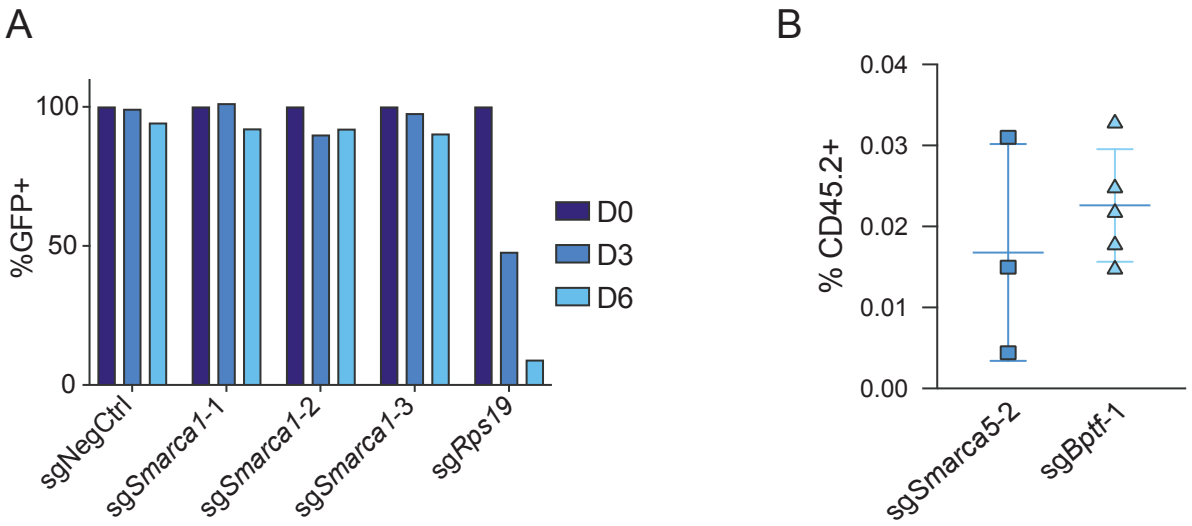
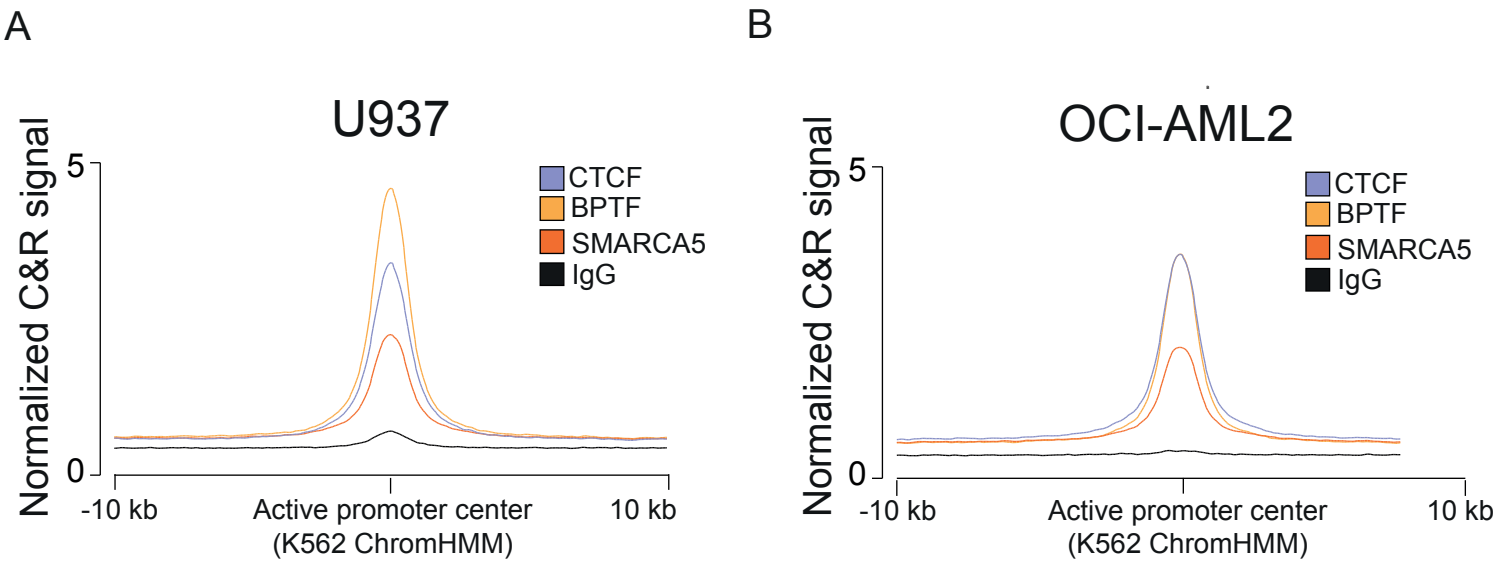
Appendix Figures Table of Contents

Appendix Figure S1



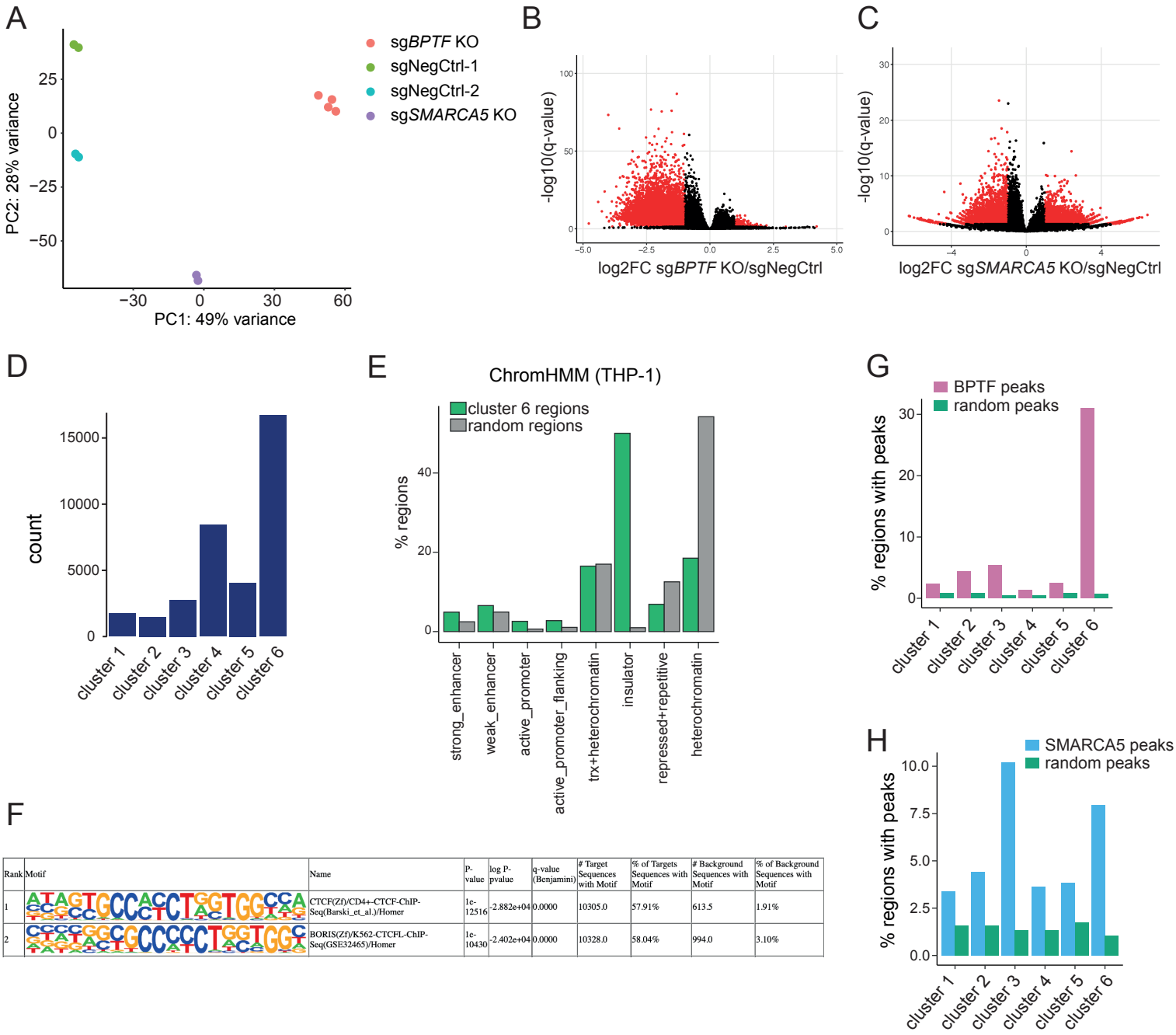
Appendix Figure S1. BPTF and SMARCA5 are essential for maintaining AML in vivo. A) Competition assay after *Smarca1* KO in mouse MLL-AF9 cells with inducible wtCas9 expression. The cells were transduced with the lentiviral cassettes expressing the corresponding sgRNAs and GFP and mixed with untransduced cells. The percentage of GFP-positive cells was measured over time. The data were normalized to Day 0. The results were validated in human AML cells, see Source data. B) Percentages of CD45.2+ (donor) cells present in the blood of the 8 surviving mice before experiment termination. Data are shown as mean ±SD.

Appendix Figure S2



Appendix Figure S2. BPTF and SMARCA5 bind active promoter regions in U937 and OCI-AML2 cells. A-B) Average profiles of the CTCF, BPTF, and SMARCA5 Cut&Run signal in U937 (A) and OCI-AML2 (B) cells at the insulator regions predicted by the ChromHMM in K562 cells.

Appendix Figure S3



Rank	Motif	Name	P-value	log P-pvalue	q-value (Benjamini)	# Target Sequences with Motif	% of Targets Sequences with Motif	# Background Sequences with Motif	% of Background Sequences with Motif
1		CTCF(Zf)/CD4+-CTCF-ChIP-Seq(Barski_et_al.)/Homer	1e-12516	-2.882e+04	0.0000	10305.0	57.91%	613.5	1.91%
2		BORIS(Zf)/K562-CTCFL-ChIP-Seq(GSE32465)/Homer	1e-10430	-2.402e+04	0.0000	10328.0	58.04%	994.0	3.10%

Appendix Figure S3. BPTF and SMARCA5 together remodel insulator regions in AML cells. A) PCA plot of the ATAC-sequencing samples. B-C) Volcano plots comparing ATAC-seq changes between the *BPTF* (B) or *SMARCA5* (C) KOs and wild-type cells. The peaks with an absolute log2 fold change over 1 and a q-value < 0.01 are highlighted in red. D) Number of regions in the differential ATAC-seq clusters described in Figure 4F. E) Bar plot illustrating the percentage of regions in cluster 6 overlapping chromatin domain categories defined by the ChromHMM in THP1 cells. A corresponding set of random regions of the same average length and size was generated and shown in green. Some regions may overlap several categories; hence, the total percentage does not equal 100. 'trx' stands for transcription. F) Two top hits of the motif analysis in the differential ATAC-seq cluster 6. G-H) Bar plots illustrating the percentage of regions in differential ATAC-seq clusters overlapping with BPTF (G) or HA-SMARCA5 (H) peaks. A corresponding set of random regions of the same average lengths and sizes was generated and shown in green. All the ATAC-seq experiments were performed in two biological replicates, i.e., independent cell transductions or treatments.