Figure S4

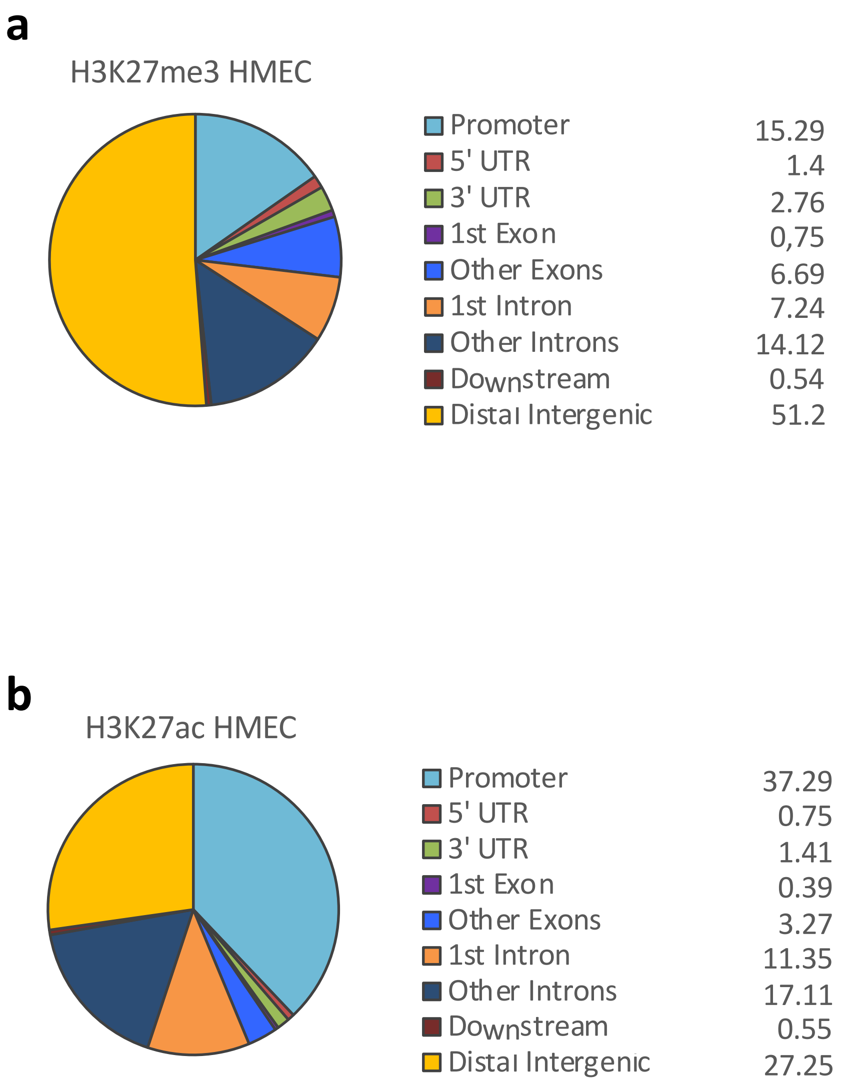

Figure S4. Analysis of H3K27me3 and H3K27ac ChIP-Seq data from ENCODE project. H3K27me3 (**a**) and H3K27ac (**b**) data set from human mammary epidermal cells (HMEC) was taken from UCSC Genome Browser and analyzed following the same pipeline used for Std PAT-ChIP and EPAT-ChIP (LRC) data sets. Pie charts depicting the distribution of peaks across genomic features with relative percentage values shown on the right. Promoters are defined as -3 Kb to +3 Kb relative to the TSS while Downstream as -3 Kb relative to the end of 3’ UTR region.