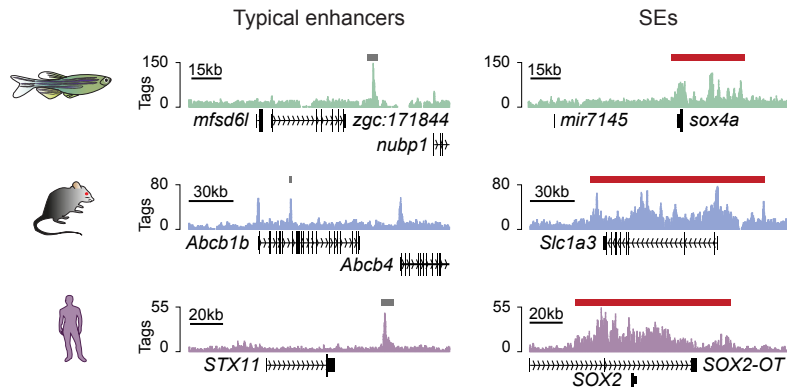
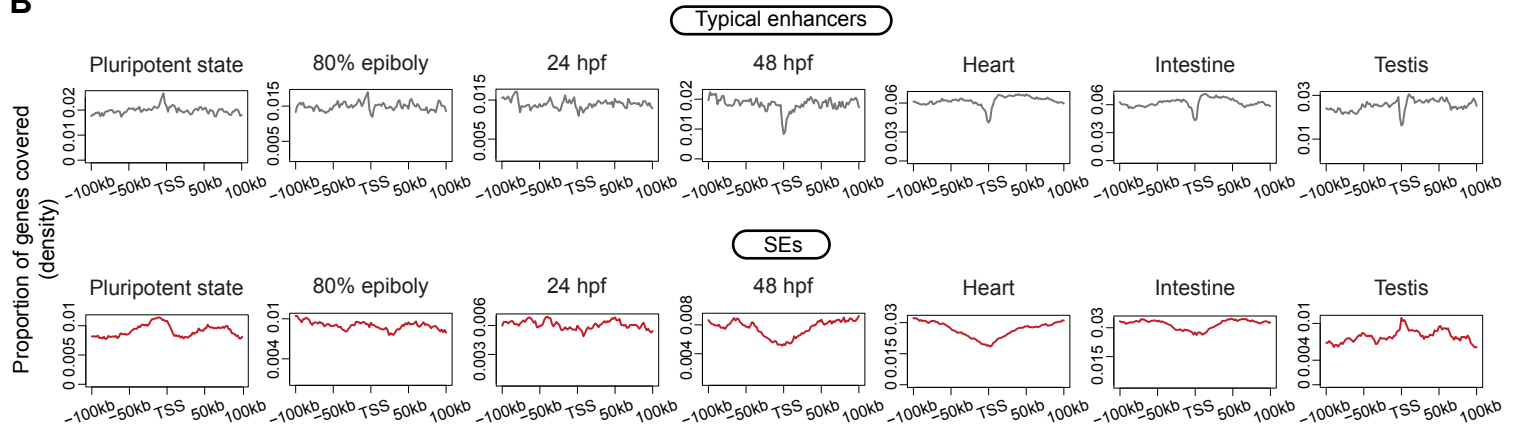


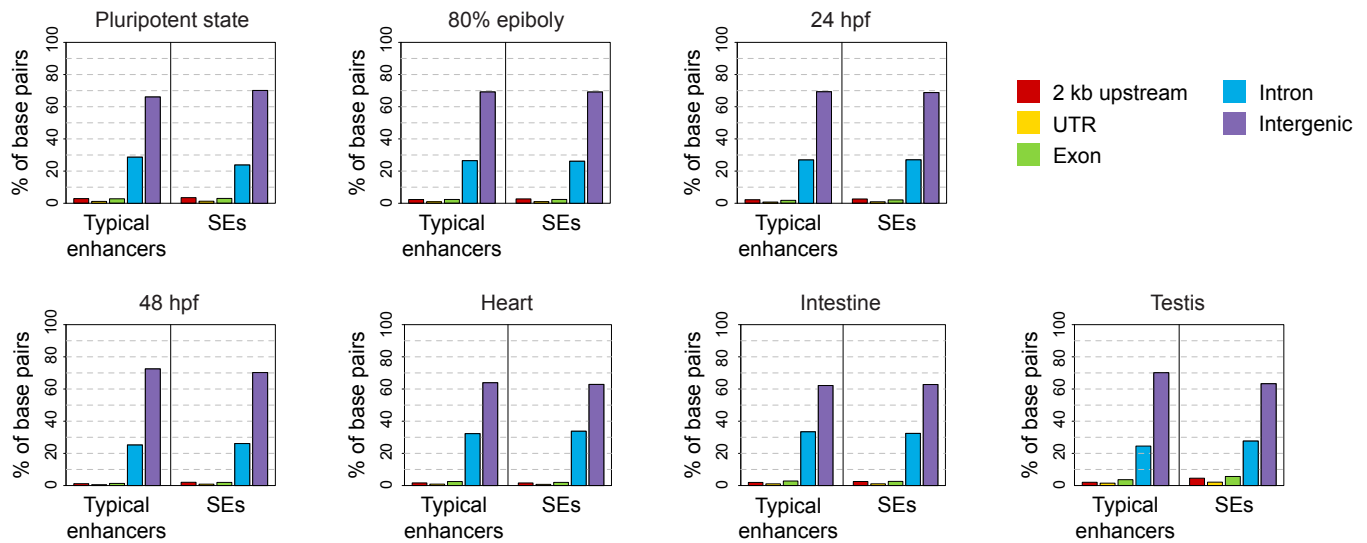
A



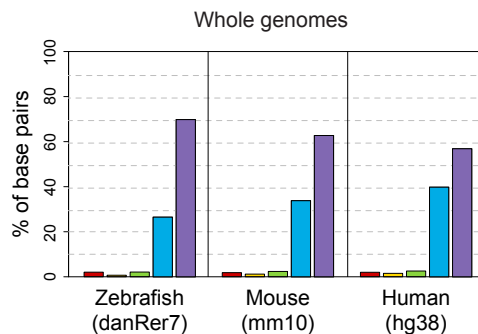
B



C



D



Supplemental Figure S2. Genomic distribution of typical enhancers and SEs. (A) Examples of H3K27ac distribution for typical enhancers (grey bars) and SEs (red bars) in the zebrafish brain, mouse forebrain and human middle frontal lobe relative to gene position. Gene positions and the corresponding raw tag count for H3K27ac distribution within the genomic region are plotted on the x-axis and y-axis, respectively. (B) Density plots representing the proportion of genes (y-axis) in the vicinity of TSSs (x-axis) covered by zebrafish typical enhancers (grey) and SEs (red). Hpf, hours post-fertilization. (C) Genomic distribution of zebrafish typical enhancers and SEs. The percentage of total typical enhancer and SE base pairs overlapping the different genomic features represented in the legend are shown on the y-axis. (D) Distribution of genomic features in the zebrafish (danRer7), mouse (mm10) and human (hg38) genomes. The y-axis shows the percentage of the genome covered by the different features represented in the legend in (C).