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Supplementary information

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A comprehensive proteogenomic pipeline for neoantigen discovery to advance personalized cancer immunotherapy

In the format provided by the authors and unedited

Supplementary table 1 : Comparison of NeoDisc 1.7.0 with pTuneos v1.0.0 and pVACtools v4.0.8: Inputs, Outputs, and Supported Features. This table provides a comparative overview of the capabilities of NeoDisc, in comparison with other established bioinformatics tools in the field. The table details the input data formats, and the features supported by each tool.

Supplementary table 2 : Comparative Analysis of Neoantigen Prediction Ranks of Immunogenic Mutations in the NCI Test Cohort. The table lists each mutation alongside the corresponding gene, amino acid change, and predicted peptide. For each tool—NeoDisc's rule-based and machine learning models, pTuneos, pVACseq, and Gartner—the ranks of the predicted neoantigens are provided, highlighting the performance and prioritization differences among the tools

Supplementary table 3 : Summary of Patient Tumor Characteristics, Diagnosis, Material available, and Neoantigen Screening Results. This table provides a summary of the patient cohort described in the paper, including clinical and molecular characteristics. For each patient, the table details the diagnosis, tumor grade, gender, HLA typing (HLA-I and HLA-II), types of assays conducted, sample type and amount, estimated tumor content, tumor mutational burden, HLA loss of heterozygosity (LOH), and specific defects in the antigen processing and presentation machinery (APPM). Additionally, the table outlines the number of neoantigens and viral peptides identified through screening, along with their immunogenic status.

Supplementary table 4 : Immunogenic Peptides Identified in Patients. This table reports all immunogenic peptides identified across the patient cohort described in the paper. For each patient, the table lists the ranking of the peptide sequence, the associated predicted HLA allele, and whether it was identified through mass spectrometry (MS). When tested, it reports whether the peptide induced tumor rejection or not, the type of T-cell response observed (CD4 or CD8), and results from ELISpot assays. Additionally, information about the gene and mutation corresponding from which each peptide derives, as well as the wild-type (WT) peptide sequence, is provided.