49A9.4	1.18	pro-2	1.2	ZK822.6	1.22
lgc-49	1.17	F25B5.3	1.18	nhr-177	1.2	Y40B1A.3	1.22
kcnl-2	1.17	clp-1	1.18	jkk-1	1.2	uev-1	1.22
rrc-1	1.17	smk-1	1.19	M01F1.9	1.2	C51E3.10	1.22
islo-1	1.17	nlp-35	1.19	ZK1127.12	1.2	R04E5.9	1.22
sam-10	1.17	F36H5.10	1.19	cest-9.2	1.2	M116.2	1.22
ccch-1	1.17	Y39A1A.3	1.19	F20C5.5	1.2	pfas-1	1.22
F09F7.5	1.17	sms-1	1.19	F26A3.4	1.2	pgrn-1	1.22
mask-1	1.17	svh-5	1.19	sop-2	1.2	fbxa-95	1.22
D2030.3	1.17	npr-31	1.19	M03C11.3	1.21	F41E7.6	1.22
T19D2.3	1.17	sad-1	1.19	aakg-3	1.21	F37B12.3	1.22
xbx-3	1.17	pcp-3	1.19	catp-5	1.21	Y105C5A.15	1.22
rgs-4	1.17	gta-1	1.19	ags-3	1.21	twk-23	1.22
F52C12.6	1.17	nep-21	1.19	Y17D7C.2	1.21	Y105C5A.24	1.22
C26E1.2	1.17	pitp-1	1.19	frpr-11	1.21	rbm-34	1.22
Y71H2B.1	1.17	col-129	1.19	K06A4.7	1.21	Y9C12A.1	1.23
C27A7.5	1.17	C35D10.17	1.19	K07E3.1	1.21	pdfr-1	1.23
din-1	1.17	C25F9.11	1.19	T16H12.3	1.21	icmt-1	1.23
K09C4.1	1.17	gpa-9	1.19	flp-26	1.21	Y69H2.10	1.23
C31H5.1	1.17	F10G2.1	1.19	atg-16.2	1.21	srbc-20	1.23
T26C5.3	1.18	C49A9.3	1.19	aexr-1	1.21	rpac-40	1.23
ubc-3	1.18	rab-14	1.19	lin-45	1.21	sbt-1	1.23
fbl-1	1.18	old-1	1.19	clec-92	1.21	hlh-10	1.23
F34H10.3	1.18	scrm-2	1.2	C06A5.3	1.21	F37C12.21	1.23
T25C12.12	1.18	Y47H10A.4	1.2	cdd-1	1.21	clec-143	1.23
acy-2	1.18	R05D3.12	1.2	lmtr-5	1.21	F28C1.3	1.23
F22H10.6	1.18	F10G2.7	1.2	C09B9.1	1.21	gldc-1	1.23
M02E1.1	1.18	sprr-2	1.2	zig-5	1.22	ugt-58	1.23

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F58B3.4	1.23	mrpl-47	1.25	F59C6.16	1.27	klp-15	1.29
T05C12.8	1.23	slcf-2	1.25	nlp-53	1.27	F17C8.3	1.29
cbp-1	1.23	K09F6.6	1.25	Y67A10A.7	1.27	dao-5	1.29
mgl-3	1.23	F35F10.1	1.25	Y4C6B.2	1.27	C17H11.6	1.3
glb-19	1.24	ugt-49	1.26	bcl-11	1.28	fbxa-222	1.3
gcst-1	1.24	T05A12.3	1.26	mlc-2	1.28	ife-1	1.3
T28B11.1	1.24	tbc-14	1.26	F29B9.12	1.28	K02E11.5	1.3
M03D4.3	1.24	R102.4	1.26	gld-2	1.28	math-35	1.3
T09F3.2	1.24	C07C7.1	1.26	F08D12.3	1.28	F58A6.2	1.3
Y67A10A.10	1.24	ctns-1	1.26	mrpl-9	1.28	tag-280	1.3
kcc-2	1.24	R151.6	1.26	nlp-18	1.28	srw-86	1.3
sri-30	1.24	pgp-1	1.26	W05F2.4	1.28	nhr-10	1.3
frpr-13	1.24	flp-32	1.26	K03A11.5	1.28	F47B8.3	1.3
amt-2	1.24	glo-4	1.26	snt-4	1.28	F54E7.9	1.3
slcf-1	1.24	sir-2.4	1.26	yars-2	1.28	T06A1.5	1.3
C04E6.13	1.24	dhs-1	1.26	cyp-33C6	1.28	rpl-16	1.3
C05C12.4	1.24	lin-41	1.26	cil-1	1.28	glb-3	1.3
F32D1.8	1.24	asna-2	1.26	kcnl-1	1.28	B0228.7	1.3
amt-3	1.24	R12E2.13	1.26	nlp-68	1.28	K04F10.7	1.3
hecd-1	1.24	atg-2	1.26	ins-17	1.29	rab-39	1.3
flp-5	1.24	T09B4.8	1.26	rlbp-1	1.29	let-70	1.3
C31C9.6	1.24	alkb-8	1.26	F46B6.5	1.29	crn-2	1.3
algn-7	1.24	Y51H7BR.4	1.26	ddl-2	1.29	F18H3.1	1.3
egl-15	1.24	math-34	1.26	clec-36	1.29	rga-6	1.3
ZK593.3	1.25	enpl-1	1.26	Y43F8A.1	1.29	ZK1320.2	1.3
clh-2	1.25	obr-4	1.26	Y38C1AA.12	1.29	R05G6.10	1.3
Y73B3A.3	1.25	T25D10.1	1.26	fbxa-172	1.29	H40L08.3	1.3
F35H8.2	1.25	W05F2.7	1.26	clec-34	1.29	lgc-12	1.3
nhr-122	1.25	piki-1	1.27	mdt-27	1.29	F42A10.6	1.3
Y39E4B.6	1.25	let-526	1.27	egl-45	1.29	acl-2	1.31
C26B9.6	1.25	acd-5	1.27	pinn-4	1.29	F46F2.5	1.31
let-19	1.25	lpd-3	1.27	noca-1	1.29	clec-60	1.31
Y51F10.3	1.25	nlp-64	1.27	Y55F3AM.13	1.29	Y39G10AR.11	1.31
fbxa-3	1.25	hpo-34	1.27	ZC190.6	1.29	Y59A8B.21	1.31
dsh-1	1.25	F10E9.12	1.27	mpz-1	1.29	lgc-38	1.31
nhr-85	1.25	osta-1	1.27	nlp-42	1.29	T04A6.1	1.31
cpna-5	1.25	rps-2	1.27	pals-38	1.29	F58E2.3	1.31
fbxc-41	1.25	fbxc-45	1.27	klu-2	1.29	nhr-227	1.31
T04F8.3	1.25	wdfy-3	1.27	Y75B8A.7	1.29	C47E8.3	1.31
rpl-2	1.25	B0303.4	1.27	arrd-14	1.29	pyr-1	1.31
T13H5.1	1.25	lin-49	1.27	kqt-2	1.29	asic-1	1.31
sre-6	1.25	C17H12.8	1.27	R12B2.2	1.29	phat-3	1.31

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
ZC47.11	1.31	fbxc-6	1.34	cif-1	1.35	gnrr-3	1.38
daf-12	1.31	dpy-22	1.34	F57C9.6	1.36	F52G2.3	1.38
Y73F8A.32	1.31	F47B10.8	1.34	nhr-8	1.36	ZK285.2	1.38
gcy-28	1.31	T27C4.1	1.34	zhit-2	1.36	pqn-15	1.38
C31H2.3	1.31	nhr-87	1.34	msi-1	1.36	F23A7.3	1.38
F53C3.6	1.32	cyld-1	1.34	nep-2	1.36	inos-1	1.38
W02H5.2	1.32	miz-1	1.34	F56F10.2	1.36	twk-2	1.38
F57B10.8	1.32	F15D4.4	1.34	rgef-1	1.36	cnx-1	1.38
kin-29	1.32	F16C3.2	1.34	F22D6.2	1.36	flr-4	1.38
C24G6.8	1.32	C15H9.2	1.34	memo-1	1.36	B0393.9	1.38
sars-1	1.32	djr-1.2	1.34	fbxa-124	1.36	plpp-1.1	1.38
C25G6.4	1.32	npr-23	1.34	linc-11	1.36	ZC449.7	1.39
gcy-12	1.32	nhr-101	1.34	unc-82	1.36	fut-1	1.39
gei-4	1.32	cpna-1	1.34	asp-12	1.36	nhr-138	1.39
Y34F4.1	1.32	lfe-2	1.34	F43D2.6	1.36	nubp-1	1.39
F22D6.14	1.32	gyf-1	1.34	rpn-6.2	1.36	mrps-5	1.39
C49F5.11	1.32	str-112	1.34	icap-1	1.36	R02F2.7	1.39
ZK792.5	1.32	C44E12.1	1.34	M18.3	1.36	flp-33	1.39
ctsa-4.1	1.32	copz-1	1.34	Y39B6A.3	1.36	eif-2gamma	1.39
ceeh-2	1.32	F54F2.7	1.34	F35G2.1	1.36	flp-18	1.39
unc-14	1.32	gap-3	1.34	C08B6.10	1.36	K09F5.6	1.39
tag-196	1.32	nep-11	1.35	irk-3	1.36	W08G11.3	1.39
cyn-5	1.33	C13B9.2	1.35	F14B6.6	1.37	glb-5	1.39
C04F12.16	1.33	T13F3.7	1.35	rnh-1.0	1.37	F40F8.4	1.39
Y45G5AM.7	1.33	linc-96	1.35	H09F14.1	1.37	mig-1	1.4
gpx-3	1.33	unc-132	1.35	C37C3.2	1.37	Y54E5A.5	1.4
mxl-1	1.33	T19C3.4	1.35	Y71F9B.13	1.37	oaz-1	1.4
osm-3	1.33	M01H9.3	1.35	R01B10.3	1.37	pab-1	1.4
T27D12.6	1.33	molo-1	1.35	dmd-7	1.37	F13B12.2	1.4
gcy-23	1.33	ima-3	1.35	C13C4.6	1.37	flp-15	1.4
pqn-20	1.33	F43G6.8	1.35	nlp-82	1.37	F46H5.7	1.4
F41E6.17	1.33	sdc-3	1.35	nlp-55	1.37	C27D6.12	1.4
K02E11.9	1.33	3/5/2020	1.35	C33E10.8	1.37	gab-1	1.4
ZK858.5	1.33	Y39B6A.34	1.35	W03A5.1	1.37	K02F2.5	1.4
T24B8.7	1.33	vps-22	1.35	dlc-3	1.37	Y111B2A.12	1.4
dab-1	1.33	F46G10.2	1.35	B0564.2	1.37	daf-8	1.4
Y119D3B.14	1.33	lpin-1	1.35	cap-2	1.37	cal-2	1.4
F46B6.4	1.33	F55C12.5	1.35	T26H5.14	1.37	T05C1.2	1.4
T16H12.9	1.33	F27C1.2	1.35	egl-47	1.37	B0250.4	1.4
drh-2	1.33	VC5.2	1.35	ins-1	1.37	C56A3.5	1.4
R10F2.4	1.33	Y92H12BM.1	1.35	pef-1	1.37	tyra-3	1.4
W05E10.5	1.34	pmt-2	1.35	Y57G11C.5	1.37	epg-6	1.41

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
T04C12.7	1.41	K05C4.2	1.43	npr-4	1.45	kgb-2	1.47
M04G7.1	1.41	fat-2	1.43	F46B6.12	1.46	T25C12.11	1.47
nhr-274	1.41	C39D10.8	1.43	T05H4.10	1.46	npr-18	1.47
tre-5	1.41	C26D10.4	1.43	Y110A2AL.3	1.46	K03H1.11	1.47
frm-4	1.41	unc-54	1.43	F36A2.14	1.46	C16C10.2	1.47
gei-3	1.41	ntr-2	1.43	C13C4.7	1.46	C34D1.4	1.48
K11H12.9	1.41	T22B7.8	1.43	Y69A2AR.22	1.46	C04F5.8	1.48
D1054.19	1.41	rbm-28	1.43	nlp-15	1.46	Y45G5AL.1	1.48
F44D12.6	1.41	klp-13	1.43	txt-5	1.46	cytb-5.2	1.48
flp-4	1.41	M03B6.5	1.43	lgg-2	1.46	rbf-1	1.48
F01G4.6	1.41	pqn-92	1.43	F19G12.9	1.46	aakg-5	1.48
ttr-1	1.41	nlp-43	1.43	eif-2alpha	1.46	M176.11	1.48
rps-20	1.41	mrpl-1	1.43	ddx-52	1.46	glb-21	1.48
C13F10.5	1.41	E04F6.8	1.44	egl-20	1.46	C47E12.9	1.48
nuaf-1	1.41	F36G3.3	1.44	T23F2.2	1.46	pcf-11	1.48
flp-2	1.41	kin-16	1.44	mltn-1	1.46	C30G12.2	1.49
vps-20	1.41	Y105E8A.1	1.44	F32D8.13	1.46	Y45F3A.9	1.49
F57B1.5	1.41	smg-1	1.44	alg-1	1.46	mekk-3	1.49
hsp-12.3	1.41	K12H4.7	1.44	K12C11.6	1.46	saeg-1	1.49
mca-2	1.42	ttr-46	1.44	pghm-1	1.46	smg-2	1.49
twk-10	1.42	dhs-17	1.44	Y53F4B.1	1.46	F29B9.1	1.49
pah-1	1.42	Y47G6A.13	1.44	gtf-2A2	1.46	sul-2	1.49
aagr-1	1.42	pqn-48	1.44	F36H2.3	1.46	gpx-6	1.49
scl-2	1.42	Y71H2B.11	1.44	W08A12.2	1.47	rla-0	1.49
cyp-13A1	1.42	C54C8.8	1.44	T26G10.1	1.47	pdcd-2	1.49
K10B3.5	1.42	smi-1	1.44	F41G3.18	1.47	daf-16	1.5
T05A8.3	1.42	F58B4.5	1.44	hsp-6	1.47	tos-1	1.5
nhr-152	1.42	C45G7.13	1.44	Y42G9A.2	1.47	Y75B8A.14	1.5
Y49F6B.2	1.42	C04H5.1	1.44	Y38F1A.1	1.47	pfk-1.2	1.5
Y105C5A.8	1.42	lron-4	1.45	F18C5.10	1.47	E02H4.5	1.5
clec-86	1.42	Y116A8C.40	1.45	srsx-19	1.47	F48E8.4	1.5
lis-1	1.42	spp-10	1.45	F55F8.2	1.47	C32E12.4	1.5
ensa-1	1.42	spin-4	1.45	C54D10.3	1.47	rpc-11	1.5
nft-1	1.42	B0403.6	1.45	F53H4.4	1.47	Y50D4A.1	1.5
nstp-1	1.42	F16B3.2	1.45	C52B11.5	1.47	pals-14	1.5
mlst-8	1.42	Y38H6C.23	1.45	trx-2	1.47	B0035.13	1.5
Y41D4A.7	1.42	ain-2	1.45	W02G9.4	1.47	lin-48	1.5
C06E1.9	1.42	Y9C9A.8	1.45	fipr-10	1.47	rgs-2	1.5
kel-1	1.42	Y39H10A.6	1.45	trxr-1	1.47	cbp-3	1.5
egl-5	1.43	mlck-1	1.45	F59B2.13	1.47	ceh-14	1.5
arrd-18	1.43	exos-8	1.45	unc-13	1.47	rpi-2	1.5
F35B3.7	1.43	rev-3	1.45	B0507.2	1.47	F33D4.4	1.5

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
plc-1	1.5	nhr-190	1.53	ctl-1	1.56	C32D5.11	1.58
Y41C4A.8	1.5	npr-24	1.53	zmp-4	1.56	gcy-21	1.59
flp-14	1.5	ZK673.1	1.53	abcf-3	1.56	ears-1	1.59
flp-6	1.5	F59E12.6	1.53	F14H12.8	1.56	kin-14	1.59
Y41D4B.1	1.51	col-91	1.53	cwp-5	1.56	tub-2	1.59
F42F12.3	1.51	C05C10.7	1.53	C05D11.1	1.56	Y92H12A.2	1.59
ttr-24	1.51	nceh-1	1.53	F52E10.4	1.56	Y54E5A.8	1.59
fozi-1	1.51	C13A10.1	1.53	F32A5.8	1.56	nuc-1	1.59
rbpl-1	1.51	nhr-100	1.53	B0454.5	1.56	F41E7.7	1.59
Y34B4A.5	1.51	C10B5.3	1.53	T03F6.9	1.56	klo-1	1.59
klf-1	1.51	spp-1	1.53	F30H5.4	1.56	T21H3.1	1.59
rnt-1	1.51	fbxa-99	1.53	rpia-1	1.56	zig-6	1.6
noa-1	1.51	F22H10.10	1.53	far-7	1.56	abhd-14	1.6
ceh-79	1.51	trk-1	1.53	pals-34	1.56	dop-5	1.6
T10C6.6	1.51	mdt-15	1.53	glb-24	1.56	sulp-5	1.6
pdzd-8	1.51	T05A10.6	1.54	Y8A9A.2	1.56	haly-1	1.6
atg-9	1.51	F49F1.14	1.54	C03H5.7	1.56	Y18D10A.23	1.6
F52E1.5	1.51	Y75B12B.3	1.54	C27H5.4	1.56	igdb-2	1.6
K08D8.7	1.51	chil-12	1.54	F59F5.3	1.56	F54D1.1	1.6
cyp-13A3	1.51	F40G9.17	1.54	nhr-144	1.57	T02B11.3	1.6
scd-2	1.51	flp-22	1.54	eef-1A.1	1.57	nhr-126	1.6
F49E2.2	1.52	F54D5.7	1.54	asm-3	1.57	ZK180.7	1.6
ikb-1	1.52	C36A4.11	1.54	C18H7.6	1.57	Y79H2A.12	1.6
fkh-7	1.52	mod-1	1.54	F02E11.7	1.57	nlp-5	1.6
T10B11.5	1.52	F09C6.1	1.54	unc-80	1.57	C17G1.5	1.6
cct-2	1.52	pfd-5	1.54	egl-43	1.57	F53B1.8	1.61
nstp-4	1.52	glb-27	1.54	byn-1	1.57	C44H9.5	1.61
spv-1	1.52	C47D2.1	1.54	rars-2	1.57	Y61A9LA.1	1.61
C18A11.2	1.52	F11C7.6	1.55	mus-81	1.57	lact-3	1.61
dgk-1	1.52	T02B11.4	1.55	bath-38	1.57	rab-21	1.61
C46H11.10	1.52	nhr-96	1.55	linc-35	1.57	ggr-3	1.61
fbxl-1	1.52	ptr-13	1.55	T03E6.8	1.58	F17H10.2	1.61
rrp-1	1.52	trm-2A	1.55	ttr-39	1.58	C32H11.3	1.61
Y18D10A.9	1.52	ceh-57	1.55	Y20C6A.1	1.58	Y92H12A.5	1.61
F32B5.6	1.52	R119.5	1.55	Y48G10A.3	1.58	F58H1.7	1.61
ugt-46	1.52	K08E5.1	1.55	spp-18	1.58	ufc-1	1.61
aakg-1	1.52	C06G3.3	1.55	Y70C5A.3	1.58	CD4.1	1.61
R10E8.8	1.52	pqn-25	1.55	K07G5.5	1.58	T07F12.1	1.61
F01D5.1	1.53	T27A10.6	1.55	deg-3	1.58	F20B6.4	1.61
adr-1	1.53	gcy-7	1.55	W02D3.12	1.58	fbxa-21	1.61
Y39H10B.2	1.53	Y61A9LA.10	1.56	ugt-18	1.58	Y51H4A.8	1.61
R10E8.7	1.53	egl-2	1.56	F57C12.2	1.58	afmd-1	1.61

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
C27H5.2	1.61	Y105E8B.7	1.65	dop-1	1.68	ubc-8	1.71
pro-3	1.61	T02C5.1	1.65	pdpr-1	1.68	flp-12	1.72
T24C2.5	1.61	ZK1240.9	1.66	pkn-1	1.68	spp-5	1.72
mlt-7	1.62	gur-3	1.66	C29F7.2	1.68	F45E10.2	1.72
nhr-83	1.62	hda-4	1.66	nas-39	1.68	C30G4.4	1.72
ZK1320.3	1.62	sptf-2	1.66	K02D10.4	1.68	F46G10.1	1.72
vbh-1	1.62	C05D11.8	1.66	scl-14	1.69	cest-31	1.72
F55A4.4	1.62	mod-5	1.66	sgk-1	1.69	nhr-48	1.72
R08B4.4	1.62	Y73E7A.1	1.66	nhr-99	1.69	M4.1	1.72
F36F2.7	1.62	F15D4.2	1.66	mtl-1	1.69	icd-2	1.72
ttr-29	1.62	cest-25	1.66	F11E6.6	1.69	sul-3	1.72
ZC404.1	1.63	ugt-52	1.66	duxl-1	1.69	egl-27	1.72
efk-1	1.63	fbxa-185	1.66	Y73B3A.18	1.69	E04F6.9	1.72
tric-1B.1	1.63	lido-13	1.66	snap-29	1.69	abcf-2	1.72
crtc-1	1.63	Y53F4B.21	1.66	hars-1	1.69	fbxa-189	1.72
rncs-1	1.63	ccdc-149	1.67	let-23	1.69	ifb-2	1.73
sel-8	1.63	D1025.10	1.67	ascc-1	1.69	nhr-5	1.73
let-611	1.63	C27B7.7	1.67	egl-21	1.69	klp-4	1.73
sma-9	1.64	F35B12.3	1.67	nlp-11	1.7	dct-11	1.73
ZK1098.11	1.64	F43C9.2	1.67	sax-1	1.7	K07D4.9	1.73
mfn-1	1.64	T28C12.2	1.67	R04E5.7	1.7	K12B6.9	1.73
F40A3.7	1.64	F17C11.4	1.67	mrpl-37	1.7	eif-3.I	1.73
sma-10	1.64	C33D9.3	1.67	B0286.1	1.7	uev-3	1.73
fbxa-140	1.64	sorf-2	1.67	Y40B1B.7	1.7	Y37F4.8	1.74
nlp-61	1.64	Y71H2AM.2	1.67	flp-3	1.7	glo-3	1.74
F02E11.2	1.64	atf-6	1.67	tag-209	1.7	nlp-80	1.74
F59C6.5	1.64	dhs-20	1.67	C38D4.7	1.7	T09E11.11	1.74
ttr-10	1.64	frpr-18	1.67	Y73B3A.9	1.7	daf-37	1.74
lipl-2	1.64	Y54G2A.10	1.67	cct-5	1.7	cyn-2	1.74
egl-10	1.65	nape-1	1.67	egl-8	1.71	hsp-90	1.74
mca-1	1.65	ugt-55	1.67	znfx-1	1.71	glct-6	1.74
cct-7	1.65	F40F12.9	1.67	C08G9.1	1.71	F02A9.1	1.74
F58G6.7	1.65	gcy-35	1.67	C25H3.11	1.71	nhr-232	1.75
fezf-1	1.65	C44H4.8	1.68	kin-10	1.71	F16B4.2	1.75
haf-4	1.65	T03G11.3	1.68	R10F2.5	1.71	lgc-25	1.75
xdh-1	1.65	F13C5.1	1.68	cest-35.1	1.71	ser-4	1.75
cpx-2	1.65	K07F5.15	1.68	Y94H6A.5	1.71	adpr-1	1.75
fbxa-74	1.65	msrp-7	1.68	lars-1	1.71	F08H9.3	1.75
mboa-7	1.65	dct-1	1.68	Y75B7AL.2	1.71	K04F10.1	1.75
ttr-40	1.65	Y39B6A.37	1.68	irld-34	1.71	C07F11.2	1.75
T24H7.2	1.65	drd-5	1.68	F10G8.9	1.71	far-5	1.75
dcp-66	1.65	T23B3.6	1.68	ampd-1	1.71	tom-1	1.75

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
nxf-1	1.75	ptl-1	1.78	T13F2.6	1.82	F20A1.6	1.87
C54F6.6	1.75	adk-1	1.78	pin-2	1.83	zip-12	1.87
frm-7	1.75	ugt-56	1.78	Y71H2AM.12	1.83	F09B12.3	1.87
clh-4	1.75	nlp-9	1.79	pde-6	1.83	aatf-1	1.87
F58G6.8	1.75	F17B5.1	1.79	glt-4	1.83	dgk-5	1.87
ccm-2	1.75	linc-56	1.79	pudl-2	1.83	tsp-6	1.87
T26H5.8	1.76	dhs-15	1.79	Y32F6A.4	1.83	Y110A2AL.9	1.87
C33G8.4	1.76	C08F11.116	1.79	nhr-128	1.84	F53F4.14	1.87
cyp-34A2	1.76	ugt-54	1.79	hizr-1	1.84	C52E2.5	1.87
glt-7	1.76	Y9C2UA.1	1.79	lin-28	1.84	osm-9	1.87
Y43C5A.2	1.76	C29G2.6	1.79	fars-3	1.84	Y46G5A.15	1.88
F16C3.1	1.76	Y73B6BL.31	1.79	ZK355.8	1.84	far-6	1.88
gpcp-1	1.76	twk-25	1.79	Y92H12BL.4	1.84	asna-1	1.88
T23G7.3	1.76	C04E7.3	1.79	F08F8.9	1.84	cct-4	1.88
zzz-1	1.76	aat-8	1.79	ccdc-47	1.84	C40H1.9	1.88
B0478.3	1.76	ric-19	1.79	flp-27	1.84	ubc-15	1.88
plc-3	1.76	nsy-1	1.79	dop-6	1.84	frk-1	1.88
pvf-1	1.76	rpl-24.2	1.8	moe-3	1.84	rabx-5	1.88
nhr-90	1.76	spp-14	1.8	gfat-1	1.84	C36B1.6	1.88
K03B4.1	1.76	pals-19	1.8	egl-3	1.84	nhr-106	1.88
nlp-17	1.76	nhr-64	1.8	F13H8.1	1.85	C29F5.3	1.88
dhp-1	1.76	gba-3	1.8	ZK131.11	1.85	crn-3	1.88
C34F6.11	1.77	eri-12	1.8	unk-1	1.85	flp-16	1.88
K01A2.10	1.77	slcr-46.1	1.8	btb-9	1.85	R151.1	1.88
npr-28	1.77	T16G1.7	1.8	gst-6	1.85	W06E11.1	1.88
bgal-2	1.77	nlp-8	1.8	shpk-1	1.85	cab-1	1.88
W08F4.5	1.77	Y39B6A.29	1.8	Y41C4A.9	1.85	xbx-5	1.89
clec-37	1.77	ZK993.2	1.8	F14D2.19	1.85	R06C1.6	1.89
pgp-11	1.78	acl-7	1.8	eef-2	1.85	T08G11.4	1.89
B0563.7	1.78	psa-3	1.8	Y67D2.5	1.85	F55H12.7	1.89
Y57G11B.2	1.78	K02A2.5	1.81	Y32H12A.8	1.85	T21F4.1	1.89
lgc-19	1.78	H10D18.1	1.81	hlh-11	1.85	sek-4	1.89
K08D10.14	1.78	F49H6.5	1.81	unc-2	1.85	cyp-37A1	1.89
ech-7	1.78	F47G3.1	1.81	K11E4.1	1.86	C42D8.1	1.89
npr-5	1.78	T21B4.15	1.81	col-184	1.86	glb-26	1.9
ncs-3	1.78	D2096.7	1.81	ftn-1	1.86	F26D11.12	1.9
nlp-38	1.78	Y116A8C.25	1.82	gstk-2	1.86	kcnl-3	1.9
apm-1	1.78	crt-1	1.82	K07H8.11	1.86	F09G2.1	1.9
unc-63	1.78	droe-4	1.82	acr-23	1.86	C01C10.2	1.9
aldo-2	1.78	clec-63	1.82	ZK930.2	1.86	tig-2	1.9
fbxa-115	1.78	frpr-8	1.82	Y22D7AR.6	1.86	eif-3.E	1.9
col-160	1.78	tat-6	1.82	ZC395.5	1.86	R01H2.7	1.9

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
mtx-2	1.9	Y47A7.2	1.95	M163.1	2	Y54F10AR.2	2.06
clec-198	1.9	T06E6.1	1.95	twk-12	2	clec-17	2.06
H10D12.2	1.9	pbo-6	1.95	C35C5.9	2	nlp-19	2.06
K09E4.4	1.91	Y59C2A.1	1.95	ZC8.6	2	del-5	2.07
T25B9.1	1.91	xpo-1	1.95	R02F2.1	2	C45G9.14	2.07
ugt-1	1.91	nhl-2	1.95	C35B8.3	2.01	F07E5.5	2.07
F32H5.1	1.91	Y95B8A.6	1.95	prmt-1	2.01	twk-8	2.07
ugt-23	1.91	ZK1128.7	1.95	nrf-5	2.01	mtq-2	2.07
hgo-1	1.91	ssu-1	1.95	F02A9.7	2.01	adss-1	2.07
F19C6.12	1.91	pals-18	1.96	des-2	2.01	endu-2	2.07
aex-5	1.91	C25G4.2	1.96	bath-43	2.01	flp-9	2.07
aakb-2	1.91	C54D10.10	1.96	F41C3.7	2.02	ubc-26	2.07
col-142	1.91	pde-4	1.96	F11E6.11	2.02	W03D8.8	2.08
pry-1	1.91	F31A3.3	1.96	W07E6.2	2.02	cdc-48.3	2.08
gpa-17	1.92	cars-1	1.96	ZK993.5	2.02	sca-1	2.08
F54D11.4	1.92	ida-1	1.96	ptr-24	2.02	clec-75	2.08
akap-1	1.92	F13G3.6	1.96	F11C7.2	2.02	D1054.3	2.08
scl-24	1.92	fbxa-175	1.97	C11D2.3	2.03	R09E10.13	2.08
K09H9.8	1.92	F46A8.13	1.97	irld-2	2.03	F28H7.2	2.08
Y48C3A.3	1.92	C07B5.3	1.97	C03H5.3	2.03	tag-229	2.08
cnnm-3	1.92	cyp-33C3	1.97	nst-1	2.03	gsa-1	2.08
T22B7.3	1.92	fbxa-163	1.97	dhs-24	2.03	coel-1	2.08
C38C3.4	1.93	fbxa-10	1.97	asp-14	2.03	Y32B12C.5	2.08
cest-5.1	1.93	ZK180.8	1.97	math-27	2.03	acs-16	2.09
memb-2	1.93	fubl-1	1.97	adt-3	2.03	mop-25.1	2.09
fkh-9	1.93	nape-2	1.97	E02H4.4	2.03	cest-13	2.09
nhr-108	1.93	gcy-11	1.97	fnip-2	2.04	ztf-7	2.09
ril-2	1.93	R186.1	1.97	nhr-221	2.04	pals-32	2.09
mrps-11	1.93	F08F3.4	1.97	tax-6	2.04	ptp-1	2.09
eif-3.G	1.93	Y51H4A.7	1.98	faah-6	2.04	C18H7.1	2.09
Y82E9BR.5	1.94	F40G12.5	1.98	nhr-55	2.04	vps-33.1	2.09
Y51H4A.24	1.94	D1044.7	1.98	plc-2	2.04	Y50D7A.8	2.1
srh-210	1.94	M01E5.3	1.98	Y56A3A.31	2.05	dhs-7	2.1
ncx-2	1.94	iff-2	1.99	sqst-2	2.05	nhr-219	2.1
ptr-21	1.94	R10H1.1	1.99	smg-3	2.05	rpom-1	2.1
C01C4.3	1.94	ist-1	1.99	chil-22	2.05	F09G2.2	2.1
C33H5.13	1.94	R02F11.2	1.99	T02G5.14	2.06	K09C8.7	2.11
nsun-2	1.94	Y66H1A.5	1.99	pgp-9	2.06	nca-2	2.11
Y105C5A.17	1.94	cyp-35B1	1.99	Y40B10B.1	2.06	ZC443.3	2.11
Y39G8B.10	1.94	aakg-4	2	timm-23	2.06	ZK512.2	2.11
ugt-2	1.94	F08G12.11	2	lipl-5	2.06	F59A7.5	2.11
col-42	1.94	W09C5.1	2	M176.4	2.06	F41E7.2	2.11

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
F41E7.20	2.11	ipla-7	2.18	nhr-94	2.26	R07C12.2	2.33
M01H9.4	2.11	T24E12.10	2.18	cps-6	2.26	scl-5	2.33
afmd-2	2.12	C35E7.6	2.19	C14A11.2	2.26	fbxa-69	2.33
ZK250.13	2.12	fshr-1	2.19	F10E7.5	2.26	F36F2.2	2.33
C25H3.18	2.12	lite-1	2.19	clec-8	2.26	T01C8.3	2.33
cat-4	2.12	B0432.14	2.19	catp-7	2.26	C10E2.2	2.34
T09F5.12	2.12	F41G4.7	2.2	asp-5	2.26	Y82E9BR.22	2.34
F14H8.4	2.12	Y54F10BM.12	2.2	F37A8.5	2.26	siah-1	2.34
glb-17	2.12	moc-2	2.2	nhr-210	2.27	Y47G6A.7	2.34
Y113G7A.13	2.12	exc-14	2.2	Y6E2A.4	2.27	tag-151	2.34
lips-15	2.12	clec-82	2.2	B0252.1	2.27	C39H7.4	2.34
peb-1	2.13	Y7A9C.1	2.2	ctn-1	2.27	Y34F4.5	2.35
D2045.8	2.13	R05A10.1	2.21	imb-3	2.27	M04D8.7	2.35
Y49E10.16	2.13	F26G1.10	2.21	F56C4.4	2.27	ZC239.16	2.35
F35B12.10	2.13	chil-23	2.21	F08A7.1	2.27	cpz-2	2.35
lact-2	2.14	ZK813.4	2.21	T28F3.8	2.27	F21H7.2	2.35
Y43F8C.3	2.14	Y106G6G.2	2.21	elpc-4	2.27	rrbs-1	2.35
K10G4.3	2.14	R09B5.11	2.21	math-37	2.27	C02F5.3	2.36
F22B7.1	2.14	unc-31	2.21	gtl-1	2.27	linc-39	2.36
skr-19	2.14	dao-6	2.22	tpra-1	2.28	rrp-8	2.36
T01D3.6	2.14	hil-1	2.22	F44A2.3	2.28	brp-1	2.37
crm-1	2.15	rars-1	2.22	wrb-1	2.28	F26A3.1	2.37
mrps-17	2.15	C06H5.8	2.22	wars-1	2.29	cct-3	2.37
ZK1307.1	2.15	T10B5.3	2.22	C28H8.3	2.29	slc-28.1	2.37
epg-5	2.15	K02A11.4	2.22	nlp-7	2.29	H35B03.1	2.37
irg-3	2.15	Y42A5A.1	2.22	ins-29	2.29	ncx-7	2.37
Y56A3A.18	2.15	nhr-35	2.22	F56D5.6	2.29	Y71H2AM.1	2.38
clec-76	2.16	nspc-19	2.22	kin-3	2.29	ttr-34	2.38
ZK971.1	2.17	lin-14	2.22	cnnm-2	2.29	T08B1.4	2.38
him-4	2.17	F33D11.16	2.23	alh-8	2.3	T20D3.6	2.38
F26F12.3	2.17	F13D11.4	2.23	D1022.4	2.3	F14H3.12	2.39
F54C8.1	2.17	R119.2	2.23	Y54F10AM.8	2.3	dohh-1	2.39
C09E7.6	2.17	alh-12	2.23	Y7A5A.6	2.3	F29C6.1	2.4
exos-9	2.17	M01F1.3	2.24	pho-4	2.31	nhr-146	2.4
riok-2	2.18	sma-2	2.24	Y6B3B.4	2.31	nap-1	2.4
pno-1	2.18	F20D6.5	2.24	W03D8.2	2.31	ZK822.4	2.4
F45E1.5	2.18	F41G4.8	2.24	nhr-119	2.31	gst-23	2.4
pals-31	2.18	nmad-1	2.25	lmd-4	2.31	Y92H12BL.1	2.41
mgl-2	2.18	mak-2	2.25	C49A9.6	2.32	bath-47	2.41
H23N18.6	2.18	nhr-80	2.25	C16A3.6	2.32	yap-1	2.41
ddx-17	2.18	lpr-2	2.25	riok-3	2.32	gpa-8	2.41
C08F11.3	2.18	Y51H4A.15	2.26	gdh-1	2.33	R09F10.1	2.42

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
gap-1	2.42	F53F10.1	2.52	T01G1.4	2.64	R10E8.6	2.8
ZK550.2	2.42	ins-35	2.52	obr-2	2.65	dph-3	2.8
nhr-170	2.42	C50F4.1	2.52	C15B12.4	2.65	T22F3.2	2.8
Y37E11B.5	2.43	clec-146	2.52	F56H9.9	2.66	clec-62	2.8
rsd-3	2.43	F35D11.3	2.53	upb-1	2.66	K02C4.5	2.8
T10H4.13	2.43	gst-22	2.53	T19C3.6	2.66	C53H9.2	2.81
ace-2	2.43	cpz-1	2.53	daf-2	2.67	C52E2.4	2.81
H34I24.2	2.43	W07A12.4	2.54	ZK430.7	2.67	lep-5	2.82
elpc-3	2.43	F30A10.9	2.54	B0507.3	2.67	nhr-103	2.82
capa-1	2.44	T19D12.2	2.54	Y47H10A.3	2.68	nlp-52	2.83
btb-17	2.45	ulp-3	2.54	lido-10	2.68	Y37H9A.5	2.83
F31E9.3	2.45	R02E4.2	2.54	lec-2	2.68	F53F1.14	2.83
C49F5.7	2.45	nlp-47	2.54	gsp-2	2.69	B0511.6	2.84
T28A11.2	2.45	twk-7	2.54	csp-2	2.69	sek-1	2.84
ugt-6	2.46	K02D10.8	2.54	asp-6	2.7	ZK1290.13	2.84
flp-20	2.46	acl-9	2.54	T07D4.2	2.7	mnk-1	2.85
R11D1.13	2.46	C23F12.4	2.55	F59A7.8	2.7	nlp-2	2.85
JC8.2	2.46	C53C11.2	2.56	T20F7.5	2.71	C49C8.8	2.85
ads-1	2.46	dph-1	2.56	mfb-1	2.71	clec-186	2.85
exos-7	2.46	K11D12.12	2.57	cgr-1	2.71	W07G4.5	2.85
Y46G5A.34	2.46	C24H12.4	2.57	Y54G2A.41	2.71	Y40C5A.4	2.86
C16D9.9	2.47	F53F4.11	2.57	W02D7.11	2.72	F21A3.11	2.86
C47D12.5	2.47	gst-3	2.58	nhr-133	2.72	K09H9.5	2.86
col-92	2.47	hpo-11	2.59	T22H9.1	2.72	Y54H5A.2	2.87
asah-1	2.47	T01B7.5	2.59	ZC443.4	2.72	Y54H5A.1	2.88
nspc-17	2.47	Y34F4.2	2.59	C34E11.4	2.72	F08F8.7	2.88
Y106G6E.4	2.48	pho-5	2.6	Y6G8.2	2.73	F16A11.5	2.88
T23D8.3	2.49	nog-1	2.61	nhr-92	2.74	gcy-15	2.88
mrpl-55	2.49	F45D11.1	2.61	tag-89	2.75	T28H10.1	2.88
eif-3.B	2.49	lnp-1	2.61	Y53C12B.7	2.75	F36A2.10	2.88
Y43C5A.3	2.5	F44G4.1	2.61	nhr-129	2.75	puf-12	2.89
smp-2	2.5	F31B12.3	2.61	btb-16	2.75	F48E8.3	2.89
aak-1	2.5	mtl-2	2.61	fbxc-7	2.76	ZK688.11	2.89
nlp-69	2.51	T10H9.8	2.62	pud-4	2.76	C53A5.17	2.9
nhl-1	2.51	F55A4.7	2.62	nnt-1	2.76	R01H10.4	2.91
C18A11.1	2.51	C36E8.1	2.62	arch-1	2.77	Y51B9A.9	2.91
asp-3	2.51	B0563.5	2.62	clec-65	2.77	Y43B11AR.3	2.92
rab-8	2.51	lpd-7	2.62	Y71G10AR.4	2.77	F49C12.6	2.92
unc-83	2.51	mps-1	2.63	Y57G11C.1135	2.77	F47H4.12	2.92
F58A3.3	2.51	T10G3.1	2.63	E02H1.1	2.78	srp-2	2.93
C16C10.8	2.51	clec-61	2.63	nlp-59	2.78	nhr-109	2.93
paqr-1	2.52	C27F2.4	2.63	smf-3	2.79	C05E11.6	2.96

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
asm-2	2.96	Y54E10BR.4	3.16	tut-1	3.46	chil-13	3.86
clec-85	2.97	metl-18	3.19	C09D4.2	3.47	W08E12.8	3.89
C15C7.4	2.97	fbxa-173	3.19	ctps-1	3.48	faah-3	3.89
cyp-34A9	2.98	nhr-88	3.21	Y15E3A.4	3.49	ttr-49	3.93
flp-10	2.98	F36A2.2	3.22	B0513.4	3.49	F35C8.5	3.93
M60.7	2.99	Y71F9AL.2	3.23	B0546.3	3.49	T26H5.4	3.97
T25G3.3	2.99	nspc-18	3.23	asah-2	3.5	arrd-11	4.01
ulp-4	3	F54D5.3	3.23	Y48G8AL.13	3.5	C45E5.4	4.04
T10B5.7	3	C25A8.5	3.24	hpo-15	3.5	D1086.2	4.07
odr-10	3	Y22D7AL.15	3.24	Y47D3A.32	3.5	C18H9.5	4.08
F42A9.18	3.02	Y39B6A.33	3.25	H06H21.8	3.52	ZK593.2	4.13
zig-9	3.02	F10G7.5	3.26	C25F9.12	3.52	exc-13	4.13
metl-2	3.02	nhr-18	3.27	W09C3.7	3.54	cyp-37B1	4.16
cpr-6	3.03	linc-43	3.28	nas-9	3.56	C05D9.9	4.18
T18D3.6	3.04	srap-1	3.28	C45E1.4	3.56	cest-1.2	4.2
Y18D10A.3	3.05	F53A2.9	3.29	C39D10.11	3.58	T10C6.15	4.24
C23H5.15	3.05	Y65B4BL.7	3.3	F47B8.4	3.58	F56H9.2	4.26
C32H11.4	3.05	ZC239.17	3.3	ncr-2	3.59	hda-5	4.3
nspc-20	3.06	fbxa-6	3.31	tts-1	3.6	B0379.7	4.34
C28G1.6	3.07	adah-1	3.31	T06C12.14	3.6	F47B8.8	4.37
gst-20	3.07	Y56A3A.33	3.32	cup-16	3.6	C32F10.4	4.37
ngp-1	3.07	pmt-1	3.32	col-181	3.61	ZC395.4	4.47
lgc-28	3.07	R10E8.1	3.33	twk-5	3.61	nspc-14	4.52
M01B2.13	3.07	nspc-16	3.34	clec-84	3.62	K05F6.10	4.63
ubc-1	3.07	C10A4.3	3.35	hrg-2	3.67	spp-8	4.68
C28H8.2	3.08	fbxa-162	3.35	acp-5	3.67	ZK185.5	4.77
Y97E10AL.1	3.11	Y52B11A.10	3.36	C17G10.6	3.68	W10G11.1	4.79
Y42G9A.1	3.11	pqn-59	3.37	spp-6	3.7	F21H7.12	4.87
col-118	3.11	Y47G6A.5	3.37	ZK470.14	3.71	srv-4	5
T12D8.5	3.12	pho-6	3.38	F18G5.6	3.71	cyp-32B1	5.16
F40F8.5	3.12	hecw-1	3.38	T26E3.4	3.71	F43C11.7	5.2
txt-3	3.13	ZK1240.2	3.39	chil-16	3.72	F56F11.1	5.37
W04E12.7	3.13	fbxa-80	3.4	F43D2.7	3.74	dpy-5	5.53
riok-1	3.13	C08F11.13	3.41	clec-264	3.74	hsp-12.6	6.52
tag-243	3.13	F56A8.5	3.41	F21C10.11	3.74		
W06H8.6	3.14	F23F12.3	3.41	col-39	3.78		
T26C11.9	3.14	R07E3.1	3.41	T08A9.13	3.79		
C03G6.17	3.14	pqn-62	3.41	F16B4.5	3.81		
C16A3.4	3.15	T09B4.6	3.42	C29G2.2	3.82		
F52E1.14	3.15	fil-1	3.44	F40E3.5	3.83		
del-9	3.16	B0524.6	3.44	W03D2.6	3.83		
fat-6	3.16	fard-1	3.45	cpr-2	3.85		

6.18. Proteome (TMT) - 4h Fed vs 48h Starved - N2 (wild-type)

Protein	log2FC	Protein	log2FC	Protein	log2FC	Protein	log2FC
H39E23.3	-10.04	Y51H4A.7	-1.98	spr-4	-1.49	Y67H2A.10	-1.2
B0379.6	-8.28	C08E8.4	-1.97	T08A11.1	-1.49	zyg-8	-1.19
E02C12.9	-6.57	athp-2	-1.95	hsb-1	-1.49	F31E3.12	-1.19
Y53F4B.21	-5.41	ppw-2	-1.91	cwc-15	-1.48	ZK353.9	-1.19
ipla-2	-5.24	M03C11.3	-1.9	grd-13	-1.48	F26E4.3	-1.18
col-39	-5.15	Y65B4A.2	-1.9	Y44A6D.2	-1.48	W05H12.1	-1.18
dpy-14	-4.84	cut-3	-1.89	sec-11	-1.47	B0035.3	-1.18
dpy-17	-4.59	col-121	-1.87	C14A4.9	-1.45	gst-29	-1.17
fipr-22	-4.58	hsp-16.48	-1.82	vps-2	-1.43	attf-4	-1.17
col-158	-4.31	unc-52	-1.81	cth-2	-1.42	F13B12.4	-1.17
cyp-33E2	-4.04	leo-1	-1.81	lars-2	-1.4	cox-5B	-1.16
F55F8.3	-3.95	lec-9	-1.8	B0495.7	-1.4	gst-15	-1.16
abts-4	-3.85	rpi-2	-1.8	capg-1	-1.39	F07C3.2	-1.16
grl-16	-3.83	sucl-2	-1.79	nep-1	-1.39	C24G6.8	-1.15
dpy-10	-3.67	tps-1	-1.77	C24H10.1	-1.38	kcc-2	-1.15
spin-1	-3.3	sph-1	-1.75	fbn-1	-1.35	psf-2	-1.15
hgap-2	-3.29	T03F1.11	-1.75	T04C9.1	-1.34	gst-20	-1.14
C44C10.9	-3.12	lin-10	-1.74	vps-60	-1.34	sptf-3	-1.12
nex-4	-3.1	Y37A1B.7	-1.73	ten-1	-1.34	C11D2.4	-1.12
hsp-16.2	-2.96	T10B10.3	-1.72	mlt-7	-1.33	T19H12.2	-1.11
rnp-6	-2.87	nbet-1	-1.71	K02F3.9	-1.33	C30H6.8	-1.11
hda-10	-2.81	cht-1	-1.71	shc-1	-1.33	num-1	-1.1
R02C2.7	-2.8	clec-266	-1.68	cubn-1	-1.32	T10H9.8	-1.1
hum-6	-2.78	acn-1	-1.68	fubl-1	-1.32	T10B5.4	-1.1
F54F7.6	-2.77	smr-1	-1.67	F22D6.2	-1.32	lea-1	-1.09
iscu-1	-2.75	dsl-3	-1.67	F36H9.7	-1.31	Y38C1AA.9	-1.09
F10D11.6	-2.7	egl-27	-1.67	tep-1	-1.3	ttc-36	-1.08
F14B4.1	-2.65	ensa-1	-1.65	F43C9.2	-1.3	lin-36	-1.08
ZK863.8	-2.5	Y48G1C.12	-1.63	gtf-2F1	-1.29	slc-36.5	-1.08
pde-5	-2.43	hmg-3	-1.61	F44E5.4	-1.29	ttr-23	-1.07
dve-1	-2.34	mlst-8	-1.6	W10C8.4	-1.29	inx-6	-1.07
C53B7.3	-2.3	C47A4.1	-1.6	lex-1	-1.27	C09F9.2	-1.06
Y39B6A.5	-2.26	scl-12	-1.58	ttr-5	-1.25	cav-2	-1.06
T21B6.3	-2.26	F59F3.6	-1.57	pdl-1	-1.24	Y92H12BL.4	-1.06
Y39A1A.21	-2.25	T18D3.1	-1.56	F29B9.5	-1.24	F36G3.2	-1.06
sod-5	-2.24	sec-10	-1.55	hmg-1.2	-1.23	viro-2	-1.06
C01G6.3	-2.19	dgk-1	-1.54	K01A2.10	-1.22	F59B10.3	-1.06
C50D2.8	-2.13	ints-7	-1.54	eif-3.K	-1.22	C16C10.4	-1.06
elpc-2	-2.12	pqn-94	-1.54	lron-9	-1.21	ncam-1	-1.06
C15C7.7	-2.09	F53E10.1	-1.51	dpy-27	-1.2	ech-8	-1.05
Y53F4B.23	-1.99	pfas-1	-1.51	hil-2	-1.2	cox-6B	-1.05

Protein	log2FC	Protein	log2FC	Protein	log2FC	Protein	log2FC
tut-1	-1.05	lbp-2	1.06	cdr-6	1.17	Y54E10A.10	1.33
daf-16	-1.04	wdr-46	1.06	glh-2	1.18	ugt-22	1.33
Y37E11B.5	-1.04	pod-2	1.06	iff-2	1.18	nola-3	1.34
lin-15B	-1.03	C05C10.3	1.06	mrpl-37	1.18	fpn-1.1	1.34
ttr-33	-1.03	hmt-1	1.06	fmo-5	1.18	rnp-1	1.35
T05F1.11	-1.03	gob-1	1.06	AC3.5	1.19	alh-8	1.35
gst-24	-1.03	taap-1	1.07	rbm-34	1.19	rps-10	1.35
F37F2.2	-1.02	lec-4	1.07	acp-6	1.2	cdr-4	1.36
C50F4.16	-1.01	Y104H12D.2	1.07	fbxa-156	1.2	pqn-22	1.37
F23H11.5	-1.01	txdc-12.2	1.08	scav-3	1.21	ttr-51	1.38
hmg-1.1	-1.01	mct-4	1.09	cpn-1	1.21	rme-2	1.38
cox-6A	-1.01	mpc-2	1.09	Y15E3A.4	1.21	gldc-1	1.39
hsp-16.11	-1.01	acdh-9	1.09	T10G3.3	1.21	pud-2.1	1.39
emb-9	-1	mrps-23	1.1	T20B12.3	1.21	cle-1	1.39
cept-2	-1	sptl-3	1.1	nuc-1	1.22	cps-6	1.39
hrpa-1	-1	Y16B4A.2	1.1	glh-4	1.22	dod-19	1.4
Y106G6H.8	1	C39D10.8	1.11	T21H3.1	1.22	mrpl-13	1.4
dut-1	1	cpr-4	1.11	msra-1	1.22	Y10G11A.1	1.41
cyp-34A9	1	T07D3.9	1.11	Y48A6C.4	1.22	msi-1	1.41
F41D9.2	1.01	csq-1	1.11	oxy-4	1.22	lec-6	1.42
otub-1	1.01	pmt-2	1.11	C10G11.8	1.23	ger-1	1.42
W01A11.1	1.01	LLC1.2	1.11	rps-25	1.23	pept-1	1.43
rps-23	1.01	ogdh-2	1.12	Y34B4A.6	1.23	F53F4.16	1.43
arf-6	1.01	T13C2.6	1.12	F37C12.3	1.24	comt-4	1.43
cka-2	1.01	ubc-14	1.12	eef-1B.1	1.24	bca-2	1.44
spp-2	1.01	tag-18	1.12	F33A8.4	1.25	rbm-3.2	1.44
Y54E2A.4	1.02	Y67D2.7	1.12	F53B1.8	1.25	mrpl-45	1.44
F57F5.1	1.02	F32D8.12	1.13	paic-1	1.26	vha-1	1.44
F33H2.6	1.02	ceh-20	1.13	lact-3	1.26	C17G1.2	1.45
sur-5	1.03	D1086.3	1.13	F54D5.12	1.26	ech-6	1.45
col-159	1.04	aps-2	1.13	R08B4.3	1.27	gst-27	1.45
spp-5	1.04	C01B10.6	1.13	coq-6	1.27	eif-2Balpha	1.45
hda-5	1.04	vha-6	1.13	lec-10	1.28	wdr-12	1.46
Y43F4B.7	1.04	R10F2.4	1.14	gst-35	1.28	oxa-1	1.46
T21C9.6	1.04	ima-2	1.14	ugt-26	1.29	rhr-1	1.47
nex-3	1.05	cest-4	1.15	T01D3.6	1.29	lron-7	1.48
rpl-25.1	1.05	F39H11.1	1.16	acp-5	1.29	pgp-3	1.5
T20H4.5	1.05	ZK1320.9	1.16	coq-3	1.31	pde-3	1.52
nas-11	1.05	T25C12.3	1.17	mig-2	1.32	nhr-130	1.53
R119.3	1.05	Y54E5A.5	1.17	gly-5	1.32	gfi-1	1.53
cpz-1	1.06	W10C8.5	1.17	C45G9.5	1.33	F09C8.1	1.53

Protein	log2FC	Protein	log2FC	Protein	log2FC
madd-3	1.53	Y7A5A.1	1.86	bigr-1	2.63
K08D8.6	1.54	cyp-13A5	1.86	T12D8.5	2.63
F09F7.6	1.54	pcp-4	1.86	ZK6.11	2.63
csn-5	1.55	C09G9.1	1.86	lys-4	2.7
nol-10	1.55	R09H10.5	1.87	grl-23	2.75
F28B4.3	1.56	elo-1	1.89	D1054.10	2.81
asp-5	1.57	Y54F10AM.8	1.9	dct-16	2.93
trpa-2	1.57	col-92	1.93	acdh-1	2.94
R193.2	1.58	F21C10.9	1.93	F17E9.5	2.96
dhs-25	1.58	C34H4.2	1.94	T28F3.8	3
mpc-1	1.59	F35C8.5	1.95	vit-3	3
F20G2.1	1.59	timm-23	1.97	Y62H9A.5	3.14
hpo-40	1.6	C14F11.4	1.97	rpc-25	3.22
M02H5.8	1.6	pud-1.1	1.98	perm-2	3.22
F33H1.4	1.6	pmp-5	1.99	cey-3	3.24
F44G4.1	1.61	vps-36	2	fip-5	3.24
far-6	1.62	C03A3.2	2.01	ilys-5	3.32
F59B1.2	1.62	argk-1	2.02	glh-1	3.36
asps-1	1.63	spp-3	2.03	cey-2	3.5
C53D5.5	1.64	B0432.7	2.08	F54E2.1	3.63
Y34B4A.9	1.65	R10H10.3	2.09	cbd-1	3.65
hpo-34	1.67	vit-1	2.09	far-2	3.67
hach-1	1.68	hphd-1	2.11	ule-1	3.69
aagr-2	1.69	ugt-62	2.11	Y39H10A.6	3.7
asp-6	1.71	pgp-1	2.11	perm-4	3.74
F19C7.1	1.71	asp-13	2.19	K12H4.7	3.83
tomm-22	1.71	F56C9.7	2.19	folt-2	4.38
cdf-1	1.72	lec-8	2.24	C01H6.8	4.77
F58B4.5	1.72	clec-63	2.27	ule-5	5.11
ldp-1	1.75	ZK813.3	2.27	Y59E9AR.1	5.28
ctsa-1.2	1.75	tba-4	2.28		
sodh-1	1.76	asp-1	2.28		
egg-1	1.76	F17E9.4	2.31		
vit-5	1.77	Y51F10.7	2.35		
Y37H2A.14	1.78	C23H5.8	2.37		
sft-1	1.79	C23H3.2	2.4		
mct-2	1.8	T26G10.1	2.45		
W04B5.3	1.81	anp-1	2.46		
let-767	1.81	hrg-7	2.47		
vit-4	1.85	clec-50	2.49		
trpp-8	1.85	W05F2.3	2.59		

6.19. Proteome (TMT) - 4h Fed vs 48h Starved – HBR227 (*aptf-1*)

Protein	log2FC	Protein	log2FC	Protein	log2FC	Protein	log2FC
B0379.6	-8.69	vit-6	-1.72	C35A5.11	-1.31	tut-1	-1.09
dpy-10	-5.79	lpr-3	-1.71	mec-1	-1.3	ifc-2	-1.08
H39E23.3	-5.21	Y47H9C.1	-1.7	dnc-3	-1.3	shc-1	-1.08
Y53F4B.21	-5.1	C14A4.9	-1.7	Y55D9A.2	-1.29	ttr-35	-1.07
fipr-22	-4.92	vit-2	-1.67	C15A11.7	-1.28	T05F1.11	-1.06
E02C12.9	-4.76	sec-10	-1.67	Y39B6A.5	-1.28	R02C2.7	-1.04
hum-6	-4.4	lin-10	-1.63	grd-13	-1.26	memo-1	-1.04
dpy-17	-4.12	acn-1	-1.62	T10G3.3	-1.25	sor-1	-1.04
ipla-2	-3.95	hcp-1	-1.61	hsp-16.48	-1.25	oig-3	-1.04
dpy-14	-3.94	cth-2	-1.6	vit-3	-1.24	hch-1	-1.03
spin-1	-3.87	vit-5	-1.59	cht-1	-1.24	tpst-1	-1.03
abts-4	-3.74	ifc-1	-1.58	T24H10.1	-1.24	mlst-8	-1.02
leo-1	-3.5	ifp-1	-1.57	grl-7	-1.24	F53E10.1	-1.02
grl-16	-3.17	Y51H4A.7	-1.56	R06F6.8	-1.23	pch-2	-1.02
cyp-33E2	-3.04	asns-2	-1.55	psf-2	-1.2	mctp-1	-1.02
F54F7.6	-3.01	mcm-5	-1.53	F43G9.12	-1.2	C49A9.9	-1.02
hgap-2	-2.92	ost-1	-1.52	M02H5.8	-1.2	noah-1	-1.01
F14B4.1	-2.69	ZK287.1	-1.51	lex-1	-1.19	T24B8.7	-1.01
C11D2.4	-2.61	lin-14	-1.51	madd-3	-1.19	natc-2	-1
hda-10	-2.56	rnp-6	-1.51	mlt-11	-1.19	Y43F4B.7	1
Y39A1A.21	-2.47	elpc-2	-1.5	fdps-1	-1.19	C46G7.2	1.01
iscu-1	-2.38	ints-7	-1.49	M03C11.3	-1.18	R07B7.9	1.01
grl-21	-2.32	Y48G1C.12	-1.47	gln-6	-1.18	ZK1058.9	1.01
nex-4	-2.31	rnr-1	-1.44	K01A2.5	-1.17	clec-13	1.02
Y69E1A.5	-2.26	F25B4.7	-1.43	lars-2	-1.17	drr-1	1.02
H20J04.1	-2.17	R74.8	-1.43	fbn-1	-1.16	gpd-3	1.02
F55F8.3	-2.12	rme-2	-1.42	W02D3.12	-1.16	ifa-4	1.03
pfas-1	-2.1	sip-1	-1.42	C25A1.1	-1.16	haao-1	1.03
sucl-2	-2.04	F20A1.1	-1.42	set-18	-1.15	tag-18	1.03
T05H10.3	-2.04	clec-266	-1.4	far-3	-1.15	pqn-22	1.03
dsl-3	-2.02	rde-12	-1.39	C39D10.8	-1.15	T23E7.2	1.03
hsp-16.2	-2.02	dut-1	-1.38	sec-6	-1.14	ZK185.5	1.03
col-39	-2.01	nasp-2	-1.38	hsp-16.11	-1.13	gst-26	1.04
C01G6.3	-2	hmp-2	-1.37	eif-3.K	-1.12	gsnl-1	1.05
C44C10.9	-1.98	dve-1	-1.36	C08E8.4	-1.12	C01H6.8	1.05
egl-27	-1.98	ZK970.7	-1.34	lin-13	-1.11	F46H5.7	1.05
pde-5	-1.93	vit-4	-1.33	Y14H12B.1	-1.11	C03A3.2	1.05
F53F8.4	-1.76	hsb-1	-1.32	nbet-1	-1.1	C25H3.9	1.06
rnr-2	-1.76	ints-13	-1.32	ttc-1	-1.09	unc-7	1.06
pad-2	-1.75	csr-1	-1.32	F22D6.2	-1.09	far-8	1.06
T21B6.3	-1.73	ppw-2	-1.32	C24H10.1	-1.09	F17H10.2	1.06
T19H12.2	-1.72	capg-1	-1.31	C47A4.1	-1.09	gpx-5	1.07

Protein	log2FC	Protein	log2FC	Protein	log2FC	Protein	log2FC
tric-1B.1	1.07	asg-2	1.22	T01D1.4	1.5	Y37H2A.14	2.9
C33G3.4	1.07	F13D12.5	1.23	tnt-2	1.51	Y54G2A.57	2.99
cpz-2	1.08	lfi-1	1.23	Y55F3BR.6	1.52	K12H4.7	3.59
C14B9.10	1.08	C01B10.6	1.23	srw-20	1.53	scl-12	3.72
T03G6.3	1.08	gst-28	1.24	paic-1	1.54	folt-2	3.75
F53B1.8	1.08	unc-98	1.26	ilys-5	1.55	T12D8.5	3.89
droe-4	1.09	D1086.3	1.26	Y106G6H.8	1.56	asp-9	4.1
gcp-2.1	1.09	W10C8.5	1.27	F17E9.5	1.57	pud-2.1	4.31
srp-1	1.09	D1054.10	1.27	Y54F10AM.8	1.6	cey-3	4.43
hsp-17	1.09	argk-1	1.27	msi-1	1.62	cut-1	4.81
tomm-22	1.09	F56D5.6	1.28	F40A3.2	1.64	pud-1.1	5.25
plpp-1.1	1.09	hex-2	1.28	imp-1	1.67	scl-11	5.52
R07B1.9	1.1	cht-4	1.28	fip-5	1.67	grl-23	5.84
mec-9	1.1	rhr-1	1.28	F58B4.5	1.7		
acp-6	1.1	Y12A6A.1	1.29	F09B12.3	1.71		
pud-3	1.1	gly-8	1.29	csq-1	1.73		
T27C4.1	1.1	rps-30	1.31	C53D6.7	1.74		
M01H9.3	1.13	R13D11.4	1.31	grd-3	1.74		
mrp-3	1.13	T28F3.8	1.32	timm-23	1.75		
C18H7.1	1.14	E04F6.9	1.33	hil-1	1.8		
cah-5	1.14	K09G1.1	1.34	dct-16	1.85		
bcl-7	1.15	D2092.4	1.34	F59B1.2	1.85		
far-6	1.15	poml-3	1.34	F45D11.15	1.91		
C53D5.5	1.15	K12C11.1	1.34	AC3.5	2		
glt-1	1.15	catp-2	1.35	C23H3.2	2.05		
mpc-1	1.15	spp-13	1.36	ZK6.11	2.05		
elo-1	1.16	gst-27	1.36	sod-3	2.08		
Y7A5A.1	1.16	srap-1	1.36	F54E2.1	2.09		
zig-11	1.16	ugt-62	1.38	cbd-1	2.19		
fld-1	1.16	lec-10	1.38	perm-4	2.32		
fipr-21	1.16	acp-5	1.39	pqn-94	2.32		
mua-6	1.17	ftn-1	1.41	Y59E9AR.1	2.34		
Y73F4A.1	1.17	unc-27	1.42	C14F11.4	2.4		
pat-10	1.18	endu-1	1.42	cey-2	2.44		
msa-1	1.19	hmt-1	1.42	glh-1	2.49		
Y43C5A.2	1.19	R13H4.2	1.44	Y62H9A.5	2.61		
ZK154.6	1.2	F53B3.6	1.45	cyp-34A9	2.61		
T10E9.3	1.2	atic-1	1.45	lec-4	2.7		
tres-1	1.2	lbp-2	1.47	lec-8	2.7		
R53.5	1.2	cest-4	1.48	far-2	2.7		
pqn-68	1.21	cal-5	1.48	ule-5	2.84		
rpl-25.1	1.21	lec-6	1.5	perm-2	2.87		

6.20. Proteome (TMT) - 4h Fed vs 48h Starved – HBR1777 (*flp-11*::EGL-1)

Protein	log2FC	Protein	log2FC	Protein	log2FC	Protein	log2FC
B0379.6	-6.8	rnp-6	-1.47	F25B4.7	-1.02	exp-2	1.76
Y53F4B.21	-4.68	T21B6.3	-1.47	csr-1	-1.01	C06A5.3	1.8
spin-1	-3.81	grl-21	-1.45	tep-1	-1.01	oxa-1	1.95
E02C12.9	-3.72	ilys-5	-1.44	sph-1	-1	egg-1	1.99
cyp-33E2	-2.98	Y62H9A.5	-1.43	cka-2	1.02	M01H9.3	2.07
hgap-2	-2.98	C39D10.8	-1.36	gstk-1	1.02	scl-11	2.16
ipla-2	-2.92	Y51H4A.7	-1.36	ent-1	1.03	hil-1	2.52
Y67D2.7	-2.67	egl-27	-1.35	tag-65	1.03	mec-9	2.68
leo-1	-2.46	ost-1	-1.33	lbp-2	1.03	T12D8.5	2.75
dpy-14	-2.31	athp-2	-1.32	C53B7.3	1.04		
R10H10.3	-2.23	trpa-2	-1.31	unc-51	1.04		
abts-4	-2.2	elpc-2	-1.28	F17H10.2	1.05		
F55F8.3	-2.19	soap-1	-1.27	pde-6	1.05		
pfas-1	-2.17	sucl-2	-1.27	srap-1	1.08		
F54F7.6	-2.15	pfs-2	-1.26	sodh-1	1.09		
nex-4	-2.15	T05H10.3	-1.26	clec-87	1.09		
hum-6	-2.12	fkb-5	-1.24	tomm-22	1.1		
dpy-10	-2.11	vms-1	-1.22	mtl-1	1.11		
mlt-7	-2.02	ifc-2	-1.22	bli-4	1.11		
Y39A1A.21	-1.97	unc-52	-1.21	T04C9.1	1.12		
hda-10	-1.96	sec-10	-1.21	cid-1	1.13		
dpy-17	-1.93	nhl-1	-1.2	zwl-1	1.13		
C44C10.9	-1.89	set-18	-1.2	asp-9	1.13		
H39E23.3	-1.85	C32E8.5	-1.19	F55G1.9	1.14		
col-92	-1.8	cth-2	-1.18	Y52E8A.3	1.19		
col-39	-1.8	far-8	-1.17	far-6	1.2		
T08A11.1	-1.77	T10B10.3	-1.17	C18H7.1	1.22		
C11D2.4	-1.73	ints-7	-1.17	clec-91	1.24		
far-3	-1.71	lec-9	-1.13	srp-2	1.26		
ifc-1	-1.65	C15A11.7	-1.13	gst-19	1.26		
F10D11.6	-1.65	acn-1	-1.13	F59B1.2	1.31		
Y75B8A.14	-1.64	dve-1	-1.12	sir-2.4	1.39		
ifp-1	-1.64	Y48A6B.7	-1.11	cey-3	1.43		
iscu-1	-1.64	C08E8.4	-1.11	pqbp-1.1	1.45		
cpr-4	-1.62	C47A4.1	-1.1	scl-3	1.47		
grl-16	-1.61	nbet-1	-1.1	vit-1	1.49		
sod-5	-1.6	tut-1	-1.08	cnnm-1	1.53		
immp-1	-1.56	rde-12	-1.06	vit-3	1.54		
F47B8.2	-1.56	atg-16.2	-1.04	ttr-35	1.6		
sor-1	-1.51	col-121	-1.04	sod-4	1.63		
grd-13	-1.49	C14A4.9	-1.04	hmg-3	1.68		
fmo-5	-1.49	hsp-16.2	-1.04	clec-13	1.7		

6.21. RNA-seq (MPI-MG) - N2 (wild-type) vs HBR227 (*aptf-1*) - 48h Starved

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
lmd-4	-2.53	K01A6.7	-1.24	ttr-50	-1.11	F41G3.3	-1.03
F14F9.2	-2.35	col-131	-1.23	fbxc-51	-1.11	K08H2.4	-1.03
ZK354.3	-2.1	F19B2.12	-1.23	fbxc-24	-1.1	nas-15	-1.03
aptf-1	-1.79	F36H5.13	-1.22	Y75B7AR.1	-1.09	Y39D8A.1	-1.03
flp-11	-1.77	C09B8.4	-1.22	B0207.5	-1.09	R12A1.3	-1.02
F32A7.8	-1.73	W03A5.1	-1.21	wrt-10	-1.09	fbxb-33	-1.02
acd-2	-1.68	M02G9.1	-1.21	Y17D7C.4	-1.09	F40G9.9	-1.02
acdh-2	-1.66	fbxb-116	-1.21	F21C10.11	-1.09	C07G3.10	-1.02
argk-1	-1.58	C10C5.3	-1.2	K02E7.6	-1.09	F35A5.4	-1.02
clec-180	-1.58	F45D11.16	-1.2	abf-2	-1.08	K08H2.2	-1.02
arrd-11	-1.57	F45D11.15	-1.2	dpy-3	-1.08	clec-174	-1.02
W03F9.4	-1.53	F45D11.14	-1.2	Y105C5A.2	-1.08	mltn-9	-1.02
F40G12.5	-1.5	pqn-26	-1.19	sams-5	-1.07	C08F1.6	-1.02
F23A7.8	-1.46	Y71A12B.11	-1.19	C08F1.10	-1.07	F12A10.1	-1.02
Y39G10AR.15	-1.46	Y38E10A.3	-1.19	Y82E9BR.17	-1.07	K08E3.2	-1.01
snet-1	-1.45	ZK675.4	-1.18	Y19D2B.2	-1.07	fbxb-94	-1.01
T14B4.19	-1.44	C38D9.8	-1.18	lgx-1	-1.07	his-16	-1.01
txdc-12.2	-1.44	F48E3.6	-1.17	C47E12.9	-1.07	skr-8	-1.01
hsp-12.6	-1.43	col-176	-1.17	fbxb-62	-1.06	W10D9.2	-1.01
F01D4.8	-1.42	fbxb-78	-1.17	M153.3	-1.06	Y57A10B.6	-1.01
F59C12.4	-1.41	H39E23.3	-1.17	W02H5.8	-1.06	lgc-27	-1.01
atz-1	-1.38	K03H6.2	-1.16	fbxb-57	-1.06	C45E5.1	-1.01
Y6E2A.4	-1.37	F33D4.6	-1.16	F22E5.20	-1.06	C24B5.4	-1.01
aman-1	-1.36	R05H5.7	-1.16	F43D9.1	-1.06	R12E2.8	-1
C35E7.5	-1.34	cutl-2	-1.15	W04A8.9	-1.06	T26E3.8	-1
qua-1	-1.33	Y17G9B.2	-1.15	bath-31	-1.06	fbxb-18	-1
dsl-3	-1.33	col-172	-1.14	F55C9.5	-1.06	Y47G6A.31	-1
asns-2	-1.32	ZC334.7	-1.13	R01E6.2	-1.05	fipr-7	1
ugt-53	-1.31	F39G3.2	-1.13	C10C5.5	-1.05	F49H6.5	1
F21E9.2	-1.31	F55G11.8	-1.13	Y41D4B.26	-1.05	D1054.18	1
M02G9.2	-1.3	Y65A5A.1	-1.13	sym-1	-1.05	F58F12.12	1.01
C46C11.4	-1.29	dpy-7	-1.12	pqn-13	-1.05	F10C1.9	1.01
F45B8.3	-1.29	R04A9.7	-1.12	fbxb-7	-1.04	mif-4	1.02
ZK105.13	-1.29	F16B3.2	-1.12	hch-1	-1.04	pgp-9	1.02
K02E11.15	-1.29	fbxb-35	-1.12	C40A11.2	-1.04	clec-57	1.03
C35E7.9	-1.29	F56F4.8	-1.12	T01D1.8	-1.04	K12D9.1	1.03
mtl-1	-1.28	F40E10.5	-1.12	skr-15	-1.04	E02H4.4	1.04
Y82E9BR.1	-1.27	zipt-17	-1.11	nas-12	-1.04	C25F9.4	1.04
sdz-30	-1.26	Y57G7A.2	-1.11	C06C3.7	-1.04	col-153	1.05
fkb-5	-1.26	C55B7.3	-1.11	fbxb-96	-1.03	F57H12.6	1.06

Gene	log2FC	Gene	log2FC
F18E3.13	1.06	slc-17.3	1.26
nspc-19	1.07	K08D10.14	1.27
cpr-1	1.07	C05D12.3	1.28
F18E3.12	1.07	clec-61	1.29
irg-5	1.07	C34H4.2	1.29
lron-4	1.07	ilys-2	1.29
scl-14	1.08	fbxa-166	1.3
capa-1	1.08	fipr-9	1.34
F53B3.6	1.08	dct-5	1.35
mfb-1	1.08	srd-14	1.36
fipr-8	1.08	cpr-4	1.36
T04C12.32	1.09	F28E10.5	1.37
Y69A2AR.19	1.1	clec-80	1.4
clec-230	1.1	R07C12.1	1.42
nspc-17	1.1	str-112	1.44
K01D12.9	1.11	nspc-15	1.46
F20B6.5	1.11	nspc-12	1.46
math-18	1.11	nspc-14	1.53
Y46H3A.5	1.12	F46A8.1	1.53
T16G1.6	1.12	C23G10.11	1.54
wrt-8	1.14	asp-16	1.57
F53F4.1	1.16	nspc-18	1.58
T04C12.7	1.16	lipl-3	1.6
pcp-3	1.17	fbxa-136	1.62
nspe-6	1.17	F10A3.4	1.7
nspc-20	1.17	hsp-16.48	1.77
T20F5.5	1.17	col-106	1.81
T16G1.4	1.18	hsp-16.49	1.89
clec-42	1.19	ZK218.1	2.57
dnj-20	1.19		
gtf-2H1	1.2		
H02F09.3	1.2		
gba-2	1.21		
tag-244	1.23		
nspc-16	1.23		
clec-25	1.23		
chil-22	1.23		
C50F7.5	1.24		
ZC204.1	1.25		
C45E1.4	1.25		

6.22. RNA-seq (MPI-MG) - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 48h Starved

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
dmsr-2	-3.81	T23F6.1	-1.89	T13C2.2	-1.63	wht-3	-1.43
F12E12.12	-2.73	gst-12	-1.87	T19D12.3	-1.62	abu-6	-1.42
M03E7.4	-2.57	gst-39	-1.85	cyp-13A3	-1.62	F42A8.1	-1.42
C04G6.7	-2.41	gsto-2	-1.85	F33H12.7	-1.62	Y102A11A.7	-1.42
R05D8.7	-2.4	ZK1010.4	-1.85	cdr-4	-1.61	F20B10.3	-1.41
pqn-26	-2.37	pqn-29	-1.84	C03F11.2	-1.6	R04B3.3	-1.41
F35A5.4	-2.34	B0205.13	-1.84	plpr-1	-1.59	K08D12.4	-1.4
M153.3	-2.34	pqn-63	-1.82	lgx-1	-1.59	nas-13	-1.4
T05H4.7	-2.28	W08E12.6	-1.82	T06D8.10	-1.59	col-113	-1.4
D2096.6	-2.28	sri-39	-1.82	gst-33	-1.58	W08E12.3	-1.4
F41G3.3	-2.28	C35A5.10	-1.82	W06H8.2	-1.58	F59B10.3	-1.39
gst-37	-2.26	gst-30	-1.81	T28C12.6	-1.58	pqn-67	-1.39
R12A1.3	-2.26	R03C1.1	-1.8	C25F6.8	-1.56	numr-2	-1.38
F12E12.11	-2.23	gst-25	-1.78	drd-1	-1.56	numr-1	-1.38
abu-14	-2.22	T06E4.8	-1.77	C34E11.2	-1.55	col-89	-1.38
T24C12.4	-2.14	Y43F8B.3	-1.77	K01A6.7	-1.55	W08E12.4	-1.37
F07H5.8	-2.13	W08E12.2	-1.77	W03F9.4	-1.55	W08E12.5	-1.37
T20B6.3	-2.12	cyp-13A10	-1.76	C18E9.7	-1.52	grl-6	-1.37
M195.2	-2.1	ZC334.7	-1.75	C54D2.1	-1.52	F55G1.1	-1.37
K08D12.8	-2.08	C36B7.5	-1.75	lact-7	-1.52	C08E8.10	-1.37
ZK354.3	-2.07	C26B2.8	-1.73	ora-1	-1.5	abu-7	-1.36
ZK662.2	-2.06	R09E12.9	-1.72	F20G2.1	-1.5	twk-11	-1.35
M02G9.1	-2.03	phat-2	-1.72	col-172	-1.5	abu-8	-1.34
gst-31	-2.02	pqn-74	-1.72	K09B3.1	-1.49	cpt-5	-1.34
C06E4.6	-1.99	C56C10.4	-1.71	F52A8.3	-1.49	F55F8.8	-1.33
nas-15	-1.96	F25D1.5	-1.71	F32A7.8	-1.49	D1054.8	-1.33
Y50D4B.2	-1.96	E01G6.1	-1.71	gpdh-1	-1.48	R07E3.2	-1.32
Y53F4B.36	-1.95	C06E4.3	-1.7	asns-1	-1.47	F40F11.4	-1.32
K10H10.6	-1.95	T25E4.1	-1.7	lron-2	-1.47	T06E4.14	-1.32
gst-8	-1.95	K01D12.5	-1.7	phg-1	-1.46	sri-36	-1.32
R02F11.1	-1.93	M02G9.2	-1.69	C06G1.2	-1.45	T22F3.11	-1.32
gst-5	-1.93	Y47D3B.6	-1.68	F59B1.8	-1.45	clec-163	-1.32
R13H4.8	-1.92	abu-11	-1.68	gst-21	-1.45	F57H12.6	-1.31
grl-1	-1.92	chs-2	-1.67	abu-15	-1.45	stdh-2	-1.31
nas-14	-1.9	T01G6.1	-1.66	Y75B7AR.1	-1.45	ZK742.4	-1.31
sdz-8	-1.9	cutl-12	-1.65	col-69	-1.44	T13F3.8	-1.3
acd-2	-1.9	Y65B4BL.6	-1.65	gst-16	-1.44	asic-2	-1.3
B0205.14	-1.9	F41E6.11	-1.65	F07B7.8	-1.43	comt-3	-1.29
D2092.8	-1.89	C29G2.3	-1.65	nhr-237	-1.43	C56C10.6	-1.29
T10E10.4	-1.89	F40E10.5	-1.65	K06C4.1	-1.43	pqn-13	-1.29

Gene	log2FC	Gene	log2FC	Gene	log2FC	Gene	log2FC
gpx-2	-1.28	cpg-9	-1.14	nep-12	-1.06	F45D11.15	1.02
gst-40	-1.28	C30A5.10	-1.13	Y48G1BM.8	-1.06	F45D11.16	1.02
gst-26	-1.28	grd-12	-1.13	R08A2.5	-1.06	mex-1	1.02
aip-1	-1.27	C55A6.6	-1.13	Y39G10AR.15	-1.06	F45D11.14	1.02
gst-35	-1.27	col-51	-1.13	gba-2	-1.05	clec-13	1.02
dhs-23	-1.26	ugt-25	-1.13	abu-12	-1.05	W05F2.3	1.02
hmit-1.2	-1.26	Y53F4B.27	-1.13	Y52E8A.3	-1.05	T02G5.14	1.02
fmo-5	-1.25	Y73C8B.1	-1.13	his-18	-1.04	B0024.4	1.02
irg-3	-1.25	clec-174	-1.12	C15F1.5	-1.04	F15D4.5	1.03
H12D21.2	-1.24	fbxb-36	-1.12	otpl-1	-1.04	W09C3.7	1.03
folt-2	-1.24	col-176	-1.12	rpr-1	-1.04	C45B11.7	1.03
fpn-1.2	-1.24	sri-38	-1.12	Y113G7B.15	-1.04	C17E7.4	1.04
ZC412.9	-1.24	spl-2	-1.12	F23F12.8	-1.04	R11D1.3	1.04
arf-1.1	-1.23	F23A7.8	-1.12	ZC21.10	-1.04	F07B7.2	1.05
cutl-27	-1.23	cyp-13A2	-1.11	H10E21.4	-1.03	W09B7.2	1.05
slc-17.8	-1.23	nas-1	-1.11	comt-5	-1.03	irg-5	1.05
gst-7	-1.23	K02D10.2	-1.11	R08F11.4	-1.03	sip-1	1.05
zipt-17	-1.22	lagr-1	-1.11	ptr-19	-1.03	M60.7	1.06
K08E3.2	-1.21	pqn-36	-1.11	dhs-8	-1.03	Y43F8B.24	1.06
gst-4	-1.21	exc-6	-1.11	npax-2	-1.02	K01D12.3	1.06
D1007.13	-1.21	ram-5	-1.1	gst-38	-1.02	asm-3	1.07
B0554.5	-1.21	gpx-1	-1.1	qua-1	-1.02	scl-14	1.07
cat-2	-1.21	F59C12.4	-1.1	K02E11.15	-1.01	D1054.18	1.08
dhs-9	-1.2	D2005.6	-1.09	F53B3.3	-1.01	F26D11.12	1.08
T06E4.9	-1.19	F56F4.8	-1.09	T17H7.7	-1.01	C35A5.5	1.08
T07A5.1	-1.19	M88.4	-1.09	tts-2	-1.01	T10G3.4	1.08
lgc-27	-1.19	F53C3.3	-1.09	K01A12.4	-1.01	M02E1.4	1.09
lrx-1	-1.19	F08D12.2	-1.08	C09B8.4	-1.01	clec-87	1.09
jud-4	-1.18	T06A4.1	-1.08	nas-8	-1.01	srap-1	1.1
T16A9.3	-1.18	R02C2.7	-1.08	col-111	-1.01	meg-1	1.11
phat-1	-1.17	acox-1.2	-1.08	Y57G7A.2	-1.01	F15H10.8	1.12
gst-9	-1.17	F26D2.15	-1.07	K08D8.4	-1	F29C6.1	1.13
his-5	-1.17	twk-34	-1.07	acox-1.1	-1	C06E8.5	1.13
grd-15	-1.16	F53H4.3	-1.07	C42D4.13	1	F21H7.12	1.14
Y57G11B.4	-1.16	Y32G9B.1	-1.07	Y68A4B.3	1.01	sri-31	1.14
D2063.1	-1.16	col-54	-1.06	C45E5.4	1.01	meg-2	1.14
Y76B12C.4	-1.16	her-1	-1.06	gln-6	1.01	srd-14	1.15
pqn-71	-1.15	F07A11.1	-1.06	lmd-4	1.01	cpg-2	1.16
col-48	-1.15	Y37F4.1	-1.06	clec-15	1.01	fipr-6	1.16
F23D12.11	-1.14	col-186	-1.06	nhr-219	1.02	T19D7.6	1.17

Gene	log2FC	Gene	log2FC
E02H4.4	1.17	dct-5	1.66
C24H10.3	1.17	nspc-19	1.71
lipl-3	1.18	unc-119	1.72
skr-5	1.18	nspc-20	2.03
F08H9.3	1.19	hsp-16.48	2.05
col-138	1.2	nspc-16	2.07
fipr-8	1.2	nspc-15	2.15
fipr-7	1.21	nspc-12	2.15
acbp-4	1.21	hsp-16.49	2.18
K03D3.2	1.22	nspc-18	2.54
T28A11.19	1.22	nspc-14	2.89
math-38	1.23	col-108	3.1
ZK381.2	1.23	ZK218.1	3.43
T28A11.5	1.24	egl-1	4.59
capa-1	1.24		
fbxa-136	1.26		
C05D9.9	1.26		
tyr-3	1.27		
cey-2	1.27		
fipr-5	1.3		
cpg-1	1.3		
fipr-10	1.31		
C04E6.8	1.34		
ugt-15	1.34		
C27A7.2	1.36		
lron-4	1.37		
Y46H3A.5	1.38		
ZC204.1	1.4		
fbxa-185	1.4		
F35G2.5	1.42		
far-5	1.44		
gmn-1	1.45		
fipr-9	1.45		
sre-6	1.45		
F41E7.20	1.52		
asp-16	1.54		
pud-4	1.56		
col-106	1.58		
F07H5.13	1.59		
nspc-17	1.6		

6.23. Proteome (LFQ) - N2 (wild-type) vs HBR227 (*aptf-1*) - 48h Starved

Protein	log2FC
grd-5	-1.82
hsp-12.6	-1.41
ttr-47	-1.3
pud-1.1	-1.21
ttr-16	-1.21
unc-44	-1.05
F45D11.15	-1.03
misc-1	-1.02
acox-3	-1.01
lim-8	1.03
dpy-28	1.22
sfxn-1.5	1.22
K08D12.3	1.26
dao-5	1.29
gck-1	1.37

6.24. Proteome (LFQ) - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 48h Starved

Protein	log2FC
rbm-3.1	-2.21
hsp-12.6	-2.12
hsp-16.48	-1.7
hsp-16.11	-1.6
vpr-1	-1.38
T20H4.5	-1.33
ostd-1	-1.32
zfp-1	-1.27
msa-1	-1.26
C32D5.8	-1.26
tni-4	-1.24
ctsa-3.1	-1.2
unc-44	-1.18
mif-1	-1.16
kdp-1	-1.16
zig-12	-1.12
rho-1	-1.12
T03F1.11	-1.1
phat-5	-1.1
dnj-13	-1.09
lsm-3	-1.09
rps-21	-1.06
ufm-1	-1.04
ttr-16	-1.03
F40A3.3	-1.03
tli-1	-1.02
tdo-2	1
pqn-87	1.01
csnk-1	1.02
C49A1.10	1.02
cku-80	1.02
vrk-1	1.03
ifet-1	1.03
K09F5.6	1.04
swsn-7	1.05
vha-14	1.05
K09G1.1	1.06
eif-3.I	1.06
eif-3.F	1.07
cox-6C	1.09
swan-1	1.1
xrn-1	1.11
wago-1	1.11
inx-3	1.12
dod-19	1.12
T18D3.1	1.14
vit-4	1.15
F56F11.4	1.17
T16G1.9	1.17
lim-8	1.18
gck-1	1.19
mrps-2	1.25
vit-3	1.26
rab-8	1.36
taap-1	1.37
acox-1.5	1.37
vit-5	1.39
K11H12.8	1.5
rab-10	1.67

6.25. Metabolome - N2 (wild-type) vs HBR227 (*aptf-1*) - 48h Starved

Metabolite	log2FC
Sphingomyelin (d18:0/16:1(9Z))	-1.89
Glycerol 3-phosphate	-1.51
Sphingomyelin (d18:1/26:1(17Z)), Sphingomyelin (d18:0/26:1(17Z))	-1.44
Sphingomyelin (d18:0/18:0)	-1.43
L-Methionine	-1.37
Sphingomyelin (d18:0/12:0)	-1.35
L-Proline	-1.29
Sphingomyelin (d18:0/22:3(10Z,13Z,16Z))	-1.11
Sphingomyelin (d18:0/14:0)	-1.09
Uracil	-0.87
Sphingomyelin (d18:0/22:1(13Z)(OH))	-0.84
Sphingomyelin (d17:1/24:0)	-0.79
Sphingomyelin (d19:1/24:1(15Z))	-0.78
Sphingomyelin (d18:1/18:1(9Z)), Sphingomyelin (d18:1/18:1(11Z))	-0.76
Sphingomyelin (d18:1/22:1(13Z))	-0.76
Sphingomyelin (d18:1/22:0), Sphingomyelin (d18:0/22:1(13Z))	-0.64
Sphingomyelin (d18:0/26:0)	-0.58
Sphingomyelin (d18:1/24:1(15Z))	-0.53
Sphingomyelin (d18:1/12:0)	0.62
Adenosine monophosphate	0.64
Choline	0.78
L-Arginine	1.01
Butyrylcarnitine, Isobutyryl-L-carnitine	1.09
Propionylcarnitine	1.1
L-Phenylalanine	1.42
Uric acid	1.43
Allantoin	1.46
Succinic acid	1.47
Sphingomyelin (d18:1/26:0)	1.93
5'-Methylthioadenosine	1.95
Glutathione	2.23
Methylmalonylcarnitine	2.23
L-Tryptophan	2.53

6.26. Metabolome - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 48h Starved

Metabolite	log2FC
L-Methionine	-3.16

6.27. Metabolome - N2 (wild-type) vs HBR227 (*aptf-1*) - 6 days Starved

Metabolite	log2FC
Uridine diphosphate-N-acetylglucosamine	-1.24
Trehalose	-1.18
Methylmalonylcarnitine	-1
L-Tyrosine	-0.82
Sphingomyelin (d18:0/16:1(9Z))	-0.78
L-Valine	-0.73
Sphingomyelin (d18:0/22:2(13Z,16Z)(OH))	-0.58
Sphingomyelin (d18:0/24:1(15Z)(OH)), Sphingomyelin (d18:1/25:0)	-0.55
FAD	-0.55
Nicotinic acid	0.64
L-Tryptophan	0.67
Cytidine	0.78
Niacinamide	0.88
3-Dehydroxycarnitine	0.89
CDP-choline	1.07
Hypoxanthine	1.09
L-Serine	1.2
Flavin Mononucleotide	1.3
Deoxyguanosine	1.39
Guanosine	1.73
Kynurenic acid	1.78
Guanine	2.38
Inosine	2.51

6.28. Metabolome - N2 (wild-type) vs HBR1777 (*flp-11*::EGL-1) - 6 days Starved

Metabolite	log2FC
Methylmalonylcarnitine	-4.27
Tyramine	-4.2
Adenylsuccinic acid	-3.34
Pyroglutamic acid	-3.24
Kynurenic acid	-3.12
Thiamine	-2.92
L-Cystathionine	-2.34
Fumaric acid	-2.17
3-Aminoisobutanoic acid	-2.02
Ophthalmic acid	-2
NADP	-1.96
Methylmalonic acid	-1.79
L-Tyrosine	-1.4
Hydroxypyruvic acid	-1.21
L-Proline	-1.17
L-Valine	-1.1
Riboflavin	-1.09
Hypoxanthine	-1.05
Sphingomyelin (d18:0/20:2(11Z,14Z))	-0.85
Sphingomyelin (d18:0/24:1(15Z)(OH)), Sphingomyelin (d18:1/25:0)	-0.84
L-Phenylalanine	-0.76
Sphingomyelin (d18:1/23:0)	-0.74
Sphingomyelin (d18:0/20:0)	-0.72
Sphingomyelin (d18:0/22:3(10Z,13Z,16Z))	-0.68
Sphingomyelin (d18:0/22:1(13Z)(OH))	-0.68
Sphingomyelin (d18:1/18:0)	-0.67
Sphingomyelin (d17:1/24:1(15Z))	-0.64
Sphingomyelin (d18:1/22:0), Sphingomyelin (d18:0/22:1(13Z))	-0.64
Sphingomyelin (d18:1/22:1(13Z))	-0.62
Pyridoxal	1.25
Butyrylcarnitine, Isobutyryl-L-carnitine	1.28
Pantothenic acid	1.42
L-Carnitine	1.46
Nicotinic acid	1.65
Uracil	1.73
L-Serine	1.73
L-Targinine	1.78
L-Acetylcarnitine	2.05
ADP	2.36
L-Glutamine	2.45

Metabolite	log2FC
Glycerol 3-phosphate	2.52
Guanine	2.55
Flavin Mononucleotide	2.81
L-Tryptophan	3.1
2-Aminobenzoic acid	3.21
CDP-choline	3.53
L-Glycine	3.59

6.29. Genetic screen for quiescence phenotypes

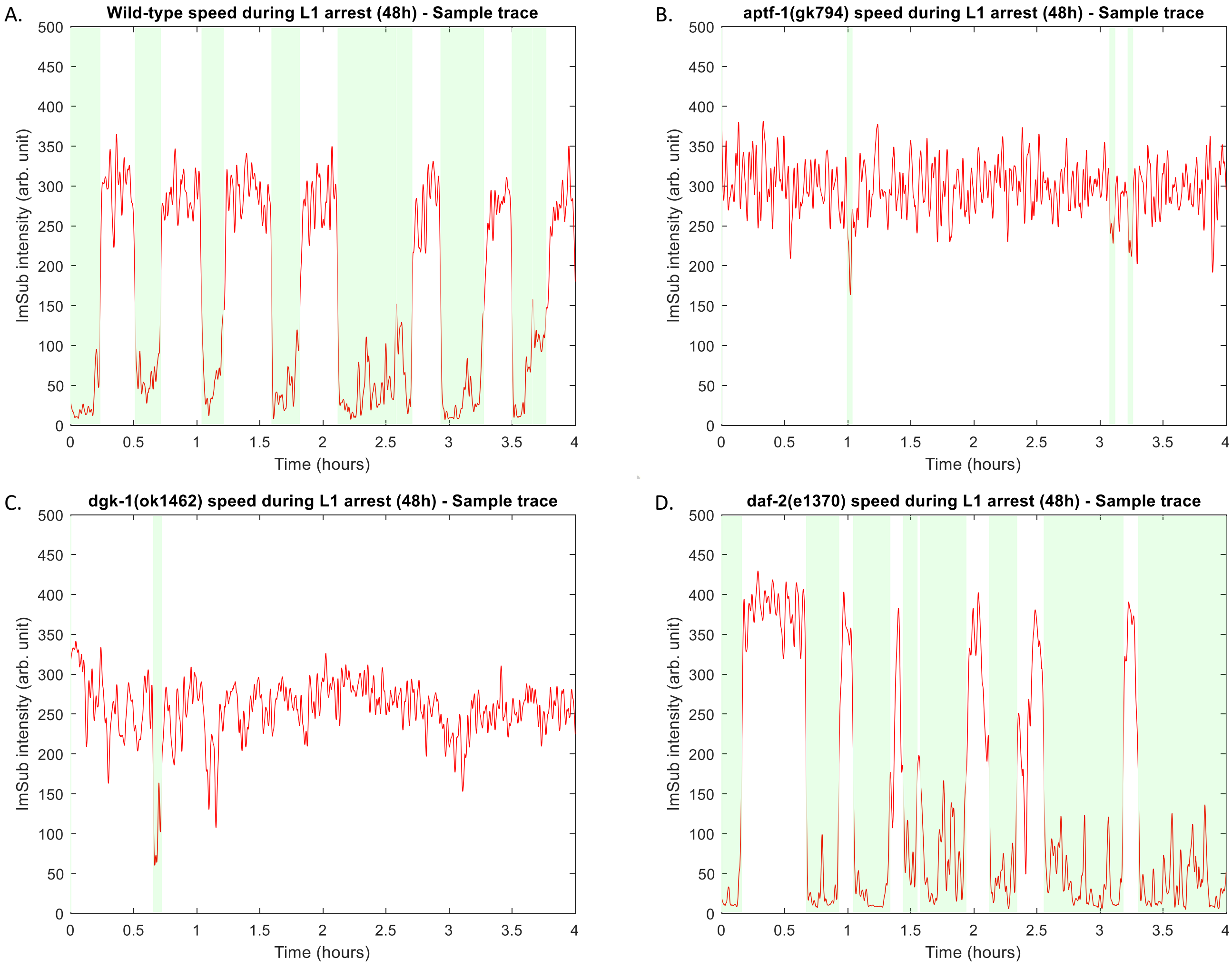
Strain	Gene	Allele	Effect size
HBR2315	aptf-1; tdc-1	gk794;n3420	-3.08
HBR2050	dgk-1	ok1462	-2.94
HBR2269	flp-11; tdc-1	tm2706;n3420	-2.8
HBR227	aptf-1	gk794	-2.75
HBR2286	aptf-1; ser-2	gk794;pk1357	-2.73
HBR1777	flp-11::EGL-1	goeIs384	-2.7
RB1690	ser-2	ok2103	-2.64
VC1339	efhc-1	ok1856	-2.62
HBR1010	nas-38	ok3407	-2.53
HBR2242	aptf-1; elpc-1	tm2149; gk794	-2.45
HBR507	flp-11	tm2706	-2.45
HBR2122	dgk-1	sy428	-2.37
RB737	snt-4	ok503	-2.34
SCL1	mcp-1	tm2679	-2.23
HBR2233	aptf-1; tut-1	gk794; tm1297	-2.23
RB1400	tre-3	ok394	-2.2
VC225	tps-1	ok373	-2.18
CB156	unc-25	e156	-2.18
VM487	nmr-1	ak4	-2.18
CF1038	daf-16	mu86	-2.17
DA609	npr-1	ad609	-2.16
RB2105	ntr-1	ok2780	-2.16
HBR2312	aptf-1; glp-1	gk794;ar202	-2.15
RB1073	dgk-4	ok1031	-2.14
HBR2374	aptf-1; ztf-20	gk263563;gk794	-2.09
RB1932	tofu-7	ok2535	-2.04
RB2277	ser-5	ok3087	-2.04
VC1876	pcyt-2.2	ok2179	-2.04
RB1942	ace-2	ok2545	-2.01
RB608	tag-96	ok336	-2
NL1832	ucr-2.3	pk732	-1.98
RB1974	smd-1	ok2602	-1.94
RB1326	unc-129	ok1443	-1.93
HBR1403	aptf-1; daf-2	e1370; gk794	-1.92
RB1036	hyl-1	ok976	-1.92
VC1198	Y39G8B.1	ok1682	-1.91
VC912	jmjd-3.1	gk387	-1.91
ZG31	hif-1	ia4	-1.9
VC2210	cbl-1	ok2954	-1.9
HBR2372	aptf-1; xbp-1	zc12;gk794	-1.9
RB1482	gpdh-2	ok1733	-1.89
VC2171	tkr-1	ok2886	-1.89

Strain	Gene	Allele	Effect size
RB1053	sgt-1	ok1000	-1.86
RB1160	ckb-4	ok1195	-1.86
RB775	plpp-1.2	ok555	-1.83
MT8347	ced-3	n2452	-1.83
VC138	elo-1	gk48	-1.81
RB2061	ora-1	ok2724	-1.8
RB1083	F27C8.5	ok1050	-1.79
RB938	vha-12	ok281	-1.79
RB1588	mxl-3	ok1947	-1.79
RB2135	F33D4.4	ok2843	-1.79
KG2730	clu-1	ok2	-1.79
RB748	gta-1	ok517	-1.79
HS184	swsn-4	os13	-1.74
RB2071	ced-3	ok2734	-1.73
VB674	nnt-1	sv34	-1.72
OH313	ser-2	pk1357	-1.72
MH1090	pnc-1	ku212	-1.71
MQ989	isp-1; ctb-1	qm150; qm189	-1.71
VC2520	aagr-2	ok3193	-1.7
RB2128	idh-1	ok2832	-1.7
RB1404	lec-1	ok1597	-1.69
CB5602	vhl-1	ok161	-1.69
RB2550	ugt-23	ok3541	-1.67
RB1795	fat-1	ok2323	-1.67
RB1704	acp-2	ok2129	-1.66
RB2549	sms-3	ok3540	-1.66
RB1134	hpo-13	ok1157	-1.66
HBR12	goa-1	sa734	-1.65
RB2625	F40F12.7	ok3684	-1.65
RB512	mce-1	ok243	-1.64
RB1373	gpdh-1	ok1558	-1.64
FX06710	pho-5	tm6710	-1.63
RB910	elo-3	ok777	-1.62
VC1896	ckb-3	ok2310	-1.58
RB1498	hyl-2	ok1766	-1.58
JT307	egl-9	sa307	-1.56
RB1031	fat-4	ok958	-1.54
VC26	pgp-12	gk19	-1.53
GR1307	daf-16	mgDf50	-1.52
RB1170	C04B4.2	ok1212	-1.51
TU55	mec-14	u55	-1.51
BC119	blmp-1	s71	-1.5

Gene	Allele	Effect size
mmcm-1	ok1637	-1.49
dot-1.1	ok2154	-1.48
ugt-1	ok2718	-1.48
sptl-3	ok1927	-1.46
gba-1	gk399608	-1.45
gpd-3	ok2870	-1.44
fasn-1	g43	-1.42
amx-2	ok1235	-1.42
met-2	ok2307	-1.42
C27A7.3	tm6393	-1.41
dgk-5	ok2366	-1.41
acs-19	tm4853	-1.39
trpa-1	ok999	-1.39
pcbd-1	tm5924	-1.38
rabn-5	ok1555	-1.37
lin-42	n1089	-1.36
tkt-1	ok3624	-1.34
ced-3	n717	-1.34
pnk-4	ok1832	-1.33
egl-9	n586	-1.33
aldo-2	gk944084	-1.33
nnt-1	tm358	-1.31
elo-4	ok1346	-1.3
vab-3	ju468	-1.29
hosl-1	gk278589	-1.28
ZC155.4; hxk-3	gk961143; gk961144	-1.28
egl-9; hif-1	sa307; ia4	-1.27
haf-9	gk23	-1.27
asns-2	ok3108	-1.27
acly-2	tm5123	-1.26
lagr-1	gk327	-1.26
capa-1	ok3065	-1.24
glod-4	gk189	-1.23
set-21	ok2327	-1.22
gpd-1	gk152785	-1.22
ace-1	ok663	-1.21
idh-2	ok3184	-1.21
Y94H6A.7	gk925915	1.22
gln-5	gk875298	1.28
elo-5	gk208	1.31
ace-4	gk942942	1.31
aqp-2	ok2159	1.44

Strain	Gene	Allele	Effect size
CB1370	daf-2	e1370	1.47
EG9631	unc-13	s69	1.58
VL1176	alh-8	ww48	1.63

6.30. Representative mobility traces and quiescence bouts



(**A**-**D**) Mobility traces of wild-type, *aptf-1*(gk794), *dgk-1*(ok1462) and *daf-2*(e1370) worms. Movement (shown in red) is reduced when the worm goes in a quiescence bout (shown in green). Loss of function of the AP2 transcription factor *aptf-1* and diacylglycerol kinase DGKθ homolog *dgk-1* ablates sleep, while loss of function of the insulin receptor *daf-2* increases the amount of sleep.

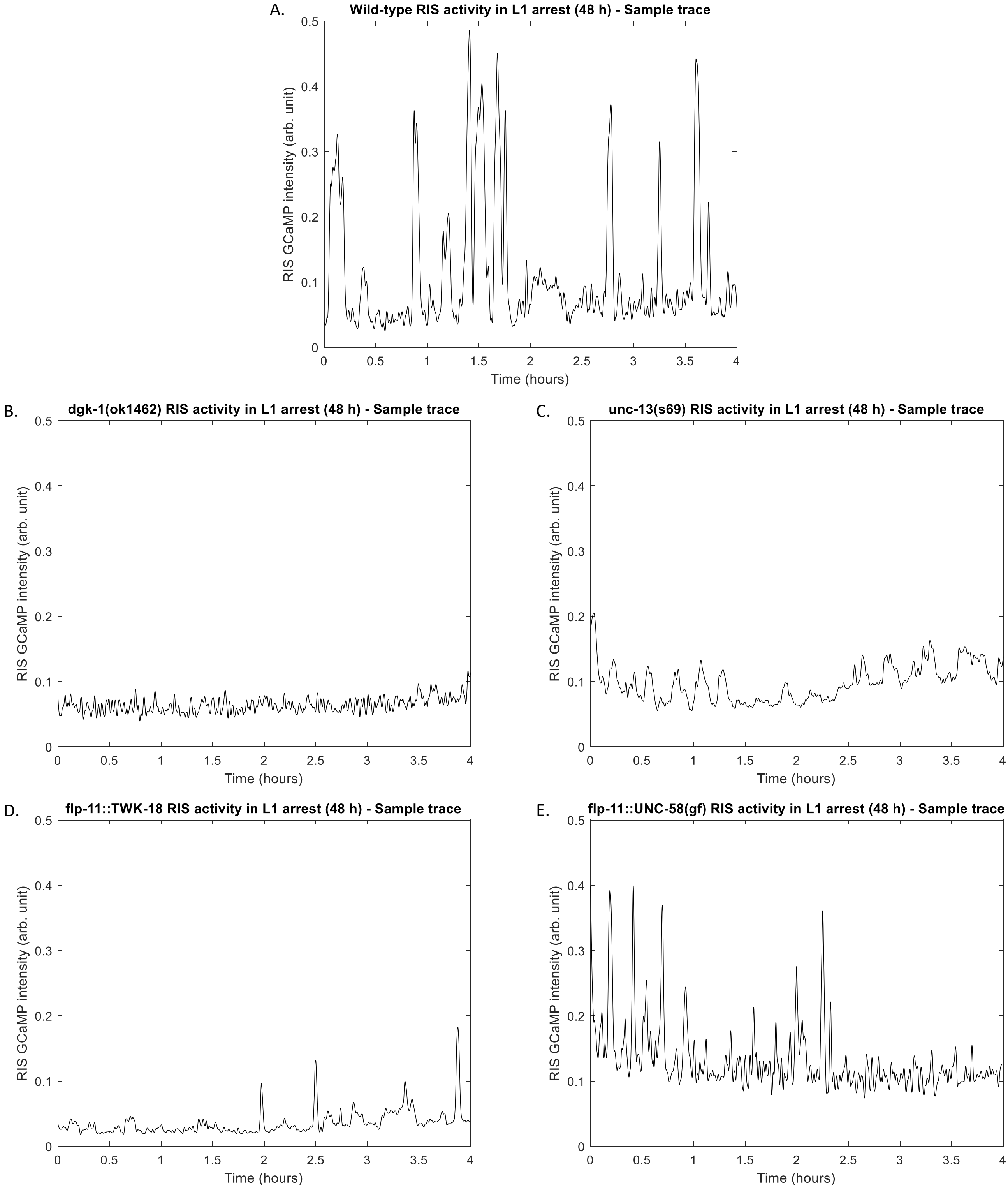
6.31. Quiescence assessment of wild-type animals after supplementation with methionine, glycine and glutamate

Treatment	Effect size
Methionine 10 mM	-1.19
Methionine 12.5 mM	-1.17
Glycine 10 mM	-0.66
Methionine 25 mM	-0.64
Glutamate 10 mM	-0.63
Glycine 1mM	-0.52
Glycine 0.1 mM	-0.45
Methionine 1mM	0.48

6.32. Impact of maternal growth conditions in the quiescence fraction of the offspring in the wild-type background

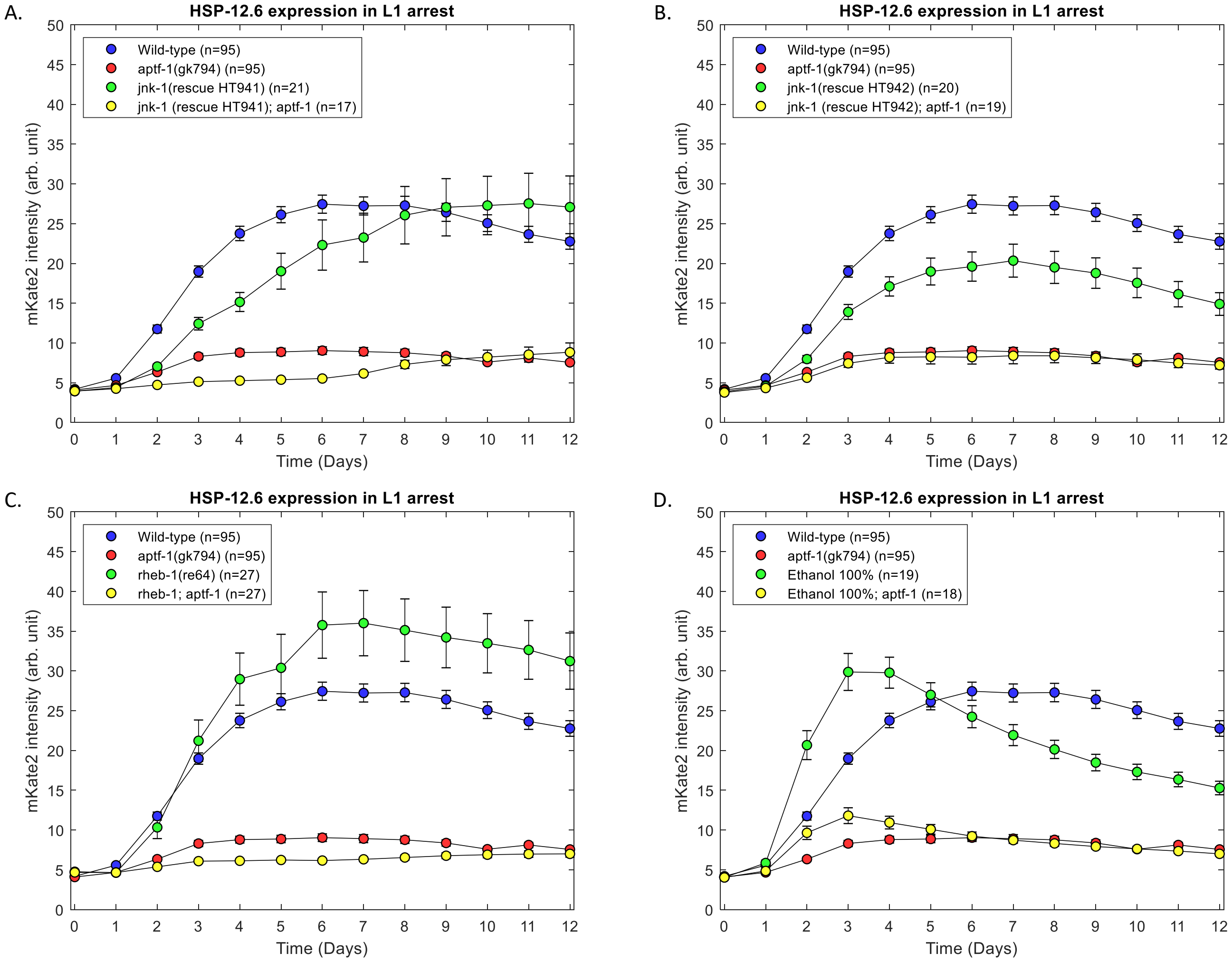
Temperature (°C)	Food	Effect size
15	OP50	0.43
25	OP50	-0.41
20	Na22	-0.43
20	DL41	0.41

6.33. Representative RIS intensity GCaMP traces

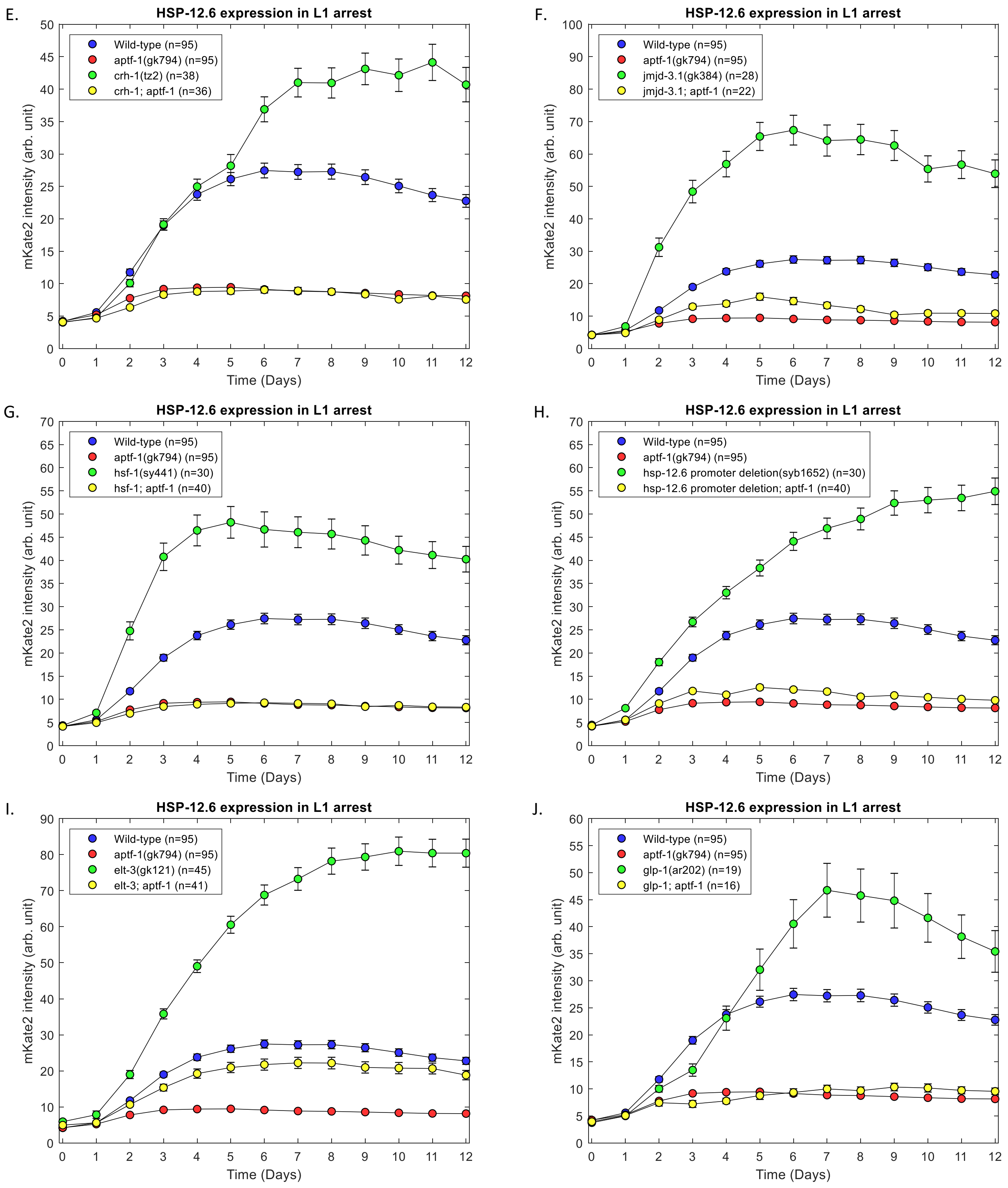


(**A**) In the wild-type worm characteristic peaks in RIS activity indicate sleep bouts.
(**B**-**C**) RIS peaks are absent after loss of function of *dgk-1* and *unc-13*.
(**D**-**E**) RIS peaks are also absent in the engineered flp-11::TWK-18 strain as expected. In the RIS-hyperactive flp-11::UNC-58(gf) strain RIS does not activate as strong as the wild-type.

6.34. HSP-12.6 expression screening in L1 arrest



(**A**) Overexpression of *jnk-1*, only causes significant downregulation of HSP-12.6 expression from day 2 to day 7 (FDR < 0.05) in both wild-type and *aptf-1*(gk794) backgrounds.
(**B**) Overexpression of *jnk-1* with a different strain, causes significant downregulation of HSP-12.6 expression only in the wild-type (FDR < 0.05, except for days 0 and 1).
(**C**) *rheb-1* loss of function upregulates HSP-12.6 expression in the wild-type (FDR < 0.05 from day 6 to day 12) but not in the *aptf-1*(gk794).
(**D**) Ethanol (100%) treatment changes the kinetics of HSP-12.6 expression in a similar way in wild-type and *aptf-1*(gk794).



(**E**) *crh-1* loss of function only affects the expression of HSP-12.6 in the wild type after 6 days (FDR < 0.05 from day 6 to day 12)

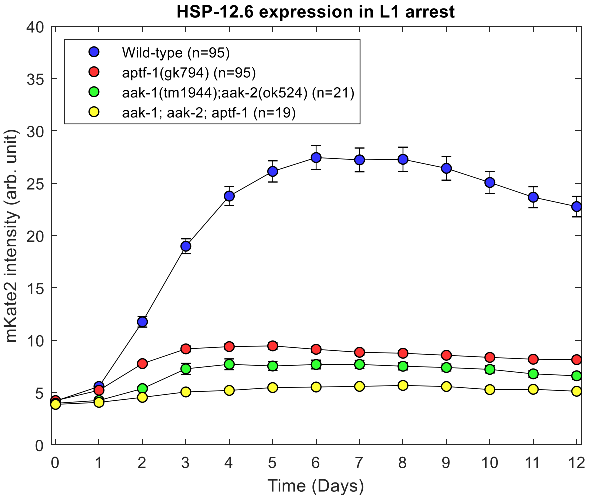
(**F**) *jmjd-3.1* loss of function increases the expression of HSP-12.6 in the wild type (FDR < 0.05, except for days 0 and 1) and less in the *aptf-1*(gk794) (FDR < 0.05 from day 3 to day 7)

(**G-H**) Loss of function of *hsf-1* or a 4kb deletion of the promoter region of HSP-12.6 increase HSP-12.6 expression in the wild-type (FDR < 0.05, except for days 0 and 1)

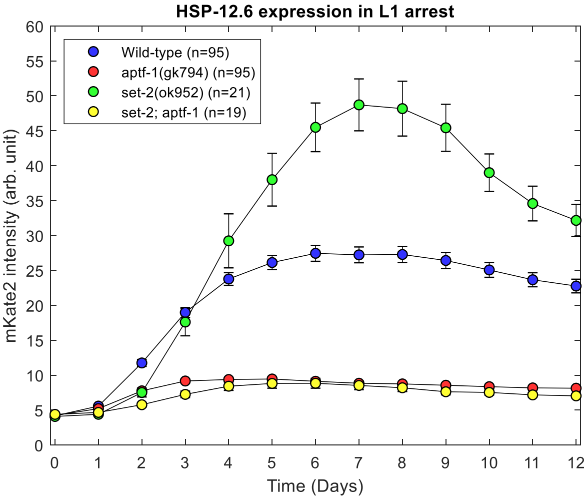
(**I**) *elt-3* loss of function causes upregulation of HSP-12.6 expression in both the wild-type and the *aptf-1*(gk794) backgrounds (FDR < 0.05, except for days 0 and 1)

(**J**) Gain of function of *glp-1* increases HSP-12.6 expression only in the wild type starting from day 6 (FDR < 0.05, except for days 0 and 1)

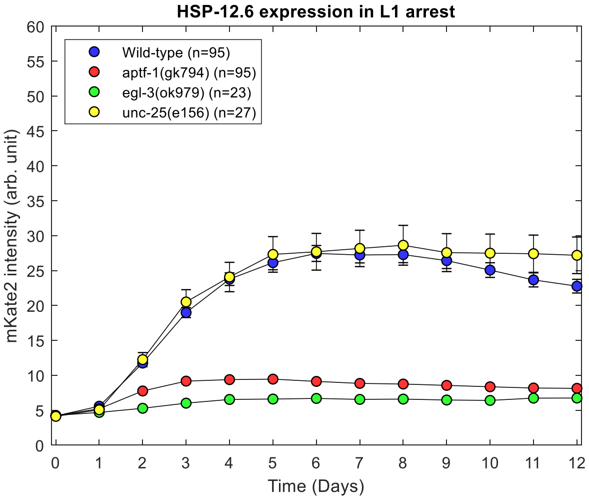
K.



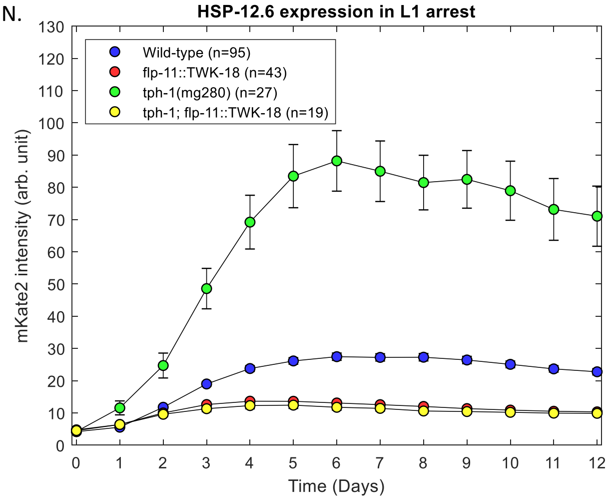
L.



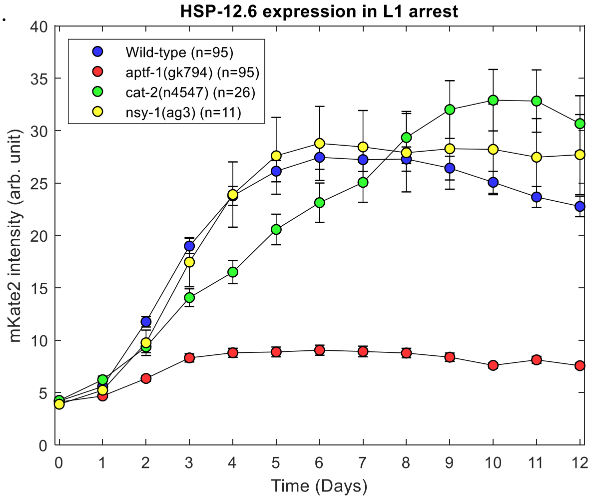
M.



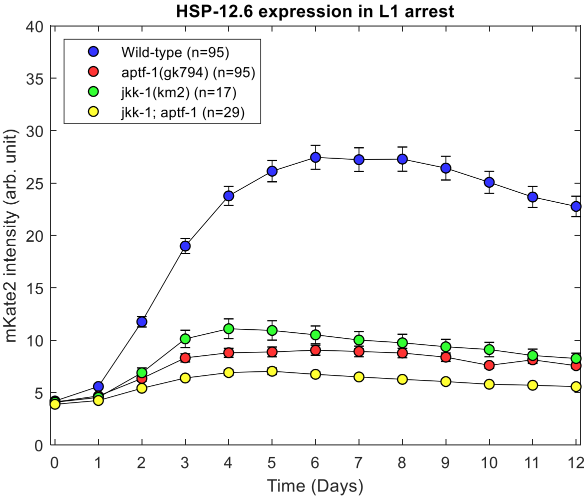
N.



O.



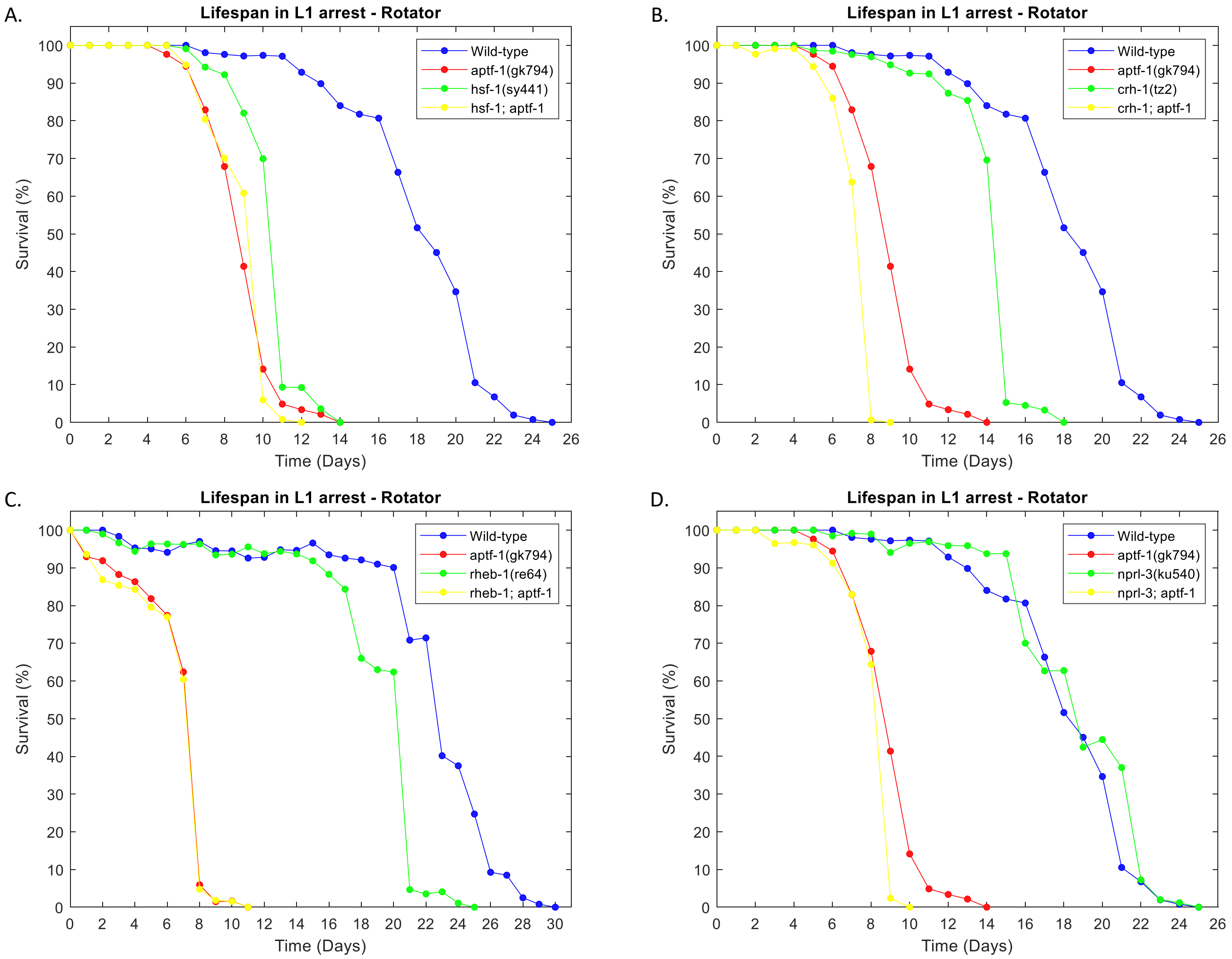
P.



(**K**) Loss of function of *aak-1* and *aak-2* reduce HSP-12.6 expression in both wild type and *aptf-1*(gk794) (FDR < 0.05, except days 0 and 1)
(**L**) *set-2* loss of function increases the expression of HSP-12.6 only in the wild type (FDR < 0.05 from day 5 to day 12)

(**M**) *egl-3* loss of function downregulates the expression of HSP-12.6 (FDR < 0.05, except for day 0 and 1), while *unc-25* loss of function does not affect it.
(**N**) *tph-1* loss of function decreases HSP-12.6 expression only in the wild type (FDR < 0.05, except day 0)
(**O**) *cat-2* loss of function decreases HSP-12.6 expression from day 2 to day 6 (FDR < 0.05) and increases it from day 10 to day 12 (FDR < 0.05). *nsy-1* loss of function does not affect the expression of HSP-12.6
(**P**) *jkk-1* loss of function decreases the expression of HSP-12.6 in the wild-type and aptf-1(gk794) (FDR < 0.05, except days 0 and 1)

6.35. Lifespan screening in L1 arrest



(**A**) *hsf-1* loss of function decreases the lifespan of the wild type (FDR < 0.05 at day 12)
(**B**) *crh-1* loss of function decreases the lifespan of both the wild-type and the *aptf-1*(gk794) strains (FDR < 0.05 at day 16 and 7 respectively)
(C) *rheb-1* loss of function decreases the lifespan of the wild-type (FDR < 0.05 at day 23)
(D) *nprl-3* loss of function does not alter the lifespan of either the wild type or the *aptf-1*(gk794)

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PUBLICATIONS

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CONFERENCES – PRESENTATIONS - SCHOLARSHIPS

1st prize - poster presentation: "Metabolic regulation of sleep" (11/2018) 10th anniversary of GGNB (Göttingen Graduate center for Neurosciences, Biophysics and Molecular Biosciences)

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Scholarship from the "Department of Studies of Aristotle University of Thessaloniki", for excellent performance and conduct, as a graduate student (2013- 2014)

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