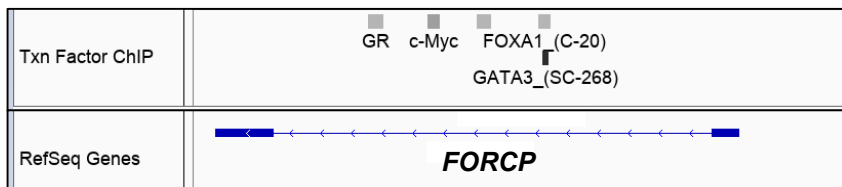
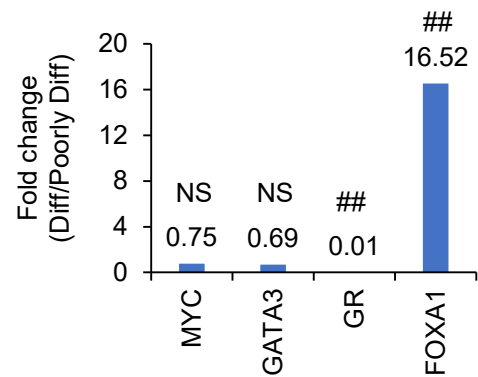
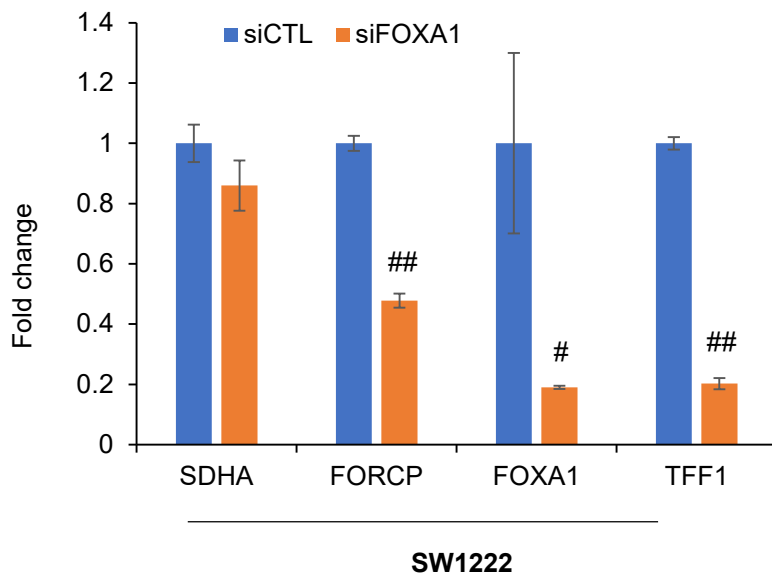
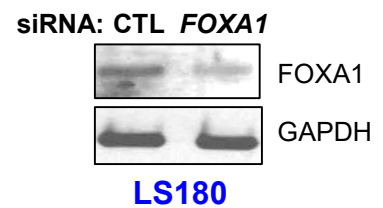
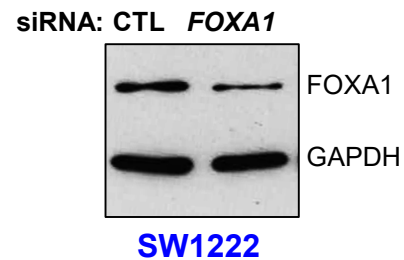


**A****ENCODE ChIP-seq**

chr17:10,697,839

10,709,420

**B****C****D****E****Figure 1-figure supplement 3.**

(A) IGV snapshot of ENCODE ChIP-seq data depicting ChIP-seq peaks of FOXA1, GR, c-Myc, and GATA3 at the *FORCP* locus. (B) Relative abundance of FOXA1, GR, MYC and GATA3 in well-differentiated (Diff) vs poorly-differentiated (Poorly Diff) CRC lines was assessed by RNA-seq (also see Supplementary file 2).

(C) qRT-PCR analysis normalized to *GAPDH* is shown from SW1222 cells transfected with CTL siRNA or FOXA1 siRNAs for 48 hr. (D, E) Immunoblotting from whole cell lysates was performed from LS180 (D) and SW1222 cells (E) transfected with CTL siRNA or FOXA1 siRNAs for 48 hr. GAPDH was used as loading control. Error bars in panel C represent SD from 3 experiments. # $p < 0.01$ , ## $p < 0.001$ .