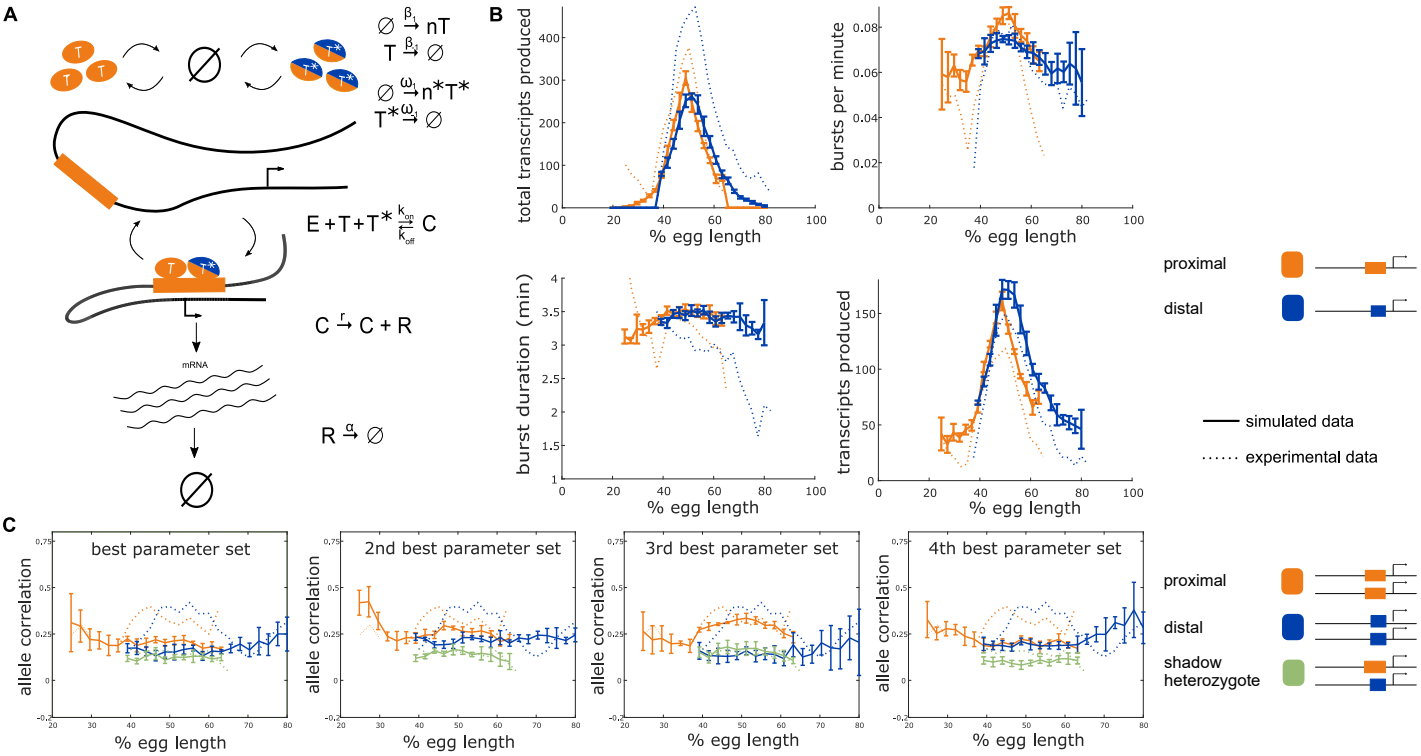

Figure 2 - figure supplement 2: Incorporating a common TF into the model yields nonzero heterozygote allele correlations. To determine whether the observed nonzero heterozygote correlation can be explained by common TF activity, we incorporated into our model a TF that can bind to both the proximal and distal enhancers. **A.** Schematic of a model that includes an additional TF denoted T^* which can bind to both the proximal and distal enhancers. The production of T^* occurs at a rate ω_l which varies across the embryo in a similar manner to β_l. T^* degrades linearly at a rate ω_{-l} and appears in bursts of size n^*. The presence of both the enhancer-specific TF T_i and the common TF T^* are necessary to initiate transcription. **B.** The addition of a common TF does not hinder the model from recapitulating the experimentally observed burst properties of single enhancer constructs. Simulated data is created using the second-best parameter set for each enhancer. The data shown is the average of five simulated embryos that have 80 transcriptional spots per AP bin. In B, C, and D simulated data are shown by solid lines, experimental data are shown by dotted lines. **C.** The addition of the common TF T* consistently produces nonzero heterozygote allele correlations. However, some of the best parameter sets do not conserve the experimental relationship between homozygote and heterozygote correlations. Other parameter sets do not match the experimental data well suggesting that the model accepts a narrower range of parameter combinations than the bursting TF model. Error bars in B and C represent 95% confidence intervals.