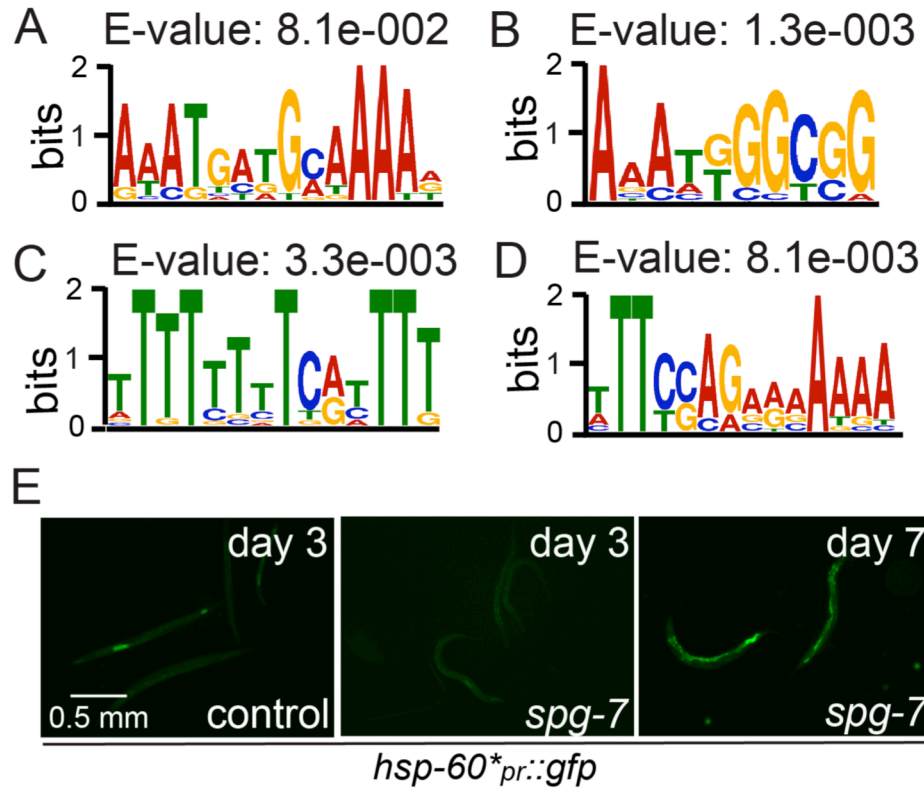


**Figure S1. ATFS-1 interacts with the promoters of mitochondrial-protective genes induced during mitochondrial stress. Related to Figure 1.**

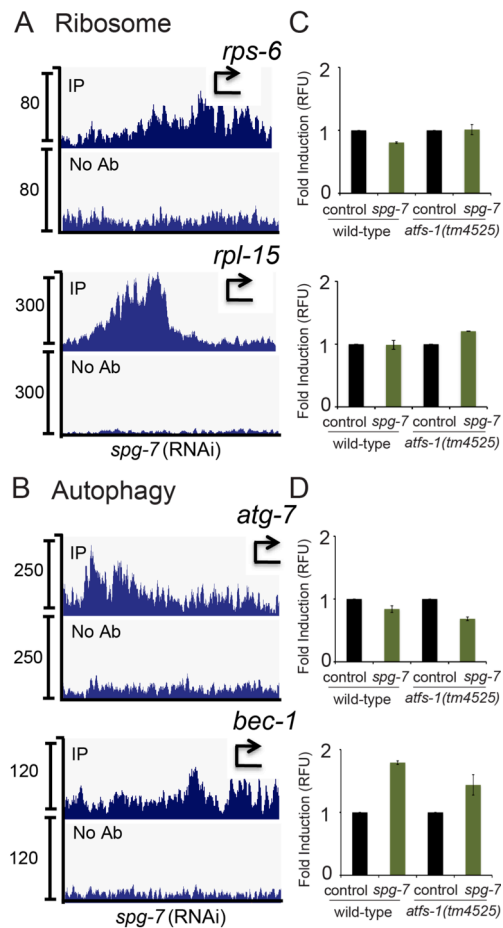
**A-E.** In the left column are ChIP-seq profiles of the *dnj-10*, *drp-1*, *timm-17*, *timm-23*, and *skn-1* promoters in wild-type worms raised on *spg-7*(RNAi), using ATFS-1-specific antibody (upper panel) or no antibody (lower panel). The y-axis is the number of sequence reads and the x-axis is approximately 2.5 kilobases with the start codon marked with an arrowhead. In the right column are the corresponding expression levels of *dnj-10*, *drp-1*, *timm-17*, *timm-23*, and *skn-1* mRNA in wild-type or *atfs-1(tm4525)* worms raised on control or *spg-7*(RNAi) determined by qRT-PCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05) (right panels).



**Figure S2. Potential ATFS-1 binding sites and UPR<sup>mt</sup> regulatory elements. Related to Figure 2.**

**A-D.** Motifs enriched within the promoters of mitochondrial protective genes in the ATFS-1 bound regions as determined by ChIP-seq, obtained using MEME. The motifs are in descending order based on the enrichment (E)-value generated by MEME. It should be noted that the sequence in Figure S2A also appears in Figure 2A.

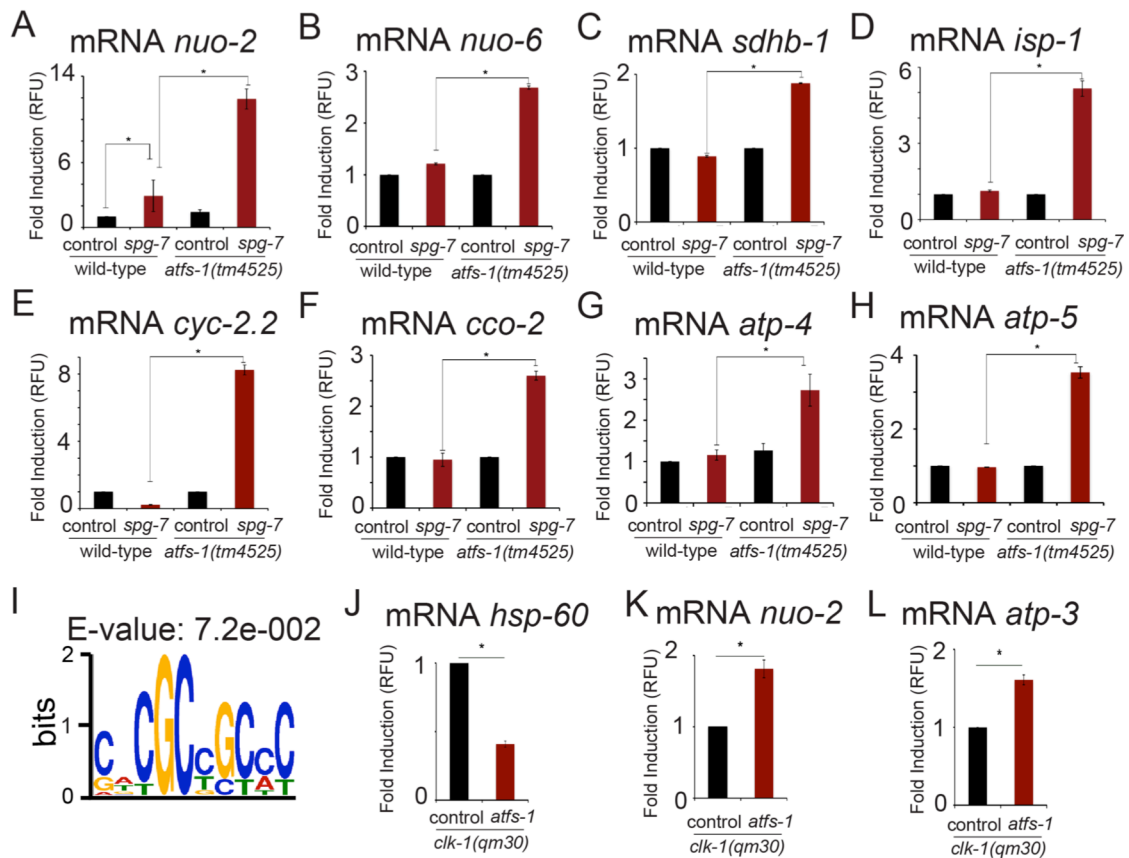
**E.** Photomicrographs of *hsp-60\*<sub>pr</sub>::gfp* transgenic worms lacking a single UPR<sup>mt</sup> worms raised on control or *spg-7*(RNAi) for 3 or 7 days. Scale bar, 0.5 mm.



**Figure S3. ATFS-1 binds ribosome and autophagy gene promoters with no obvious effect on transcription. Related to Figure 3.**

**A-B.** ChIP-seq profiles of the *rps-6*, *rpl-15*, *atg-7* and *bec-1* promoters in wild-type worms raised on *spg-7*(RNAi), using ATFS-1-specific antibody (upper panel) or no antibody (lower panel). The y-axis is the number of sequence reads and the x-axis is approximately 2.5 kilobases with the start codon marked with an arrowhead.

**C-D.** Expression levels of *rps-6*, *rpl-15*, *atg-7* and *bec-1* mRNA in wild-type or *atfs-1(tm4525)* worms raised on control or *spg-7*(RNAi) determined by qRT-PCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05).

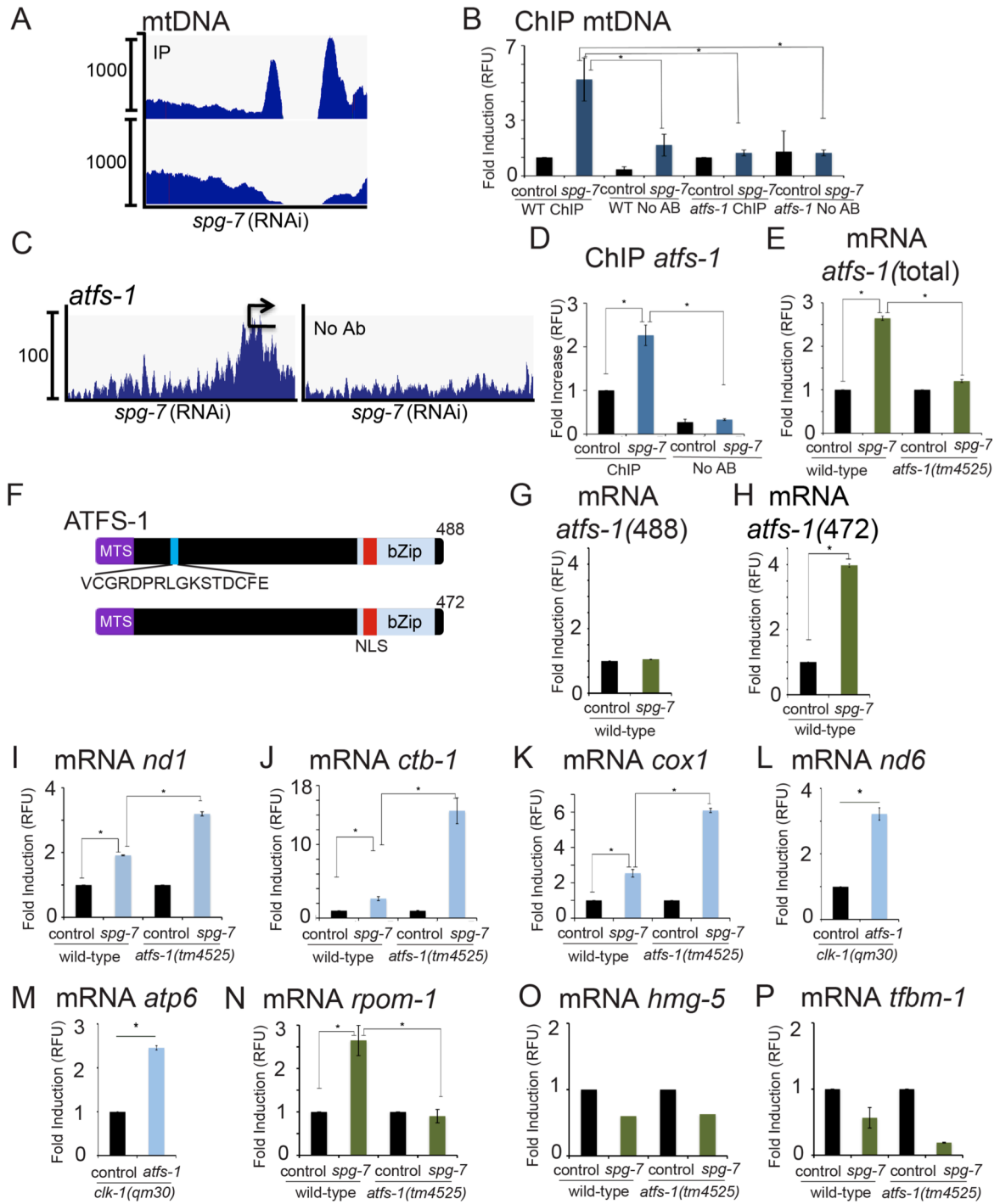


**Figure S4. ATFS-1 limits nuclear-encoded OXPPOS transcript accumulation during mitochondrial stress. Related to Figure 4.**

**A-H.** Expression levels of *nuo-2*, *nuo-6*, *sdhb-1*, *isp-1*, *cyc-2.2*, *cco-2*, *atp-4*, and *atp-5* mRNA in wild-type or *atfs-1(tm4525)* worms raised on control or *spg-7*(RNAi) determined by qRT-PCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05).

**I.** The only significantly enriched motif found within the promoters of nuclear encoded OXPPOS and TCA cycle genes in the ATFS-1 bound regions as determined by ChiP-seq, obtained using MEME.

**J-L.** Expression levels of *hsp-60*, *nuo-2*, and *atp-3* mRNA in *clk-1(qm30)* worms raised on control or *atfs-1*(RNAi) determined by qRT-PCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05)



**Figure S5. ATFS-1 directly binds mtDNA and impairs mtDNA-encoded transcript accumulation. Related to Figure 5.**

**A.** ChIP-seq profiles of the mtDNA non-coding region in wild-type worms raised on *spg-7*(RNAi),

using ATFS-1-specific antibody (upper panel) or no antibody (lower panel). In this profile the CHIP-seq reads that also mapped to the *C. elegans* nuclear genome were removed. Despite the extra stringency, ATFS-1 binding is enriched in this region of the mtDNA. The y-axis is the number of sequence reads and the x-axis is approximately 0.8 kilobases including the mtDNA region lacking protein or RNA coding segments.

**B.** ATFS-1 ChIP of the mtDNA non-coding region in wild-type and *atfs-1(tm4525)* worms, raised on control or *spg-7(RNAi)*, using ATFS-1-specific antibody or no antibody (No AB) as measured by qPCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05). These results demonstrate that the increased interaction of ATFS-1 with mtDNA during mitochondrial stress, as obtained by ChIP-qPCR, requires *spg-7(RNAi)*, ATFS-1-specific antibodies and the *atfs-1* gene.

**C.** ChIP-seq profiles of the *atfs-1* promoter in wild-type worms raised on *spg-7(RNAi)*, using ATFS-1-specific antibody (upper panel) or no antibody (lower panel). The y-axis is the number of sequence reads and the x-axis is approximately 2.5 kilobases with the start codon marked with an arrowhead.

**D.** ChIP of the *atfs-1* promoter in the presence or absence of ATFS-1-specific antibody from wild-type worms raised on control or *spg-7(RNAi)* as measured by qPCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05).

**E.** Expression level of *atfs-1* mRNA in wild-type or *atfs-1(tm4525)* worms raised on control or *spg-7(RNAi)* determined by qRT-PCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05).

**F.** Schematic of two ATFS-1 isoforms with the same mitochondrial targeting sequence (MTS) encoded by mRNA two splice variants. The 472 amino acid isoform lacks a 16 amino acid sequence (blue box) located near the MTS as indicated.

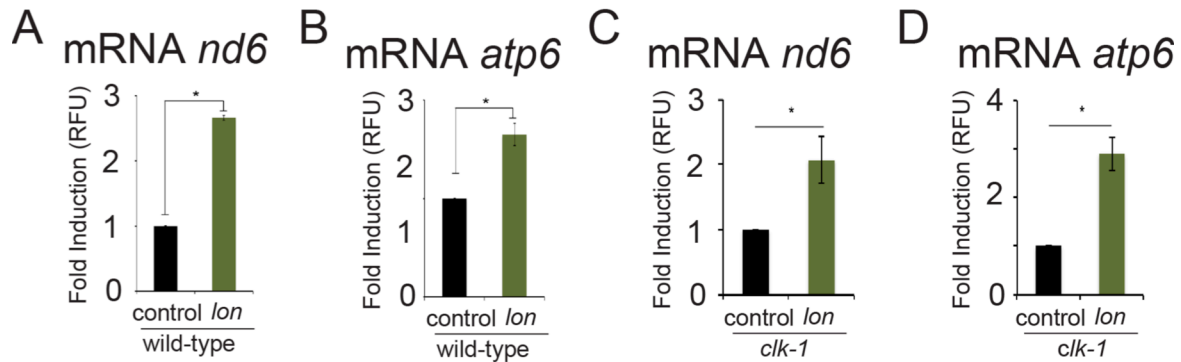
**G-H.** Expression level of the two *atfs-1* splice variant mRNAs depicted in Figure S5F in worms raised on control or *spg-7(RNAi)* as measured by qRT-PCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05).

**I-K.** Expression levels of mtDNA-encoded *nd1*, *ctb-1* and *cox1* mRNA in wild-type or *atfs-*

*1(tm4525)* worms raised on control or *spg-7*(RNAi) determined by qRT-PCR (N = 3, ± SD, p\* (student t-test) < 0.05).

**L-M.** Expression levels of *nd6* and *atp6* mRNA in *clk-1(qm30)* worms raised on control or *atfs-1*(RNAi) determined by qRT-PCR (N = 3, ± SD, p\* (student t-test) < 0.05).

**N-P.** Expression levels of *rpom-1* (the mitochondrial RNA polymerase), *hmg-5* (TFAM ortholog) and *tfbm-1* mRNA in in wild-type or *atfs-1(tm4525)* worms raised on control or *spg-7*(RNAi) determined by qRT-PCR (N = 3, ± SD, p\* (student t-test) < 0.05).



**Figure S6. *Lon* inhibition does not impair mtDNA-encoded transcript accumulation.**

**Related to Figure 7.**

**A-D.** Expression levels of *nd6* and *atp6* mRNA in wild-type and *clk-1*(*qm30*) worms raised on control or *lon*(RNAi) determined by qRT-PCR (N = 3,  $\pm$  SD,  $p^*$  (student t-test) < 0.05). While *lon*(RNAi) causes a ~55 kD species of ATFS-1 (lowest molecular weight form of ATFS-1 as observed in Figure 5E) to accumulate, the accumulation of mtDNA-encoded mRNAs is not decreased suggesting *Lon*-mediated degradation of this ATFS-1 species does not affect the regulation of mtDNA-encoded mRNAs.

**Table S1.** Promoters of genes that ATFS-1 interacted with during *spg-7*(RNAi) exposure as determined by ATFS-1 ChIP-seq.



**Table S2** . ATFS-1 directly binds and up-regulates genes during mitochondrial stress.

Related to Figure 1.

Sequence Name	Gene symbol	KOG title, protein domain or function	Fold Enrichment DNA-ChIP Wild-type <i>spg-</i> 7(RNAi)/control	Fold Induction Transcription Wild-type <i>spg-</i> 7(RNAi)/control
<b>Detoxification/stress response</b>				
ZK1290.5		Aldo/keto reductase family proteins	4.38	2.83203
K10D2.6	emb-8	NADP/FAD dependent oxidoreductase UDP-glucuronosyl and UDP-glucosyl transferase	4.91	2.38339
K08B4.3	ugt-19	transferase	7.54	26.7691
AC3.8	ugt-2	UDP-GlucuronosylTransferase UDP-glucuronosyl and UDP-glucosyl transferase	4.72	25.4083
M88.1	ugt-62	transferase	2.6	11.1567
F39G3.1	ugt-61	UDP-glucuronosyl and UDP-glucosyl transferase	3.1	9.46427
T07C5.1	ugt-50	UDP-GlucuronosylTransferase	8.97	5.17449
R04D3.1	cyp-14A4	Cytochrome P450 CYP2 subfamily	2.51	100.474
K09A11.2	cyp-14A1	Cytochrome P450 CYP2 subfamily	3.1	23.8354
R08F11.3	cyp-33C8	Cytochrome P450 CYP2 subfamily	9.44	52.7502
Y17D7A.4	cyp-33D3	Cytochrome P450 CYP2 subfamily	3.95	4.19634
F40F8.7	pqm-1	paraquat responsive	2.95	3.752
C54D10.1	cdr-2	glutathione S-transferase-like protein	6.34	15.2001
K01D12.11	cdr-4	cadmium responsive	5.9	11.9017
F52E1.13		Oxidation resistance protein	3.06	1.71515
Y73F8A.27		Ferredoxin	4.89	1.86338
<b>Signaling/Peptide</b>				
ZK488.2	nhr-90	Nuclear Hormone Receptor family	3.98	4.64094
F57G8.6	nhr-193	Nuclear Hormone Receptor family	5.83	5.66826
R11G11.1	nhr-132	Nuclear Hormone Receptor family	7.48	3.15044
R11G11.12	nhr-210	Nuclear Hormone Receptor family	2.68	5.76655
vhp-1	vhp-1	Dual specificity phosphatase	3.05	2.39868
F26G5.9	tam-1	Predicted E3 ubiquitin ligase Serine/threonine specific protein phosphatase	3.43	1.73396
F56C9.1	gsp-2, kap-1	PP1	2.62	4.35203
<b>Transporters</b>				
F57A10.3	haf-3	ABC transporter family Mitochondrial import inner membrane translocase, subunit TIM23	6.59	2.08411
F15D3.7		Mitochondrial import inner membrane translocase, subunit TIM17	7.57	2.12536
E04A4.5		translocase, subunit TIM17	5	1.9311
T09F3.2		Mitochondrial carrier protein - Rim2p/Mrs12p	6.04	1.82836
F25B4.7		Mitochondrial ADP/ATP carrier proteins	2.62	2.37832
T28F3.4		Permease of the major facilitator superfamily Synaptic vesicle transporter SVOP and related transporters	4.21	5.30959
C46C2.2		transporters	9.01	2.25887
C47A10.1	pgp-9	Multidrug/pheromone exporter	4.85	10.8474
<b>Mitochondrial quality control</b>				
M03C11.5	ymel-1	YME1-Like (Yeast Mitochondrial Escape) AAA protease)	13.08	1.44121
F55F8.6	mff-2	Mitochondrial fission factor	2.98	6.03495
T12E12.4	drp-1	dynammin-related protein	5.53	2.63286
F56C11.3		Mitochondrial sulfhydryl oxidase	8.5	2.19908

C14F5.1	dct-1	Similarity to the mammalian BNIP3 proteins	3.89	2.23187
<b>Protein folding/degradation</b>				
T09B4.10	chn-1	Chaperone-dependent E3 ubiquitin protein ligase	8.12	2.45897
ZK593.6	lgg-2	Microtubule-associated anchor protein involved in autophagy	2.61	2.14331
<b>Metabolism</b>				
F09F7.7		2-Oxoglutarate- and iron-dependent dioxygenase-related proteins	2.7	2.50844
M28.6	lact-3	Predicted esterase	2.98	2.12752
F15A8.6		Carboxylesterase and related proteins	2.93	3.59892
F54D5.1	pcs-1	PhytoChelatin Synthase	5.06	2.67404
<b>Metabolism: Ubiquinone biosynthesis</b>				
C24A11.9	coq-1	Polyprenyl synthetase	3.74	3.9627
<b>Metabolism: carbohydrates</b>				
K10B3.9	mai-1	ATPase inhibitory factor	7.5	3.08519
K10B3.9	gpd-2	Glyceraldehyde 3 Phosphate dehydrogenase	7.5	3.13691
F13D12.2	ldh-1	Lactate dehydrogenase	7.09	2.64655
<b>Metabolism: lipids</b>				
C36A4.9	acs-19	Acyl-CoA synthetase	2.55	2.00316
M01F1.3		Lipoate synthase	2.88	1.93466
<b>Orphans</b>				
C06A5.7	unc-94	Tropomodulin and leiomodulin	3.19	1.56777
B0546.4		Predicted Yippee-type zinc-binding protein	3.42	1.82517
F58B4.5		Predicted small molecule kinase	2.76	6.59003
T12G3.1		contains ZZ-type Zn-finger	4.03	5.74038
F54F2.8	prx-19	farnesylated protein associated with peroxisomes	4.3	1.72993
<b>Transcription regulators</b>				
ZC376.7	atfs-1	bZip transcription factor	3.62	1.84076
T19E7.2	skn-1	bZIP transcription factor NRF1	6.69	1.83395
W07G1.3	zip-3	bZip transcription factor	5.41	1.9944
F40G9.11	mxl-2	HLHZip transcription factor BIGMAX	4.62	2.00943
F19B2.5		Helicase-like transcription factor		3.81204
<b>Unknowns</b>				
C49A9.6		Uncharacterized protein with ubiquitin fold	3.19	2.42714
F15B9.10			6.34	1.34891
Y95B8A.6			3.41	1.67149
F22H10.2			4.88	7.33184
C32F10.4			4.88	4.21816
ZK470.2			9.56	2.13876
T28B8.1			3.57	1.98455
F26F12.3			2.46	1.7378
H28G03.2			11.53	2.56769
C41G7.9			3.42	1.99333
R08E5.1			3.83	2.30598
R102.5			4.24	4.2808
R102.5			4.24	4.2808

**Table S3.** Pathways enriched in ChIP-Seq dataset of ATFS-1 binding during spg-7(RNAi) exposure. Related to Figure 3.

**Entrez GeneID Gene symbol KOG title, protein domain or function**

**Ribosomes**

178352	rpl-29	Large ribosomal subunit L29 protein
176891	rpl-15	Large ribosomal subunit L15 protein
173235	rpl-31	Large ribosomal subunit L31 protein
3564813	M01F1.3	
171853	rpl-1	Large ribosomal subunit L10a protein
176097	rpl-35	Large ribosomal subunit L35 protein
171949	rpl-13	Large ribosomal subunit L13 protein
177203	rpl-7A	Large ribosomal subunit L7A protein
172074	rpl-4	Large ribosomal subunit L4 protein
171602	rpl-7	Large ribosomal subunit L7 protein
171692	rpl-17	Large ribosomal subunit L17 protein
175786	rps-12	Small ribosomal subunit S12 protein
173342	rps-26	Small ribosomal subunit S26 protein
172061	rps-10	Small ribosomal subunit S10 protein
173260	rps-6	Small ribosomal subunit S6 protein
173309	rps-20	Small ribosomal subunit S20 protein
177481	rps-4	Small ribosomal subunit S4 protein
176975	rps-28	Small ribosomal subunit S28 protein
175413	ubl-1	ubiquitin like/ ribosomal protein S27a
171767	Y37E3.8	

**Glycolysis/Gluconeogenesis**

175500	acs-19	fatty Acid CoA Synthetase family
174423	enol-1	Enolase
172751	F14B4.2	Hexokinase
172376	ipgm-1	cofactor-independent phosphoglycerate mutase
176788	aldo-1	Fructose-bisphosphate aldolase 1
175827	aldo-2	Fructose-bisphosphate aldolase 2
3565504	gpd-2	GPD (glyceraldehyde 3-phosphate dehydrogenase)
173227	gpi-1	Glucose-6-Phosphate Isomerase
174798	ldh-1	Lactate DeHydrogenase
172744	pyk-1	Pyruvate kinase
179627	sodh-1	Sorbitol DeHydrogenase family
174844	tpi-1	Triose Phosphate Isomerase

**Oxidative Phosphorylation**

177038	Y69A2AR.18	ATP synthase gamma chain
172195	atp-3	ATP5O subunit of mitochondrial ATP synthase
175716	atp-2	catalytic F1 portion of ATP synthase
173134	H28O16.1	ATP synthase alpha
174059	F58F12.1	ATP16, epsilon/delta subunit
176707	cco-2	COX Va
172832	cco-1	COX5b
178404	nuo-3	NDUFA6
176001	nuo-4	NDUFA10
172734	nduf-7	NDUFS7
184827	nduf-6	NDUFS6
188912	nduf-2.2	NDUFS2
181108	sdha-1	Succinate DeHydrogenase complex subunit A
175038	Y51H1A.3	NDUFB8
175371	Y54F10AM.5	NDUFA8

**Vacuolar ATPase**

3564970	vha-13	vacuolar proton-translocating ATPase
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180692 vha-12	vacuolar proton-translocating ATPase
177442 vha-8	Vacuolar H ATPase
176383 vha-1	Vacuolar H ATPase
174596 vha-9	Vacuolar H ATPase
177017 vha-11	Vacuolar H ATPase
180534 vha-15	Vacuolar H ATPase

#### **TCA (Citric Acid Cycle)**

176121 aco-2	Aconitase
176437 cts-1	Citrate Synthase
177775 idh-1	Isocitrate Dehydrogenase
179041 mdh-1	Malate dehydrogenase
179616 pyc-1	Pyruvate Carboxylase
180485 D1005.1	Probable ATP-citrate synthase
181570 sucl-1	Succinyl-CoA Ligase, alpha subunit
181108 sdha-1	Succinate Dehydrogenase complex subunit A
179063 dlst-1	DihydroLipoamide S-SuccinylTransferase

#### **Regulation of Autophagy**

181727 aak-2	AMP-Activated Kinase
178005 atg-7	AuTophagy (yeast Atg homolog)
177345 bec-1	Beclin (human autophagy) homolog
174050 lgg-1	LC3, GABARAP and GATE-16 family
180311 unc-51	serine/threonine protein kinase orthologous to Saccharomyces cerevisiae autophagy protein Atg1p

**Table S4.** ATFS-1 directly interacts with some OXPHOS genes during mitochondrial stress. Related to Figure 4.

<b>Human Name</b>	<b>Worm Name</b>	<b>ATFS-1 Binding</b>
<b>Complex I</b>		
<b>NADH-ubiquinone oxidoreductase</b>		
NDUFA5	C33A12.1	NO
NDUFA6	Y57G11C.12	NUO-3
NDUFA7	F45H10.3	NO
NDUFA8	Y54F10AM.5	YES
NDUFA9	Y53G8AL.2	NO
NDUFA10	K04G7.4	NUO-4
NDUFA12	Y94H6A.8	NO
NDUFA13	C34B2.8	NO
NDUFAB1	Y56A3A.19	NO
NDUFAF1	C50B8.3	NUAF-1
NDUFAF2	Y94H6A.8	NO
NDUFAF3	R07H5.3	NUAF-3
NDUFAF4	B0035.15	YES
NDUFB2	F44G4.2	NO
NDUFB4	W01A8.4	NUO-6
NDUFB5	C25H3.9	NO
NDUFB7	D2030.4	NO
NDUFB8	Y51H1A.3	YES
NDUFB9	C16A3.5	NO
NDUFB10	F59C6.5	NO
NDUFB11	F42G8.10	NO
NDUFC2	Y71H2AM.4	YES
NDUFS1	Y45G12B.1	NUO-5
NDUFS2	T26A5.3	NDUF-2.2
	K09A9.5	GAS-1
NDUFS3	T10E9.7	NUO-2
NDUFS4	ZK973.10	NDUF-4
NDUFS5	Y54E10BL.5	NDUF-5
NDUFS6	F22D6.4	NDUF-6
NDUFS7	W10D5.2	NDUF-7
NDUFS8	T20H4.5	NO
NDUFV1	C09H10.3	NUO-1
NDUFV2	F53F4.10	NO
<b>Complex II</b>		
<b>Succinate dehydrogenase</b>		
SDHA	C03G5.1	SDHA-1
		YES

SDHB	F42A8.2	SDHB-1	NO
SDHC	T07C4.7	MEV-1	NO
SDHD	F33A8.5	SDHD-1	NO

### Complex III

#### Cytochrome c reductase

RIP1/Rieske Fe-S protein	F42G8.12	ISP-1	NO
cytochrome c	E04A4.7	CYC-2.1	YES
cytochrome c	ZC116.2	CYC-2.2	NO
cytochrome b-c1 complex subunit 7	T02H6.11		NO
cytochrome b-c1 complex subunit 6	T27E9.2		YES
Cytochrome b-c1 complex subunit 2	T10B10.2	UCR-2.2	NO
Cytochrome b-c1 complex subunit 2	T24C4.1	UCR-2.3	NO
Cytochrome b-c1 complex subunit 2	VW06B3R.1	UCR-2.1	YES
Cytochrome b-c1 complex subunit 1	F56D2.1	UCR-1	NO
tetratricopeptide repeat protein 19	Y54G11A.8	DDL-3	NO

### Complex IV

#### Cytochrome c oxidoreductase

Co4, COX4	W09C5.8		NO
COX5b	F26E4.9	CCO-1	YES
COX Va	Y37D8A.14	CCO-2	YES
COX Vib	Y71H2AM.5		YES

### Complex V

#### ATP synthase

F1 Beta subunit	C34E10.6	ATP-2	YES
delta subunit	F27C1.7	ATP-3	YES
ATP synthase alpha	H28O16.1		YES
ATP16, epsilon/delta subunit	F58F12.1		YES
ATP15	ZC262.5		NO
gamma subunit	Y69A2AR.18		YES
	R05D3.6		NO
	F32D1.2		No
ATP4	F02E8.1	ASB-1	NO
ATP4	F35G12.10	ASB-2	NO
ATP9	Y82E9BR.3		YES
	R04F11.2		NO
subunit f	R53.4		NO
subunit g, F0, ATP20	C53B7.4	asg-2	NO
subunit g, F0, ATP20	K07A12.3	asg-1	NO
	C05C8.1		NO

**Table S5.** Sequences of primers used in ChIP quantitative real time PCR. Related to Experimental Procedures.

<b>Gene</b>	<b>Primer Sequence</b>
<i>mthsp-70</i>	F: 5'-GCATCATTATTCTCCTAAAACCTTG-3' R: 5'-GTGCCTGAAAGAAAATTGCATC-3'
<i>ymel-1</i>	F: 5' ATGCCGGTTTTATTTAGCCAAC 3' R: 5' GAGCGAGAGTCCAGTGGAGC 3'
<i>gpd-2</i>	F: 5' GCATCATCATTTTTCAATTTTCC 3' R: 5' GACGAAACATGTGCAGTAAGC 3'
<i>hsp-4</i>	F: 5' GAGTCCATCGTGGTGCCG 3' R: 5' GACATCGGGTCTCGACACG 3'
<i>hsp-60</i>	F: 5'-TCTCGTGCGGCAAACCTTG-3' R: 5'-ATGGCTAATTTACATCAGAATAGACT-3'
<i>chrM</i>	F: 5'-GACGGTCAATTGTGAATTGTC-3' R: 5'-GCCTAGAAGCTTCCATCATGC-3'
<i>hsp-70</i>	F: 5' CGAGCATCGGGCACAATG 3' R: 5' CTCGAAAATCGCTGCAGTGTG 3'
<i>atfs-1</i>	F:5' GACGGTCAATTGTGAATTGTC 3' R:5' GCCTAGAAGCTTCCATCATGC 3'
<i>mtDNA-ctrl</i>	F: 5'-GCCGTGAGCTATTCTAGTTATTG-3' R: 5'-GCATCTTTACCTAAGTACTCAGGTC-3'

**Table S6.** Sequences of primers used in quantitative RT real time PCR reactions. Related to Experimental Procedures.

<b>Gene</b>	<b>Primer Sequence</b>
<i>act-3</i>	F: 5'-ATCCGTAAGGACTTGTACGCCAAC-3' R: 5'-CGATGATCTTGATCTTCATGGTTC-3'
<i>mthsp-70</i>	F: 5'-GAAGATACGAAGACCCAGAGGTTTC-3' R: 5'-CAACCTGAGATGGGGAATACACT-3'
<i>yme-1</i>	F: 5'-GCTGGATCAGAATTTGATGAAGTAC-3' R: 5'-ACTGAATCGATTTCGTCGATG-3'
<i>gpd-2</i>	F: 5'-TGAAATCCAATGGGGAGCCTC-3' R: 5'-GGAGCAGAGATGATGACCTTCTTG-3'
<i>hsp-4</i>	F: 5' GAGTTGAAATCATCGCCAACG 3' R: 5' GTCGCTCTCCTTGATCTCCG 3'
<i>hsp-60</i>	F: 5'-AGGGATTCGAGAGCATTCTGCAAG-3' R: 5'-TGTGGCGACTTGAGCGATCTCTTC-3'
<i>dnj-10</i>	F: 5'-GCGGGCTCATTTCATCGATCTGTAC-3' R: 5'-CAGATTTTTTGTGACACCCAAAG-3'
<i>drp-1</i>	F: 5'-TGGATTCCTTGGATTATTCGGC-3' R: 5'-AGTTGCGTCTCTGGCACTTCTG-3'
<i>timm-17</i>	F: 5'-GATTGTTGTCTTGTGCGCCATCC-3' R: 5'-ATCACCTTTGGTCCTGAACGG-3'
<i>timm-23</i>	F: 5'-CAACTGAAATCTGCTGGAGTAGGAG-3' R: 5'-GGCATAATGTATTGCGGCTGC-3'
<i>skn-1</i>	F: 5'-TCCACCAGCATCTCCATTCG-3 R: 5'-CTCCATAGCACATCAATCAAGTCG-3'
<i>enol-1</i>	F :5' GCAGTTCCATCTGGAGCTTCTACTG 3' R :5' GTTGATGTTGAGACGGCCTTG 3'
<i>ldh-1</i>	F :5' GATAAGTTGAAGGGAGAGATGATG 3' R :5' GACGAGCACCTGCTGTCACTAC 3'
<i>rps-6</i>	F :5' GTCGCCATCGATGCTCTCG 3' R :5' CTTCAATGGGAATCCCTGCTTG 3'
<i>rpl-15</i>	F :5' CGTGCCAAGCAAGGATTTCG 3' R :5' GTAGGTTTGTCCCTTGCACTG 3'
<i>nuo-3</i>	F: 5' GGACATCTCACCGATGTTTCG 3' R: 5' GCGTAACGGATCGATTTTCATG 3'
<i>Y69A2AR.18</i>	F :5' GCTTGTGTCTCAAGGCTTCG 3' R :5' GGATTTGGTGATCTTTGGATG 3'
<i>aco-2</i>	5' GAGCCACTTGGCTGGACCTG 3' 5' GTACGACTTCGGCTCGAATTTACTG 3'
<i>cts-1</i>	5' GCTATTCGCAGACTTATCACCAAG 3' 5' TGTGGGCTGGGATCTTCTTG 3'
<i>atg-7</i>	F:5' GCTCAATGATTGGAACTCGATGAG 3' R:5' GCTCAAACGTGCGTAACTTAAGGATAGATG 3'
<i>bec-1</i>	F :5' GATTCAGCGGATTCCGAG 3' R :5' GCTTCATGAGGTTTCGAGAATG 3'
ND6	F: 5'-AGATGAGATTTATTGGGTATTTCTAG-3' R: 5'-CACCTAGACGATTAGTTAATGCTG-3'
CO II	F: 5'-GTAGTTTATTGTTGGGAGTTTATG-3' R: 5'-CACAATAATTCACCAAACGATACTC-3'
ATP6	F: 5'-GTAGTTCATACCCTCGTTATCGTTATG-3' R: 5'-CTGCGTAAAAACACAATATAATTAAGAG-3'
<i>ctb-1</i>	F: 5'-GCCGTGAGCTATTCTAGTTATTG-3' R: 5'-GCATCTTTACCTAAGTACTCAGGTC-3'
<i>atfs-1</i>	F: 5'-CAATCACCATCAAAATCGGCG-3' R: 5'-CTTGCTCAATGTCCATTTGCAAC-3'



<i>atfs-1 (488)</i>	F: 5'-GCGGCAGAGATCCTAGATTGG-3' R: 5'-CACTGCTACCATTCTGCCATG-3'
<i>atfs-1 (472)</i>	F :5' ACGTGACGCTGGAAGCATG 3' R :5' GCGGCTGCTGACATGTCTG 3'
<i>nd-1</i>	F: 5' -AGCGTCATTT ATTGGGAAGAAGAC-3' R: 5' -AAGCTTGTGCTAATCCCATAAATGT-3'
CO I	F: 5'-GCAGCAGGGTTAAGATCTATCTTAG-3' R: 5'-CTGTTACAAATACAGTTCAAACAAAT-3'
<i>rpom-1</i>	F: 5'-TGGGAAGAGATAATGAGGGTGGAG-3' R: 5'-CTTGTTGCCGTTTTTGCTCG-3'
<i>hmg-5</i>	F: 5'-AGTGGAAGGCATTGAGTATCTCTG-3' R: 5'-GTCATCCAGCTTTTGAGCATTG-3'
<i>tfbm-1</i>	F: 5'-CTACCTGCAATGCATGTCATTG-3' R: 5'-CGTCGGTATGACATGTCACG-3'
<i>nuo-4</i>	F: 5'-CAAGGAGTTGTGCTCGAACG-3' R: 5'-GTAGTTGAGGAAGAGCATTTTTACG-3'
<i>sdha-1</i>	F: 5'-TTACCAGCGTGCTTTCGGAG-3' R: 5'-AGGGTGTGGAGAAGAGAATGACC-3'
<i>ucr-2.1</i>	F: 5'-CGCGCCCATCTGGAAGT-3' R: 5'-GAACTCCAGCAGATTTGGCTG-3'
<i>cyc-2.1</i>	F: 5'-CGGAGTTATCGGACGTACATCAG-3' R: 5'-GTCTCGCGGGTCCAGACG-3'
<i>cco-1</i>	F: 5'-GCTGGAGATGATCGTTACGAG-3' R: 5'-GCATCCAATGATTCTGAAGTCG-3'
<i>atp-3</i>	F: 5'-GTCCTCGACCCAAGTCTCAAG-3' R: 5'-GTCCAAGGAAGTTTCCAGTCTC-3'
<i>nuo-2</i>	F: 5'-TCTGCTCTGAATGATGTGCTGG-3' R: 5'-CCGTTCTTGCCAATGAGGAATC-3'
<i>nuo-6</i>	F: 5'-CTGCCAGGACATGAATACAATCTGAG-3' R: 5'-GCTATGAGGATCGTATTCACGACG-3'
<i>sdhb-1</i>	F: 5'-GCTGAACGTGATCGTCTTGATG-3' R: 5' GTAGGATGGGCATGACGTGG-3'
<i>isp-1</i>	F: 5'-GCAGAAAGATGAATGGTCCGTTG-3' R: 5'-ATCCGTGACAAGGGCAGTAATAAC-3'
<i>cyc-2.2</i>	F: 5'-CGACTATTTGGCTGATCC- 3' R: 5'-GATCAGCTCGTTCGTCAGC-3'
<i>cco-2</i>	F: 5'-GTGATACCGTCTACGCCTACATTG-3' R: 5'-GCTCTGGCACGAAGAATTCTG-3'
<i>atp-4</i>	F: 5'-AGCTCGCCAACGCCGATG-3' R: 5'-GAGCGGATTGAACTGCAGAGTC-3'
<i>atp-5</i>	F: 5'-CAAGGTCGCTGATGGACTTCAG-3' R: 5'-GCTGACGATCGAAATGTTCAACTG-3'
<i>nuaf-1</i>	F: 5'-GAGACATAACGAGGCTCGTGTTG-3' R: 5'-GAAGCCTTCTTTCCAATCACTATCG-3'
<i>lpd-8</i>	F: 5'-GTCAACAGCTTCTCCCAGACG-3' F: 5'-GCTTCACTCCGTCGACTCG-3'
Y17G9B.5	F: 5'-GTGCAGTGAAGTTCTAGATGAAATG-3' F: 5' CTTTGGCATCCAATAGAGCATACG-3'

**Primers to measure mitochondrial DNA content**

<i>ND-1</i>	F: 5' -AGCGTCATTT ATTGGGAAGAAGAC-3' R: 5' -AAGCTTGTGCTAATCCCATAAATGT-3'
<i>act-3</i>	F: 5'-TGCGACATTGATATCCGTAAGG-3' R: 5'-GGTGGTTCTCCGAAAGAA-3'

**Table S7.** Sequences of primers that were annealed and used in the EMSA experiments. Related to Experimental Procedures.

Wild-type	F: 5'-ATTTATATTATAAATATGATGAAGTACTAAAAAAAAGATG-3' R: 5'-CATCTTTTTTTTAGTACTTCATCATATTTATAATATAAAT-3'
scrambled UPRmtE	F: 5'-ATTTATATTATAAATGAAGTAATGTACTAAAAAAAAGATG-3' R: 5'-CATCTTTTTTTTAGTACATTACTTCATTTATAATATAAAT-3'