

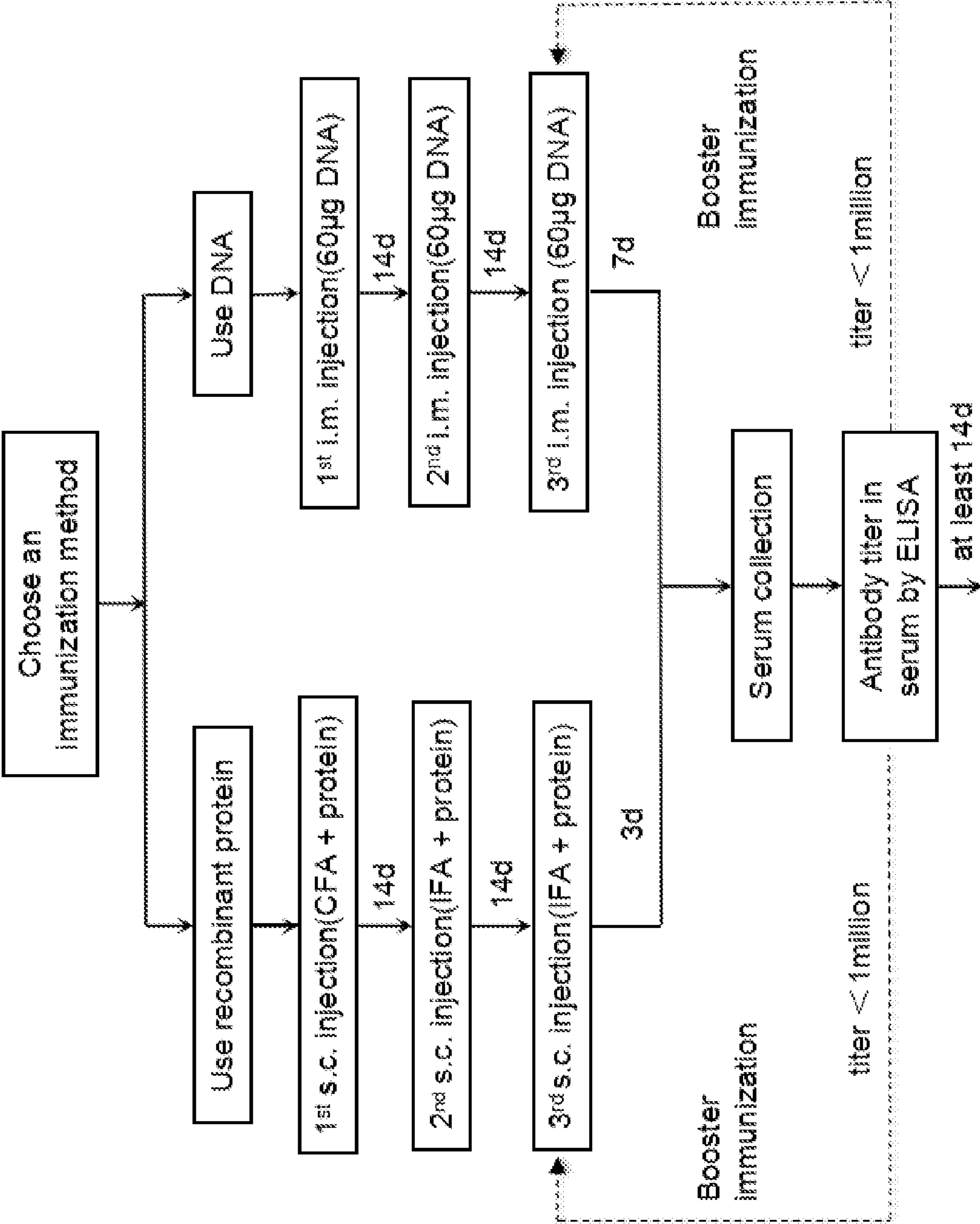


FIG. 1

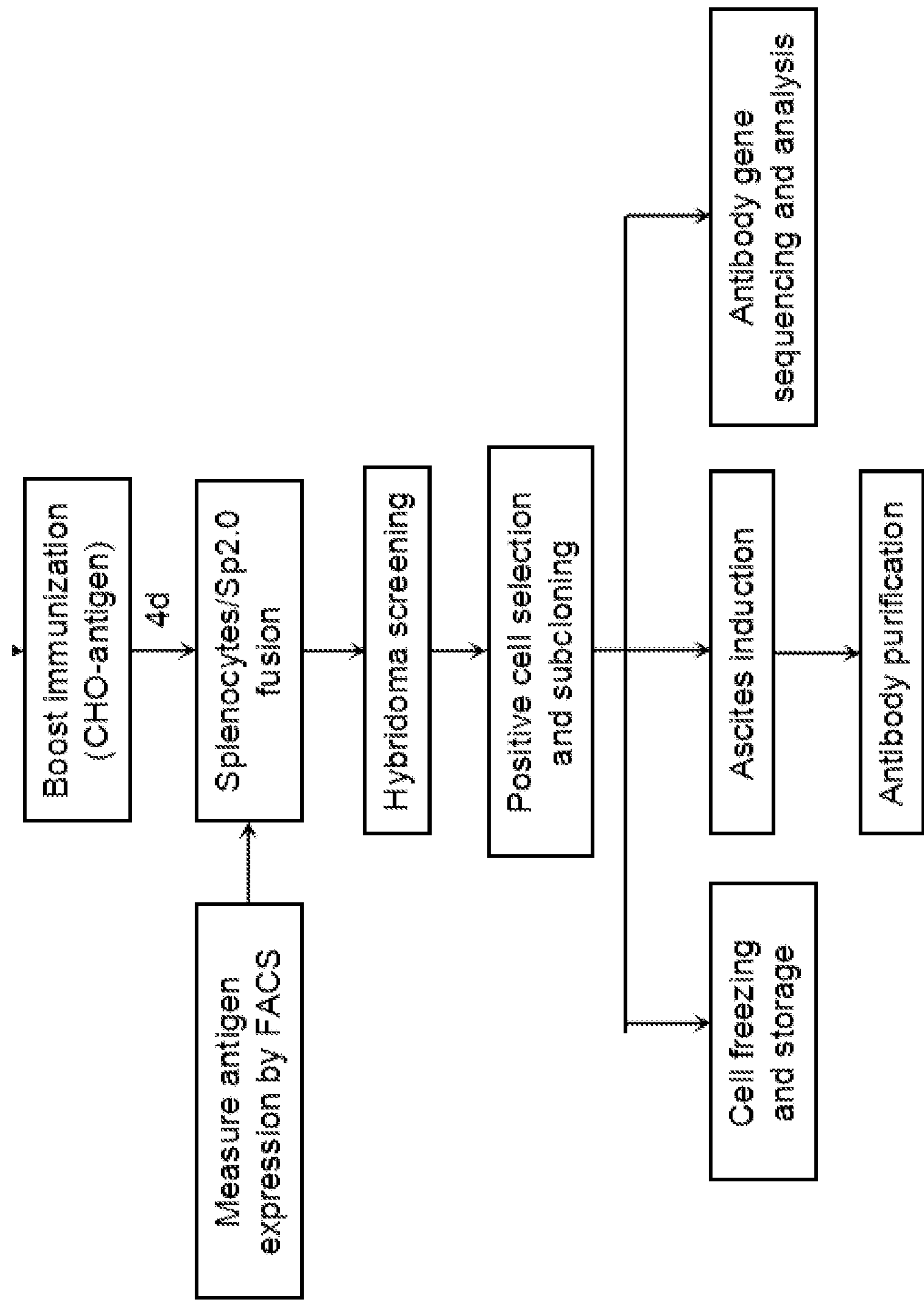


FIG. 2

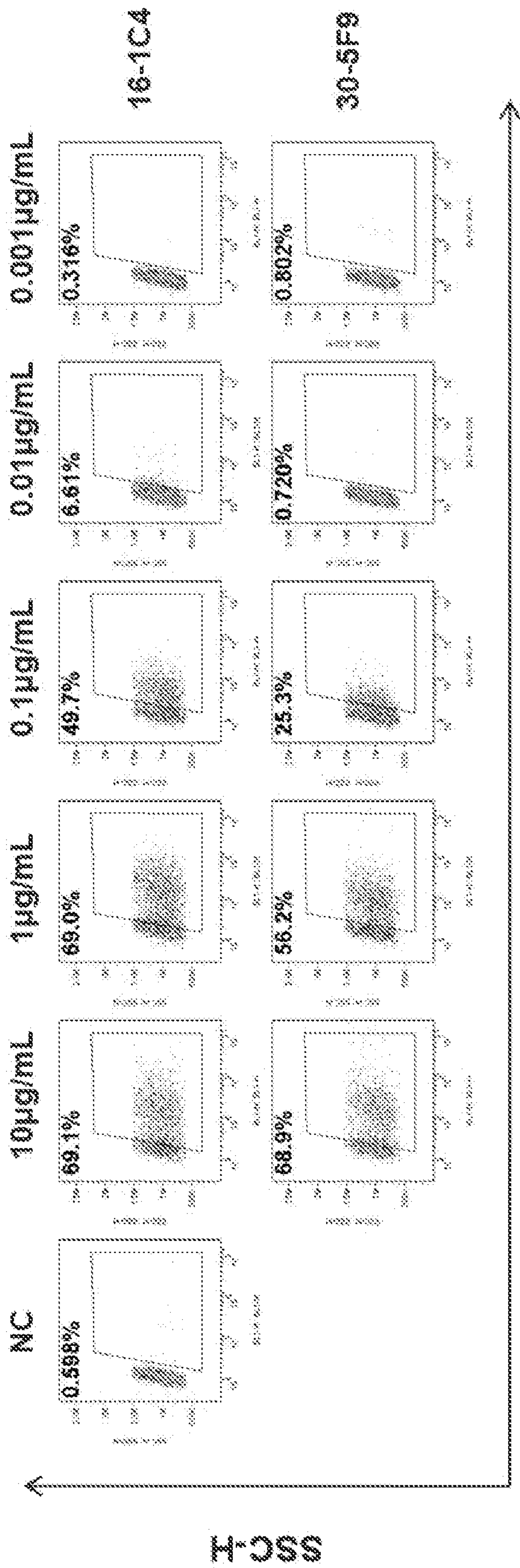


FIG. 3

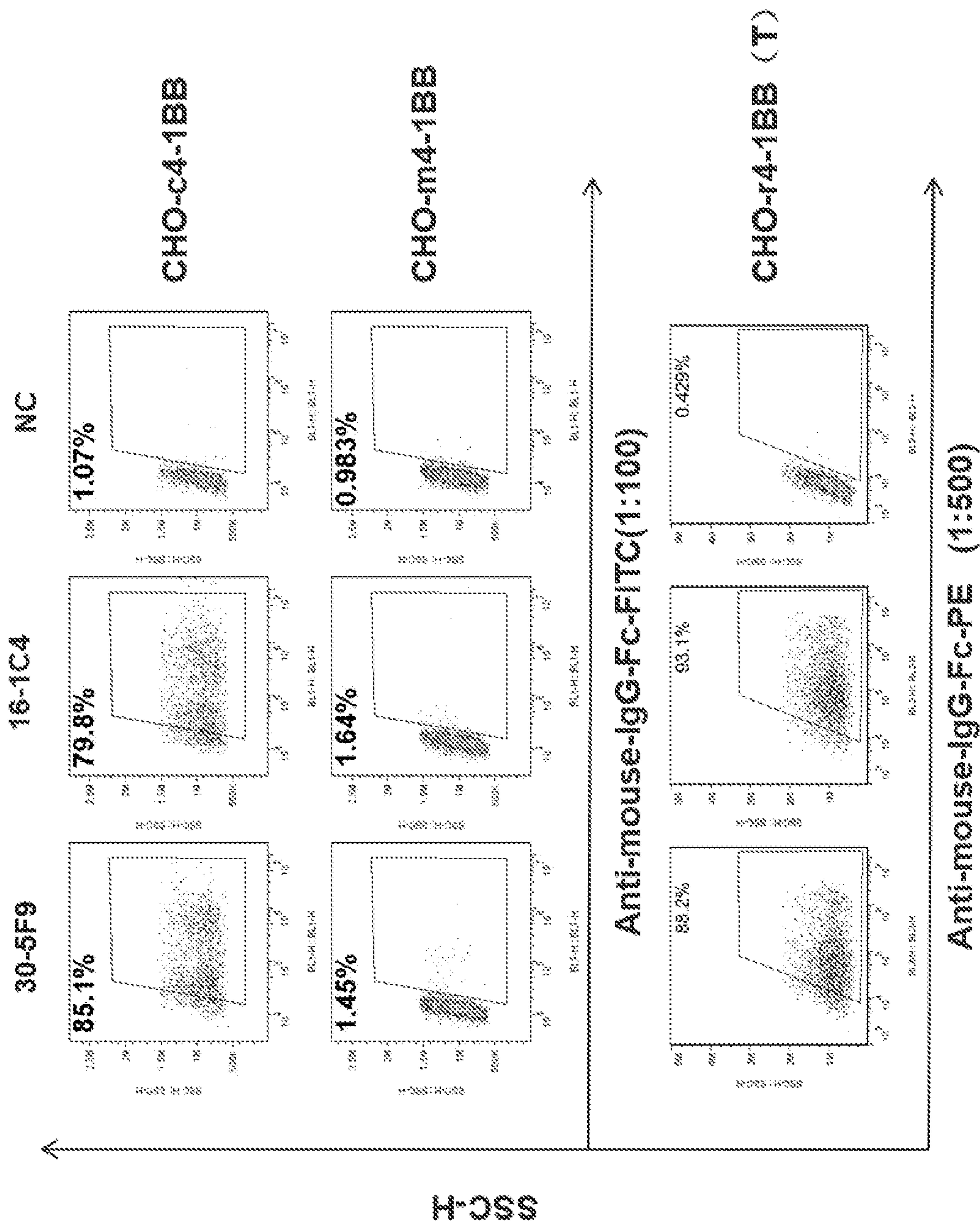


FIG. 4

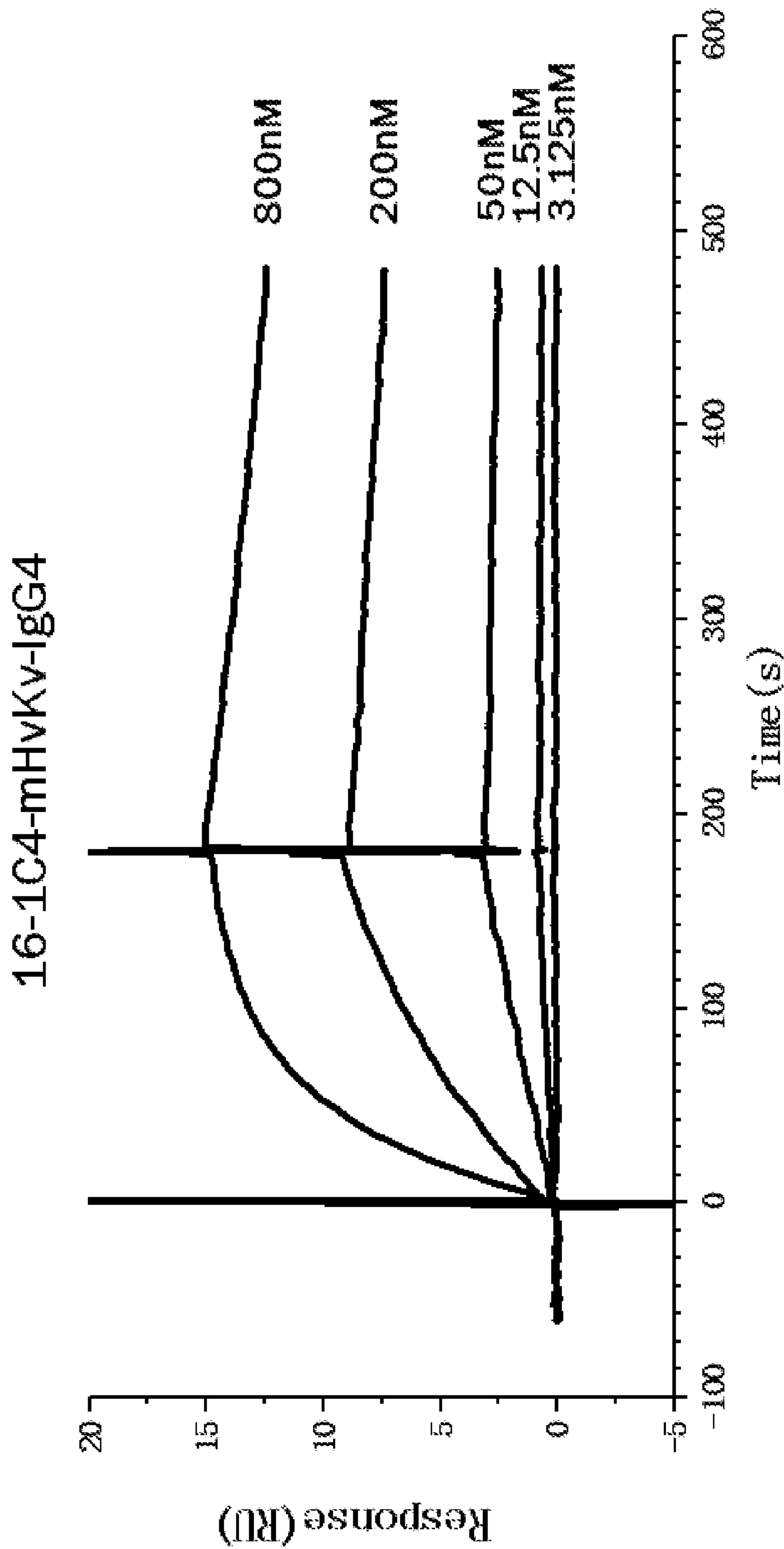


FIG. 5

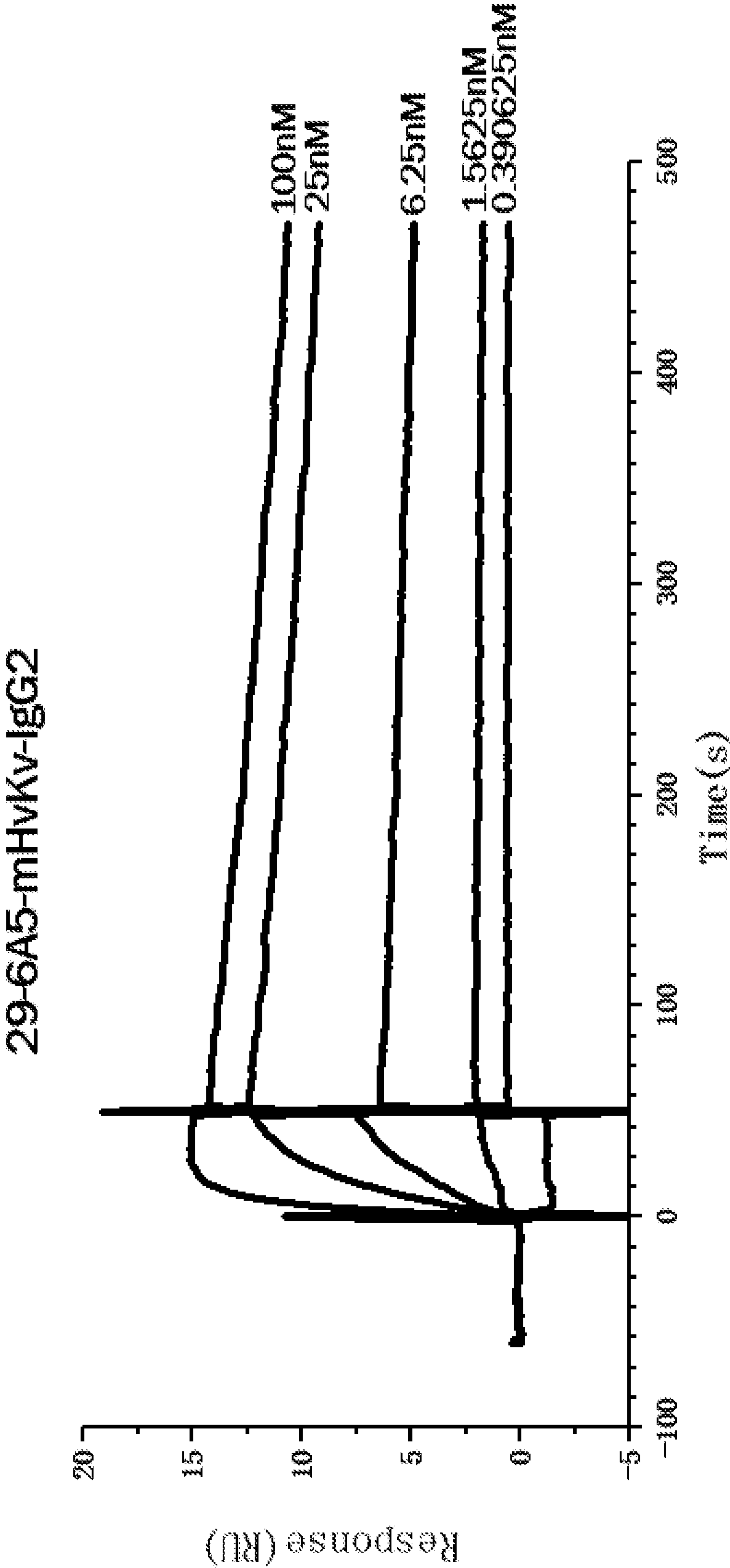


FIG. 6

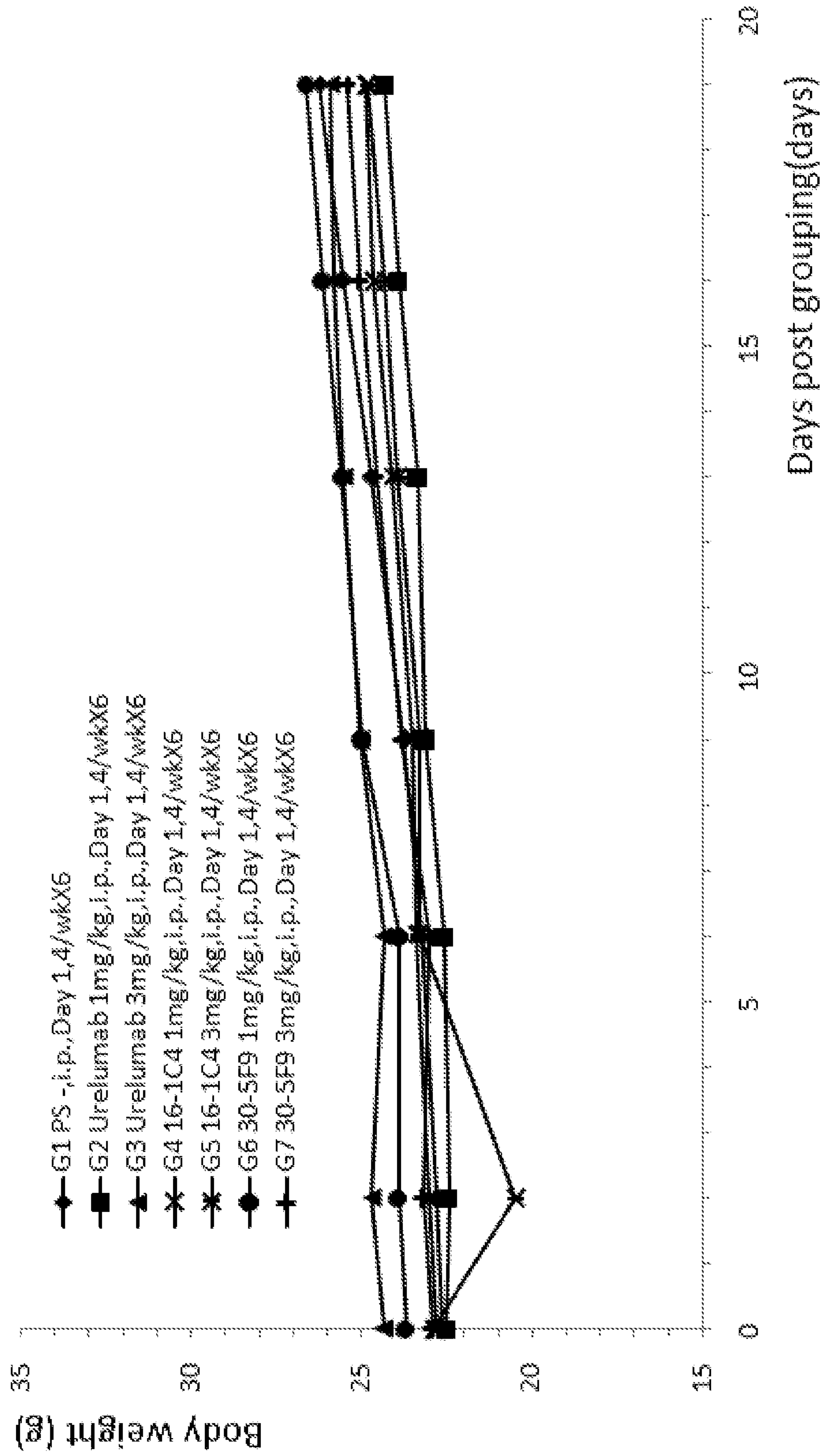


FIG. 7

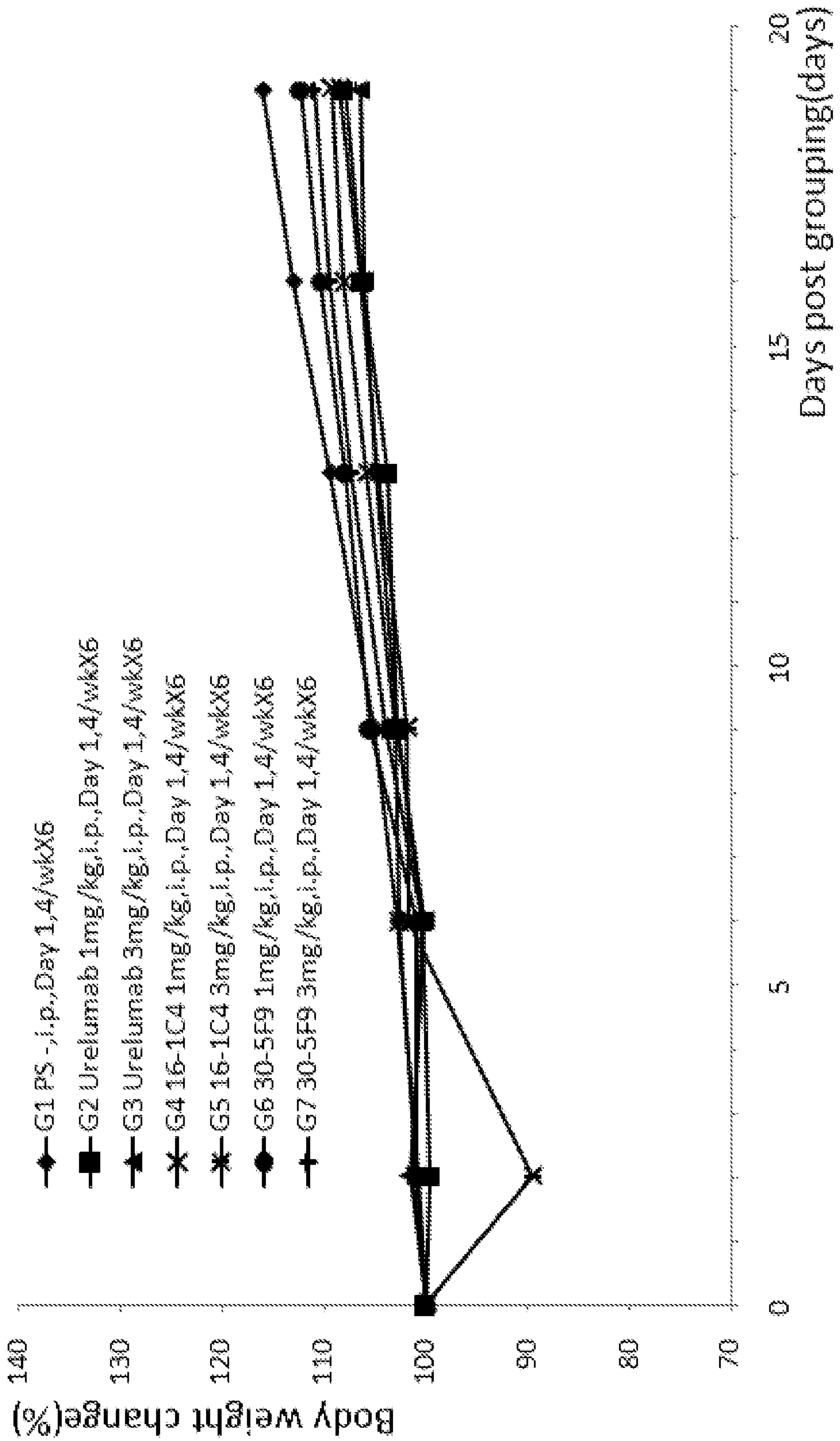


FIG. 8

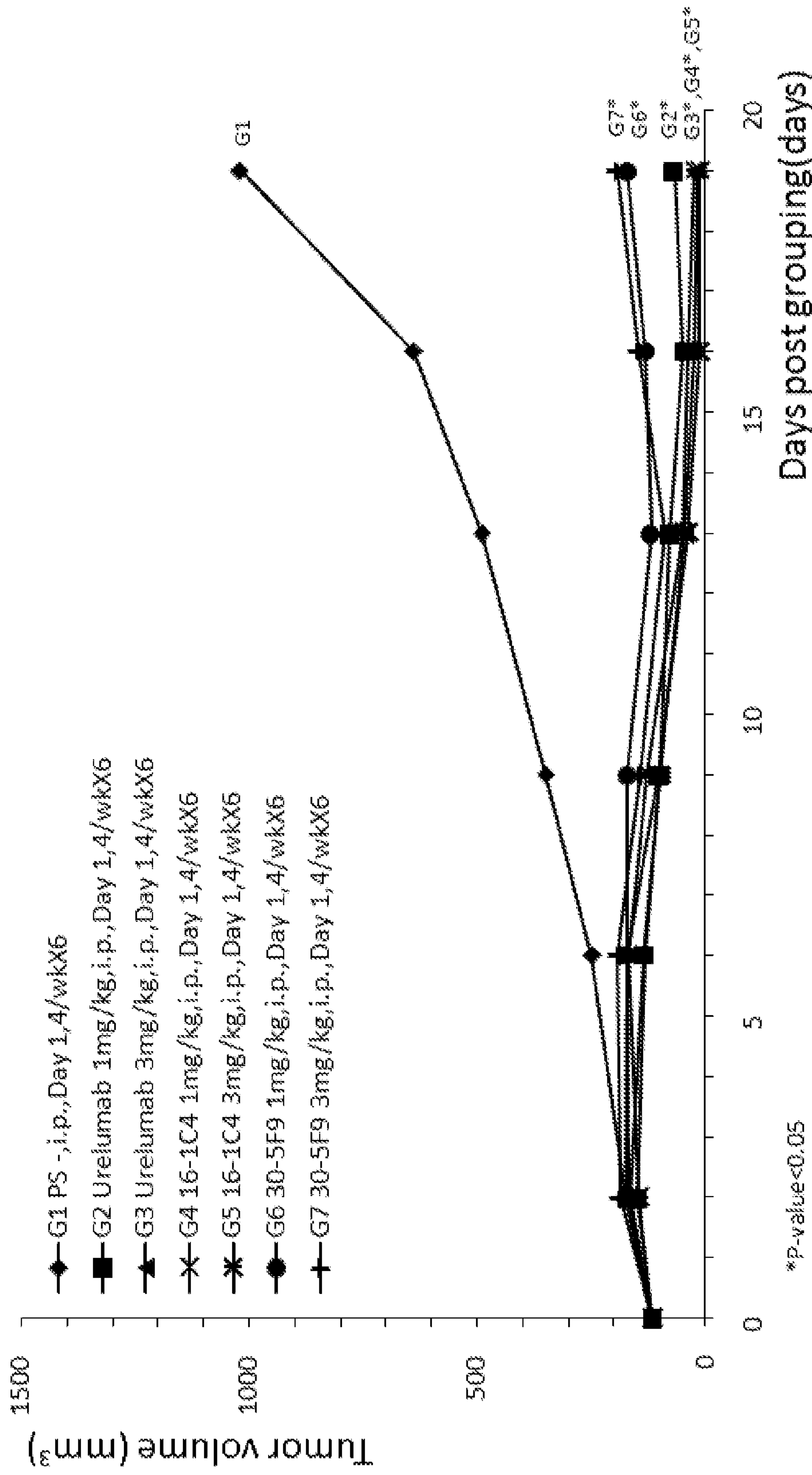


FIG. 9

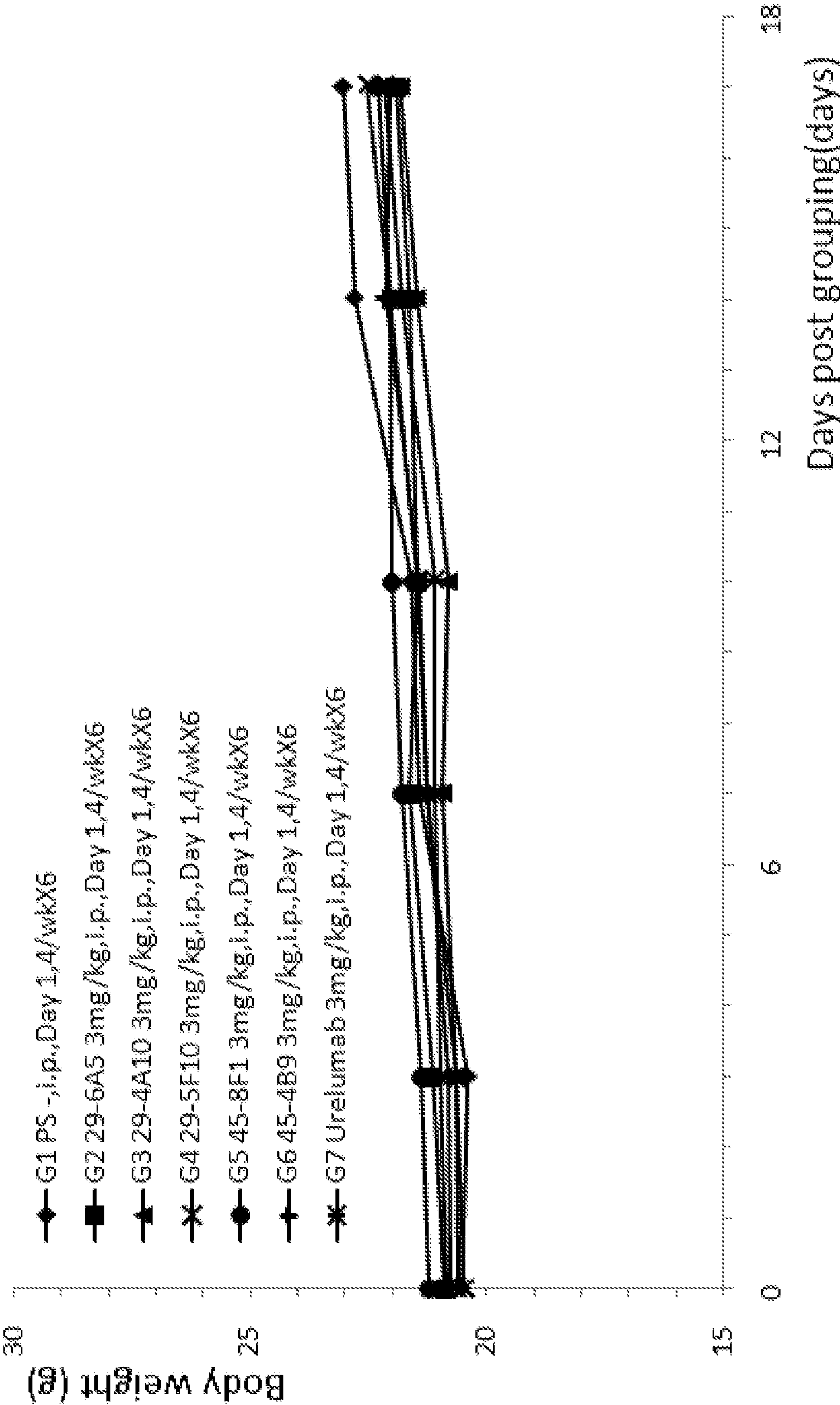


FIG. 10

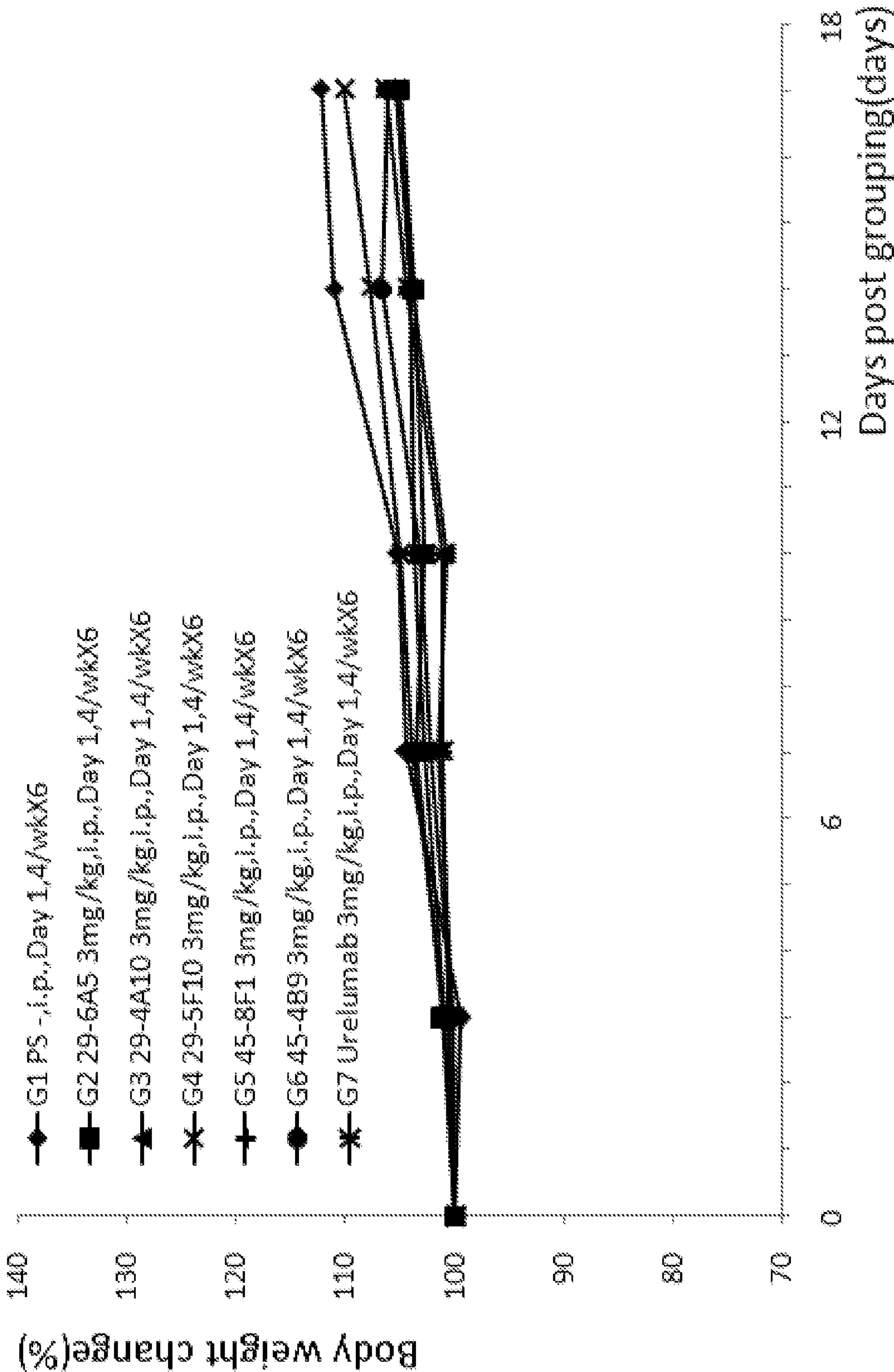


FIG. 11

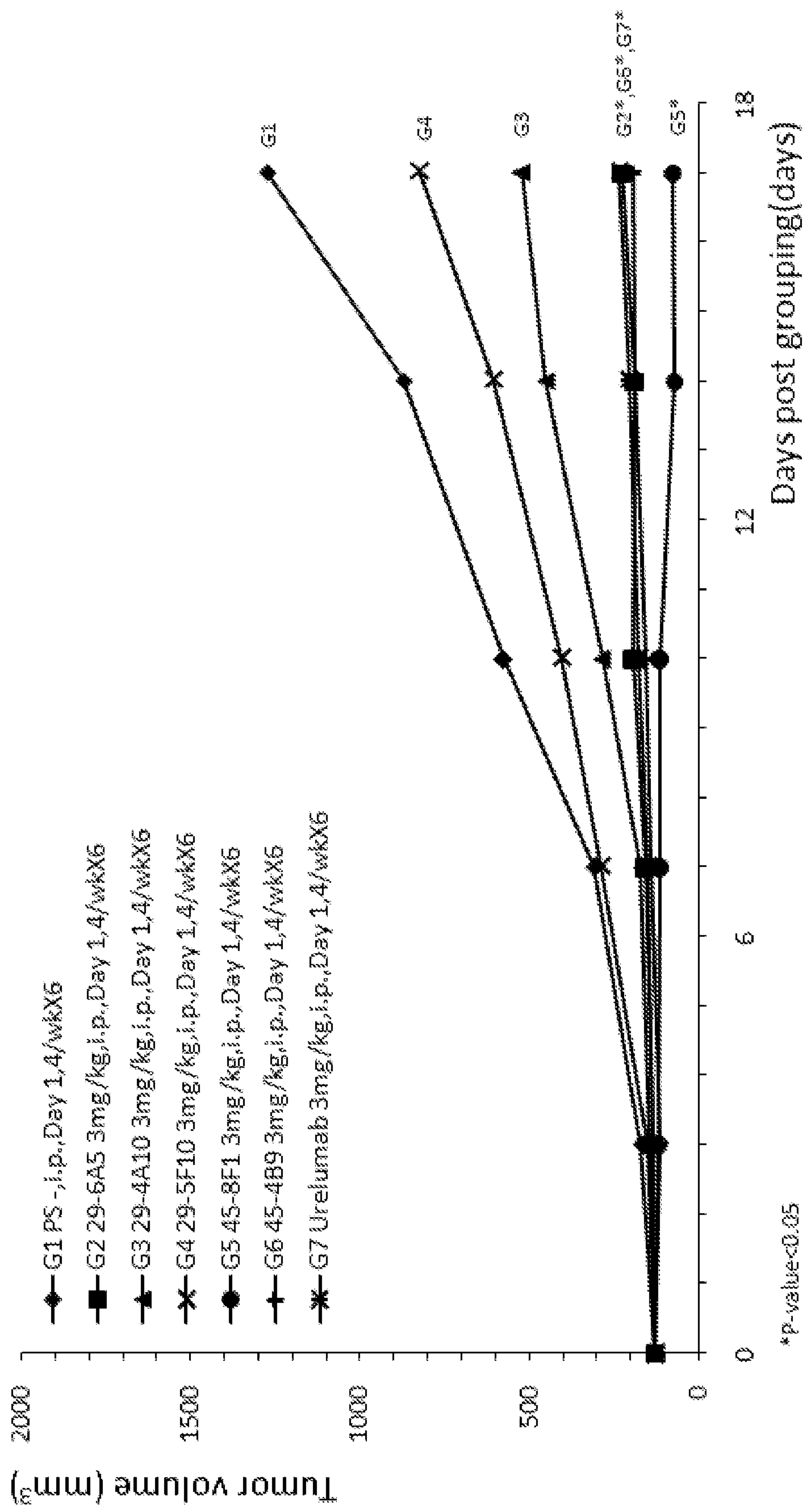


FIG. 12

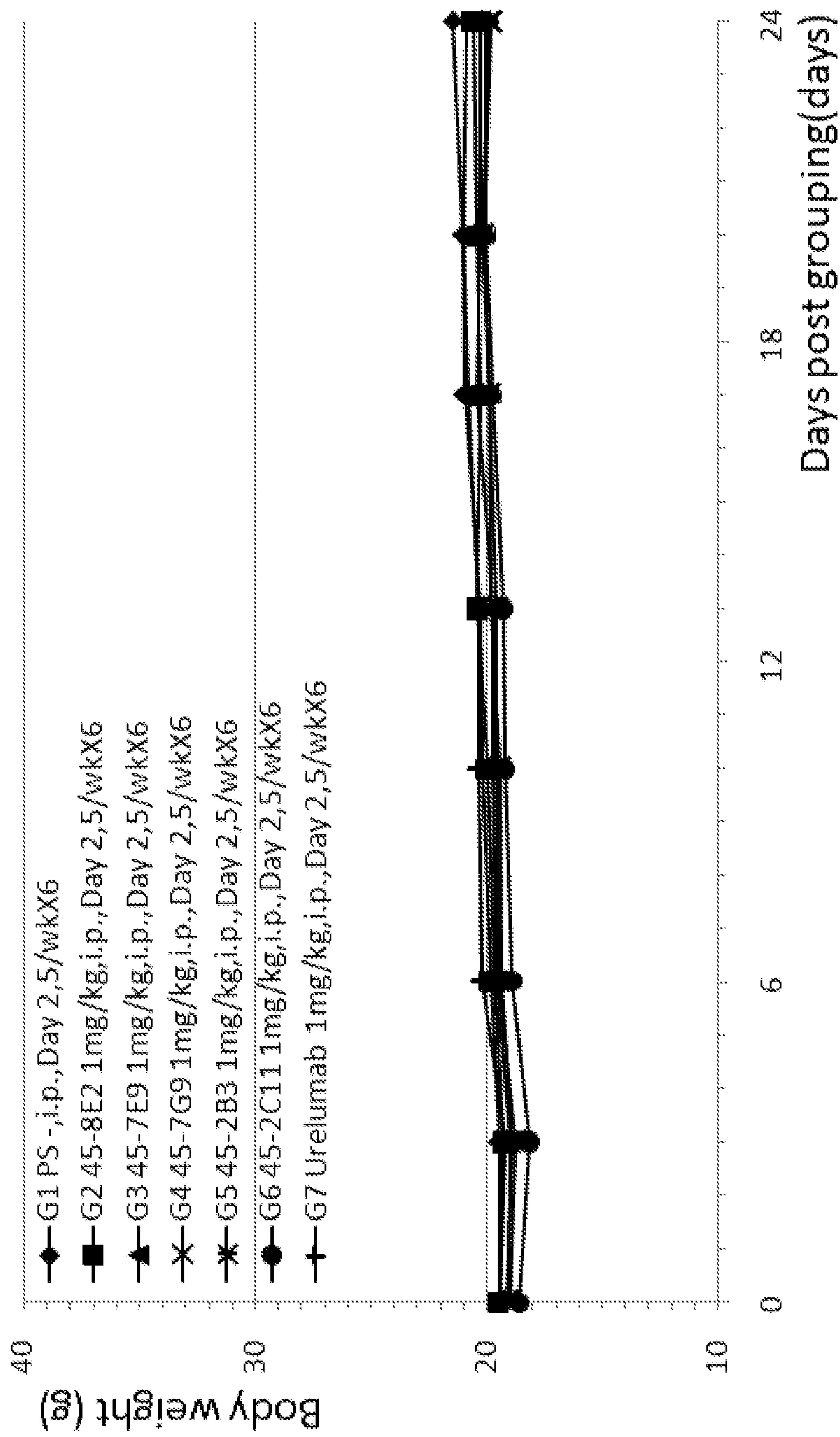


FIG. 13

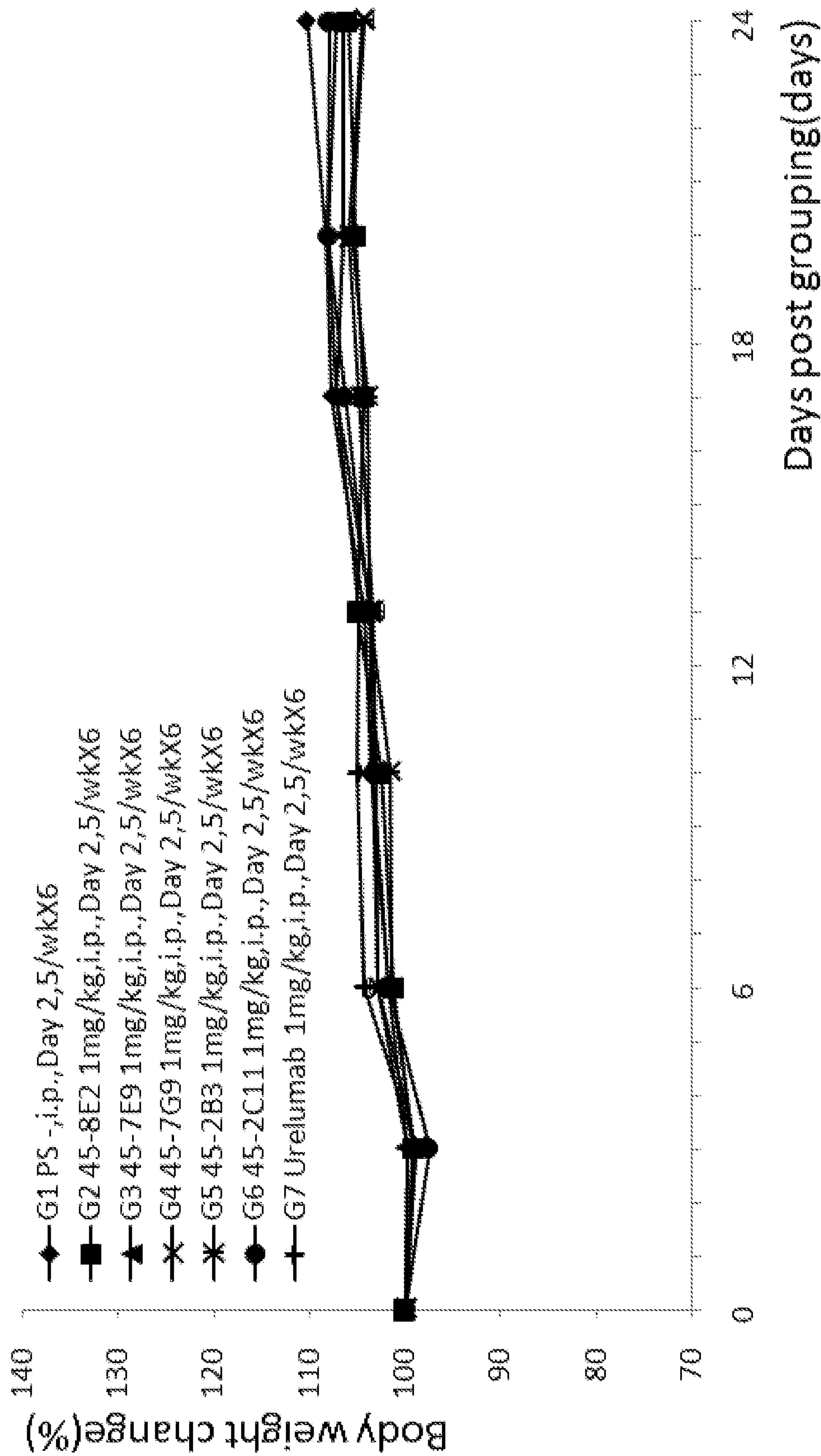


FIG. 14

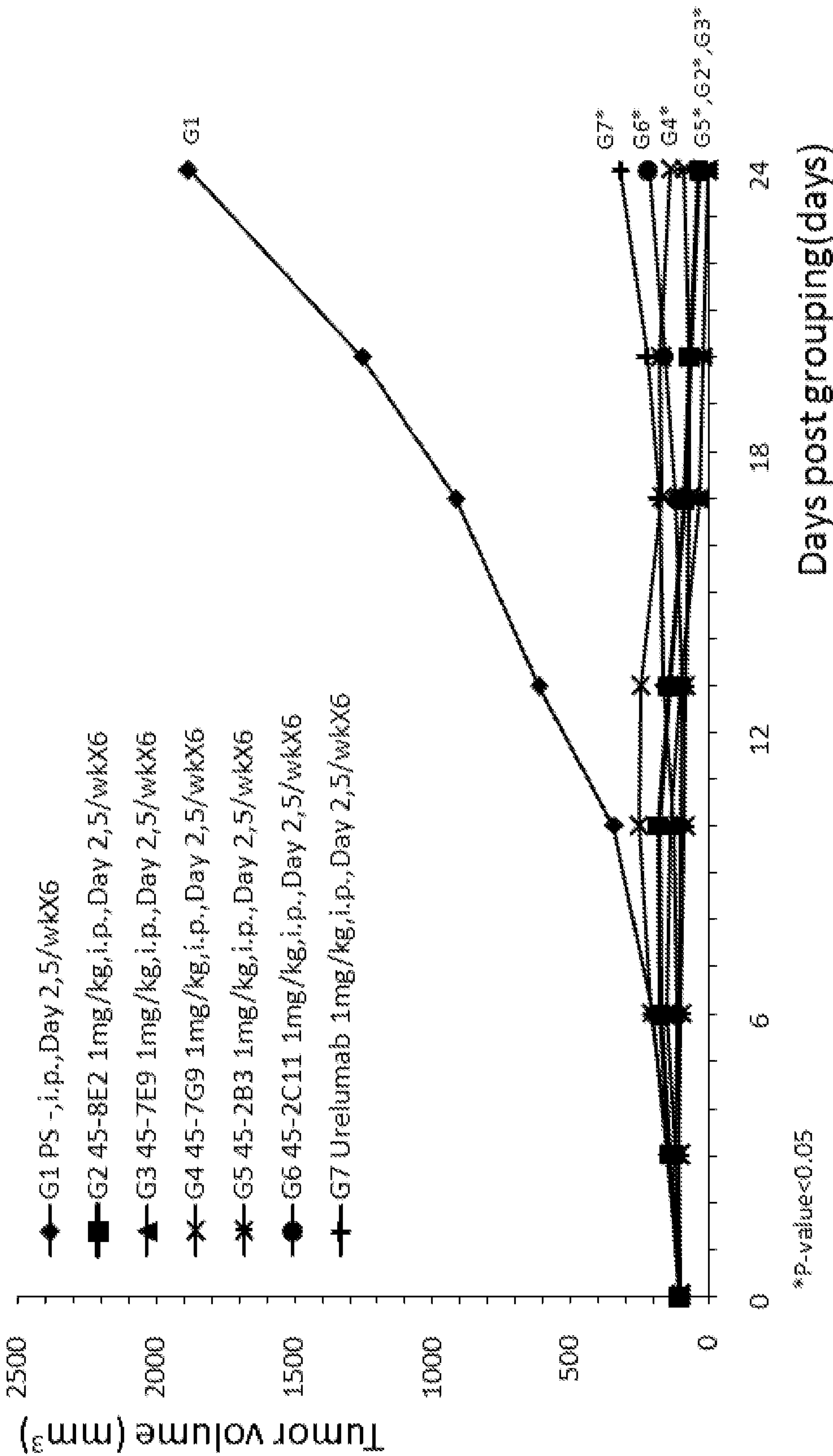


FIG. 15

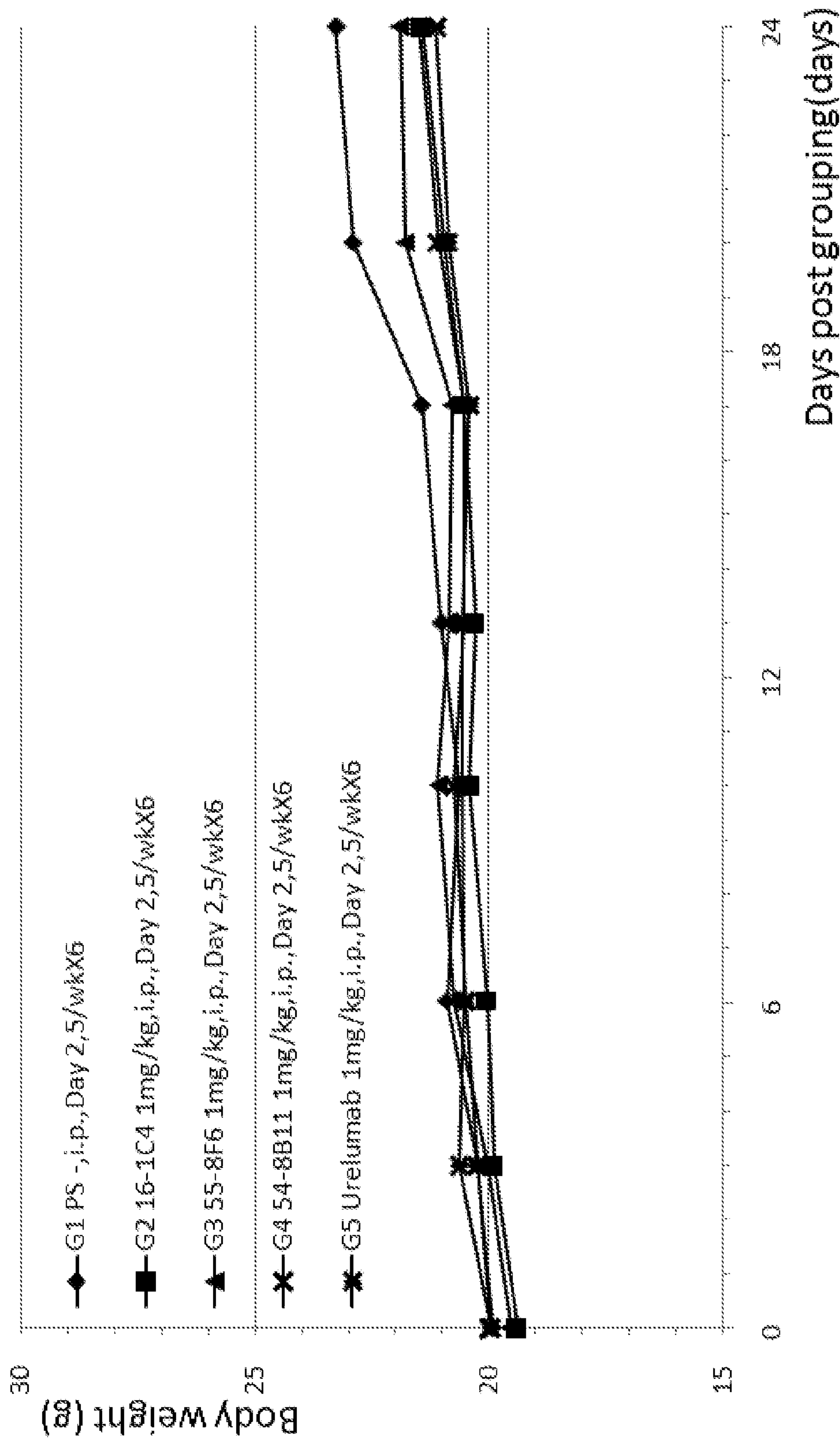


FIG. 16

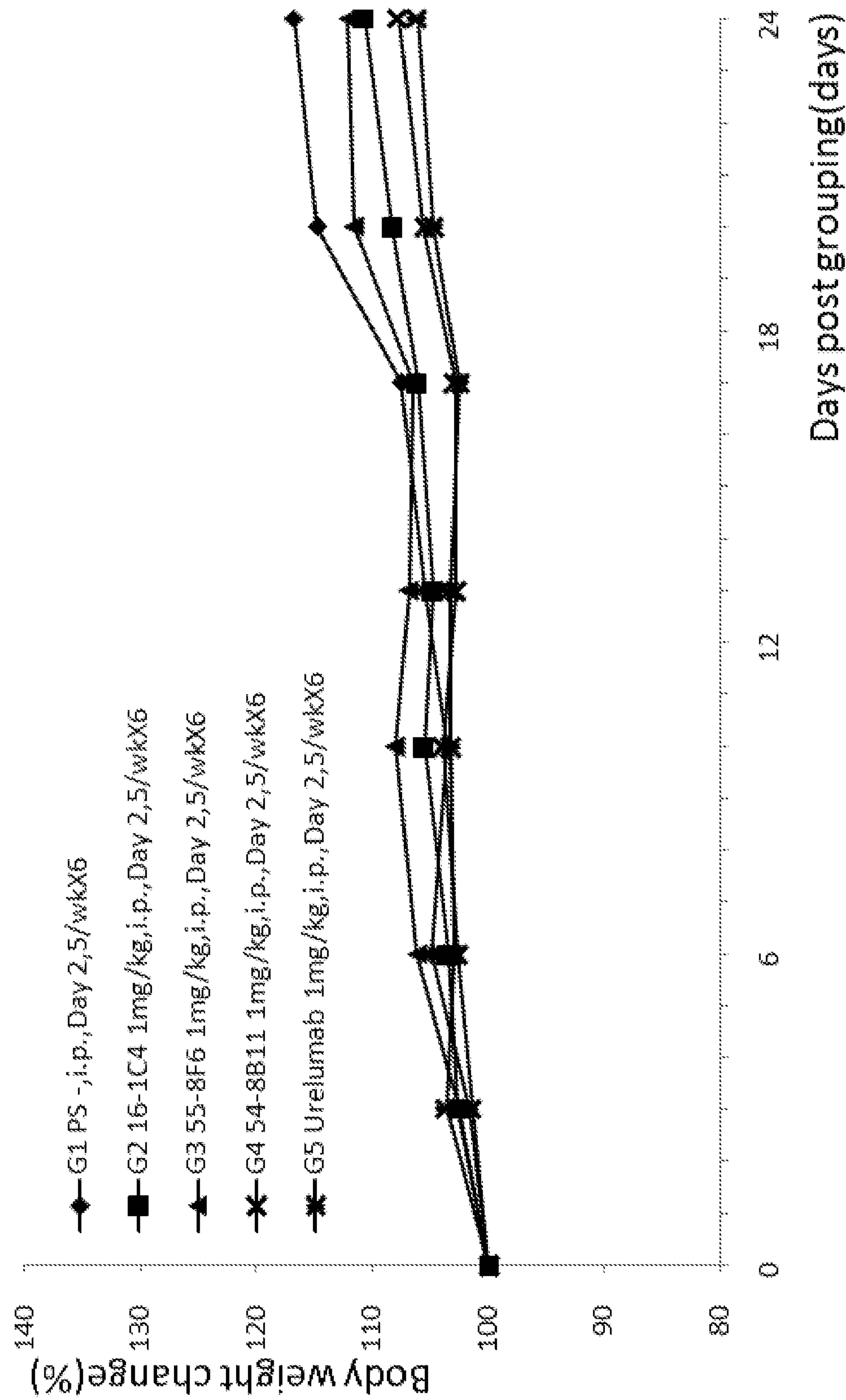


FIG. 17

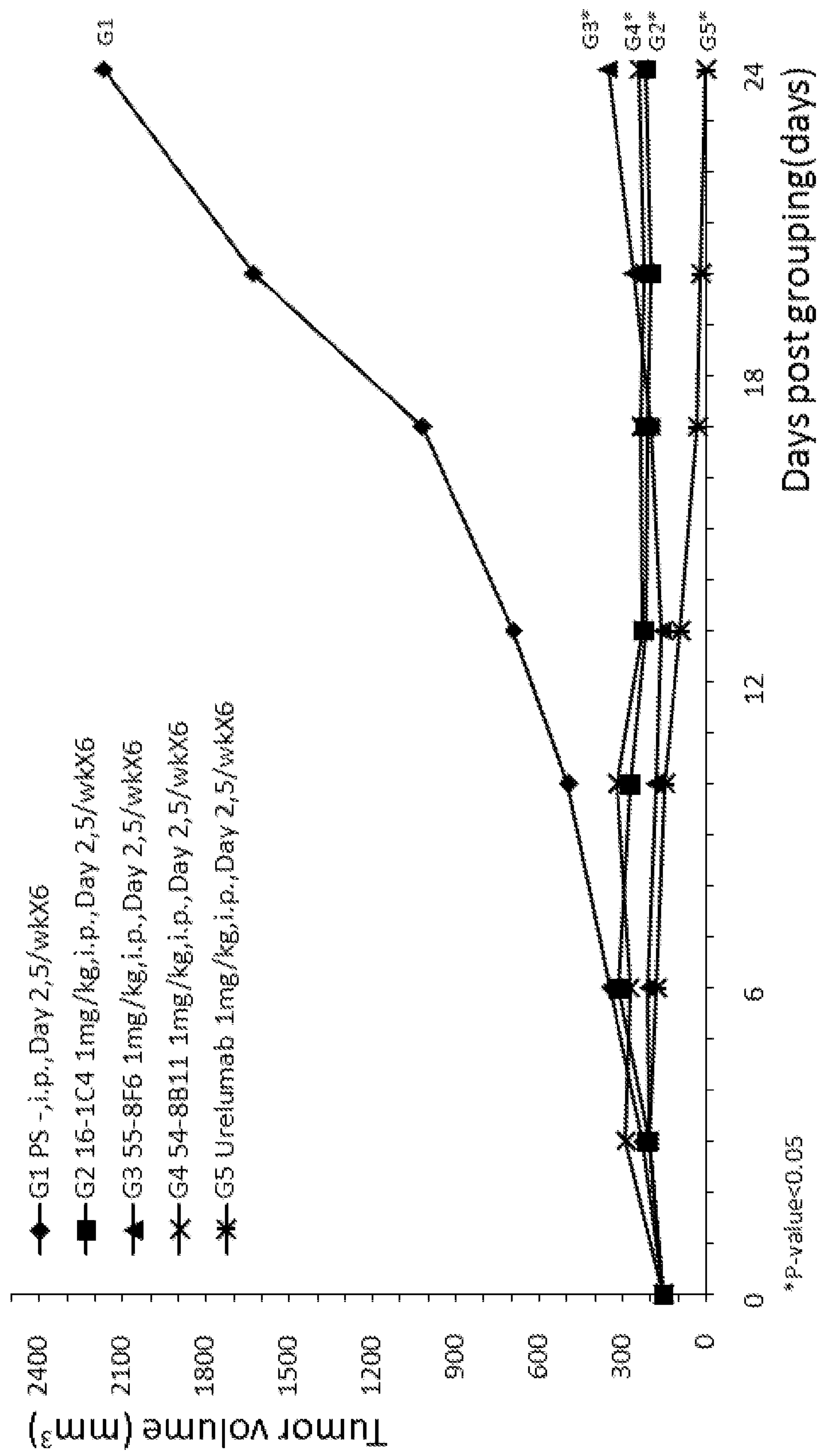


FIG. 18

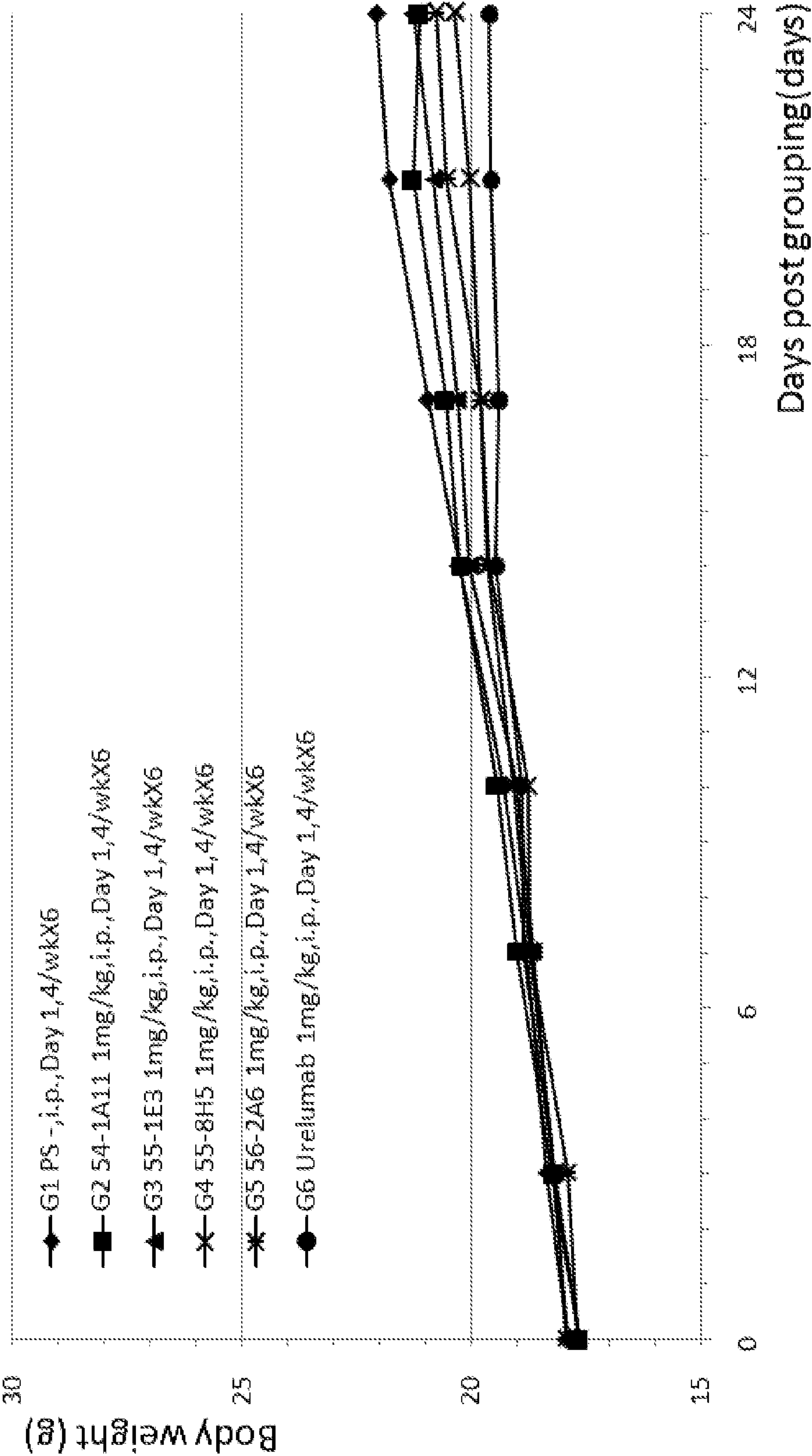


FIG. 19

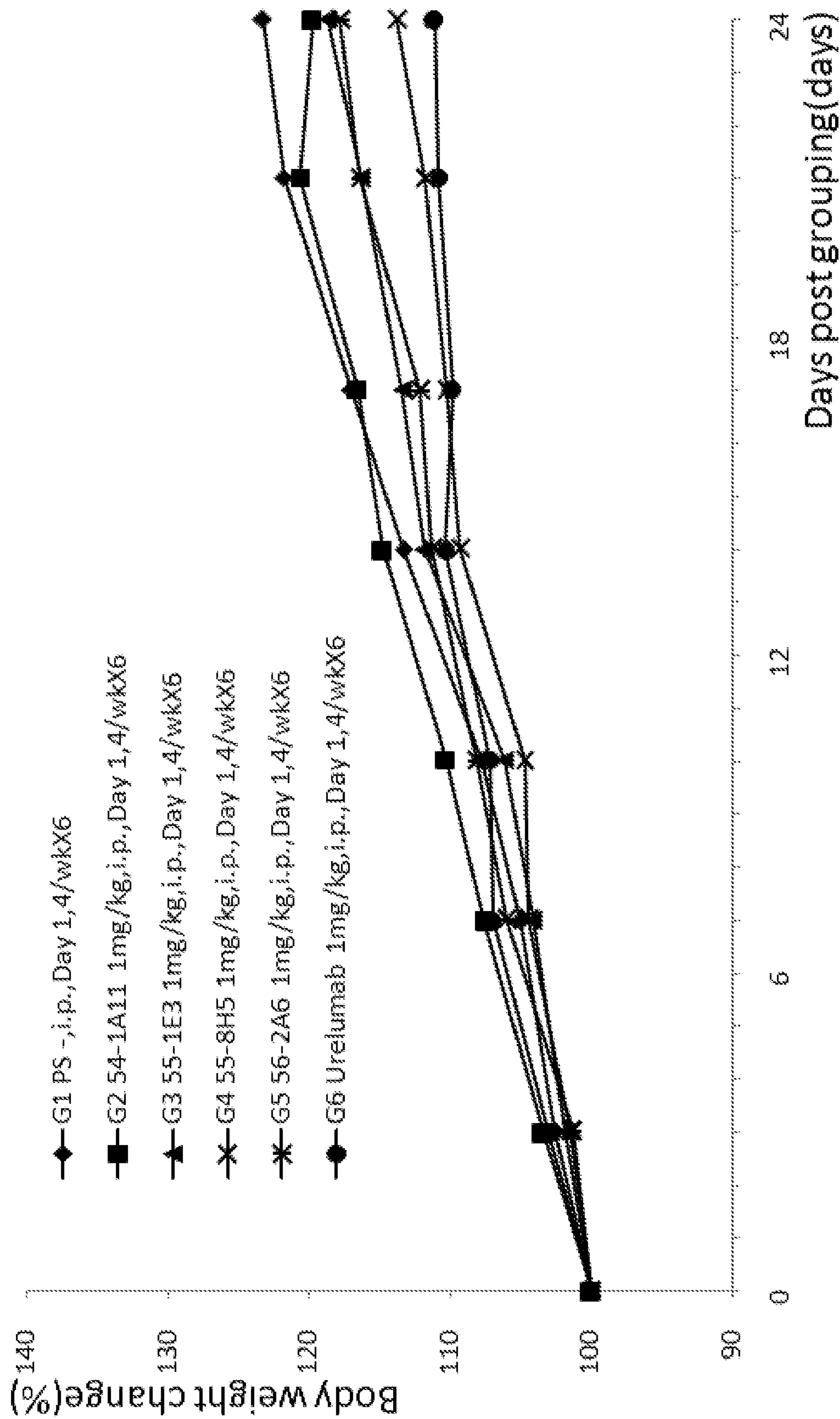


FIG. 20

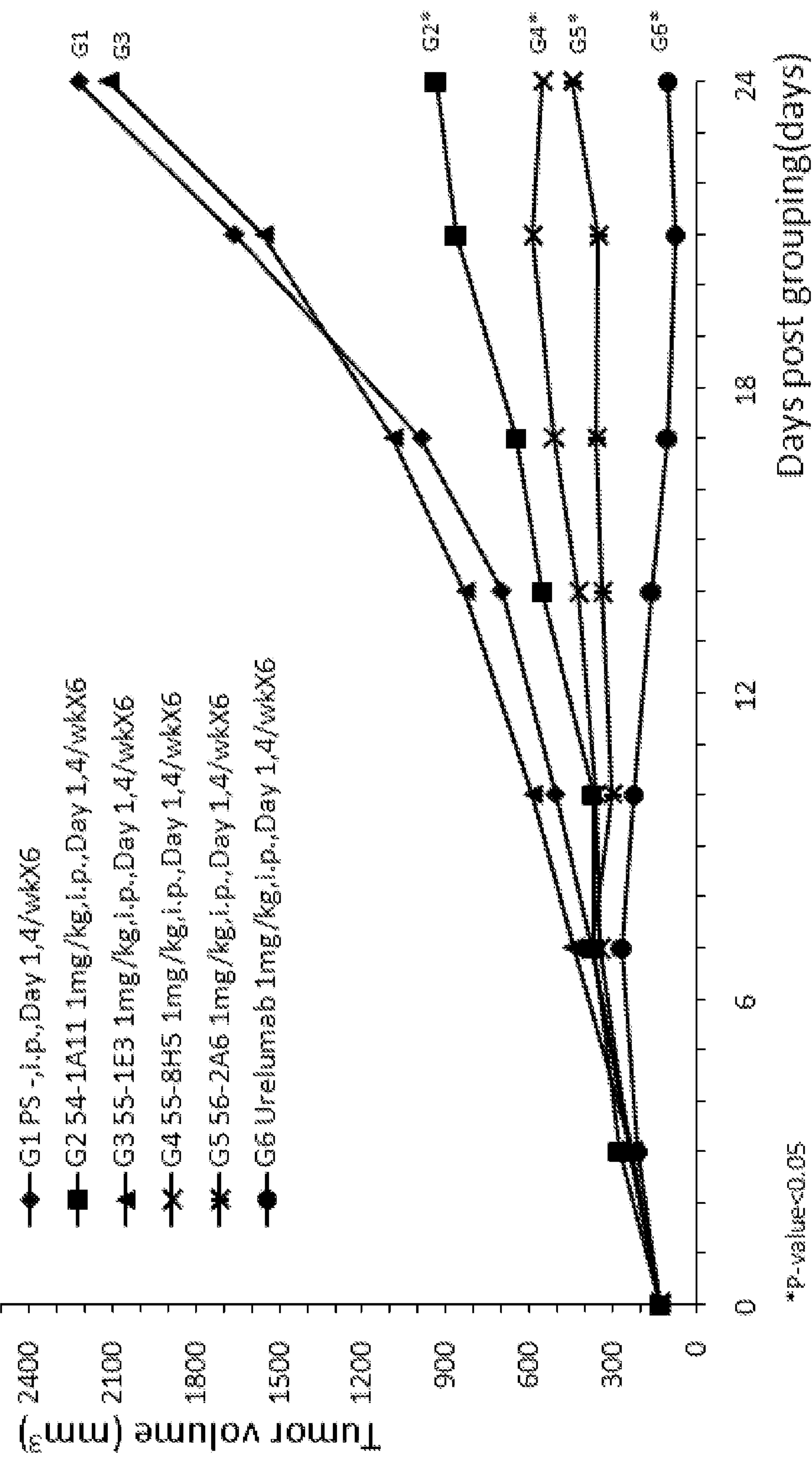


FIG. 21

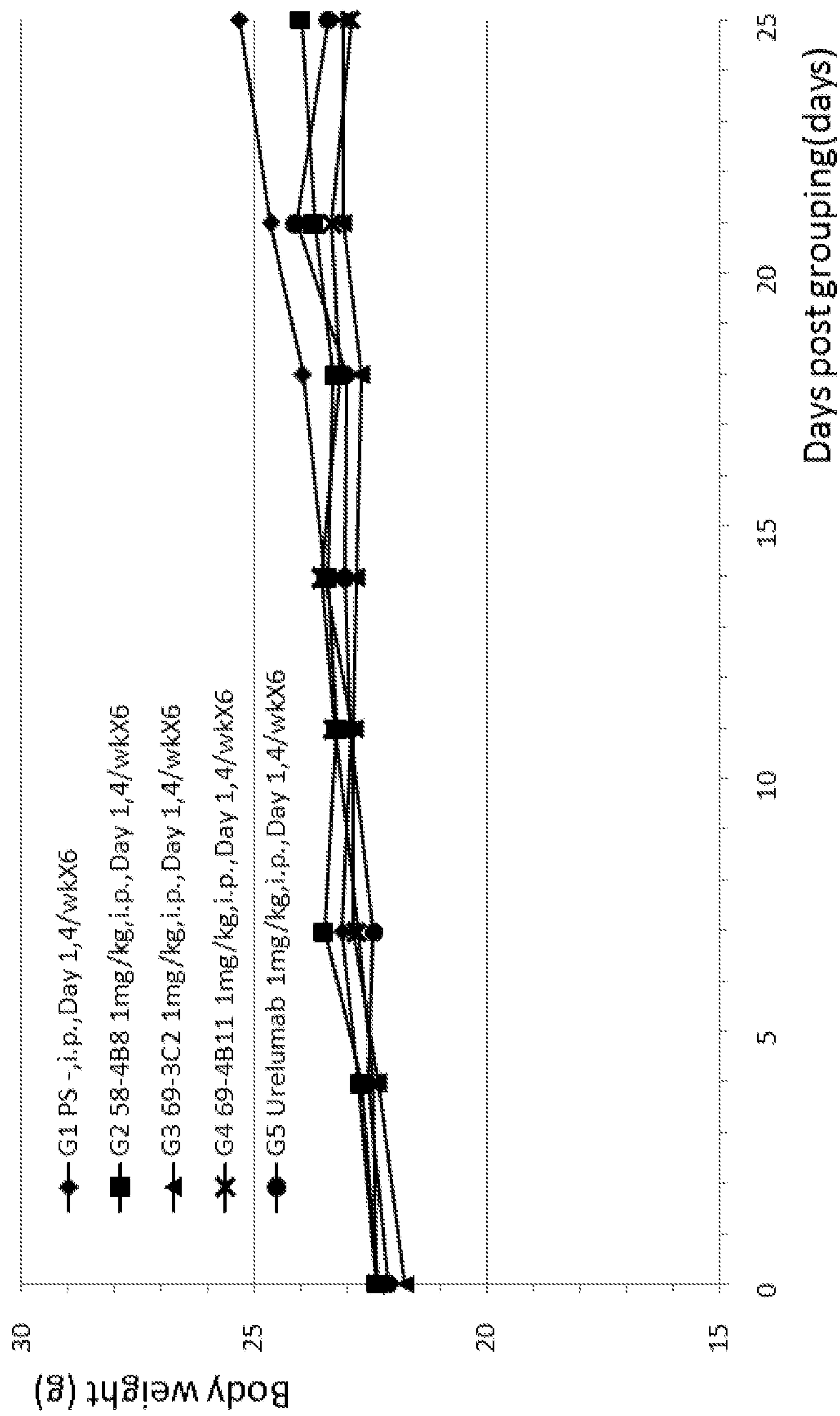


FIG. 22

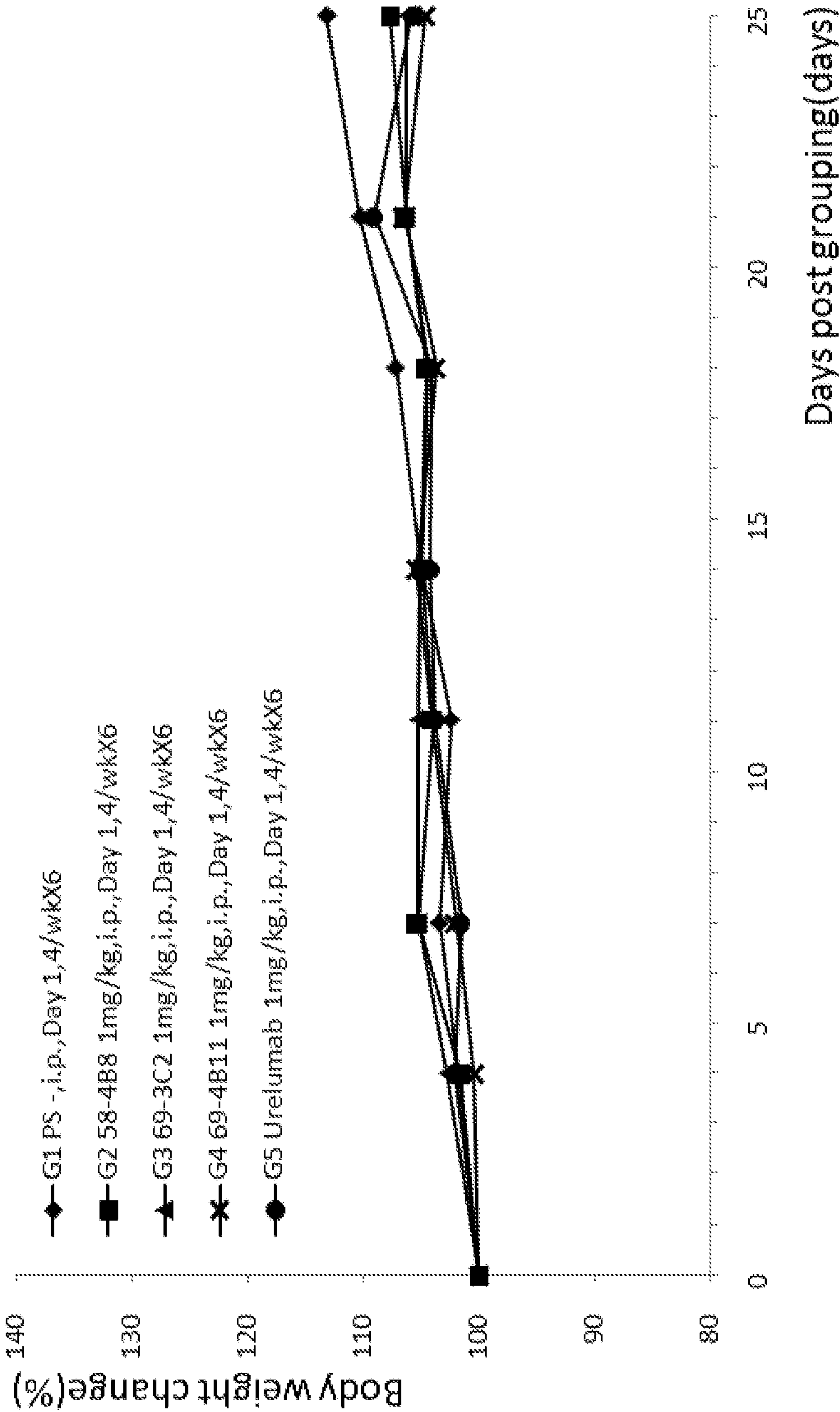


FIG. 23

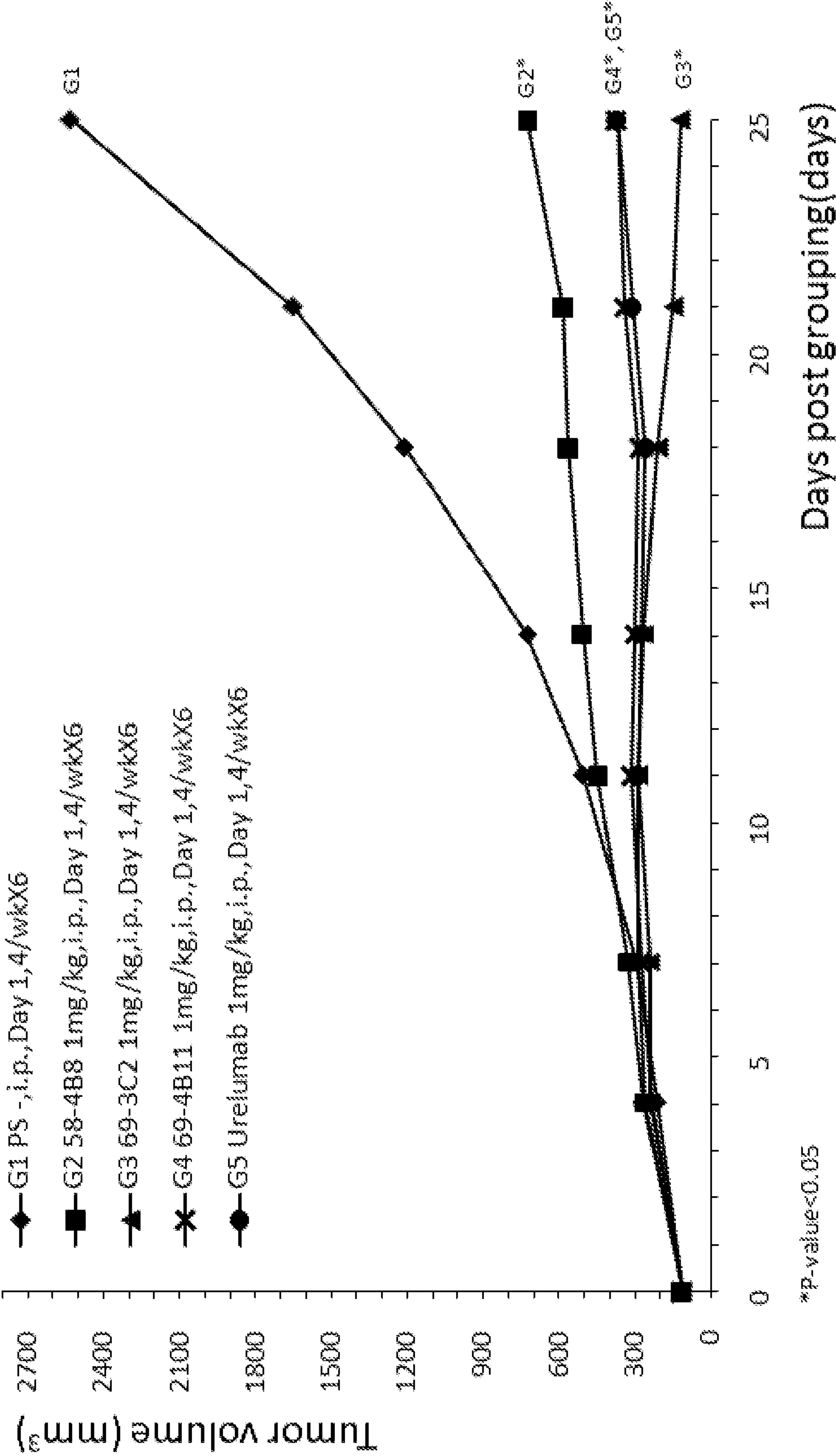


FIG. 24

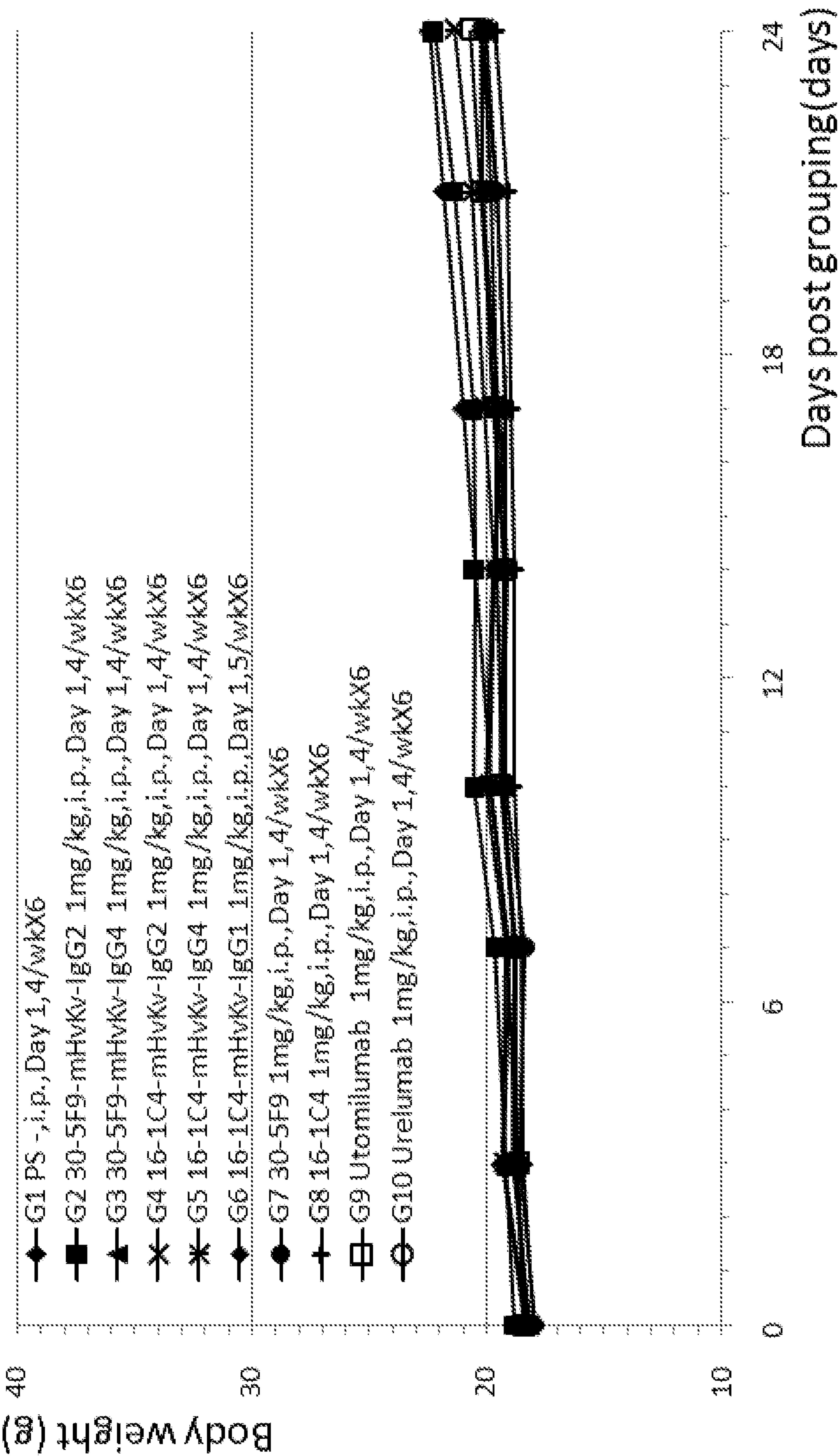


FIG. 25

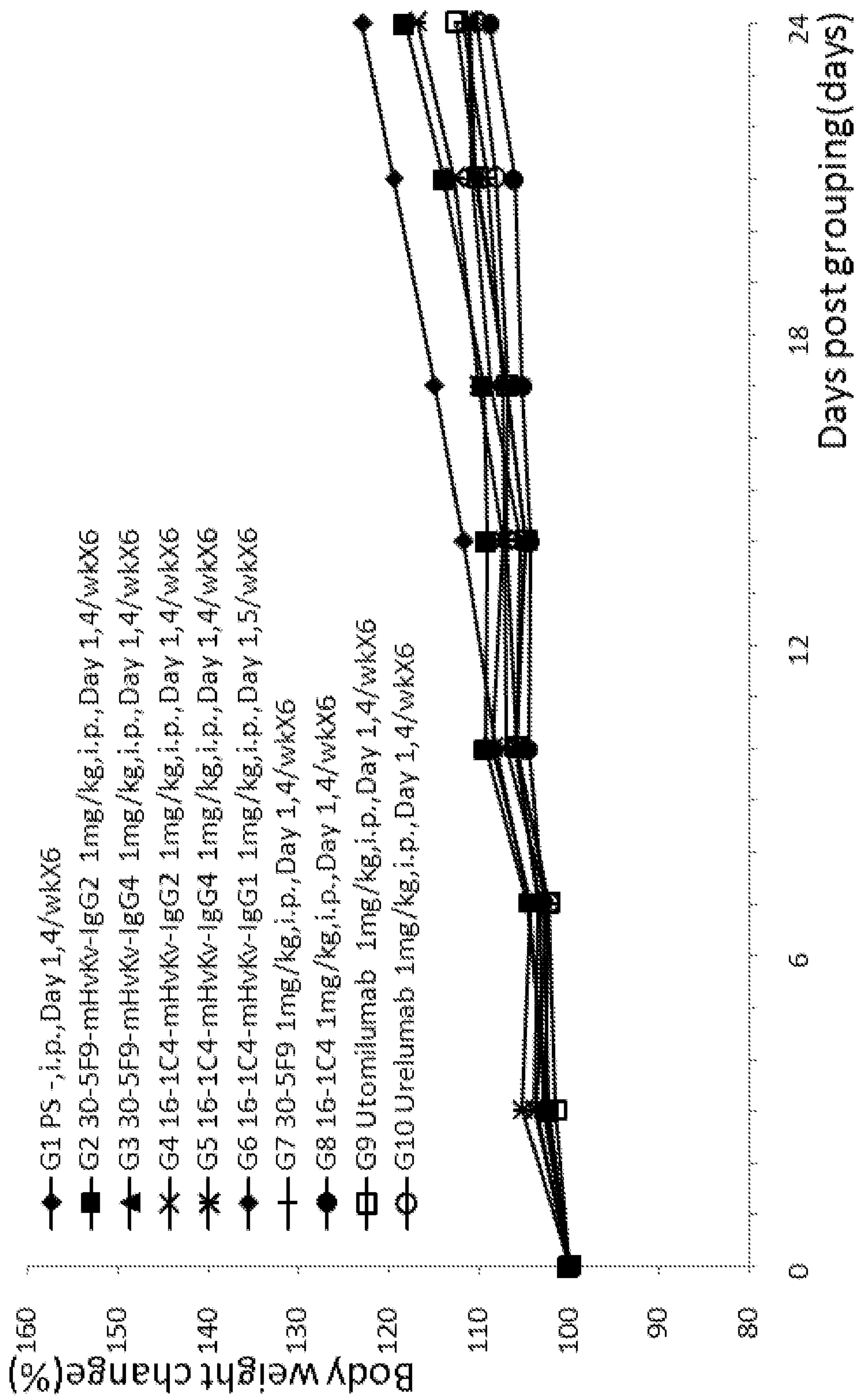


FIG. 26

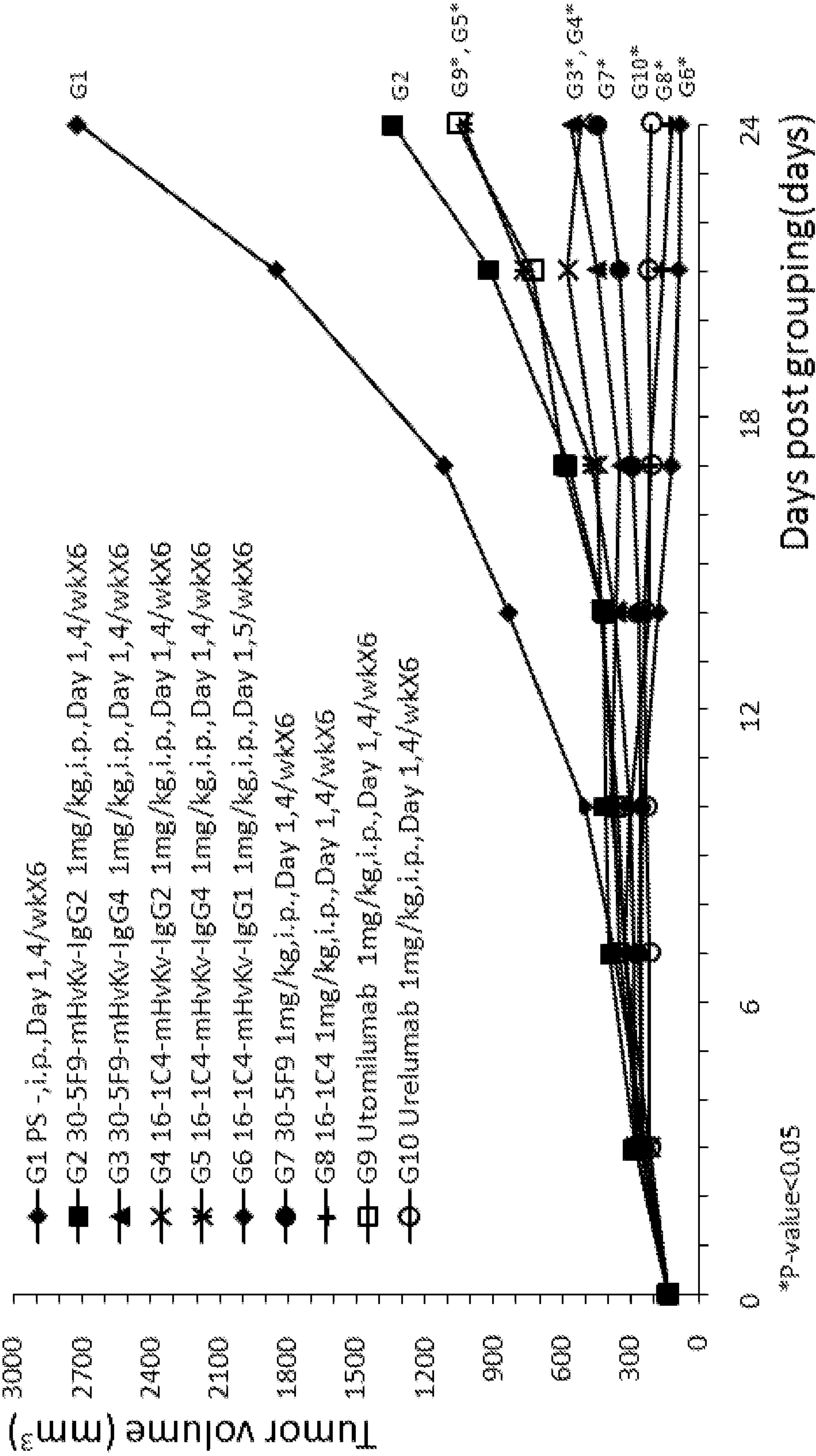


FIG. 27

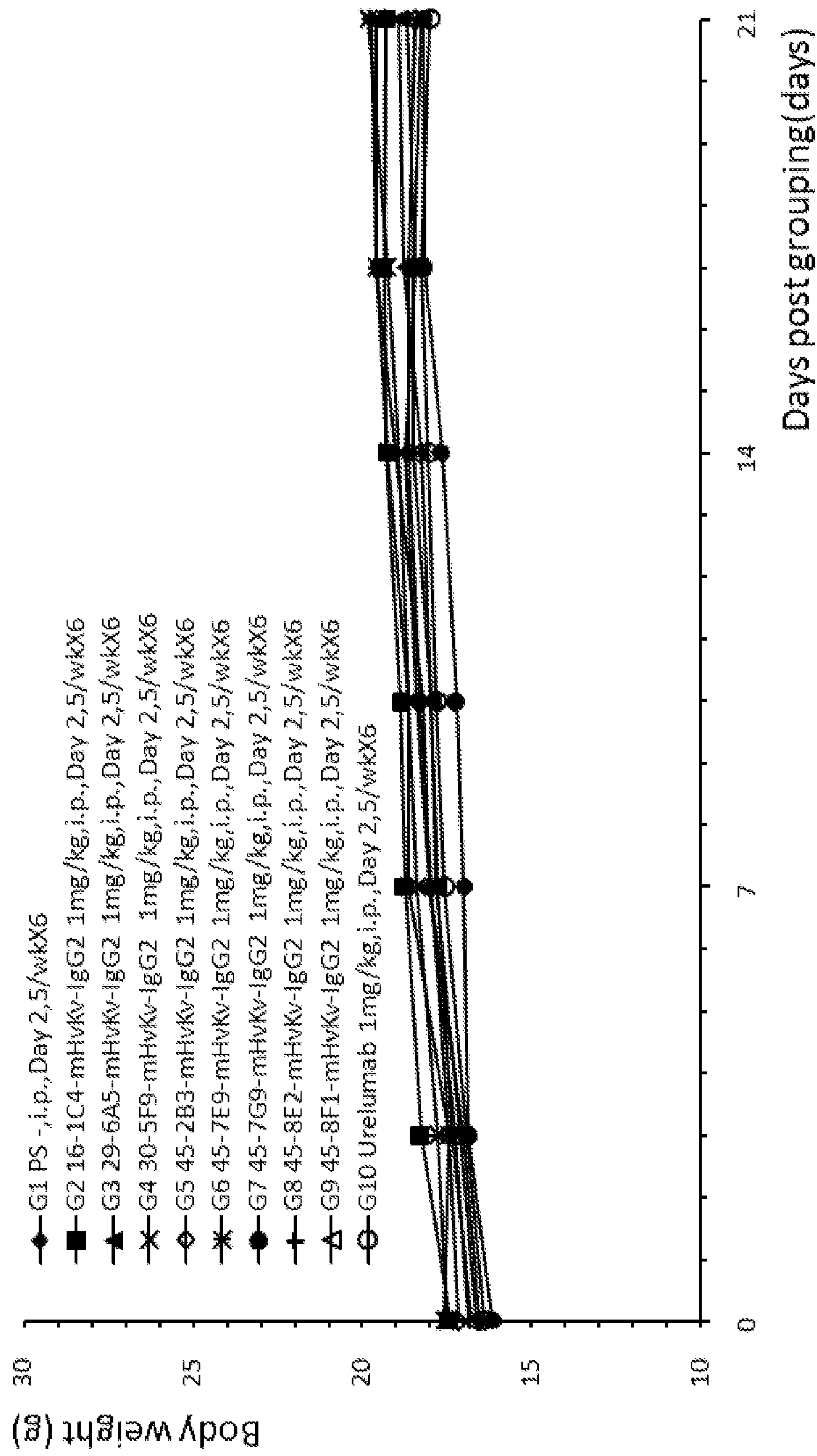


FIG. 28

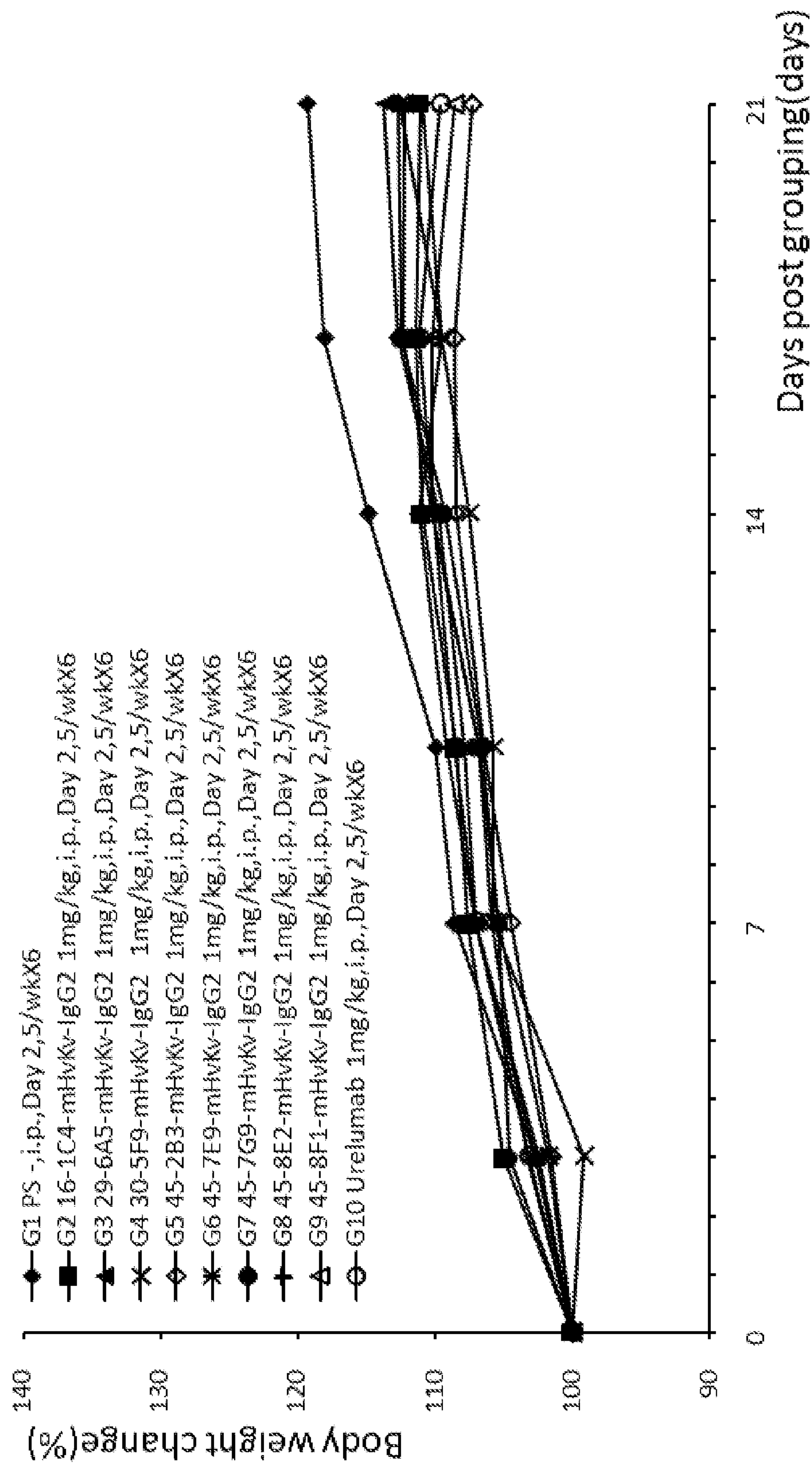


FIG. 29

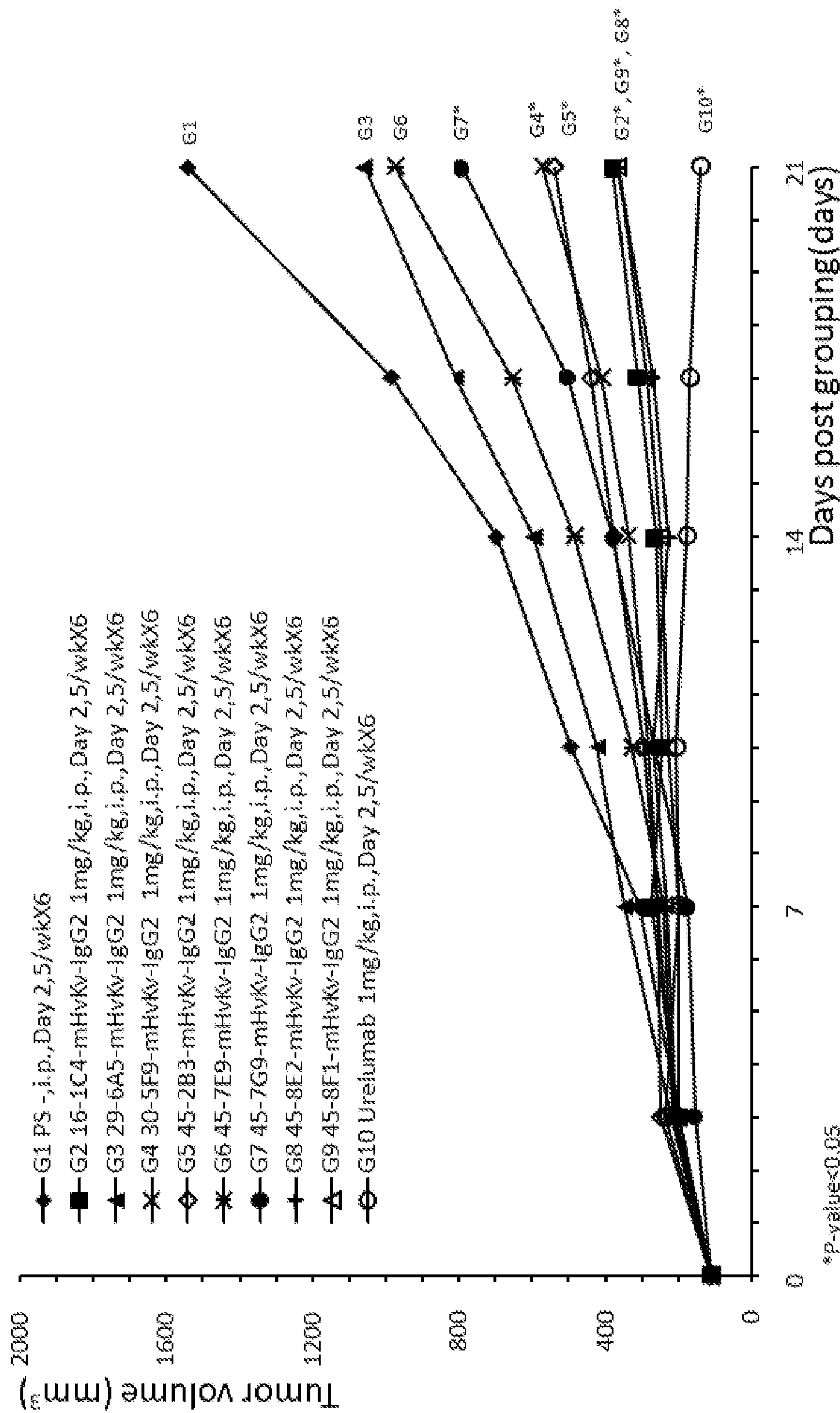


FIG. 30

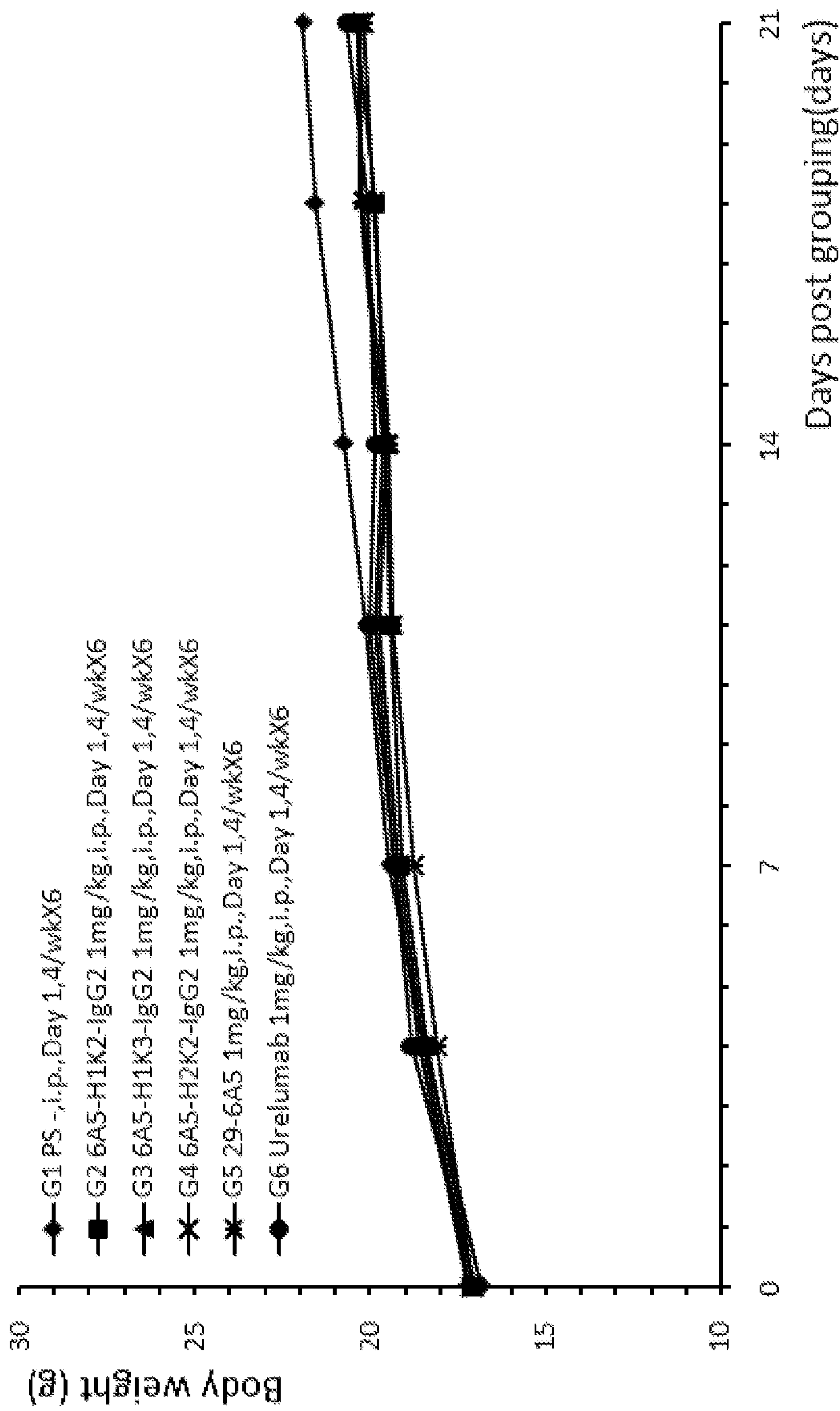


FIG. 31

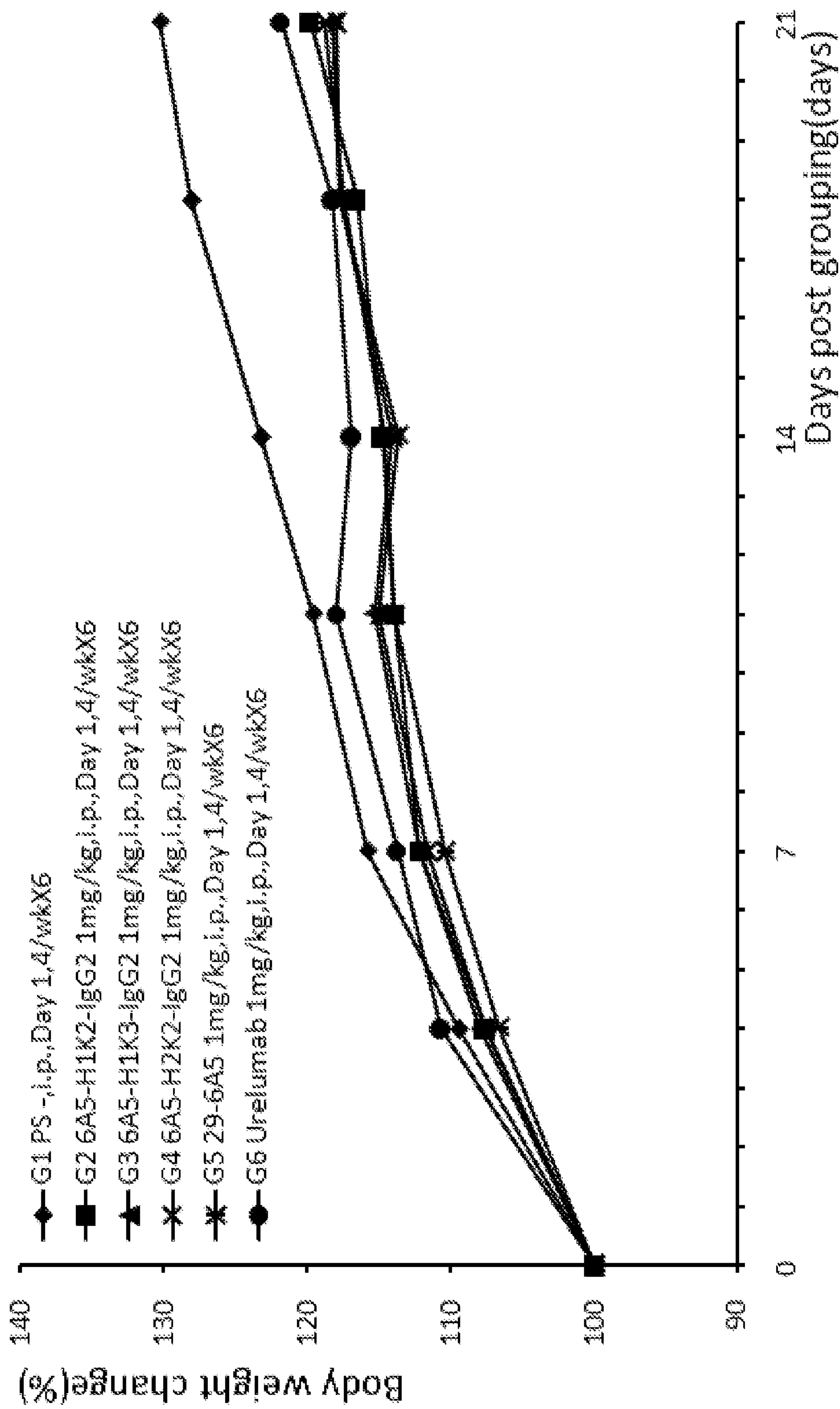


FIG. 32

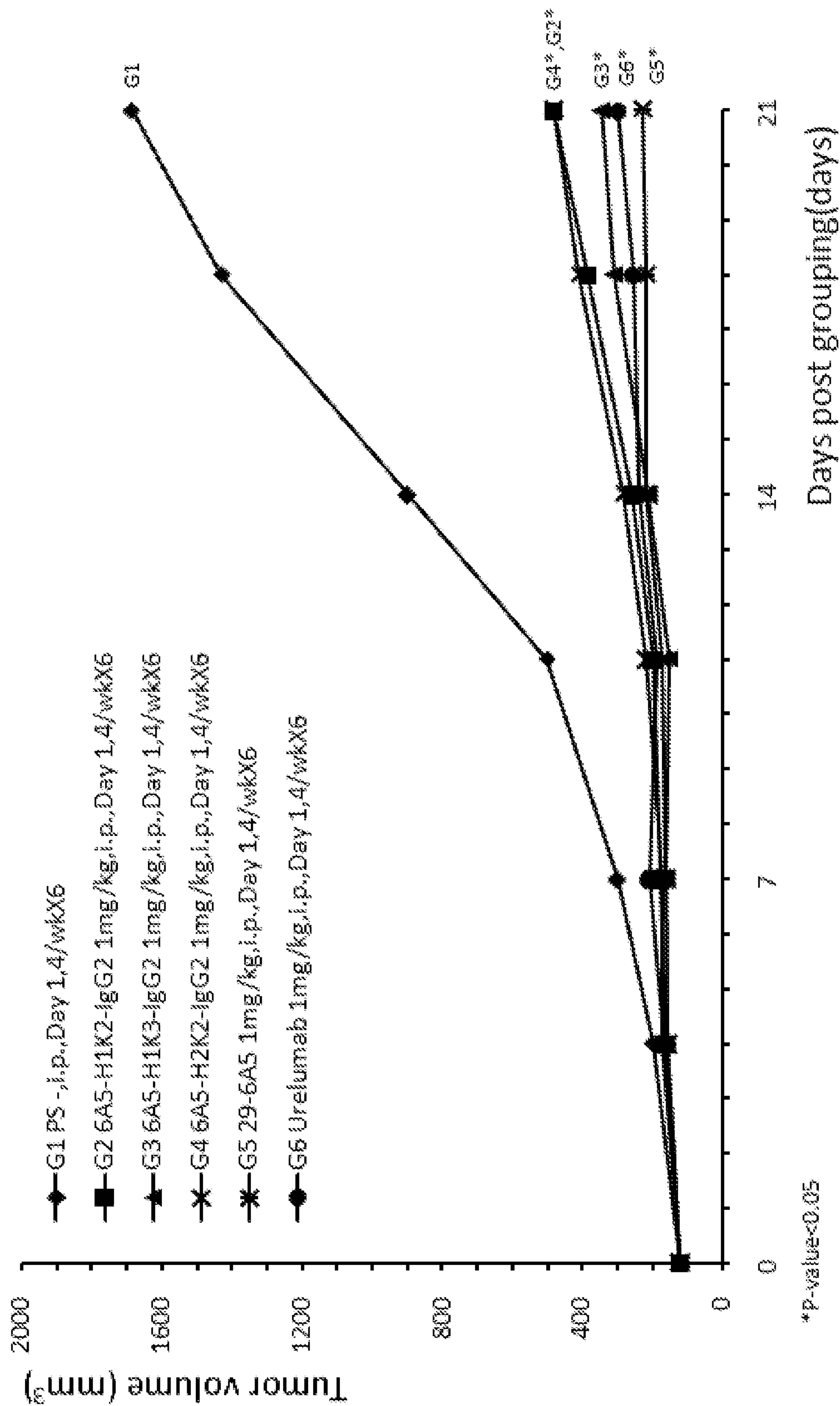


FIG. 33

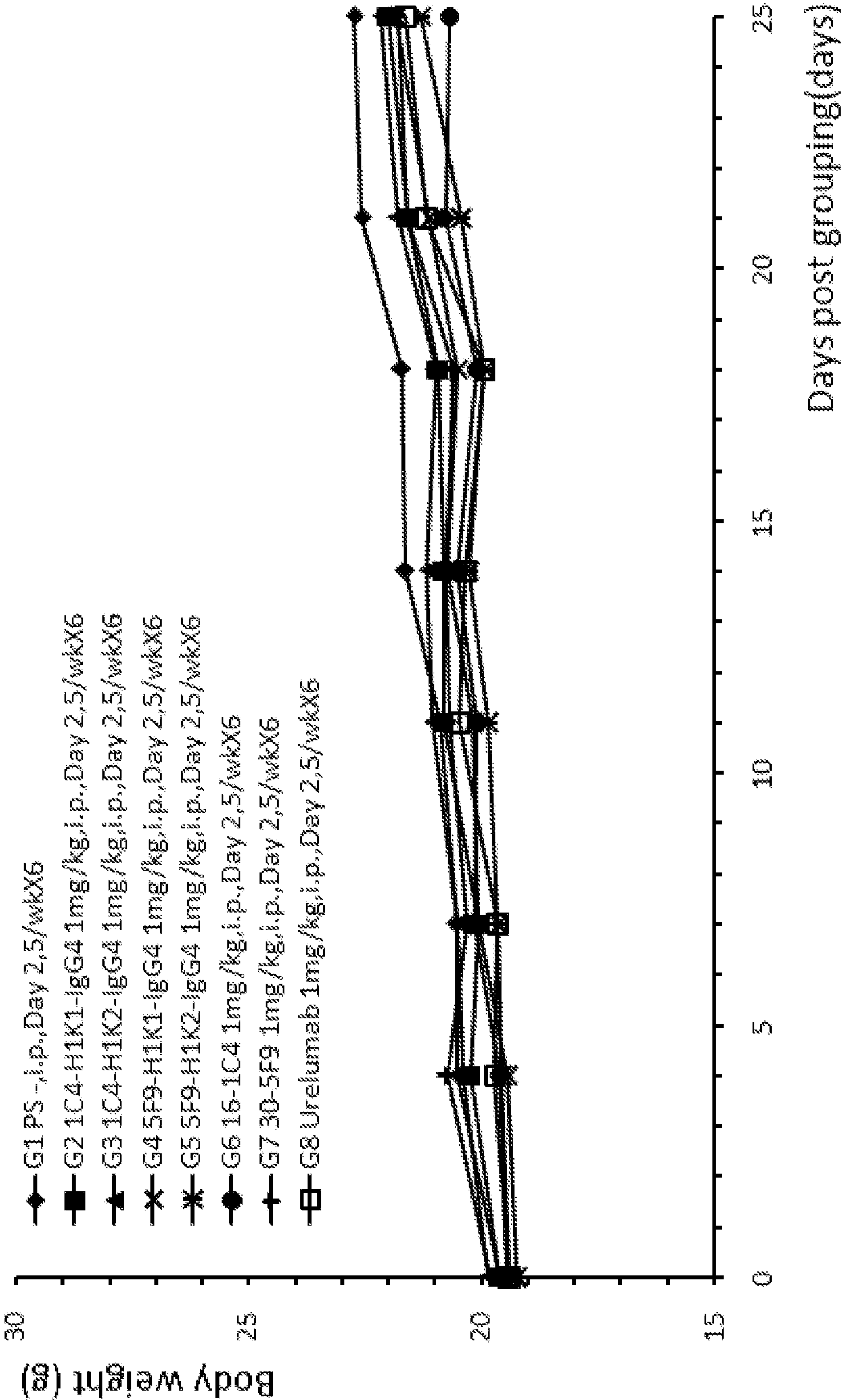


FIG. 34

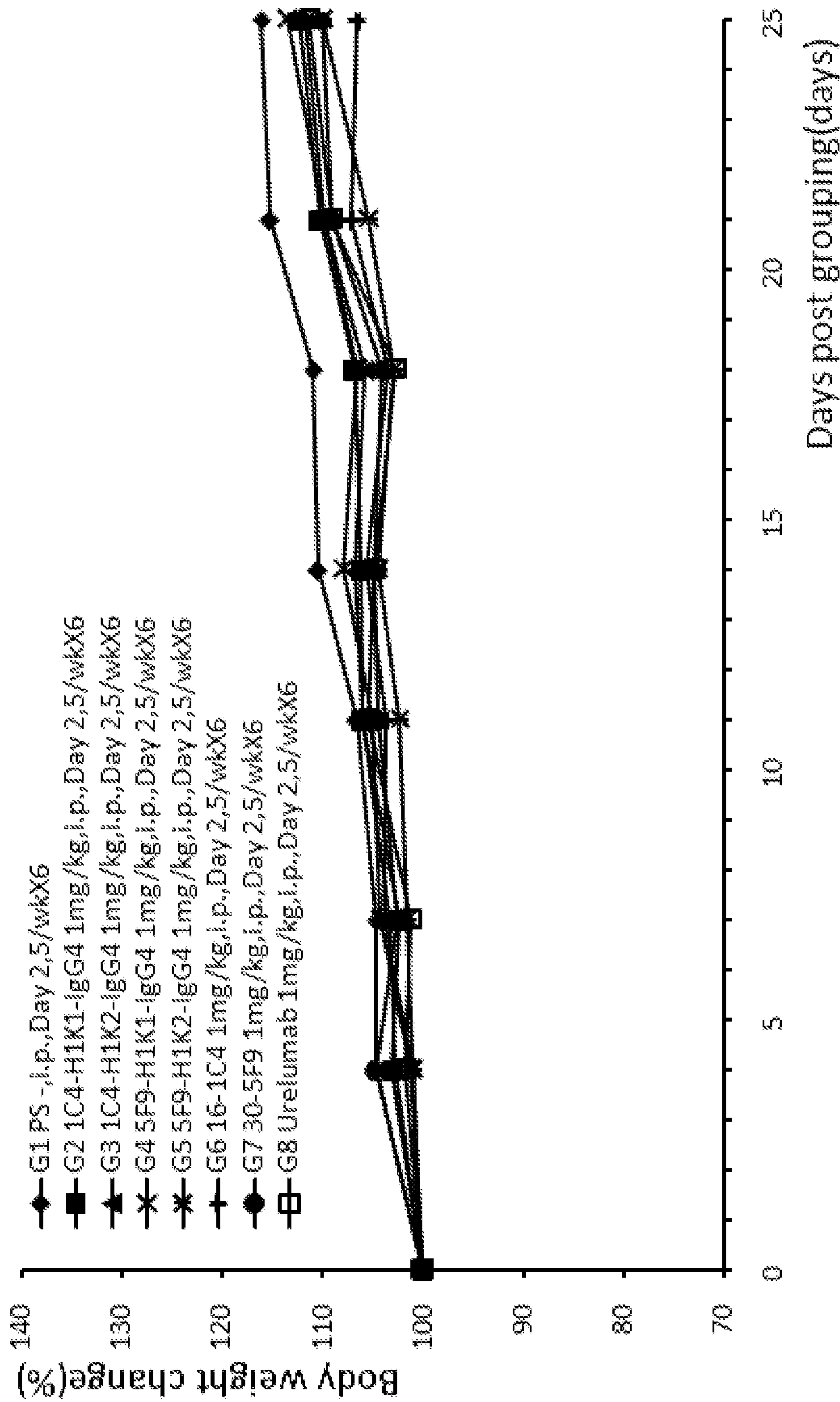


FIG. 35

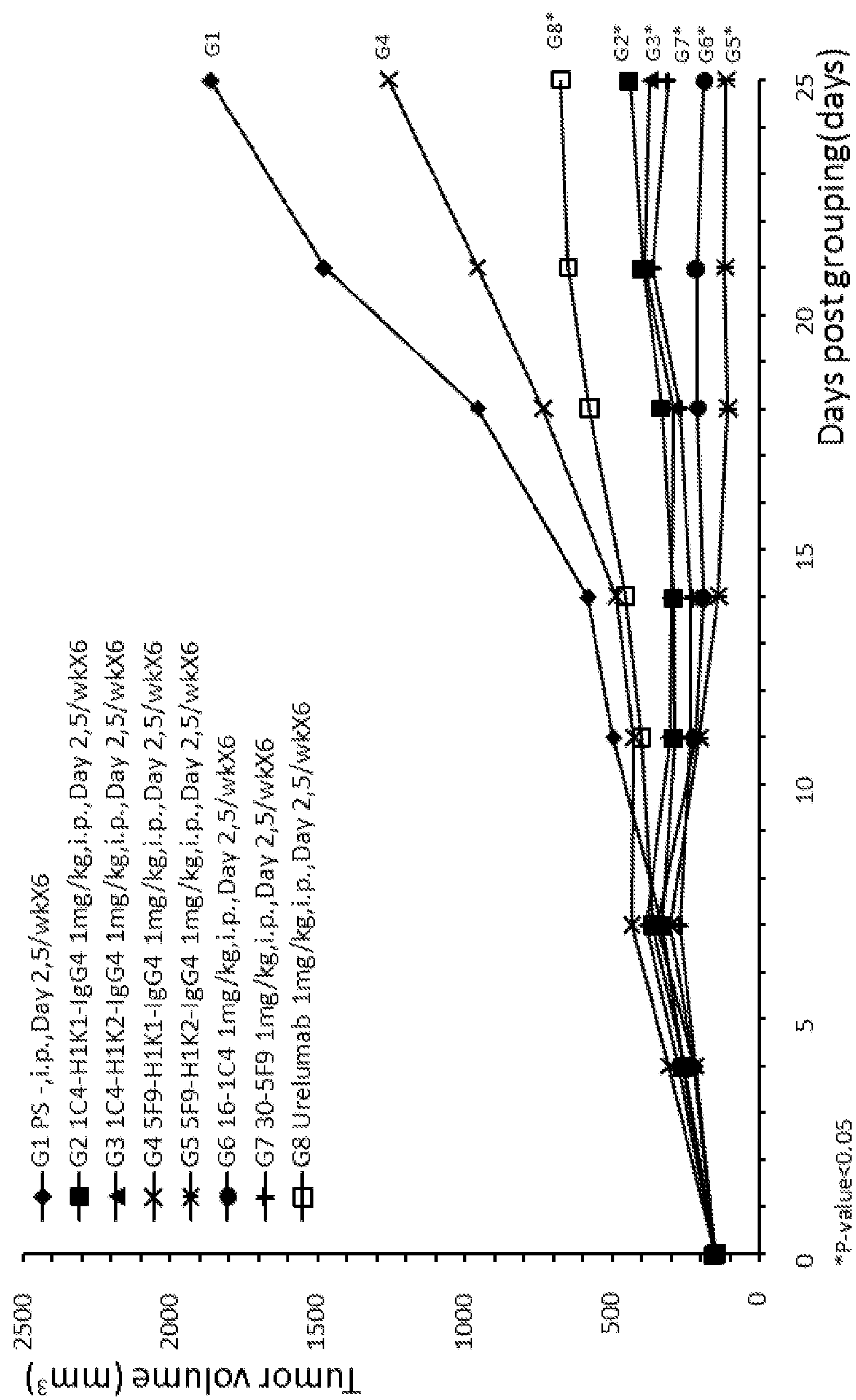


FIG. 36

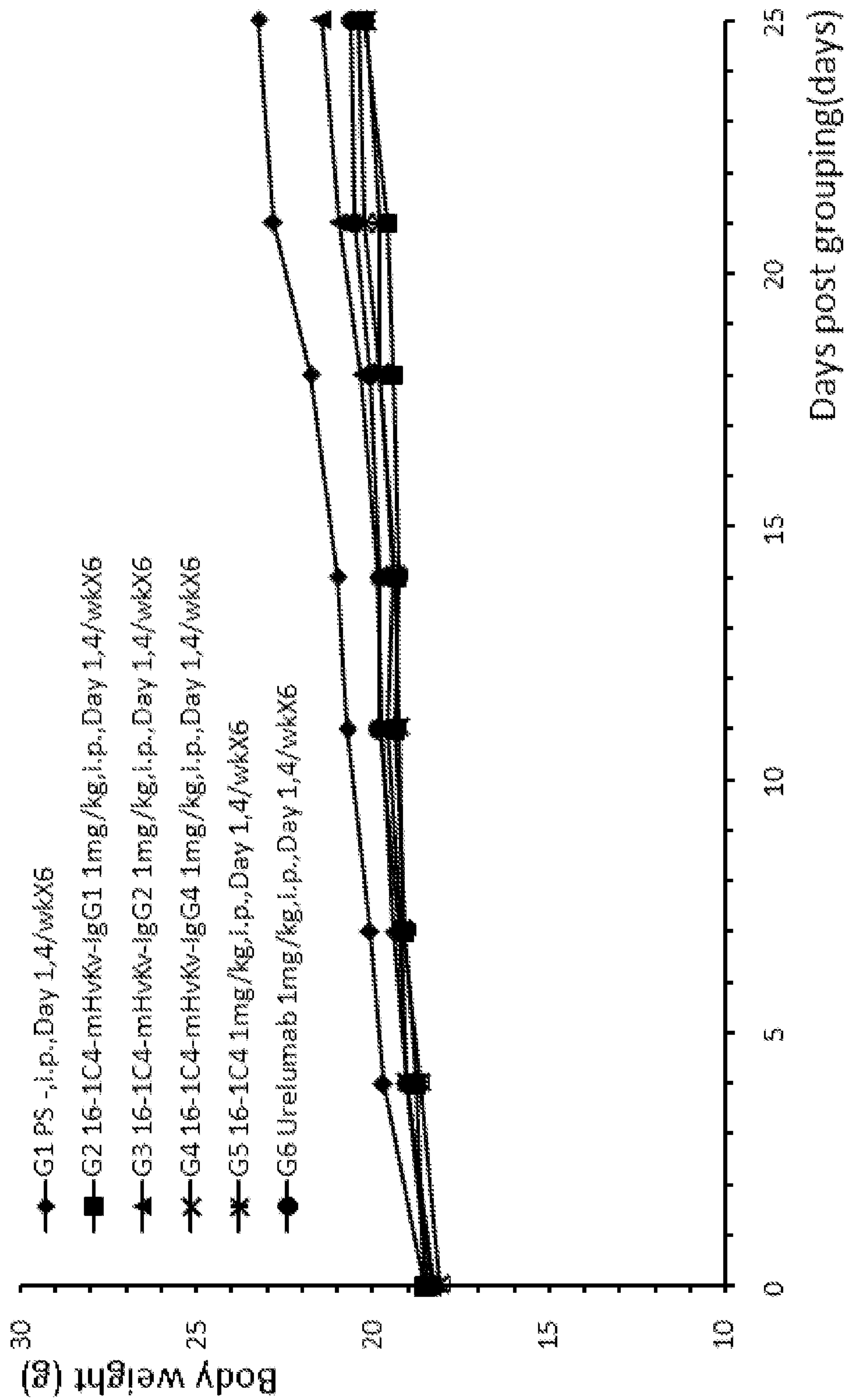


FIG. 37

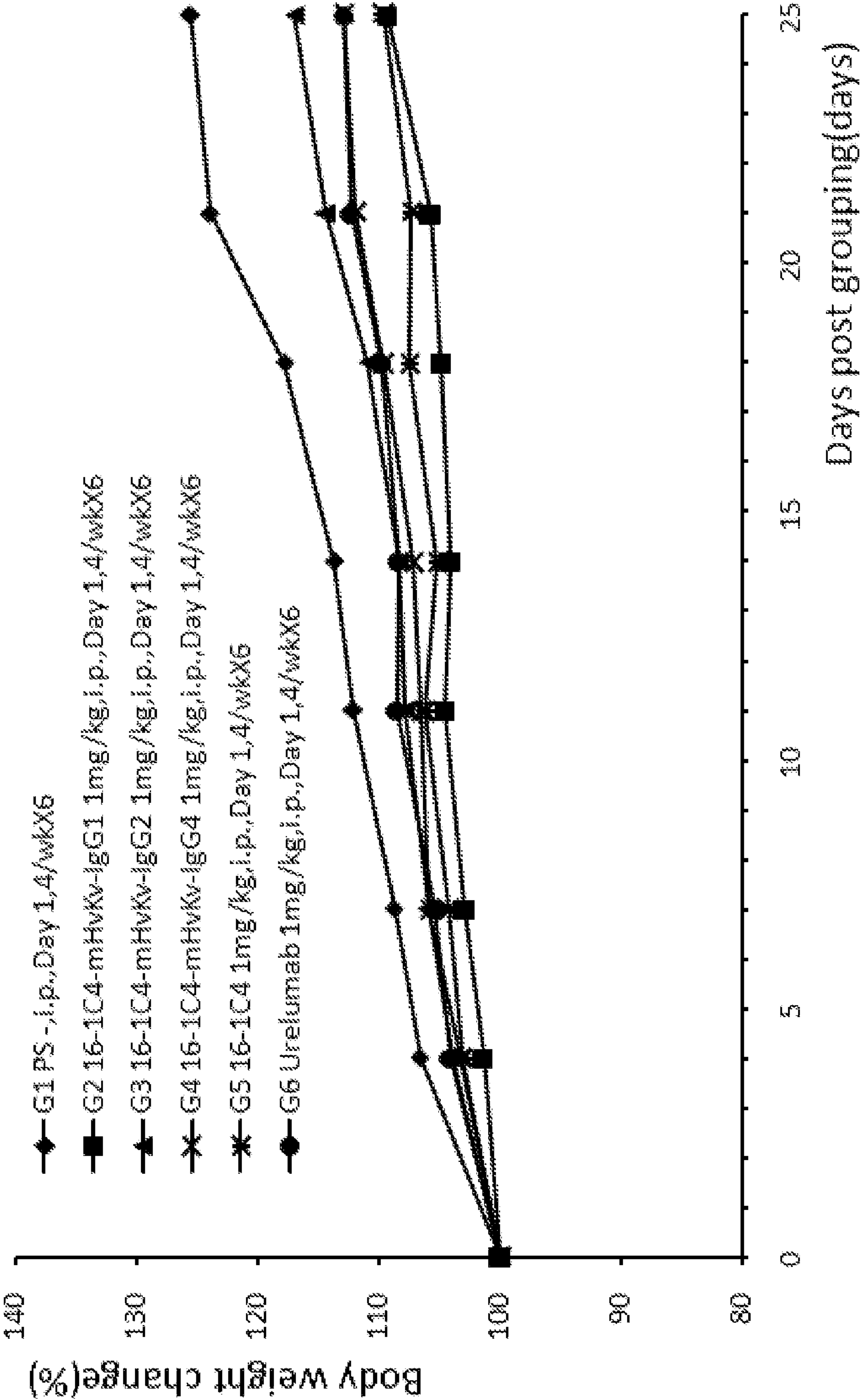


FIG. 38

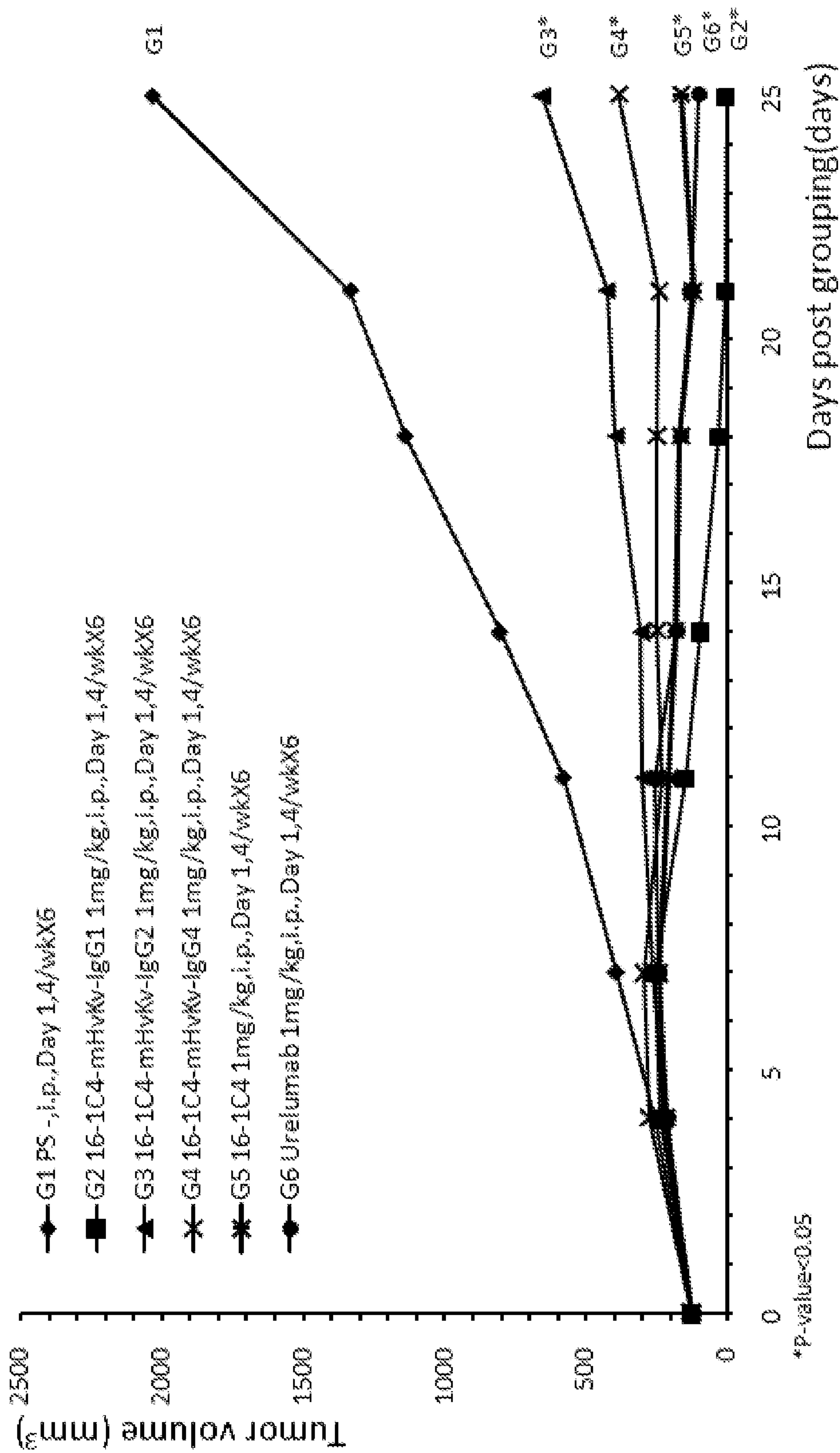


FIG. 39

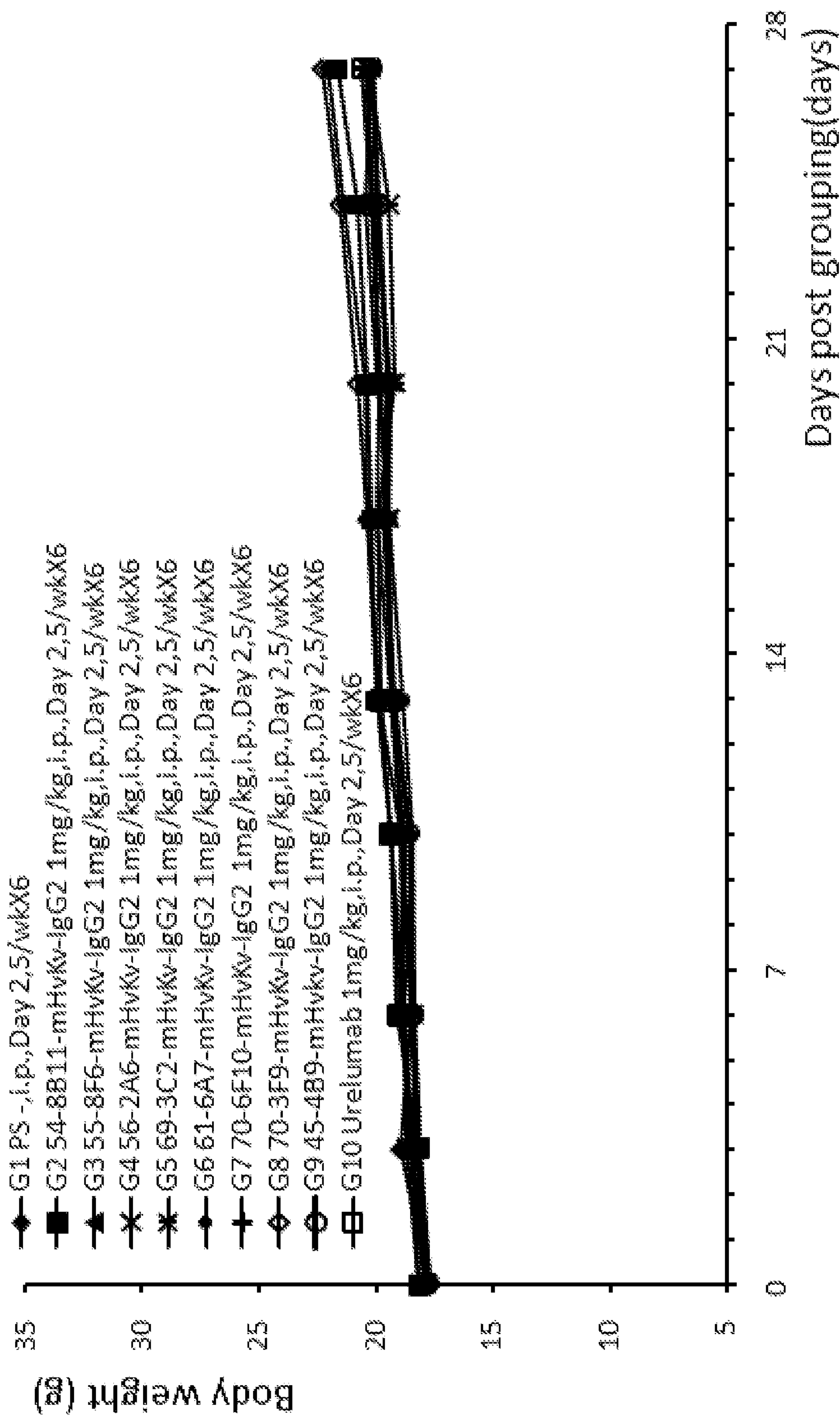


FIG. 40

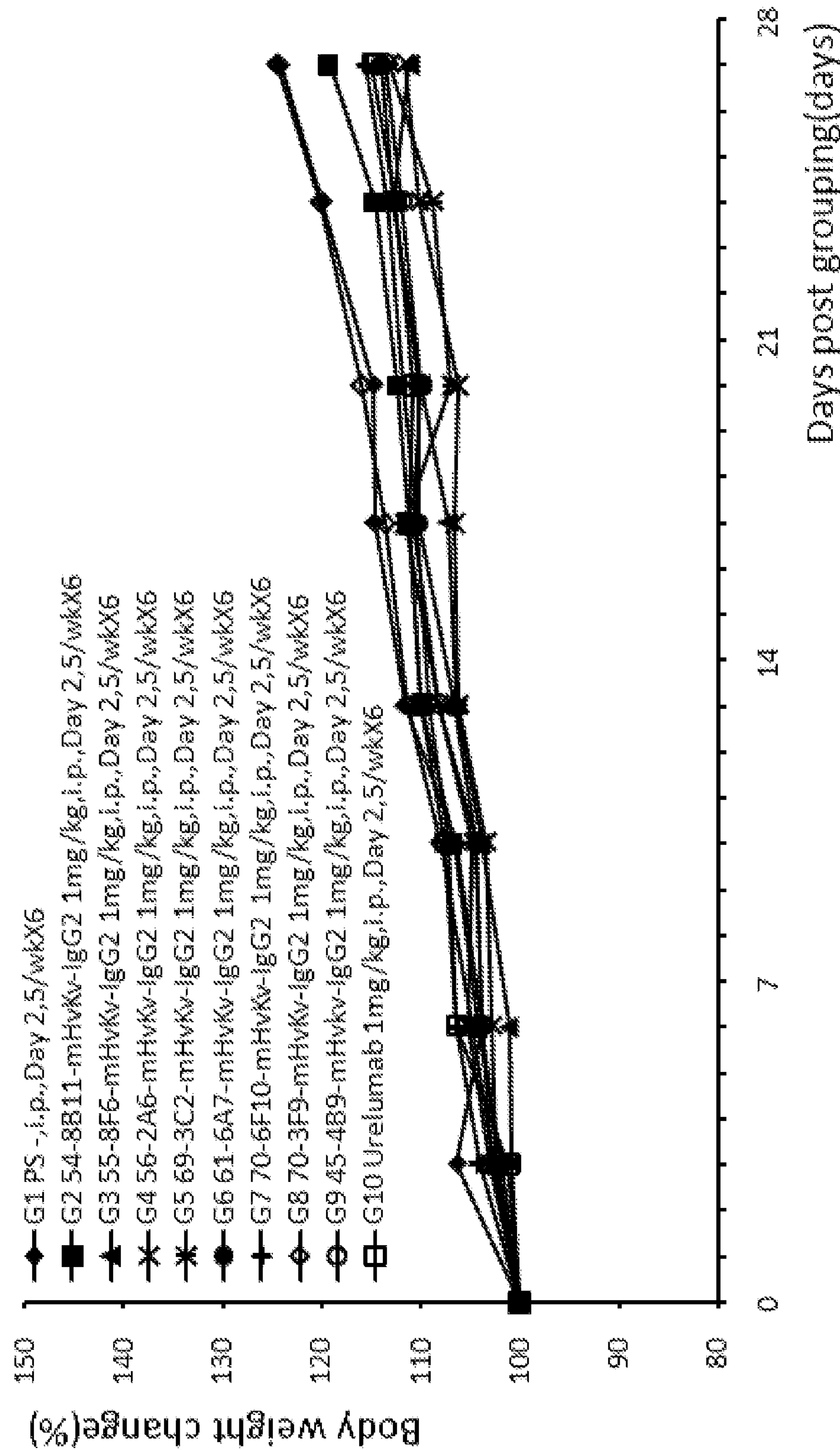


FIG. 41

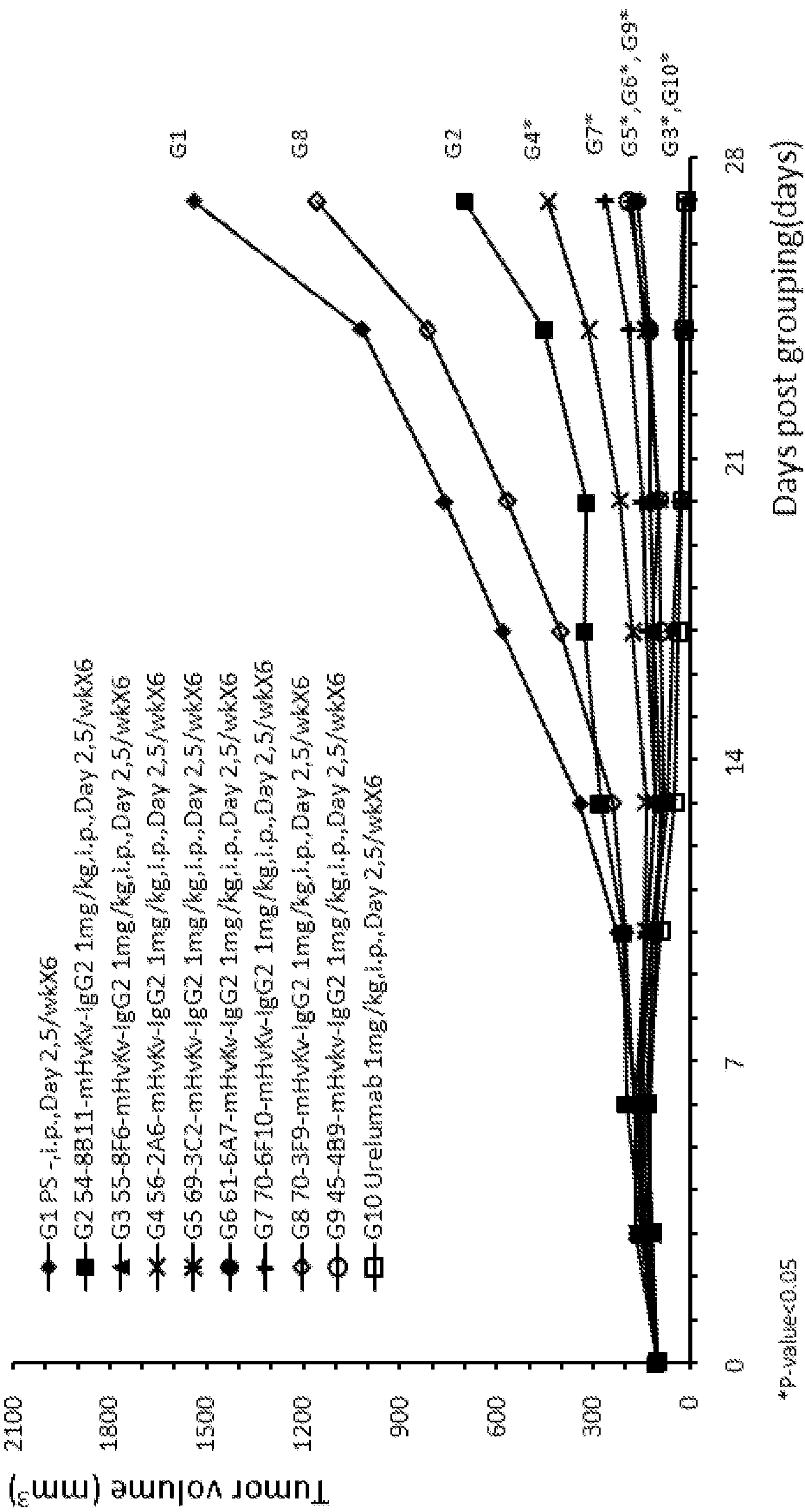


FIG. 42

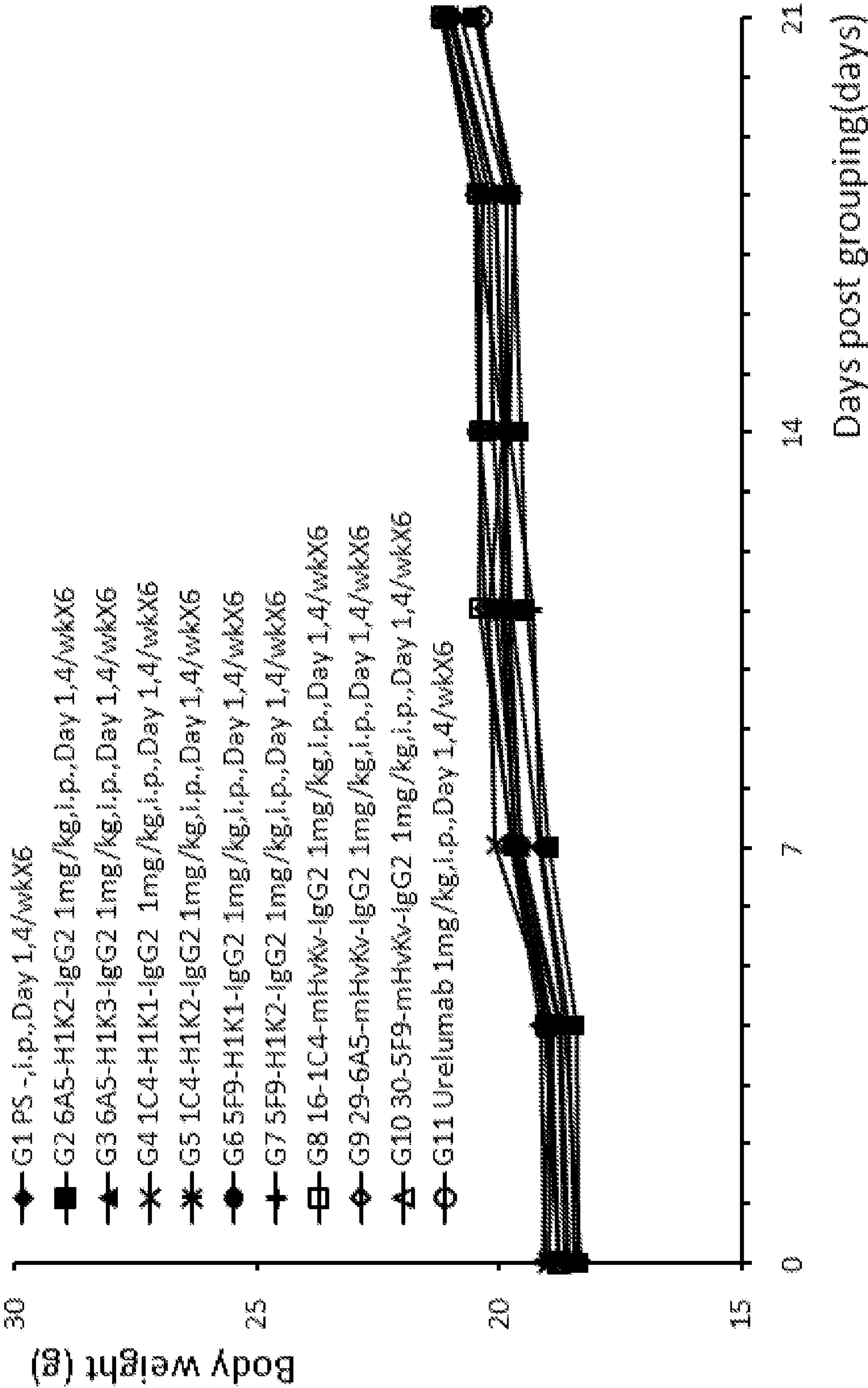


FIG. 43

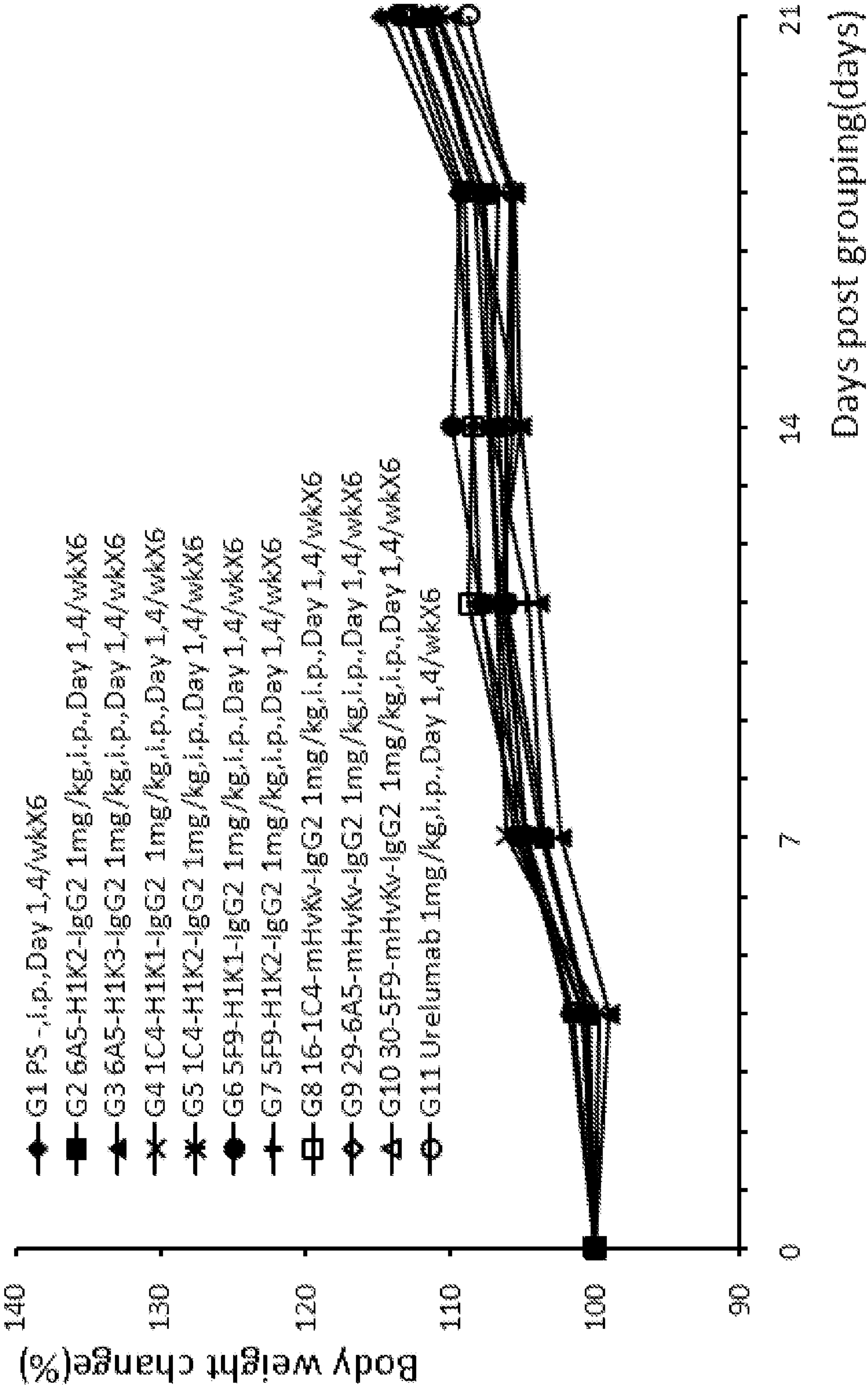


FIG. 44

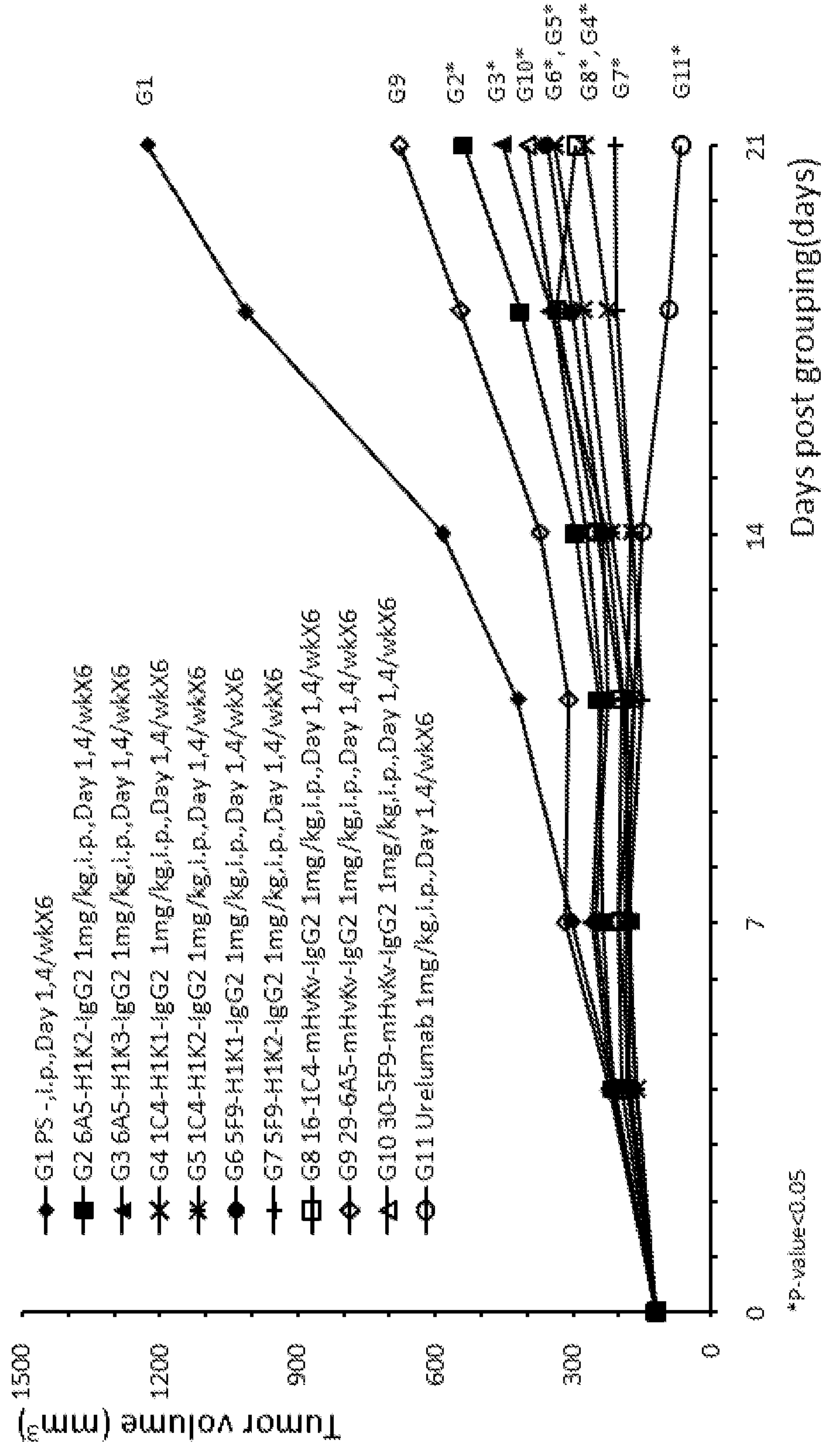


FIG. 45

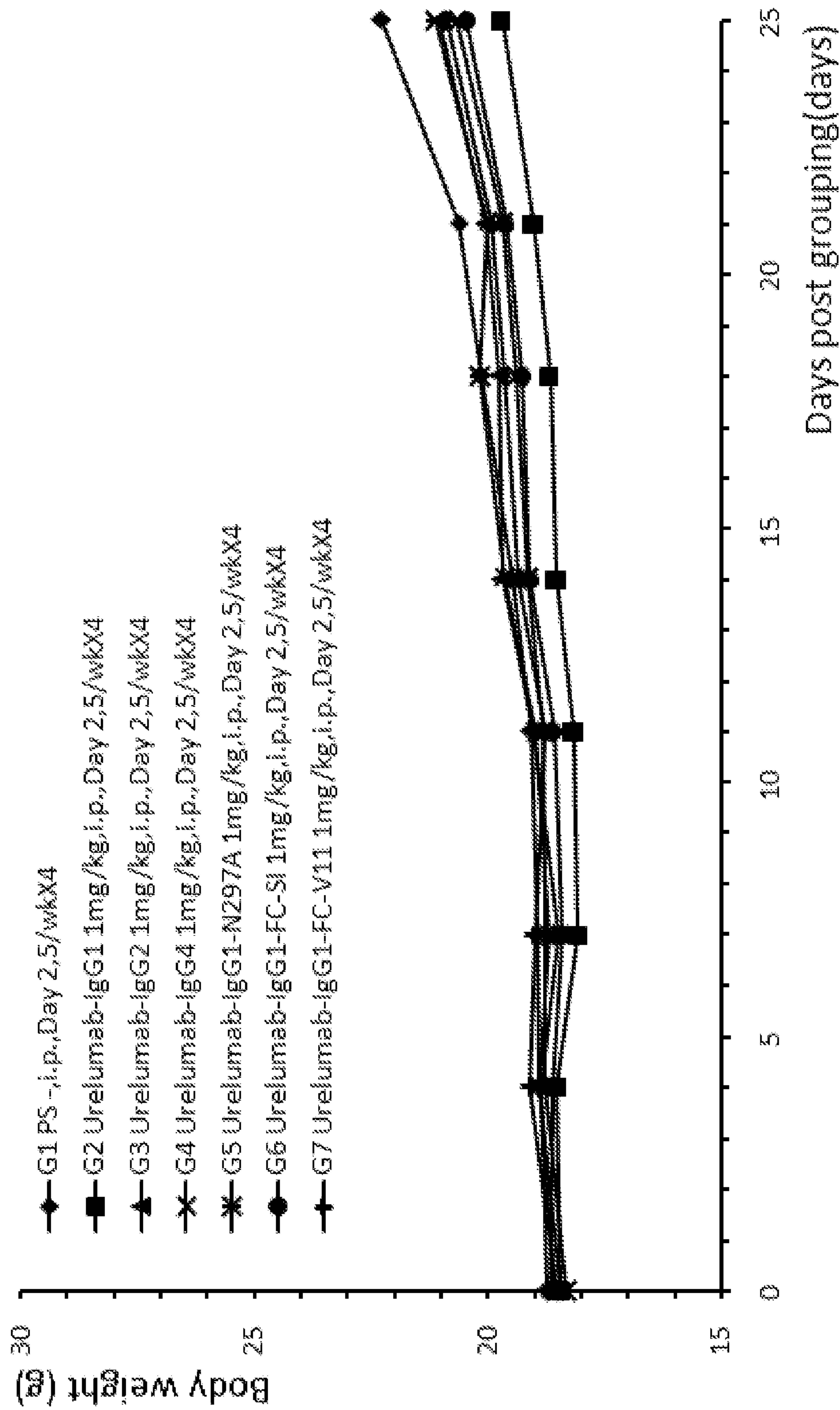


FIG. 46

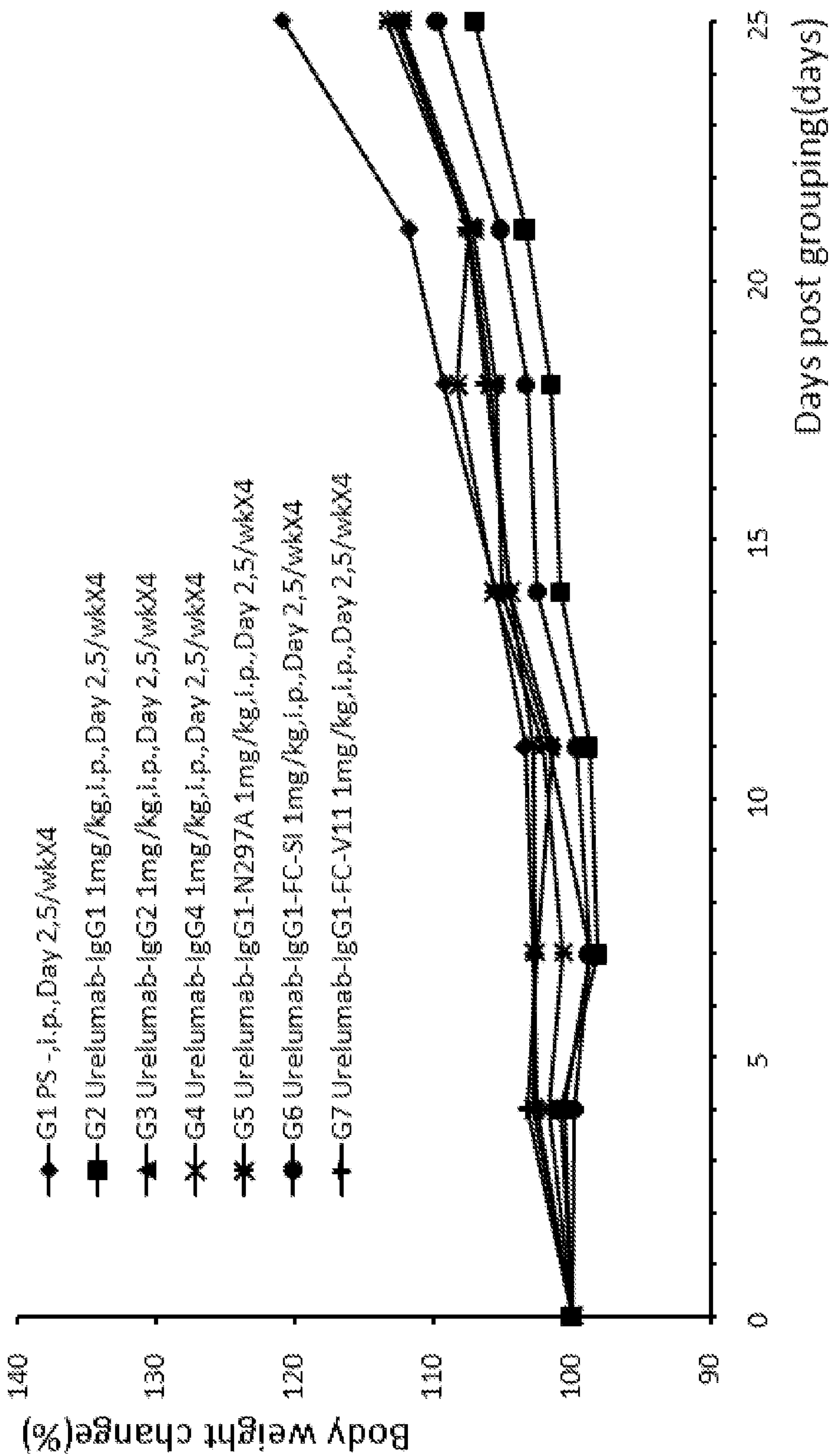


FIG. 47

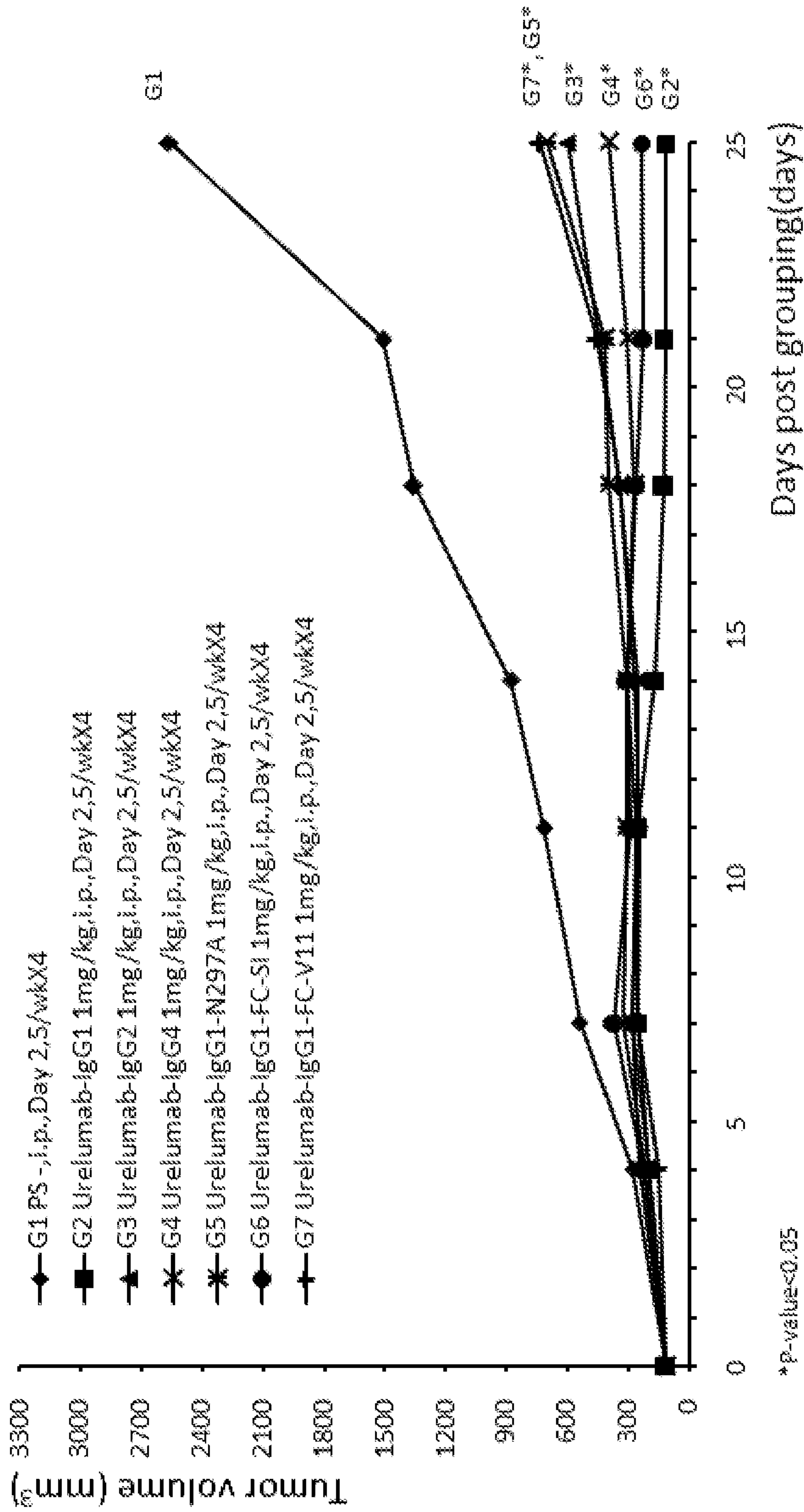


FIG. 48

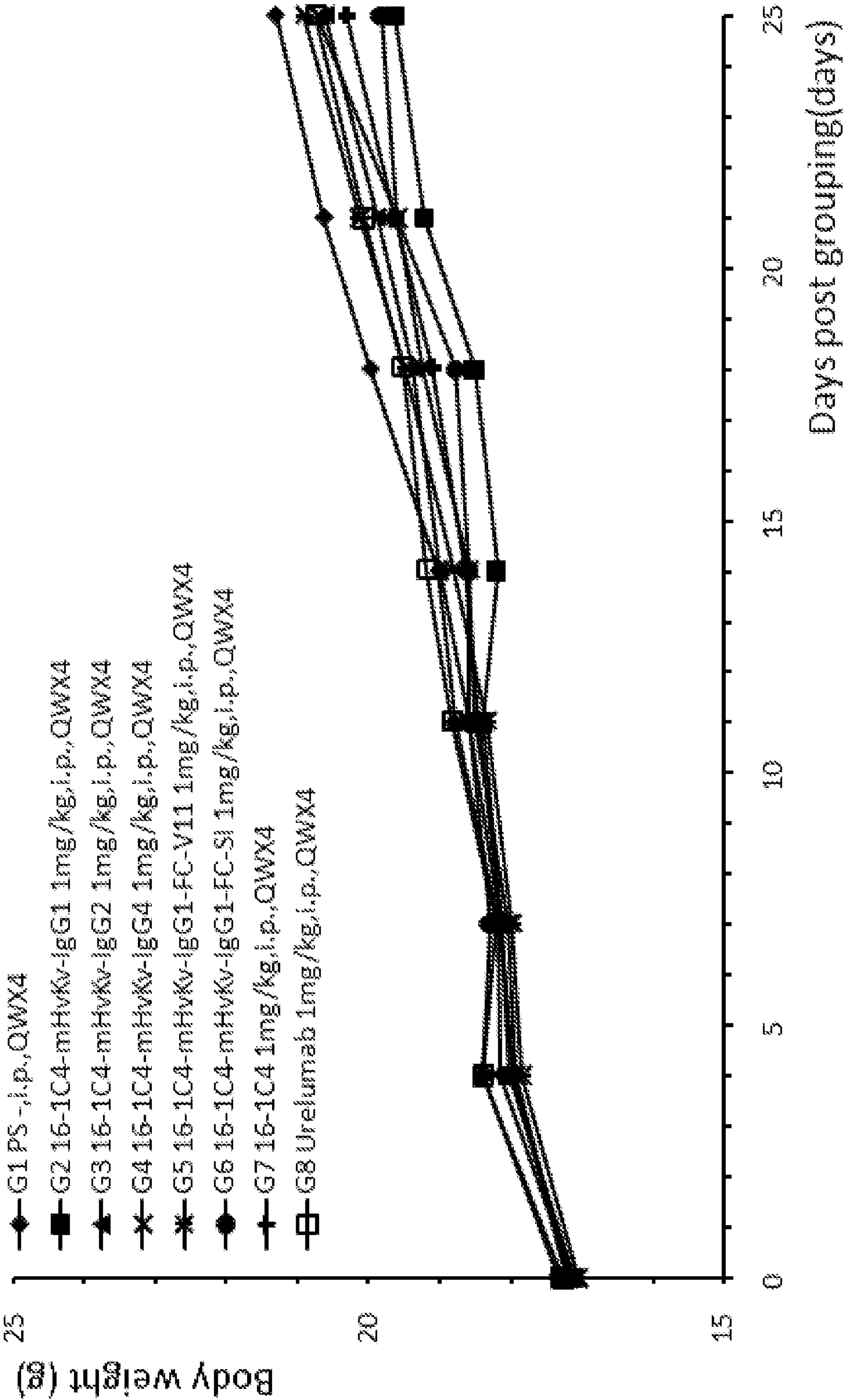


FIG. 49

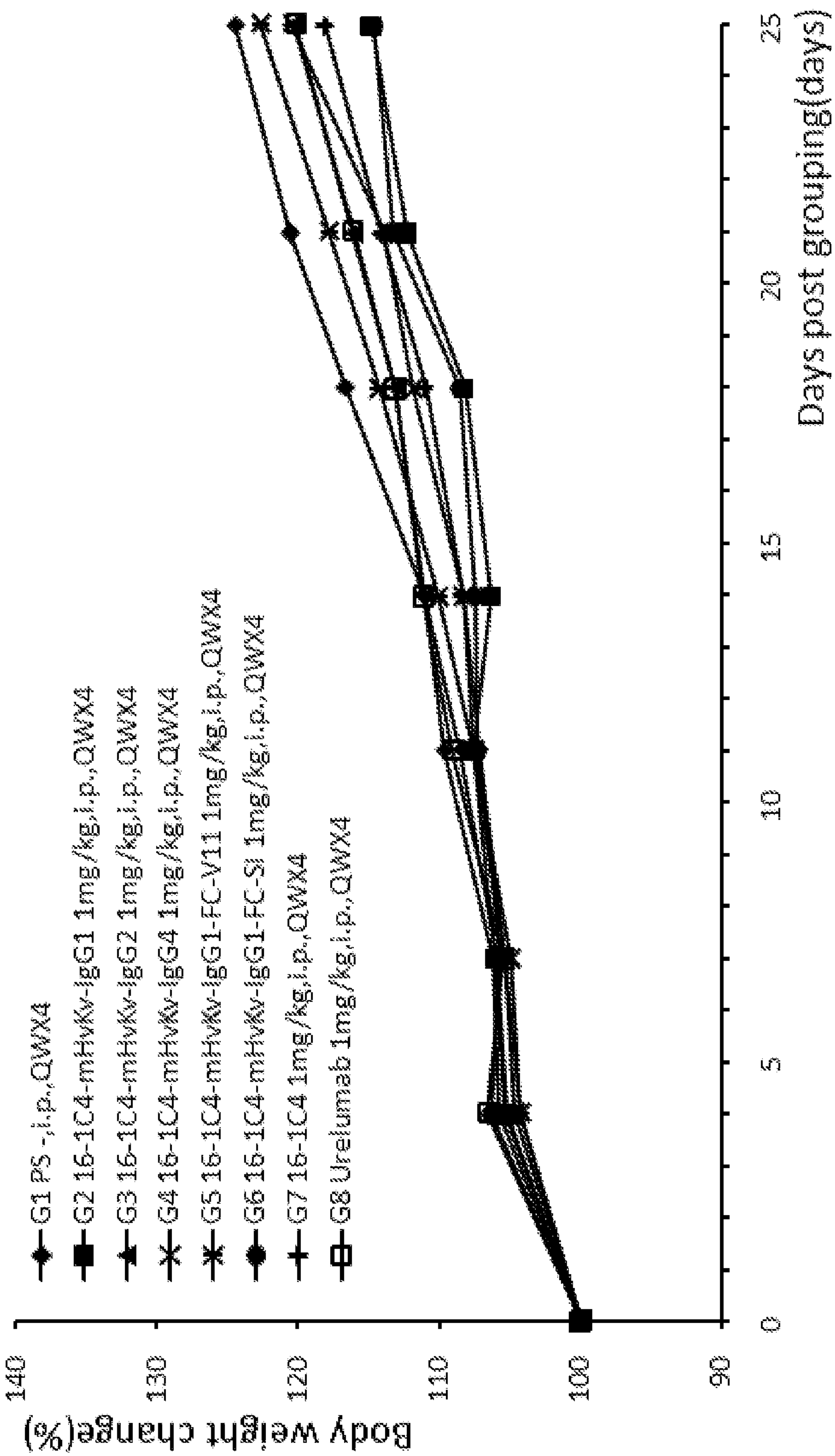


FIG. 50

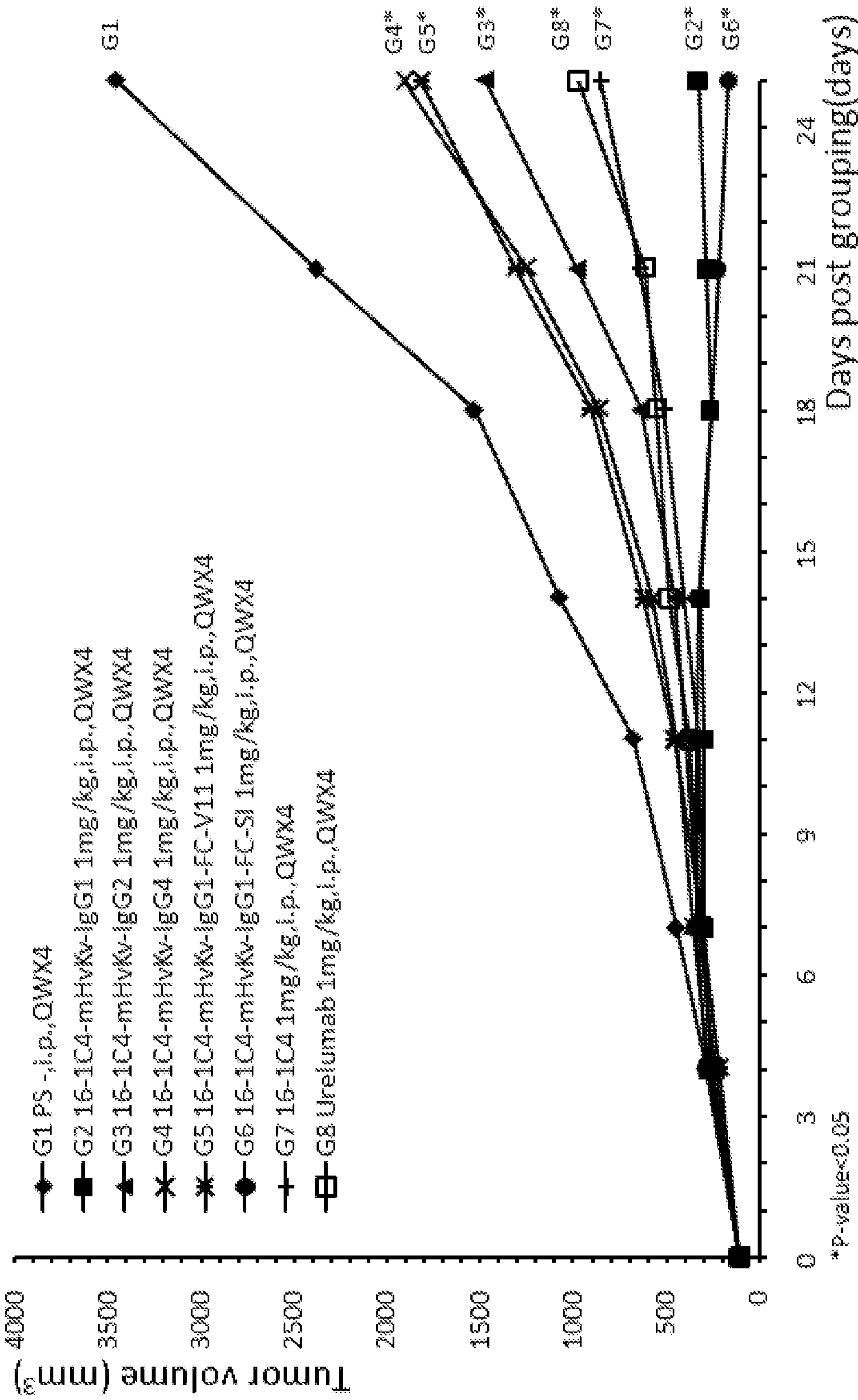


FIG. 51

FIG. 52

Kabat CDR

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:
16-1C4 or humanized 16-1C4	SSYIN	1	WIFAGTGGTYYN QKFTG	2	HSPRATLFD F	3	RASSSVNHMH	4	ATSNLAS	5	QQWSSN PYT	6
29-6A5 or humanized 29-6A5	SYWIN	7	NIYPSDSYTNYN QKFKD	8	TWEFYDSV FDY	9	KASQDINSYLS	10	RANRLVD	11	LQYDELP PT	12
30-5F9 or humanized 30-5F9	TYDIS	13	VIWTGGGTNYS SFMS	14	VDY	15	RSSQSLVHSNG NTYLH	16	KVSNRFS	17	SQNTHVP WT	18
45-2B3 or humanized 45-2B3	TSWM N	19	RIYPGDGDTDYN GRFKG	20	LDGYEVFY FDY	21	KSSQSLLYSNG KTYLN	22	LVSKLDS	23	FQGTHFP WT	24
45-4B9 or humanized 45-4B9	TYVM Y	25	YINPYNDDIRYNE KFKG	26	QGGDY	27	RASKNINKYLA	28	SGSTLQS	29	QQYNEYP LT	30
45-7E9 or humanized 45-7E9	TYGVH	31	VIWSDGNTDYN DAFIS	32	NSITSVSFDC	33	KASQNVGTTV A	34	SASYRYS	35	QQYNSYP LT	36
45-7G9 or humanized 45-7G9	NYWI H	37	NIYPASDYTNYDE KFKN	38	GYFGSLDY	39	RASQPIGTGIH	40	SASESIS	41	QQSYSW PTT	42
45-8E11 or humanized 45-8E11	SNW MH	43	VIYPGNSDTSYN QKFKG	44	GITTAPEY	45	KASENVGIYVS	46	GASNRYT	47	GHTYNYP FT	48

45-8E2 or humanized 45-8E2	RYWM S	49	EIHPDSSAINYTPS LKD	50	SYGRVFDY	51	RASQISDYLH	52	YASQIS	53	QDGHSP PT	54
45-8F1 or humanized 45-8F1	SYWM H	55	VIYPGNSDTSYN QKFKG	56	GITTAPDY	57	KASENVGIHVS	58	GASSGN	59	GQTSYP FT	60
54-8B11 or humanized 54-8B11	NYGM N	61	WINTYTGEPTYA DDFKG	62	REYYPWV FV Y	63	SASSSVSYMH	64	DTSKLAS	65	FQSGYP LT	66
55-8F6 or humanized 55-8F6	SYWIN	67	NIYPSDSYTNYN QKFKD	68	FHYGSPFD N	69	RASQDISHYLN	70	YTSRLHS	71	QQGHTL PRT	72
56-2A6 or humanized 56-2A6	NYGM N	73	WINTYTGEPTYA DDFKG	74	RDYLGAMD Y	75	RASSSVSSYL H	76	STSNLAS	77	QQYSAYL YT	78
59-5E4 or humanized 59-5E4	TYWIN	79	NIYPSDSYTNYN QKFKD	80	EAGDGT HY AIDY	81	KASENVGT YVS	82	GASNRYP	83	GQGY SYL RT	84
61-6A7 or humanized 61-6A7	DYYM H	85	WIDPENGNTIYD PKFQD	86	GLPWYFDY	87	SASSSVSDMN	88	LTSNLSS	89	QQW SGN PLT	90
69-3C2 or humanized 69-3C2	SFGM H	91	YISSGSSAIY YADT VKG	92	DWVDY	93	RASENIYS NLV	94	TATKLTN	95	QHFWD T PYT	96
70-3F9 or humanized 70-3F9	SYWIN	97	NIYPSDSYTNYN QKFKD	98	FGSSGYP DY YTM EY	99	RASGNIDN YLA	100	NAKT LAE	101	QQY WTIP YT	102
70-6F10 or humanized 70-6F10	NSW MN	103	RIYPGDGDT DYN GKFKG	104	LDGN YYYW YFDV	105	KSSQSL LSDG KTYLN	106	LVSK LDS	107	WQGT HF PQT	108

FIG. 53

Chothia CDR

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:
16-1C4 or humanized 16-1C4	GFTFS SSYIN	109	FAGTGG	110	HSPRATLFD F	111	RASSSVNHMH	112	ATSNLAS	113	QQWSSN PYT	114
29-6A5 or humanized 29-6A5	GYTFS SYWIN	115	YPSDSY	116	TWEFYDVS FDY	117	KASQDINSYLS	118	RANRLVD	119	LQYDELP PT	120
30-5F9 or humanized 30-5F9	GFSLT TYDIS	121	WTGGG	122	VDY	123	RSSQSLVHSNG NTYLH	124	KVSNRFS	125	SQNTHVP WT	126
45-2B3 or humanized 45-2B3	GYAFS TSWM N	127	YPGDGD	128	LDGYEVFY FDY	129	KSSQSLLYSNG KTYLN	130	LVSCLDS	131	FQGTHFP WT	132
45-4B9 or humanized 45-4B9	GYTFT TYVM Y	133	NPYNDD	134	QGGDY	135	RASKNINKYLA	136	SGSTLQS	137	QQYNEYP LT	138
45-7E9 or humanized 45-7E9	GFSLT TYGVH	139	WSDGN	140	NSITSVSFDC	141	KASQNVGTTV A	142	SASYRYS	143	QQYNSYP LT	144
45-7G9 or humanized 45-7G9	GYTFS NYWI H	145	YPASDY	146	GYFGSLDY	147	RASQPIGTGIH	148	SASESIS	149	QQSYSW PTT	150
45-8E11 or humanized 45-8E11	GYSFT SNW MH	151	YPGNSD	152	GITTAPEY	153	KASENVGIYVS	154	GASNRYT	155	GHTYNYP FT	156
45-8E2 or humanized 45-8E2	GFDFS RYWM S	157	HPDSSA	158	SYYGRVFDY	159	RASQSIDYLH	160	YASQSIS	161	QDGHSP PT	162

45-8F1 or humanized 45-8F1	GYSFT SYWM H	163	YPGNSD	164	GITTAPDY	165	KASENVGIHVS	166	GASSGYN	167	GQTYSP FT	168
54-8B11 or humanized 54-8B11	KFTFT NYGM N	169	NTYTGE	170	REYYPWVFV Y	171	SASSSVSYM H	172	DTSKLAS	173	FQGS GYP LT	174
55-8F6 or humanized 55-8F6	GYIFTS YWIN	175	YPSDSY	176	FHYGSSPFD N	177	RASQDISHYLN	178	YTSRLHS	179	QQGHTL PRT	180
56-2A6 or humanized 56-2A6	GYTFT NYGM N	181	NTYTGE	182	RDYLGAMD Y	183	RASSSVSSSYL H	184	STSNLAS	185	QQYSAYL YT	186
59-5E4 or humanized 59-5E4	GYTFT TYWIN	187	YPSDSY	188	EAGDGTTHY AIDY	189	KASENVGTYVS	190	GASNRYP	191	GQGYSYL RT	192
61-6A7 or humanized 61-6A7	GFNIK DYWM H	193	DPENGN	194	GLPWYFDY	195	SASSSVSDMN	196	LTSNLSS	197	QQWSGN PLT	198
69-3C2 or humanized 69-3C2	GFSFS SFGM H	199	SSGSSA	200	DWVDY	201	RASENIYSNLV	202	TATKLTN	203	QHFWDT PYT	204
70-3F9 or humanized 70-3F9	GYTFT SYWIN	205	FPSDSY	206	FGSSGYPDY YTIMEY	207	RASGNIDNYLA	208	NAKTLAE	209	QQYWTIP YT	210
70-6F10 or humanized 70-6F10	GYAFN NSW MN	211	YPGDGD	212	LDGNYYYW YFDV	213	KSSQSLDSDG KTYLN	214	LVSKLDS	215	WQGTHF PQT	216

Protein	Amino acid sequence	SEQ ID No:
Human 4-1BB (h4-1BB) NP_001552.2	MGNSCYNIVA TLLLVNFER TRSLQDPCSN CPAGTFCDNN RNQICSPCPP NSFSSAGGQR TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS MCEQDCKQGQ ELTKKGCKDC CFGTFNDQKR GICRPWTNCS LDGKSVLVNG TKERDVVCGP SPADLSPGAS SVTPPAPARE PGHSPQIISF FLALTSTALL FLLFFLTIRF SVVKRGRKKL LYIFKQPFMR PVQTTQEEDG CSCRFPEEEE GGCEL	217
Mouse 4-1BB (m4-1BB) NP_035742.1	MGNNCYNVVV IVLLVGCEK VGAVQNSCDN CQPGTFCRKY NPVCKSCPPS TFSSIGGQPN CNICRVCAGY FRKKFCSST HNAECECIEG FHCLGPQCTR CEKDCRPGQE LTKQGCKTCS LGTENDQNGT GVCRPWTNCS LDGRSVLKTG TTEKDVVCGP PVVSFSPSTT ISVTPEGGPG GHSLQVLTIF LALTSALLA LIFITLLFSV LKWIRKKFPH IFKQPFKTT GAAQEEDACS CRCPQEEEGG GGGYEL	218
Monkey 4-1BB (rm4-1BB) NP_001253057.1	MGNSCYNIVA TLLLVNFER TRSLQDLCSN CPAGTFCDNN RSQICSPCPP NSFSSAGGQR TCDICRQCKG VFKTRKECSS TSNAECDNIS GYHCLGAECs MCEQDCKQGQ ELTKKGCKDC CFGTFNDQKR GICRPWTNCS LDGKSVLVNG TKERDVVCGP SPADLSPGAS SATPPAPARE PGHSPQIIF LALTSTVVLV LFLFLVLRFS VVKRSRKKLL YIFKQPFMRP VQTTQEEDGC SCRFPEEEEG GGCEL	219
Chimeric 4-1BB (chi4-1BB) (Humanized 4-1BB)	MGNSCYNIVATLLLVNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQRTCDICRQCKGVF RTRKECSSTNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDCCFGTFNDQKRGICRPWTNCSLD GKSVLVNGTKERDVVCGPSPADLSPGASSVTPPAPAREPGHSLQVLTFLALTSALLALIFITLLFSVLKWIRK KFPHFQPFKKTGTAAQEEEDACSCRCPQEEEGGGGYEL	220

FIG. 54

FIG. 55

Humanized antibody variable domains	Description	AMINO ACID SEQUENCE	SEQ ID NO:
1C4 Humanized heavy chain variable domain (H1)	HuVHv1: humanization percentage 83.7%; top hit to human and <i>Macaca fascicularis</i>	QVQMVSQGAEVKKPGASVKLSCKASGFTFSSSYINWLRQAPGQRLE WMGWIFAGTGGTYYNQKFTGRVTITRDTSASTAYMELSSLRSEDTA IYYCARHSPRATLFD <u>EWGQGTT</u> LTVSS	221
1C4 Humanized heavy chain variable domain (H2)	HuVHv2: humanization percentage 80.6%; top hit to human and <i>Macaca fascicularis</i>	QVQMVSQGAEVKKPGASVKLSCKASGFTFSSSYINWLRQAPGQSLE WIGWIFAGTGGTYYNQKFTGRVQITRDTSASTAYMELSSLRSEDTAI YYCARHSPRATLFD <u>EWGQGTT</u> LTVSS	222
1C4 Humanized heavy chain variable domain (H3)	HuVHv3: humanization percentage 79.6%; top hit to human and <i>Macaca fascicularis</i>	QVQMVSQGAEVKKPGASVKLSCKASGFTFSSSYINWLRQAPGQSLE WIGWIFAGTGGTYYNQKFTGRAQITRDTSASTAYMELSSLRSEDTAI YYCARHSPRATLFD <u>EWGQGTT</u> LTVSS	223
1C4 Humanized heavy chain variable domain (H4)	HuVHv4: humanization percentage 74.5%; top hit to human and <i>Macaca fascicularis</i>	QVQMVSQGAEVKKPGASVKLSCKTSGFTFSSSYINWLRQAPGQSLE WIAWIFAGTGGTYYNQKFTGRAQLTVDTSASTAYMELSSLRSEDTAI YYCARHSPRATLFD <u>EWGQGTT</u> LTVSS	224
1C4 Humanized light chain variable domain (K1)	HuVLv1: humanization percentage 84.2%; top hit to human and <i>Macaca fascicularis</i>	EIVLTQSPATLSLSPGERATLSCRASSSVNHMHWYQQKPKGPAPRALI YATSNLASGIPARFSGSGSGTSFTLTISSEPEDFAVYYC <u>QQWSSNPY</u> IFGGGTKLEIK	225
1C4 Humanized light chain variable domain (K2)	HuVLv2: humanization percentage 83.2%; top hit to human and <i>Macaca fascicularis</i>	EIVLTQSPATLSLSPGERATLSCRASSSVNHMHWYQQKPKGPAPRALI YATSNLASGIPARFSGSGSGTSFTLTISSEPEDFATYVC <u>QQWSSNPYT</u> FGGGTKLEIK	226
1C4 Humanized light chain variable domain (K3)	HuVLv3: humanization percentage 78.9%; Non top hit to human and <i>Macaca fascicularis</i>	EIVLTQSPATLSLSPGERATMSCRASSSVNHMHWYQQKPGFSPRA WYATSNLASGIPARFSGSGSGTSFTLTISSEPEDFATYVC <u>QQWSSN</u> PYTFGGGTKLEIK	227
1C4 Humanized light chain variable domain (K4)	HuVLv3: humanization percentage 73.7%; Non top hit to human and <i>Macaca fascicularis</i>	EIVLTQSPATLSASPGERVMTMSCRASSSVNHMHWYQQRPGFSPRA WYATSNLASGIPARFSGSGSGTSYSLTISSEPEDFATYVC <u>QQWSSN</u> PYTFGGGTKLEIK	228

FIG. 56

Humanized antibody variable domains	Description	AMINO ACID SEQUENCE	SEQ ID NO:
6A5 Humanized heavy chain variable domain (H1)	HuVHv1: humanization percentage 82.7%; top hit to human and <i>Macaca fascicularis</i>	QVQLVQSGAEVKKPGSSVKLSCKASGYTFSSYW <u>INWVRQAPGQGL</u> EWMGNIYPSDSYTNYNQKFKD <u>RVTLTV</u> DKSTSTAYMELSSLRSEDT AVYYCTRTWFEFYD <u>SVFDYWGGQGLTV</u> VSS	229
6A5 Humanized heavy chain variable domain (H2)	HuVHv2: humanization percentage 80.6%; Non top hit to human and <i>Macaca fascicularis</i>	QVQLVQSGAEVKKPGSSVKLSCKASGYTFSSYW <u>INWVRQAPGQGL</u> EWIGNIYPSDSYTNYNQKFKD <u>RATLTV</u> DKSTSTAYMELSSLRSEDTA VYYCTRTWFEFYD <u>SVFDYWGGQGLTV</u> VSS	230
6A5 Humanized heavy chain variable domain (H3)	HuVHv3: humanization percentage 78.6%; Non top hit to human and <i>Macaca fascicularis</i>	QVQLVQSGAEVKKPGSSVKLSCKASGYTFSSYW <u>INWVKQAPGQGL</u> EWIGNIYPSDSYTNYNQKFKD <u>KATLTV</u> DKSTSTAYMELSSLRSEDTA VYYCTRTWFEFYD <u>SVFDYWGGQTTLTV</u> VSS	231
6A5 Humanized light chain variable domain (K1)	HuVLv1: humanization percentage 84.2%; Non top hit to human and <i>Macaca fascicularis</i>	DIqMTQSPSSIsASLGERVTITCKASQDINSYLSW <u>yQQKPGKaPKLIY</u> <u>RANRLVDGV</u> PSRFSGSGGQD <u>ftLTIS</u> SLqpEDiatYYCLQYDELPPTF GGGTKvEIK	232
6A5 Humanized light chain variable domain (K2)	HuVLv2: humanization percentage 83.2%; Non top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSSLSASLGERVTITCKASQDINSYLSWYQQKPGKAPKTLI Y <u>RANRLVDGV</u> PSRFSGSGGQDFTLTISSLQPEDIA <u>TYYCLQYDELPP</u> TFGGGTKVEIK	233
6A5 Humanized light chain variable domain (K3)	HuVLv3: humanization percentage 82.1%; Non top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSSLSASLGERVTITCKASQDINSYLSW <u>FQQKPGKAPKTLI</u> Y <u>RANRLVDGV</u> PSRFSGSGGQDFTLTISSLQPEDIA <u>TYYCLQYDELPP</u> TFGGGTKVEIK	234
6A5 Humanized light chain variable domain (K4)	HuVLv3: humanization percentage 81.1%; Non top hit to human and <i>Macaca fascicularis</i>	DIQMTQSPSSLSASLGERVTITCKASQDINSYLSW <u>FQQKPGKAPKTLI</u> Y <u>RANRLVDGV</u> PSRFSGSGGQDYTLTISSLQPEDIA <u>TYYCLQYDELPP</u> TFGGGTKLEIK	235

FIG. 57

Humanized antibody variable domains	Description	AMINO ACID SEQUENCE	SEQ ID NO:
5F9 Humanized heavy chain variable domain (H1)	HuVHv1: humanization percentage 82.5%; top hit to human and <i>Macaca fascicularis</i>	QVQLQESGPGLVKPSETLSLTCTVSGFSLTTYD <u>ISWVRQPPGKGLEW</u> IGV <u>I</u> WTGGGTN <u>YN</u> SSFM <u>SR</u> VTISKDTSKNQVSLKLSVTAADTA <u>V</u> Y CERVDYWGQGTTTVTVSS	236
5F9 Humanized heavy chain variable domain (H2)	HuVHv2: humanization percentage 79.4%; Non top hit to human and <i>Macaca fascicularis</i>	QVQLKESGPGLVKPSETLSLTCTVSGFSLTTYD <u>ISWVRQPPGKGLEW</u> LGV <u>I</u> WTGGGTN <u>YN</u> SSFM <u>SR</u> VTISKDTSKNQVSLKLSVTAADTA <u>V</u> Y CERVDYWGQGTTTVTVSS	237
5F9 Humanized heavy chain variable domain (H3)	HuVHv3: humanization percentage 77.3%; Non top hit to human and <i>Macaca fascicularis</i>	QVQLKESGPGLVKPSETLSITCTVSGFSLTTYD <u>ISWVRQPPGKGLEW</u> GV <u>I</u> WTGGGTN <u>YN</u> SSFM <u>SR</u> VTISKDNSKNQVSLKLSVTAADTA <u>V</u> Y ERVDYWGQGTTTLTVSS	238
5F9 Humanized light chain variable domain (K1)	HuVLv1: humanization percentage 91%; top hit to human and <i>Macaca fascicularis</i>	DVVM <u>T</u> QSP <u>L</u> SLPVTLGQPA <u>S</u> ISCRSSQSLVHSNGNTY <u>L</u> HW <u>F</u> QQRP <u>G</u> QSP <u>R</u> LL <u>I</u> YKVSNR <u>F</u> SGVPDR <u>F</u> SGSGGT <u>A</u> FTFKISRVEAEDVG <u>V</u> Y <u>C</u> <u>S</u> QNT <u>H</u> VPWTFGGG <u>T</u> KVEIK	239
5F9 Humanized light chain variable domain (K2)	HuVLv2: humanization percentage 90%; top hit to human and <i>Macaca fascicularis</i>	DVVM <u>T</u> QSP <u>L</u> SLPVTLGQPA <u>S</u> ISCRSSQSLVHSNGNTY <u>L</u> HW <u>F</u> QQRP <u>G</u> QSP <u>K</u> LL <u>I</u> YKVSNR <u>F</u> SGVPDR <u>F</u> SGSGGT <u>A</u> FTFKISRVEAEDVG <u>V</u> Y <u>C</u> <u>S</u> QNT <u>H</u> VPWTFGGG <u>T</u> KVEIK	240
5F9 Humanized light chain variable domain (K3)	HuVLv3: humanization percentage 89%; Non top hit to human and <i>Macaca fascicularis</i>	DVVM <u>T</u> QSP <u>L</u> SLPVTLGQPA <u>S</u> ISCRSSQSLVHSNGNTY <u>L</u> HW <u>Y</u> QQRP <u>G</u> QSP <u>K</u> LL <u>I</u> YKVSNR <u>F</u> SGVPDR <u>F</u> SGSGGT <u>A</u> FTFKISRVEAEDVG <u>V</u> Y <u>C</u> <u>S</u> QNT <u>H</u> VPWTFGGG <u>T</u> KLEIK	241
5F9 Humanized light chain variable domain (K4)	HuVLv3: humanization percentage 87%; Non top hit to human and <i>Macaca fascicularis</i>	DVVM <u>T</u> QSP <u>L</u> SLPVTLGDP <u>A</u> SISCRSSQSLVHSNGNTY <u>L</u> HW <u>Y</u> LQR <u>P</u> <u>G</u> QSP <u>K</u> LL <u>I</u> YKVSNR <u>F</u> SGVPDR <u>F</u> SGSGGT <u>A</u> FTFKISRVEAEDVG <u>V</u> Y <u>C</u> <u>S</u> QNT <u>H</u> VPWTFGGG <u>T</u> KLEIK	242

FIG. 58

16-1C4 ("1C4") Heavy chain variable region (SEQ ID NO: 243)
QGMQSQSGAELVKPGASVKLSCKTSGFTFSSSYINWLKQKPGQSLEWIAWIFAGTGGTYYNQKFTGKAQLTVDTSSGTAYMQFSSLTTEDSAIYYCAR
HSPRATLFDWFQGQTLLTVSS

16-1C4 ("1C4") Light chain variable region (SEQ ID NO: 244)
QIVLSQSPAILLSASPGEKVTMTCRASSSVNHHMWYQQRTGFSPKAWIYATSNLASGVPARFSGSGTSYSLTISRVEAEDAATYYCQQWSSNPYTFG
GGTKLEIK

29-6A5 ("6A5") Heavy chain variable region (SEQ ID NO: 245)
QVQLQQPGAELVRPGASVKLSCKASGYTFSSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQKFKDKATLTVDKSSSTAYMQLSPTSDDSAVYYCTR
TWEFYDYSVFDYWGQGTLLTVSS

29-6A5 ("6A5") Light chain variable region (SEQ ID NO: 246)
DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFFQQKPGKSPKTLIYRANRLVDGVPSPRFSGSGGQDYSLTISSLEYEDMGIYYCLQYDELPPTF
GGTKLEIK

30-5F9 ("5F9") Heavy chain variable region (SEQ ID NO: 247)
QVQLKESGPGLVAPSQSLSTCTVSGFSLTTYDISWVRQPPGKGLEWLGVIWTGGTNYNSSFMSRLSISKDNSKNQVFLKMNSLQVDDTAIYYCERV
DYWGQGTLLTVSS

30-5F9 ("5F9") Light chain variable region (SEQ ID NO: 248)
DVVMTQTPLSLPVSLGDAQASISCRSSQSLVHSNGNTYLHWYLVKQPGQSPKLLIYKVSNRFSGVDPDRFSGSGGTAFTEFKISRVEAEDLGVFCSQNT
VPWTFGGGTTKLEIK

45-2B3 ("2B3") Heavy chain variable region (SEQ ID NO: 249)
QVQLQQSGPELVKPGASVKISCKTSGYAFSTSWMNWVKQRPGQGLEWIGRIYPGDGDTDYNGRFKGKATLTADKSSSTAYLQLSSLTSVDSAVYFCAR
LDGYEVEVFYFDYWGQGTLLTVSS

45-2B3 ("2B3") Light chain variable region (SEQ ID NO: 250)
DVVMTQTPLTSLVTTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGIYCFQGTH
FPWTFGGGTKLEIK

45-4B9 ("4B9") Heavy chain variable region (SEQ ID NO: 251)
EVQLQQSGPELVKPGASVKMSCKASGYTFTTYVMYWKQRPQGQGLEWIGYINPYNDDIRYNEKFKGKATLTSDRSSSTAYMELSSLTSEDSAVYLCAR
QGGDYWGQGTLITVSS

45-4B9 ("4B9") Light chain variable region (SEQ ID NO: 252)
DVQITQSPSYLAASPGETITVNCRAASKNINKYLAWYQEKPGKTNKLLIYSGSTLQSGIPSRFSGSGSGTDFTLTISSLEPEDFAVYHCCQQYNEYPLTF
GAGTKLEMK

45-7E9 ("7E9") Heavy chain variable region (SEQ ID NO: 253)
QVQLKQSGPGLVQPSQSLSTCTVSGFSLTTYGVHWRQPPGKGLEWLGVWSDGNTDYNDAFISRLSITKDNSTSQVFFKMNGLQADDTAIYYCARN
SITSVSFDCWGQGTTLTVSS

45-7E9 ("7E9") Light chain variable region (SEQ ID NO: 254)
DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTTVAWYQQRPQGQSPKALICSAARYSGVDPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPLTF
GSGTKLEIK

45-7G9 ("7G9") Heavy chain variable region (SEQ ID NO: 255)
QVQLQQPGSALVRPGASVKLSCKASGYTFSNYWIHWVKQRHGQGLEWIGNIYPASDYTNYDEKFKNKGTLTVDTSSTAYMHLSSLTSEDSAVYYCSR
GYFGSLDYWGQGTSTVTVSA

45-7G9 ("7G9") Light chain variable region (SEQ ID NO: 256)
DILLTQSPAILSVNPGERVSFSCRASQPIGTGIHWYQQRTNGSPRLLIKSASEISGIPSRFSGSGSGTDFTLTINNVEDDVGDIYCCQQYSWPPTTF
GGGTKLKIN

45-8E11 ("8E11") Heavy chain variable region (SEQ ID NO: 257)
EVQLQQSGTVLARPGASVKMSCKASGYSFTSNWMHWVKQRPQGLEWIGVIYPGNSDTSYNQKFKGAKLTAVTSASTAYMELSSLTNEDSAVYYCTR
GITTAPEYWGQGTTLTVSS

45-8E11 ("8E11") Light chain variable region (SEQ ID NO: 258)
NIVMTQSPKSMMSVGERVTLSCKASENVGIYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISSVQPEDLADYHCGHTYNYPPFTF
GSGTKLEIK

45-8E2 ("8E2") Heavy chain variable region (SEQ ID NO: 259)
EVKLLSGGGLVQPGGSLKLSCAASGDFSRYSWMSWVRQAPGKGLEWIGEIHDPDSSAINYTPSLKDKFII SRDNAKNTLYLQMSKVRSEDTALYYCAR
SYYGRVFDYWGGTTLTVSS

45-8E2 ("8E2") Light chain variable region (SEQ ID NO: 260)
DIVMTQSPATLSVTPGDRVSLSCRASQISDYLHWYQQKSHESPRLLIKYASQSIGIPPRFSGSGSGDFTLSINSVEPEDVGMYYCQDGHSPPTF
GAGTKLELK

45-8F1 ("8F1") Heavy chain variable region (SEQ ID NO: 261)
EVQLQQSGTVLARPGASVKMSCKASGYSFTSYWMHWVKQRPQGLEWIGVIYPGNSDTSYNQKFKGAKLTAVTSASTAYMDLSSLTNEDSAVYYCTR
GITTAPDYWGQGTTLTVSS

45-8F1 ("8F1") Light chain variable region (SEQ ID NO: 262)
NIVMTQSPKSMMSVGERVTLSCKASENVGIHVSWYQQKPEQSPKLLIYGASSGYNGVPDRFTGSGSATDFTLTISSVQPEDLADYHCGQTSYPPFTF
GSGTKLEIK

54-8B11 ("8B11") Heavy chain variable region (SEQ ID NO: 263)
QIQLVQSGPELKKPGETVKISCKASKFTFTNYGMNWKQAPGKALKWMGWINTYTGEPTYADDFKGRFDFSLETSAATAYLQINNLLKNEDTATYFCAR
REYYPWVFVYWGQGTTLVTVSA

54-8B11 ("8B11") Light chain variable region (SEQ ID NO: 264)

ENVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSSTSPKLWIYDTSKLASGVPGRFSGSGSGNSYSLTISSMEAEADVATYYCFQQSGGYPLTFG
GGTKLEIK

55-8F6 ("8F6") Heavy chain variable region (SEQ ID NO: 265)
QVQLQQPGAELVRPGASVKLSCKASGYIFTSYWINWVKQRPQGQGLEWIGNIYPSDSYTNYNQKFKDKATLTVDKSSSTAYMQLSSPTSEDSAVYYCTR
FHYGSSPFDNWGQGTTLTVSS

55-8F6 ("8F6") Light chain variable region (SEQ ID NO: 266)
DIQMTQSTSSLSASLGDRVTISCRASQDISHYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGGTDYSLTISNLEQEDFATYFCQQGHTLPRTF
GGGTKLEIK

56-2A6 ("2A6") Heavy chain variable region (SEQ ID NO: 267)
QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWKQAPGKGFKWMGWINTYTGEPTYADDFKGRFAFSLEISASTAYLQINNLIKNETATYFCAR
RDYLGAMDYWGQGTSTVTVSS

56-2A6 ("2A6") Light chain variable region (SEQ ID NO: 268)
ENVLTQSPAIMSASPGEKVTMTCRASSSVSSSYLHWYQQKSGASPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSEVEAEADAATYYCQQYSAYLYT
FGGGTKLEIK

59-5E4 ("5E4") Heavy chain variable region (SEQ ID NO: 269)
QVQLQQPGAELVRPGASVKLSCKASGYTFTTYWINWVRQRPQGQGLEWIGNIYPSDSYTNYNQKFKDKASLTVDKSSNTAYMQLSSPTSEDSAVYYCAR
EAGDGTHYYAIDYWGGTSTVTVSS

59-5E4 ("5E4") Light chain variable region (SEQ ID NO: 270)
NIVMTQSPKSMMSVGERVTLSCKASENVGTYYVSWYQQKPEQSPKLLIYGASNRYPGVPDRFTGSGSATDFTLTISSLQAEDLADYHCGGYSYLRTF
GGGTNLEIK

61-6A7 ("6A7") Heavy chain variable region (SEQ ID NO: 271)

EVQLQQSGAELVRPGALVKLSCKASGFNIKDYMHVVKRRPEQGLEWIGWIDPENGNTIYDPKFQDKASITADTSSNTAYLQLSSLTSEDTAVYYCAE
GLPWYFDYWGGTTLLTVSS

61-6A7 ("6A7") Light chain variable region (SEQ ID NO: 272)
QIILTQSPALMSASPGGEKVTMTCSASSVSDMNNWYQQKPRSSPTPWIYLTSNLSSGVDPDRFSGSGGTSYSLTISSMEEADAATYYCQQQWSGNPLTFG
AGTRLELK

69-3C2 ("3C2") Heavy chain variable region (SEQ ID NO: 273)
DVQLVESGGGLVQPGGSRKLSCAASGFSFGMHWMRQAPEKGLEWVAYISGGSSAIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDAMYYCAR
DWVDYWGGTTLLTVSS

69-3C2 ("3C2") Light chain variable region (SEQ ID NO: 274)
DIQMTQSPASLSVSVGETVTITCRASENIYSNLVWYQQKQKSPQLLVYTATKLTNGVPSRFSGSGGTQYSLKINSLQSEDFGTYYCQHFWDTPYTF
GGGTKLEMK

70-3F9 ("3F9") Heavy chain variable region (SEQ ID NO: 275)
QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWINWVKQRPQGQGLEWIGNIFPSDSYTNYNQKFKDRAKLTVDKSSSTAYMQLSSPTSEDSAVYYCTR
FGSSGYPDYYTMEYWGGTSVTVSS

70-3F9 ("3F9") Light chain variable region (SEQ ID NO: 276)
DIQMTQSPASLSASVGETVTITCRASGNIDNLAWYQQKQKSPQLLVYNAKTLAEGVPSRFSGSGGTEYSLKINSLQPEDFGSYHCQQYWTIPYTF
GGGTKLEIK

70-6F10 ("6F10") Heavy chain variable region (SEQ ID NO: 277)
QVQLQQSGPELVKPGASVKISCKASGYAFNNSWMNWNVKQRPQGQGLEWIGRIYPGDGDTDYNGKFKGKATLTADKSSSTAYMQLSSLTSVDSAVYFCAR
LDGNYYYWYFDVWGAGTTVTVSS

70-6F10 ("6F10") Light chain variable region (SEQ ID NO: 278)
DVVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPGGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGYYCQQGTH
FPQTFGGGTKLEIK

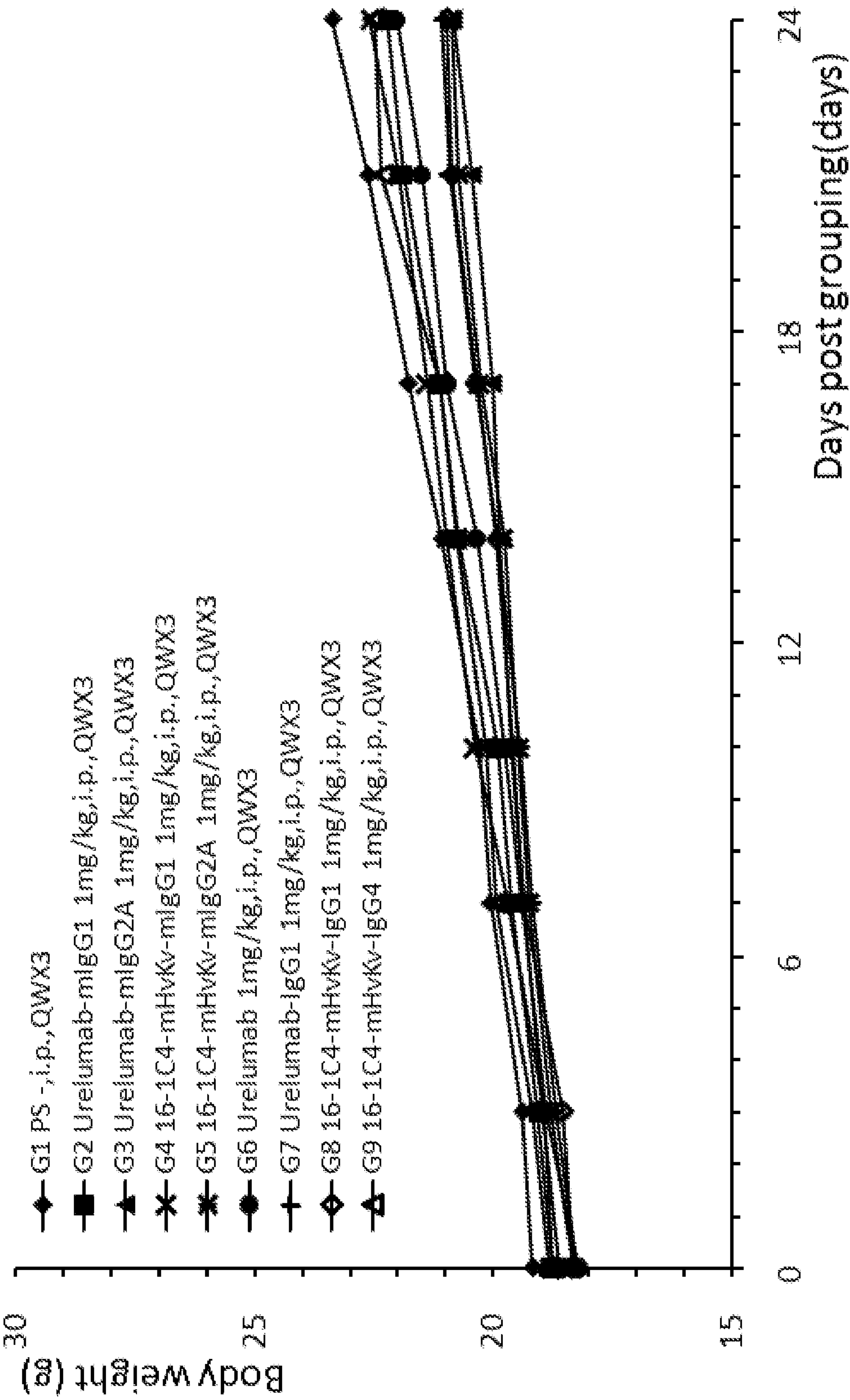


FIG. 59

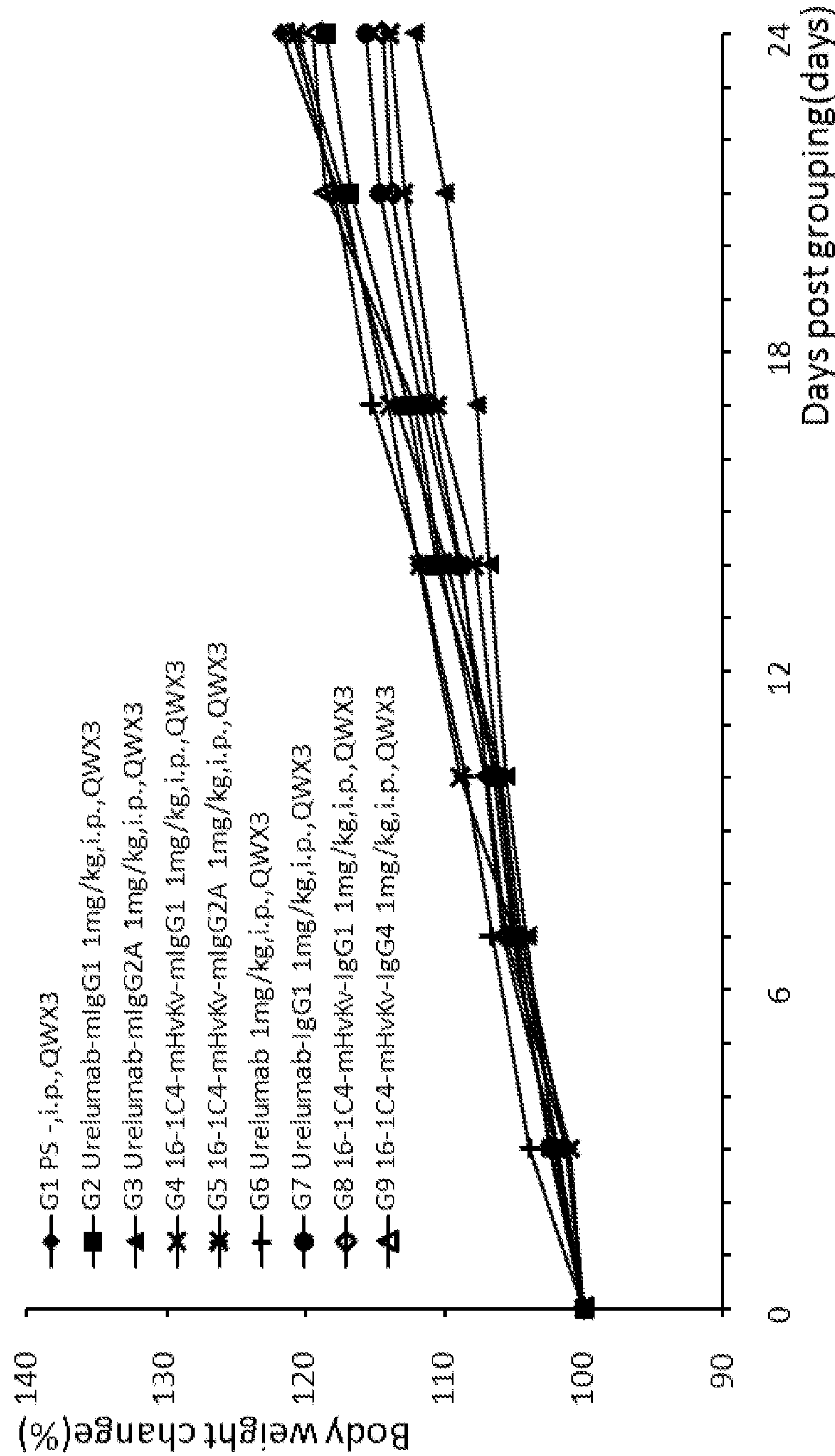


FIG. 60

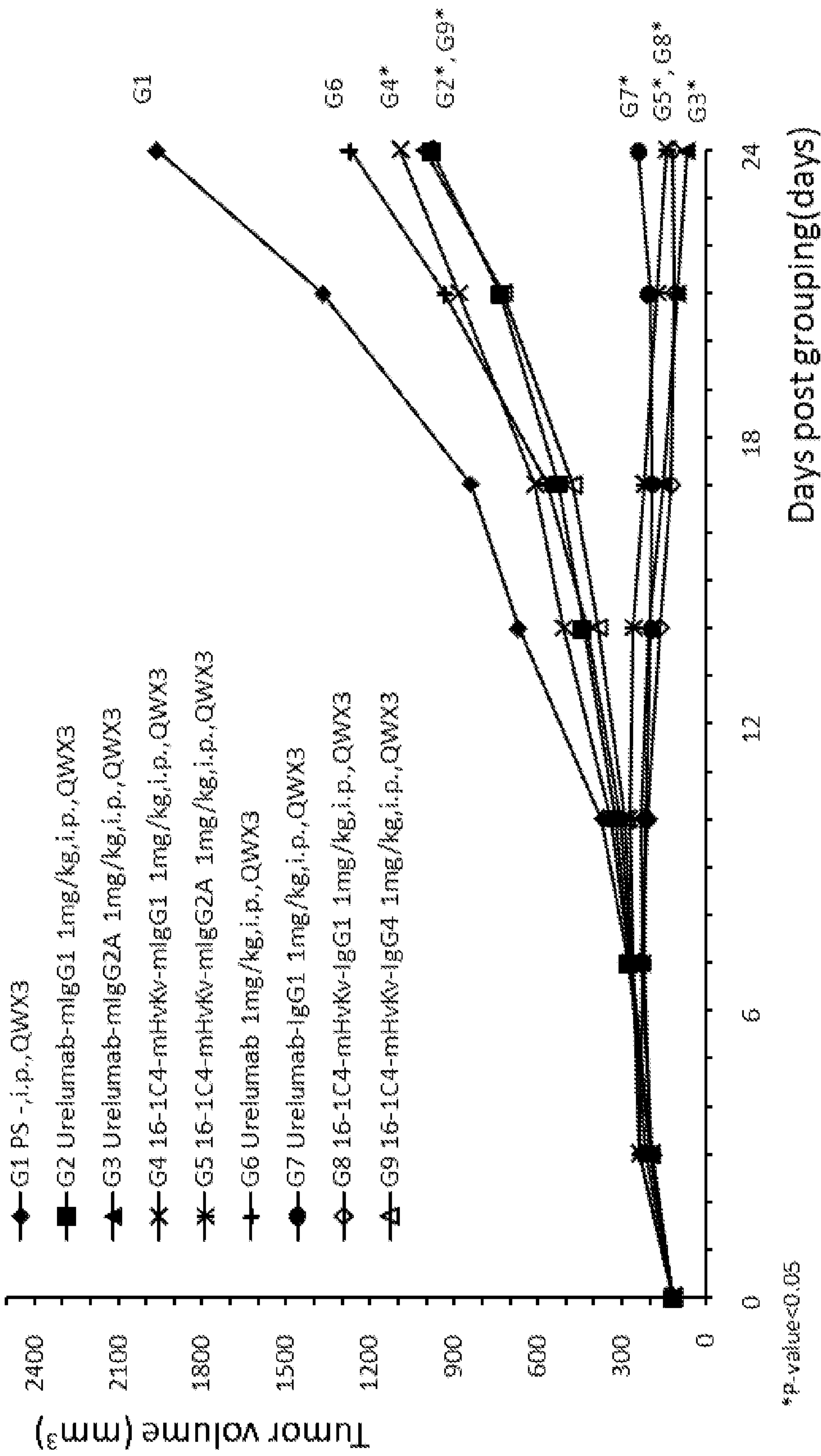


FIG. 61

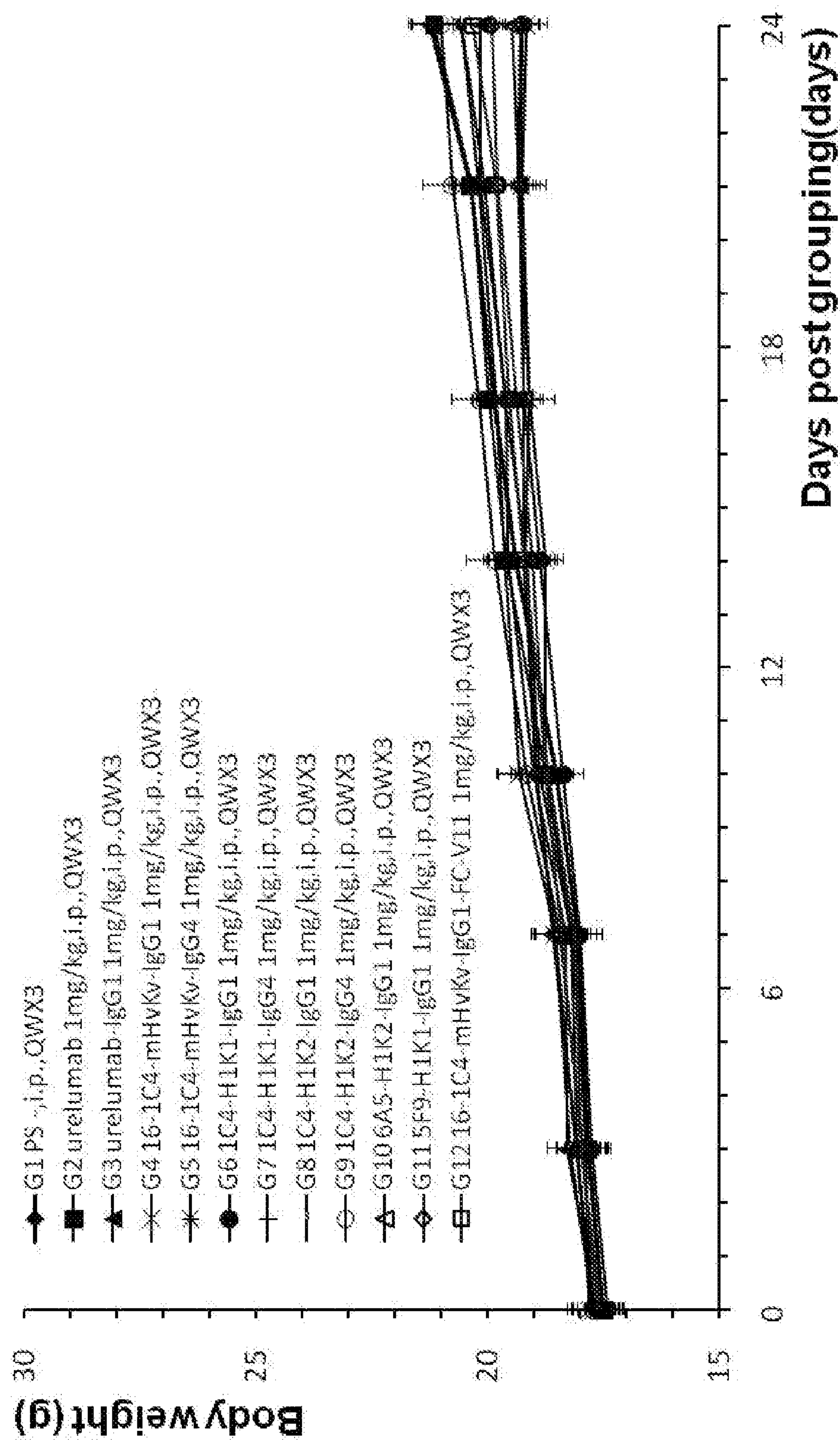


FIG. 62

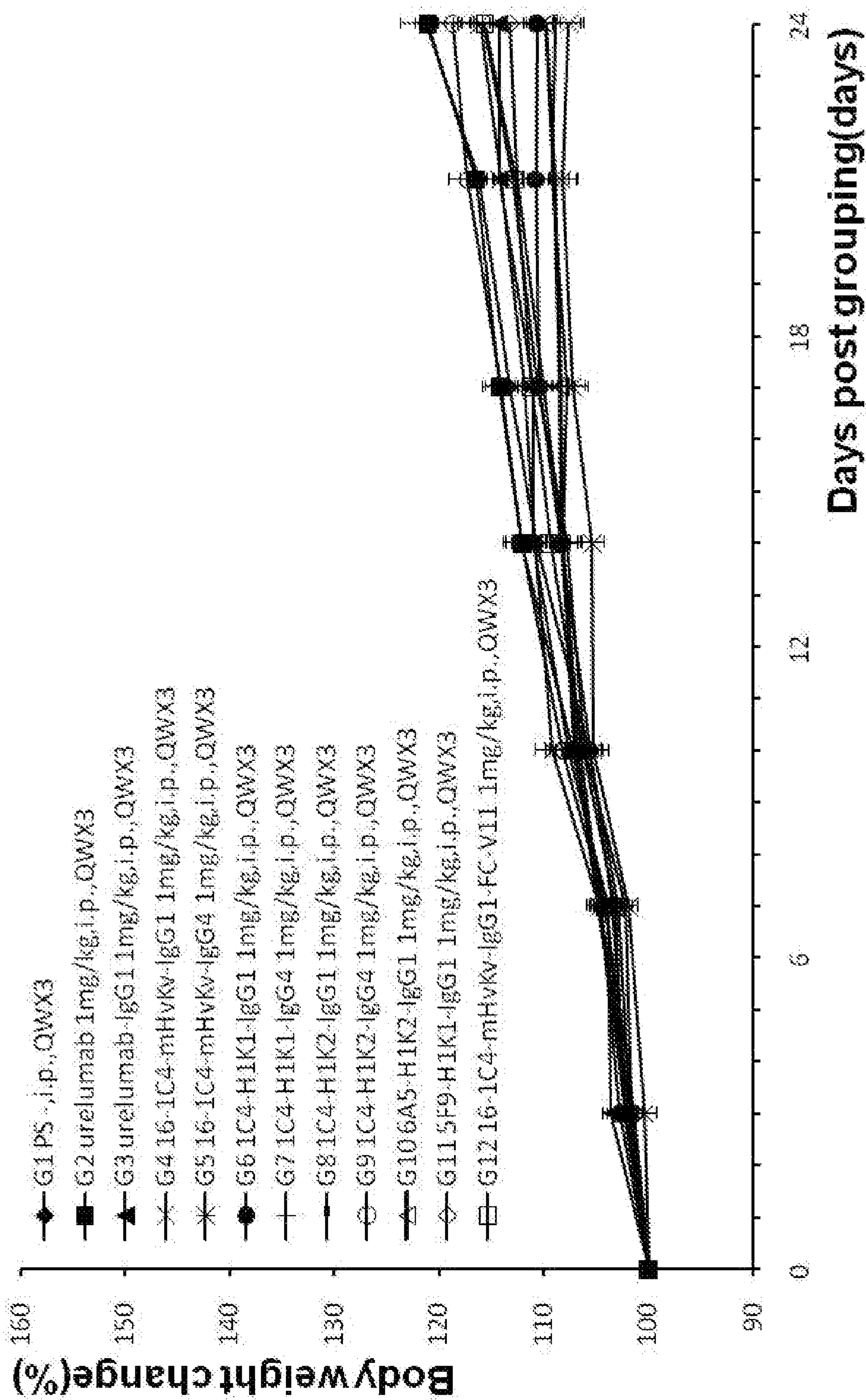


FIG. 63

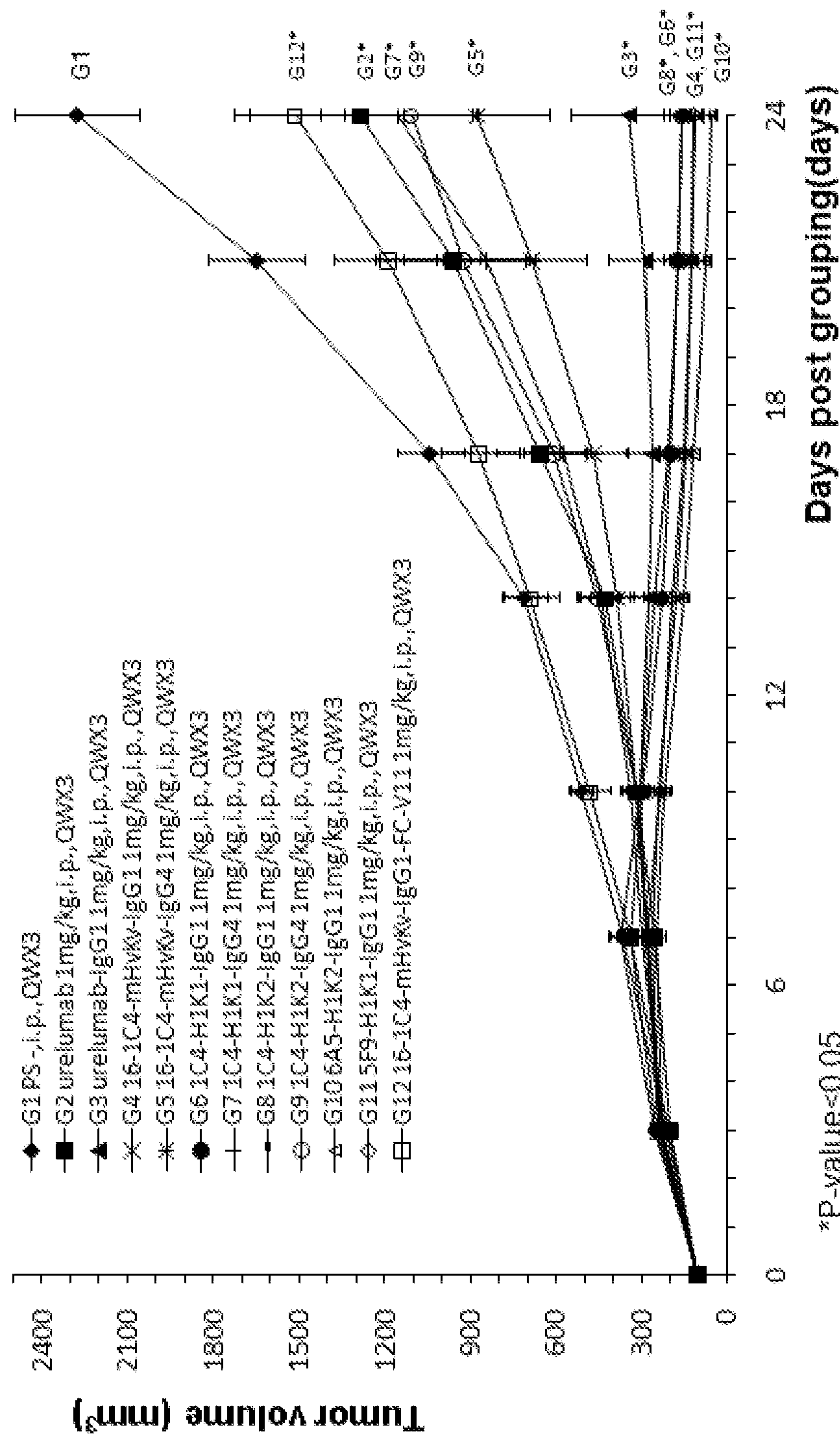


FIG. 64

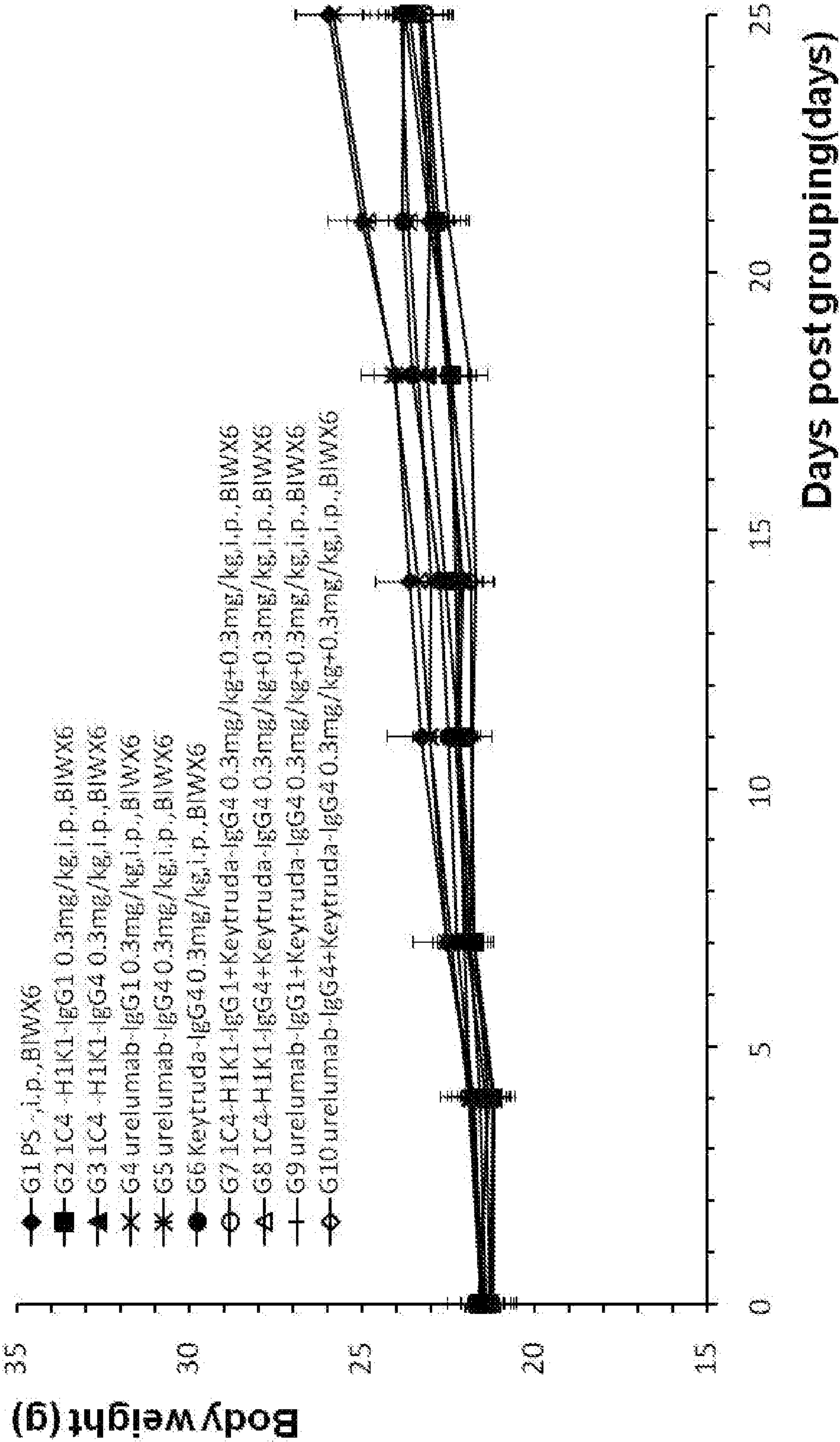


FIG. 65

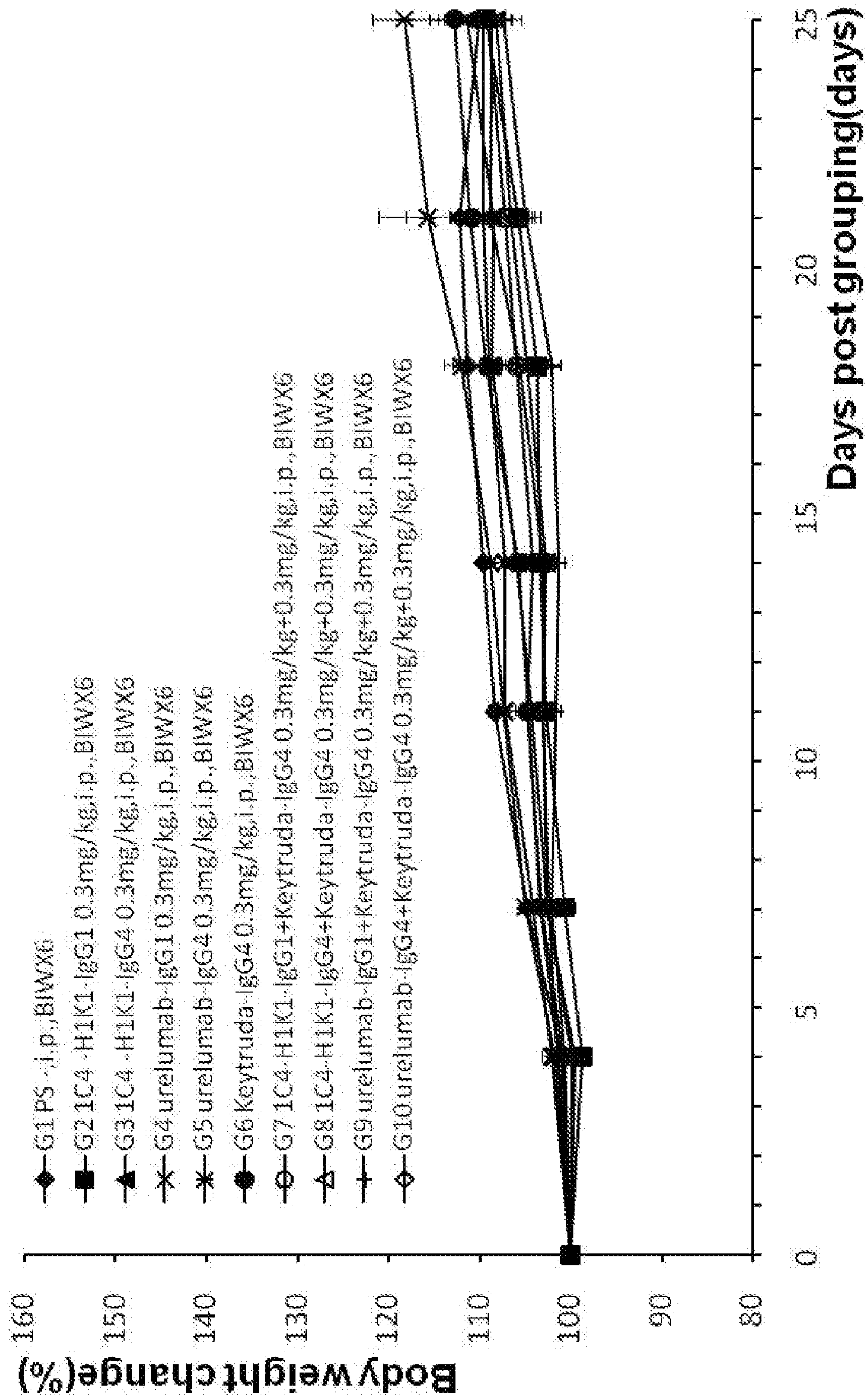


FIG. 66

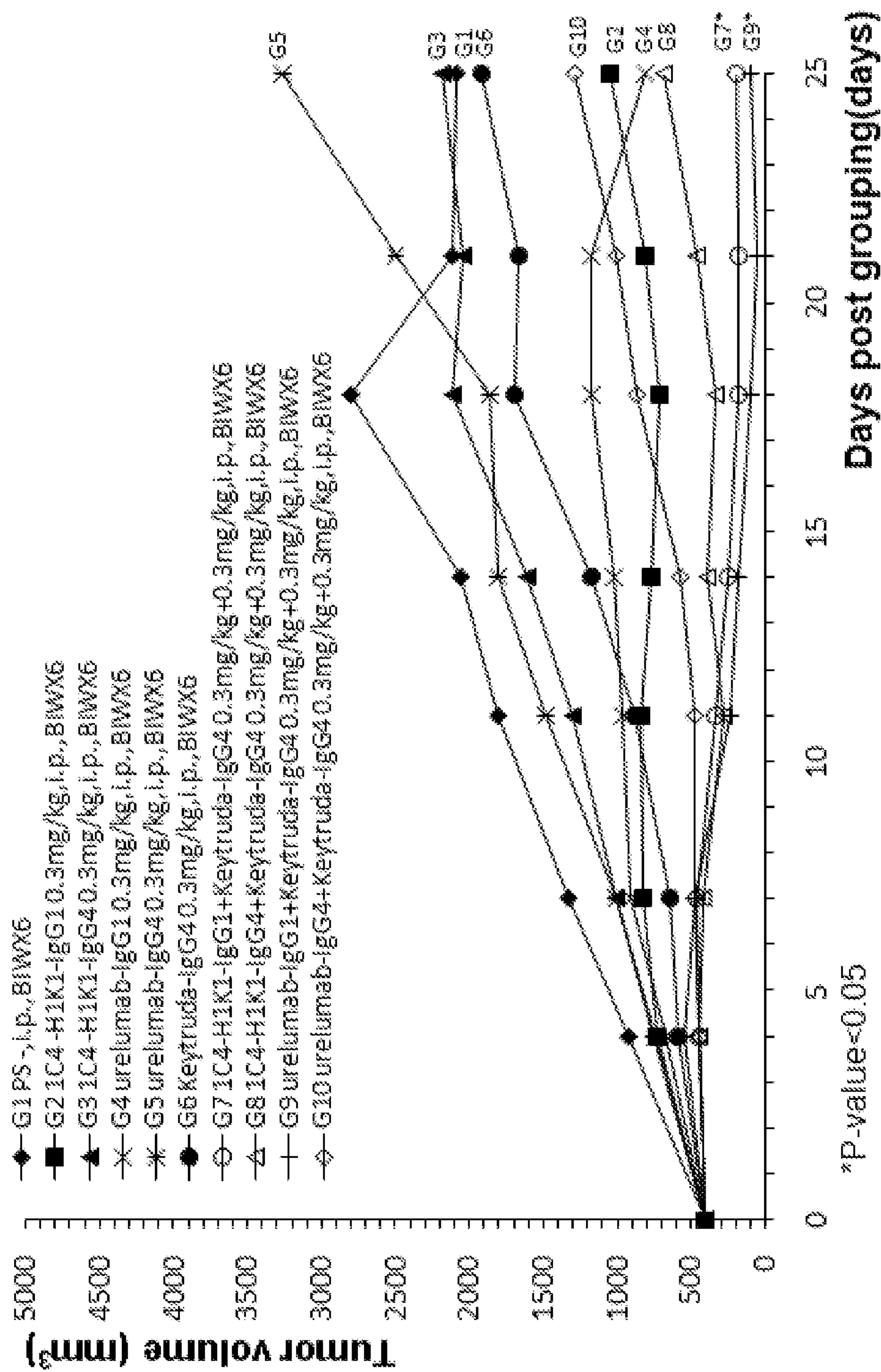


FIG. 67

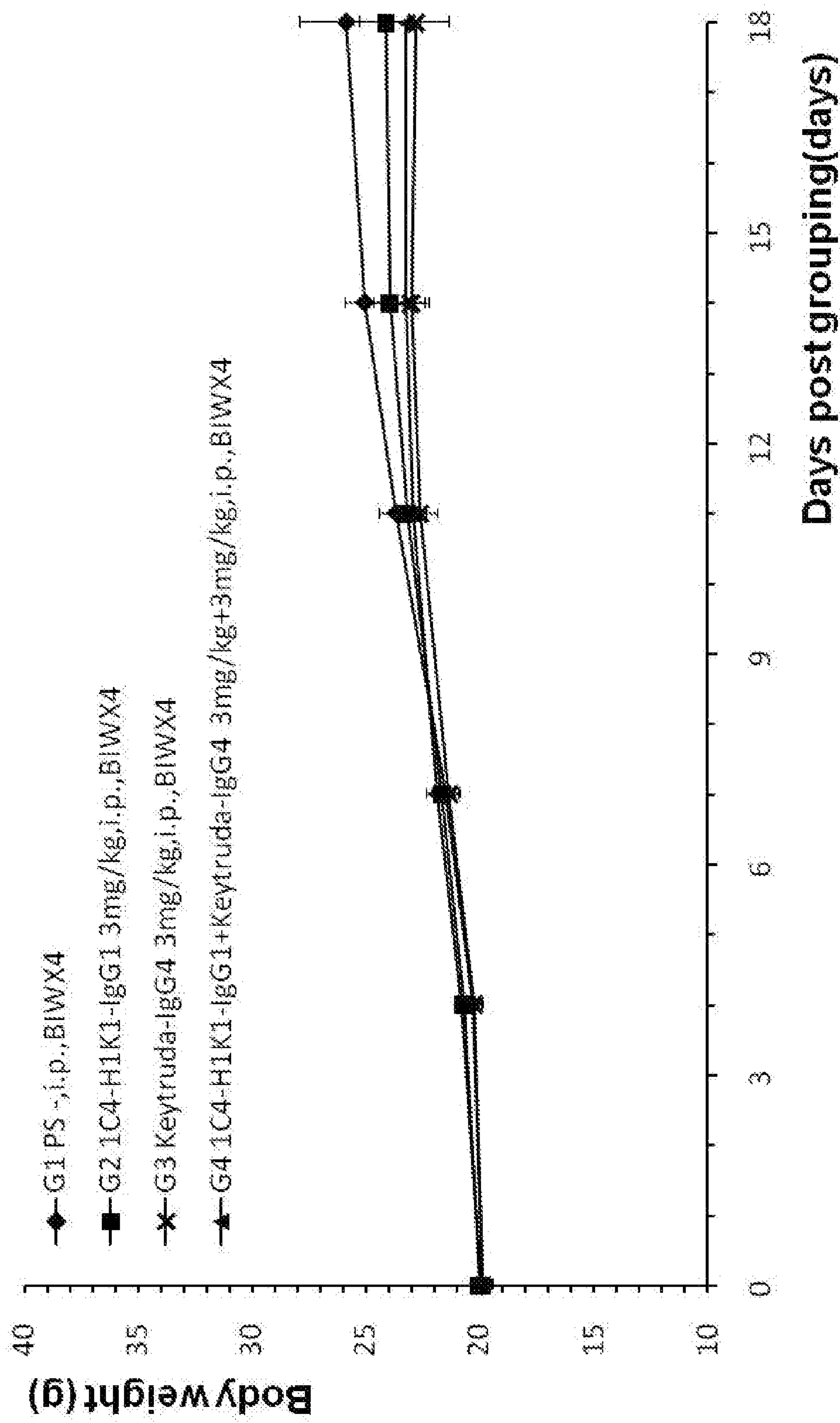


FIG. 68

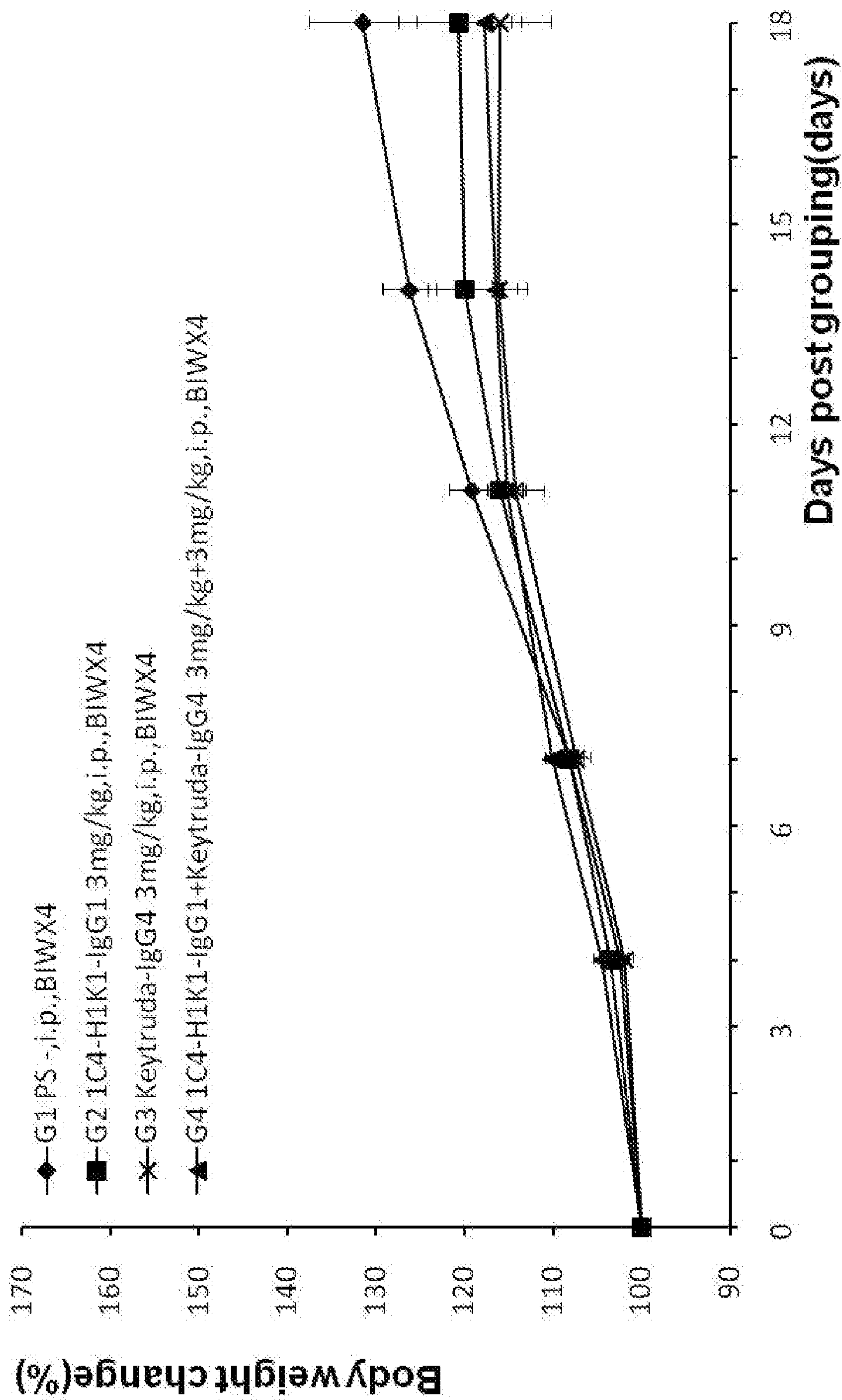


FIG. 69

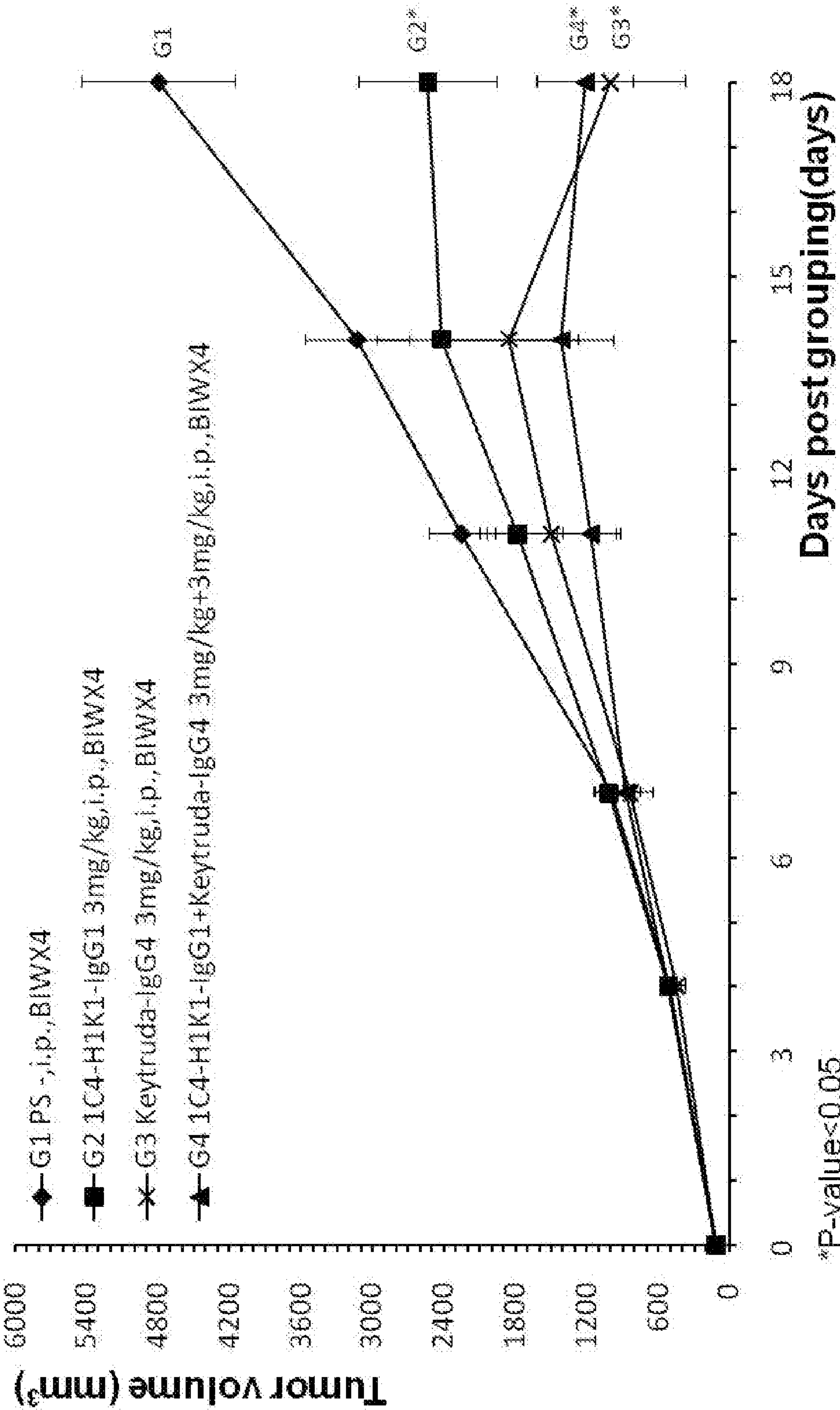


FIG. 70

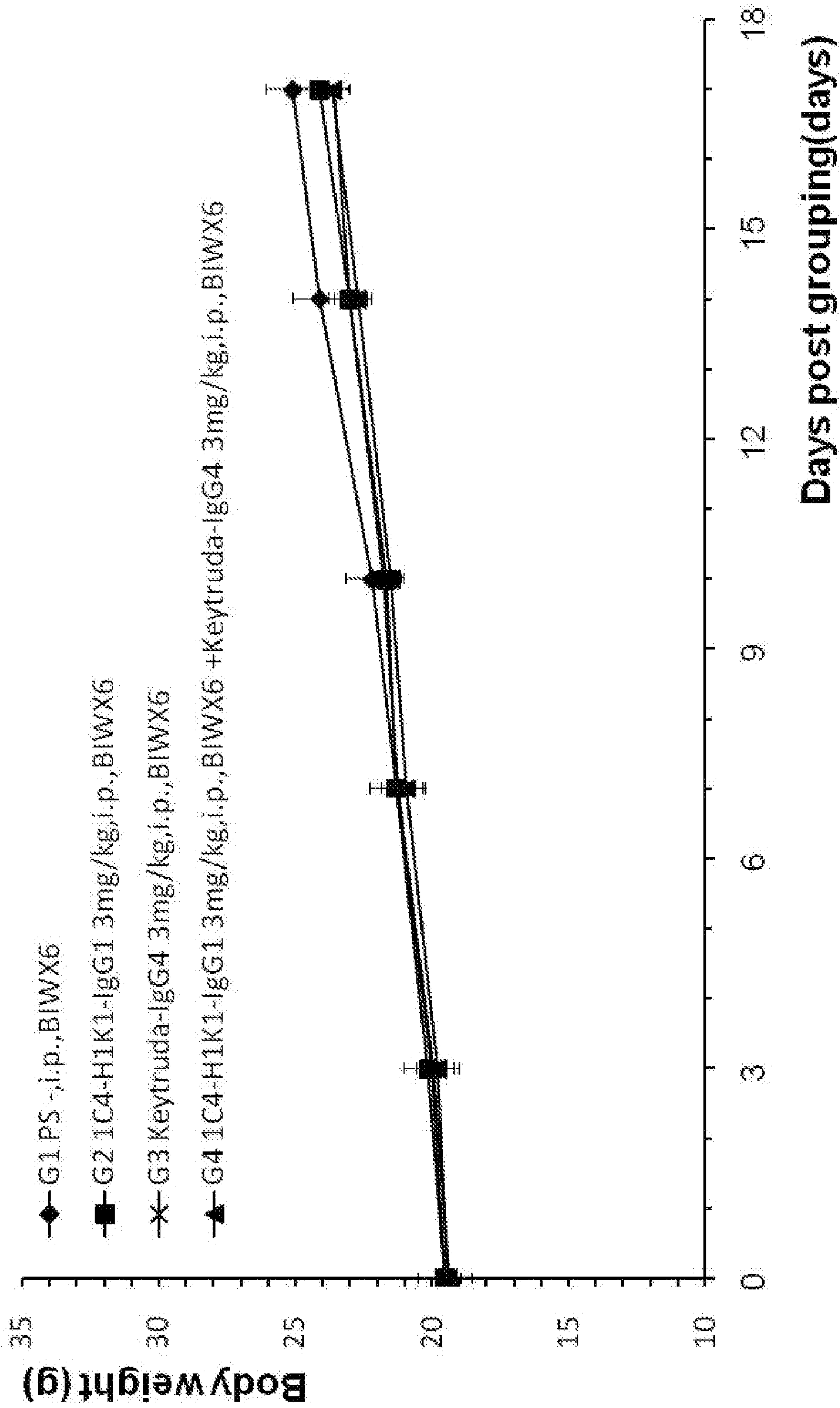


FIG. 71

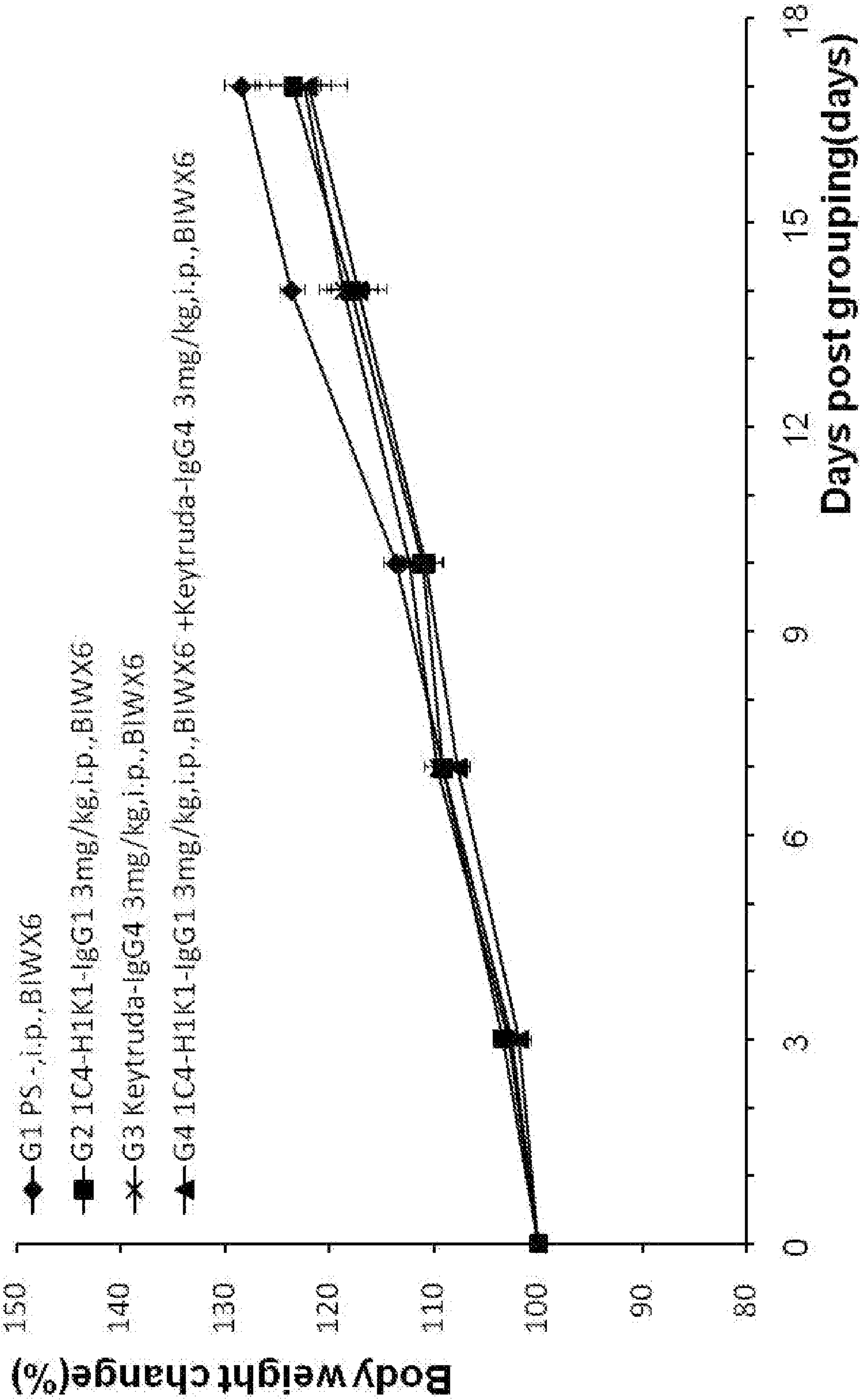


FIG. 72

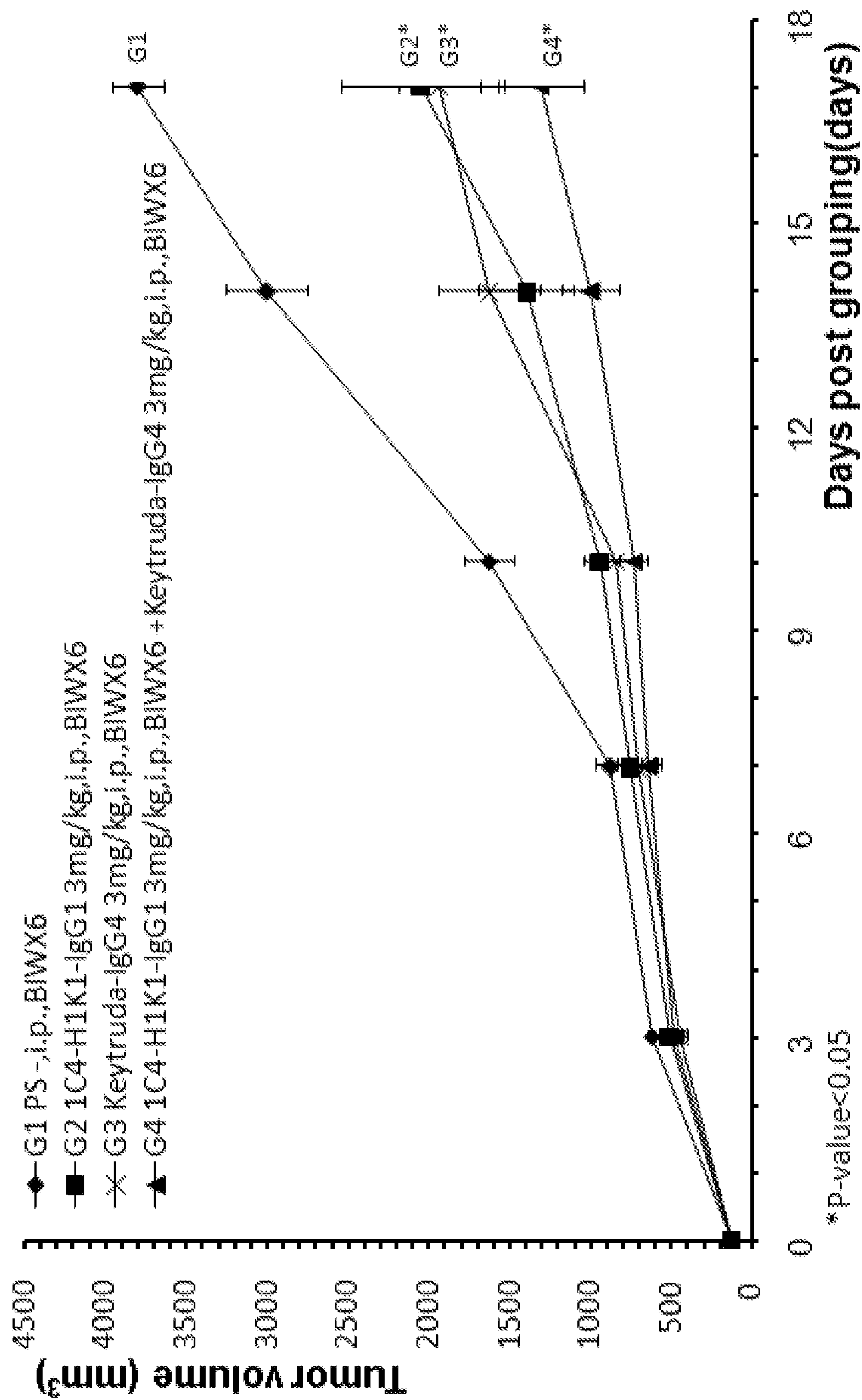


FIG. 73

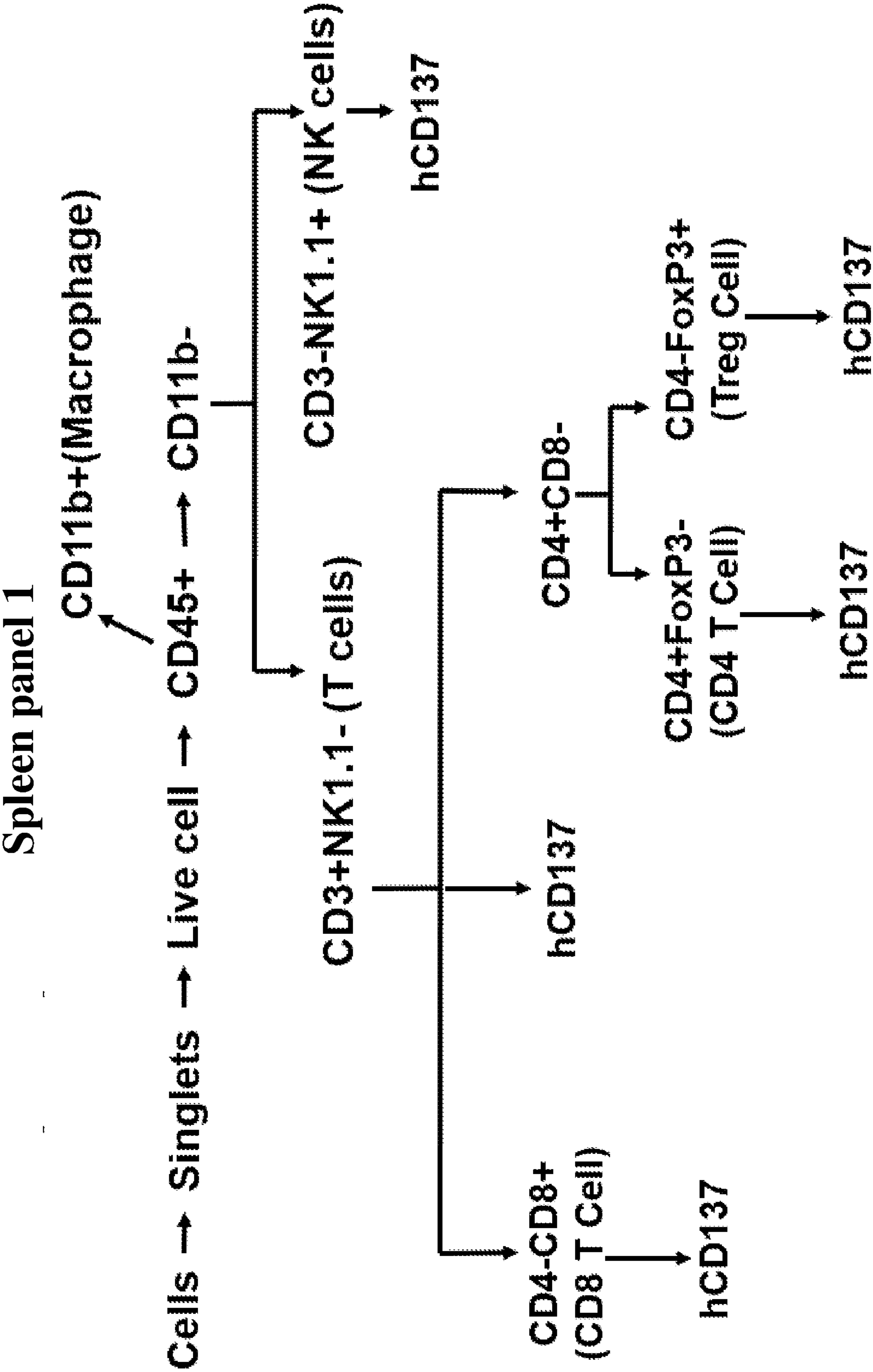


FIG. 74

Spleen panel 2

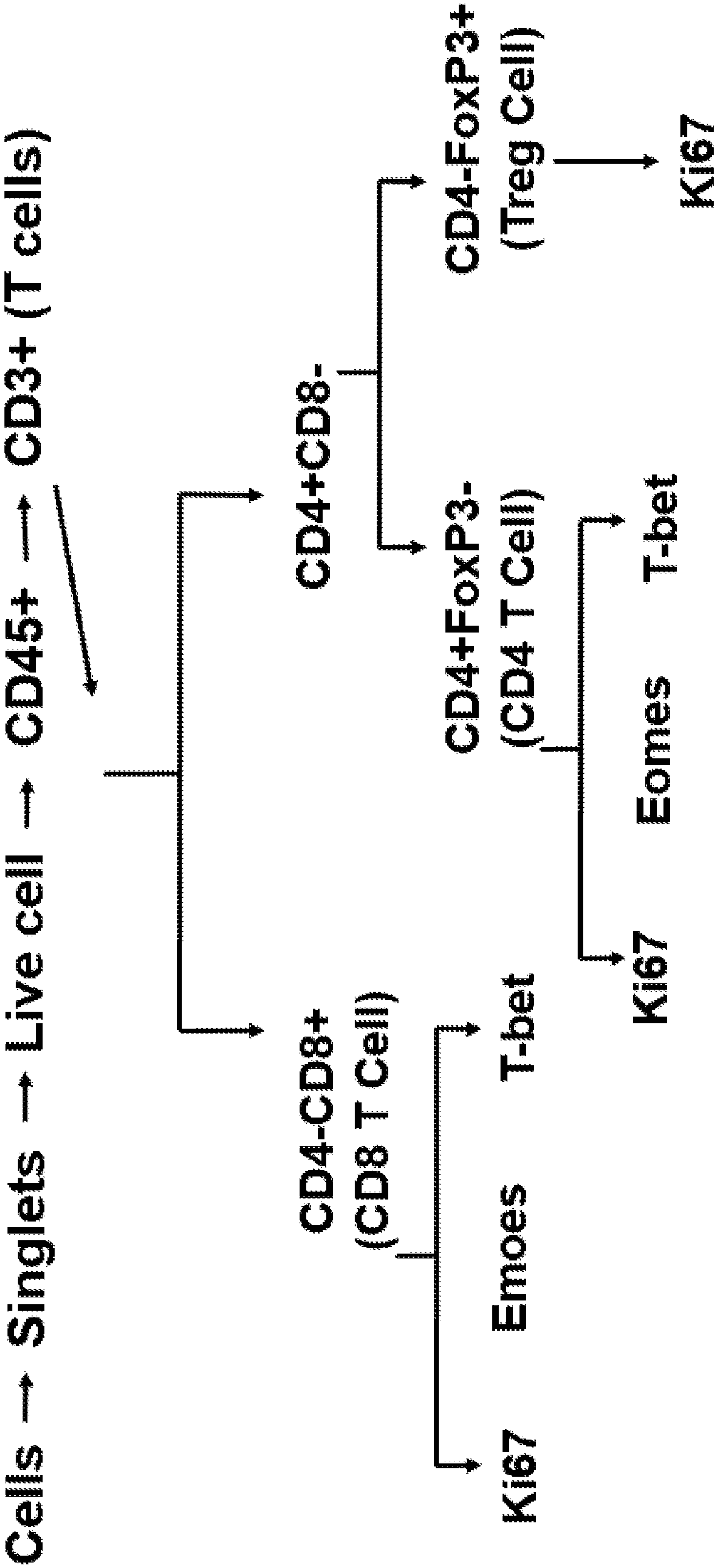


FIG. 75

Tumor panel 1

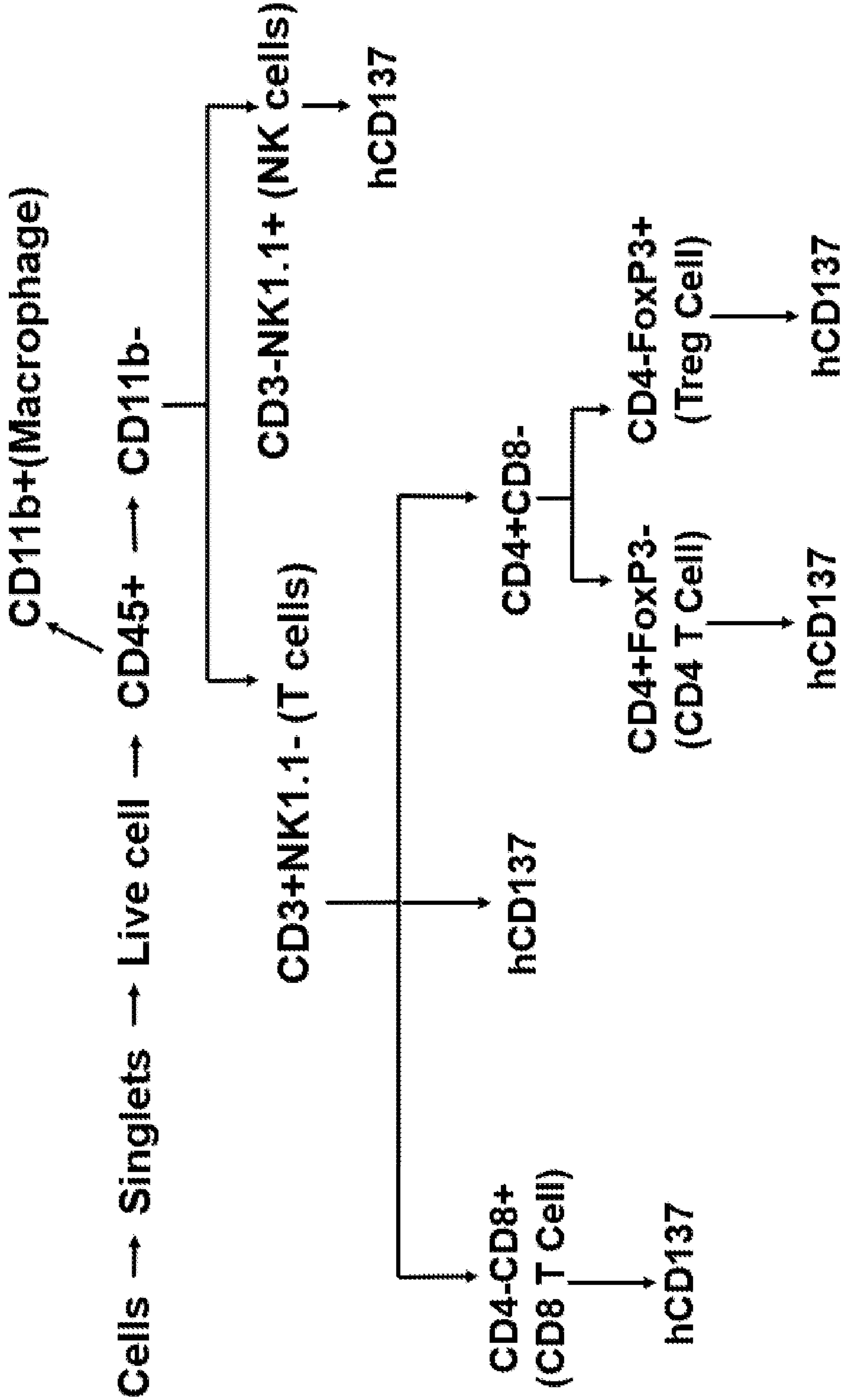


FIG. 76

Tumor panel 2

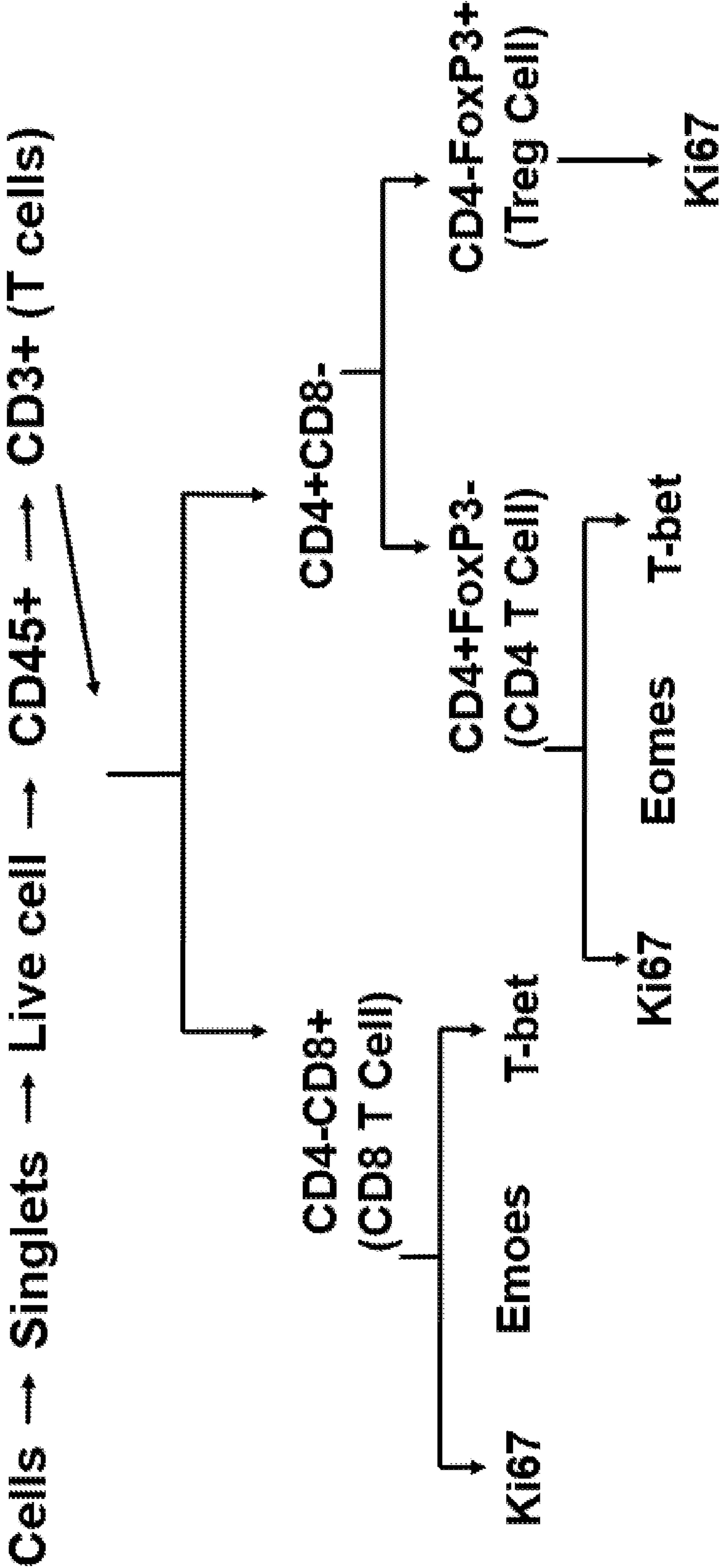


FIG. 77

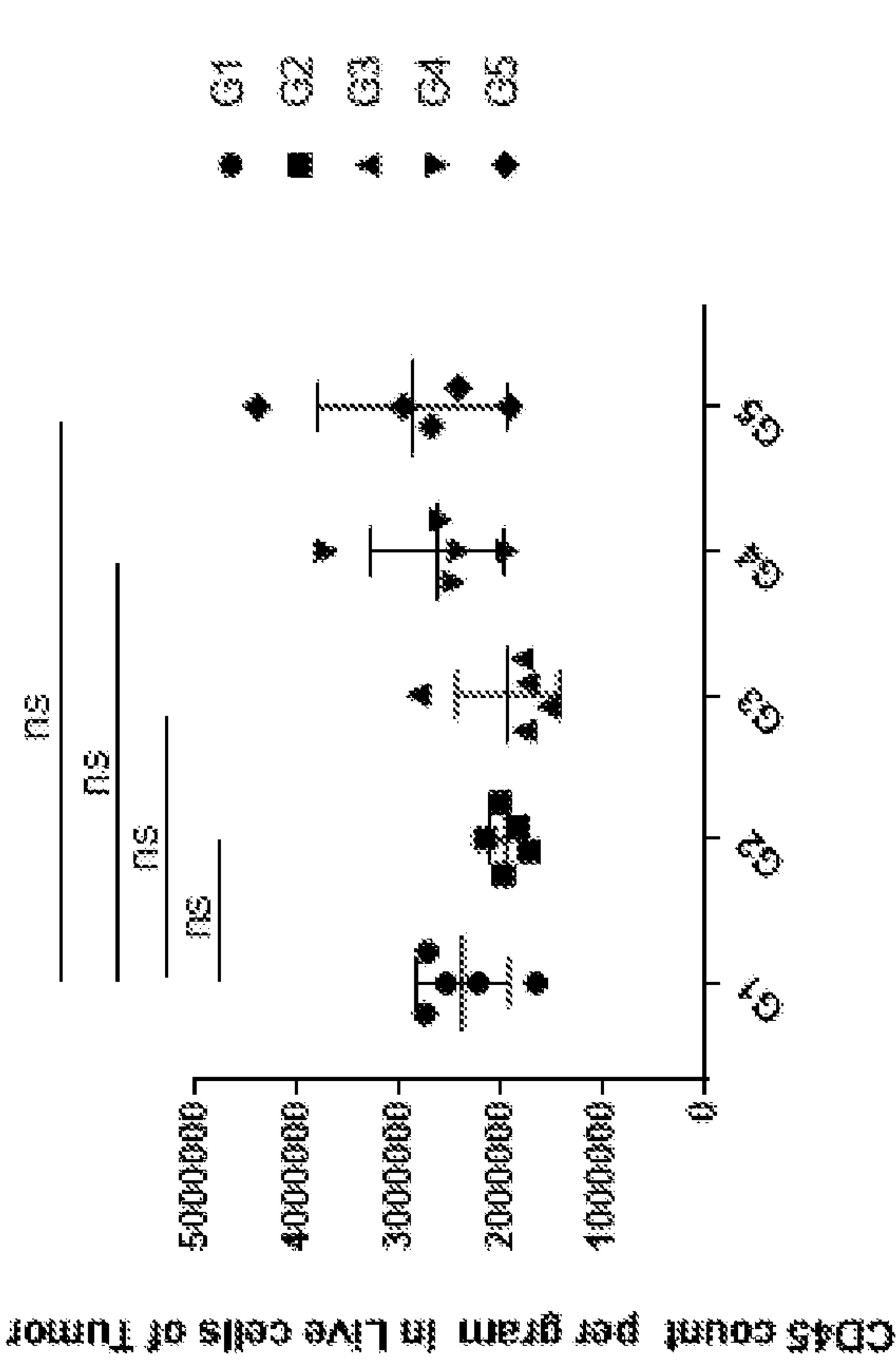


FIG. 78B

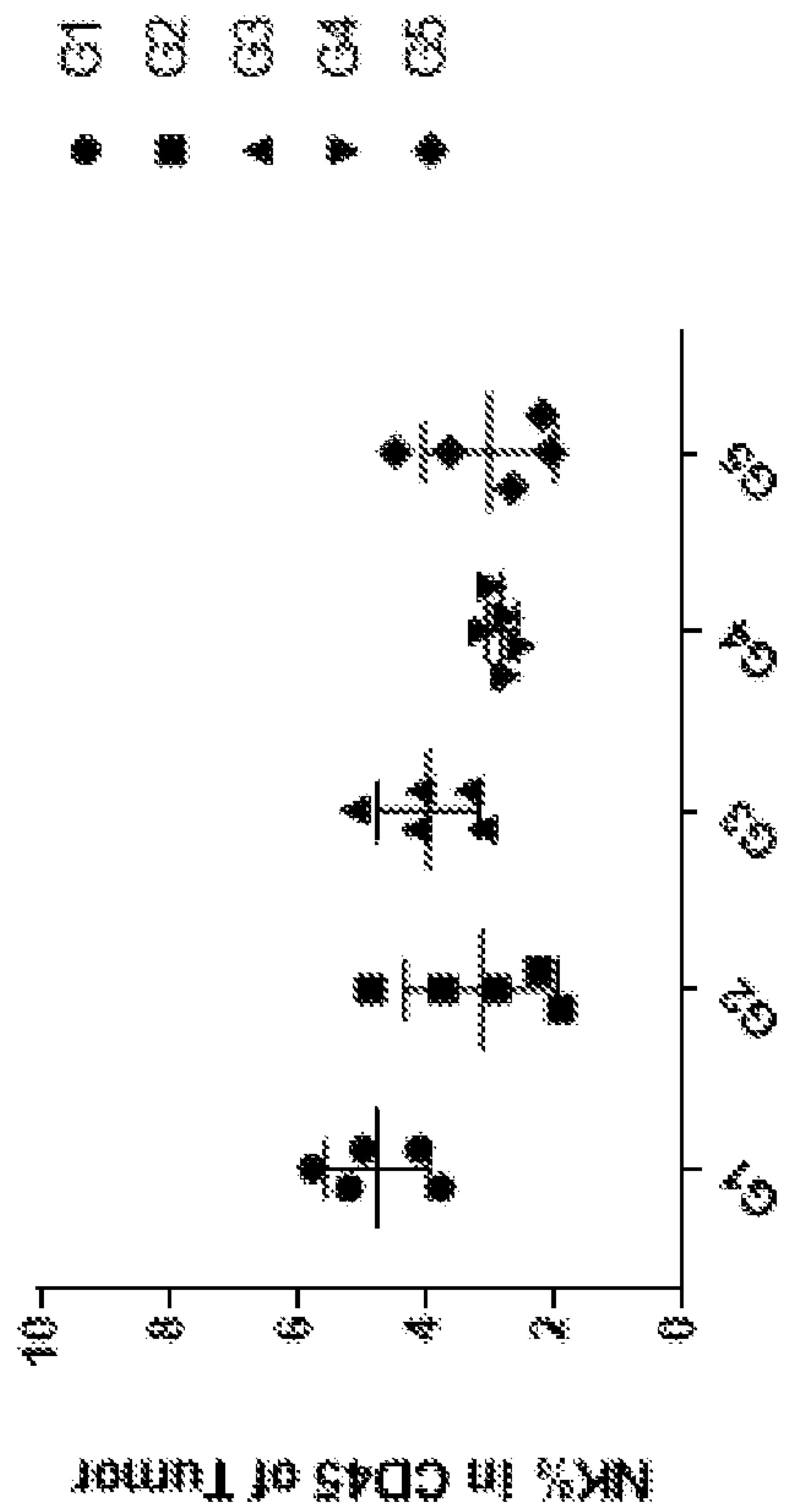


FIG. 78D

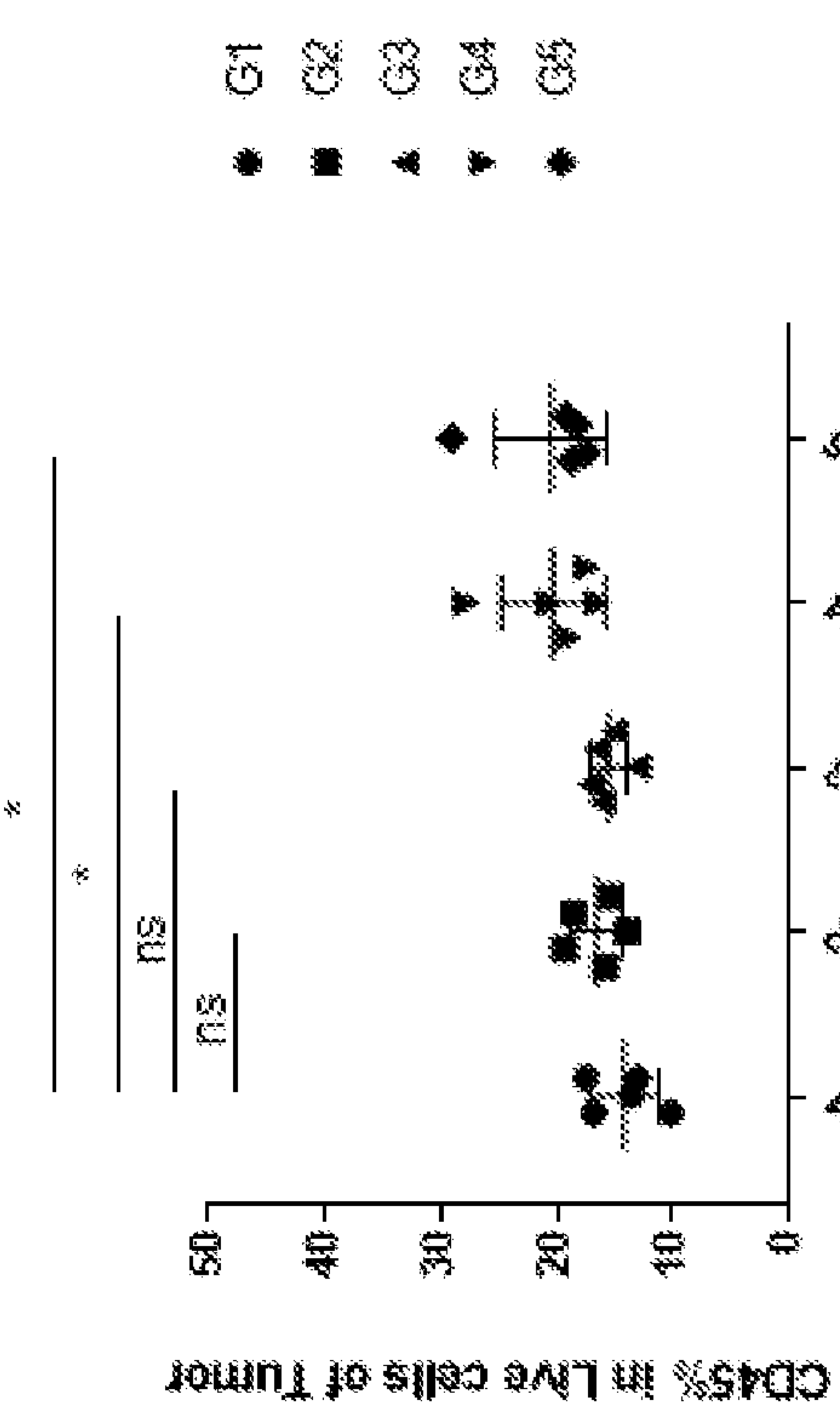


FIG. 78A

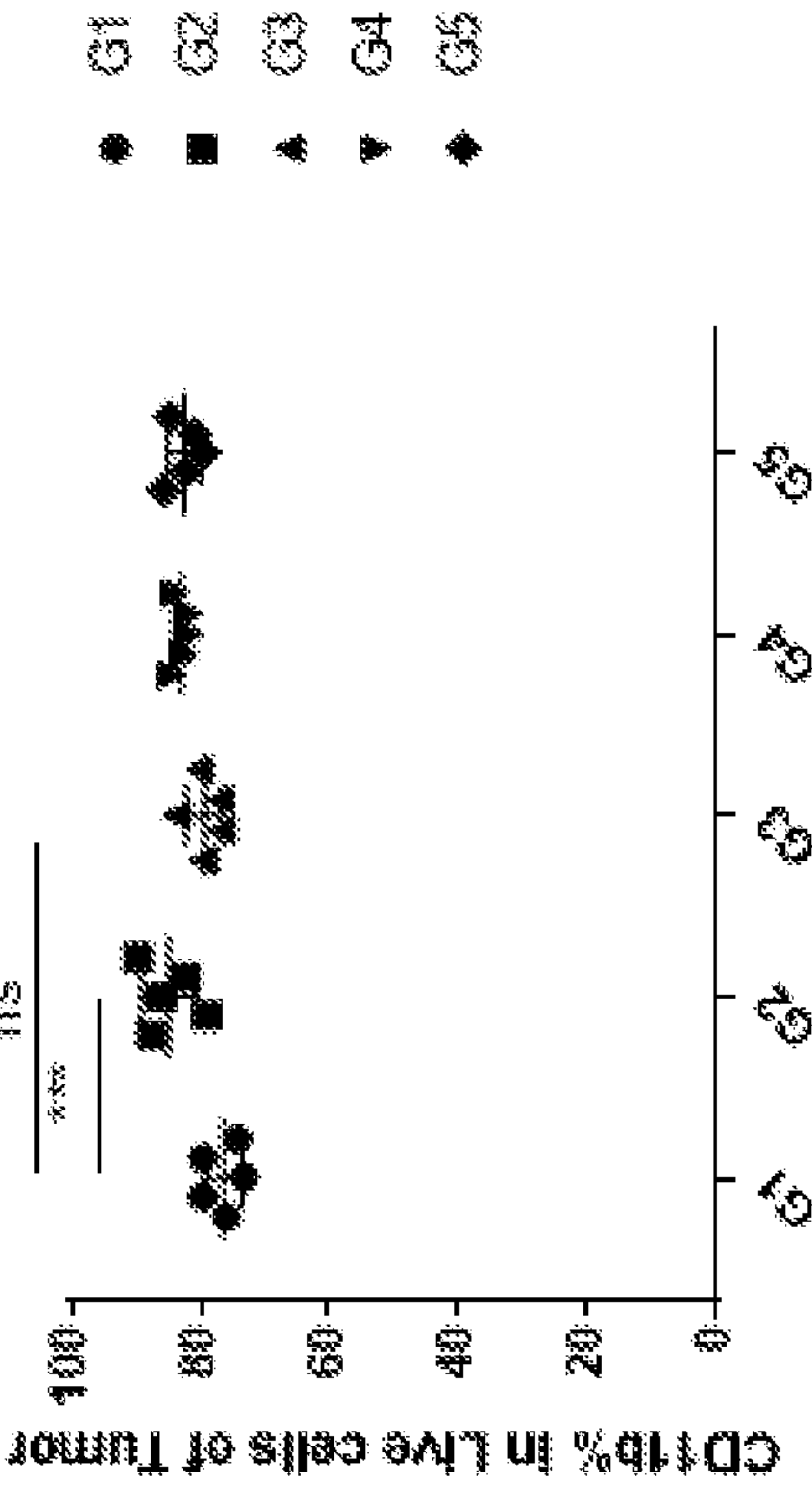


FIG. 78C

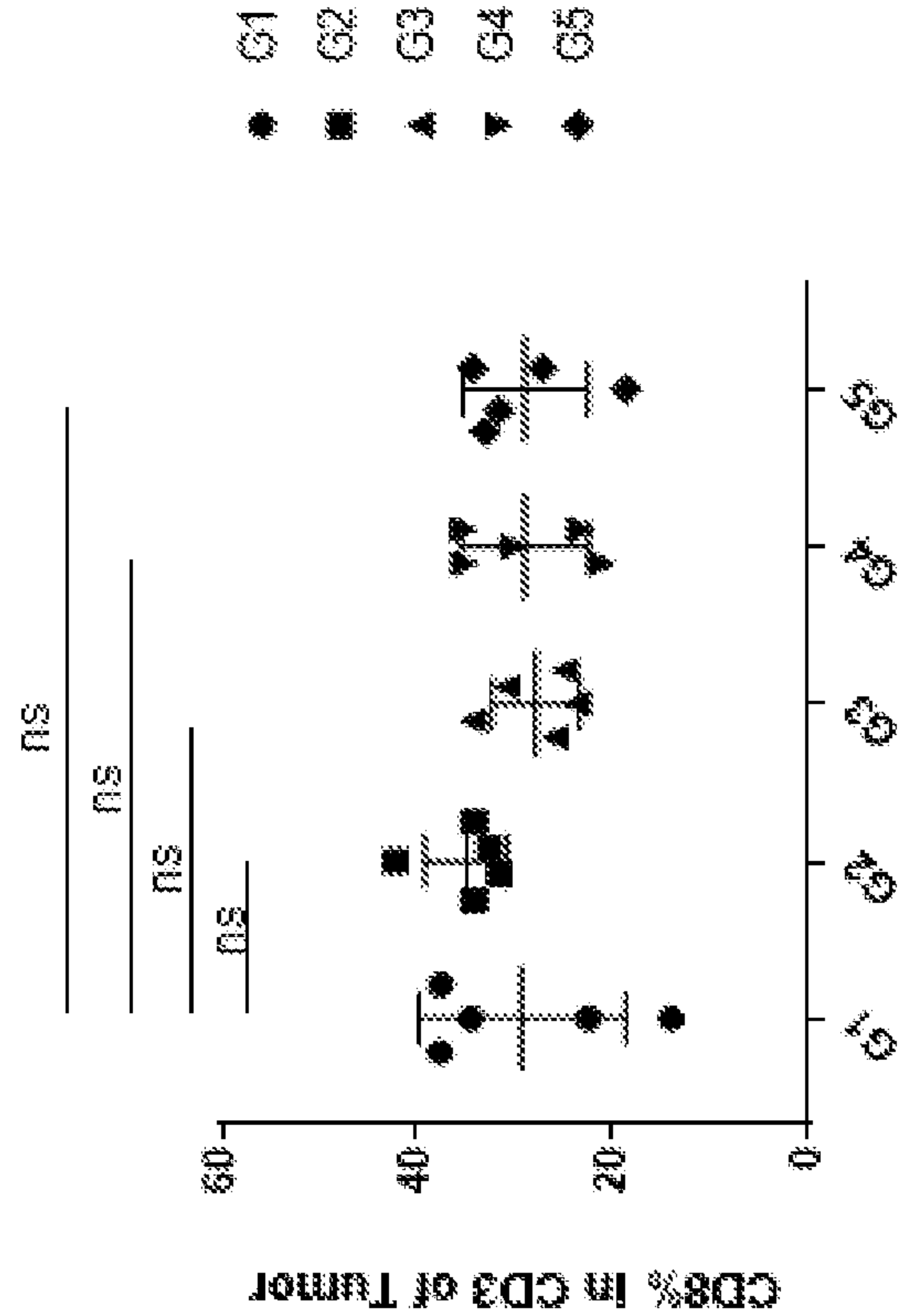


FIG. 79B

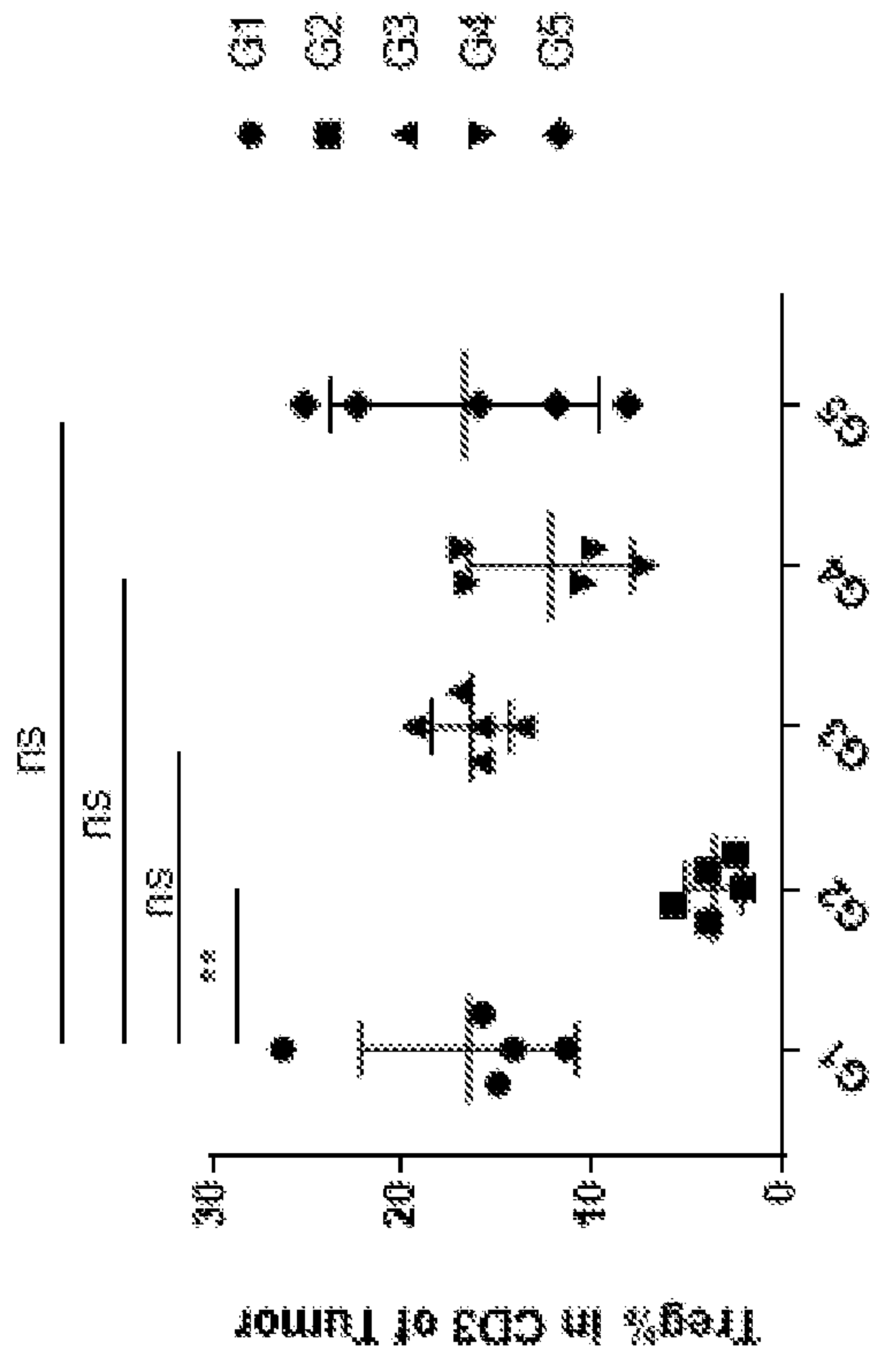


FIG. 79D

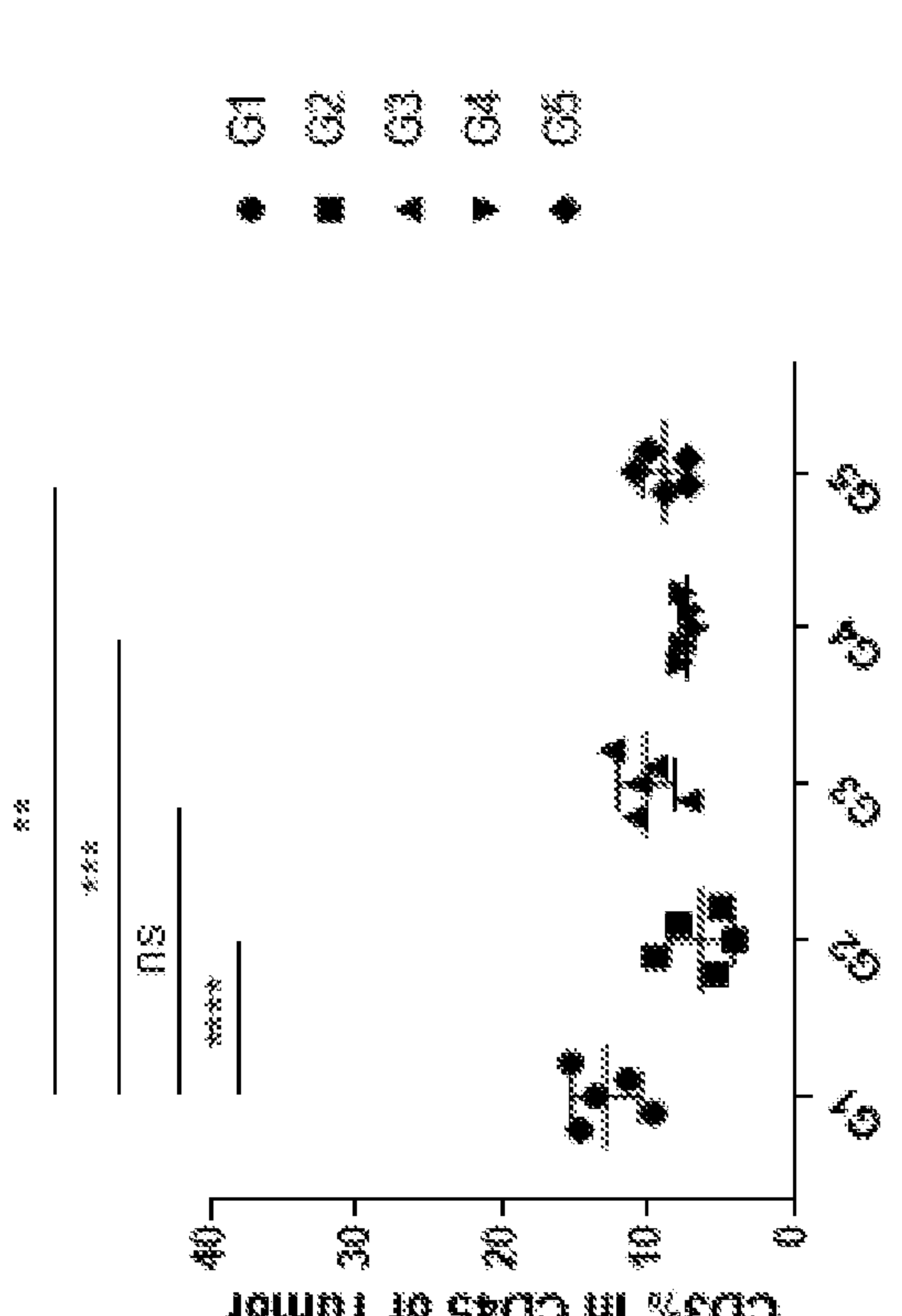


FIG. 79A

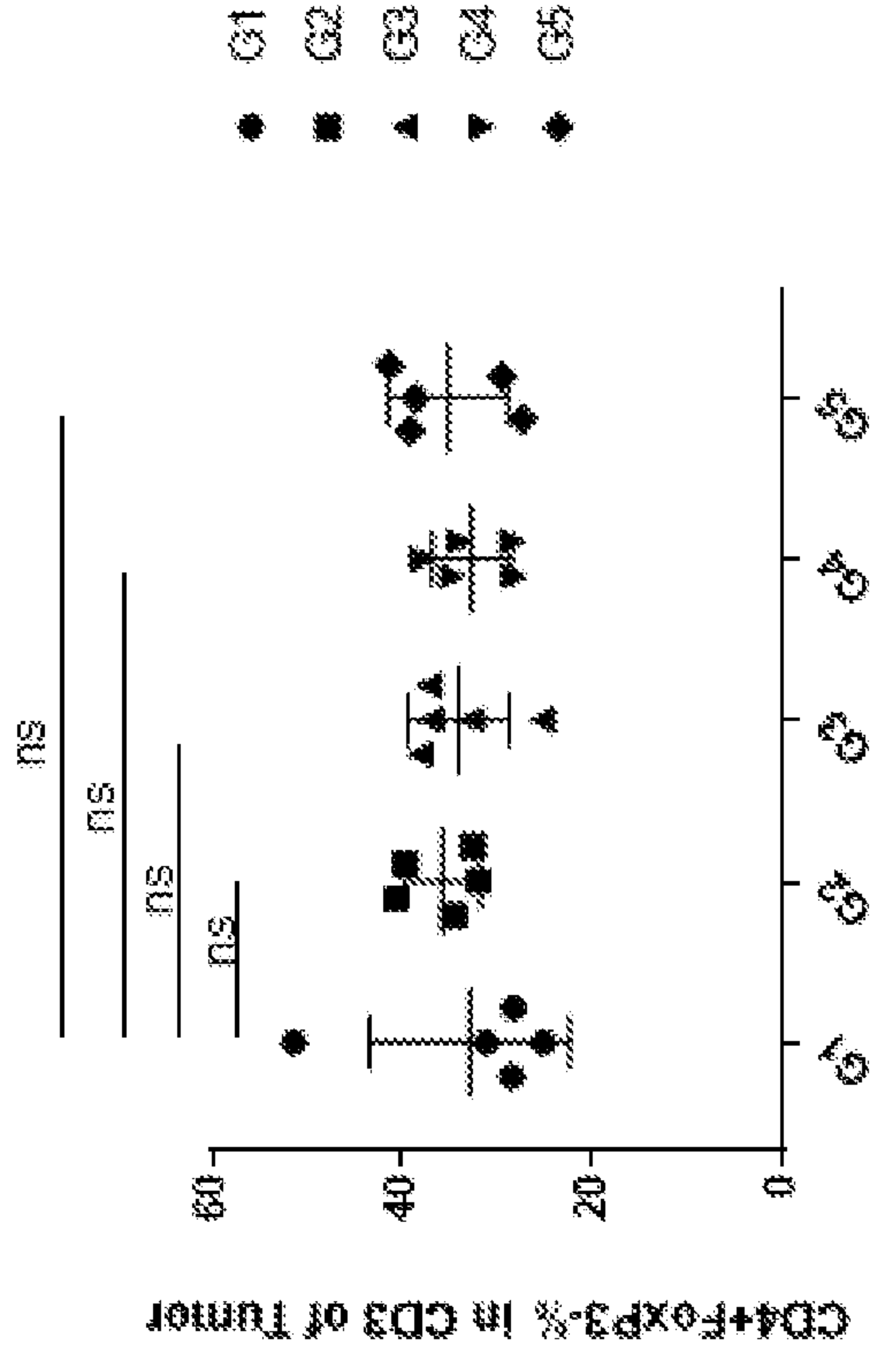


FIG. 79C

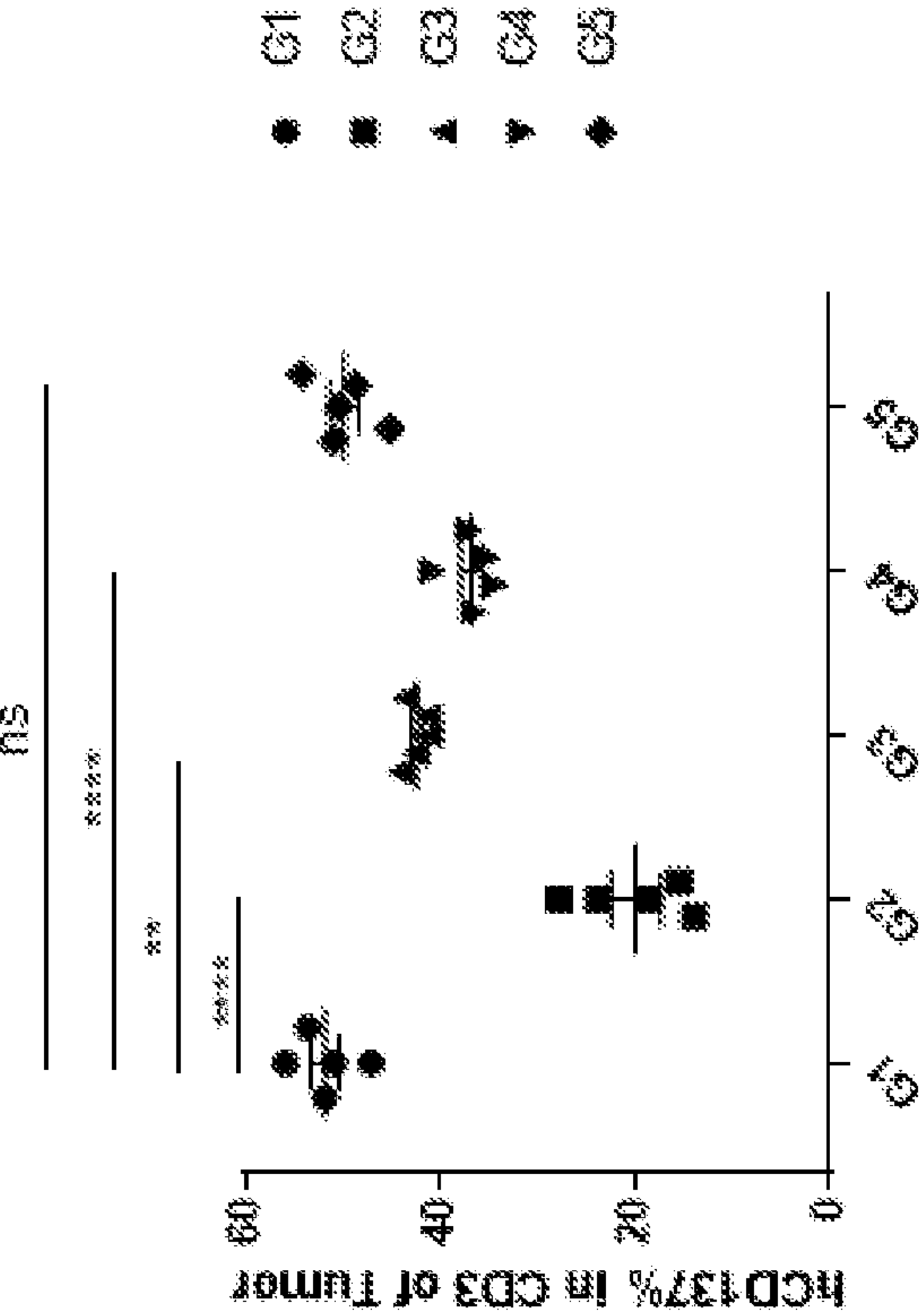


FIG. 80B

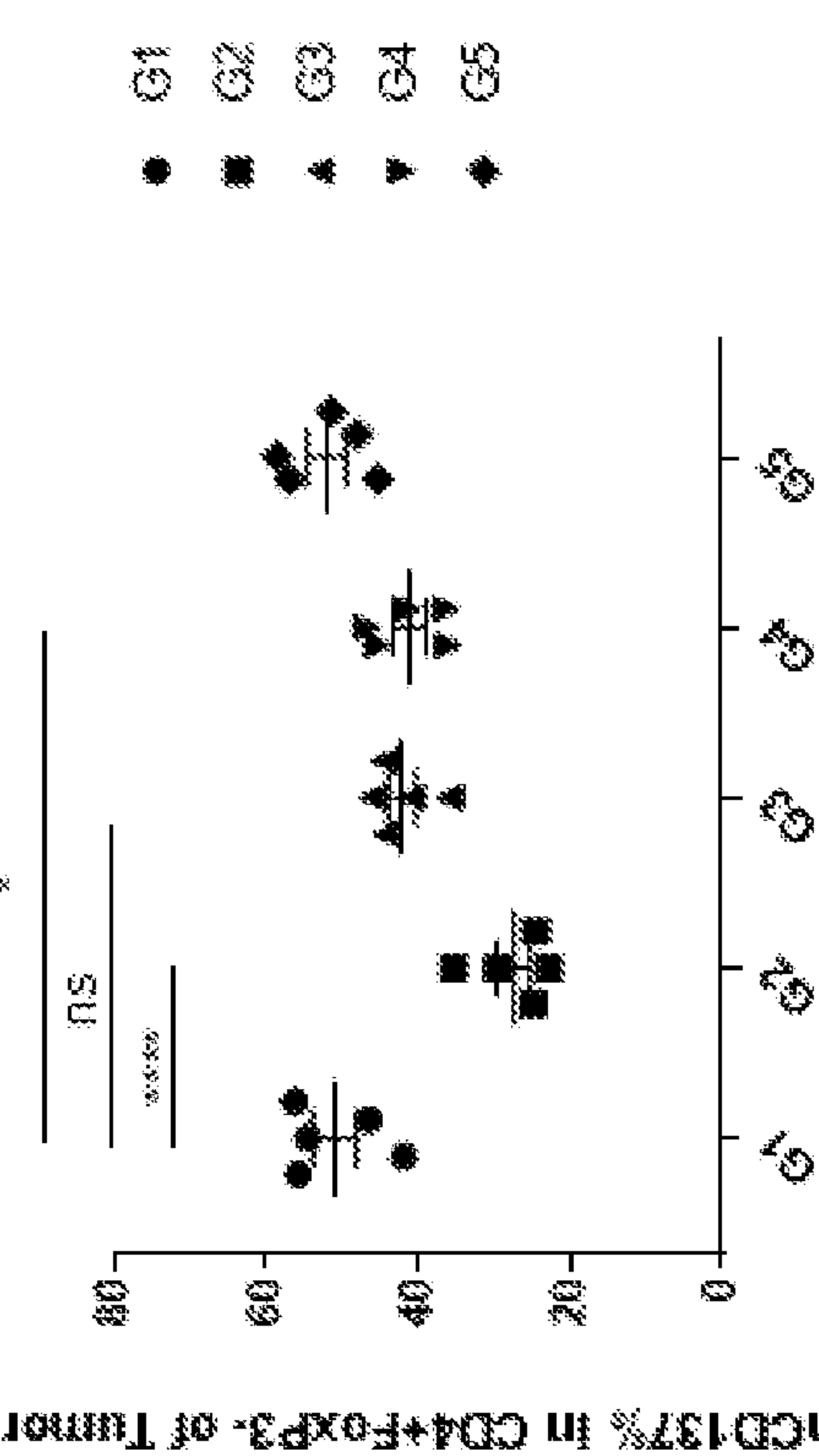


FIG. 80D

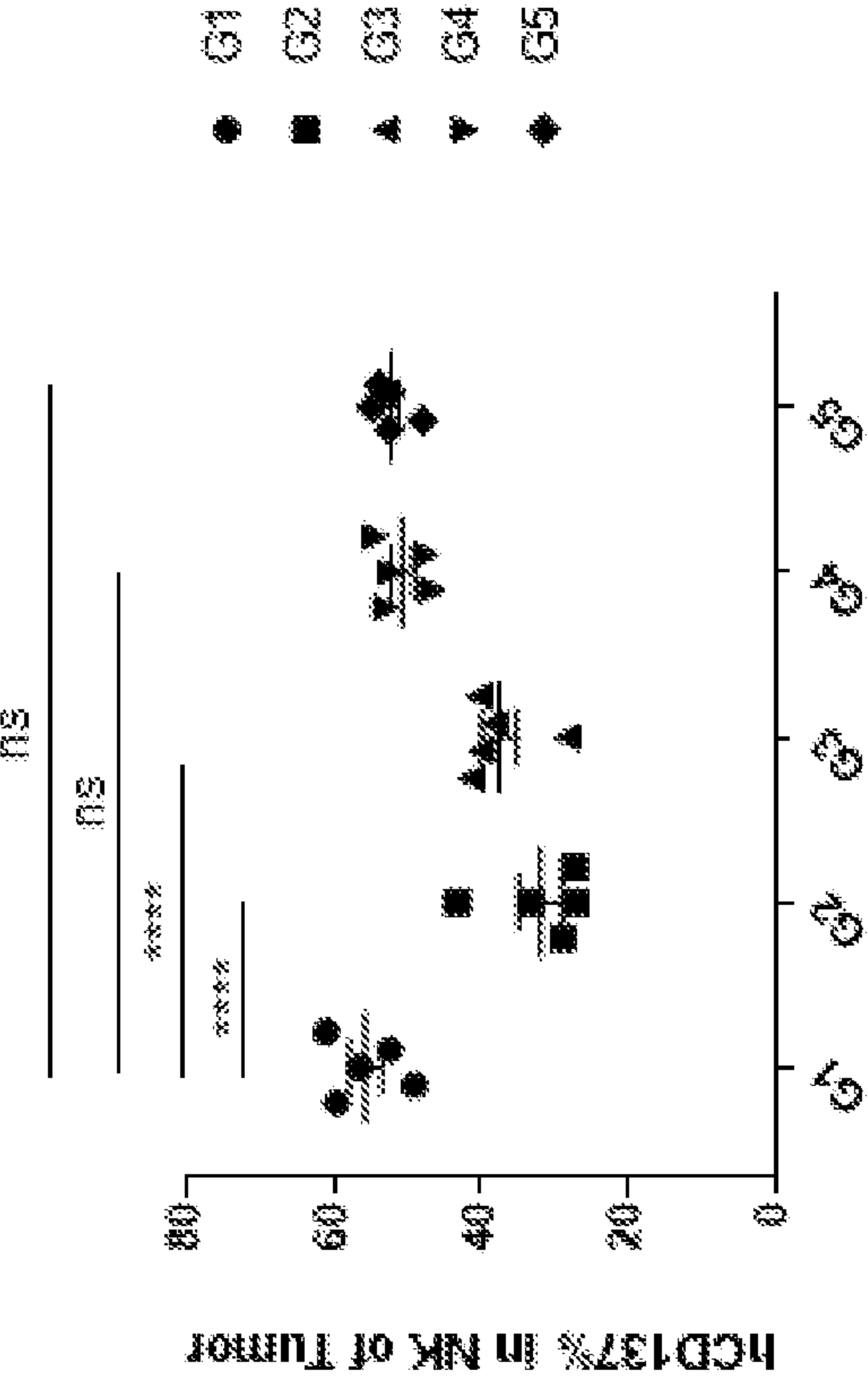


FIG. 80A

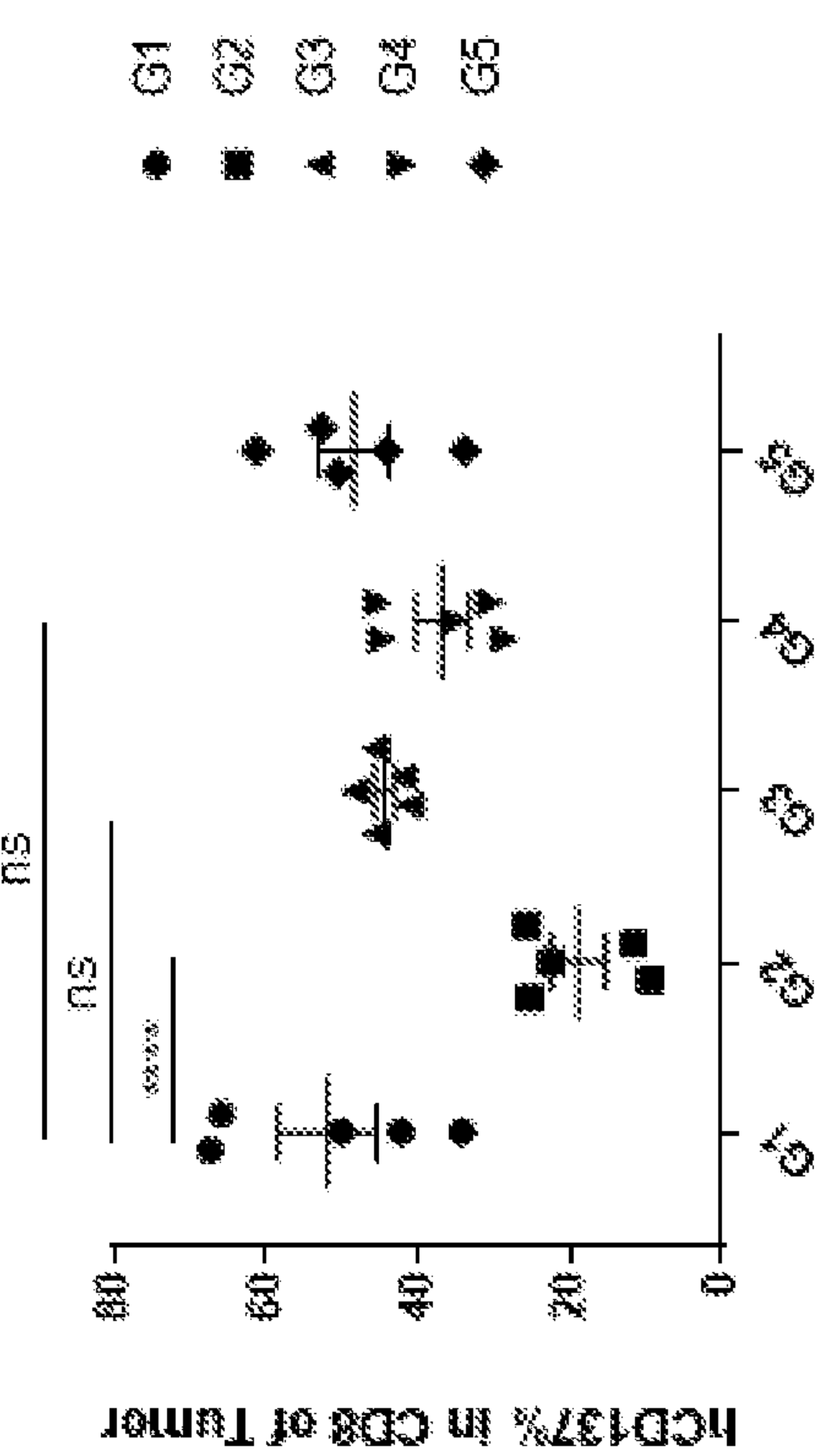


FIG. 80C

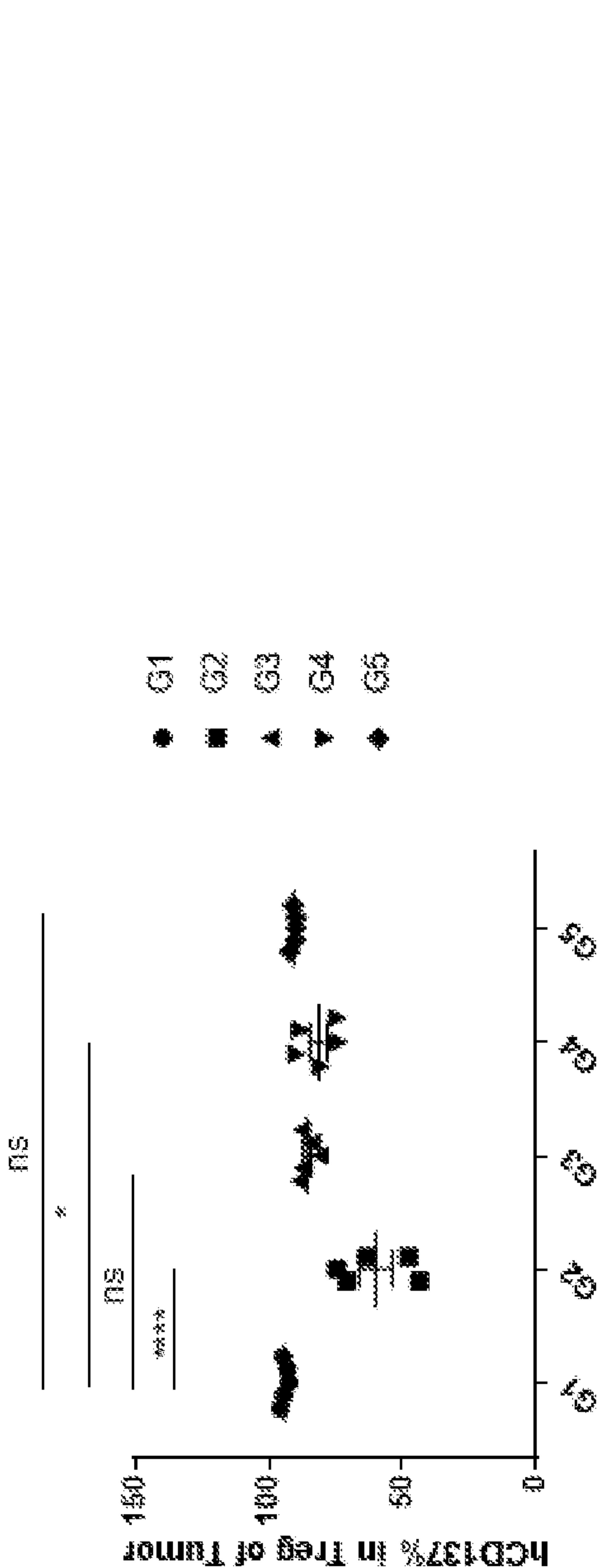


FIG. 80E

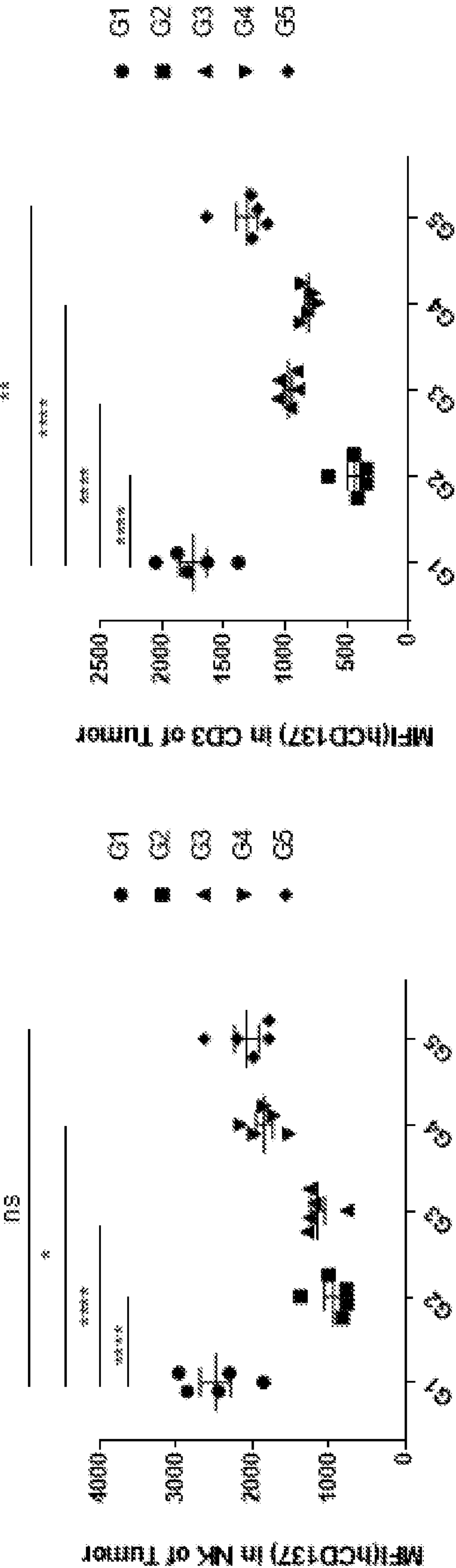
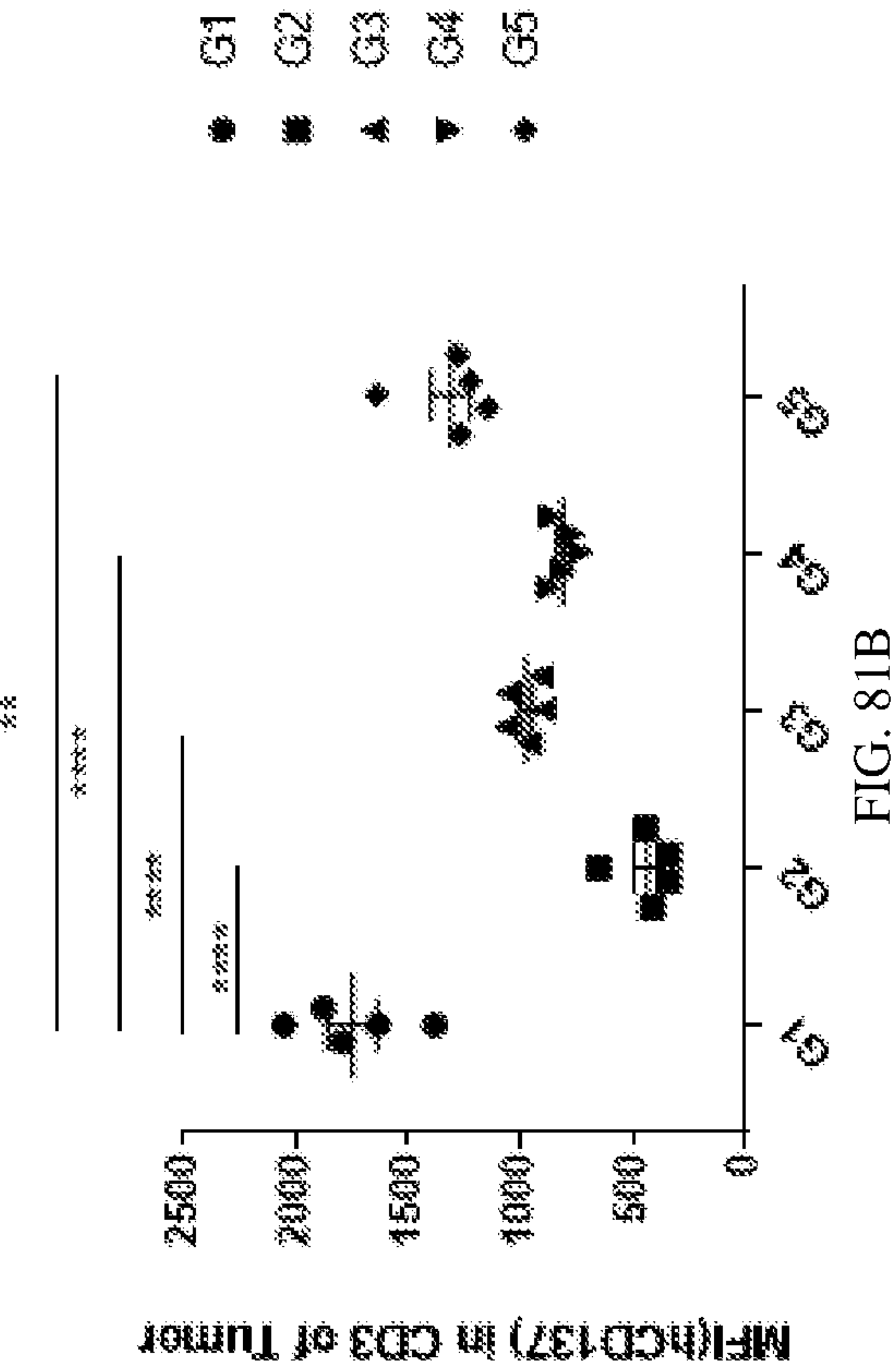


FIG. 81A



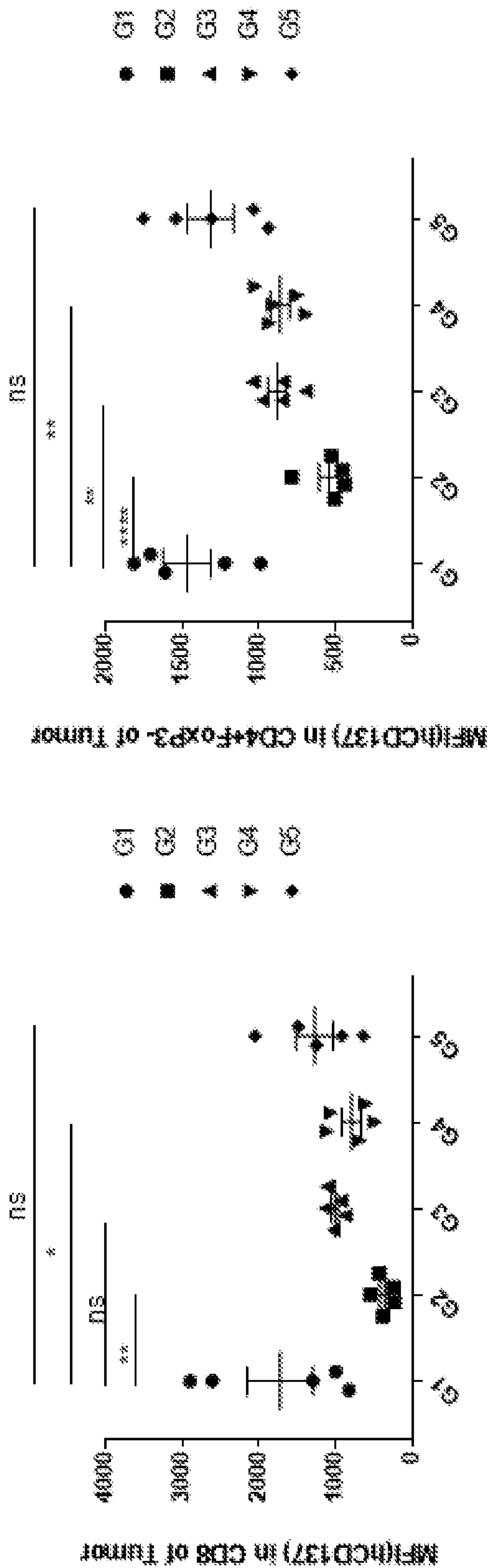


FIG. 81D

FIG. 81C

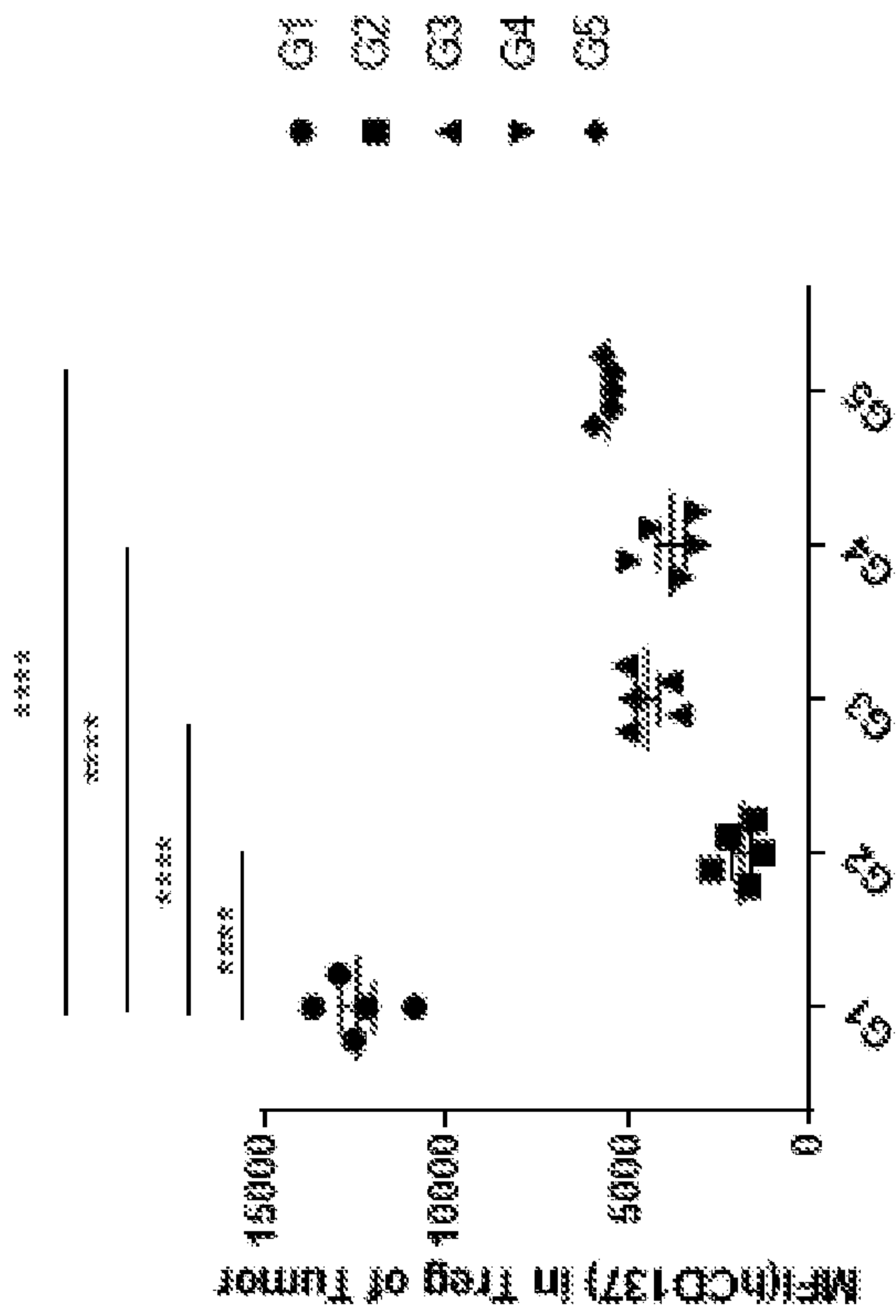


FIG. 81E

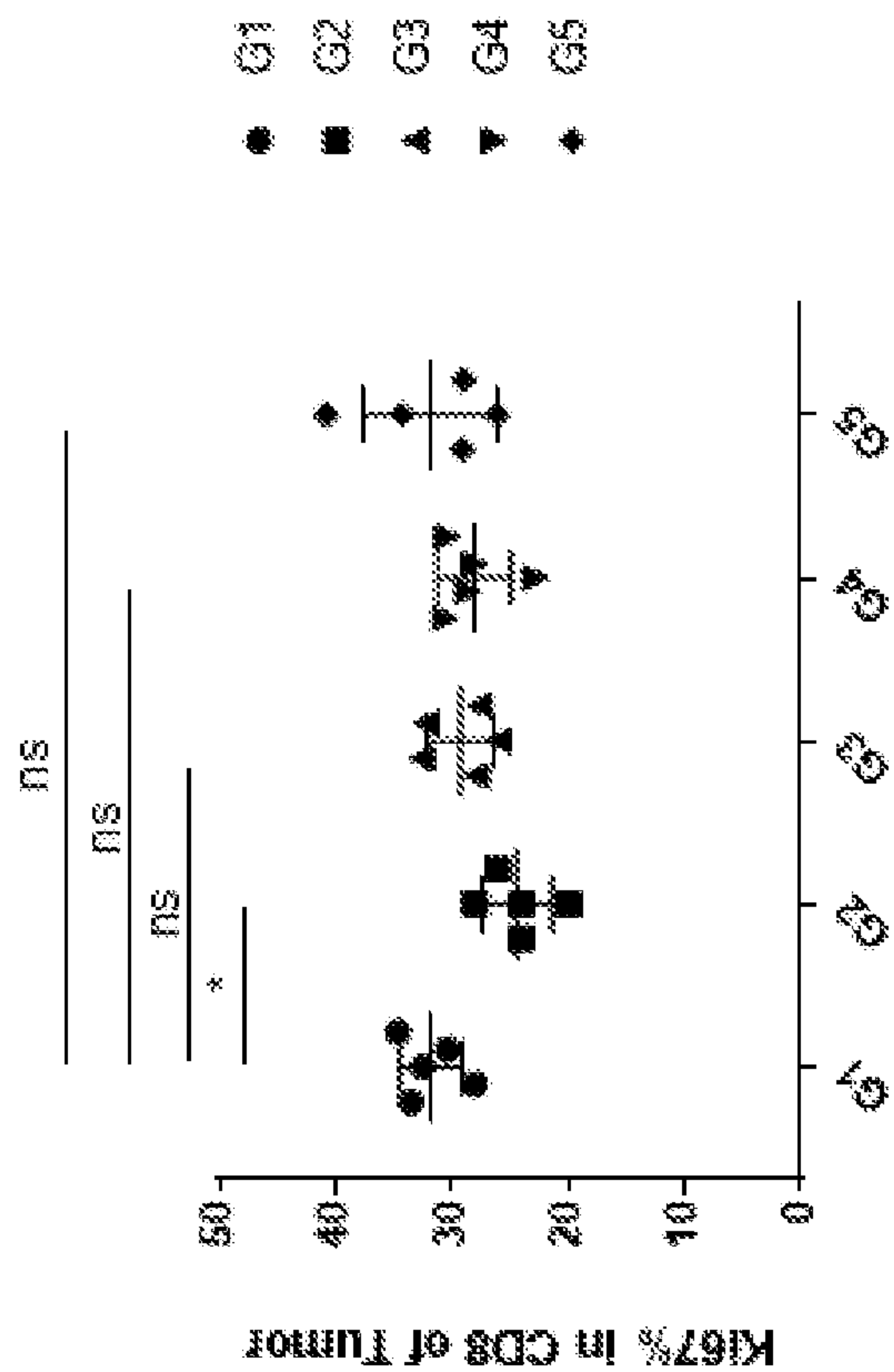


FIG. 82B

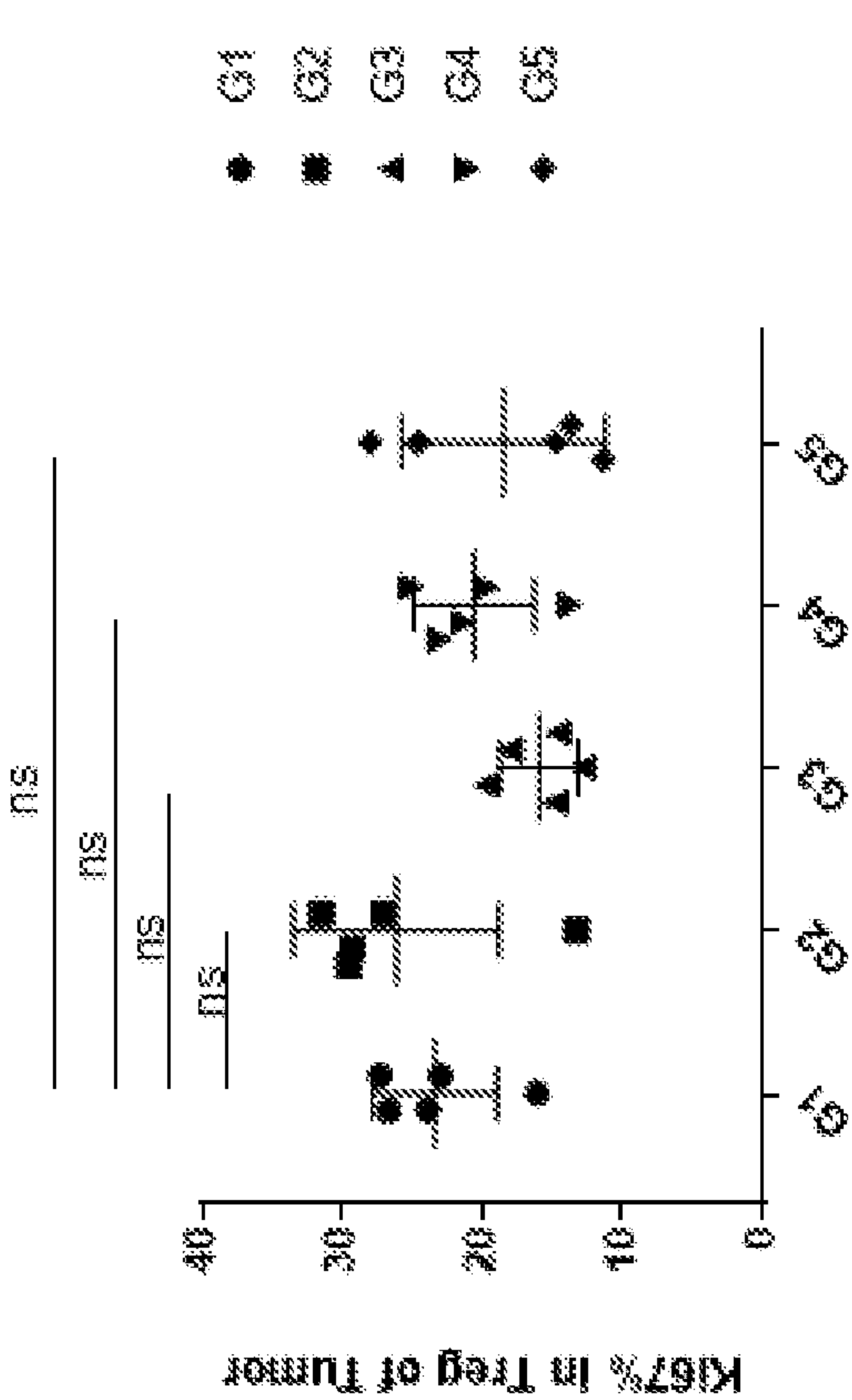


FIG. 82C

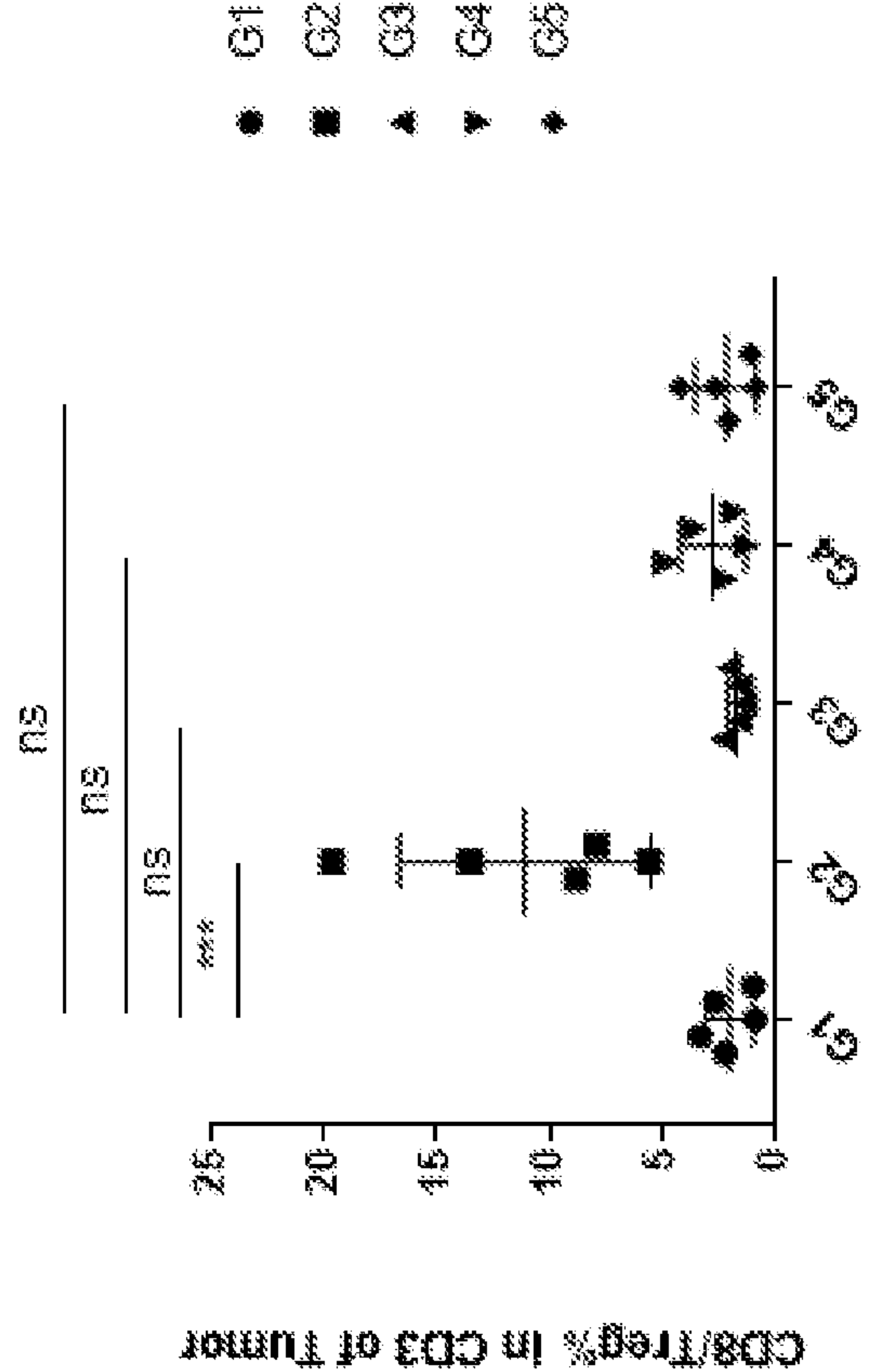
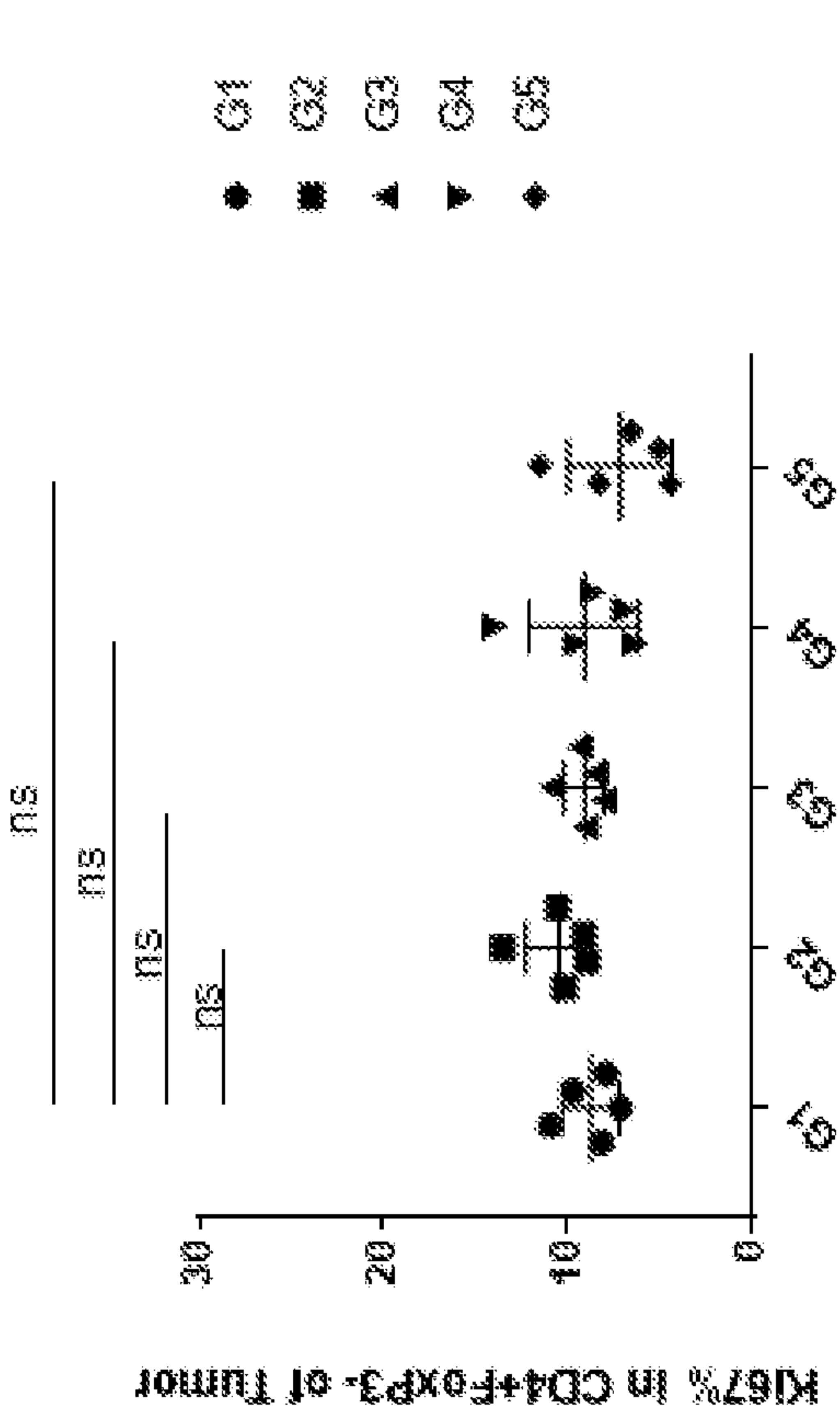


FIG. 82D



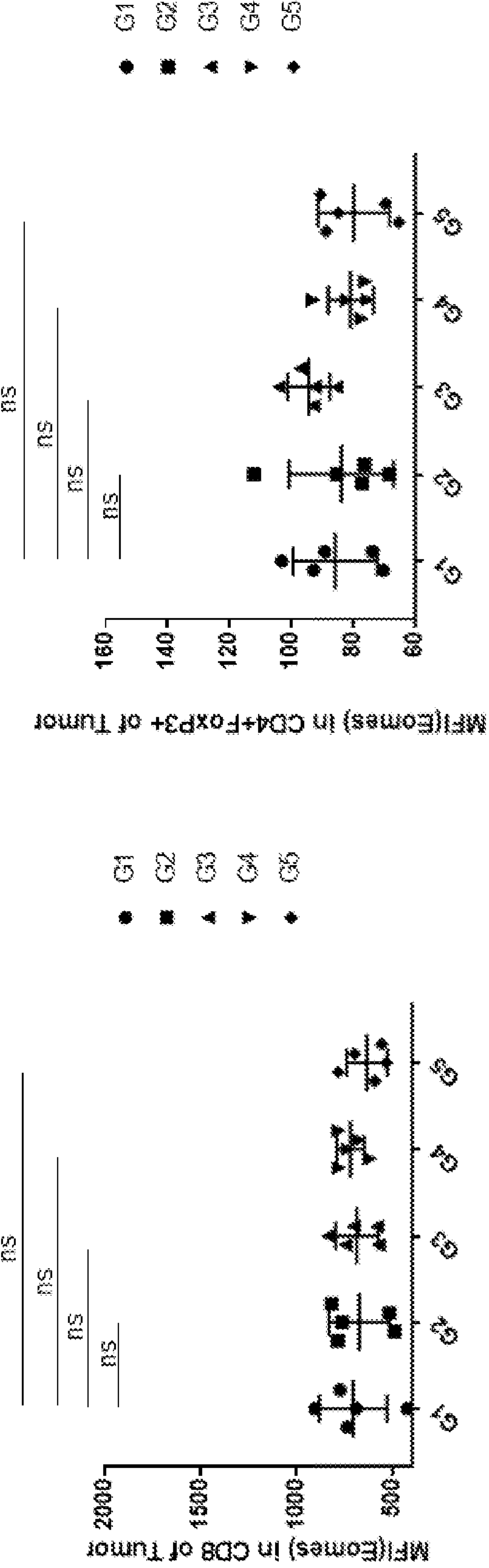


FIG. 83A

FIG. 83B

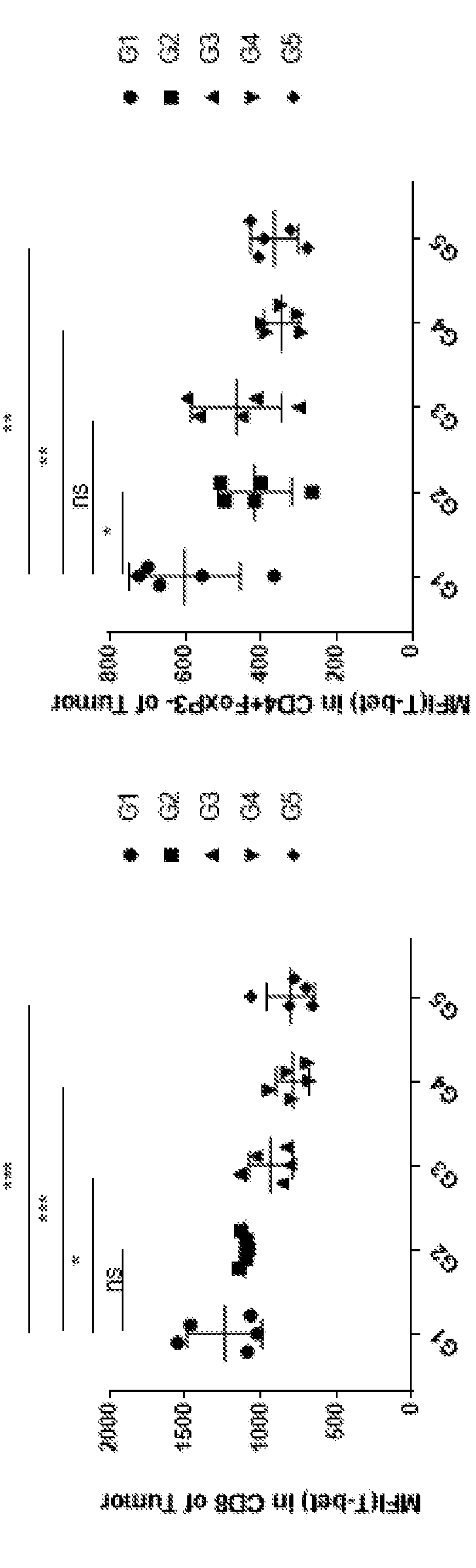


FIG. 83C

FIG. 83D