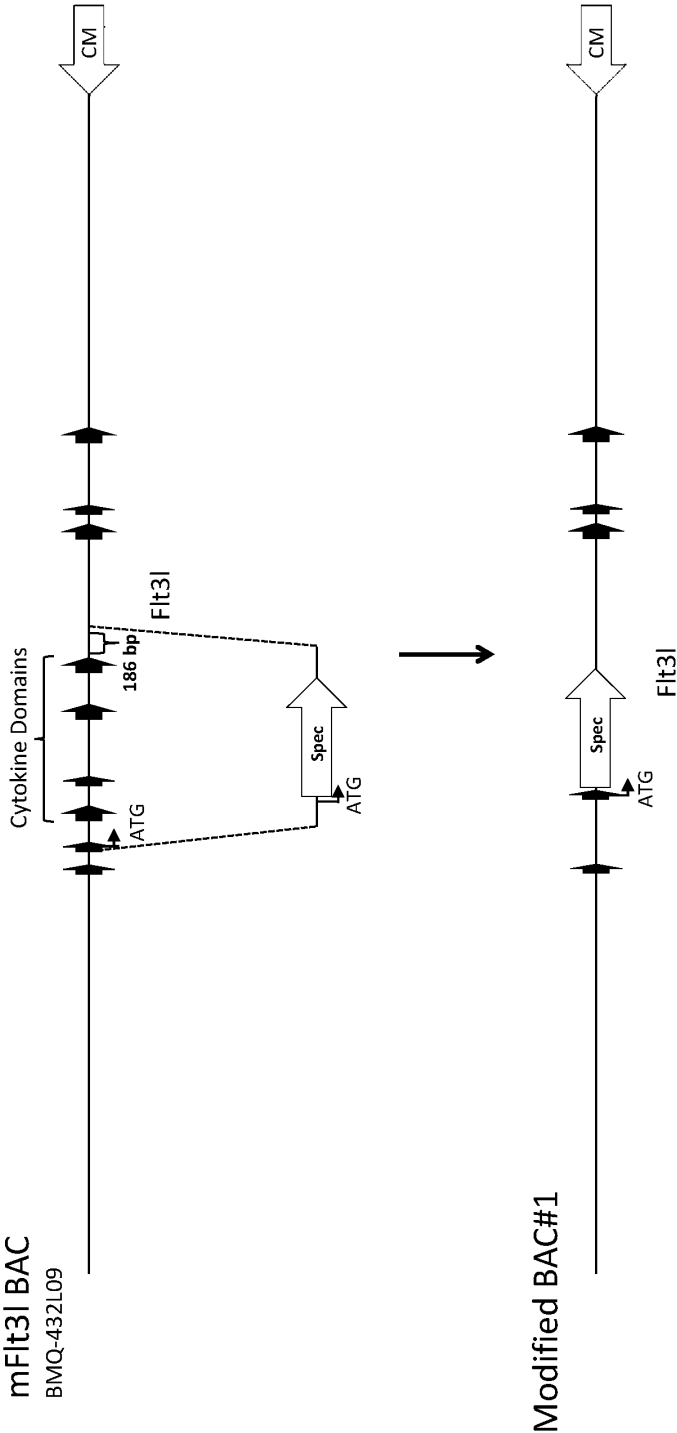


FIG. 1A



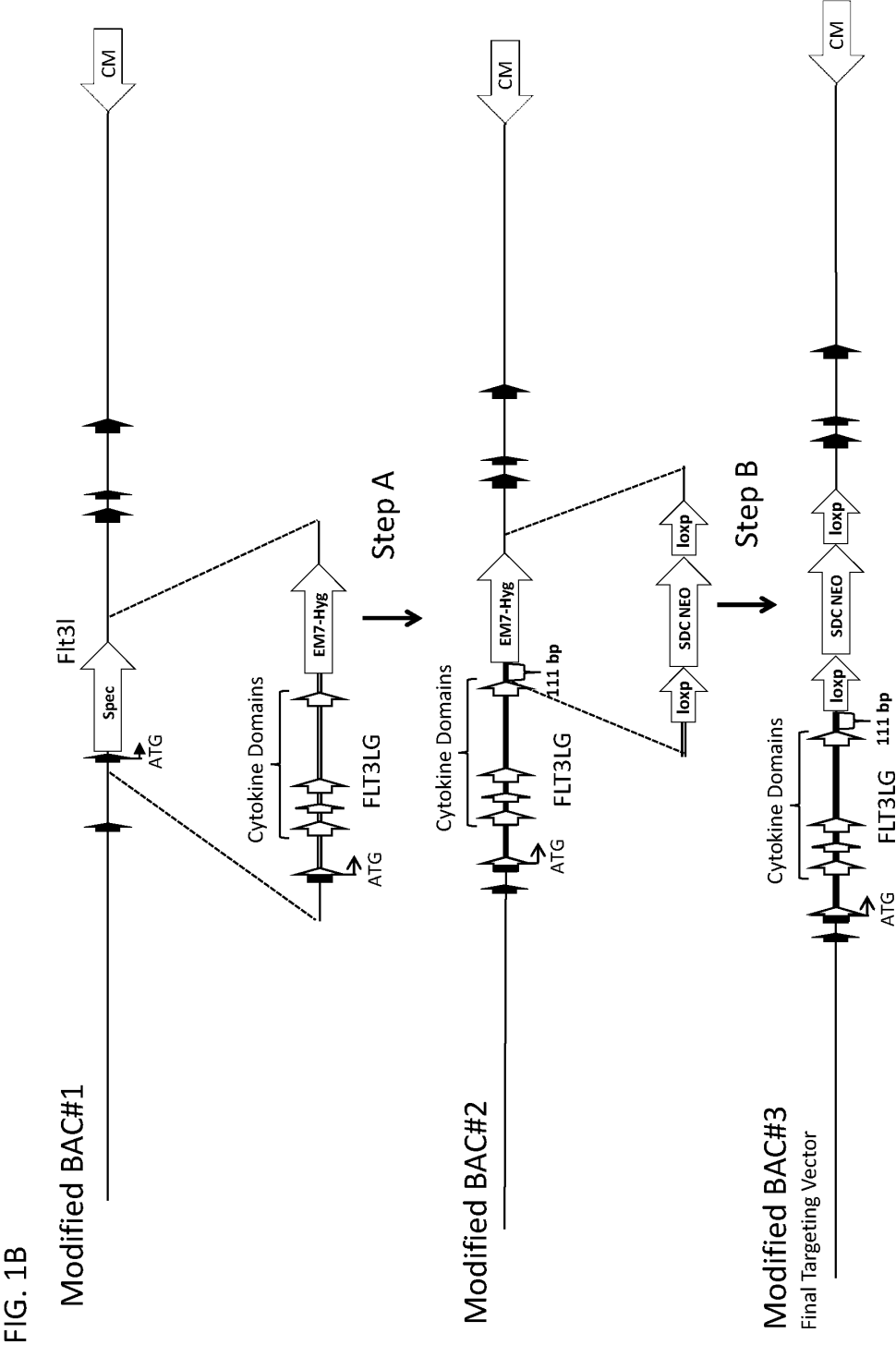


FIG. 1C

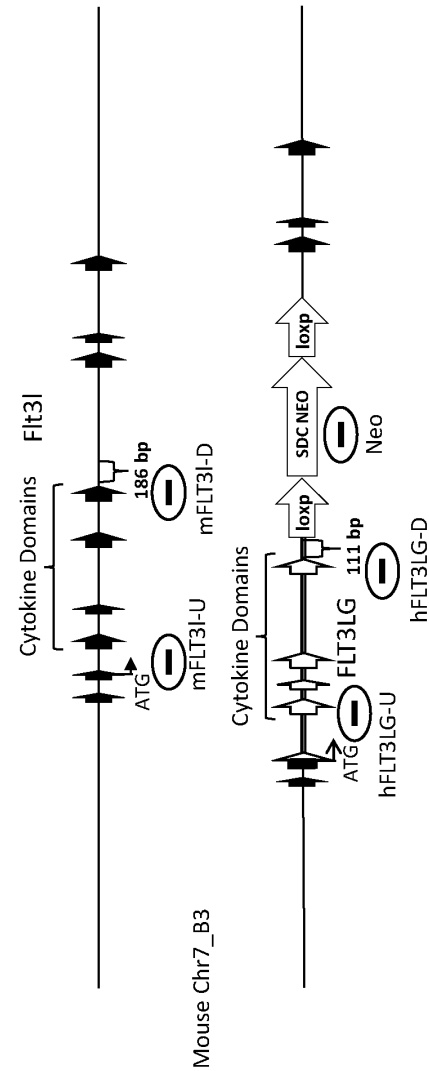


FIG. 1D

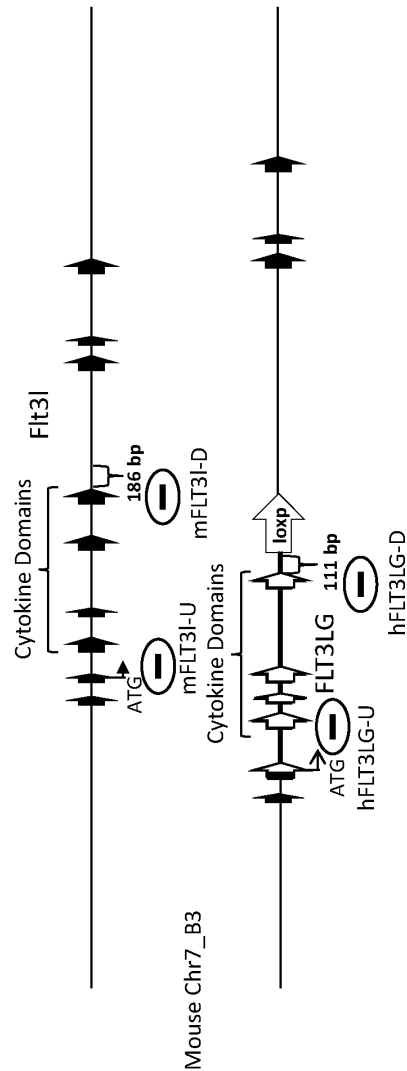


FIG. 1E

Formatted Alignments

cytokine-like core domain

Signal Peptide

mFlt3L_MB
Chimeric_Flt3LG_MB
hFlt3LG_MB

MTVLAPAWSPN	SS	L	L	L	L	L	S	P	C	R	G	T	P	D	Q	F	S	H	S	P	I	S	S	N	F	K	V	K	F	R	E	L	T	D	H	L	L	K	D	Y	P	V	T	V	A	M	N	L	Q	D	E	K		
MTVLAPAWSP	-	T	T	Y	L	L	L	L	S	S	G	L	S	G	T	Q	D	C	S	F	H	S	P	I	S	S	D	F	A	V	K	I	R	E	L	S	D	L	L	Q	D	Y	P	V	T	V	A	S	N	L	Q	D	E	E
MTVLAPAWSP	-	T	T	Y	L	L	L	L	S	S	G	L	S	G	T	Q	D	C	S	F	H	S	P	I	S	S	D	F	A	V	K	I	R	E	L	S	D	L	L	Q	D	Y	P	V	T	V	A	S	N	L	Q	D	E	E

mFlt3L_MB
Chimeric_Flt3LG_MB
hFlt3LG_MB

140	C	K	A	W	S	L	E	L	A	Q	R	W	I	E	Q	L	K	T	V	A	G	S	K	M	Q	L	L	E	D	V	N	T	E	I	H	F	V	T	S	C	I	F	Q	P	L	P	E	C	L	R	F	V	Q	T	N	I	S	H	L	K	D	T	C	J	Q	L	L	
139	C	G	G	L	W	R	L	V	L	A	Q	R	W	M	E	R	L	K	T	V	A	G	S	K	M	Q	L	L	E	R	V	N	T	E	I	H	F	V	T	K	C	A	F	P	P	P	S	C	L	R	F	V	Q	T	N	I	S	R	L	L	Q	E	T	S	E	Q	L	V
139	C	G	G	L	W	R	L	V	L	A	Q	R	W	M	E	R	L	K	T	V	A	G	S	K	M	Q	L	L	E	R	V	N	T	E	I	H	F	V	T	K	C	A	F	P	P	P	S	C	L	R	F	V	Q	T	N	I	S	R	L	L	Q	E	T	S	E	Q	L	V

Transmembrane domain

stalk

141	ALKPCTGKACQNF	SRCLEVMQCQPD	SSTLLPPRSPIA	EATELPEPR	PRQLLLLLLL	PLTLVLA	AAWG	210
140	ALKPWITR	---QNFSRCLE	QCQPD	SSTLLPPRSPIA	EATELPEPR	PRQLLLLLLL	PLTLVLA	AAWG
140	ALKPWITR	---QNFSRCLE	QCQPD	SSTLLPPRSPIA	EATELPEPR	PRQLLLLLLL	PLTLVLA	AAWG
140	ALKPWITR	---QNFSRCLE	QCQPD	SSTLLPPMSRPLEA	TAP	PP---LLLLLL	PMGLLLA	AAWC

211 LRWQRARRR- ---GELHPGVPLPSHP 232
208 LRWQRARRR- ---GELHPGVPLPSHP 229
205 LRWQRTTTRRTPRPGEQVPVPSPQDQLLVEH 235

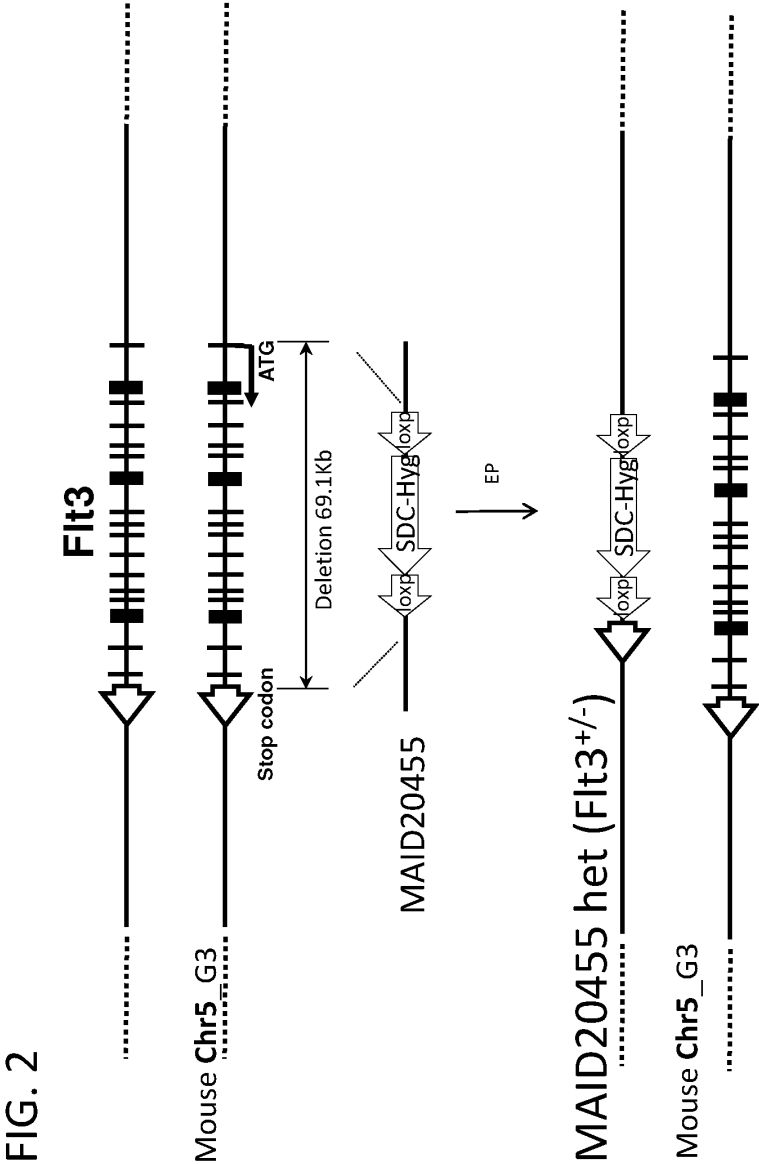
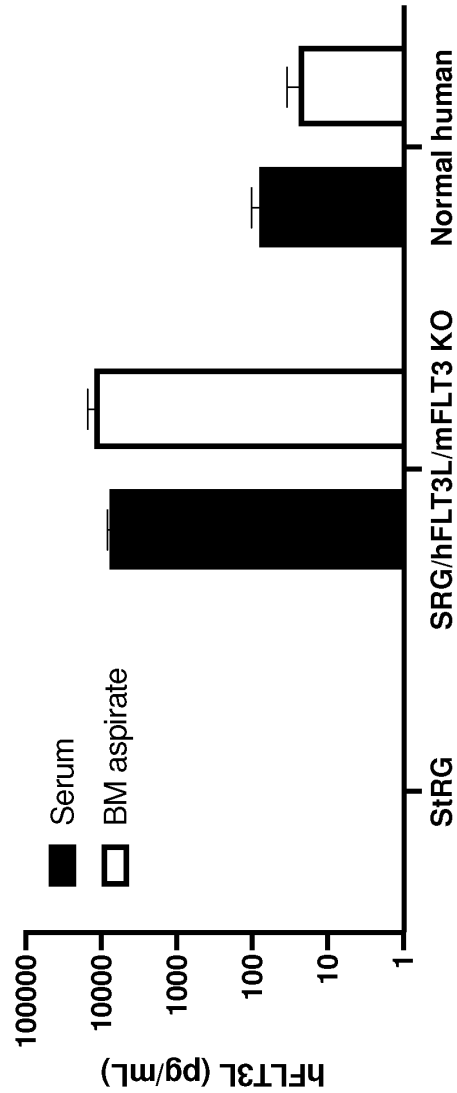


FIG. 3



- Log¹⁰ scale
- N=4 per sample
- All mice were non-engrafted

FIG. 4A

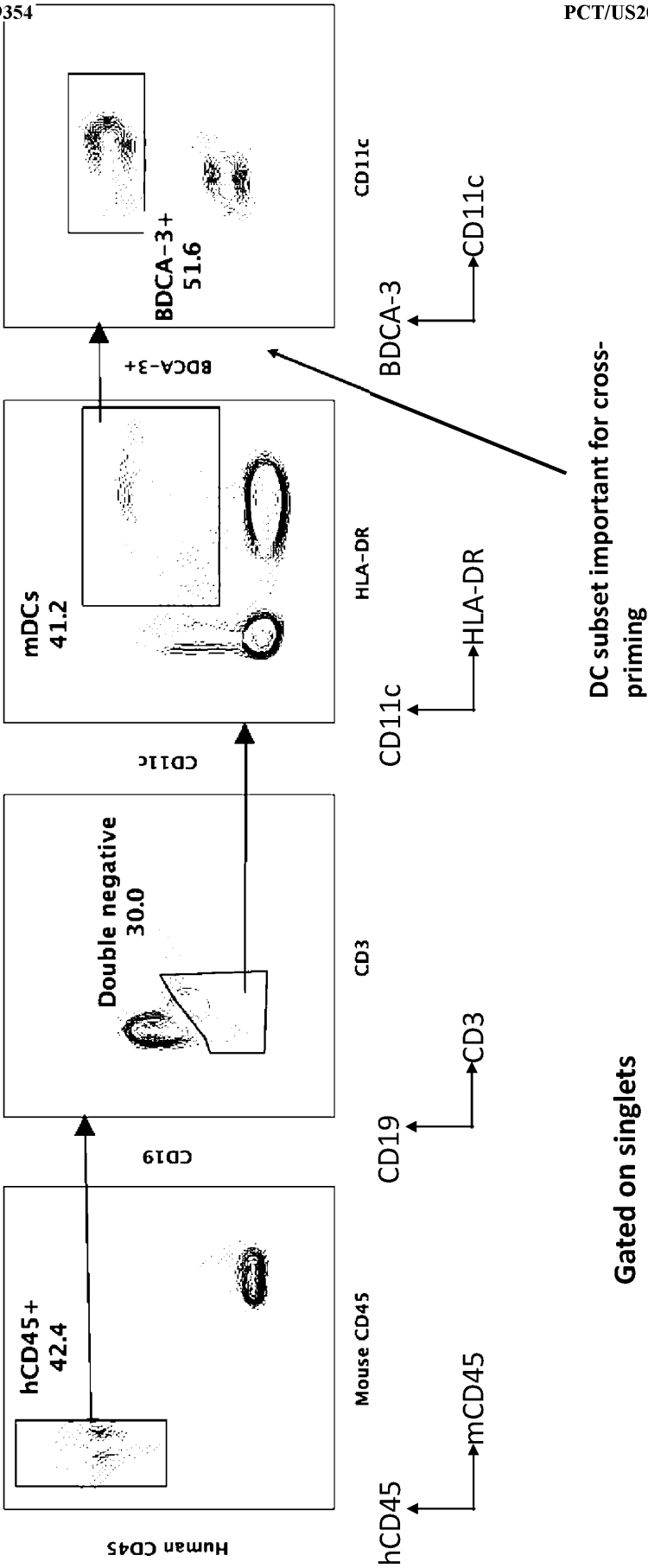
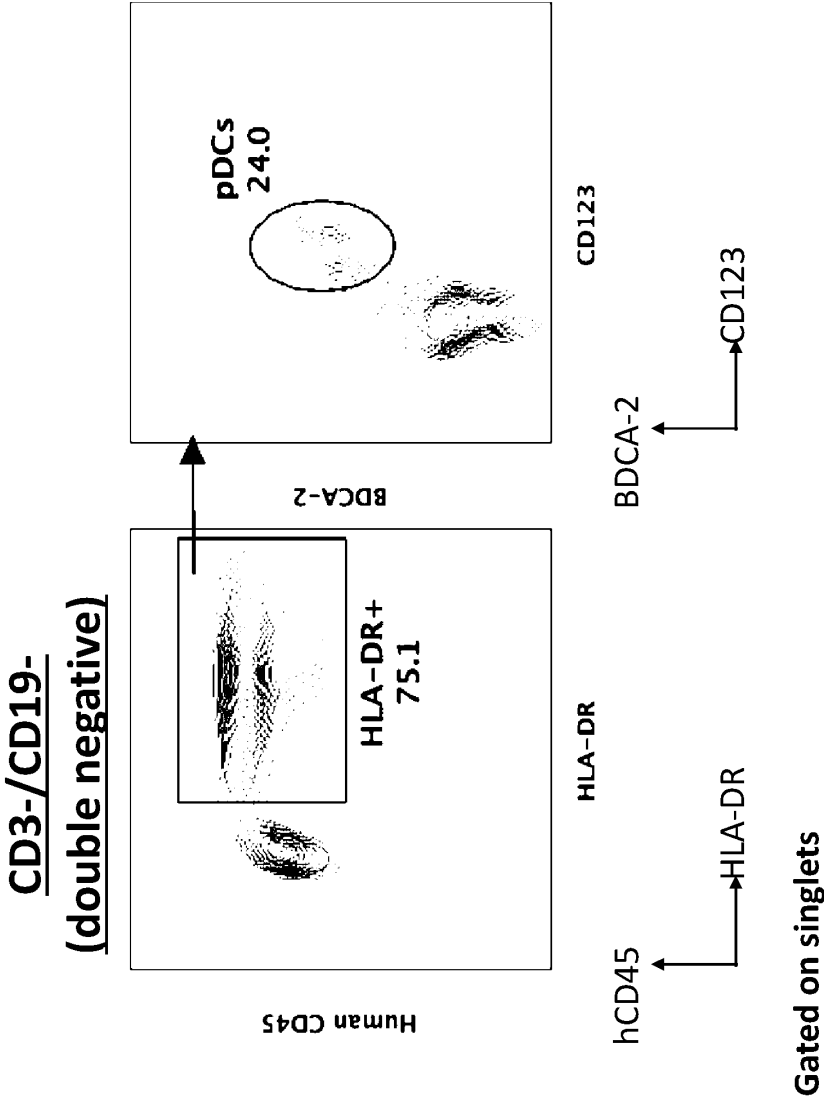


FIG. 4A (continued)



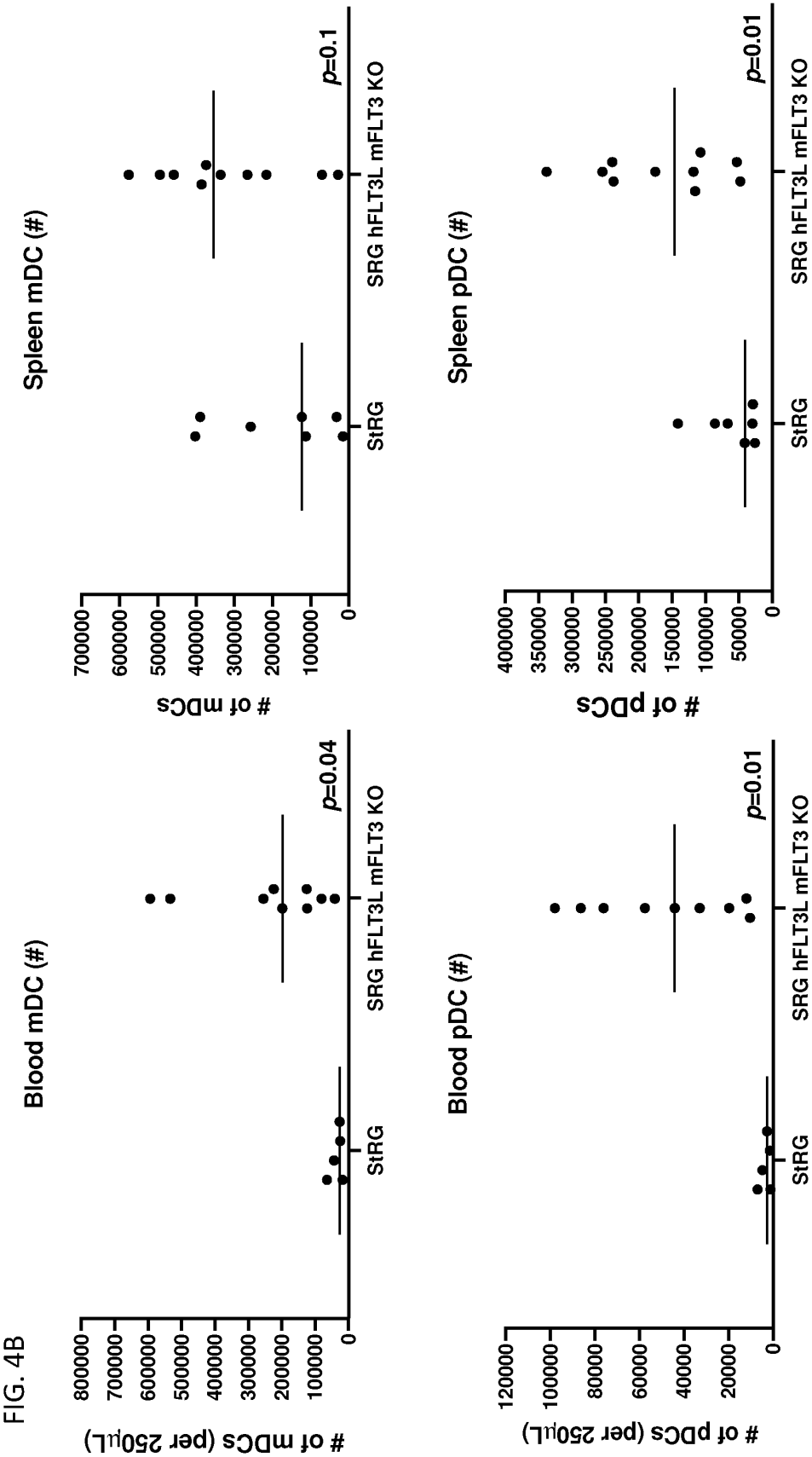


FIG. 4C

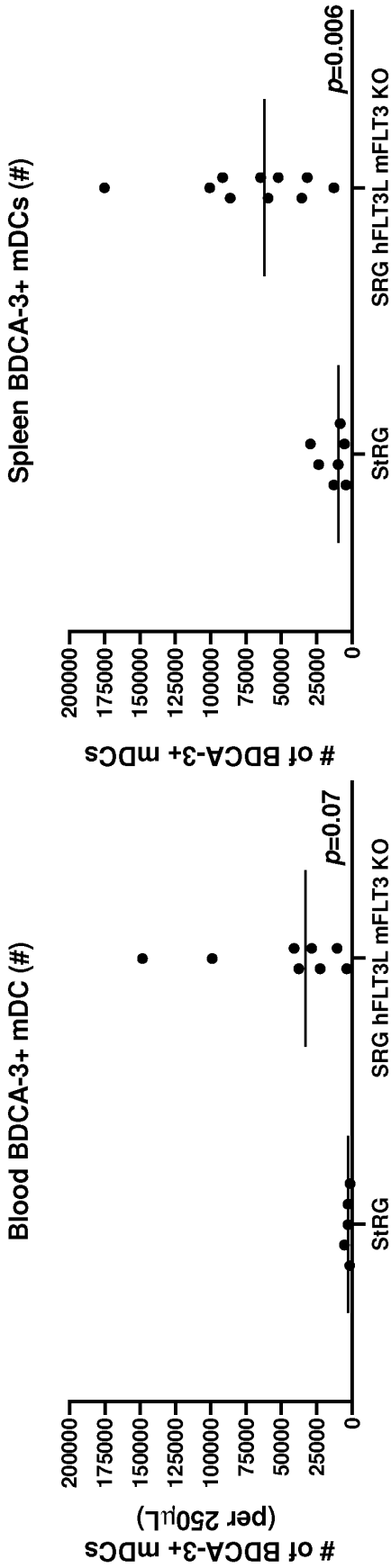


FIG. 4D

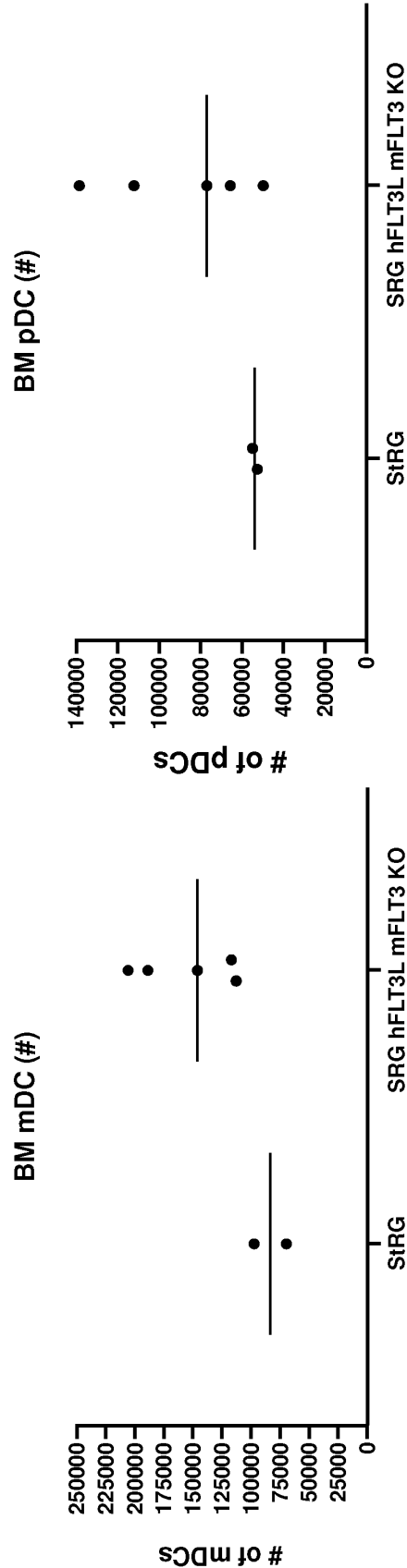


FIG. 4E



FIG. 4F

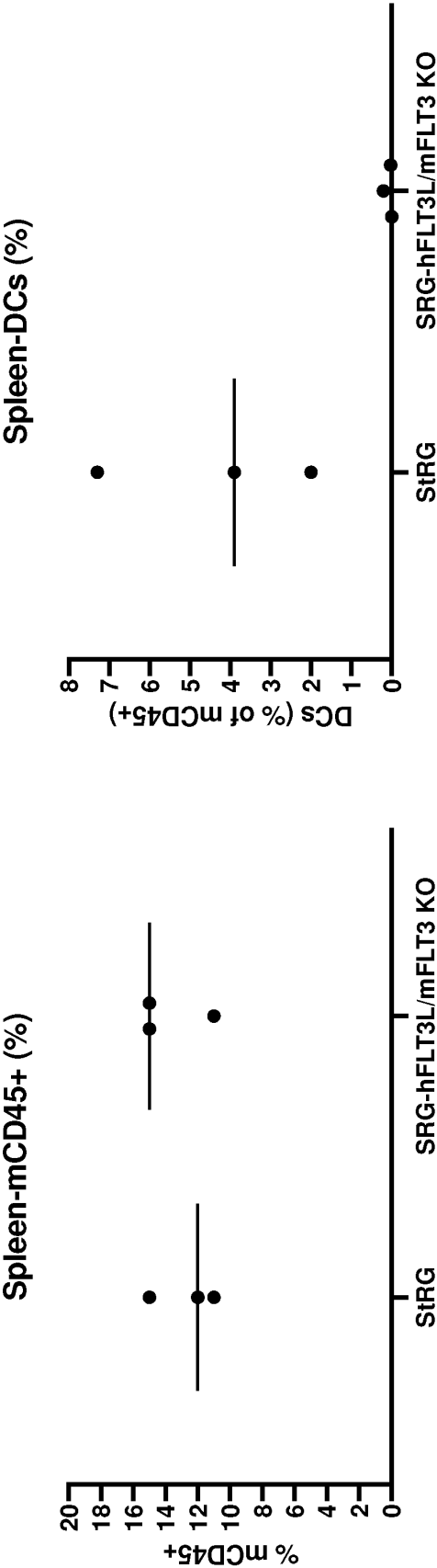


FIG. 5A

The figure consists of four dot plots arranged in a 2x2 grid, showing the number of myeloid dendritic cells (mDCs) and plasmacytoid dendritic cells (pDCs) in spleen and blood for two genotypes: *FLT3L^{m/m}* and *FLT3L^{h/h}*. Each plot includes individual data points, a horizontal line representing the mean, and a p-value indicating statistical significance.

- Spleen mDC (#):** The y-axis ranges from 0 to 700,000. The *FLT3L^{m/m}* group has a mean of approximately 100,000, while the *FLT3L^{h/h}* group has a significantly higher mean of approximately 400,000 ($p=0.006$).
- Spleen pDC (#):** The y-axis ranges from 0 to 400,000. The *FLT3L^{m/m}* group has a mean of approximately 10,000, while the *FLT3L^{h/h}* group has a significantly higher mean of approximately 100,000 ($p=0.002$).
- Blood mDC (#):** The y-axis ranges from 0 to 800,000. The *FLT3L^{m/m}* group has a mean of approximately 100,000, while the *FLT3L^{h/h}* group has a significantly higher mean of approximately 200,000 ($p=0.006$).
- Blood pDC (#):** The y-axis ranges from 0 to 120,000. The *FLT3L^{m/m}* group has a mean of approximately 10,000, while the *FLT3L^{h/h}* group has a significantly higher mean of approximately 40,000 ($p=0.002$).

Legend: *FLT3L^{m/m}* (black dots), *FLT3L^{h/h}* (grey dots). p -values are indicated above the plots.

FIG. 5B

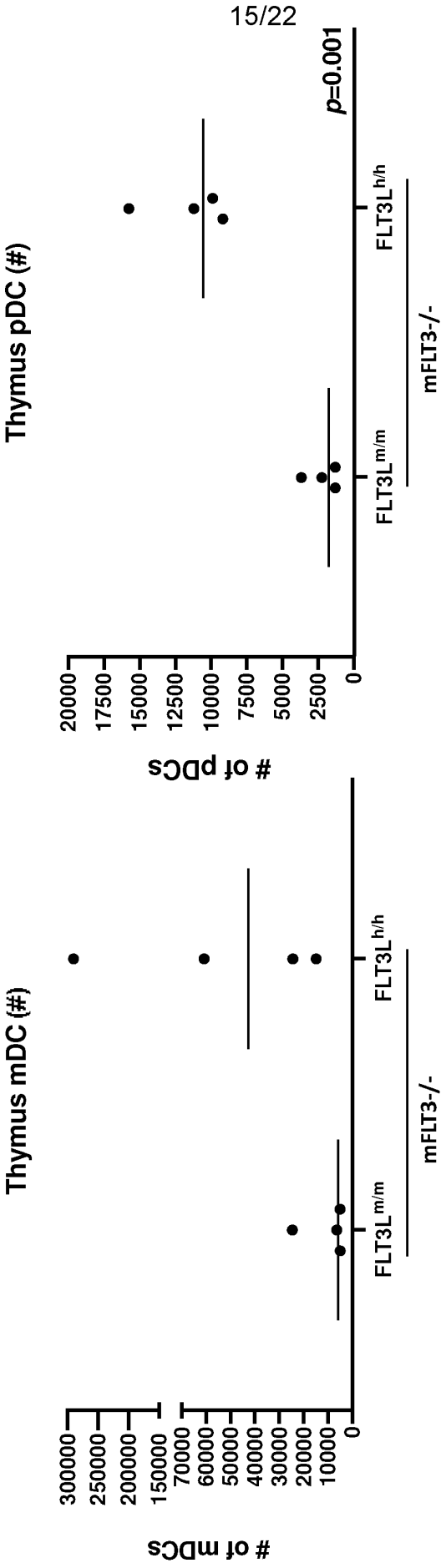
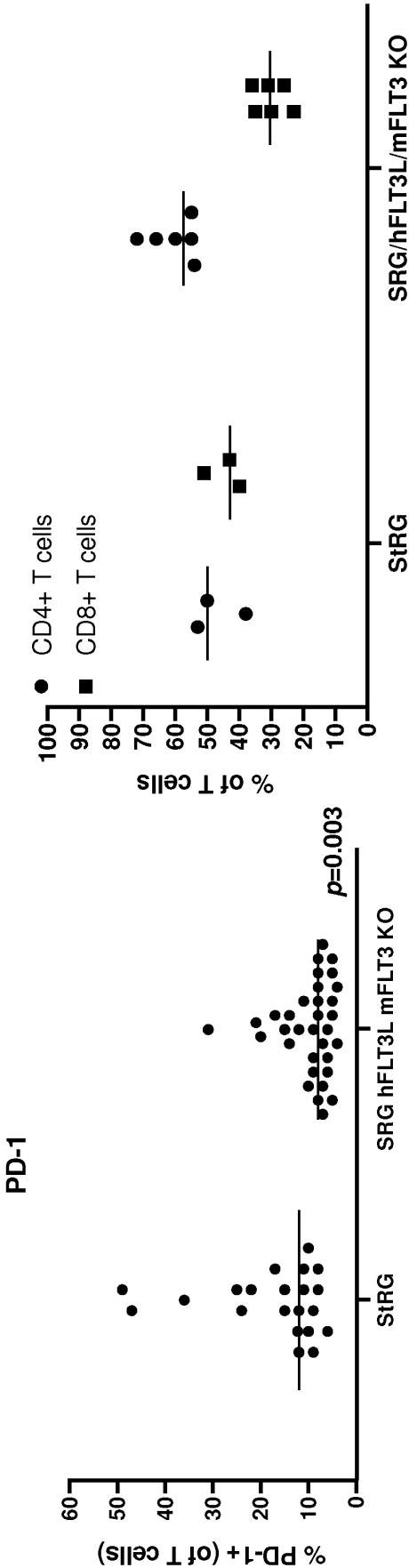


FIG. 6A



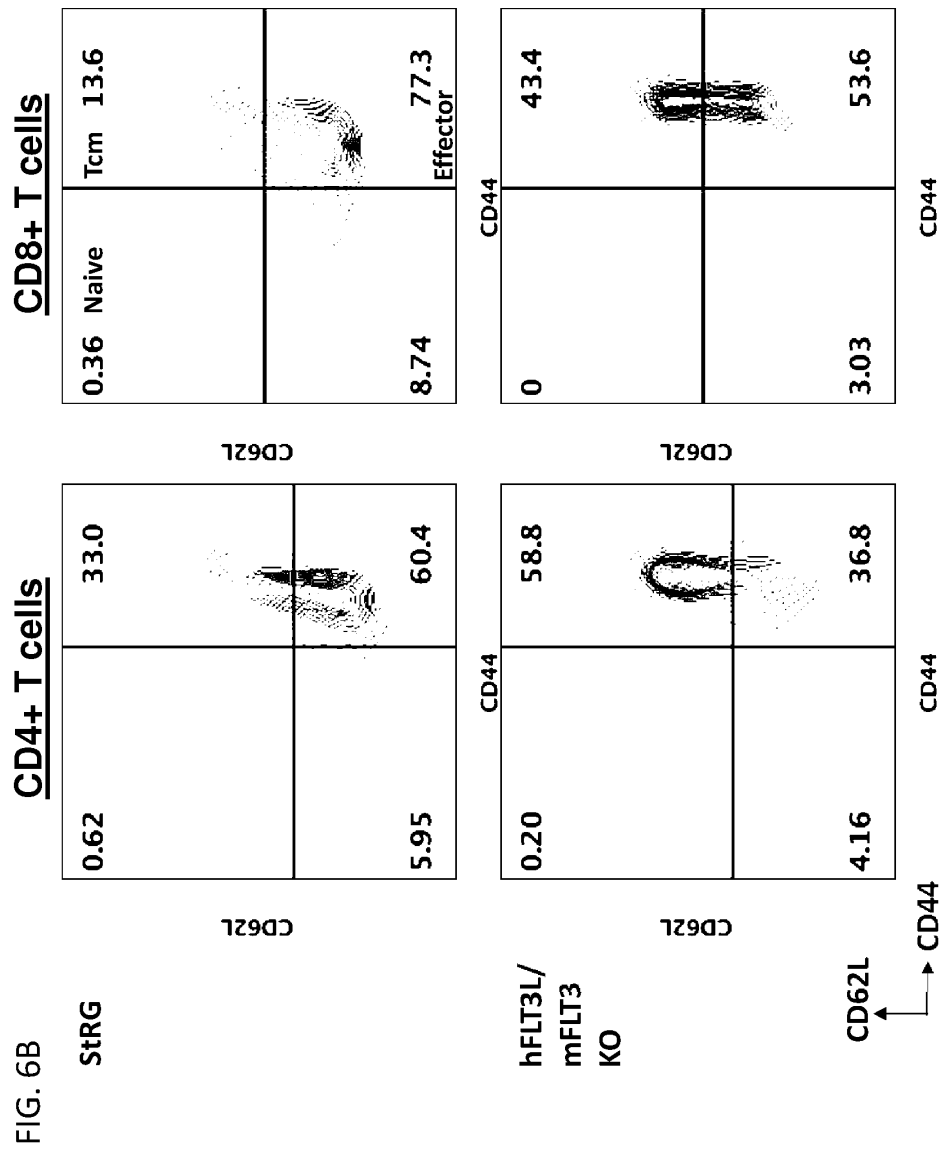


FIG. 6B (continued)

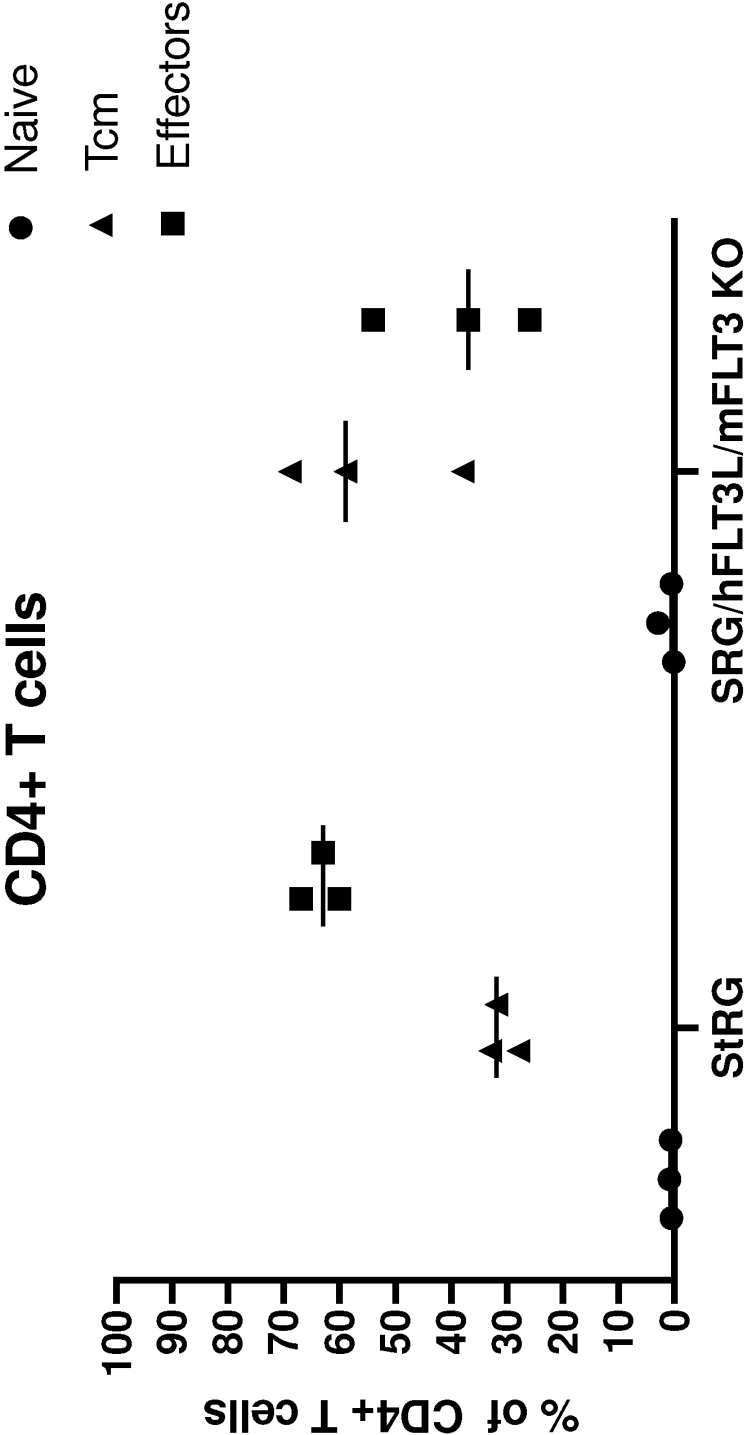


FIG. 6B (continued)

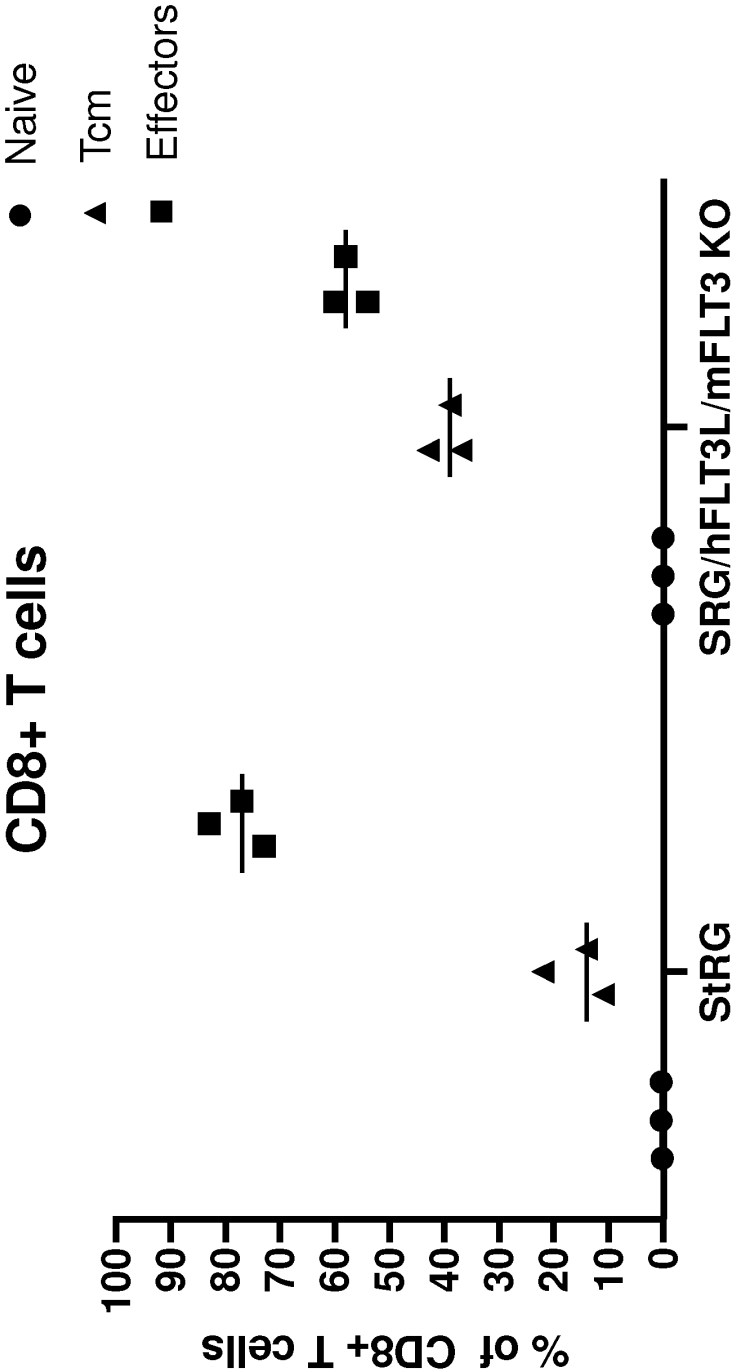


FIG. 7A

<u>DC subset</u>	<u>Human</u> <u>(blood)</u>	<u>SRG/hFLT3L/mFLT3 KO</u> <u>(blood)</u>	<u>SRG/hFLT3L/mFLT3 KO</u> <u>(spleen)</u>	<u>DC subset</u>	<u>Human</u> <u>(BM)</u>	<u>SRG/hFLT3L/mFLT3 KO</u> <u>(BM)</u>
DC_11	0.26%	46.39%	9.21%	DC_11	2.34%	1.48%
DC_CCR7	0.21%	1.25%	2.82%	DC_CCR7	0.13%	1.21%
DC_C1EC10A	51.35%	13.79%	17.11%	DC_C1EC10A	23.23%	20.09%
DC_C1EC9A_XCR1	9.19%	35.74%	53.33%	DC_C1EC9A_XCR1	3.11%	14.61%
DC_DEFA4	0.00%	0.31%	0.34%	DC_DEFA4	0.43%	12.11%
DC_S100A8	0.15%	0.63%	0.69%	DC_S100A8	43.79%	29.03%
pDC_IRF4	37.6%	0.00%	1.03%	pDC_IRF4	26.78%	1.44%
pDC_LTB	1.23%	1.88%	15.46%	pDC_LTB	0.18%	20.03%

FIG. 7B

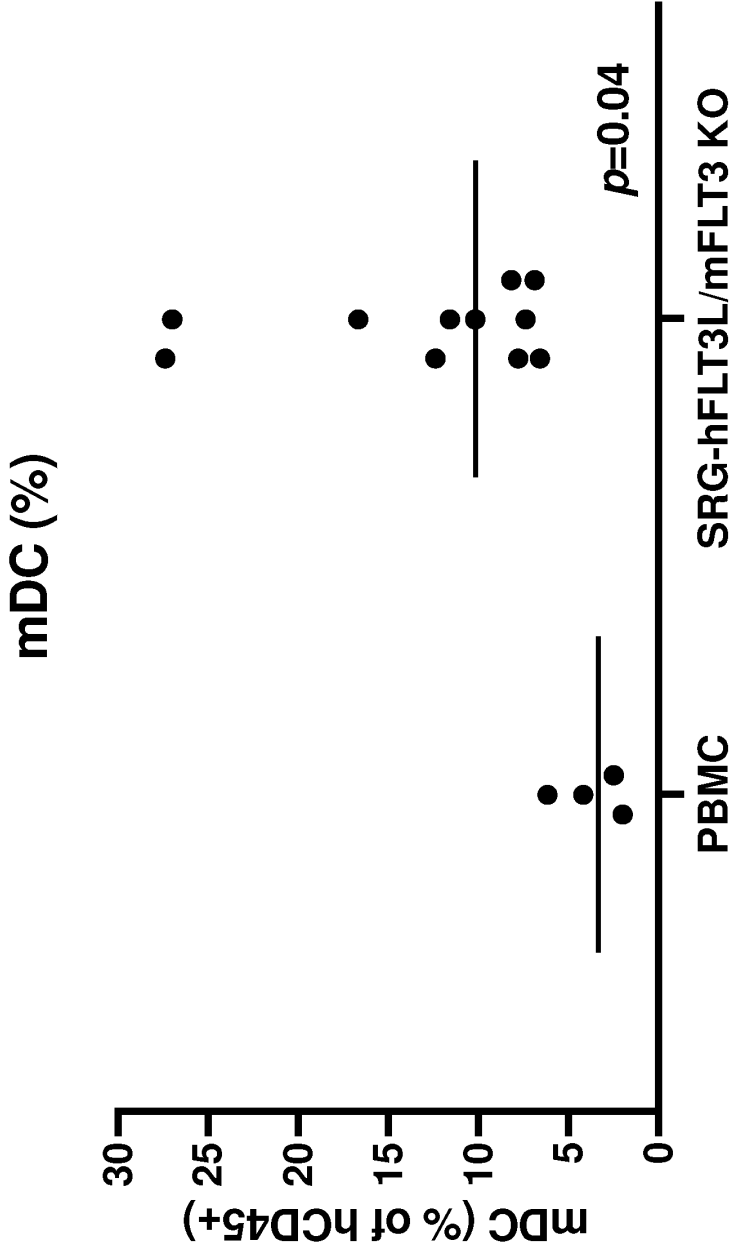


FIG. 7B (continued)

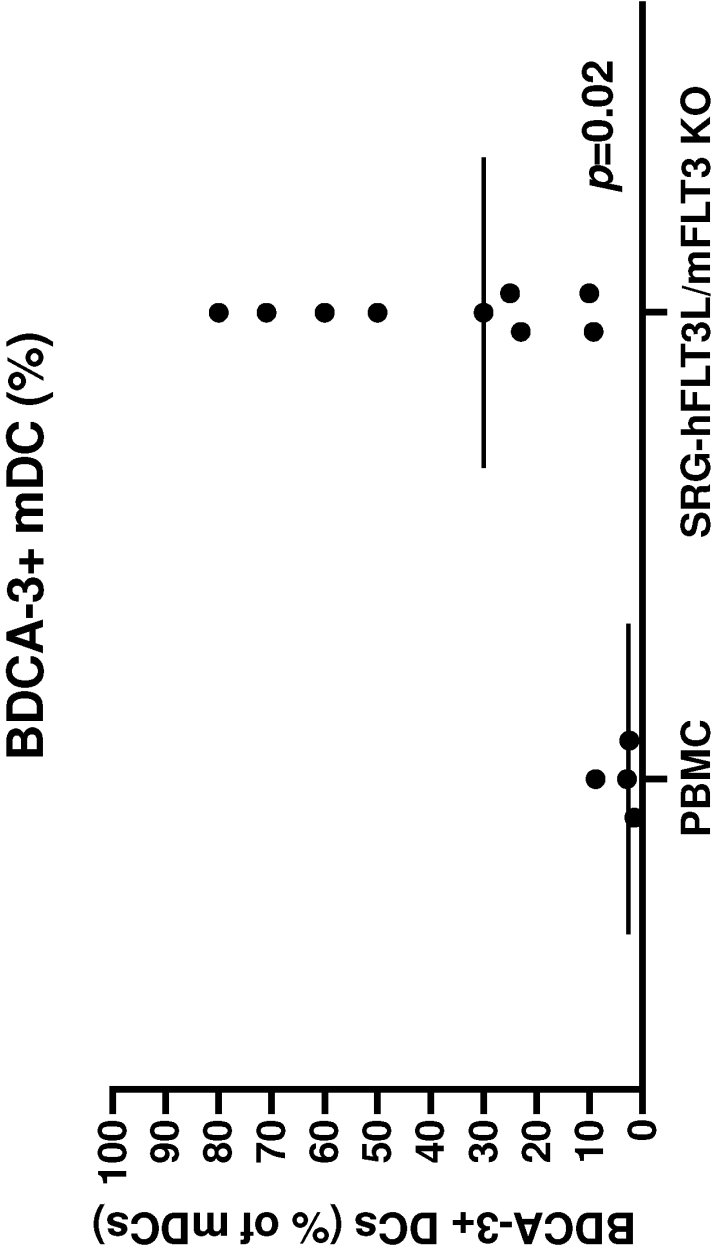
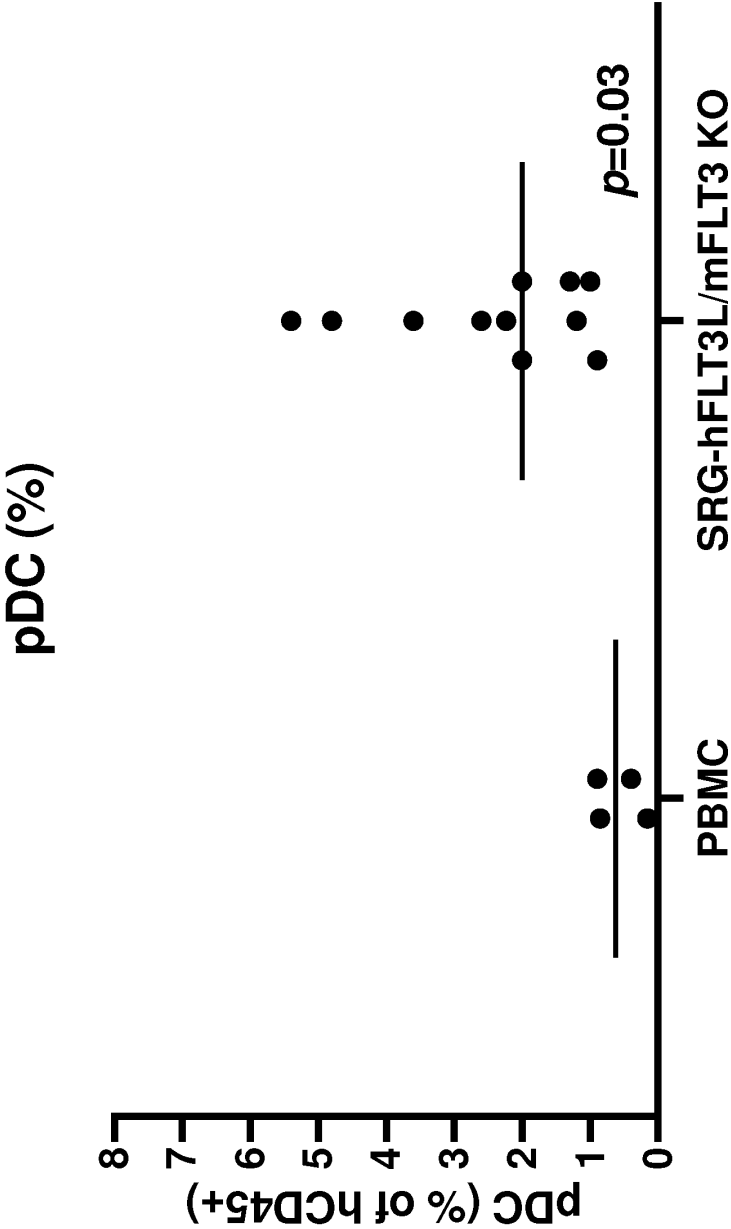


FIG. 7B (continued)



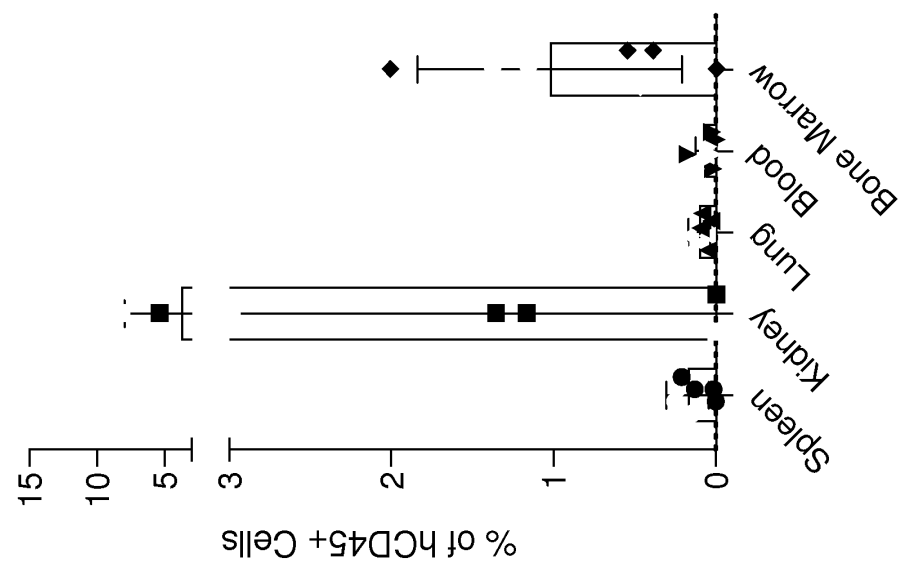


FIG. 8

FIG. 9A

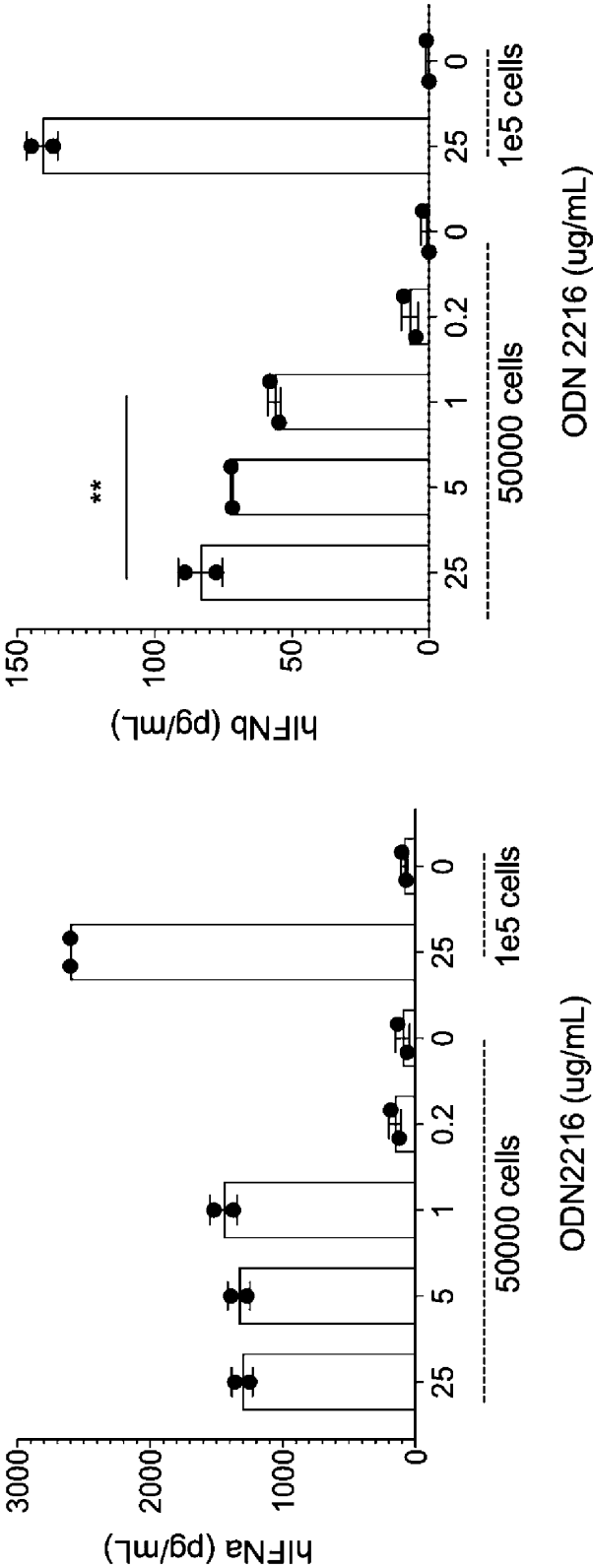


FIG. 9B

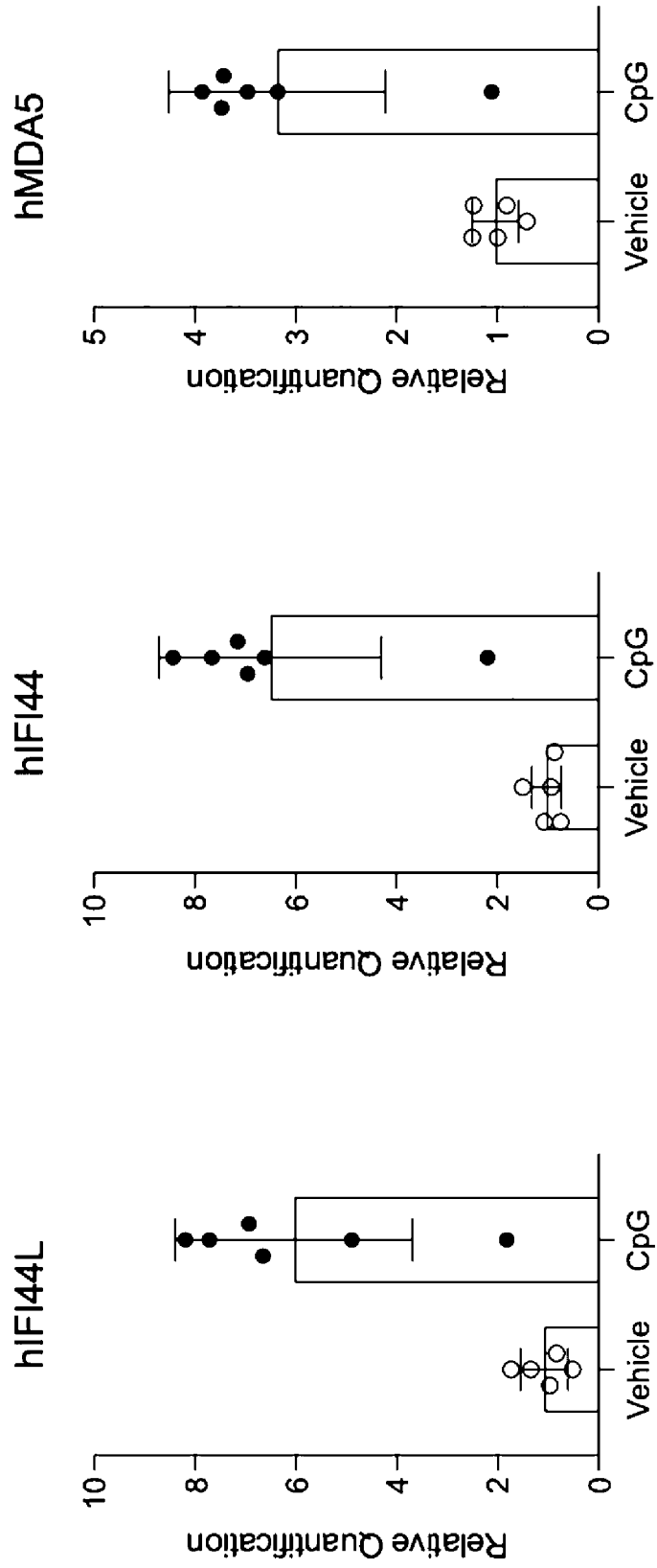


FIG. 9B (continued)

