Supplementary Table 1

Title: Summary of lifespan statistics

Experiments used in figures are indicated in the right-most column. Mean lifespan and s.e.m. were calculated by log-rank test using triplicate samples, each containing 25-35 worms. # worms: total number of worms died in this assay/(total died + total censored). Censored worms included ones underwent “matricide,” exhibited ruptured vulva, or crawled off the plates.

Supplementary Table 2

Title: List of genes analyzed in the germline RNA-seq samples

Table columns:

baseMean	mean of normalized counts across all germline samples
log2FoldChange	log2 fold change of *ash-2* RNAi vs. empty vector (Positive log2FoldChange: Higher expression in *ash-2* RNAi; Negative log2FoldChange: Higher expression in empty vector)
lfcSE	standard error
stat	Wald statistic
pvalue	Wald test p-value
padj	FDR-adjusted p-value

Supplementary Table 3

Title: List of genes analyzed in the intestine RNA-seq samples

Table columns:

baseMean	mean of normalized counts across all intestine samples
log2FoldChange	log2 fold change of *ash-2* RNAi vs. empty vector (Positive log2FoldChange: Higher expression in *ash-2* RNAi; Negative log2FoldChange: Higher expression in empty vector)
lfcSE	standard error
stat	Wald statistic
pvalue	Wald test p-value
padj	FDR-adjusted p-value

Supplementary Table 4

Title: List of “germline-enriched” genes

Genes were determined “germline-enriched” if the lowest expression value (log2(FPKM+1)) observed in the germline empty vector samples was at least 2-fold higher than the highest expression value observed in the intestine empty vector samples (5,494 genes). Showing log2(FPKM+1) values for all “germline-enriched” genes and all samples.

Supplementary Table 5

Title: List of “intestine-enriched” genes

Genes were determined “intestine-enriched” if the lowest expression value (log2(FPKM+1)) observed in the intestine empty vector samples was at least 2-fold higher than the highest expression value observed in the germline empty vector samples (1,418 genes). Showing log2(FPKM+1) values for all “intestine-enriched” genes and all samples.

Supplementary Table 6

Title: List of *C. elegans* strains used in this study

List of published and newly generated *C. elegans* strains used in this study.

Supplementary Table 7

Title: List of primers used in this study

List of RT-qPCR and genotyping primers used in this study.

Supplementary Table 8

Title: Raw data obtained from GC-MS in this study

Raw data generated by GC-MS experiments shown in this manuscript.