



Figure S9. Characterization of the TSS associated NDRs in a replicate experiment. (A) A heat map showing the normalized and standardized z-scores at 6kb regions centered at the TSS of 5731 genes that are occupied by H3K4me3, H3K9ac, and H3K27ac. The regions were manually divided into four groups and the percentage of regions in each group is shown in parentheses. **(B)** Metagene plots showing the average occupancy of each modification in each group. **(C)** Boxplot showing the difference in the GC content at the TSS for groups 1-3. The difference between group 1 and both 2 and 3 is highly significant (p -value = 2.01×10^{-103} and 5.32×10^{-64} ; t -test, and effect size = 0.76 and 0.95, respectively).