**SUMMARY OF SUPPLEMENTARY FIGURES**

**Figure S1. GO Analysis of upregulated genes from *sams-1(RNAi)* animals by Gene Set Enrichment Analysis.** Bar graph showing GO categories returned from *sams-1(RNAi)* upregulated genes (Ding *et al.* 2015) by the WormBase Gene Set Enrichment Analysis tool (Angeles-Albores *et al.* 2016).

**Figure S2. WormCat verifies known category enrichments from *sams-1(RNAi)* downregulated genes**. (**A-B**) Semantic graphs of GO analysis generated by GOrilla (Eden *et al.* 2009) and visualized by REVIGO (Supek *et al.* 2011) of *sams-1(RNAi)* downregulated genes from untreated (**A**) and choline (Ch) treated (**B**) animals. (**C**) WormCat bubble heat plots comparing *sams-1(RNAi)* with and without choline. Gene expression microarray data for **A-C** were obtained from Ding *et al*., 2015. Bubble heat plot key is the same as **Fig 1D**. CUB, Complement C1r/C1s, Uegf, Bmp1 Domain; PUF, Pumilio, and *fem-3* mRNA Binding Factor; ZF, Zinc Finger. (**D**) Venn diagrams showing overlap between *Stress Response* genes in *sams-1(RNAi)* up (pink) or downregulated genes (blue).

**Figure S3: WormCat analysis of germline-specific microarray data identifies the tau tubulin kinase family as a male-specific category**. (**A**) Category 1 analysis of Oogenic (Oo) or Spermatogenic (Sp) data sets ordered by most enriched in Oo data. Breakdown of data from the Category 1 level for Cell cycle (**B**), Development (**C**), mRNA Functions (**D**), or Cytoskeleton (**E**). All data is from Reinke *et al.*  Gen. Trans. Machinery, General Transcription Machinery; Trans. Chromatin, Transcription: Chromatin; ZF, zinc finger.

**Figure S4: GO analysis visualized by REVIGO of germline RNA-seq data from Ortiz *et al*.** Semantic graphs of GO analysis generated by GOrilla(Eden *et al.* 2009)and visualized by REVIGO of Gender Neutral (**A**), Oogenic (**B**) and Spermatogenic (**C**) germlines.

**Figure S5: GO analysis visualized by REVIGO of germline microarray data from Reinke *et al*.** Semantic graphs of GO analysis generated by GOrilla and visualized by REVIGO of Oogenic (**A**) and Spermatogenic (**B**) germlines.

**Figure S6: GO analysis visualized by REVIGO of larval tissue-specific microarray data from Spencer *et al*.** Semantic graphs of GO analysis generated by GOrilla and visualized by REVIGO of microarray from larval Muscle (BWM, body wall muscle) (**A**) Intestine (Int) (**B**), Hypodermis (Hyp) (**C**), Excretory cells (Exc) (**D**), or Neurons (**E**).

**Figure S7: GO analysis visualized by REVIGO of adult tissue-specific RNA-seq data from Kaletsky, *et al*.** Semantic graphs of GO analysis generated by GOrilla and visualized by REVIGO of RNA-seq data from adult Muscle (Mus) (**A**) Intestine (Int) (**B**), Hypodermis (Hyp) (**C**), or Neurons (**D**).

**Figure S8: GO analysis visualized by REVIGO of larval neuronal subtype microarray data from Spencer, et al.** Semantic graphs of GO analysis generated by GOrilla and visualized by REVIGO of microarray from larval dopaminergic (Dopa) (**A**) GABAergic (GABA) (**B**), *glr-1* expressing (*glr-1*) (**C**), or Class A motor neurons (Motor) (**D**).

**Figure S9: WormCat analysis of upregulated genes in *C. elegans* treated with triple combinations of lifespan-changing drugs**. Category 1, 2, and 3 analysis of upregulated genes found by RNA-seq from triple-drug combinations (Admasu *et al.* 2018). Pink box denotes drug combination that causes premature death. Allan, allantoin; CYP, Cytochrome P450; EC Material, Extracellular Material; Maj Sperm Protein, Major Sperm Protein; Neur Function; Neuronal Function; NHR, Nuclear Hormone Receptor; Prot General, Proteolysis General; Psora, Psora-4; Rapa, Rapamycin; Rifa, Rifampicin; Short Chain Dehydr., Short Chain Dehydrogenase; Trans Factor, Transcription Factor; TYR kinase, Tyrosine Kinase; ugt, UDP-glycosyltransferase.

**Figure S10: WormCat analysis of downregulated genes in *C. elegans* treated with triple combinations of lifespan-changing drugs**. Category 1, 2, and 3 analysis of downregulated genes found by RNA-seq from triple-drug combinations (Admasu *et al.* 2018). Pink box denotes drug combination that causes premature death. Allan, Allantoin; Psora, Psora-4; Rapa, Rapamycin; Rifa, Rifampicin.

**Figure S11: GO analysis visualized by REVIGO of upregulated genes from RNA-seq data from *C. elegans* treated with triple combinations of lifespan-extending drugs from Admasu *et al*.** Semantic graphs of GO analysis generated by GOrilla and visualized by REVIGO of RNA-seq data from Rifa, Psora, Allan treated (**A**) Rifa, Rapa, Allan treated (**B**), or Rifa, Rapa, Psora treated (**C**).

**Figure S12: GO analysis visualized by REVIGO of RNA-seq data from a *C. elegans* RNAi screen for glycogen storage from LaMacchia *et al*.** Semantic graphs of GO analysis generated by GOrilla and visualized by REVIGO of *C. elegans* showing low glycogen storage in an RNAi screen.

**SUMMARY OF SUPPLEMENTARY TABLES**

**Supplemental Table 1:** **WormCat annotations.** xlsx file containing *C. elegans* genes arranged alphabetically by Categories with Sequence ID, WormBase ID, and Category 1, 2, and 3 annotations along with WormBase descriptions (WormBase version WS270).

**Supplemental Table 2:** **WormCat annotation definitions**. xlsx file containing annotation definitions.

**Supplemental Table 3: Random gene analysis.** xlsx file with tabs containing lists of randomly generated WormBase IDs of 100 (tabs 1-4), 500 (tabs 5-8), 1000 (tabs 9-12, and 1500 (tabs 13-16) genes with Category 1, 2 and 3 analysis. NA genes on these tables reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene.

**Supplemental Table 4: GO analysis of *sams-1(RNAi)* regulated genes.** xlsx file containing GO terms produced by GOrilla (Eden *et al.* 2009) from microarray data for *sams-1(RNAi)* up genes (tab 1), *sams-1(RNAi)* up plus choline (CH) (tab 2), *sams-1(RNAi)* down (tab 3), *sams-1(RNAi)* down plus CH (tab 4), and the *sams-1(RNAi)* up genes identified by GOrilla as lipid metabolism with corresponding WormCat annotations (tab 5). Data from Ding *et al.,* 2015*.*

**Supplemental Table 5: WormCat analysis of *sams-1(RNAi)* regulated genes.** xlsx file containing Category 1, 2, and 3 analysis from microarray data for *sams-1(RNAi)* up and down genes with or without choline (CH, tabs 1-3) from Ding *et al*., 2015. Tabs 4-7 contain input genes with WormCat annotations for each gene. NA genes on these tables reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene.

**Supplemental Table 6: WormCat analysis of *sams-1(RNAi)* regulated genes that were excluded by GSEA analysis.** xlxs file containing Category 1, 2, and 3 analysis from microarray data for *sams-1(RNAi)* upregulated genes (see **Table S5**, Tab 4) that were excluded by the GSEA tool on WormBase. Data from Ding *et al*., 2015.

**Supplemental Table 7: WormCat analysis of germline-expressed genes from Oritz *et al*.** xlxs file containing Category 1, 2, and 3 analysis from RNA-seq data for Germline Neutral (GN), Oogenic (Oo) or Spermatogenic (Sp) datasets (tabs 1-3). Tabs 4-6 contain input genes with WormCat annotations for each gene. NA genes on these tables reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene. Tabs 7-10 contain GO analysis by GOrilla for Germline Neutral (GN), Oogenic (Oo), or Spermatogenic (Sp) datasets.

**Supplemental Table 8:**  **WormCat analysis of germline-expressed genes from Reinke *et al*.** xlxs file containing Category 1, 2, and 3 analysis from microarray data of Oogenic (Oo) or Spermatogenic (Sp) datasets (tabs1-3). Tabs 4-5 contain input genes with WormCat annotations for each gene. NA genes on these tables reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene. Tabs 6-7 contain GO analysis by GOrilla for Oogenic (Oo) or Spermatogenic (Sp) datasets.

**Supplemental Table 9:**  **WormCat analysis of larval tissue-specific genes from Spencer *et al*.** xlsx file containing Category 1, 2, and 3 analysis from microarray data from *"selective enriched*" datasets (tabs 1-3). Tabs 4-12 contain input genes with WormCat annotations for each gene for all tissue and cell types examined. NA genes on these tables reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene. Tabs 13-22 contain GO analysis by GOrilla from selective enriched datasets from Muscle (BWM, body wall muscle), Intestine (Int), Hypodermis (Hyp), Excretory cells (Exc), Neurons (Neuro, pan-neuronal), Dopaminergic (Dopa), GABAergic (GABA), *glr-1* expressing (*glr-1*) or Class A Motor neurons (Motor).

**Supplemental Table 10:**  **WormCat analysis of adult tissue-specific genes from Kaletsky *et al*.** xlsx file containing Category 1, 2, and 3 analysis from RNA-seq data of enriched (en) and unique (un) datasets (tabs 1-3). Tabs 4-11 contain input genes with WormCat annotations for each gene for all tissue and cell types examined. NA genes on these tables reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene. Tabs 12-16 contain GO analysis by GOrilla of enriched genes from Muscle (Mus), Intestine (Int), Hypodermis (Hyp), or Neuron (Neur).

**Supplemental Table 11: WormCat analysis of upregulated genes from a combinatorial RNA-seq study of lifespan enhancing drugs.** xlsx file analysis of data from Admasu *et al.* comparing upregulated genes from single, double, and triple combinations of lifespan inducing drugs. Tabs 1-3: Category 1-3 analysis of genes upregulated by single drugs. Tabs 4-7: Input genes with WormCat annotations for each single drug treatment. Tabs 8-10: Category 1-3 analysis of upregulated genes by double drug combinations. Tabs 11-14: Input genes with WormCat annotations for each double combination drug treatment. Tabs 15-17: Category 1-3 analysis of upregulated genes by triple-drug combinations. Tab 18: Genes from the *Metabolism: lipid: sterol* category from the Rifa/Rapa/Psora set with corresponding lifespan data from Murphy *et al*. (yellow) (Murphy *et al.* 2003). Tabs 19-21: Input genes with WormCat annotations for each triple combination drug treatment. NA genes on these tabs reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene. Tabs 22-24: GO analysis by GOrilla (Eden *et al.* 2009) for each triple combination drug treatment.

**Supplemental Table 12: WormCat analysis of downregulated genes from a combinatorial RNA-seq study of lifespan enhancing drugs.** xlsx file analysis of data from Admasu *et al*. comparing downregulated genes from single, double, and triple combinations of lifespan inducing drugs. Tabs 1-3: Category 1-3 analysis of genes downregulated by single drugs. Tabs 4-7: Input genes with WormCat annotations for each single drug treatment. Tabs 8-10: Category 1-3 analysis of downregulated genes by double drug combinations. Tabs 11-14: Input genes with WormCat annotations for each double combination drug treatment. Tabs 15-17: Category 1-3 analysis of downregulated genes by triple-drug combinations. Tabs 18-20: input genes with WormCat annotations for each triple combination drug treatment. NA genes on these tabs reflect WormBase IDs that have been merged, marked as dead, or updated as not corresponding to a protein-coding gene.

**Supplemental Table 13: WormCat annotations for genes in the Ahringer RNAi library**. xlsx file containing gene and WormBase IDs along with Category 1, 2, and 3 annotations for the clones represented in the Ahringer RNAi library (Kamath *et al.* 2003).

**Supplemental Table 14: WormCat analysis of a genome-scale RNAi screen from LaMacchia *et al*.** xlsx file containing Category 1, 2, and 3 analysis of RNAi screen data of all, high and low glycogen stained animals (Tabs 1-3). Tabs 4-6 contain input genes with WormCat annotations for each gene. Tab 7 is "Glycogen low" genes analyzed by GOrilla. Tabs 8-11 show GO terms with multiple categories containing *cyc-1*, *vha-6*, *pbs-7*, and Y71F9AL.17.