Representative term (GO, INTERPRO, KEGG PATHWAY)	**Enrichment score**	***P* value**
Downregulated in *daf-2(e1370)*		
GO:0030529~ribonucleoprotein complex	24.30	8.32E-34
GO:0009792~embryonic development ending in birth or egg hatching	15.26	3.09E-17
GO:0018988~molting cycle, protein-based cuticle	5.57	2.65E-06
GO:0045735~nutrient reservoir activity	5.07	3.47E-08
GO:0010259~multicellular organismal aging	4.99	1.03E-05
GO:0070001~aspartic-type peptidase activity	2.76	3.00E-05
GO:0008233~peptidase activity	2.39	1.71E-03
GO:0040019~positive regulation of embryonic development	1.82	1.89E-04
GO:0051082~unfolded protein binding	1.64	2.23E-02
GO:0043039~tRNA aminoacylation	1.44	2.89E-02
Upregulated in *daf-2(e1370)*		
GO:0005739~mitochondrion	20.70	5.93E-25
GO:0006091~generation of precursor metabolites and energy	13.16	8.43E-24
GO:0006006~glucose metabolic process	7.60	6.25E-11
GO:0022900~electron transport chain	7.60	4.11E-08
IPR002198:Short-chain dehydrogenase/reductase SDR	6.40	2.96E-12
GO:0005509~calcium ion binding	3.45	2.52E-08
KEGG_PATHWAY cel00071:Fatty acid metabolism	2.93	9.07E-05
GO:0006572~tyrosine catabolic process	2.63	2.89E-05
GO:0045927~positive regulation of growth	2.62	5.18E-04
GO:0003779~actin binding, SP_PIR_KEYWORDS muscle proteins	2.46	9.01E-06
GO:0030239~myofibril assembly	2.06	2.69E-03
GO:0002119~nematode larval development	1.89	5.73E-03
KEGG_PATHWAY cel00480:Glutathione metabolism	1.76	3.32E-03
GO:0006098~pentose-phosphate shunt	1.62	8.38E-03
GO:0005529~sugar binding, SP_PIR_KEYWORDS Lectin, IPR001079 Galectin carbohydrate recognition site	1.51	2.43E-04
GO:0008340~determination of adult life span	1.51	3.09E-02
IPR002328:Alcohol dehydrogenase, zinc-containing, conserved site	1.36	3.96E-03
Upregulated in DR		
GO:0002119~nematode larval development	7.88	2.12E-10
GO:0016459~myosin complex	5.22	5.42E-10
GO:0005839~proteasome core complex	4.00	4.45E-08
GO:0048581~negative regulation of post-embryonic development	2.87	7.05E-06
GO:0008380~RNA splicing, KEGG PATHWAY cel03040:Spliceosome	2.64	1.37E-04
GO:0055114~oxidation reduction, GO:0045333~cellular respiration	2.36	5.69E-05
GO:0045111~intermediate filament cytoskeleton	2.15	1.57E-03
GO:0051536~iron-sulfur cluster binding	2.02	8.95E-03
GO:0000166~nucleotide binding	1.97	3.22E-04
GO:0042625~ATPase activity, coupled to transmembrane movement of ions	1.85	8.00E-04

GO:0008340~determination of adult life span	1.71	1.91E-02
GO:0018988~molting cycle, protein-based cuticle	1.67	2.11E-02
Downregulated in DR		
GO:0005840~ribosome	26.35	1.23E-49
GO:0010259~multicellular organismal aging	6.20	6.21E-07
GO:0018988~molting cycle, protein-based cuticle	4.65	2.19E-05
GO:0045735~nutrient reservoir activity, IPR015816: Vitellinogen	3.23	1.24E-06
GO:0019843~rRNA binding	2.99	4.09E-04
GO:0055114~oxidation reduction	2.71	2.20E-04
GO:0046394~carboxylic acid biosynthetic process	2.33	9.79E-04
GO:0070001~aspartic-type peptidase activity	2.26	2.60E-07
GO:0019842~vitamin binding, GO:0070279~vitamin B6 binding	2.15	1.30E-02
IPR002198:Short-chain dehydrogenase/reductase SDR	2.10	1.57E-04
GO:0005783~endoplasmic reticulum, INTERPRO IPR006662:Thioredoxin-like subdomain	1.83	1.16E-03
GO:0045927~positive regulation of growth	1.68	1.85E-02
KEGG PATHWAY cel00640:Propanoate metabolism	1.43	3.30E-02

Supplemental table 1: Gene ontology information from Database for Annotation, Visualization and Integrated Discovery (DAVID) Bioinformatics Resource 6.7 (http://david.abcc.ncifcrf.gov/) of proteins that are respectively down- or up-regulated in *daf-2* or diet-restricted nematodes, respectively. Reported *P* value is the modified Fisher Exact *P* value or EASE score. Only clusters with Enrichment score > 1.3 are shown.