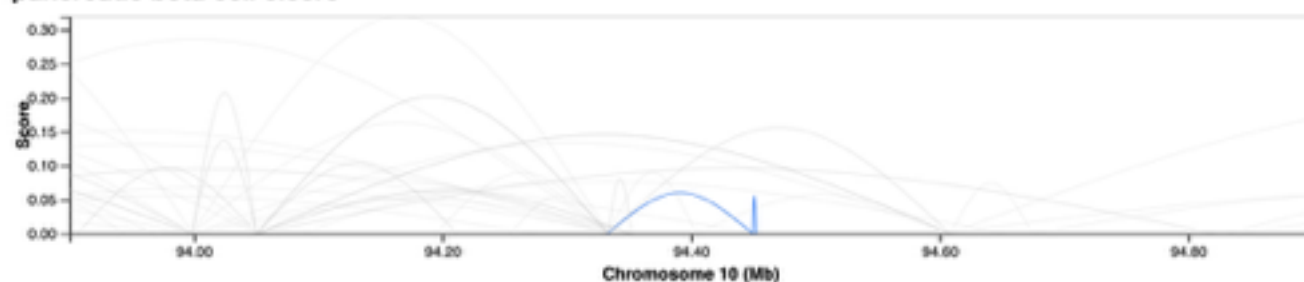
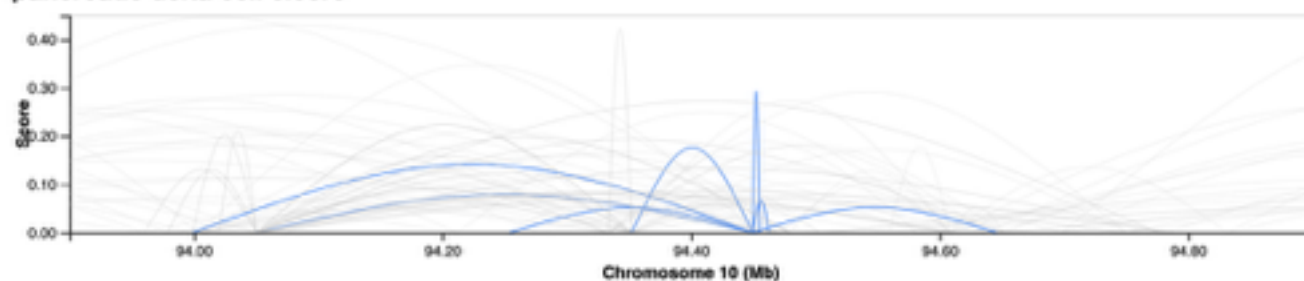


Supplementary Figure 1. Beta cell (top) and alpha cell (middle) co-accessibility between pairs of accessible chromatin sites and high-confidence promoter capture Hi-C interactions from bulk islets (bottom) anchored at the PDX1 promoter.

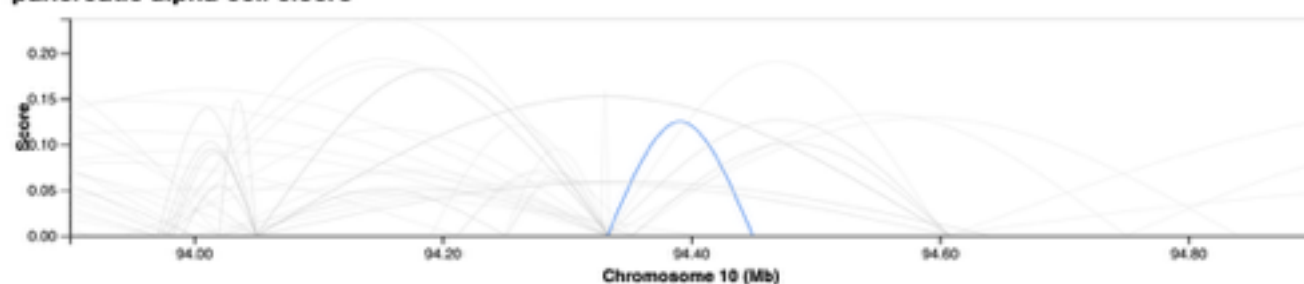
pancreatic beta cell cicero



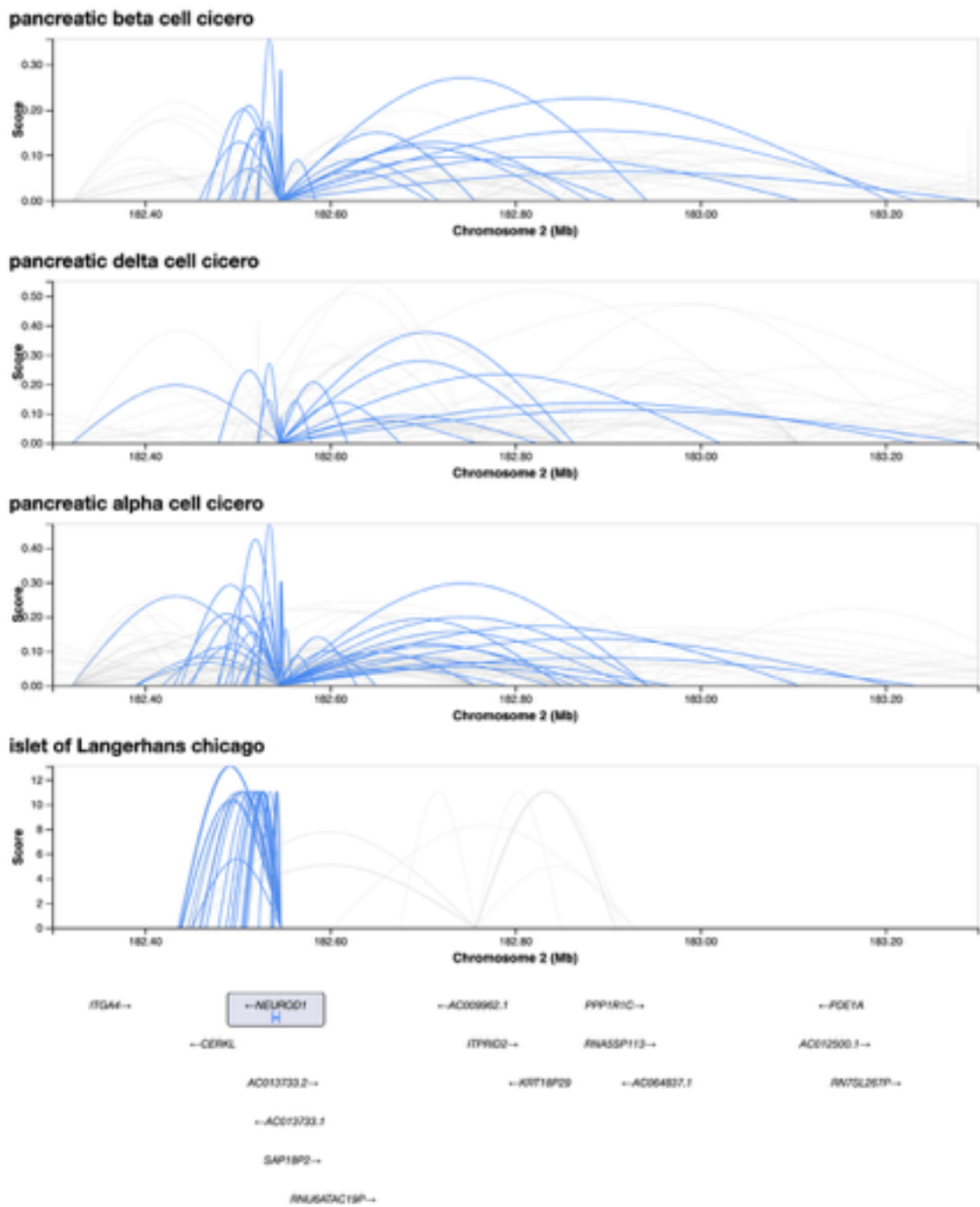
pancreatic delta cell cicero



pancreatic alpha cell cicero



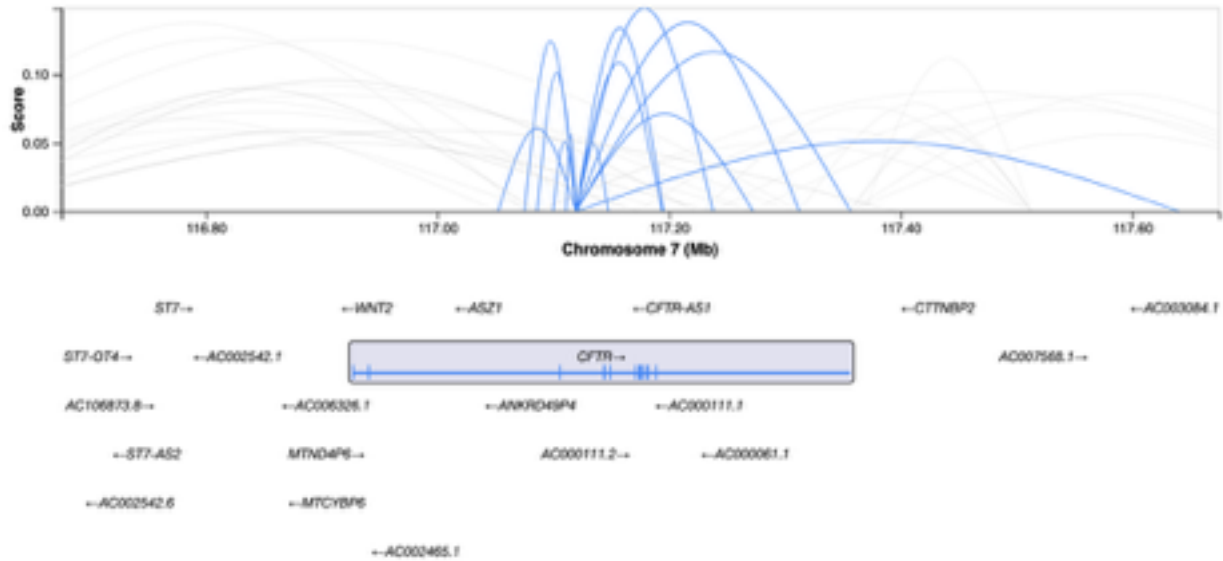
Supplementary Figure 2. An example of co-accessibility anchored at the promoter for the delta cell identity TF *HHEX* (region shown: chr10:93,900,000-94,900,000, hg19). Co-accessibility for beta, delta, and alpha cells



Supplementary Figure 3. An example of shared co-accessibility anchored at the promoter for the shared islet identity TF NEUROD1 (region shown: chr2:182,100,000-183,500,000, hg19)

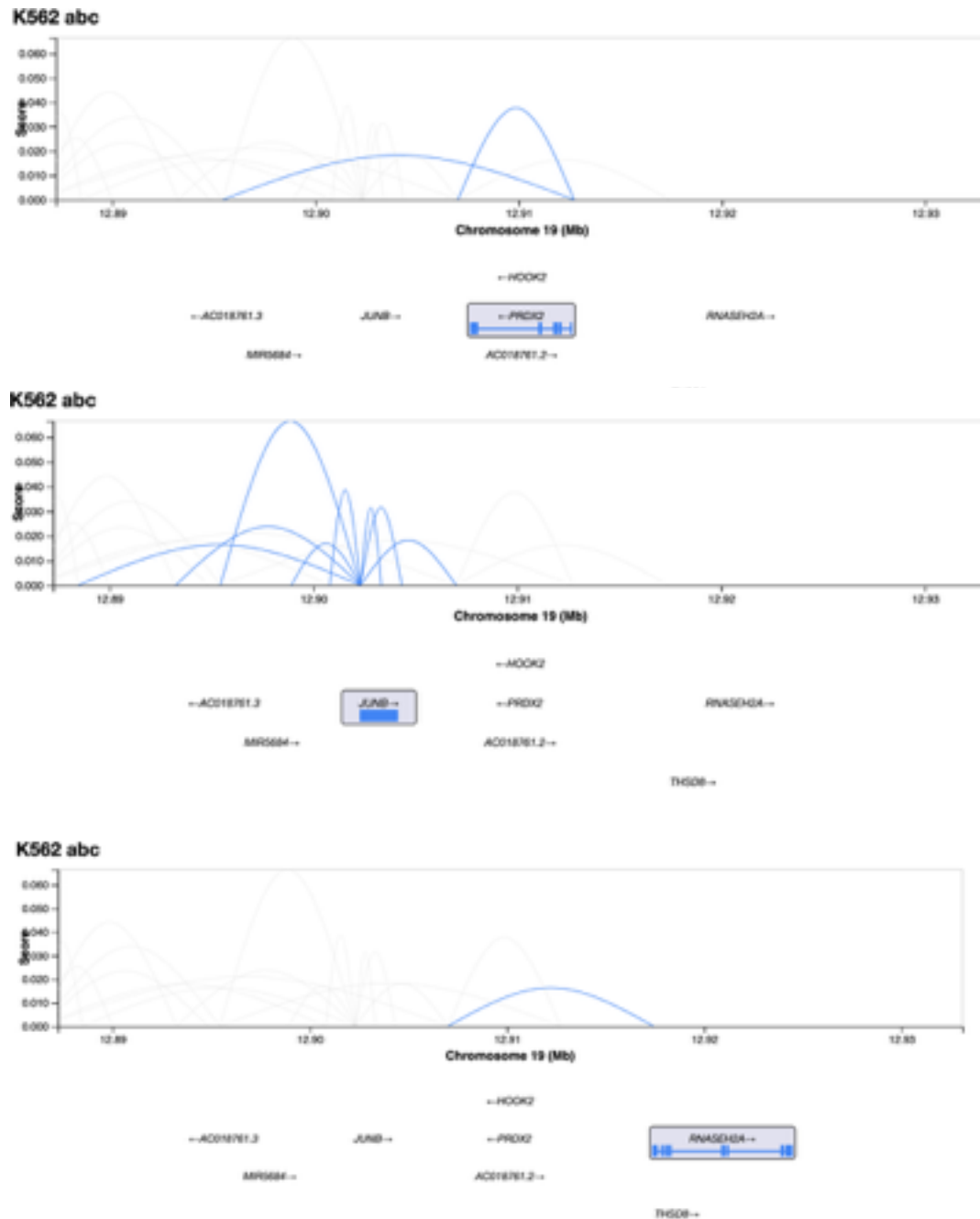
Large-scale genetic association study and single cell chromatin map identifies novel loci and cell types affecting type 1 diabetes risk

T1D pancreatic ductal cell cicero

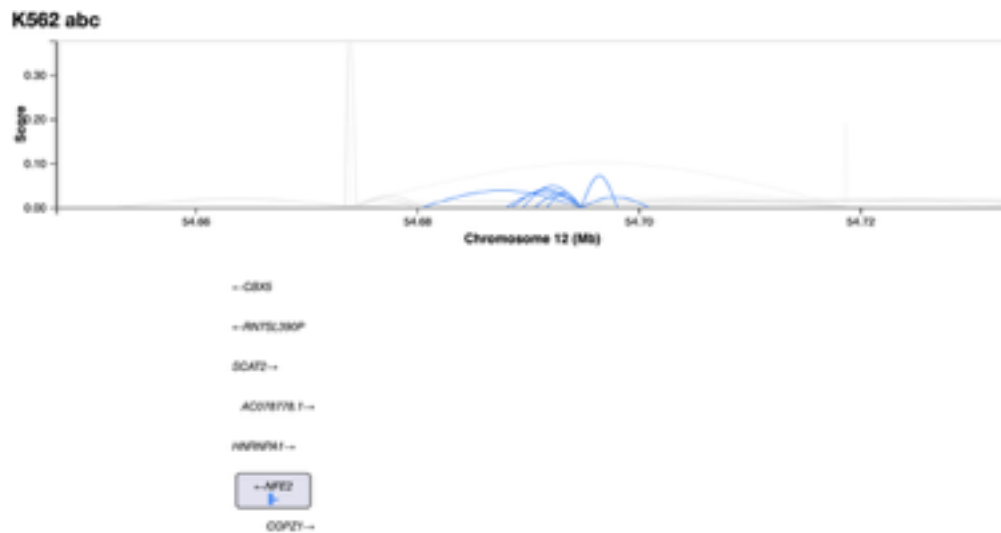
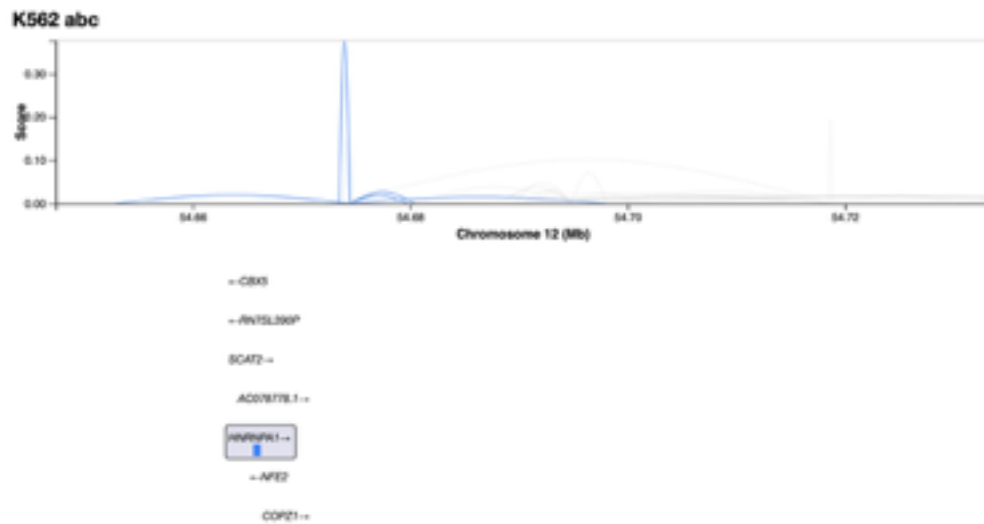
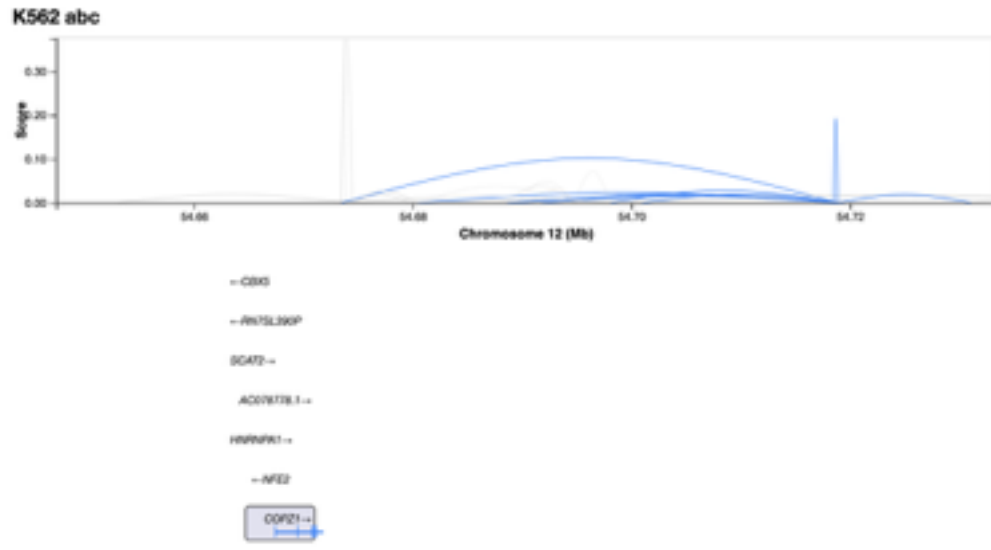


Supplementary Figure 5. (region shown: chr7:116,490,000-117,860,000). The cCRE is located approximately 33 kb upstream of the CFTR promoter.

Activity-by-Contact model of enhancer specificity from thousands of CRISPR perturbations



Supplementary Figure 6. Example of CRISPRi-FlowFISH screen data. DE-G connections are elements affecting the expression of JUNB, PRDX2, and RNASEH2A in CRISPRi-FlowFISH screens in K562 cells (region shown: chr19:1,22,80,001-1,37,00,000) The width of the arc corresponds to the effect size. Tested genes refer to genes for which CRISPRi-FlowFISH experiments were performed



Supplementary Figure 7. Same as (Supplementary Figure 6.) for the genes HNRNPA1, NFE2, and COPZ1. (region shown: chr12:54,647,404-5,47,33,396)