Supplemental Figure S18 Comparison of the coverage by computationally predicted TFBSs between four TSS groups. The computationally predicted TFBSs in human genome were from ENCODE project (http://compbio.mit.edu/encode-motifs/). Note that the TFBSs predicted by computational methods are based on binding motifs, usually smaller than the called peaks in the TF ChIP-seq data that were used for generating **Fig. 4**.