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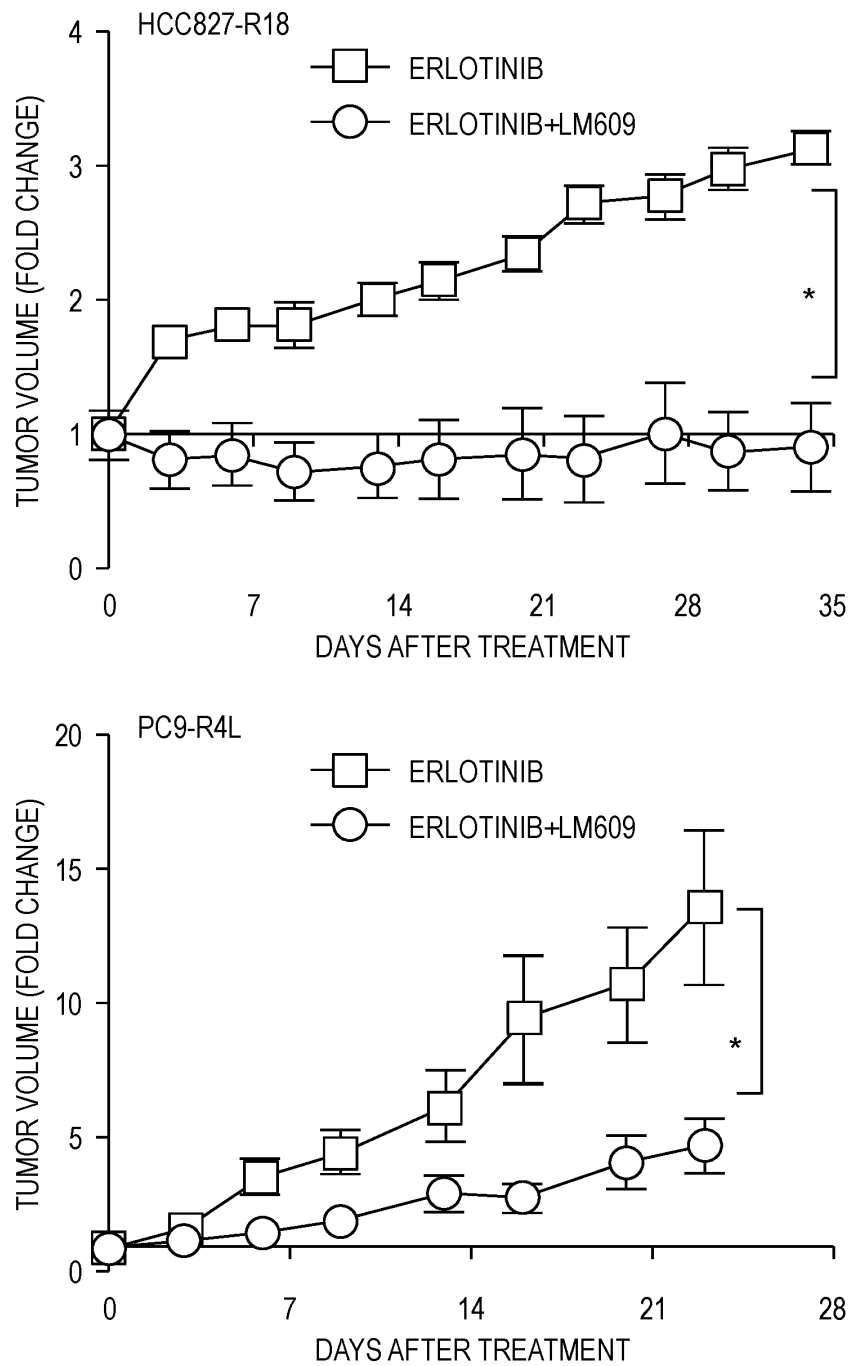


FIG. 1

mAb LM609-mIgG1			
H-GAMMA-1		HEAVY CHAIN: AMINO ACID SEQUENCE (460 AA)	
		SIGNAL PEPTIDE-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-CONSTANT REGION-STOP CODON	
VH	1-117	MNFGRLRI FLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQI PEKRLEWV AKVSSGGGSTYYLDTVQGRFTISRDNAKNTLYLQMSLSNSEDAMYYCARHNYGSFAYWGQGTLLTVV SA	
CH1	118-215	AKTTPPSVYPLAPGSAAQTNMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLS SSVTVPSSSTWPSETVTCNVAHPASSTKVDKKI	
HINGE		VPRDCGCKPCICT	
CH2	231-340	VPEVSSVFI FPPKPKDVLITIL TPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCR VNSAAFPAPIEKTISKTK	
CH3	341-445	GRP KAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITV EWQWNGQPAE NYKNTQPIMDTDGSYFVYSKLNQKSNWEAGNTFTCSVLHEGLHHHTEKSLSHSP	
CS	341-445	GK	
L-KAPPA		LIGHT CHAIN: AMINO ACID SEQUENCE (234 AA)	
		SIGNAL PEPTIDE-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-CONSTANT REGION-STOP CODON	
V-KAPPA	1-107	MVF T P Q I L G L M L F W I S A S R G D I V L T Q S P A T L S V T P G D S V S L S C R A S Q S I S N H L H W Y Q Q K S H E S P R L L I K Y A S Q S I S G I P S R F S G S G S G T D F T L S I N S V E T E D F G M Y F C Q Q S N S W P H T F G G G T K L E I K R A D A A P T	
C-KAPPA	108-214	V S I F P P S S E Q L T S G G A S V V C F L N N F Y P K D I N V K W K I D G S E R Q N G V L N S W T D Q D S K D S T Y S M S S T L T L T K D E Y E R H N S Y T C E A T H K T S T S P I V K S F N R N E C	

FIG. 2

hLM609-hlgG1-WT

IMGT.ORG CHAIN ID: INN 8862_H

H-GAMMA-1 (VH (1-117)[D1]+CH1 (118-215)[D2]+CH2 (231-340)[D3]+CH3 (341-445)[D4])

QVQLVESGGGVVQPGRSLRLSCAASGFTSSYDMSWVRQAPGKGLEWVAKVSSGGSTYY 60

LDTVQGRFTISRDNKNTLYLQMNSLRAEDTAVYFCARHLHGSFASWGQGT'TVTVSSAST 120

KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

SLSSVTVFPSSSLGTQYICNVNHPKPSNTKVDKRVKPKSCDKTHTCPPCPAPELLGGPSV 240

FLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 300

RVVSVLTVQLHQLDNLNGKEYCKKVSNAKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTK 360

NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG 420

NVFSCSVMEALHNHYTQKSLSLSPGK 447

IMGT.ORG CHAIN ID: INN 8862_L

L-KAPPA (V-KAPPA (1-107)[D1]+C-KAPPA (108-214)[D2])

EIVLTQSPATLSLSPGERATLSCQASQSI SNFLHWYQQRPQGAPRLLIRYRSQISGIPA 60

RFSGSGGTDFLTITSSLEPEDFAVYQCQSGSWPLTFGGGTKEIKRTVAAPSVFIFPP 120

SDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLT 180

LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

FIG. 3

[illegible][illegible]

FIG. 4

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hLM609-hIgG4-S228P

H-GAMMA-1 (VH (1-117)[D1]+CH1 (118-215)[D2]+CH2 (231-340)[D3]+CH3 (341-445)[D4])

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVS
SGGGSTYYLDTVQGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARHLHGSF
ASWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSN
TKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTC
LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE
GNVFSCSVMHEALHNHYTQKSLSLSLGK

L-KAPPA (V-KAPPA (1-107)[D1]+C-KAPPA (108-214)[D2])

EIVLTQSPATLSLSPGERATLSCQASQSI SNFLHWYQQRPGQAPRLLIRYS
QSI SGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQSGSWPLTFGGGTKV
EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
FNRGEC

FIG. 5

SCORE	EXPECT	METHOD	IDENTITIES	POSITIVES	GAPS
816 BITS(2109)	0.0	COMPOSITIONAL MATRIX ADJUST.	418/447 (94%)	427/447 (95%)	3/447 (0%)
VH (1-117)					
hlgG1 WT	1	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVAKVSSGGGSTYY			60
hlgG4-S228P	1				60
VH (1-117)					
hlgG1 WT	61	LDTVQGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARHLHGSEFASWGQGTIVTVSSAST			120
hlgG4-S228P	61				120
CH1 (118-215)					
hlgG1 WT	121	KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY			180
hlgG4-S228P	121	C.R...ES.....			180
CH1 (118-215) HINGE CH2					
hlgG1 WT	181	SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCTPPCPAPELLGGPSV			240
hlgG4-S228P	181	K...T...D.....S.YGPPCPP.....F.....			237
CH2 (231-340)					
hlgG1 WT	241	FLFPPKPKDTIMI SRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY			300
hlgG4-S228P	238	Q.....Q.....F.....			297
CH2 (231-340) CH3 (341-445)					
hlgG1 WT	301	RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTK			360
hlgG4-S228P	298	G..SS.....Q.....			357
CH3 (341-445)					
hlgG1 WT	361	NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG			420
hlgG4-S228P	358	R.....E..			417
CH3 (341-445)					
hlgG1 WT	421	NVFSCVMHEALHNHYTQKSLSLSPGK			447
hlgG4-S228P	418	L... 444			444

FIG. 6

FIG. 6

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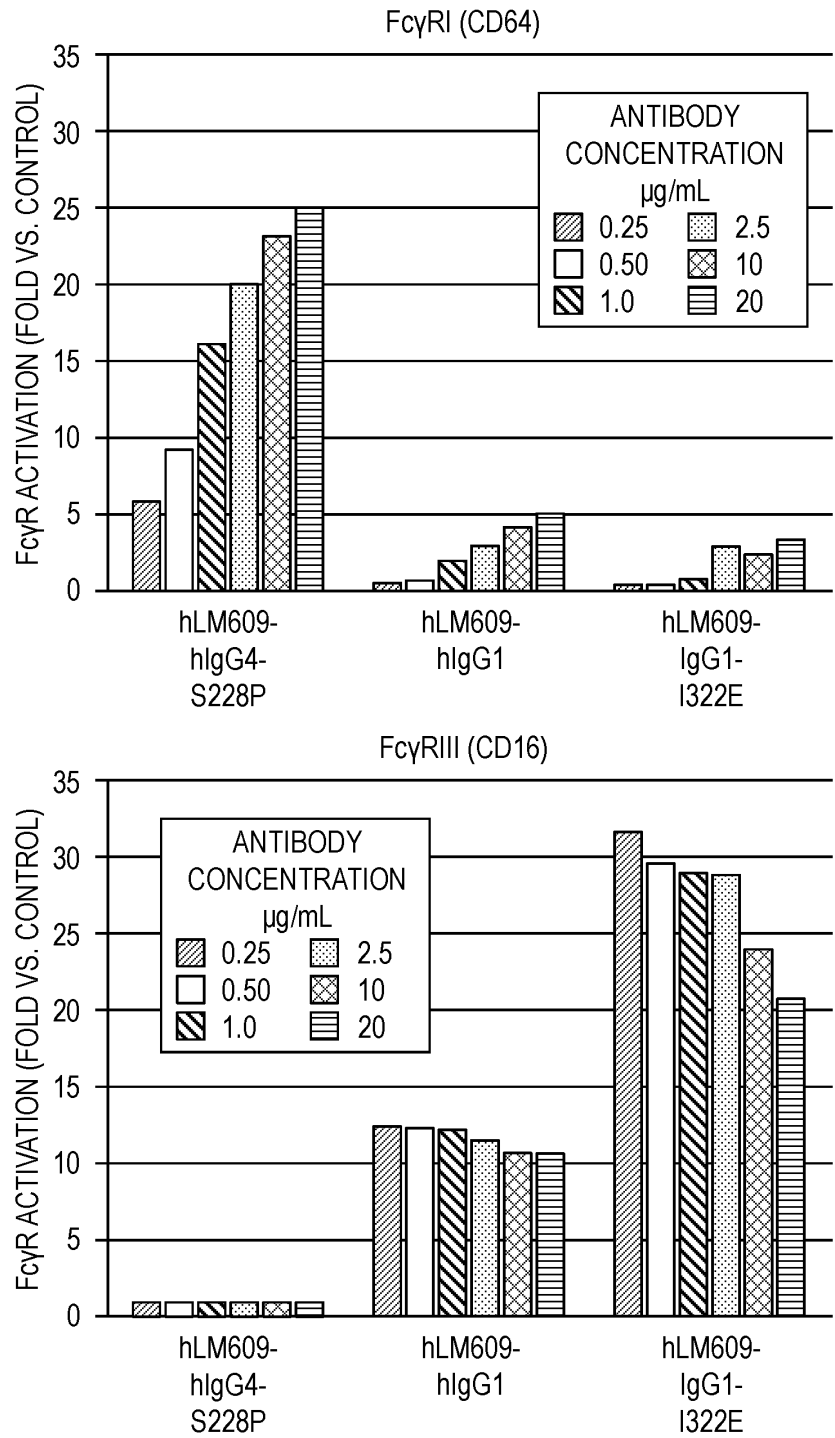


FIG. 7

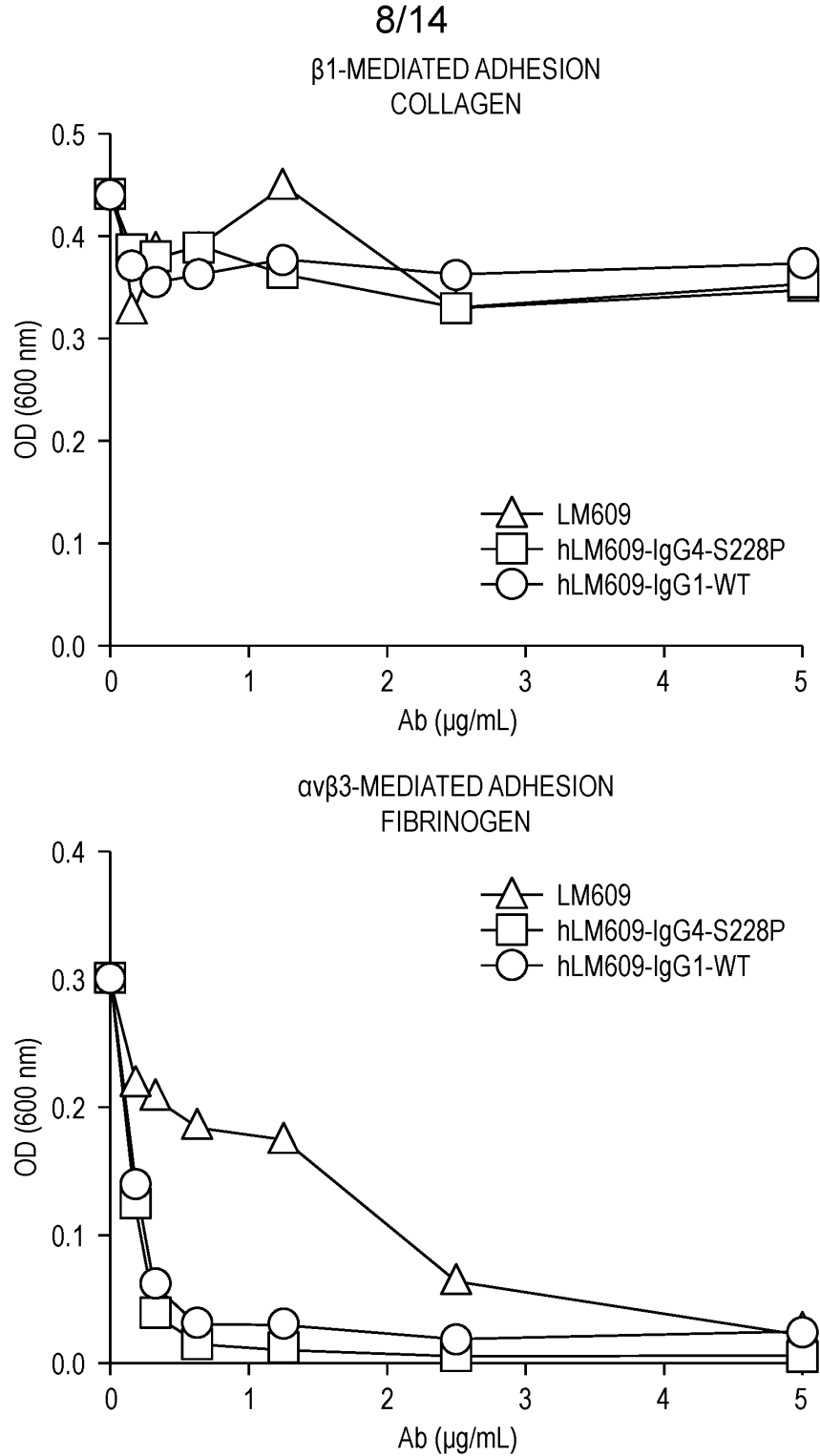


FIG. 8

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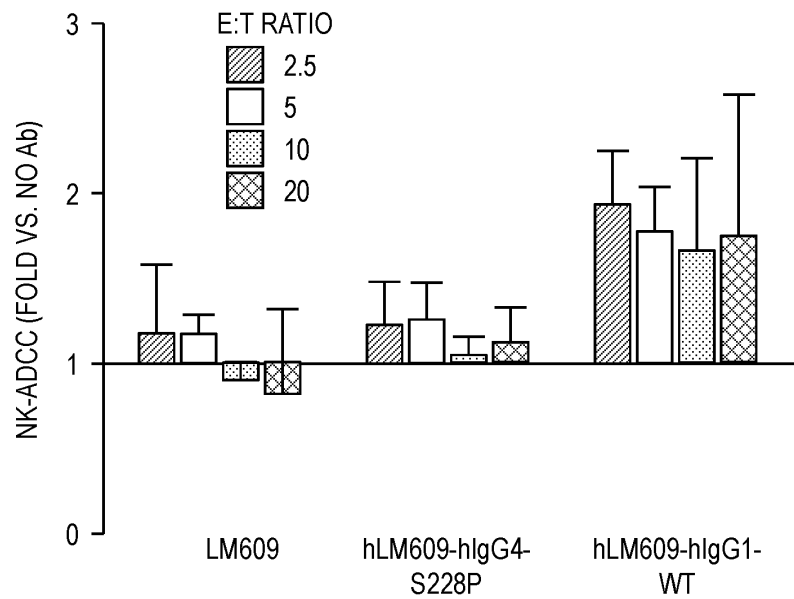


FIG. 9A

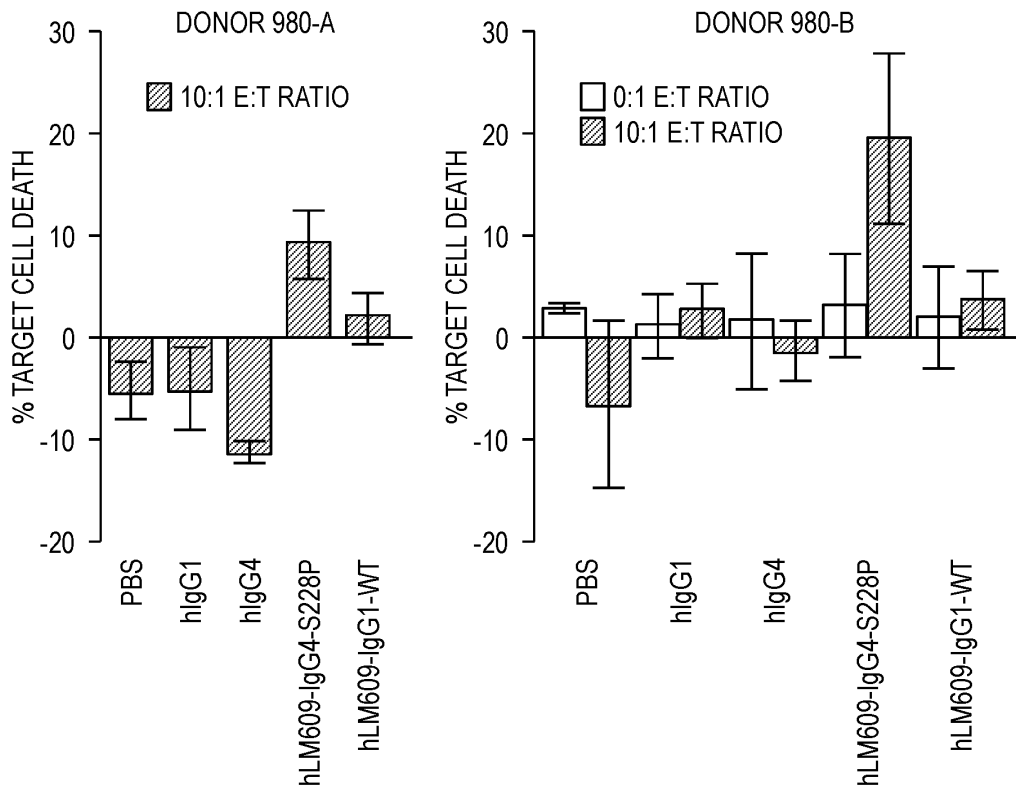
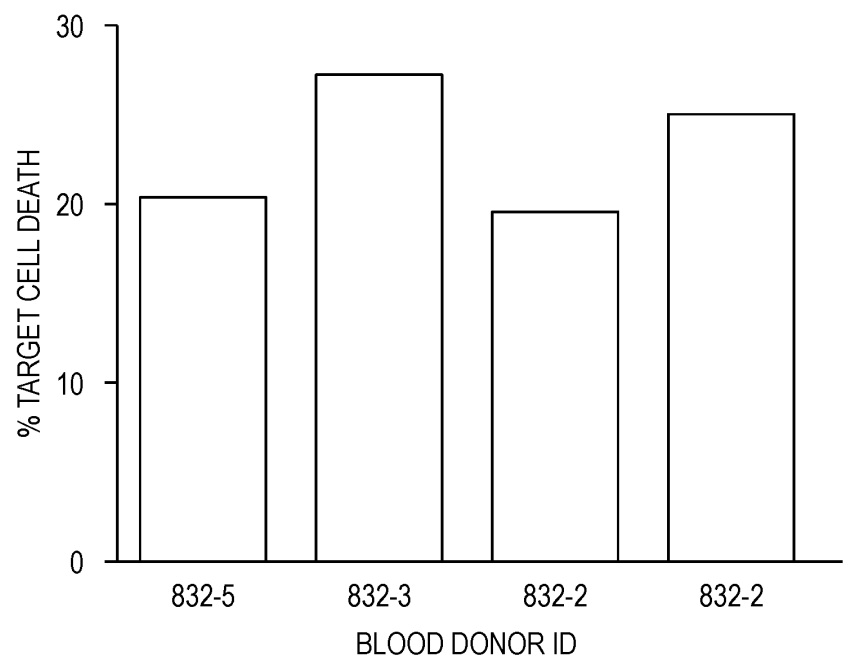


FIG. 9B

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MACROPHAGE-ADCC FOR hLM609-hIgG4-S228P

DONOR POLYMORPHIC VARIANTS:		
	<u>CD32</u>	<u>CD16</u>
832-2	H131 (HI)	F158 (LO)
832-3	H131 (HI)	F158/V158 (HET)
832-5	R131 (LO)	F158 (LO)

FIG. 9C

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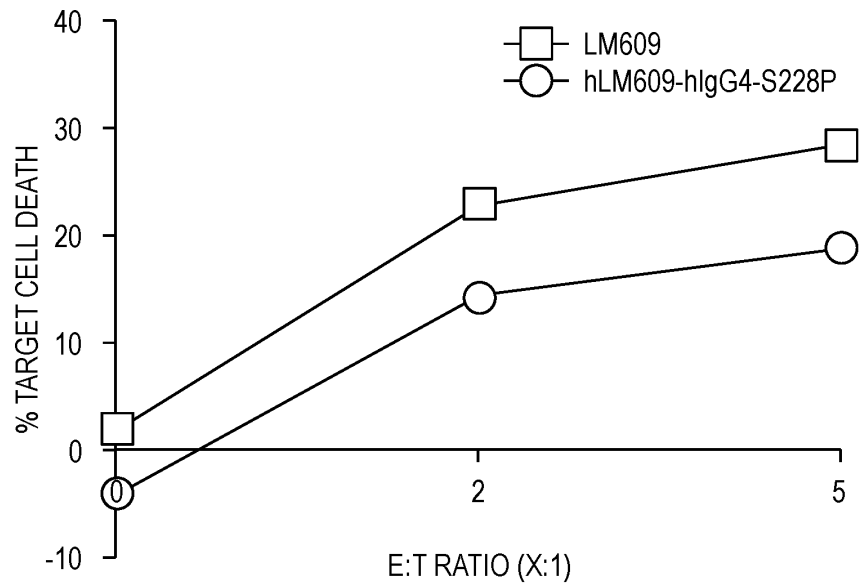


FIG. 10A

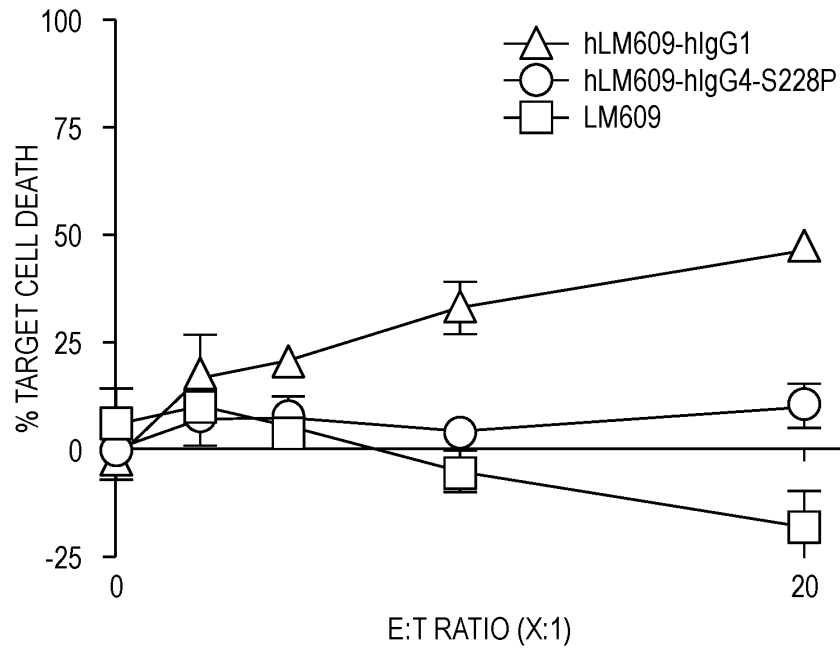


FIG. 10B

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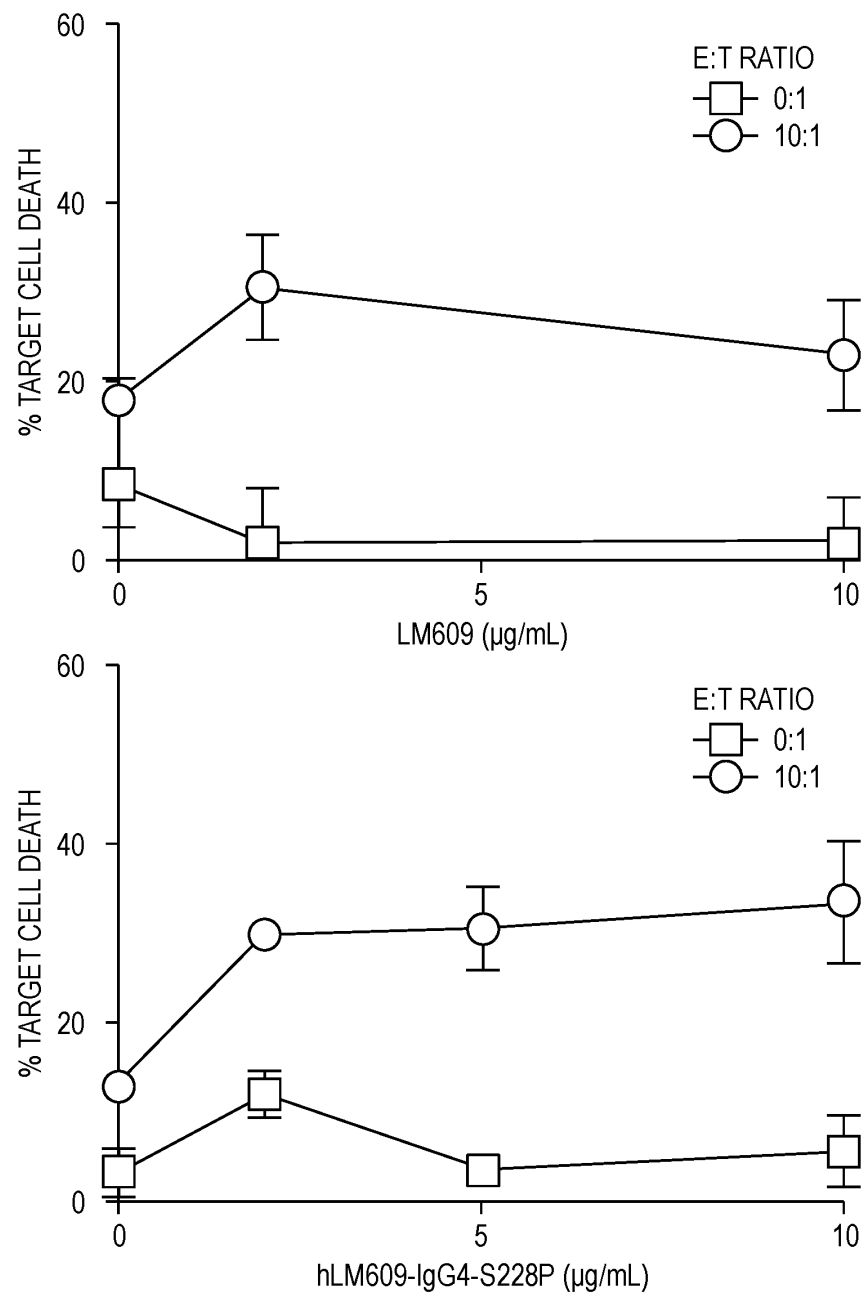


FIG. 11

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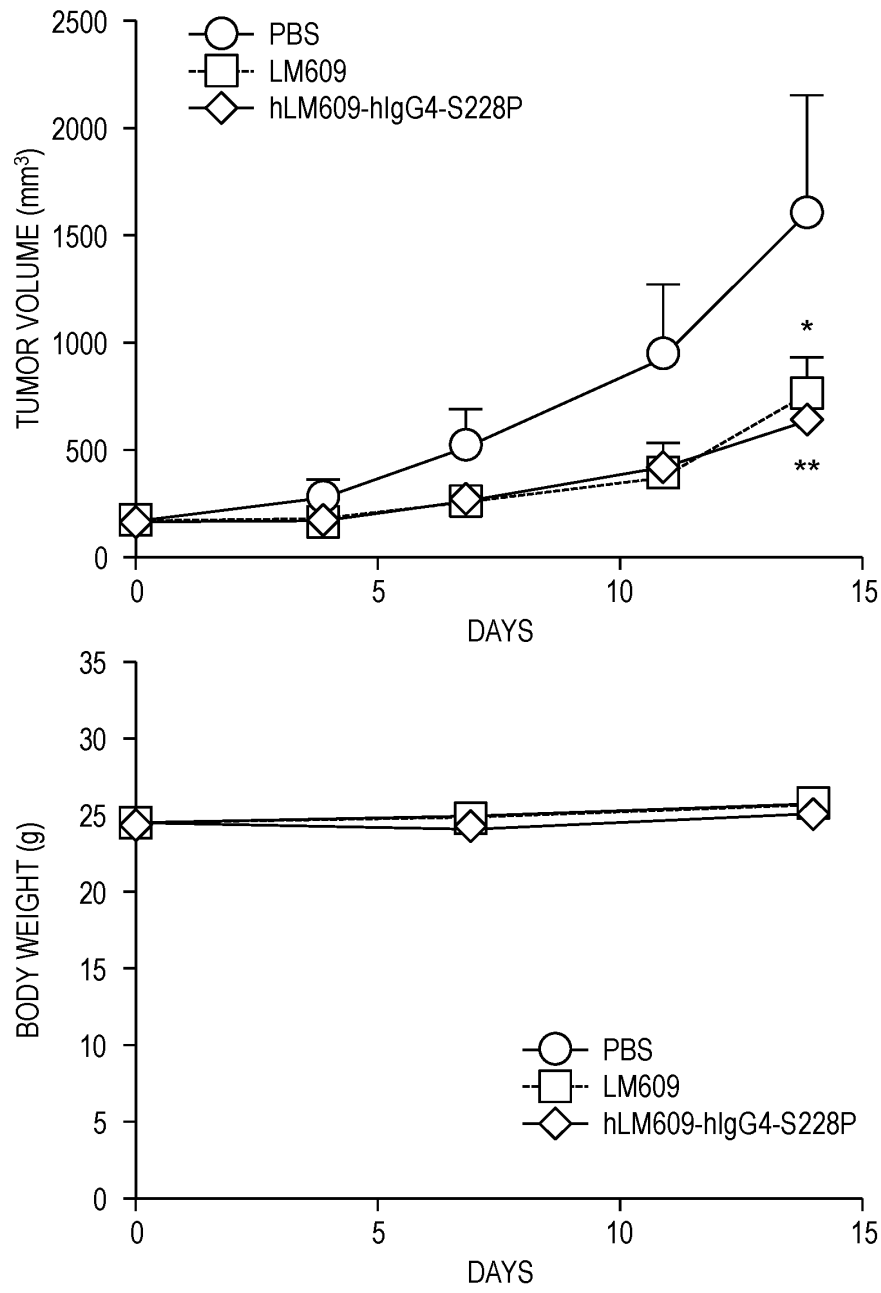


FIG. 12

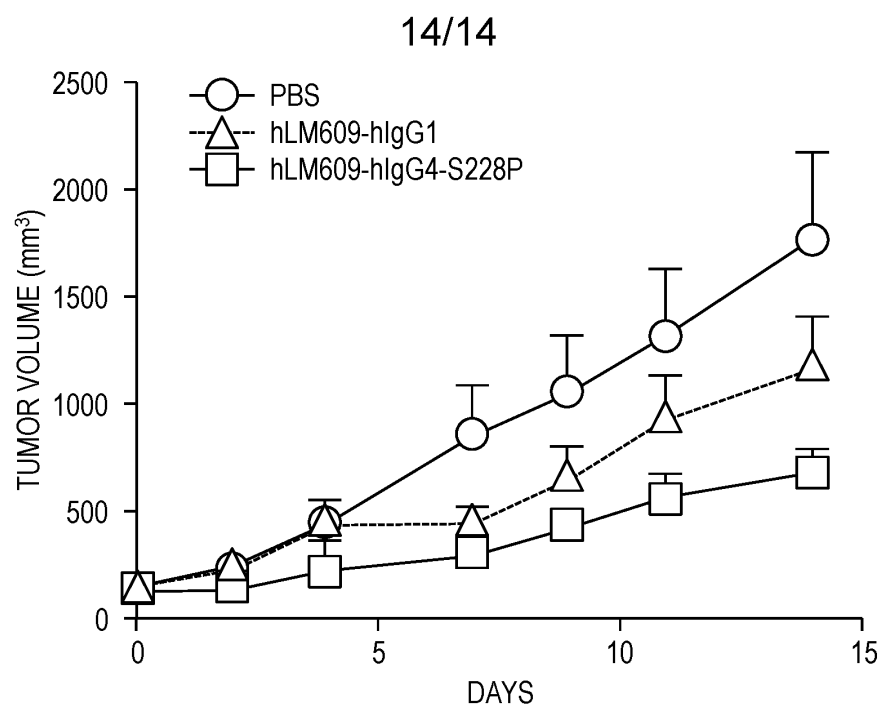


FIG. 13

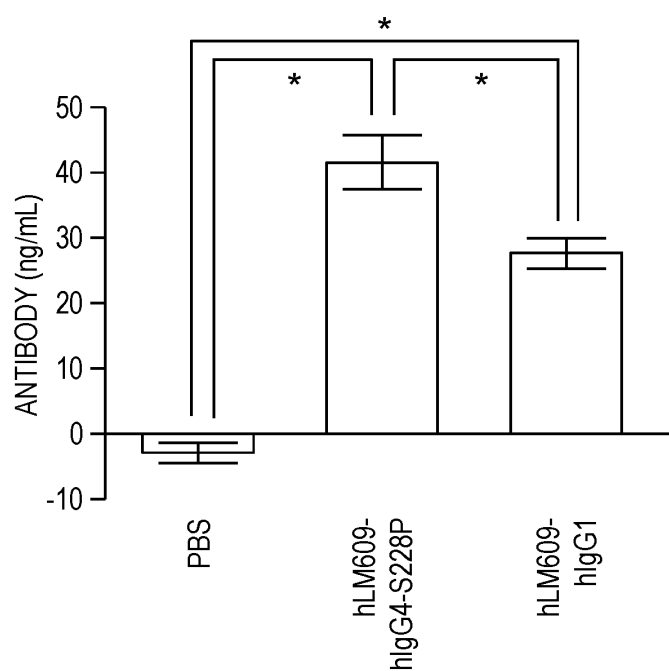


FIG. 14