LEADER
FR1 - IMGT
CDR1 - IMGT
FR2 - IMGT
CDR2 - IMGT
FR3 - IMGT
FG129_29H

Figure 1a

Figure 1a continued

```
                76  F  T  I  S  R  D  D  S  Q  S  M  L  Y  L  Q
FG129_29H       ttc acc ata tcc aga gat gat tca caa agc atg ctc tat ctg caa

                ----------------------------  FR3 - IMGT  ----------------->
                91  M  N  S  L  K  T  E  D  T  A  M  Y  Y  C  V
FG129_29H       atg aac aac ttg aaa acg gag gac aca gcc atg tat tac tgt gta

                    CDR3 - IMGT
                106 G  Y  G  S  G  S  G  G  N  Y  W  G  Q  G
FG129_29H       ggg tac ggt agt ggg gga aac tac tgg ggt caa gga ... ... ...

                121 T  S  V  T. V. S. S. A  K  T  T  P  A  S  V
FG129_29H       acc tca gtc acc gtc tcc tca gcc aaa acg aca ccc cca tct gtc

                136 Y  A  L  A  P  G  S  A  A  Q  T  N  S  M  V
FG129_29H       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  A  E  P  V  T
FG129_29H       acc ctg gga tgc ctg gtc aag ggc tat ttc cct gag cca gtg aca

                166 V  T  W  N  S  G  S  L  S  S  G  V  H  T  F
FG129_29H       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
FG129_29H       cca gct gtc ctg gag tct gac ctc tac act ctg agc agc tca gtg

                196 T  V  P  S  S  S  A  R  P  S  E  T  V  T  C  N
FG129_29H       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
FG129_29H       gtt gcc cac ccg gcc agc agc acc aag gtg gac aag aaa att gtg

                226 P  R  D  C  G  C  K  P  C  I  C  T  V  P  E
```

Figure 1a continued

```
FG129_29H       ccc agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa
                241  V   S   S   V   F   I   E   P   P   K   P   K   D   V   L
FG129_29H       gta tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc
                256  T   I   T   L   T   P   K   V   T   C   V   V   V   D   I
FG129_29H       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
FG129_29H       agc aag gat gat ccc gag gtc cag ttc agc tgg ttt gta gat gat
                286  V   E   V   H   T   A   Q   T   Q   P   R   E   E   Q   F
FG129_29H       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
FG129_29H       aac agc act ttc cgc tca gtc agt gaa ctt ccc atc atg cac cag
                316  D   W   L   N   G   K   E   F   K   C   R   V   N   S   A
FG129_29H       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
FG129_29H       gct ttc cct gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggc
                346  R   P   K   A   P   Q   V   Y   T   I   P   P   P   K   E
FG129_29H       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
FG129_29H       cag atg gcc aag gat aaa gtc agt ctg acc tgc atg ata aca gac
                376  F   F   P   E   D   I   T   V   E   W   Q   W   N   G   Q
FG129_29H       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
```

Figure 1a continued

```
FG129_29H     cca gcg gag aac tac aag aac act cag ccc atc atg aac acg aat
                 P  A  E  N  Y  K  N  T  Q  P  I  M  N  T  N
              406 G  S  Y  F  V  Y  S  K  L  N  V  Q  K  S  N
FG129_29H        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
FG129_29H        tgg gag gca gga aat act ttc acc tgc tct gtg tta cat gag ggc
              436 L  H  N  H  H  T  E  K  S  L  S  H  S  P  G
FG129_29H        ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt
              451 K
FG129_29H        aaa
```

Figure 1b

```
                                                  -20  M   E   S   Q   T
                                                      atg gaa tca cag act

                                 LEADER
            -15  Q   V   L   M   S   L   L   F   W   V   S   G   T   C   G
FG129_29K       cag gtc ctc atg tcc ctg ctg ttc tgg gta tct ggt acc tgt ggg

                <------------------------ FR1 - IMGT ---------------------
              1  D   I   V   M   T   Q   S   P   S   S   L   T   V   T   A
FG129_29K       gac att gtg atg aca cag tct cca tcc tcc ctg act gtg aca gca

                --------------- FR1 - IMGT ------------->    CDR1 - IMGT
             16  G   E   K   V   T   M   S   C   K   S   S   Q   S   L   L
FG129_29K       gga gag aag gtc act atg agc tgc aag tcc agt cag agt ctg tta

                        CDR1 - IMGT            <--------- FR2 - IMGT ----
             31  N   S   G   N   Q   K   N   Y   L   T   W   Y   Q   Q   K
FG129_29K       aac agt gga aat caa aag aac tac ttg acc tgg tac cag cag aaa

               ------------- FR2 - IMGT ------------>     CDR2 - IMGT
             46  P   G   Q   P   P   K   V   L   I   Y   W   A
FG129_29K       cca ggg cag cct cct aaa gtg ttg atc tac tgg gca ... ... ...

                     CDR2 - IMGT        <-------------- FR3 - IMGT ----------
             61                      S   T   R   E   S   G   V   P       D   R
FG129_29K       ... ... ... ... tcc act agg gaa tct ggg gtc cct ... gat cgc

                ------------------------ FR3 - IMGT ---------------------
             76  F   T   G   S   G           S   G   T   D   F   T   L   T
FG129_29K       ttc aca ggc agt gga ... ... tct gga aca gat ttc act ctc acc
```

Figure 1b continued

```
                    -------------------- FR3 - IMGT -------------------> ___
               91   I   S   S   V   Q   A   E   D   L   A   V   Y   Y   C   Q
FG129_29K          atc agc agt gtg cag gct gaa gac ctg gca gtt tat tac tgt cag

                   _______ CDR3 - IMGT ___________
              106   N   D   Y   S   S   P   F   T   F   G   S   G   T   K   L
FG129_29K          aat gat tat agt tct cca ttc acg ttc ggc tcg ggg aca aag ttg

              121   E   I   K   R   A   D   A   A   P   T   V   S   I   F   P
FG129_29K          gaa ata aaa cgg gct gat gct gca cca act gta tcc atc ttc cca

              136   P   S   S   E   Q   L   T   S   G   G   A   S   V   V   C
FG129_29K          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
FG129_29K          ttc ttg aac aac ttc tac ccc aaa gac atc aat gtc aag tgg aag

              166   I   D   G   S   E   R   Q   N   G   V   L   N   S   W   T
FG129_29K          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
FG129_29K          gat cag gac agc aaa gac agc acc tac agc atg agc agc acc ctc

              196   T   L   T   K   D   E   Y   E   R   H   N   S   Y   T   C
FG129_29K          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
FG129_29K          gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc

              226   N   R   N   E   C
FG129_29K          aac agg aat gag tgt
```

Figure 2a

```
                                                            -19 ·M· ·L· ·L· ·G·
Ch129_29H                                                       atg ctg ttg ggg

                                       LEADER
               ·L· ·K· ·W· ·V· ·F· ·F· ·V· ·V· ·F· ·Y· ·Q· ·G· ·V· ·H· ·C·
Ch129_29H      ctg aag tgg gtt ttc ttt gtt gtt ttt tat caa ggt gtg cat tgt

               <------------------------- FR1 - IMGT -------------------
            1  E   V   Q   L   V   E   S   G   G       G   L   V   Q   P
Ch129_29H      gag gtg cag ctt gtt gag tct ggt gga ... gga ttg gtg cag cct

               ------------- FR1 - IMGT ----------------->   CDR1 - IMGT
           16  K   G   S   L   K   L   S   C   A   A   S   G   F   T   F
Ch129_29H      aaa ggg tca ttg aaa ctc tca tgt gca gcc tct gga ttc acc ttc

                   CDR1 - IMGT               <------------ FR2 - IMGT --
           31                      N   T   Y   A   M   N   W   V   R   Q   A
Ch129_29H      ... ... ... ... aat acc tac gcc atg aac tgg gtc cgc cag gct

               --------- FR2 - IMGT --------------->   CDR2 - IMGT
           46  P   G   K   G   L   E   W   V   A   R   I   R   S   K   S
Ch129_29H      cca gga aag ggt ttg gaa tgg gtt gct cgc ata aga agt aaa agt

                   CDR2 - IMGT       <-------------- FR3 - IMGT ----------
           61  N   N   Y   A   T   Y   Y   A   D   S   V   K       D   R
Ch129_29H      aat aat tat gca aca tat tat gcc gat tca gtg aaa ... gac agg

               ------------------------- FR3 - IMGT -------------------
```

Figure 2a continued

```
                76  F  T  I  S  R  D  D  S  Q  S  M  T  L  Q
Ch129_29H       ttc acc ata tcc aga gat gat tca caa agc atg ctc tat ctg caa

                ----------------------------  FR3 - IMGT  ----------------->  ____
                91  M  N  N  L  K  K  E  D  T  A  M  Y  Y  C  V
Ch129_29H       atg aac aac ttg aaa aag gag gac aca gcc atg tat tac tgt gta

                          CDR3 - IMGT
                          ___________
               106  G  Y  G  G  G  N  Y  W  G  Q  G
Ch129_29H       ggg tac ggt agt ggg gga aac tac tgg ggt caa gga ... ... ... ...

               121  T  S  V  T  V  S  S  A  S  T  K  G  P  S  V
Ch129_29H       acc tca gtc acc gtc tcc agc gct tcc acc aag ggc cca tcg gtc

               136  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A
Ch129_29H       ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg

               151  A  L  G  C  L  V  K  D  Y  F  P  E  P  V  T
Ch129_29H       gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg

               166  V  S  W  N  S  G  A  L  T  S  G  V  H  T  F
Ch129_20H       gtg tcg 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
Ch129_20H       ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg

               196  V  T  V  P  S  S  S  L  G  T  Q  T  Y  I  C
Ch129_29H       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
Ch129_29H       aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt

               226  E  P  K  S  C  D  K  T  H  T  C  P  P  C  P
```

```
Ch129_29H       gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca
                  E   P   K   S   C   D   K   T   H   T   C   P   P   C   P
           241  A   P   E   L   L   G   G   P   S   V   F   L   F   P   P
Ch129_29H      gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca
           256  K   P   K   D   T   L   M   I   S   R   T   P   E   V   T
Ch129_29H      aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca
           271  C   V   V   V   D   V   S   H   E   D   P   E   V   K   F
Ch129_29H      tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc
           286  N   W   Y   V   D   G   V   E   V   H   N   A   K   T   K
Ch129_29H      aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag
           301  P   R   E   E   Q   Y   N   S   T   Y   R   V   V   S   V
Ch129_29H      ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc
           316  L   T   V   L   H   Q   D   W   L   N   G   K   E   Y   K
Ch129_29H      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
Ch129_29H      tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc
           346  I   S   K   A   K   G   Q   P   R   E   P   Q   V   Y   T
Ch129_29H      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
Ch129_29H      ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg
           376  T   C   L   V   K   G   F   Y   P   S   D   I   A   V   E
Ch129_29H      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
```

Figure 2a continued

Figure 2a continued

```
Ch129_29H      tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct

          406  P   V   L   D   S   D   G   S   F   F   L   Y   S   K   L
Ch129_29H      ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc

          421  T   V   D   K   S   R   W   Q   Q   G   N   V   F   S   C
Ch129_29H      acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc

          436  S   V   M   H   E   A   L   H   N   H   Y   T   Q   K   S
Ch129_29H      tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc

          451  L   S   L   S   P   G   K
Ch129_29H      ctc tcc ctg tct ccg ggt aaa
```

LEADER
FR1 - IMGT
CDR1 - IMGT
FR2 - IMGT
CDR2 - IMGT
FR3 - IMGT
Ch129_29K

Figure 2b

Figure 2b continued

```
                76  F   T   G   S   G                   S   G   T   D   F   T   L   T
Ch129_29K           ttc aca ggc agt gga ... ... ... tct gga aca gat ttc act ctc acc
                    ~~~~~~~~~~~~~~~~~~  FR3 - IMGT  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~>
               91   I   S   S   V   Q   A   E   D   L   A   V   Y   Y   C   Q
Ch129_29K      atc agc agt gtg cag gct gaa gac ctg gca gtt tat tac tgt cag
                        CDR3 - IMGT
              106   N   D   Y   S   S   P   F   T   F   G   S   G   T   K   L
Ch129_29K     aat gat tat agt tct 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
Ch129_29K     gaa ata aaa cgt acg gta gcg gcc cca tct gtc ttc atc ttc ccg
              136   P   S   D   E   Q   L   K   S   G   T   A   S   V   V   C
Ch129_29K     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
Ch129_29K     ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag
              166   V   D   N   A   L   Q   S   G   N   S   Q   E   S   V   T
Ch129_29K     gtg gat aac gcc ctc 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
Ch129_29K     gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg
              196   T   L   S   K   A   D   Y   E   K   H   K   V   Y   A   C
Ch129_29K     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
Ch129_29K     gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc
              226   N   R   G   E   C
```

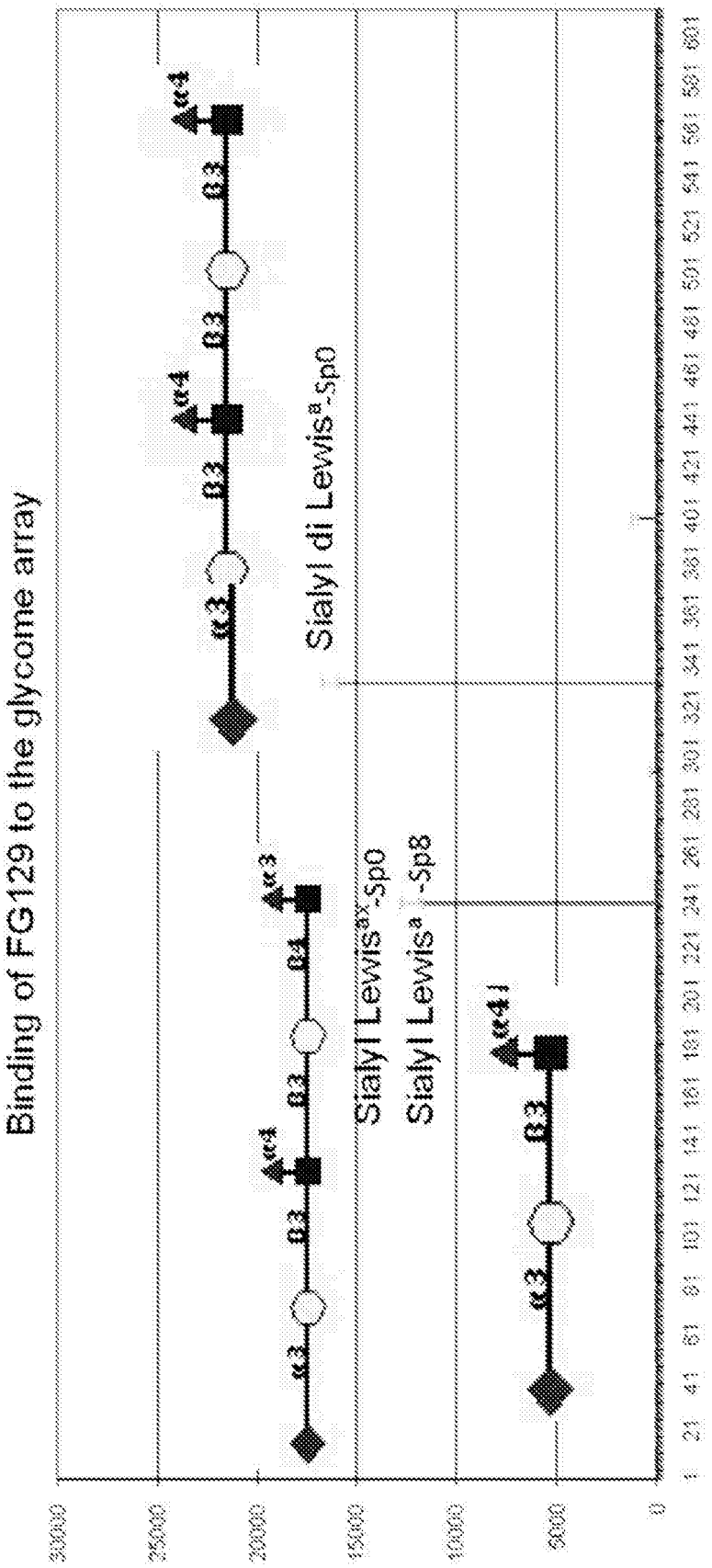

Binding of FG129 to the glycome array
Sialyl di Lewis^a-Sp0
Sialyl Lewis^{ax}-Sp0
Sialyl Lewis^a -Sp8
α3
α4
β3
β4
β2
30000
25000
20000
15000
10000
5000
0
1 21 41 61 81 101 121 141 161 181 201 221 241 261 281 301 321 341 361 381 401 421 441 461 481 501 521 541 561 581 601

Figure 3a

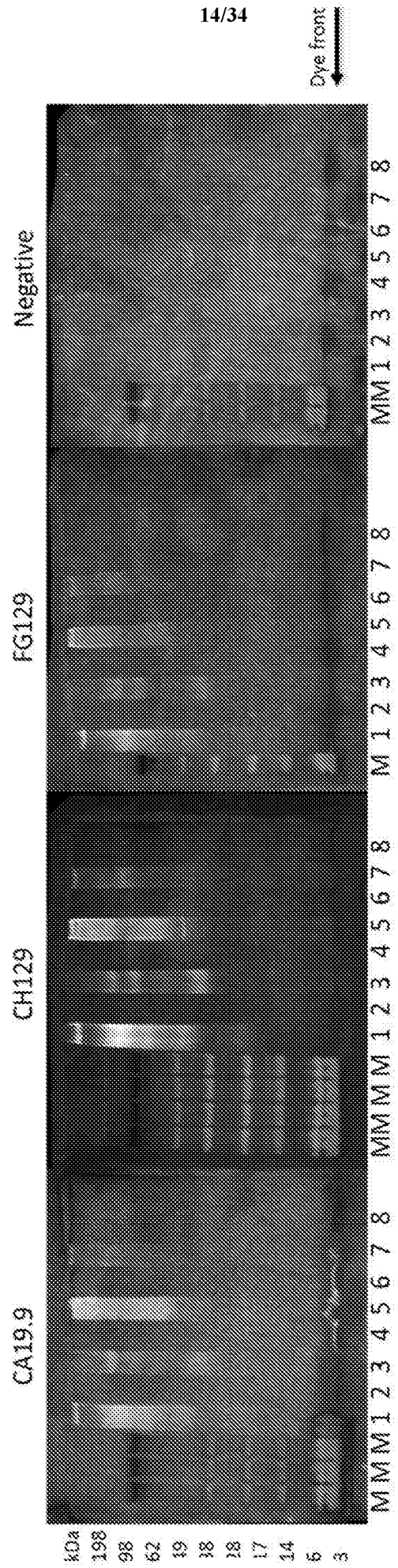

Dye front
Negative
FG129
CH129
CA19.9
M M M 1 2 3 4 5 6 7 8
M M M 1 2 3 4 5 6 7 8
M M M 1 2 3 4 5 6 7 8
M 1 2 3 4 5 6 7 8
MM 1 2 3 4 5 6 7 8
kDa
198
98
62
49
38
28
17
14
6
3

Figure 3b

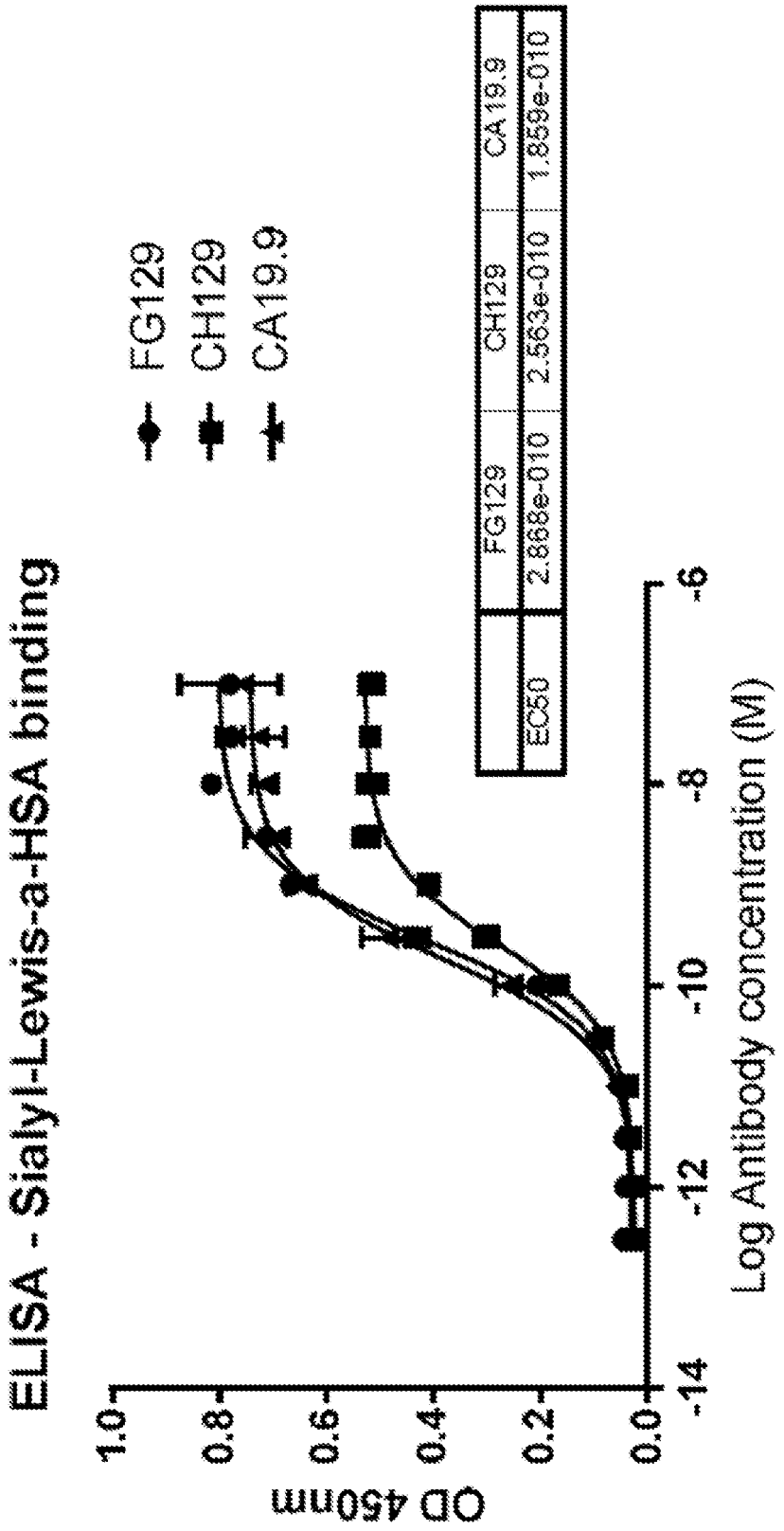

ELISA - Sialyl-Lewis-a-HSA binding
FG129
CH129
CA19.9
OD 450nm
1.0
0.8
0.6
0.4
0.2
0.0
-14
-12
-10
-8
-6
Log Antibody concentration (M)
EC50
FG129
2.868e-010
CH129
2.563e-010
CA19.9
1.859e-010

Figure 4

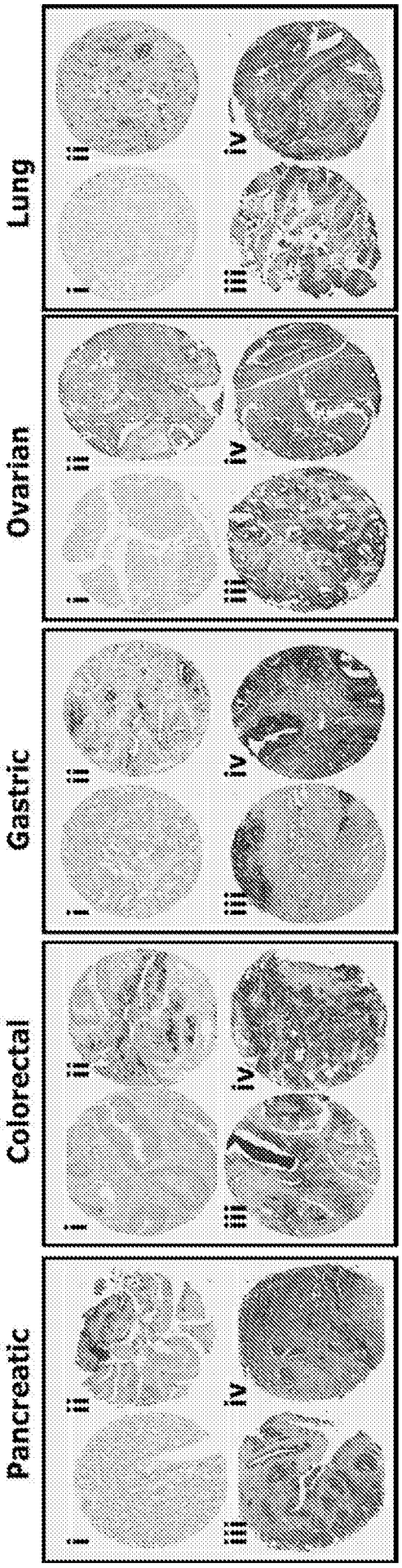

Pancreatic
i
ii
iii
iv
Colorectal
i
ii
iii
iv
Gastric
i
ii
iii
iv
Ovarian
i
ii
iii
iv
Lung
i
ii
iii
iv

Figure 5a

Pancreatic
Cumulative survival
1.0
0.8
0.6
0.4
0.2
0
negative/weak
moderate/strong
P=0.004
0
50
100
150
200
250
Survival from operation
(months)

Figure 5b

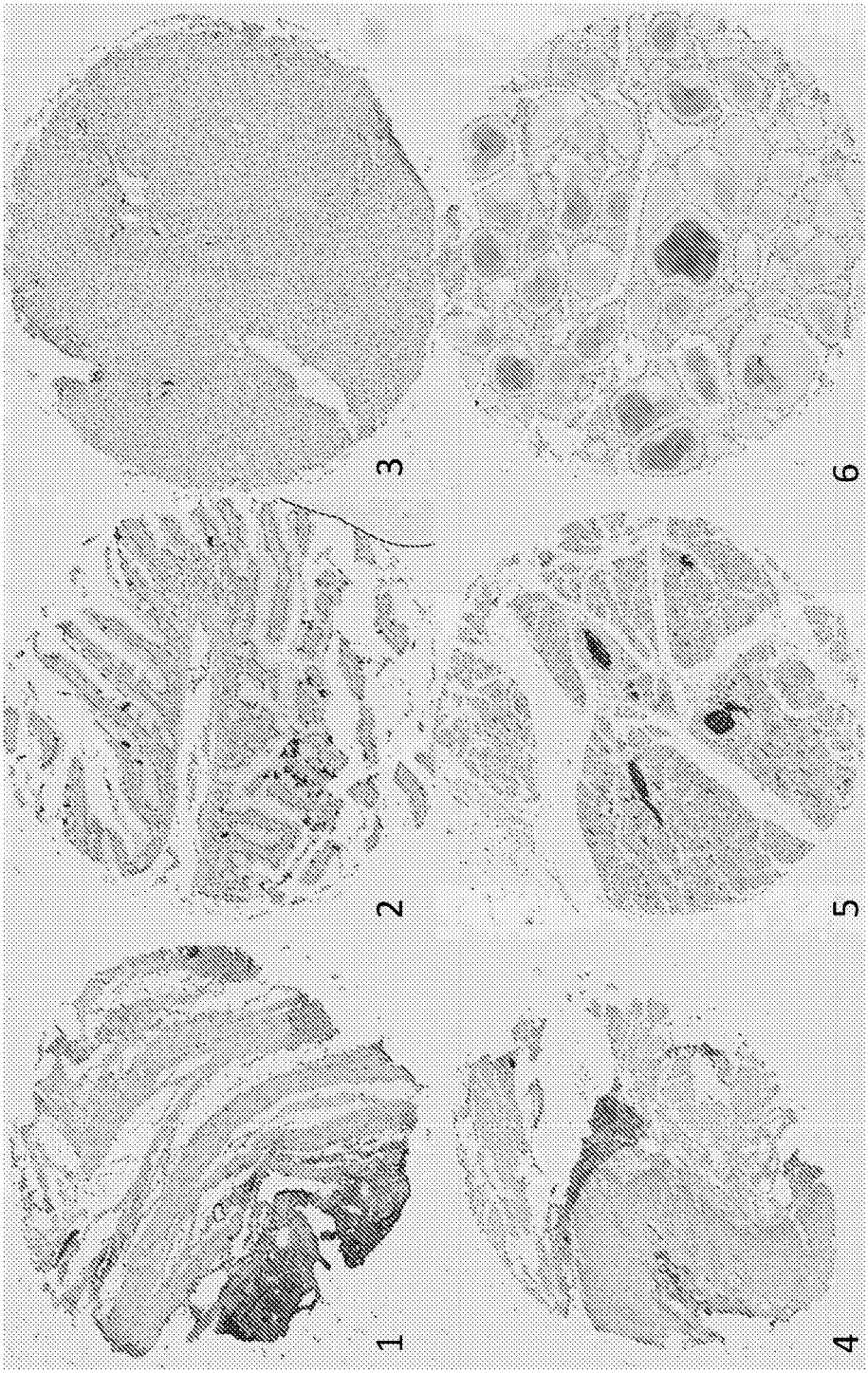


Figure 5c

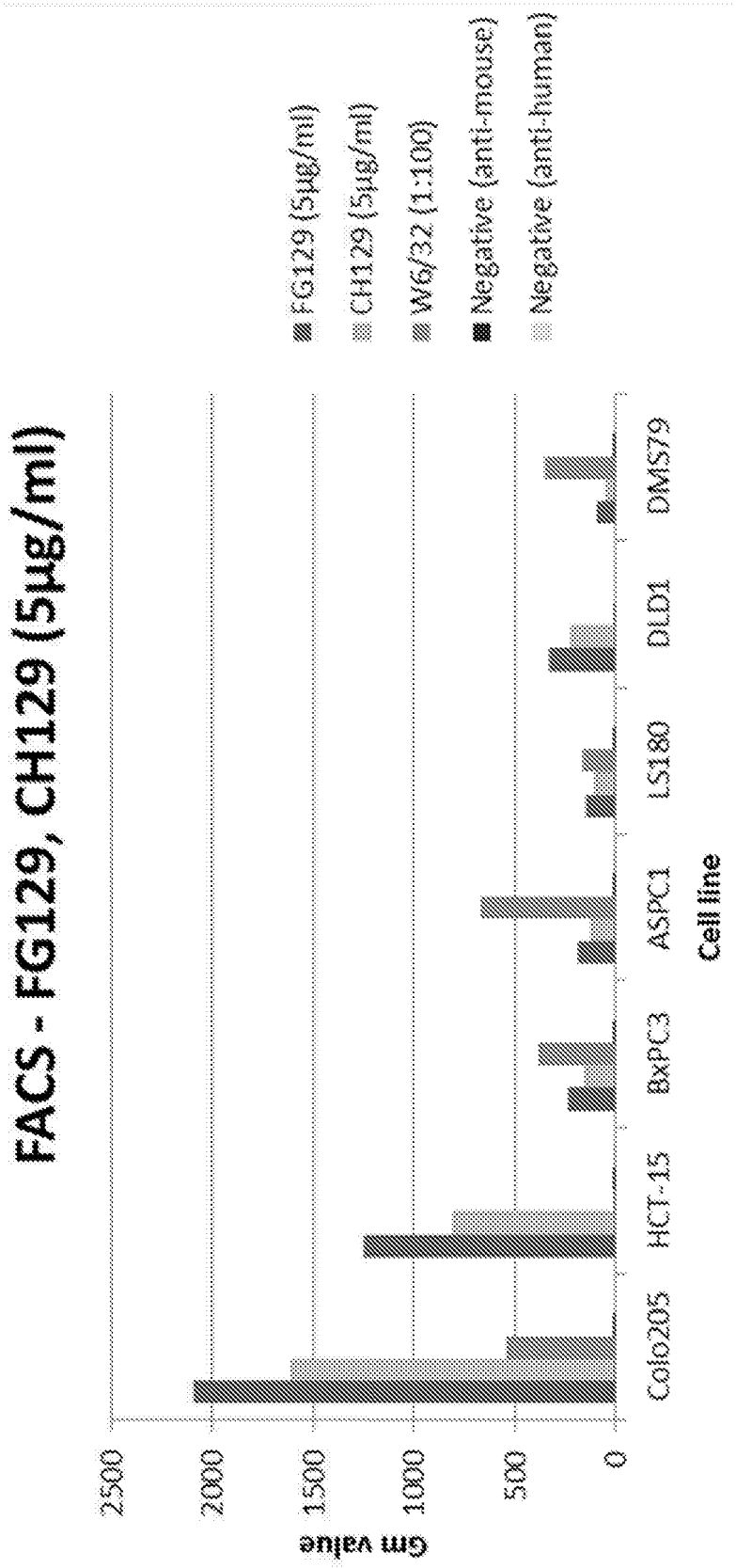

FACS - FG129, CH129 (5µg/ml)
FG129 (5µg/ml)
CH129 (5µg/ml)
W6/32 (1:100)
Negative (anti-mouse)
Negative (anti-human)
Gm value
2500
2000
1500
1000
500
0
Colo205
HCT-15
BxPC3
ASPC1
LS180
DLD1
DMS79
Cell line

Figure 6a

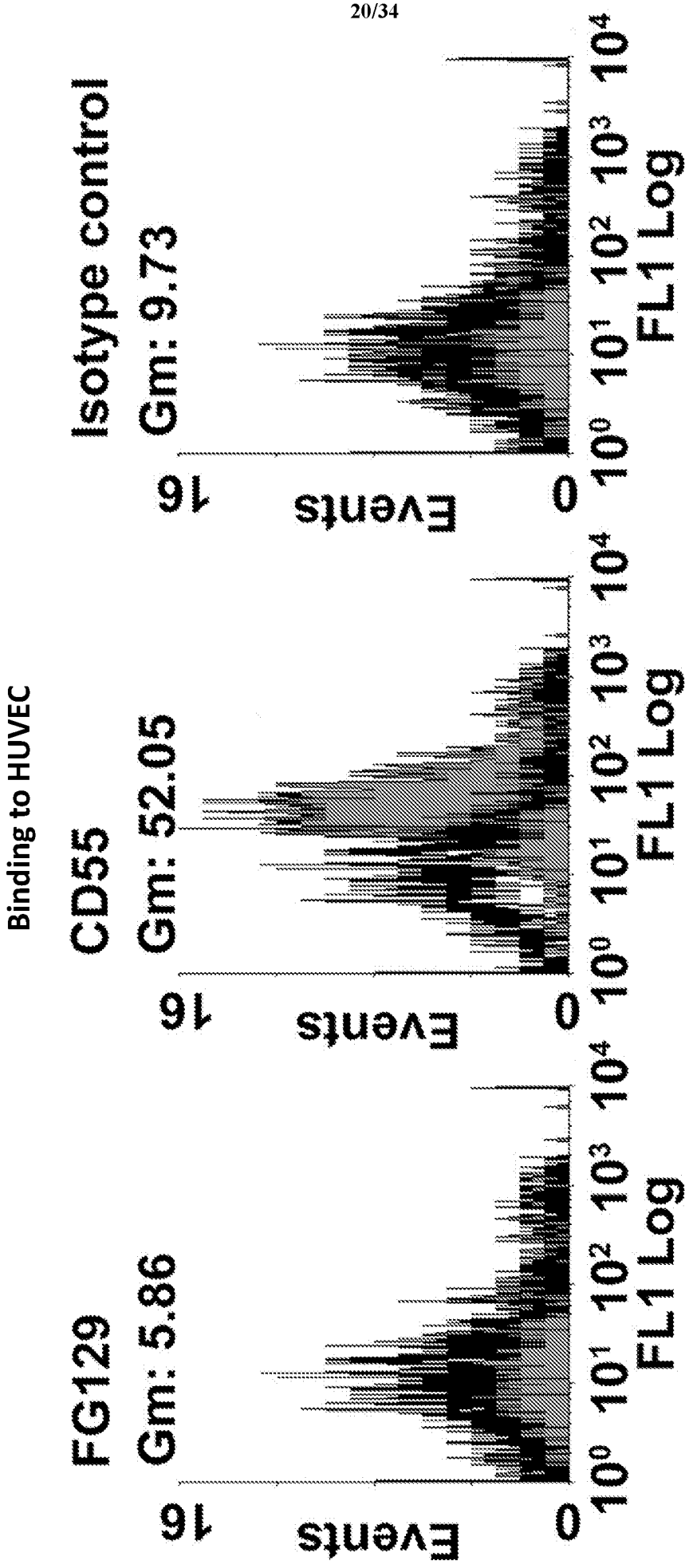

Binding to HUVEC
FG129
Gm: 5.86
CD55
Gm: 52.05
Isotype control
Gm: 9.73
Events
16
0
FL1 Log
10^0 10^1 10^2 10^3 10^4

Figure 6b

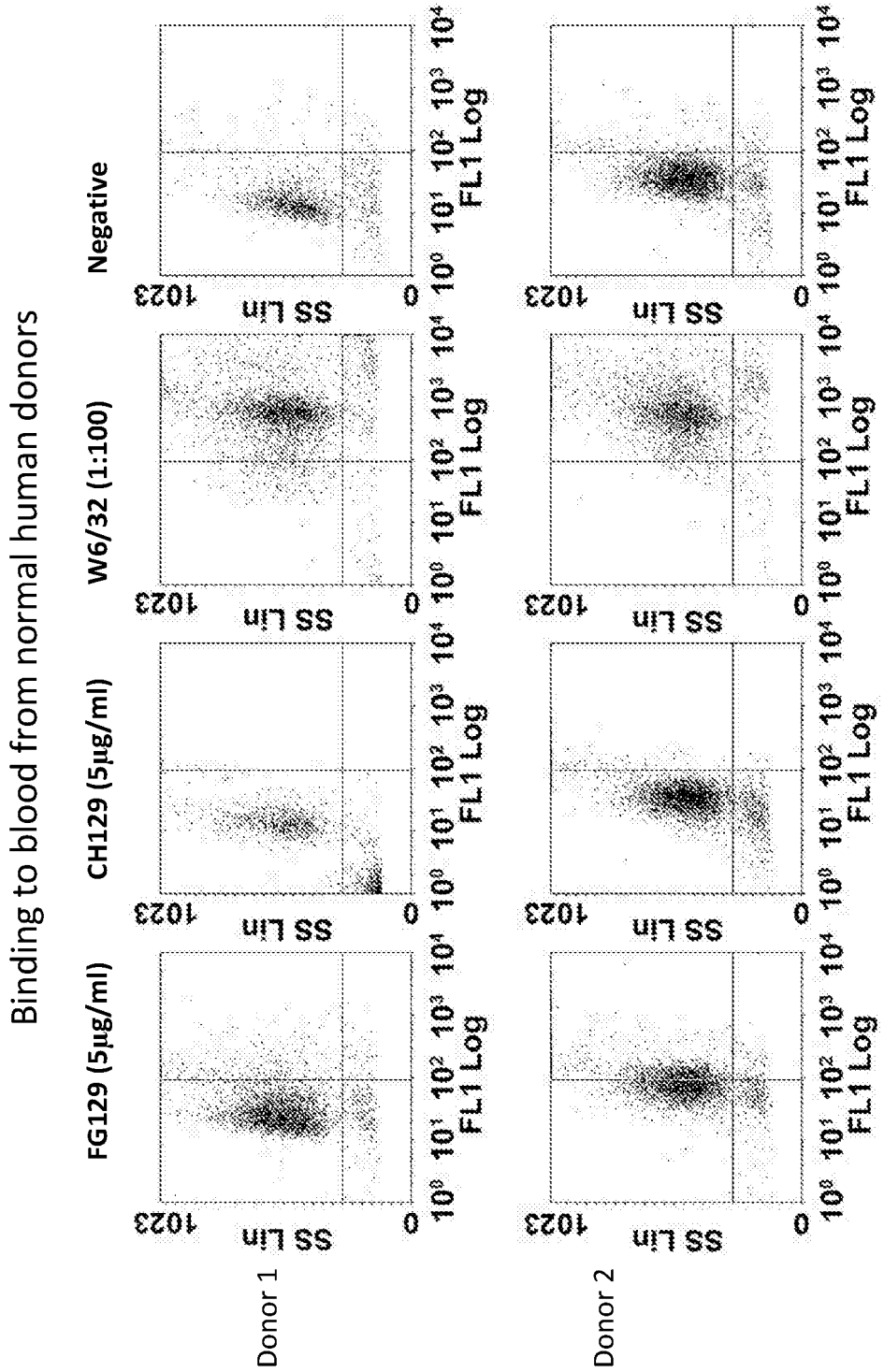

Binding to blood from normal human donors
FG129 (5µg/ml)
CH129 (5µg/ml)
W6/32 (1:100)
Negative
Donor 1
Donor 2
SS Lin
FL1 Log
0
1023
10^0 10^1 10^2 10^3 10^4

Figure 6c

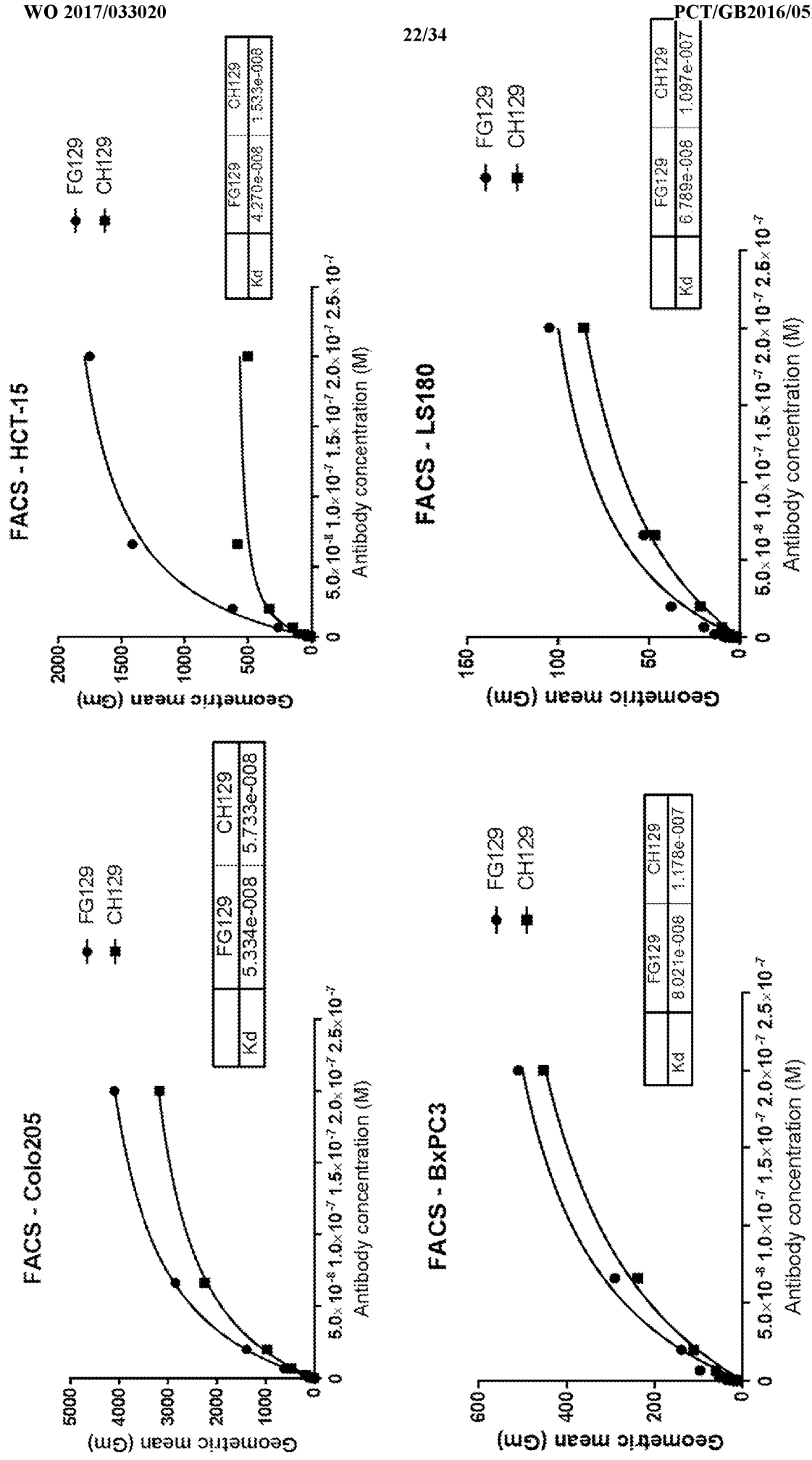

FACS - HCT-15
FG129
CH129
Geometric mean (Gm)
Antibody concentration (M)
FG129 CH129
Kd 4.270e-008 1.533e-008
FACS - LS180
FG129
CH129
Geometric mean (Gm)
Antibody concentration (M)
FG129 CH129
Kd 6.789e-008 1.097e-007
FACS - Colo205
FG129
CH129
Geometric mean (Gm)
Antibody concentration (M)
FG129 CH129
Kd 5.334e-008 5.733e-008
FACS - BxPC3
FG129
CH129
Geometric mean (Gm)
Antibody concentration (M)
FG129 CH129
Kd 8.021e-008 1.178e-007

Figure 7

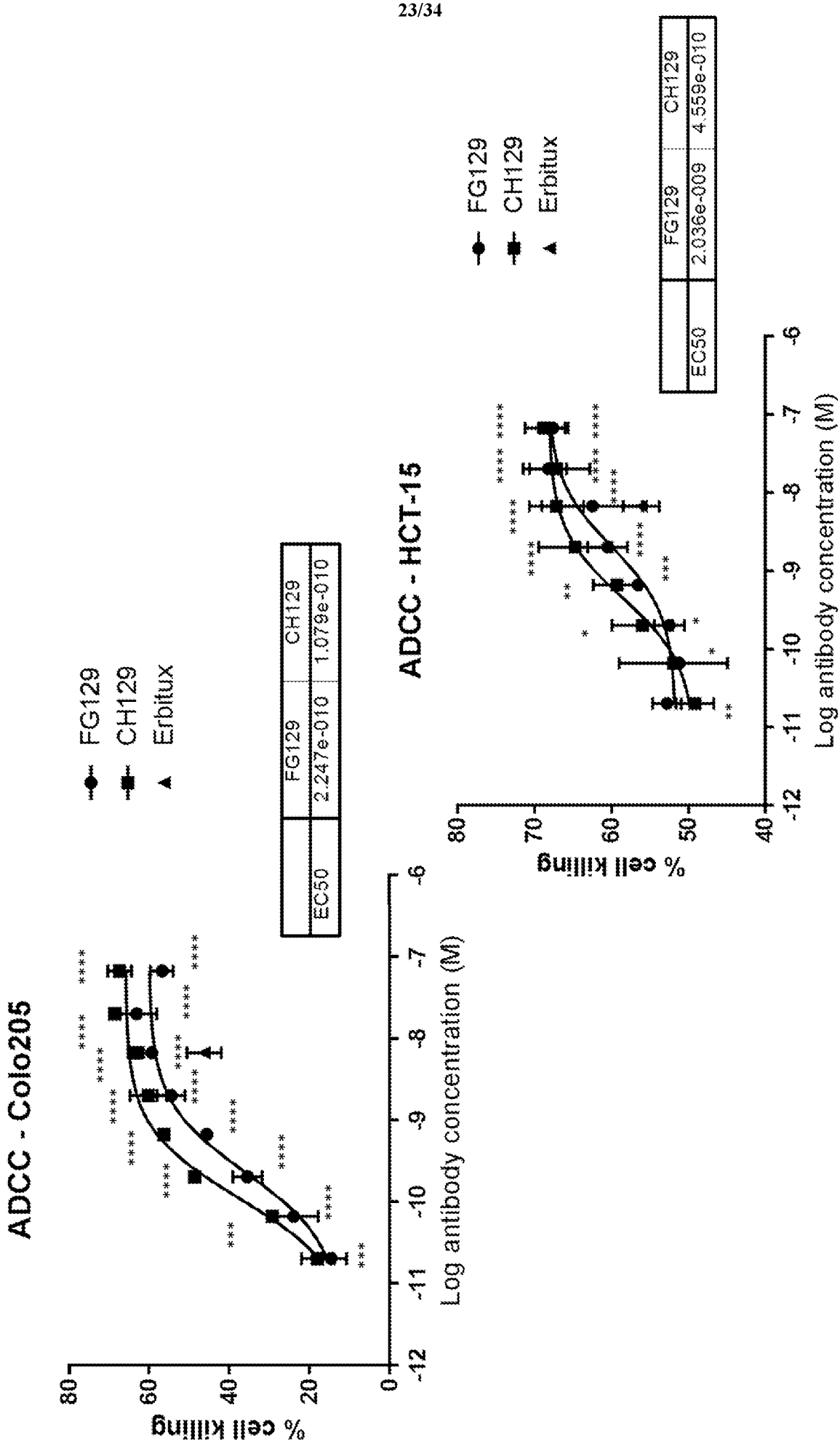

ADCC - Colo205
FG129
CH129
Erbitux
% cell killing
Log antibody concentration (M)
EC50
FG129
2.247e-010
CH129
1.079e-010
ADCC - HCT-15
FG129
CH129
Erbitux
% cell killing
Log antibody concentration (M)
EC50
FG129
2.036e-009
CH129
4.559e-010

Figure 8

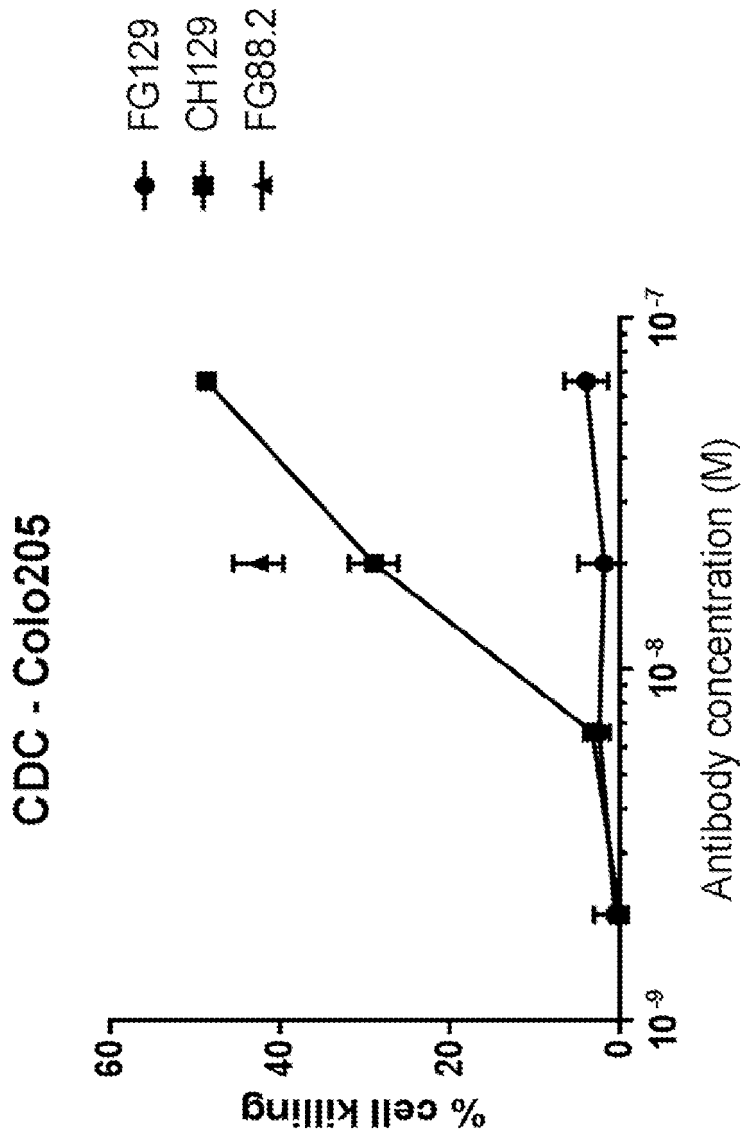

CDC - Colo205
FG129
CH129
FG88.2
% cell killing
0
20
40
60
10^{-9}
10^{-8}
10^{-7}
Antibody concentration (M)

Figure 9

Figure 10b

Figure 10a

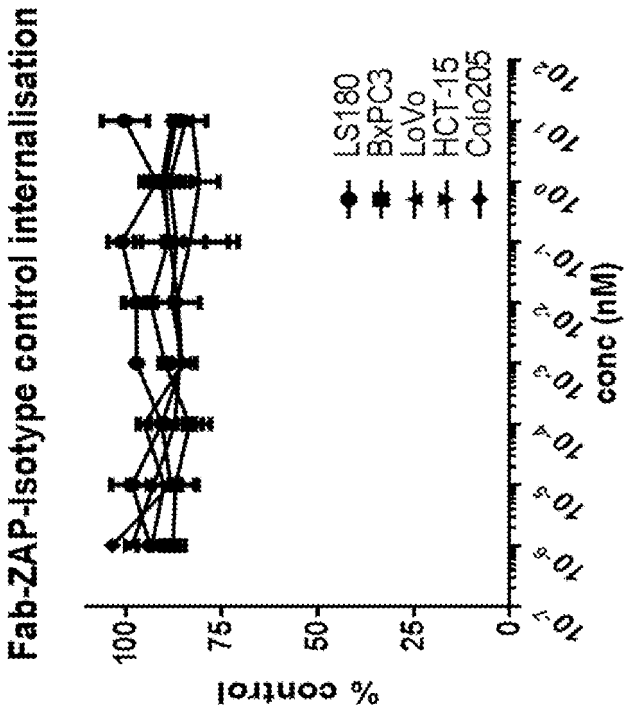


Figure 11b

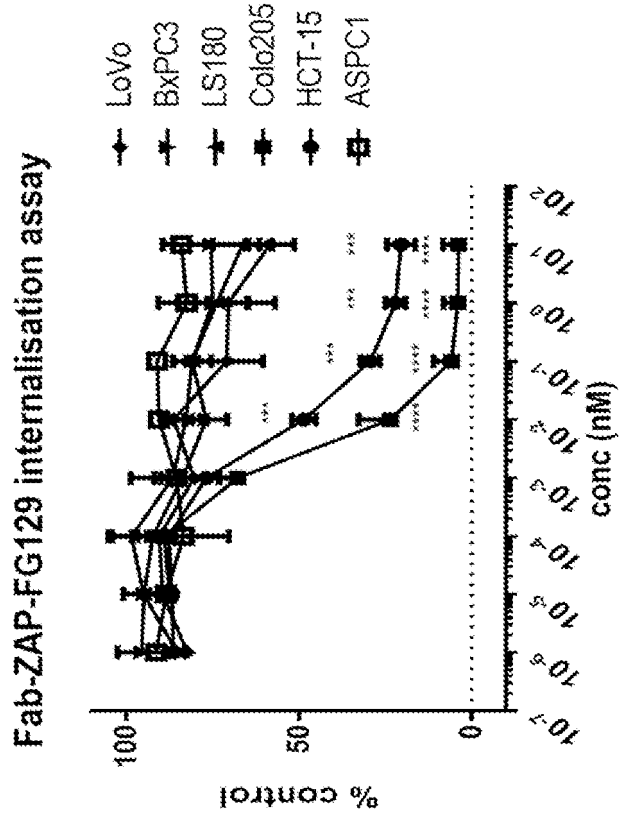


Figure 11a

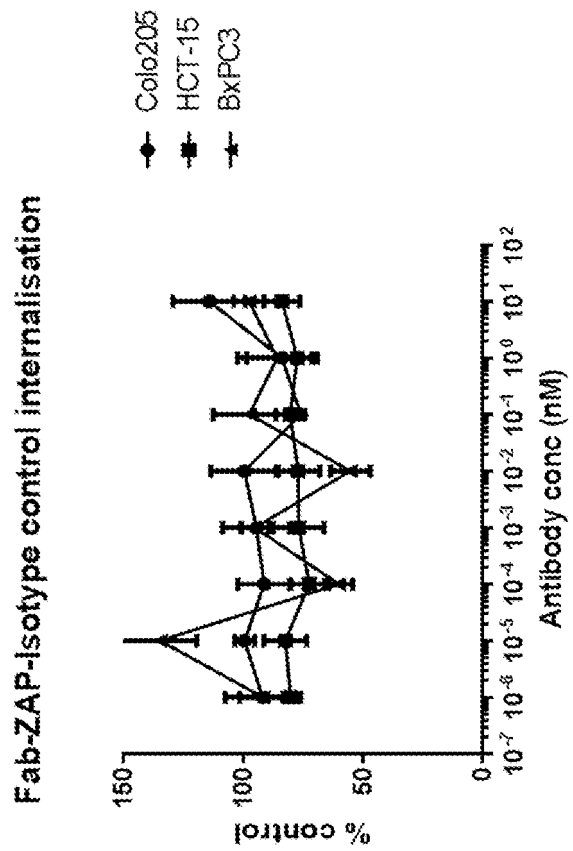


Figure 11d

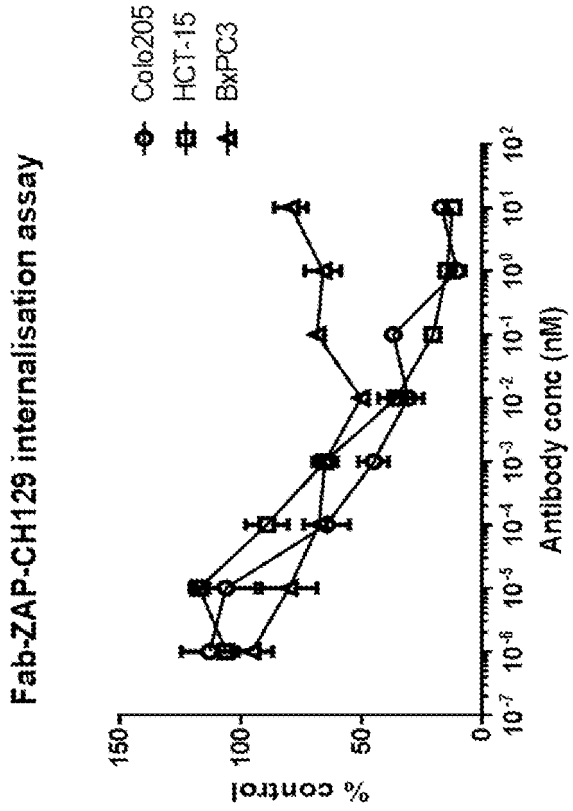
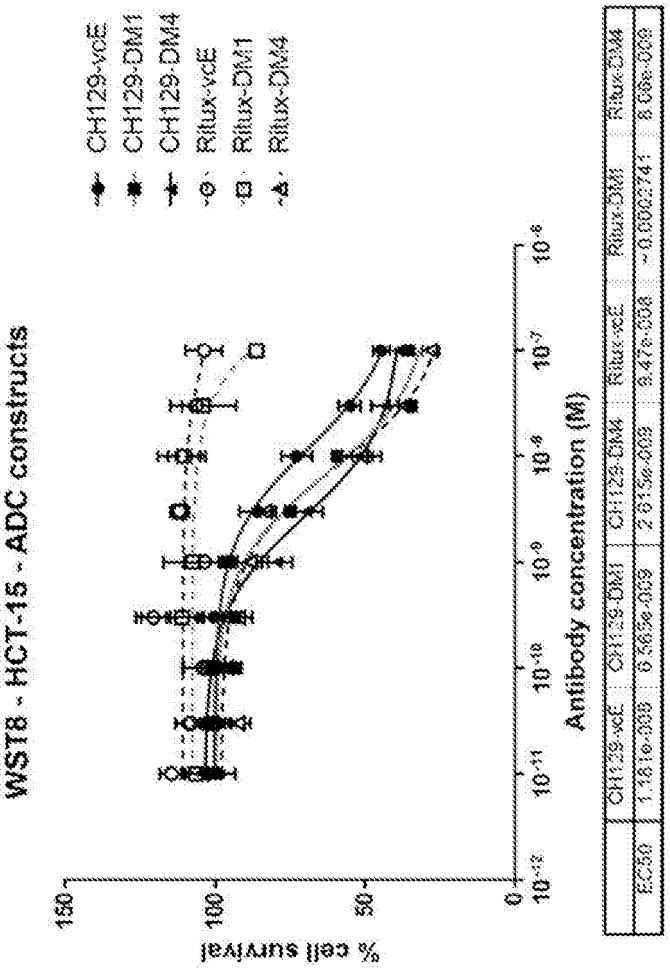
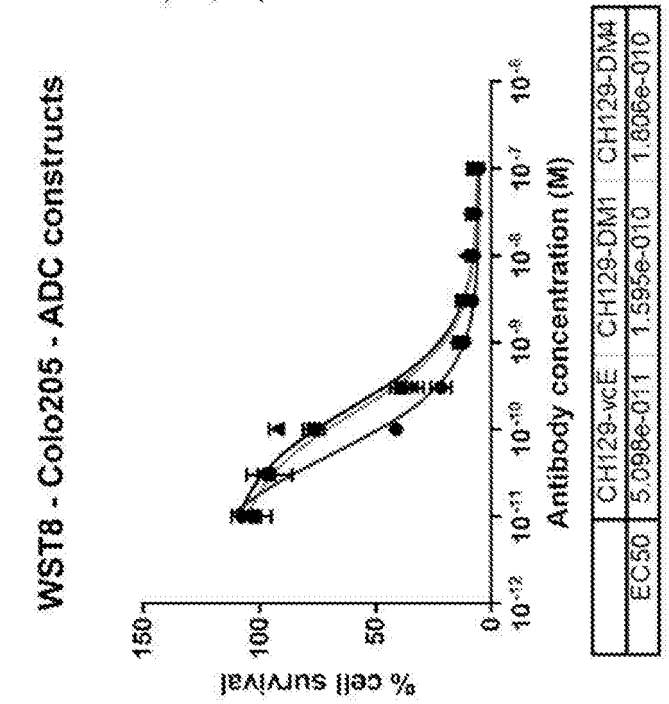


Figure 11c



	CH129-vcE	CH129-DM1	CH129-DM4	Ritux-vcE	Ritux-DM1	Ritux-DM4
EC50	1.181e-009	6.565e-009	2.915e-009	8.472e-008	~0.6002741	8.08e-009

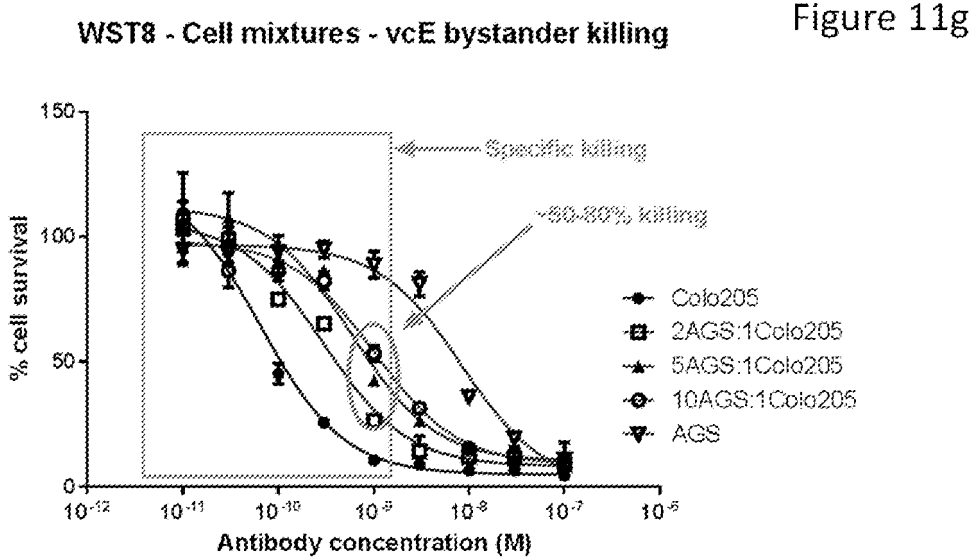
Figure 11f



	CH129-vcE	CH129-DM1	CH129-DM4
EC50	5.098e-011	1.595e-010	1.806e-010

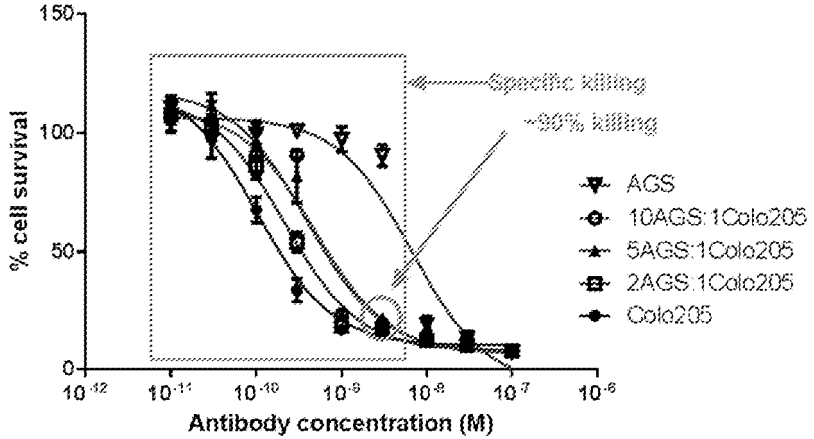
Figure 11e

Figure 11g



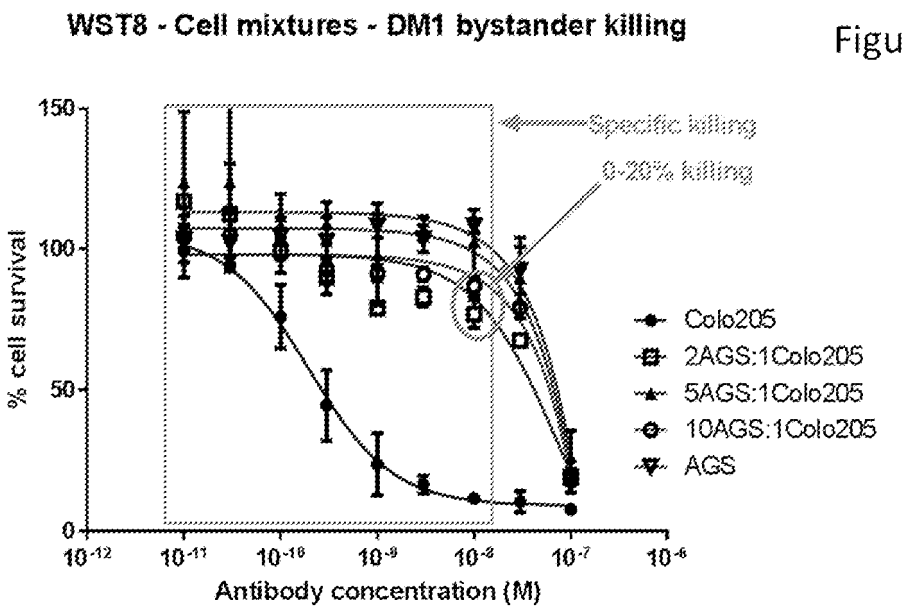
	Colo205	2AGS:1Colo205	5AGS:1Colo205	10AGS:1Colo205	AGS
EC50	6.577e-011	2.993e-010	5.814e-010	1.017e-009	8.394e-009

Figure 11h



	Colo205	2AGS:1Colo205	5AGS:1Colo205	10AGS:1Colo205	AGS
EC50	1.061e-010	2.204e-010	4.011e-010	4.963e-010	6.696e-009

Figure 11i



	Colo205	2AGS:1Colo205	5AGS:1Colo205	10AGS:1Colo205	AGS
EC50	1.961e-010	7.78e-008	~ 6.707e-005	~ 0.0003625	~ 0.001792

SUBSTITUTE SHEET (RULE 26)

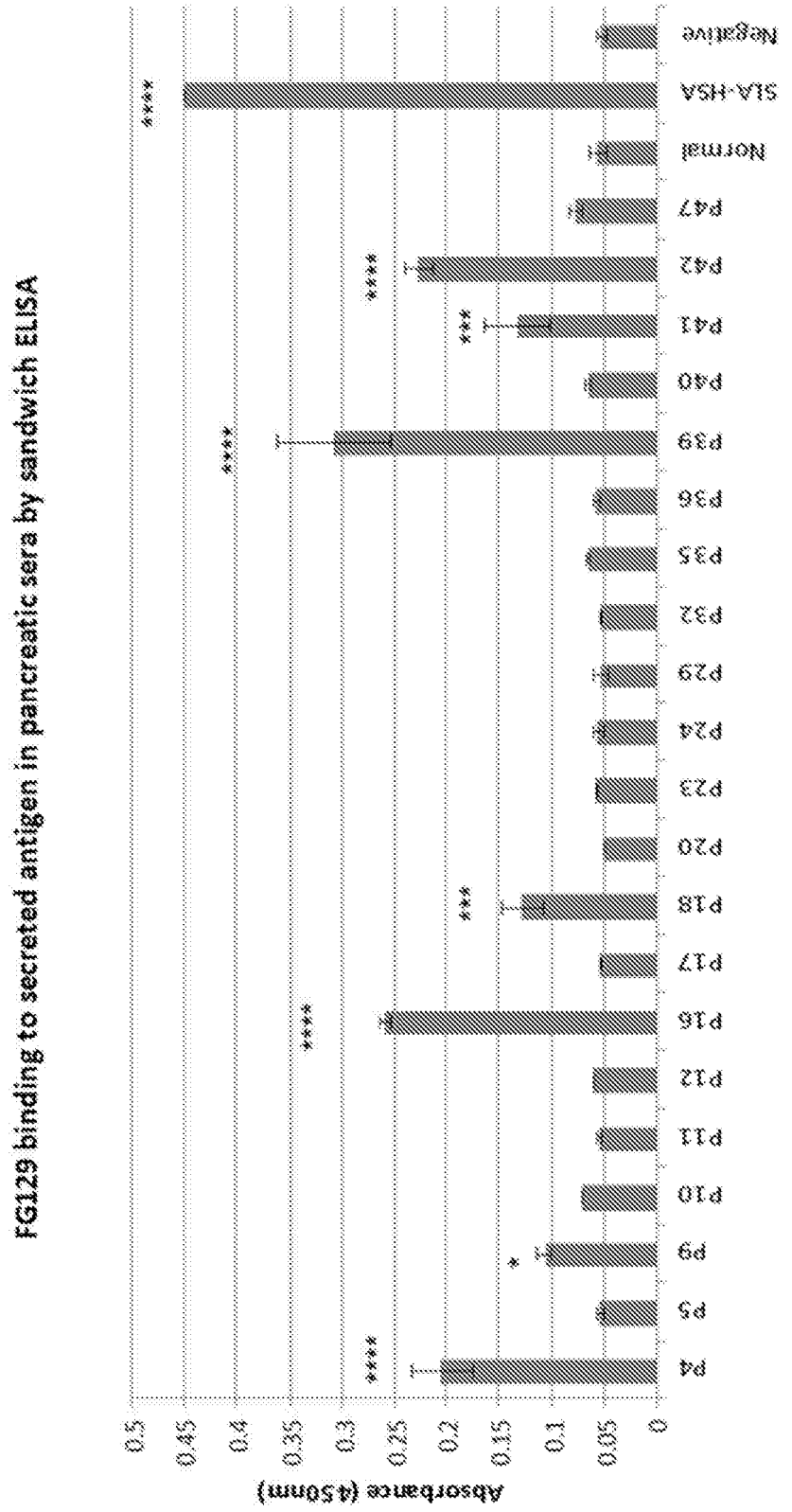

FG129 binding to secreted antigen in pancreatic sera by sandwich ELISA
Absorbance (450nm)
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
P4
P5
P9
P10
P11
P12
P16
P17
P18
P20
P23
P24
P29
P32
P35
P36
P39
P40
P41
P42
P47
Normal
SLA-HSA
Negative
****
*
****
***
****
***
****
****

Figure 12a

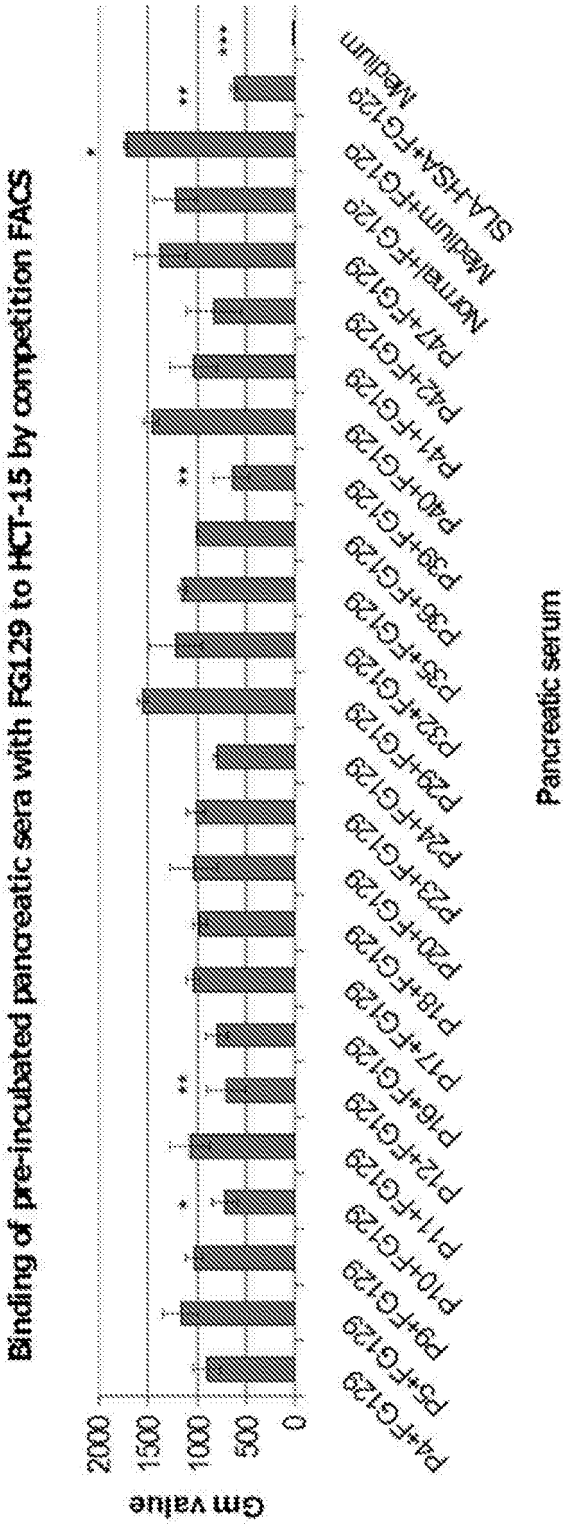

Binding of pre-incubated pancreatic sera with FG129 to HCT-15 by competition FACS
Gm value
2000
1500
1000
500
0
P4+FG129
P5+FG129
P9+FG129
P10+FG129
P11+FG129
P12+FG129
P16+FG129
P17+FG129
P18+FG129
P20+FG129
P23+FG129
P24+FG129
P29+FG129
P32+FG129
P35+FG129
P36+FG129
P39+FG129
P40+FG129
P41+FG129
P42+FG129
P47+FG129
NormalPancreatic+FG129
Medium+FG129
SLA-HSA+FG129
Medium
Pancreatic serum

Figure 12b

Figure 13a

```
                  <----------        Leader        ----------------------->
FG129-scFv        atgctgttgggggctgaagtgggttttcttgttttttctatcaaggtgtgcatctatcg
                  MetLeuLeuGlyLeuLysTrpValPhePheValValPheTyrGlnGlyValHisSerSer

                  <----------       heavy chain variable region      ------->
FG129-scFv        atggaggtgcagcttgttgagtctgggggaggattggtgcagcctaaagggtcattgaaa
                  MetGluValGlnLeuValGluSerGlyGlyLeuValGlnProLysGlySerLeuLys

                  <----------       heavy chain variable region      ------->
FG129-scFv        ctctcatgtgcagcctctggattcaccttcaatacctacgccatgaactgggtccgccag
                  LeuSerCysAlaAlaSerGlyPheThrPheAsnThrTyrAlaMetAsnTrpValArgGln

                  <----------       heavy chain variable region      ------->
FG129-scFv        gctccaggaaagggtttgtctggcataaagaagtaaaagtaaataattatgcaca
                  AlaProGlyLysGlyLeuGluTrpValAlaArgIleArgSerLysSerAsnAsnTyrAla

                  <----------       heavy chain variable region      ------->
FG129-scFv        acatattatgccgatttcagtgaaagacaggttcaccatatccagagatgattcacaaagc
                  ThrTyrTyrAlaAspSerValLysAspArgPheThrIleSerArgAspAspSerGlnSer

                  <----------       heavy chain variable region      ------->
FG129-scFv        atgctctatctgcaaatgaacaacttgaaaaaggaggacacagccatgtattactgtgta
                  MetLeuTyrLeuGlnMetAsnAsnLeuLysLysGluAspThrAlaMetTyrTyrCysVal

                  <----------       heavy chain variable region      ----><--
FG129-scFv        gggtacggtagtgggggaaactactggggtcaaggaacctcagtcaccgtctcctcaggt
                  GlyTyrGlySerGlyGlyAsnTyrTrpGlyGlnGlyThrSerValThrValSerSerGly

                  <----      3 x GGGGS linker      ----><----------------------
FG129-scFv        ggaggcggttcaggcggaggtggctctggcggtggcggatcagacattgtgatgacacag
                  GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerAspIleValMetThrGln

                  <----------       light chain variable region      ---------->
FG129-scFv        tctccatcctccctgactgtgacagcaggagagaaggtcactatgagctgcaagtccagt
                  SerProSerSerLeuThrValThrAlaGlyGluLysValThrMetSerCysLysSerSer
```

Figure 13a continued

```
                <---------- light chain variable region ----------->
FG129-scFv      cagagtctgttaaacagtggaaatcaaaagaactacttgacctggtaccagcagaaacca
                GlnSerLeuLeuAsnSerGlyAsnGlnLysAsnTyrLeuThrTrpTyrGlnGlnLysPro

                <---------- light chain variable region ----------->
FG129-scFv      gggcagcctcctaaagtgttgatctactgggcatccactagggaatctgggtccctgat
                GlyGlnProProLysValLeuIleTyrTrpAlaSerThrArgGluSerGlyValProAsp

                <---------- light chain variable region ----------->
FG129-scFv      cgcttcacaggcagtggatctggaacagatttcactctcaccatcagcagtgtgcaggct
                ArgPheThrGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerValGlnAla

                <---------- light chain variable region ----------->
FG129-scFv      gaagacctggcagtttattactgtcagaatgattatagttctccattcacgttcggctcg
                GluAspLeuAlaValTyrTyrCysGlnAsnAspTyrSerSerProPheThrPheGlySer

                <---------------------><---  poly-Ala and 6 x His tag  --->
FG129-scFv      gggacaaagttggaaataaaacggtggcggctgcagcggcatcaccatcactaa
                GlyThrLysLeuGluIleLysArgAlaAlaAlaAlaHisHisHisHisHisOc*
```

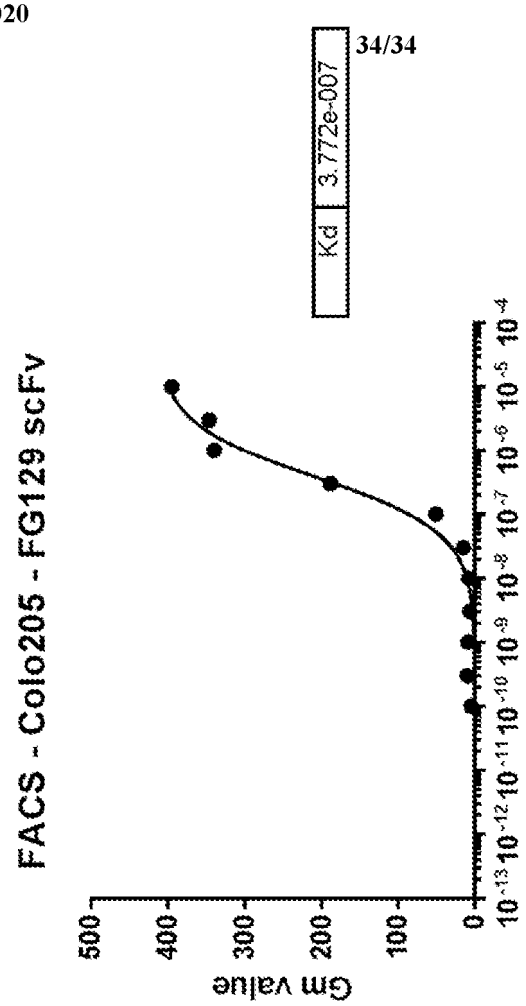


Figure 13c

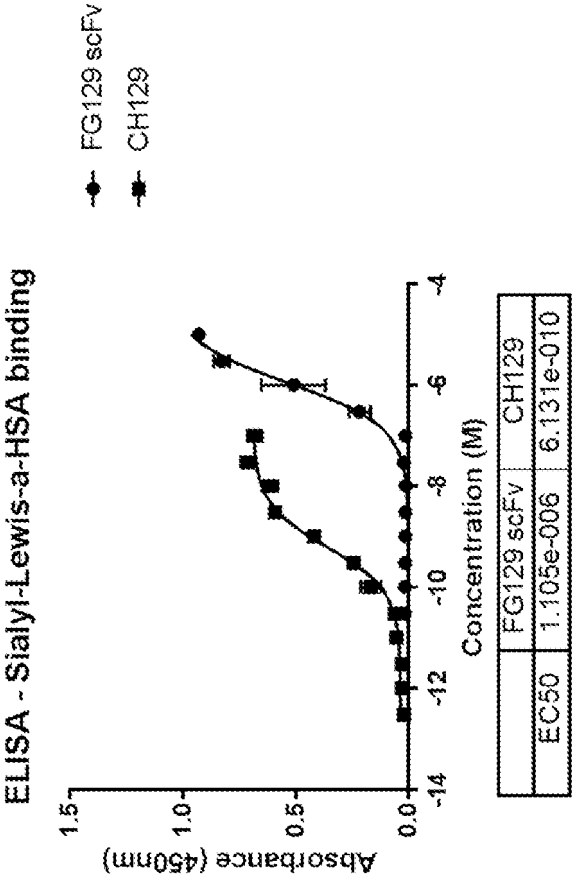


Figure 13b