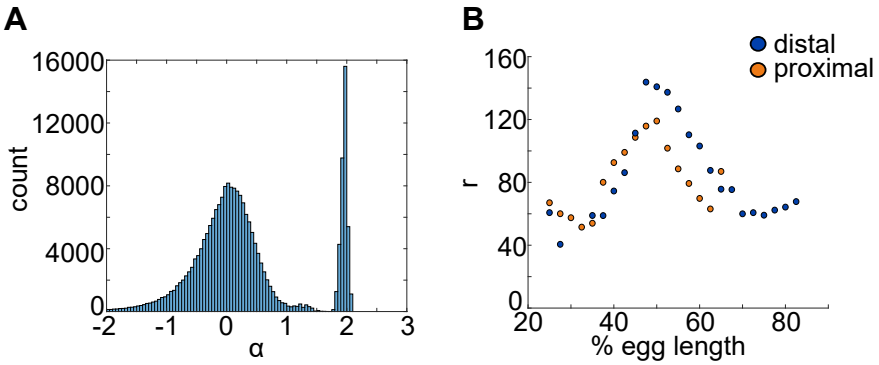

Figure 2 - figure supplement 3: mRNA production and decay rates can be directly estimated from experimental data. The mRNA degradation parameter α and production parameter r were measured directly from fluorescence data without any input from the model. A. To estimate α, we used adjacent measurements of fluorescence intensity to approximate the slope at each point in the fluorescence traces. These values are compared with an exponential rate of mRNA decay (see Methods) and the resulting predicted values are shown in the histogram. Periods of mRNA production have negative α values and periods of decay have positive values. The histogram shows a distinct peak for $\alpha > 0$, which provided us with an estimate of $\alpha \approx 1.95$. B. A similar computational approach was used to calculate values of r from fluorescence data (see Methods). We calculated different values of r for each bin to account for differences in transcriptional efficiency across the length of the embryo due to factors that are not explicitly included in the model. For example, different combinations of TF bound to the enhancer may give rise to different mRNA production rates. Different values of r were found for the proximal and distal enhancers. Notice that distal r values shown correspond to the distal enhancer at the proximal location.