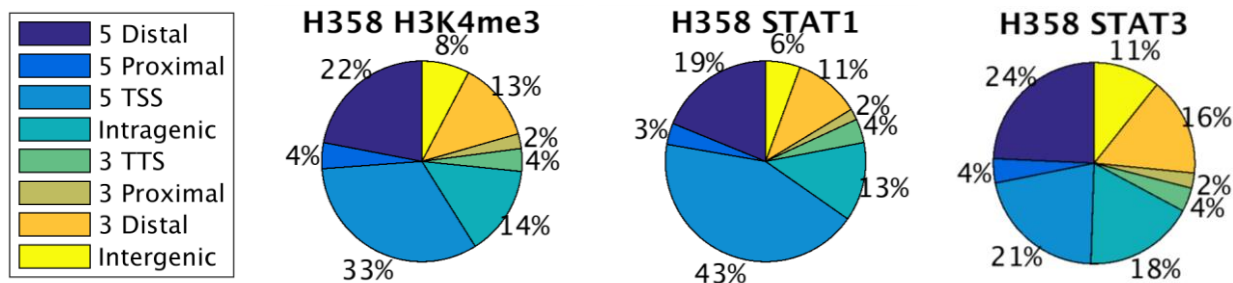
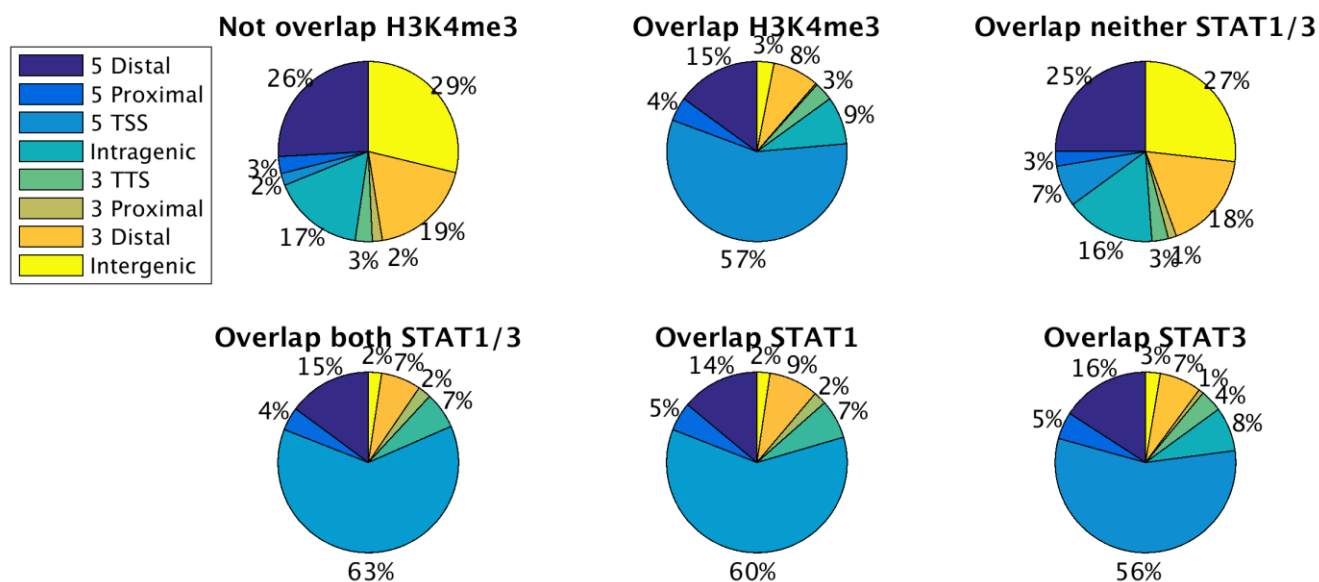


Fig 5-S2

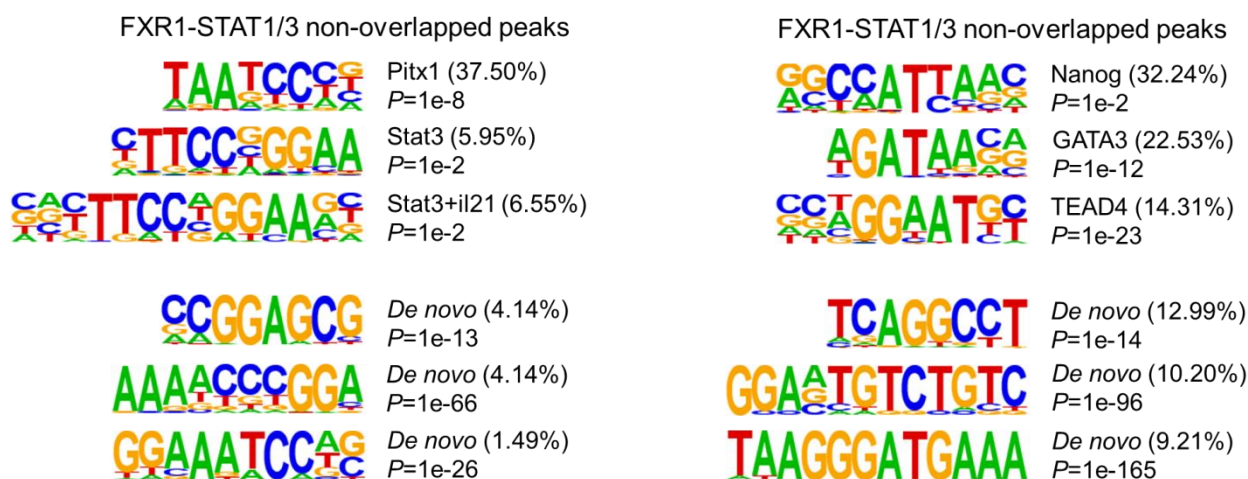
A



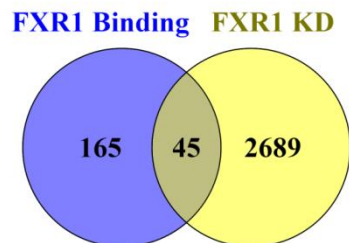
B



C



D



E

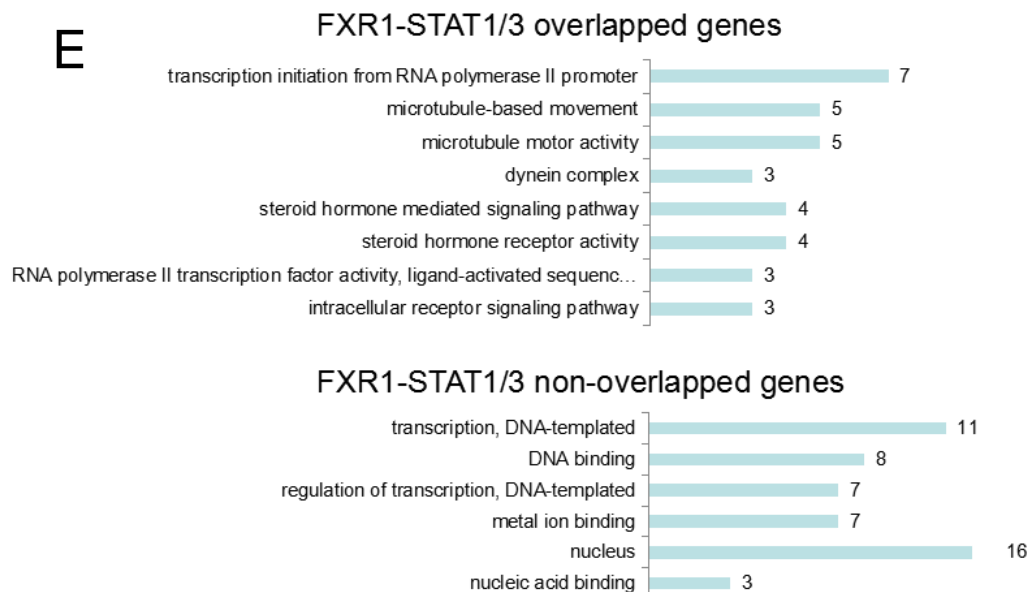


Figure 5–Figure Supplement 2. FXR1 colocalizes with H3K4me3 and STAT1/3 at gene promoter

- (A) Genomic distribution of H3K4me3, STAT1 and STAT3 ChIP-seq peaks in H358 cells.
 - (B) Genomic distribution of FXR1-H3K4me3 or FXR1-STAT1/3 overlapped or non-overlapped ChIP-seq peaks in H358 cells.
 - (C) Representative binding motifs of FXR1 from motif analysis of FXR1 and STAT1/3 overlapped regions (left) or non-overlapped regions (right) using MEME.
 - (D) Venn diagrams showing significant overlap between FXR1 regulated genes from RNA-seq result and genes with FXR1 occupancy at promoter from ChIP-seq result in H358 cells ($P<1\times e-5$). KD, knockdown.
 - (E) GO analysis of overlapped or non-overlapped genes of FXR1 with STAT1/3.
- TSS, transcription start site; TTS, transcription termination site.
- Also see Supplementary Table S6 and S7.