

Supplemental Figure S1. Distribution of 4,000 target DHS regions. (A) Histogram showing the locations of the target regions (up- or downstream) relative to the nearest transcriptional start site (TSS, indicated by arrow) based on GREAT analysis (McLean et al. 2010). The number of 'promoter-proximal' DHSs for each group is shown, as defined by DHSs that fell within -1 kb to +100 bp relative to the nearest TSS. (B) Histogram showing the basic annotations for the target regions, based on HOMER (Heinz et al. 2010). Abbreviations: UTR, untranslated region; TTS, transcription termination site; ncRNA, non-coding RNA.