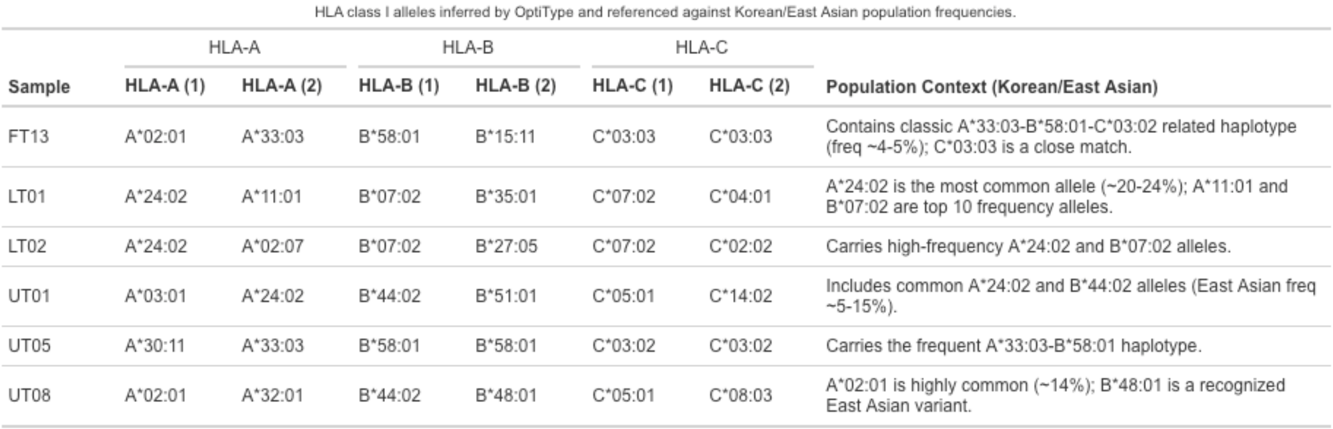
Supplemental material

Sample ID	Classification	TP53	ATRX	PTEN	CDK4
FT13	Hypermutator	WT	WT	Frameshift	WT
LT02	Hypermutator	WT	Frameshift	Splice Site	WT
UT05	Hypermutator	Missense	WT	Missense	WT
LT01	Non-Hyper	WT	WT	WT	Amplification
UT01	Non-Hyper	WT	WT	WT	WT
UT08	Non-Hyper	WT	WT	WT	WT

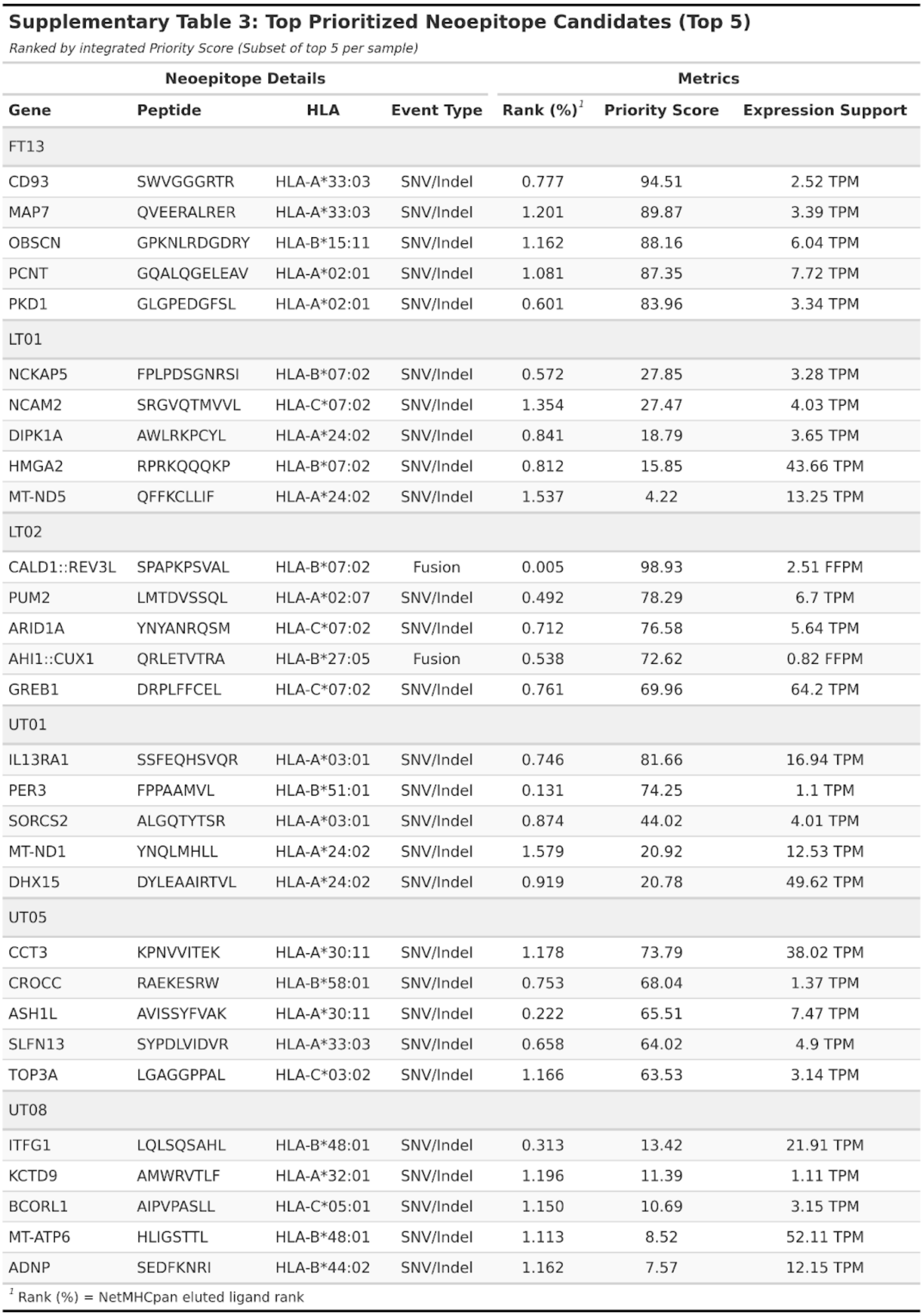
Supplementary Table S1. Verification of somatic driver landscape. Comparison of key driver gene alterations (TP53, ATRX, PTEN, CDK4) detected in this study versus the original publication (Kim et al.). Samples are grouped by hypermutator status. Alteration types (Missense, Frameshift, Splice Site, Amplification) are mentioned; "WT" indicates wild-type status. The observed landscape replicates the enrichment of PTEN/ATRX alterations in hypermutated samples and CDK4 amplification in LT01, confirming pipeline accuracy.



HLA class I alleles inferred by OptiType and referenced against Korean/East Asian population frequencies.

	HLA-A		HLA-B		HLA-C		
Sample	HLA-A (1)	HLA-A (2)	HLA-B (1)	HLA-B (2)	HLA-C (1)	HLA-C (2)	Population Context (Korean/East Asian)
FT13	A*02:01	A*33:03	B*58:01	B*15:11	C*03:03	C*03:03	Contains classic A*33:03-B*58:01-C*03:02 related haplotype (freq ~4-5%); C*03:03 is a close match.
LT01	A*24:02	A*11:01	B*07:02	B*35:01	C*07:02	C*04:01	A*24:02 is the most common allele (~20-24%); A*11:01 and B*07:02 are top 10 frequency alleles.
LT02	A*24:02	A*02:07	B*07:02	B*27:05	C*07:02	C*02:02	Carries high-frequency A*24:02 and B*07:02 alleles.
UT01	A*03:01	A*24:02	B*44:02	B*51:01	C*05:01	C*14:02	Includes common A*24:02 and B*44:02 alleles (East Asian freq ~5-15%).
UT05	A*30:11	A*33:03	B*58:01	B*58:01	C*03:02	C*03:02	Carries the frequent A*33:03-B*58:01 haplotype.
UT08	A*02:01	A*32:01	B*44:02	B*48:01	C*05:01	C*08:03	A*02:01 is highly common (~14%); B*48:01 is a recognized East Asian variant.

Supplementary Table S2. Supplementary Table S1. Inferred HLA Class I Genotypes and Population Context. HLA-A, -B, and -C alleles were determined using OptiType from tumor WXS data. The population context column relates individual genotypes to high-frequency alleles and common haplotypes reported in Korean and East Asian populations, supporting the representative nature of the cohort’s immunogenetic profile.



Supplementary Table 3: Top Prioritized Neoepitope Candidates (Top 5)

Ranked by integrated Priority Score (Subset of top 5 per sample)

Neoepitope Details				Metrics		
Gene	**Peptide**	**HLA**	**Event Type**	**Rank (%)**[1]	**Priority Score**	**Expression Support**
FT13						
CD93	SWVGGGRTR	HLA-A*33:03	SNV/Indel	0.777	94.51	2.52 TPM
MAP7	QVEERALRER	HLA-A*33:03	SNV/Indel	1.201	89.87	3.39 TPM
OBSCN	GPKNLRDGDRY	HLA-B*15:11	SNV/Indel	1.162	88.16	6.04 TPM
PCNT	GQALQGELEAV	HLA-A*02:01	SNV/Indel	1.081	87.35	7.72 TPM
PKD1	GLGPEDGFSL	HLA-A*02:01	SNV/Indel	0.601	83.96	3.34 TPM
LT01						
NCKAP5	FPLPDSGNRSI	HLA-B*07:02	SNV/Indel	0.572	27.85	3.28 TPM
NCAM2	SRGVQTMVVL	HLA-C*07:02	SNV/Indel	1.354	27.47	4.03 TPM
DIPK1A	AWLRKPCYL	HLA-A*24:02	SNV/Indel	0.841	18.79	3.65 TPM
HMGA2	RPRKQQQKP	HLA-B*07:02	SNV/Indel	0.812	15.85	43.66 TPM
MT-ND5	QFFKCLLIF	HLA-A*24:02	SNV/Indel	1.537	4.22	13.25 TPM
LT02						
CALD1::REV3L	SPAPKPSVAL	HLA-B*07:02	Fusion	0.005	98.93	2.51 FFPM
PUM2	LMTDVSSQL	HLA-A*02:07	SNV/Indel	0.492	78.29	6.7 TPM
ARID1A	YNYANRQSM	HLA-C*07:02	SNV/Indel	0.712	76.58	5.64 TPM
AHI1::CUX1	QRLETVTRA	HLA-B*27:05	Fusion	0.538	72.62	0.82 FFPM
GREB1	DRPLFFCEL	HLA-C*07:02	SNV/Indel	0.761	69.96	64.2 TPM
UT01						
IL13RA1	SSFEQHSVQR	HLA-A*03:01	SNV/Indel	0.746	81.66	16.94 TPM
PER3	FPPAAMVL	HLA-B*51:01	SNV/Indel	0.131	74.25	1.1 TPM
SORCS2	ALGQTYTSR	HLA-A*03:01	SNV/Indel	0.874	44.02	4.01 TPM
MT-ND1	YNQLMHLL	HLA-A*24:02	SNV/Indel	1.579	20.92	12.53 TPM
DHX15	DYLEAAIRTVL	HLA-A*24:02	SNV/Indel	0.919	20.78	49.62 TPM
UT05						
CCT3	KPNVVITEK	HLA-A*30:11	SNV/Indel	1.178	73.79	38.02 TPM
CROCC	RAEKESRW	HLA-B*58:01	SNV/Indel	0.753	68.04	1.37 TPM
ASH1L	AVISSYFVAK	HLA-A*30:11	SNV/Indel	0.222	65.51	7.47 TPM
SLFN13	SYPDLVIDVR	HLA-A*33:03	SNV/Indel	0.658	64.02	4.9 TPM
TOP3A	LGAGGPPAL	HLA-C*03:02	SNV/Indel	1.166	63.53	3.14 TPM
UT08						
ITFG1	LQLSQSAHL	HLA-B*48:01	SNV/Indel	0.313	13.42	21.91 TPM
KCTD9	AMWRVTLF	HLA-A*32:01	SNV/Indel	1.196	11.39	1.11 TPM
BCORL1	AIPVPASLL	HLA-C*05:01	SNV/Indel	1.150	10.69	3.15 TPM
MT-ATP6	HLIGSTTL	HLA-B*48:01	SNV/Indel	1.113	8.52	52.11 TPM
ADNP	SEDFKNRI	HLA-B*44:02	SNV/Indel	1.162	7.57	12.15 TPM

[1] Rank (%) = NetMHCpan eluted ligand rank

Supplementary table 3: Top Prioritized Neoepitope Candidates. The top 5 neoepitope candidates per sample were ranked by an integrated Priority Score combining MHC binding affinity, expression support (TPM/FFPM), and agretopicity. Only the highest-scoring peptide per somatic alteration is shown. 'Rank (%)' denotes the NetMHCpan eluted ligand rank.