

Supplementary Tables

Supplementary Table 1.

Gene	Description
<i>pfid-6*</i>	Putative prefoldin 6 subunit
C54C8.3*	An ortholog of human B3GALNT1 (beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group))
<i>vps-4*</i>	An ortholog of human VPS4A/B (vacuolar protein sorting 4 A/B)
<i>ntl-2*</i>	An ortholog of human CNOT2 (CCR4-NOT transcription complex subunit 2)
<i>fat-7*</i>	Delta-9 fatty acid desaturase
<i>inst-1</i>	Integrator complex subunit 1 homolog
T08G11.4	An ortholog of human Tgs1 (trimethylguanosine synthase 1)
<i>rae-1</i>	An ortholog of human Rae1 (ribonucleic acid export 1)
<i>ekl-4</i>	An ortholog of human DMAP1 (DNA methyltransferase 1 associated protein 1)
<i>srpa-72</i>	An ortholog of human Srp72 (signal recognition particle 72)
<i>ulp-2</i>	An ortholog of human SENP6/7 (SUMO1/sentrin specific peptidase 6/7)
<i>ulp-4</i>	An ortholog of human SENP3-EIF4A1 (SENP3-EIF4A1 readthrough (NMD candidate))
<i>cap-2</i>	Beta subunit of actin capping protein

hmg-1.2 An ortholog of members of the human canonical high mobility group family including HMGB2

C02B10.5 An ortholog of human PYGO1/2 (pygopus family PHD finger 1/2)

K07F5.14 Putative human ortholog of NOL8 (nucleolar protein 8)

sec-6 An ortholog of human EXOC3L1 (exocyst complex component 3 like 1) and EXOC3 (exocyst complex component 3)

*: RNAi targeting each gene decreased the lifespan of *daf-2* mutants compared to wild-type.

Supplementary Table 2. Analysis of lifespan assay results related to Figure 1 and Figure

S1.

Strain	Mean lifespan \pm s.e.m. (days)	75th percentile	% change	Number of animals that died/total	<i>p</i> value vs. control	Figure in text
WT/control RNAi	20.2 \pm 0.6	22		29/60		Fig.1B,1D,1E,1F
WT/ <i>daf-16</i> RNAi	18.6 \pm 0.3	20	-8%	67/90	0.0125	
WT/ <i>inst-1</i> RNAi	16.1 \pm 0.4	18	-20%	43/60	<0.0001	
WT/ <i>pfid-6</i> RNAi	18.6 \pm 0.5	20	-8%	36/90	0.0244	Fig.1B
WT/T08G11.4 RNAi	15.6 \pm 0.2	20	-23%	48/90	<0.0001	
WT/ <i>rae-1</i> RNAi	16.8 \pm 0.4	20	-17%	34/90	<0.0001	
WT/C54C8.3 RNAi	18.1 \pm 0.5	20	-10%	38/60	0.0036	Fig.1D
WT/ <i>ekl-4</i> RNAi	19.1 \pm 0.8	24	-5%	25/90	0.2201	

WT/ <i>vps-4</i> RNAi	12.4±0.2	16	-38%	72/90	<0.0001	Fig. 1E
WT/ <i>srpa-72</i> RNAi	21.1±0.6	24	5%	67/90	0.2143	
WT/ <i>ntl-2</i> RNAi	17.1±0.3	20	-15%	60/90	<0.0001	Fig. 1F
<i>daf-2(e1370)</i> /control RNAi@	44.6±1.1	48	121%	40/75	<0.0001	Fig. 1B, 1D, 1E, 1F
<i>daf-2(e1370)</i> / <i>daf-16</i> RNAi	22.3±0.6	25	-50% ^{<i>daf-2</i>}	20/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>hsf-1</i> RNAi	24.0±0.6	28	-46% ^{<i>daf-2</i>}	62/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>inst-1</i> RNAi	33.9±0.8	38	-24% ^{<i>daf-2</i>}	52/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>pfid-6</i> RNAi	32.1±1.3	38	-28% ^{<i>daf-2</i>}	9/75	<0.0001 ^{<i>daf-2</i>}	Fig. 1B
<i>daf-2(e1370)</i> /T08G11.4 RNAi	38.7±0.7	42	-13% ^{<i>daf-2</i>}	41/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>rae-1</i> RNAi	41.7±1.3	45	-7% ^{<i>daf-2</i>}	24/75	0.0241 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> /C54C8.3 RNAi	28.8±0.9	31	-36% ^{<i>daf-2</i>}	28/75	<0.0001 ^{<i>daf-2</i>}	Fig. 1D
<i>daf-2(e1370)</i> / <i>ekl-4</i> RNAi	42.4±0.9	48	-5% ^{<i>daf-2</i>}	38/75	0.0136 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>vps-4</i> RNAi	22.9±0.6	28	-49% ^{<i>daf-2</i>}	23/75	<0.0001 ^{<i>daf-2</i>}	Fig. 1E
<i>daf-2(e1370)</i> / <i>srpa-72</i> RNAi	44.8±1.2	50	0% ^{<i>daf-2</i>}	37/75	0.9535 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>ntl-2</i> RNAi	30.9±0.9	35	-31% ^{<i>daf-2</i>}	14/75	<0.0001 ^{<i>daf-2</i>}	Fig. 1F
WT/control RNAi	19.0±0.6	23		42/90		
WT/ <i>daf-16</i> RNAi	17.9±0.5	21	-5%	60/90	0.1854	
WT/ <i>hsf-1</i> RNAi	14.5±0.3	17	-24%	62/90	<0.0001	
WT/ <i>ulp-2</i> RNAi	19.2±0.7	21	1%	36/90	0.7640	
WT/ <i>sec-6</i> RNAi	17.8±0.6	21	-6%	41/88	0.1337	
WT/ <i>ulp-4</i> RNAi	17.4±0.3	21	-8%	33/90	0.0139	
WT/ <i>cap-2</i> RNAi	14.7±0.2	17	-22%	63/90	<0.0001	
WT/ <i>hmg-1.2</i> RNAi	15.4±0.4	19	-19%	36/60	<0.0001	

WT/C02B10.5 RNAi	19.4±0.6	23	2%	35/60	0.6470	
WT/K07F5.14 RNAi	18.3±0.5	21	-3%	51/90	0.3263	
WT/ <i>fat-7</i> RNAi	16.4±0.4	19	-14%	66/90	0.0008	
<i>daf-2(e1370)</i> /control RNAi@	44.6±1.1	48	135%	40/75	<0.0001	
<i>daf-2(e1370)</i> / <i>ulp-2</i> RNAi	48.6±1.8	53	9% ^{<i>daf-2</i>}	23/75	0.0163 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>sec-6</i> RNAi	38.8±1.1	45	-13% ^{<i>daf-2</i>}	35/75	0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>ulp-4</i> RNAi	39.1±1.0	45	-12% ^{<i>daf-2</i>}	42/75	0.0004 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>cap-2</i> RNAi	36.3±1.4	42	-19% ^{<i>daf-2</i>}	35/75	0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>hmg-1.2</i> RNAi	40.3±0.8	45	-10% ^{<i>daf-2</i>}	40/75	0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> /C02B10.5 RNAi	45.8±1.3	50	3% ^{<i>daf-2</i>}	45/75	0.1955 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> /K07F5.14 RNAi	43.9±1.7	50	-2% ^{<i>daf-2</i>}	25/74	0.8712 ^{<i>daf-2</i>}	
<i>daf-2(e1370)</i> / <i>fat-7</i> RNAi	33.4±2.6	45	-25% ^{<i>daf-2</i>}	19/75	0.0001 ^{<i>daf-2</i>}	
WT/control RNAi	20.5±0.6	24		75/105		
WT/ <i>hsf-1</i> RNAi	16.2±0.3	20	-21%	87/105	<0.0001	
WT/ <i>inst-1</i> RNAi	19.7±0.5	24	-4%	76/105	0.3378	
WT/ <i>pfid-6</i> RNAi	20.1±0.5	22	-2%	58/105	0.3019	
WT/T08G11.4 RNAi	17.8±0.3	20	-13%	75/104	<0.0001	
WT/ <i>rae-1</i> RNAi	18.8±0.4	22	-8%	73/105	0.0039	
WT/C54C8.3 RNAi	17.2±0.3	20	-16%	69/105	<0.0001	
WT/ <i>ekl-4</i> RNAi	18.6±0.4	22	-9%	71/99	0.0006	
WT/ <i>vps-4</i> RNAi	14.3±0.3	17	-31%	40/50	<0.0001	
WT/ <i>srpa-72</i> RNAi	19.7±0.6	22	-4%	49/99	0.2088	
<i>daf-2(e1370)</i> /control RNAi	48.3±1.6	60	136%	45/75	<0.0001	

<i>daf-2(e1370)/daf-16</i> RNAi	24.2±0.5	29	-50% ^{<i>daf-2</i>}	49/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/hsf-1</i> RNAi	27.8±0.7	33	-42% ^{<i>daf-2</i>}	57/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/inst-1</i> RNAi	42.3±1.0	52	-12% ^{<i>daf-2</i>}	70/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/pfd-6</i> RNAi	41.6±0.9	49	-14% ^{<i>daf-2</i>}	65/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/T08G11.4</i> RNAi	44.6±0.8	49	-8% ^{<i>daf-2</i>}	68/75	0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/rae-1</i> RNAi	46.8±1.2	52	-3% ^{<i>daf-2</i>}	60/75	0.1158 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/C54C8.3</i> RNAi	29.6±0.7	33	-39% ^{<i>daf-2</i>}	54/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/ekl-4</i> RNAi	46.1±1.5	52	-5% ^{<i>daf-2</i>}	49/75	0.1303 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/vps-4</i> RNAi	22.6±0.4	26	-53% ^{<i>daf-2</i>}	64/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/srpa-72</i> RNAi	45.8±1.3	52	-5% ^{<i>daf-2</i>}	64/75	0.0209 ^{<i>daf-2</i>}	
WT/control RNAi	20.0±0.6	23		69/105		Fig.1C
WT/ <i>hsf-1</i> RNAi	17.6±0.3	21	-12%	88/105	<0.0001	
WT/ <i>ntl-2</i> RNAi	20.2±0.5	23	1%	70/88	0.9101	
WT/ <i>ulp-2</i> RNAi	20.5±0.6	23	2%	43/73	0.9773	
WT/ <i>sec-6</i> RNAi	22.5±0.6	27	12%	61/105	0.0203	
WT/ <i>ulp-4</i> RNAi	20.1±0.5	23	0%	79/105	0.7294	
WT/ <i>cap-2</i> RNAi	21.2±0.5	23	6%	83/105	0.3609	
WT/ <i>hmg-1.2</i> RNAi	18.9±0.4	21	-6%	65/101	0.0182	
WT/C02B10.5 RNAi	22.4±0.7	27	12%	60/104	0.0204	
WT/K07F5.14 RNAi	19.3±0.4	21	-4%	70/105	0.0868	
WT/ <i>fat-7</i> RNAi	18.7±0.4	21	-7%	77/100	0.0296	Fig.1C
<i>daf-2(e1370)/control</i> RNAi	47.1±1.5	52	135%	39/50	<0.0001	Fig.1C

<i>daf-2(e1370)/daf-16</i> RNAi	25.9±0.6	31	-45% ^{<i>daf-2</i>}	60/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/hsf-1</i> RNAi	27.7±0.7	31	-41% ^{<i>daf-2</i>}	60/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/ntl-2</i> RNAi	31.8±0.9	38	-33% ^{<i>daf-2</i>}	50/75	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/ulp-2</i> RNAi	46.7±1.6	56	-1% ^{<i>daf-2</i>}	62/75	0.3256 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/sec-6</i> RNAi	47.0±1.2	49	0% ^{<i>daf-2</i>}	62/75	0.8945 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/ulp-4</i> RNAi	43.8±1.1	49	-7% ^{<i>daf-2</i>}	56/75	0.0243 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/cap-2</i> RNAi	43.5±1.1	49	-8% ^{<i>daf-2</i>}	69/75	0.0183 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/hmg-1.2</i> RNAi	42.4±1.2	49	-10% ^{<i>daf-2</i>}	51/75	0.0018 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/C02B10.5</i> RNAi	46.8±1.5	56	-1% ^{<i>daf-2</i>}	55/75	0.5308 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/K07F5.14</i> RNAi	42.9±1.6	52	-9% ^{<i>daf-2</i>}	58/75	0.4089 ^{<i>daf-2</i>}	
<i>daf-2(e1370)/fat-7</i> RNAi	37.6±1.9	49	-19% ^{<i>daf-2</i>}	49/75	0.0029 ^{<i>daf-2</i>}	Fig.1C
WT	23.5±0.9	30		87/120		Fig. S1B,S1D
<i>pfid-6(gk493446)</i>	21.9±0.7	26	-7%	85/120	0.0114	
<i>fat-7(wa36)</i>	27.2±0.9	34	16%	105/150	0.0012	Fig. S1B
<i>ntl-2(gk390728)</i>	23.9±0.6	29	1%	120/150	0.7974	Fig. S1D
<i>daf-2(e1370)</i>	43.5±1.2	53	85%	99/120	<0.0001	Fig. S1B,S1D
<i>pfid-6(gk493446); daf-2(e1370)</i>	30.1±1.0	41	-31% ^{<i>daf-2</i>}	89/120	<0.0001 ^{<i>daf-2</i>}	
<i>daf-2(e1370); fat-7(wa36)</i>	31.4±1.3	41	-28% ^{<i>daf-2</i>}	93/120	<0.0001 ^{<i>daf-2</i>}	Fig. S1B
<i>ntl-2(gk390728); daf-2(e1370)</i>	38.7±1.7	53	-11% ^{<i>daf-2</i>}	95/120	0.8200 ^{<i>daf-2</i>}	Fig. S1D
WT	25.2±0.6	24		135/140		Fig. S1A
<i>pfid-6(gk493446)</i>	19.8±0.5	19	-21%	128/140	<0.0001	Fig. S1A

<i>fat-7(wa36)</i>	25.7±0.9	26	2%	93/105	0.0607	
<i>ntl-2(gk390728)</i>	21.1±0.8	19	-16%	63/70	<0.0001	
<i>daf-2(e1370)</i>	49.9±1.0	51	98%	118/140	<0.0001	Fig. S1A
<i>pfd-6(gk493446); daf-2(e1370)</i>	33.6±0.9	32	-33% ^{<i>daf-2</i>}	124/140	<0.0001 ^{<i>daf-2</i>}	Fig. S1A
<i>daf-2(e1370); fat-7(wa36)</i>	46.6±1.3	48	-7% ^{<i>daf-2</i>}	111/140	0.5324 ^{<i>daf-2</i>}	
<i>ntl-2(gk390728); daf-2(e1370)</i>	52.2±1.6	60	5% ^{<i>daf-2</i>}	121/140	<0.0001 ^{<i>daf-2</i>}	
WT	20.3±0.5	25		114/120		Fig. S1C
<i>C54C8.3(gk896531)</i>	21.0±0.5	24	4%	118/150	0.1762	Fig. S1C
<i>daf-2(e1370)</i>	41.5±1.5	55	105%	97/120	<0.0001	Fig. S1C
<i>C54C8.3(gk896531); daf-2(e1370)</i>	37.7±1.2	50	-9% ^{<i>daf-2</i>}	129/150	0.0013 ^{<i>daf-2</i>}	Fig. S1C
WT	21.3±0.6	25		93/120		
<i>C54C8.3(gk896531)</i>	21.5±0.6	26	1%	111/150	0.6291	
<i>daf-2(e1370)</i>	49.6±1.6	64	132%	97/120	<0.0001	
<i>C54C8.3(gk896531); daf-2(e1370)</i>	41.7±1.4	58	-16% ^{<i>daf-2</i>}	119/150	<0.0001 ^{<i>daf-2</i>}	

Lifespan data within solid lines are the same experimental sets.

@: These lifespan results are from the same trials, but written in tables twice for different comparisons.

p values were calculated within the sets by using the log-rank (Mantel-Cox) method.

Percent (%) changes and *p* values were calculated with each control that is located in the first row within the solid line. The other comparisons used for calculating % changes and *p* values were indicated as superscripts.

Number of animals that died indicates the number of worms that counted as dead, and total indicates the number of worms that were initially used for our lifespan assays, including censored worms.

Supplementary Table 3. Analysis of lifespan assay results related to Figure 2 and Figure S2.

Strain	Mean lifespan \pm s.e.m. (days)	75th percentile	% change	Number of animals that died/total	<i>p</i> value vs. control	Figure in text
WT/control RNAi	17.9 \pm 0.4	22		60/120		Fig. 2A
<i>pfδ-6(gk493446)</i> /control RNAi	18.1 \pm 0.4	22	1%	84/120	0.7028	Fig. 2A
<i>pfδ-6(gk493446)</i> / <i>pfδ-6</i> RNAi	17.8 \pm 0.4	22	0%	81/120	0.9826	Fig. 2A
<i>daf-2(e1370)</i> /control RNAi	49.6 \pm 0.9	54	178%	67/120	<0.0001	Fig. 2A
<i>pfδ-6(gk493446); daf-2(e1370)</i> /control RNAi	30.5 \pm 0.7	36	-30% ^{<i>daf-2</i>}	80/120	<0.0001 ^{<i>daf-2</i>}	Fig. 2A
<i>pfδ-6(gk493446); daf-2(e1370)</i> / <i>pfδ-6</i> RNAi	27.8 \pm 0.6	33	-44% ^{<i>daf-2</i>}	94/120	<0.0001 ^{<i>daf-2</i>}	Fig. 2A
WT/control RNAi	19.2 \pm 0.5	22		51/90		
<i>pfδ-6(gk493446)</i> /control RNAi	15.7 \pm 0.4	18	-18%	83/120	<0.0001	
<i>pfδ-6(gk493446)</i> / <i>pfδ-6</i> RNAi	15.1 \pm 0.4	18	-21%	70/110	<0.0001	

<i>daf-2(e1370)/control</i> RNAi	45.6±1.2	53	137%	62/120	<0.0001	
<i>pfid-6(gk493446); daf-2(e1370)/control</i> RNAi	36.7±0.9	44	-16% ^{<i>daf-2</i>}	96/120	<0.0001 ^{<i>daf-2</i>}	
<i>pfid-6(gk493446); daf-2(e1370)/pfid-6</i> RNAi	33.9±0.8	41	-26% ^{<i>daf-2</i>}	109/120	<0.0001 ^{<i>daf-2</i>}	
WT/control RNAi	20.1±0.5	22		52/120		
<i>pfid-6(gk493446)/pfid-6</i> RNAi	17.9±0.3	23	-11%	85/120	<0.0001	
<i>daf-2(e1370)/control</i> RNAi	47.7±1.1	55	138%	65/90	<0.0001	
<i>pfid-6(gk493446); daf-2(e1370)/pfid-6</i> RNAi	33.6±0.6	41	-30% ^{<i>daf-2</i>}	90/120	<0.0001 ^{<i>daf-2</i>}	
WT/control RNAi	18.5±0.4	22		70/120		
<i>pfid-6(gk493446)/pfid-6</i> RNAi	18.2±0.3	21	-2%	93/120	0.7732	
<i>daf-2(e1370)/control</i> RNAi	48.1±1.1	58	159%	107/120	<0.0001	
<i>pfid-6(gk493446); daf-2(e1370)/pfid-6</i> RNAi	42.1±0.9	48	-12% ^{<i>daf-2</i>}	96/120	<0.0001 ^{<i>daf-2</i>}	
WT/control RNAi without FUDR	19.0±0.6	23		67/140		Fig. 2B
<i>pfid-6(gk493446)/pfid-6</i> RNAi without FUDR	16.5±0.5	18	-13%	73/138	0.0018	Fig. 2B
<i>daf-2(e1370)/control</i> RNAi without FUDR	47.0±1.5	56	147%	66/122	<0.0001	Fig. 2B
<i>pfid-6(gk493446); daf-2(e1370)/pfid-6</i> RNAi without FUDR	31.9±1.0	38	-32% ^{<i>daf-2</i>}	86/139	<0.0001 ^{<i>daf-2</i>}	Fig. 2B
WT/control RNAi without FUDR	18.6±0.7	23		96/140		

<i>pdf-6(gk493446)/pdf-6</i> RNAi without FUdR	18.6±0.6	23	0%	100/140	0.7833	
<i>daf-2(e1370)/control</i> RNAi without FUdR	46.9±1.9	60	153%	58/140	<0.0001	
<i>pdf-6(gk493446); daf-2(e1370)/pdf-6</i> RNAi without FUdR	32.0±0.7	38	-32% ^{<i>daf-2</i>}	103/140	<0.0001 ^{<i>daf-2</i>}	
WT/control RNAi	18.6±0.5	21		48/60		Fig. 2C-E,G
WT/ <i>pdf-6</i> RNAi	16.6±0.5	19	-11%	81/90	0.0646	Fig. 2C-E,G
<i>osm-5(p813)/control</i> RNAi	34.9±1.5	46	45%	36/90	<0.0001	Fig. 2C
<i>osm-5(p813)/pdf-6</i> RNAi	29.6±1.1	35	10% ^{<i>osm-5</i>}	43/97	0.0866 ^{<i>osm-5</i>}	Fig. 2C
<i>osm-5(p813)/control</i> RNAi	28.4±1.1	32	53%	48/60	<0.0001	
<i>osm-5(p813)/pdf-6</i> RNAi	23.8±0.9	27	-16% ^{<i>osm-5</i>}	35/115	0.0027 ^{<i>osm-5</i>}	
<i>eat-2(ad1116)/control</i> RNAi	21.0±0.7	26	13%	32/90	0.0048	Fig. 2D
<i>eat-2(ad1116)/pdf-6</i> RNAi	24.7±0.9	29	18% ^{<i>eat-2</i>}	29/90	0.0036 ^{<i>eat-2</i>}	Fig. 2D
<i>isp-1(qm150)/control</i> RNAi	31.1±1.2	42	67%	61/75	<0.0001	Fig. 2E
<i>isp-1(qm150)/pdf-6</i> RNAi	30.6±1.0	36	-2% ^{<i>isp-1</i>}	59/75	0.2331 ^{<i>isp-1</i>}	Fig. 2E
<i>vhl-1(ok161)/control</i> RNAi	24.1±0.7	28	30%	40/75	<0.0001	Fig. 2G
<i>vhl-1(ok161)/pdf-6</i> RNAi	25.7±0.6	28	7% ^{<i>vhl-1</i>}	39/50	0.1415 ^{<i>vhl-1</i>}	Fig. 2G
WT/control RNAi	23.4±0.4	27		88/90		
WT/ <i>pdf-6</i> RNAi	22.4±0.5	25	-4%	70/91	0.6485	

<i>osm-5(p813)/control</i> RNAi	30.1±1.5	41	29%	37/81	<0.0001	
<i>osm-5(p813)/pfd-6</i> RNAi	24.0±1.1	29	-20% ^{<i>osm-5</i>}	39/90	0.0019 ^{<i>osm-5</i>}	
<i>eat-2(ad1116)/control</i> RNAi	24.5±0.8	30	10%	38/70	0.0116	
<i>eat-2(ad1116)/pfd-6</i> RNAi	30.8±0.8	35	20% ^{<i>eat-2</i>}	54/75	0.0020 ^{<i>eat-2</i>}	
<i>isp-1(qm150)/control</i> RNAi	31.0±1.3	38	33%	74/75	<0.0001	
<i>isp-1(qm150)/pfd-6</i> RNAi	29.9±1.3	38	-4% ^{<i>isp-1</i>}	74/75	0.7607 ^{<i>isp-1</i>}	
WT/control RNAi	21.8±0.7	24		51/89		
WT/ <i>pfd-6</i> RNAi	17.7±0.8	21	-19%	23/40	0.0003	
<i>osm-5(p813)/control</i> RNAi	34.9±1.5	46	60%	36/90	<0.0001	
<i>osm-5(p813)/pfd-6</i> RNAi	27.7±1.3	31	-21% ^{<i>osm-5</i>}	34/90	0.0002 ^{<i>osm-5</i>}	
<i>vhl-1(ok161)/control</i> RNAi	23.5±0.6	28	7%	63/90	0.1022	
<i>vhl-1(ok161)/pfd-6</i> RNAi	26.3±0.5	30	12% ^{<i>vhl-1</i>}	80/90	0.0017 ^{<i>vhl-1</i>}	
WT/control RNAi*	16.7±0.3	21		56/90		Fig. 2F
<i>pfd-6</i> RNAi*	17.0±0.3	21	2%	63/120	0.4988	Fig. 2F
<i>rsk-1(tm1714) pfd-6</i> RNAi*	23.1±0.5	26	38%	100/120	<0.0001	Fig. 2F
<i>rsk-1(tm1714)/control</i> RNAi*	23.1±0.5	28	0% ^{<i>rsk-1</i>}	97/120	0.7448 ^{<i>rsk-1</i>}	Fig. 2F
WT/control RNAi*	18.0±0.3	21		86/120		
<i>pfd-6</i> RNAi*	17.8±0.3	21	-1%	80/120	0.5127	
<i>rsk-1(tm1714)/control</i> RNAi*	24.0±0.6	29	33%	99/112	<0.0001	

<i>rsk-1(tm1714) pfd-6</i> RNAi*	23.9±0.6	29	0% <i>rsk-1</i>	77/104	0.9656 <i>rsk-1</i>	
WT	19.3±0.5	23		88/120		Fig. 2H
<i>pfd-6(gk493446)</i>	19.3±0.5	23	0%	71/120	0.7921	Fig. 2H
<i>hsb-1(cg116)</i>	21.4±0.7	24	11%	83/120	0.0098	Fig. 2H
<i>pfd-6(gk493446); hsb-1(cg116)</i>	24.7±0.7	31	15% <i>hsb-1</i>	97/120	0.0016 <i>hsb-1</i>	Fig. 2H
WT	19.3±0.4	22		99/118		
<i>pfd-6(gk493446)</i>	18.9±0.4	22	-2%	97/120	0.4007	
<i>hsb-1(cg116)</i>	22.6±0.7	26	17%	84/120	<0.0001	
<i>pfd-6(gk493446); hsb-1(cg116)</i>	25.7±0.5	29	14% <i>hsb-1</i>	96/120	0.0016 <i>hsb-1</i>	
WT/control RNAi without FUdR	21.9±0.6	25		75/120		Fig. S2F
WT/ <i>pfd-6</i> RNAi without FUdR	22.4±0.6	25	2%	71/120	0.5843	Fig. S2F
<i>daf-2(e1370)/</i> control RNAi without FUdR	53.7±1.4	63	145%	67/120	<0.0001	Fig. S2F
<i>daf-2(e1370)/pfd-6</i> RNAi without FUdR	35.0±0.7	40	-35% <i>daf-2</i>	72/120	<0.0001 <i>daf-2</i>	Fig. S2F
WT/control RNAi without FUdR	18.1±0.5	23		78/140		
WT/ <i>pfd-6</i> RNAi without FUdR	18.0±0.5	21	-1%	67/140	0.6462	
<i>daf-2(e1370)/</i> control RNAi without FUdR	44.4±1.6	52	145%	44/120	<0.0001	
<i>daf-2(e1370)/pfd-6</i> RNAi without FUdR	32.2±0.8	38	-27% <i>daf-2</i>	42/120	<0.0001 <i>daf-2</i>	
WT without FUdR	20.2±0.5	23		63/120		Fig. S2G
<i>pfd-6(gk493446)</i> without FUdR	19.4±0.5	23	-4%	74/120	0.1674	Fig. S2G

<i>daf-2(e1370)</i> without FUdR	50.5±1.3	58	150%	63/120	<0.0001	Fig. S2G
<i>pfid-6(gk493446); daf-2(e1370)</i> without FUdR	37.4±1.1	45	-26% ^{<i>daf-2</i>}	83/120	<0.0001 ^{<i>daf-2</i>}	Fig. S2G
WT without FUdR	16.5±0.5	19		67/120		
<i>pfid-6(gk493446)</i> without FUdR	13.0±0.5	16	-21%	80/120	0.0001	
<i>daf-2(e1370)</i> without FUdR	41.9±1.4	54	154%	83/120	<0.0001	
<i>pfid-6(gk493446); daf-2(e1370)</i> without FUdR	32.3±1.3	41	-23% ^{<i>daf-2</i>}	69/120	<0.0001 ^{<i>daf-2</i>}	
WT/control RNAi	16.0±0.6	19		69/72		Fig. S2H
WT/ <i>pfid-6</i> RNAi	17.1±0.5	19	7%	65/68	0.4042	Fig. S2H
<i>hsb-1(cg116)</i> /control RNAi	20.9±0.9	27	30%	56/72	<0.0001	Fig. S2H
<i>hsb-1(cg116)/pfid-6</i> RNAi	22.0±0.8	25	5% ^{<i>hsb-1</i>}	57/69	0.5584 ^{<i>hsb-1</i>}	Fig. S2H
WT/control RNAi	17.1±0.5	21		71/72		
WT/ <i>pfid-6</i> RNAi	18.3±0.6	21	7%	71/72	0.1424	
<i>hsb-1(cg116)</i> /control RNAi	20.0±0.8	26	17%	64/72	0.0011	
<i>hsb-1(cg116)/pfid-6</i> RNAi	21.4±0.7	26	7% ^{<i>hsb-1</i>}	71/72	0.4640 ^{<i>hsb-1</i>}	

Lifespan data within solid lines are the same experimental sets.

*: These lifespan assays were carried out at 22.5°C.

p values were calculated within the sets by using the log-rank (Mantel-Cox) method.

Percent (%) changes and *p* values were calculated with each control that is located in the first row within the solid line. The other comparisons used for calculating % changes and *p* values were indicated as superscripts.

Number of animals that died indicates the number of worms that counted as dead, and total indicates the number of worms that were initially used for our lifespan assays, including censored worms.

Supplementary Table 4. Analysis of lifespan assay results related to Figure 3 and Figure S3.

Strain	Mean lifespan \pm s.e.m. (days)	75th percentile	% change	Number of animals that died/total	<i>p</i> value vs. control	Figure in text
Intestine/control RNAi	23.4 \pm 0.6	27		49/103		Fig. 3B
Intestine/ <i>pf</i> d-6 RNAi	23.6 \pm 0.6	27	1%	70/120	0.4104	Fig. 3B
<i>daf-2(e1370)</i> Intestine/control RNAi	49.4 \pm 0.8	57	111%	89/120	<0.0001	Fig. 3B
<i>daf-2(e1370)</i> Intestine/ <i>pf</i> d-6 RNAi	39.3 \pm 0.5	42	-20% ^{<i>daf-2(-)</i>}	76/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 3B
<i>daf-2(e1370)</i> Intestine/control RNAi	50.8 \pm 0.9	58	117%	97/120	<0.0001	
<i>daf-2(e1370)</i> Intestine/ <i>pf</i> d-6 RNAi	39.3 \pm 0.6	43	-23% ^{<i>daf-2(-)</i>}	102/120	<0.0001 ^{<i>daf-2(-)</i>}	
Intestine/control RNAi	18.3 \pm 0.5	21		89/120		
Intestine/ <i>pf</i> d-6 RNAi	19.6 \pm 0.6	23	7%	73/120	0.0526	

<i>daf-2(e1370)</i> Intestine/control RNAi	44.7±1.2	53	145%	93/120	<0.0001	
<i>daf-2(e1370)</i> Intestine/ <i>pdf-6</i> RNAi	35.7±0.6	41	-20% ^{<i>daf-2(-)</i>}	113/122	<0.0001 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)</i> Intestine/control RNAi	35.9±1.0	43	96%	96/120	<0.0001	
<i>daf-2(e1370)</i> Intestine/ <i>pdf-6</i> RNAi	29.8±0.8	36	-17% ^{<i>daf-2(-)</i>}	98/120	<0.0001 ^{<i>daf-2(-)</i>}	
Hypodermis/control RNAi	18.9±0.5	21		53/90		Fig. 3C
Hypodermis/ <i>pdf-6</i> RNAi	19.4±0.5	23	3%	81/120	0.1756	Fig. 3C
<i>daf-2(e1370)</i> Hypodermis/control RNAi	46.5±0.7	53	147%	95/120	<0.0001	Fig. 3C
<i>daf-2(e1370)</i> Hypodermis/ <i>pdf-6</i> RNAi	39.6±0.5	42	-15% ^{<i>daf-2(-)</i>}	90/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 3C
<i>daf-2(e1370)</i> Hypodermis/control RNAi	49.6±1.5	61	163%	73/90	<0.0001	
<i>daf-2(e1370)</i> Hypodermis/ <i>pdf-6</i> RNAi	40.5±0.5	46	-18% ^{<i>daf-2(-)</i>}	93/120	<0.0001 ^{<i>daf-2(-)</i>}	
Hypodermis/control RNAi	21.4±0.6	26		81/121		
Hypodermis/ <i>pdf-6</i> RNAi	18.2±0.8	23	-15%	69/90	0.0033	
<i>daf-2(e1370)</i> Hypodermis/control RNAi	39.6±1.4	49	85%	82/120	<0.0001	
<i>daf-2(e1370)</i> Hypodermis/ <i>pdf-6</i> RNAi	31.3±0.8	37	-21% ^{<i>daf-2(-)</i>}	104/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)</i> Hypodermis/control RNAi	39.2±0.8	46	83%	96/120	<0.0001	

<i>daf-2(e1370)</i> Hypodermis/ <i>pfid-6</i> RNAi	32.0±0.8	39	-18% ^{<i>daf-2(-)</i>}	105/120	<0.0001 ^{<i>daf-2(-)</i>}	
Muscle/control RNAi	17.1±1.0	21		23/50		Fig. 3D
Muscle/ <i>pfid-6</i> RNAi	18.1±0.7	21	6%	36/50	0.5195	Fig. 3D
<i>daf-2(e1370)</i> Muscle/control RNAi	49.0±1.2	61	187%	99/119	<0.0001	Fig. 3D
<i>daf-2(e1370)</i> Muscle/ <i>pfid-6</i> RNAi	50.7±1.2	61	3% ^{<i>daf-2(-)</i>}	92/119	0.4865 ^{<i>daf-2(-)</i>}	Fig. 3D
Muscle/control RNAi	16.8±0.8	21		31/60		
Muscle/ <i>pfid-6</i> RNAi	17.2±0.9	21	2%	40/60	0.6825	
<i>daf-2(e1370)</i> Muscle/control RNAi	45.4±1.7	58	170%	101/120	<0.0001	
<i>daf-2(e1370)</i> Muscle/ <i>pfid-6</i> RNAi	48.8±1.5	62	8% ^{<i>daf-2(-)</i>}	106/124	0.5884 ^{<i>daf-2(-)</i>}	
Neuron/control RNAi	22.8±0.6	27		80/120		Fig. 3E
Neuron/ <i>pfid-6</i> RNAi	23.5±0.5	27	3%	80/120	0.6029	Fig. 3E
<i>daf-2(e1370)</i> Neuron/control RNAi	44.5±1.2	50	95%	76/120	<0.0001	Fig. 3E
<i>daf-2(e1370)</i> Neuron/ <i>pfid-6</i> RNAi	45.5±0.9	50	2% ^{<i>daf-2(-)</i>}	88/120	0.9774 ^{<i>daf-2(-)</i>}	Fig. 3E
Neuron/control RNAi	21.1±0.6	24		82/120		
Neuron/ <i>pfid-6</i> RNAi	22.6±0.5	27	7%	73/120	0.0788	
<i>daf-2(e1370)</i> Neuron/control RNAi	41.4±1.2	49	96%	86/120	<0.0001	
<i>daf-2(e1370)</i> Neuron/ <i>pfid-6</i> RNAi	39.2±1.1	46	-5% ^{<i>daf-2(-)</i>}	88/120	0.0531 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)</i>	38.6±1.5	49		71/120		Fig. S3B
<i>pfid-6(gk493446); daf-2(e1370)</i>	31.8±1.0	38	-18%	64/120	0.0001	Fig. S3B

<i>pdf-6(gk493446); daf-2(e1370); yhEX133[pfd-6p::pfd-6::gfp]</i>	37.3±1.3	48	-3% (17% ^{<i>pdf-6(-); daf-2(-)</i>})	68/120	0.1520 (0.0014 ^{<i>pdf-6(-); daf-2(-)</i>})	Fig. S3B
<i>pdf-6(gk493446); daf-2(e1370); yhEX134[pfd-6p::pfd-6::gfp]</i>	39.9±1.9	55	3% (25% ^{<i>pdf-6(-); daf-2(-)</i>})	47/120	0.7275 (0.0005 ^{<i>pdf-6(-); daf-2(-)</i>})	Fig. S3B
<i>daf-2(e1370)</i>	37.1±1.4	48		68/120		
<i>pdf-6(gk493446); daf-2(e1370)</i>	25.1±0.9	28	-32%	75/120	<0.0001	
<i>pdf-6(gk493446); daf-2(e1370); yhEX133[pfd-6p::pfd-6::gfp]</i>	32.3±1.1	42	-13% (29% ^{<i>pdf-6(-); daf-2(-)</i>})	102/120	0.0134 (<0.0001 ^{<i>pdf-6(-); daf-2(-)</i>})	
<i>pdf-6(gk493446); daf-2(e1370); yhEX134[pfd-6p::pfd-6::gfp]</i>	39.3±1.1	47	6% (57% ^{<i>pdf-6(-); daf-2(-)</i>})	119/140	0.1621 (<0.0001 ^{<i>pdf-6(-); daf-2(-)</i>})	
WT	20.9±0.6	25		97/150		Fig. S3C
<i>yhEX132[pfd-6p::pfd-6::gfp]</i>	24.2±0.6	28	16%	77/120	0.0007	Fig. S3C
<i>yhEX133[pfd-6p::pfd-6::gfp]</i>	22.9±0.7	28	10%	82/120	0.0250	Fig. S3C
<i>yhEX134[pfd-6p::pfd-6::gfp]</i>	23.0±0.7	28	10%	78/135	0.0110	Fig. S3C
WT	19.0±0.5	24		103/120		
<i>yhEX132[pfd-6p::pfd-6::gfp]</i>	21.9±0.6	26	15%	102/120	0.0001	
<i>yhEX133[pfd-6p::pfd-6::gfp]</i>	20.6±0.6	26	8%	115/150	0.0133	
<i>yhEX134[pfd-6p::pfd-6::gfp]</i>	20.7±0.6	26	9%	110/150	0.0041	
WT	24.3±0.6	30		104/121		
<i>yhEX132[pfd-6p::pfd-6::gfp]</i>	27.2±0.7	31	12%	86/121	0.0249	
<i>yhEX133[pfd-6p::pfd-6::gfp]</i>	21.3±0.7	29	-12%	107/151	0.0050	

<i>yhEX134[pfd-6p::pfd-6::gfp]</i>	22.2±0.8	27	9%	108/135	0.3257	
<i>rde-1(ne219)/control RNAi</i>	18.0±0.3	21		103/120		Fig. S3D
<i>rde-1(ne219)/pfd-6 RNAi</i>	18.1±0.3	21	1%	89/120	0.6756	Fig. S3D
<i>daf-2(e1370); rde-1(ne219)/control RNAi</i>	43.5±1.1	53	142%	85/120	<0.0001	Fig. S3D
<i>daf-2(e1370); rde-1(ne219)/pfd-6 RNAi</i>	41.8±0.8	49	-4% ^{<i>daf-2(-)</i>}	86/120	0.0073 ^{<i>daf-2(-)</i>}	Fig. S3D
<i>daf-2(e1370); rde-1(ne219)/control RNAi</i>	39.9±0.7	46	122%	87/120	<0.0001	
<i>daf-2(e1370); rde-1(ne219)/pfd-6 RNAi</i>	36.3±0.6	40	-9% ^{<i>daf-2(-)</i>}	81/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>rde-1(ne219)/control RNAi</i>	17.2±0.4	21		106/120		
<i>rde-1(ne219)/pfd-6 RNAi</i>	16.9±0.5	21	-2%	110/121	0.8954	
<i>daf-2(e1370); rde-1(ne219)/control RNAi</i>	36.8±1.0	44	114%	71/120	<0.0001	
<i>daf-2(e1370); rde-1(ne219)/pfd-6 RNAi</i>	32.8±0.9	37	-11% ^{<i>daf-2(-)</i>}	100/120	0.0010 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370); rde-1(ne219)/control RNAi</i>	31.6±1.2	39	84%	70/120	<0.0001	
<i>daf-2(e1370); rde-1(ne219)/pfd-6 RNAi</i>	24.9±1.0	32	-21% ^{<i>daf-2(-)</i>}	60/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>sid-1(pk3321)/control RNAi</i>	19.6±0.5	22		64/120		Fig. S3E
<i>sid-1(pk3321)/pfd-6 RNAi</i>	20.5±0.6	25	5%	64/120	0.1618	Fig. S3E
<i>daf-2(e1370); sid-1(pk3321)/control RNAi</i>	41.1±1.0	50	110%	72/100	<0.0001	Fig. S3E
<i>daf-2(e1370); sid-1(pk3321)/pfd-6 RNAi</i>	44.1±1.0	50	7% ^{<i>daf-2(-)</i>}	67/90	0.0353 ^{<i>daf-2(-)</i>}	Fig. S3E
<i>sid-1(pk3321)/control RNAi</i>	19.5±0.8	24		39/90		

<i>sid-1(pk3321)/pfd-6</i> RNAi	19.9±0.6	24	2%	50/120	0.7150	
<i>daf-2(e1370); sid-1(pk3321)/control</i> RNAi	41.9±1.3	52	115%	63/85	<0.0001	
<i>daf-2(e1370); sid-1(pk3321)/pfd-6</i> RNAi	42.4±1.3	49	1% ^{<i>daf-2(-)</i>}	78/90	0.8462 ^{<i>daf-2(-)</i>}	

Lifespan data within solid lines are the same experimental sets.

p values were calculated within the sets by using the log-rank (Mantel-Cox) method.

Percent (%) changes and *p* values were calculated with each control that is located in the first row within the solid line. The other comparisons used for calculating % changes and *p* values were indicated as superscripts.

Number of animals that died indicates the number of worms that counted as dead, and total indicates the number of worms that were initially used for our lifespan assays, including censored worms.

Supplementary Table 5. Analysis of lifespan assay results related to Figure 4 and Figure S4.

Strain	Mean lifespan ±s.e.m. (days)	75th percentile	% change	Number of animals that died/total	<i>p</i> value vs. control	Figure in text
WT/control RNAi	22.7±0.4	27		119/140		Fig. 4C-4E, S4C
WT/ <i>ruvb-1</i> RNAi	21.6±0.2	24	-5%	125/140	0.0012	Fig. 4C

WT/ <i>ruvb-2</i> RNAi	21.5±0.3	24	-5	119/140	0.0066	Fig. 4D
WT/ <i>uri-1</i> RNAi	25.8±0.5	31	14	106/120	<0.0001	Fig. 4E
WT/F35H10.6 (<i>UXT</i>) RNAi	23.7±0.4	27	5%	113/140	0.0266	Fig. S4C
<i>daf-2(e1370)</i> /control RNAi	53.7±1.9	59	137%	15/30	<0.0001	Fig. 4C-4E, S4C
<i>daf-2(e1370)/ruvb-1</i> RNAi	41.2±0.8	48	-23% ^{<i>daf-2(-)</i>}	104/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 4C
<i>daf-2(e1370)/ruvb-2</i> RNAi	39.0±0.5	42	-27% ^{<i>daf-2(-)</i>}	76/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 4D
<i>daf-2(e1370)/uri-1</i> RNAi	42.3±1.1	49	-21% ^{<i>daf-2(-)</i>}	22/90	0.0001 ^{<i>daf-2(-)</i>}	Fig. 4E
<i>daf-2(e1370)/ F35H10.6 (UXT)</i> RNAi	51.3±1.8	59	-5% ^{<i>daf-2(-)</i>}	50/90	0.7559 ^{<i>daf-2(-)</i>}	Fig. S4C
WT/control RNAi	20.9±0.4	24		119/140		
WT/ <i>ruvb-1</i> RNAi	20.1±0.4	24	-4%	127/140	0.0914	
WT/ <i>ruvb-2</i> RNAi	20.9±0.4	24	0%	121/140	0.7597	
WT/ <i>uri-1</i> RNAi	27.3±0.5	33	30%	107/120	<0.0001	
WT/F35H10.6 (<i>UXT</i>) RNAi	21.7±0.4	24	4%	127/140	0.3375	
<i>daf-2(e1370)</i> /control RNAi	49.2±1.4	56	135%	58/100	<0.0001	
<i>daf-2(e1370)/ruvb-1</i> RNAi	41.9±1.0	49	-15% ^{<i>daf-2(-)</i>}	90/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/ruvb-2</i> RNAi	43.1±0.9	51	-12% ^{<i>daf-2(-)</i>}	100/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/uri-1</i> RNAi	40.9±0.6	45	-17% ^{<i>daf-2(-)</i>}	100/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/ F35H10.6 (UXT)</i> RNAi	49.8±1.4	59	1% ^{<i>daf-2(-)</i>}	82/100	0.1634 ^{<i>daf-2(-)</i>}	
<i>pfid-6(gk493446)</i> /control RNAi	20.4±0.4	22		103/120		Fig. S4D, S4E, S4G

<i>pfid-6(gk493446)/ruvb-1</i> RNAi	19.6±0.2	22	-4%	121/140	0.0109	Fig. S4D
<i>pfid-6(gk493446)/ruvb-2</i> RNAi	20.2±0.3	22	-1%	116/140	0.4116	Fig. S4E
<i>pfid-6(gk493446)/uri-1</i> RNAi	20.2±0.4	25	-1%	99/120	0.8768	
<i>pfid-6(gk493446)/F35H10.6 (UXT)</i> RNAi	20.7±0.3	22	1%	117/136	0.7488	Fig. S4G
<i>pfid-6(gk493446); daf-2(e1370)/control</i> RNAi	33.9±1.1	44	66%	108/120	<0.0001	Fig. S4D, S4E, S4G
<i>pfid-6(gk493446); daf-2(e1370)/ruvb-1</i> RNAi	32.6±1.1	38	-4% ^{<i>pfid-6(-); daf-2(-)</i>}	45/90	0.1055 ^{<i>pfid-6(-); daf-2(-)</i>}	Fig. S4D
<i>pfid-6(gk493446); daf-2(e1370)/ruvb-2</i> RNAi	34.1±1.0	40	1% ^{<i>pfid-6(-); daf-2(-)</i>}	89/120	0.6539 ^{<i>pfid-6(-); daf-2(-)</i>}	Fig. S4E
<i>pfid-6(gk493446); daf-2(e1370)/uri-1</i> RNAi	31.7±0.5	35	-6% ^{<i>pfid-6(-); daf-2(-)</i>}	104/120	<0.0001 ^{<i>pfid-6(-); daf-2(-)</i>}	
<i>pfid-6(gk493446); daf-2(e1370)/F35H10.6 (UXT)</i> RNAi	36.2±1.0	44	7% ^{<i>pfid-6(-); daf-2(-)</i>}	109/120	0.2116 ^{<i>pfid-6(-); daf-2(-)</i>}	Fig. S4G
<i>pfid-6(gk493446)/control</i> RNAi	16.4±0.3	27		102/140		Fig. S4F
<i>pfid-6(gk493446)/ruvb-1</i> RNAi	17.5±0.4	22	7%	120/140	0.0116	
<i>pfid-6(gk493446)/ruvb-2</i> RNAi	18.5±0.3	21	13%	135/140	<0.0001	
<i>pfid-6(gk493446)/uri-1</i> RNAi	19.2±0.3	22	17%	74/90	<0.0001	Fig. S4F
<i>pfid-6(gk493446)/F35H10.6 (utx-1)</i> RNAi	17.3±0.2	19	5%	108/140	0.0740	
<i>pfid-6(gk493446); daf-2(e1370)/control</i> RNAi	28.6±1.0	38	74%	109/120	<0.0001	Fig. S4F
<i>pfid-6(gk493446); daf-2(e1370)/ruvb-1</i> RNAi	29.4±0.9	35	3% ^{<i>pfid-6(-); daf-2(-)</i>}	79/90	0.6712 ^{<i>pfid-6(-); daf-2(-)</i>}	

<i>pfid-6(gk493446); daf-2(e1370)/ruvb-2</i> RNAi	29.3±1.0	35	2% ^{<i>pfid-6(-); daf-2(-)</i>}	80/90	0.8391 ^{<i>pfid-6(-); daf-2(-)</i>}	
<i>pfid-6(gk493446); daf-2(e1370)/uri-1</i> RNAi	31.5±0.6	35	10% ^{<i>pfid-6(-); daf-2(-)</i>}	82/90	0.9375 ^{<i>pfid-6(-); daf-2(-)</i>}	Fig. S4F
<i>pfid-6(gk493446); daf-2(e1370)/F35H10.6 (utx-1)</i> RNAi	28.8±1.0	38	1% ^{<i>pfid-6(-); daf-2(-)</i>}	101/118	0.6003 ^{<i>pfid-6(-); daf-2(-)</i>}	
WT/control RNAi	21.9±0.4	25		120/150		Fig. S4H,S4I,S4K
WT/ <i>pfid-1</i> RNAi	21.6±0.4	25	-1%	123/150	0.4568	Fig. S4H
WT/ <i>pfid-2</i> RNAi	21.0±0.4	23	-4%	119/150	0.0526	
WT/ <i>pfid-3</i> RNAi	20.0±0.4	23	-8%	110/151	0.0061	Fig. S4I
WT/ <i>pfid-5</i> RNAi	20.7±0.4	23	-5%	115/150	0.0156	Fig. S4K
<i>daf-2(e1370)/control</i> RNAi	42.9±1.0	50	96%	124/152	<0.0001	Fig. S4H,S4I,S4K
<i>daf-2(e1370)/pfid-1</i> RNAi	42.3±0.9	50	-2% ^{<i>daf-2(-)</i>}	127/150	0.1526 ^{<i>daf-2(-)</i>}	Fig. S4H
<i>daf-2(e1370)/pfid-2</i> RNAi	41.0±1.0	50	-5% ^{<i>daf-2(-)</i>}	114/150	0.2088 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfid-3</i> RNAi	42.4±0.9	47	-1% ^{<i>daf-2(-)</i>}	119/146	0.4578 ^{<i>daf-2(-)</i>}	Fig. S4I
<i>daf-2(e1370)/pfid-5</i> RNAi	43.2±0.9	50	1% ^{<i>daf-2(-)</i>}	140/149	0.8799 ^{<i>daf-2(-)</i>}	Fig. S4K
WT/control RNAi	23.8±0.6	29		113/150		
WT/ <i>pfid-1</i> RNAi	24.9±0.6	31	5%	107/150	0.1637	
WT/ <i>pfid-2</i> RNAi	24.4±0.6	29	2%	108/151	0.6647	
WT/ <i>pfid-3</i> RNAi	24.1±0.6	31	1%	105/150	0.4517	
WT/ <i>pfid-5</i> RNAi	26.4±0.6	31	11%	105/150	0.0003	
<i>daf-2(e1370)/control</i> RNAi	44.4±0.8	51	87%	136/150	<0.0001	
<i>daf-2(e1370)/pfid-1</i> RNAi	42.9±0.8	51	-3% ^{<i>daf-2(-)</i>}	132/150	0.0336 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfid-2</i> RNAi	40.0±0.8	46	-10% ^{<i>daf-2(-)</i>}	125/149	<0.0001 ^{<i>daf-2(-)</i>}	

<i>daf-2(e1370)/pfd-3</i> RNAi	45.4±0.8	51	2% ^{<i>daf-2(-)</i>}	132/150	0.4791 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfd-5</i> RNAi	45.4±0.8	51	2% ^{<i>daf-2(-)</i>}	128/149	0.4145 ^{<i>daf-2(-)</i>}	
WT/control RNAi	23.0±0.6	27		97/112		
WT/ <i>pfd-1</i> RNAi	24.3±0.6	29	6%	68/90	0.3045	
WT/ <i>pfd-2</i> RNAi	22.8±0.6	27	-1%	87/120	0.8569	
WT/ <i>pfd-6</i> RNAi	23.6±0.7	29	3%	82/120	0.2716	
<i>daf-2(e1370)/control</i> RNAi	49.4±1.1	57	115%	75/96	<0.0001	
<i>daf-2(e1370)/pfd-1</i> RNAi	49.0±1.0	57	-1% ^{<i>daf-2(-)</i>}	107/120	0.7571 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfd-2</i> RNAi	46.9±1.1	54	-5% ^{<i>daf-2(-)</i>}	105/122	0.2922 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfd-6</i> RNAi	42.3±0.8	48	-14% ^{<i>daf-2(-)</i>}	104/120	<0.0001 ^{<i>daf-2(-)</i>}	
WT/control RNAi	23.6±0.6	29		71/125		Fig. 4F
WT/ <i>pfd-1</i> RNAi	22.3±0.6	25	-5%	57/124	0.1238	
WT/ <i>pfd-2</i> RNAi	23.6±0.7	27	0%	44/93	0.6723	Fig. 4F
WT/ <i>pfd-6</i> RNAi	23.5±0.7	27	0%	64/124	0.9507	
<i>daf-2(e1370)/control</i> RNAi	47.4±0.9	52	100%	86/118	<0.0001	Fig. 4F
<i>daf-2(e1370)/pfd-1</i> RNAi	45.1±0.9	52	-5% ^{<i>daf-2(-)</i>}	96/122	0.0120 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfd-2</i> RNAi	43.0±1.0	52	-9% ^{<i>daf-2(-)</i>}	100/120	0.0005 ^{<i>daf-2(-)</i>}	Fig. 4F
<i>daf-2(e1370)/pfd-6</i> RNAi	40.4±0.7	46	-15% ^{<i>daf-2(-)</i>}	85/120	<0.0001 ^{<i>daf-2(-)</i>}	
WT/control RNAi	22.1±0.5	26		59/120		
WT/ <i>pfd-1</i> RNAi	21.3±0.4	23	-4%	53/120	0.1665	
WT/ <i>pfd-2</i> RNAi	22.3±0.5	26	1%	53/120	0.7472	
WT/ <i>pfd-6</i> RNAi	22.8±0.6	26	3%	34/120	0.4693	
<i>daf-2(e1370)/control</i> RNAi	47.6±1.3	55	116%	85/121	<0.0001	
<i>daf-2(e1370)/pfd-1</i> RNAi	47.0±1.3	59	-1% ^{<i>daf-2(-)</i>}	92/120	0.7017 ^{<i>daf-2(-)</i>}	

<i>daf-2(e1370)/pfd-2</i> RNAi	42.7±1.6	53	-10% ^{<i>daf-2(-)</i>}	64/120	0.0181 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfd-6</i> RNAi	32.7±0.8	38	-31% ^{<i>daf-2(-)</i>}	71/120	<0.0001 ^{<i>daf-2(-)</i>}	
WT/control RNAi	21.5±0.5	25		104/120		Fig. S4J
WT/ <i>pfd-4</i> RNAi	22.1±0.5	25	3%	70/90	0.7361	Fig. S4J
WT/ <i>pfd-6</i> RNAi	20.2±0.4	25	-6%	104/120	0.0070	
<i>daf-2(e1370)/control</i> RNAi	45.7±0.7	53	114%	119/121	<0.0001	Fig. S4J
<i>daf-2(e1370)/pfd-4</i> RNAi	43.9±0.7	49	-4% ^{<i>daf-2(-)</i>}	116/120	0.0944 ^{<i>daf-2(-)</i>}	Fig. S4J
<i>daf-2(e1370)/pfd-6</i> RNAi	39.4±0.6	52	-14% ^{<i>daf-2(-)</i>}	112/121	<0.0001 ^{<i>daf-2(-)</i>}	
WT/control RNAi	22.6±0.5	27		97/120		
WT/ <i>pfd-4</i> RNAi	23.7±0.5	27	5%	84/120	0.1233	
WT/ <i>pfd-6</i> RNAi	23.5±0.7	29	4%	87/120	0.0156	
<i>daf-2(e1370)/control</i> RNAi	53.0±0.9	56	135%	102/120	<0.0001	
<i>daf-2(e1370)/pfd-4</i> RNAi	48.8±1.0	56	-8% ^{<i>daf-2(-)</i>}	104/120	0.0006 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfd-6</i> RNAi	42.5±0.5	48	-22% ^{<i>daf-2(-)</i>}	107/121	<0.0001 ^{<i>daf-2(-)</i>}	
WT/control RNAi	25.2±0.7	30		60/120		
WT/ <i>pfd-4</i> RNAi	25.1±0.7	30	0%	65/120	0.9941	
WT/ <i>pfd-6</i> RNAi	23.2±0.6	27	-8%	75/120	0.0266	
<i>daf-2(e1370)/control</i> RNAi	46.2±0.9	52	83%	64/120	<0.0001	
<i>daf-2(e1370)/pfd-4</i> RNAi	46.2±0.8	55	0% ^{<i>daf-2(-)</i>}	92/120	0.7002 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)/pfd-6</i> RNAi	37.0±0.5	42	-20% ^{<i>daf-2(-)</i>}	76/120	<0.0001 ^{<i>daf-2(-)</i>}	

Lifespan data within solid lines are the same experimental sets.

p values were calculated within the sets by using the log-rank (Mantel-Cox) method.

Percent (%) changes and *p* values were calculated with each control that is located in the first row within the solid line. The other comparisons used for calculating % changes and *p* values were indicated as superscripts.

Number of animals that died indicates the number of worms that counted as dead, and total indicates the number of worms that were initially used for our lifespan assays, including censored worms.

Supplementary Table 6. Analysis of lifespan assay results related to Figure 7 and Figure S7.

Strain	Mean lifespan ±s.e.m. (days)	75th percentile	% change	Number of animals that died/total	<i>p</i> value vs. control	Figure in text
Intestine/control RNAi	18.4±0.3	22	0%	96/120		Fig. 7A, 7B
Intestine/ <i>hsf-1</i> RNAi	11.3±0.2	16	-38%	98/120	<0.0001	Fig. 7A
Intestine/ <i>daf-16</i> RNAi	17.3±0.4	22	-6%	81/120	0.0667	Fig. 7B
<i>daf-2(e1370)</i> Intestine/control RNAi	36.3±1.0	43	98%	87/120	<0.0001	Fig. 7A, 7B
<i>daf-2(e1370)</i> Intestine/ <i>hsf-1</i> RNAi	11.4±0.2	16	-69% ^{<i>daf-2(-)</i>}	115/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 7A
<i>daf-2(e1370)</i> Intestine/ <i>daf-16</i> RNAi	18.6±0.7	22	-49% ^{<i>daf-2(-)</i>}	91/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 7B
Intestine/control RNAi	17.1±0.3	20		102/120		

Intestine/ <i>hsf-1</i> RNAi	11.5±0.2	-	-33%	103/120	<0.0001	
Intestine/ <i>daf-16</i> RNAi	16.3±0.3	18	-5%	88/120	0.3599	
<i>daf-2(e1370)</i> Intestine/control RNAi	38.0±0.8	45	122%	97/120	<0.0001	
<i>daf-2(e1370)</i> Intestine/ <i>hsf-1</i> RNAi	11.4±0.2	17	-70% ^{<i>daf-2(-)</i>}	100/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)</i> Intestine/ <i>daf-16</i> RNAi	18.8±0.7	23	-51% ^{<i>daf-2(-)</i>}	102/120	<0.0001 ^{<i>daf-2(-)</i>}	
Hypodermis/control RNAi	18.9±0.4	22		81/120		Fig. 7C, 7D
Hypodermis/ <i>hsf-1</i> RNAi	12.0±0.2	16	-8%	110/120	0.0002	Fig. 7C
Hypodermis/ <i>daf-16</i> RNAi	15.8±0.4	19	-9%	89/120	0.0113	Fig. 7D
<i>daf-2(e1370)</i> Hypodermis/control RNAi	41.5±0.8	49	107%	90/120	<0.0001	Fig. 7C, 7D
<i>daf-2(e1370)</i> Hypodermis/ <i>hsf-1</i> RNAi	34.2±0.8	40	-17% ^{<i>daf-2(-)</i>}	88/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 7C
<i>daf-2(e1370)</i> Hypodermis/ <i>daf-16</i> RNAi	29.5±0.6	34	-29% ^{<i>daf-2(-)</i>}	86/120	<0.0001 ^{<i>daf-2(-)</i>}	Fig. 7D
Hypodermis/control RNAi	18.6±0.3	22		114/120		
Hypodermis/ <i>hsf-1</i> RNAi	16.3±0.2	18	-13%	98/120	<0.0001	
Hypodermis/ <i>daf-16</i> RNAi	14.9±0.3	18	-20%	79/120	<0.0001	
<i>daf-2(e1370)</i> Hypodermis/control RNAi	42.2±1.1	51	127%	98/120	<0.0001	
<i>daf-2(e1370)</i> Hypodermis/ <i>hsf-1</i> RNAi	31.2±0.5	34	-26% ^{<i>daf-2(-)</i>}	97/120	<0.0001 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370)</i> Hypodermis/ <i>daf-16</i> RNAi	30.9±0.7	34	-27% ^{<i>daf-2(-)</i>}	83/120	<0.0001 ^{<i>daf-2(-)</i>}	

<i>rde-1(ne219)/control</i> RNAi	18.4±0.3	22		90/120		Fig. S7A, S7B
<i>rde-1(ne219)/hsf-1</i> RNAi	18.5±0.4	22	1%	95/120	0.6095	Fig. S7A
<i>rde-1(ne219)/daf-16</i> RNAi	18.1±0.3	22	-1%	99/120	0.6389	Fig. S7B
<i>daf-2(e1370); rde-1(ne219)/control</i> RNAi	35.4±1.1	43	93%	59/120	<0.0001	Fig. S7A, S7B
<i>daf-2(e1370); rde-1(ne219)/hsf-1</i> RNAi	34.2±1.0	40	-3% ^{<i>daf-2(-)</i>}	62/120	0.2345 ^{<i>daf-2(-)</i>}	Fig. S7A
<i>daf-2(e1370); rde-1(ne219)/daf-16</i> RNAi	33.4±1.2	40	-6% ^{<i>daf-2(-)</i>}	55/120	0.2446 ^{<i>daf-2(-)</i>}	Fig. S7B
<i>rde-1(ne219)/control</i> RNAi	17.9±0.3	20		105/120		
<i>rde-1(ne219)/hsf-1</i> RNAi	17.5±0.4	20	-2%	68/120	0.6517	
<i>rde-1(ne219)/daf-16</i> RNAi	17.3±0.3	20	-3%	93/120	0.1287	
<i>daf-2(e1370); rde-1(ne219)/control</i> RNAi	32.8±0.8	40	83%	92/120	<0.0001	
<i>daf-2(e1370); rde-1(ne219)/hsf-1</i> RNAi	31.1±0.7	37	-5% ^{<i>daf-2(-)</i>}	89/120	0.0101 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370); rde-1(ne219)/daf-16</i> RNAi	32.6±1.0	37	-1% ^{<i>daf-2(-)</i>}	63/120	0.7565 ^{<i>daf-2(-)</i>}	
<i>daf-2(e1370);</i> Intestine/control RNAi	35.8±1.4	47		79/120		
<i>daf-2(e1370)</i> Intestine/ <i>hsf-1</i> RNAi	14.0±0.4	19	-61%	114/120	<0.0001	
<i>daf-2(e1370)</i> Intestine/ <i>daf-16</i> RNAi	22.4±1.0	30	-37%	111/120	<0.0001	
<i>daf-2(e1370)</i> Intestine/control RNAi	34.1±1.1	41		60/120		
<i>daf-2(e1370)</i> Intestine/ <i>hsf-1</i> RNAi	11.86±0.39	17	-65%	54/120	<0.0001	
<i>daf-2(e1370)</i> Intestine/ <i>daf-16</i> RNAi	22.5±0.7	28	-34%	78/120	<0.0001	

<i>daf-2(e1370)</i> Hypodermis/control RNAi	36.4±1.3	47		89/102		
<i>daf-2(e1370)</i> Hypodermis/ <i>hsf-1</i> RNAi	31.4±1.0	41	-14%	94/120	0.0013	
<i>daf-2(e1370)</i> Hypodermis/ <i>daf-16</i> RNAi	31.9±1.2	41	-12%	95/110	<0.0001	
<i>daf-2(e1370)</i> Hypodermis/control RNAi	40.1±1.0	48		87/120		
<i>daf-2(e1370)</i> Hypodermis/ <i>hsf-1</i> RNAi	26.4±0.6	31	-34%	88/120	<0.0001	
<i>daf-2(e1370)</i> Hypodermis/ <i>daf-16</i> RNAi	34.1±1.1	41	-15%	72/119	<0.0001	
<i>daf-2(e1370); rde-1(ne219)</i> /control RNAi	38.3±0.8	47		79/120		
<i>daf-2(e1370); rde-1(ne219)/hsf-1</i> RNAi	35.0±1.0	44	-9%	87/120	0.0121	
<i>daf-2(e1370); rde-1(ne219)/daf-16</i> RNAi	34.9±1.0	44	-9%	93/120	0.0082	
<i>daf-2(e1370); rde-1(ne219)</i> /control RNAi	33.0±0.7	38		54/120		
<i>daf-2(e1370); rde-1(ne219)/hsf-1</i> RNAi	32.8±0.8	38	0%	65/120	0.8162	
<i>daf-2(e1370); rde-1(ne219)/daf-16</i> RNAi	30.4±0.8	38	-8%	56/120	0.0359	
Muscle/control RNAi	15.9±0.4	19		96/160		Fig. S7C, S7D
Muscle/ <i>hsf-1</i> RNAi	16.5±0.5	22	4%	74/160	0.1072	Fig. S7C
Muscle/ <i>daf-16</i> RNAi	15.6±0.4	19	-2%	84/160	0.6293	Fig. S7D
<i>daf-2(e1370)</i> Muscle/control RNAi	37.6±0.9	46	137%	86/160	<0.0001	Fig. S7C, S7D
<i>daf-2(e1370)</i> Muscle/ <i>hsf-1</i> RNAi	28.7±1.1	37	-24% ^{<i>daf-2(-)</i>}	75/160	<0.0001 ^{<i>daf-2(-)</i>}	Fig. S7C
Muscle/ <i>daf-16</i> RNAi	25.9±0.8	31	-31% ^{<i>daf-2(-)</i>}	77/160	<0.0001 ^{<i>daf-2(-)</i>}	Fig. S7D

Muscle/control RNAi	11.0±0.2	16		124/160		
Muscle/ <i>hsf-1</i> RNAi	11.4±0.2	16	4%	81/160	0.2086	
Muscle/ <i>daf-16</i> RNAi	11.1±0.3	16	1%	100/151	0.5596	
<i>daf-2(e1370)</i> Muscle/control RNAi	28.9±1.0	37	163%	102/160	<0.0001	
<i>daf-2(e1370)</i> Muscle/ <i>hsf-1</i> RNAi	22.4±0.6	23	-22% ^{<i>daf-2(-)</i>}	126/160	<0.0001 ^{<i>daf-2(-)</i>}	
Muscle/ <i>daf-16</i> RNAi	23.5±0.9	28	-19% ^{<i>daf-2(-)</i>}	69/160	0.0001 ^{<i>daf-2(-)</i>}	

Lifespan data within solid lines are the same experimental sets.

p values were calculated within the sets by using the log-rank (Mantel-Cox) method.

Percent (%) changes and *p* values were calculated with each control that is located in the first row within the solid line. The other comparisons used for calculating % changes and *p* values were indicated as superscripts.

Number of animals that died indicates the number of worms that counted as dead, and total indicates the number of worms that were initially used for our lifespan assays, including censored worms.

Supplementary Table 7. List of potential PFD-6-interacting partners identified from a yeast two-hybrid screen, related to Figure 4

Gene	Description	Number of Clone (75)	Type of Clone
<i>ifc-2</i>	Intermediate filament	7	4

<i>ifd-1</i>	Intermediate filament	10	2 [^]
<i>ifd-2</i>	Intermediate filament	10	4 [^]
<i>dsbn-1</i>	Human dysbindin	1	1
<i>pfd-5</i>	Prefoldin subunit 5	6	4
F35H10.6/ <i>UXT</i>	Protein UXT isoform 1	27	4
T18D3.7	TSC22	1	1
<i>eef-1B.2</i>	Translation elongation factor	1	1
R06F6.12		3	2
B0336.7	THAP or THAP-like domain	7	3
<i>col-76</i>	Collagen	2	2 [^]

[^]: These clones were confirmed by sequencing. The other clones were confirmed by using restriction enzymes.