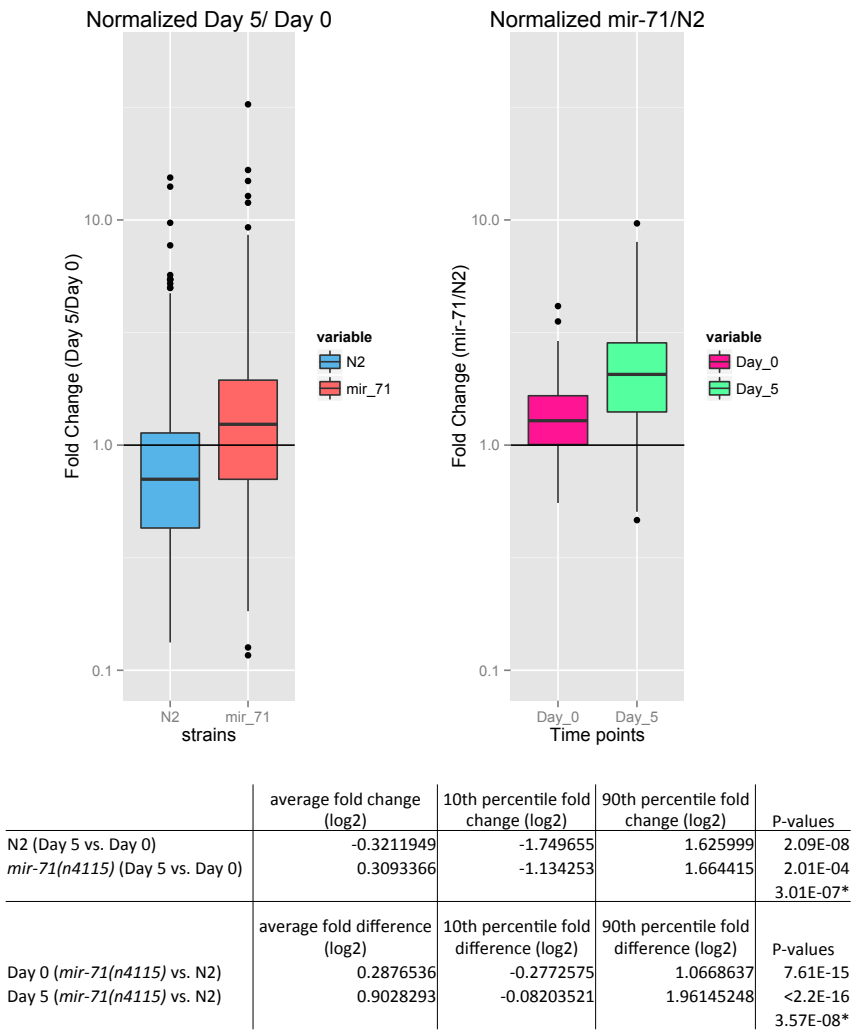


A



B

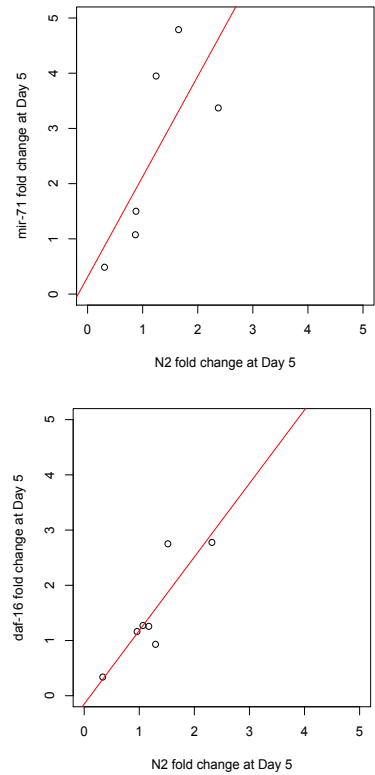


Figure S3: miRNA Expression Fold Changes/Differences during Aging and between Strains. Related to Figure 3.

(A) Top: Box whisker plots of miRNA fold change/fold difference. Left: miRNA expression fold change during aging (Day 5/Day0) for each strain. The two distributions are significantly different (Welch two-sample t-test, P-value 3.01×10^{-7}). Right: miRNA expression fold differences between the two strains (*mir-71*/N2) at each time point. The two distributions are significantly different (Welch two-sample t-test, P-value 3.57×10^{-8}).

Bottom: Table summarizing the average fold change/fold difference between conditions and relevant P-values. P-values obtained from binomial tests comparing the number of miRNAs demonstrating negative or positive fold change/fold difference. P-values marked by * were obtained from Welch two-sample t-tests comparing distributions of fold change/fold difference.

(B) Shift in miRNA abundance is not a hallmark of short-lived strains. Comparison of TaqMan qPCR results for select miRNAs, as in Figure 3C. Points are fold differences between Day 5 and Day 0 or Day 0/1. Red lines: linear fit. Left: Expression fold difference for N2 vs. *mir-71*(n4115), data same as in Figure 3C. Right: Expression fold difference for N2 vs. *daf-16*(mu86).