



Figure 6 - figure supplement 1: Fraction of nuclei with negative covariance of allele activity. To identify the likely cause of the observed negative covariance between allele activity in some nuclei, we calculated the fraction of nuclei displaying negative covariance out of all nuclei that had active reporter transcription. Graphs show the fraction of transcribing nuclei with negative covariance as a function of egg length for each reporter construct, with a black circle indicating the position along the embryo of maximal expression for that construct. A. Distal; B. Proximal; C. 2x Proximal; D. 2x Distal; E. Shadow pair. Note that for all constructs, the highest rates of negative covariance are outside of the region of maximal reporter expression. MCP-GFP is expressed uniformly along the length of the embryo and we would therefore expect if MCP-GFP were the limiting factor, we would see the highest rates of negative covariance in the center of the expression pattern, where the highest number of transcripts are produced. Instead, the highest rates of negative covariance are seen at the edges of the Kr expression pattern, suggesting a spatially patterned factor, such as a TF, may be what is limiting.