

	Ab#	Control 3	Bin 6	Bin 7	Bin 1	Bin 3	Bin 2	Bin 5	
			MBA001	MBN005	MBN001	MBN004	MBN002	MBV002	PBST
	Control 3	-0.2098	0.9789	0.7824	0.8244	-0.0582	0.8321	0.7855	-0.3099
Bin 6	MBA001	0.852	-0.3265	0.5705	0.6645	1.0393	1.4165	0.6581	-0.4274
Bin 7	MBN005	0.9697	1.0029	-0.3881	0.8364	1.1846	1.6827	0.7306	-0.4427
Bin 1	MBN001	1.0304	1.0149	0.7758	-0.2185	1.1801	1.3824	0.7127	-0.2724
Bin 3	MBN004	-0.1677	0.9315	0.8456	0.7465	-0.0564	0.8324	0.7526	-0.2672
Bin 2	MBN002	0.1891	0.6704	0.609	0.5325	0.2701	0.1461	0.5274	-0.053
Bin 5	MBV002	1.1007	1.0253	0.8381	0.9074	1.2824	1.6045	0.0042	-0.0717

FIG. 1A

	CEACAM5	CEACAM1	CEACAM6
Bin1	+	-	-
Bin2	+	-	-
Bin3	+	-	-
Bin4	+	+	-
Bin5	+	-	-
Bin6	+	-	+
Bin7	+	+	-
Bin8	+	+	-

FIG. 1B

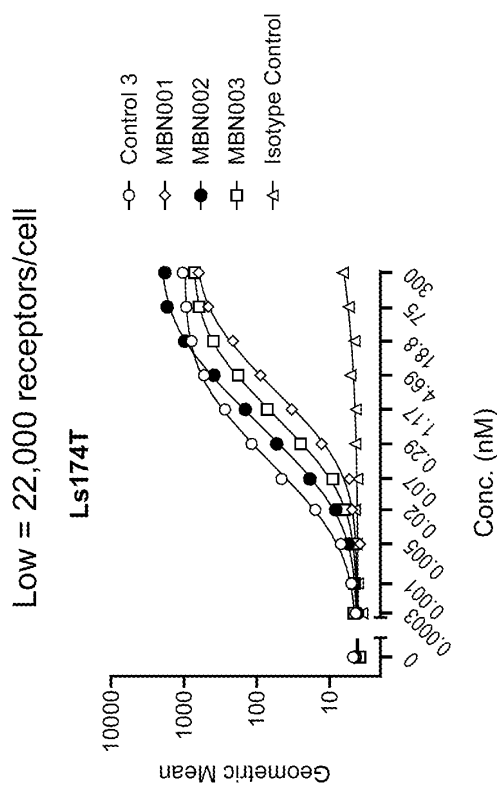


FIG. 2B

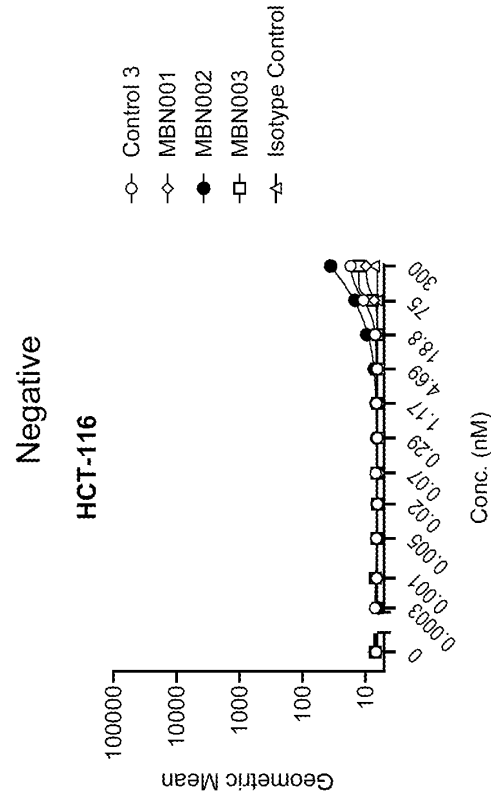


FIG. 2D

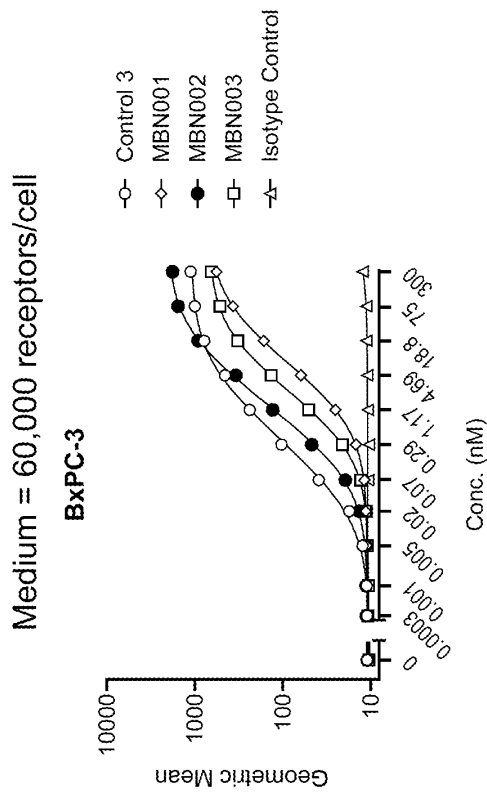


FIG. 2A

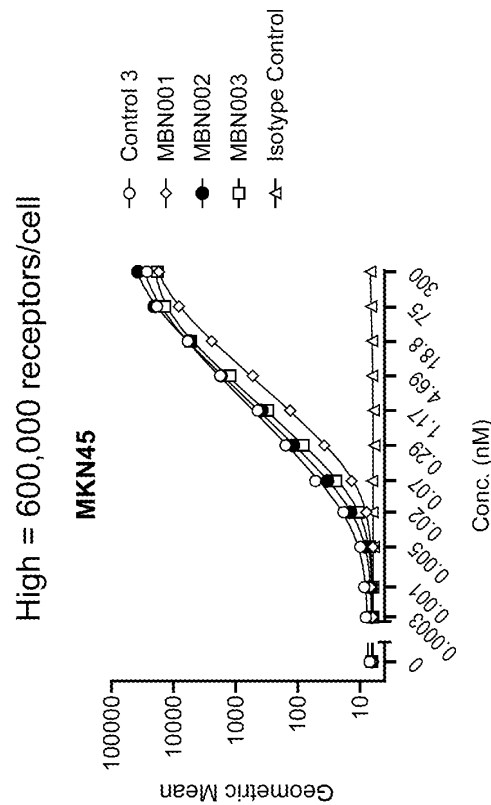


FIG. 2C

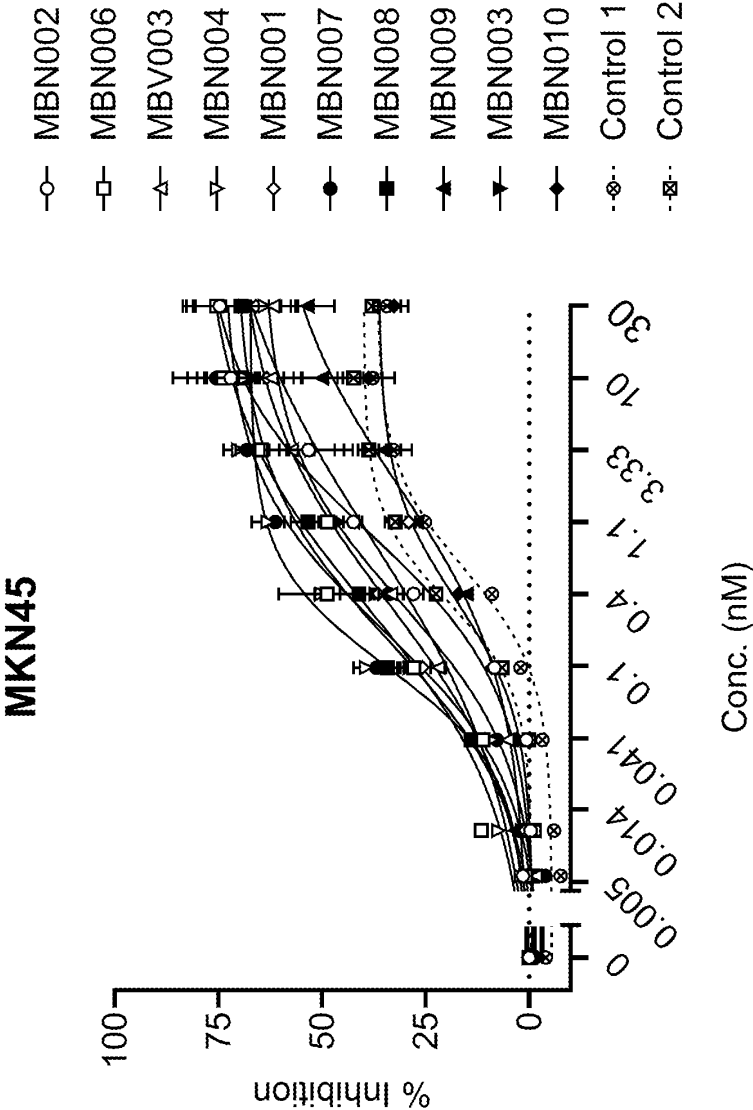


FIG. 3A

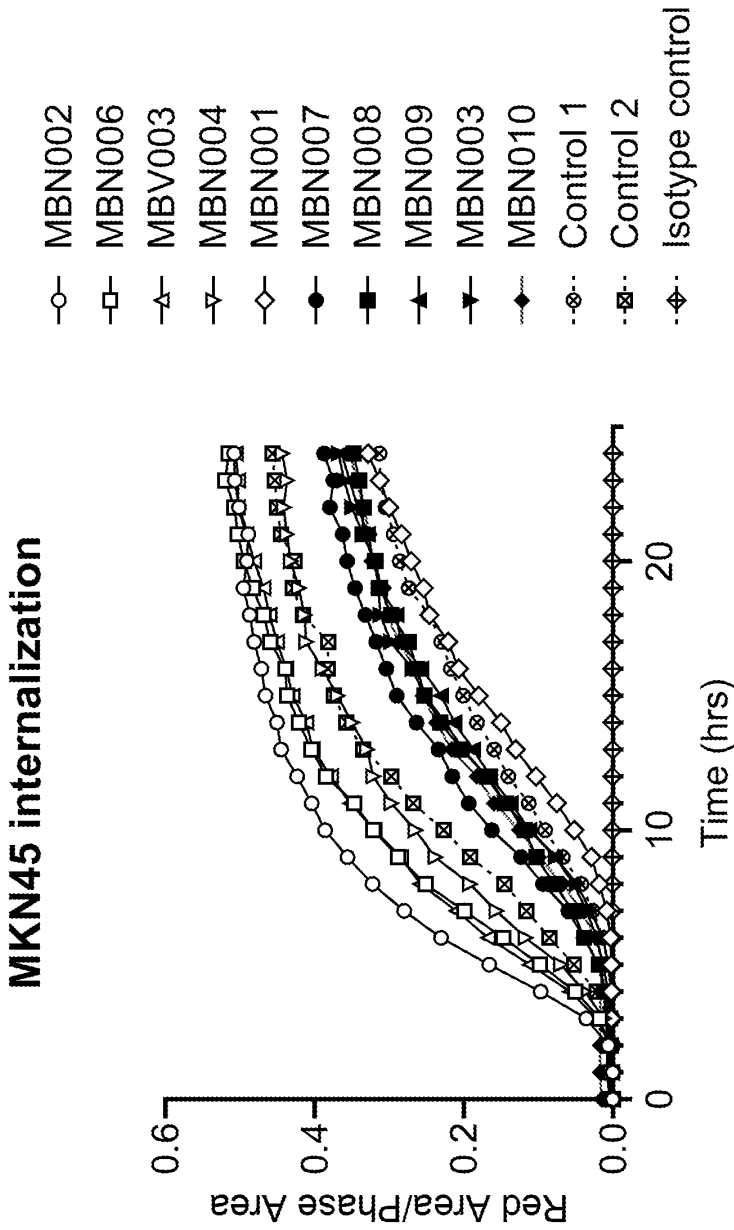


FIG. 3B

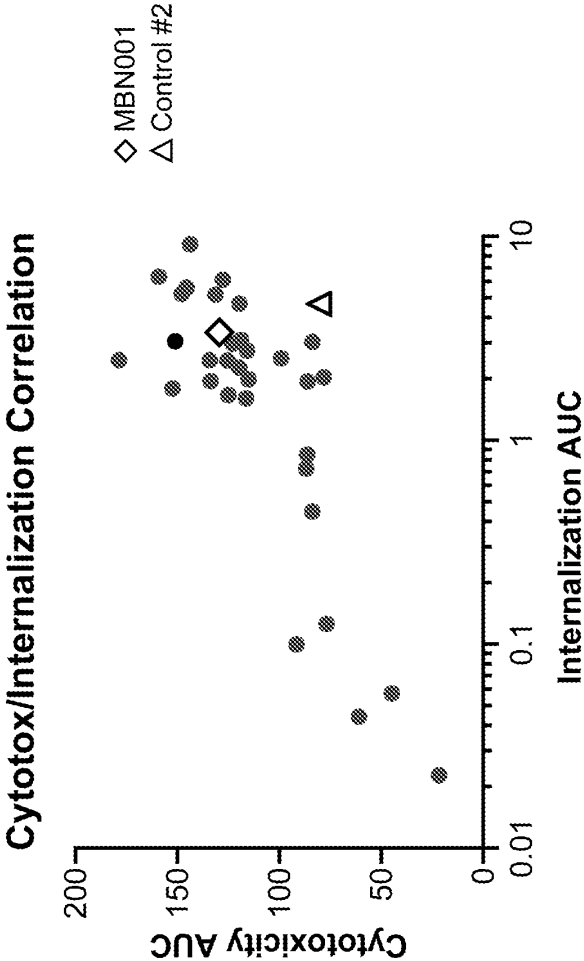


FIG. 3C

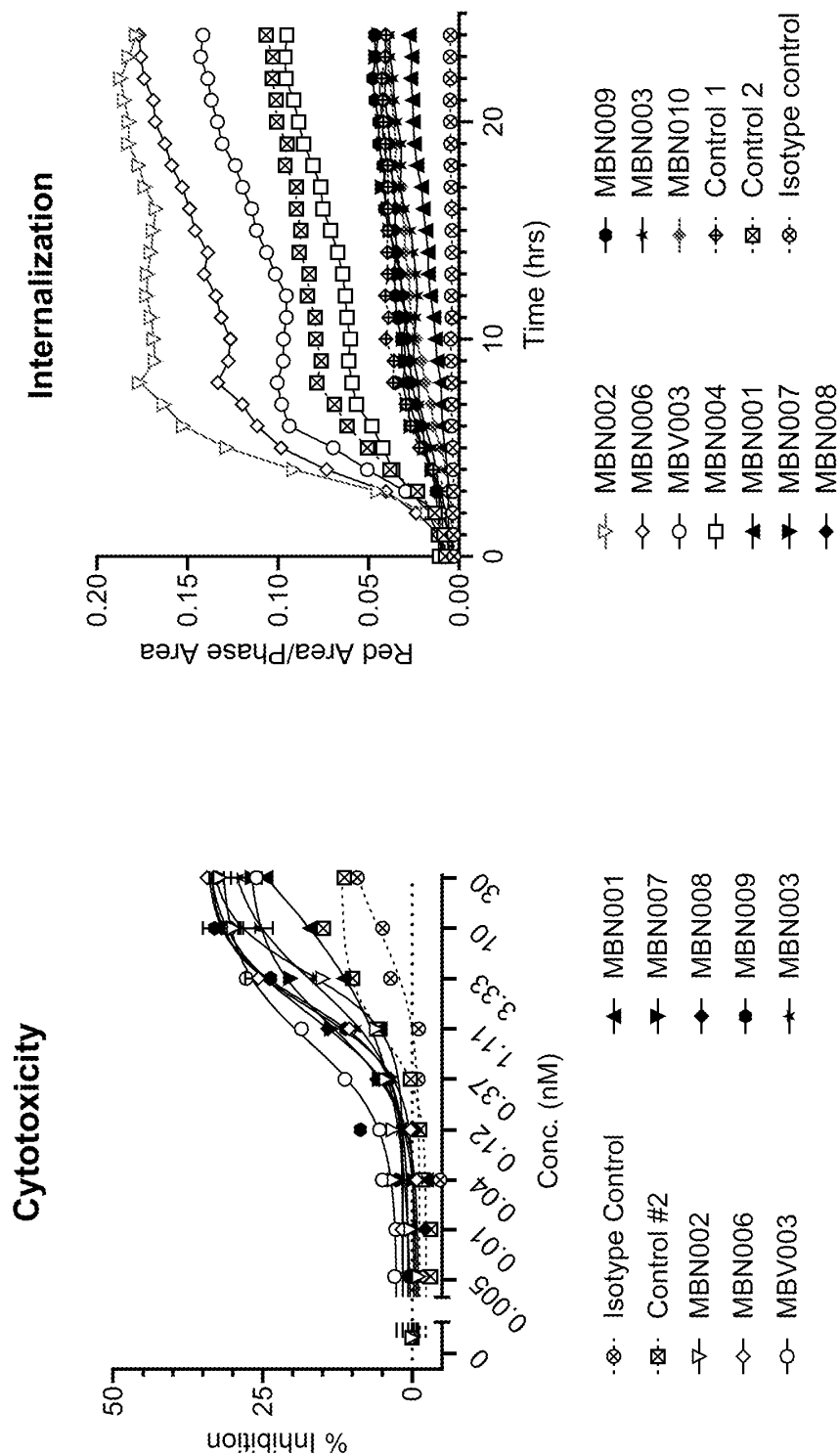


FIG. 4A

FIG. 4B

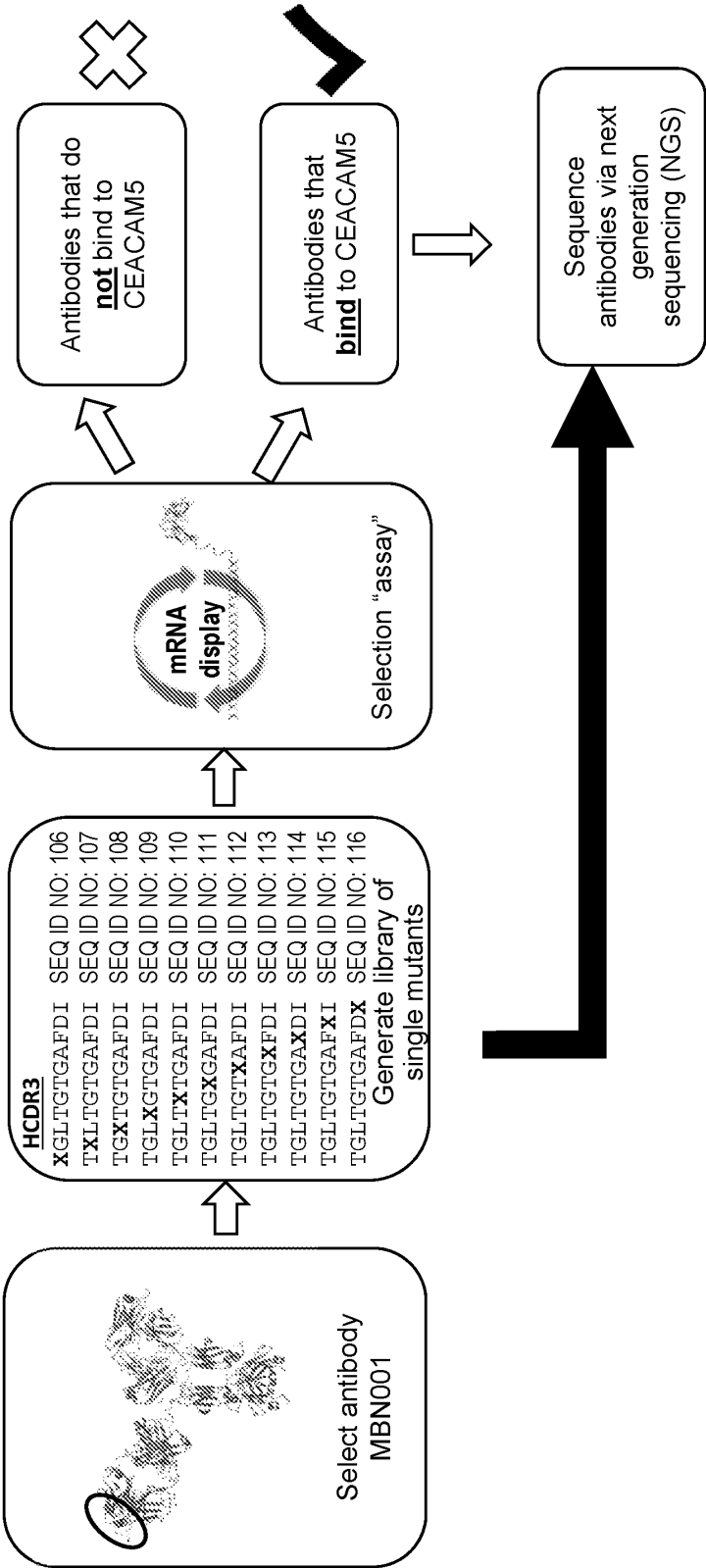


FIG. 5A

Heavy Chain	
HCDR1	26 27 28 29 30 31 32 G I T F S S H SEQ ID NO: 61
HCDR2	49 50 51 52 52a 53 54 55 56 57 58 59 60 61 62 63 64 65 T F I S Y D G S Y K S Y V D S V K G SEQ ID NO: 62
HCDR3	94 95 96 97 98 99 100 100a100b 101 102 T G L T G T G A F D I SEQ ID NO: 63
Light Chain	
LCDR1	24 25 26 27 27a 28 29 30 31 32 33 34 R A S Q S V S S S Y L A SEQ ID NO: 64
LCDR2	50 51 52 53 54 55 56 G A S S R A T SEQ ID NO: 65
LCDR3	89 90 91 92 93 94 95 96 Q Q Y G S S P Y SEQ ID NO: 66

Mutations to germline VH: T7S, S40A, A68T, P84A

FIG. 5B

MBN001 HCDR1
Human CEACAM5

SEQ ID NO: 61																		
Germline Parental	--	F	--	T	--	F	--	S	--	S	--	S	--	H				
	26	27	28	28	29	30	31	32										
Normalized Enrichment Ratio																		
*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.51	0.00					
P	0.06	0.07	0.28	0.00	0.00	0.33	0.07	0.45										
G	1.00	0.04	1.32	0.03	0.53	0.16	0.02											
A	0.46	0.08	0.92	0.00	0.24	0.38	0.00											
C	0.35	0.00	1.45	0.16	0.36	0.76	0.00											
S	0.26	0.00	1.11	0.03	1.00	1.00	0.09											
T	0.67	0.05	1.00	0.00	0.43	0.22	0.09											
V	0.49	0.28	0.79	0.12	0.24	0.29	0.12											
L	0.18	1.25	3.86	0.02	0.25	0.75	0.50											
I	0.17	1.00	3.29	0.07	0.45	2.68	0.17											
M	0.09	0.27	3.97	0.00	0.42	1.67	0.08											
K	0.62	0.15	0.32	0.20	0.00	0.42	0.05											
R	0.44	0.09	3.55	0.03	0.18	0.35	0.10											
H	0.34	0.00	2.55	0.00	0.00	5.51	1.00											
F	0.09	0.09	4.12	1.00	0.00	8.08	0.16											
Y	0.40	0.00	8.19	1.24	0.52	15.50	0.59											
W	0.20	0.09	0.00	0.25	0.42	14.41	0.00											
N	0.51	0.08	1.91	0.00	1.24	0.94	0.68											
D	0.44	0.00	3.73	0.00	4.06	2.70	0.17											
E	0.67	0.00	1.64	0.13	0.86	8.62	0.08											
Q	0.54	0.00	1.10	0.00	0.40	1.52	0.25											

Legend

Favorable	>2
Neutral	} 0.5 to 2
Unfavorable	<0.5

FIG. 5C

MBN001 HCDR1
Cynomolgus CEACAM5

SEQ ID NO: 61												
Germline	~	F			~	~	~	~	~	~	~	Y
Parental	G	I	T	F	T	F	S	S	S	S	H	H
	26	27	28	29	30	31	32					
Normalized Enrichment Ratio												
*	0.19	0.00	0.00	0.00	0.00	0.00	0.76	0.00	0.00	0.00	0.00	0.00
P	0.00	0.16	0.44	0.00	0.00	0.00	0.26	0.66	0.00	0.00	0.00	0.66
G	1.00	0.10	0.97	0.19	0.72	0.35	0.35	0.22	0.00	0.00	0.00	0.22
A	0.43	0.17	0.52	0.31	0.00	0.29	0.29	0.06	0.00	0.00	0.00	0.06
C	0.23	0.17	2.44	0.19	2.14	0.43	0.43	0.17	0.00	0.00	0.00	0.17
S	0.70	0.10	1.88	0.10	1.00	1.00	1.00	0.08	0.00	0.00	0.00	0.08
T	0.53	0.00	1.00	0.44	0.74	1.27	1.27	0.08	0.00	0.00	0.00	0.08
V	0.40	0.21	1.74	0.30	0.58	0.89	0.89	0.12	0.00	0.00	0.00	0.12
L	0.33	1.19	3.59	0.22	0.56	0.58	0.58	0.52	0.00	0.00	0.00	0.52
I	0.35	1.00	8.73	0.29	0.19	1.86	1.86	0.38	0.00	0.00	0.00	0.38
M	0.48	0.27	3.30	0.28	0.35	0.67	0.67	0.29	0.00	0.00	0.00	0.29
K	0.57	0.14	0.41	0.00	0.35	0.66	0.66	0.11	0.00	0.00	0.00	0.11
R	0.44	0.16	1.63	0.06	0.57	0.52	0.52	0.19	0.00	0.00	0.00	0.19
H	0.50	0.13	4.28	0.00	0.27	3.48	3.48	1.00	0.00	0.00	0.00	1.00
F	0.14	0.19	32.19	1.00	0.00	4.46	4.46	0.29	0.00	0.00	0.00	0.29
Y	0.58	0.00	48.51	0.85	0.00	7.19	7.19	0.69	0.00	0.00	0.00	0.69
W	0.28	0.11	1.29	0.38	2.71	17.45	17.45	0.15	0.00	0.00	0.00	0.15
N	0.71	0.13	6.49	0.00	0.00	0.91	0.91	0.66	0.00	0.00	0.00	0.66
D	0.33	0.00	1.51	0.00	1.27	1.07	1.07	0.26	0.00	0.00	0.00	0.26
E	0.57	0.11	0.69	0.00	0.50	3.23	3.23	0.31	0.00	0.00	0.00	0.31
Q	0.36	0.30	1.51	0.00	0.00	0.63	0.63	0.46	0.00	0.00	0.00	0.46

Legend

Favorable

Neutral

Unfavorable

>2

0.5 to 2

<0.5

FIG. 5D

		SEQ ID NO: 62														
Germline Parental	A	V	I	S	Y	D	G	S	N	K	Y	S	Y	A	D	G
	T	F	50	51	52	52a	53	54	55	56	57	58	59	60	61	65
Normalized Enrichment Ratio																
*	0.00	0.00	0.00	0.00	0.00	0.24	0.40	0.00	0.00	0.23	0.20	0.60	0.52	0.18	0.15	0.00
P	0.27	0.06	0.06	0.40	0.07	0.16	0.00	0.13	0.00	2.15	0.39	0.25	0.49	1.59	0.92	0.19
G	0.55	0.27	0.69	0.08	0.00	0.12	1.00	0.06	0.08	0.44	1.21	0.81	0.35	0.86	1.06	0.43
A	0.97	0.19	3.85	0.24	0.00	0.08	1.80	0.08	0.05	0.90	0.57	1.10	0.50	0.76	0.71	0.32
C	0.70	0.53	0.44	0.07	0.13	0.09	1.31	0.05	0.09	1.28	1.27	0.90	0.67	1.05	1.06	0.32
S	0.84	0.16	3.59	1.00	0.06	0.10	1.90	1.00	0.17	0.73	1.00	1.14	0.76	0.91	1.00	0.24
T	1.00	0.14	1.94	2.58	0.00	0.11	0.59	0.56	0.07	1.54	4.02	1.12	0.74	0.68	1.34	0.24
V	1.19	0.35	1.75	1.39	0.05	0.09	0.15	0.06	0.43	2.41	1.21	0.94	1.00	1.03	1.06	0.20
L	1.26	0.33	0.85	0.09	0.05	0.14	0.26	0.07	1.27	3.34	7.72	1.57	1.41	0.88	0.85	0.30
I	1.39	0.24	1.00	0.11	0.13	0.20	0.07	0.05	3.76	3.85	4.67	1.34	1.47	0.66	0.79	0.41
M	0.87	1.40	0.69	0.00	0.11	0.17	0.58	0.08	3.55	1.99	5.92	1.62	1.25	0.62	1.14	0.45
K	0.34	0.00	0.19	0.00	0.00	0.11	0.24	0.00	0.00	1.00	4.57	0.52	0.37	0.79	0.66	1.00
R	0.35	0.06	0.05	0.03	0.00	0.06	0.41	0.10	0.00	1.13	1.15	1.40	0.38	0.75	0.96	0.86
H	0.33	0.00	0.00	0.37	0.31	0.11	0.32	0.00	0.31	1.59	0.60	1.75	0.48	0.48	1.41	1.30
F	0.99	1.00	0.19	0.15	0.41	0.09	0.19	0.07	0.39	1.22	0.96	1.42	0.68	0.89	0.79	1.78
Y	1.02	0.87	0.25	0.10	1.00	0.25	0.39	0.17	1.00	1.81	0.12	1.00	0.69	0.84	0.91	1.59
W	0.35	0.39	0.06	0.06	0.18	0.09	0.35	0.11	0.79	1.39	1.22	1.07	0.76	1.37	0.81	2.74
N	2.00	0.06	0.16	0.00	0.09	0.14	0.24	0.11	0.09	0.97	0.68	0.61	0.36	0.88	0.62	1.50
D	1.02	0.17	1.09	0.00	0.14	1.00	0.32	0.06	0.00	0.70	0.05	0.61	0.57	1.00	1.00	1.09
E	0.96	0.57	0.93	0.00	0.00	0.15	1.06	0.00	0.00	1.45	0.00	0.70	0.83	1.33	0.66	0.60
Q	0.48	0.21	0.11	0.00	0.00	0.21	1.97	0.00	0.57	0.21	9.58	1.91	0.46	0.72	0.76	0.62

Legend

Favorable	>2
Neutral	} 0.5 to 2
Unfavorable	<0.5

FIG. 5E

MBN001 HCDR2
Cynomolgus CEACAM5

SEQ ID NO: 62

Germline Parental	A	V	T	F	I	S	Y	D	G	S	N	Y	Y	A	D	S	V	K	G
	49	50	51	52	52a	53	54	55	56	57	58	59	60	61	62	63	64	65	
Normalized Enrichment Ratio																			
*	0.00	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00	0.59	0.54	1.38	0.49	0.00	0.15	0.00	0.00	0.51	0.00
P	0.58	0.32	0.11	0.00	0.12	0.32	0.16	0.23	0.40	1.50	1.42	0.24	0.86	0.88	1.15	0.79	0.78	1.01	
G	0.49	0.18	1.22	0.38	0.07	0.27	1.00	0.19	0.10	0.43	1.02	0.75	0.31	1.03	0.77	0.62	0.61	1.00	
A	0.93	0.22	4.51	0.26	0.00	0.18	1.75	0.19	0.06	0.66	1.27	1.29	1.05	1.65	1.04	0.95	0.60	0.96	
C	0.68	0.44	0.45	0.17	0.13	0.23	1.31	0.09	0.38	1.67	0.95	1.58	0.71	2.01	0.84	1.01	0.24	1.16	
S	0.94	0.19	6.18	1.00	0.21	0.33	2.87	1.00	0.17	0.54	1.00	0.46	0.62	0.95	1.00	0.63	0.56	1.09	
T	1.00	0.22	1.59	2.34	0.35	0.37	0.48	0.73	0.43	1.05	9.46	1.18	0.57	1.07	1.10	2.71	0.62	1.44	
V	1.11	0.31	1.27	0.81	0.12	0.15	0.41	0.19	0.38	2.23	1.05	1.14	1.00	1.14	1.26	1.00	0.36	0.91	
L	1.06	0.45	1.12	0.35	0.12	0.43	0.54	0.20	1.39	3.52	20.15	1.00	1.13	1.26	0.79	0.66	0.33	0.86	
I	0.98	0.77	1.00	0.21	0.00	0.28	0.30	0.19	13.42	6.98	4.97	1.27	1.64	0.77	1.19	1.25	0.23	1.02	
M	0.96	0.87	1.00	0.28	0.12	0.47	0.53	0.10	11.09	1.87	10.49	1.45	0.40	0.57	0.62	0.63	0.35	1.04	
K	0.70	0.00	0.00	0.00	0.20	0.25	1.02	0.00	0.00	1.00	3.54	0.50	0.53	0.83	0.80	0.60	1.00	0.90	
R	0.47	0.20	0.36	0.25	0.11	0.14	0.37	0.18	0.13	1.19	1.13	1.07	0.25	0.85	0.67	0.35	1.00	1.15	
H	1.01	0.22	0.00	0.00	0.58	0.00	0.82	0.11	0.58	0.91	0.32	1.33	0.44	1.21	1.21	0.60	0.70	0.61	
F	1.57	1.00	0.58	0.34	0.47	0.31	0.41	0.26	0.37	0.84	0.97	1.89	0.62	0.70	0.79	0.73	0.40	1.00	
Y	1.33	0.53	0.47	0.23	1.00	0.33	0.29	0.23	1.00	1.40	0.26	1.00	0.46	1.08	0.80	0.66	0.86	1.07	
W	0.28	0.72	0.24	0.35	0.39	0.18	0.48	0.17	1.07	1.05	1.03	0.59	0.80	1.47	0.71	0.53	0.34	2.12	
N	1.39	0.22	0.38	0.11	0.07	0.34	0.46	0.27	0.18	0.89	0.54	0.76	0.35	1.40	0.36	0.78	0.60	1.09	
D	1.11	0.15	0.95	0.08	0.34	1.00	0.38	0.14	0.13	0.49	0.26	0.34	0.70	1.00	0.78	0.57	0.22	0.79	
E	0.50	0.40	0.79	0.11	0.14	0.33	0.92	0.06	0.29	1.07	0.12	0.28	0.75	1.57	0.48	0.62	0.31	0.54	
Q	0.63	0.00	0.85	0.00	0.00	0.52	1.43	0.25	0.00	0.46	11.91	1.06	0.23	0.90	0.98	0.39	0.24	1.14	

Legend

Favorable

Neutral

Unfavorable

>2
} 0.5 to 2
<0.5

FIG. 5F

MBN001 HCDR3
Human CEACAM5

SEQ ID NO: 63

Germline Parental	T	G	L	T	G	T	G	A	F	D	I	
	94	95	96	97	98	99	100	100a	100b	101	102	
Normalized Enrichment Ratio												
*	0.00	ND	ND	0.00	0.00	ND	0.00	0.00	0.00	0.00	0.00	0.00
P	0.14	0.00	0.00	0.00	0.00	0.11	1.78	0.07	0.00	0.00	0.00	0.00
G	0.00	1.00	0.05	0.05	1.00	0.00	1.00	0.15	0.18	0.27	0.08	
A	0.14	0.07	0.13	0.00	0.00	0.29	0.19	1.00	0.63	0.05	0.00	
C	0.00	0.11	1.40	0.19	0.00	0.07	0.84	0.08	1.23	0.17	0.00	
S	0.05	0.03	0.03	0.04	0.03	0.06	0.22	0.21	2.59	0.14	0.09	
T	1.00	0.06	0.00	1.00	0.00	1.00	0.10	0.04	1.64	0.00	0.00	
V	0.03	0.00	0.13	0.11	0.07	0.14	0.59	0.08	2.64	0.21	1.24	
L	0.04	0.08	1.00	0.03	0.00	0.15	2.49	0.06	3.16	0.00	0.10	
I	0.09	0.00	0.00	0.22	0.08	0.26	1.16	0.13	1.28	0.00	1.00	
M	0.07	0.00	0.36	0.10	0.00	0.00	0.31	0.00	3.07	0.00	0.16	
K	0.00	0.00	0.00	0.00	0.32	0.00	0.00	0.00	3.26	0.00	0.19	
R	0.00	0.04	0.00	0.00	0.00	0.00	0.12	0.09	0.00	0.00	0.00	
H	0.00	0.00	0.00	0.00	0.00	0.23	0.00	0.25	2.74	0.14	0.00	
F	0.06	0.05	0.11	0.06	0.00	0.00	0.00	0.09	1.00	0.12	0.15	
Y	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.10	4.01	0.00	0.00	
W	0.09	0.21	0.00	0.00	0.17	0.04	0.29	0.18	0.64	0.08	0.00	
N	0.24	0.13	0.25	0.14	0.00	0.14	3.68	0.00	7.04	0.12	0.00	
D	0.08	0.00	0.04	0.00	0.06	0.00	0.66	0.04	1.15	1.00	0.00	
E	0.06	0.11	0.08	0.00	0.00	0.20	0.12	0.00	0.11	0.40	0.00	
Q	0.00	0.13	0.34	0.00	0.12	0.00	0.26	0.00	1.55	0.00	0.30	

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

FIG. 5G

Legend

Favorable

Neutral

Unfavorable

>2
} 0.5 to 2
<0.5

SEQ ID NO: 63

Germline		T	G	L	T	G	T	G	T	G	A	F	D	I
Parental		94	95	96	97	98	99	100	100a	100b	101	102		
Normalized Enrichment Ratio		0.00	ND	ND	0.00	0.00	ND	0.00	0.00	0.00	0.00	0.00	0.00	0.00
*	P	0.16	0.15	0.15	0.00	0.19	0.11	0.62	0.00	0.00	0.00	0.00	0.00	0.00
	G	0.26	1.00	0.25	0.06	1.00	0.12	1.00	0.22	0.07	0.33	0.11		
	A	0.07	0.00	0.19	0.14	0.08	0.35	0.26	1.00	1.03	0.08	0.33		
	C	0.16	0.20	2.58	0.00	<u>0.11</u>	0.00	0.40	0.27	1.94	0.43	0.33		
	S	<u>0.11</u>	0.23	0.18	0.22	0.18	0.28	0.46	0.28	2.16	0.68	0.17		
	T	1.00	0.20	0.30	1.00	0.00	1.00	0.00	0.08	0.90	0.38	<u>0.00</u>		
	V	<u>0.04</u>	0.14	0.25	<u>0.04</u>	<u>0.09</u>	0.23	0.48	0.15	3.11	0.27	1.10		
	L	<u>0.13</u>	<u>0.14</u>	1.00	0.13	0.10	0.11	0.96	0.15	5.23	0.00	<u>0.11</u>		
	I	0.00	0.21	0.26	0.21	0.33	0.14	0.27	0.12	1.30	0.00	1.00		
	M	0.14	0.16	0.44	0.19	0.00	0.00	0.24	<u>0.11</u>	5.08	0.00	<u>0.00</u>		
	K	<u>0.00</u>	0.15	<u>0.00</u>	0.00	0.00	0.00	0.00	0.15	3.43	0.00	<u>0.00</u>		
	R	<u>0.11</u>	0.15	0.19	0.06	0.00	0.19	0.11	0.24	0.23	0.00	0.15		
	H	0.00	0.00	0.00	0.23	0.00	0.36	0.00	0.67	3.10	0.00	<u>0.00</u>		
	F	0.24	0.14	0.21	0.34	0.10	0.35	0.27	0.08	1.00	0.00	0.51		
	Y	0.22	0.14	0.17	0.17	0.21	0.32	0.38	0.28	4.49	0.18	0.19		
	W	0.24	0.12	0.12	0.18	0.39	0.07	0.17	0.20	0.50	0.25	0.50		
	N	0.32	0.35	0.00	0.25	0.19	0.22	19.17	0.00	22.72	0.00	0.21		
	D	0.26	0.38	0.00	0.00	0.00	0.00	0.92	0.28	1.64	1.00	0.00		
	E	0.00	<u>0.13</u>	0.22	0.00	0.00	0.00	0.22	0.09	0.28	0.37	<u>0.00</u>		
	Q	0.25	0.39	0.98	0.00	0.00	0.00	0.14	0.00	0.78	0.00	<u>0.00</u>		

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

Legend

Favorable	>2
Neutral	} 0.5 to 2
Unfavorable	<0.5

FIG. 5H

		SEQ ID NO: 64													
Germline Parental	R	A	S	24	25	26	27	27a	28	29	30	31	32	33	34
	24	25	26	27	27a	28	29	30	31	32	33	34			
Normalized Enrichment Ratio															
*	0.21	ND	0.00	0.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	ND
P	0.47	2.56	0.77	1.23	0.68	2.27	0.47	1.79	2.20	2.20	0.00	0.00	2.20	0.00	0.00
G	1.19	0.70	1.25	0.54	0.97	0.35	1.61	0.40	0.90	2.68	2.01	0.39			
A	0.94	1.00	1.20	0.56	0.83	0.44	0.90	1.19	1.16	0.53	2.20	1.00			
C	1.03	3.03	0.75	0.82	1.01	2.44	1.19	0.14	1.70	0.10	0.80	0.71			
S	1.04	0.86	1.00	0.59	1.00	0.75	1.00	1.00	1.00	0.61	1.82	0.72			
T	0.75	1.58	0.55	1.01	0.66	2.00	0.28	0.49	1.26	0.57	0.86	0.22			
V	0.73	1.38	0.79	1.11	0.77	1.00	0.37	0.87	2.48	0.64	1.45	0.00			
L	0.82	1.98	1.12	0.65	0.61	1.62	0.72	0.30	1.81	0.09	1.00	0.00			
I	1.05	1.55	1.13	1.20	0.59	1.66	0.48	0.57	6.43	0.84	2.32	0.00			
M	0.78	1.99	1.40	0.73	0.52	2.73	0.41	0.19	1.54	0.95	1.88	0.00			
K	0.94	0.29	1.12	0.90	0.85	0.55	0.19	0.22	1.15	0.08	0.57	0.00			
R	1.00	0.12	0.97	0.55	0.95	0.24	0.10	0.37	0.61	0.13	0.75	0.00			
H	0.72	0.34	1.57	0.64	1.32	0.44	0.57	0.00	0.73	0.75	0.34	0.00			
F	1.31	1.42	1.04	0.56	1.39	2.23	0.39	0.11	0.75	0.91	1.67	0.00			
Y	1.13	0.37	1.46	0.59	1.55	0.63	0.56	0.27	1.02	1.00	1.85	0.00			
W	1.10	0.31	0.87	0.43	0.82	0.49	0.46	0.08	6.16	0.89	1.96	0.30			
N	0.98	0.57	0.75	0.52	0.51	0.36	0.66	0.27	0.00	0.84	0.52	0.00			
D	0.62	0.50	1.11	0.63	0.68	0.69	1.12	0.55	0.31	0.76	1.19	0.00			
E	1.05	0.28	1.48	1.14	0.64	0.26	1.53	0.26	0.88	0.37	1.74	0.00			
Q	0.73	0.83	1.49	1.00	0.95	0.75	0.80	0.19	ND	0.33	0.84	ND			

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

Legend

Favorable

Neutral

Unfavorable

>2
} 0.5 to 2
<0.5

FIG. 5I

SEQ ID NO: 64

Germline Parental	Normalized Enrichment Ratio																							
	R	A	S	Q	S	V	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	
*	0.00	ND	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.36	0.00	0.00	0.00	0.00	0.00	ND	
P	0.89	3.13	0.61	0.98	1.03	0.77	0.77	0.59	2.12	1.78	1.84	0.00	0.00	0.00	0.00	0.00	0.00	1.84	0.00	0.00	0.00	0.00	0.00	
G	0.82	0.53	1.27	0.50	0.71	0.14	2.54	0.08	0.00	1.33	1.15	0.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
A	0.63	1.00	0.92	0.49	1.19	0.49	0.41	1.92	1.60	0.25	1.39	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
C	1.23	2.85	0.85	0.54	1.20	1.22	0.86	0.26	1.52	0.73	0.24	1.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
S	0.68	1.34	1.00	0.62	1.00	0.44	1.00	1.00	1.00	0.79	0.61	0.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
T	0.50	1.95	0.82	0.89	0.60	2.11	0.27	0.81	1.31	0.57	0.34	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
V	0.63	1.38	0.87	1.23	0.60	1.00	0.13	0.99	3.15	0.91	1.81	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
L	0.65	3.20	0.51	0.62	0.62	1.41	0.45	0.11	1.79	0.05	1.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
I	0.99	2.09	1.03	1.12	0.88	1.77	0.15	0.91	10.62	1.24	3.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
M	0.66	2.77	1.52	1.08	1.24	2.69	0.00	0.25	1.56	1.05	2.86	0.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
K	0.45	0.40	1.71	0.82	0.00	0.76	0.00	0.00	2.62	0.00	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
R	1.00	0.44	0.89	0.80	0.96	0.36	0.60	0.13	0.76	0.00	0.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
H	0.38	0.62	0.46	0.64	1.17	0.29	0.36	0.00	1.13	0.48	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
F	1.49	1.80	1.14	0.44	1.47	2.20	0.34	0.00	0.24	0.77	1.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Y	0.59	0.70	0.98	0.78	3.51	0.53	0.11	0.21	0.71	1.00	2.11	0.58	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
W	0.73	0.52	0.74	0.87	4.29	0.36	0.67	0.61	12.32	1.65	2.76	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
N	1.95	0.73	0.84	0.55	0.54	0.35	0.68	0.00	0.00	0.59	0.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
D	0.63	0.24	0.80	0.41	0.35	0.00	1.18	0.00	0.18	0.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
E	1.12	0.65	0.84	0.50	0.37	0.00	0.87	0.35	0.00	0.00	1.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Q	0.62	0.45	1.70	1.00	0.73	0.00	0.00	0.39	ND	0.68	1.06	ND	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

Legend

Favorable

Neutral

Unfavorable

>2
} 0.5 to 2
<0.5

FIG. 5J

MBN001 Lcdr2
Human CEACAM5

SEQ ID NO: 65											
Germline Parental	G	A	S	S	S	R	A	T			
	50	51	52	53	54	55	56	56			
Normalized Enrichment Ratio											
*	ND	ND	<u>0.00</u>	<u>0.00</u>	<u>0.00</u>	<u>0.00</u>	<u>0.00</u>	<u>0.00</u>	<u>0.00</u>	<u>0.00</u>	<u>0.00</u>
P	ND	2.98	0.16	0.59	0.53	0.62	1.52				
G	1.00	3.07	0.52	0.55	0.47	0.82	0.37				
A	4.16	1.00	0.85	1.19	0.53	1.00	0.32				
C	0.91	2.36	0.86	0.64	0.50	<u>0.19</u>	0.50				
S	2.43	0.91	1.00	1.00	0.49	0.74	0.50				
T	0.79	1.80	0.73	1.64	0.74	0.45	1.00				
V	1.92	0.24	0.96	1.50	0.79	0.48	0.76				
L	<u>0.14</u>	0.76	1.04	<u>0.04</u>	1.10	2.21	0.55				
I	0.35	<u>0.00</u>	0.56	0.44	0.87	0.49	0.56				
M	4.11	0.67	0.38	0.60	1.22	1.67	0.59				
K	<u>0.00</u>	0.27	0.81	<u>0.00</u>	0.83	0.22	0.22				
R	0.71	0.47	0.66	<u>0.07</u>	1.00	0.29	0.70				
H	1.58	1.20	0.43	1.71	1.32	2.25	0.44				
F	7.10	0.23	1.37	2.52	0.83	0.31	0.59				
Y	6.97	0.25	2.35	4.04	1.10	1.57	0.51				
W	8.12	1.61	1.66	5.71	0.80	0.62	0.97				
N	0.80	1.08	0.64	1.19	0.62	1.60	1.20				
D	<u>0.00</u>	0.42	0.65	<u>0.09</u>	0.32	2.76	0.66				
E	<u>0.00</u>	0.47	0.62	0.42	0.53	<u>0.19</u>	0.34				
Q	0.91	0.53	2.41	0.88	0.79	1.13	0.66				

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

Legend

Favorable	>2
Neutral	} 0.5 to 2
Unfavorable	<0.5

FIG. 5K

Germline		G		A		S		S		R		A		T	
Parental	50	51	52	53	54	55	56	SEQ ID NO: 65							
Normalized Enrichment Ratio															
*	ND	ND	1.46	0.00	0.00	0.36	0.00								
P	ND	2.92	0.49	0.52	1.19	0.79	2.79								
G	1.00	2.79	0.28	0.31	0.40	0.76	0.74								
A	2.75	1.00	1.03	1.84	0.40	1.00	0.85								
C	4.63	3.14	1.16	0.20	0.53	0.43	2.08								
S	4.64	1.66	1.00	1.00	0.13	0.74	0.74								
T	0.26	1.61	0.19	1.06	1.03	0.65	1.00								
V	4.74	0.00	1.01	0.32	0.44	0.42	0.45								
L	0.55	0.77	1.05	0.00	1.08	2.67	0.92								
I	0.28	0.00	1.22	0.00	0.57	0.42	0.51								
M	12.30	0.67	1.06	0.22	0.79	10.37	0.21								
K	0.00	1.12	0.30	0.21	0.78	0.00	1.18								
R	0.62	0.85	0.11	0.17	1.00	0.18	1.07								
H	0.59	2.45	0.00	1.13	0.44	0.92	0.90								
F	21.52	0.22	3.24	1.58	0.61	2.90	0.67								
Y	32.14	0.00	4.09	1.85	0.19	7.46	1.48								
W	45.22	1.20	2.13	10.33	0.91	0.36	3.29								
N	0.00	0.21	0.26	0.55	0.81	8.97	2.10								
D	0.16	0.00	0.00	0.10	0.49	5.65	0.16								
E	0.44	0.14	0.64	0.21	0.15	0.24	0.48								
Q	0.35	0.51	3.50	1.37	1.05	0.49	0.00								

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

Legend

Favorable

Neutral

Unfavorable

>2
} 0.5 to 2
<0.5

FIG. 5L

SEQ ID NO: 66														
Germline Parental	Q	Q	Y	G	S	S	P	Y						
	89	90	91	92	93	94	95	96						
Normalized Enrichment Ratio														
*	0.00	0.49	0.44	0.53	ND	ND	ND	0.00	0.00	0.00				
P	0.38	0.10	0.00	0.07	7.51	0.80	1.00	1.98						
G	1.74	0.09	1.49	1.00	0.20	0.77	0.14	1.27						
A	1.04	0.00	1.42	1.97	0.91	0.85	1.02	1.10						
C	0.00	0.00	1.52	2.47	1.90	1.77	1.12	1.68						
S	2.56	0.07	3.34	1.74	1.00	1.00	0.48	3.11						
T	0.35	0.00	2.76	0.98	1.85	1.19	1.44	3.02						
V	0.03	0.10	0.62	2.63	2.47	1.49	2.39	2.52						
L	0.43	0.17	0.08	4.75	4.94	3.46	1.71	0.85						
I	0.00	0.12	0.11	3.43	3.51	3.58	1.75	3.12						
M	2.23	0.23	0.25	3.49	2.43	1.59	2.09	5.58						
K	0.95	0.00	0.00	4.04	0.72	0.46	3.10	0.00						
R	0.22	0.10	0.15	2.66	3.39	1.32	2.13	0.08						
H	3.22	0.16	0.27	1.16	2.01	1.64	2.16	2.46						
F	4.29	0.15	0.55	3.53	3.04	3.06	1.66	0.29						
Y	2.50	0.10	1.00	3.87	2.72	3.35	1.53	1.00						
W	0.26	0.16	0.10	3.65	1.37	1.14	1.78	2.97						
N	2.68	0.00	3.24	1.35	1.53	1.69	1.22	3.56						
D	2.70	0.09	1.60	0.94	0.44	0.29	0.20	3.19						
E	1.32	0.27	0.31	1.94	0.49	0.00	1.31	1.46						
Q	1.00	1.00	1.92	1.45	2.71	1.79	3.79	4.11						

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

Legend

Favorable	>2
Neutral	} 0.5 to 2
Unfavorable	<0.5

FIG. 5M

SEQ ID NO: 66

Germline Parental	Normalized Enrichment Ratio														
	Q	89	90	91	92	G	S	93	94	95	P	Y	96		
*	0.00	0.00	0.00	0.51	0.68	ND	ND	ND	ND	0.00	0.00	0.00	0.00		
P	0.65	0.00	0.00	0.00	0.07	43.51	0.47	1.00	1.17	0.00	0.00	0.00	1.17		
G	1.24	0.17	4.40	1.00	0.32	0.54	0.23	0.42							
A	1.46	0.07	1.07	1.09	0.59	0.79	0.77	0.73							
C	0.00	0.19	2.61	1.47	3.50	2.72	0.61	0.51							
S	2.03	0.10	3.81	1.07	1.00	1.00	0.32	0.87							
T	0.00	0.00	2.68	0.63	5.66	1.01	1.05	1.42							
V	0.25	0.00	0.36	1.61	8.10	1.69	0.85	0.89							
L	0.26	0.05	0.00	6.63	16.69	8.11	1.04	0.49							
I	0.00	0.25	0.00	3.92	15.44	2.52	2.19	1.67							
M	0.73	0.00	0.35	2.97	4.31	2.02	1.46	2.10							
K	0.51	0.00	0.00	29.40	3.63	0.00	3.58	0.20							
R	0.08	0.05	0.35	9.73	33.98	1.08	1.36	0.10							
H	4.56	0.00	0.62	0.40	6.28	1.25	0.64	0.00							
F	1.14	0.00	0.39	1.82	3.58	5.30	1.12	0.42							
Y	0.77	0.00	1.00	2.44	6.25	2.80	0.36	1.00							
W	0.20	0.00	0.13	3.08	2.67	1.09	1.19	1.79							
N	0.80	0.00	20.59	2.10	2.75	0.47	1.19	3.42							
D	2.77	0.48	1.14	0.22	0.00	0.00	0.21	2.32							
E	1.49	0.27	0.00	0.41	0.17	0.00	0.60	2.34							
Q	1.00	1.00	2.27	1.06	4.12	2.68	0.88	1.90							

ND= Enrichment ratios could not be determined because NGS counts in the starting library were too low

FIG. 5N

Legend

Favorable	>2
Neutral	} 0.5 to 2
Unfavorable	<0.5

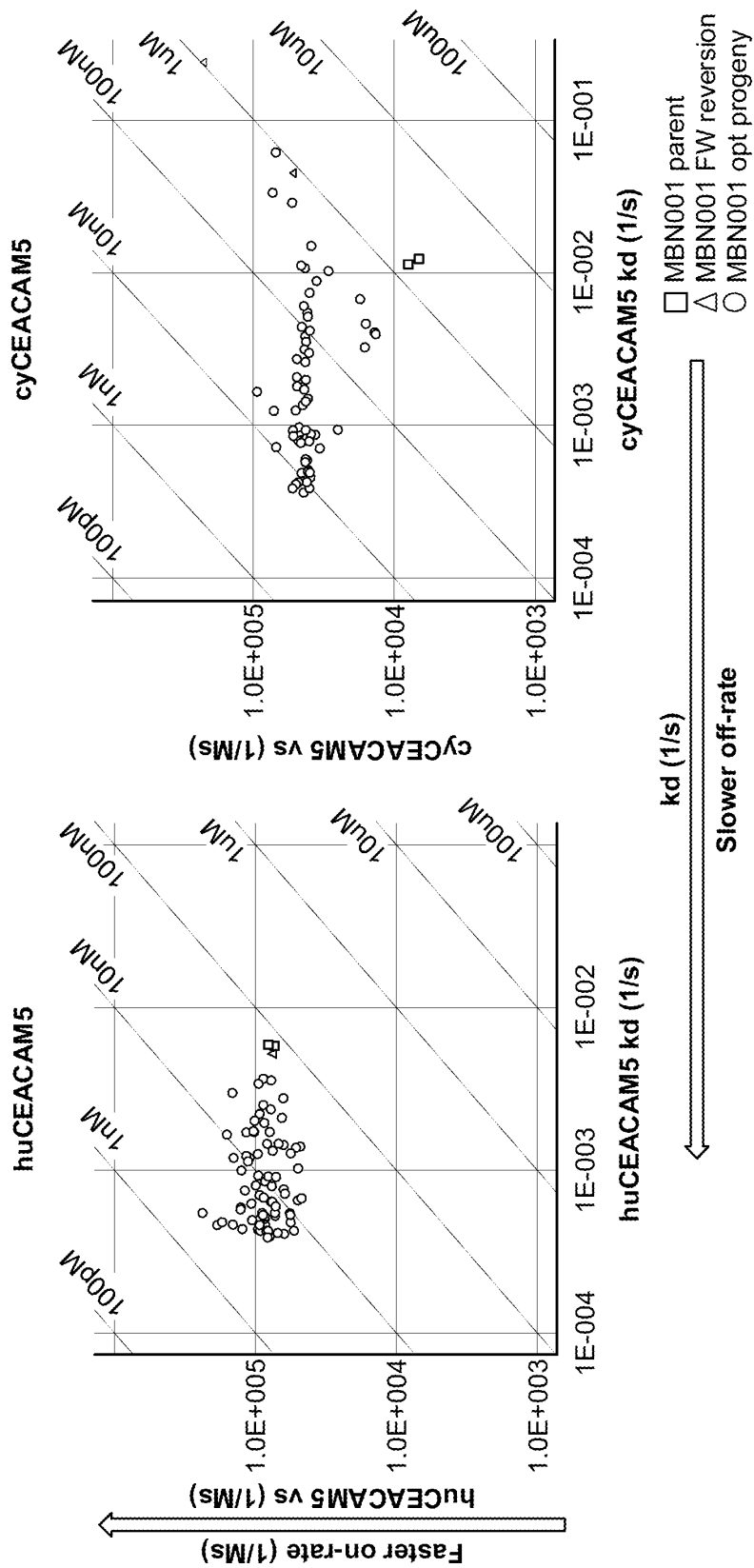


FIG. 6B

FIG. 6A

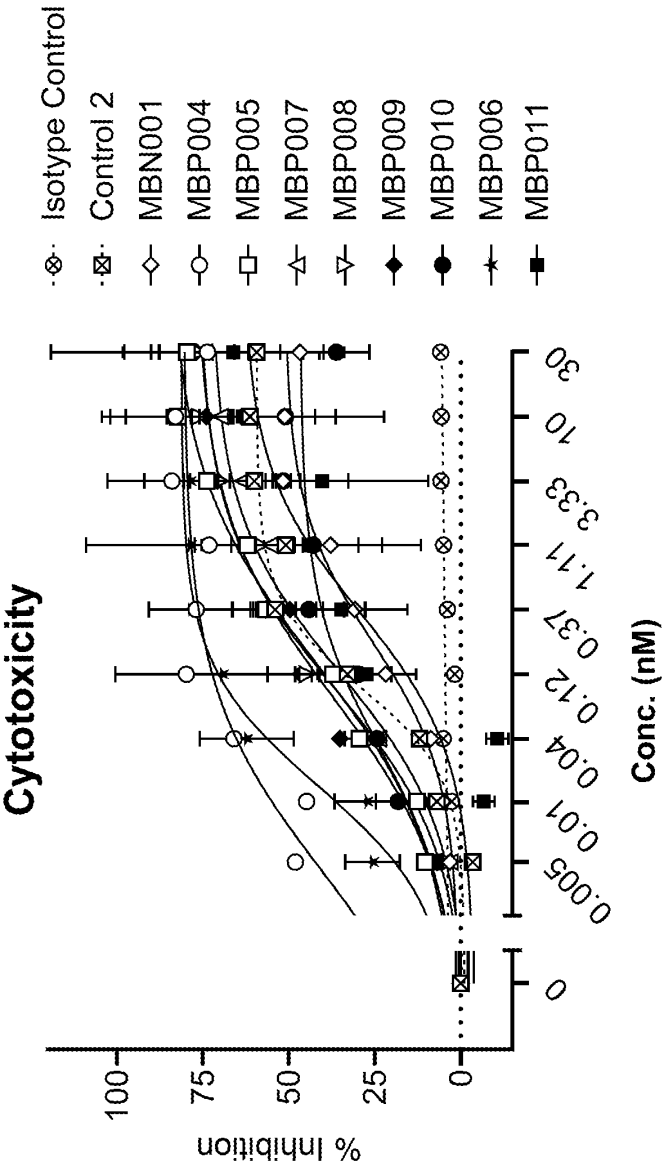


FIG. 7A

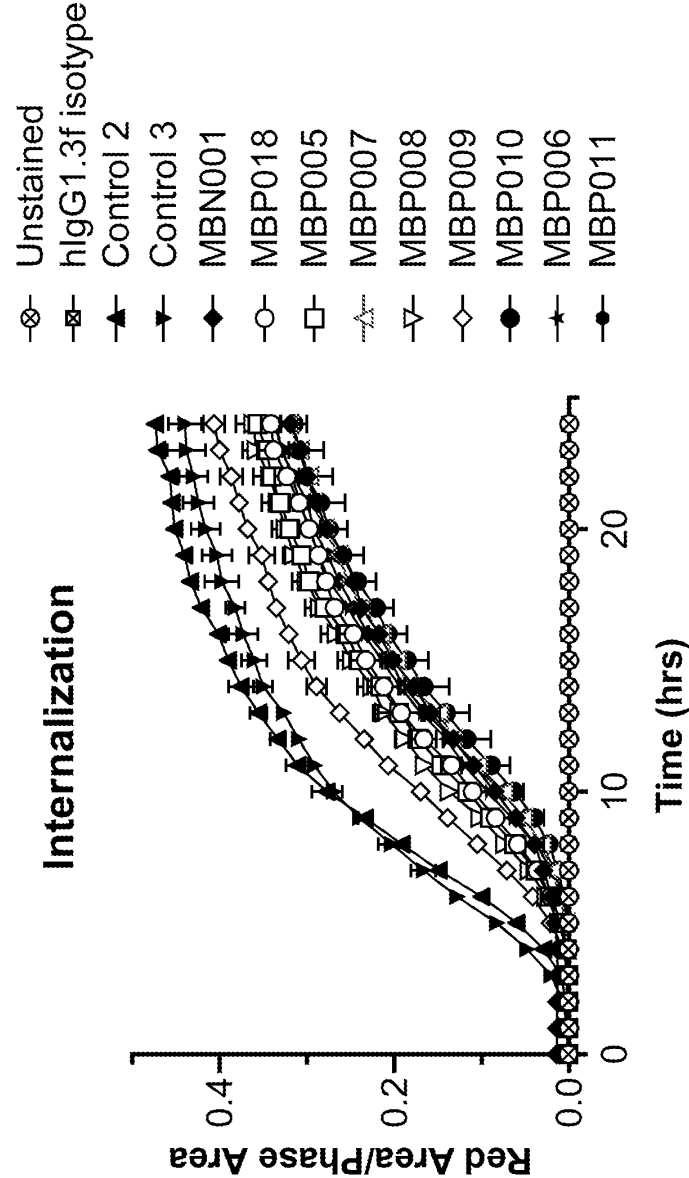


FIG. 7B

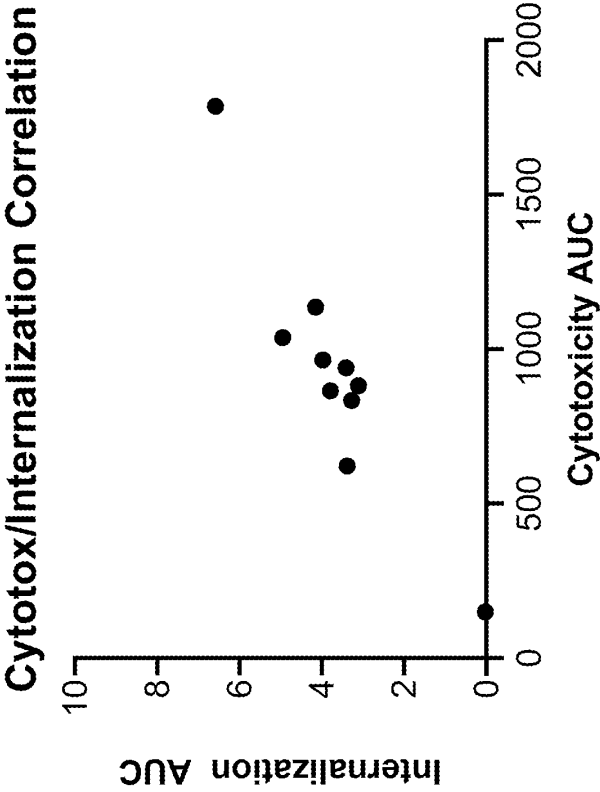


FIG. 7C

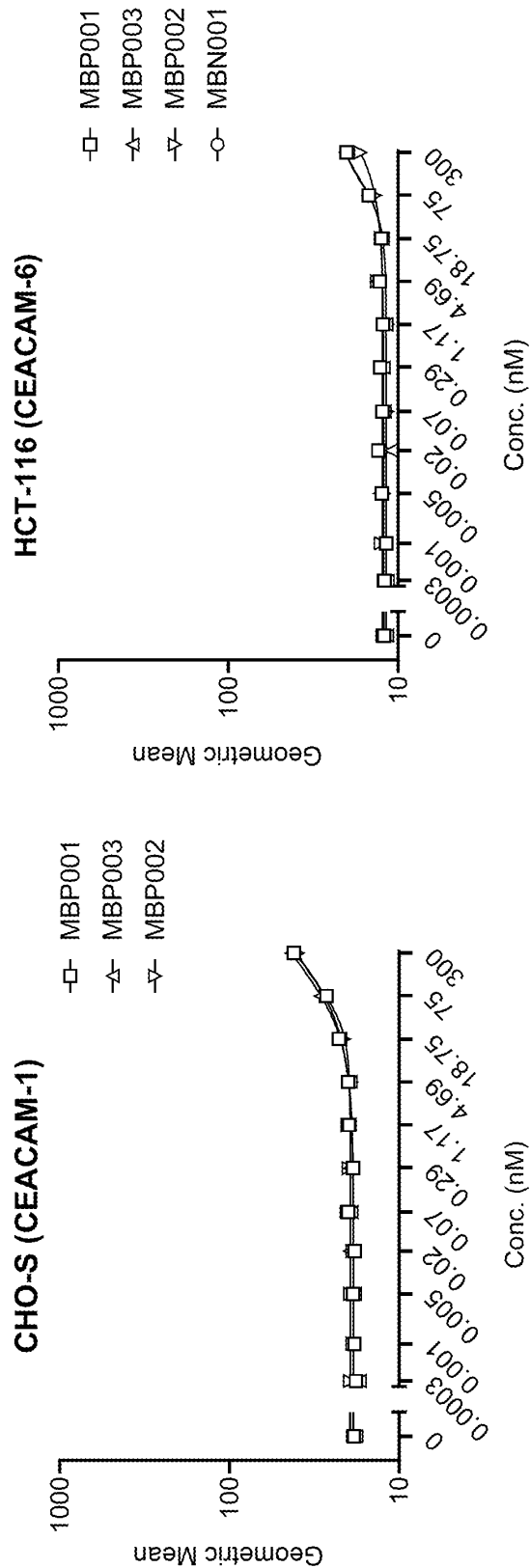


FIG. 8B

FIG. 8A

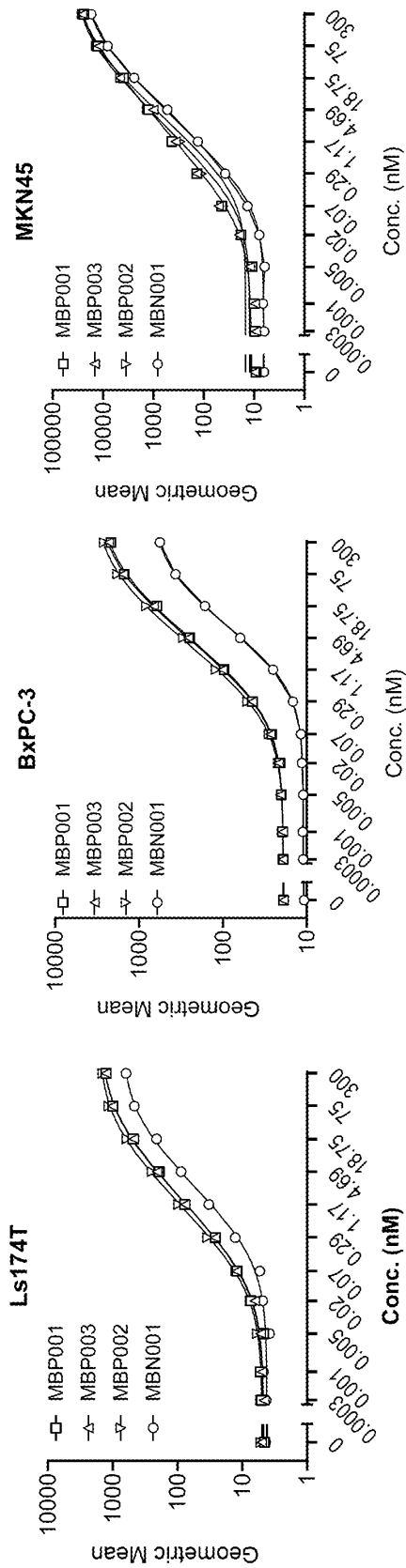


FIG. 9C

FIG. 9B

FIG. 9A

Clone name	LS174T EC50 (nM)	BxPC3 EC50 (nM)	MKN45 EC50 (nM)
MBN001	1.7	1.8	2.2
MBP003	1.7	1.9	2.4
MBP001	1.7	1.9	2.0
MBP002	1.5	1.9	2.1

FIG. 9D

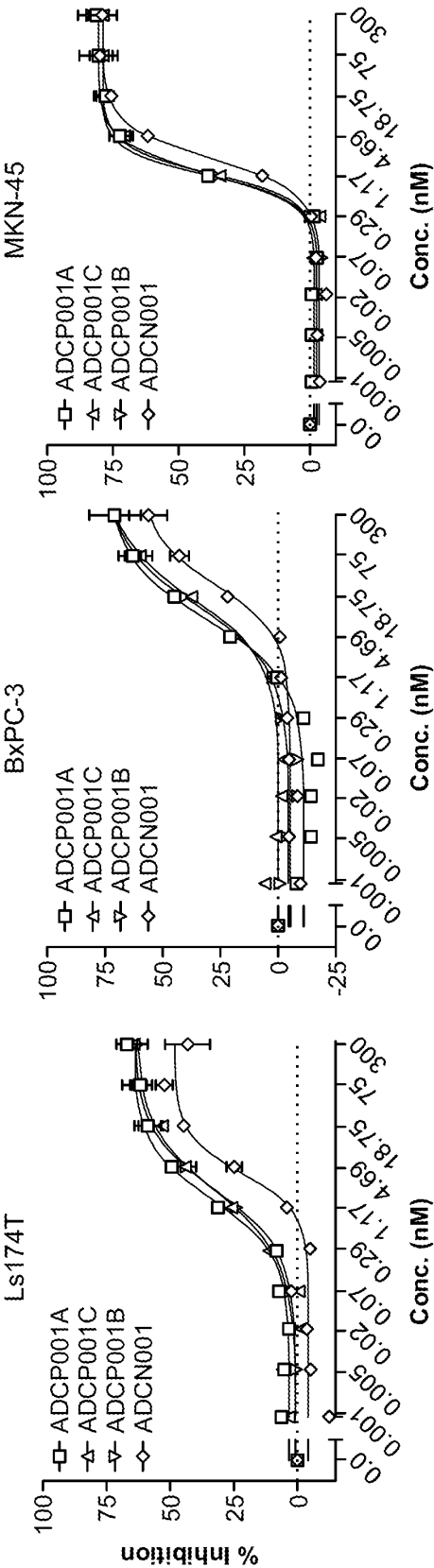


FIG. 10A

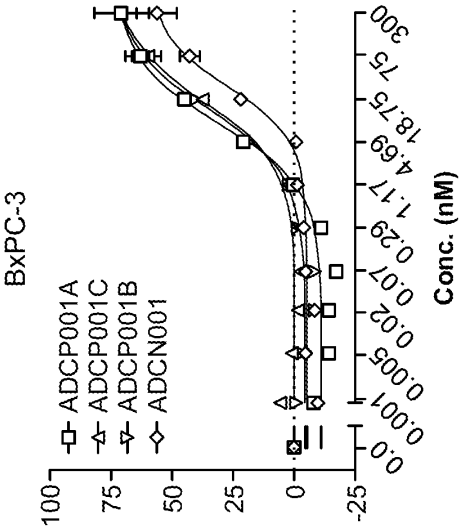


FIG. 10B

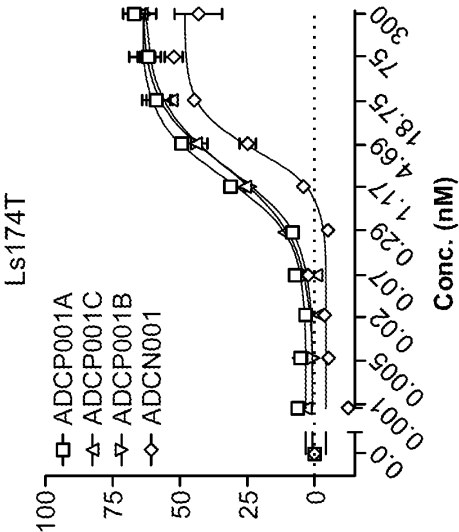


FIG. 10C

Clone name	LS174T IC50 (nM)	BxPC3 IC50 (nM)	MKN45 IC50 (nM)
ADCN001	3.9	27.5	2.2
ADCP001C	2.2	13.4	1.3
ADCP001A	2.0	16.8	1.3
ADCP001B	1.6	8.3	1.2

FIG. 10D

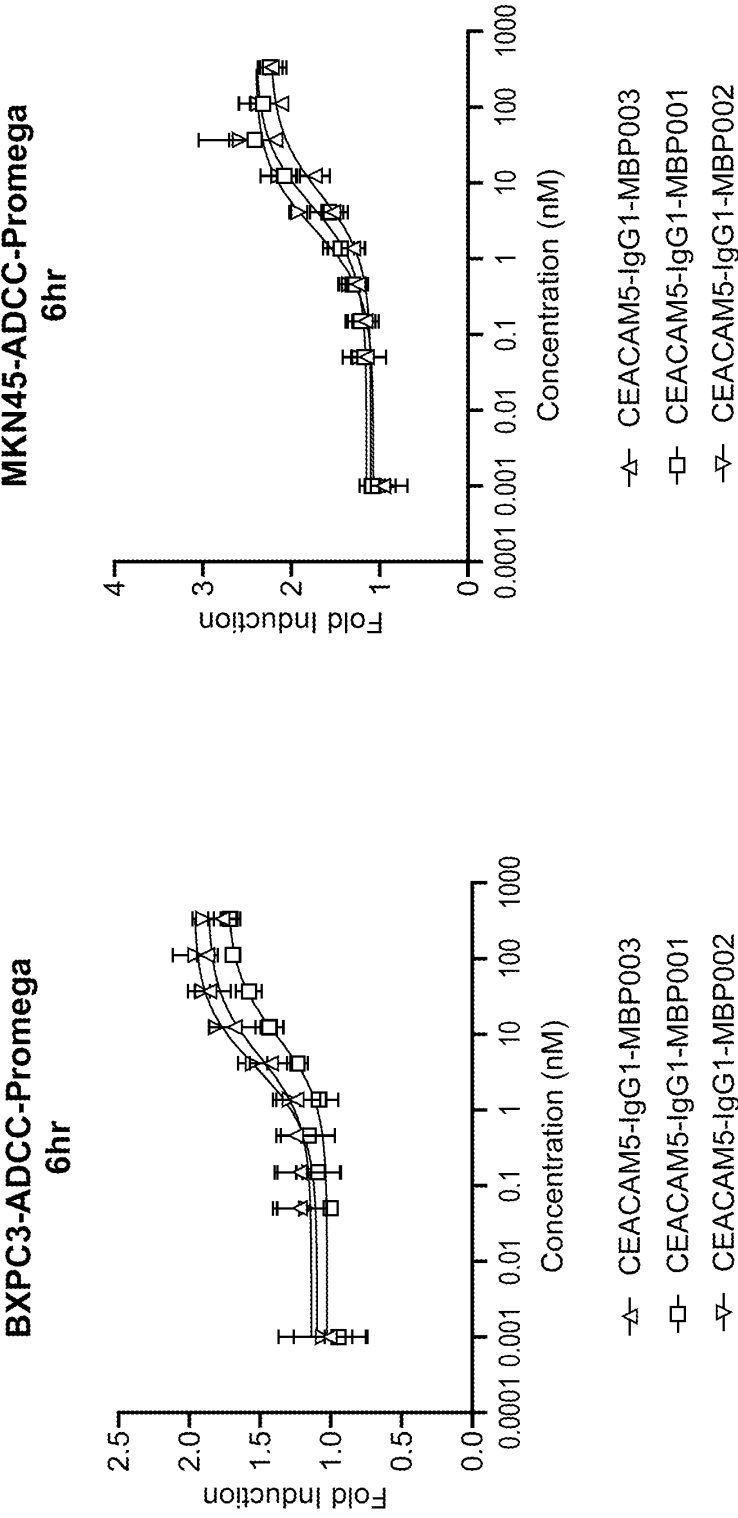


FIG. 11A

FIG. 11B

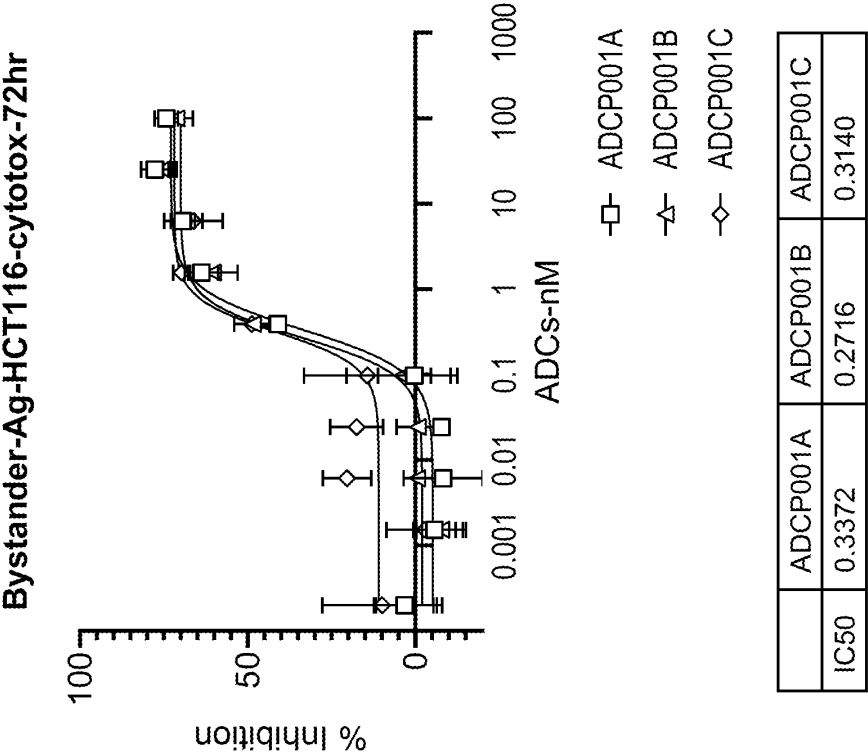


FIG. 12B

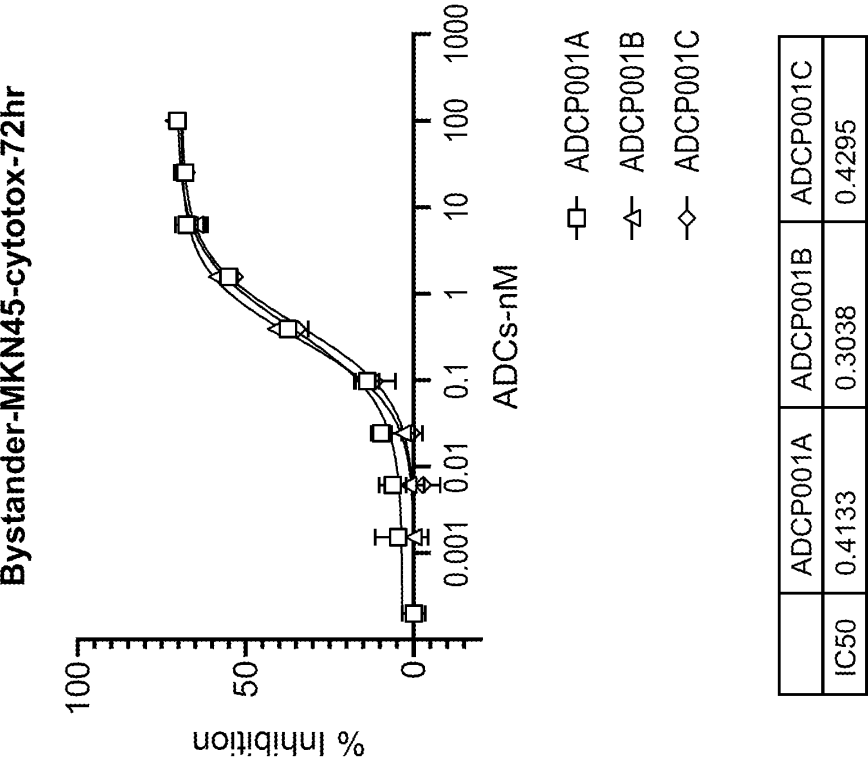


FIG. 12A

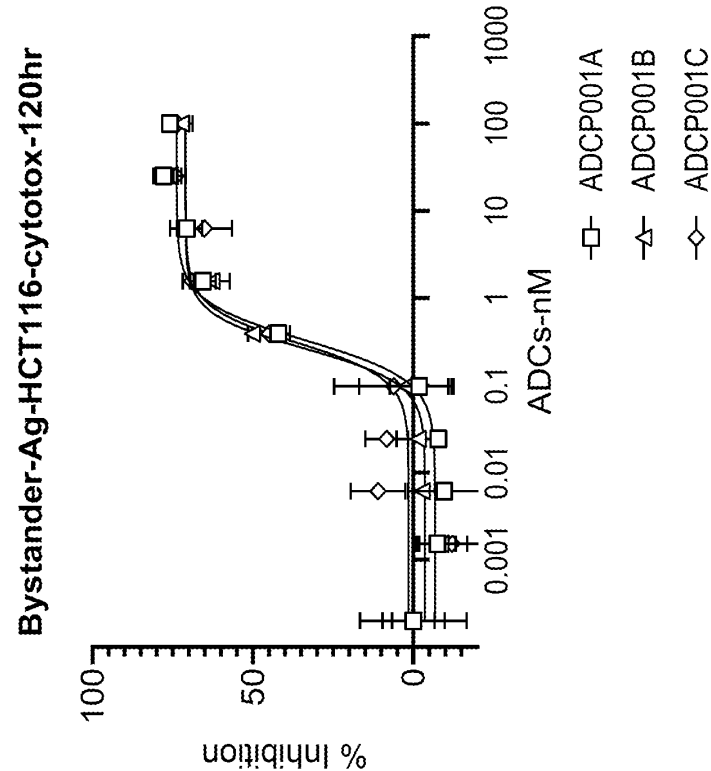


FIG. 12D

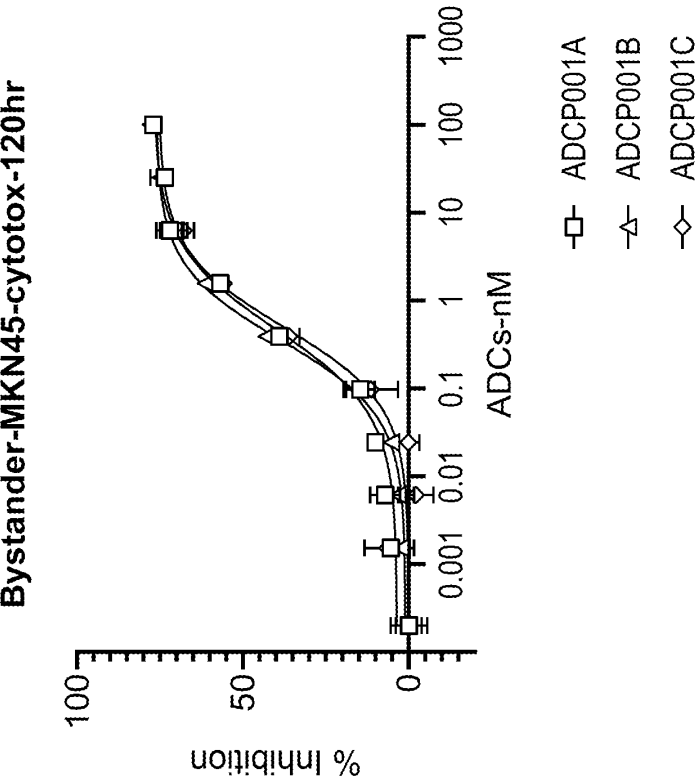


FIG. 12C

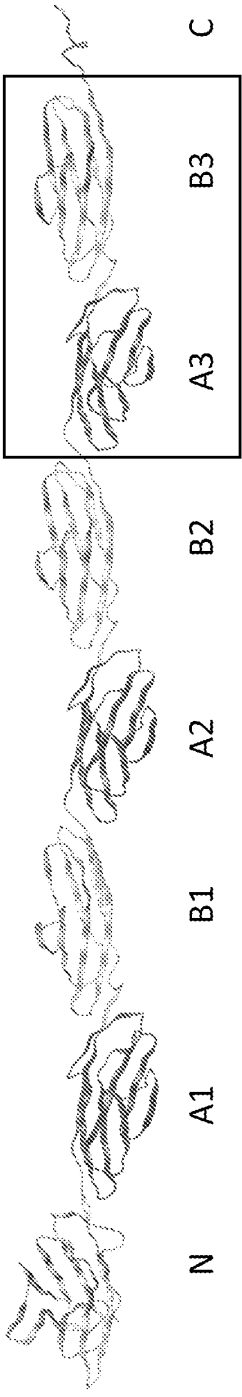


FIG. 13A

```
>sp|P06731|CEAM5_HUMAN
KLTIESTPENVAEGKEVLLLVHNLPOHLFGYSWKGERVDGNRQIIIGYVIGTQQATPGPAYSGREIIYPNASLLI N
QNIIQNDTGFTLHVLIKSDLVNEEATGQFRVYPELPKPSISSNNSKPEDKDAVAFTCEPETQDATYLWWVNNQS A1
LPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISP LNTSYRSGENLNLSC B1
HAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNNSGSYTCQAHNSDTGLNR TTTTITVYAEPPKPFITSNNSNP A2
VEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPrLQLSNDNR TLTLLSVTRNDVGPYECGIQNELSVDHSDPVIL
NVLYGPDPTISPSTYTYRPGVNL SLSCHAAASNPPAQYSWLIDGNIQQHTQELFISNITEKNSGLYTCQANNSAS B2
GHSRTTVKTTITVSAELPKPSISSNNSKPEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPrLQLSNGNRTLTLF A3
NVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTP IISPDDSSYLSGANLNL SCHSASNPPQYSWRINGIPQ B3
QHTQVLFIAKITPNNNGTYACFVSNLATGRNNSIVKSI TVSASGTSPGLSAGATVGIMIGLVGVALI C
```

(SEQ ID NO: 105)

FIG. 13B

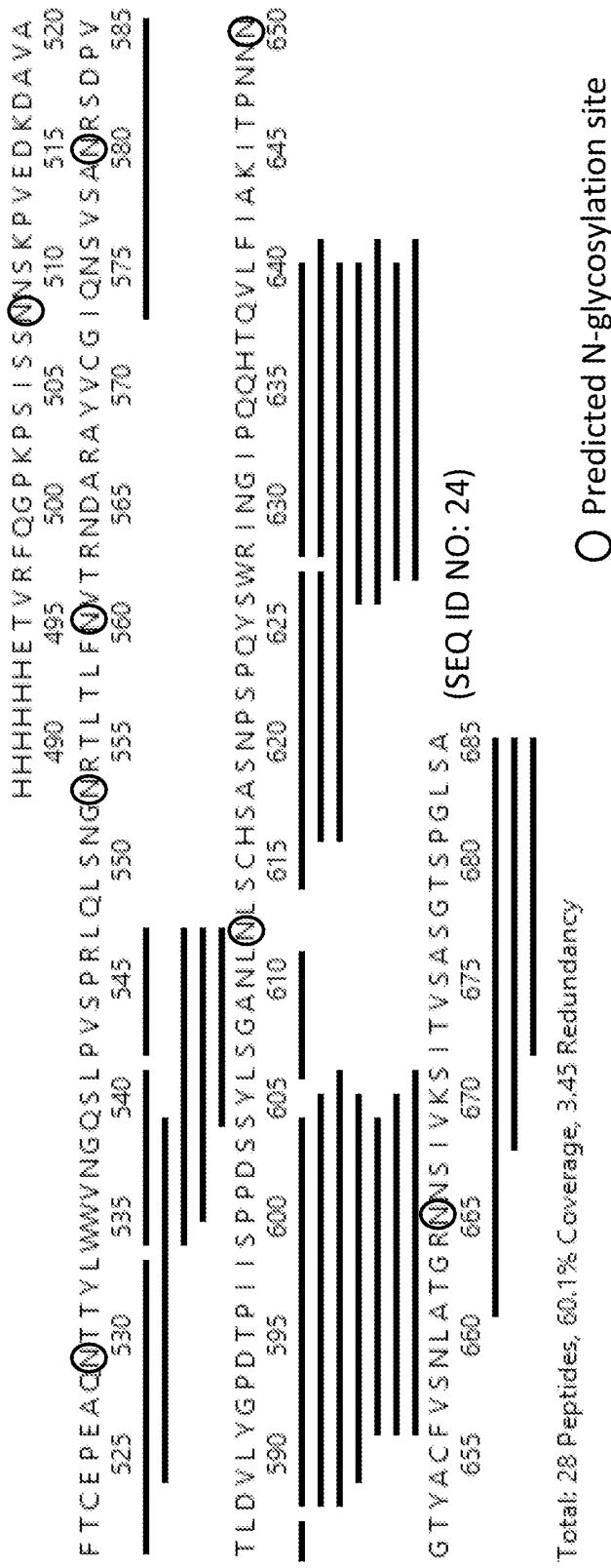


FIG. 13C

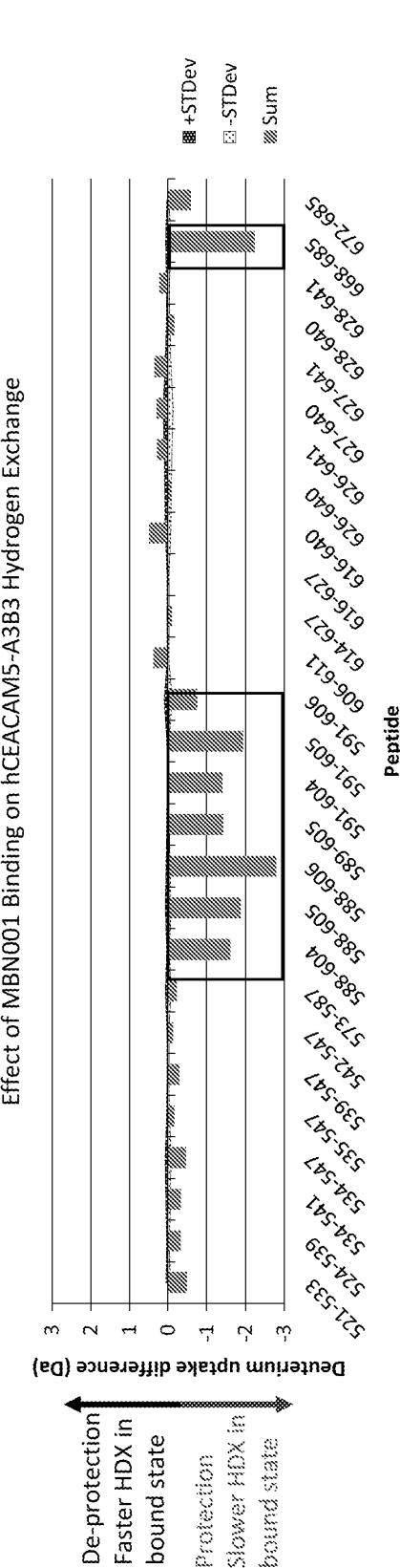


FIG. 13D

hCEACAM5 A3-B3-CT:
HHHHHHETVRFQGPKESSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFENVTRNDA
RAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISSYLSGANLNLSCHSASNPSPQYSWRINGIPQQHTQVLFIAKITPNN
NGTYACFVSNLATGRNNSIVKSITVSASGTPGLSA (SEQ ID NO: 24)

FIG. 13E

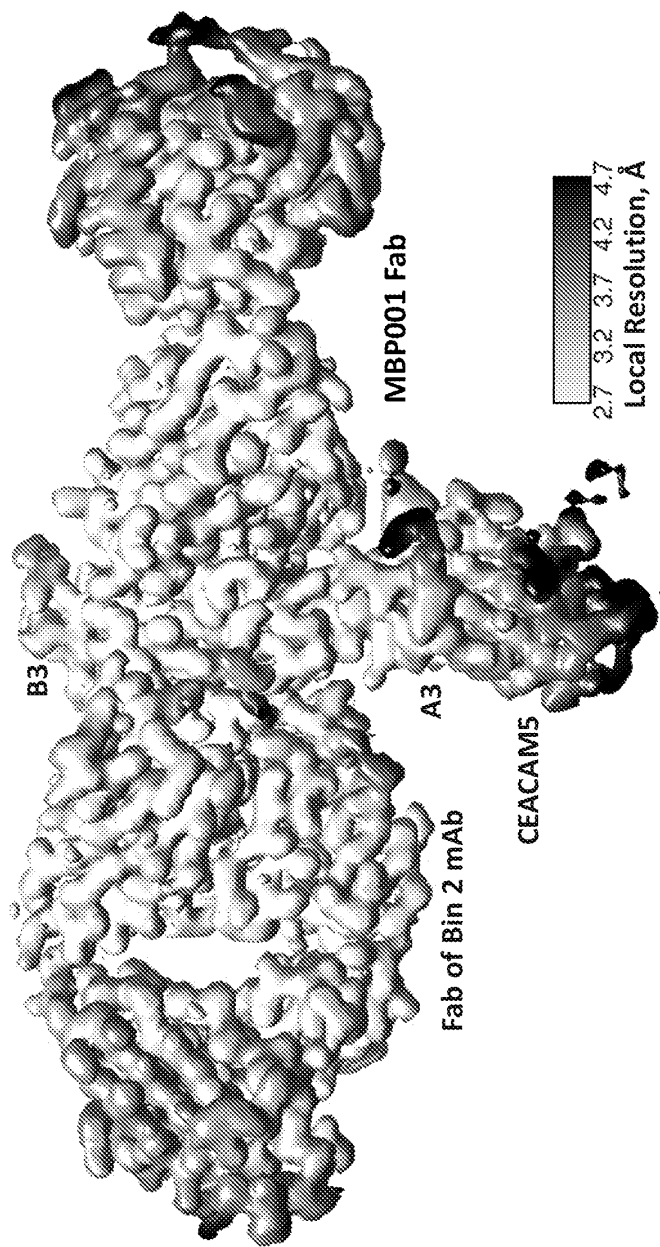


FIG. 14A

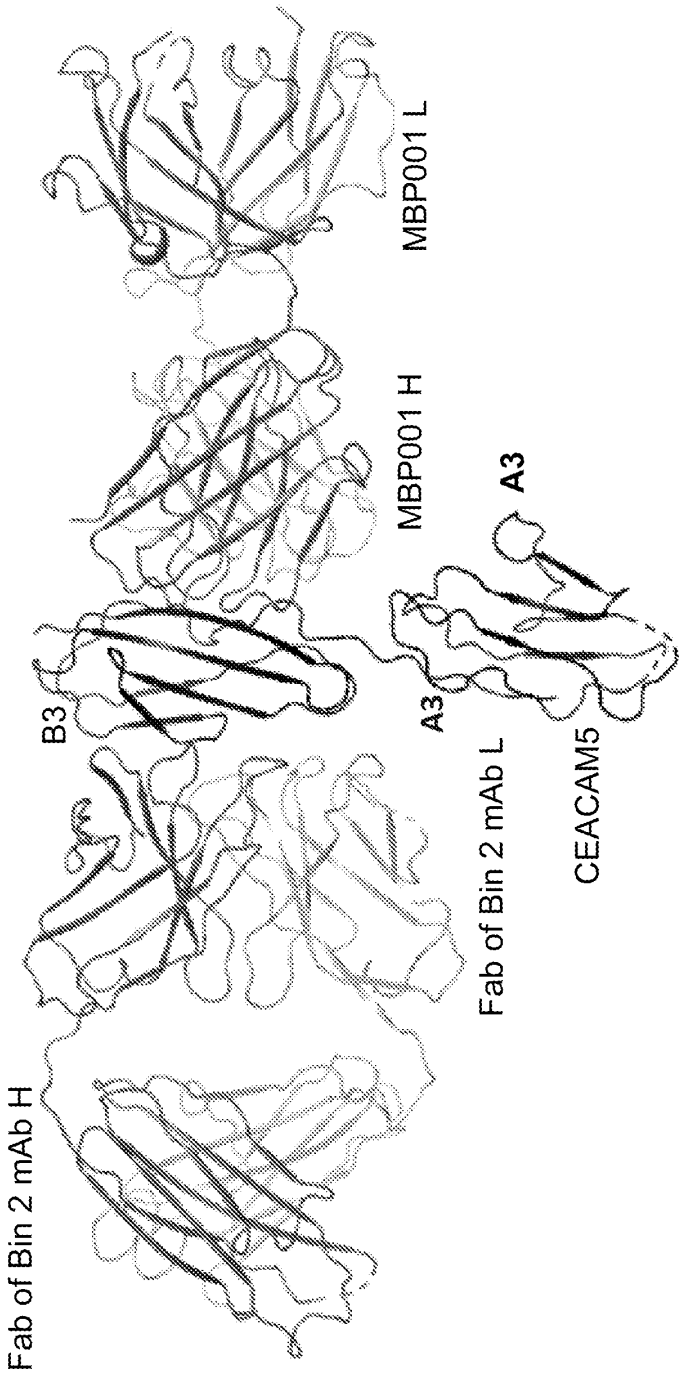
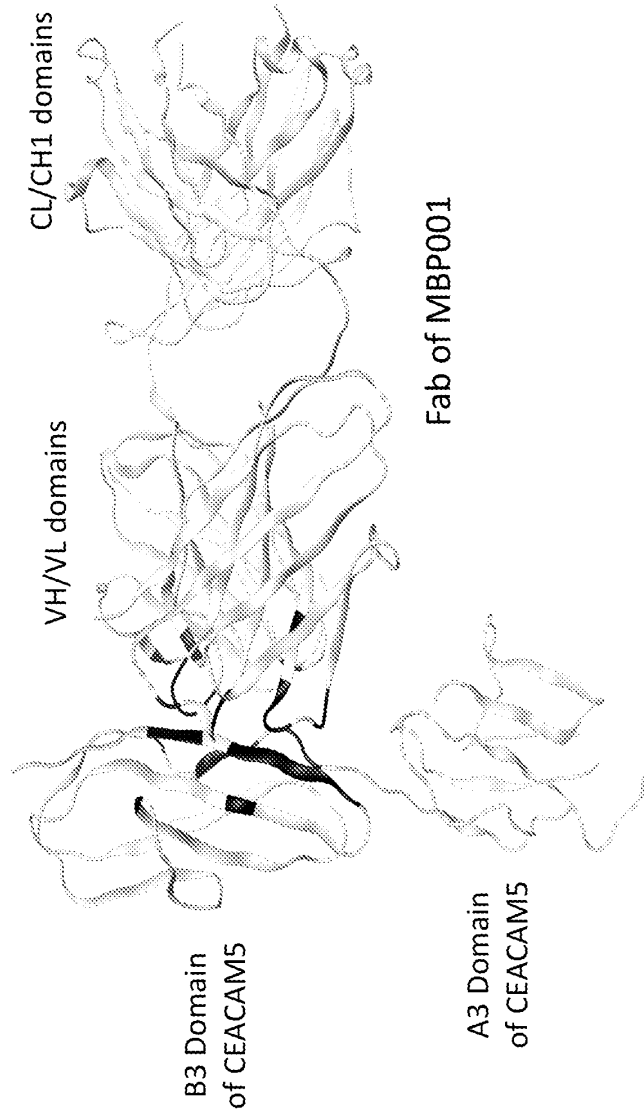


FIG. 14B



6xHis-A3-B3 huCEACAM5 (MBP001 epitope residues bolded)

HHHHHETVRFQGPKEPSNNNSKPVEDKDAVAFTEPAQNTTYLWVNGQSLPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYG**PD**TPIISPPDSSY
LSGANLNSCHSASNPSPQYSWRINGIPQQTQVLFIAKITPNNNGTYACFVSNLAT**GRNNSIV**KSITVSASGTSPLSA (SEQ ID NO: 24)

MBP001 VL (paratope residues bolded; CDRs underlined)

EIVLTQSPGTLSLSPGERATLSCRASQSVSS**SYLA**WYQQKPGQAPRLLIYGASSRAIGIPDRFSGSGSGTDFTLTISRLEPEDFAVWY**CCQYGSS**PYTFGQGTKEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 46)

MBP001 VH (paratope residues bolded; CDRs underlined)

QVQLVESGGGVVQPGRSLRLSCAASGIF**SSH**GMHWVRQAPGKGLEWV**TEISYD**GSYKSYVD**SV**KGRTISRDNKNTLYLQMNSLRAEDTAVVYCAT**GLTGT**GAFDIWGQGTMTV
TVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKSCGG (SEQ ID NO: 100)

FIG. 14C

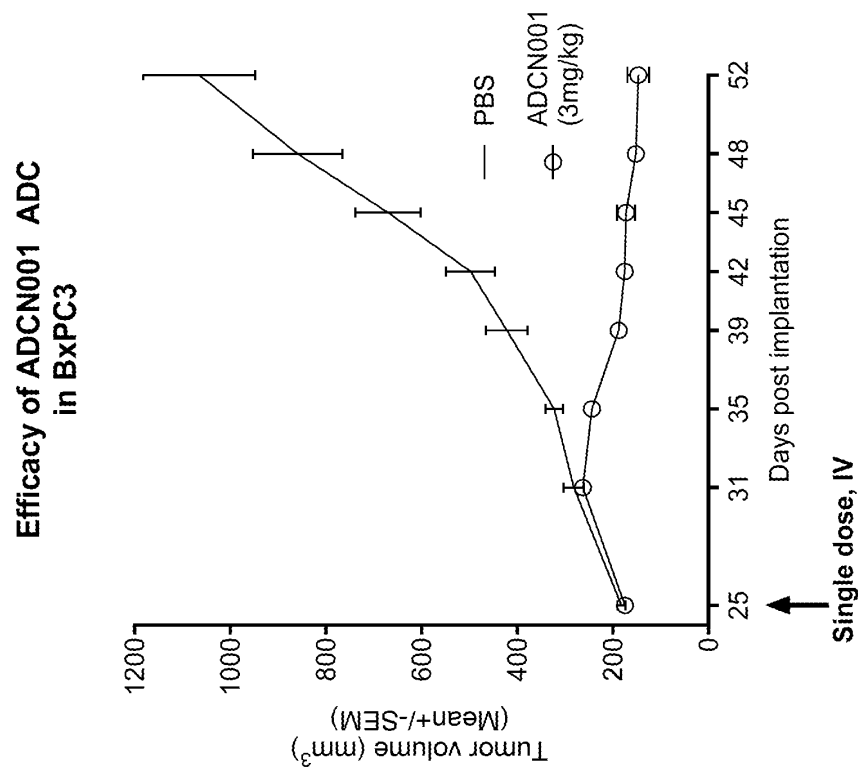


FIG. 15B

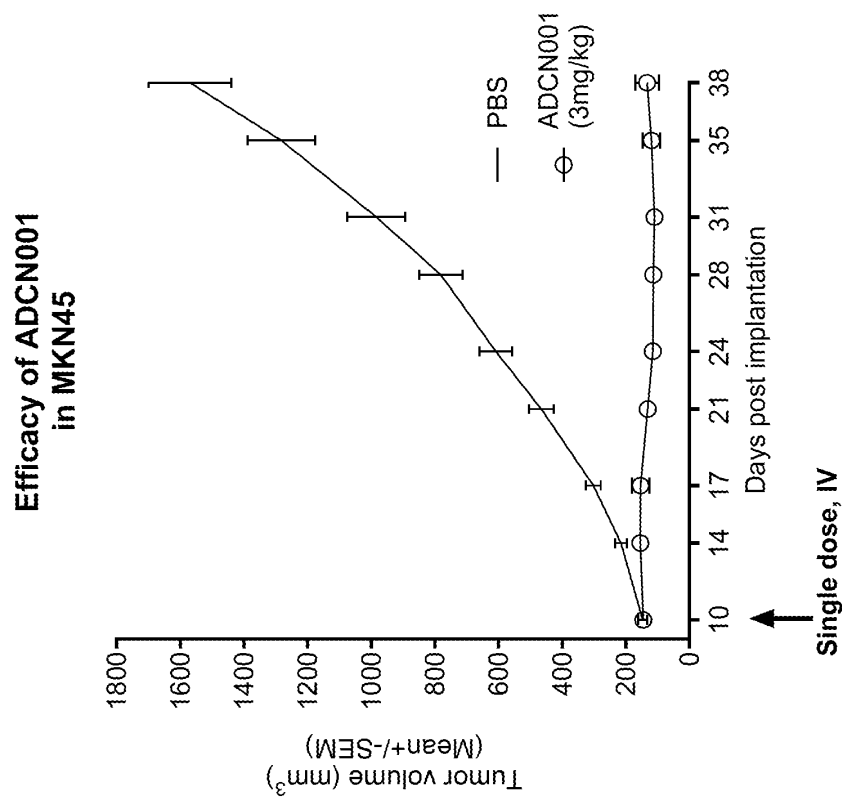


FIG. 15A

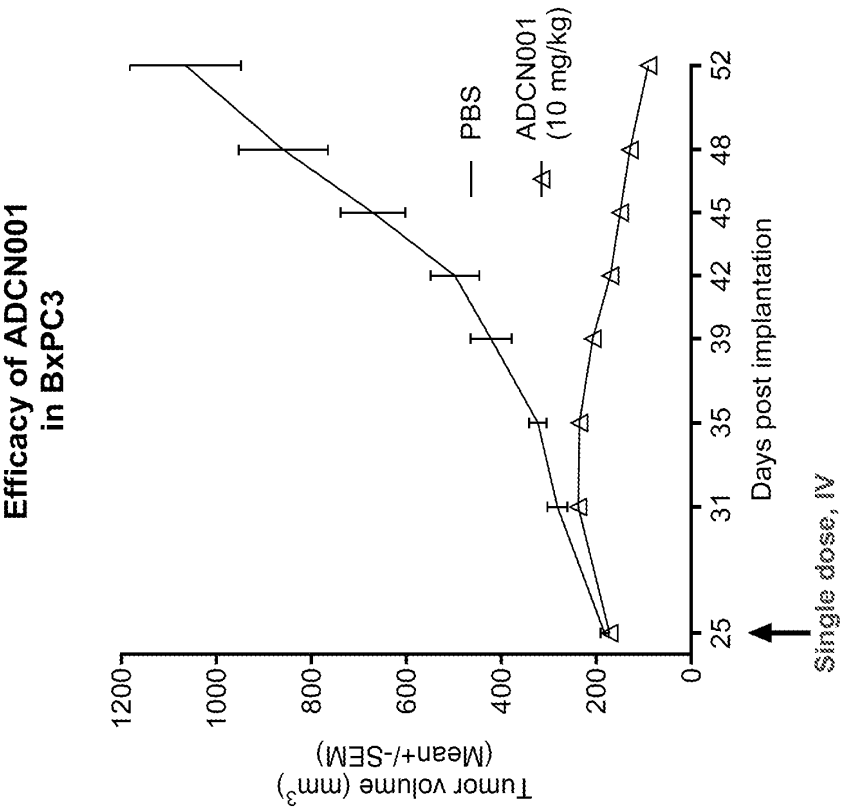


FIG. 15D

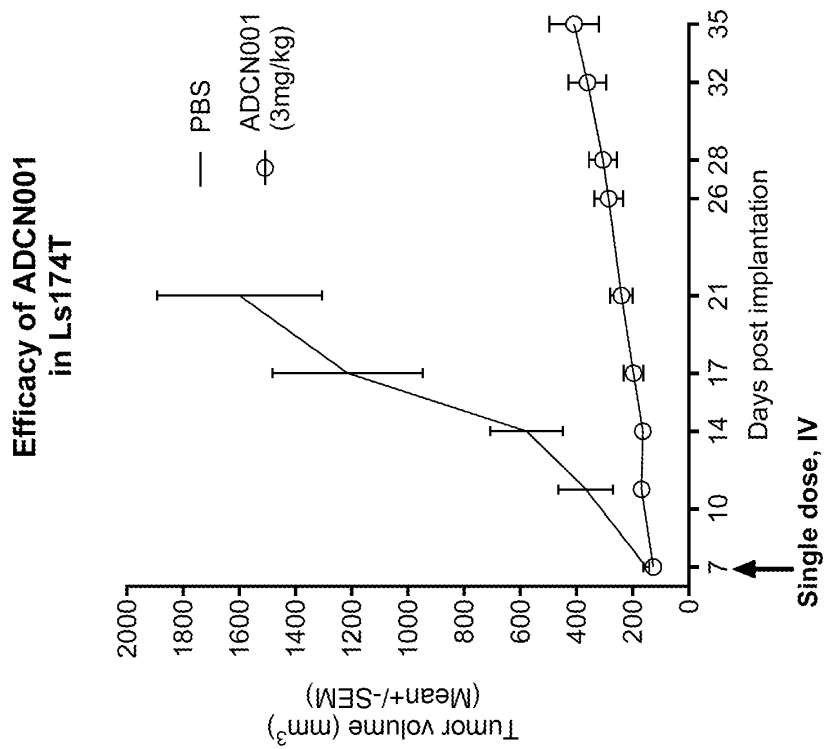


FIG. 15C

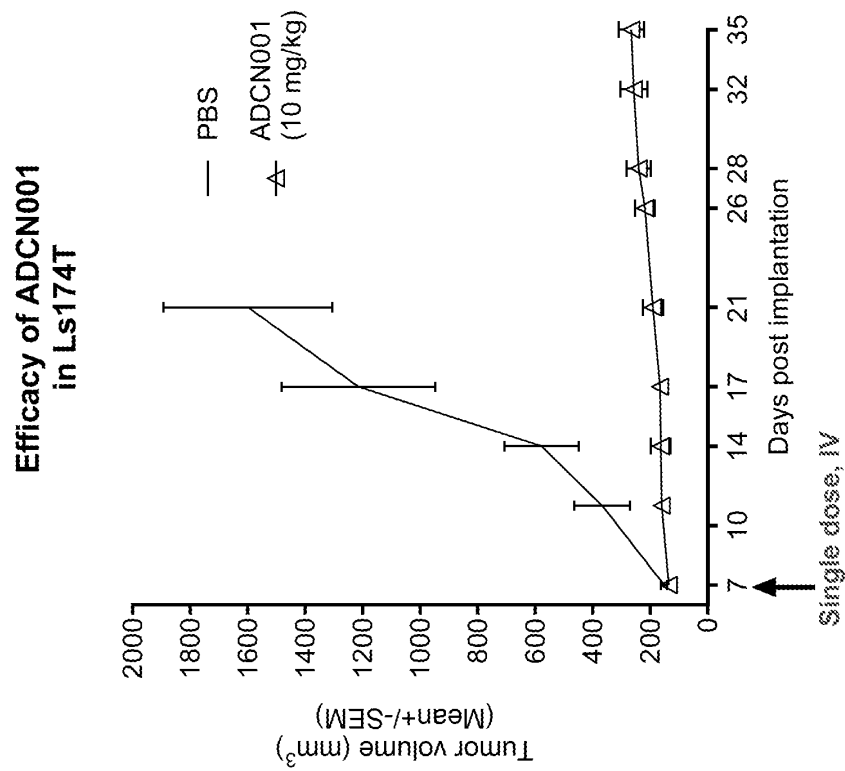


FIG. 15E

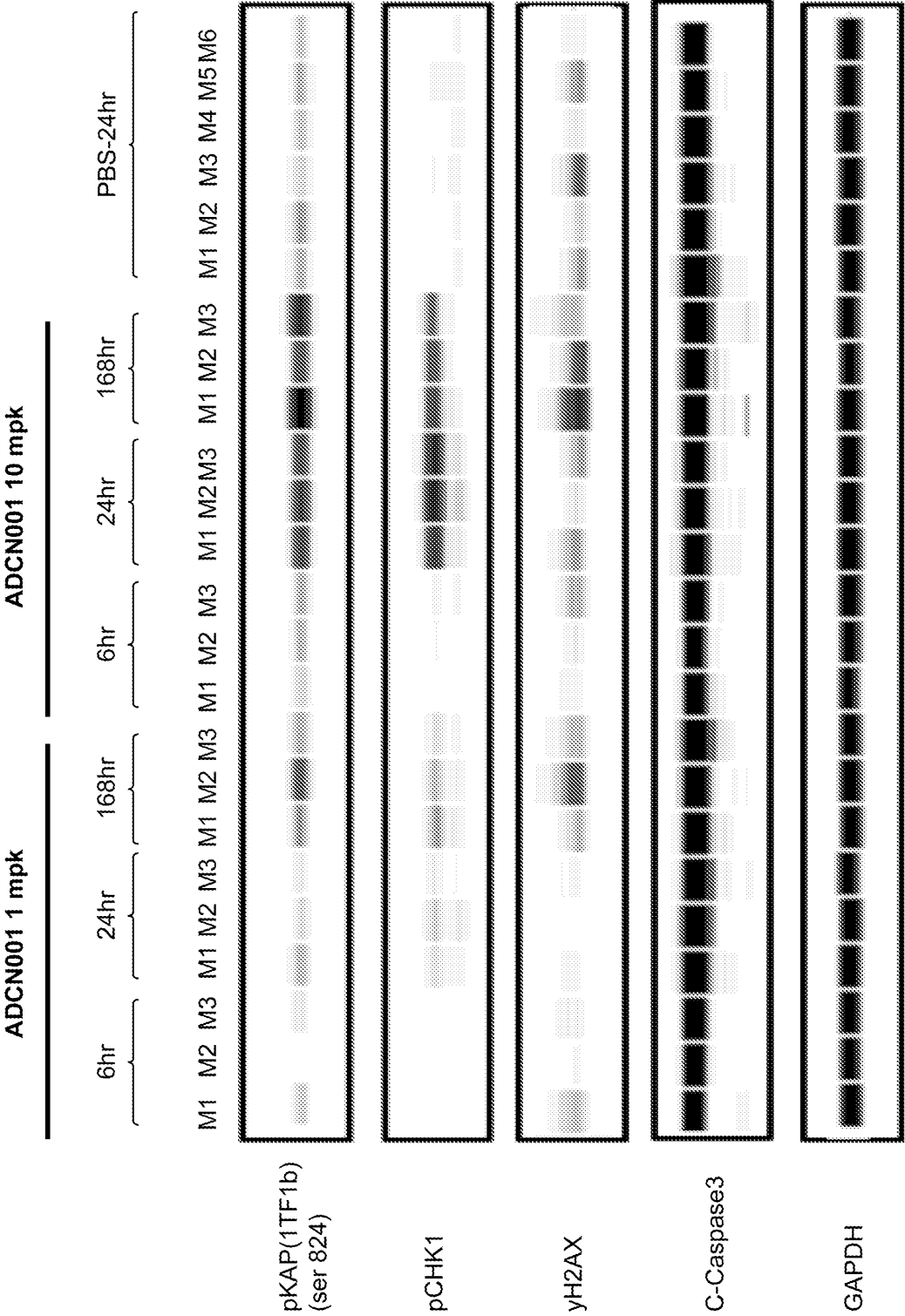


FIG. 16A

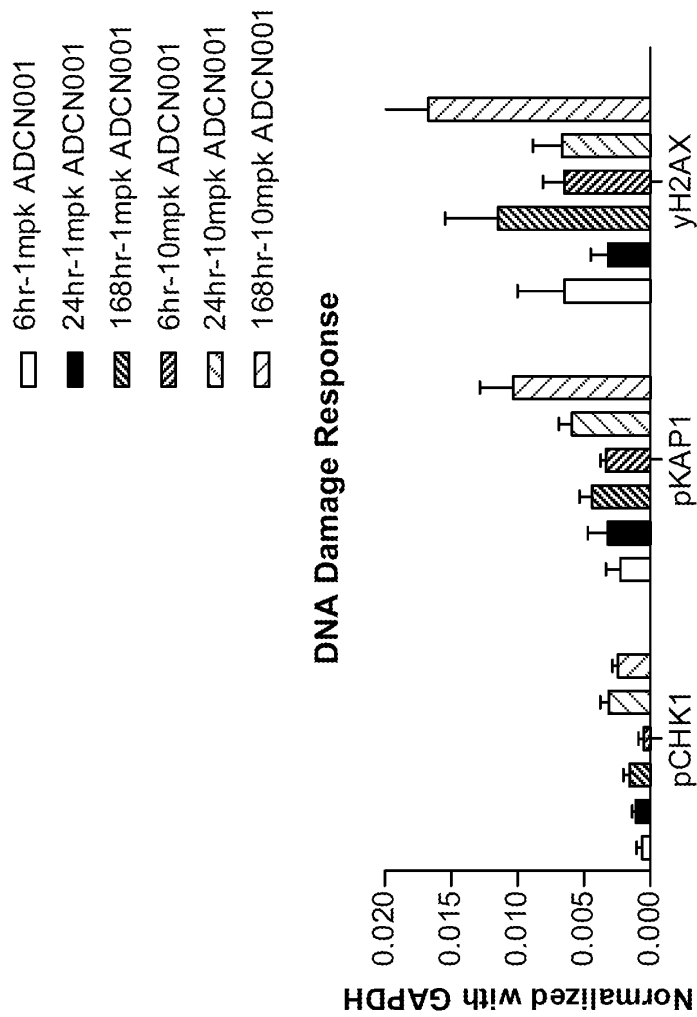


FIG. 16B

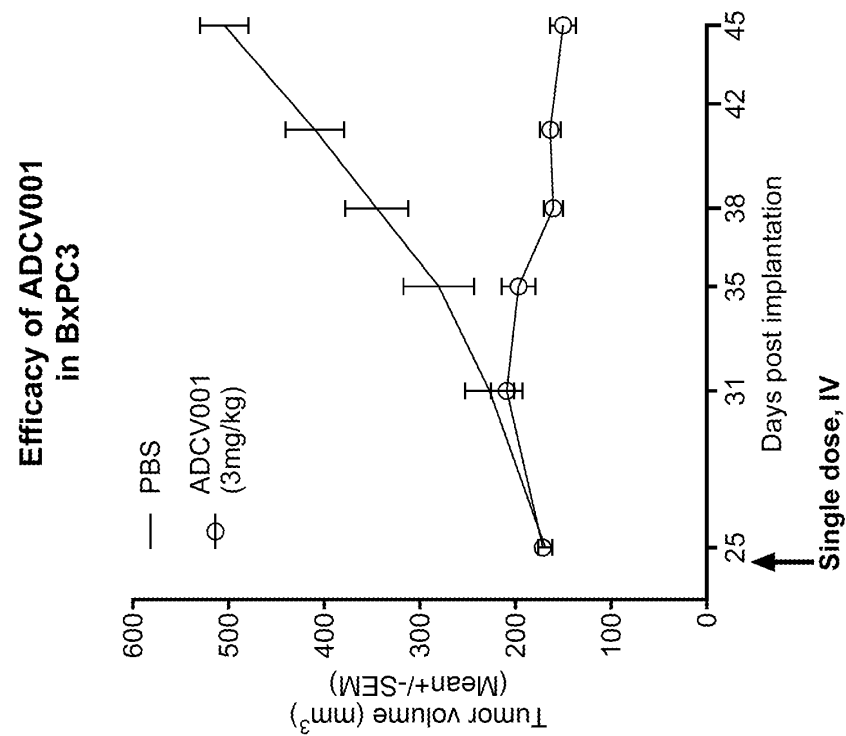


FIG. 17B

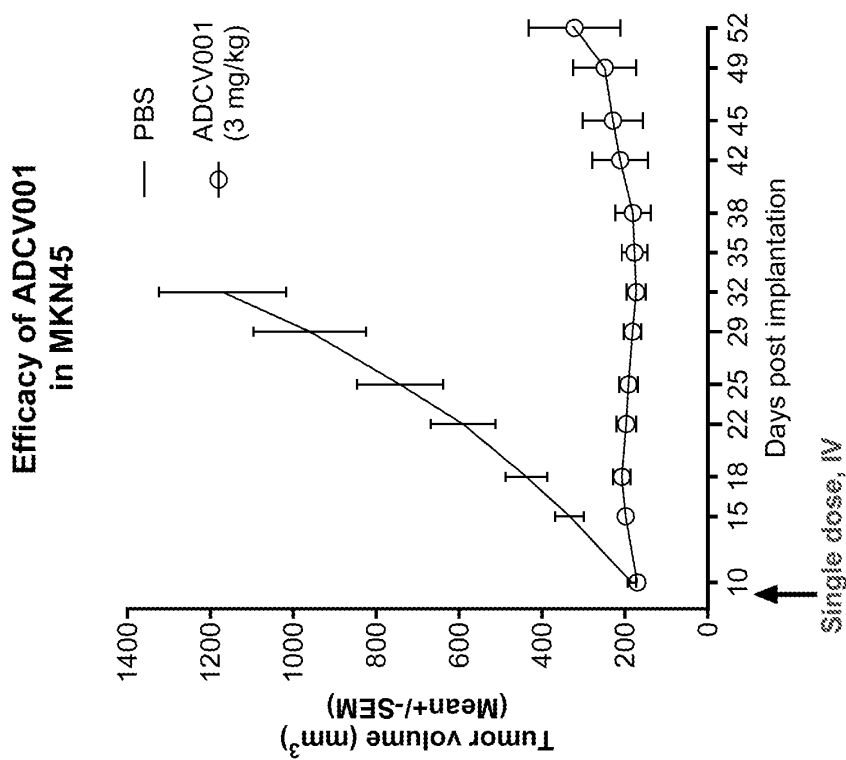


FIG. 17A

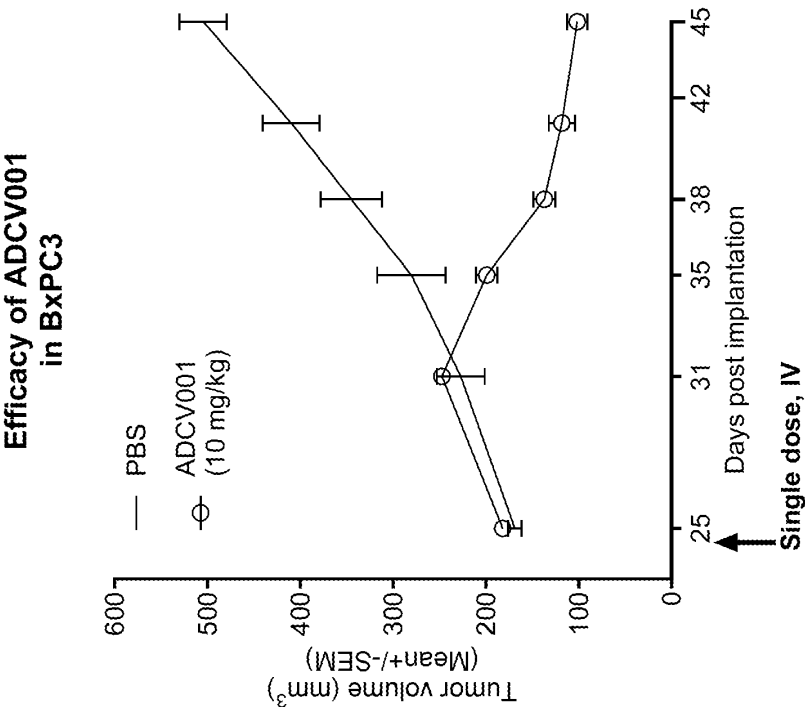


FIG. 17D

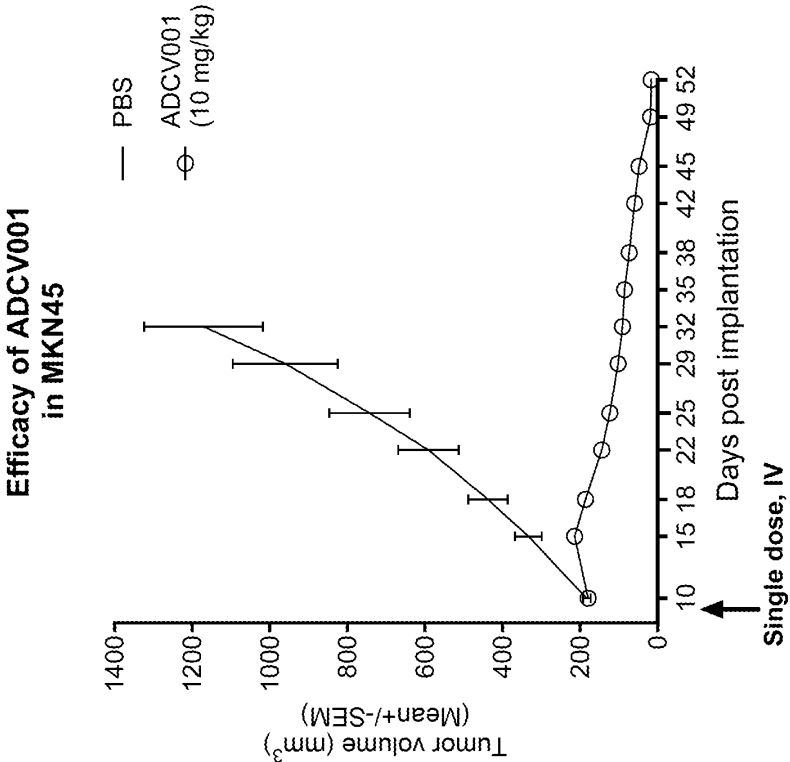


FIG. 17C

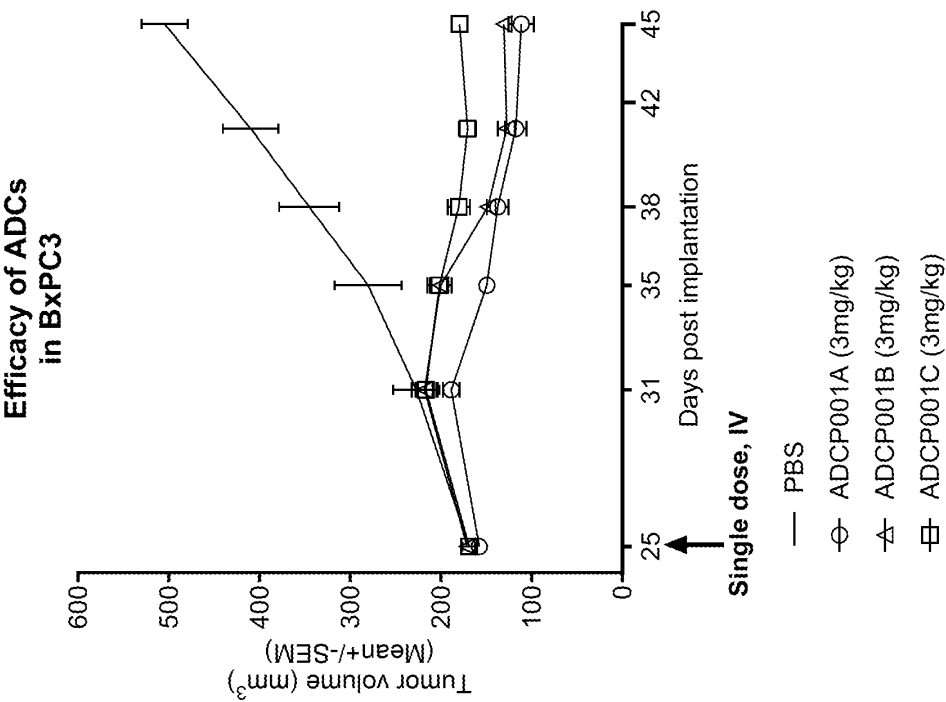


FIG. 18B

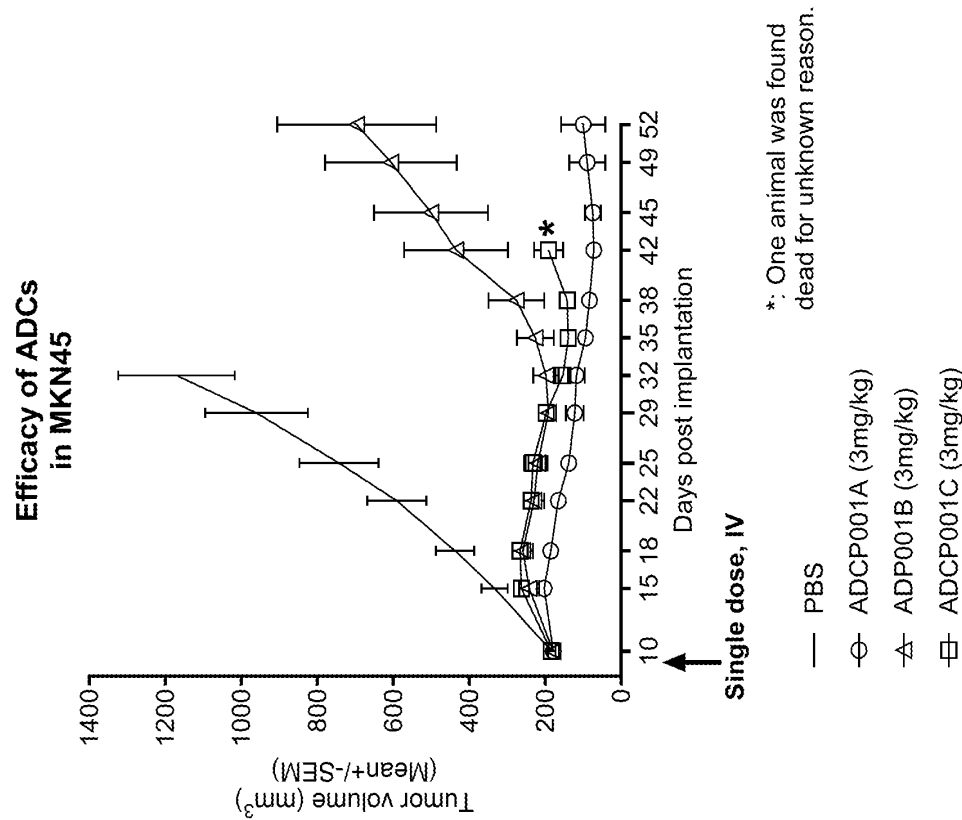


FIG. 18A

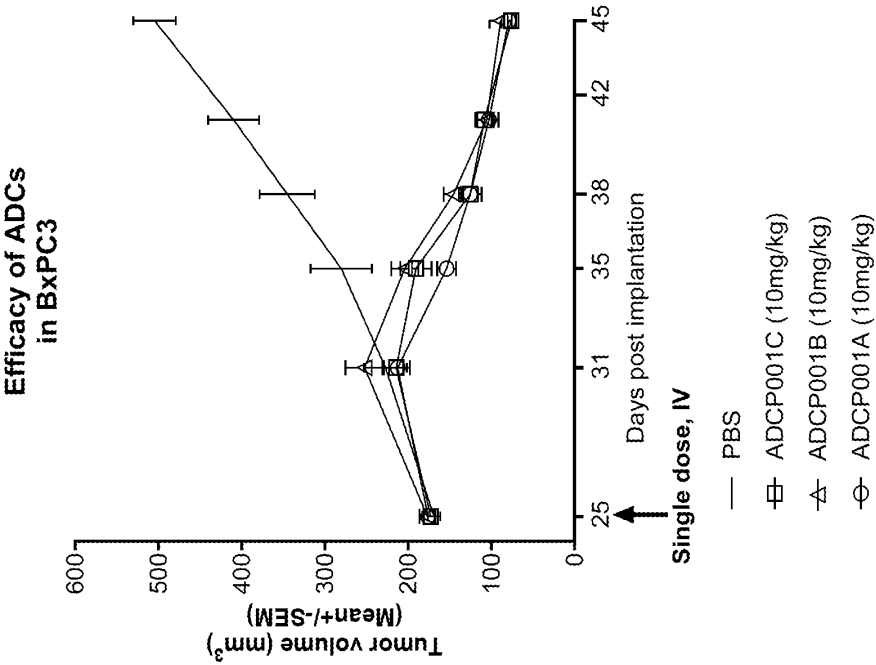


FIG. 18D

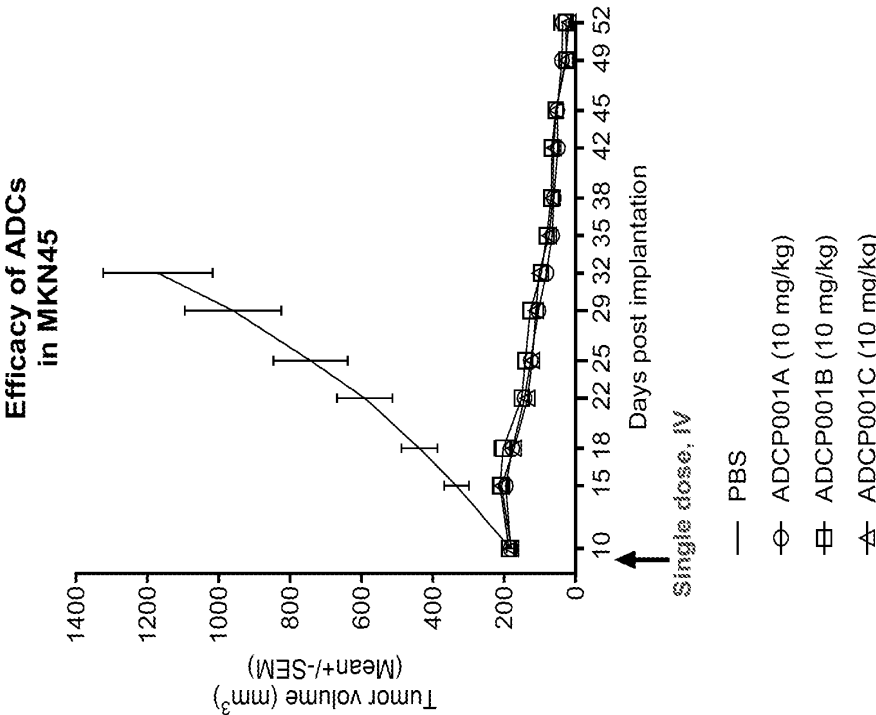


FIG. 18C

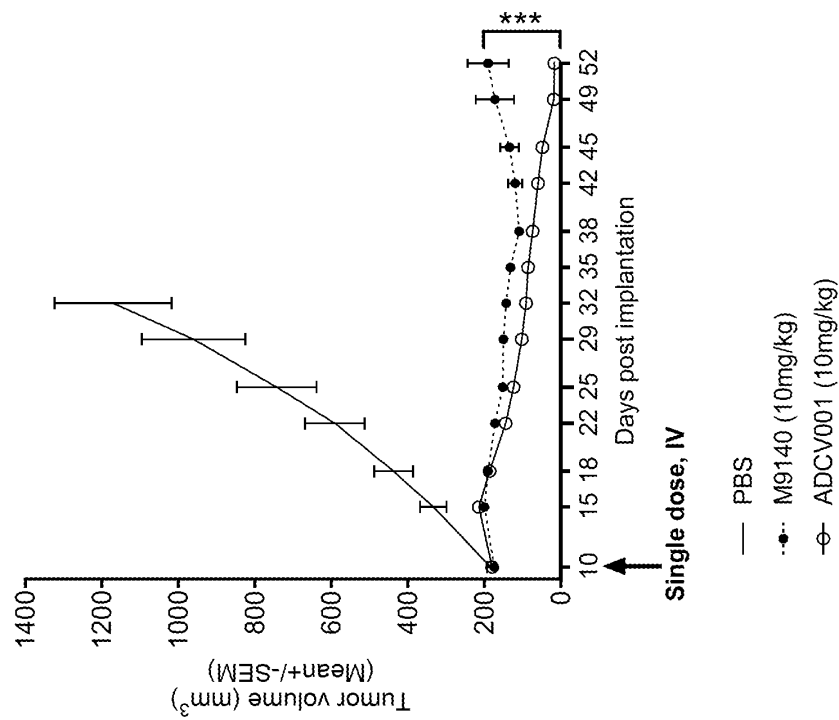


FIG. 19B

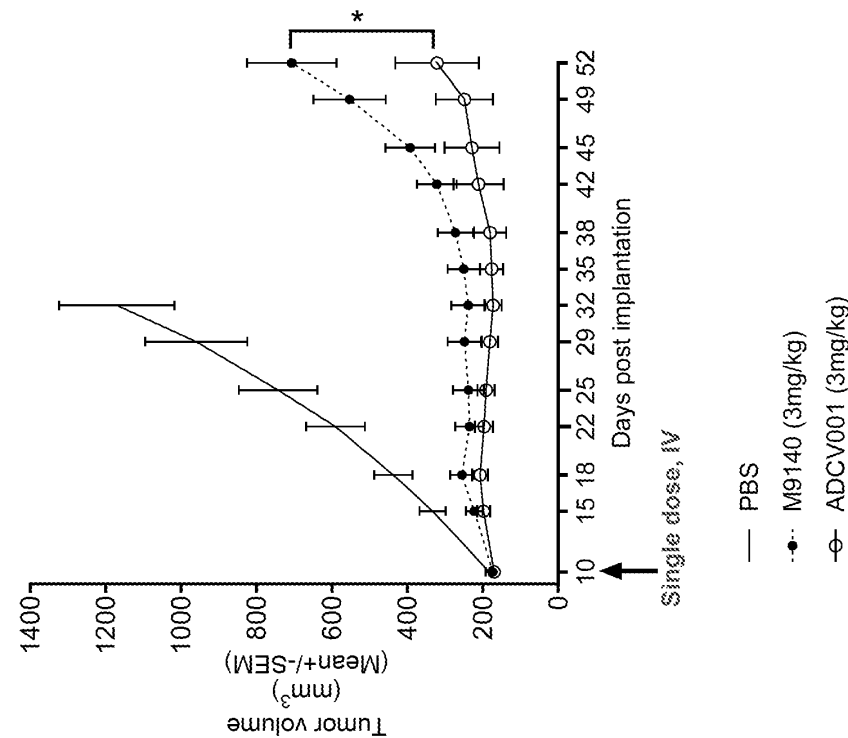


FIG. 19A

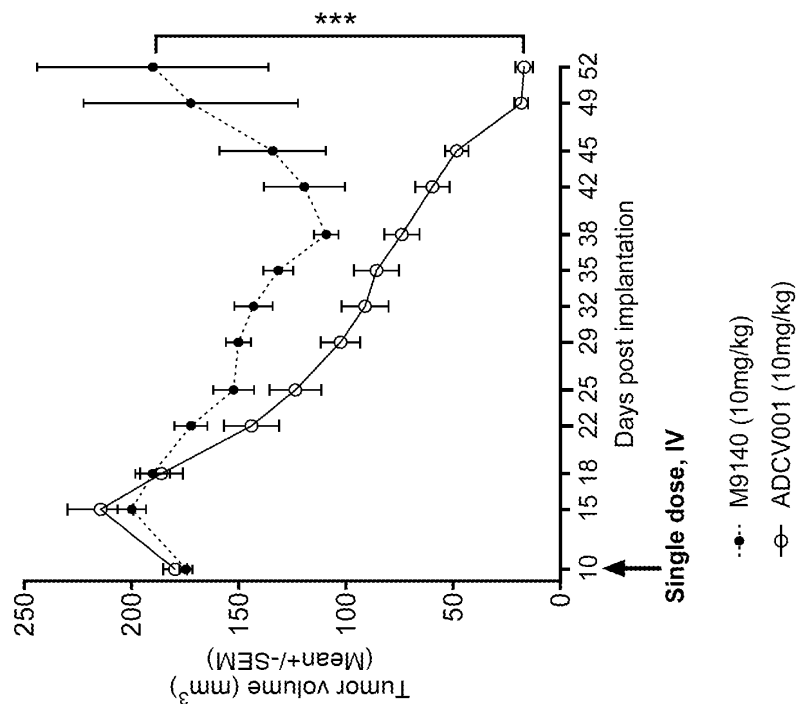


FIG. 19C

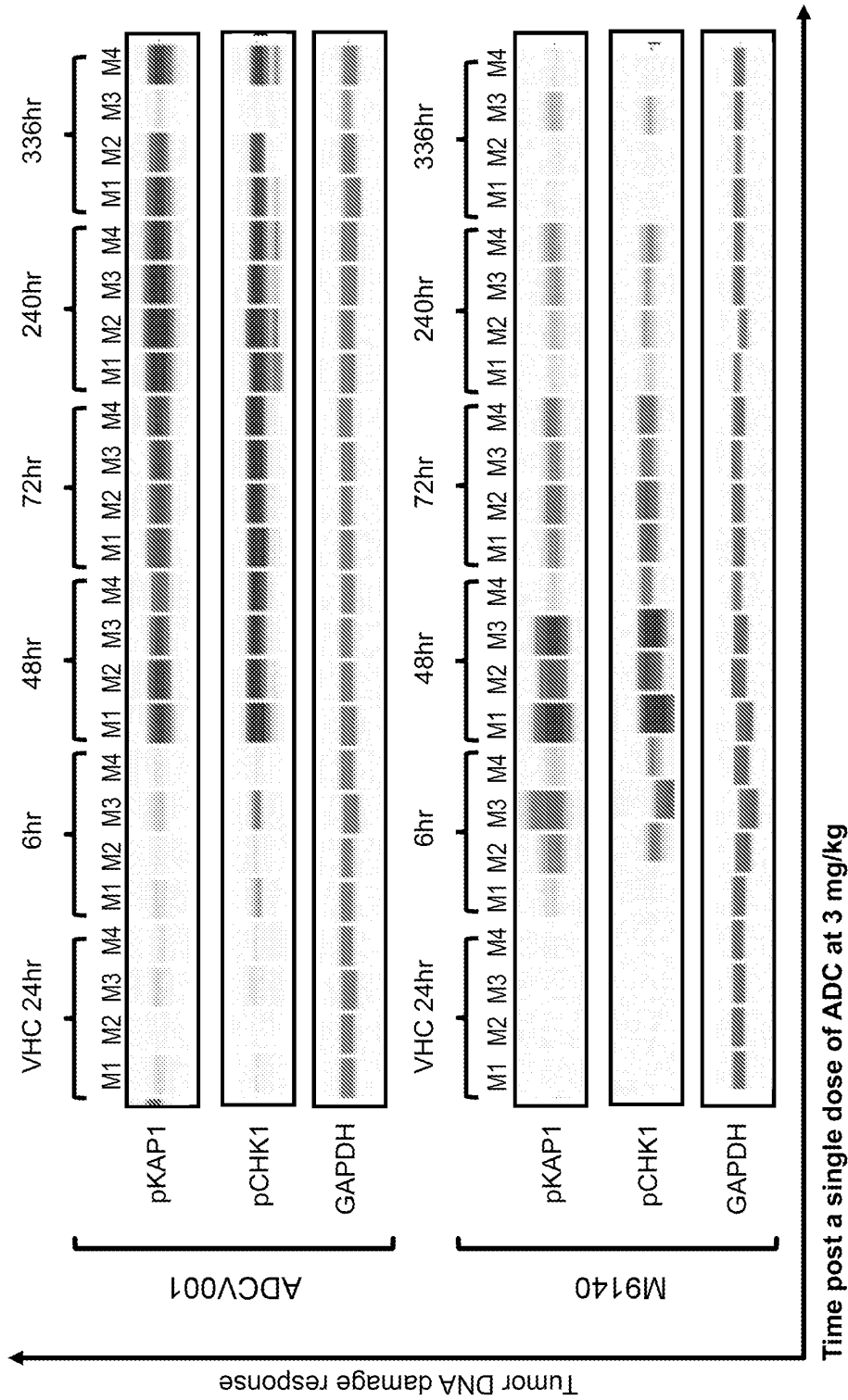


FIG. 20