

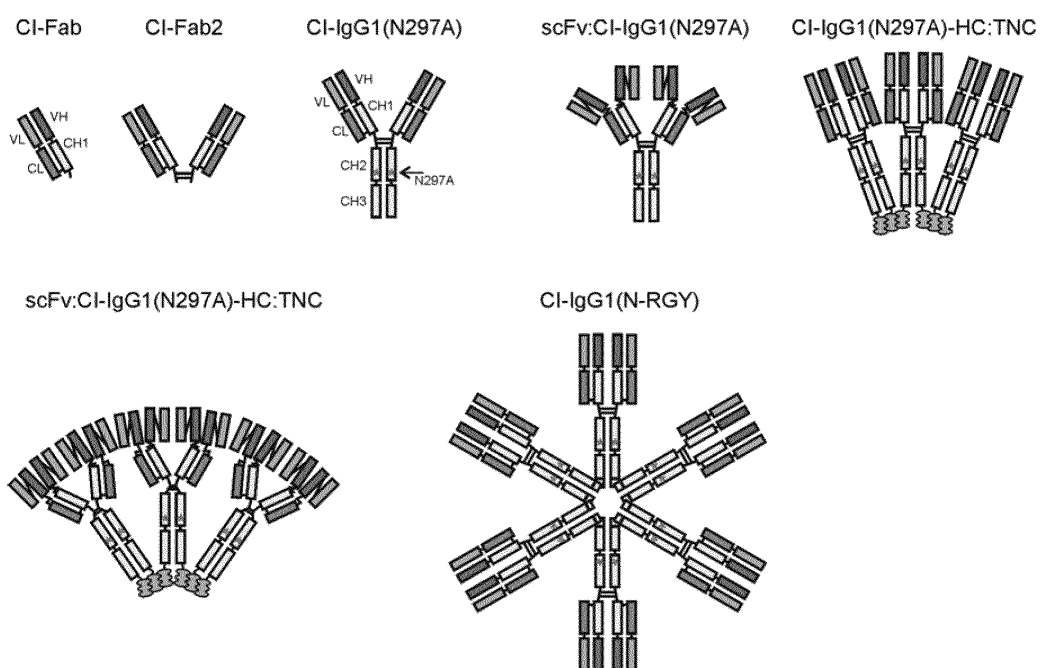
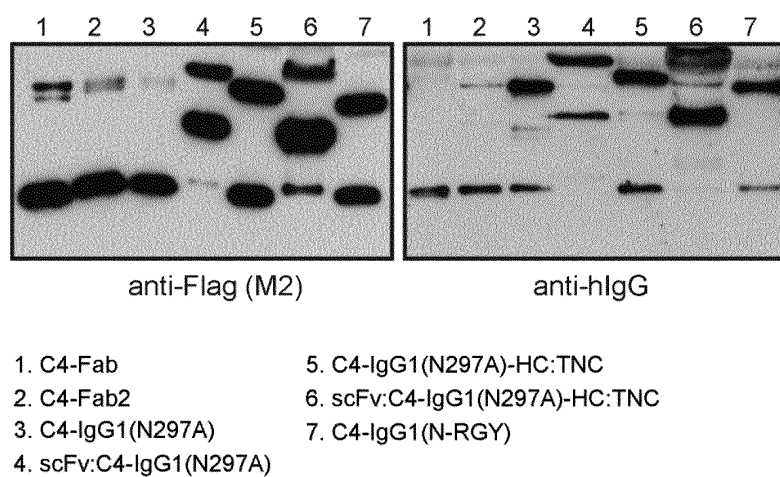


FIGURE 1

**FIGURE 2**

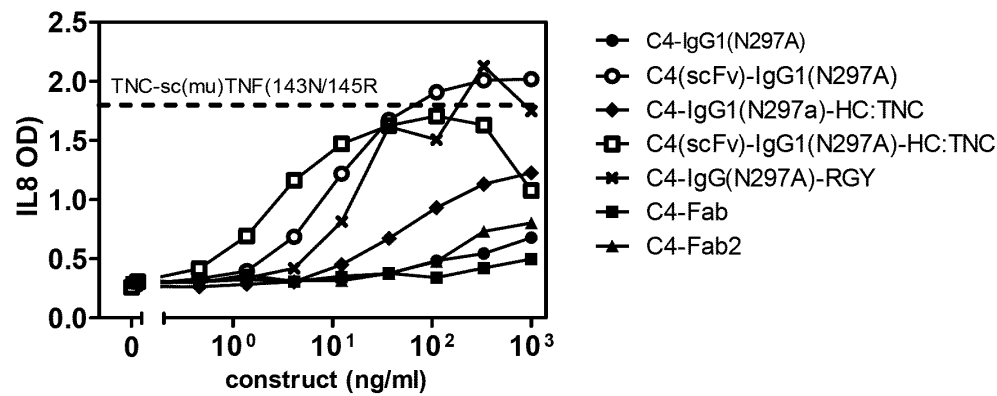


FIGURE 3

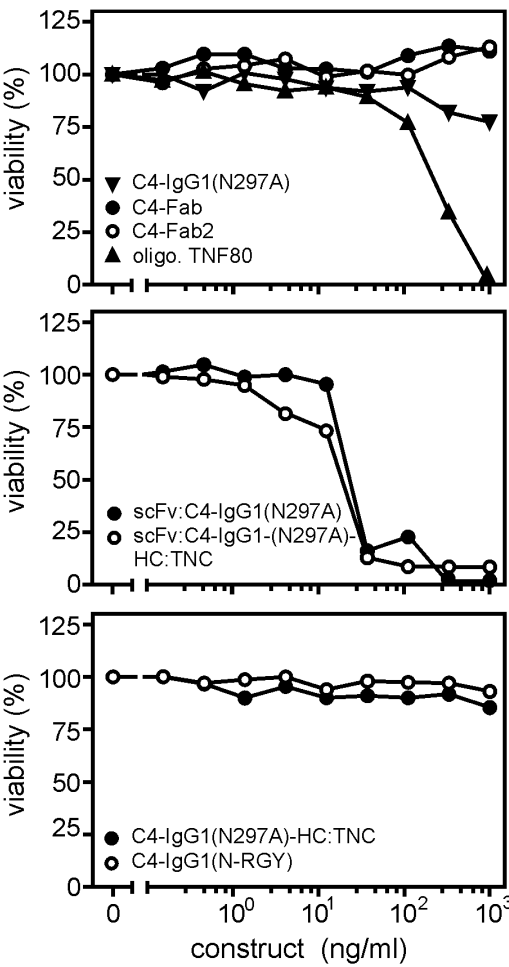
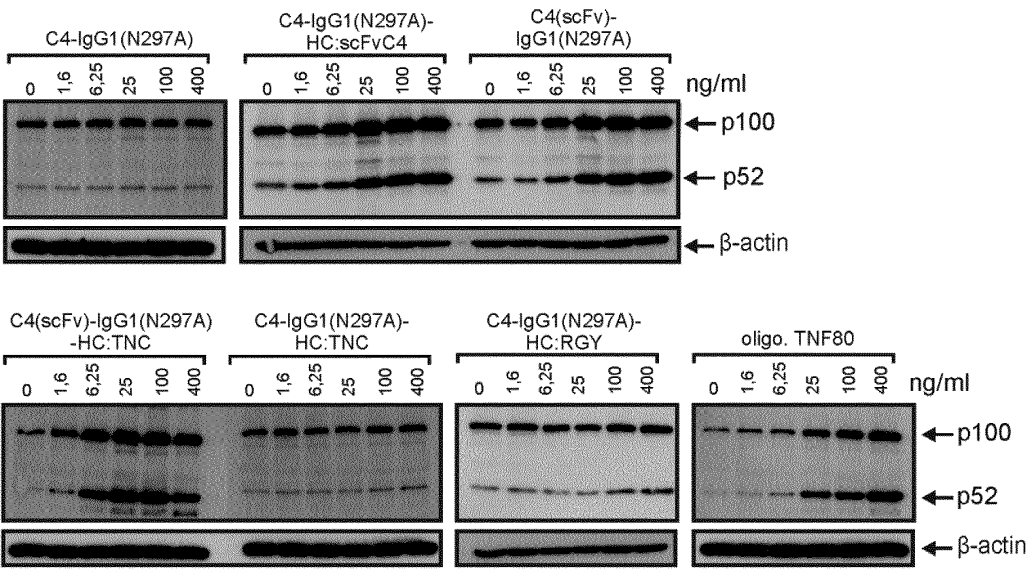


FIGURE 4



Patent-figure-5-lea-v1

FIGURE 5

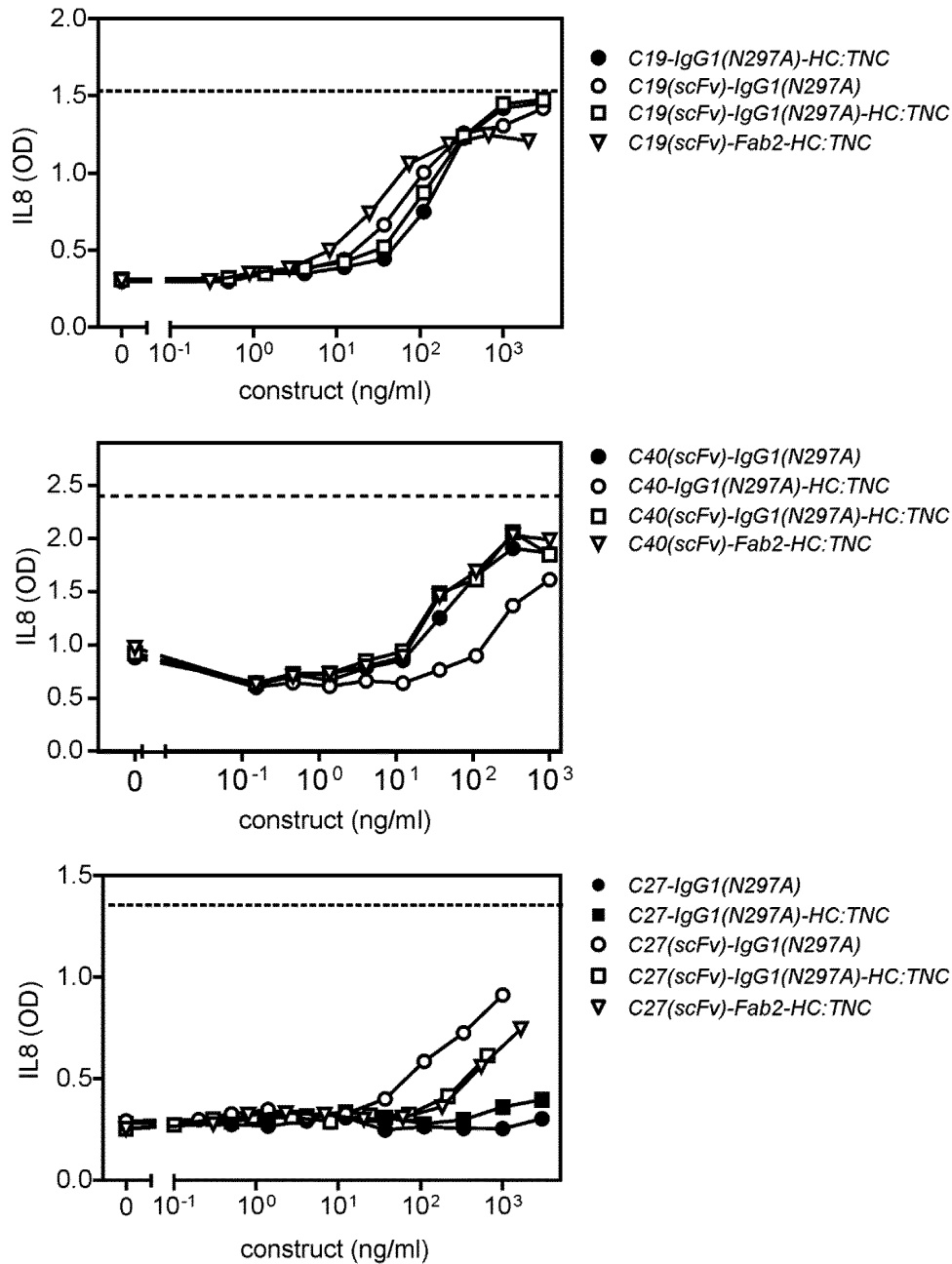


FIGURE 6

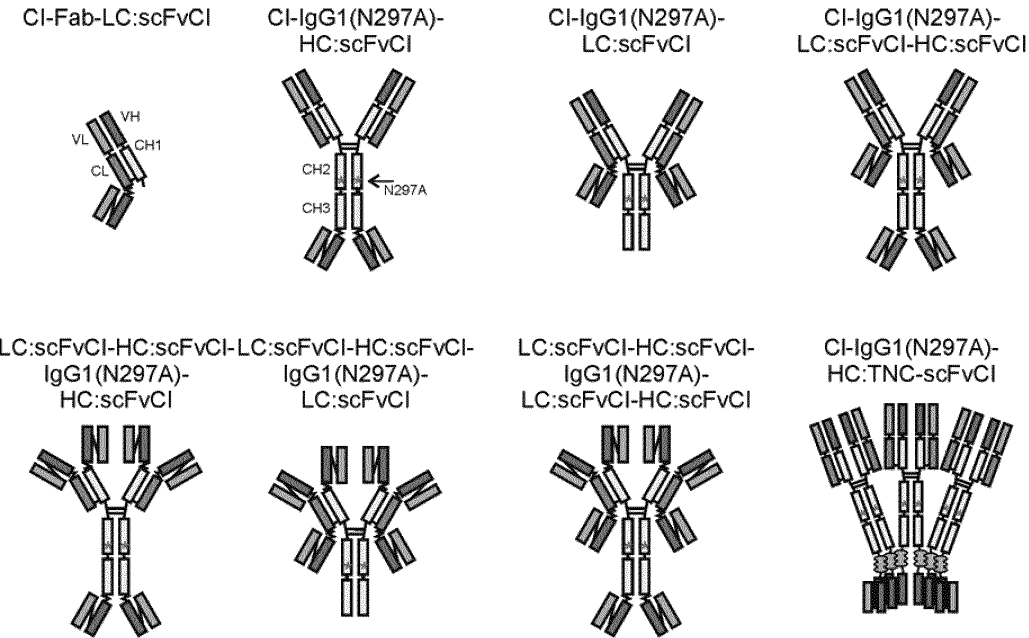
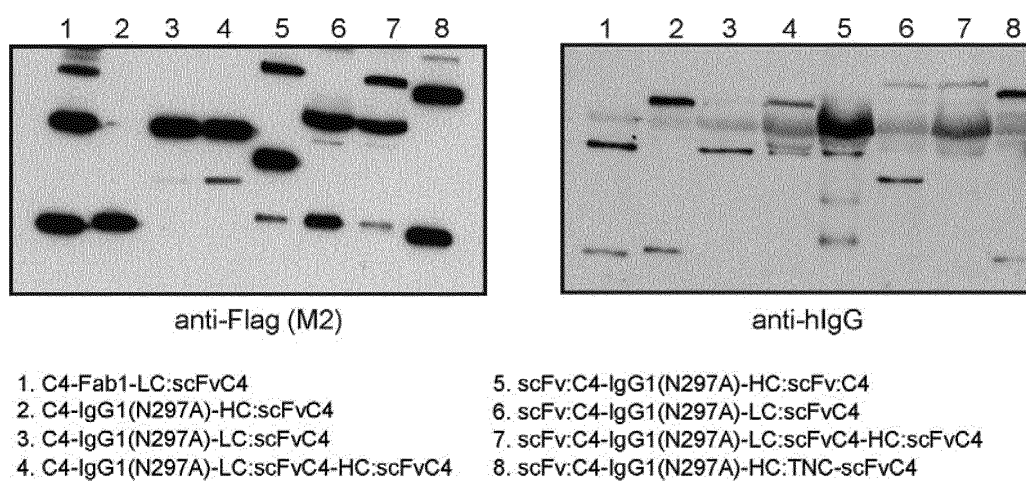


FIGURE 7

**FIGURE 8**

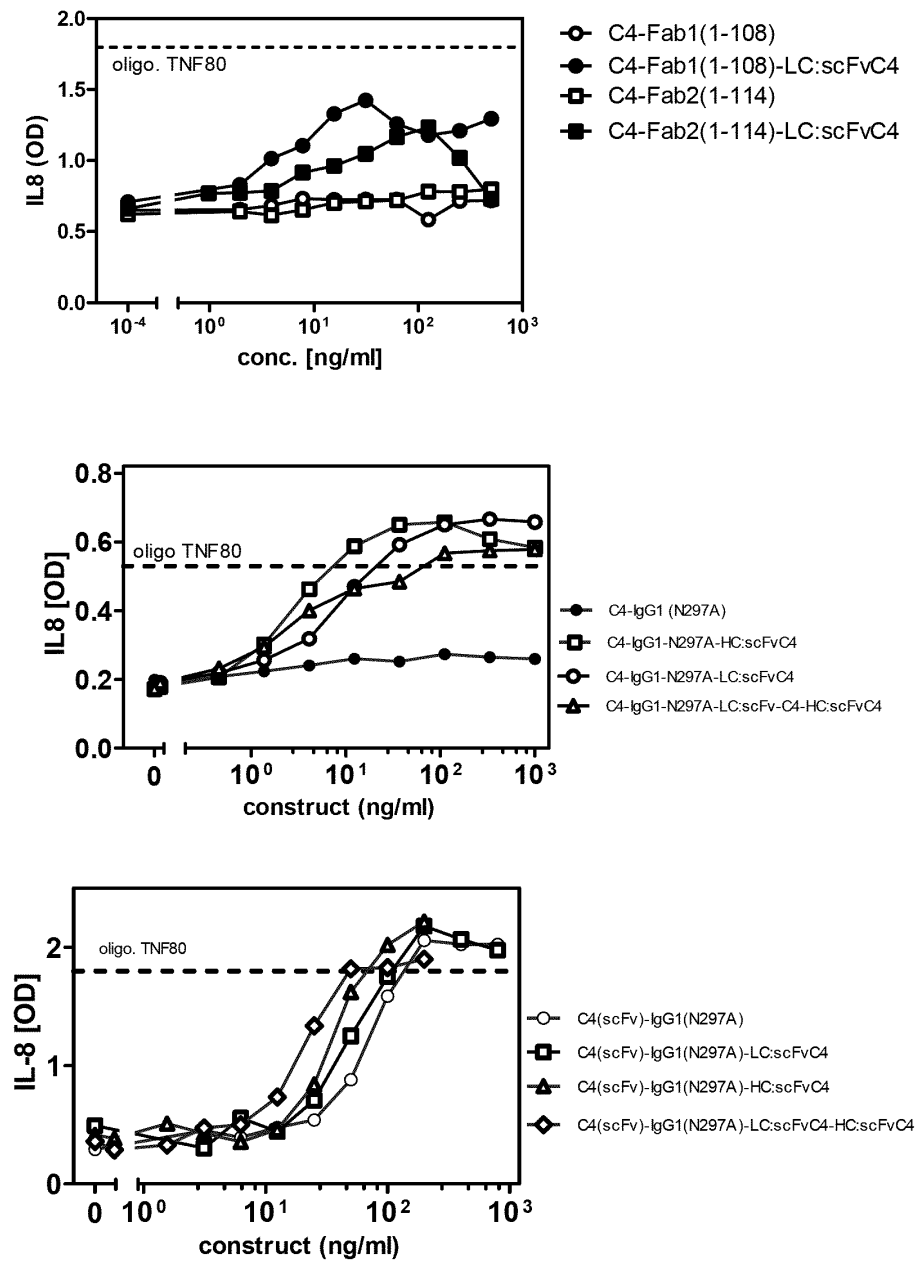


FIGURE 9

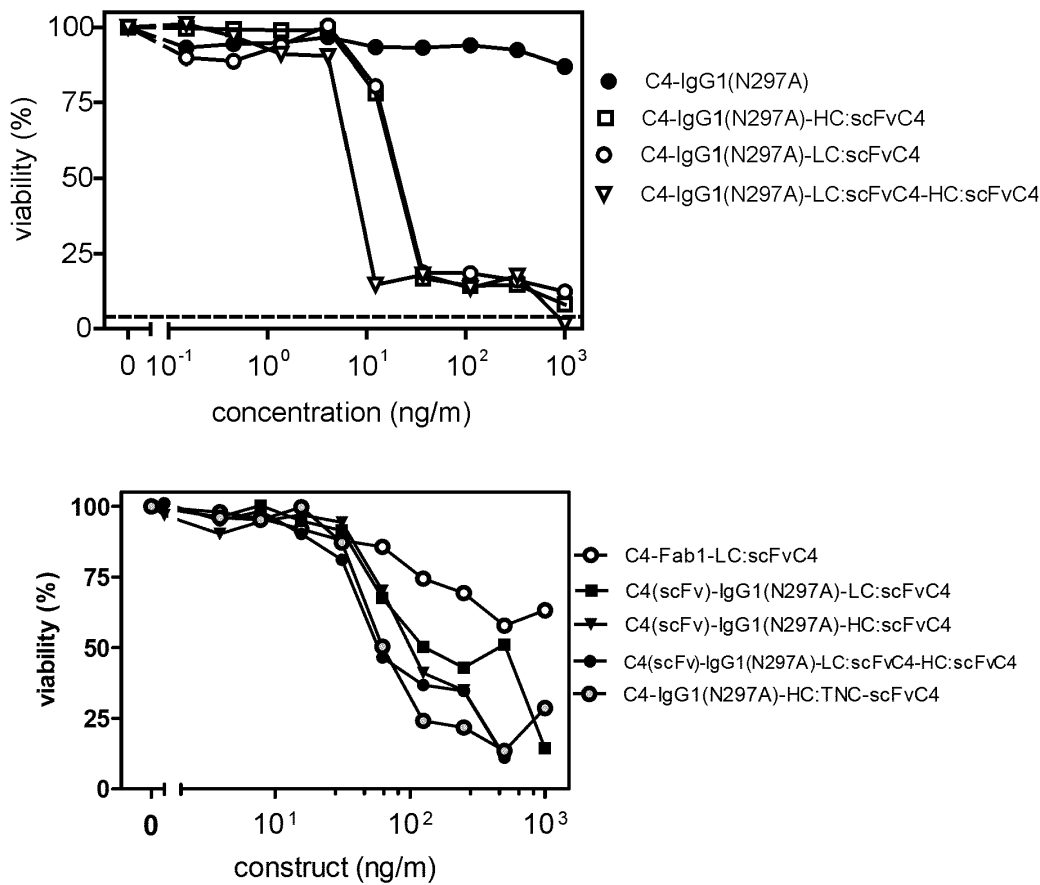


FIGURE 10



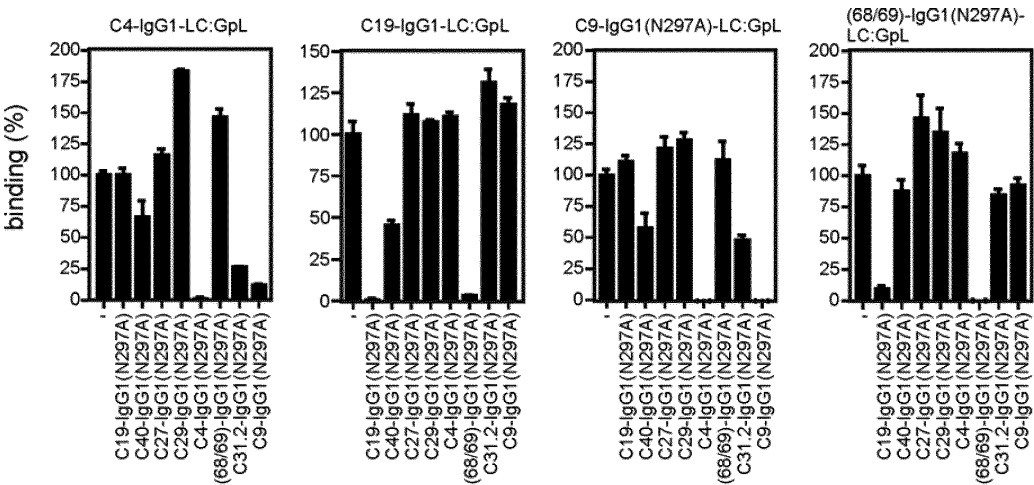


FIGURE 12

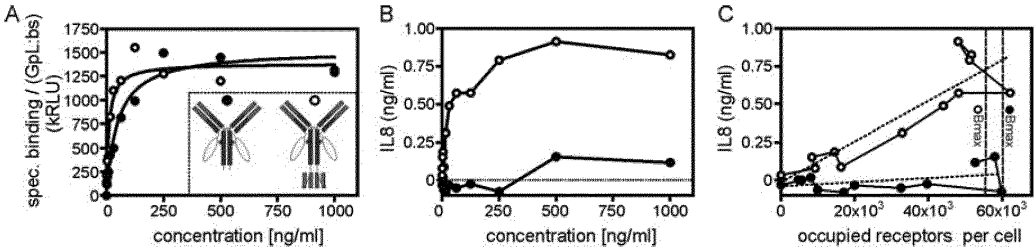


FIGURE 13

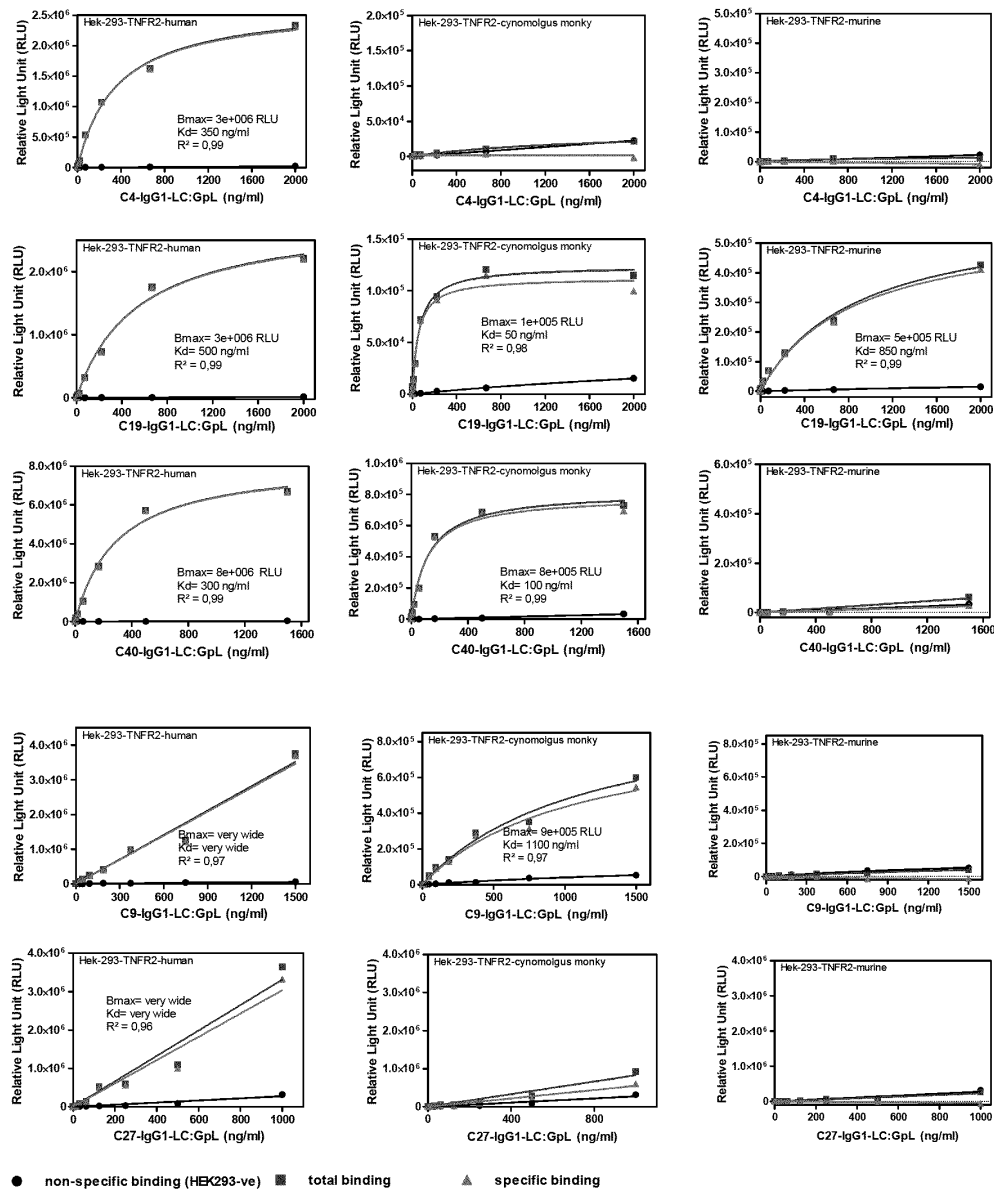
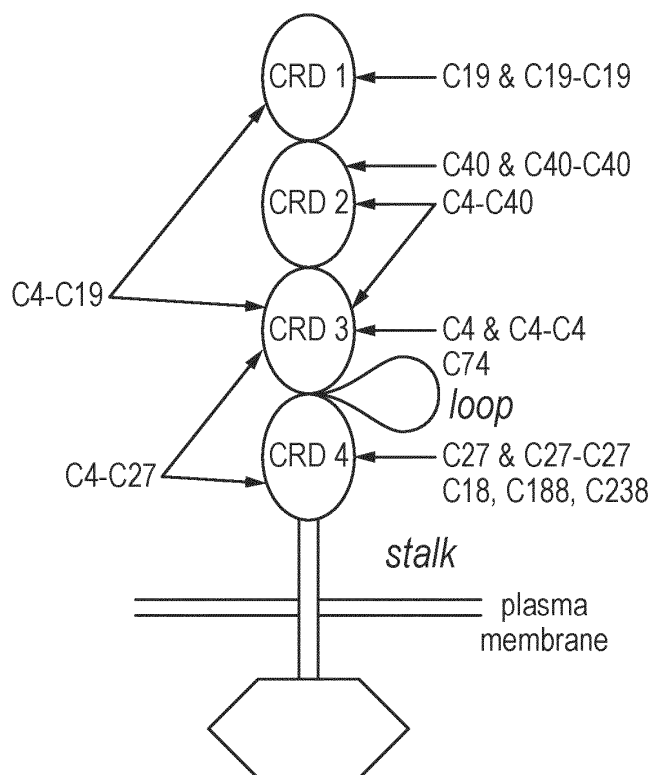


FIGURE 14

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**FIGURE 15**

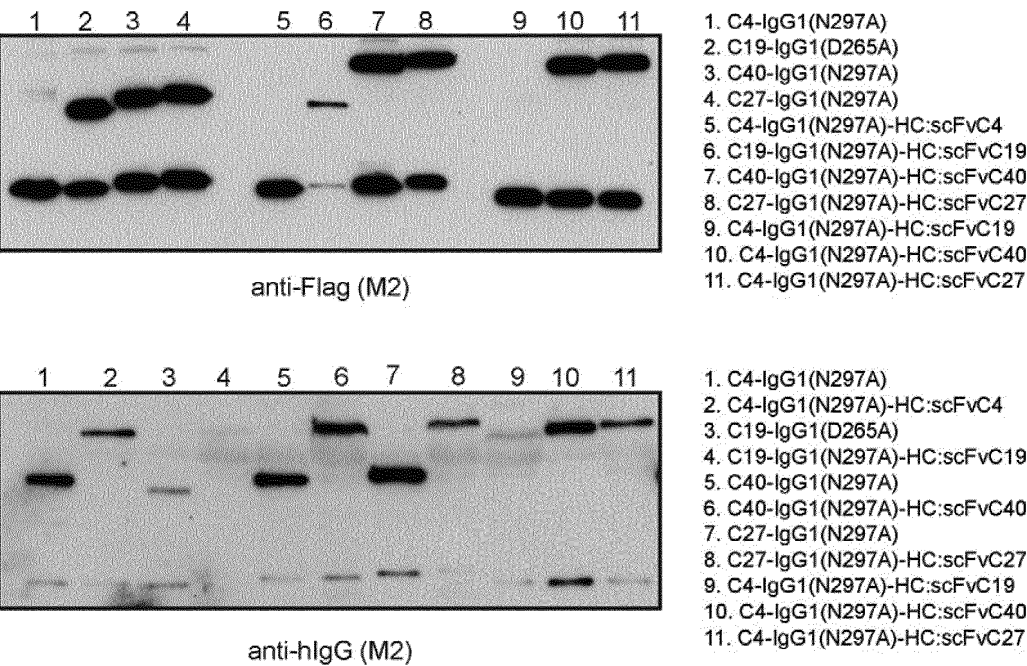


FIGURE 16

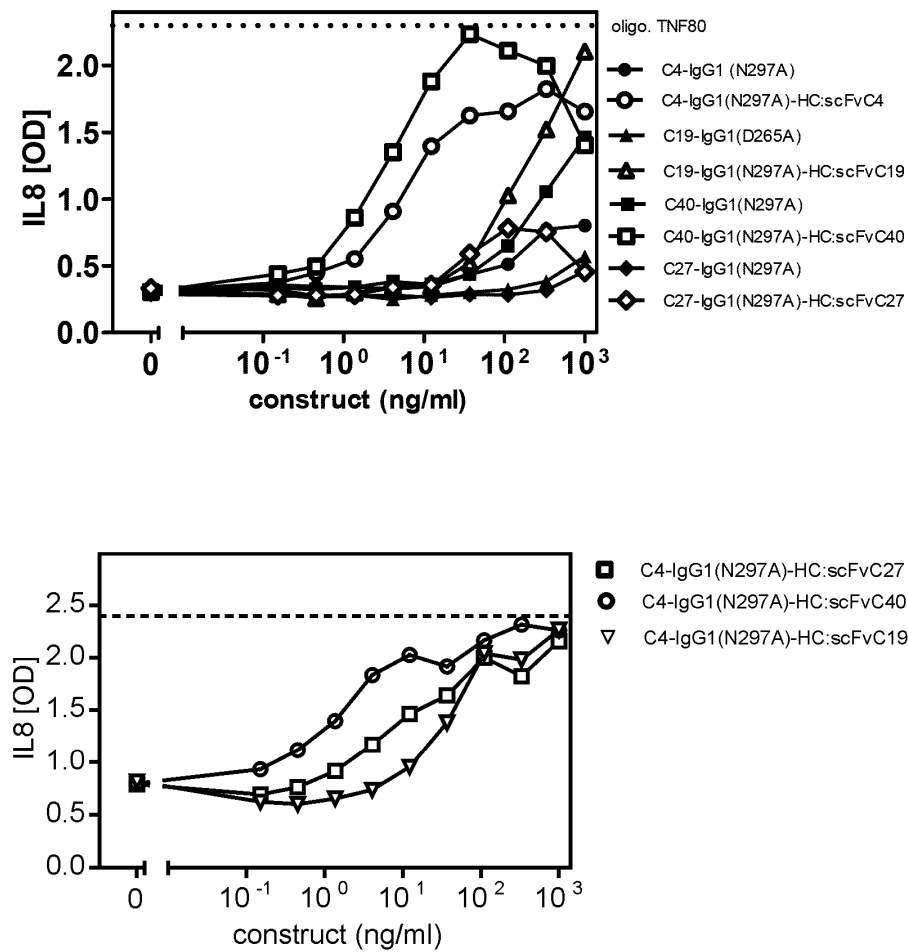


FIGURE 17

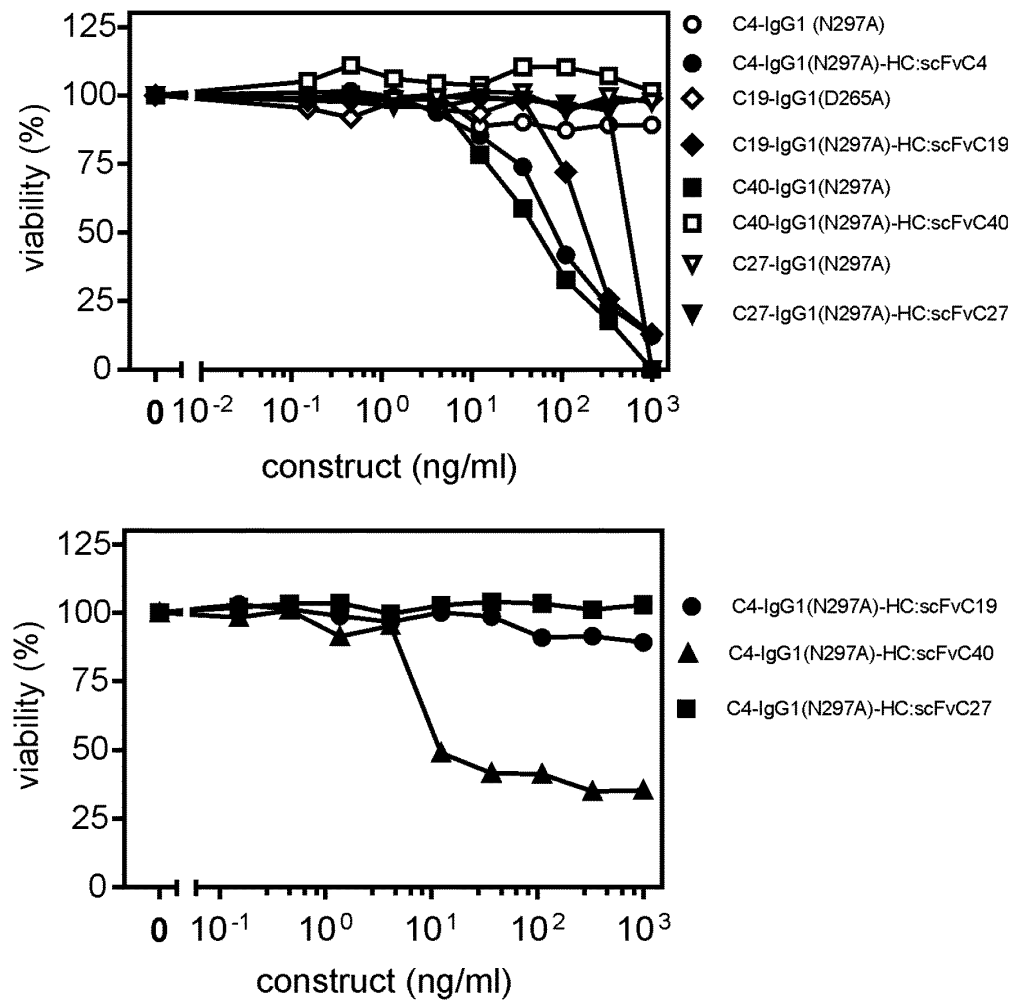


FIGURE 18

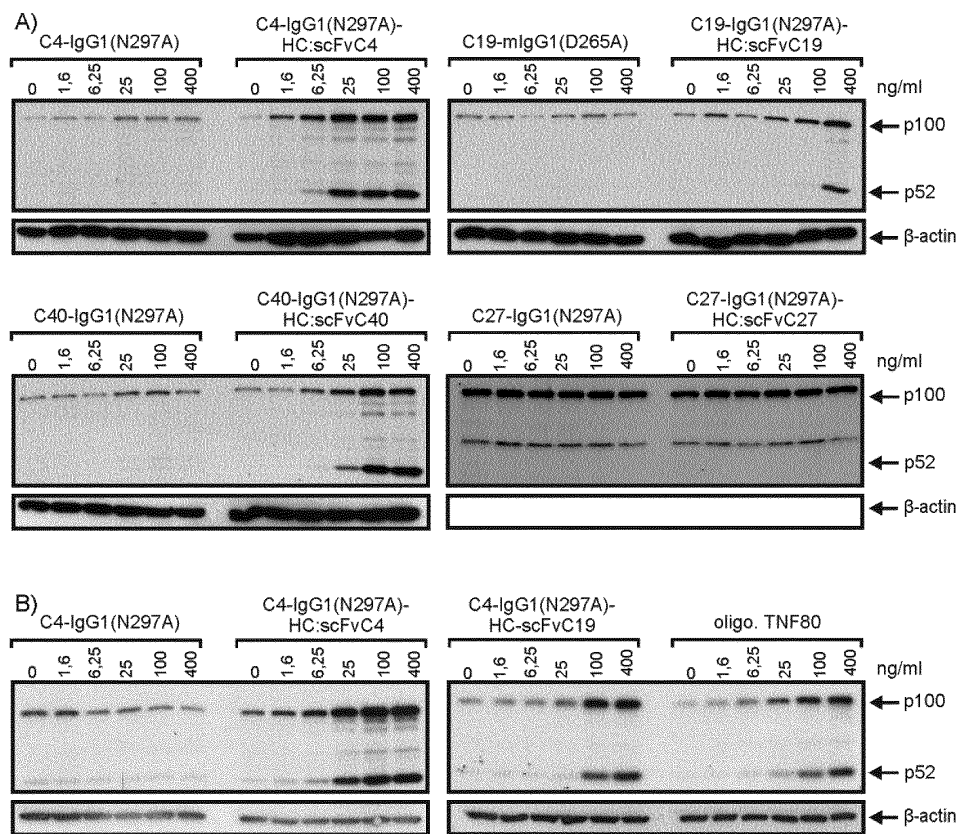


FIGURE 19

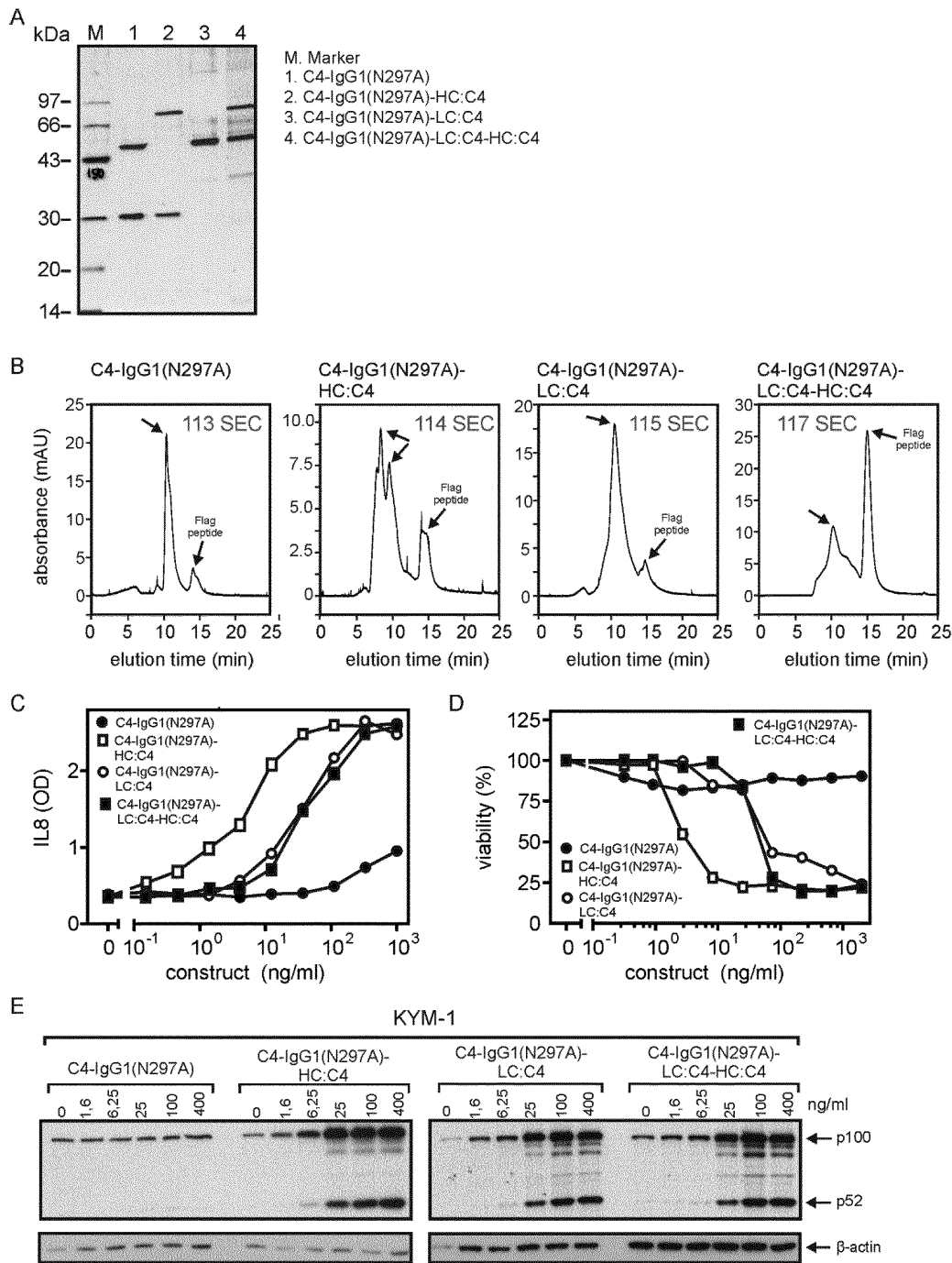


FIGURE 20

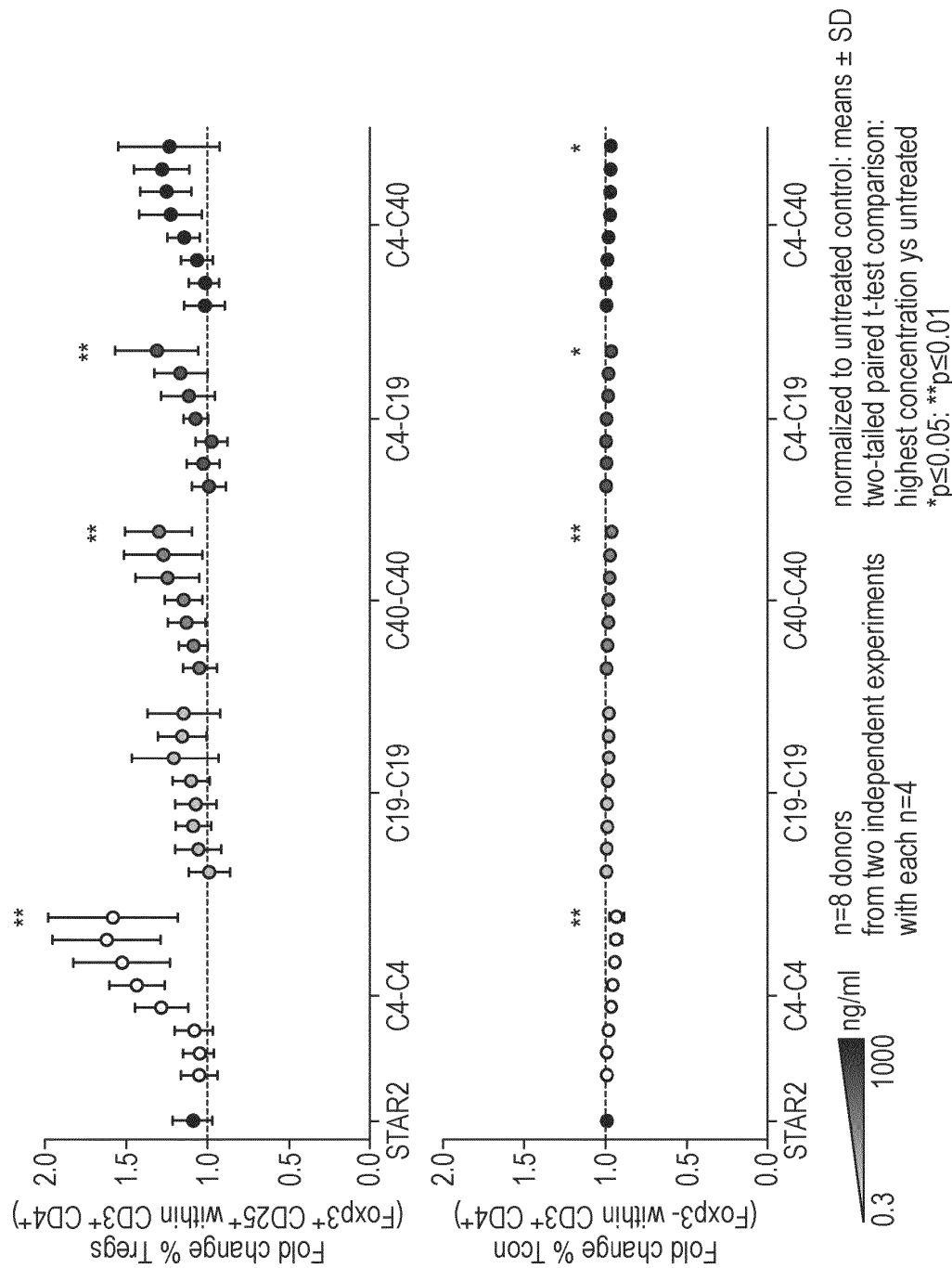
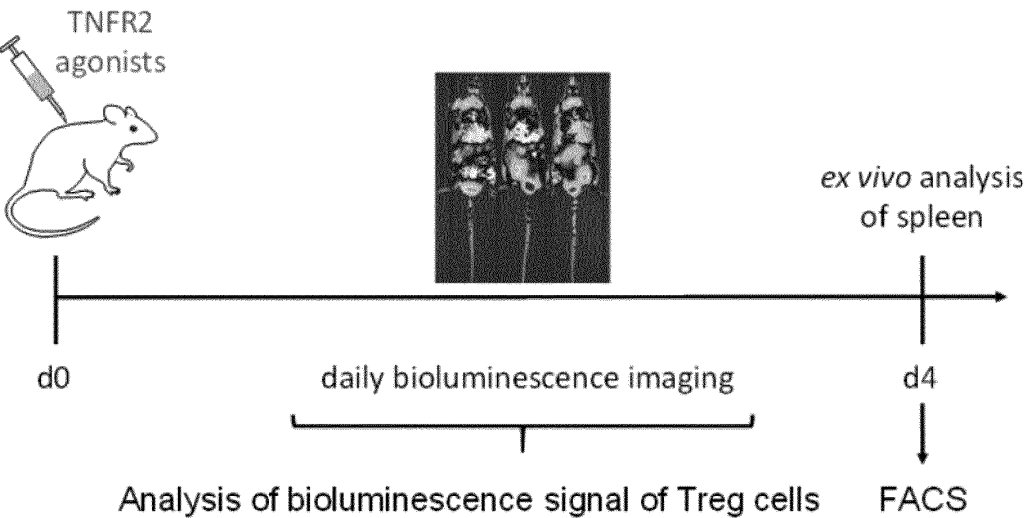


FIGURE 21

(A)



(B)

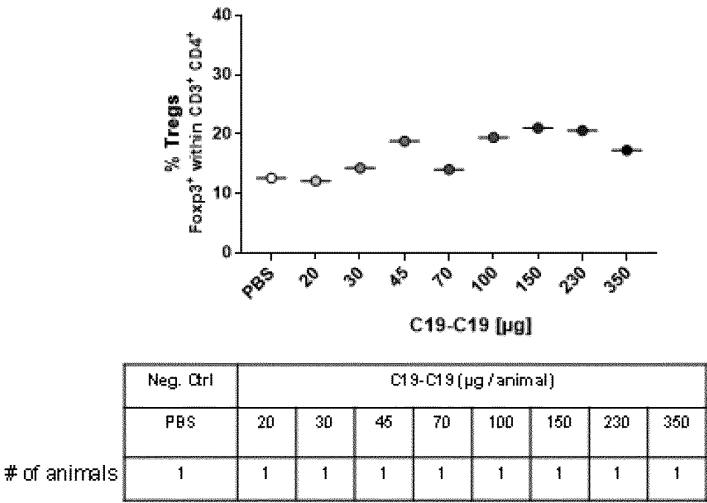


Figure 22

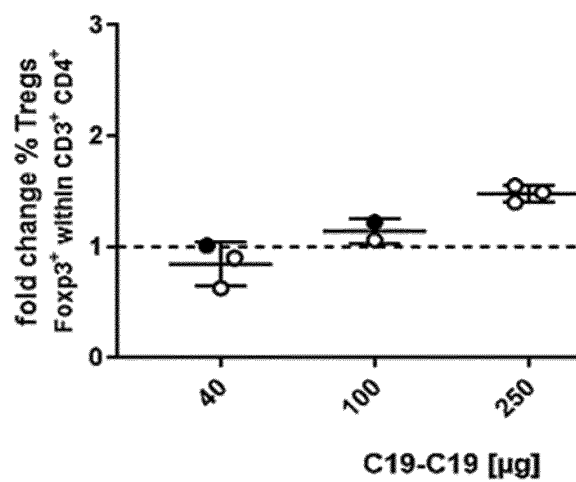


FIGURE 23

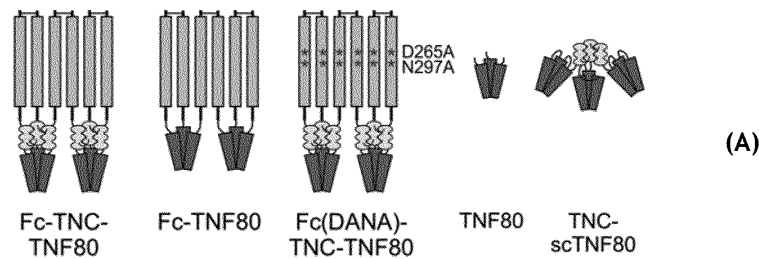
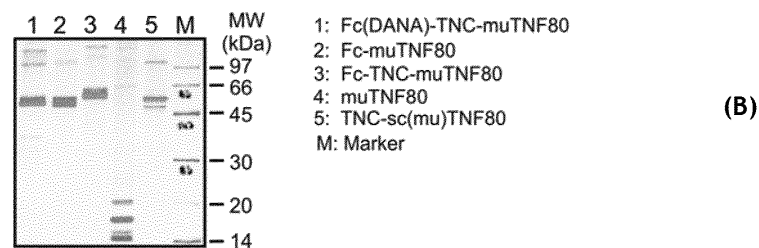
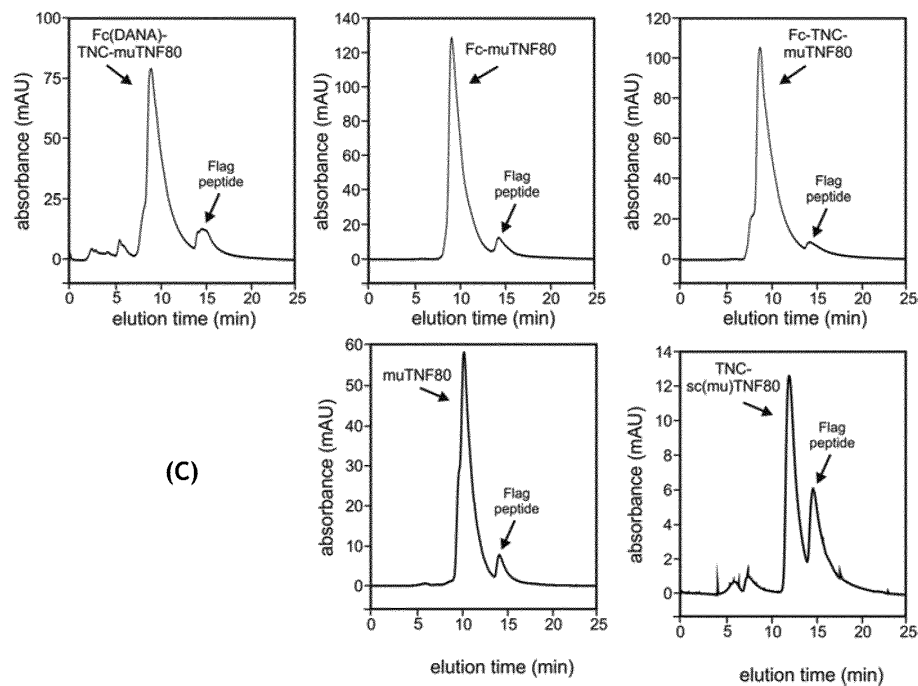


FIGURE 24

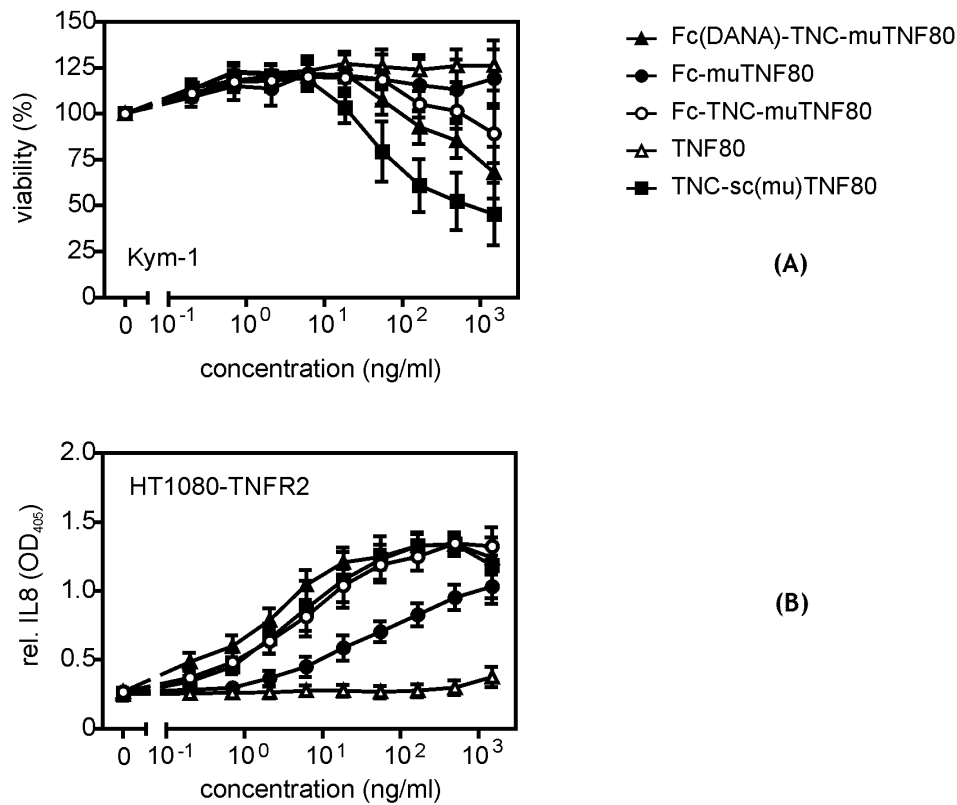


FIGURE 25

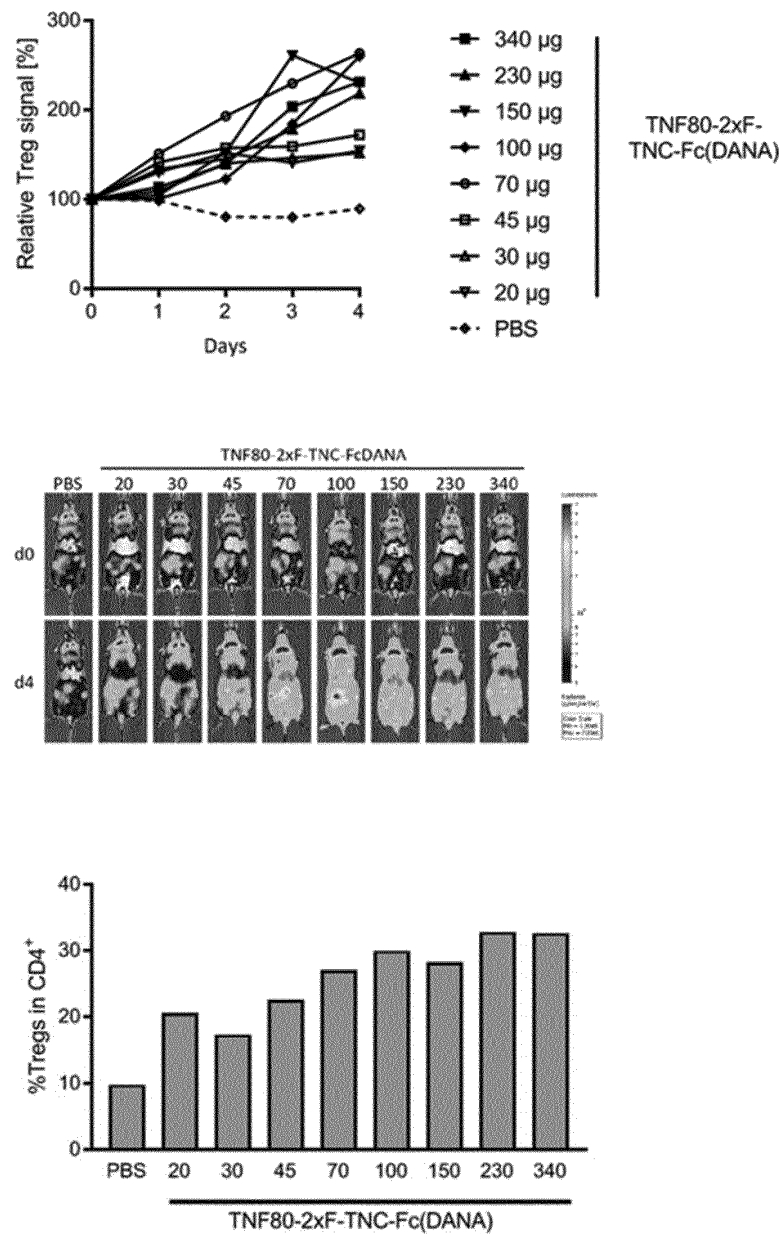


FIGURE 26

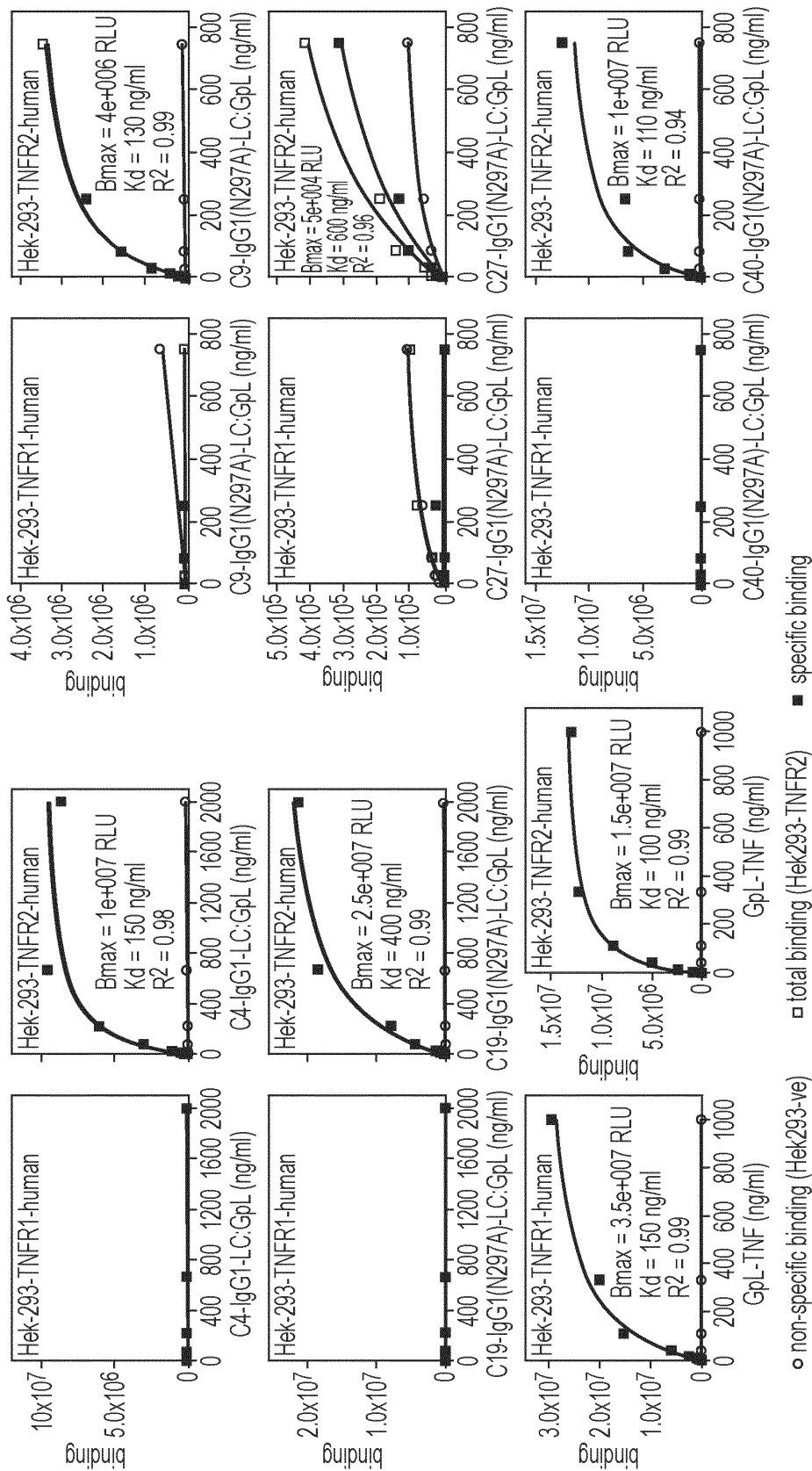


FIGURE 27

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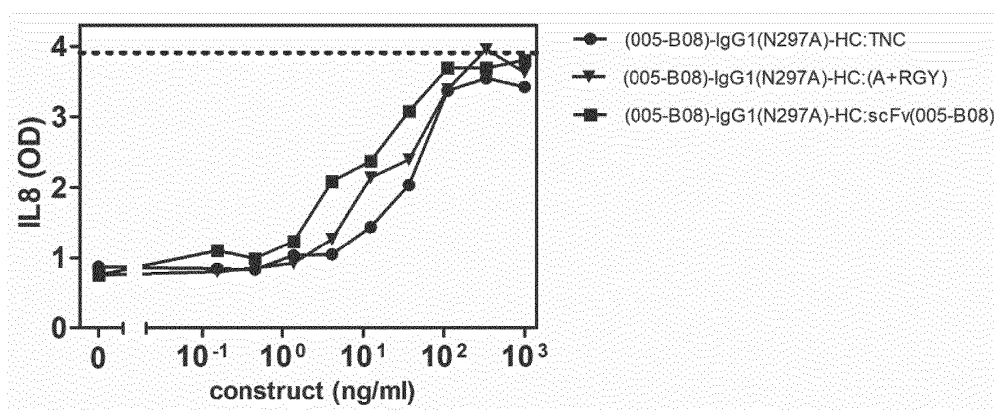
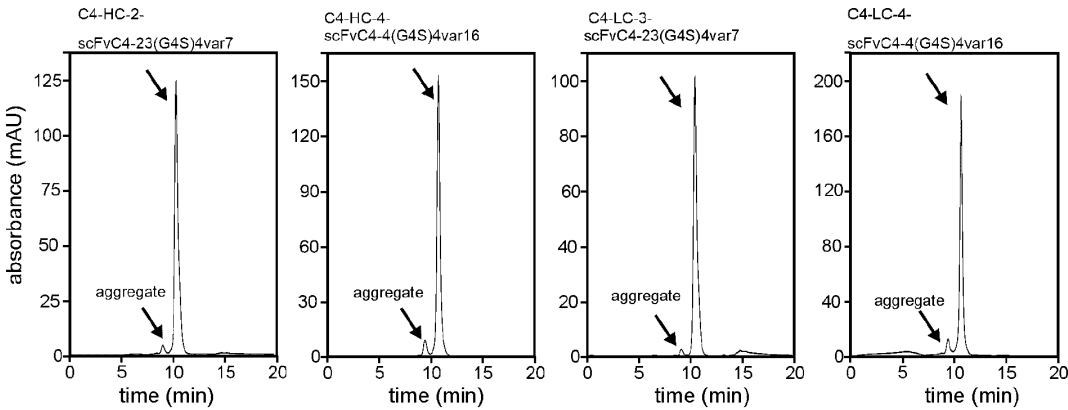


FIGURE 28

(A)



(B)

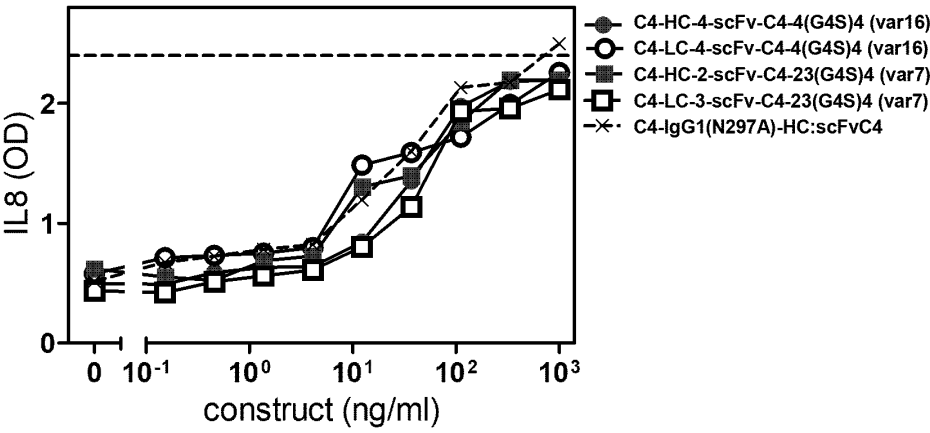


FIGURE 30

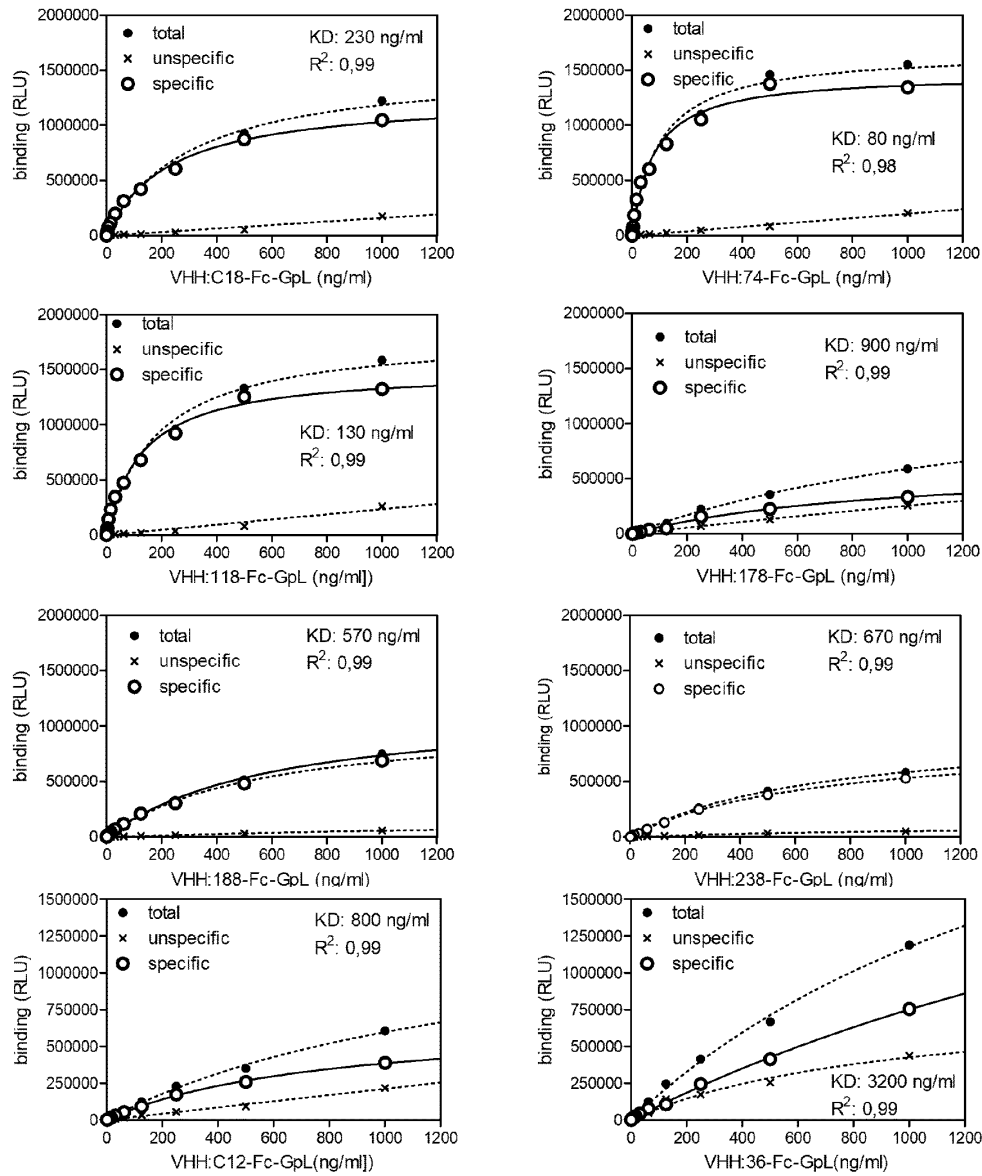


FIGURE 31

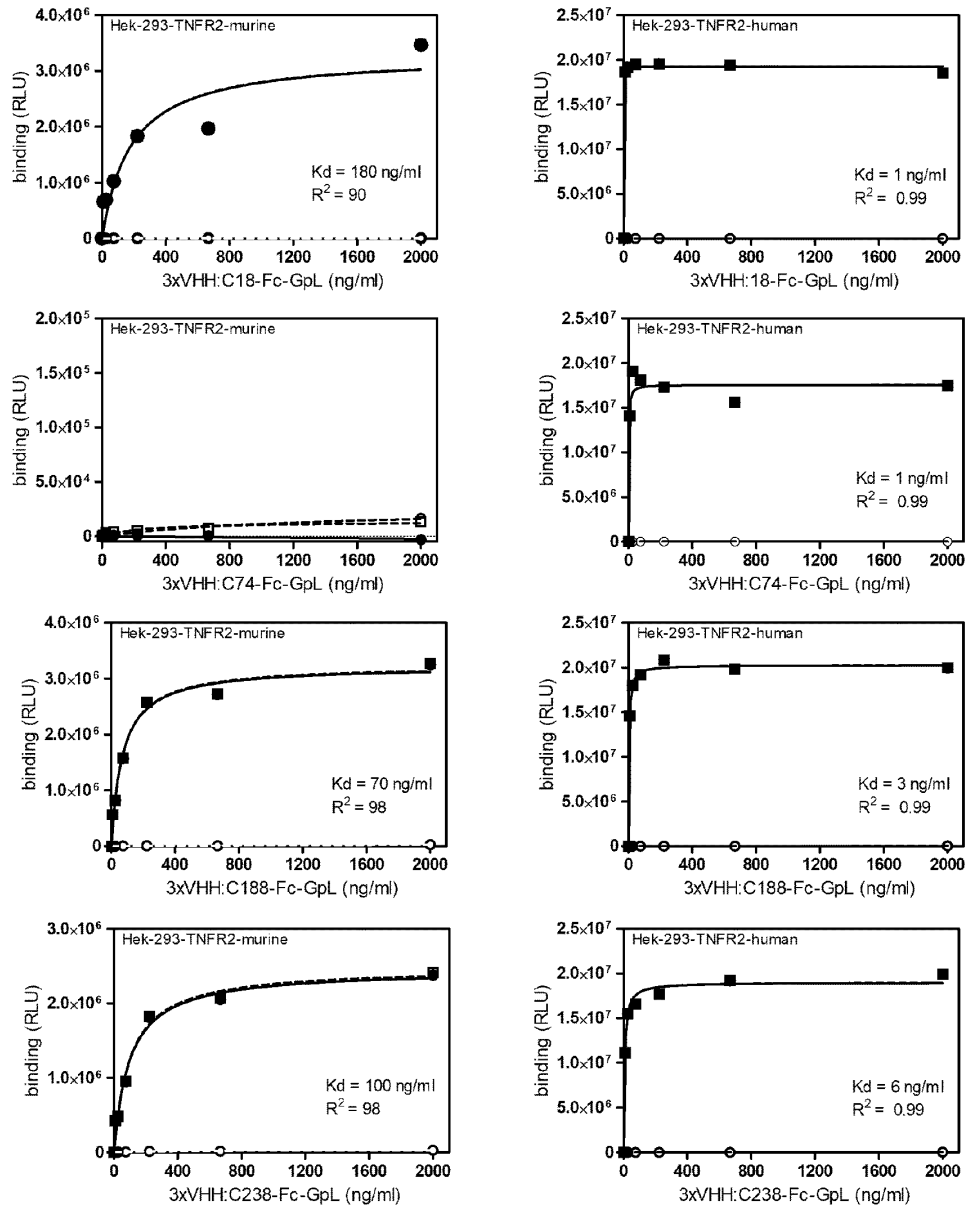
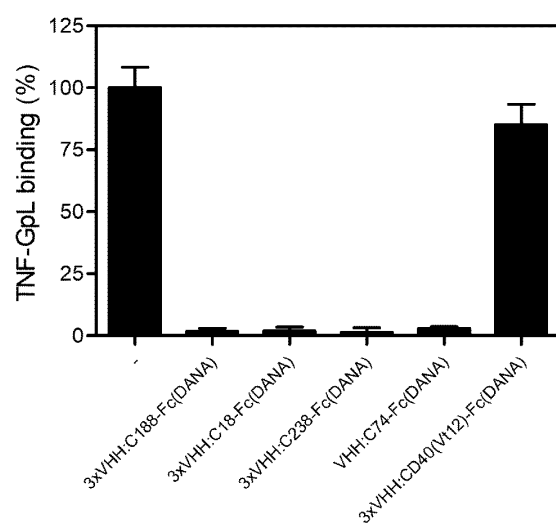


FIGURE 32

**FIGURE 33**

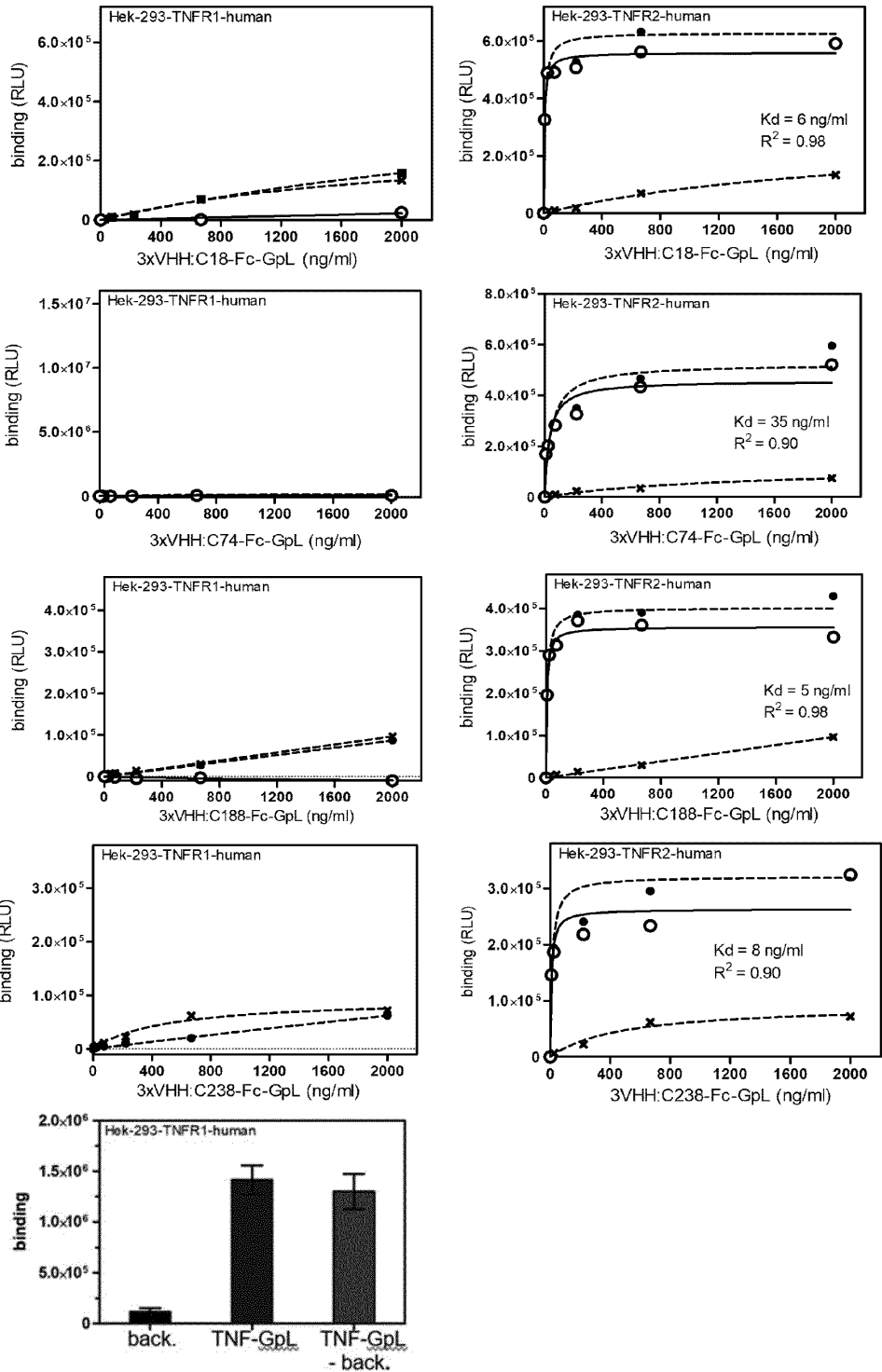


FIGURE 34

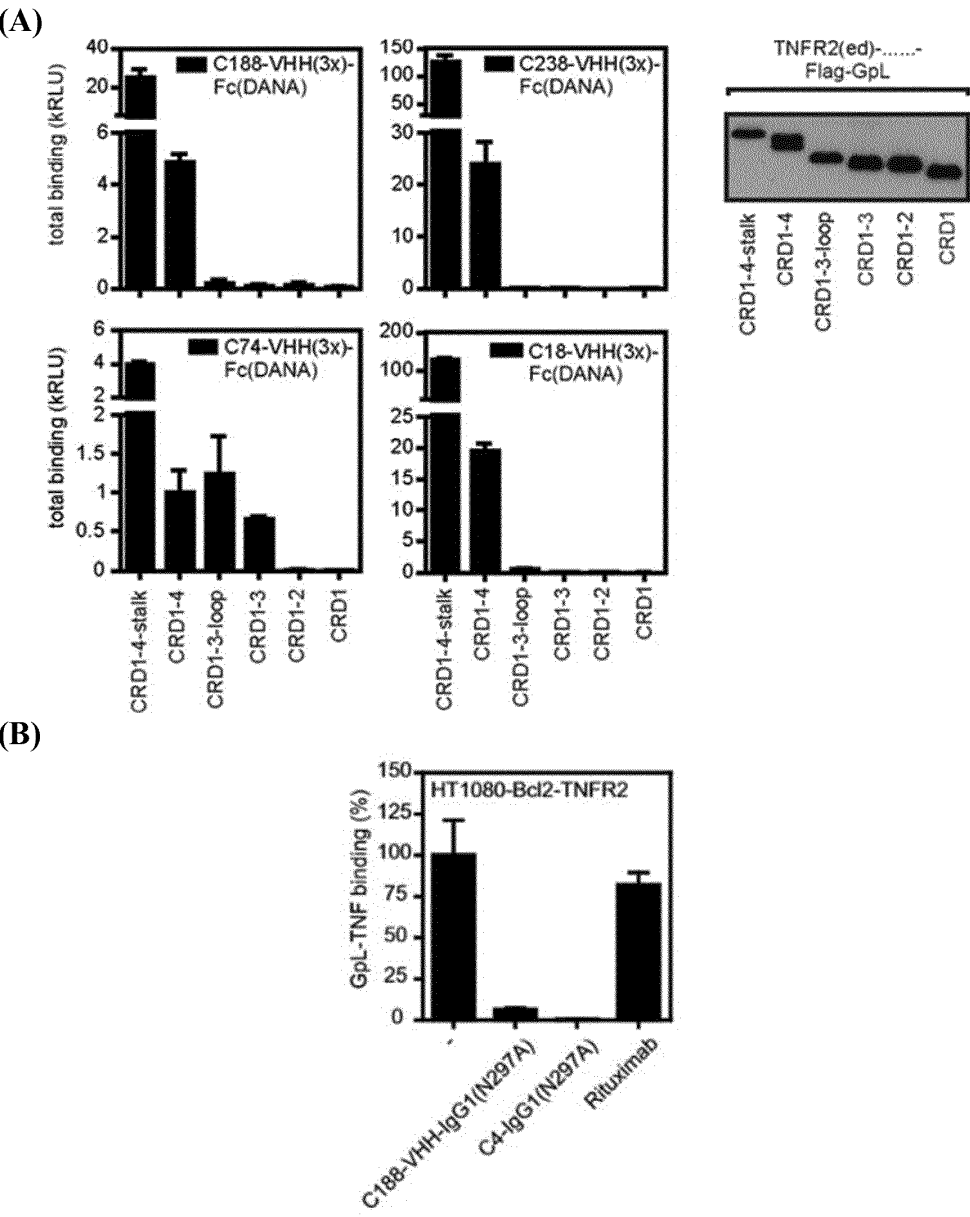


FIGURE 35

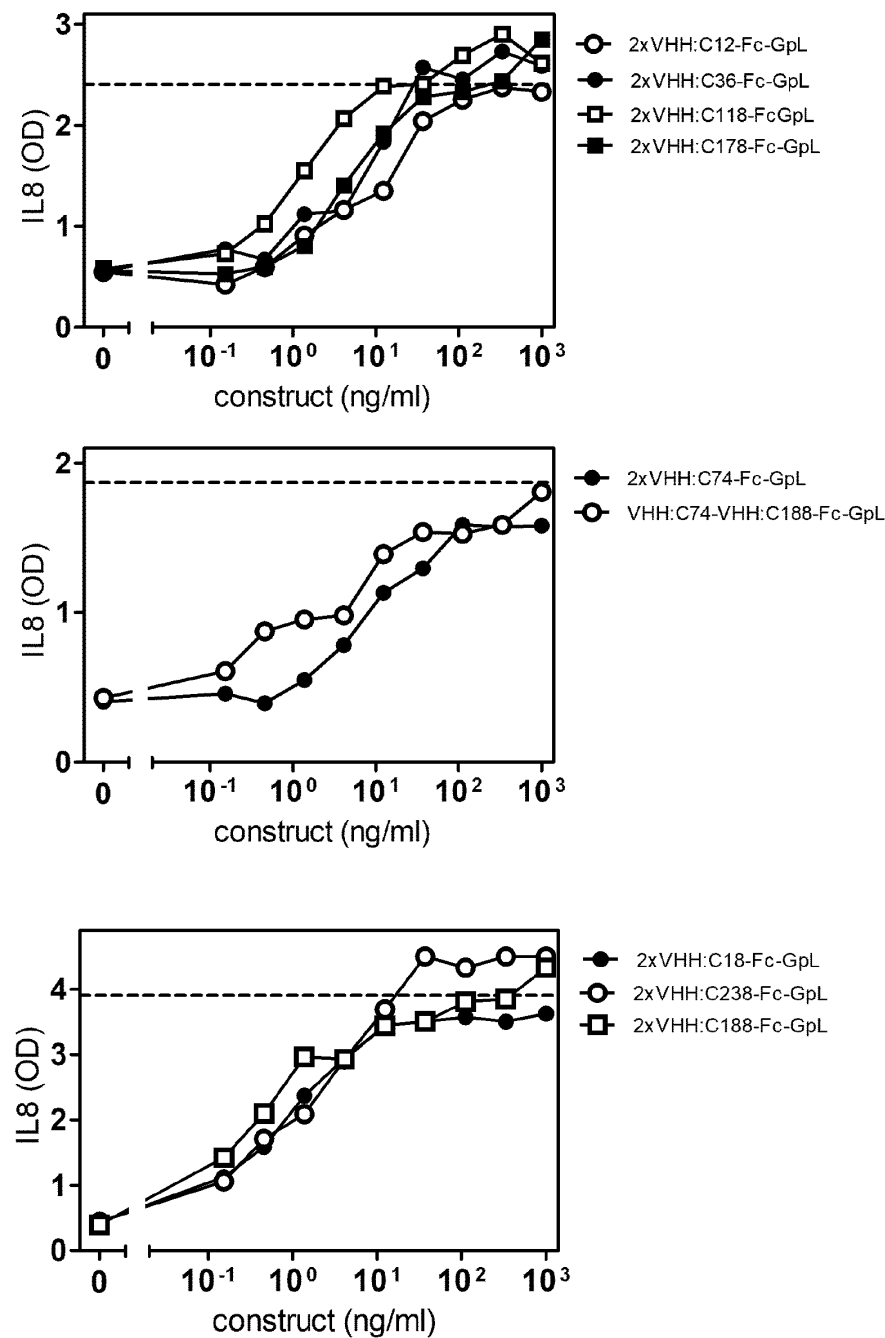
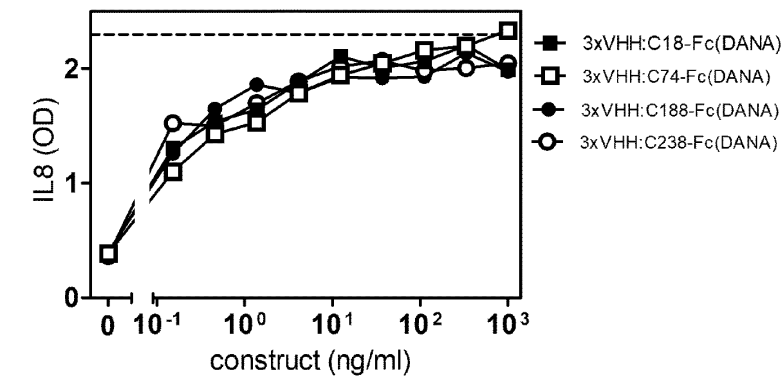


FIGURE 36

(A)



(B)

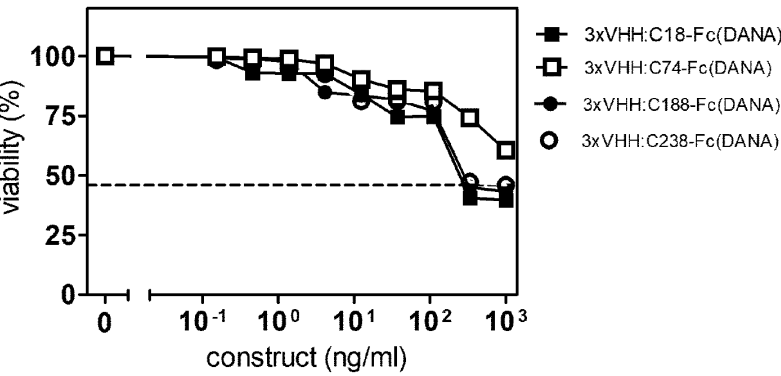
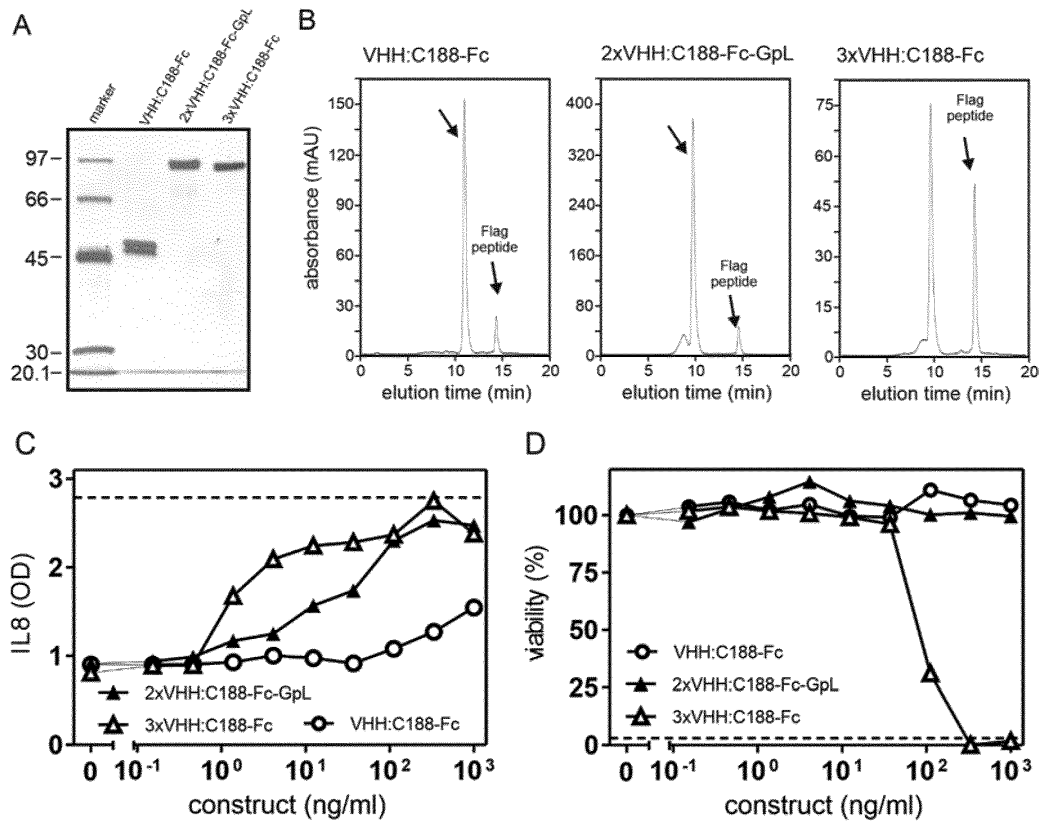


FIGURE 37



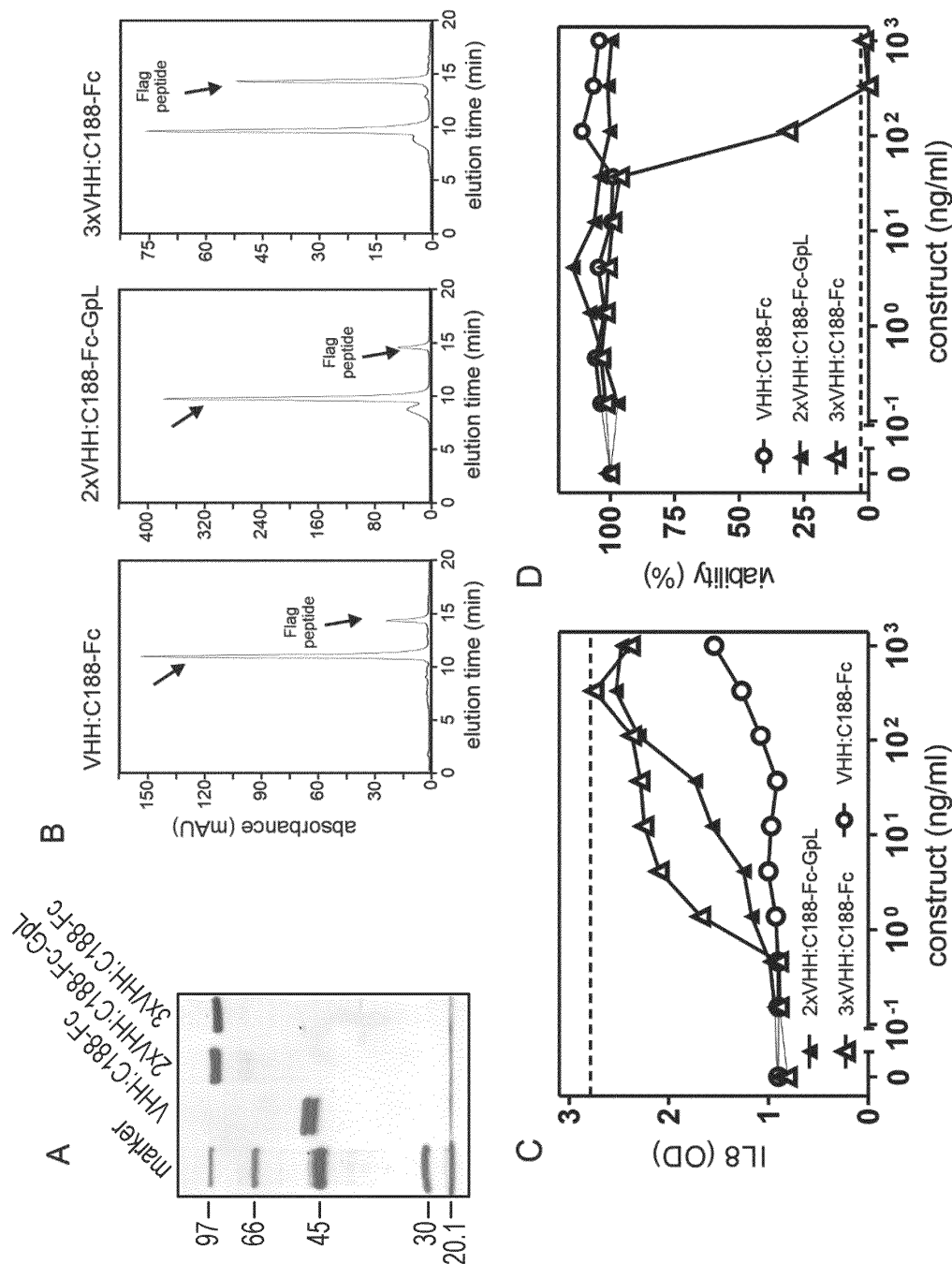


FIGURE 38

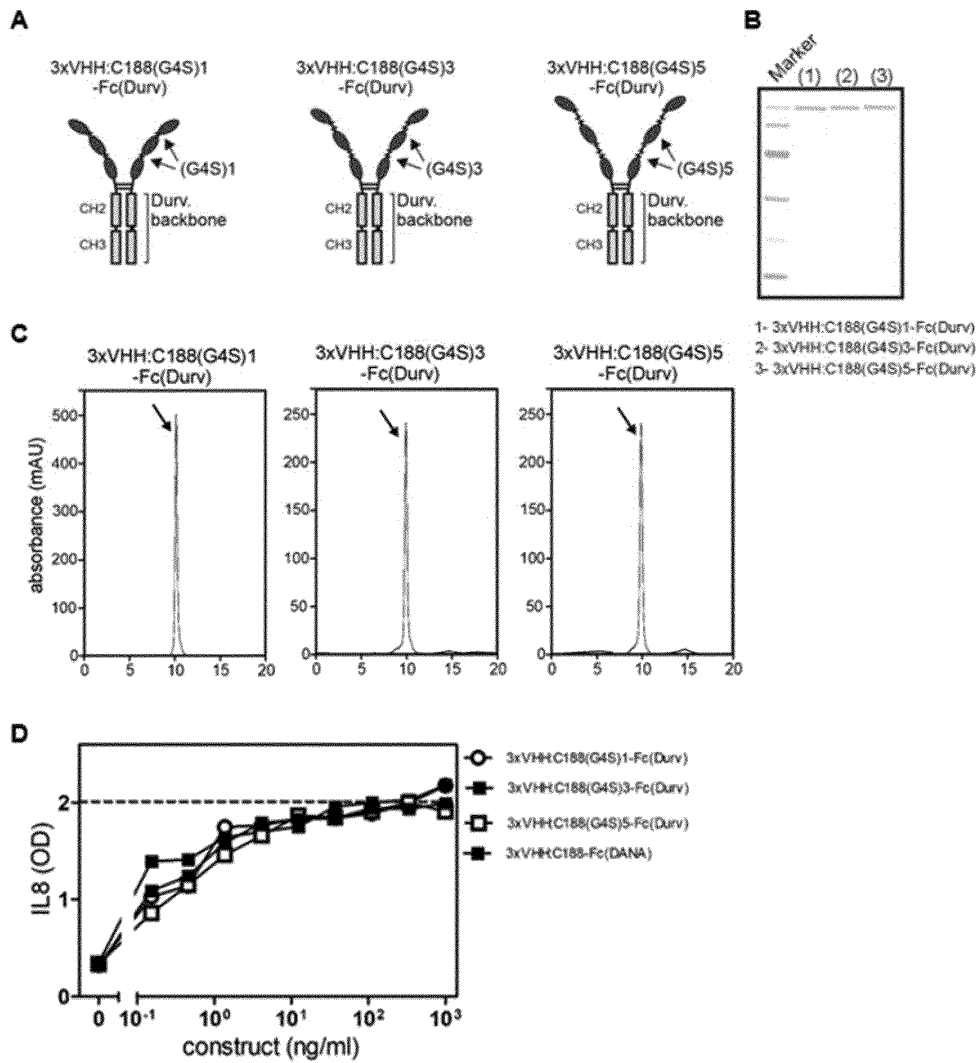


FIGURE 40

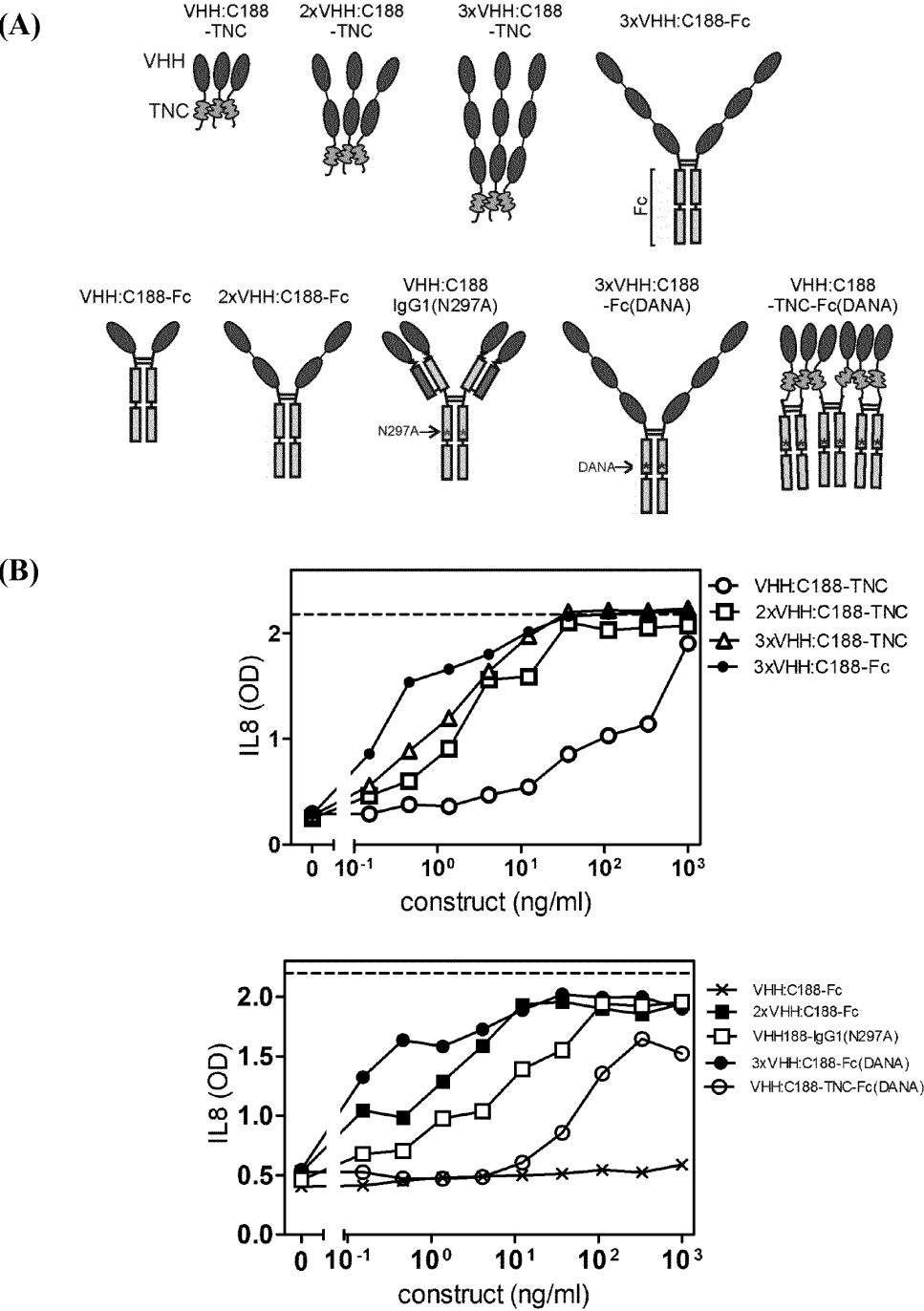


FIGURE 41

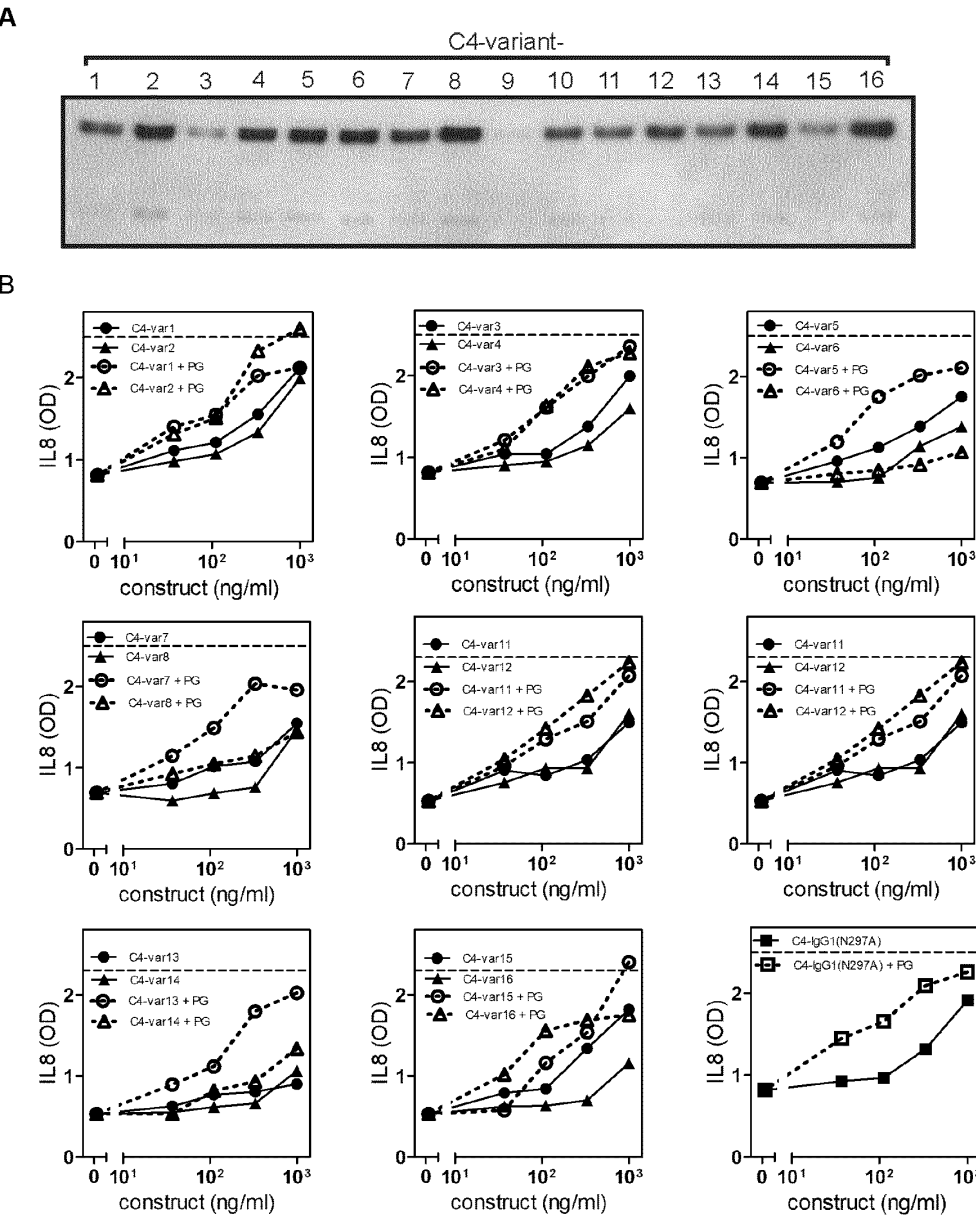


FIGURE 42

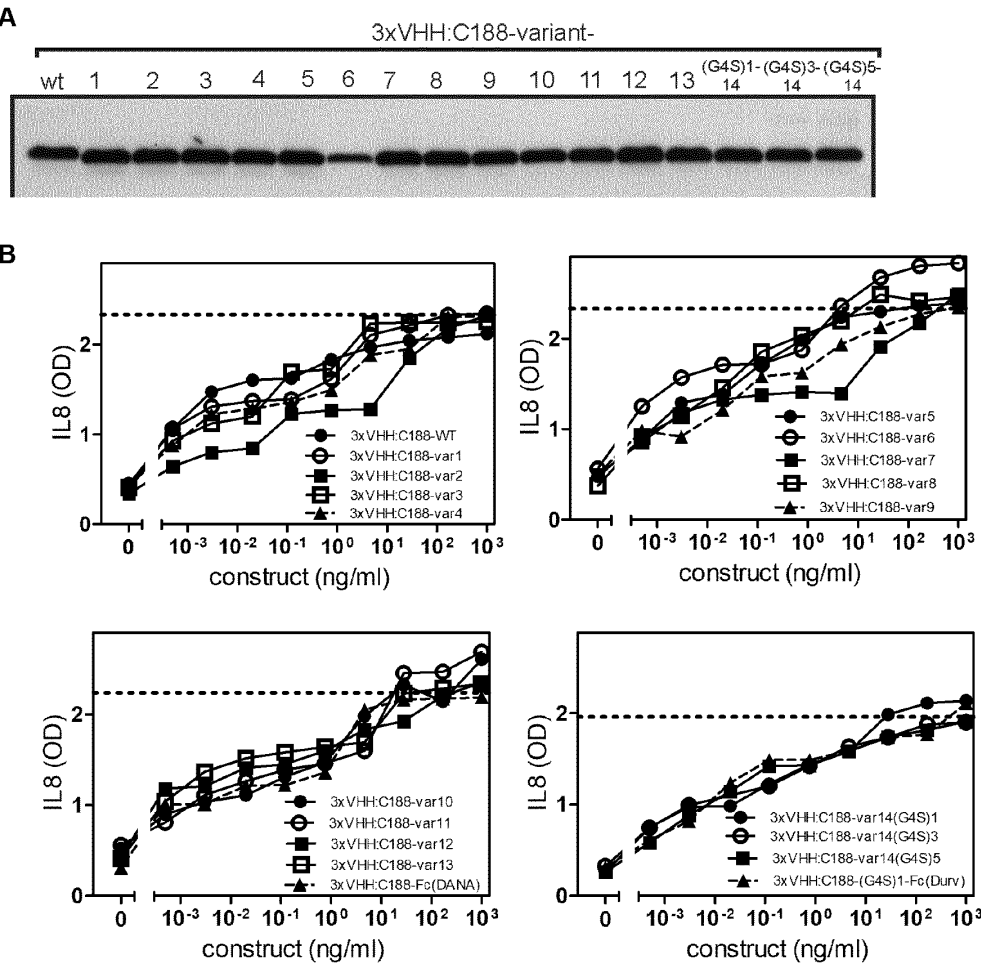


FIGURE 43

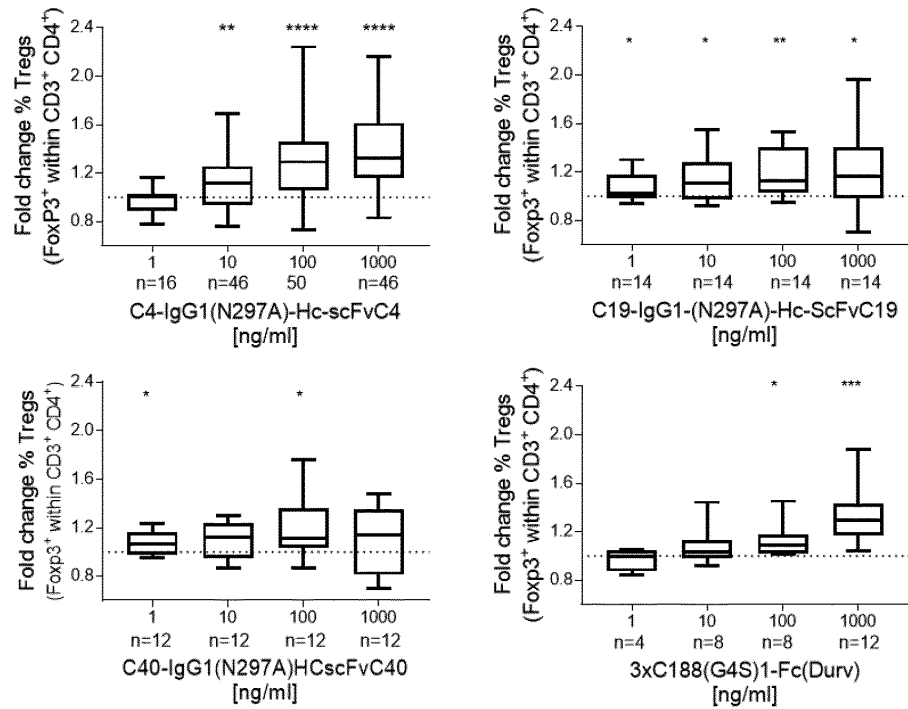


FIGURE 44

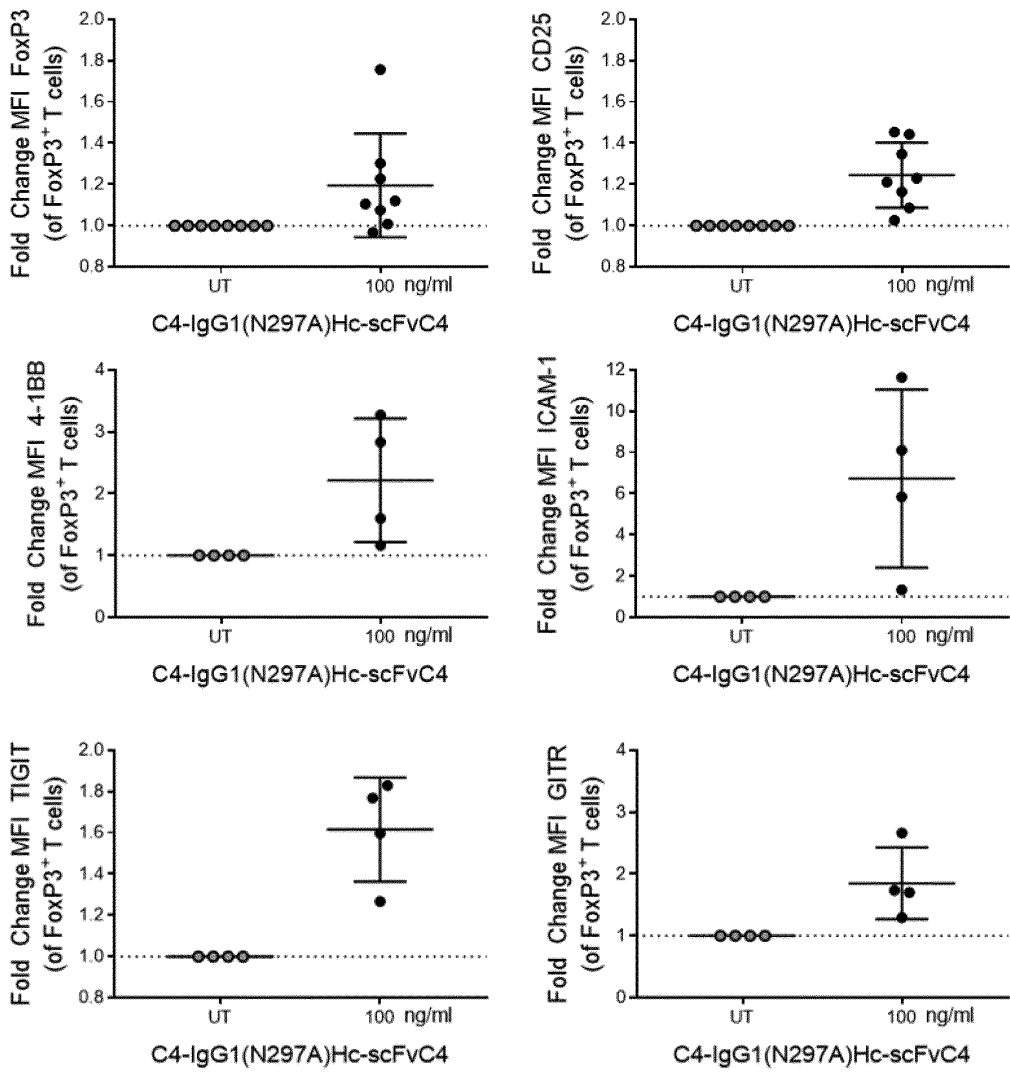


FIGURE 45

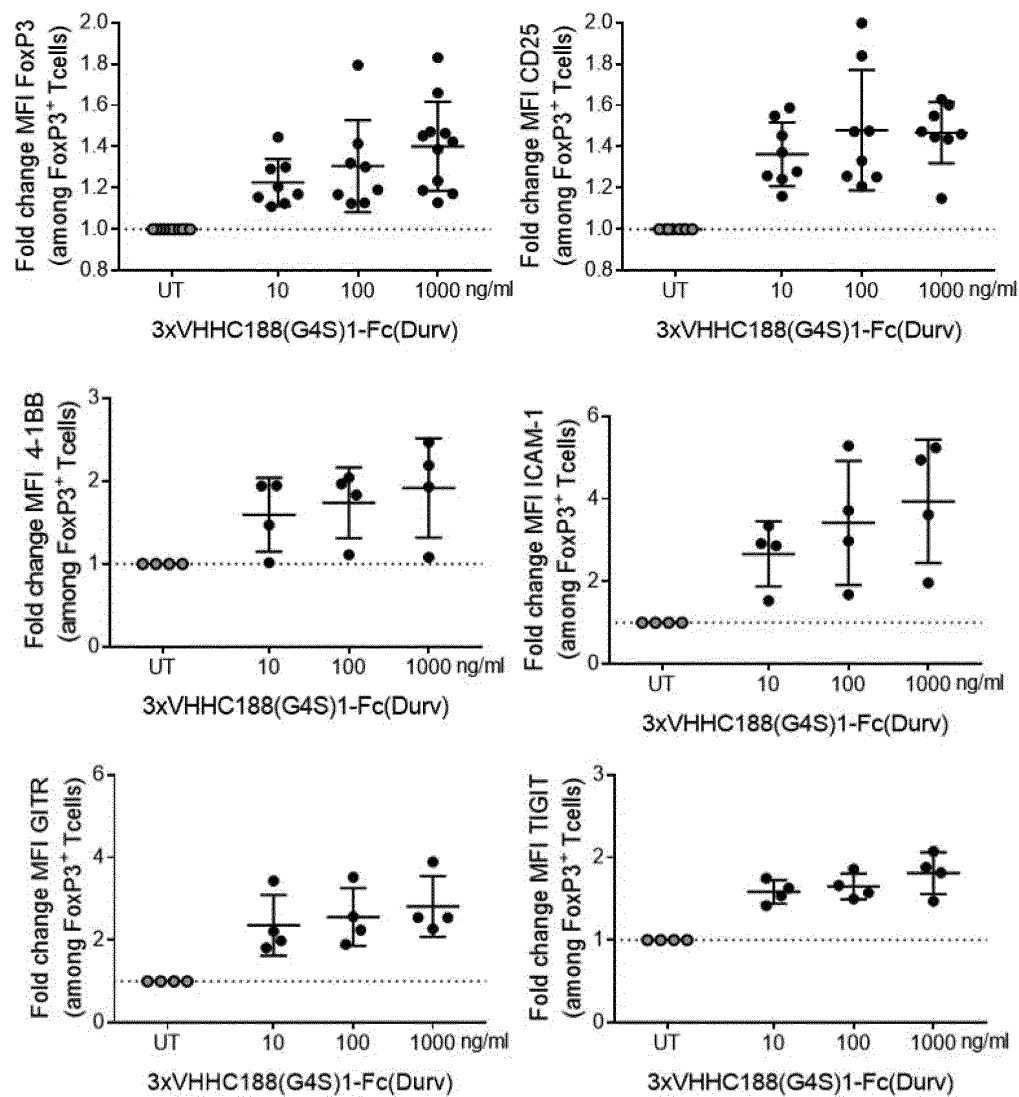


FIGURE 46

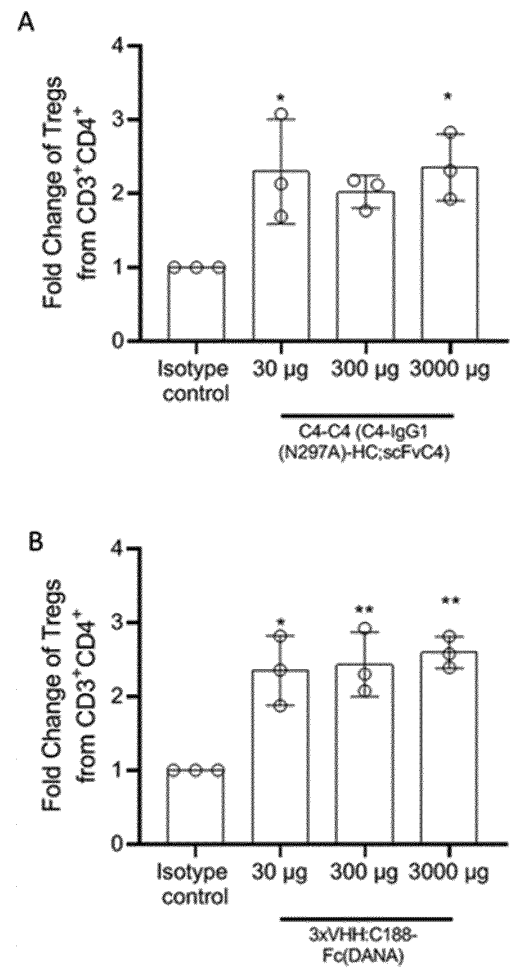


FIGURE 47

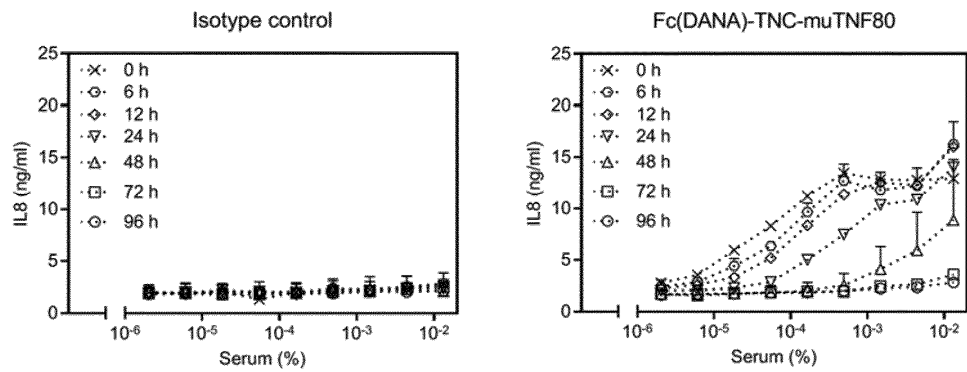


FIGURE 48

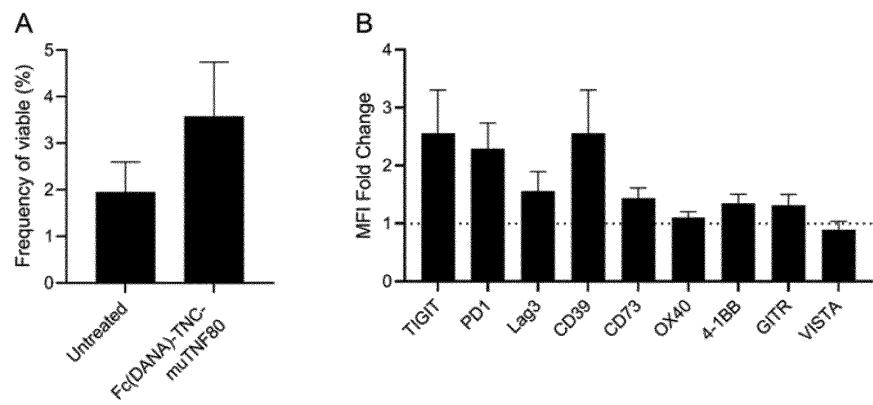
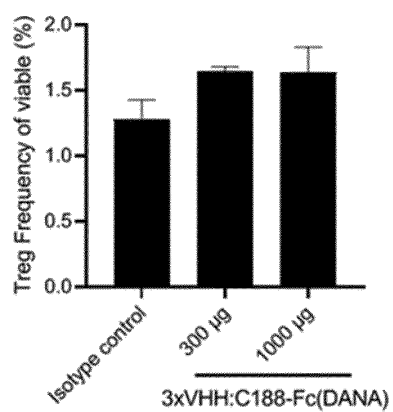


FIGURE 49

(A)



(B)

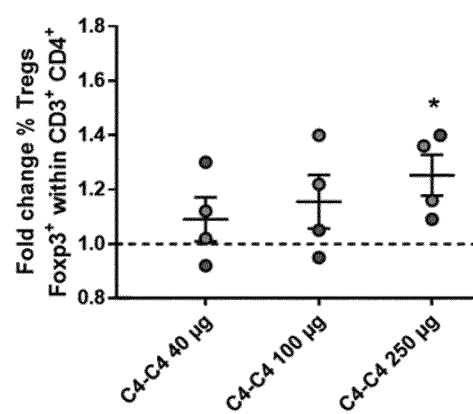


FIGURE 50

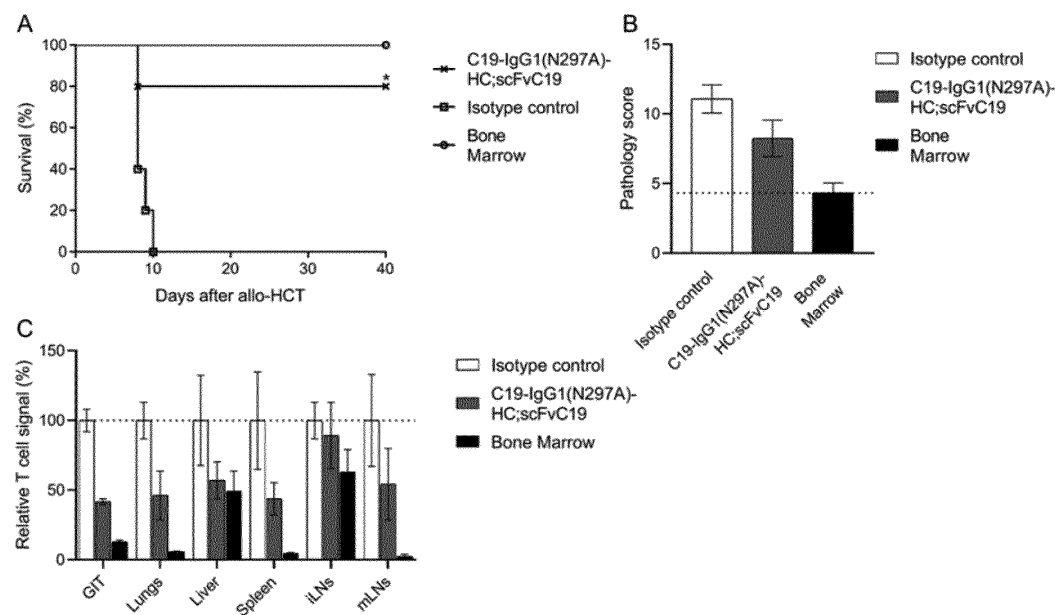


FIGURE 51

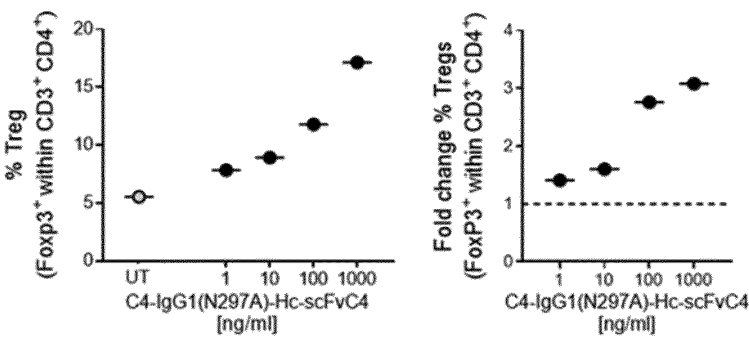


FIGURE 52

3XVHHC188(G4S)1-Fc(Durv) - SEQ ID NO: 330*(C188parental + G4S + C188parental + G4S + C188parental + hinge + Fc(Durvalumab))*

DVQLVESGGGSVQTGGSLTLSCAISGSTSERYCLGWFRQAPGREREGVAATSLTGRGAQFYADSVKGRFTISLDDA
 KNTLYLQMDSLRLPDDTAVYYCAEDVGFLCGYDSNDPFYDWGQGTQVTVSSGGGSDVQLVESGGGSVQTGGSL
 TLSCAISGSTSERYCLGWFRQAPGREREGVAATSLTGRGAQFYADSVKGRFTISLDDAKNTLYLQMDSLRLPDDTA
 VYYCAEDVGFLCGYDSNDPFYDWGQGTQVTVSSGGGSDVQLVESGGGSVQTGGSLTLSCAISGSTSERYCLG
 WFRQAPGREREGVAATSLTGRGAQFYADSVKGRFTISLDDAKNTLYLQMDSLRLPDDTAVYYCAEDVGFLCGYDS
 NDPFYDWGQGTQVTVSSEPKSDKTHTCPPCPAPFEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK * **SEQ ID NO: 163**

3XVHHC188-var14(G4S)1-Fc(Durv) - SEQ ID NO: 331*(C188variant14 + G4S + C188variant14 + G4S + C188variant14 + hinge + Fc(Durvalumab))*

EVQLVESGGGLVQPGGSLRLSCAISGSTSERYCLGWFRQAPGKGREGVAATSLTGRGAQFYADSVKGRFTISLDD
 AKNTLYLQMNSLRAEDTAVYYCAEDVGFLCGYDNDNEPFYDWGQGTQVTVSSGGGSEVQLVESGGGLVQPG
 GSLRLSCAISGSTSERYCLGWFRQAPGKGREGVAATSLTGRGAQFYADSVKGRFTISLDDAKNTLYLQMNSLRAE
 DTAVYYCAEDVGFLCGYDNDNEPFYDWGQGTQVTVSSGGGSEVQLVESGGGLVQPGGSLRLSCAISGSTSERY
 CLGWFRQAPGKGREGVAATSLTGRGAQFYADSVKGRFTISLDDAKNTLYLQMNSLRAEDTAVYYCAEDVGFLC
 GYDNDNEPFYDWGQGTQVTVSSEPKSDKTHTCPPCPAPFEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF
FLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

FIGURE 53

C4-IgG1(Durv)-HC:scFvC4(G4S)4

Light chain (C4-VL + durva-CL) - SEQ ID NO: 332

DIVMTQSHKFMSTSVGDRVSITCKASQDVDTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGS
GSGTDYTLTISSVQAEDLARYYCQQYYSPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVT
HQGLSSPVTKSFNRGEC* **SEQ ID NO: 164**

*Heavy chain (C4-VH + DURVA[CH1 + Hinge + CH2 + CH3] + scFvC4(C4-Vh-linker-C4-VL)-)
- SEQ ID NO: 333*

QVQLLQSGPELVKPGASVKLSCKASGYSFTSYDINWVKQRPQGQLEWVGWIYPRDGDTKYNEKFK
GKAILTVDTSSNTAYMNLHSLTSEDSAVYFCARLTGPYWFYFDVWGTGTTVTVSSASTKGPSVFPLA
PSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ
TYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSGDGSFFLYSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGKQVQLLQSGPELVK
GASVKLSCKASGYSFTSYDINWVKQRPQGQLEWVGWIYPRDGDTKYNEKFKGKAILTVDTSSNTA
YMNLHSLTSEDSAVYFCARLTGPYWFYFDVWGTGTTVTVSSGGGGSGGGGSGGGGSGGGGSDIVM
TQSHKFMSTSVGDRVSITCKASQDVDTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGT
DYTLTISSVQAEDLARYYCQQYYSPWTFGGGTKVEIK* **SEQ ID NO: 165**

FIGURE 54

C4var7-IgG1(Durv)-HC:scFvC4var7(G4S)4*Light chain* ~ = C4var7-VL + durva-CL) -) - SEQ ID NO: 334

DIQMTQSPSSLSTSVGDRVTITCKASQDQDVTAVAWYQQKPGQSPKLLIYWASTRHTGVPSRFSGSGS
 GTDYTLTISSLQPEDVATYYCQQYYSPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL
 LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQG
 LSSPVTKSFNRGEC*

Heavy chain ~ = C4var7-VH + DURVA[CH1 + Hinge + CH2 + CH3] + scFvC4var7[C4-Vh 2-
 linker-C4-VL 3] =) - SEQ ID NO: 335

QVQLVQSGPEVKKPGASVKVSCASGYSTSYDINWVRQAPGQGLEWMGWYIPRDGDTKYAEKF
 QGRVTLTVDTSSSTAYMELSSLRSEDATYFCARLTGPYWFYFDVWGQGLTVTVSSASTKGPSVFPL
 APSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVV
 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
 ALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGKQVQLVQSGPEVK
 KPGASVKVSCASGYSTSYDINWVRQAPGQGLEWMGWYIPRDGDTKYAEKFQGRVTLTVDTSSS
 TAYMELSSLRSEDATYFCARLTGPYWFYFDVWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSDIQ
 MTQSPSSLSTSVGDRVTITCKASQDQDVTAVAWYQQKPGQSPKLLIYWASTRHTGVPSRFSGSGSGT
 DYTTLTISSLQPEDVATYYCQQYYSPPTFGGGTKLEIK

C4var16-IgG1(Durv)-LC:scFvC4var16(G4S)4

Light chain ~ = C4var16-VL + durva-CL + scFvC4var16[C4-Vh 4-linker-C4-VL 4] -) - SEQ ID
 NO: 336

DIQMTQSPSSLSASVGDRVTITCKASQDQDVTAVAWYQQKPGQSPKLLIYWASTRHTGVPSRFSGSGS
 GTDYTLTISSLQPEDVATYYCQQYYSPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL
 LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQG
 LSSPVTKSFNRGECQVQLVQSGPEVKKPGASVKVSCASGYSTSYDINWVRQAPGQGLEWMGWI
 YPREGDTKYAEKFQGRVTLTVDTSSSTAYMELSSLRSEDATYFCARLTGPYWFYFDVWGQGLTVT
 VSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCKASQDQDVTAVAWYQQKPGQ
 SPKLLIYWASTRHTGVPSRFSGSGSGTDYTTLTISSLQPEDVATYYCQQYYSPPTFGGGTKLEIK*

Heavy chain ~ = C4var16-VH + DURVA[CH1 + Hinge + CH2 + CH3] -) - SEQ ID NO: 337
 QVQLVQSGPEVKKPGASVKVSCASGYSTSYDINWVRQAPGQGLEWMGWYIPREGDTKYAEKF
 QGRVTLTVDTSSSTAYMELSSLRSEDATYFCARLTGPYWFYFDVWGQGLTVTVSSASTKGPSVFPL
 APSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT
 QTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVV
 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
 ALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK*

FIGURE 55