Figure 1:

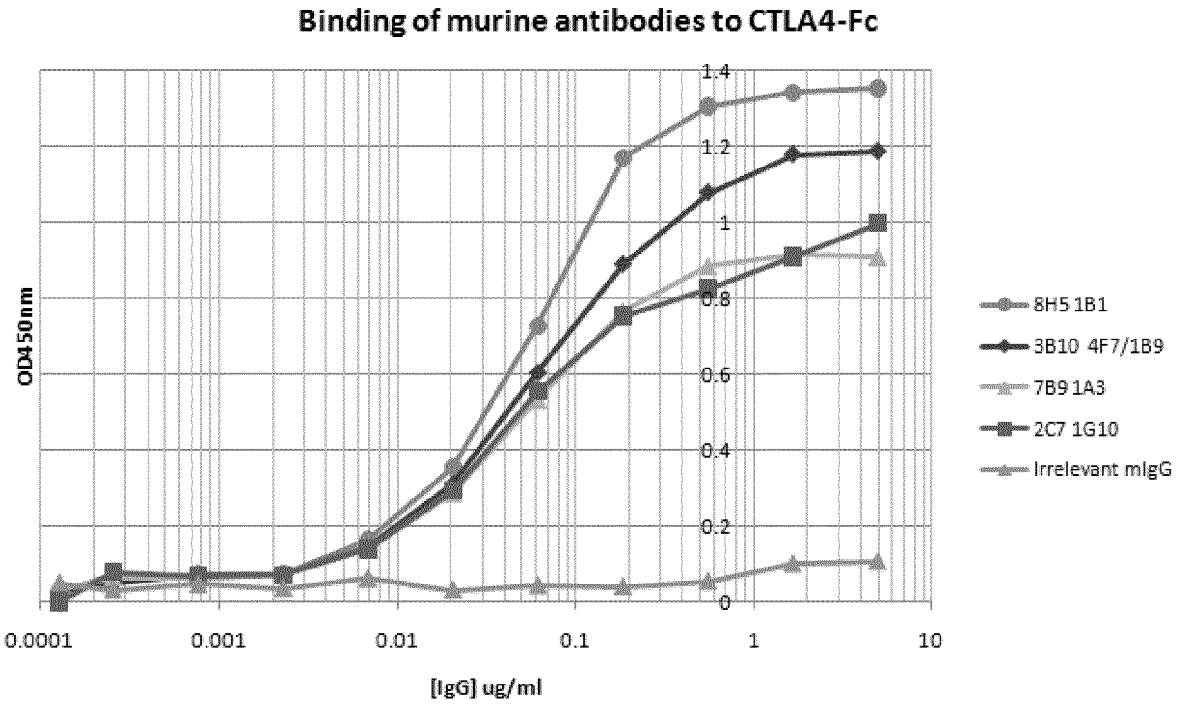

Binding of murine antibodies to CTLA4-Fc
OD450nm
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.0001
0.001
0.01
0.1
1
10
[IgG] ug/ml
8H5 1B1
3B10 4F7/1B9
7B9 1A3
2C7 1G10
Irrelevant mIgG

Figure 2:

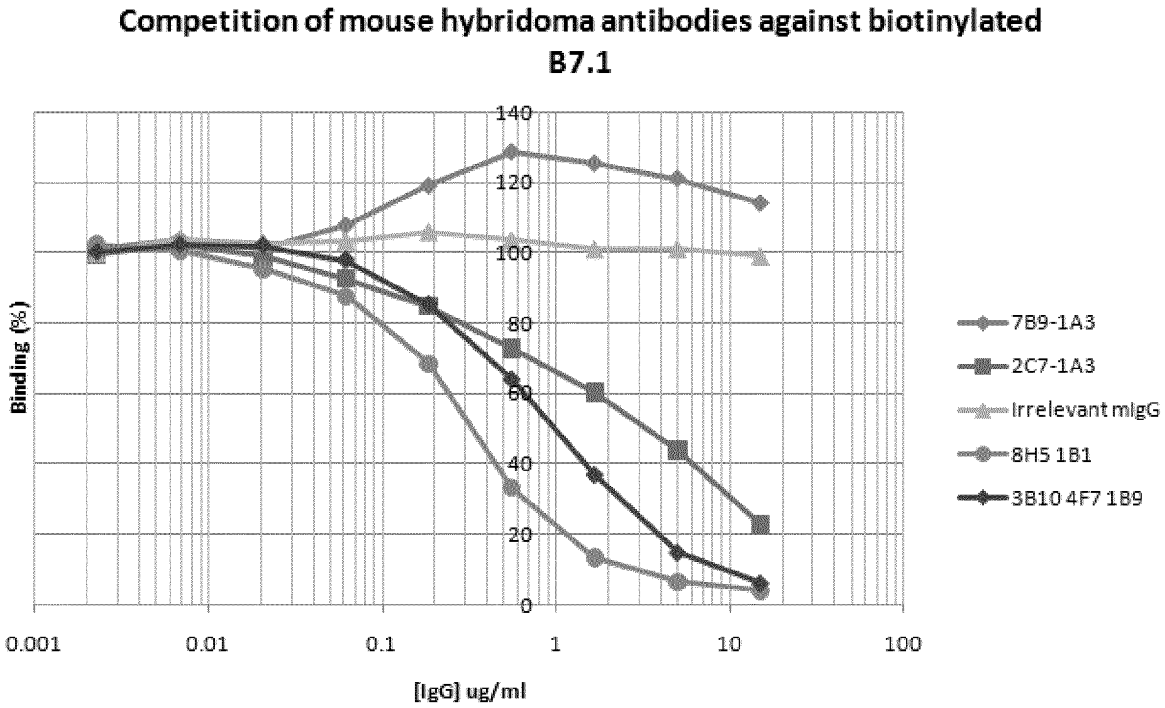

Competition of mouse hybridoma antibodies against biotinylated B7.1
Binding (%)
140
120
100
80
60
40
20
0
0.001
0.01
0.1
1
10
100
[IgG] ug/ml
7B9-1A3
2C7-1A3
Irrelevant mIgG
8H5 1B1
3B10 4F7 1B9

Figure 3:

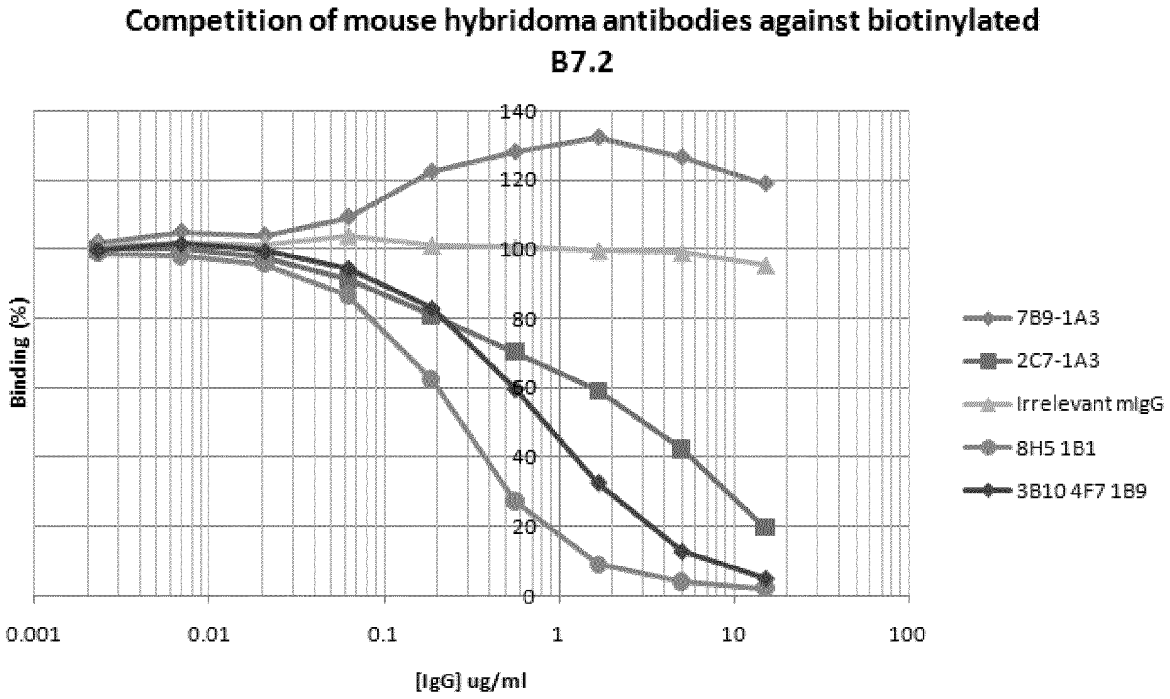

Competition of mouse hybridoma antibodies against biotinylated B7.2
Binding (%)
140
120
100
80
60
40
20
0
0.001
0.01
0.1
1
10
100
[IgG] ug/ml
7B9-1A3
2C7-1A3
Irrelevant mIgG
8H5 1B1
3B10 4F7 1B9

Figure 4:

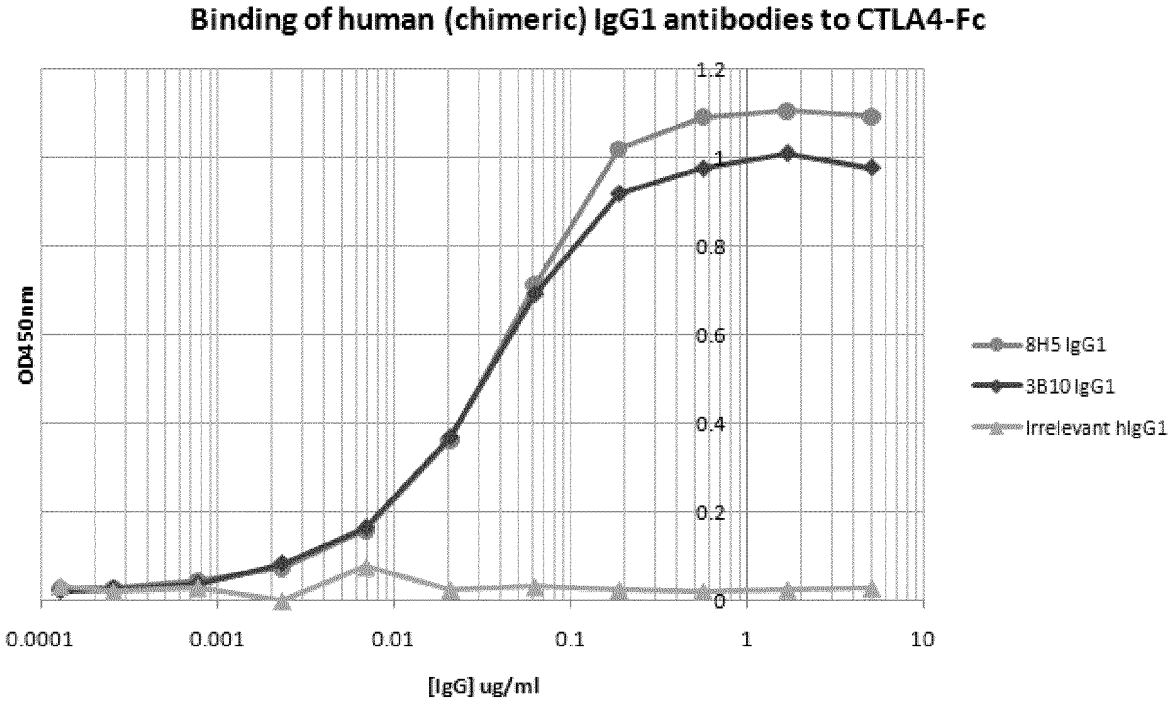

Binding of human (chimeric) IgG1 antibodies to CTLA4-Fc
OD450nm
1.2
1
0.8
0.6
0.4
0.2
0
0.0001
0.001
0.01
0.1
1
10
[IgG] ug/ml
8H5 IgG1
3B10 IgG1
Irrelevant hIgG1

Figure 5:

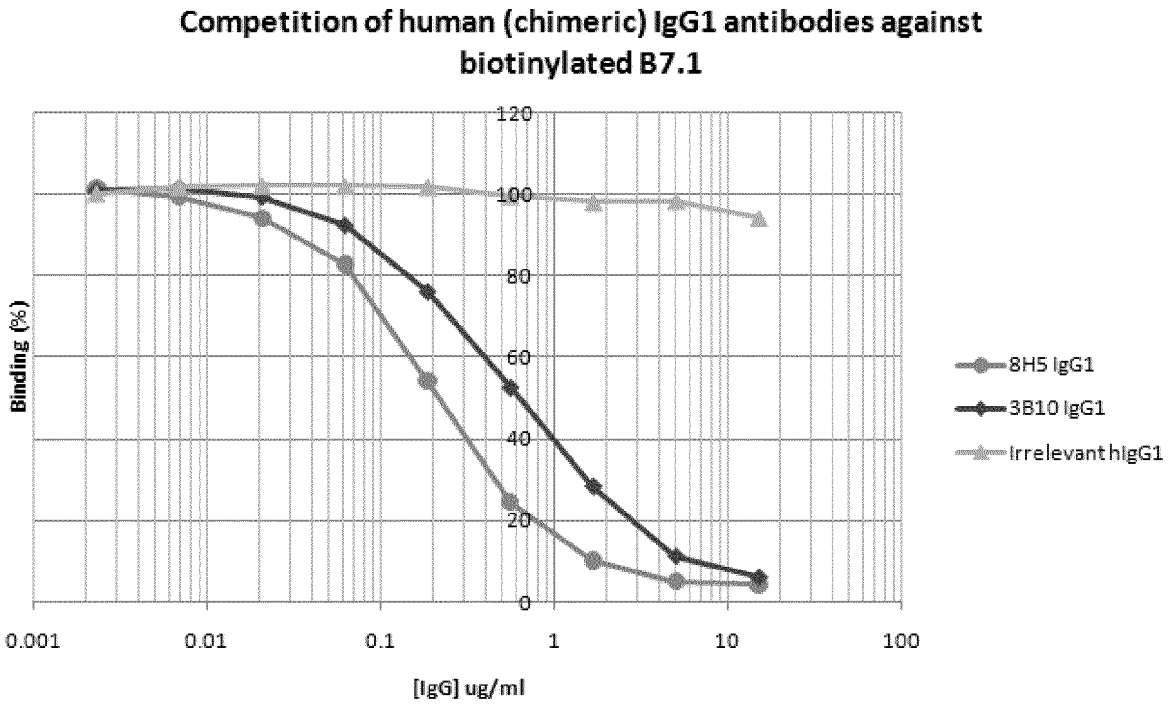

Competition of human (chimeric) IgG1 antibodies against biotinylated B7.1
Binding (%)
120
100
80
60
40
20
0
0.001
0.01
0.1
1
10
100
[IgG] ug/ml
8H5 IgG1
3B10 IgG1
Irrelevant hIgG1

Figure 6:

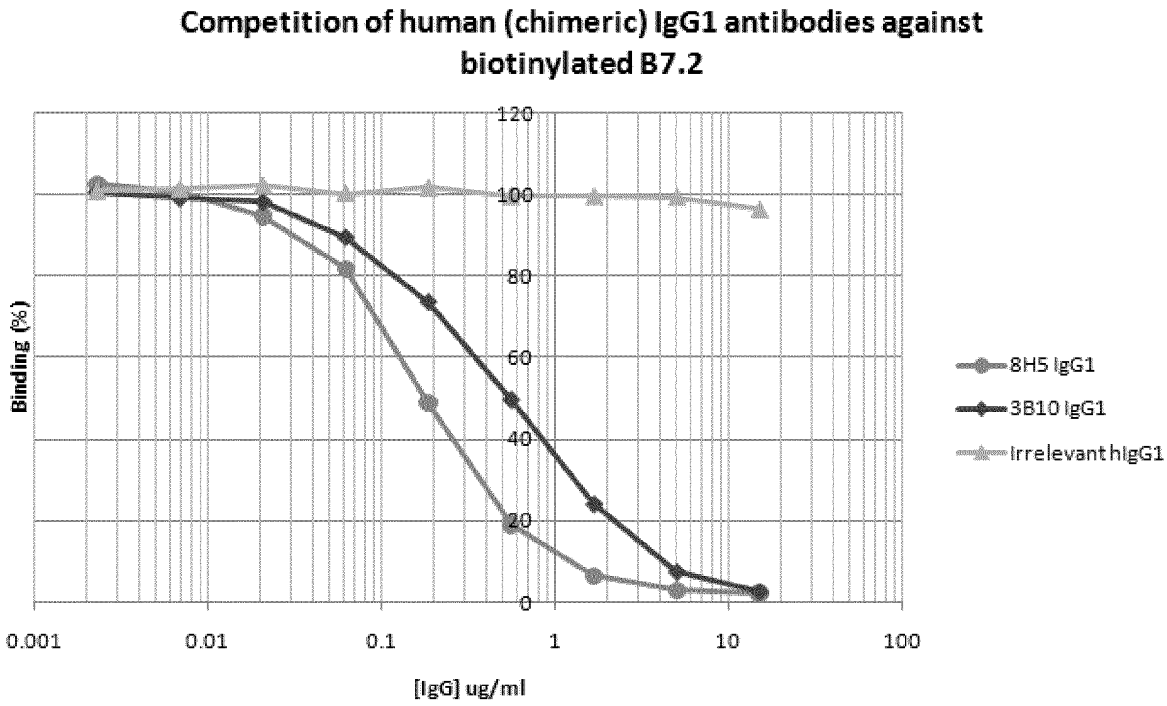

Competition of human (chimeric) IgG1 antibodies against biotinylated B7.2
Binding (%)
120
100
80
60
40
20
0
0.001
0.01
0.1
1
10
100
[IgG] ug/ml
8H5 IgG1
3B10 IgG1
Irrelevant hIgG1

Figure 7:

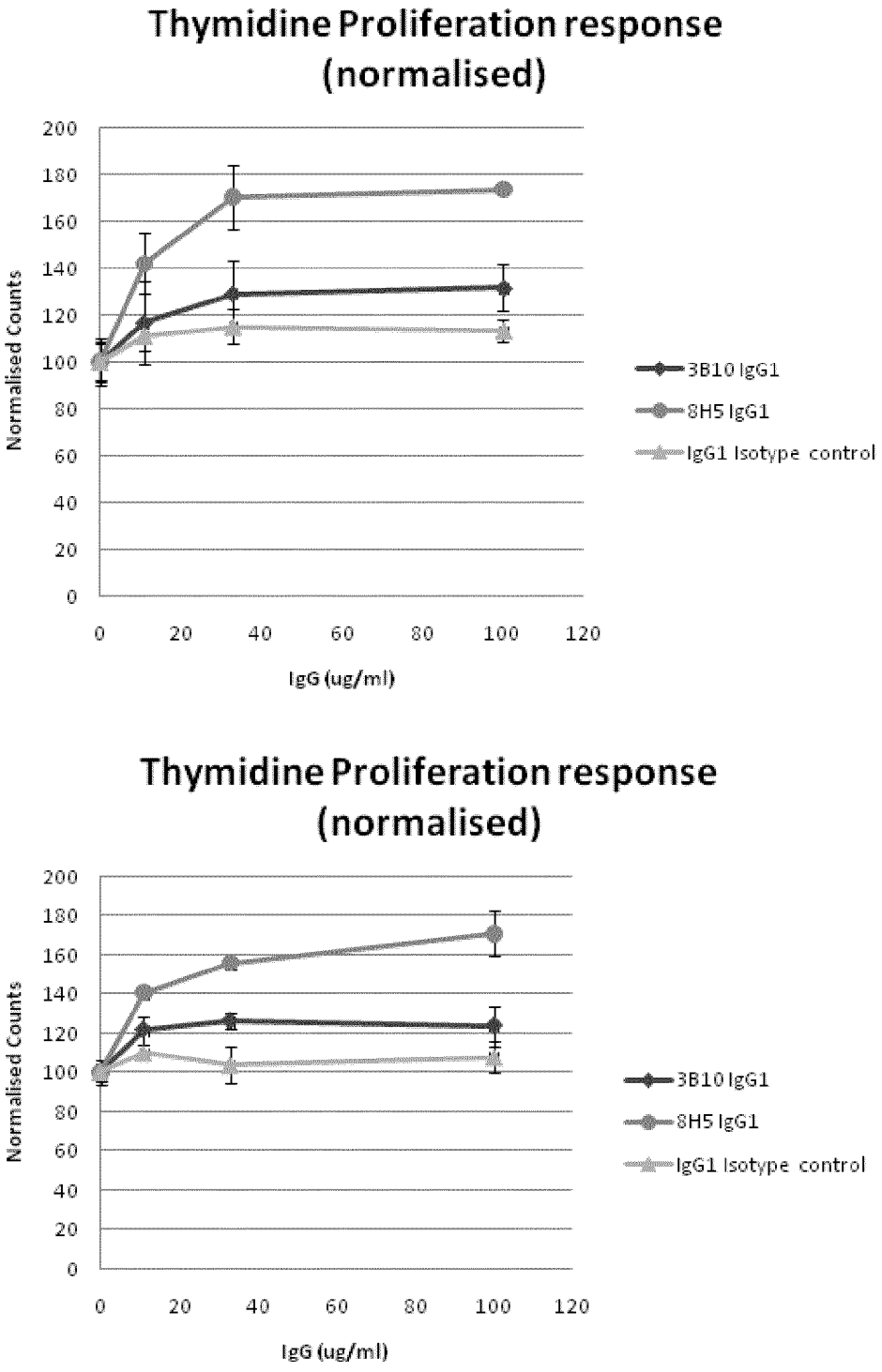
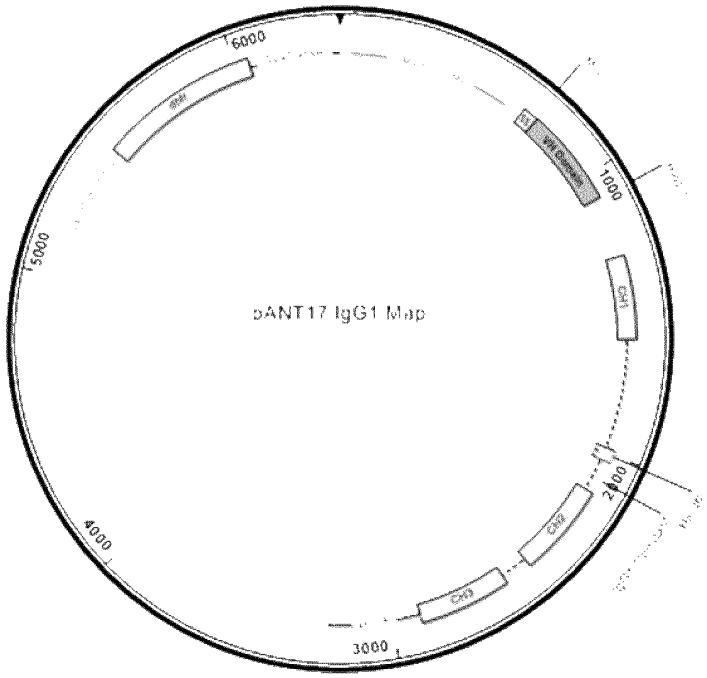

Thymidine Proliferation response (normalised)
Normalised Counts
IgG (ug/ml)
3B10 IgG1
8H5 IgG1
IgG1 Isotype control
Thymidine Proliferation response (normalised)
Normalised Counts
IgG (ug/ml)
3B10 IgG1
8H5 IgG1
IgG1 Isotype control

Figure 8:


pANT17 IgG1 Map
6000
1000
2000
3000
4000
5000
CH1
CH2
CH3

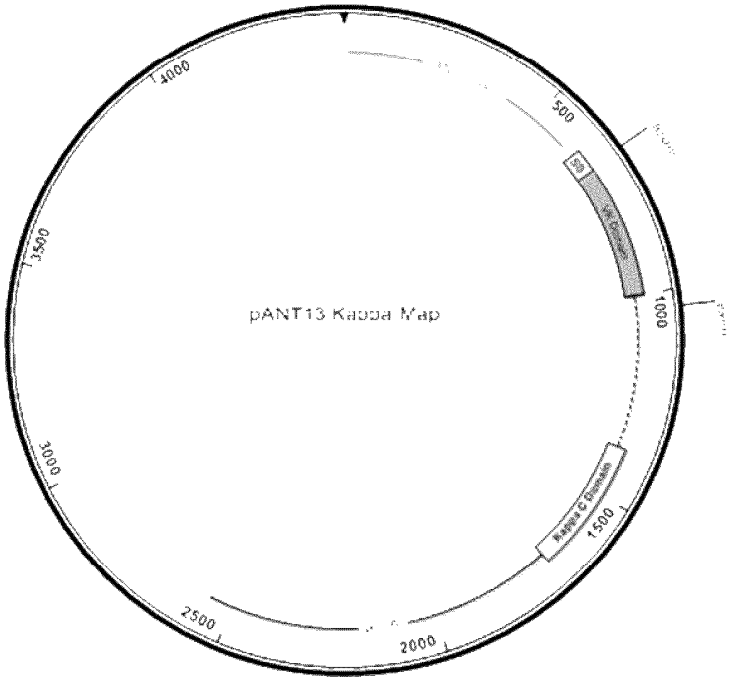

pANT13 Kappa Map
500
1000
1500
2000
2500
3000
3500
4000

Figure 9:

3B10 Hybridoma VH DNA (SEQ ID No. 1)

```
GAGGTCCAGC TGCAACAGTT TGGAGCTGAA CTGGTGAAGC CTGGGGCTTC   50
AGTGAAGATG TCCTGCAAGG CTTCTGGCTA CACATTCACT GACTACAACA  100
TGGACTGGGT GAGGCAGAGC CATGGAAAGA GTCTTGAGTG GATCGGAAAT  150
ATTAATCCTA ACTCTGAGAG TACTAGTTAC AACCAGAAGT TCAAGGGAAA  200
GGCCACATTG ACTGTAGACA AGTCCTCCAG CACAGCCTAC ATGGAGCTCC  250
GCAGCCTGAC ATCTGATGAC ACTGCAGTCT ATTACTGTAC AAGAGACGGG  300
AATAGGTACG ACGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC  350
TGTCTCCTCA                                              360
```

3B10 Hybridoma VK DNA (SEQ ID No. 2)

```
CAGATTGTTC TCACCCAGTC TCCAGCAATC ATGTCTGCAT CTCCAGGGGA   50
GAAGGTCACC ATGACCTGCA GTGCCAGCTC AAGTGTTACT TACATGCACT  100
GGTTCCAGCA GAAGCCAGGC ACTTCTCCCA AACTCTGGAT TTATAGCACA  150
TCCATCCTGG CTTCTGGAGT CCCTGCTCGC TTCAGTGGCA GTGGATCTGG  200
GACCTCTTAC TCTCTCACAA TCAGCCGAAT GGAGGCTGAA GATGCTGCCA  250
CTTATTACTG CCAGCAAAGG ACTAGTTACC CGCTCACGTT CGGTACTGGG  300
ACCAAGCTGG AGCTGAAA                                     318
```

Figure 10:

8H5 Hybridoma VH DNA (SEQ ID No. 5)

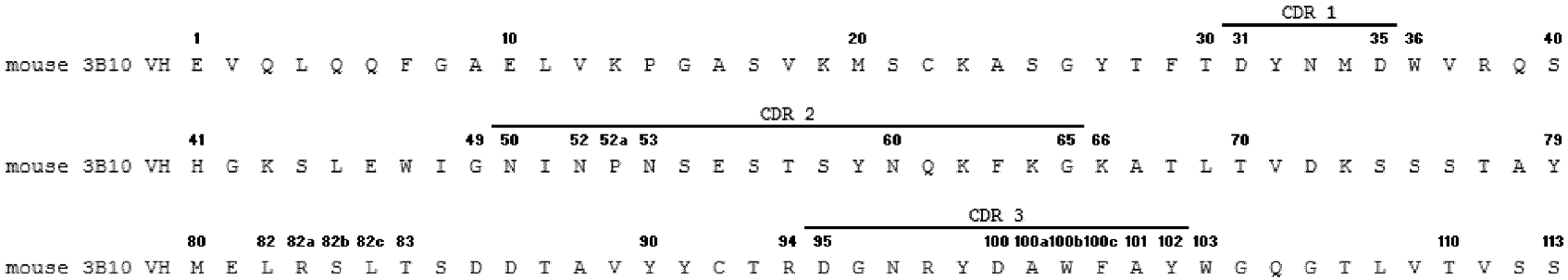
```
CAGGTCCAGC TGCAACAGTC TGGAGATGAT CTGGTAAAGC CTGGGGCCTC   50
AGTGAAGCTG TCCTGCAAGG CTTCTGGCTA CACCTTCACC AGCTACTGGA  100
TTAACTGGAT AAAACAGAGG CCTGGACAGG GCCTTGAGTG GATAGGACGT  150
ATTGCTCCTG GAAGTGGTAC TACTTACTAC AATGAAGTGT TCAAGGGCAA  200
GGCAACACTG ACTGTAGACA AATATTCCAG CACAGCCTAC ATTCAGCTCA  250
GCAGCCTGTC ATCTGAGGAC TCTGCTGTCT ATTTCTGTGC AAGAGGGGAC  300
TATGGTTCTT ACTGGGGCCA AGGGACTCTG GTCACTGTCT CCTCA       345
```

8H5 Hybridoma VK DNA (SEQ ID No. 6)

```
CAAATTGTTC TCACCCAGTC TCCAGCAATC ATGTCTGCAT CTCCAGGGGA   50
GAAGGTCACC ATGACCTGCA GTGCCAGCTC AAGTATAAGT TACATGCACT  100
GGTTCCAGCA GAAGCCAGGC ACCTCCCCCA AAAGATGGAT TTATGACACA  150
TCCAAACTGG CTTCTGGAGT CCCTGCTCGC TTCAGTGGCA GTGGGTCTGG  200
GACCTCTTAT TCTCTCACAA TCAACAGCAT GGAGGCTGAA GATGCTGCCA  250
CTTATTACTG CCATCAGCGG ACTAGTTACC CACTCACGTT CGGTGCTGGG  300
ACCAAGCTGG AGCTGAAA                                    318
```

Figure 11:

3B10 Hybridoma VH Amino Acid (SEQ ID No. 3)



3B10 Hybridoma VK Amino Acid (SEQ ID No. 4)

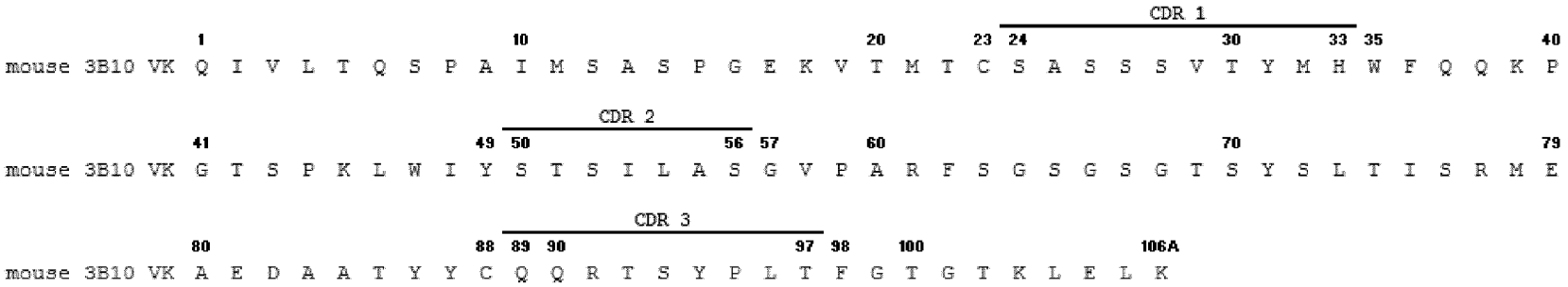
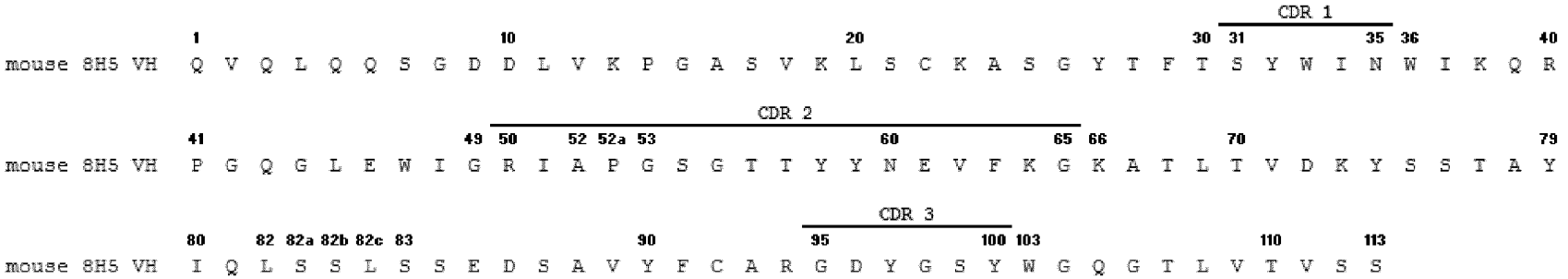


Figure 12:

8H5 Hybridoma VH Amino Acid (SEQ ID No. 7)



8H5 Hybridoma VK Amino Acid (SEQ ID No. 8)

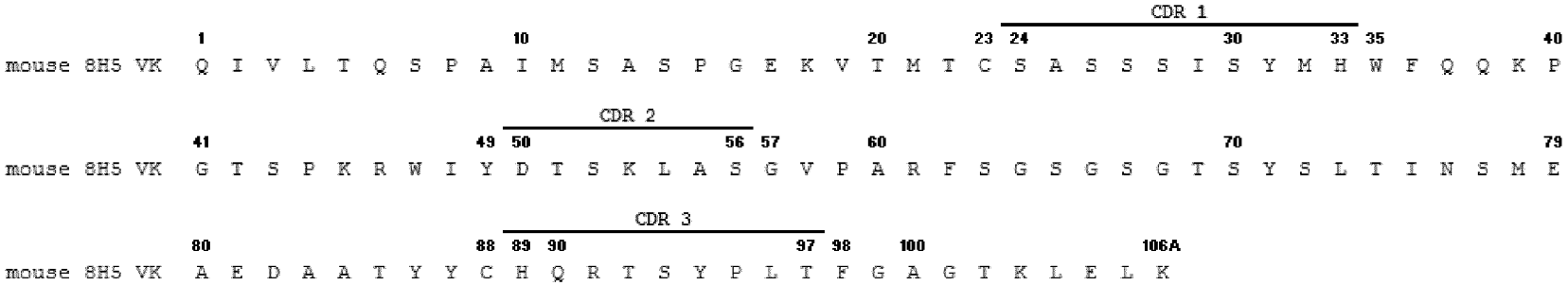


Figure 13:

Humanised 3B10 variant VH amino acid sequences (SEQ ID Nos 3 and 31 to 35)

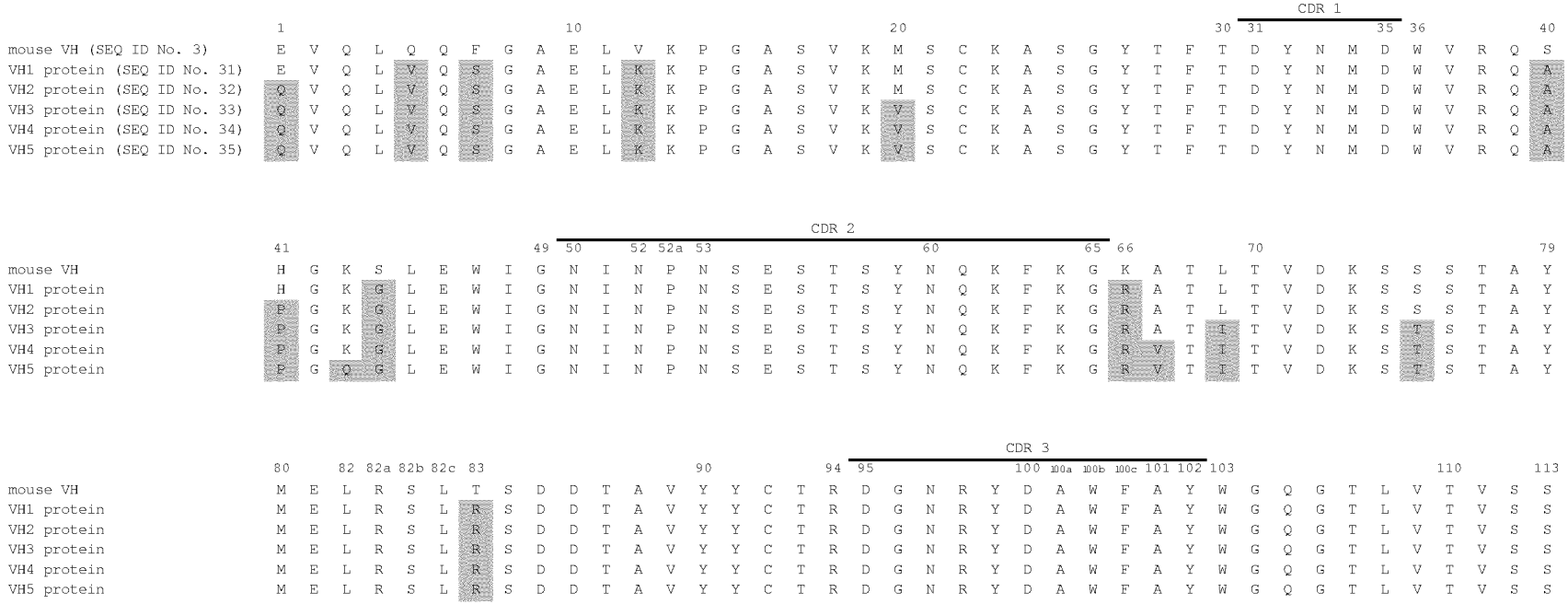


Figure 14:

Humanised 3B10 variant VK amino acid sequences (SEQ ID Nos 4 and 36 to 40)

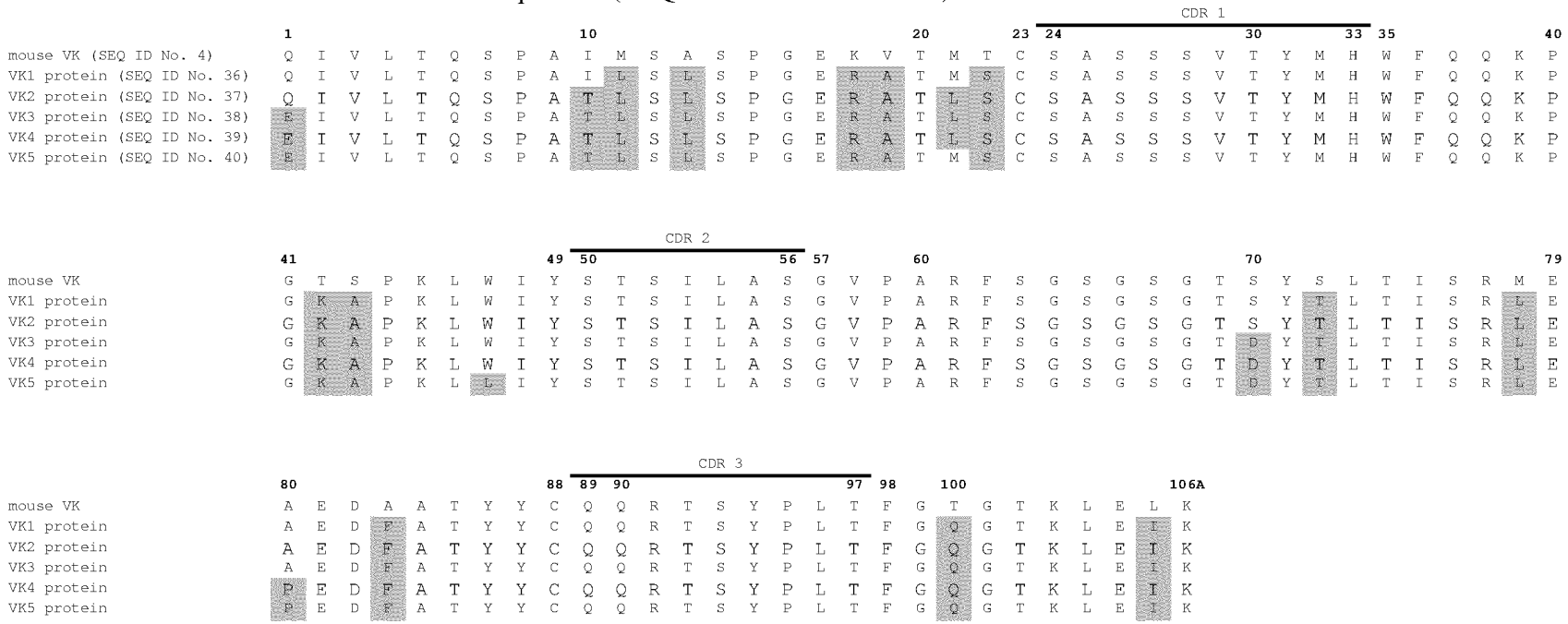


Figure 15:

Humanised 8H5 variant VH amino acid sequences (SEQ ID Nos 7 and 41 to 45)

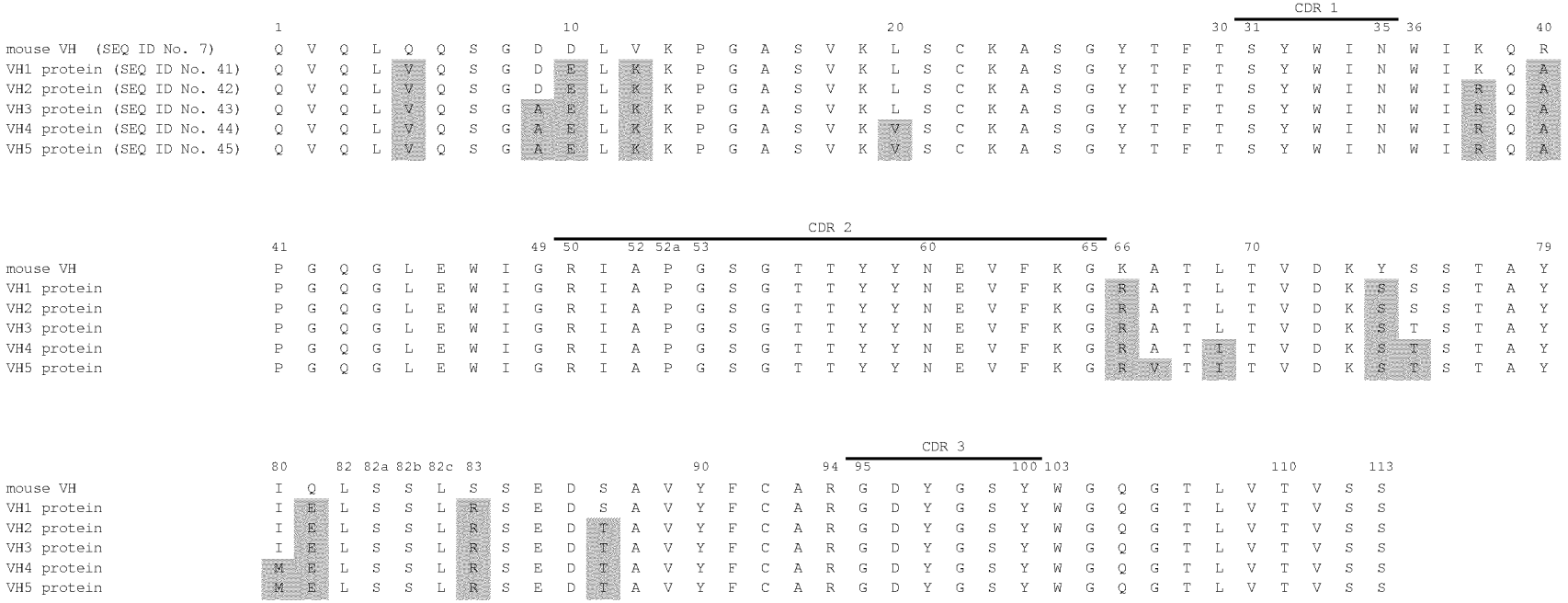


Figure 16:

Humanised 8H5 variant VK amino acid sequences (SEQ ID Nos 8 and 46-50)

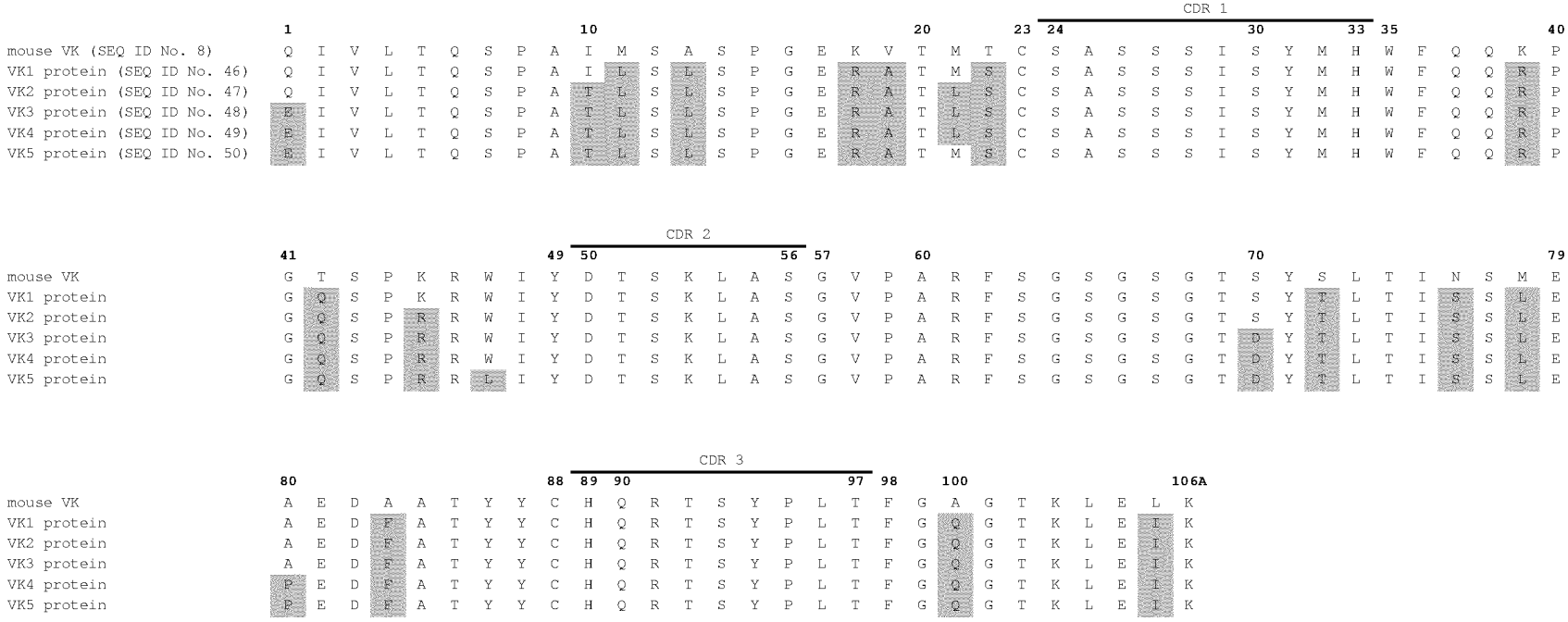
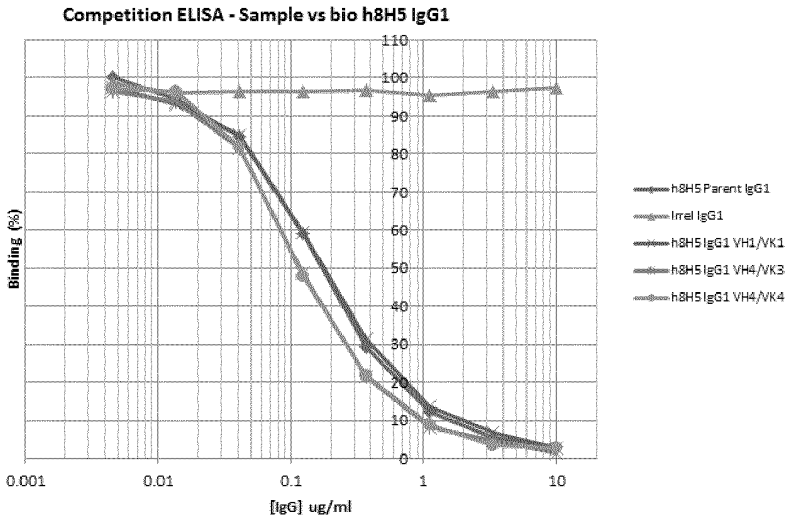
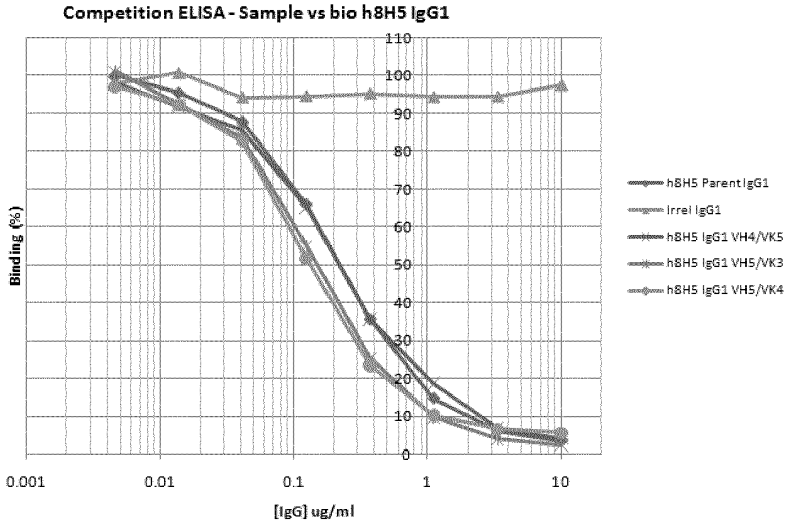


Figure 17:


Competition ELISA - Sample vs bio h8H5 IgG1
Binding (%)
[IgG] ug/ml
h8H5 Parent IgG1
Irrel IgG1
h8H5 IgG1 VH1/VK1
h8H5 IgG1 VH4/VK3
h8H5 IgG1 VH4/VK4


Competition ELISA - Sample vs bio h8H5 IgG1
Binding (%)
[IgG] ug/ml
h8H5 Parent IgG1
Irrel IgG1
h8H5 IgG1 VH4/VK5
h8H5 IgG1 VH5/VK3
h8H5 IgG1 VH5/VK4

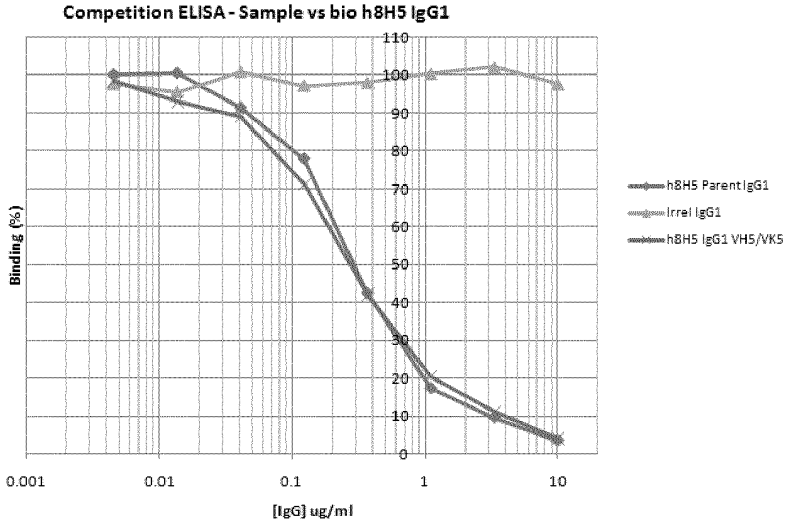

Competition ELISA - Sample vs bio h8H5 IgG1
Binding (%)
[IgG] ug/ml
h8H5 Parent IgG1
Irrel IgG1
h8H5 IgG1 VH5/VK5

Figure 18: Human Mixed Lymphocyte Reaction Model

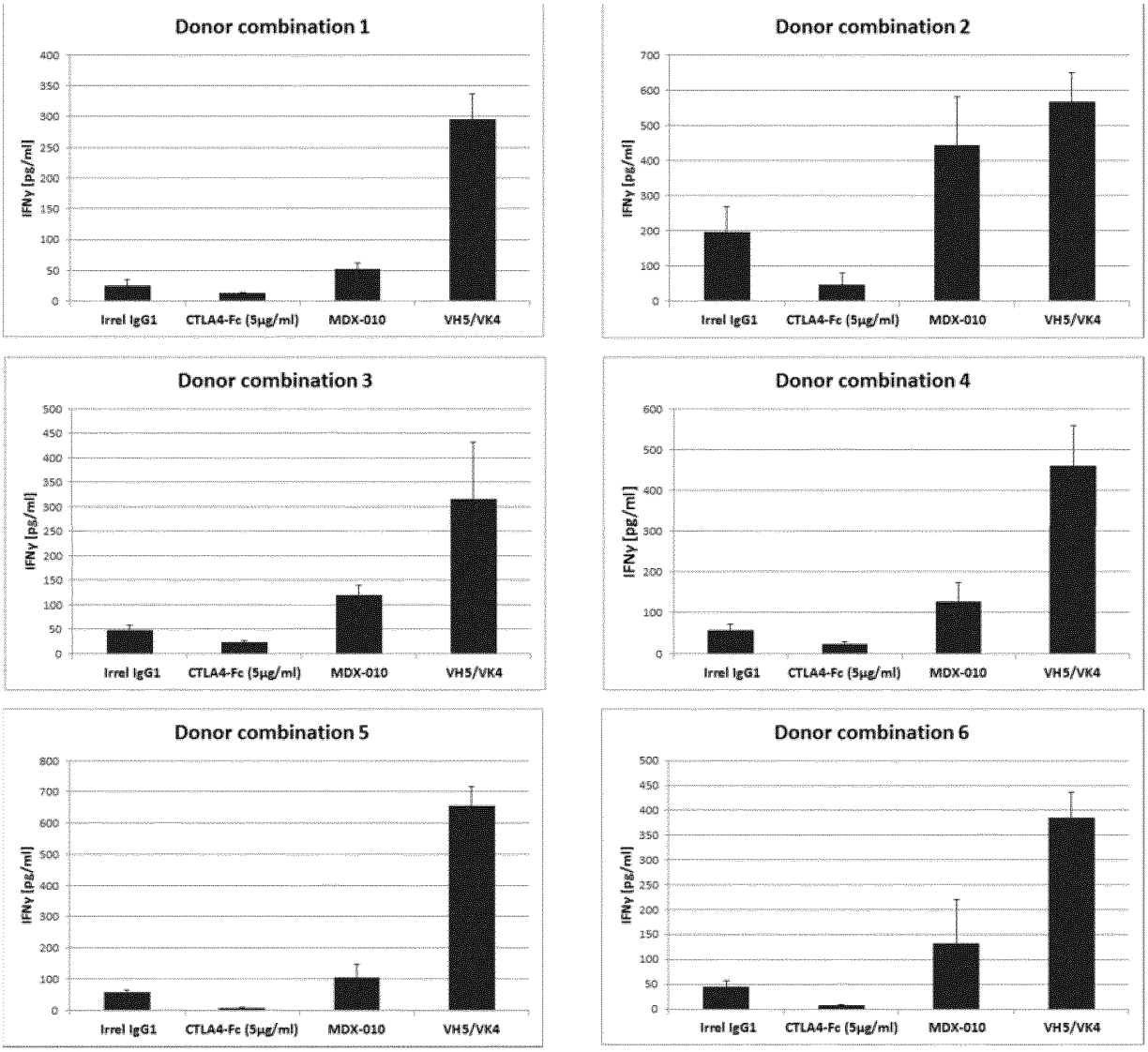
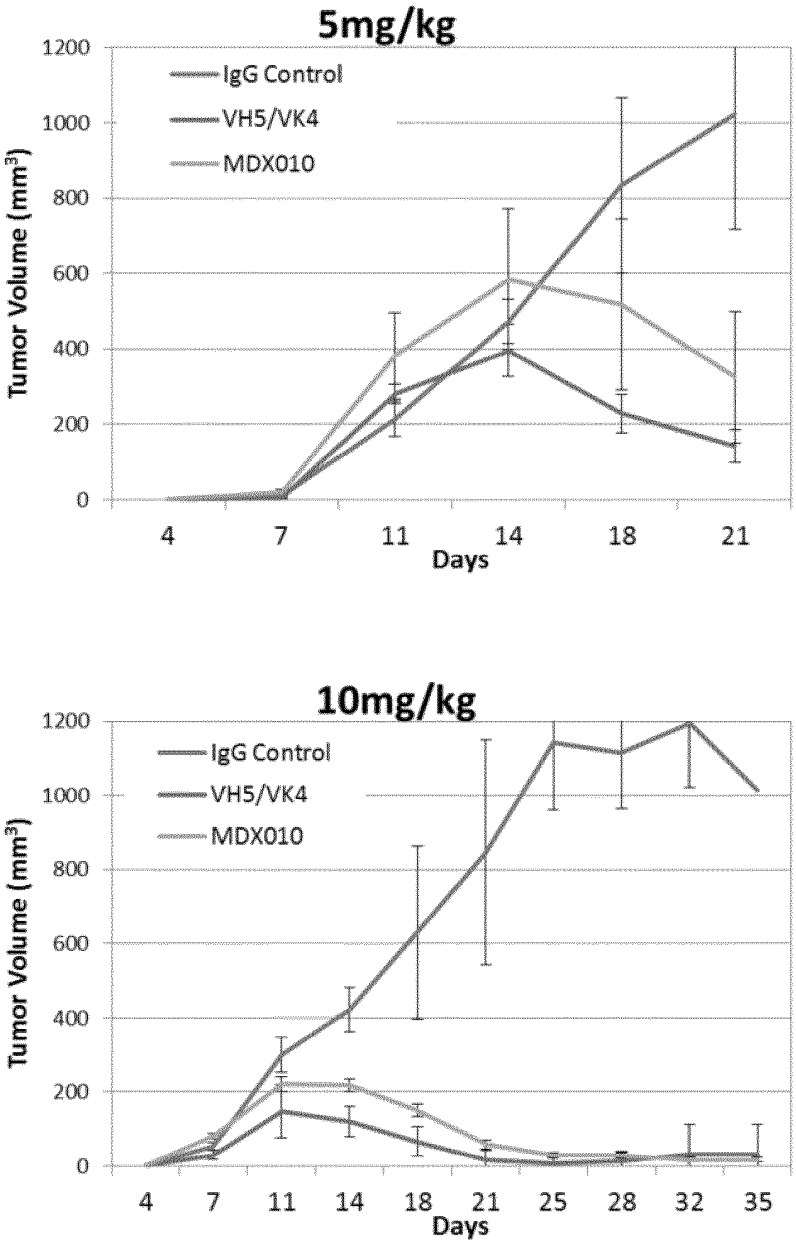


Figure 19: Tumour Animal Model



Sequence	Name-Pool
ATGRASTTSKGGYTMARCTKGRTTT	MuIgV$_H$5'-A
ATGRAATGSASCTGGGTYWTYCTCTT	MuIgV$_H$5'-B
ATGGACTCCAGGCTCAATTTAGTTTTCCT	MuIgV$_H$5'-C
ATGGCTGTCYTRGBGCTGYTCYTCTG	MuIgV$_H$5'-C
ATGGVTTGGSTGTGGAMCTTGCYATTCCT	MuIgV$_H$5'-C
ATGAAATGCAGCTGGRTYATSTTCTT	MuIgV$_H$5'-D
ATGGRCAGRCTTACWTYYTCATTCCT	MuIgV$_H$5'-D
ATGATGGTGTTAAGTCTTCTGTACCT	MuIgV$_H$5'-D
ATGGGATGGAGCTRTATCATSYTCTT	MuIgV$_H$5'-E
ATGAAGWTGTGGBTRAACTGGRT	MuIgV$_H$5'-E
ATGGRATGGASCKKIRTCTTTMTCT	MuIgV$_H$5'-E
ATGAACTTYGGGYTSAGMTTGRTTT	MuIgV$_H$5'-F
ATGTACTTGGGACTGAGCTGTGTAT	MuIgV$_H$5'-F
ATGAGAGTGCTGATTCTTTTGTG	MuIgV$_H$5'-F
ATGGATTTTGGGCTGATTTTTTTTATTG	MuIgV$_H$5'-F
CCAGGGRCCARKGGATARACIGRTGG	MuIgGV$_H$3'-2
ATGRAGWCACAKWCYCAGGTCTTT	MuIgkV$_L$5'-A
ATGGAGACAGACACACTCCTGCTAT	MuIgkV$_L$5'-B
ATGGAGWCAGACACACTSCTGYTATGGGT	MuIgkV$_L$5'-C
ATGAGGRCCCCTGCTCAGWTTYTTGGIWTCTT	MuIgkV$_L$5'-D
ATGGGCWTCAAGATGRAGTCACAKWYYCWGG	MuIgkV$_L$5'-D
ATGAGTGTGCYCACTCAGGTCCTGGSGTT	MuIgkV$_L$5'-E
ATGTGGGGAYCGKTTTYAMMCTTTTCAATTG	MuIgkV$_L$5'-E
ATGGAAGCCCCAGCTCAGCTTCTCTTCC	MuIgkV$_L$5'-E
ATGAGIMMKTCIMTTCAITTCYTGGG	MuIgkV$_L$5'-F
ATGAKGTHCYCIGCTCAGYTYCTIRG	MuIgkV$_L$5'-F
ATGGTRTCCWCASCTCAGTTCCTTG	MuIgkV$_L$5'-F
ATGTATATATGTTTGTTGTCTATTTCT	MuIgkV$_L$5'-F
ATGAAGTTGCCTGTTAGGCTGTTGGTGCT	MuIgkV$_L$5'-G
ATGGATTTWCARGTGCAGATTWTCAGCTT	MuIgkV$_L$5'-G
ATGGTYCTYATVTCCTTGCTGTTCTGG	MuIgkV$_L$5'-G
ATGGTYCTYATVTTRCTGCTGCTATGG	MuIgkV$_L$5'-G
ACTGGATGGTGGGAAGATGGA	MuIgkV$_L$3'-1

Table 1

Table 2

Sequence	Name
ctgttgctacgcgtgtccactccGAGGTCCAGCTGCAACAG	3B10 VH 5’
ctgccccagaaagcttaccTGAGGAGACAGTGACCAGAG	3B10 VH 3’
ggctcccaggcgcgcgatgtCAGATTGTTCTCACCCAGTC	3B10 VK 5’
tagaattgcgggatccaactgaggaagcaaagtttaaattctactcacgTTTCAGCTCCAGCTTGGTC	3B10 VK 3’
ctgttgctacgcgtgtccactccCAGGTCCAGCTGCAACAG	8H5 VH 5’
ctgccccagaaagcttaccTGAGGAGACAGTGACCAGAG	8H5 VH 3’
ggctcccaggcgcgcgatgtCAAATTGTTCTCACCCAGTCTC	8H5 VK 5’
tagaattgcgggatccaactgaggaagcaaagtttaaattctactcacgTTTCAGCTCCAGCTTGGTCC	8H5 VK 3’