

FIGURE 1**Figure 1A**

DIQMTQSPSSLSASVGDRVITITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVP
SRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPTFGGQGTKVEIK
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDYSLSSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 1B

gacatccagatgacccagtcctccatcctccctgtctgcatctgtaggagacagagtcacc
D I Q M T Q S P S S L S A S V G D R V T
atcacttgccgggcaagtcagagcatttagcagctacttaaattggtatcagcagaaacca
I T C R A S Q S I S S Y L N W Y Q Q K P
gggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtgggtcccatca
G K A P K L L I Y A A S S L Q S G V P S
aggttcagtggcagtggtatctgggacagatttcactctcaccatcagcagctctgcaacct
R F S G S G S G T D F T L T I S S L Q P
gaagattttgcaacttactactgtcaacagagttacagtacccctccaacgttcggccaa
E D F A T Y Y C Q Q S Y S T P P T F G Q
gggaccaaggtggagatcaaa
G T K V E I K

Figure 1C

cgaactgtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatct
R T V A A P S V F I F P P S D E Q L K S
ggaactgcctctgttggtgtgctgaataacttctatcccagagaggccaaagtacag
G T A S V V C L L N N F Y P R E A K V Q
tggaaggtggataacgcctccaatcgggtaactcccaggagagtggtcacagagcaggac
W K V D N A L Q S G N S Q E S V T E Q D
agcaaggacagcacctacagcctcagcagcaccctgacgctgagcaaagcagactacgag
S K D S T Y S L S S T L T L S K A D Y E
aaacacaaagtctacgcctgcgaagtcacccatcagggcctgagctcgcccgtcacaaag
K H K V Y A C E V T H Q G L S S P V T K
agcttcaacaggggagagtggttag
S F N R G E C -

Figure 1D

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG
TDFTLTISLQPEDFATYYCQQSYSTPPITFGQGTRLEIK

Figure 1E

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSG
TDFTLTISLQPEDFATYYCQQSYSTP

FIGURE 2**Figure 2A**

VH: dependent on the MF (target): Figure 3.

Figure 2B

```
gctagcaccaagggcccatcggtcttccccctggcaccctcctccaagagcacctctggg
A S T K G P S V F P L A P S S K S T S G
ggcacagcgggccctgggctgcttgggtcaaggactacttccccgaaccggtgacggtgtcg
G T A A L G C L V K D Y F P E P V T V S
tggaactcaggcgccctgaccagcggtgcacaccttcccggtgtcctacagtcctca
W N S G A L T S G V H T F P A V L Q S S
ggactctactccctcagcagcgctcgtgaccgtgccctccagcagcttgggcaccagacc
G L Y S L S S V V T V P S S S L G T Q T
tacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagtt
Y I C N V N H K P S N T K V D K R V
```

Figure 2C

```
gagcccaaactcttgtgacaaaactcacacatgcccaccgtgccc
E P K S C D K T H T C P P C P
```

Figure 2D

```
gcacctgaactcctgggggggaccgtcagttcttcttccccccaaaacccaaggacacc
A P E L L G G P S V F L F P P K P K D T
ctcatgatctcccggaaccttgaggtcacatgcgtgggtgggacgtgagccacgaagac
L M I S R T P E V T C V V V D V S H E D
cctgaggtcaagttcaactggtacgtggacggcggtggaggtgcataatgccaagacaaag
P E V K F N W Y V D G V E V H N A K T K
ccgcgaggaggagcagtacaacagcacgtaccgtgtgggtcagcgctcctcaccgtcctgcac
P R E E Q Y N S T Y R V V S V L T V L H
caggactgggtgaatggcaaggagtacaagtgaagggtctccaacaaagccctcccagcc
Q D W L N G K E Y K C K V S N K A L P A
cccatcgagaaaaccatctccaaagccaaa
P I E K T I S K A K
```

Figure 2E

gcacctgaactcggcaggggacgcgtcagttcttcttccccccaaaacccaaggacacc
A P E L G R G P S V F L F P P K P K D T
ctcatgatctcccggaacctgaggtcacatgcgtggtggtggacgtgagccacgaagac
L M I S R T P E V T C V V V D V S H E D
cctgaggtcaagttcaactggtagcgtggacggcgtggaggtgcataatgccaagacaaag
P E V K F N W Y V D G V E V H N A K T K
ccgcgaggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcacgcgtcctgcac
P R E E Q Y N S T Y R V V S V L T V L H
caggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcc
Q D W L N G K E Y K C K V S N K A L P A
cccatcgagaaaaccatctccaaagccaaa
P I E K T I S K A K

Figure 2F

gggcagccccgagaaccacaggtgtacaccaagcccccatcccgggaggagatgaccaag
G Q P R E P Q V Y T K P P S R E E M T K
aaccaggtcagcctgaagtgcctgggtcaaaggcttctatcccagcgacatcgccgtggag
N Q V S L K C L V K G F Y P S D I A V E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
W E S N G Q P E N N Y K T T P P V L D S
gacggctccttcttctctatagcaagctcacgcgtggacaagagcaggtggcagcagggg
D G S F F L Y S K L T V D K S R W Q Q G
aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
N V F S C S V M H E A L H N H Y T Q K S
ctctccctgtctccgggttga
L S L S P G -

Figure 2G

gggcagccccgagaaccacaggtgtacacgcaccccccatcccgggaggagatgaccaag
G Q P R E P Q V Y T D P P S R E E M T K
aaccaggtcagcctgacctgcgaggtcaaaggcttctatcccagcgacatcgccgtggag
N Q V S L T C E V K G F Y P S D I A V E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
W E S N G Q P E N N Y K T T P P V L D S
gacggctccttcttctctatagcaagctcaccggtggacaagagcaggtggcagcagggg
D G S F F L Y S K L T V D K S R W Q Q G
aacgtcttctcatgctccgtgatgcatgaggtctgcacaaccactacacgcagaagagc
N V F S C S V M H E A L H N H Y T Q K S
ctctccctgtctccgggttga
L S L S P G -

FIGURE 3**Figure 3A**

MF6076

QVQLQESGPGLVKPSETLSLTCTVSTDSLGEYFWSWIRQPPGKGLEWIGYIYYSGSAN
FNPSLKSRVTMSIDTSNNQFSLKLRSVTAADTAVYFCARGGYTGYGGDWFDPWGQG
TLVTVSS

MF6226

QVQLQESGPGLVKPSETLSLTCTVSGDSIGYYFWSWIRQPPGKGLEWIGYVYYSGSNN
LNPSLKSRVTLSVDTSKNQFSLRLNSMTAADTAVYYCARGGYSGYGGDSFDLWGQGT
TVTVSS

MF6236

QVQLQESGPGLVKPSETLSLTCTVSGGSIGYYFWSWIRQPPGKGLEWIGYIYYSGSTN
FNPSLKSRVTMSVDTSKNQFSLNLRSVTTADTAVYYCARGGYTGHGGDWFDPWGQG
TLVTVSS

MF6256

EVQLVQSGAEVKKPGSSMKVSCKASGGTFSSYVISWVRQAPGQGLEWMGMIIPVFDT
SSYEKKFQGRITIIADKSTSTVYLELSSLRSEDAAVYYCARGTVEATLLEFDFWGQGTLV
TVSS

MF6930

EVQLVQSGAEVKKPGSSMKVSCKASGGTFSSYVISWVRQAPGQGLEWMGMIIPVFET
ATYEKKFQGRVTIIADKSTSTVYMELSSLRSEDAAVYYCARGTVEATLLEFDYWGQGT
VTVSS

MF6932

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGMIIPFFDT
ANYAQKFQGRVTITADKSTSTASMELRSLRSEDTAVYYCARGTVSATLLEFDYWGQGT
LTVSS

MF6935

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYVISWVRQAPGQGLEWMGMIIPIFDT
ANYAQKFQGRVTITADKSTSTASMELRSLRSED~~TAVYYCARGTVSGTLVF~~EDYWGQGT
LVTVSS

MF6936

EVQLVQSGAEVKKPGSSVKVSCKASGDTFSNYVINWVRQAPGQGLEWMGMIIIPVFDT
TSYERKFQGRVTITADKSTSTAYMELTSLRSED~~TAVYYCARGTVGATLL~~FDN~~WGQGT~~
LVTVSS

MF6972

EVQLQESGPGLVKPSETLSLTCTVSGGSISTYFWSWIRQPPGKGLEWIGYIIYSGSTNY
NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSGYGGDDFDI~~WGQGT~~M
VTVSS

MF6974

EVQLVESGGDLVQPGGSLRLSCAASGFTFNSYAMSWVRQAPGKGLEWVSTISGGGA
NIYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYFCASPYGSGYFDV~~WGQGT~~L
VTVSS

MF6982

EVQLVESGGDLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGGGTN
IYYADSVKGRFTISRDNSKNTLFLQMNSLRAGDTAVYYCASPYGSGYLDV~~WGQGT~~LV
TVSS

Figure 3B

MF7100

EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDTHWVRQAPGKGLEWVAVISYDGSN
KYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCARERGWDVFDIWGQGTL
VTVSS

MF7111

QVQLQESGPGLVKPSETLSLTCTVSDDSISDYYWSWIRQPPGKGLEWIGYIYYSGNTK
YNPSLKNRVTISVDTSKSKQFSLKLTSVTAADTAVYYCARIPLTGEFDYWAQGTLVTVSS

MF7116

EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYHGS
DKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDGDNDVFDIWGQG
TLVTVSS

MF7118

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSISGGGVS
TFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIVPAAATPSGTYYWIFDL
WGRGTLVTVSS

MF7134

EVQLVQSGSELKKPGASVKVSCKASGYTFTTNALNWVRQAPGQGLEWMGWINTHTG
NPTYAQGFIGRFVFSLDTSVSTAYLQIRSLKAEDTAVYYCAREPNWGVYFDYWGQGTL
LTVTVSS

MF7136

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSAISGSGRS
TTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDSTYYTSGSYSVFDY
WGQGTLVTVSS

MF7137

QVQLVQSGAEVKRPGASVKVSCVSGYTLTELSMHWVRQAPGKGLEWMGGSDPEH
GETVDAQKFQGRVTMTEDTSTD TAYMELSSLRSEDTAVYYCTTGGTYYYGSGSYITL
DFWGQGTLLTVSS

MF7142

QVQLVQSGAEVRKPGSSVMVSCKASGGTFNTYAINWVRQAPGQGLEWMGGIPIFGT
PYYGQRFQGRVTITADKSTNTVFMELSSLRSEDTAMYFCARERDIGSLYYFDSWGQG
TLTVSS

MF7146

EVQLVQSGAEVKKPGSSVKVSCKASGGTFNNYFITWVRQAPGQGLEWMGGIIPSEFGT
GNYAQKFQGRVAITADKSTNTAYMELSSLRSEDTAIYYCVRDREVGAIYYFDYWGQG
TMVTVSS

MF7165

QVQLVQSGAEVRKPGASVKVSCVSGYTLTELSIHWVRQAPGKGLEWMGAFDPEDG
ETIYAQKFQGRVTMTEDTSTD TAYMELSSLRSEDTAVYFCATGGTYYYGSGSYITLDY
WGQGTLLTVSS

MF7167

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGSGVS
TYYADSVKGRFTISRDN SKNTLYLQMNTLRAEDTAVYYCAKDRGYDYSYHNWFD
PWGQGTLLTVSS

MF7185

QVQLVQSGAEVKKPGSSVKVSCKTSGGTFSNYA FSWVRQAPGQGLEWMGGIPIFGS
TNYAQSFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDREMGTLYFFDQWGQG
TTVTVSS

MF7443

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGS
TTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDTSTWQRGGYKAFDY
WGQGTLVTVSS

MF7444

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGS
TTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDTGQSWSNYYHAFDY
WGQGTLVTVSS

MF7515

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYSG
NTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARRPGPALGDLDSWGQ
GTLVTVSS

MF7518

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYSG
NTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARDGSGWDDFDYWGQ
GTLVTVSS

MF7096

QVQLQESGPGLVRPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIDYSGSTNY
NPSLKSRVTISVDTSKTQFSLKLSSVSAADTAVYYCAKDLLYKWNYVEGFDIWGQGT
TVSS

MF7097

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIDYSGTTN
FNPSLKSRVTISVDTSKTQFSLKLSSVSAADTAVYYCAKDLLYKWNYVEGFDIWGQGT
MTVSS

MF7106

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSKYVVSWVRQAPGQGFDWMGGIIPMEG
TANYAQMFQGRVTITADKSTSTVNMELSSLRSEDTAVYYCVRDKAVAGLYYFDSWGQ
GTLVTVSS

MF7120

QVQLVQSGAEVKKPGSSVKVSCKASGDTFSTYAINWIRQAPGQGLEWMGGIPIFGTA
YYAQEFQDRVTITADKSTSTGYMEMSSLISEDTAVYYCARERELGALYAFDIWGQGT
MVTVSS

MF7133

EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHAISWVRQVPGQGLEWMGGIIPLFDT
AKNAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARDRETGTLYYFDYWGQG
TLVTVSS

MF7139

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNFAFSWVRQAPGQGLEWMGGIIPMFD
TAKYAQKFQGRVTIADKSTNTAYMDLNSLRSEDTAVYYCVRDDRAIGTLYYFDYWGQ
GTLVTVSS

MF7144

QVQLVQSGAEVRKPGSSVMVSCKASGGTFSTYAINWLRQAPGQGLEWMGGIPIFGT
PYYGQRFQGRVTITADKSTNTVFMELSSLRSEDTAIYYCARDDRDSGGLYYFDSWGQG
TLVTVSS

MF7524

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYSG
NTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDTAVYYCARGSILAAQMWGDIWG
QGTTLVTVSS

FIGURE 4

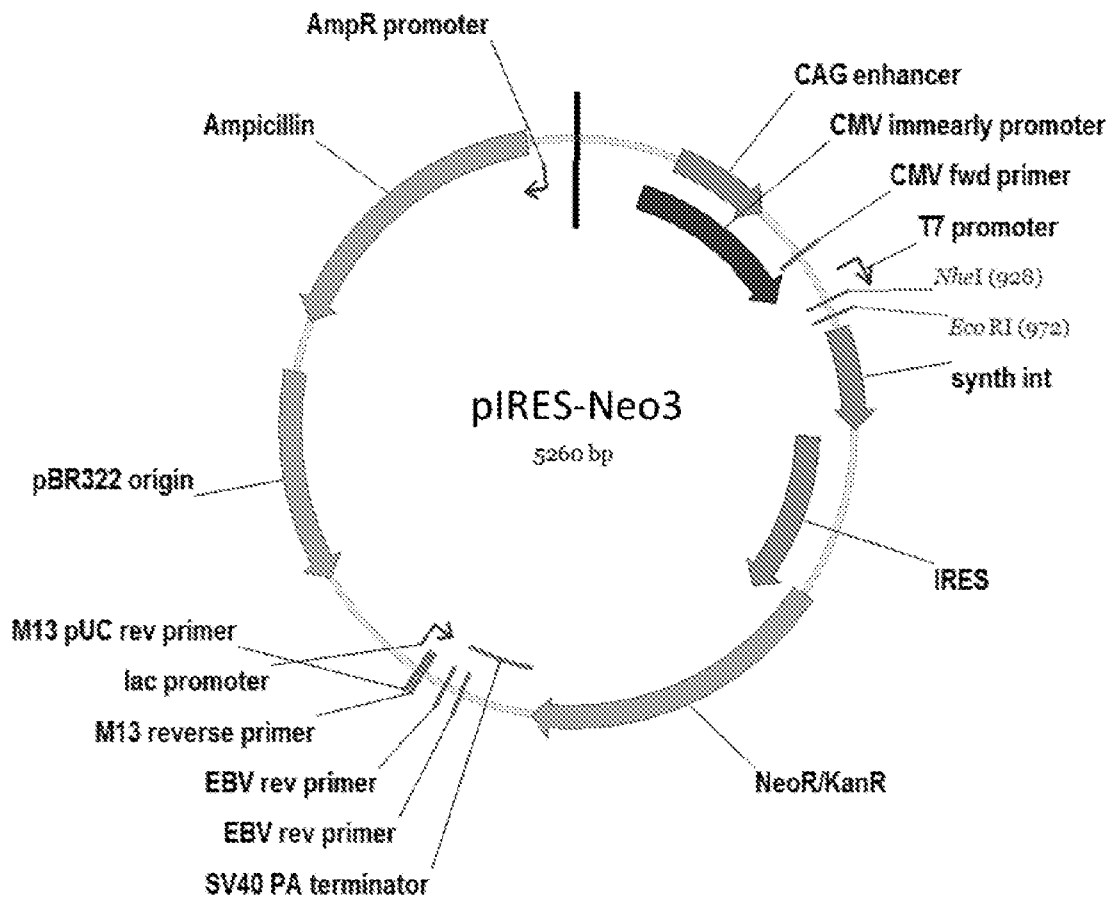


FIGURE 5

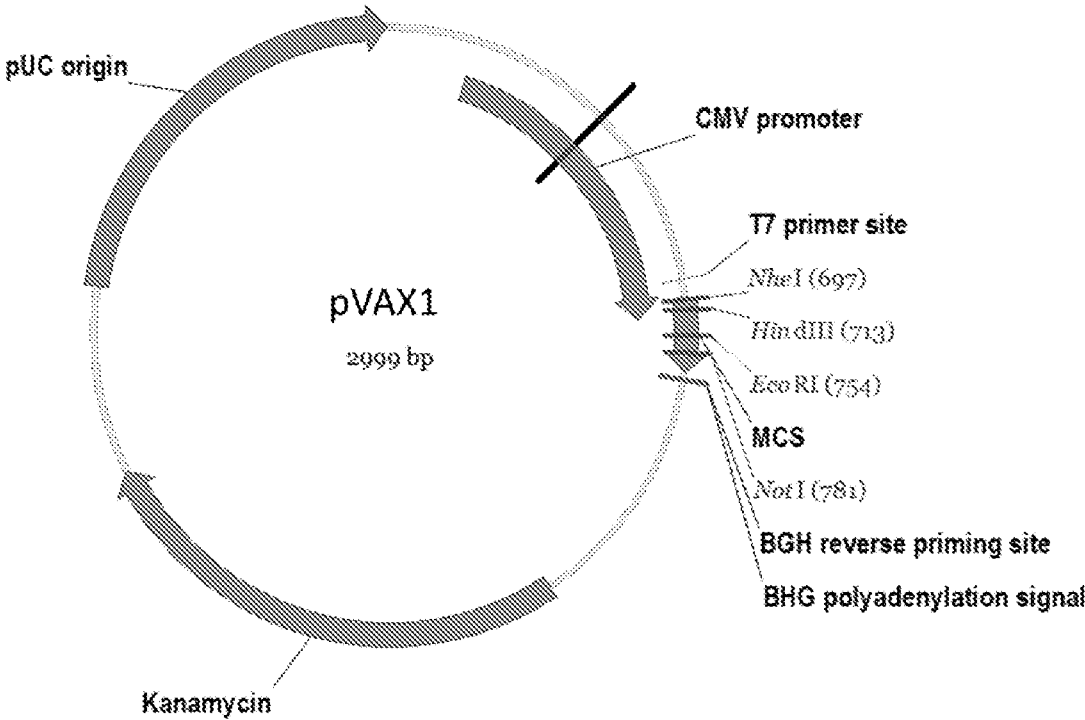


FIGURE 6

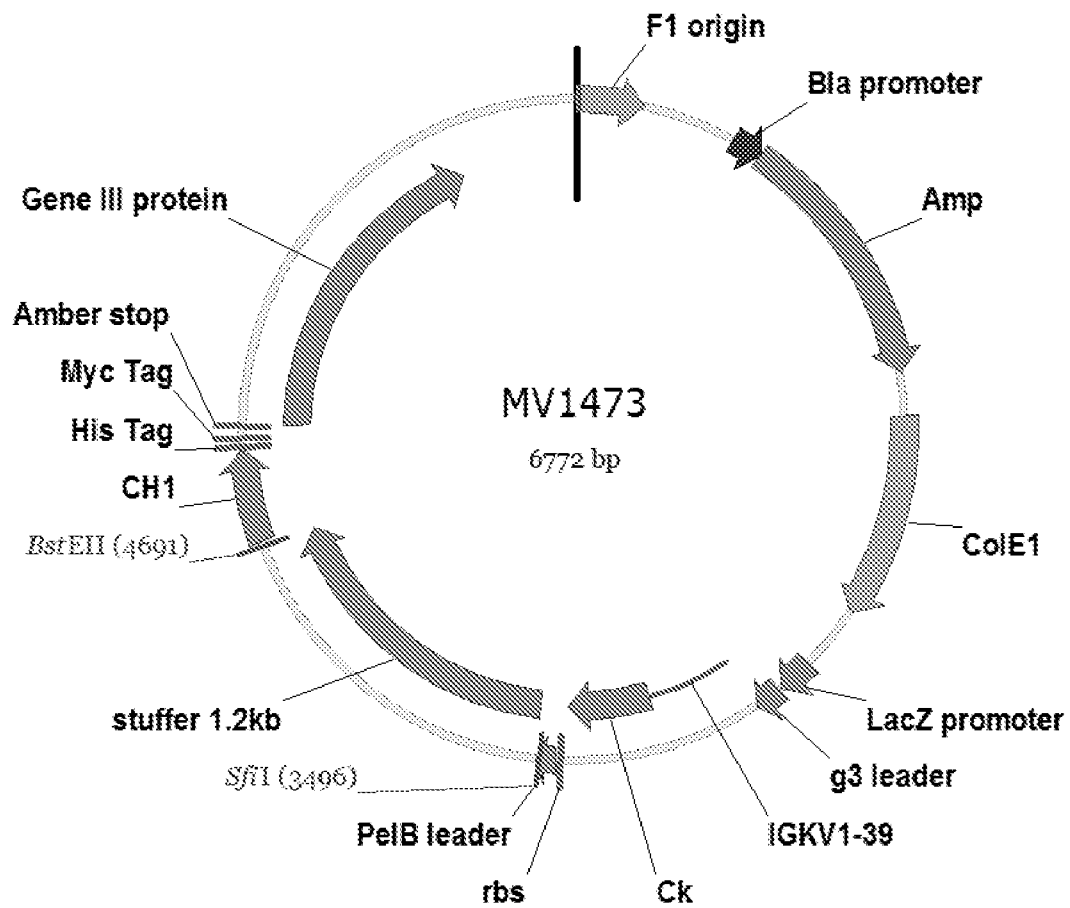


FIGURE 7

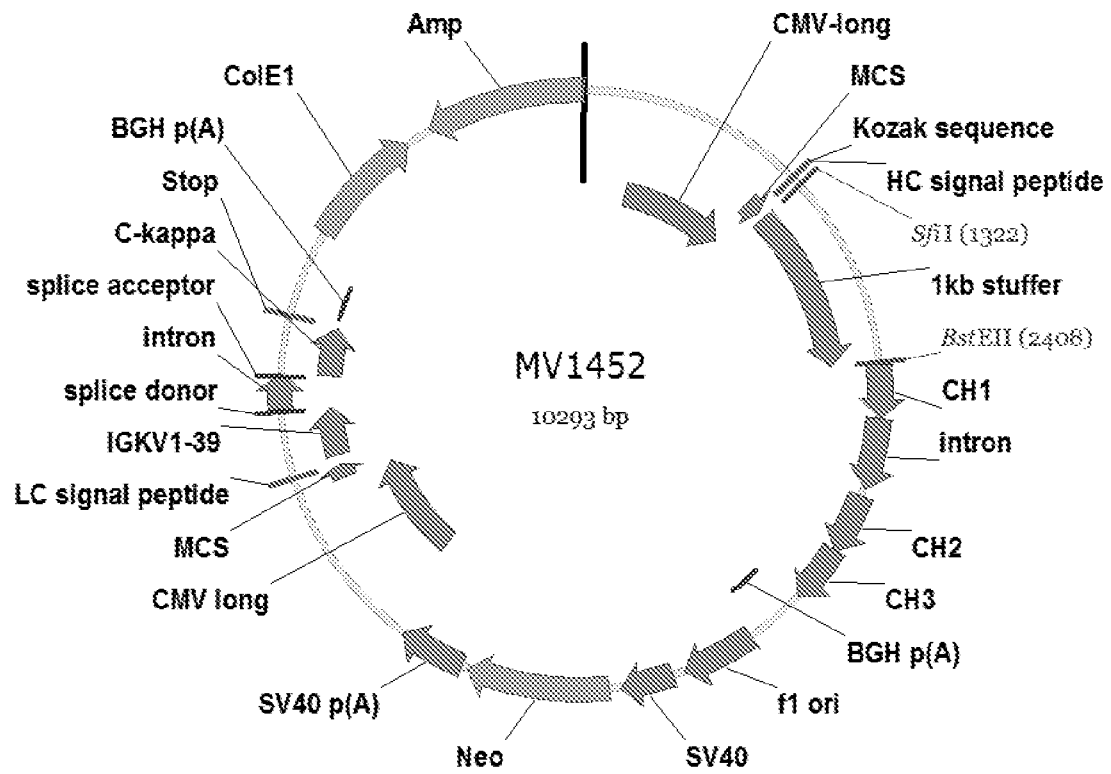


FIGURE 8

EVQLVETGAEVKKPGASVKVSCKASDYIFTKYDINWVRQAPGQGLEWMGWMSANTGNIGYAQKFQGRVTMTRDTS
INTAYMELSSLTSGDTAVYFCARSSLFKTETAPYYHFALDVWGQGTTVTVSS

FIGURE 9

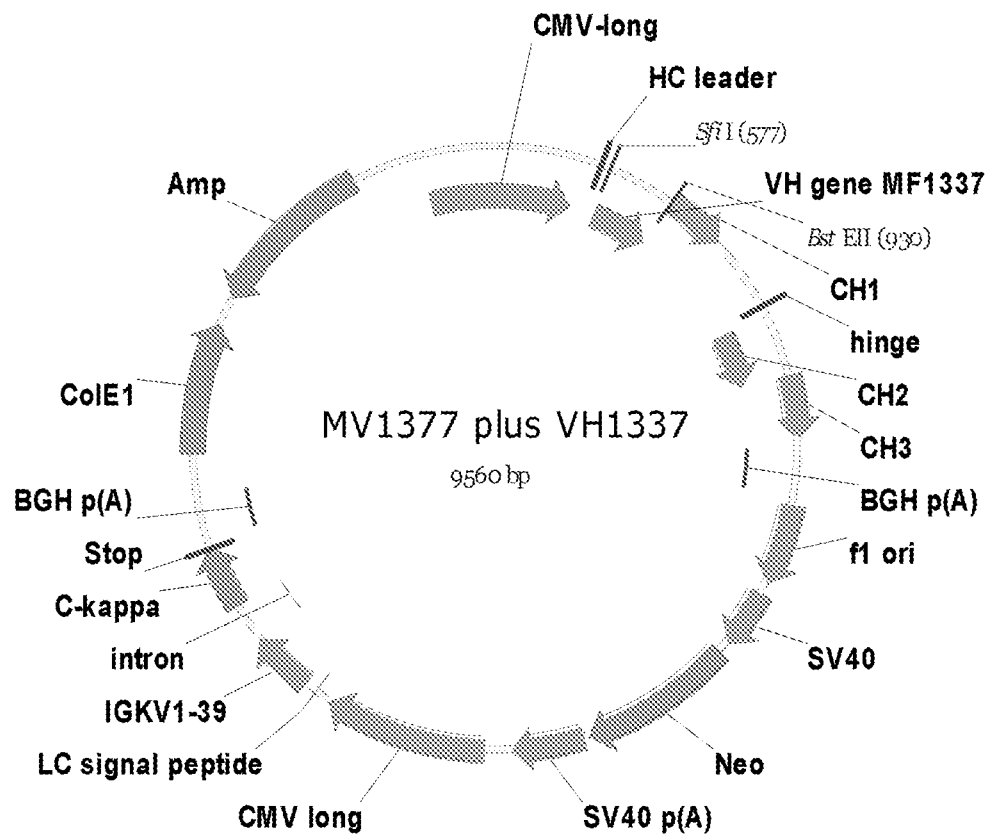


FIGURE 10

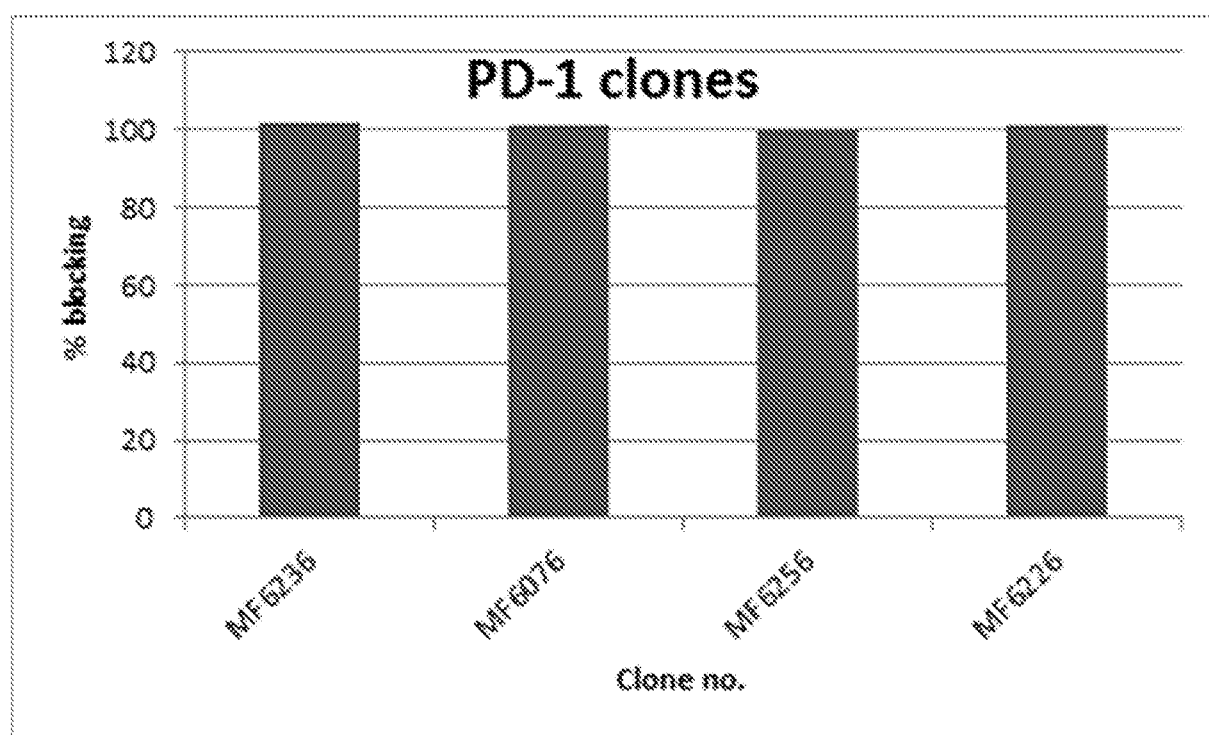


FIGURE 11

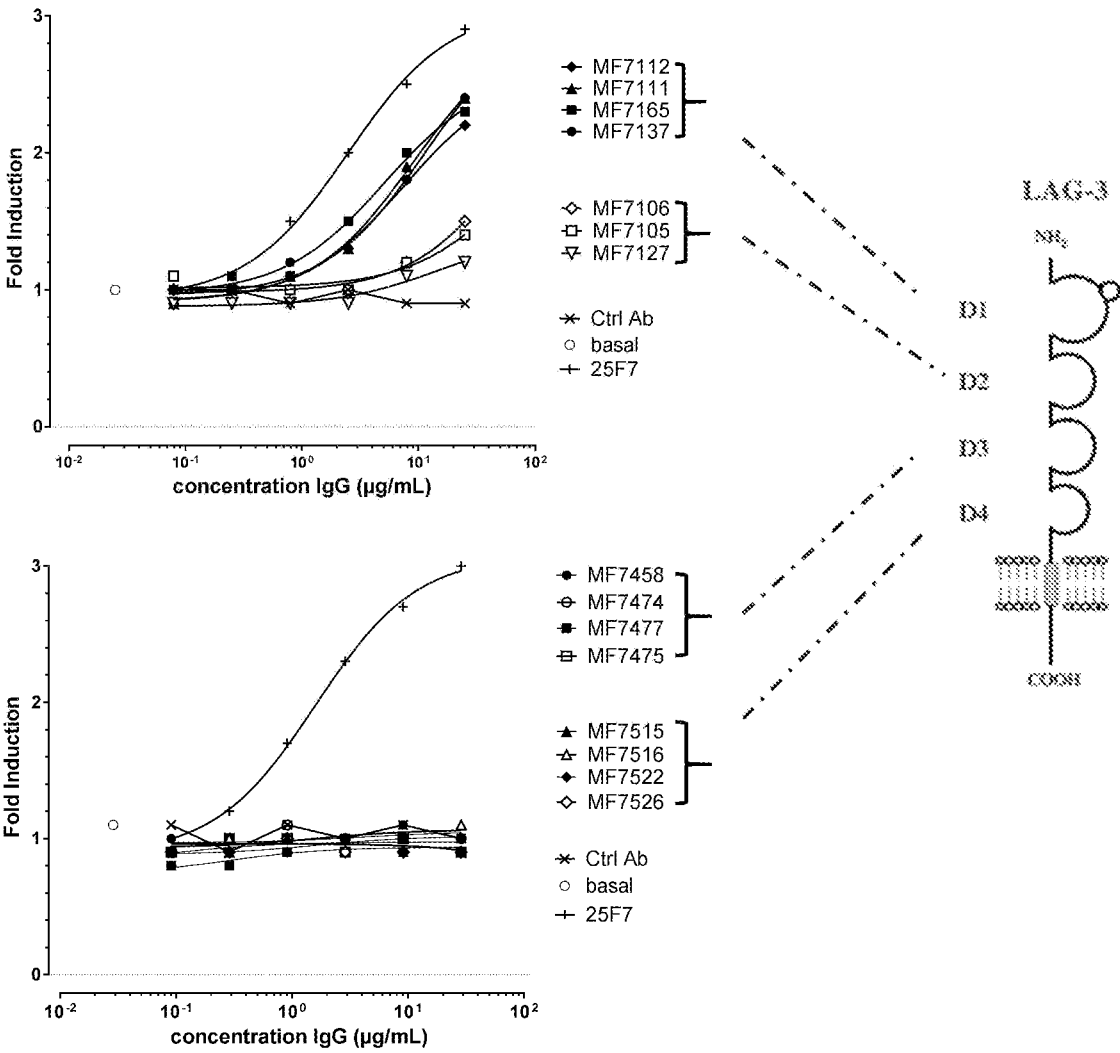


FIGURE 12

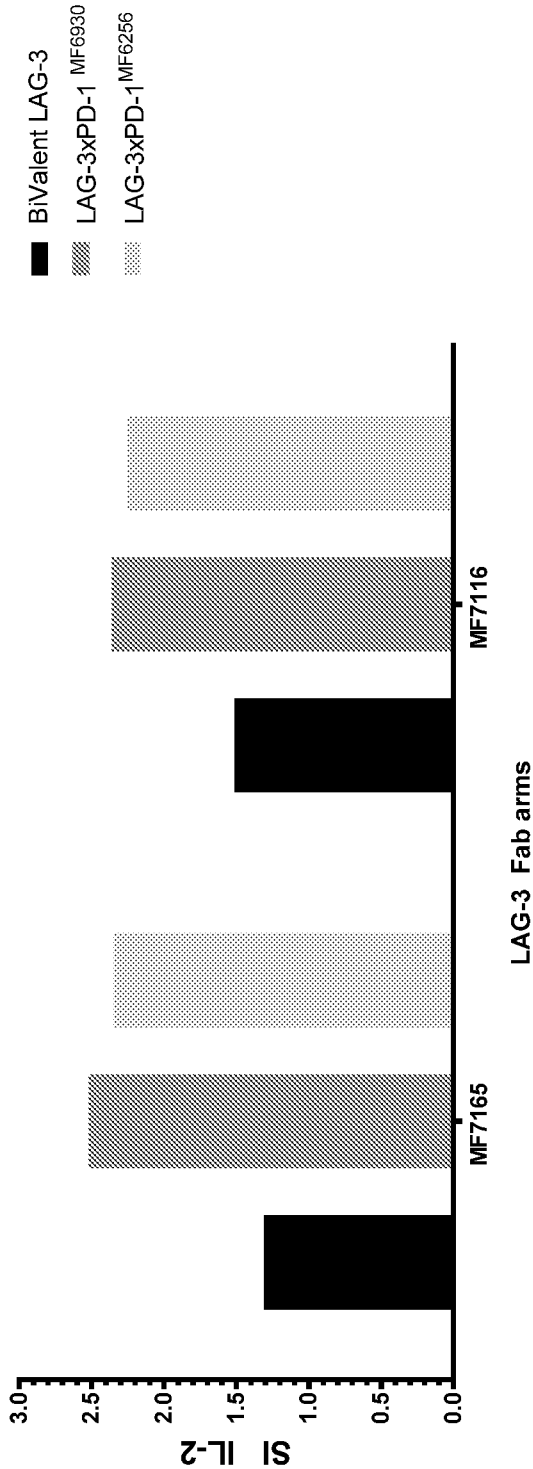


FIGURE 13

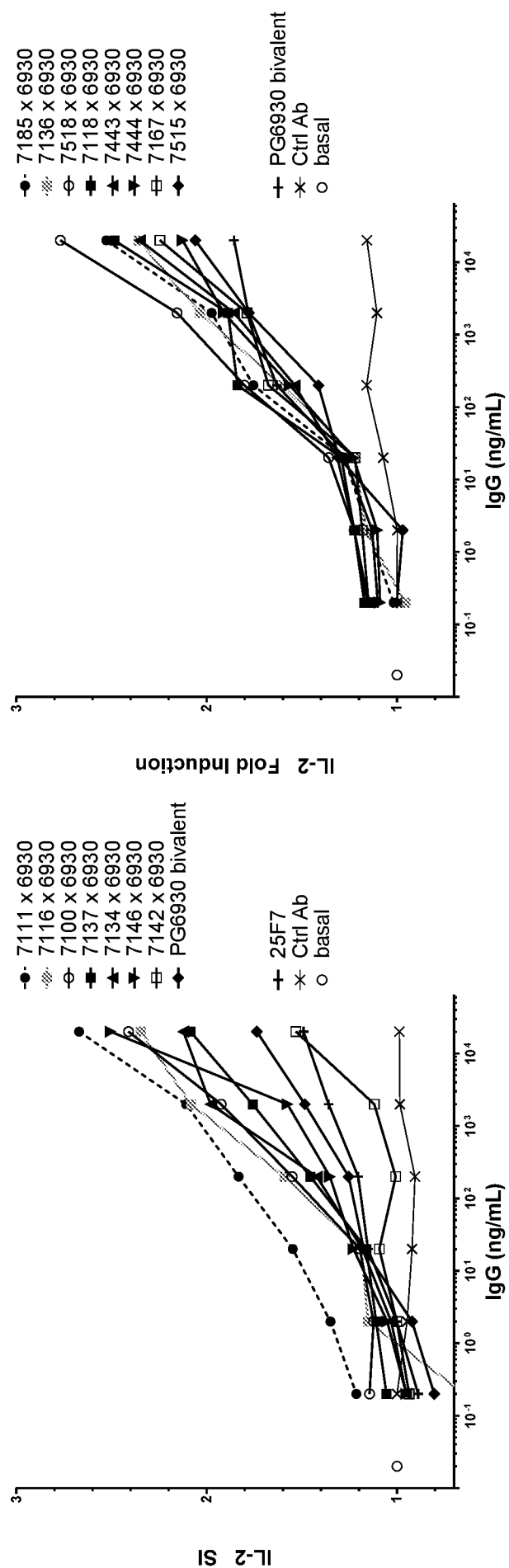


FIGURE 14

Antibody	IgG format
25F7* (PG7431)	p02 = IgG1 WT
Relatlimab*	IgG4 with S228P stabilizing mutation
H4sH15482P*	IgG4 with S228P stabilizing mutation

* Surrogate antibodies

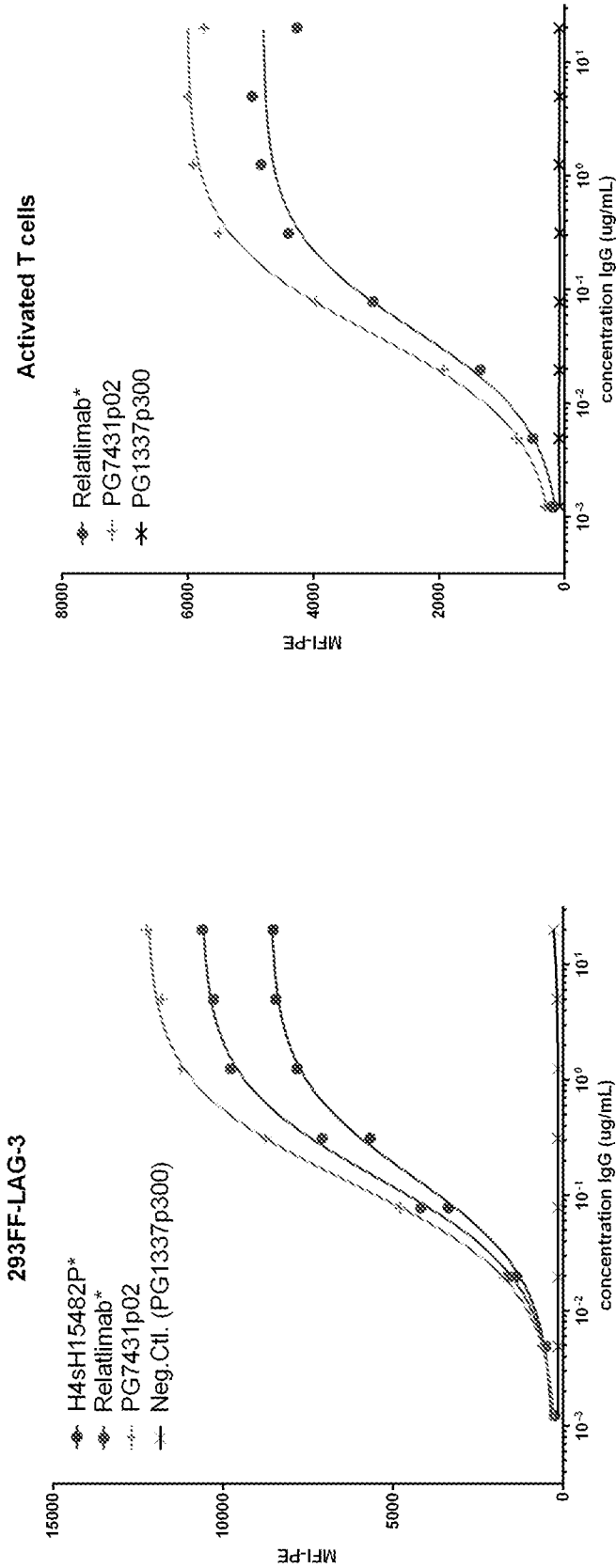


FIGURE 15

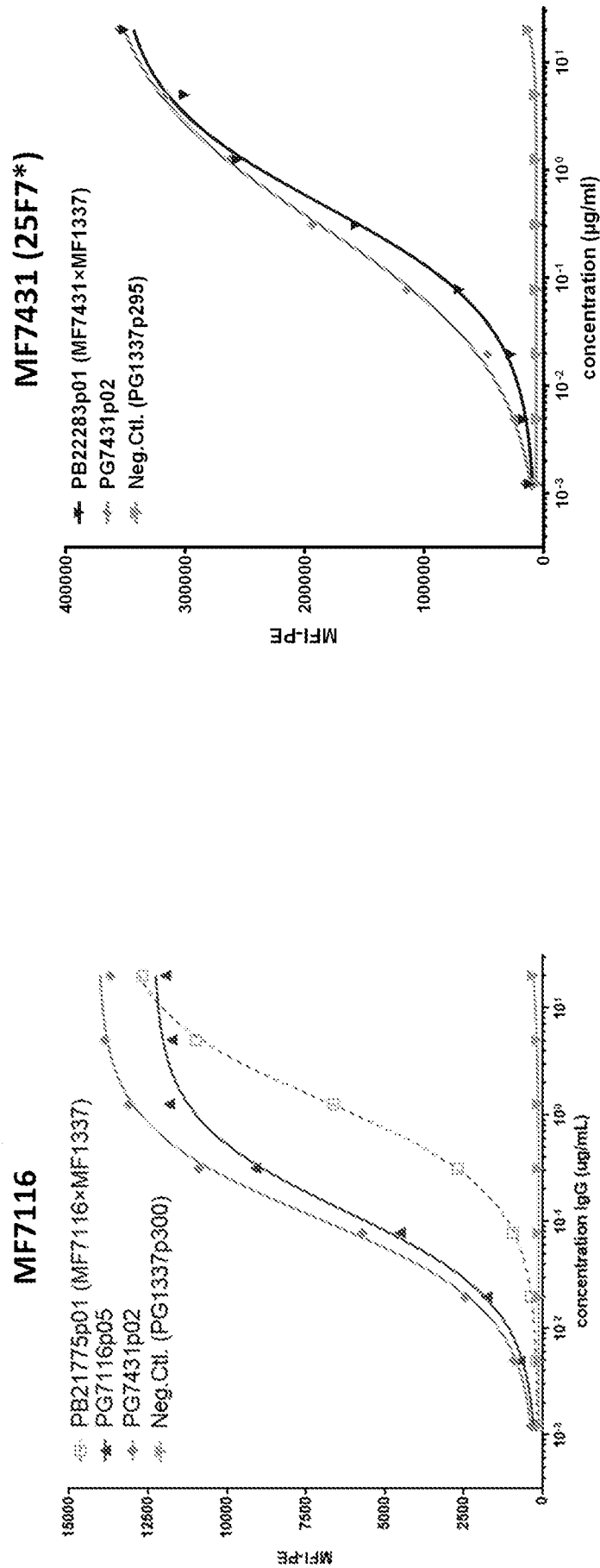


FIGURE 16

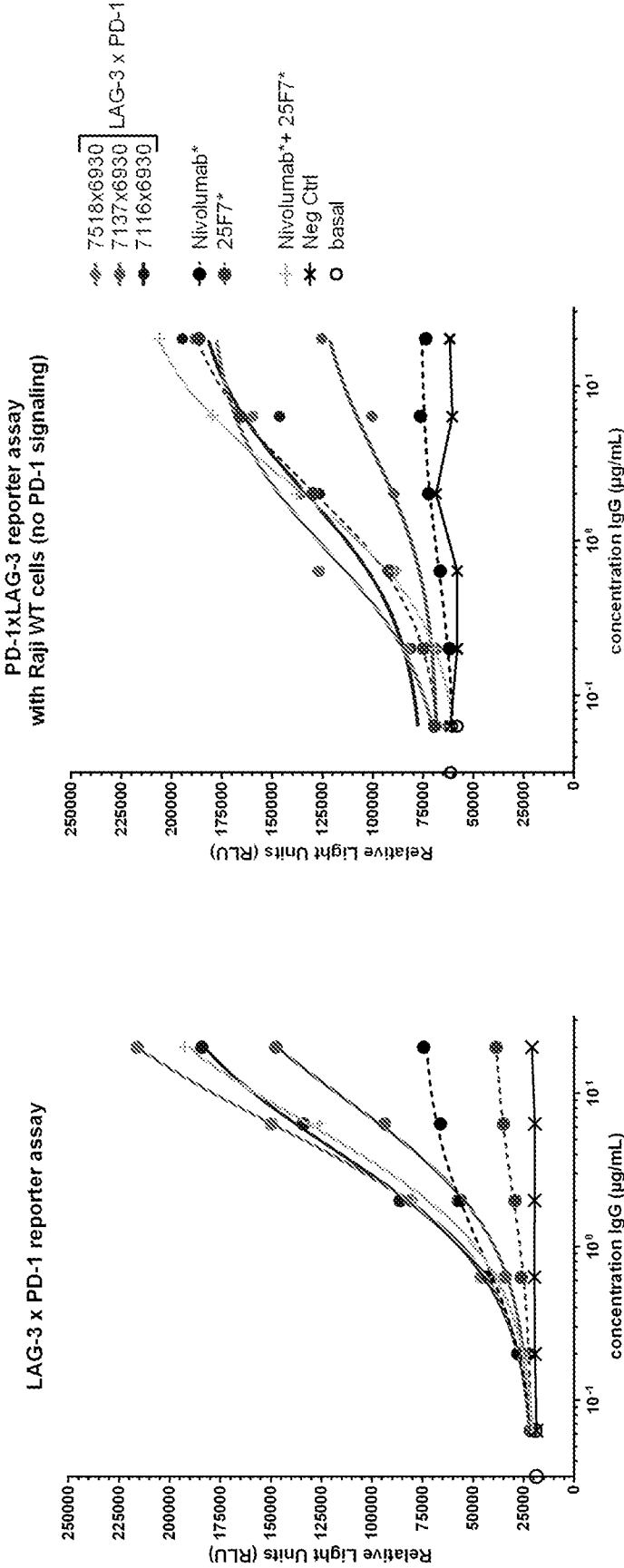


FIGURE17A

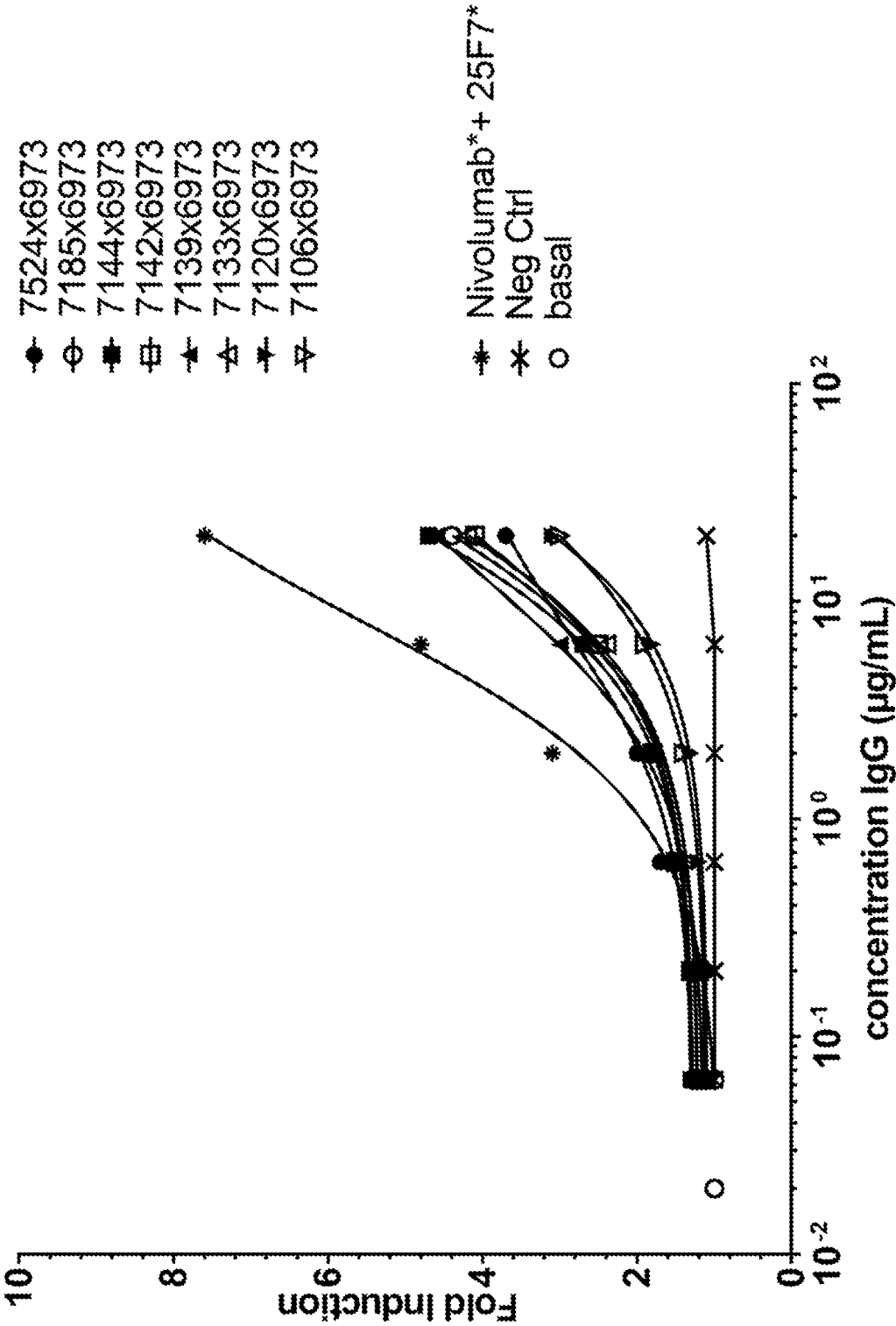


FIGURE 17B

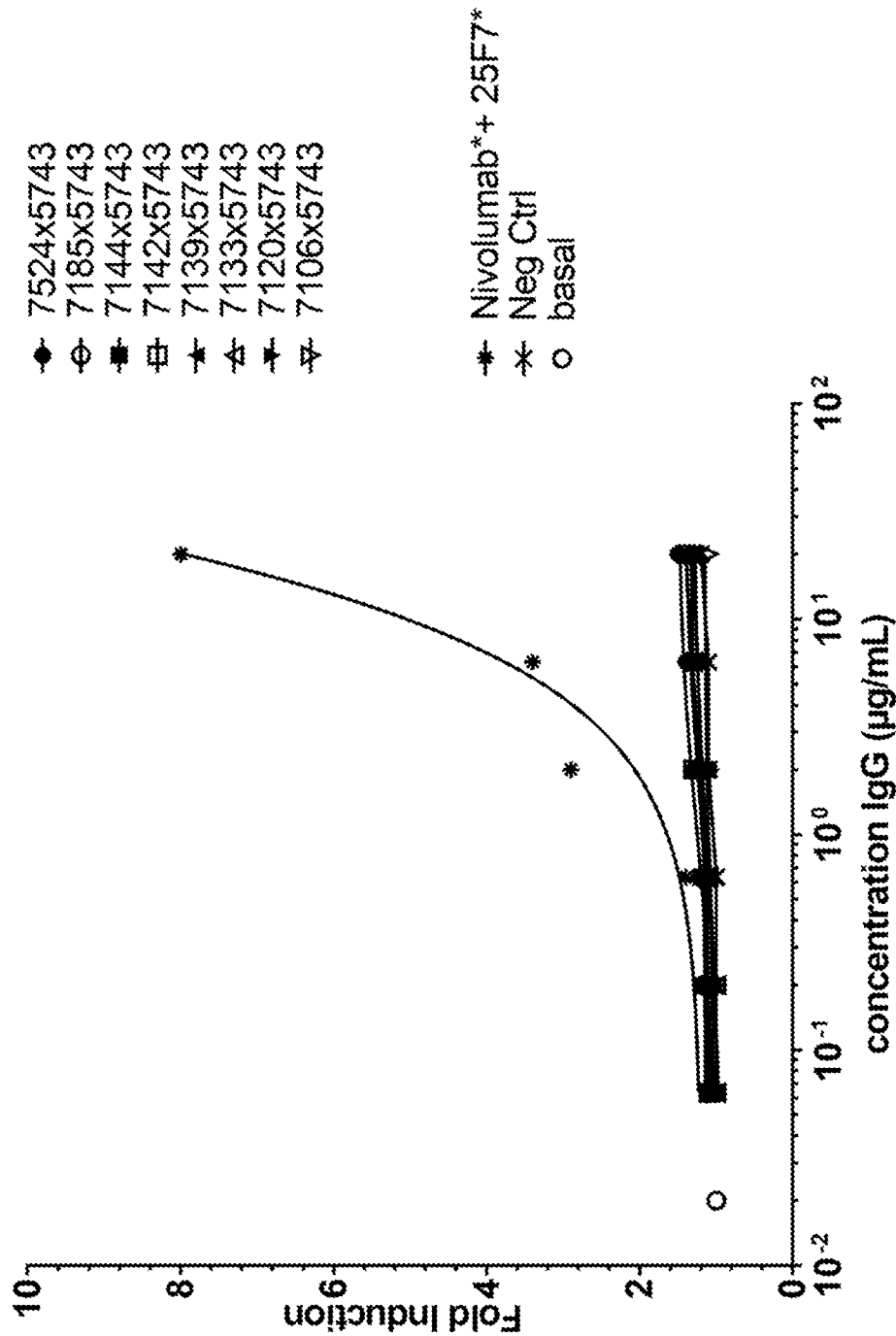


FIGURE 17C

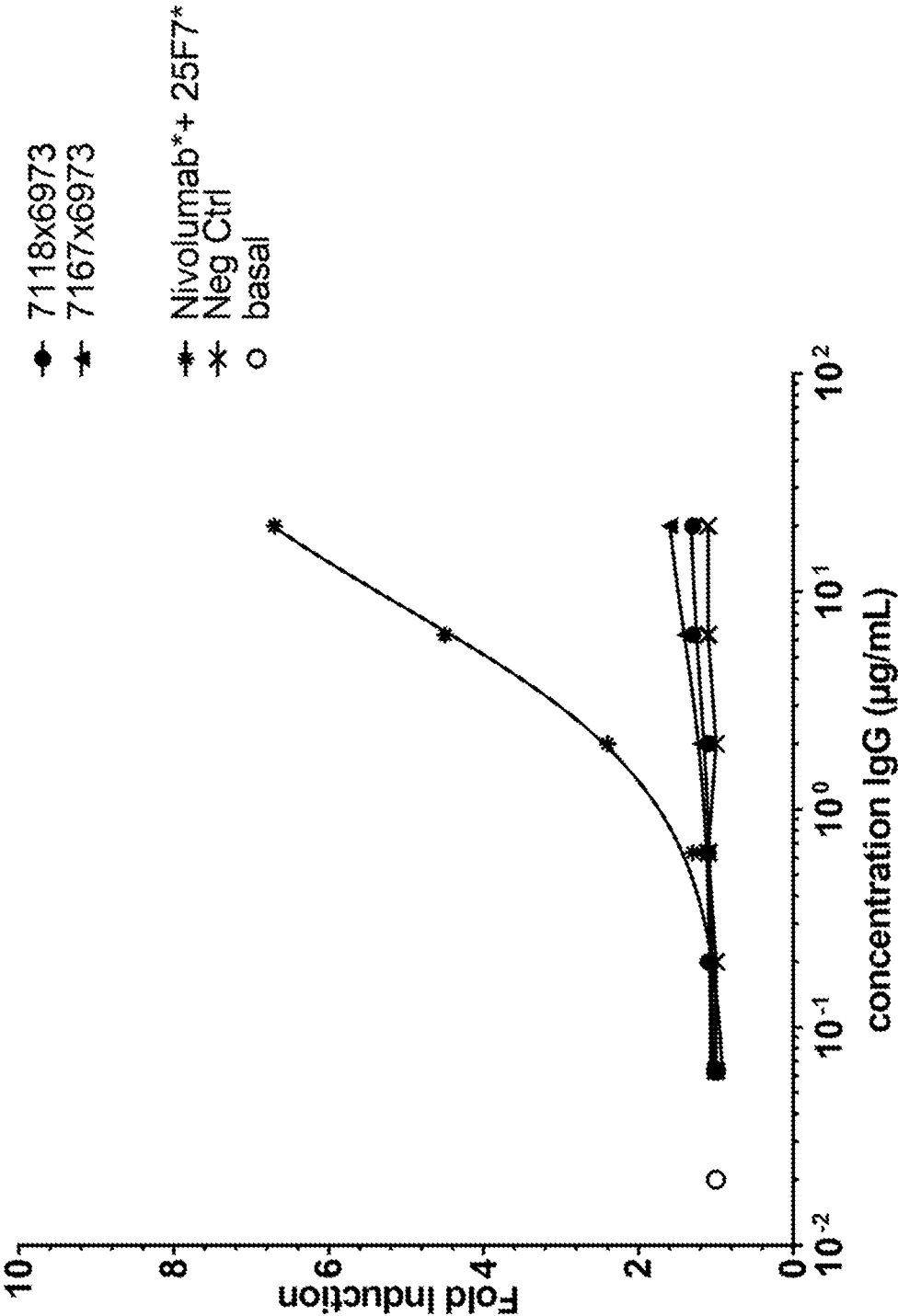


FIGURE 18

→ LAG-3
→ PD-1
Arms ranked on (high to low) functionality as bivalent Ab in reporter assay

		Higher than (%)		30.00	
		Lower than (%)		15.00	
		Higher than (%)		30.00	
		Lower than (%)		15.00	
Reporters		1st MLAG-3			
		2nd MLAG-3			
		3rd MLAG-3			
		4th MLAG-3			
		5th MLAG-3			
		6th MLAG-3			
		7th MLAG-3			
		8th MLAG-3			
		9th MLAG-3			
		10th MLAG-3			
		11th MLAG-3			
		12th MLAG-3			
		13th MLAG-3			
		14th MLAG-3			
		15th MLAG-3			
		16th MLAG-3			
		17th MLAG-3			
		18th MLAG-3			
		19th MLAG-3			
		20th MLAG-3			
		21st MLAG-3			
		22nd MLAG-3			
		23rd MLAG-3			
		24th MLAG-3			
		25th MLAG-3			
		26th MLAG-3			
		27th MLAG-3			
		28th MLAG-3			
		29th MLAG-3			
		30th MLAG-3			
		31st MLAG-3			
		32nd MLAG-3			
		33rd MLAG-3			
		34th MLAG-3			
		35th MLAG-3			
		36th MLAG-3			
		37th MLAG-3			
		38th MLAG-3			
		39th MLAG-3			
		40th MLAG-3			
		41st MLAG-3			
		42nd MLAG-3			
		43rd MLAG-3			
		44th MLAG-3			
		45th MLAG-3			
		46th MLAG-3			
		47th MLAG-3			
		48th MLAG-3			
		49th MLAG-3			
		50th MLAG-3			
		51st MLAG-3			
		52nd MLAG-3			
		53rd MLAG-3			
		54th MLAG-3			
		55th MLAG-3			
		56th MLAG-3			
		57th MLAG-3			
		58th MLAG-3			
		59th MLAG-3			
		60th MLAG-3			
		61st MLAG-3			
		62nd MLAG-3			
		63rd MLAG-3			
		64th MLAG-3			
		65th MLAG-3			
		66th MLAG-3			
		67th MLAG-3			
		68th MLAG-3			
		69th MLAG-3			
		70th MLAG-3			
		71st MLAG-3			
		72nd MLAG-3			
		73rd MLAG-3			
		74th MLAG-3			
		75th MLAG-3			
		76th MLAG-3			
		77th MLAG-3			
		78th MLAG-3			
		79th MLAG-3			
		80th MLAG-3			
		81st MLAG-3			
		82nd MLAG-3			
		83rd MLAG-3			
		84th MLAG-3			
		85th MLAG-3			
		86th MLAG-3			
		87th MLAG-3			
		88th MLAG-3			
		89th MLAG-3			
		90th MLAG-3			
		91st MLAG-3			
		92nd MLAG-3			
		93rd MLAG-3			
		94th MLAG-3			
		95th MLAG-3			
		96th MLAG-3			
		97th MLAG-3			
		98th MLAG-3			
		99th MLAG-3			
		100th MLAG-3			

FIGURE 19A

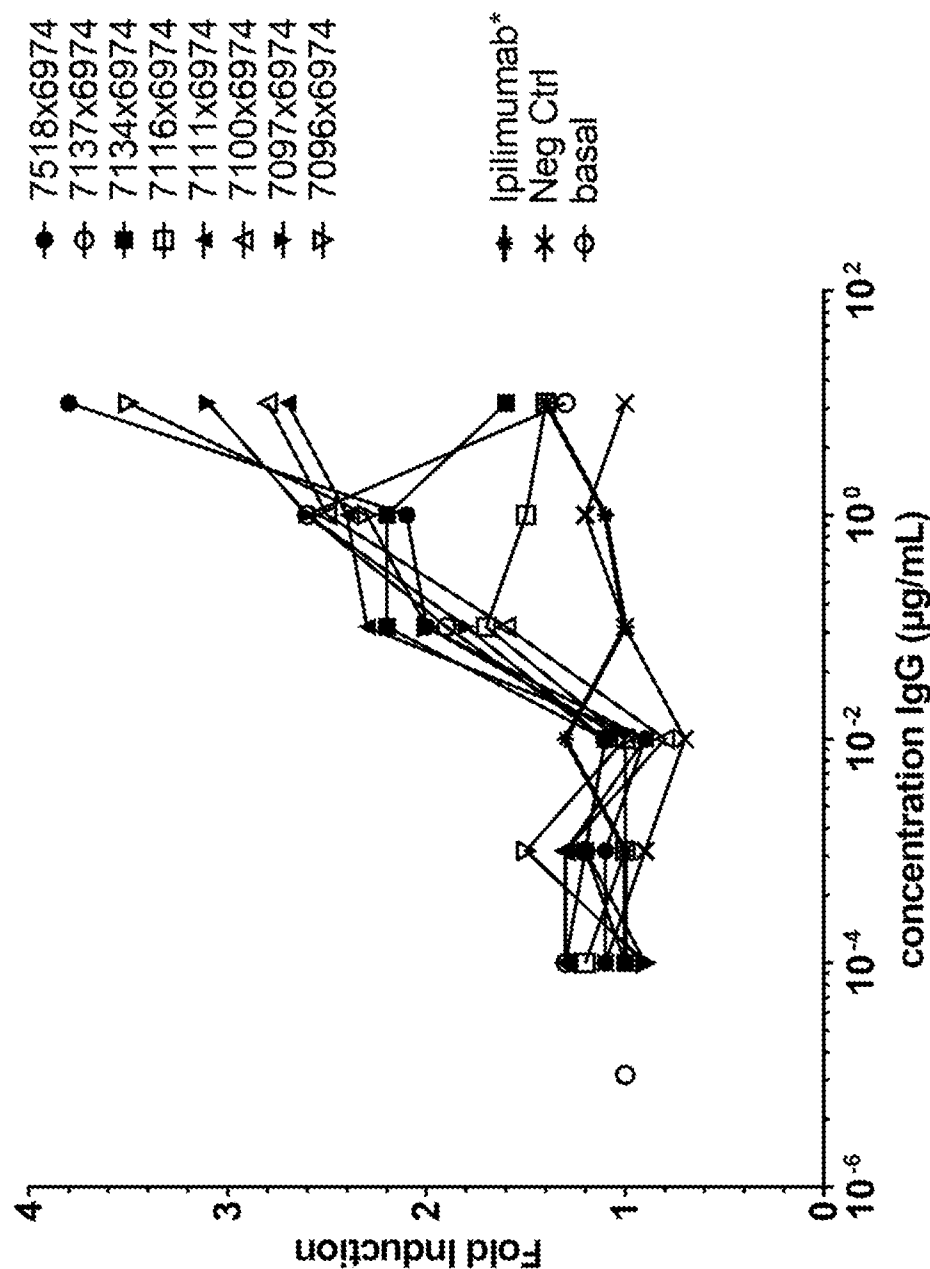


FIGURE 19B

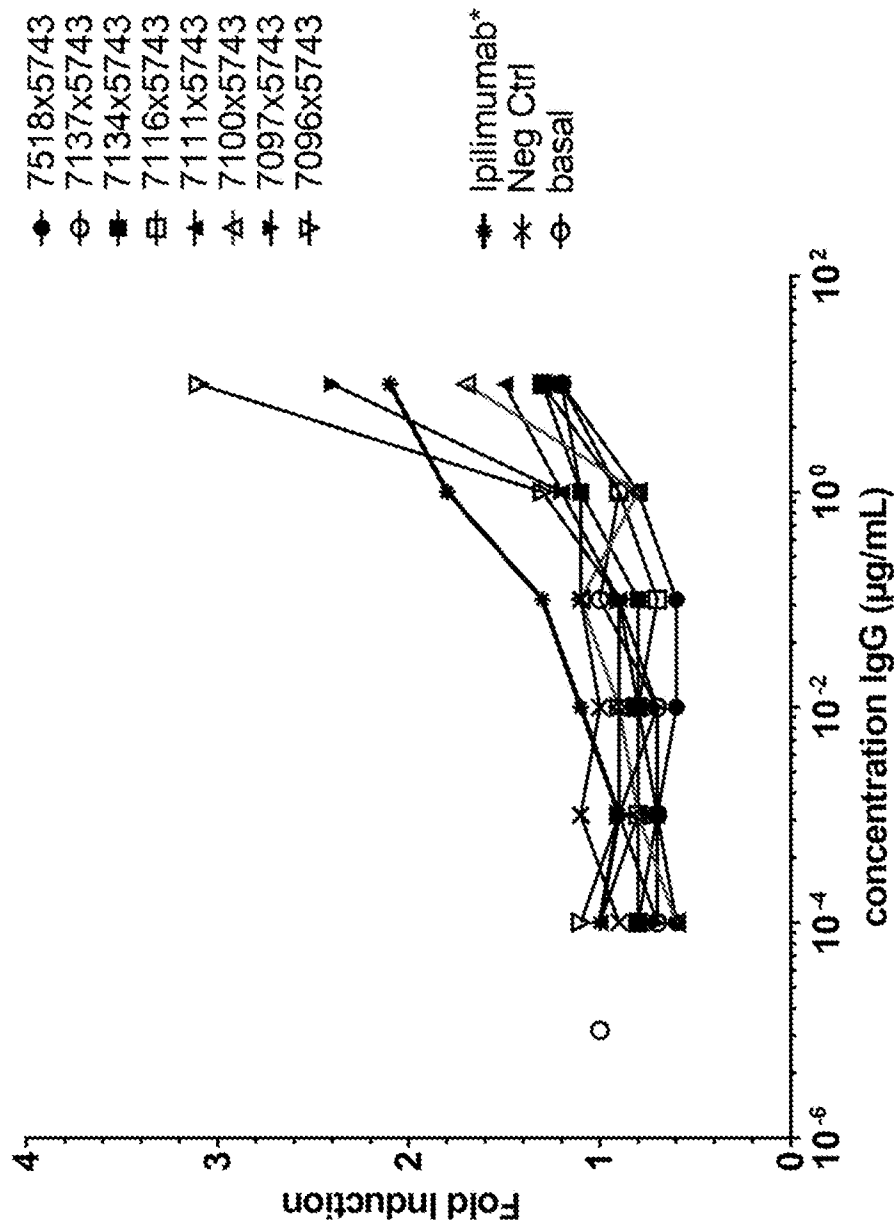


FIGURE 19C

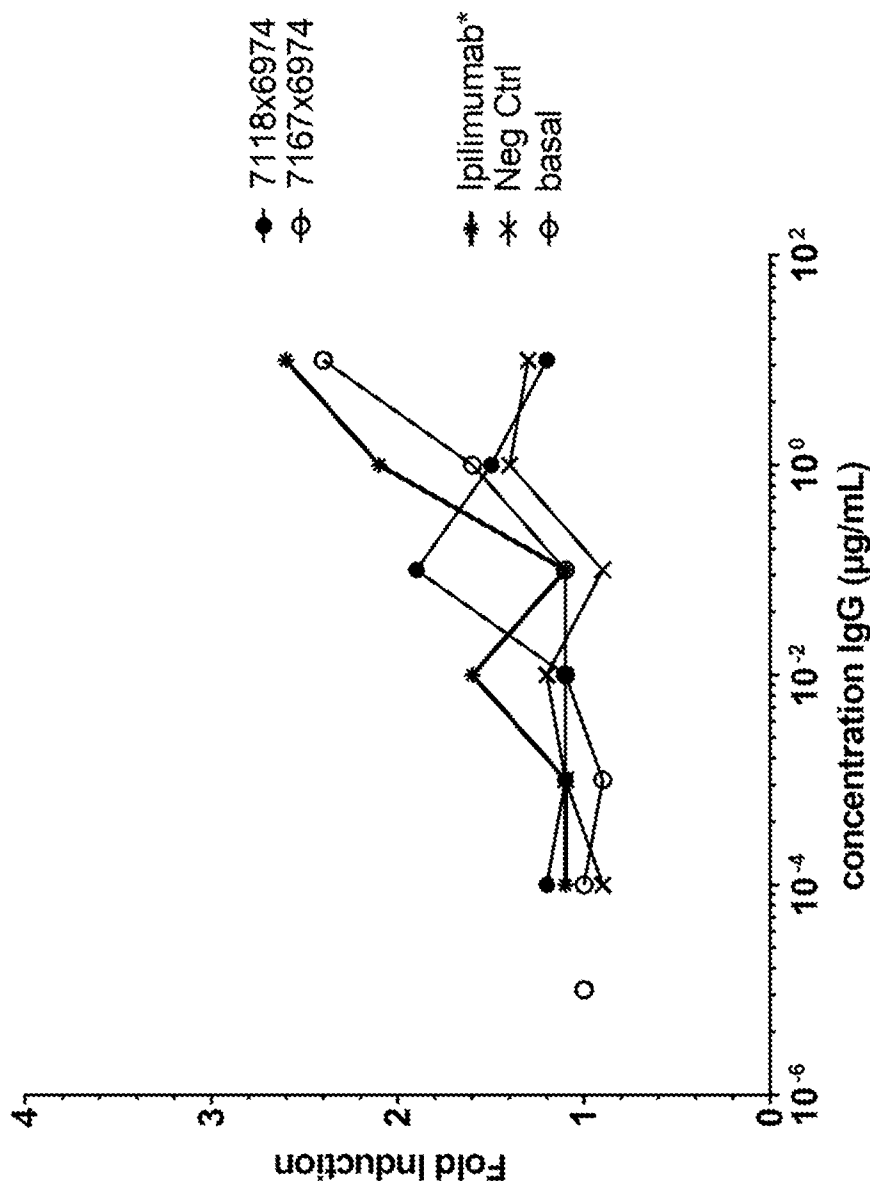


FIGURE 20

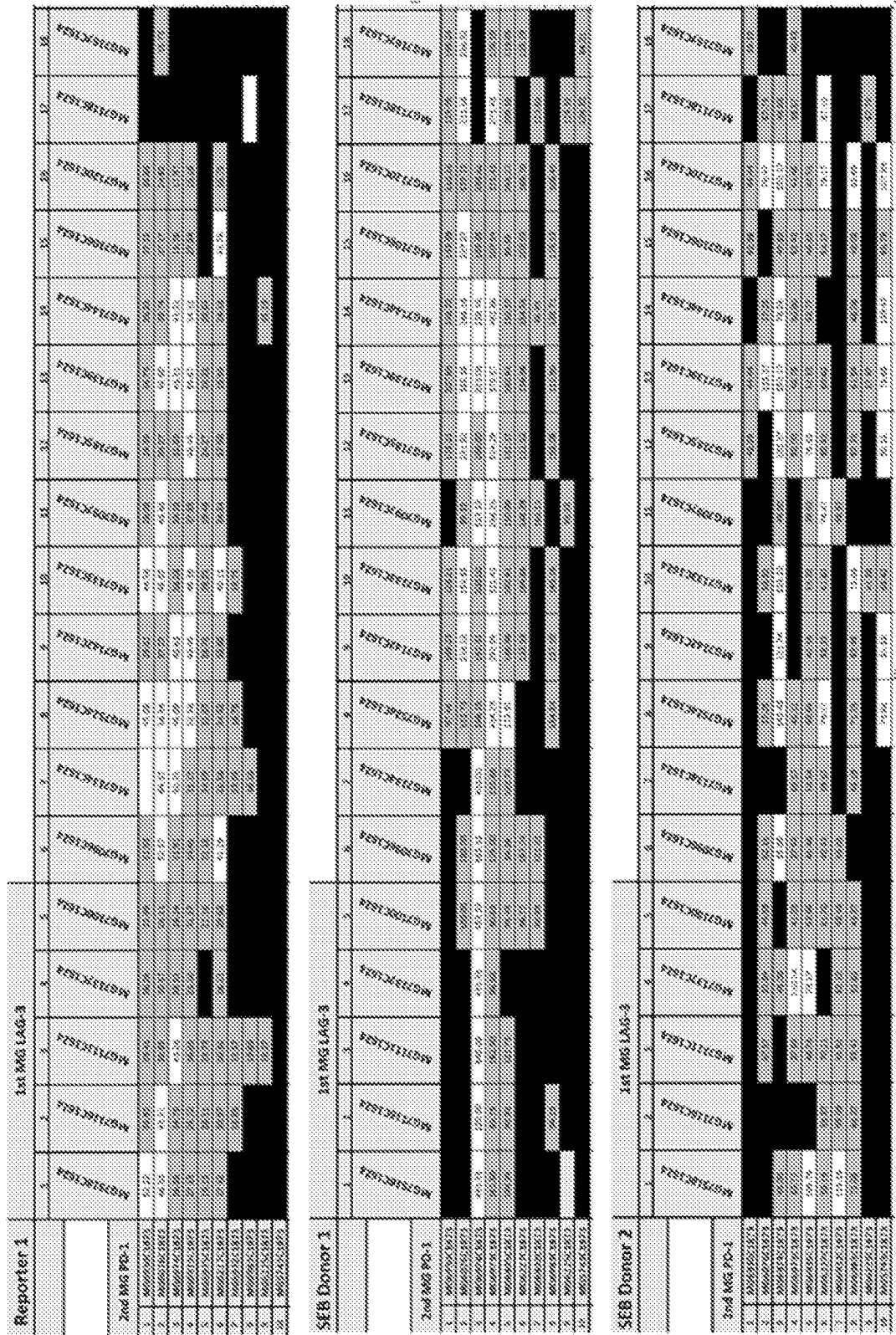


FIGURE 21

	Reporter	SEB donor 1	SEB donor 2	Sum	Average
MG6930C1873	3	0	0	3	1.0
MG6076C1873	8	8	2	18	6.0
MG6974C1873	6	10	8	24	8.0
MG6973C1873	6	8	1	15	5.0
MG6935C1873	0	1	3	4	1.3
MG6227C1873	3	0	4	7	2.3
MG6932C1873	0	0	1	1	0.3
MG6983C1873	0	0	2	2	0.7
MG6225C1873	0	0	0	0	0.0
MG5743C1873	0	0	6	6	2.0

FIGURE 22

	Reporter	SEB donor 1	SEB donor 2	Sum	Average	Ranking		Reporter	SEB donor 1	SEB donor 2	Sum	Average
MG7518C1624	2	1	2	5	1.7	7	MG7518C1624	3	2	5	10	3.3
MG7116C1624	1	1	0	2	0.7		MG7116C1624	3	1	1	5	1.7
MG7111C1624	1	1	0	2	0.7		MG7111C1624	4	1	2	7	2.3
MG7137C1624	0	1	2	3	1.0		MG7137C1624	0	1	2	3	1.0
MG7100C1624	0	1	0	1	0.3		MG7100C1624	0	1	0	1	0.3
MG7096C1624	2	1	1	4	1.3	10	MG7096C1624	2	2	2	6	2.0
MG7134C1624	2	1	0	3	1.0		MG7134C1624	2	1	1	4	1.3
MG7524C1624	4	2	3	9	3.0	2	MG7524C1624	5	2	4	11	3.7
MG7142C1624	2	2	2	6	2.0	5	MG7142C1624	3	5	3	11	3.7
MG7133C1624	4	2	2	8	2.7	3	MG7133C1624	5	5	3	13	4.3
MG7097C1624	1	2	1	4	1.3	9	MG7097C1624	3	2	1	6	2.0
MG7185C1624	1	2	3	6	2.0	6	MG7185C1624	2	3	4	9	3.0
MG7139C1624	3	3	3	9	3.0	1	MG7139C1624	4	5	3	12	4.0
MG7144C1624	2	3	2	7	2.3	4	MG7144C1624	4	3	3	10	3.3
MG7106C1624	1	1	0	2	0.7		MG7106C1624	3	2	3	8	2.7
MG7120C1624	0	0	5	5	1.7	8	MG7120C1624	2	2	5	9	3.0
MG7118C1624	0	2	1	3	1.0		MG7118C1624	0	3	3	6	2.0
MG7167C1624	0	1	0	1	0.3		MG7167C1624	0	4	0	4	1.3

FIGURE 23

Monospecific activity
(as bivalent IgG)

Clone information

Screening results

MF	CDR3	CDR3 length	Germline	% AUC of pos ctrl	Ranking reporter	Ranking SEB assay
MF6076	GGYTG YGGDW FDP	13	IGHV4-59	49.2	1	2
MF6974	PYSGYFDV	9	IGHV3-23	46.5	2/3	1
MF6973	PYSGYFDV	9	IGHV3-23	39.1	2/3	3
MF6930	GTVEA TLFDY	11	IGHV1-69	51.5	4	
MF6227	GGYSG YGGDD FDI	13	IGHV4-59	21.5	5	
MF6935	GTVSG TLVFDY	11	IGHV1-69	32.0		
MF6932	GTVSA TLVFDY	11	IGHV1-69	15.9		
MF6983	PYDSGYFDV	9	IGHV3-23	11.1		
MF6225	GGYSG YGGDSMDV	13	IGHV4-59	7.7		
MF5743	AYCSGN SCYTDYFDY	15	IGHV3-13			

FIGURE 24

MF	CDR3	Domain specificity	Activity bivalent (AUC, % of control)	T cell binding (AUC) monovalent t	EC50 monovalent t (ug/ml)	Ranking SEB and reporter
MG7139	DRAIGTLVYFDY	hu D2	20.00	2854	5.71	1
MG7524	GSILAAQMWGDI	hu/mo cross-reactive - mo D1	29.41	5551	4.2	2
MG7133	DRETGTLVYFDY	hu D2	26.67	4611	11.23	3
MG7144	DRDSGGLVYFDS	hu D2	19.39	1896	10.19	4
MG7142	ERDIGSLVYFDS	hu D2	27.62	5276	3.45	5
MG7185	DREMGTLVFFDQ	hu D2	20.95	2796	4.49	6
MG7518	DGSGWDDFDY	Hu D1 + D4	64.71	12450	0.9	7
MG7120	EREIGALVAFDI	hu D2	14.29	1597	66.19	8
MG7097	DILLYKWNVVEGFDI	hu D1	21.43	5400	2.7	9
MG7096	DILLYKWNVVEGFDI	hu D1	35.71	5950	1.66	10
MG7111	IPLTGEFDY	hu D1	51.16	11445	1.52	>10
MG7100	ERGWDVFDI	hu D1	39.80	10615	1.14	>10
MG7134	EPNWWGVYFDY	hu D1	34.29	10368	0.49	>10
MG7116	DGDNWDDVFDI	hu D1	57.14	10307	0.68	>10
MG7137	GGTYVYSGSYTLDI	hu D1	51.16	8588	1.68	>10
MG7106	DKAVAGLYFDS	hu D2	16.28	2883	26.52	>10
MG7118	VPAAATPSGTYWIFDL	hu D3	2.04	ND	ND	>10
MG7167	DRGYDYSGSYHNWFDI	hu D4	-1.33	ND	ND	>10
MG7444	DTGQSWSNYYHAFDY	hu/mo cross-reactive - hu D3	-4.35	ND	ND	ND

FIGURE 25

