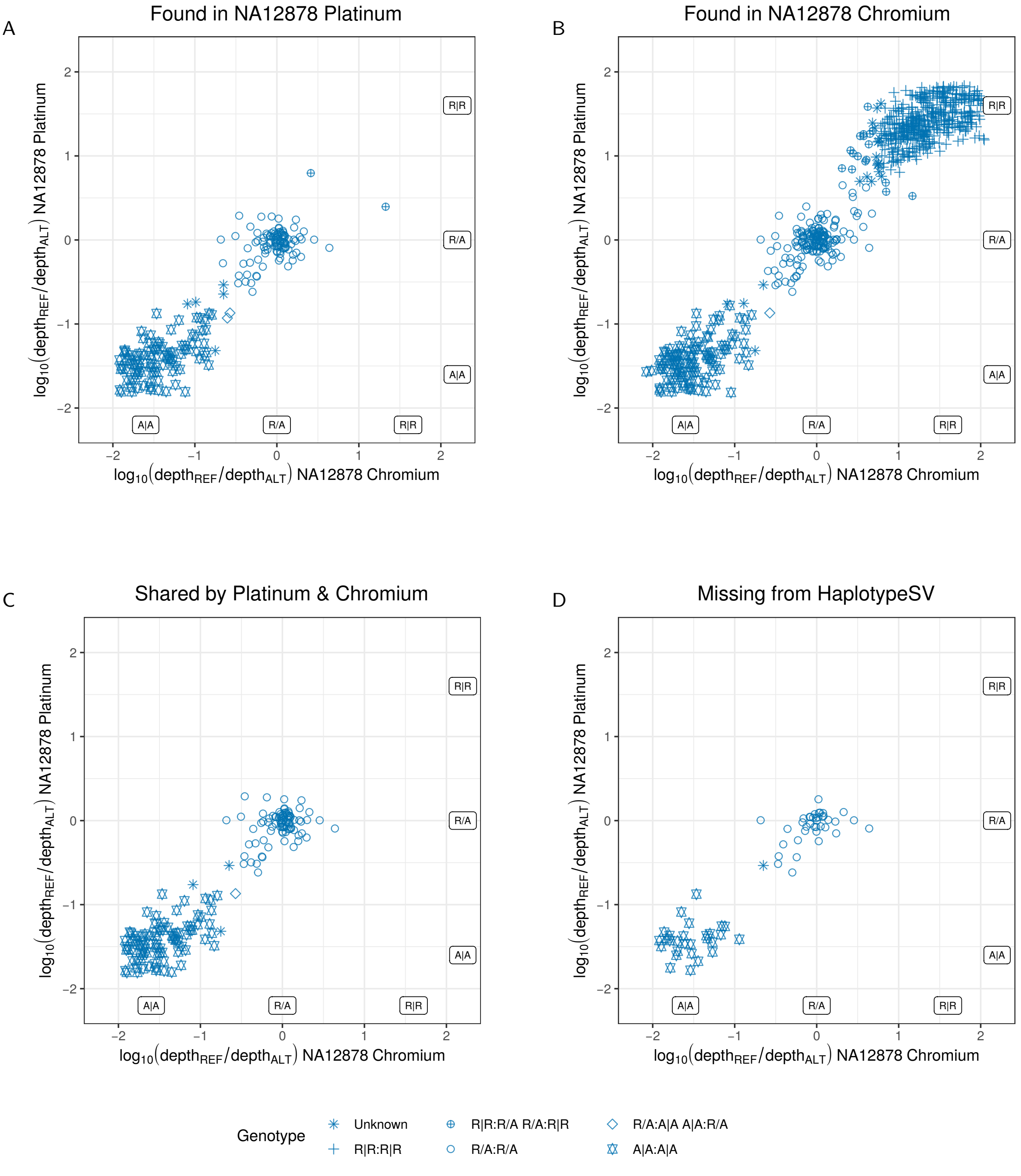

Fig S7. Genotyping of the TSM candidate loci found with short-read data. (**A**) The 211 candidate TSM loci found in NA12878 Platinum data passing the sequence-based filtering. Ratio of REF and ALT allele mapping coverage ($r = depth_{\mathrm{REF}}/depth_{\mathrm{ALT}}$) reflects the genotype: $r \approx 1$ (and thus $log_{10}(r) \approx 0$) for a heterozygote; $r \ll 1$ and $r \gg 1$ for the two types of homozygotes. The Log10-ratios agree for the NA12878 Platinum and Chromium datasets, and 105 and 96 loci (of the total 211) are called heterozygous and homozygous for ALT by both datasets. (**B**) Of the 755 candidate TSM loci found in NA12878 Chromium data, 438 are called homozygous for REF by both methods. (**C**) The 176 loci found in both short-read datasets. (**D**) The 67 loci found in both short-read datasets but not in HaplotypeSV dataset.