Table S1. Effect of *skn-1* RNAi on Genes Up-Regulated by Oxidative Stress[a]

Sequence Name	Gene Name[b]	Gene Symbol	Fold Δ[c]	*P*[d]	% *skn-1*[e]
Antioxidant Response					
Y54G11A.5	catalase 2, peroxisomal	*ctl-2*	2.7	0.001	80*
Y54G11A.13	catalase 3	*ctl-3*	2.8	0.001	0
C15F1.7	superoxide dismutase 1	*sod-1*	1.4	0.007	100*
ZK637.10	thioredoxin reductase 2	*trxr-2*	1.4	0.017	-42
R03G5.5	*glutathione peroxidase*		3.0	0.000	68*
F26E4.12	*glutathione peroxidase*		1.7	0.004	100*
C46F11.2	*pyridine nucleotide-disulphide oxidoreductase*		1.2	0.021	76
Glutathione S-transferase					
R107.7	glutathione S-transferase 1	*gst-1*	1.7	0.001	53
K08F4.7	glutathione S-transferase 4	*gst-4*	12.4	0.000	79*
R03D7.6	glutathione S-transferase 5	*gst-5*	5.4	0.027	60
F11G11.3	glutathione S-transferase 6	*gst-6*	4.8	0.004	41
R05F9.5	glutathione S-transferase 9	*gst-9*	9.2	0.009	64
Y45G12C.2	glutathione S-transferase 10	*gst-10*	3.0	0.000	100*
Y45G12C.2	glutathione S-transferase 10	*gst-10*	2.9	0.000	100*
F37B1.2	glutathione S-transferase 12	*gst-12*	9.2	0.000	100*
T26C5.1	glutathione S-transferase 13	*gst-13*	4.9	0.001	100*
F37B1.3	glutathione S-transferase 14	*gst-14*	15.9	0.000	85*
F37B1.4	glutathione S-transferase 15	*gst-15*	6.4	0.025	45
F37B1.5	glutathione S-transferase 16	*gst-16*	3.7	0.002	61
F21H7.1	glutathione S-transferase 22	*gst-22*	3.0	0.019	4
Y53F4B.32	glutathione S-transferase 29	*gst-29*	2.4	0.027	69
ZK546.11	glutathione S-transferase 30	*gst-30*	20.6	0.000	20
Y53F4B.35	glutathione S-transferase 31	*gst-31*	3.9	0.006	72
Y53F4B.37	glutathione S-transferase 32	*gst-32*	18.9	0.001	99*
F35E8.8	glutathione S-transferase 38	*gst-38*	3.9	0.000	100*
Y53F4B.33	glutathione S-transferase 39	*gst-39*	6.1	0.000	69*
K10F12.4	*glutathione S-transferase*		1.7	0.028	-100
Heat Shock Response					
T27E4.8	heat shock protein 16.1	*hsp-16.1*	5.2	0.019	-36
Y46H3A.3	heat shock protein 16.2	*hsp-16.2*	3.7	0.001	-100
Y46H3A.2	heat shock protein 16.41	*hsp-16.41*	4.7	0.010	-100
T27E4.9	heat shock protein 16.49	*hsp-16.49*	5.7	0.000	-15
F08H9.3	*Unknown*		4.0	0.002	-53
F08H9.4	*Unknown*		3.3	0.022	38
Electron Transport					
Y54G11A.13	catalase 3	*ctl-3*	2.8	0.001	0
K09A11.2	cytochrome P450 family 14A1	*cyp-14A1*	4.6	0.017	-80
K09A11.3	cytochrome P450 family 14A2	*cyp-14A2*	2.4	0.007	71*
R04D3.1	cytochrome P450 family 14A4	*cyp-14A4*	13.8	0.003	-20
Y5H2B.5	cytochrome P450 family 32B1	*cyp-32B1*	3.2	0.020	82
R08F11.3	cytochrome P450 family 33C8	*cyp-33C8*	41.9	0.004	56
T09H2.1	cytochrome P450 family 34A4	*cyp-34A4*	6.3	0.011	-33
B0213.15	cytochrome P450 family 34A9	*cyp-34A9*	3.1	0.018	75
F01D5.9	cytochrome P450 family 37A1	*cyp-37A1*	1.9	0.006	95
F28G4.1	cytochrome P450 family 37B1	*cyp-37B1*	3.5	0.001	77
Y80D3A.5	cytochrome P450 family 42A1	*cyp-42A1*	3.9	0.006	43

E03E2.1	cytochrome P450 family 43A1	*cyp-43A1*	5.3	0.017	72
K08C7.2	flavin-containing monoxygenase family 1	*fmo-1*	3.5	0.023	28
F53F4.5	flavin-containing monoxygenase family 4	*fmo-4*	1.5	0.011	100
C05E4.9	GEX Interacting protein 7	*gei-7*	4.0	0.028	83
Y34D9A.6	glutaredoxin 10	*glrx-10*	2.2	0.001	78*
K10B3.9	mitochondrial ATPase inhibitor family 1	*mai-1*	4.0	0.028	58
C15H9.1	nicotinamide nucleotide transhydrogenase 1	*nnt-1*	2.9	0.001	18
B0222.9	*xanthine dehydrogenase*		8.0	0.001	73*
F55B11.1	*xanthine dehydrogenase*		1.9	0.019	100
F56D5.3	*NADH:flavin oxidoreductase/12-oxophytodienoate reductase*		15.5	0.000	93*
F17A9.4	*NADH:flavin oxidoreductase/12-oxophytodienoate reductase*		4.9	0.000	85*
W06H8.2	*NADH:flavin oxidoreductase/12-oxophytodienoate reductase*		57.3	0.007	51
W01B11.6	*Thioredoxin*		4.5	0.001	-54
C35B1.5	*thioredoxin, nucleoredoxin and related proteins*		2.4	0.000	100*
F28A10.6	*medium-chain acyl-CoA dehydrogenase*		1.5	0.004	23
F58F9.7	*pristanoyl-CoA/acyl-CoA oxidase*		2.6	0.007	51
F41E6.5	*glycolate oxidase*		3.2	0.004	36
M153.1	*pyrroline-5-carboxylate reductase*		3.6	0.002	39
C15B12.1	*FAD-dependent oxidoreductase*		1.9	0.030	94
C46F11.2	*pyridine nucleotide-disulphide oxidoreductase*		1.2	0.021	76
F47B8.4	*glutaredoxin-related protein*		16.3	0.004	53
C24G6.6	*flavin-containing amine oxidase*		2.6	0.028	60
C49G7.10	*Unknown*		39.1	0.034	68
Neuropeptide Signaling					
Y48D7A.2	FMRF-like peptide 18	*flp-18*	2.3	0.002	17
T23E7.4	neuropeptide like protein 6	*nlp-6*	1.2	0.028	-93
F18E9.2	neuropeptide like protein 7	*nlp-7*	1.2	0.025	100*
D1009.4	neuropeptide like protein 14	*nlp-14*	2.2	0.018	2
T13A10.5	neuropeptide like protein 16	*nlp-16*	2.8	0.002	59
T03D8.3	seven B two homolog 1	*sbt-1*	1.5	0.032	-98

[a] This table shows subsets of up-regulated genes involved in selected functional classes. Significant genes and fold change were determined by SAM. Functional classification was determined by DAVID.

[b] The predicted gene titles for unknown genes are shown in Italics.

[c] Fold change under oxidative stress.

[d] Determined by T-test.

[e] % inhibition effect of *skn-1* knockdown.
Negative value means *skn-1* RNAi further increases the expression compared to oxidative-stressed control.

Asterisk (*) indicates the % effect of *skn-1* knockdown is statistically significant (SAM).

Table S2. Effect of *skn-1* RNAi on Genes Down-Regulated by Oxidative Stress[a]

Sequence Name	Gene Name[b]	Gene Symbol	Fold Δ[c]	*P*[d]	% *skn-1*[e]
Homeostasis					
B0495.4	NA(+)/H(+) exchanger 2	*nhx-2*	0.3	0.000	31*
T17E9.2	N-myristoyl transferase homolog 1	*nmt-1*	0.7	0.016	100*
K04E7.2	oligopeptide transporter 2	*opt-2*	0.1	0.004	10
C54H2.5	surfeit homolog 4	*sft-4*	0.6	0.016	52*
Y66H1B.4	sphingosine phosphate lyase 1	*spl-1*	0.5	0.015	43*
F55A11.2	syntaxin 3	*syn-3*	0.9	0.005	100*
C16A11.4	*PHD Zn-finger proteins*[6]		0.6	0.000	73*
H41C03.1	*Phosphatidylinositol transfer protein SEC14 and related proteins*		0.4	0.008	20
F54C9.6	*AAA+-type ATPase*		0.8	0.004	5
Y38E10A.24	*unknown*		0.7	0.001	-21
F58G1.4	*unknown*		0.2	0.001	-7
C24G6.8	*unknown*		0.8	0.016	25
Post-embryonic development					
C53B4.7	BT (bacillus thuringiensis) toxin resistant 1	*bre-1*	0.7	0.008	2
W05B2.5	collagen 93	*col-93*	0.6	0.019	-19
W05B2.1	collagen 94	*col-94*	0.6	0.014	-43
W05B2.1	collagen 94	*col-94*	0.6	0.019	-30
F30B5.1	dumpy: shorter than wild-type 13	*dpy-13*	0.5	0.012	-54
F32D8.6	endomitotic oocytes 1	*emo-1*	0.7	0.018	-29
T08B2.9	phenylalanyl tRNA synthetase 1	*frs-1*	0.8	0.020	22
T21G5.3	germ-line helicase 1	*glh-1*	0.5	0.000	20
T21G5.3	germ-line helicase 1	*glh-1*	0.6	0.002	15
T09A5.10	abnormal cell lineage 5	*lin-5*	0.7	0.015	2
C08B11.4	nose resistant to fluoxetine 6	*nrf-6*	0.6	0.014	22
R12C12.2	associated with RAN (nuclear import/export) function 5	*ran-5*	0.8	0.009	94*
W02B12.2	SR protein (splicing factor) 2	*rsp-2*	0.8	0.012	-34
F23H12.4	squat 3	*sqt-3*	0.6	0.011	-41
F57B1.2	SUN (S. pombe sad1/Ce-UNC-84) domain protein 1	*sun-1*	0.7	0.003	72*
R06C7.5	*adenylosuccinate lyase*		0.6	0.002	37*
F28C6.2	*transcription factor AP-2*		0.7	0.020	39
Y19D10A.4	*unknown*		0.5	0.002	-41
F33H1.3	*unknown*		0.8	0.014	-35
F42A8.1	*unknown*		0.4	0.000	57*
Reproduction					
C53B4.7	BT (bacillus thuringiensis) toxin resistant 1	*bre-1*	0.7	0.008	2
T05G5.3	cyclin-dependent kinase family 1	*cdk-1*	0.7	0.005	71*
F56D1.7	human DAZ (deleted in azoospermia) homolog 1	*daz-1*	0.7	0.001	14
B0244.8	egg sterile (unfertilizable) 1	*egg-1*	0.7	0.005	20
R08D7.3	eukaryotic initiation factor 3D	*eif-3.D*	0.7	0.001	7
F32D8.6	endomitotic oocytes 1	*emo-1*	0.7	0.018	-29
ZK809.4	equilibrative nucleoside transporter 1	*ent-1*	0.6	0.009	63*
Y39A1A.19	favin-containing monooxygenase family 3	*fmo-3*	0.3	0.000	9
T08B2.9	phenylalanyl tRNA synthetase 1	*frs-1*	0.8	0.020	22
T23G11.3	defective in germ line development 1	*gld-1*	0.8	0.018	49
T21G5.3	germ-line helicase 1	*glh-1*	0.5	0.000	20
C34E10.2	gro-1 operon gene 2	*gop-2*	0.8	0.009	60*
K03A1.6	histone 38	*his-38*	0.6	0.011	-18

K08E7.3	lethal 99	*let-99*	0.7	0.000	-4
B0495.4	NA(+)/H(+) exchanger 2	*nhx-2*	0.3	0.000	31*
T17E9.2	N-myristoyl transferase homolog 1	*nmt-1*	0.7	0.016	100*
C32E8.8	patched related family 2	*ptr-2*	0.7	0.004	50*
K01G5.4	associated with RAN (nuclear import/export) function 1	*ran-1*	0.8	0.004	-41
F23F12.6	proteasome regulatory particle, ATPase-like 3	*rpt-3*	0.8	0.004	62*
W02B12.3	SR protein (splicing factor) 1	*rsp-1*	0.7	0.018	100*
W02B12.2	SR protein (splicing factor) 2	*rsp-2*	0.8	0.012	-34
F10G7.4	yeast SCC (mitotic condensin subunit) homolog 1	*scc-1*	0.8	0.015	100*
Y41D4B.12	SET (trithorax/polycomb) domain containing 23	*set-23*	0.3	0.003	-22
C54H2.5	surfeit homolog 4	*sft-4*	0.6	0.016	52*
F55A11.2	syntaxin 3	*syn-3*	0.9	0.005	100*
C14B1.4	temporarily assigned gene name 125	*tag-125*	0.8	0.009	100*
F29B9.6	ubiquitin-conjugating enzyme 9	*ubc-9*	0.7	0.016	72*
F19B6.2	ubiquitin fusion degradation (yeast UFD homolog) 1	*ufd-1*	0.8	0.015	-8
R10E11.8	vacuolar H ATPase 1	*vha-1*	0.8	0.010	-100
F46F11.5	vacuolar H ATPase 10	*vha-10*	0.6	0.004	-30
Y49A3A.2	vacuolar H ATPase 13	*vha-13*	0.6	0.011	-42
F49C12.13	vacuolar H ATPase 17	*vha-17*	0.8	0.012	-67
C29E4.8	*adenylate kinase*		0.6	0.010	5
F44F4.2	*alternative splicing factor SRp55/B52/SRp75 (RRM superfamily)*		0.8	0.005	5
C18E9.6	*translocase of outer mitochondrial membrane complex, subunit TOM40*		0.6	0.008	11
K08D12.3	*E3 ubiquitin ligase interacting with arginine methyltransferase*		0.7	0.005	-23
Y54E10BR.5	*signal peptidase I*		0.8	0.018	72
F43G9.5	*mRNA cleavage factor I subunit*		0.6	0.001	19
F55A12.8	*predicted P-loop ATPase fused to an acetyltransferase*		0.7	0.005	32
H41C03.1	*phosphatidylinositol transfer protein SEC14 and related proteins*		0.4	0.008	20
R06C7.5	*adenylosuccinate lyase*		0.6	0.002	37*
C06E7.1	*S-adenosylmethionine synthetase*		0.6	0.009	41
Y105C5B.12	*unknown*		0.6	0.007	16
F32D8.5	*unknown*		0.7	0.004	32
C53H9.2	*unknown*		0.5	0.013	5
C50E3.5	*unknown*		0.7	0.017	96*
F37B12.1	*unknown*		0.3	0.006	34
W03F9.2	*unknown*		0.7	0.005	-5
C09H10.10	*unknown*		0.6	0.001	93*
F33H1.3	*unknown*		0.8	0.014	-35
Y110A7A.19	*unknown*		0.7	0.018	-7

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[a] This table shows subsets of down-regulated genes involved in selected functional classes. Significant genes and fold change were determined by SAM. Functional classification was determined by DAVID.

[b] The predicted gene titles for unknown genes are shown in Italics.

[c] Fold change under oxidative stress.

[d] Determined by T-test.

[e] % inhibition effect of *skn-1* knockdown.
Negative value means *skn-1* RNAi further decreases the expression compared to oxidative-stressed control.

Asterisk (*) indicates the % effect of *skn-1* knockdown is statistically significant (SAM).

Table S3. Comparison of expression levels of selected genes between microarray and quantitaive RT-PCR

	Microarray[a]			qRT-PCR[b]			qRT-PCR[b]		
Gene Name	**C**	**O**	**SO**	**C**	**O**	**SO**	**C**	**P**	**SP**
gst-4	365.45	4528.35	1240.40	1.00	220.69	7.26	1.00	6.00	0.54
hsp-16.2	15.58	58.28	221.10	1.00	162.43	24.07	1.00	1.99	1.84
nlp-7	133.18	154.20	122.30	1.00	22.37	2.26	1.00	1.60	1.56
cup-4	65.85	101.15	61.53	1.00	4.55	1.87	1.00	1.36	1.99
nhx-2	113.00	28.38	54.33	1.00	0.03	0.36	1.00	1.03	0.99
ent-1	1058.33	681.50	918.23	1.00	0.59	2.23	1.00	0.60	0.92

[a] Average signal intensities of each gene in each group.

[b] Relative expression compared to C.

C: unstressed control.

O: worms stressed with 6 hours of hyperbaric oxygen exposure

SO: worms treated with *skn-1* RNAi and stressed with 6 hours of hyperbaric oxygen exposure.

P: worms stressed with 6 hours of 20 mM paraquat exposure.

SP: worms treated with *skn-1* RNAi and stressed with 6 hours of 20 mM paraquat exposure.

Table S4. Overlaps Between Genes Regulated by Oxidative Stress and Aging

Sequence Name	Gene Name	Gene Symbol	Biological Function
Up-regulated genes by oxidative stress			
C05E4.9	GEX interacting protein 7	*gei-7*	metabolism
C10H11.3	UDP-glucuronosyltransferase 25	*ugt-25*	metabolism
F10D2.11	UDP-glucuronosyltransferase 41	*ugt-41*	metabolism
C45B11.3	dehydrogenases, short chain 18	*dhs-18*	metabolism
K01C8.1	*threonine/serine dehydratases*		metabolism
R04B5.5	*sorbitol dehydogenase*		metabolism
Y48A6B.9	*Zn2+ binding dehydrogenase*		metabolism
C17C3.1	*acyl-CoA thioesterase*		acyl-CoA metabolism
C12C8.2	*cystathionine beta-lyases/ cystathionine gamma-lyases*		amino acid metabolism
Y22F5A.5	lysozyme 2	*lys-2*	carbohydrate metabolism
C02A12.4	lysozyme 7	*lys-7*	carbohydrate metabolism
C17G10.5	lysozyme 8	*lys-8*	carbohydrate metabolism
C25A8.4	*chitinase*		carbohydrate metabolism
C50F7.10	*beta-glucosidase,*		carbohydrate metabolism
K10B3.6	*predicted starch-binding protein*		carbohydrate metabolism
R11F4.1	*ribulose kinase and related carbohydrate kinases*		carbohydrate metabolism
F01G10.2	enoyl-CoA hydratase 8	*ech-8*	fatty acid metabolism
F01G10.3	enoyl-CoA hydratase 9	*ech-9*	fatty acid metabolism
F58F9.7	*pristanoyl-CoA/acyl-CoA oxidase*		fatty acid metabolism
H17B01.3	lipase related 14	*lips-14*	lipid catabolism
W02A2.1	fatty acid desaturase 2	*fat-2*	lipid metabolism
W06D4.1	homogentisate oxidase 1	*hgo-1*	L-phenylalanine catabolism
ZK1058.6	nitrilase 1	*nit-1*	nitrogen compound metabolism
K02D7.1	*purine nucleoside phosphorylase*		nucleic acid metabolism
F43E2.5	*peptide methionine sulfoxide reductase*		protein metabolism
C28C12.5	saposin-like protein family 8	*spp-8*	growth
C37A5.8	FIP related 24	*fipr-24*	growth
C49G7.4	pharyngeal gland toxin-related 3	*phat-3*	growth
F40E10.3	calsequestrin 1	*csq-1*	growth
K02E7.9	BTB domain protein 10	*btb-10*	growth
R09B5.9	caenacin 4	*cnc-4*	growth
R06A4.6	SKN-1 dependent zygotic transcript 26	*sdz-26*	development
T04D3.2	SKN-1 dependent zygotic transcript 30	*sdz-30*	development
F37B4.7	folate transporter family 2	*folt-2*	transport
R07E3.4	*mitochondrial ADP/ATP carrier proteins*		transport
M110.1	collagen 76	*col-76*	phosphate transport
M195.1	collagen 77	*col-77*	phosphate transport
F17E9.1	collagen 116	*col-116*	phosphate transport
C09H5.2	*Na+/K+ ATPase, alpha subunit*		cation transport
F55F3.3	*Na+/K+ ATPase, beta subunit*		cation transport
R08F11.3	cytochrome P450 family 33C8	*cyp-33C8*	electron transport
B0213.15	cytochrome P450 family 34A9	*cyp-34A9*	electron transport
C24G6.6	*flavin-containing amine oxidase*		electron transport
C37H5.9	nematode astacin protease 9	*nas-9*	proteolysis
C52E4.1	cysteine protease related 1	*cpr-1*	proteolysis

F44C4.3	cysteine protease related 4	*cpr-4*	proteolysis
T28H10.3	*asparaginyl peptidase*		proteolysis
F10D7.3	*glutaredoxin and related proteins*		cell redox homeostasis
W01B11.6	*thioredoxin*		cell redox homeostasis
ZC581.1	NEK like 2	*nekl-2*	body morphogenesis
B0286.3	*phosphoribosylamidoimidazole-succinocarboxamide synthase*		de novo' IMP biosynthesis
C02C2.3	coelomocyte uptake defective 7	*cup-4*	endocytosis
D1054.8	*reductase*		enterobactin biosynthetic process
T27E4.8	heat shock protein 16.1	*hsp-16.1*	heat shock response
T04H1.9	beta-tubulin	*tbb-6*	microtubule-based movement
B0213.4	neuropeptide-like protein	*nlp-29*	nematode larval development
C28H8.11	*tryptophan 2,3-deoxygenase*		oxidation reduction
ZK1251.2	insulin related 7	*ins-7*	physiological process
C54D10.1	cadmium responsive 2	*cdr-2*	
F49E11.10	SCP-like extracellular protein 2	*scl-2*	
W06B11.3	DAF-16/FOXO controlled, germline tumor affecting 11	*dct-11*	
K10D11.1	downstream of DAF-16 17	*dod-17*	
C24B9.9	downstream of DAF-16 3	*dod-3*	
T12B5.10	F-box A protein 60	*fbxa-60*	
C06H5.1	F-box A protein 156	*fbxa-156*	
F54D10.2	F-box B protein 24	*fbxb-24*	
K05F6.7	F-box B protein 54	*fbxb-54*	
F40F4.1	F-box B protein 71	*fbxb-71*	
C32B5.14	F-box C protein 18	*fbxc-18*	
R07C3.2	F-box C protein 36	*fbxc-36*	
K08F4.7	glutathione S-transferase 4	*gst-4*	
T26C5.1	glutathione S-transferase 13	*gst-13*	
F21H7.1	glutathione S-transferase 22	*gst-22*	
ZK1320.1	glutathione S-transferase keppa protein 1	*gstk-1*	
C45G7.3	invertebrate lysozyme 3	*ilys-3*	
K11D12.3	serpentine receptor, class R 4	*srr-4*	
F28D1.5	thaumatin family 2	*thn-2*	
F36A4.8	trans thyretin-related family domain 20	*ttr-20*	
T21F4.1	*arginase*		
Y48A6B.7	*cytosine deaminase FCY1 and related enzymes*		
C01B10.3	*inositol polyphosphate 5-phosphatase, type 1*		
C08F11.13	*integral membrane O-acyltransferase*		
ZK550.6	*peroxisomal phytanoyl-CoA hydroxylase*		
Y69E1A.5	*phosphatidylethanolamine binding protein*		
C42D4.1	*predicted alpha-helical protein*		
T24A6.7	*predicted riboflavin biosynthesis protein*		
F21A3.2	*purple acid phosphatase*		
H28G03.1	*RRM domain*		
F01D5.1	*screted surface protein*		
F01D5.2	*screted surface protein*		
F01D5.5	*screted surface protein*		
C35B1.5	*thioredoxin, nucleoredoxin and related proteins*		

F22B8.7	*uncharacterized Fe-S protein*		
B0281.3	*unknown*		
C07H4.1	*unknown*		
C17H12.8	*unknown*		
C18A11.1	*unknown*		
C32H11.4	*unknown*		
C33A12.4	*unknown*		
C34C6.7	*unknown*		
C39E9.8	*unknown*		
C49G7.5	*unknown*		
C50F7.5	*unknown*		
C53B7.3	*unknown*		
F08B12.4	*unknown*		
F09B12.3	*unknown*		
F13D12.3	*unknown*		
F15E6.4	*unknown*		
F17H10.2	*unknown*		
F23F1.7	*unknown*		
F29G9.1	*unknown*		
F41B4.3	*unknown*		
F43H9.4	*unknown*		
F47B10.9	*unknown*		
F47B8.8	*unknown*		
F48D6.4	*unknown*		
F52E1.5	*unknown*		
F53A9.6	*unknown*		
F54D5.4	*unknown*		
F55G11.4	*unknown*		
F55G11.8	*unknown*		
F58E10.7	*unknown*		
F59E11.7	*unknown*		
R10D12.9	*unknown*		
T11B7.2	*unknown*		
T12G3.1	*unknown*		
T24B8.5	*unknown*		
T28F4.5	*unknown*		
W01F3.2	*unknown*		
W04B5.1	*unknown*		
Y106G6H.10	*unknown*		
Y75B8A.23	*unknown*		
ZC395.5	*unknown*		
ZC410.5	*unknown*		

Down-regulated genes by oxidative stress

F11H8.3	collagen 8	*col-8*	phosphate transport
B0222.8	collagen 10	*col-10*	phosphate transport
F15H10.1	collagen 12	*col-12*	phosphate transport
F11G11.10	collagen 17	*col-17*	phosphate transport
F11G11.11	collagen 20	*col-20*	phosphate transport
ZC513.8	collagen 43	*col-43*	phosphate transport
W05G11.3	collagen 88	*col-88*	phosphate transport
W05B2.5	collagen 93	*col-93*	phosphate transport

F14F7.1	collagen 98	*col-98*	phosphate transport
C29F4.1	collagen 125	*col-125*	phosphate transport
B0222.6	collagen 144	*col-144*	phosphate transport
F15A2.1	collagen 184	*col-184*	phosphate transport
F56B3.1	collagen 103	*col-103*	phosphate transport
K02D7.3	collagen 101	*col-101*	phosphate transport
T10E10.1	collagen 168	*col-168*	phosphate transport
W03G11.1	collagen 181	*col-181*	phosphate transport
C12D12.2	glutamate transporter family 1	*glt-1*	dicarboxylic acid transport
Y49A3A.2	vacuolar H ATPase 13	*vha-13*	proton transport
W02D3.5	lipid binding protein 6	*lbp-6*	transport
F10C1.2	intermediate filament, B 1	*ifb-1*	body morphogenesis
F25B4.9	C-type lectin 1	*clec-1*	body morphogenesis
Y41E3.2	dumpy 4	*dyp-4*	body morphogenesis
F30B5.1	dumpy 13	*dyp-13*	body morphogenesis
F08H9.7	C-type lectin 56	*clec-56*	body morphogenesis
ZK858.3	C-type lectin 91	*clec-91*	body morphogenesis
F01F1.6	aldehyde dehydrogenase 9	*alh-9*	metabolism
F54D11.1	phosphoethanolamine methyltransferase	*pmt-2*	metabolism
Y76A2B.3	fatty acid CoA synthetase family 5	*acs-5*	metabolism
F47B10.1	*succinyl-CoA synthetase, beta subunit*		metabolism
K09H11.7	*p-nitropheny phosphatase*		metabolism
F22B8.6	*cystathionine beta-lyases/ cystathionine gamma-lyases*		amino acid metabolism
C16A3.10	*ornithine aminotransferase*		arginine metabolic process
F52A8.5	*glycine cleavage system H protein*		glycine catabolism
R12C12.1	*glycine dehydrogenase*		glycine metabolism
T05A12.2	trehalase 2	*tre-2*	trehalose metabolism
F11C1.3	*plasma membrane glycoprotein CD36 and related membrane receptors*		cell adhesion
T25C12.3	*unknown*		cell adhesion
W05E7.1	groundhog 3	*grd-3*	cell communication
F41E6.2	groundhog 5	*grd-5*	cell communication
R09B5.8	caenacin 3	*cnc-3*	development
F41E7.8	caenacin 8	*cnc-8*	development
C36A4.1	cytochrome P450 family 25A1	*cyp-25A1*	electron transport
C36A4.2	cytochrome P450 family 25A2	*cyp-25A2*	electron transport
C25F6.3	dihydropyrimidine dehydrogenase 1	*dpyd-1*	electron transport
C15H9.7	*L-kynurenine hydrolase*		NAD biosynthesis
K03A1.6	histone 38	*his-38*	nucleosome assembly
C06E7.1	*S-adenosylmethionine synthetase*		one-carbon compound metabolism
F32A5.3	*serine carboxypeptidases*		proteolysis
R07B1.4	glutathione S-transferase 36	*gst-36*	
T19D7.1	ligand-gated ion channel 32	*lgc-32*	
C44C1.5	*alpha/beta hydrolase*		
F32B5.1	*creatine kinases*		
T25B9.1	*glycine C-acetyltransferase/ 2-amino-3-ketobutyrate-CoA ligase*		
K09G1.1	*members of chemokine-like factor super familly and related proteins*		
ZK682.2	*permease of the major facilitator superfamily*		

C52G5.2	*unknown*
D1086.3	*unknown*
F16B4.4	*unknown*
F46F2.3	*unknown*
F55H12.4	*unknown*
K08H2.3	*unknown*
T03G11.6	*unknown*
T28D6.3	*unknown*
Y25C1A.6	*unknown*
ZK1307.1	*unknown*
ZK512.7	*unknown*

The predicted gene title for unknown gene is shown in Italic.

Table S5. Overlaps Between Genes Regulated by Oxidative Stress and *daf-16*

Sequence Name	Gene Name	Gene Symbol	Biological Function
Up-regulated genes by oxidative stress			
Y54G11A.5	catalase 2	*ctl-2*	response to oxidative stress
Y54G11A.6	catalase 3	*ctl-3*	response to oxidative stress
T27E4.8	heat shock protein 16.1	*hsp-16.1*	heat shock response
Y46H3A.3	heat shock protein 16.2	*hsp-16.2*	heat shock response
K11G9.6	metallothionein 1	*mtl-1*	response to heat
B0213.15	cytochrome P450 family 34A9	*cyp-34A9*	electron transport
C15H9.1	nicotinamide nucleotide transhydrogenase 1	*nnt-1*	electron transport
C24G6.6	*flavin-containing amine oxidase*		electron transport
F18E3.7	*D-aspartate oxidase*		electron transport
F47B8.4	*glutaredoxin-related protein*		electron transport
C46F4.2	fatty acid CoA synthetase family 17	*acs-17*	metabolism
C45B11.3	dehydrogenases, short chain 18	*dhs-18*	metabolism
C05E4.9	GEX interacting protein 7	*gei-7*	metabolism
ZK54.2	trehalose 6-phosphate synthase 1	*tps-1*	metabolism
F10D2.11	UDP-glucuronosyltransferase 41	*ugt-41*	metabolism
M02D8.4	*asparagine synthase*		metabolism
Y51A2B.1	*predicted riboflavin biosynthesis protein*		metabolism
C12C8.2	*cystathionine beta-lyases/cystathionine gamma-synthases*		amino acid metabolism
T21C12.2	4-hydroxyphenylpyruvate dioxygenase 1	*hpd-1*	aromatic amino acid metabolism
C37H5.2	*predicted hydrolase/acyltransferase*		aromatic compound metabolism
C02A12.4	lysozyme 7	*lys-7*	carbohydrate metabolism
C17G10.5	lysozyme 8	*lys-8*	carbohydrate metabolism
C50F7.10	*beta-glucosidase,* *lactase phlorizinhydrolase*		carbohydrate metabolism
W06D4.1	homogentisate oxidase 1	*hgo-1*	L-phenylalanine catabolism
C54C8.9	neuropeptide-like protein 39	*nlp-39*	development
F09F7.7	*2-Oxoglutarate- and iron-dependent dioxygenase-related proteins*		development
C09G12.8	cell death abnormality 10	*ced-10*	protein transport
C52E4.1	cysteine protease related 1	*cpr-1*	proteolysis
C30G7.1	histone H1 like 1	*hil-1*	nucleosome assembly
ZK1251.2	insulin related 7	*ins-7*	physiological process
F28D1.3	thaumatin family 1	*thn-1*	defense response
B0286.3	*phosphoribosylamidoimidazole-succinocarboxamide synthase*		de novo' IMP biosynthesis
W01B11.6	*thioredoxin*		cell redox homeostasis
Y56A3A.33	*3'-5' exonuclease*		DNA repair
T21D12.9	*membrane glycoprotein LIG-1*		regulation of cell growth
F53A9.1	*unknown*		proteolysis
ZC247.1	*unknown*		cell adhesion
W06B11.3	DAF-16/FOXO controlled, germline tumor affecting 11	*dct-11*	
C54D10.1	cadmium responsive 2	*cdr-2*	
F56D6.2	C-type lectin 67	*clec-67*	
K10D11.1	downstream of DAF-16 17	*dod-17*	

C24B9.9	downstream of DAF-16 3	*dod-3*	
F40F4.1	F-box B protein 71	*fbxb-71*	
K08F4.7	glutathione S-transferase 4	*gst-4*	
C45G7.3	invertebrate lysozyme 3	*ilys-3*	
F47H4.10	skp1 related 5	*skr-5*	
F28D1.5	thaumatin family 2	*thn-2*	
B0238.1	*carboxylesterase*		
C05C9.1	*BPI/LBP/CETP family protein*		
C08E8.4	*predicted riboflavin biosynthesis protein*		
F52H3.5	*TPR repeat-containing protein*		
T23B3.2	*stress responsive protein*		
ZK550.6	*peroxisomal phytanoyl-CoA hydroxylase*		
C31A11.5	*predicted acyltransferase*		
C18A11.1	*unknown*		
C34C6.7	*unknown*		
C40H1.5	*unknown*		
C50F7.5	*unknown*		
C53B7.3	*unknown*		
F08B12.4	*unknown*		
F09B12.3	*unknown*		
F09F7.6	*unknown*		
F15E6.4	*unknown*		
F21C10.10	*unknown*		
F32A5.4	*unknown*		
F36F2.2	*unknown*		
F43H9.4	*unknown*		
F45D3.4	*unknown*		
F48D6.4	*unknown*		
F54F7.3	*unknown*		
JC8.8	*unknown*		
K01A2.2	*unknown*		
T21C9.8	*unknown*		
T28F4.5	*unknown*		
W05H9.1	*unknown*		
Y43C5A.3	*unknown*		
Y51A2D.11	*unknown*		
Y51B9A.8	*unknown*		
ZC395.5	*unknown*		
ZC410.5	*unknown*		
C08B6.10	*unknown*		
C17H12.8	*unknown*		
C32H11.4	*unknown*		
F35E12.9	*unknown*		
F36F2.1	*unknown*		
F54E2.1	*unknown*		
F55G11.8	*unknown*		
T24B8.5	*unknown*		
Y106G6H.9	*unknown*		
Down-regulated genes by oxidative stress			
K04E7.2	oligopeptide transporter 2	*opt-2*	oligopeptide transport
T10E10.2	collagen 167	*col-167*	phosphate transport

C08B11.4	nose resistant to fluoxetine 6	*nrf-6*	transport
T23G5.2	*unknown*		transport
T03F6.1	quinoid dihyropteridine reductase 1	*qdpr-1*	metabolism
C16A3.10	*ornithine aminotransferase*		arginine metabolic process
C15H9.7	*L-kynurenine hydrolase*		NAD biosynthesis
C25F6.3	dihydropyrimidine dehydrogenase 1	*dpyd-1*	electron transport
F02H6.5	*unknown*		electron transport
EGAP2.3	intestinal acid phosphatase 1	*pho-1*	development
F58G1.4	*unknown*		osmoregulation
T16G12.1	*puromycin-sensitive aminopeptidase*		proteolysis
T25C12.3	*unknown*		cell adhesion
D1086.3	*unknown*		

The predicted gene title for unknown gene is shown in Italic.

Table S6. Overlaps Among Genes Regulated by Oxidative Stress, Aging, and *daf-16*

Sequence Name	Gene Name	Gene Symbol	Biological Function
Up-regulated genes by oxidative stress			
B0213.15	cytochrome P450 family 34A9	*cyp-34A9*	electron transport
C24G6.6	*flavin-containing amine oxidase*		electron transport
C45B11.3	dehydrogenases, short chain 18	*dhs-18*	metabolism
F10D2.11	UDP-glucuronosyltransferase 41	*ugt-41*	metabolism
C05E4.9	GEX interacting protein 7	*gei-7*	metabolism
C02A12.4	lysozyme 7	*lys-7*	carbohydrate metabolism
W06D4.1	homogentisate oxidase 1	*hgo-1*	L-phenylalanine catabolism
C17G10.5	lysozyme 8	*lys-8*	carbohydrate metabolism
C50F7.10	*beta-glucosidase,*		carbohydrate metabolism
C12C8.2	*cystathionine beta-lyases/ cystathionine gamma-lyases*		amino acid metabolism
C52E4.1	cysteine protease related 1	*cpr-1*	proteolysis
ZK1251.2	insulin related 7	*ins-7*	physiological process
T27E4.8	heat shock protein 16.1	*hsp-16.1*	heat shock response
B0286.3	*phosphoribosylamidoimidazole-succinocarboxamide synthase*		de novo' IMP biosynthesis
W01B11.6	*thioredoxin*		cell redox homeostasis
C54D10.1	cadmium responsive 2	*cdr-2*	
K08F4.7	glutathione S-transferase 4	*gst-4*	
F28D1.5	thaumatin family 2	*thn-2*	
C45G7.3	invertebrate lysozyme 3	*ilys-3*	
C24B9.9	dowmstream of DAF-16 3	*dod-3*	
K10D11.1	dowmstream of DAF-16 17	*dod-17*	
F40F4.1	F-box B protein 71	*fbxb-71*	
W06B11.3	DAF-16/FOXO controlled, germline tumor affecting 11	*dct-11*	
C17H12.8	*unknown*		
C18A11.1	*unknown*		
C32H11.4	*unknown*		
C34C6.7	*unknown*		
C50F7.5	*unknown*		
C53B7.3	*unknown*		
F08B12.4	*unknown*		
F09B12.3	*unknown*		
F15E6.4	*unknown*		
F43H9.4	*unknown*		
F48D6.4	*unknown*		
F55G11.8	*unknown*		
T24B8.5	*unknown*		
T28F4.5	*unknown*		
ZC395.5	*unknown*		
ZC410.5	*unknown*		
ZK550.6	*peroxisomal phytanoyl-CoA hydroxylase*		
Down-regulated genes by oxidative stress			
C25F6.3	dihydropyrimidine dehydrogenase 1	*dpyd-1*	electron transport
C15H9.7	*L-kynurenine hydrolase*		NAD biosynthesis
T25C12.3	*unknown*		cell adhesion

C16A3.10	*ornithine aminotransferase*	arginine metabolic process
D1086.3	*unknown*	

The predicted gene title for unknown gene is shown in Italic.

Table S7. Common Genes in Oxidative Stress Response in *C. elegans & D. melanogaster*

Sequence Name	Gene Name	Gene Symbol	Biological Function
F26E4.12	*glutathione peroxidase*		response to oxidative stress
C36A4.2	cytochrome P450 family 25A2	*cyp-25A2*	electron transport
Y5H2B.5	cytochrome P450 family 32B1	*cyp-32B1*	electron transport
F01D5.9	cytochrome P450 family 37A1	*cyp-37A1*	electron transport
F28G4.1	cytochrome P450 family 37B1	*cyp-37B1*	electron transport
C55A6.5	SKN-1 dependent zygotic transcript 8	*sdz-8*	metabolism
F35H8.6	UDP-glucuronosyltransferase 58	*ugt-58*	metabolism
F13G3.5	abnormal thermotaxis 7	*ttx-7*	metabolism
C55A6.6	*short chain-type dehydrogenase*		metabolism
F20G2.1	*short chain-type dehydrogenase*		metabolism
C37H5.2	*hydrolase/acyltransferase*		aromatic compound metabolism
C37H5.3	*hydrolase/acyltransferase*		aromatic compound metabolism
T21C12.2	4-hydroxyphenylpyruvate dioxygenase 1	*hpd-1*	aromatic amino acid family metabolism
F22A3.6	invertebrate lysozyme 5	*ilys-5*	development
T24H10.7	*Transcriptional activator of the JUN family*		development
C09C7.1	2 (zwei) Ig-domain protein 4	*zig-4*	neuron development
K04G2.1	eIF2 beta translation initiation factor 1	*iftb-1*	translational initiation
Y38C9A.2	Caenorhabditis GTP-binding protein 1	*cgp-1*	protein biosynthesis

The predicted gene title for unknown gene is shown in Italic.

Table S8. Primer sets used for quantitative RT-PCR

Gene Name	**Primer**	**Sequence**
ama-1	forward	5'-CGG AGC AGC CAG GAA CTT C-3'
	reverse	5'-AAC GGG AAA AAT CTT ATG AAT-3'
gst-4	forward	5'-GCT GAA GCC AAC GAC TCC AT-3'
	reverse	5'-GAC CGA ATT GTT CTC CAT CGA-3'
hsp-16.2	forward	5'-TGG TGC AGT TGC TTC GAA TC-3'
	reverse	5'-TTG AAC CGC TTC TTT CTT TGG-3'
nlp-7	forward	5'-GCG TTG CTC ATT GTG GTT CTC-3'
	reverse	5'-TCG GCT TGC TTC AAA TAC AAA G-3'
cup-4	forward	5'-CAC TTC ATC GGC CCC AAT T-3'
	reverse	5'-AAC TGA CAG TAA CTG CCA GC-3'
nhx-2	forward	5'-TGC TGC CAT GCG TCA GTA CT-3'
	reverse	5'-TGA TGA ATG ATT CTG TGG CTT TTA C-3'
ent-1	forward	5'-CCC GTT CAC TTC CCG TCT T-3'
	reverse	5'-TCG AGG CGG CGA TAA TGA-3'