

Evolutionary Landscapes of Human cis-regulatory Elements and Transcription Factor Binding Sites in the Mammalian Lineage

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Date: Monday, Oct. 3rd, 2022

The ENCODE Project has generated tens of thousands of DNase-seq, ChIP-seq, RNA-seq datasets in humans and mice. As part of the ENCODE consortium, we developed a registry of human and mouse candidate cis-regulatory elements (cCREs), covering 10% of their respective genomes, by integrating selected datatypes associated with gene regulation (The ENCODE Consortium et al., Nature, 2020). We built a web-based server named SCREEN (<http://screen.encodeproject.org>) to provide flexible, user-defined access to the registry of cCREs and related genomic annotations generated by ENCODE. We created a similar resource, Factorbook (<https://factorbook.org>), which focused on transcription factors and their binding sites and motifs derived from ENCODE ChIP-seq data. Recently, we leveraged the genomes of 240 mammals sequenced by the Zoonomia consortium to annotate further cCREs and transcription factor binding sites. I will describe how these resources aid our interpretation of human variants associated with traits and diseases.