

FIGURE 1A

```

1 NEPACGAPCRLGPLLCLLLAASCANSCVACEEELQVIOQPKSVLVAAGETATLRCATSL 60
1 NEPACGAPCRLGPLLCLLLAASCANSCVACEEELQVIOQPKSVLVAAGESAIIHCVTSL 60
*****
61 IPVGPIONFRGACPCRELIIYNQKECHFPRTVTVSDLTKRNNMDFSIRIGNITPADACTYY 120
61 IPVGPIONFRGACPCRELIIYNQKECHFPRTVTVSESTKRENMDFSISISNITPADACTYY 120
*****
121 CVKFRKQSPDDVEFKSCACTELSVRAKPSAPVVSQPAARATPQHTVSFTCESHGCFSPRDI 180
121 CVKFRKQSPD~TEFKSCACTELSVRAKPSAPVVSQPAARATPQHTVSFTCESHGCFSPRDI 179
*****
181 TLKWFKNONELSDFTQNVDPVGESVSYSHSTAKVVLTRDVDHSQVICEVAHVTLQGDPL 240
180 TLKWFKNONELSDFTQNVDPVGESVSYSHSTAKVVLTRDVDHSQVICEVAHVTLQGDPL 239
*****
241 RGTANLSETIRVPPTLEVTOQPVRAENQVNVTCQVRKFYPQRLQLTWLENCNVSEHTETAS 300
240 RGTANLSETIRVPPTLEVTOQPVRAENQVNVTCQVRKFYPQRLQLTWLENCNVSEHTETAS 299
*****
301 TVTENKDGTYNWNMSWLLVNVSAHRDDVKLTQVEHDCQPAVSKSHDLKVSANHPKEQCSNT 360
300 TVTENKDGTYNWNMSWLLVNVSAHRDDVKLTQVEHDCQPAVSKSHDLKVSANHPKEQCSNT 359
*****
361 AAENTGCSNERNIYIVGVVCTLLVALLMAALYLVRIRQKKAQGSTSSSTRLHEPEKNAREI 420
360 AAENTGCSNERNIYIVGVVCTLLVALLMAALYLVRIRQKKAQGSTSSSTRLHEPEKNAREI 419
*****
421 TQDTNDITYADLNLPKCKKPAQAAEPNNHTEYASIQTSQPASEDTLTYADLQWHLNR 480
420 TQDTNDITYADLNLPKCKKPAQAAEPNNHTEYASIQTSQPASEDTLTYADLQWHLNR 479
*****
481 TPKQAPKPEPSFSEYASVQVPRK 504
480 TPKQAPKPEPSFSEYASVQVPRK 503
*****

```

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FIGURE 1B

```

MEPAGAPACRLGPELLCILLAAACNWSVACEHELOVQDPKSVLVAGETATLCTATSL 60
MPVPASWPHLPSPFL~LMTLLGLRLTOVACEDELOVQPEKSVSVAGESATLRCAMTSL 59
* . * .*: * :*****;*****;*** *****;*****; ***
IPVQPIQWFRACAGPCRELIYNQKECHFPRVTTVSOLTKRNNMDFSRIGNITPADACTYY 120
IPVQPIWFRACACARELIYNQKECHFPRVTTVSELTKRNNLDFSSISNITPADACTYY 119
***** *****;*****;*****;***** * ,*****
CVNFRKCSDDVEFKSGACTELSVRAKPSAPVVSQPAARATPQHTVSVTCESHGFSRDI 180
CVNFRKCSDDVEFKSGACTELSVRAKPSAPVVSQPAVRATPENTVSVTCESHGFSRDI 179
***** *****;*****;*****;***** *****
TLNWFKNONELSDPQTNVDPVGSVSIHSTAKVVLTRZEDVHSQVCEVAHVTLQODPL 240
TLNWFKNONELSDPQTNVDPACDSVSIHSTARVVLTRCDVHSQVCEIAHITLQODPL 239
***** *****;*****;***** *****;*****
ROTNANLSETIRVPTLEVTQOPVRAENQNVTCQVRKFYPQRLQLTWLENQNVSRTEAS 300
ROTNANLSEAIRVPTLEVTQOPHRAENQNVTCQVSNFYPRCLQLTWLENQNVSRTEAS 299
*****;*****;*****;*****;***** *****
TVTENKDCGTYNWMSKLLVNVSAHRDDVKLTQVEHDCQPAVSKSHDLKVSAPHEQCSNT 360
TLIENKDCGTYNWMSKLLVNTCAHRDDVVLTCQVEHDCQQAQVSKSYALEISAHQKEHCSDI 359
*; *****;***** ***** *****; *;*** **:***;
AAENTCSNERNIYTVGVVCTLLVALLMAALYLVRIRQKKAQCSSTSLHEPEKNAREI 420
THEAALAPTAPLLVALLGPKLLLVGVSAIYICWKORA----- 398
: * : : :*: : :*:*: : :
TOOTNDITYADLNLPKCKPAPQAAEPNNHTEYASIQTSQPASEDTLYADLDXVHLNR 480

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```

TPKQAPKPEPFSFYASVQVPRK 504

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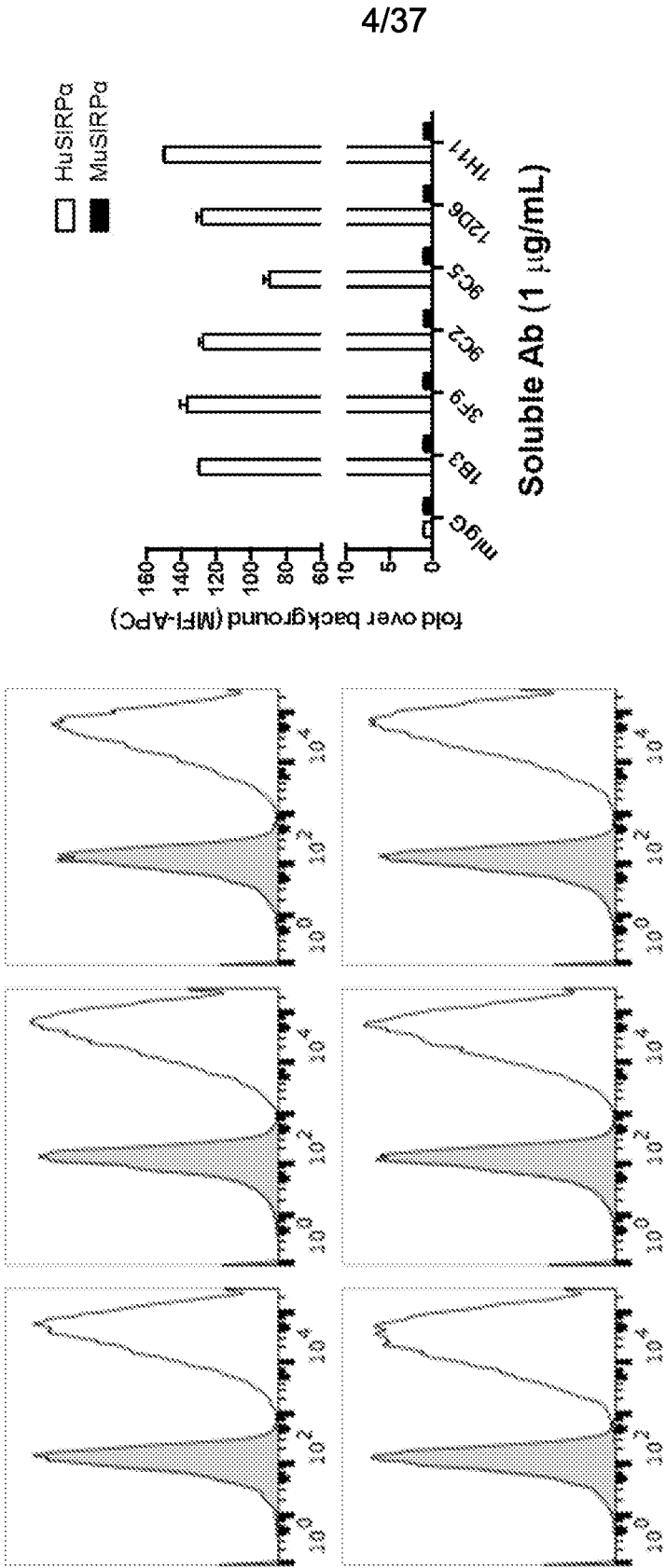
FIGURE 2

```

1  MEPAGPAPGRLOPL~LCILLAAACAWSCVAGEEELQVIOPOKSVLYAAGETATLACTATS      59
1  MEPAGPAPGRLOPL~LCILLASACFCCTATC~KELRVTOPEKSVSVAACDSVILNCILTS      59
   *****;*** ;*.1* :**.* **;* ** *****;*. ** **
60  LIPVGPIONFRGACPCRELIYNQKEGFFRVTVVSOLTKRNNMDFEIRIGNITPADACTY      119
60  LLPVCPIRWYRGVCPFSRLIYSPAGEIVPRIENVSDTKRNNMDFEIRISNVTPADAGIY      119
   *;*****;*. **.* ***, ;. **; .*** *****;*. ***** *
120  YCVKFRKQSP~DOVEFKSCACTELSVRAKPSAPVVGPAARATPQHTVSTCESHCFSFR      178
120  YCVKFRKQSCSEPDTEIQSCCCTEVYVLAKPSPPEVSCPADRCIPDOKVNFCKSHCFSPR      179
   *****;*** *.**.* ***, * ***** * ***** *. **.*.***;*****
179  DITLKWPFNGNELSDPCTNVDPVGRSVSYSHSTAKVLTREDVHSQVCEVAHVTLQCD      238
180  NITLWFKDQELHLETTVNFSGKNVSYNISSTVAVVLNSMDVNSKVCEVAHITLDRS      239
   ;*****;*. ** ;*. **.* **.* **.*.***. **.*;*****;*. *
239  PLRGIANLSETRVPTLEVTQOPVRAENQVNVTCQVRKFPQRLQLTLWENGVSKTER      298
240  PLRGIANLSNFIKVSPTVKVTCQSPTEMNQVNLTCRAERFYFEDQLIWLGNVSHNDT      299
   *****; *** **.* **.* **.* **.* **.* **.* **.* **.* **.* **.* **.*
299  ASTVTENKDCITYNMWELLVNVSAHRDDVWLTQOVENDQOPAVSKSHDLKVSANRKEQGS      358
300  PKNLTKNITDQTYNTSLFLVNSSAHRDVFVTCQVKHQOPAITRNHTVLQFANSSDQGS      359
   .**.*;*****; * ;*** *****; ** ;*****; ** *****; ** .;***
359  NT~AAGENTCSNERNIYIVGVVCTLLVALLMAALYLVAIROKKAQGSTSSTRLHEPEKNA      417
360  MQTFPNNATHNNVFIQGVACALLVLLMAALYLIRIKOKKAGSTSSSTRLHEPEKNA      419
   ;*.1.1. ;*;* **.* **.*.*****;*. *****;*****
418  REITQ~-----DTNDITYADINLPKCKPAPQAAEPNNHTEYASIQTSQPASEDTLTYAD      472
420  REITQIQDTNDINDITYADINLPKCKPAPRAPEPNNHTEYASIECKVFPEDTLTYAD      479
   ***** * ***** ***** *****; * *****;*. * *****
473  LDMVHLNRTPKQAPAKPEPSEFSEYASVOVPRK      504
480  LDMVHLSRA~--QAPAKPEPSEFSEYASVOVQRK      509
   *****.*; *****

```

FIGURE 3A



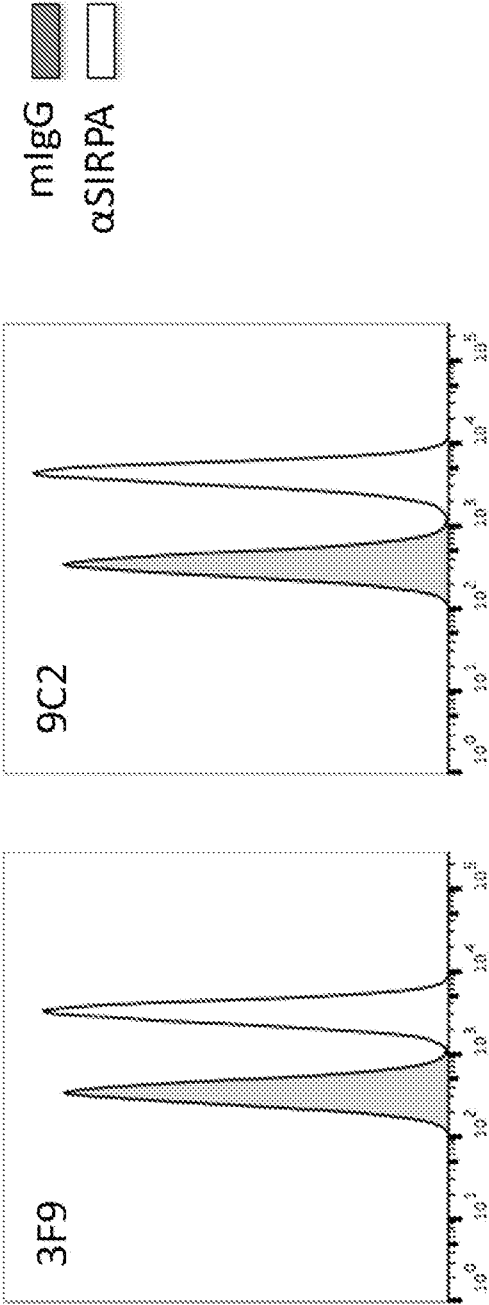


FIGURE 3B

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FIGURE 3C

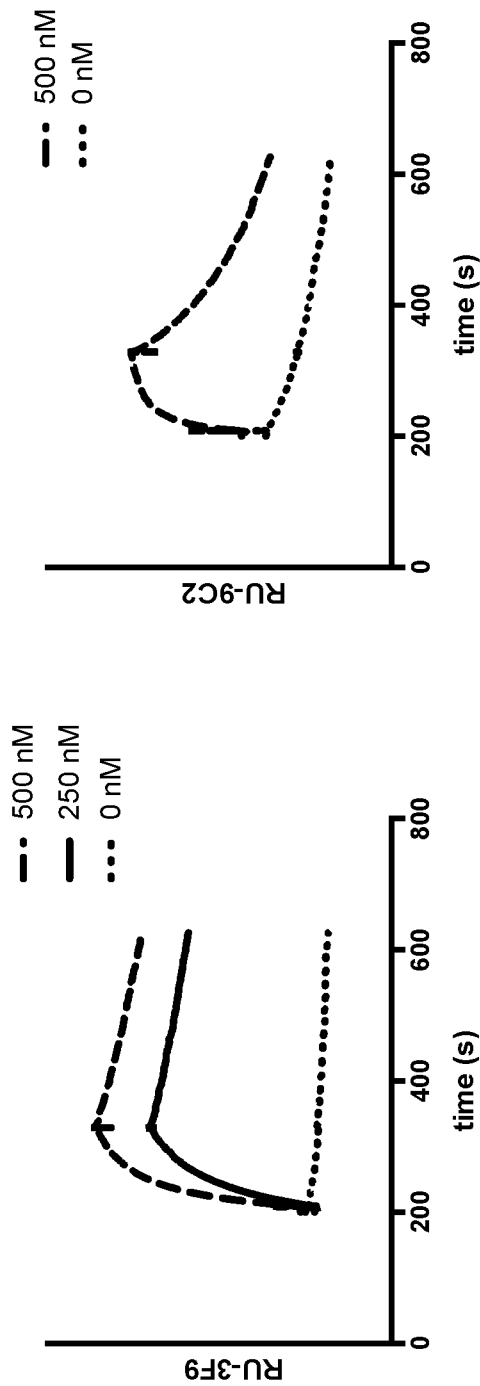


FIGURE 3D

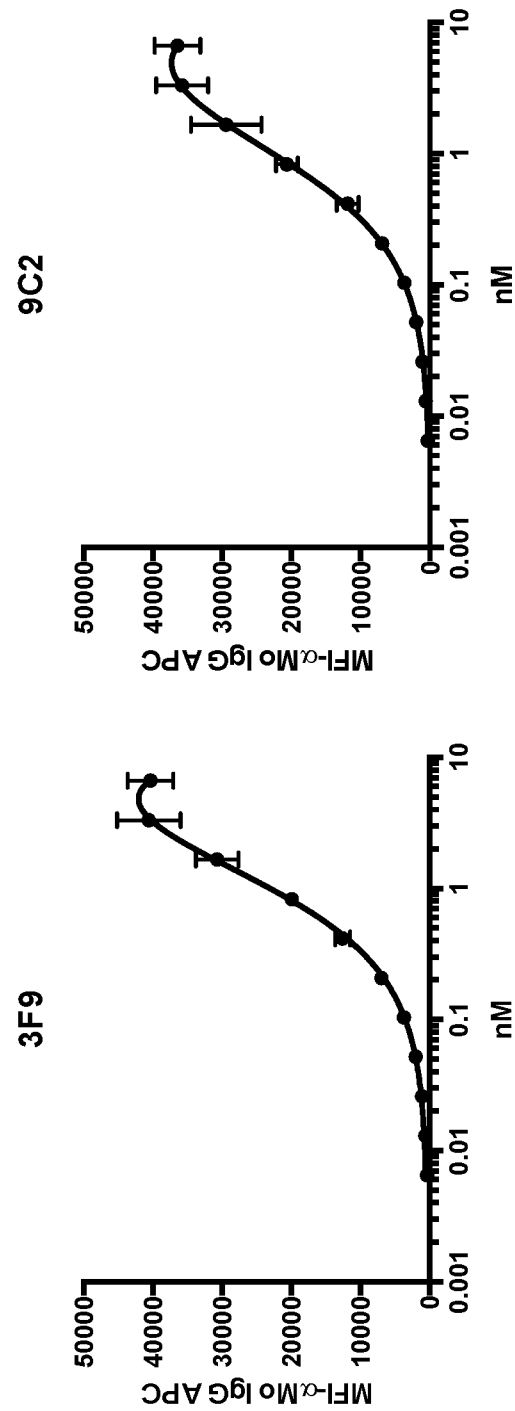


FIGURE 4A

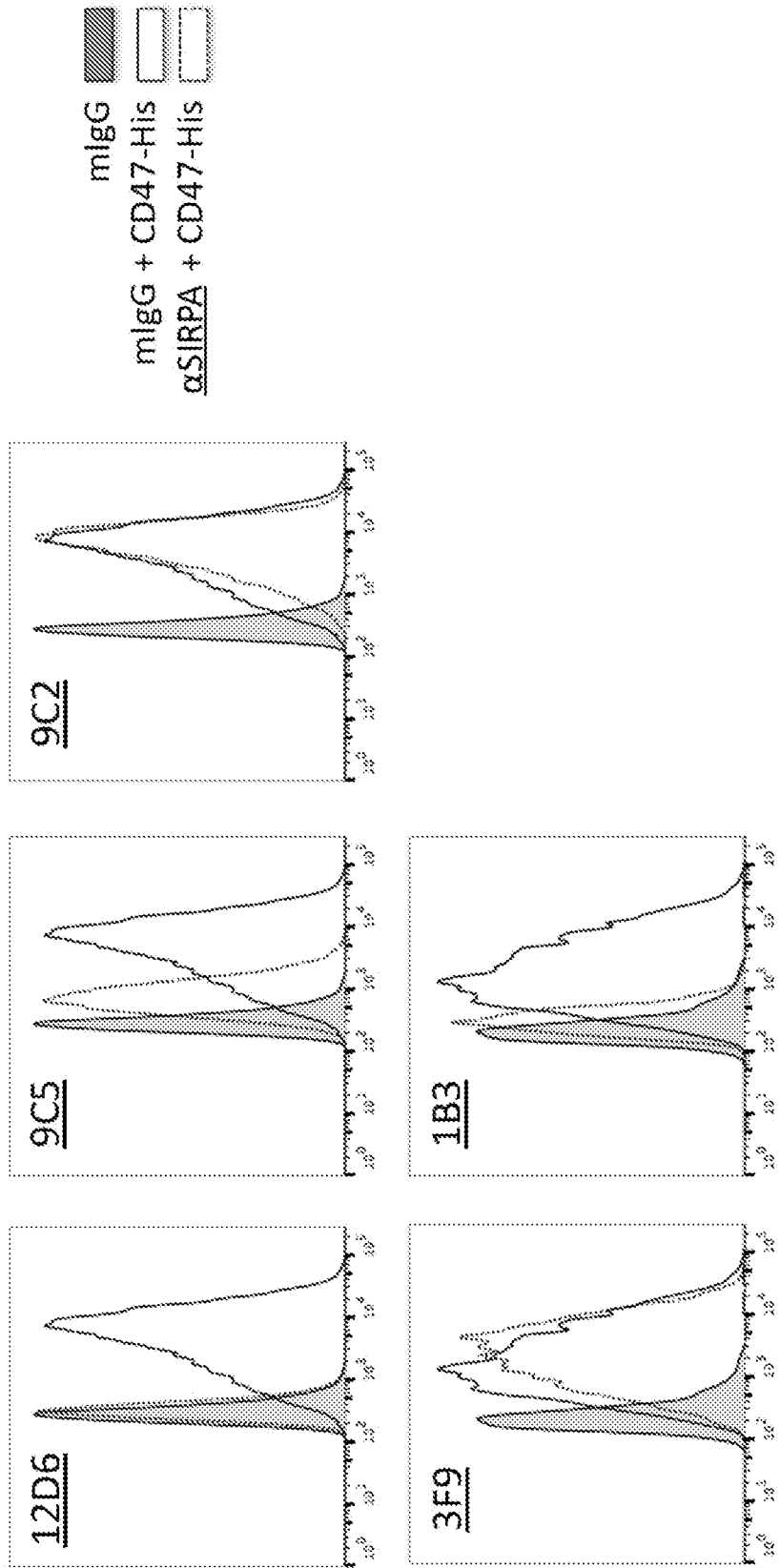
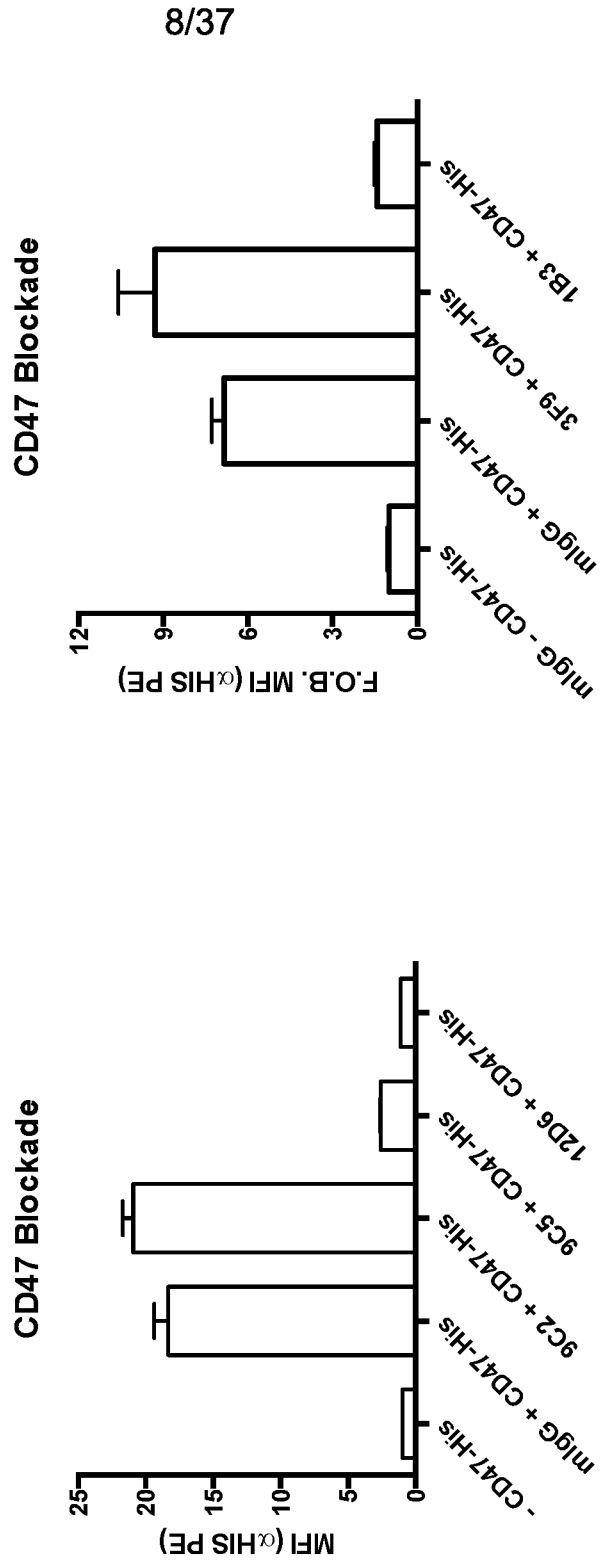


FIGURE 4B



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FIGURE 5A

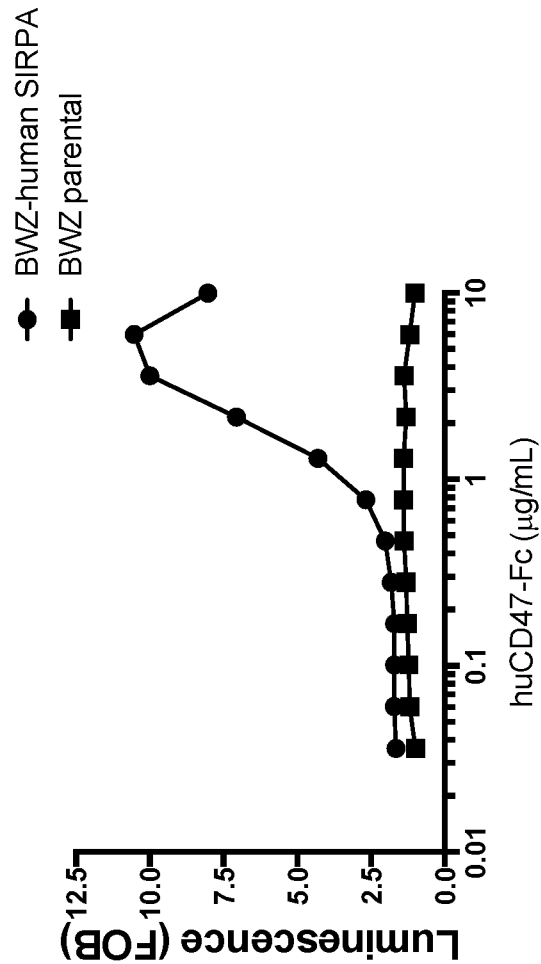


FIGURE 5B

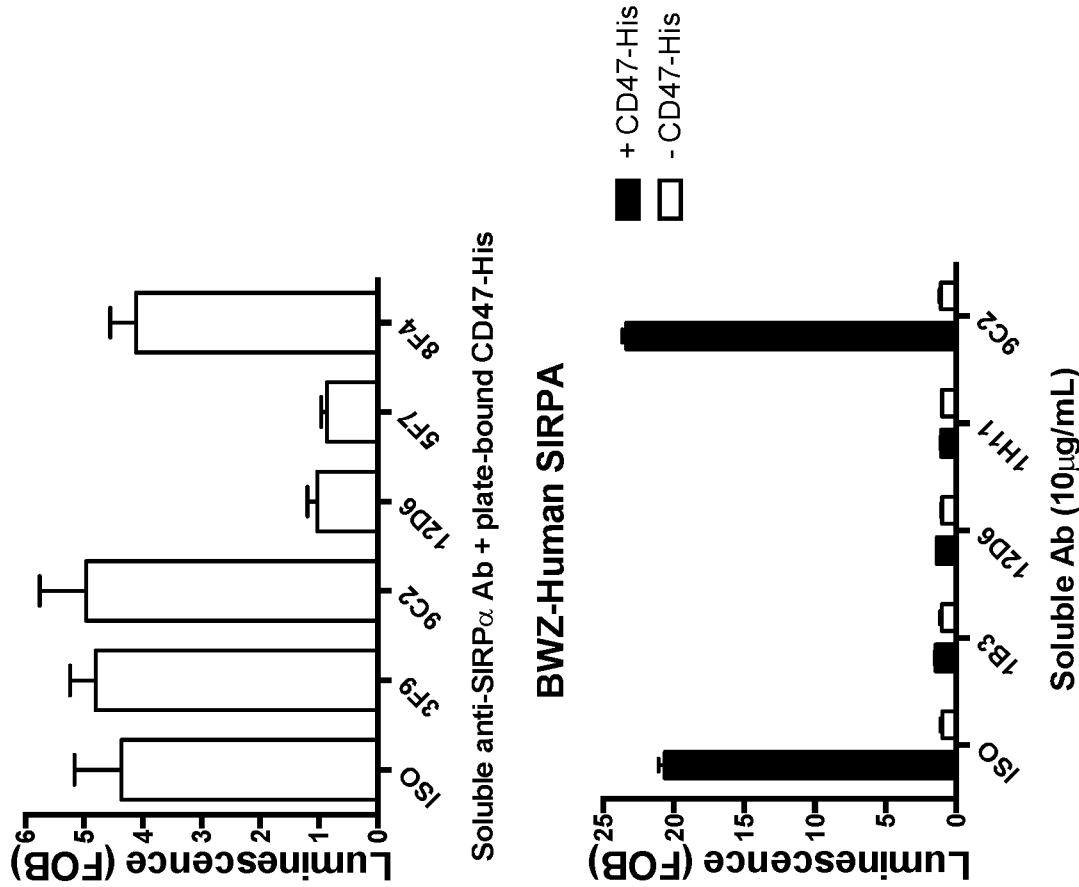


FIGURE 6A

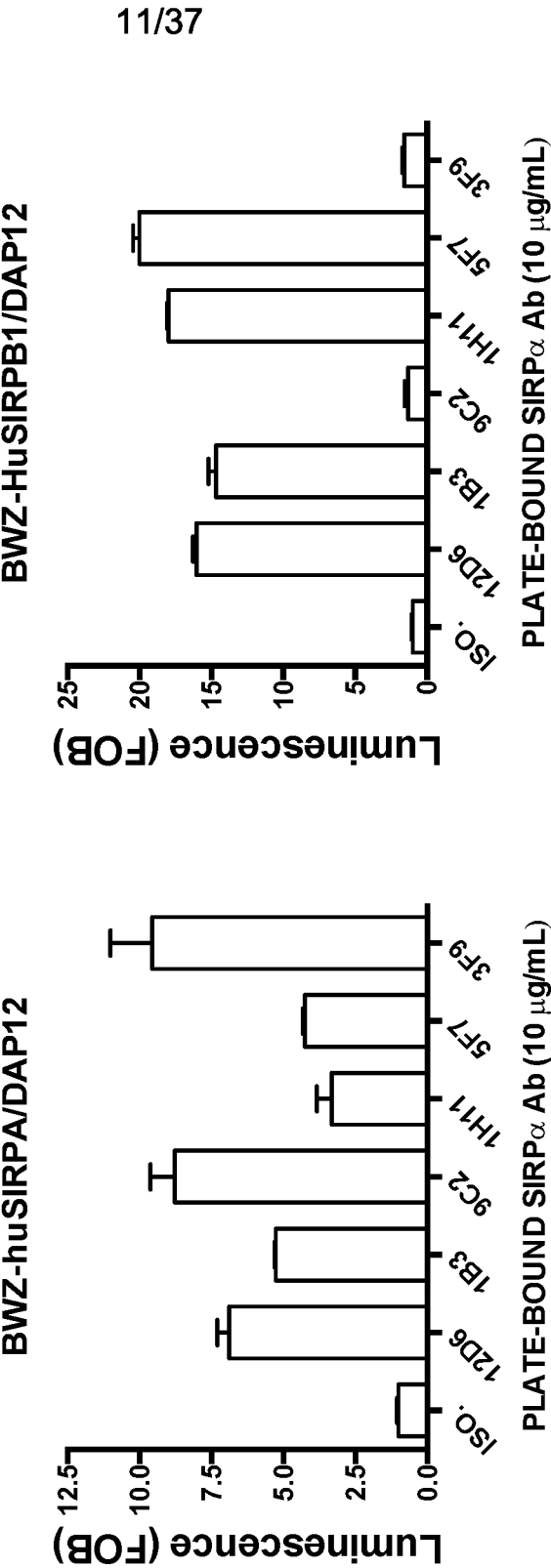


FIGURE 6B

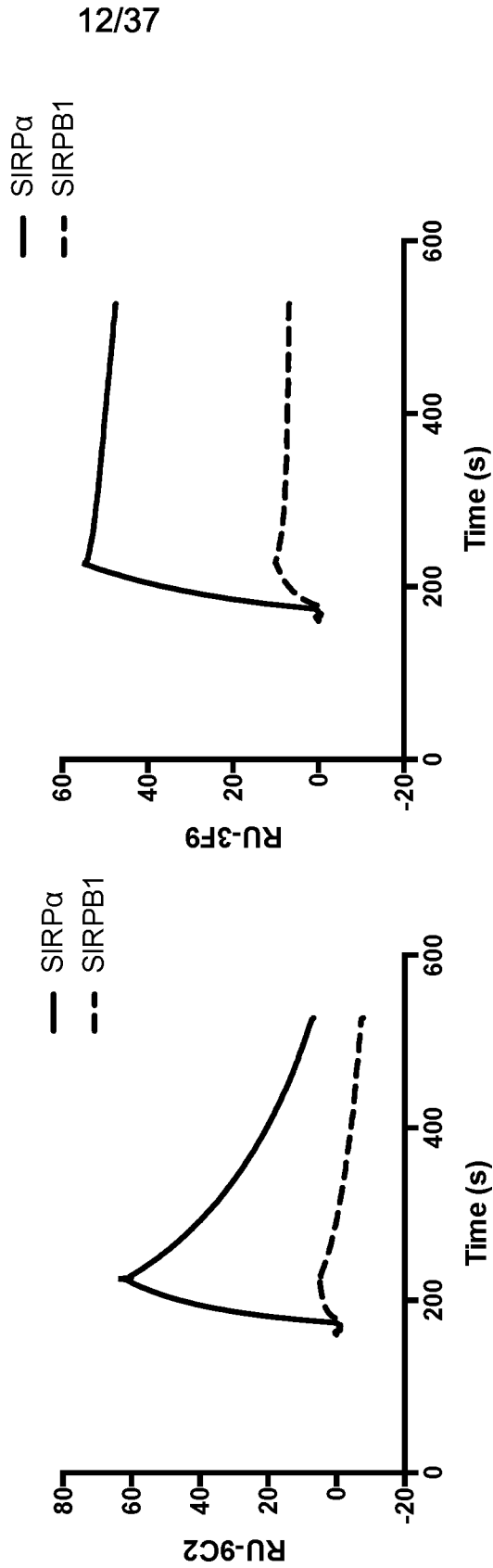


FIGURE 7A

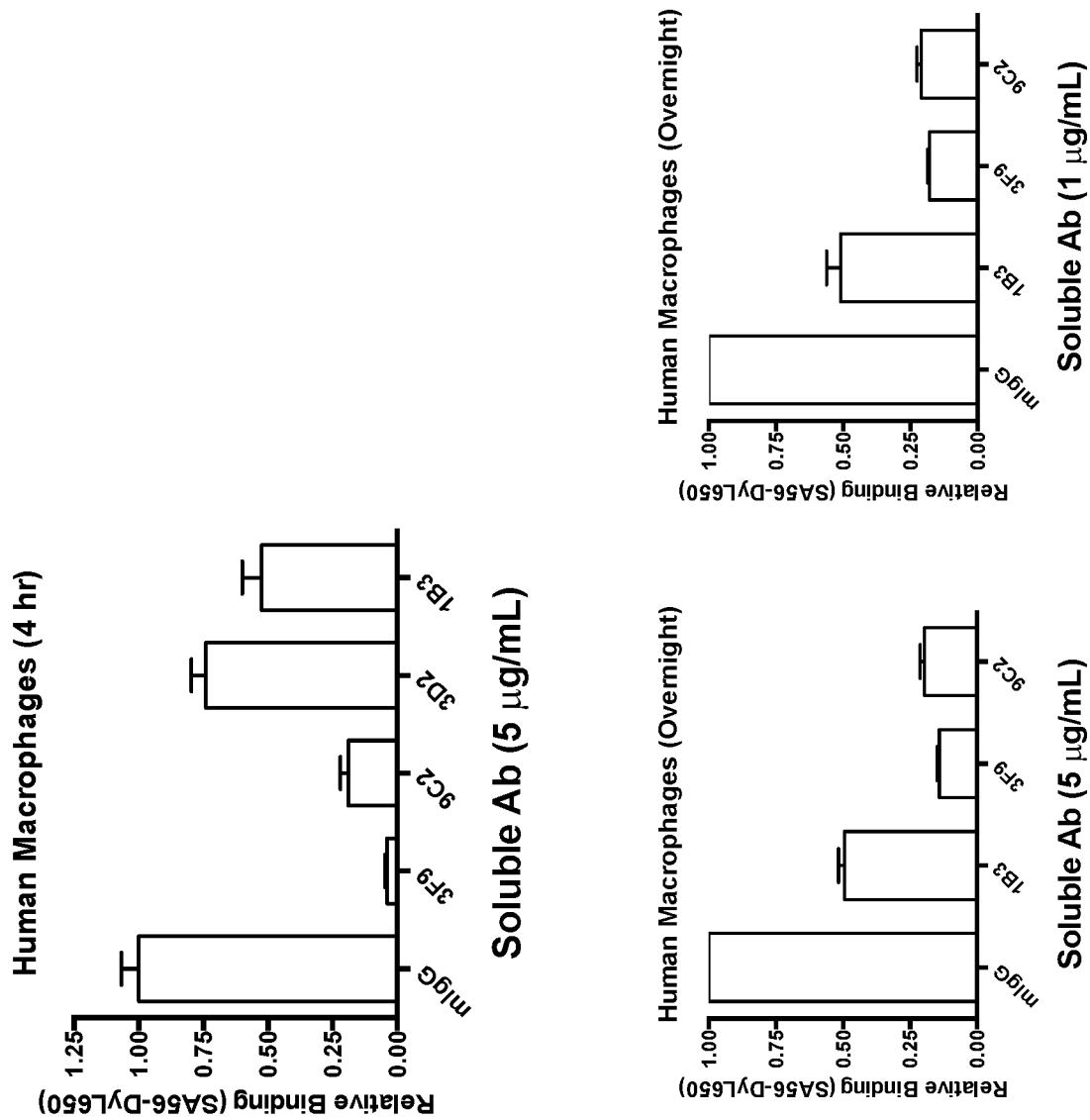


FIGURE 7B

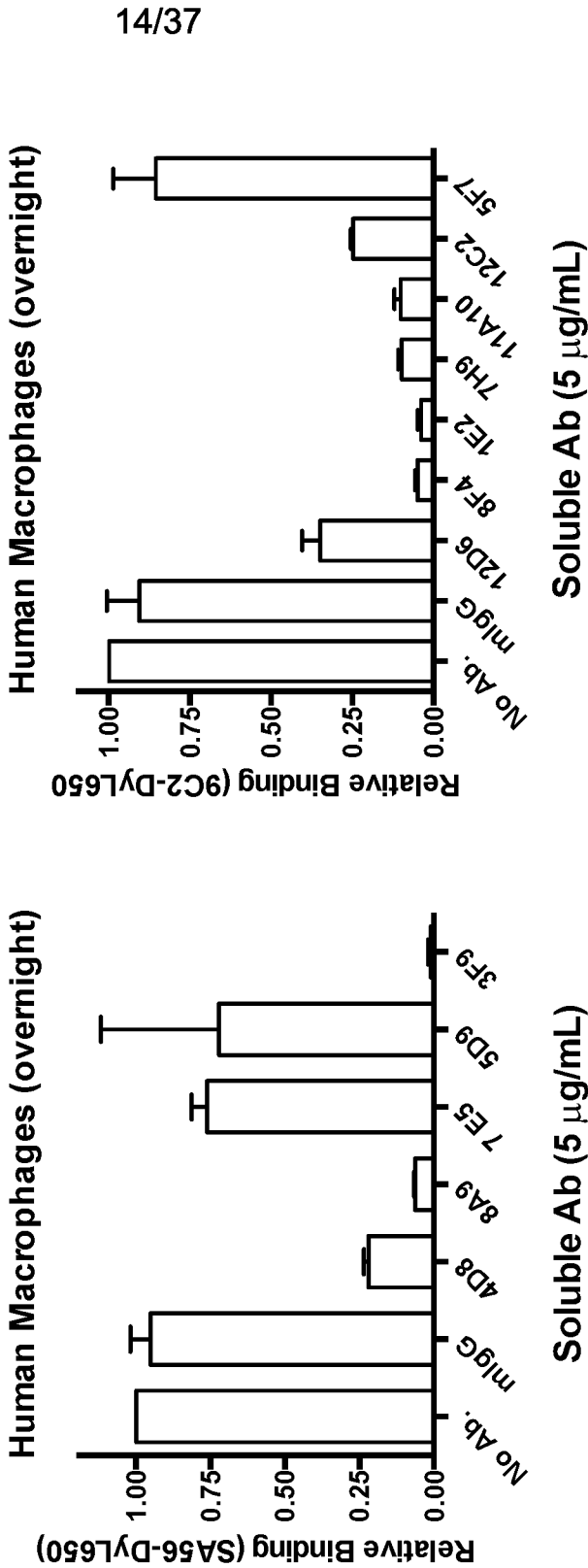


FIGURE 8A

Enhanced phagocytosis of phrodo-labeled Raji cells with CD20

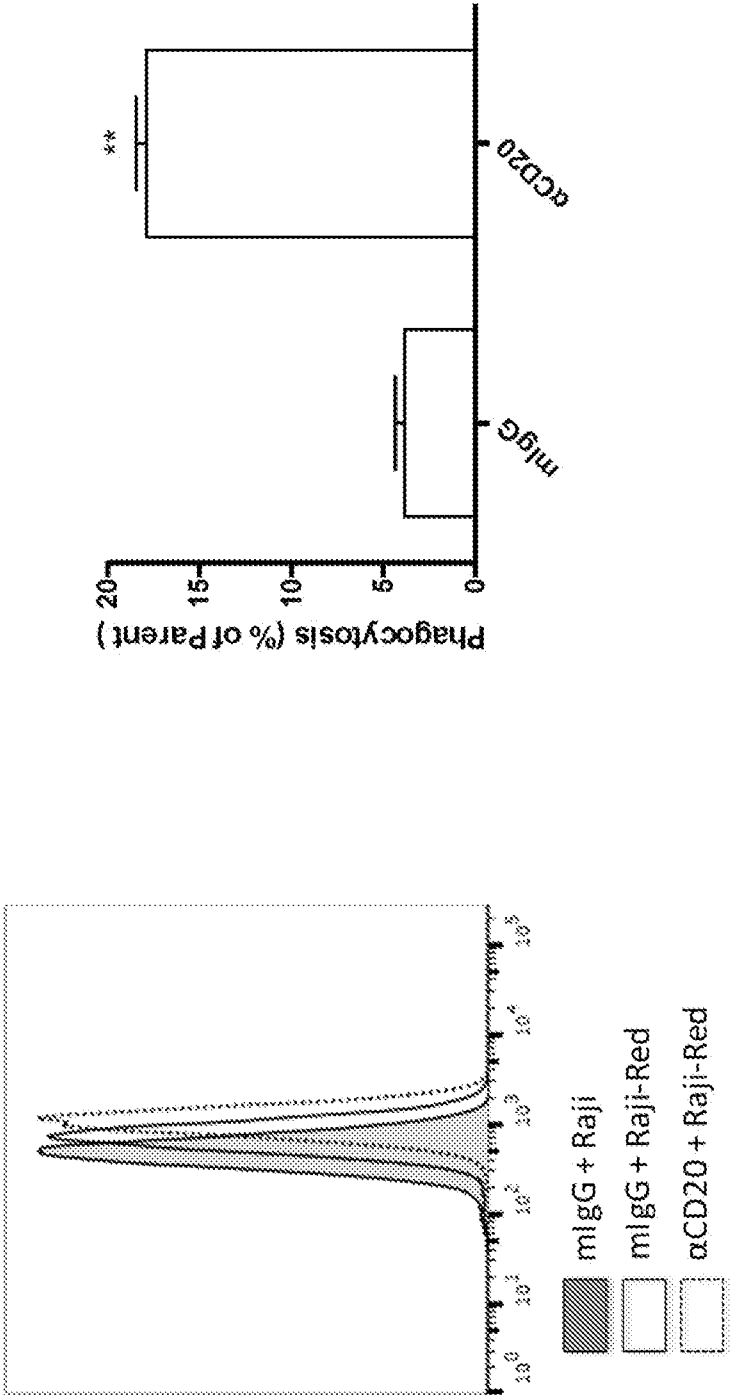
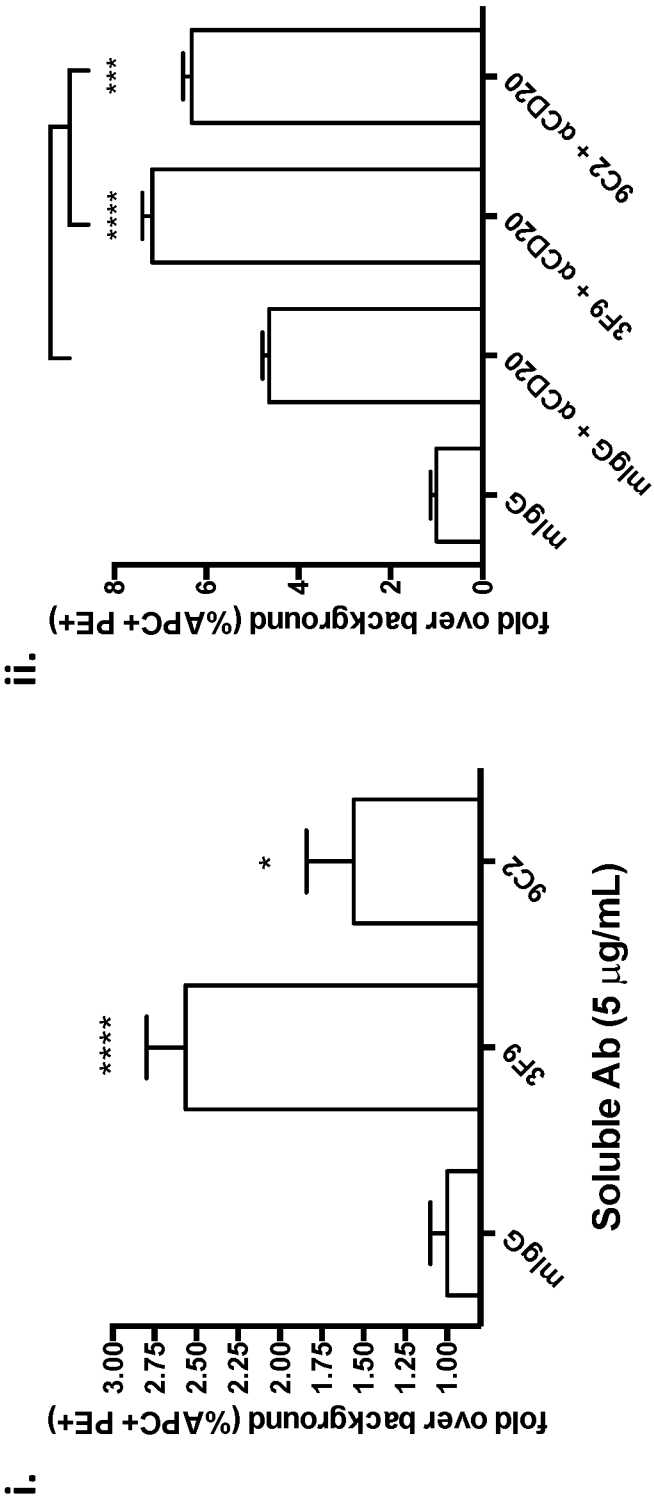


FIGURE 8B



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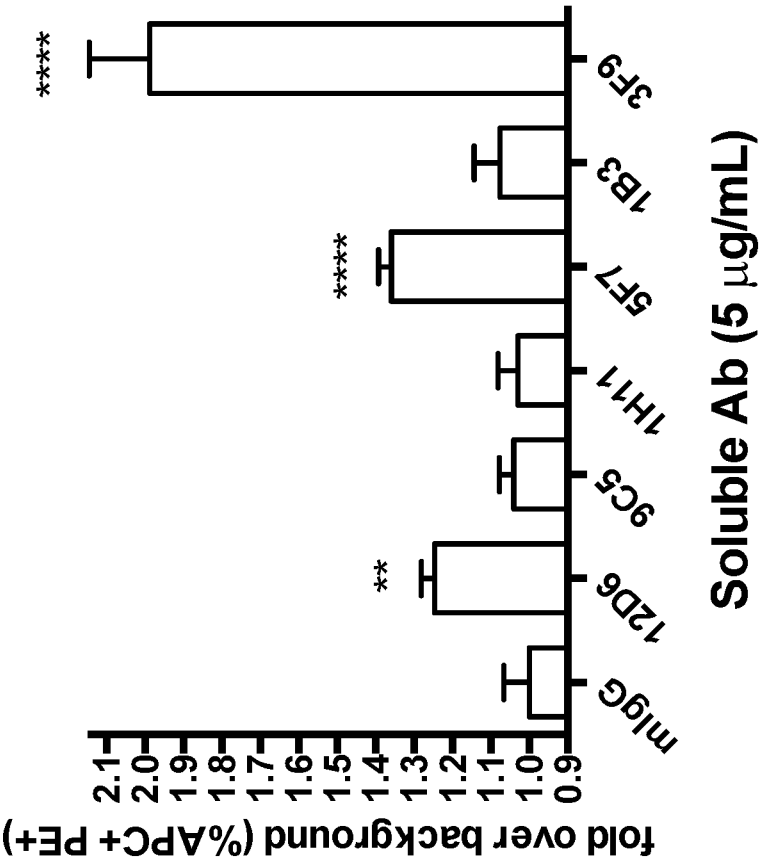


FIGURE 8C

FIGURE 9A

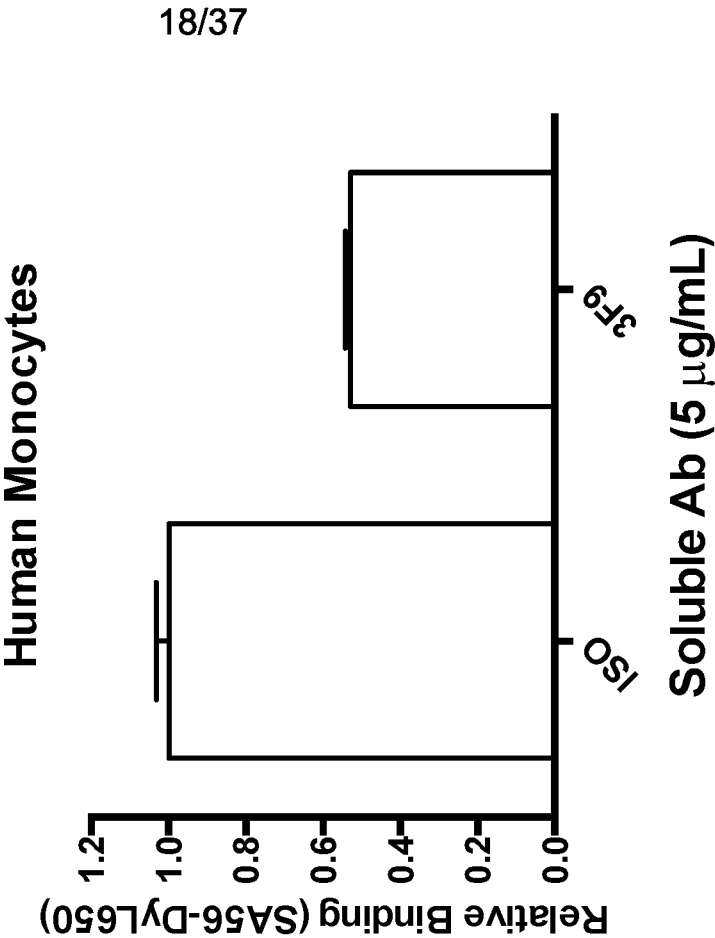


FIGURE 9B

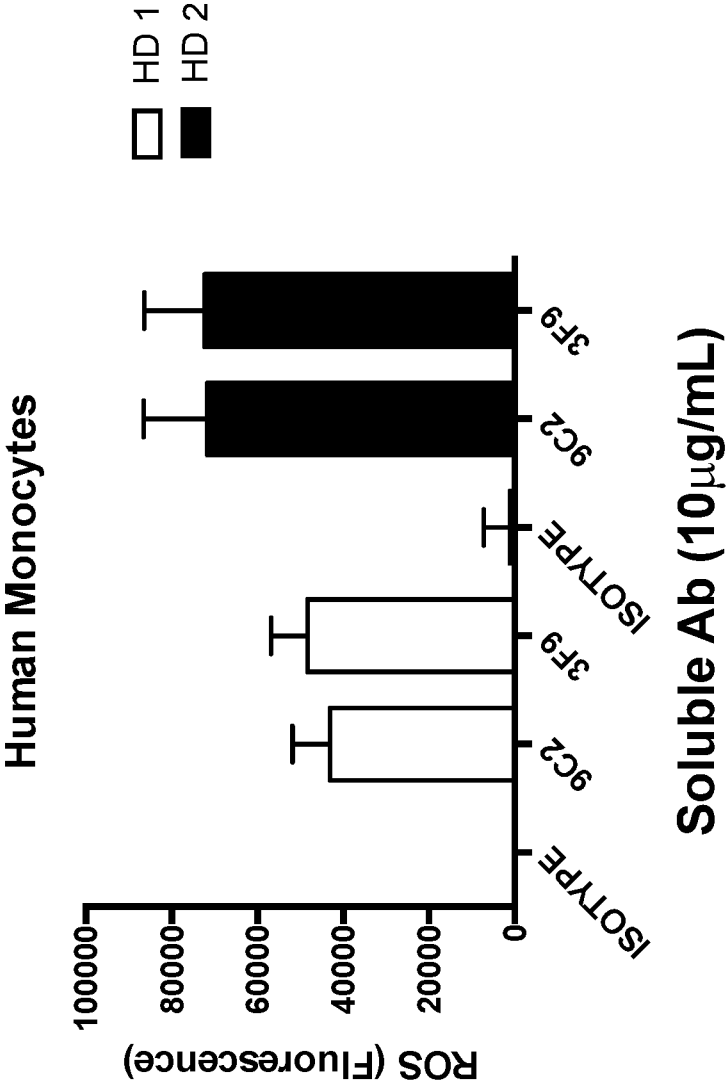


FIGURE 9C

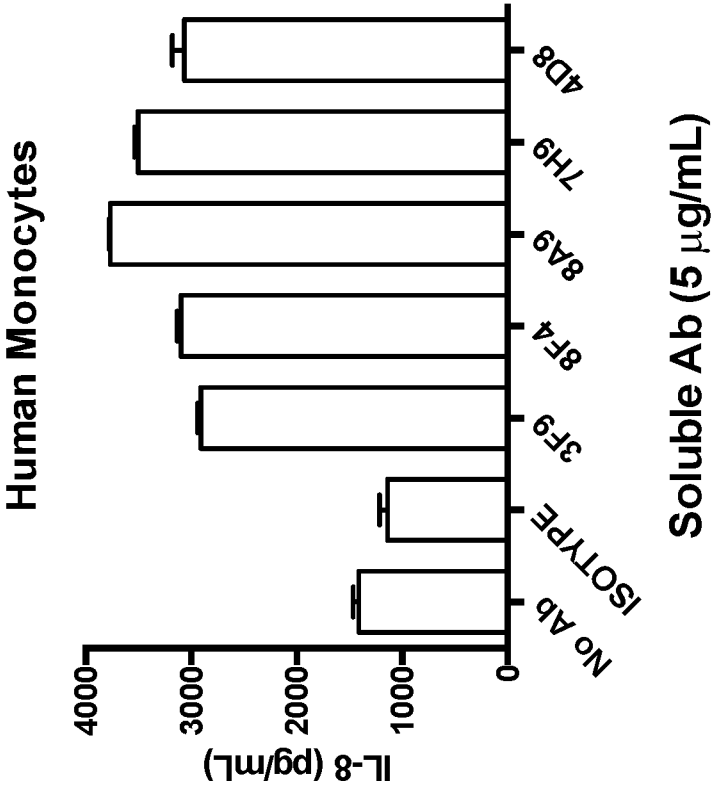


FIGURE 10A

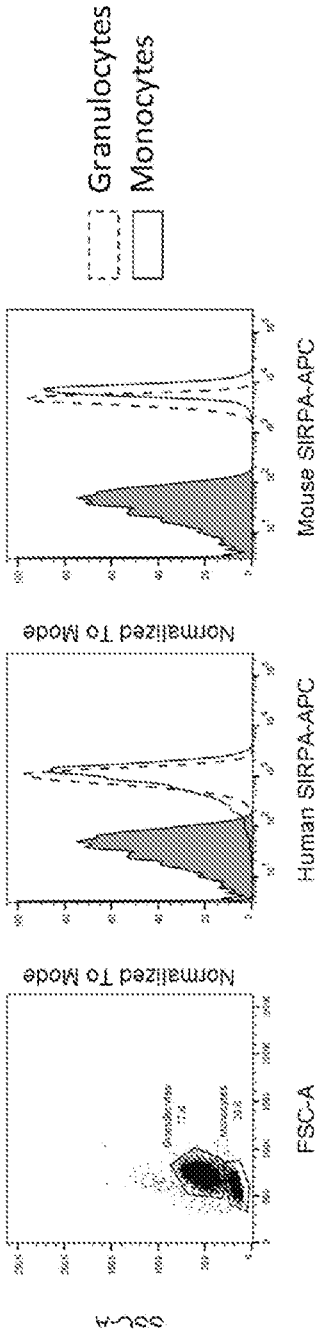


FIGURE 10B

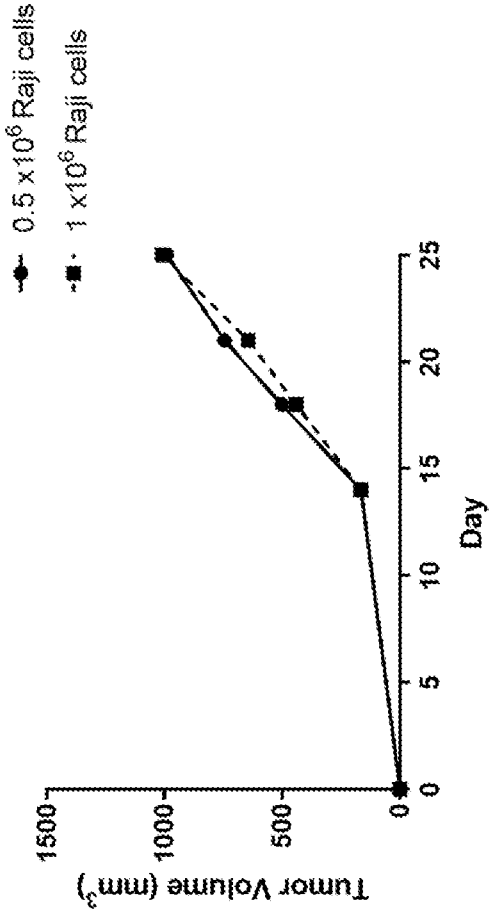


FIGURE 10C

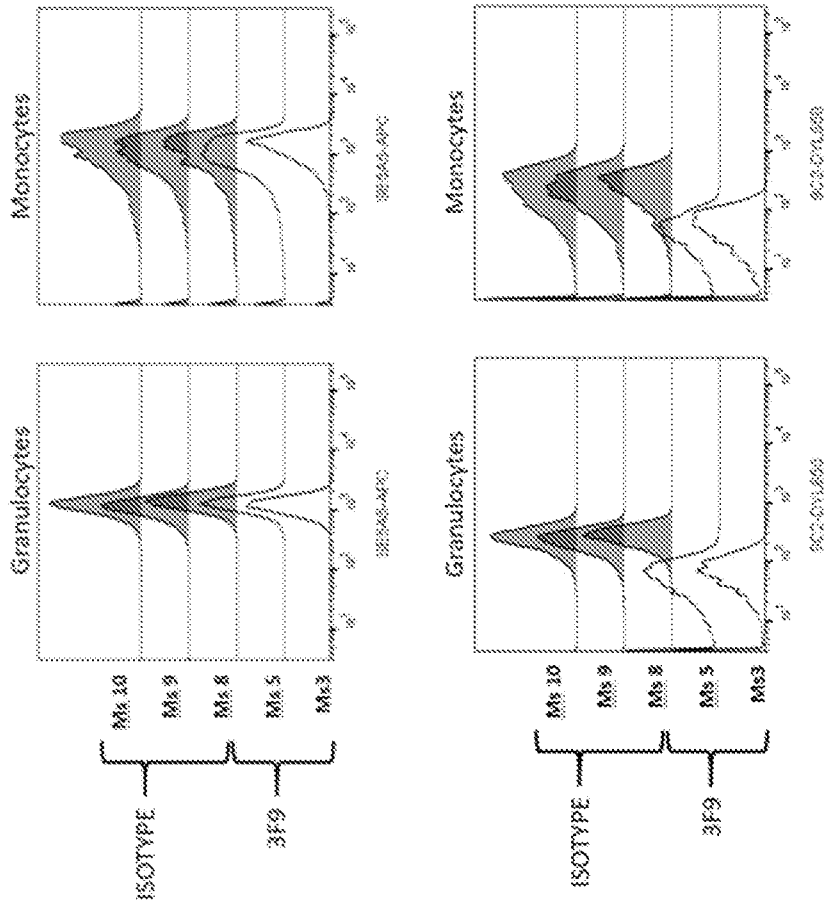


FIGURE 10D

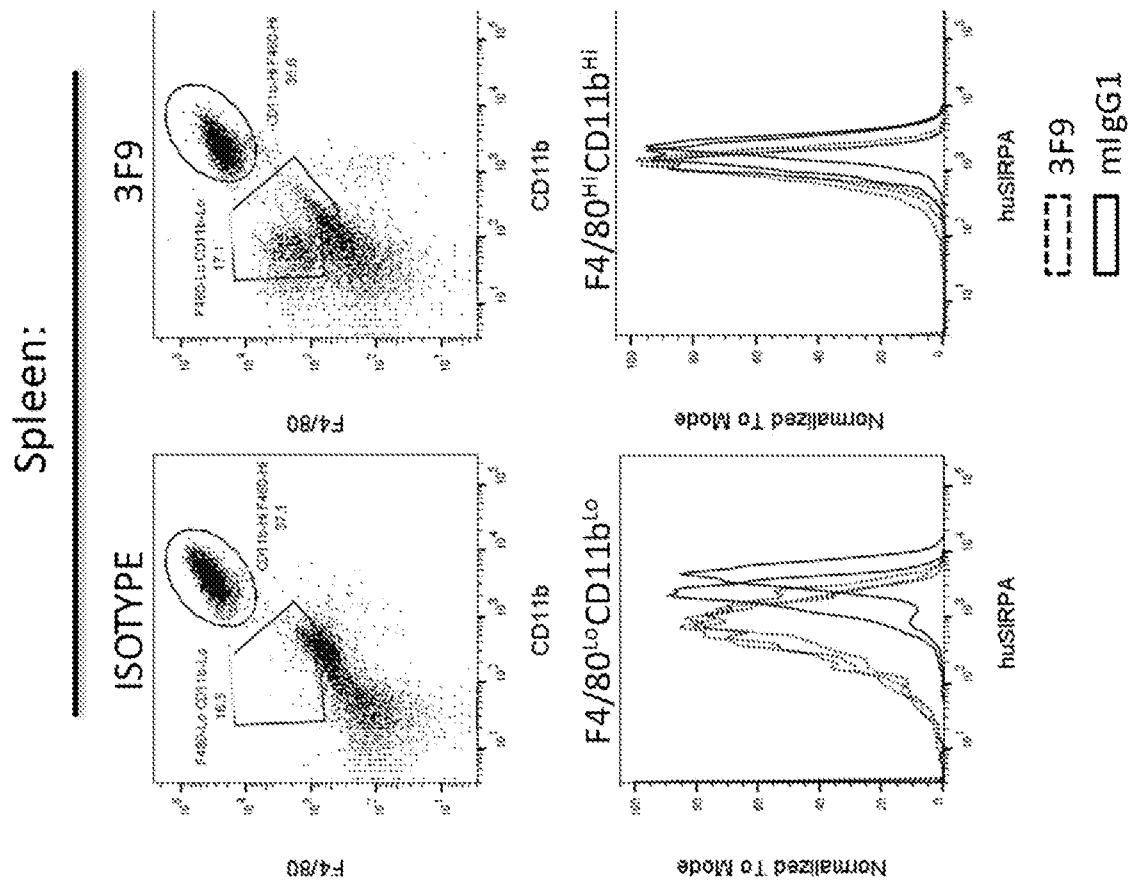


FIGURE 11A

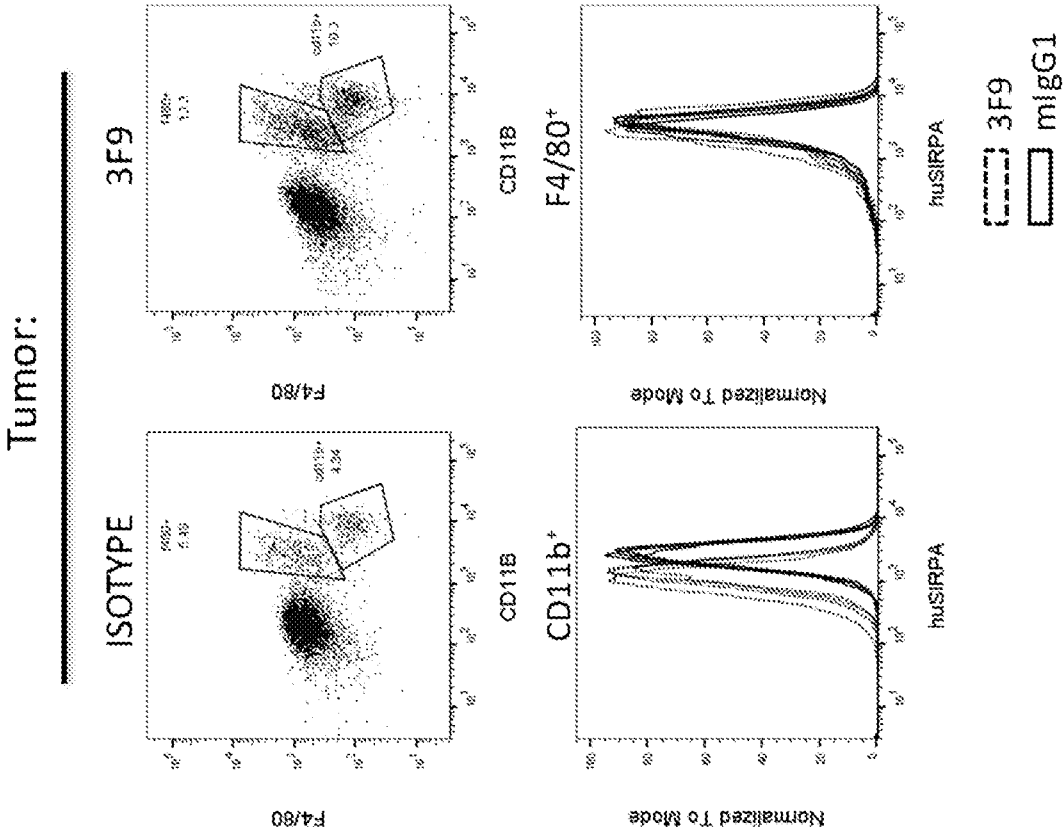


FIGURE 11B

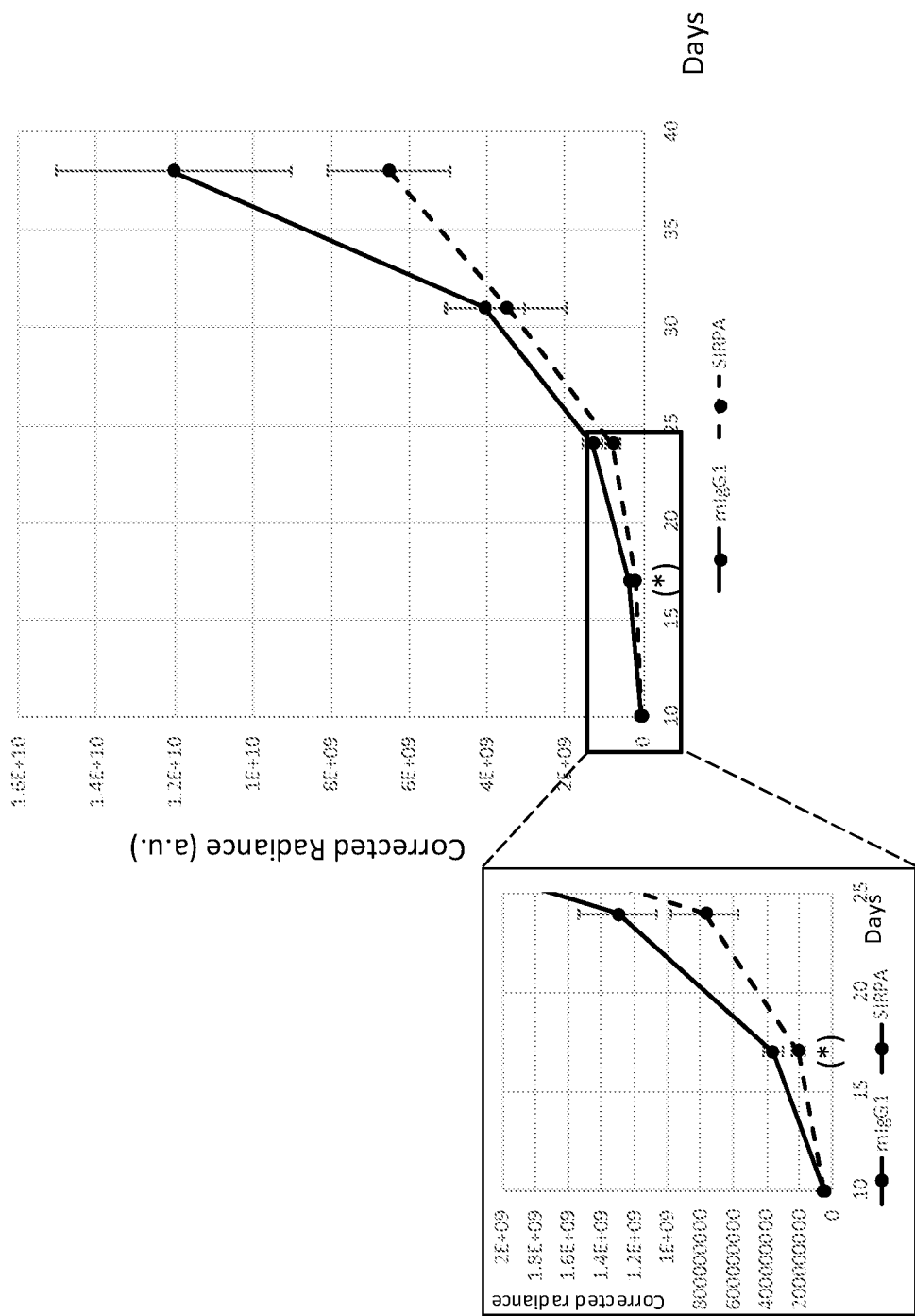


FIGURE 12A

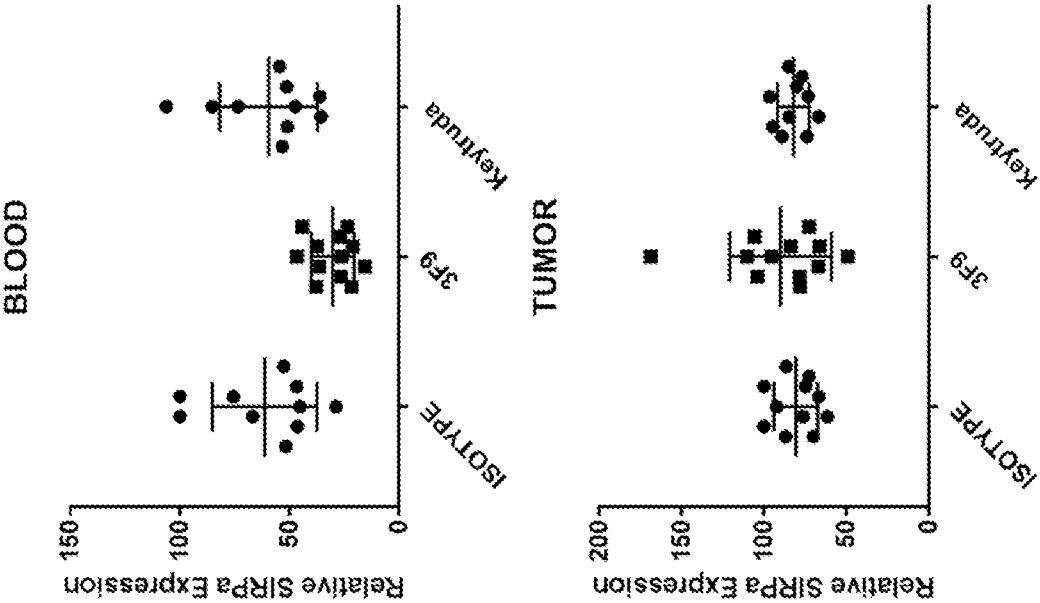


FIGURE 12B

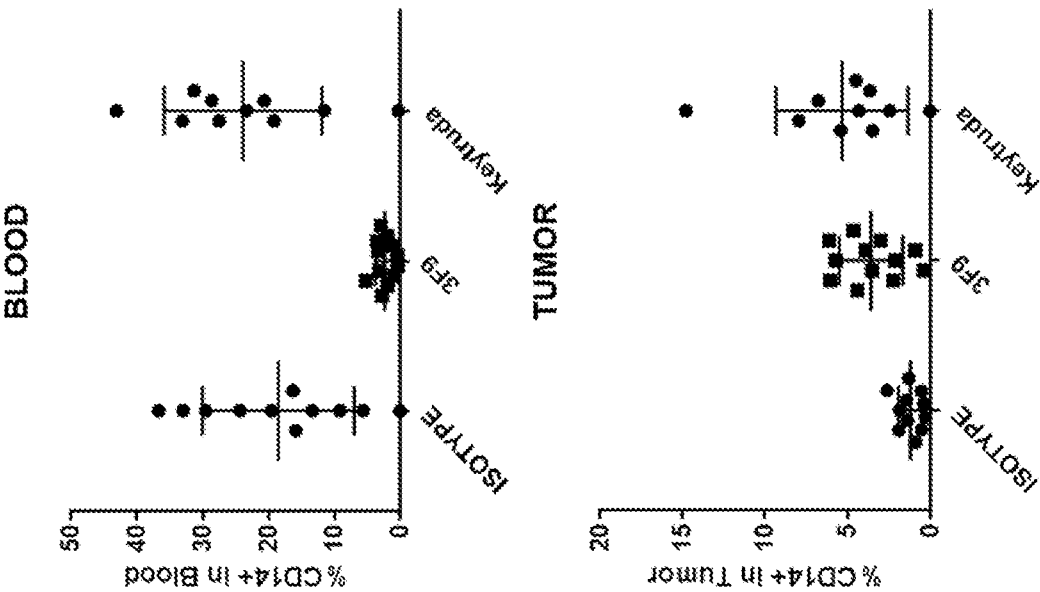
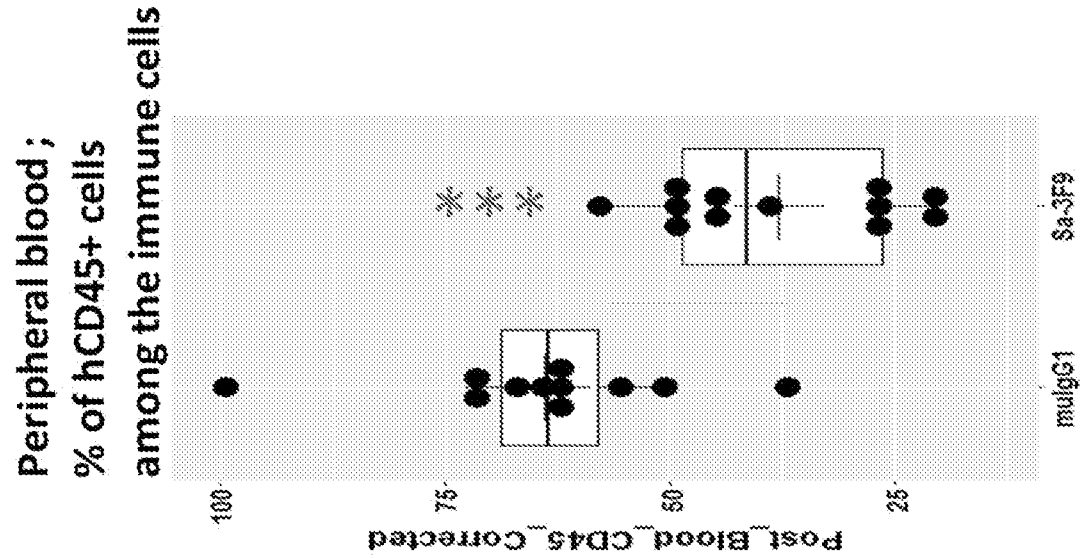
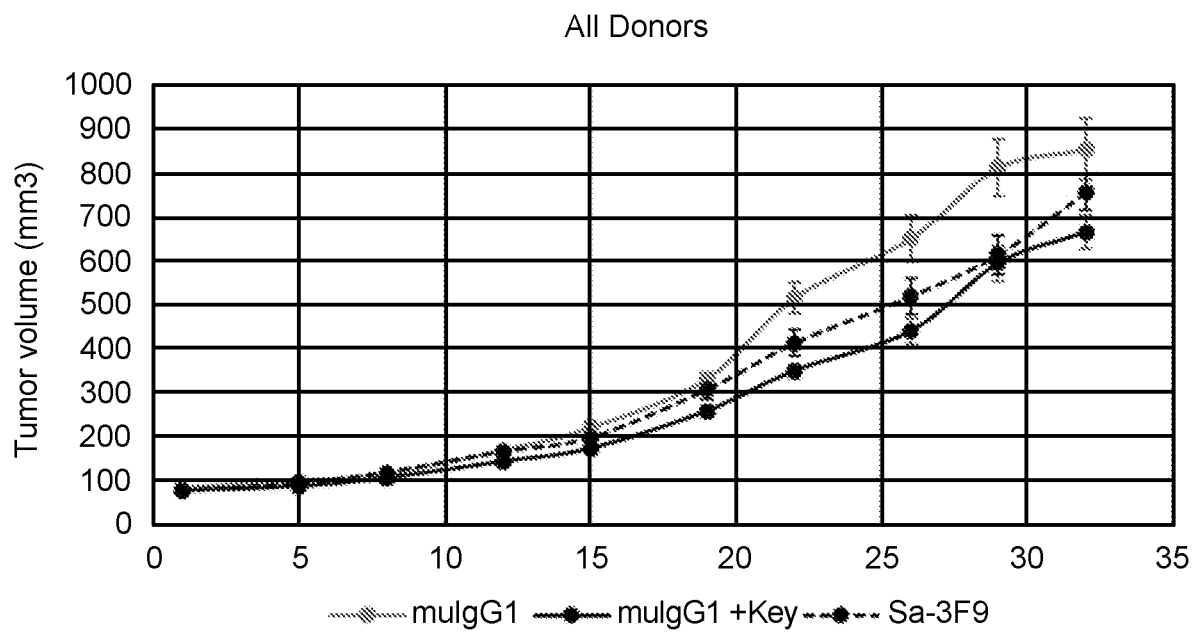


Figure 12C



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FIGURE 13A



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FIGURE 13B

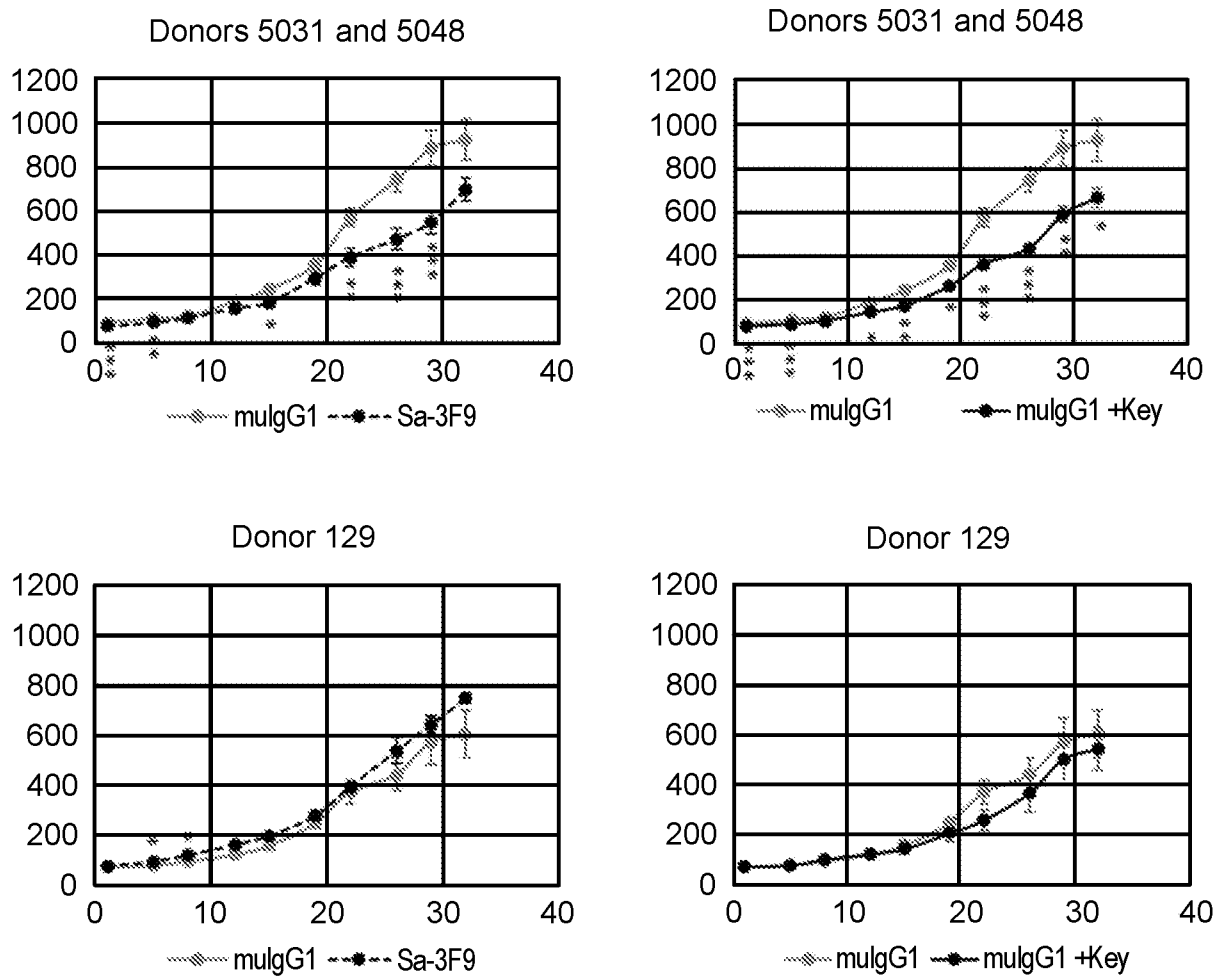


FIGURE 14B

Potential humanized sequence based on IGKV3-11*01 acceptor framework (AbM CDR definition)

IGKV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRA

GIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPP

Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

seq	10	20	30	40	50	60
AbM	10	20	30abcd	40	50	60
	b b b	p p	b b b b	b i b i	i i i b b i	i
SB-3F9	DIVLTQSPASLAVSLQQRATISC RASKSVSSSSGYSYMH WYQKPGQAPRLLIY LASNLES					
	*	* * * *	*	*	*	*
3-11*01	EIVLTQSPATLSLSPGERATLSC RASQSVS----SYLA WYQKPGQAPRLLIY DASNRA					
hSB-3F9-L1	EIVLTQSPATLSLSPGERATLSC RASKSVSSSSGYSYMH WYQKPGQAPRLLIY LASNLES					
hSB-3F9-L2	EIVLTQSPATLSLSPGERATLSC RASKSVSSSSGYSYMH WYQKPGQAPRLLIY LASNLES					
hSB-3F9-L3	EIVLTQSPATLSLSPGERATLSC RASKSVSSSSGYSYMH WYQKPGQAPRLLIY LASNLES					

seq	70	80	90	100	110
AbM	60	70	80	90	100
	b b	b b b b	i b i b i	b b b	b b b
SB-3F9	GVPARFSGSGSGTDFTLTINIHVFEEDAAATYYC QHNREL PCT FCGGTKLEIK				
	*	* * * *	*	*	*
3-11*01	GIPARFSGSGSGTDFTLTISSELPEDFAVYYC QQRSNWPP				
hSB-3F9-L1	GIPARFSGSGSGTDFTLTISSELPEDFAVYYC QHNREL PCT FCGGTKLEIK				
hSB-3F9-L2	GVPARFSGSGSGTDFTLTISSELPEDFAVYYC QHNREL PCT FCGGTKLEIK				
hSB-3F9-L3	GVPARFSGSGSGTDFTLTISSELPEDFAVYYC QHNREL PCT FCGGTKLEIK				

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FIGURE 14C

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

RVTMTSDTSTVYMELSSLRSEDTAVYYCAR

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGLTVTVSS

seq	10	20	30	40	50
AbM	10	20	30	40	50 a
	b b b	p p b b b	b b b	b i i	i i b b b
SB-9C2	EFQLQSGAEIVKPGASVKISCKAS	GYSLTGYNMN	WVKQSRGKSLIEWIG	NINPHYGSST	
	** *	** *	** *	** *	*
IGHV1-46*01	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTSYIMH	WVRQAPGQGLEWMG	IINPSGGSTS	
hSB-9C2-H1	QVQLVQSGAEVKKPGASVKVSCKAS	GYSLTGYNMN	WVRQAPGQGLEWMG	NINPHYGSST	
hSB-9C2-H2	QVQLVQSGAEVKKPGASVKVSCKAS	GYSLTGYNMN	WVRQAPGQGLEWMG	NINPHYGSST	
hSB-9C2-H3	QVQLVQSGAEVKKPGASVKISCKAS	GYSLTGYNMN	WVRQAPGQGLEWMG	NINPHYGSST	
hSB-9C2-H4	QVQLVQSGAEVKKPGASVKISCKAS	GYSLTGYNMN	WVRQAPGQGLEWMG	NINPHYGSST	
F		V			# #

seq	60	70	80	90	100	110
AbM	60	70	80 abc	90	100a	110
	i b	b b b x	b b b b	b i b i b b	i b b b	
SB-9C2	YNQNFKDKATLTVDKSSSAAYMQFNLSLTSEDSAVYYCAR	EGYDGVFDY	WGQGLTVTVSS			
	* * * * *	* * * * *	* * *	*		
IGHV1-46*01	YAQKFPQGRVTMTSDTSTVYMELSSLRSEDTAVYYCAR					
hSB-9C2-H1	YAQKFPQGRVTMTSDTSTVYMELSSLRSEDTAVYYCAR	EGYDGVFDY	WGQGLTVTVSS			
hSB-9C2-H2	YAQKFPQGRVTMTSDTSTVYMELSSLRSEDTAVYYCAR	EGYDGVFDY	WGQGLTVTVSS			
hSB-9C2-H3	YAQKFPQGRATLTVDKSSSAAYMQFNLSLTSEDTAVYYCAR	EGYDGVFDY	WGQGLTVTVSS			
hSB-9C2-H4	YAQKFPQGRATLTVDKSSSAAYMQFNLSLTSEDTAVYYCAR	EGYDGVFDY	WGQGLTVTVSS			
N						

FIGURE 14D

Potential humanized sequence based on IGV3-11*01 acceptor framework (AbM CDR definition)
 IGV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAT
 GIPARFSGSGSGTDFTLTISGLEPEDFAVYYCQQRSNWPP
 Joining region IMGT J00242|IGKJ2*01|YTFGGGTKLEIK

seq	10	20	30	40	50
AbM	10	20	30	40	50
SB-9C2	b b b p p b b b b b b i i i b b i i				
	QIVLSQSPAILASAPGKVTMC RASSSVS-YMH WYQKPGSSPKFWIY VTSNLAS				
	* * * * * ** *				
3-11*01	EIVLTQSPATLSLSPGERATLSC RASQSVSSYLA WYQKPGQAPRLLIY DASNRAT				
hSB-9C2-L1	EIVLTQSPATLSLSPGERATLSC RASSSVS-YMH WYQKPGQAPRLLIY VTSNLAS				
hSB-9C2-L2	EIVLTQSPATLSLSPGERATLSC RASSSVS-YMH WYQKPGQAPRLLIY VTSNLAS				
hSB-9C2-L3	EIVLTQSPATLSLSPGERATLSC RASSSVS-YMH WYQKPGQAPRLLIY VTSNLAS				
hSB-9C2-L4	EIVLTQSPATLSLSPGERVTMTC RASSSVS-YMH WYQKPGQAPRLLIY VTSNLAS				
	A		S		#

seq	60	70	80	90	100
AbM	60	70	80	90	100
SB-9C2	b b b b b b b b i b i i b i b b b				
	GVPTRFSGSGSGTSSYSLTISRVEAEDAATYYC QQWSSNPRT FGGGTKLEIK				
	* * *** ** * *				*
3-11*01	GIPARFSGSGSGTDFTLTISGLEPEDFAVYYC QQRSNWPP				
hSB-9C2-L1	GIPARFSGSGSGTDFTLTISGLEPEDFAVYYC QQWSSNPRT FGGGTKLEIK				
hSB-9C2-L2	GIPARFSGSGSGTDFTLTISGLEPEDFAVYYC QQWSSNPRT FGGGTKLEIK				
hSB-9C2-L3	GIPARFSGSGSGTDFTLTISGLEPEDFAVYYC QQWSSNPRT FGGGTKLEIK				
hSB-9C2-L4	GVPTRFSGSGSGTDFTLTISGLEPEDFAVYYC QQWSSNPRT FGGGTKLEIK				
	A		^		#

Figure 15A

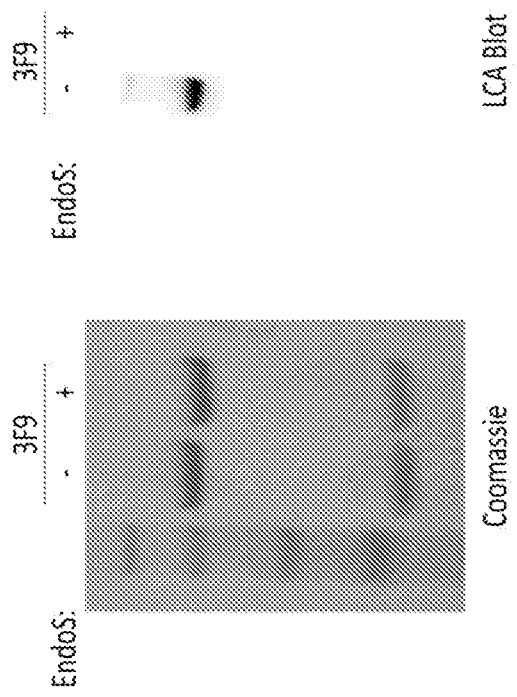
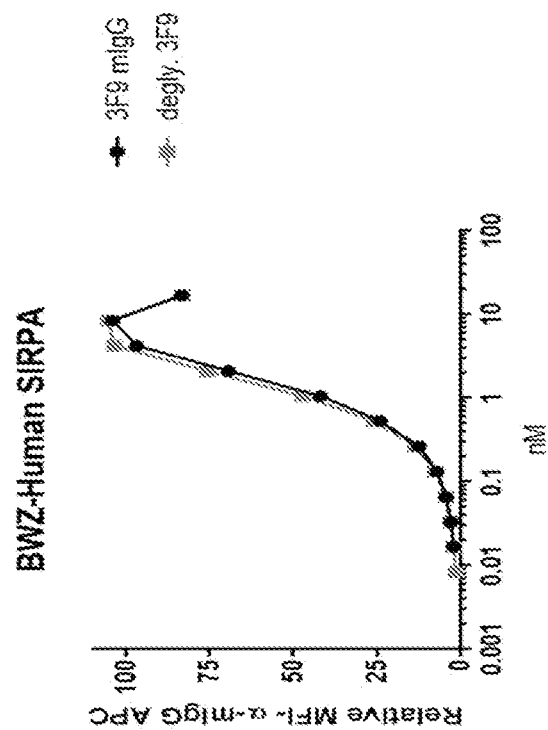


Figure 15B



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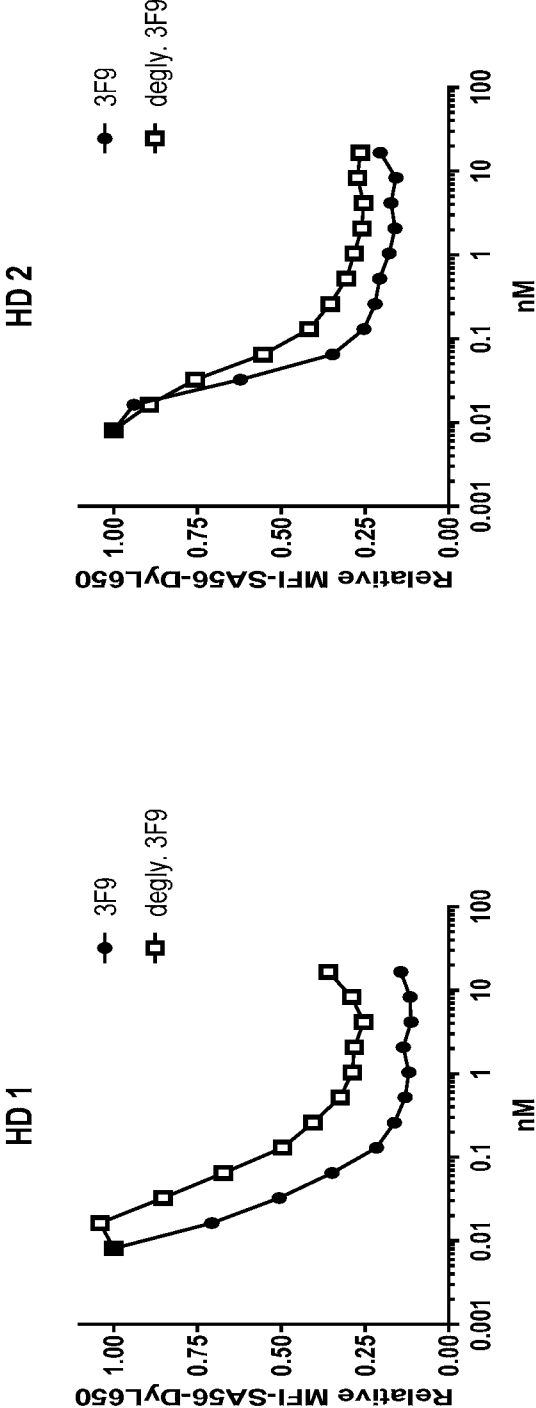


Figure 16

Figure 17A

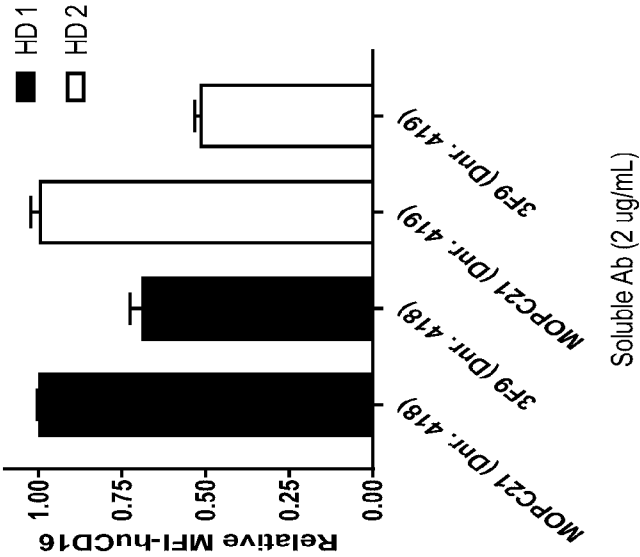


Figure 17B

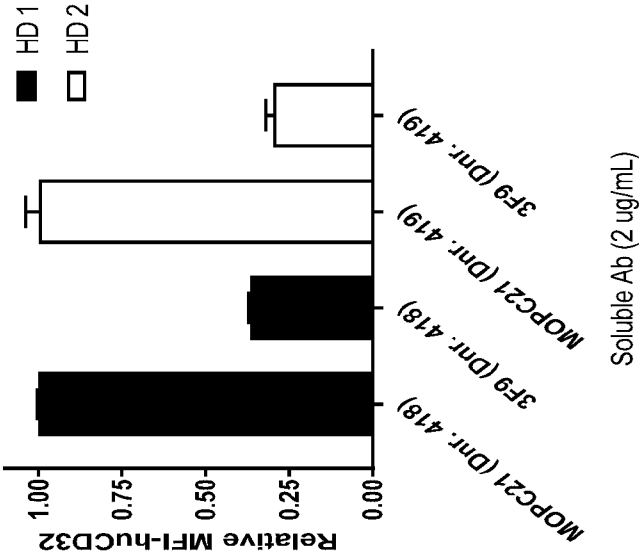


Figure 18

