

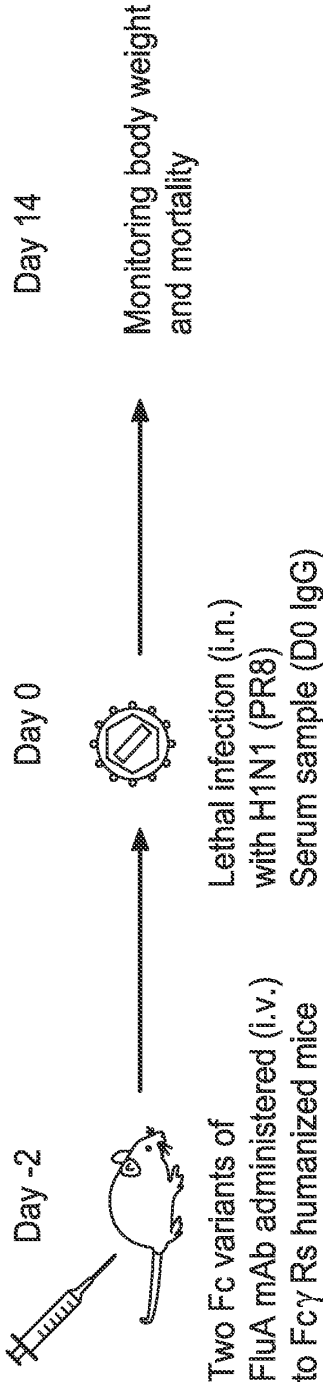


FIG. 1A

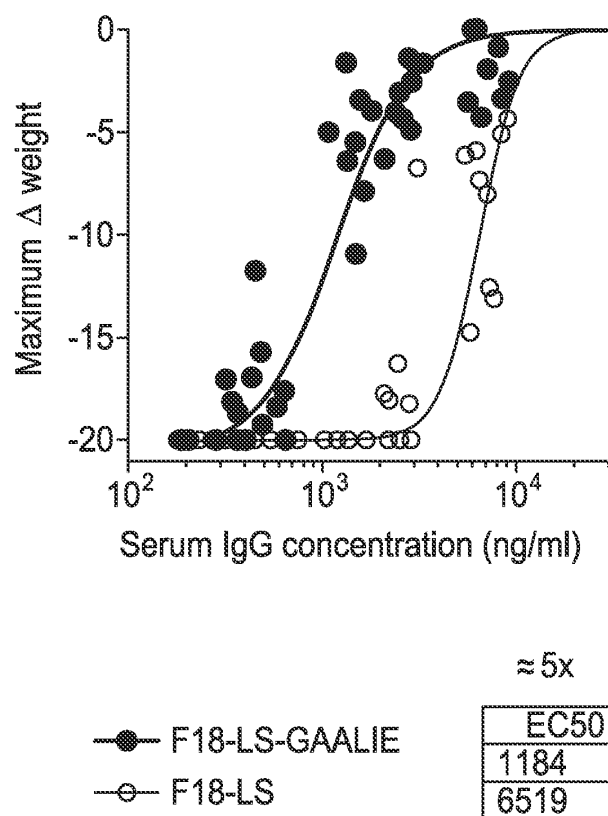


FIG. 1B

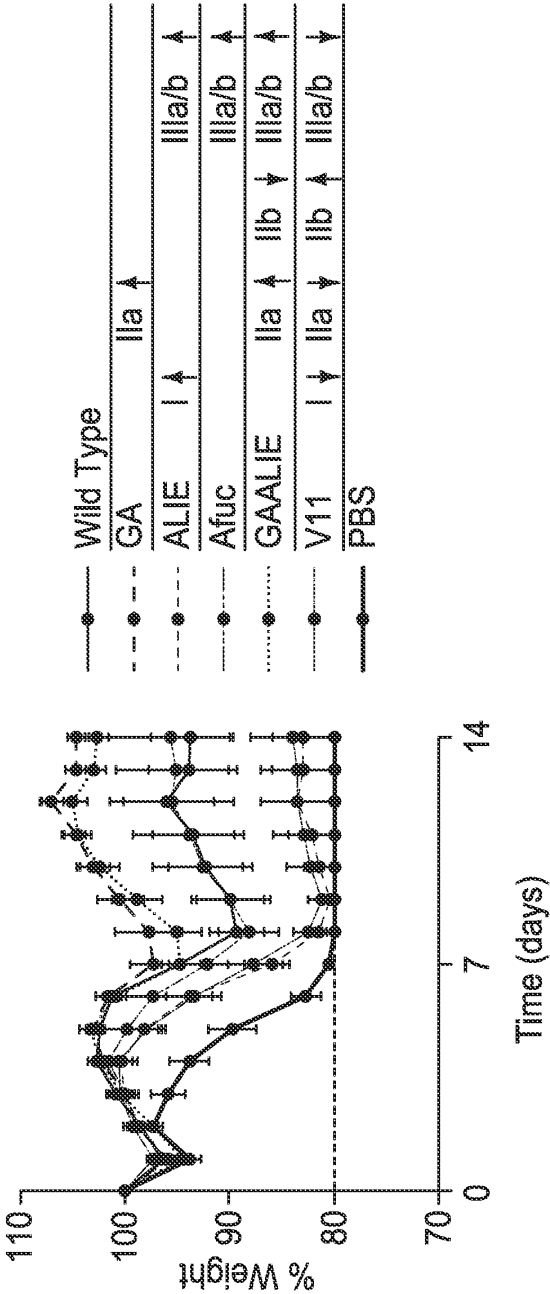


FIG. 1C

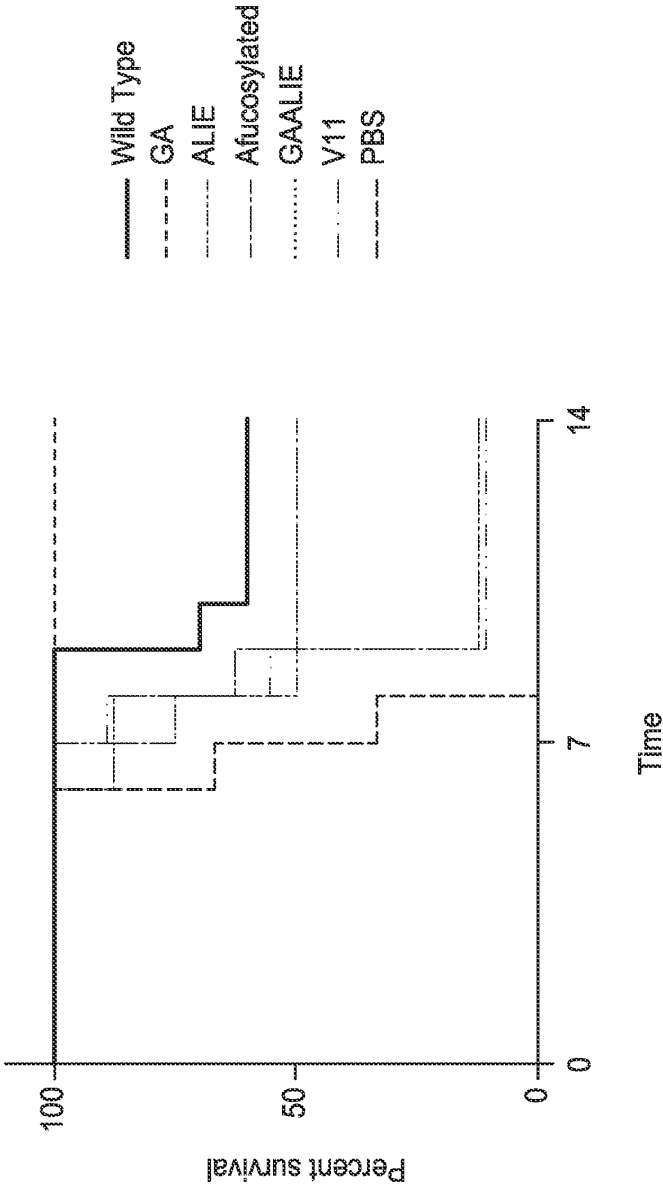


FIG. 1D

Fc variant	FcγRI	FcγRIIIa	FcγRIIb	FcγRIIIa/b
WT	++++	++	++	++
GRLR	—	—	—	—
GA	+++	+++++	++	++
ALIE	+++++	++	++	+++++
Afuc	+++++	++	++	+++++
GAALIE	+++++	+++++	+	+++++
V11	+	+	+++++	—

FIG. 1E

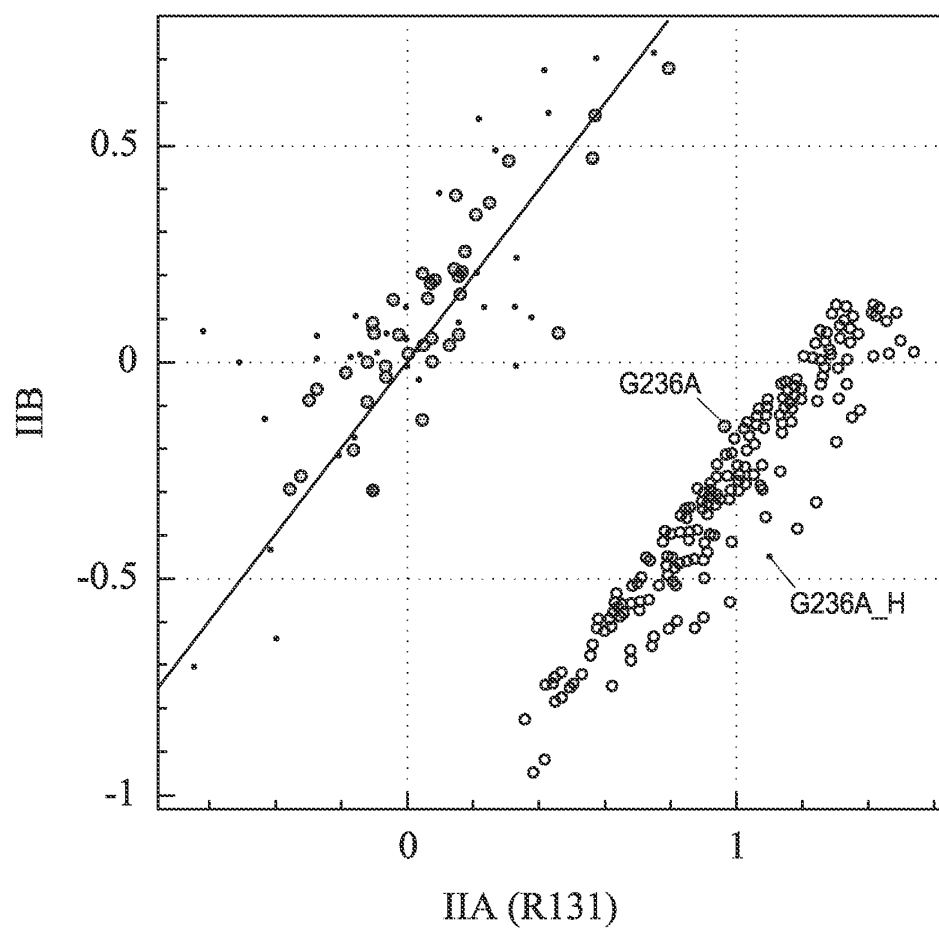


FIG. 2

	IIA_H	IIB	IIA_R	IIIA_V	IIIA_F	IIB	FcRn	IIA/IIB	Titer mg/mL	Tm (°C)
G236A A330L I332E	4.3	0.61	1.62	2.38	13.35	1.98	0.93		-0.0039	-13.305
G236A A330L I332E	2.91	0.60	1.19	1.69	11.25	1.6	0.94		-0.0181	-13.725
G236A E272Y S298N	0.63	0.19	0.38	0.06	0.31	0.62	0.98	3.24	0.0255	-2.985
G236A K334A Q295E	5.01	0.4	2.88	0.27	0.74	0.72	1.02	12.59	0.0245	-8.055
G236A L328V Q295E	7.76	0.81	10.72	0.36	0.52	0.71	1.07	9.55	0.0145	-11.265
G236A P230A Q295E	7.59	0.48	4.57	0.31	0.48	0.72	0.93	15.85	0.0245	-6.185
G236A Q295E S298N	1.82	0.23	0.65	0.07	0.35	0.76	0.93	7.76	0.0425	-3.225
K334A Q295E S298N	0.22	0.47	0.28	0.09	0.37	0.93	0.91	0.47		
L234D G236D K326E	0.14	0.28	0.3	0.05	0.35	0.6	0.83	0.51		
L234D V264R K326E	0.14	0.5	0.25	0.05	0.27	0.6	0.83	0.28		
L328V Q295E S298N	0.26	0.32	0.33	0.08	0.28	0.79	1.02	0.79		
P245A Q295E S298N	0.28	0.31	0.3	0.1	0.34	0.89	0.85	0.91		

FIG. 3

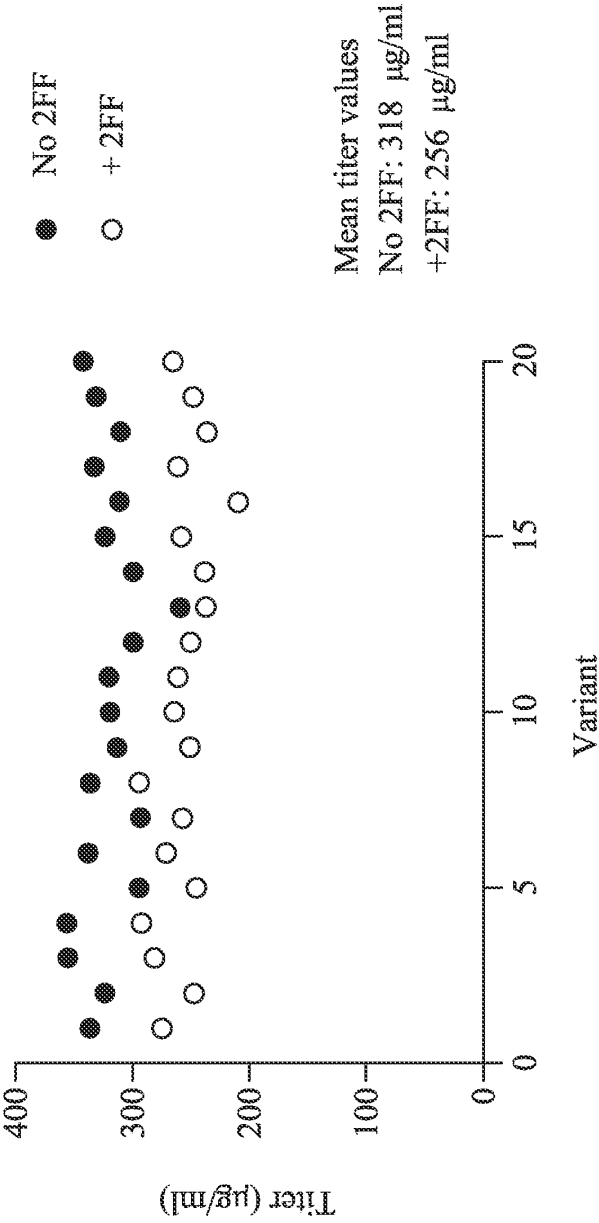


FIG. 4A

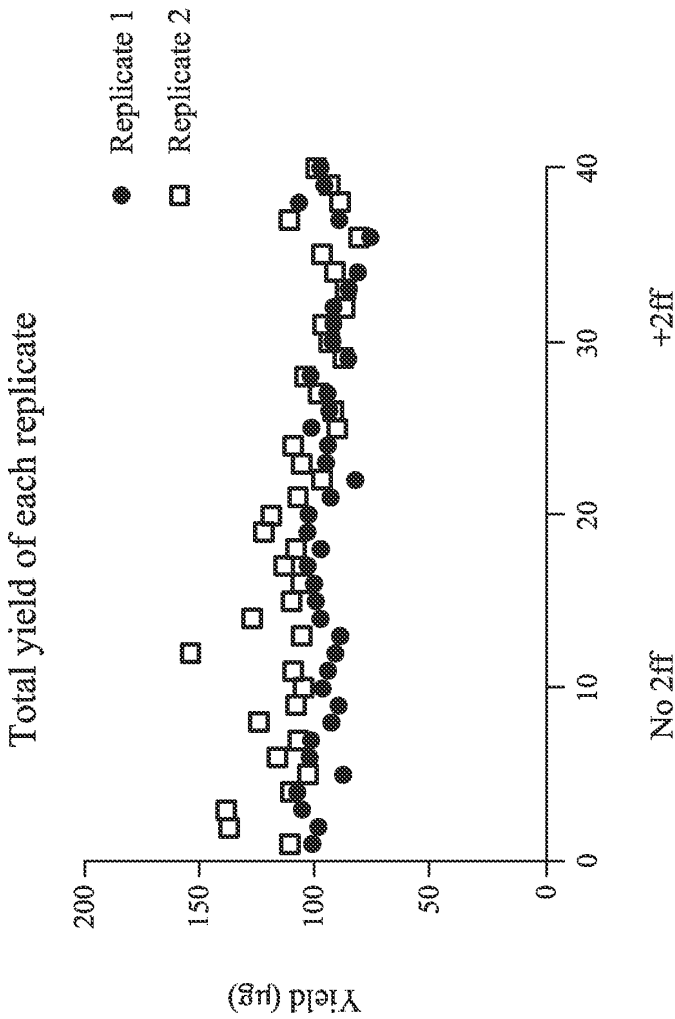


FIG. 4B

Purification	Theo.Avg Max Yield (µg)	Avg Yield (µg)	Avg Recovery	Avg Conc. Elution 2 (mg/mL)
No 2FF 1	286	98	34%	0.61
No 2FF 2	286	117	41%	0.68
+2FF 1	230	92	40%	0.54
+2FF 2	230	96	42%	0.55

FIG. 4C

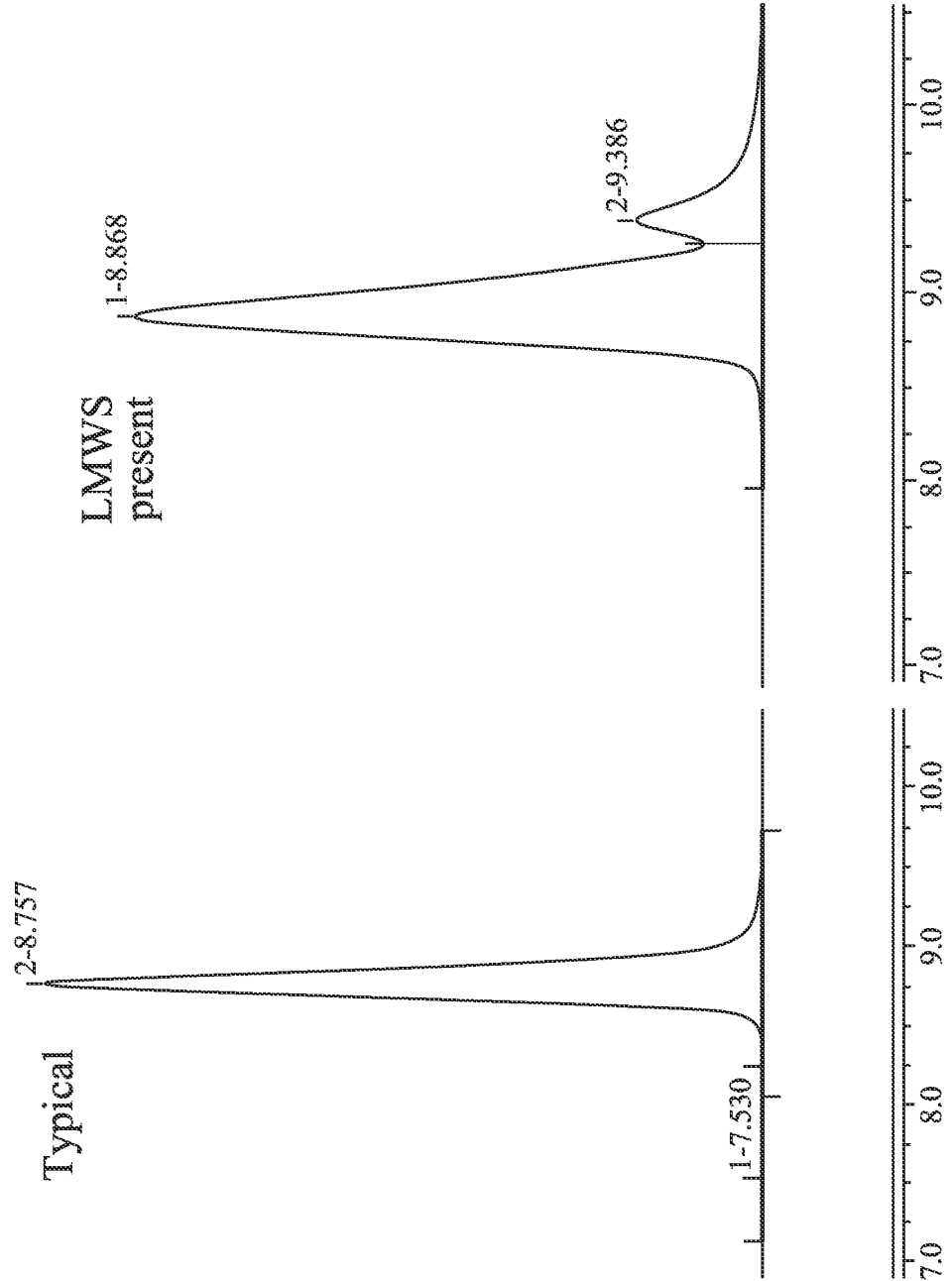


FIG. 5

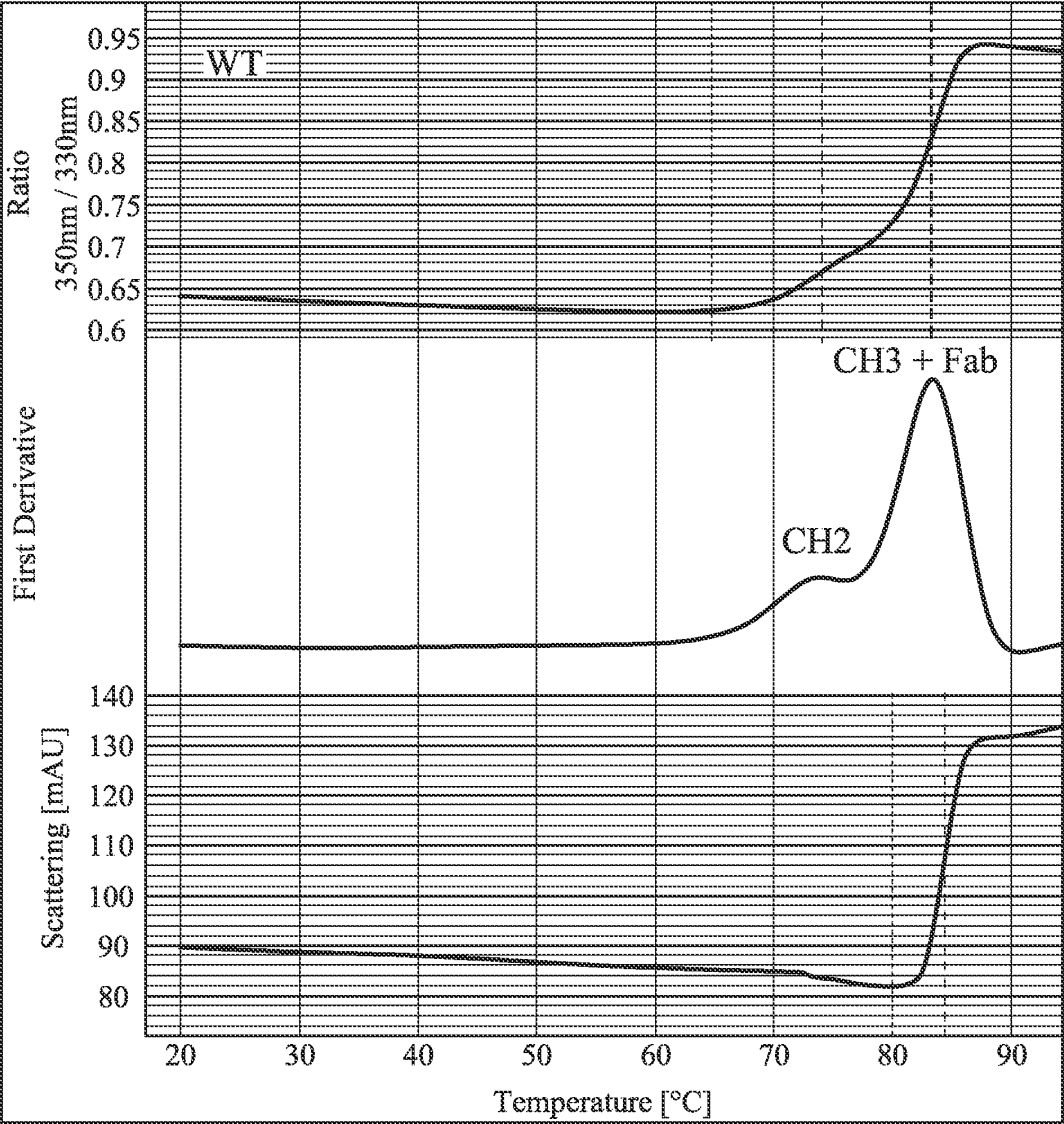


FIG. 6A

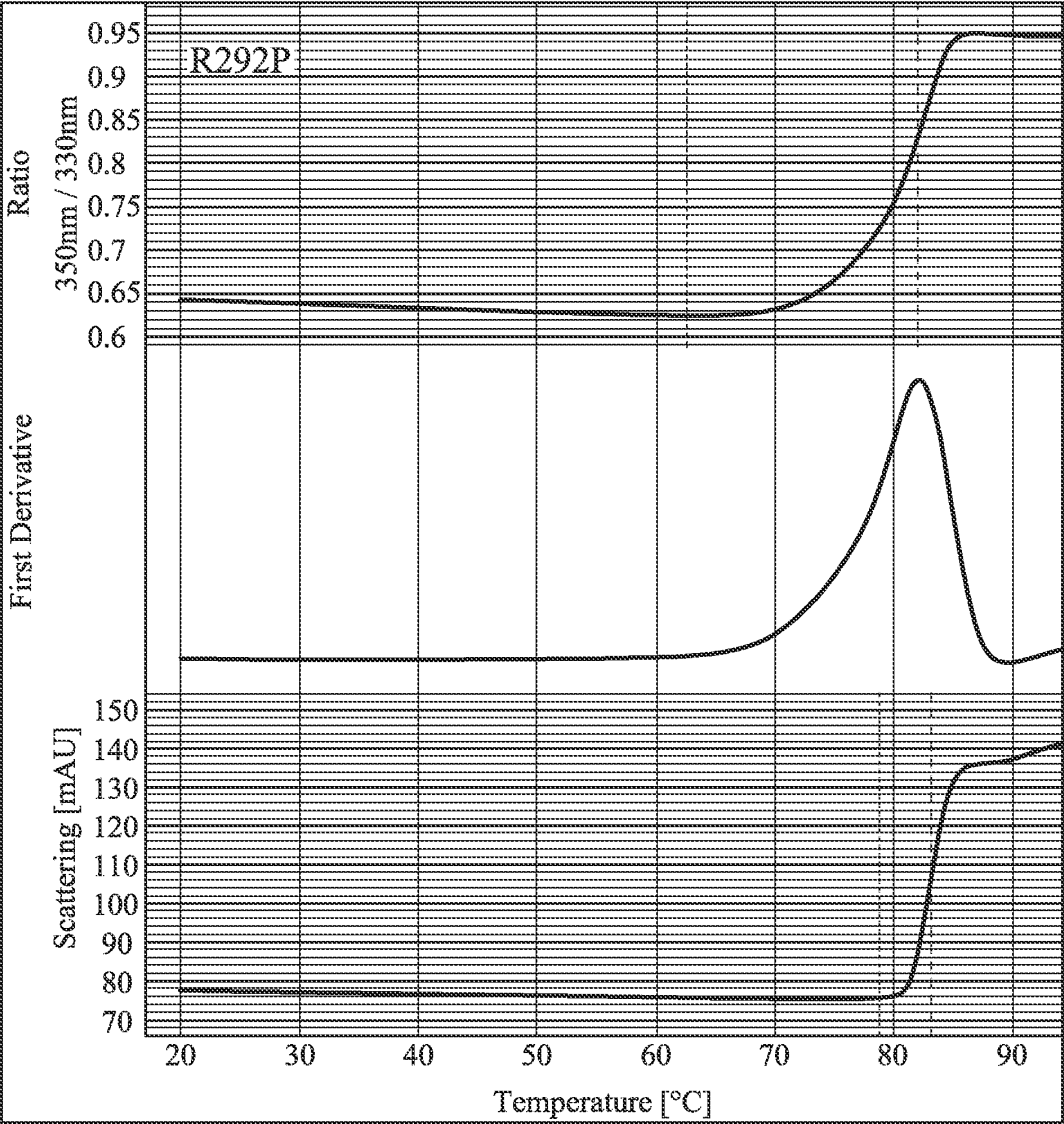


FIG. 6B

Fc variant Name (no 2FF) Fold-change to WT Fc	FcgRIIA-H (high affinity)	FcgRIIA-R (low affinity)	FcgRIIB
WT	1.000	1.000	1.000
R292P	0.577	0.454	0.541
Y300L	1.860	0.822	1.176
A431G	1.761	1.377	1.499
C220P	1.167	1.037	1.210
G446E	1.114	1.047	1.168
G236A	12.090	6.310	1.053
G236S	9.143	2.635	1.099
G236W	1.061	0.469	0.652
G236L	0.435	1.416	0.395
G236Y	0.735	0.418	0.547
R292P_Y300L	1.399	0.682	0.900
G236A_R292P	5.647	1.037	0.446
G236A_Y300L	18.188	4.606	1.054
R292P_G446E	0.628	0.450	0.562
G236A_R292P_Y300L	14.186	2.708	0.940
G236A_R292P_G446E	4.544	0.986	0.512
G236A_R292P_I377N	7.833	1.345	0.549
G236S_R292P_Y300L	10.853	1.341	0.817
G236A_R292P_A431G	5.212	0.939	0.511

FIG. 7A

Fc variant Name (no 2FF) Fold-change to WT Fc	FcgRIIIA-V (high affinity)	FcgRIIIA-F (low affinity)	FcRn PH 6
WT	1.000	1.000	1.000
R292P	0.917	0.790	0.898
Y300L	1.620	1.245	1.060
A431G	1.611	1.231	0.916
C220P	1.326	0.990	0.991
G446E	1.422	1.103	1.056
G236A	0.638	0.776	0.977
G236S	0.179	0.466	0.991
G236W	0.117	0.541	1.088
G236L	0.083	0.345	0.949
G236Y	0.116	0.559	1.051
R292P_Y300L	4.848	5.286	0.879
G236A_R292P	0.411	0.603	0.809
G236A_Y300L	0.871	0.997	0.981
R292P_G446E	0.916	0.779	0.884
G236A_R292P_Y300L	2.685	3.714	0.828
G236A_R292P_G446E	0.415	0.552	0.851
G236A_R292P_I377N	1.024	1.107	0.879
G236A_R292P_Y300L	0.753	1.059	0.870
G236A_R292P_A431G	0.394	0.569	0.674

FIG. 7A (cont'd)

Fc variant Name (no 2FF) Fold-change to WT Fc	FcgRIIA-H (high affinity)	FcgRIIB	IIA/IIIB ratio	FcgRIIA-V (high affinity)
WT	1.000	1.000	1.000	1.000
R292P	0.577	0.541	1.067	0.917
Y300L	1.860	1.176	1.582	1.620
A431G	1.761	1.499	1.175	1.611
C220P	1.167	1.210	0.964	1.326
G446E	1.114	1.168	0.954	1.422
G236A	12.090	1.053	11.483	0.638
G236S	9.143	1.099	8.317	0.179
G236W	1.061	0.652	1.628	0.117
G236L	0.435	0.395	1.102	0.083
G236Y	0.735	0.547	1.345	0.116
R292P_Y300L	1.399	0.900	1.554	4.848
G236A_R292P	5.647	0.446	12.658	0.411
G236A_Y300L	18.188	1.054	17.260	0.871
R292P_G446E	0.628	0.562	1.117	0.916
G236A_R292P_Y300L	14.186	0.940	15.098	2.685
G236A_R292P_G446E	4.544	0.512	8.881	0.415
G236A_R292P_I377N	7.833	0.549	14.268	1.024
G236S_R292P_Y300L	10.853	0.817	13.283	0.753
G236A_R292P_A431G	5.212	0.511	10.191	0.394
GAALIE (AVG2, 1st plate)	3.605	0.605	5.955	2.039
GAALIE-LS (1st plate)	2.888	0.422	6.848	1.563

FIG. 7B

Fc variant Name (no 2FF) Fold-change to WT Fc	FcRn PH 6	Clq binding	CDC
WT	1.000	1.000	1.000
R292P	0.898	0.549	0.656
Y300L	1.060	2.157	0.887
A431G	0.916	0.824	NA
C220P	0.991	0.761	NA
G446E	1.056	0.840	NA
G236A	0.977	0.358	0.488
G236S	0.991	0.391	NA
G236W	1.088	3.662	1.035
G236L	0.949	1.480	NA
G236Y	1.051	3.252	1.065
R292P_Y300L	0.879	2.088	1.254
G236A_R292P	0.809	0.125	0.613
G236A_Y300L	0.981	0.981	NA
R292P_G446E	0.884	0.391	NA
G236A_R292P_Y300L	0.828	1.012	0.935
G236A_R292P_G446E	0.851	0.099	0.522
G236A_R292P_I377N	0.879	0.235	0.809
G236S_R292P_Y300L	0.870	1.976	0.936
G236A_R292P_A431G	0.674	0.100	0.581
GAALIE (AVG2, 1st plate)	0.937	-0.004	0.364
GAALIE-LS (1st plate)	12.327	FLGEPLSE (1st)	1.463

FIG. 7B (cont'd)

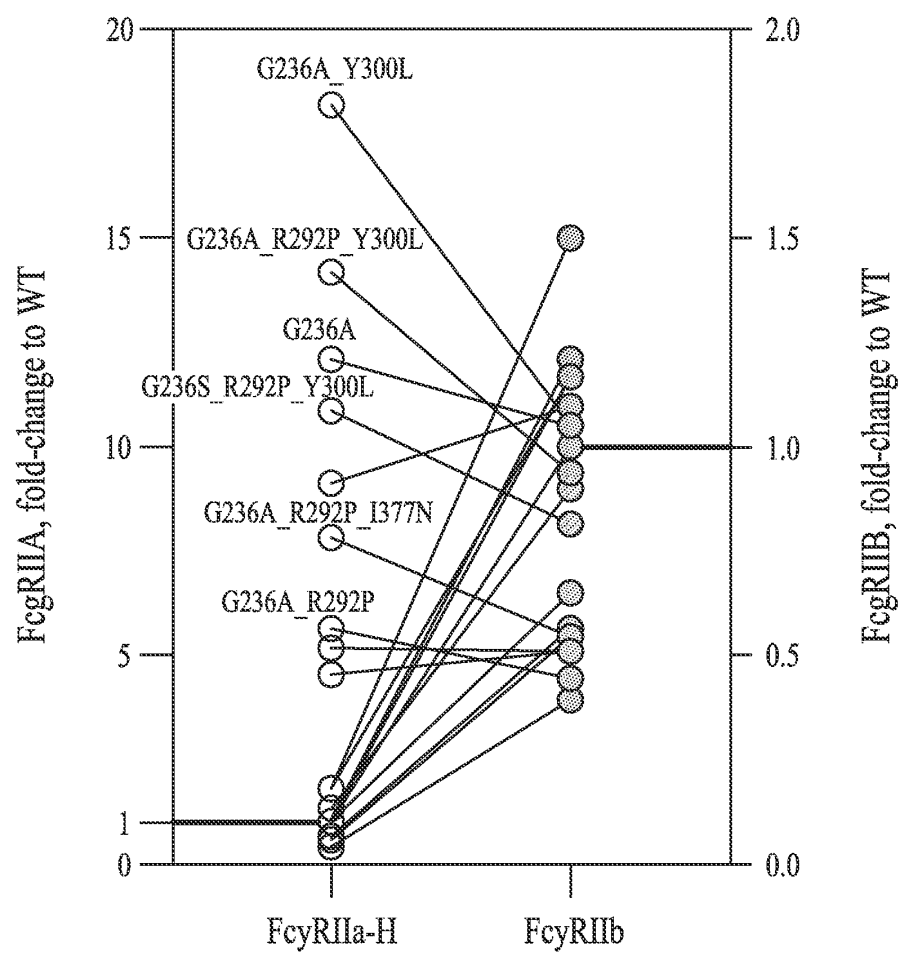


FIG. 8

	IIA-H	IIB	ratio
WT	1.00	1.00	1.00
GAALIE (1st)	2.20	1.58	1.39
R292P	0.63	0.13	4.89
Y300L	1.33	1.05	1.27
G236A	2.52	1.27	1.99
G236W	1.53	0.24	6.40
G236Y	1.02	0.05	22.21
R292P_Y300L	1.36	0.96	1.41
G236A_R292P	2.06	0.18	11.28
G236A_R292P_Y300L	2.45	1.30	1.88
G236A_R292P_G446E	1.95	0.09	21.63
G236A_R292P_I377N	1.96	0.28	6.94
G236A_R292P_Y300L	2.02	0.75	2.70
G236A_R292P_A431G	1.87	0.16	11.38
A431G	1.20	1.38	0.87
C220P	1.65	1.75	0.94
G446E	1.48	1.16	1.28
G236S	2.23	1.27	1.75
G236L	0.25	0.02	11.67
G236A_Y300L	2.52	1.65	1.53
R292P_G446E	0.81	0.12	6.57
	fuc	fuc	fuc

FIG. 9A

	IIIA-V		IIIA-F	
WT	1.00	5.20	1.00	16.45
GAALIE (1st)	3.54	6.44	13.92	29.86
R292P	0.98	3.24	0.46	5.10
Y300L	1.12	4.61	1.40	12.02
G236A	0.58	4.14	0.34	9.81
G236W	0.02	2.09	0.07	6.60
G236Y	0.02	1.34	0.07	4.07
R292P_Y300L	3.80	4.90	8.29	13.76
G236A_R292P	0.56	2.92	0.33	6.72
G236A_R292P_Y300L	3.00	4.06	7.16	11.37
G236A_R292P_G446E	0.51	2.76	0.36	4.12
G236A_R292P_I377N	0.99	3.56	0.93	6.44
G236A_R292P_Y300L	1.18	2.58	1.01	4.35
G236A_R292P_A431G	0.47	2.14	0.12	2.89
A431G	1.20	5.61	fuc	afuc
C220P	1.18	4.77		
G446E	1.21	4.63		
G236S	0.13	3.36		
G236L	0.02	0.03		
G236A_Y300L	0.87	4.10		
R292P_G446E	1.22	3.53		
	fuc	afuc		

FIG. 9B

Variants	IIA_H	IIA_R	IIB	IIA-H/IIB	IIA-R/IIB	IIIA_V	IIIA_F	IIIB
High IIA/IIB, low IIB				Calculated	Calculated			
G236A	8.50	5.53	0.81	10.49	6.83	0.49	0.69	0.82
G236A_L328V_Q295E	7.80	10.78	0.86	9.07	12.53	0.36	0.52	0.70
G236A_P230A_Q295E	7.67	4.57	0.54	14.20	8.46	0.31	0.48	0.72
G236A_R292P_I377N	7.83	1.34	0.55	14.24	2.44	1.02	1.11	0.96
G236A_K334A_Q295E	4.96	2.92	0.67	7.40	4.36	0.27	0.74	0.72
G236S_R292P_Y300L	10.85	1.34	0.82	13.23	1.63	0.75	1.06	1.04
Strong increase IIA, no change IIB								
G236S	9.14	2.63	1.10	8.31	2.39	0.18	0.47	0.92
G236A_Y300L	18.19	4.61	1.05	17.32	4.39	0.87	1.00	0.97
Strong decrease IIB								
G236S_G420V_G446E_L309T	4.85	1.47	0.39	12.44	3.77	0.09	0.32	0.56
G236A_R292P	5.65	1.04	0.45	12.56	2.31	0.41	0.60	0.95
High IIA/IIB, low IIB, increase IIIA								
G236A_A330L_I332E	3.54	1.39	0.61	5.80	2.28	2.01	12.25	1.78
G236A_A330L_I332E_M428L_N434S	2.89	1.27	0.42	6.88	3.02	1.56	9.41	1.40

FIG. 10A-1

FIG. 10A-1	FIG. 10A-3
FIG. 10A-2	FIG. 10A-4

FIG. 10A

Variants	IIA_H	IIA_R	IB	IIA-H/IB	IIA-R/IB	IIIA_V	IIIA_F	IIIB
				Calculated	Calculated			
High IIA, little/no change IB, increase IIIA, has C1q								
G236A_R292P_Y300L	14.19	2.71	0.94	15.10	2.88	2.69	3.71	1.03
High increase IIIA, Tm drops in most								
R292P_Y300L	1.40	0.68	0.90	1.56	0.76	4.85	5.29	1.72
A330L_I332E	0.42	0.52	0.66	0.64	0.79	3.52	11.90	5.19
G236A_S239D_A330L_I332E	5.15	9.68	1.94	2.65	4.99	8.03	55.13	13.99
Abrogate FcγR binding (same as background)								
G236R_L328R	0.14	0.22	0.16	0.88	1.38	0.05	0.26	0.61
Other controls								
L309T_P238D_P396L_T366A	0.17	0.50	3.08	0.06	0.16	0.05	0.26	0.58
S239D_H268E_G236A	11.72	53.52	5.09	2.30	10.51	7.90	16.33	3.04
R292P	0.58	0.45	0.54	0.92	0.83	0.79	0.93	0.9
Y300L	1.86	0.82	1.18	1.62	0.69	1.24	1.01	1.06

FIG. 10A-2

Variants	FcRn	C1q	Tm	titer	signaling_IIA_H	signaling_IIB	signaling_IIIA_V	signaling_IIIA_F
High IIA/IIB, low IIB								
G236A	0.99	0.06	-1.30	-0.06	2.51	1.06	0.65	0.46
G236A_L328V_Q295E	1.08	0.07	-11.26	0.01	2.18	0.66	0.03	0.02
G236A_P230A_Q295E	0.93	0.30	-6.19	0.02	2.29	0.56	0.06	0.02
G236A_R292P_I377N	0.88	0.24	-1.08	-0.03	2.15	0.35	0.11	1.40
G236A_K334A_Q295E	1.02	0.90	-8.06	0.02	2.13	0.80	0.36	0.23
G236S_R292P_Y300L	0.87	1.98	-4.00	-0.01	2.24	0.93	1.32	1.52
Strong increase IIA, no change IIB								
G236S	0.99	0.39	-2.36	0.00	1.95	1.37	0.11	NaN
G236A_Y300L	0.98	0.98	-4.45	-0.04	2.21	1.78	0.74	NaN
Strong decrease IIB								
G236S_G420V_G446E_L309T	0.77	0.21	1.89	-0.01	2.56	0.22	0.06	0.03
G236A_R292P	0.81	0.13	-4.00	-0.08	1.47	0.15	0.54	0.29
High IIA/IIB, low IIB, increase IIIA								
G236A_A330L_I332E	0.94	0.00	-13.51	-0.01	1.98	0.55	3.24	9.57
G236A_A330L_I332E_M428L_N434S	12.33	0.00	-14.26	0.00	2.32	0.35	3.92	13.51

FIG. 10A-3

Variants	FcRn	C1q	Tm	titer	signaling_IIA_H	signaling_IIB	signaling_IIIA_V	signaling_IIIA_F
High IIA, little/no change IIB, increase IIIA, has C1q								
G236A_R292P_Y300L	0.83	1.01	-4.00	-0.02	1.87	1.01	2.83	6.15
High increase IIIA, Tm drops in most								
R292P_Y300L	0.88	2.09	-4.00	-0.04	0.98	0.72	3.66	7.42
A330L_I332E	1.12	0.03	-12.98	-0.02	0.71	0.69	4.38	11.91
G236A_S239D_A330L_I332E	1.02	0.00	-23.37	-0.04	2.47	1.20	6.02	19.43
Abrogate FcγR binding (same as background)								
G236R_L328R	1.03	NaN	-3.73	0.03	0.05	0.04	0.02	0.27
Other controls								
L309T_P238D_P396L_T366A	0.88	0.01	-13.37	-0.01	0.04	0.91	0.01	0.05
S239D_H268E_G236A	0.91	0.40	-8.34	0.00	2.15	1.80	5.22	12.85
R292P	0.55	0.55	-0.01	0.71	0.16	0.69		1.13
Y300L	2.16	2.16	0.02	1.52	1.3	2.1		1.27

FIG. 10A-4

Variants (fold to wt-fucose)	IIA_H	IIA_R	IIB	IIIA-V	IIIA-F	IIIB	FcRn	C1q
High IIA/IIB, low IIB								
G236A-afuc	7.59	7.91	0.91	10.20	25.67	1.92	0.95	NaN
G236A_L328V_Q295E-afuc	7.54	10.07	1.13	8.41	12.71	2.31	1.09	NaN
G236A_P230A_Q295E-afuc	8.94	6.04	0.67	10.84	26.73	1.80	1.02	NaN
G236A_R292P_I377N-afuc	5.54	1.35	0.60	7.14	14.79	1.20	0.80	NaN
G236A_K334A_Q295E-afuc	5.32	3.75	0.55	7.93	27.49	1.62	1.11	NaN
G236S_R292P_Y300L-afuc	8.13	1.50	0.72	3.17	5.47	1.04	0.80	NaN
Strong increase IIA, no change IIB								
G236S-afuc	7.37	4.39	1.08	4.63	10.60	1.37	0.85	NaN
G236A_Y300L-afuc	14.86	3.95	0.93	13.73	30.09	2.55	0.92	NaN
Strong decrease IIB								
G236S_G420V_G446E_L309T-afuc	3.62	1.70	0.44	1.99	3.35	0.86	0.77	NaN
G236A_R292P-afuc	3.05	1.04	0.51	3.37	5.83	1.15	0.73	NaN
High IIA/IIB, low IIB, increase IIIA								
G236A_A330L_I332E-afuc	3.45	1.65	0.67	31.96	259.43	14.14	1.09	NaN
G236A_A330L_I332E_M428L_N434S-afuc	2.56	1.20	0.41	34.46	275.26	11.77	7.37	NaN

FIG. 10B-1

FIG. 10B-1	FIG. 10B-3
FIG. 10B-2	FIG. 10B-4

FIG. 10B

Variants (fold to wt-fucose)	IIA_H	IIA_R	IIB	IIIA-V	IIIA-F	IIIB	FcRn	C1q
High IIA, little/no change IIB, increase IIIA, has C1q								
G236A_R292P_Y300L-afuc	11.22	2.22	1.03	9.13	19.74	1.83	0.80	NaN
High increase IIIA, Tm drops in most								
R292P_Y300L-afuc	1.27	0.72	1.05	16.14	26.54	4.53	0.82	NaN
A330L_I332E-afuc	0.42	0.53	0.61	37.80	191.41	37.41	1.00	NaN
G236A_S239D_A330L_I332E-afuc	3.58	7.58	1.21	75.61	729.90	94.34	0.96	NaN
Abrogate FcγR binding (same as background)								
G236R_L328R-afuc	0.16	0.24	0.17	0.07	0.33	0.60	1.09	NaN
Other controls								
L309T_P238D_P396L_T366A-afuc	0.18	0.34	1.71	0.09	0.49	0.64	0.95	NaN
S239D_H268E_G236A-afuc	13.60	61.96	6.35	84.91	424.82	38.06	1.01	NaN

FIG. 10B-2

Variants (fold to wt-fucose)	Tm	titer	signaling_IIA_H	signaling_IIB	signaling_IIIA_V	signaling_IIIA_F
High IIA/IIB, low IIB						
G236A-afuc	-0.15	-0.01	NaN	NaN	5.01	13.36
G236A_L328V_Q295E-afuc	-10.82	-0.04	NaN	NaN	5.31	6.79
G236A_P230A_Q295E-afuc	-5.84	0.02	NaN	NaN	5.54	10.95
G236A_R292P_I377N-afuc	1.64	-0.04	NaN	NaN	3.94	9.68
G236A_K334A_Q295E-afuc	-7.73	0.03	NaN	NaN	5.54	12.73
G236S_R292P_Y300L-afuc	NaN	-0.03	NaN	NaN	2.87	6.54
Strong increase IIA, no change IIB						
G236S-afuc	-0.26	0.02	NaN	NaN	2.86	NaN
G236A_Y300L-afuc	-2.92	-0.04	NaN	NaN	3.49	NaN
Strong decrease IIB						
G236S_G420V_G446E_L309T-afuc	3.12	0.02	NaN	NaN	4.00	4.41
G236A_R292P-afuc	NaN	-0.04	NaN	NaN	2.18	3.34
High IIA/IIB, low IIB, increase IIIA						
G236A_A330L_I332E-afuc	-13.03	-0.01	NaN	NaN	5.27	14.81
G236A_A330L_I332E_M428L_N434S-afuc	-13.95	0.01	NaN	NaN	6.20	16.38

FIG. 10B-3

Variants (fold to wt-fucose)	Tm	titer	signaling_IIA_H	signaling_IIB	signaling_IIIA_V	signaling_IIIA_F
High IIA, little/no change IIB, increase IIIA, has C1q						
G236A_R292P_Y300L-afuc	NaN	-0.07	NaN	NaN	3.85	9.46
High increase IIIA, Tm drops in most						
R292P_Y300L-afuc	NaN	-0.03	NaN	NaN	4.52	10.64
A330L_I332E-afuc	-12.76	0.02	NaN	NaN	6.34	16.91
G236A_S239D_A330L_I332E-afuc	-22.70	-0.02	NaN	NaN	5.16	11.51
Abrogate FcγR binding (same as background)						
G236R_L328R-afuc	-3.57	0.03	NaN	NaN	0.20	0.05
Other controls						
L309T_P238D_P396L_T366A-afuc	-13.57	0.01	NaN	NaN	0.16	0.04
S239D_H268E_G236A-afuc	-7.94	-0.02	NaN	NaN	5.65	11.64

FIG. 10B-4

CDC & C1q	IIA_H	IIA_R	IIB	IIA/IIB	IIIA_V	IIIA_F	FcRn	C1q	Tm
G236S_R292P_Y300L	10.85	1.34	0.82	13.24	0.75	1.06	0.87	1.96	-4.00
R292P_Y300L	1.40	0.68	0.90	1.56	4.85	5.29	0.88	2.07	-4.00
Y300L	1.86	0.82	1.18	1.58	1.62	1.24	1.06	2.14	-2.96
E345K_G236S_L235Y_S267E	0.53	9.22	1.71	0.34	0.05	0.29	0.90	2.35	NaN
E272R_L309T_S219Y_S267E	0.33	10.65	4.77	0.10	0.11	0.37	0.98	2.53	NaN
G236Y	0.74	0.42	0.55	1.35	0.12	0.56	1.05	3.22	-3.24
G236W	1.06	0.47	0.65	1.63	0.12	0.54	1.09	3.63	-4.19
F243L_G446E_P396L_S267E	0.77	31.05	15.73	0.07	0.24	0.63	1.05	4.17	NaN

FIG. 10C

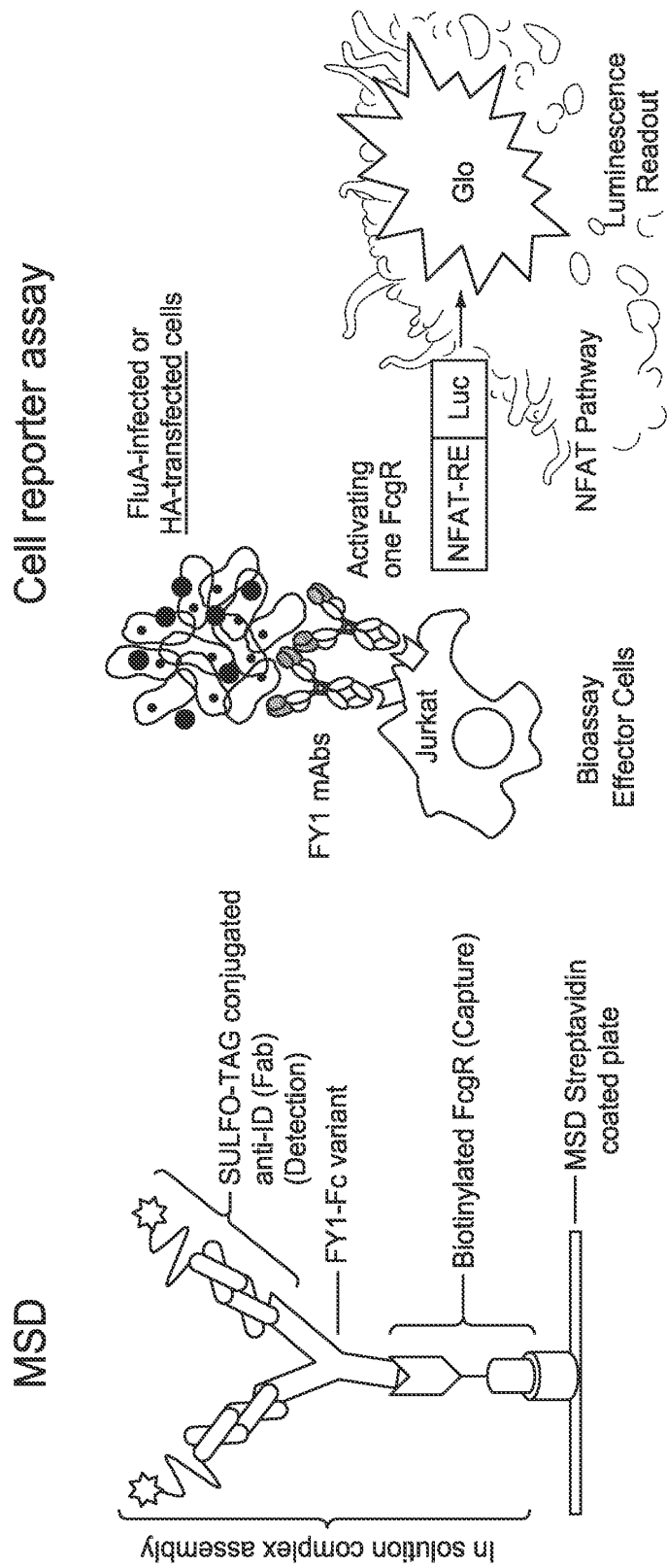


FIG. 11

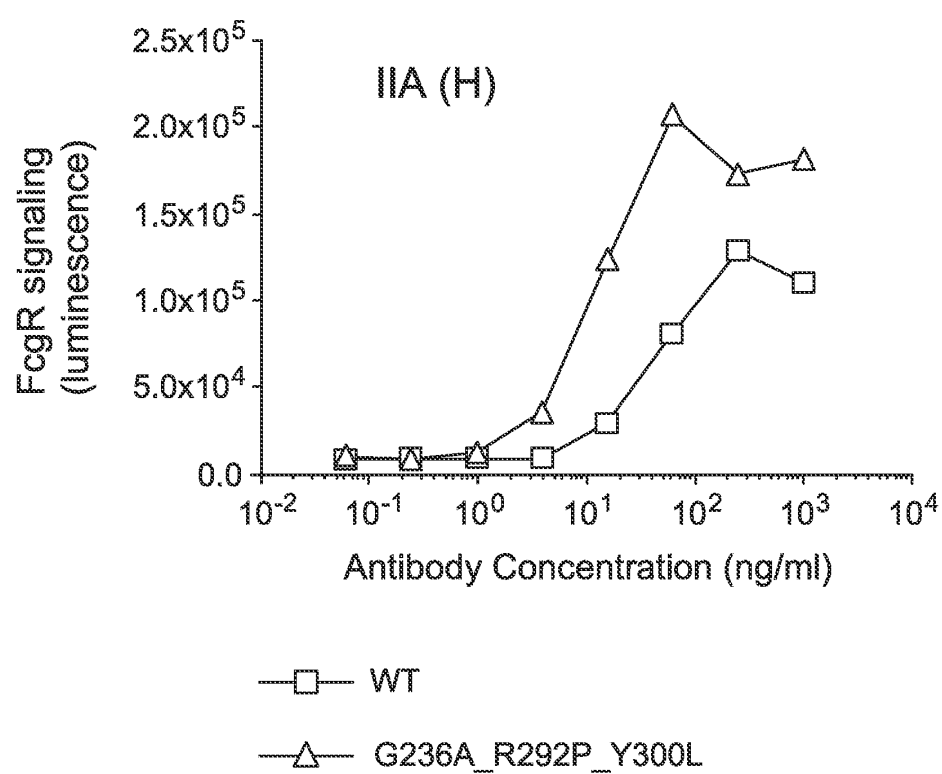


FIG. 12A

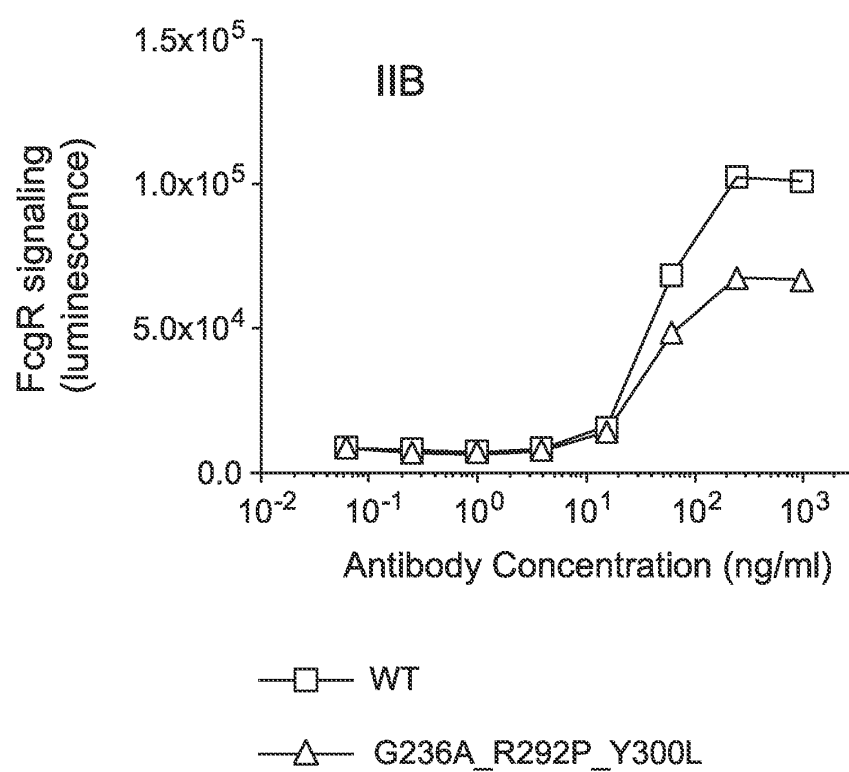


FIG. 12B

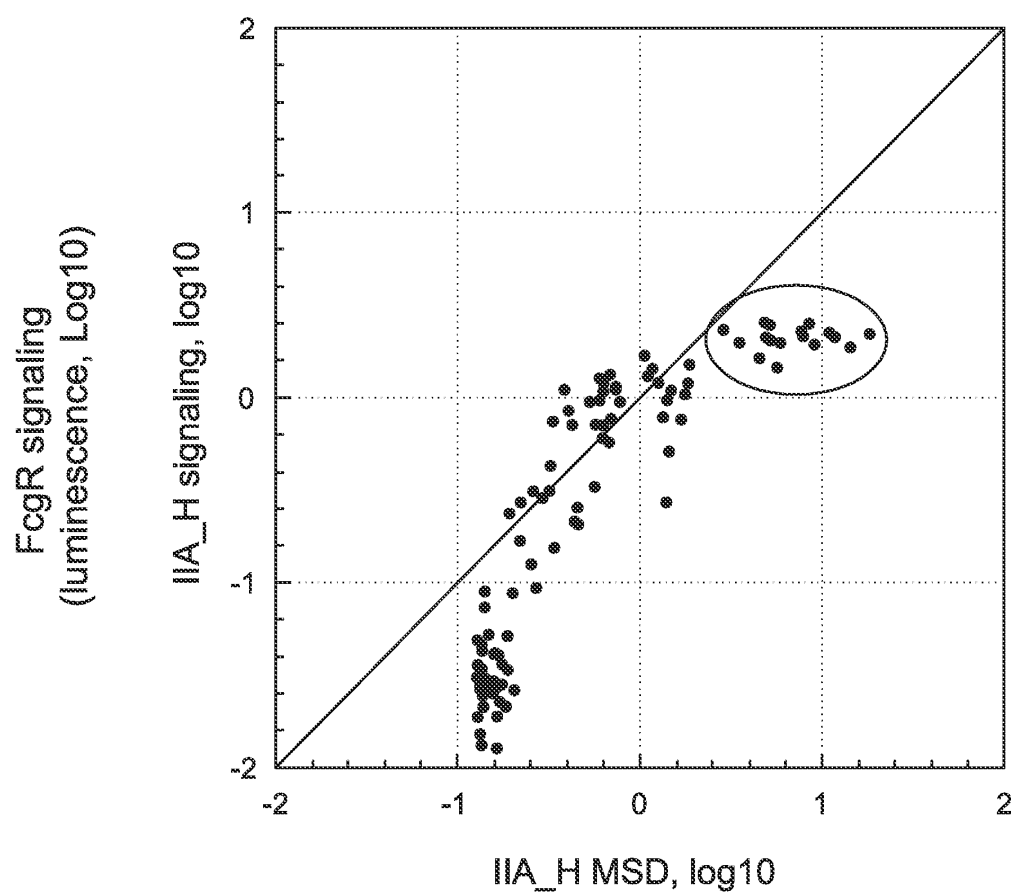


FIG. 13A

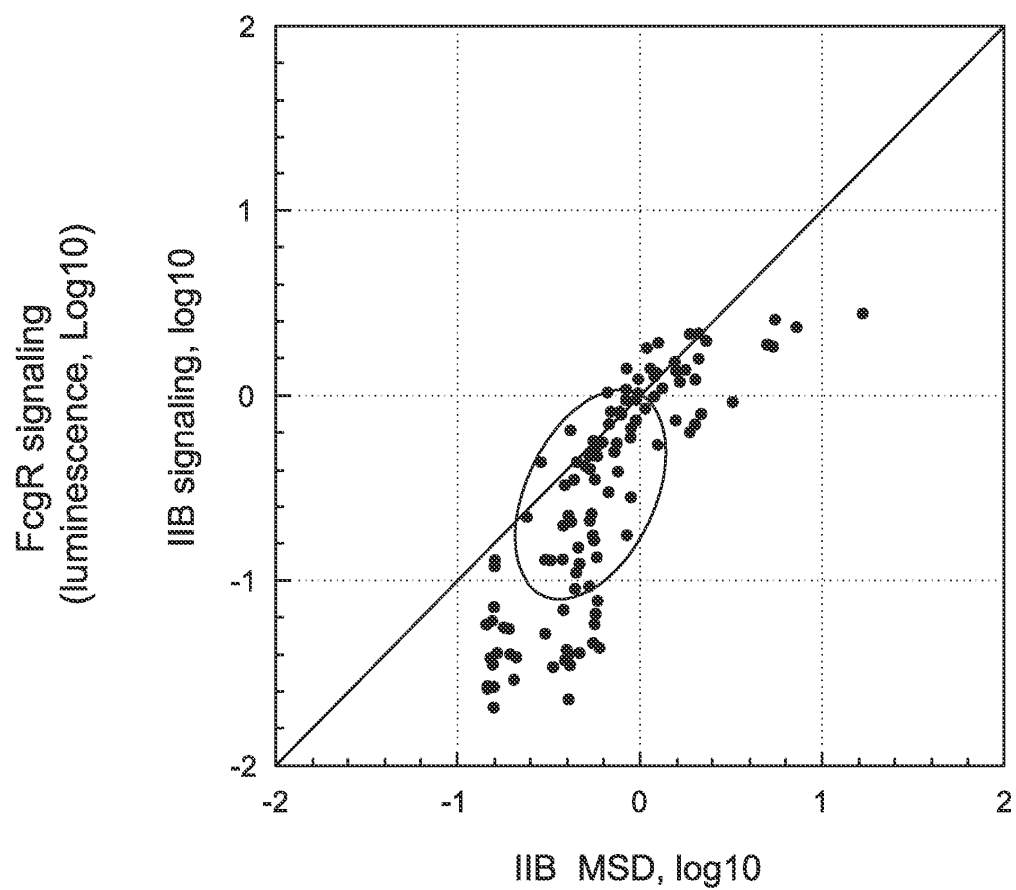


FIG. 13B

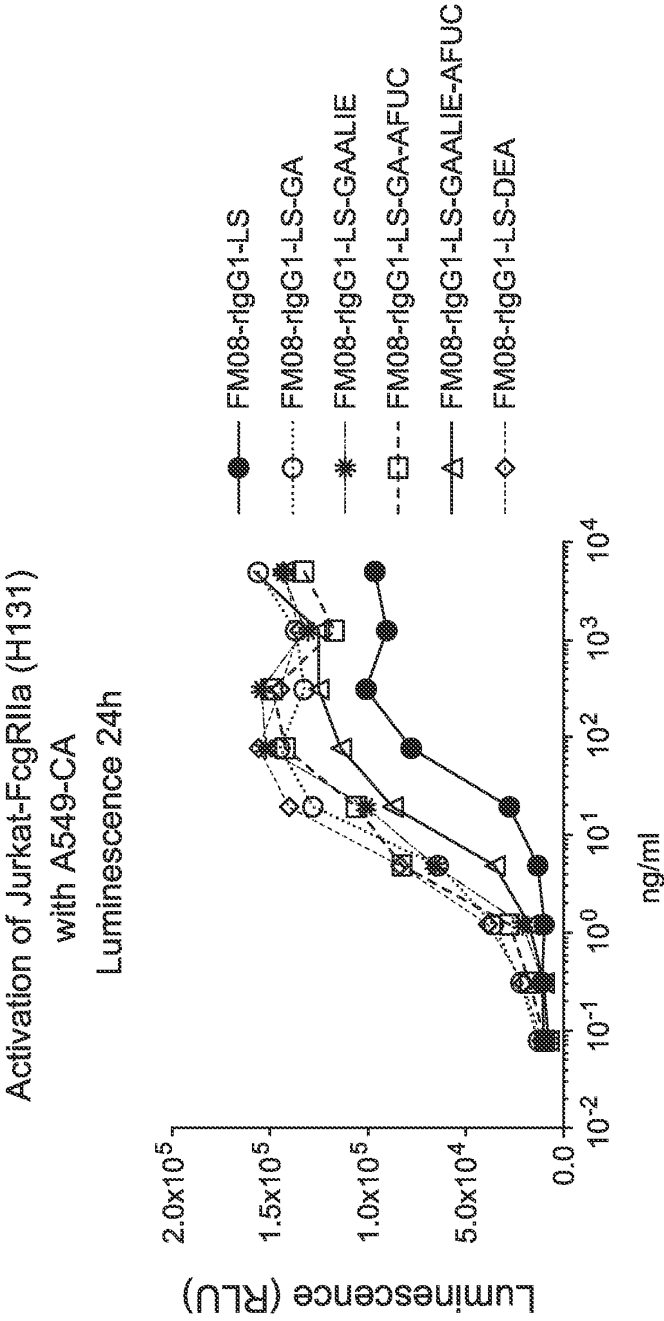


FIG. 14A

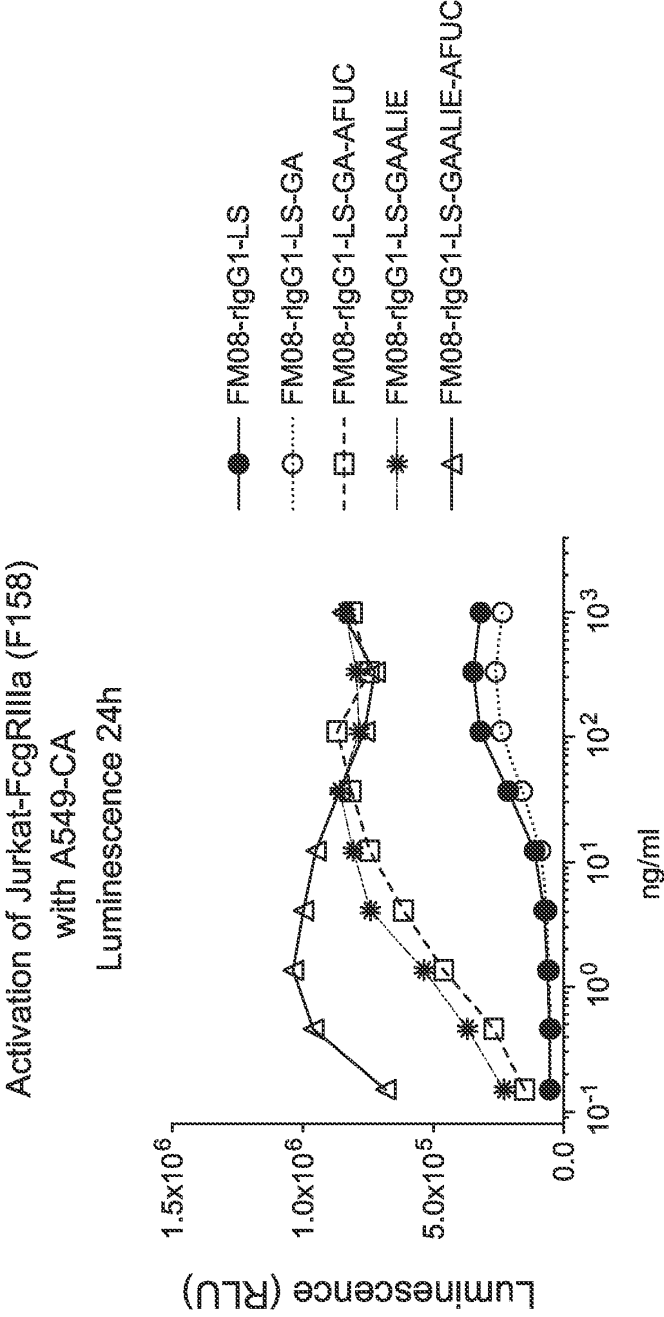


FIG. 14B

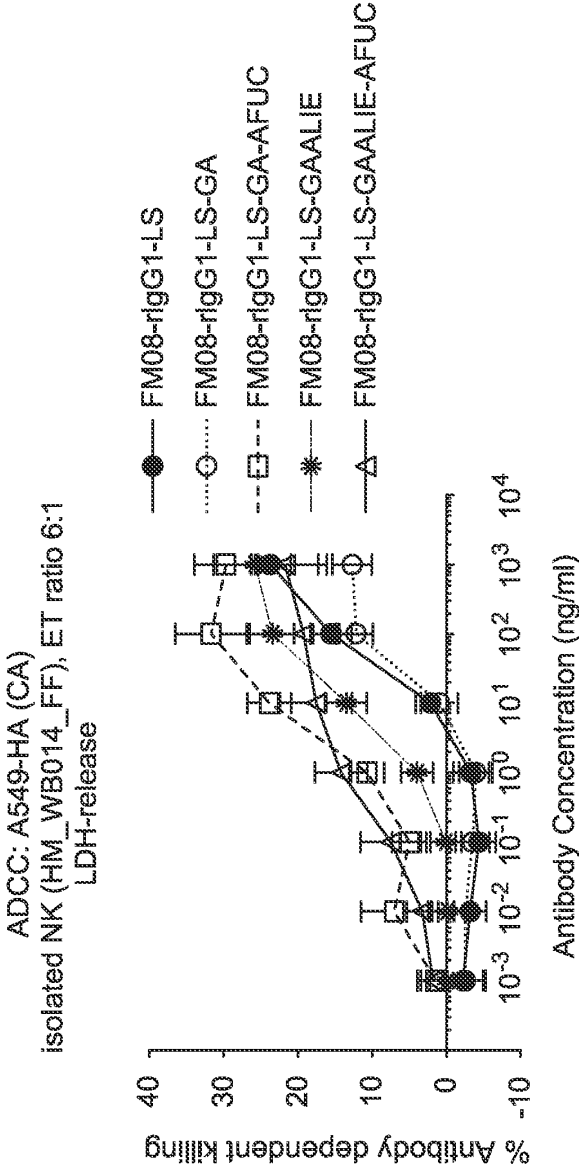


FIG. 14C

Fc variant	Response	Fold change to LS
FY1-rlgG1m3-LS	0.251	1.00
FY1-rlgG1m3-LS-G236A	0.087	0.35
FY1-rlgG1m3-LS-G236A-A330L-I332E	-0.008	-0.03
FY1-rlgG1m3-LS-A330L-I332E	-0.008	-0.03
FY1-rlgG1m3-LS-G326R-L328R	-0.008	-0.03

FIG. 15

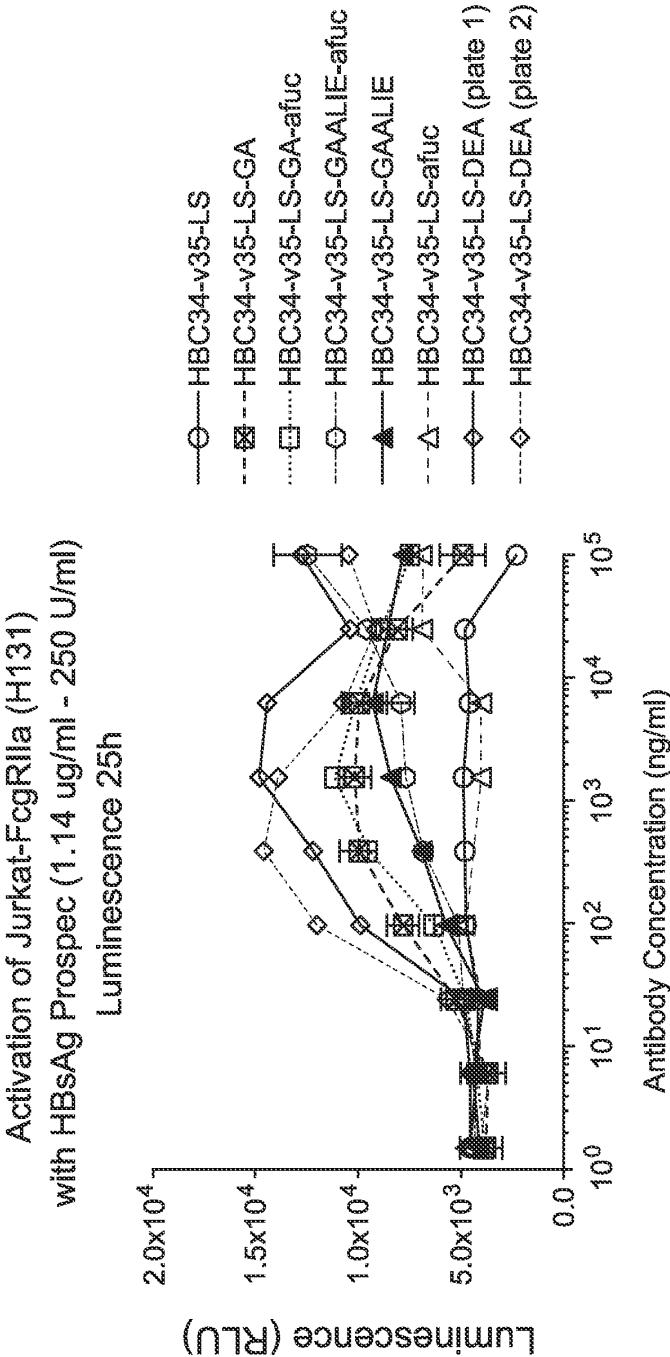


FIG. 16A

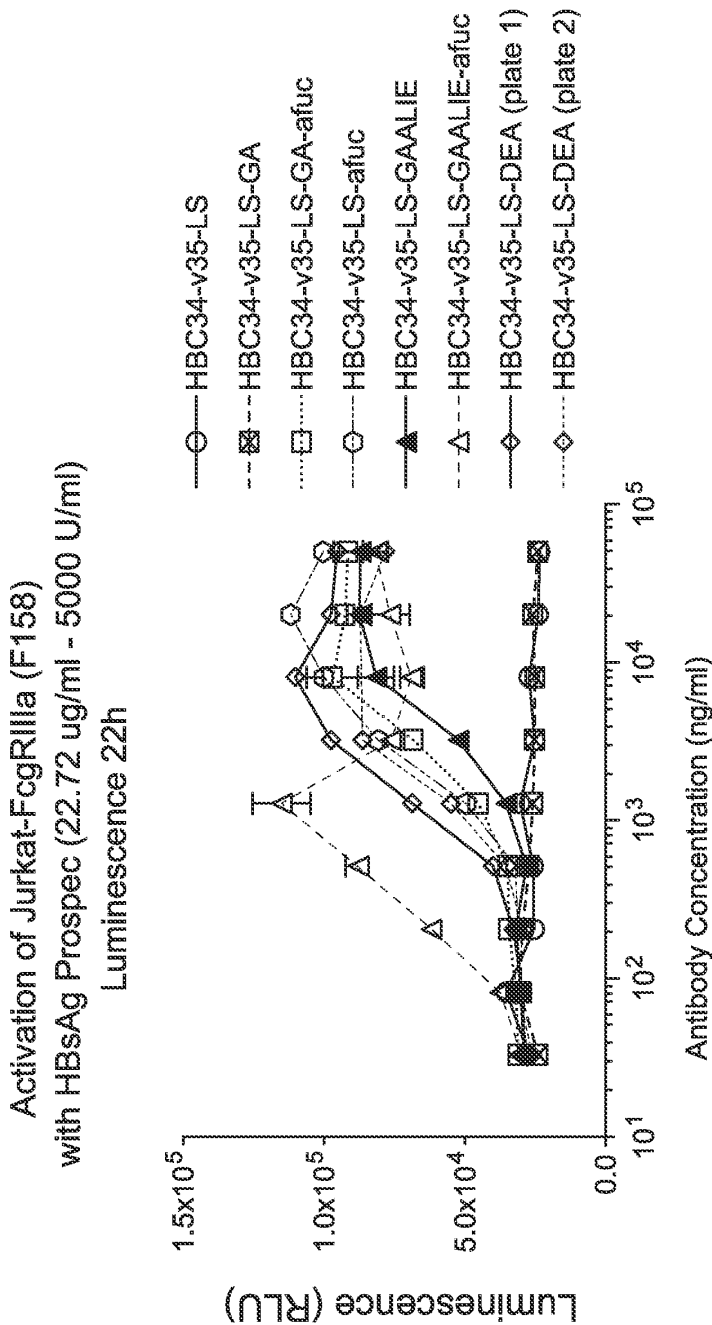


FIG. 16B

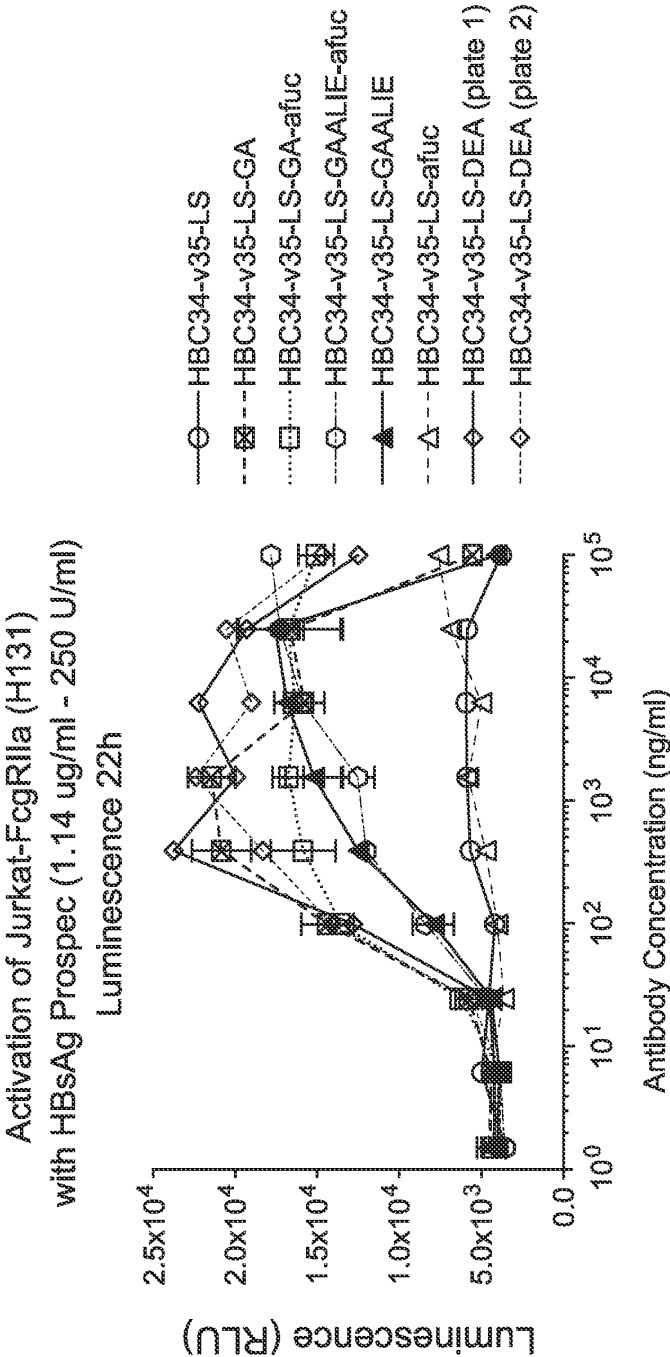


FIG. 17A

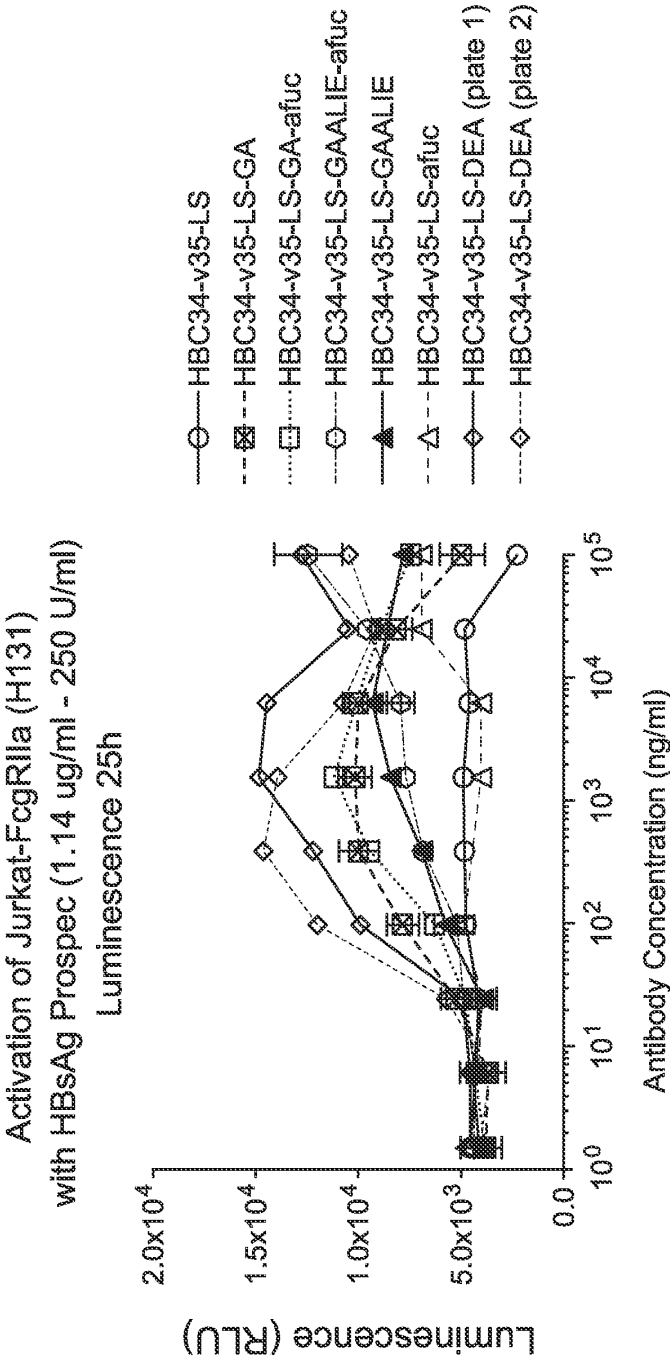


FIG. 17B

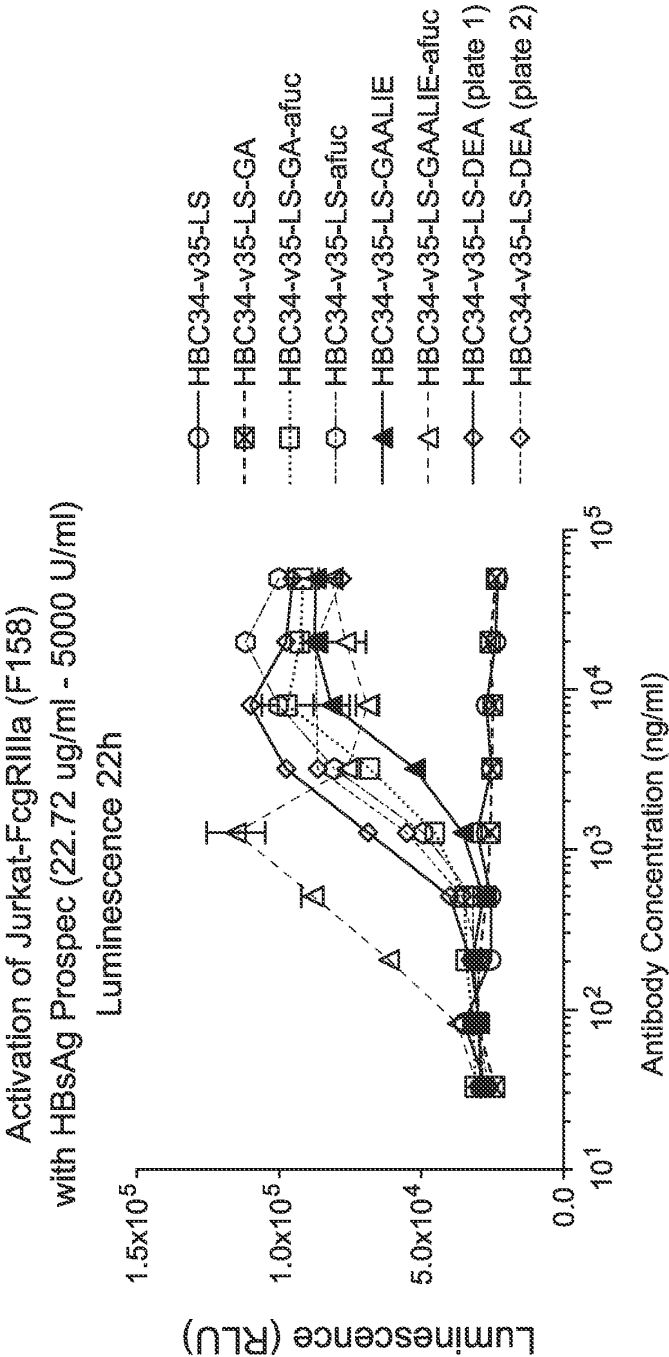


FIG. 17C

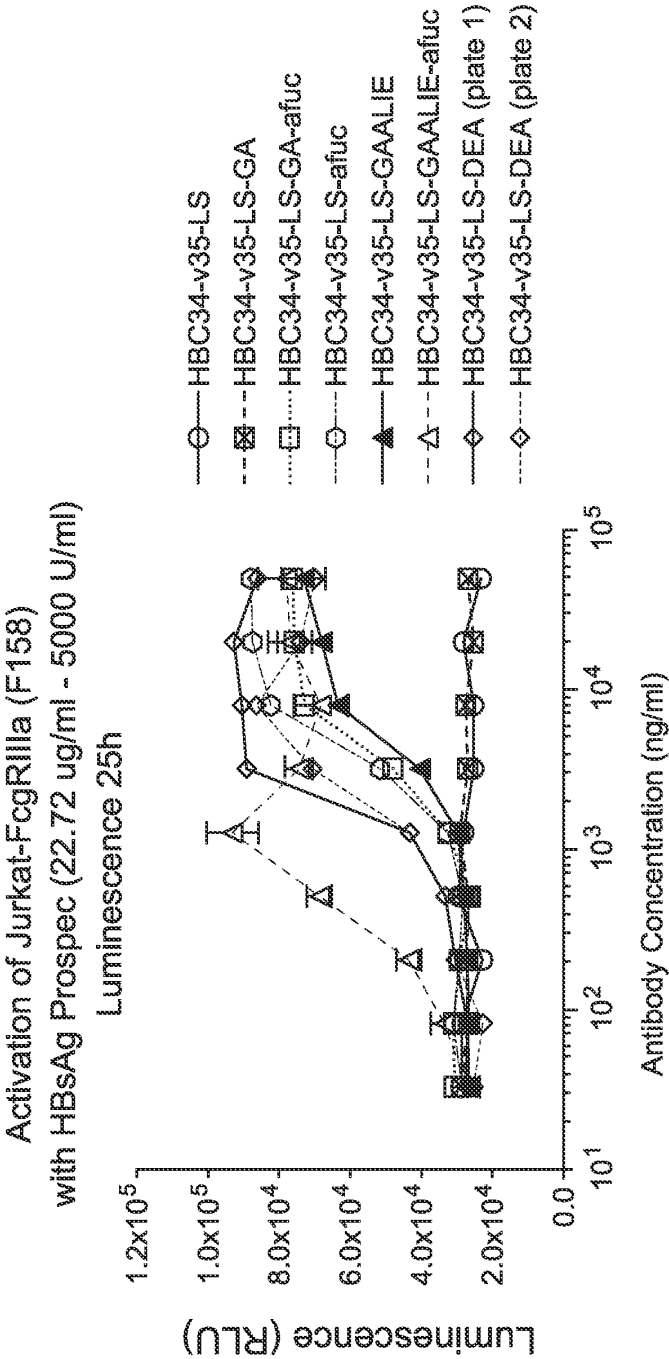


FIG. 17D

Fc-LS	IIA-H	IIA-R	IIB	IIA _H /IIB _{IIA-R/IIB} ratio	IIIA-V	IIIA-F	IIB	C1q	T _m °C	FcRn
GAALIE	3.8	2.5	0.8	4.7	2.1	14.4	1.9	NB	56.5	0.68
GA	10	6.9	1.1	9.9	0.52	0.93	0.84	0.35	68.4	0.95
GRLR	0.28	0.38	0.38	0.72	0.08	0.25	0.70	NB	65.7	0.69
GALVQE	11	14	1.1	10	0.16	0.27	0.88	0.08	61.1	0.81
GAYL	16	3.7	1.0	17	0.48	0.78	0.85	1.09	65.9	0.88
GARPYL	9.9	2.4	0.85	12	1.8	3.4	1.1	1.39	69.3	0.60
GARPIN	22	5.4	0.6	37	1.3	1.5	0.84	0.29	69.8	1.54

FIG. 18

Fc	IIA-H	IIA-R	IIB	IIA _W /IIB ratio	IIA _Q /IIB ratio	IIIA-V	IIIA-F	IIIB	C1q	Tm °C	FcRn
GAALIE	3.6	1.4	0.6	6.0	2.3	2.0	12.2	1.8	NB	58.8	0.9
GAALIE-LS	2.9	1.3	0.4	6.8	3.0	1.6	9.4	1.4	NB	58.0	12.3
GA	5.9	4.8	0.6	9.4	7.7	0.4	0.6	NB	0.59	72.6	1.0
GA	12.1	6.3	1.1	11.5	6.0	0.6	0.8	0.82	0.36	71.1	1.0
GRLR	NB	NB	0.2	NA	NA	NB	NB	0.61	NB	68.6	1.0
GALVQE	7.8	10.8	0.9	9.0	12.5	0.4	0.5	0.70	0.07	61.0	1.1
GAYL	18.2	4.6	1.1	17.3	4.4	0.9	1.0	0.97	0.98	69.6	1.0
GARPYL	14.2	2.7	0.9	15.1	2.9	2.7	3.7	1.03	1.01	>70	0.8
GARPIN	7.8	1.3	0.5	14.3	2.4	1.0	1.1	0.96	0.24	72.9	0.9

FIG. 19

Fc	IIA-H	IIA-R	IIB	IIA _r /IIB ratio	IIA _r /IIB ratio	IIIA_V	IIIA_F	III_B	C1q	Tm °C
GAALIE-afuc	3.1	1.6	0.6	5.1	2.6	28.0	242	14.8	NB	59.4
GAALIE-LS-afuc	2.3	1.1	0.4	6.5	3.3	30.2	256	12.3	NB	58.5
GA-afuc	5.4	6.1	0.6	8.4	9.5	6.7	17.2	2.1	0.16	73.0
GA-afuc	9.5	9.9	1.1	8.4	8.7	13.6	35.6	1.8	NA	71.6
GRLR-afuc	NB	NB	0.2	NA	NA	NB	NB	NB	NA	68.9
GALVQE-afuc	6.7	9.6	1.0	6.8	9.8	7.4	11.8	2.4	NA	61.6
GAYL-afuc	14.9	4.0	0.9	16.0	4.2	13.7	30.1	2.6	NA	69.6
GARPYL-afuc	11.2	2.2	1.0	11.0	2.2	9.1	19.7	1.8	NA	>70
GARPIN-afuc	5.5	1.4	0.6	9.2	2.3	7.1	14.8	1.2	NA	74.2

FIG. 20

Targets: A549 expressing Flua H1N1 HA
Jurkat reporter cells FcγR1a (H131) activation

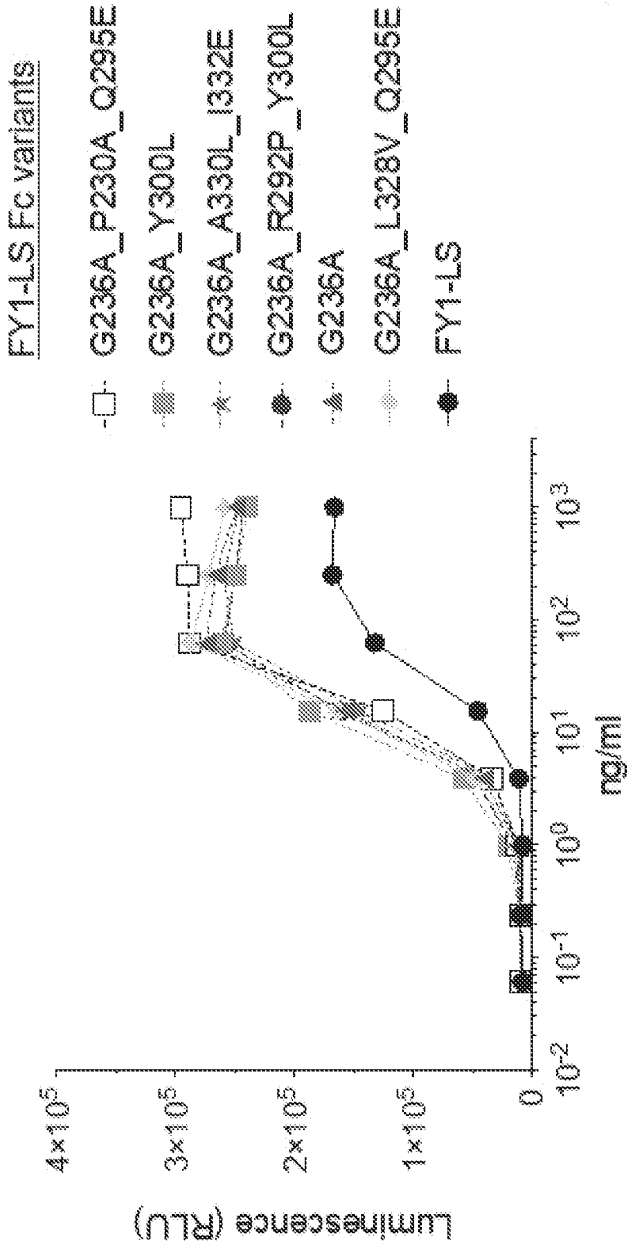


FIG. 21

Targets: A549 expressing FluA H1N1 HA
Jurkat reporter cells FcγRIIIa (F158, low affinity) activation

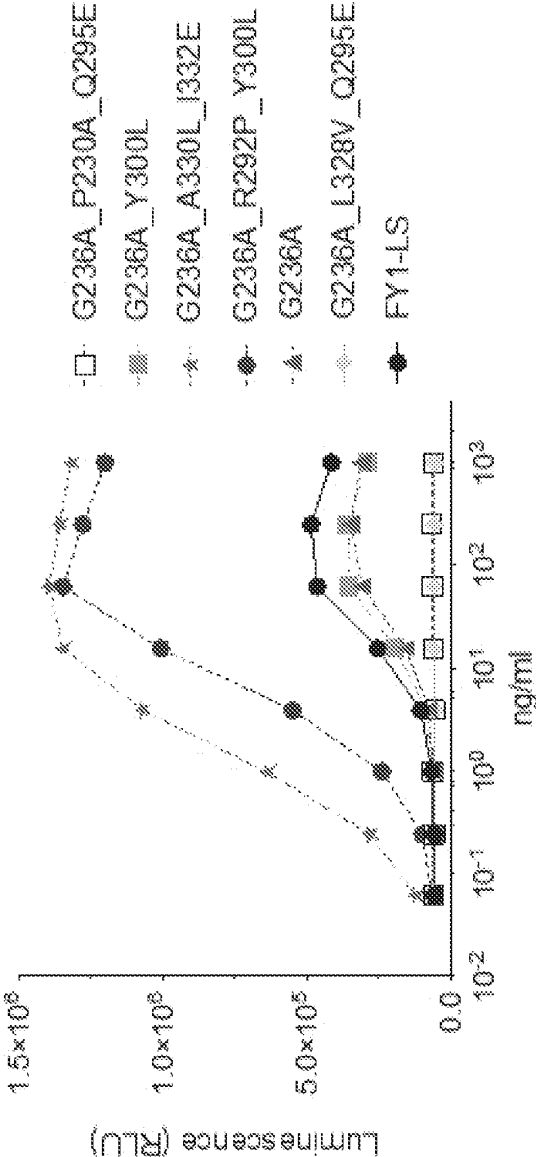


FIG. 22A

Targets: A549 expressing FluA H1N1 HA
Jurkat reporter cells FcγRIIIa (V158, higher affinity)
activation

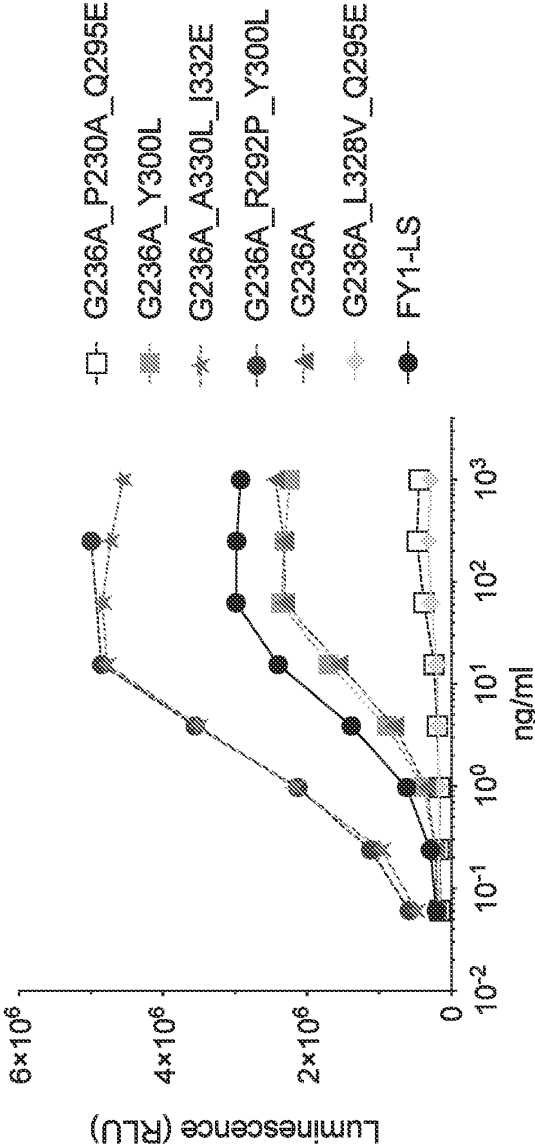


FIG. 22B

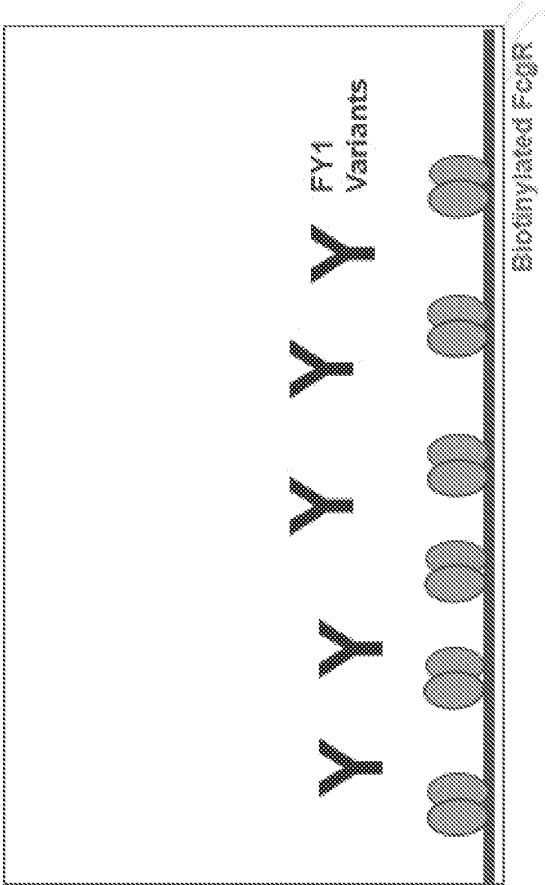


FIG. 23

FY1 Variant	FcgRI FC	FcgRIIa (H) FC	FcgRIIa (R) FC	FcgRIIb FC	FcgRIIa (V) FC	FcgRIIa (F) FC
FY1-rIgG1m3-LS	1.00	1.00	1.00	1.00	1.00	1.00
FY1-rIgG1m3-LS-G236A-K334A-Q295E	0.55	4.00	2.44	0.97	0.24	-
FY1-rIgG1m3-LS-G236S-G420V-G446E-L309T	0.10	3.85	1.79	0.85	0.12	-
FY1-rIgG1m3-LS-G236A	0.25	5.56	3.45	1.61	0.59	1.09
FY1-rIgG1m3-LS-Q295E	0.87	1.04	0.85	-	0.49	1.35
FY1-rIgG1m3-LS-R292P	0.67	0.40	-	-	0.98	0.91
FY1-rIgG1m3-LS-G236A-R292P-I377N	0.25	3.33	1.16	-	0.81	-
FY1-rIgG1m3-LS-L328V	0.92	0.72	1.35	-	0.78	1.33
FY1-rIgG1m3-LS-K334A	1.79	0.56	0.55	1.45	2.17	2.22
FY1-rIgG1m3-LS-G236A-A330L-I332E	1.54	2.70	1.69	-	2.50	6.25
FY1-rIgG1m3-LS-A330L-I332E	3.13	0.43	0.14	0.30	5.00	7.14
FY1-rIgG1m3-LS-P230A	0.89	-	0.94	-	-	1.28
FY1-rIgG1m3-LS-S239D-H268E-G236A	1.61	10.00	20.00	10.71	4.76	5.88
FY1-rIgG1m3-LS-G236A-Y300L	0.32	7.14	3.13	0.33	0.53	0.74
FY1-rIgG1m3-LS-G236A-R292P-Y300L	0.34	6.67	2.63	0.85	1.69	2.17
FY1-rIgG1m3-LS-G446E	0.88	0.89	0.92	0.97	1.16	1.04
FY1-rIgG1m3-LS-G236A-P230A-Q295E	0.30	5.26	2.70	0.54	-	-
FY1-rIgG1m3-LS-Y300L	1.12	1.47	0.68	0.64	1.33	1.47
FY1-rIgG1m3-LS-L309T-P238D-P396L-T366A	0.06	-	-	5.85	-	-
FY1-rIgG1m3-LS-I377N	1.04	1.30	1.25	2.15	1.64	1.79
FY1-rIgG1m3-LS-G236R-L328R	-	-	-	-	-	-
FY1-rIgG1m3-LS-G236A-L328V-Q295E	0.23	4.76	4.00	0.62	-	-

FIG. 24

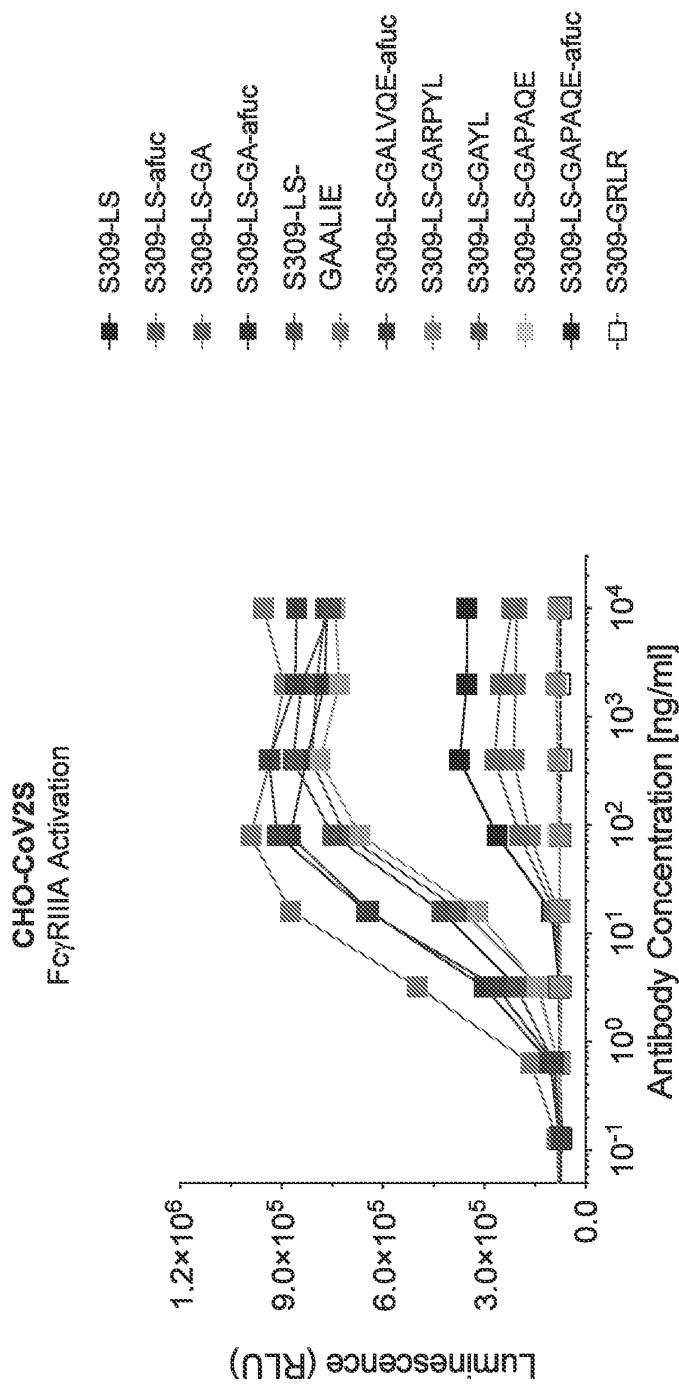


FIG. 25A

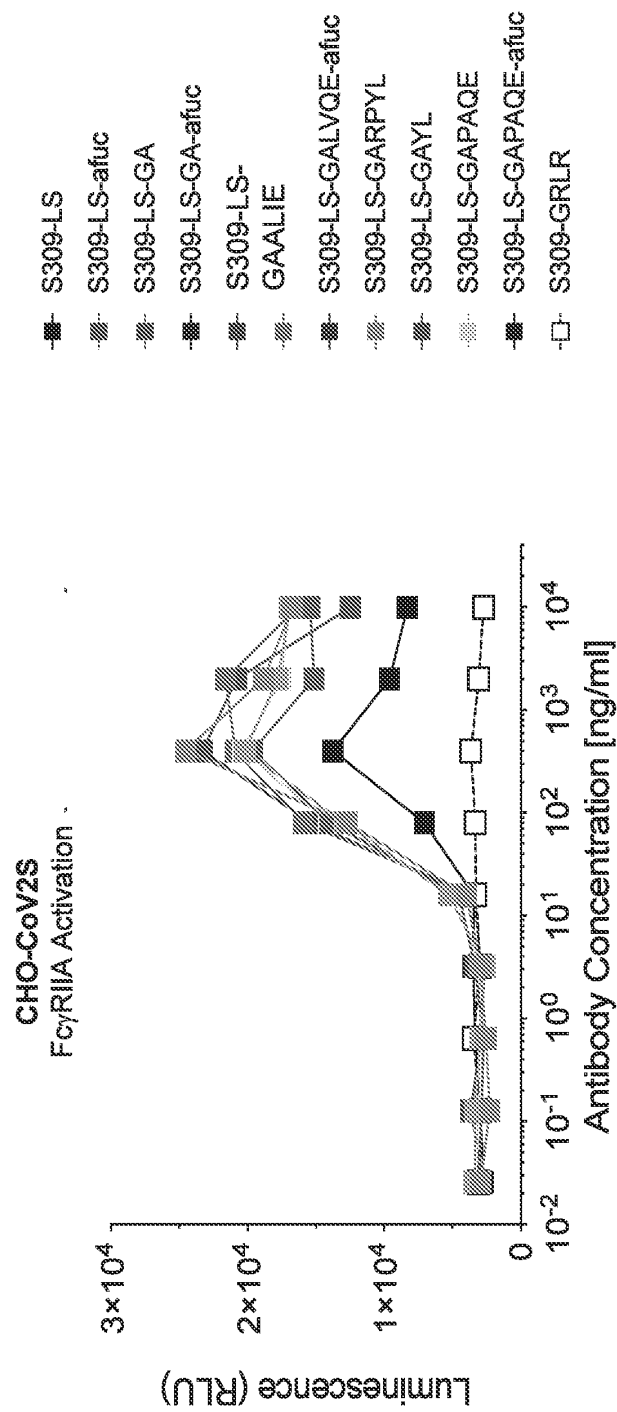


FIG. 25B

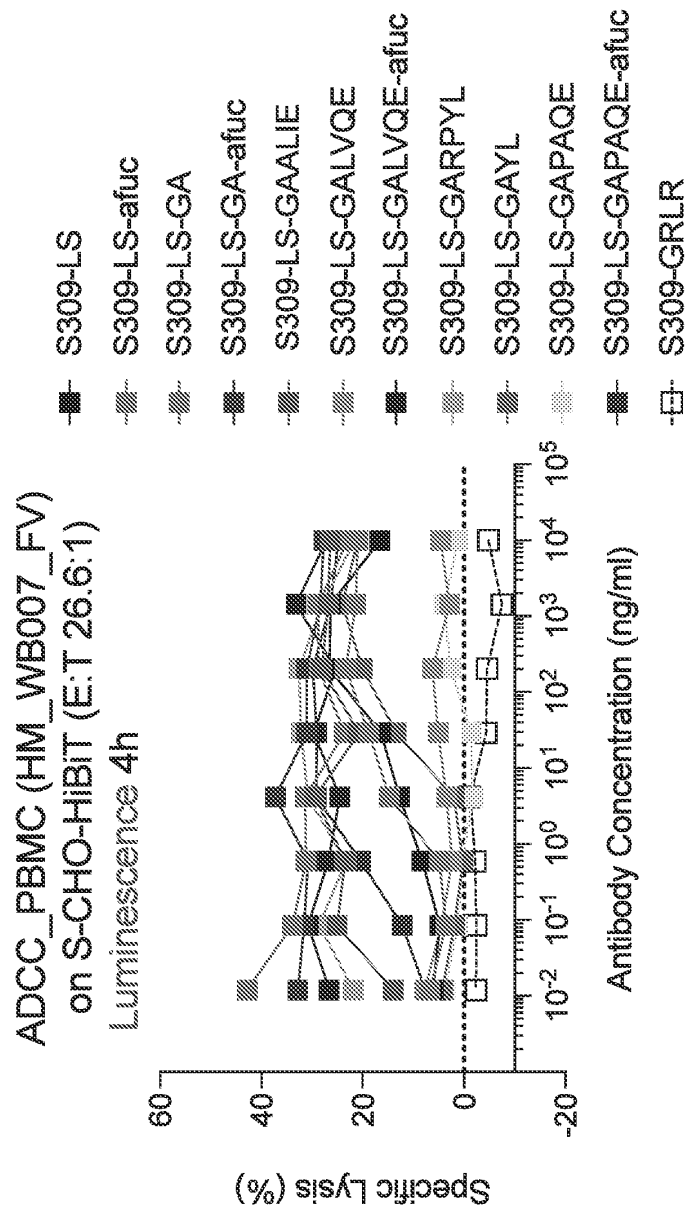


FIG. 25C

Targets: CHO expressing SARS-CoV-2-Spike
Jurkat reporter cells FcγRIIIa (H131) activation
(fucosylated)

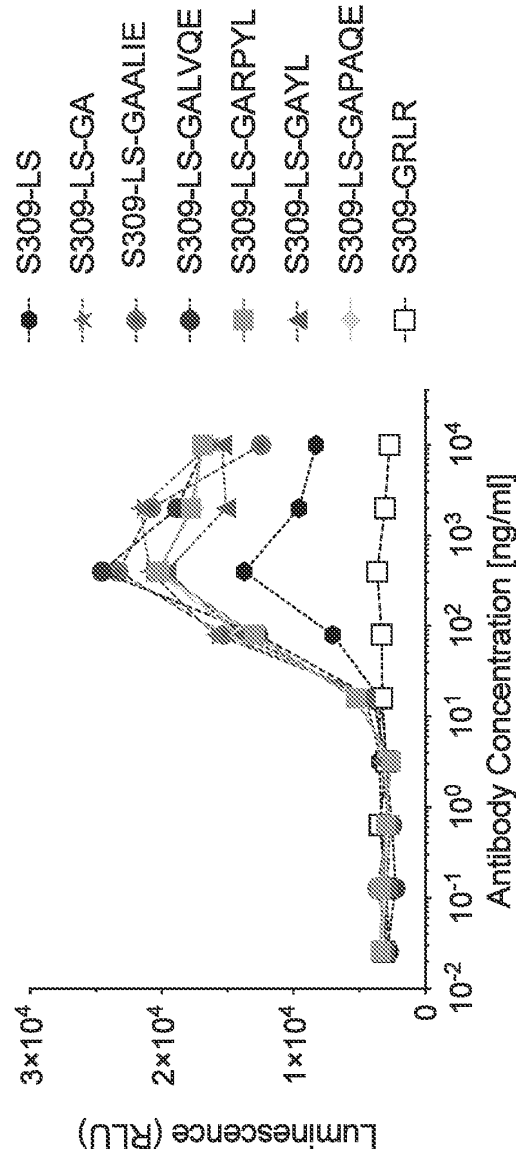


FIG. 26A

Targets: CHO expressing SARS-CoV-2-Spike
Jurkat reporter cells FcγRIIIa (H131) activation
(afucosylated Fc variants)

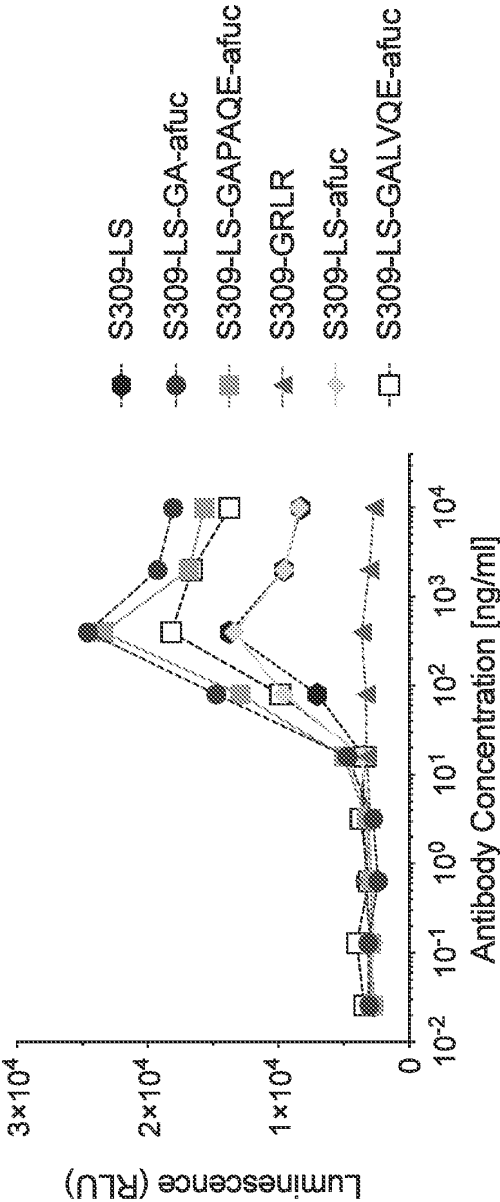


FIG. 26B

Targets: CHO expressing SARS-CoV-2-Spike
Jurkat reporter cells FcγRIIIa (V158) activation
(fucosylated)

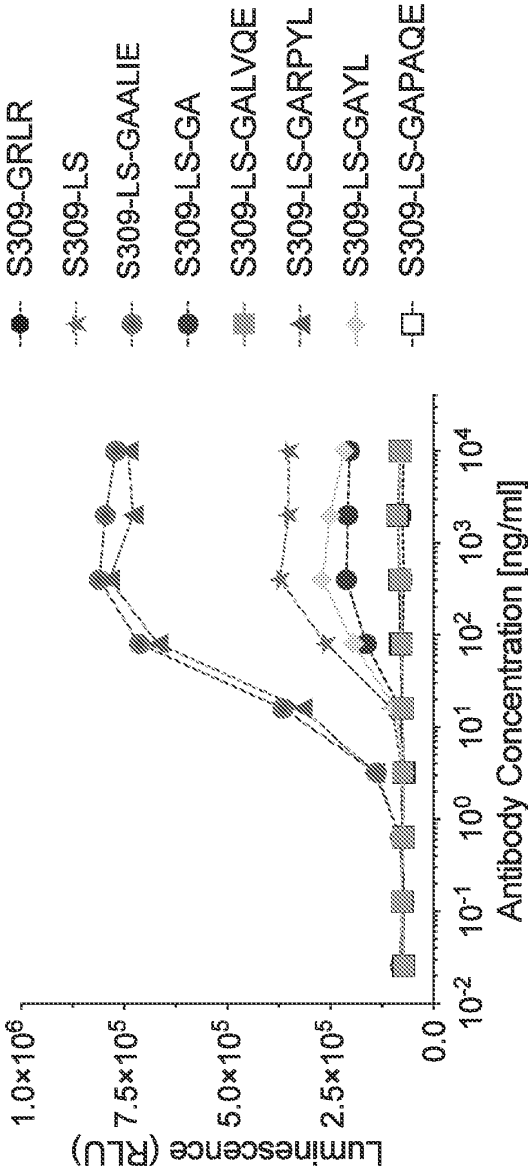


FIG. 26C

Targets: CHO expressing SARS-CoV-2-Spike
Jurkat reporter cells FcγRIIIa (V158) activation
(afucosylated Fc variants)

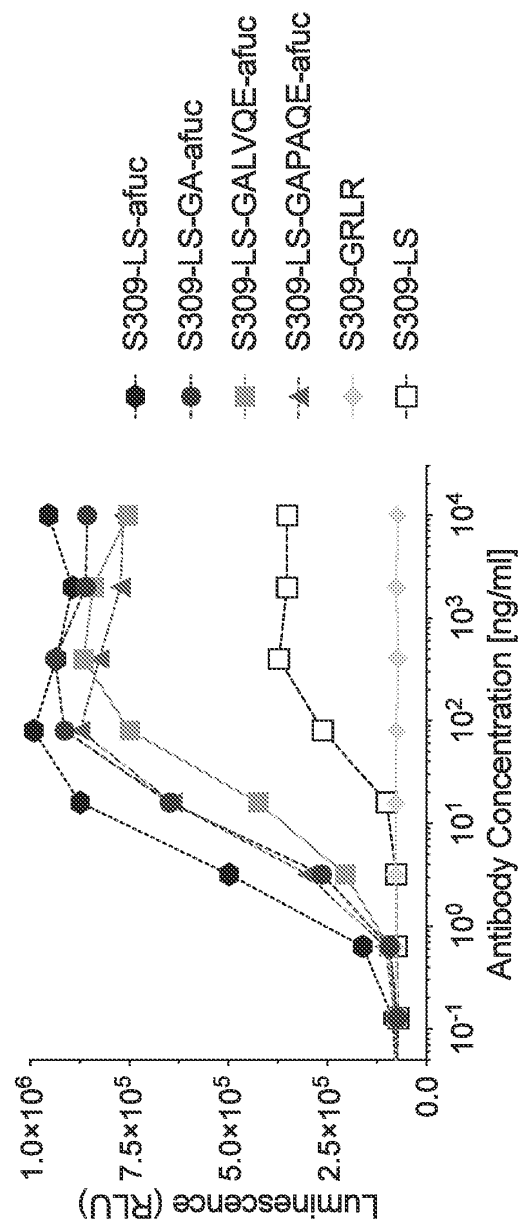


FIG. 26D

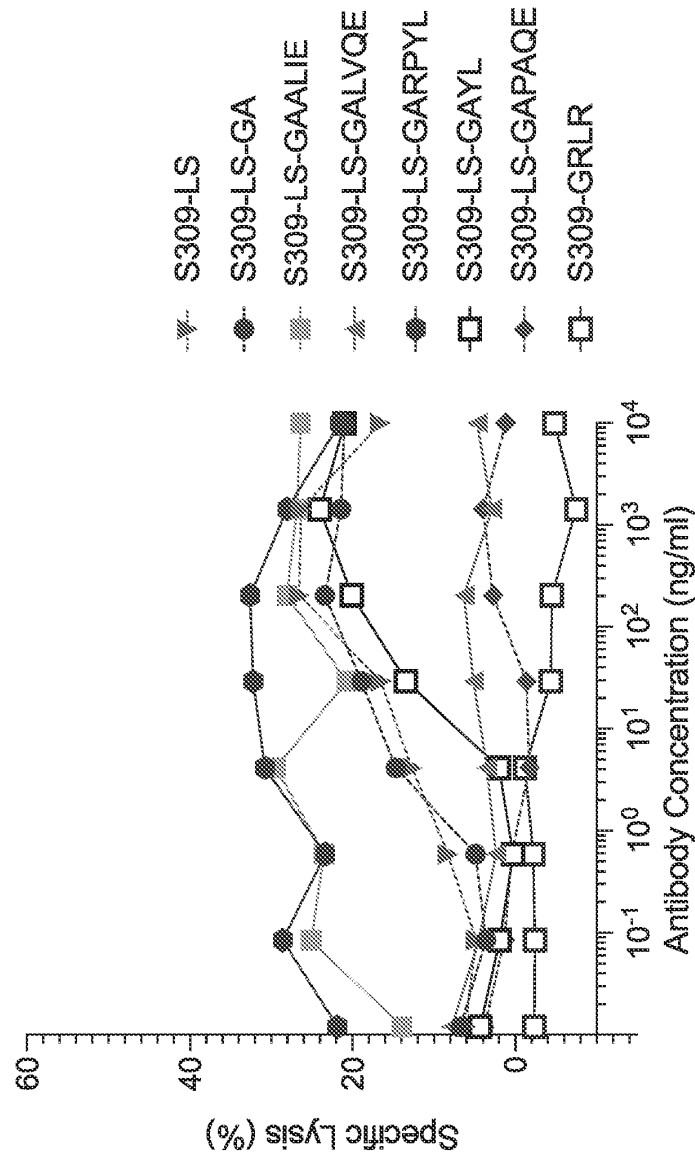


FIG. 26E

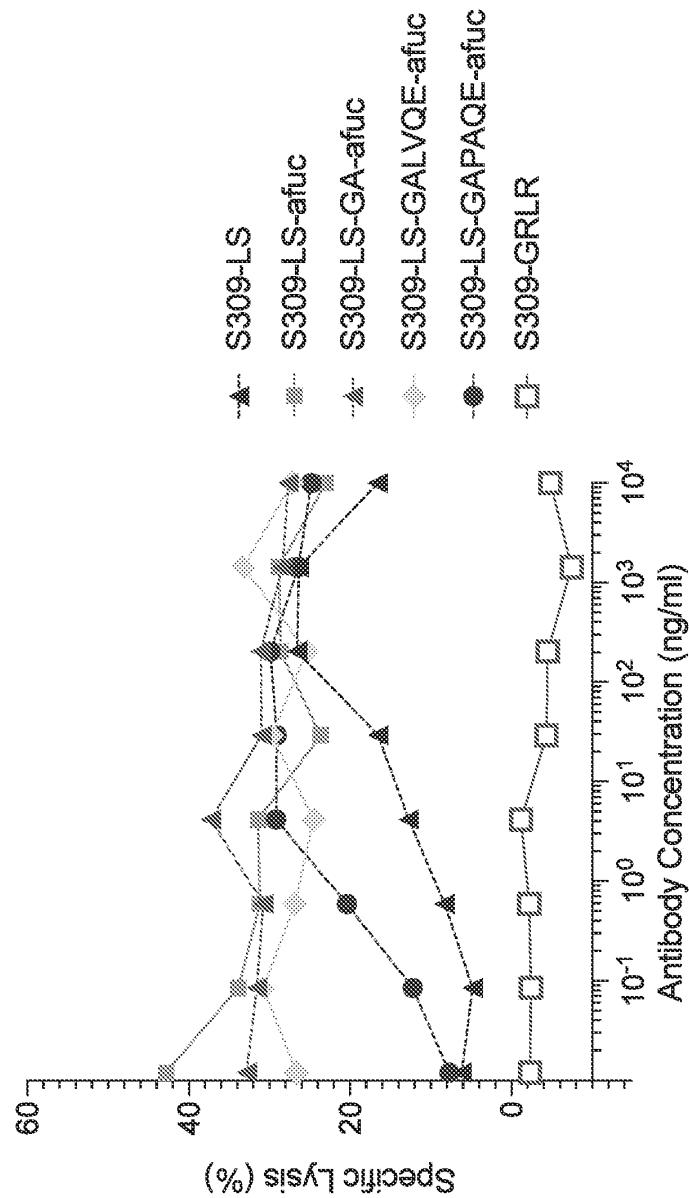


FIG. 26F

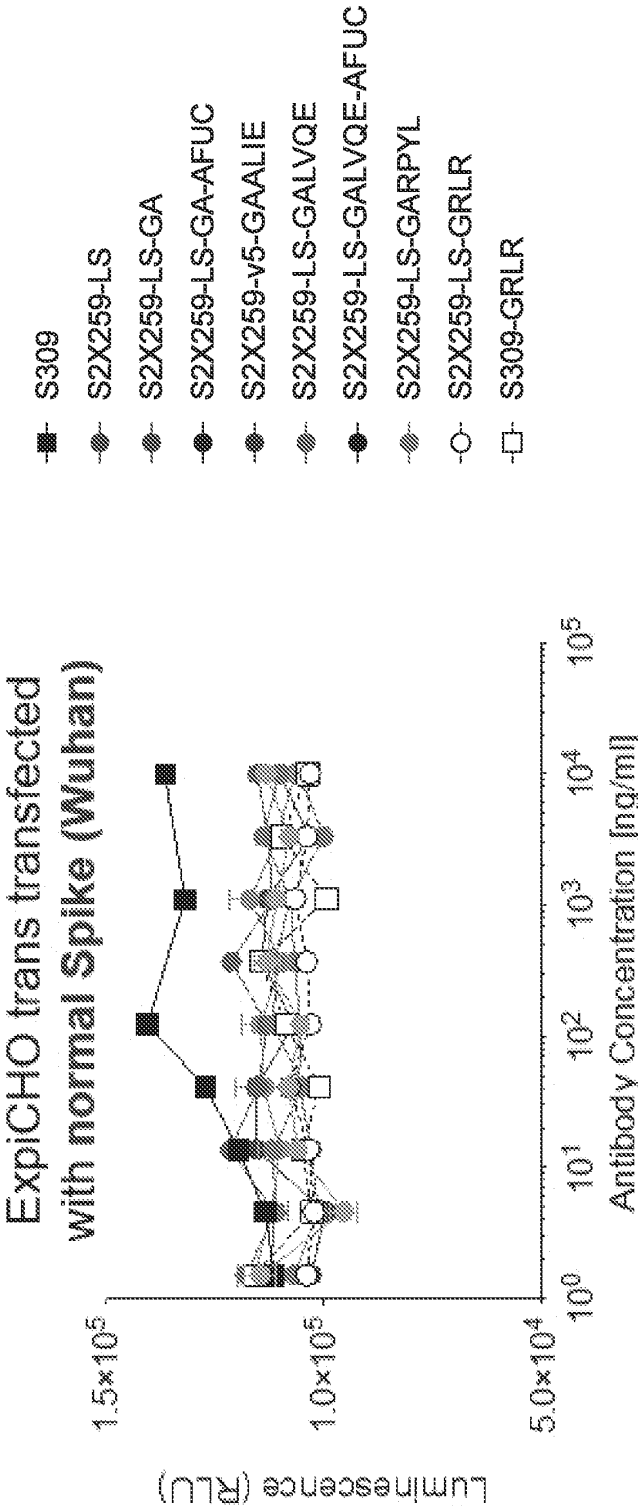


FIG. 27A

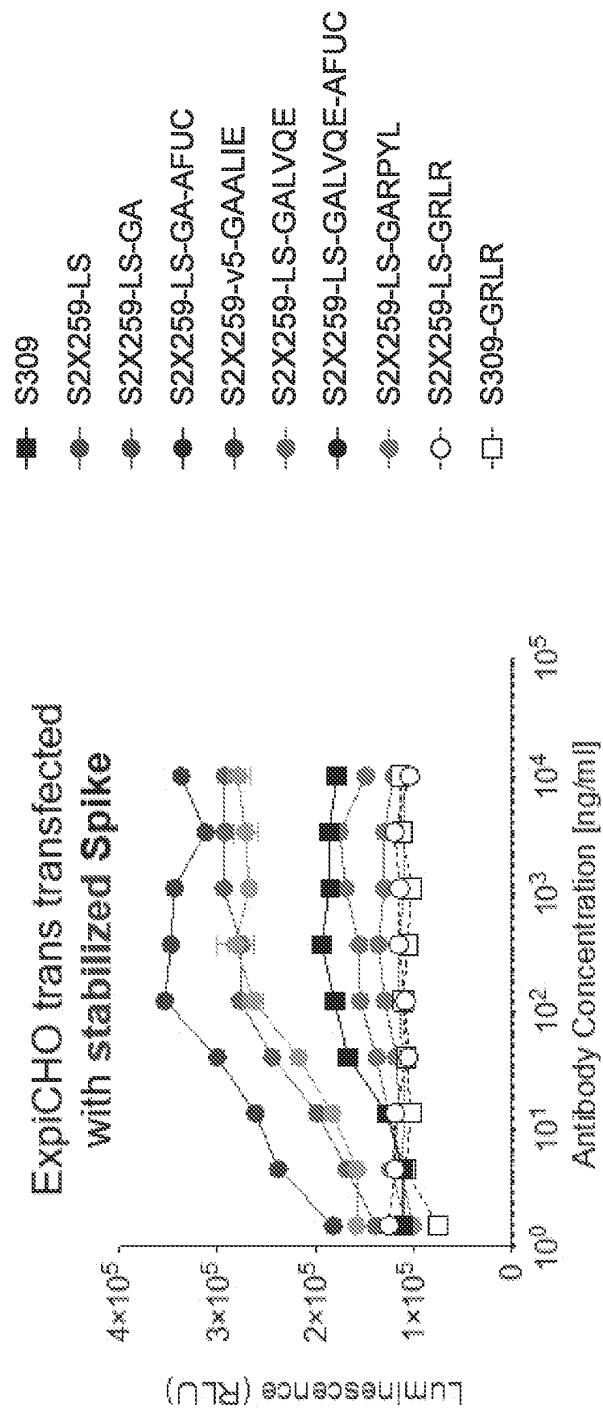


FIG. 27B

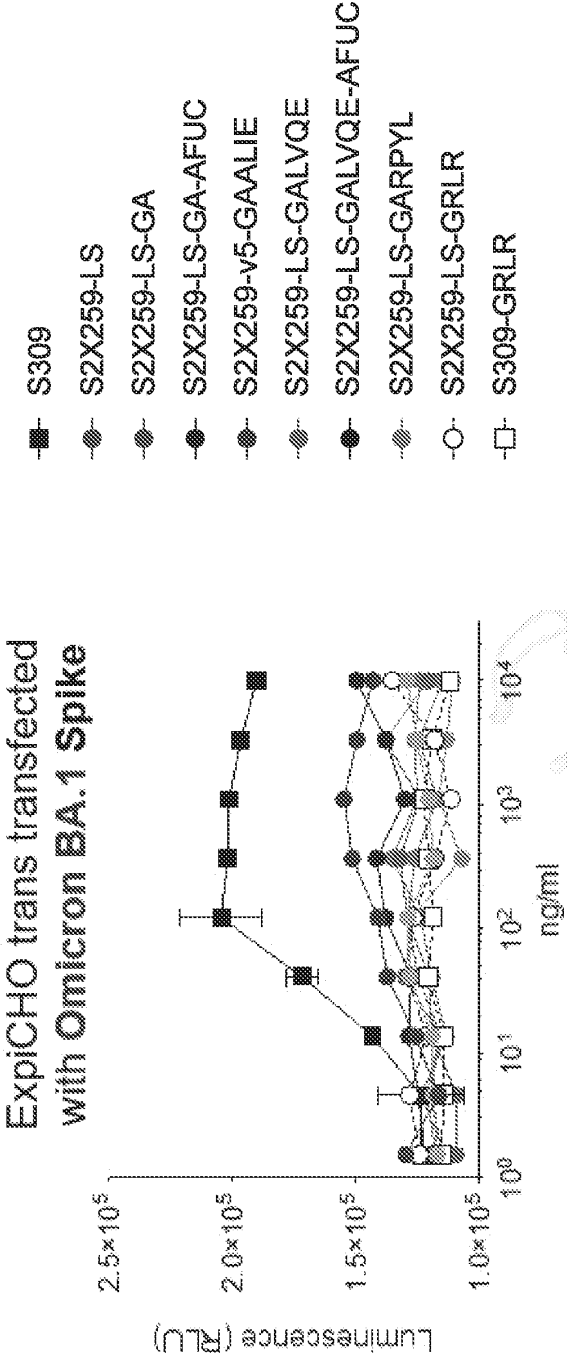


FIG. 27C

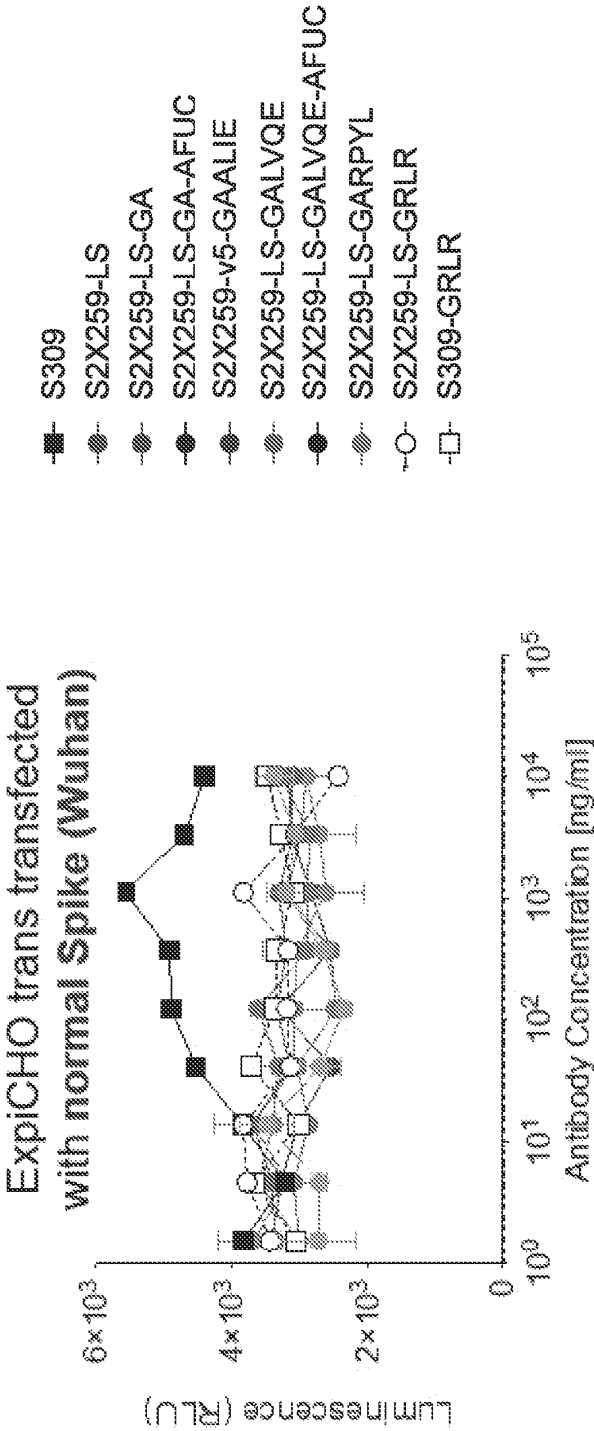


FIG. 27D

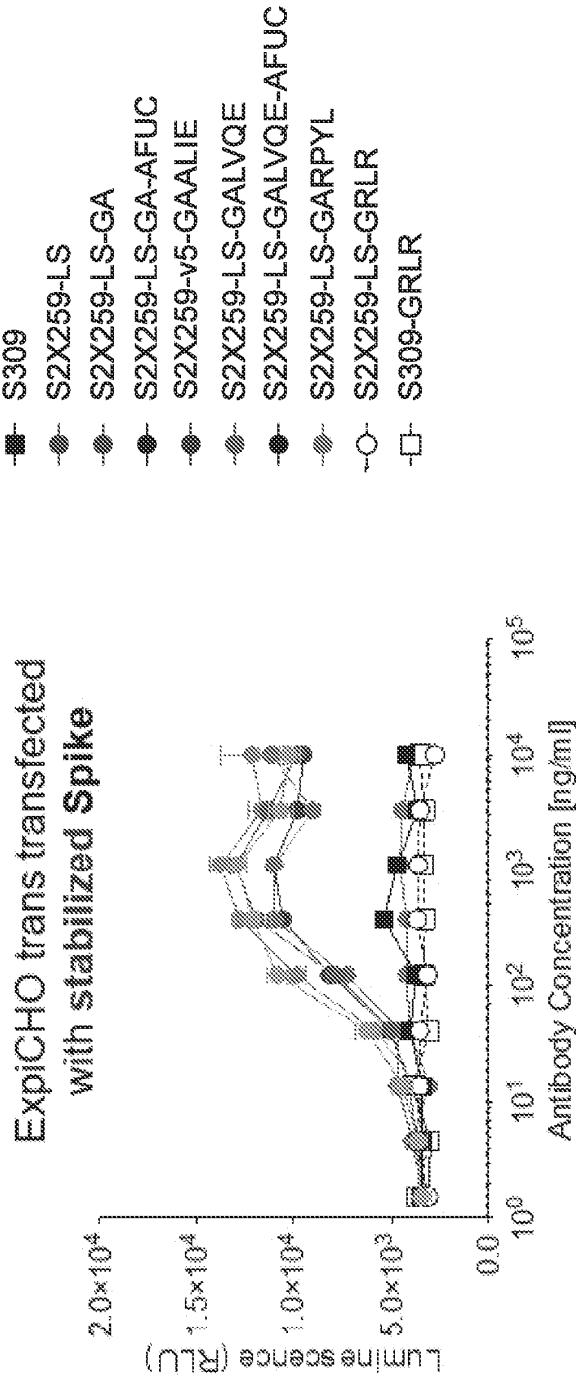


FIG. 27E

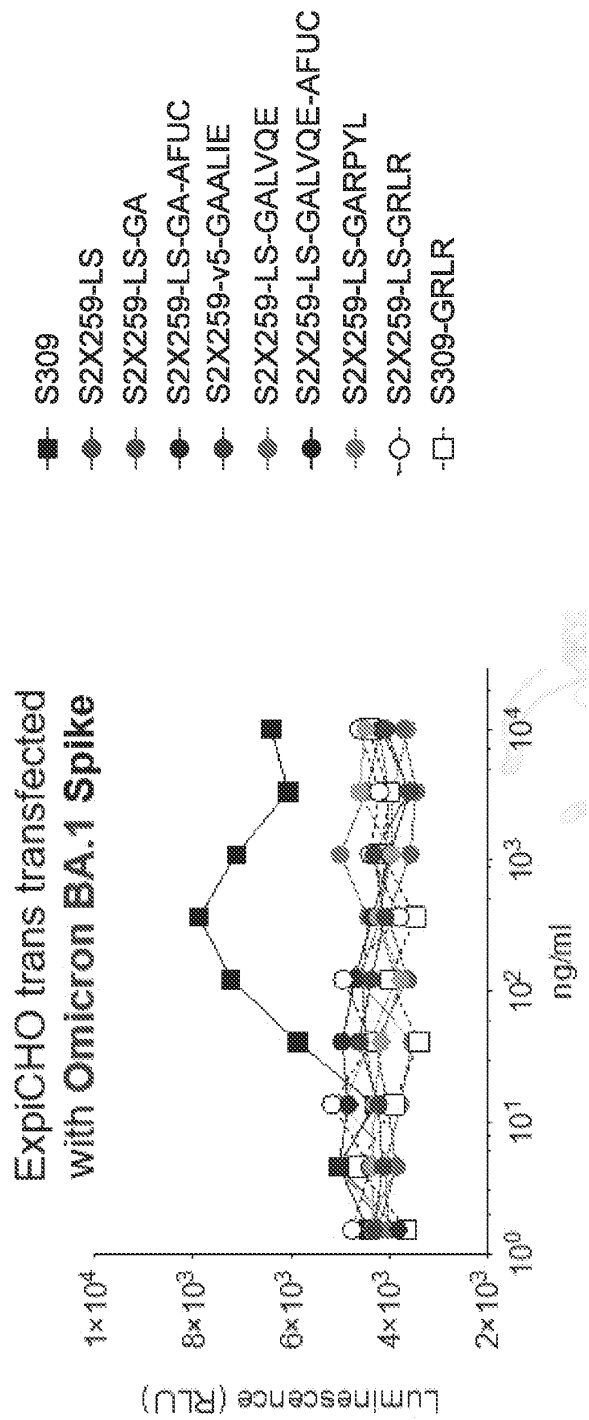


FIG. 27F

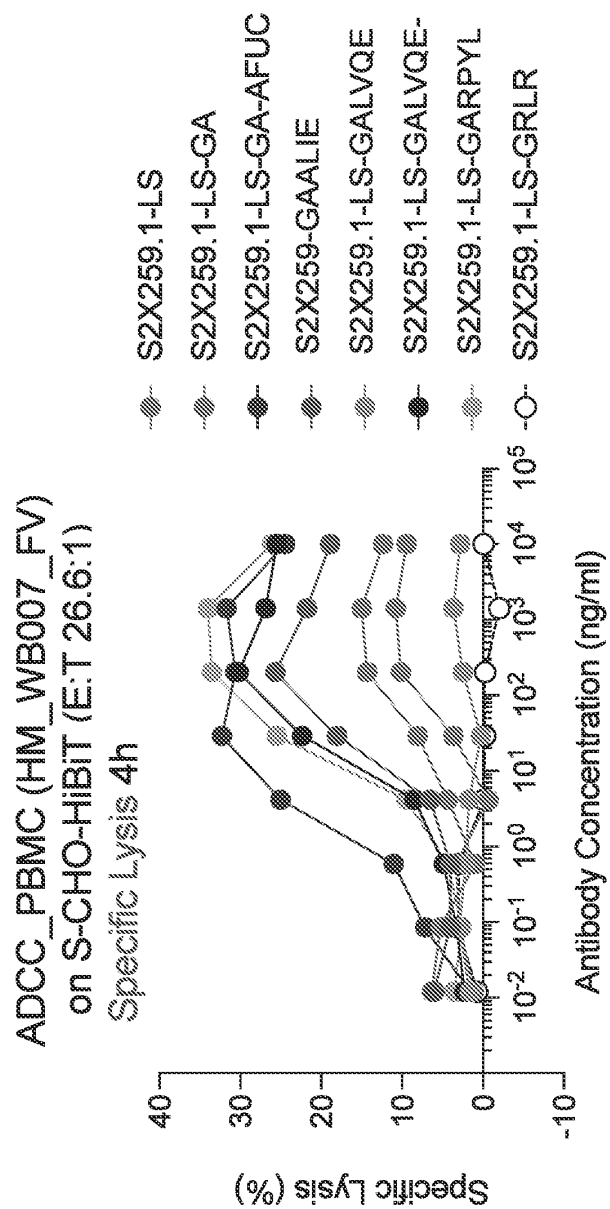


FIG. 27G

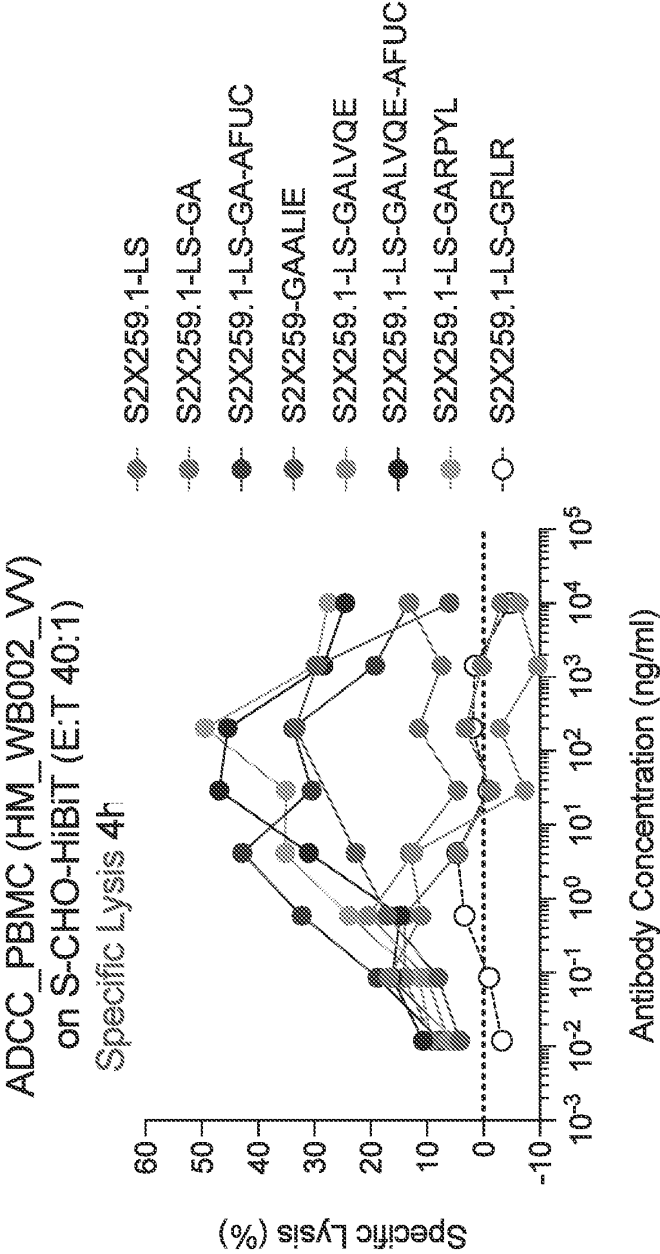
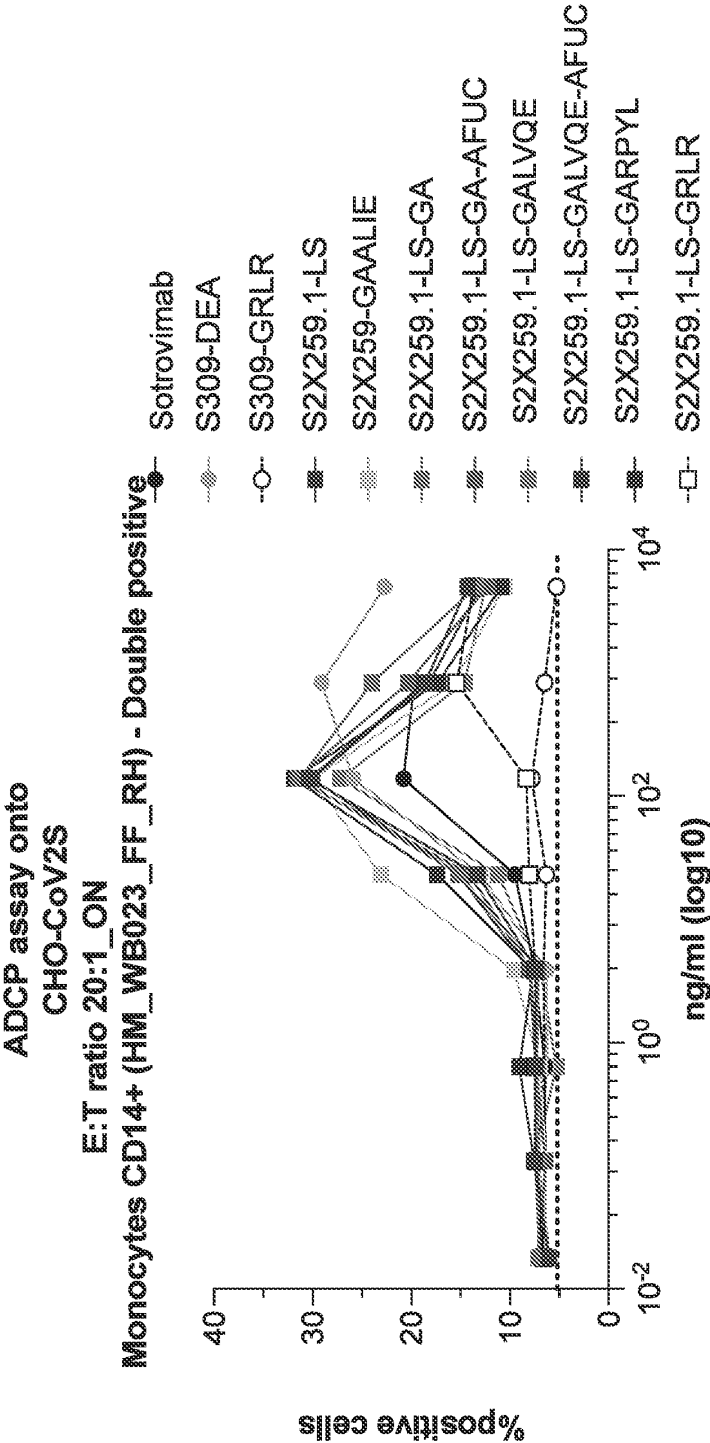
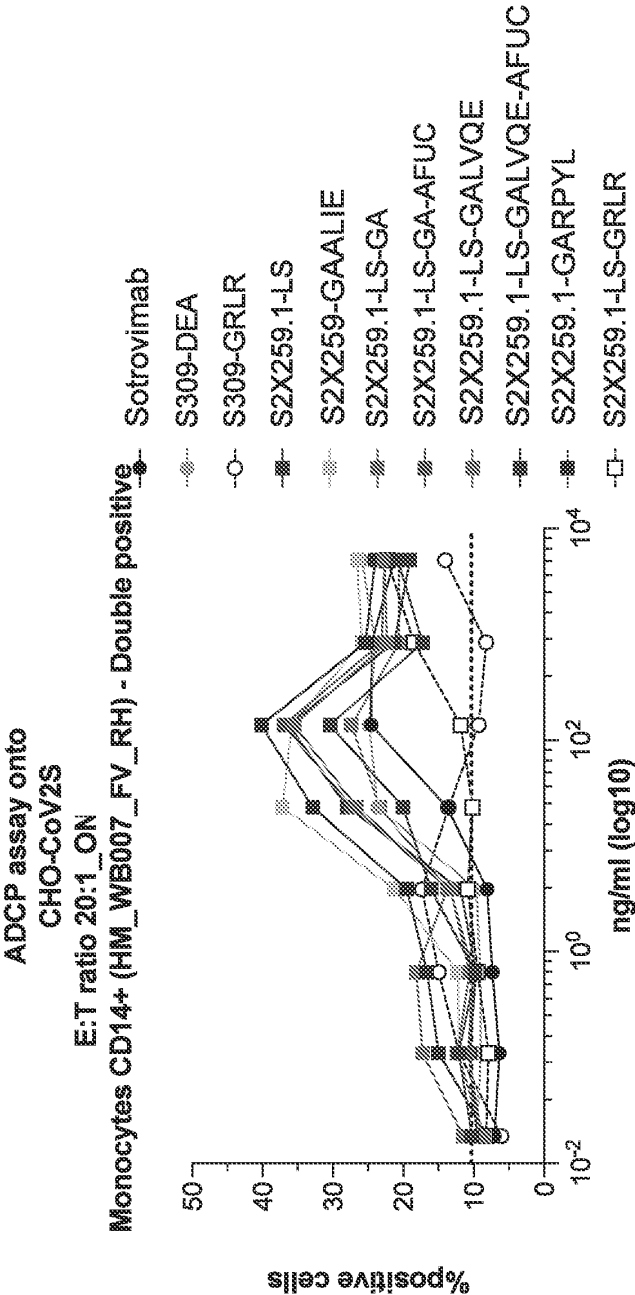


FIG. 27H



dashed line indicates value for target+effector without antibody

FIG. 27I



dashed line indicates value for target+effector without antibody

FIG. 27J

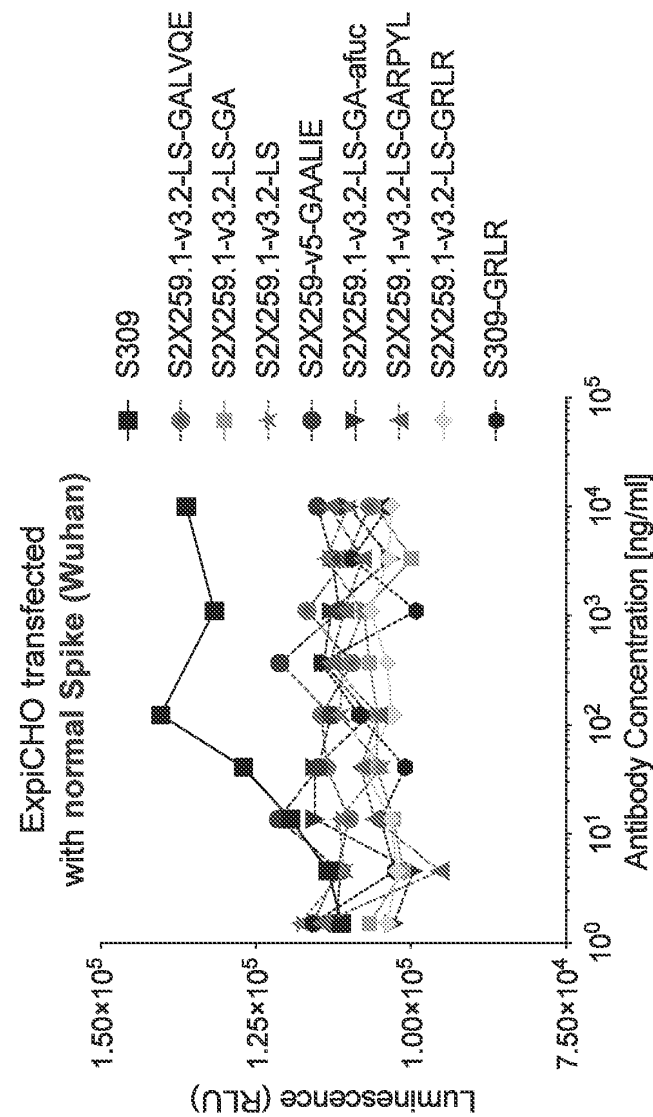


FIG. 28A

ExpCHO transfected
with stabilized Spike

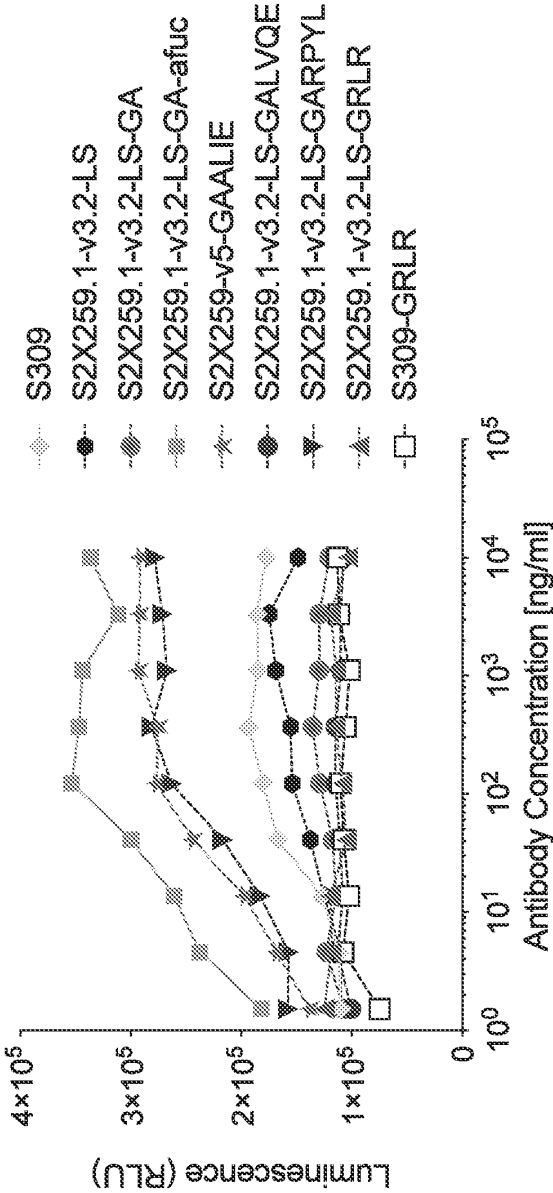


FIG. 28B

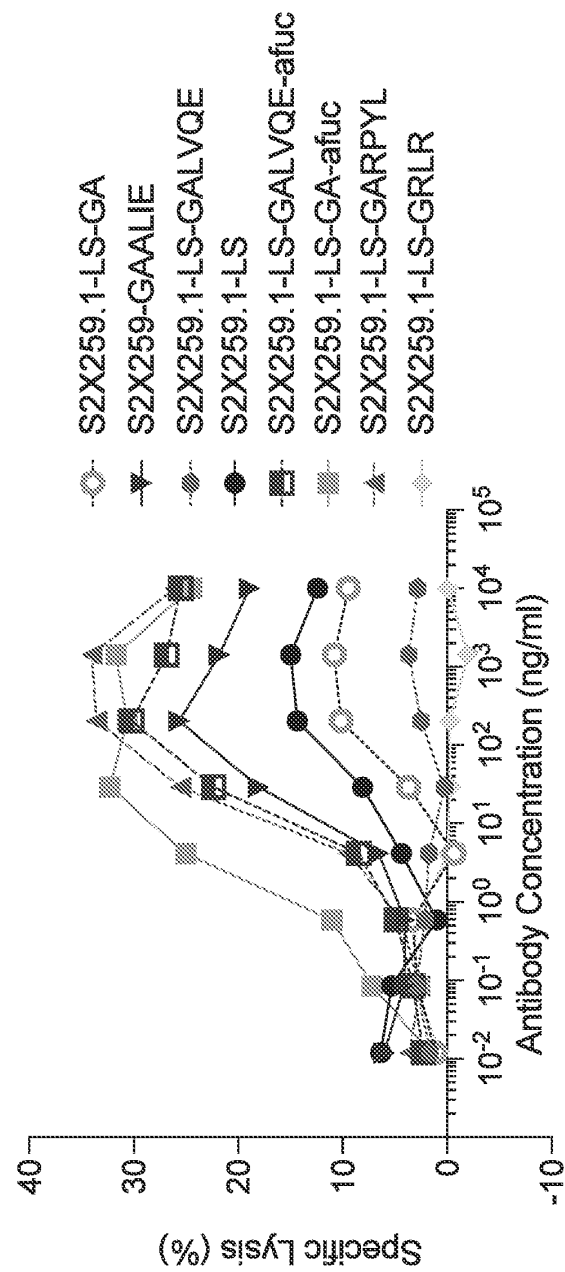


FIG. 28C

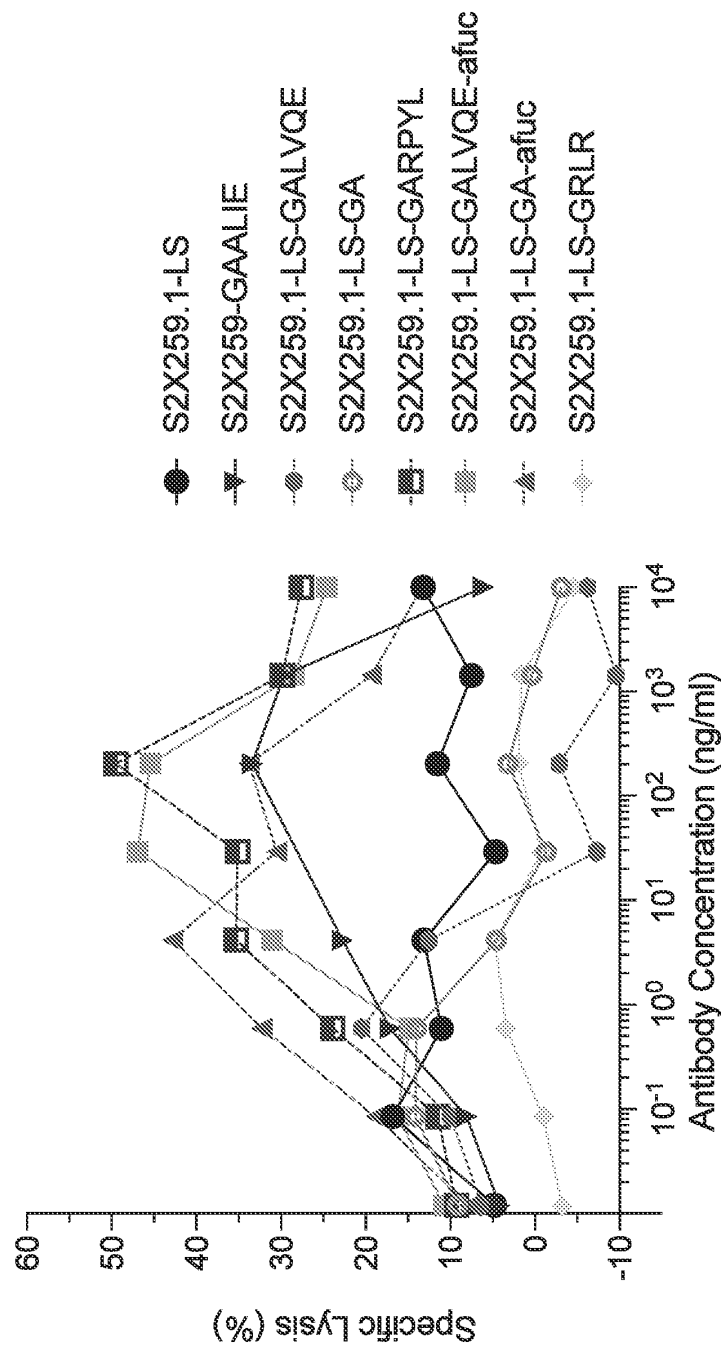


FIG. 28D

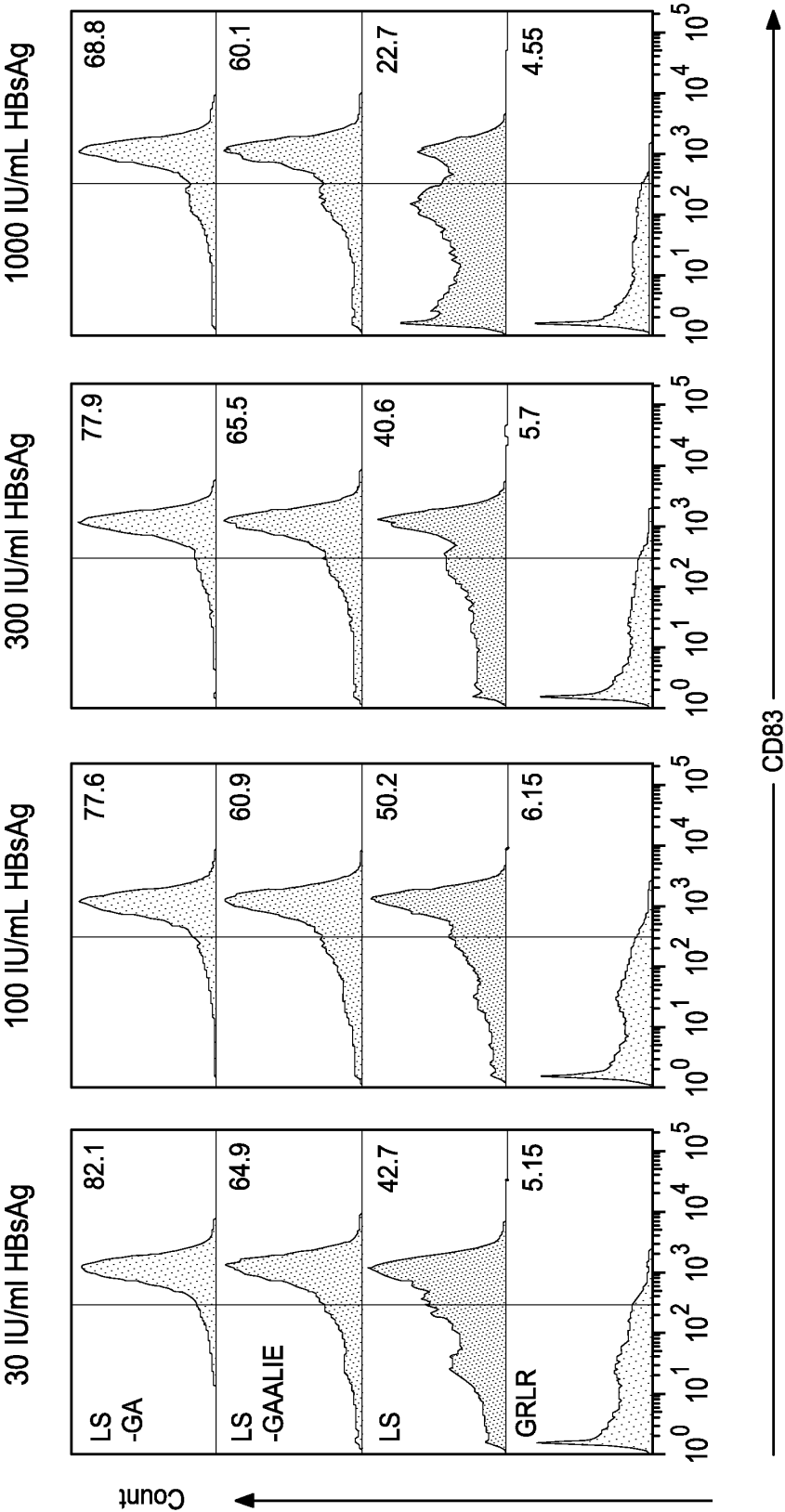


FIG. 29A

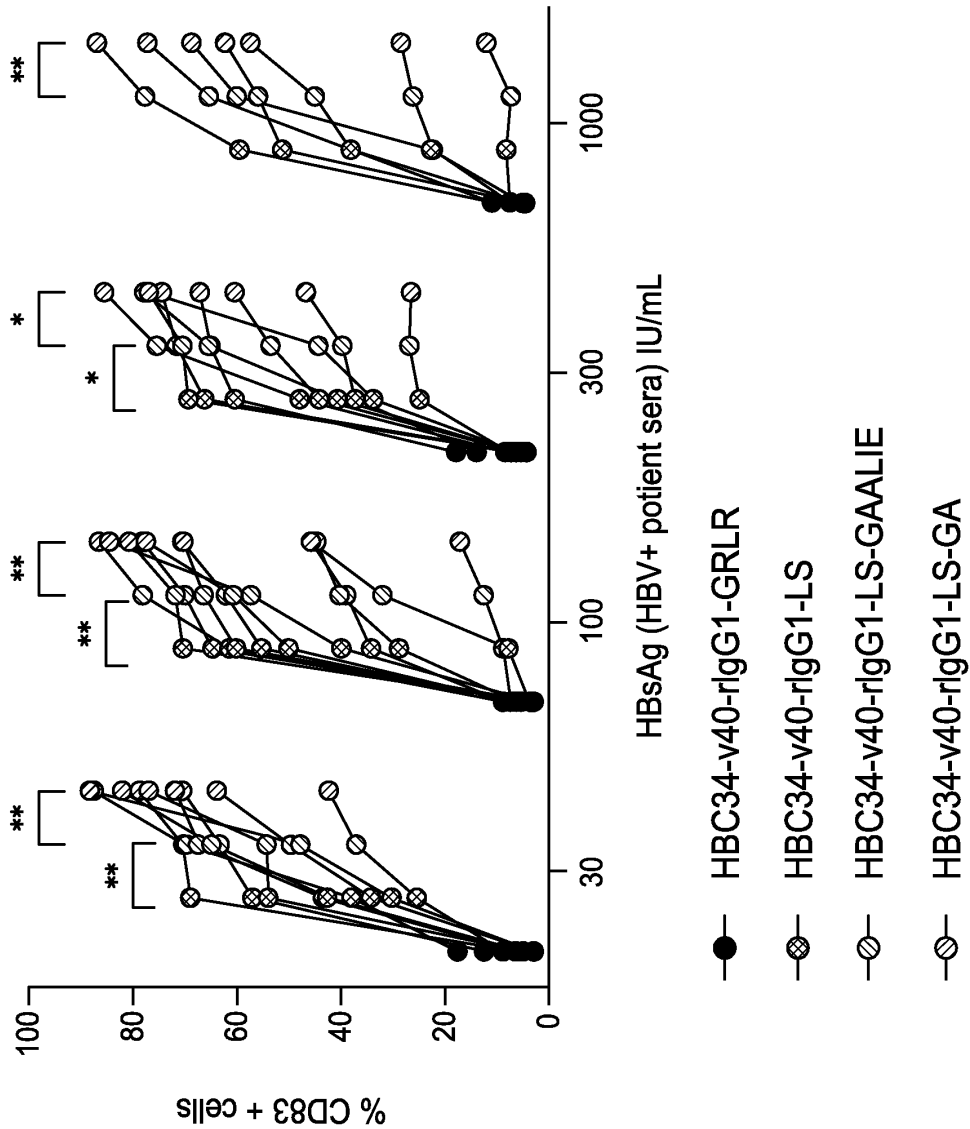
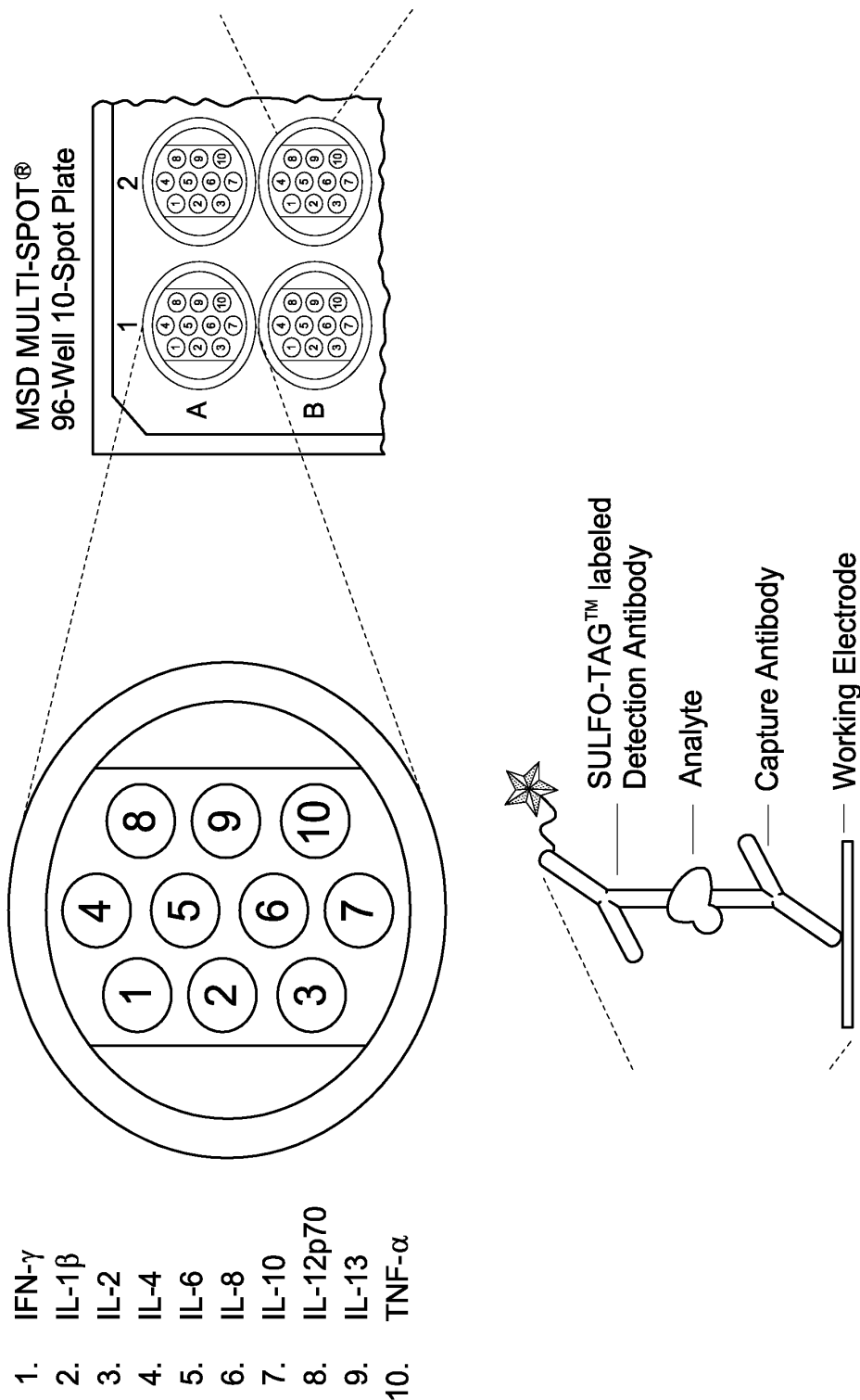


FIG. 29B



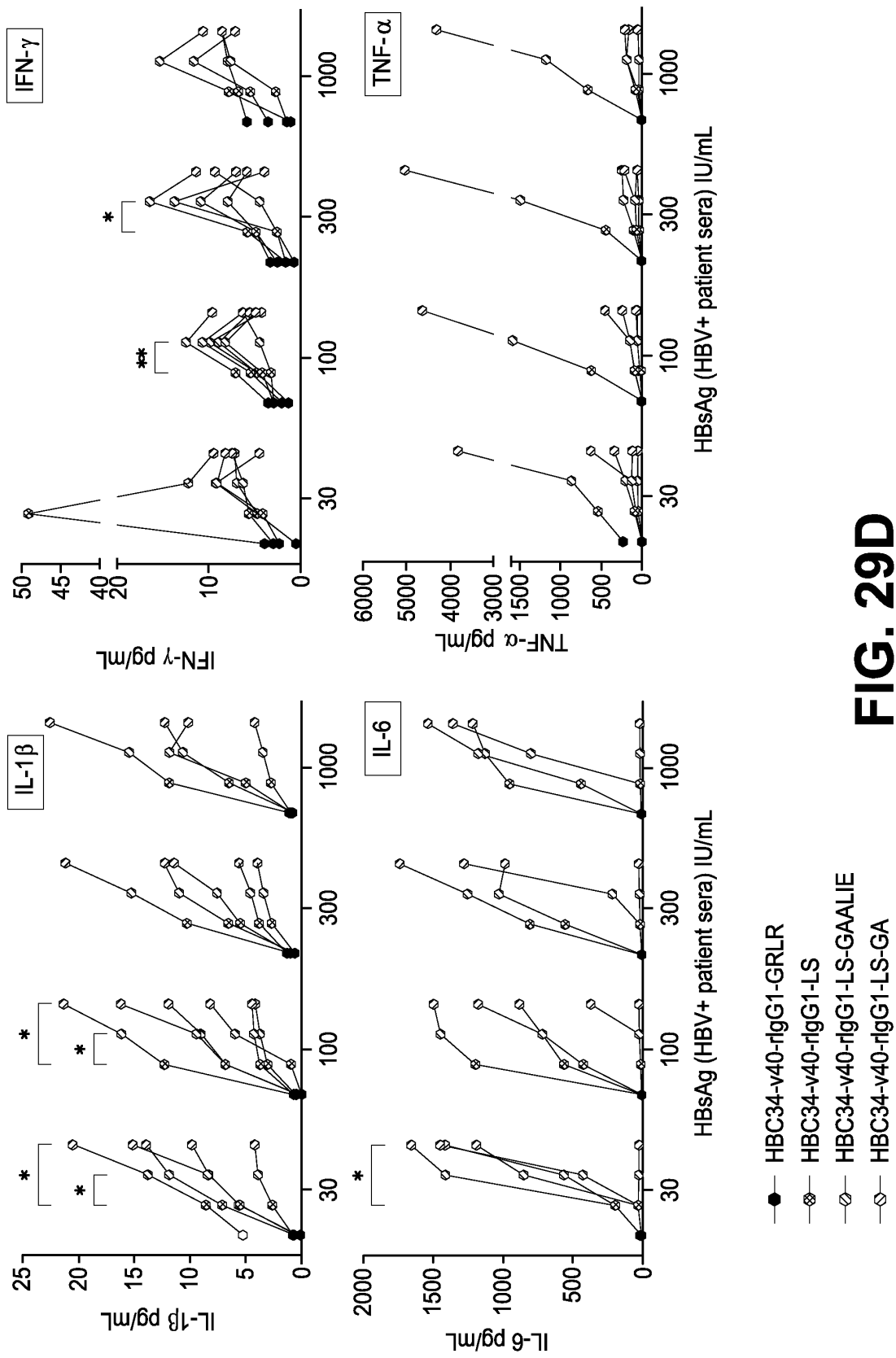


FIG. 29D

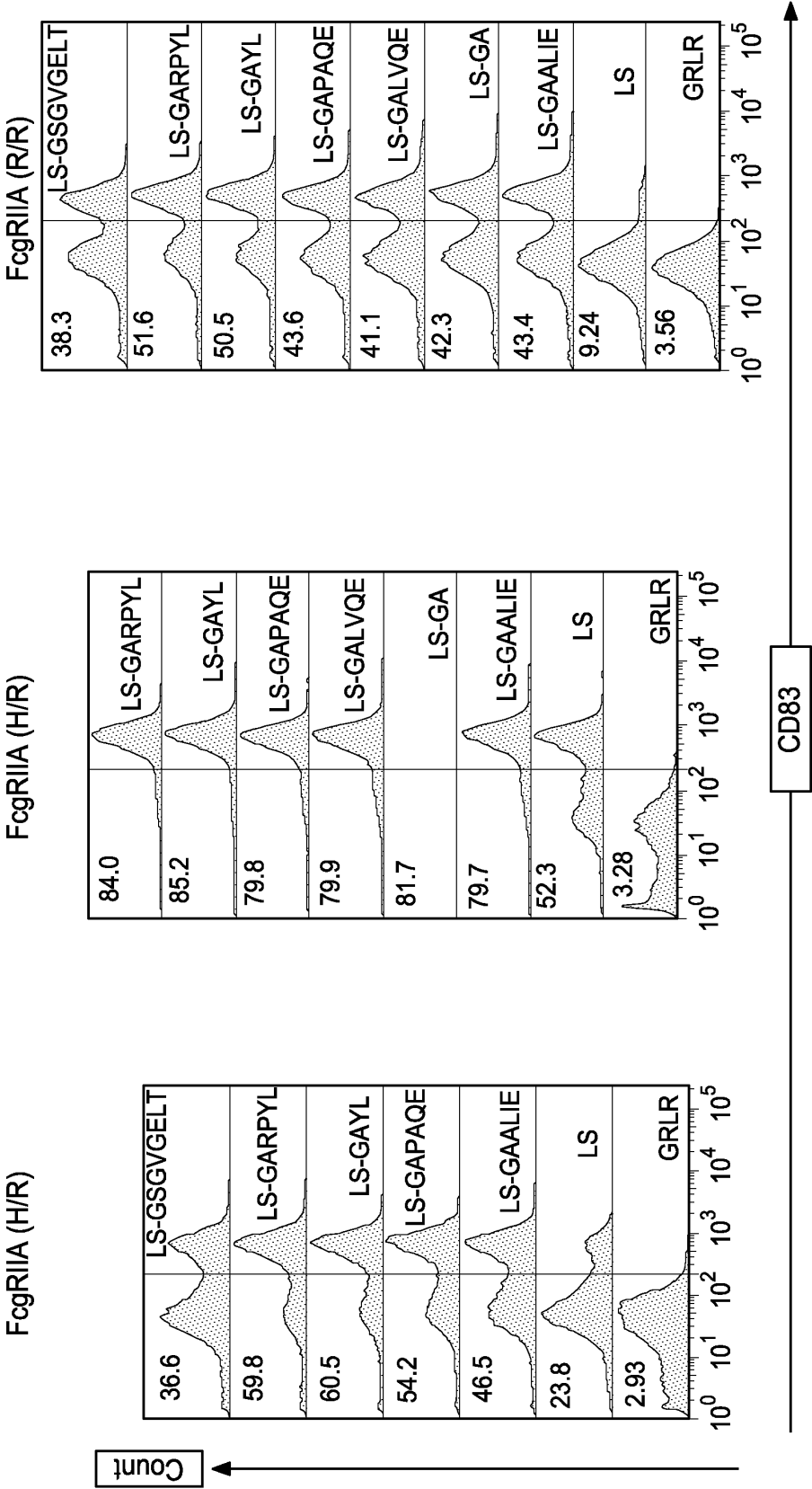


FIG. 29E

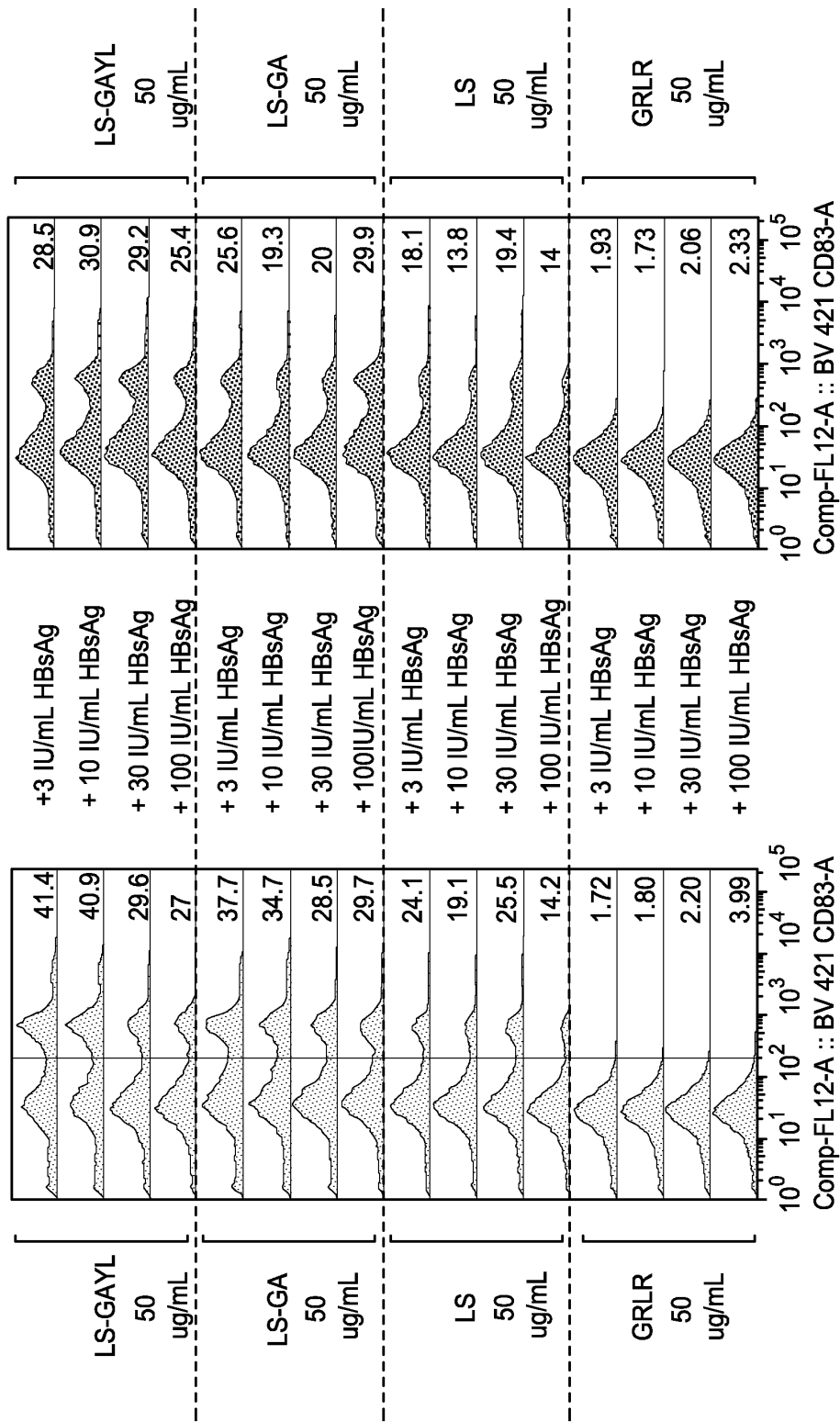


FIG. 29F

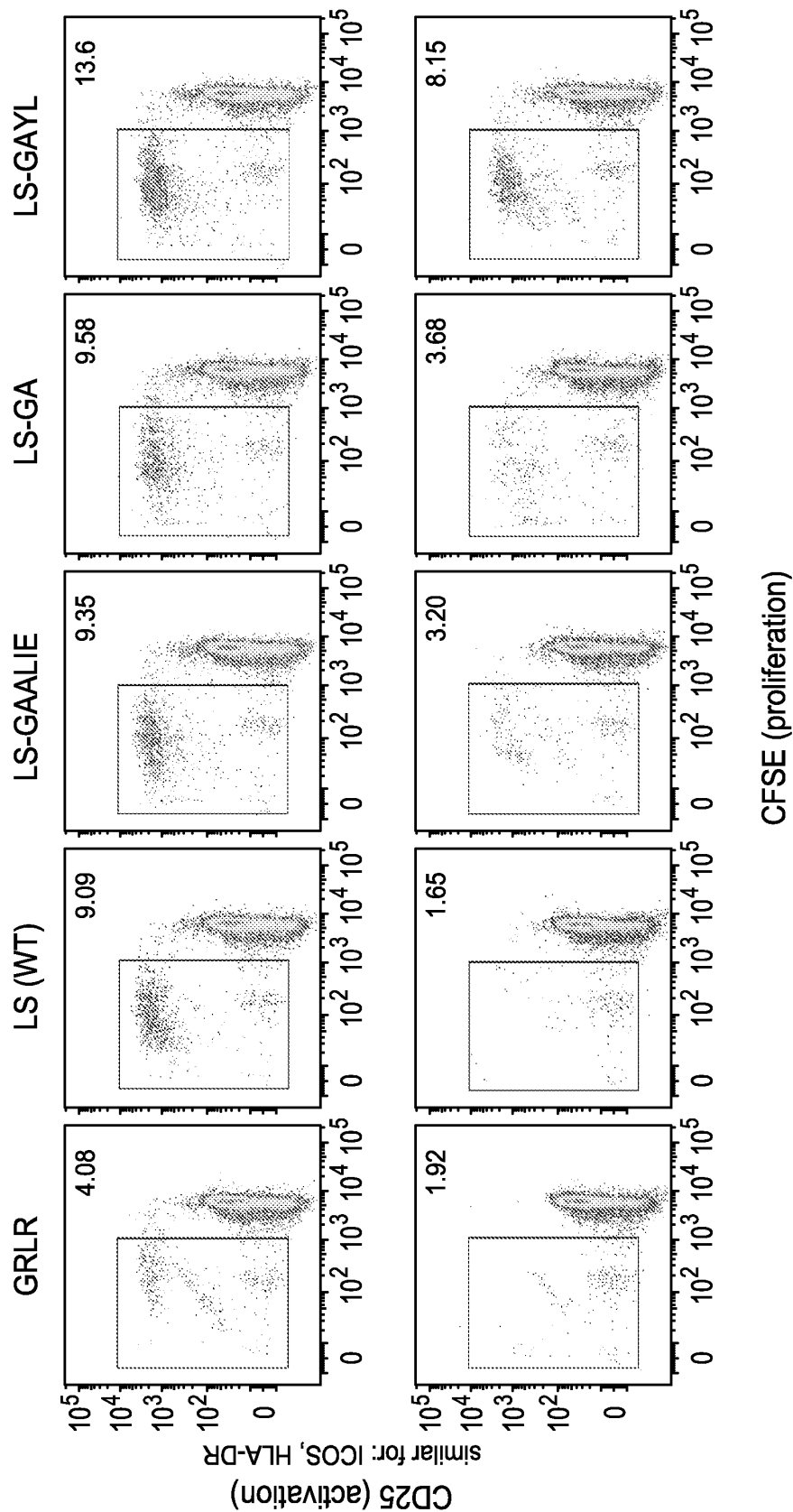


FIG. 29G

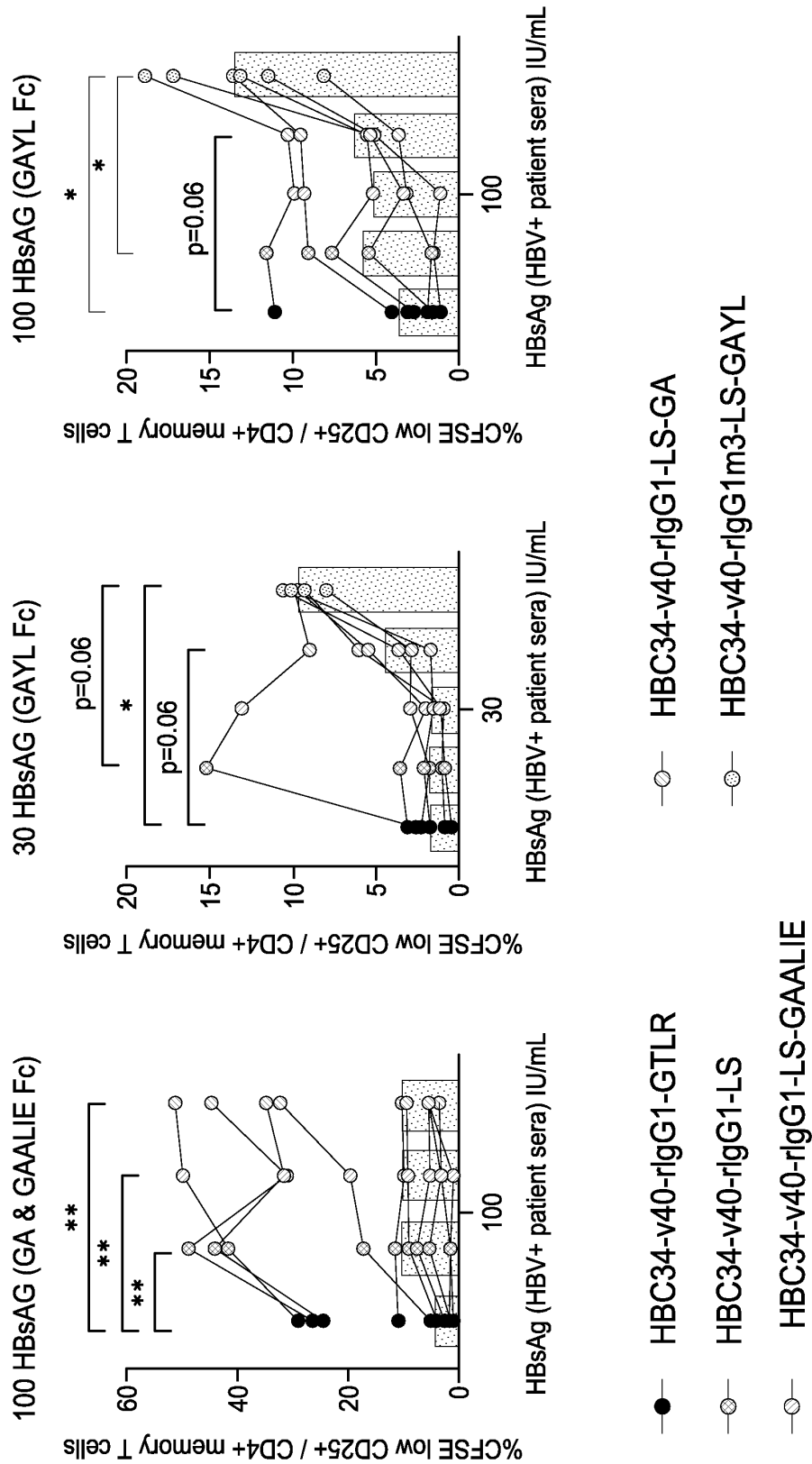


FIG. 29H

HBC34 titration + 1000IU/ml (PLC sup.)

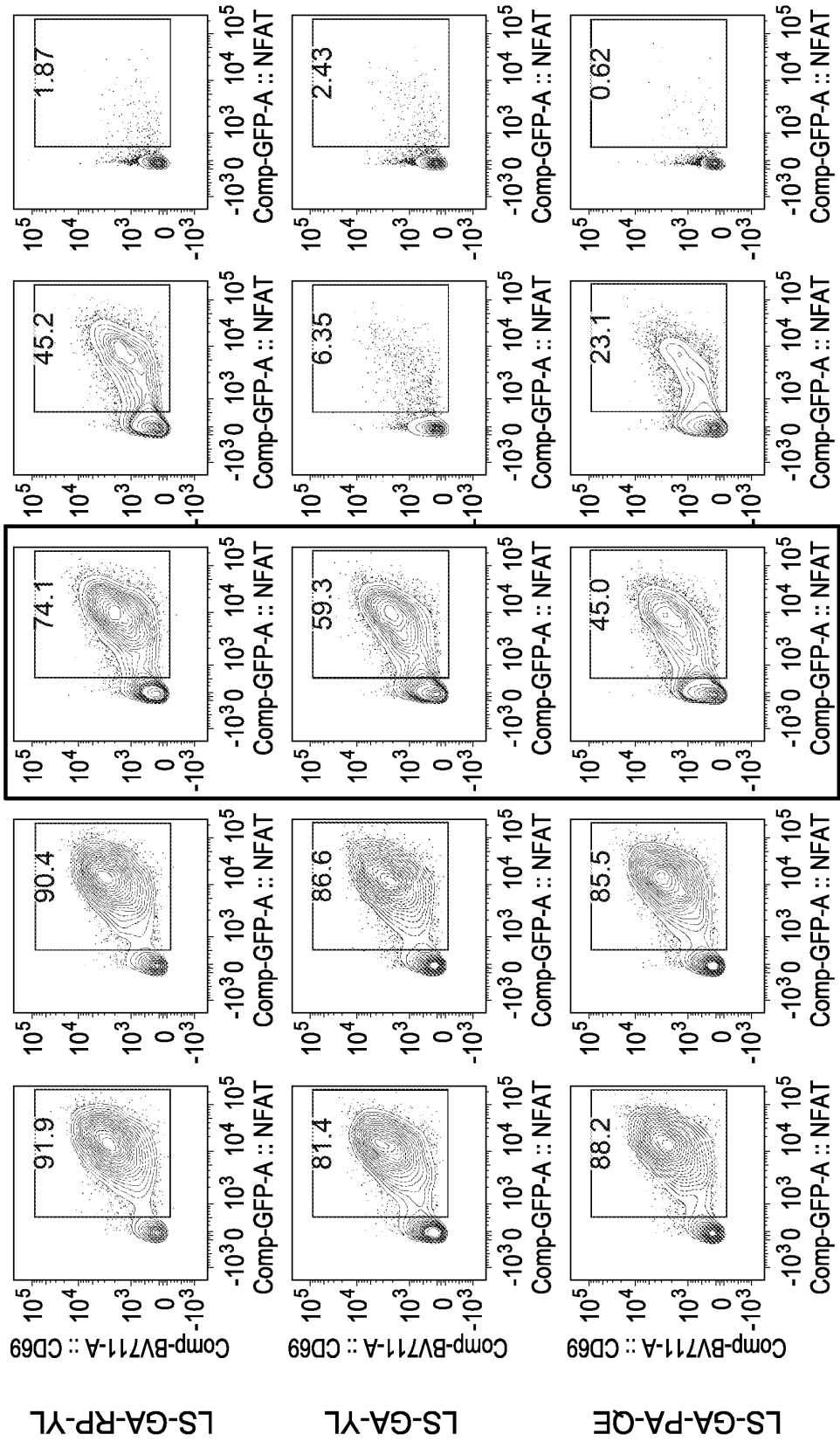


FIG. 29I

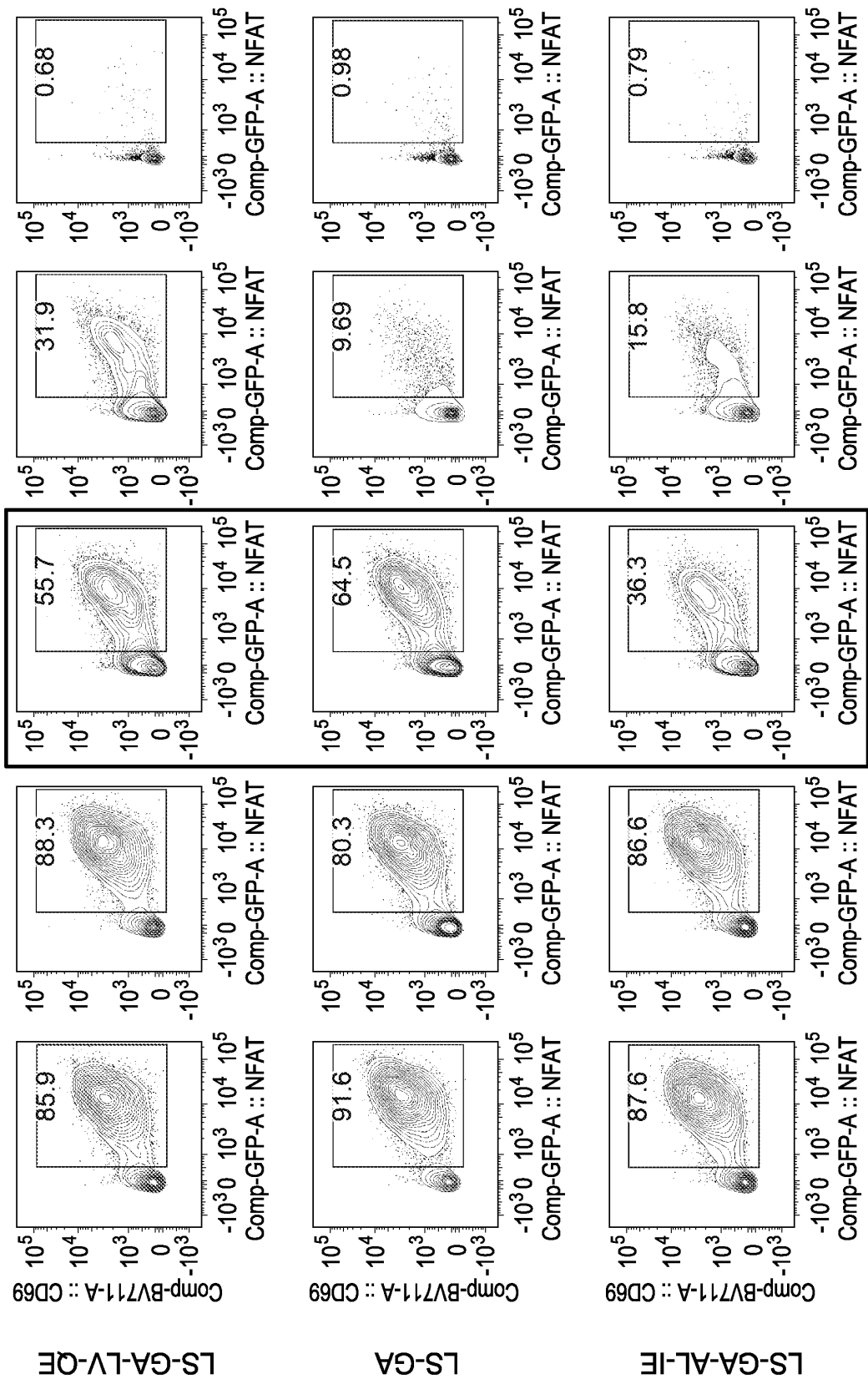


FIG. 29I (cont'd)

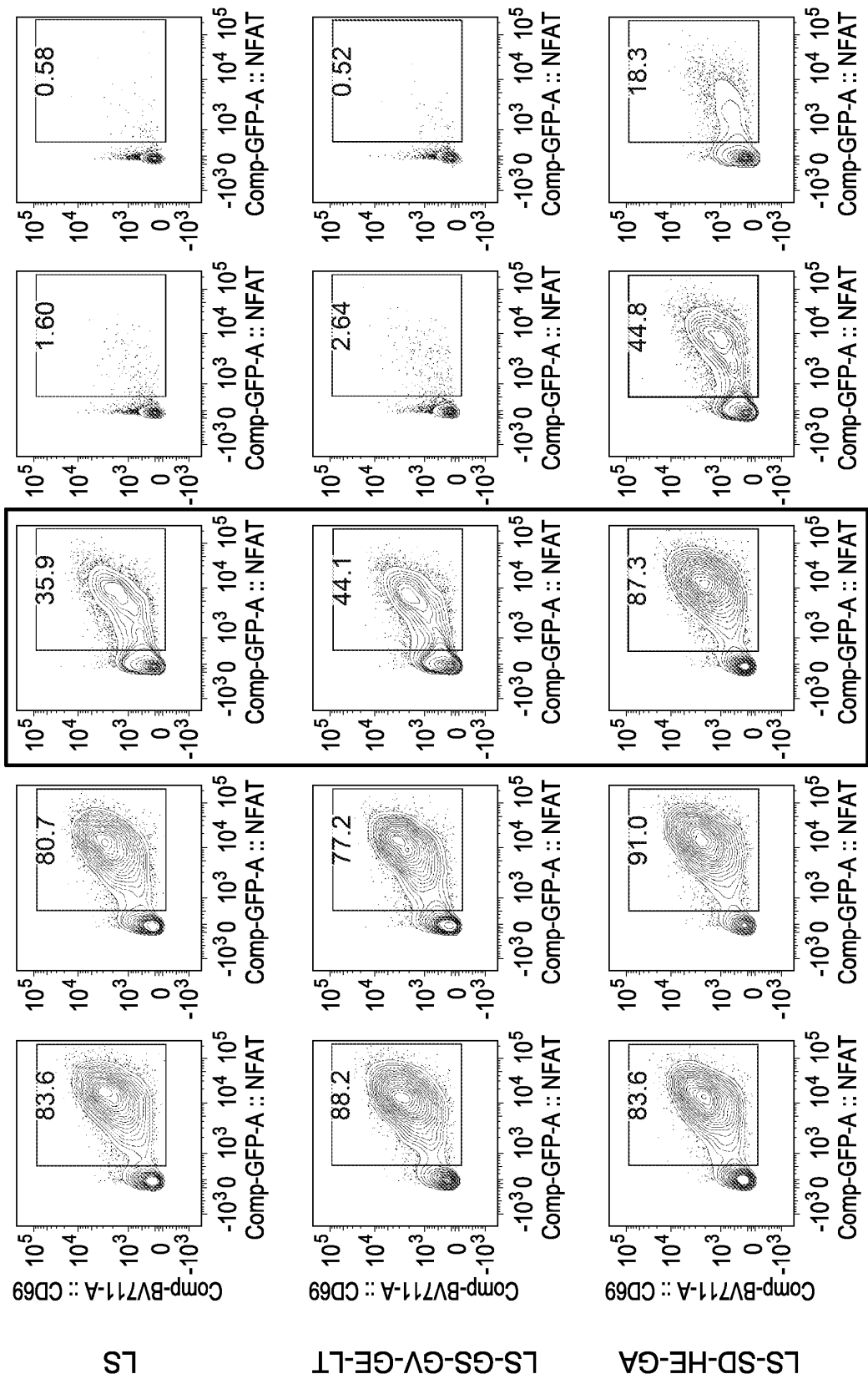


FIG. 29I (cont'd)

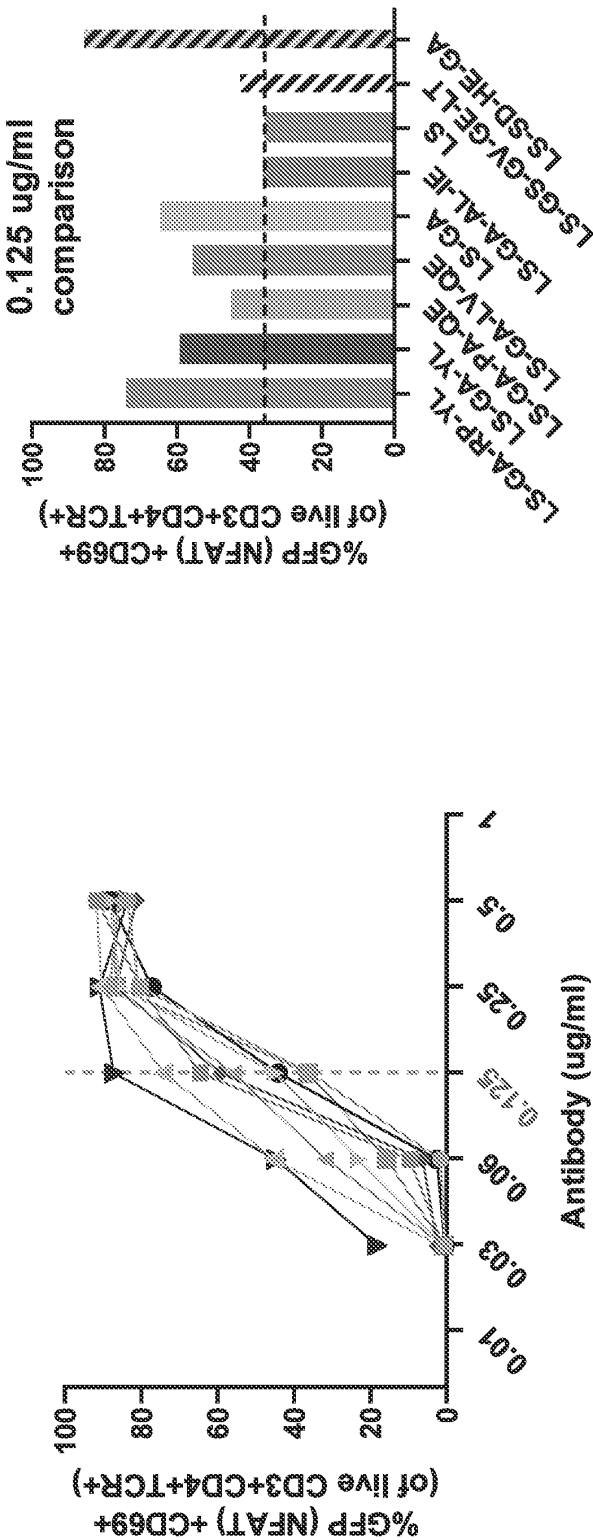


FIG. 29J

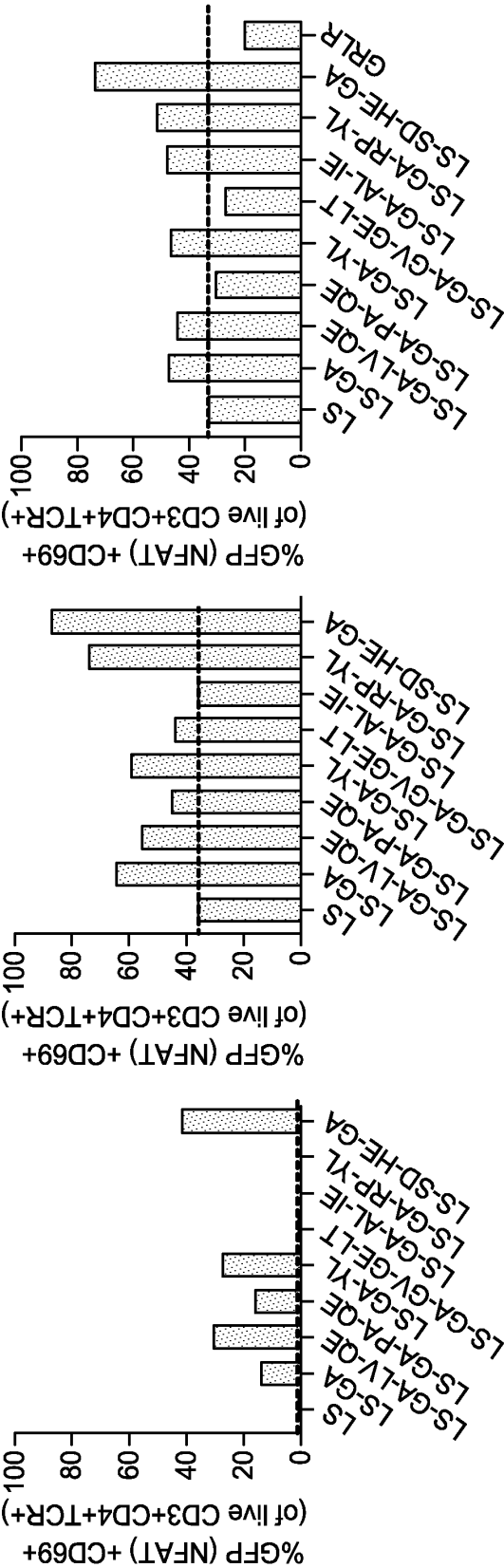


FIG. 29K

*signal lower than expected

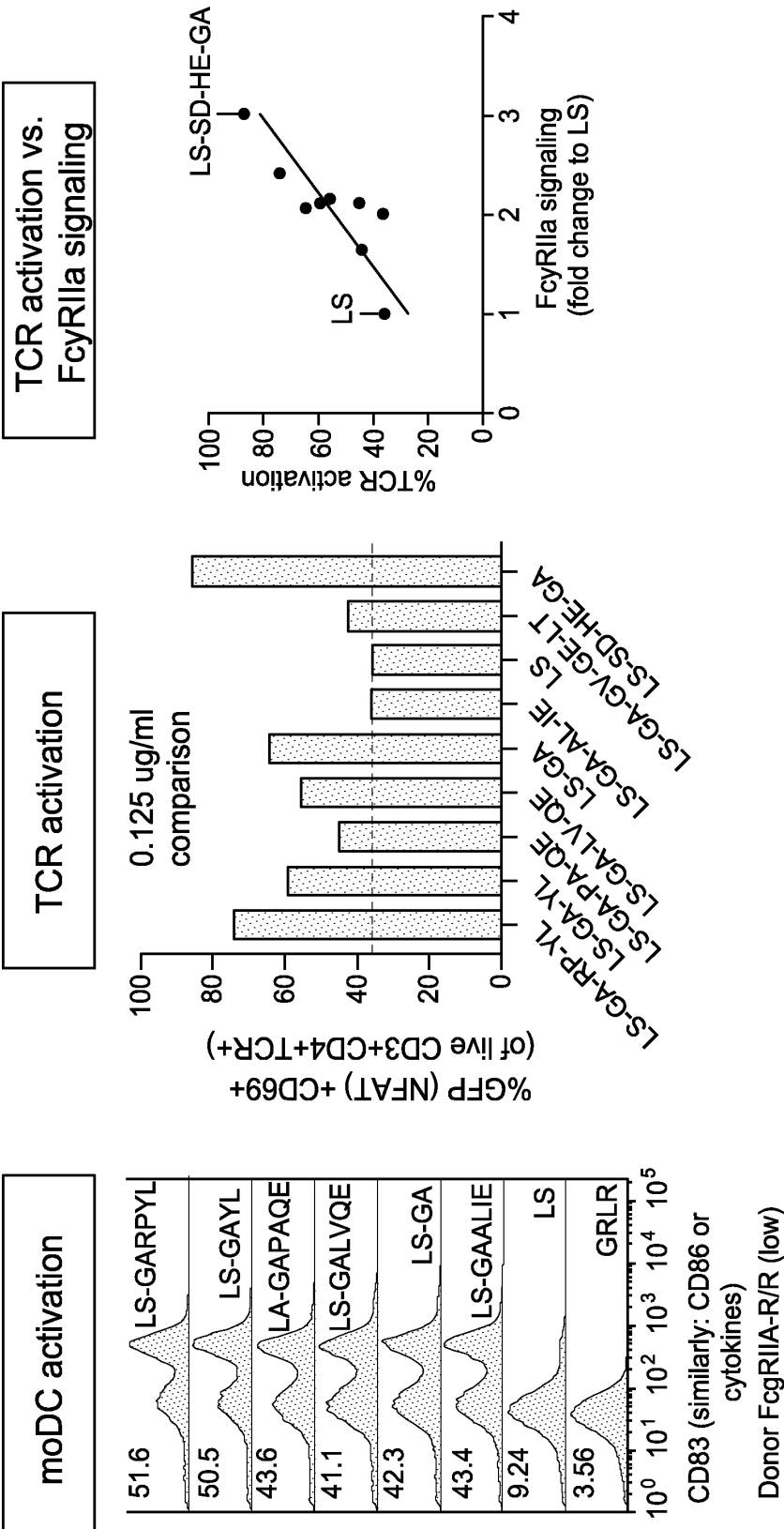


FIG. 29L

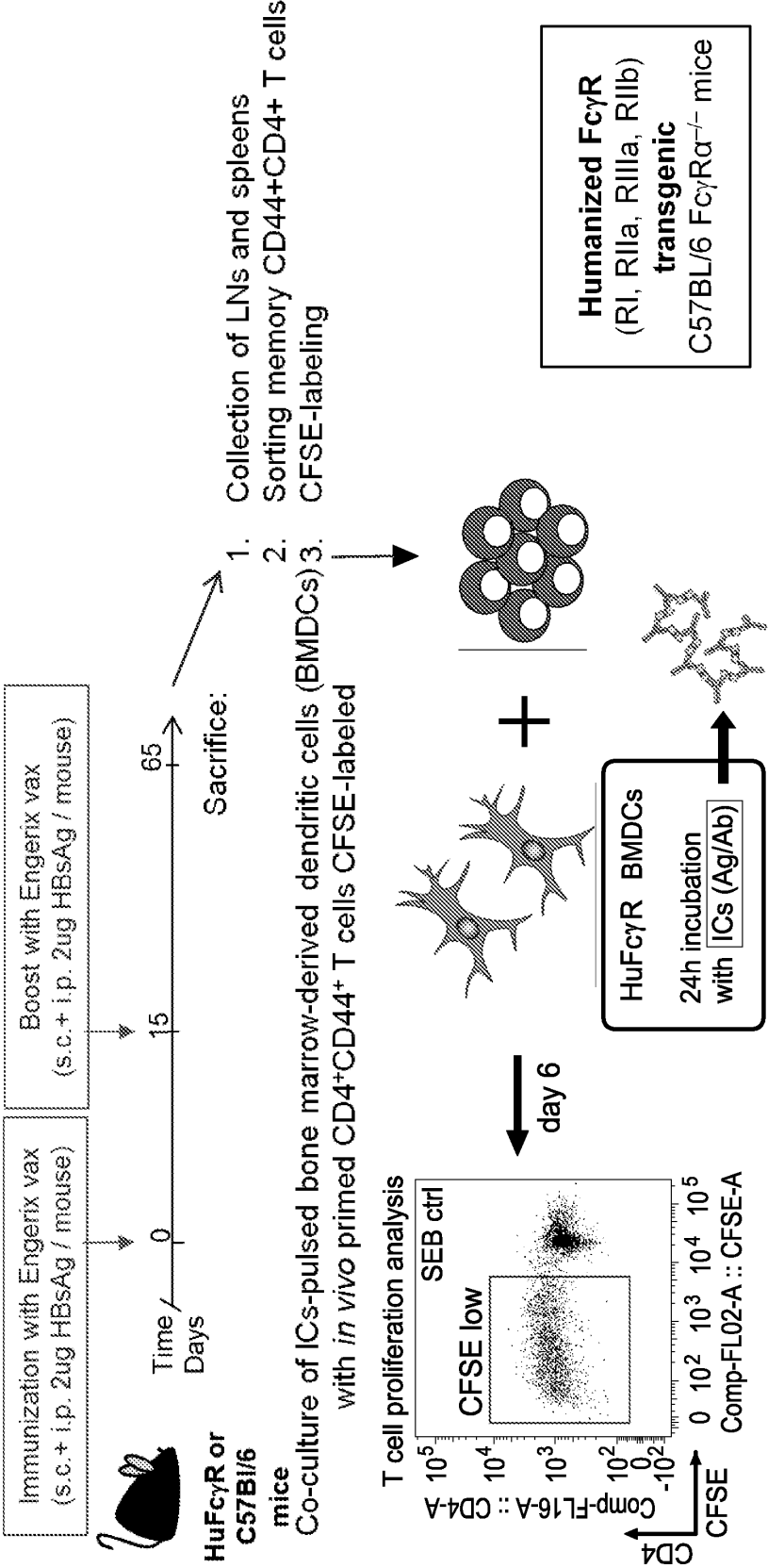
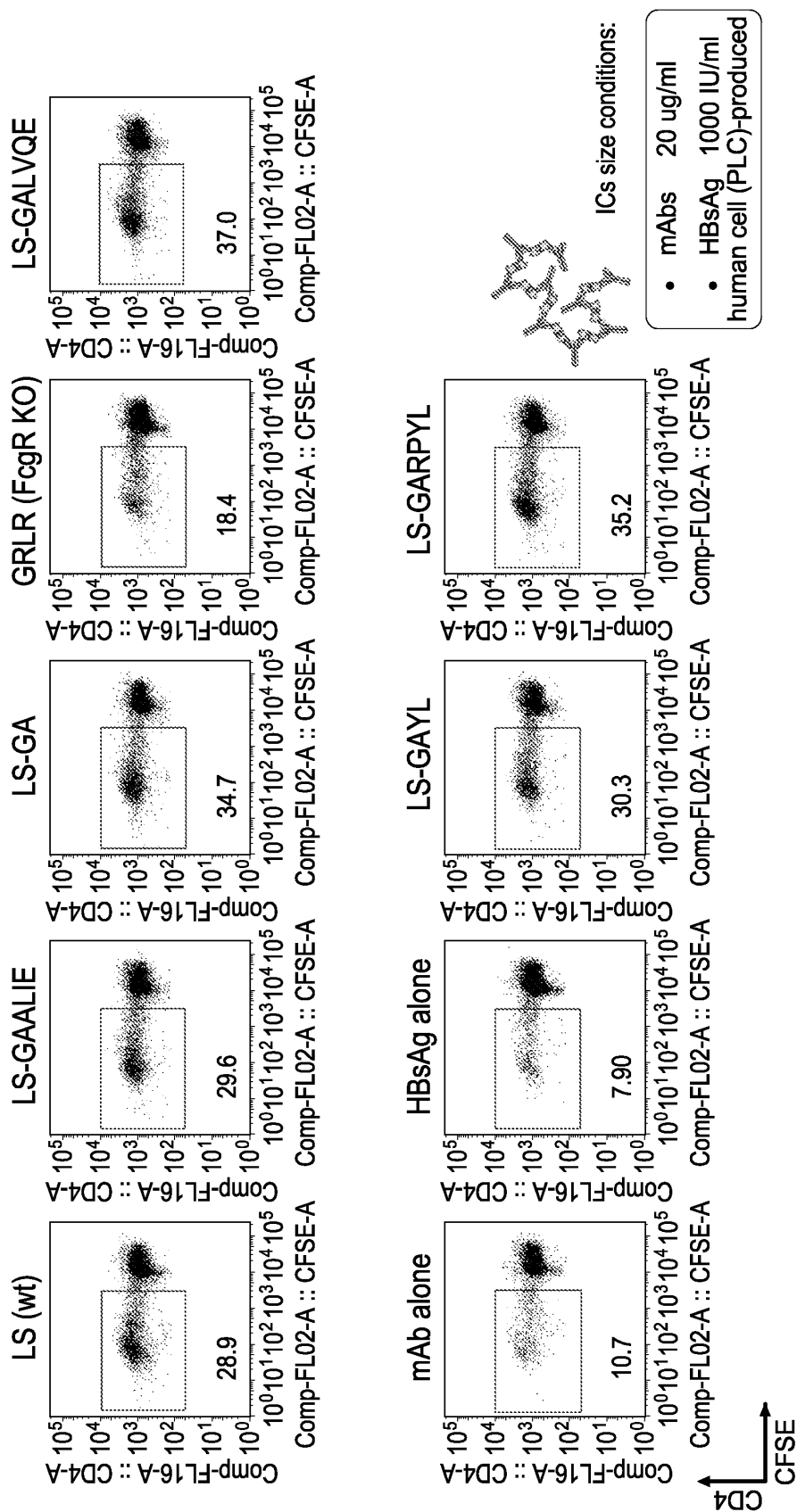
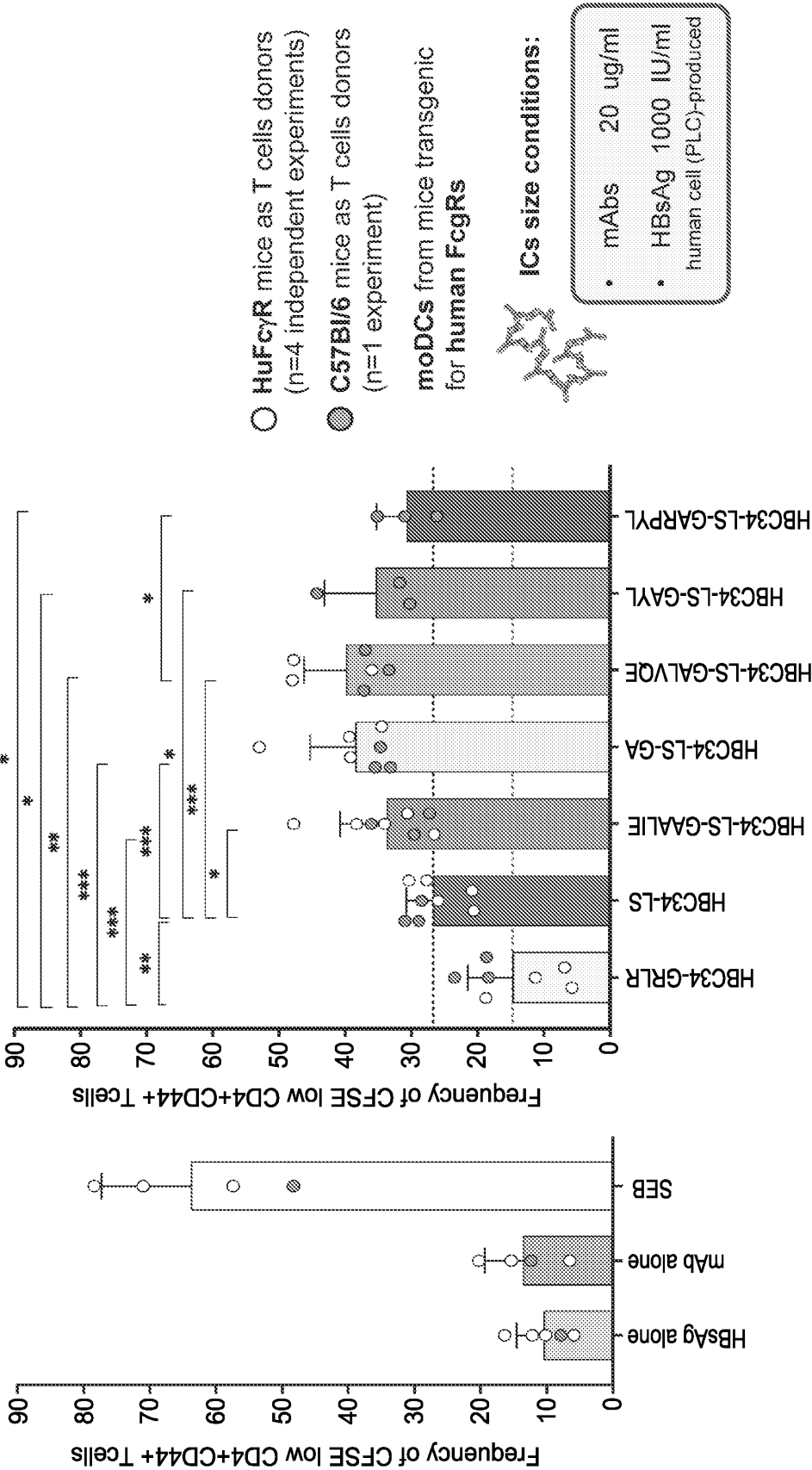


FIG. 29M





(five independent experiments, 50k BMDCs + 500k T cells)

FIG. 290

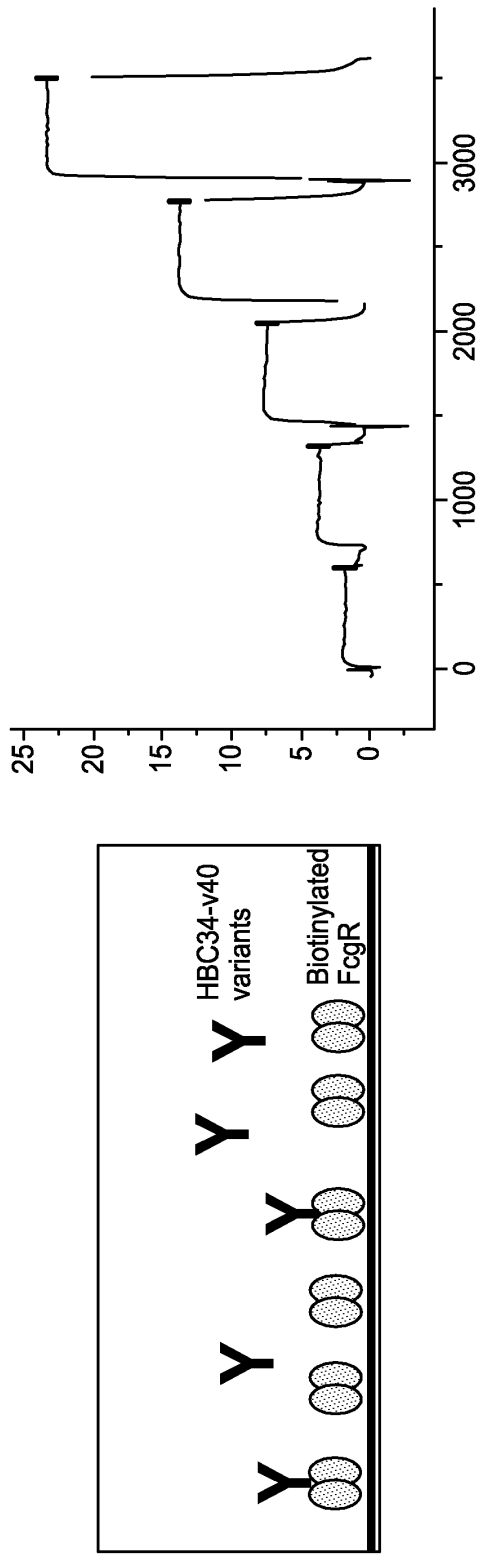


FIG. 29P

HBC34-v40 Variant	FcGR1 FC	FcGR1a (H) FC	FcGR1a (R) FC	FcGR1b FC	FcGR1a (V) FC	FcGR1a (F) FC
HBC34-v40-rlgG1m3-LS	1.00	1.00	1.00	1.00	1.00	1.00
HBC34-v40-rlgG1m3-LS-G236A-I328V-Q295E	0.20	5.17	4.51	1.00	0.31	0.47
HBC34-v40-rlgG1m3-LS-G236A-P230A-Q295E	0.23	5.79	3.01	0.92	0.30	1.62
HBC34-v40-rlgG1m3-LS-G236A-A330L-I332E	1.60	2.87	2.10	0.92	2.60	8.46
HBC34-v40-rlgG1m3-LS-G236A	0.29	5.88	4.54	0.73	0.60	0.99
HBC34-v40-rlgG1m3-LS-G236A-Y300L	0.40	7.73	4.02	0.80	0.51	0.64
HBC34-v40-rlgG1m3-LS-G236A-R292P-Y300L	0.43	7.06	3.67	0.84	2.11	3.14
HBC34-v40-rlgG1m3-LS-afuc	0.80	1.01	1.37	1.27	9.90	9.21
HBC34-v40-rlgG1m3-LS-G236A-R292P-I377N-afuc	0.36	3.37	1.74	0.78	3.22	5.17
HBC34-v40-rlgG1m3-LS-G236A-R292P-Y300L-afuc	0.45	6.25	3.33	0.62	4.46	6.96
HBC34-v40-rlgG1m3-LS-G236A-A330L-I332E-afuc	1.68	2.56	2.08	0.83	22.78	62.86
HBC34-v40-rlgG1m3-LS-G236A-Y300L-afuc	0.31	8.16	2.60	1.34	5.86	4.78
HBC34-v40-rlgG1m3-LS-G236A-afuc	0.24	5.38	3.83	1.31	5.52	5.70
HBC34-v40-rlgG1m3-LS-G236A-I328V-Q295E-afuc	0.30	5.22	5.95	1.13	4.47	4.10
HBC34-v40-rlgG1m3-LS-G236A-R292P-I377N	0.34	3.81	2.12	0.77	0.87	1.40
HBC34-v40-rlgG1m3-LS-G236R-I328R	-	-	-	-	-	-
HBC34-v40-rlgG1m3-LS-G236S-G420V-G446E-I309T	0.09	4.25	1.80	0.69	0.23	0.65
HBC34-v40-rlgG1m3-LS-S239D-H268E-G236A	1.01	9.27	22.56	7.07	4.88	6.76

FIG. 29Q