

FIGURE 1

SEQ ID	Description	Sequence
1	Heavy Chain Variable Region	QVQLQQPGAELVKPGASVKMSCKASGYFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTSAA
2	Heavy Chain Constant Region – Option 1	STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
3	Heavy Chain Constant Region – Option 2	STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
4	Heavy Chain, Full Length Sequence with signal – Option 1	<u>MMRP</u> IVLVLLFATSALA <u>QVQLQQPGAELVKPGASVKMSCKASGYFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTSAA</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
5	Heavy Chain, Full Length Sequence with signal – Option 2	<u>MMRP</u> IVLVLLFATSALA <u>QVQLQQPGAELVKPGASVKMSCKASGYFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTSAA</u> STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 1- Cont.

SEQ ID	Description	Sequence
6	Heavy Chain, Full Length Sequence – Option 1	QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIG AIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYY GGDWYFNVWGAGTTVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV N HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVAVSHEDPEVKFNWYVDGVEVHNAKTPREEQYASTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK
7	Heavy Chain, Full Length Sequence – Option 2	QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIG AIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYY GGDWYFNVWGAGTTVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV N HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISR RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPSRDEL TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK
8	Light Chain Variable Region	QIVLSQSPAILSASPGEKVTMTCRASSSVYIHWFFQKQPGSSPKPWIYATSNL ASGVPPVRFSGSGSGTSYSLTISRVEAEDAATYYCQWTSNPPTFGGGTKLEIK
9	Light Chain Constant Region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSYSLSSLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
10	Linker	APTSSSGGGGS
11	A1-A2 Domain (NQ)	EPHSLSYDITVIPKFRPGPRWCAVQGQVDEKTFLLHYDCGQKTVTPVSPLGKK LQVTTAWKAQNPVLRVVDILTEQLWDIQLENYTPKEPLTLQARMSCEQKA EGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKV VAT KLYLWSMGDCIGWLEDFLMGMDSTLEPS
12	Light Chain, Full Length Fusion Sequence with signal	MMRPVIVLLFATSALA QIVLSQSPAILSASPGEKVTMTCRASSSVYIHWFF QKPGSSPKPWIYATSNLASGVPPVRFSGSGSGTSYSLTISRVEAEDAATYY CQWTSNPPTFGGGTKLEIK RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSLTSLKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC APTSSSGGGGSE PHSLSYDITVIPKFRPGP RWCAVQGQVDEKTFLLHYDCGQKTVTPVSPLGKKLQVTTAWKAQNPVLRV VDILTEQLWDIQLENYTPKEPLTLQARMSCEQKAEGHSSGSWQFSFDGQIFL LFDSEKRMWTTVHPGARKMKEKWENDKV VATKLYLWSMGDCIGWLEDFL MGMDSTLEPS

FIGURE 1- Cont.

SEQ ID	Description	Sequence
13	Light Chain, Full Length Fusion Sequence with A1-A2 domain and linker	QIVLSQSPAILASAPGEKVTMTCRASSSVSYIHWFAQKPGSSPKPWYATS NLASGVVPRFSGSGSGTSYSLTISRVEAEDAATYYCQWTSNPPTFGGGT KLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGECAPTSSSGGGGSEPHSLSYDITVIPKFRPGPRWCVAVQGVDEKTFLLHY DCGQKTVTPVSPGKLLQVTTAWKAQNPVLREVVDILTEQLWDIQLENYTP KEPLTLQARMSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGA RKMKEKWENDKVATKLYLWSMGDCIGWLEDFLMGMDSTLEPS
14	Linker	GGGS
15	iNKG2D domain	<i>LFNQEVQIPLTESYCGPCPNWICYKNNCYQFFDESKNWYESQASCM SQNA SLLKVYSKEDQDLLKLVKSAHWMGLVHIPTNGSWQWEDGSILSPNLLTIEM QKGDICALYASSFKGYIENCSTPNTYICMQRTV</i>
16	CD8a hinge/tm domain	TTTPAPRPPTAPTASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLA GTCGVLLSLVITLYCSL
17	4-1BB domain	<u><i>KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEGGGCEL</i></u>
18	CD3 ζ domain	RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKP RRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATK DTYDALHMQALPPR
19	iNKG2D domain + CD8a hinge/tm domain + 4-1BB domain + CD3 ζ domain	<i>LFNQEVQIPLTESYCGPCPNWICYKNNCYQFFDESKNWYESQASCM SQNA SLLKVYSKEDQDLLKLVKSAHWMGLVHIPTNGSWQWEDGSILSPNLLTIEM QKGDICALYASSFKGYIENCSTPNTYICMQRTVTTTPAPRPPTAPTASQPLSL RPEACRPAAGGAVHTRGLDFACDIYWAPLAGTCGVLLSLVITLYCSL</i> <u><i>KRGR KKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEGGGCEL</i></u> RVKFSRSADAPAYK QGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL QKDKMAEAYSEIGMKGERRRGKGGHDGLYQGLSTATKDTYDALHMQALP PR
20	Signal sequence + iNKG2D domain + CD8a hinge/tm domain + 4-1BB domain + CD3 ζ domain + linker + eGFP	<u><i>MALPVTALLPLALLHAARPLFNQEVQIPLTESYCGPCPNWICYKNNCYQF FDESKNWYESQASCM SQNASLLKVYSKEDQDLLKLVKSAHWMGLVHIPTN GSWQWEDGSILSPNLLTIEMQKGDICALYASSFKGYIENCSTPNTYICMQRTV TTTPAPRPPTAPTASQPLSLRPEACRPAAGGAVHTRGLDFACDIYWAPLA GTCGVLLSLVITLYCSL</i></u> <u><i>KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCEL</i></u> RVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGGHDGLYQ GLSTATKDTYDALHMQALPPRSGSGSGSGSMVSKGEELFTGVVPILVELDG DVNGHKFSVSGEGDATYGKLTCLKICTTGKLPVPWPTLVTTLTLYGVQCFS RYPDHMKQHDFKSAPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRI ELKGIDFKEDGNILGHKLEYNNSHNVIYIMADKQKNGIKANFKIRHNIEDGS VQLADHYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDMVLLFVTA AGITLGMDELYK

FIGURE 1- Cont.

SEQ ID	Description	Sequence
21	Light Chain, Full Length	QIVLSQSPAILSASPGKVTMTCRASSSVSIHWFQQKPGSSPKPWYATS NLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGT KLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSF NRGEC
30	A1-A2 domain	EPHSLSYDITVIPKFRPGPRWCAVQGQVDEKTFLLHYDCGNKTVTPVSPLGKK LNVTTAWKAQNPVLREVVDILTEQLWDIQLENYTPKEPLTLQARMSCEQKA EGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAT KLYLWSMGDCIGWLEDFLMGMDSTLEPS
31	A1-A2 domain (AYT)	EPHSLSYDITVIPKFRPGPRWCAVQGQVDEKTFLLHYDCGQKTVTPVSPLGKK LQVTTAWKAQNPVLREVVDILTEQLWDIQLAYTPKEPLTLQARMSCEQKA EGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAT KLYLWSMGDCIGWLEDFLMGMDSTLEPS
32	A1-A2 domain (QYT)	EPHSLSYDITVIPKFRPGPRWCAVQGQVDEKTFLLHYDCGQKTVTPVSPLGKK LQVTTAWKAQNPVLREVVDILTEQLWDIQLQYTPKEPLTLQARMSCEQKA EGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAT KLYLWSMGDCIGWLEDFLMGMDSTLEPS

FIGURE 2A

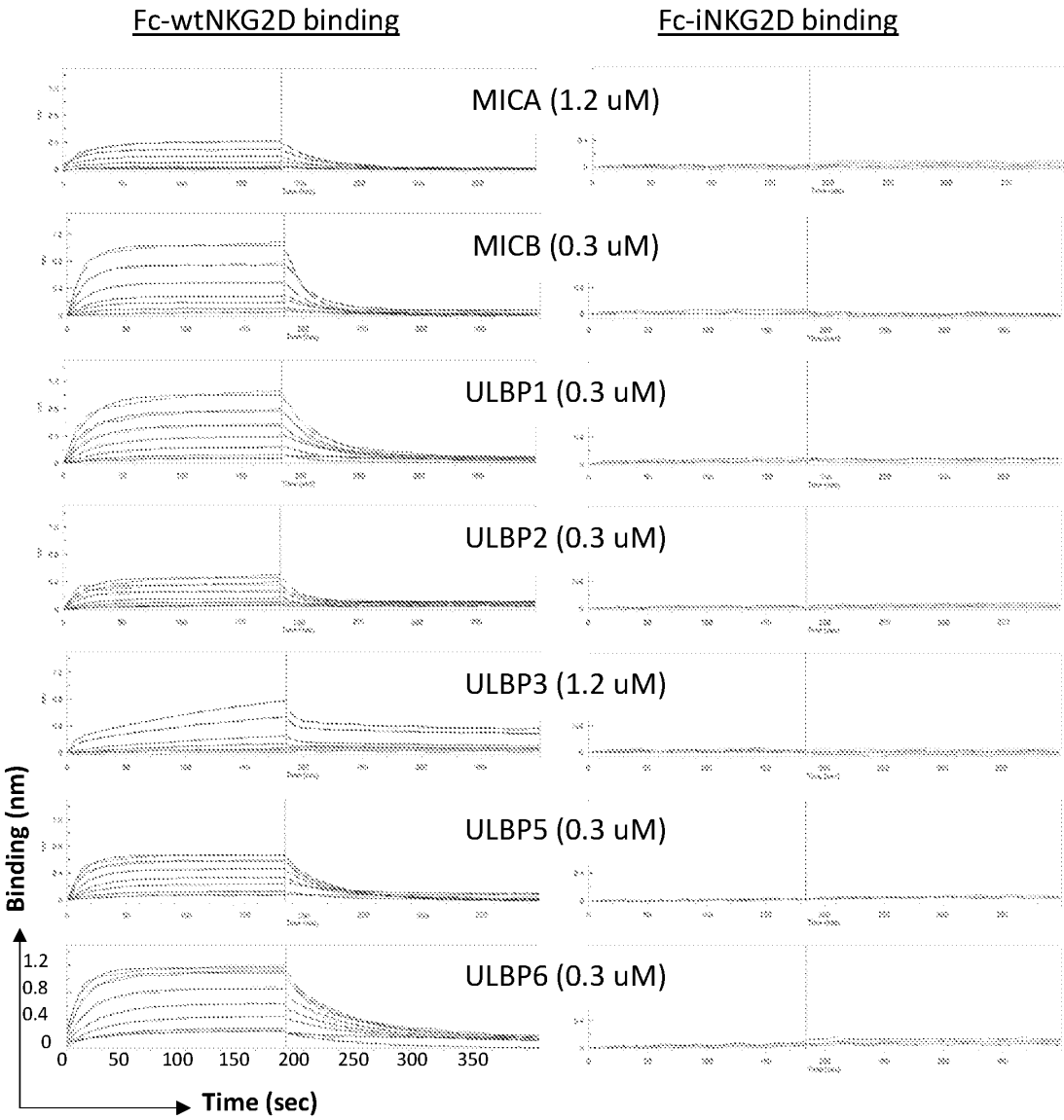


FIGURE 2B

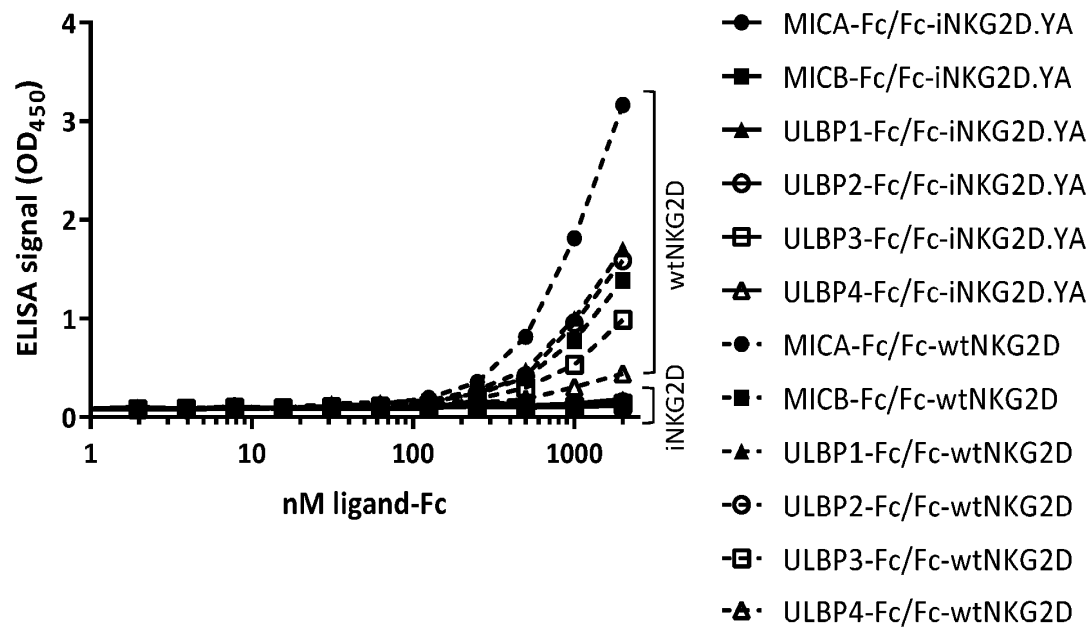


FIGURE 3A

◆ MICA ◆ MICB ◆ ULBP1 ✕ ULBP2 ✖ ULBP3 ◆ ULBP4

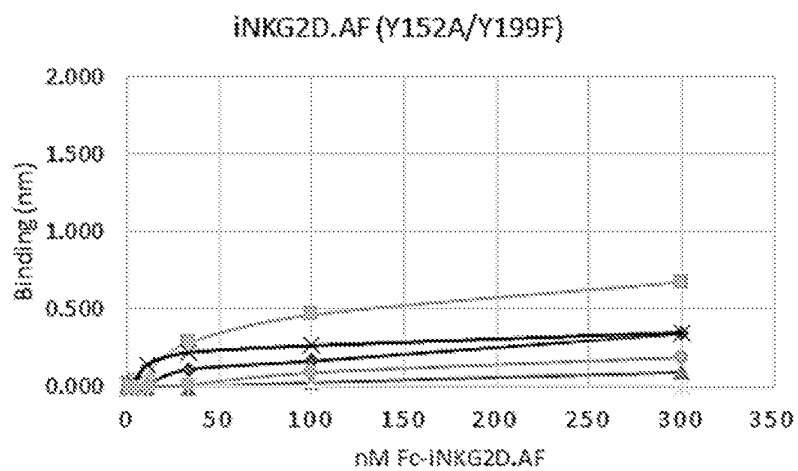
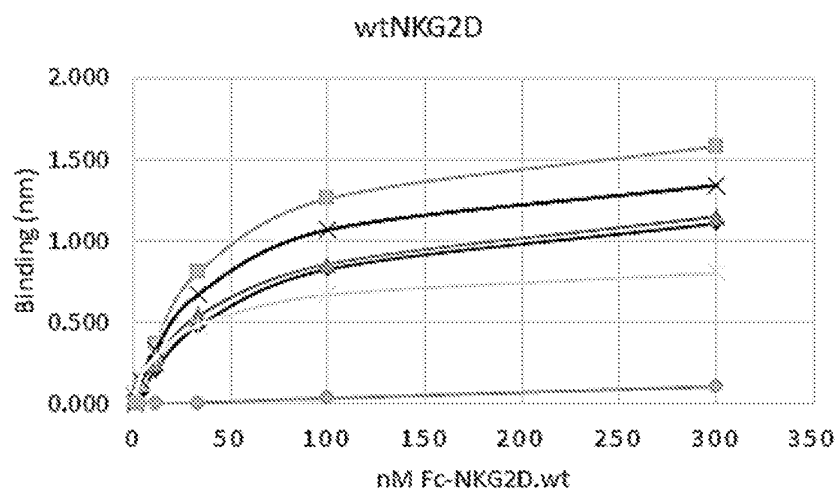


FIGURE 3B

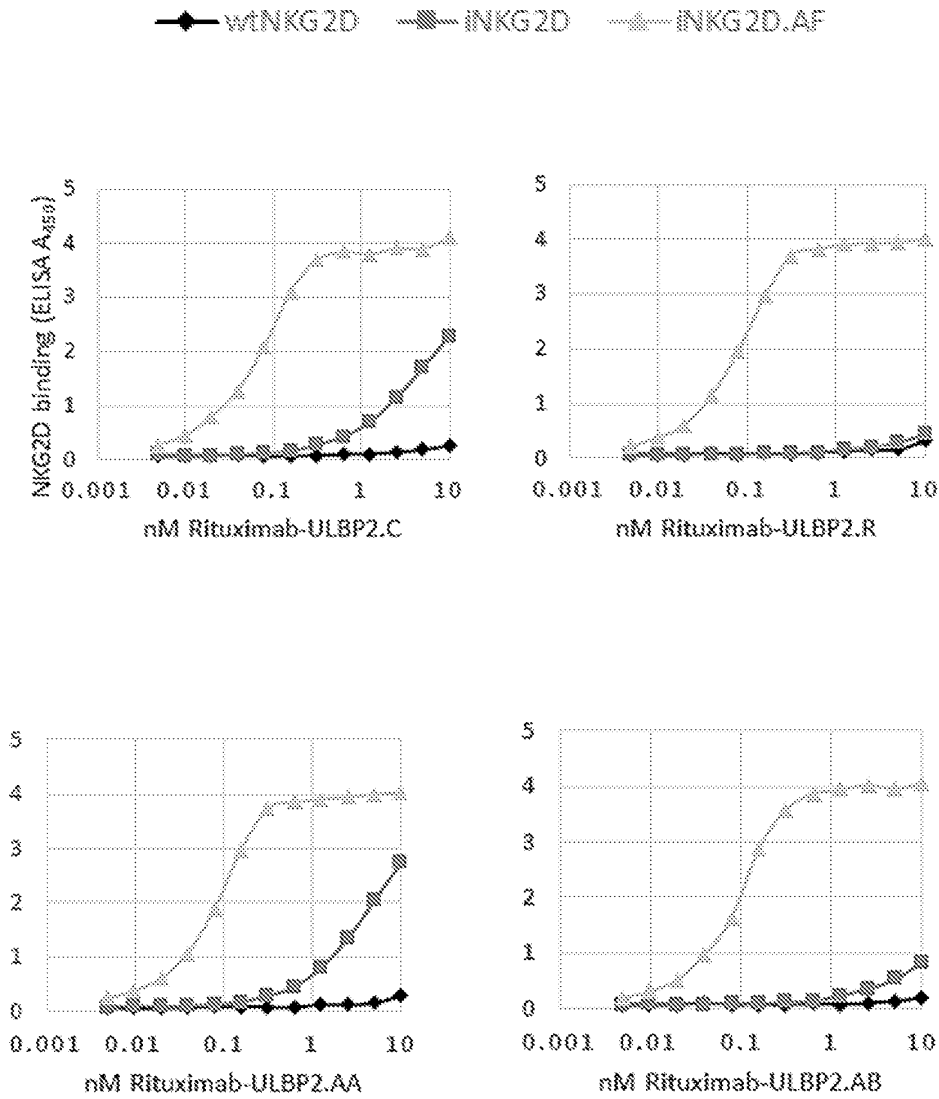


FIGURE 3C

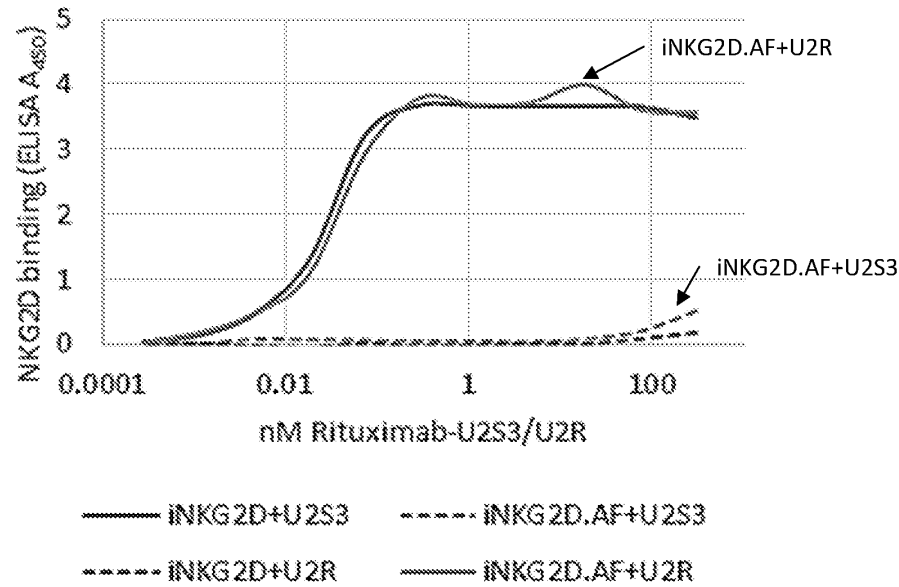
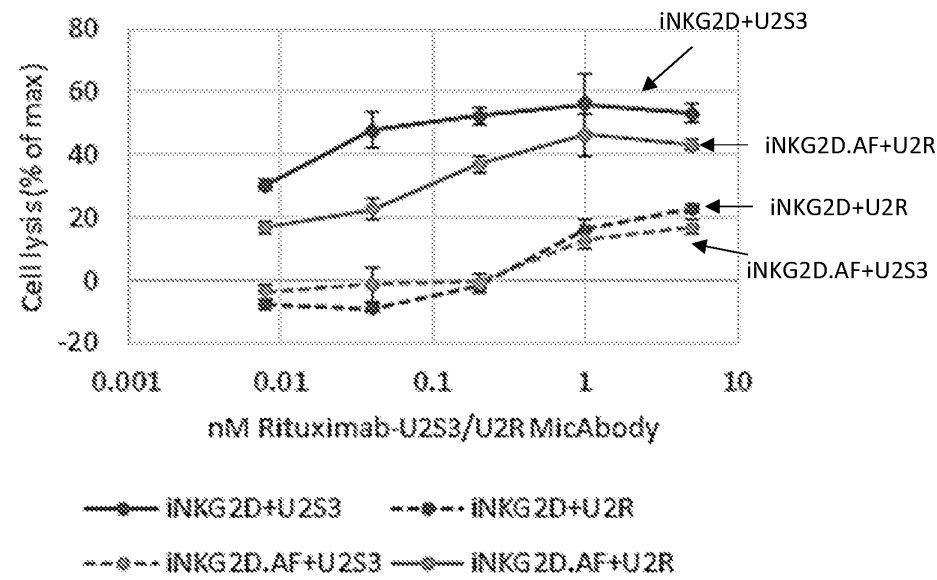


FIGURE 3D



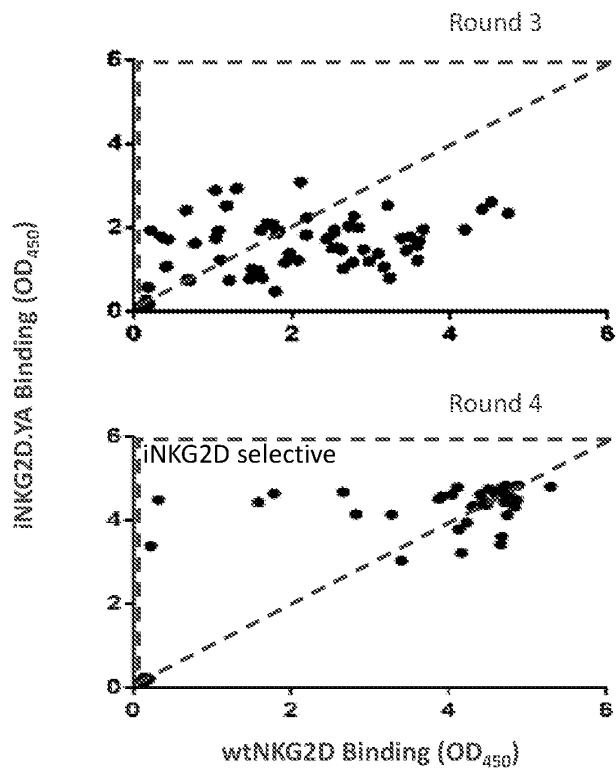


FIGURE 4A

FIGURE 4B

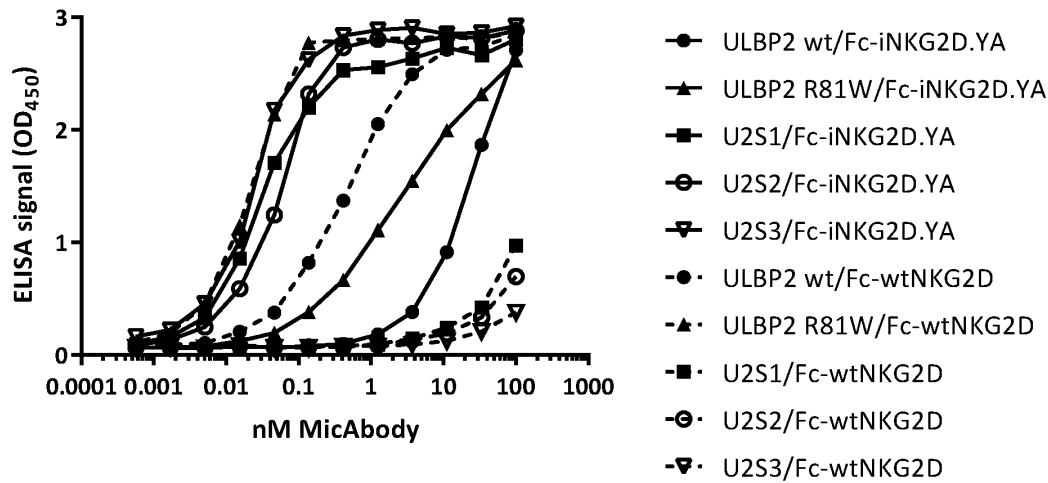


FIGURE 4C

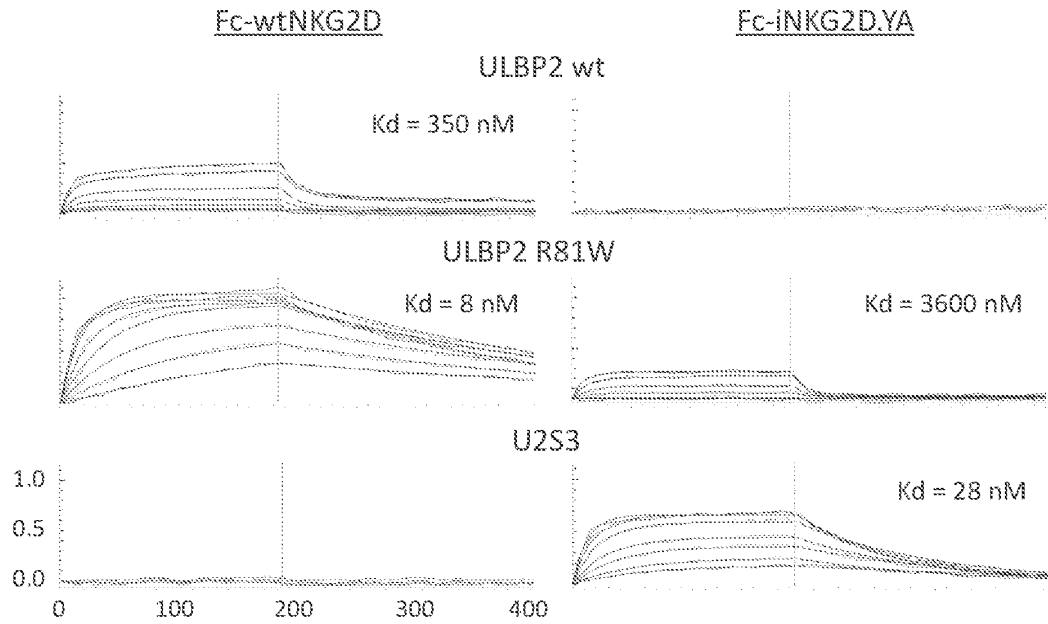


FIGURE 5

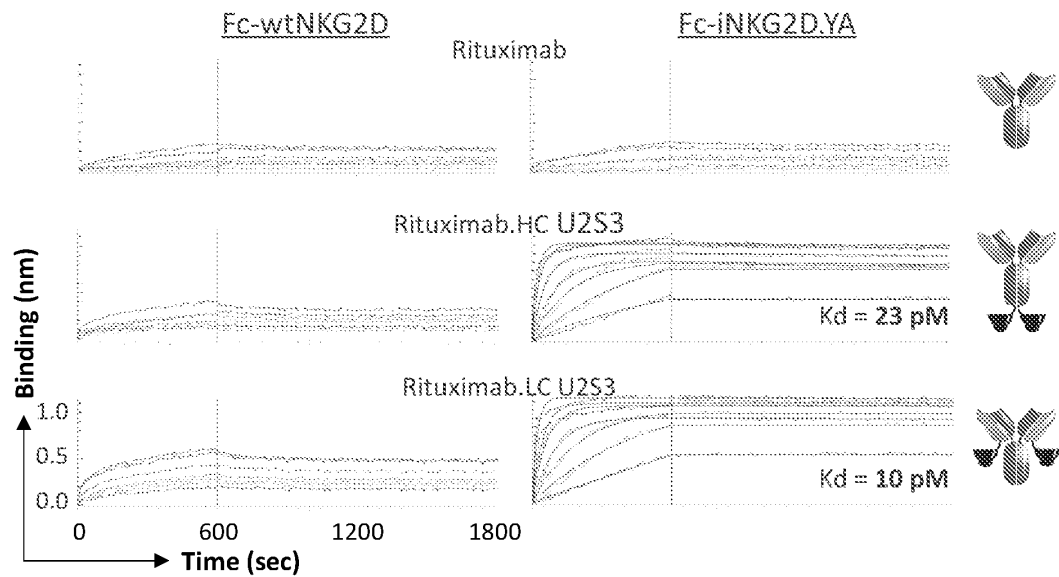
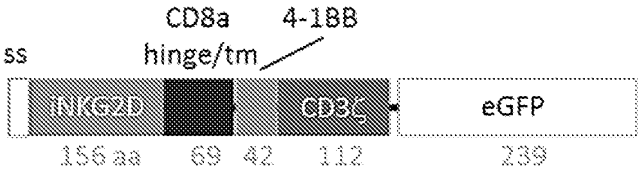


FIGURE 6



MALPVTALLPLALLHAARPLFNQEVQIPLTESYCGPCPNWICYKNNCYQFFDESKNWWYESQAS
CMSQNASLLKVYSKEDQDLLKLVKSAHWMGLVHIPTNGSWQWEDGSILSPNLLTIEMQKGDCA
LYASSFKGYIENCSTPNTYICMQRVTTPAPRPPTPAPTASQPLSLRPEACRPAAGGAVHTRGLD
FACDIYWAPLAGTCGVLLLSLVITLYCSLKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGG
CELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLY
NELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPRSGSGSGSGS
MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLT
YGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFK
EDGNILGHKLEYNNSHNVYIMADKQKNGIKANFKIRHNIEDGSVQLADHYQQNTPIGDGPVLL
PDNHYSTQSALSKDPNEKRDHMVLLFVTAAGITLGMDELYK (SEQ ID NO: 20)

FIGURE 7A

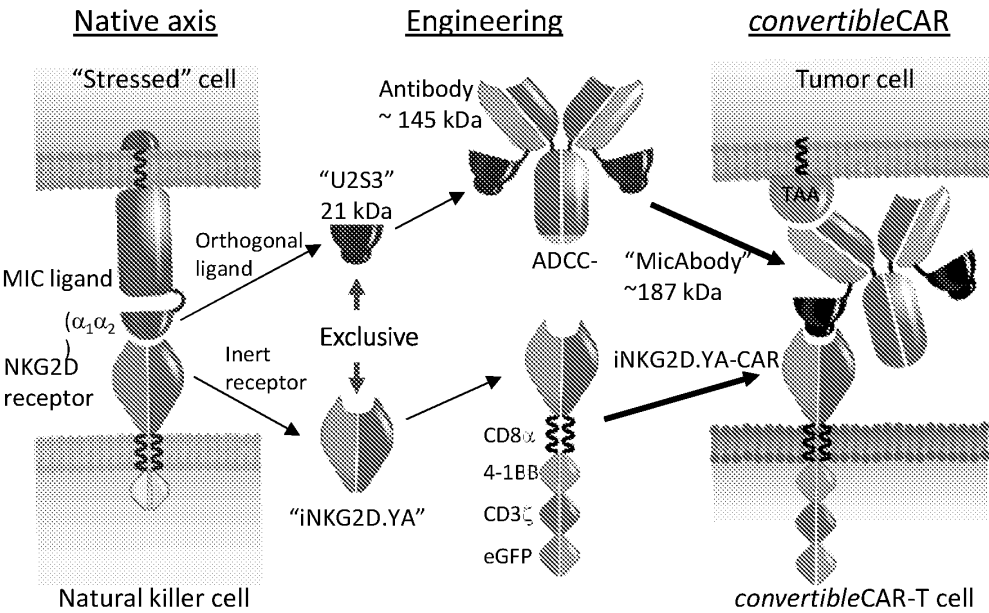


FIGURE 7B

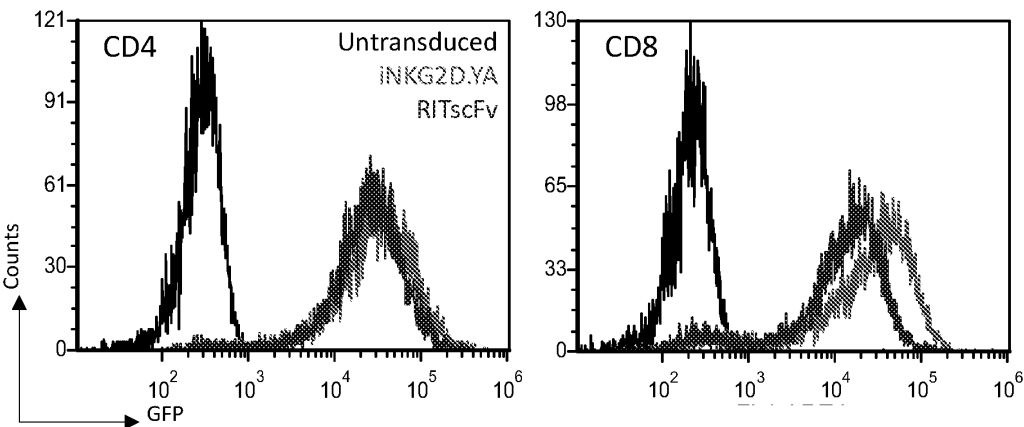


FIGURE 7C

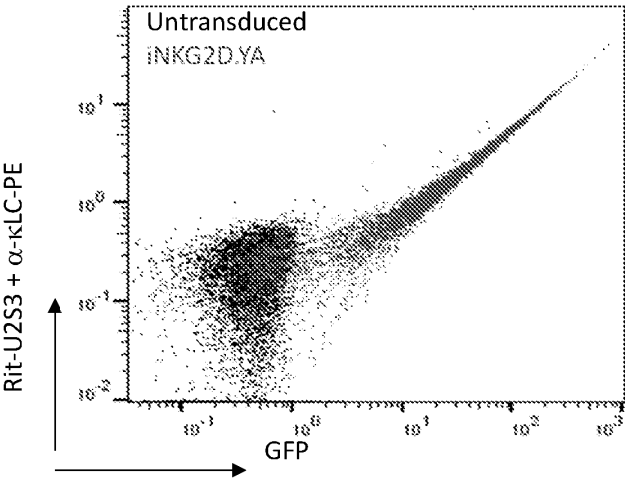


FIGURE 8A

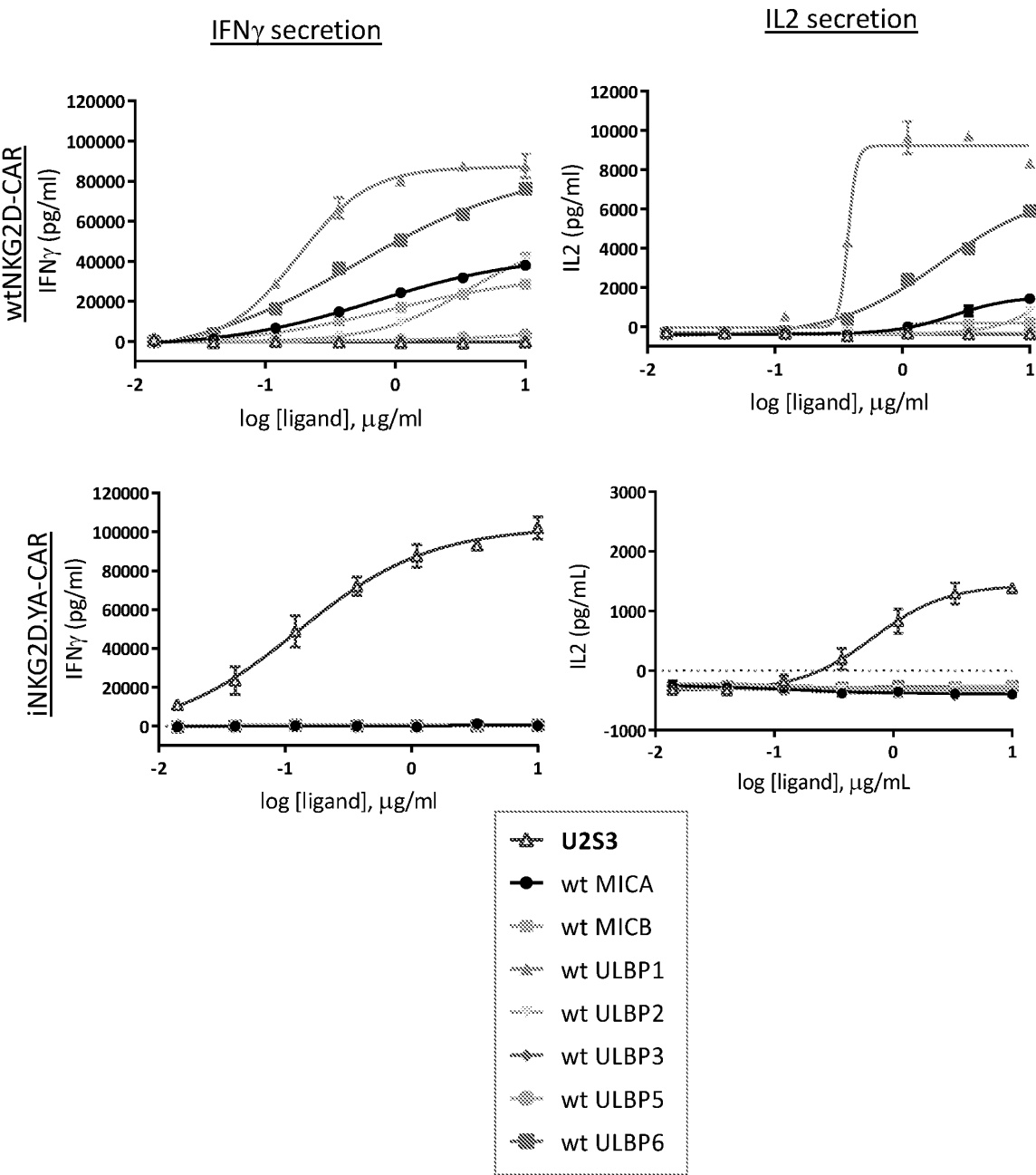


FIGURE 8C

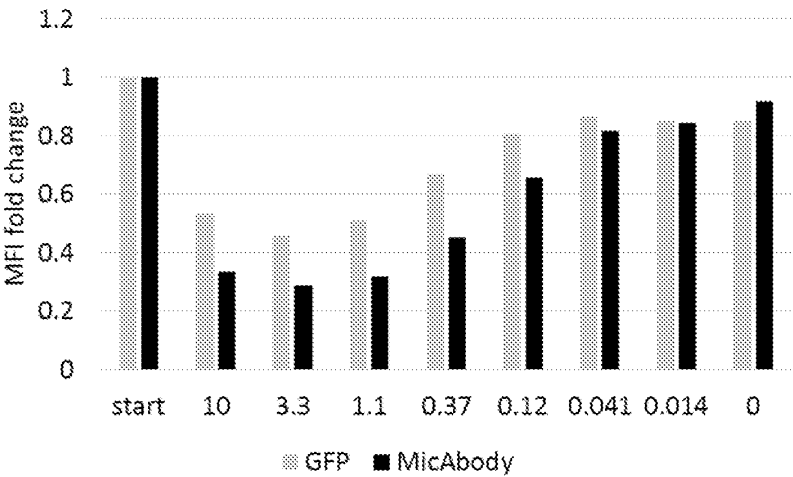
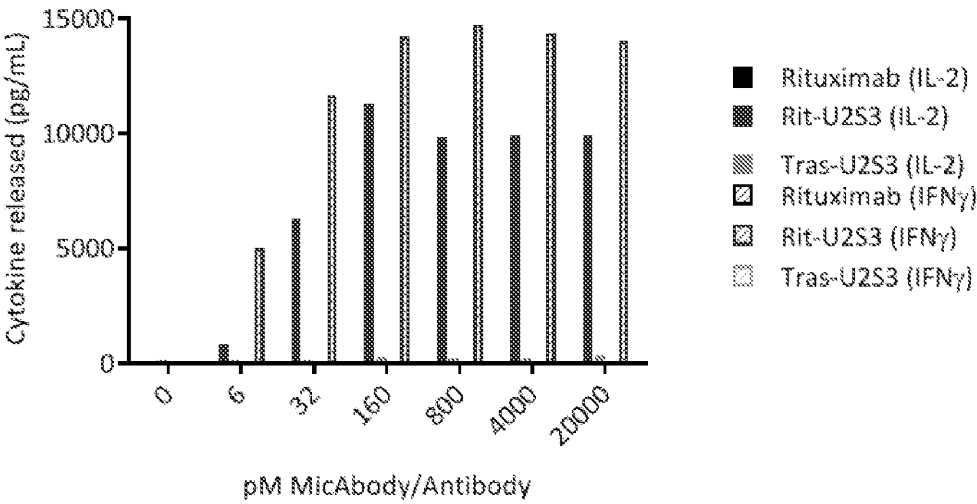


FIGURE 9A



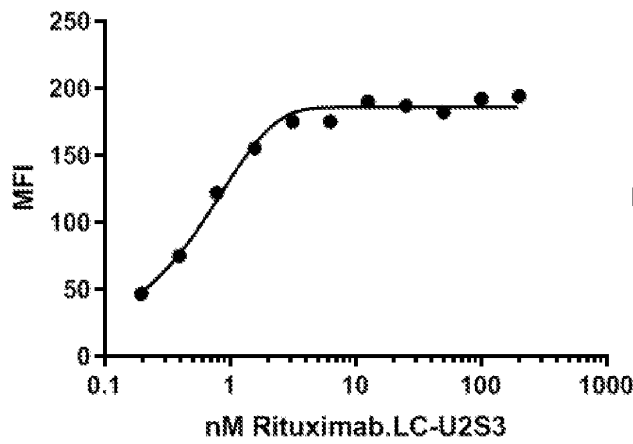


FIGURE 9B

FIGURE 9C

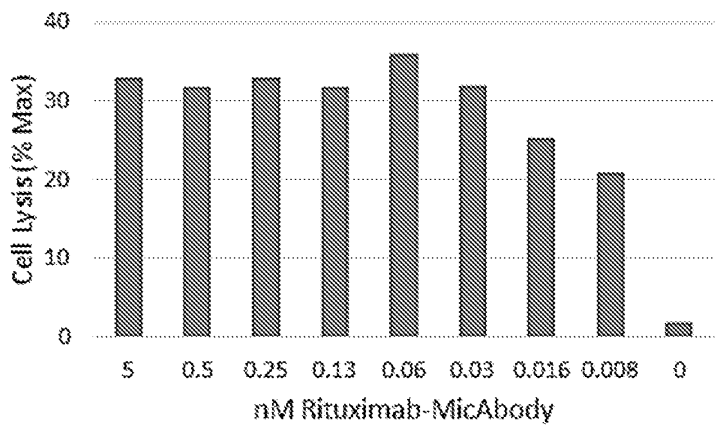
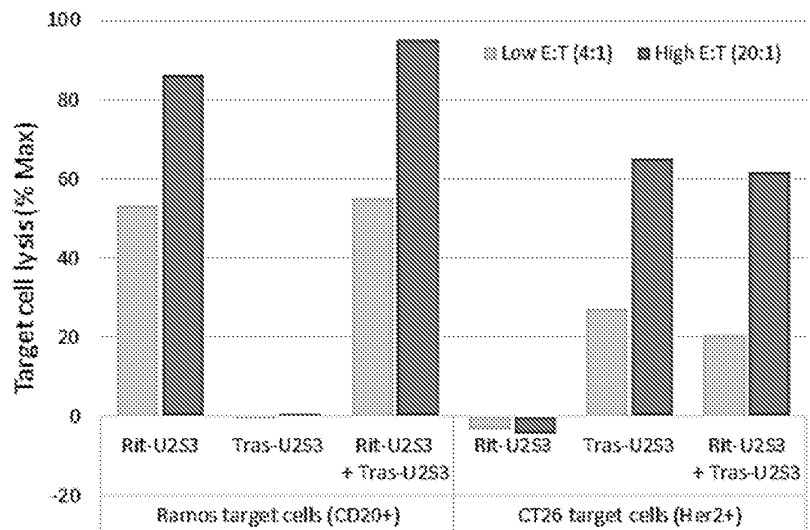


FIGURE 9D

FIGURE 10A

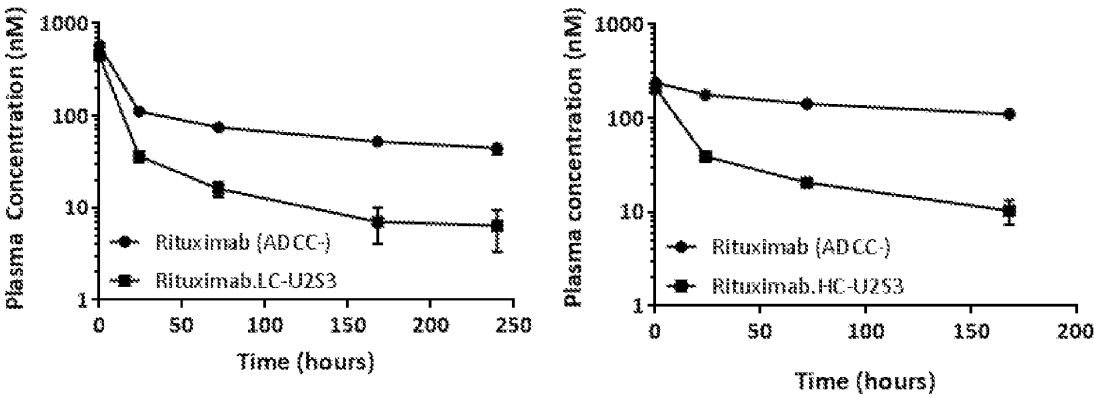


FIGURE 10B

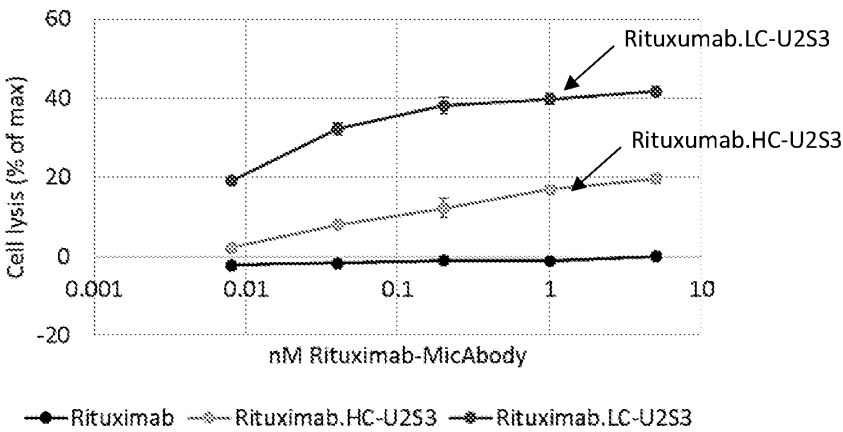
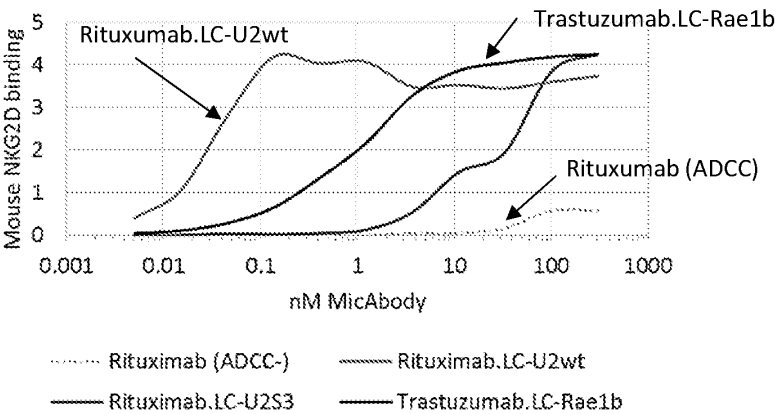
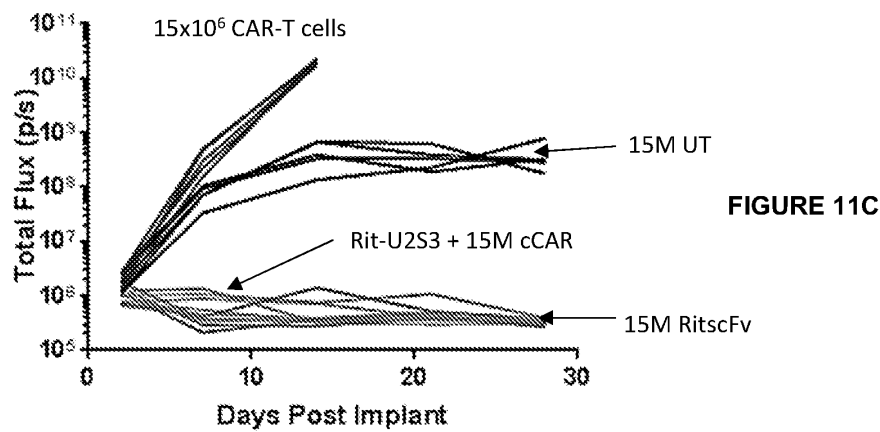
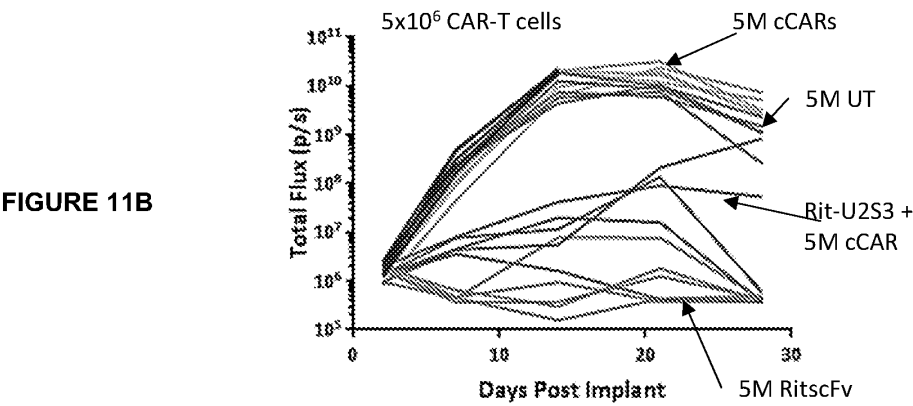
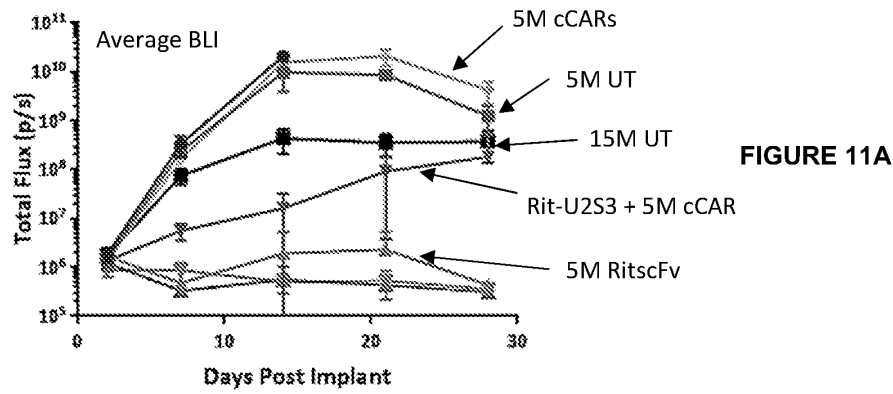
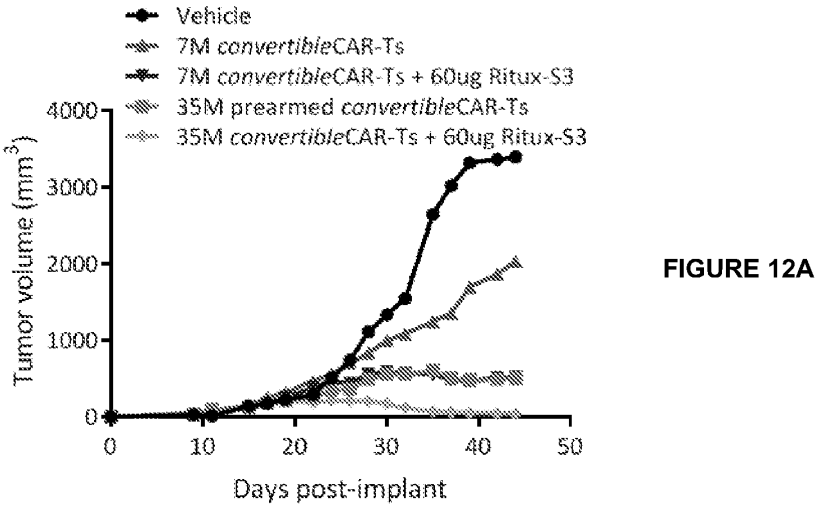
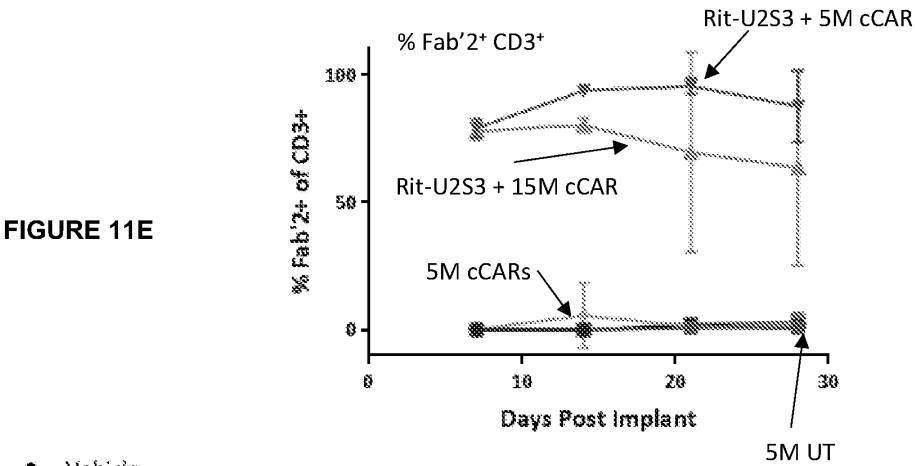
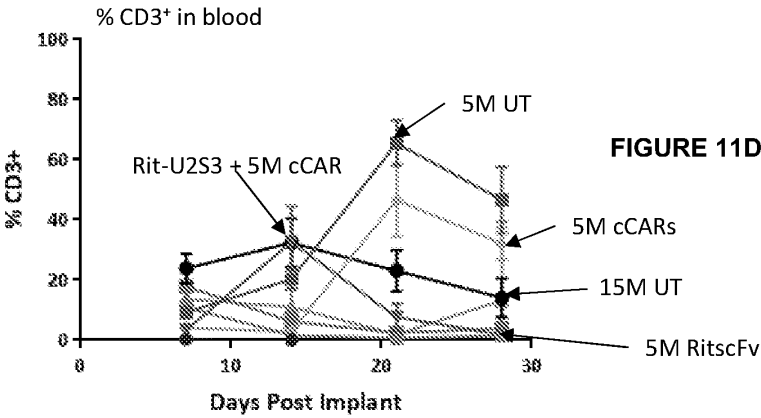
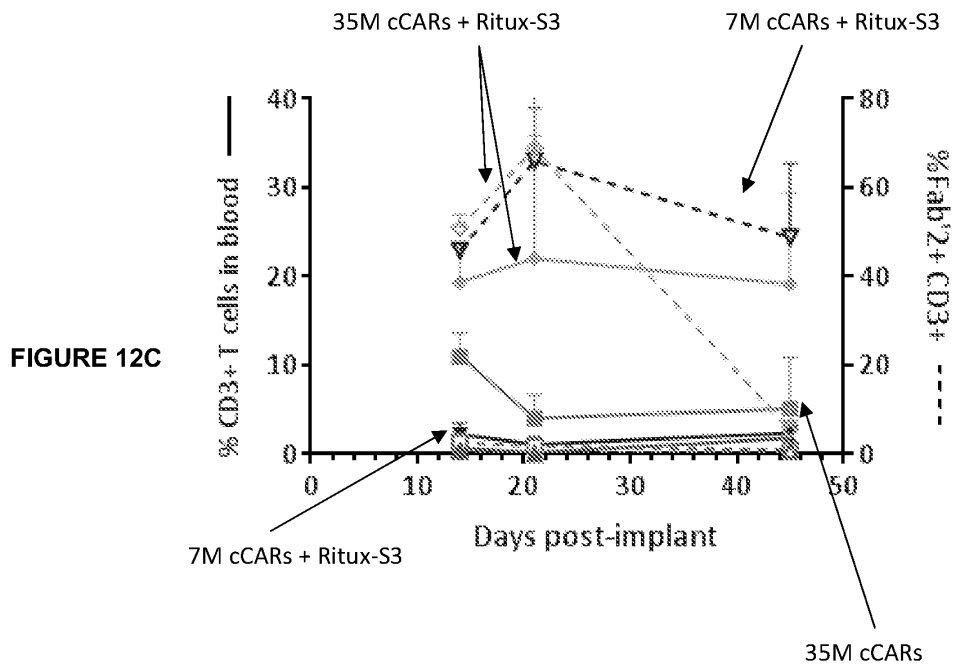
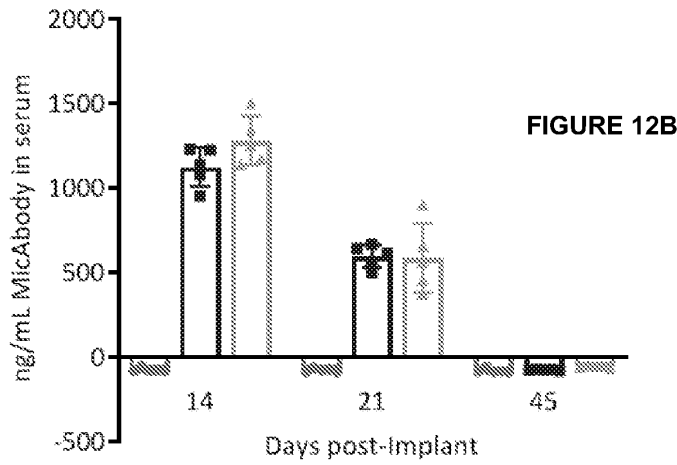


FIGURE 10C









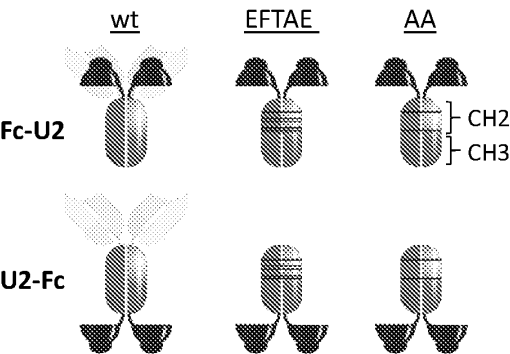
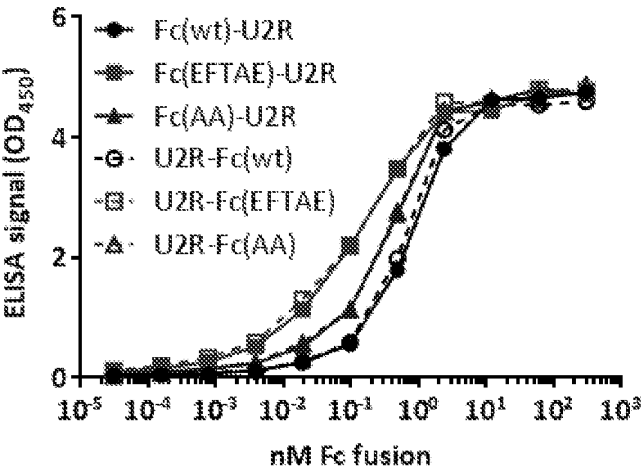


FIGURE 13A

FIGURE 13B



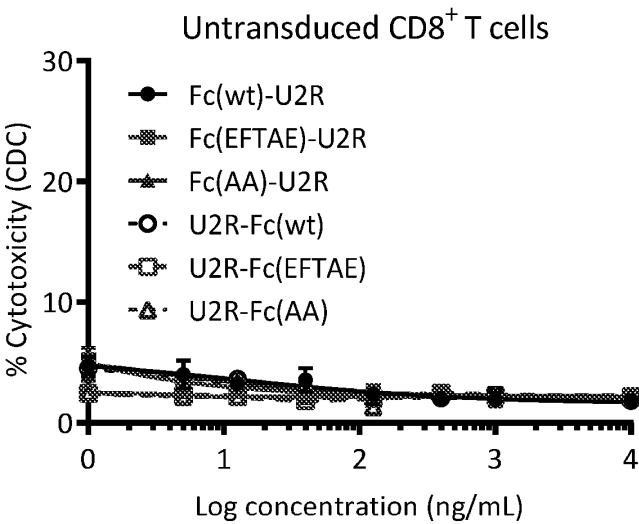


FIGURE 13C

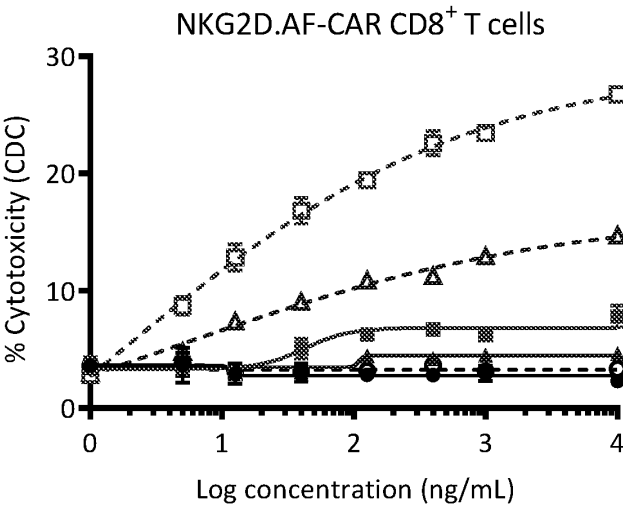


FIGURE 13D

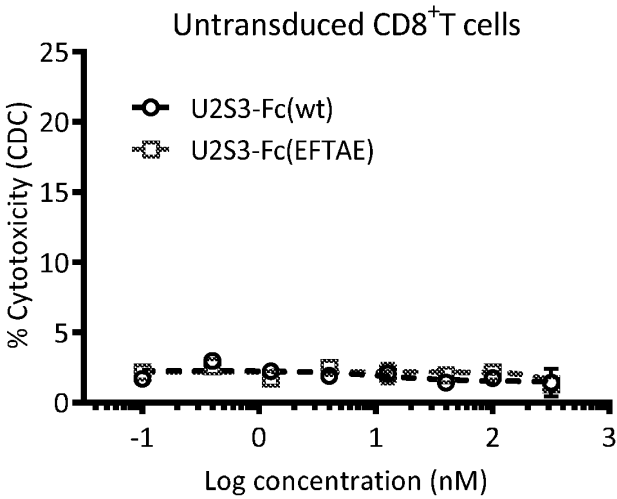


FIGURE 13E

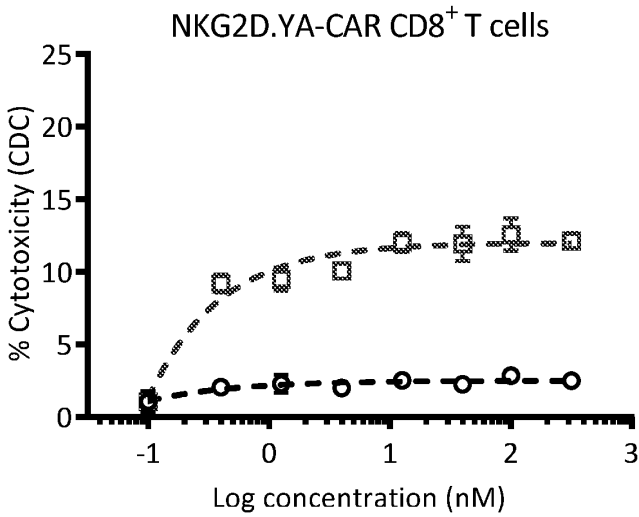


FIGURE 13F

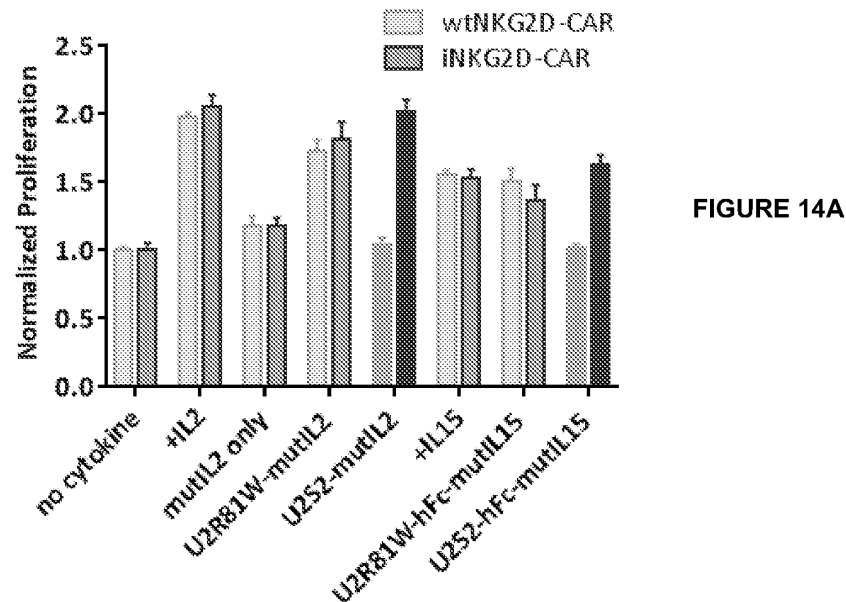
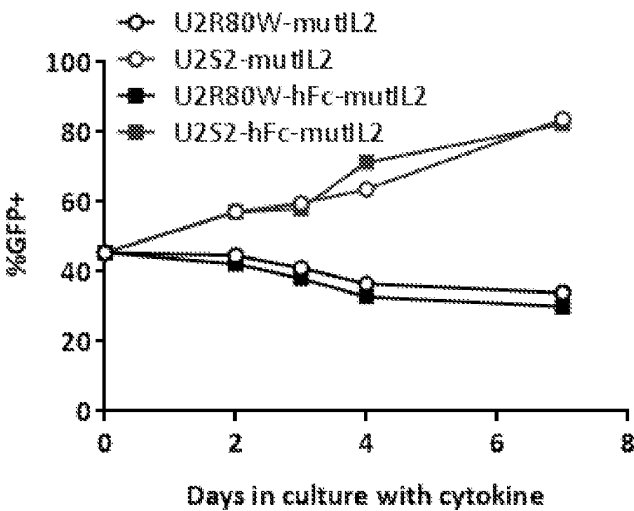


FIGURE 14B



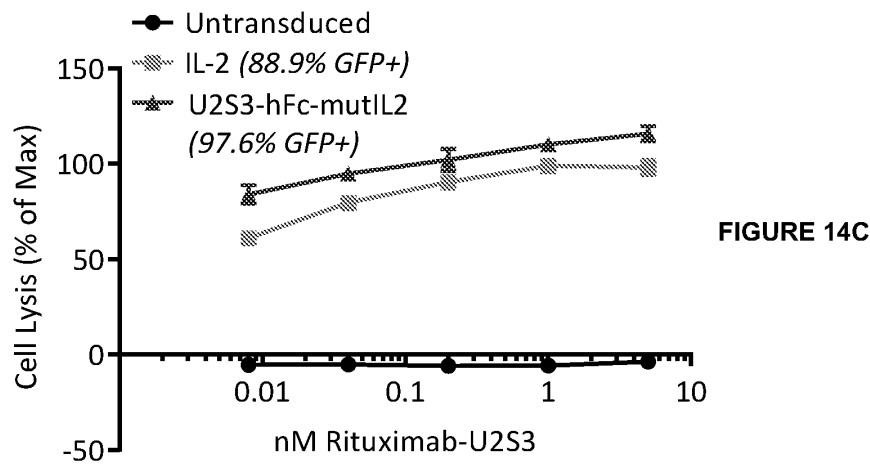


FIGURE 14C

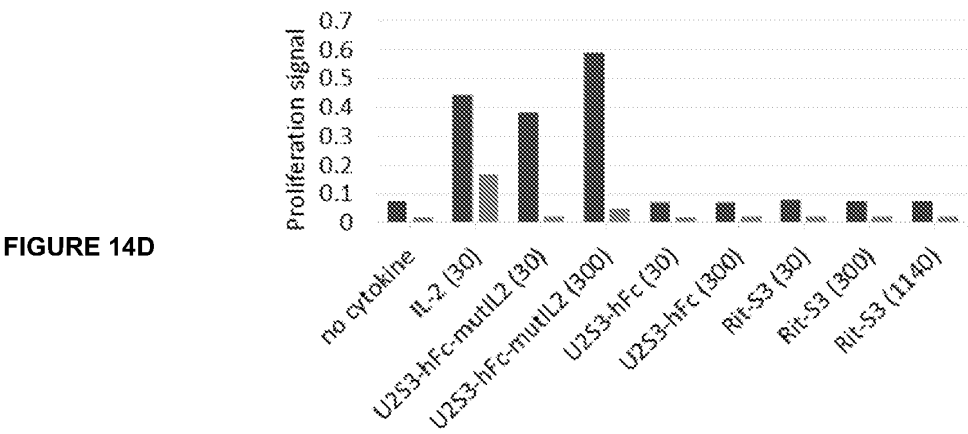


FIGURE 14D

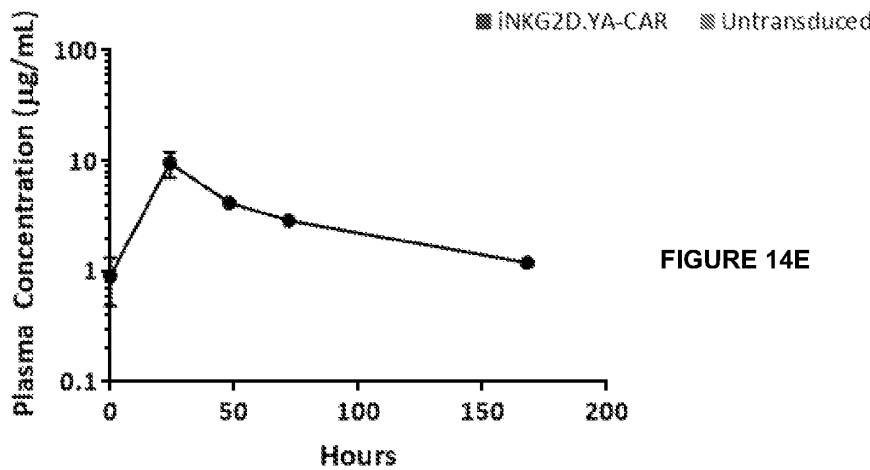


FIGURE 14E

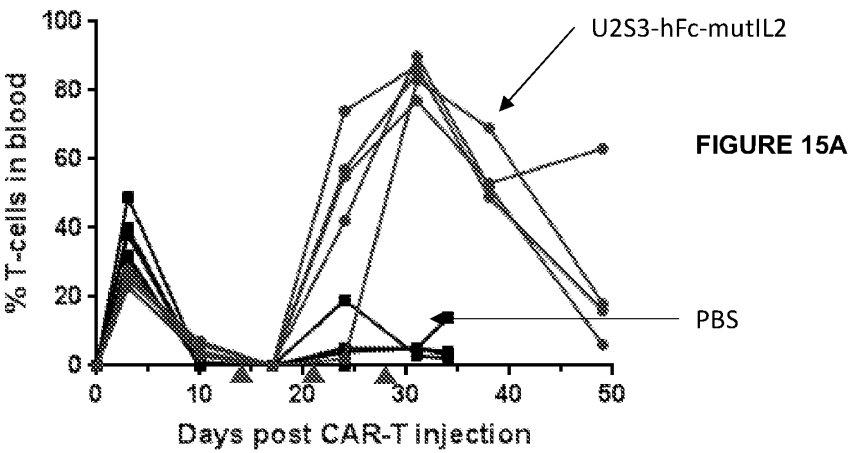


FIGURE 15B

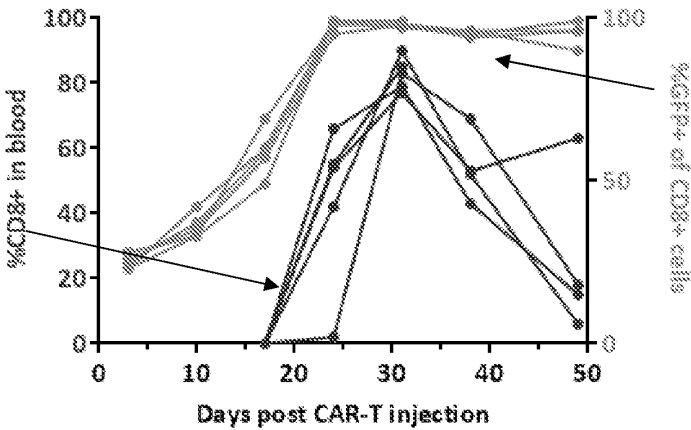


FIGURE 16

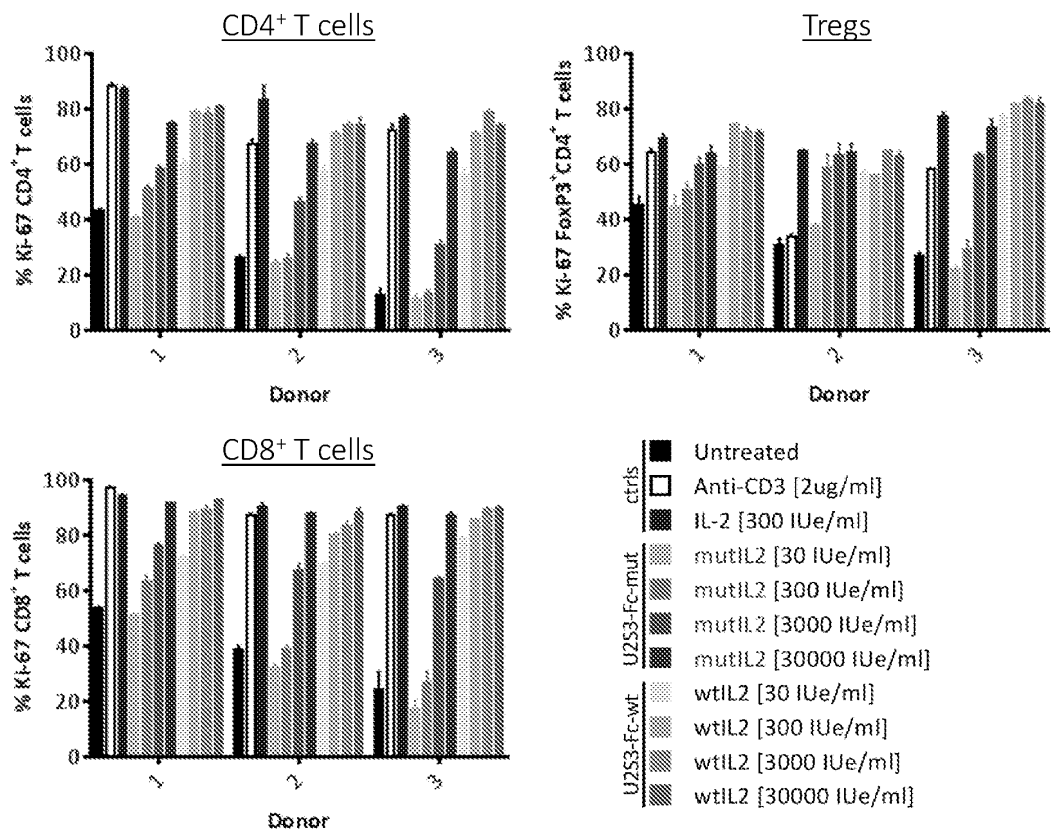


FIGURE 17A

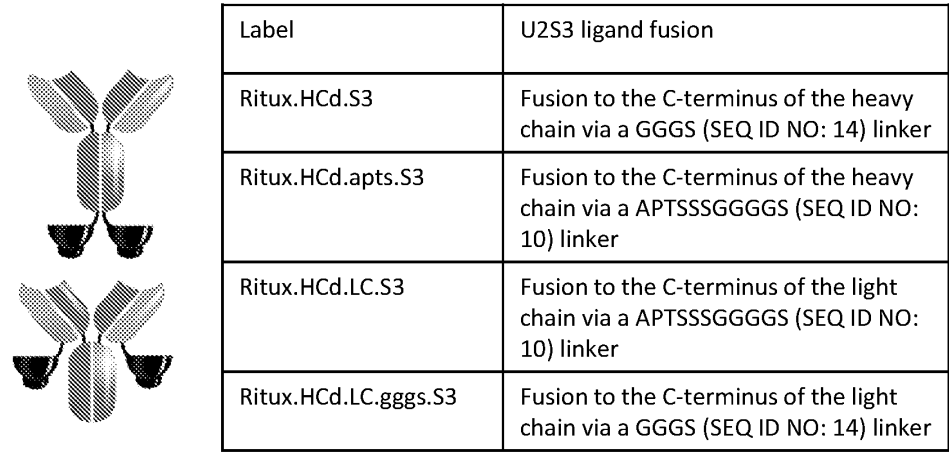


FIGURE 17B

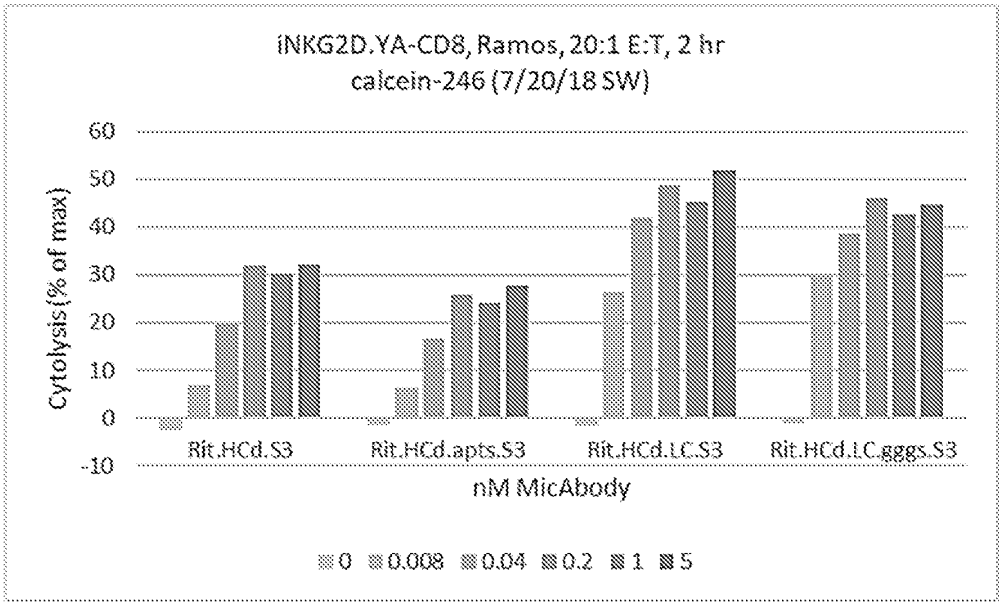


FIGURE 18

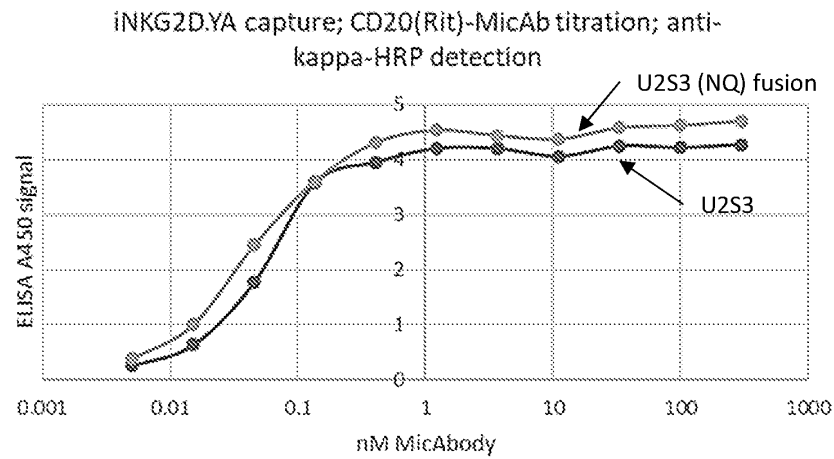


FIGURE 19

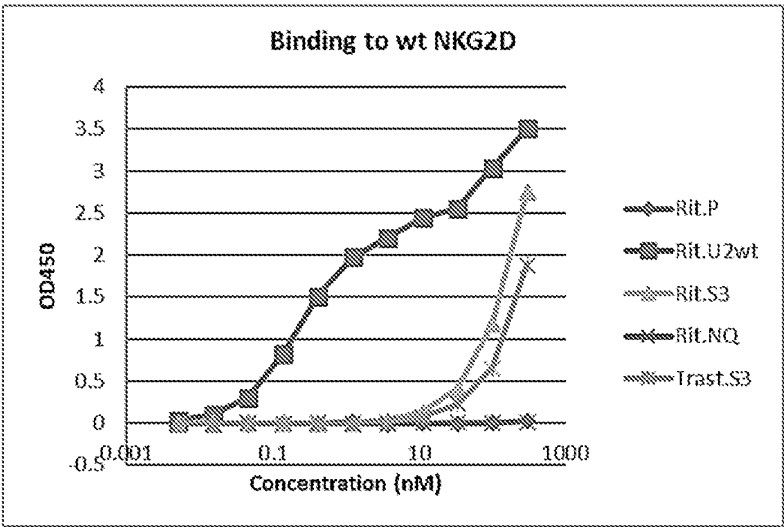


FIGURE 20

