

# Retina

All retina DHSs in retina

All brain DHSs in retina

All heart DHSs in retina

All liver DHSs in retina

# Cerebral cortex

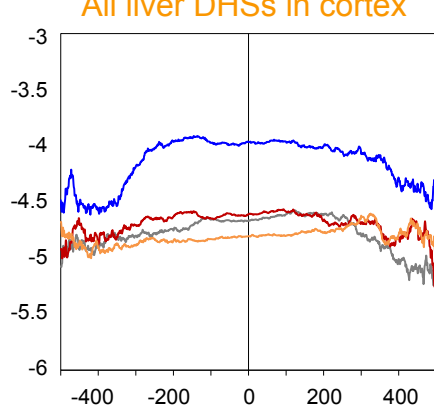
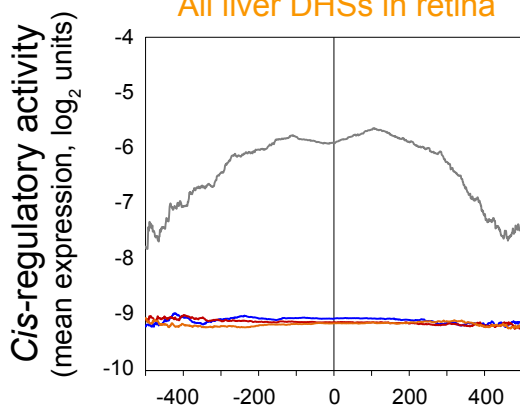
All retina DHSs in cortex

All brain DHSs in cortex

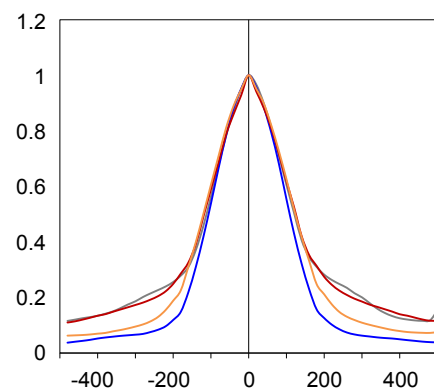
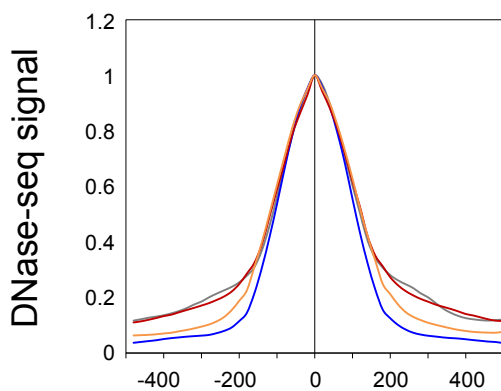
All heart DHSs in cortex

All liver DHSs in cortex

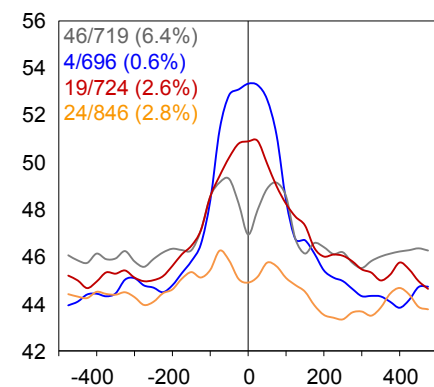
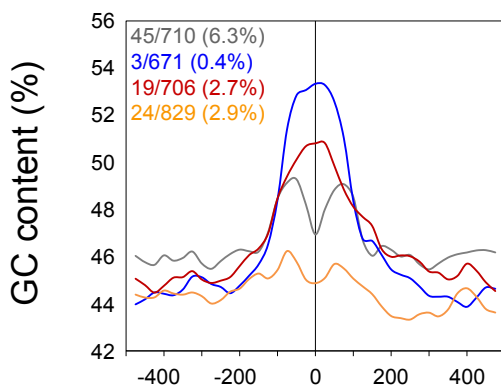
## A



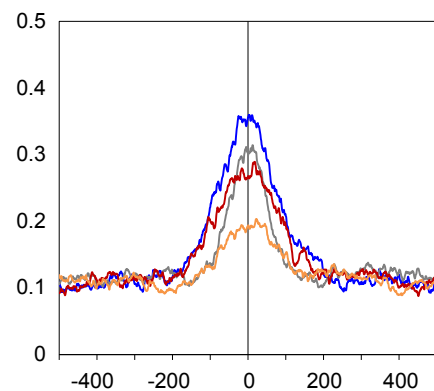
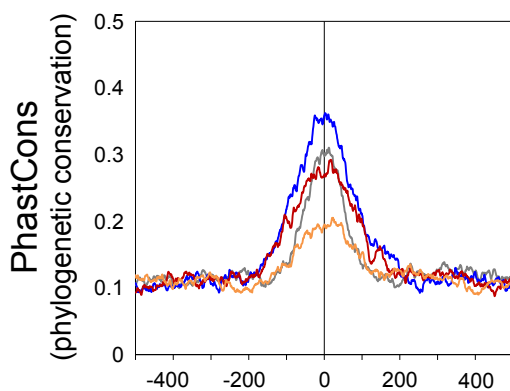
## B



## C



## D



Position (bp)

Position (bp)

### Supplemental Figure S5. CRE activity, DNase-seq signal, GC content, and phylogenetic conservation of assayed DHSs in a 1 kb centered window.

Retina, brain, heart, and liver DHSs were assayed in the retina (left) and cerebral cortex (right). Each panel shows a 1 kb centered window. Only DHSs with at least 2 barcodes were included in this analysis, i.e., in the retina, 710 retinal DHSs, 671 brain DHSs, 706 heart DHSs, and 829 liver DHSs, and in the cerebral cortex, 719 retinal DHSs, 696 brain DHSs, 724 heart DHSs, and 846 liver DHSs. (A) Cis-regulatory activity, as measured by mean expression in log<sub>2</sub> units. For each assayed DHS, at each base position across the 1 kb window, the expression values of the individual barcoded constructs whose CREs overlapped the position were averaged across biological replicates. (B) DNase-seq score, normalized to the peak height. (C) GC content, calculated in 50 bp windows, sliding 25 bp at a time. The fractions denote the proportion of DHSs that were promoter-proximal (i.e., located within -1 kb to +100 bp relative to the nearest TSS) based on GREAT annotations (McLean et al. 2010). (D) Phylogenetic conservation as measured by 30-way vertebrate PhastCons (Siepel et al. 2005).