

supplementary Table 4. List of in silico predicted neoantigenic peptides based on identified SNVs (mutated amino acid in red)

Table with columns: ATTR #, rsid/clinvar, chromosome, gene, UniProt ID, position in protein, Wildtype, Mutation, Reference, Best sequence, Best HLA allele, IEDB score, VaxDen score, NetMHCbind affinity, NetMHCpan affinity, NetMHCbind score, NetMHCpan score. The table lists numerous entries for different attributes (ATTR #) and SNVs (rsid/clinvar), detailing their genomic location, protein context, mutation, and predicted immunogenicity across various HLA alleles and scoring systems.

Table with 16 columns: ID, Type, Gene, RefSeq, Protein, UniProt, Ensembl, RefSeq, UniProt, Ensembl, RefSeq, UniProt, Ensembl, RefSeq, UniProt, Ensembl. Contains genomic coordinates and gene names for various samples.



