**Fig1. Identification of ASB.** A) Schematics of detecting allele-specifc TF binding by ATAC-seq. B) For each putative AS-TFBS, ASB event will be identified by using the number of retro-transposes cutting sites (used in ATAC-seq) falling into two regions: a – candidate binding sites, and c – flanking region). Number of cutting sites in region b (site shoulders) will not be considered to tolerate the variability of the size of the binding motifs.

**Fig2. Workflow of RegSNPs-ASB.** a) The basic inputs for RegSNPs-ASB are ATAC-seq raw read counts in a standard BAM alignment format and a set of priori TF binding motifs. b)

**Fig3. Allele-specific TF binding events are widespread in genome.** A) Two samples of allele-specific TF binding events. Orange and blue histogram represented the observed ATAC-seq profile in reference allele and alternative allele, respectively. B) Scatter diagram shows

Most of mutations lead TFs losing of binding affinity.

**Fig4. TF motif clustering analysis.** a) Cluster all TF motifs that probably binding on RegSNPs by sequence similarity. b) Show a representation of all the 53 RegSNPs and corresponding potential binding TFs on them. c) The relative expression of TFs in each clustered motif group. A higher expression value means more relevant to corresponding disease.

**Fig5. One example of RegSNP that is in strong LD (r^2 > 0.8) with one of the GWAS SNPs in strongest association with breast cancer.** A) rs7943121 genotypes are correlated with SPTY2D1 expression. B) Linkage disequilibrium plots show the amount of correlation between a sentinel variant and its surrounding variants. The y-axis shows the correlation coefficient (r2), the x-axis shows chromosomal position of each SNP.SNP rs7943121 is the top eSNP in the same haloptype region. The SNP rs10832963 (highlighted in red) is one of the most associated GWAS hits for breast cancer susceptibility, and rs7943121 is in strong LD with it.C) The allele C of rs7943121 is predicted to compromise the binding of HY5, which is consistent with RegSNP-ASB predicted.

Fig6.