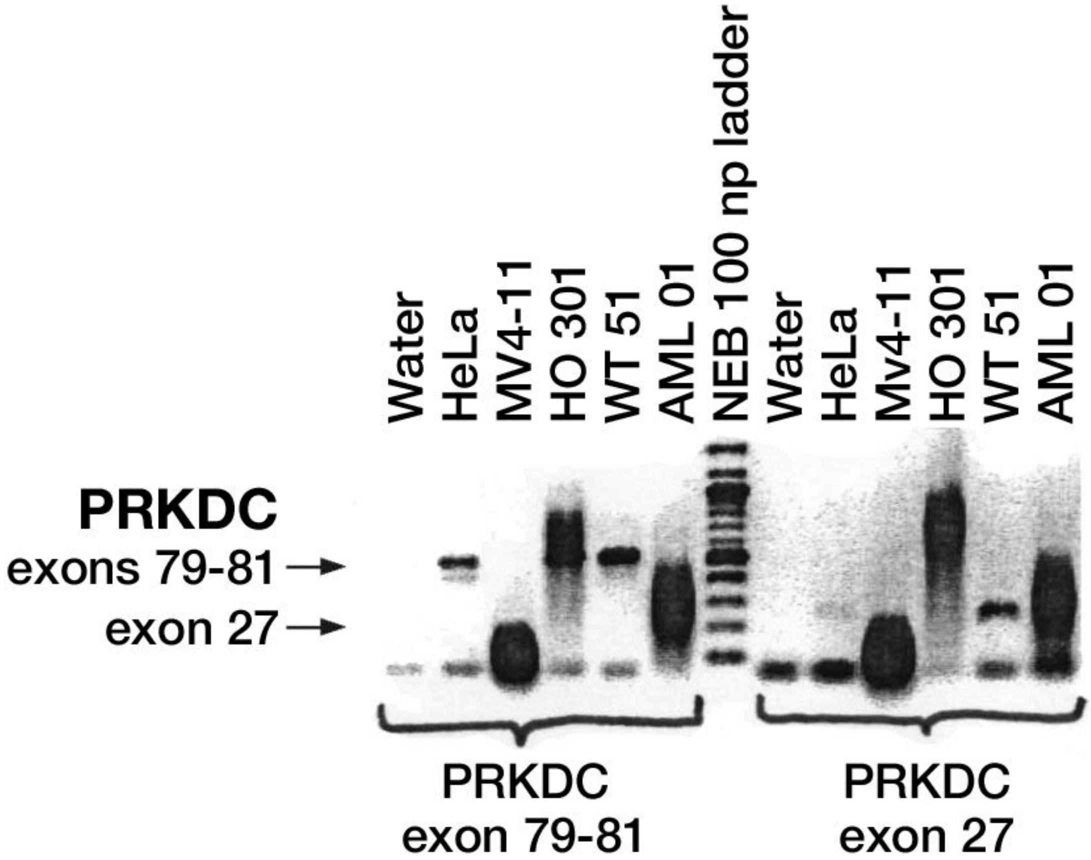

Supplemental Figure 1: mRNA expression of PRKDC in different tumor cell lines.

Both transcripts of PRKDC could be detected in the EBV-transformed B cell line WT51.

Cancer Immunology, Immunotherapy (submitted in 2013) – A. Neumann *et al*.

Supplemental Table 1: HLA ligands characterized after elution from immunopurified HLA molecules of lung cancer tissue.

Peptide	**HLA**	**gene symbol**	**gene**	**cancer associated (ref. / PMID)**	**n-fold overexpression**					
					LCA008	LCA010	LCA011	LCA018	LCA020	LCA021
VHYDRSGRSL	B*14	THOC4	THO complex 4	n	n.a.					
NTDRNIDKY	A*01	C3orf63	chromosome 3 open reading frame 63 (retinoblastoma-associated protein 140)	n	1.6	1.5	1.3	1.4	0.9	1.1
ILDKKVEKV	A*02	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	19047110	0.5	1.0	0.8	0.9	0.4	0.6
ERAIHQAL	B*14	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	19690133	0.9	0.2	1.9	1.7	9.2	0.2
DVAALHKAI	A*02	ANXA1	annexin A1	16899607	0.8	0.1	1.2	1.7	1.4	0.2
VLASMFHVTL	A*02	CLEC12A	C-type lectin domain family 12, member A	n	n.a.					
DQLRHGGL	n.a.	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	n	0.1	0.4	0.3	0.3	0.2	0.2
HPISDHEATL	B*35	HLA-A	major histocompatibility complex, class I, A	n	2.3	2.1	3.7	0.9	1.3	0.8
RQDVDNASL	n.a.	VIM	vimentin	n	0.5	0.2	0.9	0.4	1.5	0.5
DRRERVLKL	B*14	EAF2	ELL associated factor 2 (testosterone regulated apoptosis inducer and tumor suppressor)	12907652	1.0	0.3	0.7	0.7	1.5	0.4
NGATRKLAL	n.a.	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	n	0.5	0.5	0.9	0.9	0.3	0.3
VTEIDQDKY	A*01	FLNA	filamin A, alpha (actin binding protein 280)	19690385	0.5	0.2	1.1	0.5	1.1	5.7
ALADGVQKV	A*02	APOL1	apolipoprotein L, 1	n	0.6	0.1	0.4	0.4	0.4	0.1
KMAGIGIREA	A*02	KRT15	keratin 15	n	90.5	1.3	6.5	0.6	0.0	0.0
QENSSDYQSNLA	n.a.	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')	n	1.4	1.1	1.1	0.8	1.1	1.2
NTEEEGLKY	A*01	BCLAF1	BCL2-associated transcription factor 1	n	6.5	6.5	4.9	3.2	4.6	2.8
NTDSPLRY	A*01	RPSA	ribosomal protein SA	12386810	0.9	0.9	0.8	1.1	0.9	0.8
ERVVHYEI	B*14	NDUFB8	NADH dehydrogenase (ubiquinone) 1	n	0.7	0.7	0.7	0.8	0.8	1.3

			beta subcomplex, 8, 19kDa							
RPFERTITM	B*35	SDCBP	syndecan binding protein (syntenin) (Melanoma differentiation- associated protein 9)	18832467	0.5	0.4	0.7	0.9	0.9	0.4
IADMGHLKY	A*01	PCNA	proliferating cell nuclear antigen	(18), (28)	4.9	5.3	3.5	7.5	2.8	1.6
SRIARALAL	B*14	CYR61	cysteine-rich, angiogenic inducer, 61	11751417	0.5	0.1	0.7	0.2	1.2	0.6
RFDHVITNM	n.a.	C1QB	complement component 1, q subcomponent, B chain	n	1.7	0.3	4.0	2.8	3.7	0.3
LTDRELEEY	A*01	ADD1	adducin 1 (alpha)	n	0.9	0.7	1.2	0.8	1.2	2.6
RLASYLDKV	A*02	KRT17	keratin 17	16638858	42.2	0.1	0.1	1.2	1.1	0.1
DRVLRAML	B*14	CCND1	cyclin D1	(19), (29), (30)	1.6	4.9	4.9	0.4	4.3	1.4
LRFQSSAVM	B*14	HIST1H3B	histone cluster 1, H3b	n	0.9	2.0	1.9	0.7	1.6	0.2
DRVAHILL	B*14	VPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)	n	1.5	1.4	1.9	3.0	2.0	1.3
YIDEQFERY	A*01	SEPT2	septin 2	16682951	1.6	1.6	2.0	1.1	2.0	1.1
NRFPAVNSL	B*14	GOSR1	golgi SNAP receptor complex member 1	n	2.1	1.5	3.0	1.2	2.0	2.5
VTELHVISY	A*01	RNF213	ring finger protein 213	n	n.a.					
DTDHYFLRY	A*01	PIGT	phosphatidylinositol glycan anchor biosynthesis, class T	n	0.9	4.0	1.5	1.9	1.5	1.4
DRVALRNLL	B*14	HLA-F	major histocompatibility complex, class I, F	n	0.6	0.6	1.1	0.7	0.7	0.3
VMAPRTLVL	E	HLA-A	major histocompatibility complex, class I, A	n	2.3	2.1	3.7	0.9	1.3	0.8
DRYISKMFL	B*14	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	n	1.7	2.0	1.5	1.4	1.2	1.2
DRFLRQLDF	B*14	COPA	coatomer protein complex, subunit alpha	n	1.5	1.1	1.4	1.3	1.1	0.9
MPVGPDAILRY	B*35	BAT3	HLA-B associated transcript 3	18978787	0.9	1.9	1.7	1.9	1.1	1.6
FLALLAGAHA	A*02	PLTP	phospholipid transfer protein	n	4.6	0.9	6.5	1.2	17.1	2.1
FGGRNPFDTF	n.a.	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	n	0.5	0.2	0.3	0.3	0.1	0.1
VLIENVASL	A*02	GPX2	glutathione peroxidase 2 (gastrointestinal)	19047153	73.5	42.2	0.8	0.5	0.2	0.4
TLSDLRVYL	A*02	SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	n	n.a.					
VLWDRTFSL	A*02	STAT1	signal transducer and activator of transcription 1, 91kDa	(25) - (27)	7.0	2.6	9.2	5.7	2.5	0.6

DPFKDIILY	B*35	BZW1	basic leucine zipper and W2 domains 1	n	1.2	1.9	1.6	1.1	1.2	0.5
VRFLGNLVL	B*14	RRAGB	Ras-related GTP binding B	n	0.9	0.9	1.1	0.7	1.9	2.1
SIIGRLLEV	A*02	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	n	0.9	0.9	1.7	1.0	0.8	0.3
LPFLPSTEDVY	B*35	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	n	2.6	0.2	0.0	1.0	2.1	0.1
FVHDLVLYL	A*02	CLTC	clathrin, heavy chain (Hc)	n	1.3	0.9	1.7	0.8	1.1	0.9
KLLEPVLLL	A*02	RPS16	ribosomal protein S16	n	0.8	0.8	0.7	0.8	0.6	0.8
DPVHKLLTL	B*35	KIAA0317	KIAA0317	n	1.1	1.4	1.2	1.1	1.1	0.7
TLADIIARL	A*02	NYNRIN	NYN domain and retroviral integrase containing	n	0.6	0.4	0.8	0.1	0.4	0.4
GLWHDVIFI	A*02	LAMA4	laminin, alpha 4	15915502	1.1	0.5	2.8	0.9	6.5	6.1
WRFPGLLL	B*14	CD46	CD46 molecule, complement regulatory protein	14712499	1.2	1.3	1.7	2.1	0.4	0.1
MRLSLPLLL	B*14	MGC29506	hypothetical protein MGC29506 (proapoptotic caspase adaptor protein)	12792799	9.2	0.2	1.2	3.5	9.8	0.0
PTASPFPLLLL	n.a.	SEMA4F	semaphorin 4F	n	1.9	1.1	2.0	1.1	1.3	0.7
AVASFPKKQE	artefact	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	n	0.9	1.1	0.8	0.7	0.8	0.9
ILDKKVEKV	A*02	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	19047110	0.5	1.0	0.8	0.9	0.4	0.6
FVQMMTAK	n.a.	CALM3	calmodulin 3 (phosphorylase kinase, delta)	n	1.3	2.0	2.6	1.4	3.7	4.3
QRFSHQTL	B*14	MED12	mediator complex subunit 12	n	0.8	1.5	0.9	0.9	0.4	0.8
TRLESRTQL	B*14	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	n	3.0	1.4	3.5	1.9	2.5	2.8
MRVERSTL	B*14	ZMAT2	zinc finger, matrin type 2	n	n.a.					
DRFRNNSL	B*14	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	n	1.2	0.2	1.2	0.9	1.7	0.2
TPGIKGEKGLPGL	B*35	C1QB	complement component 1, q subcomponent, B chain	n	1.7	0.3	4.0	2.8	3.7	0.3
INFDGHVVL	n.a.	CNTNAP2	contactin associated protein-like 2	n	39.4	48.5	1.4	0.9	1.1	0.8
RPAGLPEKY	B*35	SAA2	serum amyloid A2	n	0.9	0.1	0.2	0.0	0.1	0.2
IYNEALKG	n.a.	S100A6	S100 calcium binding protein A6	18620780	0.9	0.5	1.2	0.2	0.9	0.8
DRTTISRAL	B*14	GOLGA2	golgi autoantigen, golgin subfamily a, 2	n	1.9	1.5	1.9	1.6	2.3	2.1
RVAPEEHPVL	A*02	ACTB	actin, beta	n	0.7	0.6	0.9	0.9	1.0	0.9
YEVSQLKD	artefact	CNDP2	CNDP dipeptidase 2 (metallopeptidase	n	0.7	0.7	2.1	1.3	0.7	0.3

			M20 family)							
VPNVHGAL	B*35	PTBP1	polypyrimidine tract binding protein 1	n	0.6	1.1	0.7	0.8	0.4	0.1
DQVTHIRI	B*14	PTPN6	protein tyrosine phosphatase, non-receptor type 6	15870198	1.5	0.9	2.3	1.1	1.6	0.4
ILMEHIHKL	A*02	RPL19	ribosomal protein L19	16609016	1.4	1.1	1.0	1.1	1.1	1.1
DRVAHMEF	B*14	SPTBN1	spectrin, beta, non-erythrocytic 1	n	0.5	1.6	1.1	0.4	0.9	0.7
QLEDGRTLSDY	A*01	UBB	ubiquitin B	n	0.6	0.5	0.8	0.3	0.7	0.7
DRALRSFKL	B*14	HDLBP	high density lipoprotein binding protein (vigilin)	n	1.4	1.7	2.0	1.1	2.0	1.3
LLDQGQLNKY	A*01	CLTC	clathrin, heavy chain (Hc)	n	1.3	0.9	1.7	0.8	1.1	0.9
DRMVGQVL	B*14	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	n	0.2	0.9	0.4	0.5	0.4	0.2
LPFIHHEL	B*35	OSGIN1	oxidative stress induced growth inhibitor 1	16924236	8.6	0.9	0.5	0.2	0.2	0.8
LRPIQALGTEY	B*14	FCGBP	Fc fragment of IgG binding protein	n	3.5	0.7	9.2	0.3	1.1	0.4
DQVSRLVTI	B*14	UGDH	UDP-glucose dehydrogenase	19676054	2.5	0.8	1.1	0.8	1.0	1.0
LASVSTVLTSKY	B*35	HBA1	hemoglobin, alpha 1	n	0.1	0.1	0.4	0.2	0.9	0.1
VELDDLGKDEL	n.a.	PDIA6	protein disulfide isomerase family A, member 6	17495932	1.0	1.7	1.7	1.4	1.1	0.8
LRYPMAVGL	B*14	RPL36	ribosomal protein L36	n	2.6	2.6	1.3	1.9	2.0	1.7
DVELDDLGKDEL	A*02	PDIA6	protein disulfide isomerase family A, member 6	17495932	1.0	1.7	1.7	1.4	1.1	0.8
LVVYPWTQRF	artefact	HBB	hemoglobin, beta	n	0.1	0.1	0.3	0.1	0.9	0.1
GFSDEGGWLTRL	A*01	SQSTM1	sequestosome 1	(17)	3.2	0.6	0.9	1.0	0.6	1.3
LRLLPFLGVL	B*14	CISD2	CDGSH iron sulfur domain 2	n	n.a.					
VVRHQLLKT	A*02	COX7C	cytochrome c oxidase subunit VIIc	n	1.5	0.7	1.4	0.9	1.1	2.3
DRLNKKVVL	B*14	SNRNP200	small nuclear ribonucleoprotein 200kDa (U5)	n	2.5	1.9	2.5	1.4	2.5	0.9
FSDEGGWLTRL	A*01	SQSTM1	sequestosome 1	(17)	3.2	0.6	0.9	1.0	0.6	1.3
YLLPAIVHI	A*02	DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	n	1.5	0.9	1.9	1.1	1.7	1.1
LLPAGWILSHL	A*02	COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	n	1.2	0.8	1.3	0.9	0.8	1.2
ERIDTRNEL	B*14	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	16912156	1.1	1.1	1.9	1.7	1.1	0.7
LQTTRQEL	B*14	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	n	2.5	2.8	3.0	2.6	1.6	1.7
NRSIHRVF	B*14	PNPLA6	patatin-like phospholipase domain	n	1.0	1.3	2.6	0.7	0.9	1.0

			containing 6							
NLFQHQII	A*02	ZNF7	zinc finger protein 7	n	6.1	4.6	4.6	4.0	3.7	4.3
VRHGRSLAL	B*14	GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	n	1.7	2.5	2.6	4.0	2.1	2.8
LIDVGFTDDV	A*02	KIAA0174 / IST1	KIAA0174 (MAPK activating protein PM28)	19001599	1.3	1.1	1.1	0.9	1.2	1.1
NPLEHKTI	B*35	ARHGAP26	Rho GTPase activating protein 26	10908648	1.4	2.0	2.1	0.7	2.0	0.4
KTDLHNEGY	A*01	RFTN1	raftlin, lipid raft linker 1	n	0.7	0.2	1.4	0.4	2.1	0.4
SRVIRNAL	B*14	NCKAP1L	NCK-associated protein 1-like	17875758	9.2	3.0	18.4	8.6	18.4	9.8
SMVKHIAL	A*02	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	18688030	0.6	111.4	0.5	0.3	1.6	0.5
DRLLALNSL	B*14	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	(49) - (51)	2.5	4.9	1.4	2.1	1.0	1.5
ALPSRILLWK	A*03	MXRA8	matrix-remodelling associated 8	n	1.2	0.3	1.9	0.2	8.6	1.1
GEHTEALSKK	artefact	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	n	0.1	0.0	0.1	0.0	0.4	0.6
HIHKSLIGK	A*03	H2AFV	H2A histone family, member V	n	0.8	2.5	1.4	1.0	1.4	3.0
IIYKGGTSR	A*03	GSN	gelsolin (amyloidosis, Finnish type)	9921973	1.1	0.6	2.8	0.6	3.7	1.6
EEYTKKLNTQ	n.a.	APOA1	apolipoprotein A-I	n	0.6	2.6	1.6	0.5	3.2	3.5
KASGTLREY	n.a.	RPL18A	ribosomal protein L18a	n	0.9	0.8	0.5	0.8	0.6	0.5
ATYHGSFSTK	A*03	COL6A3	collagen, type VI, alpha 3	n	1.6	0.6	2.0	0.6	3.2	2.0
KLDPVPAAR	A*03	PJA1	praja 1	n	1.3	1.4	1.6	0.9	1.2	2.1
EEVHDLERKY	B*44	NAP1L4	nucleosome assembly protein 1-like 4	n	3.2	3.0	2.6	2.5	2.1	2.8
QLYWSHPRK	A*03	RPS29	ribosomal protein S29	12705879	0.7	0.7	0.6	0.8	0.7	0.6
QIFVKTLTGK	A*03	RPS27A	ribosomal protein S27a	1660345	1.3	1.2	1.1	1.1	1.2	1.3
YYRYPTGESY	A*29	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	16115917	0.5	0.2	0.7	0.4	0.4	0.1
NVIRDAVTY	A*03	HIST2H4B	histone cluster 2, H4b	n	0.3	0.2	2.5	0.4	1.1	0.3
GTMTGMLYK	A*03	TIMM23B	translocase of inner mitochondrial membrane 23 homolog B (yeast)	n	1.2	1.6	1.5	1.9	1.6	1.1
KLLNYAPLEK	A*03	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	n	1.7	2.5	3.0	4.0	1.5	1.7
IIAIPTGVK	A*03	MT-COI	mitochondrially encoded cytochrome c oxidase I	n	n.a.					
GVAPFTIAR	A*03	COL6A3	collagen, type VI, alpha 3	n	1.6	0.6	2.0	0.6	3.2	2.0
NEVSKIVQTY	B*44	ACTN1	actinin, alpha 1	n	2.3	2.8	2.8	3.0	2.3	2.0
RLFVGSIPK	A*03	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	19137262	3.0	6.5	1.7	2.0	2.5	7.0

AYVHMVTHF	A*29	TMBIM6	transmembrane BAX inhibitor motif containing 6	16353209	0.8	0.7	1.4	0.8	0.8	0.7
GVAPFTIAR	A*03	COL6A3	collagen, type VI, alpha 3	n	1.6	0.6	2.0	0.6	3.2	2.0
VTYVPVTTFK	A*03	RPL31	ribosomal protein L31	n	1.6	1.7	1.5	0.4	1.1	1.1
GEHTLLVTV	B*49	C7orf59	chromosome 7 open reading frame 59	n	n.a.					
REYQDLLNV	B*49	INA	internexin neuronal intermediate filament protein, alpha	12209604	3.0	0.1	0.4	0.5	0.4	0.1
NYIDKVRFL	A*29	VIM	vimentin	n	0.5	0.2	0.9	0.4	1.5	0.5
KIADRFLLY	A*03	LMO4	LIM domain only 4	n	3.7	1.1	2.0	3.7	2.8	3.7
ALPSRILLWK	A*03	MXRA8	matrix-remodelling associated 8	n	1.2	0.3	1.9	0.2	8.6	1.1
SEMHSFIQI	B*49	PYHIN1	pyrin and HIN domain family, member 1	15122330	1.1	0.4	1.0	0.8	1.1	0.5
MPVGPDAILRY	B*35	BAT3	HLA-B associated transcript 3	18055229	0.9	1.9	1.7	1.9	1.1	1.6
KEIFLRELI	B*49	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	17545519	0.9	1.4	2.0	2.0	1.3	0.5
APSAILPLPGQSVER	DRB1*01	ITIH4	inter-alpha (globulin) inhibitor H4	n	7.0	0.4	1.9	0.9	9.8	18.4
AILPLPGQSVER	DRB1*01	ITIH4	inter-alpha (globulin) inhibitor H4	n	7.0	0.4	1.9	0.9	9.8	18.4
PAILSEASAPIPH	DRB1*01	SDCBP	syndecan binding protein (syntenin)	18832467	0.5	0.4	0.7	0.9	0.9	0.4
ARKLIGDPNLEF	DRB1*15	RAN	RAN, member RAS oncogene family	(14), (22), (23)	1.1	1.7	1.3	1.5	0.9	0.7
WTTGTIISSQRF	DRB1*01	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	(16)	3.0	0.2	1.2	0.1	0.8	1.3
YDNEFGYSNRVVDL	DRB1*15	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	n	0.8	0.7	0.8	0.8	0.8	0.8
VVYPWTQRF	artefact	HBB	hemoglobin, beta	n	0.1	0.1	0.3	0.1	0.9	0.1
LEEFGRAFSFEAQG	DRB1*15	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	n	0.7	0.1	1.5	0.9	1.1	0.3
SGTLVLLQGARGFA	DRB1*01	CD14	CD14 molecule	n	0.5	0.1	0.9	0.3	1.6	0.2
IIVNWVNETLRE	DRB1*15	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	16287074	0.8	0.1	1.3	1.1	0.6	0.1
TRQQDLVGLVLG	DRB1*01	GSQS6193	GSQS6193	n	n.a.					
LVVYPWTQRF	artefact	HBB	hemoglobin, beta	n	0.1	0.1	0.3	0.1	0.9	0.1
LVVYPWTQRFFES	DRB1*15	HBB	hemoglobin, beta	n	0.1	0.1	0.3	0.1	0.9	0.1
FSLPIKESEIIDF	DRB1*01	RPS2	ribosomal protein S2	19138403	1.1	1.0	0.9	1.1	1.0	0.8
DDIIVNWVNETLRE	DRB1*15	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	16287074	0.8	0.1	1.3	1.1	0.6	0.1
NKMPSLSPIDKN	DRB1*15	MYO1B	myosin IB	n	1.2	1.0	2.5	0.4	1.6	0.3
VTFLLPAGWILSHLET	DRB1*01	COX8A	cytochrome c oxidase subunit 8A	n	1.2	0.8	1.3	0.9	0.8	1.2

			(ubiquitous)							
GQSVVQLQGSRVVVG	DRB1*01	ITGAM	integrin, alpha M	12485936	0.5	0.1	1.5	0.4	0.9	0.3
EPVAVLKANRVWG	DRB1*01	HEXB	hexosaminidase B (beta polypeptide)	n	1.7	1.1	3.7	5.3	2.5	1.1
LVVYPWTQRF	artefact	HBB	hemoglobin, beta	n	0.1	0.1	0.3	0.1	0.9	0.1
SSEFVAASEQFLSTM	DRB1*15	DUOX1	dual oxidase 1	18281478	2.1	0.4	2.3	1.2	0.2	0.0
FGRAFSFEAQG	DRB1*15	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	n	0.7	0.1	1.5	0.9	1.1	0.3
KTGKLVSLSAQNLVD	DRB1*01	CTSS	cathepsin S	16550604	2.6	0.9	4.3	2.5	3.5	0.3
QVTQPTVGMNFKTPRGP	DRB1*01	RPS17	ribosomal protein S17	n	0.8	0.7	0.6	0.8	0.9	0.8
GPTEEIRALHAAIGGIP	DRB1*01	NAPSA	napsin A aspartic peptidase	(15), (24)	n.a.					
SPNIVIALAGNKAFDL	DRB1*01	RAB5C	RAB5C, member RAS oncogene family	n	1.5	1.1	2.5	1.2	2.3	1.0
ANWGKVNVDEVGGEALGRL	DRB1*15	HBB	hemoglobin, beta	n	0.1	0.1	0.3	0.1	0.9	0.1
VSGTLVLLQGARGFA	DRB1*01	CD14	CD14 molecule	n	0.5	0.1	0.9	0.3	1.6	0.2