Figure S1

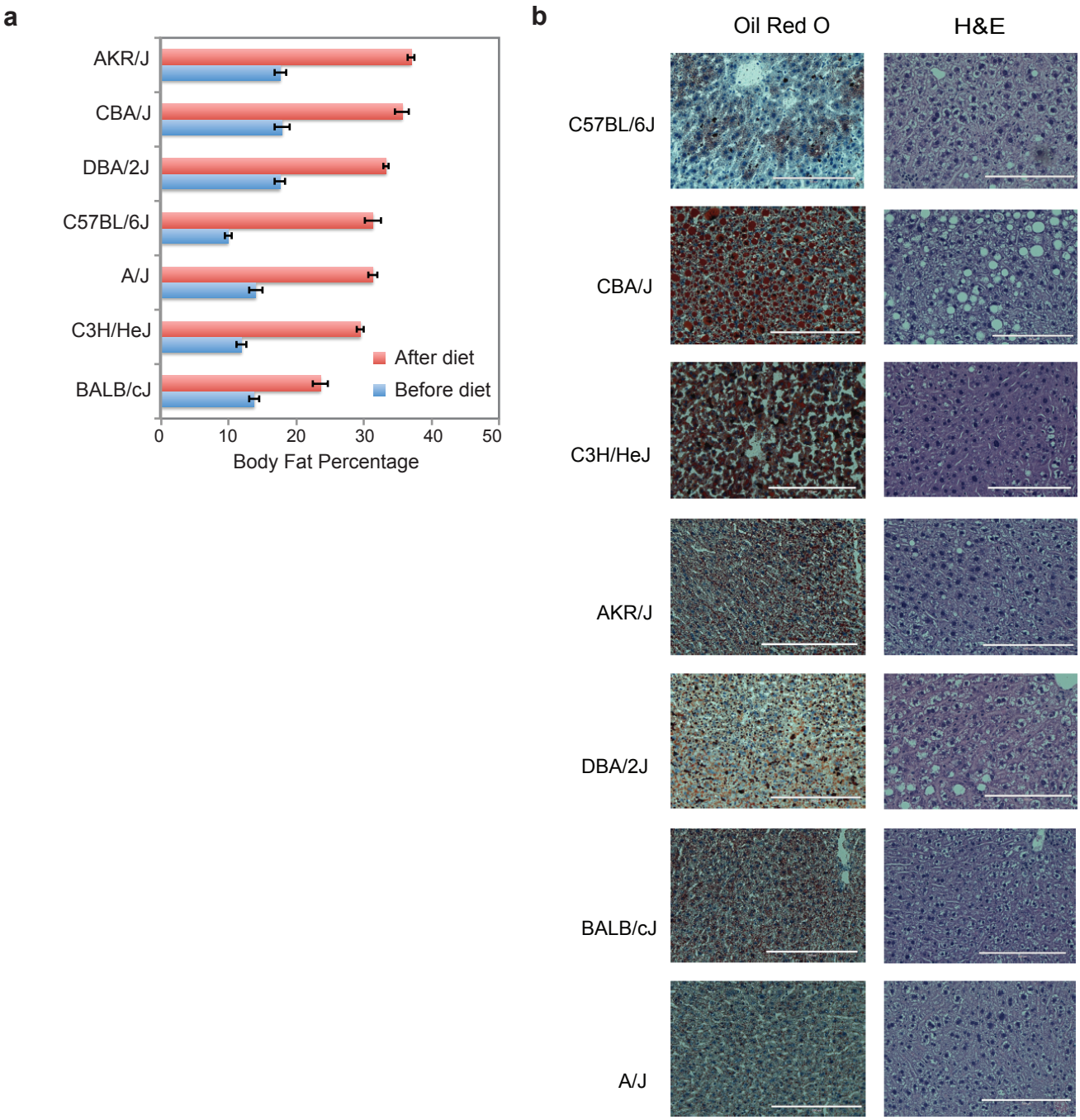

Figure S1. Phenotypic diversity in different inbred strains. (**a**) Body fat percentage of 7 inbred mouse strains before and after 8 weeks of HF/HS diet (from Parks et al. *Cell Metab*, 2013 17(1), pp. 141-152). (**b**) Oil red O and H&E staining of liver sections from mice after HF/HS diet.

Figure S2

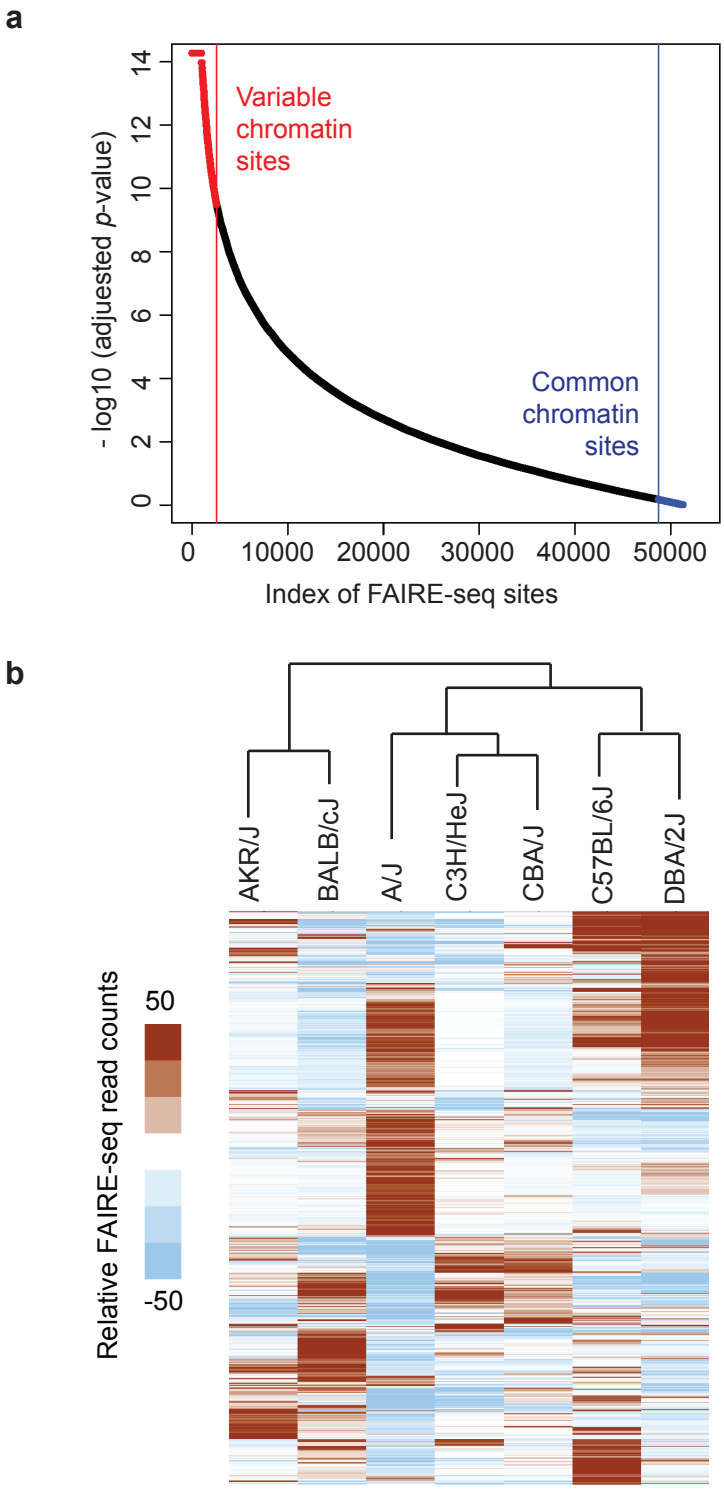

Figure S2. Chromatin variability across strains of mice. (**a**) Distribution of *p*-values of each chromatin sites from DEseq analysis. (**b**) Unsupervised hierarchical clustering of relative FAIRE-seq read counts at variable chromatin sites (red data points in **a**) across seven strains of mice.

Figure S3

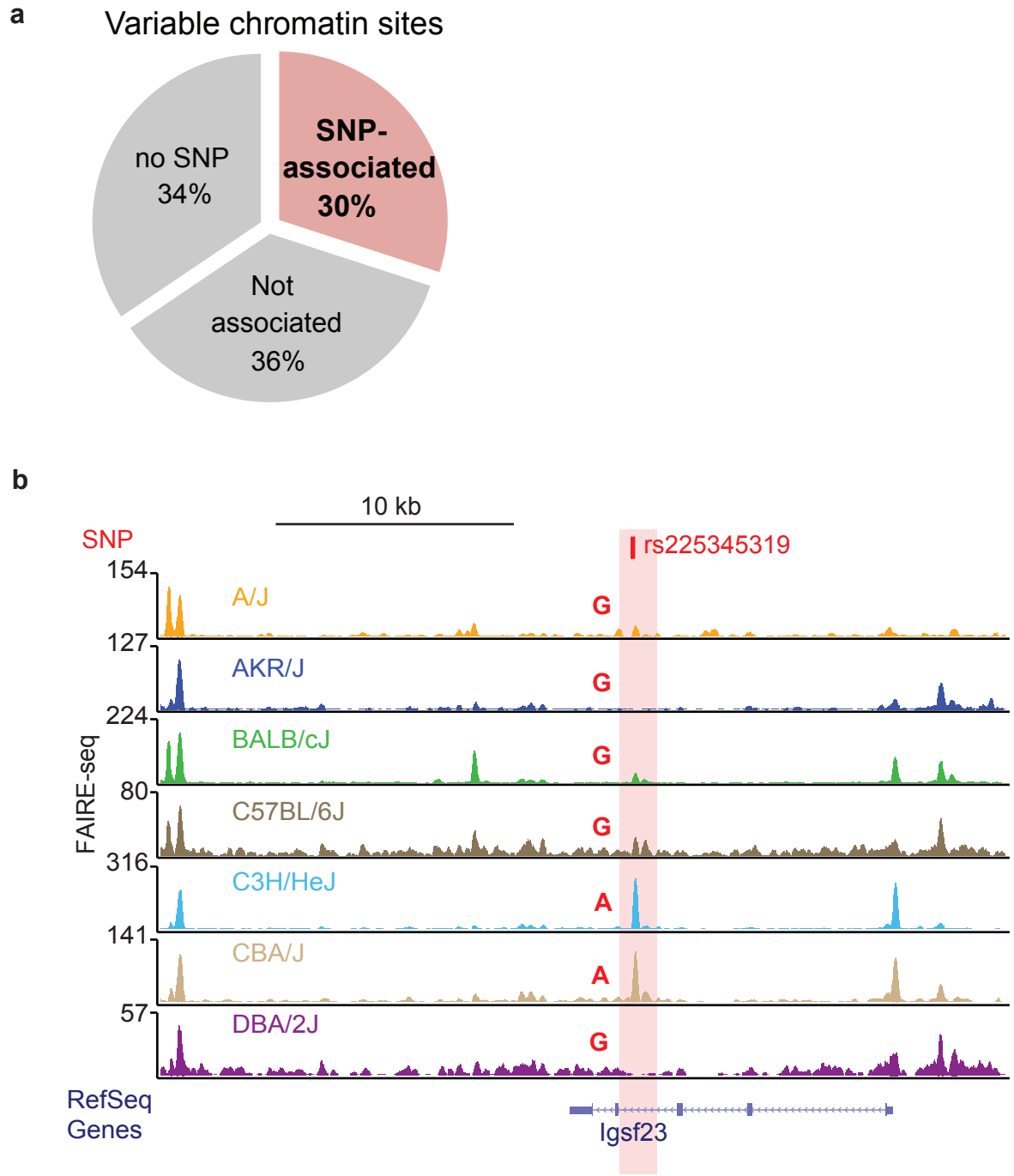

Figure S3. Association between chromatin variation and SNPs. (**a**) Fraction of most variable chromatin sites associated with underlying SNPs. (**b**) Genome browser view of **a** variable chromatin sites associated with SNP rs225345319 in the 7 strains.

Figure S4

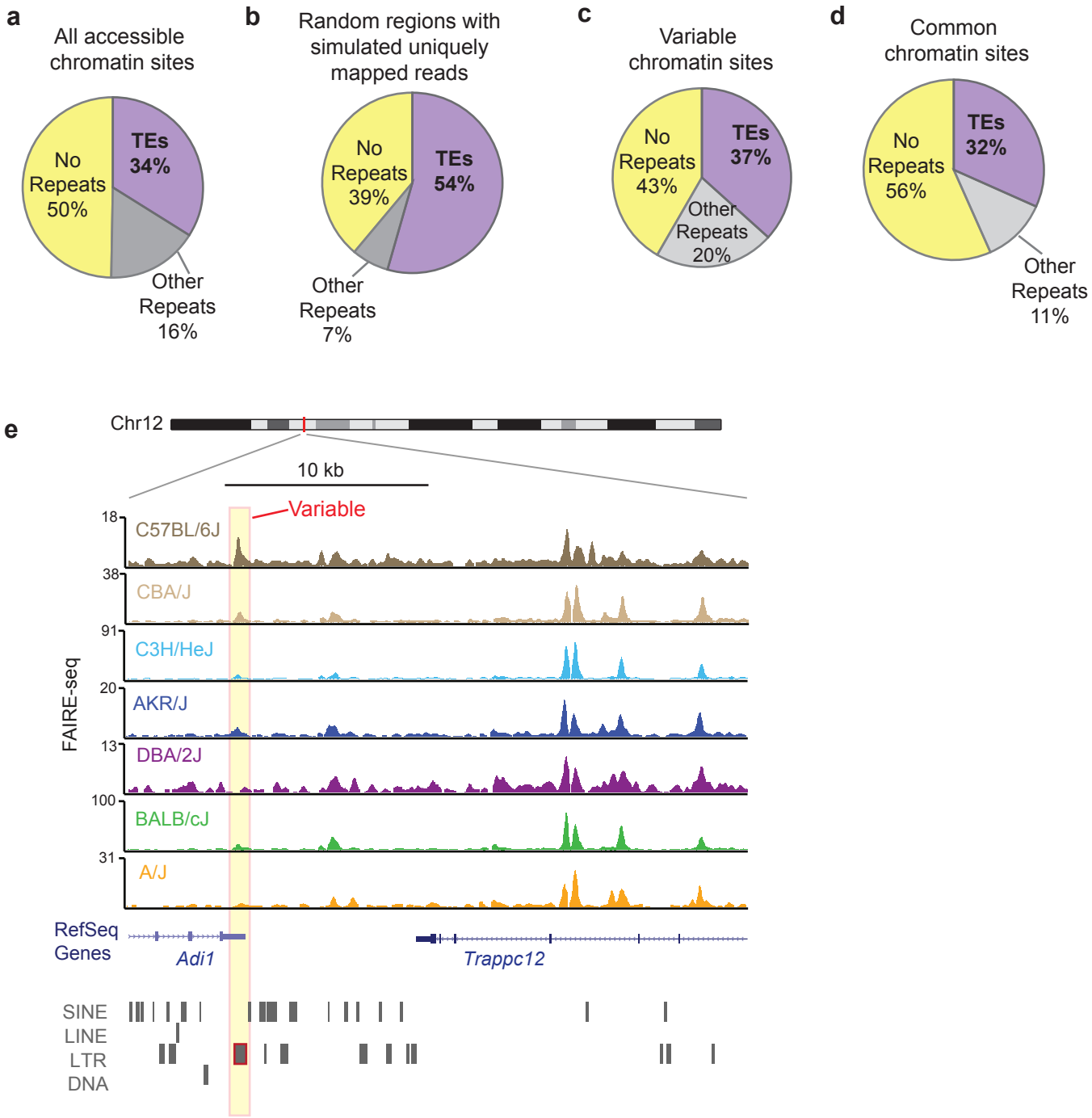

Figure S4. Accessible chromatin sites and TE sequences. (**a, b**) Proportion of all accessible chromatin sites (**a**) and random genomic regions (**b**) that overlap with overlap with TEs, other repeat elements (RepeatMasker annotated, non-TE elements), or non-repetitive elements. (**c, d**) Proportion of variable (**c**) and common (**d**) chromatin sites that overlap with TEs, other repeat elements, or none of them. e Genome browser view of variable chromatin site in Fig. 1**b** coincides with a LTR.

Figure S5

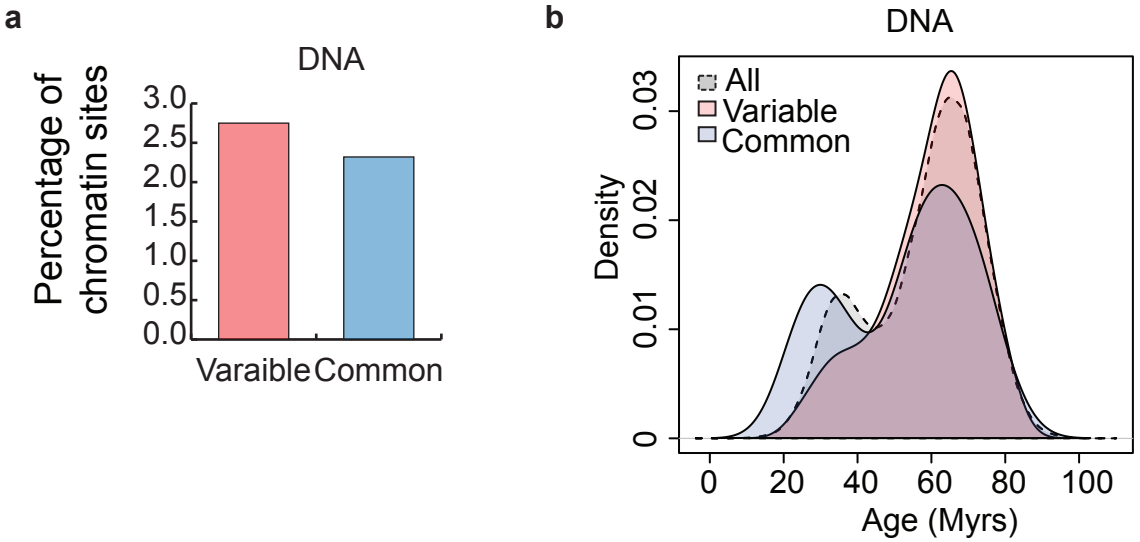

Figure S5. DNA transposon and chromatin accessibility variation. (**a**) Percentage of variable and common chromatin sites overlapping DNA transposons. (**b**) Age distribution of all TEs, TEs at variable or common chromatin sites for DNA transposons.

Figure S6

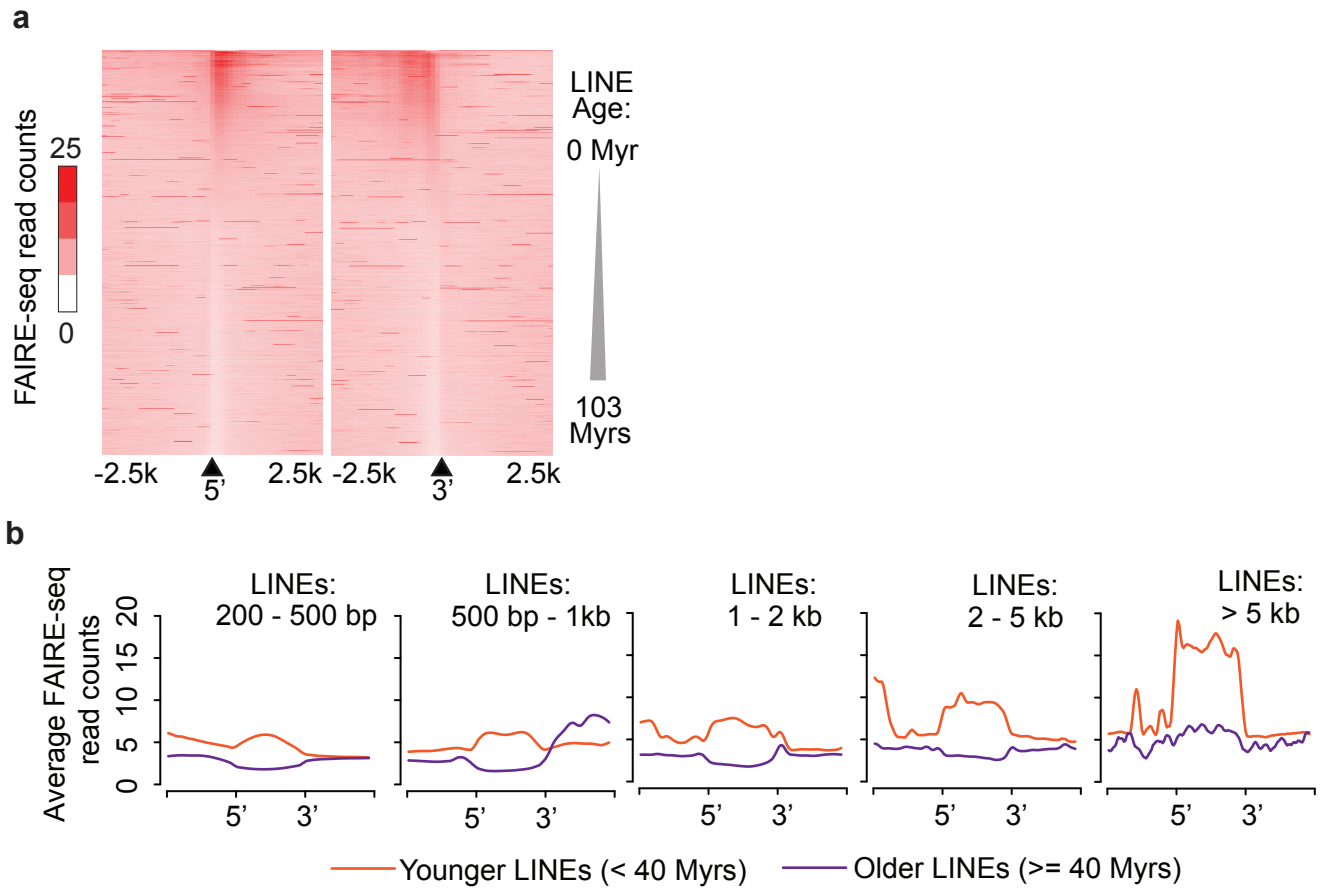

Figure S6. Differential chromatin accessibility profile at younger and older LINEs in A/J. (**a**) Heatmap showing FAIRE-seq read counts from A/J mice liver around 5' (left) and 3' (right) regions of LINEs. LINEs are sorted by their evolutionary age. Black triangles denote the 5' (left) or the 3' (right) end of LINEs, with plots extending +/- 2,500 bp upstream and downstream. (**b**) Aggregate plots of average FAIRE-seq read counts upstream, downstream and within LINEs, organized by size of LINEs.