

Fig. S1

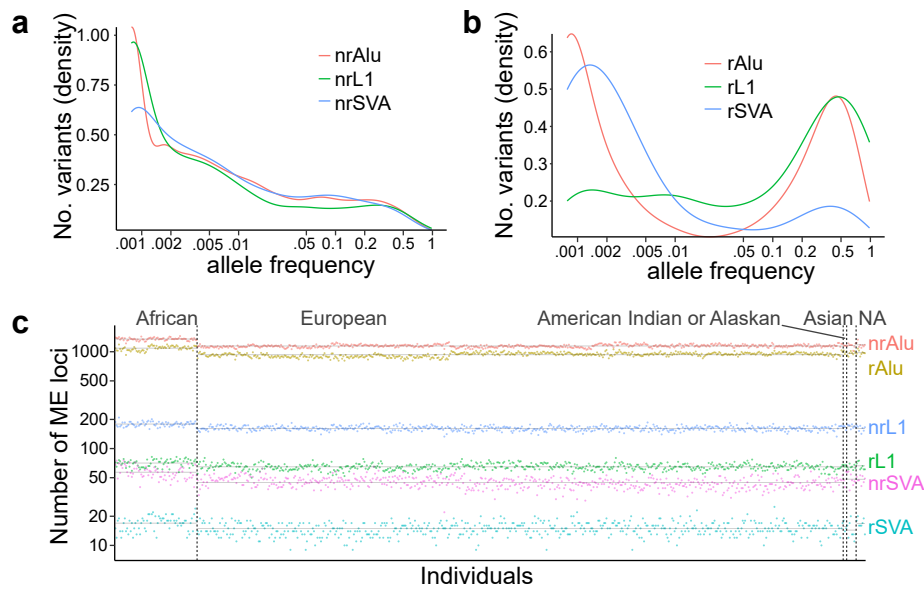


Fig. S1 Overview of high confidence pMEIs in GTEx individuals. (a, b) Allele frequency distribution of nrMEIs (a) and rMEIs (b). (c) Counts of nrMEIs (nrAlu, nrL1, nrSVA) and rMEIs (rAlu, rL1, rSVA) relative to the reference genome (GRCh38) in each individual. Individuals are grouped based on ethnic groups. NA, ethnic group unavailable.

Fig. S2

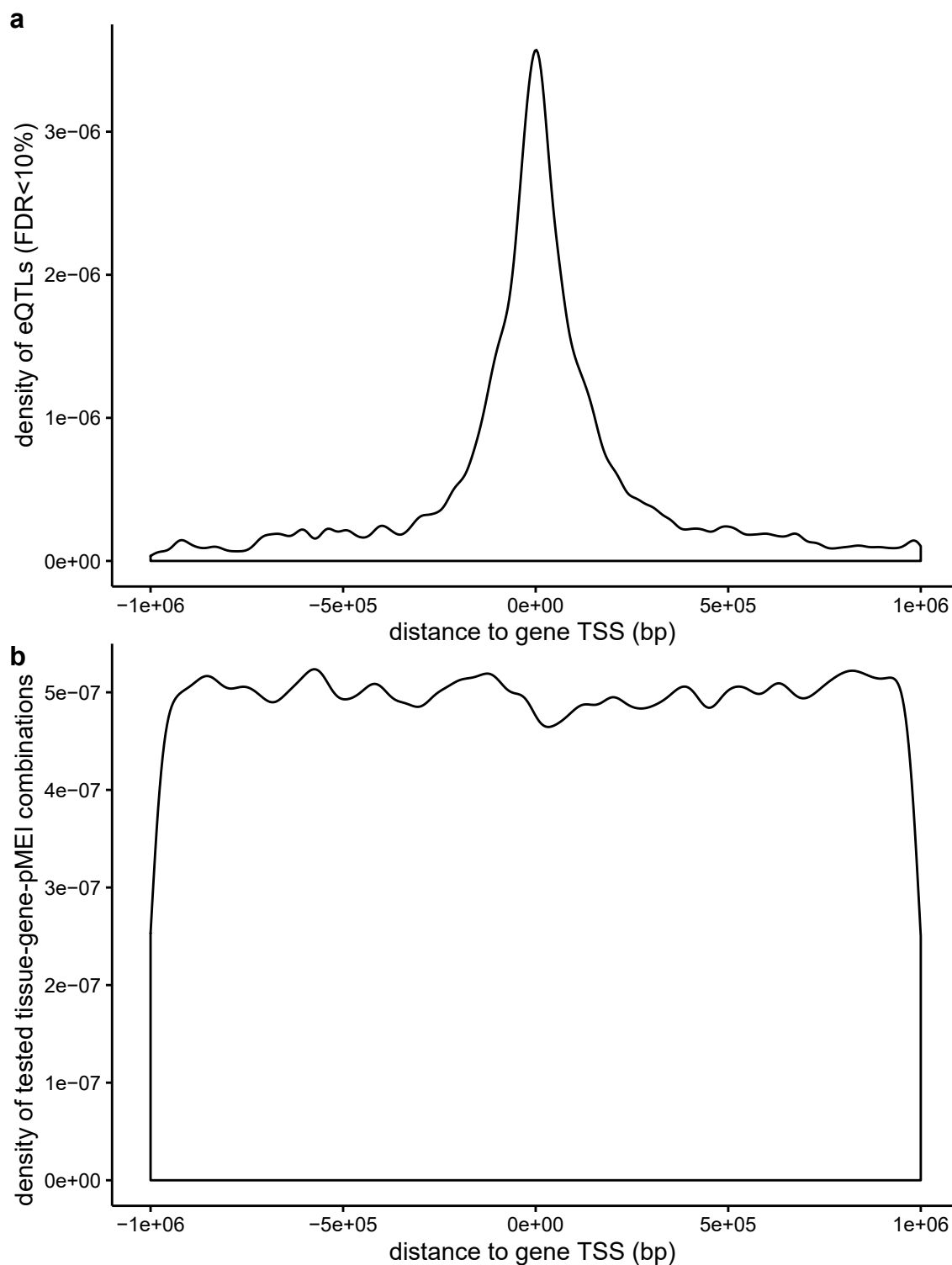


Fig. S2 Enrichment of pMEIs around Transcription Starting Sites (TSSs) of genes. (a) Density of pMEIs associated with eQTLs (tissue-gene-pMEI combinations with $FDR < 0.1$) around TSSs. (b) Density of pMEIs in all possible tissue-gene-pMEI combinations examined by Matrix eQTL around TSSs.

Fig. S3

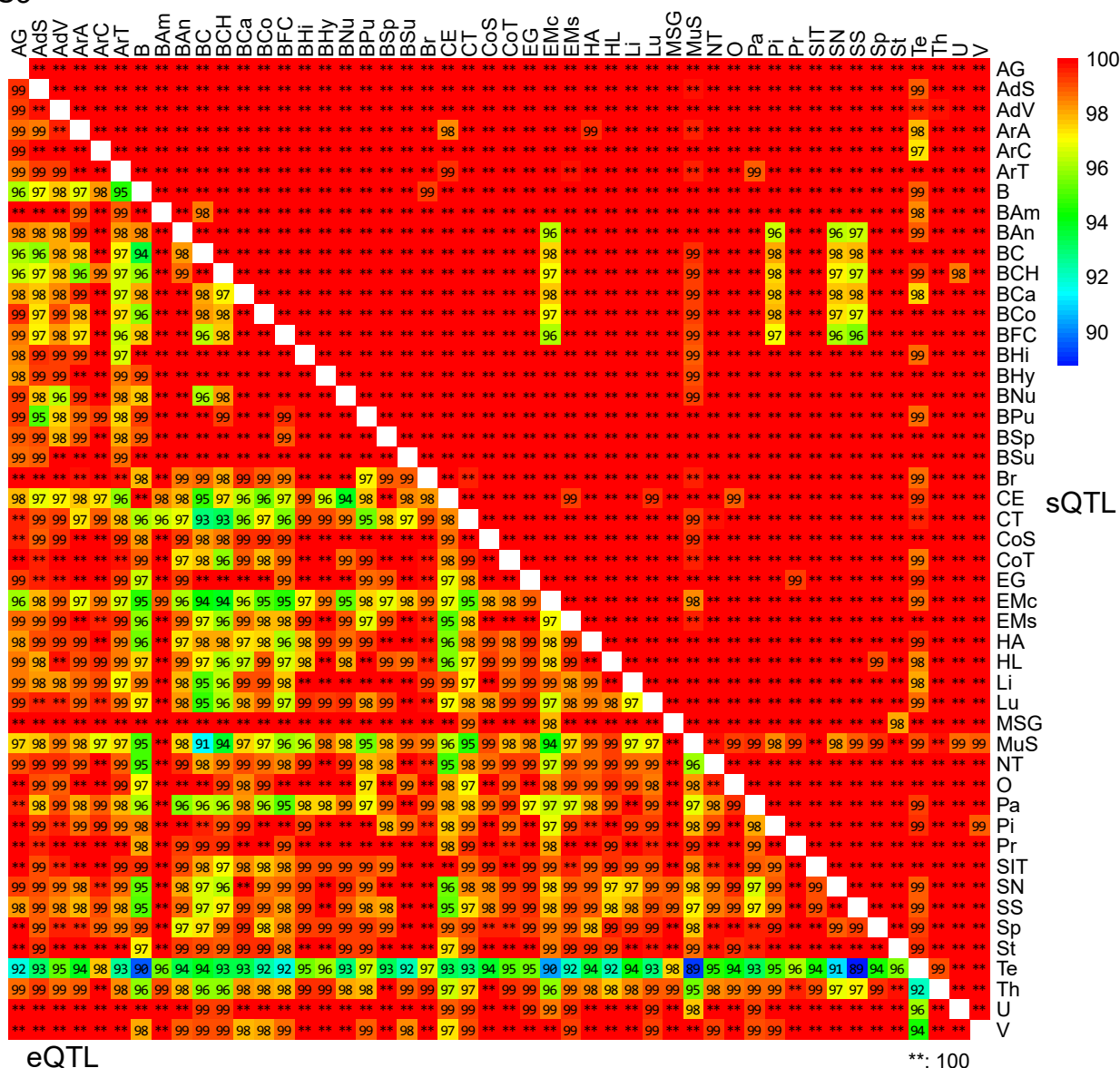


Fig. S3 Agreement of the effect direction between a pair of tissues for eQTLs (lower-left) and sQTLs (upper-right). Numbers are the percentage of shared eQTL/sQTL of two tissues with the same impact direction (the sign of beta value). Tissue abbreviations were the same as in Fig. 1. **=100% shared.