

**Figure 1a**

|          |     | LEADER                                                                                                                  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|----------|-----|-------------------------------------------------------------------------------------------------------------------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|          |     | atg aac ttc tgg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt gtc cag tgt                                             |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|          |     | -19 M N F W L S L I F L V L V L K G V Q C                                                                               |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|          |     | <----- FR1 - IMGT ----->                                                                                                |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 1   | E                                                                                                                       | V | K | L | V | E | S | G | G | G | L | V | Q | P | G | G | S | L | K | L | S | C | A | T | S | G | F | T | F |   |
|          |     | gaa gtg aag ctg gtg gag tct ggg gga ... ggc tta gtg cag cct gga ggg tcc ctg aaa ctc tcc tgt gca acc tct gga ttc act ttc |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|          |     | _____ CDR1 - IMGT _____<----- FR2 - IMGT ----->_____ CDR2 S                                                             |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 31  |                                                                                                                         |   |   |   | H | Y | Y | M | Y | W | V | R | Q | T | P | E | K | R | L | E | W | V | A | Y | I | S | N | D |   |   |
|          |     | ... .. agt cac tat tac atg tat tgg gtt cgc cag act cca gag aag agg ctg gag tgg gtc gca tac att agt aat gat ...          |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|          |     | - IMGT _____<----- FR3 - IMGT ----->                                                                                    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 61  | G                                                                                                                       | D | N | T | Y | Y | P | D | T | I | R | G | R | F | T | I | S | R | D | N | A | R | N | T | L | Y | L | Q |   |   |
|          |     | ... ggt gat aac acc tat tat cca gac act ata agg ... ggc cga ttc acc atc tcc aga gac aat gcc agg aac acc ctg tac ctg caa |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|          |     | ----->_____ CDR3 - IMGT _____                                                                                           |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 91  | M                                                                                                                       | S | R | L | K | S | E | D | T | A | M | Y | Y | C | A | R | G | K | Y | D | G | A | W | F | A | Y | W | G | Q | G |
|          |     | atg agc cgt ctg aag tct gag gac aca gcc atg tat tac tgt gca aga ggg aag tac gac ggg gcc tgg ttt gct tac tgg ggc caa ggg |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 121 | T                                                                                                                       | L | V | T | V | S | A | A | T | T | T | A | F | S | V | Y | P | L | V | P | G | C | S | D | T | S | G | S | S | V |
|          |     | act ctg gtc act gtc tct gca gct aca aca aca gcc cca tct gtc tat ccc ttg gtc cct ggc tgc agt gac aca tct gga tcc tgg gtg |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 151 | T                                                                                                                       | L | G | C | L | V | K | G | Y | F | P | E | P | V | T | V | K | W | N | Y | G | A | L | S | S | G | V | R | T | V |
|          |     | aca ctg gga tgc ctt gtc aaa ggc tac ttc cct gag ccg gta act gta aaa tgg aac tat gga gcc ctg tcc agc ggt gtg cgc aca gtc |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 181 | S                                                                                                                       | S | V | L | Q | S | G | F | Y | S | L | S | S | L | V | T | V | P | S | S | T | W | P | S | Q | T | V | I | C | N |
|          |     | tca tct gtc ctg cag tct ggg ttc tat tcc ctc agc agc ttg gtg act gta ccc tcc agc acc tgg ccc agc cag act gtc atc tgc aac |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 211 | V                                                                                                                       | A | H | P | A | S | K | T | E | L | I | K | R | I | E | P | R | I | P | K | P | S | T | P | P | G | S | S | C | P |
|          |     | gta gcc cac cca gcc agc aag act gag ttg atc aag aga atc gag cct aga ata ccc aag ccc agt acc ccc cca ggt tct tca tgc cca |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 241 | P                                                                                                                       | G | N | I | L | G | G | P | S | V | F | I | F | P | P | K | P | K | D | A | L | M | I | S | L | T | P | K | V | T |
|          |     | cct ggt aac atc ttg ggt gga cca tcc gtc ttc atc ttc ccc cca aag ccc aag gat gca ctc atg atc tcc cta acc ccc aag gtt acg |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 271 | C                                                                                                                       | V | V | V | D | V | S | E | D | D | P | D | V | H | V | S | W | F | V | D | N | K | E | V | H | T | A | W | T | Q |
|          |     | tgt gtg gtg gtg gat gtg agc gag gat gac cca gat gtc cat gtc agc tgg ttt gtg gac aac aaa gaa gta cac aca gcc tgg aca cag |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 301 | P                                                                                                                       | R | E | A | Q | Y | N | S | T | F | R | V | V | S | A | L | P | I | Q | H | Q | D | W | M | R | G | K | E | F | K |
|          |     | ccc cgt gaa gct cag tac aac agt acc ttc cga gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agg ggc aag gag ttc aaa |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 331 | C                                                                                                                       | K | V | N | N | K | A | L | P | A | P | I | E | R | T | I | S | K | P | K | G | R | A | Q | T | P | Q | V | Y | T |
|          |     | tgc aag gtc aac aac aaa gcc ctc cca gcc ccc atc gag aga acc atc tca aaa ccc aaa gga aga gcc cag aca cct caa gta tac acc |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 361 | I                                                                                                                       | P | P | P | R | E | Q | M | S | K | K | K | V | S | L | T | C | L | V | T | N | F | F | S | E | A | I | S | V | E |
|          |     | ata ccc cca cct cgt gaa caa atg tcc aag aag aag gtt agt ctg acc tgc ctg gtc acc aac ttc ttc tct gaa gcc atc agt gtg gag |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 391 | W                                                                                                                       | E | R | N | G | E | L | E | Q | D | Y | K | N | T | P | P | I | L | D | S | D | G | T | Y | F | L | Y | S | K | L |
|          |     | tgg gaa agg aac gga gaa ctg gag cag gat tac aag aac act cca ccc atc ctg gac tca gat ggg acc tac ttc ctc tac agc aag ctc |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 421 | T                                                                                                                       | V | D | T | D | S | W | L | Q | G | E | I | F | T | C | S | V | V | H | E | A | L | H | N | H | H | T | Q | K | N |
|          |     | act gtg gat aca gac agt tgg ttg caa gga gaa att ttt acc tgc tcc gtg gtg cat gag gct ctc cat aac cac cac aca cag aag aac |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FG27_10H | 451 | L                                                                                                                       | S | R | S | F | G | K |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|          |     | ctg tct cgc tcc cct ggt aaa                                                                                             |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

Figure 1b

```

                                     LEADER
      atg aac ttc tgg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt gtc cag tgt
-19 M N F W L S L I F L V L V L K G V Q C

<-----FR1 - IMGT----->
1 E V K L V E S G G G L V Q P G G S L K L S C A T S G F T F
FG27_18H gaa gtg aag ctg gtg gag tct ggg gga ... ggc tta gtg cag cct gga ggg tcc ctg aaa ctc tcc tgt gca acc tct gga ttc act ttc

      CDR1 - IMGT      <-----FR2 - IMGT----->      CDR2 S
31 H Y Y M Y W V R Q T P E K R L E W V A Y I S N D
FG27_18H ... .. agt cac tat tac atg tat tgg gtt cgc cag act cca gag aag agg ctg gag tgg gtc gca tac att agt aat gat ...

      - IMGT      <-----FR3 - IMGT----->
61 G D N T Y Y P D T I R G R F T I S R D N A R N T L Y L Q
FG27_18H ... ggt gat aac acc tat tat cca gac act ata agg ... ggc cga ttc acc atc tcc aga gac aat gcc agg aac acc ctg tac ctg caa

----->      CDR3 - IMGT
91 M S R L K S E D T A M Y Y C A R G K Y D G A W F A Y W G Q G
FG27_18H atg agc cgt ctg aag tct gag gac aca gcc atg tat tac tgt gca aga ggg aag tac gac ggg gcc tgg ttt gct tac tgg ggc caa ggg

121 T L V T V S A A K T T P P S V Y P L A P G S A A Q T N S M V
FG27_18H act ctg gtc act gtc tct gca gcc aaa acg aca ccc cca tct gtc tat cca ctg gcc cct gga tct gct gcc caa act aac tcc atg gtg

151 T L G C L V K G Y F P E P V T V T W N S G S L S S G V H T F
FG27_18H acc ctg gga tgc ctg gtc aag ggc tat ttc cct gag cca gtg aca gtg acc tgg aac tct gga tcc ctg tcc agc ggt gtg cac acc ttc

181 P A V L E S D L Y T L S S S V T V P S S P R P S E T V T C N
FG27_18H cca gct gtc ctg gag tct gac ctc tac act ctg agc agc tca gtg act gtc ccc tcc agc cct cgg ccc agc gag acc gtc acc tgc aac

211 V A H P A S S T K V D K K I V P R D C G C K P C I C T V P E
FG27_18H gtt gcc cac ccg gcc agc agc acc aag gtg gac aag aaa att gtg ccc agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa

241 V S S V F I F P P K P K D V L T I T L T P K V T C V V V D I
FG27_18H gta tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc att act ctg act cct aag gtc acg tgt gtt gtg gta gac atc

271 S K D D P E V Q F S W F V D D V E V H T A Q T Q P R E E Q F
FG27_18H agc aag gat gat ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg cac aca gct cag acg caa ccc cgg gag gag cag ttc

301 N S T F R S V S E L P I M H Q D W L N G K E F K C R V N S A
FG27_18H aac agc act ttc cgc tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc aag gag ttc aaa tgc agg gtc aac agt gca

331 A F P A P I E K T I S K T K G R P K A P Q V Y T I P P P K E
FG27_18H gct ttc cct gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac acc att cca cct ccc aag gag

361 Q M A K D K V S L T C M I T D F F P E D I T V E W Q W N G Q
FG27_18H cag atg gcc aag gat aaa gtc agt ctg acc tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag tgg cag tgg aat ggg cag

391 P A E N Y K N T Q P I M N T N G S Y F V Y S K L N V Q K S N
FG27_18H cca gcg gag aac tac aag aac act cag ccc atc atg aac acg aat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag aag agc aac

421 W E A G N T F T C S V L H E G L H N H H T E K S L S H S P G
FG27_18H tgg gag gca gga aat act ttc acc tgc tct gtg tta cat gag ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt

451 K
FG27_18H aaa
```

Figure 1c

```

                                     LEADER
-19 M K L P V R L L V L M F W I P A S I S
    atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct gct tcc atc agt

<-----FR1 - IMGT----->
1  D V L M T Q T P L S L P V S L G D Q A S I S C R S S Q I I V
FG27_10K   gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag atc att gta

    CDR1 - IMGT <-----FR2 - IMGT-----> CDR2
31 H T      N G N T Y L E W Y L Q K P G Q S P N L L I Y K V
FG27_10K   cat act ... aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca ggc cag tct cca aac ctc ctg atc tac aaa gtt ... ..

    - IMGT <-----FR3 - IMGT----->
61          S N R F S G V P      D R F S G S G      S G T D F T L K
FG27_10K   ... .. tcc aac cga ttt tct ggg gtc cca ... gac agg ttc agt ggc agt gga ... .. tca ggg aca gat ttc aca ctc aag

-----> CDR3 - IMGT
91 I S R V E A E D L G V Y Y C F Q G S H V P F T F G S G T K L
FG27_10K   atc agc aga gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt cca ttc acg ttc ggc tgc ggg aca aag ttg

121 E I K R A D A A P T V S I F P P S S E Q L T S G G A S V V C
FG27_10K   gaa ata aaa cgg gct gat gct gca cca act gta tcc atc ttc cca cca tcc agt gag cag tta aca tct gga ggt gcc tca gtc gtg tgc

151 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
FG27_10K   ttc ttg aac aac ttc tac ccc aaa gac atc aat gtc aag tgg aag att gat ggc agt gaa cga caa aat ggc gtc ctg aac agt tgg act

181 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
FG27_10K   gat cag gac agc aaa gac agc acc tac agc atg agc agc acc ctc acg ttg acc aag gac gag tat gaa cga cat aac agc tat acc tgt

211 E A T H K T S T S P I V K S F N R N E C
FG27_10K   gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc aac agg aat gag tgt
```

Figure 2a

```

                                     LEADER
                                     _____
                                     atg aac ttc tgg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt gtc cag tgt
                                     -19 M N F W L S L I F L V L V L K G V Q C

<-----FR1 - IMGT----->
1  E V K L V E S G G G L V Q P G G S L K L S C A T S G F T F
Ch27_10H  gaa gtg aag ctg gtg gag tct ggg gga ... ggc tta gtg cag cct gga ggg tcc ctg aaa ctc tcc tgt gca acc tct gga ttc act ttc

____CDR1 - IMGT____<-----FR2 - IMGT----->____CDR2 S
31  H Y Y M Y W V R Q T P E K R L E W V A Y I S N D
Ch27_10H  ... .. agt cac tat tac atg tat tgg gtt cgc cag act cca gag aag agg ctg gag tgg gtc gca tac att agt aat gat ...

- IMGT____<-----FR3 - IMGT----->
61  G D N T Y Y P D T I R G R F T I S R D N A R N T L Y L Q
Ch27_10H  ... ggt gat aac acc tat tat cca gac act ata agg ... ggc cga ttc acc atc tcc aga gac aat gcc agg aac acc ctg tac ctg caa

----->____CDR3 - IMGT____
91  M S R L K S E D T A M Y Y C A R G K Y D G A W F A Y W G Q G
Ch27_10H  atg agc cgt ctg aag tct gag gac aca gcc atg tat tac tgt gca aga ggg aag tac gac ggg gcc tgg ttt gct tac tgg ggc caa ggg

121  T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A
Ch27_10H  act ctg gtc act gtc tct agc gct tcc acc aag ggc cca tgg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca ggc

151  A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F
Ch27_10H  gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tgg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc

181  P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T Y I C
Ch27_10H  ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc

211  N V N H K P S N T K V D K K V E P K S C D K T H T C P P C P
Ch27_10H  aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca

241  A P E L L G G P S V F L F P P K P K D T L M I S R T P E V T
Ch27_10H  gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc ccg acc cct gag gtc aca

271  C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
Ch27_10H  tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag

301  F R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K
Ch27_10H  ccg ccg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag

331  C K V S N K A L P A P I E K T I S K A K G Q P R E F Q V Y T
Ch27_10H  tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc

361  L P P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E
Ch27_10H  ctg ccc cca tcc ccg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag

391  W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L
Ch27_10H  tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc

421  T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S
Ch27_10H  acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc

451  L S L S P G K
Ch27_10H  ctc tcc ctg tct ccg ggt aaa
```

5/40

Figure 2b

```

                                     LEADER
-19 M K L P V R L L V L M F W I P A S I S
    atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct gct tcc atc agt

<----- FR1 - IMGT ----->
1  D V L M T Q T P L S L P V S L G D Q A S I S C R S S Q I I V
Ch27_10K  gat gtt ttg atg acc caa act cca ctg tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag atc att gta

    CDR1 - IMGT <----- FR2 - IMGT -----> CDR2
31  H T      N G N T Y L E W Y L Q K P G Q S P N L L I Y K V
Ch27_10K  cat act ... aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca ggc cag tct cca aac ctg ctg atc tac aaa gtt ... ..

    - IMGT <----- FR3 - IMGT ----->
61      S N R F S G V P      D R F S G S G      S G T D F T L K
Ch27_10K  ... .. tcc aac cga ttt tct ggg gtc cca ... gac agg ttc agt ggc agt gga ... .. tca ggg aca gat ttc aca ctg aag

-----> CDR3 - IMGT -----
91  I S R V E A E D L G V Y Y C F Q G S H V P F T F G S G T K L
Ch27_10K  atc agc aga gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt cca ttc acg ttc ggc tcg ggg aca aag ttg

121 E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C
Ch27_10K  gaa ata aaa cgt acg gta gcg gcc cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc

151 L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T
Ch27_10K  ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctg caa tcg ggt aac tcc cag gag agt gtc aca

181 E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C
Ch27_10K  gag cag gac agc aag gac agc acc tac agc ctg agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc

211 E V T H Q G L S S P V T K S F N R G E C
Ch27_10K  gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt
```

CAGGTCCAGCTGGTCGAATCAGGGGGAGGCGTCTGTGCAGCCCGGAAGGTCACTGAGACTGTCTATGTGCCGCATC  
AGGGTTTACTTTCTCACTACTATATGTACTGGGTGCGACAGGCTCCAGGCAAGGGACTGGAGTGGGTGCGATA  
TATCAGCAACGACGGCGATAATACTTACTATCTGTACACCATCCGGGGGAGATTACAATCTCTAGAGATAACAG  
TAAGAACACTCTGTACCTGCAGATGAACTCTCTGAGGGCAGAAGACACCGCCGTGTACTATTGCGCCCGCGGGAA  
ATACGATGGAGCCTGGTTTGCTTATTGGGGACAGGGCACCTGGTGACAGTCAGCTCC

CDR1  
 QVQLVESGGGVVQPGRSLRLSCAASGFTFSHYMYWVVRQAPGKGLEWVAISNDGDNTYYPDTIRGRFTISRDNSKN  
 TLYLQMNSLRAEDTAVYYCARGKYDGAWFAYWGQGLTVVSS  
 CDR3

GCCTCCACCAAGGGCCCTTCCGTGTTCCCTCTGGCCCTTCTCTCAAGTCCACCTCCGGC  
 GGCACCGCCGCTCTGGGCTGCCTGGTGAAGGACTACTTCCCTGAGCCTGTGACCGTGCC  
 TGGAACTCTGGCGCCCTGACCAGCGGCGTGACACCTTCCCTGCCGTGCTGCAGTCTCC  
 GGCTGTACTCCCTGTCTCCGTGGTGACCGTGCTTCTCTCTCCCTGGGCACCCAGACC  
 TACATCTGCAACGTGAACCACAAGCCTTCCAACACCAAGGTGGACAAGAAGGTGGAGCCT  
 AAGTCTGCGACAAGACCCACACGTGCCCTCCATGCCAGCTCCCGAGCTGCTGGGCGGA  
 CCAAGCGTGTTTCTGTTCCCTCTAAGCCTAAGGACACCCTGATGATCTCCCGGACCCCT  
 GAGGTGACGTGCGTGGTGGTGGACGTGTCCACGAGGACCCAGAGGTGAAGTTCAATTGG  
 TACGTGGACGGCGTGGAGGTGCACAACGCCAAGACCAAGCCTCGGGAGGAACAGTACAAC  
 TCCACCTACCGGGTGGTGTCTGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAG  
 GAATACAAGTGCAAAGTCTCCAACAAGGCCCTGCCTGCCCCATCGAAAAGACCATCTCC  
 AAGGCCAAGGGCCAGCCTCGCGAGCCTCAGGTGTACACCCTGCCTCCAAGCAGGGAGGAA  
 ATGACCAAGAACCAGGTGTCCCTGACCTGTCTGGTGAAGGGCTTCTACCCCTCCGATATC  
 GCCGTGGAGTGGGAGTCCAACGGCCAGCCTGAGAACAATAACAAGACCACCCCTCCTGTG  
 CTGGACTCCGACGGCTCCTTCTTCTGTACTCCAAGCTGACCGTGGAACAAGTCCCGGTGG  
 CAGCAGGGCAACGTGTTCTCTGCTCCGTGATGCACGAGGGCCTGCACAACCACTACACC  
 CAGAAGAGCCTCTCCCTGTCCCCGGGTAA

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWSGALTSGVHTFPAVLQSS  
GLYLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG  
PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  
STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE  
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 3b

**FG27 RKC (DNA Sequence)**

ATGGAAGCCCCAGCGCAGCTTCTCTCCTCTGCTACTCTGGCTCCCTGATACCACCGGAGACGTCGTGATGACCC  
 AGAGCCCACTGAGCCTGCCTGTGACACCCGGCGAGCCCGCAAGTATTTCTGTAGAAGTTCCCAGATTATCGTGC  
 ACTAACGGGAATACCTACCTGGAGTGGTATCTGCAGAAGCCCGGCCAGAGTCCTCAGCTGCTGATCTACAAAG  
 TGAGTAACCGGTTCTCAGGAGTCCCAGACCGGTTTCAGCGGCTCCGGGTCTGGAACCGATTTCACACTGAAGATTA  
 GCAGGTGGAGGCCGAAGACGTGGGAGTCTACTATTGCTTTAGGGCTCCCATGTCCCTTCACATTGGCCAGG  
 GGACCAAGCTGGAAATCAAA

**FG27 RKC (Protein Sequence)**

MEAPAQLLFLLLWLPDITGDVVMQSPSLPVTGPGEASISCRSSQIIVHTNGNTYLEWYLQKPGQSPQLLIY  
 KVSNRFSVDPDRFSGSGSGTDFTLKISRVEAEDVGVYCFQGSHPFTFGQGTKLEIK

CDR1

CDR2

CDR3

**DNA SEQUENCE- HuK**

AGAACTGTGGCAGCACCAAGCGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT  
 GGAAGTGCCTCTGTTGTGTGCCTGCTGAATACTTCTATCCCAGAGAGGCCAAAGTACAG  
 TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCACAGAGCAGGAC  
 AGCAAGGACAGCACCTACAGCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAG  
 AAACACAAAGTCTACGCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG  
 AGCTTCAACAGGGGAGAGTGT

**PROTEIN SEQUENCE- HuK**

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD  
 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 4

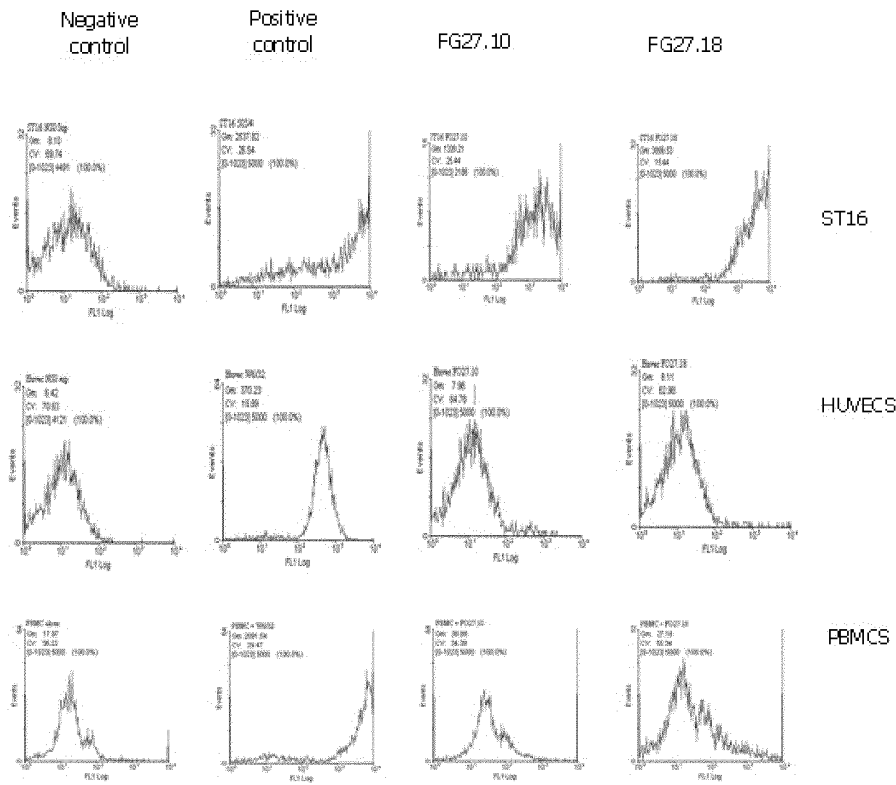


Figure 5

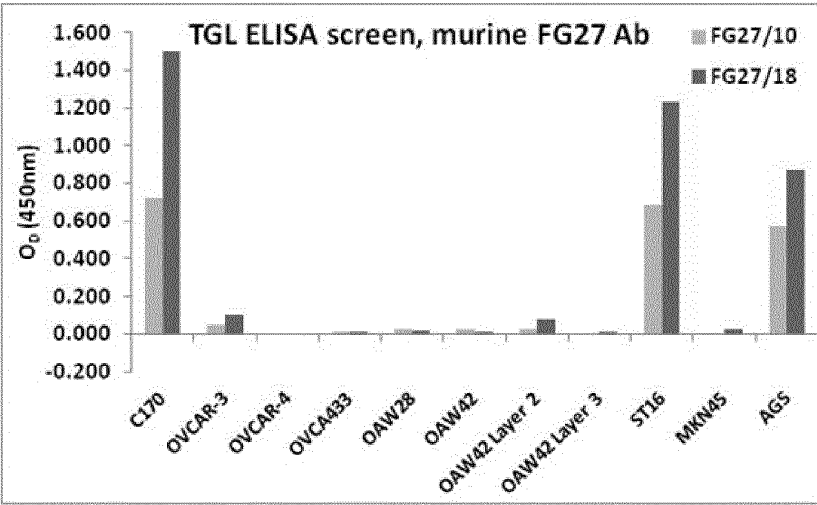


Figure 6

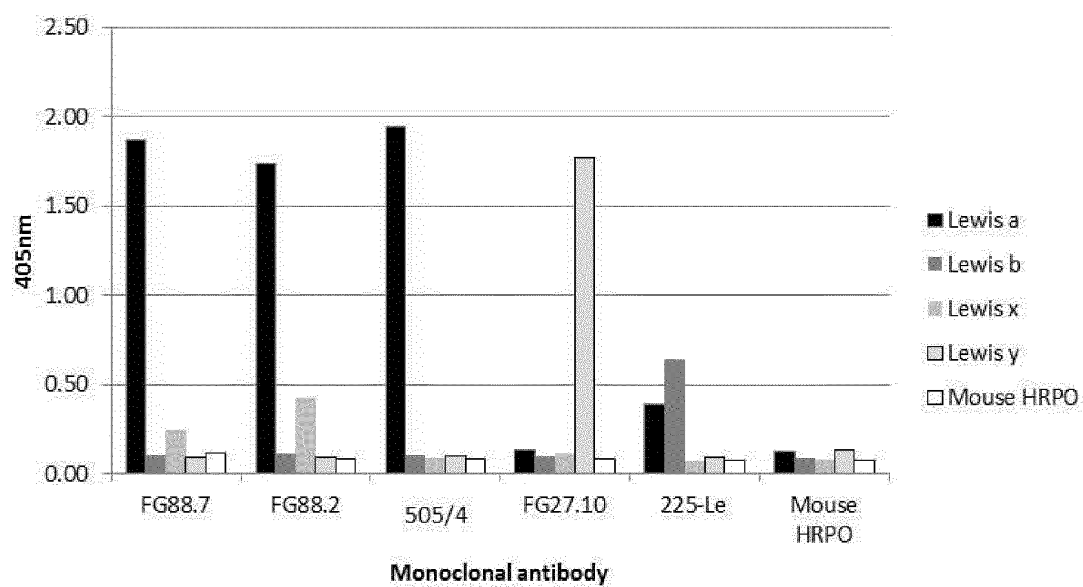


Figure 7

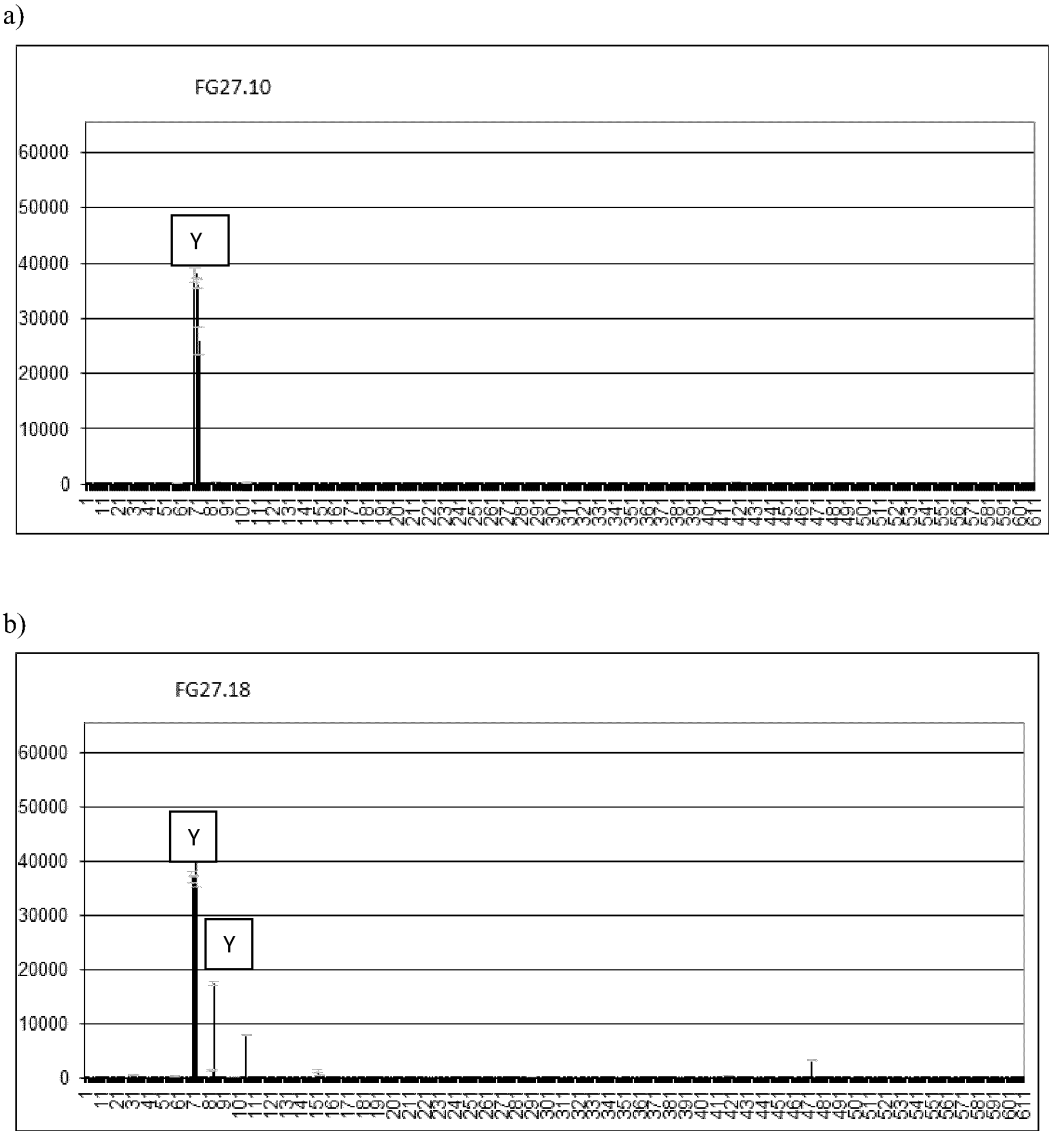
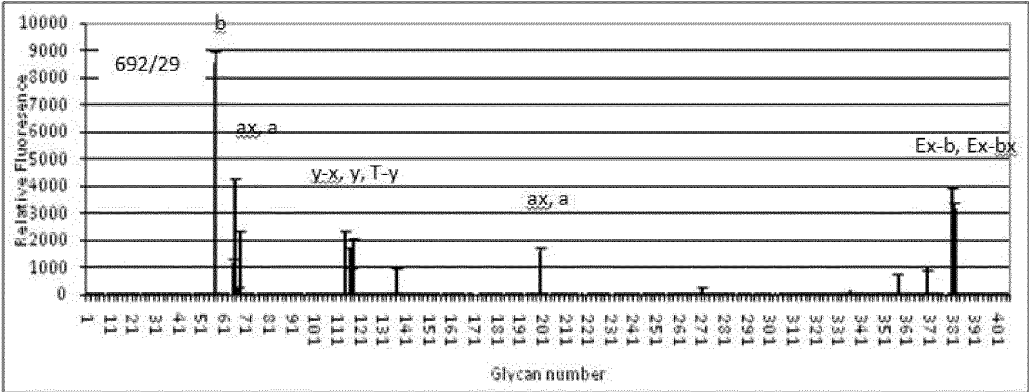


Figure 7 contd

c)



d)

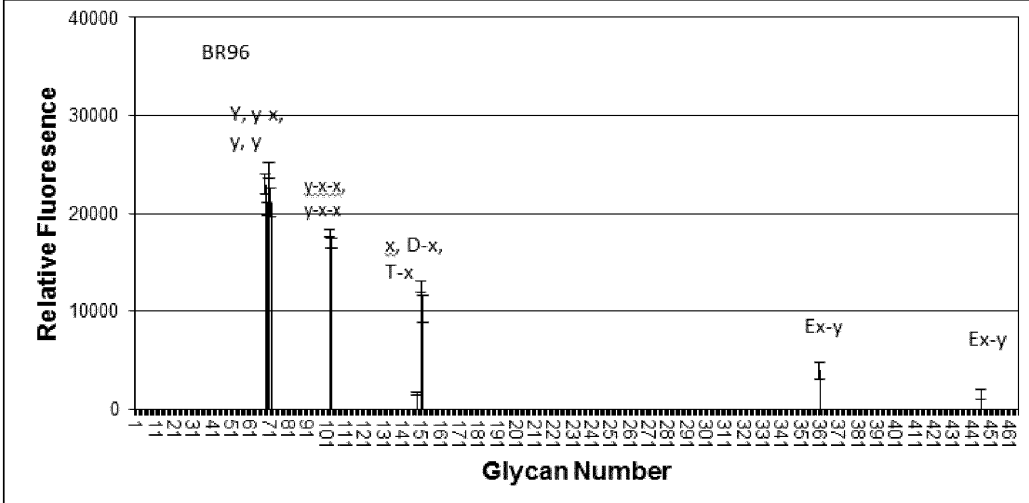


Figure 8

- M: Marker
- 1. AGS: PM
  - 2. AGS: L
  - 3. HCT15: PM
  - 4. HCT15: L
  - 5. OVCAR3: PM
  - 6. OVCAR3: L
  - 7. MCF7: PM
  - 8. MCF7: L
  - 9. H322: PM
  - 10. H322: L

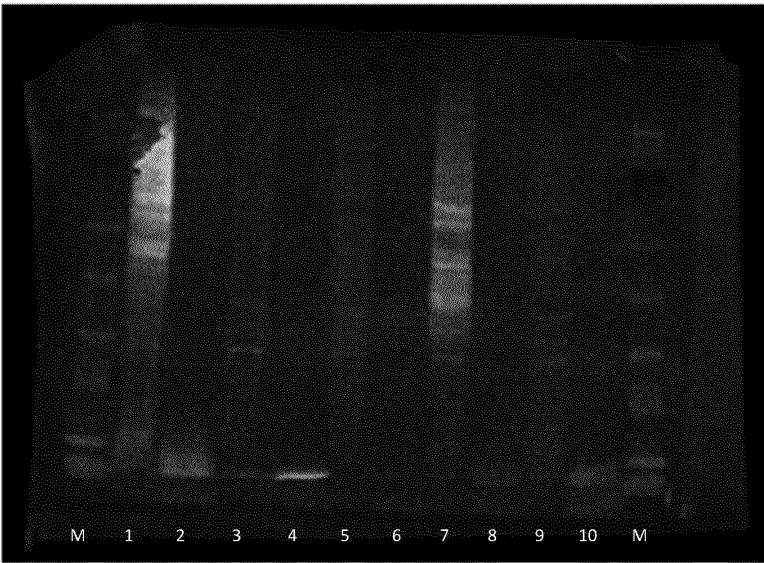
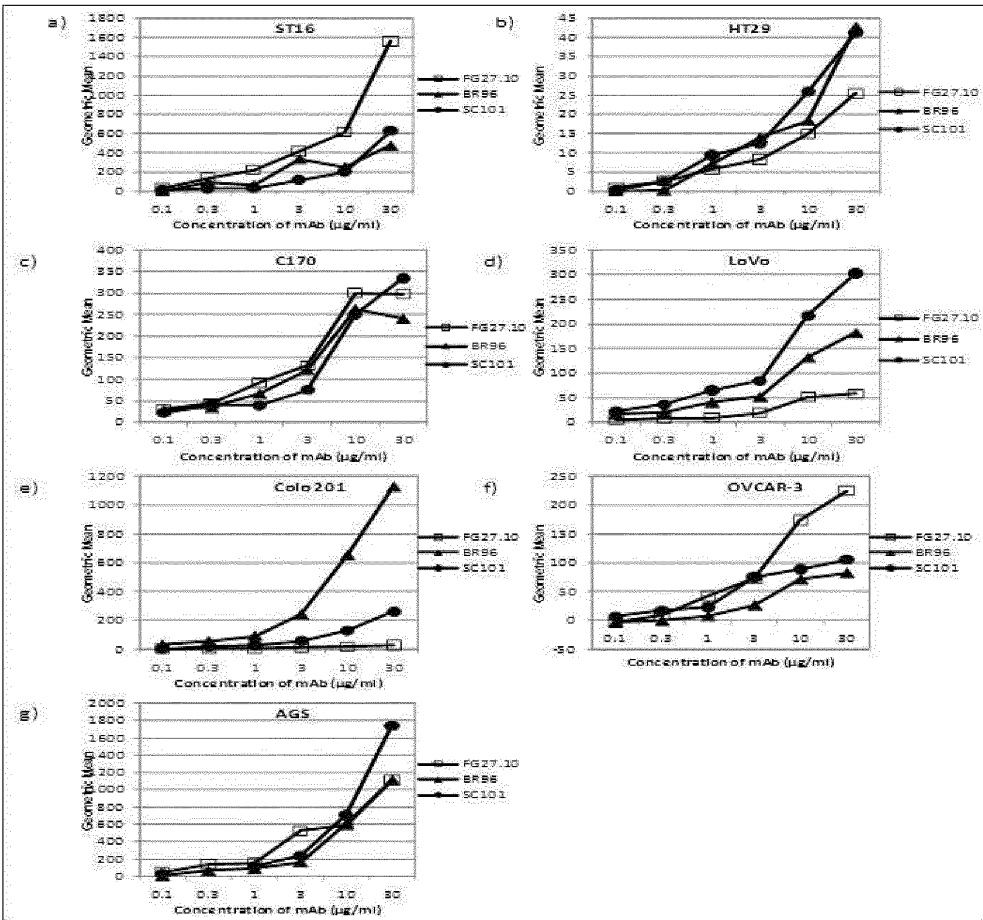


Figure 9



13/40

Figure 10

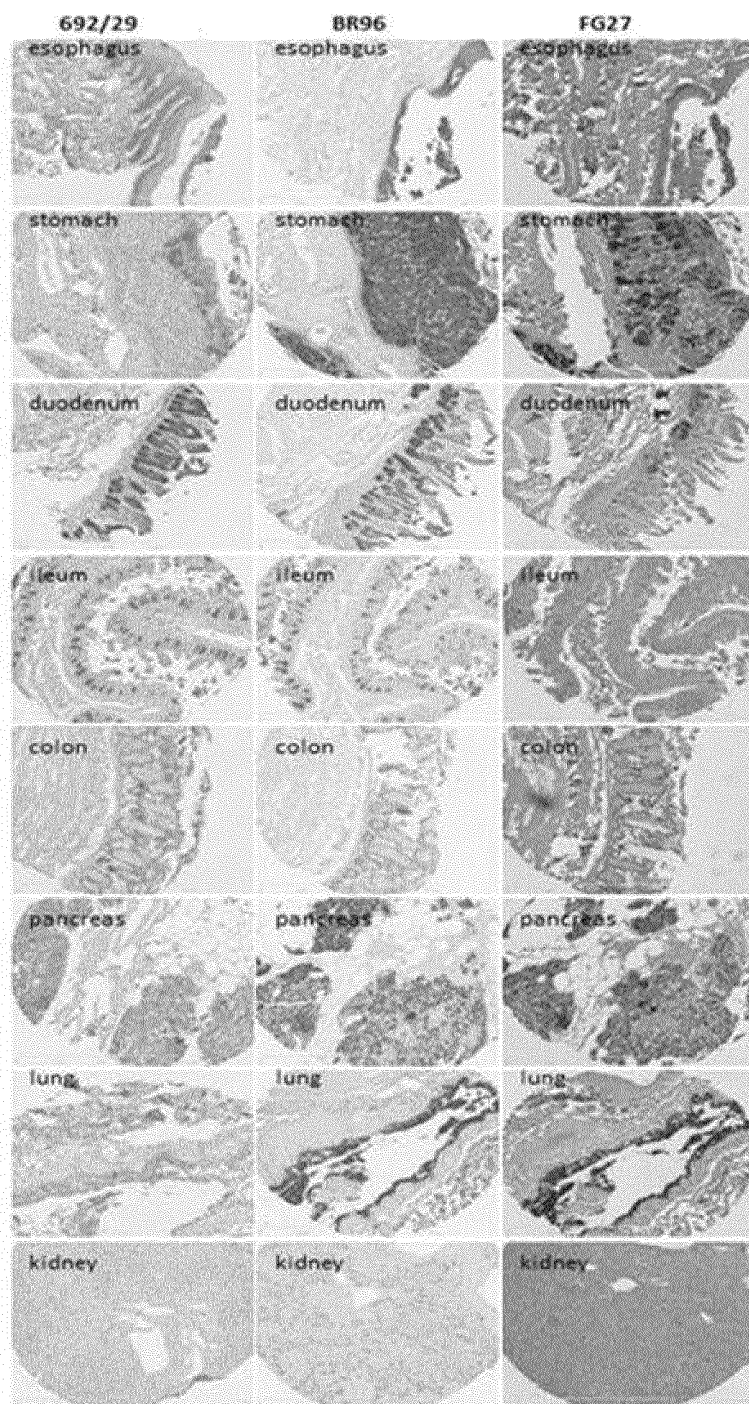


Figure 11a

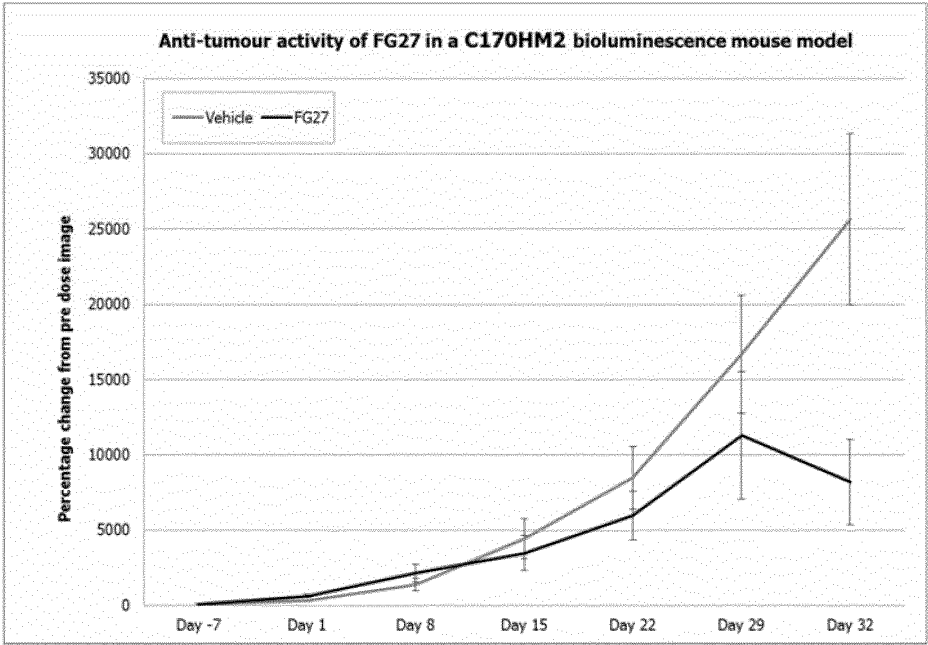


Figure 11b

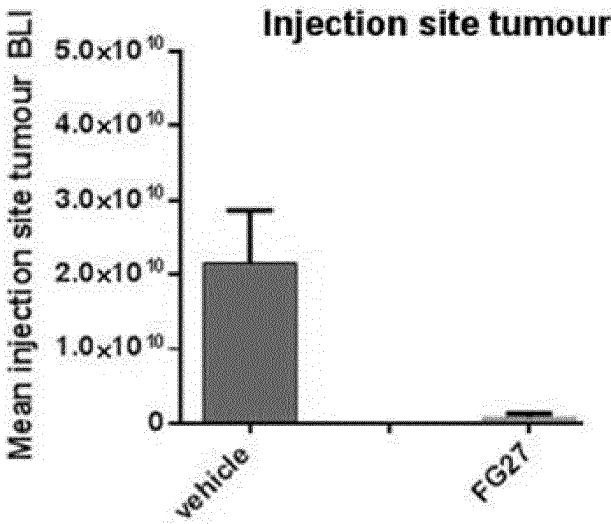


Figure 12a

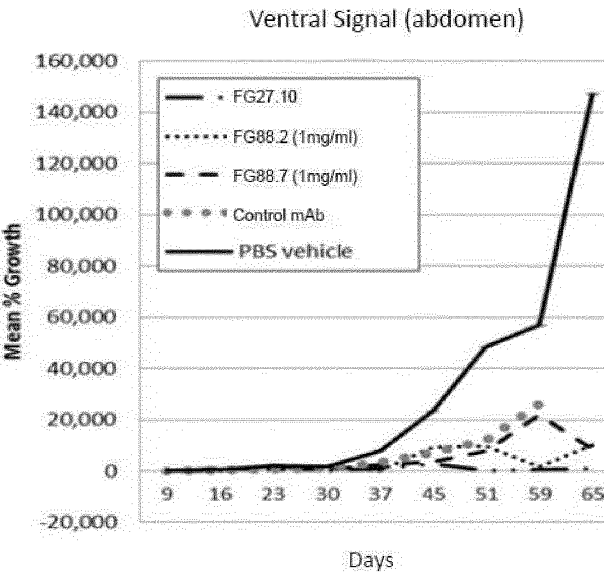


Figure 12b

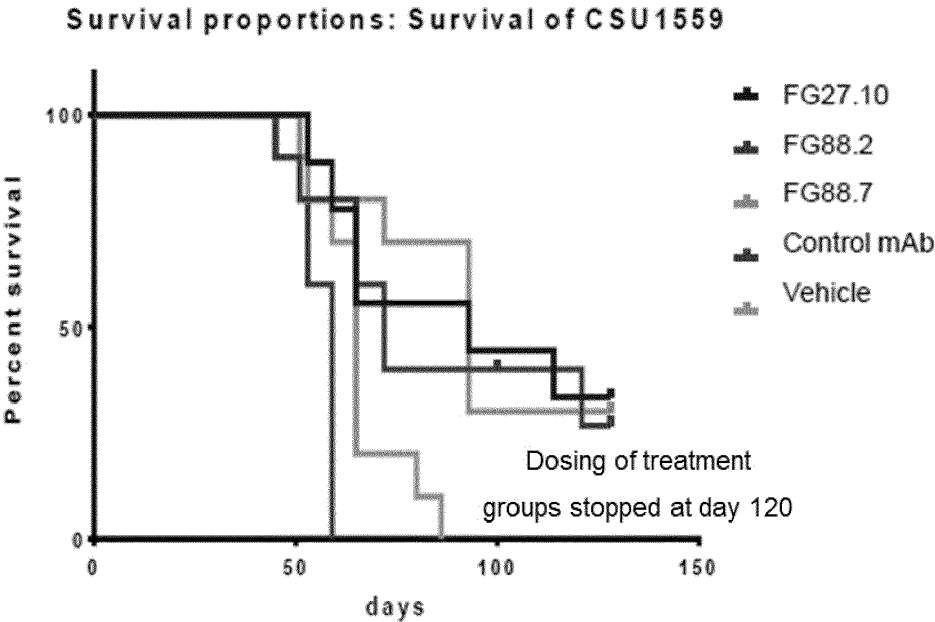


Figure 13a

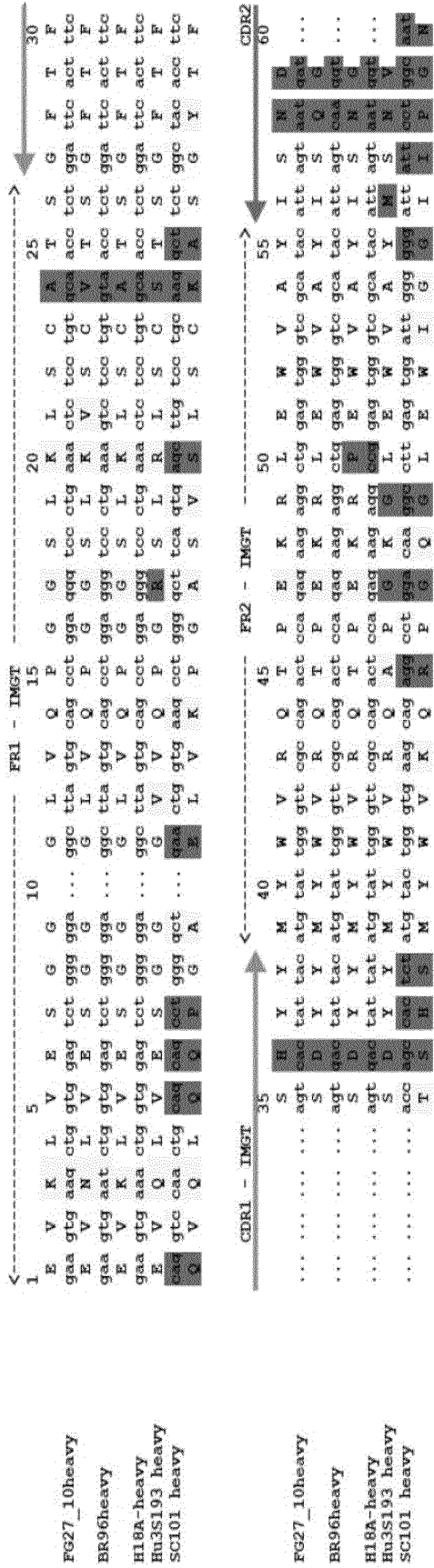
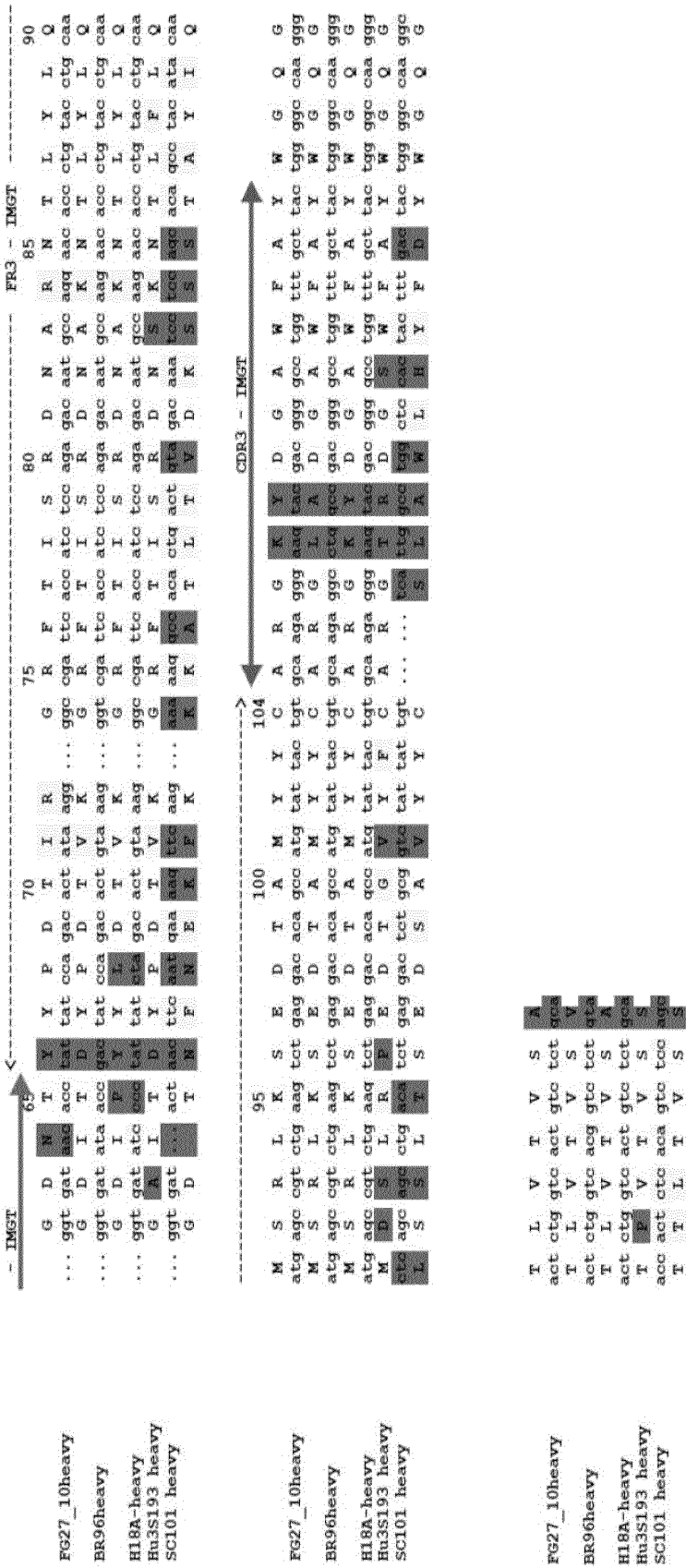


Figure 13a cont.





[illegible]

Figure 14

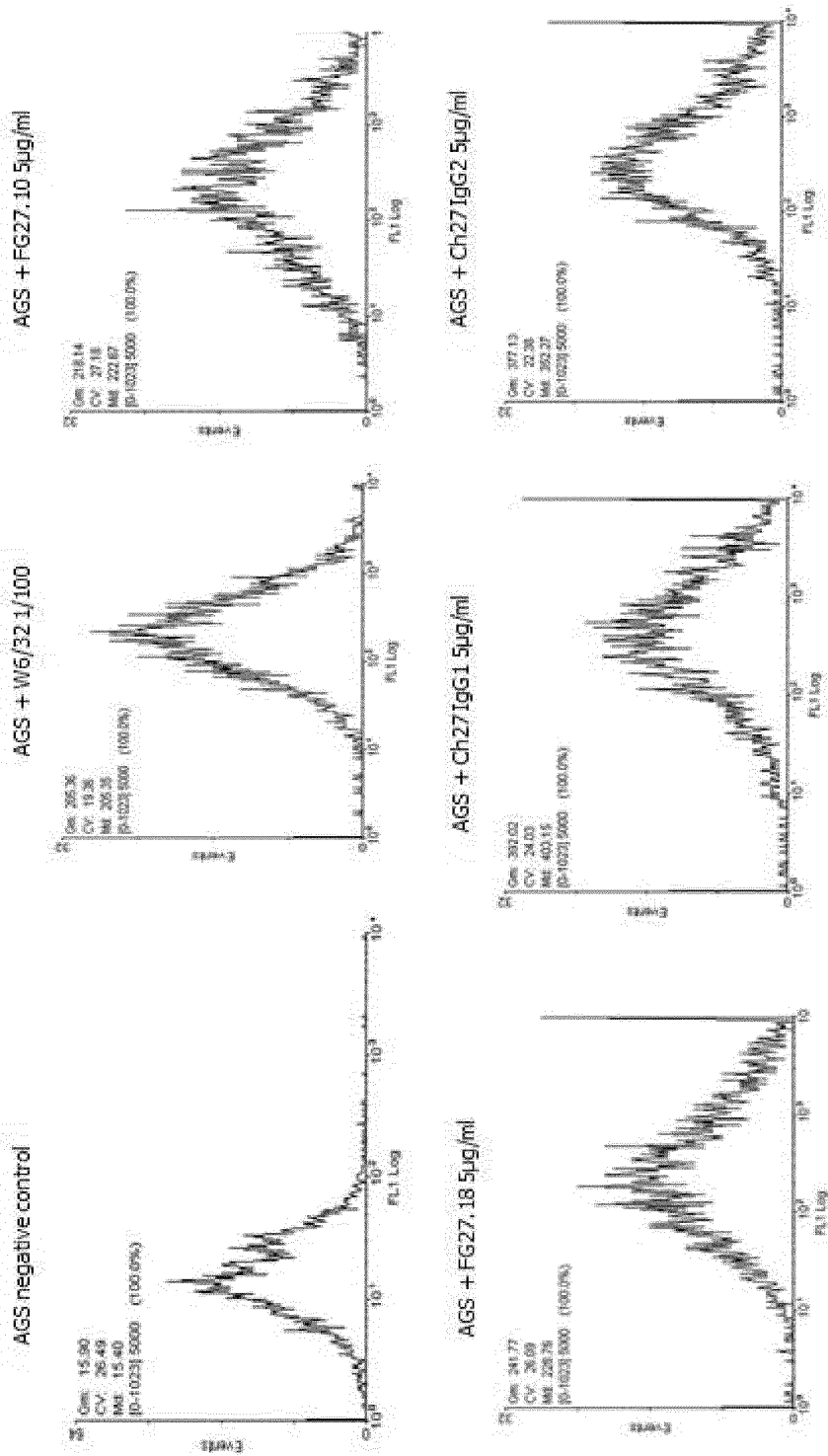


Figure 15a

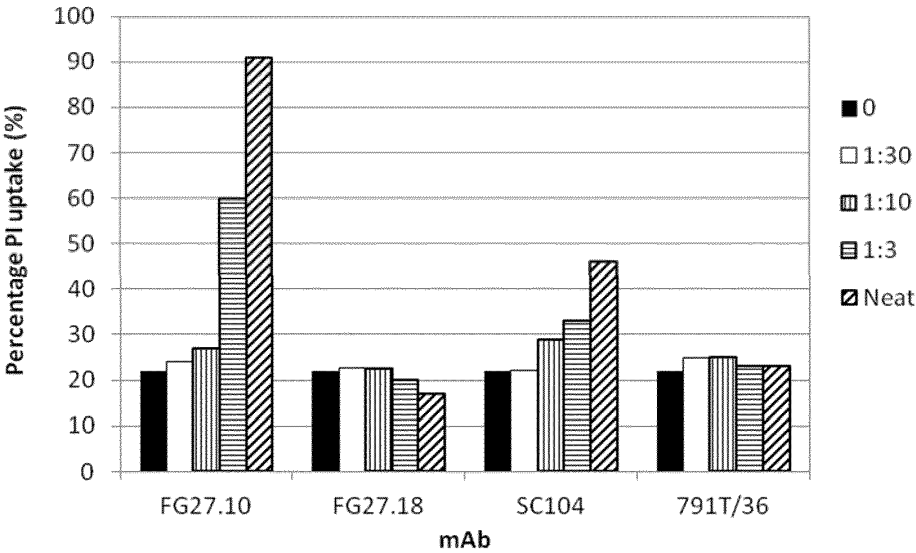


Figure 15b

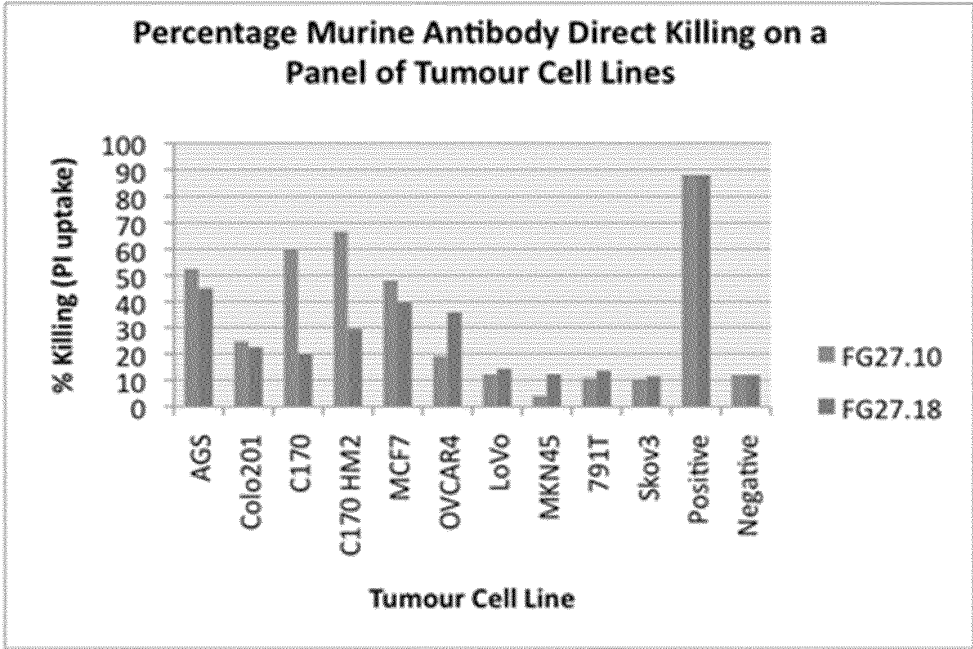


Figure 15c

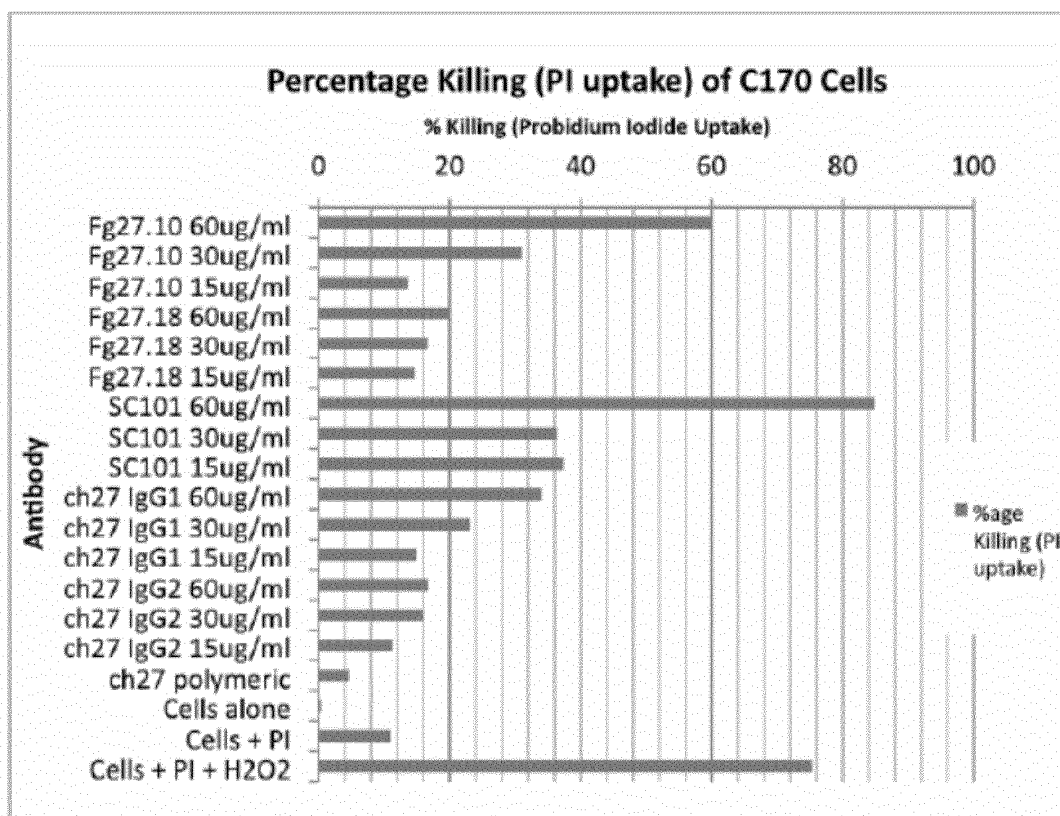


Figure 16

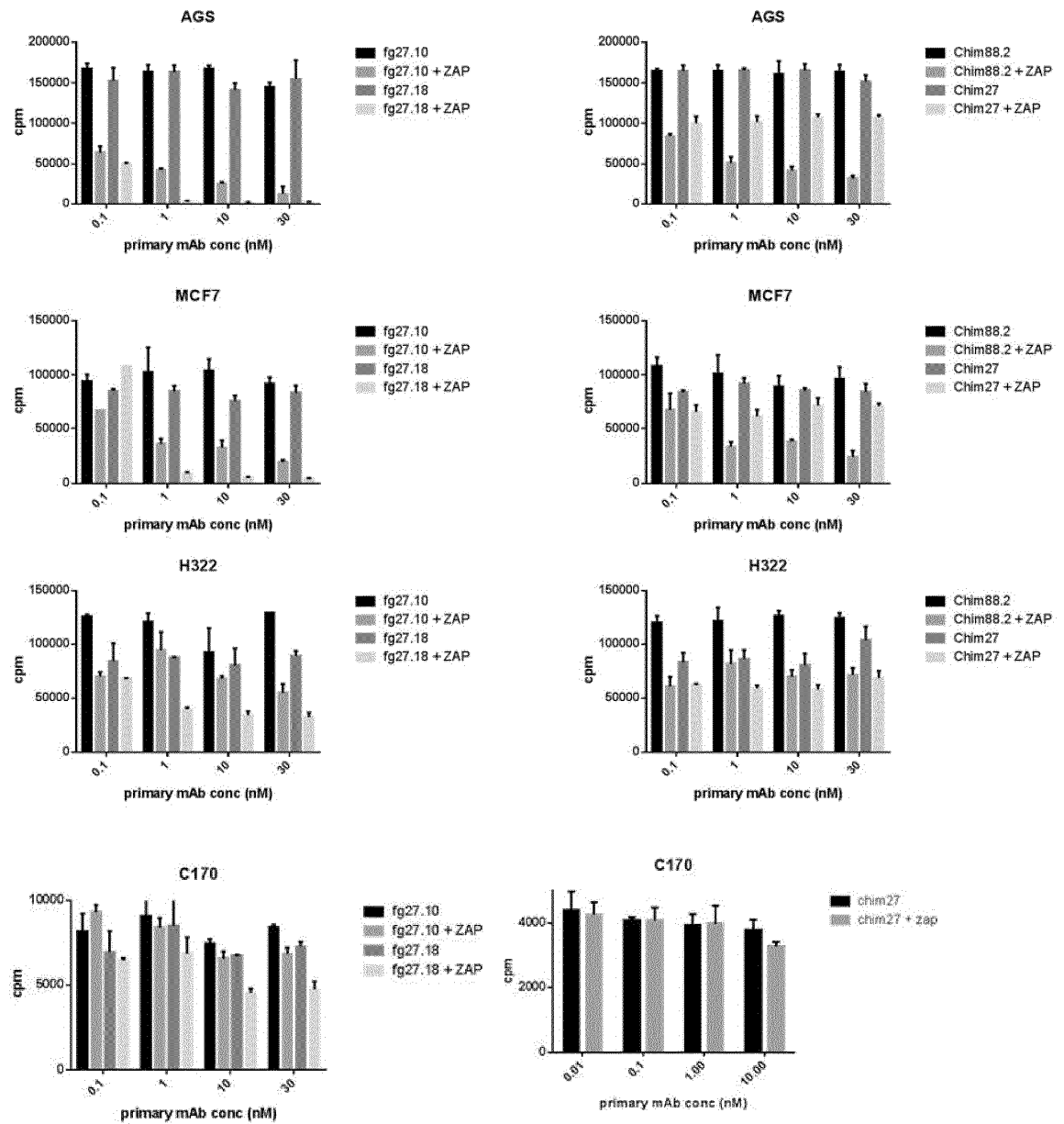


Figure 17a

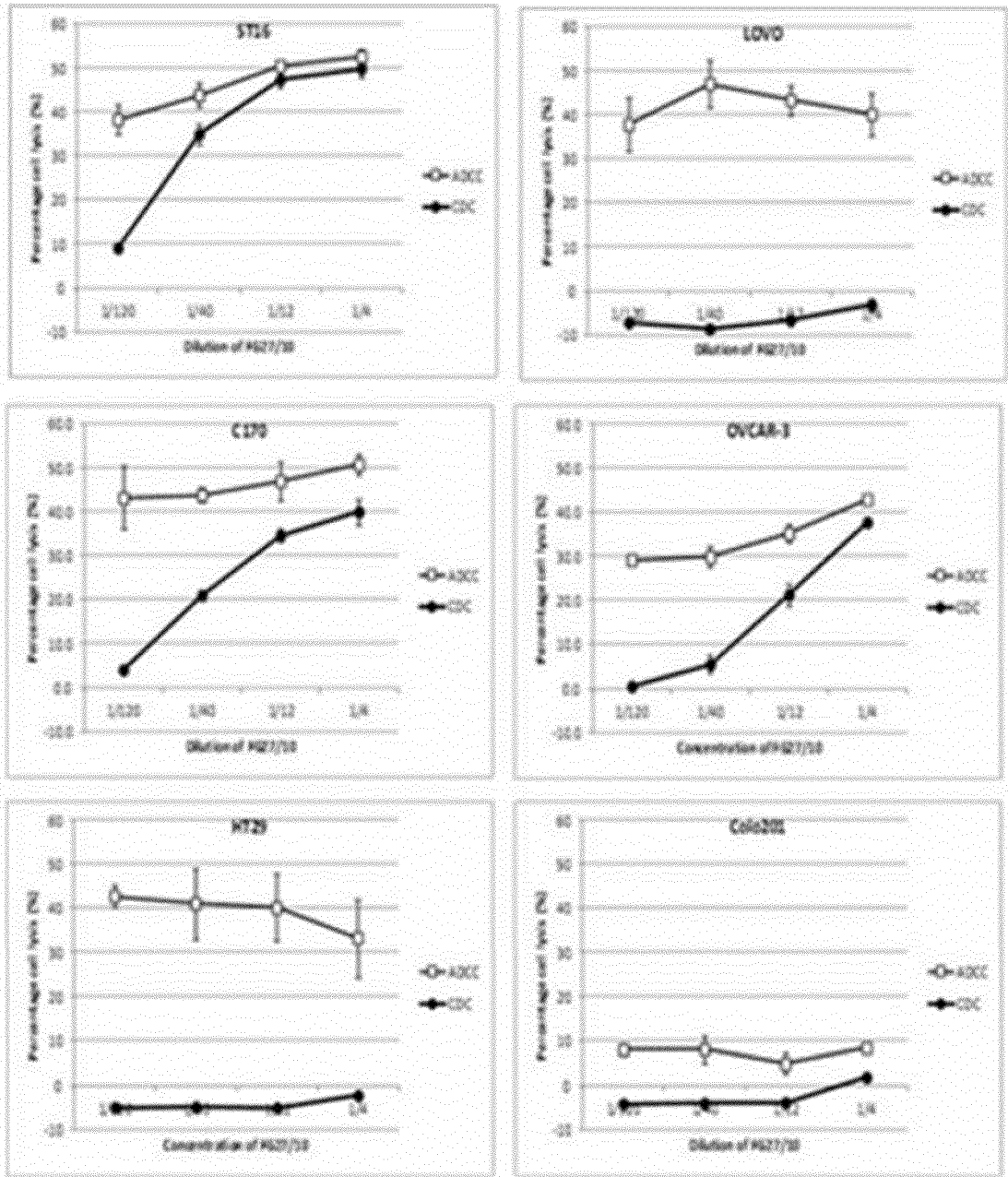


Figure 17b

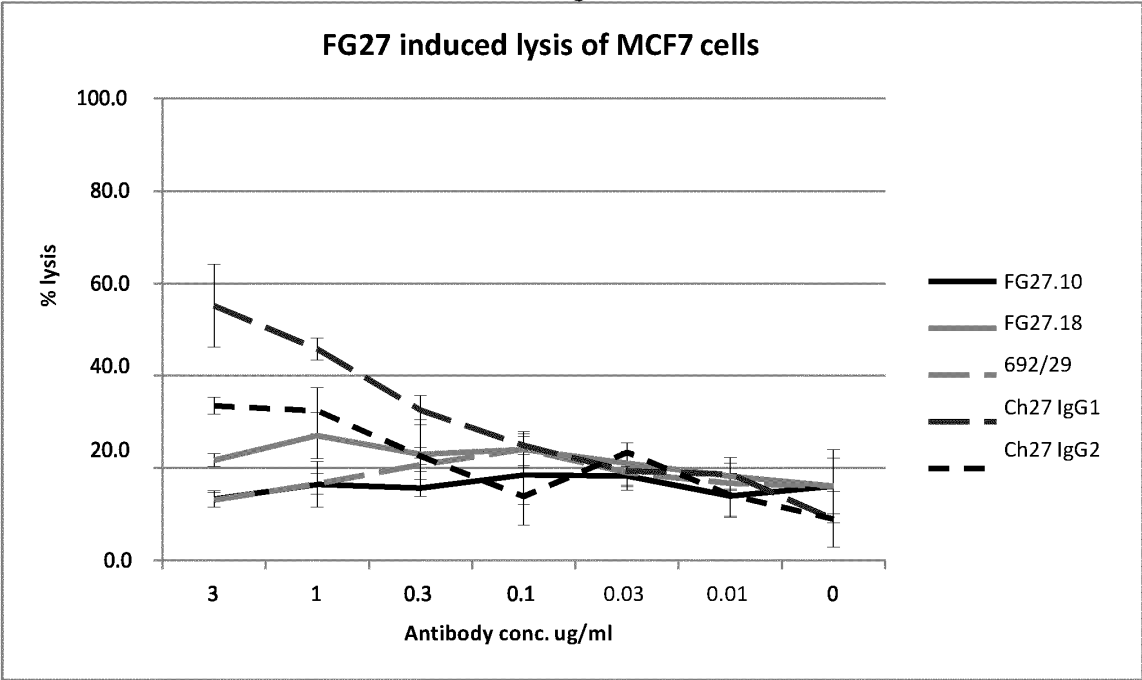


Figure 17c

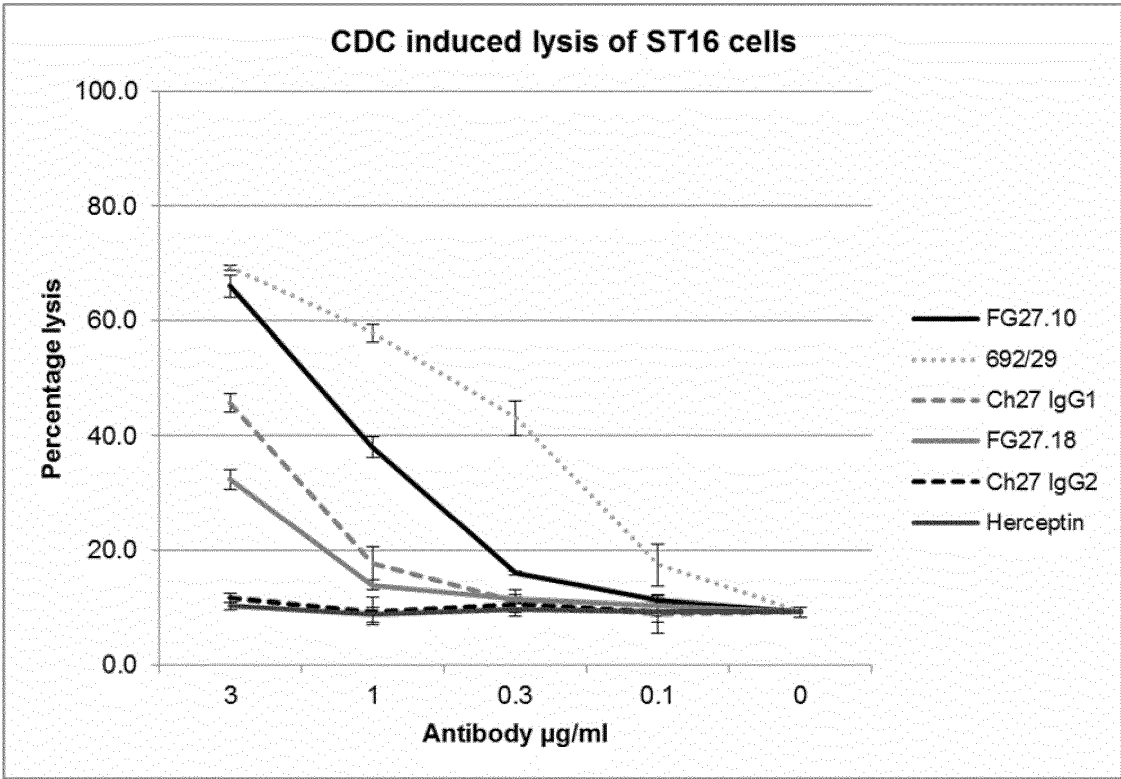


Figure 17d

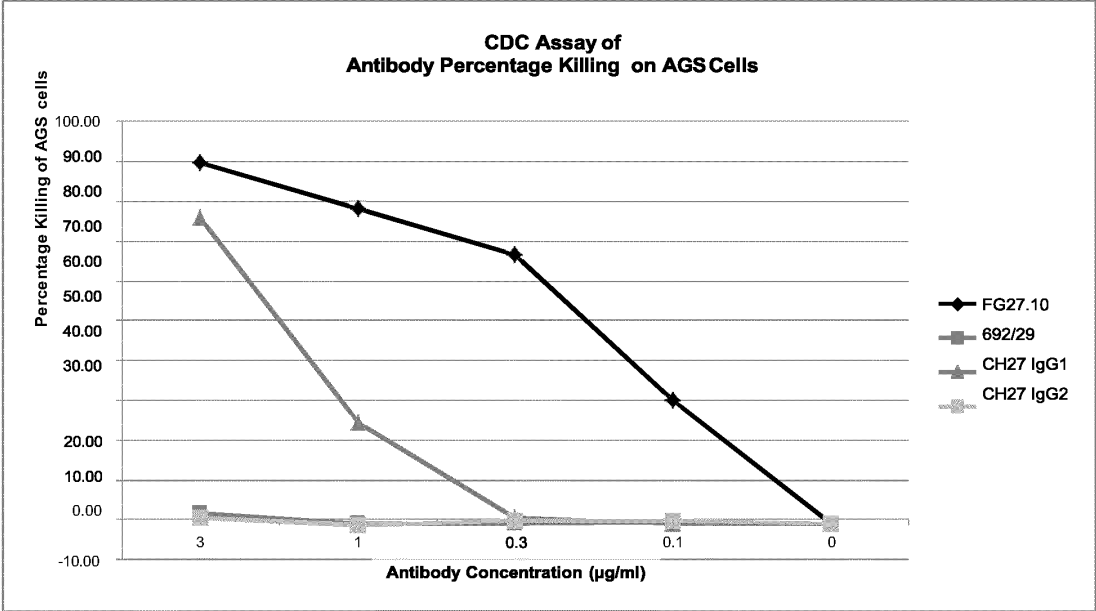




Figure 19

|                   | ID | SIM | FR | FRs | VCI | VCIs | Prox | 4Å Proximity Residues                    | H1 | H2 | H3 |
|-------------------|----|-----|----|-----|-----|------|------|------------------------------------------|----|----|----|
| <b>FG27_Heavy</b> |    |     |    |     | 22  |      |      | VLTFTEFSWVREWVARFTISRNL <sup>C</sup> ARW | 5  | 17 | 10 |
| <b>AJ579110</b>   | 82 | 450 | 70 | 381 | 21  | 115  | 25   | ..A.....                                 | 5  | 17 | 10 |
| <b>AB067239</b>   | 83 | 449 | 71 | 384 | 21  | 115  | 25   | ..A.....                                 | 5  | 17 | 10 |
| <b>DQ840852</b>   | 83 | 453 | 70 | 376 | 21  | 115  | 25   | ..A.....                                 | 5  | 7  | 10 |
| <b>AY941943</b>   | 83 | 444 | 72 | 391 | 21  | 115  | 25   | ..A.....                                 | 5  | 17 | 10 |
| <b>AB063665</b>   | 81 | 437 | 71 | 383 | 21  | 115  | 25   | ..A.....                                 | 5  | 17 | 10 |
| <b>X67908</b>     | 83 | 444 | 72 | 391 | 21  | 115  | 25   | ..A.....                                 | 5  | 17 | 10 |

Cysteine residues are outlined in White



Figure 21

| Kabat Number | 1                                                                                                                                | 10 | 20 | 30 | 40   | 50  | 60 | 70    | 80 | 90 | 100 | 110 |
|--------------|----------------------------------------------------------------------------------------------------------------------------------|----|----|----|------|-----|----|-------|----|----|-----|-----|
|              | * *                                                                                                                              |    |    | *  | **** | *** |    | ***** | *  |    | *** | *   |
| mFG27.18VH   | FYRLVESGGGLVQPPGSLRLS <b>CA</b> TSQFTFSHYMYWVRQIPKRLWVAYISNDGNTYYPDTIRGRFTISRDNRNNTLYLQMSRIKSEDTAMTYCARECKYDGAWFAYWGQGLIVTYS     |    |    |    |      |     |    |       |    |    |     |     |
| AJ579110     | QVQLVTSGGGVVQPPGESLRLS <b>CA</b> ASGFTFSYCMHWVRQAPCKGLEWVAVIWDGSKNYADSVKGRFTISRDNSKNTLYIQMNSIRAEEDTAVYYCARECKYDGAWFAYWGQGLIVTYS  |    |    |    |      |     |    |       |    |    |     |     |
| FG27.18 RHA  | QVQLVTSGGGVVQPPGESLRLS <b>CAASGFTFS</b> HYMYWVRQAPCKGLEWVAVISNDGNTYYPDTIRGRFTISRDNSKNTLYIQMNSIRAEEDTAVYYCARECKYDGAWFAYWGQGLIVTYS |    |    |    |      |     |    |       |    |    |     |     |
| FG27.18 RHB  | QVQLVTSGGGVVQPPGESLRLS <b>CA</b> TSQFTFSHYMYWVRQAPCKGLEWVAVISNDGNTYYPDTIRGRFTISRDNSKNTLYIQMNSIRAEEDTAVYYCARECKYDGAWFAYWGQGLIVTYS |    |    |    |      |     |    |       |    |    |     |     |

Structurally important residues are highlighted: Proline residues are outlined in White, Cysteine residues outlined in Black, and Asparagine residues in Grey.  
The residue outlined in Grey and in italics indicate back-translation to the Mouse Residue.



|                   | ID  | SIM | FR | FRs | VCI | VCIs | Prox | 4Å Proximity Residues         | L1 | L2 | L3 |
|-------------------|-----|-----|----|-----|-----|------|------|-------------------------------|----|----|----|
| <b>FG27_Kappa</b> |     |     |    |     | 17  |      | 28   | DVLMTWCWYLLIYGVPDFSGSGGTDFYCF | 16 | 7  | 10 |
| <b>Z46620</b>     | 82  | 425 | 70 | 378 | 16  | 99   | 26   | .IV.....                      | 16 | 7  | 9  |
| <b>35927</b>      | 101 | 528 | 74 | 391 | 17  | 100  | 28   | .....                         | 16 | 7  | 9  |
| <b>AB064105</b>   | 85  | 445 | 71 | 379 | 17  | 100  | 27   | ..V.....                      | 16 | 7  | 9  |
| <b>AX805665</b>   | 93  | 496 | 70 | 376 | 17  | 100  | 27   | ..V.....                      | 16 | 7  | 9  |
| <b>AB063934</b>   | 84  | 439 | 70 | 376 | 17  | 100  | 27   | ..V.....                      | 16 | 7  | 9  |
| <b>AY685343</b>   | 81  | 429 | 68 | 365 | 17  | 100  | 27   | ..V.....                      | 16 | 7  | 9  |
| <b>38700</b>      | 99  | 508 | 73 | 382 | 16  | 96   | 27   | .....F.....                   | 16 | 7  | 9  |
| <b>E10698</b>     | 83  | 434 | 70 | 372 | 16  | 99   | 26   | .IV.....                      | 16 | 7  | 8  |

X72449

*Closest V-REGIONS (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon plus 15 nt of the CDR3-IMGT)*

**X72449**

Closest V-REGIONS (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon plus 15 nt of the CDR3-IMGT)

|                              | Score | Identity            |
|------------------------------|-------|---------------------|
| X63397 Homsap IGKV2-28*01 F  | 1447  | 99,32% (292/294 nt) |
| X12691 Homsap IGKV2D-28*01 F | 1447  | 99,32% (292/294 nt) |
| X59314 Homsap IGKV2-40*01 F  | 1213  | 90,14% (265/294 nt) |
| X59311 Homsap IGKV2D-40*01 F | 1213  | 90,14% (265/294 nt) |
| X63400 Homsap IGKV2-18*01 P  | 1177  | 88,78% (261/294 nt) |

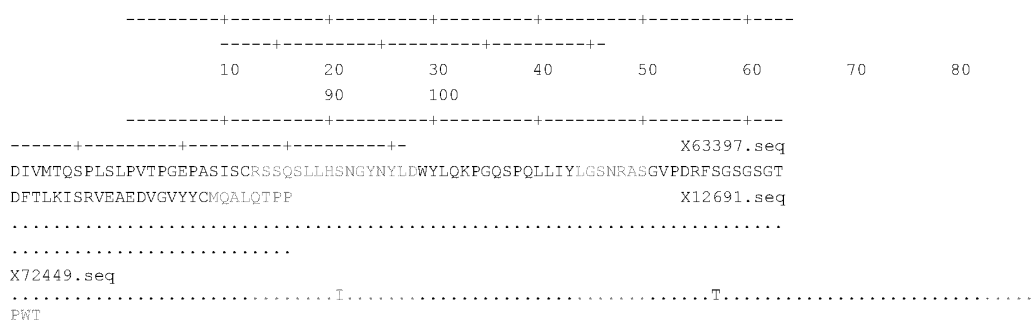
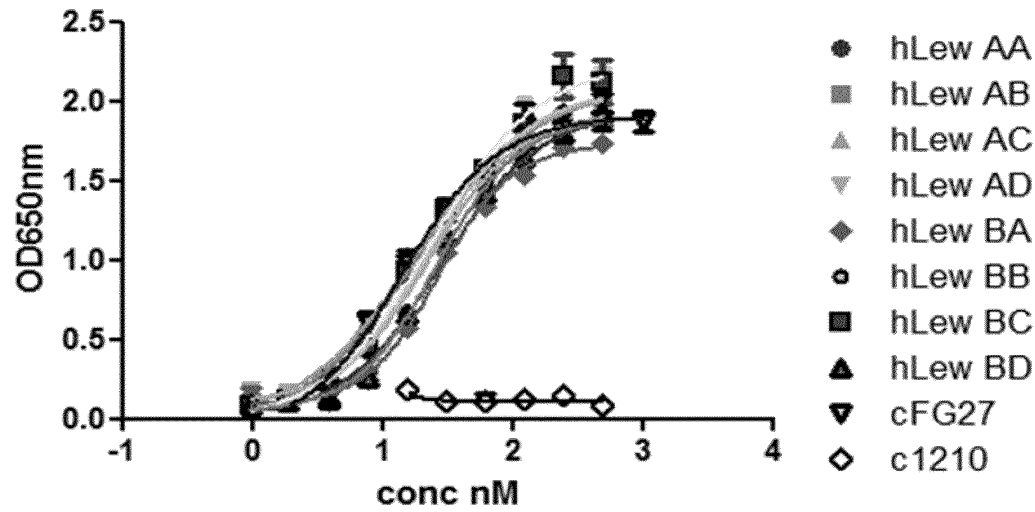


Figure 25

| 4Å Residues | *****                                                                                                                   | * | ** | **** | ***** | **** | ** | * |
|-------------|-------------------------------------------------------------------------------------------------------------------------|---|----|------|-------|------|----|---|
| mFG27.18 VK | DVIMTQTPLSLPVSLGDQASISCRSS-QIIVHTNGNTYLEWYLQKPCQSPNLIYKVSNRFSGVPPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHPV-----FTFGSGTKLEIK  |   |    |      |       |      |    |   |
| Z46620      | DIVMTQSPISLPVTPCEPASISCRSS-QSILHSNGVNYLDWYLQKPCQSPQLLIYLGSNRASGVPPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP                  |   |    |      |       |      |    |   |
| FG27.18 RKA | DIVMTQSPISLPVTPCEPASISCRSS-QIIVHTNGNTYLEWYLQKPCQSPQLLIYKVSNRFSGVPPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHPV-----FTFGSGTKLEIK |   |    |      |       |      |    |   |
| FG27.18 RKB | DVIMTQSPISLPVTPCEPASISCRSS-QIIVHTNGNTYLEWYLQKPCQSPQLLIYKVSNRFSGVPPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHPV-----FTFGSGTKLEIK |   |    |      |       |      |    |   |
| FG27.18 RKC | DVIMTQSPISLPVTPCEPASISCRSS-QIIVHTNGNTYLEWYLQKPCQSPQLLIYKVSNRFSGVPPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHPV-----FTFGSGTKLEIK |   |    |      |       |      |    |   |
| FG27.18 RKD | DIVMTQSPISLPVTPCEPASISCRSS-QIIVHTNGNTYLEWYLQKPCQSPQLLIYKVSNRFSGVPPDRFSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHPV-----FTFGSGTKLEIK |   |    |      |       |      |    |   |

Structurally important residues are highlighted: Proline residues are outlined in White and Cysteine residues are outlined in Black.  
Residues in Bold indicate back-translations to the Mouse Residue.

Figure 26



| Antibody            | hLewAA | hLewAB | hLewAC | hLewAD | hLewBA | hLewBB | hLewBC | hLewBD | cFG27 | c1210 |
|---------------------|--------|--------|--------|--------|--------|--------|--------|--------|-------|-------|
| Expression<br>µg/ml | 71     | 32     | 50     | 64     | 68     | 68     | 56     | 64     | 50    | 110   |
| EC50 nM             | 28     | 18     | 18     | 23     | 27     | 23     | 24     | 26     | 14    |       |

Legend: Comparison of antibody binding to LewisY-HSA antigen for combinations of antibody expressed as LewRHA with LewRKA, LewRKB, LewRKC or LewRKD and LewRHB with LewRKA, LewRKB, LewRKC or LewRKD, including cFG27 positive control antibody and c1210 negative control antibody.

Figure 27

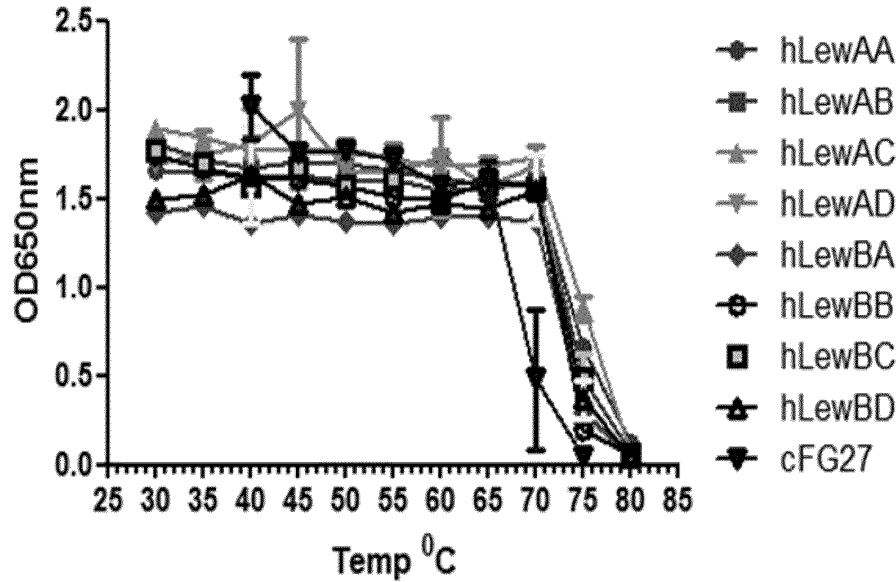
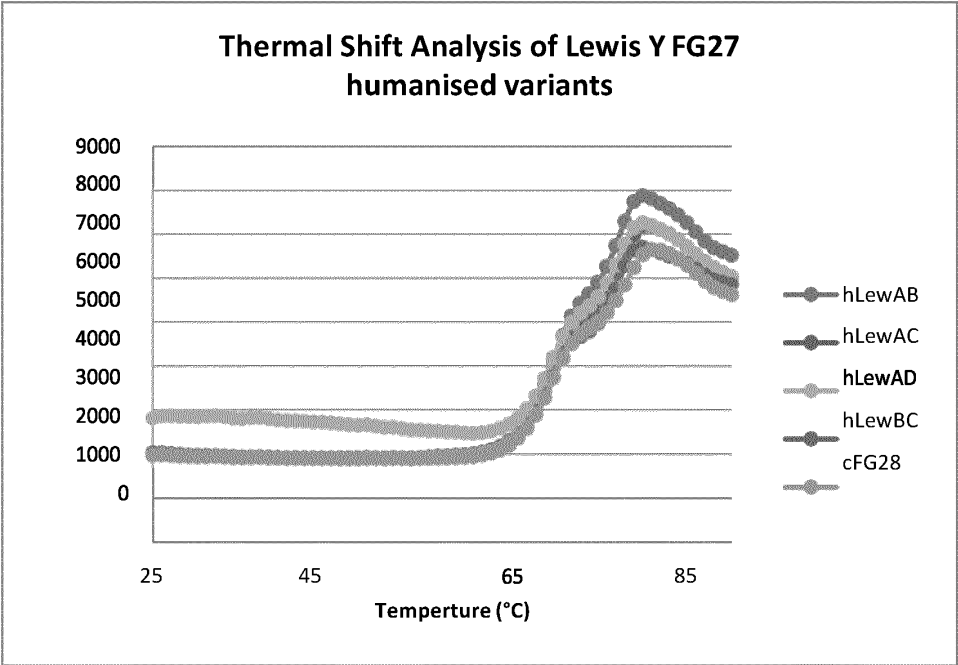
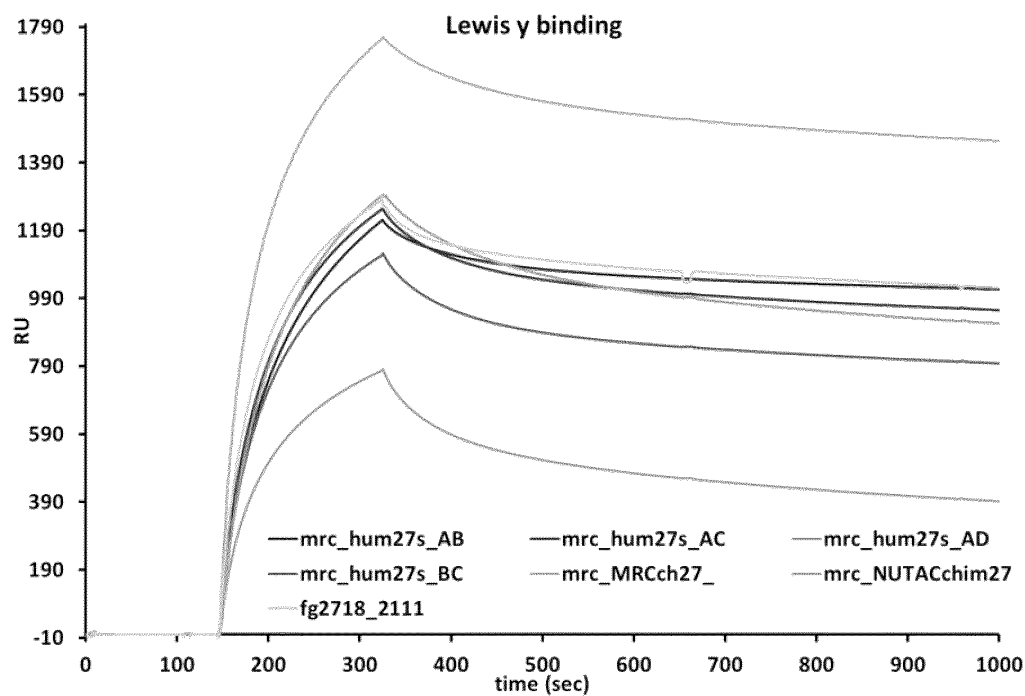


Figure 28



| Antibody | Tm (°C) |
|----------|---------|
| cFG27    | 72      |
| hLewAB   | 72      |
| hLewAC   | 72      |
| hLewAD   | 72      |
| hLewBC   | 72      |

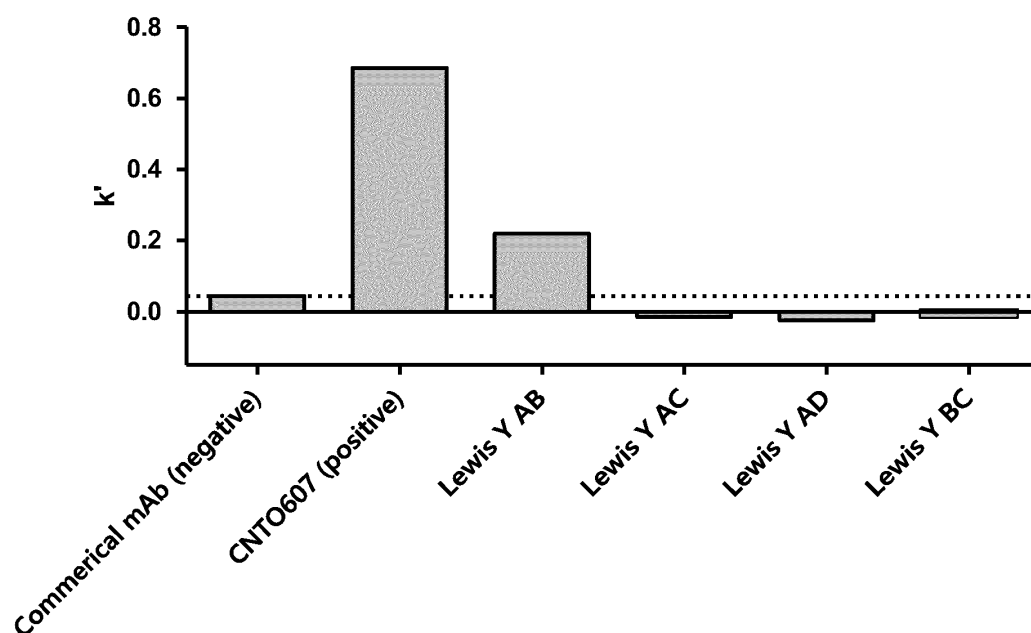
Figure 29



|            | Kon(1/Ms) | Koff (1/s) | Kd (M)  | Rmax (RU) |
|------------|-----------|------------|---------|-----------|
| Ch27_fc34  | 6.6E+04   | 2.2E-04    | 3.3E-09 | 1374      |
| MRC chim27 | 7.1E+05   | 2.8E-04    | 4.0E-10 | 1816      |
| RHA/RKD    | 3.48E+04  | 4.6E-04    | 1.3E-08 | 1040      |
| RHA/RKB    | 5.72E+04  | 8.2E-05    | 1.4E-09 | 1296      |
| RHA/RKC    | 5.9E+04   | 1.3E-04    | 2.2E-09 | 1274      |
| RHB/RKC    | 3.0E+05   | 9.5E-04    | 3.1E-09 | 1477      |

37/40

Figure 30



| Antibody   | Retention Index (k') |
|------------|----------------------|
| Commercial | 0.044                |
| CNTO607    | 0.685                |
| Lewis Y AB | 0.219                |
| Lewis Y AC | -0.014               |
| Lewis Y AD | -0.023               |
| Lewis Y BC | -0.012               |

Figure 31

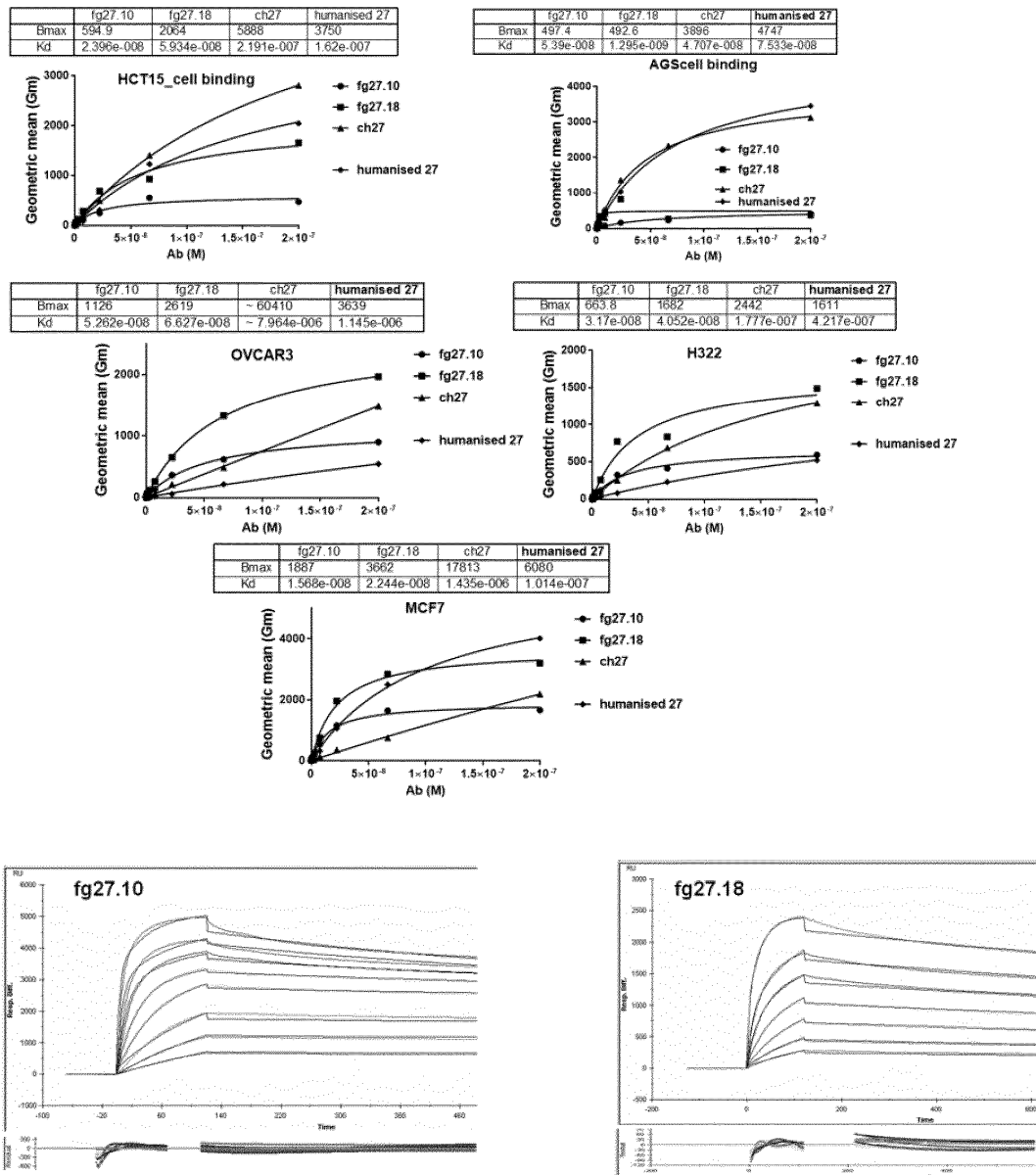


Figure 32

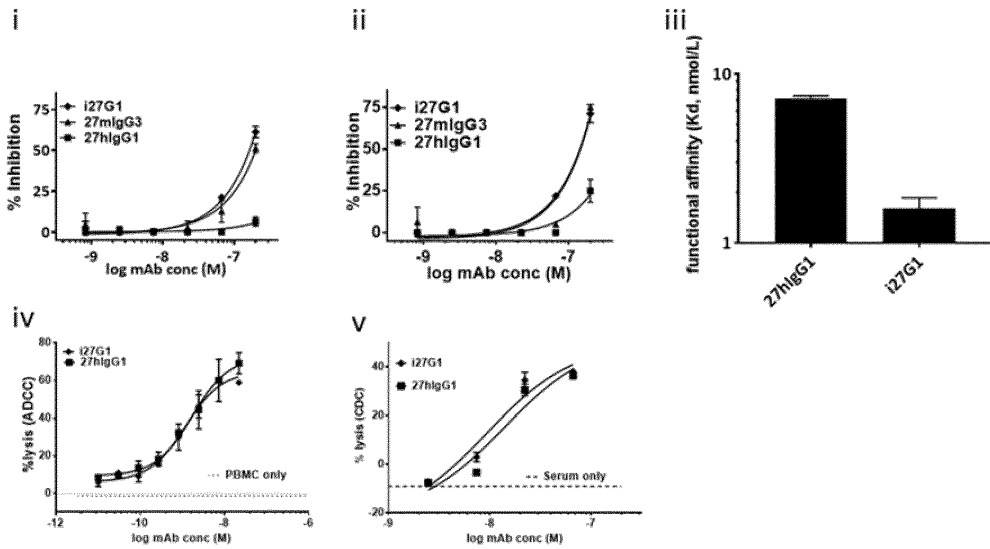


**Figure 33 27 antibody sequences****27 Light chain DNA sequence (variable region + Kappa contant)**

atgaagttgctgttaggctgttggtgctgatgttctggattcctctccatcagtgatgtttgatgacccaaactccactctccctgctgtcagt  
 ctggagatcaagcctcatctctgcagatcagtcagatcattgtacatactaatggaacacctatttagaatggtacctgcagaaaccaggc  
 cagctccaaacctctgatctacaaagttccaaccgattttctggggtcccagacaggttcagtggtgagtgatcaggacagatttcacactc  
 aagatcagcagagtggaggctgaggatctgggagtttattactgcttccaaggttcacatgttccattcacgttcggctcggggacaaagtggga  
 aataaaacgtacggtacggcccatctgtcttcatcttccgccatctgatgagcagttgaaatctggaaactgcctctgtgtgtcctgctgaat  
 aacttctatcccagagaggccaaagtacagtggaaagtggaataacgccctccaatcgggtaactccaggagagtgacacagagcaggacagc  
 aaggacagcactcagcctcagcagcacctgacgtgagcaagcagactacgagaacacaaagtctacgctgcgaagtcacccatca  
 gggcctgagctcgtccgtcacaagagcttcaacaggaggagagtgt

**27 Light chain protein sequence (variable region + Kappa contant)**

MKLPVRLVLVLMFWIPASISDVLMTQTPLSLPVS LGDQASISCRSSQIIIVHTNGNTYLEWYL  
 QKPGQSPNLLIYKVS NFRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTF  
 GSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS  
 QESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**Heavy chain DNA sequence of i27v1 (variable + 'improved' v1 constant region)**

atgaactctggctcagcttgattttcctgtccttgttttaaaaggtgtccagtgtgaagtgaagctggaggagctggggaggccttagtgagc  
 ctggagggtccctgaaactcctgtgcaacctctggattcacttcagtcactattacatgtattgggttcgacagactccagagaaaggctgg  
 agtgggtgcacatacattagtaagtgtgataacacctattatccagacactataaggggacgattcaccatctccagagacaatgccaggaa  
 caccctgtacctgcaaatgagccgtctgaagtctgaggacacagccatgtattactgtgcaagagggaagtagcaggggctgtgttcttact  
 ggggccaaaggactctgtgtcactgtcttagcgttccaccaagggtccatgggtcttcccctggcaacctcctccaagagcacctctgggggc  
 acagcgccctgggctgctgtgtaaggactacttccccgaaccgggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacacct  
 tcccgtgtctctacagtcctcaggactctactccctcagcagcgtgtgacggtgcctccagcagcttgggcacccagacctacatctgcaacg  
 tgaatcacaaagcccagcaacccaaggtggacaagaaagttgagcccaaatcttgtagaaaaactcacacatgccaccgtgccagcacctg  
 aactcctggggggacgctcagttctctcttcccccaaaacccaaggacacctcatgatctccggacccctgaggtcacatgctgtgtgtg  
 gacgtgagccacgaagacctgagggtcaagttcaactgtgtagtgacggcgtggagggtgcatacagcctggacacagccccgtgaagagca  
 gtacaacagttacctaccgagtggtcagtgctctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgaaggttccaacaaa  
 gccctcccagccccatcgagaaaacatctcacaacccaaaggaagagcccagacacctcaagtatacaccataccccacctcgtgaacaa  
 atgtccaagaagaaggttagctgacctgctgtgtcaccacattcttctgaagccatcagtggtgagtgaggagagcaatgggcagccggaga  
 acaactacaagaccagcctccgtgtgactccgacggctccttctctctacagcaagctcaccgtggacaagagcaggtggcagcaggg  
 gaactcttctcatgctcgtgatgtaggctctgcacaaccactacacgcagaagagcctcctcctgtctccgggtaaa

**Heavy chain Protein sequence of i27v1 (variable + 'improved' v1 constant region)**

MNFWLSLIFLVVLKGVQCEVKLVESGGLVQPGGSLKLSCATSGFTFSHYMYWVRQTP  
 EKRLWVAYISNDGDNYYPTIRGRFTISRDNARNTLYLQMSRLKSEDTAMYVCARGKY  
 DGAWFAYWGQGLVTVSS  
 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS  
 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTPPCPAPPELLGG  
 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHTAQTQPREEQYN  
 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKPKGRAQTPQVYTIPTPREQ  
 MSKKKVLSTCLVTNFFSEAIISVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW  
 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK