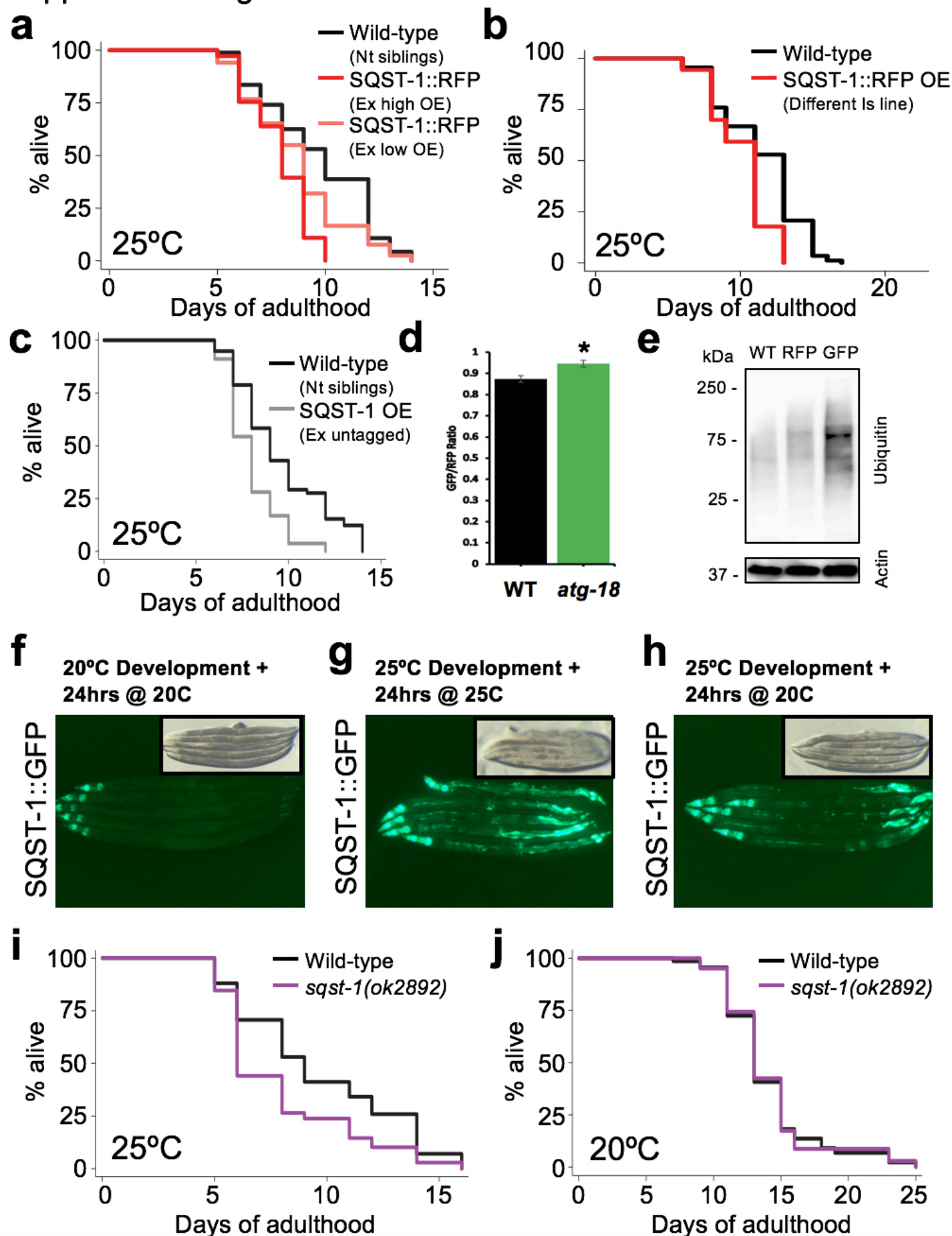
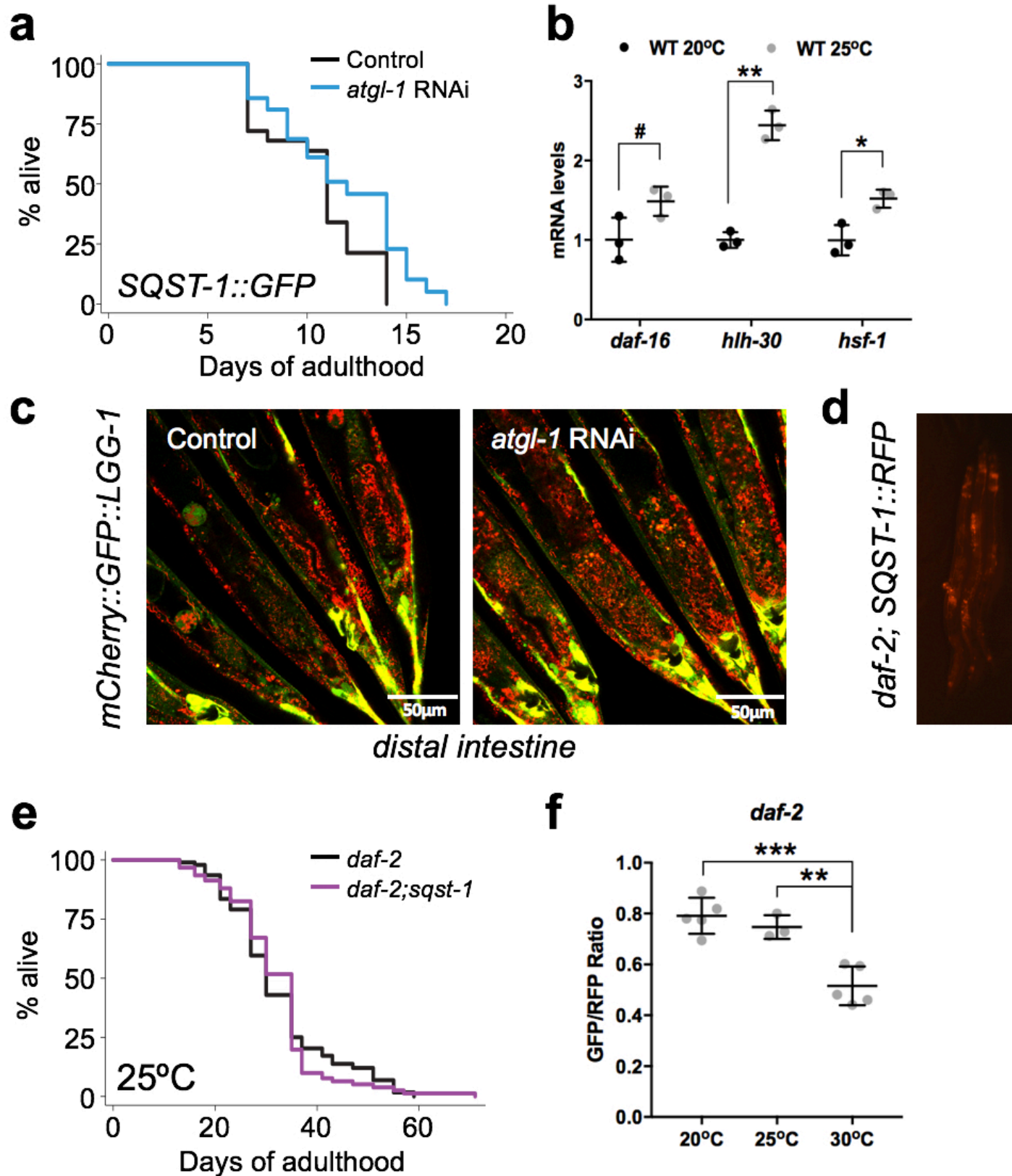


Supplemental Figure 1



Supplemental Figure 1. SQST-1 function in lifespan modulation is temperature-dependent. **a.** Lifespan analysis of wild-type animals (non-transgenic siblings) and transgenic animals over-expressing SQST-1::RFP at low and high level (Ex: Extrachromosomal array), and **b.** transgenic animals over-expressing SQST-1::RFP (Integrated strain, Is) raised at 20°C and grown at 25°C during adulthood on OP50 *E. coli*. n=100. **c.** Lifespan analysis of wild-type animals (non-transgenic siblings, Nt) and transgenic animals over-expressing SQST-1 (untagged). **d.** Quantification of the GFP and RFP signal ratio in GFP::RFP::SQST-1 over-expressing animals in a wild-type or autophagy-defective *atg-18(gk378)* background. Average of 10 worms per image, n=4 images per condition *t*-test **p*<0.05. **e.** Immunoblot of ubiquitin and actin in Day 1 wild-type (WT) animals and SQST-1::RFP (RFP) and SQST-1::GFP (GFP) over-expressing animals raised at 25°C. **f.** Images (GFP and transmitted light) of animals over-expressing SQST-1::GFP were raised at 20°C or 25°C (**f-h**) and kept or transferred to 20°C (**f, h**), or kept at 25°C (**g**) for 24 hours. Lifespan analysis of wild-type animals and *sqst-1(ok2892)* animals raised at 20°C and grown at 25°C (**i**) or 20°C (**j**) during adulthood on OP50 *E. coli*. n=100. Details on lifespan analyses and repeats are available in Supplemental Table 3.

Supplemental Figure 2



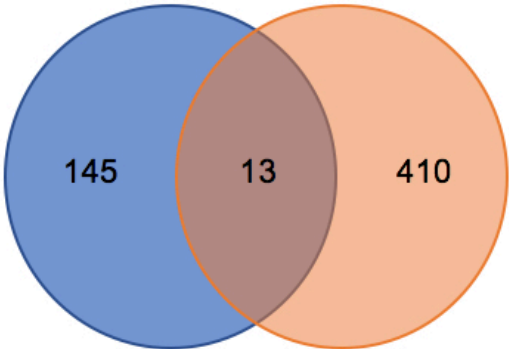
Supplemental Figure 2. Lipid droplets enhance lifespan, autophagy, and the response to heat stress

a. Lifespan analysis of transgenic animals over-expressing SQST-1::GFP grown on control bacteria or bacteria expressing dsRNA against *atgl-1*. **b.** qPCR analysis *daf-16*, *hlh-30* and *hsf-1* in Day 1 wild-type animals raised at 20°C or 25°C on OP50 *E. coli*. Biological triplicates *t*-test #*p*=0.06, **p*<0.05, ***p*<0.01 **c.** Representative confocal microscopy images of the distal intestine of animals expressing mCherry::GFP::LGG-1 and raised at 20°C and fed during adulthood control bacteria or bacteria expressing dsRNA against *atgl-1* for 2 days at 25°C. **d.** Image of *daf-2(e1370)* animals over-expressing SQST-1::RFP raised on OP50 *E. coli*. bacteria at 20°C and transferred to 25°C during adulthood for 5 days. Comparative WT image in Figure 1a. **e.** Lifespan analysis of *daf-2(e1370)* and *daf-2(e1370);sqst-1(ok2892)* raised at 20°C and grown at 25°C during adulthood on OP50 *E. coli*. bacteria (n=100). **f.** Levels of GFP and RFP were measured in transgenic tandem *daf-2;SQST-1::GFP::RFP* animals after incubating Day 1 animals at 20°C, 25°C or 30°C for 24 hours on OP50 *E. coli*. Average of 10 worms per image. n=3-5 image per condition *t*-test ***p*<0.01, ****p*<0.001. Details on lifespan analyses and repeats are available in Supplemental Tables 3 and 4.

Supplemental Figure 3

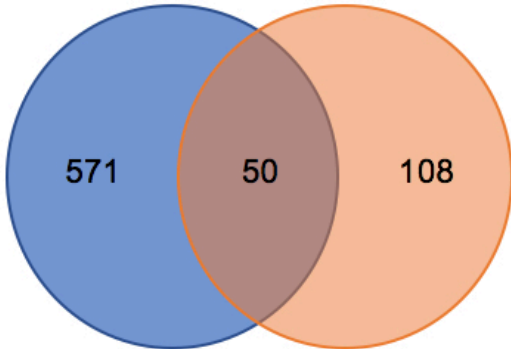
a

atgl-1 RNAi WT DEG *atgl-1* RNAi *daf-2* DEG



c

ATGL-1 OE DEG *atgl-1* RNAi DEG



b

Gene Name	Regulation in WT on <i>atgl-1</i> RNAi	Regulation in <i>daf-2</i> on <i>atgl-1</i> RNAi
<i>atgl-1</i>	Down	Down
<i>col-130</i>	Down	Up
<i>Y47D7A.13</i>	Down	Down
<i>nhx-2</i>	Down	Up
<i>T19B10.2</i>	Down	Down
<i>col-179</i>	Down	Down
<i>W03F9.4</i>	Down	Down
<i>ttr-23</i>	Up	Down
<i>mup-4</i>	Down	Down
<i>col-8</i>	Down	Up
<i>ttr-26</i>	Up	Down
<i>pvf-1</i>	Up	Up
<i>col-124</i>	Down	Down

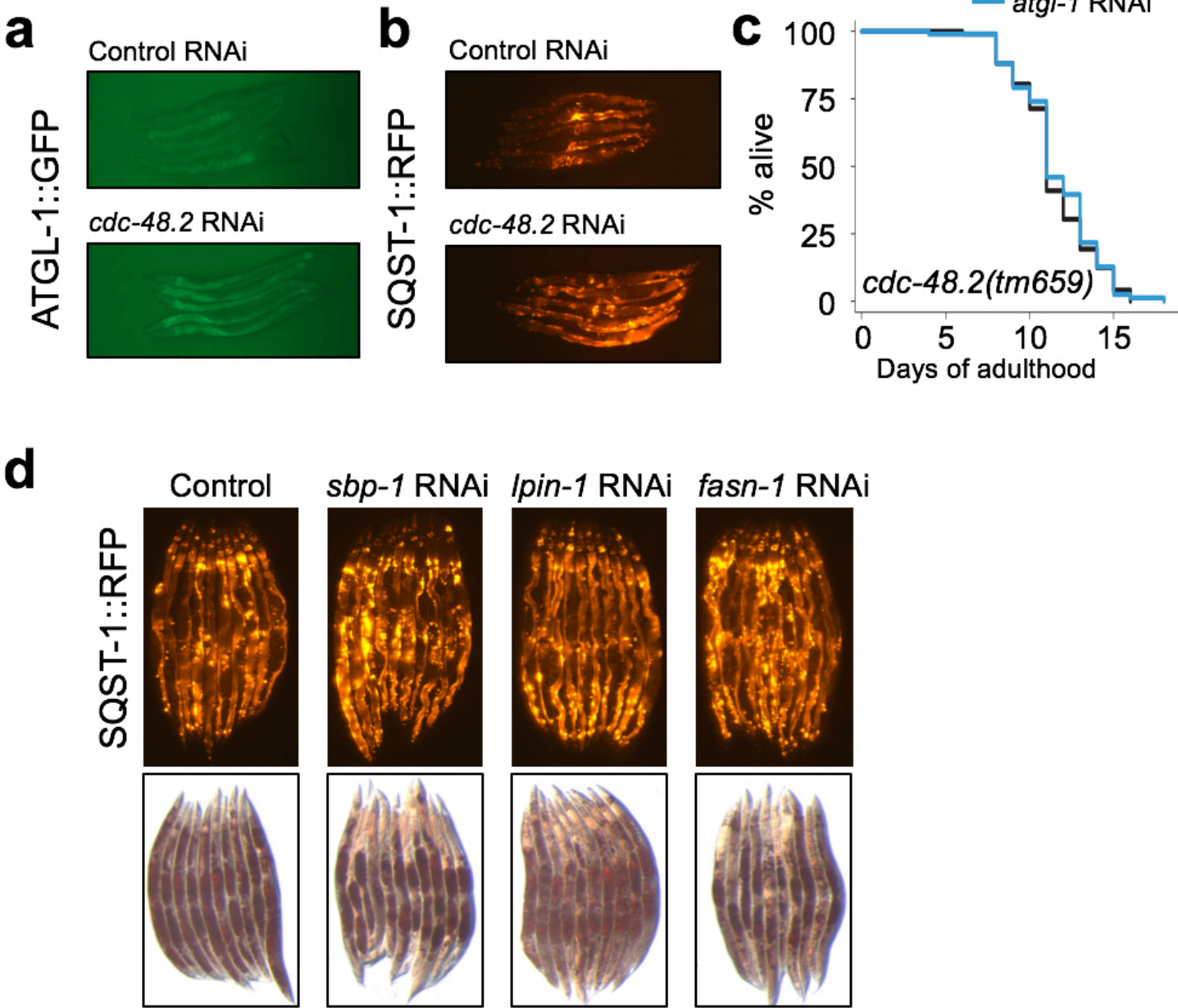
d

Gene Name	Regulation in ATGL-1 OE	Regulation in <i>atgl-1</i> RNAi
<i>atgl-1</i>	Up	Down
<i>C55A6.7</i>	Down	Down
<i>F10D2.10</i>	Up	Down
<i>col-130</i>	Down	Down
<i>cest-1</i>	Down	Down
<i>ifp-1</i>	Down	Down
<i>T19B10.2</i>	Up	Down
<i>pcp-3</i>	Down	Down
<i>col-14</i>	Down	Down
<i>grl-16</i>	Down	Down
<i>mlc-1</i>	Down	Down
<i>lys-10</i>	Down	Down
<i>W03F9.4</i>	Down	Down
<i>aldo-1</i>	Down	Down
<i>col-104</i>	Down	Down
<i>col-77</i>	Down	Down
<i>gst-1</i>	Down	Down
<i>wrt-6</i>	Down	Down
<i>C01B9.1</i>	Down	Down
<i>T05E7.1</i>	Down	Down
<i>clcc-47</i>	Up	Down
<i>npa-1</i>	Down	Down
<i>M04C3.2</i>	Down	Down
<i>ttr-26</i>	Up	Up
<i>T19D12.1</i>	Down	Down
<i>col-125</i>	Down	Down
<i>dim-1</i>	Down	Down
<i>ifc-1</i>	Down	Down
<i>col-97</i>	Down	Down
<i>M153.1</i>	Down	Down
<i>poml-3</i>	Down	Down
<i>W08A12.2</i>	Up	Up
<i>pvf-1</i>	Up	Up
<i>M153.2</i>	Down	Down
<i>Y16B4A.2</i>	Down	Down
<i>acs-7</i>	Down	Down
<i>F10D2.8</i>	Down	Down
<i>H02F09.3</i>	Down	Down
<i>wrt-4</i>	Down	Down
<i>grd-6</i>	Down	Down
<i>idhg-2</i>	Down	Down
<i>cyp-14A2</i>	Down	Down
<i>ifd-1</i>	Down	Down
<i>Y43F8B.1</i>	Down	Down
<i>col-157</i>	Down	Down
<i>haf-9</i>	Down	Down
<i>ifc-2</i>	Down	Down
<i>T23E7.2</i>	Down	Down
<i>H43E16.1</i>	Down	Down
<i>tnt-2</i>	Down	Down

Supplemental Figure 3. Transcriptomic analyses of animals with over-expressed or silenced *atgl-1* reveal limited transcriptional changes.

a. Overlap of differentially expressed genes (DEGs) in WT and *daf-2* mutant backgrounds when *atgl-1* is silenced during adulthood at 25°C for 4 days. **b.** Identity of overlapping DEGs from a. and their regulation status in each strain. **c.** Overlap of DEGs between nematodes over-expressing ATGL-1::GFP and adult-only *atgl-1* silencing in wild-type animals at 25°C for 4 days. **d.** Identity of overlapping DEGs from c. and their regulation status under each condition.

Supplemental Figure 4



Supplemental Figure 4. SQST-1 levels are modulated by CDC-48 activity and lipid droplet levels. **a.** Day 1 ATGL-1::GFP and **b.** SQST-1::RFP over-expressing nematodes were fed control bacteria or bacteria expressing dsRNA against *cdc-48.2* for 2 days at 25°C. **c.** Lifespan analysis of *cdc-48.2* mutants fed control bacteria or bacteria expressing dsRNA against *atgl-1* during adulthood at 25°C. **d.** Day 1 SQST-1::RFP over-expressing nematodes were fed control bacteria or bacteria expressing dsRNA against *sbp-1*, *lpin-1*, or *fasn-1* for 6 days at 25°C. Corresponding images of nematodes stained with Oil-Red-O. Details on lifespan analyses and repeats are available in Supplemental Table 4.

Supplemental Table 1

See Supplemental Table 1 Excel File

Supplemental Table 2

See Supplemental Table 2 Excel File

Supplemental Table 3

Strains	Transgenic Mean Lifespan	Events Observed	N2 Control Mean Lifespan	Events Observed	% Difference	P Value	Fig.
25°C							
LRL160 (<i>Ilcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>)	11.9	43/100	13.5	50/100	-11%	0.0661	
LRL160 (<i>Ilcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>)	10.5	76/100	11.5	87/100	-9%	0.0094	
LRL160 (<i>Ilcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>)	9.8	57/100	12.9	49/100	-24%	<0.0001	1a
LRL161 (<i>Ilcls13 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>)	10.1	84/100	11.5	87/100	-12%	<0.0001	S1b
MAH349 (<i>sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	7.7	50/100	9.9	53/100	-22%	<0.0001	
MAH349 (<i>sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	7.9	48/100	10.0	86/100	-21%	<0.0001	
MAH349 (<i>sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	7.9	58/100	10.6	71/100	-26%	<0.0001	1b
MAH349 (<i>sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	9.6	28/100	11.0	48/100	-13%	0.0320	
LRL132 (<i>IlcEx55 (sqst-1p::sqst-1::GFP::RFP::unc-54)</i>)	10.7	89/100	11.7	74/100	-9%	0.0017	1c
LRL132 (<i>IlcEx55 (sqst-1p::sqst-1::GFP::RFP::unc-54)</i>)	10.0	89/100	10.9	70/100	-8%	0.0030	
LRL90 (<i>IlcEx39 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>) Ex high	7.9	124/160	9.6	57/100	-18%	<0.0001	S1a
LRL90 (<i>IlcEx39 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>) Ex low	8.6	79/100	9.6	57/100	-11%	0.0250	S1a
LRL90 (<i>IlcEx39 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>) Ex high	9.8	87/100	11.2	75/100	-13%	0.0061	
LRL90 (<i>IlcEx39 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>) Ex low	9.5	69/100	11.2	75/100	-15%	0.0021	
MAH844 (<i>Exsq146 (sqst-1p::sqst-1 + rol-6)</i>)	8.0	61/100	9.6	68/100	-16%	<0.0001	S1c
VC2196 (<i>sqst-1 (ok2892) IV</i>)	7.5	87/100	9.9	53/100	-24%	<0.0001	
VC2196 (<i>sqst-1 (ok2892) IV</i>)	7.9	81/100	10.0	86/100	-21%	<0.0001	S1i
VC2196 (<i>sqst-1 (ok2892) IV</i>)	9.3	75/100	10.6	71/100	-12%	0.0420	
VC2196 (<i>sqst-1 (ok2892) IV</i>)	9.5	63/100	11.0	48/100	-14%	0.0023	
VS20 (<i>hJIs67 [atgl-1p::atgl-1::GFP + mec-7::RFP]</i>)	11.8	74/100	13.5	50/100	-12%	0.0203	4a
VS20 (<i>hJIs67 [atgl-1p::atgl-1::GFP + mec-7::RFP]</i>)	10.1	59/100	10.7	79/100	-6%	0.0312	
VS20 (<i>hJIs67 [atgl-1p::atgl-1::GFP + mec-7::RFP]</i>)	11.6	61/100	12.9	49/100	-10%	0.0035	
LRL24 (<i>daf-2(e1370) III; sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	30.7	95/100	27.9 (<i>daf-2</i>)	95/100	10%	0.1258	
LRL24 (<i>daf-2(e1370) III; sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	31.9	92/100	29.3 (<i>daf-2</i>)	89/100	9%	0.5998	3f
LRL170 (<i>daf-2(e1370) III; sqst-1 (ok2892) IV</i>)	32.0	89/100	32.5 (<i>daf-2</i>)	80/100	-2%	0.8749	S2e
20°C							
LRL160 (<i>Ilcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>)	14.0	62/100	15.1	68/100	-7%	0.1021	1d
LRL160 (<i>Ilcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>)	15.3	48/100	16.3	50/100	-6%	0.2725	
LRL161 (<i>Ilcls13 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>)	14.0	63/100	15.1	68/100	-7%	0.0904	
MAH349 (<i>sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	14.1	42/100	14.0	49/100	1%	0.6271	1e
MAH349 (<i>sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>)	15.3	48/100	14.2	30/100	7%	0.3137	
LRL132 (<i>IlcEx55 (sqst-1p::sqst-1::GFP::RFP::unc-54)</i>)	14.1	68/100	15.0	42/100	-6%	0.1409	1f
VC2196 (<i>sqst-1 (ok2892) IV</i>)	14.1	52/100	14.0	49/100	1%	0.8730	S1j
VS20 (<i>hJIs67 [atgl-1p::atgl-1::GFP + mec-7::RFP]</i>)	15.2	77/100	11.9	58/100	27%	<0.0001	

Supplemental Table 3 (continued)

Supplemental Table 3. Lifespan analyses performed on OP50 *E. coli*.
Animals were raised at 20°C and grown at 20°C or 25°C (as noted) during adulthood on OP50 *E. coli*. Statistical analyses: Mantel-Cox log-rank

Supplemental Table 4

Strains	<i>atgl-1</i> RNAi Mean Lifespan	Events Observed	Control RNAi Mean Lifespan	Events Observed	% Difference	P Value	Fig.
<i>N2</i>	16.0	59/100	13.1	53/100	22%	0.0017	3a
<i>N2</i>	11.9	75/100	10.4	79/100	14%	0.0019	
<i>N2</i>	12.6	90/100	10.6	79/100	19%	<0.0001	
<i>N2</i>	12.7	66/100	9.9	50/100	28%	<0.0001	
<i>N2</i>	11.4	52/100	10.2	60/100	12%	0.0461	
<i>N2</i>	13.1	75/100	11.1	53/100	18%	0.0231	
<i>N2</i>	12.7	62/100	10.5	61/100	21%	<0.0001	
<i>CF1037 (daf-16 (mu86) I)</i>	14.0	55/100	11.6	53/100	21% (22)	0.0010	3e
<i>CF1037 (daf-16 (mu86) I)</i>	10.1	83/100	9.0	81/100	12% (14)	0.0002	
<i>LRL31 (hlh-30 (tm1978) IV)</i>	14.7	72/100	12.1	62/100	22% (22)	<0.0001	3f
<i>LRL31 (hlh-30 (tm1978) IV)</i>	8.7	59/100	7.9	77/100	10% (14)	<0.0001	
<i>CF24905 (hsf-1 (sy441) I)</i>	12.4	36/100	11.9	35/100	4% (22)	0.5855	3g
<i>CF24905 (hsf-1 (sy441) I)</i>	10.7	86/100	10.2	85/100	5% (14)	0.3276	
<i>MAH349 (sqIs35[sqst-1p::sqst-1::GFP + unc-122p::rfp])</i>	11.8	40/100	9.8	44/100	20% (19)	0.0010	S2a
<i>LRL160 (llcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP))</i>	12.1	73/100	8.6	69/100	41% (19)	<0.0001	3c
<i>CF1041 (e1370 III)</i>	35.0	80/100	27.3	76/100	28% (18)	<0.0001	3j
<i>CF1041 (e1370 III)</i>	25.1	60/100	23.0	81/100	9% (18)	0.0312	
<i>FX544 (cdc-48.1 (tm544) II)</i>	12.4	79/100	12.3	77/100	-1 (21)	0.7901	
<i>FX659 (cdc-48.2 (tm659) II)</i>	9.4	47/100	9.5	54/100	1 (12)	0.8290	S4c
<i>FX659 (cdc-48.2 (tm659) II)</i>	11.6	79/100	11.5	76/100	1 (21)	0.5981	

Supplemental Table 4. Lifespan analyses related to *atgl-1* silencing. Animals were developed at 20°C on OP50 and transferred on control bacteria or bacteria expressing dsRNA against *atgl-1* and grown at 25°C during adulthood. Statistical analyses: Mantel-Cox log-rank

Supplemental Table 5

Published strains used in this study:		
Strain	Genotype	Strain origin
N2	Wild-type, WT	Hansen Lab
CF1037	<i>daf-16 (mu86) I</i>	Hansen Lab
CF1041	<i>daf-2(e1370) III</i>	Hansen Lab
CF2495	<i>hsf-1(sy441) I</i>	Hansen Lab
FX544	<i>cdc-48.1(tm544) II</i>	CGC, National Bioresource Project at the Tokyo Women's Medical University School of Medicine
FX659	<i>cdc-48.2(tm659) II</i>	CGC, National Bioresource Project at the Tokyo Women's Medical University School of Medicine
FX1978	<i>hlh-30 (tm1978) IV</i>	CGC, National Bioresource Project at the Tokyo Women's Medical University School of Medicine
GMC101	<i>dvls100 [unc-54p::A-beta-1-42::unc-54 3'-UTR + mtl-2p::GFP]</i>	CGC
LIU1	<i>ldrls1 (dhs-3p::dhs-3::GFP + unc-76(+))</i>	CGC
MAH215	<i>sqIs15[lgg-1p::mCherry::GFP::lgg-1 + rol-6]</i>	Hansen Lab
MAH349	<i>sqIs35[sqst-1p::sqst-1::GFP + unc-122p::rfp]</i>	Hansen Lab
MAH844	<i>sqEx146[sqst-1p::sqst-1 + rol-6]</i>	CGC
VC2196	<i>sqst-1 (ok2892) IV</i>	CGC
VS20	<i>hJIs67 [atgl-1p::atgl-1::GFP + mec-7::RFP]</i>	CGC

Supplemental Table 5. Published strains used in the study

Supplemental Table 6

New strains created for this study:		
Strain	Genotype	Comments
LRL24	<i>daf-2(e1370) III; sqIs35[pMH951/SQST::GFP/p62::GFP+pMH876/unc-122p::rfp]</i>	CF1041 x MAH349
LRL31	<i>hlh-30 (tm1978) IV</i>	FX1978 4x backcrossed to N2
LRL90	<i>llcEx39 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>	Injected N2 with 20 ng/μL pLAP26 and 5 ng/μL pLP7. pLP7 (<i>myo-2p::GFP::unc-54</i>) was obtained from Addgene (pBCN27). pLAP26 (<i>sqst-1p::sqst-1::RFP::unc-54</i>) was generated by NEBuilder® HiFi DNA Assembly Cloning Kit (New England BioLabs Inc., Ipswich, MA) by replacing the 3XFLAG-tag with the <i>RFP</i> sequence in pLP25 (<i>sqst-1p::sqst-1::3XFLAG::unc-54</i>) (unpublished). The <i>RFP</i> insert was PCR-amplified from Addgene plasmid #8938 (<i>unc-122p::RFP</i>) with HiFi-compatible forward primer LC209 (5' GATGTGCTTCAGGCGCTTCTTCACGGCTCGGGCTCGATGGTGCGCTCCTCCAAGAACG 3') and reverse primer LC210 (5' GACACCAGACAAGTTGGTAATGGCTACAGGAACAGGTGGTGGC 3'). For linearizing and amplifying linear fragments of the vector backbone <i>sqst-1p::sqst-1::unc-54</i> from pLAP25, HiFi-compatible forward primer LC207 (5' CCATTACCAACTTGTCTGGTGC 3') and reverse primer LC208 (5' GTGAAGAAGCGCCTGAAGACACATC 3') were used. Ligation of insert to the vector backbone and subsequent transformation of products into competent <i>E. coli</i> , were performed according to manufacturer's instructions.
LRL132	<i>llcEx55 (sqst-1p::sqst-1::GFP::RFP::unc-54)</i>	Injected N2 with 20 ng/μL pLAP29 (<i>sqst-1p::sqst-1::GFP::RFP::unc-54</i>). pLAP29 was generated by NEBuilder® HiFi DNA Assembly Cloning Kit (New England BioLabs Inc., Ipswich, MA) by inserting the <i>GFP</i> sequence 3' and 5' of the <i>sqst-1</i> and <i>RFP</i> sequences in pLAP26 (<i>sqst-1p::sqst-1::RFP::unc-54</i>) respectively. The <i>GFP</i> insert was PCR-amplified from plasmid #836 kindly provided by Dr Andrew Dillin (UC Berkeley) with HiFi-compatible forward primer LC251 (5' TTCAGGCGCTTCTTCACGGCTCGGGCTCGATGAGTAAGGAGAAGAACTTTTC 3') and reverse primer LC252 (5' GACGTTCTTGGAGGAGCGCACCATCGAGCCGCCGCCGCTTTGTATAGTTCATCCATGC CATG 3'). For linearizing and amplifying the vector backbone pLP26, HiFi-compatible forward primer LC244 (5' GATGGTGCCTCCTCCAAGAAGTC 3') and reverse primer LC250 (5' GCCGTGAAGAAGCGCCTGAAGACAC 3') were used. Ligation of insert to the vector backbone and subsequent transformation of products into competent <i>E. coli</i> , were performed according to manufacturer's instructions.
LRL160	<i>llcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>	UV irradiation of LRL90, 6x backcrossed to N2
LRL161	<i>llcls13 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>	UV irradiation of LRL90, 6x backcrossed to N2
LRL170	<i>daf-2(e1370) III; sqst-1 (ok2892) IV</i>	CF1041 x VC2196
LRL171	<i>daf-2(e1370) III; llcls12 (p62p::p62::RFP::unc-54 + myo-2p::GFP)</i>	CF1041 x LRL160
LRL175	<i>ldrls1 (dhs-3p::dhs-3::GFP + unc-76(+)); llcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>	LRL87 (LIU1 4x backcrossed into N2) x LRL160
LRL178	<i>hjlS67 [atgl-1p::atgl-1::GFP + mec-7::RFP]; llcls12 (sqst-1p::sqst-1::RFP::unc-54 + myo-2p::GFP)</i>	VS20 x LRL160

Supplemental Table 6. New strains created for this study

Supplemental Table 7

Genes	Direction	Sequence
<i>act-1</i>	Forward	CTACGAACTTCCTGACGGACAAG
<i>act-1</i>	Reverse	CCGGCGGACTCCATACC
<i>atgl-1</i>	Forward	CCGGACGTCTGGTTATCTCG
<i>atgl-1</i>	Reverse	GCTCGTCGTAGATTGGCTGA
<i>cyn-1</i>	Forward	GTGTCACCATGGAGTTGTTC
<i>cyn-1</i>	Reverse	TCCGTAGATTGATTCACCAC
<i>daf-16</i>	Forward	ATCCAATTGTGCCAAGCACTAA
<i>daf-16</i>	Reverse	CCACCATTTTGATAGTTTCCATAGG
<i>hlh-30</i>	Forward	CTCATCGGCCGGCGCTCATC
<i>hlh-30</i>	Reverse	AGAACGCGATGCGTGGTGGG
<i>hsf-1</i>	Forward	GCGGCTCCGTATAAGAATGCGACTAGGC
<i>hsf-1</i>	Reverse	TTAAACCAAATTAGGATCCGATGGACTTGGAGTAC
<i>sqst-1</i>	Forward	TGGCTGCTGCATCATCCGCT
<i>sqst-1</i>	Reverse	TCAATCGTGCCGAGACCGGG

Supplemental Table 7. qPCR primers sequences