

Table S1: Lifespan data.

Strain	RNAi condition	Median $\pm$ SEM (days)	\$ Max $\pm$ SEM (days)	# deaths/total	P value	
					vs control RNAi	vs <i>phb-1</i> RNAi
N2	Control RNAi	18.5 $\pm$ 1.5	22.49 $\pm$ 1.77	253/340 (2)		
	<i>atfs-1</i> RNAi	19 $\pm$ 1	22.92 $\pm$ 2.41	255/340 (2)	0.3671 (ns)	
	<i>phb-1</i> RNAi	16 $\pm$ 2	18.93 $\pm$ 2.72	186/340 (2)		
	<i>phb-1;atfs-1</i> RNAi	16 $\pm$ 2	18.93 $\pm$ 1.76	259/340 (2)		0.5462 (ns)
<i>daf-2</i>	Control RNAi	44.75 $\pm$ 2.02	53.62 $\pm$ 3.28	332/625 (4)		
	<i>atfs-1</i> RNAi	33.67 $\pm$ 4.33	39.13 $\pm$ 5.32	367/514 (3)	<0.0001 (****)	
	<i>phb-1</i> RNAi	75 $\pm$ 10	103.7 $\pm$ 1.94	211/300 (2)		
	<i>phb-1;atfs-1</i> RNAi	51 $\pm$ 7	53.64 $\pm$ 6.6	213/236 (2)		<0.0001 (****)
N2	Control RNAi	19	23.61	89/150 (1)		
	Control + <i>phb-1</i> RNAi	15	18.04	72/150 (1)	<0.0001 (****)	
<i>daf-2</i>	Control RNAi	48	60.39	105/115 (1)		
	Control + <i>phb-1</i> RNAi	65	103.5	134/160 (1)	<0.0001 (****)	
N2	Control RNAi	19 $\pm$ 1.16	26.35 $\pm$ 1.65	287/511 (3)		
	<i>znf-622</i> RNAi	17.67 $\pm$ 0.67	22.86 $\pm$ 1.38	290/600 (3)	<0.0001 (****)	
	<i>phb-1</i> RNAi	17.67 $\pm$ 0.67	23.96 $\pm$ 0.96	313/540 (3)		
	<i>phb-1;znf-622</i> RNAi	18.33 $\pm$ 0.67	24.08 $\pm$ 1.3	278/540 (3)		0.8730 (ns)
<i>daf-2</i>	Control RNAi	42 $\pm$ 3	48.37 $\pm$ 2.67	177/361 (2)		
	<i>znf-622</i> RNAi	26 $\pm$ 1	33.31 $\pm$ 2.8	237/360 (2)	<0.0001 (****)	
	<i>phb-1</i> RNAi	68 $\pm$ 6	87.32 $\pm$ 6.35	155/360 (2)		
	<i>phb-1;znf-622</i> RNAi	37.5 $\pm$ 1.5	54.51 $\pm$ 1.5	209/357 (2)		<0.0001 (****)
N2	Control RNAi	19 $\pm$ 1.16	26.35 $\pm$ 1.65	287/511 (3)		
	<i>tlf-1</i> RNAi	16 $\pm$ 1	19.70 $\pm$ 0.55	357/510 (3)	<0.0001 (****)	
	<i>phb-1</i> RNAi	17.67 $\pm$ 0.67	23.96 $\pm$ 0.96	313/540 (3)		
	<i>phb-1;tlf-1</i> RNAi	17 $\pm$ 0	22.27 $\pm$ 0.43	441/540 (3)		<0.0001 (****)
<i>daf-2</i>	Control RNAi	42 $\pm$ 3	48.37 $\pm$ 2.67	177/361 (2)		
	<i>tlf-1</i> RNAi	21.5 $\pm$ 3.5	27.16 $\pm$ 3.36	286/360 (2)	<0.0001 (****)	
	<i>phb-1</i> RNAi	68 $\pm$ 6	87.32 $\pm$ 6.35	155/360 (2)		
	<i>phb-1;tlf-1</i> RNAi	28.5 $\pm$ 0.5	44.04 $\pm$ 11.96	226/360 (2)		<0.0001 (****)
N2	Control RNAi	18 $\pm$ 1	23.05 $\pm$ 0.57	172/299 (2)		
	<i>his-65</i> RNAi	19 $\pm$ 0	23.82 $\pm$ 0.75	240/300 (2)	0.1409 (ns)	
	<i>phb-1</i> RNAi	16 $\pm$ 1	18.13 $\pm$ 0.05	136/300 (2)		
	<i>phb-1;his-65</i> RNAi	16 $\pm$ 1	17.56 $\pm$ 0.5	192/299 (2)		0.6518 (ns)
<i>daf-2</i>	Control RNAi	47.5 $\pm$ 0.5	58.88 $\pm$ 1.51	155/264 (2)		
	<i>his-65</i> RNAi	47.5 $\pm$ 0.5	61.53 $\pm$ 1.09	174/258 (2)	0.0792 (ns)	
	<i>phb-1</i> RNAi	67.5 $\pm$ 2.5	101.5 $\pm$ 0.23	235/308 (2)		
	<i>phb-1;his-65</i> RNAi	68 $\pm$ 0	96.84 $\pm$ 0.57	238/287 (2)		0.3364 (ns)
N2	Control RNAi	18 $\pm$ 1	23.05 $\pm$ 0.57	172/299 (2)		
	<i>usp-48</i> RNAi	13 $\pm$ 1	14.13 $\pm$ 1.04	160/345 (2)	<0.0001 (****)	
	<i>phb-1</i> RNAi	16 $\pm$ 1	18.13 $\pm$ 0.05	136/300 (2)		
	<i>phb-1;usp-48</i> RNAi	12 $\pm$ 2	12.90 $\pm$ 1.84	190/348 (2)		<0.0001 (****)
<i>daf-2</i>	Control RNAi	47.5 $\pm$ 0.5	58.88 $\pm$ 1.51	155/264 (2)		
	<i>usp-48</i> RNAi	16.5 $\pm$ 1.5	19.4 $\pm$ 0.34	114/321 (2)	<0.0001 (****)	
	<i>phb-1</i> RNAi	75 $\pm$ 10	103.7 $\pm$ 1.94	211/300 (2)		
	<i>phb-1;usp-48</i> RNAi	18 $\pm$ 0	20.22 $\pm$ 0.66	289/355 (2)		<0.0001 (****)
<i>daf-7</i>	Control RNAi	22 $\pm$ 1	26.32 $\pm$ 2.13	88/379 (2)		
	<i>usp-48</i> RNAi	15 $\pm$ 0	16.3 $\pm$ 0.6	73/380 (2)	<0.0001 (****)	
	<i>phb-1</i> RNAi	24 $\pm$ 1	35.03 $\pm$ 2.23	116/331 (2)		
	<i>phb-1;usp-48</i> RNAi	14 $\pm$ 1	15.96 $\pm$ 0.01	108/304 (2)		<0.0001 (****)
<i>isp-1</i>	Control RNAi	22.5 $\pm$ 1.5	25.38 $\pm$ 2.16	101/346 (2)		
	<i>usp-48</i> RNAi	15.50 $\pm$ 0.5	17.22 $\pm$ 1.2	115/351 (2)	<0.0001 (****)	
	<i>phb-1</i> RNAi	32 $\pm$ 1	46.3 $\pm$ 1.4	223/348 (2)		
	<i>phb-1;usp-48</i> RNAi	19.5 $\pm$ 0.5	22 $\pm$ 0.01	248/356 (2)		<0.0001 (****)

All ageing experiments were performed on plates seeded with HT115(DE3) *E. coli*.

P values were calculated using the log-rank (Mantel-Cox) test.

\$ Maximum life span; mean life span of the most long-lived 10% of animals.

Confirmed death events divided by the total number of animals included in the assay.

Total equals the number of animals than died plus the number of censored animals.

The number of independent lifespan assays for each strain or condition is shown in parentheses.