Supplementary Material

Figures S1-S2

Figure S1

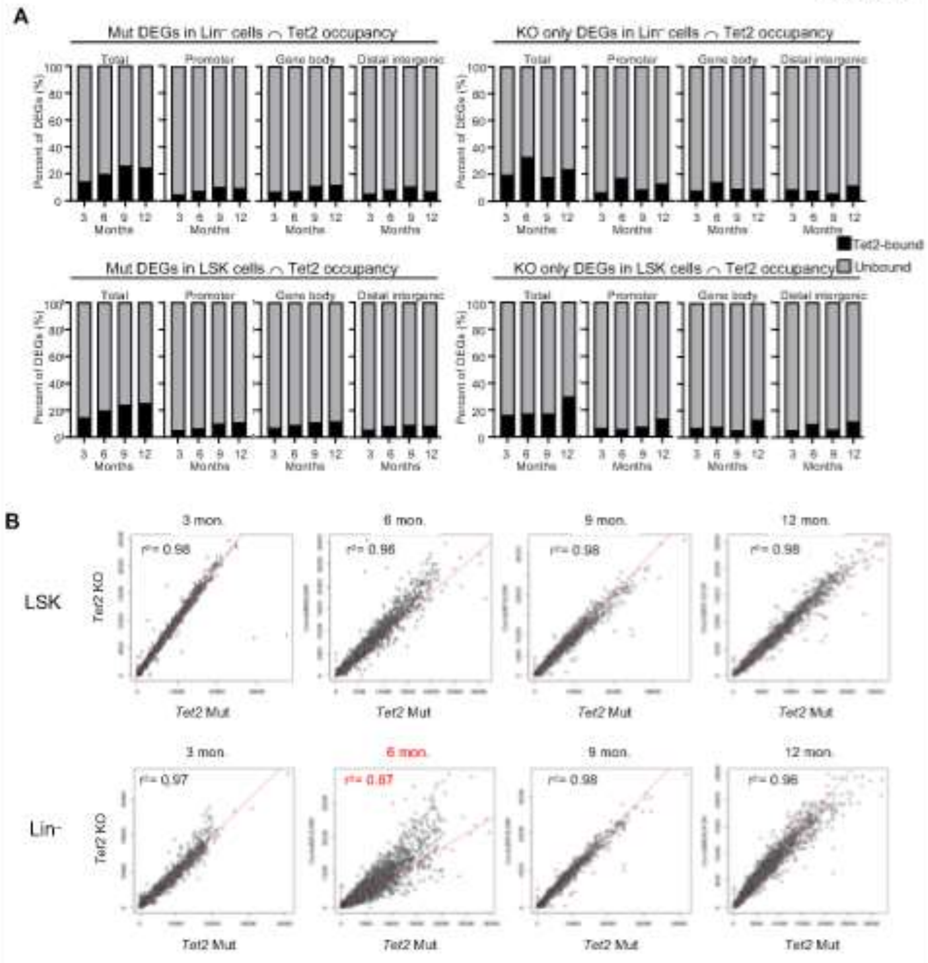


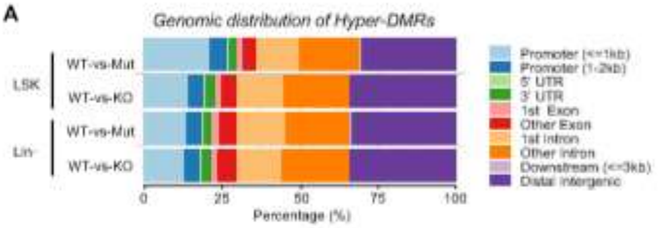
Figure S1: Transcriptomic characterization of *Tet2* Mut and KO LSK and Lin⁻ cells.

A. Integration of Tet2 occupancy in AML cells with gene expression data from *Tet2* Mut and KO LSK and Lin– cells across time points (Tet2 ChIP-seq data from Rasmussen et al., 2019). Percentages of Tet2-bound DEGs across genomic regions and time points are shown.

B. Transcriptome-wide correlation analysis between *Tet2* Mut and KO LSK and Lin⁻ cells. Note that gene expression is most divergent between genotypes at 6 months in Lin⁻ cells (lowest r^2 value).

Figure S2

A



B

Number of Hyper-DMRs at each genomic region.

Sample	Promoter	Gene body	Distal	Downstream	Total
LSK: WT-vs-Mut	1,051	1,669	1,192	4	3,916
LSK: WT-vs-KO	751	1,793	1,321	2	3,867
Lin−: WT-vs-Mut	600	1,520	1,081	1	3,202
Lin−: WT-vs-KO	695	1,799	1,294	2	3,790

C

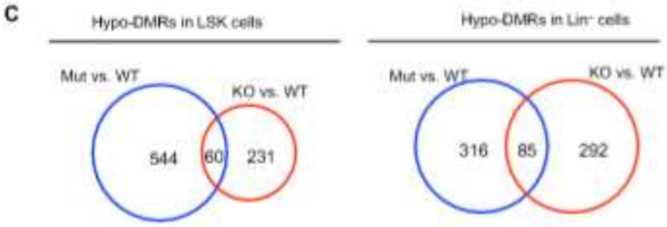


Figure S2: WGBS of *Tet2* Mut and KO LSK and Lin⁻ cells at 3 months of age

A. Genomic annotation of hyper-DMRs found in Tet2 Mut and KO LSK and Lin⁻ cells.

B. Number of hyper-DMRs at the indicated genomic regions.

C. Overlap of hypo-DMRs in Mut and KO LSK and Lin⁻ cells.