**SUPPLEMENTAL TABLES**

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| **Table S1. Survival analysis of *hs::lin-29* animals periodically induced in adulthood** | | | | | | | |
| **Time of heat shock** | ***E. coli* (diet)** | **strain** | **N** | **Mean lifespan** | | | **Abs. max (days)** |
| **days** | **SE** | **95% C.I.** |
| every 24 hrs | live | *hs::control* | 140 | 13.78 | 0.27 | 13.26 ~ 14.30 | 21 |
| *hs::lin-29* | 140 | 11.63 | 0.18 | 11.27 ~ 11.98 | 15 |
| every 24 hrs | dead | *hs::control* | 114 | 14.46 | 0.24 | 13.99 ~ 14.92 | 22 |
| *hs::lin-29* | 109 | 11.36 | 0.16 | 11.05 ~ 11.68 | 14 |
| every 48 hrs | live | *hs::control* | 174 | 14.89 | 0.21 | 14.48 ~ 15.29 | 23 |
| *hs::lin-29* | 175 | 13.07 | 0.16 | 12.75 ~ 13.39 | 18 |
| every 48 hrs | dead | *hs::control* | 115 | 16.36 | 0.32 | 15.73 ~ 16.99 | 22 |
| *hs::lin-29* | 117 | 12.11 | 0.19 | 11.73 ~ 12.49 | 18 |
| Survival was analyzed in four independent experiments following the indicated conditions. Mean lifespans were estimated for each group considered separately using the Kaplan-Meier method. SE refers to standard error. Absolute maximum lifespan is the time at which cohorts reached 100% mortality. | | | | | | | |

**Tables S2 and S3 are a separate Excel files**

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| **Table S4: Blister phenotype depends on *lin-29* function** | | |
| ***strain*** | ***RNAi treatment*** | ***Bli phenotype*** |
| N2 | control | 0% |
| N2 | *bli-1* | 63% |
| *rrf-3(pk1426)* | control | 0% |
| *rrf-3(pk1426)* | *bli-1* | 89% |
| *lin-29(xe37)* | control | 0% |
| *lin-29(xe37)* | *bli-1* | 0% |
| *lin-29(xe40)* | control | 0% |
| *lin-29(xe40)* | *bli-1* | 0% |
| N2 | control | 0% |
| N2 | *lin-29* | 0% |
| *bli-1(e769)* | control | 95% |
| *bli-1(e769)* | *lin-29* | 1% |
| N2 | *lin-29 + bli-1* | 0% |
| Hermaphrodite L4s of the strain indicated were grown on HT115 bacteria expressing dsRNA targeting *bli-1,* or *lin-29,* both *lin-29* and *bli-1* simultaneously,or no gene (control: empty RNAi vector). F1 progeny were grown on the same bacteria to adulthood and then scored for a Blister phenotype. *lin-29(xe37)* is a null allele affecting both *lin-29a* and *lin-29b* transcripts; *lin-29(xe40)* removes function of *lin-29a* only (Aeschimann *et al.* 2019). In all cases N>100 | | |

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| **Table S5. Primers used for quantitative PCR** | |
| **Primer description** | **Sequence** |
| *hacd-1* qPCR Fwd | GATTCATTGTCAACCGGCTATT |
| *hacd-1* qPCR Rev | TCGCGGAAGATTTTCAAAGTG |
| *acs-7* qPCR Fwd | GAAGCATATTAATCAGAAGCTAGCCA |
| *acs-7* qPCR Rev | CATCCAAAAACGCTTTCTTCA |
| *dhs-18* qPCR Fwd | ATTGAGAAGGCAGGAGGTCAT |
| *dhs-18* qPCR Rev | GGTAAGAGAGATGGCTGAAGCA |
| *fat-5* qPCR Fwd | GTTGGATGGGTATTCCTCCTG |
| *fat-5* qPCR Rev | CAGTATCCGTCCACTTGTGATG |
| *prx-11* qPCR Fwd | ATTCAACTCAGCGAGGCTCTA |
| *prx-11* qPCR Rev | CTTTCCAGCCCATAAAATCTTG |
| *vit-1* qPCR Fwd § | GAGGTTCGCTTTGACGGATA |
| *vit-1* qPCR Rev § | GGCTTCACATTCCTCGTTCT |
| *vit-2* qPCR Fwd Δ | GACACCGAGCTCATCCGCCCA |
| *vit-2* qPCR Rev Δ | TTCCTTCTCTCCATTGACCT |
| *vit-3* qPCR Fwd \* | CATGTGCACCATCGAAGAACTC |
| *vit-3* qPCR Rev \* | CCAATGTGGTTTCAATGACAAGTTG |
| *vit-6* qPCR Fwd \* | TTCACCCAGAAGCCAGTTC |
| *vit-6* qPCR Rev \* | AGGATGGGAGGCAGTAGAC |
| *col-38* qPCR Fwd | GGAGTCCATGACATGAAGGTG |
| *col-38* qPCR Rev | CCTTGAGAGTTGGCATCACA |
| *col-49* qPCR Fwd | TCATTTCGTTTGAGCATTCG |
| *col-49* qPCR Rev | ATCCCTTCTCTCCTGGTGGT |
| *col-63* qPCR Fwd | CTATTGTTCCAGCTATTTTTGCC |
| *col-63* qPCR Rev | GCATCTCCATATCCTCTTCTGA |
| *col-138* qPCR Fwd | AGCAAGGACCAAAGGGAGAAG |
| *col-138* qPCR Rev | ATATCCTGGAGCAGTTCTTGGT |
| *gpd-2* qPCR Fwd | CCTCTGGAGCCGACTATGTC |
| *gpd-2* qPCR Rev | TGGCATGATCGTACTTCTCG |
| ΔFrom (DePina *et al.* 2011); §From (Ding and Grosshans 2009); \*From (Dowen *et al.* 2016). | |