Gene co-expression analyses of health(span) across multiple species

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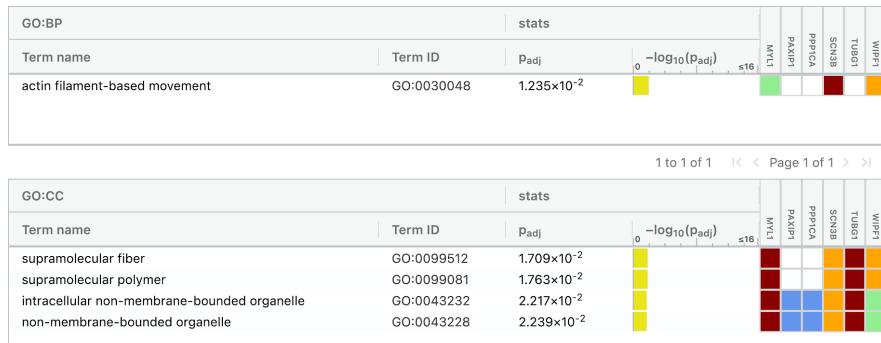[2] Humboldt-University of Berlin, Institute of Biology, Berlin, Germany

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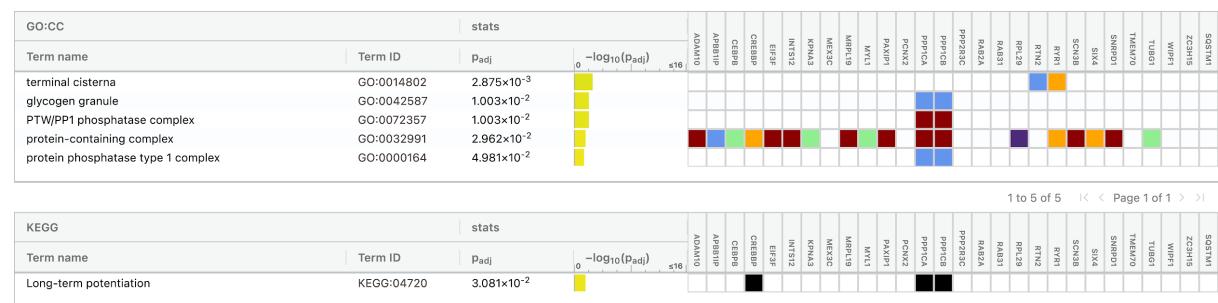
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Supplement

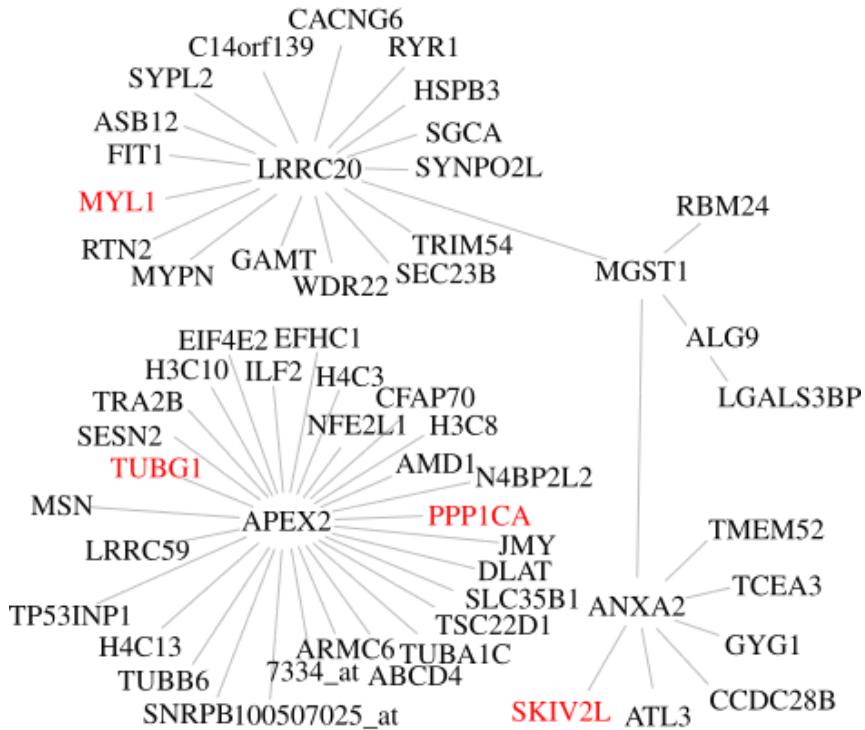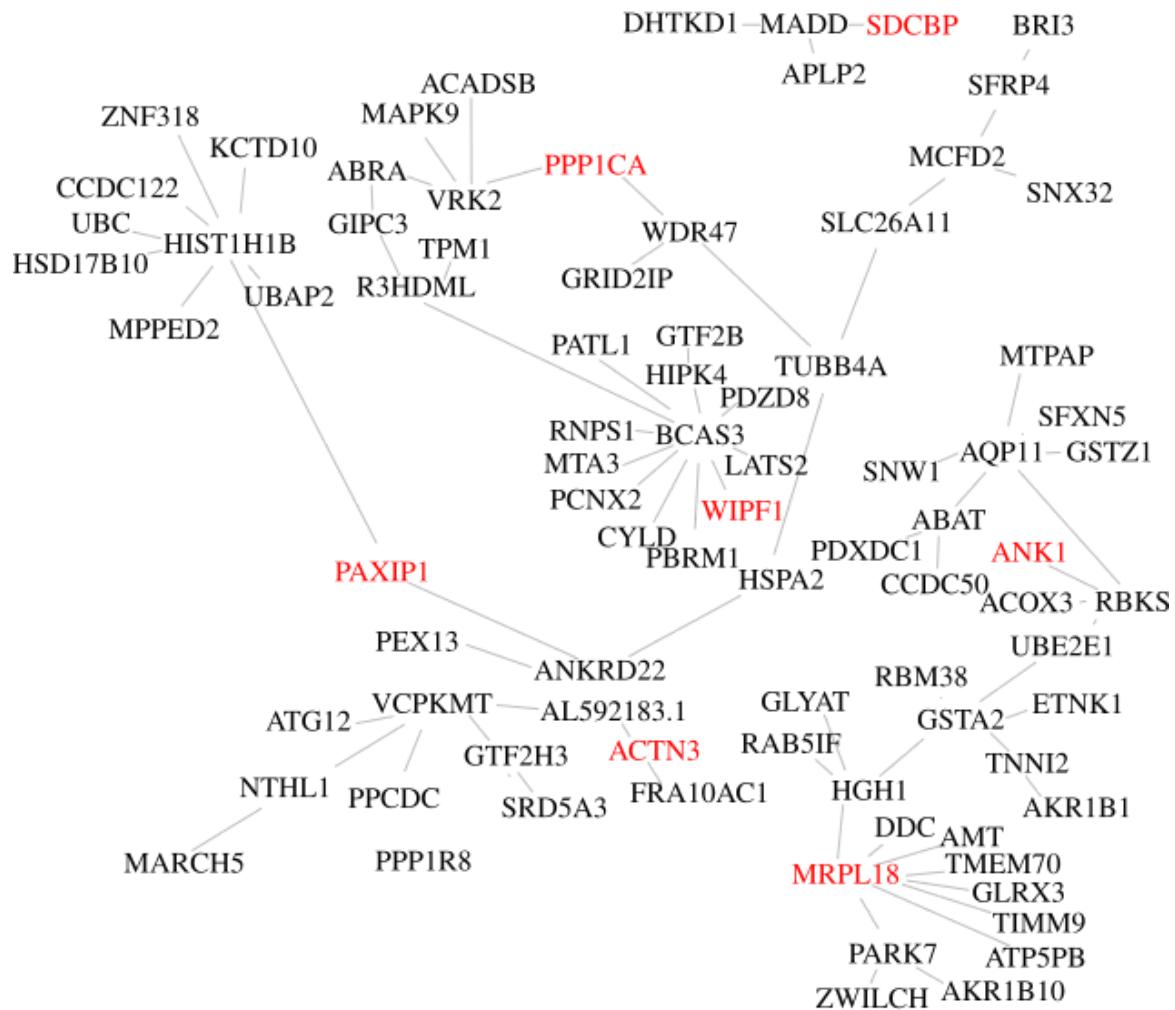### Figures

Supplement Figure 1a: g:profiler gene set enrichment analysis of genes listed jointly in Tables 2 and 3.
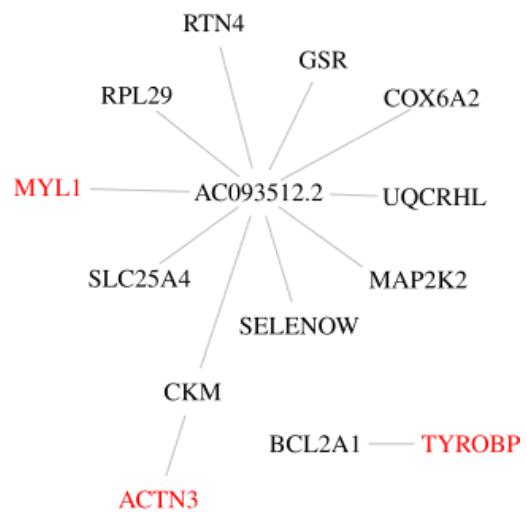

Supplement Figure 1b: g:profiler gene set enrichment analysis of genes listed in Table 3.

Supplement Figure 2a: Gene interactions observed in human. *The genes MYL1, PPP1CA, SKIV2L and TUBG1 are hub genes in WGCNA-defined modules from multiple species (cf. Figure 1, here shown in red). This graph was created iteratively with the red genes as a seed, then adding all the gene-gene interactions from WGCNA in human experiments originating from these red genes, and then transitively adding all the interacting genes of those. The resulting graph is highly interconnected before applying the minimum spanning tree algorithm. The genes interacting with hub genes across species (in red) then appear marginalized by the three human-only hub genes ANXA2, APEX2, LRRC20 and MGST1, given that the minimum spanning tree shows only the strongest correlations. ANXA2 is well described for a wide array of disease, i.e. cancer but also pulmonary fibrosis, and on a molecular level chimes in with vesicle fusion. APEX2 is a nuclease required for lymphocyte proliferation. LRRC20 is not yet described but known to interact with the also mostly undescribed TOM1 that once more is thought to be involved in intracellular trafficking and the E3 SUMO-protein ligase ZBED1. MGST1 is an enzyme located at the ER and mitochondria, a transferase of glutathione, an antioxidant.*

Supplement Figure 2b: *Gene interactions observed in worm. The figure was prepared analogously to Supplement Figure 2a from gene interactions observed in the worm. Gene names were mapped to human orthologs for an easier comparison between species.*

Supplement Figure 2c: Gene interactions observed in rat.

Supplement Figure 2d: Gene interactions observed in mouse.

GO:MF

Term name	Term ID	p_{adj}
protein-containing complex binding	GO:0044877	2.774×10^{-2}

GO:BP

Term name	Term ID	p_{adj}
leukocyte mediated immunity	GO:0002443	1.375×10^{-3}
leukocyte degranulation	GO:0043299	1.480×10^{-3}
myeloid cell activation involved in immune response	GO:0002275	1.647×10^{-3}
myeloid leukocyte mediated immunity	GO:0002444	1.774×10^{-3}
myeloid leukocyte activation	GO:0002274	5.387×10^{-3}
leukocyte activation involved in immune response	GO:0002366	7.896×10^{-3}
cell activation involved in immune response	GO:0002263	8.153×10^{-3}
regulated exocytosis	GO:0045055	1.450×10^{-2}
positive regulation of gamma-delta T cell differentiation	GO:0045588	1.513×10^{-2}
immune effector process	GO:0002252	1.810×10^{-2}
positive regulation of gamma-delta T cell activation	GO:0046645	2.017×10^{-2}
neutrophil degranulation	GO:0043312	2.191×10^{-2}
neutrophil activation involved in immune response	GO:0002283	2.258×10^{-2}
neutrophil mediated immunity	GO:0002446	2.515×10^{-2}
neutrophil activation	GO:0042119	2.564×10^{-2}
regulation of gamma-delta T cell differentiation	GO:0045586	2.592×10^{-2}
granulocyte activation	GO:0036230	2.743×10^{-2}
secretion by cell	GO:0032940	2.754×10^{-2}
regulation of gamma-delta T cell activation	GO:0046643	3.239×10^{-2}
exocytosis	GO:0006887	3.270×10^{-2}
export from cell	GO:0140352	3.535×10^{-2}
gamma-delta T cell differentiation	GO:0042492	4.747×10^{-2}

GO:CC

Term name	Term ID	p_{adj}
external side of plasma membrane	GO:0009897	2.121×10^{-5}
cell surface	GO:0009986	1.031×10^{-4}
side of membrane	GO:0098552	2.327×10^{-4}
ficolin-1-rich granule	GO:0101002	7.090×10^{-4}
vesicle	GO:0031982	3.815×10^{-3}
cytoplasmic vesicle	GO:0031410	6.422×10^{-3}
intracellular vesicle	GO:0097708	6.500×10^{-3}
intrinsic component of plasma membrane	GO:0031226	6.681×10^{-3}
secretory granule	GO:0030141	2.167×10^{-2}

REAC

Term name	Term ID	p_{adj}
Neutrophil degranulation	REAC:R-HSA-6…	3.042×10^{-2}

WP

Term name	Term ID	p_{adj}
TYROBP Causal Network	WP:WP3945	2.593×10^{-3}

CORUM

Term name	Term ID	p_{adj}
ITGB2-RACK1 complex	CORUM:7013	4.999×10^{-2}

Supplement Figure 3a: g:Profiler GSEA on genes connecting hub genes TYROBP and SDCBP.

GO:MF

Term name	Term ID	p_{adj}
protein-containing complex binding	GO:0044877	2.774×10^{-2}

GO:BP

Term name	Term ID	p_{adj}
leukocyte mediated immunity	GO:0002443	1.375×10^{-3}
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granulocyte activation	GO:0036230	2.743×10^{-2}
secretion by cell	GO:0032940	2.754×10^{-2}
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export from cell	GO:0140352	3.535×10^{-2}
gamma-delta T cell differentiation	GO:0042492	4.747×10^{-2}

GO:CC

Term name	Term ID	p_{adj}
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cell surface	GO:0009986	1.031×10^{-4}
side of membrane	GO:0098552	2.327×10^{-4}
ficolin-1-rich granule	GO:0101002	7.090×10^{-4}
vesicle	GO:0031982	3.815×10^{-3}
cytoplasmic vesicle	GO:0031410	6.422×10^{-3}
intracellular vesicle	GO:0097708	6.500×10^{-3}
intrinsic component of plasma membrane	GO:0031226	6.681×10^{-3}
secretory granule	GO:0030141	2.167×10^{-2}

REAC

Term name	Term ID	p_{adj}
Neutrophil degranulation	REAC:R-HSA-6…	3.042×10^{-2}

WP

Term name	Term ID	p_{adj}
TYROBP Causal Network	WP:WP3945	2.593×10^{-3}

CORUM

Term name	Term ID	p_{adj}
ITGB2-RACK1 complex	CORUM:7013	4.999×10^{-2}

Supplement Figure 3b: g:Profiler GSEA on genes connecting hub genes MYL1 and SKIV2L.

GO:BP

Term name	Term ID	p_{adj}
DNA replication-dependent nucleosome assembly	GO:0006335	1.954×10^{-4}
DNA replication-dependent nucleosome organization	GO:0034723	1.954×10^{-4}
rDNA heterochromatin assembly	GO:0000183	4.927×10^{-4}
regulation of gene silencing by miRNA	GO:0060964	1.021×10^{-3}
regulation of posttranscriptional gene silencing	GO:0060147	1.111×10^{-3}
regulation of gene silencing by RNA	GO:0060966	1.158×10^{-3}
regulation of gene silencing	GO:0060968	2.398×10^{-3}
heterochromatin assembly	GO:0031507	5.682×10^{-3}
regulation of megakaryocyte differentiation	GO:0045652	9.051×10^{-3}
heterochromatin organization	GO:0070828	9.501×10^{-3}
megakaryocyte differentiation	GO:0030219	1.994×10^{-2}
negative regulation of gene expression, epigenetic	GO:0045814	4.962×10^{-2}

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GO:CC

Term name	Term ID	p_{adj}
nucleosome	GO:0000786	3.405×10^{-3}
DNA packaging complex	GO:0044815	4.325×10^{-3}
protein-DNA complex	GO:0032993	4.086×10^{-2}

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KEGG

Term name	Term ID	p_{adj}
Systemic lupus erythematosus	KEGG:05322	1.914×10^{-4}
Alcoholism	KEGG:05034	1.991×10^{-2}

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Term ID	p_{adj}
Recycling pathway of L1 REAC:R-HSA-4...	7.327×10^{-3}

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WP

Term name	Term ID	p_{adj}
Histone Modifications	WP:WP2369	2.074×10^{-3}

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MIRNA

Term name	Term ID	p_{adj}
hsa-miR-484	MIRNA:hsa-mi...	4.270×10^{-2}

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Supplement Figure 3c: g:Profiler GSEA on genes connecting hub genes TUBG1 and PPP1CA.

Tables

Supplement Table 1: List of ArrayExpress/GEO files used as input in our study. *This table provides an overview of the transcriptomics experiments that were retrieved for this study. Each experiment was processed by a regular WGCNA workflow with unsigned correlation. Interactions were collected for the 30 most connected (hub) genes in each module. The column Modules lists the number of modules found for the experiment that feature an eigengene that correlates (with P<0.05) with the samples' health phenotype score. Within each module, only interactions with an adjacency value above the 95th percentile of an experiment were considered. The rightmost column lists the number of different hub genes that are paired in any of these interactions. Numbers in parentheses give the number of genes/interactions that could be mapped to ortholog genes in the human; for human data, the number of orthologs in worm are shown. For an interaction, both of the paired genes need to have orthologs assigned; otherwise they were not considered for the count.*

Accession	Description	Number of (with orthologs)			
Treatment groups		Samples [total[1] / per group]	Modules	Inter-actions	Genes

a) Mouse experiments on healthspan

Accession	Treatment groups	Description	Samples [total[1] / per group]	Modules	Inter-actions	Genes
E-GEOD-19102 (array)	i) high-fat diet + 100mg/kg SRT1720, ii) high-fat diet + 30mg/kg SRT1720, iii) high-fat diet, iv) standard AIN-93G diet	An activator of Sirt1, SRT1720, extends healthspan and lifespan in diet-induced obese mice; samples: liver tissue from strain C57BL/6J	12/3	10	324 (182)	28 (20)
E-GEOD-34773 (array)	i) PGC-1a skeletal muscle specific knockout, ii) PGC-1a skeletal muscle specific knockout + CR, iii) WT, iv) WT + CR	PGC-1a is a transcriptional coactivator that regulates mitochondrial function and is induced by CR; PGC-1a mediates mitochondrial, but not metabolic, changes during calorie restriction (Finley *et al.*, 2012)	26/6-7	12	0 (0)	0 (0)
E-GEOD-40936 (array)	i) ad libitum diet, muscle tissue, ii) ad libitum diet + 0.1% w/w metformin, muscle tissue, iii) 40% calorically restricted diet, muscle tissue, iv) ad libitum diet, liver tissue, v) ad libitum diet + 0.1% w/w metformin, liver tissue, vi) 40% calorically restricted diet, liver tissue	Chronic treatment with low dose of metformin (0.1% w/w in diet) starting at one year of age extends health and lifespan in male mice, while a higher dose (1% w/w) was toxic	30/5	1	434 (0)	29 (23)
E-GEOD-49000 (array)	i) standard diet, muscle tissue, ii) standard diet liver tissue, iii) standard diet + SRT2104, muscle tissue, iv) standard diet + SRT2104, liver tissue, v) 40% Caloric restriction, muscle tissue, vi) 40% Caloric restriction, liver tissue	SRT2104, a synthetic small molecule activator of SIRT1, extends survival of male mice on a standard diet and preserves bone and muscle mass (Mercken *et al.*, 2014)	30/5		no modules found	

E-GEOD-54853 (RNA-seq)	i) 10 g/kg D-Glucoseamine, ii) untreated	D-Glucoseamine mimics a ketogenic diet and extends lifespan of aging C57BL/6 mice	12/6	1	435 (0)	30 (19)
E-GEOD-55272 (array)	i) WT, 5 months, liver tissue, ii) WT, 24 months, liver tissue, iii) WT, 5 months, muscle tissue, iv) WT, 24 months, muscle tissue, v) WT, 5 months, adipose tissue, vi) WT, 24 months, adipose tissue, vii) Myc+/- , 5 months, liver tissue, viii) Myc+/- , 24 months, liver tissue, ix) Myc+/- , 5 months, muscle tissue, x) Myc+/- 24 months, muscle tissue, xi) Myc+/- , 5 months, adipose tissue, xii) Myc+/- , 24 months, adipose tissue	The pleiotropic transcription factor MYC is a proto-oncogene and Myc+/- heterozygous mice have extended lifespan and improved healthspan	36/3	6	567 (377)	79 (64)
E-MTAB-6578 (RNA-seq)	female heart tissue: i) 10 weeks, HGPS-/- mutants, ii) 10 weeks, HGPS-/-; NAT10-/- double mutants, iii) 10 weeks, NAT10-/- mutants, iv) 10 weeks, HGPS-/- mutants + 100 mg/kg remodelin, v) 104 weeks, WT, vi) 10 weeks, WT	Targeting NAT10 enhances healthspan and lifespan in a mouse model of human accelerated aging syndrome (Hutchinson-Gilford progeria syndrome)	12/2	1	0 (0)	0 (0)

b) Rat experiments on healthspan

E-GEOD-38062 (array)	i) fed ad libitum, ii) fed 40% CR	Muscle specimens of rats following a calorie restriction (40%) diet vs ad libitum fed rats; age: from 2-27 months (Mercken et al., 2013)	10/5	8	467 (81)	57 (24)

c) Human experiments on healthspan

E-GEOD-38012 (array)	i) middle-aged humans under CR diet, ii) middle-aged humans under western diet	Skeletal muscle specimens of humans following a calorie restriction diet vs humans following a Western diet	25/10-15	2	405 (324)	28 (25)
E-GEOD-66236 (array)	i) adipocytes proliferating in culture, ii) adipocytes in gamma-irradiation induced senescence	Difference between senescent and non-senescent cells in order to develop senolytic drugs	16/8	1	435 (276)	30 (24)

d) Worm experiments on healthspan

E-GEOD-8696 (array)	i) 4 μM, ii) 20 μM, & iii) 500 μM hemin	To understand heme homeostasis, genes transcriptionally regulated by heme should be identified	9/3	4	22 (0)	20 (7)

(Rajagopal *et al.*, 2008)

ID	Conditions	Description				
E-GEOD-9246 (array)	i) *slr-2*(ku297) mutants, ii) WT	Transcription profiling of *C. elegans slr-2* (C2H2 Zn-finger protein) mutants at L1 stage	6/3	1	434 (104)	29 (14)
E-GEOD-9301 (array)	i) 99% O2 (oxidative stress), ii) 99% O2 + *skn-1* RNAi, iii) untreated	*C. elegans* treated with oxidative stress in absence and presence of the transcription factor SKN-1, which is involved in response to oxidative stress	11/3-4		no modules found	
E-GEOD-21531 (array)	i) *unc-32; glp-1* double mutants (excess proliferation), ii) *unc-32* mutants	Analysis of germ cell proliferation in *unc-32*(e189);*glp-1*(oz112gf) double mutants (excess germ cell proliferation) compared to *unc-32*(e189) mutants as control (Waters *et al.*, 2010)	8/4		no modules found	
E-GEOD-30505 (array)	i) L3, WT, EV, ii) L3, WT, *ash-2* RNAi, iii) L3, *glp-1*(e2141ts) mutants, EV, iv) L3, *glp-1*(e2141ts) mutants, *ash-2* RNAi, v) day 8, WT, EV, vi) day 8, WT, *ash-2* RNAi, vii) day 8, *glp-1*(e2141ts) mutants, EV, viii) day 8, *glp-1*(e2141ts) mutants, *ash-2* RNAi	The ASH-2 trithorax complex trimethylates histone H3 at lysine 4 (H3K4); *ash-2* knock-down increases lifespan in a germline dependent manner. *ash-2* knock-down was compared in young and old as well as in WT and germline deficient (*glp-1*) mutants (Greer et al., 2010)	23/2-3	4	854 (146)	60 (20)
E-GEOD-32031 (array)	i) *nhr-23* RNAi, ii) untreated	Inhibition of *nhr-32*, important for growth and molting, in L2 larvae	6/3	1	124 (2)	27 (5)
E-GEOD-32339 (array)	i) L3 WT, ii) L3 *nep-1* mutants, iii) adult WT, iv) adult *nep-1* mutants	Comparison between wild-type and *nep-1* (homologue of human ECE1 (endothelin-converting enzyme 1) mutant strain	10/2-3	3	867 (173)	57 (25)
E-GEOD-35939 (array)	embryonic touch-receptor cells with i) mutant Huntingtin (128Q) vs normal Huntingtin (19Q), ii) normal Huntingtin (19Q) vs GFP only	Comparison of purified touch receptor neurons expressing mutant Huntingtin N-terminal fragment (expanded polyGlutamine) with normal Huntingtin N-terminal fragment	12/6		no modules found	
E-GEOD-36494 (RNA-seq)	i) WT, ii) WT + TAP (tobacco acid pyrophosphatase), iii) *rde-10* mutant, iv) *rde-10* mutant + TAP, v) *rde-11* mutant, vi) *rde-11* mutant + TAP)	The RDE-10/RDE-11 complex triggers RNAi induced mRNA degradation by association with target mRNA in *C. elegans* (Yang et al., 2012)	12/2		no modules found	
E-GEOD-38877 (array)	centrifuged at i) 1g, ii) 5g, iii) 10g, iv) 15g	Worms spun in centrifuge at elevated g values	18/3-9		no modules found	
E-GEOD-40459 (array)	i) *rsd-2* (yp10) mutants, 25 °C, late generation, ii) *rsd-2* (yp10) mutants, 25 °C, early generation, iii) *rsd-2* (pk3307) mutants, 25°C, late generation, iv) *rsd-2* (pk3307) mutants, 25°C, early generation, v) *rsd-6* (pk3300) mutants, 25°C, late generation, vi) *rsd-6* (pk3300) mutants, 25°C, early generation, vii) *rsd-2* (yp10) mutants, 20 °C, late	Effects of transgeneration aging studied in early and late generation *rsd-2* and *rsd-6* mutants at the restrictive temperature of 25°C and the permissive temperature of 20°C	36/3		no modules found	

ID	Conditions	Description				
	generation, viii) *rsd-2* (yp10) mutants, 20 °C, early generation, ix) *rsd-2* (pk3307) mutants, 20°C, late generation, x) *rsd-2* (pk3307) mutants, 20°C, early generation, xi) *rsd-6* (pk3300) mutants, 20°C, late generation, xii) *rsd-6* (pk3300) mutants, 20°C, early generation					
E-GEOD-42192 (array)	i) fed with E.coli OP50 for 3 days or ii) 10 days, iii) fed with Lactobacillus rhamnosus CNCM I-3690 for 3 days or iv) 10 days, v) fed with Lactobacillus rhamnosus CNCM I-4317 for 3 days or vi) 10 days	The lactic acid bacteria *Lactobacillus rhamnosus* (CNCM I-3690) increase worm's lifespan by antioxidative actions	18/3	2	868 (71)	58 (15)
E-GEOD-43864 (array)	i) *nhr-114* RNAi, ii) *glp-1*(q224ts) mutants, iii) WT untreated, iv) WT + tryptophan	The nuclear receptor *nhr-114*/HNF4 protects germline stem cells from dietary metabolites. The downregulation of *nhr-114* results in germline defects and sterility, which depends on tryptophan. Sterile *glp-1* mutants are used for comparison. animals	12/3	9	1287 (263)	73 (31)
E-GEOD-46051 (RNA-seq)	i) day 1, ii) day 1 + 100 nM rotenone, iii) day 5, iv) day 5 + 100 nM rotenone, v) day 10, vi) day 10 + 100 nM rotenone, vii) day 20, viii) day 20 + 100 nM rotenone	Deep sequencing of endogenous mRNA from Caenorhabditis elegans in the presence and absence of rotenone at 4 different time points (Schmeisser *et al.*, 2013)	22/2-3	21	3123 (474)	264 (74)
E-GEOD-51502 (array)	i) genetically activated beta-catenin, ii) WT	Use of an activated beta-catenin to identify Wnt/beta-catenin pathway target genes (Jackson *et al.*, 2014)	6/3	3	1302 (112)	86 (27)
E-GEOD-52340 (array)	i) WT, ii) *rsks-1* mutants, iii) *daf-2* mutants, iv) daf-2;rsks-1 double mutants, v) daf-16;daf-2;rsks-1 triple mutants	Synergistic lifespan extension in daf-2;rsks-1 double mutants requires DAF-16 and the germline was identified as the key tissue for this synergistic longevity (Chen *et al.*, 2013)	47/9-10		no modules found	
E-GEOD-54853 (RNA-seq)	i) 100 µM D-Glucosamine, ii) untreated	D-Glucosamine extends C. elegans lifespan by impairing glucose metabolism to activate AMP-activated protein kinase	12/6	2	870 (0)	60 (20)
E-GEOD-57739 (RNA-seq)	i) WT + standard food (OP50), ii) WT + *S. aureus*, iii) *hlh-30* mutants + OP50, iv) *hlh-30* mutants + *S. aureus*	HLH-30/TFEB is a transcription factor in the host response to infections and regulates the transcription of cytoprotective and antimicrobial genes (Visvikis *et al.*, 2014)	8/2		685 (55)	90 (28)
E-GEOD-85342 (array)	i) 5-fluorouracil, ii) DMSO	Treatment with 5-fluorouracil inhibits growth of *P. aeruginosa* and reduces pyoverdine biosynthesis	6/3		no modules found	
E-MEXP-479 (array)	i) fed with standard food for 12h or ii) 24h, iii) fed with *Drechmeria coniospora* for	Exposure to the fungal pathogen Drechmeria coniospora for 12 and 24 hours (Pujol *et al.*, 2008)	64/16		no modules found	

	12h or iv) 24h				
E-MTAB-1333 (array)	pash-1(mj100) mutants at restrictive temperature (25 °C) for i) 0, ii) 6, iii) 12 or iv) 24 hours, pash-1(mj100); pash-1::gfp mutants at 25 °C for v) 0, vi) 6, vii) 12 or viii) 24 hours	Reversible inactivation of miRNA synthesis via DGCR8/pash-1 conditional mutants (Lehrbach et al., 2012)	24/3	6	1715 (440) 119 (58)
E-MEXP-1808 (array)	i) strain DR1350, ii) strain DR1350 + dauer pheromone, iii) WT N2, iv) WT N2 + dauer pheromone	Wild type isolates treated with dauer larva-inducing pheromone (Harvey et al., 2009)	12/3		no modules found
E-MEXP-1810 (array)	i) strain RIL-14, ii) strain RIL-14 + dauer pheromone, iii) strain RIL-17, iv) strain RIL-17 + dauer pheromone	Wild type isolates treated with dauer larva-inducing pheromone	12/3	6	261 (108) 65 (37)

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[1] total: total samples in this experiment; per group: samples per treatment-group (biological replicates)

Supplement Table 2: Genes correlating with eigengene representation (module membership) *of those modules that are correlating with the health score. The table lists all genes that appear in at least two experiments among the top 30 and a P value below 0.05. If the expression of the gene correlates positively with the health score then the gene is tagged as positive. The columns "cor" and "P val" list the values as determined by WGCNA. A negative correlation with a positive tag indicates that eigengene of the module is negatively correlated with the health score.*

Gene	health	cor	P val	Experiment	module
0610006I08Rik	negative	0.907	4.64e-05	E-GEOD-19102	darkmagenta
0610006I08Rik	negative	0.942	4.57e-06	E-GEOD-19102	skyblue3
2010107E04Rik	positive	0.951	6.24e-19	E-GEOD-55272	black
2010107E04Rik	positive	-0.947	2.10e-18	E-GEOD-55272	magenta
ABAT	positive	0.988	2.21e-18	E-GEOD-30505	blue
ABAT	positive	-0.980	1.42e-12	E-GEOD-42192	turquoise
ABCG1	negative	-0.900	6.76e-05	E-GEOD-19102	sienna2
ABCG1	negative	0.974	1.68e-23	E-GEOD-55272	red
ABRA	negative	0.996	4.41e-12	E-GEOD-43864	brown
ABRA	negative	0.989	2.90e-06	E-GEOD-57739	turquoise
ABRA	positive	-0.968	1.12e-14	E-MTAB-1333	blue
abu-14	positive	0.993	5.68e-21	E-GEOD-30505	turquoise
abu-14	positive	0.999	7.55e-07	E-GEOD-9246	turquoise
AC068831.7	negative	-0.868	2.48e-04	E-GEOD-19102	yellow3
AC068831.7	negative	0.986	1.28e-18	E-MTAB-1333	turquoise
AC106774.4	negative	-0.873	2.13e-04	E-MEXP-1810	plum1
AC106774.4	negative	0.938	6.73e-06	E-MEXP-1810	royalblue
ADAM10	negative	-0.871	7.20e-09	E-GEOD-34773	greenyellow
ADAM10	positive	0.998	4.87e-13	E-GEOD-43864	turquoise
AGO1	negative	-0.995	2.14e-09	E-GEOD-32339	blue
AGO1	negative	-0.879	1.53e-08	E-MTAB-1333	black
ain-1	negative	0.921	4.24e-04	E-GEOD-8696	cyan
ain-1	negative	0.965	2.56e-05	E-GEOD-8696	royalblue
APBB1IP	positive	0.987	2.78e-09	E-GEOD-54853-CEL	yellow
APBB1IP	negative	0.970	1.68e-07	E-MTA-B6578	blue
AQP11	positive	0.997	2.57e-24	E-GEOD-30505	blue
AQP11	negative	0.951	1.98e-06	E-MEXP-1810	brown
ARMC1	positive	-0.850	3.97e-08	E-GEOD-34773	darkgrey
ARMC1	positive	0.874	5.48e-09	E-GEOD-34773	greenyellow
asns-2	negative	-0.993	7.01e-05	E-GEOD-51502	black
asns-2	positive	0.984	8.21e-09	EGEOD54853-CEL	brown
ATP6V1B2	negative	0.978	4.00e-08	E-GEOD-43864	paleturquoise
ATP6V1B2	negative	0.967	2.76e-07	E-GEOD-43864	paleturquoise
ATP6V1B2	positive	0.999	2.07e-06	E-GEOD-9246	turquoise
B2M	negative	0.927	1.03e-11	E-GEOD-34773	lightyellow
B2M	negative	0.922	2.13e-11	E-GEOD-34773	lightyellow
B2M	negative	0.975	6.82e-08	EMTAB6578	blue
C02E7.6	positive	0.993	4.20e-21	E-GEOD-30505	turquoise
C02E7.6	positive	0.990	9.63e-10	E-GEOD-43864	yellow
C09B9.2	negative	0.990	2.56e-06	E-GEOD-57739	turquoise
C09B9.2	positive	0.989	1.36e-19	E-MTAB-1333	yellow
C26F1.1	positive	0.989	1.13e-09	E-GEOD-43864	yellow
C26F1.1	negative	0.982	4.60e-04	E-GEOD-51502	turquoise
C46F2.1	negative	-0.869	2.45e-04	E-MEXP-1810	plum1
C46F2.1	negative	0.921	2.15e-05	E-MEXP-1810	royalblue

C46G7.1	positive	-0.979	1.62e-12	E-GEOD-42192	turquoise
C46G7.1	negative	0.928	8.98e-04	E-GEOD-57739	darkgreen
CAD	negative	-0.875	1.93e-04	E-MEXP-1810	plum1
CAD	negative	0.902	6.02e-05	E-MEXP-1810	royalblue
CD151	negative	0.934	8.51e-06	E-GEOD-19102	darkmagenta
CD151	negative	-0.905	2.28e-10	E-GEOD-34773	tan
CEBPB	positive	0.940	1.65e-04	E-GEOD-38062	salmon
CEBPB	negative	0.812	5.27e-08	E-GEOD-40936	grey
CLIC5	negative	0.842	6.00e-04	E-GEOD-19102	green3
CLIC5	negative	-0.883	2.42e-09	E-GEOD-34773	greenyellow
comp-1	negative	0.991	2.09e-06	E-GEOD-57739	turquoise
comp-1	positive	0.991	9.50e-21	E-MTAB-1333	yellow
COX15	positive	-0.890	1.19e-09	E-GEOD-34773	darkgrey
COX15	positive	-0.879	3.61e-09	E-GEOD-34773	darkgrey
COX15	positive	0.923	1.79e-11	E-GEOD-34773	greenyellow
cpg-2	negative	-0.994	5.19e-09	E-GEOD-32339	blue
cpg-2	positive	0.961	3.76e-05	E-GEOD-8696	red
CRB1	negative	-0.958	1.85e-04	E-GEOD-57739	darkorange
CRB1	positive	0.989	1.48e-09	EGEOD54853-CEL	yellow
CREBBP	negative	0.953	1.96e-05	E-GEOD-32339	pink
CREBBP	negative	0.937	1.75e-12	E-GEOD-34773	red
CREBBP	negative	0.958	4.89e-05	E-GEOD-8696	purple
D2062.7	positive	-0.969	4.07e-11	E-GEOD-42192	blue
D2062.7	positive	0.985	1.99e-18	E-MTAB-1333	yellow
DCP2	negative	0.928	1.74e-10	E-GEOD-30505	black
DCP2	negative	-0.997	2.13e-10	E-GEOD-32339	blue
DDX4	positive	-0.998	3.10e-13	E-GEOD-43864	blue
DDX4	negative	-0.877	1.77e-04	E-MEXP-1810	lightcyan
DEPDC1B	negative	0.915	9.48e-10	E-GEOD-30505	black
DEPDC1B	positive	-0.934	2.28e-04	E-GEOD-8696	cyan
dnj-3	positive	0.940	5.49e-06	E-GEOD-43864	royalblue
dnj-3	negative	0.924	1.05e-03	E-GEOD-57739	darkgreen
dnj-3	negative	0.974	9.23e-16	E-MTAB-1333	brown
DRG1	negative	0.993	6.92e-05	E-GEOD-51502	turquoise
DRG1	negative	0.925	1.64e-05	E-MEXP-1810	brown
EEF1B2	negative	-0.866	2.71e-04	E-GEOD-19102	deeppink
EEF1B2	positive	0.948	1.93e-13	E-GEOD-34773	green
egg-2	positive	-0.998	8.73e-14	E-GEOD-43864	blue
egg-2	positive	-0.998	2.95e-13	E-GEOD-43864	blue
egg-2	positive	0.964	2.85e-05	E-GEOD-8696	red
EIF3F	positive	-0.929	7.24e-12	E-GEOD-34773	purple
EIF3F	positive	0.999	9.64e-07	E-GEOD-9246	turquoise
EMC3	negative	-0.915	5.49e-04	E-GEOD-38062	darkgreen
EMC3	negative	0.954	6.54e-05	E-GEOD-38062	plum1
F45D3.4	positive	0.935	8.05e-06	E-MEXP-1810	darkmagenta
F45D3.4	positive	-0.917	2.69e-05	E-MEXP-1810	royalblue
F55A3.2	positive	0.867	2.62e-04	E-MEXP-1810	darkmagenta
F55A3.2	positive	0.876	1.89e-04	E-MEXP-1810	darkolivegreen
FBLN7	negative	0.877	1.83e-04	E-GEOD-19102	green3
FBLN7	negative	0.909	1.37e-10	E-GEOD-34773	magenta
fkb-7	positive	-0.995	4.39e-05	E-GEOD-51502	turquoise
fkb-7	positive	0.965	1.05e-04	E-GEOD-57739	sienna3
flp-15	positive	0.959	8.29e-07	E-MEXP-1810	plum1
flp-15	positive	0.914	3.14e-05	E-MEXP-1810	plum1

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flp-15      positive -0.898 7.43e-05   E-MEXP-1810         royalblue
 GMFG       negative  0.892 9.67e-05   E-GEOD-19102       darkmagenta
 GMFG       negative  0.984 6.89e-27   E-GEOD-55272               red
GNG10       negative  0.927 1.40e-05   E-GEOD-19102       darkmagenta
GNG10       positive  0.959 3.66e-20   E-GEOD-55272            yellow
GPR142      negative  0.990 7.71e-10   E-GEOD-43864        lightgreen
GPR142      negative  0.979 3.46e-08   E-GEOD-43864        lightgreen
GPR142      negative  0.925 3.56e-04    E-GEOD-8696              cyan
grl-7       positive  0.992 4.32e-20   E-GEOD-30505         turquoise
grl-7       positive  0.993 1.22e-10   E-GEOD-43864            yellow
grl-7       positive  0.991 3.61e-10   E-GEOD-43864            yellow
grl-7       positive  0.991 3.91e-10   E-GEOD-43864            yellow
GSTA2       positive  0.992 3.59e-20   E-GEOD-30505              blue
GSTA2       negative  0.976 6.93e-06    E-GEOD-8696            purple
GSTA2       negative  0.953 1.73e-06    E-MEXP-1810            brown
H2-D1       negative  0.951 9.09e-14   E-GEOD-34773       lightyellow
H2-D1       negative  0.948 1.95e-13   E-GEOD-34773       lightyellow
H2-D1       negative  0.941 9.01e-13   E-GEOD-34773       lightyellow
H2-D1       negative  0.894 7.30e-10   E-GEOD-34773       lightyellow
H2-D1       negative  0.974 9.03e-08      EMTAB6578              blue
H42K12.3    positive  0.992 2.23e-20   E-GEOD-30505         turquoise
H42K12.3    positive  0.988 2.15e-04   E-GEOD-51502              blue
HACL1       positive  0.881 1.55e-04    E-MEXP-1810             plum1
HACL1       positive -0.963 5.25e-07    E-MEXP-1810         royalblue
HACL1       positive -0.908 4.46e-05    E-MEXP-1810         royalblue
HSDL2       positive  0.940 5.23e-04   E-GEOD-57739        darkorange
HSDL2       positive  0.949 2.39e-06    E-MEXP-1810          lightcyan
 IHH        negative  0.933 2.34e-04    E-GEOD-8696              cyan
 IHH        positive  0.999 2.32e-06    E-GEOD-9246         turquoise
INTS12      negative -0.845 5.42e-04   E-GEOD-19102           yellow3
INTS12      positive -0.980 2.32e-08   E-GEOD-43864      paleturquoise
K08C9.2     negative  0.997 8.50e-13   E-GEOD-43864             brown
K08C9.2     positive  0.986 1.88e-18    E-MTAB-1333            yellow
KPNA3       negative  0.932 4.18e-12   E-GEOD-34773               red
KPNA3       positive  0.999 2.92e-06    E-GEOD-9246         turquoise
let-2       positive  0.992 1.36e-20   E-GEOD-30505              blue
let-2       positive -0.979 1.83e-12   E-GEOD-42192         turquoise
LIAS        positive -0.921 2.67e-11   E-GEOD-34773             black
LIAS        positive  0.880 3.27e-09   E-GEOD-34773               tan
LIN28A      positive -0.998 1.06e-13   E-GEOD-43864              blue
LIN28A      positive -0.998 2.15e-13   E-GEOD-43864              blue
LIN28A      negative -0.877 1.78e-04    E-MEXP-1810     darkolivegreen
MARCKS      negative  0.967 3.10e-07   E-GEOD-19102              blue
MARCKS      negative  0.918 4.08e-11   E-GEOD-34773           magenta
MEX3C       negative -0.994 7.28e-09   E-GEOD-32339              blue
MEX3C       negative  0.948 6.71e-13   E-GEOD-38012            yellow
mig-6       positive -0.978 2.21e-12   E-GEOD-42192         turquoise
mig-6       positive  0.984 8.04e-09  EGEOD54853-CEL           yellow
 MRAS       positive  0.989 5.85e-19   E-GEOD-30505              blue
 MRAS       positive -0.965 3.01e-14    E-MTAB-1333              blue
MRPL13      positive -0.886 1.74e-09   E-GEOD-34773          darkgrey
MRPL13      positive -0.878 3.75e-09   E-GEOD-34773          darkgrey
MRPL13      positive  0.867 9.86e-09   E-GEOD-34773       greenyellow
MRPL19      positive -0.869 8.64e-09   E-GEOD-34773          darkgrey
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MRPL19   negative  0.951 1.96e-06   E-MEXP-1810            brown
MRPL30   negative  0.888 1.13e-04   E-GEOD-19102         skyblue3
MRPL30   positive  0.939 2.45e-17   E-GEOD-55272            black
 MTPAP   negative -0.992 3.65e-20   E-GEOD-30505             blue
 MTPAP   negative -0.995 2.69e-09   E-GEOD-32339             blue
Myeov2   positive  0.931 1.71e-16   E-GEOD-55272            black
Myeov2   positive -0.976 5.77e-24   E-GEOD-55272          magenta
  MYL1   positive -0.996 3.24e-25   E-GEOD-38012        turquoise
  MYL1   positive  0.985 1.49e-06   E-GEOD-38062              tan
  MYL7   negative  0.895 8.28e-05   E-GEOD-19102         skyblue3
  MYL7   negative  0.901 6.40e-05 EGEOD54853-MMU    darkturquoise
NDUFS1   positive  0.862 3.07e-04   E-GEOD-19102            coral1
NDUFS1   positive  0.877 1.77e-04   E-GEOD-19102 lightsteelblue1
 NR1H2   positive  0.983 1.22e-08   E-GEOD-43864        darkorange
 NR1H2   negative -0.909 1.75e-03   E-GEOD-57739           sienna3
 NR1H2   positive  0.883 1.42e-04   E-MEXP-1810    darkolivegreen
 NR1H2   positive  0.851 4.51e-04   E-MEXP-1810    darkolivegreen
 NR1H2   positive  0.894 3.95e-09   E-MTAB-1333            black
 NRBP1   negative  0.855 2.64e-08   E-GEOD-34773          darkgrey
 NRBP1   negative  0.969 4.13e-22   E-GEOD-55272             pink
Pabpc1   positive -0.887 1.21e-04   E-GEOD-19102       darkmagenta
Pabpc1   negative  0.969 2.22e-07      EMTAB6578             blue
PAXIP1   positive  0.890 1.03e-04   E-GEOD-19102         deeppink
PAXIP1   positive  0.998 2.67e-13   E-GEOD-43864        turquoise
 PCNX2   negative  0.962 7.78e-14   E-MTAB-1333             blue
 PCNX2   negative  0.907 4.66e-05 EGEOD54853-MMU    darkturquoise
 PDCD6   negative -0.959 8.71e-07   E-GEOD-43864        royalblue
 PDCD6   negative  0.928 6.50e-11   E-MTAB-1333            green
  PFAS   positive -0.858 2.13e-08   E-GEOD-34773          darkgrey
  PFAS   positive  0.941 8.58e-13   E-GEOD-34773       greenyellow
  PPIA   positive -0.975 6.83e-12   E-GEOD-42192             blue
  PPIA   negative  0.918 2.52e-05   E-MEXP-1810        royalblue
  PPIC   negative  0.981 1.67e-08   E-GEOD-19102             blue
  PPIC   negative  0.981 1.97e-08   E-GEOD-19102             blue
  PPIC   negative  0.917 4.55e-11   E-GEOD-34773          magenta
PPP1CA   positive  0.987 2.48e-04   E-GEOD-51502            black
PPP1CA   negative  0.991 1.68e-06   E-GEOD-57739        turquoise
PPP1CA   positive  0.993 2.02e-14   E-GEOD-66236        turquoise
PPP1CA   positive  0.989 9.26e-20   E-MTAB-1333            yellow
PPP1CB   positive -0.979 4.67e-06   E-GEOD-38062        turquoise
PPP1CB   positive  0.999 1.18e-06    E-GEOD-9246        turquoise
PPP2R3C  negative  0.944 1.38e-12   E-GEOD-38012            yellow
PPP2R3C  negative  0.966 1.31e-21   E-GEOD-55272             pink
pqn-32   positive  0.993 3.79e-21   E-GEOD-30505        turquoise
pqn-32   positive  0.993 1.60e-10   E-GEOD-43864            yellow
pqn-32   positive  0.989 1.27e-09   E-GEOD-43864            yellow
 PSMD4   positive  0.932 9.87e-06   E-GEOD-19102        lightpink2
 PSMD4   negative  0.848 4.59e-08   E-GEOD-34773          darkgrey
 ptp-2   negative -0.937 7.07e-06   E-MEXP-1810            plum1
 ptp-2   negative  0.932 1.03e-05   E-MEXP-1810        royalblue
  PUM1   negative -0.995 3.07e-09   E-GEOD-32339             blue
  PUM1   negative -0.995 3.51e-09   E-GEOD-32339             blue
  PUM1   positive  0.986 9.40e-07    E-GEOD-8696              red
R3HDML   negative -0.898 7.34e-05   E-MEXP-1810            plum1
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  R3HDML   negative   0.928 1.33e-05   E-MEXP-1810      royalblue
  R3HDML   negative   0.916 2.80e-05   E-MEXP-1810      royalblue
   RAB2A   negative   0.965 6.41e-06   E-GEOD-32339          pink
   RAB2A   negative   0.960 2.47e-20   E-GEOD-55272          pink
   RAB31   negative   0.952 1.77e-06   E-GEOD-19102          blue
   RAB31   negative   0.971 1.37e-05   E-GEOD-38062     turquoise
   RAD17   negative   0.994 5.90e-09   E-GEOD-32339     turquoise
   RAD17   negative   0.982 1.90e-17   E-MTAB-1333      turquoise
    RGL1   negative   0.956 1.25e-06   E-GEOD-19102          blue
    RGL1   positive  -0.687 2.76e-05   E-GEOD-40936          grey
   RMDN3   positive  -0.971 2.12e-11   E-GEOD-42192          blue
   RMDN3   negative   0.999 3.97e-14   E-GEOD-43864         brown
   RMDN3   negative   0.996 4.43e-12   E-GEOD-43864         brown
   RMDN3   positive   0.967 2.03e-05   E-GEOD-8696            red
   RPL11   positive   0.929 7.00e-12   E-GEOD-34773         green
   RPL11   positive   0.963 7.42e-21   E-GEOD-55272        yellow
  RPL13A   positive   0.936 2.43e-12   E-GEOD-34773         green
  RPL13A   positive  -0.959 1.11e-14   E-GEOD-34773        purple
  RPL23A   positive   0.934 3.34e-12   E-GEOD-34773         green
  RPL23A   positive   0.929 7.50e-12   E-GEOD-34773         green
  RPL23A   positive  -0.966 1.56e-15   E-GEOD-34773        purple
  RPL23A   positive  -0.939 1.26e-12   E-GEOD-34773        purple
  RPL23A   positive  -0.934 3.44e-12   E-GEOD-34773        purple
   RPL27   positive   0.930 6.54e-12   E-GEOD-34773         green
   RPL27   positive  -0.963 4.04e-15   E-GEOD-34773        purple
  Rpl27a   positive   0.935 2.52e-12   E-GEOD-34773         green
  Rpl27a   positive   0.965 2.64e-21   E-GEOD-55272        yellow
   RPL29   positive   0.940 1.09e-12   E-GEOD-34773         green
   RPL29   positive   0.976 7.35e-06   E-GEOD-38062           tan
   RPS12   positive   0.942 7.63e-13   E-GEOD-34773         green
   RPS12   positive  -0.926 1.28e-11   E-GEOD-34773        purple
   RPS21   positive   0.954 4.18e-14   E-GEOD-34773         green
   RPS21   positive   0.937 1.87e-12   E-GEOD-34773         green
   RPS21   positive  -0.923 1.82e-11   E-GEOD-34773        purple
   Rps25   positive   0.960 1.00e-14   E-GEOD-34773         green
   Rps25   positive  -0.927 1.02e-11   E-GEOD-34773        purple
   Rps29   positive   0.935 2.90e-12   E-GEOD-34773         green
   Rps29   positive  -0.954 4.47e-14   E-GEOD-34773        purple
    RPS7   negative  -0.905 5.22e-05   E-GEOD-19102      deeppink
    RPS7   positive  -0.923 1.92e-11   E-GEOD-34773        purple
    RTN2   negative   0.861 1.66e-08   E-GEOD-34773      darkgrey
    RTN2   positive  -0.995 2.44e-24   E-GEOD-38012     turquoise
    RYR1   positive   0.883 1.43e-04   E-GEOD-19102       sienna2
    RYR1   positive  -0.994 2.21e-23   E-GEOD-38012     turquoise
   SCN3B   positive  -0.879 1.67e-04   E-GEOD-19102        green3
   SCN3B   positive  -0.956 5.85e-05   E-GEOD-38062   yellowgreen
  SFT2D2   negative  -0.929 2.73e-16   E-GEOD-55272         black
  SFT2D2   negative   0.975 8.14e-24   E-GEOD-55272       magenta
   sgo-1   positive  -0.998 1.68e-13   E-GEOD-43864          blue
   sgo-1   negative   0.985 3.18e-18   E-MTAB-1333      turquoise
   SIK1B   negative   0.992 1.18e-06   E-GEOD-57739     turquoise
   SIK1B   positive   0.989 1.13e-19   E-MTAB-1333         yellow
    SIX4   negative   0.954 1.74e-12   E-GEOD-30505           red
    SIX4   negative  -0.871 7.31e-09   E-GEOD-34773   greenyellow
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    SKP1    negative   0.995 2.19e-09     E-GEOD-32339         turquoise
    SKP1    negative   0.940 9.01e-12     E-MTAB-1333             green
    SKP1    negative   0.924 1.21e-10     E-MTAB-1333             green
  SLC16A9   positive   0.989 1.02e-18     E-GEOD-30505              blue
  SLC16A9   negative  -0.911 3.81e-05     E-MEXP-1810        darkmagenta
  SLC7A11   negative   0.960 1.19e-13     E-MTAB-1333              blue
  SLC7A11   positive   0.987 2.50e-09    EGEOD54853-CEL            brown
    smz-2   positive  -0.970 3.19e-11     E-GEOD-42192              blue
    smz-2   positive   0.988 2.18e-19     E-MTAB-1333            yellow
   SNRPD1   negative  -0.875 1.91e-04     E-GEOD-19102    lightsteelblue1
   SNRPD1   negative   0.954 6.08e-13     E-MTAB-1333             brown
   somi-1   positive   0.917 2.74e-05     E-MEXP-1810             plum1
   somi-1   positive   0.993 1.50e-10    EGEOD54853-CEL          yellow
   spe-38   negative  -0.976 6.37e-08     E-GEOD-43864        darkorange
   spe-38   negative   0.992 2.98e-10     E-GEOD-43864        lightgreen
   SQSTM1   negative   0.959 1.07e-14     E-GEOD-34773             black
   SQSTM1   negative   0.924 3.74e-04     E-GEOD-38062       yellowgreen
   SQSTM1   positive   0.885 1.29e-04     E-MEXP-1810          lightcyan
    sss-2   positive  -0.970 3.11e-11     E-GEOD-42192              blue
    sss-2   positive   0.990 5.42e-20     E-MTAB-1333            yellow
  T14G11.1  negative  -0.955 2.26e-04     E-GEOD-57739        darkorange
  T14G11.1  negative  -0.909 7.81e-10     E-MTAB-1333             black
  T19D12.2  negative   0.979 6.61e-04     E-GEOD-51502         turquoise
  T19D12.2  positive  -0.892 9.42e-05     E-MEXP-1810          royalblue
   T22B3.3  negative   0.998 3.30e-08     E-GEOD-57739         turquoise
   T22B3.3  positive   0.989 1.42e-19     E-MTAB-1333            yellow
  T28B11.1  positive  -0.928 1.39e-05     E-MEXP-1810             brown
  T28B11.1  negative   0.964 3.65e-14     E-MTAB-1333              blue
  T28H11.7  positive  -0.981 8.69e-13     E-GEOD-42192              blue
  T28H11.7  positive   0.987 4.02e-19     E-MTAB-1333            yellow
    TGIF2   negative   0.964 7.01e-06     E-GEOD-32339              pink
    TGIF2   positive   0.883 1.08e-08     E-MTAB-1333             black
   TMEM70   positive  -0.913 8.24e-11     E-GEOD-34773          darkgrey
   TMEM70   negative   0.952 1.87e-06     E-MEXP-1810             brown
    TNNI2   positive   0.905 5.22e-05     E-MEXP-1810             plum1
    TNNI2   positive   0.870 2.34e-04     E-MEXP-1810             plum1
    TNNI2   positive   0.992 3.43e-10    EGEOD54853-CEL           brown
   TOMM70   positive  -0.917 2.70e-05     E-GEOD-19102       darkmagenta
   TOMM70   positive   0.879 1.65e-04     E-GEOD-19102          deeppink
    TUBG1   negative   0.948 1.03e-04     E-GEOD-38062             plum1
    TUBG1   positive   0.987 1.43e-12     E-GEOD-66236         turquoise
    UBE2E1  negative  -0.989 7.37e-19     E-GEOD-30505              blue
    UBE2E1  negative  -0.993 8.90e-09     E-GEOD-32339              blue
    UGT3A1  positive  -0.979 1.55e-12     E-GEOD-42192         turquoise
    UGT3A1  positive   0.935 6.68e-04     E-GEOD-57739           sienna3
      UTY   negative   0.986 2.97e-04     E-GEOD-51502         turquoise
      UTY   positive   0.985 6.35e-09    EGEOD54853-CEL          yellow
    VAMP3   negative  -0.912 9.32e-11     E-GEOD-34773       greenyellow
    VAMP3   negative  -0.885 1.96e-09     E-GEOD-34773               tan
     VRK2   positive  -0.972 1.70e-11     E-GEOD-42192              blue
     VRK2   negative  -0.935 8.29e-06     E-GEOD-43864        darkorange
     VRK2   negative   0.996 1.77e-07     E-GEOD-57739         turquoise
     VRK2   negative   0.993 9.81e-07     E-GEOD-57739         turquoise
     VRK2   negative   0.982 2.26e-17     E-MTAB-1333          turquoise
```

```
      VRK2     positive   0.990 3.87e-20    E-MTAB-1333           yellow
      VRK2     positive   0.989 1.44e-19    E-MTAB-1333           yellow
      VRK2     positive   0.986 1.55e-18    E-MTAB-1333           yellow
   W03G11.4    positive   0.993 1.43e-10    E-GEOD-43864          yellow
   W03G11.4    positive   0.990 8.23e-10    E-GEOD-43864          yellow
   W03G11.4    positive   0.998 3.84e-06    E-GEOD-9246         turquoise
   W03G11.4    positive   0.990 6.47e-10   EGEOD54853-CEL         yellow
     WDR47     negative  -0.993 6.36e-05    E-GEOD-51502          black
     WDR47     positive   0.947 2.94e-06    E-MEXP-1810        darkmagenta
     WIPF1     negative   0.954 1.55e-06    E-GEOD-19102           blue
     WIPF1     negative   0.919 3.60e-11    E-GEOD-34773         magenta
     WIPF1     negative   0.962 6.73e-14    E-MTAB-1333            blue
   Y42H9AR.4   negative   0.942 2.15e-11    E-GEOD-30505          black
   Y42H9AR.4   negative  -0.996 1.78e-09    E-GEOD-32339           blue
     ZC3H15    negative   0.982 1.56e-08    E-GEOD-43864      midnightblue
     ZC3H15    negative  -0.978 7.07e-25    E-GEOD-55272          yellow
     ZFP36     negative  -0.994 4.29e-09    E-GEOD-32339           blue
     ZFP36     negative  -0.994 4.60e-09    E-GEOD-32339           blue
     ZFP36     positive   0.971 1.33e-05    E-GEOD-8696            red
```

Supplement Table 3: Hub genes found by quantile normalization with an export of 60 genes per health-associated module. *67 genes were identified as hub genes with the same WGCNA cross-species consensus protocol when a quantile normalization was performed on the expression data. Only 13 genes were found in a cross-species consensus when 30 genes were exported.*

```
ABCD4        worm,human
ABCE1        mouse,worm
AKR7L        mouse,rat
AL669918.1   mouse,worm
ANXA2        mouse,human
ATF2         mouse,worm
BAP1         mouse,worm
BRD8         mouse,worm
C4BPA        mouse,rat
CAPN7        worm,mouse
CASP1        mouse,rat
CEBPB        worm,mouse
DAB2         mouse,worm
DIMT1        mouse,worm
EIF5A        mouse,worm
ELOA         mouse,rat
EXOC6        mouse,worm
FBXO32       mouse,human
FKBP9        mouse,rat
GBP2         mouse,rat
GDF15        mouse,human
GPSM3        mouse,rat
GRASP        mouse,worm
HIST1H2BA    mouse,worm
HSPB3        mouse,human
IDH3A        rat,worm
ILF2         mouse,human
ITM2A        worm,mouse
LUZP1        rat,worm
MAP2K5       worm,human
```

MED17	worm,mouse
MFN1	mouse,rat
MRPL12	mouse,worm
MRPL51	mouse,worm
NAA25	mouse,worm
NFYA	worm,mouse
NKG7	mouse,rat
OGA	rat,human
OR2Y1	mouse,rat
PDIA4	mouse,rat
PIPOX	mouse,worm
PLD4	worm,mouse
PPP1CA	worm,human
PPP3CB	mouse,worm
PRKCZ	mouse,worm
PRPF38A	mouse,worm
PSMB9	mouse,rat
PSMD12	mouse,rat
RAB8B	mouse,worm
RAMP1	human,rat
RMI1	mouse,worm
RMND5A	worm,mouse
RPL13A	mouse,worm
RTN2	mouse,human
SCLY	mouse,rat
SCN1B	human,rat
SDCBP	mouse,worm
SDF2	mouse,worm
SERPINF1	mouse,rat
SKP1	rat,worm
SQOR	worm,mouse
SQSTM1	mouse,worm
SRD5A2	mouse,worm
SSRP1	mouse,worm
TRUB2	mouse,worm
UBC	mouse,worm
UBE4B	worm,mouse

***Supplement Table 4: Genes in interactions found by quantile normalization with an export of 60 genes per health-associated module.** 44 genes were identified as hub genes with the same WGCNA cross-species consensus protocol when a quantile normalization was performed on the expression data. Only 10 genes were found in a cross-species consensus when 30 genes were exported per module. This was not found to be significant in a permutation test.*

AASDHPPT	mouse,worm
ABCE1	mouse,worm
ACOT9	mouse,worm
ACVR1	worm,mouse
AL669918.1	mouse,worm
ANTKMT	worm,mouse
BAP1	mouse,worm
BCS1L	rat,worm
CAMK2B	human,rat
CEBPB	worm,mouse
CETN2	worm,rat
CUL1	mouse,worm

DAB2	mouse,worm
DAG1	mouse,worm
DBH	mouse,worm
EDF1	mouse,worm
FAAH	mouse,worm
FRA10AC1	mouse,worm
GTPBP10	mouse,worm
ITGA3	worm,mouse
KCNK6	mouse,worm
LMBR1L	worm,mouse
LONRF1	mouse,worm
MED11	mouse,worm
MINDY2	worm,mouse
MRPL19	mouse,worm
NF2	worm,mouse
OXSM	mouse,worm
PAXIP1	mouse,worm
PFDN1	worm,mouse
PPP1CA	worm,human
PRPF38A	mouse,worm
RFK	worm,mouse
RMND5A	mouse,worm
RNF7	worm,mouse
SLC35B1	worm,human
SLC38A10	worm,mouse
SOX2	mouse,worm
SSRP1	mouse,worm
STAT1	mouse,worm
TIMP3	mouse,worm
VPS11	mouse,worm
ILF2	mouse,human,worm