Expanded View Figures

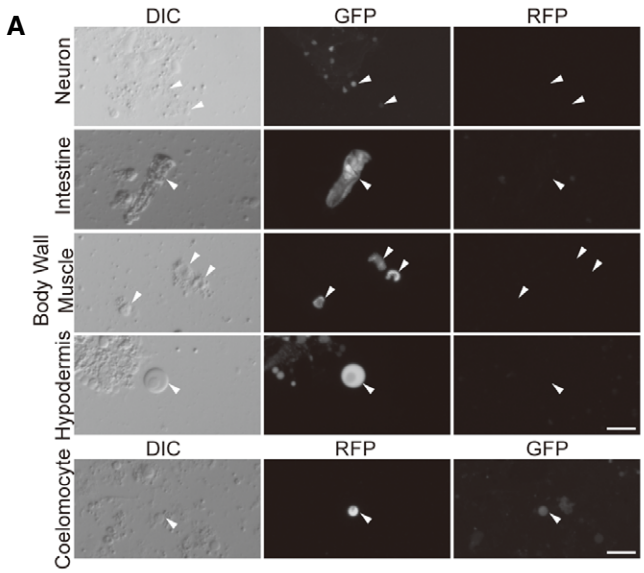
Figure EV1. The validation of isolated tissues for transcriptomic profiling.

A Cell viability assay of isolated worm cells. Cells from neurons, intestine, body wall muscle and hypodermis were labelled with tissue-specific GFP reporters. Dead cells in their preparations (RFP) were labelled by ethidium homodimer-1 staining (RFP). In the preparation of coelomocytes, coelomocytes and live cells were labelled with RFP and Calcein AM (GFP) respectively. Arrow heads denote the cells of interest. Scale bar: 20 μm.

B The list of tissue-specific genes used.

C–F RT–qPCR of indicated tissue-specific genes in the isolated intestine (C), body wall muscle (D), hypodermis (E) and coelomocytes (F). ND: Ct > 40. Mean ± SD. $n = 3$ biological replicates.

G RT–qPCR (left) or RNA-Seq reads (right) of tissue-specific genes indicate that the isolated neurons are of comparable purity as previously reported. ND: Ct > 40. D1: day 1 of adulthood. D8: day 8 of adulthood. Mean ± SD. $n = 3$ biological replicates. Unpaired *t*-test, two-tailed.



B

Tissue	Gene
Neuron (Neu)	*rab-3, rgef-1*
Intestine (Int)	*vha-6*
Body Wall Muscle (BWM)	*myo-3*
Hypodermis (Hyp)	*dpy-7, semo-1*
Coelomocyte (Coel)	*unc-122*
Mutiple tissues	*act-1*

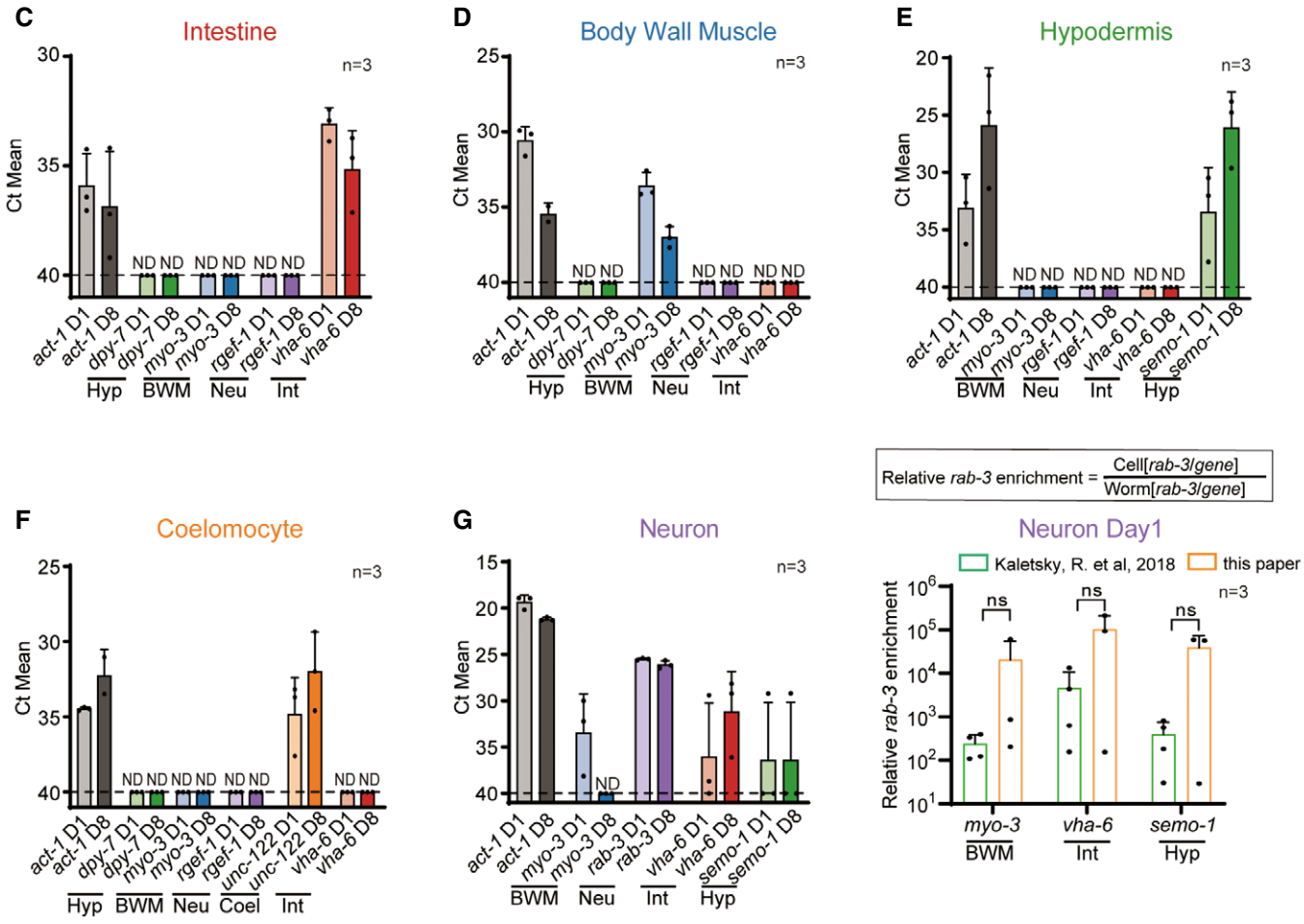
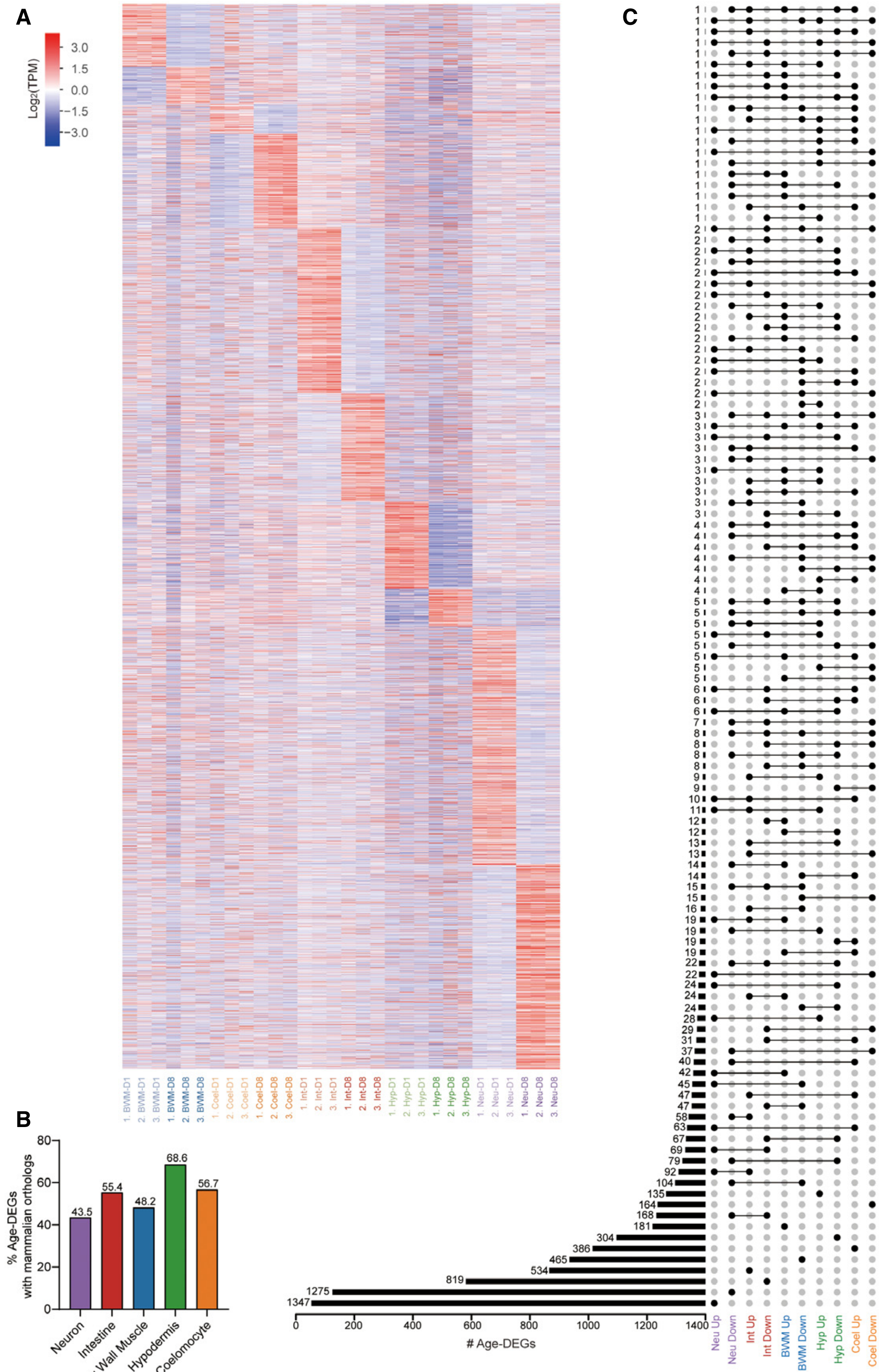


Figure EV1.

Figure EV2. Ageing induces significant transcriptomic changes across *C. elegans tissues.*

A A heatmap depicting the transcriptomic changes in the indicated tissues during ageing.
B Age-DEGs in worm tissues are highly conserved.
C A comparison of Age-DEGs in the indicated tissues.



A
Log2(TPM)
3.0
1.5
0.0
−1.5
−3.0
B
% Age-DEGs with mammalian orthologs
43.5
55.4
48.2
68.6
56.7
Neuron
Intestine
Body Wall Muscle
Hypodermis
Coelomocyte
C
Age-DEGs
Neu Up
Neu Down
Int Up
Int Down
BWM Up
BWM Down
Hyp Up
Hyp Down
Coel Up
Coel Down

Figure EV2.

Figure EV3. Age-DEGs in the whole worm have a limited overlap with those in individual tissues.

A, B The overlap of upregulated (A) and downregulated (B) Age-DEGs in the worm and the analysed tissues. The Age-DEGs in the worm are from a previous report by Hou *et al* (2016), by comparing the transcriptomes of WT worms at day 2 and day 8 of adulthood. The number and ratio of Age-DEGs are shown in the corresponding Venn diagrams. Hypergeometric test.

C, D The comparison of Age-DEGs in the indicated samples. (C): The analysis using the worm RNA-Seq data obtained in this study (Worm). (D): The analysis using the reported worm RNA-Seq data by Hou *et al* (2016). (Worm (H)). Red lines denote the common Age-DEGs between the whole worm and individual tissues.

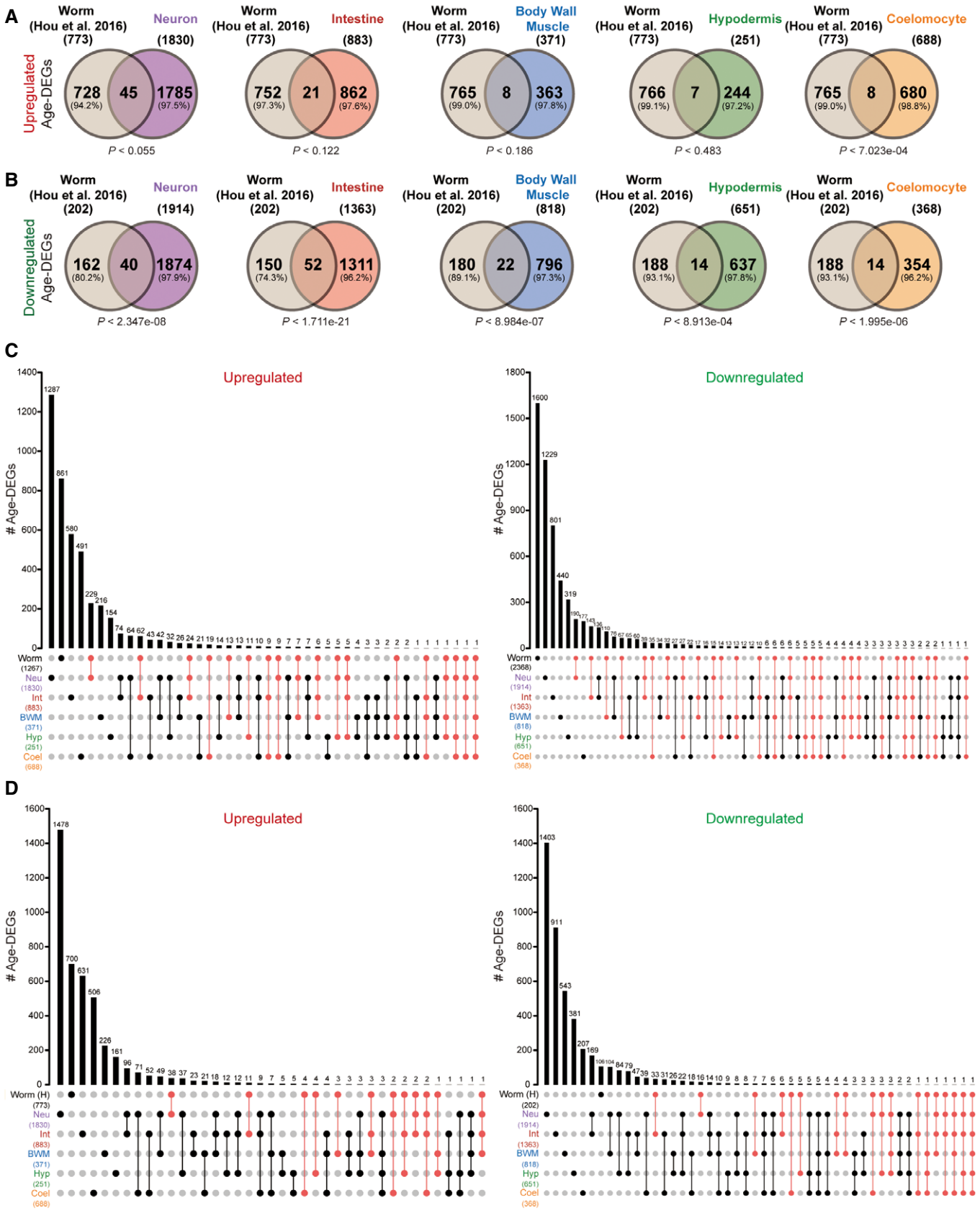


Figure EV3.

Figure EV4. The common Age-BPs are regulated in different manners across tissues.

A, B The common Age-BPs upregulated (A) or downregulated (B) in the indicated tissues. Age-BPs were from the enriched gene sets analysed by WormCat. Categories 1 and 2 are differentiated by capitalisation and bold fonts. Category 2 are shown below the corresponding Category 1.

C–K Venn diagrams showing the number of Age-DEGs of corresponding Age-BPs across indicated tissues as labelled in (A) and (B).

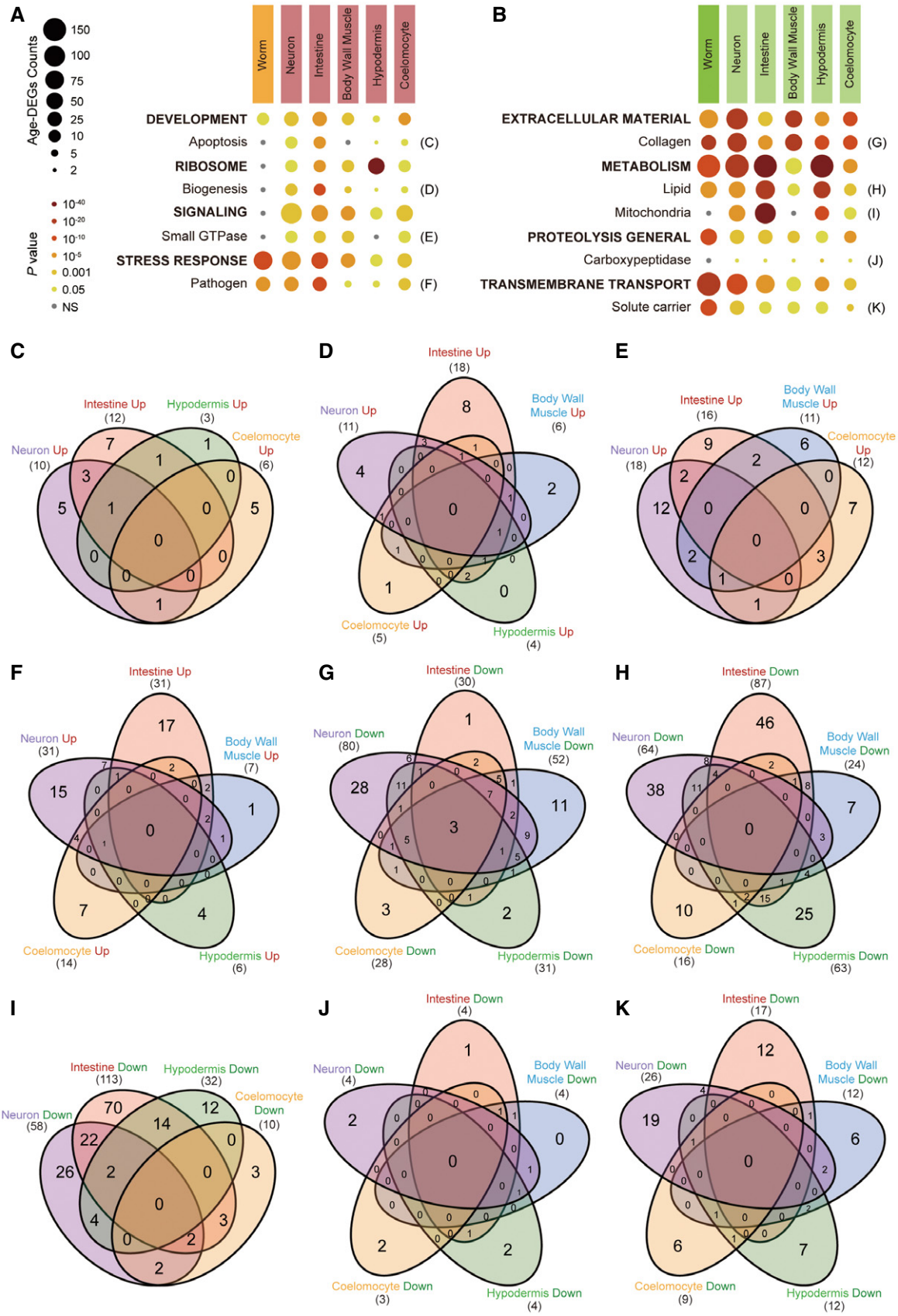


Figure EV4.

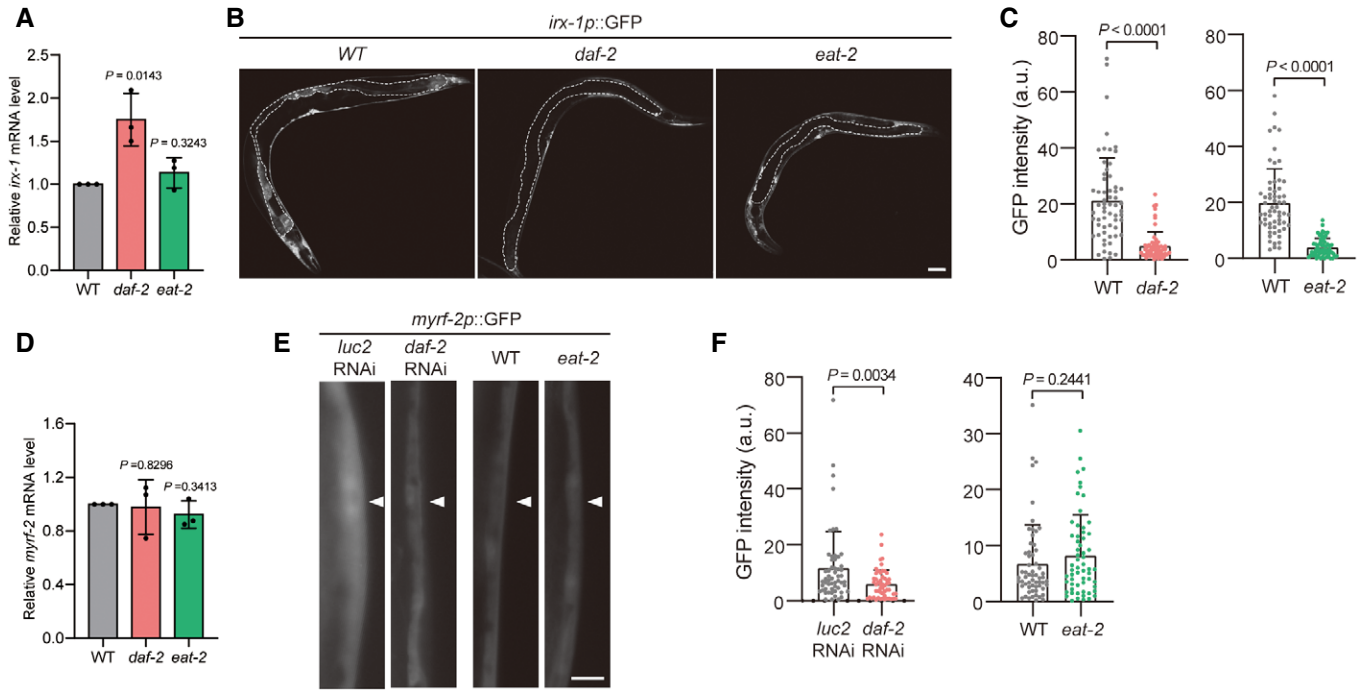


Figure EV5. The expression of *irx-1* and *myrf-2* upon the suppression of IIS or the treatment of dietary restriction.

A The mRNA levels of *irx-1* from the whole worm of the indicated strains. $n = 3$ biological replicates.

B, C Mutating *daf-2* or *eat-2* decreases the expression of *irx-1* in the intestine. The GFP is driven by the native promoter of *irx-1*. Dotted lines outline the intestine. Scale Bar: 50 μm. $n \geq 60$ worms.

D RT–qPCR of *myrf-2* in the indicated strains. $n = 3$ biological replicates.

E, F The expression of a GFP reporter driven by *myrf-2* promoter in BWM upon the indicated treatment. Arrowheads denote the myocytes. Scale Bar: 10 μm. $n \geq 53$ worms in the *daf-2* RNAi assay. $n = 60$ worms in the *eat-2* mutants assay.

Data information: In all panels, Mean ± SD, unpaired *t*-test, two-tailed.