

supplementary Table 5: Results of the DAVID 6.8 database search regarding biological process (BP)

Ligandom_MHC_I (n=53)		Term	Count	%	PValue
GOTERM_BP_DIRECT		GO:0007218~neuropeptide signaling pathway	3	5,70	#####
GOTERM_BP_DIRECT		GO:0002042~cell migration involved in sprouting angiogenesis	2	3,80	#####
GOTERM_BP_DIRECT		GO:0045776~negative regulation of blood pressure	2	3,80	#####
Ligandom_MHC_II (n=123)		Term	Count	%	PValue
GOTERM_BP_DIRECT		GO:0030154~cell differentiation	7	5,7	0.060052910
GOTERM_BP_DIRECT		GO:0035556~intracellular signal transduction	6	4,9	0.095834061
GOTERM_BP_DIRECT		GO:0007268~chemical synaptic transmission	5	4,1	0.056875200
GOTERM_BP_DIRECT		GO:0035690~cellular response to drug	3	2,4	0.064804355
GOTERM_BP_DIRECT		GO:0001558~regulation of cell growth	3	2,4	0.083710410
GOTERM_BP_DIRECT		GO:0006890~retrograde vesicle-mediated transport, Golgi to ER	3	2,4	0.087310380
GOTERM_BP_DIRECT		GO:0006919~activation of cysteine-type endopeptidase activity inv	3	2,4	0.089127662
GOTERM_BP_DIRECT		GO:0060355~positive regulation of cell adhesion molecule producti	2	1,6	0.023844990
GOTERM_BP_DIRECT		GO:0060294~cilium movement involved in cell motility	2	1,6	0.035555498
GOTERM_BP_DIRECT		GO:0046512~sphingosine biosynthetic process	2	1,6	0.047126890
GOTERM_BP_DIRECT		GO:0045086~positive regulation of interleukin-2 biosynthetic proce	2	1,6	0.069858878
Neoantigenic (n=357)		Term	Count	%	PValue
GOTERM_BP_DIRECT		GO:0043547~positive regulation of GTPase activity	21	5,9	0.003465011
GOTERM_BP_DIRECT		GO:0007155~cell adhesion	19	5,3	0.001841595
GOTERM_BP_DIRECT		GO:0006955~immune response	14	3,9	0.043239300
GOTERM_BP_DIRECT		GO:0035556~intracellular signal transduction	13	3,6	0.063736696
GOTERM_BP_DIRECT		GO:0019882~antigen processing and presentation	11	3,1	4,64E+08
GOTERM_BP_DIRECT		GO:0060333~interferon-gamma-mediated signaling pathway	11	3,1	5,68E+08
GOTERM_BP_DIRECT		GO:0007268~chemical synaptic transmission	11	3,1	0.012299544
GOTERM_BP_DIRECT		GO:0007411~axon guidance	10	2,8	0.002472512
GOTERM_BP_DIRECT		GO:0098609~cell-cell adhesion	10	2,8	0.058731936
GOTERM_BP_DIRECT		GO:0016032~viral process	10	2,8	0.094343976
GOTERM_BP_DIRECT		GO:0019886~antigen processing and presentation of exogenous pe	9	2,5	2,62E+11
GOTERM_BP_DIRECT		GO:0006974~cellular response to DNA damage stimulus	9	2,5	0.035887767
GOTERM_BP_DIRECT		GO:0030198~extracellular matrix organization	8	2,2	0.066012168
GOTERM_BP_DIRECT		GO:0034220~ion transmembrane transport	8	2,2	0.087526195
GOTERM_BP_DIRECT		GO:0002504~antigen processing and presentation of peptide or pol	7	2,0	3,51E+08

supplementary Table 5: Results of the DAVID 6.8 database search regarding cellular compartment (CC)

Ligandom_MHC_I (n=53)	Term	Count	%	PValue	Genes
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	35,8	19,0	0.04356707	A8K3F7_HUM
Ligandom_MHC_II (n=123)	Term	Count	%	PValue	Genes
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	27,6	34,0	0.06844827	Q86XB2_HUM
GOTERM_CC_DIRECT	GO:0005576~extracellular region	13,0	16,0	0.07690256	F8VXR5_HUM
GOTERM_CC_DIRECT	GO:0030054~cell junction	7,3	9,0	0.00821206	D6RDX5_HUM
GOTERM_CC_DIRECT	GO:0043231~intracellular membrane-bounded organelle	6,5	8,0	0.06098284	C9J6M1_HUM
GOTERM_CC_DIRECT	GO:0000151~ubiquitin ligase complex	4,1	5,0	0.00472469	A0A087X0C6
GOTERM_CC_DIRECT	GO:0030666~endocytic vesicle membrane	2,4	3,0	0.06423374	D6RFM6_HUM
GOTERM_CC_DIRECT	GO:0030141~secretory granule	2,4	3,0	0.07835515	H0Y332_HUM
Neoantigenic (n=357)	Term	Count	%	PValue	Genes
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	32,20	115	0.00839777	253914956
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	27,70	99	0.00173449	15629141945
GOTERM_CC_DIRECT	GO:0016020~membrane	17,60	63	2,71E+11	
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	9,50	34	0.08228878	737164072
GOTERM_CC_DIRECT	GO:0009986~cell surface	7,30	26	2,08E+11	
GOTERM_CC_DIRECT	GO:0000139~Golgi membrane	5,30	19	0.02369699	3647115815
GOTERM_CC_DIRECT	GO:0005765~lysosomal membrane	4,20	15	5,12E+11	
GOTERM_CC_DIRECT	GO:0030054~cell junction	3,90	14	0.07682308	487897786
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	3,40	12	0.03509148	222155779
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	2,80	10	0.08628603	86666289
GOTERM_CC_DIRECT	GO:0042613~MHC class II protein complex	2,50	9	2,79E+07	
GOTERM_CC_DIRECT	GO:0071556~integral component of lumenal side of endo	2,50	9	3,35E+08	
GOTERM_CC_DIRECT	GO:0012507~ER to Golgi transport vesicle membrane	2,50	9	4,08E+09	
GOTERM_CC_DIRECT	GO:0030018~Z disc	2,20	8	0.00578947	670451794
GOTERM_CC_DIRECT	GO:0010008~endosome membrane	2,20	8	0.05241370	4564529595
GOTERM_CC_DIRECT	GO:0030666~endocytic vesicle membrane	2,00	7	0.00124751	35934179747
GOTERM_CC_DIRECT	GO:0030658~transport vesicle membrane	1,70	6	5,88E+10	
GOTERM_CC_DIRECT	GO:0030669~clathrin-coated endocytic vesicle membran	1,70	6	8,40E+11	
GOTERM_CC_DIRECT	GO:0032588~trans-Golgi network membrane	1,70	6	0.01759229	32861812
GOTERM_CC_DIRECT	GO:0001726~ruffle	1,70	6	0.02406304	288415928
GOTERM_CC_DIRECT	GO:0012505~endomembrane system	1,70	6	0.05695437	2031701735

supplementary Table 5: Results of the DAVID 6.8 database search regarding molecular function (MF)**Ligandom_MHC_I (n=53)** none found

Ligandom_MHC_II (n=123)	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichme	Bonferroni	Benjamini	FDR
GOTERM_MF_DIRECT	GO:0005515~protein binding	62		50,4	0.0858491094 K7ELE0_HUMA	104	8785	16881	1,1	0.9999999928	0.9765281314	6,8
GOTERM_MF_DIRECT	GO:0016874~ligase activity	7		5,7	0.0062164289 C9J6M1_HUMA	104	270	16881	4,2	0.7283630264	0.4788119594	7,6
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	5		4,1	0.0295323728 Q6PJ10_HUMA	104	191	16881	4,2	0.9980987464	0.8761165345	3,2
GOTERM_MF_DIRECT	GO:0005520~insulin-like growth factor binding	3		2,4	0.0052927192 NOV_HUMAN,	104	18	16881	27,1	0.6701495953	0.6701495953	6,5
GOTERM_MF_DIRECT	GO:0003777~microtubule motor activity	3		2,4	0.0857825048 H7C506_HUMA	104	80	16881	6,1	0.9999999927	0.990777298	6,8

Neoantigenic (n=357)	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichme	Bonferroni	Benjamini	FDR
GOTERM_MF_DIRECT	GO:0005524~ATP binding	39		10,90	0.022897646311181793	309	1495	16881	1,40	0.9999985705	0.8140497288	29,0
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	22		6,20	0.022704774934432643	309	717	16881	1,70	0.9999983968	0.8513587050	29,0
GOTERM_MF_DIRECT	GO:0004674~protein serine/threonine kinase act	13		3,60	0.043937162117497576	309	376	16881	1,90	0.9999999999	0.9068186262	48,0
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-ce	11		3,10	0.040700453795372515	309	290	16881	2,10	0.9999999999	0.9105580441	46,0
GOTERM_MF_DIRECT	GO:0042605~peptide antigen binding	8		2,20	5,36E+08				15,60			0,0008
GOTERM_MF_DIRECT	GO:0016887~ATPase activity	8		2,20	0.05099901372151747	309	183	16881	2,40	0.9999999999	0.9206900565	54,0
GOTERM_MF_DIRECT	GO:0005215~transporter activity	8		2,20	0.07746897997553727	309	202	16881	2,20	1.0	0.9464977835	69,0
GOTERM_MF_DIRECT	GO:0001618~virus receptor activity	7		2,00	0.0017299458733675617				5,50			2,5
GOTERM_MF_DIRECT	GO:0051015~actin filament binding	7		2,00	0.034132045112144724	309	132	16881	2,90	0.9999999982	0.8937430231	40,0
GOTERM_MF_DIRECT	GO:0032395~MHC class II receptor activity	6		1,70	5,06E+09				21,90			0,0074
GOTERM_MF_DIRECT	GO:0005085~guanyl-nucleotide exchange factor	6		1,70	0.06506405173825588	309	118	16881	2,80	1.0	0.9261613081	63,0
GOTERM_MF_DIRECT	GO:0003777~microtubule motor activity	5		1,40	0.058526832974908995	309	80	16881	3,40	0.9999999999	0.9181479073	59,0
GOTERM_MF_DIRECT	GO:0043621~protein self-association	4		1,10	0.05136113493993911	309	46	16881	4,80	0.9999999999	0.9052483074	54,0
GOTERM_MF_DIRECT	GO:0005518~collagen binding	4		1,10	0.09650906435900997	309	60	16881	3,60	1.0	0.9688375897	78,0
GOTERM_MF_DIRECT	GO:0046977~TAP binding	3		0,80	9,83E+11				54,60			1,4
GOTERM_MF_DIRECT	GO:0030881~beta-2-microglobulin binding	3		0,80	0.01636964075781915				14,90			22,0
GOTERM_MF_DIRECT	GO:0050321~tau-protein kinase activity	3		0,80	0.01940936334341533	309	12	16881	13,70	0.9999886661	0.8501248320	25,0

Cryptic (n=67)	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichme	Bonferroni	Benjamini	FDR
GOTERM_MF_DIRECT	GO:0005524~ATP binding	12		17,90	0.011870463182022332	59	1495	16881	2,30	0.8143233643	0.4295042420	13,0
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	12		17,90	0.09191027432081117	59	2069	16881	1,70	0.9999987521	0.8565853112	68,0
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	6		9,00	0.007708616142669461	59	359	16881	4,80	0.6641618176	0.6641618176	8,7
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	4		6,00	0.010760876199650679	59	133	16881	8,60	0.7824890825	0.5336193432	12,0
GOTERM_MF_DIRECT	GO:0005088~Ras guanyl-nucleotide exchange fa	3		4,50	0.05941500830964671	59	115	16881	7,50	0.9998225302	0.7629423086	52,0
GOTERM_MF_DIRECT	GO:0004716~receptor signaling protein tyrosine	2		3,00	0.033840657720354064	59	10	16881	57,20	0.9922039461	0.7028548083	33,0
GOTERM_MF_DIRECT	GO:0016805~dipeptidase activity	2		3,00	0.04377156529840589	59	13	16881	44,00	0.9981836760	0.7169659805	41,0