



Figure 1 - figure supplement 2: Correspondence of observed and expected number of spots. To ensure that we can accurately measure two spots of expression in the embryo, we compared the number of transcriptional spots seen in embryos hemizygous or homozygous for each construct. Our rationale was that in the absence of transvection, the number of transcriptional spots in homozygous embryos should be twice the number in embryos expressing the reporter on only one allele. The number of transcriptional spots tracked during nc14 in the AP bin of maximum expression was counted for all embryos imaged for each homozygous and hemizygous construct. The graph shows the average of this value for homozygous embryos, divided by double the value observed in the corresponding hemizygous construct. Assuming no transvection occurs, this value should be close to 1. The ratio of observed to expected number of spots is close to 1 for all of our enhancer constructs, indicating we are reliably able to track the two individual spots of transcription in single nuclei.