

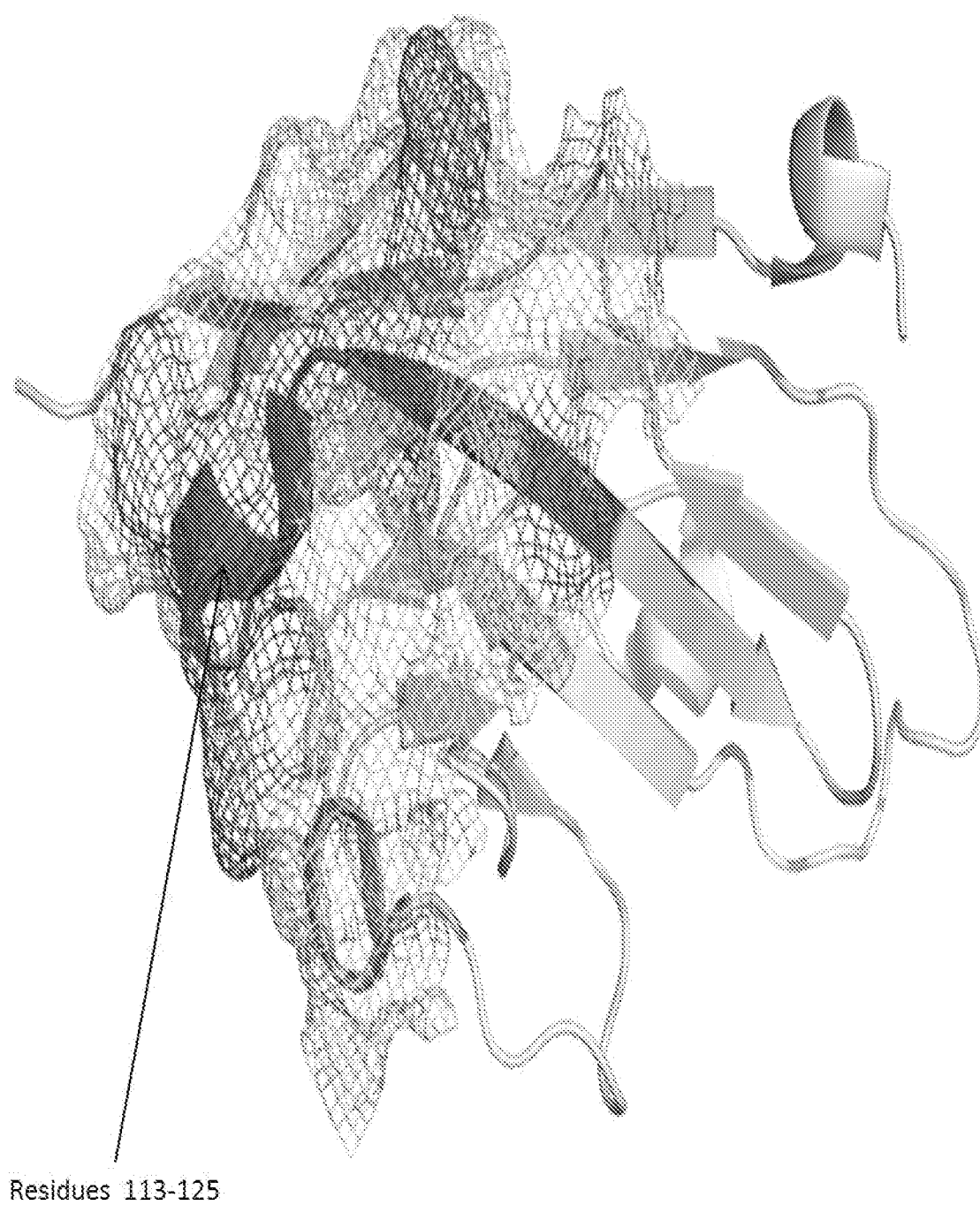


FIG. 1B

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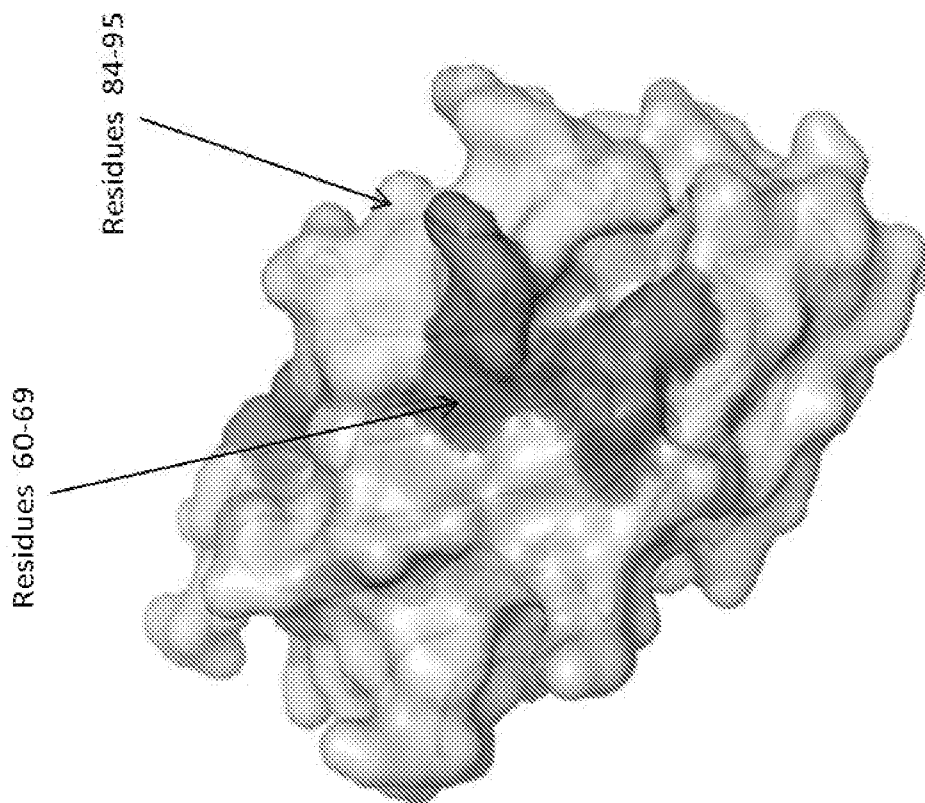


FIG. 1D

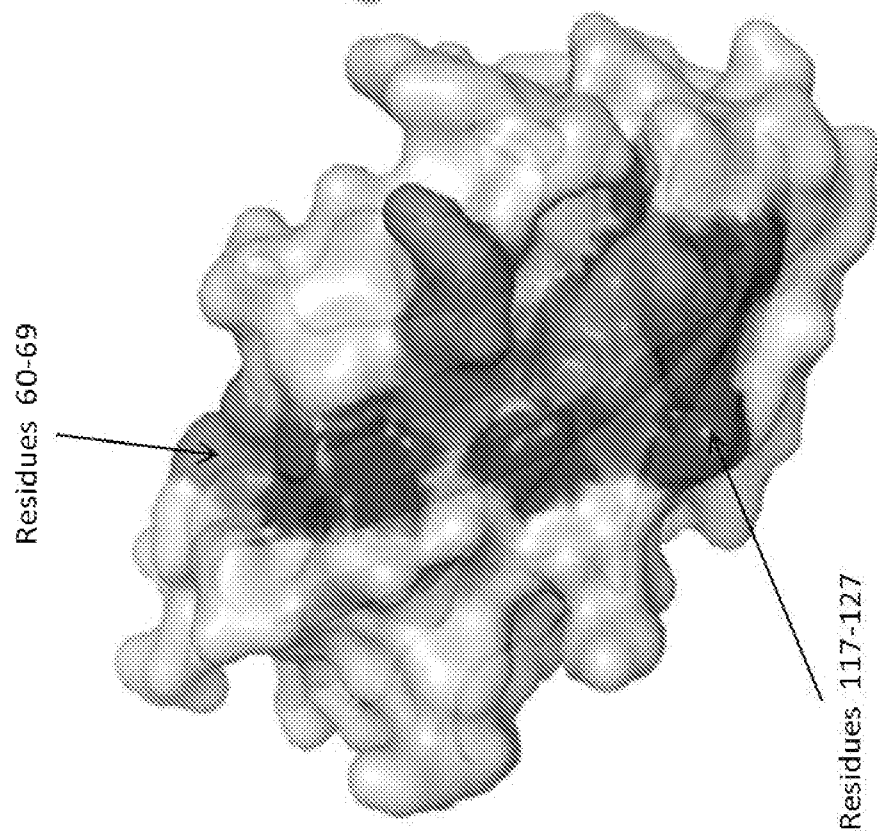


FIG. 1C

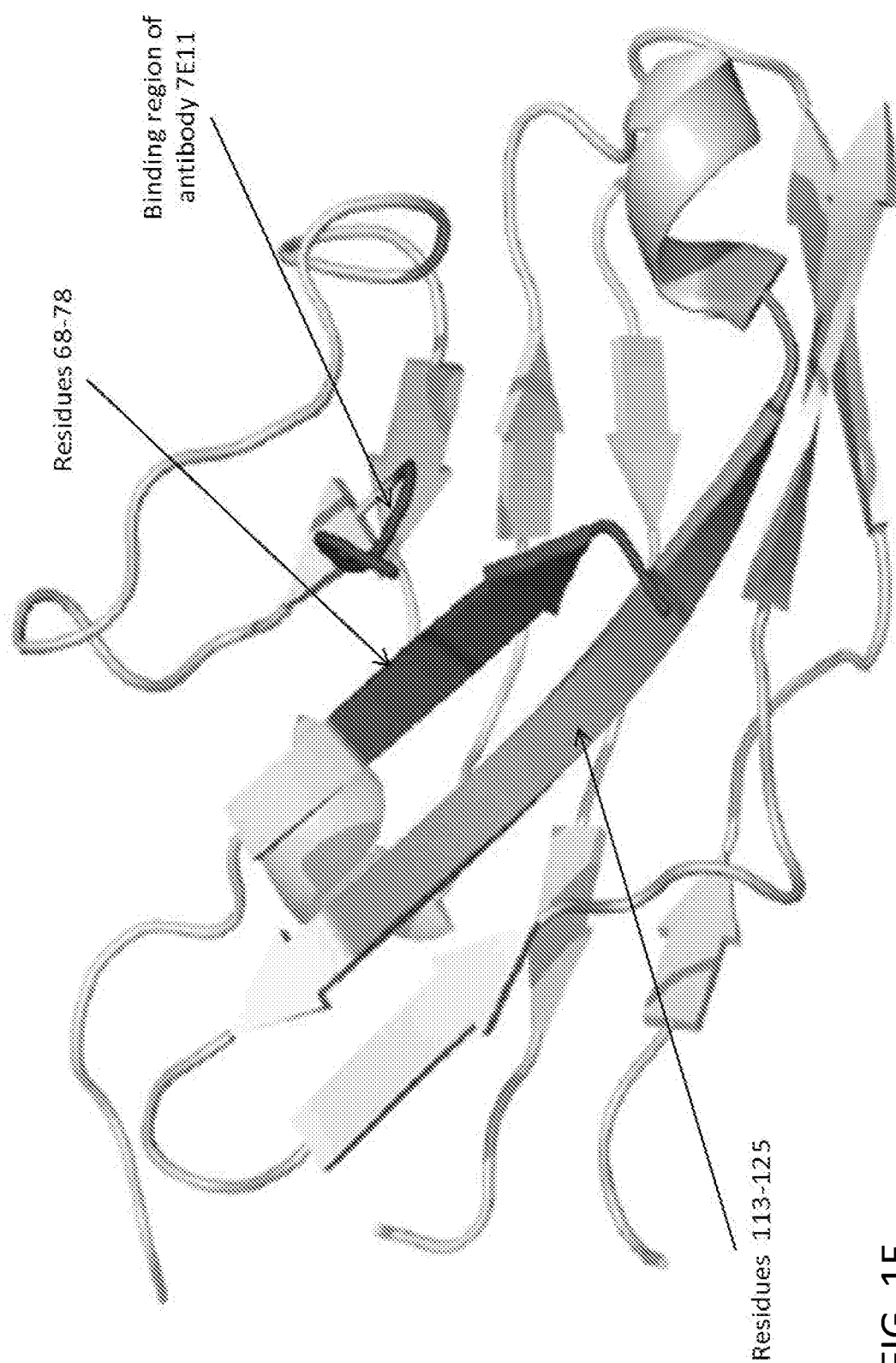


FIG. 1E

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Mutation	Binding Reactivity (% WT)				
	4E3 Fab	10B5 MAb	10B5 Fab	6-434 MAb	S7.7 MAb
M30A	122.9 (79)	89.9 (29)	20.1 (12)	84.8 (6)	100.0 (6)
Q31A	111.5 (46)	108.0 (11)	18.2 (13)	100.8 (22)	109.7 (42)
V44A	115.0 (12)	93.9 (27)	13.3 (7)	68.0 (43)	89.3 (8)
R45A	129.1 (25)	37.3 (2)	1.6 (3)	111.6 (48)	125.9 (92)
S47A	103.4 (14)	81.7 (5)	1.5 (1)	101.1 (17)	117.9 (21)
F48A	145.5 (28)	158.7 (76)	13.9 (5)	112.9 (17)	157.8 (13)
Y50A	139.2 (77)	108.5 (75)	18.2 (3)	97.9 (58)	142.3 (26)
I72A	26.5 (12)	130.1 (86)	92.8 (9)	64.2 (11)	100.7 (7)
W74A	25.7 (16)	101.0 (67)	79.8 (39)	74.9 (28)	83.7 (25)
N81A	22.0 (13)	153.1 (23)	137.7 (73)	111.6 (20)	5.6 (6)
T103A	138.9 (25)	96.3 (52)	6.3 (4)	77.5 (33)	105.7 (39)
K104A	115.0 (60)	13.6 (1)	-2.0 (5)	83.8 (7)	115.1 (67)
T107A	124.2 (105)	83.8 (17)	0.4 (10)	66.8 (8)	129.2 (9)
R124A	1.0 (4)	149.9 (22)	81.1 (42)	126.0 (48)	115.2 (4)
M185A	91.6 (62)	29.1 (5)	-2.2 (8)	69.3 (3)	74.3 (9)

FIG. 1F

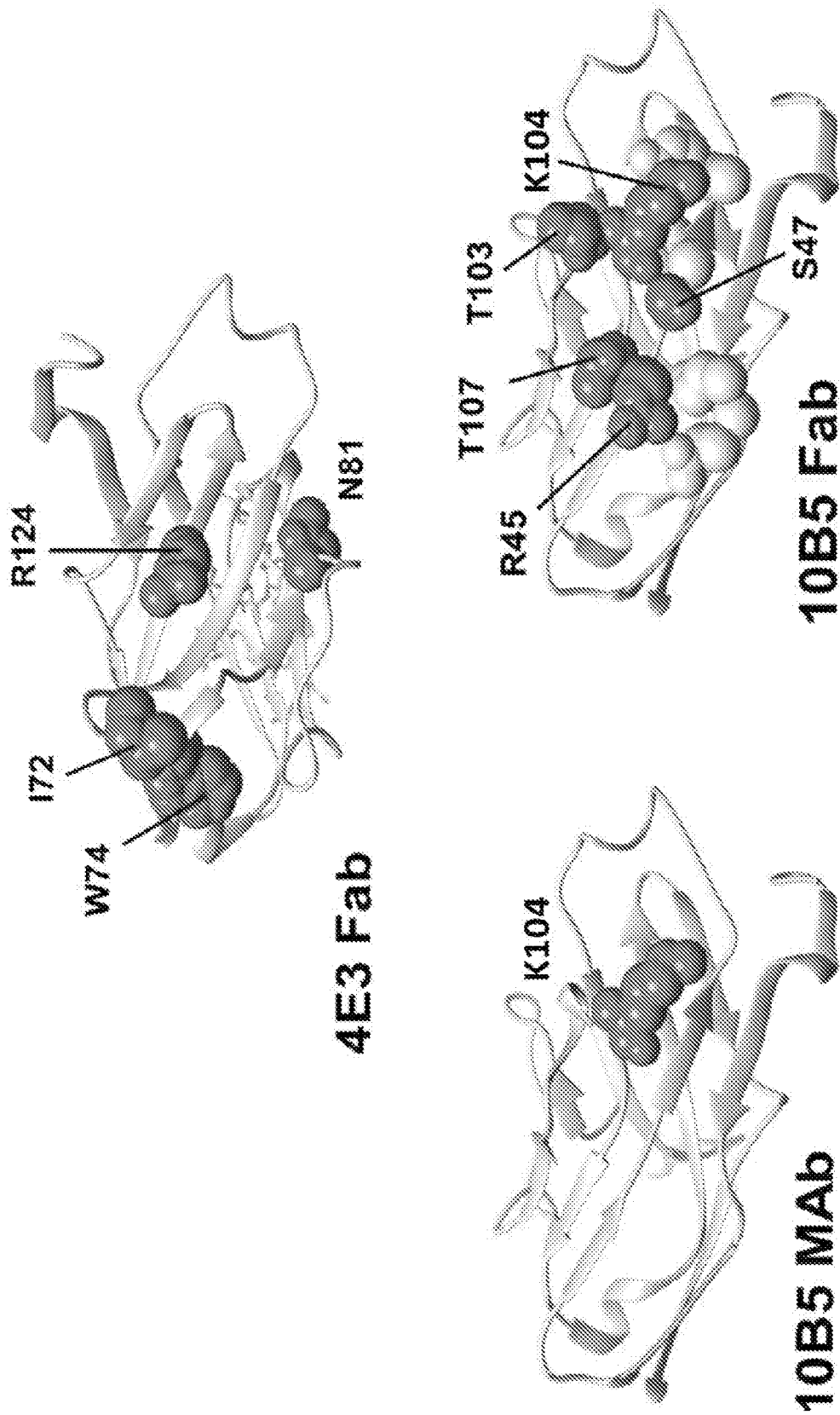


FIG. 1G

Oligosaccharide	R1	R2	R3	Relative Recognition by Human Siglec										
				1	2	3	4	5	6	7	8	9	10	11
				Legend: ◆ = Sia ○ = Gal ■ = GlcNAc ▲ = Fuc □ = GalNAc										
N-Glycan	+		+	-	++	++	-	-	-	-	-	+	+	-
O-Glycan	+			++	-	+	+	++	-	-	+	++	++	+
Glycolipid	+	+	+	+	-	+	-	-	-	++	+	+	-	++
◆α6○β4■β-R1				++	-	+	+	-	-	-	+	+	+	-
◆α3○β4■β-R1				+	-	+	-	+	-	+	+	+	-	+
◆α8◆α3○β4■β-R1				++	-	+	+	-	-	-	+	+	-	+
◆α3○β3■β-R1				+	-	+	-	-	-	-	+	+	+	-
◆α3○β4■β-R1				+	-	+	-	-	-	-	+	+	-	-
◆α3○β3□α6▲				+	-	+	+	-	-	-	-	+	-	-
◆α3○β3□β-R2/α-R3				+	-	+	+	-	-	-	-	+	-	-
◆α3○β3□β-R2/α-R3				?	?	?	++	-	-	+	-	+	?	?
◆β-R2/α-R3				+	+	+	-	-	+	+	+	+	+	-

FIG. 2

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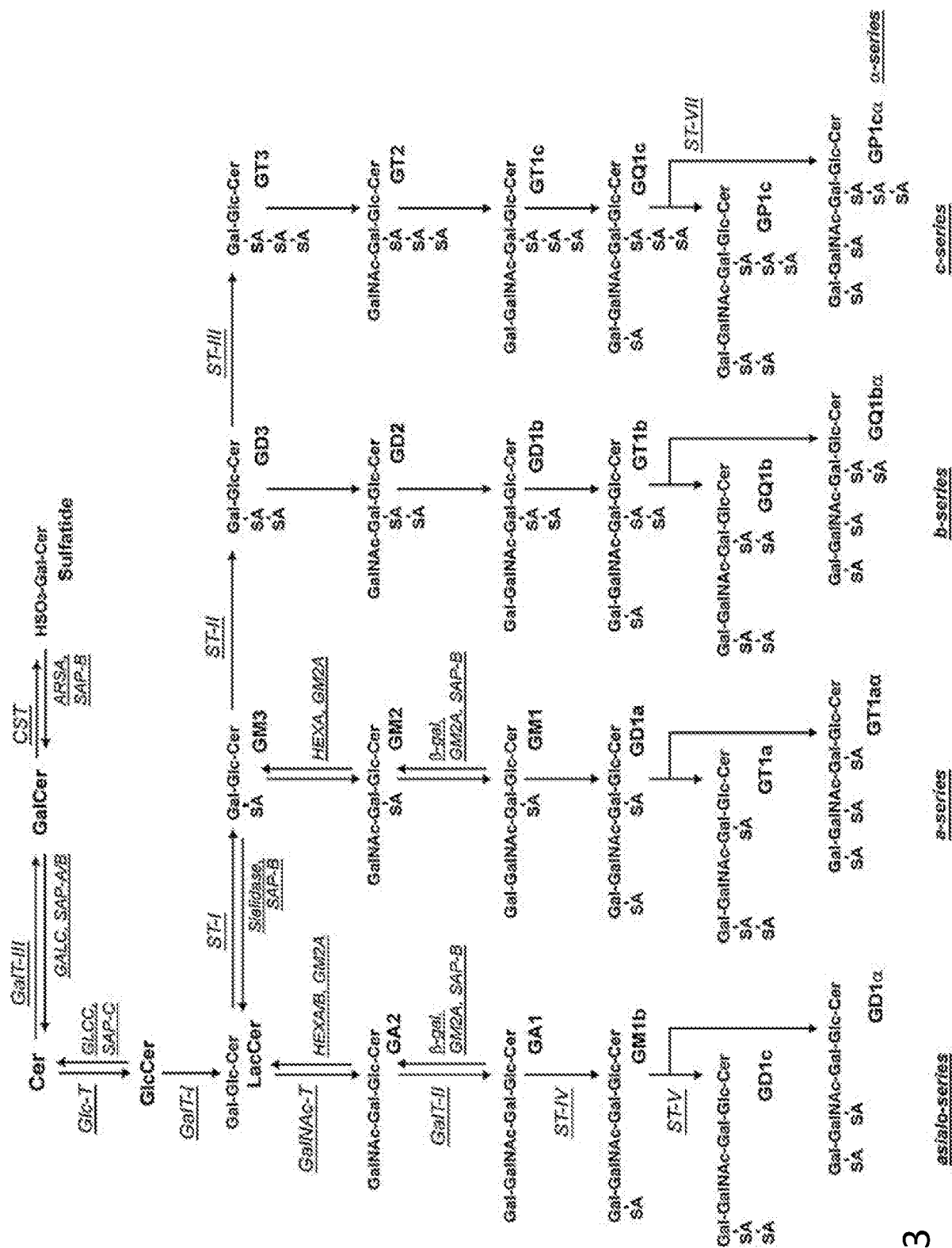
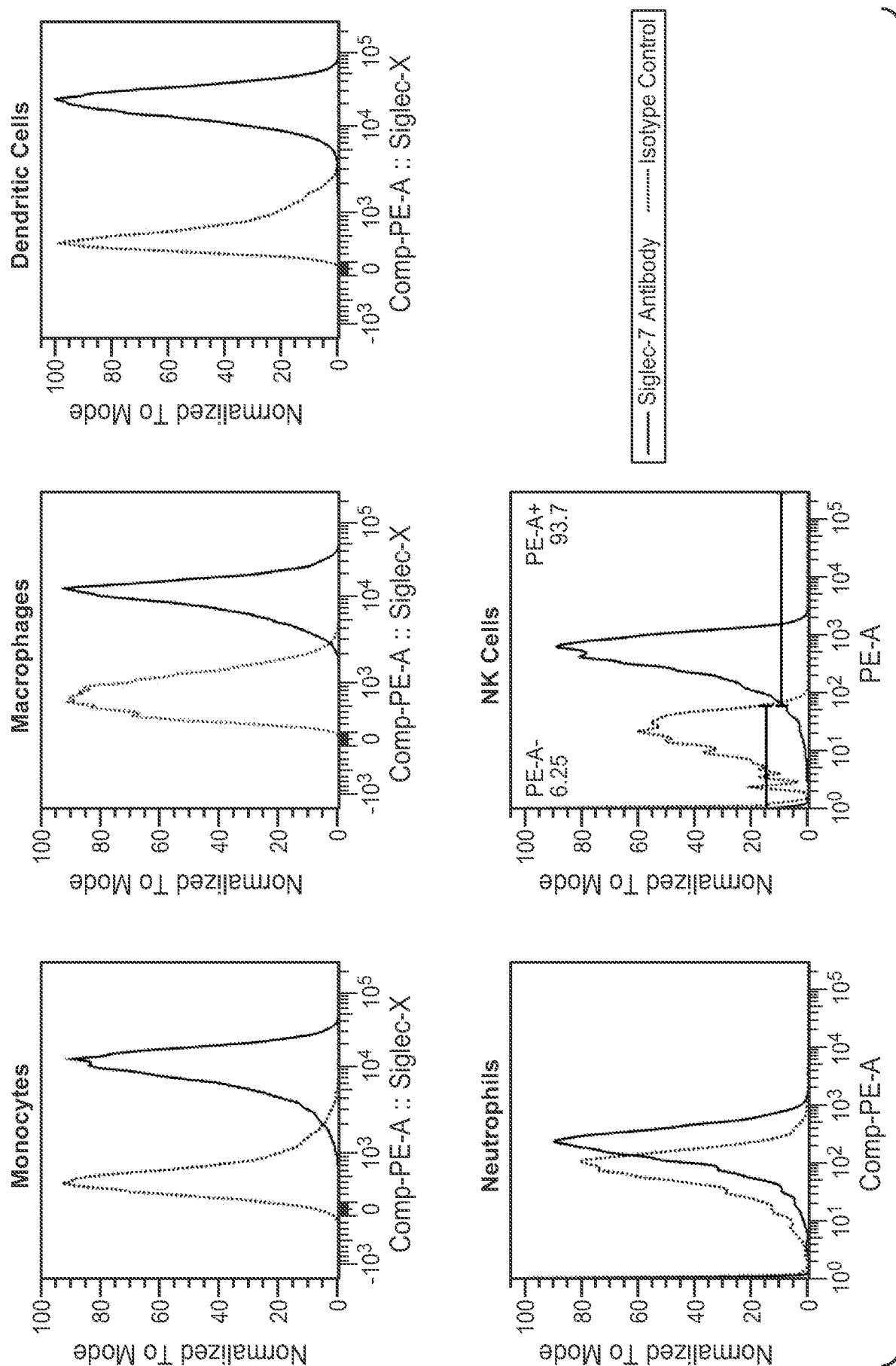
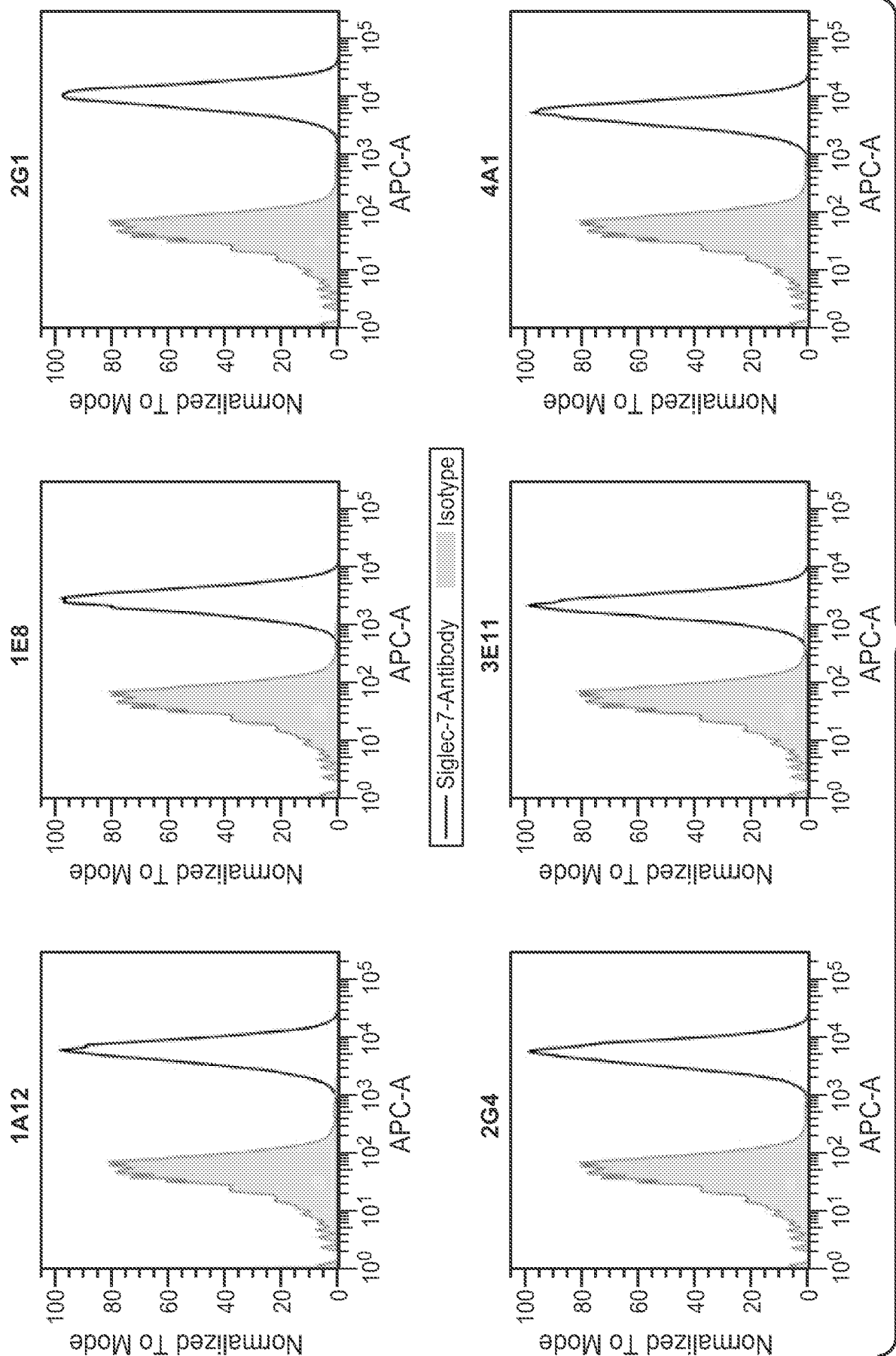
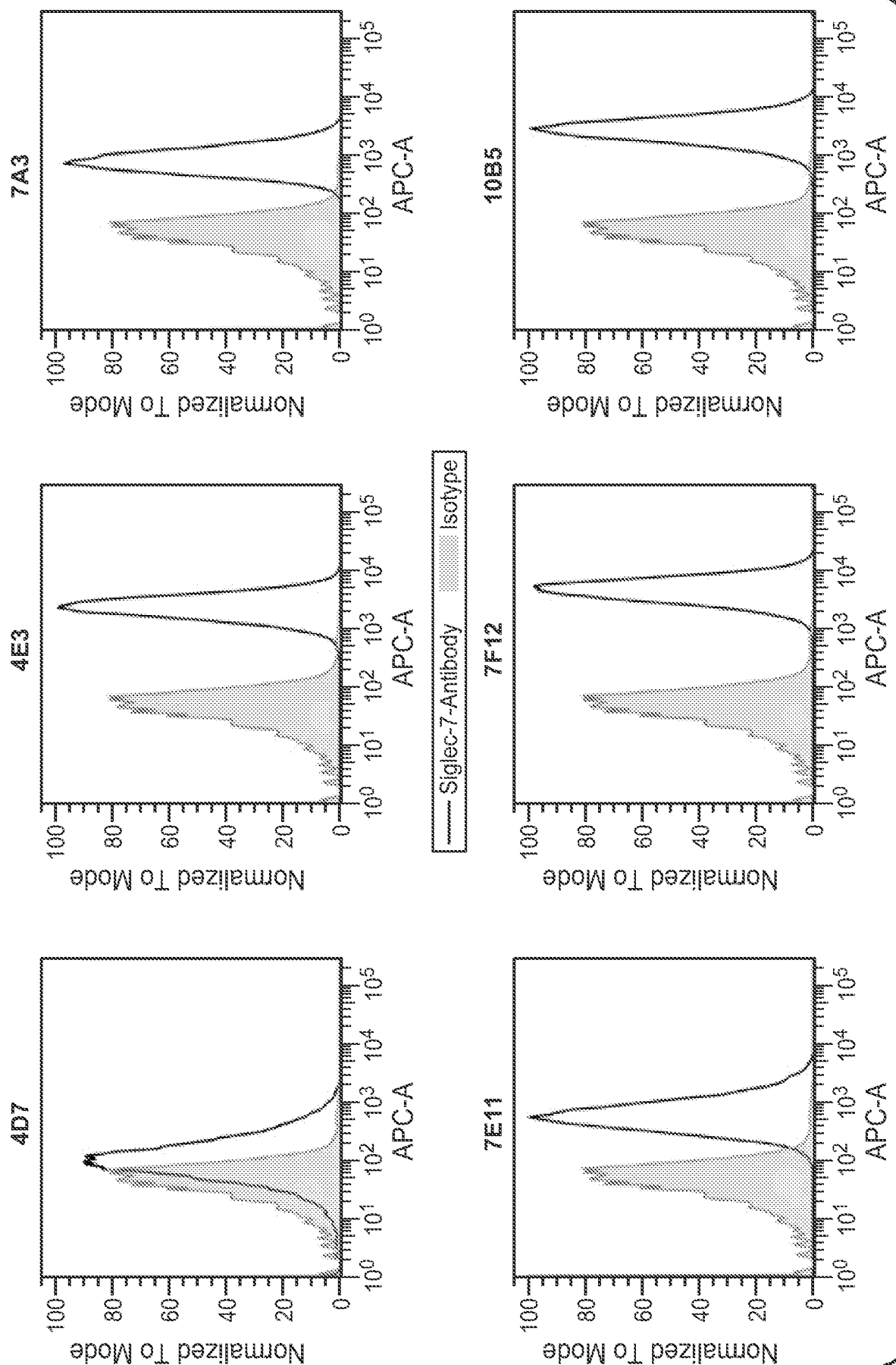


FIG. 3



**FIG. 5A**

**FIG. 5A (Cont.)**

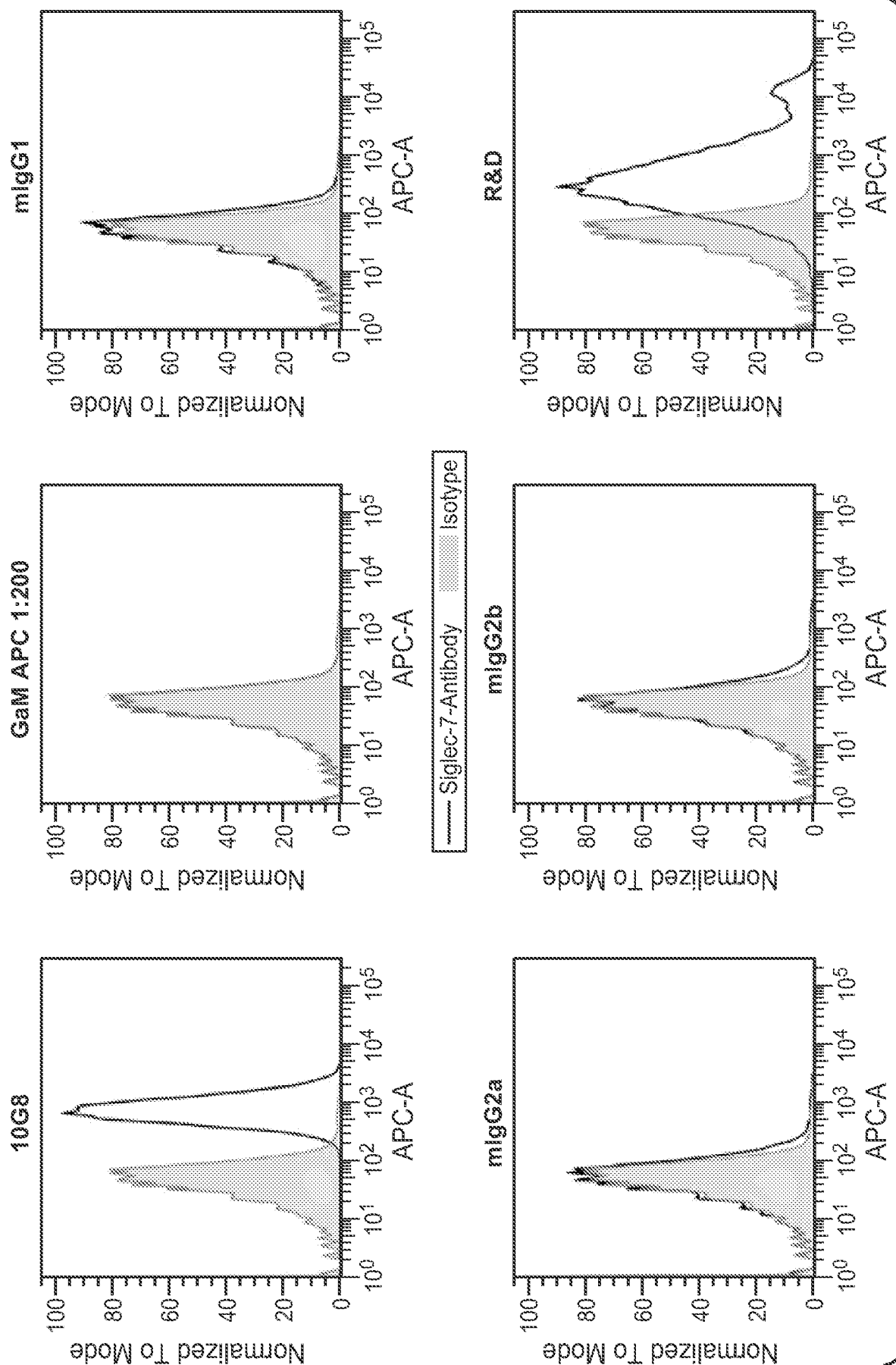


FIG. 5A (Cont.)

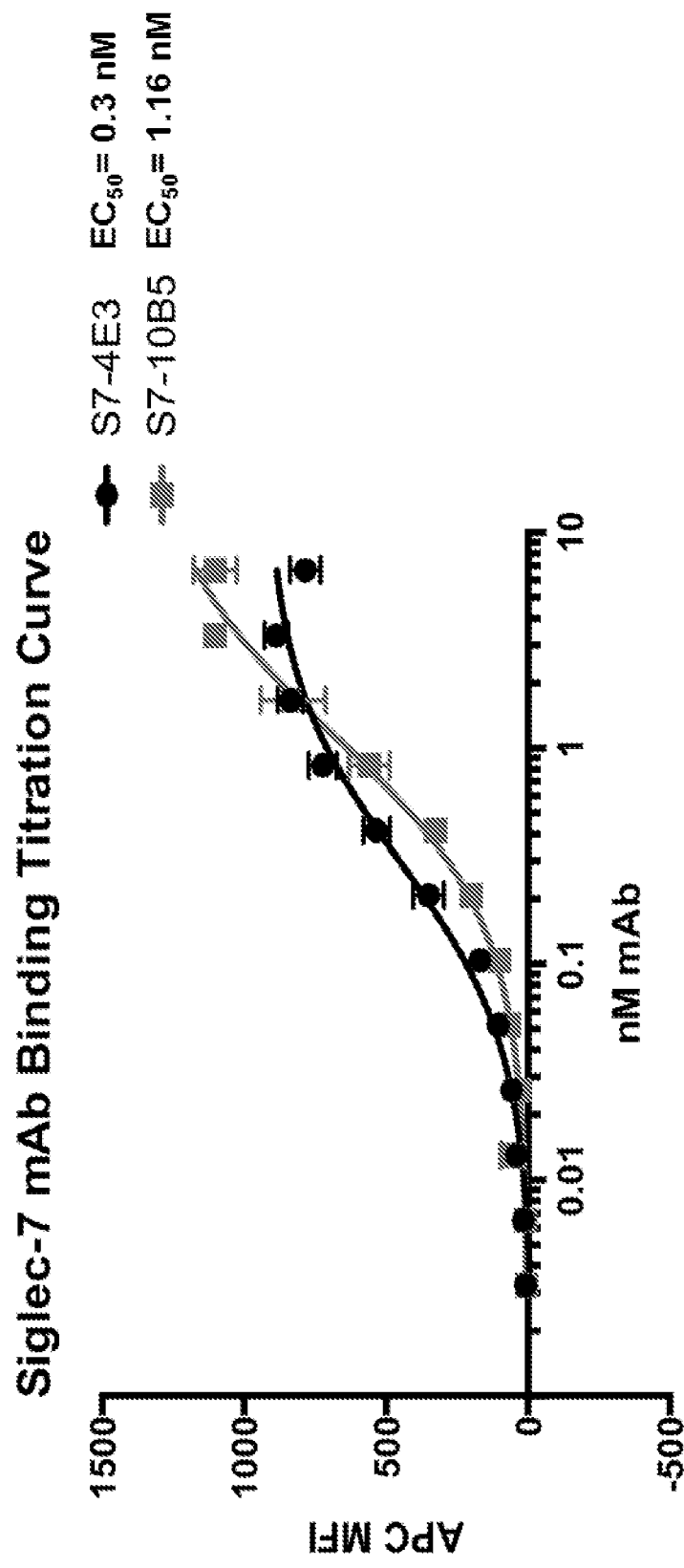


FIG. 5B

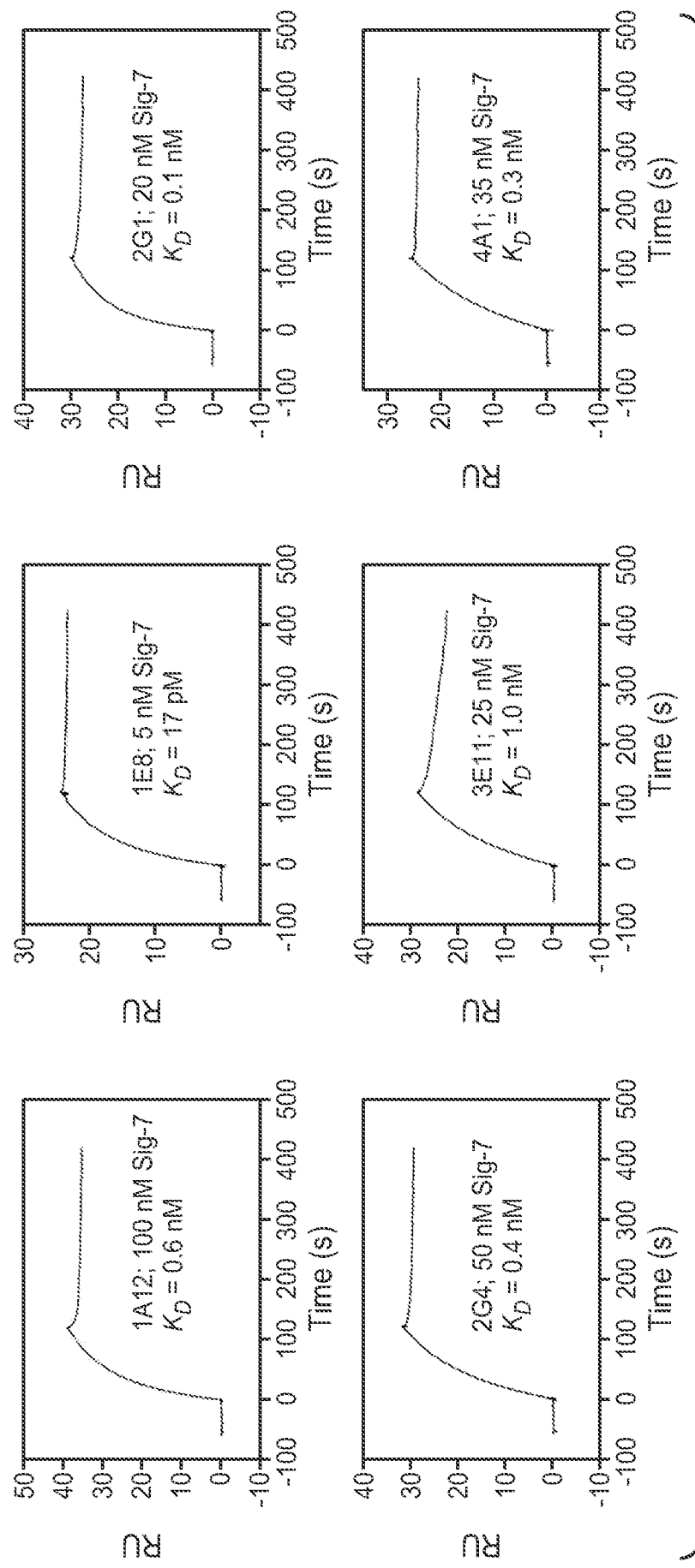


FIG. 6A

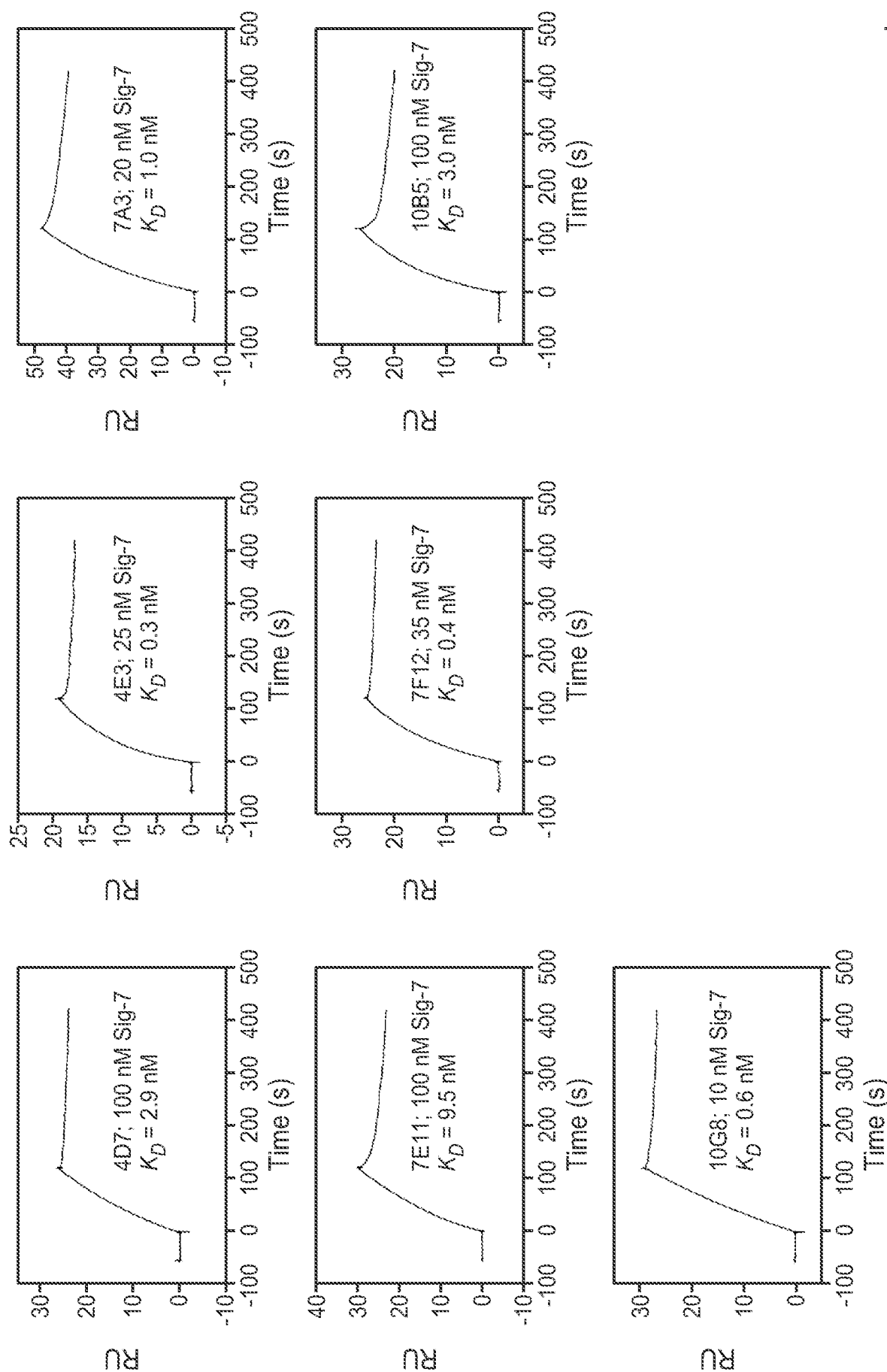


FIG. 6A (Cont.)

Potential humanized sequence based on IMGT IGKV3-11*01 acceptor framework (AbM CDR definition)
IGKV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAT
GIPARFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPP
Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50
AbM	10	20	30	40	50
	b b b	p p	b b b	b b b	i i i b b i
S7-4E3	QIVLTQSPAILASAPGEKVTMC	SANSSFTTMY	WYQQKPGSSPRLIIF	DTSNLA	S
	*	*	*	*	*
3-11*01	EIVLTQSPATLSLSPGERATLSC	RASQSVSSYLAWYQQKPGQAPRLLIY	DASNRAT		
h4E3-L1	EIVLTQSPATLSLSPGERATLSC	SANSSFTTMY	WYQQKPGQAPRLLIY	DTSNLA	S
h4E3-L2	EIVLTQSPATLSLSPGERVTMSC	SANSSFTTMY	WYQQKPGQAPRLLIY	DTSNLA	S
h4E3-L3	EIVLTQSPATLSLSPGERVTMSC	SANSSFTTMY	WYQQKPGQAPRLLIIF	DTSNLA	S

seq	60	70	80	90	100
AbM	60	70	80	90	100
	b b	b b b	ib bib	ibi iib	i b b b
S7-4E3	GVPIRFSGSGGTSTSYSLTISRMEAEATATYYC	QQWSSSPLT	FGAGTKLELK		
	*	*	*	*	*
3-11*01	GIPARFSGSGGTDFTLTISSLEPEDFAVYYC	QQRSNWPP	FGQGTKLEIK		
h4E3-L1	GIPARFSGSGGTDFTLTISSLEPEDFAVYYC	QQWSSSPLT	FGQGTKLEIK		
h4E3-L2	GVPARFSGSGGTDTYTLTISSMEPEDEFAVYYC	QQWSSSPLT	FGQGTKLEIK		
h4E3-L3	GVPARFSGSGGTDTYTLTISSMEPEDEFAVYYC	QQWSSSPLT	FGQGTKLELK		

deamidation substitutions: Q/S/A/D
^ tryptophan oxidation substitutions: H/Y/F

h4E3-L1 is a "CDR-swap" with no changes to human framework. Subsequent sequences alter framework changes shown in red (compared to sequence above it).

FIG. 6B

Potential humanized sequence based on IMGT IGHV3-21*01 acceptor framework (AbM CDR definition)

IGHV3-21*01 EVQLVESGGGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSSISSSSSIY

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS

seq	10	20	30	40	50
AbM	10	20	30	40	50 a
	b b b	p b b b b	b b b b i	i i b b b	
S7-4E3	EVQLVESGGALVKPGGSLKISCAVS	GFIFSNYDMS	WVRQNPEKRLEWVA	TISSGGGYYT	
	*	**	*	*	*
3-21*01	EVQLVESGGGLVKPGGSLRLSCAAS	GFTFSYSMN	WVRQAPGKGLEWVS	SISSSSSIY	
h4E3-H1	EVQLVESGGGLVKPGGSLRLSCAAS	GFIFSNYDMS	WVRQAPGKGLEWVS	TISSGGGYYT	
h4E3-H2	EVQLVESGGGLVKPGGSLRLSCAAS	GFIFSNYDMS	WVRQAPGKGLEWVA	TISSGGGYYT	
h4E3-H3	EVQLVESGGGLVKPGGSLRLSCAAS	GFIFSNYDMS	WVRQAPGKGLEWVA	TISSGGGYYT	

seq	60	70	80	90	100	110	120
AbM	60	70	80 abc	90			110
	i b b b b x	b b b b b	b i b b b				i b b b
S7-4E3	YDPSVKGRFTISRDNKNAKALYLQMSSLRSEDTALYYCTR	HGYGNYDWYFDV	WGAGATVTVSS				
	*	*	*	*	*	*	*
3-21*01	YADSVKGRFTISRDNKNAKNSLYLQMNSLRAEDTAVYYCAR						WGQGLTVTVSS
h4E3-H1	YADSVKGRFTISRDNKNAKNSLYLQMNSLRAEDTAVYYCAR	HGYGNYDWYFDV	WGQGLTVTVSS				
h4E3-H2	YADSVKGRFTISRDNKNAKNSLYLQMNSLRAEDTAVYYCTR	HGYGNYDWYFDV	WGQGLTVTVSS				
h4E3-H3	YADSVKGRFTISRDNKNAKNSLYLQMNSLRAEDTAVYYCTR	HGYGNYDWYFDV	WGQGLTVTVSS				
	P	L	^	#			

deamidation substitutions: Q/S/A/D

^ tryptophan oxidation substitutions: H/Y/F

h4E3-H1 is a "CDR-swap" with no changes to human framework. Subsequent sequences alter framework changes shown in red (compared to sequence above it).

FIG. 6C

Potential humanized sequence based on IMGT IGKV1-39*01 acceptor framework (AbM CDR definition)
IGKV1-39*01 DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQS
GVPSRFSGSGGTFTLTISSLQPEDFATYYCQQSYSTPP
Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50
AbM	10	20	30	40	50
	b b b	p p b b b	b b b i i i b b i	i	
S7-10B5.1	DVQMTQTSSLSASLGDRVTISC	RASQDINTYLN	WYQQKPDGTVKLLIY	YTSRLHS	
	* ** *	*	***		
1-39*01	DIQMTQSPSSLSASVGDRTITC	RASQSISSYL	WYQQKPGKAPKLLIY	AASSLQS	
h10B5-L1	DIQMTQSPSSLSASVGDRTITC	RASQDINTYLN	WYQQKPGKAPKLLIY	YTSRLHS	
h10B5-L2	DIQMTQSPSSLSASVGDRTITC	RASQDINTYLN	WYQQKPGKAPKLLIY	YTSRLHS	
h10B5-L3	DVQMTQSPSSLSASVGDRTITC	RASQDINTYLN	WYQQKPGKAPKLLIY	YTSRLHS	

seq	60	70	80	90	100
AbM	60	70	80	90	100
	b b	b b b b	ib bib ibi iib i	b b b	
S7-10B5.1	GVPSRFSGSGGTDYSLTISNLEQEDIAITYFC	QQGNITLPWT	FGGGTKLEIK		
	**	* ** *	*		
1-39*01	GVPSRFSGSGGTFTLTISSLQPEDFATYYC	QQSYSTPP	FGGGTKLEIK		
h10B5-L1	GVPSRFSGSGGTFTLTISSLQPEDFATYYC	QQGNITLPWT	FGGGTKLEIK		
h10B5-L2	GVPSRFSGSGGTFTLTISSLQPEDFATYYC	QQGNITLPWT	FGGGTKLEIK		
h10B5-L3	GVPSRFSGSGGTFTLTISSLQPEDFATYYC	QQGNITLPWT	FGGGTKLEIK		

deamidation substitutions: Q/S/A/D

h10B5-L1 is a "CDR-swap" with no changes to human framework. Subsequent sequences alter framework changes shown in red (compared to sequence above it).

FIG. 6D

Potential humanized sequence based on IMGT IGHV1-46*01 acceptor framework (AbM CDR definition)

IGHV1-46*01 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYMHVWRQAPQGQGLEWNGIINPSGGSTS

Joining region IMGT J00256|IGHJ4*01|YFDYWGGQGLTLTVSS

seq	10	20	30	40	50
AbM	10	20	30	40	50 a
	b b b	p b b b b	b b b b i	i i b b b	
S7-10B5.1	QVHLQSQGP	ELVKPGASVKISCKAS	GYAFTNCWMN	WVRQRPKGGLDNIG	RIFFGNGHTN
	* * *	* *	* * *		
1-46*01	QVQLVQSGAEVKKPGASVKVSCKAS	GYFTTSYMH	WVRQAPQGQGLEWMG	IINPSGGSTS	
h10B5-H1	QVQLVQSGAEVKKPGASVKVSCKAS	GYAFTNCWMN	WVRQAPQGQGLEWMG	RIFFGNGHTN	
h10B5-H2	QVQLVQSGAEVKKPGASVKVSCKAS	GYAFTNCWMN	WVRQAPQGQGLEWIG	RIFFGNGHTN	
h10B5-H3	QVQLVQSGAEVKKPGASVKISCKAS	GYAFTNCWMN	WVRQAPQGQGLEWIG	RIFFGNGHTN	
h10B5-H4	QVQLVQSGAEVKKPGASVKISCKAS	GYAFTNCWMN	WVRQAPQGQGLEWIG	RIFFGNGHTN	
	v				@ #
	#x^				
seq	60	70	80	90	100 110
AbM	60	70	80 abc	90	110
	i b b b b x	b b b b	bibibb	i b b b	
S7-10B5.1	YSGKFKDKATLT	EDKSSSTAYMQLSSLTSEDS	SAVYFCAR	DYSDYYFDY	WGQGTLLTVSS
	** ****	* * * *	* * *		**
1-46*01	YAQKFQGRVTMT	RTSTSTVYMELSSLRSEDT	AVYYCAR		WGQGTLLTVSS
h10B5-H1	YAQKFQGRVTMT	RTSTSTVYMELSSLRSEDT	AVYYCAR	DYSDYYFDY	WGQGTLLTVSS
h10B5-H2	YAQKFQGRVTMT	EDTSTSTVYMELSSLRSEDT	AVYYCAR	DYSDYYFDY	WGQGTLLTVSS
h10B5-H3	YAQKFQGRATLT	EDTSTSTAYMELSSLRSEDT	AVYYCAR	DYSDYYFDY	WGQGTLLTVSS
h10B5-H4	YAQKFQGRATLT	EDKSTSTAYMELSSLRSEDT	AVYYCAR	DYSDYYFDY	WGQGTLLTVSS
	S				F

deamidation substitutions: Q/S/A

@ isoaspartate substitutions: Q/S/A

^ tryptophan oxidation substitutions: H/Y/F

h10B5-H1 is a "CDR-swap" with no changes to human framework. Subsequent sequences alter framework changes shown in red (compared to sequence above it).

FIG. 6E

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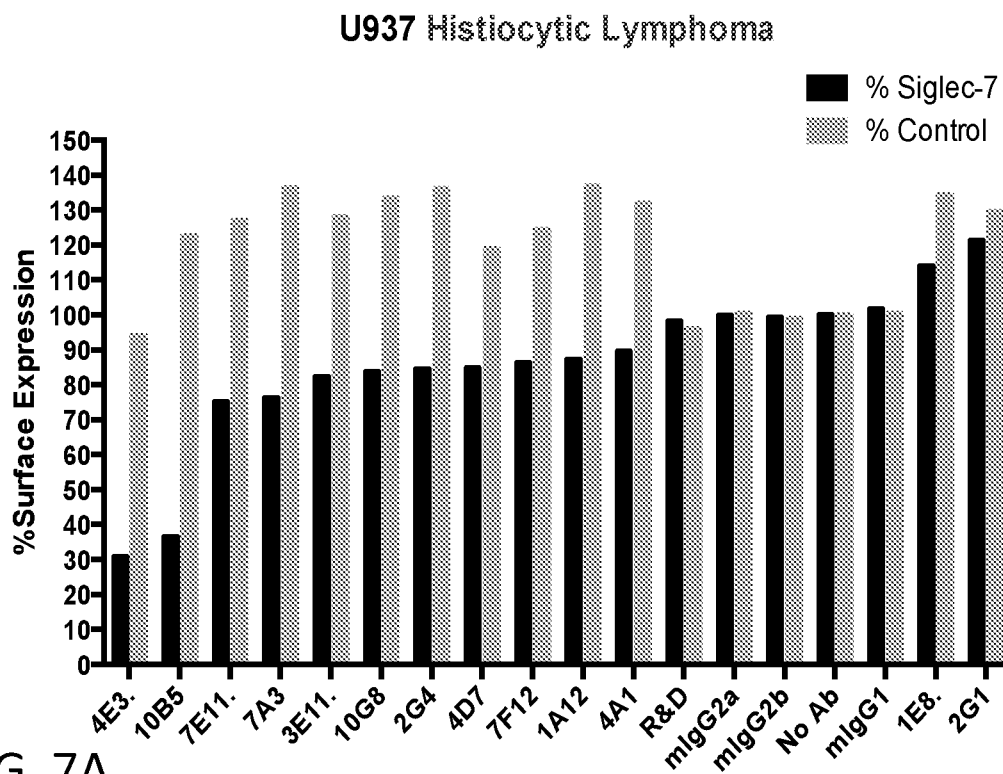


FIG. 7A

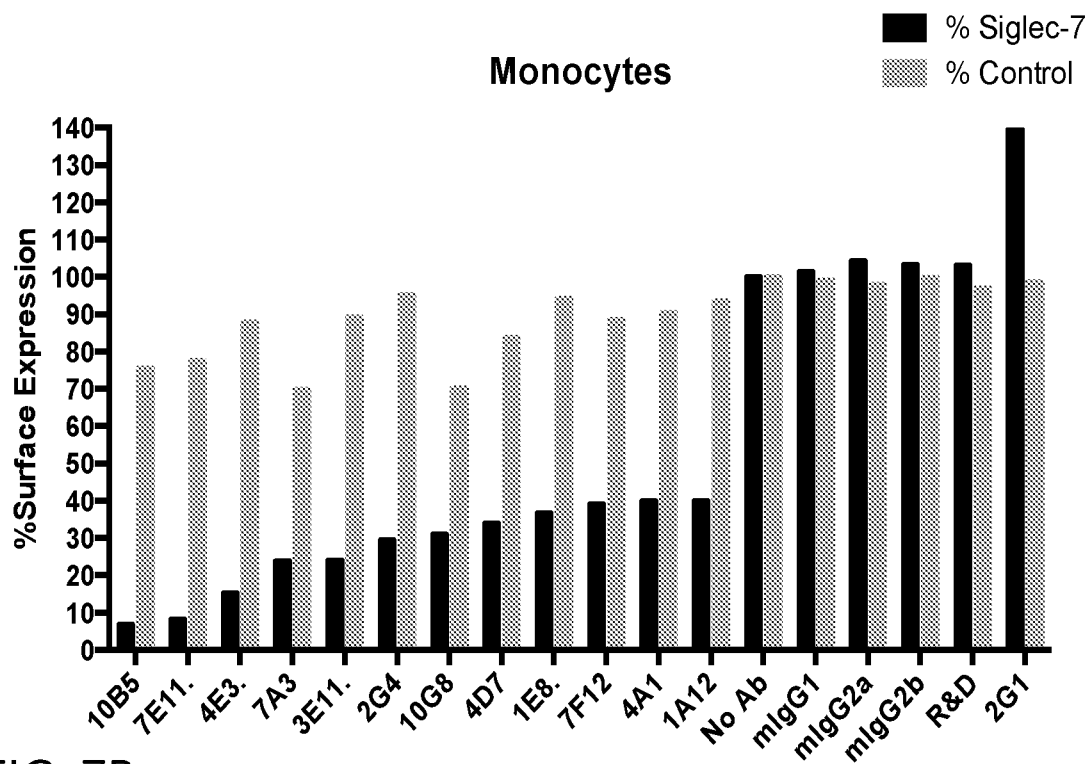


FIG. 7B

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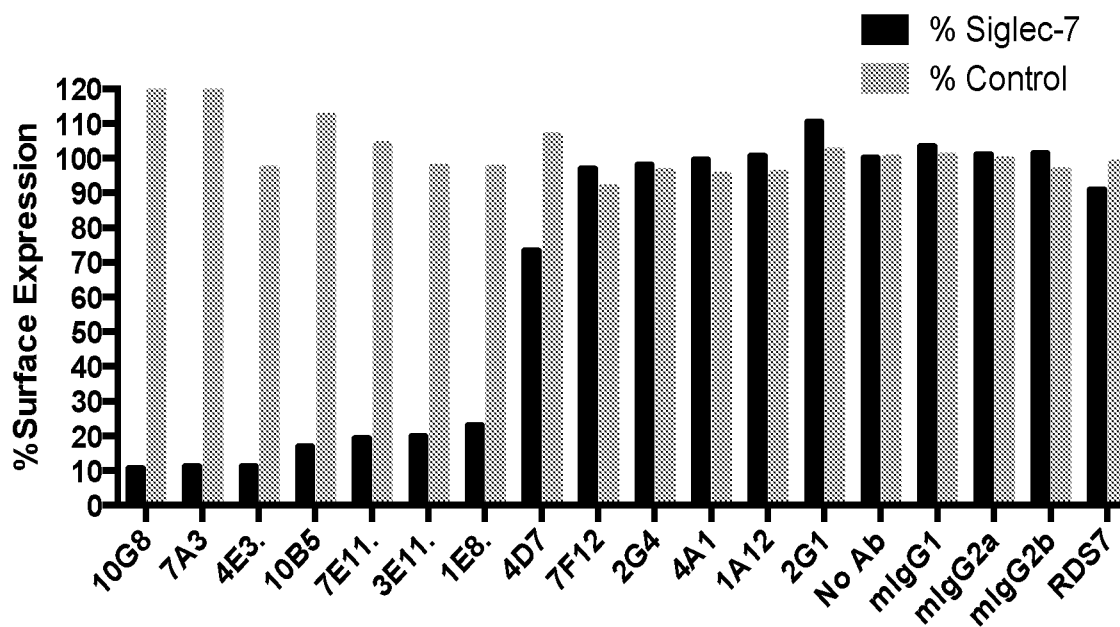
Dendritic Cells

FIG. 7C

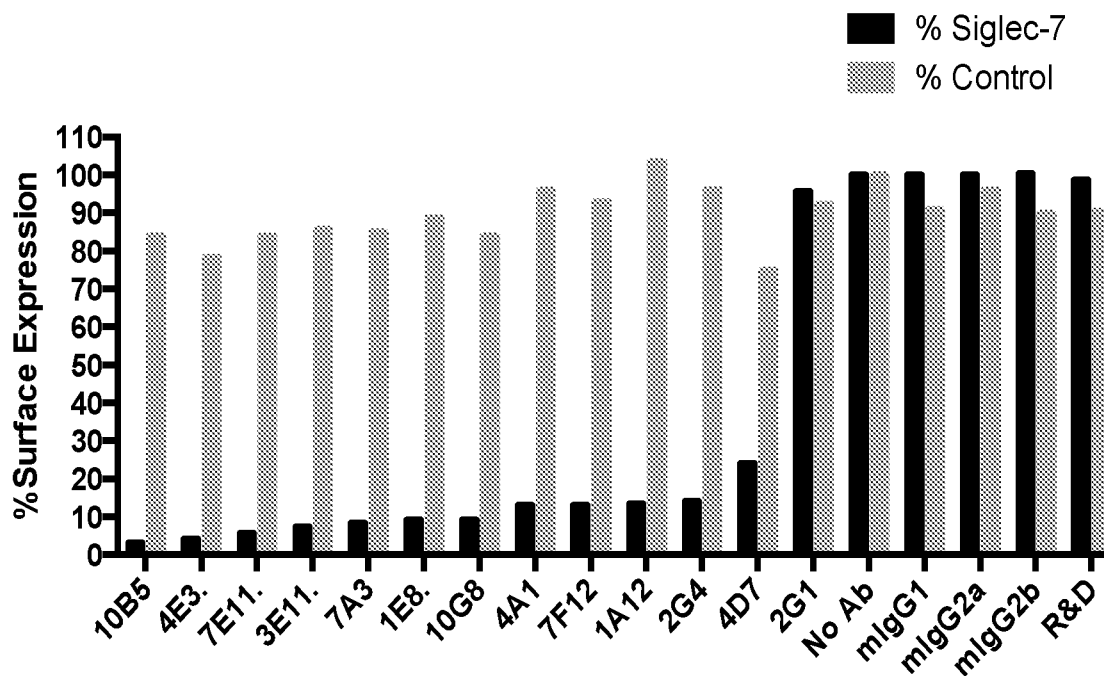
Macrophages

FIG. 7D

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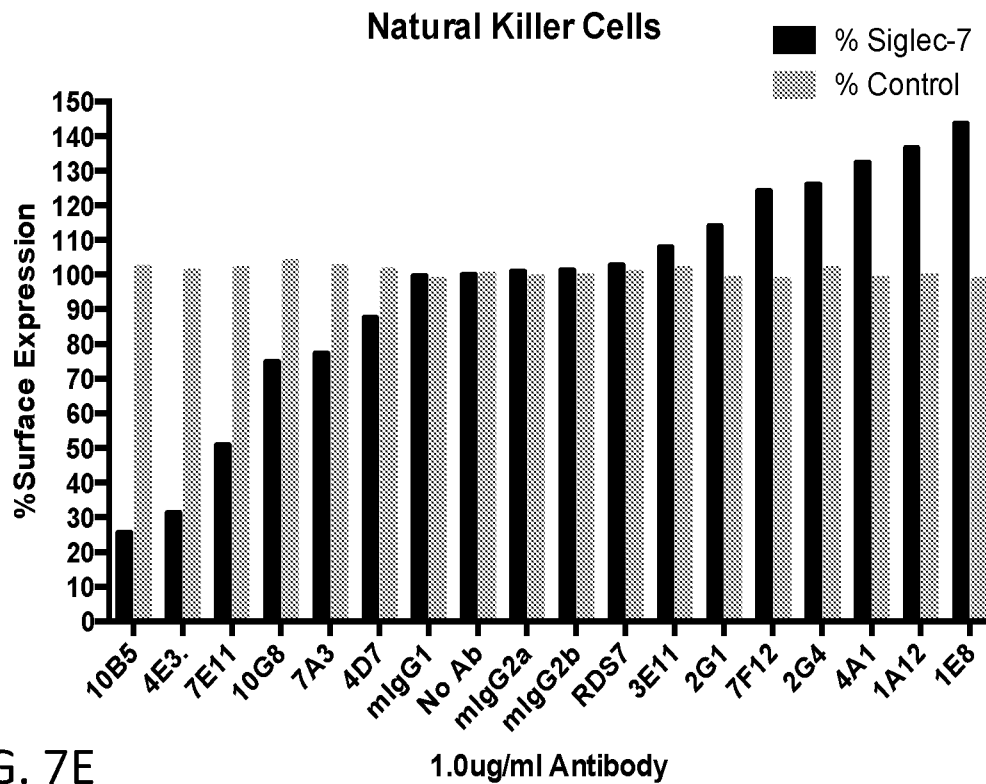


FIG. 7E

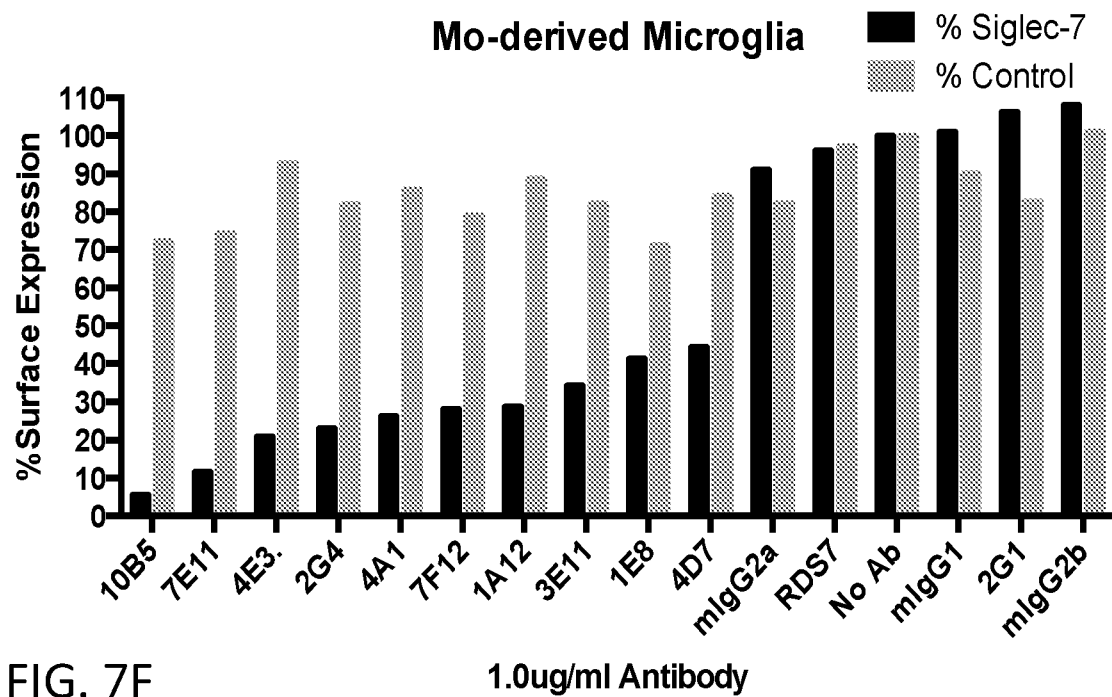


FIG. 7F

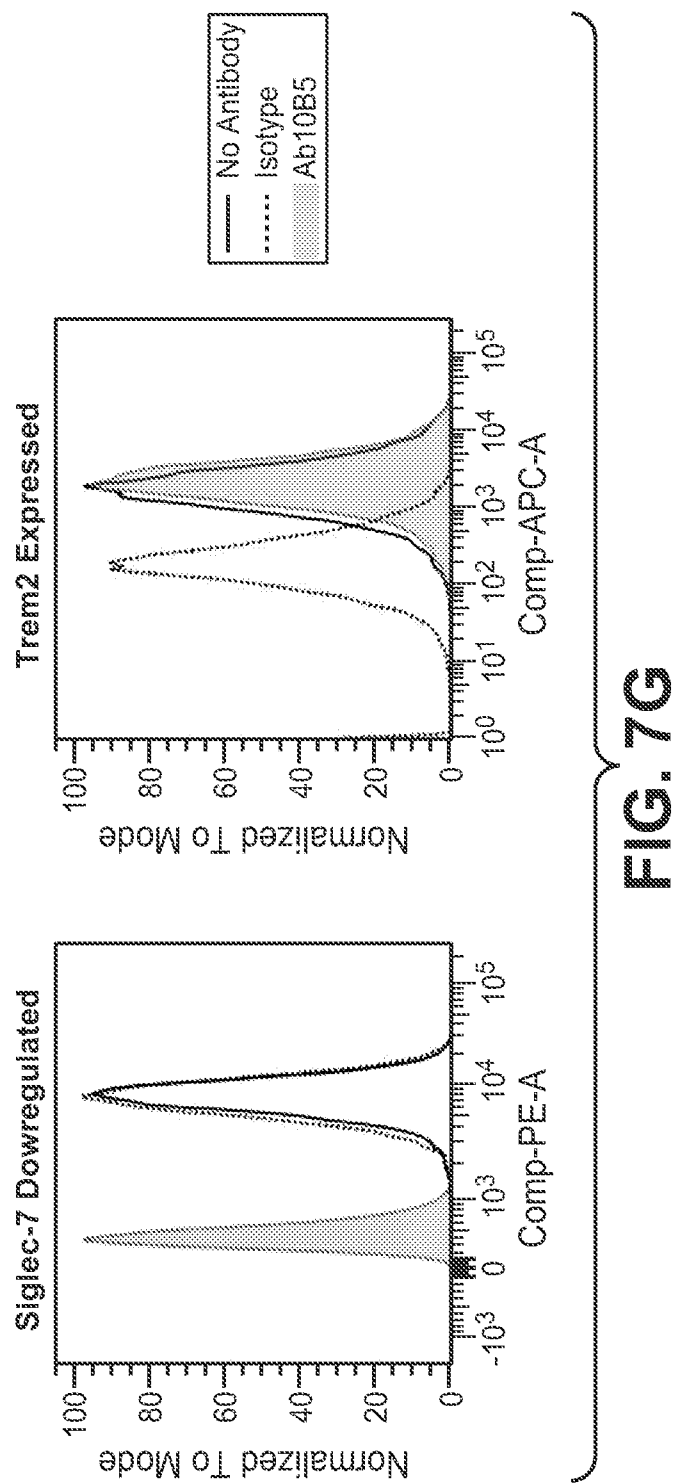


FIG. 7G

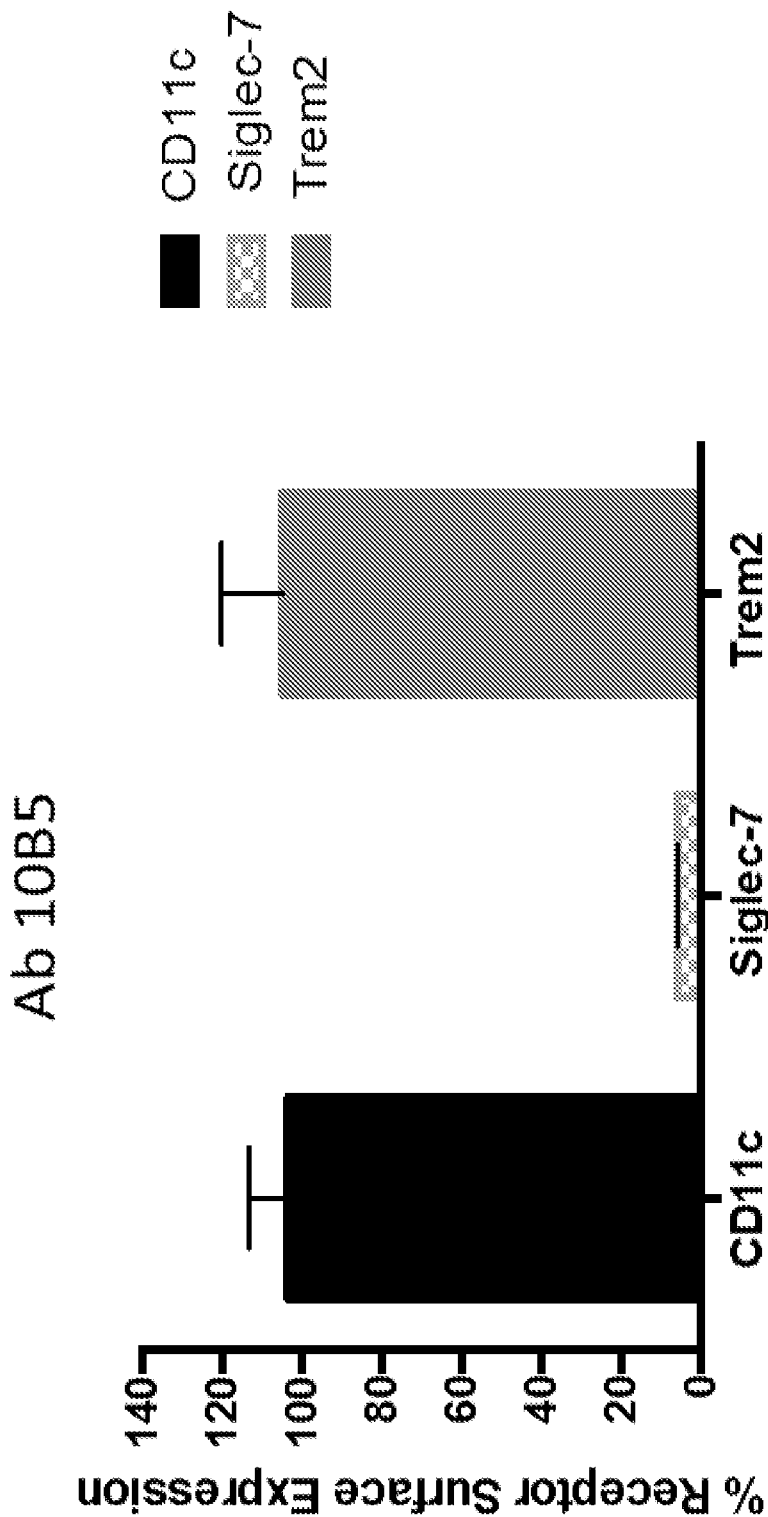
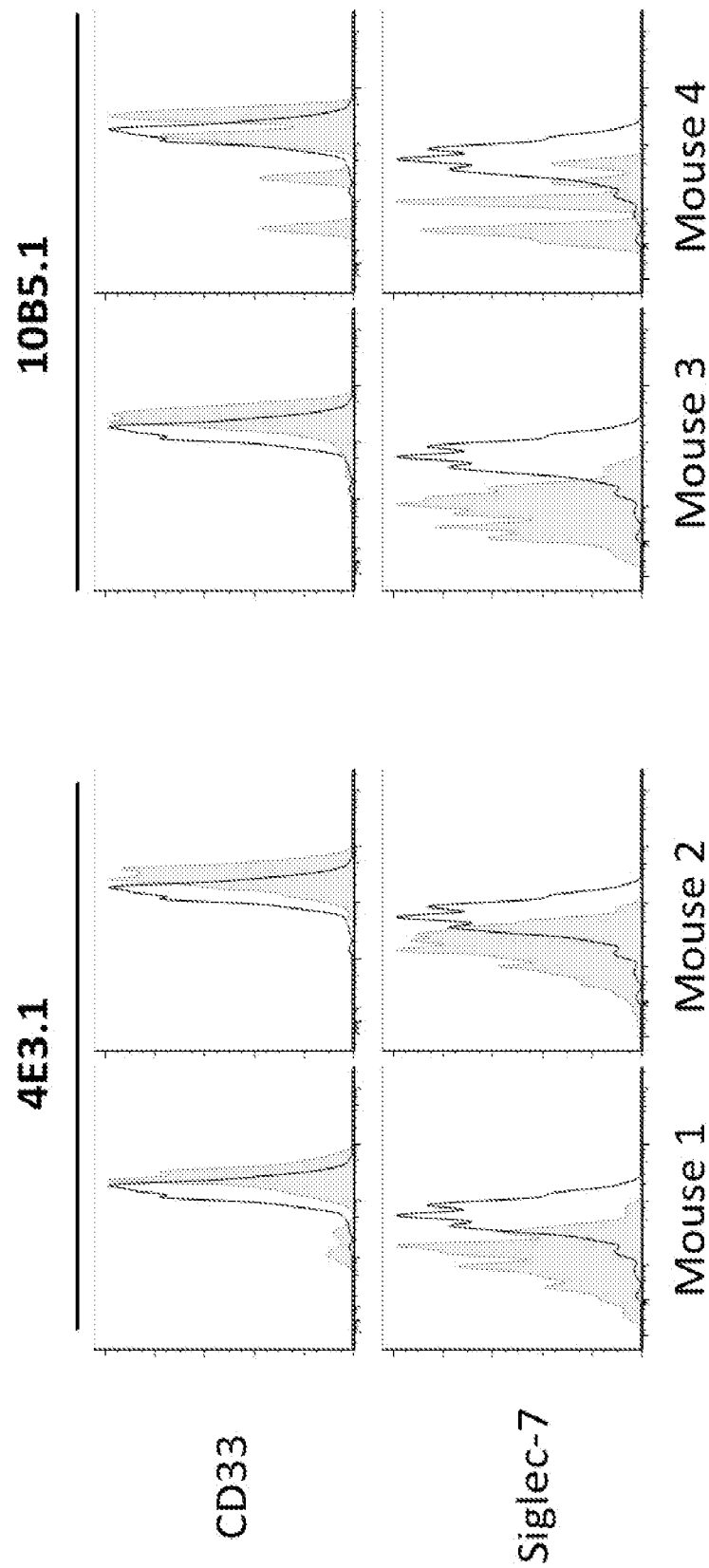


FIG. 7H



Gray Filled: Siglec-7 antibody treated
Black Line: MOPC21-treated

FIG. 7I

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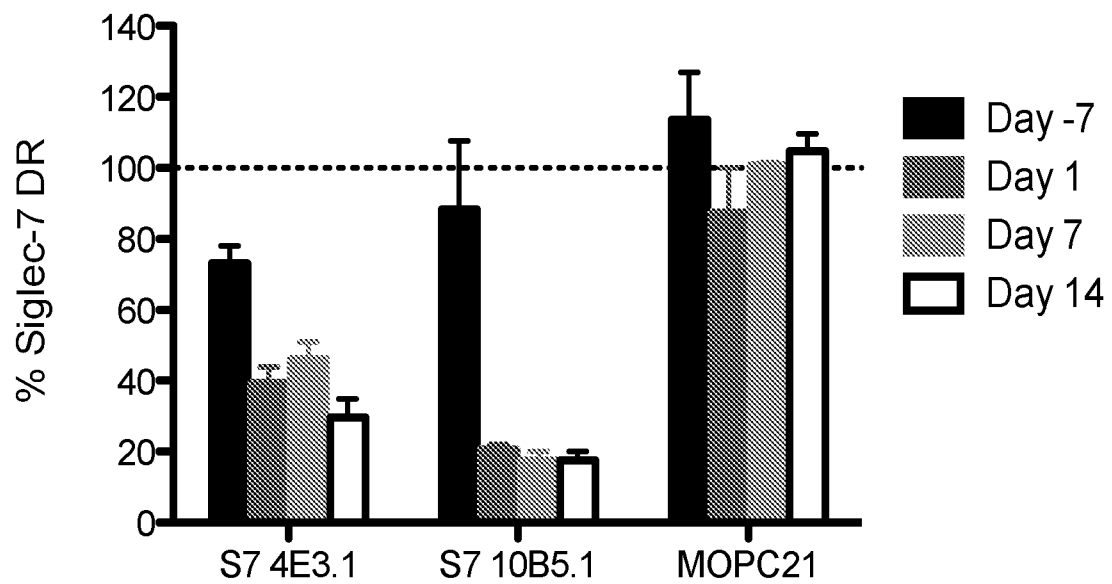


FIG. 7J

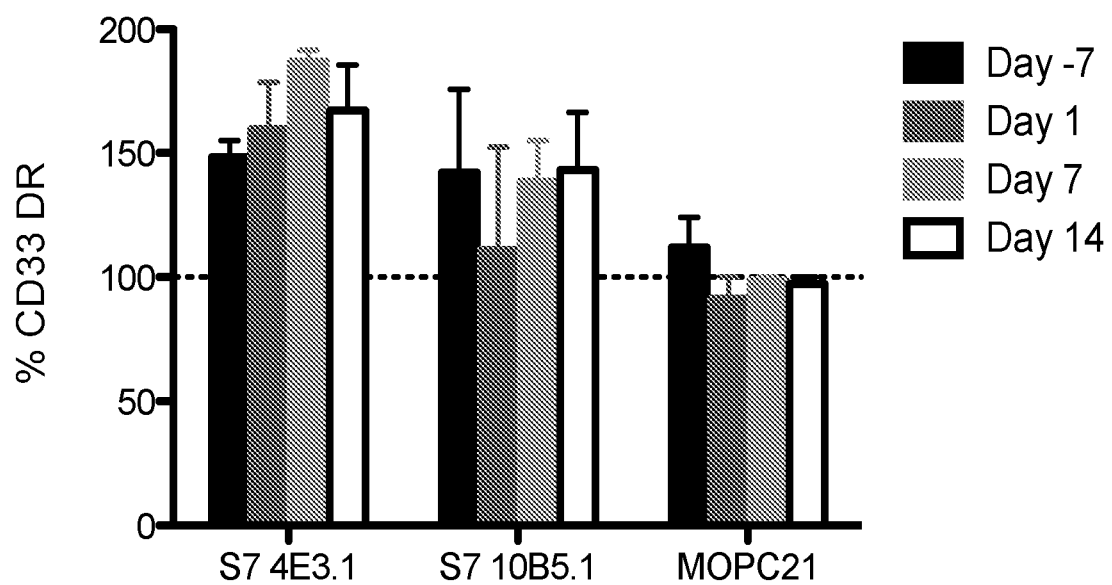


FIG. 7K

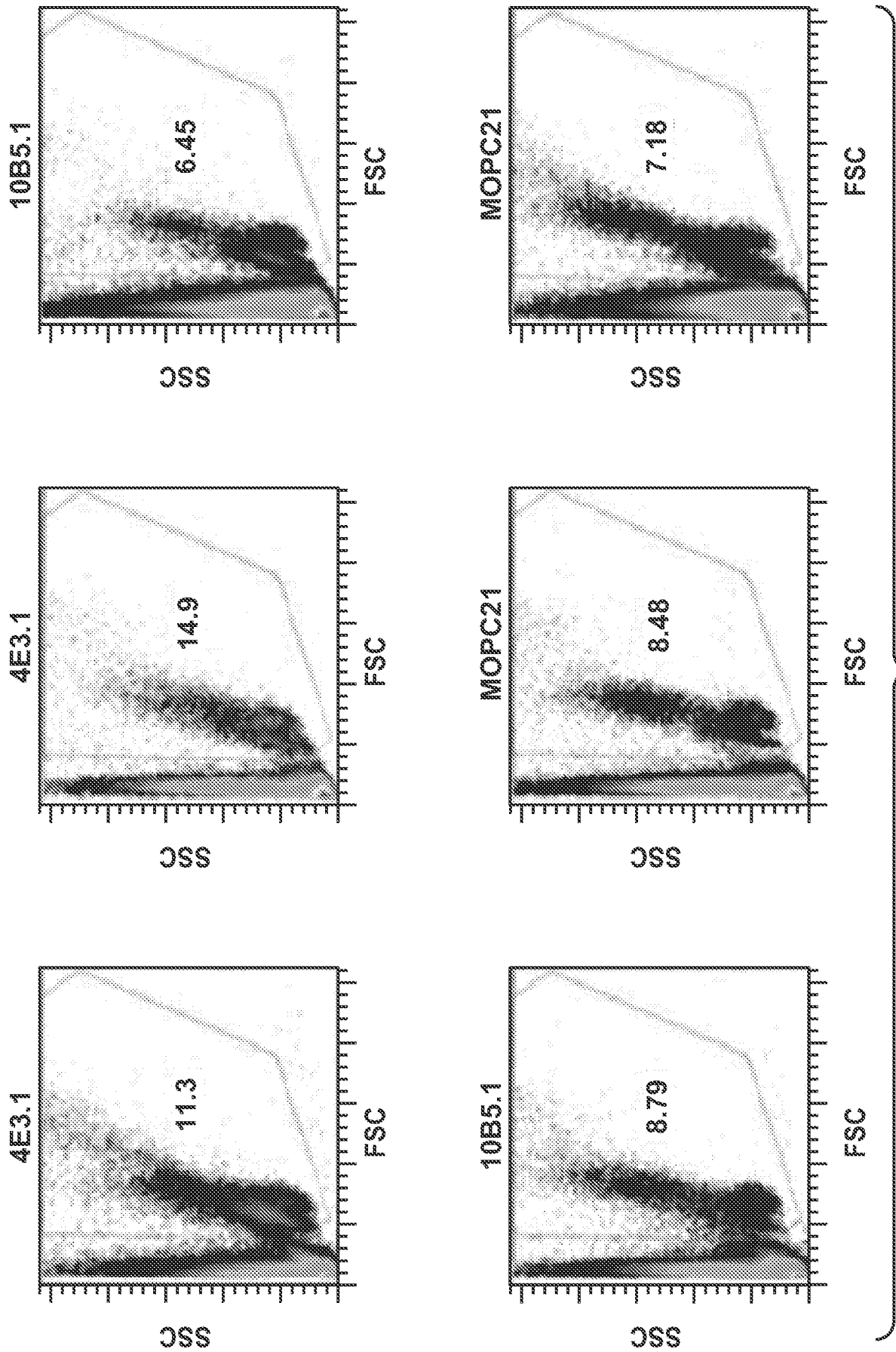


FIG. 7L

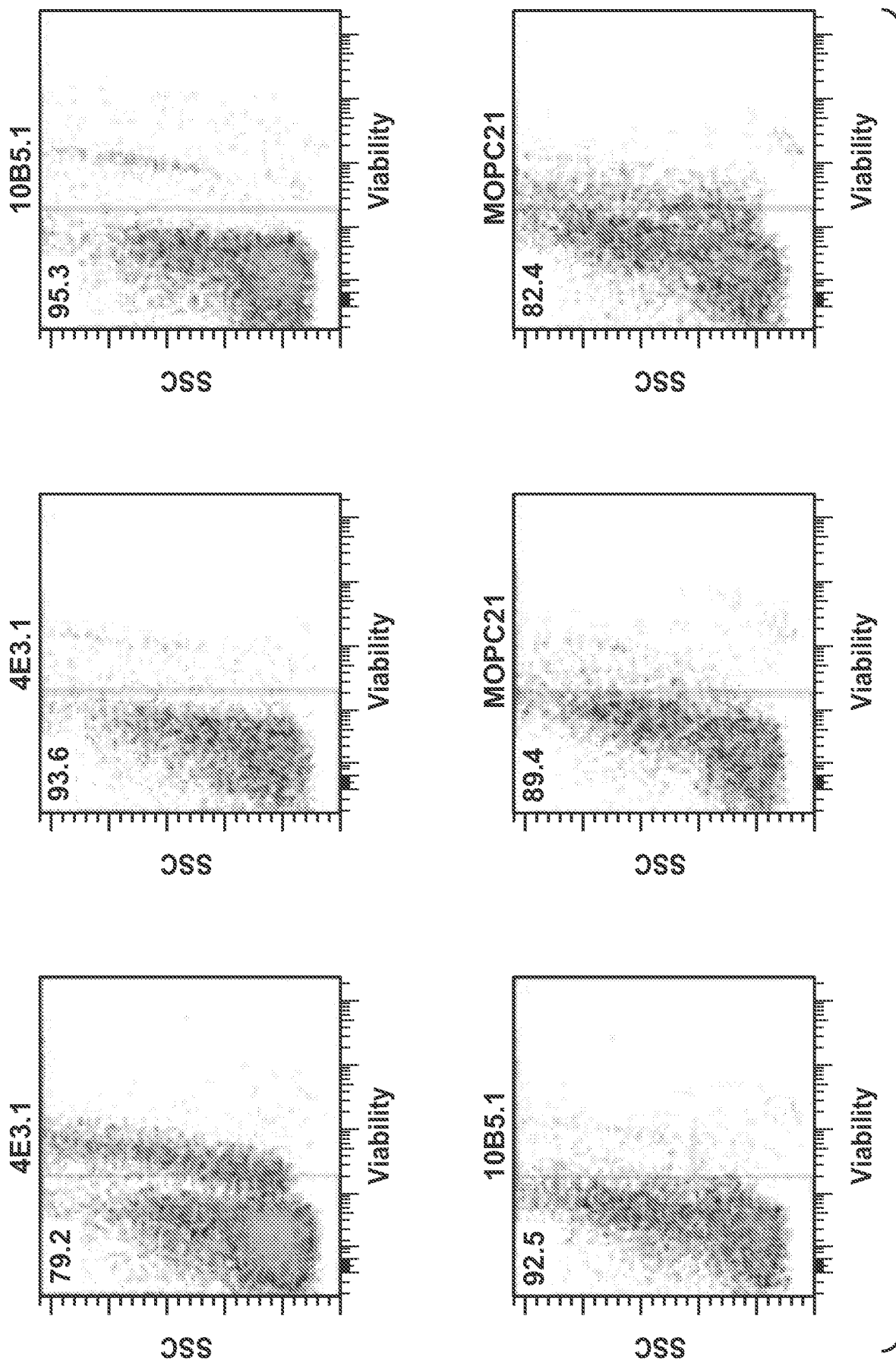
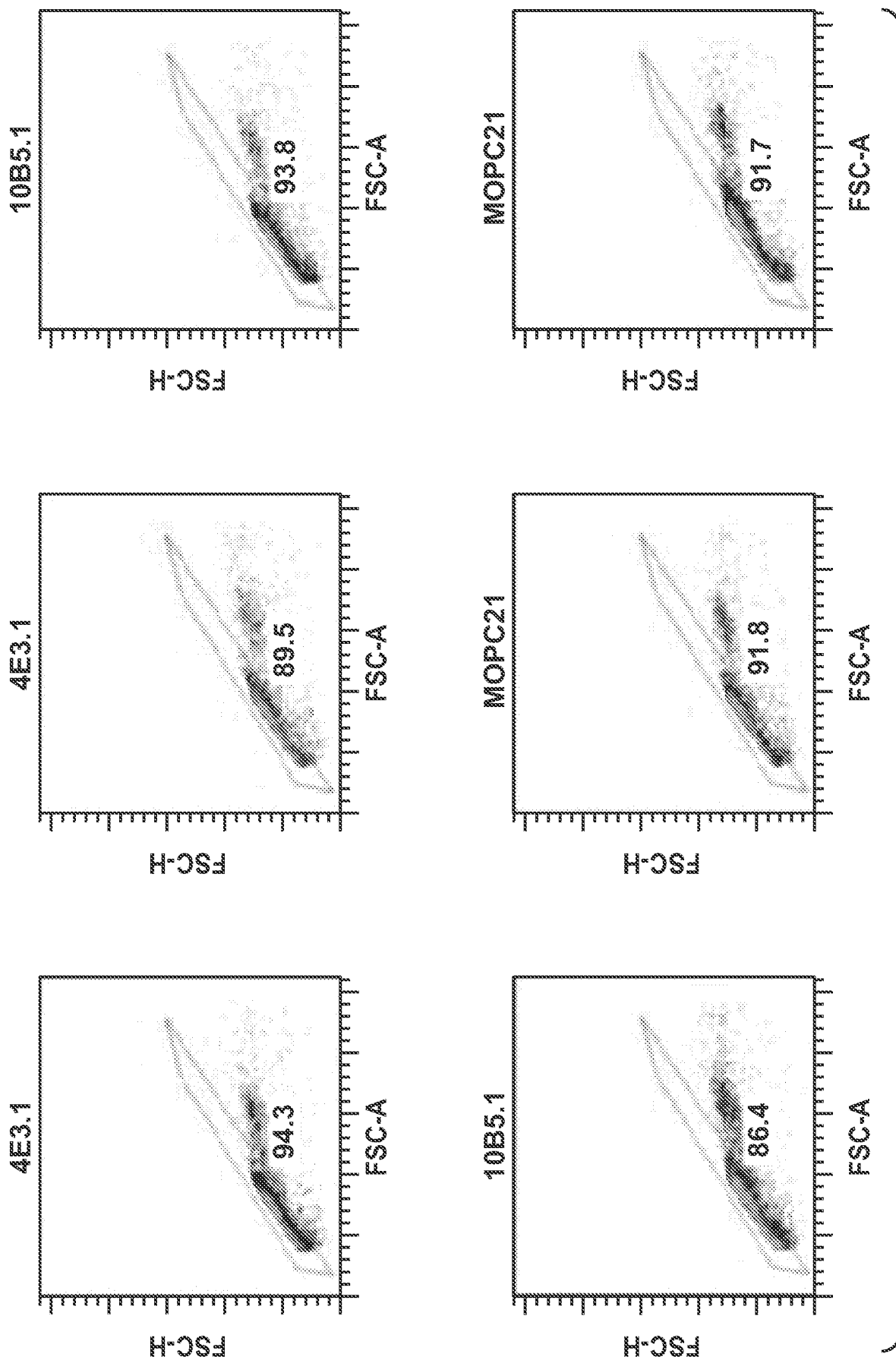


FIG. 7L (Cont.)



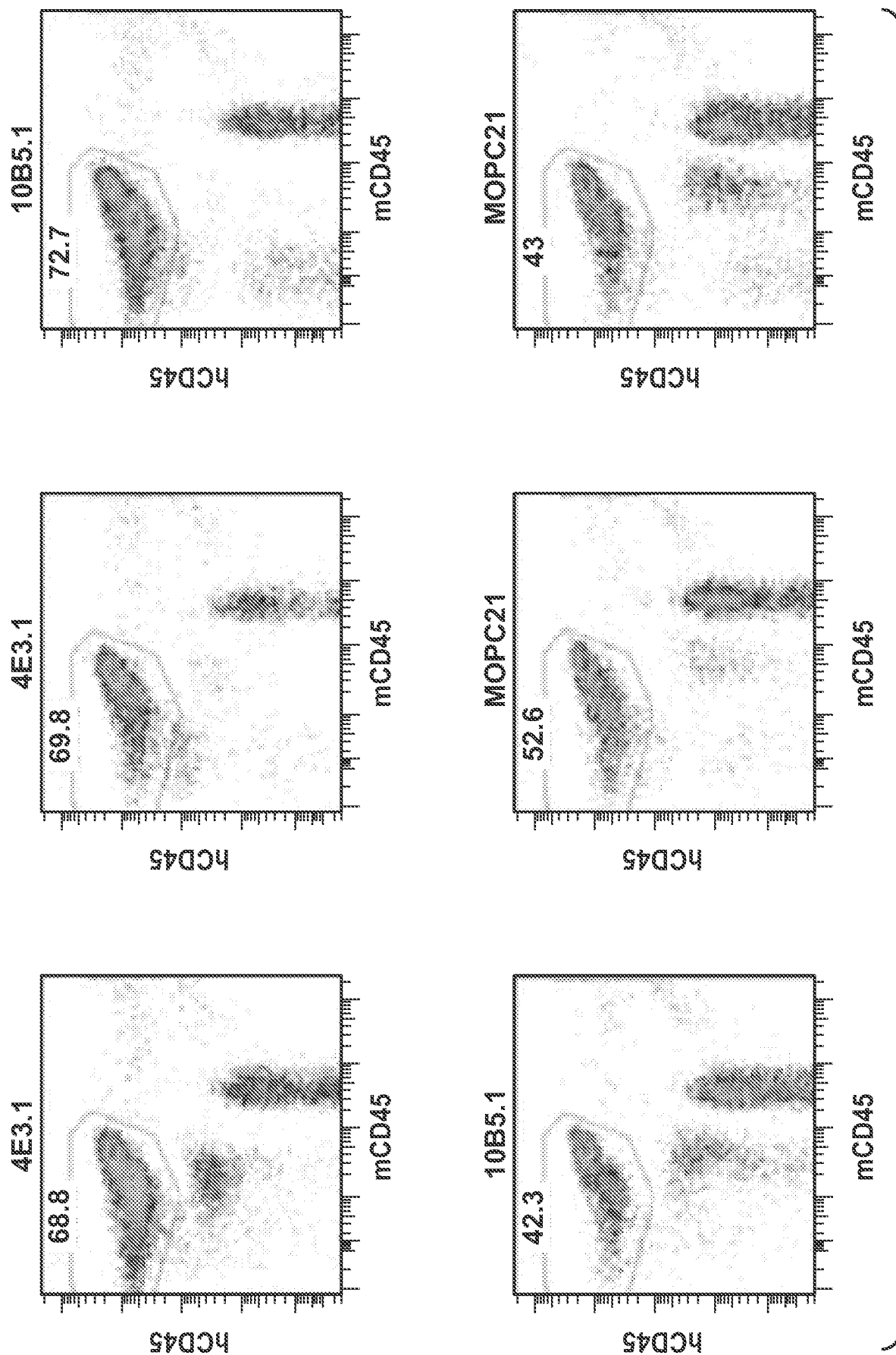


FIG. 7L (Cont.)

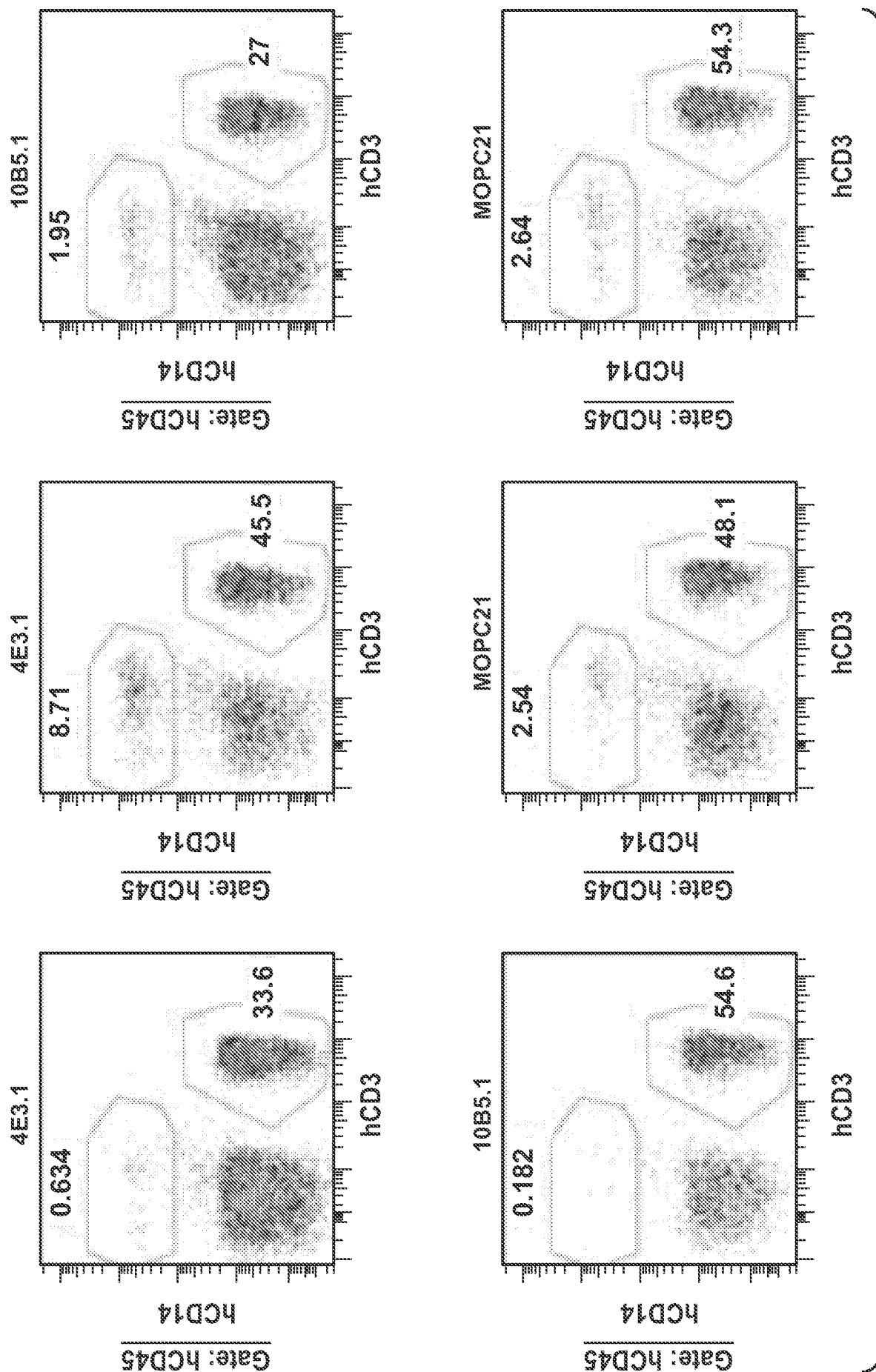


FIG. 7L (Cont.)

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Siglec-7 mAb Downregulation Titration

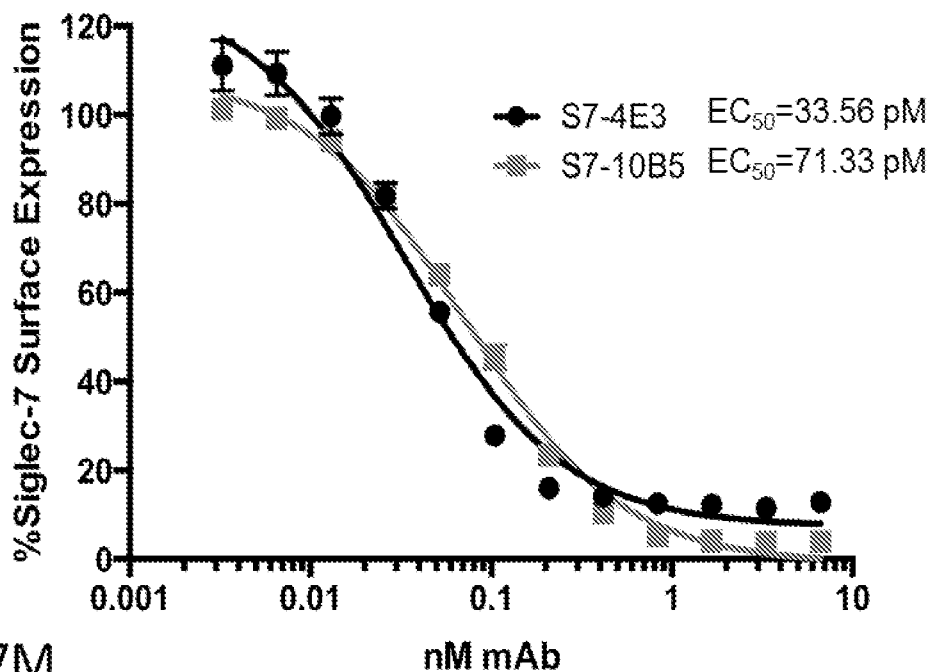


FIG. 7M

Control Receptor

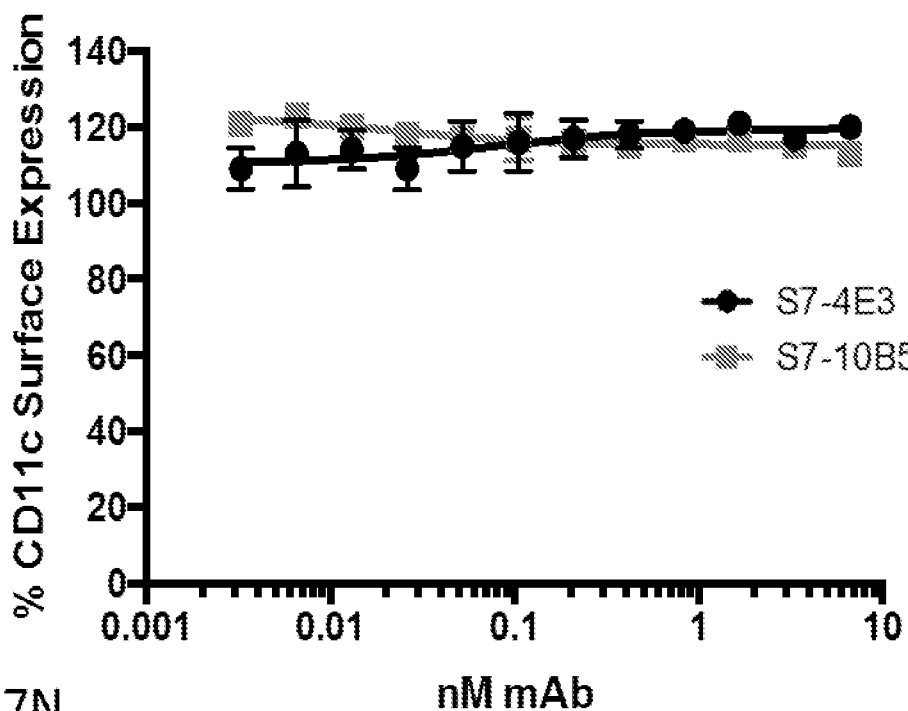


FIG. 7N

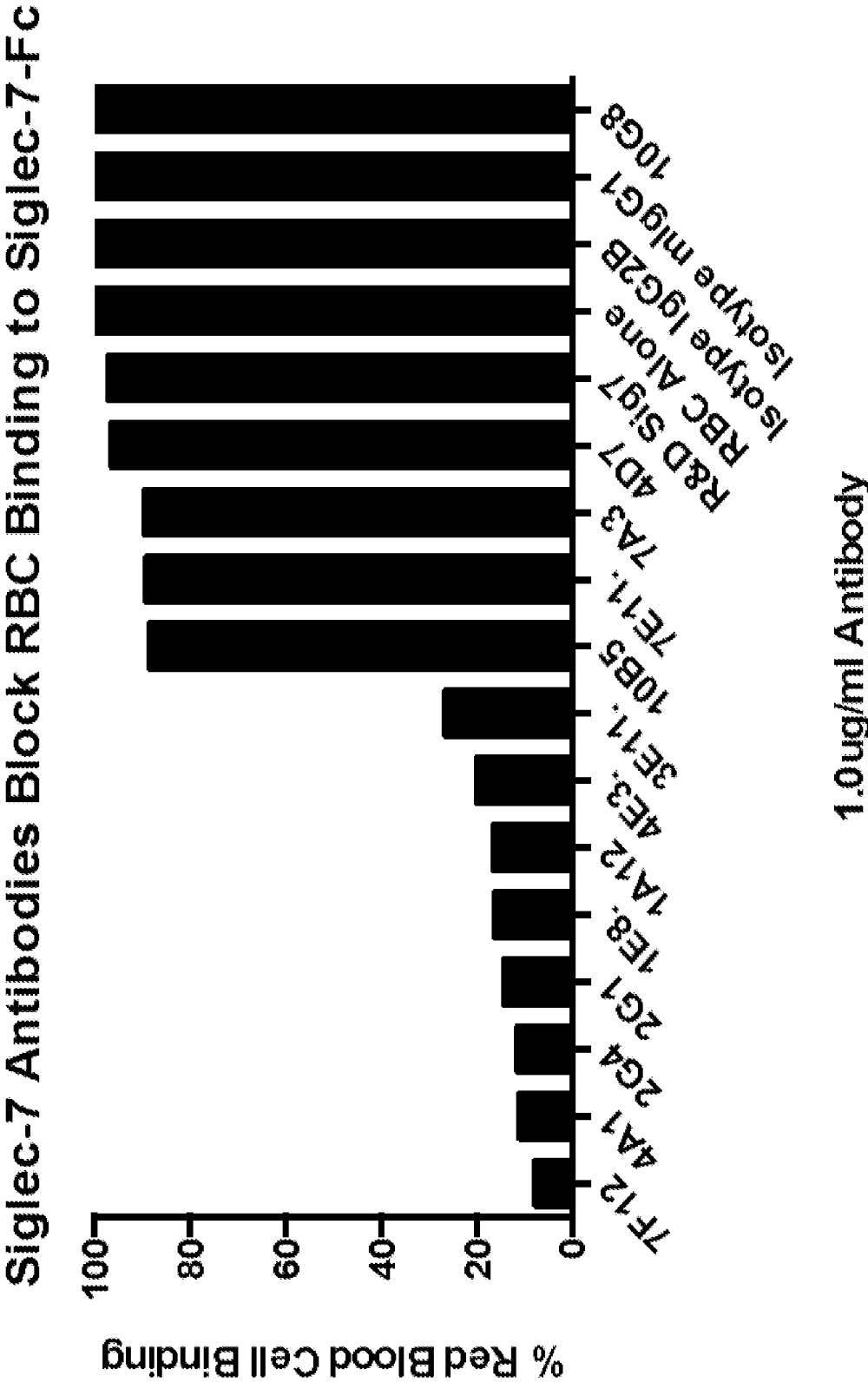
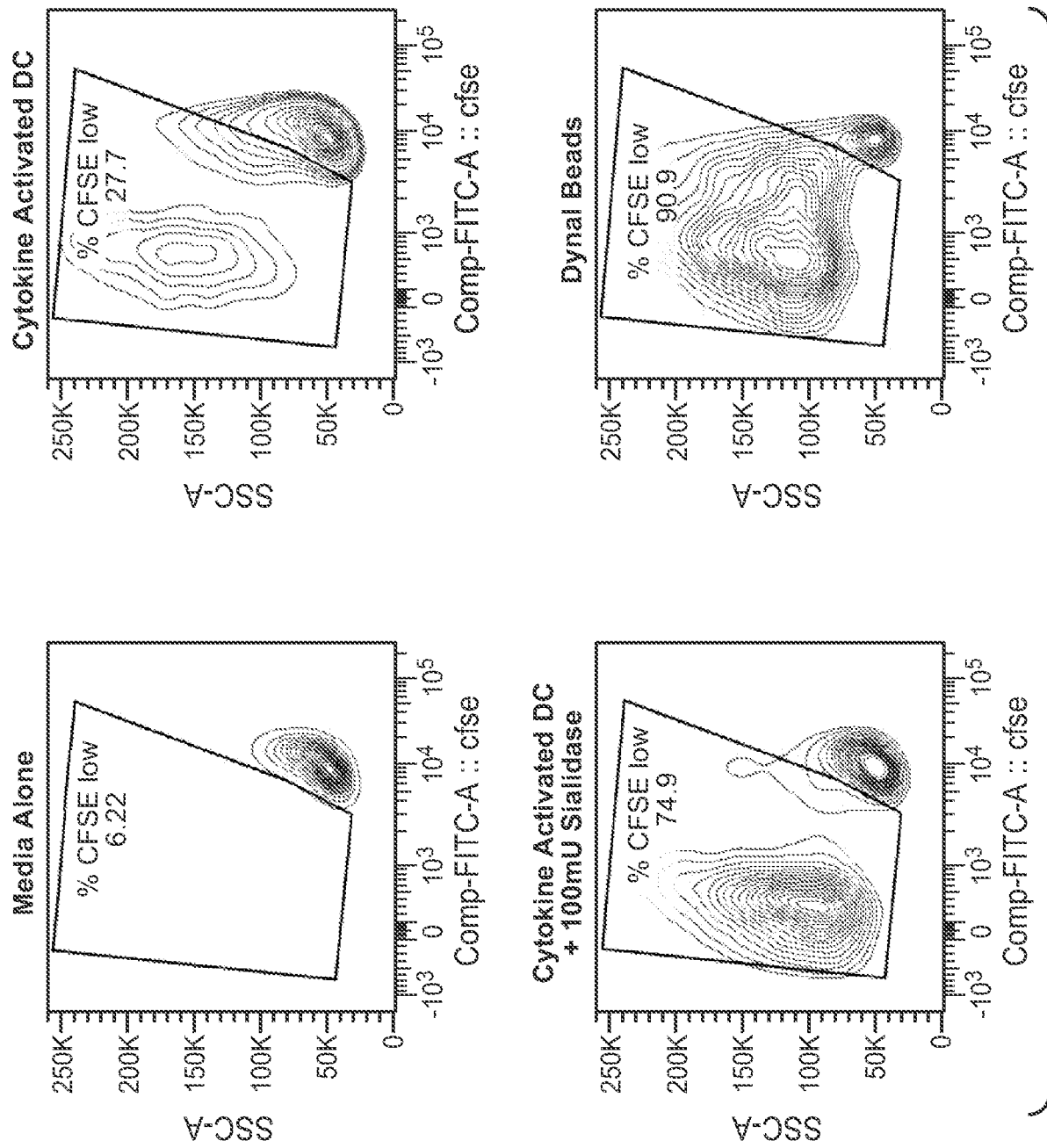


FIG. 8



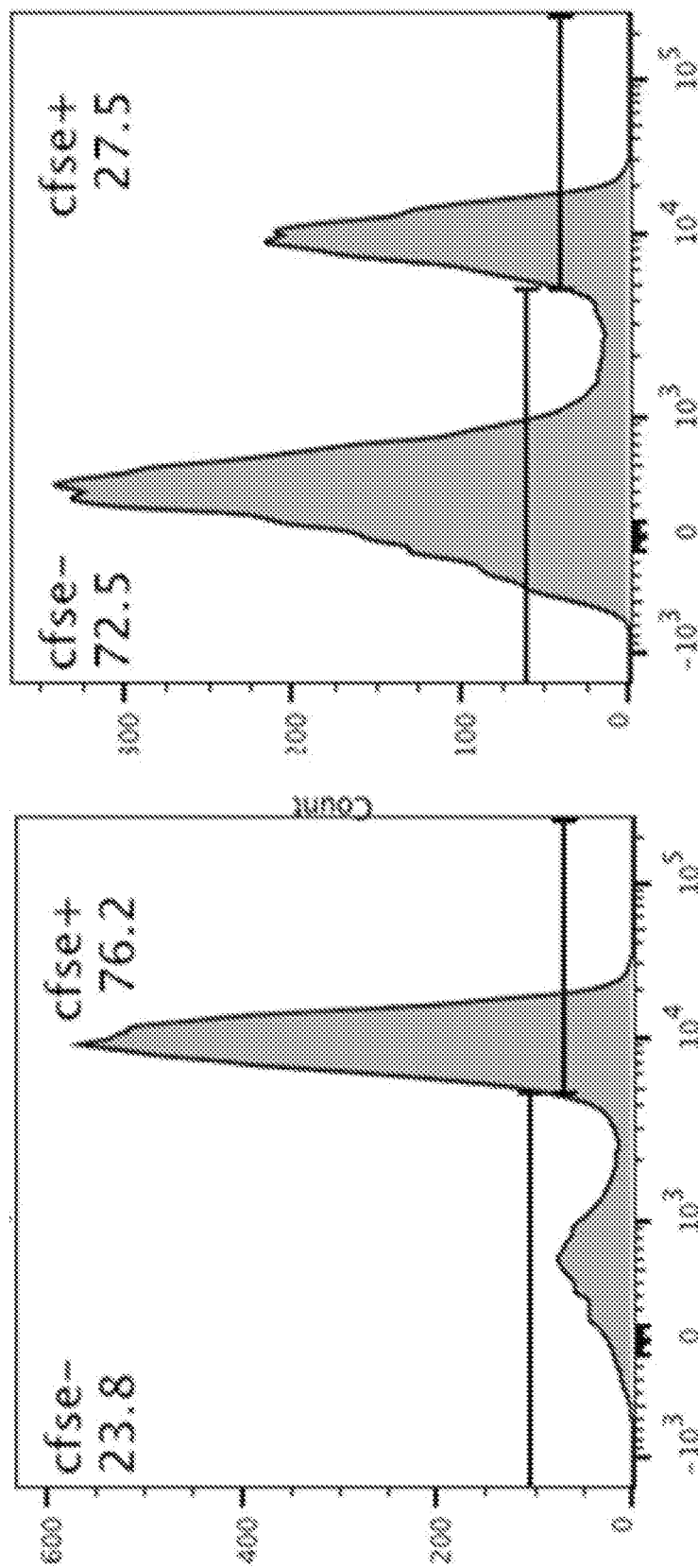


FIG. 10

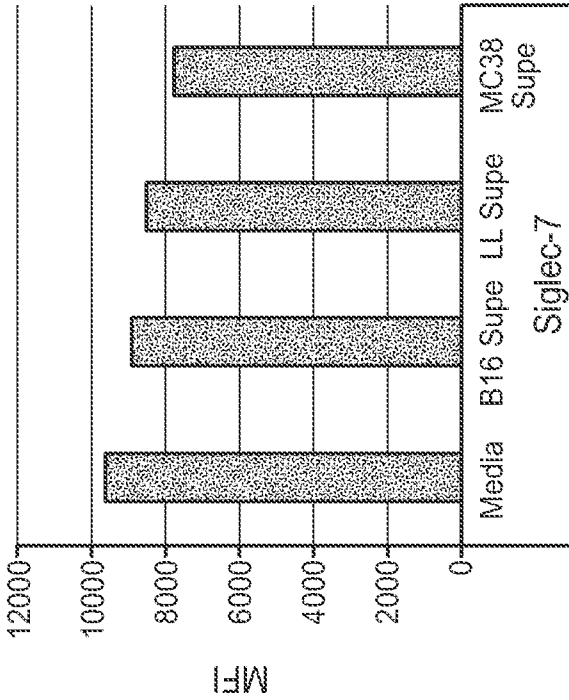
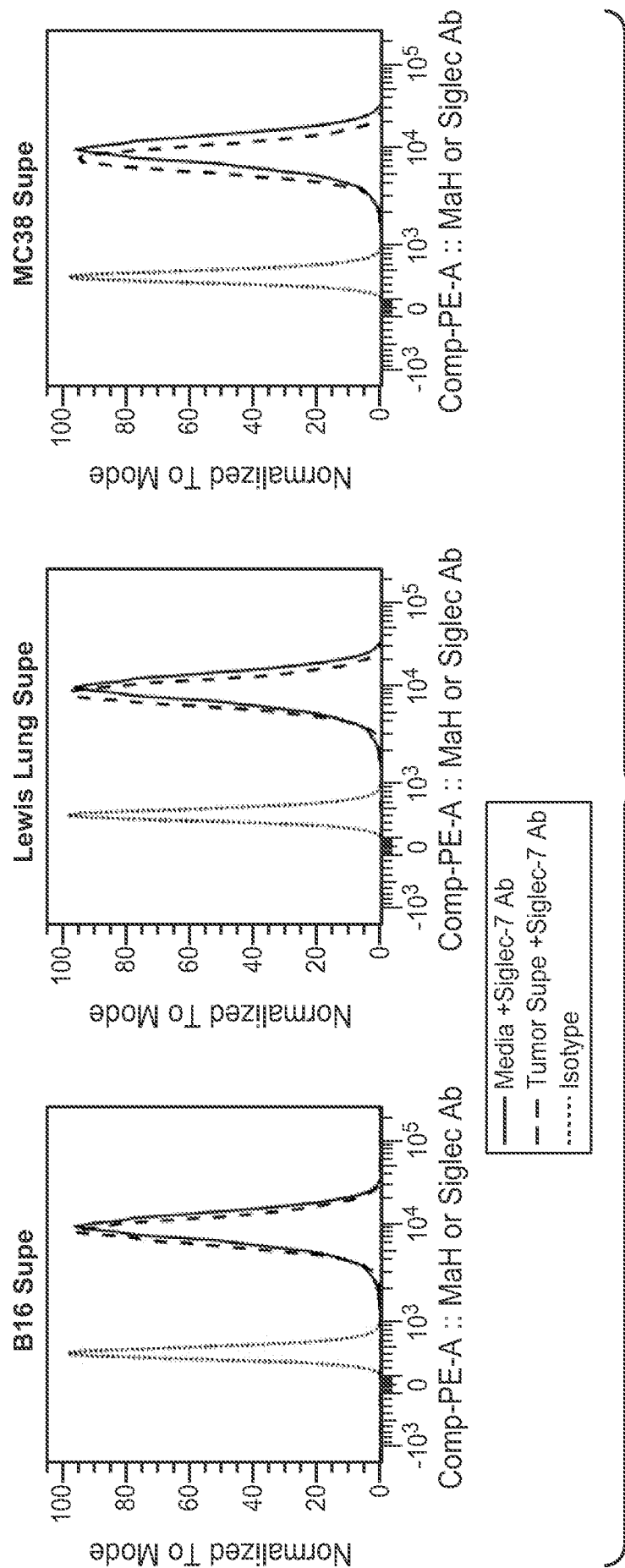


FIG. 11A



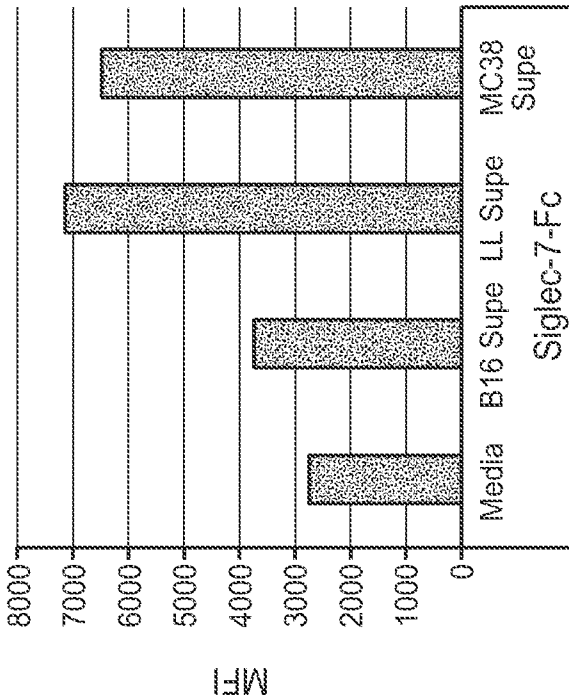


FIG. 11C

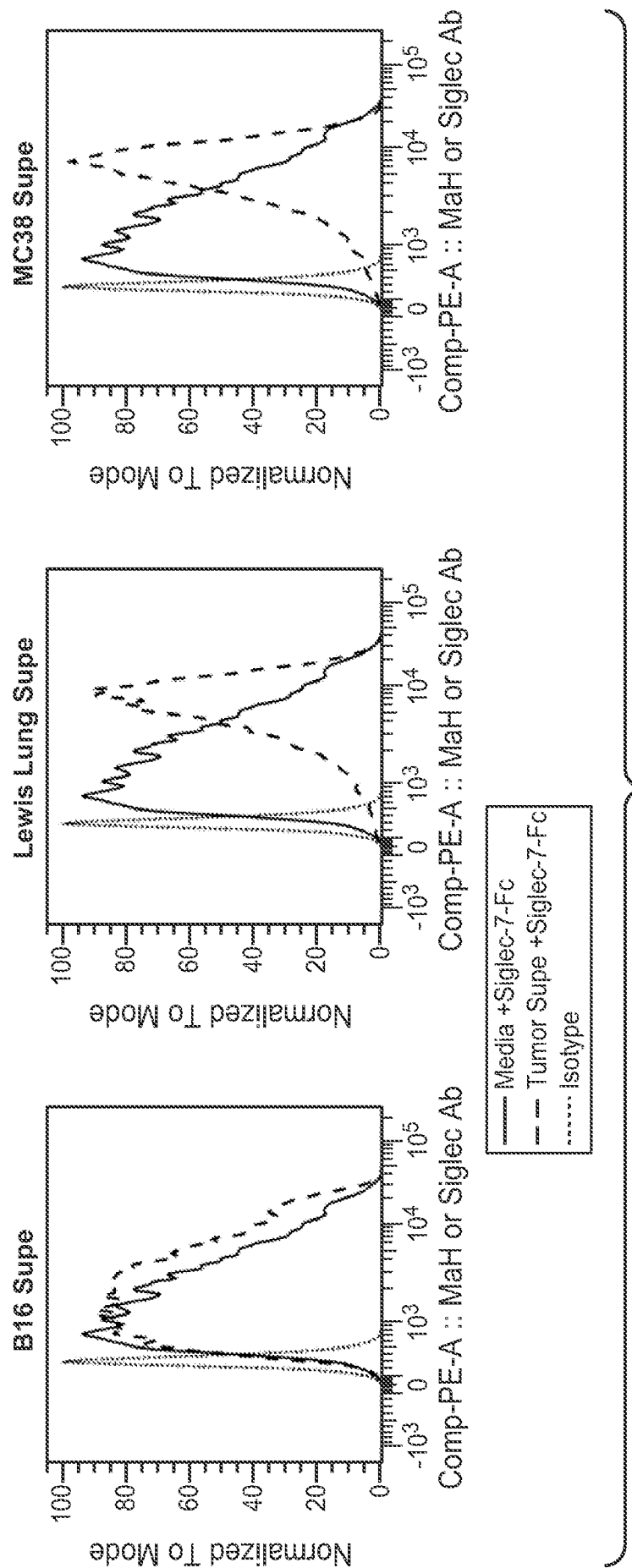


FIG. 11D

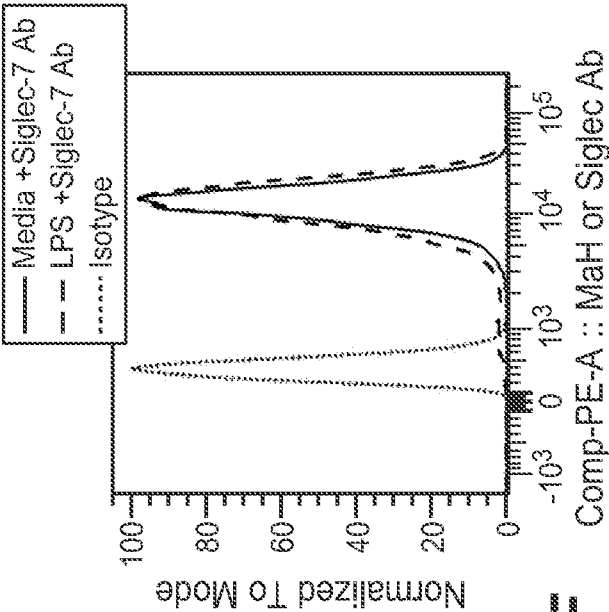


FIG. 11F

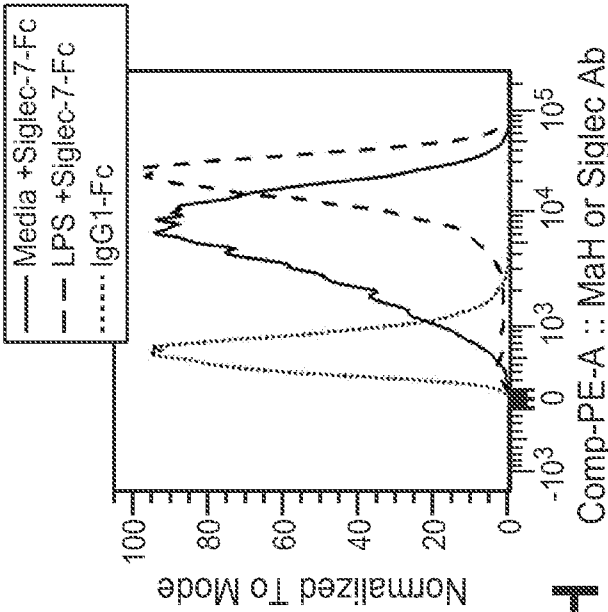


FIG. 11H

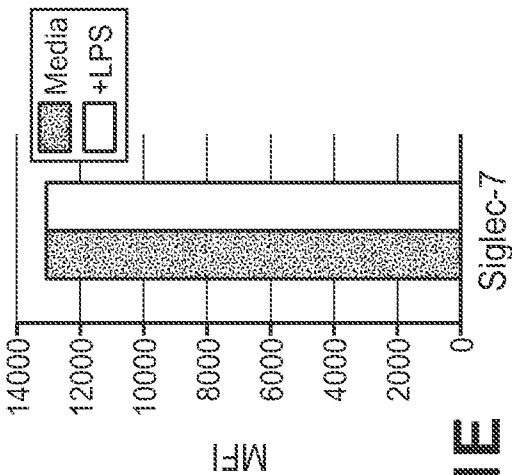


FIG. 11E

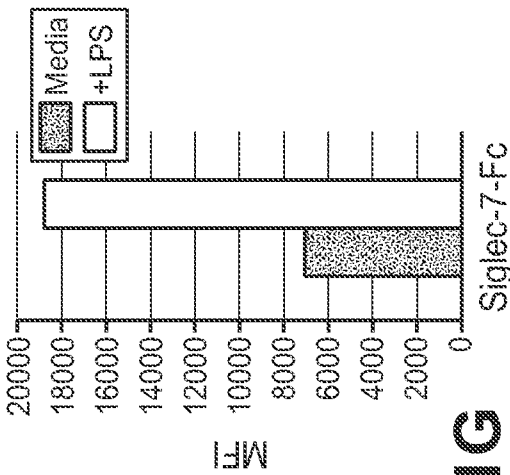


FIG. 11G

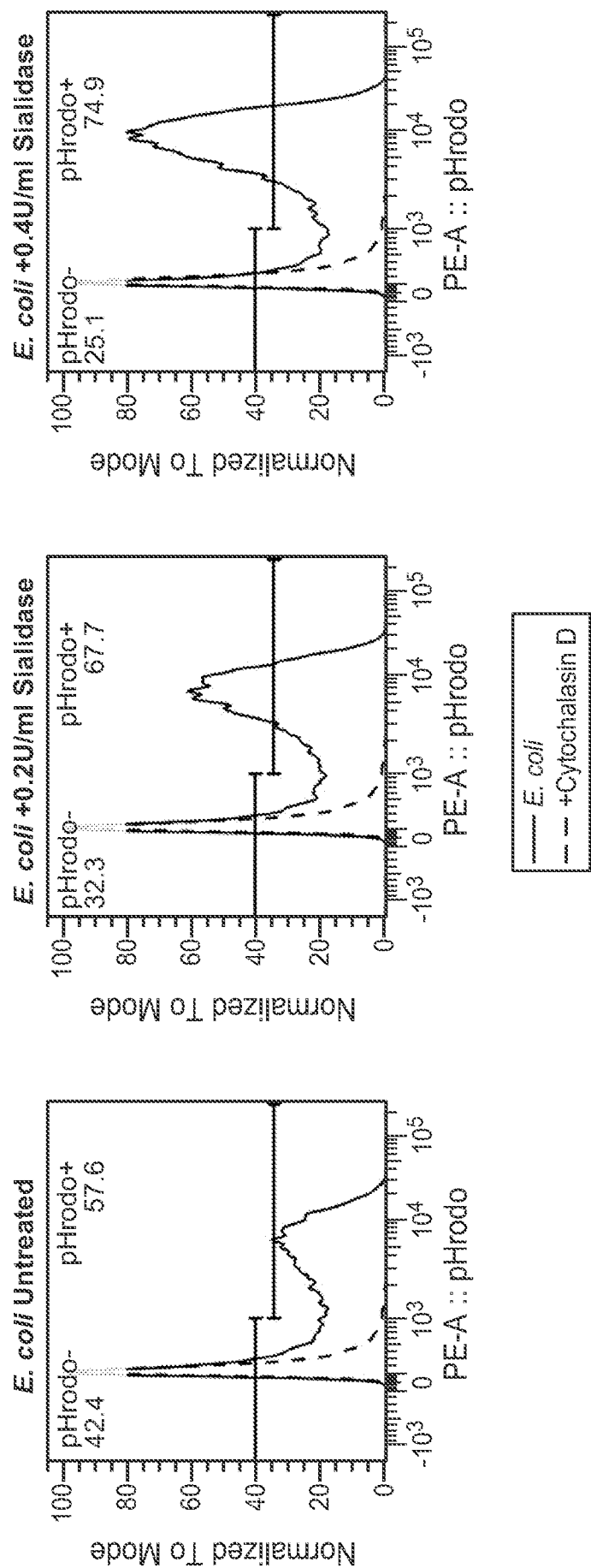


FIG. 12

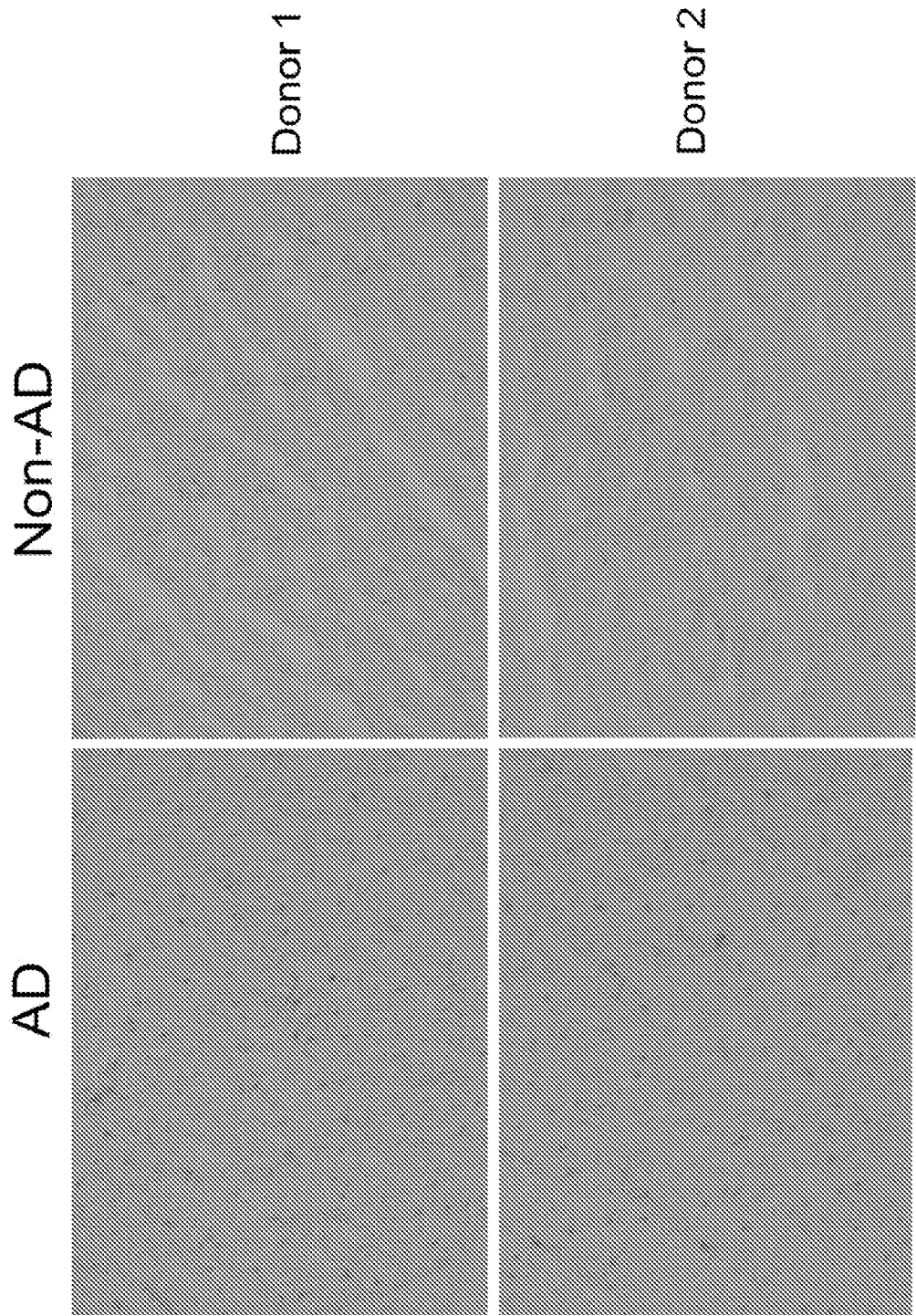


FIG. 13A

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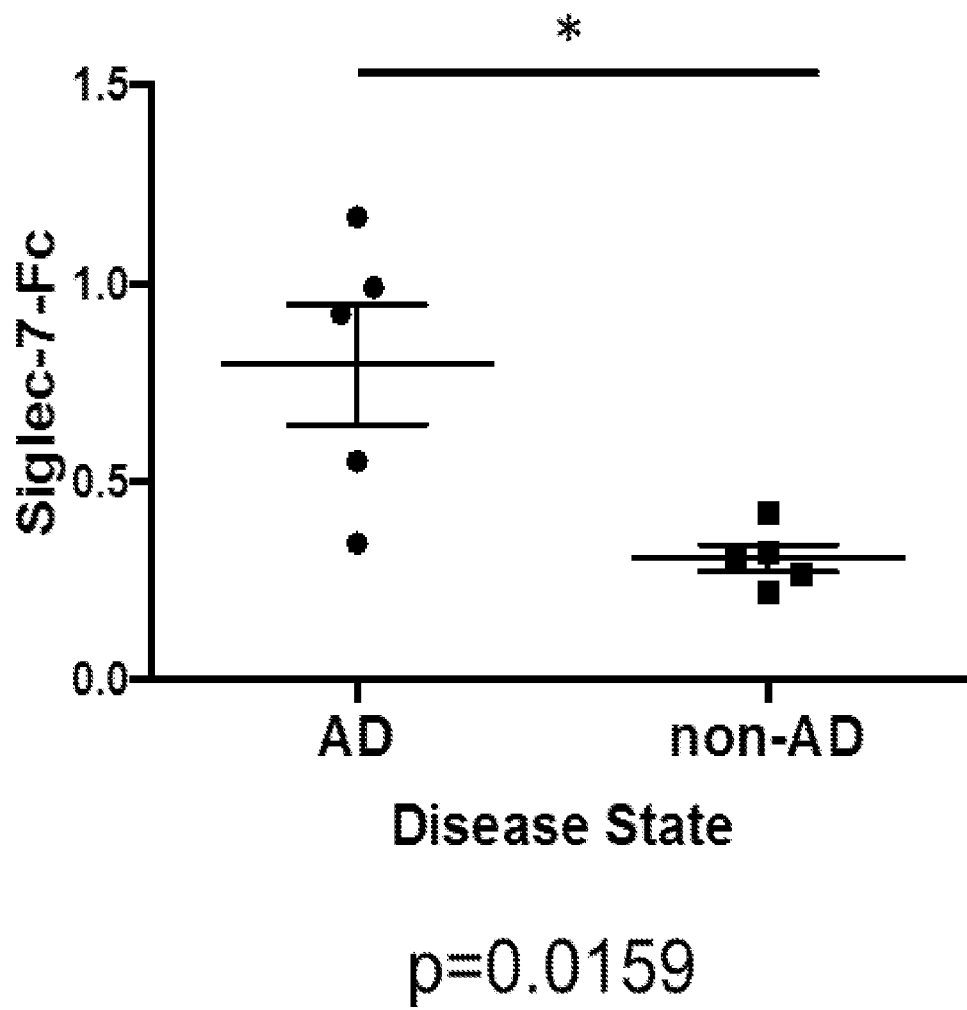


FIG. 13B

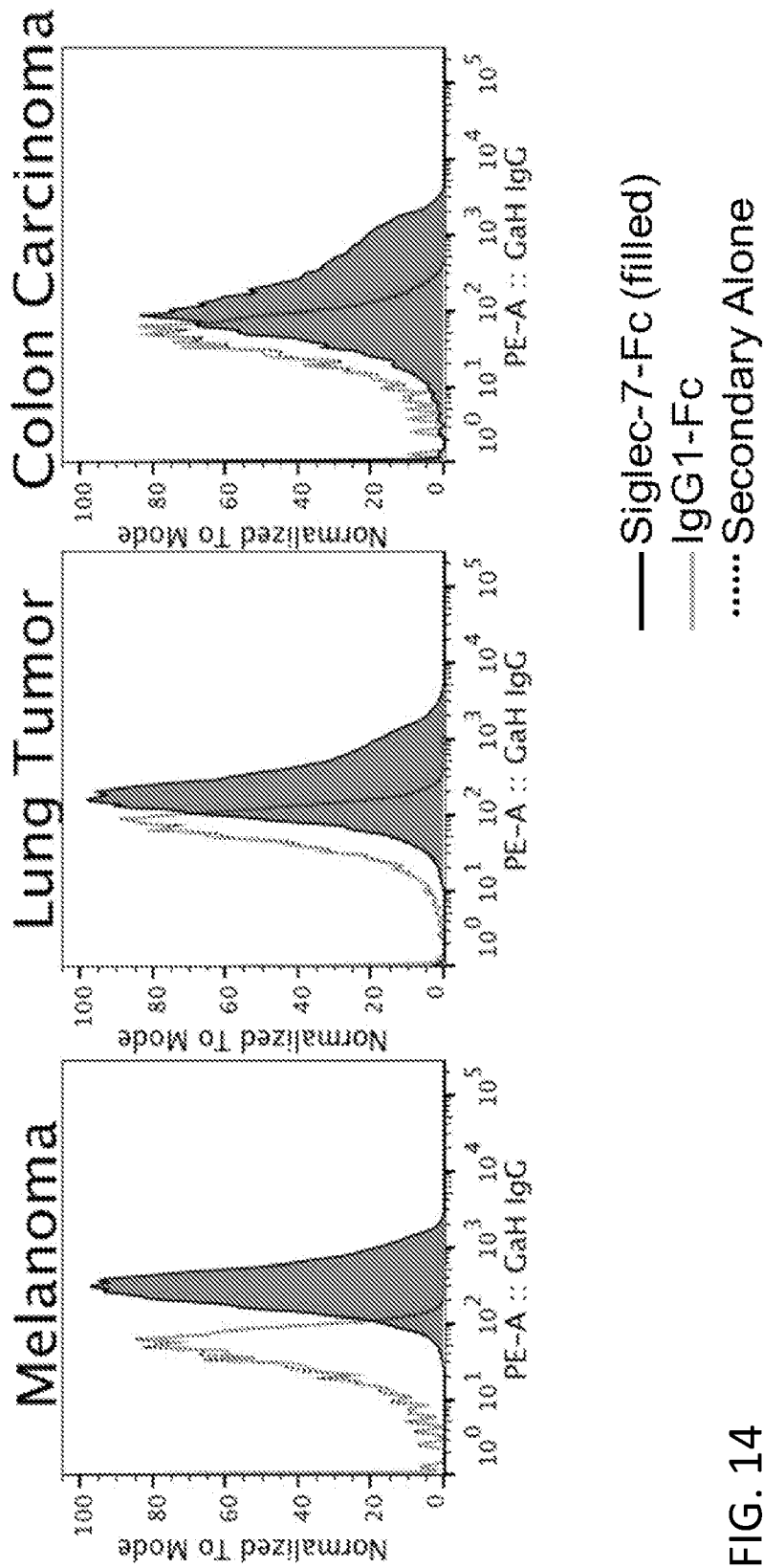


FIG. 14

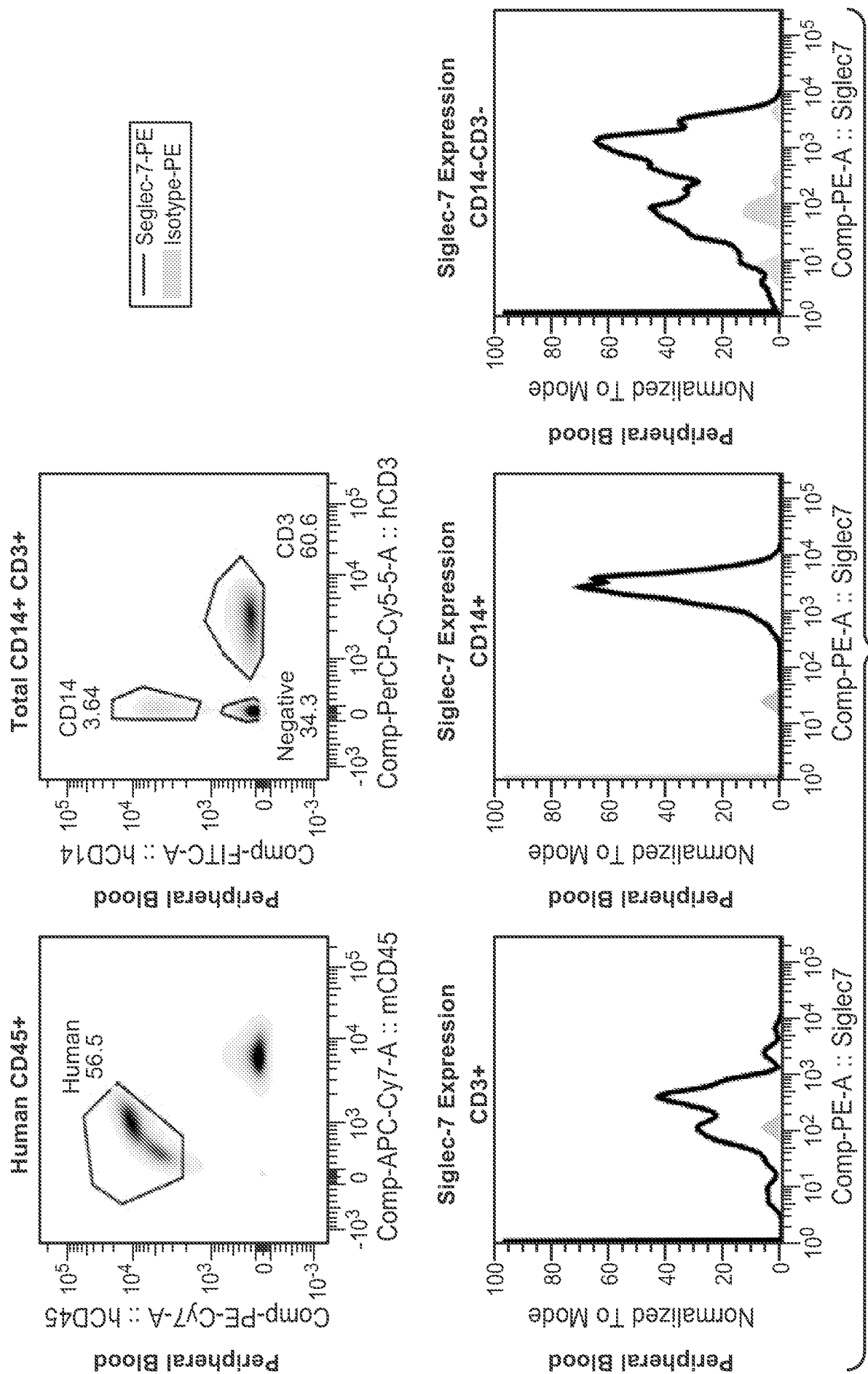


FIG. 15

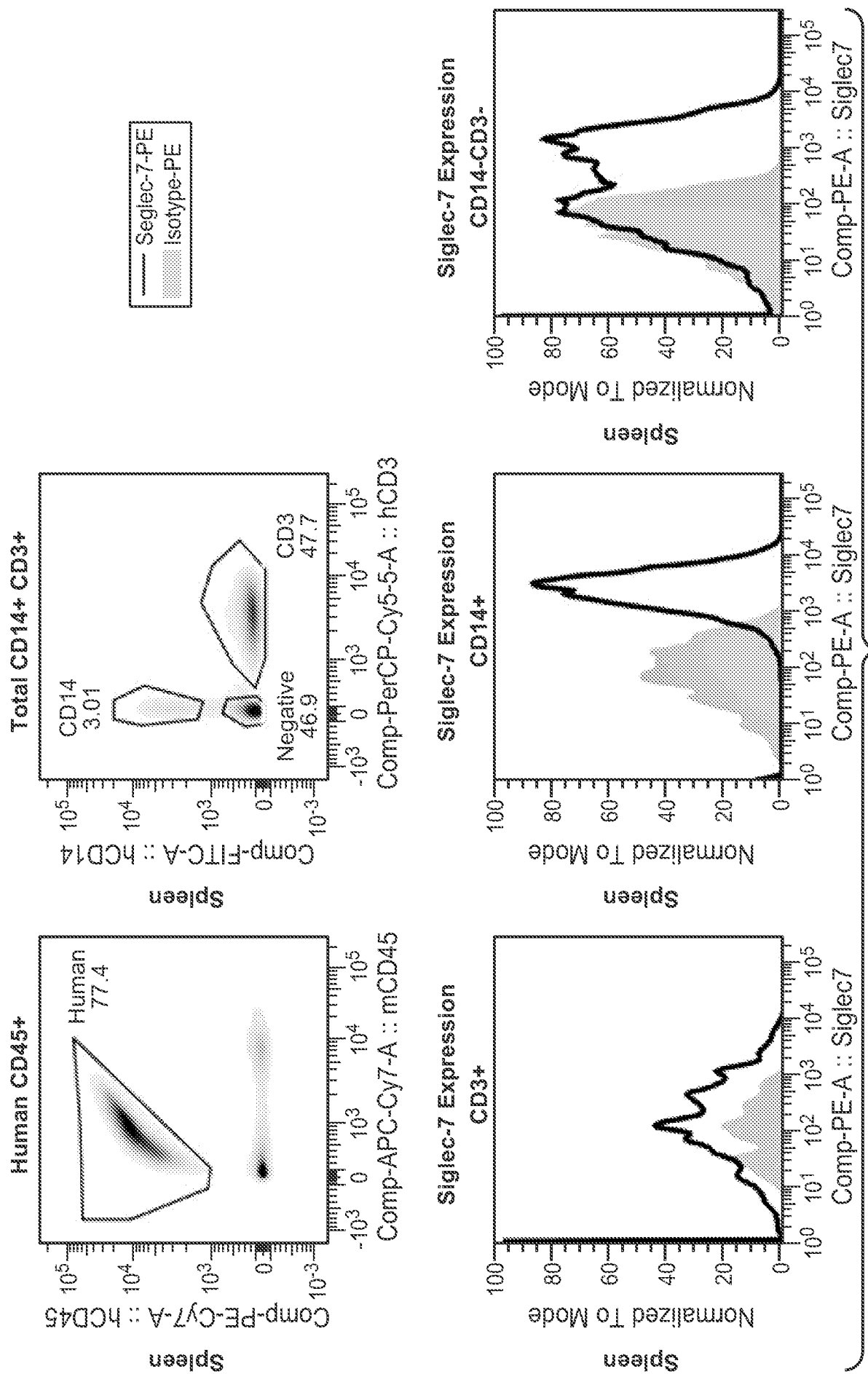


FIG. 15 (Cont.)

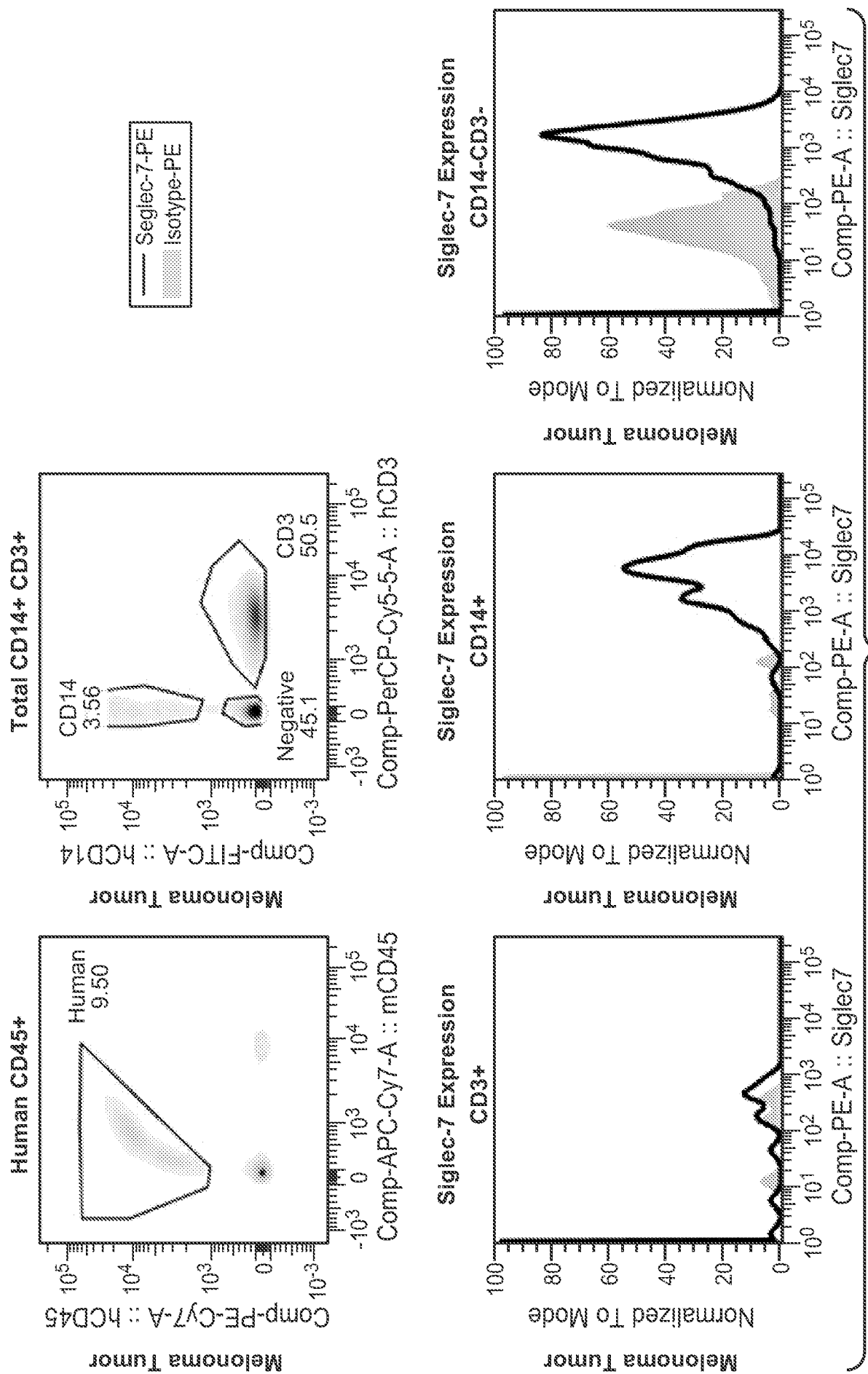


FIG. 15 (Cont.)

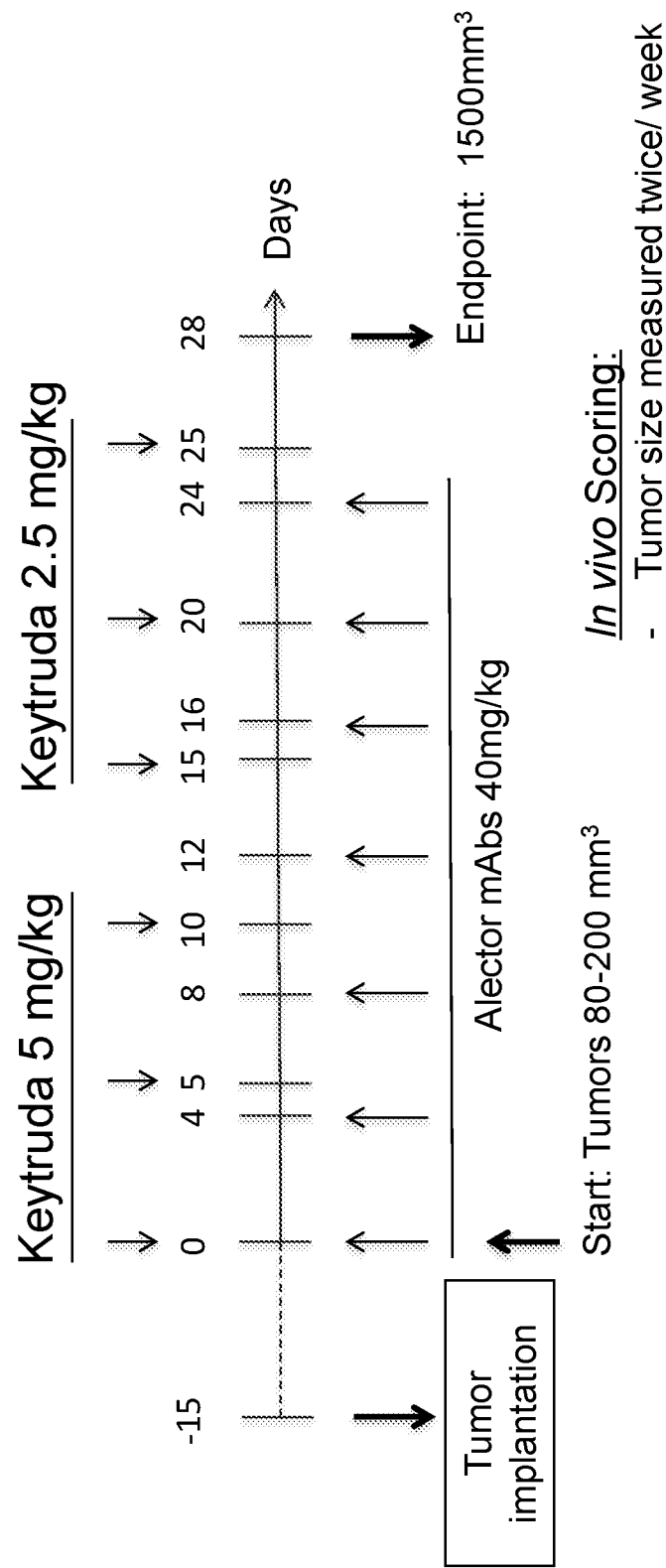


FIG. 16A

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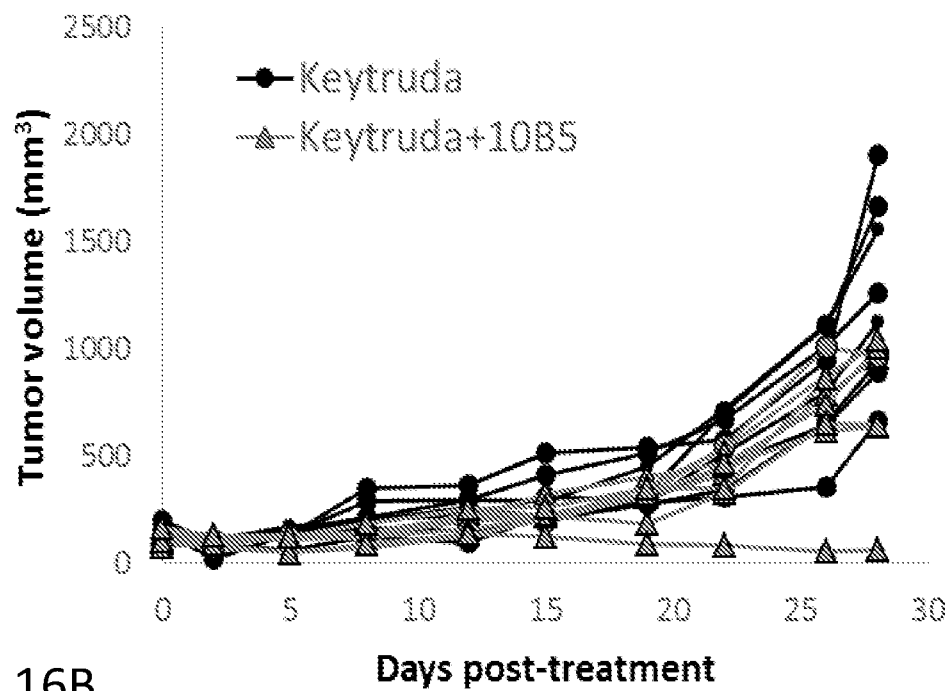


FIG. 16B

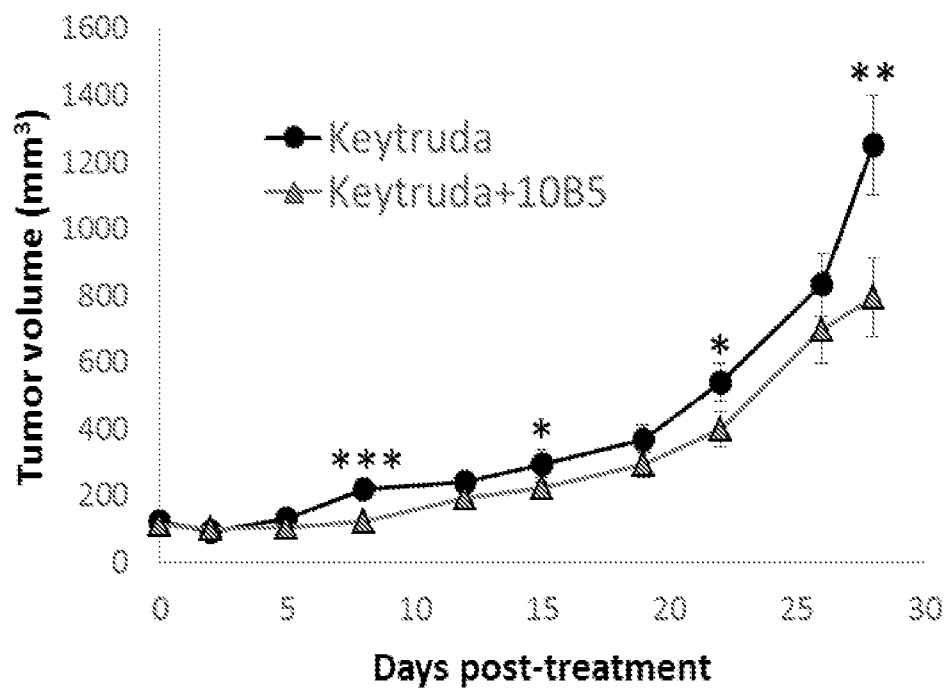


FIG. 16C

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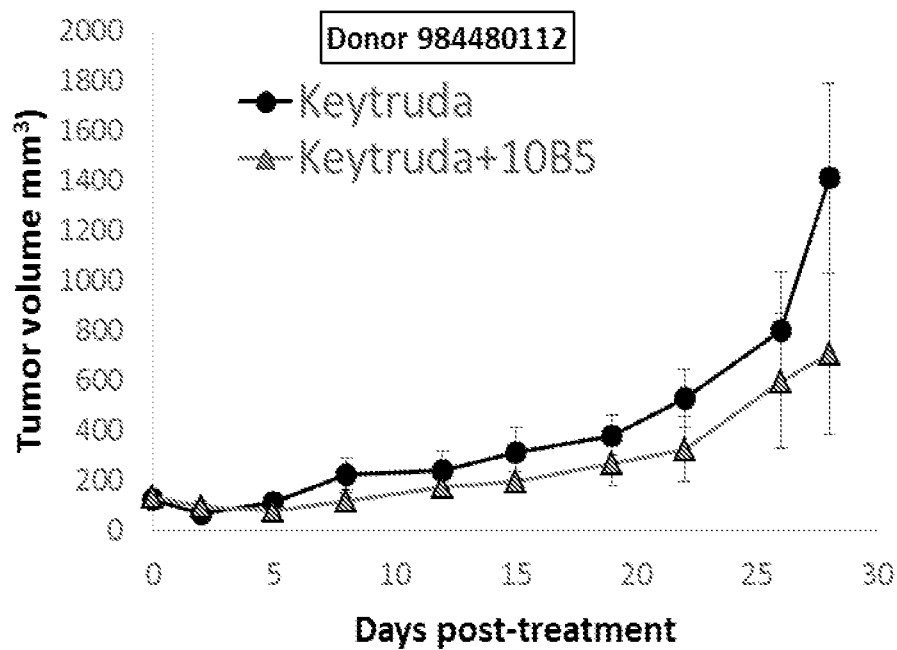


FIG. 16D

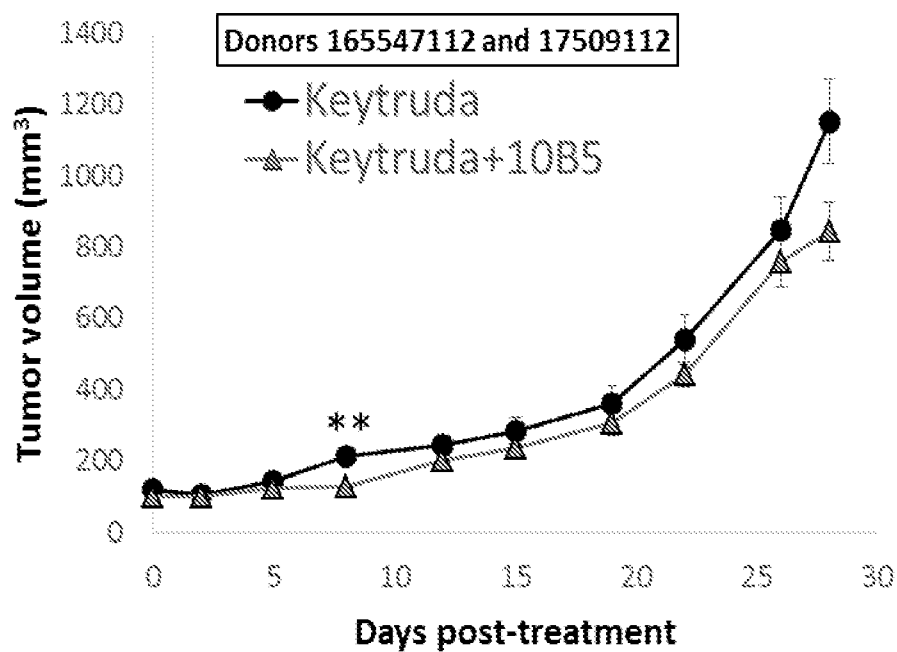


FIG. 16E

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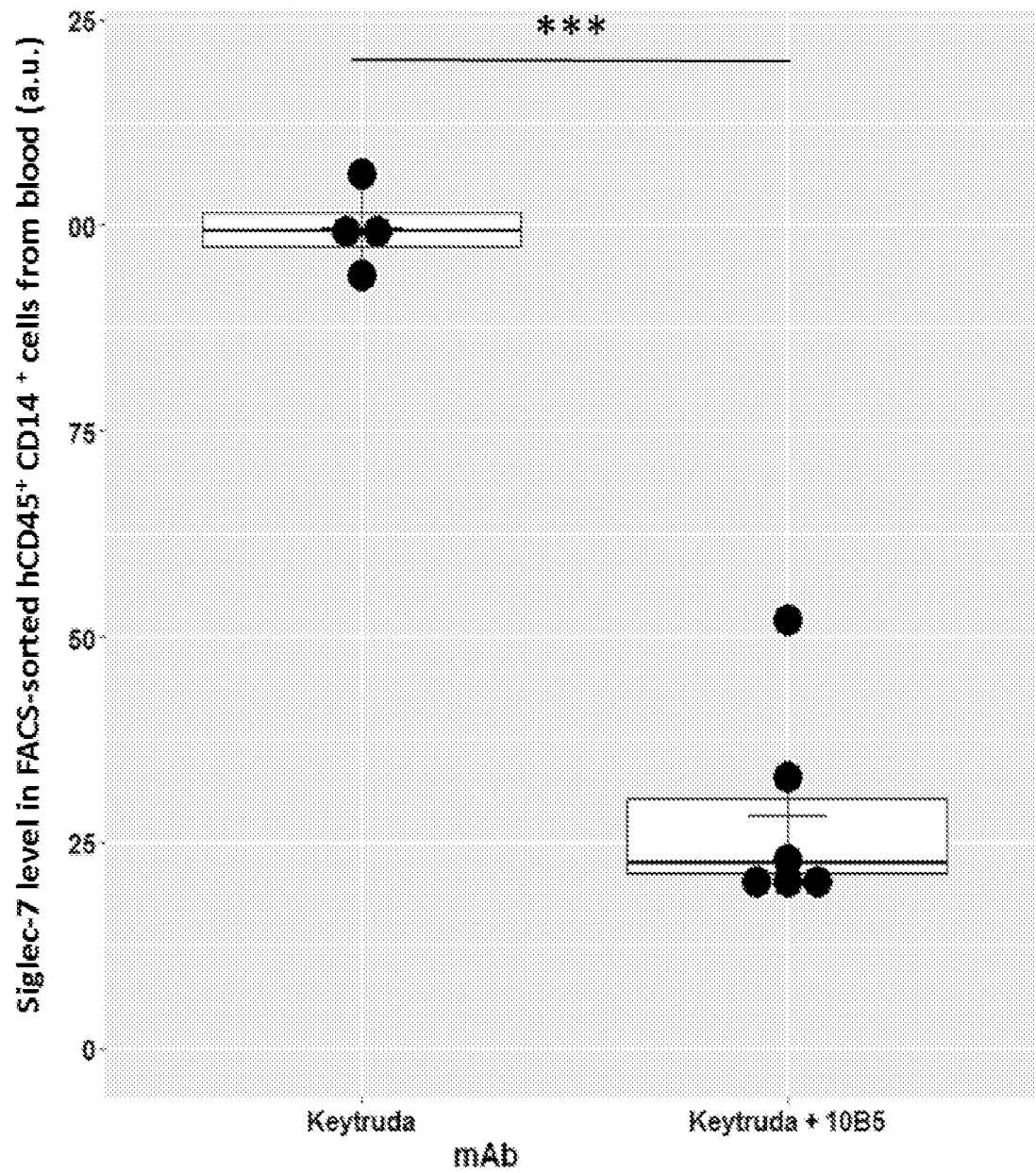


FIG. 16F

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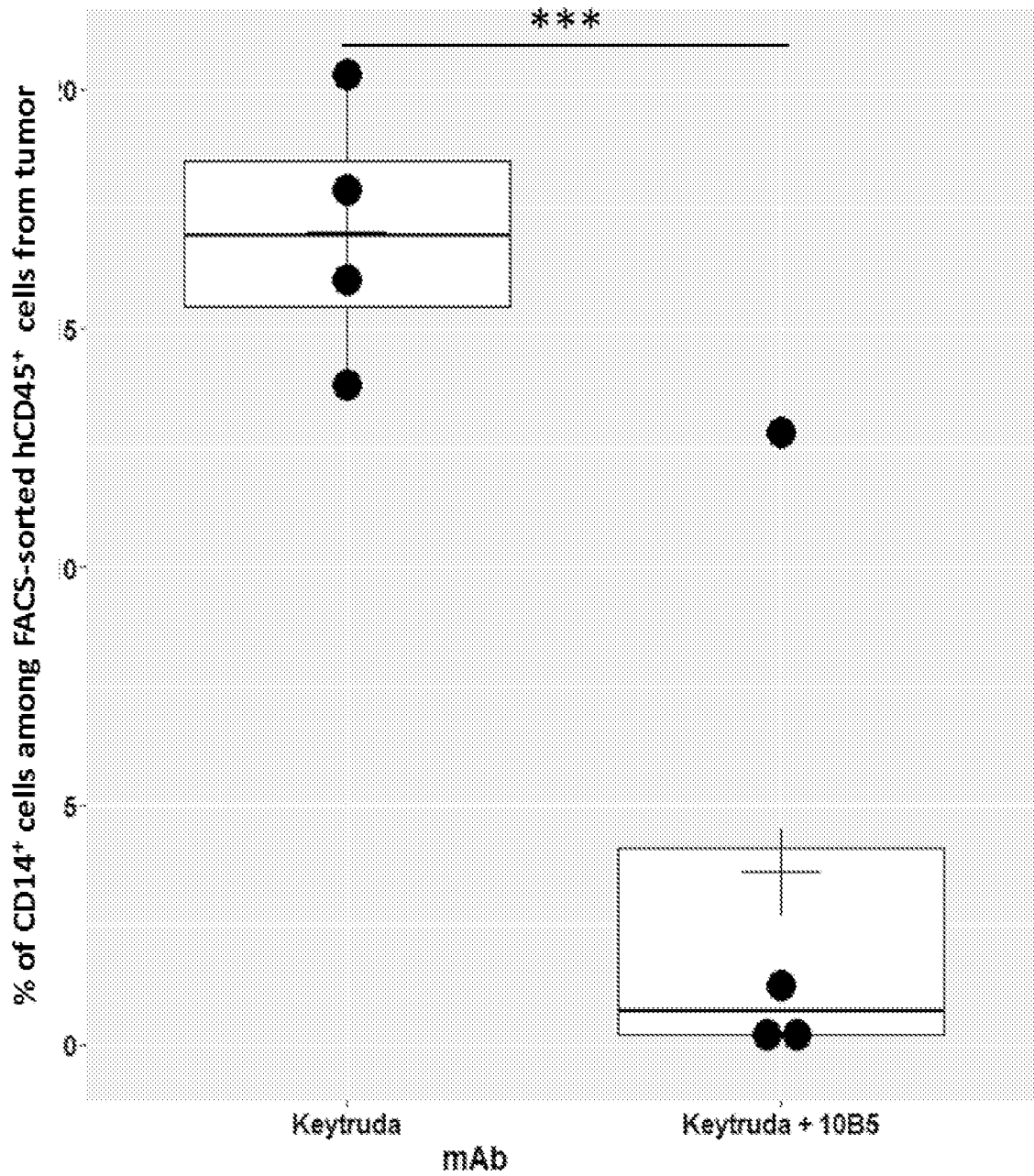


FIG. 16G

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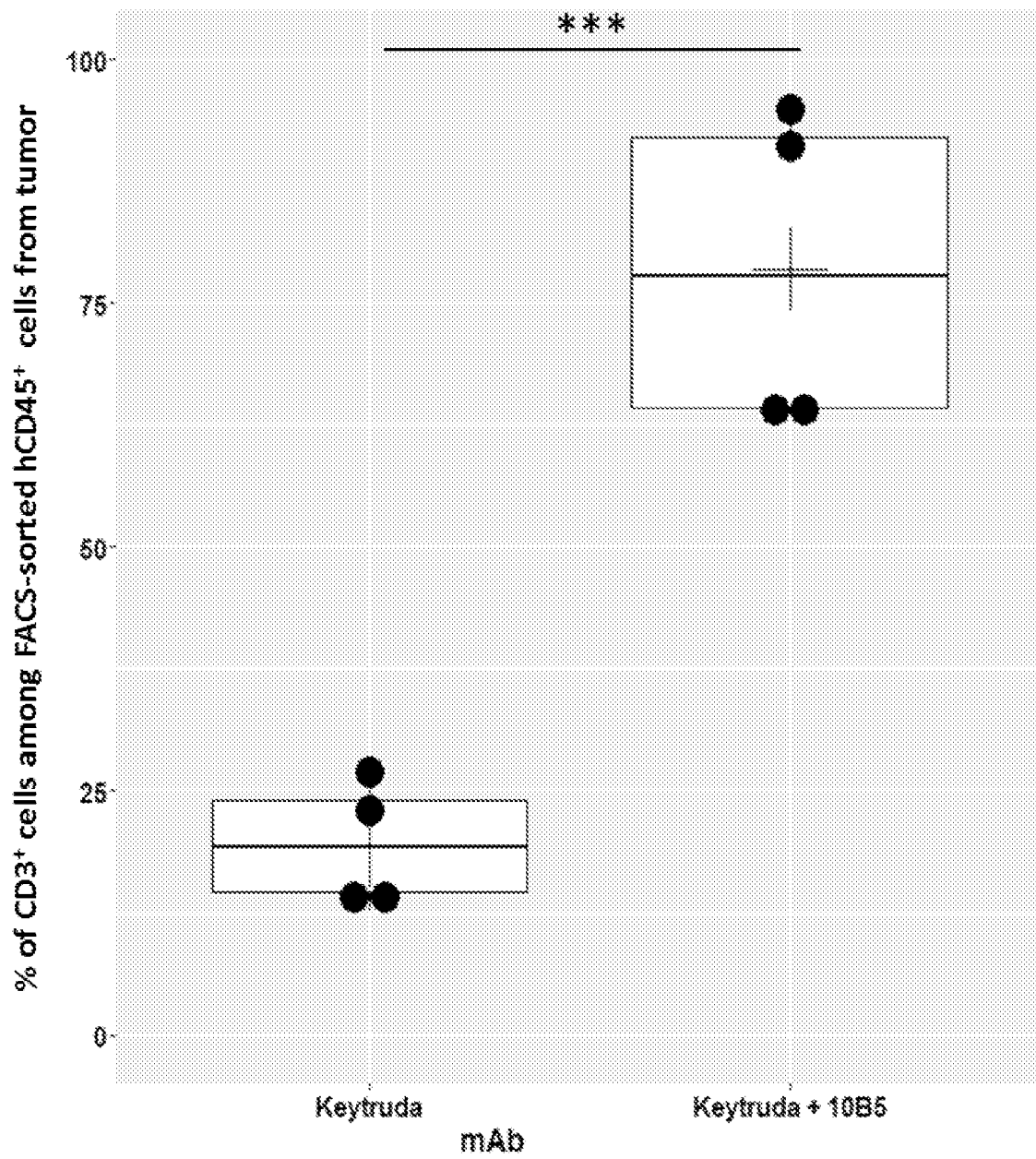


FIG. 16H

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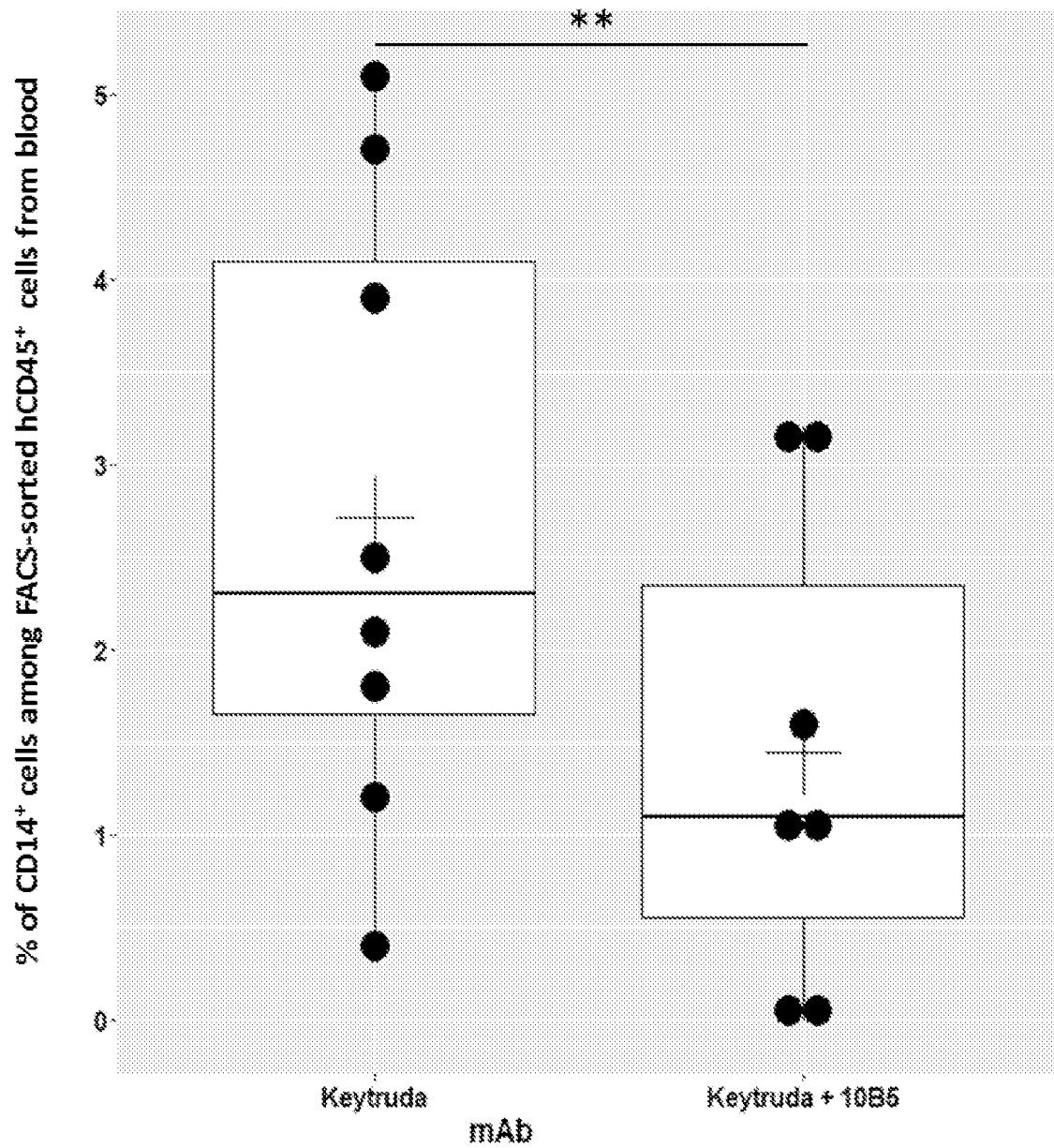


FIG. 16I

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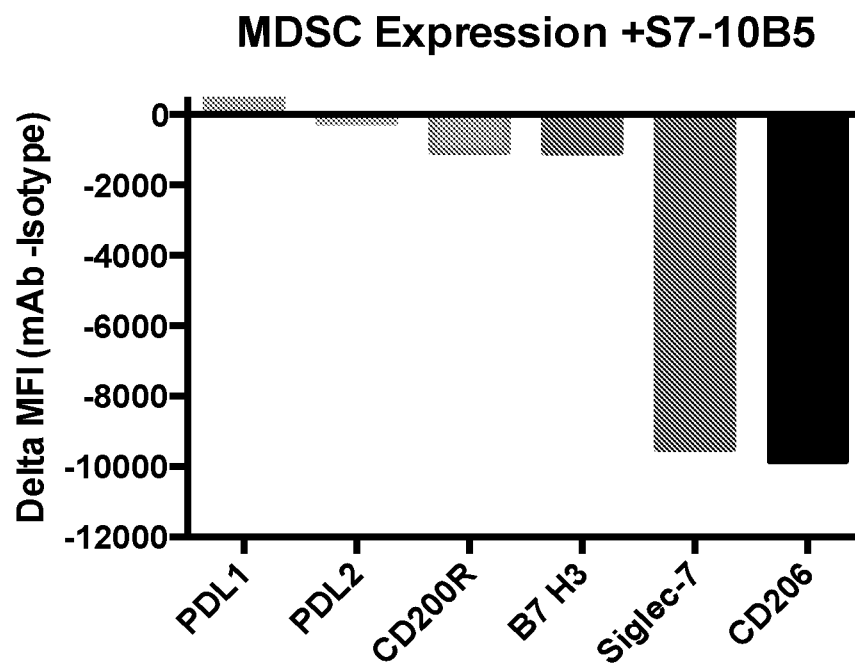


FIG. 17A

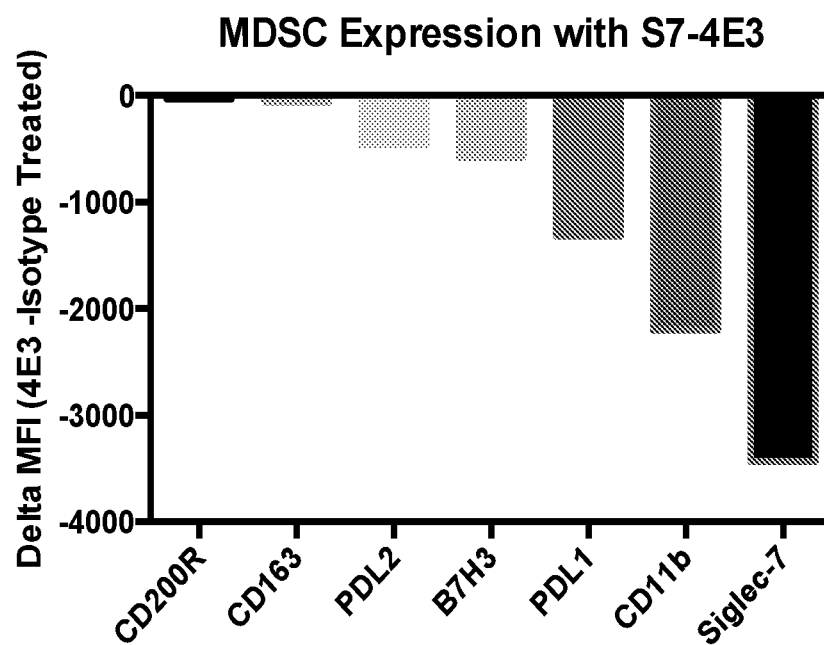


FIG. 17B

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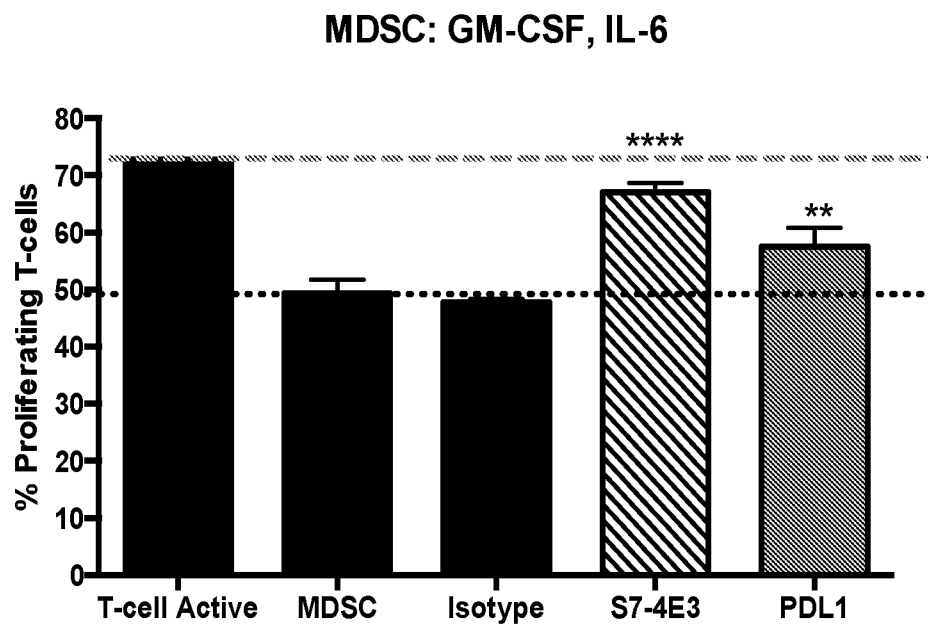


FIG. 17C

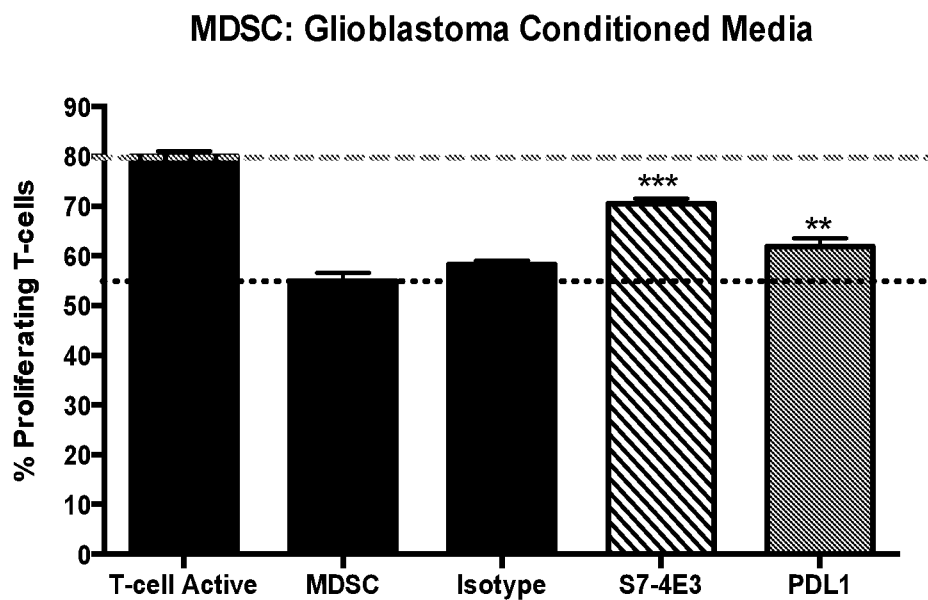


FIG. 17D

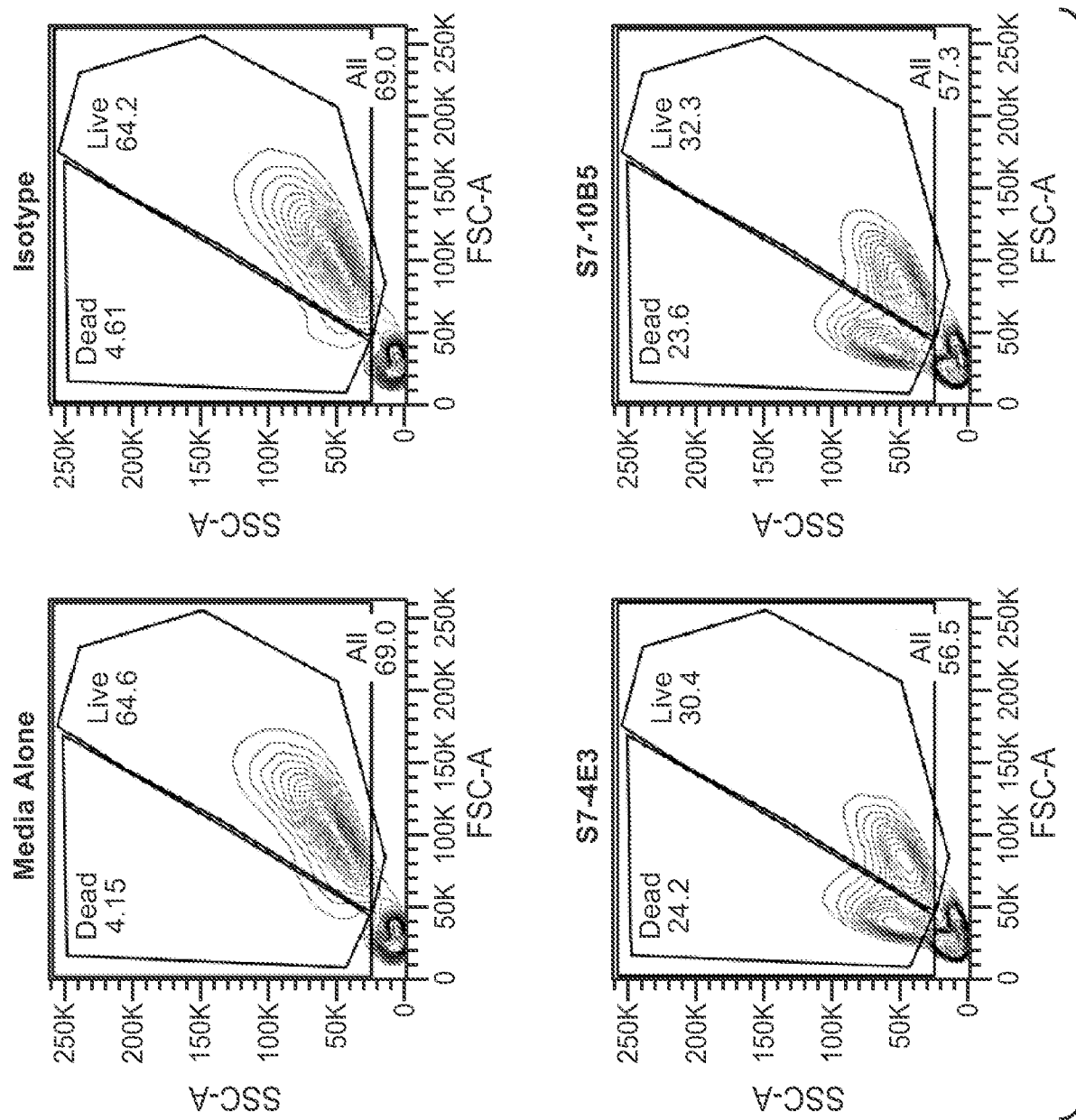


FIG. 18

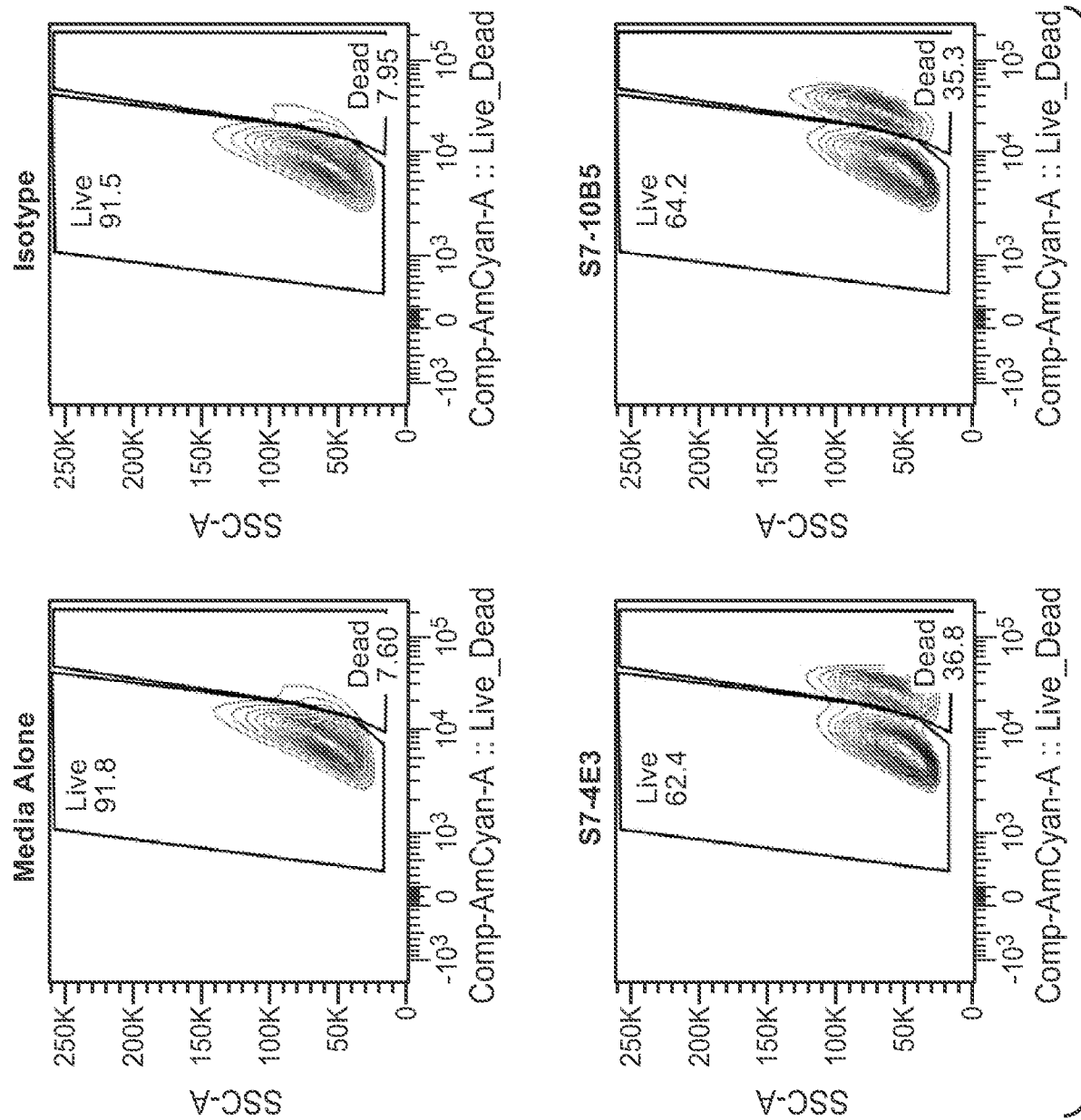


FIG. 18 (Cont.)

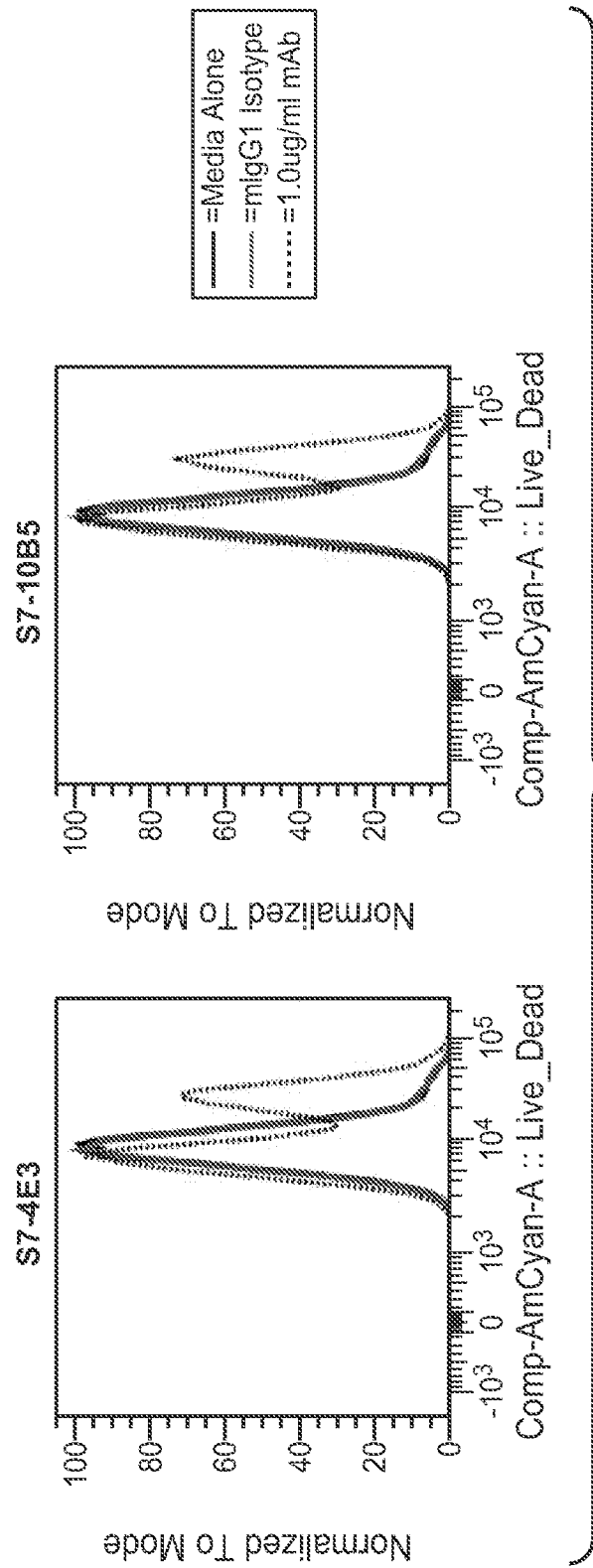


FIG. 18 (Cont.)