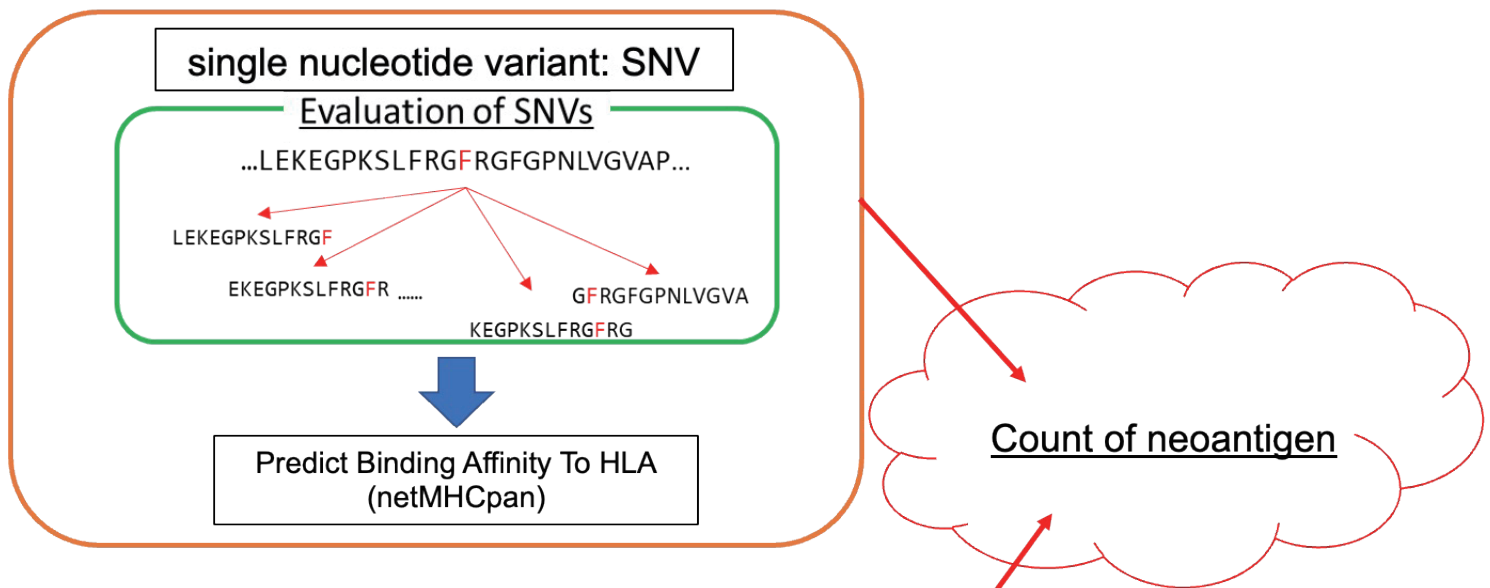


Fig. S3

WES data



RNAseq data

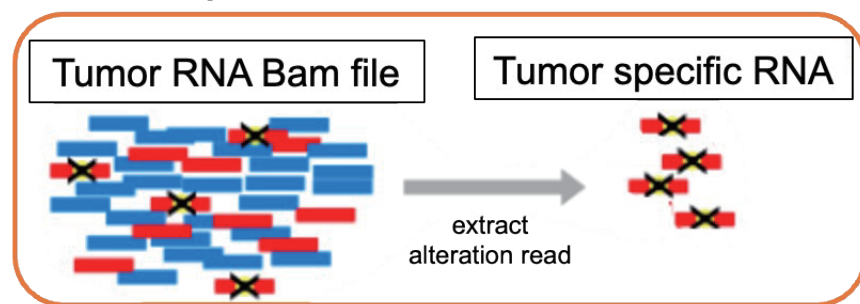


Fig. S3: Neoantigen analysis of mutated ctDNA.

Initially, we evaluated mutations to estimate neoantigen peptides in detected ctDNA at 47 points using the Neoantimon R package. Then, we estimated the binding affinity of every peptide bound to HLA, which consisted of six haplotypes (HLA-A, -B, -C) according to netMHCpan. The pipelines were established and calculated. Meanwhile, we calculated "tumor-specific RNA" using extracted altered readouts of the whole primary tumor RNA BAM file.