



Figure 5 – Figure Supplement 2

Genome browser tracks for ATAC-seq from WT, ARID1B KD, ARID1A^{-/-}, and ARID1A^{-/-} ARID1B KD cells, H3K27ac ChIP-seq data for WT, ARID1B KD, ARID1A^{-/-}, and ARID1A^{-/-} ARID1B KD cells, RNA-seq from WT, ARID1B KD, ARID1A^{-/-}, and ARID1A^{-/-} ARID1B KD cells, and GRO-seq data for WT HCT116 cells at sites with gained or stable SWI/SNF occupancy. Gray boxes indicate interacting sites of increased accessibility and/or H3K27ac. These genes show no dependence on ARID1B for accessibility, H3K27ac and RNA expression in the absence of ARID1A.