

TABLE S2. RNAi directed against known DR genes in the *mir-80*(Δ) background identify genes required for the low age pigment level phenotype.

We used RNAi to knockdown genes previously implicated in DR in the *mir-80*(Δ) background (Day 4, 20°C, three independent trials, 50 animals/trial) and quantitated age pigment levels relative to endogenous Trp levels. Since low age pigment/Trp ratios (AGE/TRP) are associated with the DR state [19], we reasoned that genetic interventions that elevated age pigment levels would help identify genes needed for the *mir-80*(Δ) DR pathway and/or for enhanced healthspan. P-values were calculated using the Unpaired two-tailed Student's T-test, values within the 90% confidence level are bold, increase or decrease indicated by arrows.

<i>mir-80</i>(Δ) Age Pigments			
RNAi Clone	Mean (AGE/TRP)	St. Error	p-value against own L4440
L4440 vector	0.459	0.02	
<i>aak-1</i>	0.643	0.03	0.04 ↑
<i>aak-2</i>	0.625	0.02	0.06 ↑
<i>bec-1</i>	0.360	0.11	0.292
<i>cbp-1</i>	0.613	0.09	0.099 ↑
<i>clk-1</i>	0.348	0.02	0.208
<i>cup-4</i>	0.414	0.01	0.603
<i>dve-1</i>	0.543	0.02	0.336
<i>hif-1</i>	0.539	0.15	0.420
<i>hsf-1</i>	0.651	0.08	0.041 ↑
<i>ire-1</i>	0.381	0.03	0.374
<i>nlp-1</i>	0.400	0.06	0.511
<i>pgp-2</i>	0.419	0.02	0.649
<i>rheb-1</i>	0.352	0.01	0.223
<i>sir-2.1</i>	0.270	0.06	0.041
<i>skn-1</i>	0.683	0.02	0.015 ↑

<i>ubc-18</i>	0.432	0.02	0.754
<i>vps-34</i>	0.599	0.05	0.121