

Supplemental Figure S8. Additional examples of truncation mutation analysis by CRE-seq. Additional examples of CRE-seq truncation mutation analysis for (A) retinal DHSs, based on retinal CRE-seq data, and (B) brain DHSs, based on cerebral cortex CRE-seq data. Individual barcoded constructs are colored by intensity (darker indicates higher expression; the heat map shown at bottom of panel A was used throughout). Critical regions are highlighted in pink. All browser images are from UCSC Genome Browser (mm9) (Karolchik et al. 2014). DNase-seq data are from Mouse ENCODE (Yue et al. 2014). PhastCons depict 30-way vertebrate phylogenetic conservation (Siepel et al. 2005).