

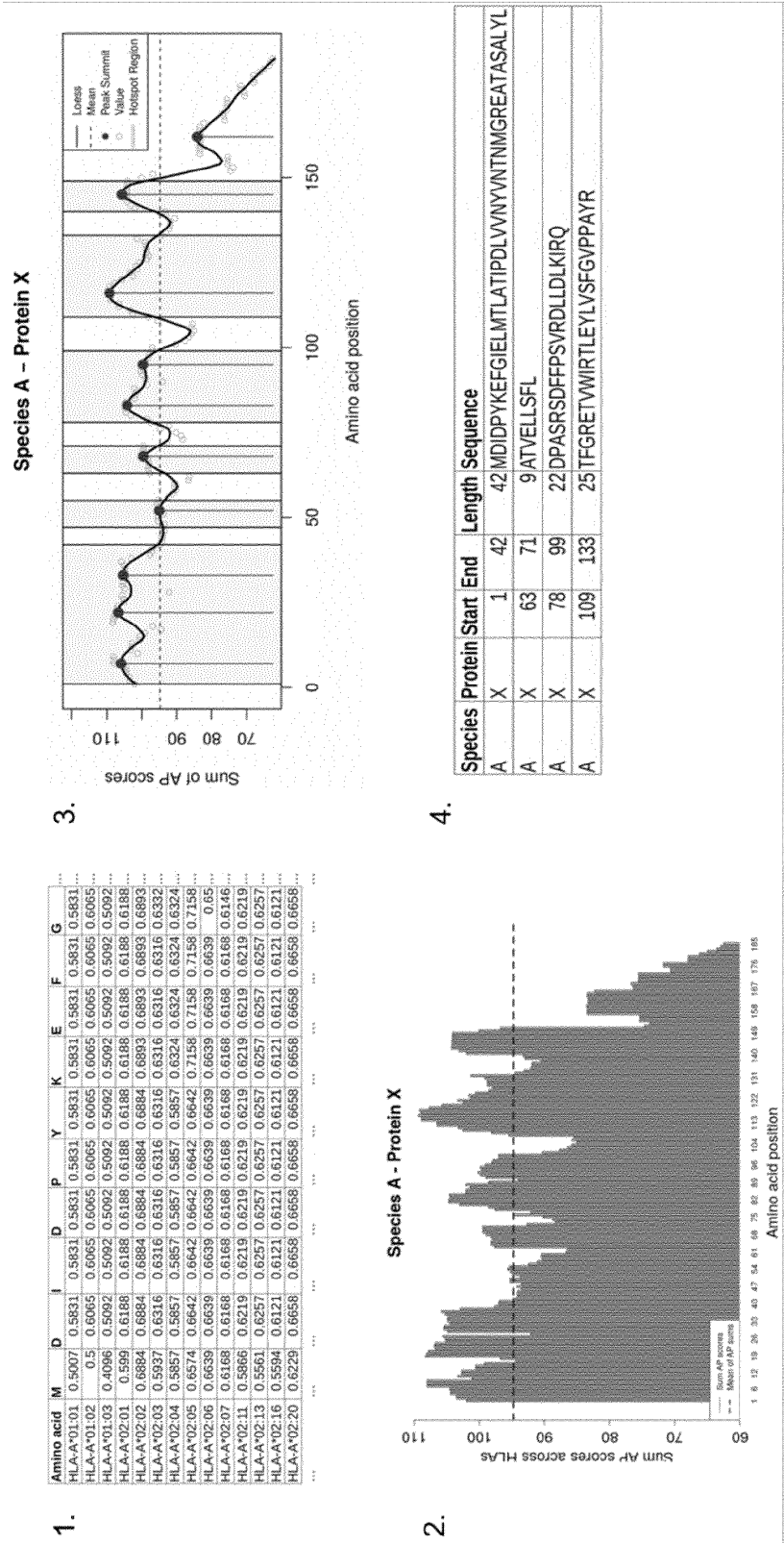


Figure 1

[illegible][illegible]

Figure 2

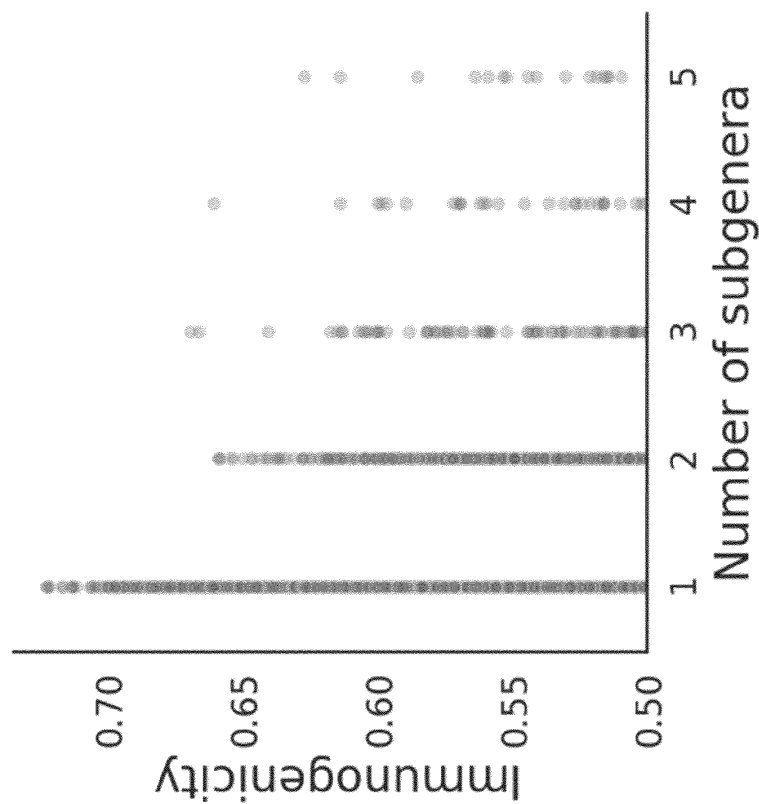


Figure 3

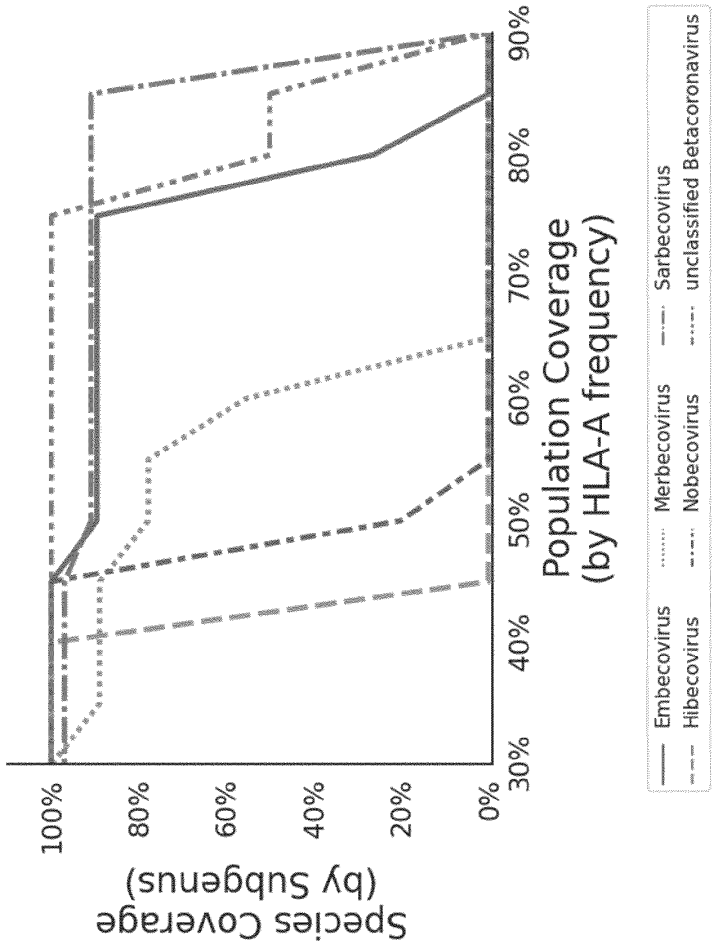


Figure 4

Polypeptide	Polypeptide aa length	SEQ ID No	Amino acid sequence	Element type	Epitope aa length
t_cell_max_marge- construct13	671	1	FVDGVPEVWSIGYHYKELGIVMNMVDVTHRYRLSLKDLLLYAADP	hotspot	45
		2	GP GPG	spacer	5
		3	NRATLQAIASEFSSLP SYAAYATAQEAY	hotspot	28
		4	GGGS	spacer	4
		5	QRVFNMYMPYVFTLLFQLCTFTKSTNSRIRASLP TTTIAKN	hotspot	40
		6	GP	spacer	2
		7	AEEHFIETVSLAGSYKDWSYSGORTELGVEFLKRGDKIVYHTVGNVIEFHMEGEV LPLEK LKTLLALRE	hotspot	100
		8	VKTIKVF TTVDNINLHTQVIDMSMTYGGQLG	spacer	5
		9	LYRLWDA YQAPPTI	hotspot	15
		10	GGGS	spacer	4
		11	GFSKFVTVQGP PGTKSHFAIGLA IYPTARVY	hotspot	34
		12	GP GPG	spacer	5
		13	LHVTYVPSQERNFTTAPAICHEGKAYFPREGV FV	hotspot	35
		14	GP GPG	spacer	5
		15	IMHVSFLVMFSGV VPLWTVLVVVV LGRHVFWFTSLCTKRTVHVGD LVFHSFQDAALQT FMLDK E V	hotspot	100
		16	LRLKREISPETYARYLALFNKYK YSGPMDTA	spacer	2
		17	TSFGPLVRKIFVDGV PFVWSTGYHFRELGVVHNQDVNLHSSRLSFKELLVYAADPAMHAASGNLLLDK	hotspot	80
		18	RTTCF SVAALTN	spacer	4
		19	GPSDASALLYLELAKRLEALEAGSKSAPKVITKKDAADAKKMRHKRVATKAYNPTQAFGLRGP	hotspot	65
		20	GP	spacer	2
		21	ARLAQMCYAGVTLDMIRINKTHYSNLIGNV PDLFTKYNYALPTNFYGCVHAYYINVT DGRYALATHYPA	hotspot	91
		22	TVITPGGROPYNSYVATV LNTV	hotspot	34
	1041		GFSKFVTVQGP PGTKSHFAIGLA IYPTARVY		

t_cell_d2-mc1000-1717	23	GP		spacer	2
	24	TFSTFEAAALCTFLLNKEMYKLRSE		hotspot	26
	25	GP GPG		spacer	5
	26	IVSVSRFNPSTWNRRFGFTQSVFKPQP		hotspot	28
	27	GP		spacer	2
	28	IVNVSLVKPTVVVYSRVKN		hotspot	19
	29	GP		spacer	2
	30	ATIPLOASLPFGWLIVGVAFVAFQSATKIALNKRWQLALYKGFQFI		hotspot	48
	31	GETALALLLLDRLNQL		hotspot	16
	32	GGGS		spacer	4
	33	VPIGGTTVVRPLVED		hotspot	15
	34	GP GPG		spacer	5
	35	KINQALHGANLRQDESVVSLY		hotspot	21
	36	GP GPG		spacer	5
	37	FAYSNRNRFYIIKLVL		hotspot	18
	38	GP		spacer	2
	39	LHVTYVPSQERNFTTAPAICHEGKAYFPREGVVF		hotspot	35
	40	GP		spacer	2
	41	LSPRWYFYLTGTGPEA		hotspot	16
	42	GGGS		spacer	4
	43	QRVFNMYMPYVFTLLFQLCTFTKSTNSRIRASLPTTIAKN		hotspot	40
	44	GGGS		spacer	4
	45	ADLYKLMGHFSWMTAFVT		hotspot	18
	46	FAGTHITMTTVYHITVSQIQLSLIKVT		hotspot	27
	47	GGGS		spacer	4
	48	RVAGSITMRSGSSPAL		hotspot	16
	49	AAIHYLNSKIVDLAQHFS		hotspot	18

		77	KIQTAPHISLAMLDIQPE	hotspot	18
		78	GGGS	spacer	4
		79	GPMLRLHLVSLWTF	hotspot	15
		80	GGGS	spacer	4
		81	VVPYYSWFSGITQFKGKEFEFAEGQGVPIAPGVPATE	hotspot	38
		82	GP	spacer	2
		83	KSAGFPFNKFGKARLYYESLSY	hotspot	22
		84	GPGPG	spacer	5
		85	ALTTFMITKDSYCKLKNLSLSDVAFNRYL	hotspot	28
		86	GPGPG	spacer	5
		87	RQKRTATKQYNVTQAFGRR	hotspot	19
		88	GPGPG	spacer	5
		89	NRATLQAIASEFSSLP SYAAYATAQEAY	hotspot	28
		90	GP	spacer	2
		91	GVAFLAVFGSATKIALNKRWQLAL	hotspot	25
		92	GPGPG	spacer	5
		93	QNKGLFYTQVYKNMAYYRSLTF	hotspot	22
t_cell_d3-mm11-104	1021	94	QGTDYKHWPIAQAFAPSASAFFGMSRIGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDAYK TFPPTTE	hotspot	74
		95	GP	spacer	2
		96	TGDSNNYMLTYNKVENMTPRDLGACIDCSARHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAA KKNNLPFKLTCTTRQVNVNVTTKIALKGGKI	hotspot	100
		97	GPGPG	spacer	5
		98	LFSTVFPLTSFGLVRKIFVDGVFPVVSTGYHFRELGVVHNQDVNLHSSRLSFKELLVYAADPAMHAAS GNLLLDKRTTCFSVAALTNNVAFQTVKPGNF	hotspot	100
		99	GPGPG	spacer	5
		100	NDVSFLAHIQWVMVMTPLVPFWITIYIICISTKHFWFFSNYLKRRVVFNGVVSFSTFEEAALCTFLLNK EMYLKLRSDVLLPFTQYNRYLALYNKYKF	hotspot	100
		101	GP	spacer	2
		102	LPSLATVAYFNMYMPASWWMRIMTWLDMVDTSLKDKCVMYASAVVLLIMTARTVYDDGARRVWT LMNVLTLYKVVYGNALDQAIMMWALISVTSN	hotspot	100

		103	GP		spacer	2
		104		RATLQAIASEFSSLPSSYAAFATAQEA YEQAVANGDSEV LK LKSLNVAKSEFDRDAAMQRKLEKMA DQAMTQMYKQARSEDKRAKVTSAMQTM LFTML	hotspot	100
		105	GGGS		spacer	4
		106		RHINAQVAKSHNIALIWNVKDFMSLEQLRKQIRSAAKNNLPFKLTCA TTRQVVNVVTTKIALKGKIV NNWLKQLIKVTLVFLFVA AIFYLITPVHVM	hotspot	100
		107	GP		spacer	2
		108		EHFIETISLAGSYKDWSSYGSGSTQLGIEFLKRGDKSVYYTSNP TTFHLDGEVITFDNLKTLLSREVRTI KVFTTVDNINLHTQVVDMSMTY GQQFGPTY	hotspot	100
		109	GGGS		spacer	4
		110		AVVYRGTTTYKLNVDYFVL TSHVMPLSAPTLPQEHYVRITGLYPTLNISDEFSSNVANYQK/GMQ KYSTLQGPPTGKSHFAIGLALYPSARIVYT	hotspot	100
		111	GP		spacer	2
		112	LPKEITVATSR TSYKLG		hotspot	19
		113		AIGKIQDSSLSTASALGKLQDVVNHNAAQALNTLVKQLSSKFGAISSVLNDILSR LDKV/AEAEVQIDRLITGR LOSLOTYVTQOLIRAAEIRASANLAATKM	hotspot	100
		114		EVVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELS LALGLKTIATHG	hotspot	57
		115	GP		spacer	2
		116		DRYFEIYDGGCLNASEVIVNNLDKSAGHPFNKFGKARVYYESLSYQEDELFA MTKRNVLP TITQMNL KYAISAKNRARTVAGVSILSTMTNRQYHQKMLKSMA	hotspot	104
		117	GP	GP	spacer	5
		118		YNSDYASKGYIANISAFQQVLYQNNVFMSEAKCWWENDINHGPHEFCSQHTMLV/KMDGDDVYLPYP DPSRILGAGCFVDDLLKTD SVLLIERFVSLAIDAY	hotspot	102
		119	GP		spacer	2
		120		EYKGPVTDV FYKETS YTTTIKPVS YKLDGVTYTIEIEPKLDGYYKKONAYVENTSITIKKPNELS LALGLKT IATHGIAAINSVPWSKILAYVKPFLGQAA	hotspot	100
		121	GP		spacer	2
		122		AEHFIETVSLAGSYKDWSSYGQRTELGVEFLKRGDKIVYHTVGNVIEFHMEGEV LPLEKLKTL LALRE VKTIKVF TTTVDNINLHTQVIDMSMTY GQQLG	hotspot	100
		123	GP	GP	spacer	5
		124		NARDGCVPLNIPLTTAAKLMVVVPDYGYKNTCEGNTFTYASALWEIQVVDADSKIVQLSEINMDNS QNLAWPLIVTALRANS AVKLQNNELSPVALR	hotspot	100
		125	GGGS		spacer	4
		126		PIEFHLDGEVLP LDKLSLSREVKTIKVFTTVDNTNLHTQLVDMSV TYGQHFQPTY	hotspot	58
		127	GP		spacer	2
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		128	KMADQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRKLNDALNNIINNARDGCVPLNIPLTTAAKL MVVVPDYGTYKNTCDGNTFTYASALWEIQVV	hotspot	100
		129	GGPG	spacer	5
		130	VSLIWNVKDYMSLSEQLRKQIRSAAKNNIPRLTCATTRQVV	hotspot	43
		131	GP	spacer	2
		132	LAYMLFTKFFYLLGLSAIMQVFFGYFASHFISN	hotspot	33
		133	GGGS	spacer	4
		134	VLKLLKSLNVAKSEFDRDAAMQRKLEKMADQAMTQMYKQARSEDKRAKVTSAMQTMFTML	hotspot	62
		135	KMADQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRKLNDALNNIINNARDGCVPLNIPLTTAAKL MVVVPDYGTYKNTCDGNTFTYASALWEIQVV	hotspot	100
		136	GGPG	spacer	5
		137	HHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNFTFTRLQSLNVAYNVNVNKGHFDGH	hotspot	60
		138	GP	spacer	2
		139	LHVTVPSQERNFTTAPAICHEGKAYFPREGVVF	hotspot	35
		140	GP	spacer	2
		141	TSFGPLVRKIFVDGVFVSTGYHFRELGVVHNQDVNLHSSRLSFKELLYAADPAMHAASGNLLLDK RTTCFSAALTN	hotspot	80
		142	GP	spacer	2
		143	VFISPYNSQNAVASKILGLPTQTVDSSQGSEYDYVIFTQTETAHSCNVNRFNVAITRAKIGILCIMSDDRD LYDKLQFTSLEIPRRNVATLQAEENVTLGFKD	hotspot	102
		144	GGGS	spacer	4
		145	EYKGPVTDVFKETSYTTTIKPVSYKLDGVTYTEIEPKLDGYKKDNAYVENTSITIKPNELSLALGLKT IATHGIAAINSVPWSKILAYVKPFLGQAA	hotspot	100
		146	GGGS	spacer	4
		147	NARDGCVPLNIPLTTAAKLMVVVPDYGTYKNTCEGNTFTYASALWEIQVVDAADSKIVQLSEINMDNS QNLAWPLVLTALRANSV/KLQNNELSPVALR	hotspot	100
		148	GGPG	spacer	5
		149	AEHFIEVSLAGSYKDWSYSGQRTLGVEFLKRGDKIVYHTVGNVIEFHMEGEVLEPLEKLTLLALRE VKTIKVTFTVDNINLHTQVIDMSMTYGQQLG	hotspot	100
		150	YNSDYASKGYIANISAFQQVLYYQNNVFMSEAKCWWENDINHGHPHEFCSQHTMLVKMDGDDVYLPYP DPSRILGAGCFVDDLLKTDSVLLIERFVSLAIDAY	hotspot	102
		151	GGPG	spacer	5
		152	DRYFEIYDGGCLNASEVIVNLDKSGAGHPFNKFGKARVYVESLSYQEDELFAMTKRNVLPTITQMNL KYAISAKNRARTVAGVSILSTMTNRQYHQKMLKSMA	hotspot	104
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t_oeil_d5-mm20-620-wf	1378		153	PIEFHLDGEVLPDLKLSLLSREVKTIKVFTTVDNTNLHTQLVDMSVTYGQHFGPTY	hotspot	58
			154	GP	spacer	2
			155	AEHFHETVSLAGSYKDWSYSGQRTELGVEFLKRGDKIVYHTVGNVIEFHMEGEVLPLEKLKTLALRE	hotspot	100
			156	VKTIKVFTTVDNINLHTQVIDMSMTYGGQLG	spacer	2
			157	HHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNTFTRLQSLNVAYNVNVKGFHFDGH	hotspot	60
			158	GP	spacer	2
			159	LAYMLFTKFFYLLGLSAIMQVFFGYFASHFISN	hotspot	33
			160	GGGS	spacer	4
			161	TKRNVLPITITQMNLKYAISAKNRARTVAGVSI	hotspot	32
			162	GP	spacer	2
			163	YNSDYASKGYIANISAFQQVLYYQNNVFMSEAKCWENDINHGPFCSQHTMLVKMDGDDVYLPYP	hotspot	102
			164	DPSRILGAGCFVDDLLKTDSVLLIERFVSLAIDAY	spacer	2
			165	GLDSLDSYPALETIQVTISSYKDLDT	hotspot	26
			166	GP	spacer	2
			167	ALTTFMITKDSYCKLKNLSLSDVAFNRYL	hotspot	28
			168	GP GPG	spacer	5
			169	PAYSFLPGVYVFLYLYTFYFTNDVSLAHLQWFAMFSPVFWIT	hotspot	46
			170	GP GPG	spacer	5
			171	NARDGCVPLNIIPLTAAKLMVVPDYGYKNTCEGNTFTTYASALWEIQVVDADSKIVQLSEINMDNIS	hotspot	100
			172	QNLAWPLIVTALRANSVAVKQNNELSPVALR	hotspot	57
			173	EVVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELSLALGLKTIATHG	spacer	4
			174	TSFGPLVRKIFVDGVPFWSTGYHFRFELGVWHNQDVNLHSSRLSFKELLYAADPAMHAASGNLLLDK	hotspot	80
			175	RTTCFSVAALTN	spacer	5
			176	GP GPG	hotspot	100
			177	EKGPFHFCSQHTMLVKMDGDEVYLPYPDPSRILGAGCFVDDLLKTDSVLLIERFVSLAIDAYPLVHHEN	spacer	5
				PEYQNVFRVYLEYIKKLYNDLGNQILDYSYV		
				GP GPG		

t_cell_d3-mc10-1375	937	178	KMADQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRKLNDALNNIINNARDGCVPLNIPLTTAAKL MVVVPDYGTYKNTCDGNTFTYASALWEIQVV	hotspot	100
		179	GP GPG	spacer	5
		180	DRYFEIYDGGCLNASEVIVNNDKSAGHPFNKFGKARVYVESLSYQEQDELFAMTKRNVLPTITQMNL KYAISAKNRARTVAGVSILSTMTNRQYHQMLKMSMA	hotspot	104
		181	GGGS	spacer	4
		182	RTVAGVSCSTMTRQFHQKLLKSIAATRGATVVGTSKFYGGWHNMMLKTVYSDVE	hotspot	56
		183	GP GPG	spacer	5
		184	EYKGPVTDVYFKETSYTTTIKPVSYKLDGVITYTEIEPKLDGYYKKONAYVENTSITIKPNELSLALGLKT IATHGIAAINSVPWSKILAYVKPFLGQAA	hotspot	100
		185	GP	spacer	2
		186	VSLIWNVKDYMSLSEQLRKQIRSAAKKNNIPRLTCATTQQW	hotspot	43
		187	GGGS	spacer	4
		188	TFSTFEEAALCTFLLNKEMYLKRSE	hotspot	26
		189	GP GPG	spacer	5
		190	VLLKLLKSLNVAKSEFDRDAAIMQRKLEKMADQAMTQMYKQARSEDKRAKVTSAMQTMFTML	hotspot	62
		191	RATLQAIASEFSSLP SYAAFATAQAEYEQAVANGDSEWVLLKLLKSLNVAKSEFDRDAAIMQRKLEKMA DQAMTQMYKQARSEDKRAKVTSAMQTMFTML	hotspot	100
		192	GP	spacer	2
		193	AVVYRGTTTTKLVNGDYFVLTSHTVMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMQ KYSTLQGPPTGKSHFAIGLALYYP SARIVYT	hotspot	100
		194	GP GPG	spacer	5
		195	NDVSFLAHIQWVMVMTPLVPFWITIAYIICISTKHFWFFSNYLKRRVFNNGVVSFTFEEAALCTFLLNK EMYLKLRSDVLLPFTQYNRYLALYNKYKF	hotspot	100
		196	GP GPG	spacer	5
		197	EHFIETISLAGSYKDWYSYSGSTQLGIEFLKRGDKSVYVTSNPTTFHLDGEVITFDNLKTLSSLREVRTI KVFTTVDNINLHTQVVDMSMTYGGQFGPTY	hotspot	100
		198	GP GPG	spacer	5
		199	LFSTVFPLTSFGPLVRKIFVDGVPFVVSSTGYHFRELGVWHNQDVNLHSSRLSKFELLVYAADPAMHAAS GNLLDKRTTCFSVAALTNNVAFQTVKPGNF	hotspot	100
		200	GP	spacer	2
		201	LPSLATVAYFNIMVYMPASWWMRIMTWLDMVDTSLKDKDCVMYASAVVLLIMTARTVYDDGARRVWT LMNVLTLYKYVYGNALDQAISMWALISVTSN	hotspot	100
		202	GP GPG	spacer	5

			203	AIGKIQDSLSSTASALGKLQDVVNHNQAQALNTLVKQLSSKFGAISSVLNDLSRLDKVEAEVQIDRLITGR LQSLQTYVTQQLIRAAEIRASANLAATKM	hotspot	100
			204	GP	spacer	2
			205	QSYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYF ASTEKSNIIRGWIFGTTLDSK	hotspot	88
			206	LPKEITVATSRTLSSYYKLG	hotspot	19
			207	GGGS	spacer	4
			208	RHINAQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKNNLPFKLTCAATTRQVVNVVTTKIALKGGKIV NNWLKQLIKVTLVFLFAAIFYLITPVHVM	hotspot	100
			209	DVLISSIVRQLFKPL	hotspot	15
			210	GGGS	spacer	4
			211	LHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVF	hotspot	35
			212	GP GPG	spacer	5
			213	AEHFIEVSLAGSYKDWSYSGQRTLGVEFLKRGDKIVYHTVGNVIEFHMEGEVLPLEKLTLLALRE VKTIKVFTTVDNINLHTQVIDMSMTYGGQLG	hotspot	100
			214	GP GPG	spacer	5
			215	LPKEITVATSRTLSSYYKLG	hotspot	19
			216	GP GPG	spacer	5
			217	DRYFEIYDGGCLNASEVIVNNDKSAGHPFNKFGKARVYVESLSYQEDELFAMTKRNVLPITITQMNL KYAISAKNRARTVAGVSILSTMTNRQYHQKMLKSMA	hotspot	104
			218	LAYMLFTKFFYLLGLSAIMQVFFGYFASHFISN	hotspot	33
			219	SVLQATLSEFSLASYAELEAAQSSYQKALNSGDASPVLLKALQKAVNIAKNAYEKDKAVARKLERMA EQAMTSMYKQARAEDKKAKIVSAMQTM	hotspot	95
			220	GGGS	spacer	4
			221	KMADQAMTQMYKQARSEDKRAKVTSAMQTMFTMLRKLNDALNNIINNARDGCVPLNIPLTTAAKL MVVVPDYGTYNKTCDGNFTTYASALWEIQQVV	hotspot	100
			222	GGGS	spacer	4
			223	HHANEYRQYLDAYNMMISAGFSLWIYKQFDTYNLWNFTFTRLQSLNVNAYNVNKGHFDGH	hotspot	60
			224	GP GPG	spacer	5
			225	NRATLQAIASEFSSLPYAAYATAQEAY	hotspot	28
			226	GP GPG	spacer	5
			227	YNSDYASKGYIANISAFQQVLVYQNNVFMSEAKCWENDINHGPHFQCSQHTMLVKMDGDDVYLPYP DPSRILGAGCFVDDLKTDVSLIERFVSLAIDAY	hotspot	102
t_cell_d4-mc20-393	1251					

	228	GP		spacer	2
	229	TSLEIPRRNVATLQAENVTLGLFKDCSKIITGLHPTQAPTHLSVDIKFKTEGLCVDIPGPKDMTYRRLISM MGFKMNYQVNGYPNMFITREEAIRHVRAW		hotspot	100
	230	GGGS		spacer	4
	231	GSNLEEEILLMLASLFGTYTWTTVLSMA		hotspot	28
	232	GGGS		spacer	4
	233	LSYFVASRFLFARTRS		hotspot	16
	234	GPGPG		spacer	5
	235	KYFKNHTSPDVLGDIS		hotspot	17
	236	GGGS		spacer	4
	237	FVDGVPFVVSIGYHYKELGIVMNMMDVDTHRYRLSKDLLLYAADP		hotspot	45
	238	GPGPG		spacer	5
	239	EYKGPVTDVFKYKETS YTTTIKPVSYKLDGVTYTEIEPKLDGYYKKDNAYVENTSITIKPNELSLALGKT IATHGIAAINSVPWSKILAYVKPFLGQAA		hotspot	100
	240	GP		spacer	2
	241	SSYMAISLKFTTSLSLHKLLOTLVLK		hotspot	26
	242	GPGPG		spacer	5
	243	RTVAGVSCSTMTRNQHFHQKLLKS/AATR GATVIGTSKFYGGWHNMLKTVYSDVE		hotspot	56
	244	GP		spacer	2
	245	VFISPYNSQNAVASKILGLPTQTVDSSQSGSEYDVYVIFTQTETTAHSCNVNRFNVATRAKIGILCIMS DRD LYDKLQFTSLEIPRRNVATLQAENVTLGLFKD		hotspot	102

Figure 5

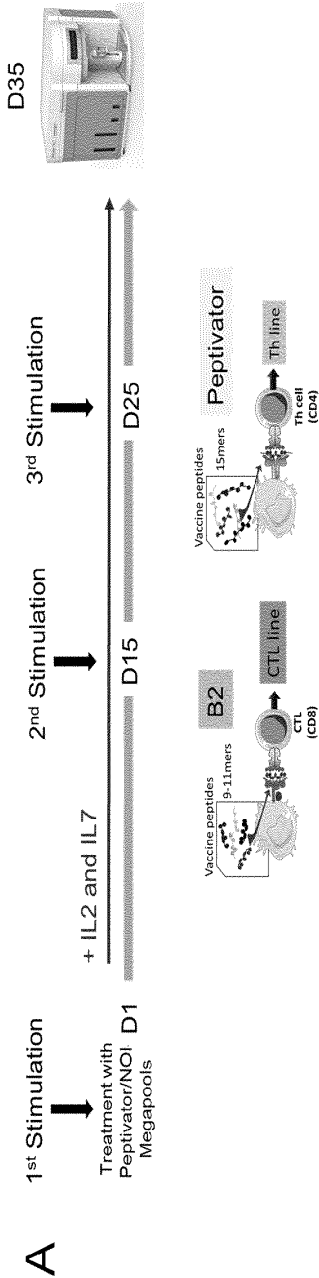


Figure 6a

B

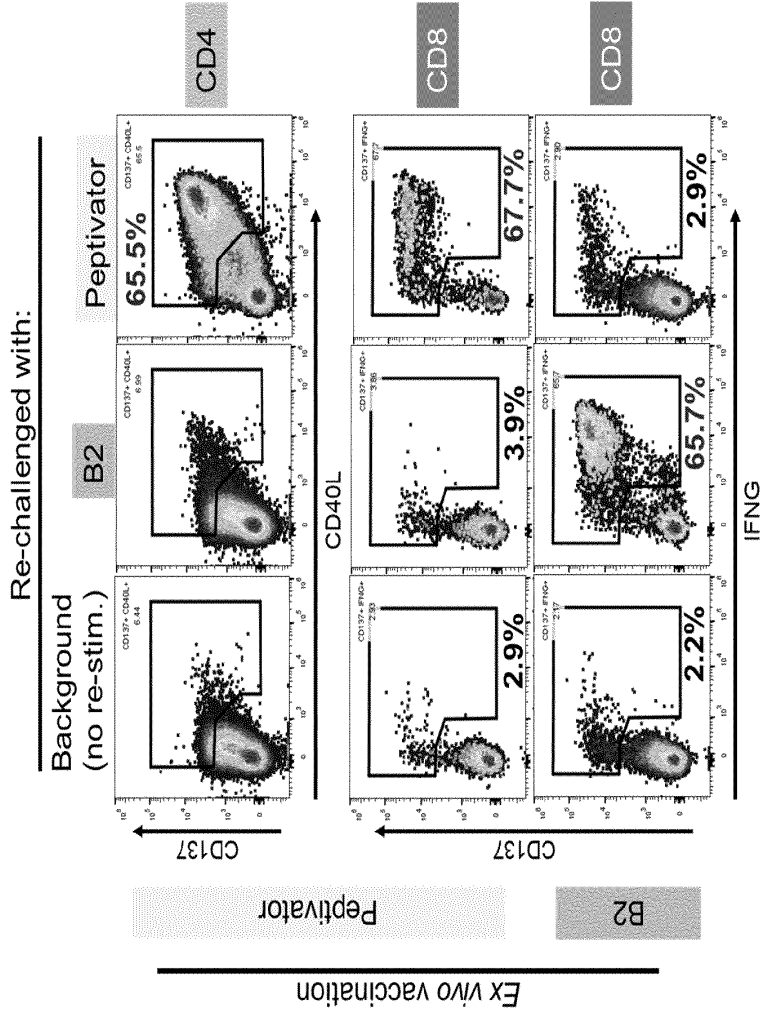


Figure 6b

Patient ID >>>																			
		BC vac 206		BC vac 207		BC vac 208		BC vac 209		BC vac 210		BC vac 211		BC vac 212		BC vac 213		BC vac 214	
Vaccine >>>		MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP
Challenge >>>		MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP	MP
CD8		BC vac 206		BC vac 207		BC vac 208		BC vac 209		BC vac 210		BC vac 211		BC vac 212		BC vac 213		BC vac 214	
CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF
-	+	+	-	72.47 %	15.00 %	15.35 %	0.00 %	4.18 %	15.96 %	26.95 %	8.95 %	29.38 %	34.57 %						
-	+	-	+	1.10 %	9.38 %	55.20 %	1.24 %	3.24 %	13.70 %	5.18 %	0.00 %	0.00 %	0.47 %						
-	+	+	+	8.04 %	8.53 %	18.38 %	85.61 %	25.56 %	13.46 %	53.86 %	5.09 %								
+	+	+	+	28.90 %	0.00 %	0.00 %	6.79 %	16.14 %	5.88 %	1.30 %	6.79 %	3.16 %							
+	+	+	-	18.47 %	5.54 %	0.00 %	0.10 %	4.79 %	2.43 %	0.32 %	5.09 %	7.16 %							
+	+	-	-	13.37 %	0.00 %	0.00 %	0.00 %	3.24 %	7.86 %	3.83 %	0.51 %	3.56 %							
-	+	-	-	12.87 %	60.13 %	24.02 %	0.00 %	29.95 %	26.95 %	65.42 %	0.00 %	45.80 %							
+	+	-	-	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %	1.57 %	0.00 %	1.21 %	0.00 %							
+	+	+	+	2.11 %	0.00 %	1.97 %	0.01 %	0.90 %	6.06 %	1.54 %	0.00 %	0.17 %							
-	+	+	+	0.02 %	0.21 %	0.00 %	1.00 %	0.00 %	0.49 %	0.00 %	0.00 %	0.01 %							
+	-	-	+	0.00 %	0.00 %	0.00 %	0.00 %	0.23 %	0.00 %	0.00 %	0.00 %	0.00 %							
-	-	-	+	0.06 %	0.00 %	0.28 %	0.58 %	0.00 %	0.00 %	0.00 %	2.04 %	0.00 %							
+	-	+	-	0.00 %	0.85 %	0.04 %	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %							
-	+	+	-	0.05 %	0.00 %	0.12 %	0.48 %	0.00 %	0.00 %	0.00 %	1.32 %	0.01 %							
+	-	+	+	0.01 %	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %							
CD4		BC vac 206		BC vac 207		BC vac 208		BC vac 209		BC vac 210		BC vac 211		BC vac 212		BC vac 213		BC vac 214	
CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF	CD40L	CD137	IFNγ	TNF
-	+	+	-	46.34 %	2.88 %	38.64 %	18.83 %	64.60 %	9.88 %	52.60 %	2.37 %	54.13 %							
-	+	-	+	0.04 %	0.00 %	0.14 %	0.07 %	0.01 %	0.27 %	0.01 %	1.22 %	0.24 %							
-	+	+	+	4.26 %	2.01 %	4.55 %	2.73 %	8.87 %	9.15 %	13.41 %	14.33 %	10.58 %							
-	+	-	+	0.22 %	1.39 %	1.12 %	0.65 %	0.39 %	1.60 %	0.65 %	1.22 %	6.53 %							
+	+	+	+	8.87 %	43.77 %	42.82 %	28.80 %	6.70 %	15.25 %	4.39 %	12.73 %	39.87 %							
+	+	+	-	0.19 %	0.00 %	0.16 %	0.36 %	0.01 %	0.56 %	0.03 %	0.00 %	0.46 %							
+	+	-	-	4.86 %	1.74 %	0.93 %	2.18 %	6.84 %	11.44 %	9.84 %	0.00 %	0.67 %							
-	+	-	-	2.55 %	21.54 %	1.04 %	2.23 %	5.20 %	8.30 %	11.63 %	7.17 %	4.21 %							
+	-	-	-	0.00 %	0.00 %	0.00 %	0.00 %	0.00 %	7.09 %	0.00 %	0.00 %	0.00 %							
+	+	+	+	56.33 %	14.24 %	44.54 %	52.22 %	59.50 %	34.34 %	36.24 %	45.11 %	19.98 %							
-	+	+	+	0.05 %	0.45 %	0.09 %	0.19 %	0.03 %	0.17 %	0.08 %	0.27 %	2.73 %							
+	+	-	+	17.91 %	6.25 %	2.30 %	5.87 %	8.67 %	7.65 %	13.13 %	12.65 %	4.33 %							
-	-	-	+	4.07 %	2.36 %	2.01 %	3.80 %	3.63 %	3.12 %	10.35 %	3.37 %	6.68 %							
+	+	-	-	0.00 %	0.00 %	0.00 %	0.27 %	0.00 %	0.16 %	0.00 %	0.65 %	0.00 %							
-	+	+	+	0.00 %	1.39 %	0.00 %	0.06 %	0.00 %	0.04 %	0.00 %	0.21 %	0.03 %							
+	+	-	+	0.65 %	4.86 %	0.29 %	0.56 %	0.15 %	0.85 %	0.43 %	1.06 %	3.70 %							

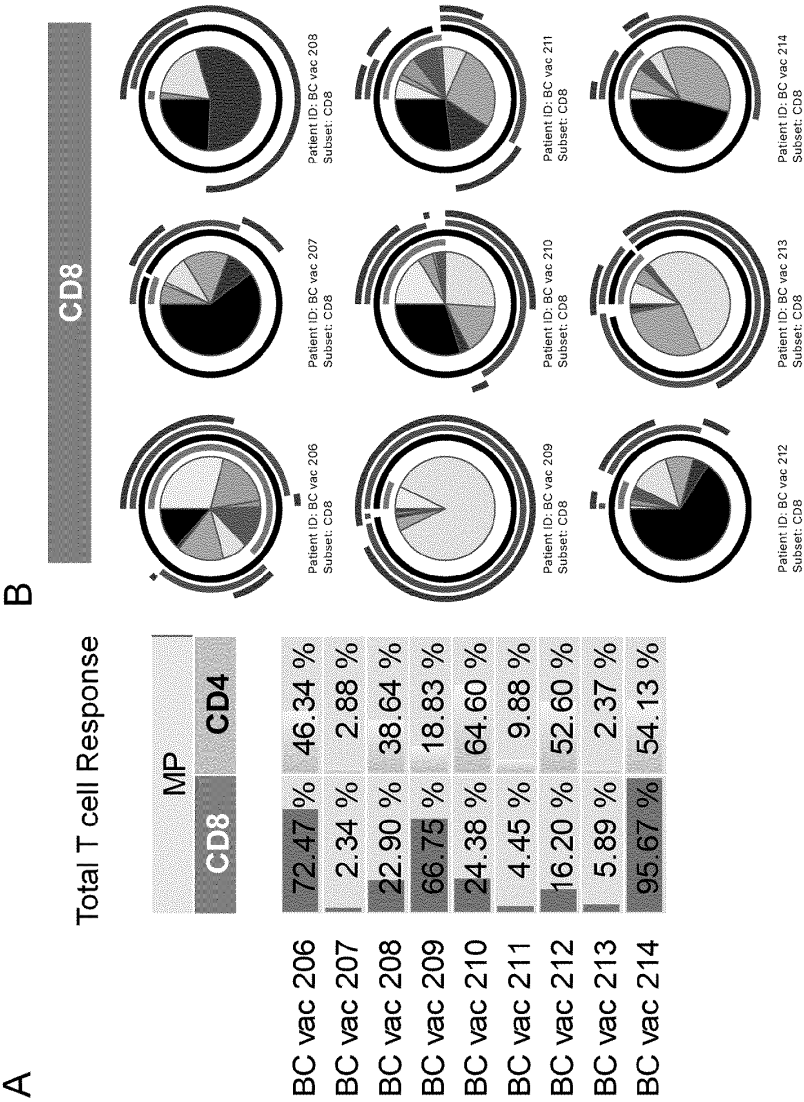


Figure 8a-b

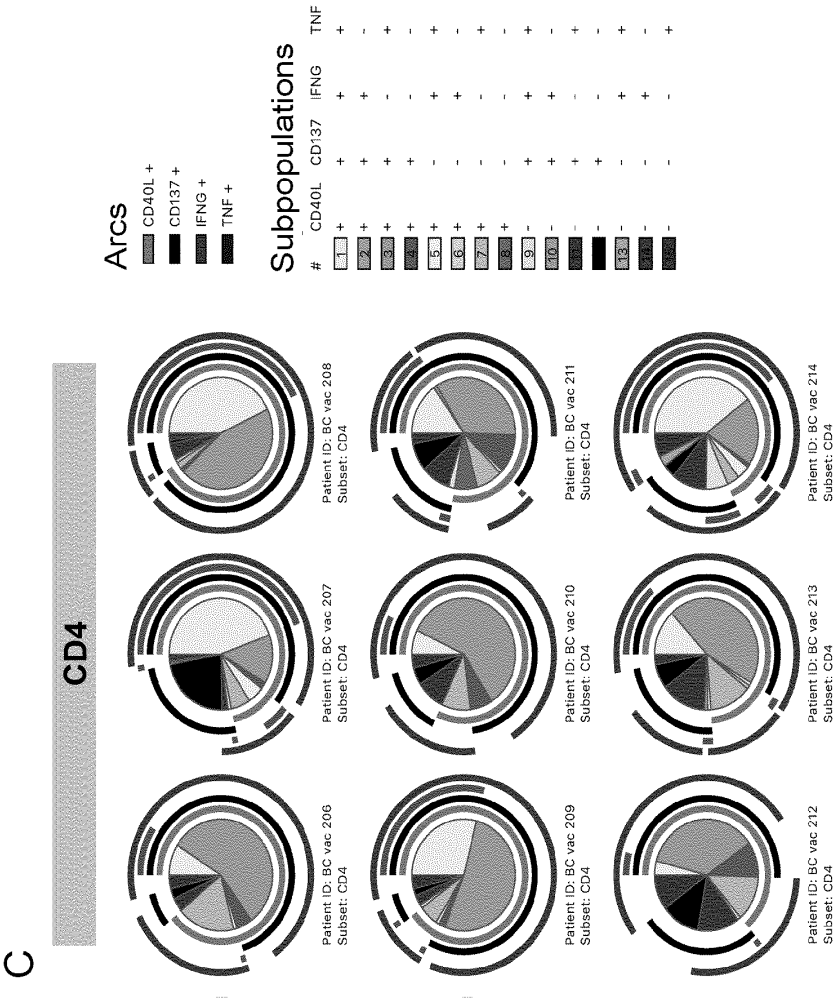


Figure 8c

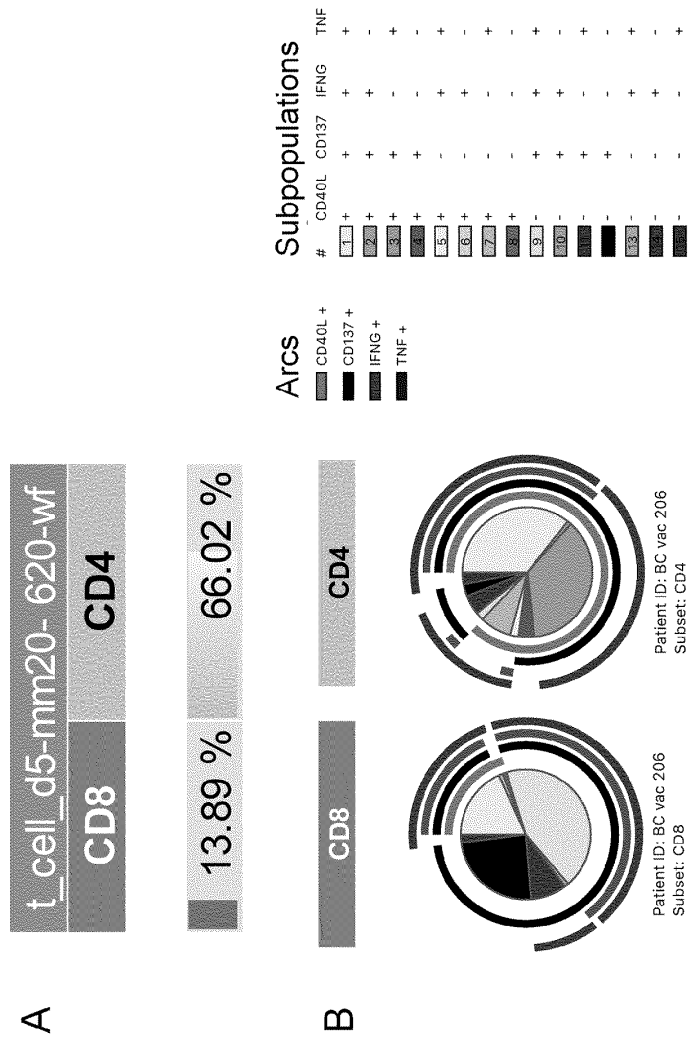


Figure 9

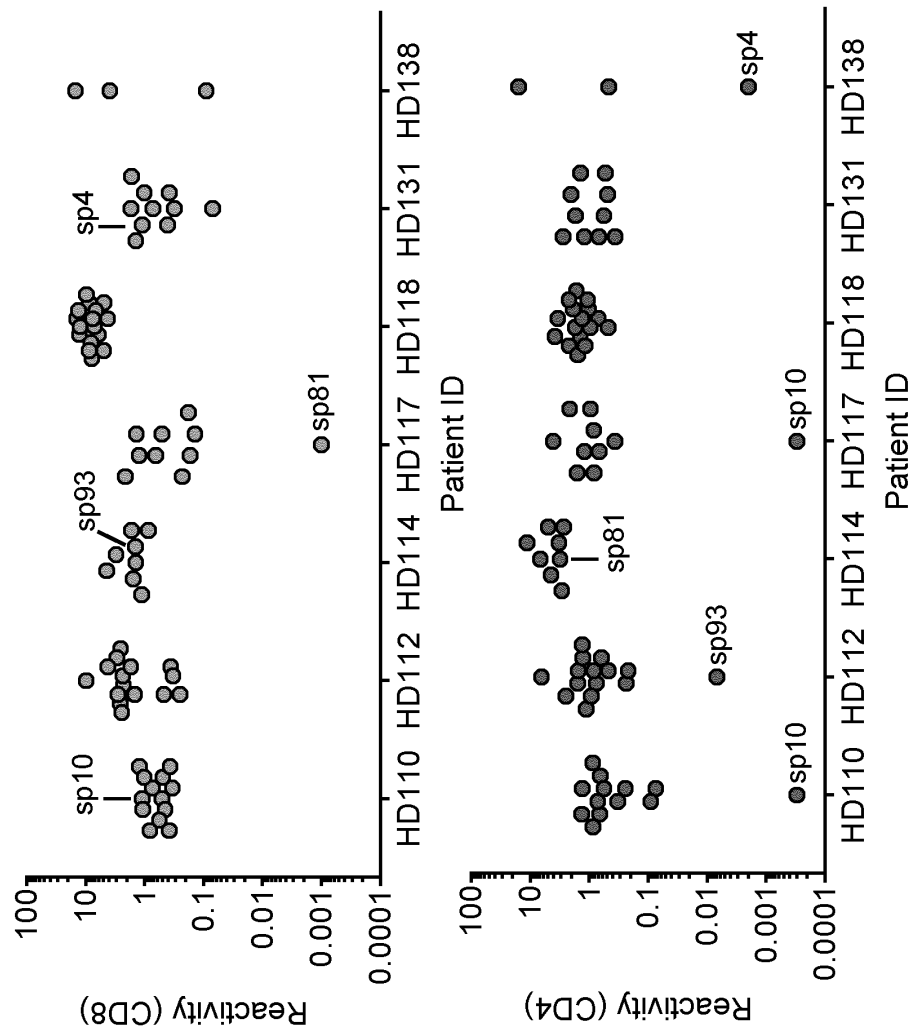


Figure 10