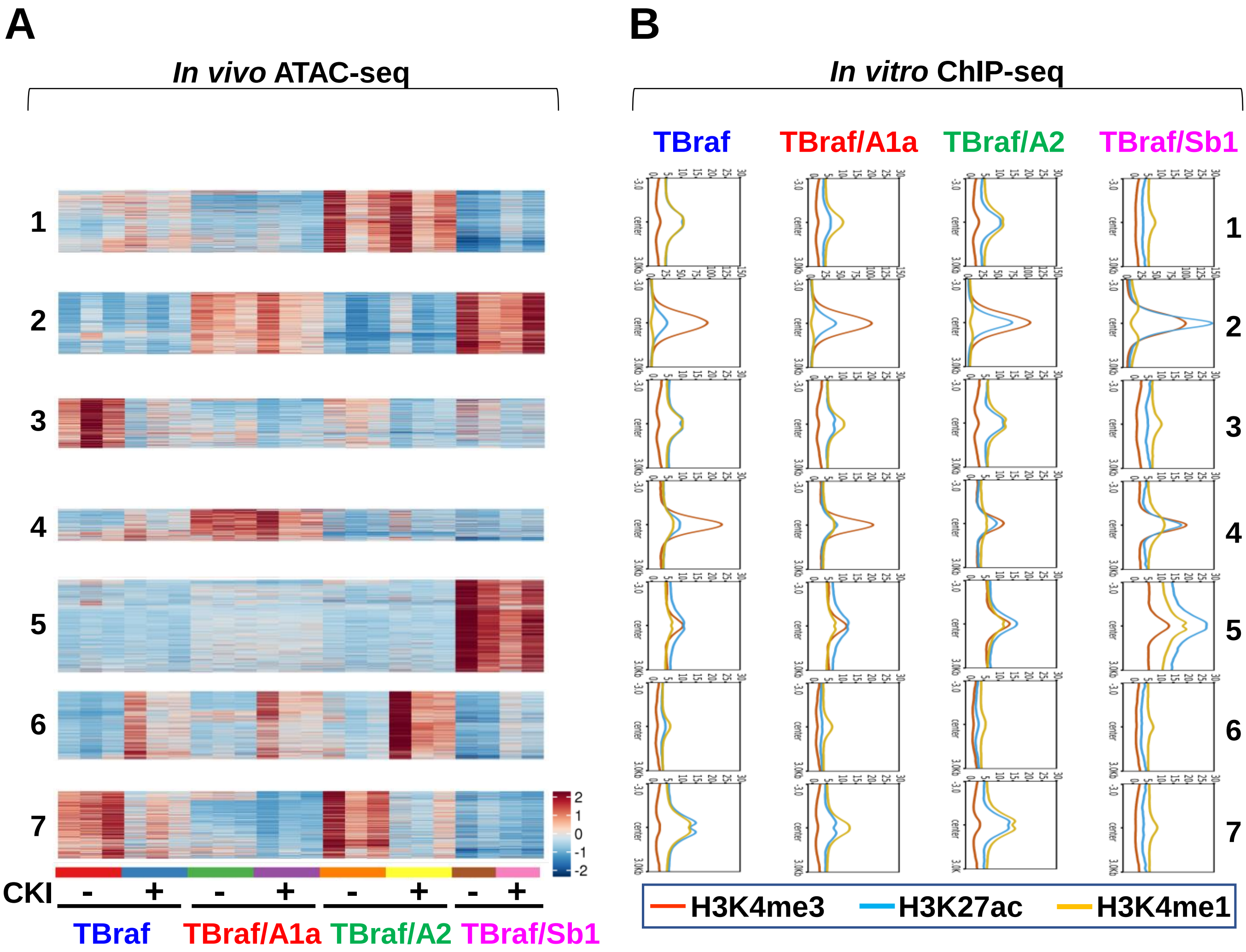

**<u>Supplementary Figure S11:</u>** ***Smarcb1* loss is associated with active enhancer/promoter marks at CTCF motif.** (A) ATAC-Seq of tumors with the indicated genotypes (from Fig 4D). (B) H3K4me3, H3K27ac, and H3K4me1 ChIP-seq was performed on cell lines derived from each tumor genotype. Shown is the ChIP-Seq average enrichment profile lying within +/-3 kb of peaks for each histone mark in the seven ATAC clusters.