



**Supplemental Figure 1. Supplement to Figure 1, part1 A.** Distribution of reference allele frequency for significant ASB variants ( $p < 0.05$ ) using bowtie2 and vg. **B.** Distribution of the difference in reads mapped between vg and bowtie2 for heterozygous variants which were found significant and discordant between the two mapping approaches. **C.** Heatmap showing the concordance in ASB identification when mapping reads with vg versus bowtie2. **D.** Distribution of the number of reads dropped from each ChIP-seq dataset because the read did not map to the same position when the heterozygous allele was flipped. **E.** The proportion of WASP-dropped reads falling in annotated ENCODE cCREs. PLS (promoter-like signal): red, pELS (proximal enhancer-like signal): orange, dELS (distal enhancer-like signal): yellow, CTCF-only: blue, DNase-H3K4me3 pink, and None: grey.