



**Supplemental Fig. S4.** (A-D) *d*NET-seq/S5P and RNA-seq profiles over the indicated pre-MBT genes. Reads that aligned to the positive strand are in blue, and reads that aligned to the negative strand are in red. The direction of transcription is indicated by an arrow. (E-G) Identification of transcriptionally active genes based on *d*NET-seq signal along the gene body in late embryos. (E) Read density distribution in intergenic regions (gene deserts). The red dashed line represents the 90th percentile of read density in all intergenic regions analysed. (F) Read density distribution per gene (RPKM) represented in Log2 scale. The 90th percentile of read density over gene deserts is set as threshold (red dashed line). (G) Comparison of read density per active gene (RPKM in log2 scale) between the indicated datasets. Total number of active genes identified in each dataset is indicated (n). Venn diagrams show common active genes between datasets.