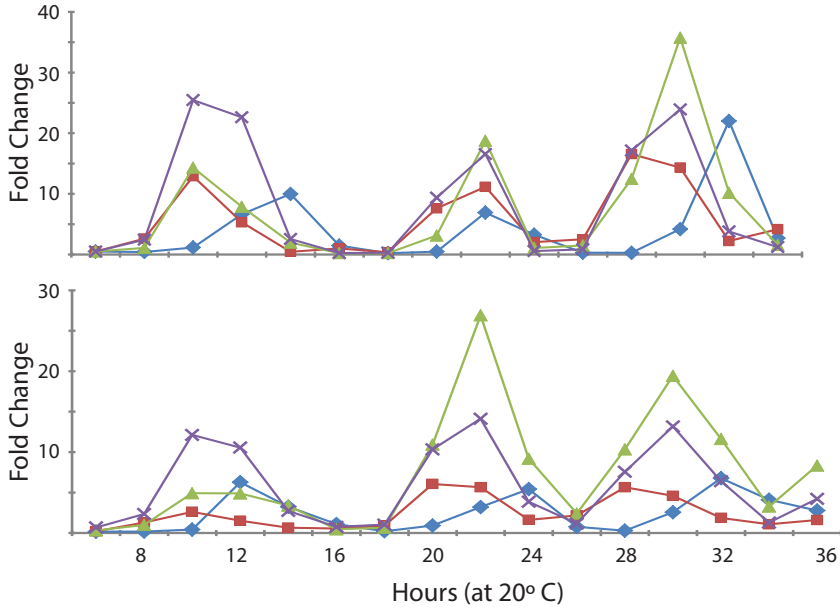
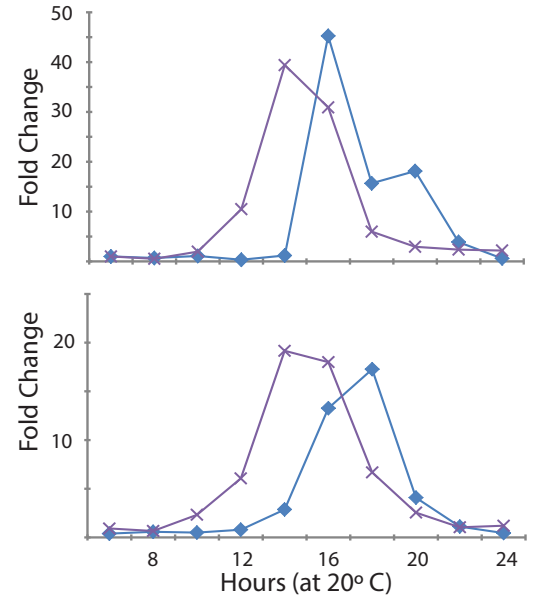


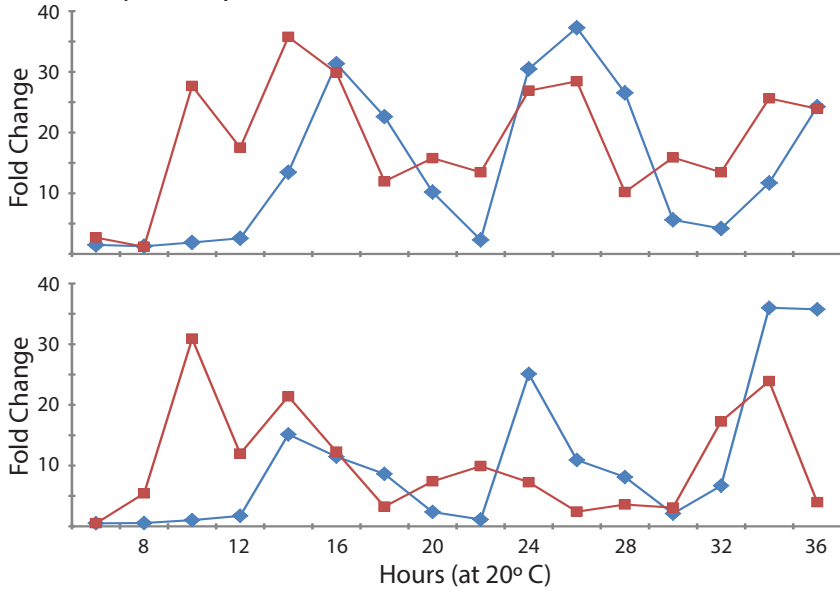
### A Wild Type



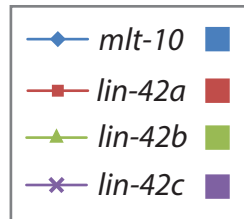
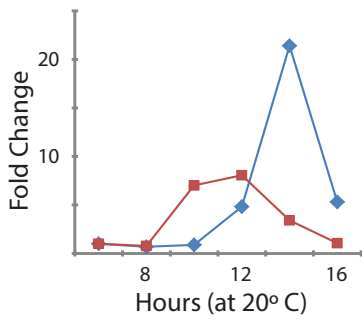
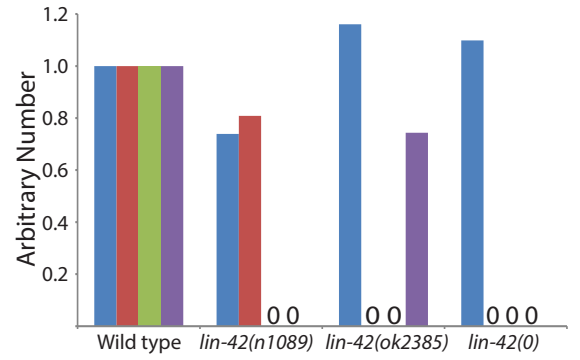
### C *lin-42(ok2385)*



### B *lin-42(n1089)*



### D Primer Controls



**Figure S1: Biological replicates of *lin-42* transcript accumulation patterns.**

(A-C) Expression of *lin-42a*, *lin-42b*, and *lin-42c* was measured relative to *mlt-10* in a total of three biological replicates (one replicate is displayed in Figure 4) for (A) wild type, (B) *lin-42(n1089)*, and (C) *lin-42(ok2385)*. Time points within each assay are normalized to 0 or 6 hr. (B) The decrease in *lin-42a* expression at 12hrs in each *lin-42(n1089)* time course is an artifact of staggering populations, since the decrease is not observed when animals were collected continuously from 6-16 hrs (third panel). (D) *lin-42* gene expression assays are specific to the intended target. Transcript levels were measured in mixed-stage populations of wild type, *lin-42(n1089)*, *lin-42(ok2385)*, and *lin-42(0)* to demonstrate the specificity of each assay.  $\Delta\text{Ct}$  values ( $[\text{target Ct}] - [\textit{ama-1} \text{ Ct}]$ ) are normalized to wild type.