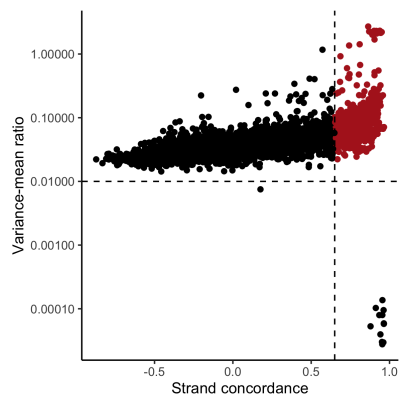
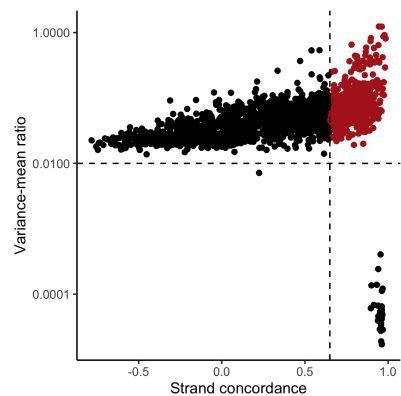


A

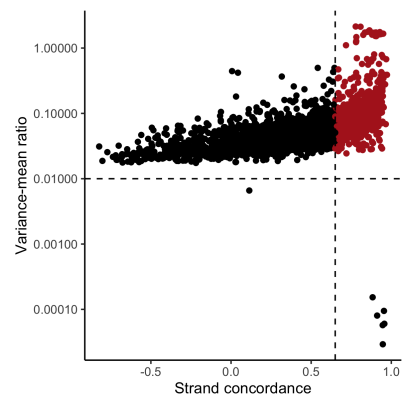
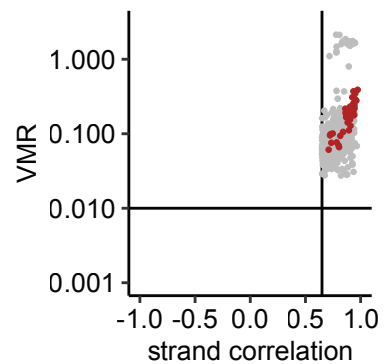
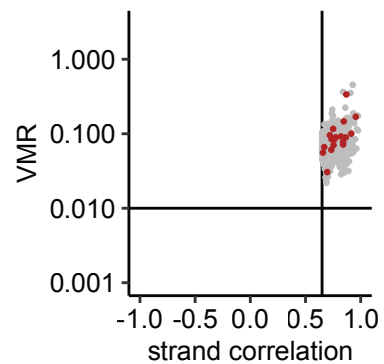
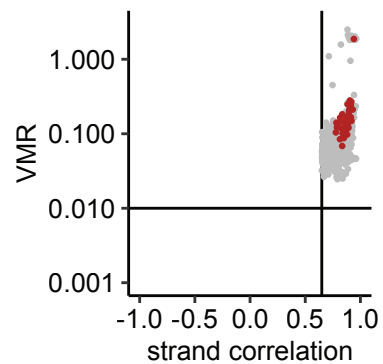
AML1010



AML1012



AML1026

**B**

Suppl. Fig. 19. Identification of high-confidence mitochondrial DNA mutations for Tapestri analysis. A High-confidence mitochondrial DNA (mtDNA) mutations (red) identified based on strand concordance and variance-mean ratio (VMR) from ASAP-seq data in AML1010, AML1012 and AML1026 served as a comparator for selection of mtDNA variants from Tapestri data. B As Tapestri amplicons do not have overlapping reads which renders analysis of strand concordance infeasible, mitochondrial DNA mutations used for analysis of Tapestri data (red) were correlated with high-confidence mtDNA mutations found using ASAP-seq (grey).