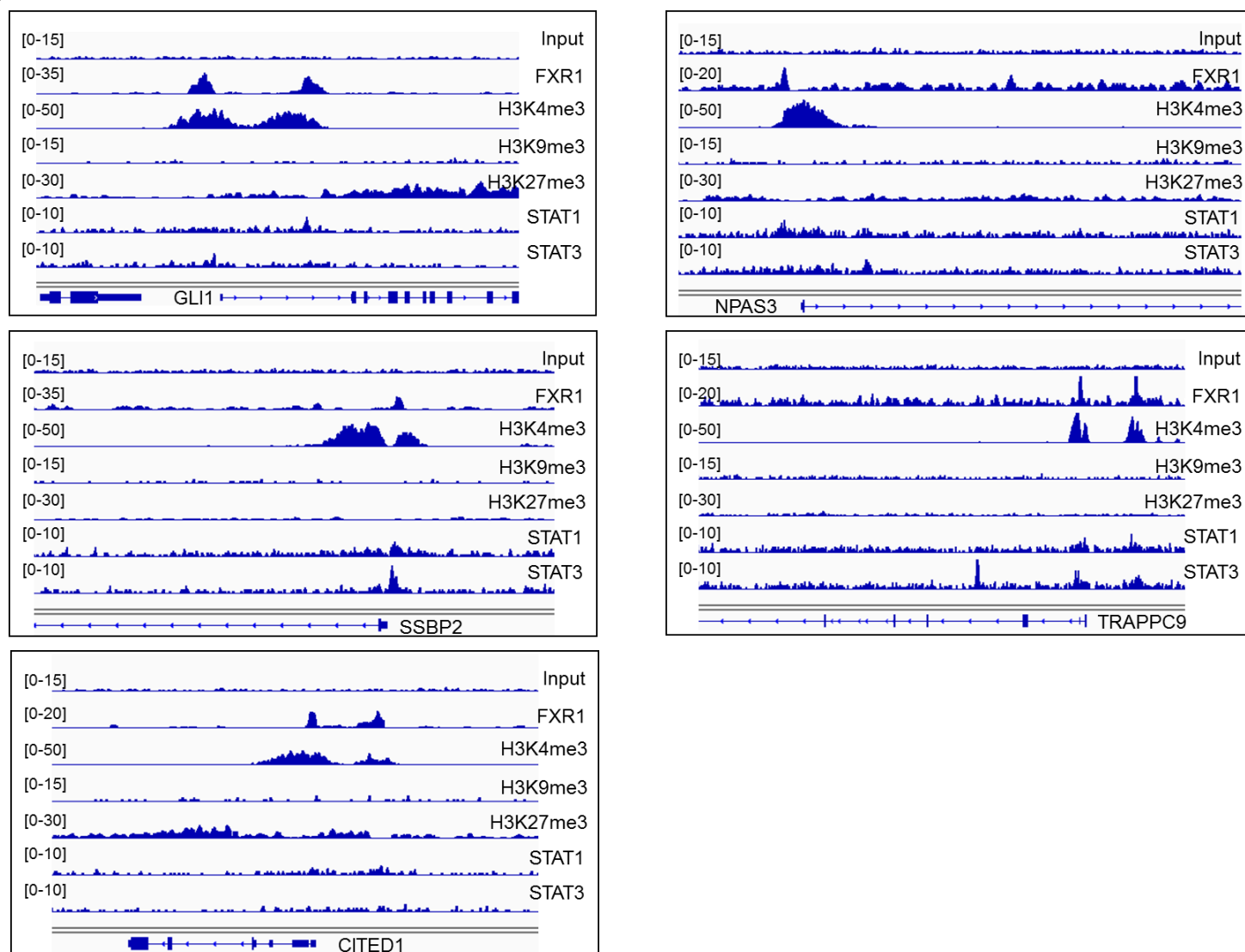


Fig 5-S1

A



B

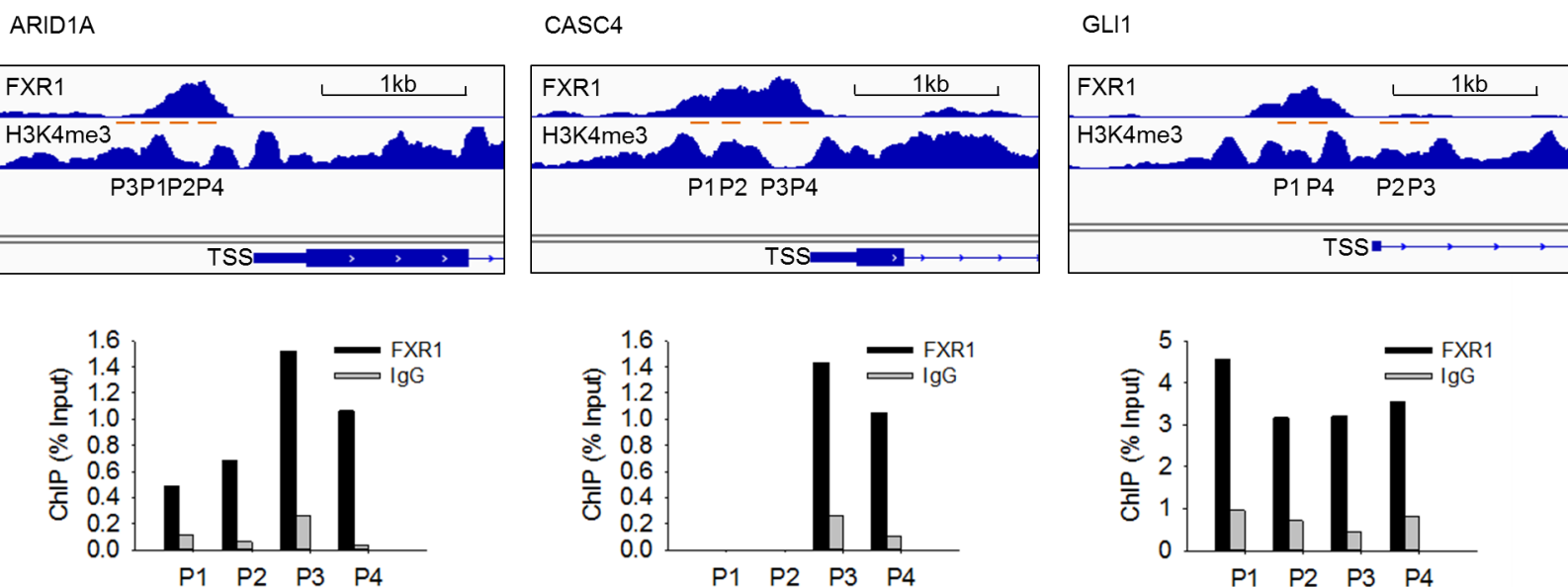


Figure 5–Figure Supplement 1. ChIP-seq peaks of FXR1, STAT1, STAT3 and histone marks (H3K4me3, H3K9me3, and H3K27me3) at validated target genes *GLI1*, *TRAPPC9*, *CITED1*, *NPAS3*, and *SSBP2*.

(A) The enrichment of FXR1, H3K4me3, H3K9me3, H3K27me3, STAT1, and STAT3 ChIP-seq peaks at gene promoter region of target genes from IGV screenshot in H358 cells.

(B) Upper, illustration of the targeting region of FXR1 ChIP-PCR primers according to FXR1 genomic peak localization at the target genes. TSS: transcription start site. Lower, evaluation of primers in FXR1 ChIP-PCR assay. IgG serves as the control of FXR1 antibody pull down. Primer design and selection for other target genes follows the same approach.