Figure 1A.

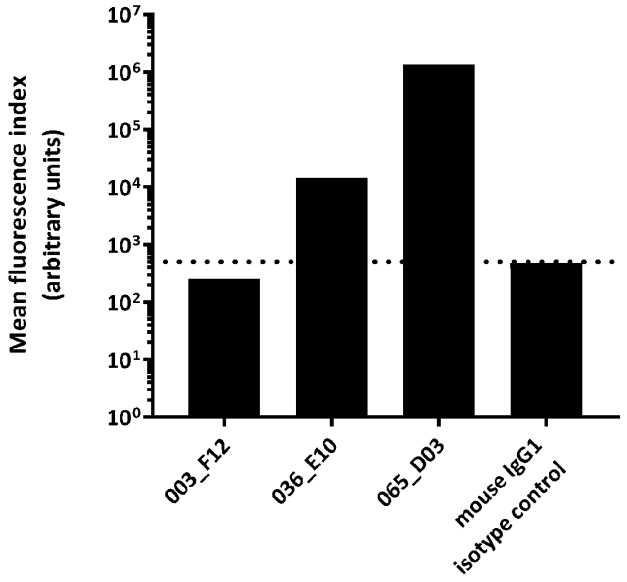

Figure 1B.

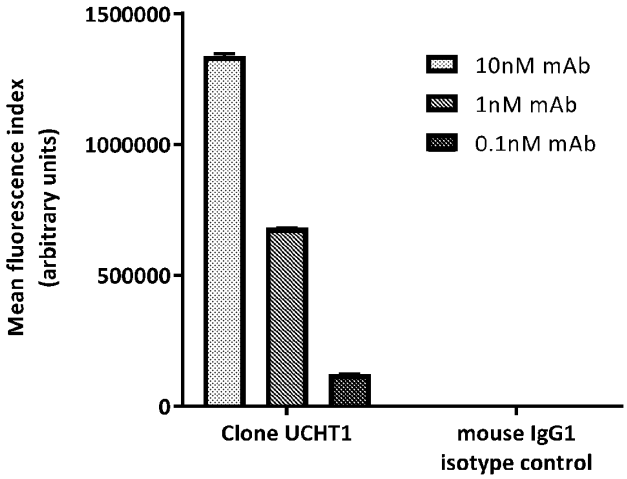

Figure 2.

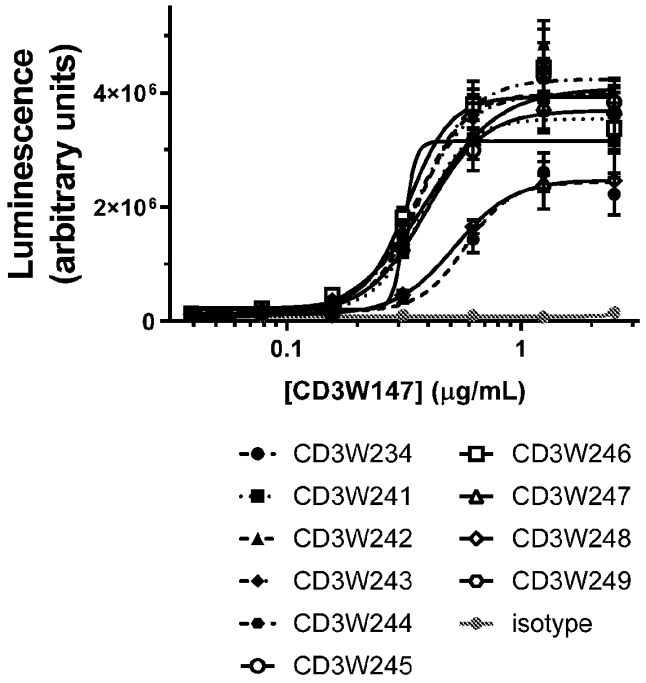
Luminescence (arbitrary units)
4×10⁶
2×10⁶
0
0.1
1
[CD3W147] (μg/mL)
CD3W234
CD3W241
CD3W242
CD3W243
CD3W244
CD3W245
CD3W246
CD3W247
CD3W248
CD3W249
isotype

Figure 3.

```
CD3B815  DILLTQSPGILSVSPGERVSFSCRARQSIGTAIHWYQQRTNGSPRLLIKYASESISGIPSRF
CD3W244  DIQMTQSPSSLSASVGDRVTITCRARQSIGTAIHWYQQKPGKAPKLLIYYASESISGVPSRF
CD3W245  DIQMTQSPSSLSASVGDRVTITCRARQSIGTAIHWYQQKPGKAPKLLIKYASESISGVPSRF
CD3W246  DIQMTQSPSSLSASVGDRVTITCRARQSIGTAIHWYQQKPGKAPKLLIKYASESISGVPSRF
CD3W247  DIQMTQSPSSLSASVGDRVTITCRARQSIGTAIHWYQQKPGKAPKLLIYYASESISGVPSRF
CD3W248  DILLTQSPGILSVSPGERVSFSCRARQSIGTAIHWYQQRTNGSPRLLIKYASESISGIPSRF
         ***:****::**:*:*:**:::*****************::::*:***:********:****


CD3B815  SGSGSGTDFTLTINSVESEDIADYYCQQSNSWPYTFGGGTKLEIK
CD3W244  SGSGSGTDFTLTISSVQPEDFATYYCQQSGSWPYTFGQGTKLEIK
CD3W245  SGSGSGTDFTLTISSLQPEDFATYYCQQSGSWPYTFGQGTKLEIK
CD3W246  SGSGSGTDFTLTISSVQPEDFATYYCQQSGSWPYTFGQGTKLEIK
CD3W247  SGSGSGTDFTLTISSLQPEDFATYYCQQSGSWPYTFGQGTKLEIK
CD3W248  SGSGSGTDFTLTINSVESEDIADYYCQQSGSWPYTFGGGTKLEIK
         *************:*:*:**:*:******:*******:*******
```

VL consensus sequence (SEQ ID NO: 103)

DIQX1TQSPX2X3LSX4SX5GX6RVX7X8X9CRARQSIGTAIHWYQQKX10X11X12X13PX14LLIX15YASESISGX16PSRFS
GSGSGTDFTLTIX17SX18QX19EDX20AX21YYCQQSX22SWPYTFGX23GTKLEIK; wherein

X1 is L or M;
X2 is G or S;
X3 is I or S;
X4 is V or A;
X5 is P or V;
X6 is E or D;
X7 is S or T;
X8 is F or I;
X9 is S or T
X10 is T or P;
X11 is N or G;
X12 is G or K;
X13 is S or A;
X14 is R or K;
X15 is K or Y;
X16 is I or V;
X17 is N or S;
X18 is V or L;
X19 is S or P;
X20 is I or F;
X21 is D or T;
X22 is N or G; or
X23 is G or Q.

Figure 4.

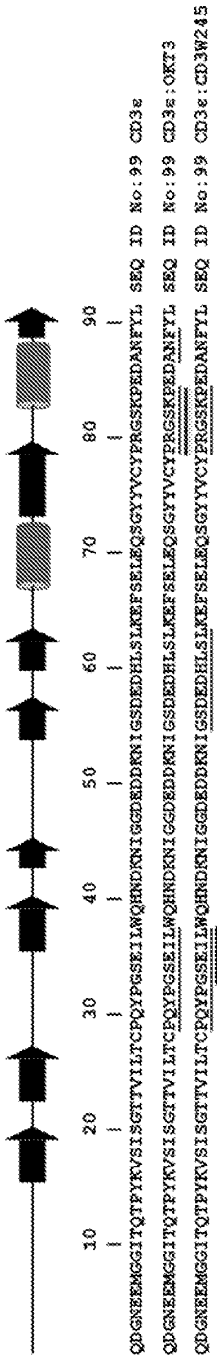
10 20 30 40 50 60 70 80 90
QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYL SEQ ID No:99 CD3ε
QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYL SEQ ID No:99 CD3ε:OKT3
QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYL SEQ ID No:99 CD3ε:CD3W245

Figure 5.

```
           1                                         45
mu11B6_VH  DVQLQESGPGLVKPSQSLSLTCTVTGNSITSDYAWNWIRQFPGNR
hu11B6_VH  QVQLQESGPGLVKPSDTLSLTCAVSGNSITSDYAWNWIRQPPGKG
KL2B357_VH QVQLQESGPGLVKPSQTLSLTCTVSGNSITSDYAWNWIRQFPGKG
KL2B358_VH QVQLQESGPGLVKPSQTLSLTCTVSGNSITSDYAWNWIRQPPGKG
KL2B359_VH QVQLQESGPGLVKPSQTLSLTCTVSGNSITSDYAWNWIRQFPGKR
KL2B360_VH QVQLQESGPGLVKPSQTLSLTCTVSGNSITSDYAWNWIRQFPGKG
      HCF3 QVQLQESGPGLVKPSDTLSLTCAVSGNSITSDYAWNWIRQFPGKG
      HCG5 QVQLQESGPGLVKPSDTLSLTCAVSGNSITSDYAWNWIRQFPGKG
       Aln :**************::*****:*:************** **:

           46                                        90
mu11B6_VH  LEWMGYISYSGSTTYSPSLKSRFSITRDTSKNQFFLQLNSVTPED
hu11B6_VH  LEWIGYISYSGSTTYNPSLKSRVTMSRDTSKNQFSLKLSSVTAVD
KL2B357_VH LEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAAD
KL2B358_VH LEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAAD
KL2B359_VH LEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAAD
KL2B360_VH LEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAAD
      HCF3 LEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTPVD
      HCG5 LEWMGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTPVD
       Aln ***:***********.******.:::******** *:*.***. *

           91                       117
mu11B6_VH  TATYFCATGYYYGSGFWGQGTLVTVSS
hu11B6_VH  TAVYYCATGYYYGSGFWGQGTLVTVSS
KL2B357_VH TAVYYCATGYYYGSGFWGQGTLVTVSS
KL2B358_VH TAVYYCATGYYYGSGFWGQGTLVTVSS
KL2B359_VH TAVYYCATGYYYGSGFWGQGTLVTVSS
KL2B360_VH TAVYYCATGYYYGSGFWGQGTLVTVSS
      HCF3 TAVYYCATGYYYGSGFWGQGTLVTVSS
      HCG5 TAVYYCATGYYYGSGFWGQGTLVTVSS
       Aln **.*:**********************
```

VH consensus sequence (SEQ ID NO: 356)

QVQLQESGPGLVKPSX_1TLSLTCX_2VSGNSITSDYAWNWIRQX_3PGKX_4LEWX_5GYISYSGSTT
YNPSLKSRVTX_6SRDTSKNQFSLKLSSVTX_7X_8DTAVYYCATGYYYGSGFWGQGTLVTVSS

X_1 is D or Q;
X_2 is A or T;
X_3 is P or F;
X_4 is G or R;
X_5 is I or M;
X_6 is I or M;
X_7 is A or P; or
X_8 is V or A.

Figure 6.

```
           1                                                       55
mu11B6_VL  DIVLTQSPASLAVSLGQRATISCRASESVEYFGTSLMHWYRQKPGQPPKLLIYAA
hu11B6_VL  DIVLTQSPDSLAVSLGERATINCKASESVEYFGTSLMHWYQQKPGQPPKLLIYAA
KL2B357_VL DIVLTQSPDSLAVSLGERATINCRASESVEYFGTSLMHWYQQKPGQPPKLLIYAA
KL2B358_VL EIVLTQSPATLSLSPGERATLSCRASESVEYFGTSLMHWYQQKPGQPPRLLIYAA
KL2B359_VL EIVLTQSPATLSLSPGERATLSCRASESVEYFGTSLMHWYQQKPGQPPRLLIYAA
KL2B360_VL EIVLTQSPATLSLSPGERATLSCRASESVEYFGTSLMHWYQQKPGQPPRLLIYAA
      LCD6 DIVLTQSPDSLAVSLGERATINCKASESVEYFGTSLMHWYQQKPGQPPKLLIYAA
      LCB7 DIVLTQSPDSLAVSLGERATINCKASESVEYFGTSLMHWYQQKPGQPPKLLIYAA
       Aln :******* :*::* *:***:.*:****************:*******:******

           56                                                     111
mu11B6_VL  SNVESGVPARFSGSGSGTDFSLNIQPVEEDDFSMYFCQQTRKVPYTFGGGTKLEIK
hu11B6_VL  SNRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQTRKVPYTFGQGTKLEIK
KL2B357_VL SNVESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQTRKVPYTFGGGTKVEIK
KL2B358_VL SNVESGIPARFSGSGSGTDFTLTISSVEPEDFAVYFCQQTRKVPYTFGGGTKVEIK
KL2B359_VL SNVESGIPARFSGSGSGTDFTLTISSVEPEDFAVYFCQQTRKVPYTFGGGTKVEIK
KL2B360_VL SNVESGIPARFSGSGSGTDFTLTISSVEPEDFAVYFCQQTRKVPYTFGGGTKVEIK
      LCD6 SNRESGVPDRFSGSGSGTDFTLTIQSVQAEDVSVYFCQQTRKVPYTFGQGTKLEIK
      LCB7 SNRESGVPDRFSGSGSGTDFTLTISSVQAEDVAVYYCQQTRKVPYTFGQGTKLEIK
       Aln ** ***:* ***********:*.*..:: :*.::*:************ ***:***
```

VL consensus sequence (SEQ ID NO: 357)

X_1IVLTQSPX_2X_3LX_4X_5SX_6GERATX_7X_8CX_9ASESVEYFGTSLMHWYQQKPGQPPX_{10}LLIYAASNX_{11}ESGX_{12}PX_{13}RFSGSGSGTDFTLTIX_{14}S$X_{15}X_{16}$QX_{17}ED$X_{18}X_{19}$VYX_{20}CQQTRKVPYTFGX_{21}GTKX_{22}EIK

X_1 is D or E; X_2 is D or A; X_3 is S or T; X_4 is A or S;
X_5 is V or L; X_6 is L or P; X_7 is I or L; X_8 is N or S;
X_9 is R or K; X_{10} is K or R; X_{11} is V or R; X_{12} is V or I;
X_{13} is A or D; X_{14} is Q or S; X_{15} is L or V; X_{16} is Q or E;
X_{17} is P or A; X_{18} is F or V; X_{19} is A or S; X_{20} is Y or F;
X_{21} is Q or G; and X_{22} is L or V.

Figure 7.

```
           1                                                  50
h11B6      VPLIEGRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL
KL2B494    VPLIEGRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL
KL2B467    VPLIEGRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL
KL2B30     VPLIEGRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL
KL2B413    VPLIEGRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL
KL2B53     VPLIEGRIVGGWECEKHSQPWQVAVYSHGWAHCGGVLVHPQWVLTAAHCL

           51                                                100
h11B6      KKNSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHQSLRPDEDS
KL2B494    KKNSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHQSLRPDEDS
KL2B467    KKNSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHQSLRPDEDS
KL2B30     KKNSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHQSLRPDEDS
KL2B413    KKNSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHQSLRPDEDS
KL2B53     KKNSQVWLGRHNLFEPEDTGQRVPVSHSFPHPLYNMSLLKHQSLRPDEDS

           101                                               150
h11B6      SHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSIEPEEFLR
KL2B494    SHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSIEPEEFLR
KL2B467    SHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSIEPEEFLR
KL2B30     SHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSIEPEEFLR
KL2B413    SHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSIEPEEFLR
KL2B53     SHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSIEPEEFLR

           151                                               200
h11B6      PRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPL
KL2B494    PRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPL
KL2B467    PRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPL
KL2B30     PRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPL
KL2B413    PRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPL
KL2B53     PRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPL

           201                                       244
H11B6      VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP
KL2B494    VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP
KL2B467    VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP
KL2B30     VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP
KL2B413    VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP
KL2B53     VCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRKWIKDTIAANP
```

Figure 8A.

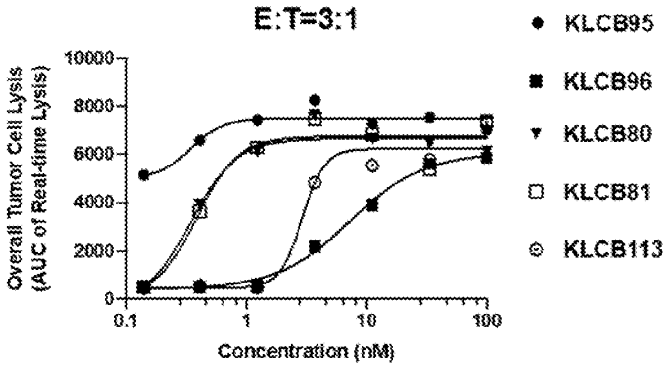
E:T=3:1
Overall Tumor Cell Lysis
(AUC of Real-time Lysis)
10000
8000
6000
4000
2000
0
0.1
1
10
100
Concentration (nM)
KLCB95
KLCB96
KLCB80
KLCB81
KLCB113

Figure 8B.

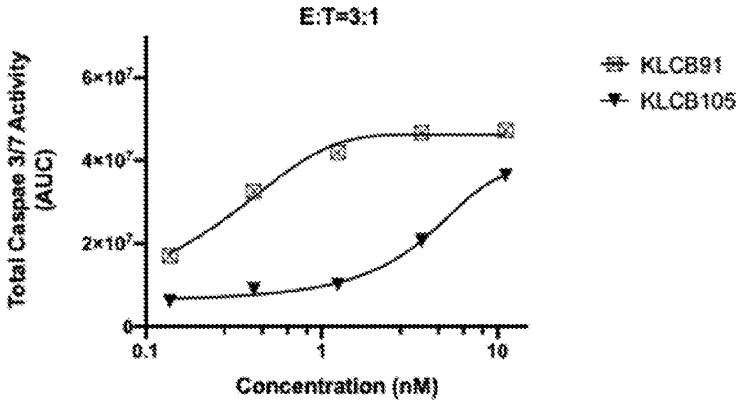
E:T=3:1
Total Caspase 3/7 Activity (AUC)
6×10⁷
4×10⁷
2×10⁷
0
0.1
1
10
Concentration (nM)
KLCB91
KLCB105

Figure 9A.

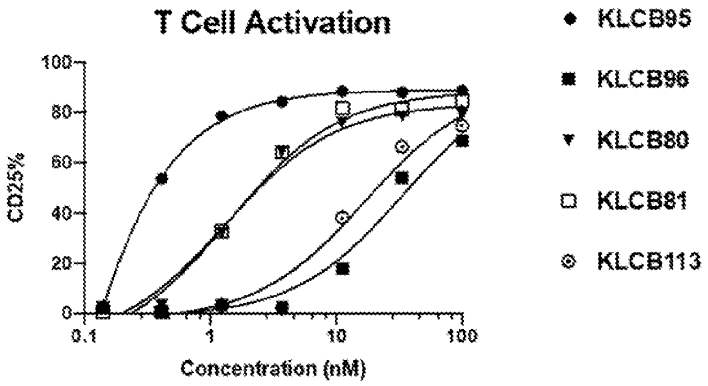
T Cell Activation
CD25%
100
80
60
40
20
0
0.1
1
10
100
Concentration (nM)
KLCB95
KLCB96
KLCB80
KLCB81
KLCB113

Figure 9B.

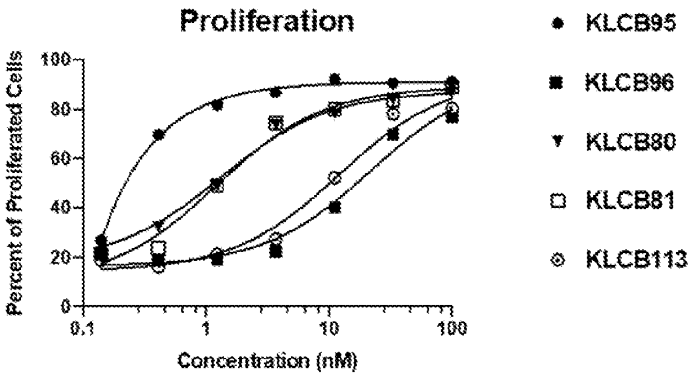
Proliferation
Percent of Proliferated Cells
100
80
60
40
20
0
0.1
1
10
100
Concentration (nM)
KLCB95
KLCB96
KLCB80
KLCB81
KLCB113

Figure 10A.

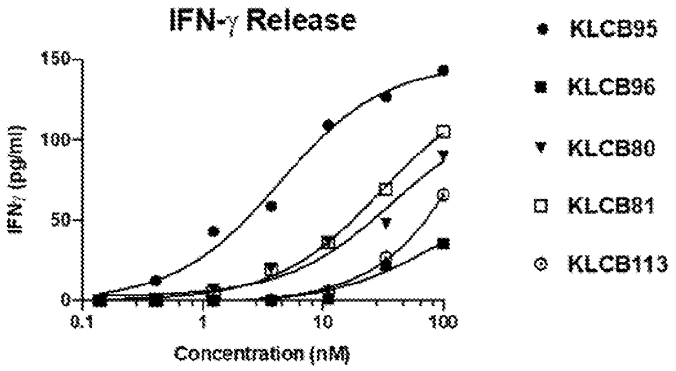
IFN-γ Release
150
100
50
0
IFNγ (pg/ml)
0.1
1
10
100
Concentration (nM)
KLCB95
KLCB96
KLCB80
KLCB81
KLCB113

Figure 10B.

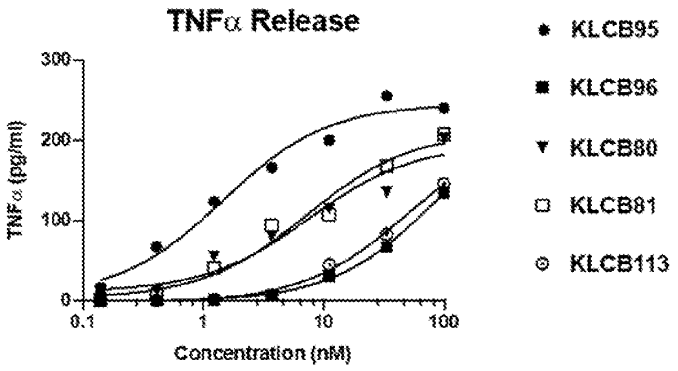
TNFα Release
300
200
100
0
TNFα (pg/ml)
0.1
1
10
100
Concentration (nM)
KLCB95
KLCB96
KLCB80
KLCB81
KLCB113

Figure 11A.

Sequence of KL2B494 (Heavy Chain)

QVQLVESGGG LVQPGGSLRL SCAASGFTFS HYAMSWVRQA PGKGLEWVST
IGGSGGSTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPH
IVMVTALLYD GMDVWGQGTM VTVSSASTKG PSVFPLAPSS KSTSGGTAAL
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS
LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP EAAGGPSVFL
FPPKPKDTLM ISRTPEVTCV VVSVSHEDPE VKFNWYVDGV EVHNAKTKPR
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ
PREPQVYTLP PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK
TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS
LSPGK

Sequence of KL2B494 (Light chain)

SSELTQPPSV SVAPGQTARI TCGGNNIGSK SVHWYQQKPG QAPVLVVYDD
SDRPSGIPER FSGSNSGNTA TLTISRVEAG DEADYYCQVW DSSSDHVVFG
GGTKLTVLGQ PKAAPSVTLF PPSSEELQAN KATLVCLISD FYPGAVTVAW
KADSSPVKAG VETTTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE
GSTVEKTVAP TECS

Figure 11B.

Sequence of KL2B467 (Heavy chain)

QVQLVESGGG VVQPGRSLRL SCAASGFTFS YYGMHWVRQA PGKGLEWVAF
ISYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAHLP
YSGSYWAFDY WGQGTQVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPEAAG GPSVFLFPPK
PKDTLMISRT PEVTCVVVSV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG
K

Sequence of KL2B467 (Light chain)

QSVLTQPPSV SVAPGQTASI TCGGDNIGSK SVHWYQQKPG QAPVLVVYDN
SDRPSGIPER FSGSNSGTTA TLTISRVEAG DEADYYCQVW DSSSDHPVVF
GGGTKVTVLG QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA
WKADSSPVKA GVETTTPSKQ SNNKYAASSY LSLTPEQWKS HRSYSCQVTH
EGSTVEKTVA PTECS

Figure 11C.

Sequence of hu11B6 (Heavy chain)

QVQLQESGPG LVKPSDTLSL TCAVSGNSIT SDYAWNWIRQ PPGKGLEWIG
YISYSGSTTY NPSLKSRVTM SRDTSKNQFS LKLSSVTAVD TAVYYCATGY
YYGSGFWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK

Sequence of hu11B6 (Light chain)

DIVLTQSPDS LAVSLGERAT INCKASESVE YFGTSLMHWY QQKPGQPPKL
LIYAASNRES GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCQQTRKVPY
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC

Figure 11D.

Sequence of KL2B413 (Heavy chain)

EVQLVESGGG LVQPGGSLRL SCAASGFTFS SYWMTWVRQP PGKGLEWVAN
IKQDGSERYF VDSVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARDQ
NYDILTGHYG MDYWGQGTTV TVSSASTKGP SVFPLAPCSR STSESTAALG
CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL
GTKTYTCNVD HKPSNTKVDK RVESKYGPPC PPCPAPEAAG GPSVFLFPPK
PKDTLMISRT PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP
QVYTLPPSQE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP
VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS VMHEALHNHY TQKSLSLSLG
K

Sequence of KL2B413 (Light chain)

EIVLTQSPSF LSASVGDRVT ITCRASQGIS SYLSWYQQKP GKAPKLLIYA
TSTLQSGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCQQ LNSYPRTFGQ
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG
LSSPVTKSFN RGEC

Figure 11E.

Sequence of KL2B30 Fab of KLCB80 bispecific (heavy chain)

QVQLQESGPG LVKPSETLSL TCTVSGGSIS SYYWSWIRQP PGKGLEWIGY
IYYSGSTNYN PSLKSRVTIS VDTSKNQFSL KLSSVTAADT AVYYCAGTTI
FGVVTPNFYY GMDVWGQGTT VTVSSASTKG PSVFPLAPSS KSTSGGTAAL
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS
LGTQTYICNV NHKPSNTKVD KKVEPKSCDK THTCPPCPAP EAAGGPSVFL
FPPKPKDTLM ISRTPEVTCV VVSVSHEDPE VKFNWYVDGV EVHNAKTKPR
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ
PREPQVYVLP PSREEMTKNQ VSLLCLVKGF YPSDIAVEWE SNGQPENNYL
TWPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS
LSPG

Sequence of KL2B30 Fab of KLCB80 bispecific (light chain)

DIQMTQSPSF LSASVGDRVT ITCRASQGIS SYLAWYQQKP GKAPKFLIYA
ASTLQSGVPS RFSGSGSGTE FTLTISSLQP EDFATYYCQQ LNSYPLTFGG
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG
LSSPVTKSFN RGEC

Figure 11F.

Sequence of KL2B353 Fab of KLCB113 bispecific (heavy chain)

EVQLVESGGG VVQPGRSLRL SCVASGFTFS SYDIHWVRQA PGKGLEWVAI
ISYDGSKKDY TDSVKGRFTI SRDNSKNTLY LQMDSLRVED SAVYSCARSS
GWSHYYYYGM DVWGQGTMVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGPSVFLFP
PKPKDTLMIS RTPEVTCVVV SVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYVLPPS REEMTKNQVS LLCLVKGFYP SDIAVEWESN GQPENNYLTW
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PG

Sequence of KL2B353 Fab of KLCB113 bispecific (heavy chain)

DIVMTQSPSS LSASVGDRVT ITCRASQDIS NYLAWYQQKP GKVPKFLIYA
ASTLHSGVPS RFSGSGSGTD FTLTISSLQP EDVATYYCQK YNSAPYTFGQ
GTRLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG
LSSPVTKSFN RGEC

Figure 12.

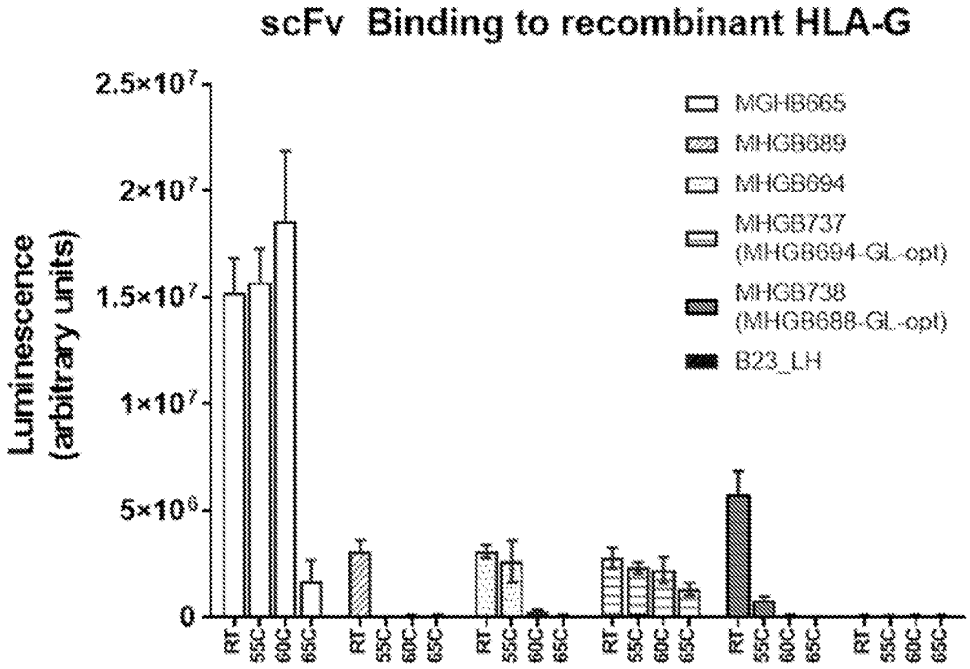
scFv Binding to recombinant HLA-G
Luminescence (arbitrary units)
2.5×10⁷
2×10⁷
1.5×10⁷
1×10⁷
5×10⁶
0
MGHB665
MHGB689
MHGB694
MHGB737 (MHGB694-GL-opt)
MHGB738 (MHGB688-GL-opt)
B23_LH
RT
55C
60C
65C

Figure 13.

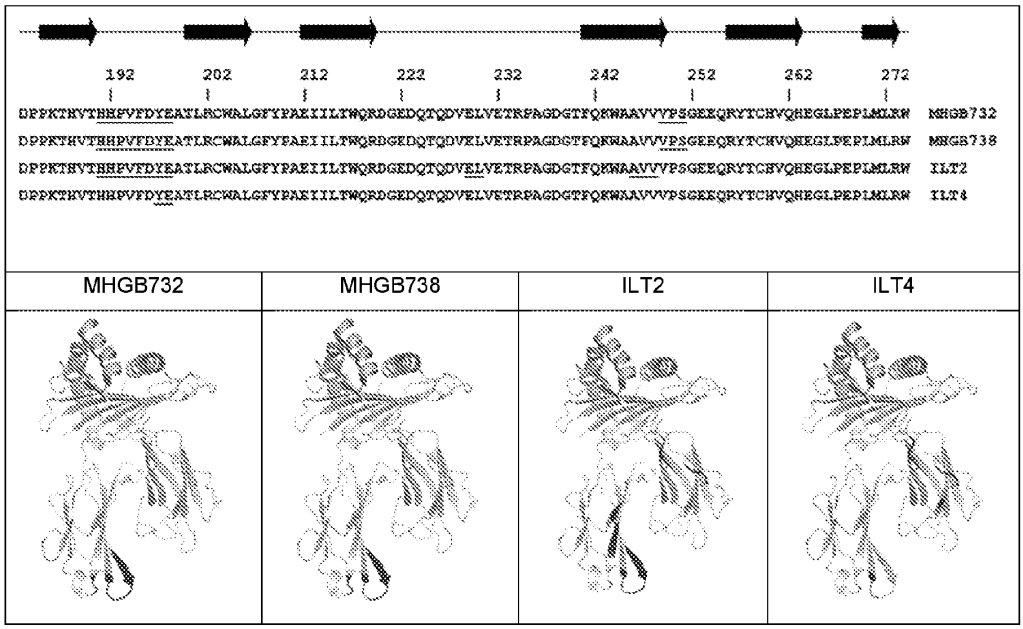
192 202 212 222 232 242 252 262 272
DPPKTHVTHHPVFDYEATLRCWALGFYPAEIILTWQRDGEDQTQDVELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLRW MHGB732
DPPKTHVTHHPVFDYEATLRCWALGFYPAEIILTWQRDGEDQTQDVELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLRW MHGB738
DPPKTHVTHHPVFDYEATLRCWALGFYPAEIILTWQRDGEDQTQDVELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLRW ILT2
DPPKTHVTHHPVFDYEATLRCWALGFYPAEIILTWQRDGEDQTQDVELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLRW ILT4
MHGB732
MHGB738
ILT2
ILT4

Figure 14A.

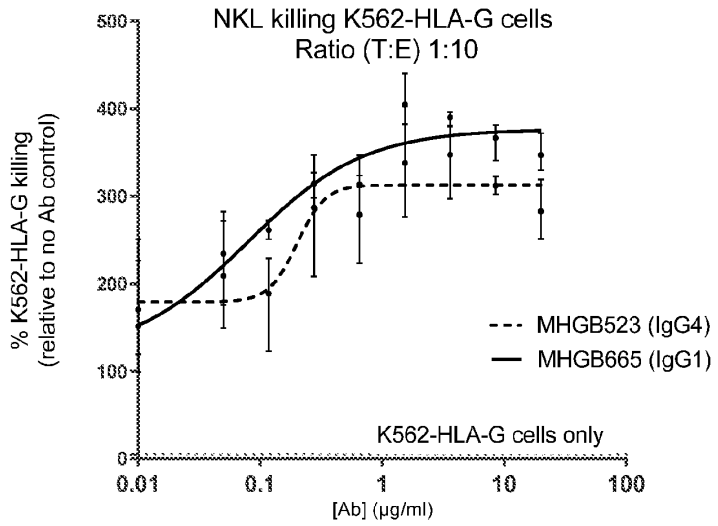

Figure 14B.

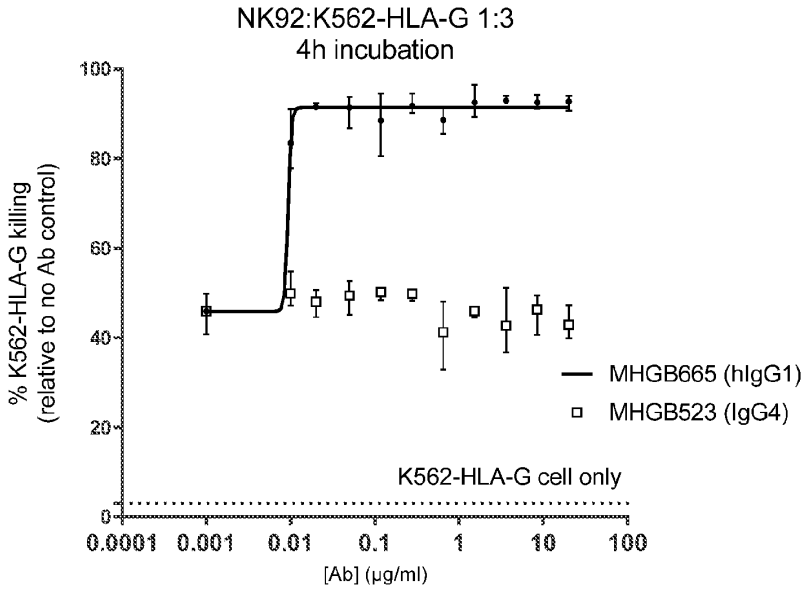

Figure 15A.

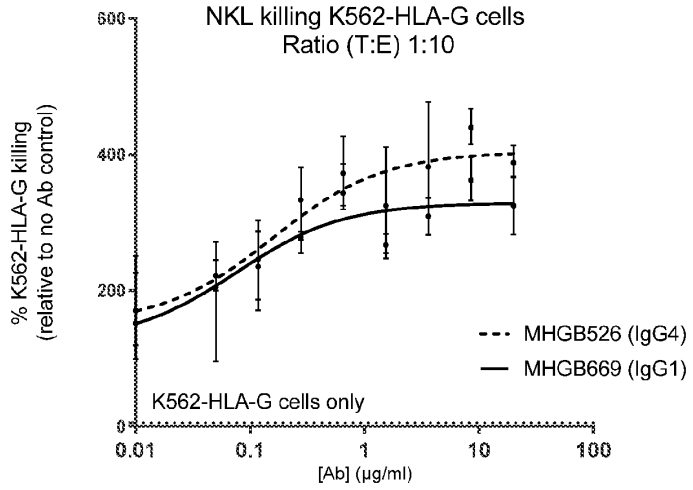

Figure 15B

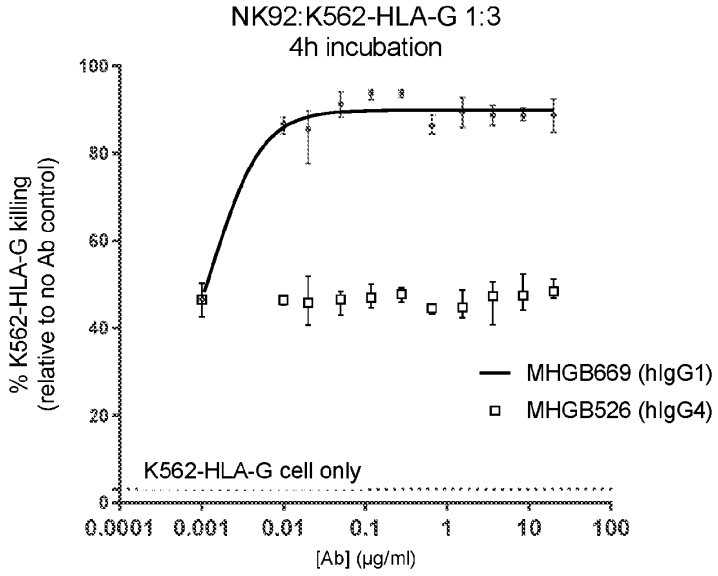

Figure 16A.

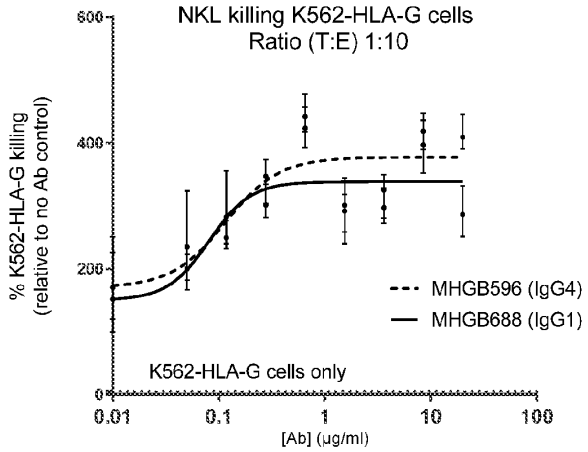

Figure 16B

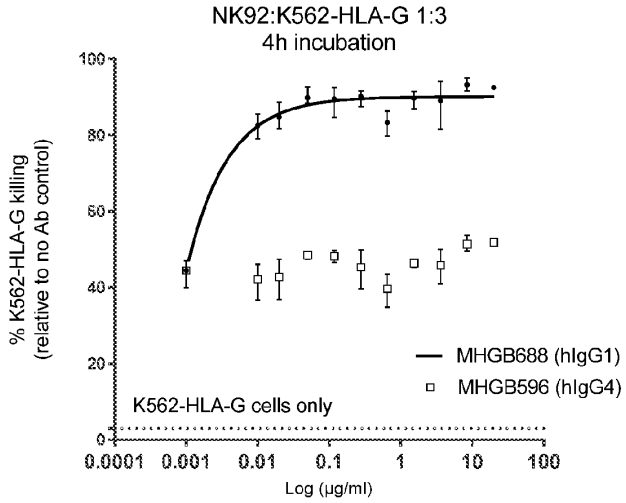

Figure 17A.

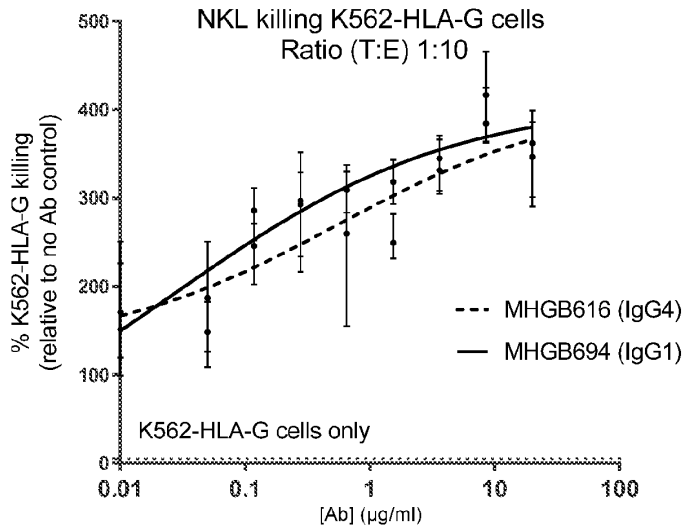

Figure 17B

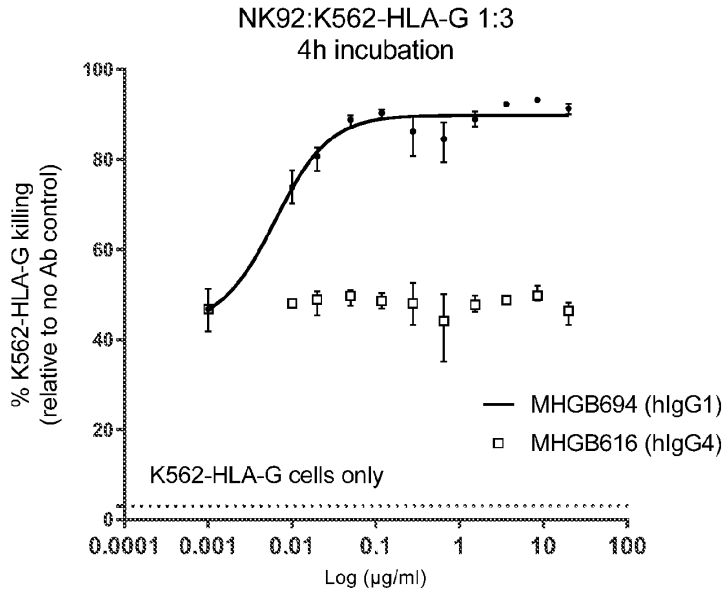

Figure 18A.

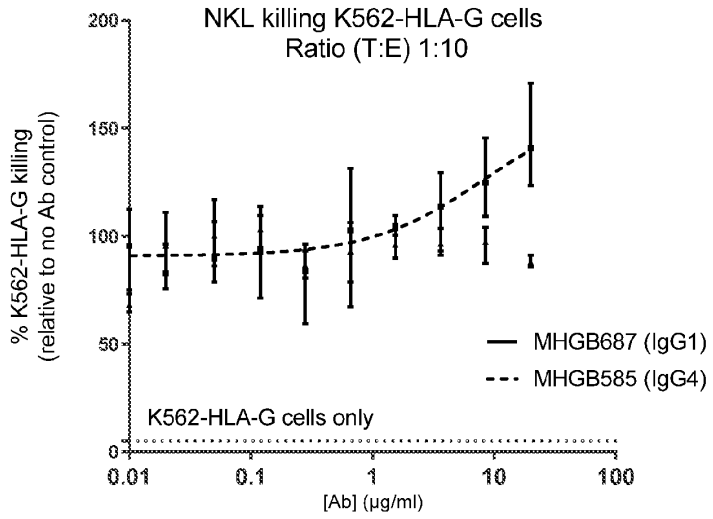

Figure 18B

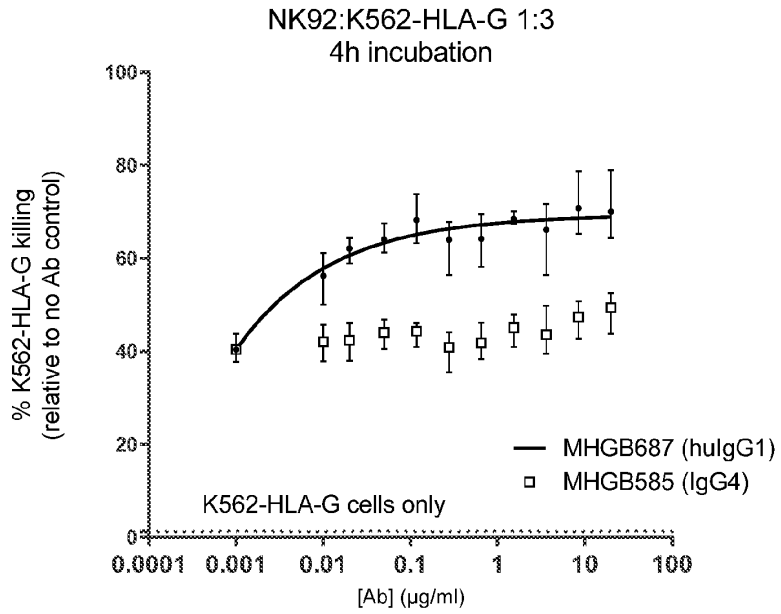

Figure 19A.

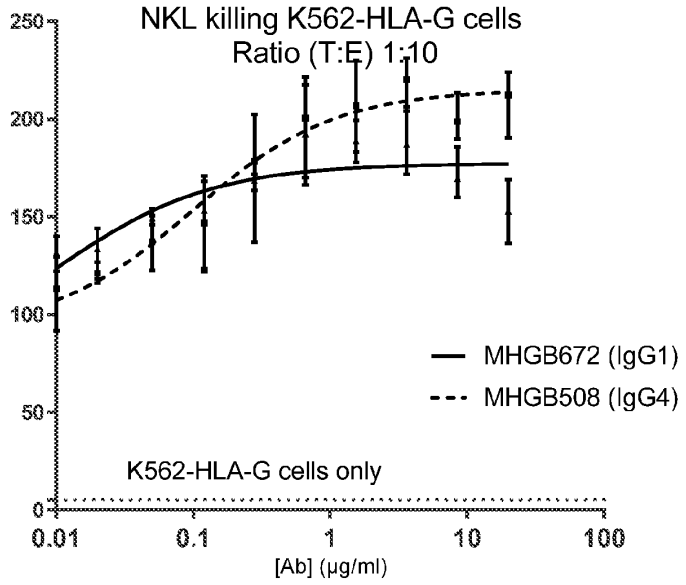

Figure 19B

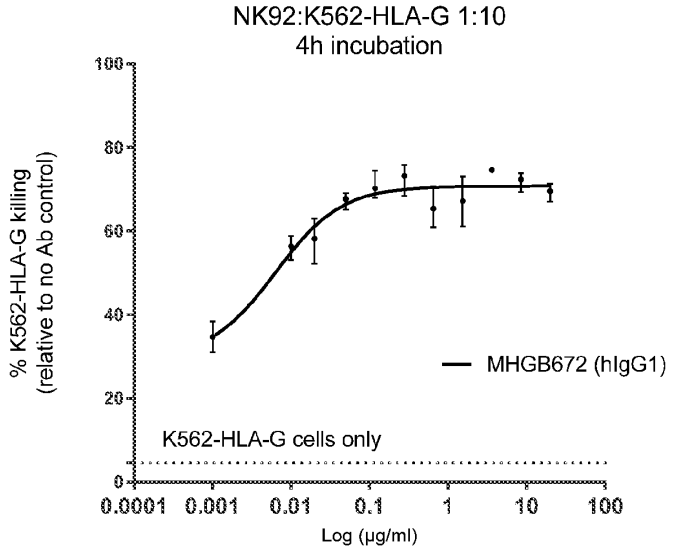

Figure 20.

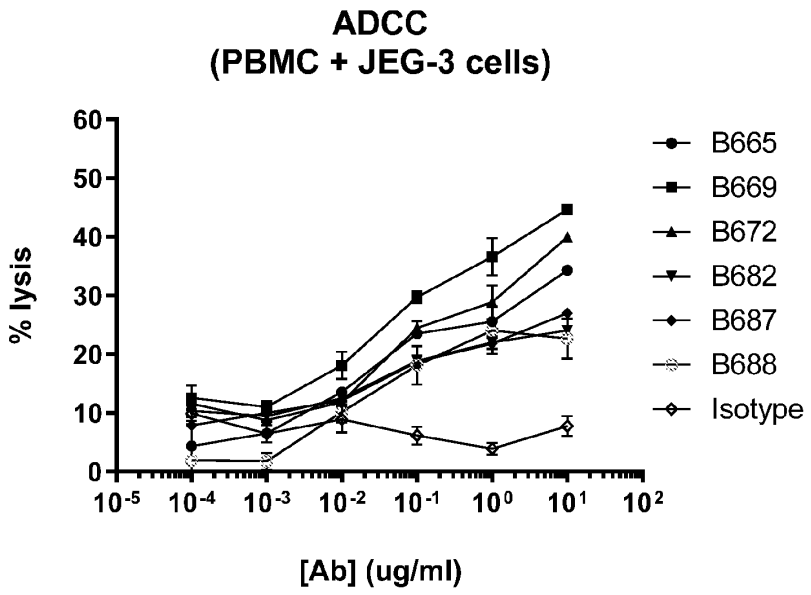
ADCC
(PBMC + JEG-3 cells)
% lysis
60
50
40
30
20
10
0
10-5
10-4
10-3
10-2
10-1
100
101
102
[Ab] (ug/ml)
B665
B669
B672
B682
B687
B688
Isotype

Figure 21A.

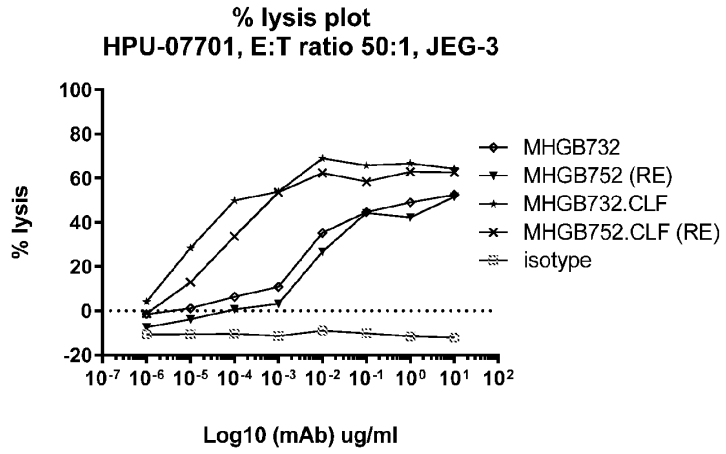

Figure 21B.

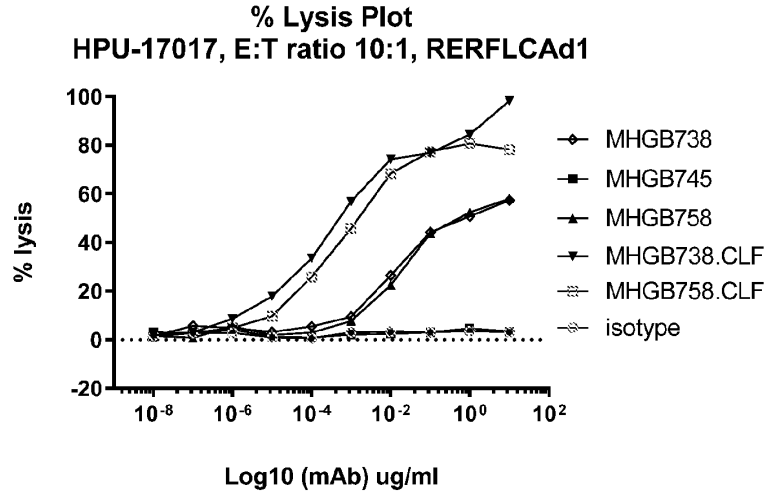

Figure 21C.

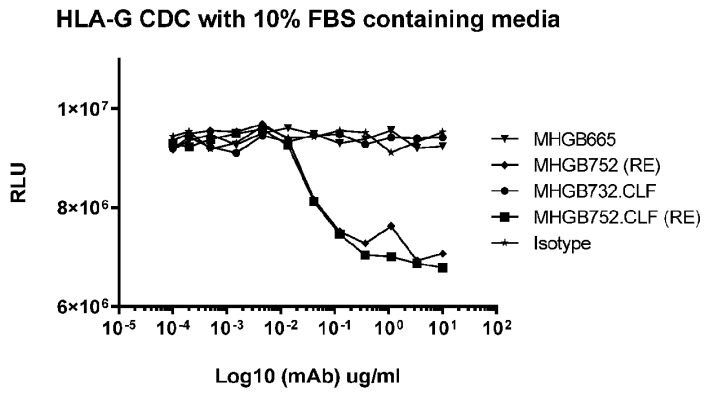

Figure 21D.

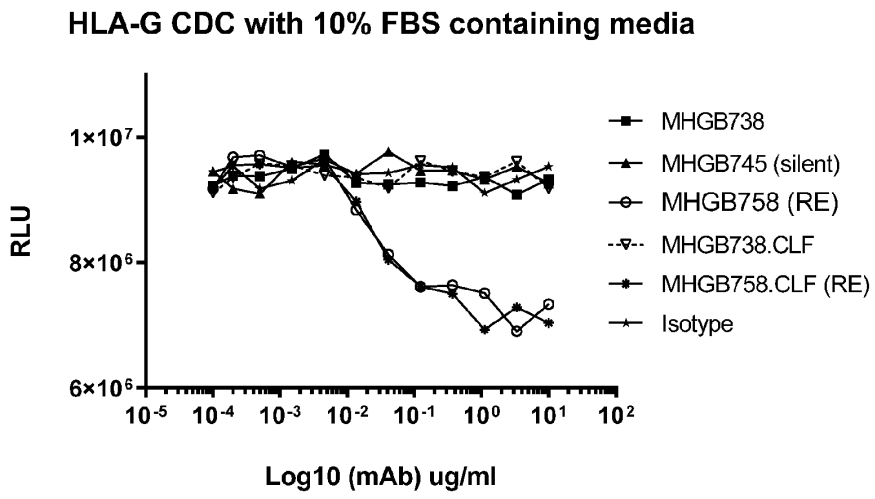

Figure 22A.

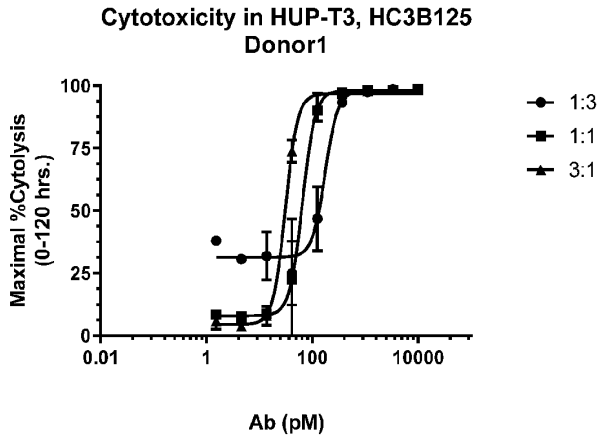

Figure 22B.

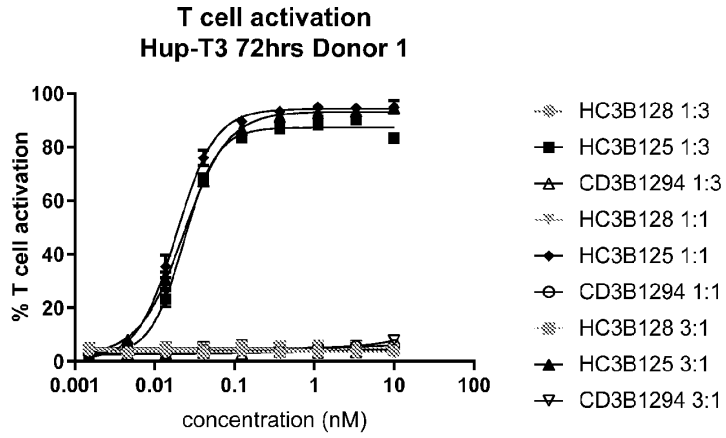

Figure 22C.

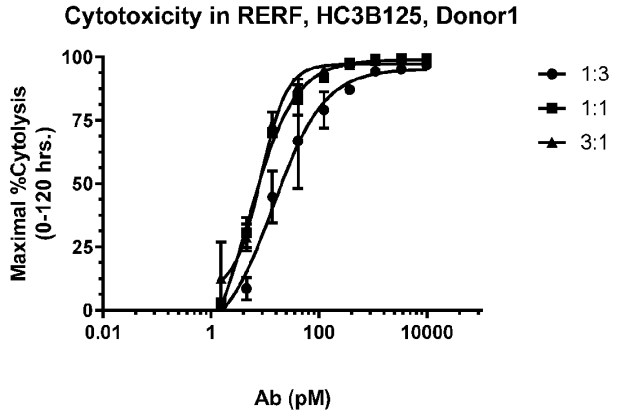

Figure 22D.

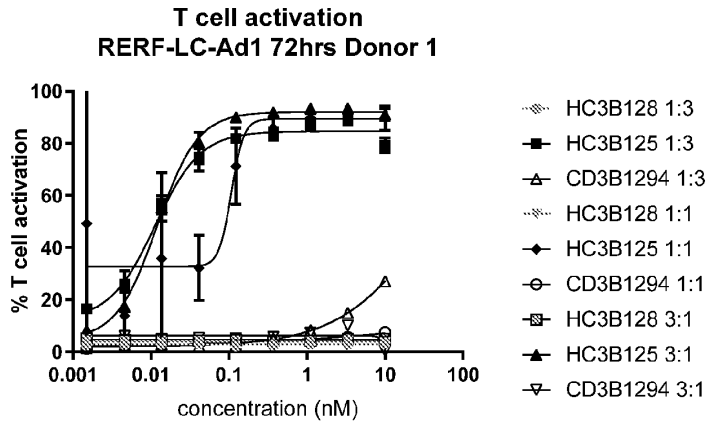

Figure 23.

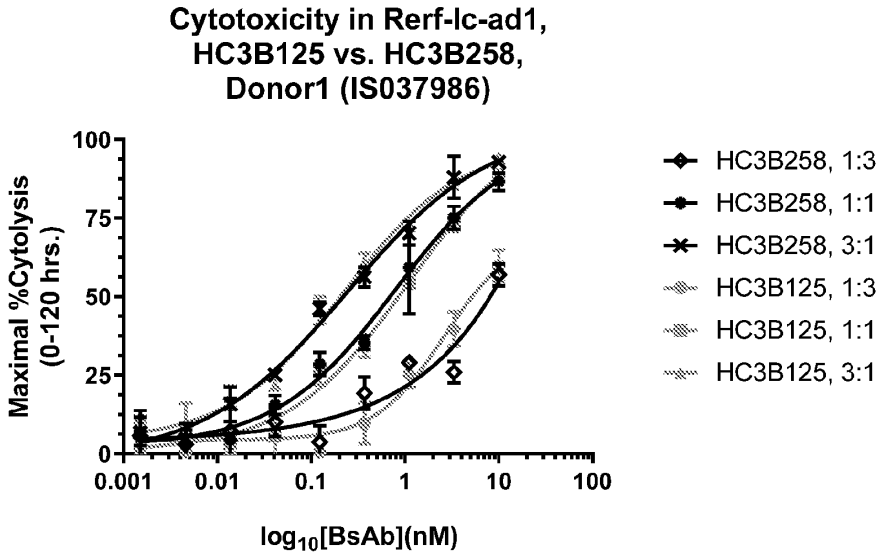
Cytotoxicity in Rerf-lc-ad1,
HC3B125 vs. HC3B258,
Donor1 (IS037986)
Maximal %Cytolysis
(0-120 hrs.)
100
75
50
25
0
0.001
0.01
0.1
1
10
100
log10[BsAb](nM)
HC3B258, 1:3
HC3B258, 1:1
HC3B258, 3:1
HC3B125, 1:3
HC3B125, 1:1
HC3B125, 3:1

Figure 24A.

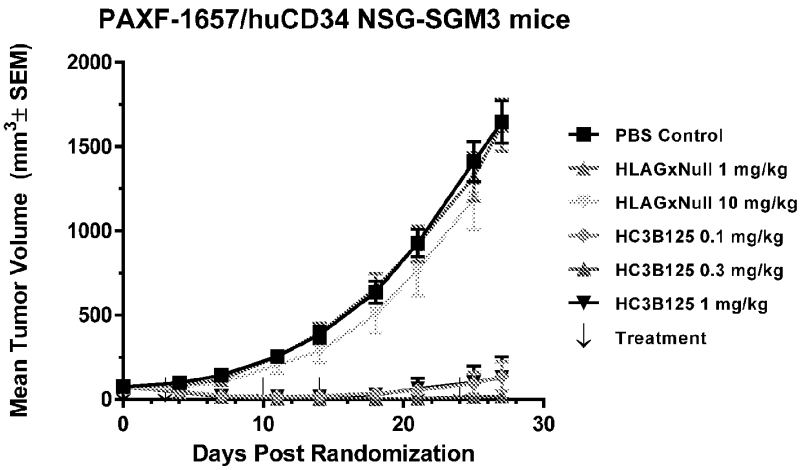

Figure 24B

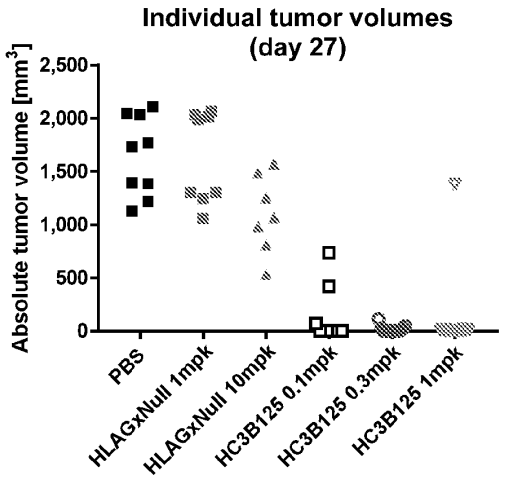

Figure 25.

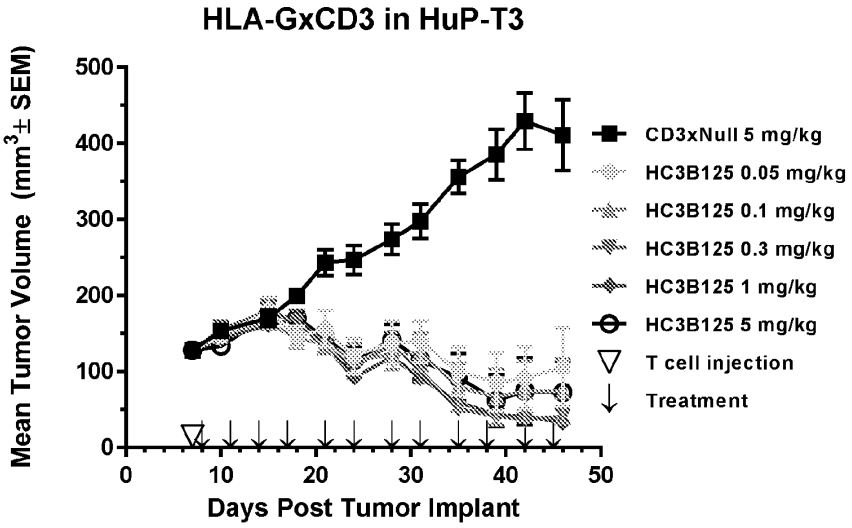
HLA-GxCD3 in HuP-T3
Mean Tumor Volume (mm3 ± SEM)
500
400
300
200
100
0
0
10
20
30
40
50
Days Post Tumor Implant
CD3xNull 5 mg/kg
HC3B125 0.05 mg/kg
HC3B125 0.1 mg/kg
HC3B125 0.3 mg/kg
HC3B125 1 mg/kg
HC3B125 5 mg/kg
T cell injection
Treatment

Figure 26A

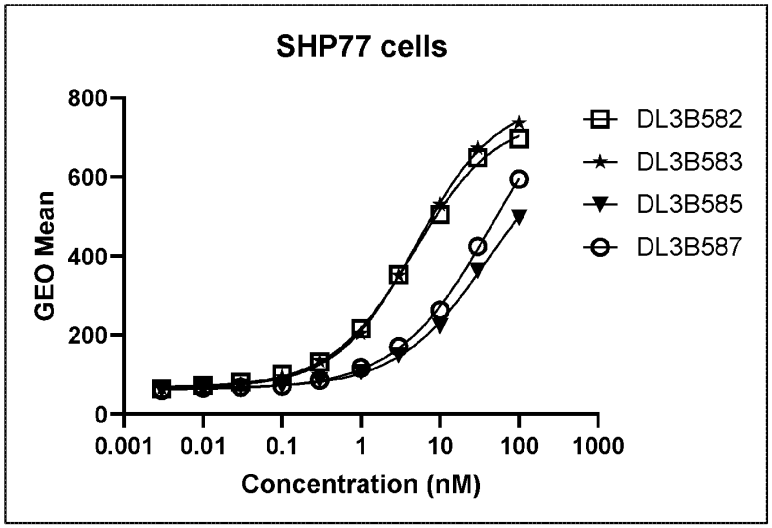

Figure 26B

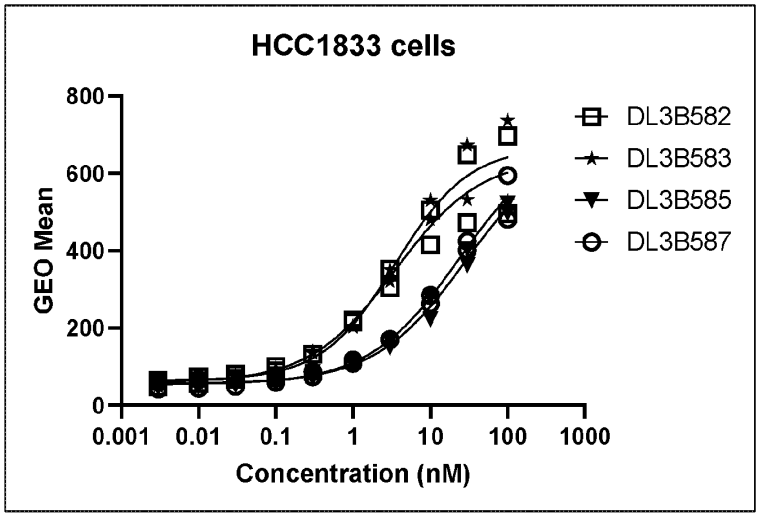

Figure 27

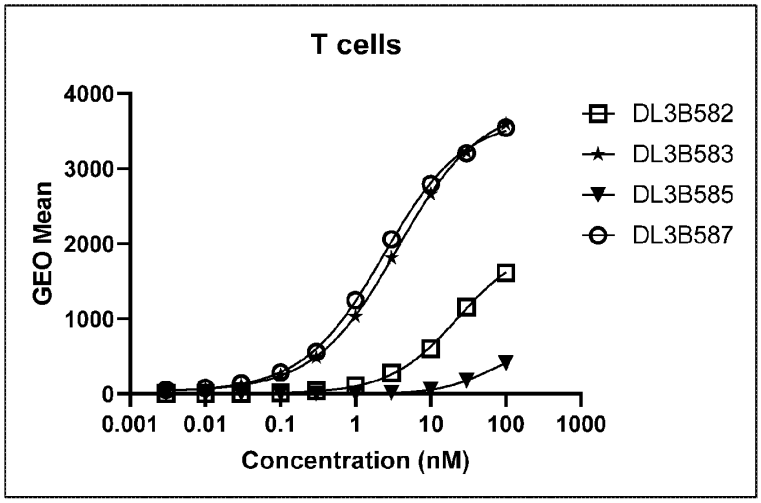
T cells
GEO Mean
4000
3000
2000
1000
0
0.001
0.01
0.1
1
10
100
1000
Concentration (nM)
DL3B582
DL3B583
DL3B585
DL3B587

Figure 28A

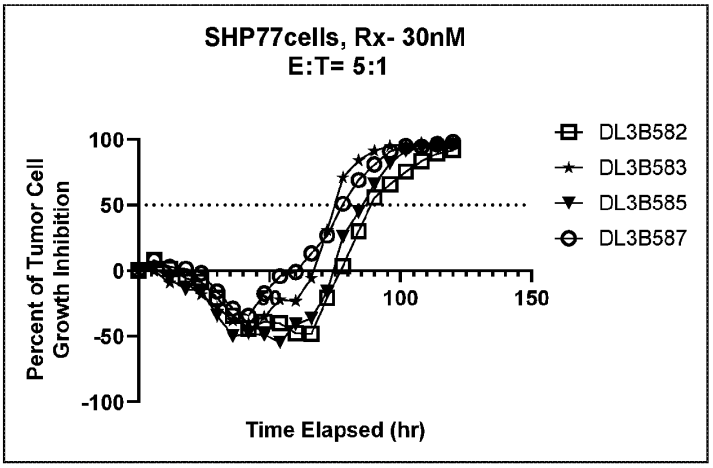

Figure 28B

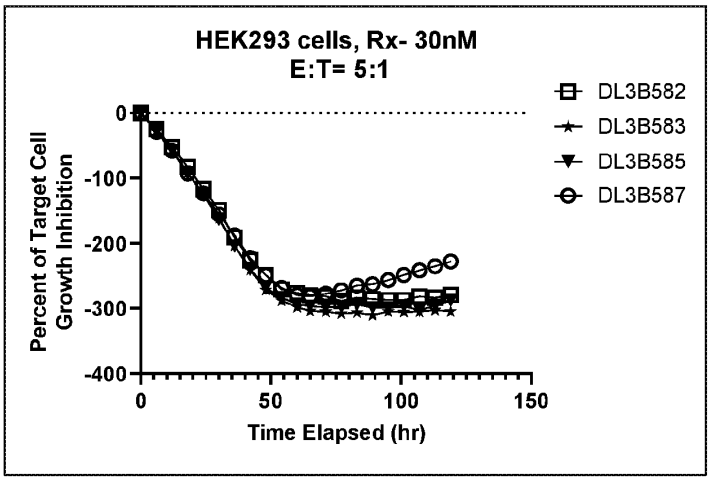

Figure 29

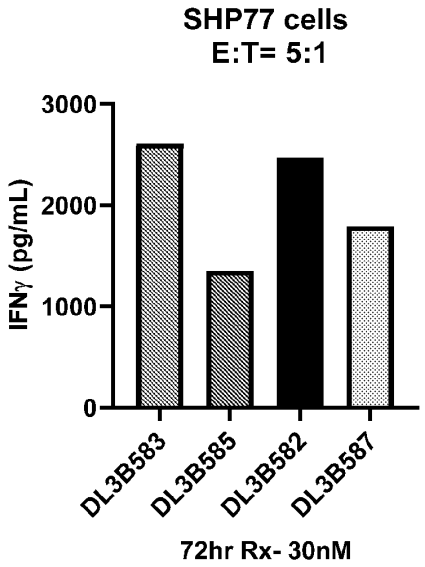
SHP77 cells
E:T= 5:1
3000
2000
1000
0
IFNγ (pg/mL)
DL3B583
DL3B585
DL3B582
DL3B587
72hr Rx- 30nM

Figure 30C

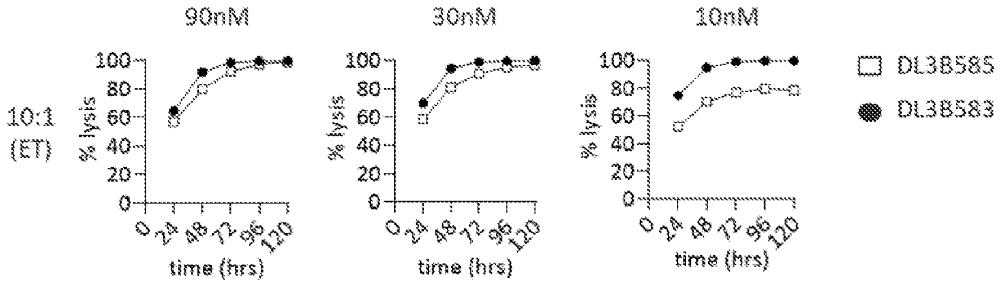

Figure 30A

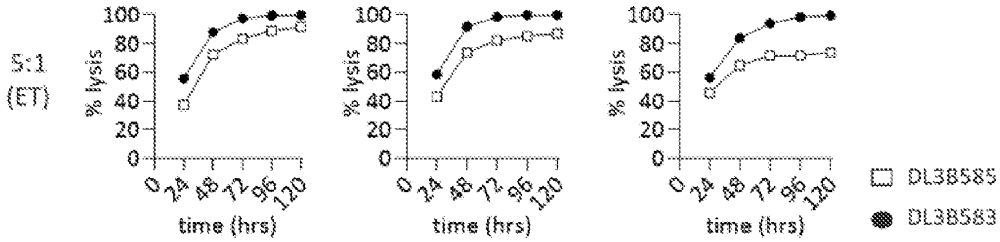

Figure 30B

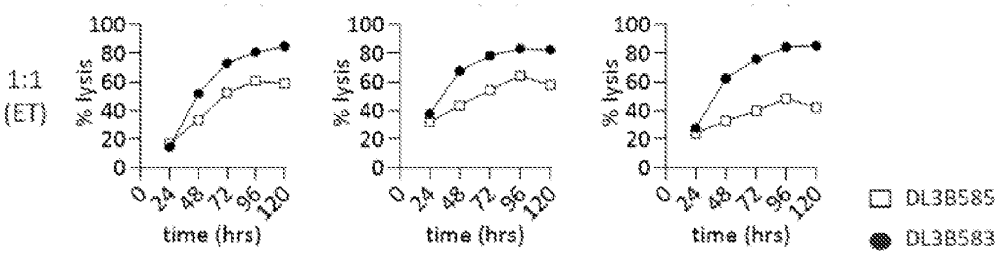

Figure 31

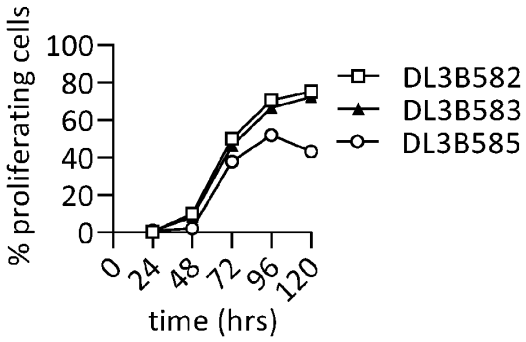

Figure 31

Figure 32A

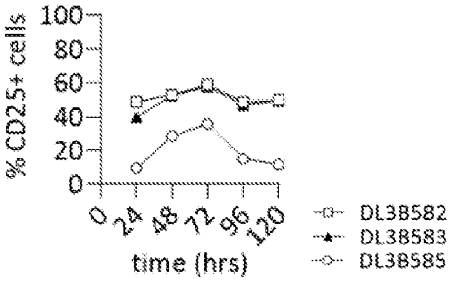

Figure 32B

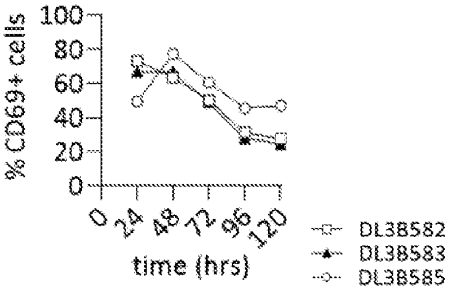

Figure 32C

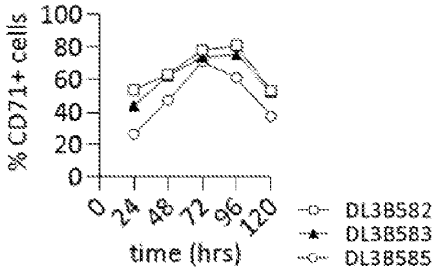

Figure 33A

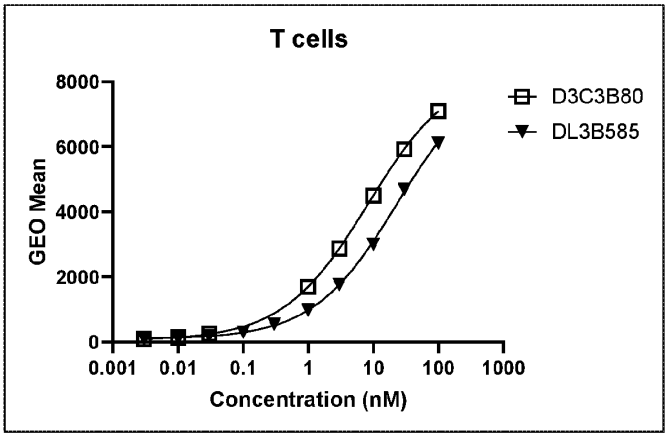
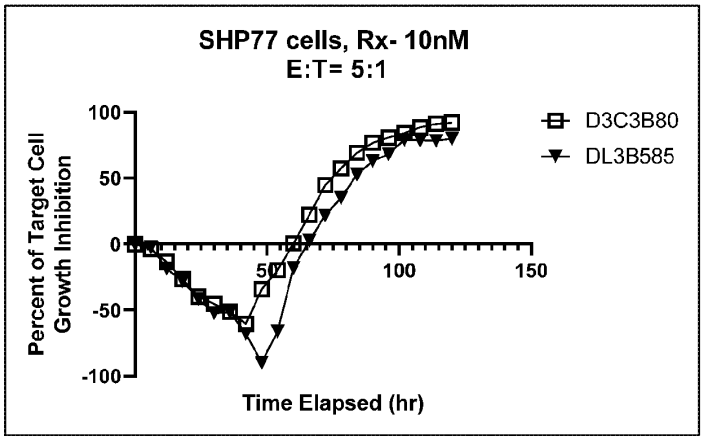
Figure 33B