

**Supplementary information for**

**Fatty acids derived from the probiotic *Lacticaseibacillus rhamnosus* HA-114 suppress age-dependent neurodegeneration**

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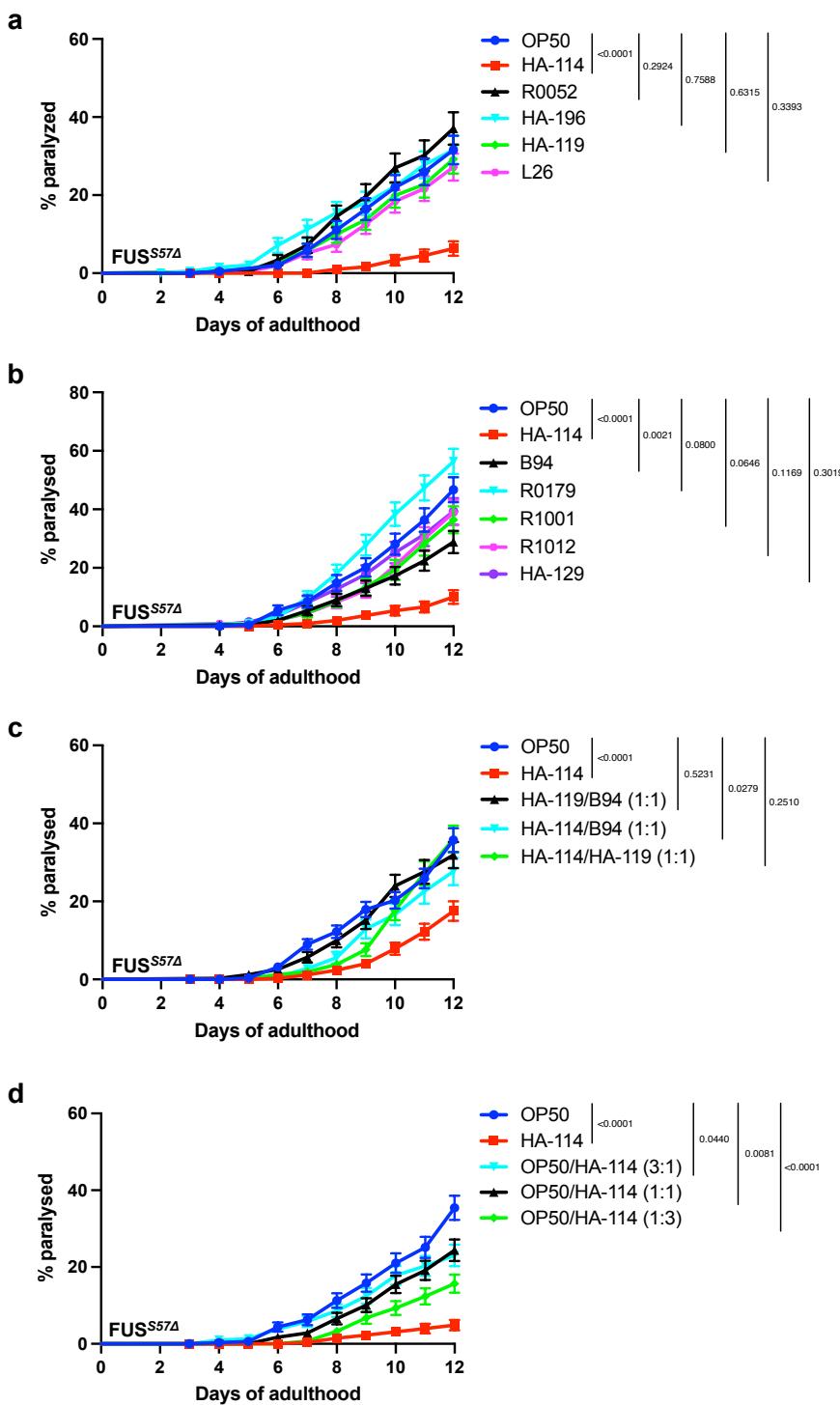
**Supplementary Table 1: List of upregulated genes in N2 worms fed with HA-114 (compared to OP50)**

**Supplementary Table 2: List of downregulated genes in N2 worms fed with HA-114 (compared to OP50)**

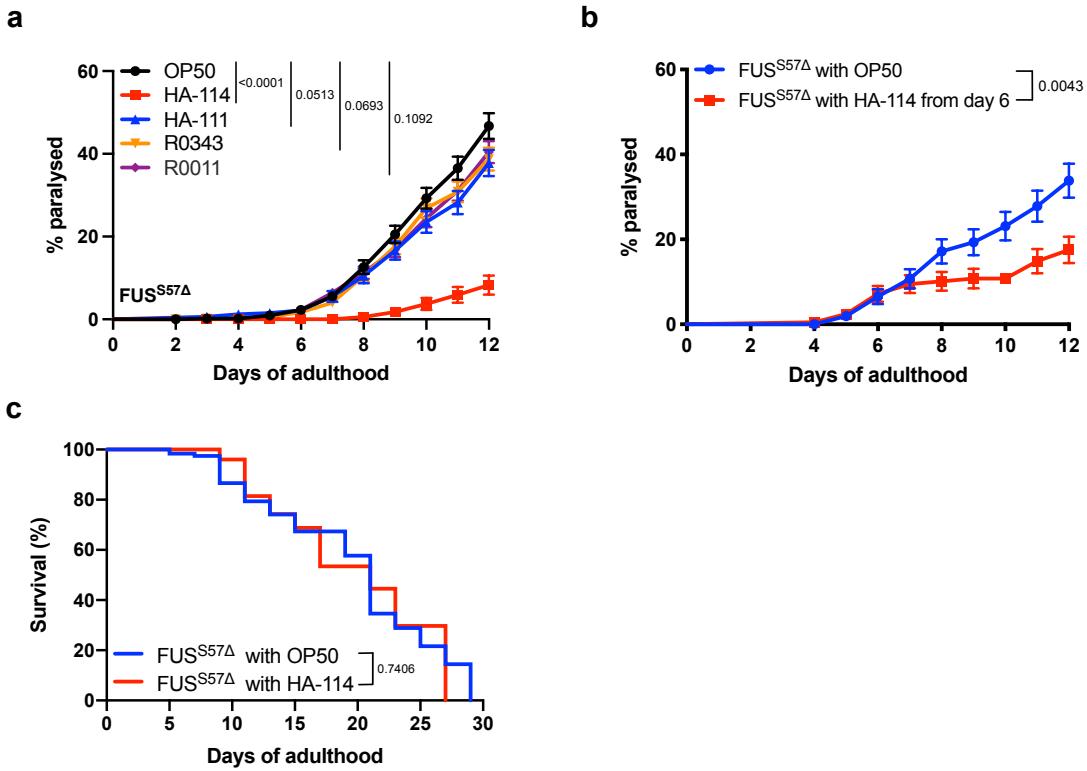
**Supplementary Table 3: List of upregulated genes in N2 worms fed with B94 (compared to OP50)**

**Supplementary Table 4: List of downregulated genes in N2 worms fed with B94 (compared to OP50)**

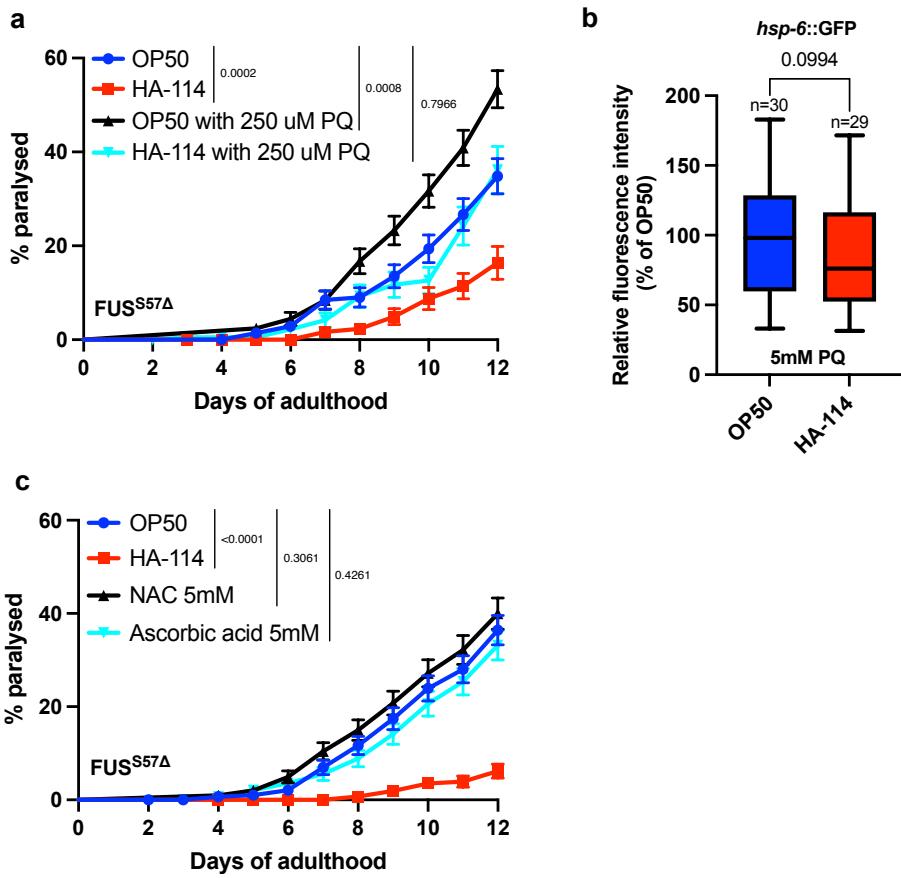
**Supplementary Table 5: List of oligo sequences used for genotyping**



**Supplementary figure 1. Probiotics screen identified *Lacticaseibacillus rhamnosus* HA-114 as a neuroprotective bacterial strain.** Transgenics were monitored from the adult stage, scored daily for paralysis. (a) FUS<sup>S57Δ</sup> worms fed with *L. helveticus* R0052, *L. paracasei* HA-196, *L. plantarum* HA-119 or *L. casei* L26 have the same paralysis rate as the worms fed with OP50, while worms fed with *L. rhamnosus* HA-114 showed less paralysis. (b) Transgenic animals fed with either, *B. subtilis* R0179, *P. acidilactici* R1001, *L. plantarum* R1012 or *B. breve* HA-129 do not show any differences in paralysis rates when compared to animals fed with OP50. Animals fed with *B. animalis* subsp. *lactis* B94 showed less paralysis than the ones fed with OP50, but showed more paralysis than animals supplemented with HA-114. (c) HA-114/B94 (1:1) is the only probiotic blend preventing paralysis in FUS<sup>S57Δ</sup> worms, at lesser extent than HA-114 alone. (d) Worms fed with blends with higher concentrations of HA-114, compared to OP50, showed less paralysis compared to transgenics expressing mutant FUS fed with OP50 alone. For paralysis (panels a-d) curves were generated and compared using the log-rank (Mantel–Cox) test. Panel a: OP50 n=211; HA-114 n=212; R0052 n=211; HA-196 n=210; HA-119 n=213; L26 n=210; . Panel b: OP50 n=210; HA-114 n=211; R0179 n=210; R1001 n=211; R1012 n=213; HA-129 n=206; B94 n=213. Panel c: OP50 n= 590; HA-114 n=382; HA-119/B94 (1:1) n=351; HA-114/B94 (1:1) n=361; HA-114/HA-119 (1:1) n=359. Panel d: OP50 n=325; HA-114 n=314; OP50/HA-114 (3:1) n= 315; OP50/HA-114 (1:1) n=312; OP50/HA-114 (1:3) n=314.

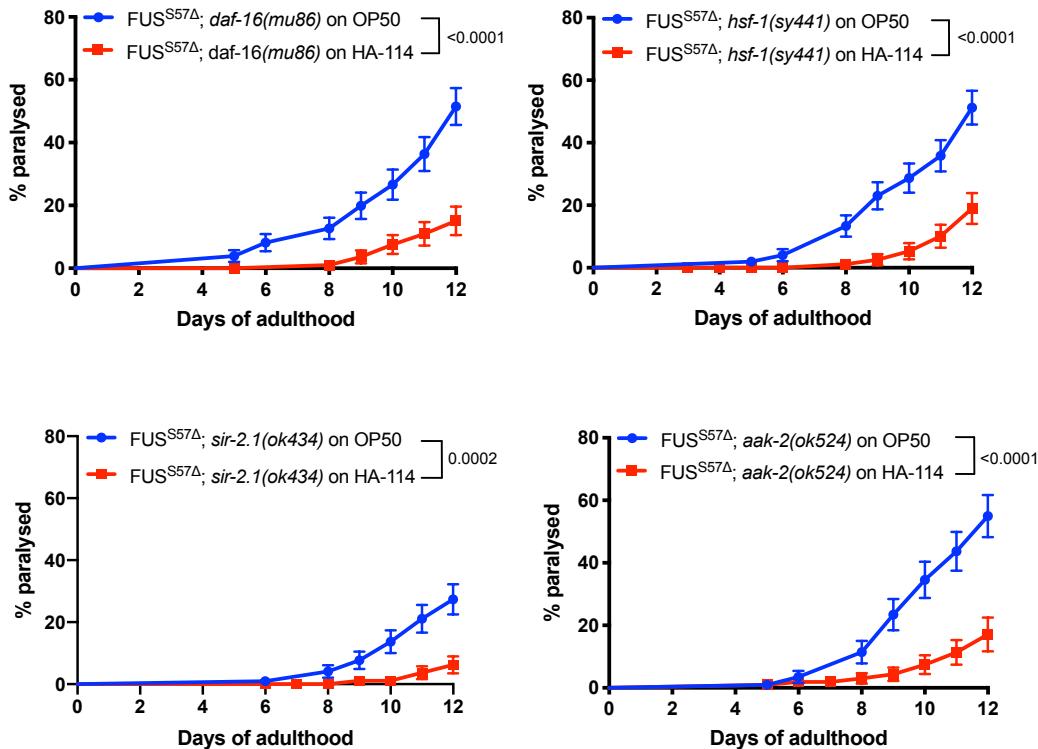


**Supplementary figure 2. *Lacticaseibacillus rhamnosus* HA-114 is the only neuroprotective *rhamnosus* strain but does not extend lifespan.** Transgenics were monitored from the adult stage, scored daily for paralysis. (a) FUS<sup>S57Δ</sup> worms fed with *L. rhamnosus* strains R0011, R0343 and HA-111 have the same paralysis rate as the worms fed with OP50. (b) Worms fed with HA-114 from day 6 (onset of paralysis) showed less paralysis compared to transgenics expressing mutant FUS fed with OP50. (c) Transgenics were monitored from the adult stage, scored every two days for mortality, and fed with control OP50 or HA-114. Mutant FUS worms fed with HA-114 do not show any lifespan extension when compared to transgenics expressing mutant FUS fed with OP50. For paralysis and lifespan assays (panels a-c) curves were generated and compared using the log-rank (Mantel–Cox) test. Panel a: OP50 n=582; HA-114 n=212; HA-111 n=331; R0343 n=585; R0011 n=588. Panel b: OP50 n=210; HA-114 from day 6 n=206. Panel c: OP50 n=126; HA-114 n=122.

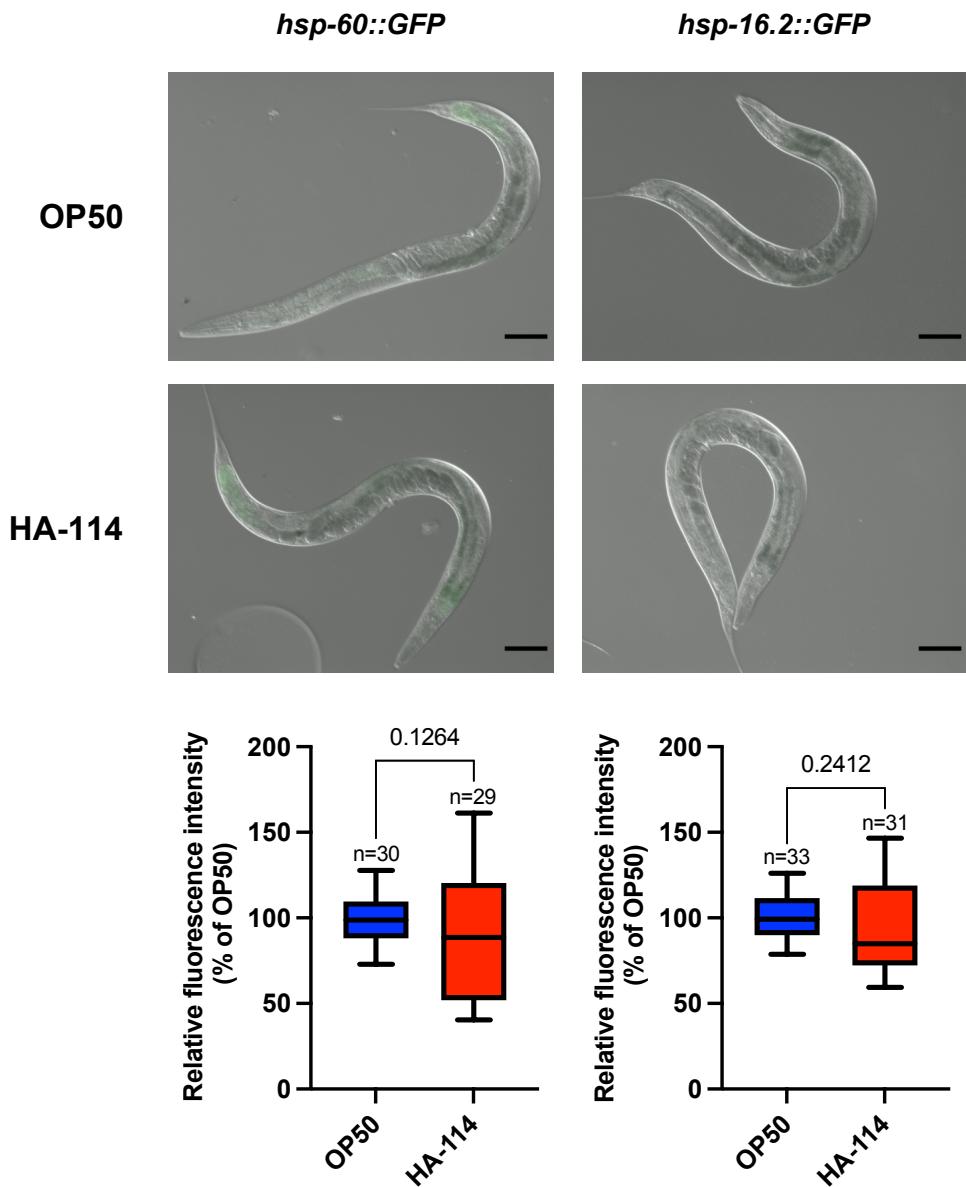


**Supplementary figure 3. *Lacticaseibacillus rhamnosus* HA-114 prevents damage from chronic oxidative stress.** (a) Transgenics were monitored from the adult stage, scored daily for paralysis. Chronic treatment of 250  $\mu$ M paraquat increased paralysis in  $FUS^{S57\Delta}$  animals. HA-114 supplementation prevents increase of paralysis from paraquat treatment. (b) HA-114 treatment did not decrease *hsp-6::GFP* signal after acute oxidative stress. (c) Worms treated with either N-acetyl cysteine (NAC) or Ascorbic acid have the same paralysis rate as the worms fed with OP50. For paralysis assays (panels a & c) curves were generated and compared using the log-rank (Mantel–Cox) test. Panel a: OP50 n=216; HA-114 n=196; OP50 with 250 $\mu$ M Paraquat n=205; HA-114 with 250 $\mu$ M Paraquat n=199. Panel c: OP50 n=312; HA-114 n=315; NAC 5mM n=310; Ascorbic acid 5mM n=303. For fluorescence quantification (panel b), an unpaired

t-test was performed, and  $n$  are indicated in the figure. For boxplots, minimum, first quartile, median, third quartile, and maximum are shown.

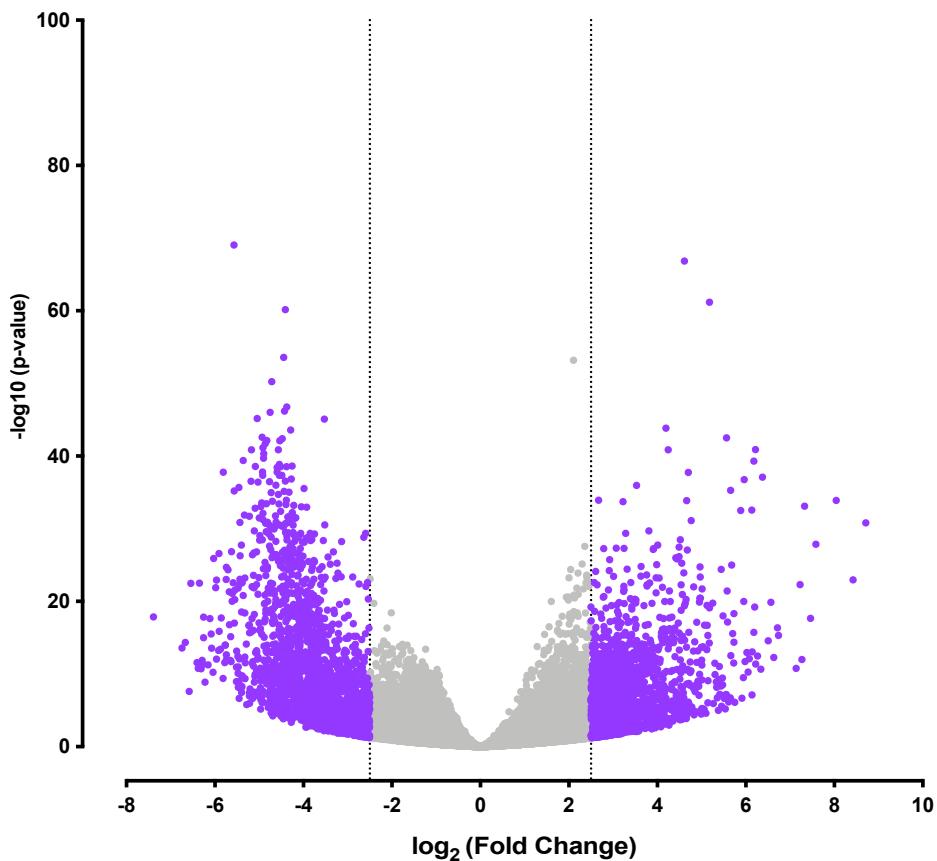


**Supplementary figure 4. HA-114 does not require classic stress and metabolic pathways in FUS<sup>S57Δ</sup> worms for neuroprotection.** Transgenics were monitored from the adult stage, scored daily for paralysis. Neuroprotection provided by *L. rhamnosus* HA-114 was unaffected by *daf-16(mu86)* deletion, nor by *hsf-1(sy441)* point mutation. Both *sir-2.1* and *aak-2* genes are not required for neuroprotection granted by HA-114 probiotics. For paralysis assays, curves were generated and compared using the log-rank (Mantel–Cox) test. FUS<sup>S57Δ</sup>; *daf-16(mu86)* on OP50 n=103; FUS<sup>S57Δ</sup>; *daf-16(mu86)* on HA-114 n=106; FUS<sup>S57Δ</sup>; *hsf-1(sy441)* on OP50 n=103; FUS<sup>S57Δ</sup>; *hsf-1(sy441)* on HA-114 n=105; FUS<sup>S57Δ</sup>; *sir-2.1(ok434)* on OP50 n=101; FUS<sup>S57Δ</sup>; *sir-2.1(ok434)* on HA-114 n=106; FUS<sup>S57Δ</sup>; *aak-2 (ok524)* on OP50 n=104; FUS<sup>S57Δ</sup>; *sir-2.1(ok524)* on HA-114 n=107.

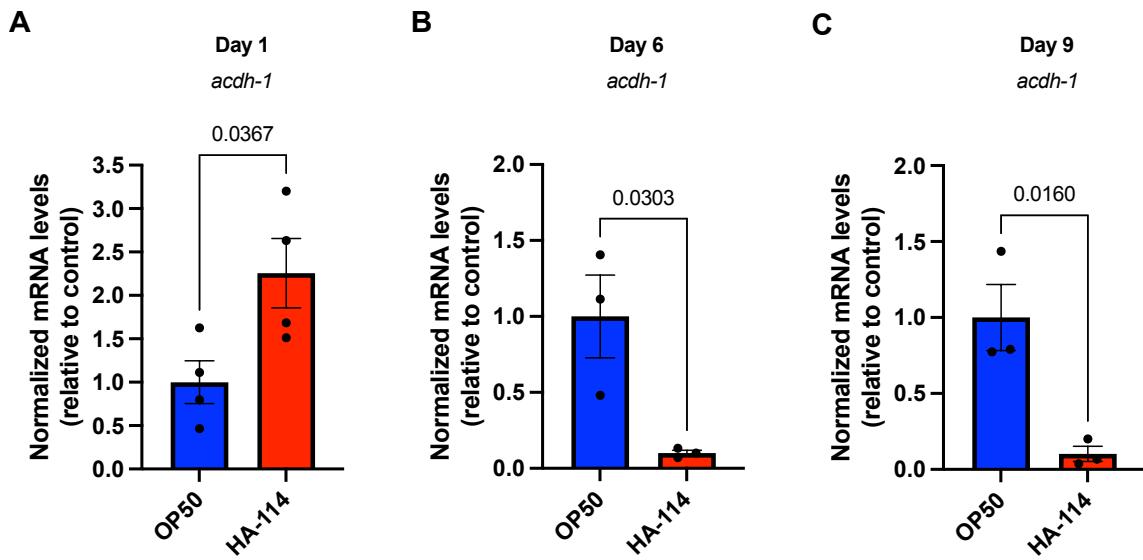


**Supplementary figure 5. HA-114 does not activate classic stress pathways in *C. elegans*.** HA-114 did not affect GFP expression of key genes of the endoplasmic reticulum unfolded protein response (UPR<sub>Mito</sub>; *hsp-60*) or cytoplasmic unfolded protein response (UPR<sub>Cyt</sub>; *hsp-16.2*). For fluorescence quantifications, unpaired t-test were performed, and *n* are indicated in the figure. Scale bar = 100  $\mu$ m. For boxplots, minimum, first quartile, median, third quartile, and maximum are shown.

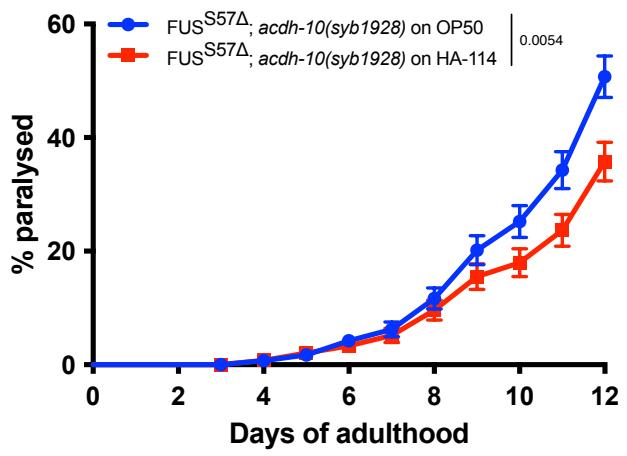
### OP50 vs B94



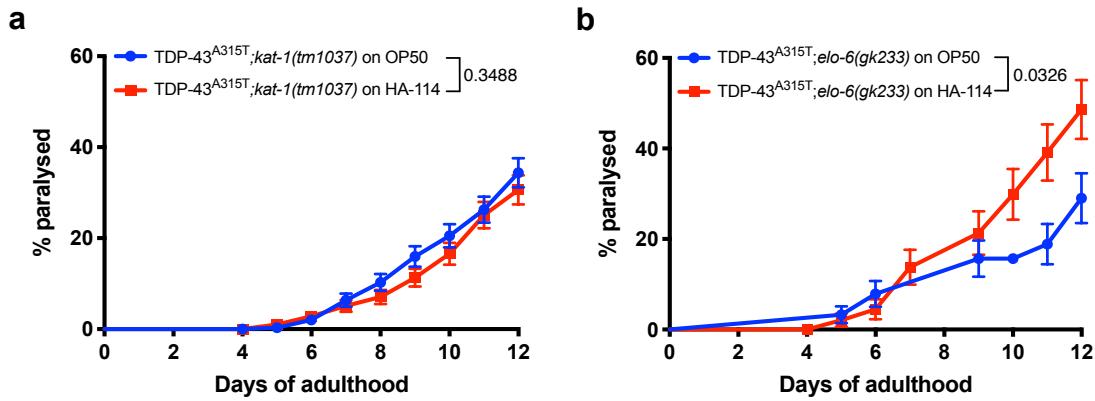
**Supplementary figure 6. *Bifidobacterium animalis* subsp. *lactis* B94 induces differential genes expression in *C. elegans*.** Volcano plot of RNA-Seq data of N2 worms fed with *Bifidobacterium animalis* subsp. *lactis* B94 and compared to worms fed with OP50. The data for all genes were plotted as  $\log_2$  fold change versus  $-\log_{10}$  of the adjusted p-value. Data: GEO accession: GSE189988; SRA study:SRP348888.



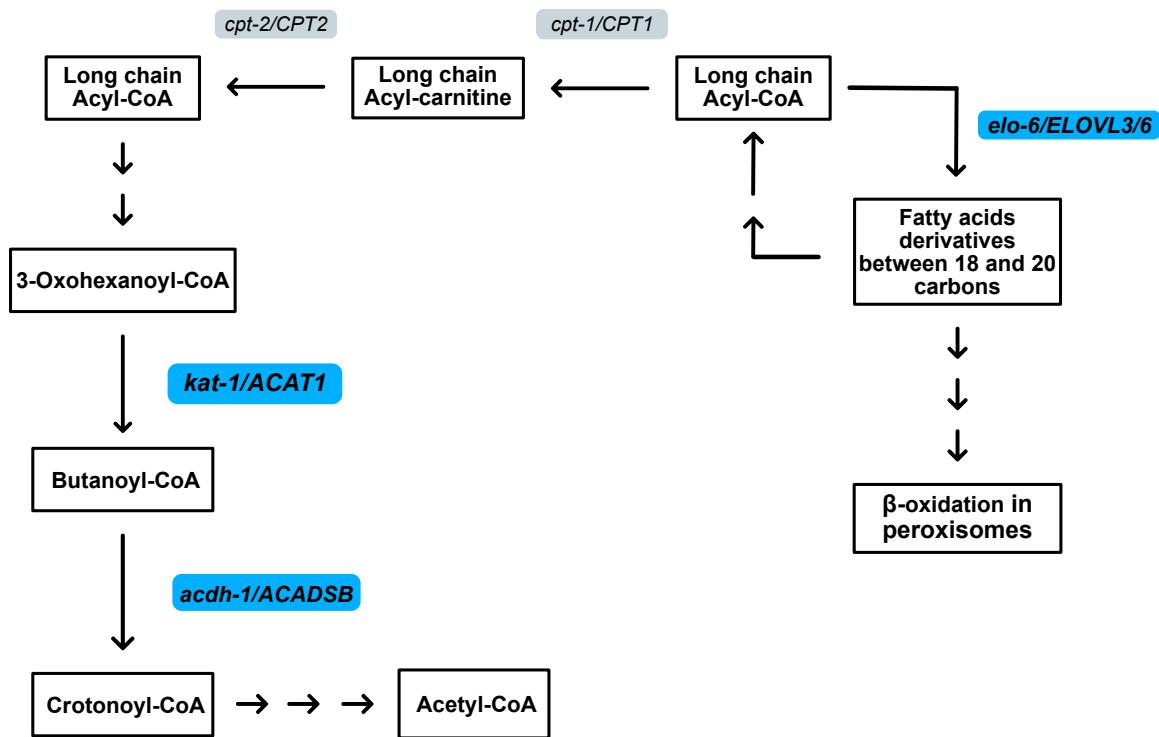
**Supplementary figure 7. HA-114 modulate *acdh-1* expression through aging in mutant FUS worms.** (a) mRNA expression of *acdh-1* was significantly increased in day 1 FUS<sup>S57Δ</sup> worms fed with HA-114 when compared to animals fed with OP50. HA-114 treatment decreased *acdh-1* expression through aging, at day 6 (b) and day 9 (c). For TaqMan assays (panels a-c), an unpaired t-test was performed. Panel a: n=4 per condition. Panel b: n=3 per condition. Panel c: n=3 per condition. Data are presented as mean ± SEM.



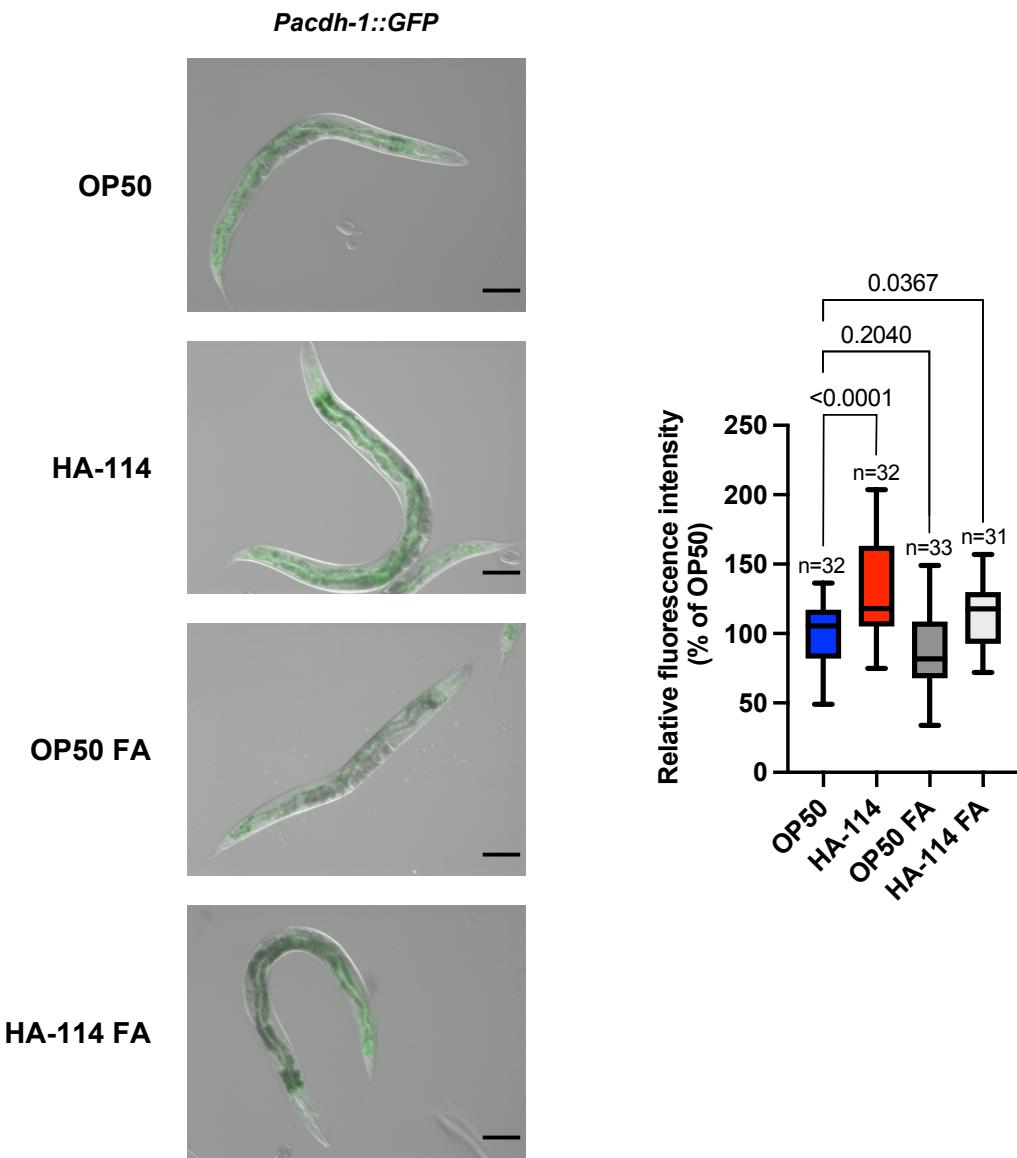
**Supplementary figure 8. *acdh-10* is not required for neuroprotection provided by HA-114 in FUS<sup>S57Δ</sup> worms.** Transgenics were monitored from the adult stage, scored daily for paralysis. Neuroprotection provided by *L. rhamnosus* HA-114 was unaffected by *acdh-10(syb1928)* nonsense mutation. Curves were generated and compared using the log-rank (Mantel–Cox) test. FUS<sup>S57Δ</sup>; *acdh-10(syb1928)* on OP50 n=419; FUS<sup>S57Δ</sup>; *acdh-10(syb1928)* on HA-114 n=421.



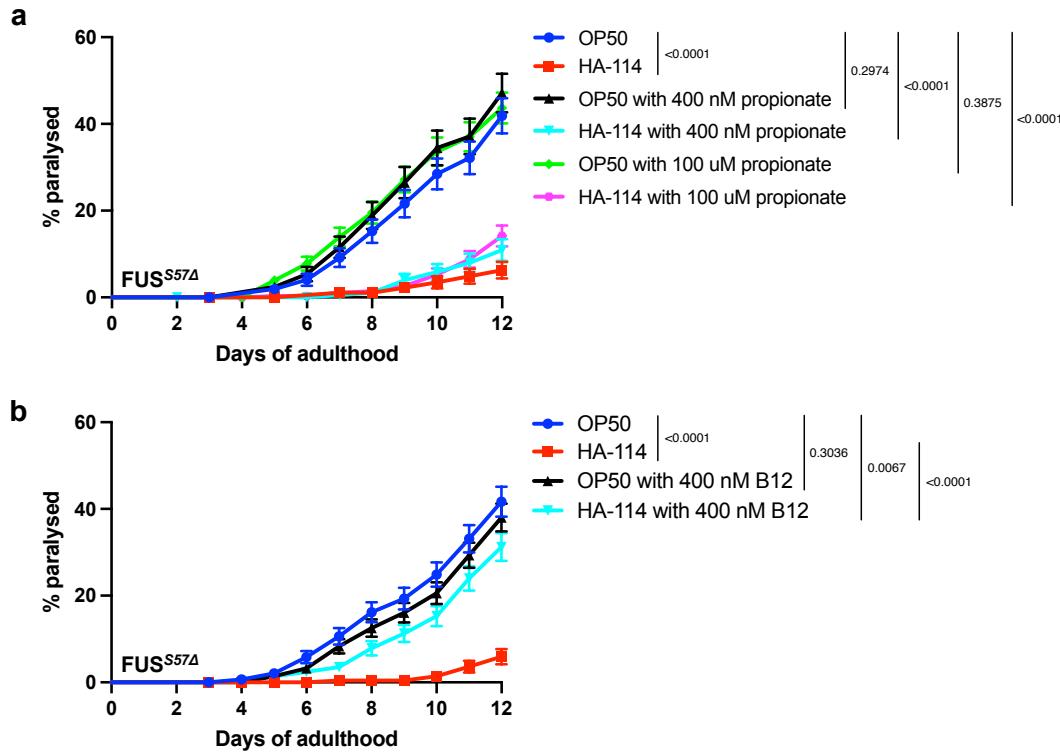
**Supplementary figure 9. *kat-1* and *elo-6* are essential for neuroprotection provided by HA-114 in TDP-43<sup>A315T</sup> ALS model.** Transgenics were monitored from the adult stage, scored daily for paralysis. Deletion of *kat-1* (a) and *elo-6* (b) altered the beneficial effect of HA-114. For paralysis assays, curves were generated and compared using the log-rank (Mantel–Cox) test. Panel a: TDP-43<sup>A315T</sup>; *kat-1(tm1037)* on OP50 n=308; TDP-43<sup>A315T</sup>; *kat-1(tm1037)* on HA-114 n=295. Panel b: TDP-43<sup>A315T</sup>; *elo-6(gk233)* on OP50 n=92; TDP-43<sup>A315T</sup>; *elo-6(gk233)* on HA-114 n=102.



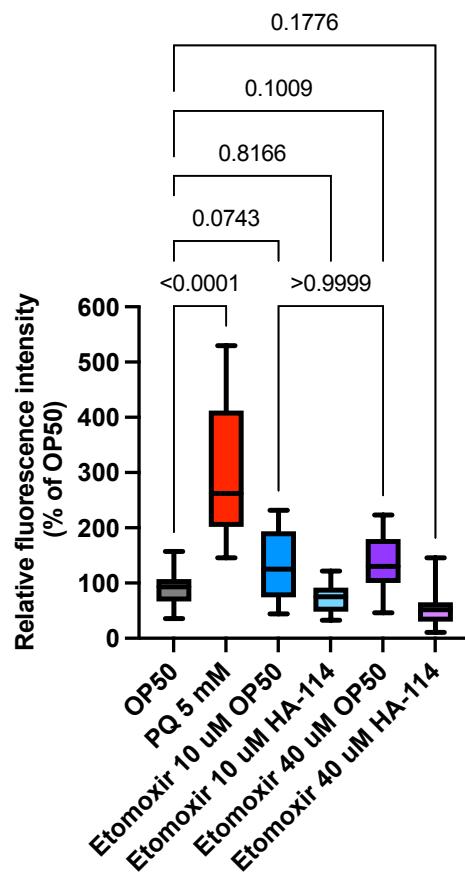
**Supplementary figure 10. Simplified pathway of fatty acids metabolism and β-oxidation in *C. elegans* and *H. sapiens*.** Enzymes names are enclosed in rounded rectangles. *acdh-1/ACADSB*: Acyl CoA dehydrogenase; *cpt-1/CPT1*: carnitine palmitoyl transferase 1; *cpt-2/CPT2* : carnitine palmitoyl transferase 2; *elo-6/ELOVL3/6*: fatty acid elongase 3/6; *kat-1/ACAT1*: 3-Ketoacyl-coA thiolase.



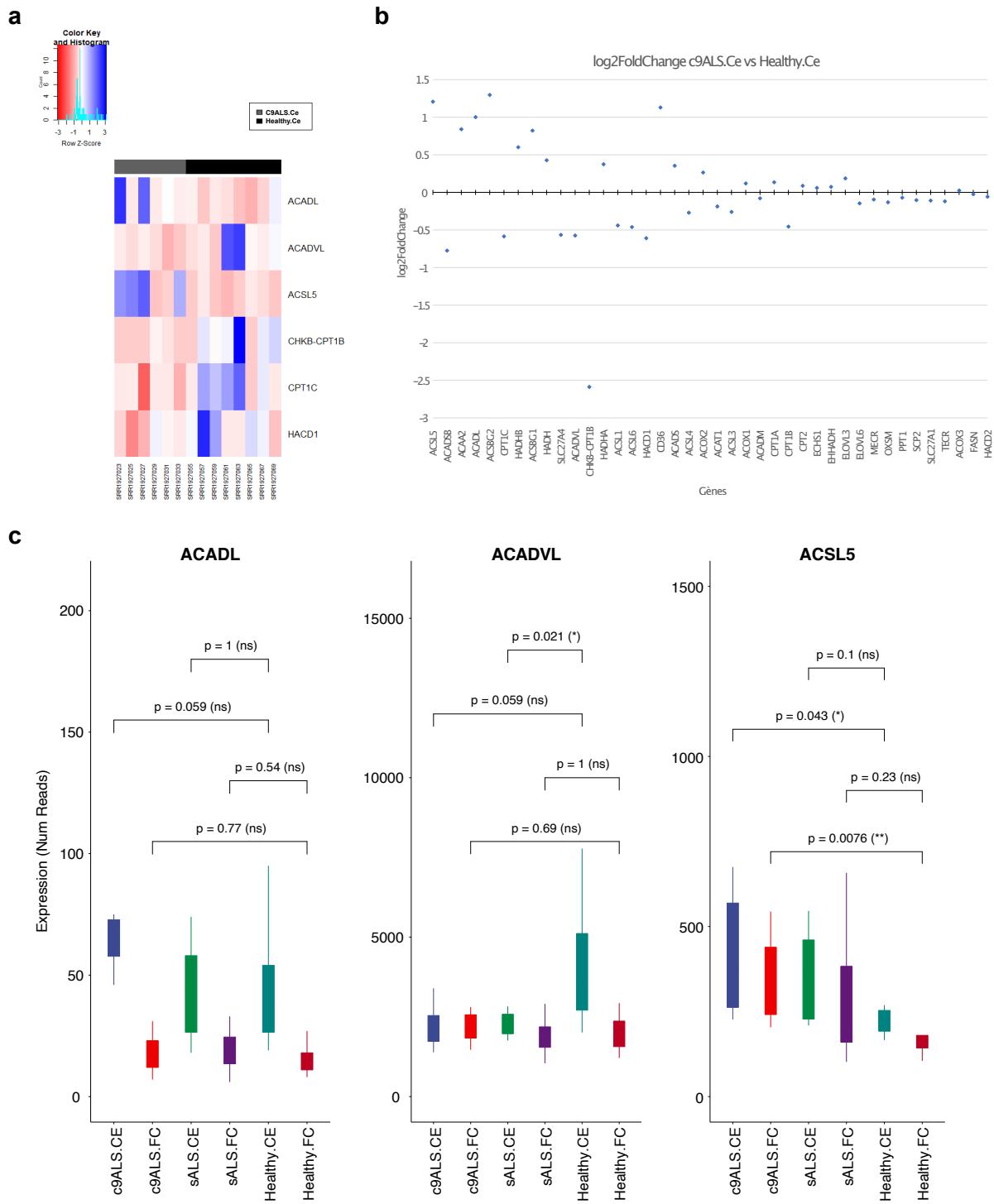
**Supplementary figure 11. *acd $h$ -1* is activated by HA-114' fatty acids.** Worms were fed with either OP50, HA-114 or a mix of OP50 and fatty acids, extracted from OP50 or HA-114, for 24h before analysis. Fatty acids from OP50 did not affect GFP expression of the *Pacd $h$ -1::GFP* reporter strain, while HA-114' fatty acids were enough to increased GFP signal. For fluorescence quantification, one-way ANOVA were performed, and n are indicated in the figure. Scale bar = 100  $\mu$ m. For boxplots, minimum, first quartile, median, third quartile, and maximum are shown.



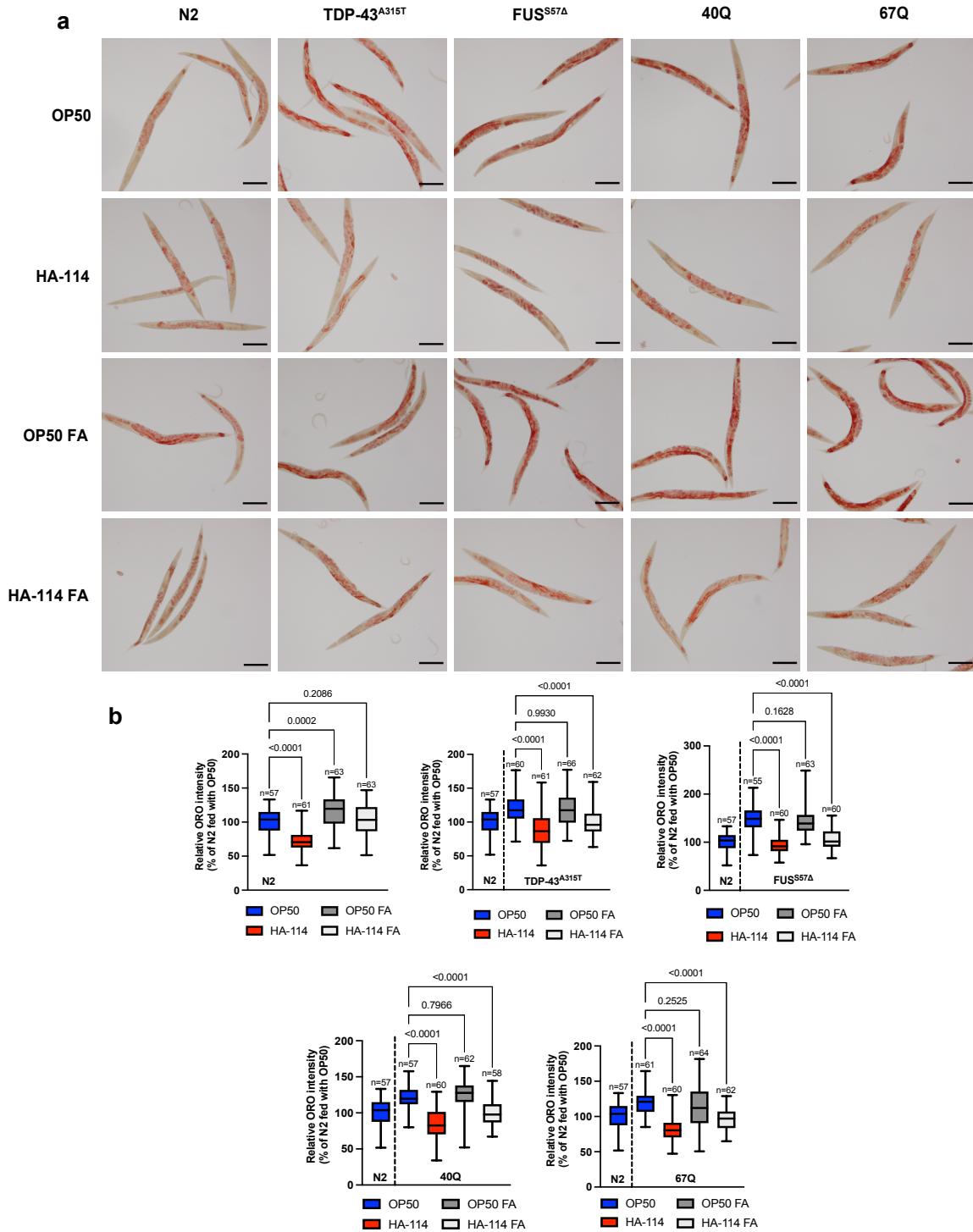
**Supplementary figure 12. Modulating *acdh-1* pathway partially affects HA-114 neuroprotective effect.** Transgenics were monitored from the adult stage, scored daily for paralysis. (a) Supplementation of propionate does not rescue paralysis phenotype in  $FUS^{S57\Delta}$  worms. Combination of HA-114 and propionate does not cause propionate toxicity in these animals. (b) Vitamin B12 supplementation prevent HA-114 to have its neuroprotective effect, but does not exacerbate paralysis phenotype in OP50 fed worms. For paralysis assays, curves were generated and compared using the log-rank (Mantel–Cox) test. Panel a: OP50 n=211; HA-114 n=208; OP50 with 400nM propionate n=212; HA-114 with 400nM propionate n=211; OP50 with 100μM propionate n=317; HA-114 with 100μM propionate n=290. Panel c: OP50 n=314; HA-114 n=262; OP50 with 400nM B12 n=300; HA-114 with 400nM B12 n=299.



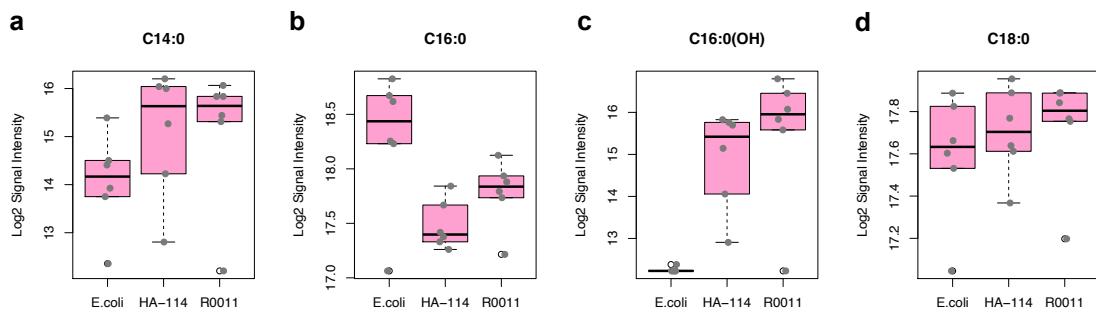
**Supplementary figure 13. Etomoxir does not cause oxidative stress in *C. elegans*.** Transgenics were treated with Etomoxir for 24h before analysis. Etomoxir does not significantly increase *hsp-6::GFP* signal, on either OP50 or HA-114 diet. For fluorescence quantification, one-way ANOVA was performed. OP50 n=30, PQ 5mM n=27, Etomoxir 10uM on OP50 n=29, Etomoxir 10uM on HA-114 n=29, Etomoxir 40uM on OP50 n=28, Etomoxir 40uM on HA-114 n=29. For boxplots, minimum, first quartile, median, third quartile, and maximum are shown.



**Supplementary figure 14: Genes associated with  $\beta$ -oxidation are differentially expressed in the cerebellum and the frontal cortex of c9ALS patients.** (a) Differentially expressed genes associated with the  $\beta$ -oxidation pathway between *C9orf72* ALS patients and healthy individuals were plotted as heatmap. Red indicates low relative expression and blue indicates high relative expression. (b) Log2 Fold change of differentially expressed genes associated with the  $\beta$ -oxidation pathway between *C9orf72* ALS patients and healthy individuals. (c) *ACADL* expression is upregulated in the cerebellum of c9ALS and *ACADVL* is downregulated in c9ALS and sALS cerebellum. Interestingly, *ACSL5* expression is upregulated in the cerebellum and the frontal cortex of c9ALS. Data: GEO accession: GSM1642314; SRA study: SRP056477. For boxplots, minimum, first quartile, third quartile, and maximum are shown.



**Supplementary figure 15. Fatty acids from HA-114 modulate lipid accumulation in worm age-dependent neurodegeneration models.** (a) Representative images of worms fed with OP50, *L. rhamnosus* HA-114, fatty acids from OP50 or fatty acids from HA-114 and stained with Oil Red O. N2 worms show a basal level of lipid accumulation. (b) Quantification of Oil Red O show same levels of fat accumulation in worms expressing  $\text{FUS}^{\text{S57}\Delta}$ ,  $\text{TDP-43}^{\text{A315T}}$ , and polyQ expansion (40Q and 67Q) when fed with either OP50 or fatty acid extract from OP50. Worms fed with fatty acids from HA-114 showed a significant decrease of lipid accumulation. For the Oil Red O quantification graphs (panel b), one-way ANOVA were performed and  $n$  are indicated in the figure. Scale bar = 100  $\mu\text{m}$ . For boxplots, minimum, first quartile, median, third quartile, and maximum are shown.



**Supplementary figure 16. Free fatty acids (FFA) annotated from OP50, HA-114 and R0011 bacterial strains.** Log2 signal intensity from (a) C14:0 myristic acid (HA-114 vs OP50  $p=0.1618594$ ; R0011 vs OP50  $p=0.1730919$ ; HA-114 vs R0011  $p=0.8966804$ ), (b) C16:0 palmitic acid (HA-114 vs OP50  $p=0.01408153$ ; R0011 vs OP50  $p=0.11738097$ ; HA-114 vs R0011  $p=0.0840674$ ), (c) C16:0(OH) hydroxypalmitic acid (HA-114 vs OP50  $p=0.0002694804$ ; R0011 vs OP50  $p=0.0007397631$ ; HA-114 vs R0011  $p=0.391468$ ), (d) C18:0 stearic acid (HA-114 vs OP50  $p=0.5338358$ ; R0011 vs OP50  $p=0.4425402$ ; HA-114 vs R0011  $p=0.901340$ ). For lipidomics analysis,  $n=6$  for each bacterial strain. Raw data and untargeted lipidomic results analysis are available in Supplementary Data 1 and 2. For boxplots, minimum, first quartile, median, third quartile, maximum and each data point are shown.

Gene	log2 (Fold Change)	-log10 (p-value)	Gene	log2 (Fold Change)	-log10 (p-value)
<b>comt-4</b>	9.87862663394132	99.7453109	<i>T07G12.5</i>	6.60805071963761	27.6992845
<b>fmo-2</b>	9.54793672826199	43.6786685	<i>Y40B10A.10</i>	6.55437120438937	9.83497546
<b>col-37</b>	8.09882592083367	23.6043977	<i>clec-101</i>	6.53234125111637	15.4291571
<b>col-51</b>	7.99974875772954	16.5212658	<i>cyp-14A4</i>	6.47819223000637	17.2524927
<b>scl-12</b>	7.77678012343102	13.627124	<i>clec-60</i>	6.46941490655043	21.5608881
<b>ZK355.8</b>	7.72806356442673	24.2158052	<i>grl-23</i>	6.45038706815409	16.1948104
<b>nlp-39</b>	7.70628621197532	41.4471206	<i>W02D7.11</i>	6.40679336017293	10.5975775
<b>scl-13</b>	7.64237045387068	12.5438689	<i>col-35</i>	6.38208805437359	16.3087854
<b>mtl-1</b>	7.63840864172396	73.3528053	<i>col-36</i>	6.36194387462439	14.6750336
<b>C54C8.12</b>	7.58426311128764	30.6444151	<i>Y57E12B.11</i>	6.35114125562006	8.84129742
<b>spp-20</b>	7.57758760470988	21.0188592	<i>Y73B6BL.37</i>	6.33850300181293	14.6128333
<b>col-2</b>	7.45257342787137	19.8318924	<i>col-108</i>	6.29215024624157	12.7314131
<b>col-185</b>	7.32752273324769	16.5394412	<i>Y50E8A.19</i>	6.24646404668113	11.6861425
<b>ZK355.3</b>	7.27234875958693	18.9184428	<i>lipl-3</i>	6.1771018660647	22.7659395
<b>col-50</b>	7.09906776970553	13.0342336	<i>M6.11</i>	6.13593697212128	9.97317931
<b>scl-11</b>	6.92409948853672	9.99911968	<i>ttr-19</i>	6.06718786890319	8.88081259
<b>col-85</b>	6.90911404977131	17.2538545	<i>Y57E12B.4</i>	6.01948735106341	13.5724462
<b>col-183</b>	6.83294309056956	28.6669326	<i>grl-20</i>	5.99933755902934	12.3038485
<b>grl-25</b>	6.75068617466407	16.5134975	<i>smf-3</i>	5.98431945049091	37.4449756
<b>col-44</b>	6.69878248210145	18.0031516	<i>C13A2.12</i>	5.95549751109163	9.2819474
<b>cut-1</b>	6.65779636590876	13.9896961	<i>gst-19</i>	5.94282889293229	12.789848
<b>col-40</b>	6.64994189406571	19.6592105	<i>F20E11.17</i>	5.93693818626582	11.7431324
<b>col-102</b>	6.63923155878408	13.4238371	<i>col-84</i>	5.88220338126241	11.4107272
<b>col-123</b>	6.63889601447437	13.4320701	<i>col-164</i>	5.88053302510974	9.39537277
<b>F57F4.2</b>	6.61010243445913	12.0319099	<i>col-114</i>	5.83481063285872	13.0582472

**Supplementary Table 1: List of upregulated genes in N2 worms fed with HA-114 (compared to OP50)**

Gene	log2 (Fold Change)	-log10 (p-value)	Gene	log2 (Fold Change)	-log10 (p-value)
<b>D1014.6</b>	-6.58130429443456	7.59723595	<i>H31G24.1</i>	-3.36110423381441	4.99501892
<i>cyp-35A3</i>	-5.26971806442959	9.8943547	<i>T26C11.3</i>	-3.35994858567097	2.10186277
<i>T20H9.6</i>	-4.77232062732769	4.86362304	<i>F49F1.8</i>	-3.34030650862598	2.68831392
<i>Y38H6C.23</i>	-4.39581701915455	5.76033539	<i>F36F12.3</i>	-3.32218550668426	2.66452973
<i>acdh-1</i>	-4.27824066606366	7.77503269	<i>mltn-3</i>	-3.30974507153072	4.11888428
<i>T24D5.5</i>	-4.27376263570936	4.90651812	<i>K08F11.6</i>	-3.29922845314491	11.3203483
<i>nspe-7</i>	-3.95673616454527	8.85512815	<i>clec-247</i>	-3.28672949400989	1.90351031
<i>Y32G9A.11</i>	-3.95309359571931	2.82279758	<i>cutl-7</i>	-3.27955819396815	8.02778931
<i>cyp-35A4</i>	-3.92865080818664	8.17889876	<i>ferl-1</i>	-3.27206188596272	2.3889255
<i>F02H6.1</i>	-3.91853525687342	10.7321835	<i>C04G6.6</i>	-3.24534306851372	5.46675923
<i>F32A11.5</i>	-3.84827550994329	6.88243496	<i>Y49E10.26</i>	-3.22848634462104	9.89937162
<i>mboa-5</i>	-3.78653834654188	2.90612659	<i>C44C10.5</i>	-3.20163254992974	4.60563122
<i>B0554.4</i>	-3.77878513898639	4.47307032	<i>dot-1.5</i>	-3.16513176281623	4.52525103
<i>C09G12.17</i>	-3.74519597364298	2.56419407	<i>B0250.11</i>	-3.15152606307824	1.95390021
<i>oac-42</i>	-3.7161674910615	3.10876041	<i>Y105C5B.1420</i>	-3.14592437731143	1.79352711
<i>F18A12.7</i>	-3.66831246728887	9.02666446	<i>C04E12.10</i>	-3.1214471921964	2.75762216
<i>ZC84.1</i>	-3.63205853382885	5.36165306	<i>Y47G6A.15</i>	-3.11295496938544	12.9674724
<i>B0554.2</i>	-3.61046784466151	2.26374503	<i>bath-23</i>	-3.08795367996044	3.29868589
<i>C04G6.13</i>	-3.57846422518453	2.3533466	<i>cutl-6</i>	-3.0868579702075	5.95140556
<i>nas-15</i>	-3.55399028351787	9.5448918	<i>F52G3.3</i>	-3.08053730032058	1.78710001
<i>ZK218.1</i>	-3.50723405639355	2.38502544	<i>Y49E10.30</i>	-3.05917236626404	3.62565075
<i>F16H6.4</i>	-3.49646819274977	2.20961034	<i>Y44A6B.3</i>	-3.04303932102096	3.02291594
<i>col-148</i>	-3.473671185875	5.30595715	<i>gcy-18</i>	-3.02977374072766	4.67264013
<i>C32H11.6</i>	-3.41679538726944	3.1785791	<i>C06A1.7</i>	-3.02194395846066	1.80489206
<i>F22H10.4</i>	-3.38583404474747	2.33439917	<i>Y20F4.8</i>	-3.01879749443978	3.73066234

**Supplementary Table 2: List of downregulated genes in N2 worms fed with HA-114 (compared to OP50)**

Gene	log2 (Fold Change)	-log10 (p-value)	Gene	log2 (Fold Change)	-log10 (p-value)
<b>fmo-2</b>	8.70956706	30.80558353	<i>cnc-11</i>	6.07894161	12.10115523
<i>ilys-3</i>	8.4244723	22.97385399	<i>C18H7.1</i>	6.04949025	10.2658901
<i>lipI-3</i>	8.04282975	33.90639009	<i>fbxa-24</i>	6.0220537	12.96771729
<b>C54C8.12</b>	7.58490125	27.87428669	<i>Y73B6BL.37</i>	5.97947893	11.71166751
<i>ilys-2</i>	7.46101799	17.66153356	<i>hsp-16.41</i>	5.96168784	36.75574214
<i>nlp-39</i>	7.32972011	33.10588398	<i>F49H6.5</i>	5.95512499	19.99147225
<b>W02D7.11</b>	7.26688977	11.98340288	<i>C08F1.8</i>	5.94529945	9.509269995
<b>clec-60</b>	7.2261522	22.32029752	<i>cyp-33C1</i>	5.91201039	6.673025068
<i>clx-1</i>	7.13852843	10.76526756	<i>acs-2</i>	5.88214796	32.50578365
<b>F40G12.5</b>	6.73873737	15.29875601	<i>Y46H3A.5</i>	5.74813101	6.115619855
<b>F57G4.11</b>	6.71539844	16.36843041	<i>Y53G8AM.5</i>	5.73195427	18.30334685
<b>W08A12.4</b>	6.63368495	12.2906029	<i>H39E23.3</i>	5.73052693	14.38396695
<b>T22F3.11</b>	6.56892797	19.87494156	<i>ZK971.1</i>	5.72632025	11.51830638
<b>spp-20</b>	6.50670072	14.56788288	<i>F07C4.12</i>	5.70130533	15.5649083
<i>tts-1</i>	6.37615852	37.09018362	<i>E02H4.4</i>	5.67989988	25.00699877
<b>rab-11.2</b>	6.34038243	10.66537805	<i>fbxa-165</i>	5.66322171	12.54398774
<b>dod-21</b>	6.26681417	12.48657479	<i>Y57E12B.11</i>	5.65483204	6.497716389
<i>lys-10</i>	6.22140365	11.37483603	<i>W03F9.4</i>	5.65472041	35.29341093
<i>mtl-1</i>	6.22053905	40.89787225	<i>Y60C6A.2</i>	5.64772622	6.738652939
<b>F46A8.13</b>	6.19936449	19.22317505	<i>scl-11</i>	5.60865357	6.147619693
<i>thn-1</i>	6.18271149	15.73992935	<i>T07G12.5</i>	5.58558481	17.13924825
<b>hsp-16.2</b>	6.18204413	39.29514003	<i>srg-31</i>	5.57982942	21.43650861
<b>F08H9.3</b>	6.14357275	13.05352608	<i>sodh-1</i>	5.56438661	42.50494404
<i>irld-36</i>	6.14111929	7.137245121	<i>C44H9.2</i>	5.55996121	7.192404706
<b>ugt-18</b>	6.1360785	32.57612213	<i>ins-8</i>	5.53446772	5.211344066

**Supplementary Table 3: List of upregulated genes in N2 worms fed with B94 (compared to OP50)**

Gene	log2 (Fold Change)	-log10 (p-value)	Gene	log2 (Fold Change)	-log10 (p-value)
<i>fipr-18</i>	-7.3899051	17.8629289	<i>ssp-19</i>	-5.9031358	15.8683656
<b>C16C8.19</b>	-6.7450299	13.5896424	<i>K02B12.6</i>	-5.8777989	13.4207461
<b>F49C5.11</b>	-6.6720748	14.3588193	<i>fipr-20</i>	-5.8562662	17.7295597
<b>D1014.6</b>	-6.5833517	7.60330179	<i>fis-1</i>	-5.8136158	9.37802511
<b>Y39B6A.9</b>	-6.5445814	22.4913188	<i>bli-1</i>	-5.8095208	37.7755119
<i>msp-71</i>	-6.4031816	11.5842834	<i>ZK970.8</i>	-5.780491	11.5692106
<b>R01E6.5</b>	-6.3793551	10.775615	<i>K08C9.1</i>	-5.768231	13.9929598
<b>T16G12.10</b>	-6.349873	22.5070685	<i>scl-7</i>	-5.763782	13.9937634
<b>ZK1025.3</b>	-6.310217	10.7349212	<i>C05B5.11</i>	-5.7464197	23.005554
<b>K12H6.8</b>	-6.2913412	11.8767872	<i>F25C8.1</i>	-5.741145	12.6612795
<b>T26E3.6</b>	-6.2636633	11.3583125	<i>col-138</i>	-5.7397982	24.6828362
<b>F46B6.13</b>	-6.255397	15.0117974	<i>R09H10.6</i>	-5.7367796	12.0214734
<b>F26D10.13</b>	-6.2547035	17.8234353	<i>rol-1</i>	-5.7045872	24.3361006
<b>Y102E9.6</b>	-6.2251704	8.86862954	<i>C48B4.12</i>	-5.6782743	21.3184496
<b>R03H10.4</b>	-6.1527173	11.2609968	<i>C09G12.5</i>	-5.671836	16.7723887
<i>clec-99</i>	-6.1141736	17.631972	<i>col-49</i>	-5.6509951	11.8762189
<i>fipr-28</i>	-6.0860342	15.5071309	<i>M176.10</i>	-5.6425164	15.1383091
<b>F43C11.2</b>	-6.0760143	13.5530852	<i>C16C8.7</i>	-5.6337892	11.7216452
<i>fipr-19</i>	-6.0407717	10.2289594	<i>try-8</i>	-5.6258549	26.8288941
<b>tag-329</b>	-6.0305397	25.8986167	<i>K12H6.4</i>	-5.6134512	20.0022469
<b>clec-207</b>	-5.9805215	21.875854	<i>clec-219</i>	-5.6047092	21.0832096
<b>clec-208</b>	-5.9653792	22.9368451	<i>F18E9.7</i>	-5.5864444	22.5636954
<b>cutl-7</b>	-5.9623714	12.0496394	<i>F35E12.5</i>	-5.5700749	69.0611886
<b>R11G10.4</b>	-5.9192587	13.2498415	<i>col-110</i>	-5.5656775	35.1928499
<b>bli-2</b>	-5.9096492	26.5864057	<i>K03D3.5</i>	-5.559995	17.0099999

**Supplementary Table 4: List of downregulated genes in N2 worms fed with B94 (compared to OP50)**

<b>Gene</b>	<b>Forward</b>	<b>Reverse</b>
<i>kat-1</i>	GCCCCGTACACCTATTGGATC	CTTCTGGTCCGATATTCCA
<i>acdh-1</i>	TCCAGCTAATGGGTGTTCATG	GTGCCTGTGGTGTTCTAC
<i>elo-6</i>	GACTCACATCGCATTCTGG	GAGACTTGTACCTTGTACCCA
<i>aak-2</i>	CCTGGCAACACCATAAGCTG	CAGGGTTCCACAAAGAAGTG
<i>daf-16</i>	TCTCCTCCTGTGTGCCTCC	CTTTATCCTCTTCTTGGCTCCG
<i>sir-2.1</i>	ACTTCTGGTCGTCTTCTCG	CTTCGCAATGTGTCTCGTG
<i>hsf-1</i>	AATCCTCGGCTCCATCATAATTG	CAGCCGCAACAAGACTATTG
<i>acs-20</i>	GAGGAACCTCTACACCATAAACAG	CCTTCTGATCGTATGTACGTCTC
<i>acdh-10</i>	ATCTTCCAAATCTACGAGGG	TTCAACAATGAGGGCAGTCT
Human <i>TARDBP</i>	GTCTCTTGTGGAGAGGACTTGATC	GGTTTGGCTCCCTCTGCATG
Human <i>FUS</i>	ATGGCCTCAAACGATTATAC	GATTATAGCTTGCTGCTGT

**Supplementary Table 5: List of oligo sequences used for genotyping**