



Supplemental Figure S1. Clusters of Start-RNAs are associated with genes that define key developmental and cell-type specific pathways. **A**, Several randomly selected unannotated TSSs that do not overlap STARR-seq regions nonetheless function as enhancers in luciferase assays. **B**, List of enriched GO categories of genes (N=568) associated with TSS clusters containing 5 or more uTSSs in S2 cells. **C**, uTSSs within larger clusters display enrichment in active histone marks. The number of H3K4me1 and H3K27ac ChIP-seq reads is shown around uTSSs (± 1 kb) within clusters of either 0-4 (black) and 5 or more sites (green). Box plots show 25th-75th percentiles and error bars depict 10-90th percentiles. P-values are from Mann-Whitney test. **D**, Distribution of the number of uTSSs associated with the 9,952 genes defined as active (observed TSSs) in *Drosophila* embryos (0-16h). A subset of genes (N=66, green) contains 4 or more associated uTSSs. **E**, List of enriched GO categories (left) and select genes (right) associated with TSS clusters containing 4 or more uTSSs in *Drosophila* embryos (0-16h). See Table S1 for full list. Related to Fig. 1.