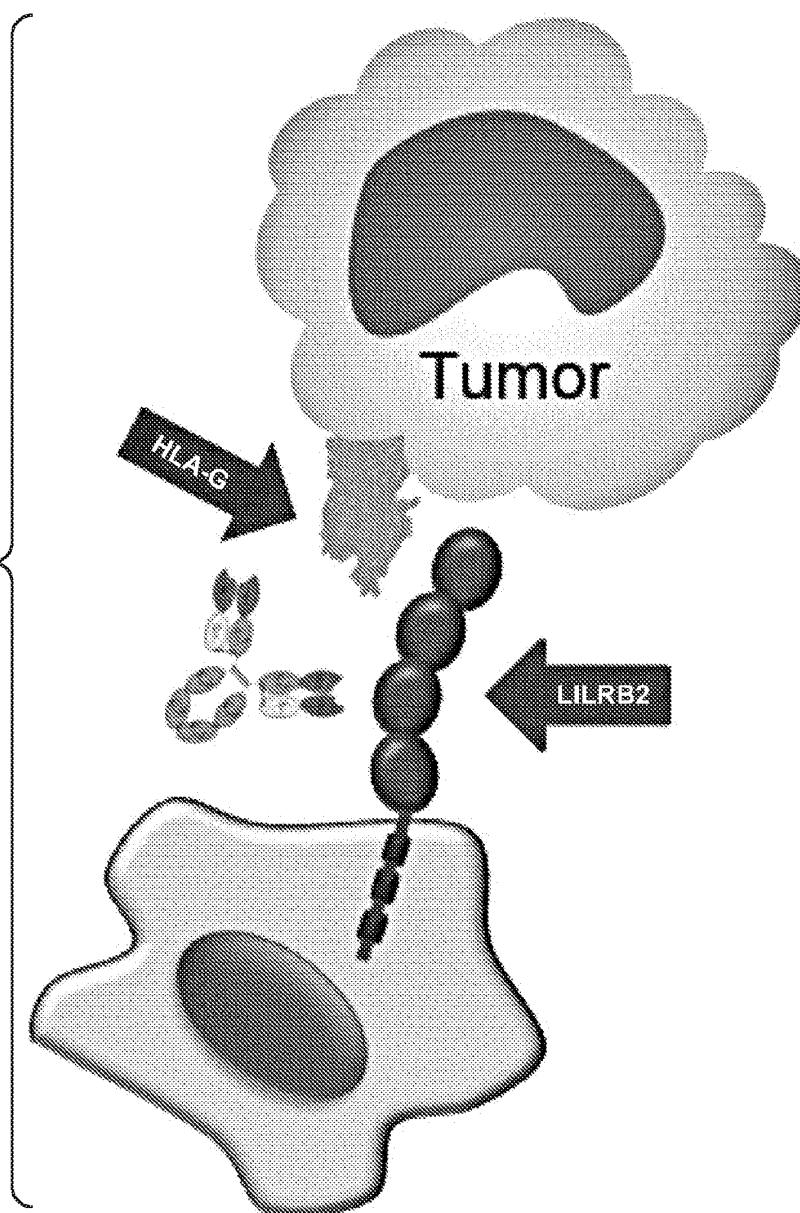


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FIG. 1



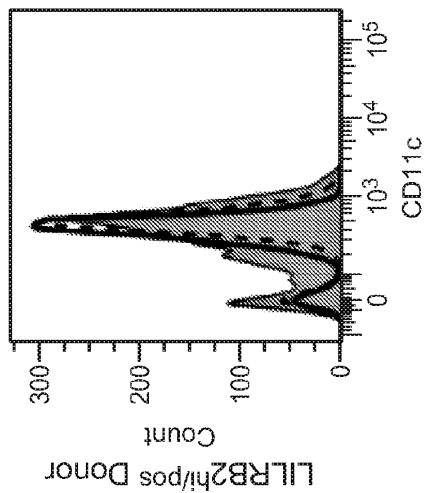


FIG. 2C

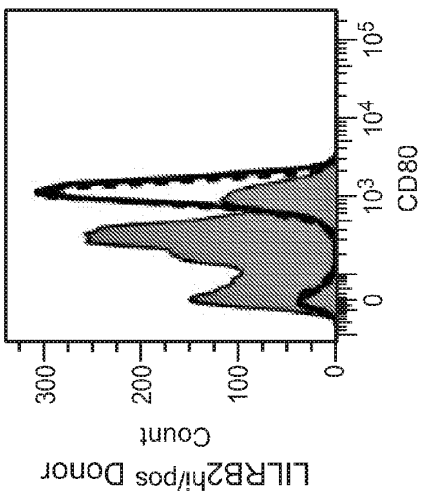


FIG. 2F

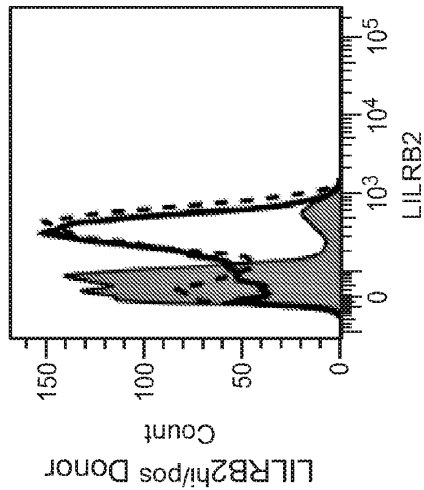


FIG. 2B

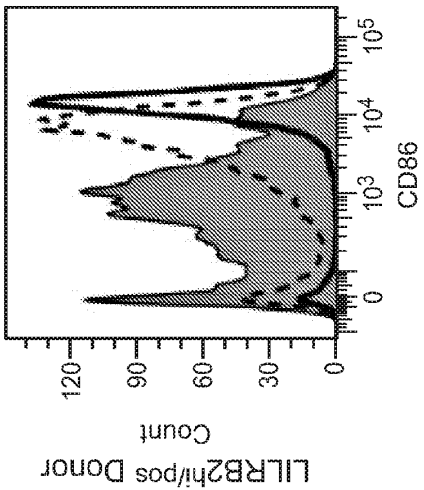


FIG. 2E

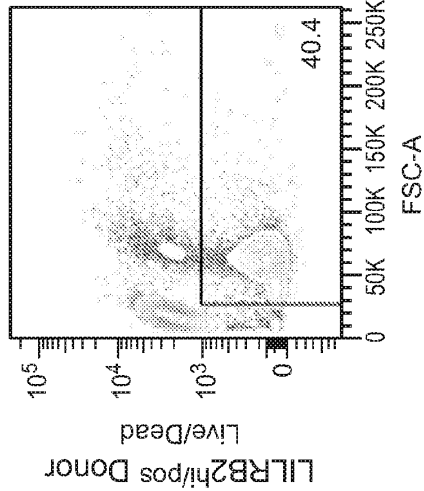


FIG. 2A

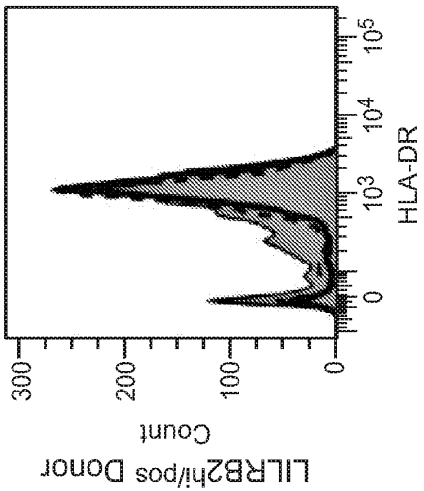


FIG. 2D

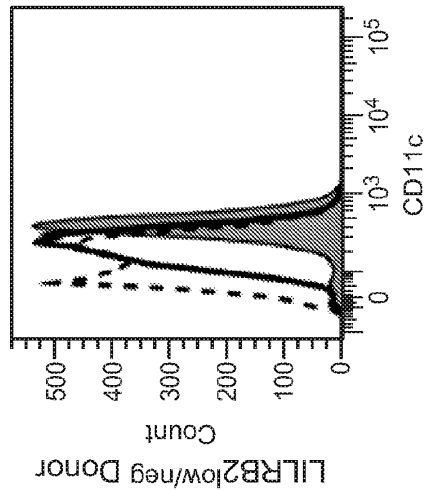


FIG. 2I

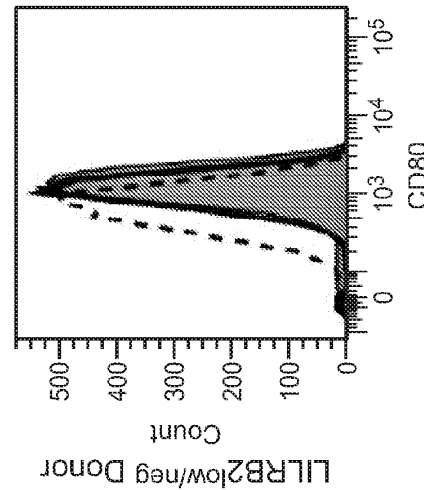


FIG. 2L

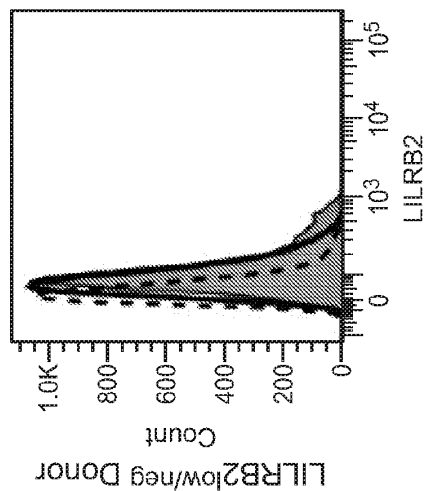


FIG. 2H

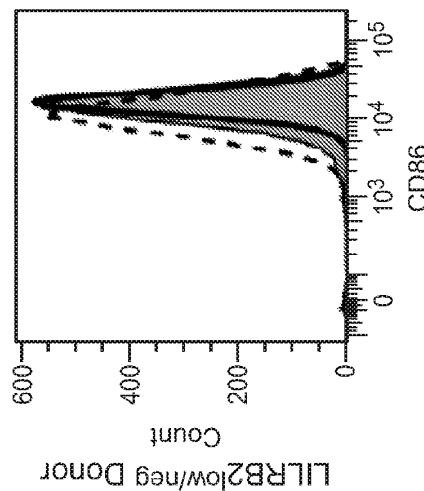


FIG. 2K

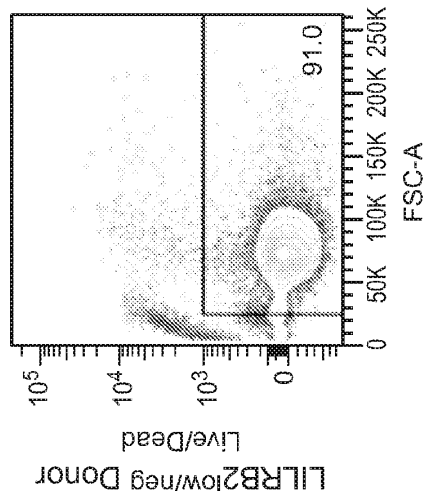


FIG. 2G

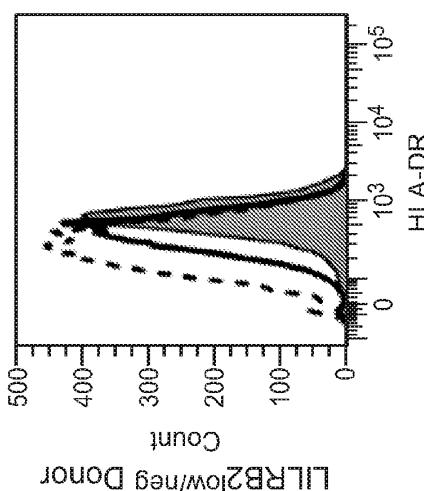


FIG. 2J

FIG. 3A

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

FIG. 3A-1

Reference	Hybridoma clone isotype	LILRB1 CHOs binding (fold over iso)	LILRB2 CHOs binding (fold over iso)	LILRB3 CHOs binding (fold over iso)	LILRB4 CHOs binding (fold over iso)	LILRB5 CHOs binding (fold over iso)	LILRA1 CHOs binding (fold over iso)
J-01	mG1	0.96	19.95	2.49	0.87	1.23	0.90
J-02	mG1	1.03	12.18	1.00	1.00	1.09	0.98
J-03	mG2b	0.94	30.14	0.97	1.02	1.00	0.89
J-04	mG2b	0.95	33.80	0.90	0.83	1.08	0.88
J-05	mG2b	0.95	25.09	0.91	0.76	1.03	0.87
J-06	mG1	0.83	9.58	0.89	0.83	1.00	1.42
J-07	mG2b	0.97	38.66	0.93	0.91	1.29	0.96
J-08	mG1	1.00	25.19	1.03	0.98	1.40	1.01
J-09	mG1	0.96	13.19	1.01	0.90	1.18	1.06
J-10	mG1	1.04	19.03	1.22	0.94	1.36	1.13
J-11	mG2b	1.07	3.49	1.09	1.03	1.22	-1.63
J-12	mG2a	0.99	1.25	0.99	0.99	0.98	1.28
J-13	mG1	0.86	14.40	0.90	0.84	1.01	0.89
J-14	mG1	0.92	25.97	0.92	1.01	1.03	0.94
J-15	mG2b	1.00	28.06	1.02	0.95	1.24	1.17
J-16	rG1	1.03	3.75	1.11	1.01	1.10	611.88
J-17	mG1	1.05	3.68	0.99	1.00	1.03	7.31

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FIG. 3A-2

LILRA2 CHOs binding (fold over iso)	LILRA3 CHOs binding (fold over iso)	LILRA4 CHOs binding (fold over iso)	LILRA5 CHOs binding (fold over iso)	LILRA6 CHOs binding (fold over iso)
1.34	1.06	1.90	0.77	1.23
1.34	1.08	1.63	1.03	1.14
1.58	1.05	2.01	0.96	1.23
1.62	0.93	2.07	0.74	1.30
1.34	0.90	1.69	0.82	1.23
1.09	1.04	1.85	0.73	1.28
1.57	1.02	1.39	0.98	1.09
1.64	1.03	0.28	1.06	1.08
1.28	1.03	1.32	0.91	0.90
1.49	1.10	1.00	0.99	0.19
-2.52	1.02	-1.27	1.34	1.00
1.24	1.23	0.20	1.12	0.41
1.08	0.99	1.93	0.76	1.19
1.42	1.01	1.46	0.99	1.17
1.86	1.17	0.43	1.19	0.92
-31.56	182.92	-35.47	3.09	0.62
-1.05	1.35	-36.53	0.82	0.94

J-18	rG1	0.98	1.23	0.81	0.96	0.97	-12.44
J-19	rG1	1.05	3.78	1.09	1.03	1.19	-3.31
J-20	rG1	1.02	3.43	1.00	0.99	1.03	375.00
J-21	mG2a	1.08	2.50	1.22	1.10	1.06	13.94
J-22	mG1	1.05	1.46	1.01	0.97	1.00	-19.25
J-23	mG2b	0.99	1.15	1.36	0.99	0.94	11.00
J-24	mG1	1.06	1.01	1.00	0.99	0.95	22.44
J-25	mG1	0.98	1.57	1.06	0.99	0.96	-6.31
Isotype		1.00	1.00	1.00	1.00	1.00	1.00
Total screened		25	25	25	25	25	25
Hit cut-off		2	2	2	2	2	2
Total hits		0	18	1	0	0	6
% hit		0.0	72.0	4.0	0.0	0.0	24.0

FIG. 3A-3

1.91	0.45	2.67	-1.93	-0.64
-0.51	0.97	-26.80	-0.62	1.07
3.12	0.18	19.73	-3.65	-0.08
-1.26	1.46	-26.33	1.63	1.21
3.03	0.51	16.00	-1.05	-0.20
0.34	1.33	-16.13	1.33	0.70
0.04	1.36	-17.67	0.59	1.19
1.85	0.51	29.73	-1.33	0.26
1.00	1.00	1.00	1.00	1.00
25	25	25	25	25
2	2	2	2	2
2	1	6	1	0
8.0	4.0	24.0	4.0	0.0

FIG. 3A-4

FIG. 3B

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

FIG. 3B-1

Reference	Hybridoma clone isotype	HLA-G:IL1RB2 CHO blocking (% blocked)	HLA-A2:IL1RB2 CHO blocking (% blocked)	TNF α production (fold over LPS alone)	IL-6 production (fold over LPS alone)	IL-10 production (fold over LPS alone)	CCL2 production (fold over LPS alone)
J-01	mG1	-40.25	15.12	3.86	2.55	0.78	0.88
J-02	mG1	50.41	43.21	1.58	1.38	0.79	0.79
J-03	mG2b	-156.17	-208.49	1.27	1.10	0.97	0.95
J-04	mG2b	-255.13	-319.42	1.18	1.36	0.95	1.00
J-05	mG2b	-21.97	15.16	1.16	1.00	1.01	1.02
J-06	mG1	-62.70	-59.10	0.56	1.10	0.92	0.84
J-07	mG2b	44.29	70.93	2.66	1.58	0.91	0.95
J-08	mG1	-186.51	-177.77	3.63	2.64	0.75	0.89
J-09	mG1	-13.66	2.46	3.32	1.68	0.90	0.92
J-10	mG1	-73.72	-34.77	2.44	1.97	1.01	1.01
J-11	mG2b	99.86	94.44	7.61	3.06	0.81	0.96
J-12	mG2a	-7.16	-10.40	0.31	0.87	0.89	0.94
J-13	mG1	-61.85	-61.85	n/a	n/a	n/a	n/a
J-14	mG1	-160.30	-204.08	0.91	2.97	0.75	0.84
J-15	mG2b	-243.96	-288.39	1.07	1.29	0.92	0.93
J-16	rG1	96.77	94.80	2.49	1.41	1.09	1.31
J-17	mG1	96.56	93.44	8.12	2.57	0.89	1.85

FIG. 3B-2

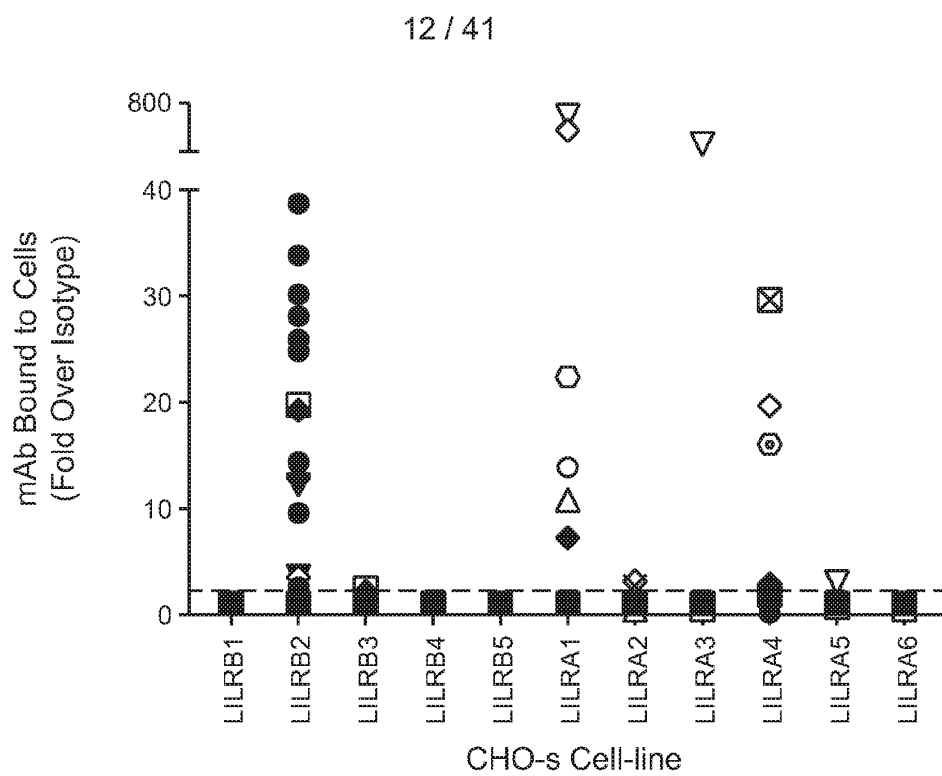
Human Monocytes binding (fold over iso)	Human Neutrophils binding (fold over iso)	Cyno Monocytes binding (fold over iso)	Cyno Neutrophils binding (fold over iso)	Rhesus Monocytes binding (fold over iso)	Rhesus Neutrophils binding (fold over iso)
8.54	2.89	0.71	0.94	0.88	0.64
11.35	4.55	0.92	0.87	1.41	1.44

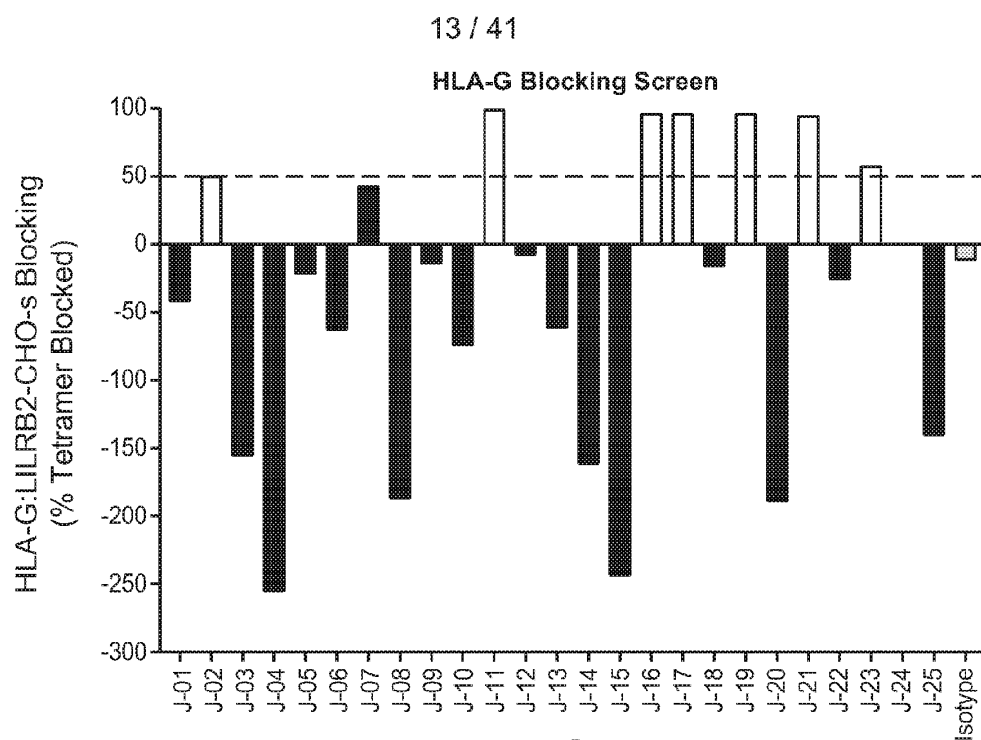
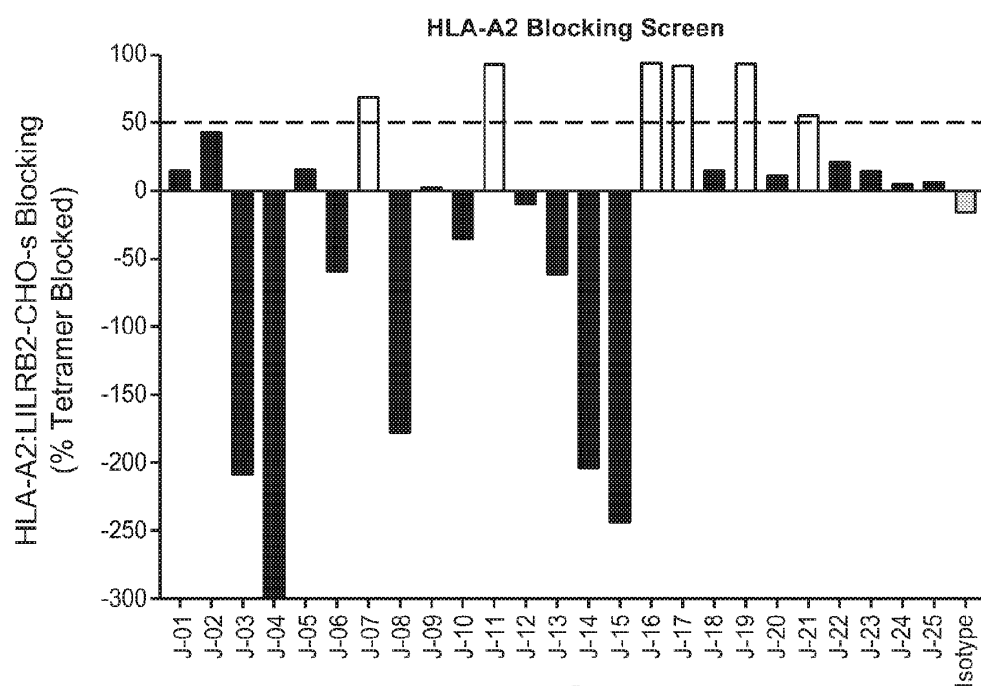
J-18	rG1	-15.14	16.04	0.92	1.08	0.99	1.00
J-19	rG1	97.01	95.32	8.90	2.72	0.80	1.69
J-20	rG1	-188.75	11.03	9.02	2.58	0.67	1.64
J-21	mG2a	95.61	56.57	5.46	2.23	1.00	1.48
J-22	mG1	-24.90	21.76	2.62	1.39	1.10	1.24
J-23	mG2b	58.97	16.27	2.07	1.14	1.03	1.12
J-24	mG1	0.08	6.30	1.16	0.84	0.83	0.87
J-25	mG1	-139.70	7.12	1.82	1.57	1.20	1.29
Isotype		-8.00	-12.49	0.82	1.08	0.96	1.02
Total screened		25	25	24	24	24	24
Hit cut-off		50	50	1.5	1.5	0.85	0.85
Total hits		7	6	15	12	8	3
% hit		28.0	24.0	62.5	50.0	33.3	12.5

FIG. 3B-3

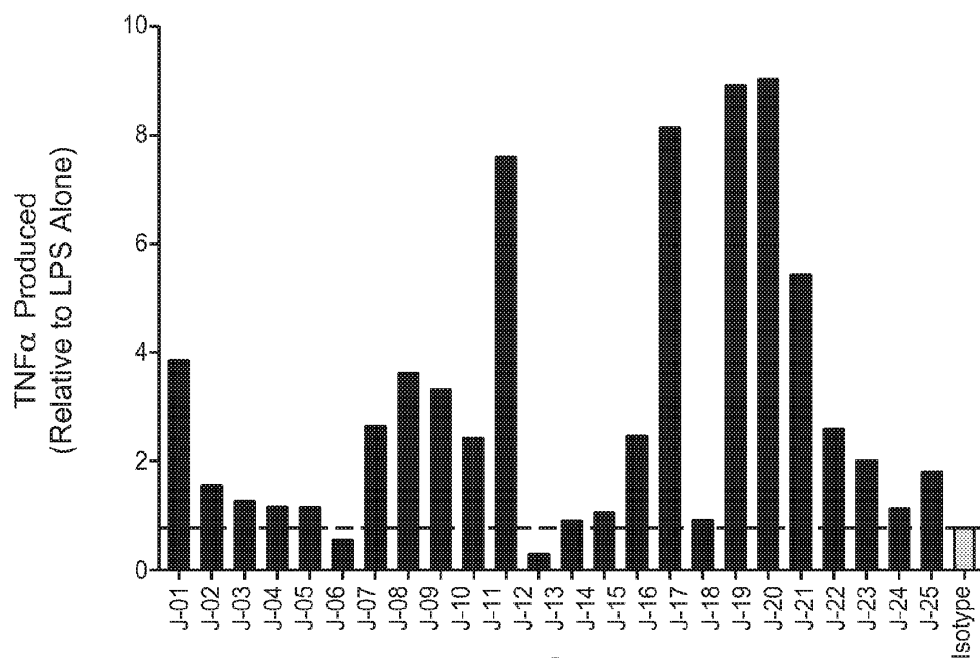
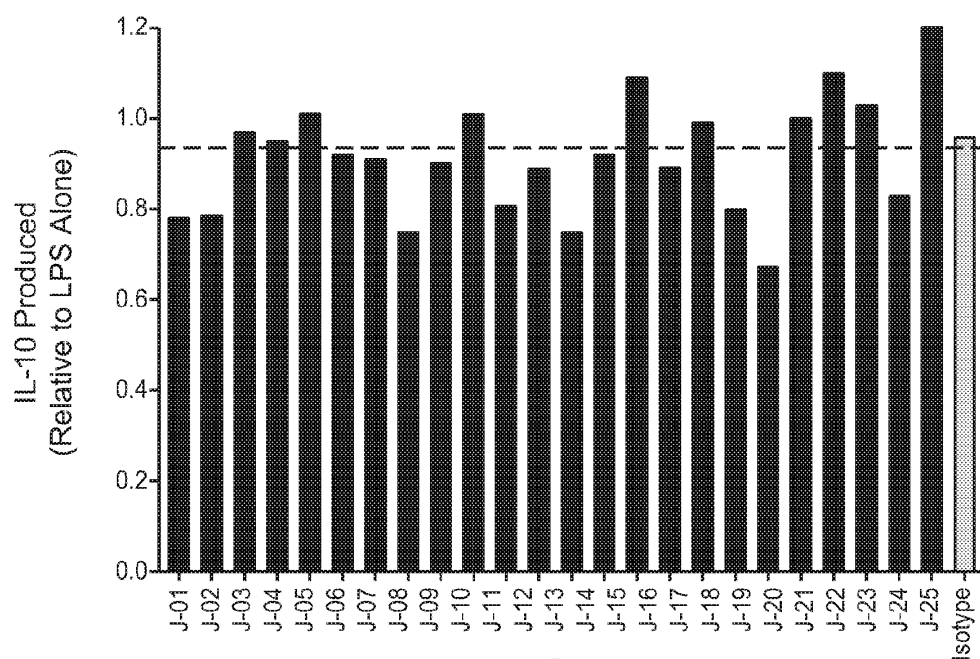
12.31	4.5	17.88	2.35	6.79	21.89
1	1	1	1	1	1
3	3	3	3	3	3
10	10	10	10	10	10
3	3	1	3	1	3
100.0		33.3		33.3	

FIG. 3B-4

**FIG. 4**

**FIG. 5****FIG. 6**

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**FIG. 7A****FIG. 7B**

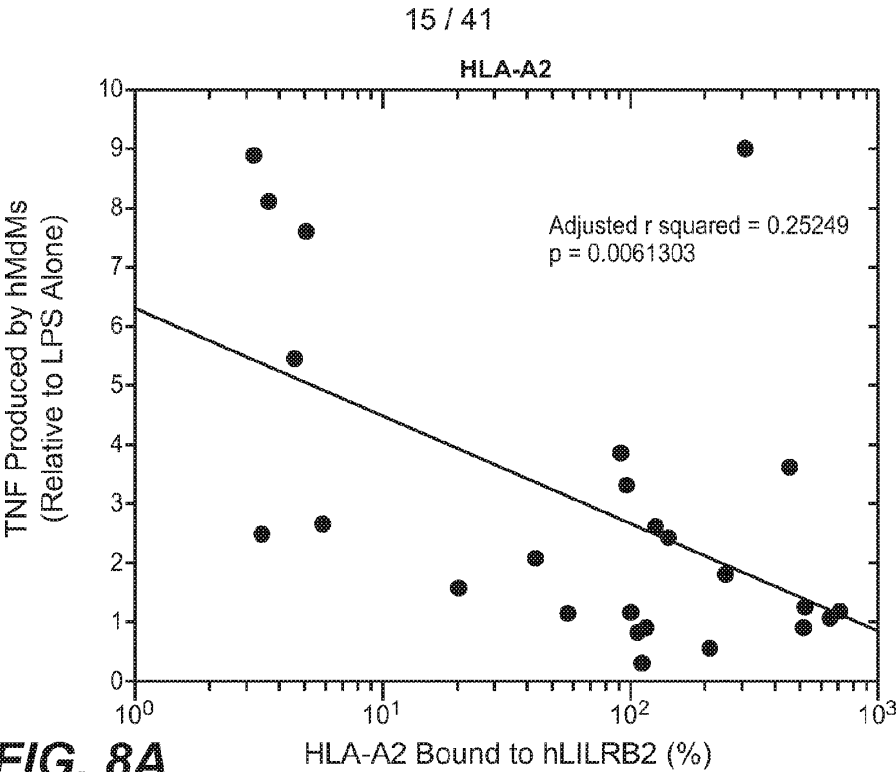


FIG. 8A

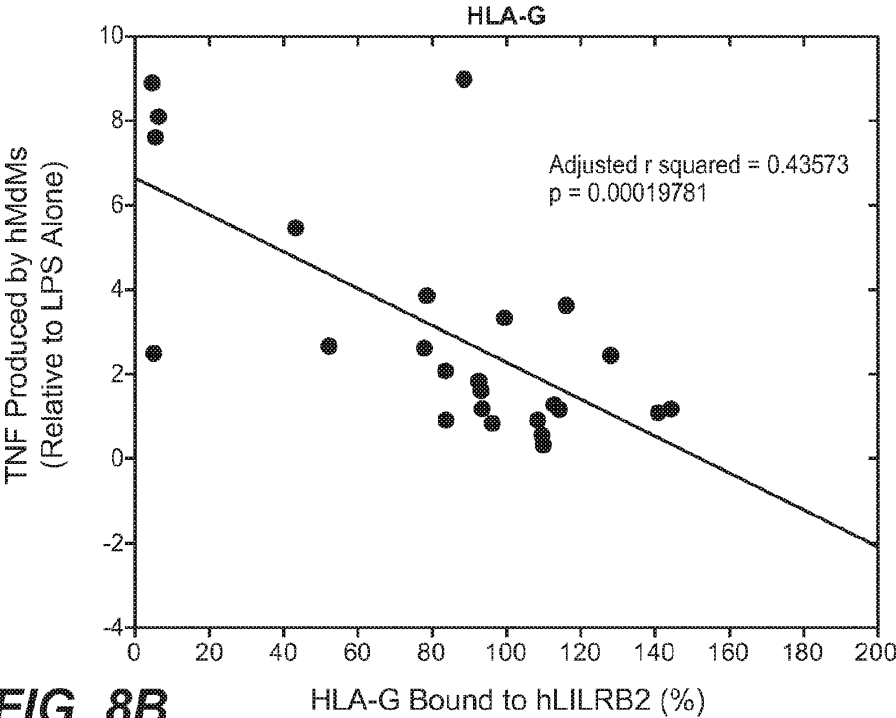
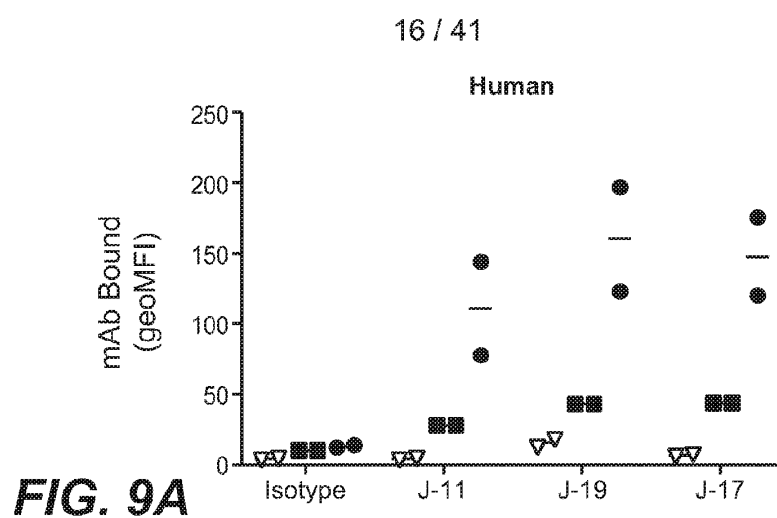
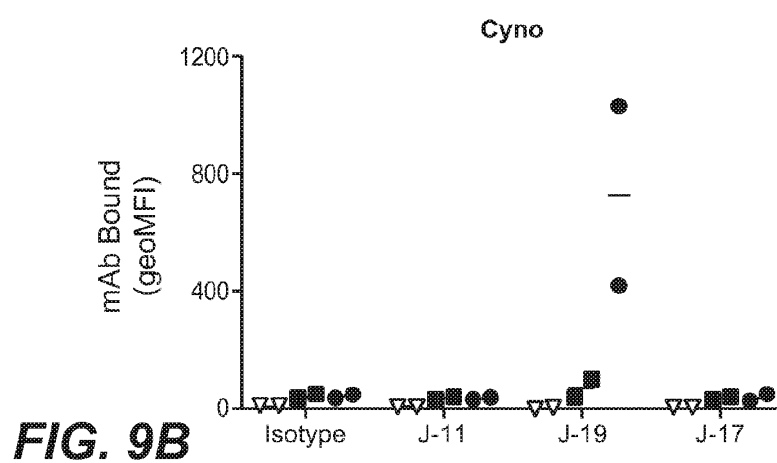
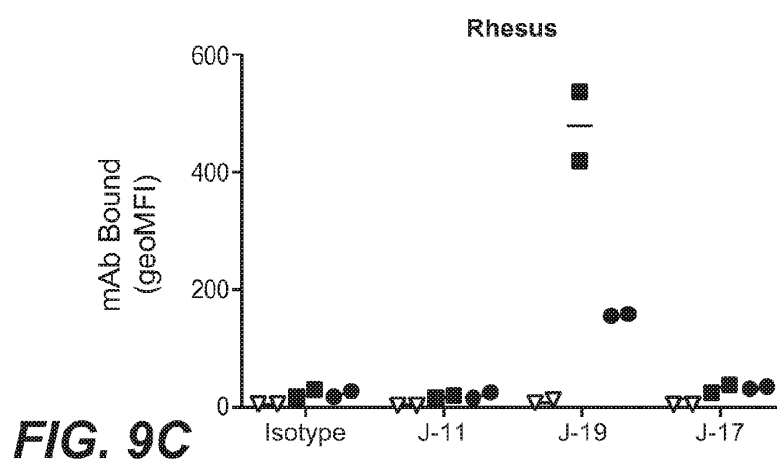
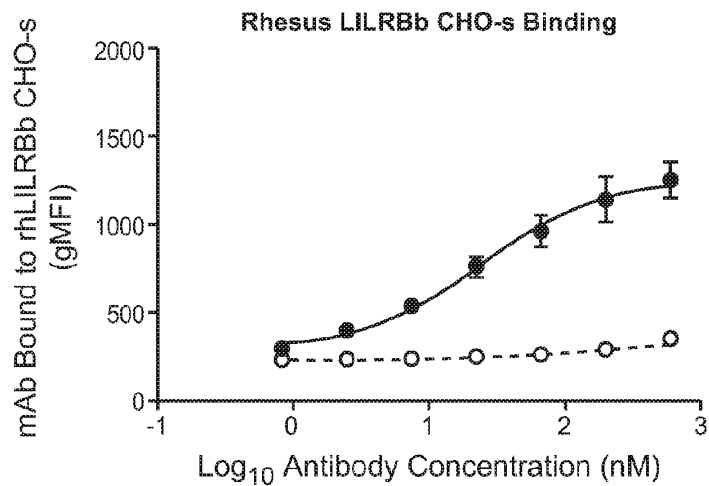
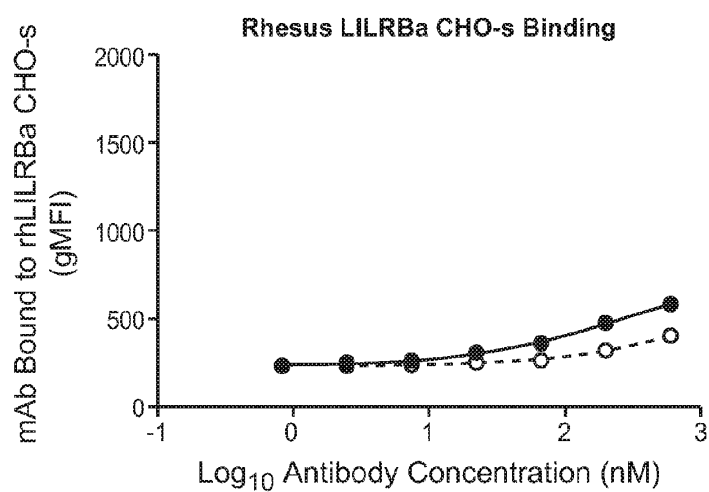


FIG. 8B

**FIG. 9A****FIG. 9B****FIG. 9C**

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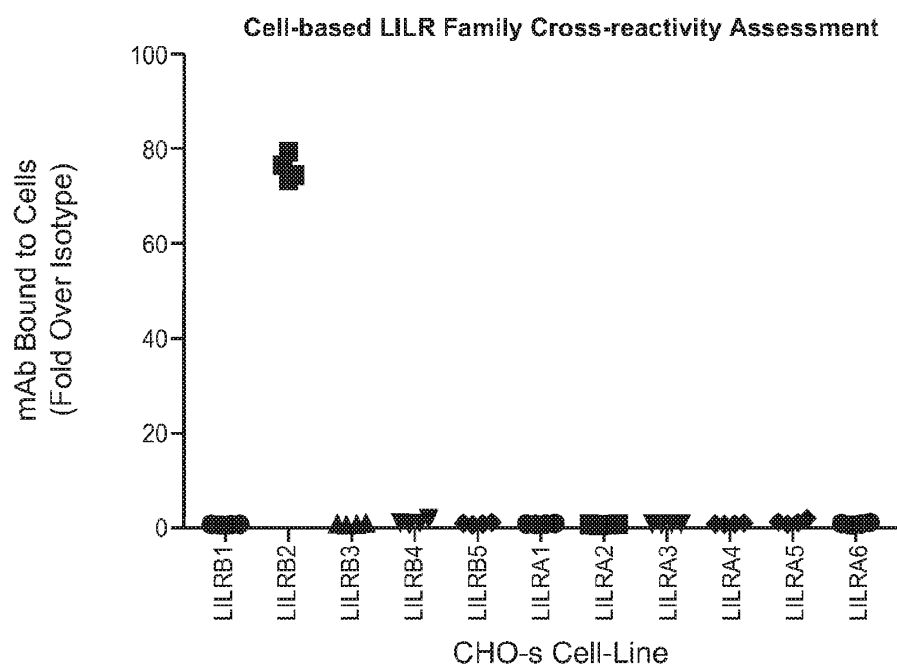
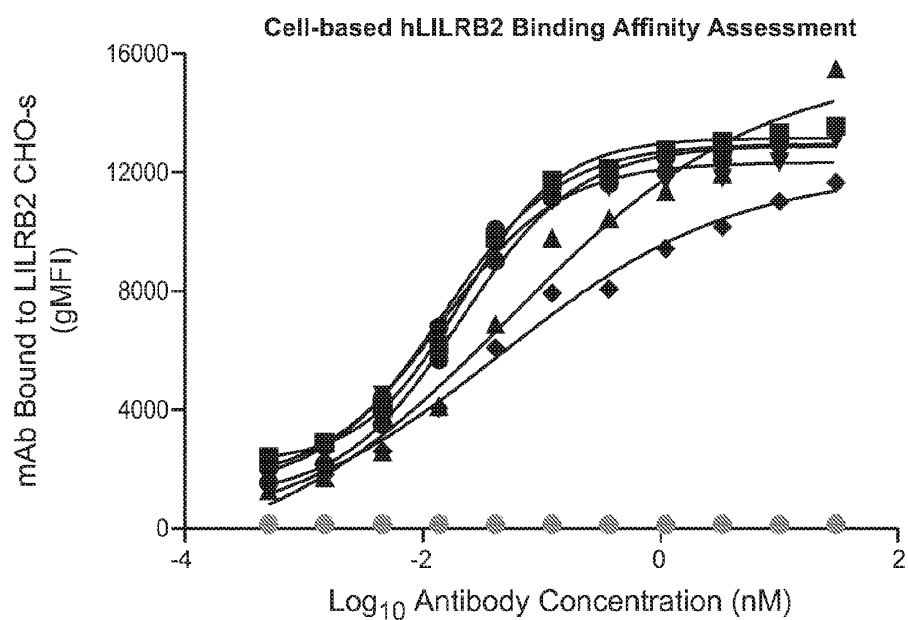
mAb	LILRB1 CHOs binding (fold over iso)	LILRB2 CHOs binding (fold over iso)	LILRB3 CHOs binding (fold over iso)	LILRB4 CHOs binding (fold over iso)	LILRB5 CHOs binding (fold over iso)	LILRA1 CHOs binding (fold over iso)	LILRA2 CHOs binding (fold over iso)	LILRA3 CHOs binding (fold over iso)	LILRA4 CHOs binding (fold over iso)	LILRA5 CHOs binding (fold over iso)	LILRA6 CHOs binding (fold over iso)
J-19.h1	0.79	73.25	1.00	1.22	1.01	0.95	0.88	0.97	0.95	1.34	0.98
J-19.h2	0.73	74.45	0.81	0.90	0.76	0.89	0.66	0.83	0.84	0.86	0.74
J-19.h3	0.84	79.40	0.97	1.16	0.95	1.00	0.83	0.92	0.99	1.22	1.03
J-19.h4	0.87	76.50	1.24	2.02	1.27	0.99	0.96	0.99	1.09	2.14	1.27
isotype	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

FIG. 11A

mAb	EC50 (nM) hLILRB2 CHOs binding	EC50 (nM) HLA-G: LILRB2 blocking	EC50 (nM) HLA-A2: LILRB2 blocking	EC50 (nM) TNFa production	EC50 (nM) IL-6 production	IC50 (nM) IL-10 production	IC50 (nM) CCL2 production
J-19.h1	0.03204	0.162	0.083	0.076	0.085	0.450	0.005
J-19.h2	0.4467	0.122	0.087	0.120	0.186	0.702	0.011
J-19.h3	0.03248	0.113	0.103	0.087	0.083	0.270	5.902
J-19.h4	0.001749	0.131	0.106	0.084	0.091	0.190	0.010
isotype	N/A	N/A	N/A	N/A	N/A	N/A	N/A

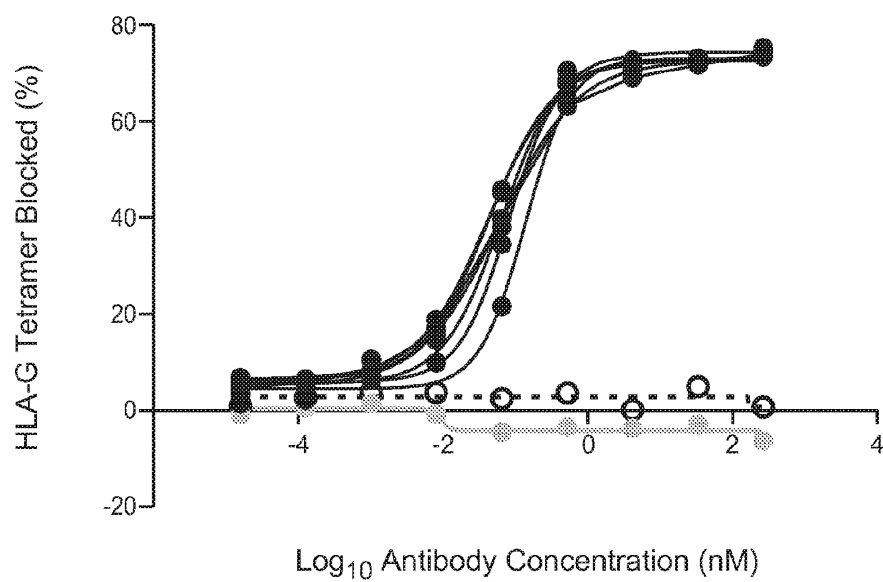
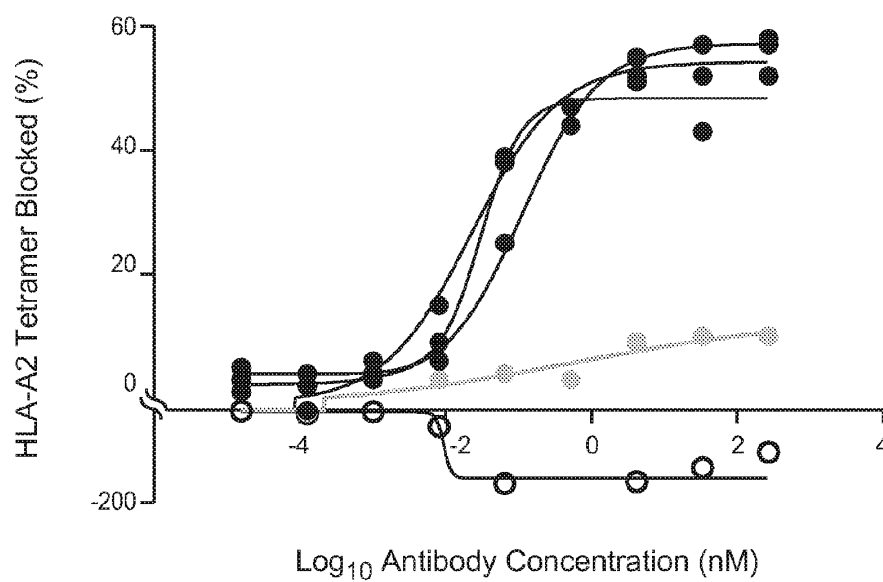
FIG. 11B

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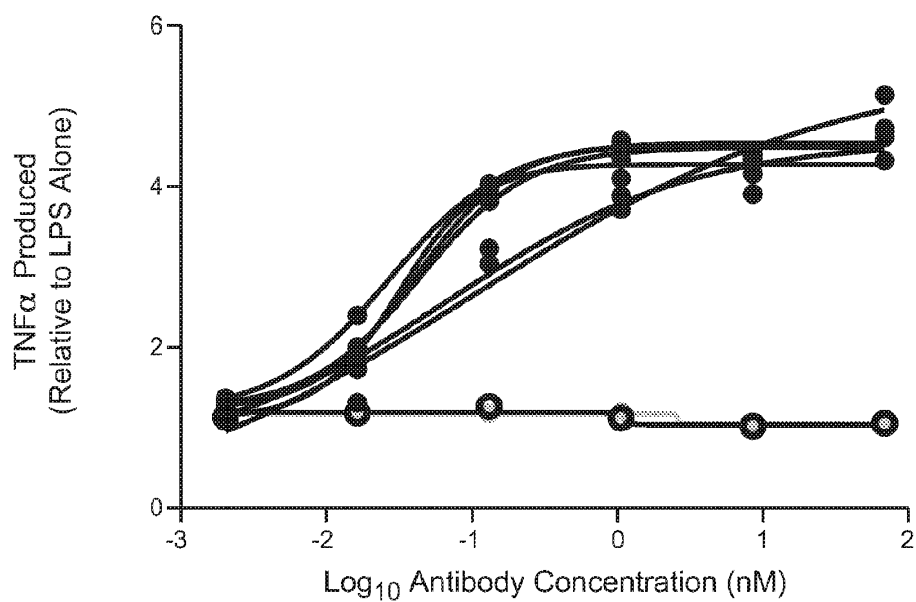
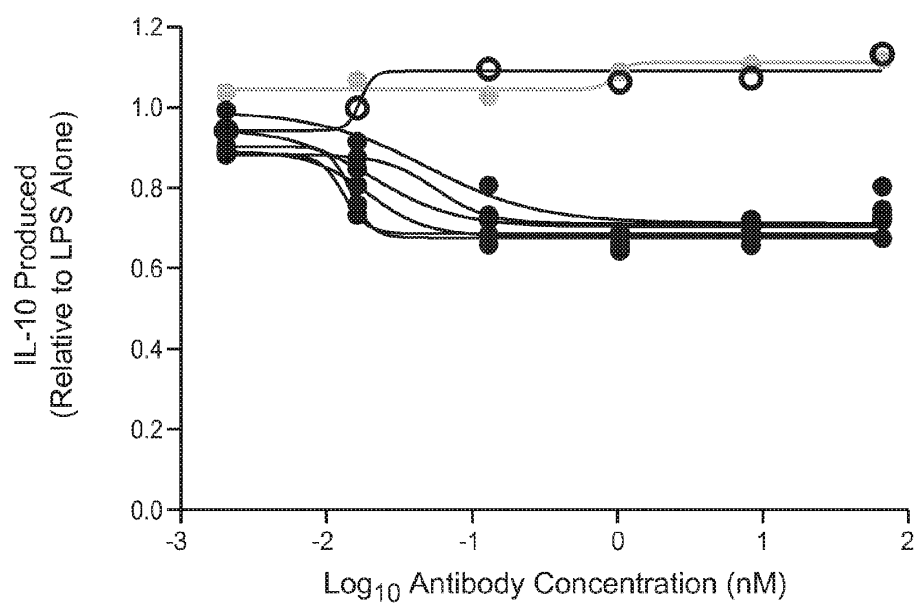
**FIG. 12****FIG. 13**

SUBSTITUTE SHEET (RULE 26)

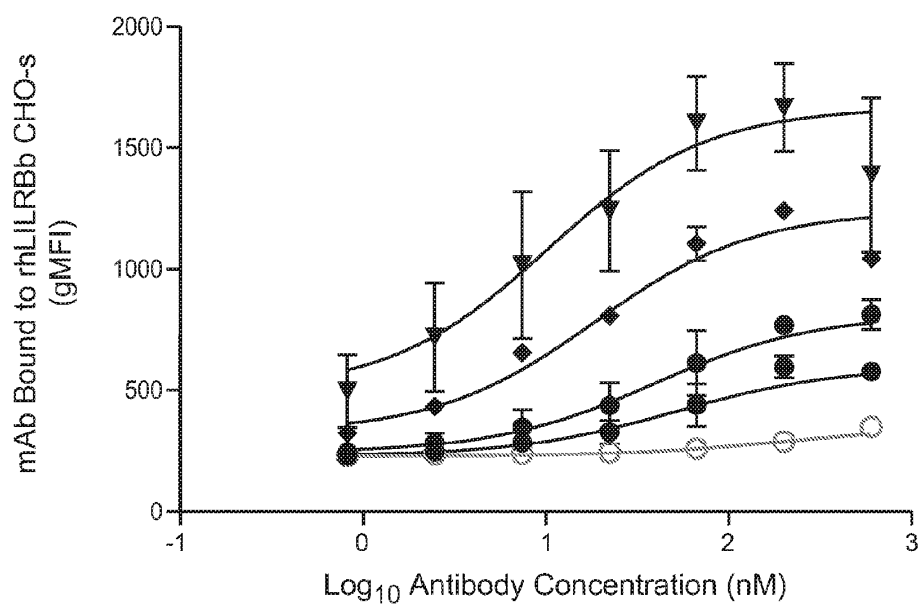
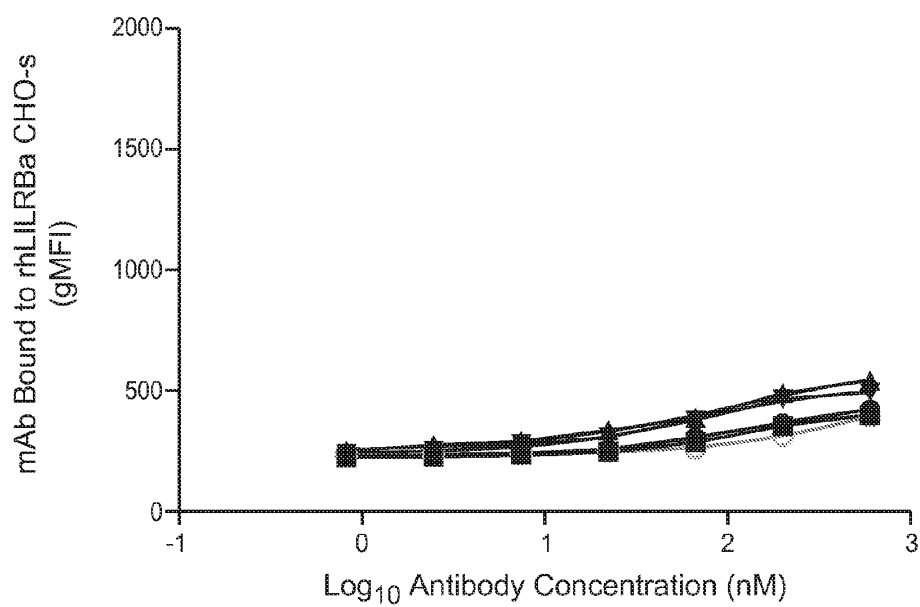
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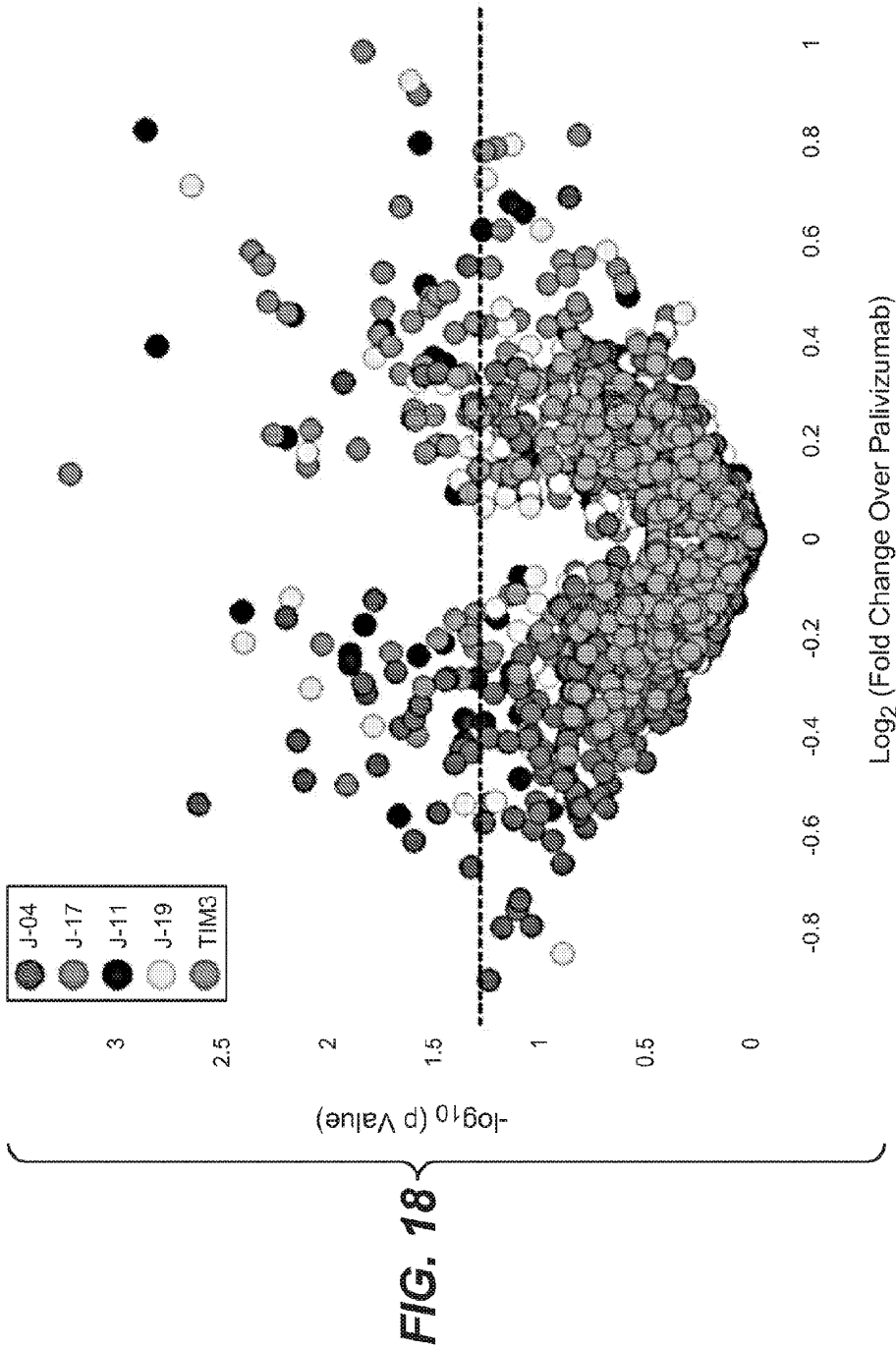
**FIG. 14****FIG. 15**

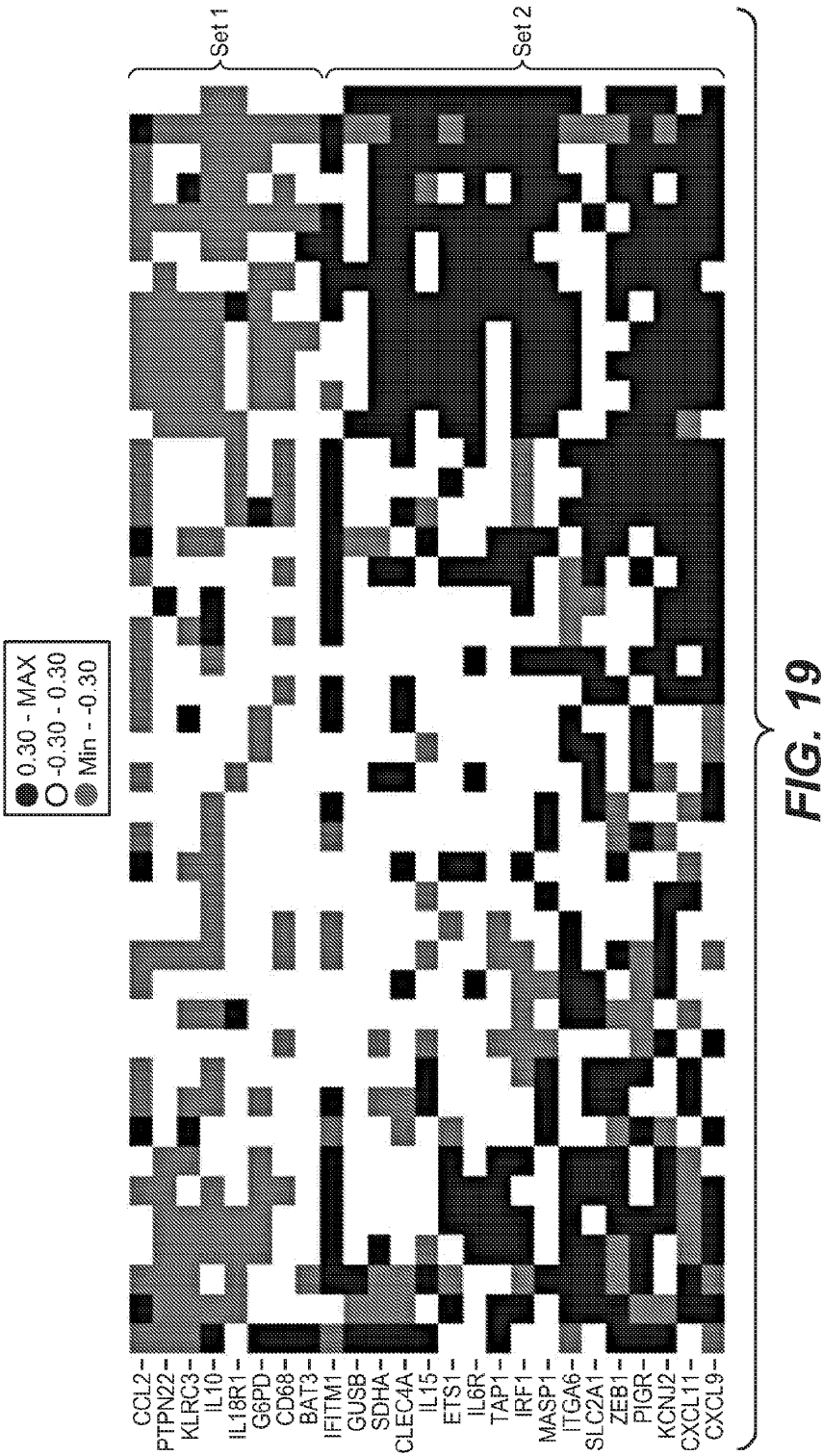
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**FIG. 16A****FIG. 16B**

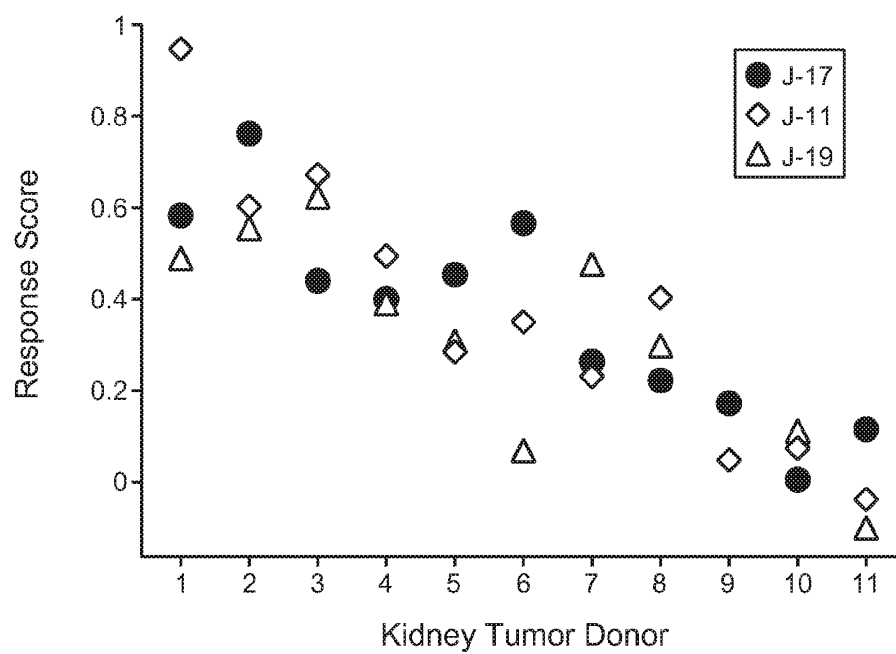
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**FIG. 17A****FIG. 17B**





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**FIG. 20**

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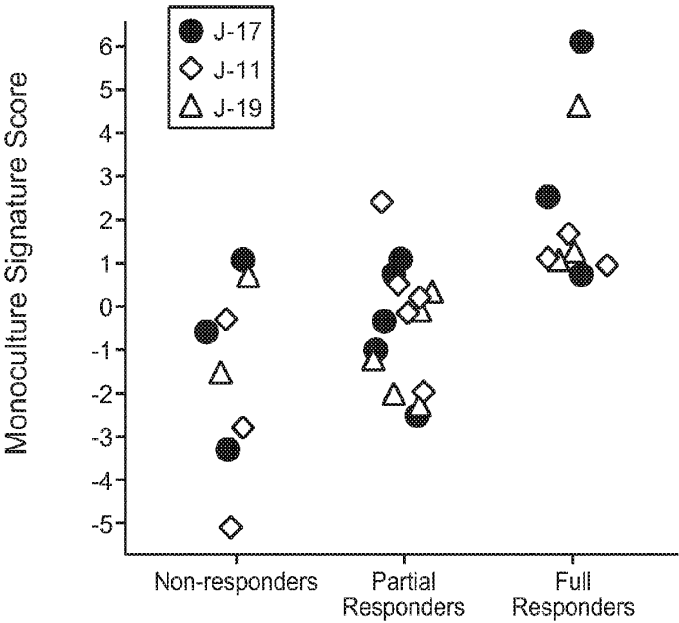


FIG. 21A

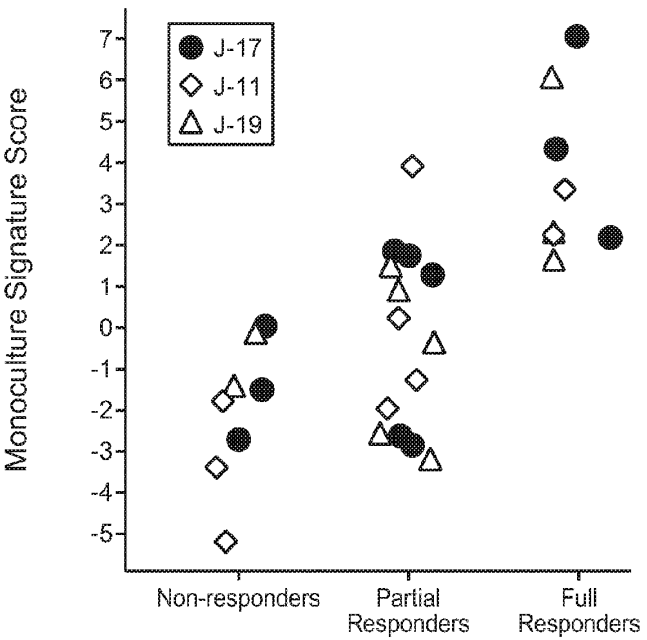
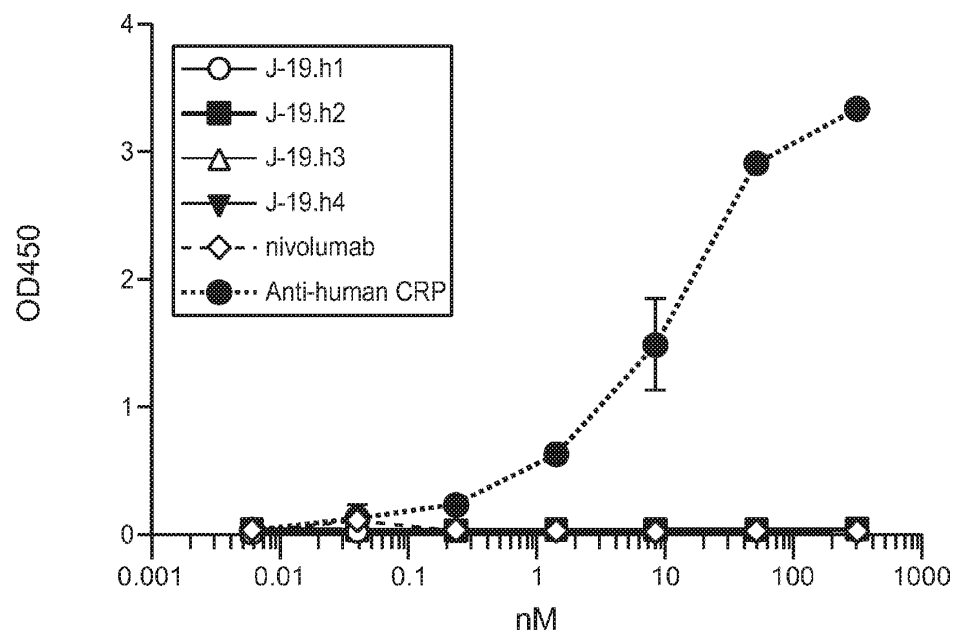


FIG. 21B

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**FIG. 22**

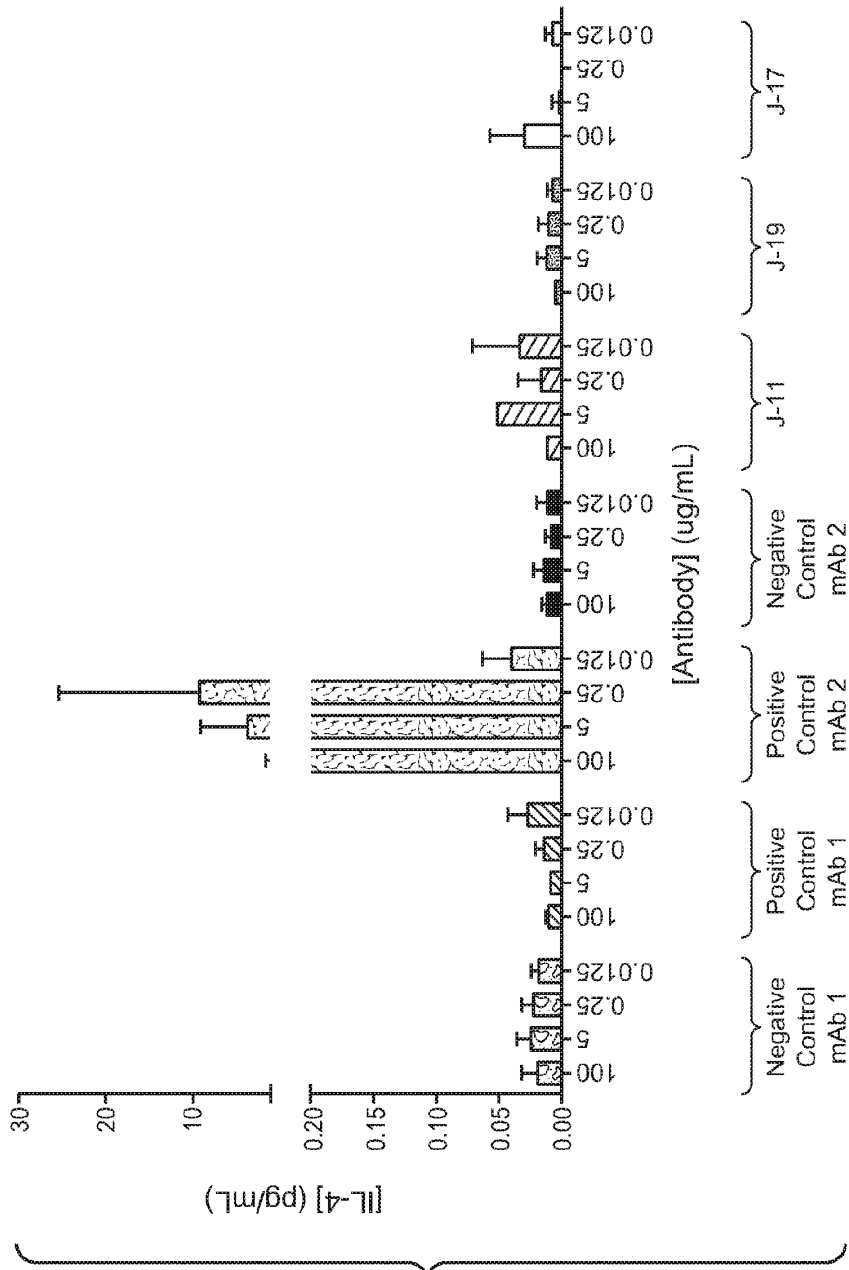
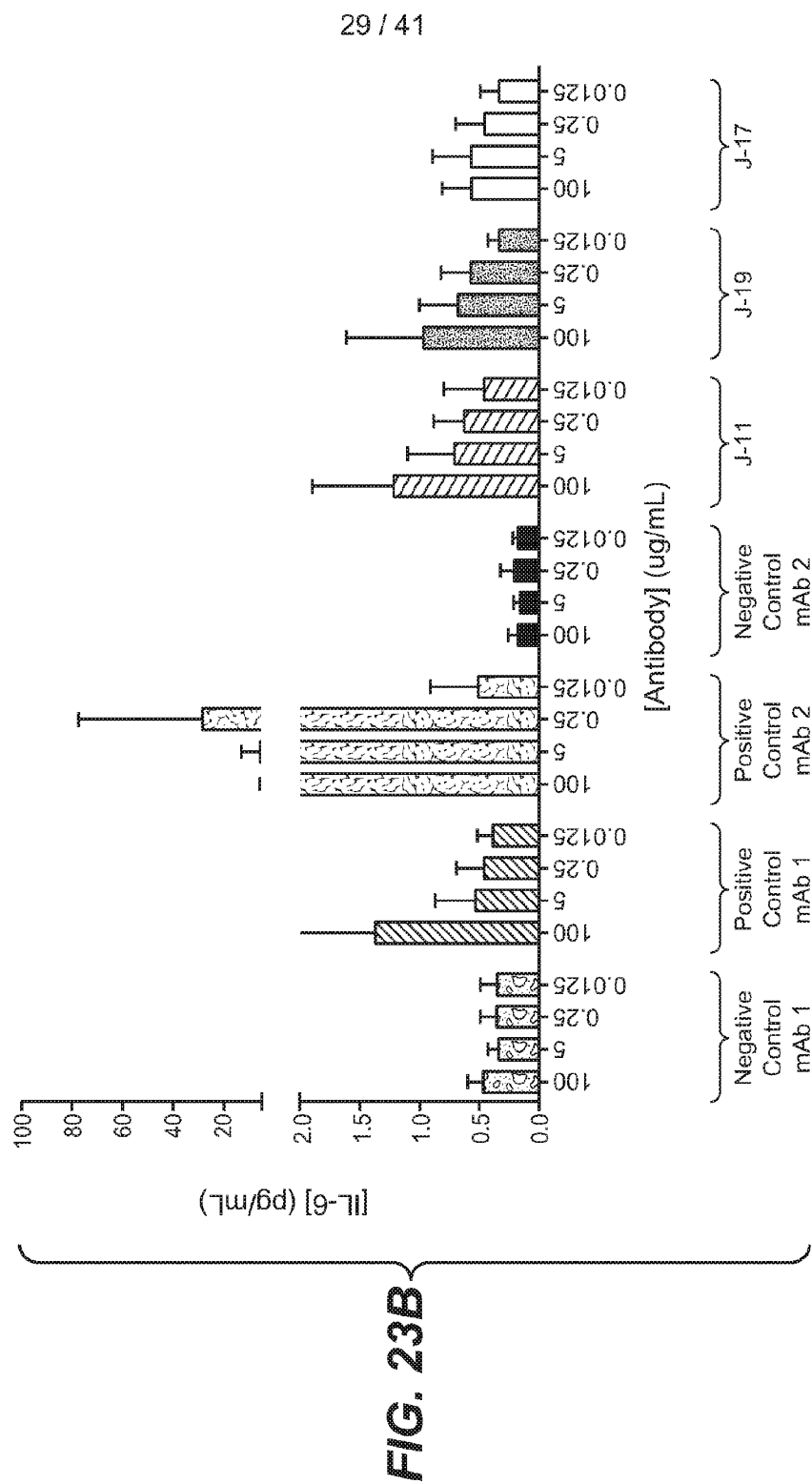


FIG. 23A



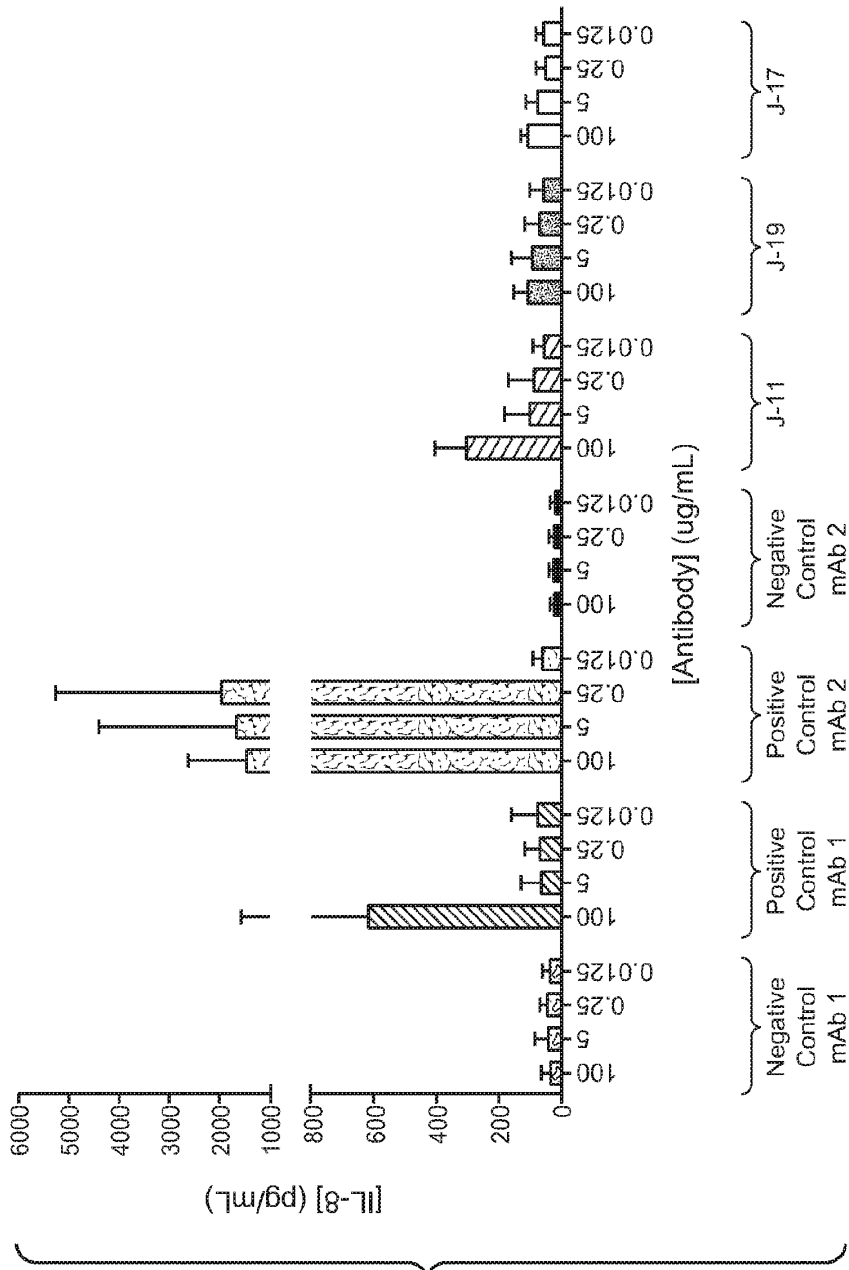


FIG. 23C

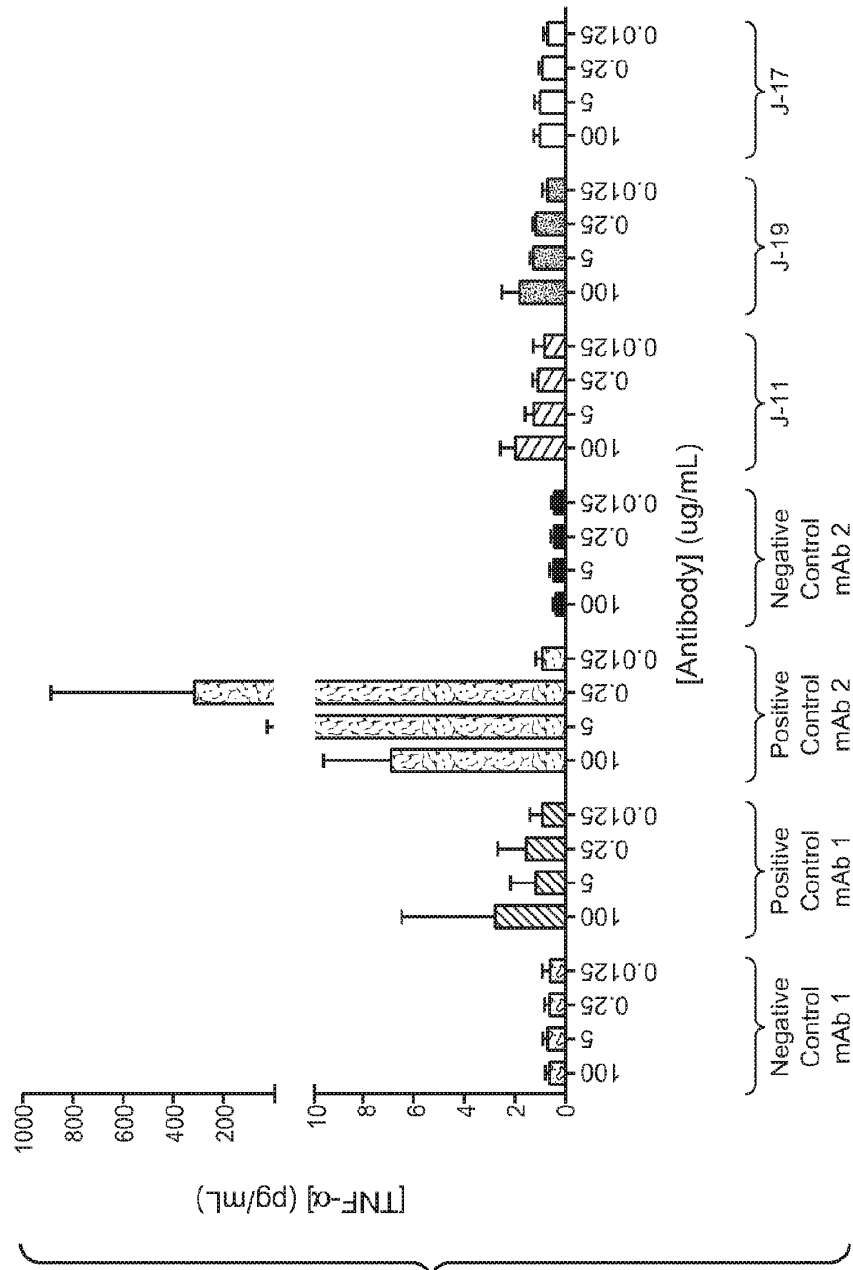


FIG. 23D

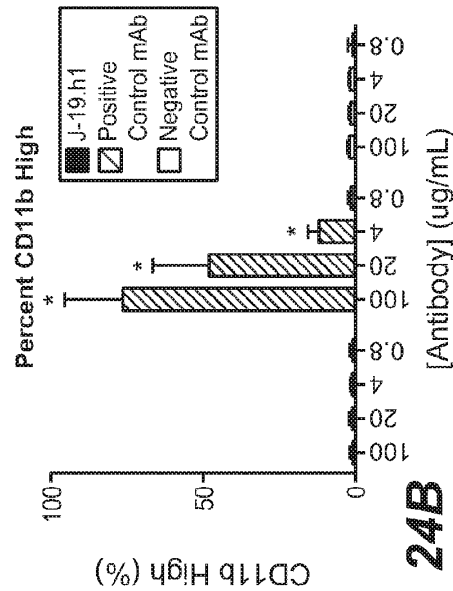


FIG. 24B

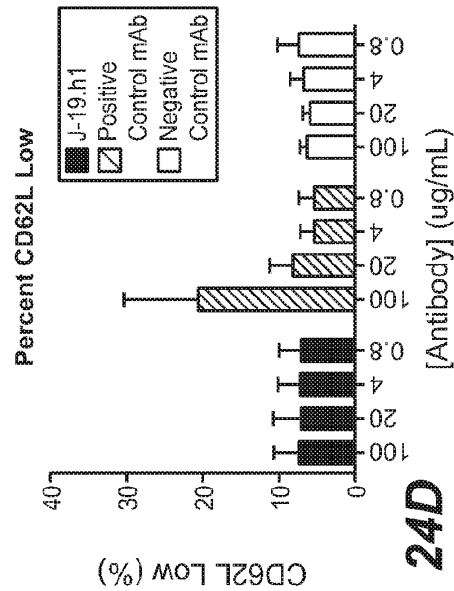


FIG. 24D

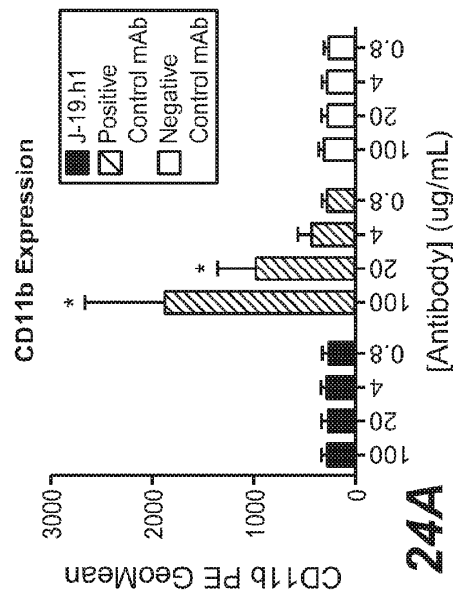


FIG. 24A

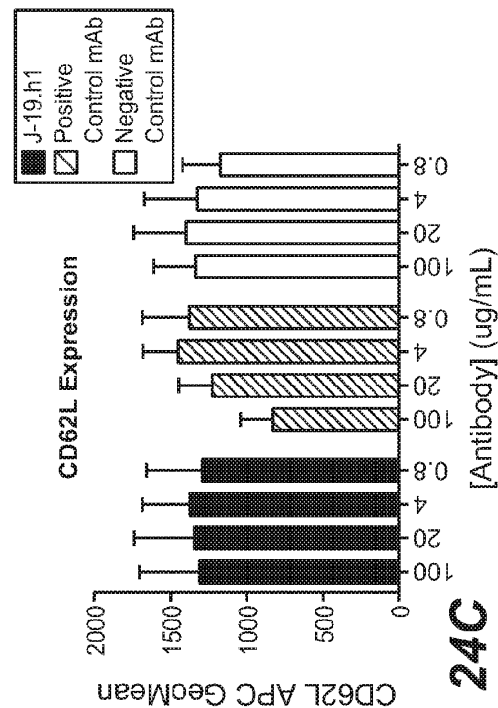
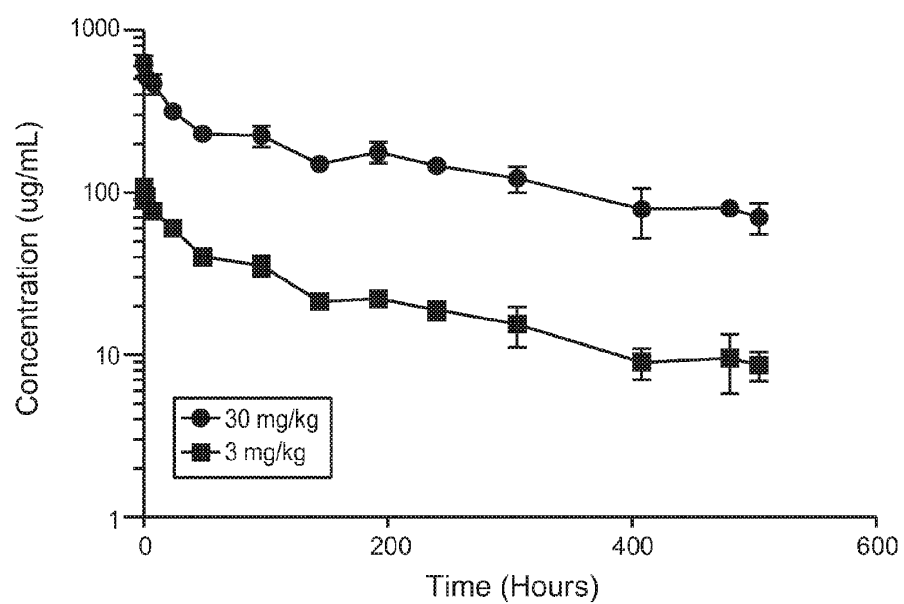


FIG. 24C

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**FIG. 25**

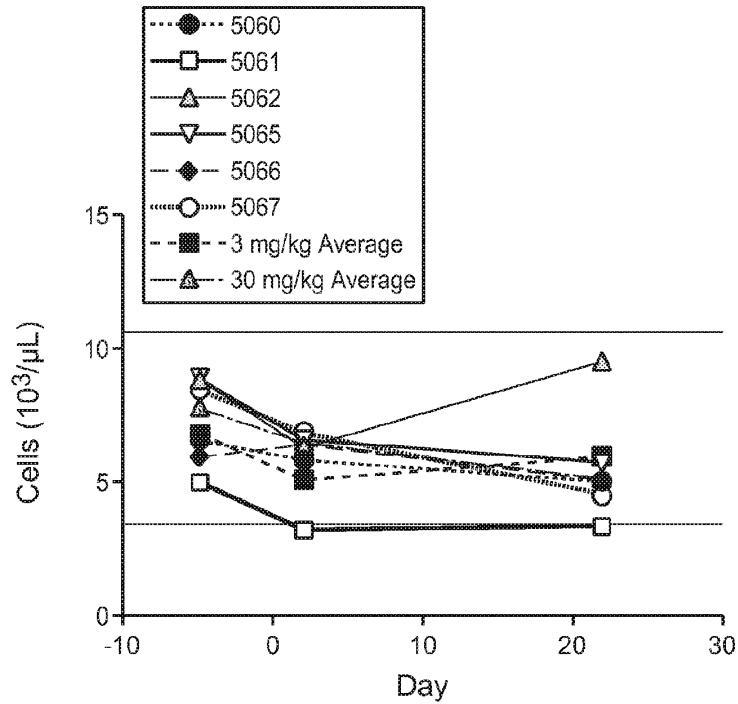


FIG. 26A

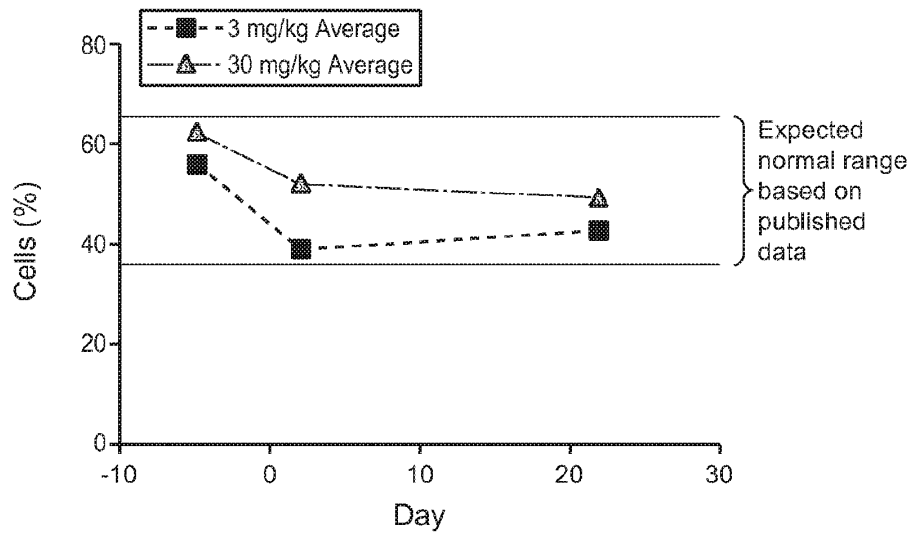
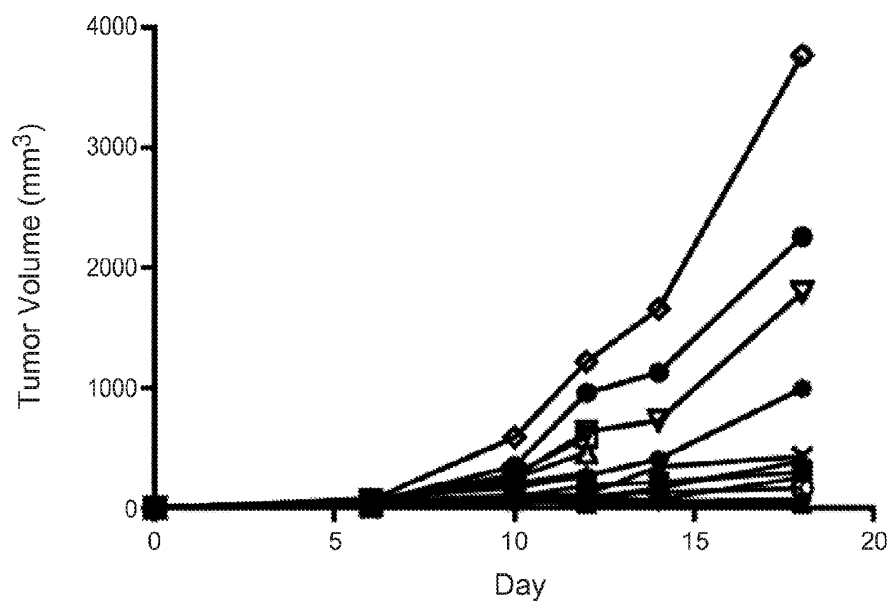
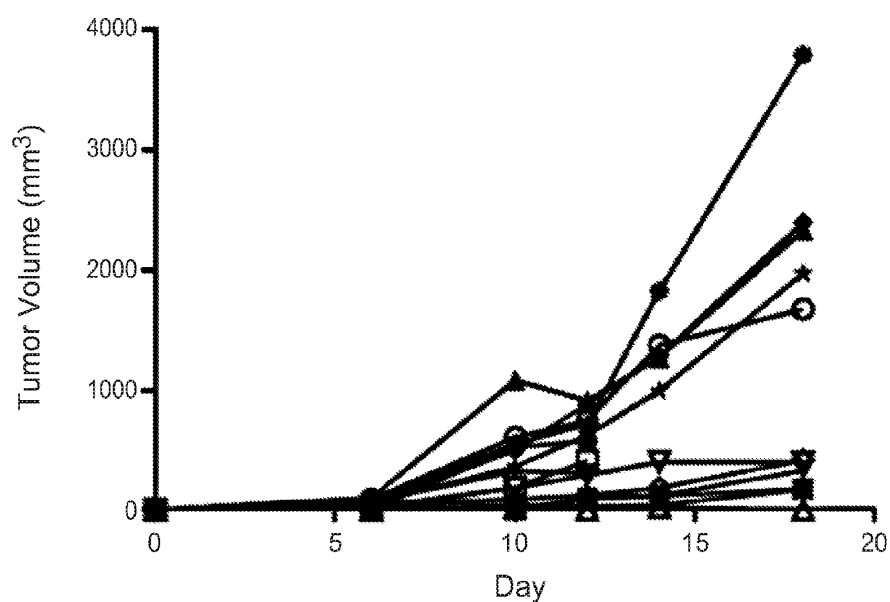
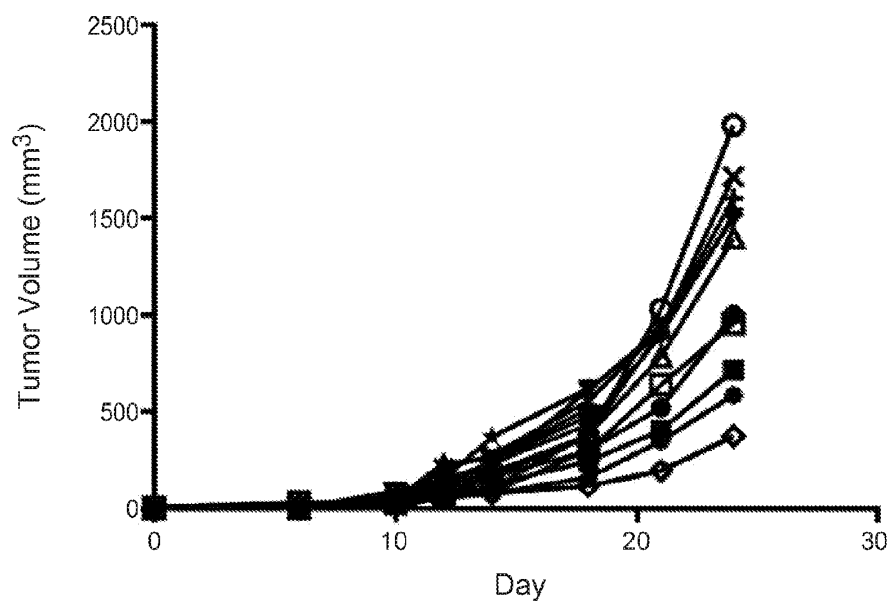
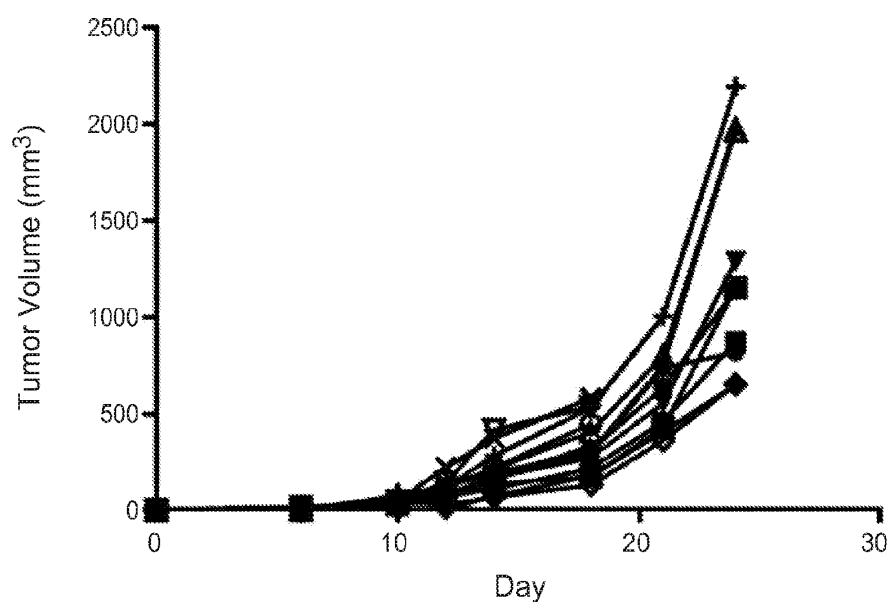


FIG. 26B

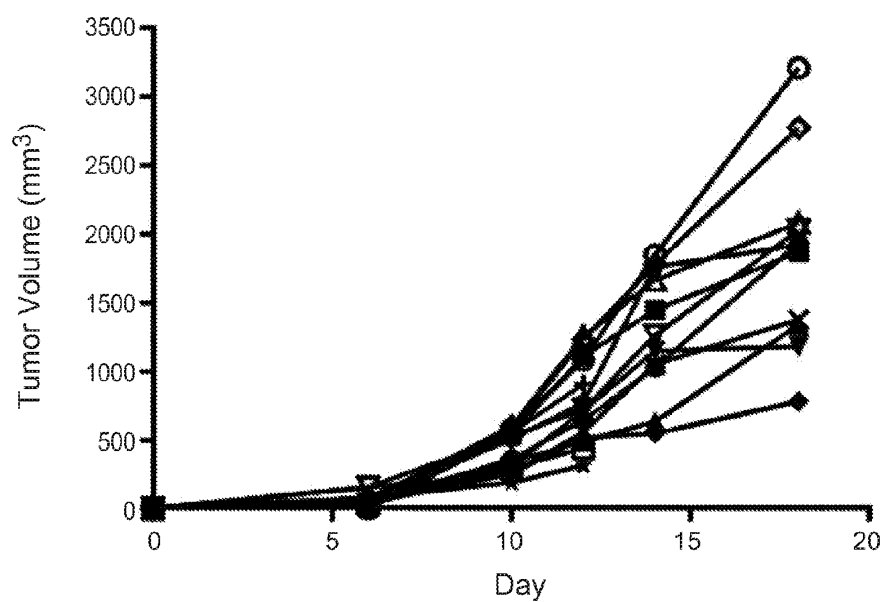
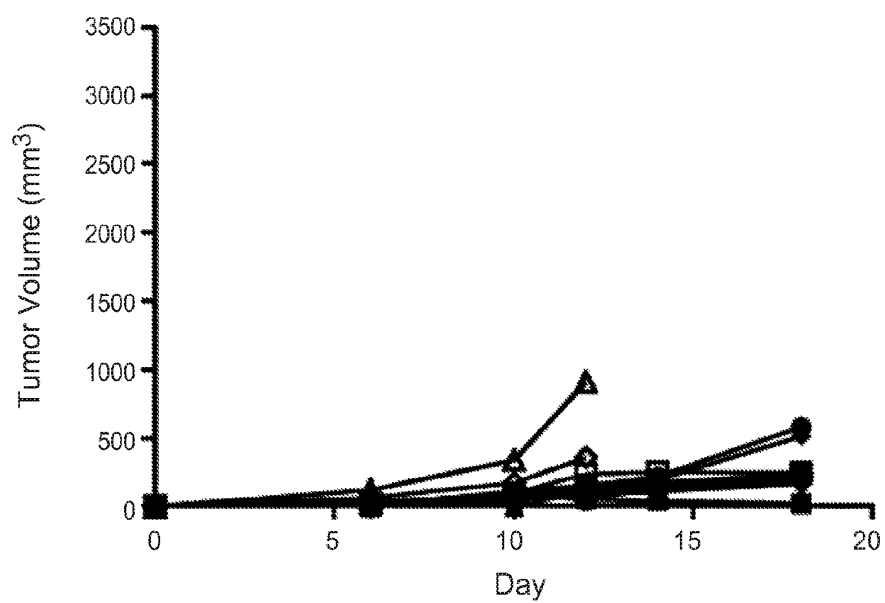
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**FIG. 27A****FIG. 27B**

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**FIG. 28A****FIG. 28B**

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**FIG. 29A****FIG. 29B**

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J-19.h1 Heavy Chain Variable Region

QITLKESGPTLVKPTQTLTLTCTFSGFSLNTYAMGVSW
IRQPPGKALEWLASIWNGNKNYNNPSLKSRLTVTKDT
SKNQVVLMTNMDPVDATYYCAHSRIIR*FTDYVMDA
WGQGTLVTVSS (SEQ ID NO: 53)

J-19.h1 Light Chain Variable Region

DIQMTQSPSSLSTSVGDRVITTCRASEDIYNDLAWYQ
QKPGKAPKLLIYNANSLHTGVASRFSGSGSGTDFTFTI
SSLQPEDVATYFCQQYYDYPLTFGQGGTKLEIK (SEQ
ID NO: 54)

FIG. 30

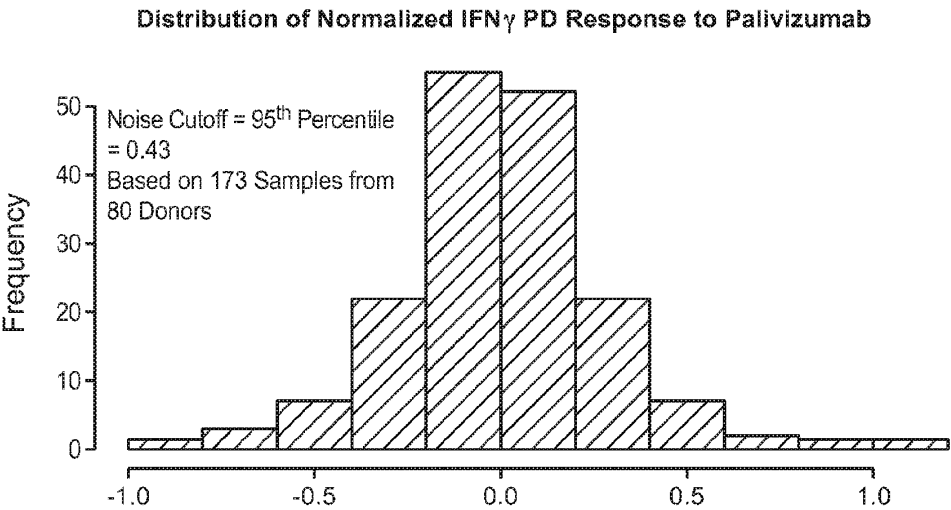


FIG. 31

PD Response Rates to J-19.h1 Across 3 Indications

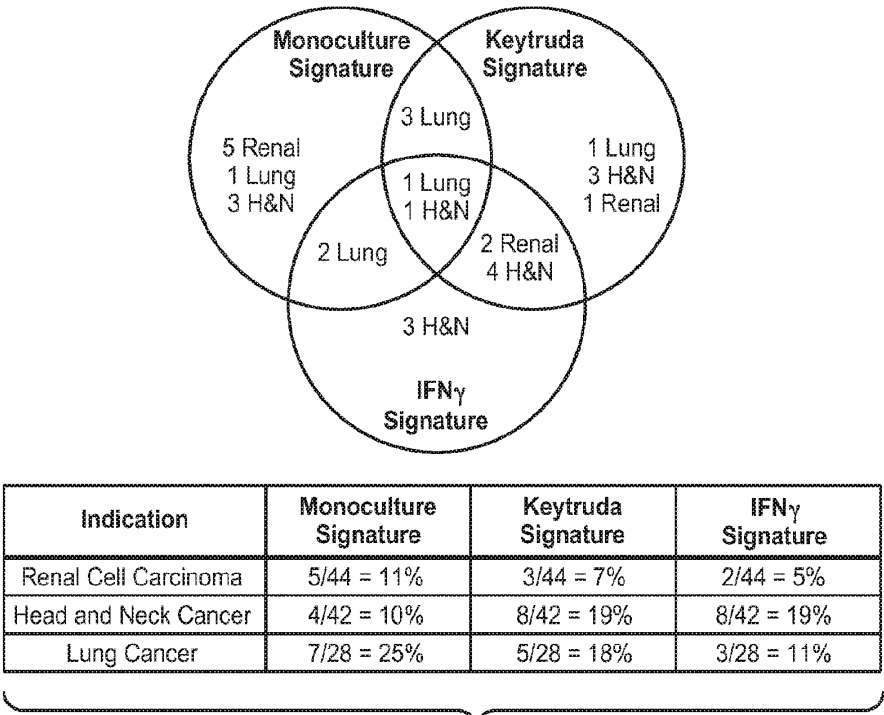


FIG. 32

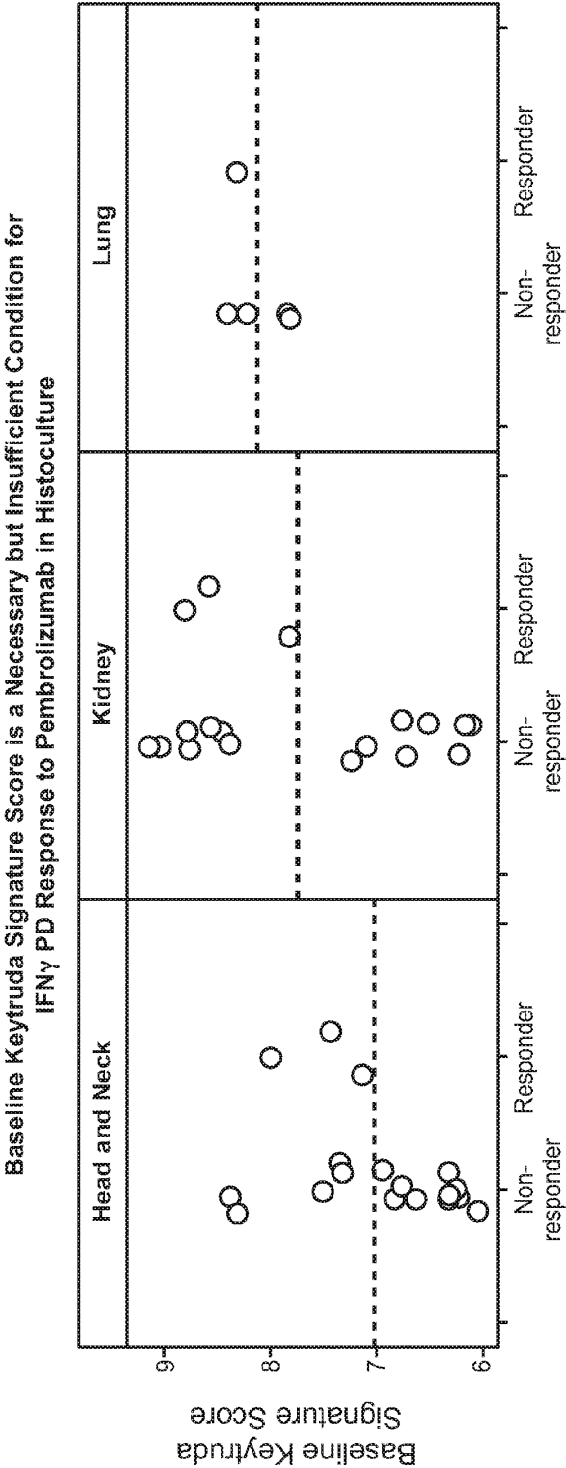


FIG. 33

