Table S2

Strains	Mean lifespan ± s.e.m. (days)	75th percentile (days)	n	P
N2; control	17.57 ± 0.24	24	57/60	-
N2; *sir-2.4(RNAi)*	18.87 ± 0.55	24	73/75	0.0638
daf-2(e1370); control	50.23 ± 0.91	63	64/90	< 0.0001
daf-2(e1370); sir-2.4(RNAi)	48.43 ± 0.61	60	68/90	< 0.0001[a]/ 0.5428[b]
N2; control	20.16 ± 1.03	23	48/59	-
N2; *cbp-1(RNAi)*	5.79 ± 0.42	7	54/60	<0.0001
sir-2.4(n5137); control	18.15 ± 1.15	23	50/71	0.1988
sir-2.4(n5137); cbp-1(RNAi)	6.16 ± 0.26	7	67/76	< 0.0001[a,b]/ 0.3274[c]
N2	16.51 ± 0.72	20	63/72	-
EQ137 (*sir-2.4::gfp* o.e.)	17.85 ± 0.66	22	53/72	0.1318
N2	20.18 ± 0.62	23	61/72	-
EQ158 (*sir-2.4* o.e.)	19.33 ± 0.63	23	57/72	0.2818

Table S2.   Effects of *sir-2.4* expression on lifespan. Adult mean lifespan ± SEM, in days, observed in lifespan analysis. Lifespan experiments were carried out at 20°C. 75th percentile is the age at which the fraction of animals alive reaches 0.25. 'n' shows the number of observed deaths relative to total number of animals started at day 1. The difference between these numbers represents the number of animals censored during the experiment, and includes animals that exploded, bagged (i.e. exhibited internal progeny hatching), or crawled off the plates. [a] *p*-Values calculated by pair-wise comparisons to N2 control of the same experiment. [b] *p*-Values calculated by pair-wise comparisons to mutants fed with control bacteria of the same experiment. [c] *p*-Values calculated by pair-wise comparisons to N2 fed with the same RNAi bacteria of the same experiment. We used Stata 8 software for statistical analysis and to determine means and percentiles. The logrank (Mantel-Cox) test was used to test the hypothesis that the survival functions among groups were equal.