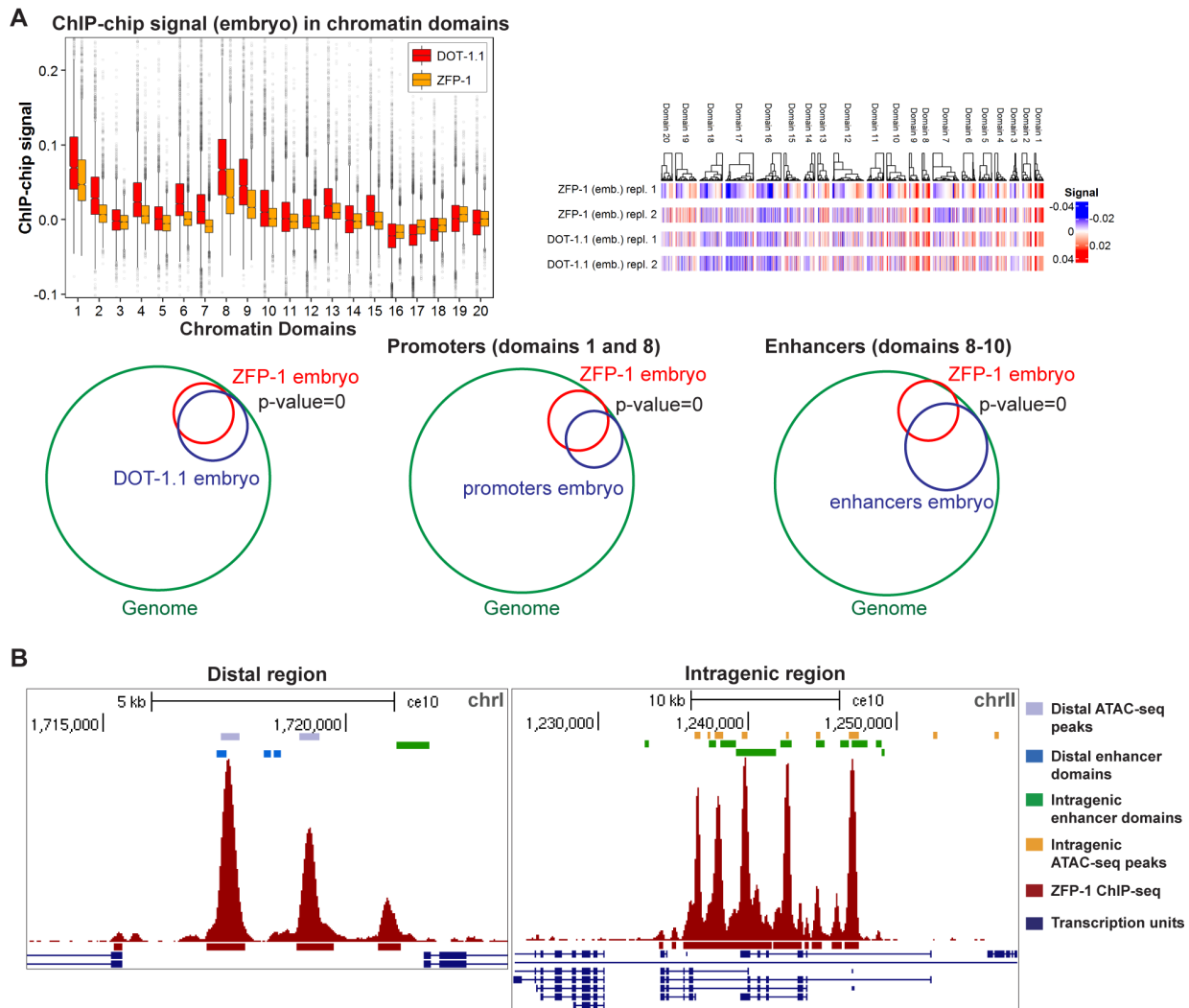




SUPPLEMENTAL FIGURE S1. ZFP-1 and DOT-1.1 localize to predicted enhancer domains and open chromatin regions detected by ATAC-seq. (A) ZFP-1/DOT-1.1 complex is enriched at promoter and enhancer chromatin domains in the embryo. Chromatin domain coordinates determined by hidden Markov models and obtained from a previously published study (Evans et al. 2016) were intersected with ZFP-1 and DOT-1.1 ChIP-chip signal tracks. Each column of the heatmap (right panel) represents a chromatin domain region and the color indicates the intersecting ZFP-1 or DOT-1.1 ChIP-chip signal as indicated in the color bar. The boxplot (left panel) represents the median (medium line), first and third quartiles (box), minimum and maximum values (whiskers), 95% interval confidence of the median (notch) and outliers (dots) of the intersecting signal (averaged across replicates) for each domain. Venn diagram (bottom left) shows that ZFP-1 and DOT-1.1 co-localize genome-wide, as previously reported (Cecere et al. 2013). ZFP-1 and DOT-1.1 ChIP-chip peak coordinates (embryo) were downloaded from modENCODE (modENCODE_2969 and modENCODE_2970, respectively) and intersected with each other and with the full genomic space (assembly WS220/ce10). Venn diagrams (bottom middle and right) show that ZFP-1 peaks co-localize with promoter domains (1) and enhancer domains (8-10) genome-wide. ZFP-1 peak coordinates (embryo) were downloaded from modENCODE (modENCODE_2969 and modENCODE_2970, respectively) and intersected with coordinates for promoter and enhancer domains and with the full genomic space (assembly WS220/ce10). The p-value was determined by a two-sided Fisher's exact test. (B) UCSC genome browser snapshots showing representative examples of overlap of ZFP-1 peaks with distal enhancer domains and ATAC-seq peaks (left panel) and with intragenic enhancer domains and ATAC-seq peaks (right panel).