



Supplemental Fig S4: The loci of transposase-accessible chromatin correlate with hypomethylated DNA and chromatin modifications of active *cis*-regulatory elements.

We used ATAC-seq to identify transposase-accessible chromatin, defining usually <1 kb regions (top left, red). The same loci show decreased DNA methylation (top, green), and local enrichment of post-translational modifications of histones, including H3K27ac (blue), H3K4me1 (gold) and H3K4me3 (purple). These histone modifications are enriched one each side of the nucleosome-free region defined by ATAC-seq, better demonstrated in the lower plot.