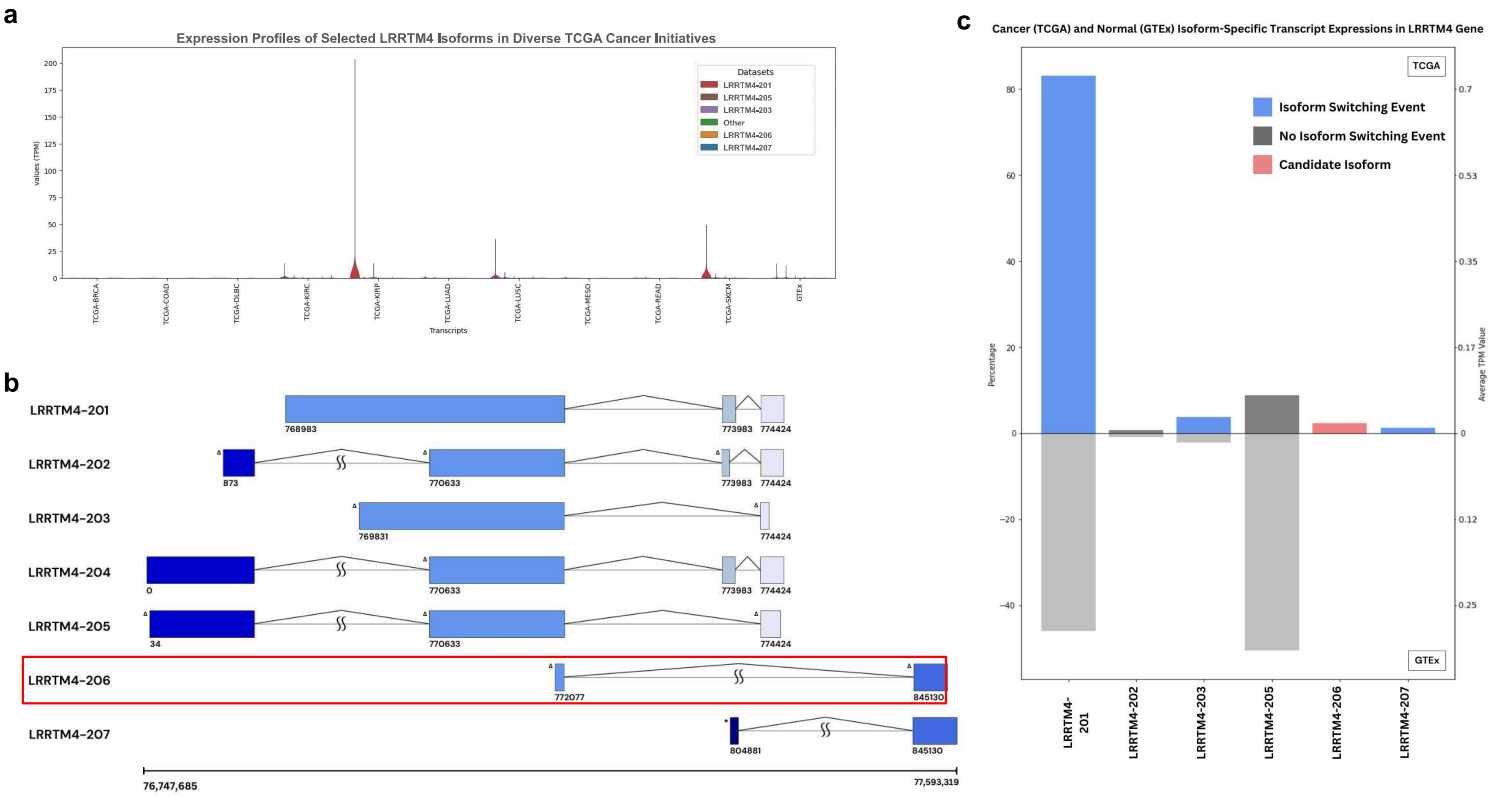
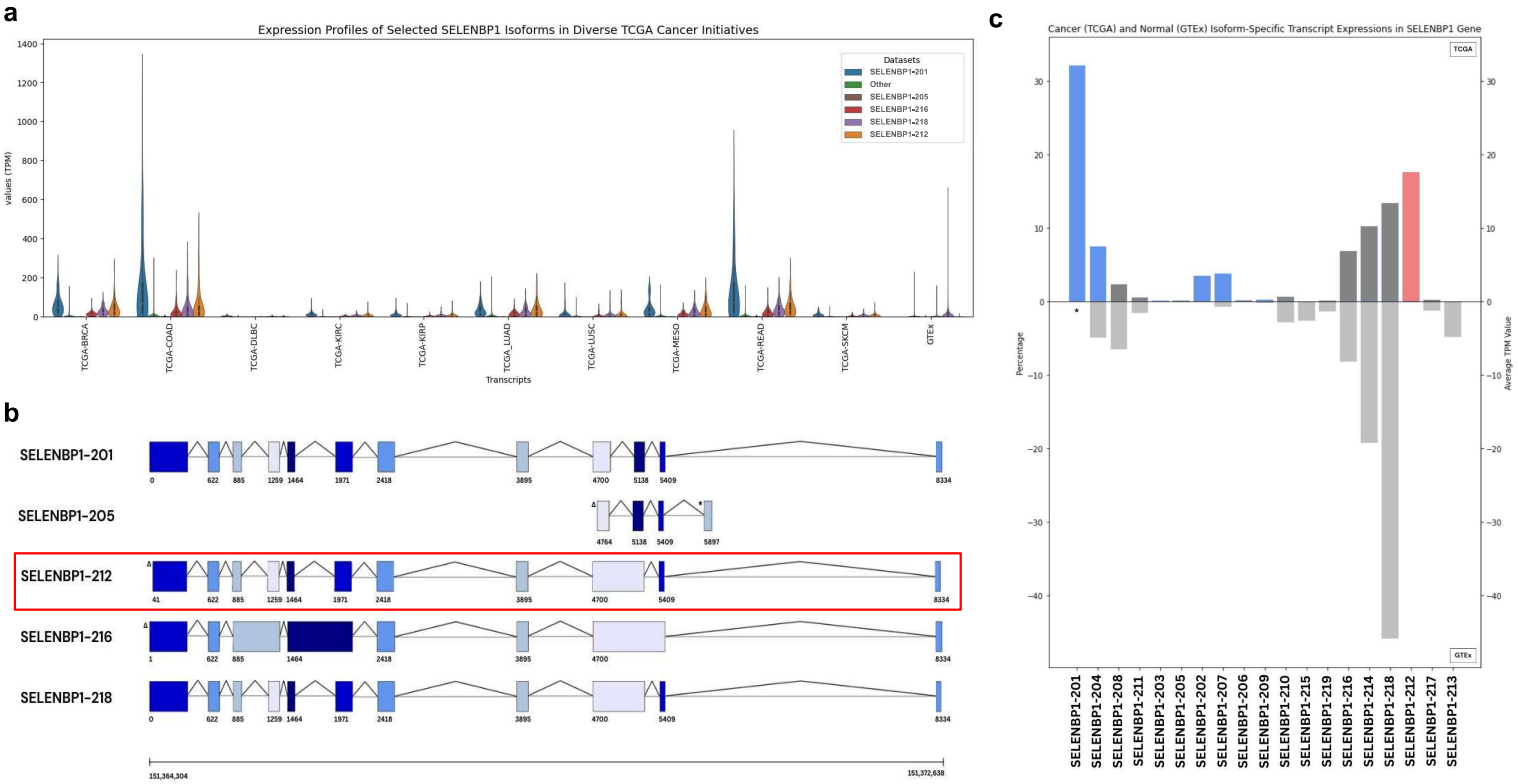
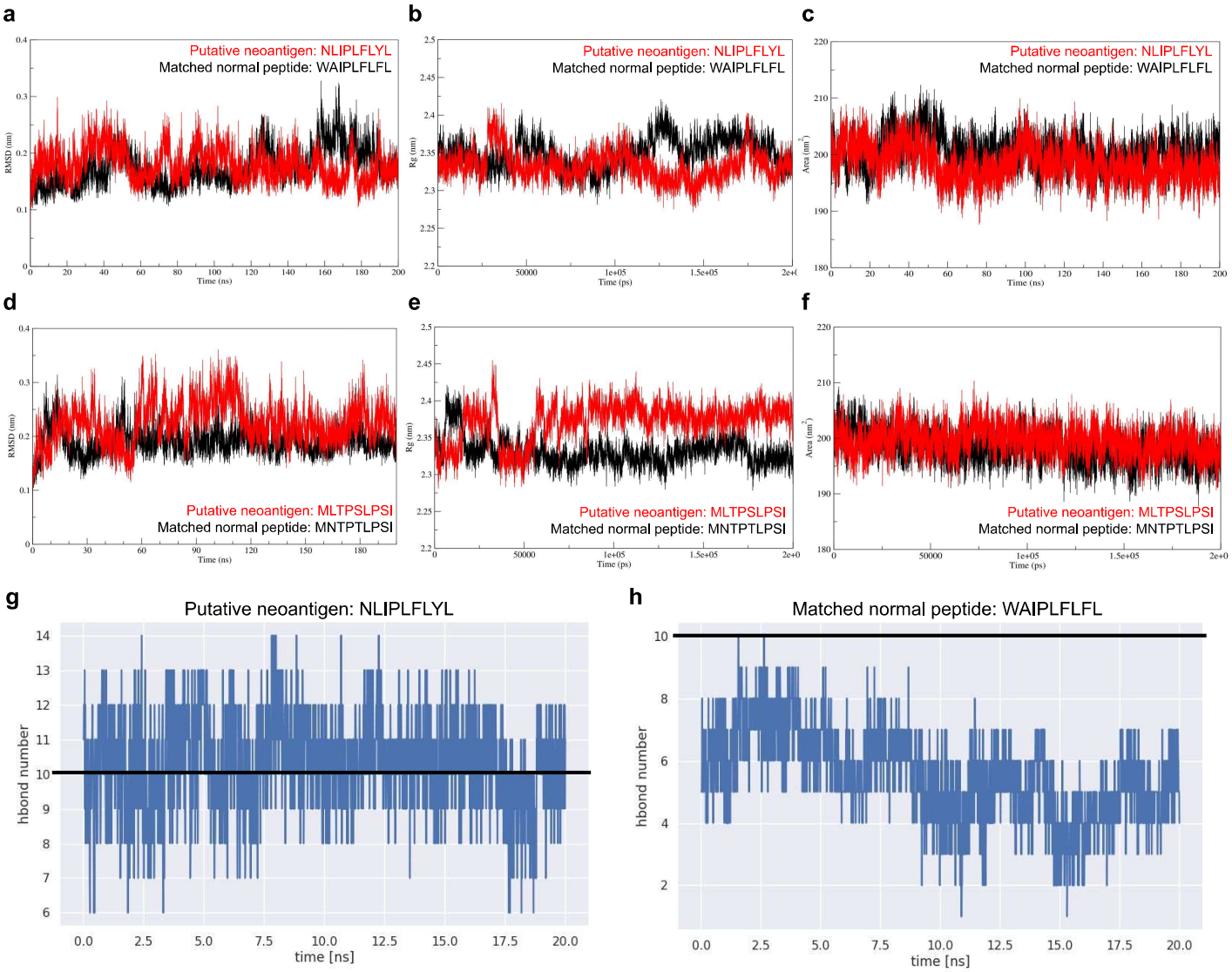


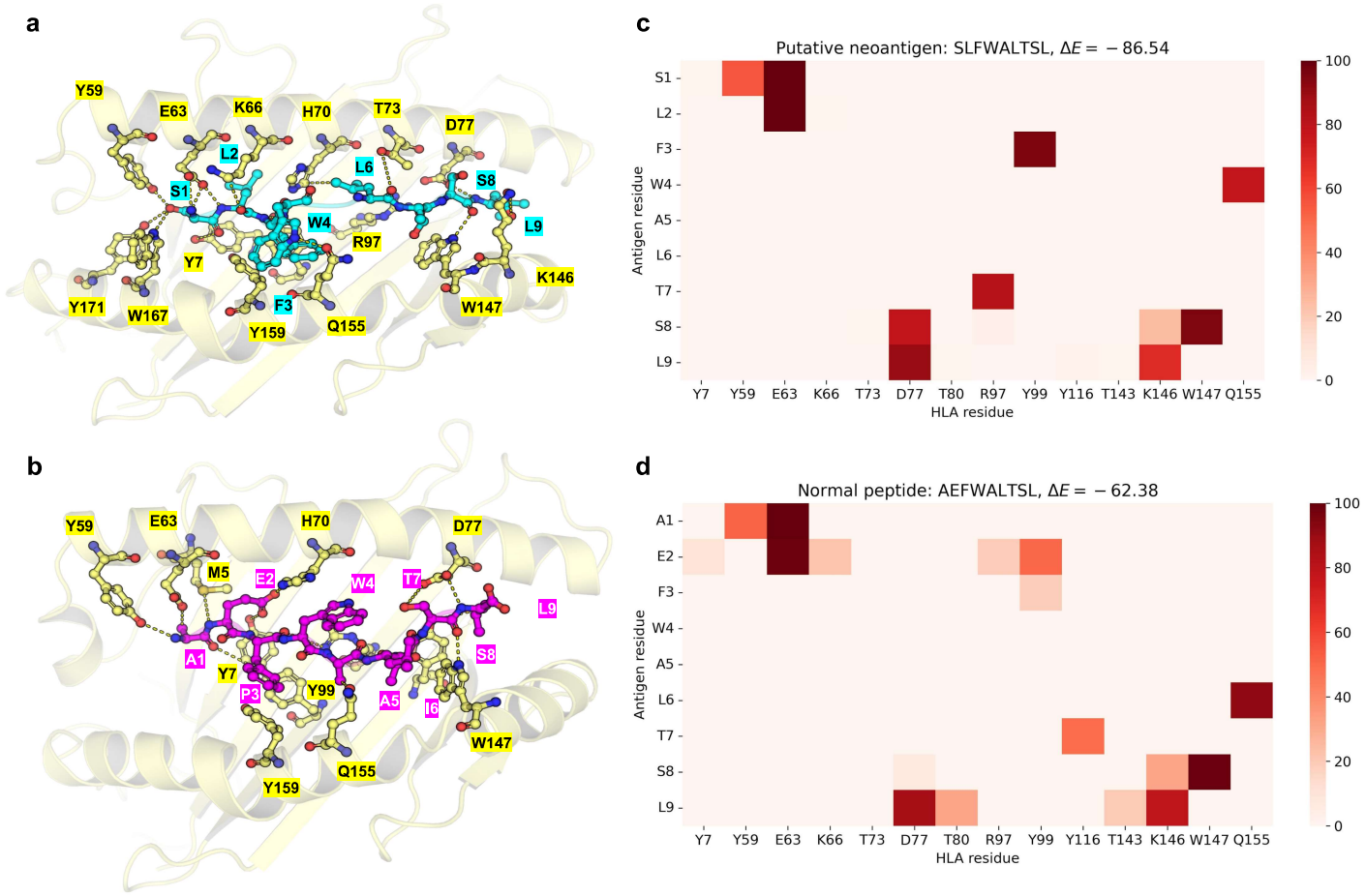
Supplementary Figure S1 Transcriptome analysis of differentially expressed gene (LRRTM4 gene). a Expression profiles of isoforms of LRRTM4 gene in TCGA cancer dataset. The orange plots represent the shared pancancer isoform of interest. **b** Exon usages in each isoform of the LRRTM4 gene, with the candidate exon represented in a red box. Triangle symbols denote nested exons, while asterisks indicate uncommon exons for the cohort. **c** Expression profile and instances of isoform switching. Comparison of isoform expression profiles between the TCGA cancer dataset and normal GTEx dataset is presented. Blue bars indicate instances of isoform switching, where cancer expression surpasses that of GTEx. The red bar represents the candidate of interest, and asterisks denote the absence of the isoform in the dataset.



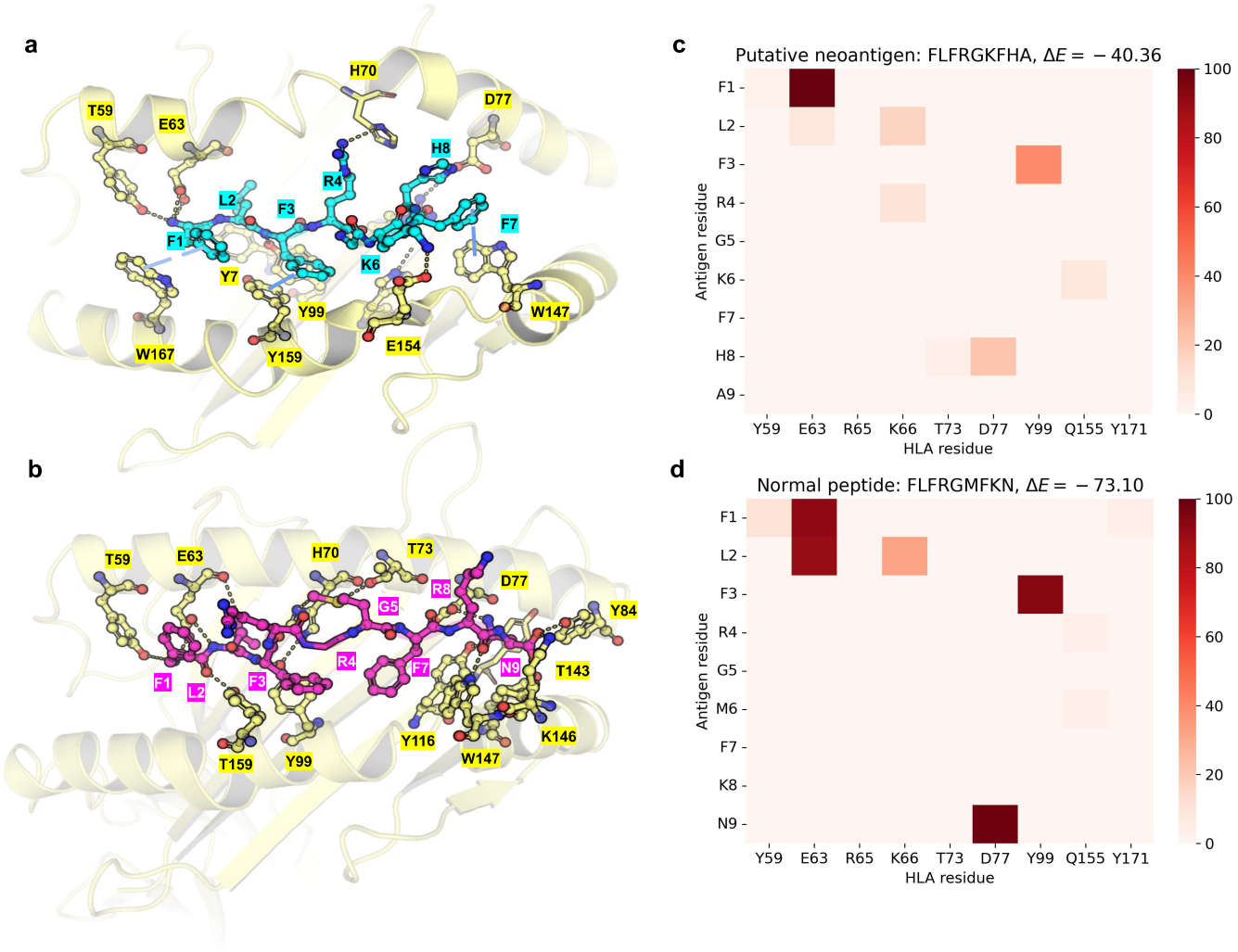
Supplementary Figure S2 Transcriptome analysis of differentially expressed gene (SELENBP1 gene). **a** Expression profiles of isoforms of SELENBP1 gene in TCGA cancer dataset. The brown plots represent the shared pancancer isoform of interest. **b** Exon usages in each isoform of the SELENBP1 gene, with the candidate exon represented in a red box. Triangle symbols denote nested exons, while asterisks indicate uncommon exons for the cohort. **c** Expression profile and instances of isoform switching. Comparison of isoform expression profiles between the TCGA cancer dataset and normal GTEx dataset is presented. Blue bars indicate instances of isoform switching, where cancer expression surpasses that of GTEx. The red bar represents the candidate of interest, and asterisks denote the absence of the isoform in the dataset.



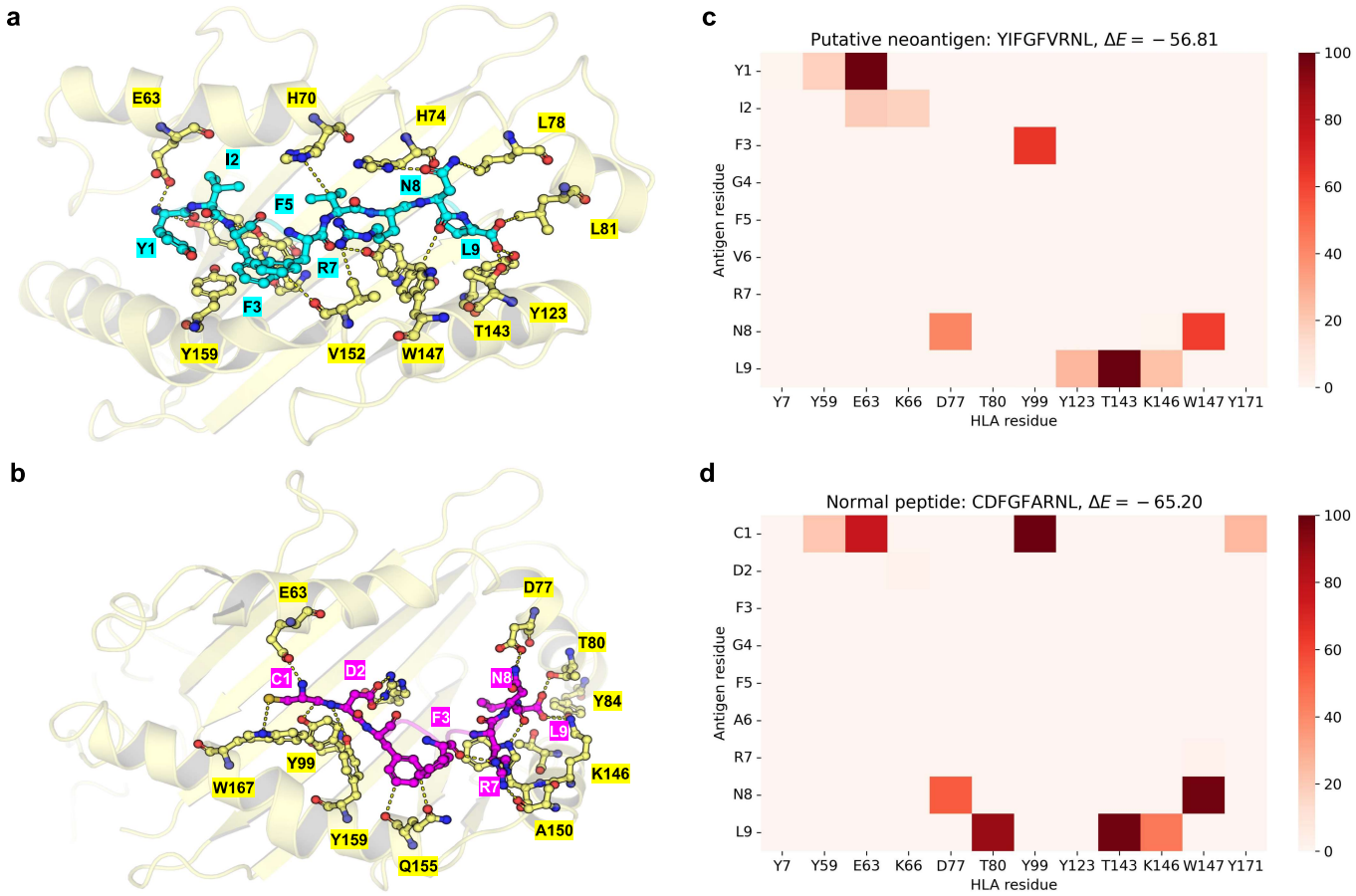
Supplementary Figure S3: Additional molecular dynamics characteristics for the most promising putative neoantigens, NLIPLFLYL and MLTPSLPSI, and matched normal peptides, WAIPLFLFL and MNTPTLPSI, shown in Figure 6 and Figure 7. a The root mean square deviations of the peptide-HLA complex between NLIPLFLYL or WAIPLFLFL with HLA-A*02:01 during the 200-ns simulation. **b** The radii of gyration of the complex during the simulation. **c** The solvent accessible surface areas of the complex during the simulation. **d-f** The same information for MLTPSLPSI and MNTPTLPSI. **g** The number of hydrogen bonds formed during the last 20 ns of the simulation between putative neoantigen NLIPLFLYL and HLA protein. **h** The number of hydrogen bonds formed between normal peptide WAIPLFLFL and HLA protein.



Supplementary Figure S4: Molecular dynamics comparison between the binding of putative neoantigen SLFWALTSL and matched normal peptide AEFWALTSL to HLA-A*02:01. **a** A final structure for putative neoantigen SLFWALTSL derived from ENST00000463664 transcript. **b** A final structure for the matched normal peptide AEFWALTSL. The side chains of the residues involved in hydrogen bonds (indicated by dashed lines) were highlighted. **c** Heatmap showing the percentage of hydrogen bond formation during the last 20 ns of the dynamics for the putative neoantigen SLFWALTSL. **d** Heatmap for the matched normal peptide AEFWALTSL.



Supplementary Figure S5: Molecular dynamics comparison between the binding of putative neoantigen FLFRGKFHA and matched normal peptide FLFRGMFKN to HLA-A*02:01. **a** A final structure for putative neoantigen FLFRGKFHA derived from ENST00000620660 transcript. **b** A final structure for the matched normal peptide FLFRGMFKN. The side chains of the residues involved in hydrogen bonds (indicated by dashed lines) were highlighted. **c** Heatmap showing the percentage of hydrogen bond formation during the last 20 ns of the dynamics for the putative neoantigen FLFRGKFHA. **d** Heatmap for the matched normal peptide FLFRGMFKN.



Supplementary Figure S6: Molecular dynamics comparison between the binding of putative neoantigen YIFGFVRNL and matched normal peptide CDFGFARNL to HLA-A*02:01. A) A final structure for putative neoantigen YIFGFVRNL derived from ENST00000556513 transcript. B) A final structure for the matched normal peptide CDFGFARNL. The side chains of the residues involved in hydrogen bonds (indicated by dashed lines) were highlighted. C) Heatmap showing the percentage of hydrogen bond formation during the last 20 ns of the dynamics for the putative neoantigen YIFGFVRNL. D) Heatmap for the matched normal peptide CDFGFARNL.