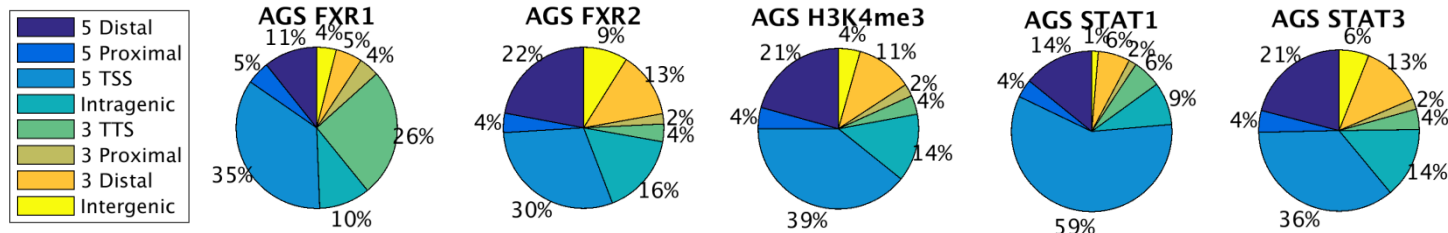
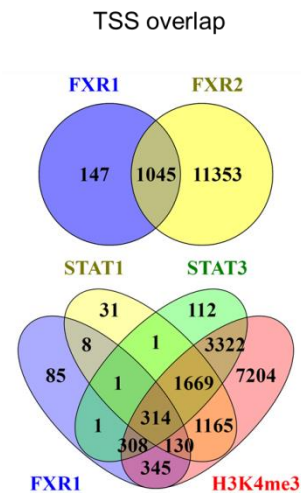


Fig 5-S4

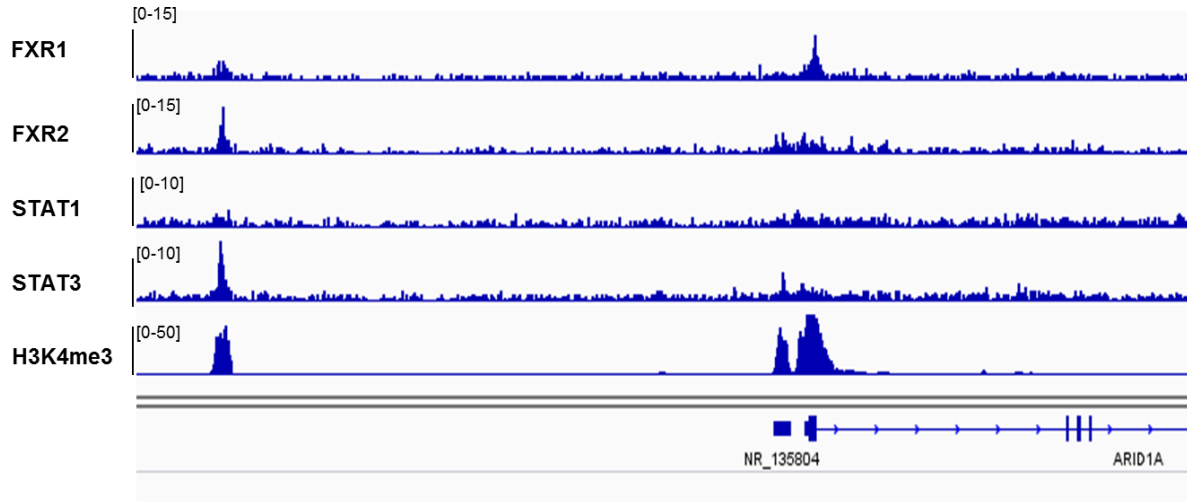
A



B

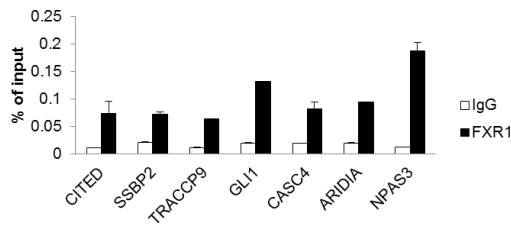


C

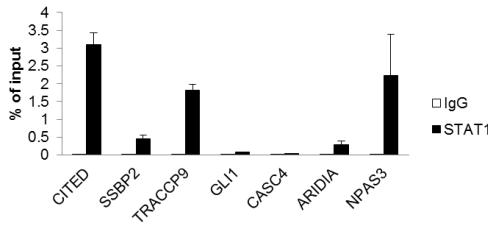


D

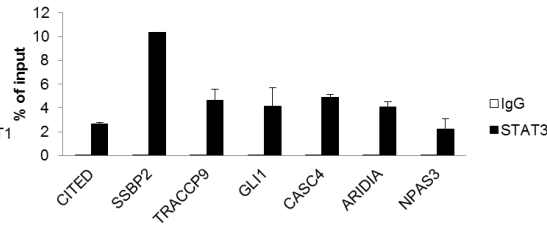
FXR1 ChIP in AGS



STAT1 ChIP in AGS



STAT3 ChIP in AGS



**Figure 5–Figure Supplement 4. FXR1 colocalizes with FXR2, STAT1/3, H3K4me3 at gene promoter in AGS cells**

(A) Genomic distribution of FXR1, FXR2, H3K4me3, STAT1 and STAT3 ChIP-seq peaks in AGS cells.

(B) Venn diagram showing significant overlap of FXR1 and FXR2 (upper), FXR1, STAT1, STAT3, and H3K4me3 (lower) ChIP-seq peaks (enriched at TSS) associated genes in AGS cells ( $P < 1 \times 10^{-5}$ ).

(C) The enrichment of FXR1, FXR2, H3K4me3, H3K9me3, H3K27me3, STAT1, and STAT3 ChIP-seq peaks at gene promoter region of *ARID1A* from IGV screenshot in AGS cells.

(D) FXR1, STAT1 and STAT3 ChIP-qPCR analyses at 7 target genes in AGS cell lines. Data are represented as mean  $\pm$  s.d. (n=3), IgG pull down is used as a negative control.

TSS, transcription start site; TTS, transcription termination site.