

FIGURE 1A

```

1 NEPACPAPCRLGPLLCLLAASCANSCVACEEELQVQPKSVLVAAGETATLRCATSL 60
1 NEPACPAPCRLGPLLCLLAASCANSCVACEEELQVQPKSVLVAAGESAIIHCVTSL 60
*****
61 IPVGPIONFRGACPCRELIIYNQKECHFPRTVTVSDLTKRNNMDFSIRIGNITPADACTYY 120
61 IPVGPIONFRGACPCARELIYNQKECHFPRTVTVSESTKRENMDFSISISNITPADACTYY 120
*****;
*****
121 CVKFRKQSPEDVEFKSCACTELSVRAKPSAPVVSQPAARATPQHTVSFTCESHGCFSPRDI 180
121 CVKFRKQSPD-TEFKSCACTELSVRAKPSAPVVSQPAARATPQHTVSFTCESHGCFSPRDI 179
*****
181 TLKWFKNONELSDFTQNVDPVGESVSYSHSTAKVLTREDVHSQVICEVAHVTLQGDPL 240
180 TLKWFKNONELSDFTQNVDPVGESVSYSHSTAKVLTREDVHSQVICEVAHVTLQGDPL 239
*****
241 RGTANLSETIRVPPTLEVTOQPVRAENQVNVTCQVRKFPQRLQLTWLENCNVSEHTETAS 300
240 RGTANLSETIRVPPTLEVTOQPVRAENQVNVTCQVRKFPQRLQLTWLENCNVSEHTETAS 299
*****
301 TVTENKDGTYNWNMSWLLVNVSAHRDDVKLTQVEHDCQPAVSKSHDLKVSANHPKEQCSNT 360
300 TVTENKDGTYNWNMSWLLVNVSAHRDDVKLTQVEHDCQPAVSKSHDLKVSANHPKEQCSNT 359
*****
361 AAENTGCSNERNIYIVGVVCTLLVALLMAALYLVRIRQKKAQGSTSSSTRLHEPEKNAREI 420
360 AAENTGCSNERNIYIVGVVCTLLVALLMAALYLVRIRQKKAQGSTSSSTRLHEPEKNAREI 419
*****
421 TQDTNDITYADLNLPKCKKPAQAAEPNNHTEYASIQTSQPASEDTLTAYADLQWHLNR 480
420 TQDTNDITYADLNLPKCKKPAQAAEPNNHTEYASIQTSQPASEDTLTAYADLQWHLNR 479
*****
481 TPKQAPAPKEPFSFSEYASVQVPRK 504
480 TPKQAPAPKEPFSFSEYASVQVPRK 503
*****

```

FIGURE 1B

```

MEPAGAPGRIGPLLCILLAAACNWSVACEHELOVQDPKSVLVAGETATLCTATSL 60
MPVPASWPHLPSPFL~LMTLLGLRLTOVACEDELOVQPEKSVSVAGESATLRCAMTSL 59
* . * .*: * :*****;*****;*** *****;*****; ***

IPVQPIQWFRGACGCHRELIYNQKECHFPRVTTVSOLTKRNNMDFSRIGNITPADACTYY 120
IPVQPIWFRGACACRELIYNQKECHFPRVTTVSELTKRNNLDFFSISNITPADACTYY 119
***** *****;*****;*****;***** *,*****
***** *****;*****;*****;*****;*****

CVKFRKCSDDVEFKSGACTELSVRAKPSAPVVSQPAARATPQHTVSTCESHGFSRDI 180
CVKFRKCSDDVEFKSGACTELSVRAKPSAPVVSQPAVRATPENTVSTCESHGFSRDI 179
***** *****;*****;*****;*****;*****

TLKWFKNONELSDPQTNVDPVCSVSYSIHSTAKVVLTRCDVHSQVICEVAHVTLQODPL 240
TLKWFKNONELSDPQTNVDPACDSVSYSIHSTARVVLTRCDVHSQVICEIAHITLQODPL 239
***** *****,*;*****;*****;***** *****;***;*****
***** *****;*****;*****;*****;*****

ROGANLSETIRVPTLEVTQOPVRAENQNVTCQVRKFYPQRLQLTWLENQNVSRTEAS 300
ROGANLSEAIRVPTLEVTQOPHRAENQNVTCQVSNFYPRCLQLTWLENQNVSRTEAS 299
*****;*****;*****;*****;*****;*****;*****
*****;*****;*****;*****;*****;*****

TVTENKDCGTYNWMSKLLVNVSAHRDDVKLTQVEHDCQPAVSKSHDLKVSAPHEQCSNT 360
TLIENKDCGTYNWMSKLLVNTCAHRDDVVLTQVEHDCQQAQVSKSYALEISAHQKEHCSDI 359
*; *****;*****;***** ***** *****; *;*** **;***;

AAENTCSNERNIYTVGVVCTLLVALLMAALYLVRIRQKKAQCSSTSLHEPEKNAREI 420
THEAALAPTAPLLVALLGPKLLVVGVSAIYICWKORA----- 398
: * : : :*: : :*:*: :*:*: :*:*: :*:*: :*:*:

TOOTNDITYADLNLPKCKPAPQAAEPNNHTEYASIQTSQPASEDTLYADLDXVHLNR 480
-----

TPKQAPKPEPFSFYASVQVPRK 504
-----

```

FIGURE 2

```

1  MEPAGPAPGRLOPL~LCILLAAACAWSCVAGEEELQVIOPOKSVLYAACETATLACTATS      59
1  MEPAGPAPGRLOPL~LCILLASCFCTOATC~KELRVTOPEKSVSVAACDSVYLNCTLTS      59
   ***** ;*.*.* *;*.* *;*.* *;*.* *;*.* *;*.* *;*.* *;*.* *;*.* *
60  LIPVGPIONFRGACPCRELIYNOKEGFFRVTVTSOLTKRNNMDFEIRIGNITPADACTY      119
60  LLPVCPIRWYRGVCPFSRLIYSPAGEYVPIRIYVSDTKRNNMDFEIRISNVTPADAGIY      119
   *;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*
120  YCVKFRKQSP~DOVEFKSCACTELSVRAKPSAPVVGPAARATPQHTVSTCESHOFSPR      178
120  YCVKFOKCSSEPDTEIOSCCTEVYVLAKPSPPEVSCPADRCIPDOKVNFCKSHGFSR      179
   ***** ;*.*.*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*
179  DITLKWFNCGNELSDPCTNVDPVGRSVSYSHSTAKVLTREDVHSQVCEVAHVTLQCD      238
180  NITLWFKDQELHLETTVNFSGKNVSYNISSTVAVVLNSMDVNSKVCEVAHITLORS      239
   ;*****;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*
239  PLRGTANLSEITRVPTLEVTOQVRAENQVNVTCQVRKFPQALQLTLWENGVSKTER      298
240  PLRGLANLSNFIRVSETVKVTQSQSTEMNQVNLTCRAERFYFEDQLIWLGNVSHNDT      299
   ***** ;*.*.*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*
299  ASTVTENKDCITYNMWELLVNVSAHRDDVWLTCQVEHDCQPAVSKSHDLKVSANRKEQGS      358
300  PKNLTKNITDQTYNTSLFLVNSSAHRDVFVTCQVKHQDQPAITRNHTVLOFANSSDQGS      359
   *.*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*
359  NT~AAGENTCSNERNIYVVGVCILLVALLMAALYLVAIROKKAQGSTSSTRLHEPEKNA      417
360  MQTFPNNATHNNNVFIGVCVACALLVLLMAALYLIRIKOKKAGSTSSSTRLHEPEKNA      419
   ;*.*.*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*;*
418  REITQ~-----DTNDITYADINLPKCKPAPQAAEPNNHTEYASIQTSQPASEDTLTYAD      472
420  REITQIQDTNDINDITYADINLPKCKPAPRAPEPNNHTEYASIECTCKVFPEDTLTYAD      479
   ***** * ***** * ***** * ***** * ***** * ***** *
473  LDMVHLNRTPKQAPAKPEPSPSEYASVOVPRK      504
480  LDMVHLSRA~--QAPAKPEPSPSEYASVOVQRK      509
   *****;*;* *****

```

FIGURE 3A

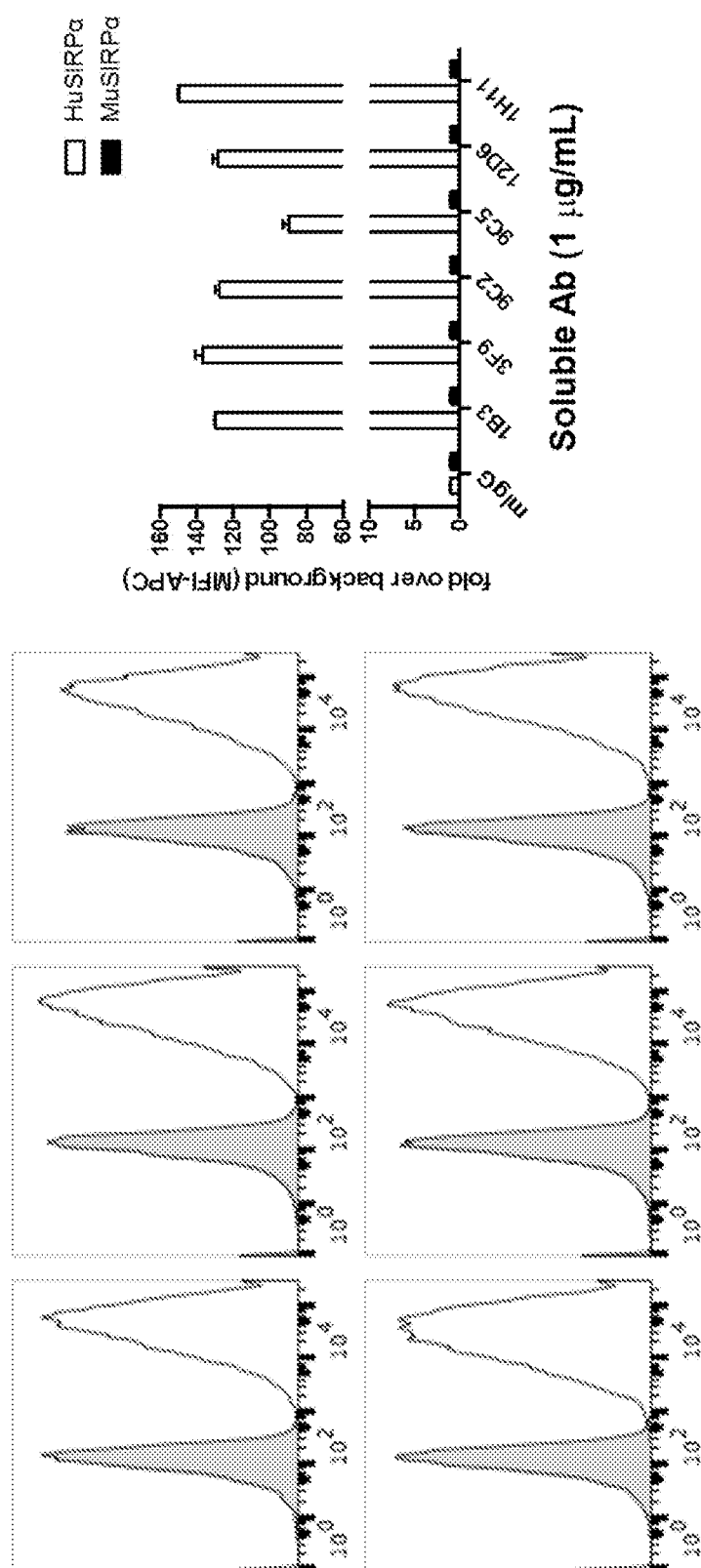


FIGURE 3B

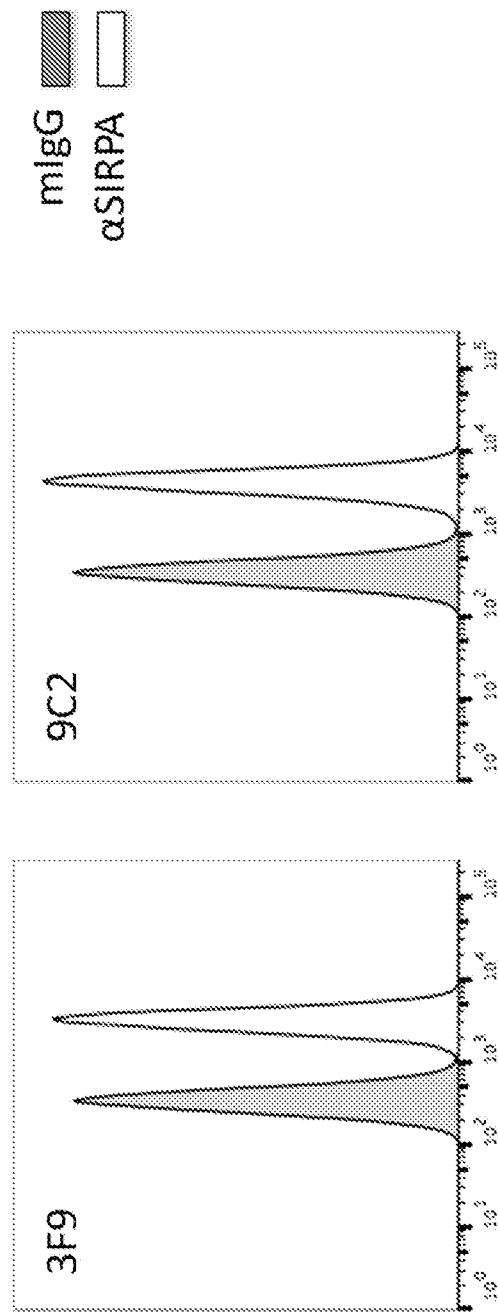


FIGURE 3C

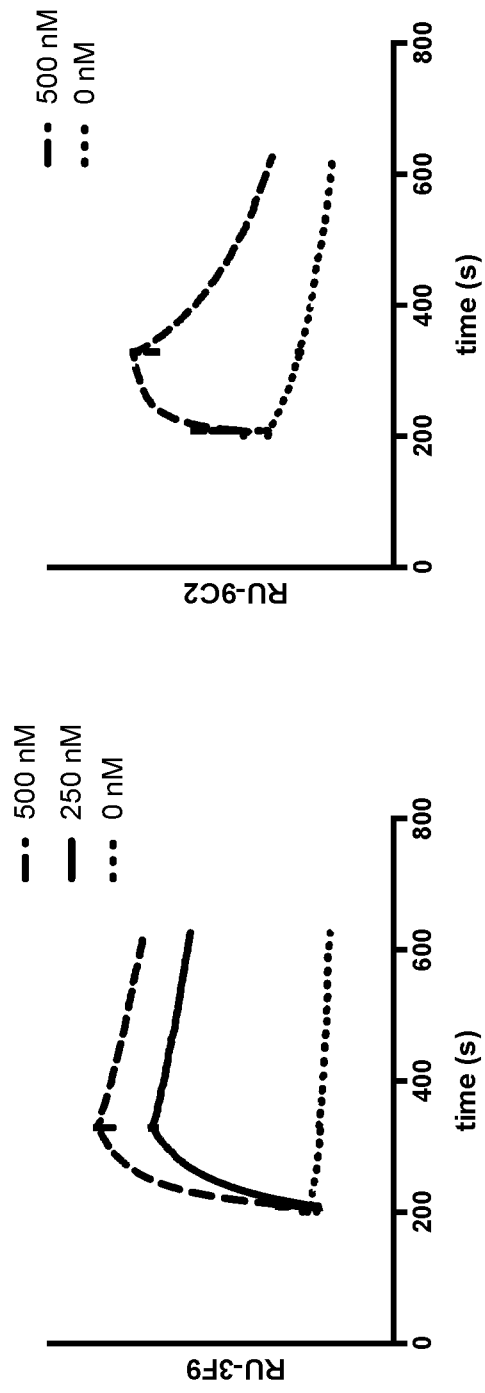


FIGURE 3D

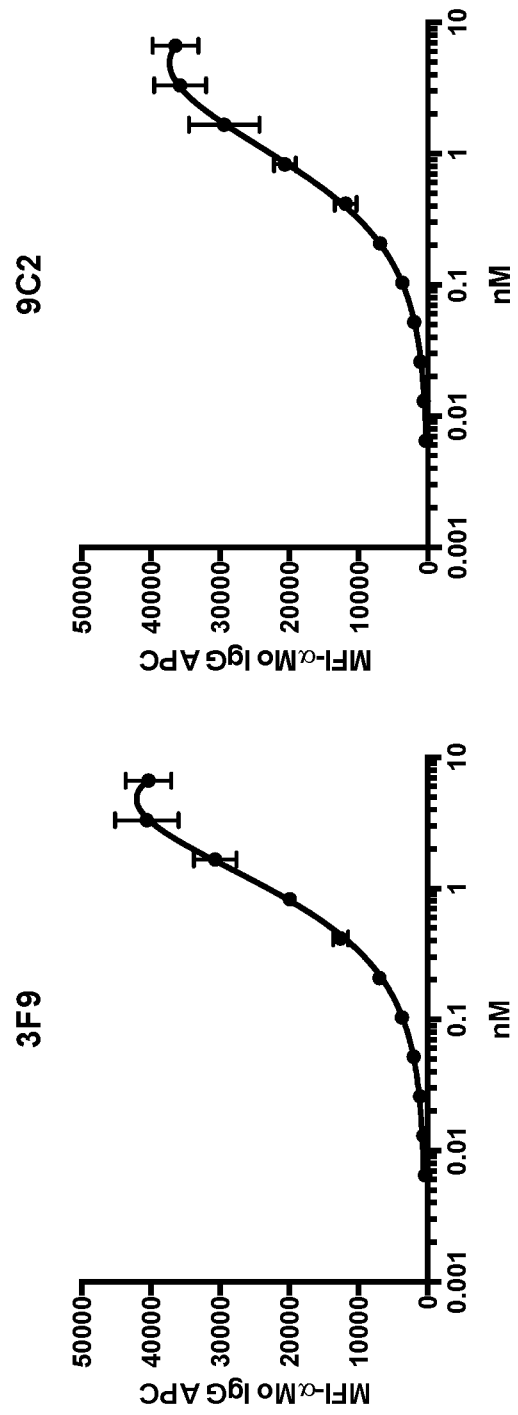


FIGURE 4A

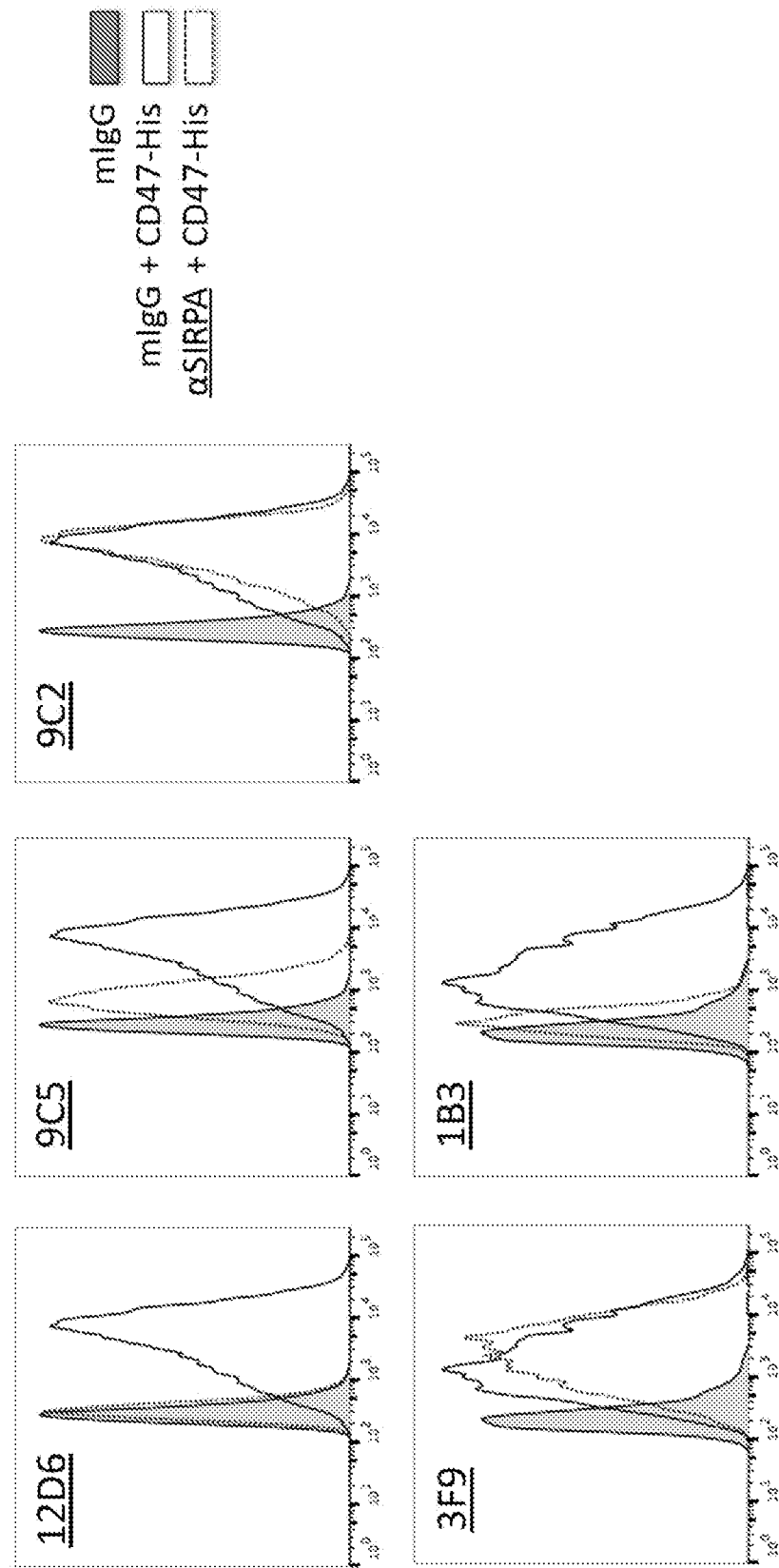


FIGURE 4B

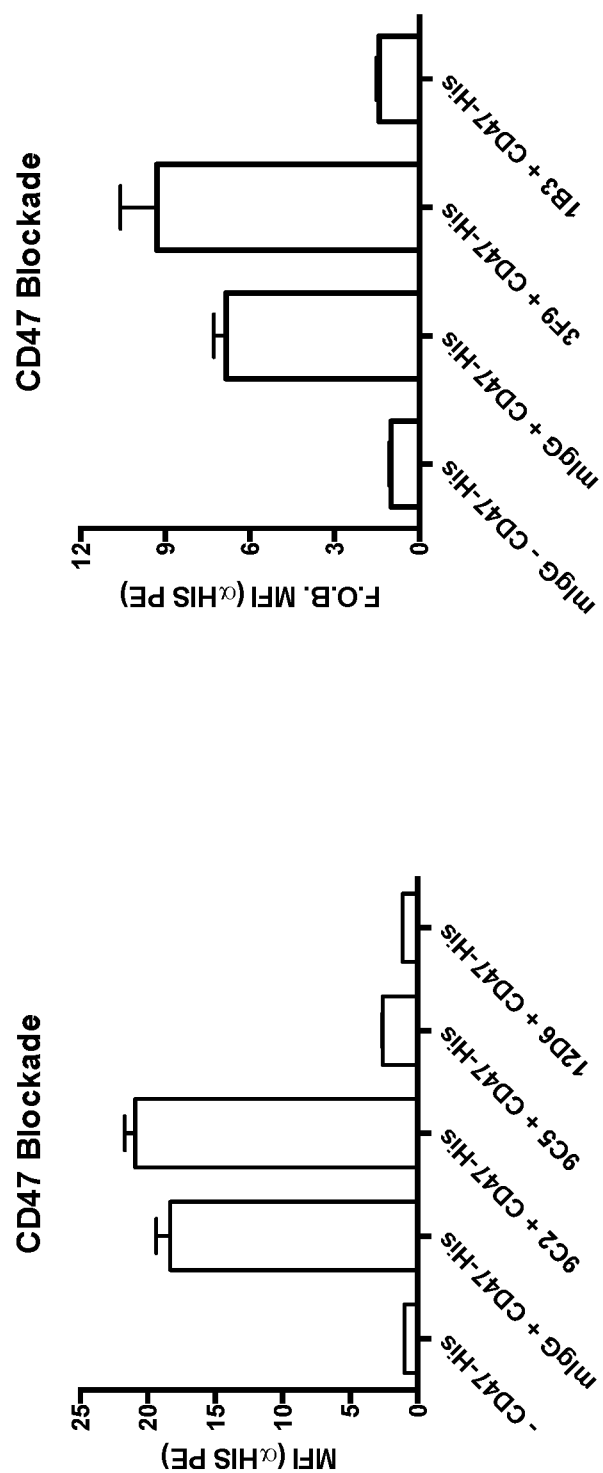


FIGURE 5A

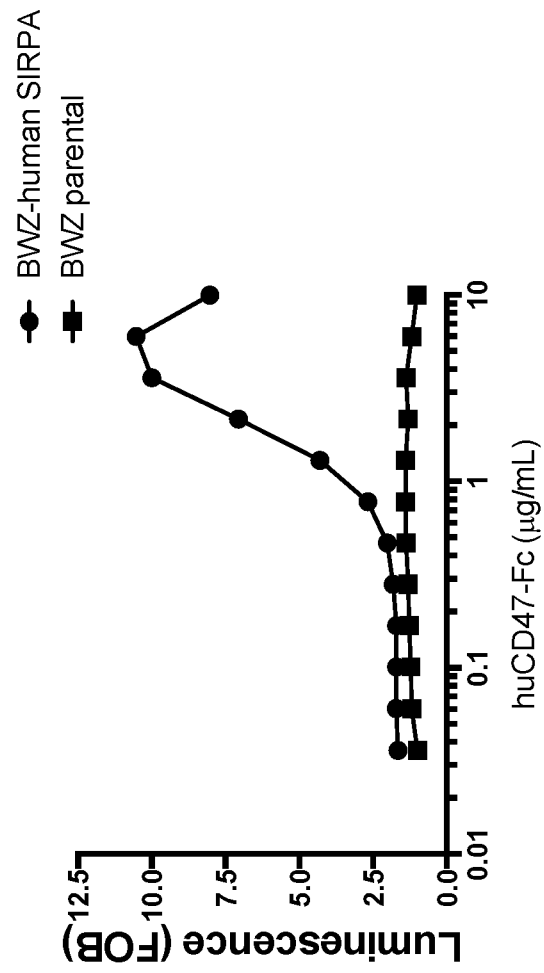


FIGURE 5B

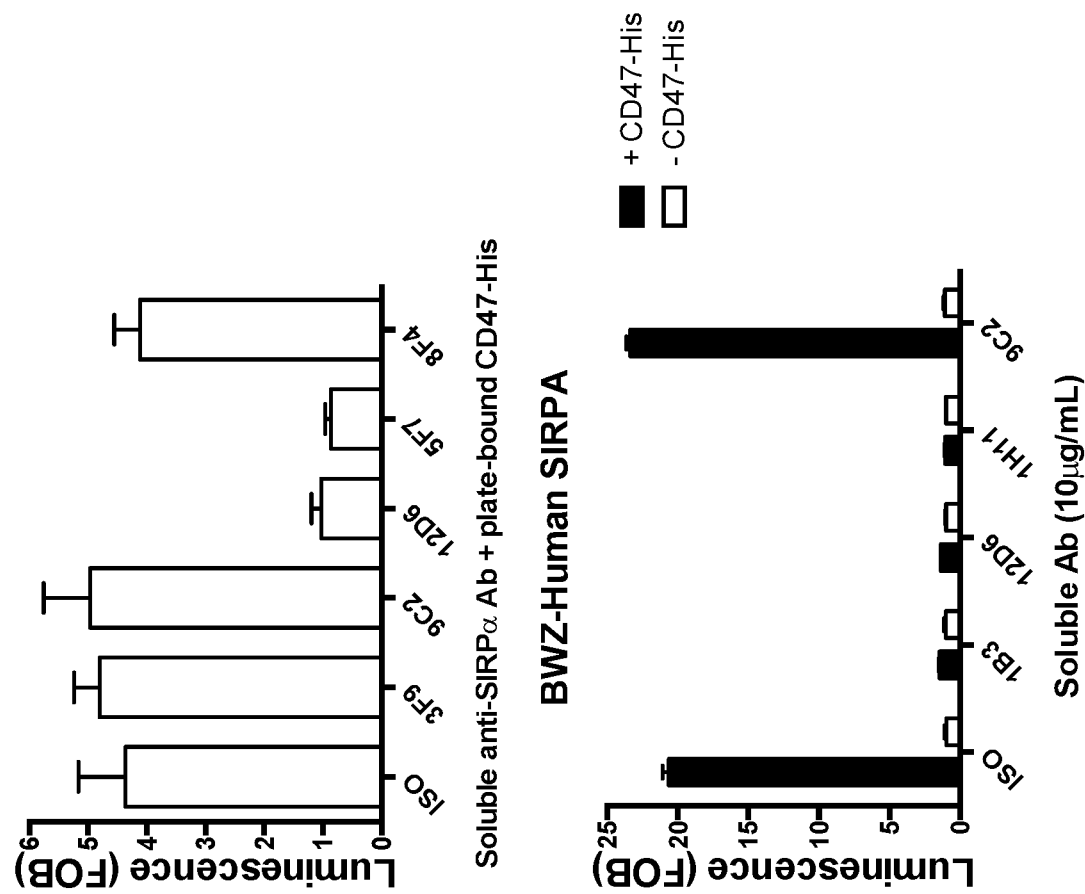


FIGURE 6A

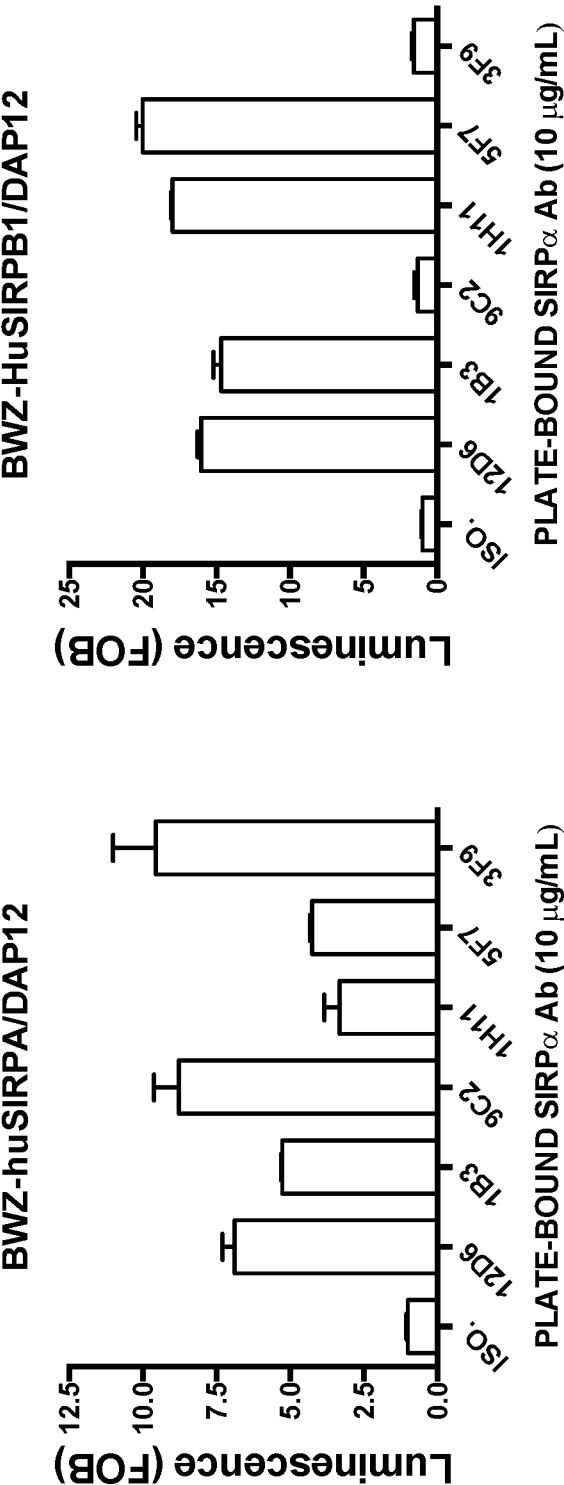


FIGURE 6B

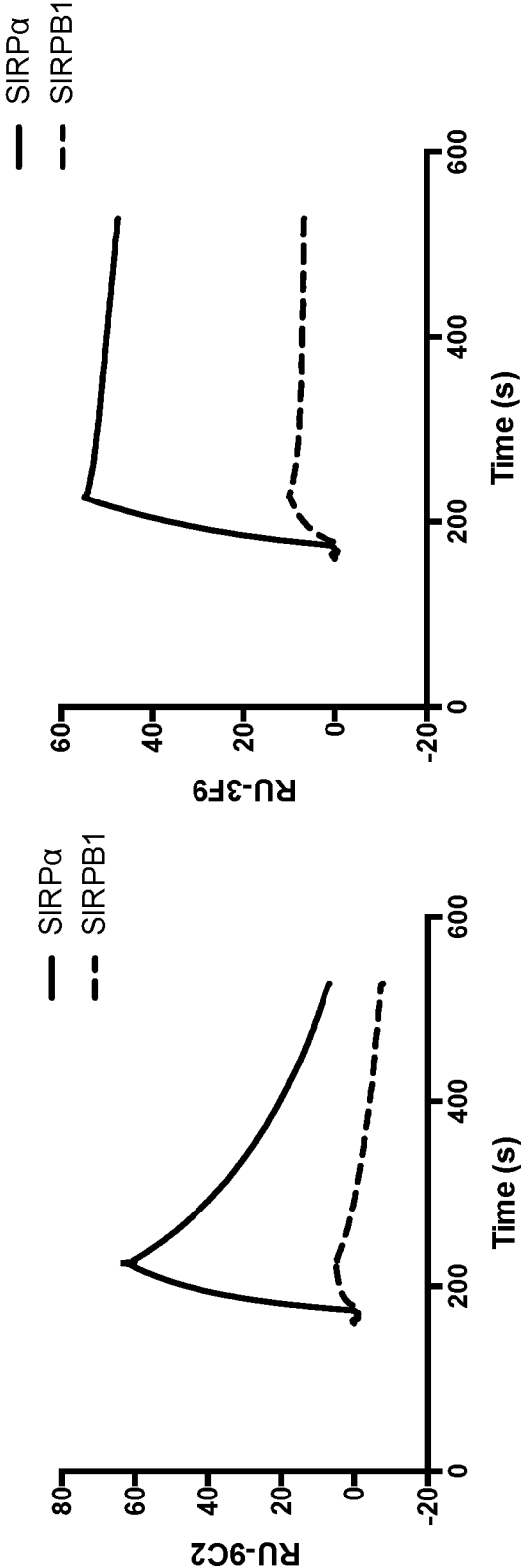


FIGURE 7A

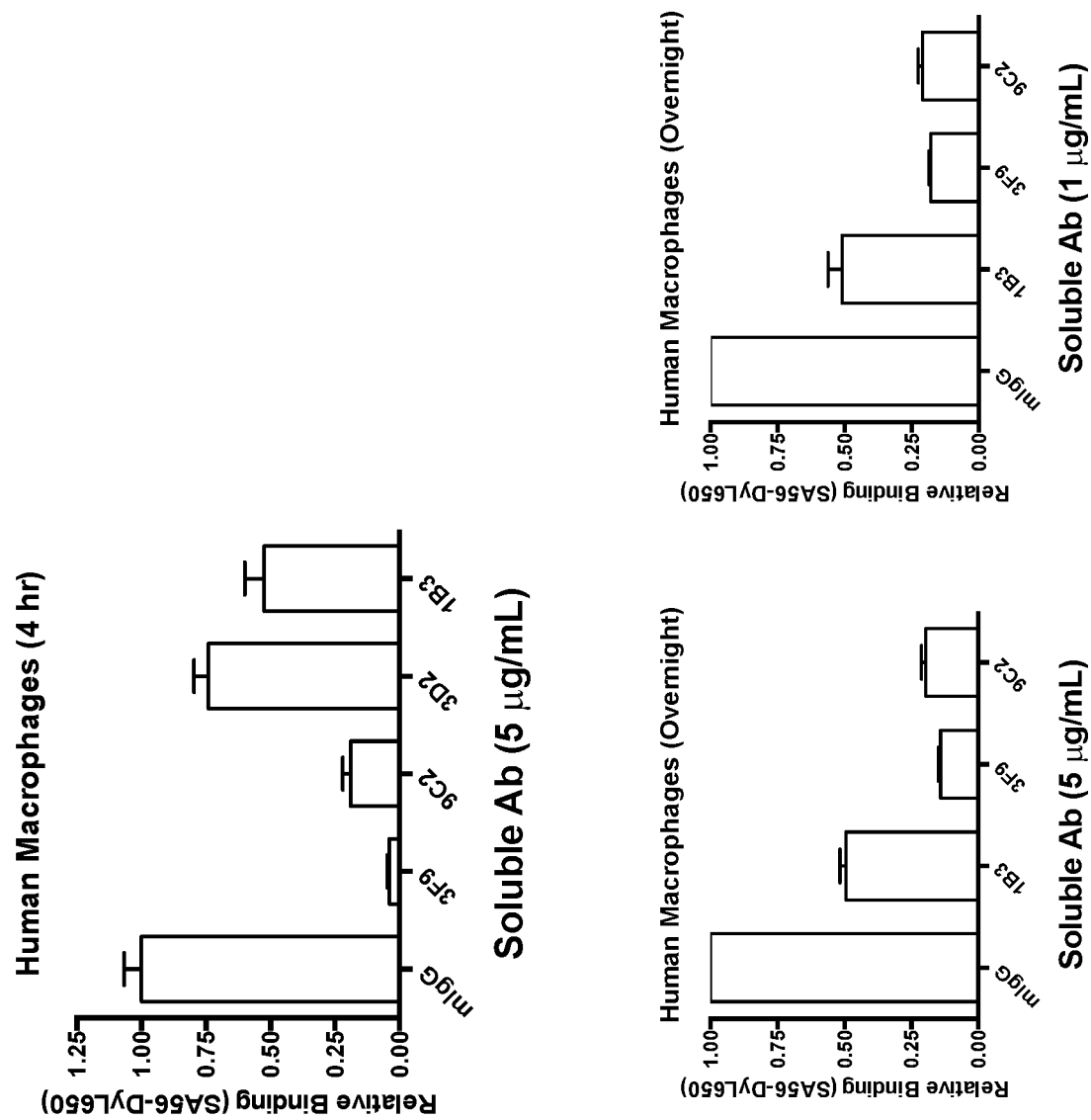


FIGURE 7B

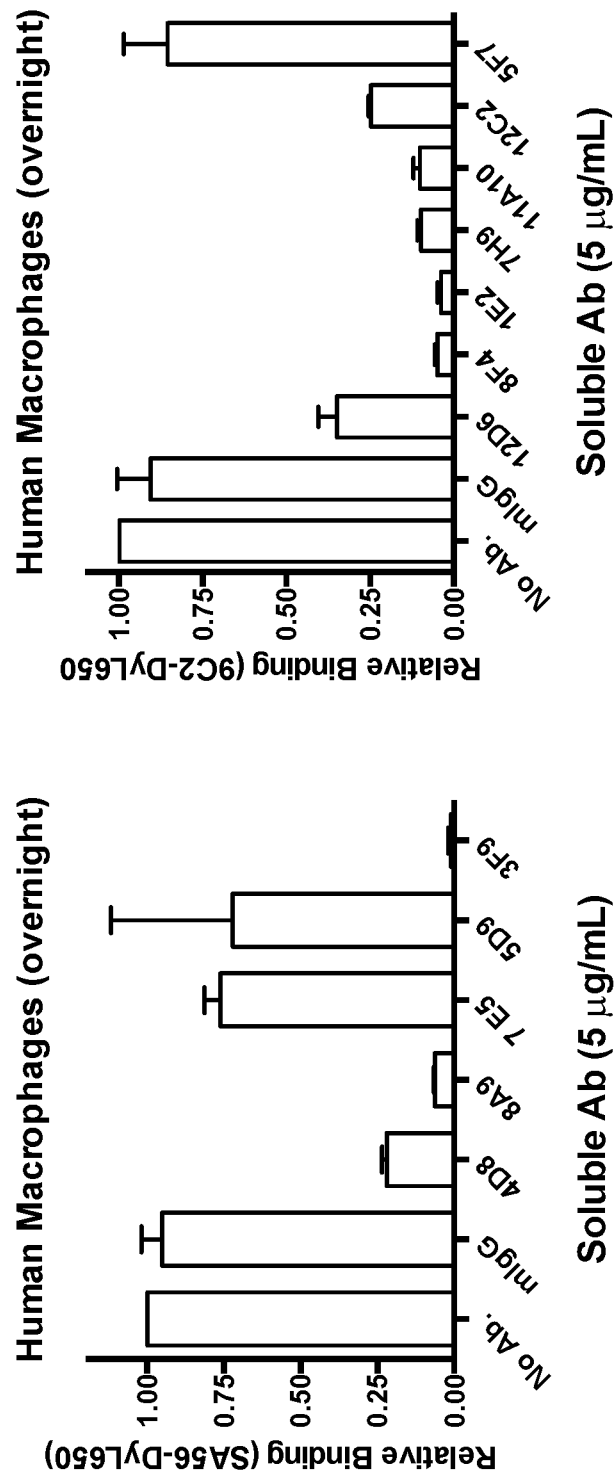


FIGURE 8A

Enhanced phagocytosis of phrodo-labeled Raji cells with CD20

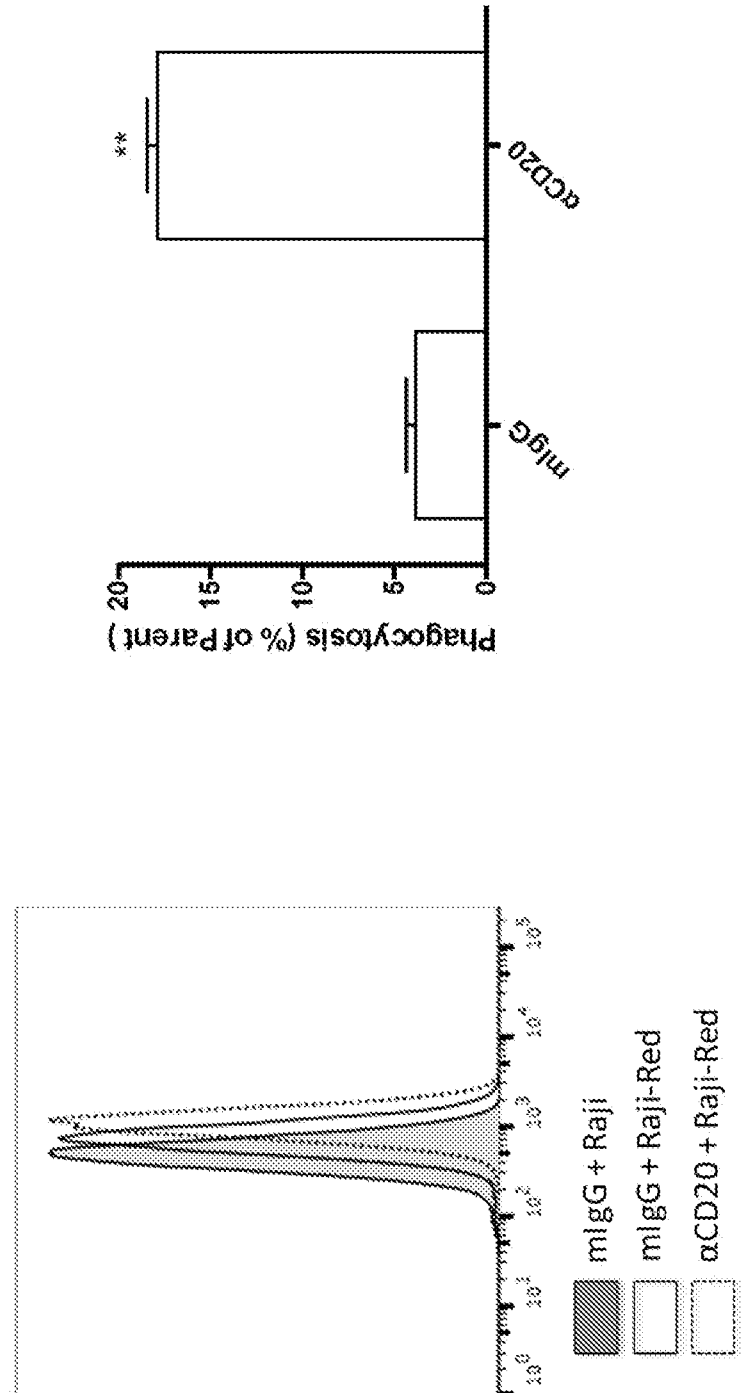


FIGURE 8B

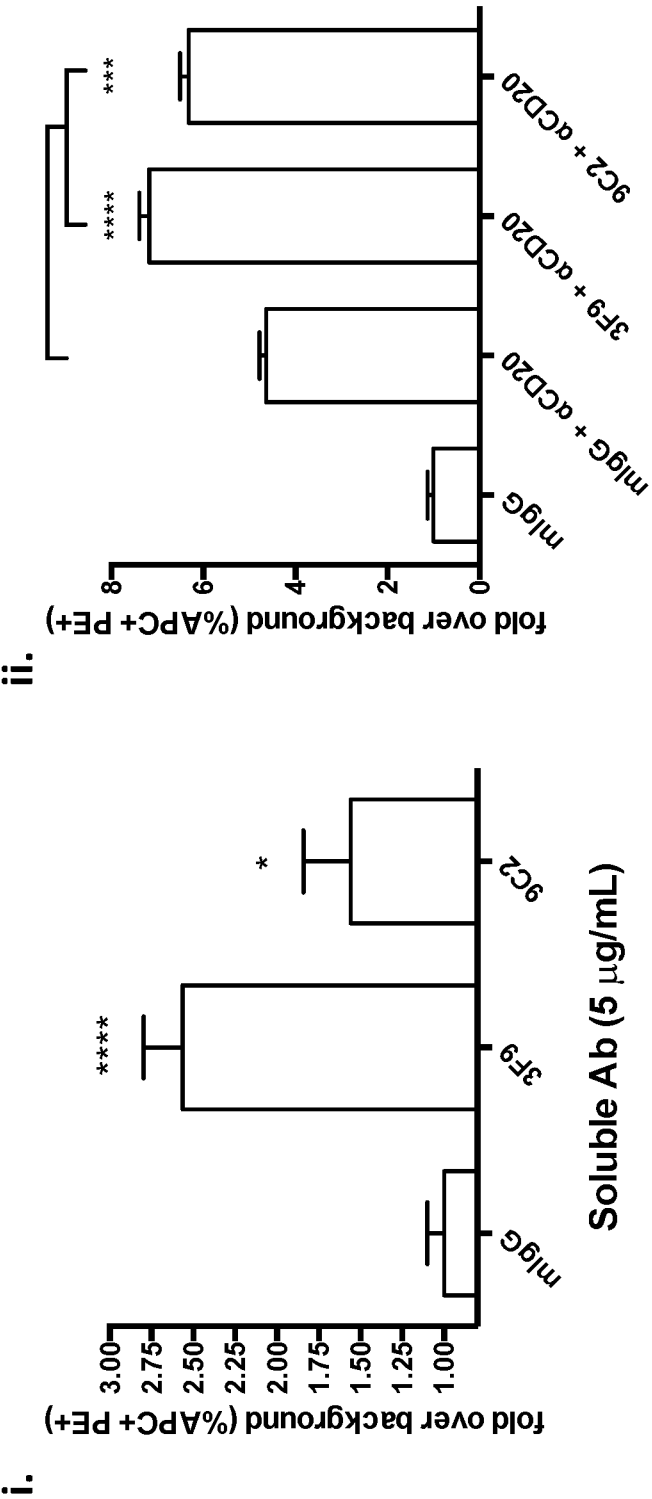


FIGURE 8C

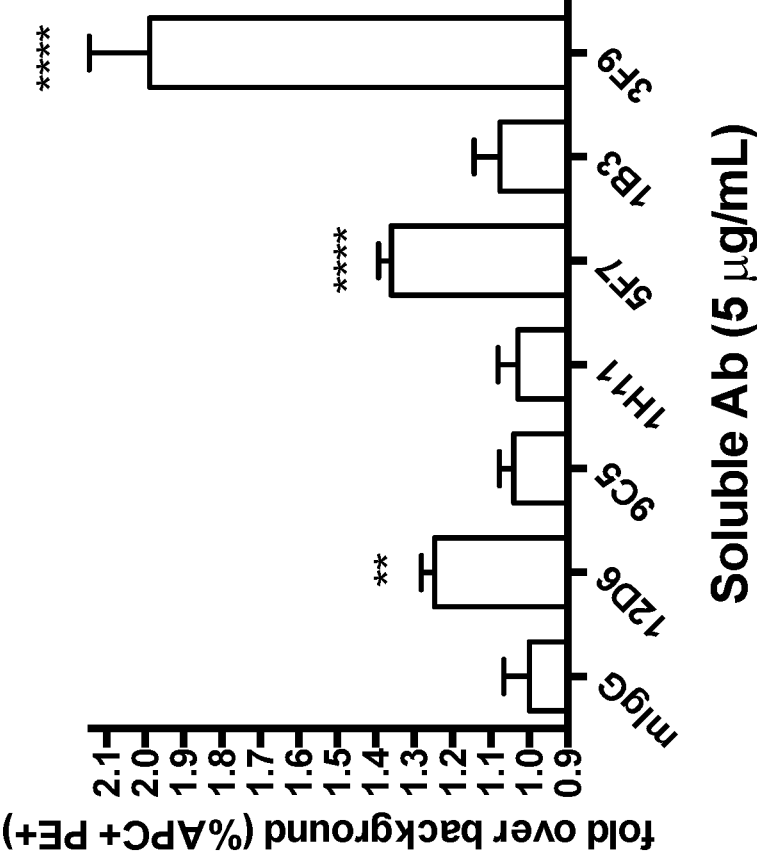


FIGURE 9A

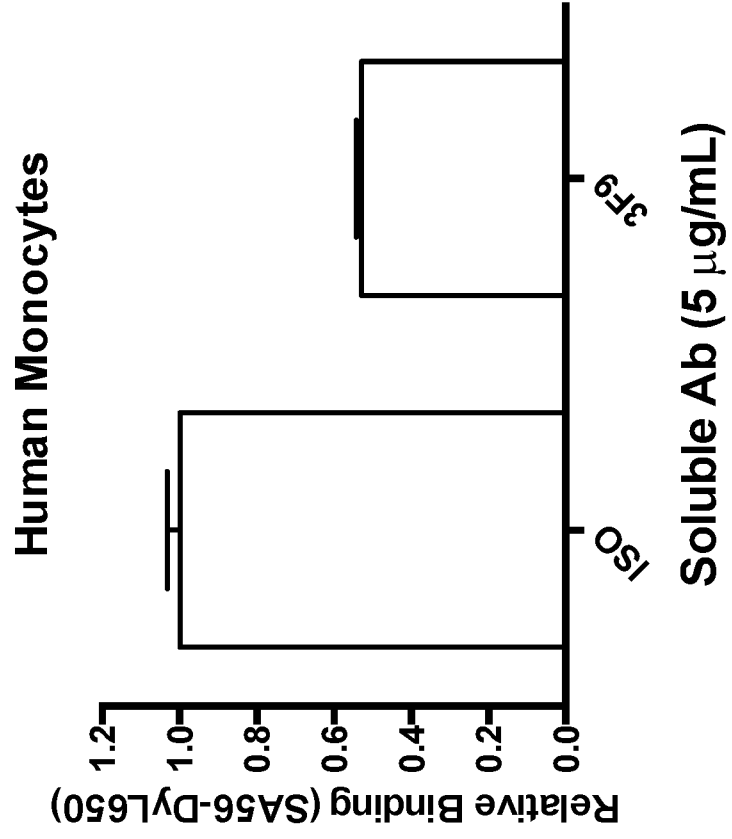


FIGURE 9B

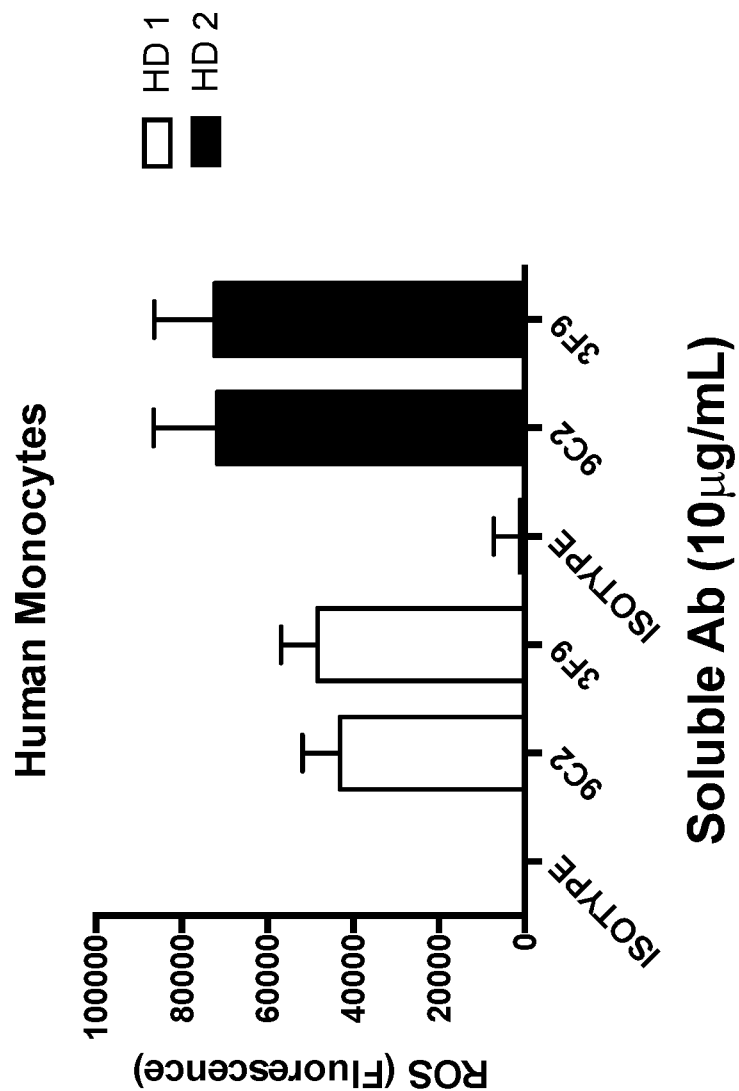


FIGURE 9C

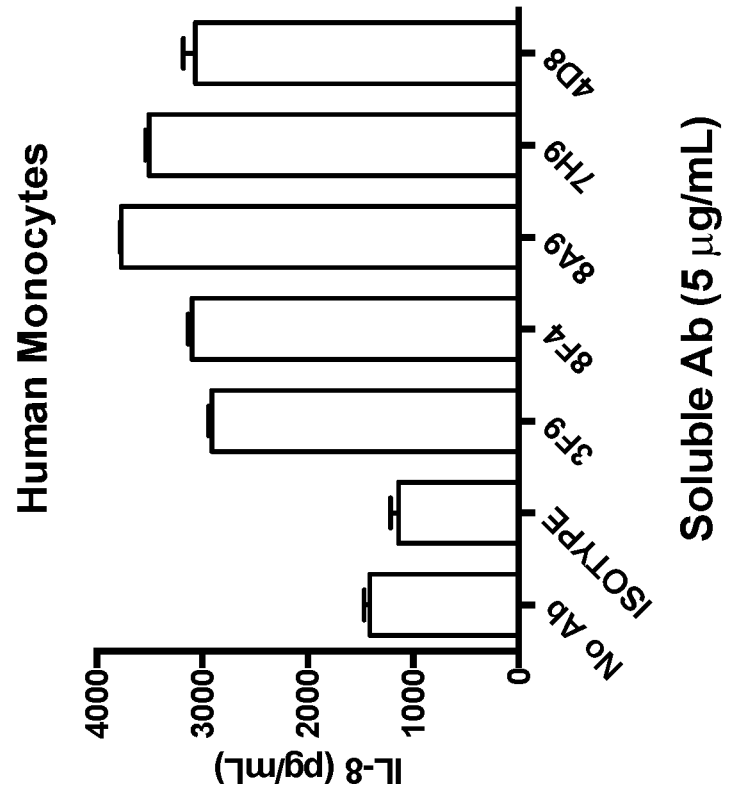


FIGURE 10A

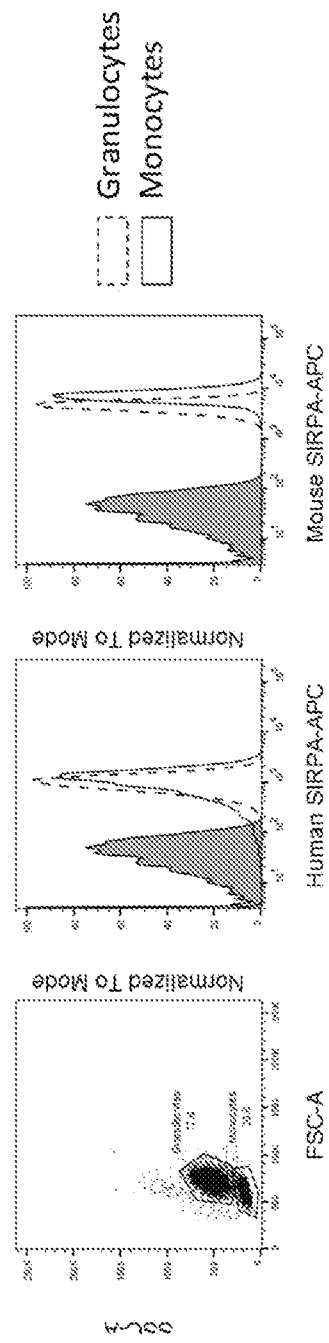


FIGURE 10B

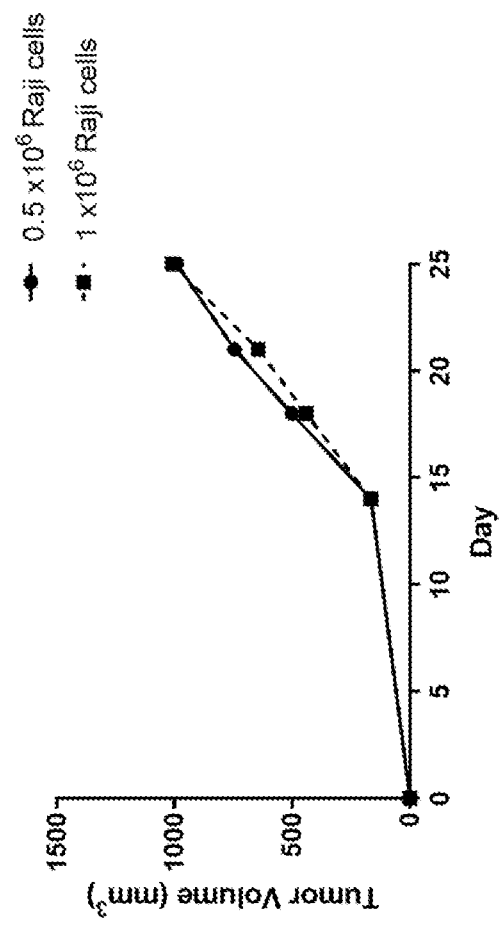


FIGURE 10C

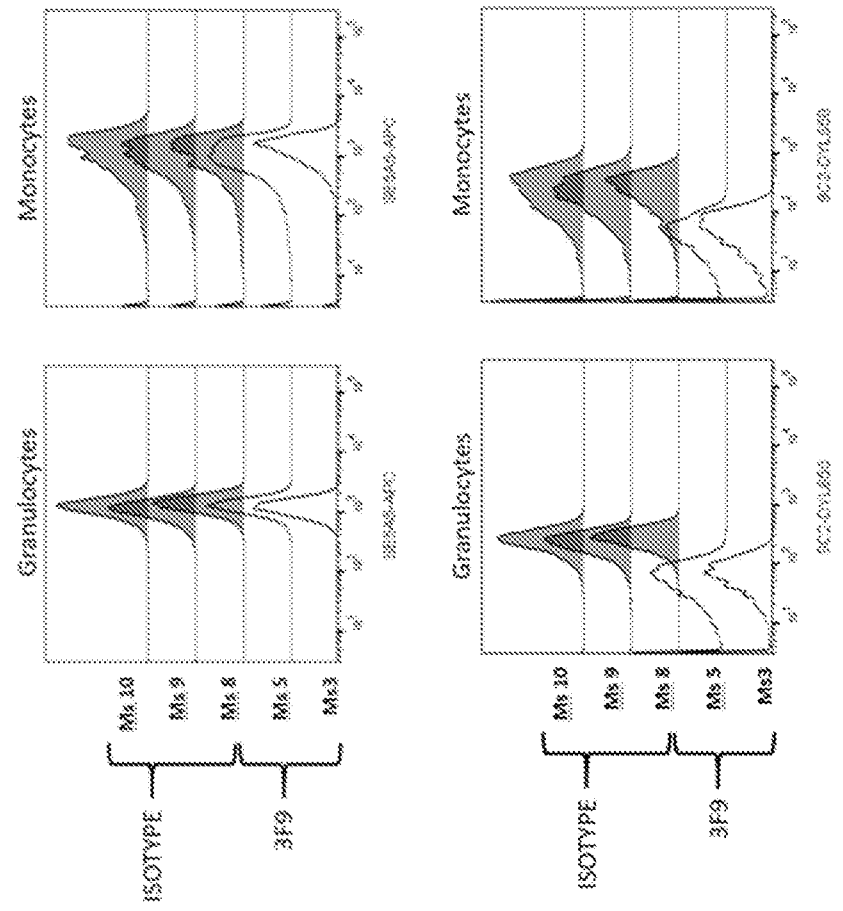


FIGURE 10D

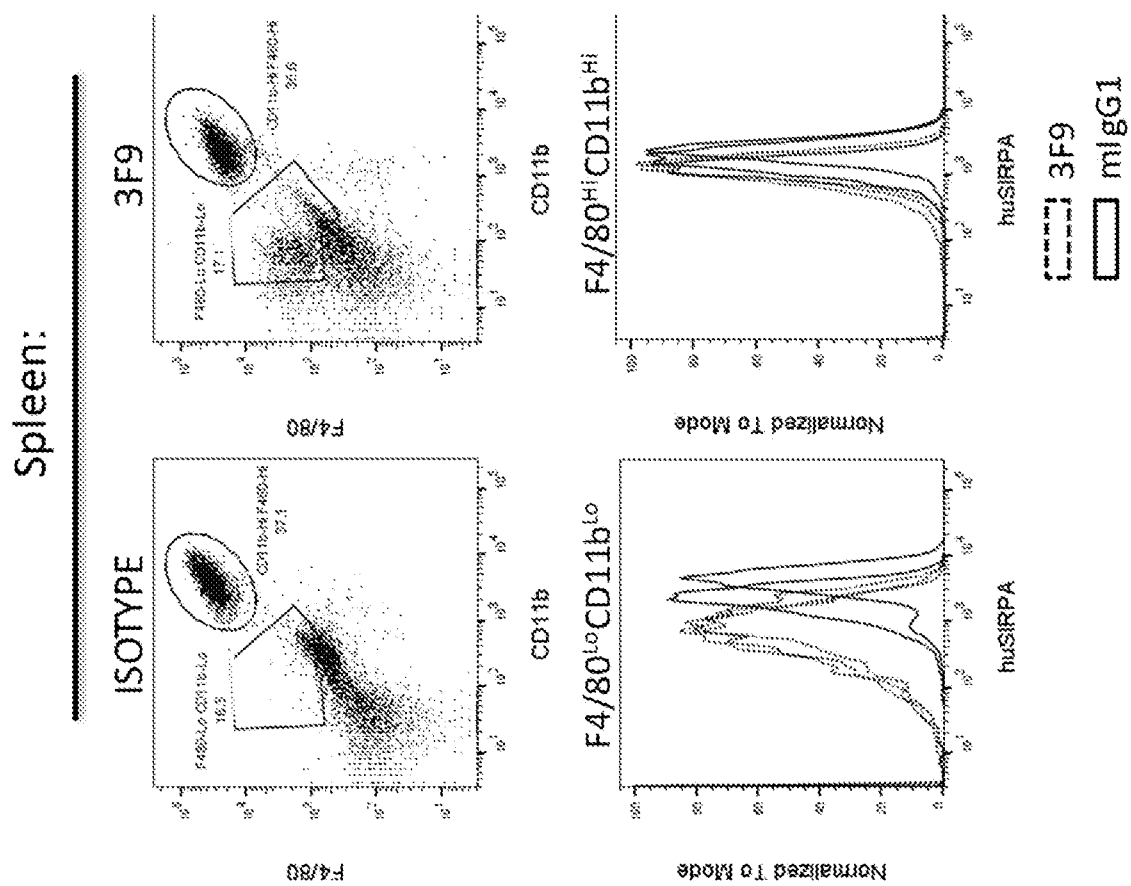


FIGURE 11A

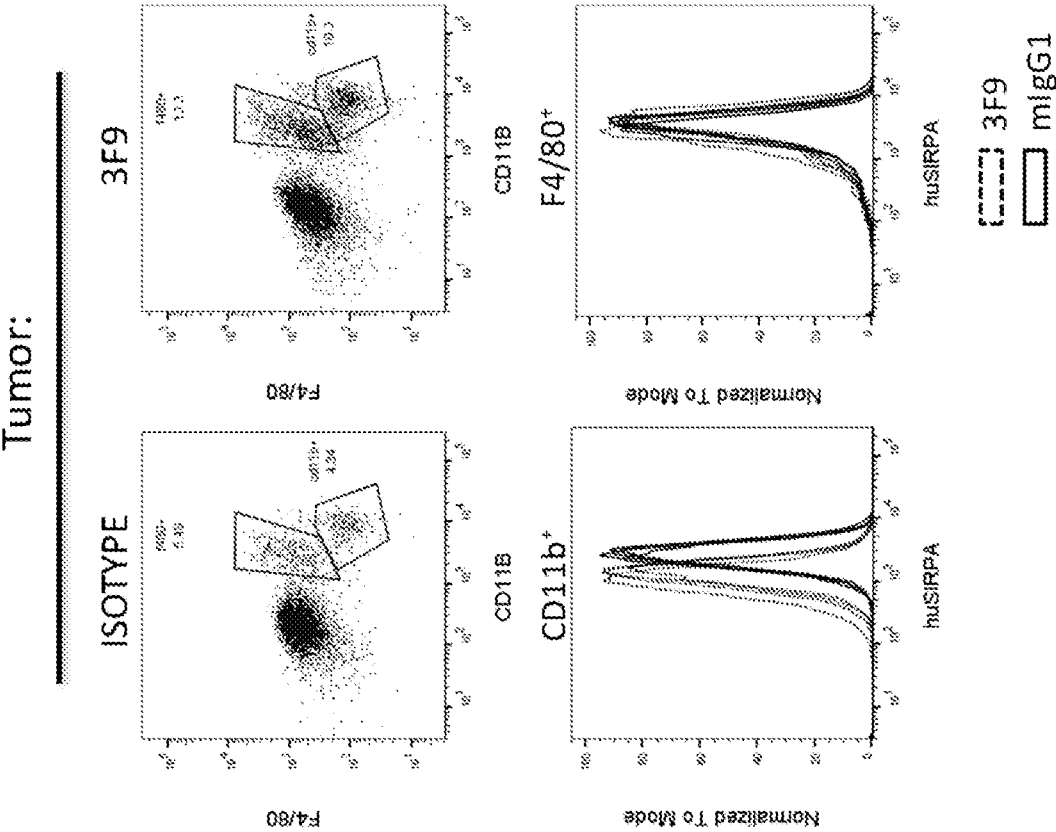


FIGURE 11B

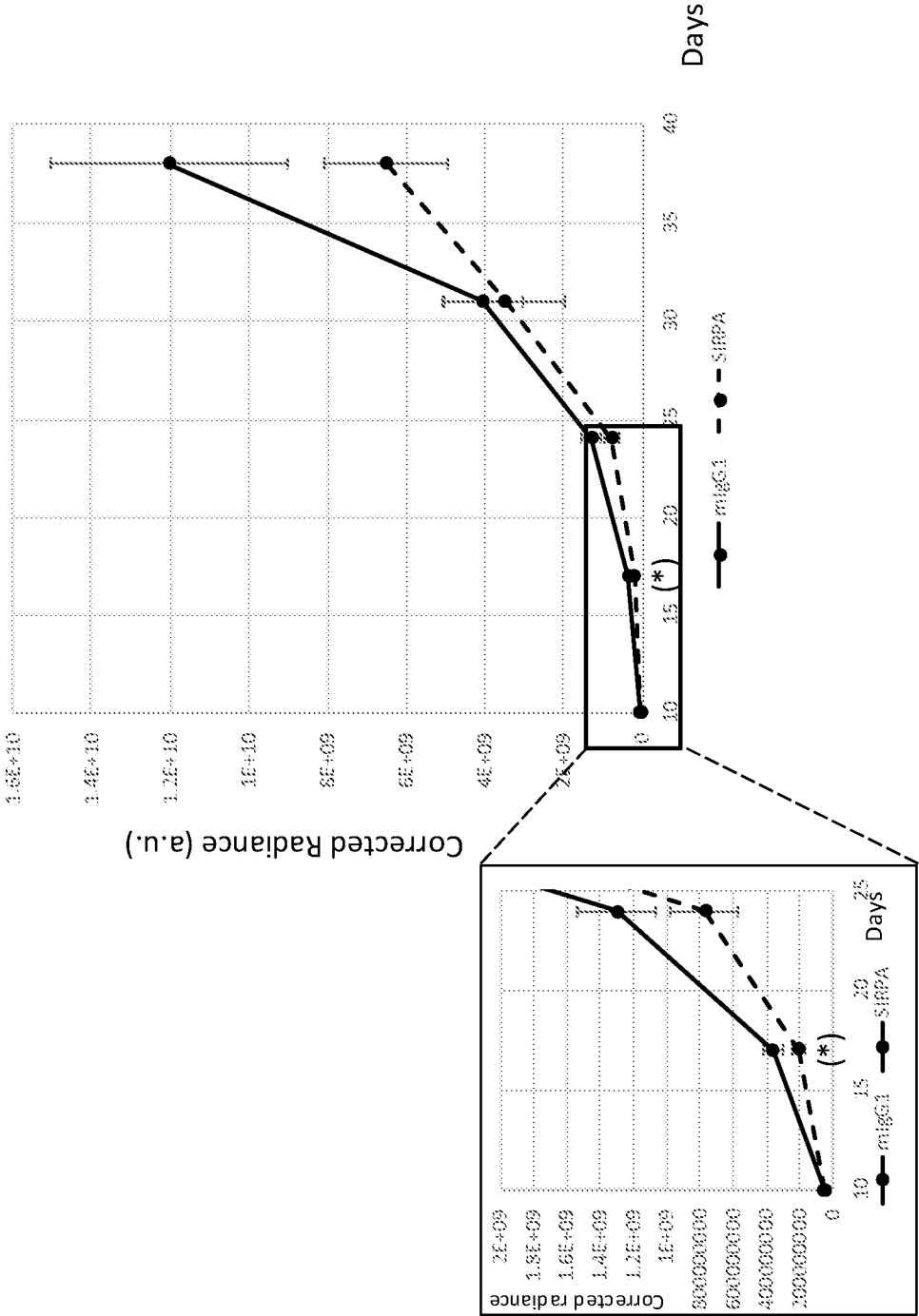


FIGURE 12B

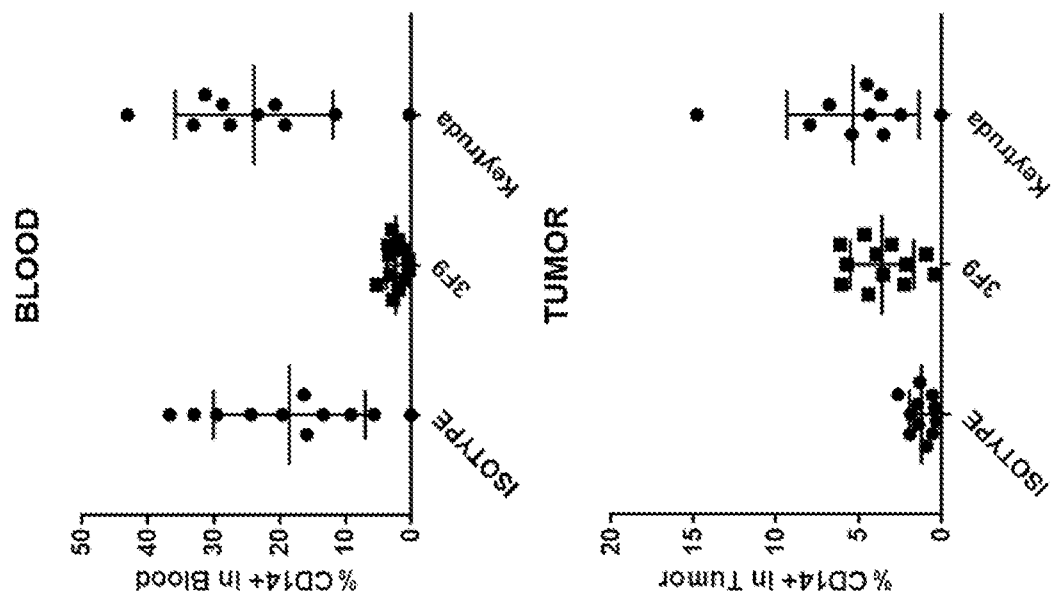


FIGURE 12A

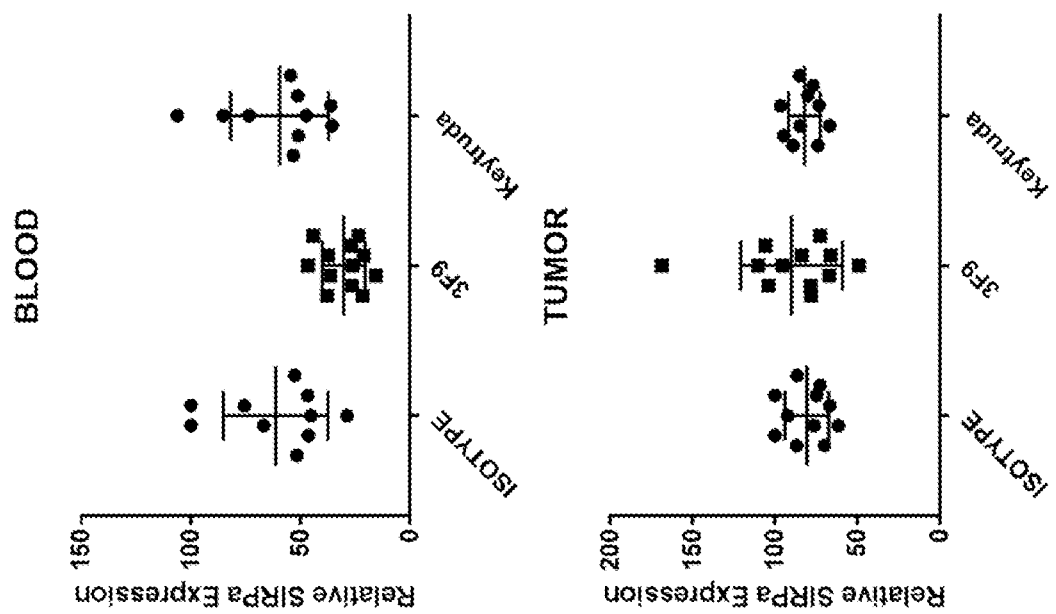


Figure 12C

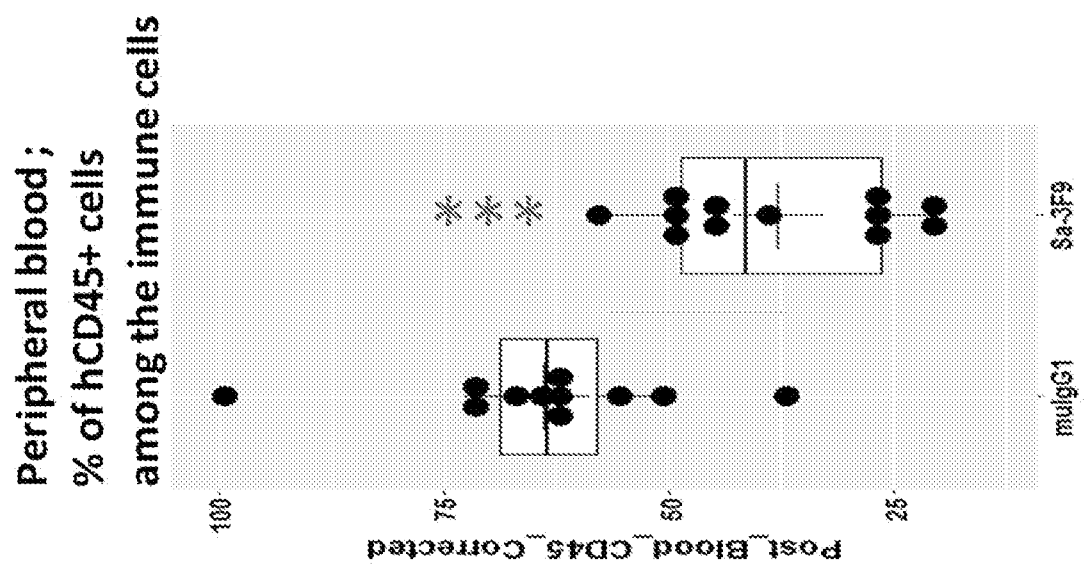


FIGURE 13A

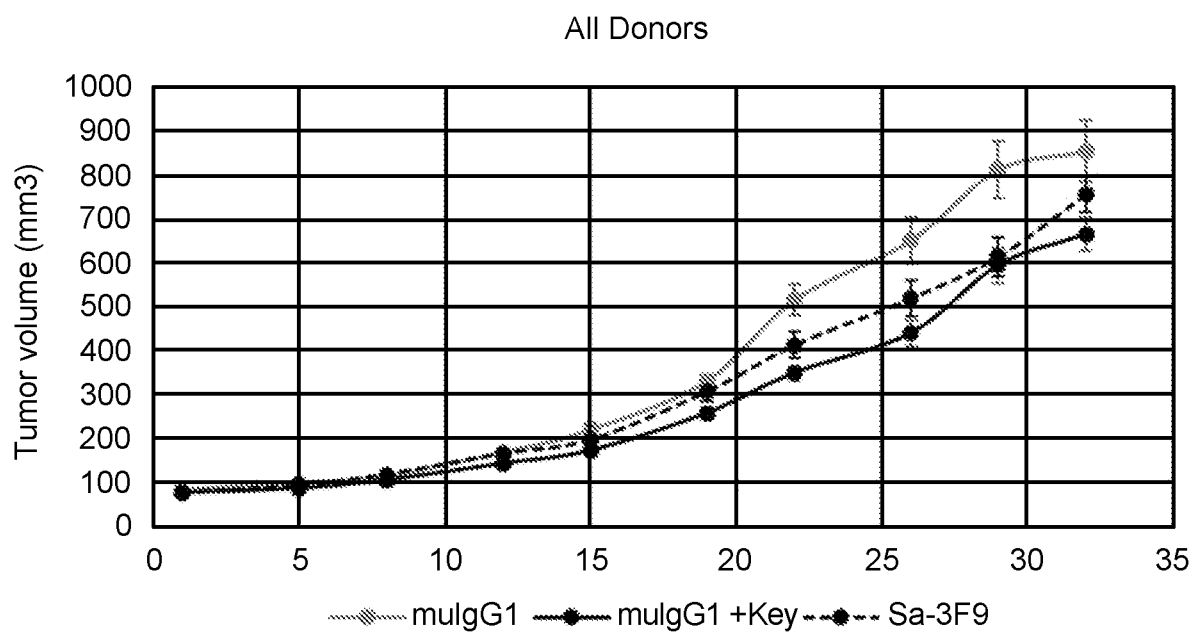


FIGURE 13B

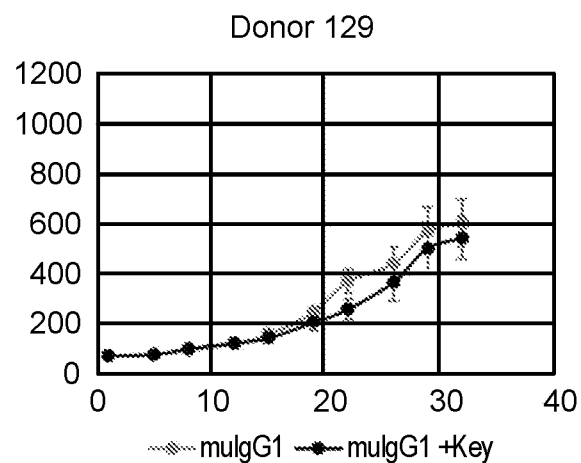
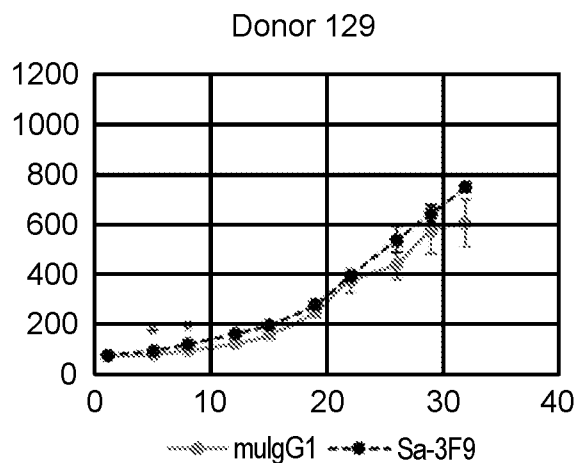
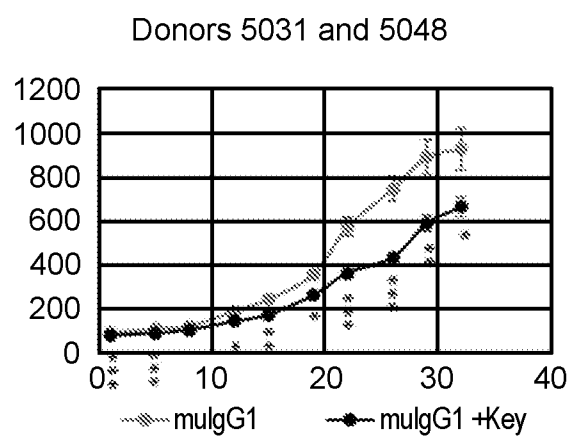
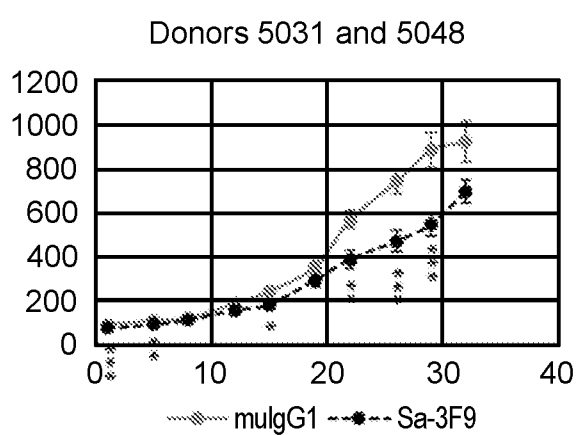


FIGURE 14A

Potential humanized sequence based on IGHV3-23*01 acceptor framework (AbM CDR definition)
 IGHV3-23*01 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPCKGLEWVSAISGSGSTYYADSVKQ
 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK

Joining region IMGT J00256|IGHJ4*01|YFDYWGQGGLVTVSS

seq	10	20	30	40	50	60
AbM	10	20	30	40	50	ab
	b b b	p p b b b	b b b	b i i	i i b b	b
SB-3F9						
	EVKLVESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQTPCKRLEWVA	TISDYGGSYTY		
	* * *	*	* * *	*		
IGHV3-23*01	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPCKGLEWVS	AISG-SGGSTY		
hSB-3F9-H1	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPCKGLEWVS	TISDYGGSYTY		
hSB-3F9-H2	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPCKGLEWVA	TISDYGGSYTY		

seq	70	80	90	100	110	120
AbM	60	70	80	abc	90	100abcd
	i b	b b b x	b b b b	b i b i b b	i b b b	
SB-3F9						
	YPDSVKGRFTISRDN	AKYTLYLQMNSLRS	EDTALYYCAR	PPYDDIYGGFAY	WCQGTILVTVSA	*
	*	* * *	* * *	*		
IGHV3-23*01	YADSVKGRFTISRDN	SKNTLYLQMNSLRAED	TAVYYCAK			
hSB-3F9-H1	YADSVKGRFTISRDN	SKNTLYLQMNSLRAED	TAVYYCAK	PPYDDIYGGFAY	WCQGTILVTVSS	
hSB-3F9-H2	YADSVKGRFTISRDN	SKNTLYLQMNSLRAED	TAVYYCAR	PPYDDIYGGFAY	WCQGTILVTVSS	

L

FIGURE 14B

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

IGKV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRAT

GIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQRSNWPP

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 b	i i i	i
SB-3F9	DIVLTQSPASLAVSLQQRATISC	RASKSVSSSGYSYMH	WYQKPGQAPRLLIY	LASNLES		
	*	* * * *	*	*	*	*
3-11*01	EIVLTQSPATLSLSPGERATLSC	RASQSVS----	SYLA	WYQKPGQAPRLLIY	DASNRAT	
hSB-3F9-L1	EIVLTQSPATLSLSPGERATLSC	RASKSVSSSGYSYMH	WYQKPGQAPRLLIY	LASNLES		
hSB-3F9-L2	EIVLTQSPATLSLSPGERATLSC	RASKSVSSSGYSYMH	WYQKPGQAPRLLIY	LASNLES		
hSB-3F9-L3	EIVLTQSPATLSLSPGERATLSC	RASKSVSSSGYSYMH	WYQKPGQAPRLLIY	LASNLES		

seq	70	80	90	100	110
AbM	60	70	80	90	100
	b b	b b b	b b b	i b i	b b b
SB-3F9	GVPARFSGSGSGTDFTLTINIHVFEEDAAATYYC	QHNREL	PCT	FCG	GTKLEIK
	*	* * * *	*	*	*
3-11*01	GIPARFSGSGSGTDFTLTISSELEPEDFAVYYC	QQRSNWPP			
hSB-3F9-L1	GIPARFSGSGSGTDFTLTISSELEPEDFAVYYC	QHNREL	PCT	FCG	GTKLEIK
hSB-3F9-L2	GVPARFSGSGSGTDFTLTISSELEPEDFAVYYC	QHNREL	PCT	FCG	GTKLEIK
hSB-3F9-L3	GVPARFSGSGSGTDFTLTISSELEPEDFAVYYC	QHNREL	PCT	FCG	GTKLEIK

FIGURE 14C

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

RVTNTRDTSTSTVYMELSSLRSEDTAVYYCAR

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	EFQLQSGAEVKKPGASVKISCKAS	GYSLTGYNMN	WVKQSRGKSLIEWIG	NINPHYGSST	
	** *	** *	** *	** *	
IGHV1-46*01	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTSYMM	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	WGQGITLVSS			
	* * * * *	* * * *	* *			
IGHV1-46*01	YAQKFPQGRVTMTNTRDTSTSTVYMELSSLRSEDTAVYYCAR					
hSB-9C2-H1	YAQKFPQGRVTMTNTRDTSTSTVYMELSSLRSEDTAVYYCAR	EGYDGVFDY	WGQGITLVSS			
hSB-9C2-H2	YAQKFPQGRVTMTNTRDTSTSTVYMELSSLRSEDTAVYYCAR	EGYDGVFDY	WGQGITLVSS			
hSB-9C2-H3	YAQKFPQGRATLTNDTSTSTAYMEFSSLRSEDTAVYYCAR	EGYDGVFDY	WGQGITLVSS			
hSB-9C2-H4	YAQKFPQGRATLTNDKSTSTAYMEFSSLRSEDTAVYYCAR	EGYDGVFDY	WGQGITLVSS			
N						

FIGURE 14D

Potential humanized sequence based on IGV3-11*01 acceptor framework (AbM CDR definition)

IGKV3-11*01 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLLIYDASNRAT

GIPARFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPP

Joining region IMGT J00242|IGKJ2*01|YTFGQGTKLEIK

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 b i i i	i i b b i	i
	QIVLSQSPAILASAPGKVTMT	RASSSVS-YMH	WYQKPGQAPRPWIY	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	WYQKPGQAPRPPWIY	VTSNLAS	
hSB-9C2-L4	EIVLTQSPATLSLSPGERVTMSC	RASSSVS-YMH	WYQKPGQAPRPPWIY	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 b b b b	i b i b i	i b i b b	b b b
	GVPTRFSGSGSGTSSYSLTISRVEADAATYYC	QQWSSNPRT	FGGGTKLEIK		
	* * * * *	** * * *	*		
3-11*01	GIPARFSGSGSGTDFTLTISLSEPEDFAVYYC	QQRSNWPP			
hSB-9C2-L1	GIPARFSGSGSGTDFTLTISLSEPEDFAVYYC	QQWSSNPRT	FGGGTKLEIK		
hSB-9C2-L2	GIPARFSGSGSGTDFTLTISLSEPEDFAVYYC	QQWSSNPRT	FGGGTKLEIK		
hSB-9C2-L3	GIPARFSGSGSGTDFTLTISLSEPEDFAVYYC	QQWSSNPRT	FGGGTKLEIK		
hSB-9C2-L4	GVPARFSGSGSGTDFTLTISLSEPEDFAVYYC	QQWSSNPRT	FGGGTKLEIK		

A

#

Figure 15A

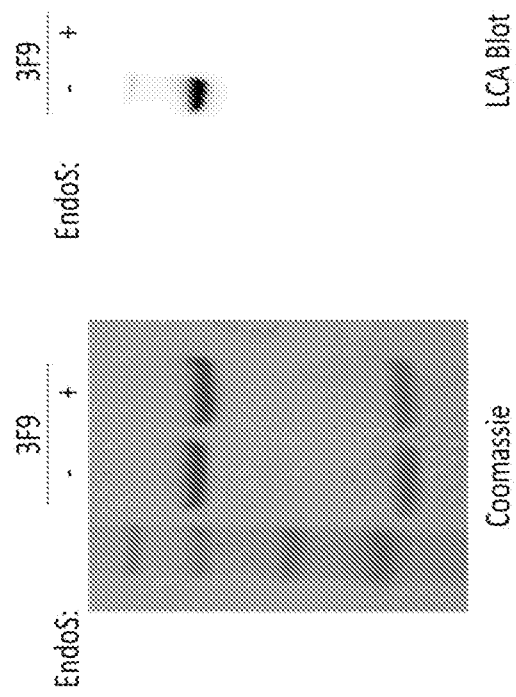


Figure 15B

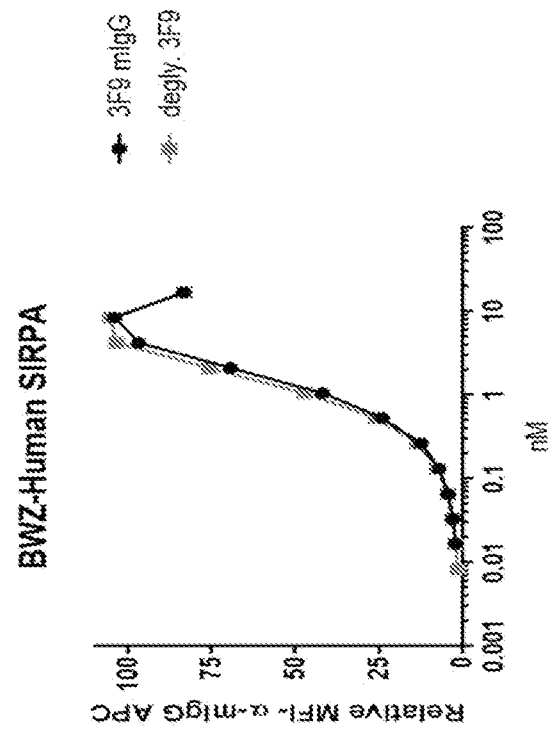


Figure 16

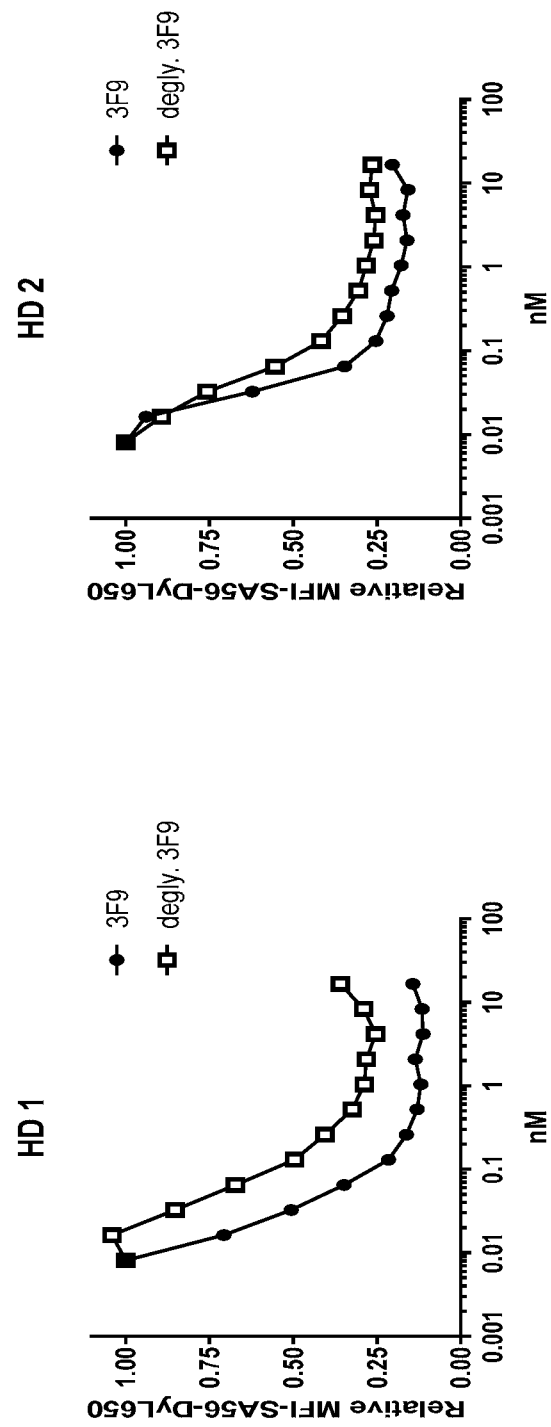


Figure 17A

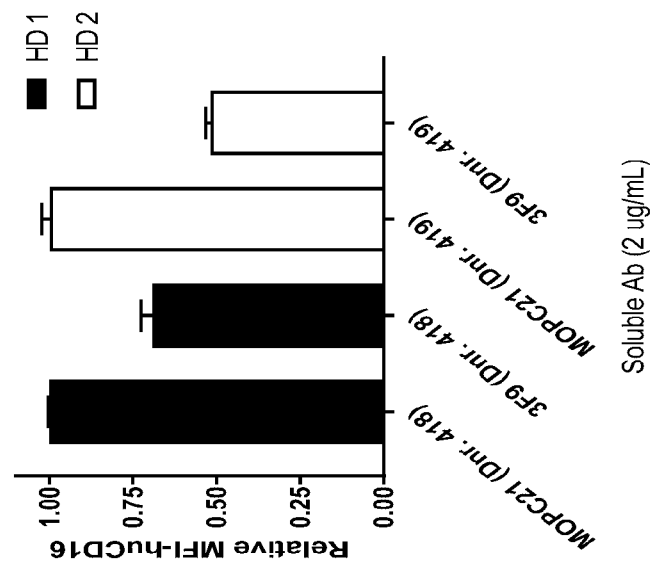


Figure 17B

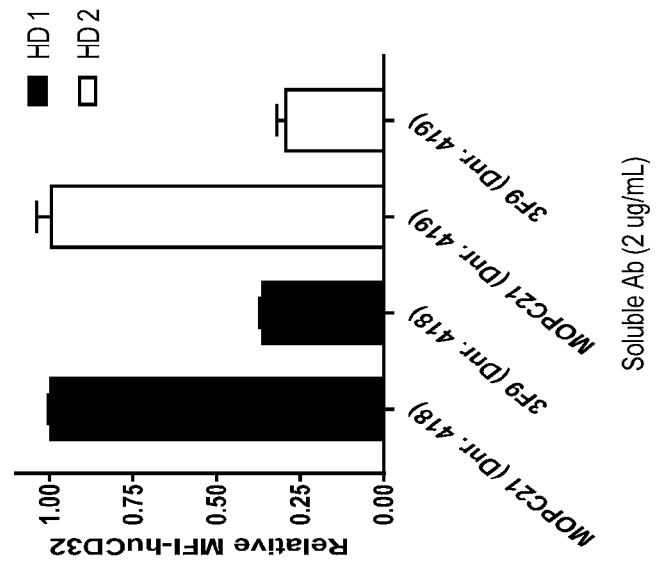


Figure 18

