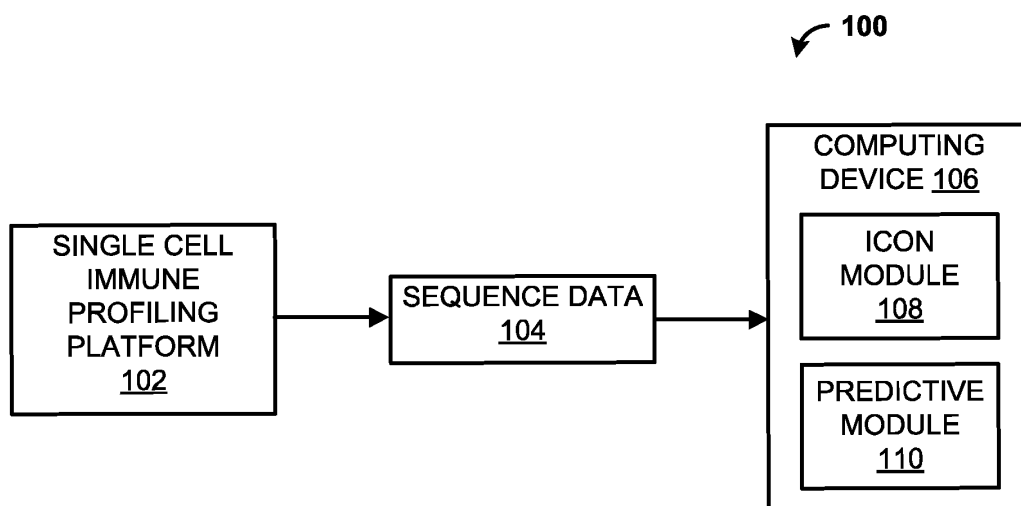


FIG. 1



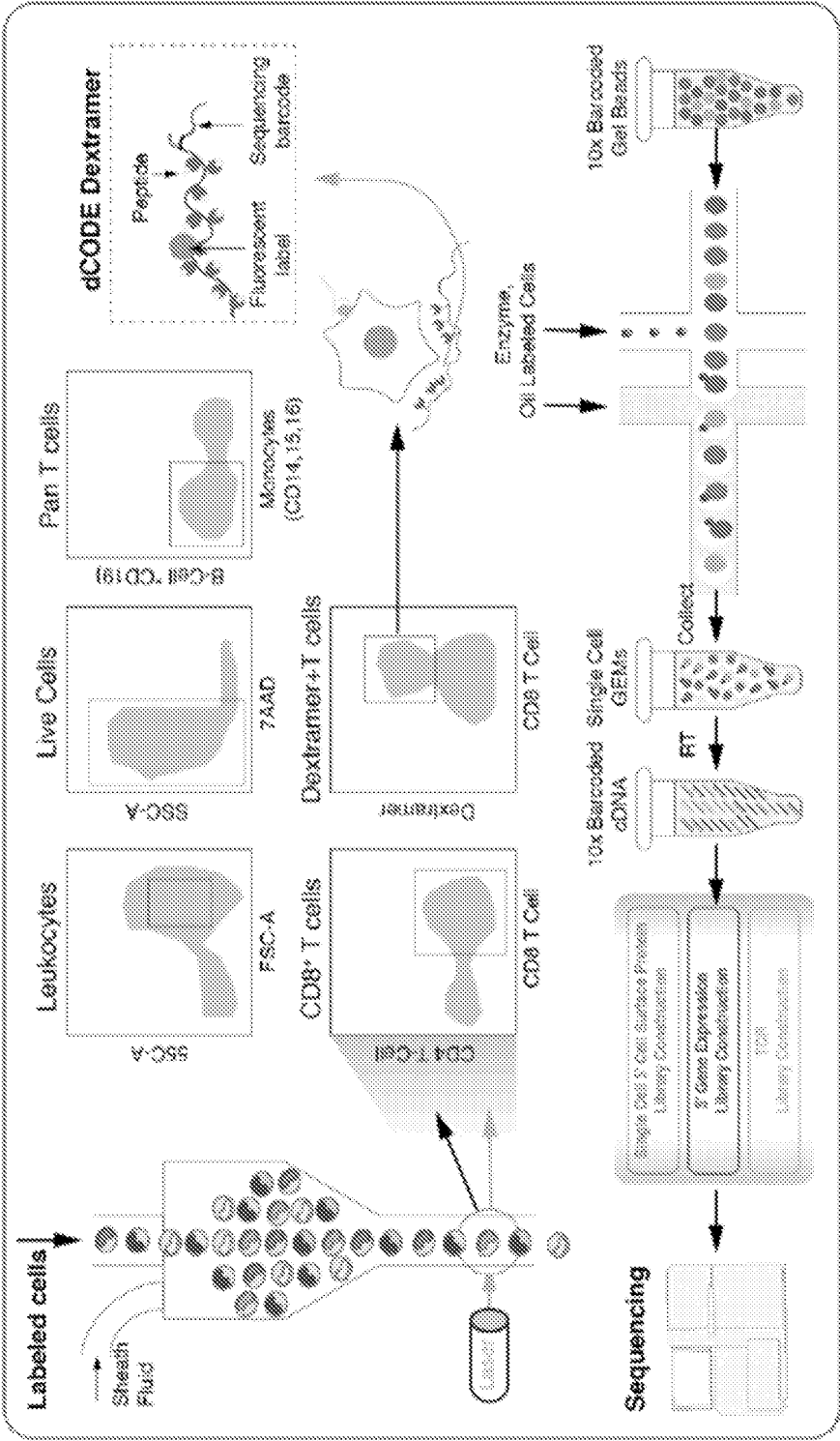
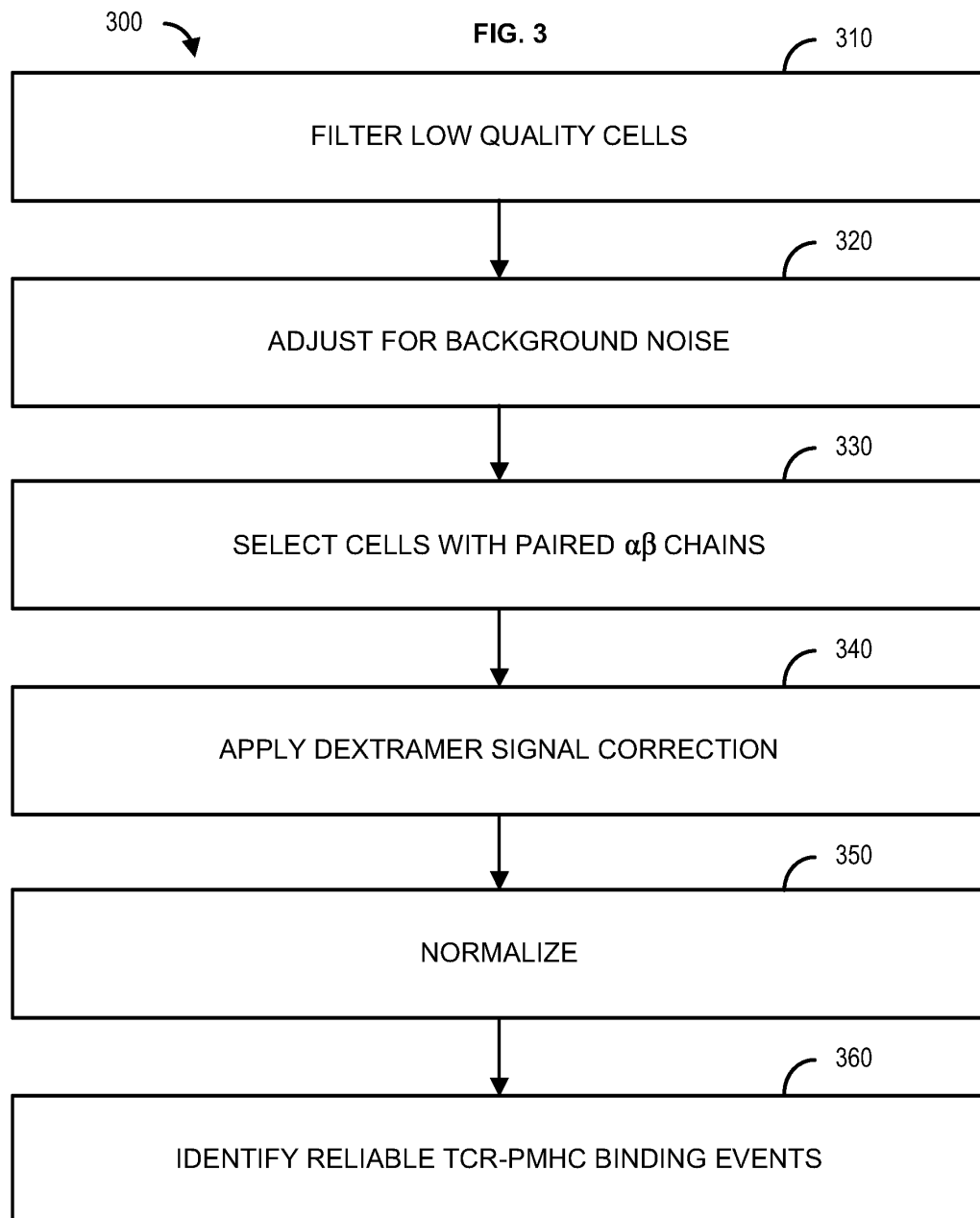


FIG. 2



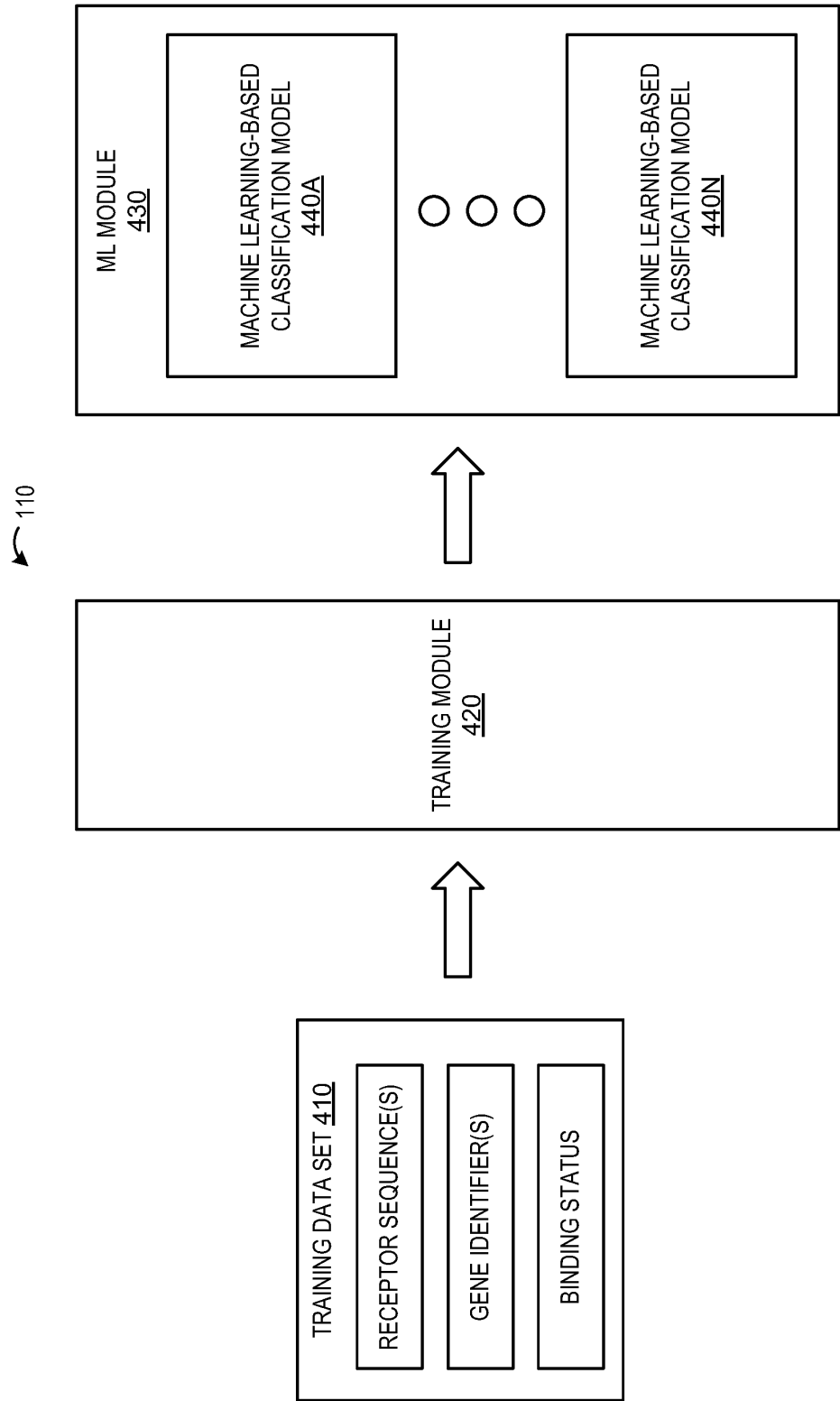
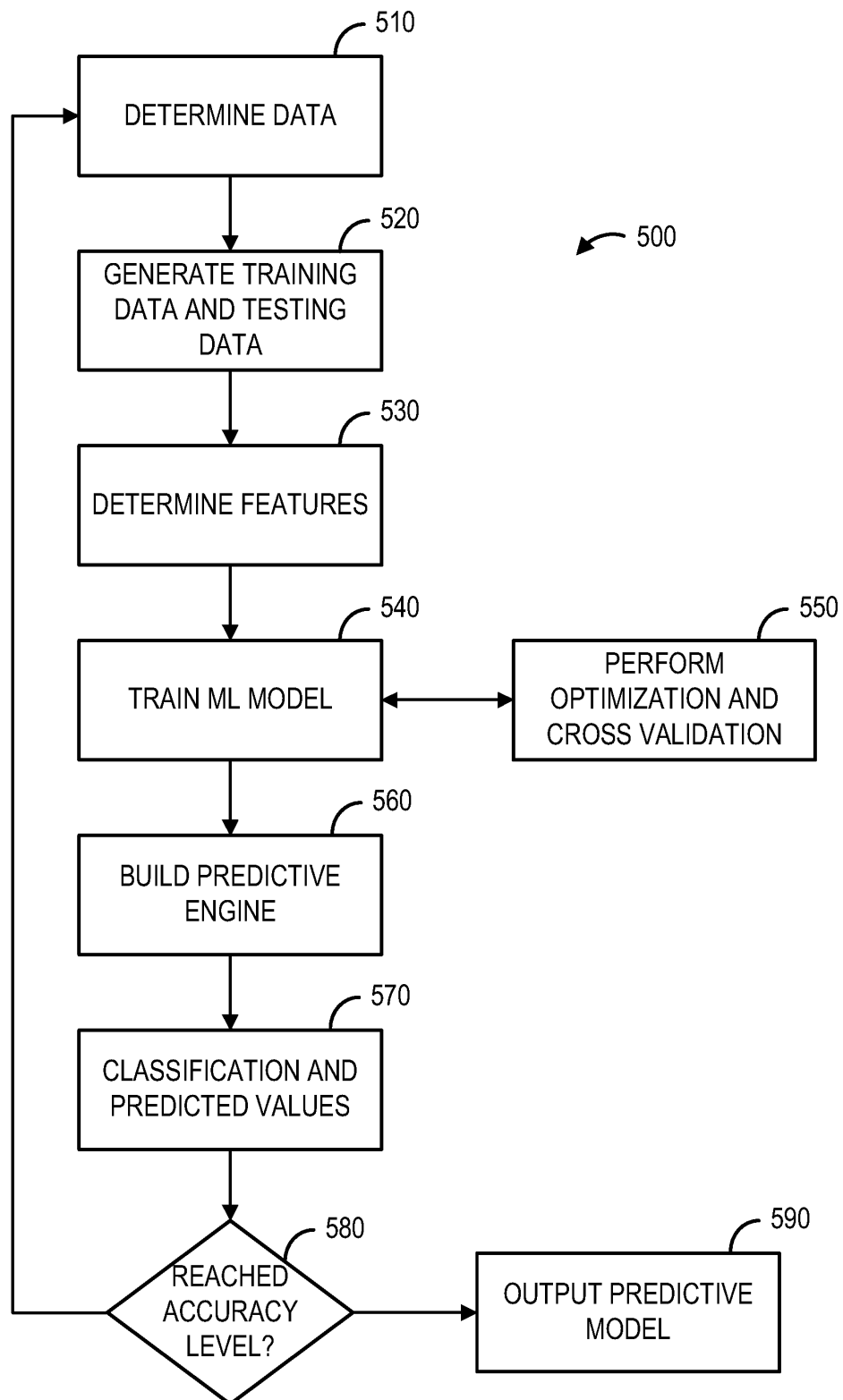


FIG. 4

FIG. 5



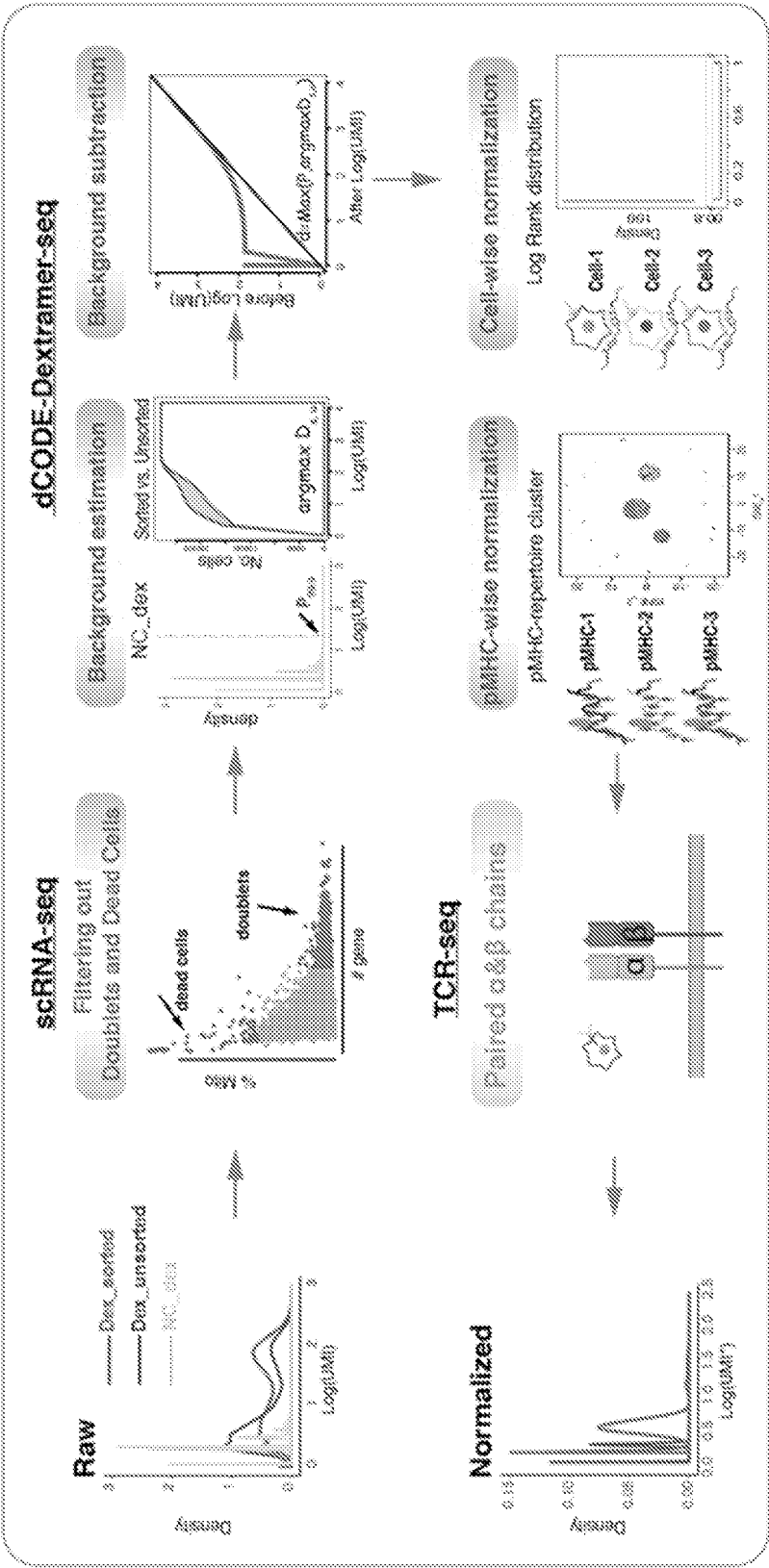


FIG. 6A

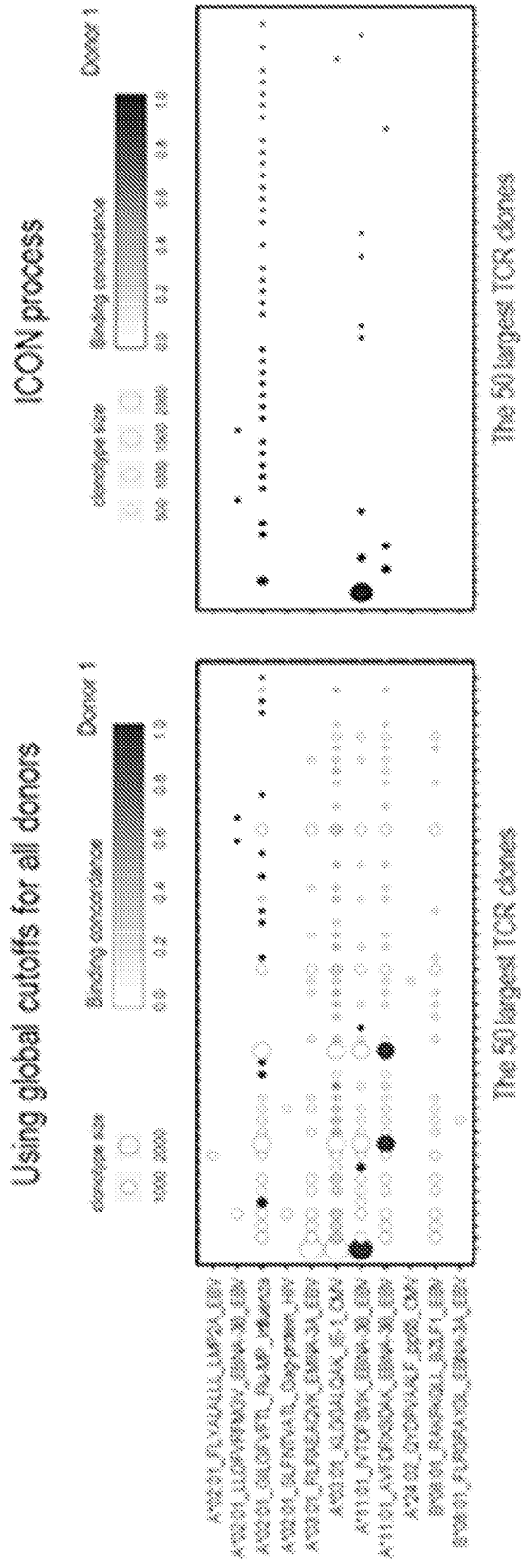


FIG. 6B

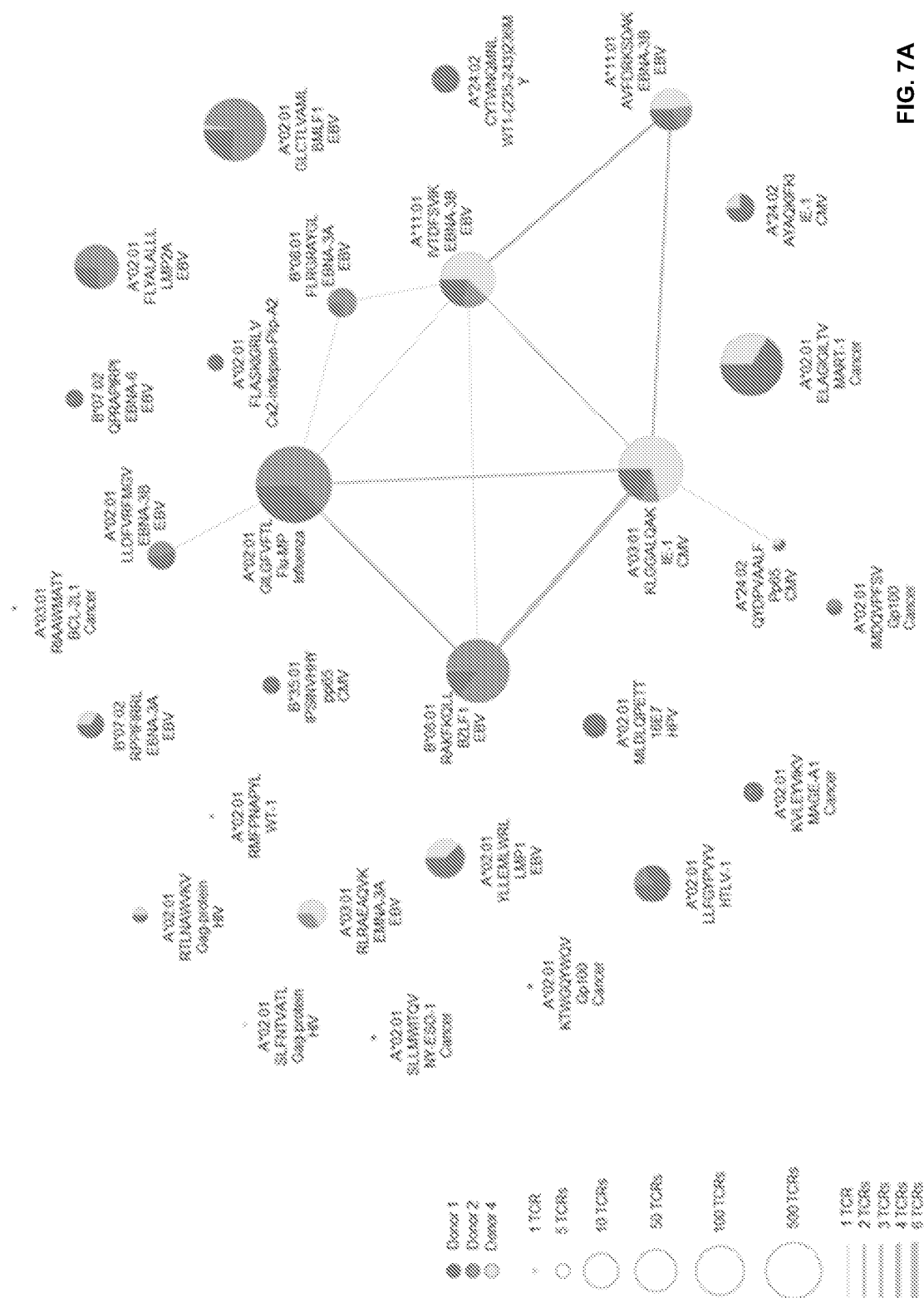


FIG. 7B

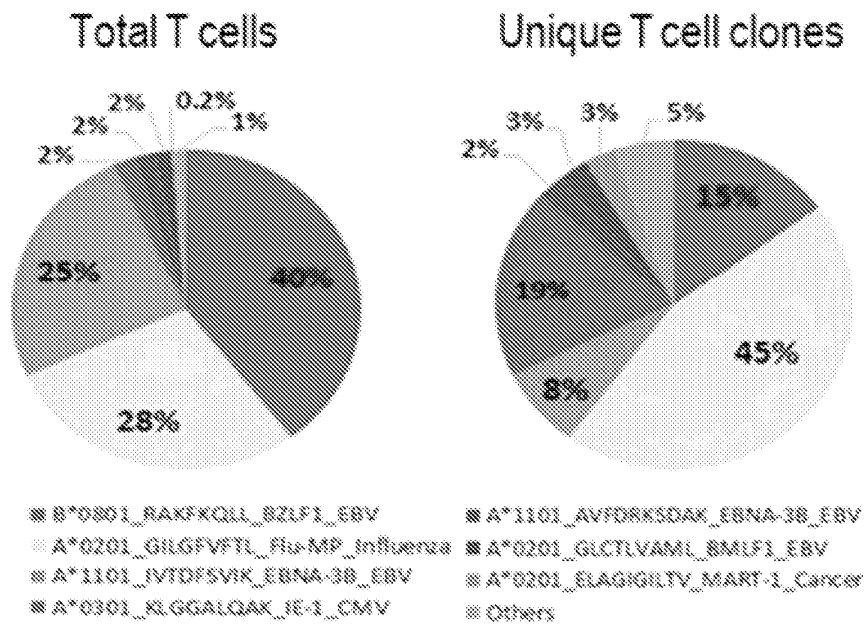


FIG. 7C

Venn diagram of unique paired binding TCRs

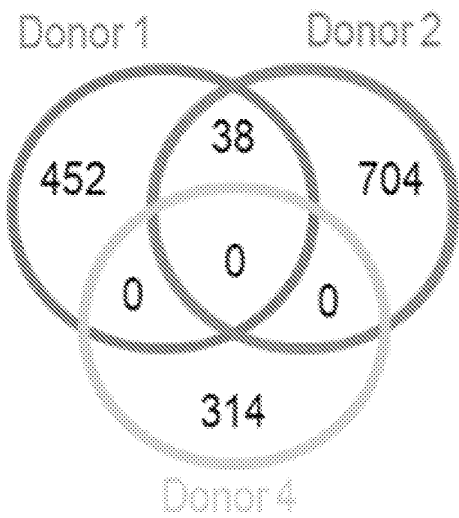


FIG. 7D

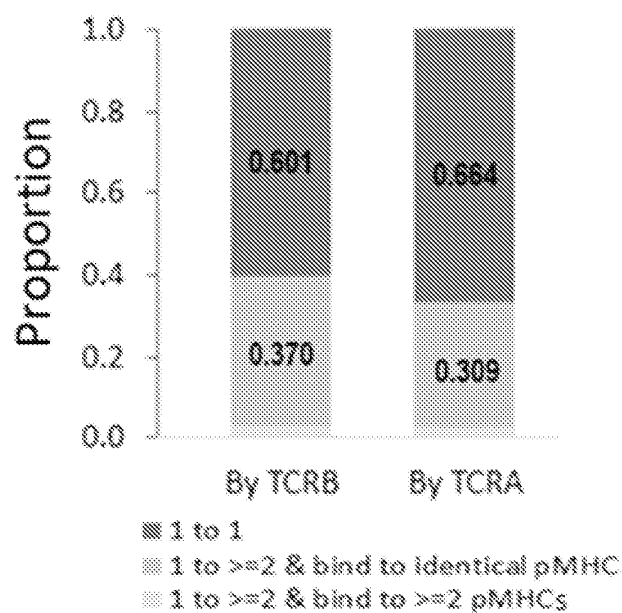
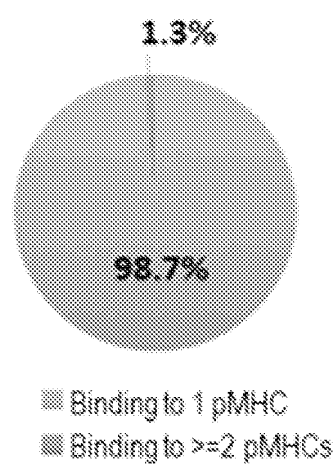
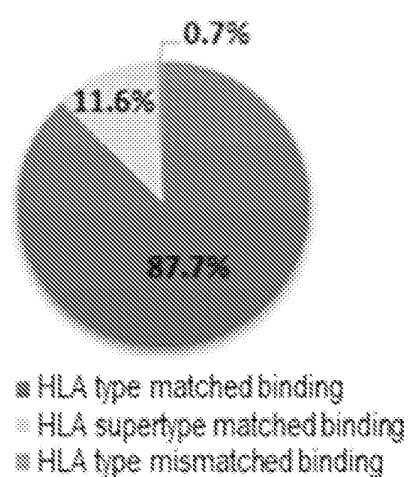


FIG. 7E

TCR-pMHC binding
specificityTCR cross-HLA
recognition

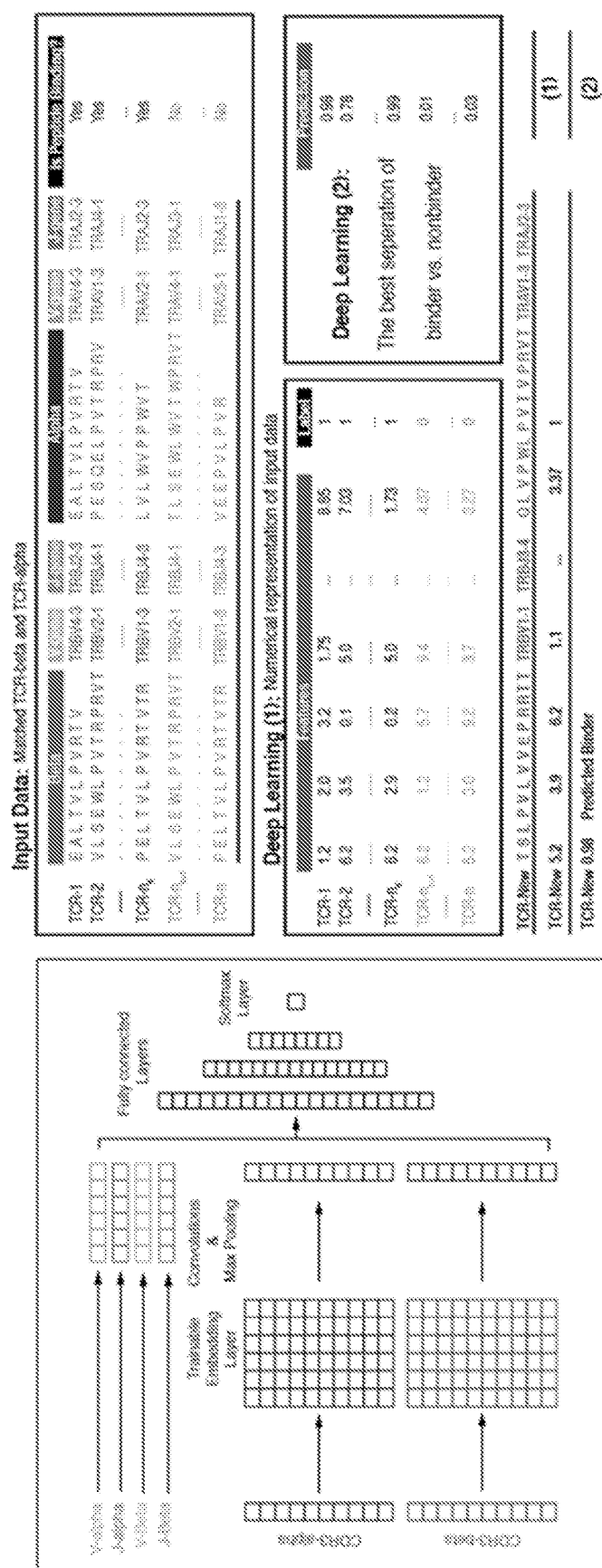


FIG. 8A

FIG. 8B

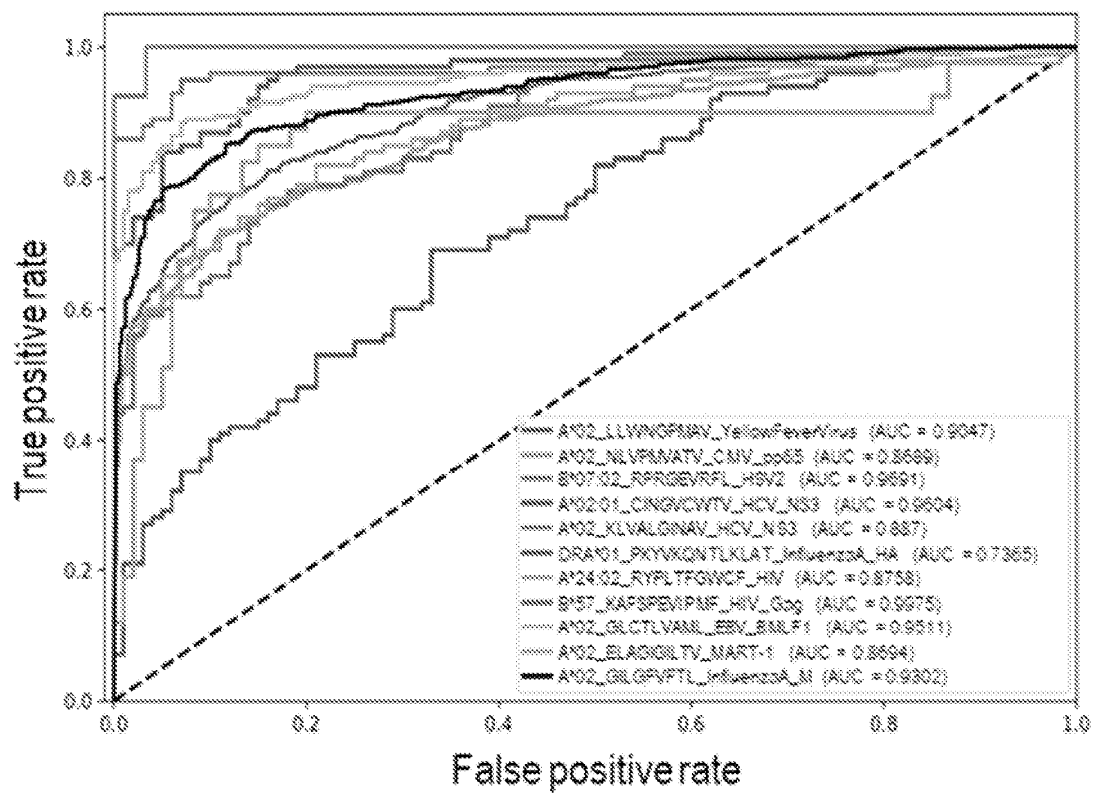


FIG. 8C

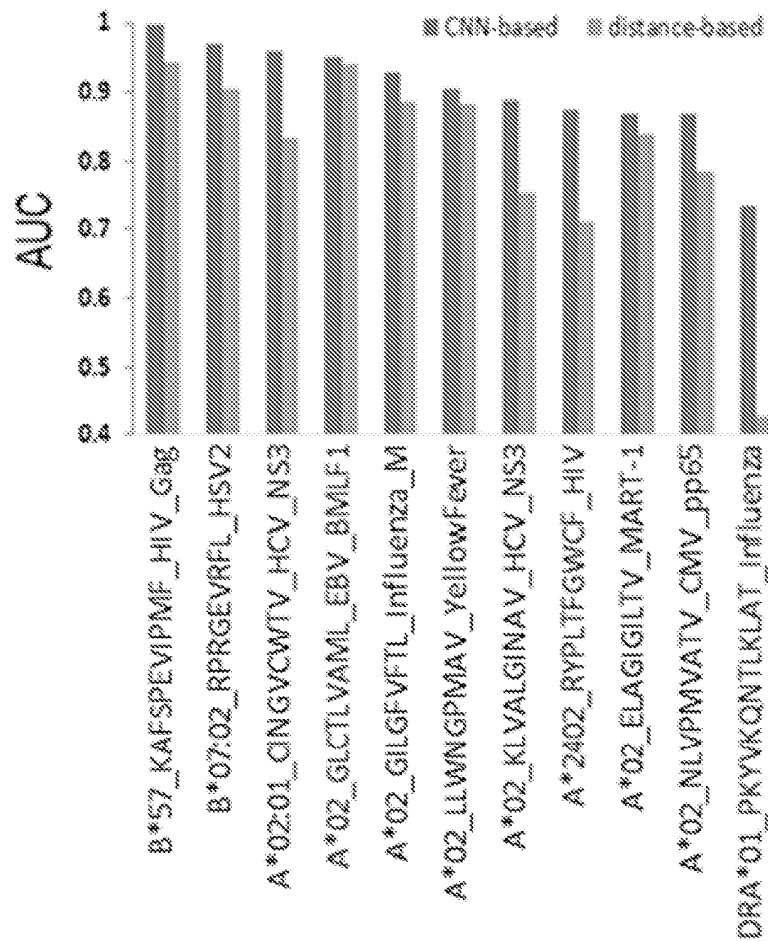


FIG. 8D

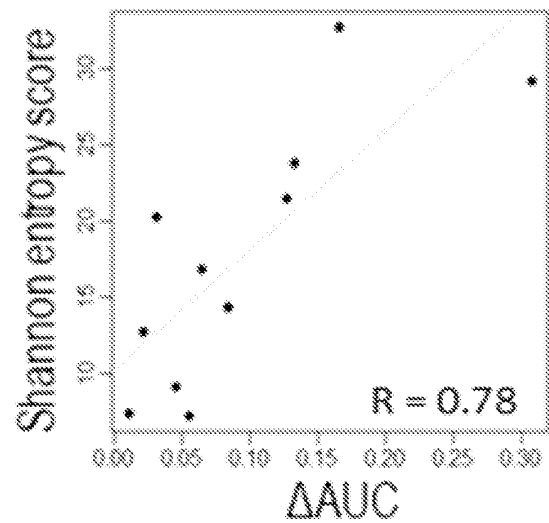


FIG. 9A

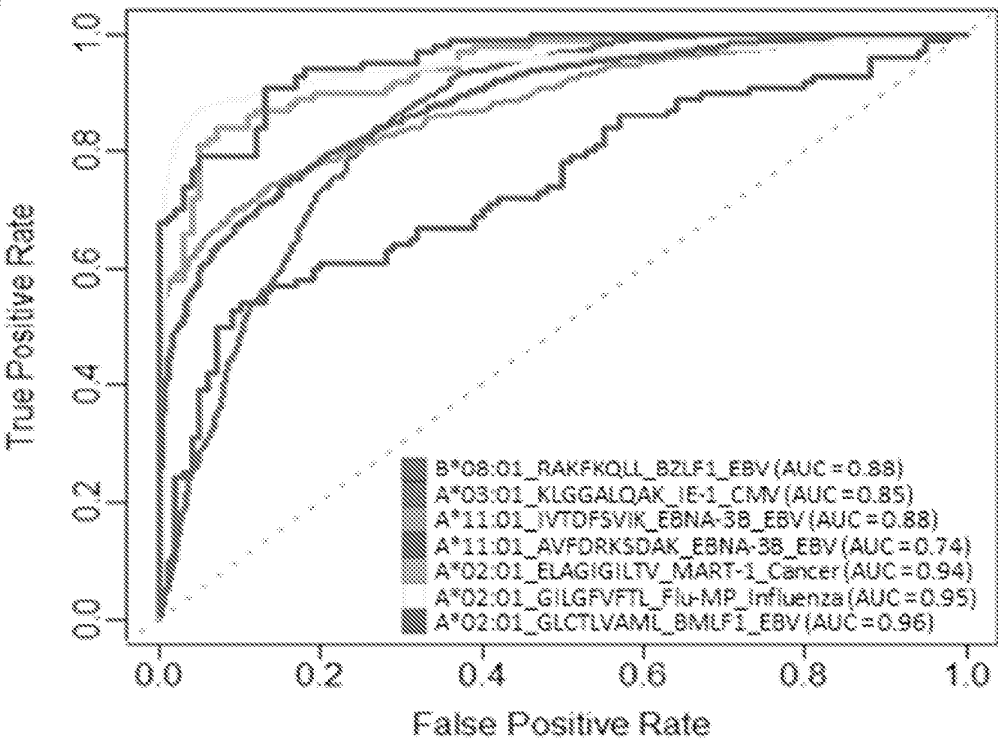


FIG. 9B

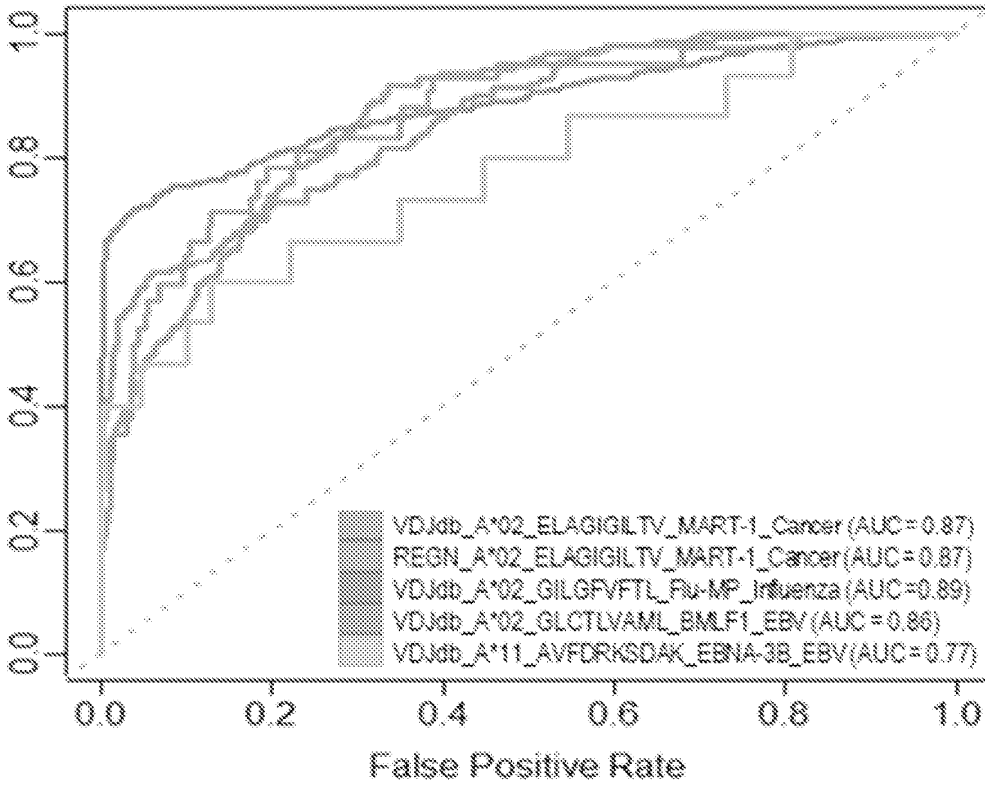
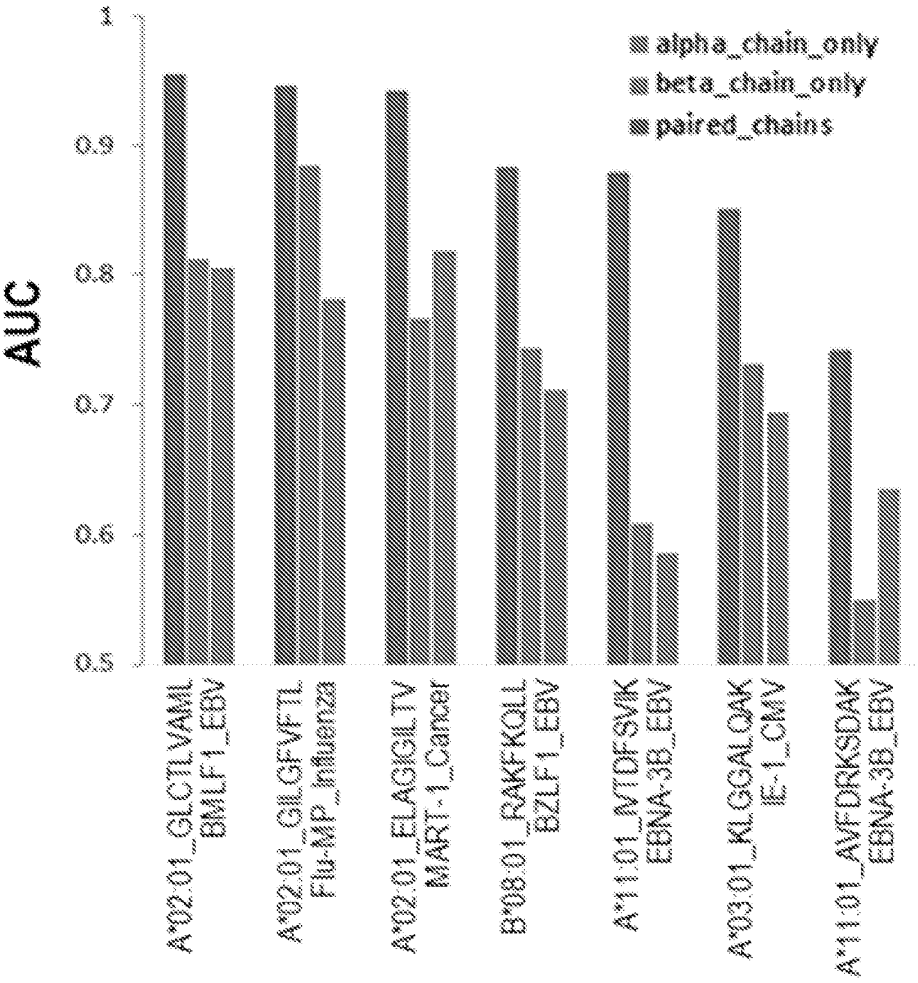


FIG. 9C



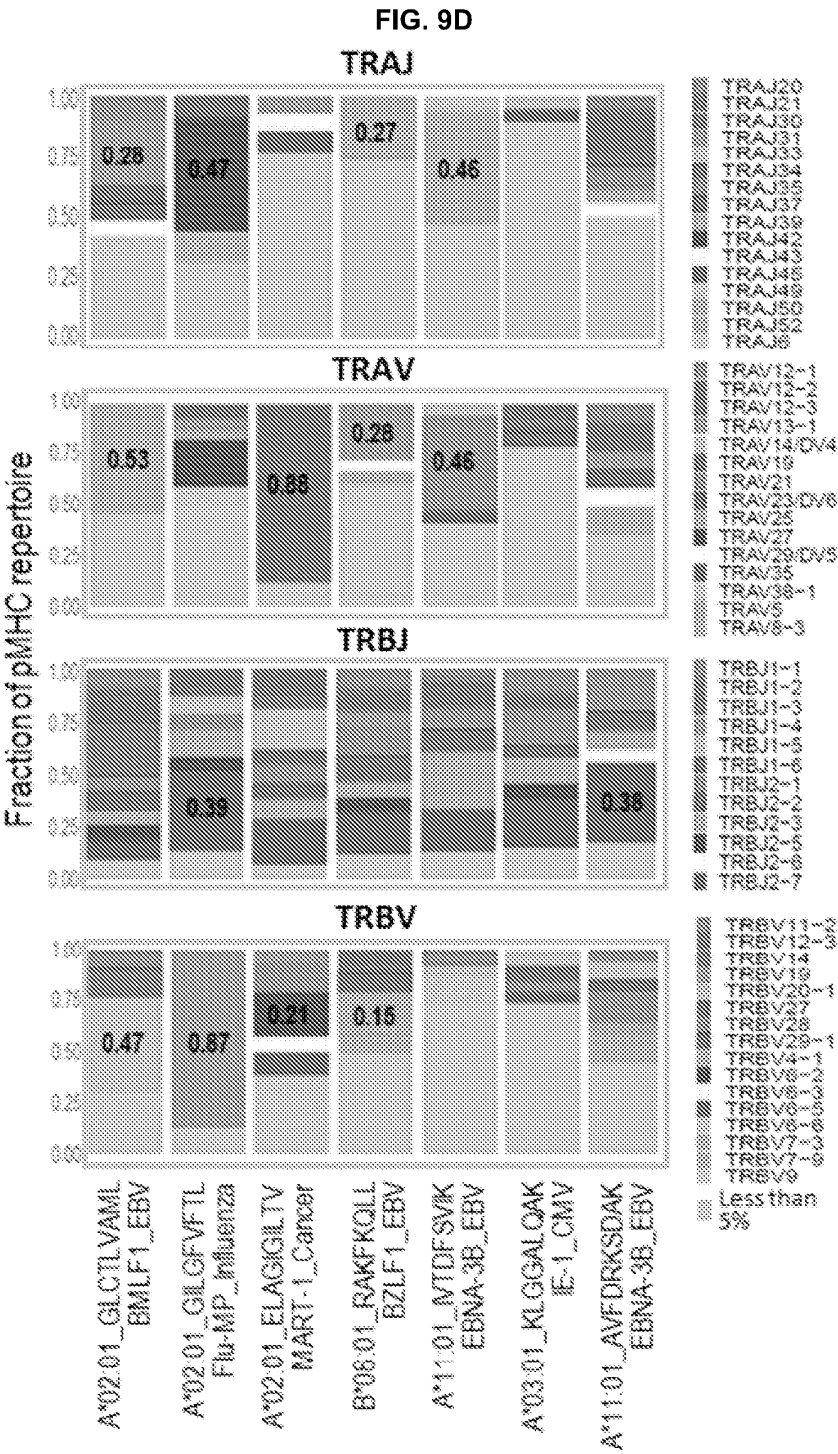


FIG. 9E

	Alpha chain CDR3 motif	Beta chain CDR3
A*11:01 AVFORKSDAK EBNA-3B_EBV	CAARVGD _W FNKE _Y F	CASS _h ATGSGANE _C OFF _W
A*02:01 GLCTLVAML BNLF1_EBV	CAEDNRNARLMF	CSARV _h PTGN _V LY _Y FF
B*08:01 RAKFKQLL BZLF1_EBV	CAAM _h GTEISYDKV _Y IF	CASS _h LA _h T _h EQ _h EFF
A*02:01 GILGFVFTL Flu-MP_influenza	CAFIL _h NA _h GGGSG _h OKL _h IF	CASS _h IR _h SGGY _h OFF _h
A*11:01 IVTDFSVIK EBNA-3B_EBV	CAVDLMKTSYDKV _Y IF	CASS _h SG _h SG _h SG _h GL _h Y _Y F
A*03:01 KLGALQAKI E-1_CMV	CAV _h EG _h NYG _h FNKE _Y F	CASRS _h SG _h EG _h EQ _h Y _Y F
A*02:01 ELAGIGILTV MART-1_Cancer	CAV _h EG _h SG _h GL _h Y _Y F	CASS _h EG _h SG _h PG _h Y _Y F

FIG. 10A

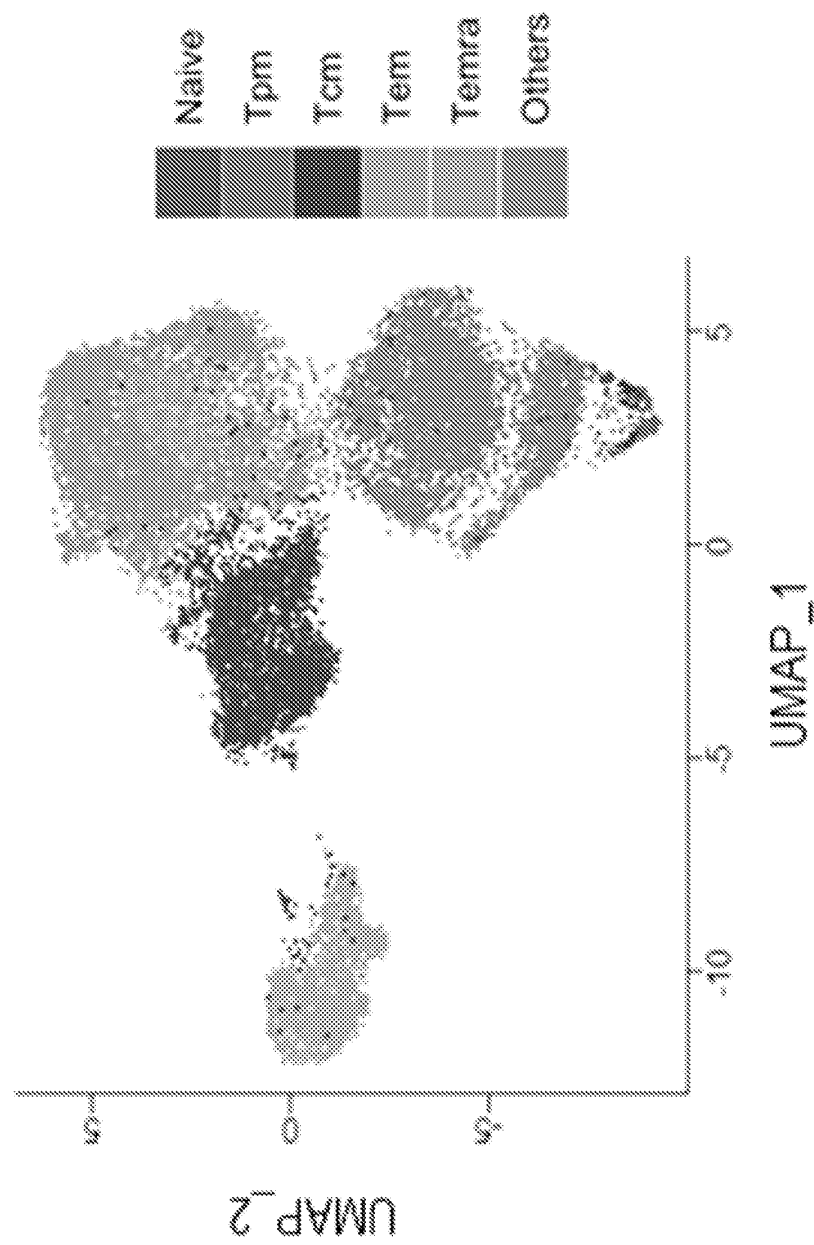


FIG. 10B

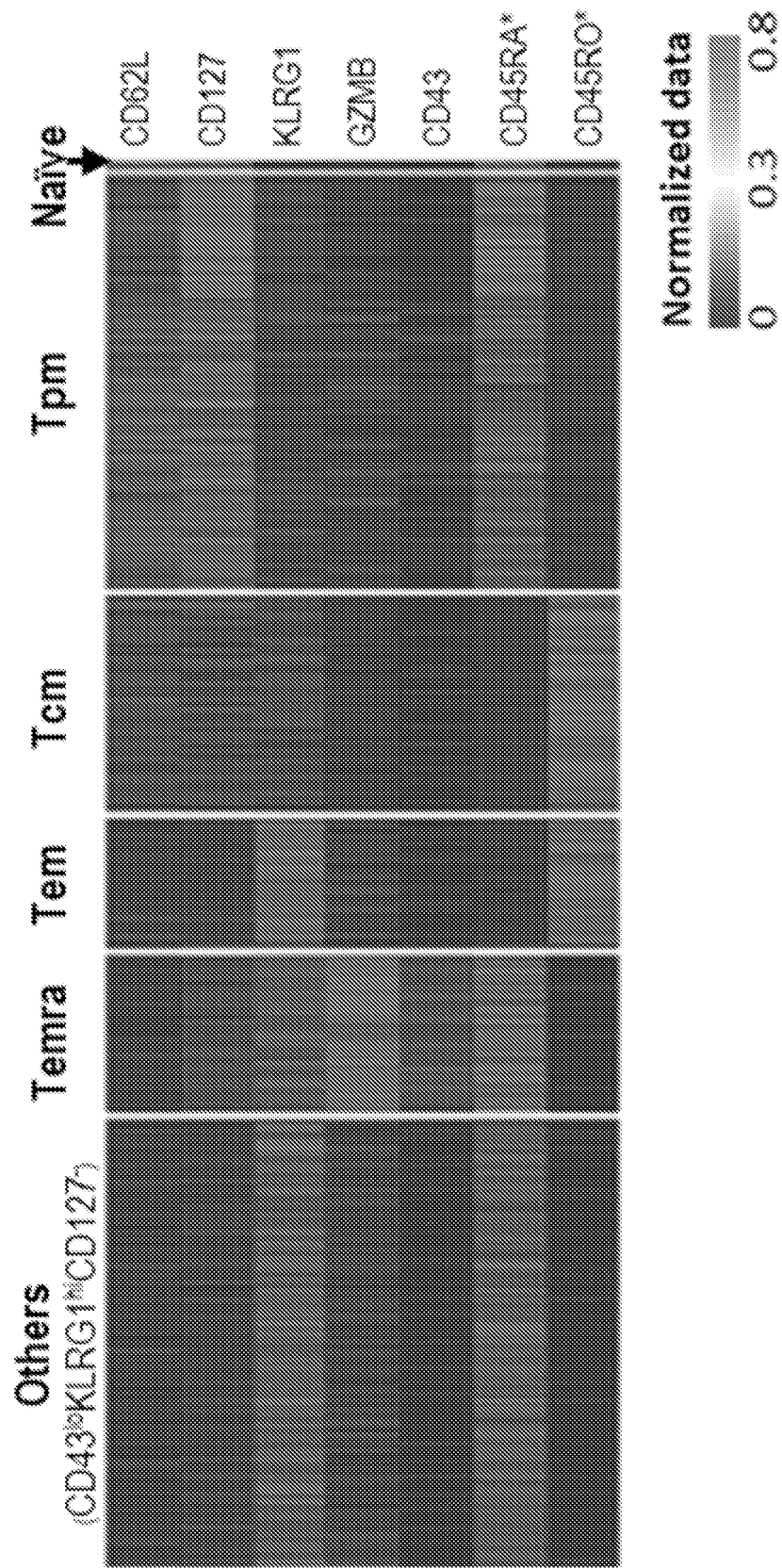
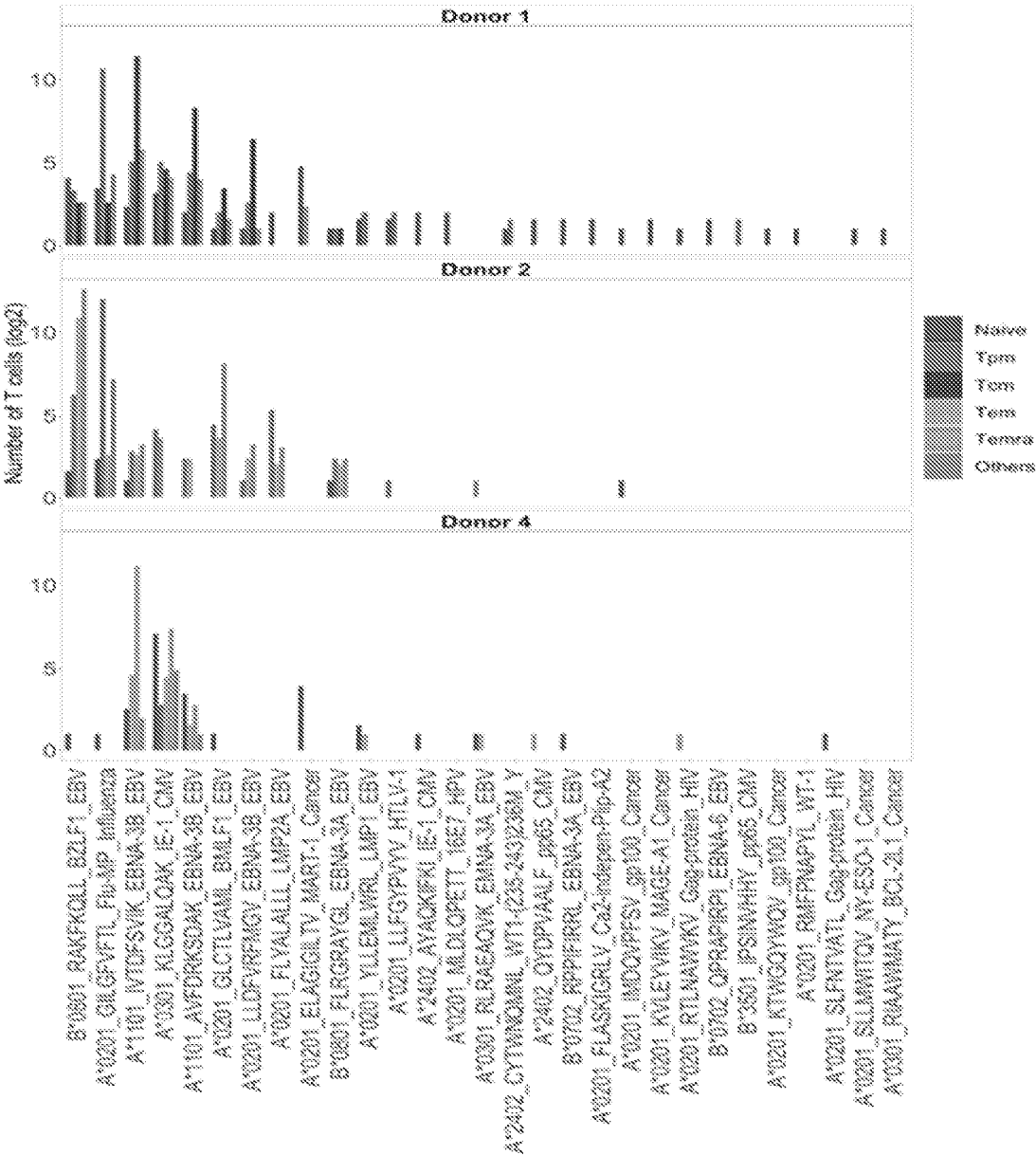


FIG. 10C



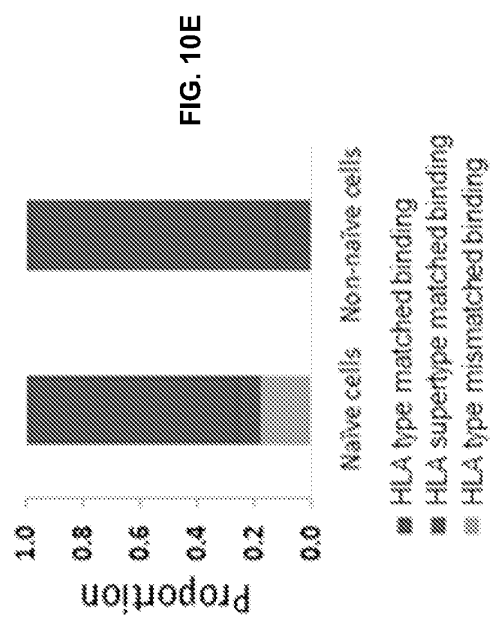
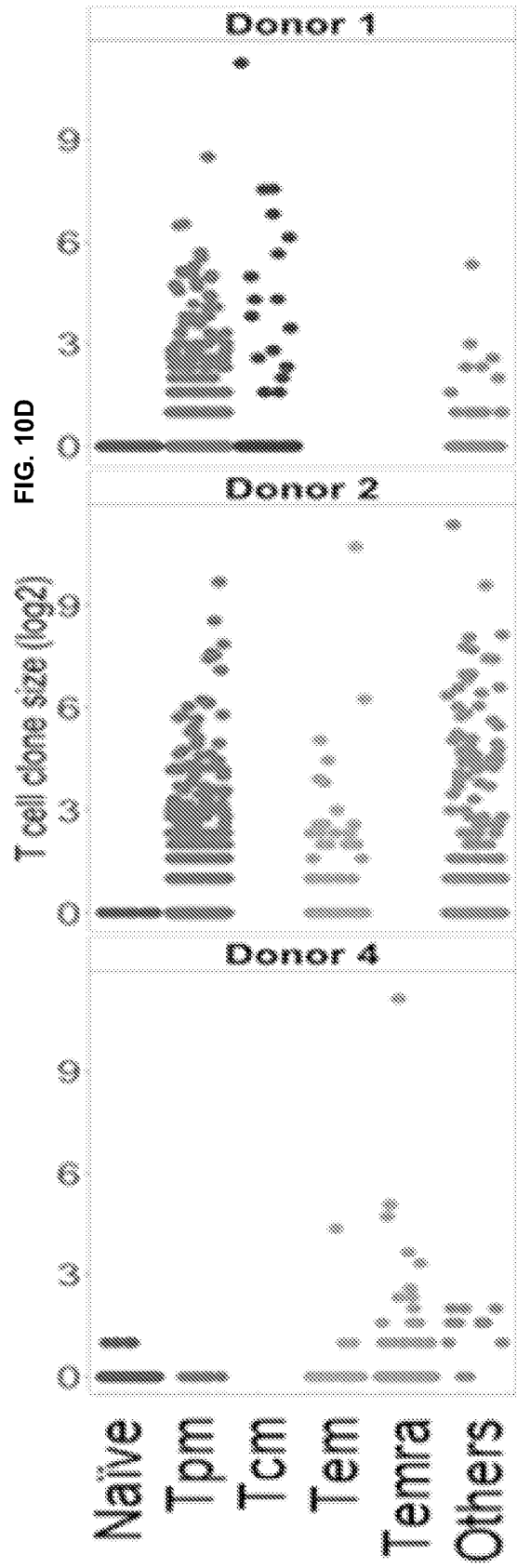


FIG. 11A

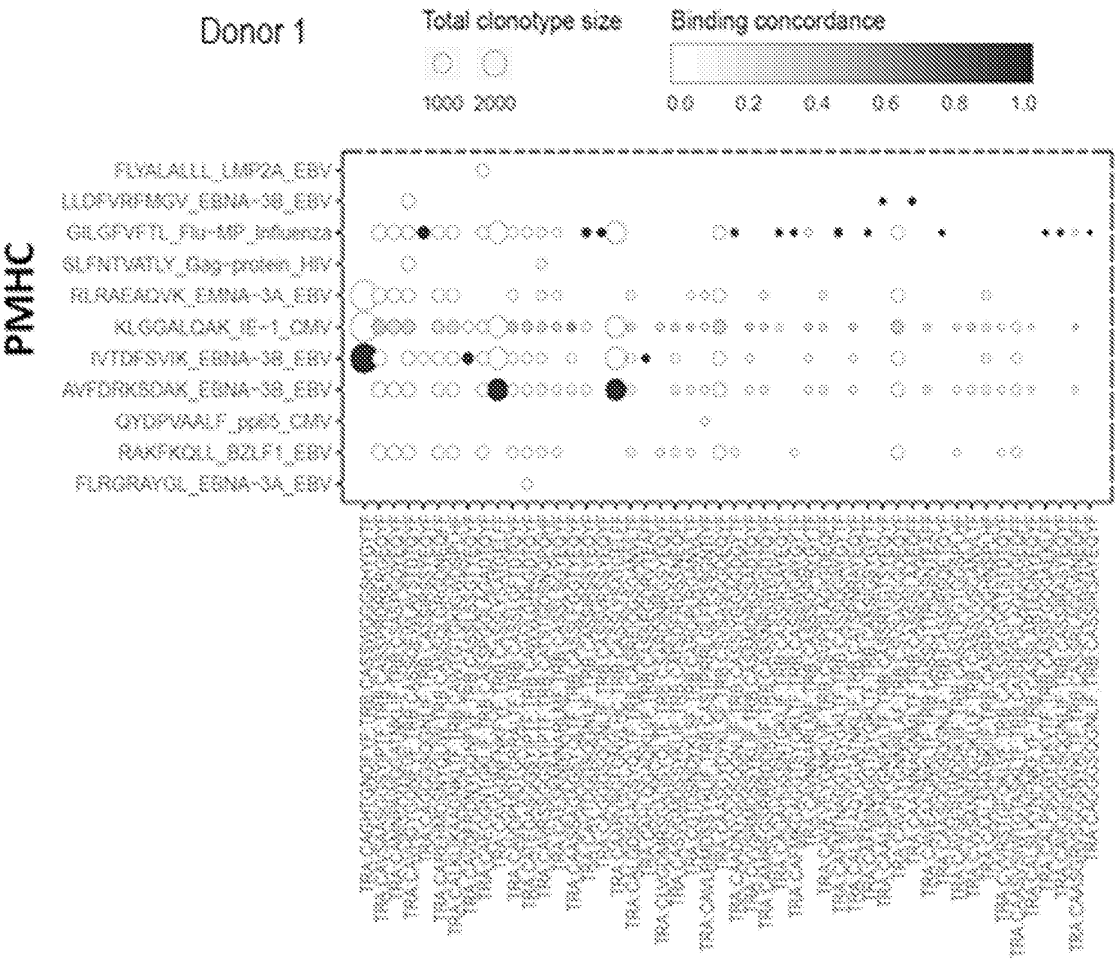


FIG. 11A
(CONTINUED)

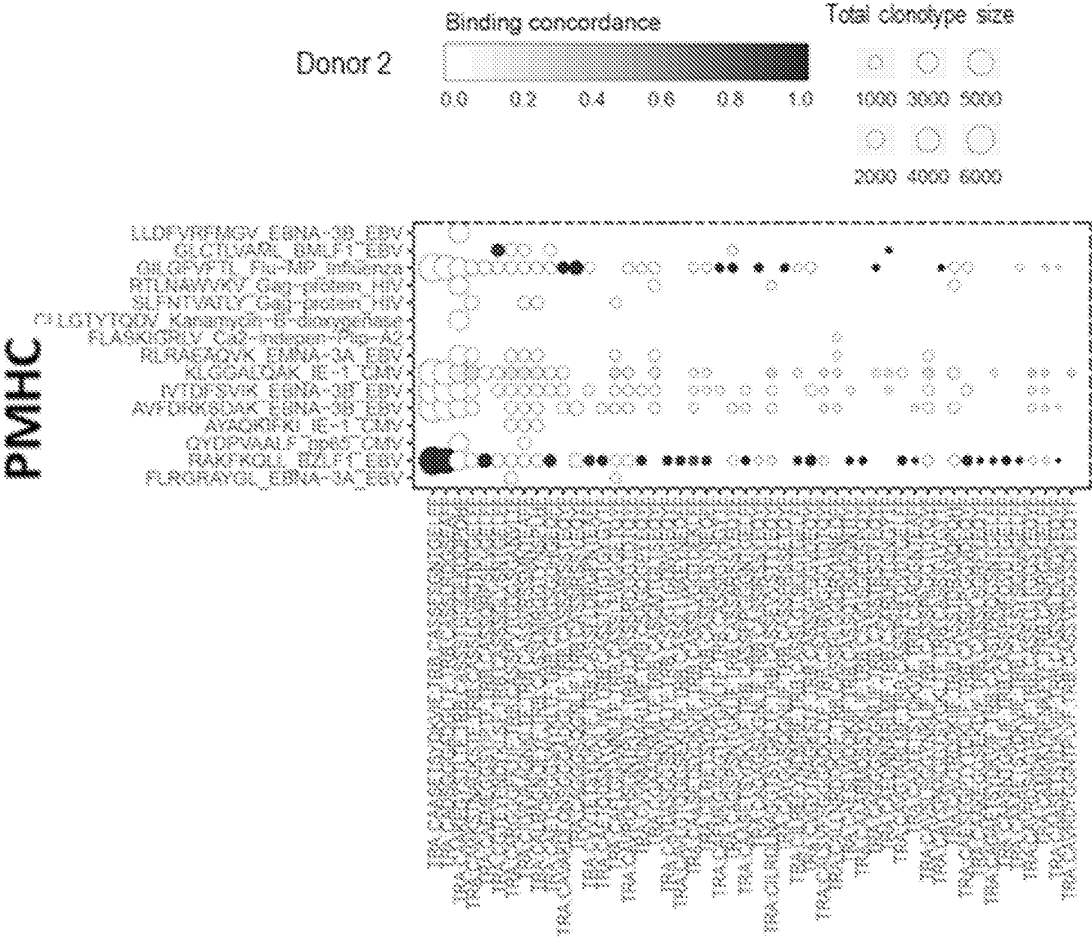


FIG. 11A
(CONTINUED)

FIG. 11A
(CONTINUED)

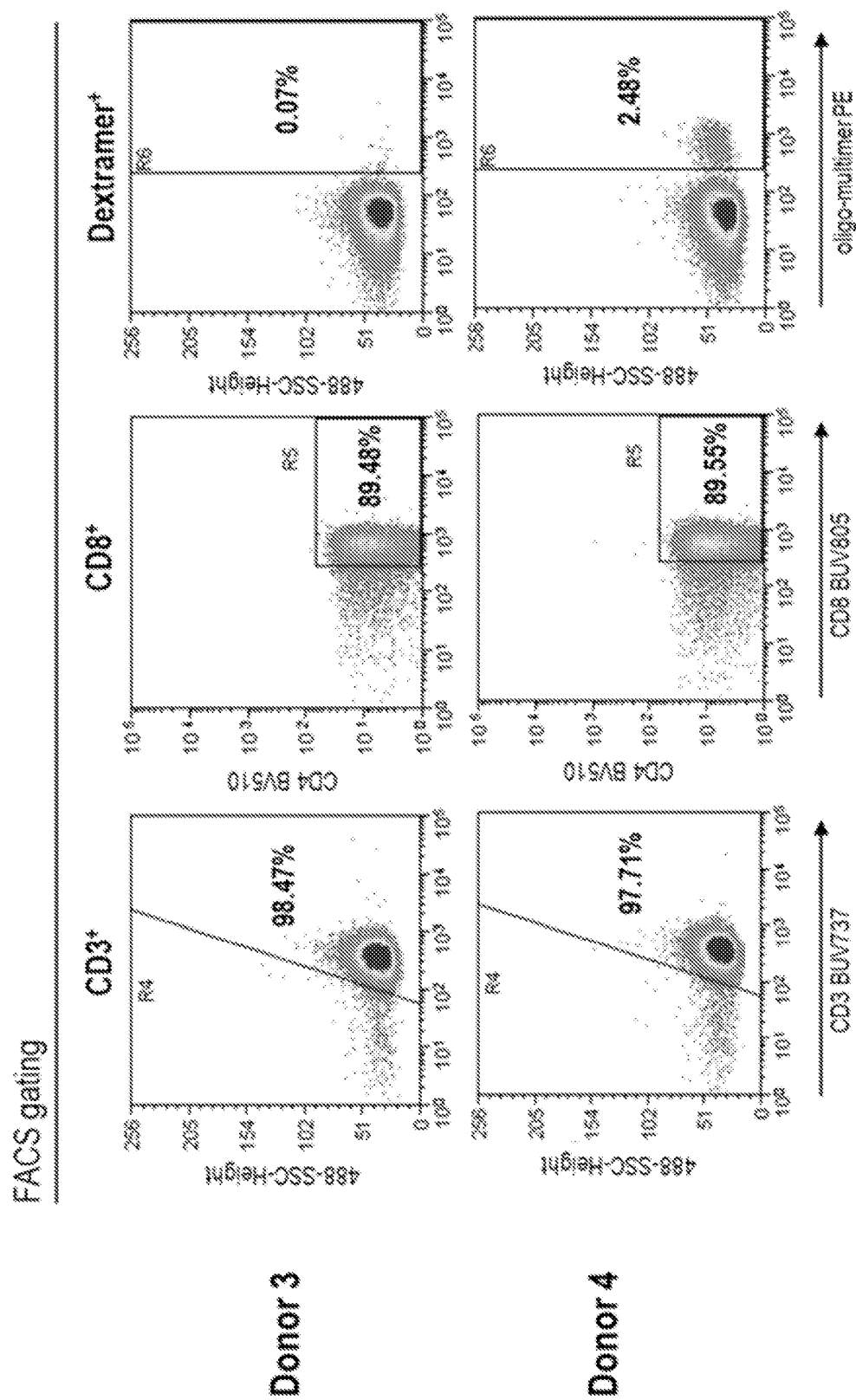


FIG. 11B

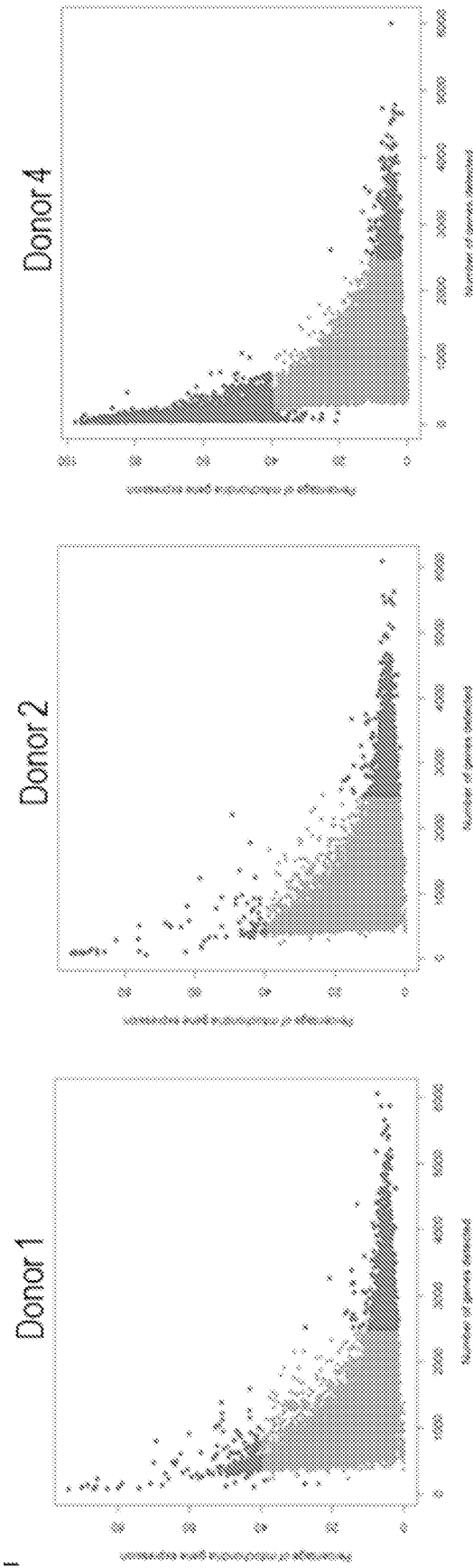


FIG. 12A

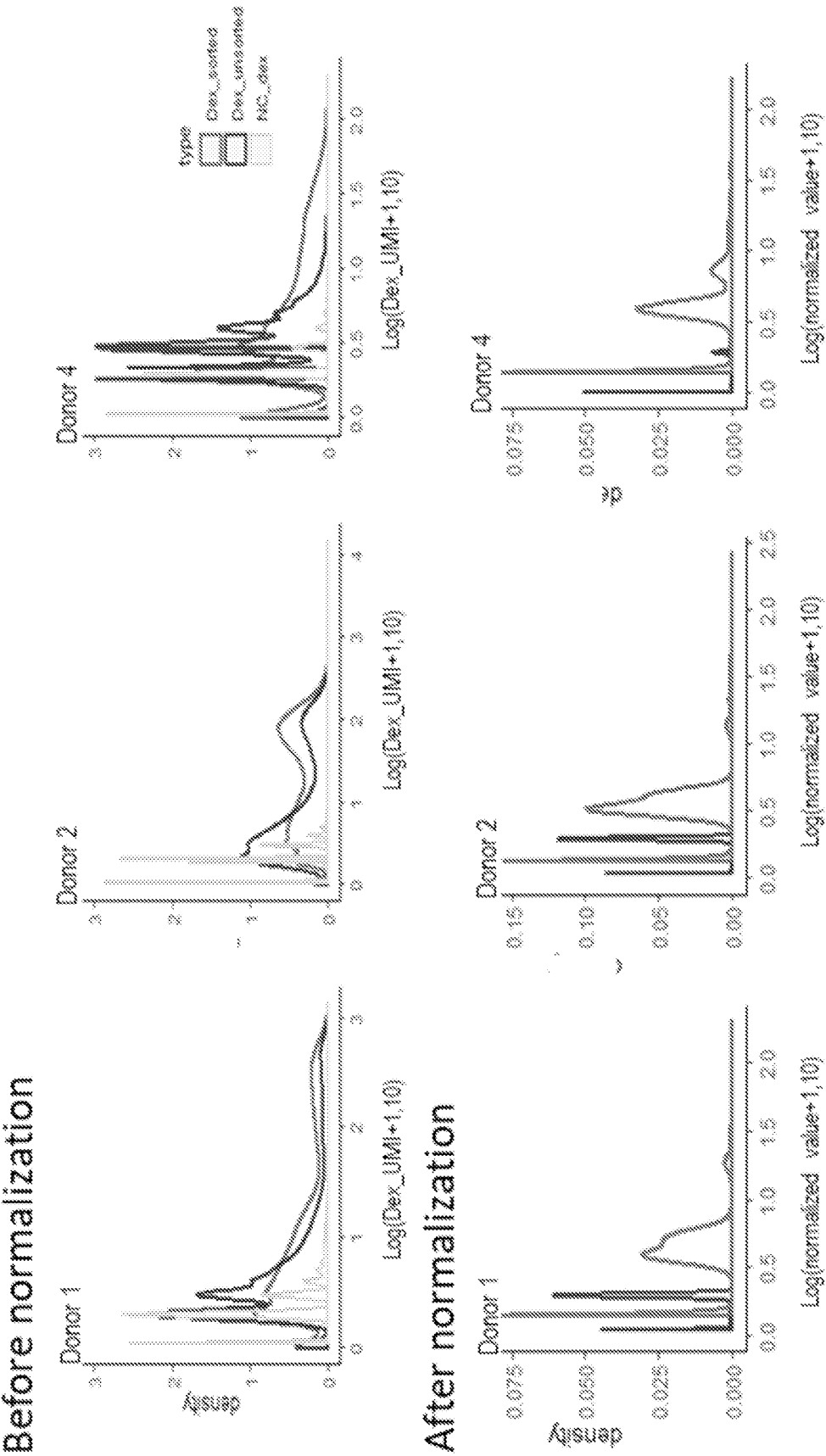
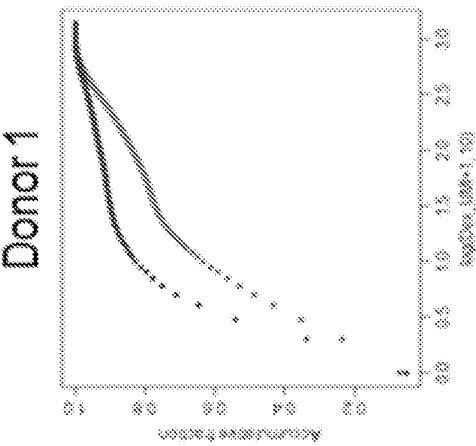
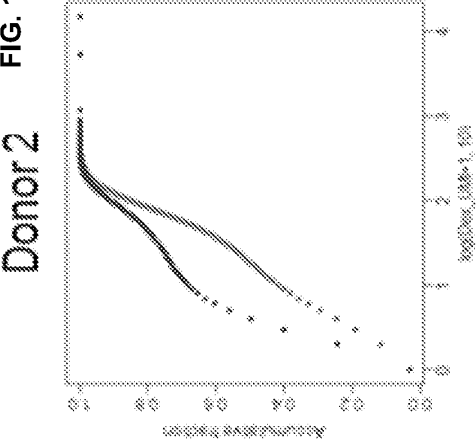
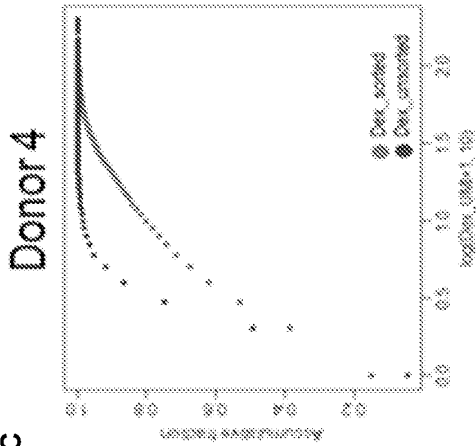
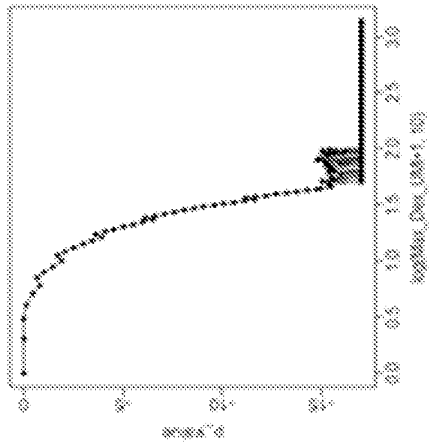
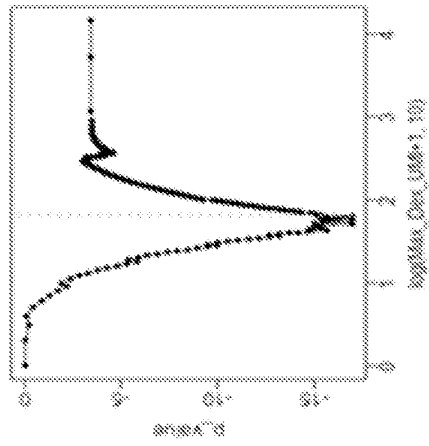
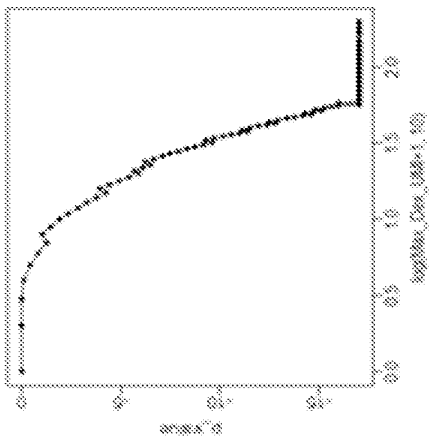


FIG. 12B



Accumulated
distribution of
Dextramer UMI

FIG. 12C



p-value
distribution of KS
test (Dex_sorted vs.
Dex_unsorted)

FIG. 12D

FIG. 12E

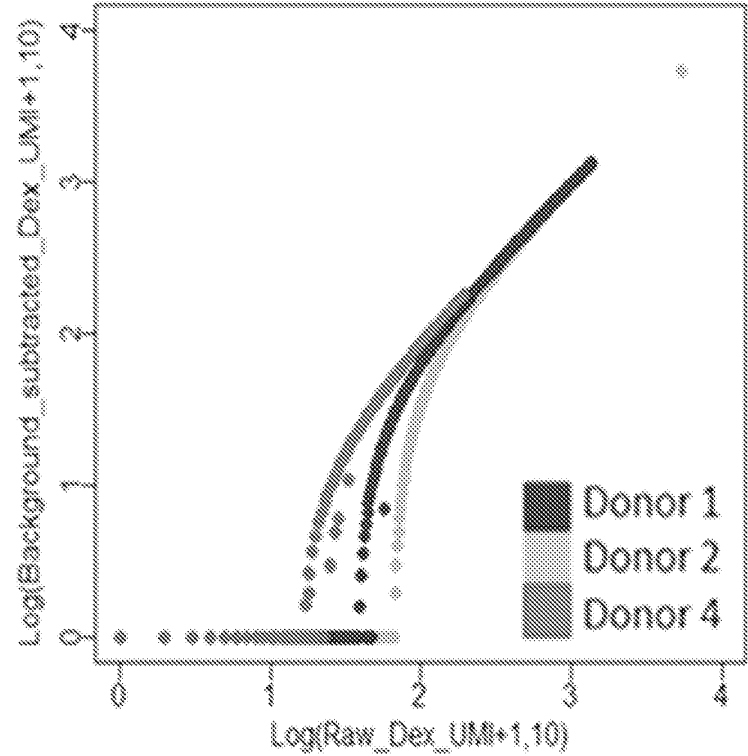


FIG. 12F

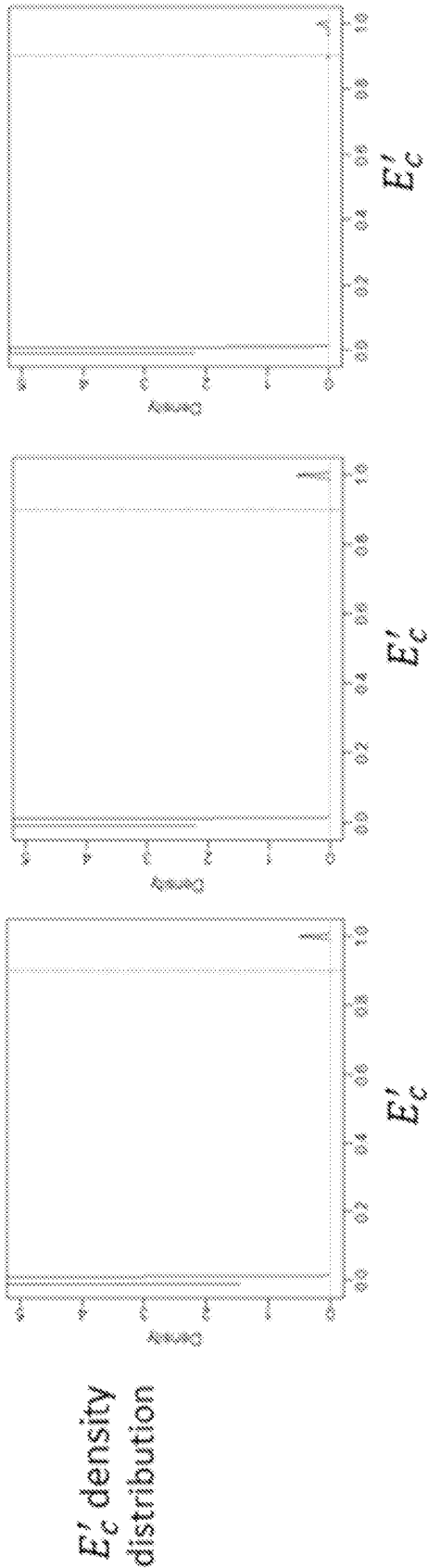


FIG. 13A

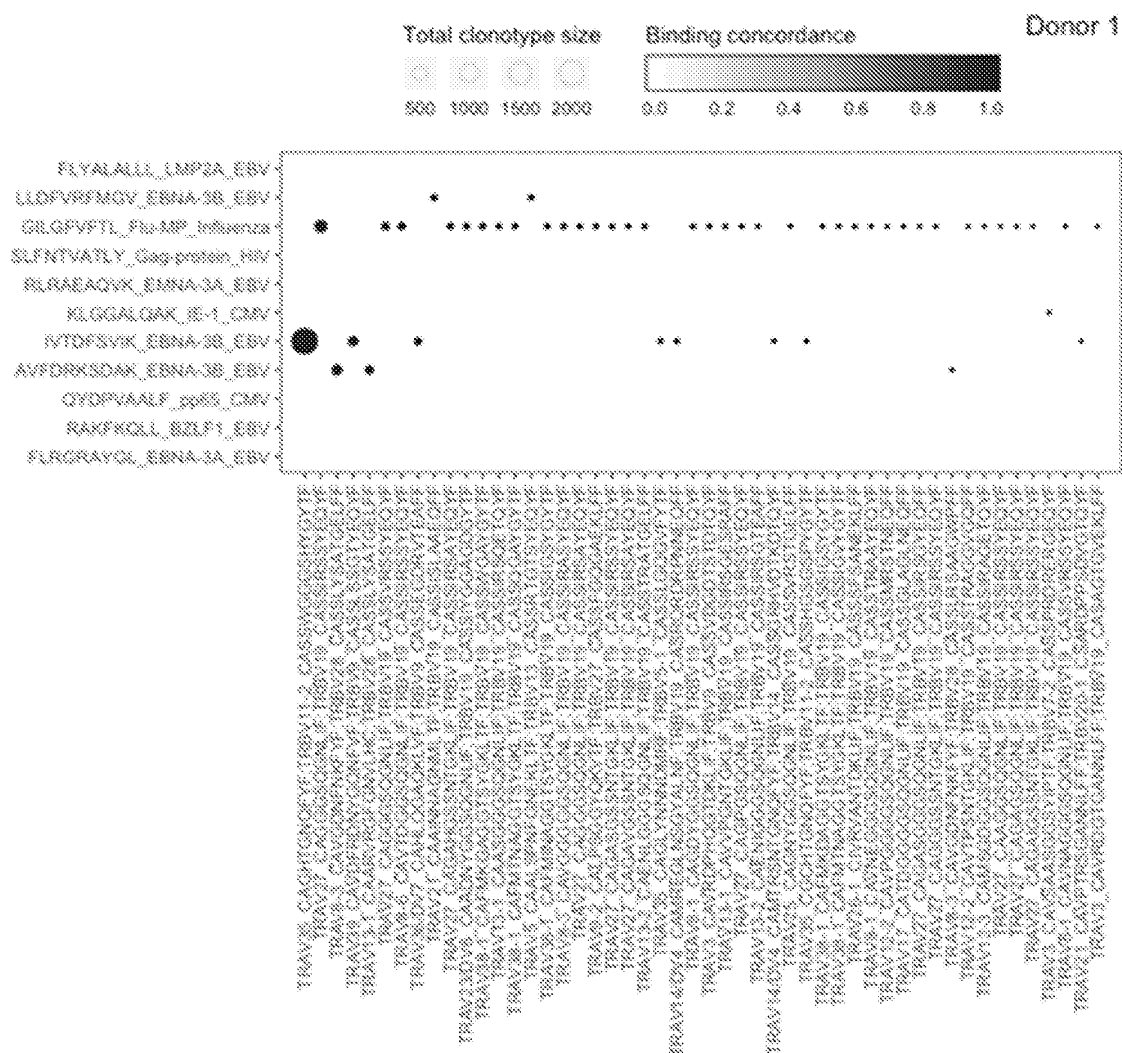


FIG. 13B

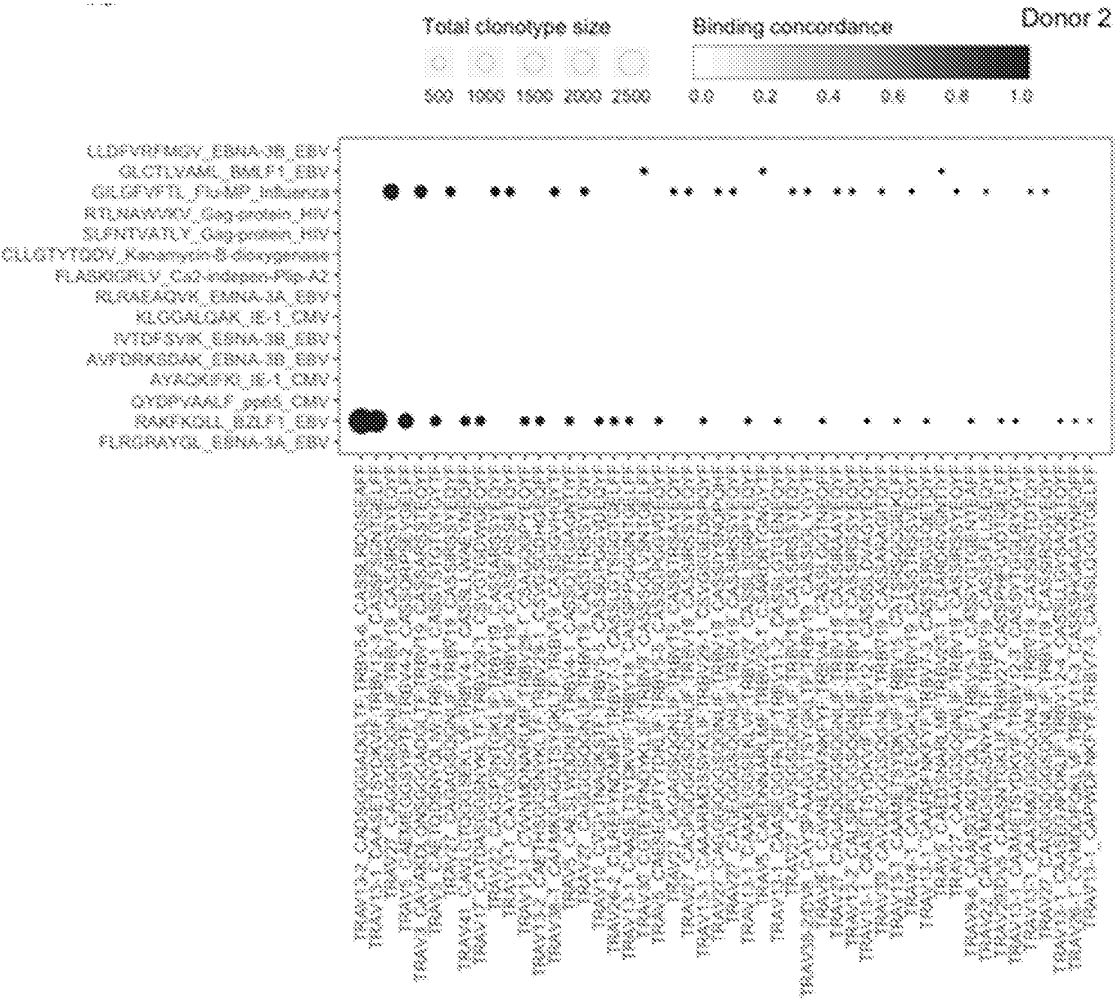


FIG. 13C

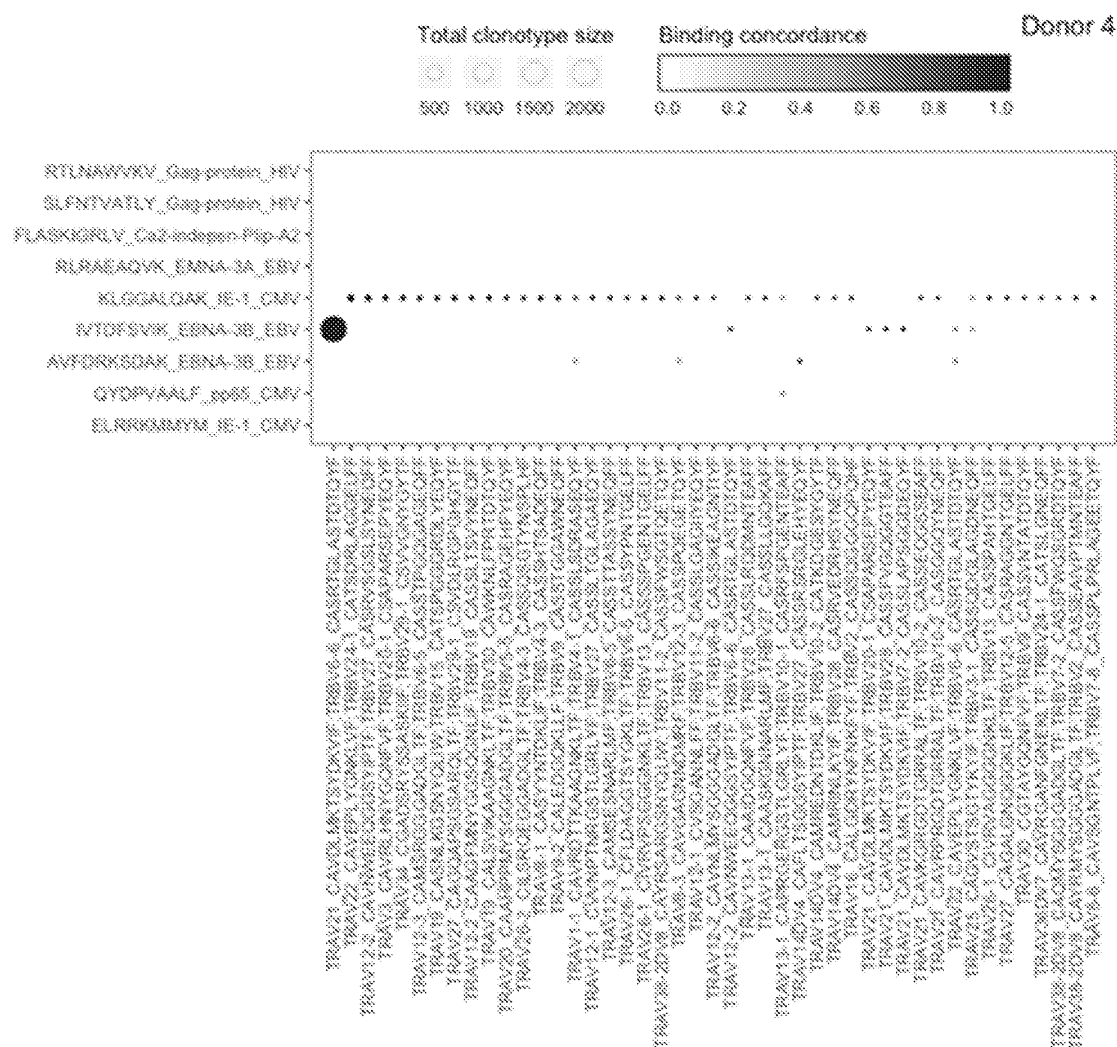


FIG. 14A

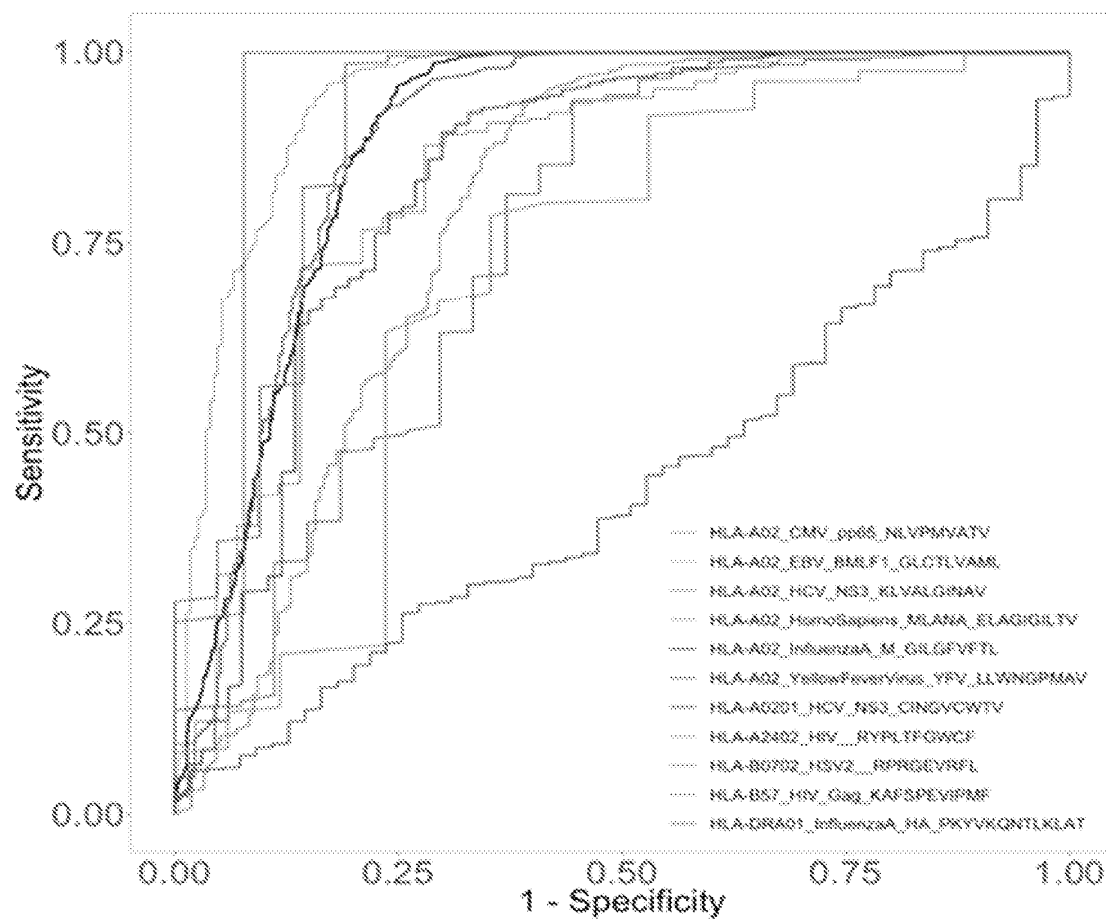


FIG. 14B

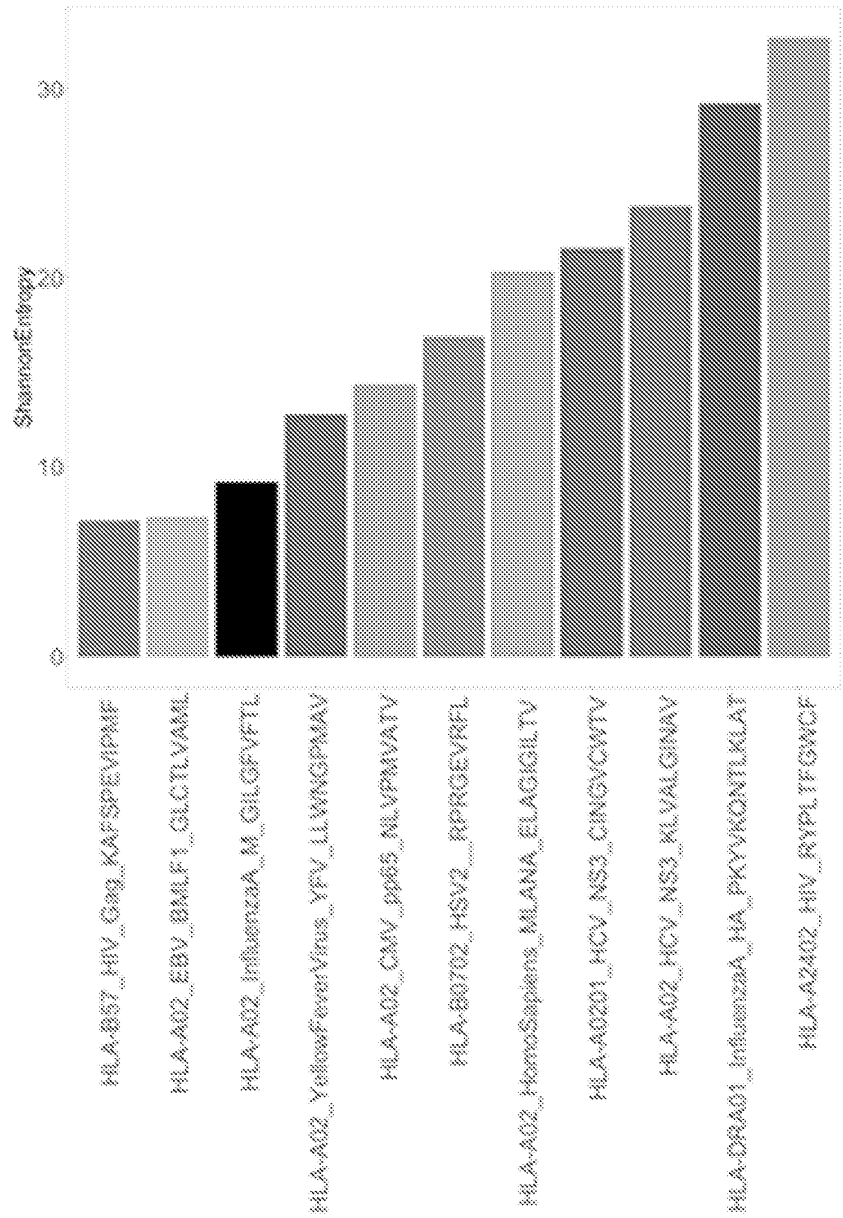


FIG. 15A

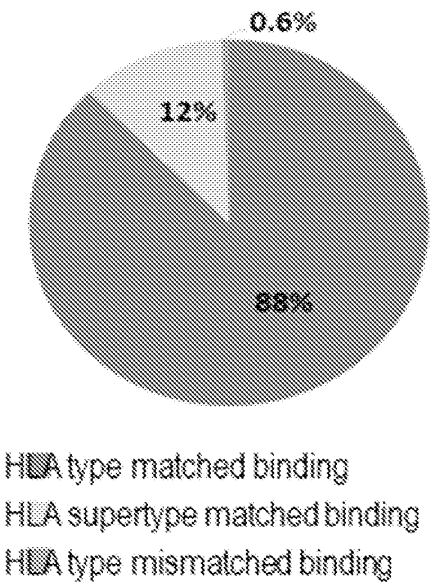
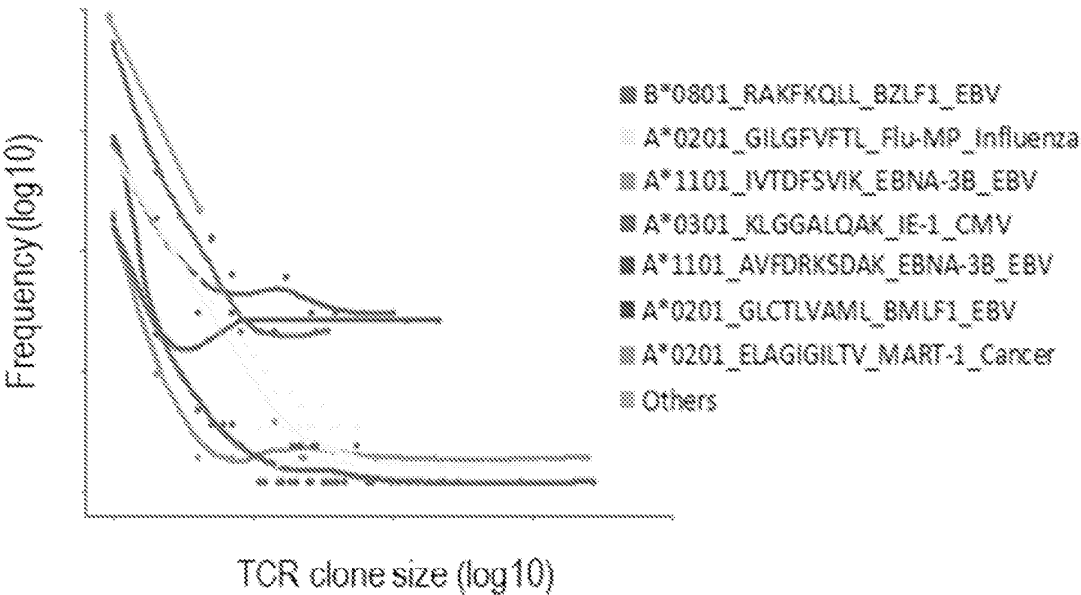


FIG. 15B



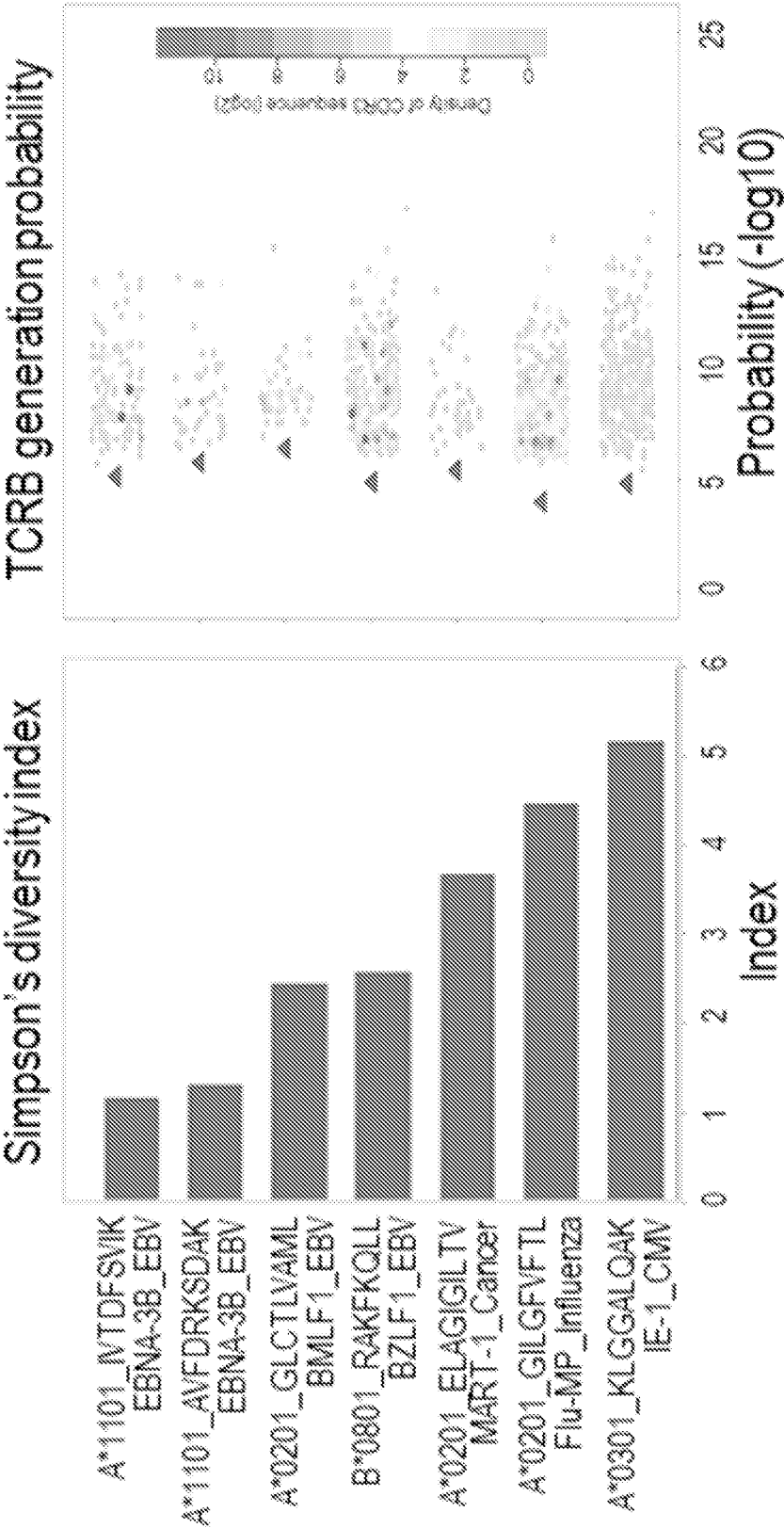


FIG. 15C

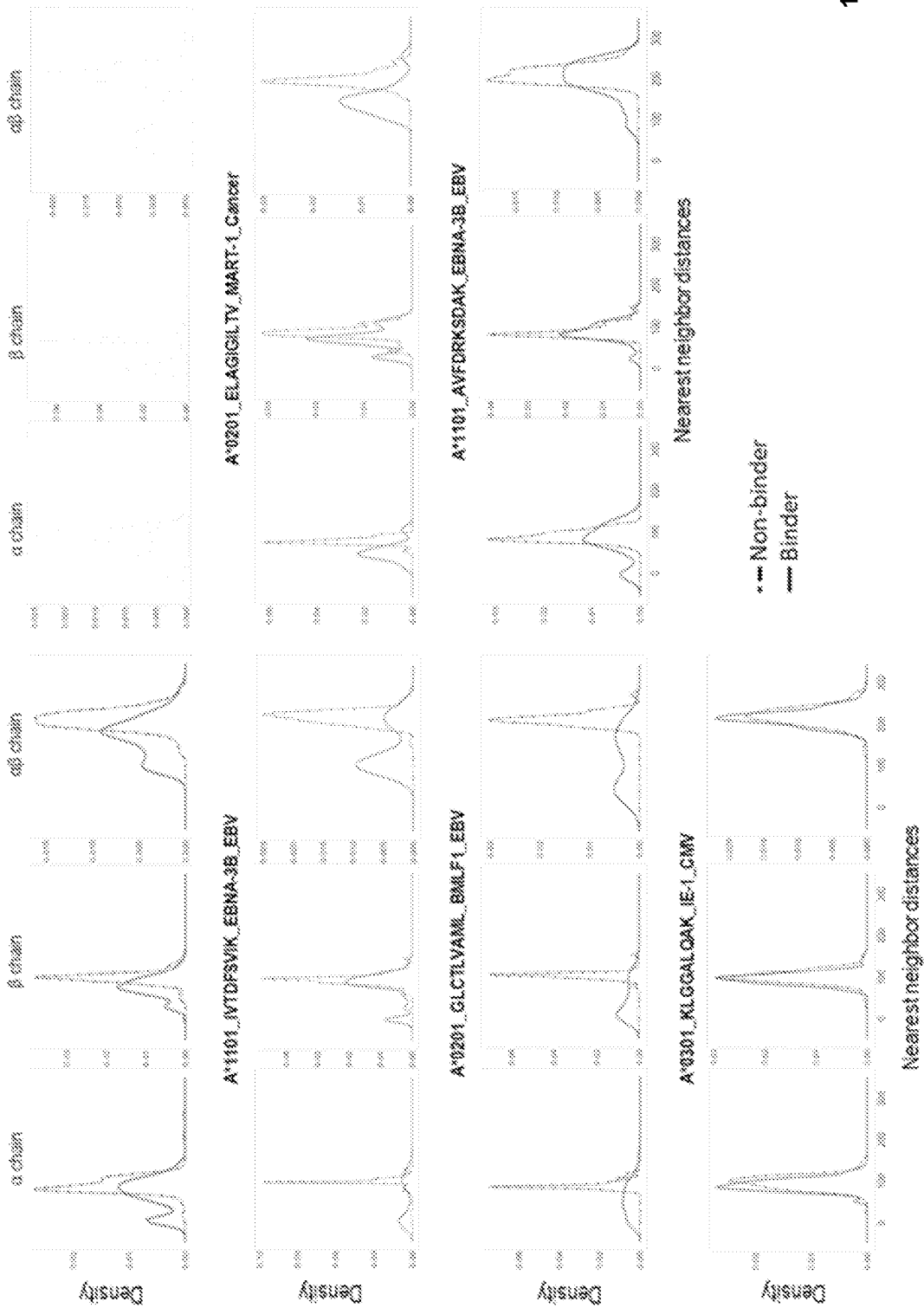


FIG. 16B

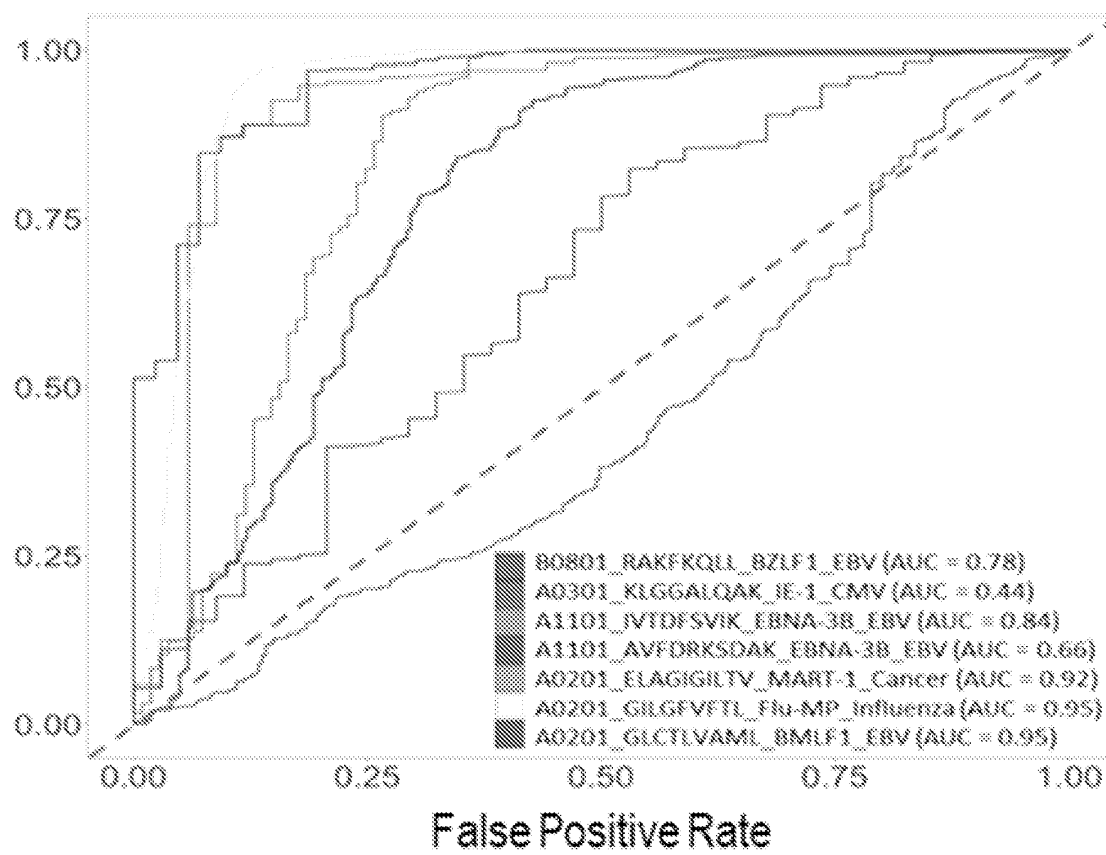
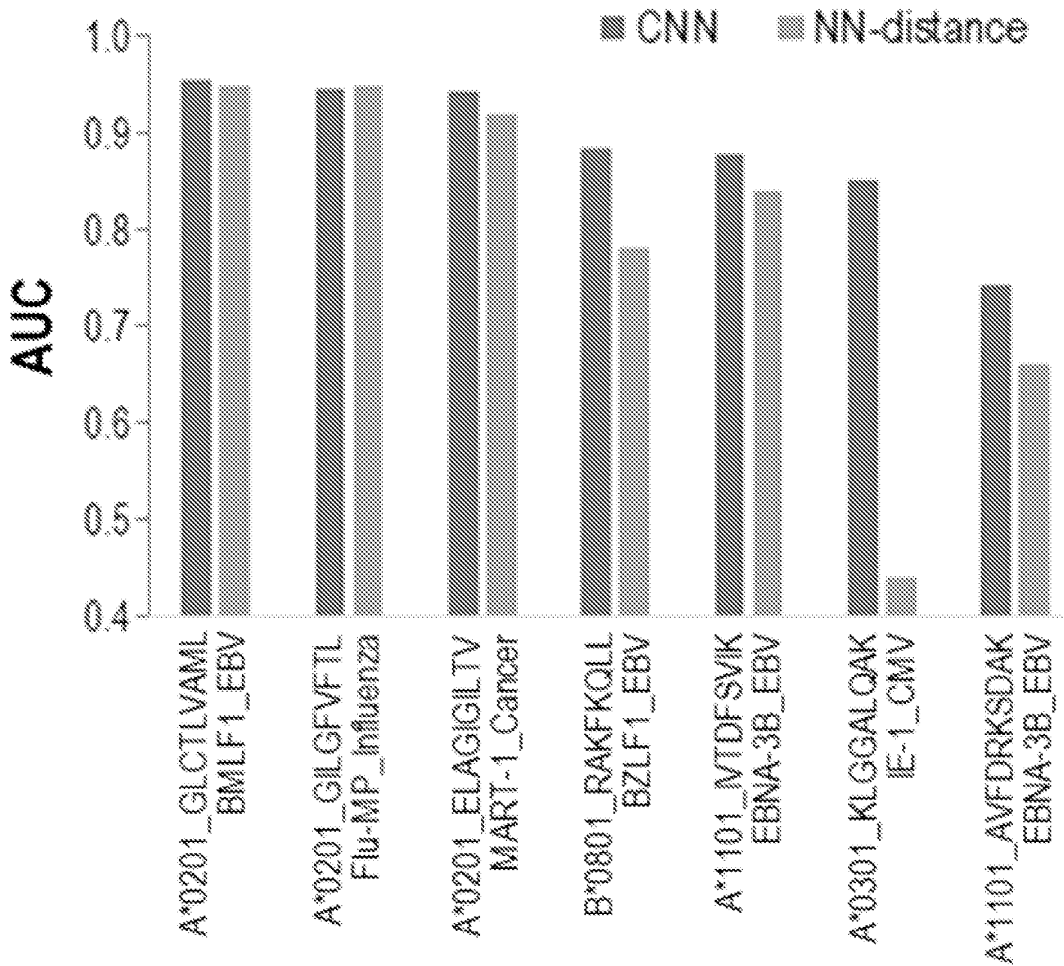


FIG. 16C



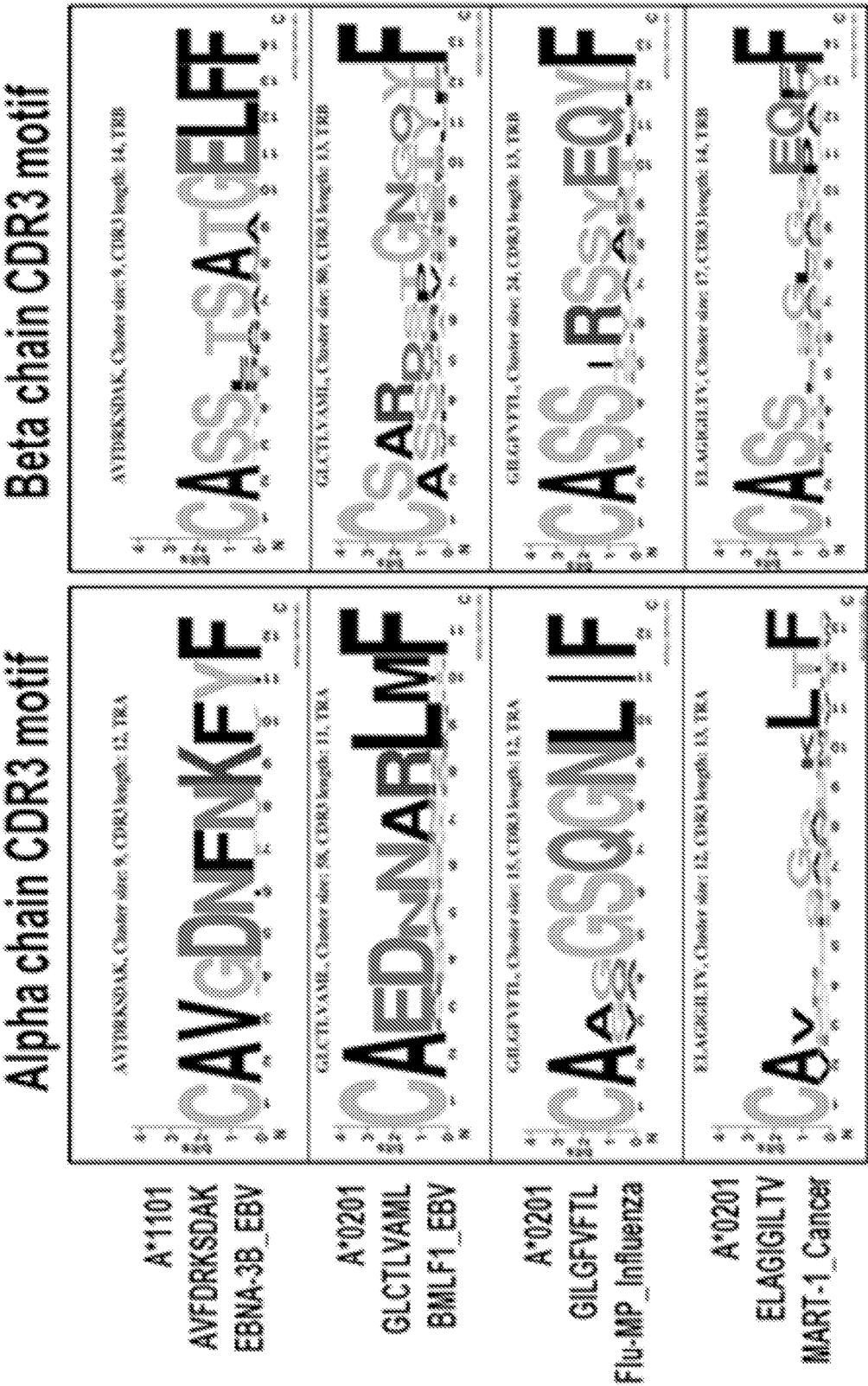


FIG. 17A

FIG. 17B

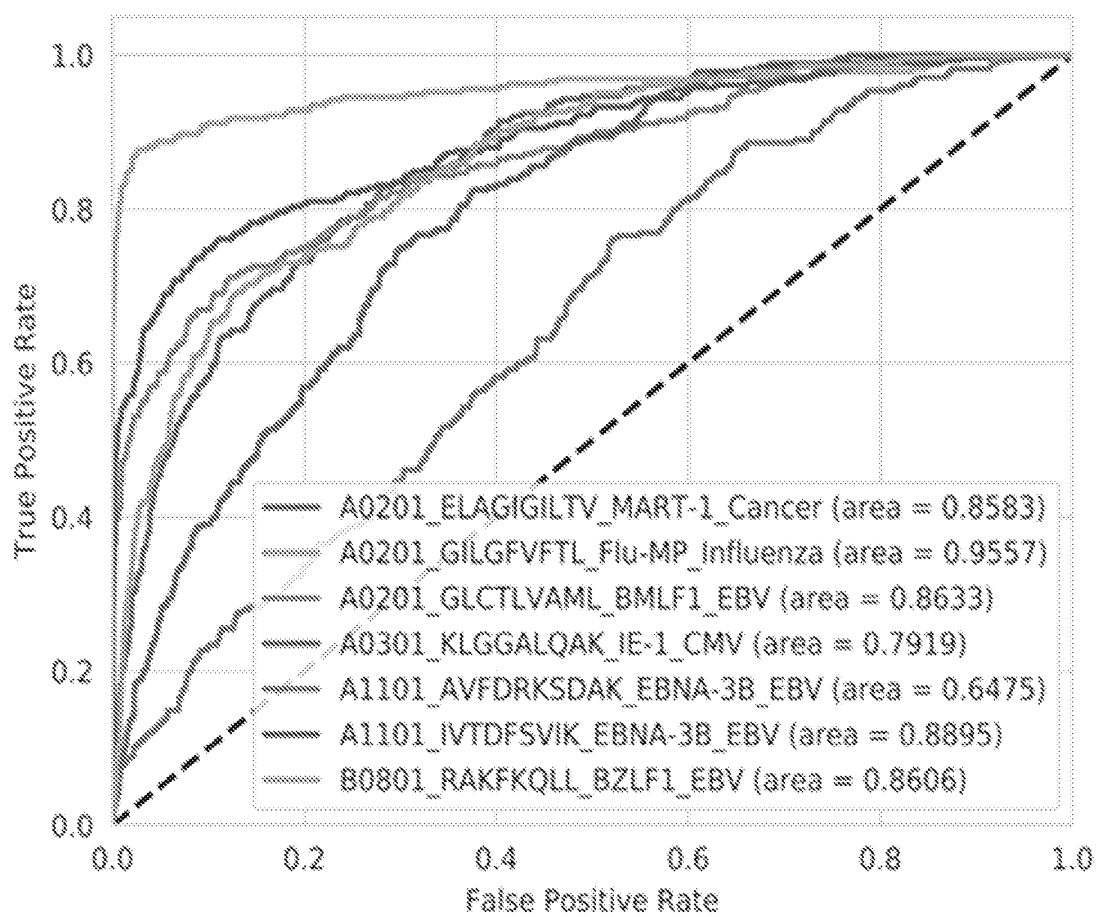


FIG. 18B

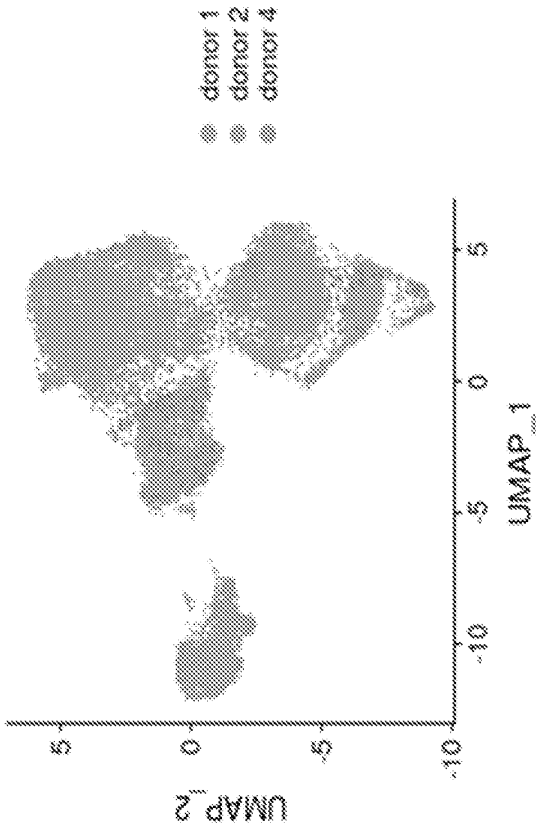
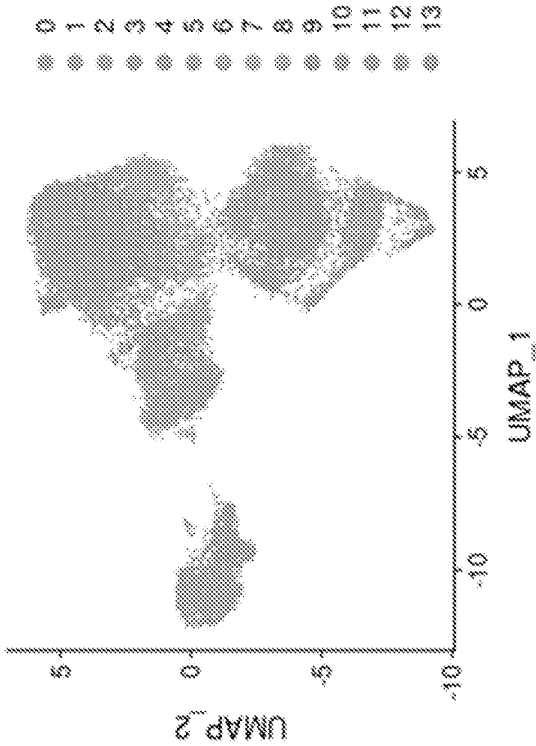


FIG. 18A



Donor	Provider	Gender	Age	Race	BMI	Smoking status	HLA alleles				Virus status		
							HLA-A1	HLA-A2	HLA-B1	HLA-B2	CMV	EBV	Others
Donor 1	StemCell Technology	Female	NA	NA	22.7	NA	2:01	11:01	35:01:00	NA	NA	NA	HIV-1, HIV-2, HCV/HCV
Donor 2		Male	NA	NA	42.5	NA	2:01	1:01	8:01	NA	NA	NA	negative
Donor 3	AllCells	Female	38	white	24	non-smoker	24:02:00	29:02:00	35:02:00	44:03:00	+	-	HIV, HIV, HCV
Donor 4		Male	31	white	35.5	non-smoker	3:01	3:01	7:02	57:01:00	-	-	negative

FIG. 19

FIG. 20

Cat#	HLA allele	Peptide	Annotation	NetMHC HLA allele prediction
WC2197	A*0301	KLGGAQAK	E-1/CMV	HLA-A0301,HLA-A1101
W02149	A*1101	AVFORKSDAK	EBNA 38/EBV	HLA-A0301,HLA-A1101
W02161	A*0201	GHGFVFTL	Flu MP/Influenza	HLA-A0201
W02148	B*0801	RAKFKQLL	BZLF1/EBV	HLA-B0801
W02175	A*1101	IVTDFSVIK	EBNA 38/EBV	HLA-A0301,HLA-A1101
W02162	A*0201	ELAGIGLTV	MART-1/Cancer/	HLA-A0201
W02130	A*0201	GLCTLVAML	BMRF1/EBV	HLA-A0201
WC2656	A*0301	RLRAEAQVK	EMNA 3A/EBV	HLA-A0301
W02143	A*0201	LLOFYKPMGV	EBNA 38/EBV	HLA-A0201,HLA-A0101,HLA-B0801
W02147	B*0801	FLRGAYGL	EBNA 3A/EBV	HLA-A0201,HLA-B0801
W03529	A*0201	PLYALALL	LMP2A/EBV	HLA-A2402,HLA-A2902,HLA-A0201
W02646	A*0201	RTLNAAVVKV	Gag protein/HIV	HLA-B5701,HLA-A1101
W02141	A*0201	LLPGYPVYV	HTLV-1	HLA-A2902,HLA-A0201
WF2196	A*2402	AYAQKIFK	E-1/CMV	HLA-A2402,HLA-B0801
W03531	A*0201	YLLEMLVRL	LMP1/EBV	HLA-A2402,HLA-A0201,HLA-B0801
W03335	A*0201	FLASKGRLV	Ca2+-independ.Plip A2	HLA-A0201,HLA-B0801
WF2133	A*2402	QYQPVAAAF	gp65/CMV	HLA-A2402,HLA-A2902
W02660	A*0201	KTWGQYWDV	gp100/Cancer/	HLA-B5701,HLA-A0201
W03474	A*0201	KVLEYVKKV	MAGE-A1/Cancer/	HLA-A0201
W02652	A*0201	MLDLQPETT	16E7/HPV	na
WH2165	B*0702	QPRAPIRPI	EBNA 6/EBV	HLA-B0702
W02158	A*0201	IMDQVPPSV	gp100/Cancer/	HLA-A0201,HLA-A0101
W03247	A*0201	SLMWITQV	NY-ESO-1/Cancer/	HLA-A0201
WH2166	B*0702	RPFHFRRL	EBNA 3A/EBV	HLA-B0702
W03340	A*0201	SLFNTVATLY	Gag protein/HIV	HLA-A2902,HLA-B3501,HLA-A0301,HLA-A0201,HLA-A1101,HLA-A0101
W02132	A*0301	NLVPMVATV	gp65/CMV	HLA-A0201
W03338	A*0201	SLFNTVATL	Gag protein/HIV	HLA-A0201
W02177	A*0201	RMFPNAPYL	WT-1	HLA-A2402,HLA-A2902,HLA-B5701,HLA-A0201
W02191	A*0201	YLNDHLEPW	BCL-X/Cancer/	HLA-A0201
W02137	B*0801	ELRRKMMYIM	E-1/CMV	HLA-B0801
WA2131	A*0101	VTEHDTLLY	E-1/CMV	HLA-A2902,HLA-B4402,HLA-A0101
W03697	A*0201	CLLW5QTSK	Tyrosinase/Cancer/	HLA-A0201
W03497	A*0201	KVAELVHFL	MAGE A3/Cancer/	HLA-A0201
W05066	A*0201	CLLGYTQDV	Kanamycin B dioxygenase	HLA-A0201,HLA-B0801
W03307	A*0201	LLMGTLSIVC	HPV 16E7, 82-91	HLA-A0201
W02144	A*0201	CLGGULTMV	LMP-2A/EBV	HLA-A0201
W02139	A*0201	RKEPVNGV	RT/HIV	HLA-A0201
WF2639	A*2402	CYTWNQMNL	WT1 (235-243)236M->Y	HLA-A2402
W02157	A*0201	KLGCVDHIV	PSA 148-154	HLA-A0201
W03339	A*0201	SLYNTVATLY	Gag protein/HIV	HLA-A2902,HLA-B3501,HLA-A0301,HLA-A0201,HLA-A1101,HLA-A0101
WC2632	A*0301	RIAAWMATY	BCL-2L1/Cancer/	HLA-A2902,HLA-B3501,HLA-A0301,HLA-B5701,HLA-A1101,HLA-A0101
WX2138	B*3501	IPSNVHHY	gp65/CMV	HLA-B3501
WH2136	B*0702	TPRYTGSGAM	gp65/CMV	HLA-B3501,HLA-B0702
WH2135	B*0702	RPHRNGFTVL	gp65/CMV	HLA-B0702,HLA-B0801
NI3233	NR(B0801)	AAKGRGAAL	NC	na
W02666	A*0201	ALIAPVHAV	NC	na
WF3231	A*2402	AYSSAGAS	NC	na
WH3397	B*0702	GPAESAAGL	NC	na
WA3580	A*0101	SLGGGGLGY	NC	na
WA3579	A*0101	STEGGGLAY	NC	na

FIG. 21

pMHC	Donor 1		Donor 2		Donor 4		All donor summary	
	total binding T	unique TCR	total binding T	unique TCR	total binding T	unique TCR	total binding T	unique TCR
	cells	clones	cells	clones	cells	clones	T cells	clones
B*08:01_RAKFKQLI_BZLF1_EBV	35	34	8,229	196	1	1	8,265	229
A*02:01_GRGFVFTL_Flu-MP_Influenza	1,673	278	4,271	447	1	1	5,945	693
A*11:01_IVTDFSVK_EBNA-38_EBV	2,860	27	20	19	2,317	76	5,197	123
A*03:01_KGGALQAK_IE-1_CMV	79	58	28	26	357	204	464	288
A*11:01_AVFORXDAK_EBNA-38_EBV	351	12	8	8	19	18	378	37
A*02:01_GLCTLVAMK_BMP1_EBV	16	10	310	33	1	1	327	43
A*02:01_ILDFVRFMGV_EBNA-38_EBV	92	6	13	5	0	0	105	11
A*02:01_FLYALALL_ILMP2A_EBV	3	3	49	8	0	0	52	11
A*02:01_ELAGIGLTV_MART-1_Cancer	31	28	0	0	14	14	45	42
B*08:01_FURGRAYGI_EBNA-3A_EBV	3	3	12	9	0	0	15	12
A*02:01_YLLEMLWBL_ILMP1_EBV	5	5	0	0	3	3	8	8
A*02:01_ILFGYPYV_HTLV-1	5	5	1	1	0	0	6	6
A*24:02_AYAQRIFK_IE-1_CMV	3	3	0	0	1	1	4	4
A*03:01_RLRASQVK_EBNA-3A_EBV	0	0	1	1	2	2	3	3
B*07:02_RPPHFRRL_EBNA-3A_EBV	2	2	0	0	1	1	3	3
A*24:02_CYTWNQMMNL_WT1-(235-243)2X	3	3	0	0	0	0	3	3
A*02:01_MLDLQPETT_15E7_HPV	3	3	0	0	0	0	3	3
A*24:02_QYDPMVAALF_pp65_CMV	2	2	0	0	1	1	3	3
A*02:01_RTLNAAWVKV_Gag-protein_HIV	1	1	0	0	1	1	2	2
A*07:01_IMDQVPPSV_gp100_Cancer	1	1	1	1	0	0	2	2
B*07:02_GPMAPRPI_EBNA-6_EBV	2	2	0	0	0	0	2	2
A*02:01_FLASNGRLV_Ca2-indepen-Plp-A	2	2	0	0	0	0	2	2
A*02:01_KVLEYVVKV_MAGE-A1_Cancer	2	2	0	0	0	0	2	2
B*35:01_IPSINVHHY_pp65_CMV	2	2	0	0	0	0	2	2
A*02:01_SLPNTVATL_Gag-protein_HIV	0	0	0	0	1	1	1	1
A*02:01_KTWGQFWQV_gp100_Cancer	1	1	0	0	0	0	1	1
A*02:01_SLSMWITQV_WT-630-1_Cancer	1	1	0	0	0	0	1	1
A*02:01_RMFPPAPYL_WT-1	1	1	0	0	0	0	1	1
A*03:01_RAAAWMATY_BCL-2L1_Cancer	1	1	0	0	0	0	1	1

FIG. 22

pMHC	Peptide Hydrophobicity		Peptide polarity		Peptide bulkiness	
	average of TCR contact positions only	average of all positions	average of TCR contact positions only	average of all positions	average of TCR contact positions only	average of all positions
KLGGALQAK_IE-1_CMV	-0.08	-0.10	8.88	8.54	10.21	13.16
GILGFVFTL_Flu-MP_Influenza	1.13	2.27	7.00	6.43	14.69	16.44
ELAGIGILTV_MART-1_Cancer	2.05	1.76	7.10	7.30	12.40	15.48
RAKFKQLL_BZLF1_EBV	1.03	-0.45	6.87	8.33	18.55	16.78
GLCTLVAML_BMLF1_EBV	1.70	2.30	6.80	6.38	16.23	16.24
AVFDKSDAK_EBNA-3B_EBV	-3.18	-0.95	11.00	9.54	12.79	14.29
IVTDFSVIK_EBNA-3B_EBV	2.00	1.26	7.33	7.72	18.61	17.60

FIG. 23

pMHC	Peptide	Number of unique TCR
A*02_InfluenzaA_M_GILGFVFTL	GILGFVFTL	1187
A*02_YellowFeverVirus_YFV_LLWNGPMAV	LLWNGPMAV	525
A*02_CMV_pp65_NLVPMVATV	NLVPMVATV	390
A*02_EBV_BMLF1_GLCTLVAML	GLCTLVAML	274
B*07:02_HSV2__RPRGEVRFL	RPRGEVRFL	127
A*02:01_HCV_NS3_CINGVCWTV	CINGVCWTV	83
A*02_HCV_NS3_KLVALGINAV	KLVALGINAV	75
DRA*01_InfluenzaA_HA_PKYVKQNTLKLAT	PKYVKQNTLKLAT	70
A*02_HomoSapiens_MLANA_ELAGIGILTV	ELAGIGILTV	57
B*57_HIV_Gag_KAFSPEVIPMF	KAFSPEVIPMF	33
A*24:02_HIV_RYPLTFGWCF	RYPLTFGWCF	30

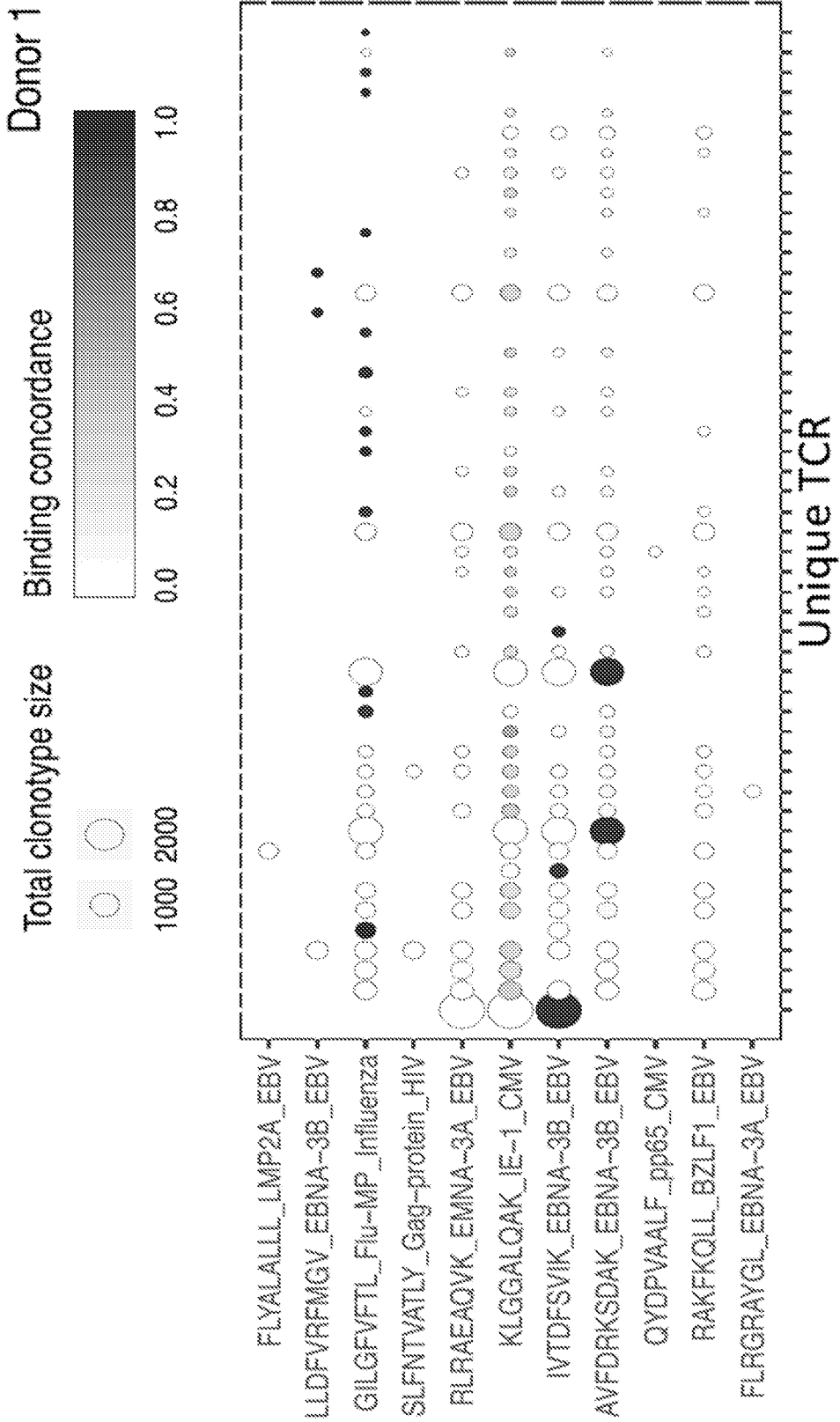


FIG. 24

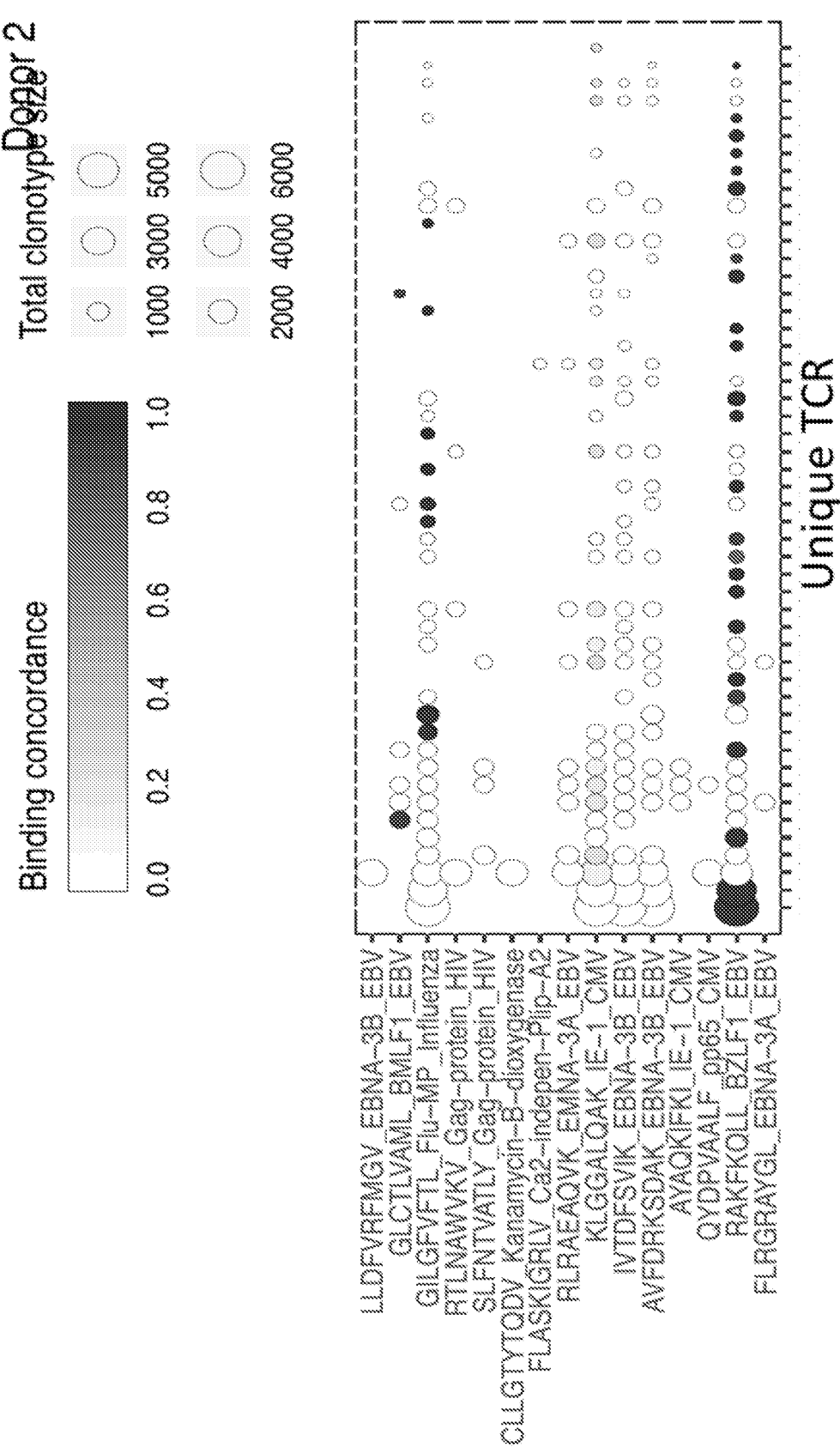


FIG. 24
(CONTINUED)

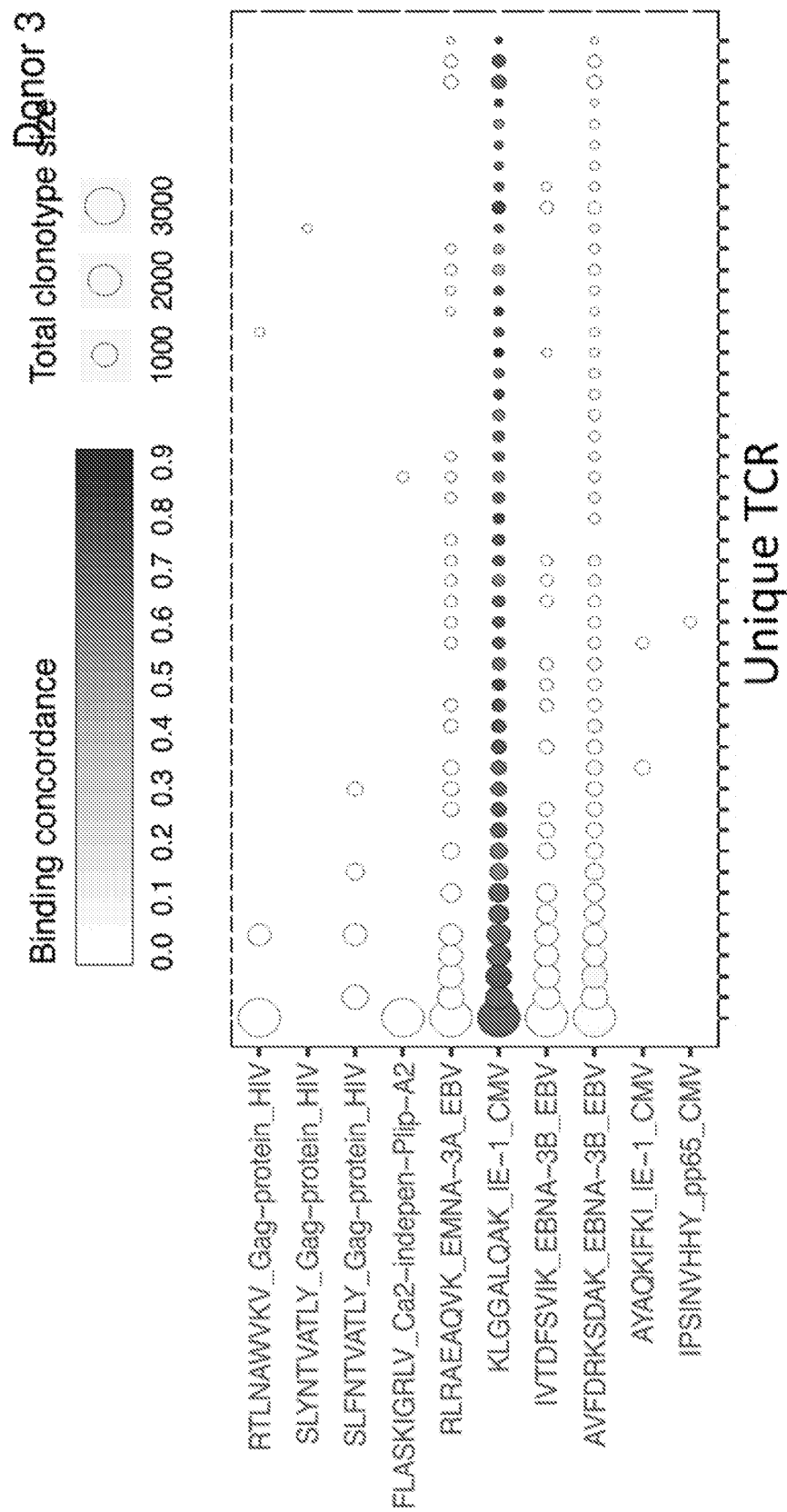


FIG. 24
(CONTINUED)

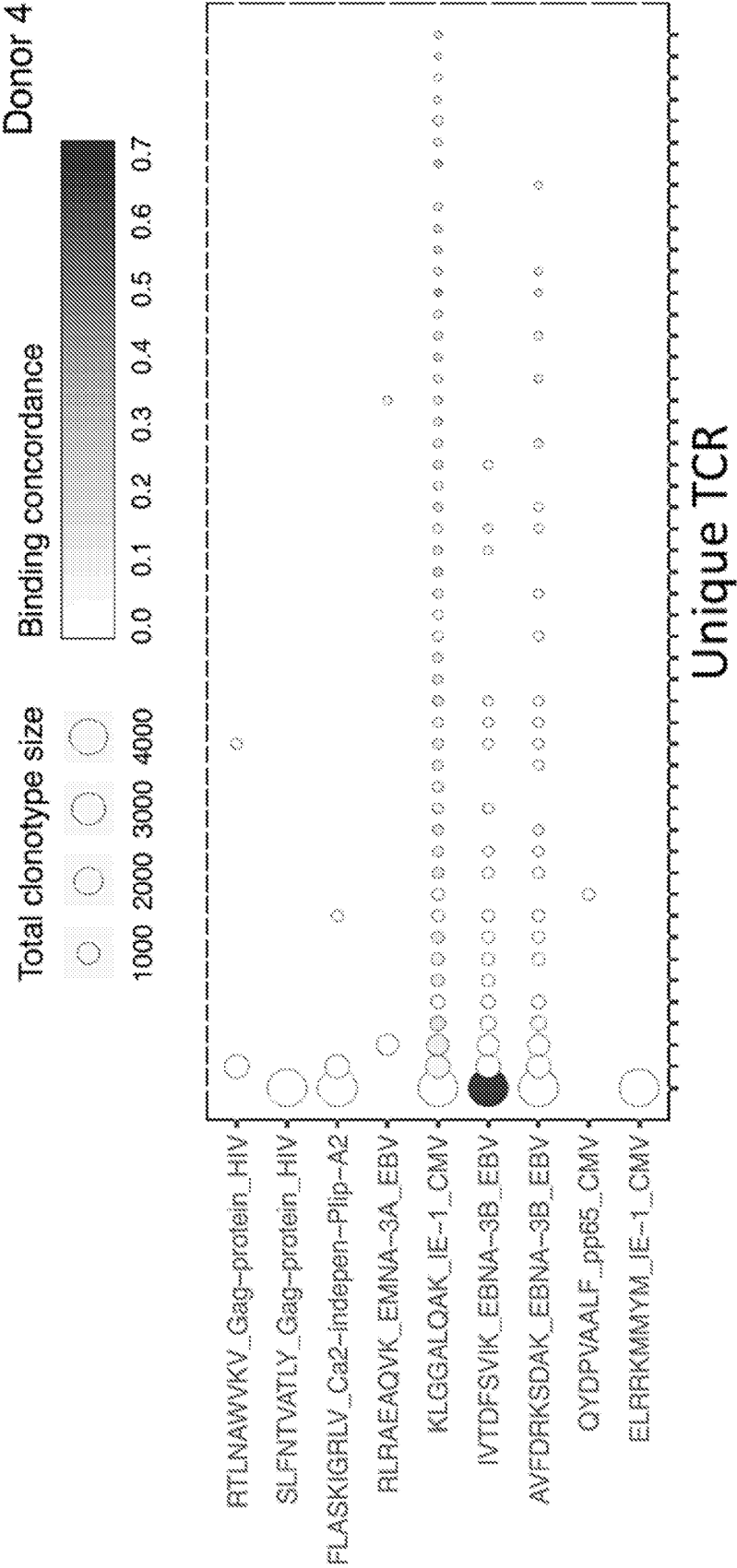


FIG. 24
(CONTINUED)

ICON (Integrative Context-specific Normalization)

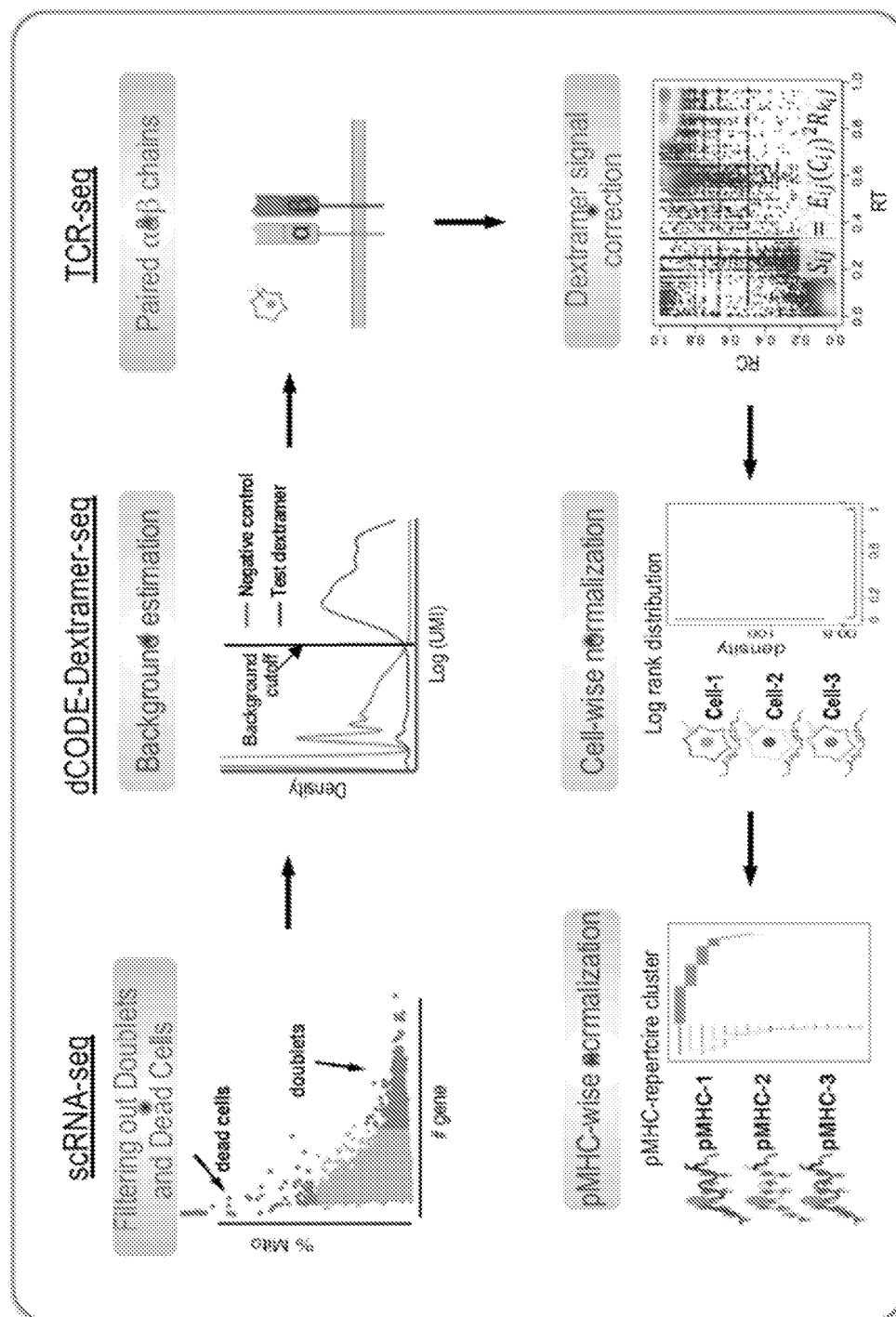


FIG. 25A

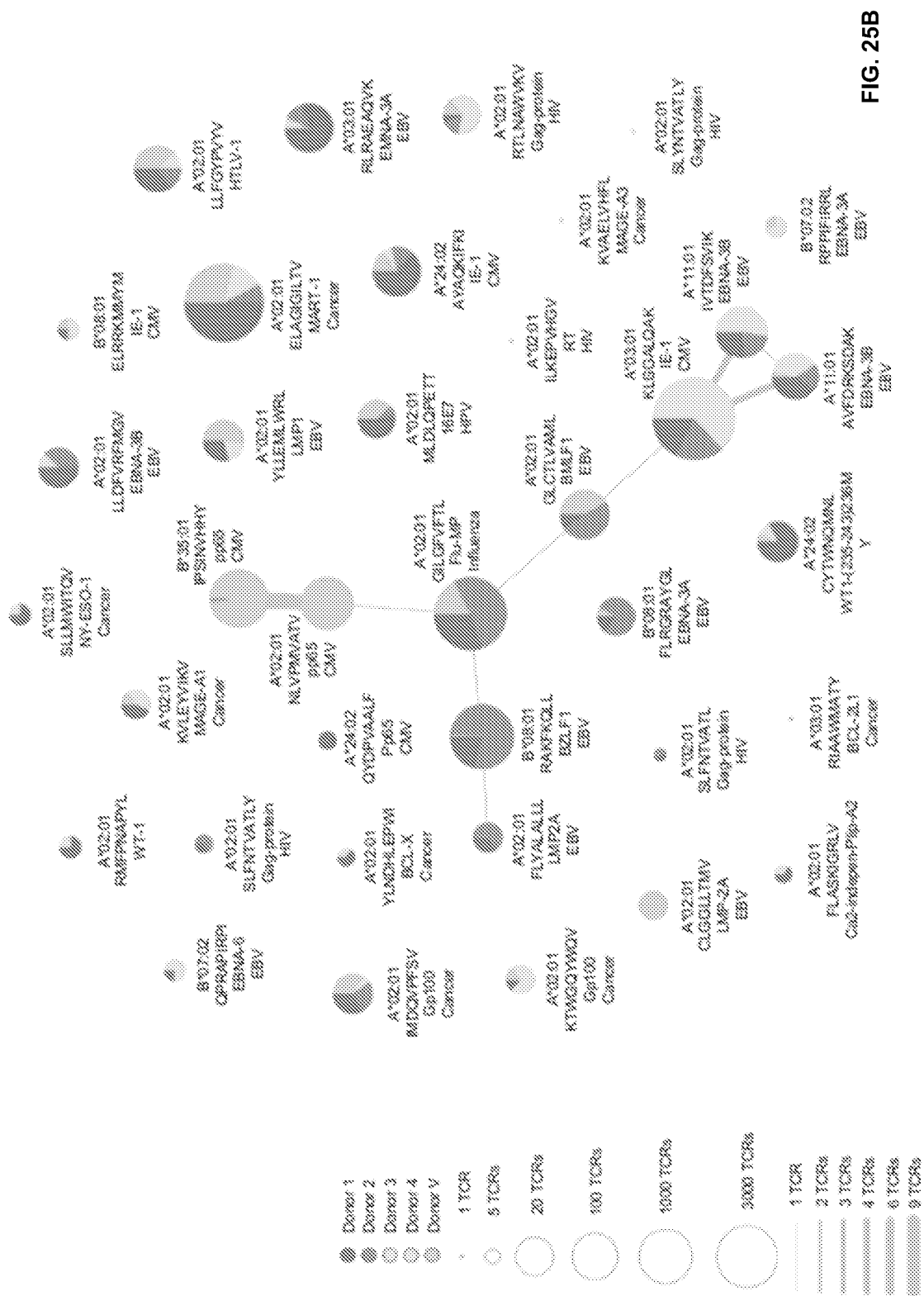
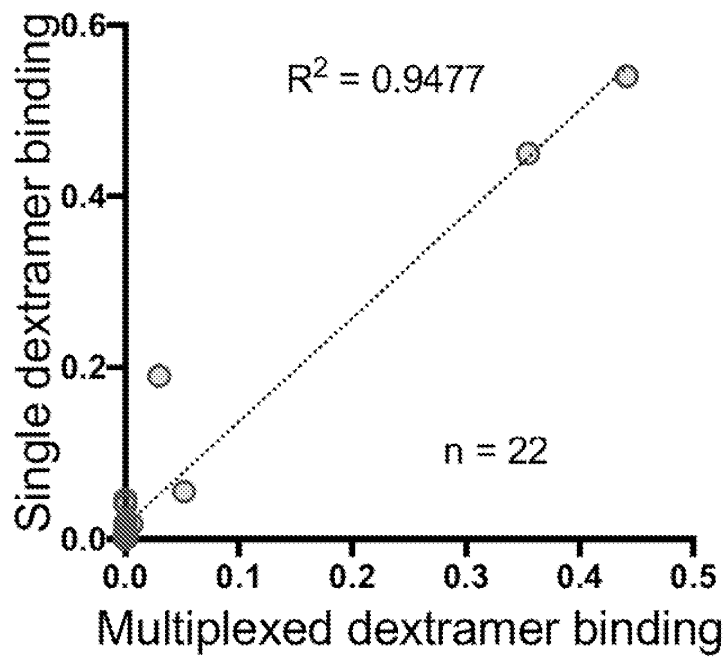


FIG. 25C



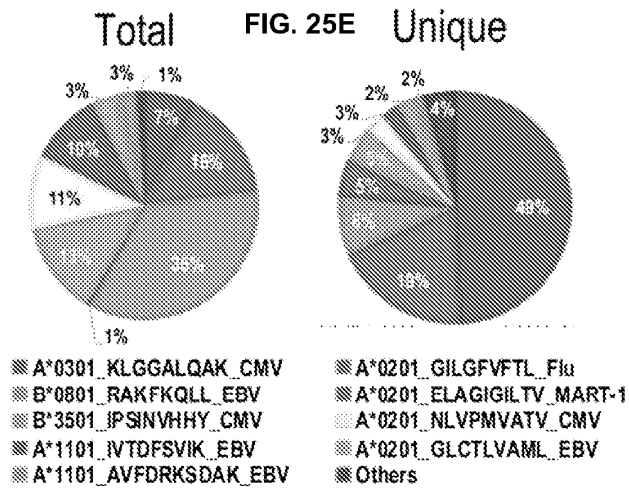
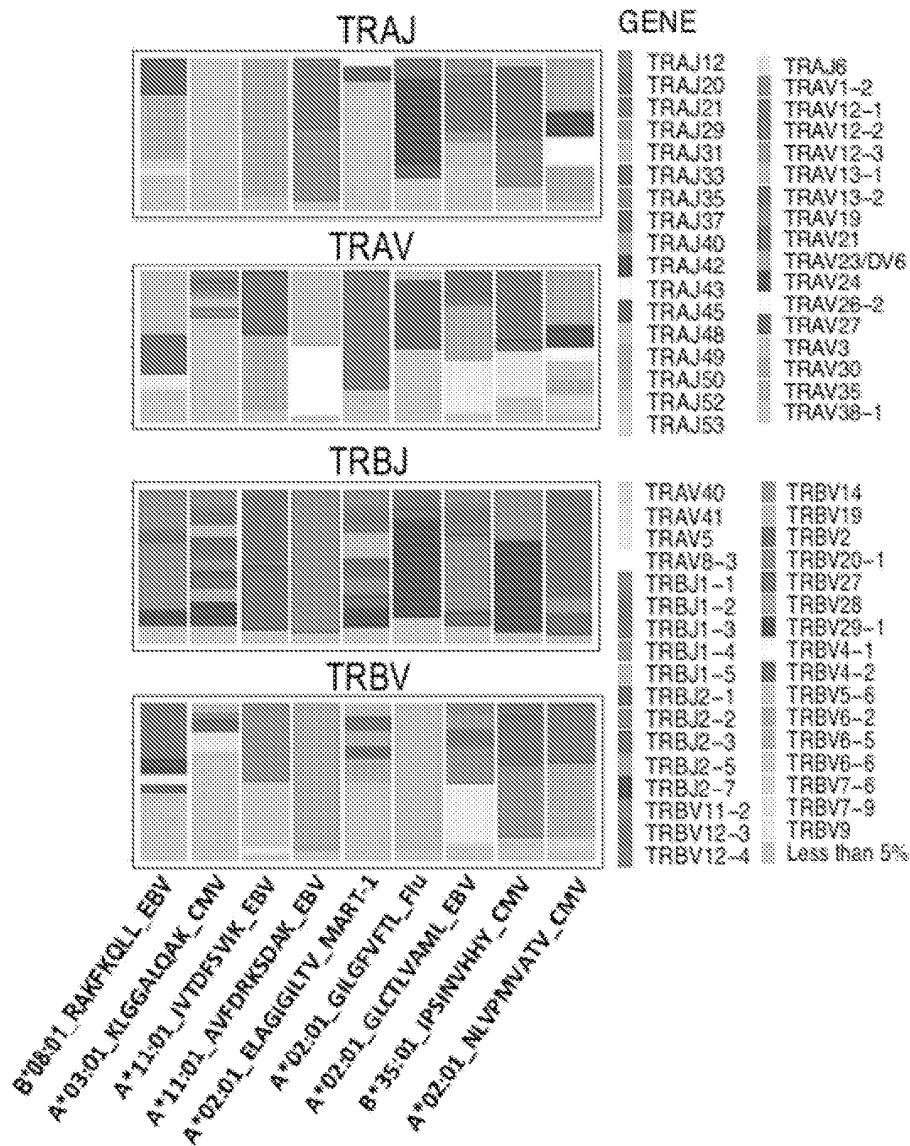


FIG. 25F



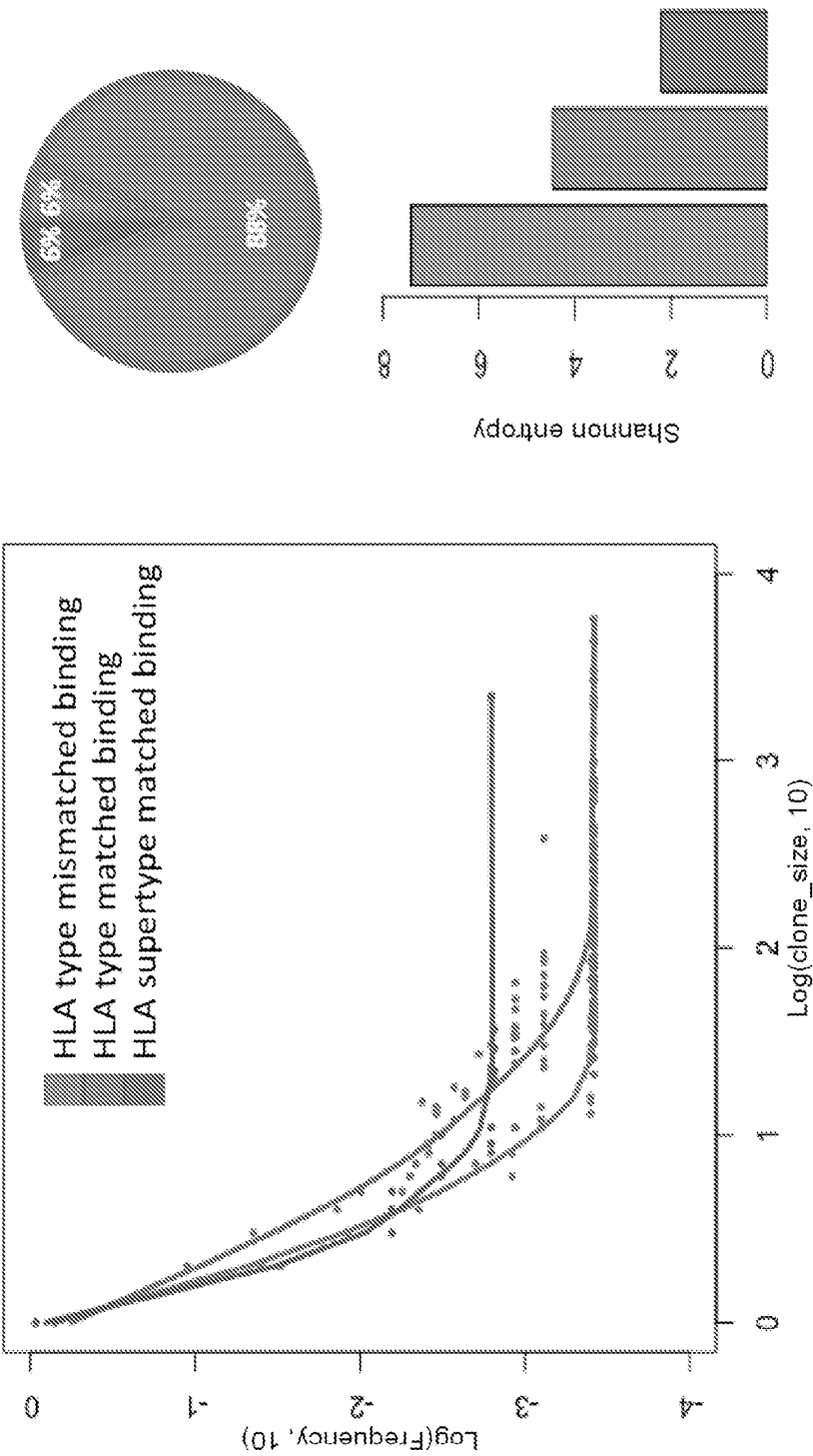


FIG. 25G

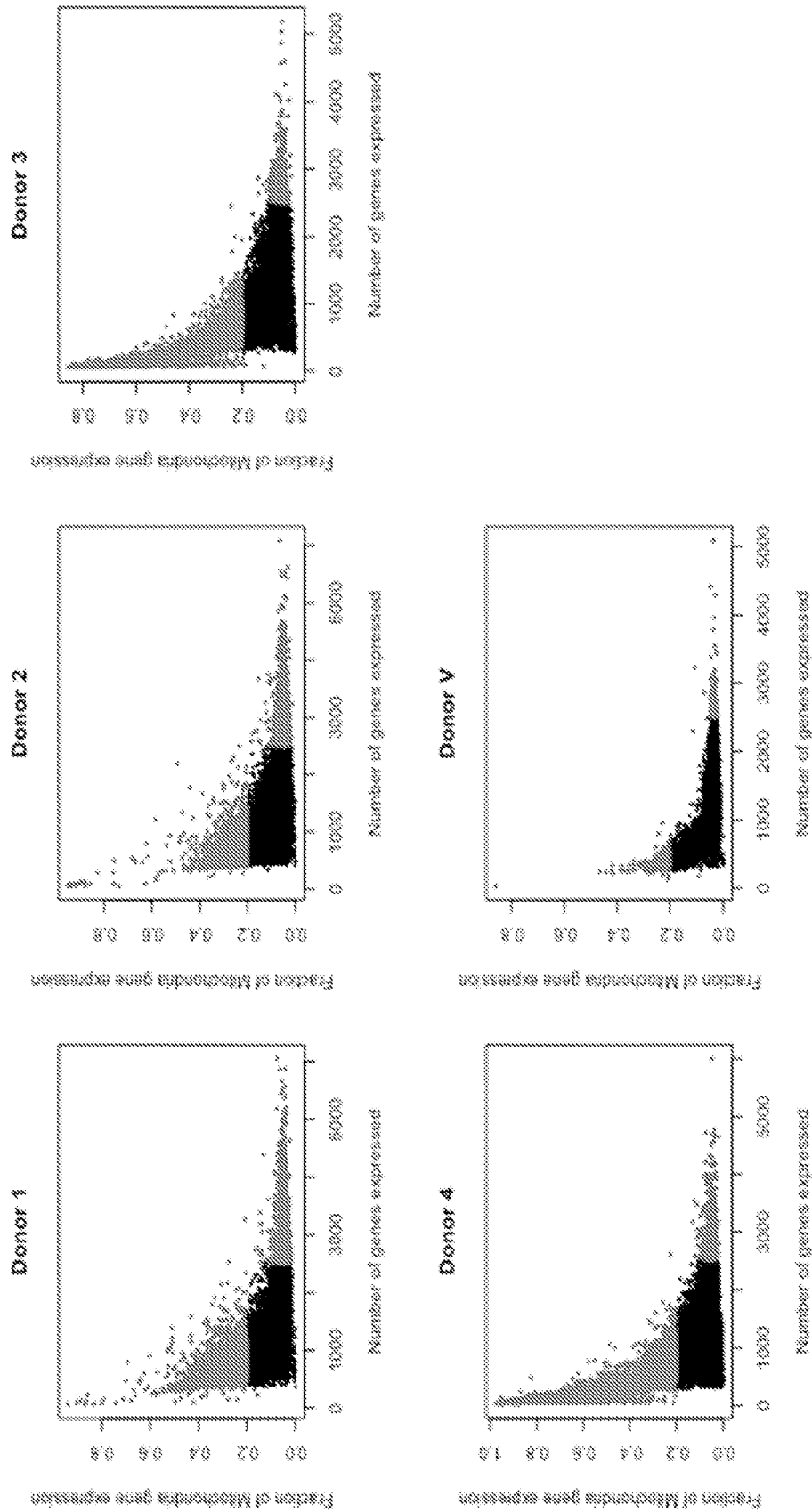


FIG. 26A

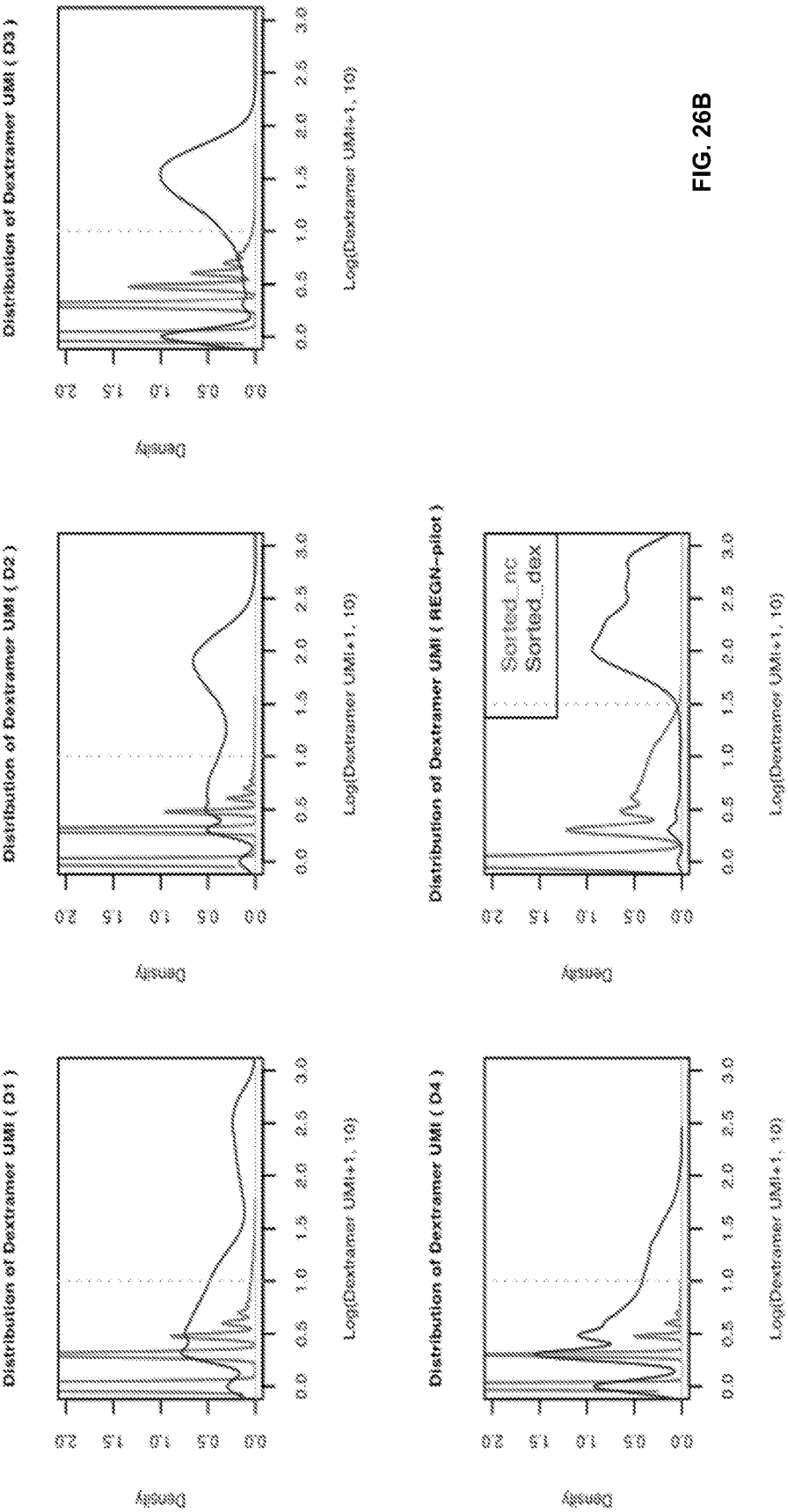
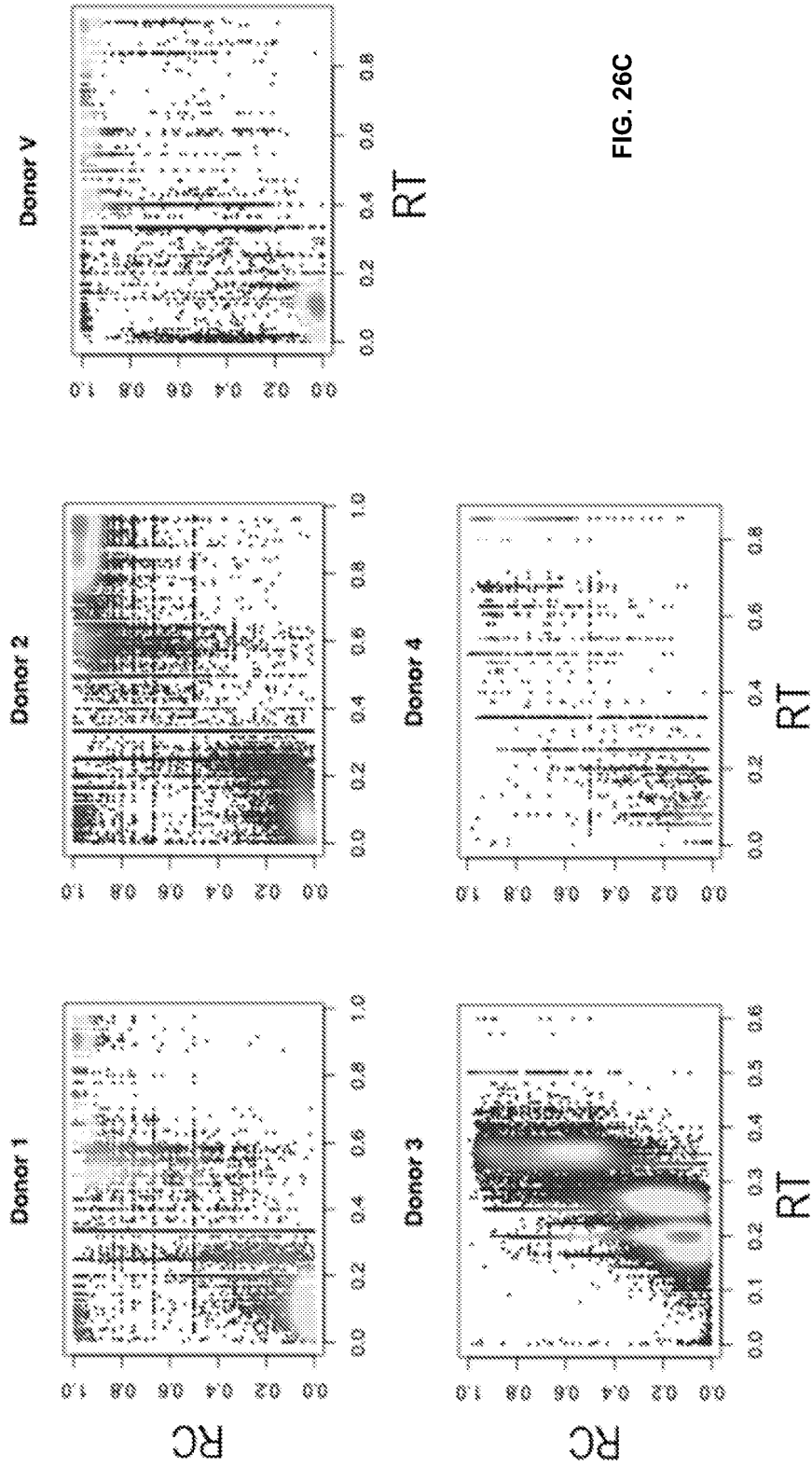


FIG. 26B



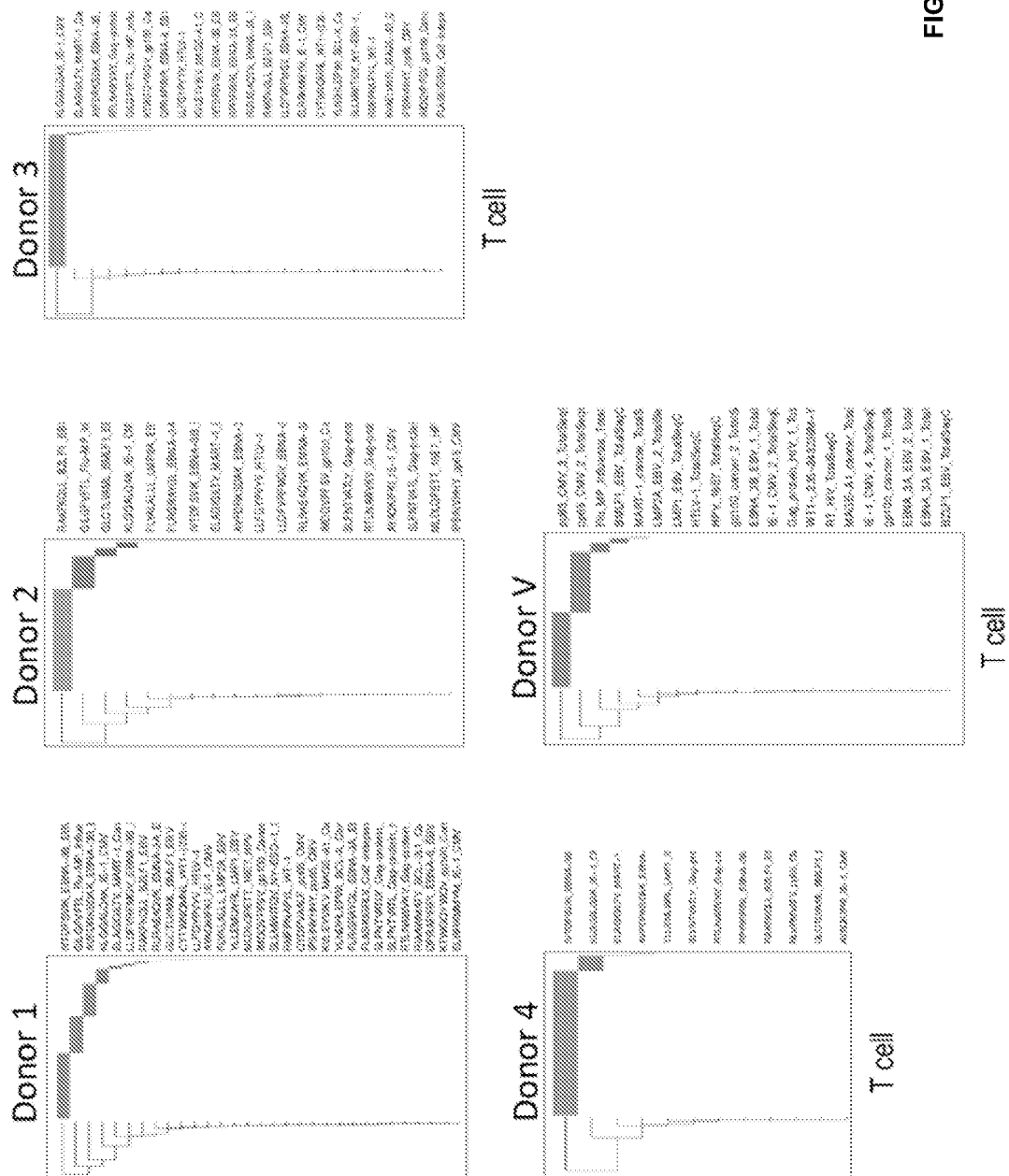
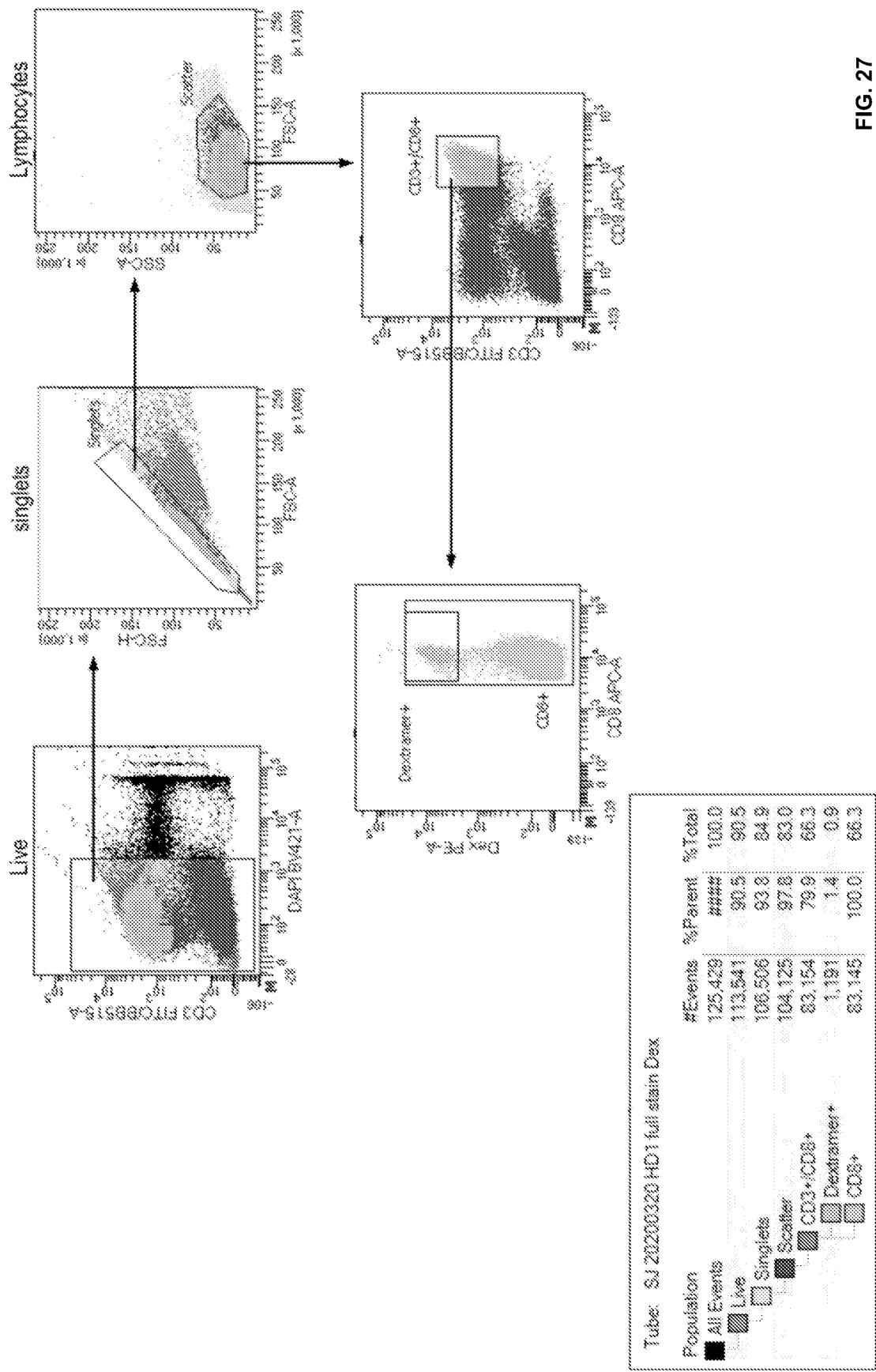


FIG. 26D



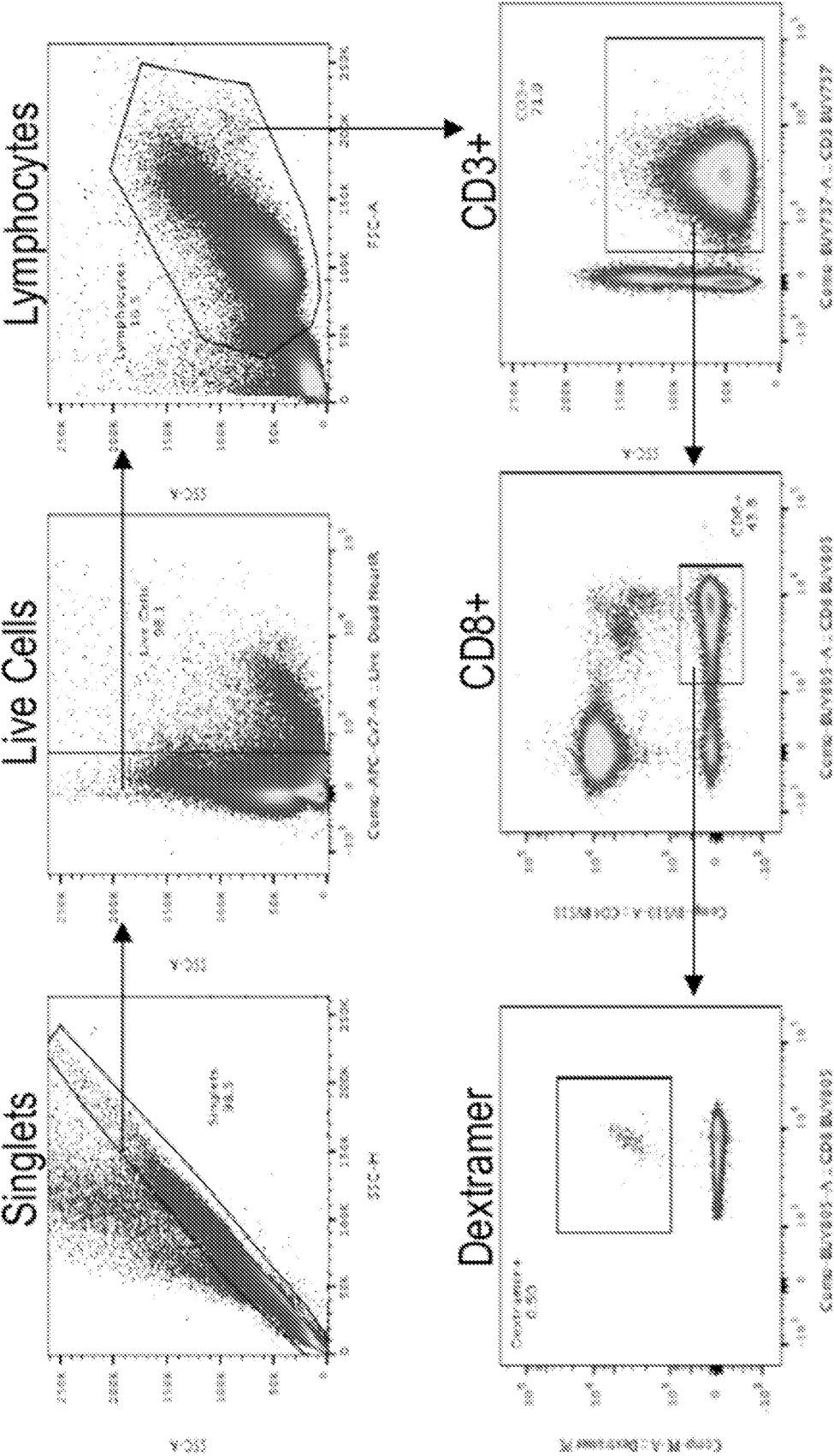


FIG. 28A

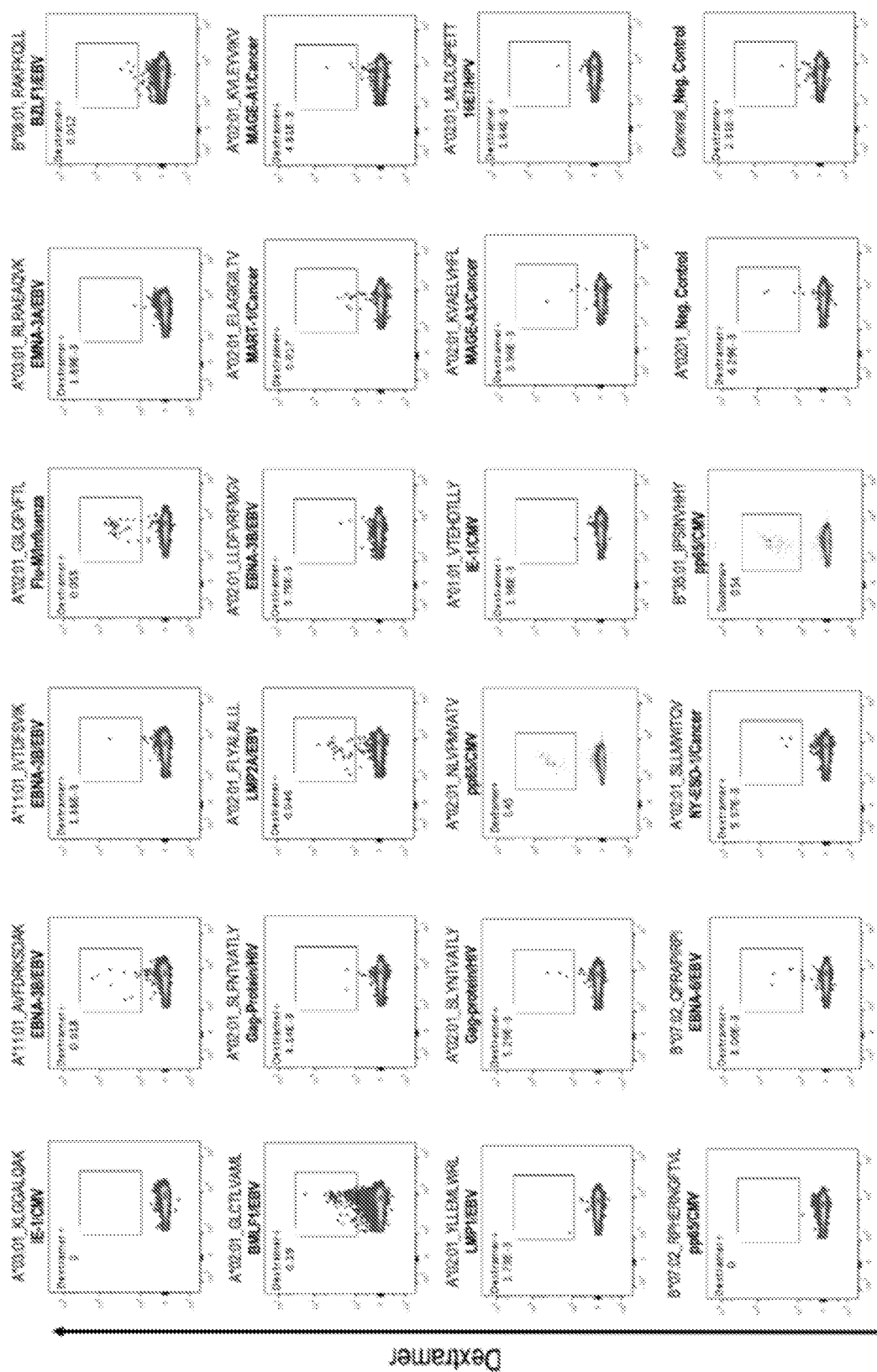


FIG. 28B

COO⁺1 cells

FIG. 29

pRNC	Donor 1		Donor 2		Donor 3		Donor 4		Donor 5		All donor summary	
	total	unique	total	unique	total	unique	total	unique	total	unique	total	unique
A108-01_BARTKBL_BMP1_FBV	1,03	104	1,835	371	2	2	1	1	1	1	1,848	479
A102-01_GAGPVT1_PuBP_influence	1,756	336	5,782	571	7	7	0	0	821	181	8,365	1,090
A105-01_SFBNV18V_golG_OAV	3	3	1	1	1	1	0	0	6,981	275	8,986	285
A102-01_NLPMVAATV_golG_OAV	0	0	0	0	0	0	0	0	1,611	163	5,512	164
A111-01_NYMSVAK_BBA 38_FBV	3,110	401	53	30	3	3	2,293	70	0	0	5,436	164
A103-01_KLGALGAK_R-1_OAV	999	511	1,136	247	1,833	1,584	241	163	0	0	3,899	2,863
A102-01_SACTVAMM_BMP1_FBV	15	13	1,336	53	0	0	1	1	475	47	1,886	117
A115-01_AVWOKSQW_BBA 38_FBV	1,116	38	22	38	34	24	13	12	4	3	1,579	99
A102-01_SAGGRTV_MART-1_Cancer	146	146	24	24	25	25	14	14	88	84	297	297
A102-01_GWVRMAGV_BBA 38_FBV	117	8	14	8	2	2	0	0	0	0	130	14
A102-01_FvAIAALL_CMLA_FBV	8	6	130	12	0	0	0	0	0	0	148	14
A108-01_FIRGRAV1_BBA 3A_FBV	2	2	38	32	0	0	0	0	1	1	41	17
A102-01_LARGPVVY_HIV-1	9	9	16	4	3	3	0	0	10	10	38	20
A103-01_BLRACQVW_BBA 3A_FBV	24	24	4	4	2	2	0	0	0	0	30	26
A102-01_CUGGLTAV_BMP-2A_FBV	0	0	0	0	0	0	0	0	27	7	27	7
A102-01_YLIRACWOL_BMP1_FBV	7	5	0	0	0	0	3	3	13	9	23	17
A124-02_CYPWONMAY_WT1 (235-243)	14	14	0	0	2	2	0	0	1	1	17	17
A103-01_BAK1VHREY_golG_cancer	5	1	4	1	1	1	0	0	0	0	25	15
A124-02_AVAG2HFKI_R-1_OAV	9	8	2	2	0	0	1	1	2	2	14	14
A102-01_BTINAVVWV_Sag protein_FBV	1	1	2	2	8	8	1	1	3	3	16	14
A103-01_MLEKQATT_16V_HPV	7	7	3	1	0	0	0	0	0	0	10	12
A102-01_KVSEVWV_MAGE-A1_cancer	3	3	0	0	3	3	0	0	1	1	7	7
A102-01_KTIGQIYVWV_golG_cancer	1	1	0	0	0	0	1	1	0	0	2	2
A108-01_CARRKMMYK-16_1_OAV	1	1	0	0	2	2	0	0	1	1	4	4
A107-02_NPPHSH1_BBA 3A_FBV	0	0	0	0	2	2	1	1	1	1	4	4
A102-01_LLMWYITGV_NY 450-2_cancer	3	3	0	0	1	1	1	1	0	0	6	6
A107-02_NPNAWPP1_BBA 6_FBV	1	1	0	0	3	3	0	0	0	0	4	4
A102-01_NAPFNAH_WT-3	3	3	0	0	1	1	0	0	0	0	4	4
A103-01_SIFNTVATV_Sag protein_FBV	1	1	2	2	0	0	0	0	0	0	3	3
A102-01_YAGQIEPAA_BCL-2_cancer	2	2	0	0	1	1	0	0	0	0	3	3
A102-01_FIASGGRV_Cd2+indepn.Pho	0	0	0	0	1	1	0	0	0	0	1	1
A124-02_QYGVVAVV_golG_OAV	3	3	0	0	0	0	0	0	0	0	3	3
A102-01_SIFNTVATV_Sag protein_FBV	1	1	1	1	0	0	0	0	0	0	2	2
A102-01_KKSPVHGV_RT_HIV	0	0	0	0	0	0	0	0	1	1	1	1
A102-01_SIFNTVATV_Sag protein_FBV	0	0	0	0	0	0	1	1	0	0	1	1
A102-01_NVALVHPI_MAGE-A3_cancer	0	0	0	0	1	1	0	0	0	0	1	1
A103-01_BAAWBRATV_BCL-2L1_cancer	1	1	0	0	0	0	0	0	0	0	1	1

FIG. 30A

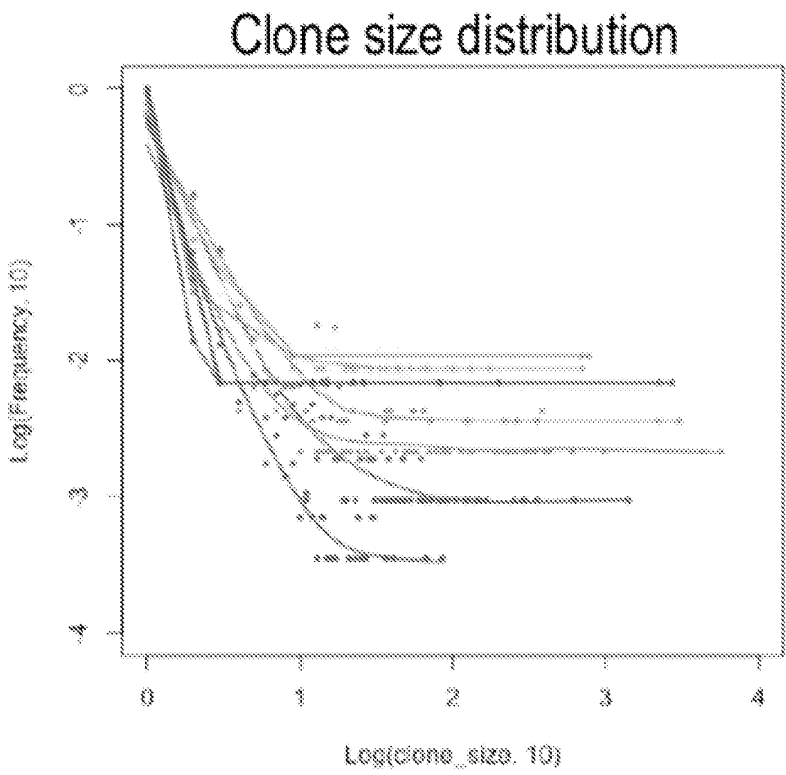
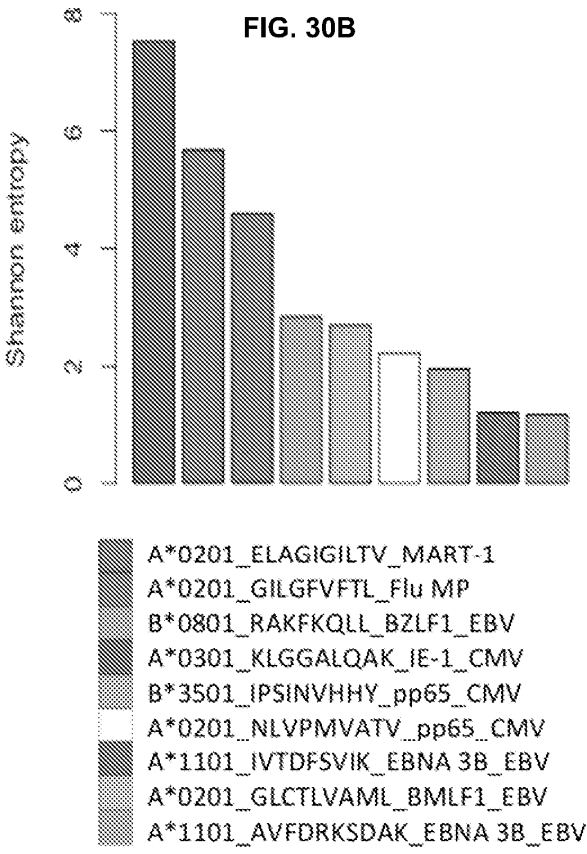


FIG. 30B



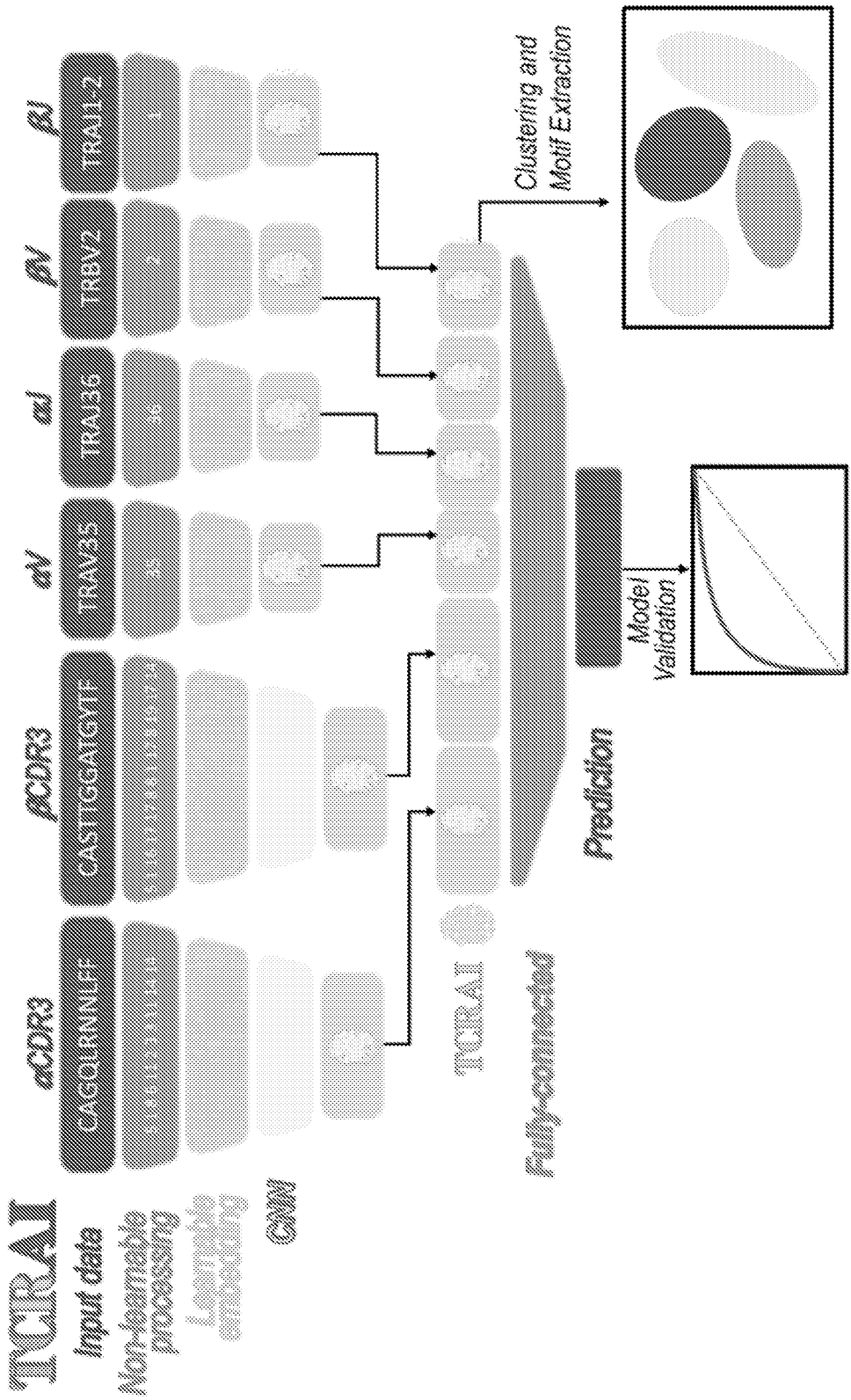


FIG. 31A

FIG. 31B

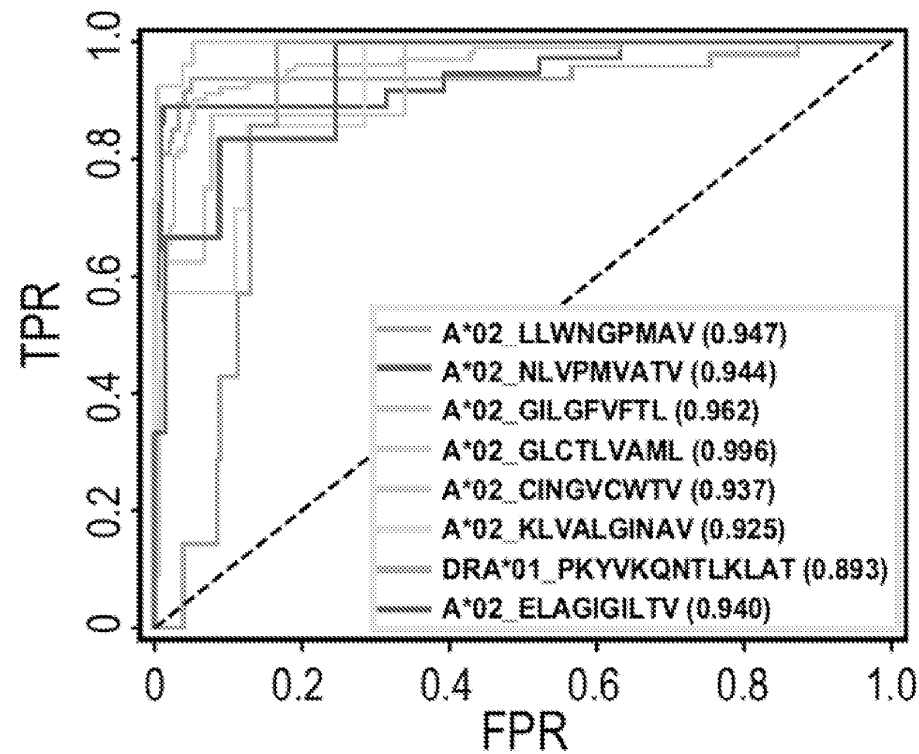


FIG. 31C

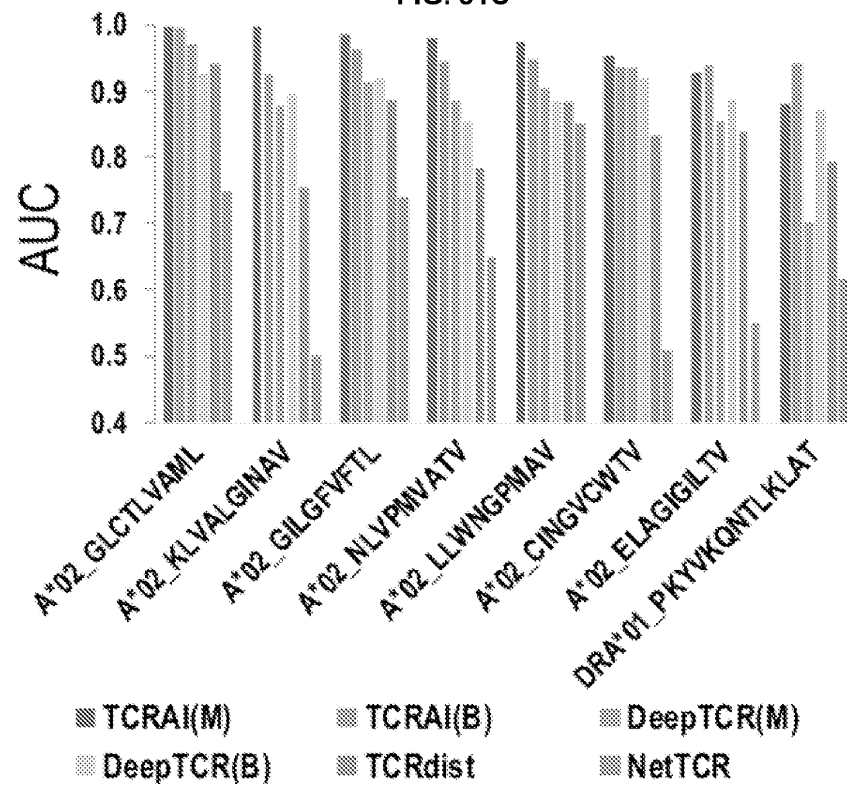


FIG. 32A

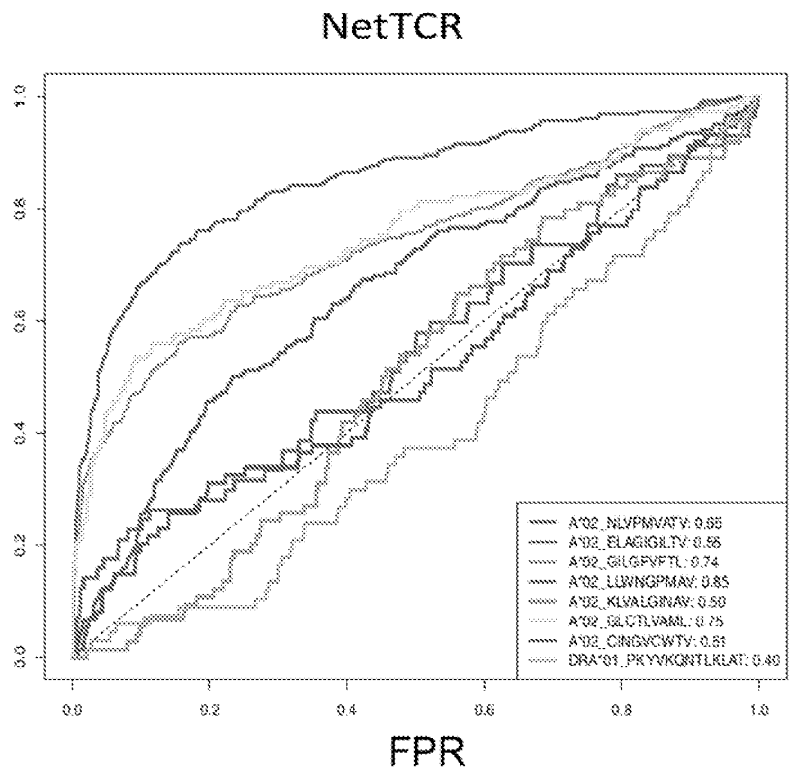
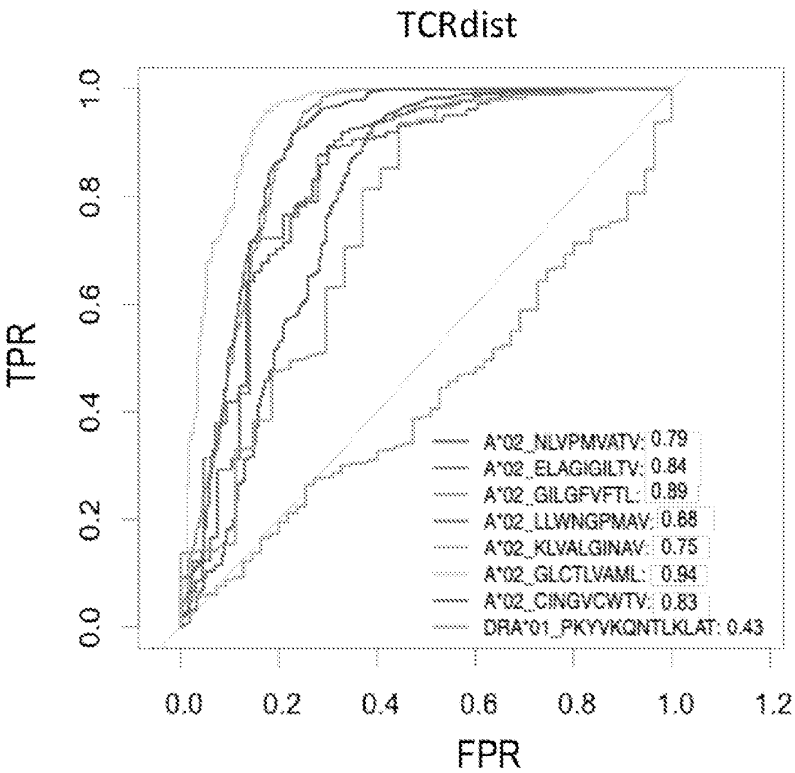


FIG. 32A
(CONTINUED)

DeepTCR(B)

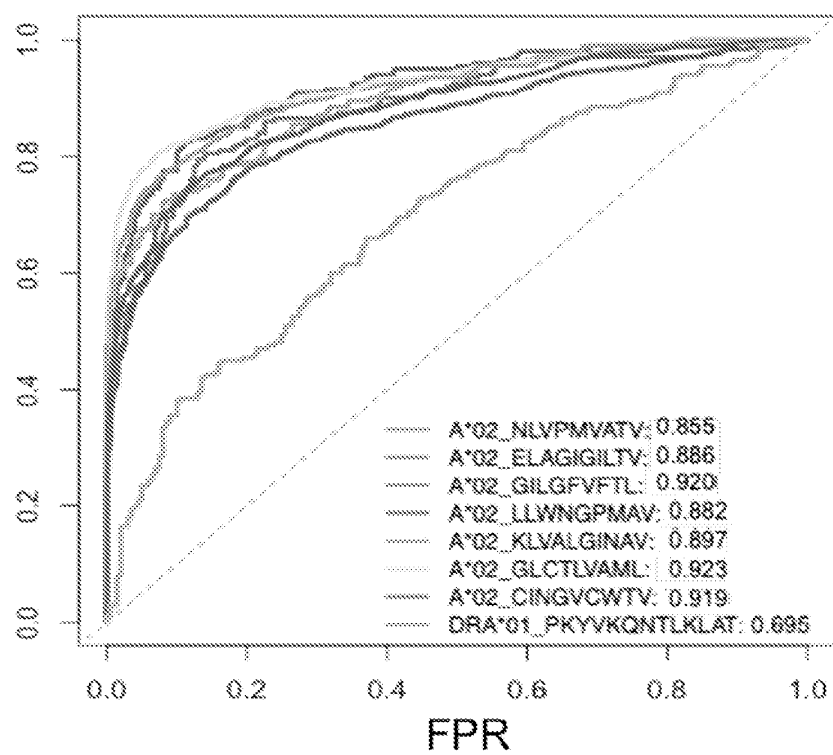


FIG. 32B

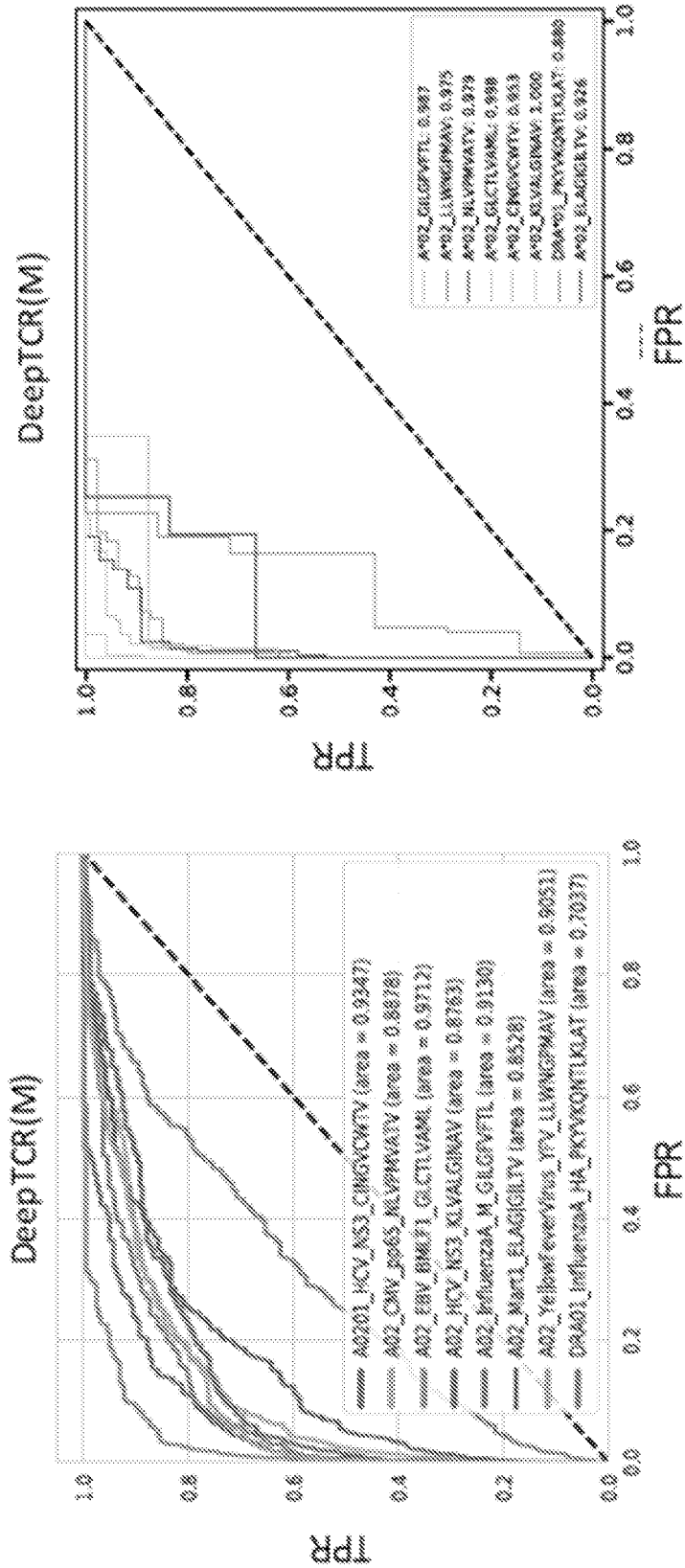
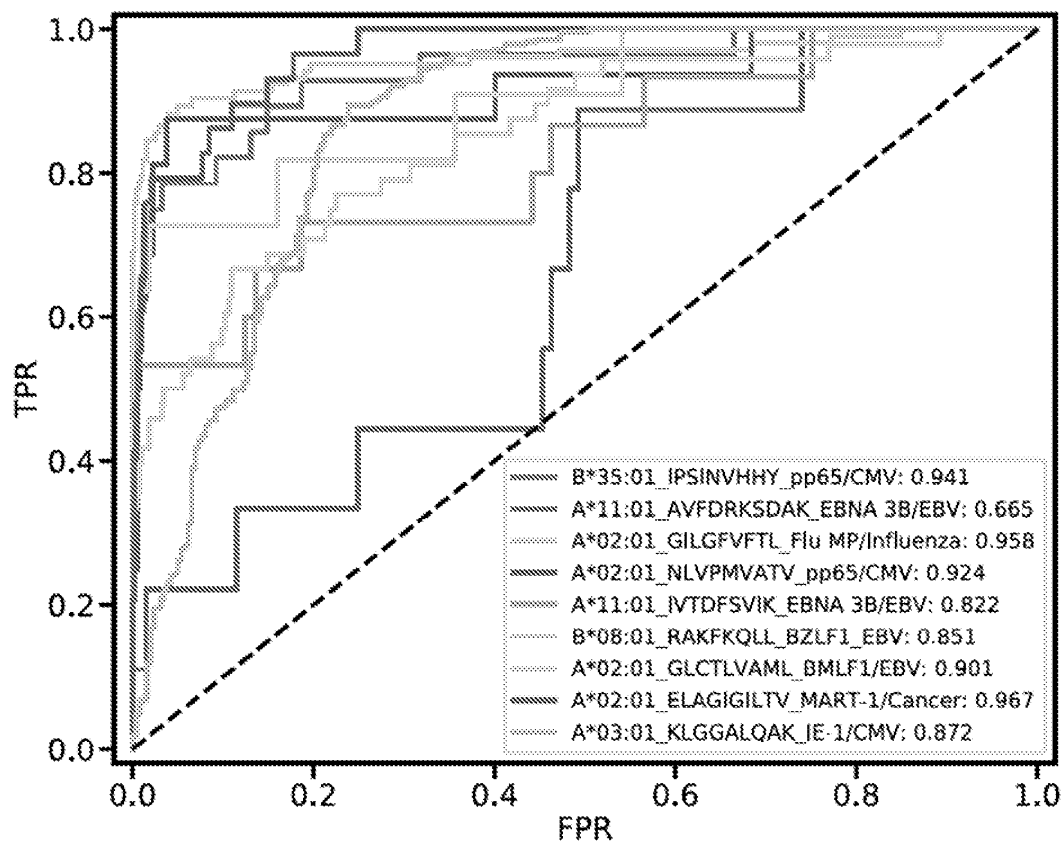


FIG. 32C



pMHC	GLIPH2		NetTCR		TCRdist		DeepTCR		TCRAI	
	sensitivity	specificity	sensitivity	specificity	sensitivity	specificity	sensitivity	specificity	sensitivity	specificity
A*02_NLVPMVATV	0.246	0.997	0.500	0.767	0.937	0.606	0.885	0.697	0.889	0.988
A*02_ELAGIGITV	0.000	1.000	0.263	0.888	0.878	0.721	0.870	0.795	0.833	0.912
A*02_GILGFVFTL	0.867	0.988	0.562	0.845	0.955	0.751	0.928	0.763	0.902	0.947
A*02_LLWNGPMAV	0.119	1.000	0.738	0.843	0.920	0.770	0.874	0.757	0.936	0.951
A*02_KLVALGINAV	0.000	1.000	0.784	0.316	0.935	0.556	0.920	0.720	0.857	0.873
A*02_GLCTIVAML	0.646	0.999	0.559	0.885	0.957	0.830	0.928	0.806	1.000	0.947
A*02_CINGVCWTV	0.191	1.000	0.257	0.860	0.895	0.701	0.890	0.825	0.875	0.922
DRA*01_PKYVKQNTKLAT	0.000	1.000	1.000	0.006	0.048	1.000	0.630	0.660	1.000	0.831
Average of HLA-A*02 binders	0.296	0.998	0.523	0.772	0.925	0.705	0.899	0.766	0.899	0.934
Average of all binders	0.259	0.998	0.583	0.676	0.816	0.742	0.866	0.753	0.912	0.922

FIG. 33

FIG. 34A

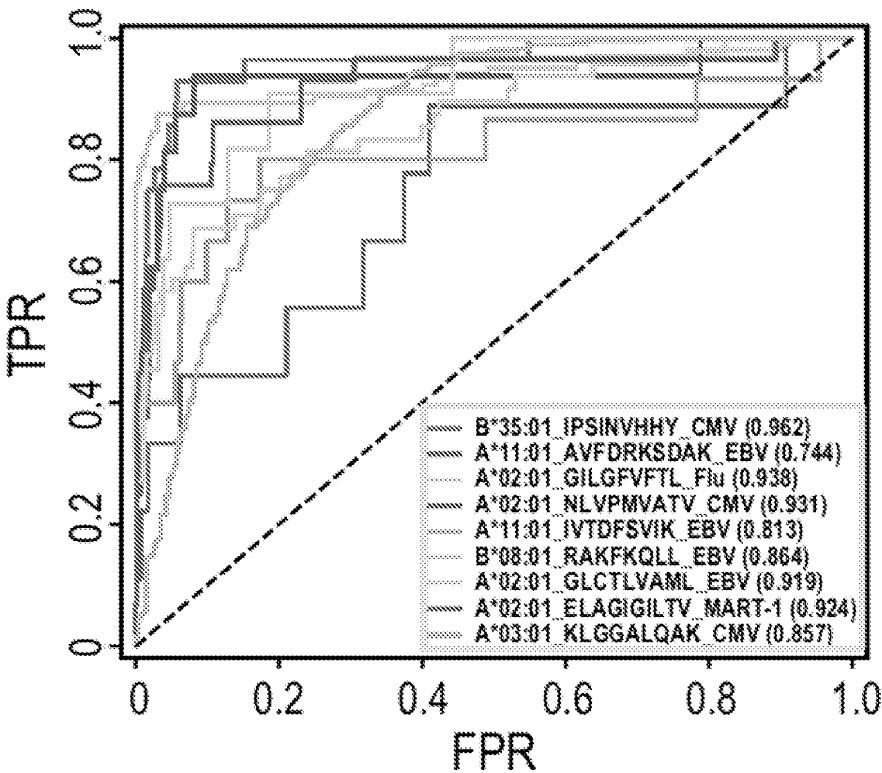


FIG. 34B

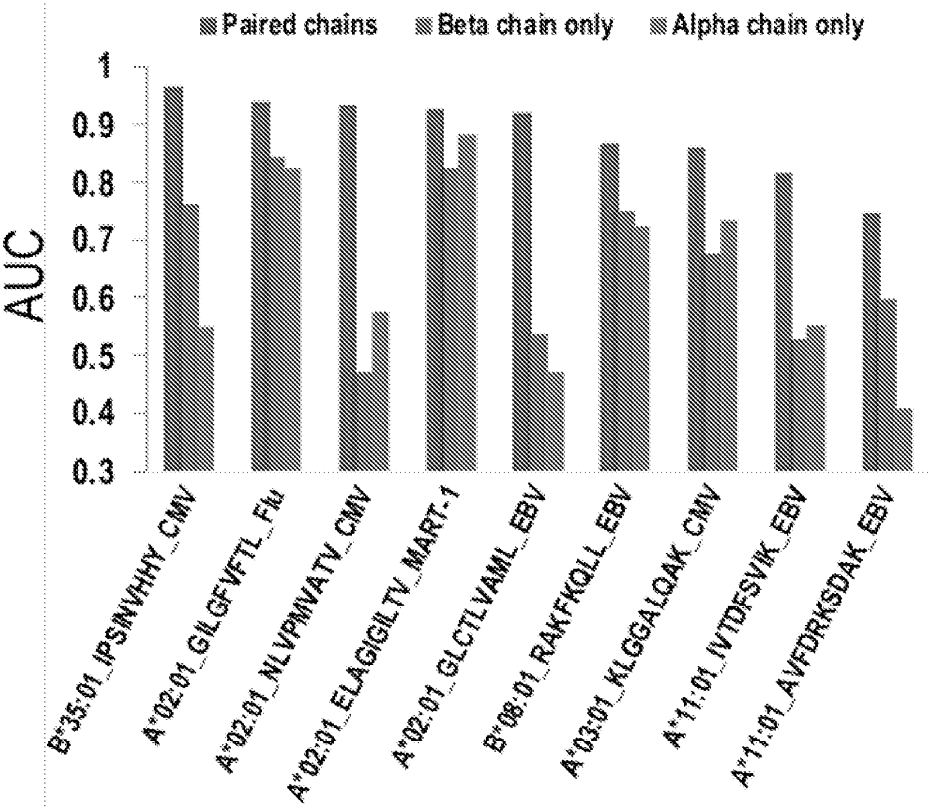


FIG. 34C

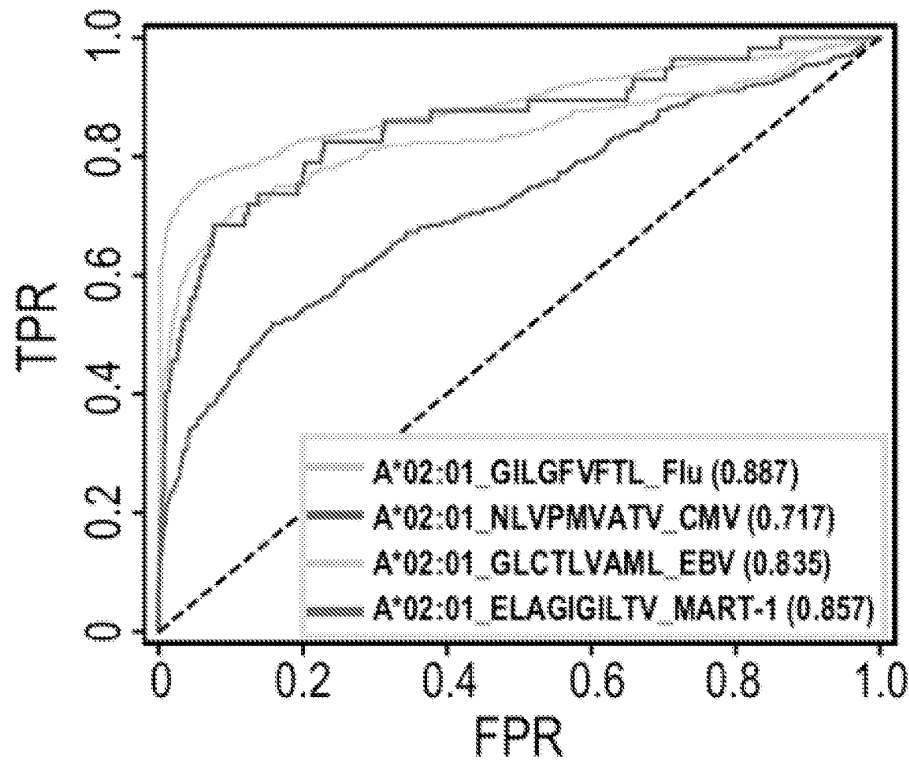


FIG. 34D

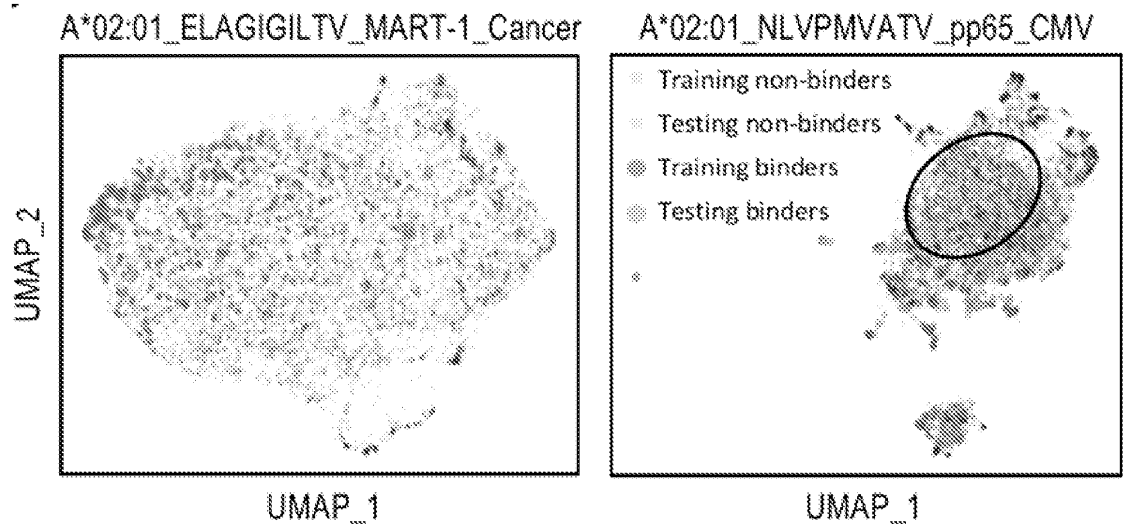


FIG. 35

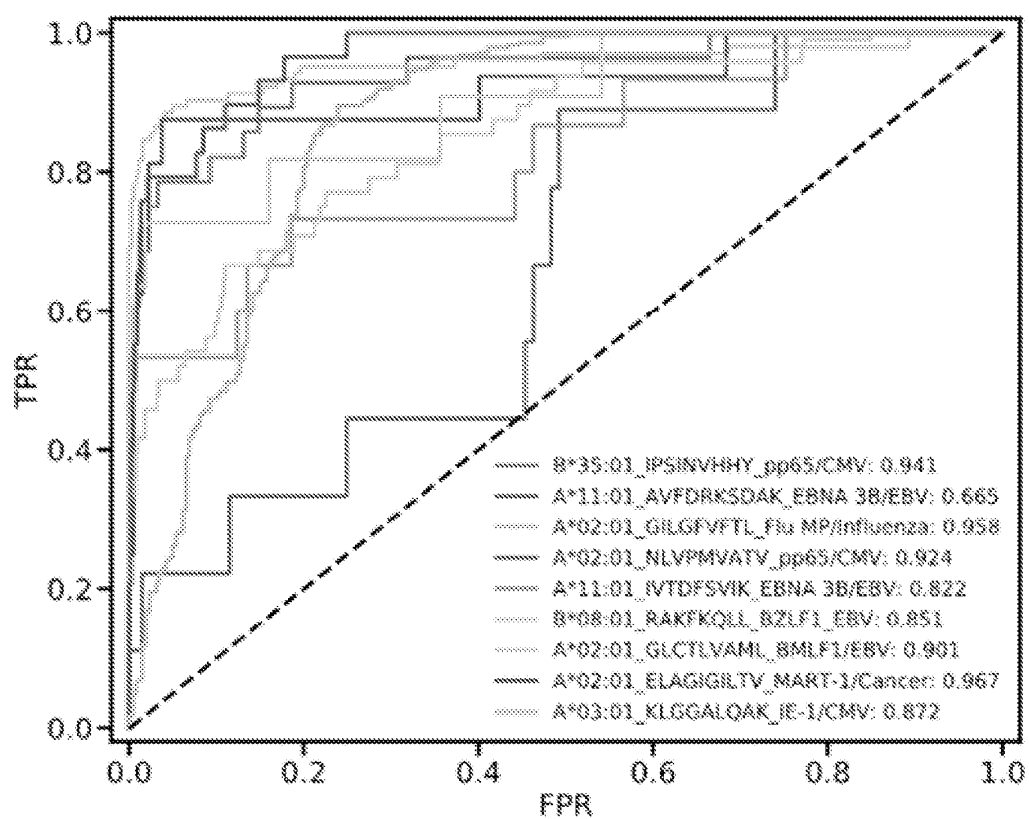


FIG. 36A

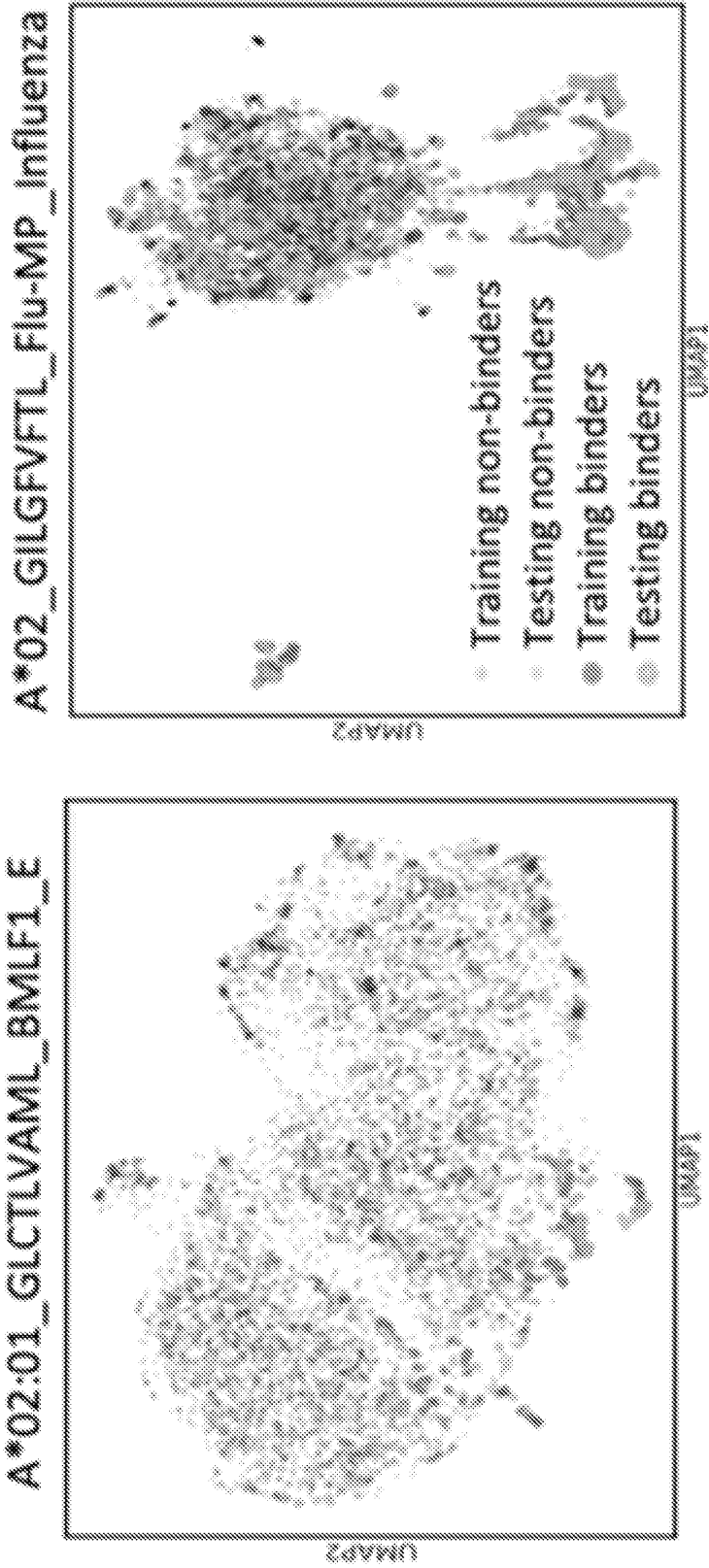


FIG. 36B

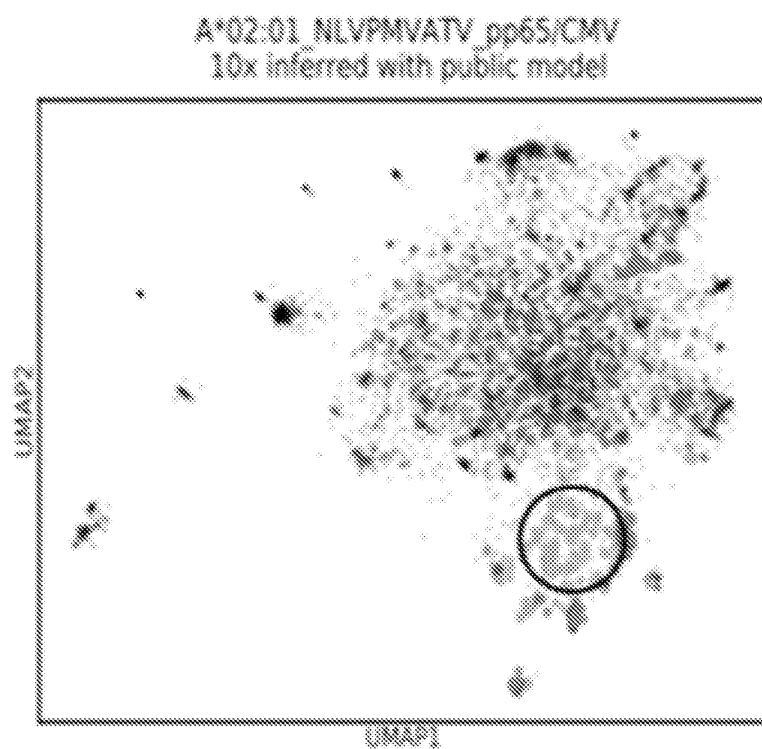


FIG. 37A

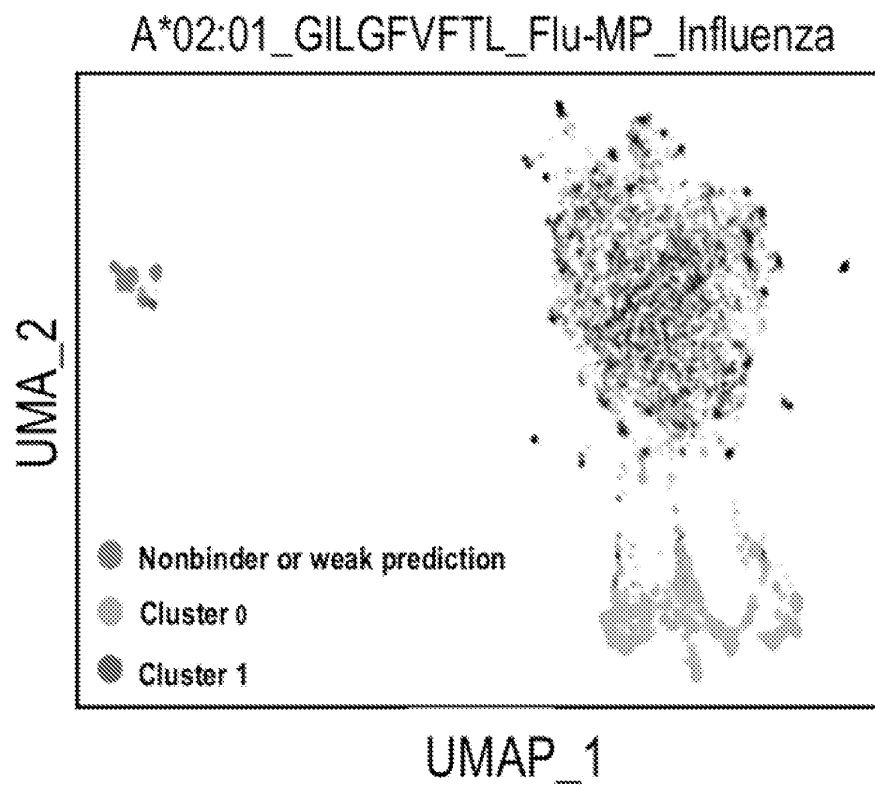
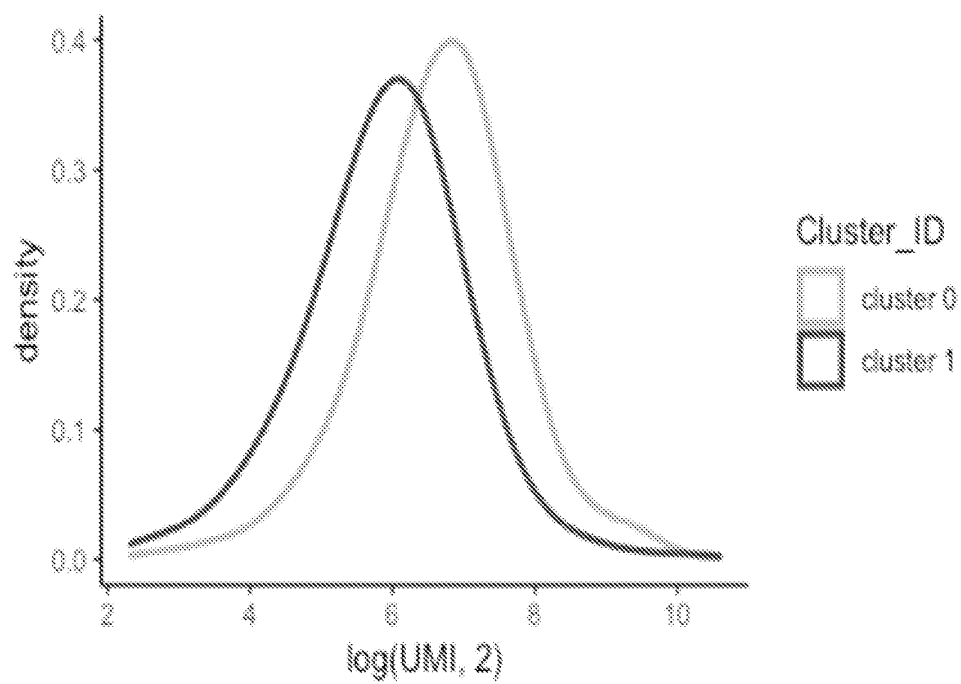


FIG. 37B



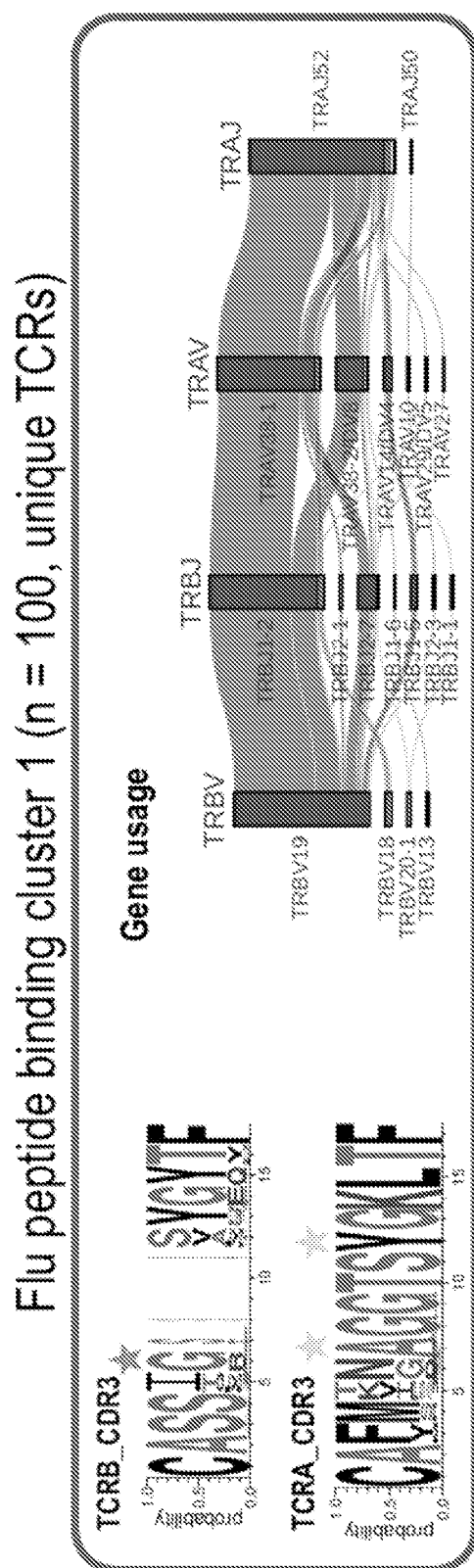
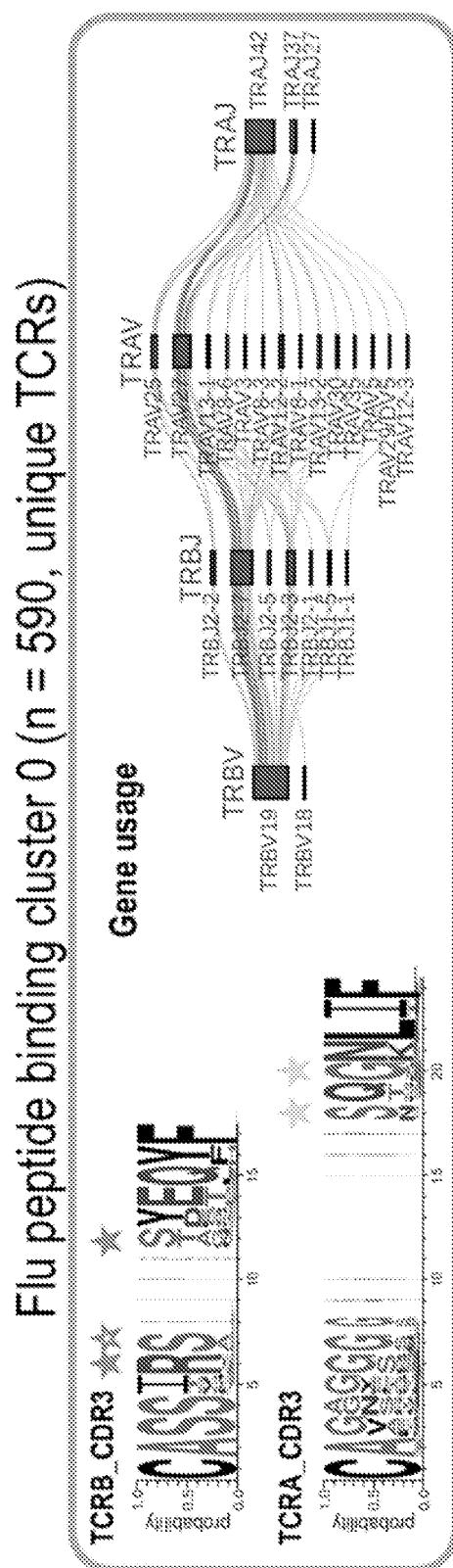


FIG. 37C

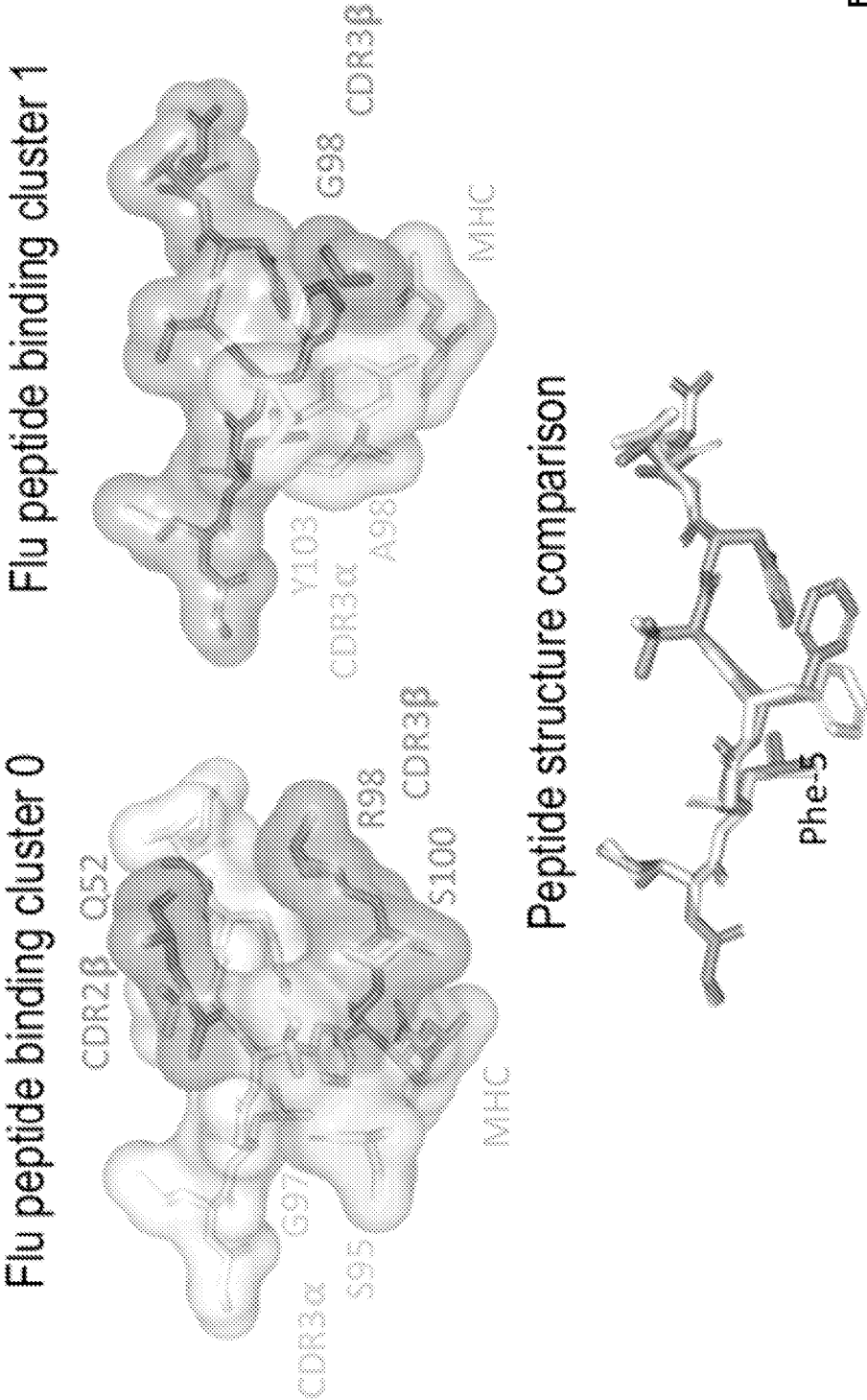


FIG. 37D

FIG. 37E

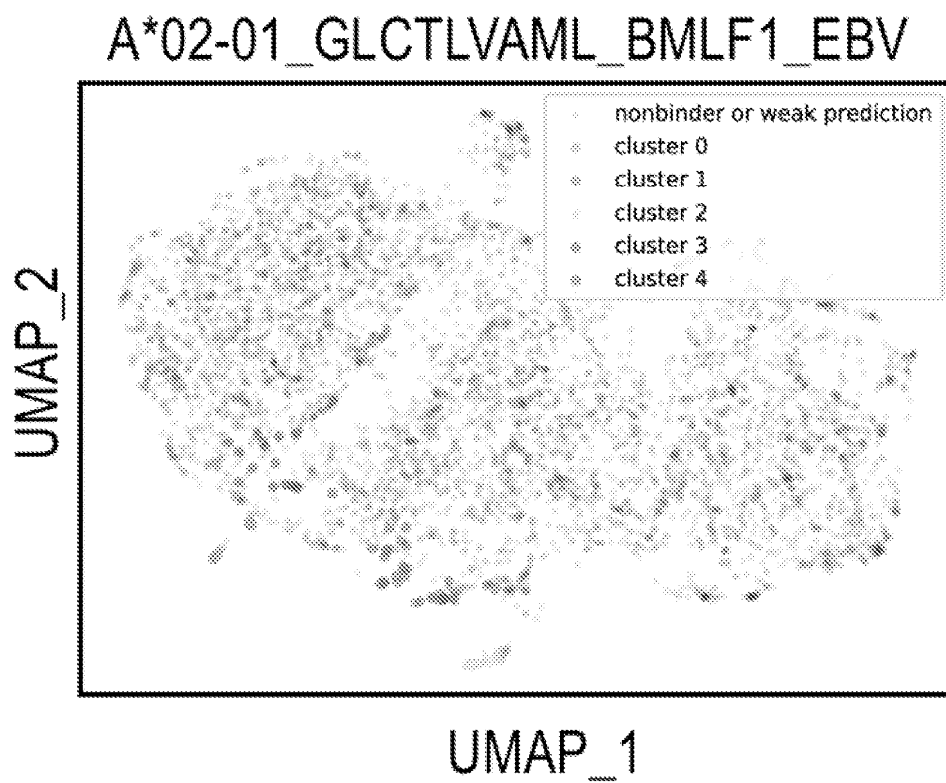


FIG. 37F

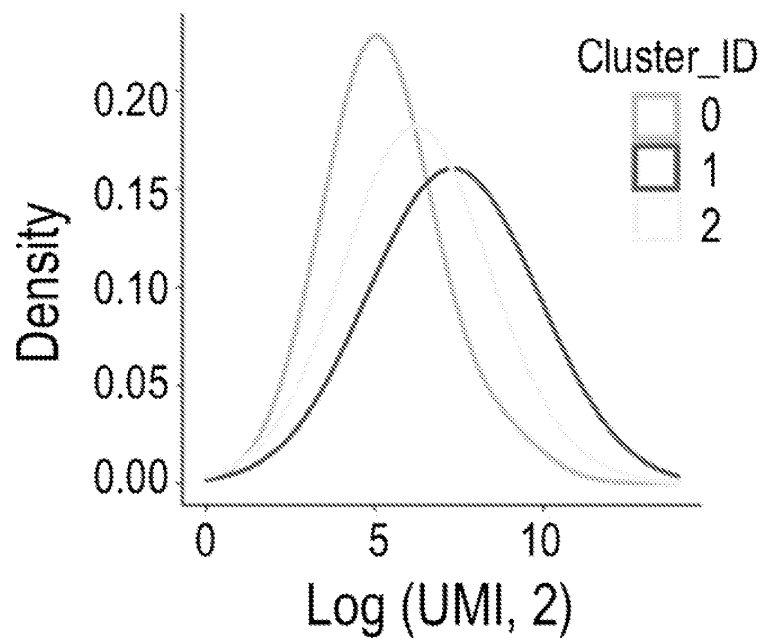
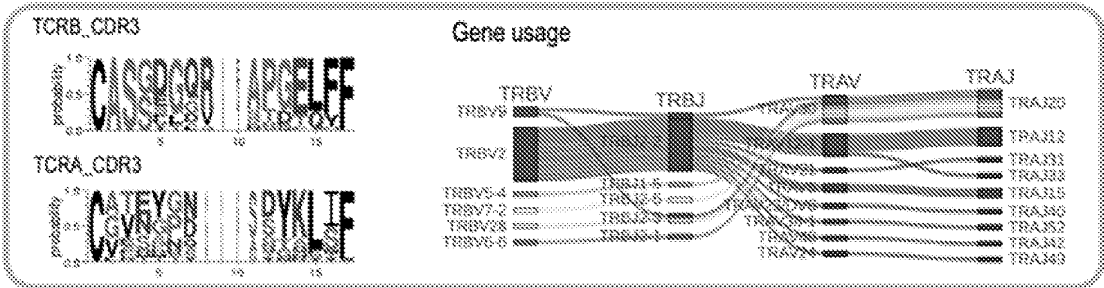
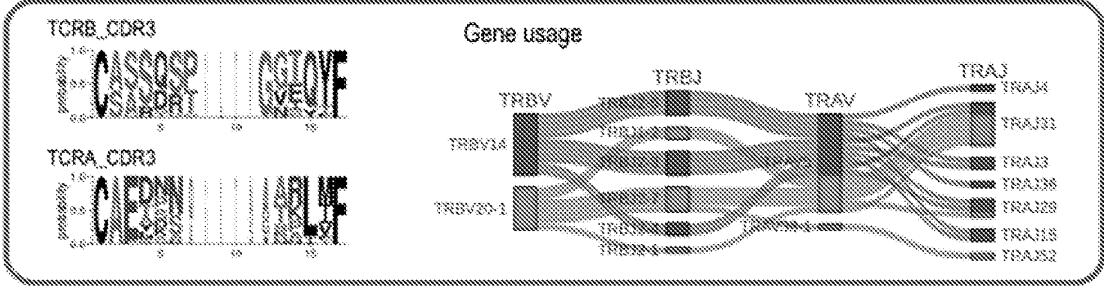


FIG. 37G

EBV peptide binding Cluster 0 (n = 18, unique TCRs)



EBV peptide binding Cluster 1 (n = 17, unique TCRs)



EBV peptide binding Cluster 2 (n = 16, unique TCRs)

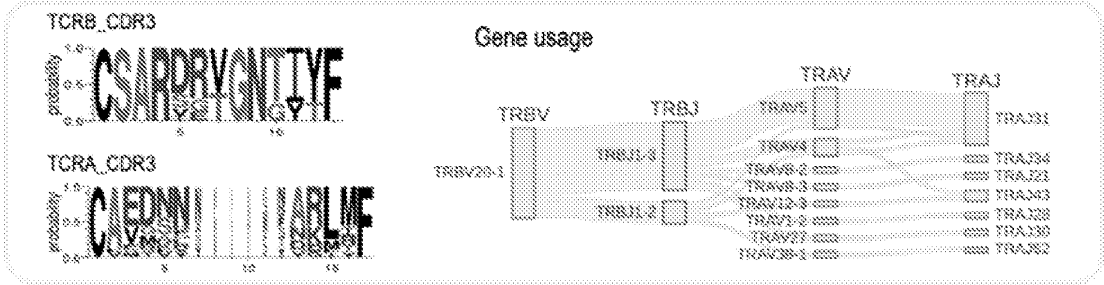
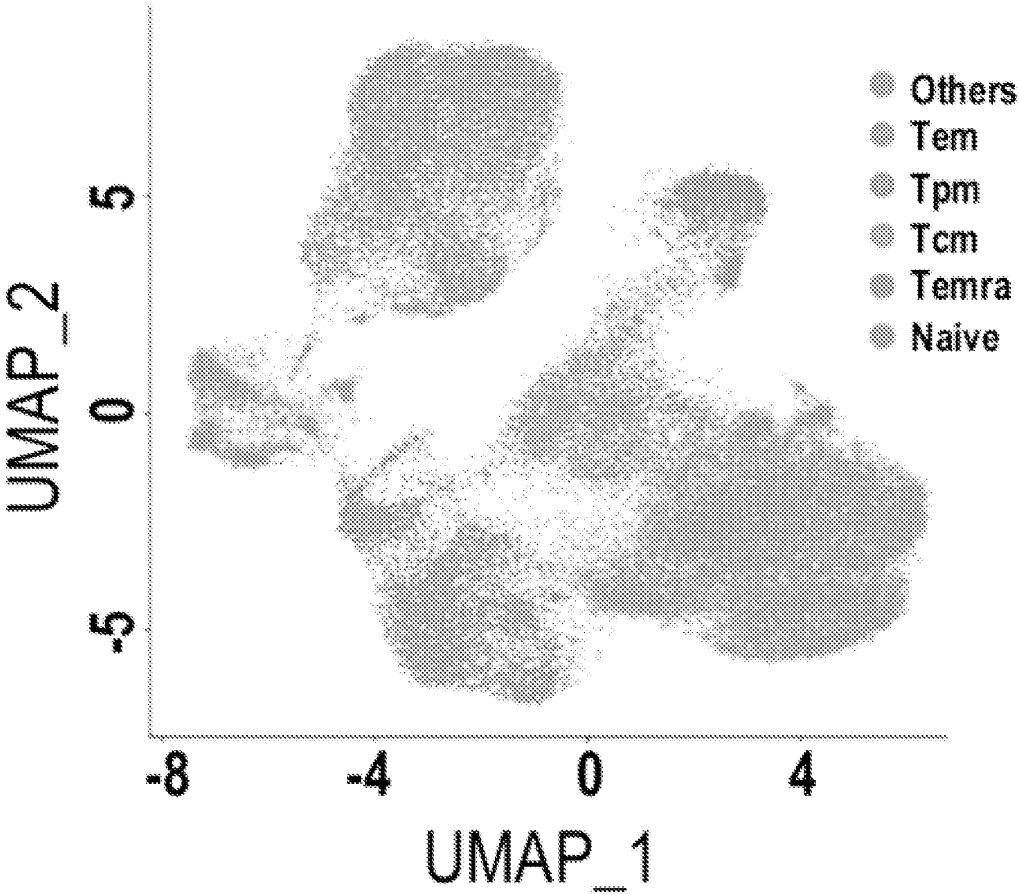


FIG. 38A



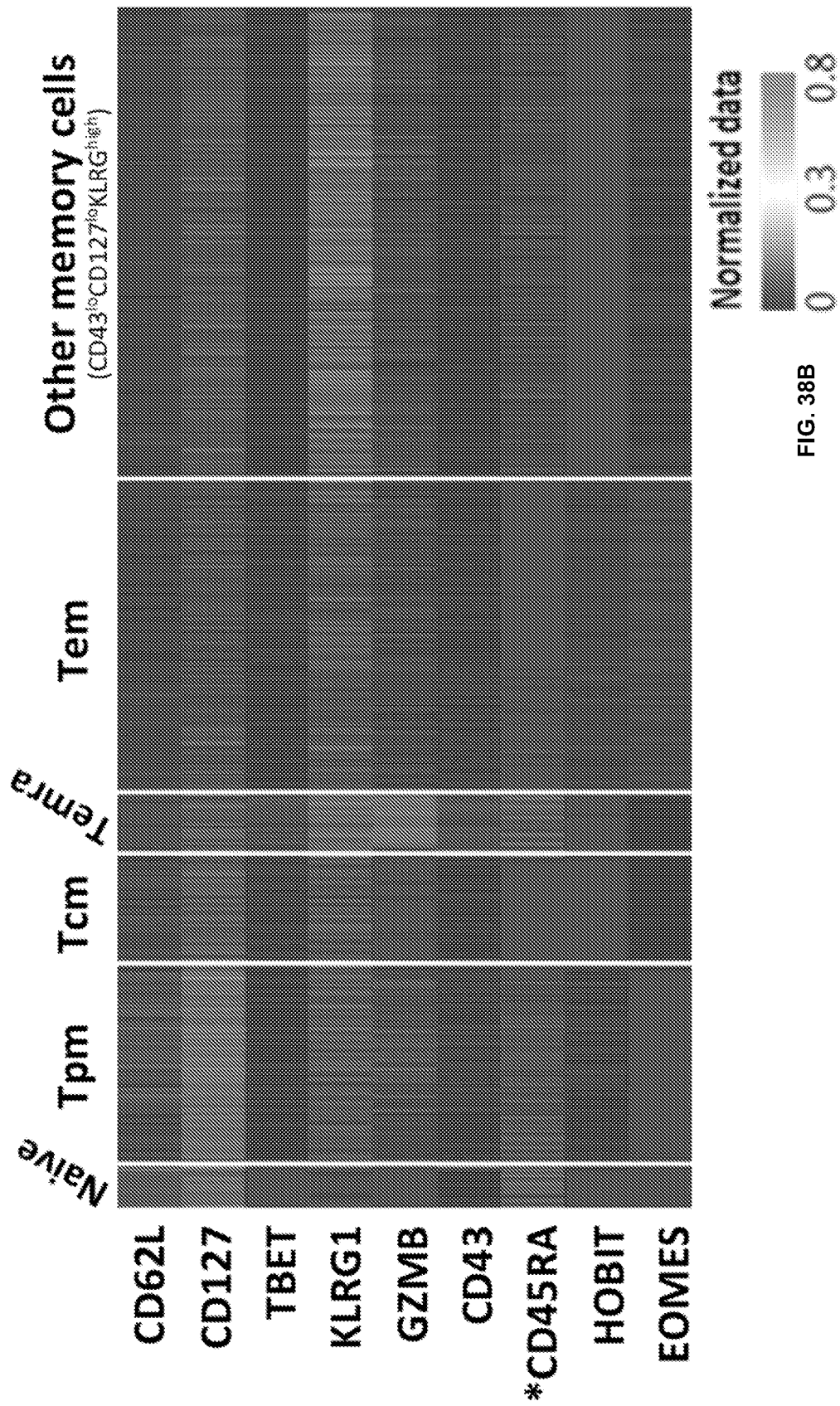
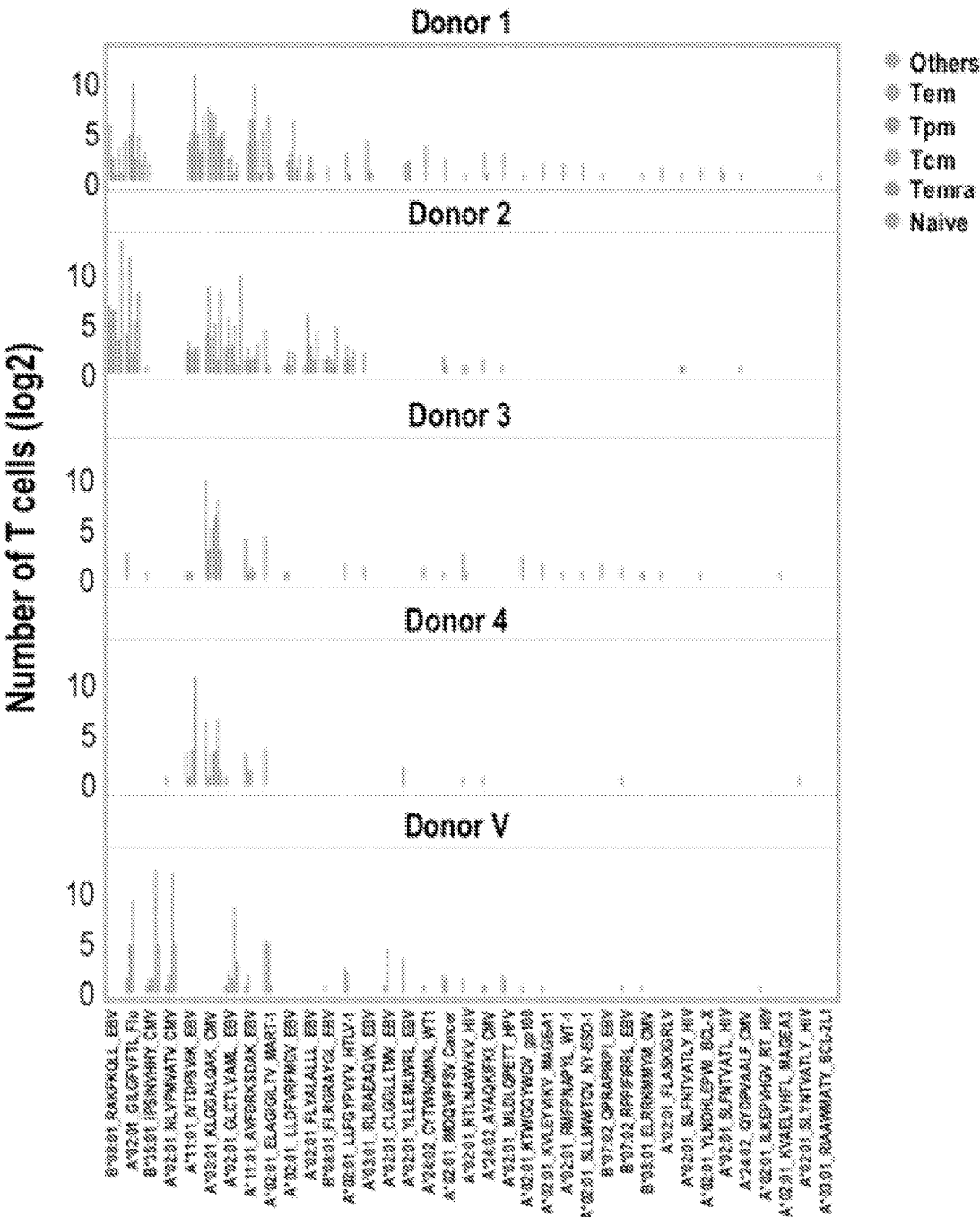


FIG. 38B

FIG. 38C



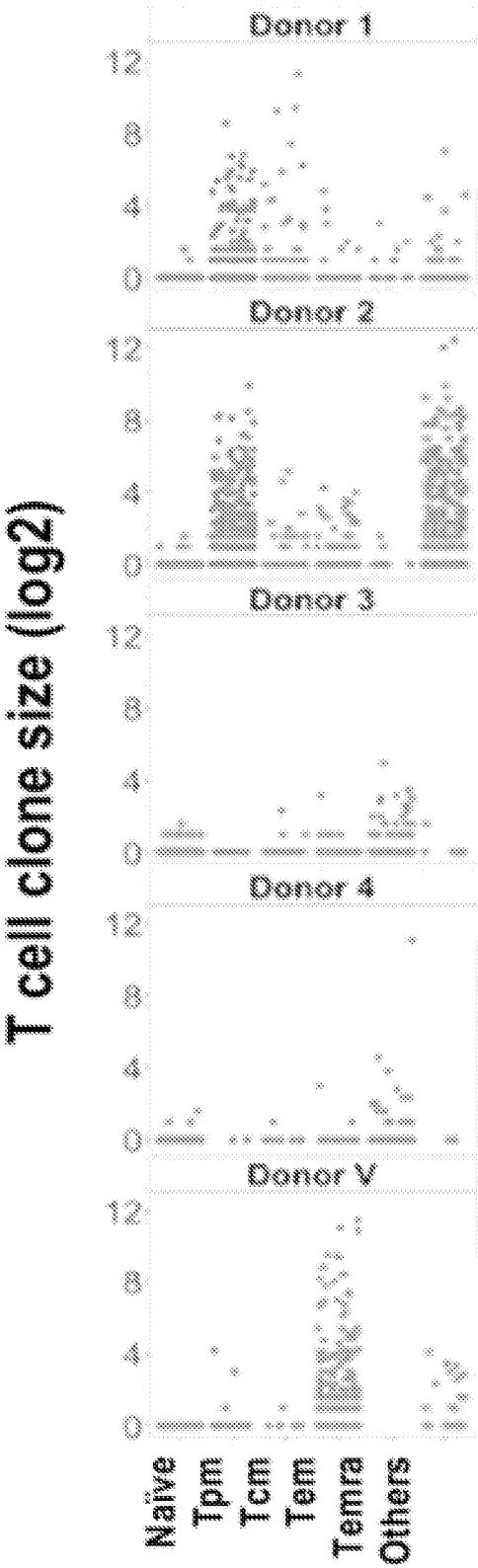


FIG. 38D

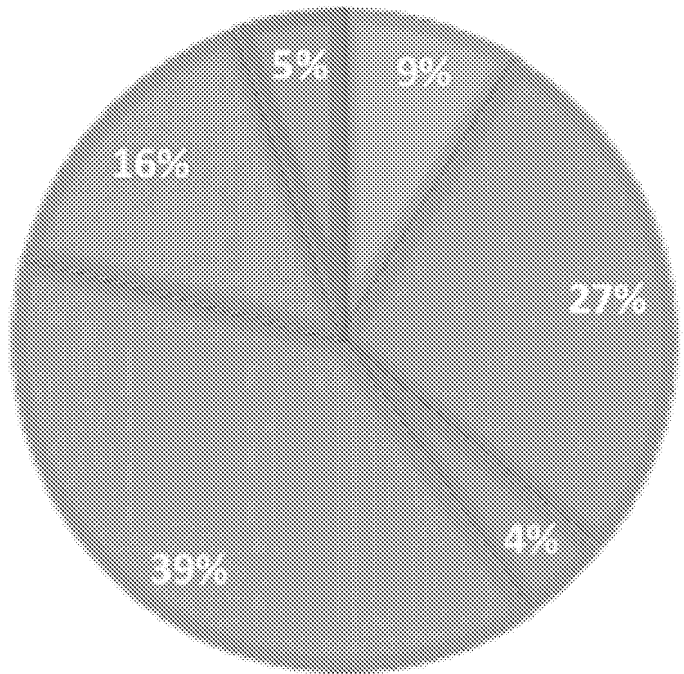


FIG. 38F

- Tcm
- Tem
- Naïve
- Others
- Tpm
- Temra

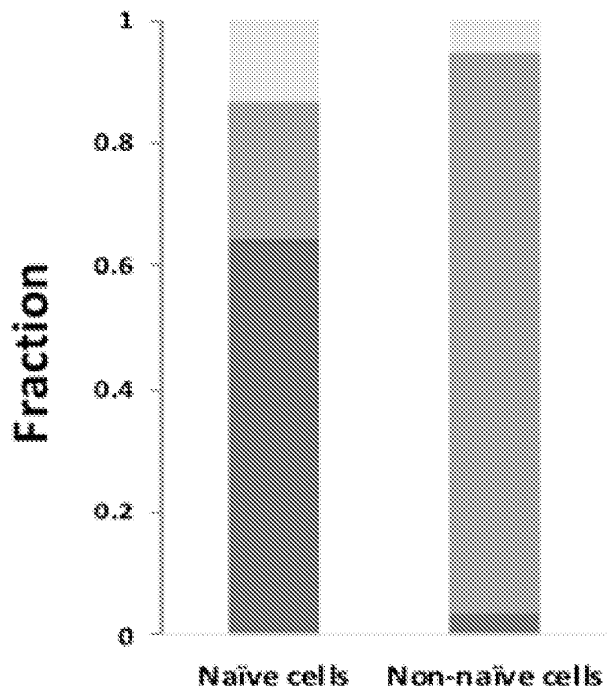


FIG. 38E

- HLA supertype matched binding
- HLA type matched binding
- HLA type mismatched binding

FIG. 39

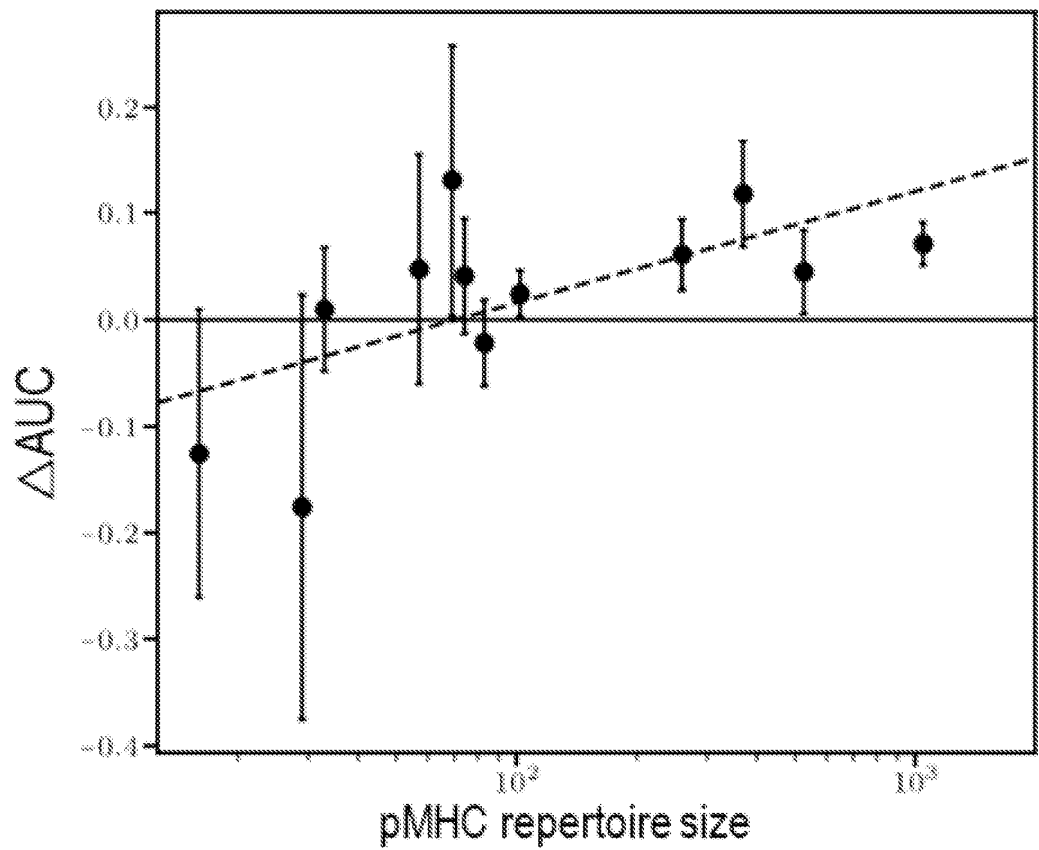
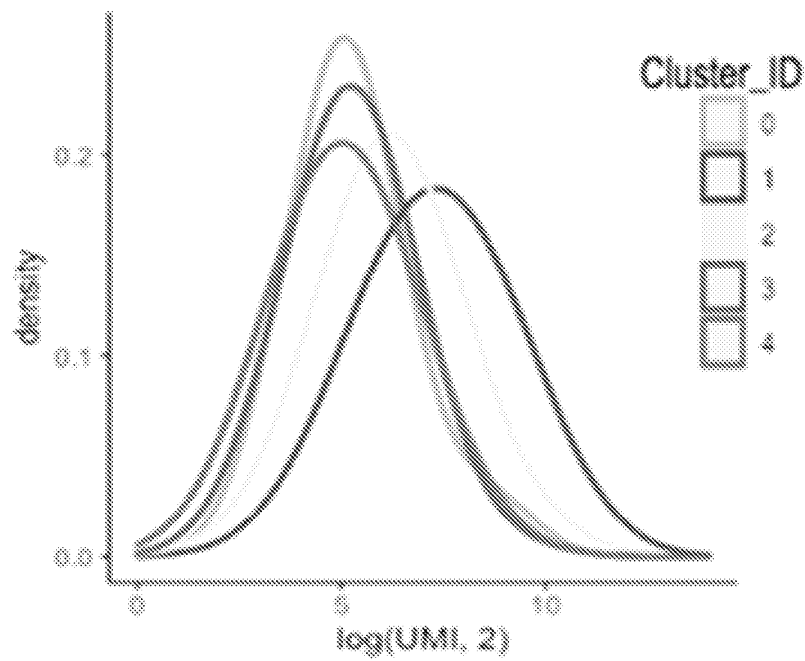
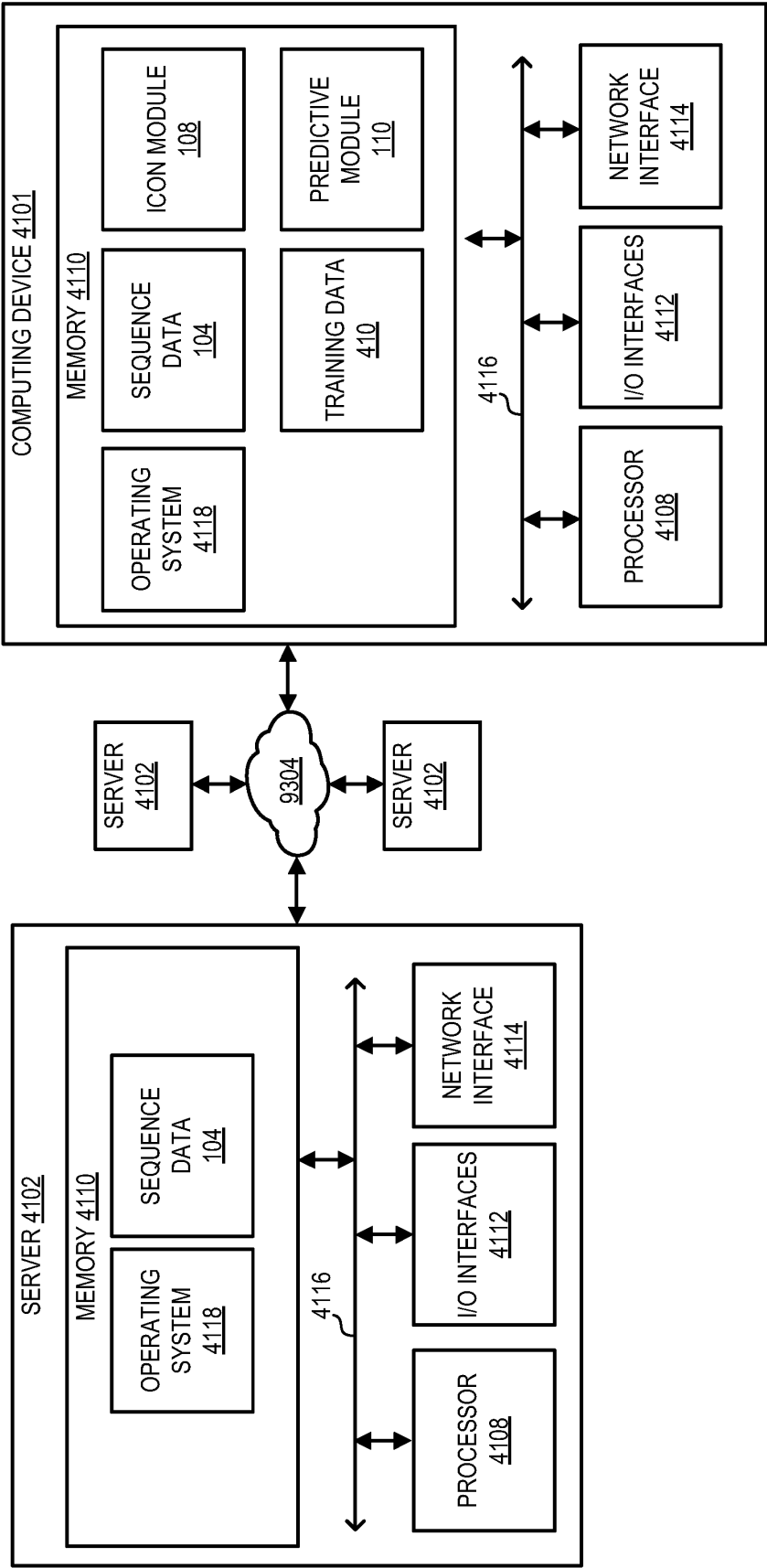


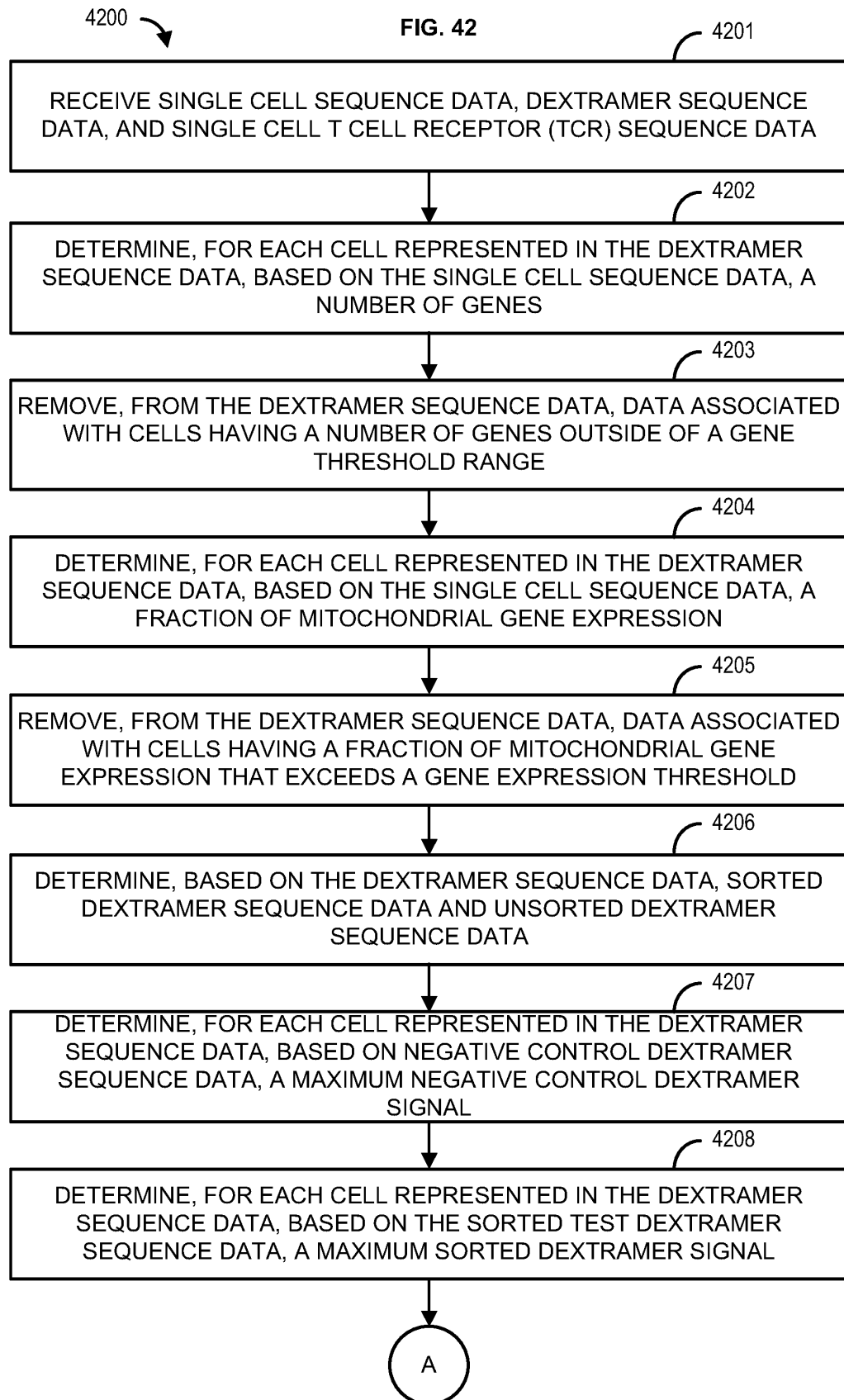
FIG. 40A



4100

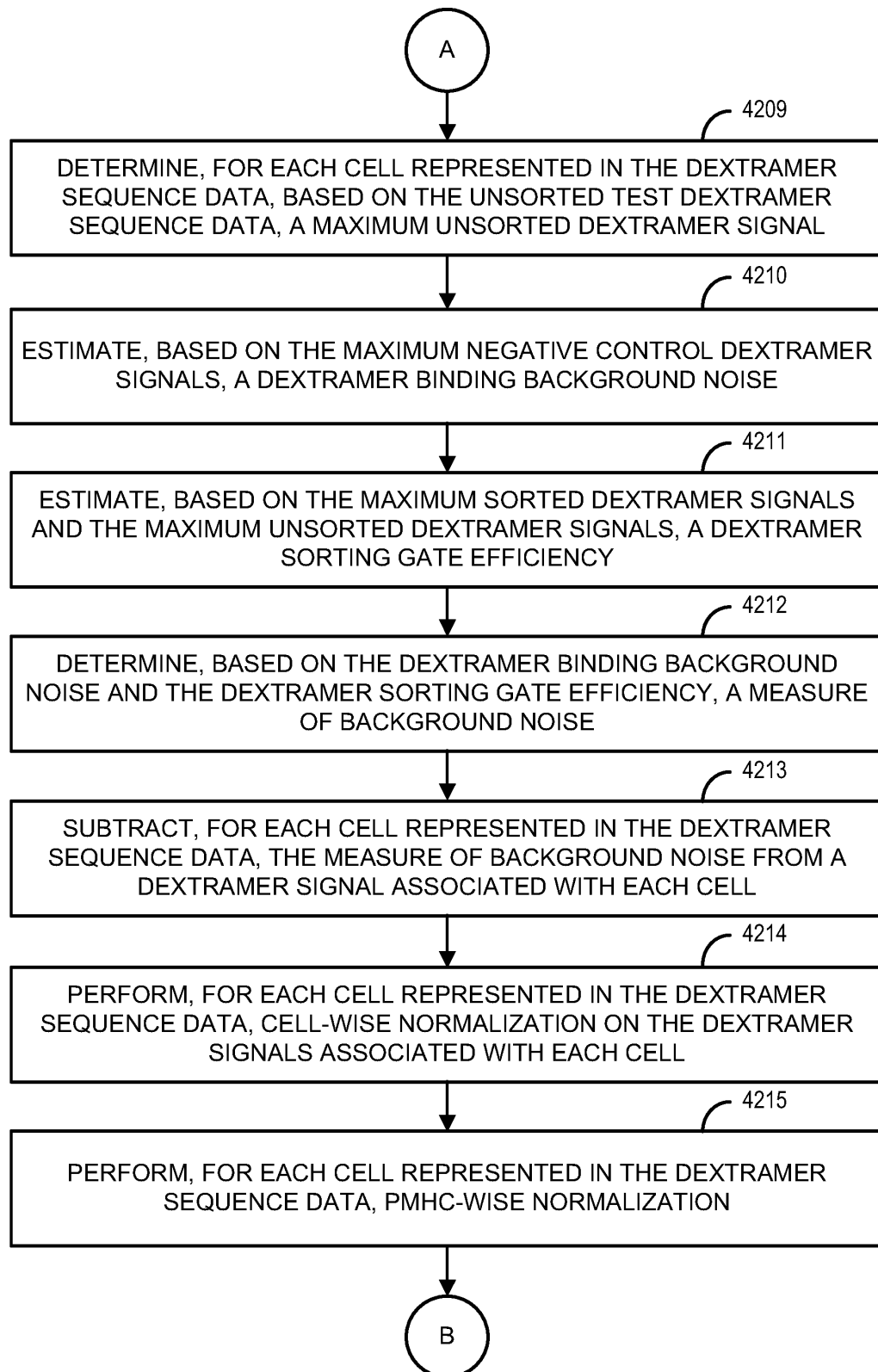
FIG. 41





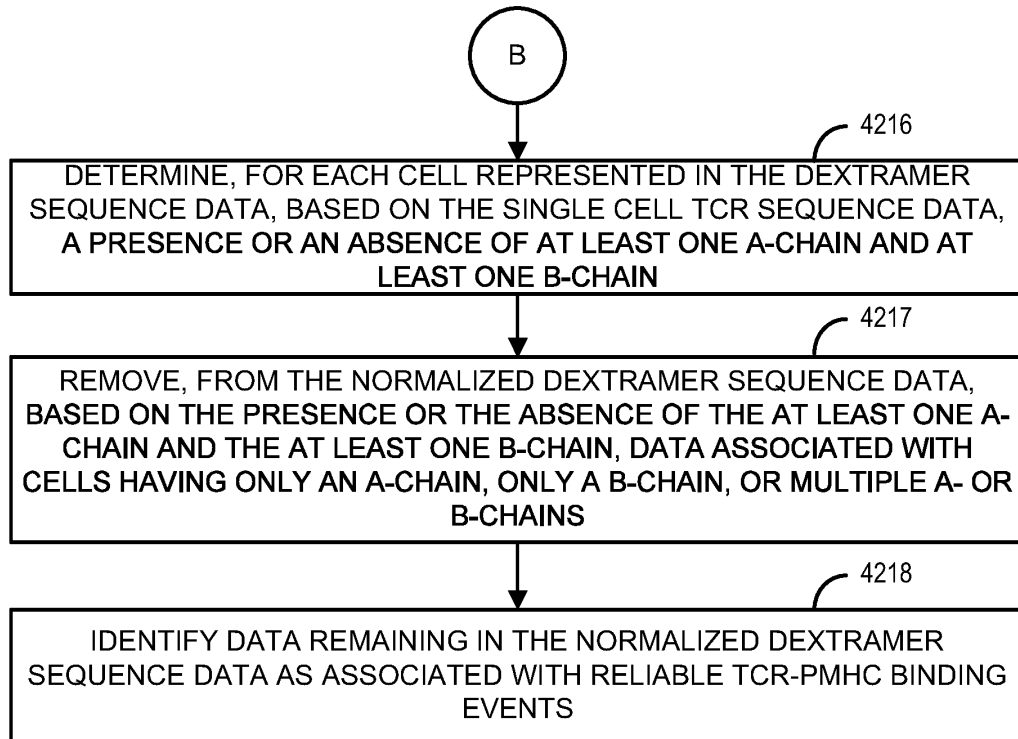
4200 ↗

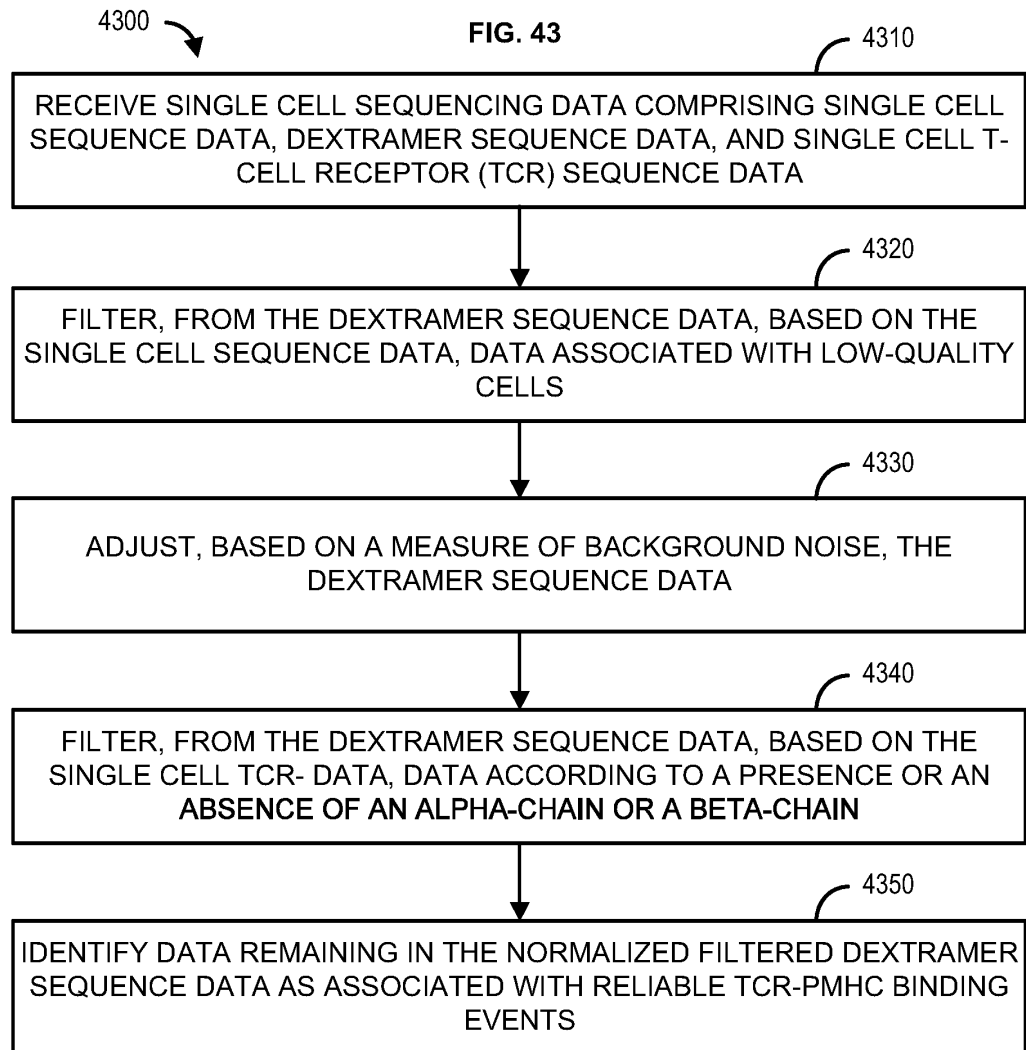
FIG. 42 (CONT'D)

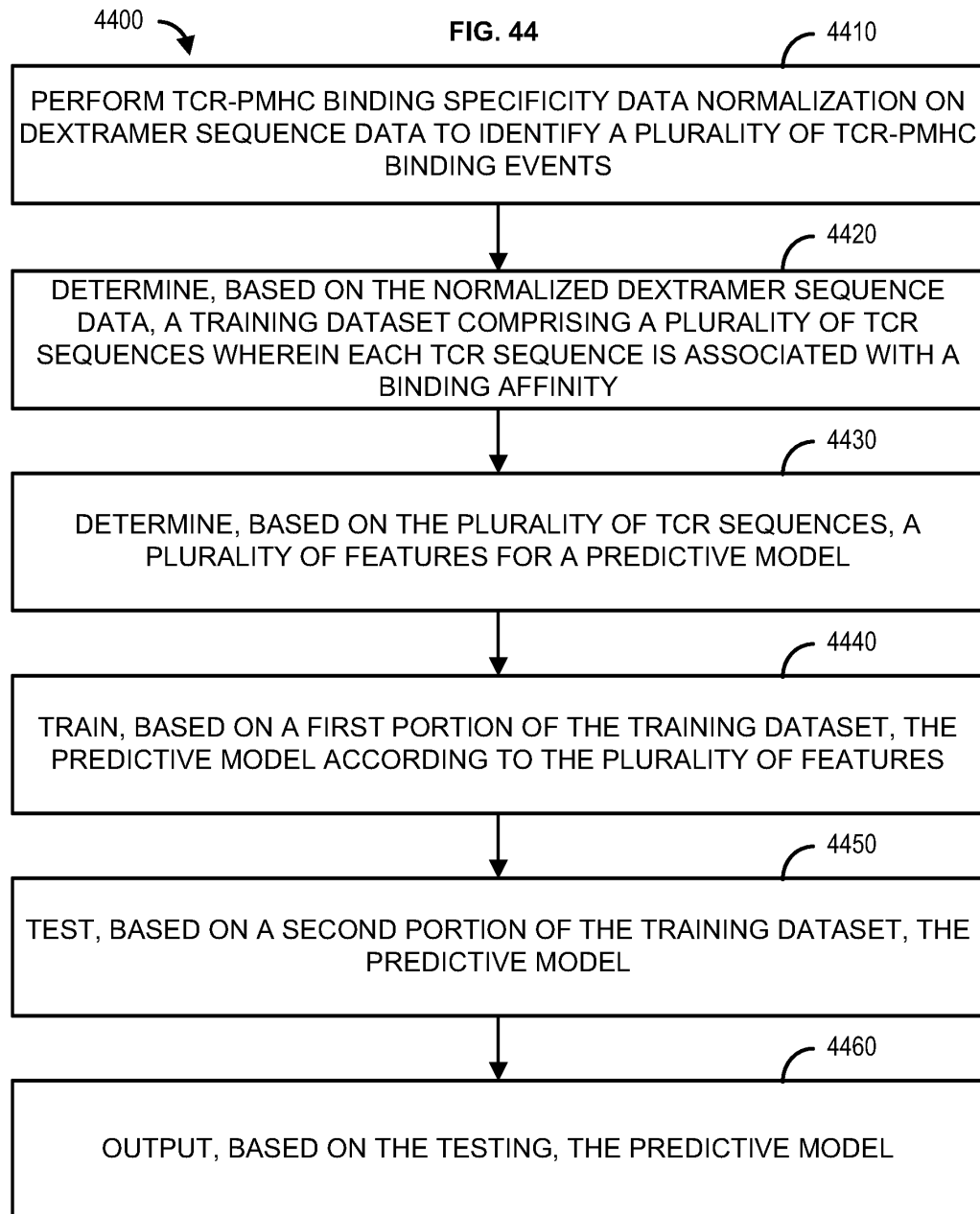


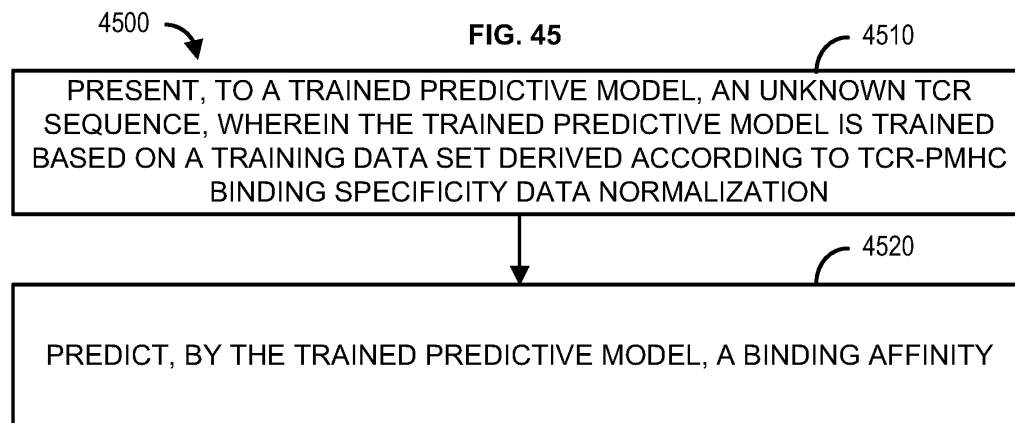
4200 ↗

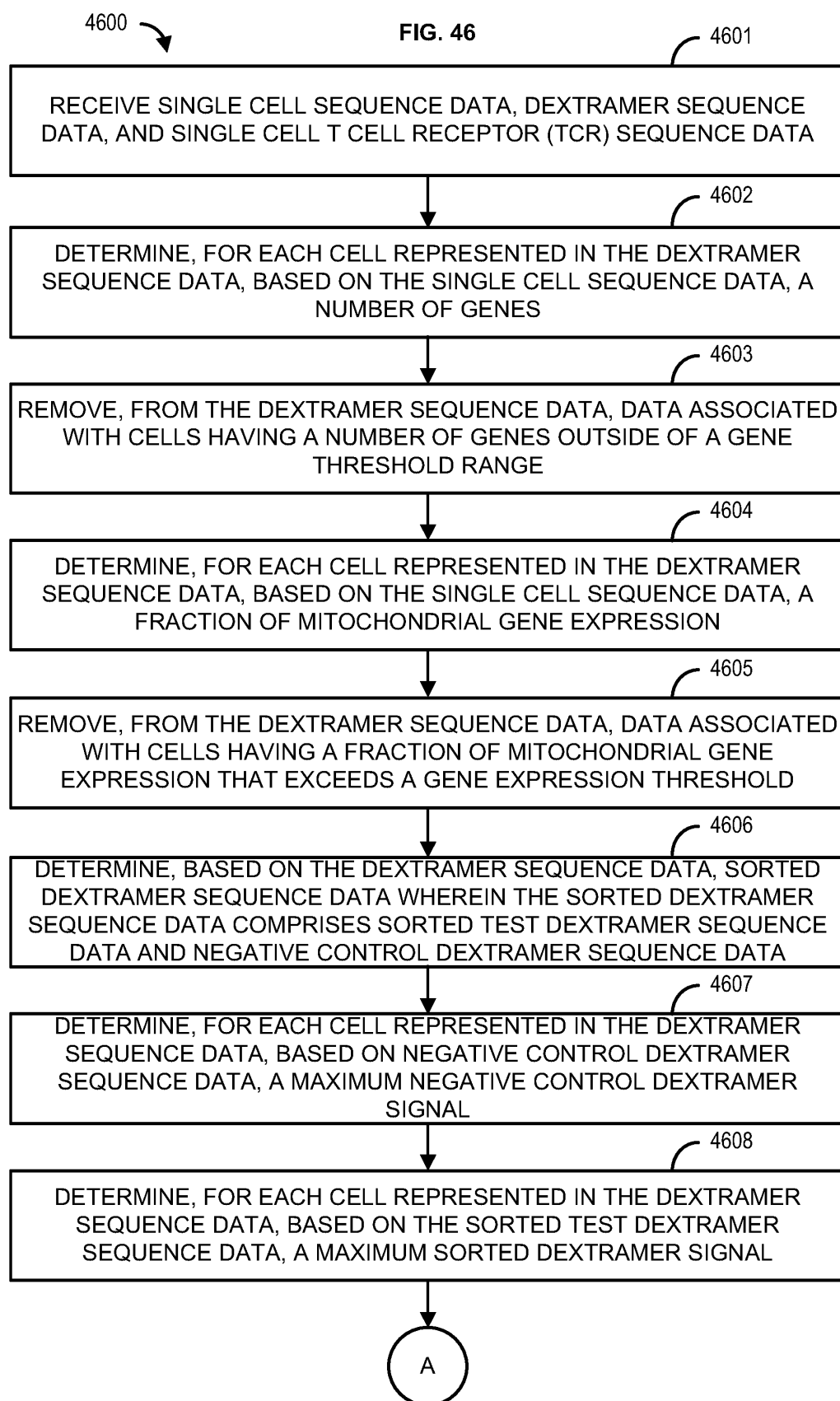
FIG. 42 (CONT'D)





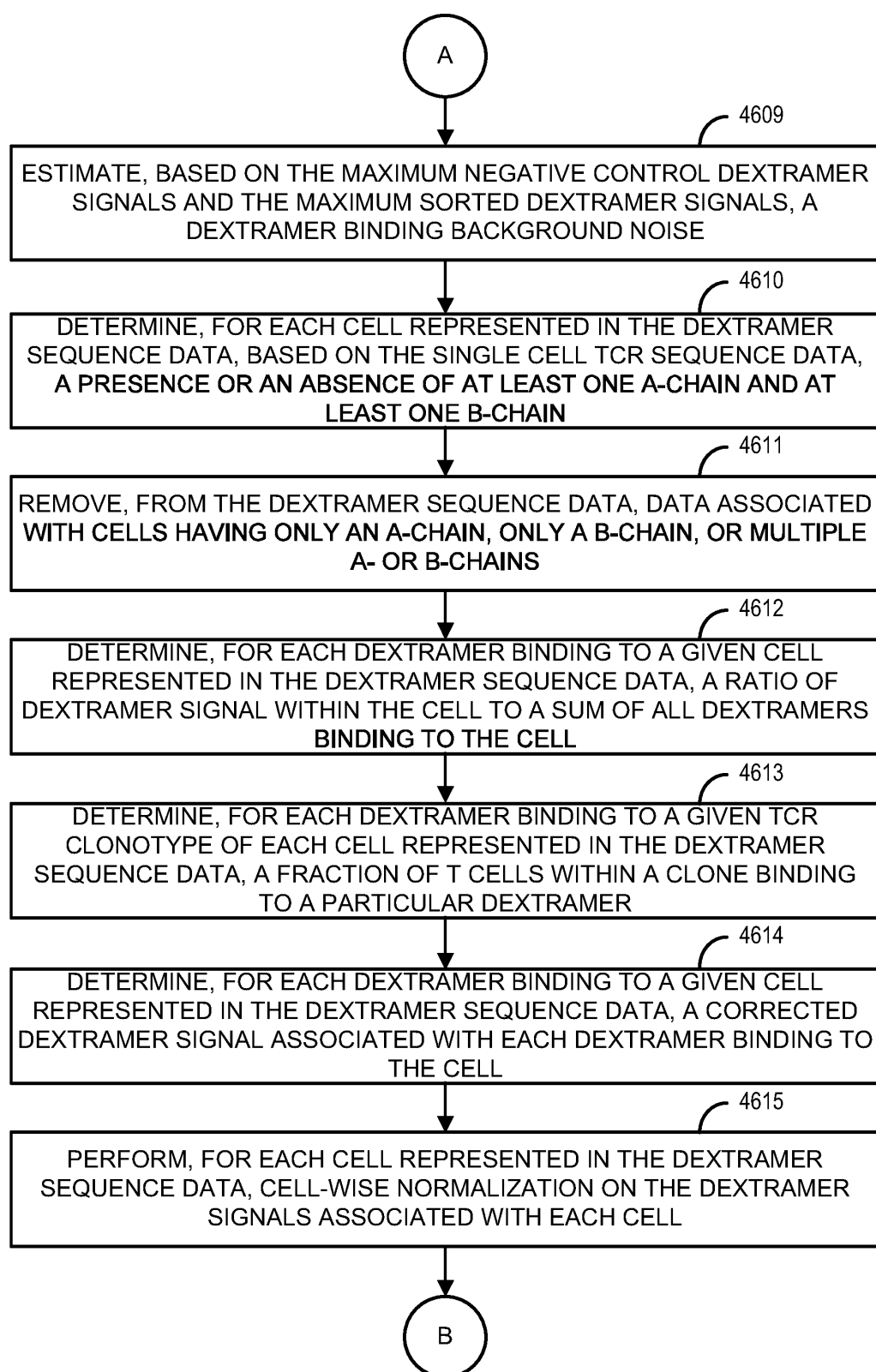






4600

FIG. 46 (CONT'D)



4600

FIG. 46 (CONT'D)

