

Supplemental Table 1: Haplotype-level allele-specific chromatin accessibility measures using ATAC-seq and DHS-seq data aggregated across three heterozygous adipocyte lines. For each line of an individual heterozygous for the haplotype, the number of reads aggregated across 19 non-coding SNPs in the haplotype, are shown.

Heterozygous line	Measure	strandBias	Haplotype_1_Count	Haplotype_2_Count
hWAT	ATAC-seq	0.5957447	47	0
MSC	DHS-seq	0.5909091	29	15
AMSC	ATAC-seq	0.475	50	30