

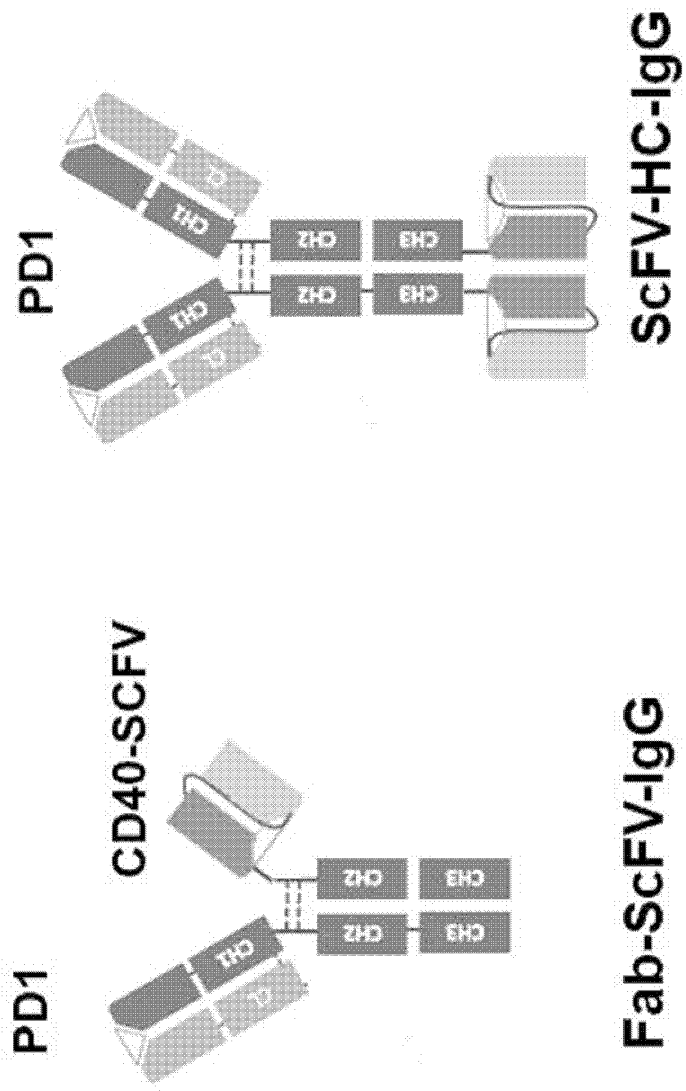


FIG. 1B

FIG. 1A

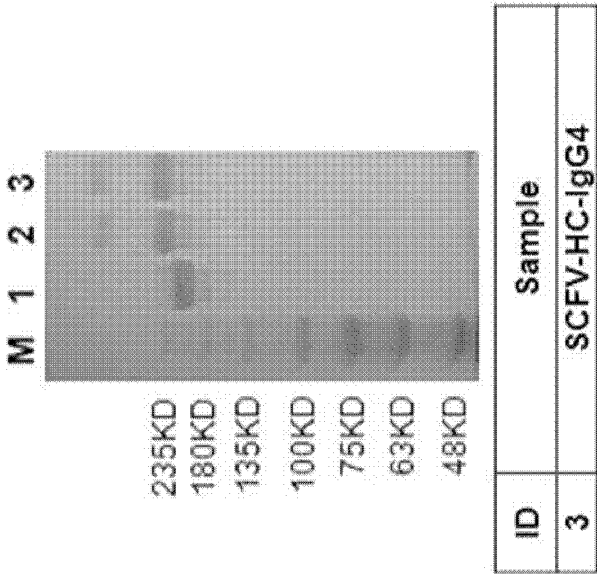


FIG. 2B

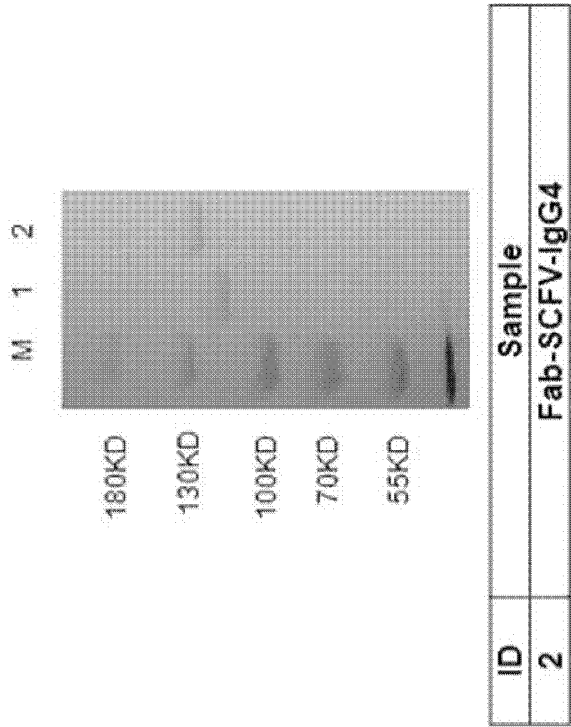


FIG. 2A

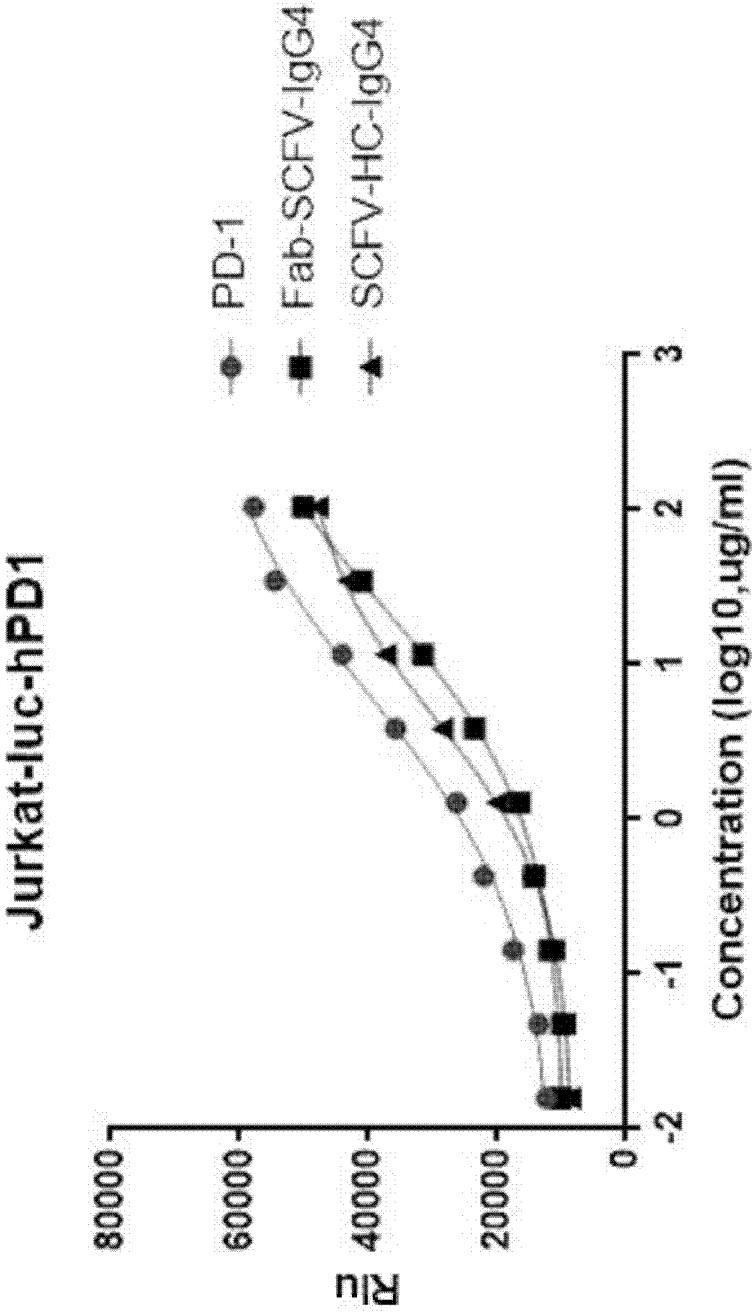


FIG. 3

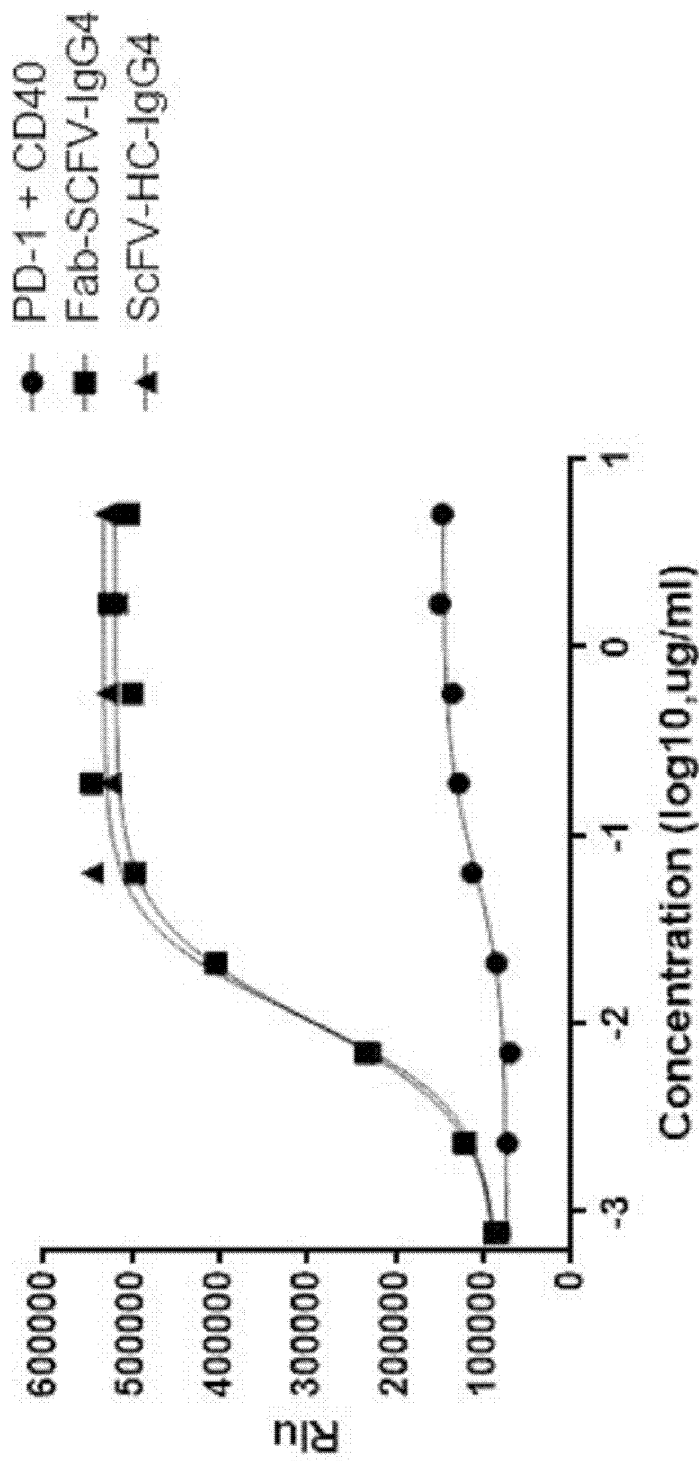


FIG. 4A

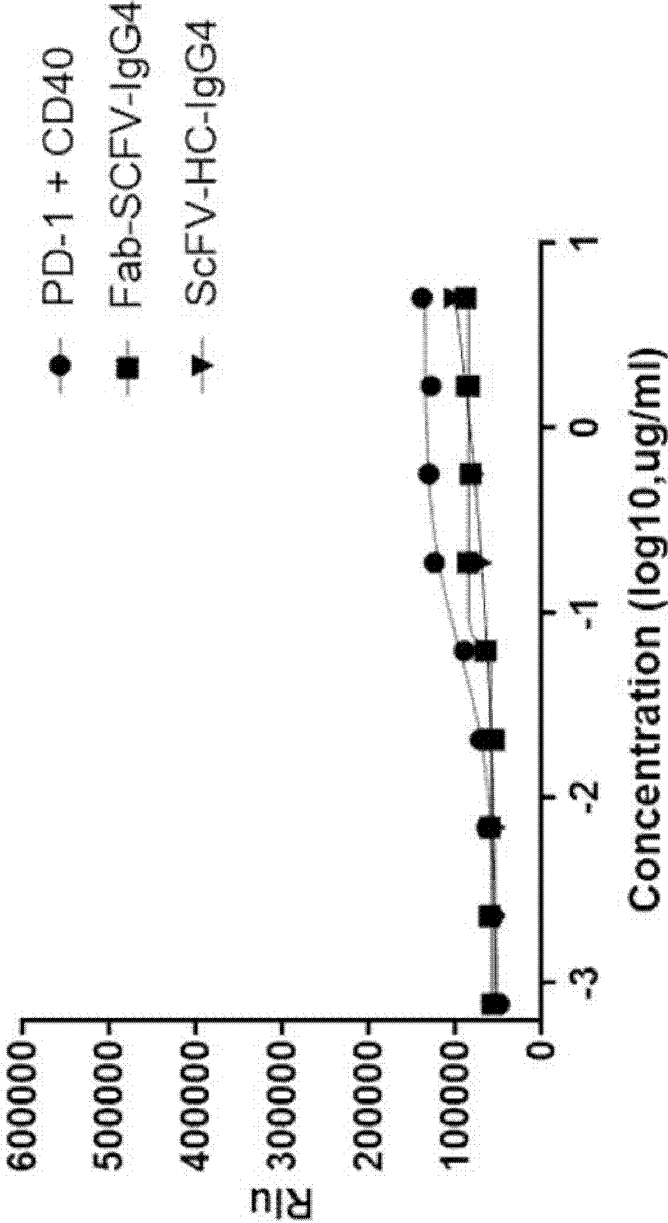


FIG. 4B

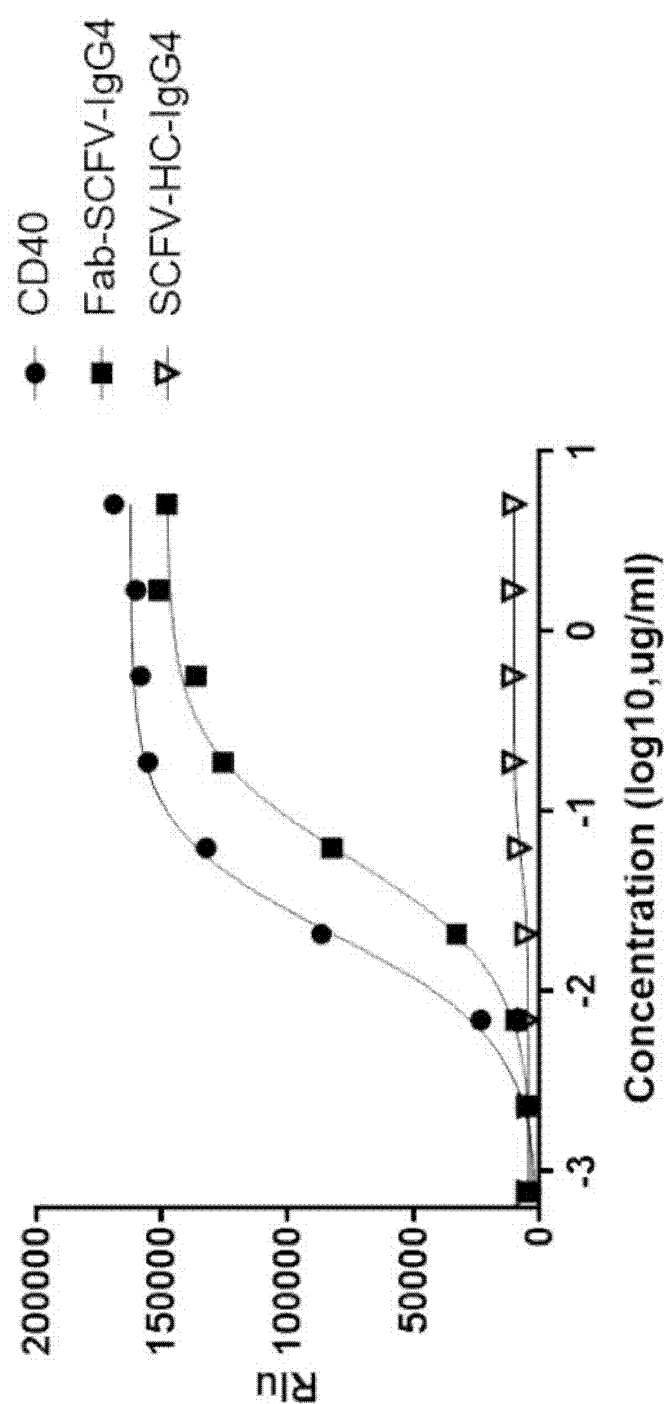
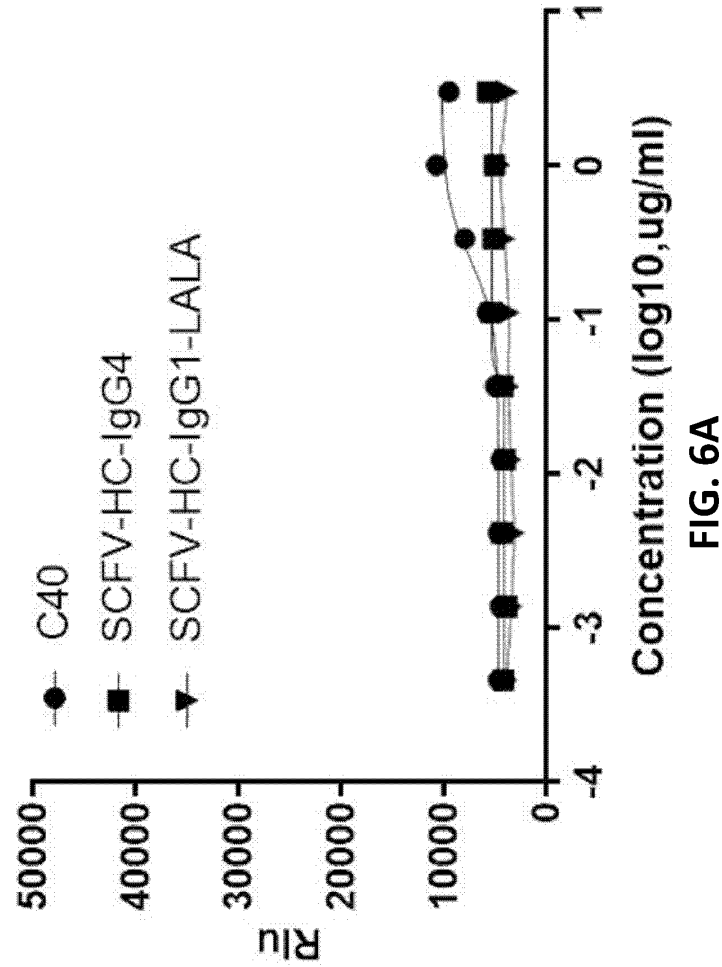


FIG. 5



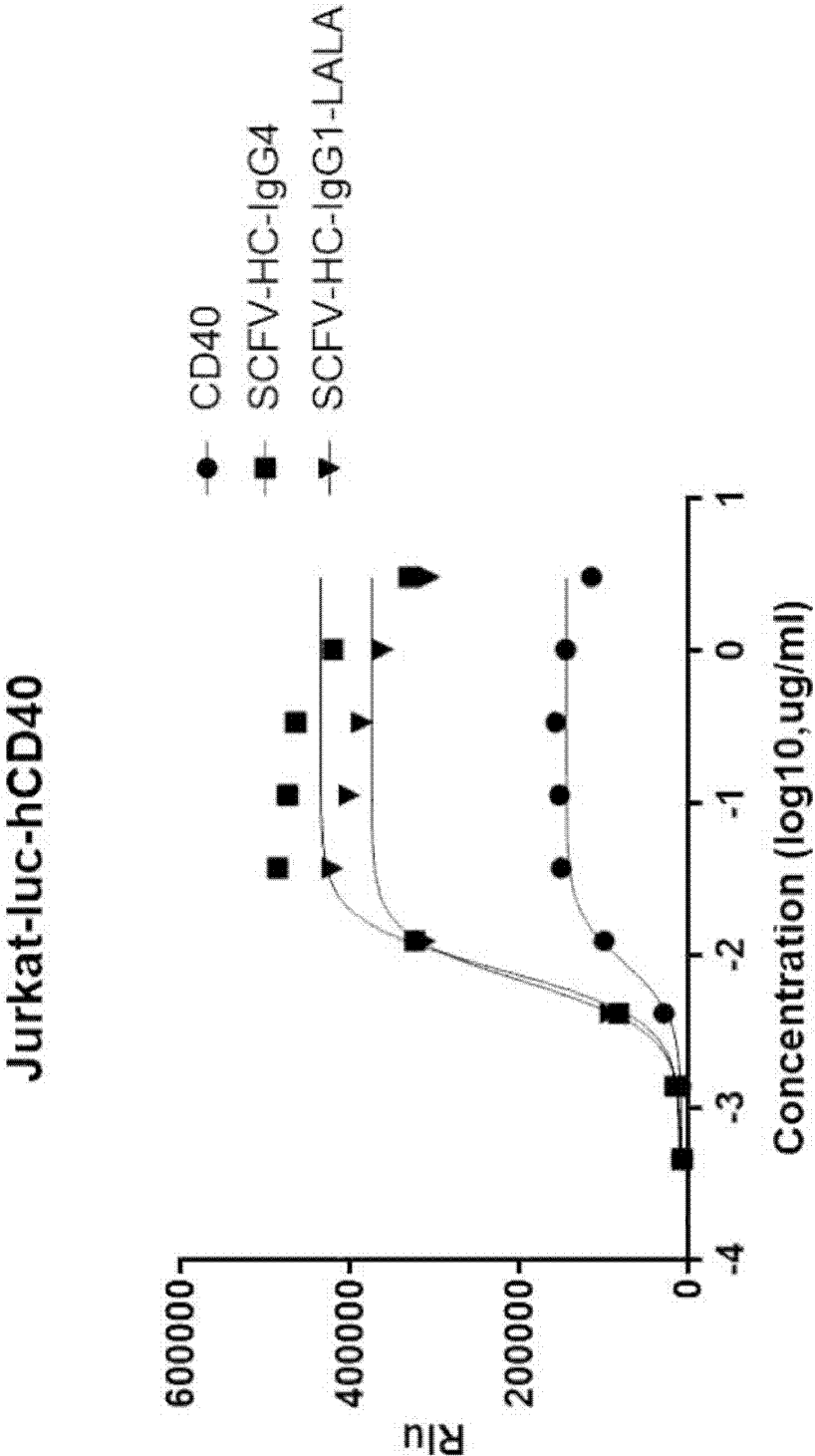


FIG. 6B

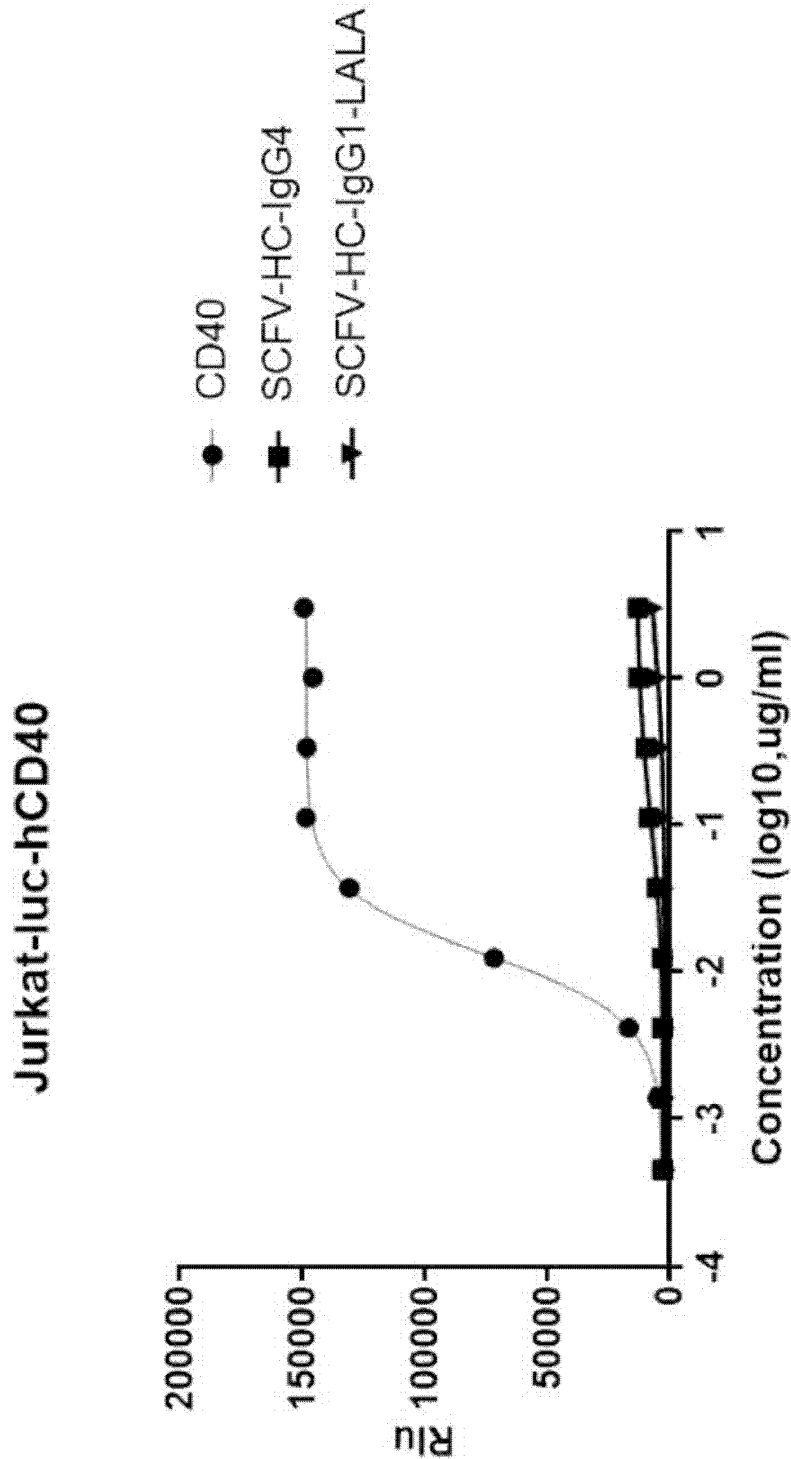


FIG. 6C

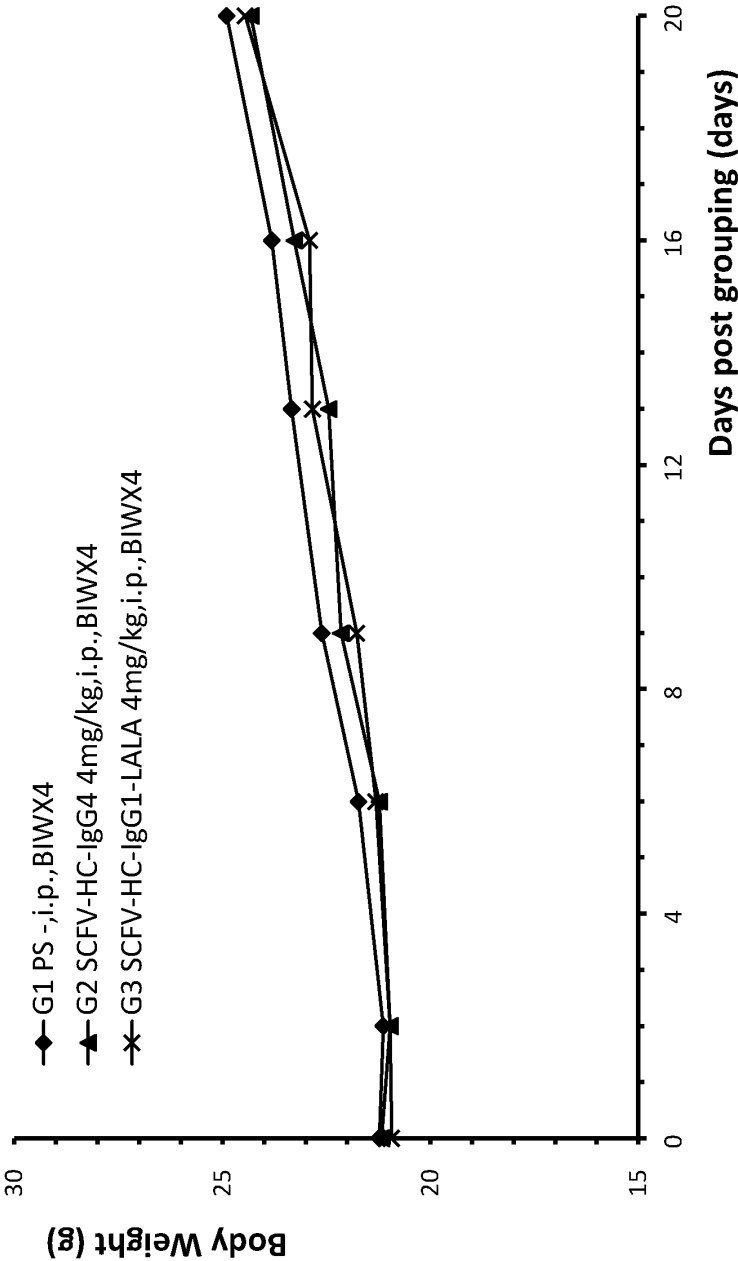


FIG. 7

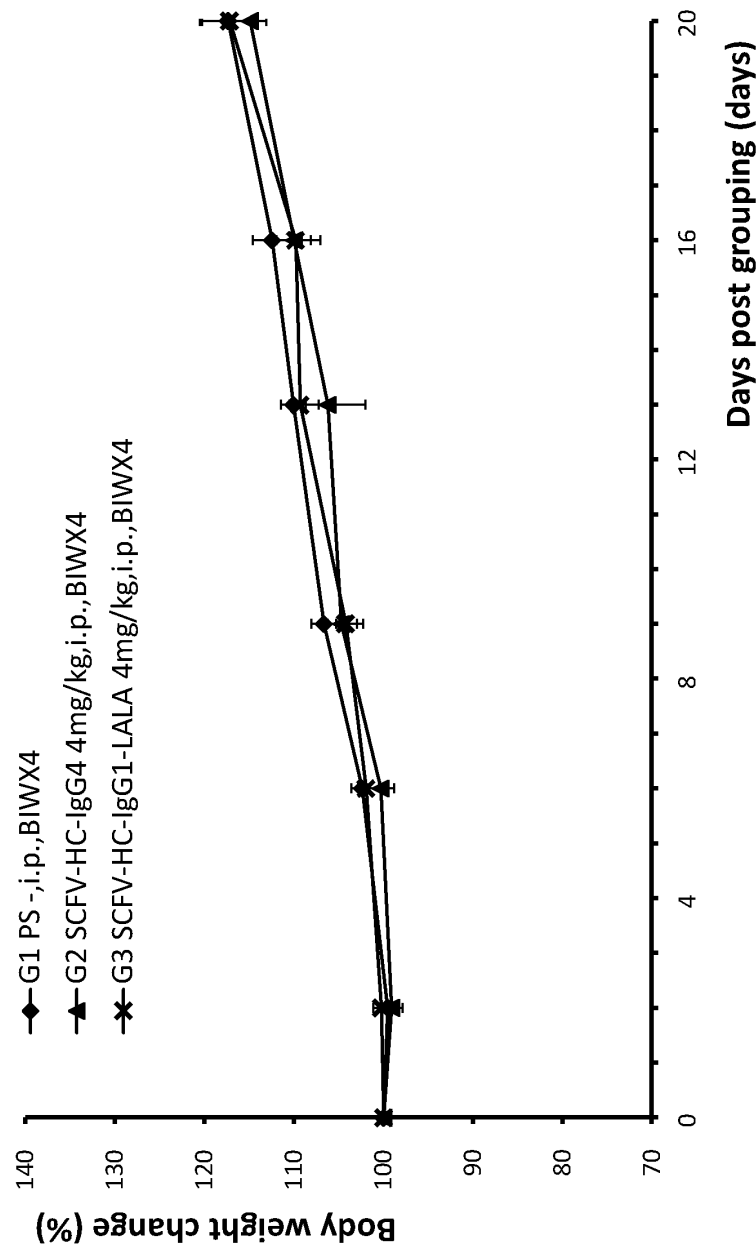


FIG. 8

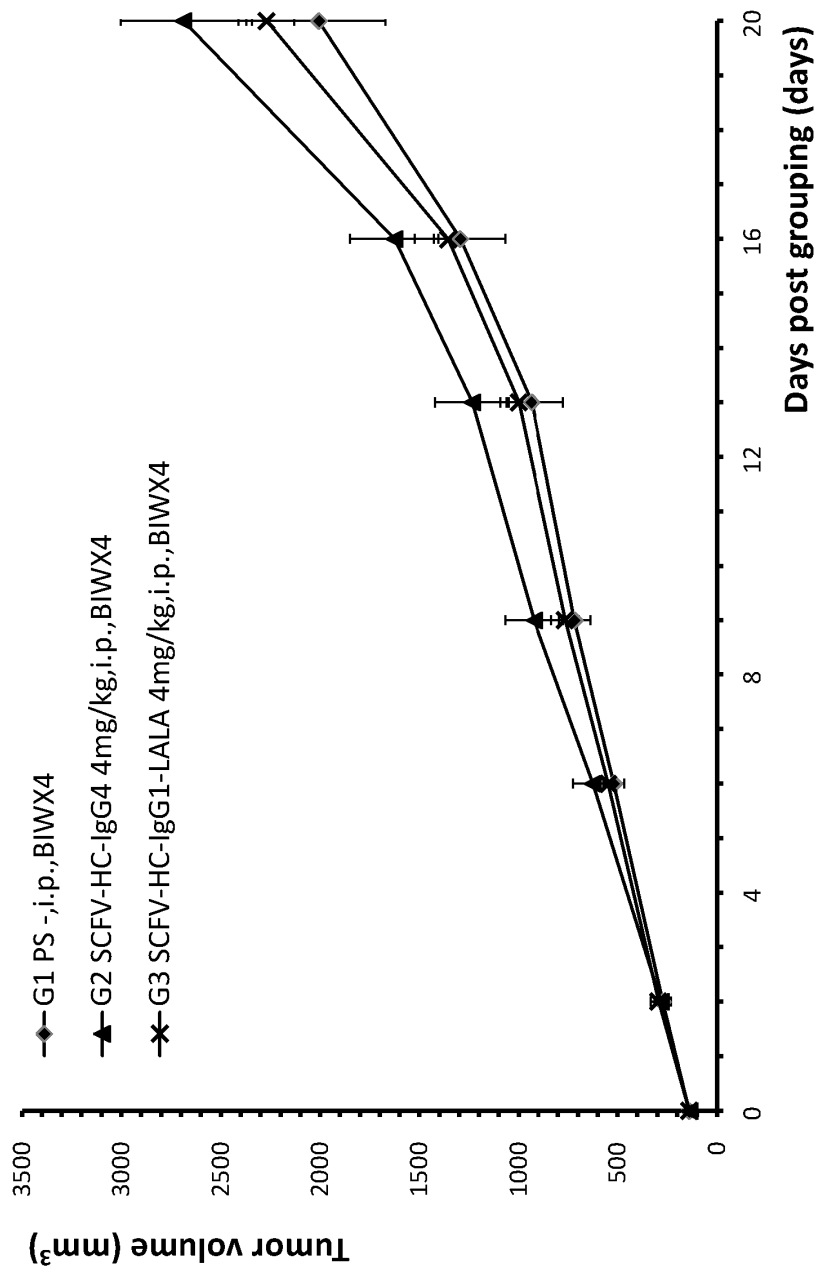


FIG. 9

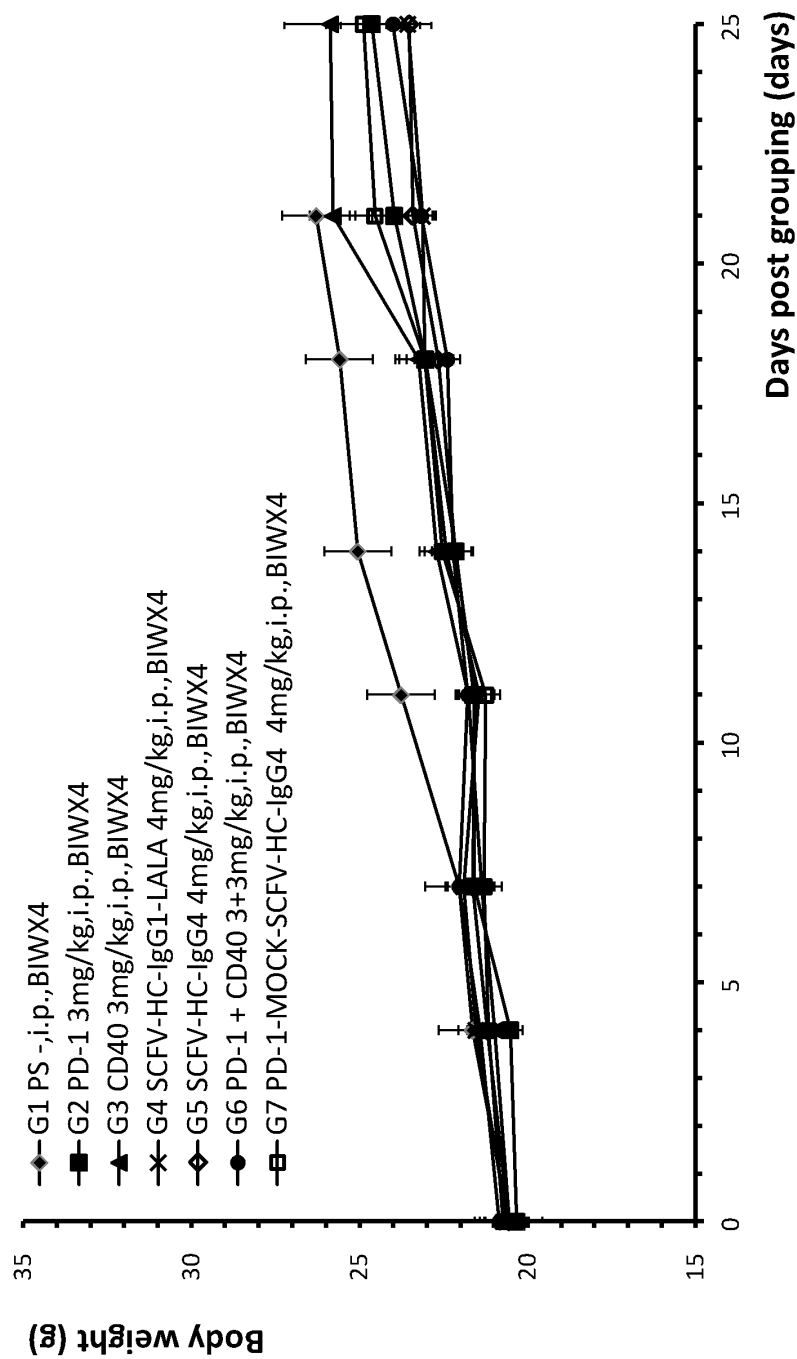


FIG. 10

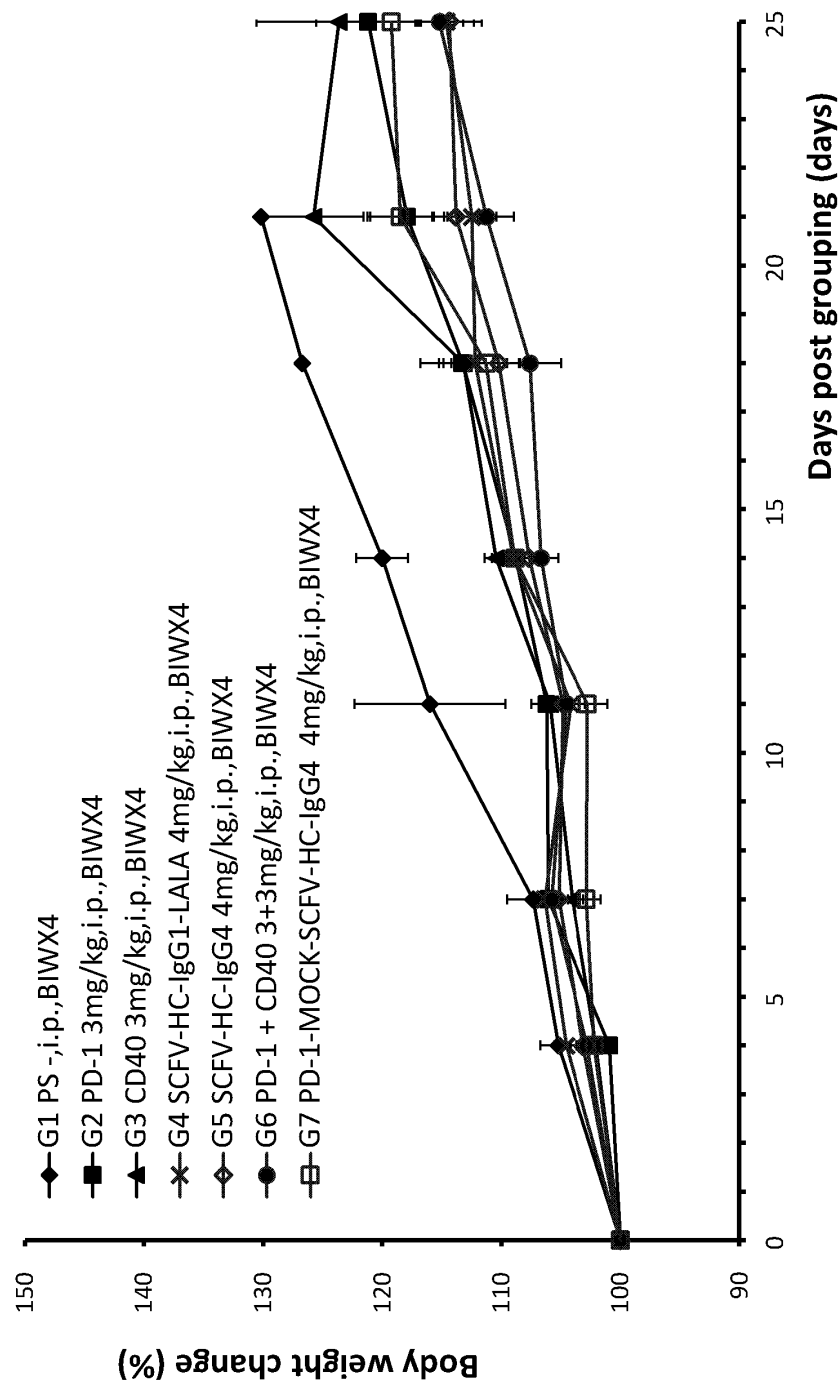


FIG. 11

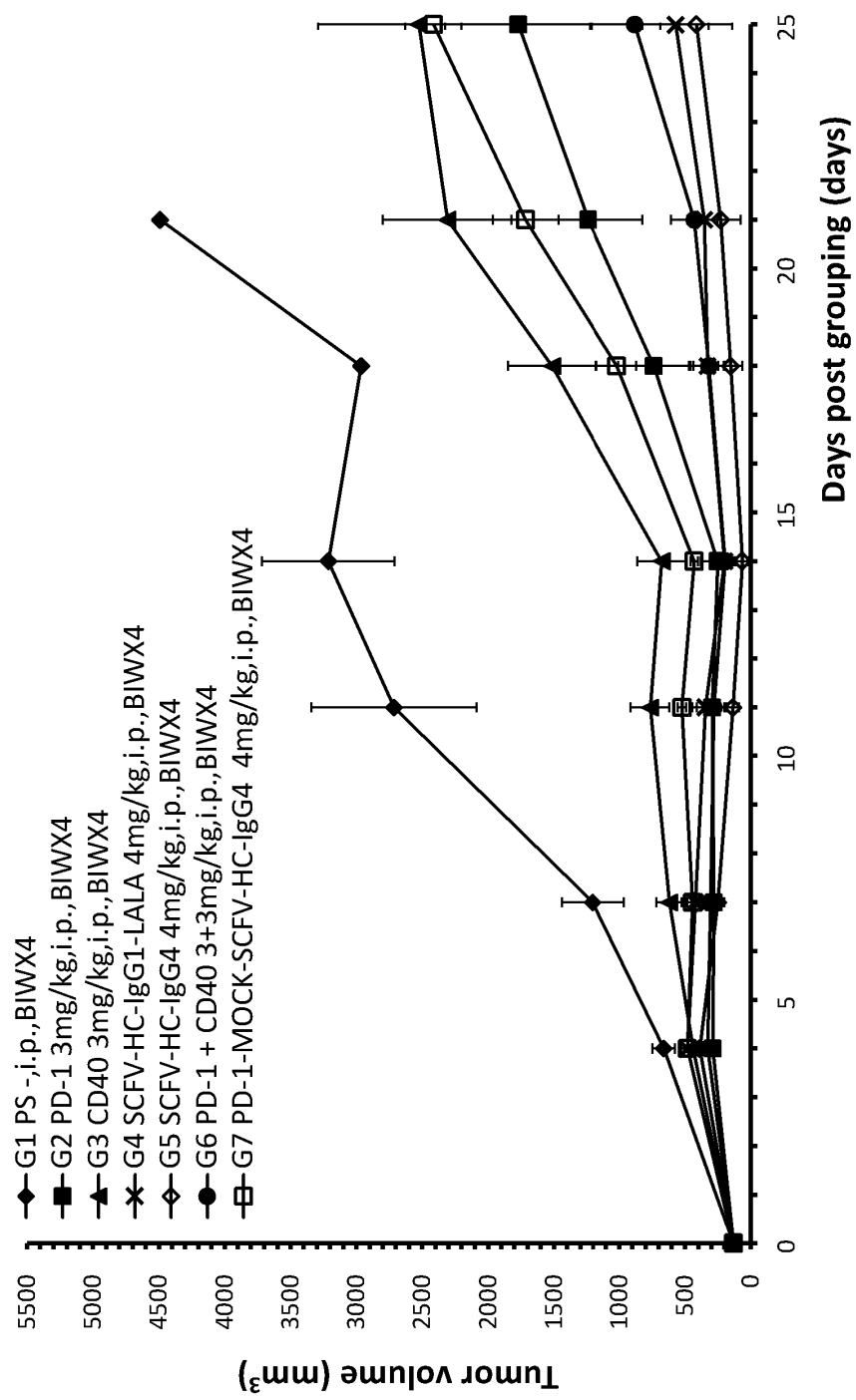


FIG. 12

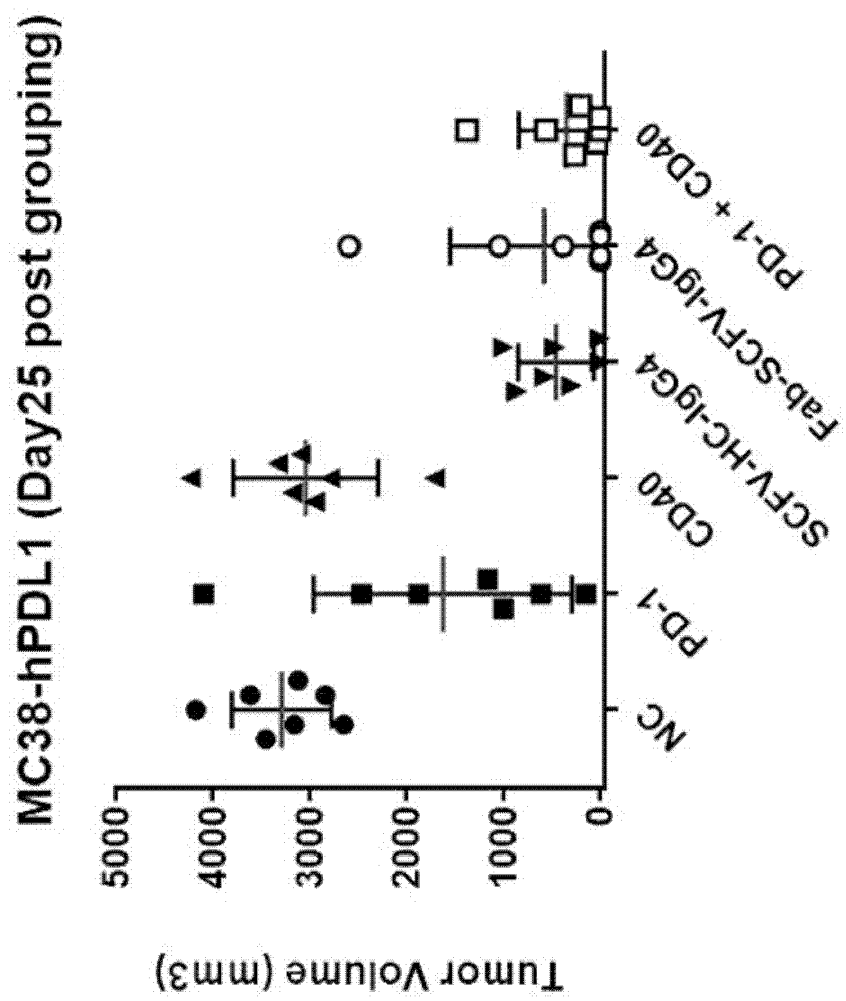


FIG. 13

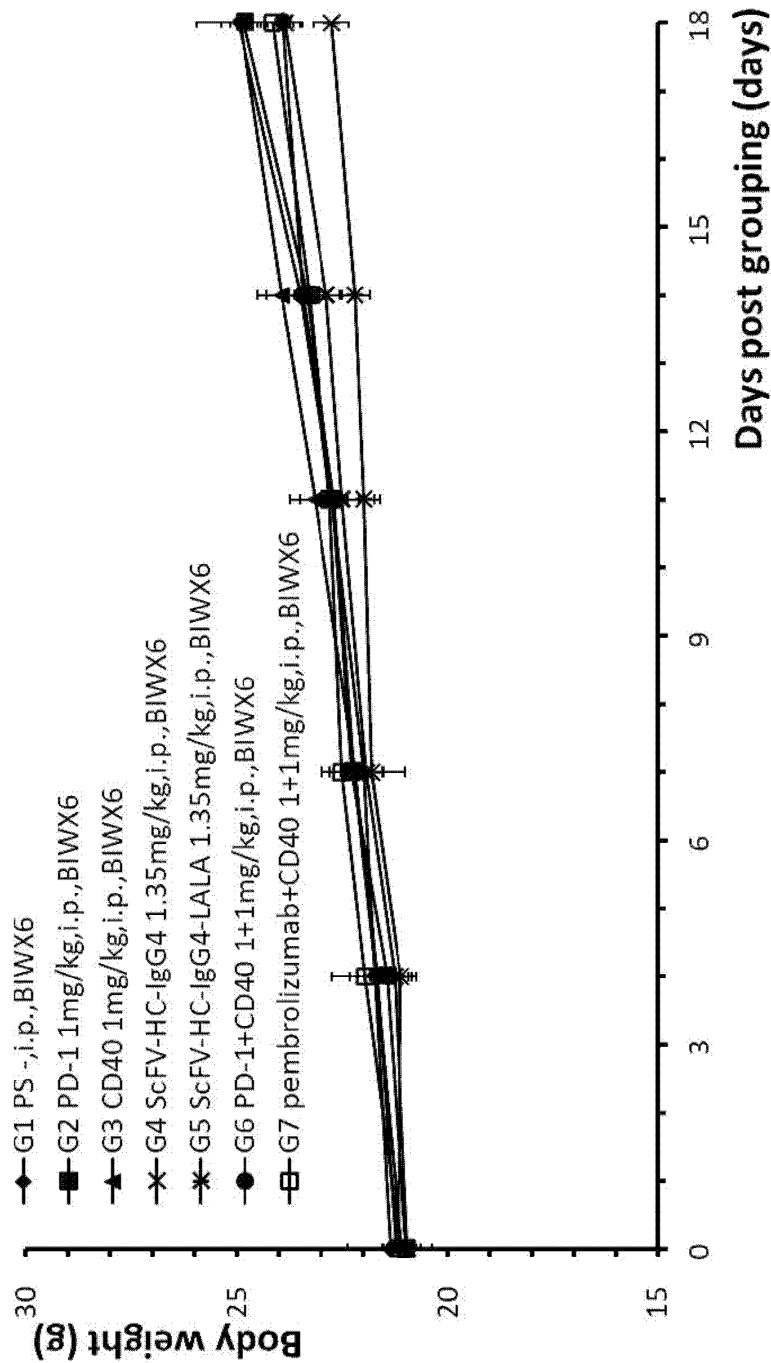


FIG. 14

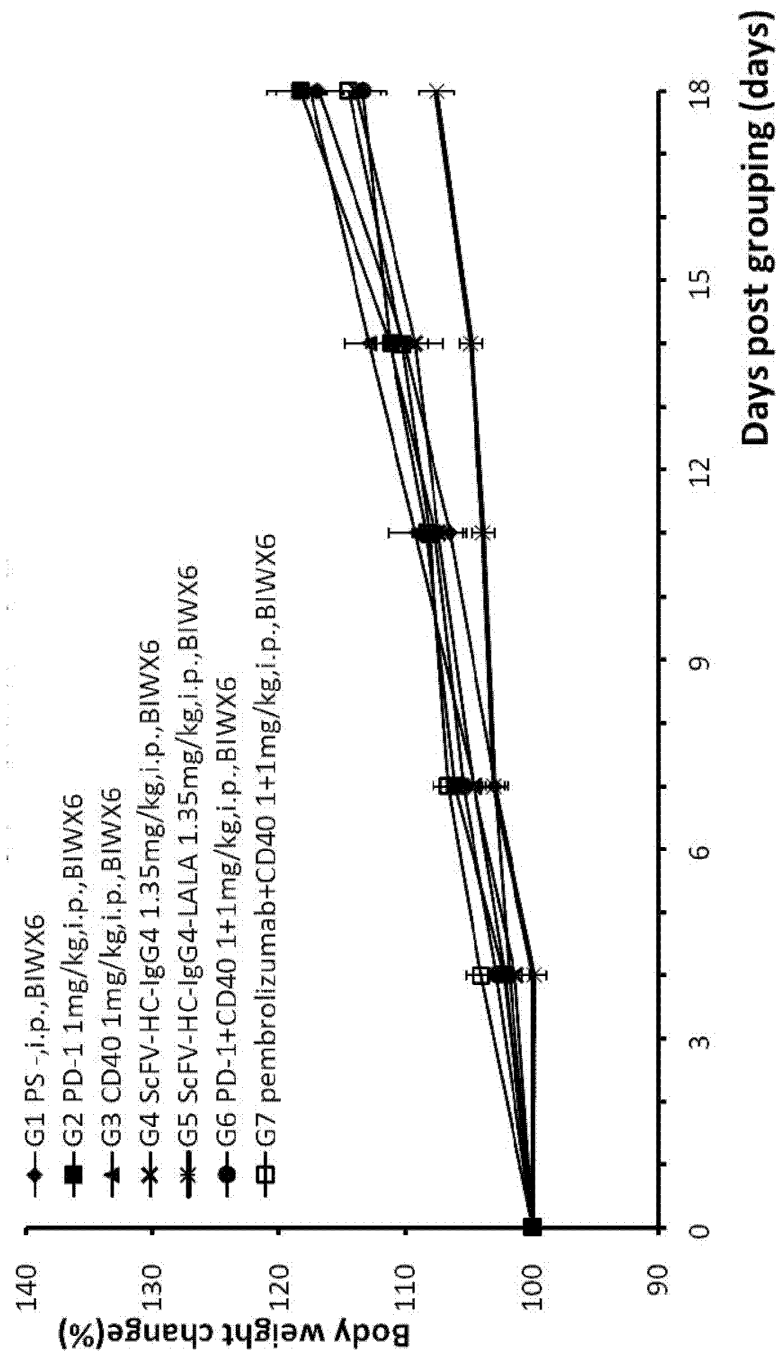


FIG. 15

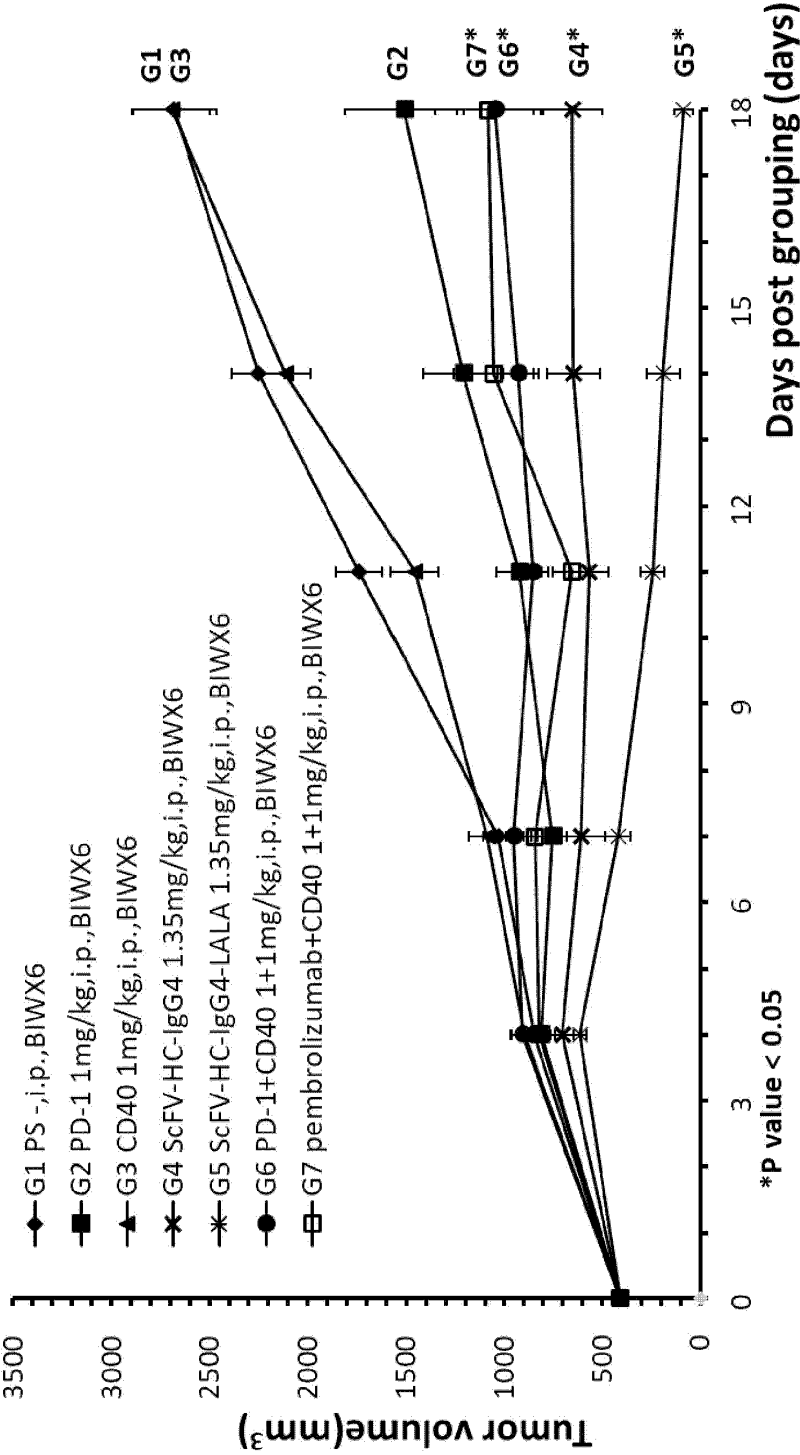


FIG. 16

Day13

ALT

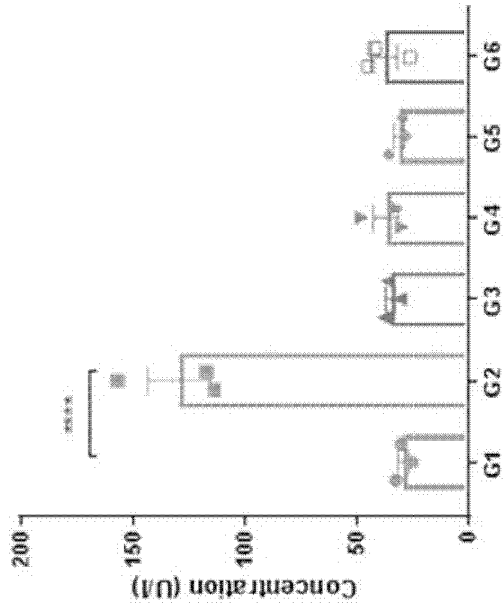


FIG. 17B

Day7

ALT

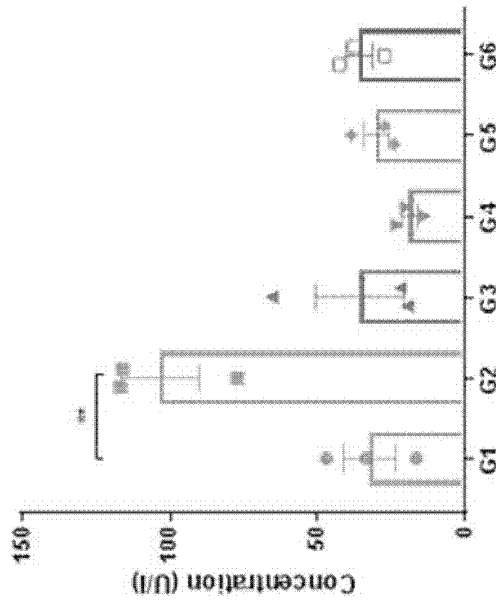


FIG. 17A

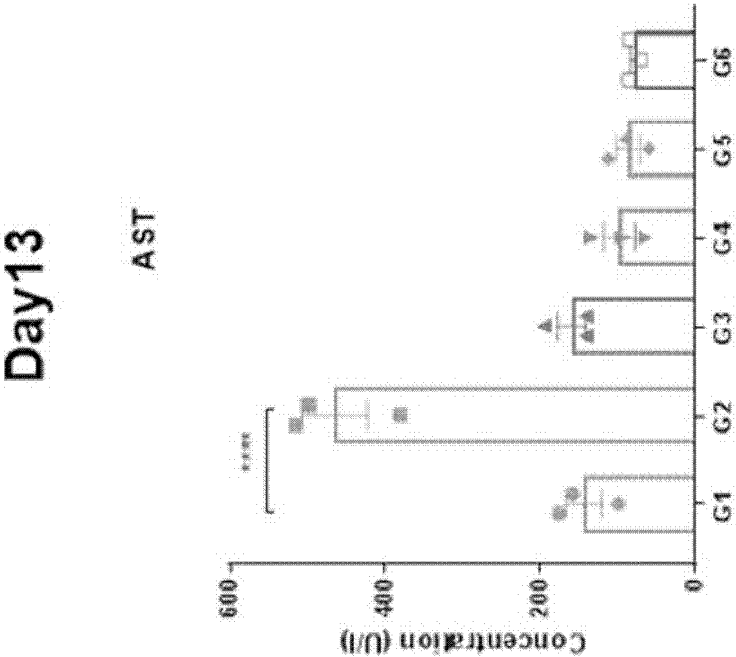


FIG. 17D

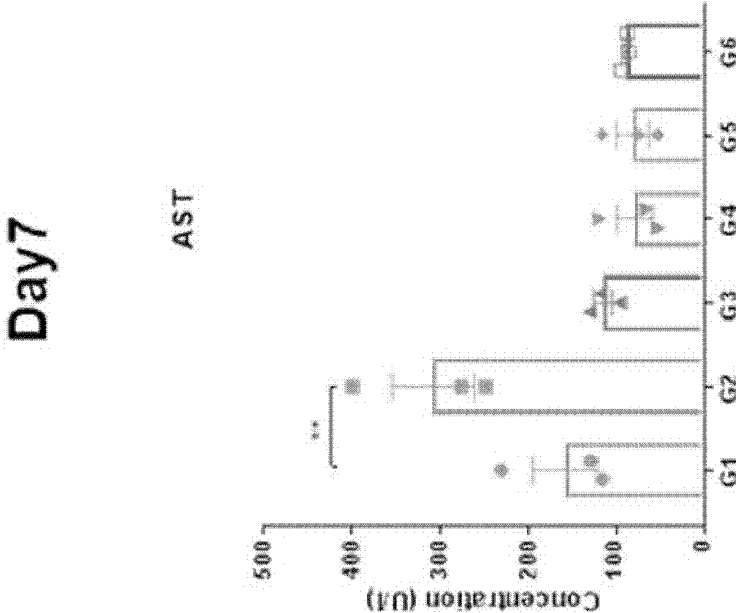
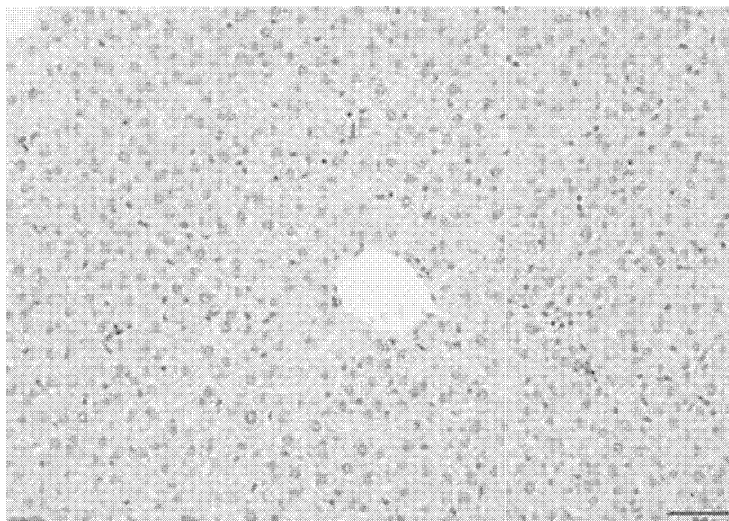


FIG. 17C

G1 PBS

Liver



Kidney

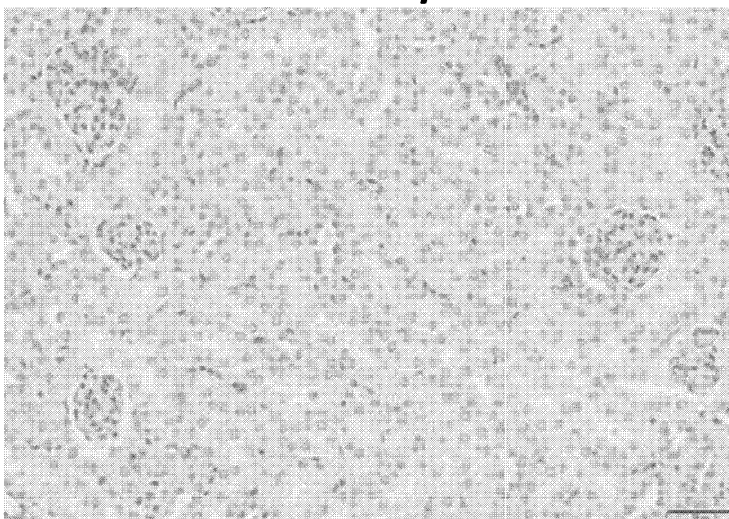
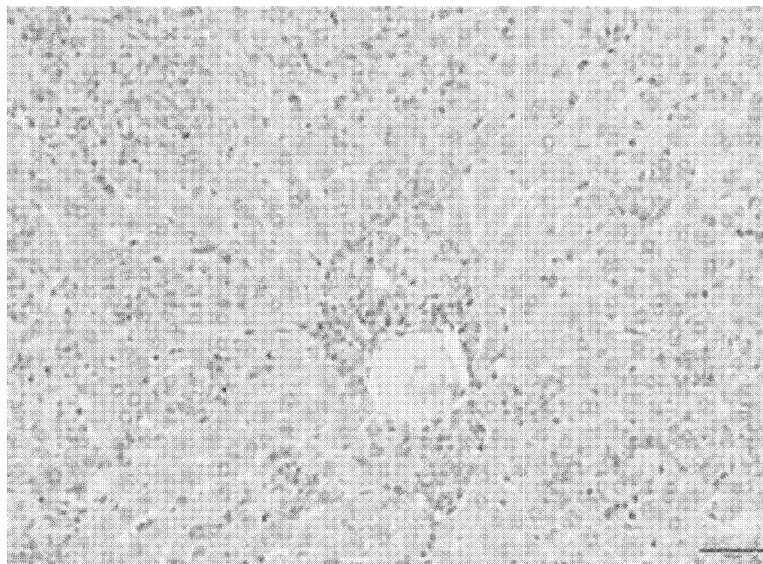


FIG. 17E

G2 Selicrelumab

Liver



Kidney

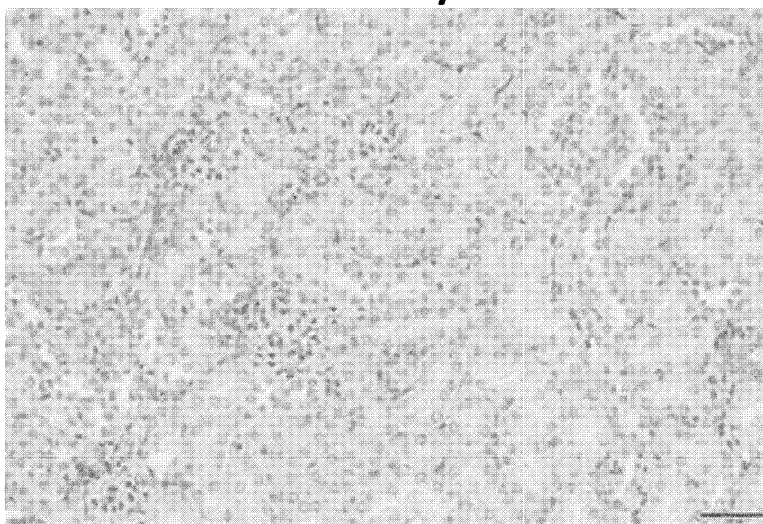
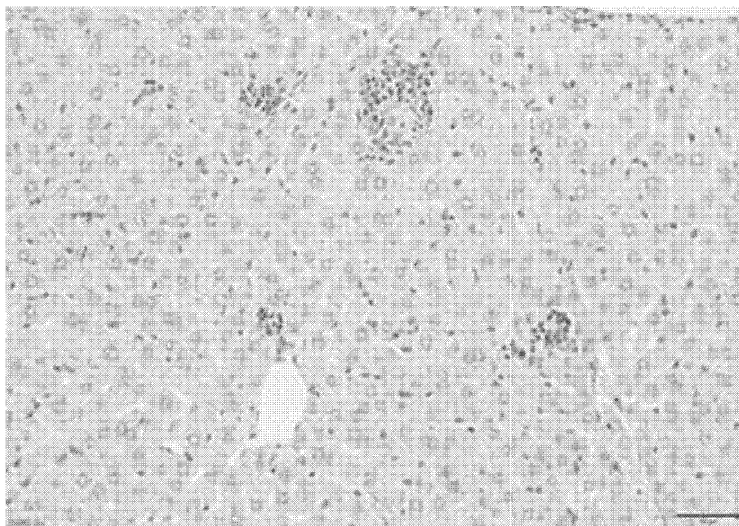


FIG. 17F

G3 6A7-H4K2-IgG2 (anti-CD40 mAb)

Liver



Kidney

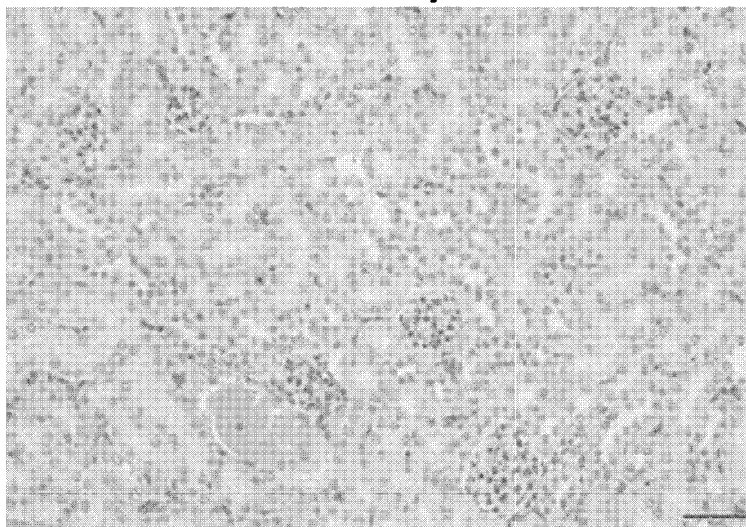
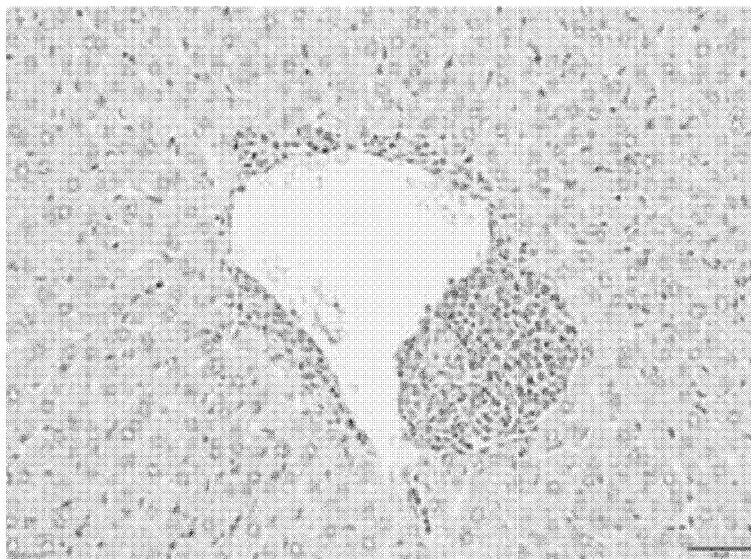


FIG. 17G

G4 1A7-H2K3-IgG4 (anti PD-1 mAb)

Liver



Kidney

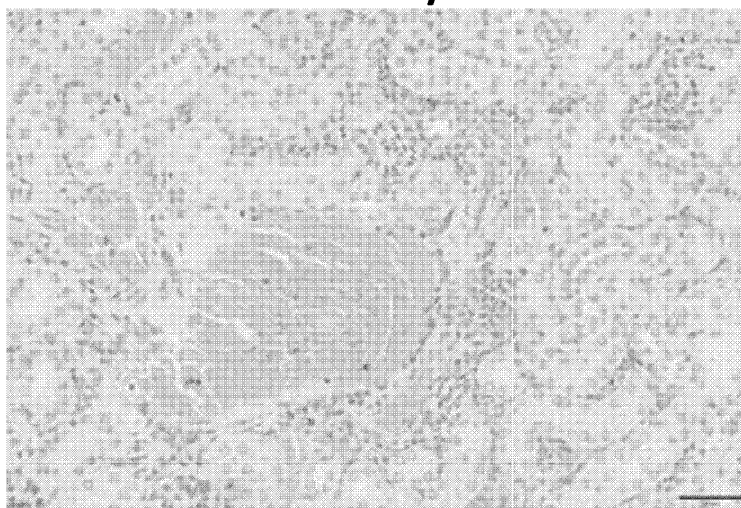
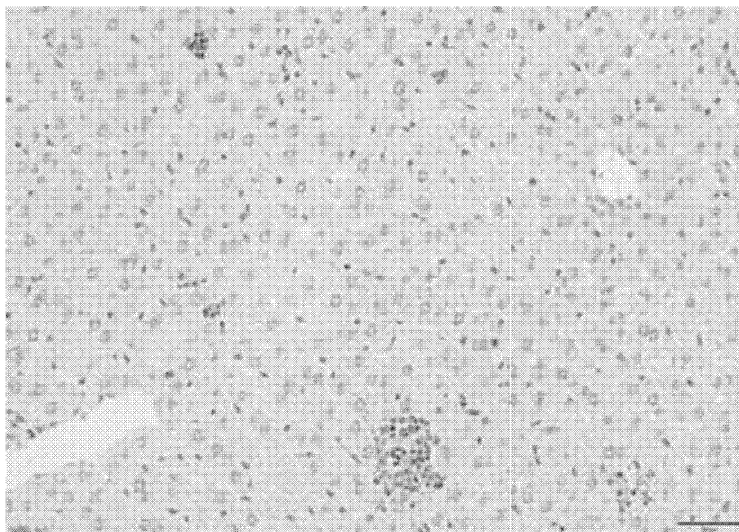


FIG. 17H

G5 SCFV-HC-IgG4

Liver



Kidney

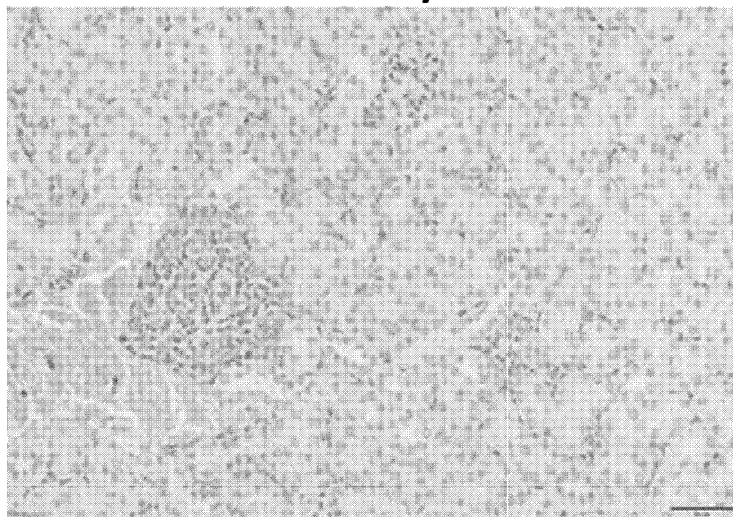
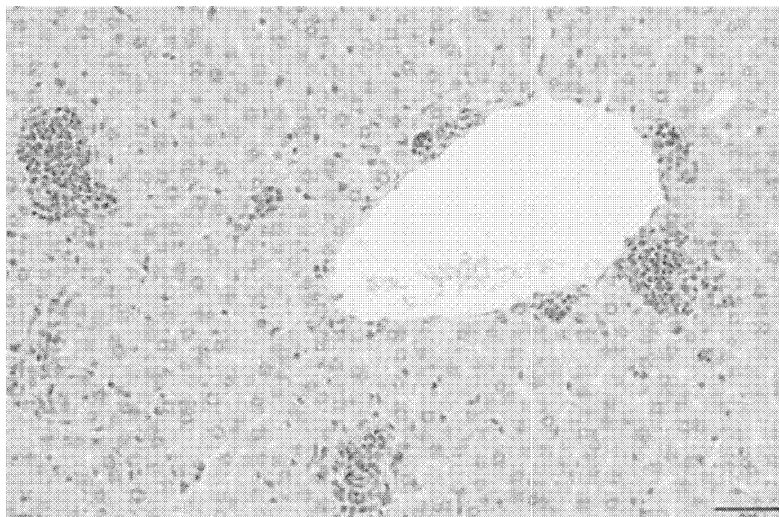


FIG. 17I

G6 Combo

Liver



Kidney

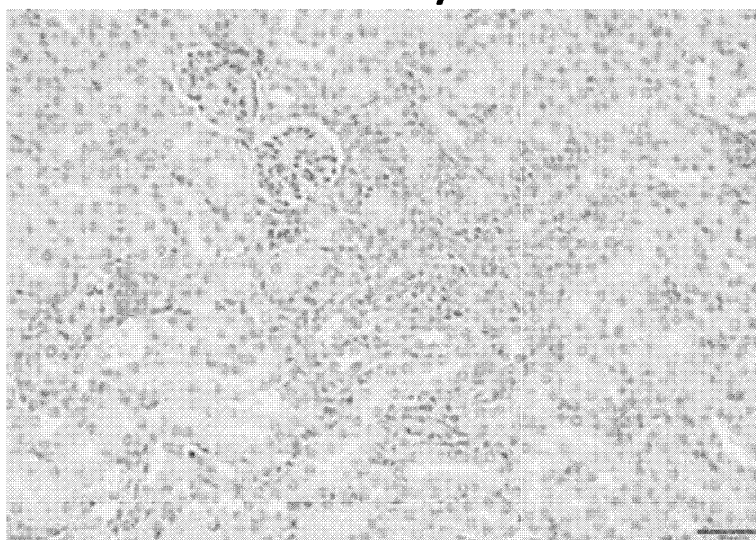
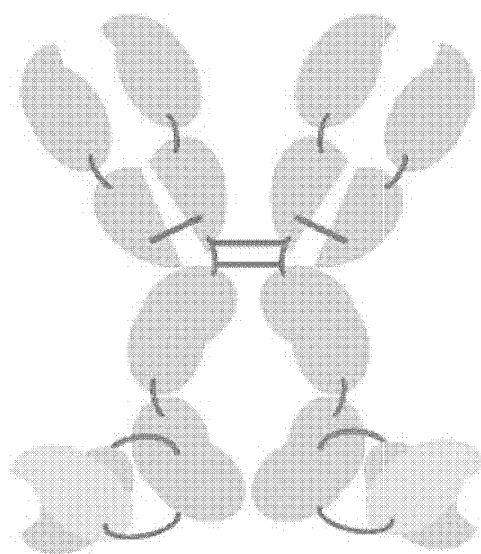


FIG. 17J



PD1-C40-6A7-FV3A

FIG. 18A

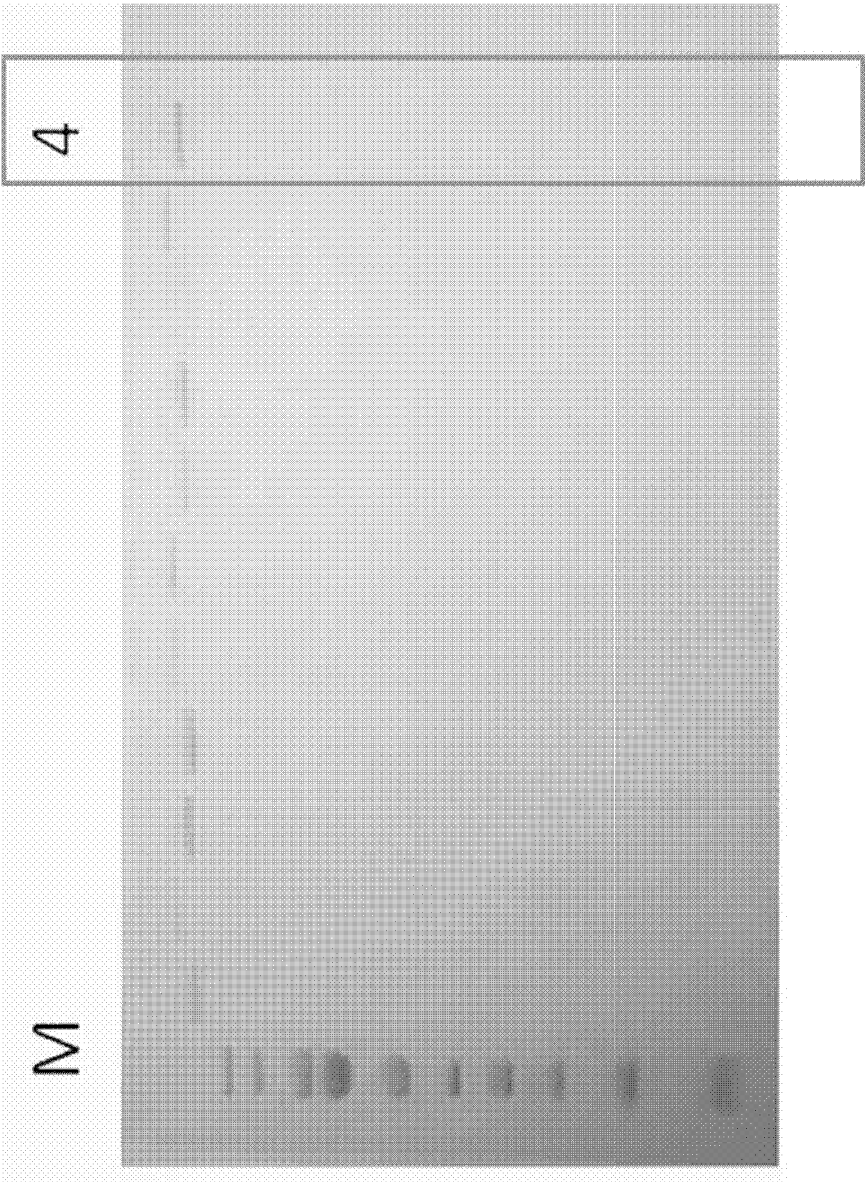


FIG. 18B

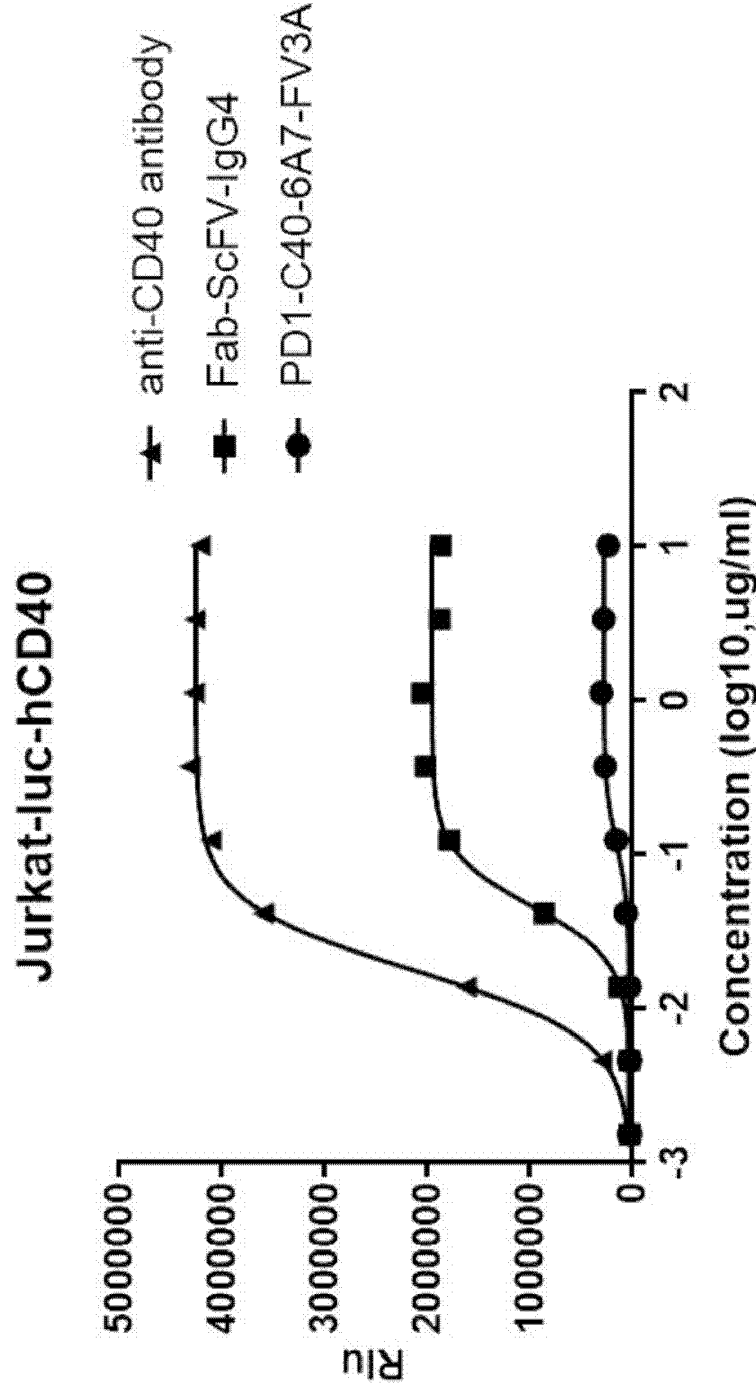


FIG. 18C

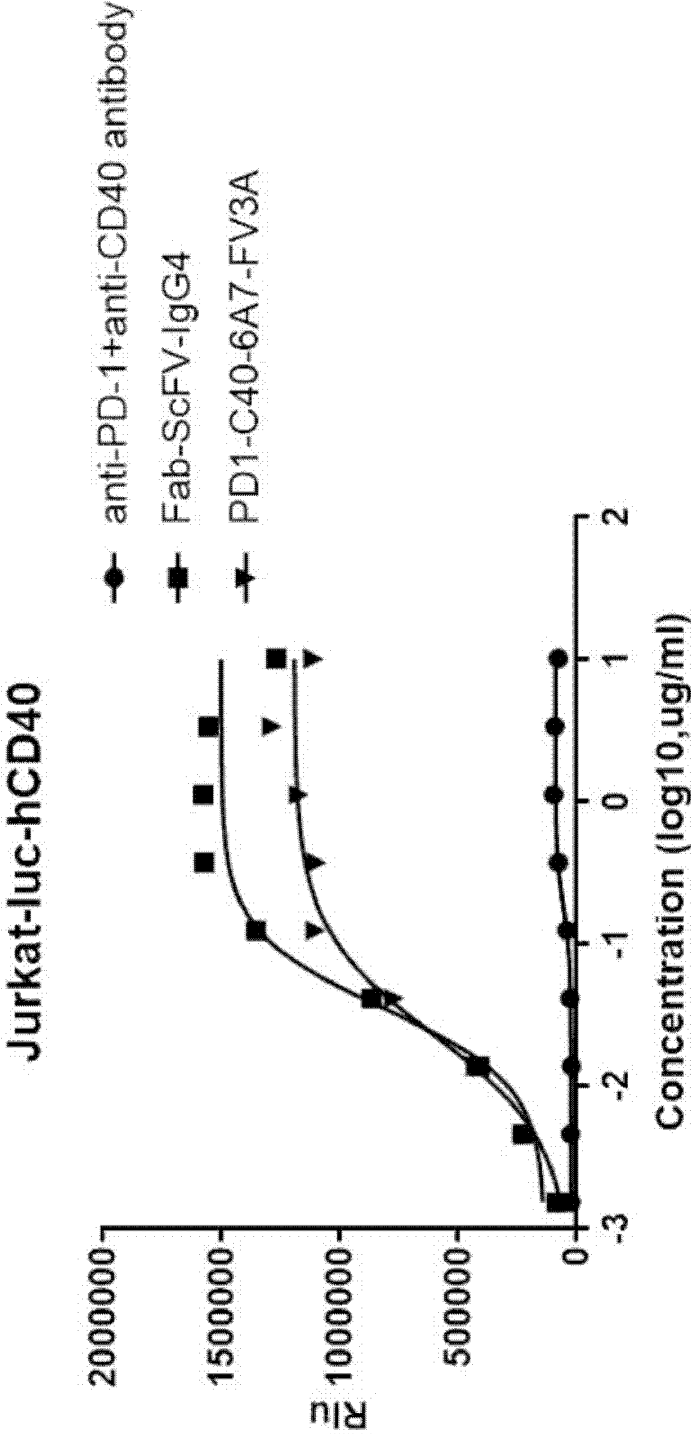


FIG. 18D

Kabat CDR for anti-PD1 antibodies

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Mouse anti-PD-1 antibody 25-1A7 and humanized 25-1A7	SYSMS	1	HISGGGSSTYYPD TVKG	2	QFYGGSEFW YFDV	3	KASQSVDFDG DSYMN	4	AASNLES	5	QQSNED PPT	6
Mouse anti-PD-1 antibody 18-3F1 and humanized 18-3F1	SYWM H	7	YINPSTGYTEYNQ KFKD	8	GVRYYFDY	9	KSSQSLLNSRT RKNYLA	10	WASTRES	11	KQSYNLL T	12
Mouse anti-PD-1 antibody 3-6G1 and humanized 3-6G1	SYWM H	13	YINPNTGYTEYN QKFKD	14	GTAYYFDY	15	KSSQSLLNSRT RKNYLA	16	WASTRES	17	KQSYNLLQ T	18

FIG. 19

Chothia CDR for anti-PD1 antibodies

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
Mouse anti-PD-1 antibody 25-1A7 and humanized 25-1A7	GFTFS SYSMS	19	SSGGSS	20	QFYYGSSFW YFDV	21	KASQSVDFDG DSYMN	22	AASNLES	23	QQSNED PPT	24
Mouse anti-PD-1 antibody 18-3F1 and humanized 18-3F1	GYTFT SYWM H	25	NPSTGY	26	GVRYYFDY	27	KSSQSLNSRT RKNYLA	28	WASTRES	29	KQSYNLL T	30
Mouse anti-PD-1 antibody 3-6G1 and humanized 3-6G1	GYTLT SYWM H	31	NPNTGY	32	GTAYYFDY	33	KSSQSLNSRT RKNYLA	34	WASTRES	35	KQSYNLQ T	36

FIG. 20

Protein	Amino acid sequence	SEQ ID NO
Human PD-1 (hPD-1) NP_005009.2	MQIPQAPWVWVAVLQLGWRPGWFLDSPDPWNPPTFSPALLVVTEGDNATFTCSFSNTSESVLNWYRMSPSNQTDKLAAF PEDRSQPGQDCRFRVTQLPNGRDFHMSVVRARRNDGTYLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSPSRPAG QFQTLVVGVGGLLGLVLLVWVLAVICSRRAAGTTGARRTGQPLKEDPSAVPVFSDYGELEDQFQWREKTPPEPPVPCVPEQT EYATIVFPSGMGTSSPARRGSADGPRSAQPLRPEDGHCSWPL	37
Mouse PD-1 (mPD-1) NP_032824.1	MWVRQVPWSFTWAVLQLSWQSGWLLLEVNGPWRSLTFYPAMLTVSEGANATFTCSLSNWSEDLMLNWNRLSPSNQTEKQAAF CNGLSQPVQDARFQIIQLPNRHD FHMNIIDTRRNDGTYLCGAISLHPKAKIEESPGAELVVTERILETS TRYPSPSPKPEG RFQGMVIGIMSA LVGIPVLLLLAWALAVFCSTSMSEARGAGSKDDTLKEEPSAAPVPSVAYEELDFQGREKTPELPTACVHT EYATIVFTEGLGASAMGRRGSADGLQGP RP RHEDGHCSWPL	38
Chimeric PD-1 (chiPD-1)	MWVRQVPWSFTWAVLQLSWQSGWLLLEVNGPWNPTFSPALLVVTEGDNATFTCSFSNTSESVLNWYRMSPSNQTDKLAAF PEDRSQPGQDCRFRVTQLPNGRDFHMSVVRARRNDGTYLCGAISLAPKAQIKESLRAELVVTERILETS TRYPSPSPKPEG RFQGMVIGIMSA LVGIPVLLLLAWALAVFCSTSMSEARGAGSKDDTLKEEPSAAPVPSVAYEELDFQGREKTPELPTACVHT EYATIVFTEGLGASAMGRRGSADGLQGP RP RHEDGHCSWPL	39

FIG. 21

FIG. 22

Humanized antibody variable domains	Description	AMINO ACID SEQUENCE	SEQ ID NO:
Humanized heavy chain variable domain H1 based on 25-1A7	HuVHv1: humanization percentage 89.8%; top hit to human and <i>Macaca fascicularis</i>	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQA PGKRLEWVAHISGGSSSTYYPD ^{SS} TVKGRFTISRDNKNTLY LQMNSLRAEDTAMYICTRQFYFGSSFWYFDVWGQGT ^{SS} TVTV	40
Humanized heavy chain variable domain H2 based on 25-1A7	HuVHv2: humanization percentage 88.8%; top hit to human and <i>Macaca fascicularis</i>	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQA PGKRLEWVAHISGGSSSTYYPD ^{SS} TVKGRFTISRDNKNTLY LQMNSLRAEDTAMYICTRQFYFGSSFWYFDVWGAGT ^{SS} TVTV	41
Humanized heavy chain variable domain H3 based on 25-1A7	HuVHv3: humanization percentage 87.8%; not top hit to human and <i>Macaca fascicularis</i>	EVKLIVESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQA PGKRLEWVAHISGGSSSTYYPD ^{SS} TVKGRFTISRDNKNTLY LQMNSLRAEDTAMYICTRQFYFGSSFWYFDVWGAGT ^{SS} TVTV	42
Humanized light chain variable domain K1 based on 25-1A7	HuVLv1: humanization percentage 84.8%; top hit to human and <i>Macaca fascicularis</i>	DNVLTQSPATLSLSPGERATLSCKASQSVDFDGD ^{SS} SYMNWY QQKPGQPPRLLIYAASNLESGIPARFSGSGPGTDF ^{SS} TLTIS SLEPEDFATYYCQQSNEDPPTFGGGTKVEIK	43
Humanized light chain variable domain K2 based on 25-1A7	HuVLv2: humanization percentage 83.7%; not top hit to human and <i>Macaca fascicularis</i>	DNVLTQSPATLSVSPGERATLSCKASQSVDFDGD ^{SS} SYMNWY QQKPGQPPRLLIYAASNLESGIPARFSGSGPGTDF ^{SS} TLTIS SLEPEDFATYYCQQSNEDPPTFGGGTKVEIK	44
Humanized light chain variable domain K3 based on 25-1A7	HuVLv3: humanization percentage 81.5%; not top hit to human and <i>Macaca fascicularis</i>	DNVLTQSPATLSVSPGERATLSCKASQSVDFDGD ^{SS} SYMNWY QQKPGQPPRLLIYAASNLESGIPARFSGSGSGTDF ^{SS} TLTIS SVEPEDFATYYCQQSNEDPPTFGGGTKVEIK	45
Humanized heavy chain variable domain H1 based on 3F1	HuVHv1: humanization percentage 84.7%; Not top hit to human and <i>Macaca fascicularis</i>	QVQLQQSGAEVKKPGASVKMSCKASGYTFTSYMMHWVRQA PGQGLEWIGYINPSTGYEYNQKFKDRATLTADTSTSTAY MELSSLRSEDTAVYYCAFGVRYFYFDYWGQGT ^{SS} LVTVSS	46
Humanized heavy chain variable domain H2 based on 3F1	HuVHv2: humanization percentage 81.6%; Not top hit to human and <i>Macaca fascicularis</i>	QVQLQQSGAEVKKPGASVKMSCKASGYTFTSYMMHWVKQR PGQGLEWIGYINPSTGYEYNQKFKDRATLTADKSTSTAY MELSSLRSEDTAVYYCAFGVRYFYFDYWGQGT ^{SS} LVTVSS	47

Humanized heavy chain variable domain H3 based on 3F1	HuVhV3: humanization percentage 81.6 % ; not top hit to human and <i>Macaca fascicularis</i>	QVQLQQSGAEVAKPGASVKMSCKASGYTFTSYMMHWVKQR PGQGLEWIGYINPSTGYEYNQKFKDRATLTADTSTSTAY MELSSLRSEDTAVYYCARGVRYFFDYWGQGTLLTVSS	48
Humanized heavy chain variable domain H4 based on 3F1	HuVhV3: humanization percentage 79.6 % ; not top hit to human and <i>Macaca fascicularis</i>	QVQLQQSGAEVAKPGASVKMSCKASGYTFTSYMMHWVKQR PGQGLEWIGYINPSTGYEYNQKFKDRATLTADTSTSTAY MELSSLTSEDTAVYYCARGVRYFFDYWGQGTLLTVSS	49
Humanized light chain variable domain K1 based on 3F1	HuVlV1: humanization percentage 88.9 % ; Not top hit to human and <i>Macaca fascicularis</i>	DIVMTQSPDLSAVSLGERATISCKSSQSLNLSRTRKKNYLA WYQKPGQSPKLLIYMASTRESGVPDRFSGSGSGTDFTLT I SSVQAEDVAVYYCKQSYNLLTFGQGT KLELK	50
Humanized light chain variable domain K2 based on 3F1	HuVlV2: humanization percentage 87.9 % ; not top hit to human and <i>Macaca fascicularis</i>	DIVMTQSPDLSAVSLGERATMSCKSSQSLNLSRTRKKNYLA WYQKPGQSPKLLIYMASTRESGVPDRFSGSGSGTDFTLT I SSVQAEDVAVYYCKQSYNLLTFGQGT KLELK	51
Humanized light chain variable domain K3 based on 3F1	HuVlV3: humanization percentage 84.8 % ; not top hit to human and <i>Macaca fascicularis</i>	DIVMTQSPSSLAVERVMTMSCKSSQSLNLSRTRKKNYLA WYQKPGQSPKLLIYMASTRESGVPDRFSGSGSGTDFTLT I SSVQAEDVAVYYCKQSYNLLTFGQGT KLELK	52
25-1A7("1A7")	Mouse heavy chain variable region	EVKLIVSGGGLVQPGGSLKLSAASGFTFSSYSMSWVRQT PEKRLWVAHISGGSSSTYPDTVKGRFTISRDNARNTLY LQMSSLKSEDTAMYCYTRQFYGYSSFWYFDVWGAGTTVTV SS	53
25-1A7("1A7")	Mouse light chain variable region	DNVLTQSPVSLAVSLGQRATISCKASQSVDFDGDSYMNNWY QKPGQSPKLLIYAASNLESGIPARFSGSGSGTDFTLNIIH PVEEDAATYYCQQSNEDPPTFGGGTKLEIK	54
18-3F1 ("3F1")	Mouse heavy chain variable region	QVQLQQSGAEELAKPGASVKMSCKASGYTFTSYMMHWVKQR PGQGLEWIGYINPSTGYEYNQKFKDKATLTADKSSSTAY MQLSSLTSEDSAVYYCARGVRYFFDYWGQGTLLTVSS	55
18-3F1("3F1")	Mouse light chain variable region	DIVMSQSPSSLAVERVMTMSCKSSQSLNLSRTRKKNYLA WYQKPGQSPKLLIYMASTRESGVPDRFTGSGSGTDFTLT I SSVQAEDLAVYYCKQSYNLLTFGAGTKLELK	56
3-6G1("6G1")	Mouse heavy chain variable region	QVQLQQSGAEELAKPGASVKMSCKASGYTFTSYMMHWVKQR PGQGLEWIGYINPNTGYEYNQKFKDKATLTADKSSSTAY MQLSSLTSEDSAVYYCARGTAYFFDYWGQGTLLTVSS	57

3-6G1("6G1")	Mouse light chain variable region	DIVMSQSPSSLAVSAGEKVTMSCKSSQSLNSRTRKNYLA WYQOKPGQSPKLLIYMASTRESGVPDRFTGSGGDTFLT ISSVQAEDLAVYYCKQSYNLTQTFGGGTKLEIK	58
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Kabat CDR for anti-CD40 antibodies

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
03-7F10 or humanized 03-7F10	DYYM Y	59	YISYGGDSTFYPD TVRG	60	PAPSAHSYY LDY	61	RASQDISNYLN	62	YYTSRLHS	63	QQGKTLP FT	64
06-6A7 or humanized 06-6A7	SYIY	65	GINPRNGGTNFN EKFS	66	HGNGVY	67	RSSQSLLHSNG NTYLH	68	QVSNRFS	69	SQTTHVP WT	70
07-4H6 or humanized 07-4H6	SGYW N	71	FISYSGSTYYTPSL KS	72	FRYDDGVD Y	73	RASHEISGYLS	74	AASTLAS	75	LQYSSYP WT	76

FIG. 23

Chothia CDR for anti-CD40 antibodies

Ab	VH CDR1	SEQ ID:	VH CDR2	SEQ ID:	VH CDR3	SEQ ID:	VL CDR1	SEQ ID:	VL CDR2	SEQ ID:	VL CDR3	SEQ ID:
03-7F10 or humanized 03-7F10	GFTFSD YYMY	77	SYGGDS	78	PAPSAHSYY LDY	79	RASQDISNYLN	80	YTSRLHS	81	QQGKTLP FT	82
06-6A7 or humanized 06-6A7	GYTFISY YIY	83	NPRNGG	84	HGNGVY	85	RSSQSLHHSNG NTYLH	86	QVSNRFS	87	SQTTHVP WT	88
07-4H6 or humanized 07-4H6	GDSVSS GYWN	89	SYSGS	90	FRYDDGVD Y	91	RASHEISGYLS	92	AASTLAS	93	LQYSSYP WT	94

FIG. 24

Protein	Amino acid sequence	SEQ ID NO:
Human CD40 (hCD40) NP_001241.1	MVRLPLQCVLWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTETETECCLPCGESEFL DTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESCVLHRSCSPGFGVKQIAT GVSDTICEPCPVGFFSNVSSAFKCHPWTSCETKDLVVQAGTNKTDVCGPQDRLRALVVIPIIFGI LFAILLVLFIKKVAKKPTNKAPHPKQEPQEIFPDDLPGSNTAAPVQETLHGCQPVQTQEDGKESRIS VQERQ	95
Mouse CD40 (mCD40) NP_035741.2	MVSLPRLCALWGCLLTAVHLGCVTCSDKQYLHDGQCCLCPGSRSLTSHCTALEKTQCHPCDSGEFS AQWNREIRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGHCTSKDCEACAQHTPCIPGFGVMEMAT ETTDVCHPCPVGFFSNQSSLEKCYPWTSCEDKNLEVLQKGTSTQTNVICGLKSRMRALLVIPVVMGI LITIFGVFLYIKKVVKKPKDNEILPPAARRQDPQEMEDYPGHNTAAPVQETLHGCQPVQTQEDGKESRI SVQERQVTDSIALRPLV	96
Chimeric CD40 (chiCD40) (Humanized CD40)	MVSLPRLCALWGCLLTAVHPEPTACREKQYLINSQCCLCPGQKLVSDCTETETECCLPCGESEFL DTWNRETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEACESCVLHRSCSPGFGVKQIAT GVSDTICEPCPVGFFSNVSSAFKCHPWTSCETKDLVVQAGTNKTDVCGPQDRLRALVVIPIVVMGI LITIFGVFLYIKKVVKKPKDNEILPPAARRQDPQEMEDYPGHNTAAPVQETLHGCQPVQTQEDGKESRI SVQERQVTDSIALRPLV	97

FIG. 25

FIG. 26

Humanized antibody variable domains	Description	AMINO ACID SEQUENCE	SEQ ID NO:
Humanized heavy chain variable domain (H1) based on 7F10	HuVHv1: humanization percentage 84.7%; Not top hit to human and <i>Macaca fascicularis</i>	EVQLVESGGGLVQPGGSLRLSCATSGFTFSDYYMWVRQAPG KRLWVAYISYGGDSTFYDPDVRGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARPAPSAHSYYLDYWGQGTLTIVSS	98
Humanized heavy chain variable domain (H2) based on 7F10	HuVHv2: humanization percentage 82.7%; Not top hit to human and <i>Macaca fascicularis</i>	EVQLVESGGGLVQPGGSLRLSCATSGFTFSDYYMWVRQAPG KRLWVAYISYGGDSTFYDPDVRGRFTISRDNAKNSLYLQMS SLKAEDTAVYYCARPAPSAHSYYLDYWGQGTLTIVSS	99
Humanized heavy chain variable domain (H3) based on 7F10	HuVHv3: humanization percentage 78.6%; Not top hit to human and <i>Macaca fascicularis</i>	EVQLVESGGGLVQPGGSLRLSCATSGFTFSDYYMWVRQAPG KRLWVAYISYGGDSTFYDPDVRGRFTISRDNAKNSLYLQMS RLKAEDTAVYYCARPAPSAHSYYLDYWGQGTLTIVSS	100
Humanized light chain variable domain (K1) based on 7F10	HuVLv1: humanization percentage 85.3%; top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSSLSASVGRVITICRASQDISNYLNWYQQKPGG AVKLLIYYTSRLHSGLPSRFSGSGGTDTFTISSLQPEDIA TYCQQGKTLPTTFASGTKLEIK	101
Humanized light chain variable domain (K2) based on 7F10	HuVLv2: humanization percentage 84.2%; Not top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSSLSASVGRVITICRASQDISNYLNWYQQKPGG AVKLLIYYTSRLHSGLPSRFSGSGGTDTFTISSLQPEDIA TYCQQGKTLPTTFASGTKLEIK	102
Humanized light chain variable domain (K3) based on 7F10	HuVLv3: humanization percentage 82.1%; Not top hit to human and <i>Macaca fascicularis</i>	DIQMTQSTSSLSASVGRVITICRASQDISNYLNWYQQKPGG AVKLLIYYTSRLHSGLPSRFSGSGGTDTFTISSLQQEDIA TYCQQGKTLPTTFASGTKLEIK	103
Humanized light chain variable domain (K4) based on 7F10	HuVLv4: humanization percentage 80%; Not top hit to human and <i>Macaca fascicularis</i>	DIQMTQSTSSLSASVGRVITICRASQDISNYLNWYQQKPDG TVKLLIYYTSRLHSGLPSRFSGSGGTDTFTISSLQQEDIA TYCQQGKTLPTTFASGTKLEIK	104

Humanized heavy chain variable domain (H1) based on 6A7	HuVHv1: humanization percentage 84.7%; top hit to human and <i>Macaca fascicularis</i>	QVQLVQSGAEVKKPGASVKVSCKASGYTFISYYIYWVRQAPG QGLEWMGGINPRNGGTFNEKFKSRVTLTVDTSISTAYMELS RLRSEDVAVYICARHNGVYWGQGTITVTVSS	105
Humanized heavy chain variable domain (H2) based on 6A7	HuVHv2: humanization percentage 82.7%; top hit to human and <i>Macaca fascicularis</i>	QVQLVQSGAEVKKPGASVKVSCKASGYTFISYYIYWVRQAPG QGLEWIGGINPRNGGTFNEKFKSRATLTVDTSISTAYMELS RLRSEDVAVYICARHNGVYWGQGTITVTVSS	106
Humanized heavy chain variable domain (H3) based on 6A7	HuVHv3: humanization percentage 81.6%; top hit to human and <i>Macaca fascicularis</i>	QVQLVQSGAEVKKPGASVKVSCKASGYTFISYYIYWVRQAPG QGLEWIGGINPRNGGTFNEKFKSRATLTVDTSISTAYMELS RLRSEDVAVYICARHNGVYWGQGTITVTVSS	107
Humanized heavy chain variable domain (H4) based on 6A7	HuVHv4: humanization percentage 79.6%; top hit to human and <i>Macaca fascicularis</i>	QVQLVQSGAEVKKPGASVKLSCKASGYTFISYYIYWVRQAPG QGLEWIGGINPRNGGTFNEKFKSRATLTVDTSISTAYMELS RLRSEDVAVYICARHNGVYWGQGTITVTVSS	108
Humanized light chain variable domain (K1) based on 6A7	HuVLv1: humanization percentage 91%; top hit to human and <i>Macaca fascicularis</i>	DVMTQSPSLPVTLGQPAISCRSSQSLHLSNGNTYLHWfQ QrPGQSPRHIIYQVSNRFSGVDPDRFSGSGGTDTLTKISRVE AEDVGVYFCSTTHVPTWTFGGGTKEIK	109
Humanized light chain variable domain (K2) based on 6A7	HuVLv2: humanization percentage 88%; Not top hit to human and <i>Macaca fascicularis</i>	DVMTQSPSLPVTLGQPAISCRSSQSLHLSNGNTYLHWYQ QRPQSPNHLIIYQVSNRFSGVDPDRFSGSGGTDTLTKISRVE AEDVGVYFCSTTHVPTWTFGGGTKEIK	110
Humanized light chain variable domain (K3) based on 6A7	HuVLv3: humanization percentage 87%; Not top hit to human and <i>Macaca fascicularis</i>	DVMTQSPSLPVTLGQPAISCRSSQSLHLSNGNTYLHWYQ QRPQSPNHLIIYQVSNRFSGVDPDRFSGSGGTDTLTKISRVE AEDVGVYFCSTTHVPTWTFGGGTKEIK	111
Humanized heavy chain variable domain (H1) based on 4H6	HuVHv1: humanization percentage 88.9%; top hit to human and <i>Macaca fascicularis</i>	QVQLQESGPGLVKPSQTLSTCTVSGDSVSSGYWNWIRKHPG KKLEWIGFISYSGSTYYTSPSLKSRVTISRDTSKNQFSLKLSS VTAADTAVYICARFRYYDDGVDYWGQGTITVTVSS	112
Humanized heavy chain variable domain (H2) based on 4H6	HuVHv2: humanization percentage 87.9%; top hit to human and <i>Macaca fascicularis</i>	EVQLQESGPGLVKPSQTLSTCTVSGDSVSSGYWNWIRKHPG KKLEWIGFISYSGSTYYTSPSLKSRVTISRDTSKNQFSLKLSS VTAADTAVYICARFRYYDDGVDYWGQGTITVTVSS	113

Humanized heavy chain variable domain (H3) based on 4H6	HuVHv3: humanization percentage 83.8%; top hit to human and <i>Macaca fascicularis</i>	EVQLQESGPGLVKPSQTLISLTCTVSGDSVSSGYWNWIRKHPG KKLEYMGFI SYSGSTYTPSLKSRITISRDTSKNQFSLKLSS VTAADTAVYFCARFRYYDDGVDYWGQGLTVTVSS	114
Humanized heavy chain variable domain (H4) based on 4H6	HuVHv4: humanization percentage 82.8%; top hit to human and <i>Macaca fascicularis</i>	EVQLQESGPGLVKPSQTLISLTCTVSGDSVSSGYWNWIRKFP KKLEYMGFI SYSGSTYTPSLKSRITISRDTSKNQFSLKLSS VTAADTAVYFCARFRYYDDGVDYWGQGLTVTVSS	115
Humanized light chain variable domain (K1) based on 4H6	HuVLv1: humanization percentage 87.4%; top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSAMSASVGDRTVITCRASHEISGYLSWIFQKPGG VIKRLINAASTLASGVPSRFSRSGTEFTLTISLSLQPEDFA tYYCLQYSSYPWTFGGKLEIK	116
Humanized light chain variable domain (K2) based on 4H6	HuVLv2: humanization percentage 84.2%; top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSAMSASVGDRTVITCRASHEISGYLSWIFQKPGG TIKRLINAASTLASGVPSRFSRSGTEFTLTISLSLQPEDFA DYYCLQYSSYPWTFGGKLEIK	117
Humanized light chain variable domain (K3) based on 4H6	HuVLv3: humanization percentage 83.2%; top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSAMSASVGDRTVITCRASHEISGYLSWIFQKPGG TIKRLINAASTLASGVPSRFSRSGTEFTLTISLSLQPEDFA DYYCLQYSSYPWTFGGKLEIK	118
Humanized light chain variable domain (K4) based on 4H6	HuVLv4: humanization percentage 82.1%; Not top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSAMSASVGDRTVITCRASHEISGYLSWIFQKPGG TIKRLINAASTLASGVPSRFSRSGTEFTLTISLSLQPEDFA DYYCLQYSSYPWTFGGKLEIK	119
03-7F10 ("7F10")	Mouse heavy chain variable region	EVKLVEGGGLVQPGGSLKLSKATSGFTFSDYMYWVRQTPE KRLWVAYI SYGGDSTFYPDTVRGFTISRDNALYIQLMS RLKSEDTAVYYCARPAPSAHSYYLDYWGQGLTVTVSS	120
03-7F10 ("7F10")	Mouse light chain variable region	DIQMTQTTSSLASLGRVTISCRASQDISNYLNWYQKQPDG TVKLLIYTSRLHSLGFSRFSRSGSDYSLTISNLEQEDIA TYCQQGKTLPTFASGKLEIK	121
06-6A7 ("6A7")	Mouse heavy chain variable region	QVQLQQPAGELVKPGASVKLSCKASGYTFISYIYWKQRP QGLEWIGGINPRNGGTNFEKFKSKATLTVDKSSSTAYMQLS SLTSEDSAVYYCTRHNGVYWGQGLTVTVSS	122

06-6A7 ("6A7")	Mouse light chain variable region	DVMTQTPLSLPVSLGDAQASISCRSSQSLHNSGNTYLHWYL QKPGQSPNHLIYQVSNRFGVDPDRFSGSGGTDFTLKISRVE AEDLGVIYFCSQTTHVPTWTFGGGTKLEIK	123
07-4H6 ("4H6")	Mouse heavy chain variable region	EVKLQESGPSLVKPSQLSLTCSVTGDSVSSGYWNWIRKFP NKLEYMGFIYSYSGTYYTSPSLKSRISITRDTSKNQFYQLNS VTEDTATYFCARFRYDDVDYWGQGTTLTVSS	124
07-4H6 ("4H6")	Mouse light chain variable region	DIQMTQSPSSLSASLGERVSLTCSRASHEISGYLSWIIQQKPDG TIKRLINAASTIASGVPRFSGSRSGSEYSLTINSLESEDF DYCLQYSSYPWTFGGGTKLEIK	125
Humanized heavy chain variable domain (H4) based on 6A7 mutant	Humanized heavy chain variable region H4 mutant	QVQLVQSGAEVKKPGASVKLSCKASGYTFISYIYVWVKQAPG QCLEWIGGINPRNGGTFNEKFKSRATLTVDTSISTAYMELS RLRSEDNAVYYCTRHGNGVYWGQGTTLTVSS	126
Humanized light chain variable domain (K2) based on 6A7 mutant	Humanized light chain variable region K2 mutant	DVMTQSPSLPVTLGQPASISCRSSQSLHNSGNTYLHWYQ QKPGQSPNHLIYQVSNRFGVDPDRFSGSGGTDFTLKISRVE AEDVGVIYFCSQTTHVPTWTFGGGTKVEIK	127
06-6A7 ("6A7") mutant	Mouse heavy chain variable region mutant	QVQLQPGAEVLPKPGASVKLSCKASGYTFISYIYVWVKQRP QCLEWIGGINPRNGGTFNEKFKSKATLTVDKSSSTAYMQLS SLTSEDSAVYYCTRHGNGVYWGQGTTLTVSS	128
06-6A7 ("6A7") mutant	Mouse light chain variable region mutant	DVMTQTPLSLPVSLGDAQASISCRSSQSLHNSGNTYLHWYL QKPGQSPNHLIYQVSNRFGVDPDRFSGSGGTDFTLKISRVE AEDLGVIYFCSQTTHVPTWTFGGGTKLEIK	129

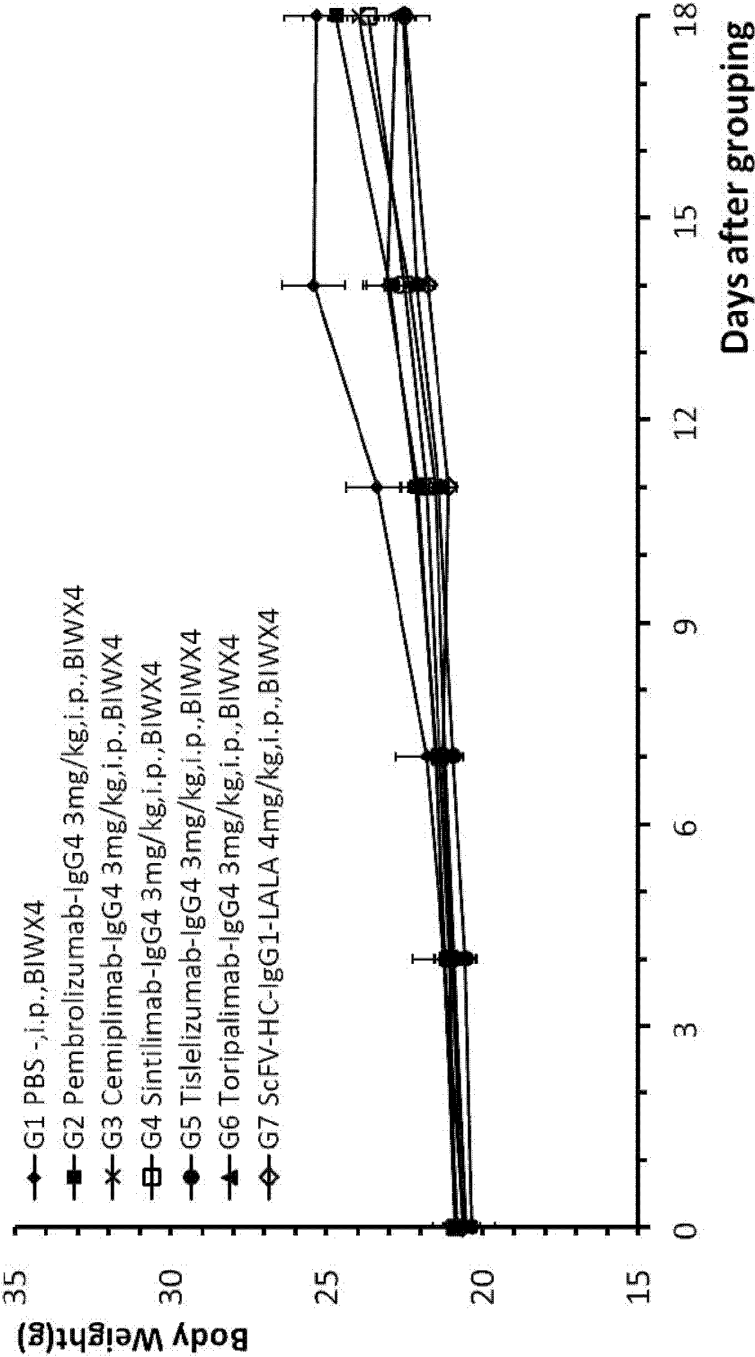


FIG. 27

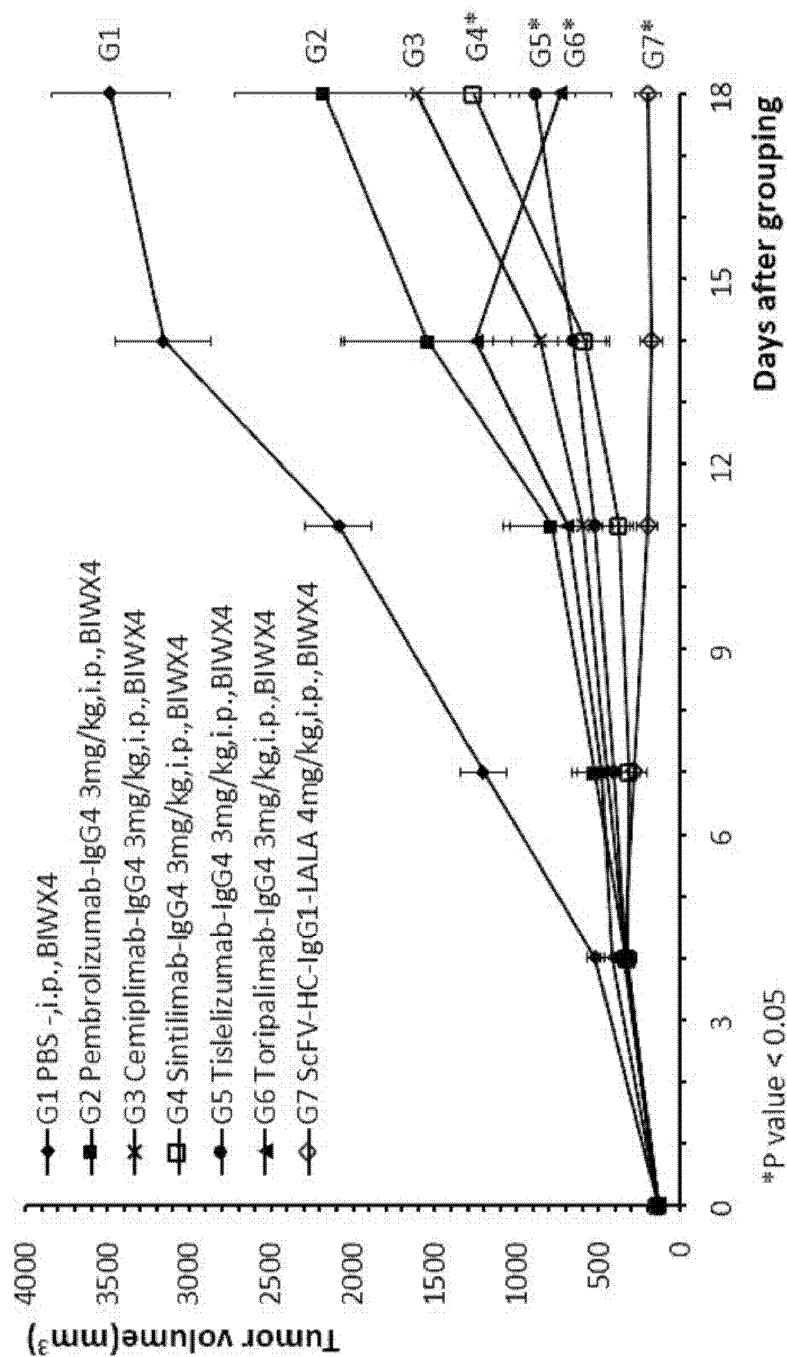


FIG. 28

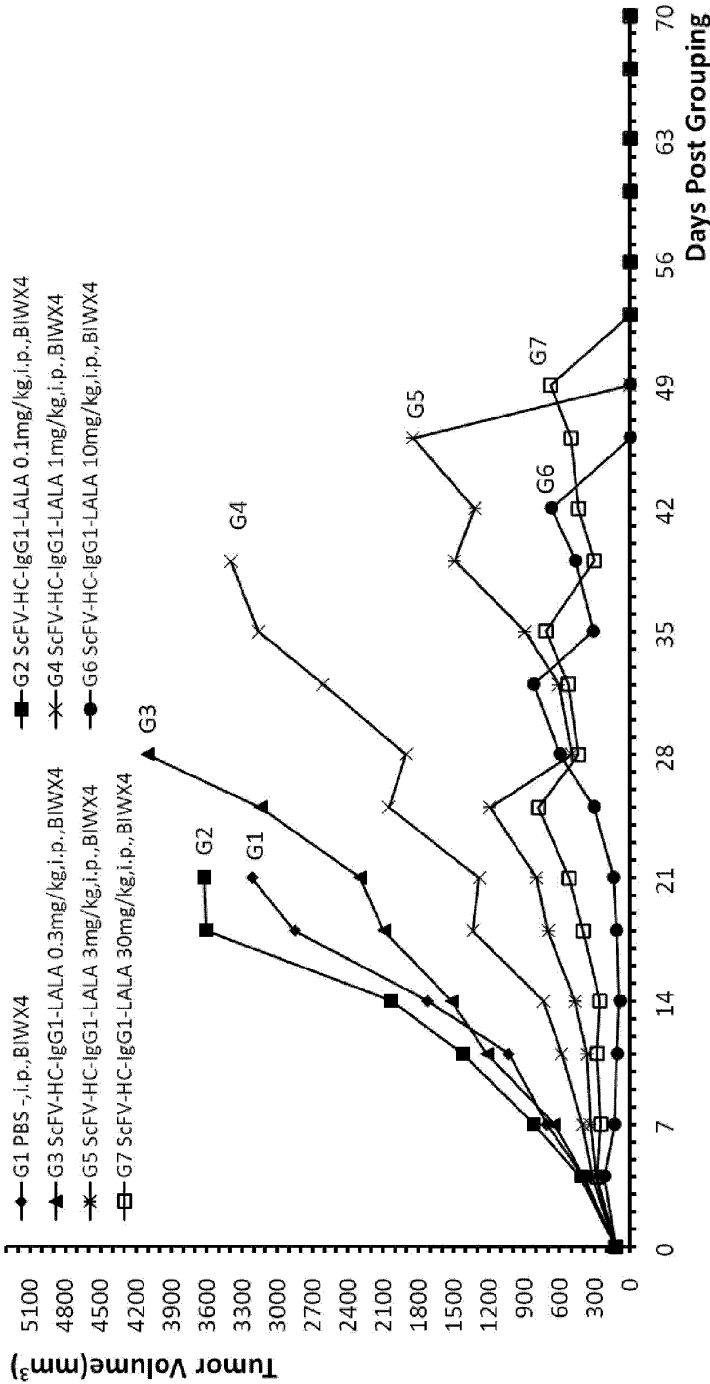


FIG. 29A

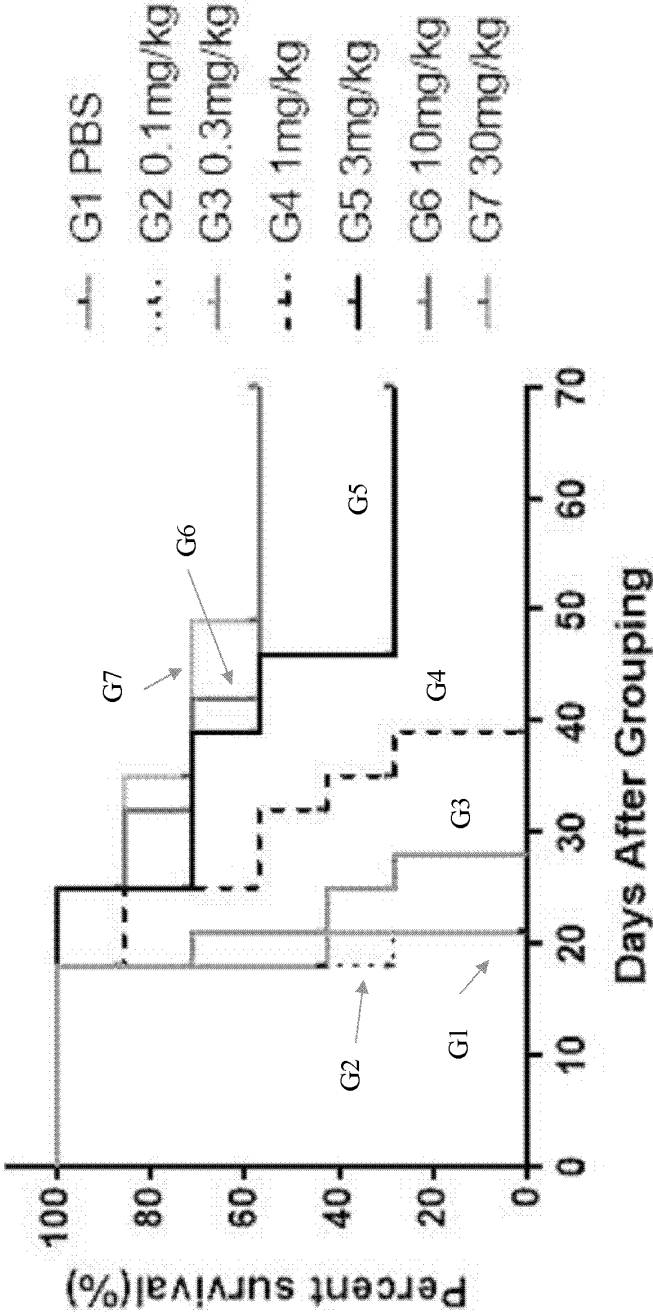
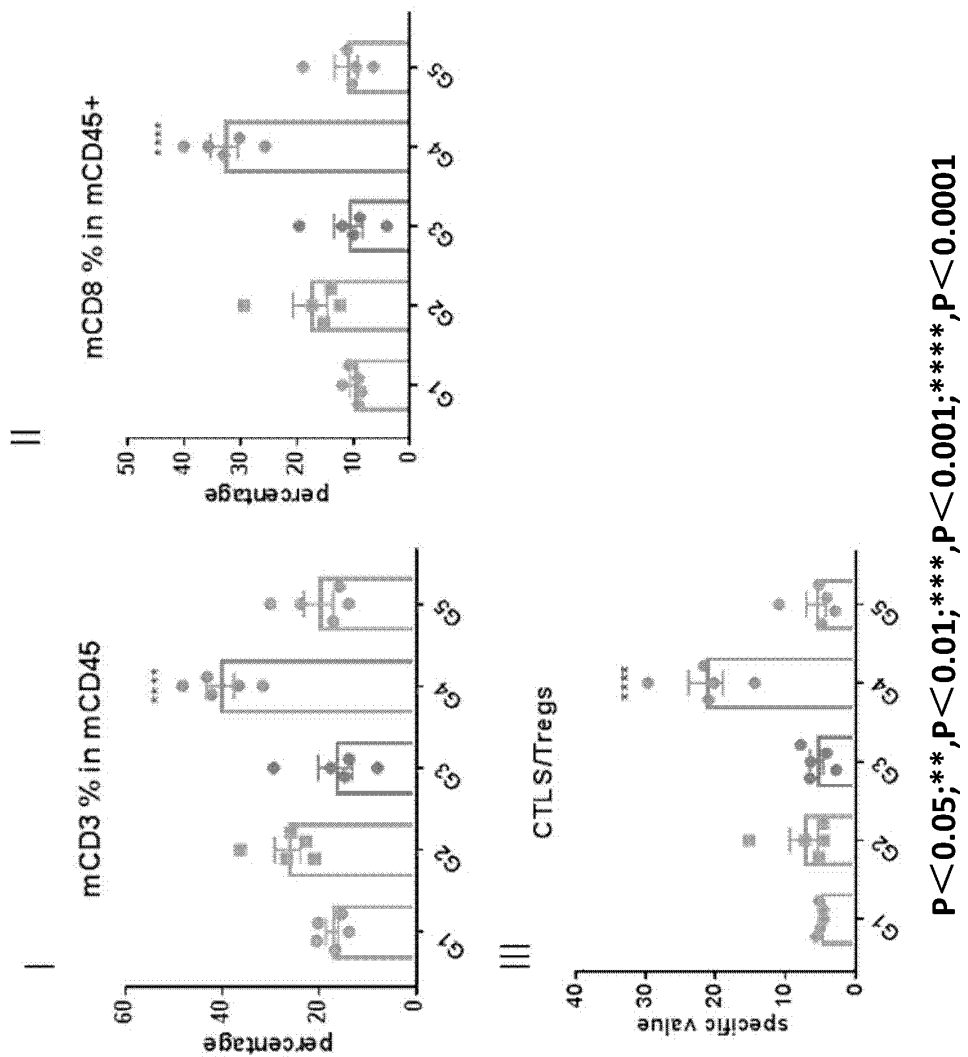


FIG. 29B



$P < 0.05; *, P < 0.01; **, P < 0.001; ***, P < 0.0001$
FIG. 30A

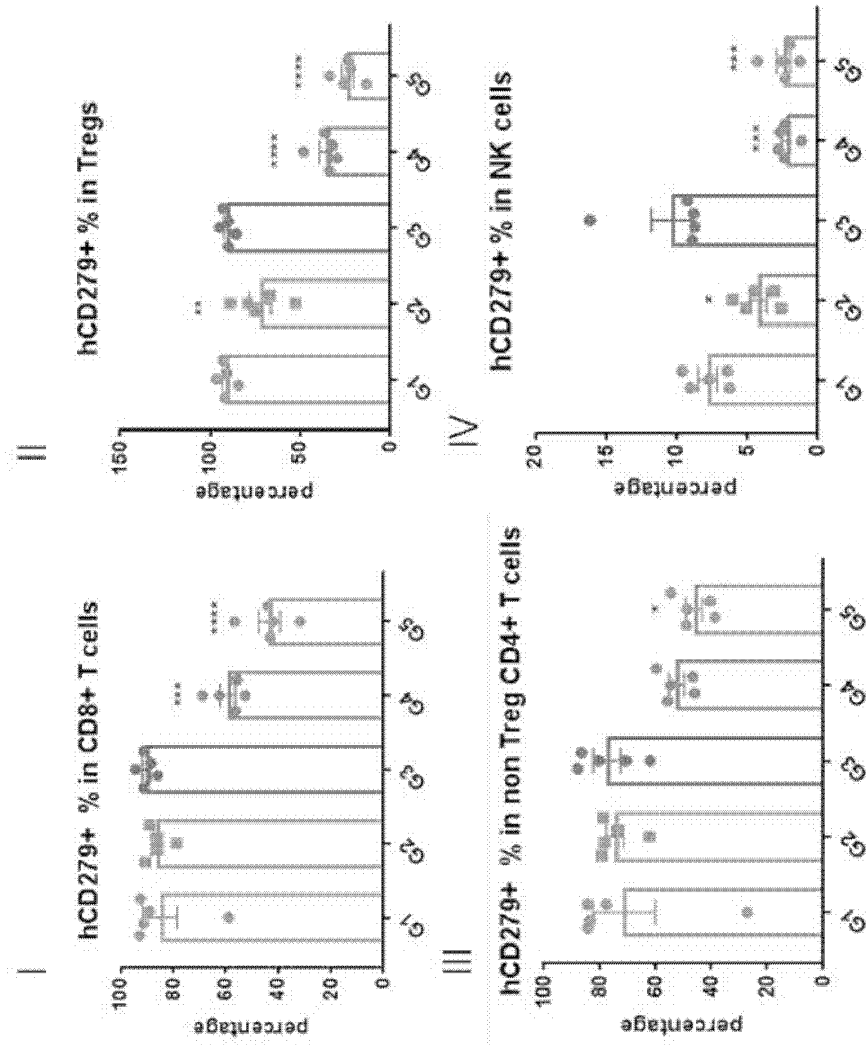


FIG. 30B

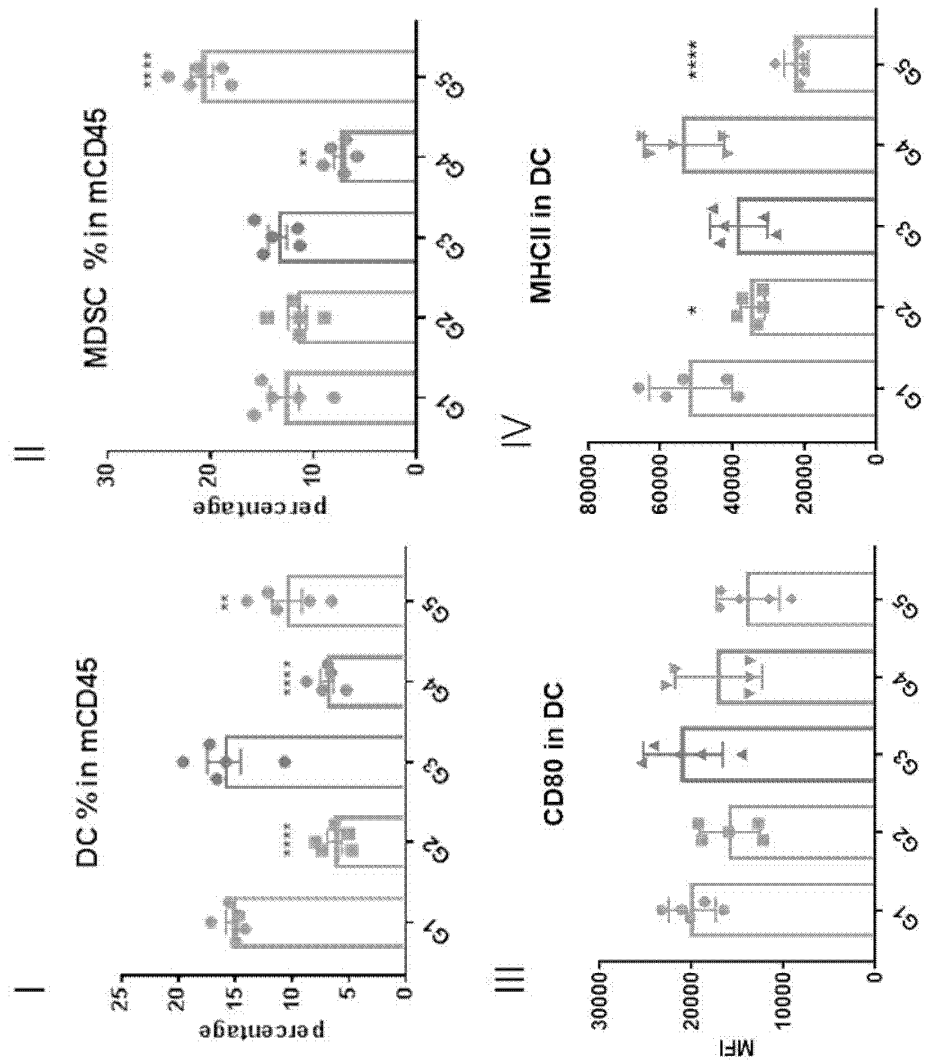


FIG. 30C



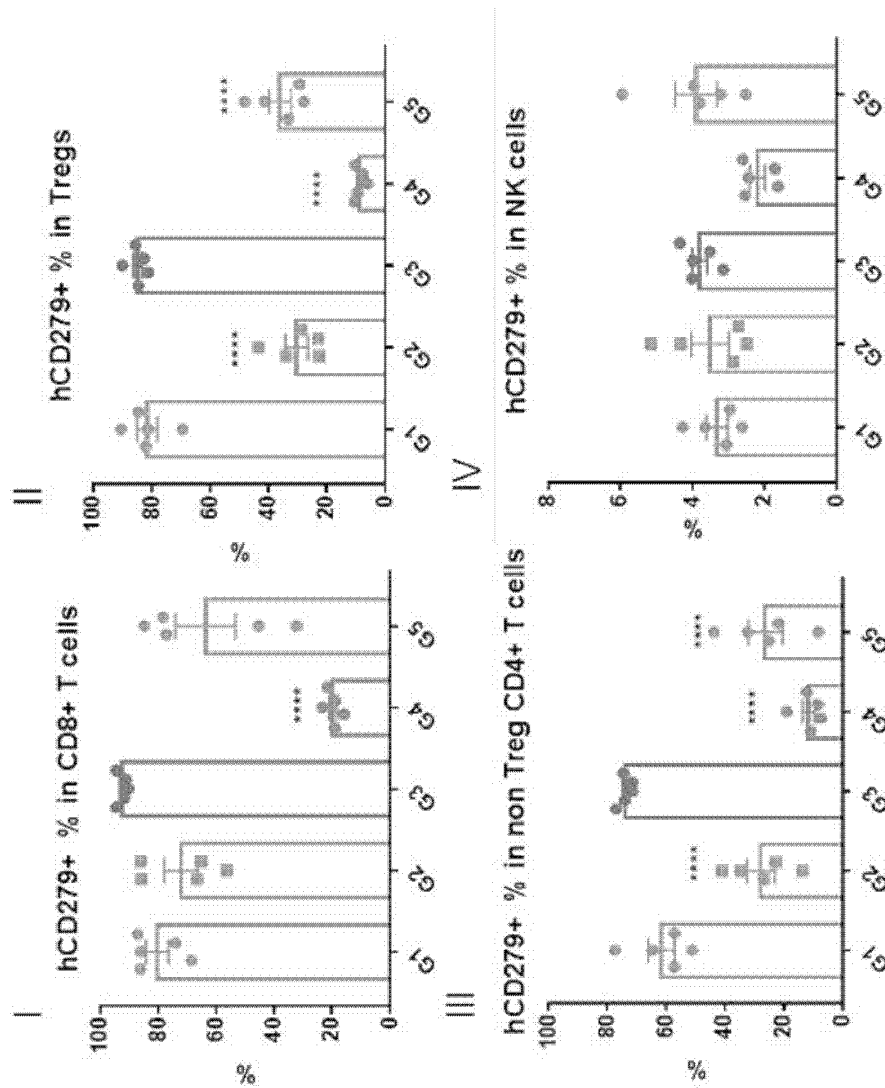


FIG. 30E

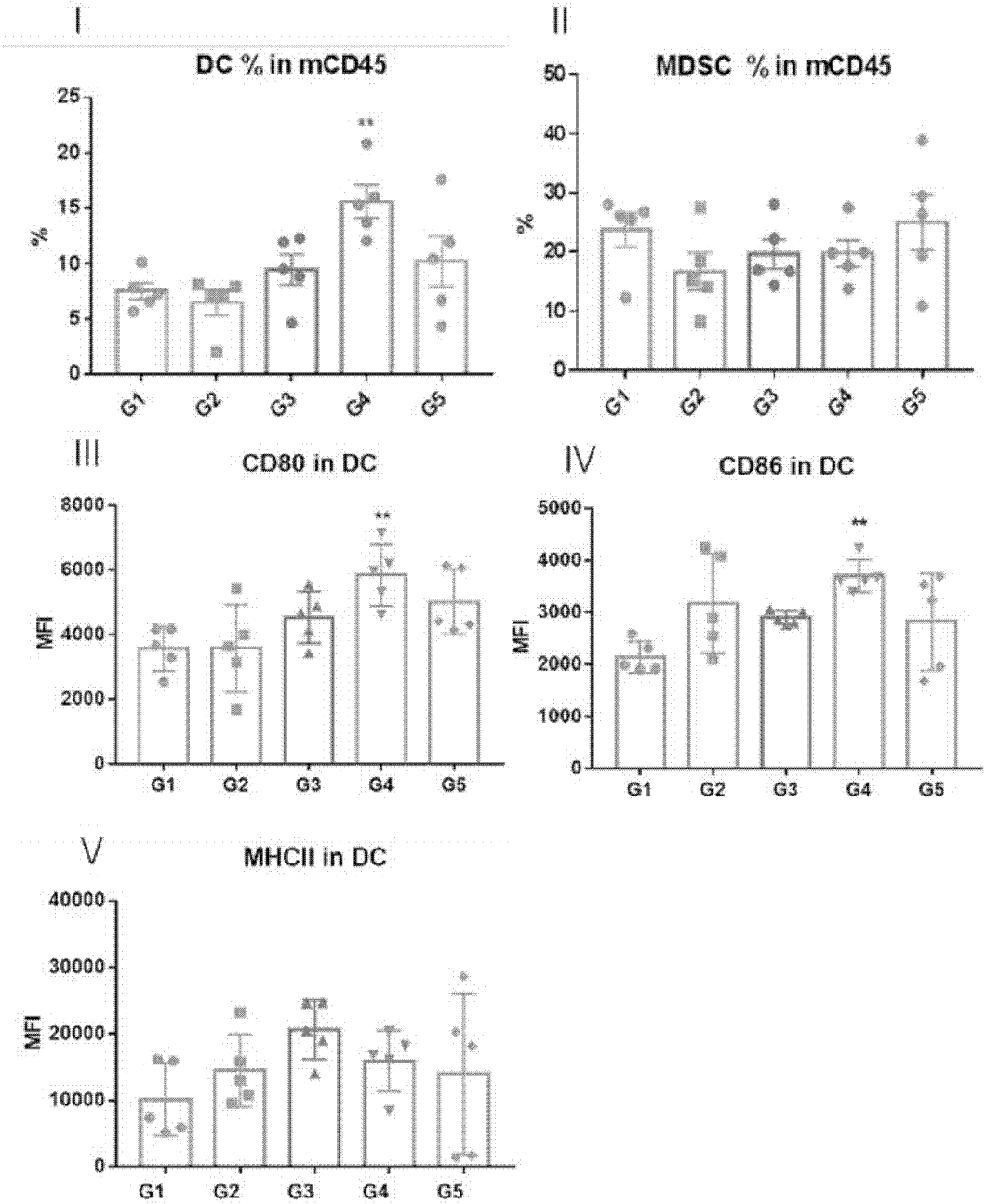


FIG. 30F

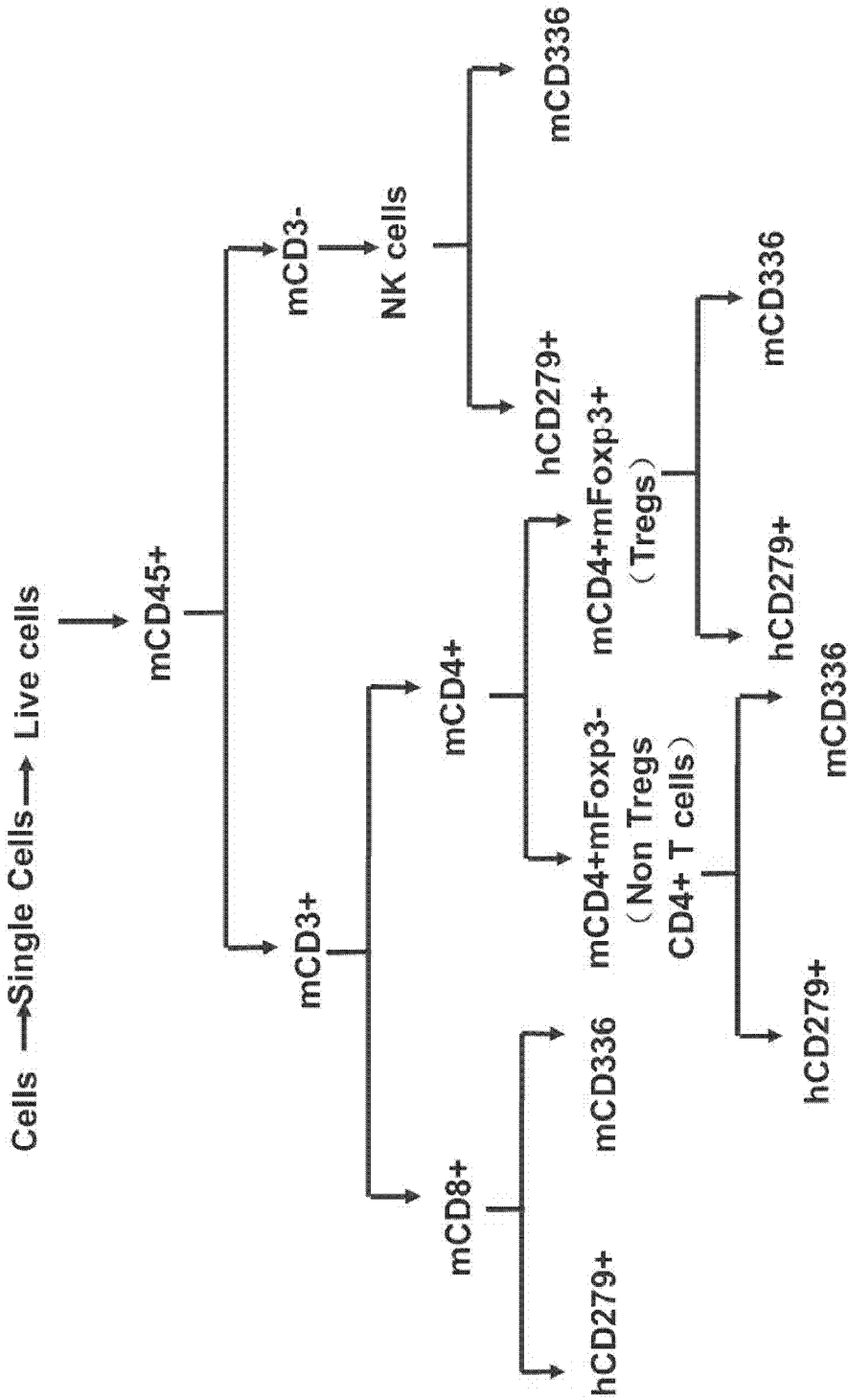


FIG. 31A

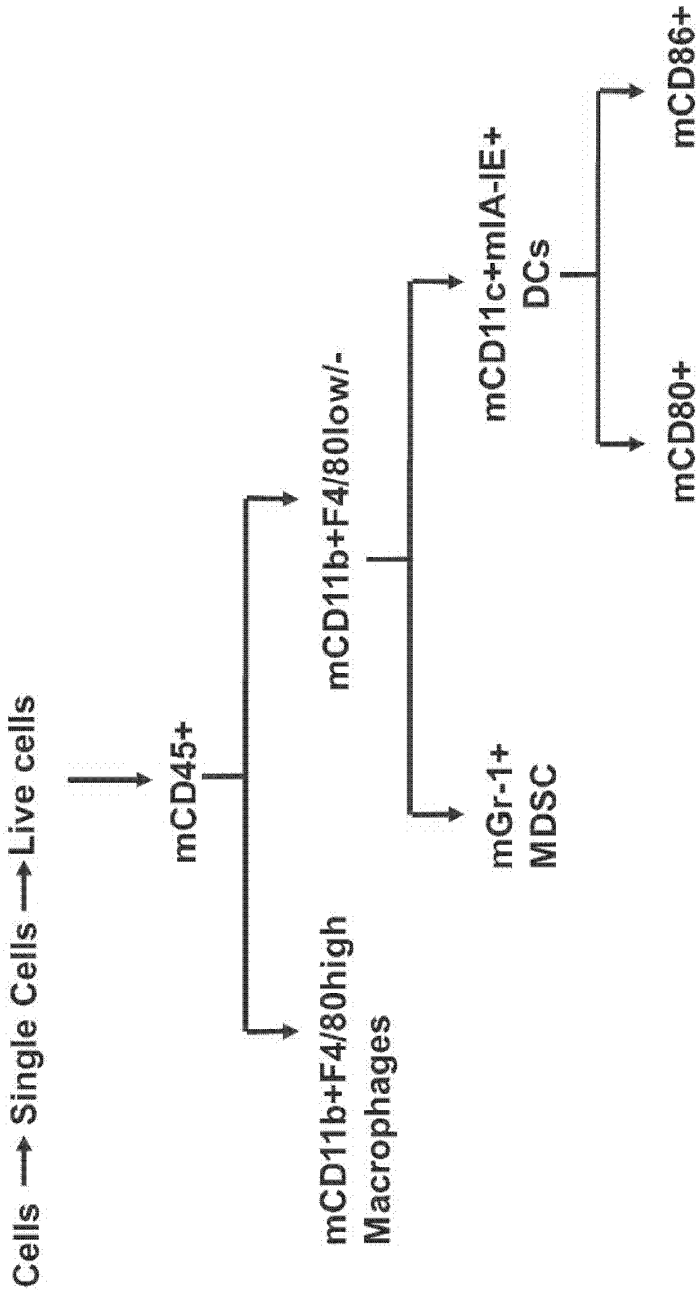


FIG. 31B

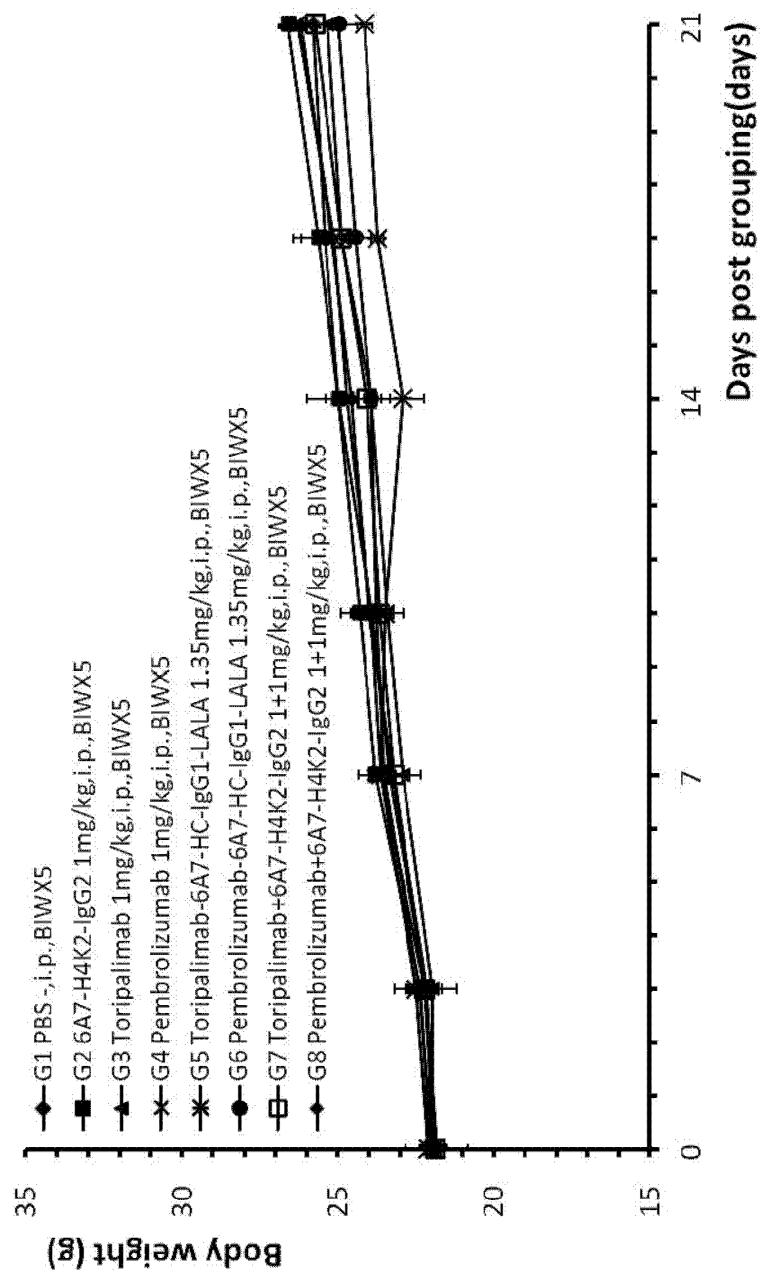


FIG. 32

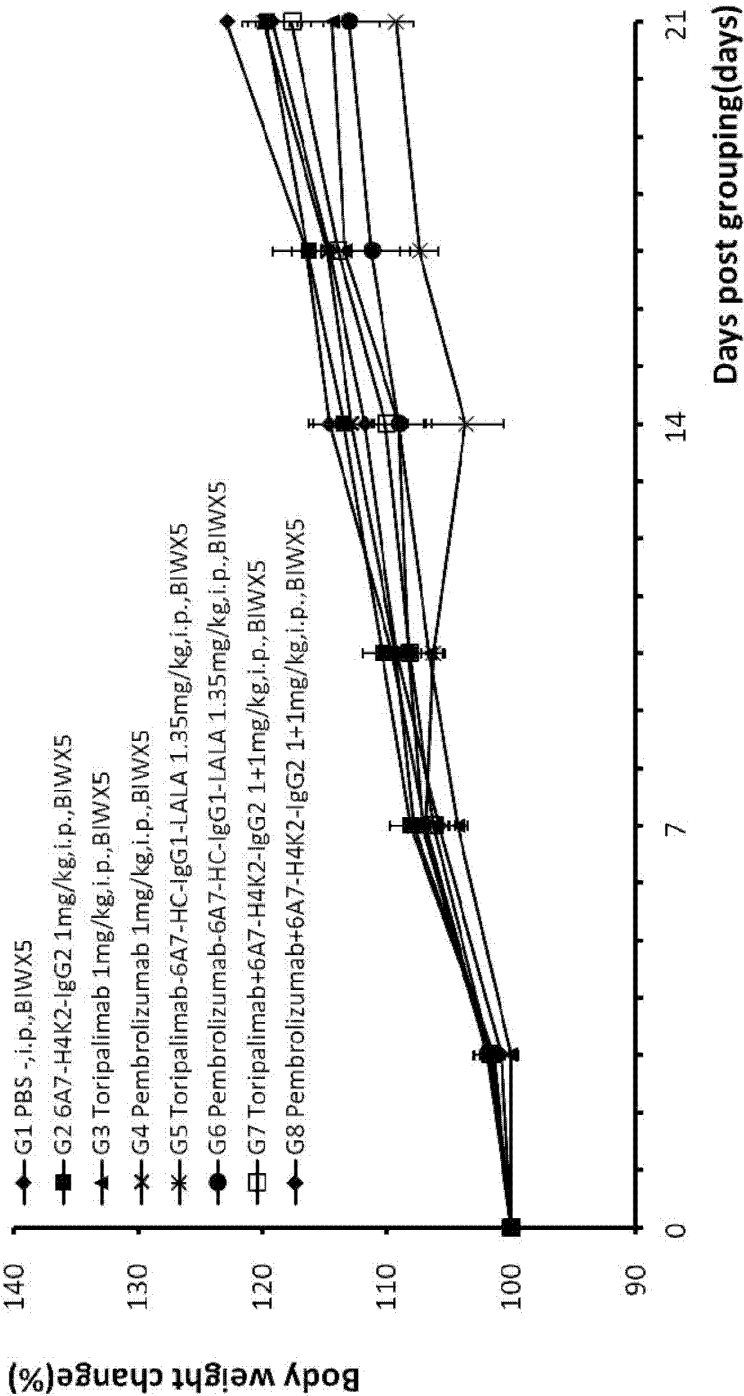


FIG. 33

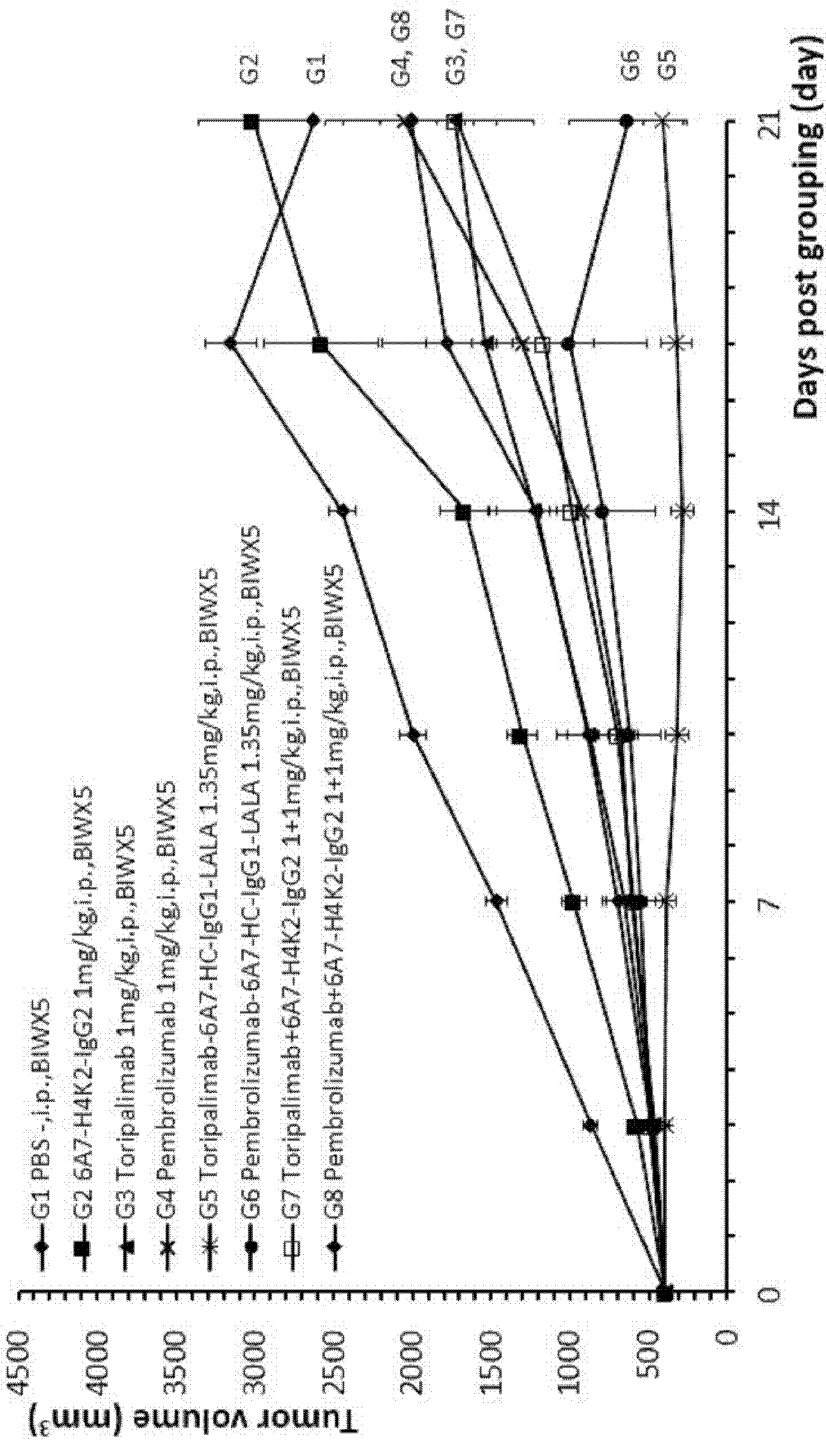


FIG. 34

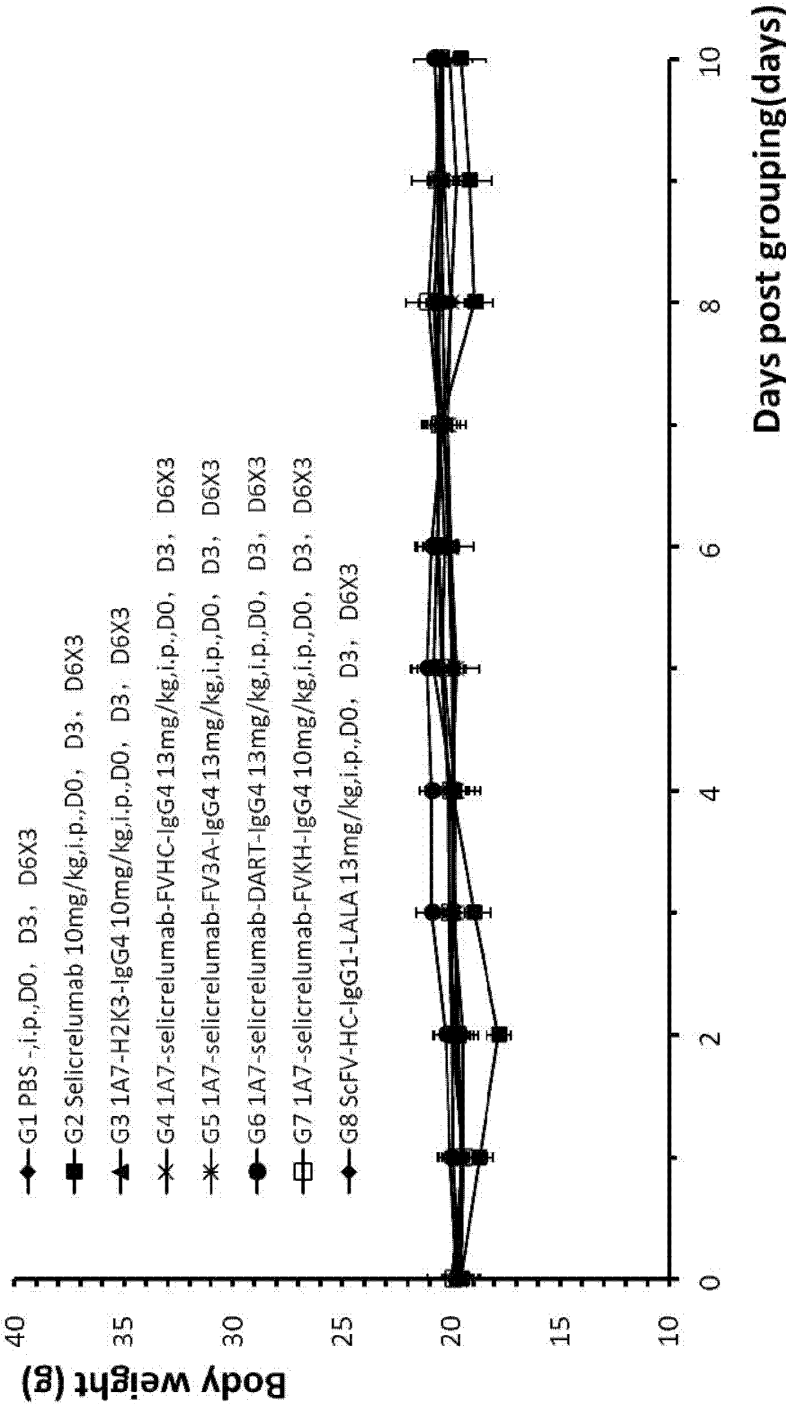


FIG. 35

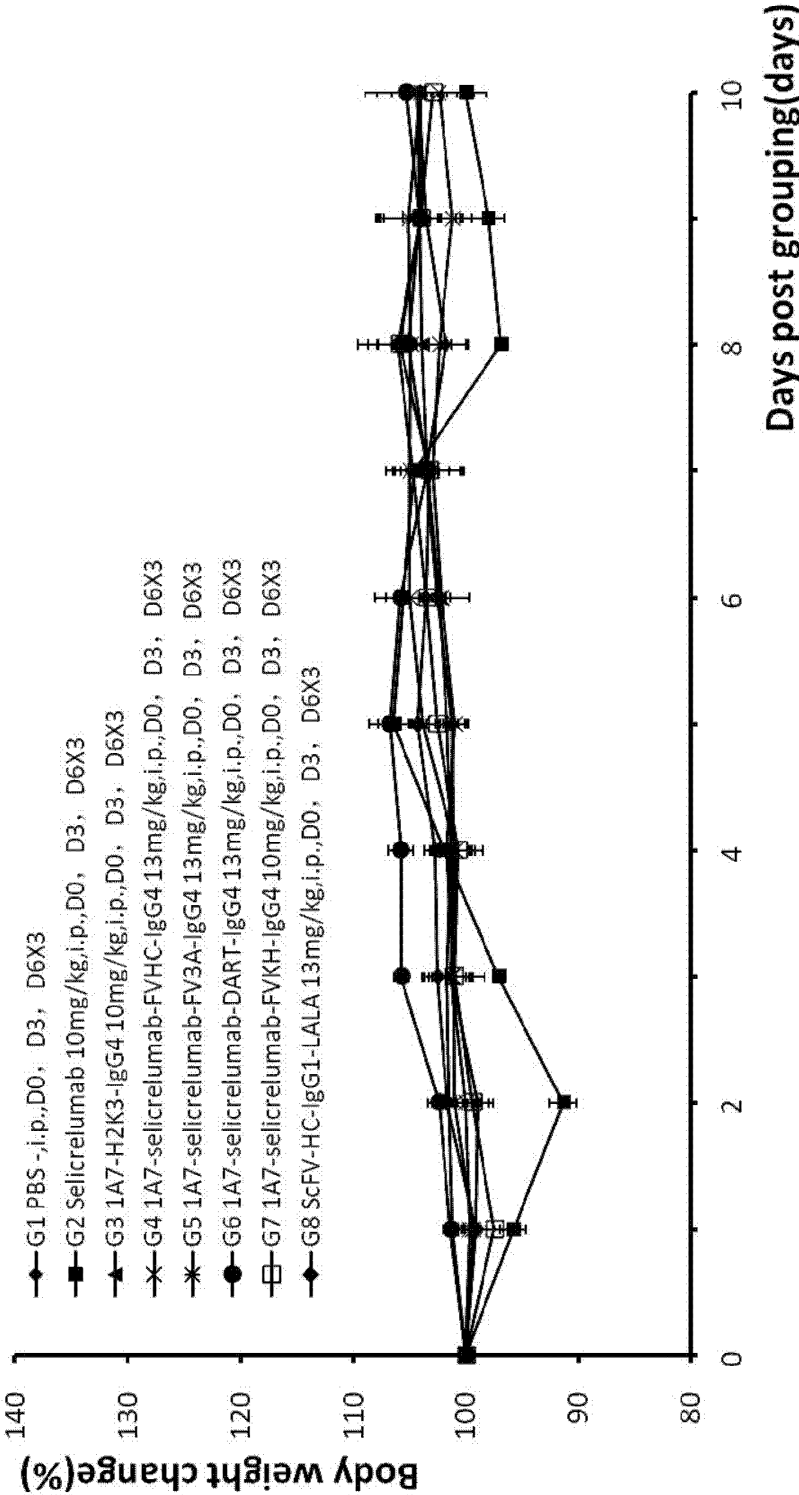


FIG. 36

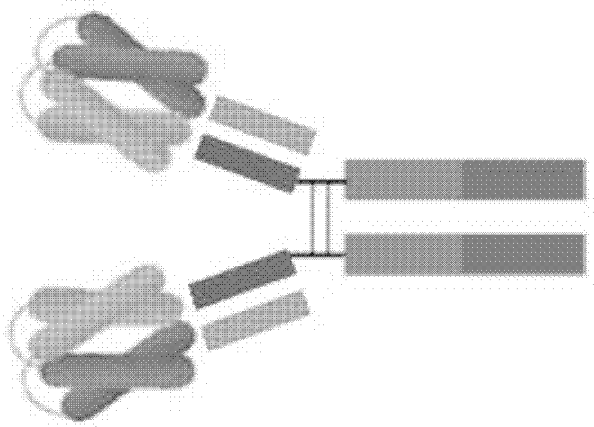


FIG. 37

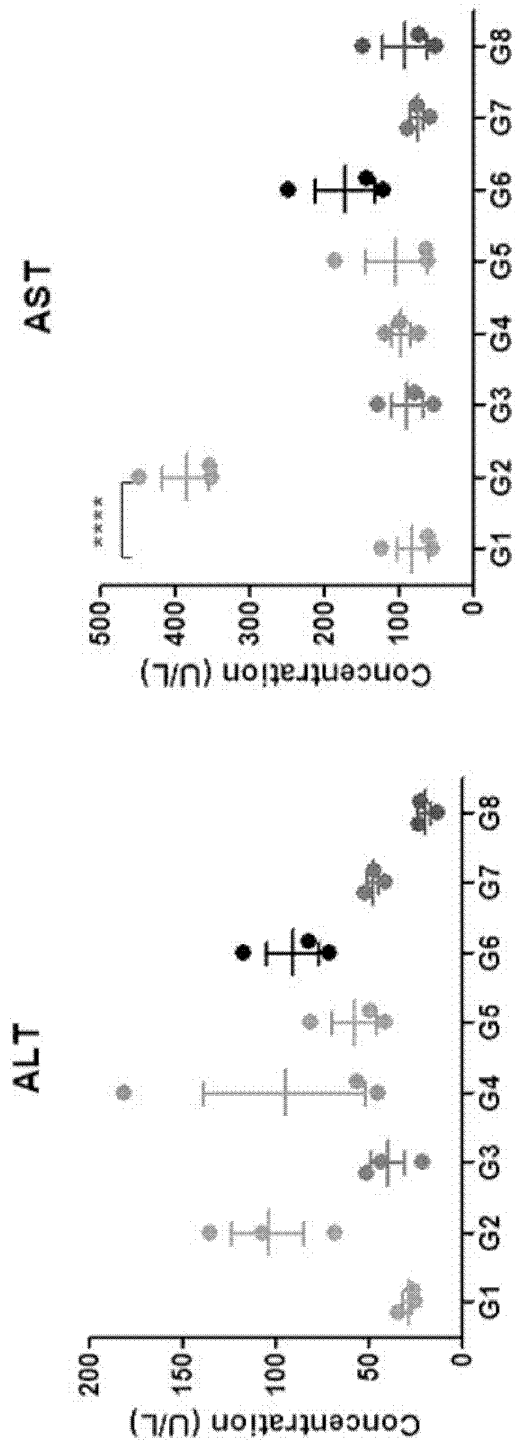


FIG. 38B

FIG. 38A

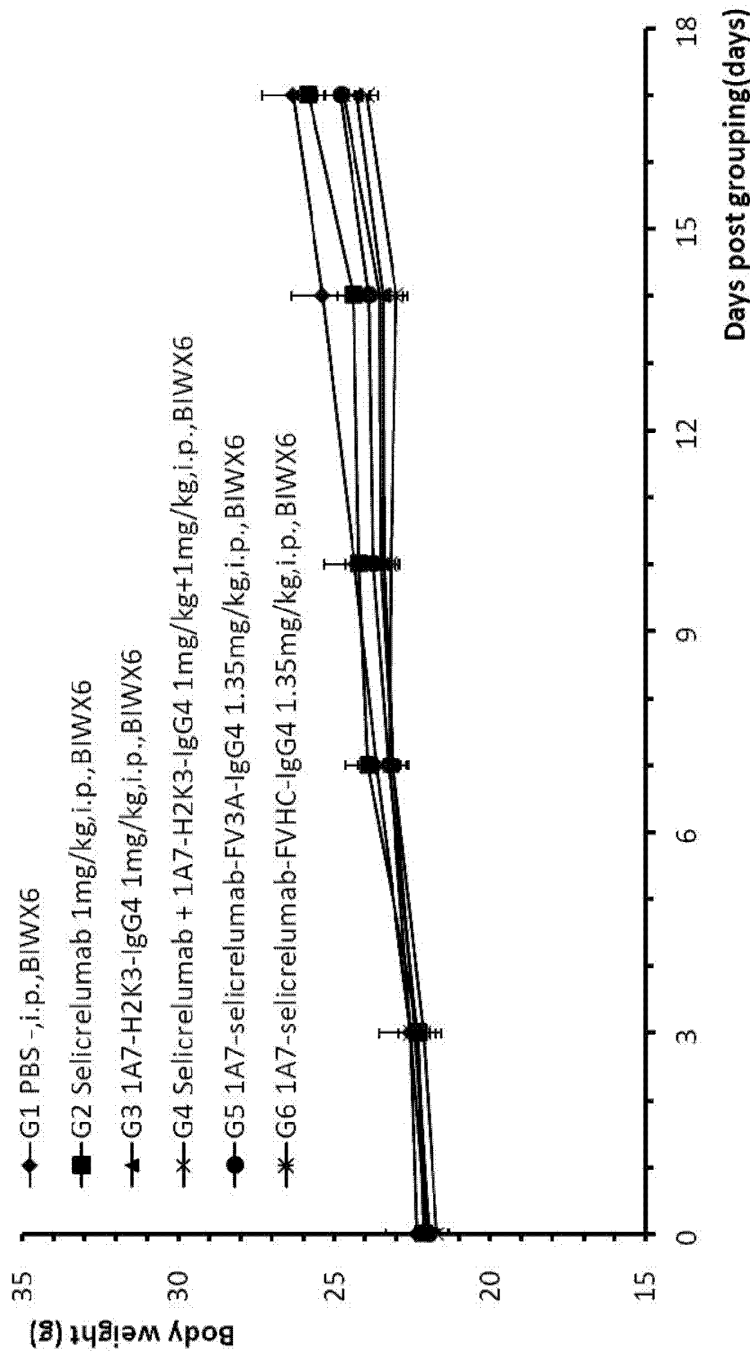


FIG. 39

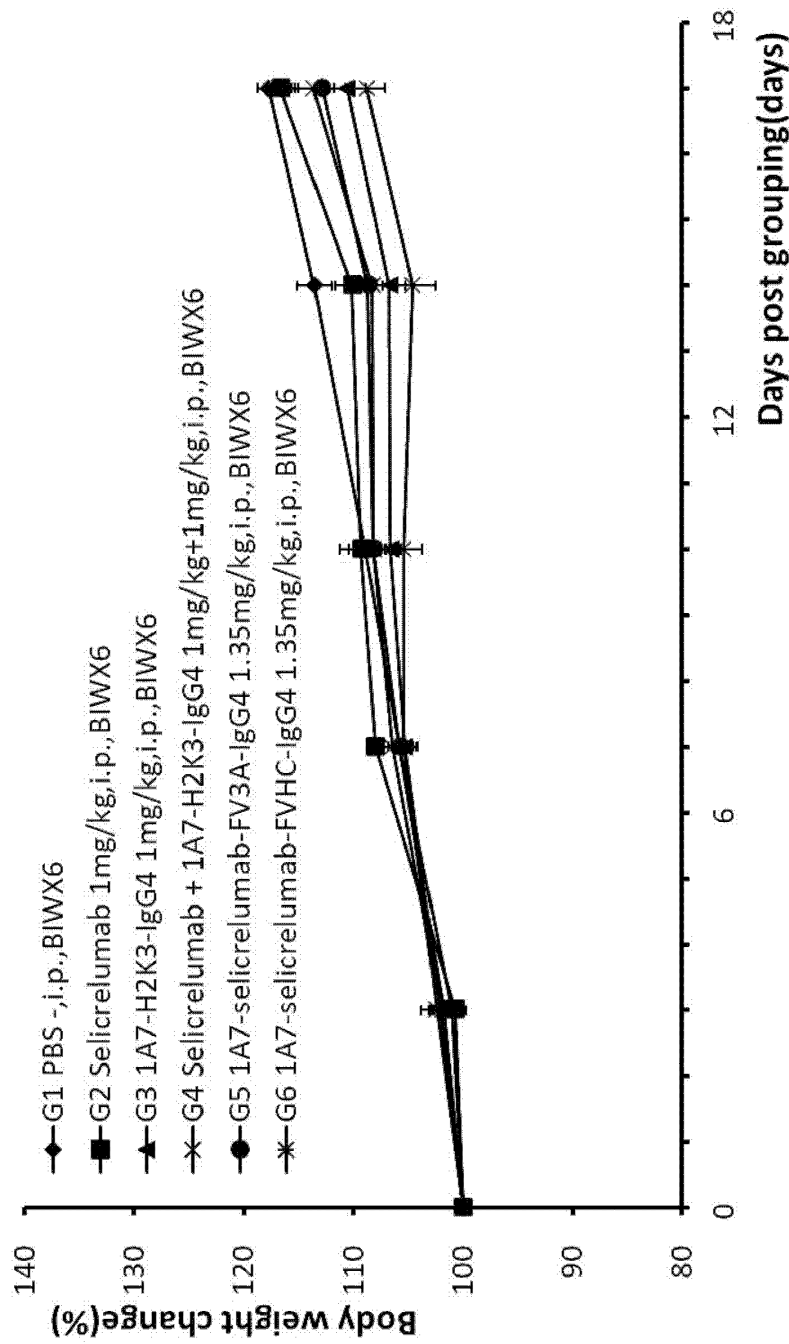


FIG. 40

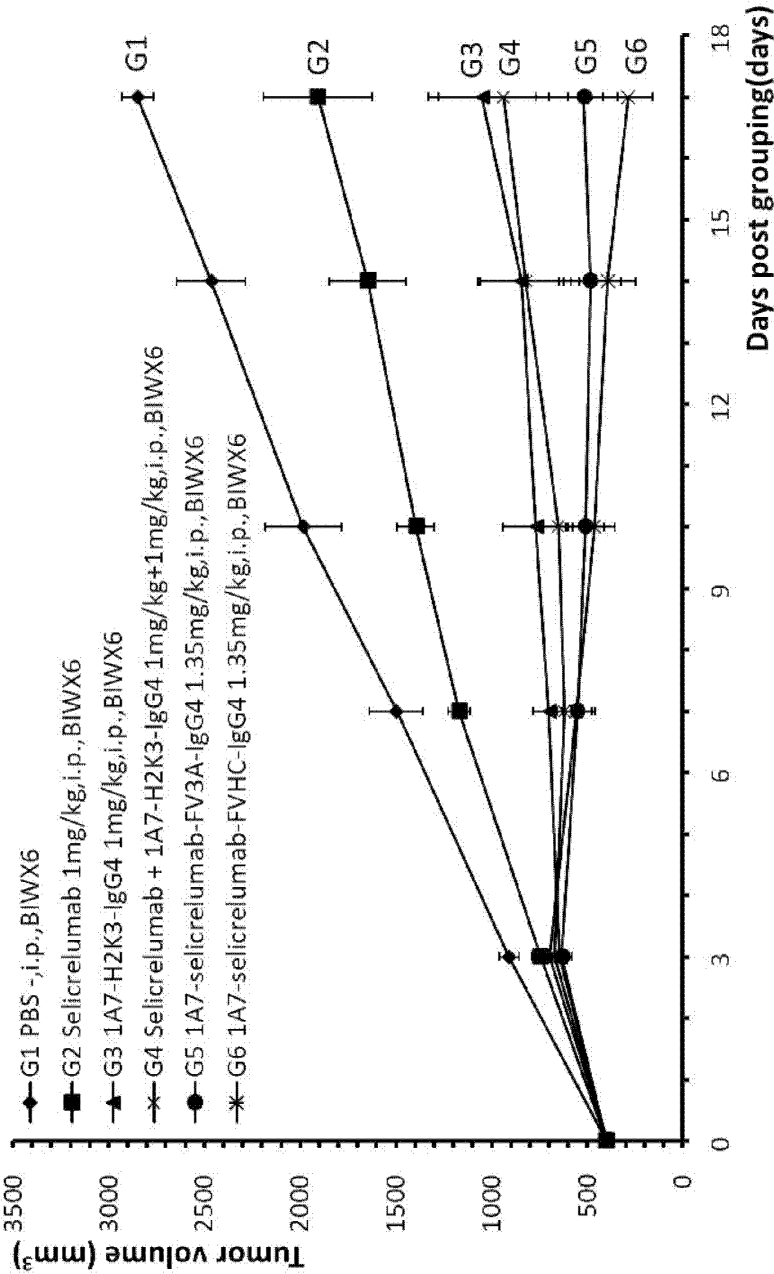


FIG. 41

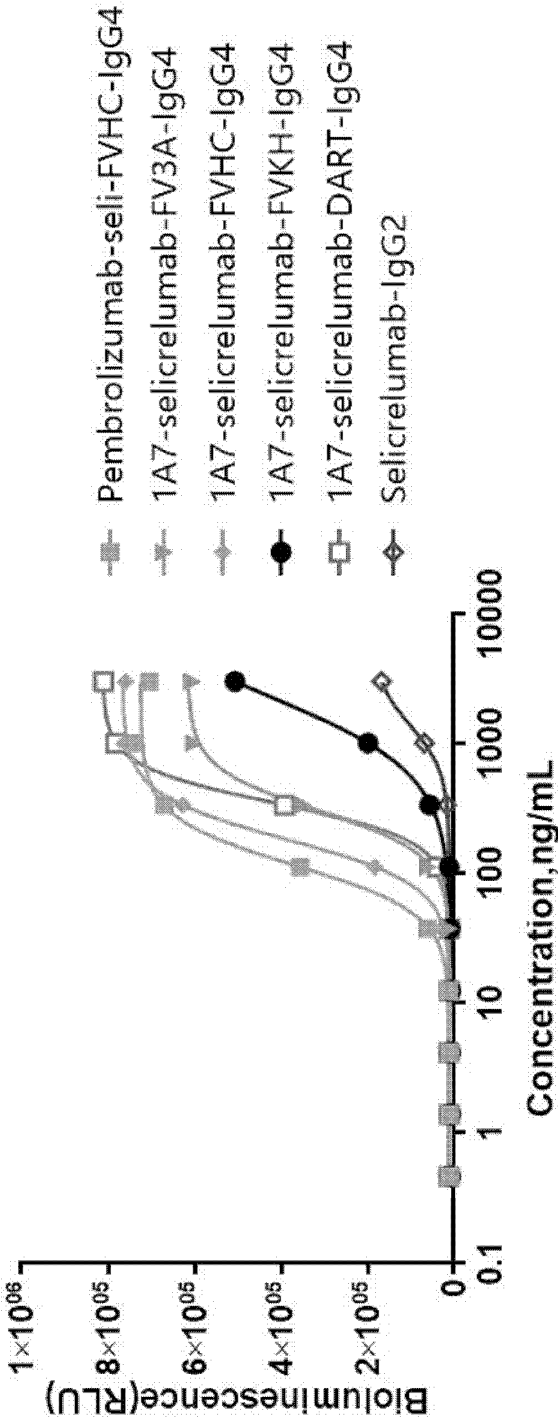


FIG. 42A

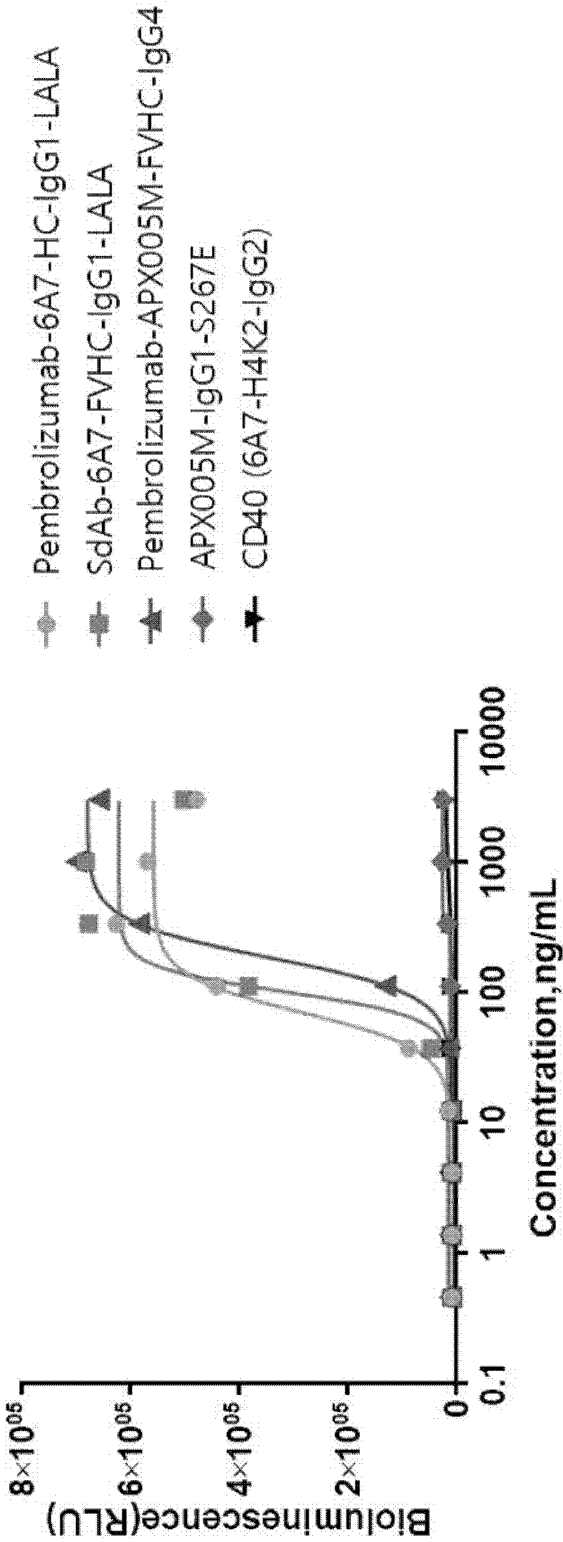


FIG. 42B

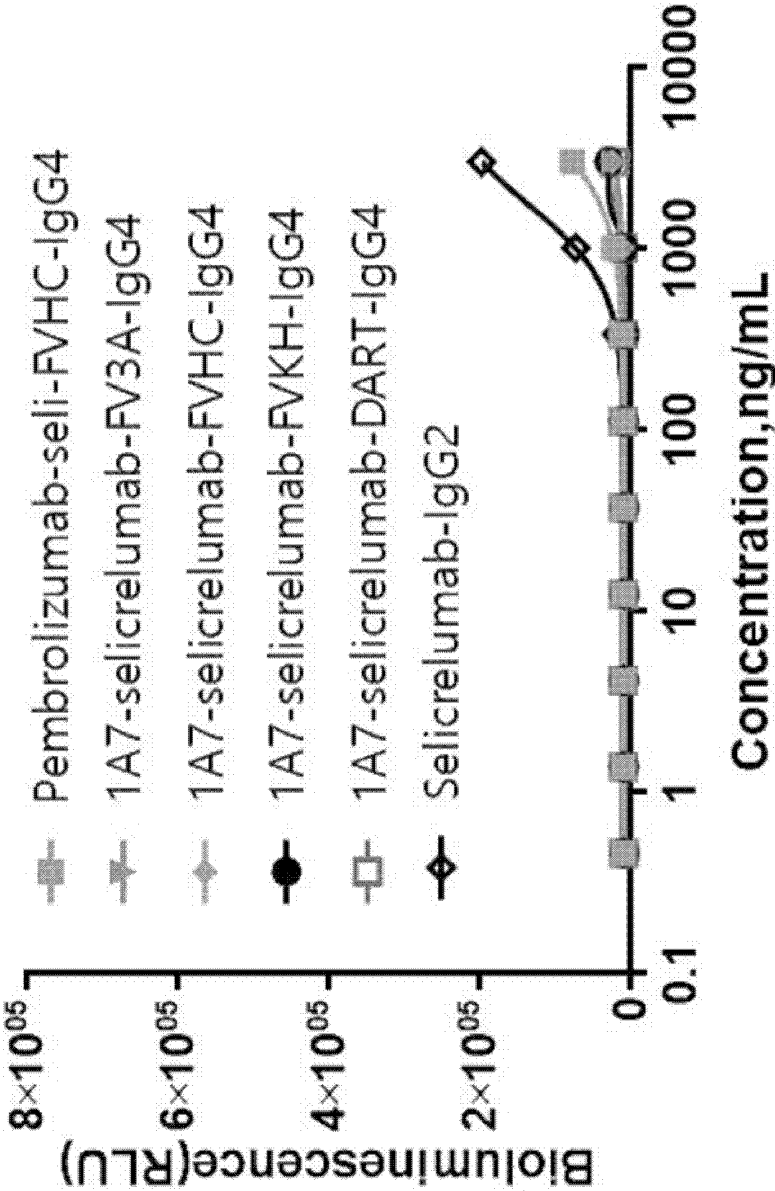


FIG. 42C

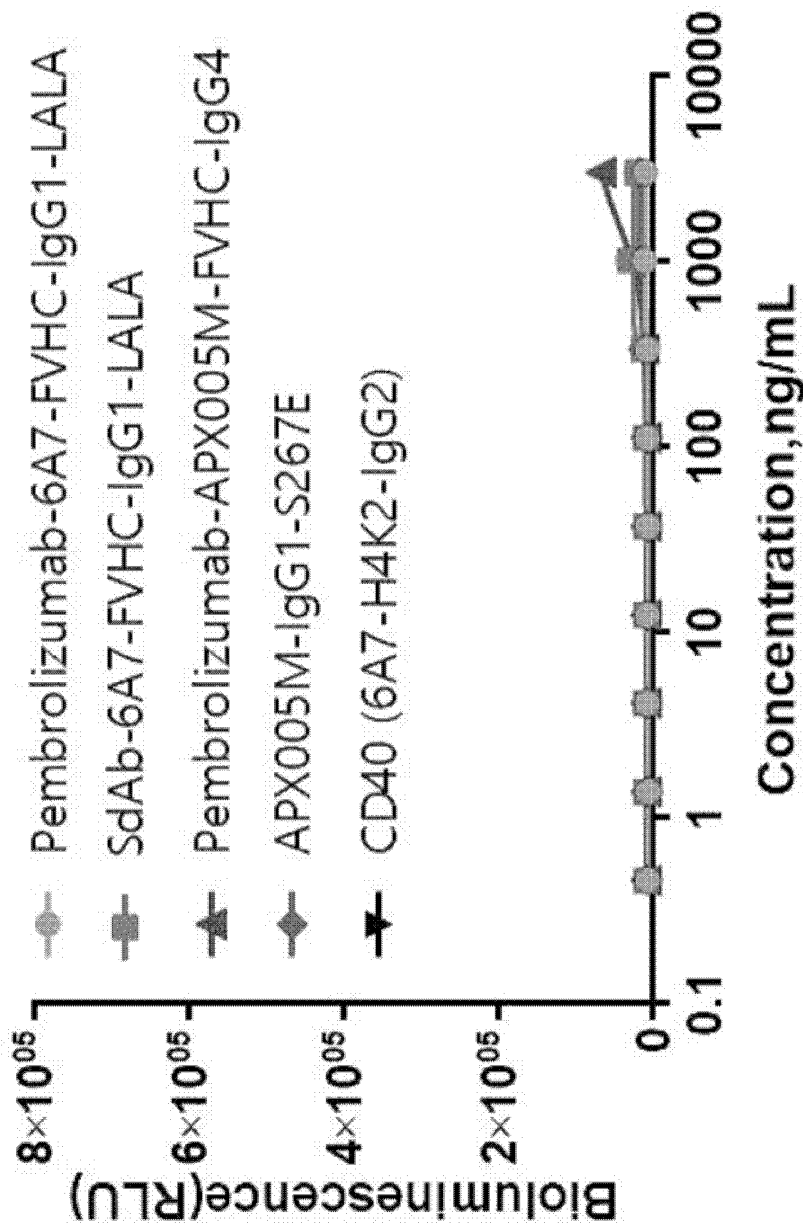
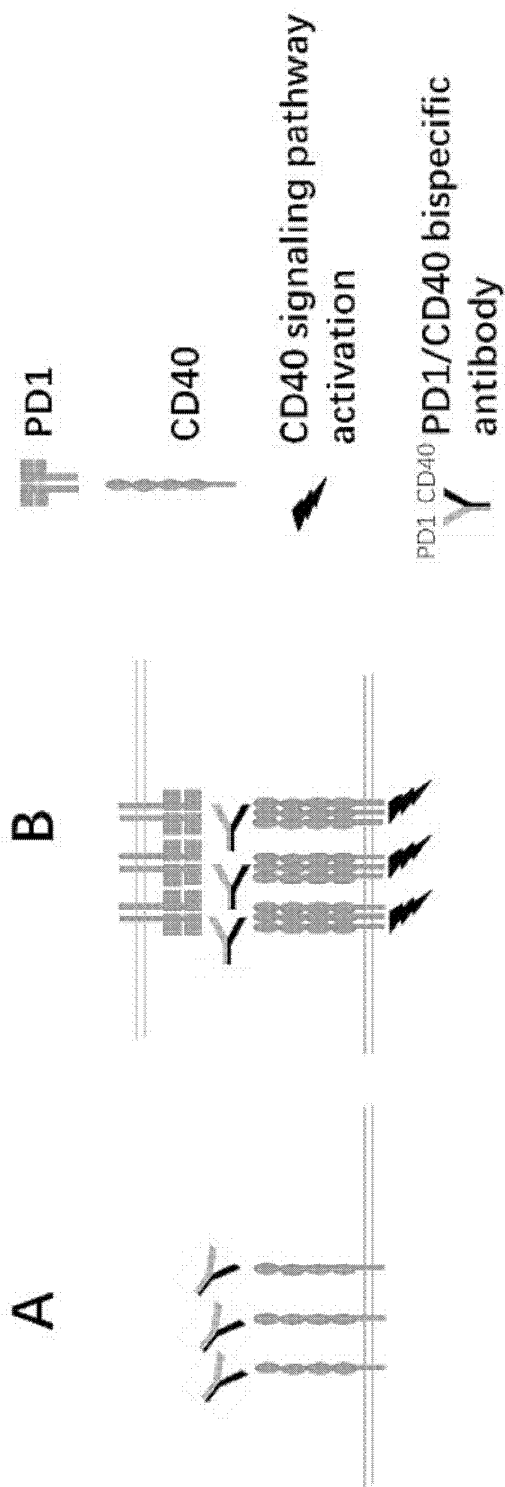


FIG. 42D



FIGS. 43A-43B

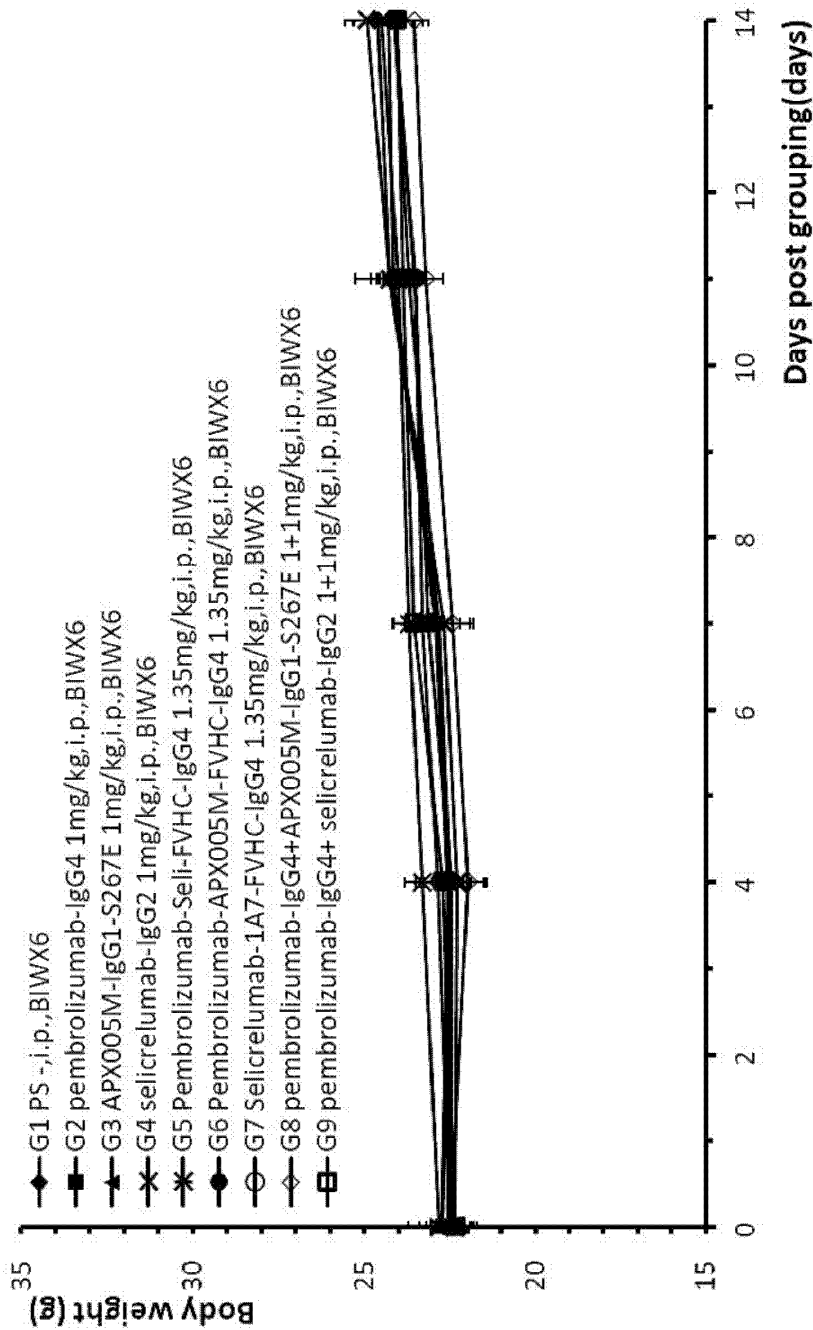


FIG. 44A

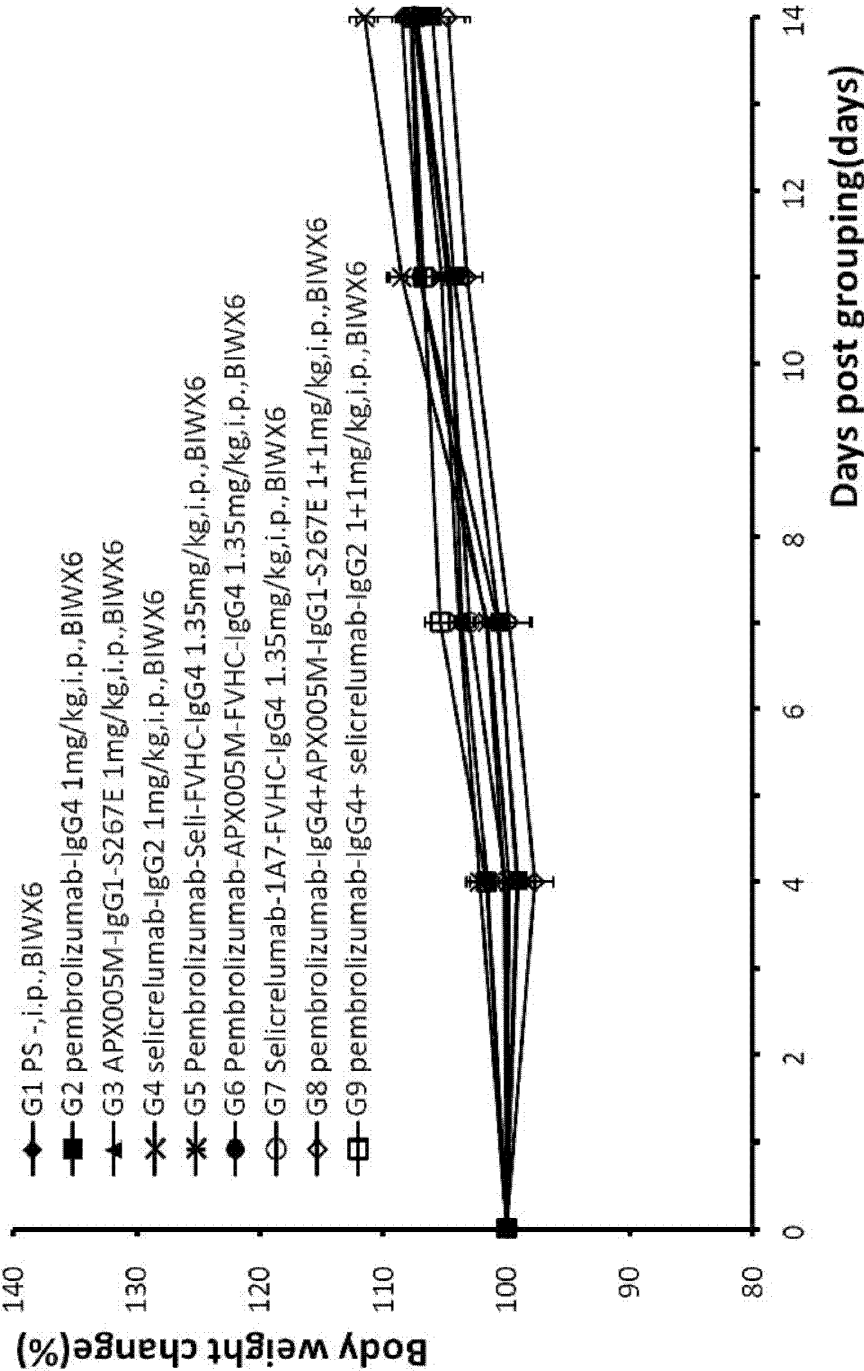


FIG. 44B

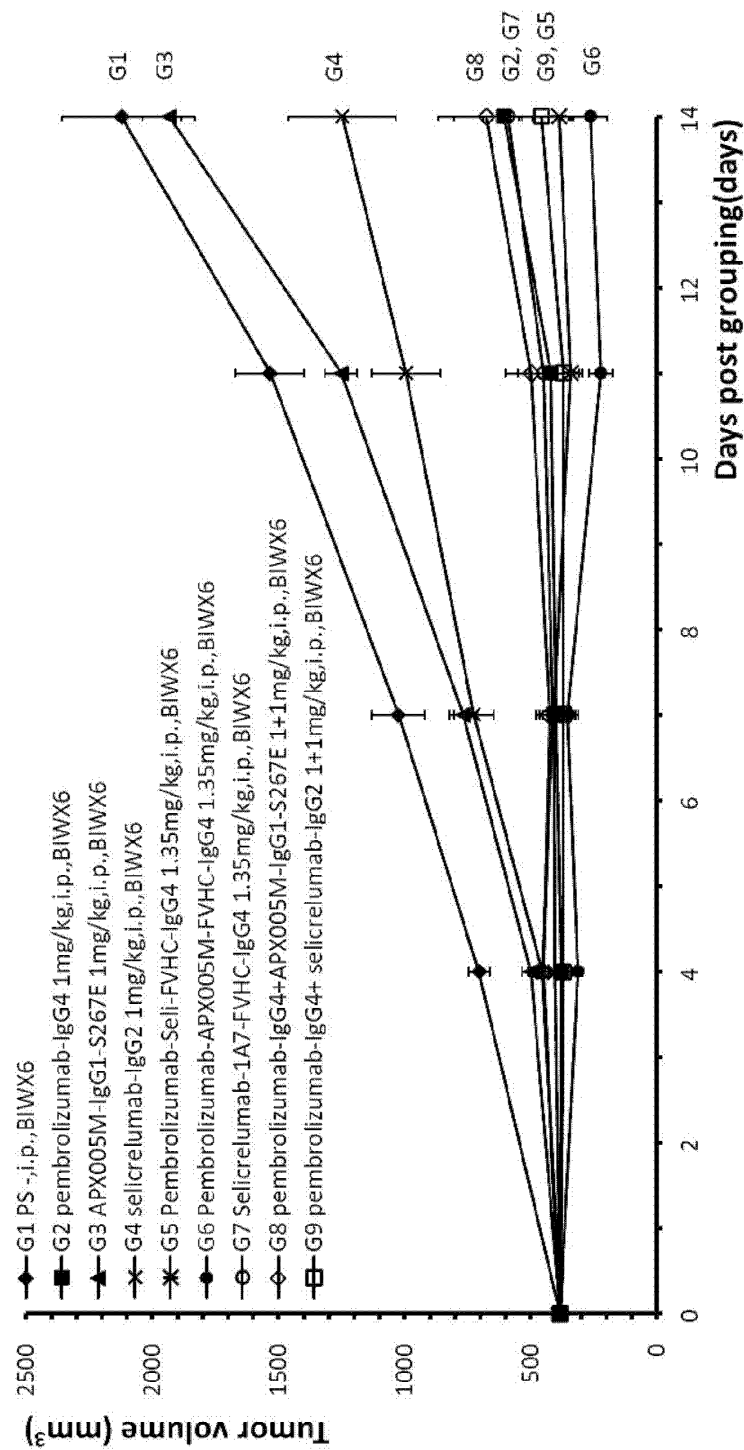


FIG. 44C

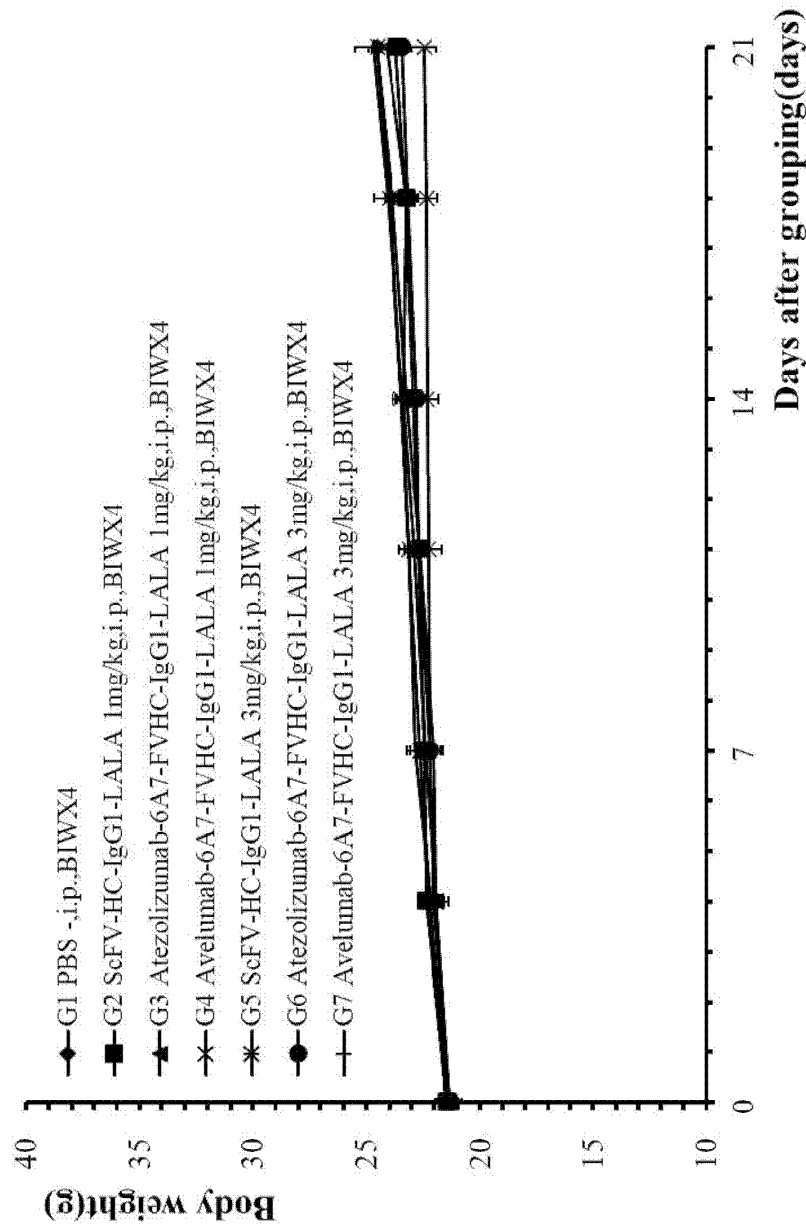


FIG. 45

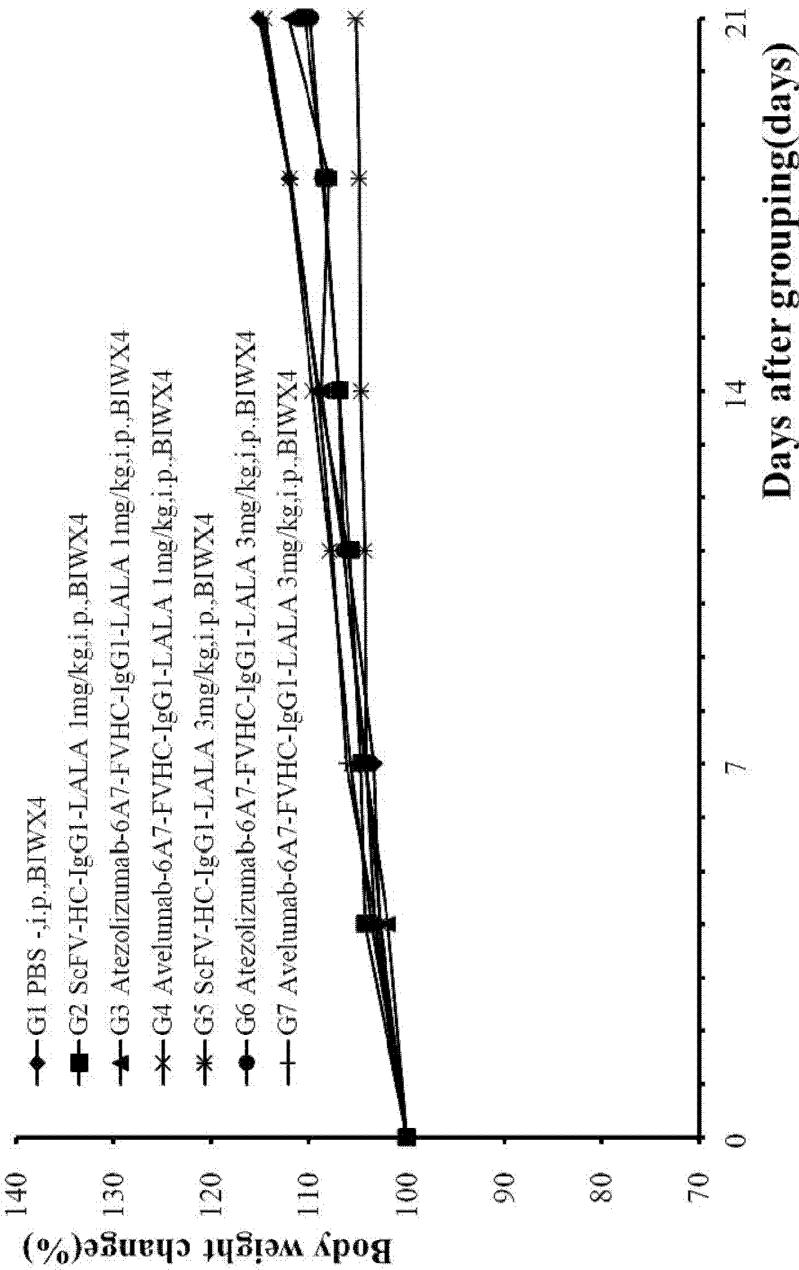


FIG. 46

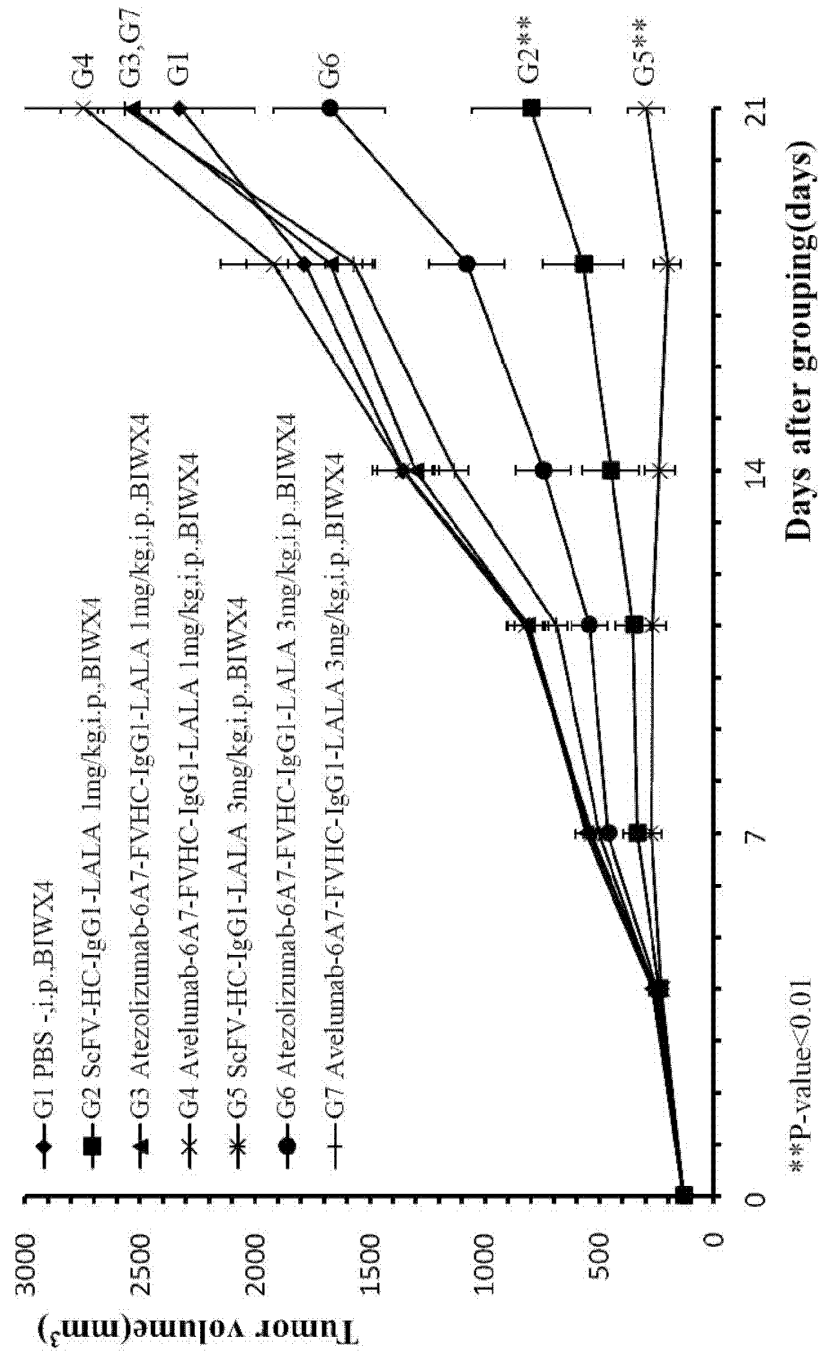


FIG. 47

FIG. 48

Full-length PD-1 heavy chain of Fab-SCFV-IgG4 (SEQ ID NO: 130)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKRLWEVAHISGGSSYYPDTVKGRFTISRDNKNTLYLQMNSLRAE
 EDTAMYCYTRQFYYGSSFWYFDVWAGTTTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV
 LQSSGLYSLSVTVPSSSLGTKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPPKPKDITLMISRTPEVTCVVVD
 VSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGPQPREPQVYTLPPC
 QEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCVMHEALHNHYTQKSLSL
 LGLG

Full-length PD-1 light chain of Fab-SCFV-IgG4 (SEQ ID NO: 131)
 DDNVLTSQPATLSVSPGERATLSCKASQSVDFDGDSYMNWYQQKPGQPRLLIYAASNLESGIPARFSGSGSGTFTLTLTISSEPEDFAT
 LSSLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC

Full-length CD40 arm (version 2) of Fab-SCFV-IgG4 (SEQ ID NO: 132)

QVQLVQSGAEVKKPGASVKLSCKASGYFISYYIWVKQAPGQCLEWIGGINPRNGGTNNEKFKSRATLTVDTSISTAYMELSRRLRSE
 DDTAVYCTRHGNGVYWGGGTTLVSSASTGGGGGGGGGGGGSDVMTQSPLSPLVTLGQPASISCRSSQSLLHSNGNTYLLHW
 YQQRPQGQSPNHLIYQVSNRFSGVDPDRFSGSGSGTFTLKISRVEAEDVGYFCSQTTHVPWTFGCGTKVEIKDKRVESKYGPPCPPCPA
 DEFLGGPSVFLPPPKPDKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVTLHQDLNNGKEYK
 CKVSNKGLPSSIEKTIISKAKGQPREPQVCTLPPSQEEMTKNQVSLSCAVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLVSR
 LTVDKSRWQEGNVFSCSVMHREALHNNHYTKQSLSLSLGK

Full-length CD40 arm (version 1) of Fab-SCFV-IgG4 (SEQ ID NO: 133)

Full-length modified heavy chain (version 2) of ScFv-HC-IgG4 (SEQ ID NO: 134)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKRLEWVAHISGGSTYYPDVTVKGRFTISRDN SKNTLYLQMN SLRAE
DTAMYYCTRQFYFGSSFWYFDVWGAGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV
LQSSGLYSLSVTVPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVD
VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPS
QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGN VFSCVMHEALHNYTQKSLSL
SPGGGGGGGGGGSDVMTQSPSLPVTILGQPASISCRSSQSLHNSNGNTYLHWYQQRPQGSPNHLIIYQVSNRFSGVDPDRFSGS
SGTDFTLKISRVEAEDVGVYFCSQTHVPWTFGGGTKEIKGGGGGGGGGGGSGGGSQVLVQSGAEVKKPGASVKLSCKASGYT
FISYIYWVKQAPGQCLEWIGGINPRNGGTNFEKFKSRATLTVDTSISTAYMELSLRSED TAVYYCTR HNGVYWGQG TLTIVSS

Full-length modified heavy chain (version 1) of ScFv-HC-IgG4 (SEQ ID NO: 135)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKRLEWVAHISGGSTYYPDVTVKGRFTISRDN SKNTLYLQMN SLRAE
DTAMYYCTRQFYFGSSFWYFDVWGAGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV
LQSSGLYSLSVTVPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVD
VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPS
QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGN VFSCVMHEALHNYTQKSLSL
SPGGGGGGGGGGSDVMTQSPSLPVTILGQPASISCRSSQSLHNSNGNTYLHWYQQRPQGSPNHLIIYQVSNRFSGVDPDRFSGS
SGTDFTLKISRVEAEDVGVYFCSQTHVPWTFGGGTKEIKGGGGGGGGGGGSGGGSQVLVQSGAEVKKPGASVKLSCKASGYT
FISYIYWVKQAPGQGLEWIGGINPRNGGTNFEKFKSRATLTVDTSISTAYMELSLRSED TAVYYCTR HNGVYWGQG TLTIVSS

Full-length light chain of ScFv-HC-IgG4 (SEQ ID NO: 136)

DNVLTQSPATLSVSPGERATLSCKASQSVDFDGD SYMNWYQOKPGQPPRLIIYAASNLESGIPARFSGSGSGTDFTLTISSEPEDEFAF
YYCQQSNEDEPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS
LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Full-length modified heavy chain (version 2) of ScFv-HC-IgG1-LALA (SEQ ID NO: 137)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSWVRQAPGKRLEWVAHISGGSTYYPDVTVKGRFTISRDN SKNTLYLQMN SLRAE
DTAMYYCTRQFYFGSSFWYFDVWGAGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV
LQSSGLYSLSVTVPSSSLGKTYTCNVNPKPSNTKVDKRVESKYGPPCPPAPAEAGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGN VFSCVMHEALHNYTQKS
LSLSPGGGGGGGGGGSDVMTQSPSLPVTILGQPASISCRSSQSLHNSNGNTYLHWYQQRPQGSPNHLIIYQVSNRFSGVDPDRFS
GSGSGTDFTLKISRVEAEDVGVYFCSQTHVPWTFGGGTKEIKGGGGGGGGGGGSGGGSQVLVQSGAEVKKPGASVKLSCKAS
GYTFISYIYWVKQAPGQCLEWIGGINPRNGGTNFEKFKSRATLTVDTSISTAYMELSLRSED TAVYYCTR HNGVYWGQG TLTIVS

S

Full-length modified heavy chain (version 1) of ScFv-HC-IgG1-LALA (SEQ ID NO: 138)
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMSVWRQAPGKRLEWVAHISGGSTYYPDTVKGRFTISRDNKNTLYLQMNSLRAE
 DTAMYYCTRFYGGSSFWYFDVWGAGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
 LQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHTCPPCPAPEAAGPSVFLFPPKPKDITLMISRTPEVTCV
 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYITL
 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS
 LSLSPGGGGGGGGGGSDVMTQSPSLPVLTLGQPASISCRSSQSLHNGNTYLNHWYQORPGQSPNHLIYQVSNRFSFGVPDRFS
 GSGSGDTFTLKISRVEAEDVGYFCSTTHVPWTFGGGTKEIKGGGGGGGGGGGGGGQVQLVQSGAEVKKPGASVKLSCKAS
 GYTFISYIYWVKQAPGGQGLEWIGGINPRNGGTNFEKFKSRATITVDTSI STAYMELSRLRSEDTAVYYCTRHNQGVYWGQGTTLTVS
 S

Full-length light chain of ScFv-HC-IgG1-LALA (SEQ ID NO: 139)
 DNVLTSQSPATLSVSPGERATLSCKASQSVDFDGDYSYMNWYQQKPGQPPRLIYAASNLESGIPARFSGSGSGTDFTLTISSEVEPEDFAT
 YYCQQSNEDPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYS
 LSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

IgG4, IgG2 and IgG1 light chain constant region (CL) (SEQ ID NO: 146)
 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEV
 THQGLSSPVTKSFNRGEC

IgG1 heavy chain constant region (SEQ ID NO: 147)
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKV
 EPKSCDKTHTCPPCPAPELIGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
 LNKKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLT
 VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

IgG1 heavy chain constant region with LALA mutations (SEQ ID NO: 148)
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKV
 EPKSCDKTHTCPPCPAPEAAGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
 LNKKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLT
 VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

IgG4 heavy chain constant region (SEQ ID NO: 149)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTTCNVDPHKPSNTKVDKRV
 ESKYGPCCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG
 KEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDK
 SRWQEGNVFSCVMHEALHNYTQKSLSLSPGK

IgG4 constant region with KIH mutations (SEQ ID NO: 150)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTTCNVDPHKP
 SNTKVDKRVEKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQP
 ENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCVMHEALHNYTQKSLSLSLGGK

IgG4 Fc (CH1 region deleted) region with KIH mutations (SEQ ID NO: 151)

DKRVEKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVV
 SVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVCTLPSPSQEEMTKNQVSLCAVKGFYPSDIAVEWESNGQPENNYK
 TTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCVMHEALHNYTQKSLSLSLGGK

Atezolizumab VH (SEQ ID NO: 211)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLRAE
 DTAVYVCARRHWPGGFDYWGQGLTVTVSS

Atezolizumab VL (SEQ ID NO: 212)

DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPKAPKLLIYSASFYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQ
 QYLYHPATFGQGTKEIK

Avelumab VH (SEQ ID NO: 213)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPGGITFYADTVKGRFTISRDNKNTLYLQMNSLRAE
 DTAVYICARIKLGTVTTVDYWGQGLTVTVSS

Avelumab VL (SEQ ID NO: 214)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY
 CSSYTSSTRVFGTGTKVTVL

Atezolizumab-6A7-FVHC-IgG1-LALA (heavy chain) (SEQ ID NO: 215)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWRQAPGKGLWVAVWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLRAE
DTAVYICARRHWPGGFDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSL
PGGGSGGGGGGSDVMTQSPSLPVTLLGQPASISCRSSQLLHNSNGNTYLNHWYQORPGQSPNHLIIYQVSNRFGSPDRFSGSG
GTDFTLKISRVEAEDVGVYFCSTTHVPWTFGGCTKVEIKGGGGGGGGGGGQVQLVQSGAEVKKPGASVKLSCKASGYTF
ISYIYWVKQAPGQCLEWIGGINPRNGGTNFEKFKSRATLTVDTSISTAYMELSLRSEDYAVYYCTRHNGVYWGQGTTLTVSS

Atezolizumab-6A7-FVHC-IgG1-LALA (light chain) (SEQ ID NO: 216)

DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQ
QYLHPATFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLST
LTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Avelumab-6A7-FVHC-IgG1-LALA (heavy chain) (SEQ ID NO: 217)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLWVSSIYPSSGGITFYADTVKGRFTISRDNKNTLYLQMNSLRAE
DTAVYICARIKLTGTTTVDYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP
SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSL
LSPGGGGSGGGGGSDVMTQSPSLPVTLLGQPASISCRSSQLLHNSNGNTYLNHWYQORPGQSPNHLIIYQVSNRFGSPDRFSGS
GSGTDFTLKISRVEAEDVGVYFCSTTHVPWTFGGCTKVEIKGGGGGGGGGGGQVQLVQSGAEVKKPGASVKLSCKASGY
TFISYIYWVKQAPGQCLEWIGGINPRNGGTNFEKFKSRATLTVDTSISTAYMELSLRSEDYAVYYCTRHNGVYWGQGTTLTVSS

Avelumab-6A7-FVHC-IgG1-LALA (light chain) (SEQ ID NO: 218)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMITYDVSNRPSGVSNRFGSGKSGNTASLTISGLQAEDEADYY
CSSYTSSTRVFGTGTKVTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKNKYAA
SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS