

Figure 1

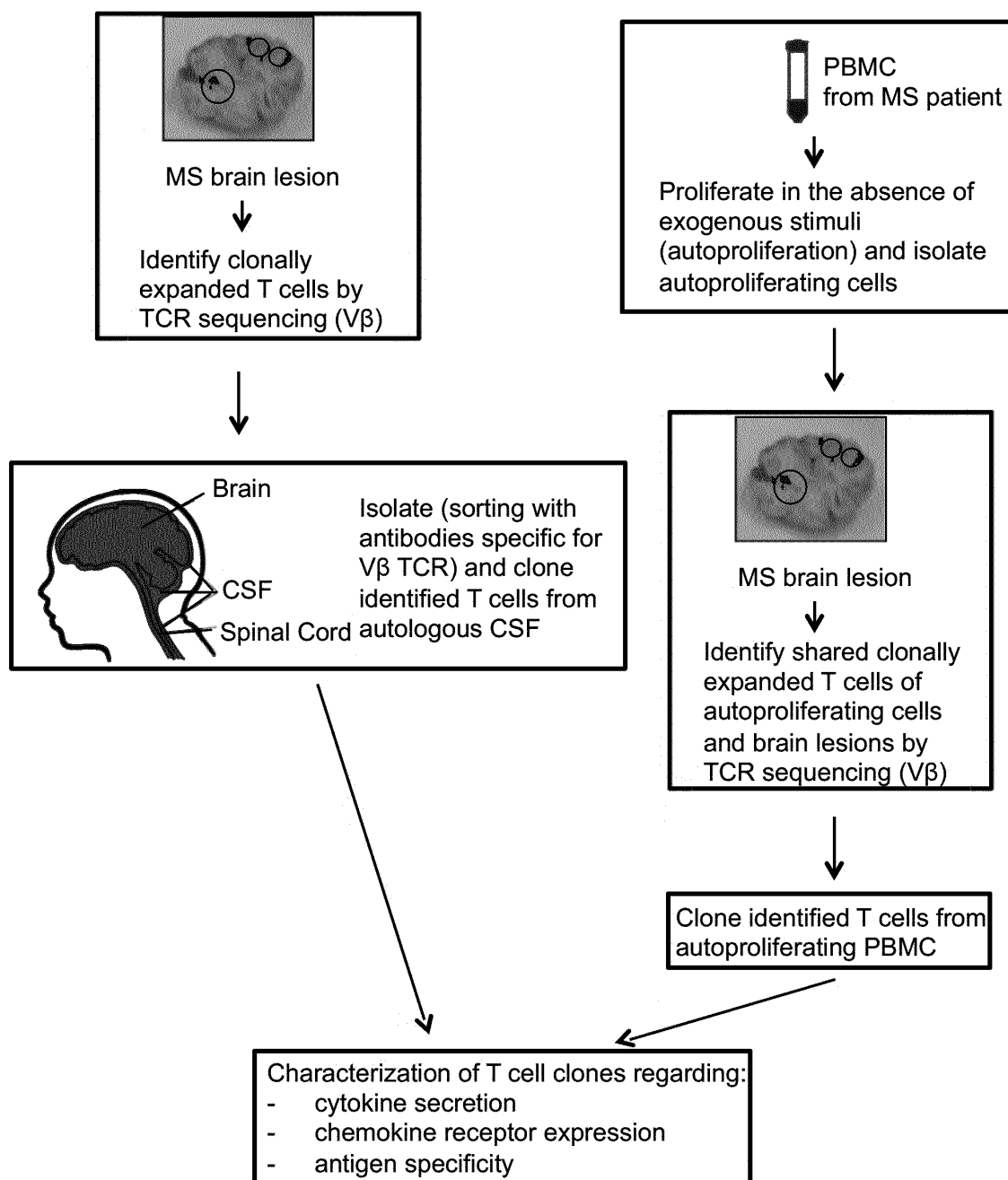
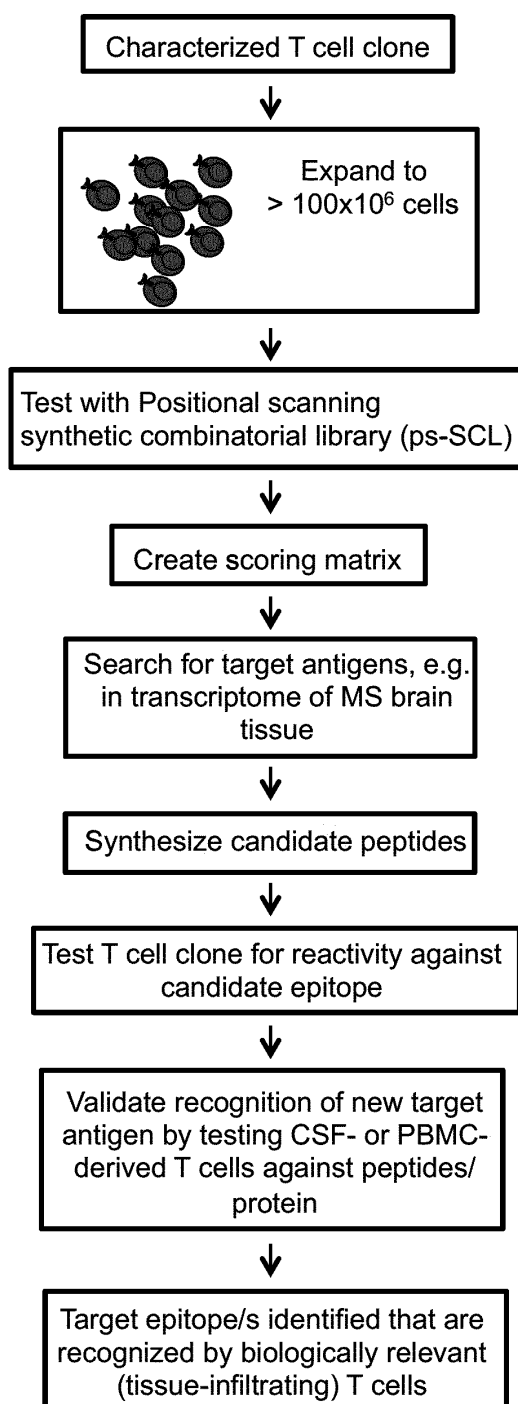
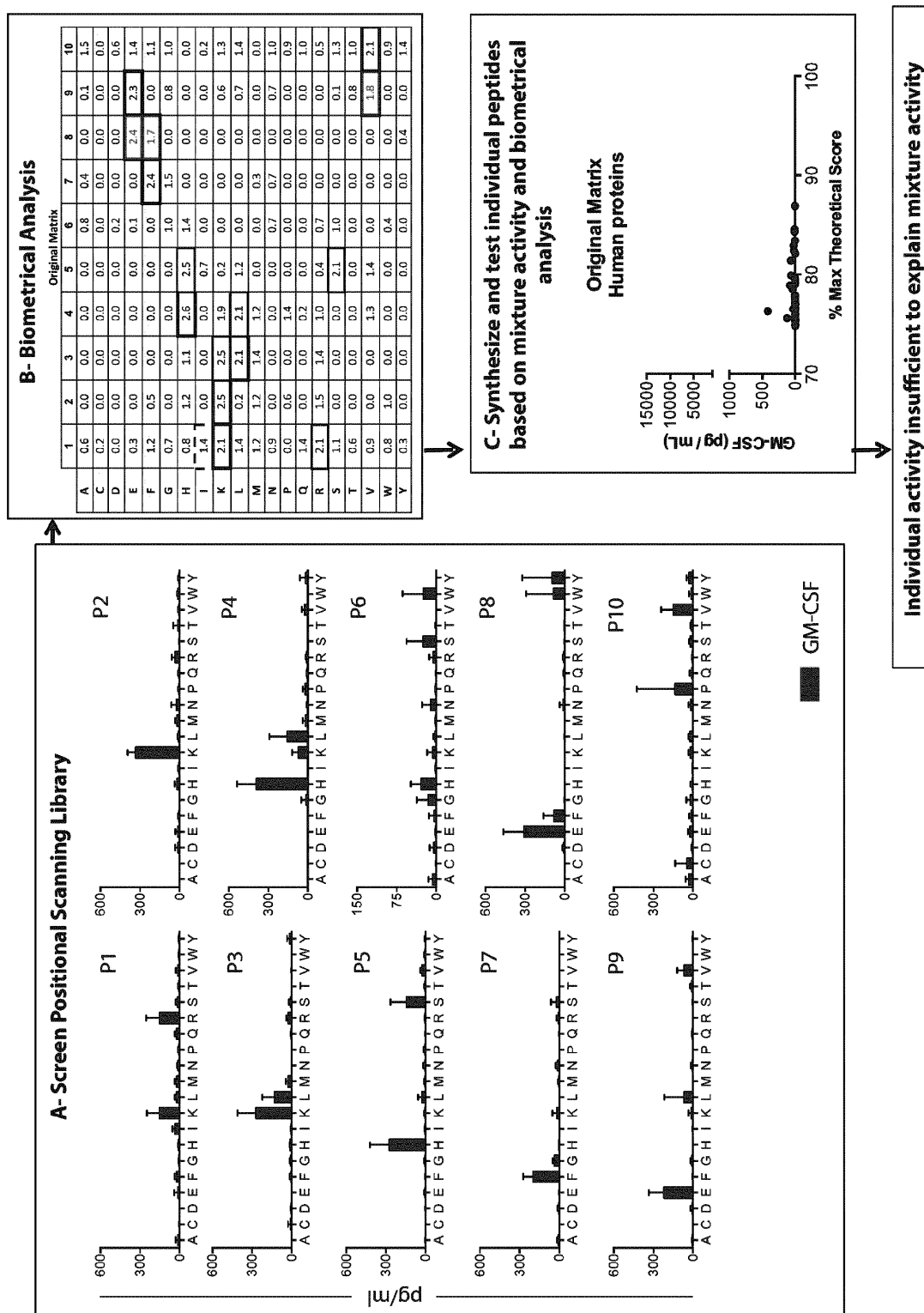


Figure 2



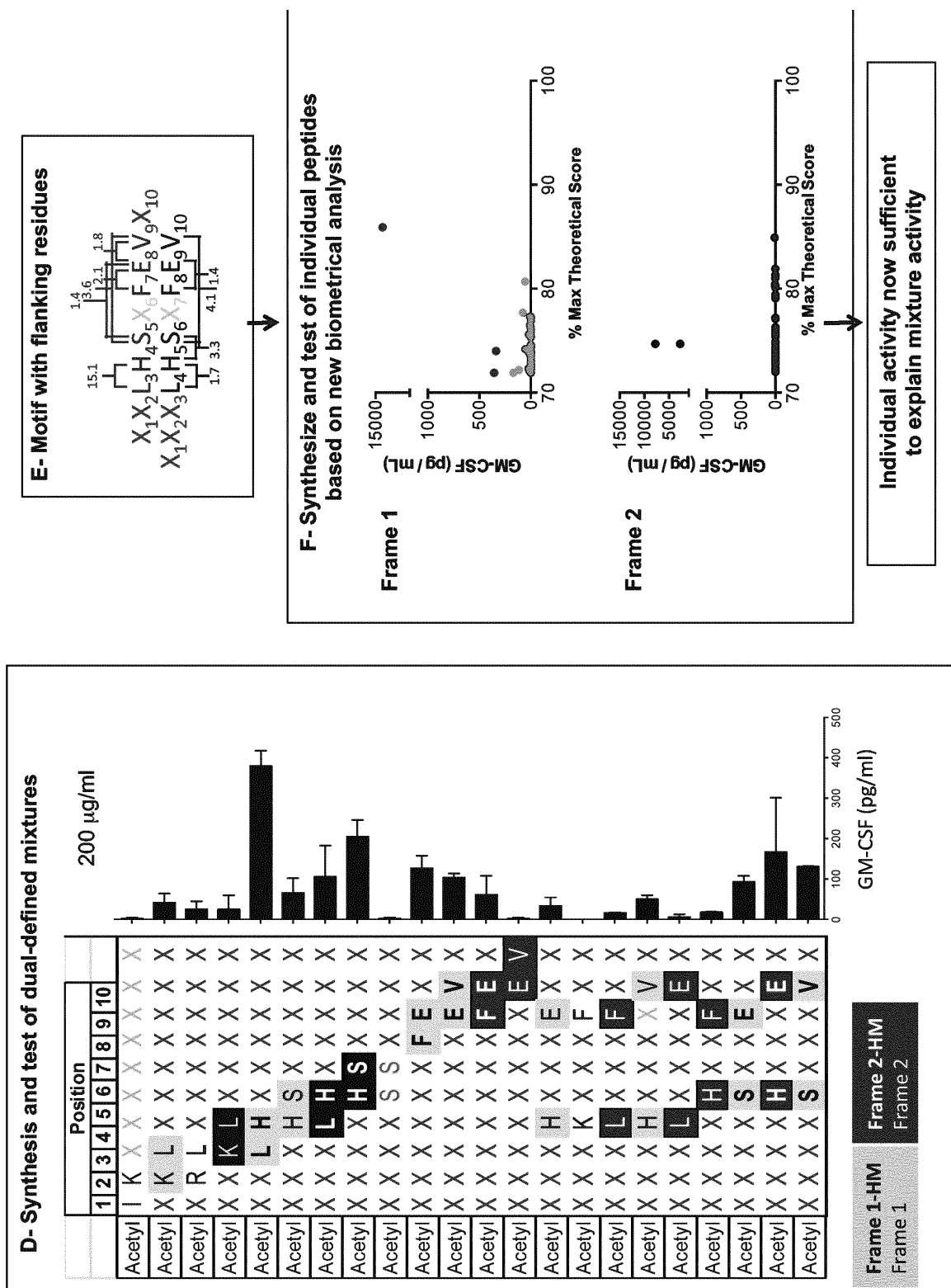


Figure 4 (I)

PEPTIDES FROM HUMAN PROTEINS		Peptides tested at 5 mg/ml Mean GM-CSF (pg/ml)
10mer	Protein	
HM Boost Frame 1		
NVLHSAFEVG	IQ13630 FCL_HUMAN GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1	12.111
RKLHSFEVKG	IQ5VST9 OBSCN_HUMAN Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3	56
LKLHSRYEL	IQ75838 CIB2_HUMAN Calcium and Integrin-binding family member 2 OS=Homo sapiens GN=CIB2 PE=1 SV=1	55
QKKHSGFEDE	IP10645 CMGA_HUMAN Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	9
LALHSVFEGL	IQ9NY26 S39A1_HUMAN Zinc transporter ZIP1 OS=Homo sapiens GN=SLC39A1 PE=1 SV=1	0
RRLHSPPEVE	IA8MT33 SYCL1_HUMAN Synaptonemal complex central element protein 1-like OS=Homo sapiens GN=SYCE1L PE=2 SV=3	0
LSLHRMFEVV	IQ8WXF8 DEDD2_HUMAN DNA-binding death effector domain-containing protein 2 OS=Homo sapiens GN=DEDD2 PE=1 SV=1	0
QKLHLHFERL	IQ9BYH1 SE6L1_HUMAN Seizure 6-like protein OS=Homo sapiens GN=SEZ6L PE=1 SV=1	10
QRLHLHFEKV	IQ53EL9 SEZ6_HUMAN Seizure protein 6 homolog OS=Homo sapiens GN=SEZ6 PE=1 SV=2	5
LLHLSIFELN	IH7C3K9 H7C3K9_HUMAN Melanophilin (Fragment) OS=Homo sapiens GN=MLPH PE=2 SV=1	0
NGLHSHSEVL	IQ9HCH5 SYTL2_HUMAN Synaptotagmin-like protein 2 OS=Homo sapiens GN=SYTL2 PE=1 SV=3	0
RRLHLHFERV	IQ6UXD5 SE6L2_HUMAN Seizure 6-like protein 2 OS=Homo sapiens GN=SEZ6L2 PE=1 SV=2	3
LRLHSPPEVT	IQ9NZ20 PA2G3_HUMAN Group 3 secretory phospholipase A2 OS=Homo sapiens GN=PLA2G3 PE=1 SV=2	0
SHLHSLFRVL	IQ8NGR2 OR1L6_HUMAN Olfactory receptor 1L6 OS=Homo sapiens GN=OR1L6 PE=2 SV=2	0
VELHSHSEVP	IQ92551 IP6K1_HUMAN Inositol hexakisphosphate kinase 1 OS=Homo sapiens GN=IP6K1 PE=1 SV=3	0
GHLHSQLEVS	IQ6ZTK2 YP015_HUMAN Putative uncharacterized protein LOC400499 OS=Homo sapiens GN=PE=2 SV=1	0
EKKVSSFEVF	IQ9UHG0 DCDC2_HUMAN Doublecortin domain-containing protein 2 OS=Homo sapiens GN=DCDC2 PE=1 SV=2	0
DGLHSSNEVL	IQ5TDP6 LGSN_HUMAN Lengsin OS=Homo sapiens GN=LGSN PE=1 SV=1	0
LSLHSLFELR	IQ6U841 S4A10_HUMAN Sodium-driven chloride bicarbonate exchanger OS=Homo sapiens GN=SLC4A10 PE=2 SV=1	0
FTPHSRFEVL	IQ9P2E5 CHPF2_HUMAN Chondroitin sulfate glucuronyltransferase OS=Homo sapiens GN=CHPF2 PE=2 SV=2	0
IKLPSSFEEKV	IQ0P6D6 CCD15_HUMAN Coiled-coil domain-containing protein 15 OS=Homo sapiens GN=CCDC15 PE=2 SV=2	54
VMLLSLFEEE	IQ9P2P5 HECW2_HUMAN E3 ubiquitin-protein ligase HECW2 OS=Homo sapiens GN=HECW2 PE=1 SV=2	0
FALHSLFEAK	IQ96PN7 TREF1_HUMAN Transcriptional-regulating factor 1 OS=Homo sapiens GN=TREF1 PE=1 SV=1	0
RKLKASFEVS	IQ8TDX9 PK1L1_HUMAN Polycystic kidney disease protein 1-like 1 OS=Homo sapiens GN=PKD1L1 PE=1 SV=1	338
KALHSDHFVK	IP52333 IAK3_HUMAN Tyrosine-protein kinase IAK3 OS=Homo sapiens GN=IAK3 PE=1 SV=2	0
KKLRSSFESS	IQ5JTI3 COA6_HUMAN Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens GN=COA6 PE=1 SV=1	23
LQLHSPFERG	IQ8TDY3 ACTT2_HUMAN Actin-related protein T2 OS=Homo sapiens GN=ACTR2 PE=2 SV=2	0
RKHSSSGEVQ	IQ8N5D0 WDTC1_HUMAN WD and tetrapeptide repeats protein 1 OS=Homo sapiens GN=WDTC1 PE=1 SV=2	4
RKLSDFPVV	IQ4LDE5 SVEP1_HUMAN Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3	7

Figure 4 (II)

KKRHSYFEKP	Q13123 RED_HUMAN Protein Red OS=Homo sapiens GN=K PE=1 SV=3	11
VHLHSFFAVG	Q86VM1 S22AG_HUMAN Solute carrier family 22 member 16 OS=Homo sapiens GN=SLC22A16 PE=1 SV=1	0
EALLSGFEVI	O60503 ADCY9_HUMAN Adenylate cyclase type 9 OS=Homo sapiens GN=ADCY9 PE=1 SV=4	0
EKLFSQFEVD	Q9NXB0 MKSI_HUMAN Meckel syndrome type 1 protein OS=Homo sapiens GN=MKS1 PE=1 SV=2	0
GDLKSGFEV	Q1XH10 SKDA1_HUMAN SKI/DACH domain-containing protein 1 OS=Homo sapiens GN=SKIDA1 PE=2 SV=1	0
KGLHSSKEVP	Q7KZF4 SND1_HUMAN Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	0
EFLASSFEVS	Q15269 PWP2_HUMAN Periodic tyrophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2	0
GVLHSEFWVV	Q96BZ4 PLD4_HUMAN Phospholipase D4 OS=Homo sapiens GN=PLD4 PE=2 SV=2	0
KQLVHHFEVD	F8WAS2 F8WAS2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=IH1 PE=2 SV=1	0
RHLHSLLEEL	A1L168 CT202_HUMAN Uncharacterized protein C20orf202 OS=Homo sapiens GN=C20orf202 PE=2 SV=2	0
RLSSGFEV	O60518 RNBP6_HUMAN Ran-binding protein 6 OS=Homo sapiens GN=RNBP6 PE=1 SV=2	24
QMLHPIFEFA	Q9BS26 ERP44_HUMAN Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	0
RRLHSTHEEL	Q03001 DYST_HUMAN Dystonin OS=Homo sapiens GN=DST PE=1 SV=4	7
RKLHWFELL	Q14997 PSME4_HUMAN Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2	116
VELHSDMEVT	P04275 VWF_HUMAN von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4	0
RKLLHRFETE	O15327 INP4B_HUMAN Type II inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4	14
NKLISEFEVE	Q8NE09 RGS22_HUMAN Regulator of G-protein signaling 22 OS=Homo sapiens GN=RGS22 PE=1 SV=3	357
SKLVSNKEVV	Q15751 HERC1_HUMAN Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens GN=HERC1 PE=1 SV=2	171
LLHLSLPVP	Q9UJ68 MSRA_HUMAN Mitochondrial peptide methionine sulfoxide reductase OS=Homo sapiens GN=MSRA PE=1 SV=1	0
RKLDVSFEER	P14780 MMP9_HUMAN Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3	0
RFKHSSTEVL	A7KAX9 RHG32_HUMAN Rho GTPase-activating protein 32 OS=Homo sapiens GN=ARHGAP32 PE=1 SV=1 EXP=0.271770	0

7/25
Figure 4 (III)

PEPTIDES FROM HUMAN PROTEINS		Peptides tested at 5 mg/ml Mean GM-CSF (pg/ml)
10mer	Protein	
HM Boost Frame 2		
RRKLHSFVEV	Q5VST9 OBSCN_HUMAN Obscurin OS=Homo sapiens GN=OBSCN PE=1 SV=3	13
RKLLSSGFEL	Q8N8A2 ANR44_HUMAN Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit B OS=Homo sapiens GN=ANKRD44 PE=1 SV=3	5
RRLSSGFEE	O60518 RNBP6_HUMAN Ran-binding protein 6 OS=Homo sapiens GN=RNBP6 PE=1 SV=2	3
RKLLHKFEET	Q96PE3 INP4A_HUMAN Type I inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4A PE=1 SV=1	3
LKLLHDFEEQ	Q98X84 TRPM6_HUMAN Transient receptor potential cation channel subfamily M member 6 OS=Homo sapiens GN=TRPM6 PE=1 SV=2	9
GLLLHSIFEL	H7C3K9 H7C3K9_HUMAN Melanophilin (Fragment) OS=Homo sapiens GN=MLPH PE=2 SV=1	0
QKLLHDFEEQ	Q96QT4 TRPM7_HUMAN Transient receptor potential cation channel subfamily M member 7 OS=Homo sapiens GN=TRPM7 PE=1 SV=1	9
QKLLSSGEEK	Q15858 SCN9A_HUMAN Sodium channel protein type 9 subunit alpha OS=Homo sapiens GN=SCN9A PE=1 SV=3	4
RKLLHSGQEA	Q5JTD0 TJAP1_HUMAN Tight junction-associated protein 1 OS=Homo sapiens GN=TJAP1 PE=1 SV=1	0
QKLVHSLFES	O15067 PUR4_HUMAN Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4	0
CYLLHSFEFF	Q4LDE5 SVEP1_HUMAN Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3	0
SKTLHSVEEK	Q8TBZ0 CC110_HUMAN Coiled-coil domain-containing protein 110 OS=Homo sapiens GN=CCDC110 PE=2 SV=1	0
LKRLHFEFEQ	Q7Z4N2 TRPM1_HUMAN Transient receptor potential cation channel subfamily M member 1 OS=Homo sapiens GN=TRPM1 PE=1 SV=2	6
VKELHSAEEG	O60941 DTNB_HUMAN Dystrobrevin beta OS=Homo sapiens GN=DTNB PE=1 SV=1	0
SLLLHSQEEK	Q8IWZ3 ANKH1_HUMAN Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1	0
AVHLHSGEEL	Q92519 TRIB2_HUMAN Tribbles homolog 2 OS=Homo sapiens GN=TRIB2 PE=2 SV=1	0
HTRLHSGEEP	Q6IV72 ZN425_HUMAN Zinc finger protein 425 OS=Homo sapiens GN=ZNF425 PE=2 SV=1	0
MPLLHAIFEV	O43592 XPOT_HUMAN Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	1
EKKRHSYFEK	Q13123 RED_HUMAN Protein Red OS=Homo sapiens GN=IK PE=1 SV=3	0
OAKLHSQEEED	Q4V328 GRAP1_HUMAN GRIP1-associated protein 1 OS=Homo sapiens GN=GRIPAP1 PE=1 SV=1	0
QQKHSQFEED	P10645 CMGA_HUMAN Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	2
LKLLHQQFEM	Q9UQ26-8 RIMS2_HUMAN Isoform 8 of Regulating synaptic membrane exocytosis protein 2 OS=Homo sapiens GN=RIMS2	0
KLLHSGVEN	Q8N1W0 YF005_HUMAN Transmembrane protein FLJ37396 OS=Homo sapiens PE=2 SV=2	2.779

Figure 4 (IV)

DNVLSAFEV	IQ13630 FCL_HUMAN GDP-L-fucose synthase OS=Homo sapiens GN=ISTA3 PE=1 SV=1	7.817
FKLHTFEV	IQ96JB1 DYH8_HUMAN Dynein heavy chain 8, axonemal OS=Homo sapiens GN=DNAH8 PE=1 SV=2	0
QAKLSFEET	IQ5TB80 CE162_HUMAN Centrosomal protein of 162 kDa OS=Homo sapiens GN=KIAA1009 PE=1 SV=2	0
SLALSHVFEF	IQ9NY26 S39A1_HUMAN Zinc transporter ZIP1 OS=Homo sapiens GN=SLC39A1 PE=1 SV=1	0
EFALHSLFEA	IQ96PN7 TREF1_HUMAN Transcriptional-regulating factor 1 OS=Homo sapiens GN=TREF1 PE=1 SV=1	0
MRHLKSFEFA	IQ7Z7H5 TMED4_HUMAN Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens GN=TMED4 PE=1 SV=1	0
QKKRHSFELES	IQ49MG5 MAP9_HUMAN Microtubule-associated protein 9 OS=Homo sapiens GN=MAP9 PE=1 SV=3	0
QKKLHHFFIG	IQ81WB1 IPRI_HUMAN Inositol 1,4,5-trisphosphate receptor-interacting protein OS=Homo sapiens GN=ITPRIP PE=1 SV=1	0
TLSLHSLFEL	IQ6U841 S4A10_HUMAN Sodium-driven chloride bicarbonate exchanger OS=Homo sapiens GN=SLC4A10 PE=2 SV=1	0
LRLHSHFEEL	IQ9UIY3 RWD2A_HUMAN RWD domain-containing protein 2A OS=Homo sapiens GN=RWD2A PE=1 SV=1	0
QKELHSHFVA	IQ9UIV8 SPB13_HUMAN Serpin B13 OS=Homo sapiens GN=SERPINB13 PE=1 SV=2	0
AWLLHSGPEG	IQ43299 AP5Z1_HUMAN AP-5 complex subunit zeta-1 OS=Homo sapiens GN=AP5Z1 PE=1 SV=2	0
TKLLHRTTEL	IQ68CJ6 SLIP_HUMAN Nuclear GTPase SLIP-GC OS=Homo sapiens GN=NUGGC PE=2 SV=3	0
FKTLSSKFEL	IQ8WWM7 ATX2L_HUMAN Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	0
KRRLHLVFEY	IQ00532 CDKL1_HUMAN Cyclin-dependent kinase-like 1 OS=Homo sapiens GN=CDKL1 PE=1 SV=5	0
EHLNLSGFEV	IA7KAX9 RHG32_HUMAN Rho GTPase-activating protein 32 OS=Homo sapiens GN=ARHGAP32 PE=1 SV=1	0
VMKLLSIFES	IQ3B7T1 EDRF1_HUMAN Erythroid differentiation-related factor 1 OS=Homo sapiens GN=EDRF1 PE=1 SV=1	0
KLELHSSFEA	IQ6TFL3 CC171_HUMAN Coiled-coil domain-containing protein 171 OS=Homo sapiens GN=CCDC171 PE=2 SV=1	0
KLP LHSSEEA	IP57721 PCBP3_HUMAN Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 PE=2 SV=2	0
LKRLLSNEEE	IQ14976 GAK_HUMAN Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=1 SV=2	0
TTRLHLSLEEK	IQ723Z0 K1C25_HUMAN Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1	0
HARLHLSLEET	IQ5T160 SYRM_HUMAN Probable arginine-tRNA ligase, mitochondrial OS=Homo sapiens GN=RARS2 PE=1 SV=1	0
LPRLHGHFEQ	IQ9UPU7 TBD2B_HUMAN TBC1 domain family member 2B OS=Homo sapiens GN=TBC1D2B PE=1 SV=2	0
VKTLHHKEEV	IQ6ZMW2 ZN782_HUMAN Zinc finger protein 782 OS=Homo sapiens GN=ZN782 PE=2 SV=1	0
SPSLHSREEA	IB7Z7H5 B7Z7H5_HUMAN Coiled-coil domain-containing protein 116 OS=Homo sapiens GN=CCDC116 PE=2 SV=1	0
PRKLHWLFEEL	IQ14997 PSME4_HUMAN Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2	0
LKLLSFAEN	IQ5W041 ARMC3_HUMAN Armadillo repeat-containing protein 3 OS=Homo sapiens GN=ARMC3 PE=2 SV=2	0

Figure 5

GDP-L-fucose synthase transcripts and peptides identified in brain tissue.

Protein	Gene ID	Transcriptome			UniProt ID	Peptide sequence	Residues	Proteome (PSM ³)				Distinct peptides #	Protein coverage %		
		RPKM ¹	LI ²	LII ²				WM	GM	WM	GM			Non-MS	Total
GDP-L-fucose synthase	TSTA3	2.17	2.02	2.67	Q13630	ILVTGGSLVGR	10 - 21	12	12	12	12	48	17	56.0	
						VVADGAGLPGEDWVFVSSK	26 - 44	12	12	12	12	48			
						DADLTDTAQR	45 - 55	12	12	12	12	48			
						VQPTHVIHLAAMVGGLFR	61 - 78	-	9	9	9	27			
						YNLDFWR	82 - 88	12	12	12	12	48			
						YNLDFWRK	82 - 89	-	-	-	1	1			
						NVHMNDNLHSAFEVGAR	90 - 107	-	13	13	13	39			
						NVHMNDNLHSAFEVGARK	90 - 108	-	-	-	3	3			
						VVSLSTCIFFDK	109 - 121	-	-	-	3	3			
						MIDVQNR	149 - 155	-	2	-	2	4			
						RMIDVQNR	148 - 155	-	-	2	2	4			
						SSGSALTWGTGNPR	200 - 214	3	-	-	-	3			
						SSGSALTWGTGNFR	200 - 215	-	-	1	-	1			
						TTYPIDETMIHNGPPHNSFGYSYAK	222 - 247	-	-	3	-	3			
						EYNEVEPIILSVGEEDVBSIK	233 - 253	-	3	-	-	3			
						TYLFDPR	291 - 297	12	12	12	12	48			
						LRTYLPDPR	289 - 297	-	-	-	2	2			
								63	87	88	95	333			
Myelin basic protein	MBP	37.20	28.97	59.21	P02586			993	871	985	865	3714	80	79.6	
	PLP1	458.31	341.43	431.91	P60201			148	153	129	157	587	13	30.6	
	MOG	-	-	-	Q16653			216	199	222	216	853	28	49.8	
	MAG	16.29	10.83	26.84	P20916			243	232	221	243	939	34	36.9	
	MOBP	14.48	11.16	19.82	Q13875			20	12	27	14	73	6	26.2	
	Oligodendrocyte myelin glycoprotein	OMG	5.21	5.07	3.26	P23515			144	155	136	155	590	13	28.8
	2',3'-cyclic-nucleotide phosphodiesterase	CNP	-	-	-	P09543			1168	985	1157	1060	4370	112	96.4

¹ RPKM, reads per kilobase of exon model per million mapped reads. ² LI and LII, active lesions in which TCC21.1 was clonally expanded. LII, inactive lesion in which TCC21.1 was not identified. ³ PSM, peptide spectrum matches. Proteome data correspond to white matter (WM) and grey matter (GM) from multiple sclerosis patients (MS, n=15) and non-MS controls (Non-MS, n=9). In bold are GDP-L-fucose synthase values.

Figure 6 (I)**GDP-L-fucose synthase, Myelin and CEF Peptides**

GDP-L-fucose synthase	
GDP-L-fucose synthase 1-15	MGEFQGS MRILVTGG
GDP-L-fucose synthase 6-20	GSMRILVTGG SGLVG
GDP-L-fucose synthase 11-25	LVTGG SGLVGKAIQK
GDP-L-fucose synthase 16-30	SGLVGKAIQKV VADG
GDP-L-fucose synthase 21-35	KAIQKV VADGAGLPG
GDP-L-fucose synthase 26-40	VVADGAGLPGEDWVF
GDP-L-fucose synthase 31-45	AGLPGEDWVFVSSKD
GDP-L-fucose synthase 36-50	EDWVFVSSKDADLTD
GDP-L-fucose synthase 41-55	VSSKDADLTDTAQTR
GDP-L-fucose synthase 46-60	ADLTDTAQTRALFEK
GDP-L-fucose synthase 51-65	TAQTRALFEKVQPTH
GDP-L-fucose synthase 56-70	ALFEKVQPTHVIHLA
GDP-L-fucose synthase 61-75	VQPTHVIHLAAMVGG
GDP-L-fucose synthase 66-80	VIHLAAMVGGLFRNI
GDP-L-fucose synthase 71-85	AMVGGLFRNIKYNLD
GDP-L-fucose synthase 76-90	LFRNIKYNLDFWRKN
GDP-L-fucose synthase 81-95	KYNLDFWRKNVHMND
GDP-L-fucose synthase 86-100	FWRKNVHMNDNVLHS
GDP-L-fucose synthase 91-105	VHMNDNVLHSAFEVG
GDP-L-fucose synthase 96-110	NVLHSAFEVGARKVV
GDP-L-fucose synthase 101-115	AFEVGARKVV SCLST
GDP-L-fucose synthase 106-120	ARKVVSCLSTC IFPD
GDP-L-fucose synthase 111-125	SCLSTC IFPDKTTYP
GDP-L-fucose synthase 116-130	CIFPDKTTYPIDETM
GDP-L-fucose synthase 121-135	KTTYPIDETMIHNGP
GDP-L-fucose synthase 126-140	IDETMIHNGPPHNSN
GDP-L-fucose synthase 131-145	IHNGPPHNSNFGYSY
GDP-L-fucose synthase 136-150	PHNSNFGYSYAKRMI
GDP-L-fucose synthase 141-155	FGYSYAKRMIDVQNR
GDP-L-fucose synthase 146-160	AKRMIDVQNRAYFQQ
GDP-L-fucose synthase 151-165	DVQNRAYFQQYGCTF
GDP-L-fucose synthase 156-170	AYFQQYGCTFTAVIP
GDP-L-fucose synthase 161-175	YGCTFTAVIPTNVFG
GDP-L-fucose synthase 166-180	TAVIPTNVFGPHDNF
GDP-L-fucose synthase 171-185	TNVFGPHDNFNIEDG
GDP-L-fucose synthase 176-190	PHDNFNIEDGHVLP
GDP-L-fucose synthase 181-195	NIEDGHVLPGLIHKV
GDP-L-fucose synthase 186-200	HVLPGLIHKVHLAKS
GDP-L-fucose synthase 191-205	LIHKVHLAKSSGSAL
GDP-L-fucose synthase 196-210	HLAKSSGSALTVWGT
GDP-L-fucose synthase 201-215	SGSALTVWGTGNPRR
GDP-L-fucose synthase 206-220	TVWGTGNPRRQFIYS
GDP-L-fucose synthase 211-225	GNPRRQFIYSLDLAQ
GDP-L-fucose synthase 216-230	QFIYSLDLAQLFIWV
GDP-L-fucose synthase 221-235	LDLAQLFIWVLRN
GDP-L-fucose synthase 226-240	LFIWVLRNREYNEVEPI
GDP-L-fucose synthase 231-245	LREYNEVEPIILSVG
GDP-L-fucose synthase 236-250	EVEPIILSVGEEDEV
GDP-L-fucose synthase 241-255	ILSVGEEDEVSIKEA
GDP-L-fucose synthase 246-260	EEDEVSIKEAAEAVV
GDP-L-fucose synthase 251-265	SIKEAAEAVVEAMDF
GDP-L-fucose synthase 256-270	AEAVVEAMDFHGEVT
GDP-L-fucose synthase 261-275	EAMDFHGEVTFDITK

Figure 6 (II)

GDP-L-fucose synthase 266-280	HGEVTFD'TTKSDGQF
GDP-L-fucose synthase 271-285	FD'TTKSDGQFKKTAS
GDP-L-fucose synthase 276-290	SDGQFKKTASNSKLR
GDP-L-fucose synthase 281-295	KKTASNSKLR'TYLPD
GDP-L-fucose synthase 286-300	NSKLR'TYLPDFRFTP
GDP-L-fucose synthase 291-305	TYLPDFRFTP'FKQAV
GDP-L-fucose synthase 296-310	FRFTP'FKQAVKETCA
GDP-L-fucose synthase 301-315	FKQAVKETCAWFTDN
GDP-L-fucose synthase 306-321	KETCAWFTDN'YEQARK
Myelin	
MOG 1-20	GQFRVIGPRHP'IRALVGDEV
MOG 35-55	MEVGWYRPP'FSRVVHLYRNGK
MBP 13-32	KYLATASTMDHARHG'FLPRH
MBP 83-99	ENPVVHFFKNI'VTPRTP
MBP 111-129	LSRFSWGAEGQR'PGFGYGG
MBP 146-170	AQGTLSKIFKL'GGRDSRSGSPMARR
PLP 139-154	HCLGKWLGH'PDKFVGI
CEFT2 Mix (CEF)	
Influenza A	FVFTLTVP'SER
Influenza A	SGPLKAEIAQ'RLEDV
Influenza A	YDVPDYASLR'SLVASS
Influenza B	PYYTGEHAKA'IGN
Tetanus	GQIGNDPNR'DIL
Influenza A	PKYVKQNTL'KLA
Influenza A	PKYVKQNTL'KLAT
Influenza A	DRLRRDQ'KS
EBV	AGLTLSLLV'ICSYLFISRG
Tetanus	QYIKANSKFI'GITEL
Tetanus	QYIKANSKFI'GITE
Tetanus	FNNFTVSF'WLRVPKVSASHLE
EBV	TSLYNLRRG'TALA
Tetanus	KFIKRYTPN'NEIDSF
Tetanus	VSIDKFRI'FCKALNPK
EBV	VPGLYSPCRA'FFNKEELL
HCMV	DKREMWMAC'IKELH
EBV	TGHGARTST'EPTTDY
EBV	KELKRQY'EKKLRO
Influenza A	RGYFKMRTG'KSSIMRS
EBV	TVFYNI'PPMPL
EBV	AEGLRALLAR'SHVER
EBV	PGPLRESIVCY'FMVFLQTHI

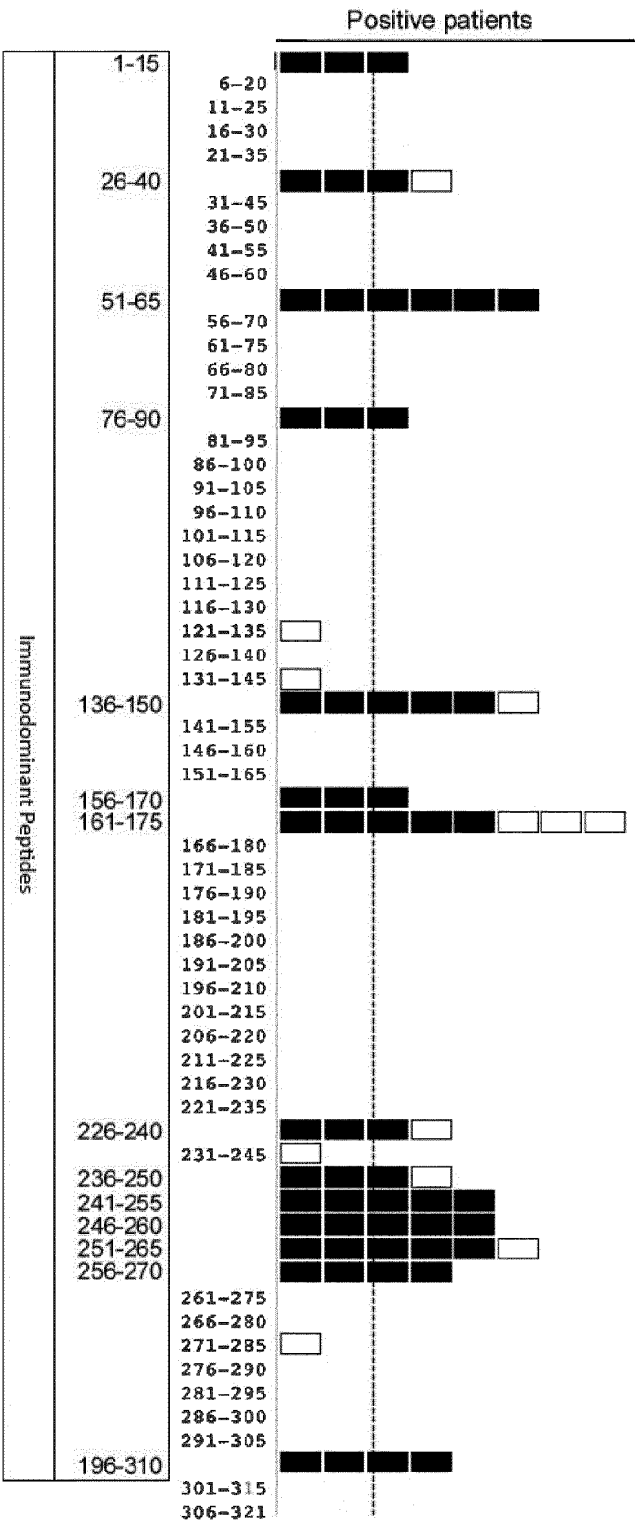


Figure 7

Figure 8

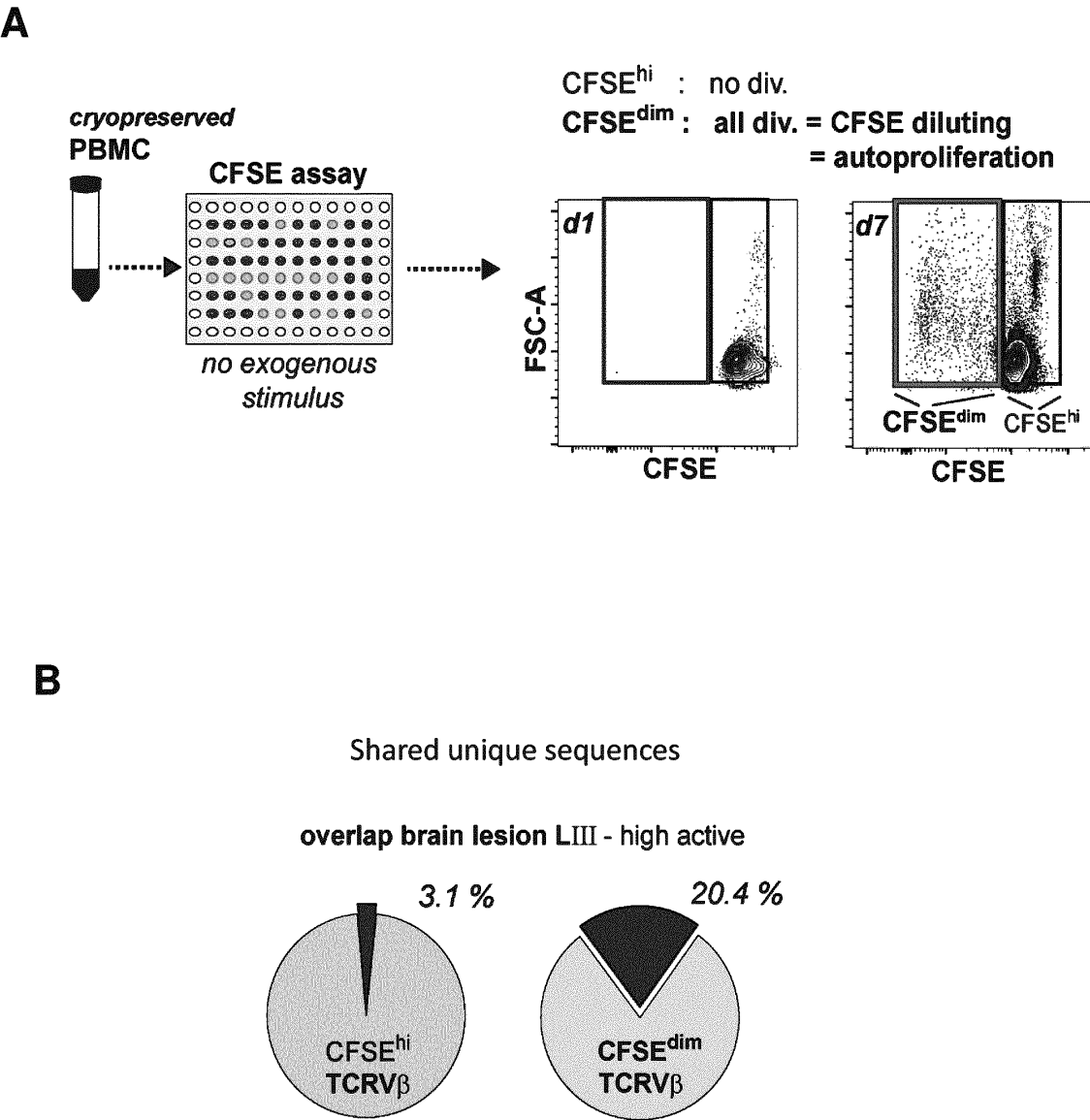
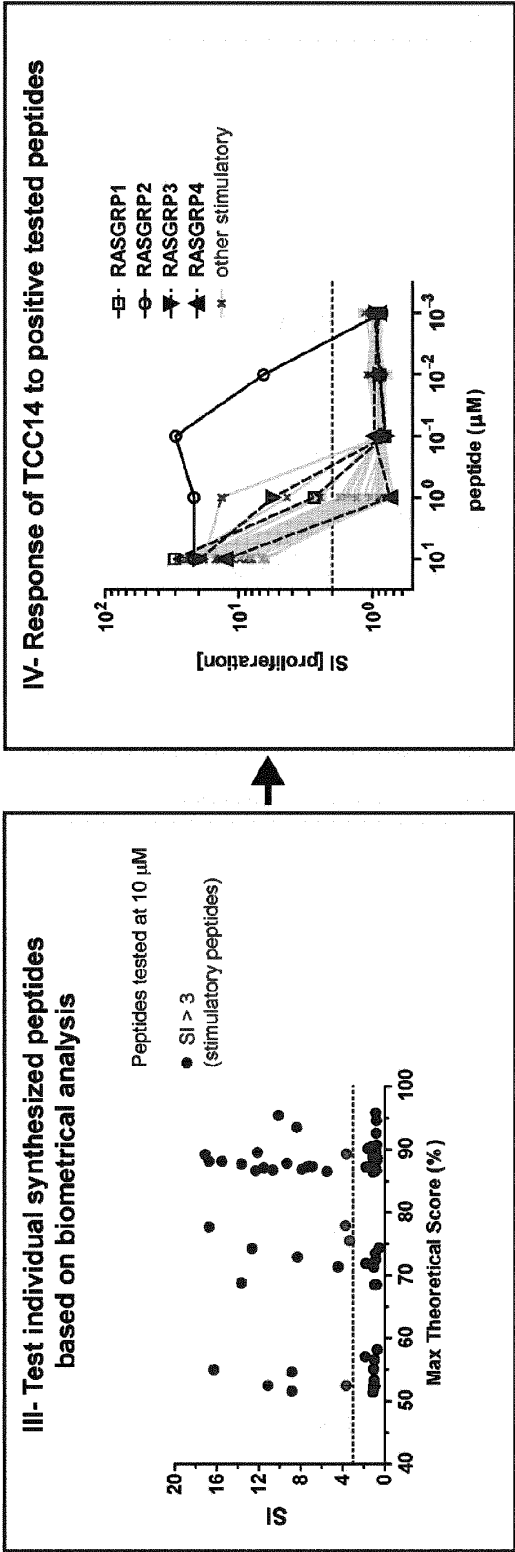


Figure 9 (II)



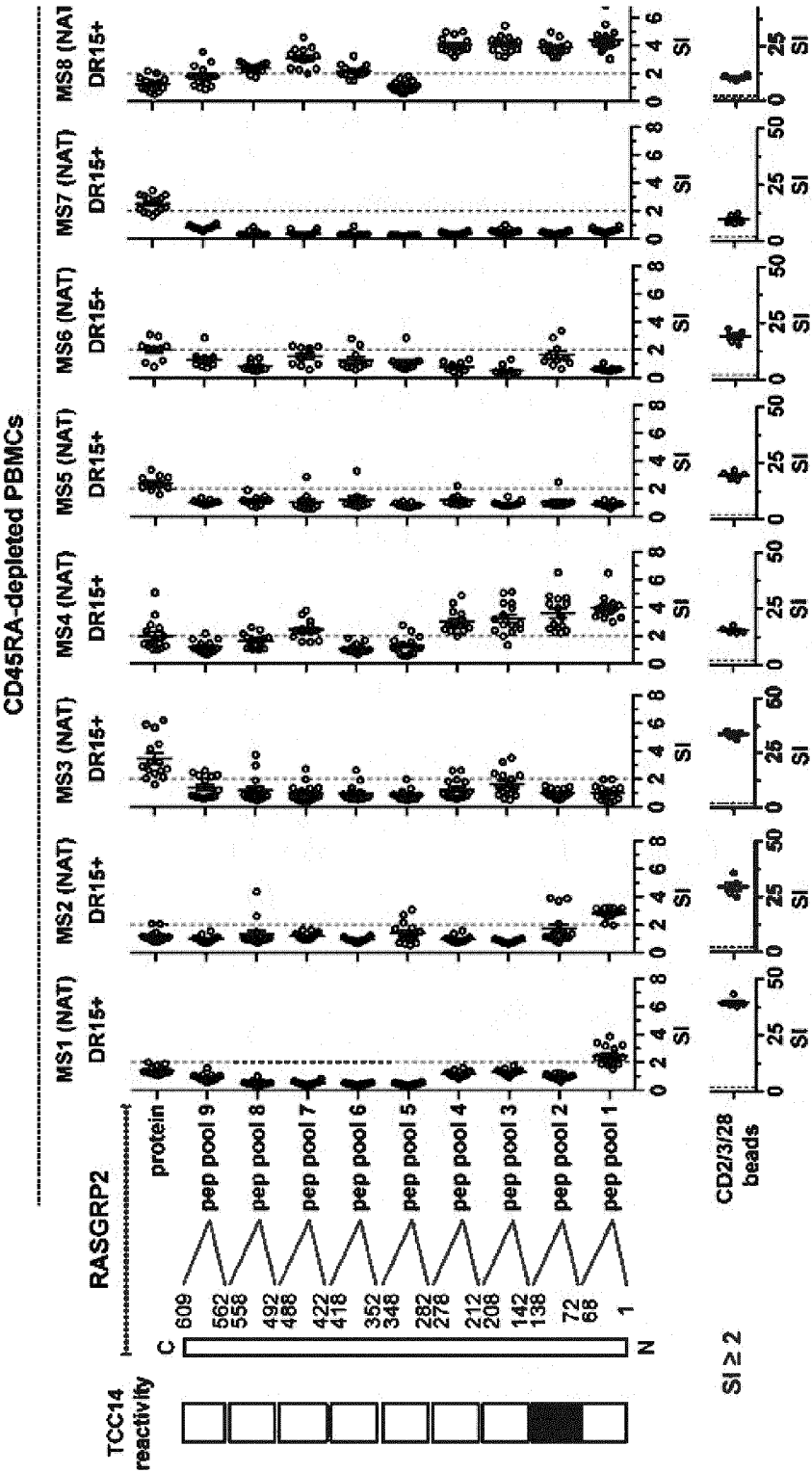


Figure 11

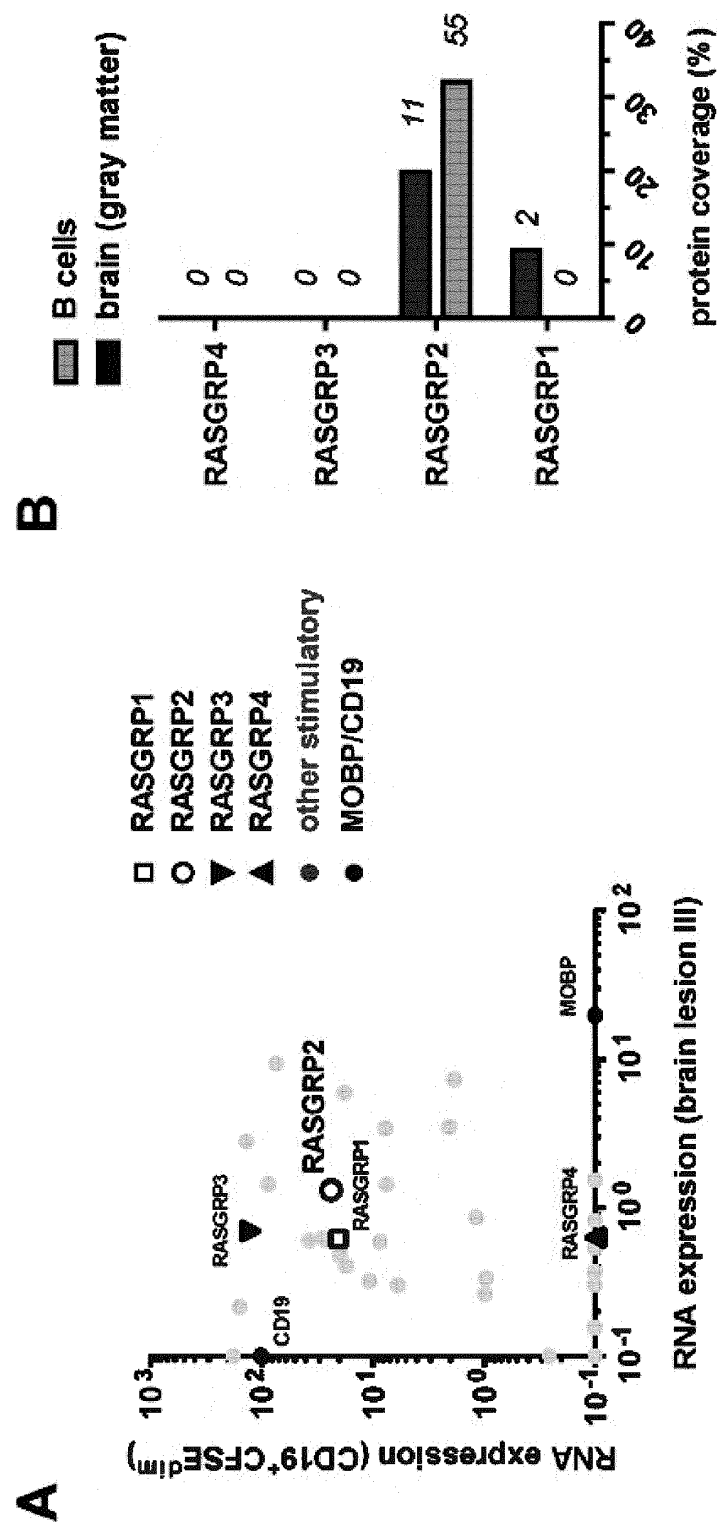
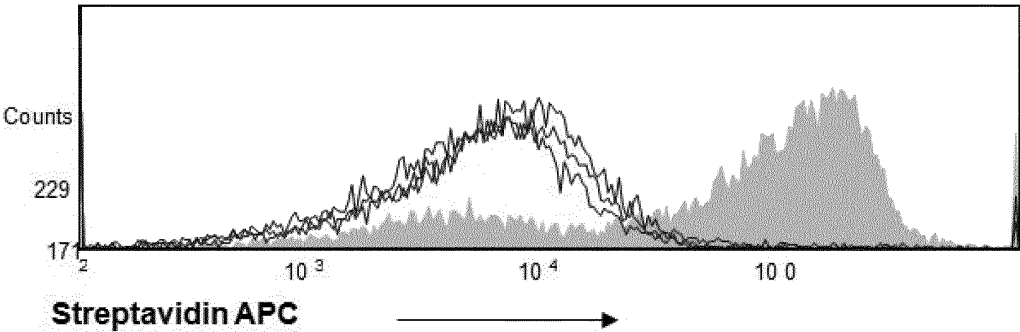


Figure 12

Antigen	Sequence	Position
RASGRP1	DLLHAPEEGPFTFPNGEAVEHGEESK	621-646
	IVISSAELLQK	95-105
	VSLFDHLEPEELSEHLTYLEFK	197-219
RASGRP2	AFSFSLPRPGR	627-637
	ALILGIYK	570-577
	ALLDQEGNRR	158-167
	ALVITHFVHVAEK	274-286
	DLVALQLALPDWLDPAR	363-379
	DNSNSLQVK	119-127
	HSSLIDIDSVPTYK	168-181
	KDNSNSLQVK	118-127
	LDQALVVEHIEK	471-482
	LLHIYQQSR	109-117
	LLQLQNFNTLMAVVGGLSHSSISR	287-310
	LWEGLTELVTATGNYGNYR	325-343
	MFLMMHPWYIPSSQLAAK	91-108
	VRDPQLVR	83-90
	YWISAFPAEFDLNPELAEQIK	134-154
RASGRP3	LSLVLEPR	376-383

Figure 13



	biotinPLP1	EDC
1 open histogram	-	-
2 open histogram	-	+
3 open histogram	+	-
4 filled histogram	+	+

Figure 14 (I)

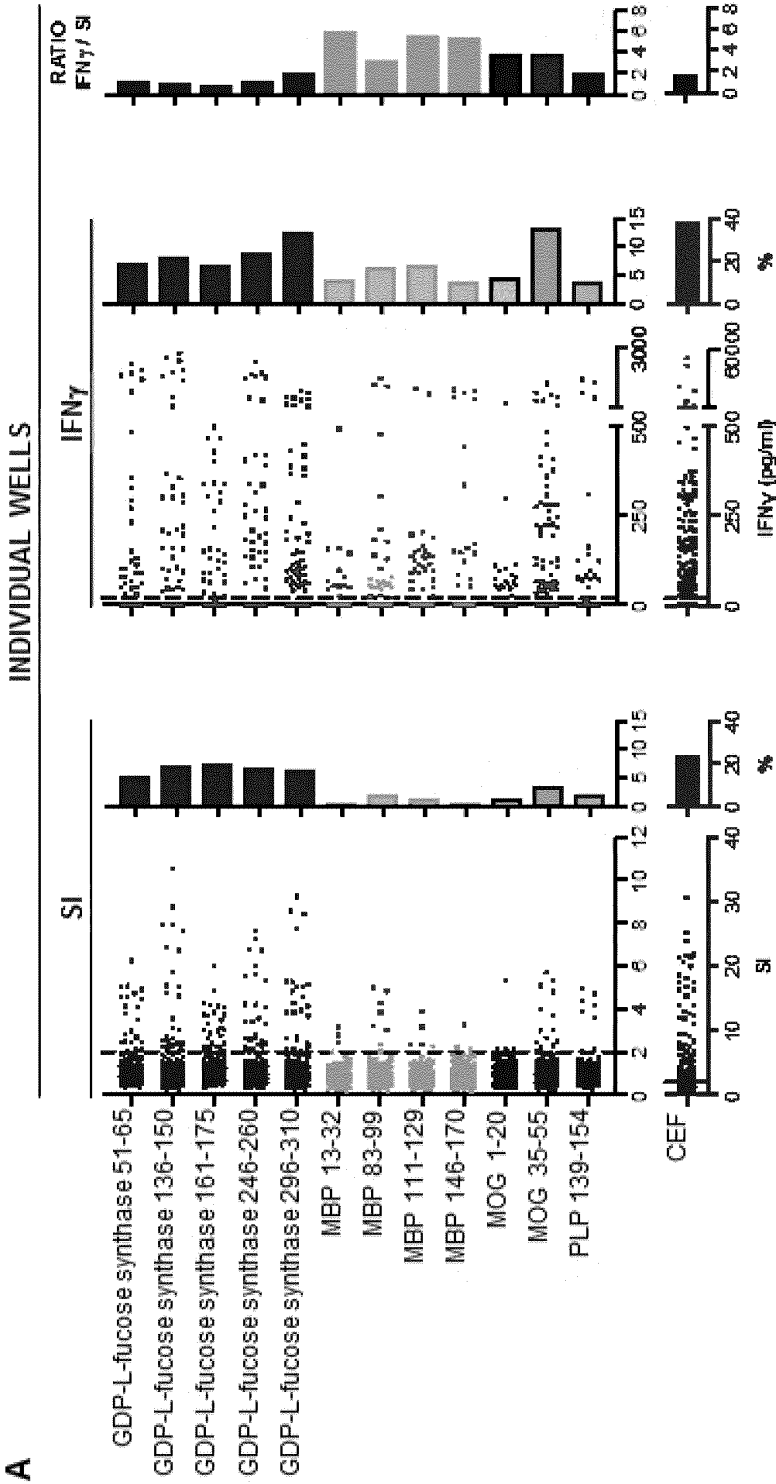


Figure 14 (II)

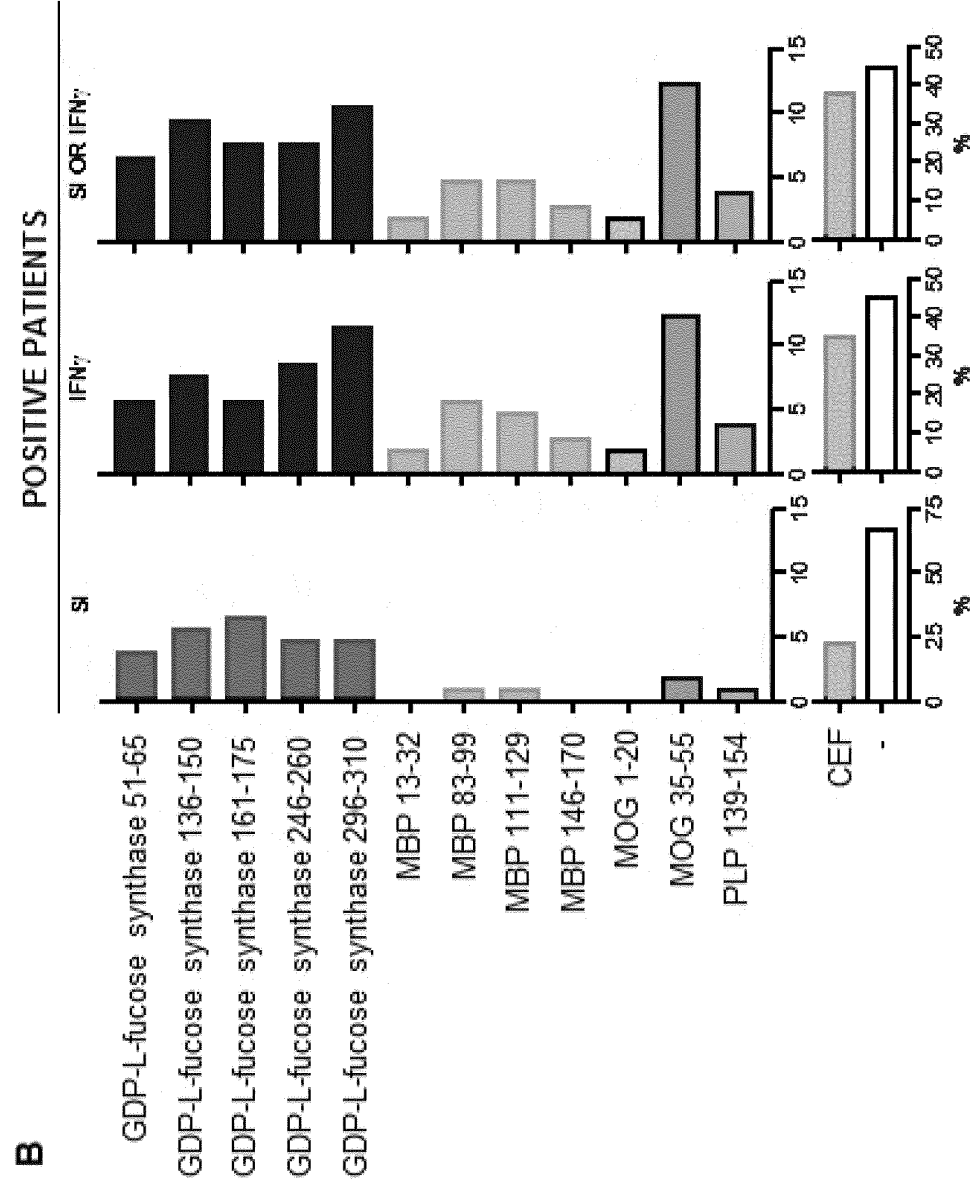
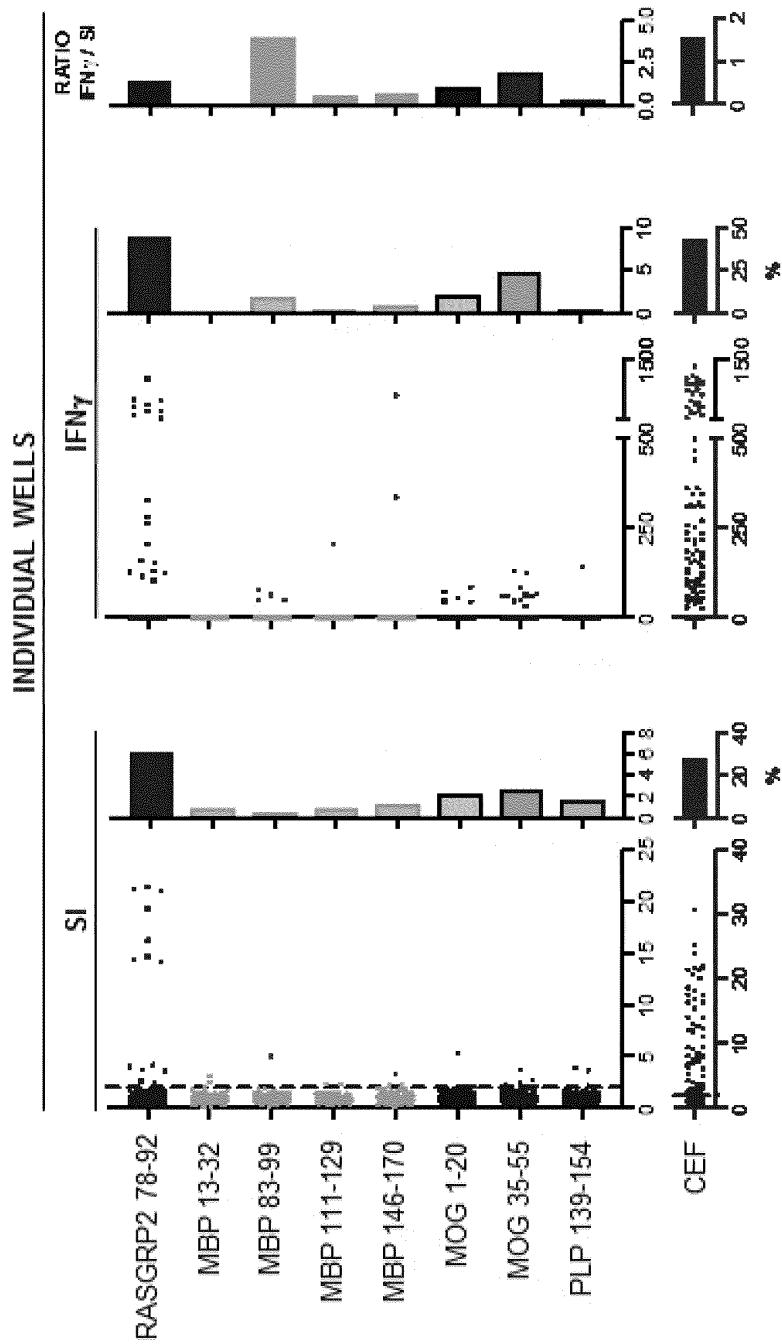
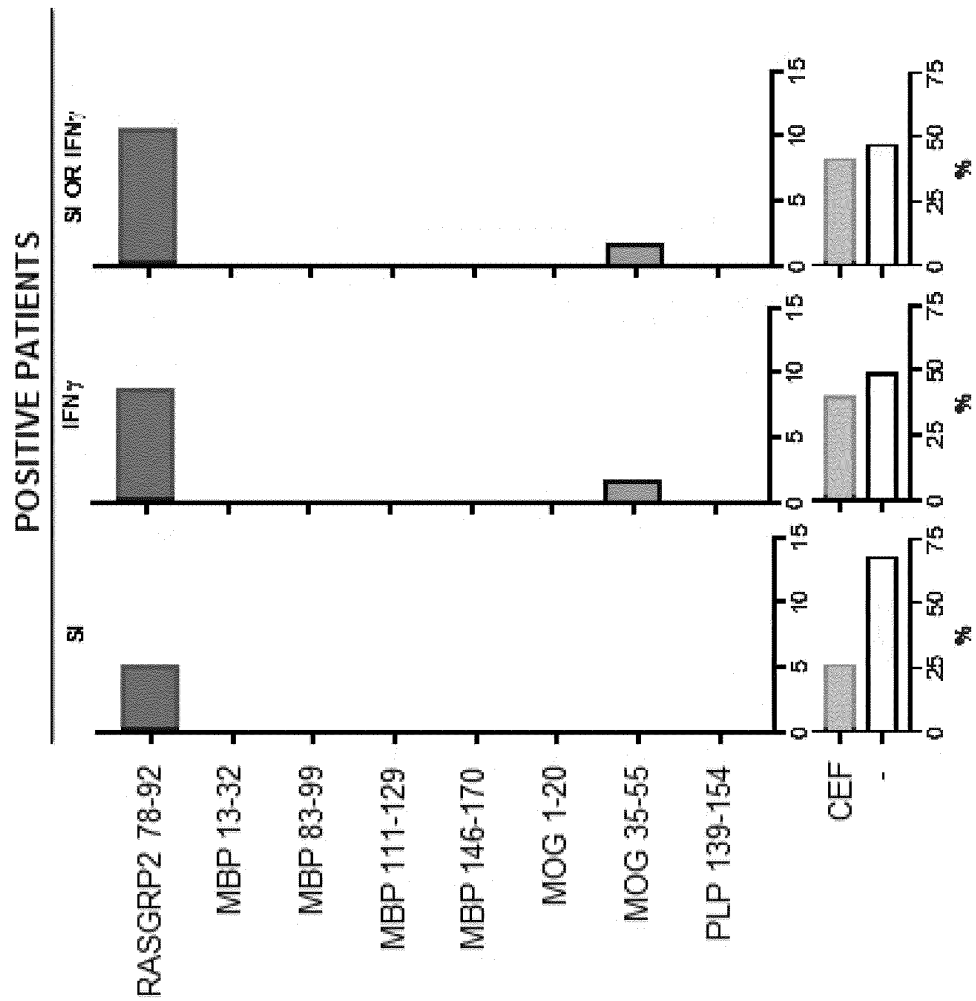


Figure 15 (I)



A

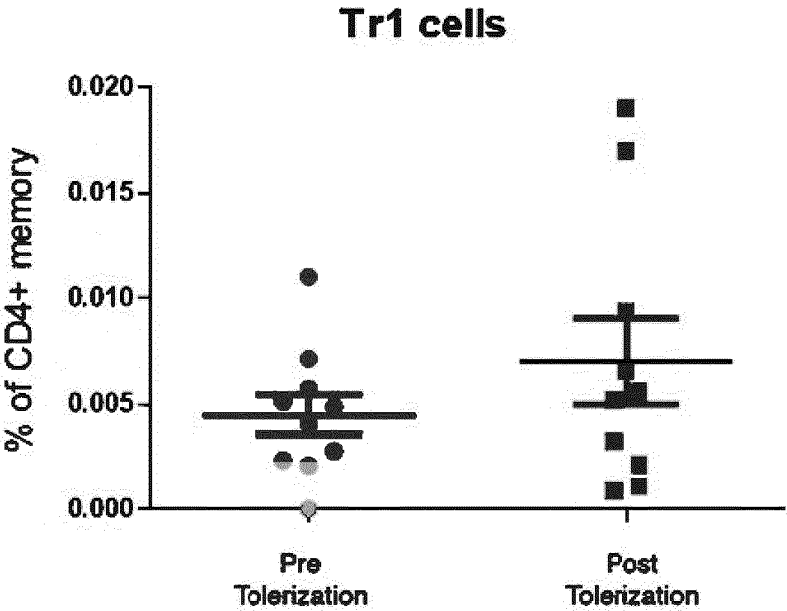
Figure 15 (II)



B

Figure 16 (I)

A



B

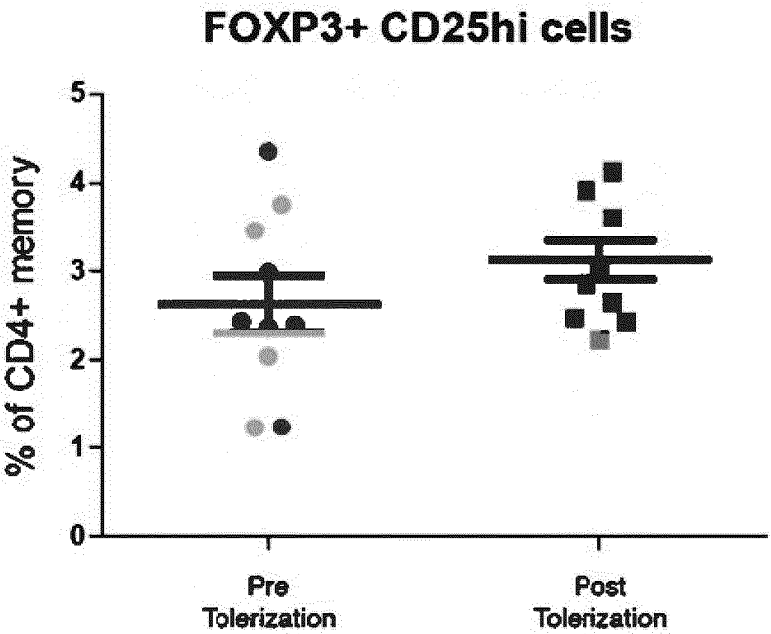


Figure 16 (II)

C

