

Mangalagarthi et al., 2020. Mutational landscape of oesophageal squamous cell carcinoma in an Indian cohort
 Supplementary Table 6. List of annotations predicted using TSNAP

Software	Variant accession	Position	HLA subtype	Wild type peptide	Wild binding	wild binding level	Mutant peptide	Mutant binding	Mutant rank	Mutant binding level	Gene symbol	Variant information	Habit	Sample ID	OneMD	COSMIC	dbSNP	EXAC	EXAC_SAS	1000G	1000G_SAS	SIFT	Polypeh2	CONDEL	VEP	LRT	Phat'non'W3	Total read depth in Normal	Reference read support in Normal	Alternative read support in Normal	Total read depth in Tumor	Reference read support in Tumor	Alternative read support in Tumor	Alternate allele frequency		
HLA	ADPKC_K4997	10HLA-A*01:01	NPYVEVIER	4579	4.6301		NPYVEVIER	483	0.1833	58	ADPKC	K497	Smoker	4248	NA	NA	NA	NA	NA	NA	NA	T	BN	N	MODERATE	NA	0.533	165	165	0	159	116	43	27.04		
TSNAD	ADPKC_K4997	10HLA-A*01:01	NPYVEVIER	7168	5.1418		NPYVEVIER	153	0.1499	58	ADPKC	K497	Smoker	4248	NA	NA	NA	NA	NA	NA	NA	T	BN	N	MODERATE	NA	0.533	165	165	0	159	116	43	27.04		
TSNAD	ADPKC_K4997	10HLA-A*01:01	NPYVEVIER	3803	5.2814		NPYVEVIER	45	0.1778	58	ADPKC	K497	Smoker	4248	NA	NA	NA	NA	NA	NA	NA	T	BN	N	MODERATE	NA	0.533	165	165	0	159	116	43	27.04		
TSNAD	ADPKC_K4997	10HLA-A*01:01	NPYVEVIER	2579	5.2814		NPYVEVIER	153	0.1499	58	ADPKC	K497	Smoker	4248	NA	NA	NA	NA	NA	NA	NA	T	BN	N	MODERATE	NA	0.533	165	165	0	159	116	43	27.04		
HLA	AF14_T973K	2HLA-A*11:01	KSPFYMYSET	2256	9.4487		KSPFYMYSET	29	0.1734	58	AF14	T973K	Chester	4245	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.977	248	247	1	155	145	10	6.45		
TSNAD	AF14_T973K	2HLA-A*11:01	KSPFYMYSET	1689	5.1686		KSPFYMYSET	25	0.1868	58	AF14	T973K	Chester	4247	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.977	248	247	1	155	145	10	6.45		
TSNAD	AF14_T973K	2HLA-A*01:01	KSPFYMYSET	2927	21.6078		KSPFYMYSET	43	0.1623	58	AF14	T973K	Chester	4245	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.977	248	247	1	155	145	10	6.45		
HLA	AKAP1_E784K	1HLA-A*01:01	RAOVYASVE	2266	9.4487		RAOVYASVE	29	0.1734	58	AKAP1	E784K	Chester	4245	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.977	248	247	1	155	145	10	6.45		
TSNAD	AKAP1_E784K	1HLA-A*01:01	RAOVYASVE	16797	12.9687		RAOVYASVE	69	0.2029	58	AKAP1	E784K	notfound	5699	NA	NA	0.0001997	0.000066	0	0.00019981	0	T	BN	BN	MODERATE	NA	0.984	172	171	0	243	234	18	7.41		
TSNAD	AKAP1_E784K	1HLA-A*01:01	RAOVYASVE	16797	12.9687		RAOVYASVE	69	0.2029	58	AKAP1	E784K	notfound	5699	NA	NA	0.0001997	0.000066	0	0.00019981	0	T	BN	BN	MODERATE	NA	0.984	172	171	0	243	234	18	7.41		
TSNAD	AKAP1_E784K	1HLA-A*01:01	RAOVYASVE	2266	9.4487		RAOVYASVE	29	0.1734	58	AKAP1	E784K	notfound	5699	NA	NA	0.0001997	0.000066	0	0.00019981	0	T	BN	BN	MODERATE	NA	0.984	172	171	0	243	234	18	7.41		
TSNAD	AKAP1_E784K	1HLA-A*01:01	RAOVYASVE	7089	9.5233		RAOVYASVE	69	0.2029	58	AKAP1	E784K	notfound	5699	NA	NA	0.0001997	0.000066	0	0.00019981	0	T	BN	BN	MODERATE	NA	0.984	172	171	0	243	234	18	7.41		
TSNAD	AKAP1_E784K	1HLA-A*01:01	RAOVYASVE	7101	11.9388		RAOVYASVE	34	0.2084	58	AKAP1	E784K	notfound	5699	NA	NA	0.0001997	0.000066	0	0.00019981	0	T	BN	BN	MODERATE	NA	0.984	172	171	0	243	234	18	7.41		
HLA	AMACR_N1251	10HLA-A*02:01	NYLALSGV	4368	8.7462		NYLALSGV	39	0.4728	58	AMACR	N1251	notfound	4288	NA	NA	NA	NA	NA	NA	NA	D	DL	DL	MODERATE	NA	NA	NA	NA	NA	NA	61	51	11	18.03	
TSNAD	AMACR_N1251	10HLA-A*02:01	NYLALSGV	626	5.3145		NYLALSGV	34	0.0871	58	AMACR	N1251	notfound	4288	NA	NA	0.0000083	0	NA	NA	NA	D	DL	DL	MODERATE	NA	NA	NA	NA	NA	61	51	11	18.03		
TSNAD	AMACR_N1251	10HLA-A*02:01	NYLALSGV	2103	9.8977		NYLALSGV	7	0.4048	58	AMACR	N1251	notfound	4288	NA	NA	0.0000083	0	NA	NA	NA	D	DL	DL	MODERATE	NA	NA	NA	NA	NA	61	51	11	18.03		
TSNAD	AMACR_N1251	10HLA-A*02:01	NYLALSGV	4368	8.7462		NYLALSGV	39	0.4728	58	AMACR	N1251	notfound	4288	NA	NA	NA	NA	NA	NA	NA	D	DL	DL	MODERATE	NA	NA	NA	NA	NA	61	51	11	18.03		
HLA	ARHGFE4_K34R	3HLA-A*11:01	VYKSGTHFK	901	8.2897		VYKSGTHFK	52	0.4453	58	ARHGFE4	K34R	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	NA	NA	NA	NA	NA	NA	100	60	40	40
TSNAD	ARHGFE4_K34R	3HLA-A*11:01	VYKSGTHFK	901	8.2897		VYKSGTHFK	52	0.4453	58	ARHGFE4	K34R	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	NA	NA	NA	NA	NA	NA	100	60	40	40
HLA	ASTN2_G121R	3HLA-A*08:01	NYNGYSTR	32703	5.2532		NYNGYSTR	48	0.4673	58	ASTN2	G121R	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.950	80	80	0	101	92	8	7.92		
TSNAD	ASTN2_G121R	3HLA-A*08:01	NYNGYSTR	32703	5.2532		NYNGYSTR	48	0.4673	58	ASTN2	G121R	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.950	80	80	0	101	92	8	7.92		
TSNAD	ASTN2_G121R	3HLA-A*08:01	NYNGYSTR	2480	25.793		NYNGYSTR	26	0.0841	58	ASTN2	G121R	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.950	80	80	0	101	92	8	7.92		
TSNAD	ASTN2_G121R	3HLA-A*01:01	NYNGYSTR	26018	35.6749		NYNGYSTR	51	0.4524	58	ASTN2	G121R	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.950	80	80	0	101	92	8	7.92		
TSNAD	ASTN2_G121R	3HLA-A*08:01	NYNGYSTR	32703	42.5212		NYNGYSTR	48	0.4673	58	ASTN2	G121R	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.950	80	80	0	101	92	8	7.92		
HLA	AT16_G391V	2HLA-A*02:01	VLAFHNVV	1576	8.8113		VLAFHNVV	5	0.3118	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
TSNAD	AT16_G391V	2HLA-A*02:01	VLAFHNVV	4857	8.7309		VLAFHNVV	19	0.2692	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
TSNAD	AT16_G391V	2HLA-A*02:01	VLAFHNVV	194	6.2692		VLAFHNVV	19	0.2692	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
TSNAD	AT16_G391V	2HLA-A*02:01	VLAFHNVV	903	4.6097		VLAFHNVV	7	0.1199	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
TSNAD	AT16_G391V	2HLA-A*08:02	LAFHNVV	6128	9.44		LAFHNVV	37	0.3311	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
TSNAD	AT16_G391V	2HLA-A*02:01	VLAFHNVV	1481	5.2683		VLAFHNVV	31	0.1978	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
TSNAD	AT16_G391V	2HLA-A*02:01	VLAFHNVV	1576	8.8113		VLAFHNVV	5	0.3118	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
TSNAD	AT16_G391V	2HLA-A*02:01	VLAFHNVV	4857	8.7309		VLAFHNVV	19	0.2692	58	AT16	G391V	notfound	5697	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.902	101	37	64	56	3	53	94.64		
HLA	BMP2K_Q541K	1HLA-A*01:01	SOYFPMAPQV	7188	8.6967		SOYFPMAPQV	21	0.1188	58	BMP2K	Q541K	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	UN	UN	MODERATE	NA	1	65	65	0	64	48	16	25		
TSNAD	BMP2K_Q541K	1HLA-A*01:01	SOYFPMAPQV	4286	8.7848		SOYFPMAPQV	21	0.1188	58	BMP2K	Q541K	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	UN	UN	MODERATE	NA	1	65	65	0	64	48	16	25		
TSNAD	BMP2K_Q541K	1HLA-A*01:01	SOYFPMAPQV	7614	4.1483		SOYFPMAPQV	34	0.1813	58	BMP2K	Q541K	Chester	4248	NA	NA	NA	NA	NA	NA	NA	D	UN	UN	MODERATE	NA	1	65	65	0	64	48	16	25		
HLA	BP2HG_G61R	2HLA-A*01:01	TPVHLDWSR	24825	7.1282		TPVHLDWSR	41	0.1584	58	BP2HG	G61R	Smoker	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.037	65	65	0	42	28	13	30.95		
TSNAD	BP2HG_G61R	2HLA-A*01:01	TPVHLDWSR	24825	7.1282		TPVHLDWSR	41	0.1584	58	BP2HG	G61R	Smoker	4248	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	MODERATE	NA	0.037	65	65	0	42	28	13	30.95		
TSNAD	BP2HG_G61R	2HLA-A*01:01	TPVHLDWSR	26218	19.3451		TPVHLDWSR	69	0.1938	58	BP2HG	G61R	Smoker	4248	NA																					

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 Supplementary Table 6. List of annotations predicted using TSSAD

Software	Variant accession	Position	HLA subtype	Wtd binding	Wtd read	w/d binding level	Mutant peptide	Mutant binding	Mutant rank	Mutant binding level	Gene symbol	Variant information	Habit	Sample ID	OneoMD	COSMIC	dbSNP	EXAC	EXAC_SAS	1000G	1000G_SAS	SIFT	PhyloP2	CONDEL	VEP	LRT	Phac'netWay	Total read depth in Normal	Reference read support in Normal	Alternative read support in Normal	Total read depth in Tumor	Reference read support in Tumor	Alternate read support in Tumor	Alternate allele frequency in Tumor		
TSSAD	ELFP_E3306	3	HLA-A*01:01	VRITGLYK	7363	4.6067	VRITGLYK	22.0	0.1198	58	ELP3	E3306	notfound	42497	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	D	1	60	60	46	33	13	28.26		
TSSAD	ELFP_E3306	2	HLA-A*01:01	VRITGLYK	7265	4.6073	VRITGLYK	24.0	0.0514	38	ELP3	E3306	notfound	42497	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	D	1	60	60	46	33	13	28.26		
TSSAD	ELFP_E3306	2	HLA-A*01:01	VRITGLYK	2521	4.6273	VRITGLYK	34.0	0.0281	38	ELP3	E3306	notfound	42497	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	D	1	60	60	46	33	13	28.26		
HLA	FAM13A_P78	3	HLA-A*01:01	TQDYLNR	37227	4.7003	TQDYLNR	30.0	0.0923	38	FAM13A	P78	Smoker	42498	NA	NA	NA	NA	NA	NA	NA	D	DL	DL	D	MODERATE	D	1	60	60	46	33	13	28.26		
TSSAD	FAM13A_P78	3	HLA-A*01:01	TQDYLNR	36267	4.7003	TQDYLNR	42.0	0.4797	38	FAM13A	P78	Smoker	42498	NA	NA	NA	NA	NA	NA	NA	D	DL	DL	D	MODERATE	D	1	60	60	46	33	13	28.26		
TSSAD	FAM13A_P78	3	HLA-A*01:01	TQDYLNR	37122	4.7003	TQDYLNR	50.0	0.1197	38	FAM13A	P78	Smoker	42498	NA	NA	NA	NA	NA	NA	NA	D	DL	DL	D	MODERATE	D	1	60	60	46	33	13	28.26		
HLA	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	19758	4.8680	MMALKVLG	75.0	0.4031	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38		
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	13578	4.8680	MMALKVLG	30.0	0.0943	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38		
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	26669	4.8680	MMALKVLG	9.0	0.0778	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38		
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	20586	4.8680	MMALKVLG	11.0	0.0178	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38		
TSSAD	FAM46D_G348	2	HLA-A*01:01	MMALKVLG	16786	4.8680	MMALKVLG	71.2	0.2944	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	17244	4.8680	MMALKVLG	9.2	0.0138	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	4	HLA-A*01:01	MMALKVLG	33609	4.8680	MMALKVLG	9.0	0.2099	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	19758	4.8680	MMALKVLG	75.0	0.4031	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	22914	4.8680	MMALKVLG	27.0	0.0992	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	22335	4.8680	MMALKVLG	57.0	0.4133	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	21061	4.8680	MMALKVLG	98.0	0.6688	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	19521	4.8680	MMALKVLG	98.0	0.6138	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	4	HLA-A*01:01	MMALKVLG	23292	4.8680	MMALKVLG	70.0	0.2734	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	16786	4.8680	MMALKVLG	11.0	0.0688	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	19521	4.8680	MMALKVLG	98.0	0.6138	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	21061	4.8680	MMALKVLG	98.0	0.6688	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	2	HLA-A*01:01	MMALKVLG	21484	4.8680	MMALKVLG	19.0	0.2488	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	6295	4.8680	MMALKVLG	6.0	0.0201	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
TSSAD	FAM46D_G348	3	HLA-A*01:01	MMALKVLG	21266	4.8680	MMALKVLG	16.0	0.1966	38	FAM46D	G348	notfound	42499	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	234	234	206	202	44	14.38	
HLA	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	792	4.9994	DPMPKXHLV	8.0	0.1709	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	10184	4.9994	DPMPKXHLV	4.0	0.2944	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	2207	4.9994	DPMPKXHLV	8.0	0.1425	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	8883	4.9994	DPMPKXHLV	98.0	0.2925	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	13224	4.9994	DPMPKXHLV	70.0	0.2925	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	703	4.9994	DPMPKXHLV	70.0	0.1328	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	2	HLA-A*29:01	TYELVYKYY	10184	4.9994	TYELVYKYY	4.0	0.2944	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	818	4.9994	DPMPKXHLV	4.0	0.0212	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	10	HLA-A*01:01	YPMRKYHLV	10089	4.9994	YPMRKYHLV	33.0	0.3441	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	792	4.9994	DPMPKXHLV	8.0	0.1709	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	4676	4.9994	DPMPKXHLV	99.0	0.0778	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	2945	4.9994	DPMPKXHLV	32.0	0.4627	38	FOLH1	D567	Smoker	42500	NA	NA	NA	NA	NA	NA	NA	NA	D	PD	PD	D	MODERATE	D	1	88	88	87	88	89	19	21.99
TSSAD	FOLH1_D567	11	HLA-A*02:01	DPMPKXHLV	1636	4.9994	DPMPKXHLV	34.0	0.0214	38	FOLH1																									

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 Supplementary Table 6. List of annotations predicted using TSSAD

Software	Variant accession	Position	HLA subtype	Wild type peptide	Wild binding	Wild rank	wild binding level	Mutant peptide	Mutant binding	Mutant rank	Mutant binding level	Gene symbol	Variant information	Habit	Sample ID	OneMD	COSMIC	dNSP	EXAC	EXAC_SAS	1000G	1000G_SAS	SIFT	PhyPhe2	CONDEL	VEP	LRT	Phast'n/UC	Total read depth in Normal	Reference read support in Normal	Alternate read support in Normal	Total read depth in Tumor	Reference read support in Tumor	Alternate read support in Tumor	Alternate allele frequency in Tumor
HLA	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	5481	4.8162		TVRVPMMLA	209	0.0134	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	4178	5.5002		TVRVPMMLK	229	0.1346	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	1622	4.997		TVRVPMMLK	17	0.1119	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	4427	4.8067		TVRVPMMLK	44	0.1744	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	10418	9.0776		TVRVPMMLK	923	0.2721	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	4452	4.365		TVRVPMMLK	23	0.0318	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	1761	2.7444		TVRVPMMLK	25	0.1419	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	4811	4.8162		TVRVPMMLK	1039	0.0114	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	1208	2.1215		TVRVPMMLK	23	0.0124	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SEPNP4A_Q248K	2	HLA-A*11:01	TVRVPMMLQ	4927	5.8229		TVRVPMMLK	29	0.0928	SEPNP4A_Q248K	missense		4249	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
HLA	SKI_S664L	10	HLA-A*24:01	YSAGIEDGV	4915	3.1327		YLAGIEDGV	21	0.2984	SKI_S664L	missense		5697	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SKI_S664L	10	HLA-A*24:01	YSAGIEDGV	2199	9.646		YLAGIEDGV	14	0.3382	SKI_S664L	missense		5697	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SKI_S664L	10	HLA-A*24:01	YSAGIEDGV	574	3.9519		YLAGIEDGV	66	0.0871	SKI_S664L	missense		5697	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SKI_S664L	10	HLA-A*24:01	YSAGIEDGV	2628	0.8567		YLAGIEDGV	7	0.4483	SKI_S664L	missense		5697	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SKI_S664L	10	HLA-A*24:01	YSAGIEDGV	4915	9.5813		YLAGIEDGV	21	0.2988	SKI_S664L	missense		5697	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
TSNAD	SKI_S664L	10	HLA-A*24:01	YSAGIEDGV	4915	9.5813		YLAGIEDGV	21	0.2988	SKI_S664L	missense		5697	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.015	65	65	56	51	5	8.93		
HLA	SLC12A9_T36M	8	HLA-A*24:01	YVTVGVANVF	576	1.1329		YVTVGVANVF	44	0.2149	SLC12A9_T36M	Chewer	4248	chr7:10045648	chr7:10045648	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.986	54	54	81	56	25	30.86		
TSNAD	SLC12A9_T36M	8	HLA-A*24:01	YVTVGVANVF	661	0.8152		YVTVGVANVF	44	0.2623	SLC12A9_T36M	Chewer	4248	chr7:10045648	chr7:10045648	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.986	54	54	81	56	25	30.86		
TSNAD	SLC12A9_T36M	8	HLA-A*24:01	YVTVGVANVF	576	1.1329		YVTVGVANVF	44	0.2149	SLC12A9_T36M	Chewer	4248	chr7:10045648	chr7:10045648	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.986	54	54	81	56	25	30.86		
TSNAD	SLC12A9_T36M	8	HLA-A*24:01	YVTVGVANVF	780	1.3509		YVTVGVANVF	46	0.1853	SLC12A9_T36M	Chewer	4248	chr7:10045648	chr7:10045648	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.986	54	54	81	56	25	30.86		
TSNAD	SLC12A9_T36M	8	HLA-A*24:01	YVTVGVANVF	1051	0.8779		YVTVGVANVF	19	0.4642	SLC12A9_T36M	Chewer	4248	chr7:10045648	chr7:10045648	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.986	54	54	81	56	25	30.86		
TSNAD	SLC12A9_T36M	8	HLA-A*24:01	YVTVGVANVF	971	6.234		YVTVGVANVF	17	0.4455	SLC12A9_T36M	Chewer	4248	chr7:10045648	chr7:10045648	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.986	54	54	81	56	25	30.86		
HLA	SLC22A1_W14L	10	HLA-A*24:01	GVFKQKAL	1701	12.6184		GVFKQKAL	6	0.3462	SLC22A1_W14L	Chewer	4248	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.99	90	90	104	89	14	13.68		
TSNAD	SLC22A1_W14L	10	HLA-A*24:01	GVFKQKAL	3701	12.6184		GVFKQKAL	6	0.3462	SLC22A1_W14L	Chewer	4248	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.99	90	90	104	89	14	13.68		
TSNAD	SLC22A1_W14L	10	HLA-A*24:01	GVFKQKAL	3190	11.9487		GVFKQKAL	13	0.2982	SLC22A1_W14L	Chewer	4248	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.99	90	90	104	89	14	13.68		
HLA	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	5170	3.1684		DIHMAGFI	85	0.2102	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
HLA	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	1068	2.6787		DIHMAGFI	85	0.2102	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	1068	2.6787		DIHMAGFI	85	0.2102	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	3973	4.1108		DIHMAGFI	83	0.1193	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	7204	5.2473		DIHMAGFI	62	0.2939	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	4520	4.5201		DIHMAGFI	43	0.178	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	7204	5.2473		DIHMAGFI	62	0.2939	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	1980	2.4999		DIHMAGFI	85	0.1419	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	4917	3.9992		DIHMAGFI	42	0.1199	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	601	4.5218		DIHMAGFI	48	0.1238	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	5170	3.1684		DIHMAGFI	85	0.2102	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	1068	2.6787		DIHMAGFI	85	0.2102	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	4847	0.6992		DIHMAGFI	85	0.2102	SLC6A3_H32Y	Snaker	4247	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	D	MODERATE	N	0.991	161	161	166	131	32	19.28		
TSNAD	SLC6A3_H32Y	9	HLA-A*24:01	DIHMAGFI	2834	4.5485		DIHMAGFI	75	0.4462	SLC6A3_H32Y	Snaker																							

Software	Variant accession	Position	HLA subtype	Wild type peptide	Wild binding	Wild rank	wild binding level	Mutant peptide	Mutant binding	Mutant rank	Mutant binding level	Gene symbol	Variant information	Habit	Sample ID	OncoMD	COSMIC	dbSNP	EXAC	EXAC_SAS	1000G	1000G_SAS	SIFT	PolyPhen2	CONDEL	VEP	LRT	PhastCons7Way	Total read depth in Normal	Reference read support in Normal	Alternative read support in Normal	Total read depth in Tumor	Reference read support in Tumor	Alternate read support in Tumor	Alternate allele frequency in Tumor	
TSSAD	YARS P49L	10	HLA-A*03:02	KPMAKGPAAK	8966.5	7.6447		KLMAGKPAK	262	0.3803	SB	YARS	P349L	noLabel	4250	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	N	0.817	76	76	0	44	31	13	29.55
TSSAD	YARS P49L	3	HLA-B*07:01	YPDPSKQKP	1292.2	11.8972		YPDPSKQKL	763	0.2812	SB	YARS	P349L	noLabel	4250	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	N	0.817	76	76	0	44	31	13	29.55
TSSAD	YARS P49L	10	HLA-A*01:01	KPMAKGPAAK	8525	8.8637		KLMAGKPAK	642	0.3893	SB	YARS	P349L	noLabel	4250	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	N	0.817	76	76	0	44	31	13	29.55
TSSAD	YARS P49L	9	HLA-A*03:01	QKPMKAGPAK	16150.5	12.3207		QKLMKAGPAK	562	0.2117	SB	YARS	P349L	noLabel	4250	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	N	0.817	76	76	0	44	31	13	29.55
TSSAD	YARS P49L	10	HLA-A*03:01	KPMAKGPAAK	7520.5	6.1843		KLMAGKPAK	114	0.6139	SB	YARS	P349L	noLabel	4250	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	N	0.817	76	76	0	44	31	13	29.55
TSSAD	YARS P49L	10	HLA-A*01:01	KPMAKGPAAK	744	2.7886		KLMAGKPAK	259	0.114	SB	YARS	P349L	noLabel	4250	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	N	0.817	76	76	0	44	31	13	29.55
TSSAD	YARS P49L	8	HLA-A*01:01	KQPMKAGPAK	234.1	1.5817	WB	KQKLMKAGPAK	87	0.3273	SB	YARS	P349L	noLabel	4250	NA	NA	NA	NA	NA	NA	NA	T	BN	BN	N	MODERATE	N	0.817	76	76	0	44	31	13	29.55
HLA	ZNF277-G184R	3	HLA-A*11:01	MCNCEFLG	16446.4	19.3663		MCNCEFLR	449	0.3718	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	2	HLA-A*11:01	CMFCNCEFLG	14140.5	16.4844		CMFCNCEFLR	409	0.3373	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	2	HLA-A*11:01	CMFCNCEFLG	2391.1	15.8138		CMFCNCEFLR	75	0.2301	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	3	HLA-A*13:03	MCNCEFLG	19334.2	14.9347		MCNCEFLR	439	0.1646	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	2	HLA-A*13:01	MCNCEFLG	19149.3	11.8792		MCNCEFLR	443	0.1288	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	3	HLA-B*08:01	FLGNRSVIL	907.8	1.2377	WB	FLGNRSVIL	299	0.0489	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	2	HLA-A*11:01	CMFCNCEFLG	14140.5	16.4844		CMFCNCEFLR	409	0.3373	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	2	HLA-A*13:03	CMFCNCEFLG	22380.3	18.3506		CMFCNCEFLR	63	0.2458	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	3	HLA-A*11:01	MCNCEFLG	16446.4	19.3663		MCNCEFLR	449	0.3718	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	9	HLA-B*08:01	FLGNRSVIL	2366.2	2.7653		FLGNRSVIL	61	0.1101	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60
TSSAD	ZNF277-G184R	9	HLA-B*04:01	FLGNRSVIL	972.7	1.8428	WB	FLGNRSVIL	62	0.2973	SB	ZNF277	G184R	Chever	4240	NA	NA	NA	0.0000165	0.000121462	NA	NA	D	P/D	P/D	D	MODERATE	D	0.744	50	50	0	45	17	27	60