



Supplemental Figure S5. Transcription of long genes in the cortex tends to pause less. (A) Heatmap of normalized GRO-seq signals across the sense strand of gene bodies and 500 bp flanking regions of the expressed genes. The genes were ordered by length (from long to short). Gene bodies were divided into 1000 equal bins. (B) Diagram representation of the definitions of promoter-proximal regions (from -30 bp to +300 bp around the TSS) and gene body regions used for the calculation of pausing index. (C-D) Browser representations of GRO-seq signals at three short gene loci (C) and nine long gene loci (D). (E) Browser representations of enhancer RNA-like transcripts (highlighted by the orange boxes). (F) Boxplots of numbers of gene body enhancer RNA-like transcripts in non-BELD control genes and BELD genes. P , P value, one-tailed t -test. (G) Boxplots of percentages of chromatin-chromatin interactions that are within the regions of super enhancers and BELD genes in the mouse cortex. P , P value, one-tailed t -test.