



Figure 5 – Figure Supplement 1
 Genome browser tracks for POLR2A ChIA-PET interactions for WT HCT116 cells, ATAC-seq from WT, ARID1B KD, ARID1A^{-/-}, and ARID1A^{-/-} ARID1B KD cells, FRA1, SMARCA4 and SMARCC1 ChIP-seq data from WT HCT116 cells, H3K27ac ChIP-seq data for WT, ARID1B KD, ARID1A^{-/-}, and ARID1A^{-/-} ARID1B KD cells, GRO-seq data for WT HCT116 cells, and RNA-seq from WT, ARID1B KD, ARID1A^{-/-}, and ARID1A^{-/-} ARID1B KD cells at the *TGFA*, *TGFBR2*, *PLAU*, and *EGFR* genes. Gray boxes indicate examples of intergenic accessible regions with SMARCA4, SMARCC1, and FRA1 binding in WT HCT116 cells, decreased accessibility and H3K27ac levels in ARID1A^{-/-} ARID1B KD cells, which exhibit POLR2A ChIA-PET interactions to promoters of genes downregulated in ARID1A^{-/-} ARID1B KD cells.