



Supplemental Figure S2. High-throughput profiling in the mouse cortex. (A) Length distributions of known ASD linked genes from SFARI database (SFARI) and all human genes (All). Only protein-coding genes were included in this analysis. (B) Boxplot of length of ASD linked genes (SFARI) and all human genes (All). P , P value, one-tailed t -test. (C) Normalized signals (reads per 30 million uniquely mapped reads, RP30M) of ATAC-seq and ChIP-seq around the TSS regions of the expressed genes. Genes were classified into four groups based on their gene length. (D-E) Browser representations of GRO-seq, ChIP-seq, ATAC-seq, mC, and hmC signals at seven BELD genes (E, scale bar is 100 kb) and six short genes (F, scale bar is 10 kb). (F) Distribution of gene body H3K4me1 signals (RPM) according to their H3K27ac ranking. (G) Distribution of gene body ATAC-seq signals (RPM) according to their H3K27ac ranking.