

Description of Additional Supplementary Files:

Supplementary Data 1: Inventory of epigenomic and transcriptomic data sources.

Supplementary Data 2: K562 CRISPR benchmarking dataset. *P*-values were derived from two-sided *t*-tests comparing control and treated groups and adjusted for multiple comparisons using the False Discovery Rate (FDR).

Supplementary Data 3: Sum of Single Effects (SuSiE) fine-mapped GTEx variants.

Supplementary Data 4: EPInformer-PE-Activity performance using ATAC-seq versus DNase-seq and H3K27ac.

Supplementary Data 5: Effect of genomic distance range on EPInformer gene expression prediction performance.