

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: small RNA levels in animals with a catalytically active or inactive transgene introduced to cause mtDNA double-stranded breaks. A raw count table of selected sequences for each sample was generated for edgeR to perform the differential expression analysis between each group. EdgeR used a trimmed mean of M-values to compute scale factors for library size normalization and used the Cox-Reid profile-adjusted likelihood method to estimate dispersions and the quasi-likelihood F-test to determine differential expression (two-sided comparison).

File Name: Supplementary Data 2

Description: Significantly differentially expressed genes (FDR<0.05) in wild-type animal vs miR-71 knock-out animal with and without azide stress. Sequencing was carried out using a 2x150bp paired-end (PE) configuration; image analysis and base calling were conducted by the HiSeq Control Software (HCS) + OLB + GAPipeline-1.6 (Illumina) on the HiSeq instrument. The sequences were processed and analyzed by GENEWIZ (two-sided comparisons).

File Name: Supplementary Data 3

Description: list of genes knocked down to find signalling molecule in muscle-to-glia stress signalling

File Name: Supplementary Data 4

Description: C. elegans strains used for this study

File Name: Supplementary Data 5

Description: plasmids used for this study

File Name: Supplementary Data 6

Description: primers used for this study