

Figure 1

Mutation position	Mutation																			
	D	E	K	R	H	S	T	N	Q	G	A	V	L	I	C	M	P	F	Y	W
HC_N30X	0.97			0.97	0.94	1.01	0.96	1.01	1.00	0.98	0.96	0.95	1.01	0.99		0.94		0.99	1.01	0.97
HC_T31X		0.66	0.58	0.92	0.89	0.89	0.97	1.00	0.93	0.88	0.93	0.92	0.91	0.68	0.86	0.43	0.78	0.87	0.78	0.67
HC_Y32X				0.24	0.15	1.05	0.46	0.54	1.00	0.57	0.61	0.28	0.55	0.38	0.30	0.09	0.86	0.32	1.05	0.76
HC_N57X		0.94	0.88	0.93	0.90		1.06	0.93	1.00	1.01	0.90	0.96	0.87	0.97	0.94	0.74	0.94	0.48	0.88	0.98
HC_A59X		0.94	0.82	0.99	0.95	1.00	0.98	0.74	1.03	0.95	1.00	1.00	0.96	1.02		0.92	1.00	0.81	0.99	1.00
HC_H101X				0.47	0.00	1.00	0.86	0.37	0.56	0.16	0.07	0.92	0.68	0.43	0.32	0.10		0.23	0.00	0.00
HC_G105X			1.11		1.07	1.16	0.34	0.22	1.15	1.26	1.00	1.22	1.14	1.11	1.15	0.38	1.07	1.35	1.11	1.10
HC_S110X			0.00	0.00	0.00	0.00	1.00	0.32	0.00	0.00	0.19	0.71	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
HC_Y114X			0.88	0.86	0.79	1.06	1.05	0.99	1.02	0.92	0.43	0.97	0.90	0.95	0.96	0.98	0.88	0.11	1.03	0.99
LC_T31X		0.79	0.98	0.75	1.01	0.97	1.03	1.00	0.94	0.89	1.01	1.02	1.01	0.72	0.98		0.97	0.92	1.00	0.93
LC_I92X		0.06	0.45	0.44	0.09		0.87	0.95	0.81		0.76	0.89	0.94	1.00	0.96	1.00	0.93	0.21	0.98	0.50
LC_I97X		1.04	0.98	1.01	1.01	0.96	0.96	0.97	0.97	1.01	0.99		0.98	1.00		0.92	0.94	0.93	0.96	0.94

Figure 2

SEQ alignment

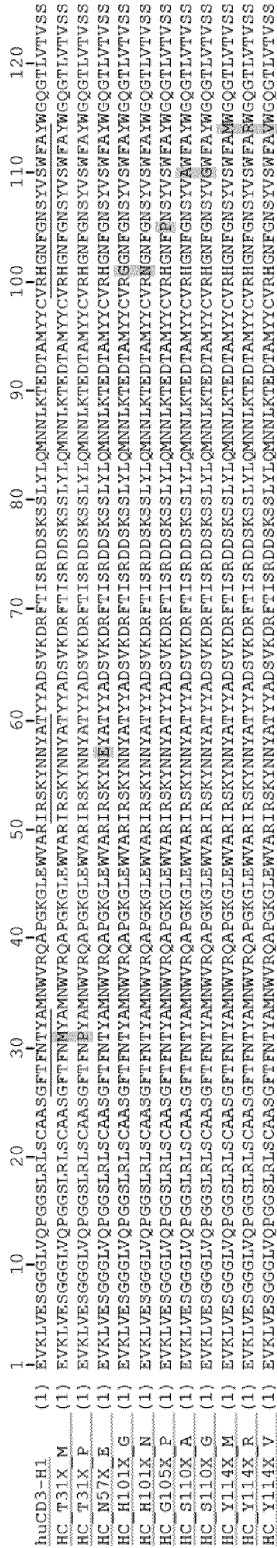


Figure 3

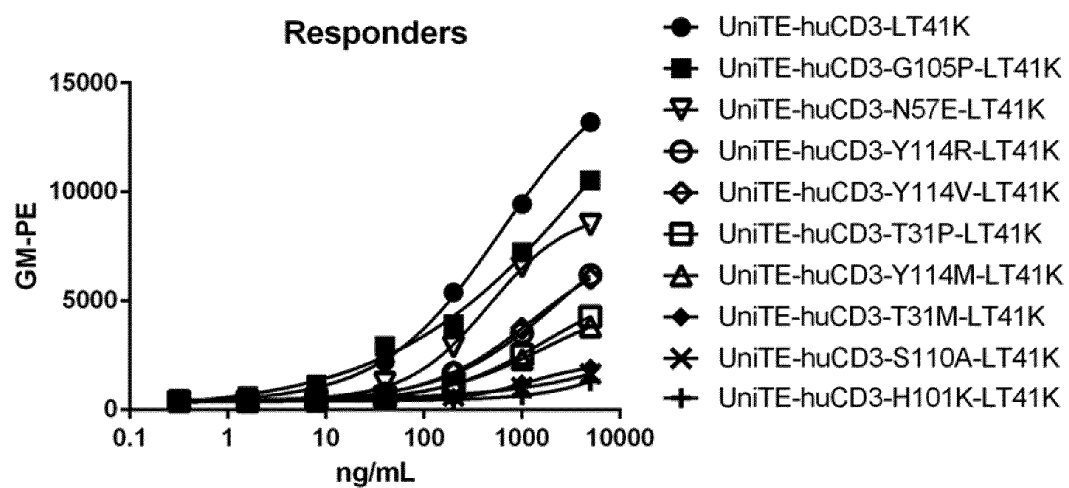


Figure 4

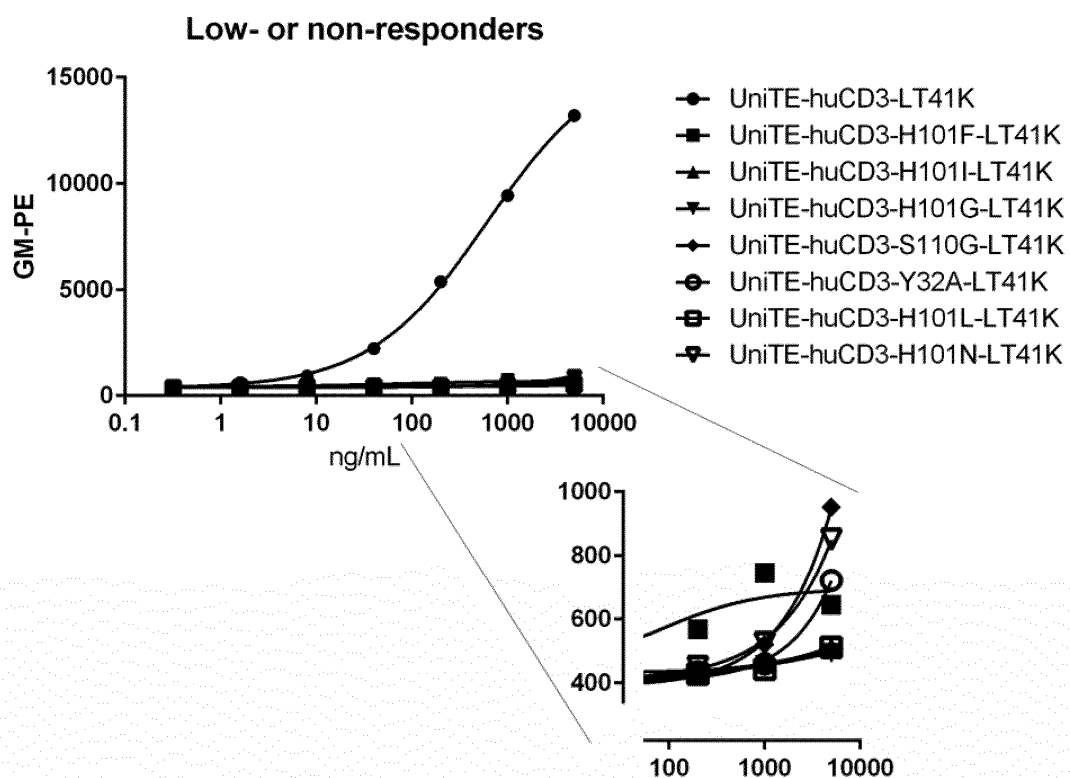


Figure 5

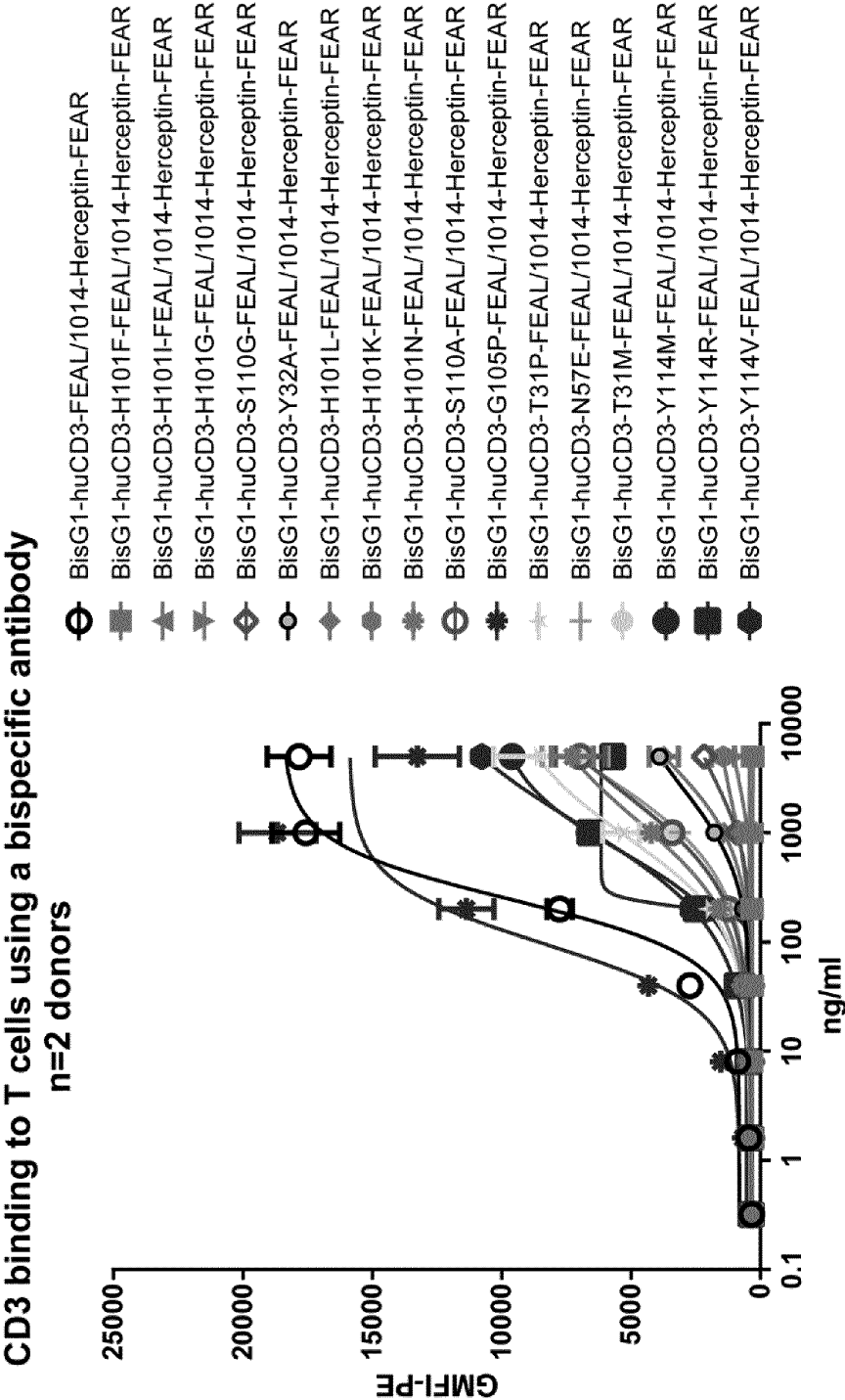


Figure 6A

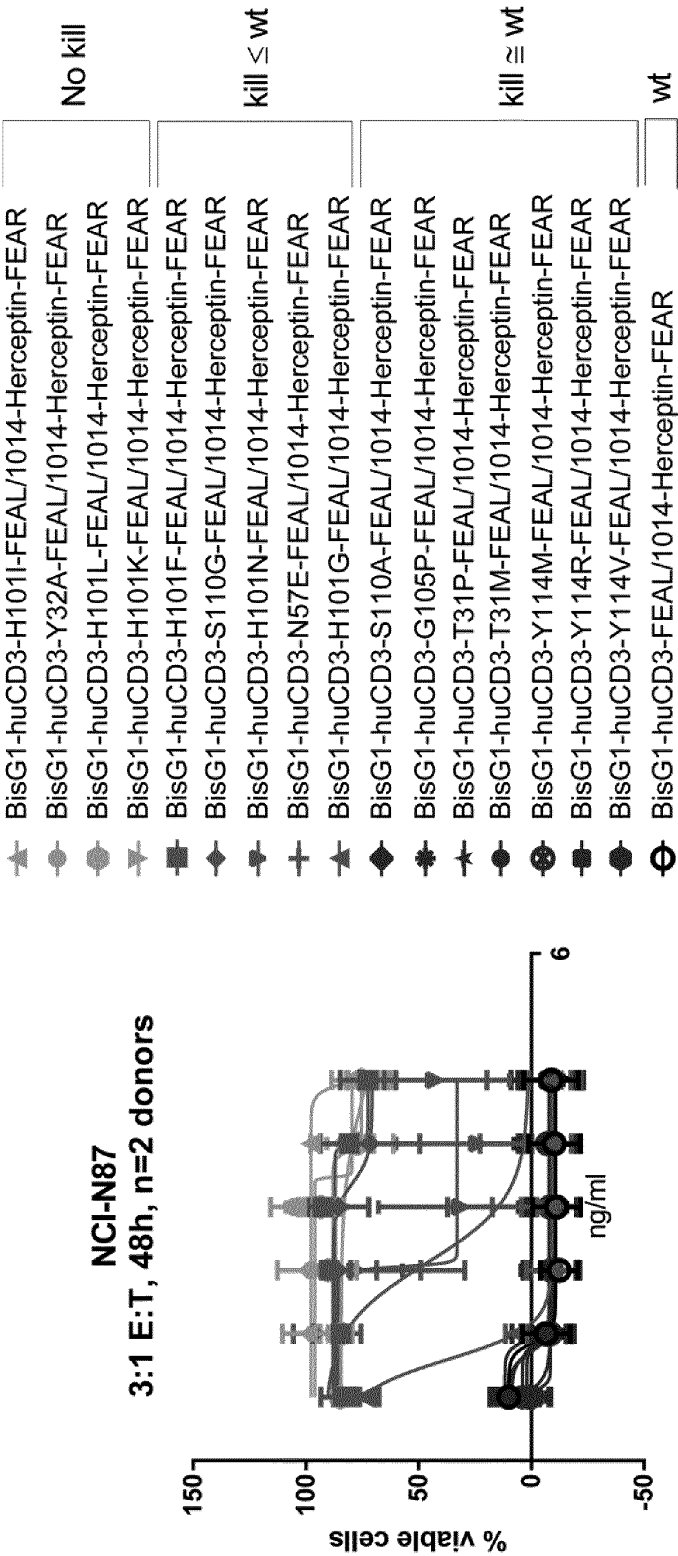


Figure 6B

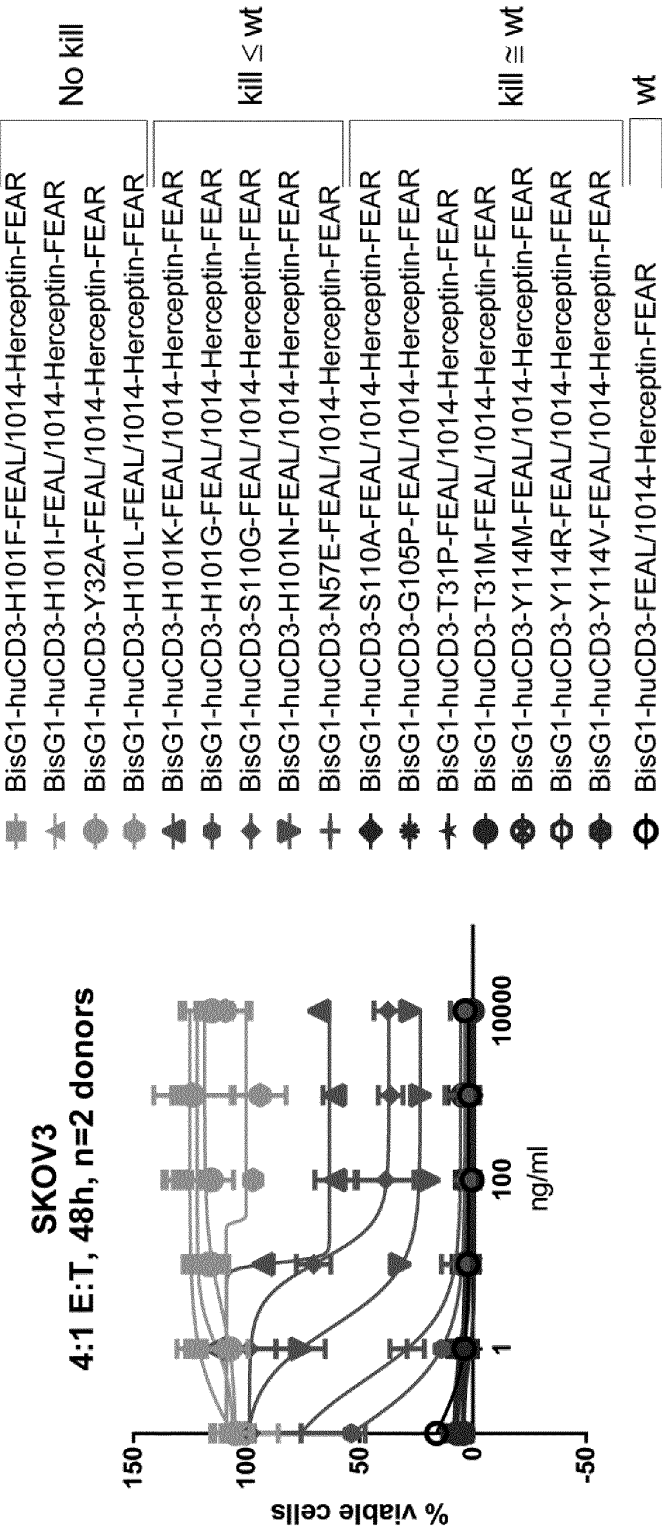


Figure 6C

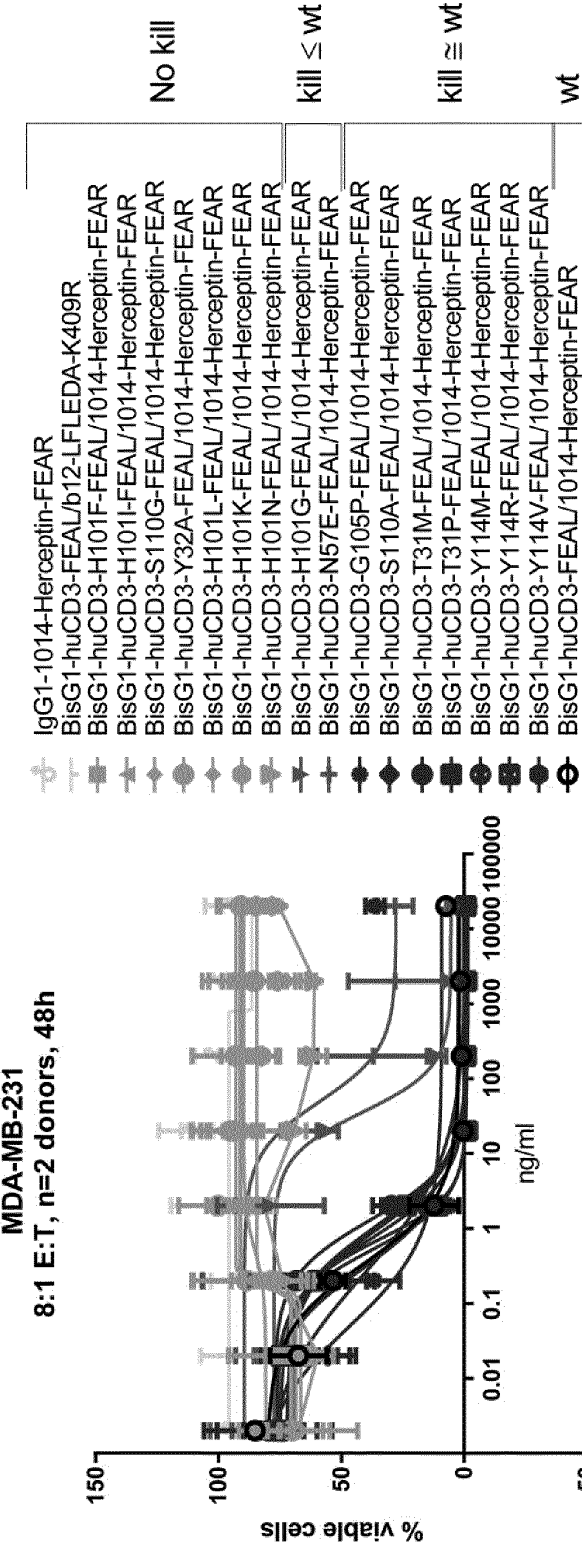


Figure 7

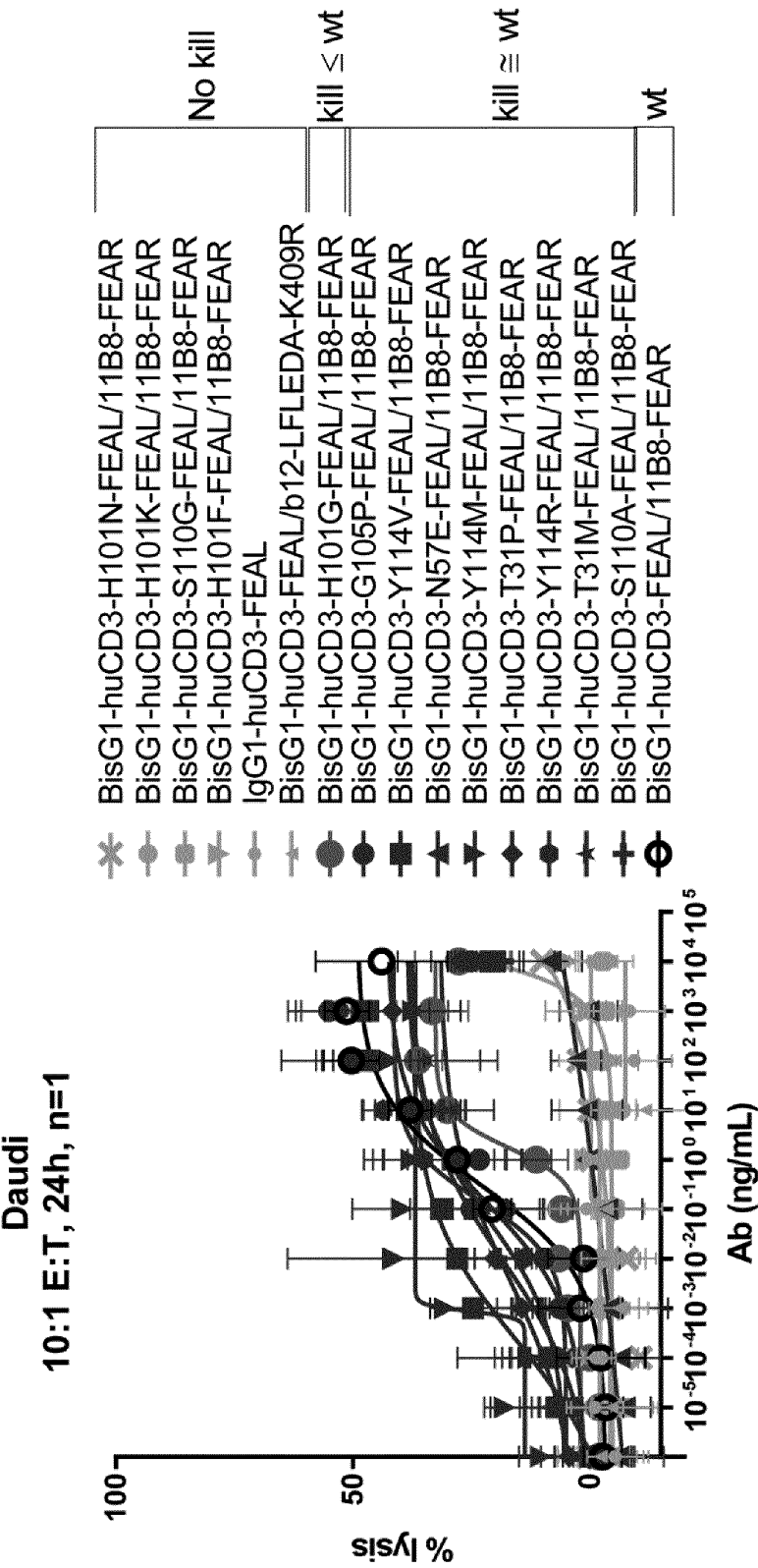


Figure 8a

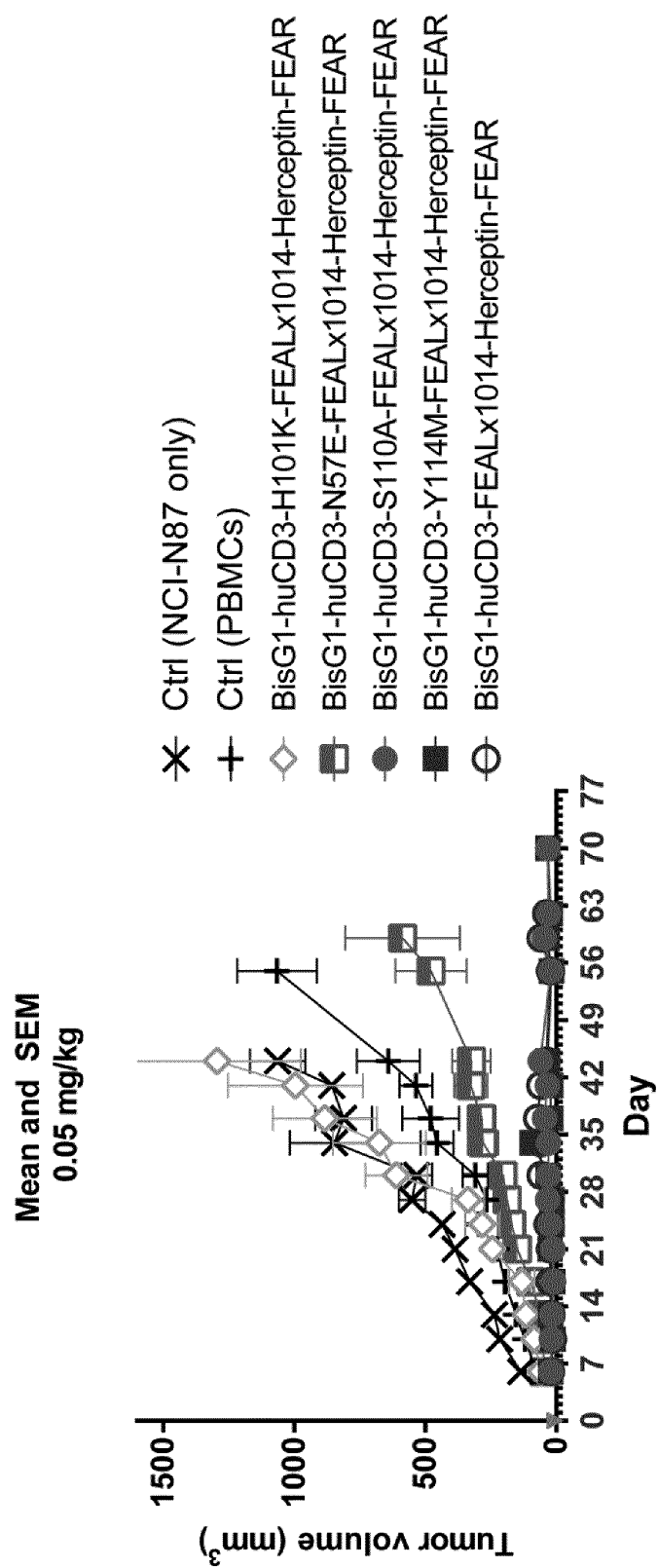


Figure 8b

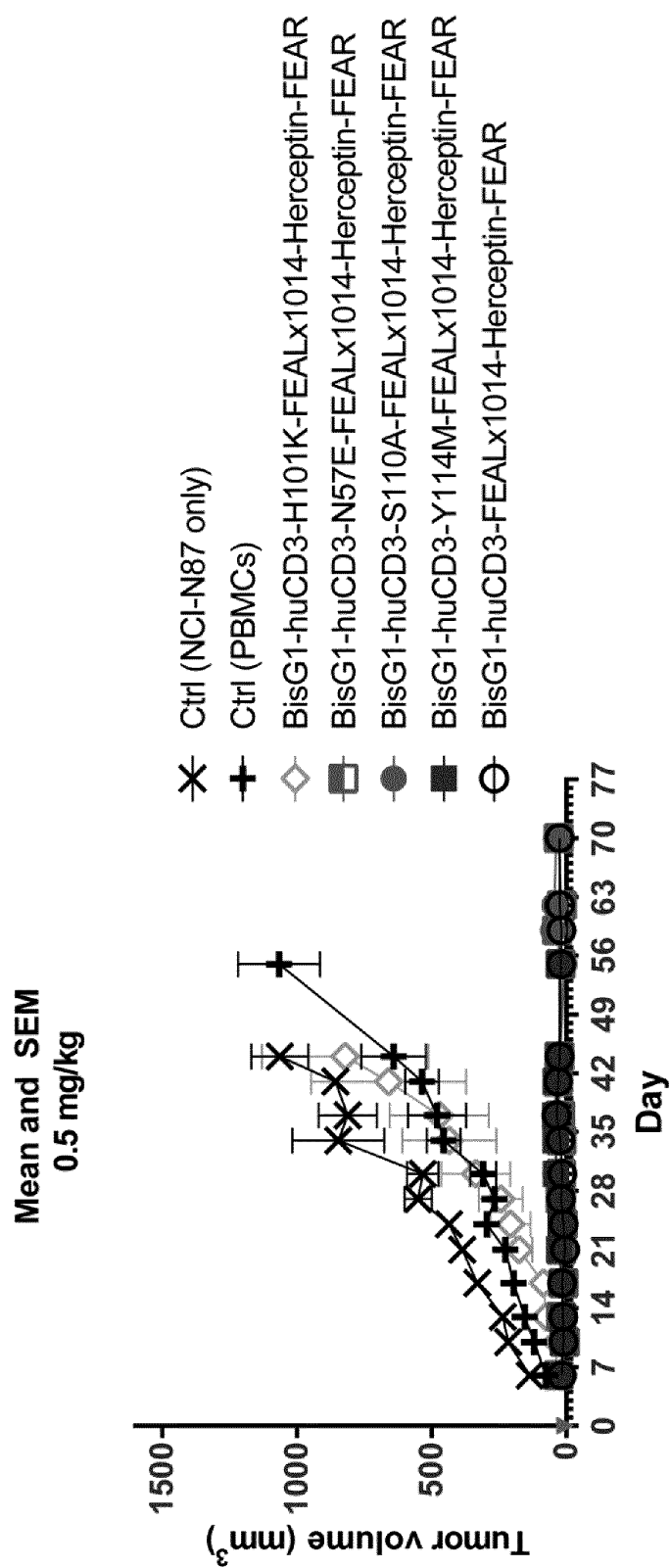


Figure 8c

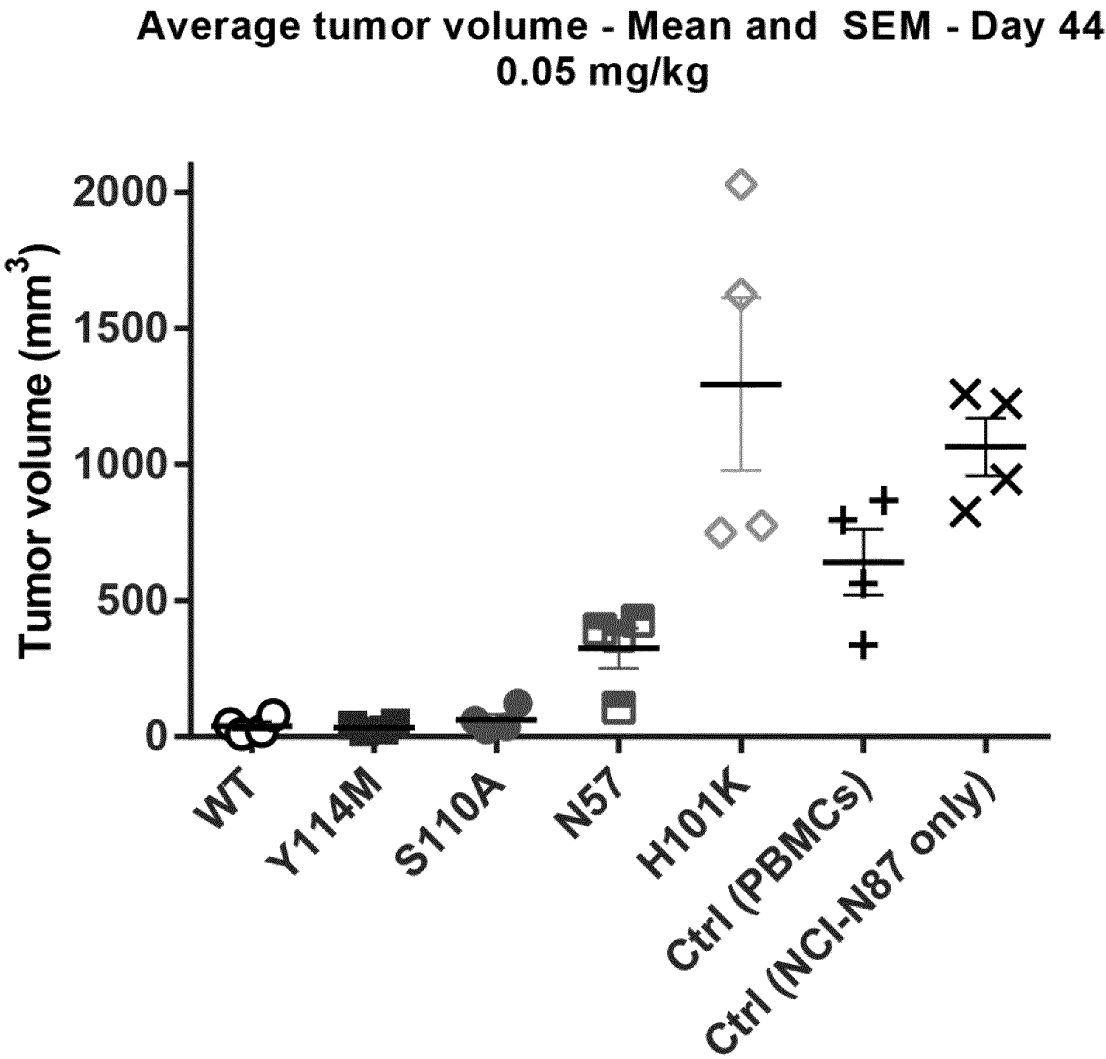


Figure 8d

