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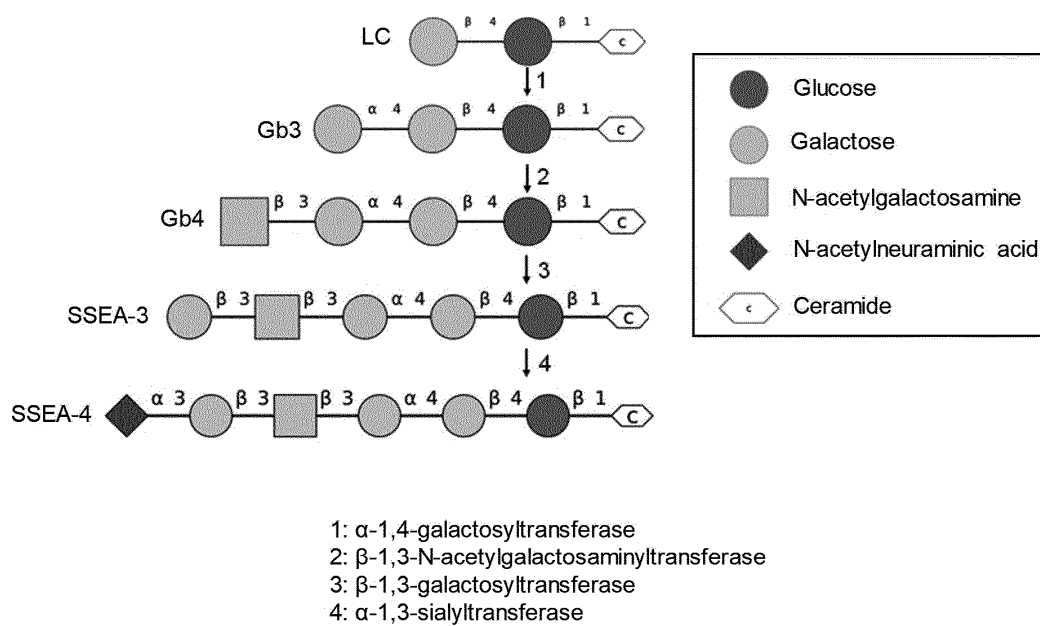


Fig. 1

**Schematic diagram of the generation of SSEA-3 and SSEA-4 glycans from lactosylceramide (LC).**

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A

FG28/11/72 heavy chain versus germline (Musmus IGHV2-3\*01)

```

<-----FR1 - IMGT-----
      1       5       10       15
      Q   V   Q   L   K   E   S   G   P       G   L   V   A   P
FG28_11H cag gtg cag ctg aag gag tca gga cct ... ggc ctg gtg gcg ccc
Germline --- -- -- -- -- -- -- -- -- -- -- -- -- -- -- --

```

```

----->-----
    20 25 30
      S   Q   S   L   S   I   T   C   T   V   S   G   F   S   L
FG28_11H tca cag agc ctg tcc atc aca tgc act gtc tca ggg ttc tca tta
Germline --- -- -- -- -- -- -- -- -- -- -- -- -- -- -- --

```

```

    CDR1 - IMGT
      35       40       45
      N   S   Y   G   V   S   W   V   R   Q   P
FG28_11H ... .. aac agt tat ggt gta agc tgg gtt cgc cag cct
Germline ... .. -c- --c -- -- -- -- -- -- -- -- -- --

```

```

      FR2 - IMGT ----->----- CDR2
      50       55       60
      P   G   K   G   L   E   W   L   G   V   I   W   G   D
FG28_11H cca gga aag ggt ctg gaa tgg ctg gga gta ata tgg ggt gac ...
Germline --- -- -- -- -- -- -g -- -- -- -- -- -- -- -- -- --

```

```

    - IMGT -----<-----
      65       70       75
      G   S   T   N   Y   H   S   A   L   M       S   R
FG28_11H ... .. ggg agc aca aat tat cat tca gct ctc atg ... tcc aga
Germline ... .. --a ... -- -- -- -- -- -- -- -- -- --

```

```

-----FR3 - IMGT-----
      80       85       90
      L   R   I   S   K   D   N   S   K   R   Q   V   F   L   K
FG28_11H ctg cgc atc agt aag gac aac tcc aag aga caa gtt ttc tta aaa
Germline --- a-- --c --t -- -- -- --c -- -- -- -- --

```

```

----->-----
      95       100       104
      L   N   S   L   Q   T   D   D   T   A   T   Y   Y   C   T
FG28_11H ctg aac agt ctg caa act gat gac aca gcc acg tac tac tgt acc
Germline --- -- -- -- -- -- -- -- -- -- -- -- -- -- -- A

```

```

    CDR3 - IMGT
      K   P   G   S   G   Y   A   F   A   Y   W   G   Q   G   T
FG28_11H aaa ccg ggc tcg ggc tac gcg ttt gct tac tgg ggc caa ggg act
Germline --- -- -- -- -- -- -- -- -- -- -- -- -- -- --

```

```

      L   V   T   V   S   S
FG28_11H ctg gtc act gtc tct tca

```

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# B

|             |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|             | FR1 - IMGT |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |  |
|             | 1          |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |  |
|             | E          | N   | V   | L   | T   | Q   | S   | P   | A   | I   | M   | S   | A   | S   | P   |  |
| FG28_11K    | gaa        | aat | gtt | ctc | acc | cag | tct | cca | gca | atc | atg | tct | gca | tct | cca |  |
| Germline    | ---        | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             |            |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |  |
|             | G          | E   | K   | V   | T   | M   | T   | C   | S   | A   | S   | S   | S   | V   |     |  |
| FG28_11K    | ggg        | gaa | aaa | gtc | acc | atg | acc | tgc | agt | gcc | agt | tca | agt | gtt | ... |  |
| Germline    | ---        | --- | -g  | --- | --- | --- | --- | --- | --- | --- | -c  | --- | --- | -a  | ... |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| CDR1 - IMGT |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             |            |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |  |
|             |            |     |     |     |     | N   | Y   | M   | H   | W   | Y   | Q   | Q   | K   |     |  |
| FG28_11K    | ...        | ... | ... | ... | ... | aat | tac | atg | cac | tgg | tac | cag | cag | aag |     |  |
| Germline    | ...        | ... | ... | ... | ... | S   | -g  | --- | --- | --- | --- | --- | --- | --- | --- |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| FR2 - IMGT  |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             |            |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |
|             | S          | S   | T   | S   | P   | K   | L   | W   | I   | Y   | D   | T   |     |     |     |  |
| FG28_11K    | tca        | agc | acc | tcc | ccc | aaa | ctc | tgg | att | tat | gac | aca | ... | ... | ... |  |
| Germline    | ---        | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| - IMGT      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             |            |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |
|             |            |     |     |     | S   | K   | L   | A   | S   | G   | V   | P   |     | G   | R   |  |
| FG28_11K    | ...        | ... | ... | ... | tcc | aaa | ctg | gct | tct | gga | gtc | cca | ... | ggt | cgc |  |
| Germline    | ...        | ... | ... | ... | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| FR3 - IMGT  |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             |            |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |
|             | F          | S   | G   | S   | G   |     |     | S   | G   | N   | S   | Y   | S   | L   | T   |  |
| FG28_11K    | ttc        | agt | ggc | agt | ggg | ... | ... | tct | gga | aac | tct | tac | tct | ctc | acg |  |
| Germline    | ---        | --- | --- | --- | --- | ... | ... | --- | --- | --- | --- | --- | --- | --- | --- |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             |            |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 104 |  |
|             | I          | R   | T   | M   | E   | A   | E   | D   | V   | A   | T   | Y   | F   | C   | F   |  |
| FG28_11K    | atc        | agg | acc | atg | gag | gct | gaa | gat | gtt | gcc | act | tat | ttc | tgt | ttt |  |
| Germline    | ---        | -c  | -g  | --- | --- | --- | --- | --- | --- | --- | --- | --- | -a  | --- | --- |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| CDR3 - IMGT |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             | Q          | A   | S   | G   | Y   | P   | L   | T   | F   | G   | G   | G   | T   | K   | L   |  |
| FG28_11K    | cag        | gcg | agt | ggg | tac | ccg | ctc | acg | ttc | ggt | ggt | ggg | acc | aag | ctg |  |
| Germline    | ---        | -g  | --- | --- | --- | -a  | --- | --- | --- | --- | --- | --- | --- | --- | --- |  |
| ----->      |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|             | E          | L   | K   |     |     |     |     |     |     |     |     |     |     |     |     |  |
| FG28_11K    | gag        | ctg | aaa | c   |     |     |     |     |     |     |     |     |     |     |     |  |

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**C** mlgG1 constant region (ALIGNMENT)

```

      A K T T P P S V Y P L A P G S A A Q T N
      GCTAAAACGACACCCCATCTGTCTATCCACTGGCCCCTGGTTCTGCTGCCCAAACCTAAC
1  -----!-----!-----!-----!-----!-----! 60
      CGATTTTGCTGTGGGGGTAGACAGATAGGTGACCGGGGACCAAGACGACGGGTTTGATTG

      S M V T L G C L V K G Y F P E P V T V T
      TCCATGGTGACCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACC
61 -----!-----!-----!-----!-----!-----! 120
      AGGTACCACTGGGACCCTACGGACCAGTTCGCGATAAAGGGACTCGGTCACTGTCACTGG

      W N S G S L S S G V H T F P A V L Q S D
      TGGAACTCTGGTTCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTGCAGTCTGAC
121 -----!-----!-----!-----!-----!-----! 180
      ACCTTGAGACCAAGGGACAGGTCGCCACACGTGTGGAAGGTCGACAGGACGTCAGACTG

      L Y T L S S S V T V P S S T W P S E T V
      CTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTC
181 -----!-----!-----!-----!-----!-----! 240
      GAGATGTGAGACTCGTCGAGTCACTGACAGGGGAGGTCGTGGACCGGGTCGCTCTGGCAG

      T C N V A H P A S S T K V D K K I V P R
      ACCTGCAACGTTGCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGG
241 -----!-----!-----!-----!-----!-----! 300
      TGGACGTTGCAACGGGTGGGCCGTCGTCGTGGTTCCACCTGTTCTTTAACACGGGTCC

      D C G C K P C I C T V P E V S S V F I F
      GATTGTGGTTGTAAGCCTTGTCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCTTC
301 -----!-----!-----!-----!-----!-----! 360
      CTAACACCAACATTTCGGAACGTATACATGTGAGGGTCTTCATAGTAGACAGAAGTAGAAG

      P P K P K D V L T I T L T P K V T C V V
      CCCCCAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTG
361 -----!-----!-----!-----!-----!-----! 420
      GGGGGTTTCGGGTTCCCTACACGAGTGGAATGAGACTGAGGATTCCAGTGACACAAACAC

      V D I S K D D P E V Q F S W F V D D V E
      GTAGACATCAGCAAGGATGATCCCAGGTCAGTTCAGCTGGTTTGTAGATGATGTGGAG
421 -----!-----!-----!-----!-----!-----! 480
      CATCTGTAGTCGTTCCCTACTAGGGCTCCAGGTCAAGTCGACCAACATCTACTACACCTC

      V H T A Q T Q P R E E Q F N S T F R S V
      GTGCACACAGCTCAGACGCAACCCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTC
481 -----!-----!-----!-----!-----!-----! 540
      CACGTGTGTCGAGTCTGCGTTGGGGCCCTCCTCGTCAAGTTGTCGTGAAAGGCGAGTCAG

      S E L P I M H Q D W L N G K E F K C R V
      AGTGAACCTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAGTTCAAATGCAGGGTC
541 -----!-----!-----!-----!-----!-----! 600
      TCACTTGAAGGGTAGTACGTGGTCCTGACCGAGTTACCGTTCCTCAAGTTTACGTCCCAG
```

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N S A A F P A P I E K T I S K T K G R P  
AACAGTGCAGCTTTCCCTGCCCCATCGAGAAAACCATCTCCAAAACCAAAGGCAGACCG  
601 -----!-----!-----!-----!-----!-----! 660  
TTGTCACGTCGAAAGGGACGGGGTAGCTCTTTGGTAGAGGTTTGGTTTCCGTCTGGC

K A P Q V Y T I P P P K E Q M A K D K V  
AAGGCTCCACAGGTGTACACCATTCACCTCCCAAGGAGCAGATGGCCAAGGATAAAGTC  
661 -----!-----!-----!-----!-----!-----! 720  
TTCCGAGGTGTCCACATGTGGTAAGGTGGAGGGTTCCTCGTCTACCGGTTCTATTTCAG

S L T C M I T D F F P E D I T V E W Q W  
AGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACTGTGGAGTGGCAGTGG  
721 -----!-----!-----!-----!-----!-----! 780  
TCAGACTGGACGTACTATTGTCTGAAGAAGGGACTTCTGTAATGACACCTCACCGTCACC

N G Q P A E N Y K N T Q P I M D T D G S  
AATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGCCCATCATGGACACAGATGGCTCT  
781 -----!-----!-----!-----!-----!-----! 840  
TTACCCGTCGGTCGCCTCTTGATGTTCTTGAGTGGGTAGTACCTGTGTCTACCGAGA

Y F V Y S K L N V Q K S N W E A G N T F  
TACTTCGTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAGGCAGGAAATACTTTC  
841 -----!-----!-----!-----!-----!-----! 900  
ATGAAGCAGATGTCGTTTCGAGTTACACGTCTTCTCGTTGACCCTCCGTCCTTTATGAAAG

T C S V L H E G L H N H H T E K S L S H  
ACCTGCTCTGTGTACATGAGGGCCTGCACAACCACCATCTGAGAAGAGCCTCTCCCAC  
901 -----!-----!-----!-----!-----!-----! 960  
TGGACGAGACACAATGTACTCCCGGACGTGTTGGTGGTATGACTCTTCTCGGAGAGGGTG

S P G K  
TCTCCTGGTAAA  
961 -----!-- 972  
AGAGGACCATT

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**D** **hlgG2 constant region (ALIGNMENT)**

```
A S T K G P S V F P L A P C S R S T S E
GCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG
1 -----!-----!-----!-----!-----!-----! 60
CGAAGGTGGTTCCCGGGTAGCCAGAAGGGGGACCGCGGGACGAGGTCCTCGTGGAGGCTC

S T A A L G C L V K D Y F P E P V T V S
AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG
61 -----!-----!-----!-----!-----!-----! 120
TCGTGTCGCCGGGACCCGACGGACCAGTTCTGATGAAGGGGCTTGCCCACTGCCACAGC

W N S G A L T S G V H T F P A V L Q S S
TGGAAGTCAGGCGCTCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCA
121 -----!-----!-----!-----!-----!-----! 180
ACCTTGAGTCCGCGAGACTGGTCGCCGCACGTGTGAAGGGCCGACAGGATGTCAGGAGT

G L Y S L S S V V T V P S S N F G T Q T
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC
181 -----!-----!-----!-----!-----!-----! 240
CCTGAGATGAGGGAGTCGTTCGCCCACTGGCACGGGAGGTCGTTGAAGCCGTGGGTCTGG

Y T C N V D H K P S N T K V D K T V E R
TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGC
241 -----!-----!-----!-----!-----!-----! 300
ATGTGGACGTTGCATCTAGTGTTCGGGTCGTTGTGGTTCCACCTGTTCTGTCAACTCGCG

K C C V E C P P C P A P P V A G P S V F
AAATGTTGTGTCGAGTGCCACCGTGCCACGACCACTGTGGCAGGACCGTCAGTCTTC
301 -----!-----!-----!-----!-----!-----! 360
TTTACAACACAGCTCACGGGTGGCACGGGTCGTGGTGGACACCGTCCTGGCAGTCAGAAG

L F P P K P K D T L M I S R T P E V T C
CTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACGTGC
361 -----!-----!-----!-----!-----!-----! 420
GAGAAGGGGGGTTTGGGTTCCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGCACG

V V V D V S H E D P E V Q F N W Y V D G
GTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC
421 -----!-----!-----!-----!-----!-----! 480
CACCACCACCTGCACTCGGTGCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTGCCG

V E V H N A K T K P R E E Q F N S T F R
GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCTG
481 -----!-----!-----!-----!-----!-----! 540
CACCTCCACGTATTACGGTTCTGTTTCGGTGCCCTCCTCGTCAAGTTGTCGTGCAAGGCA

V V S V L T V V H Q D W L N G K E Y K C
GTGGTCAGCGTCTCACCCTCGTGCACCAAGGACTGGCTGAACGGCAAGGAGTACAAGTGC
541 -----!-----!-----!-----!-----!-----! 600
CACCAGTCGCAGGAGTGGCAGCACGTGGTCCTGACCGACTTGCCGTTCTCATGTTACAG
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K V S N K G L P A P I E K T I S K T K G  
AAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGG  
601 -----!-----!-----!-----!-----!-----! 660  
TTCCAGAGGTTGTTTCCGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTTGGTTTCCC

Q P R E P Q V Y T L P P S R E E M T K N  
CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAAC  
661 -----!-----!-----!-----!-----!-----! 720  
GTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTCCTCTACTGGTTCTTG

Q V S L T C L V K G F Y P S D I A V E W  
CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGG  
721 -----!-----!-----!-----!-----!-----! 780  
GTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACC

E S N G Q P E N N Y K T T P P M L D S D  
GAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACACCTCCCATGCTGGACTCCGAC  
781 -----!-----!-----!-----!-----!-----! 840  
CTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGCTGTGGAGGGTACGACCTGAGGCTG

G S F F L Y S K L T V D K S R W Q Q G N  
GGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC  
841 -----!-----!-----!-----!-----!-----! 900  
CCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTG

V F S C S V M H E A L H N H Y T Q K S L  
GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC  
901 -----!-----!-----!-----!-----!-----! 960  
CAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAG

S L S P G K  
TCCCTGTCTCCGGGTAAA  
961 -----!----- 978  
AGGGACAGAGGCCCATTT

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**E** hlgG1 constant region (ALIGNMENT)

```

  A S T K G P S V F P L A P S S K S T S G
GCTTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG
1  -----!-----!-----!-----!-----!-----! 60
  CGAAGGTGGTTCCTGGGTAGCCAGAAGGGGGACCGTGGGAGGAGGTTCTCGTGGAGACCC

  G T A A L G C L V K D Y F P E P V T V S
GGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTG
61  -----!-----!-----!-----!-----!-----! 120
  CCGTGTCTGCCGGGACCCGACGGACCAGTTTCTGATGAAGGGGCTTGCCCACTGCCACAGC

  W N S G A L T S G V H T F P A V L Q S S
TGGAAGTCAAGGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCA
121  -----!-----!-----!-----!-----!-----! 180
  ACCTTGAGTCCGCGGGACTGGTCGCCGCACGTGTGAAGGGCCGACAGGATGTCAGGAGT

  G L Y S L S S V V T V P S S S L G T Q T
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTGGGGACCCAGACC
181  -----!-----!-----!-----!-----!-----! 240
  CCTGAGATGAGGGAGTCGTTCGCCCACTGGCACGGGAGGTCGTCGAACCCGTGGGTCTGG

  Y I C N V N H K P S N T K V D K K V E P
TACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCC
241  -----!-----!-----!-----!-----!-----! 300
  ATGTAGACGTTGCACTTAGTGTTCGGGTCGTTGTGGTTCCACCTGTTCTTTCAACTCGGG

  K S C D K T H T C P P C P A P E L L G G
AAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA
301  -----!-----!-----!-----!-----!-----! 360
  TTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCT

  P S V F L F P P K P K D T L M I S R T P
CCGTCACTCTTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCT
361  -----!-----!-----!-----!-----!-----! 420
  GGCAGTCAGAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGA

  E V T C V V V D V S H E D P E V K F N W
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGG
421  -----!-----!-----!-----!-----!-----! 480
  CTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACC

  Y V D G V E V H N A K T K P R E E Q Y N
TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
481  -----!-----!-----!-----!-----!-----! 540
  ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG

  S T Y R V V S V L T V L H Q D W L N G K
AGCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAG
541  -----!-----!-----!-----!-----!-----! 600
  TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTC
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E Y K C K V S N K A L P A P I E K T I S  
GAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCC  
601 -----!-----!-----!-----!-----!-----! 660  
CTCATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGG

K A K G Q P R E P Q V Y T L P P S R D E  
AAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG  
661 -----!-----!-----!-----!-----!-----! 720  
TTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTC

L T K N Q V S L T C L V K G F Y P S D I  
CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC  
721 -----!-----!-----!-----!-----!-----! 780  
GACTGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAG

A V E W E S N G Q P E N N Y K T T P P V  
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTG  
781 -----!-----!-----!-----!-----!-----! 840  
CGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCAC

L D S D G S F F L Y S K L T V D K S R W  
CTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGG  
841 -----!-----!-----!-----!-----!-----! 900  
GACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACC

Q Q G N V F S C S V M H E A L H N H Y T  
CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG  
901 -----!-----!-----!-----!-----!-----! 960  
GTCGTCCCCTTG CAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGC

Q K S L S L S P G K  
CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA  
961 -----!-----!-----! 990  
GTCTTCTCGGAGAGGGACAGAGGCCCATTT

10/65

**F** Murine Kappa constant region (ALIGNMENT)

```

      R A D A A P T V S I F P P S S E Q L T S
CGTGCAGATGCTGCACCAACTGTATCGATCTTCCCACCATCCAGTGAGCAGTTAACATCT
1  -----!-----!-----!-----!-----!-----! 60
      GCACGTCTACGACGTGGTTGACATAGCTAGAAGGGTGGTAGGTCACTCGTC AATTGTAGA

      G G A S V V C F L N N F Y P K D I N V K
GGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACCTTCTACCCCAAAGACATCAATGTCAAG
61 -----!-----!-----!-----!-----!-----! 120
      CCTCCACGGAGTCAGCACACGAAGAACTTGTTGAAGATGGGGTTTCTGTAGTTACAGTTC

      W K I D G S E R Q N G V L N S W T D Q D
TGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGAC
121 -----!-----!-----!-----!-----!-----! 180
      ACCTTCTAACTACCGTCACTTGCTGTTTTACCGCAGGACTTGTC AACCTGACTAGTCCTG

      S K D S T Y S M S S T L T L T K D E Y E
AGCAAAGACAGCACCTACAGCATGAGCAGCACCCCTCACGTTGACCAAGGACGAGTATGAA
181 -----!-----!-----!-----!-----!-----! 240
      TCGTTTCTGTCGTGGATGTCGTACTCGTCGTGGGAGTGCAACTGGTTCCTGCTCATACTT

      R H N S Y T C E A T H K T S T S P I V K
CGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCTACTTCACCCATTGTCAAG
241 -----!-----!-----!-----!-----!-----! 300
      GCTGTATTGTCGATATGGACACTCCGGTGAGTGTTCTGTAGATGAAGTGGGTAACAGTTC

      S F N R N E C
AGCTTCAACAGGAATGAGTGT
301 -----!-----!- 321
      TCGAAGTTGTCCTTACTCACA
```

11/65

**G Human Kappa constant region (ALIGNMENT)**

```

      R T V A A P S V F I F P P S D E Q L K S
CGTACGGTAGCGGCCCCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCT
1  -----!-----!-----!-----!-----!-----! 60
      GCATGCCATCGCCGGGGTAGACAGAAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGA

      G T A S V V C L L N N F Y P R E A K V Q
GGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG
61  -----!-----!-----!-----!-----!-----! 120
      CCTTGACGGAGACAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTC

      W K V D N A L Q S G N S Q E S V T E Q D
TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGAG
121 -----!-----!-----!-----!-----!-----! 180
      ACCTTCCACCTATTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTG

      S K D S T Y S L S S T L T L S K A D Y E
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAG
181 -----!-----!-----!-----!-----!-----! 240
      TCGTTCCTGTCTGCGGATGTCTGGAGTCGTCTGGGACTGCGACTCGTTTCGTCTGATGCTC

      K H K V Y A C E V T H Q G L S S P V T K
AAACACAAAGTCTACGCCTGCGAAGTCACCCACCAGGGCCTGAGCTCGCCCGTCACAAAG
241 -----!-----!-----!-----!-----!-----! 300
      TTTGTGTTTCAGATGCGGACGCTTCAGTGGGTGGTCCCGGACTCGAGCGGGCAGTGTTTC

      S F N R G E C
AGCTTCAACAGGGGAGAGTGT
301 -----!-----!- 321
      TCGAAGTTGTCCCCTCTCACA

```

**Fig. 2**

**Amino acid and nucleotide sequence of the FG2811.72 IgG3 heavy and kappa light chain variable regions and mIgG1, hIgG1 and hIgG2 constant regions and human and mouse kappa constant regions.**

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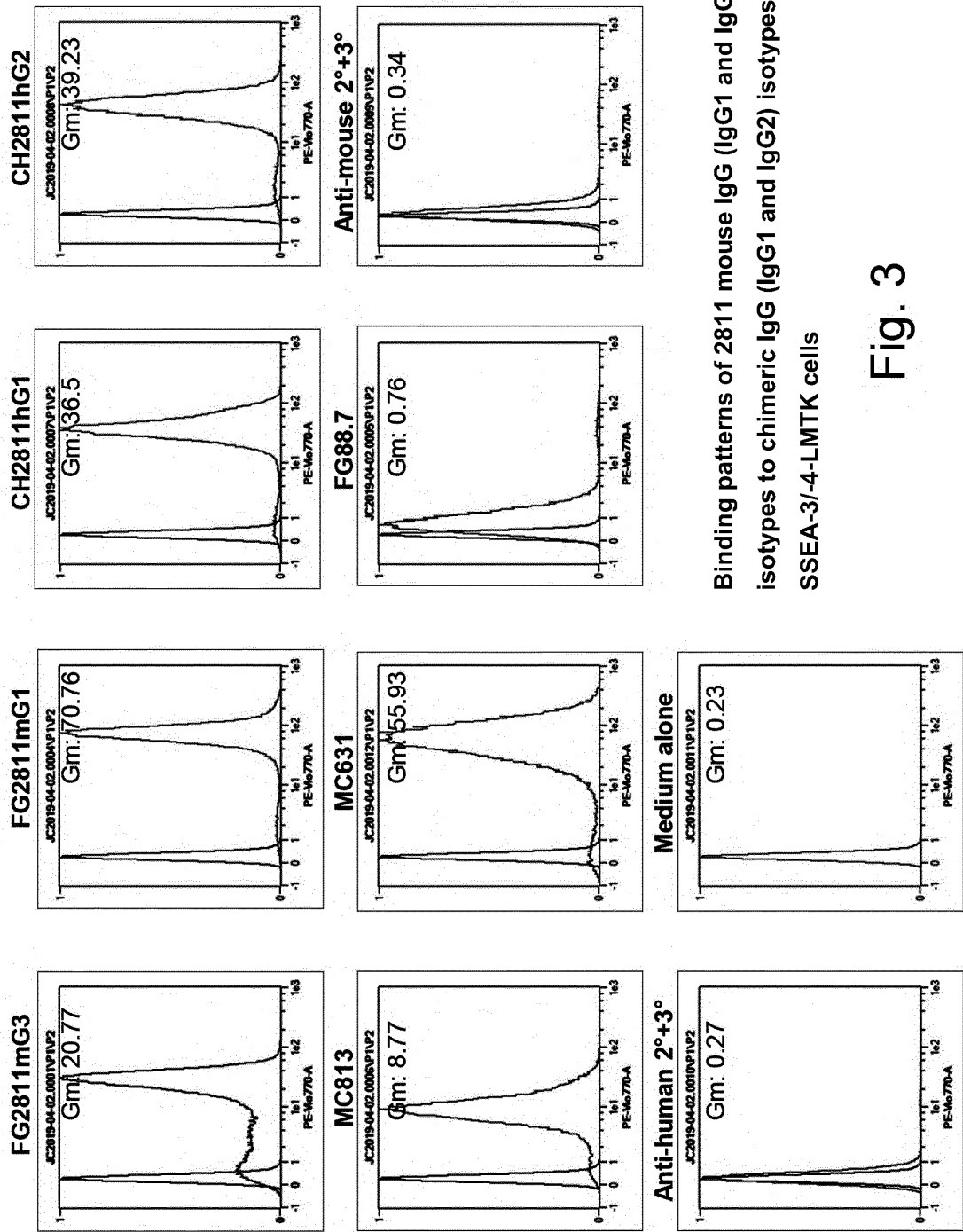


Fig. 3

Binding patterns of 2811 mouse IgG (IgG1 and IgG2) isotypes to chimeric IgG (IgG1 and IgG2) isotypes to SSEA-3/-4-LMTK cells

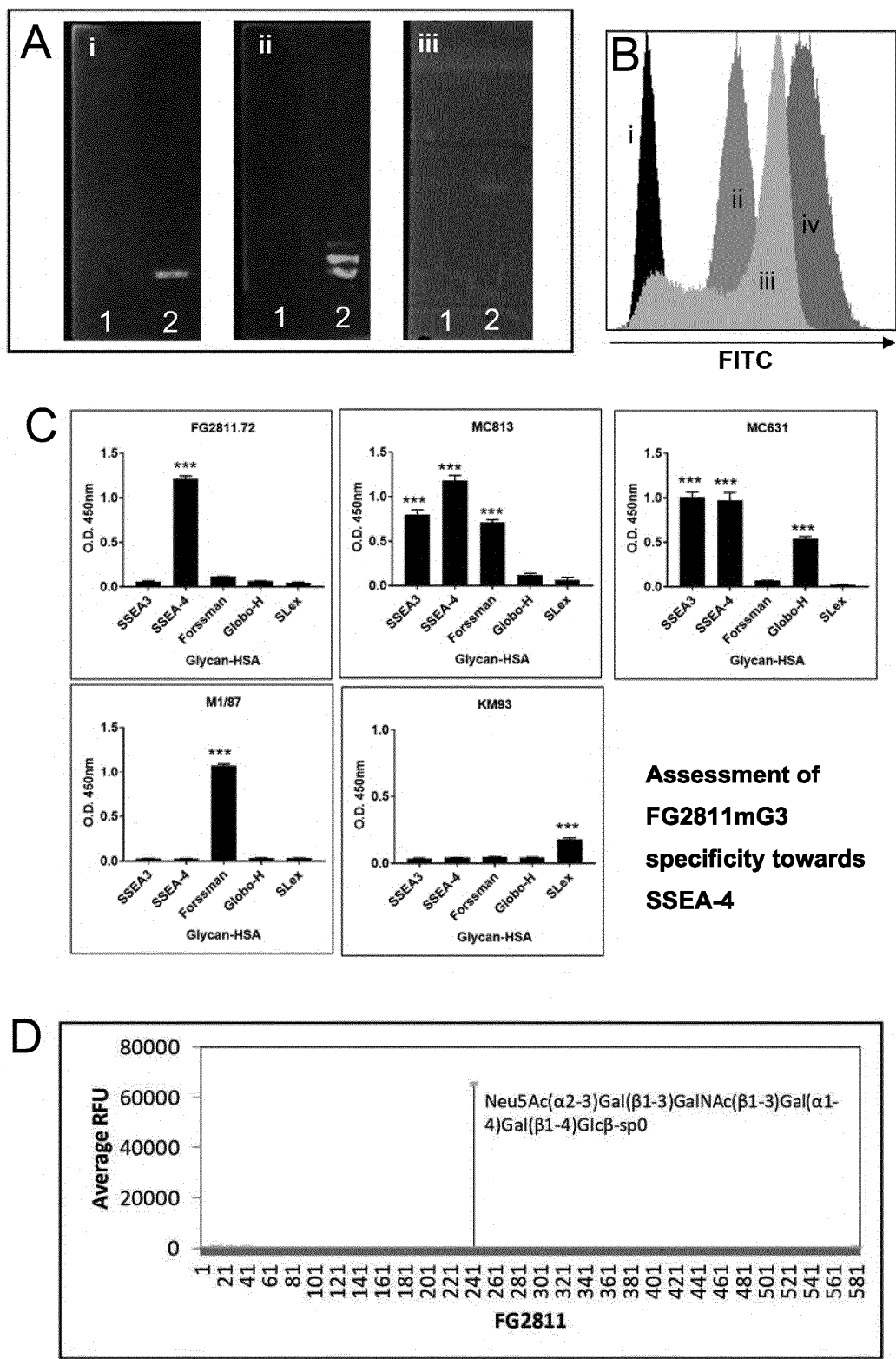
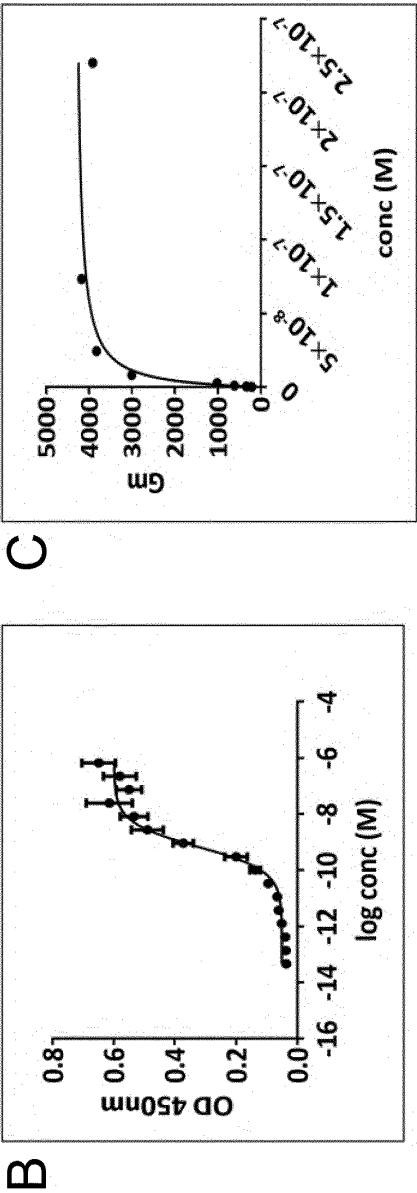
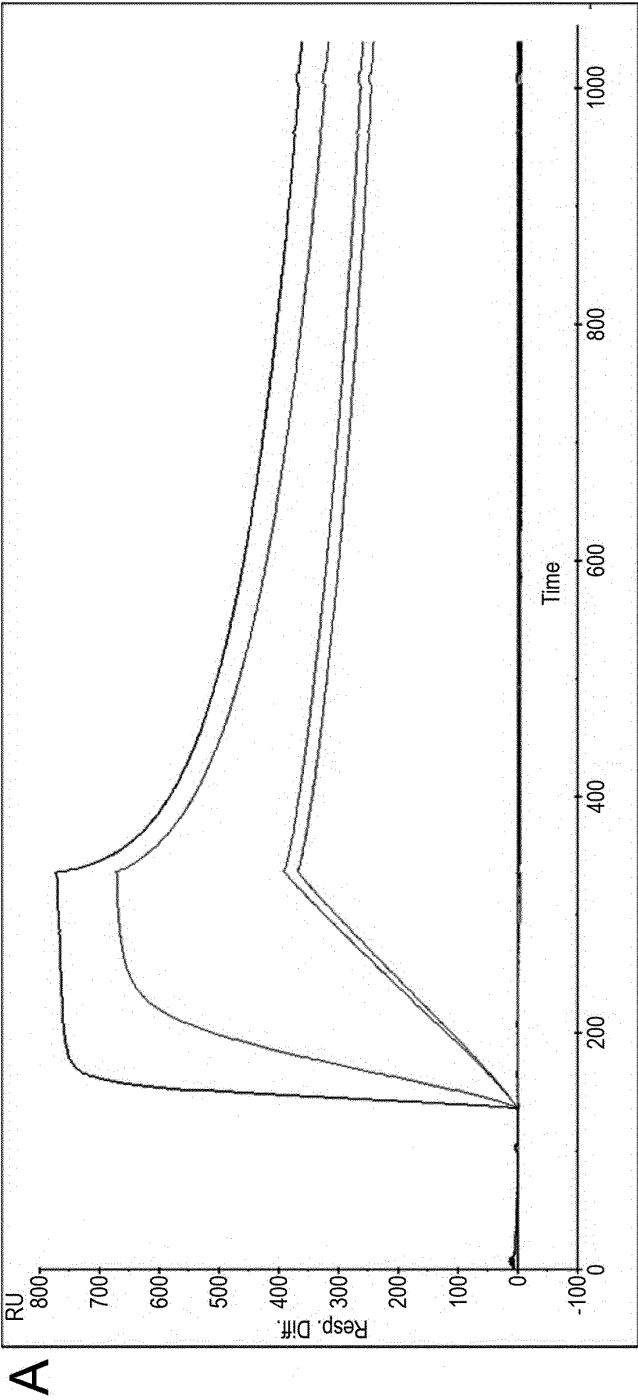
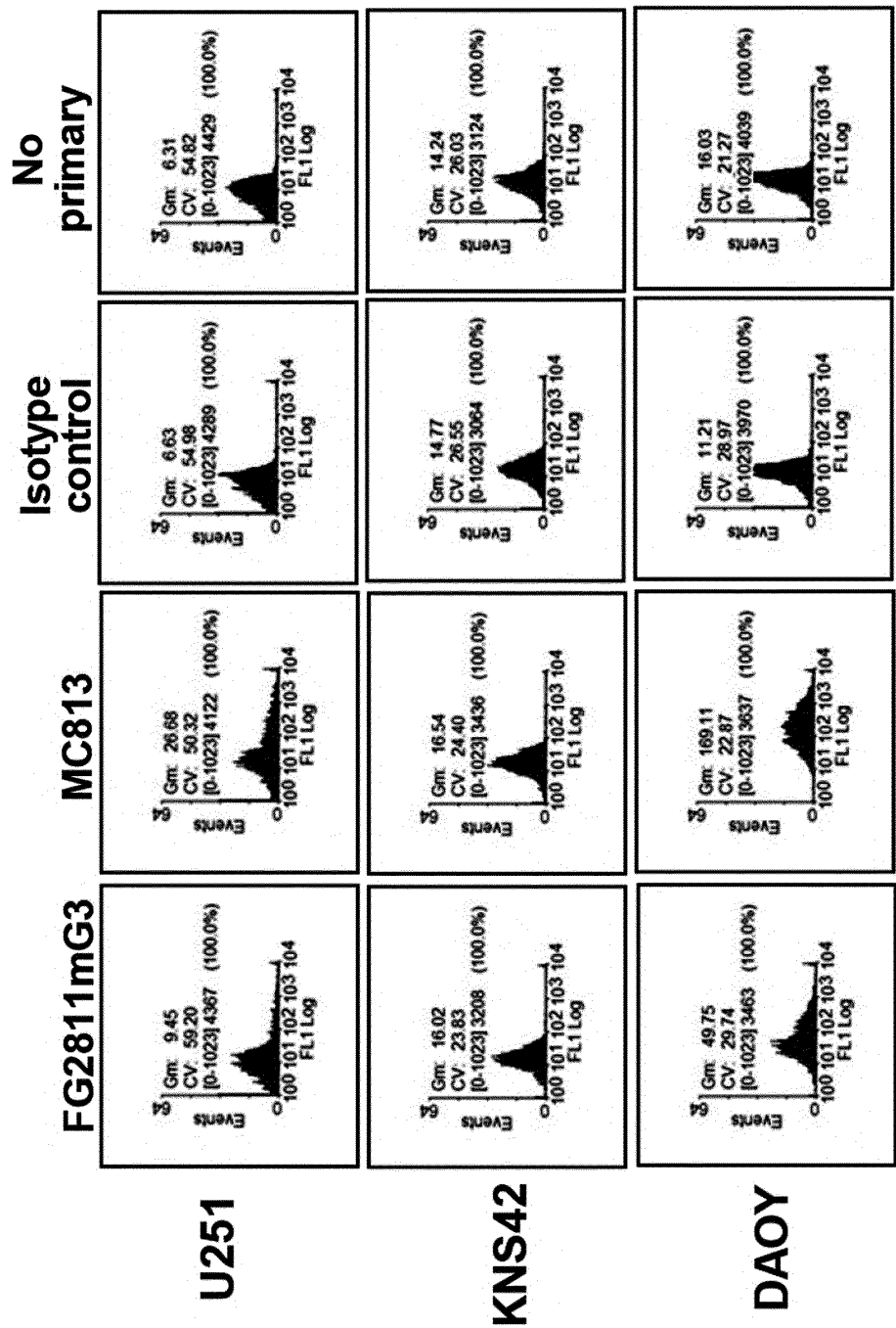


Fig. 4  
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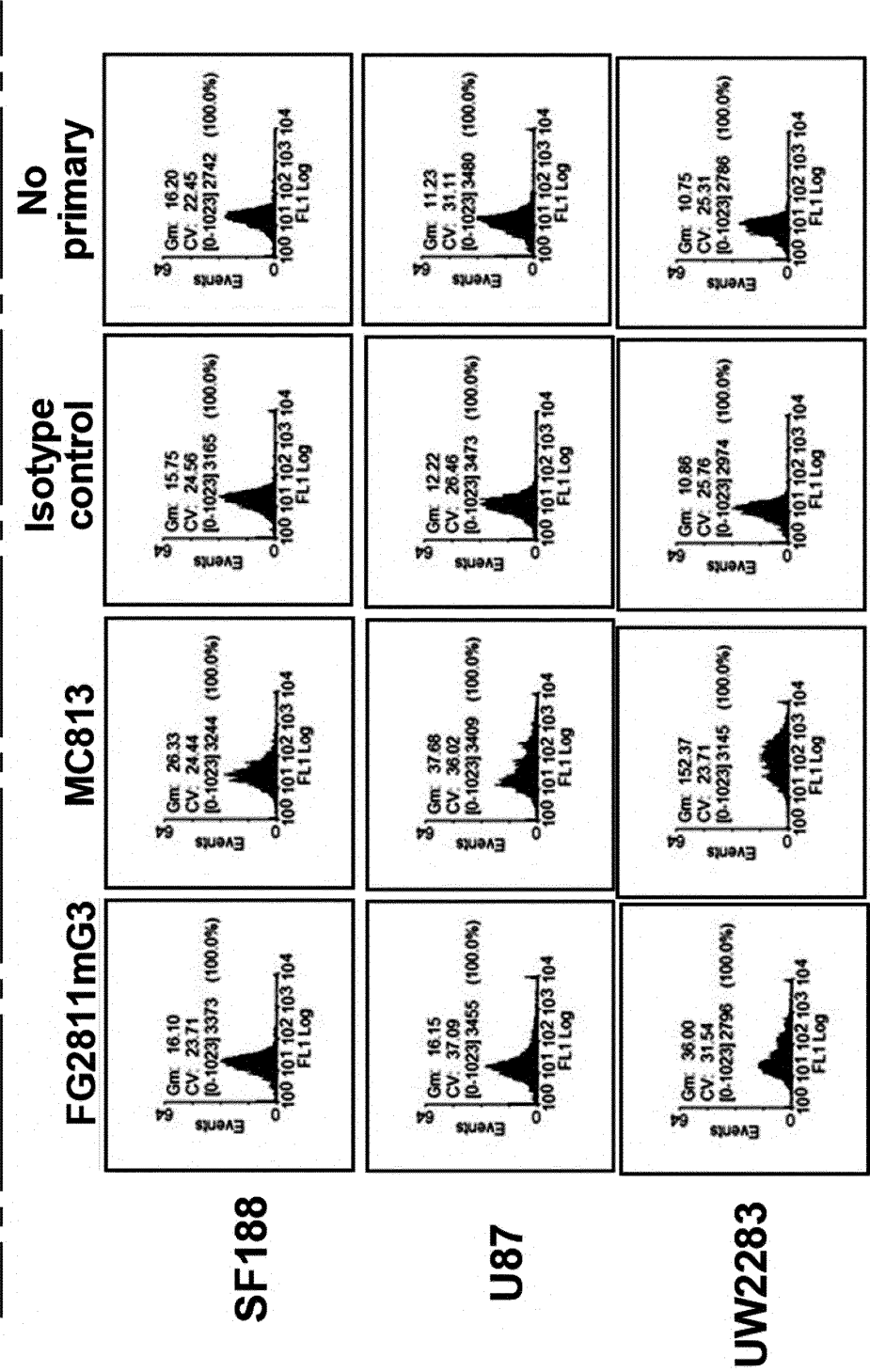
Assessment of  
FG2811mG3 affinity  
against antigen

Fig. 5



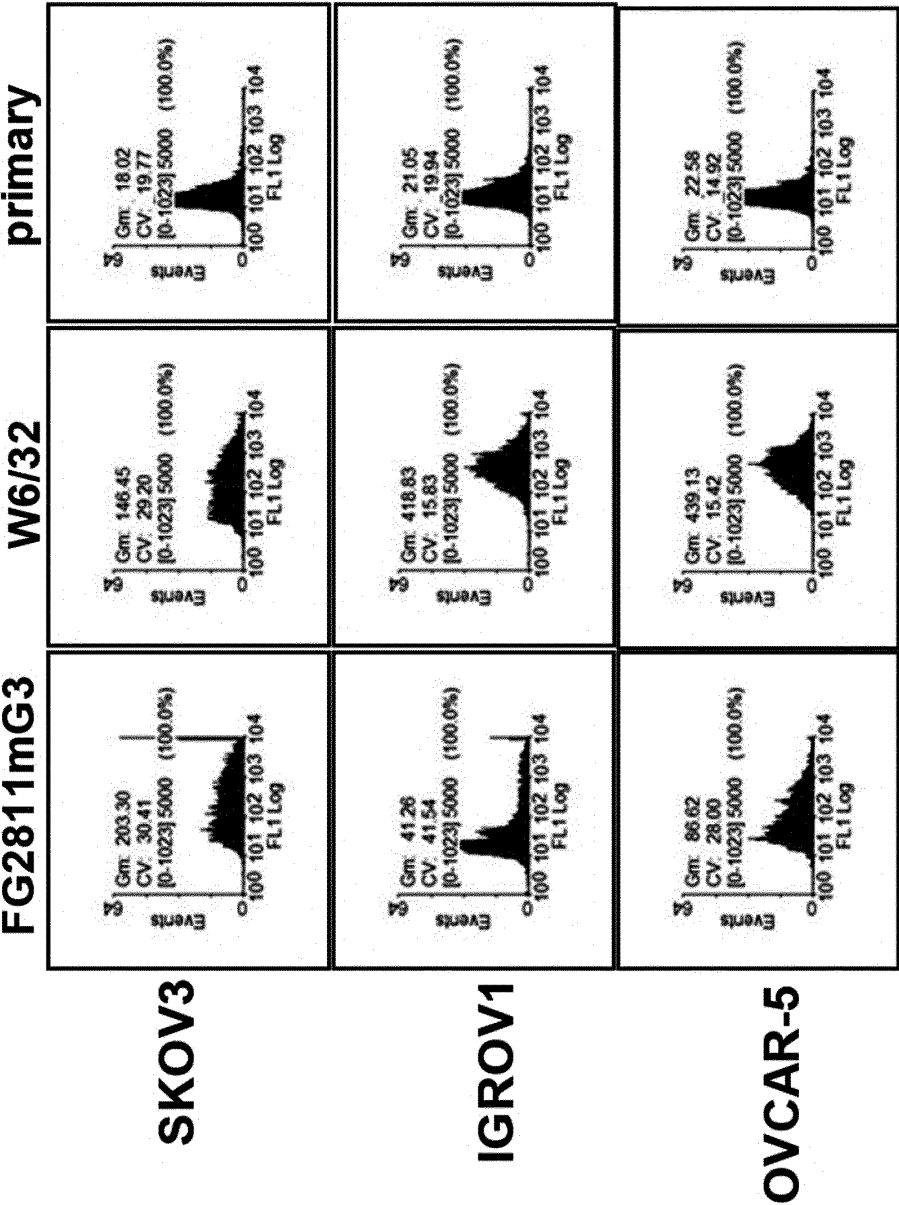
Binding of FG2811mG3 antibody to a panel of human cancer cell lines

Fig. 6A



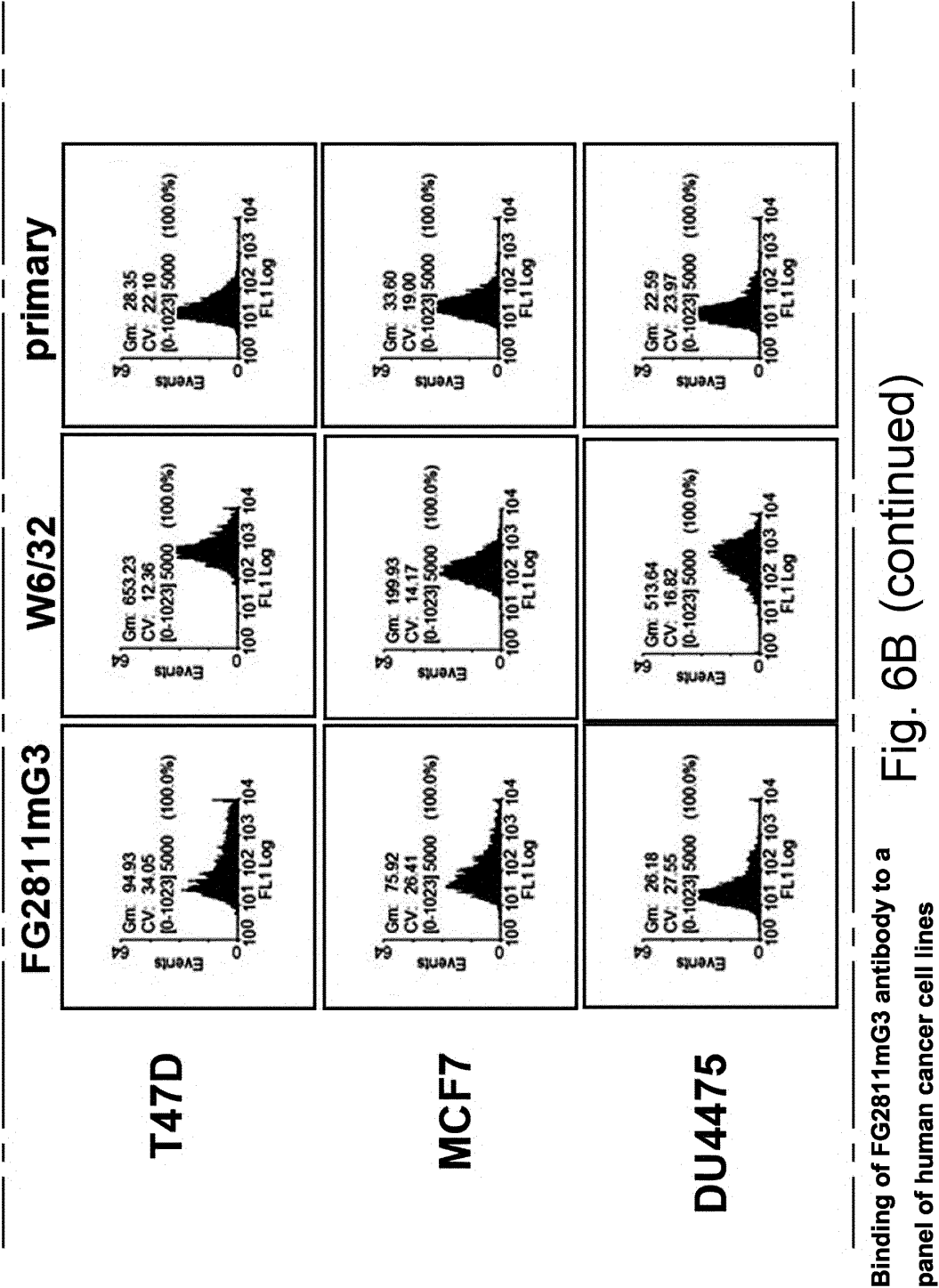
Binding of FG2811mG3 antibody to a panel of human cancer cell lines

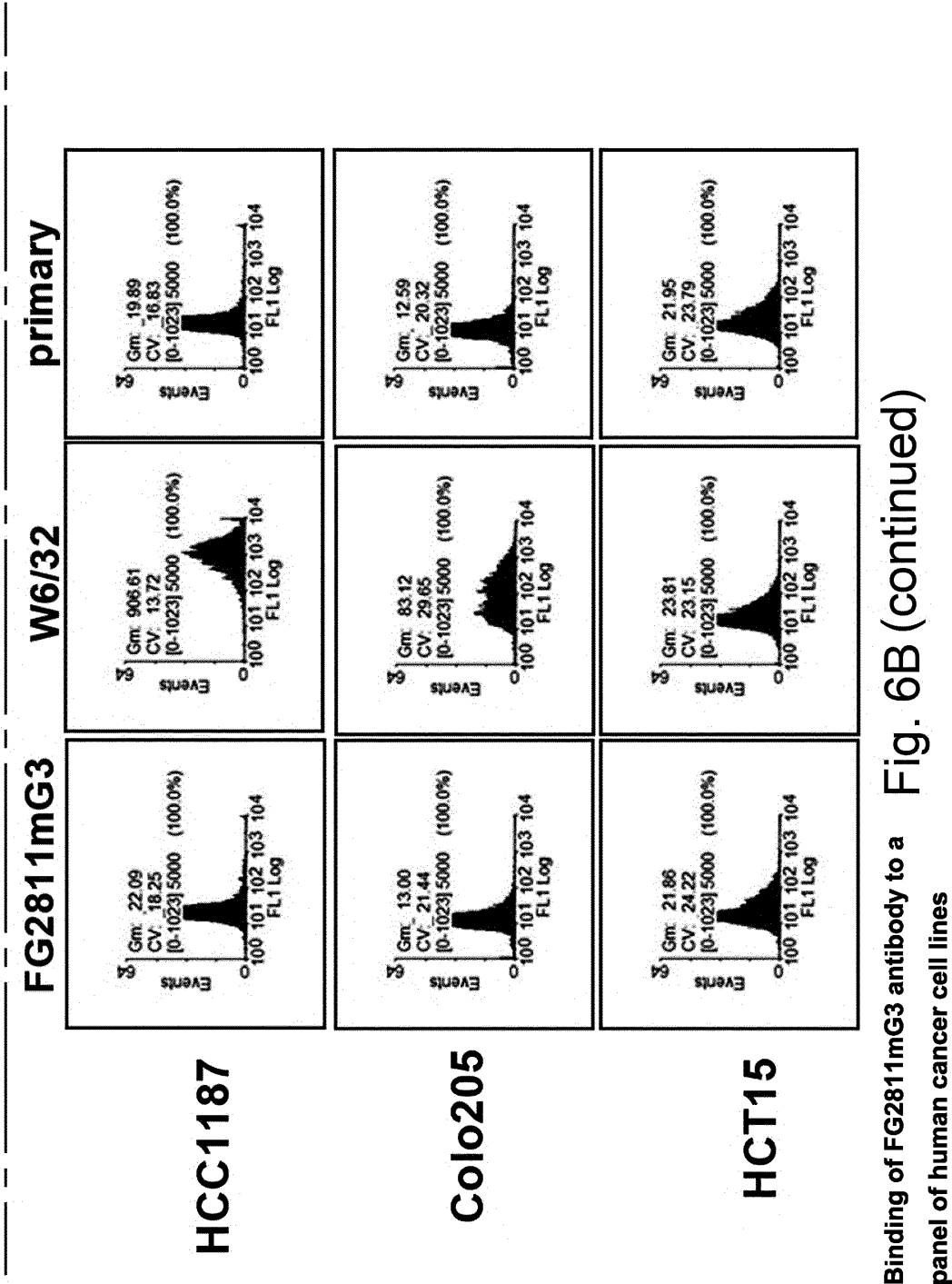
Fig. 6A (continued)

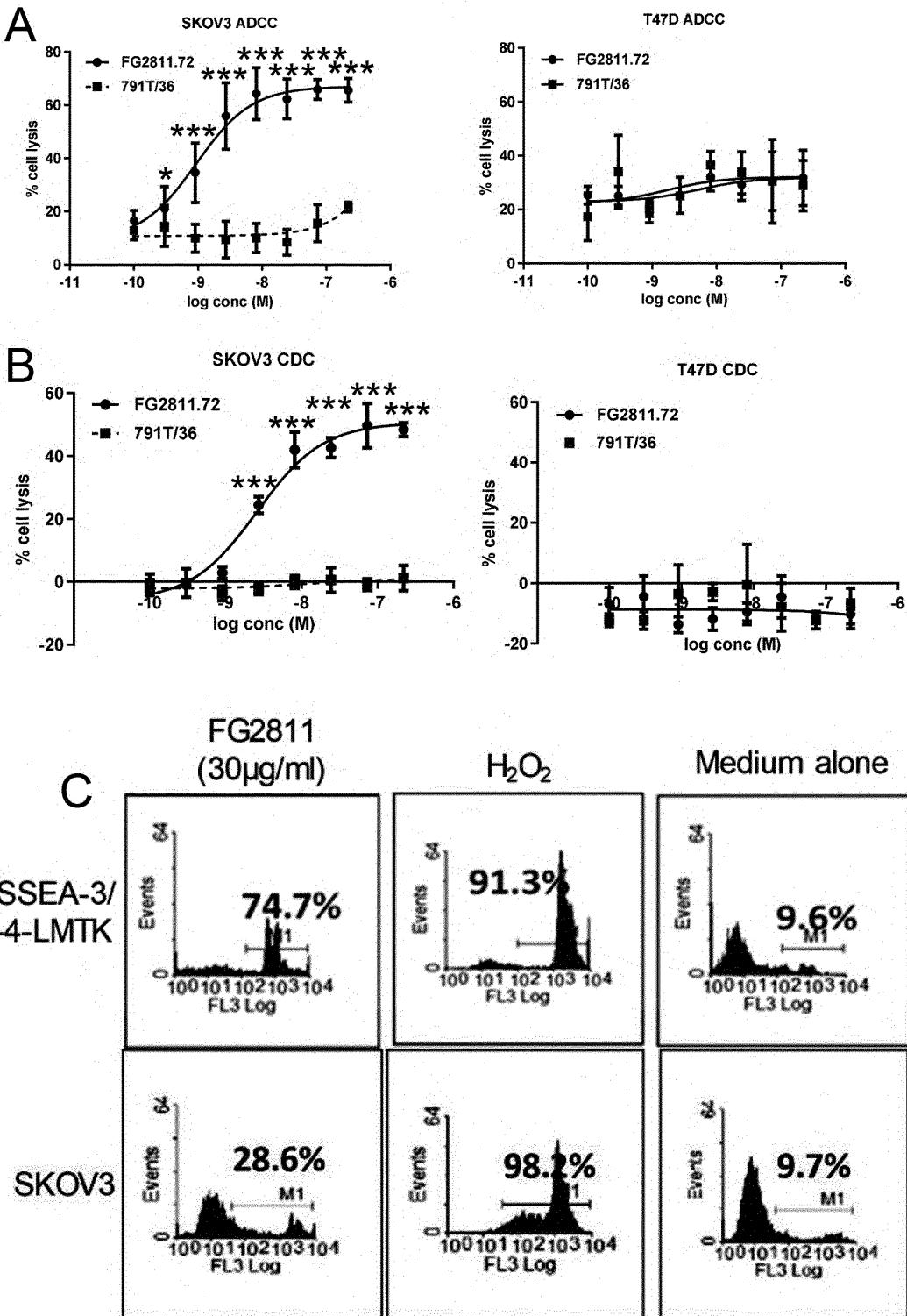


Binding of FG2811mG3 antibody to a panel of human cancer cell lines

Fig. 6B

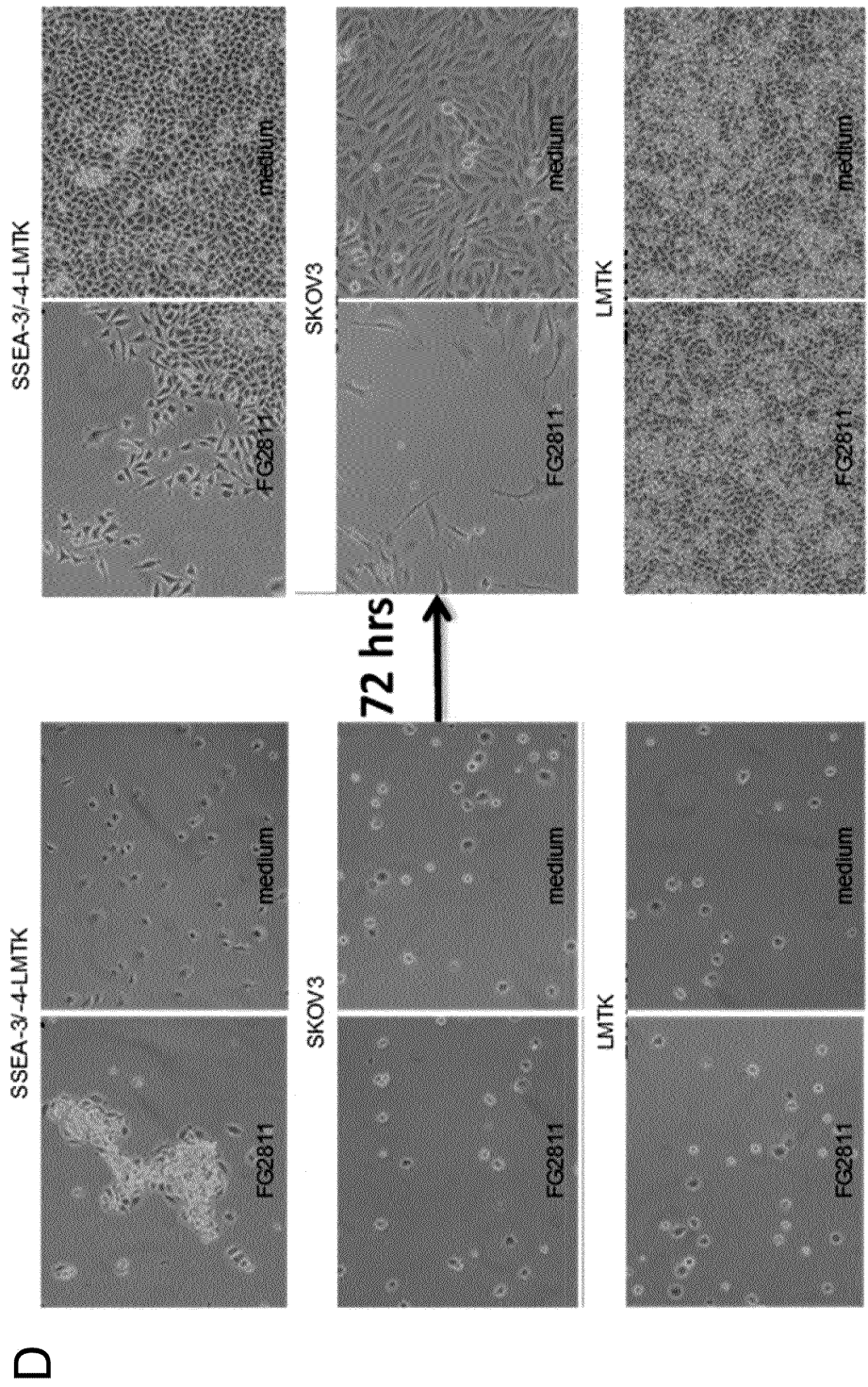






Cytotoxic activity of FG2811mG3 antibody

Fig. 7



**Fig. 7**  
**(continued)**

**Cytotoxic activity of FG2811mG3 antibody**

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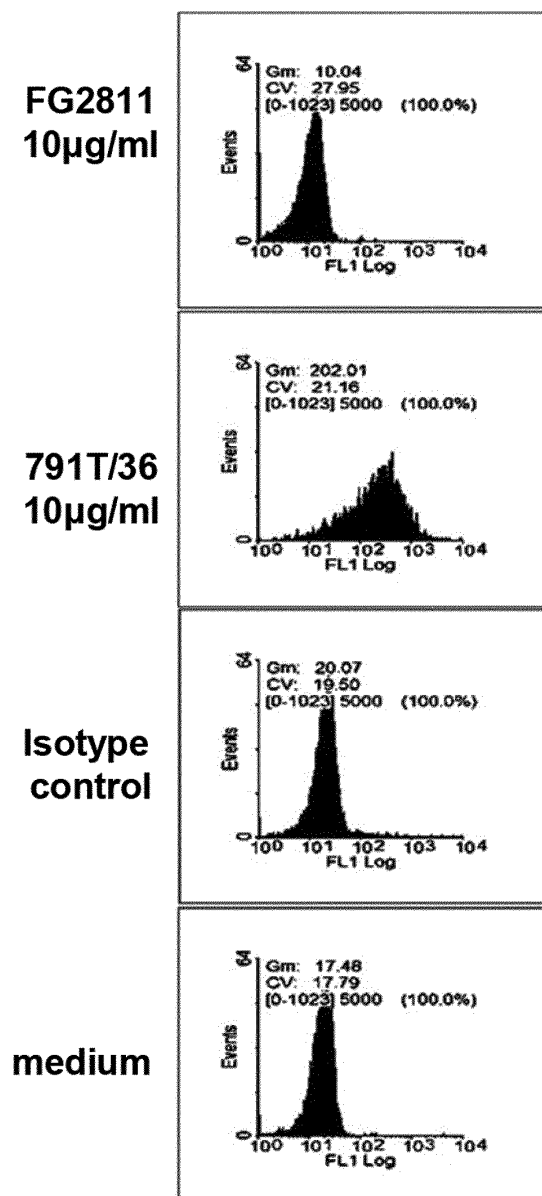
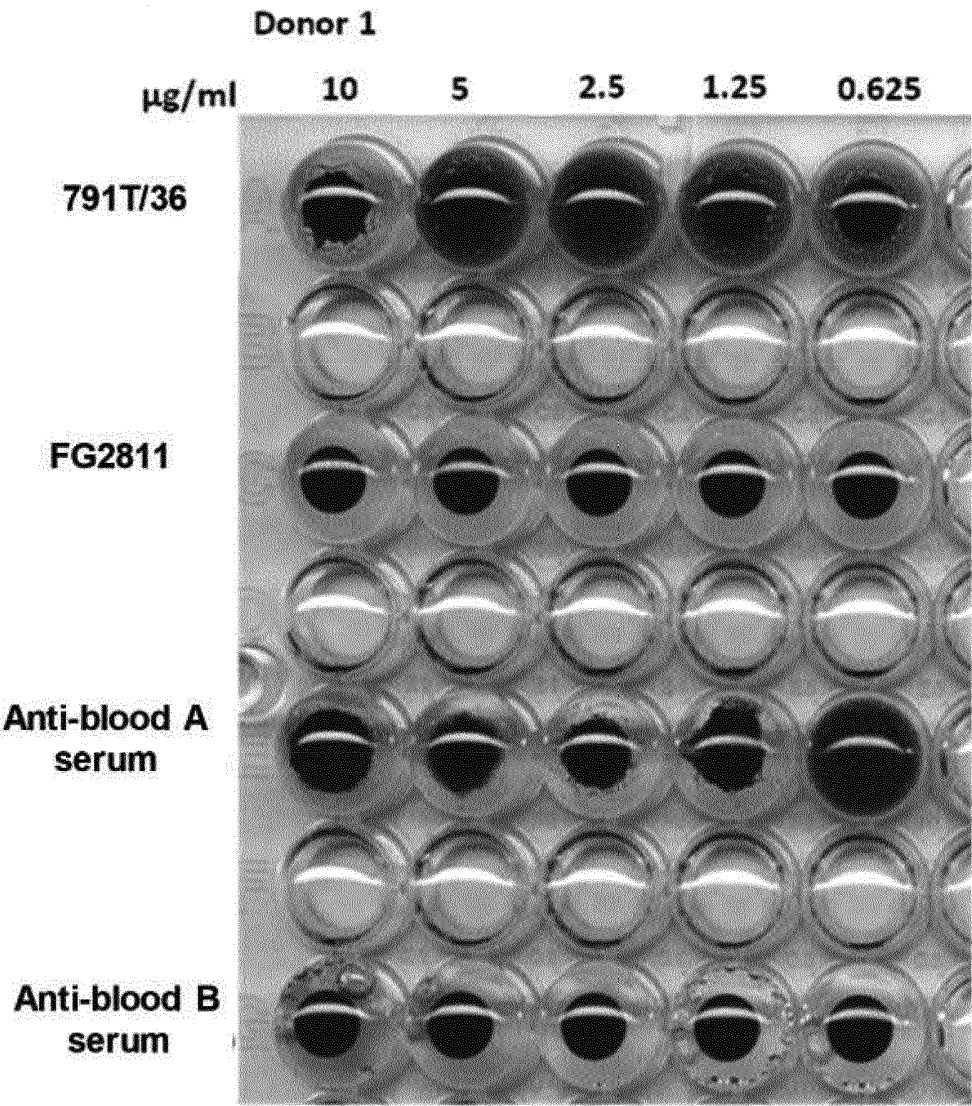


Fig. 8A

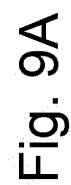
Frozen normal human tissue staining and normal erythrocyte binding

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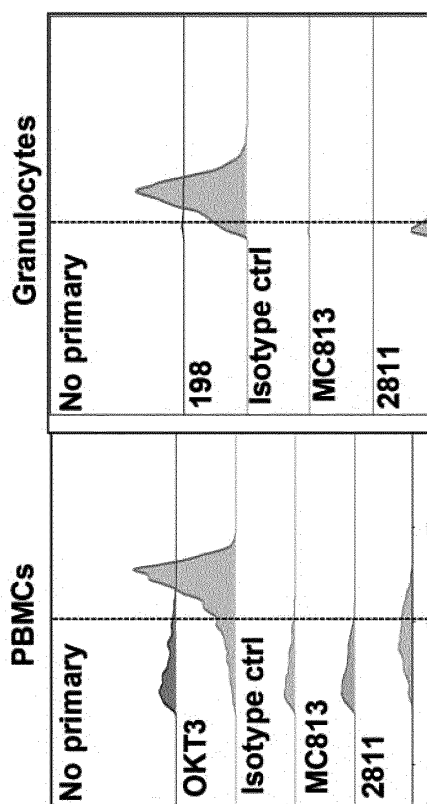


**Fig. 8B**

**Frozen normal human tissue staining and normal erythrocyte binding**



| Donor | Frequency of 2811+ PBMCs in healthy donor whole blood (%) |
|-------|-----------------------------------------------------------|
| BD3   | 2.30                                                      |
| BD13  | 0.80                                                      |
| BD18  | 2.30                                                      |
| BD27  | 1.40                                                      |
| BD38  | 1.50                                                      |
| BD96  | 0.80                                                      |
| BD31  | 1.01                                                      |



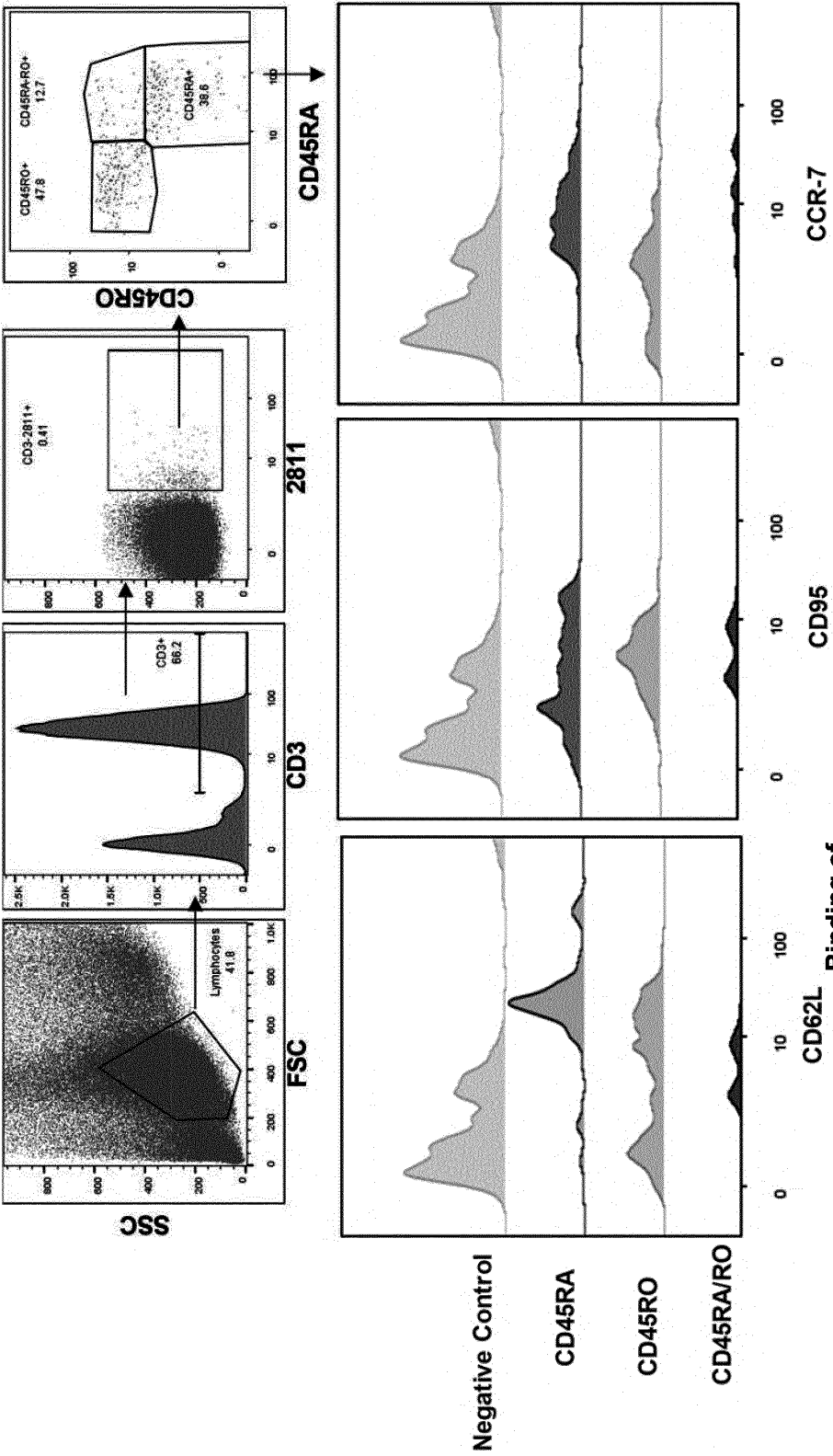


Fig. 9B

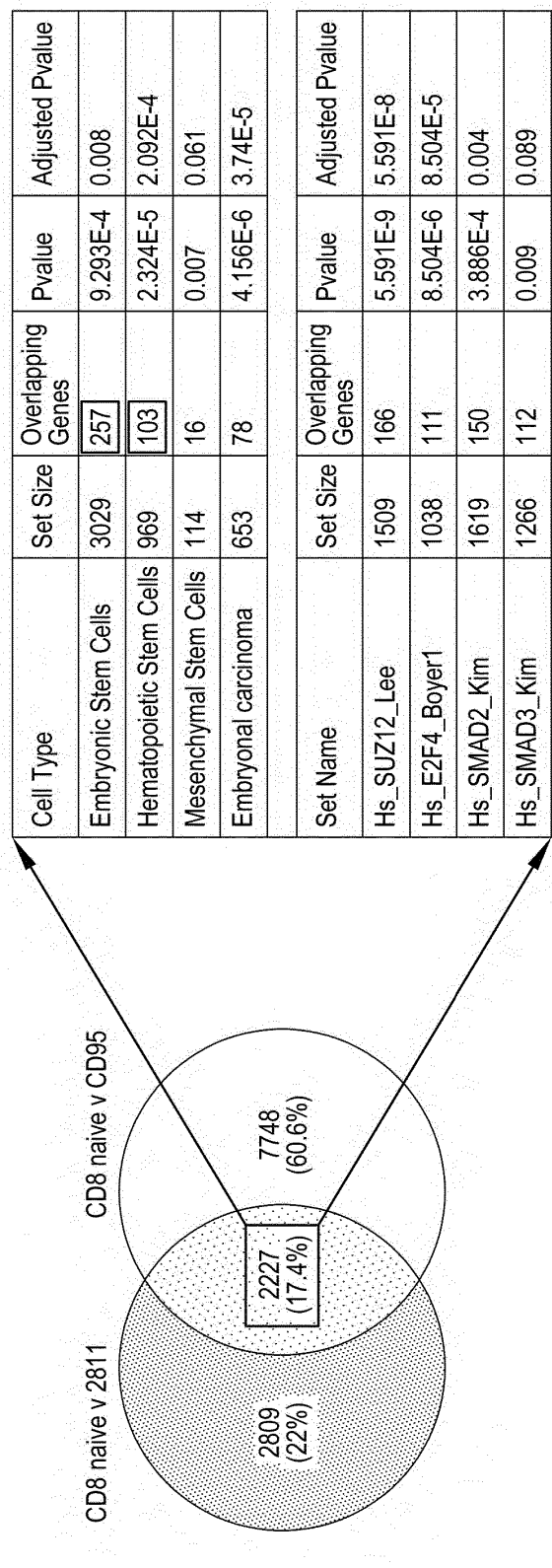


Fig. 10A

CH2811hG1-enriched naïve T cells and CD122/CD95- enriched naïve T cells, from four healthy donors were transcriptionally profiled using bulk RNAseq

CH2811hG1-enriched naïve T cells and CD122/CD95- enriched naïve T cells, from four healthy donors were transcriptionally profiled using bulk RNAseq

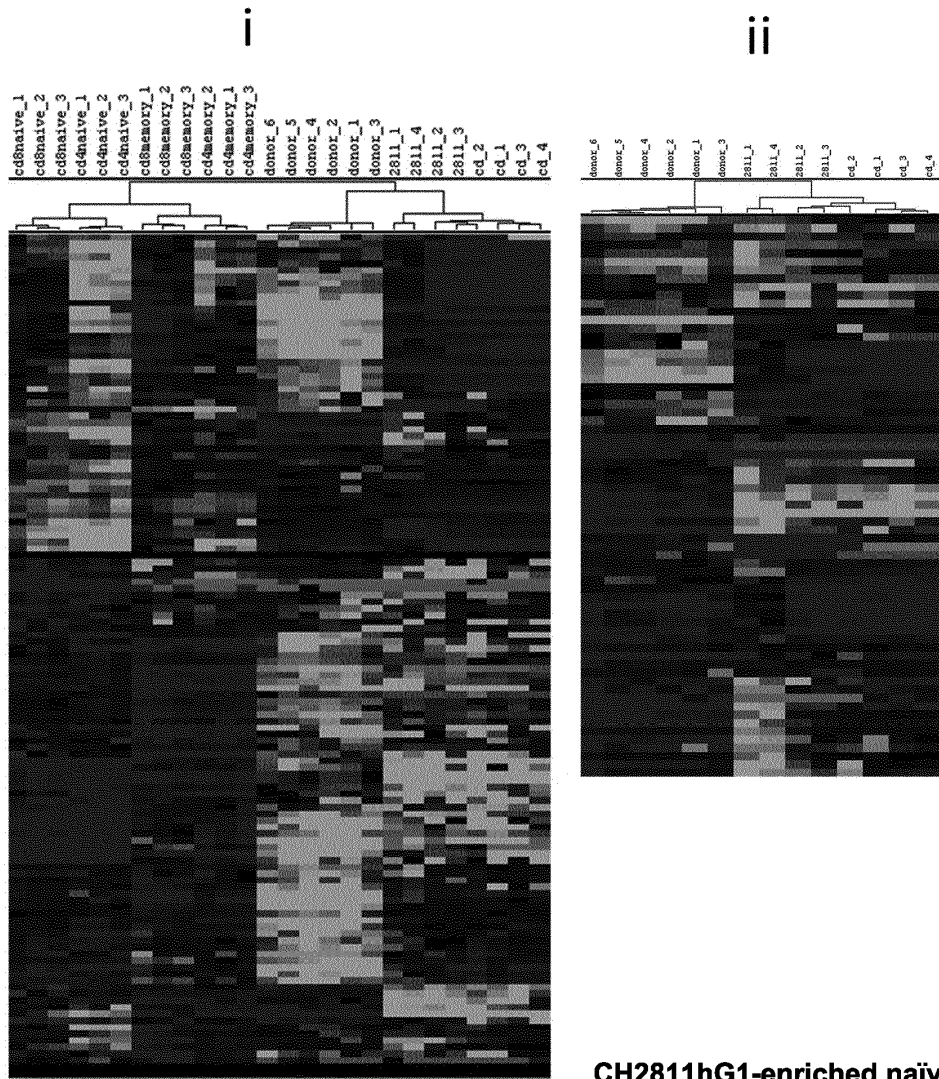
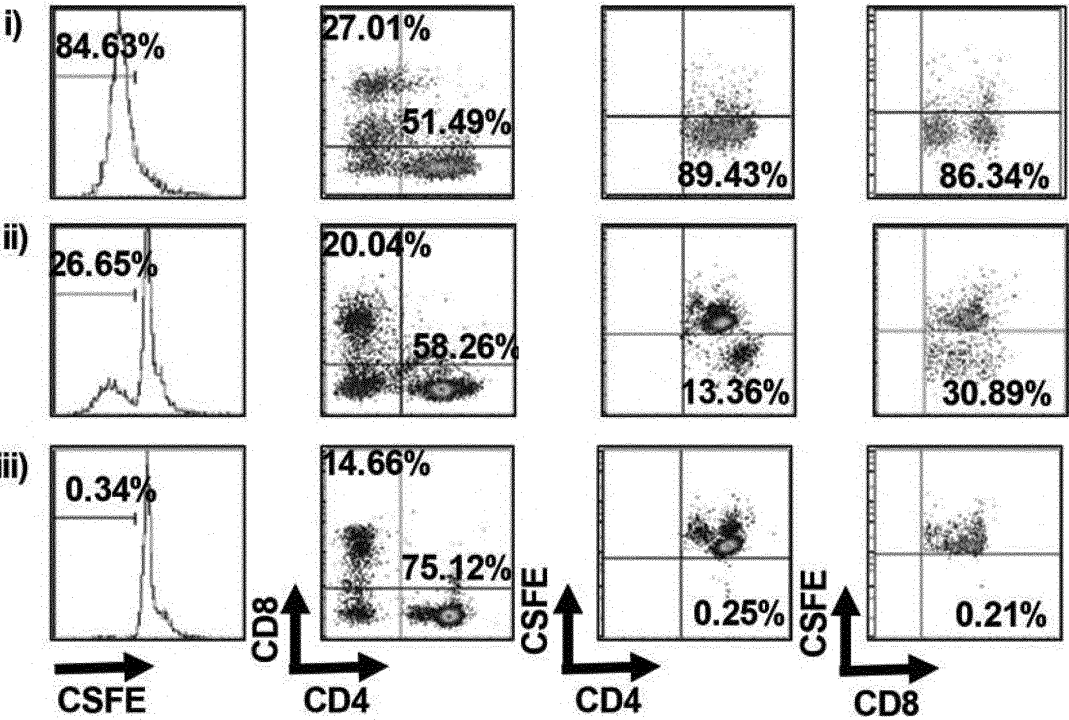


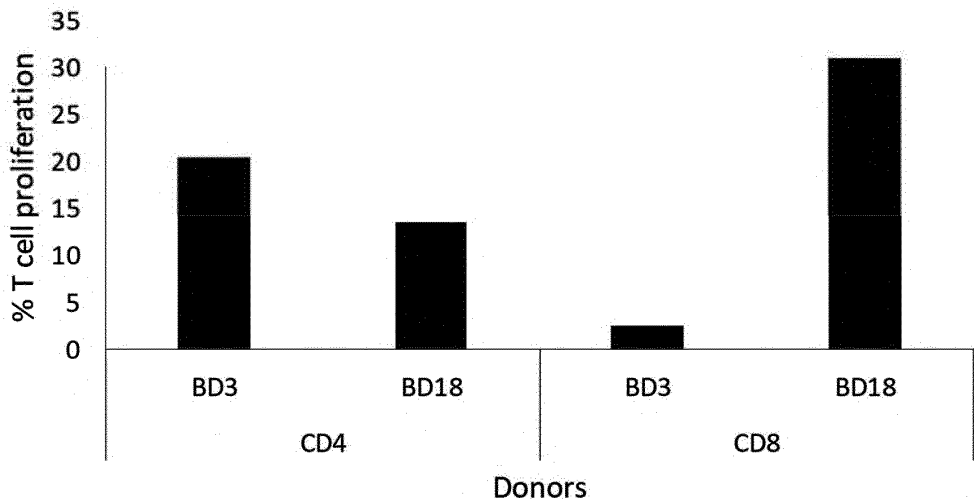
Fig. 10C

CH2811hG1-enriched naïve T cells and CD122/ CD95-enriched naïve T cells, from four healthy donors were transcriptionally profiled using bulk RNAseq

A



B



ECH2811hG1 antibody induced  
PBMCs proliferation

Fig. 11

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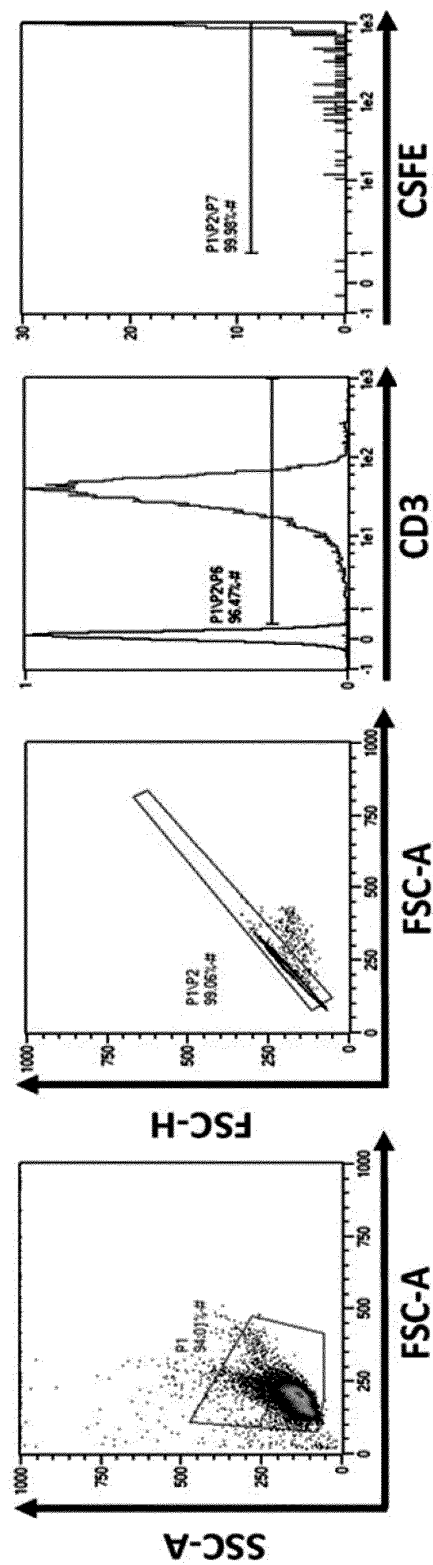
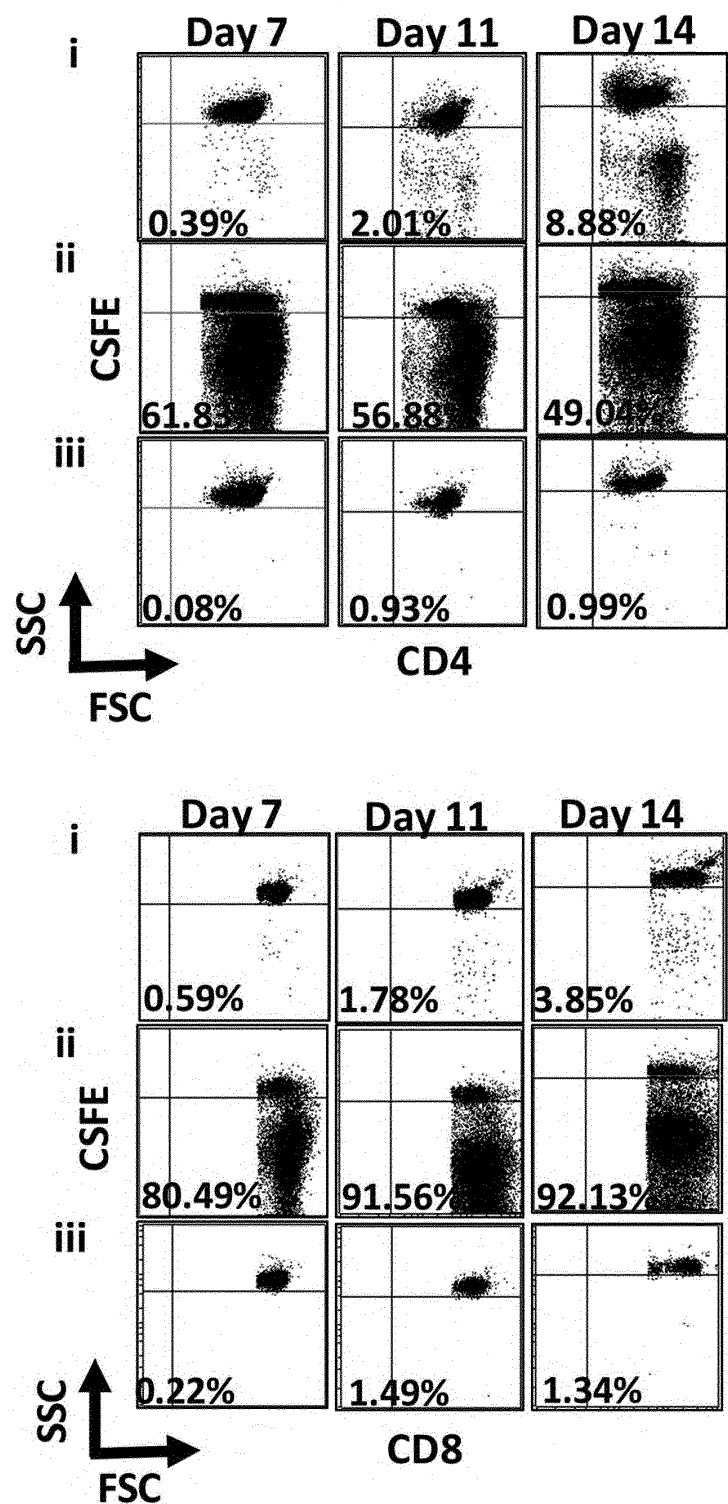


Fig. 12A

CH2811hG1 antibody induced  
T cell proliferation

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CH2811hG1 antibody induced  
T cell proliferation

Fig. 12B

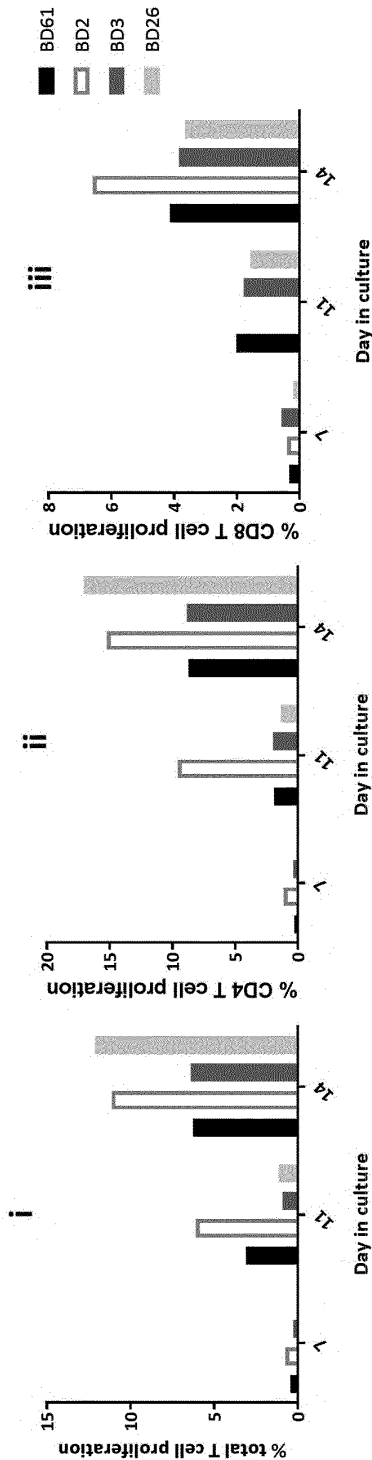


Fig. 12C

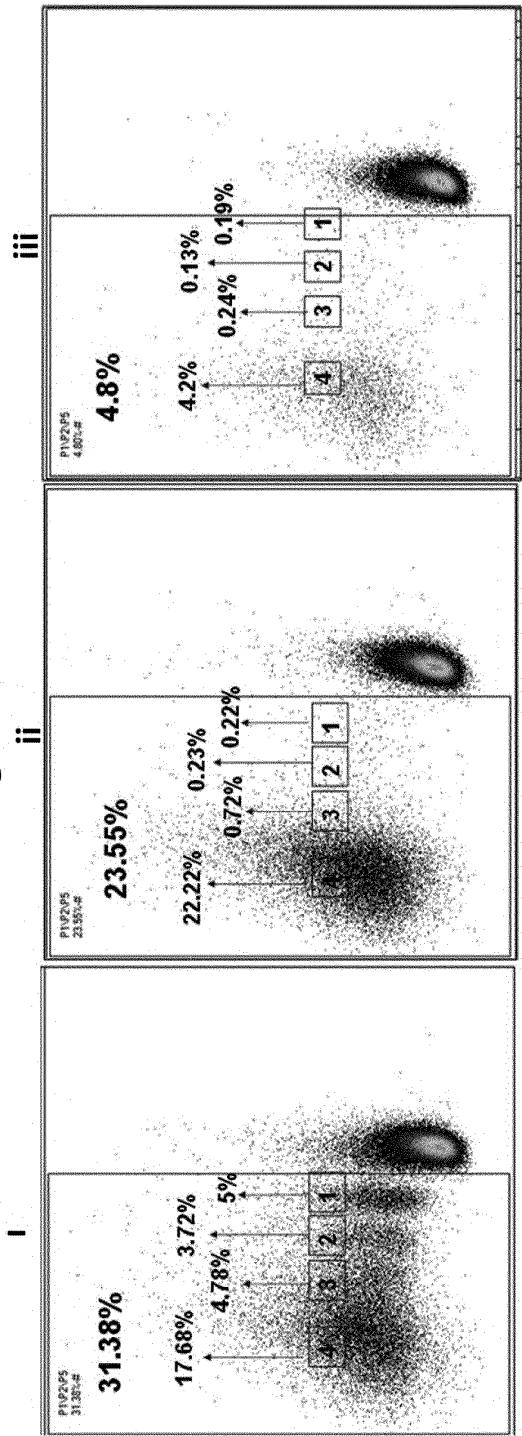
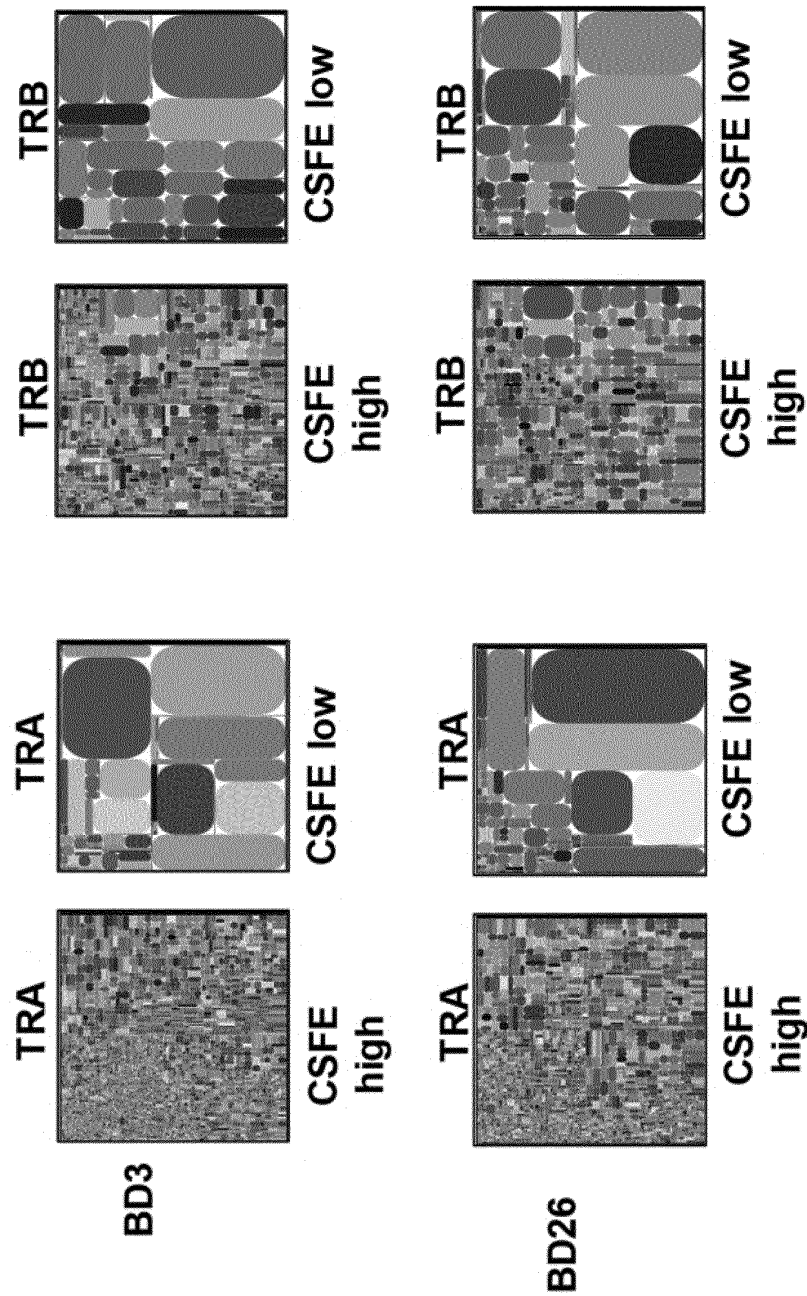


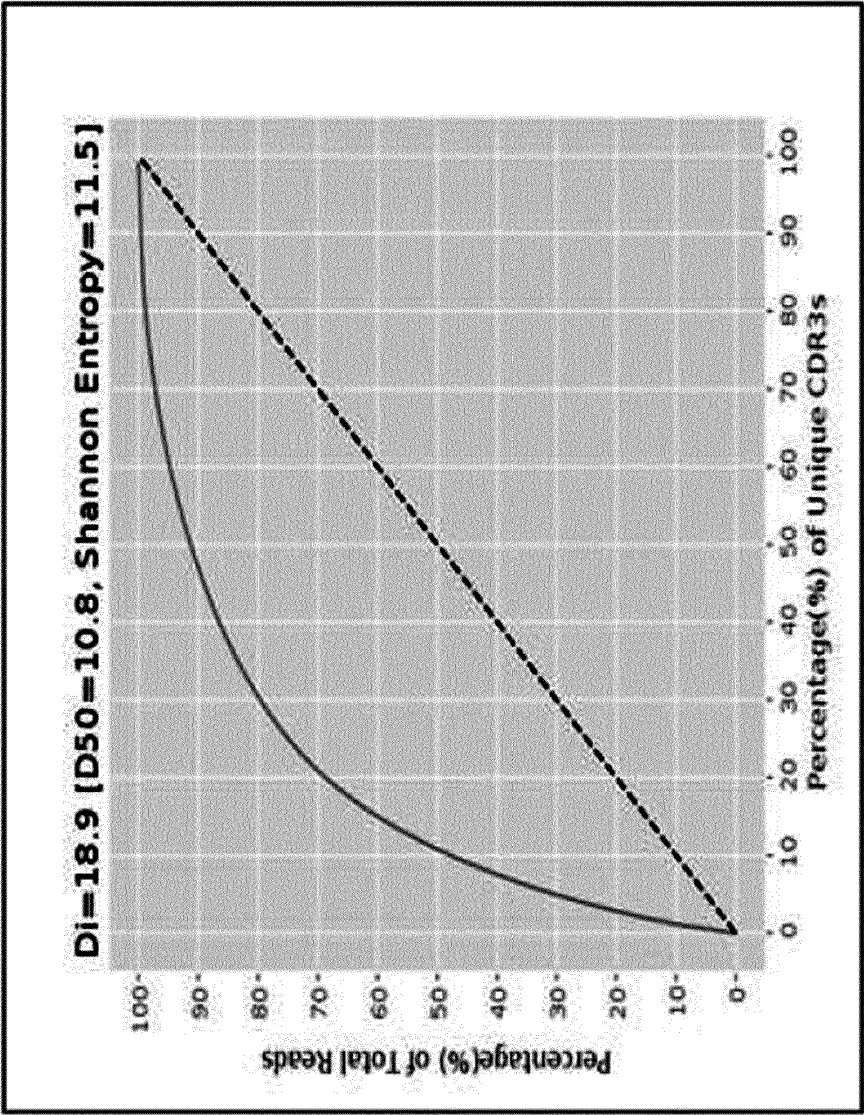
Fig. 12D

CH2811hG1 antibody induced  
T cell proliferation



Assessment of TCR repertoire clonotype in CH2811hG1 stimulated T cells Fig. 13A

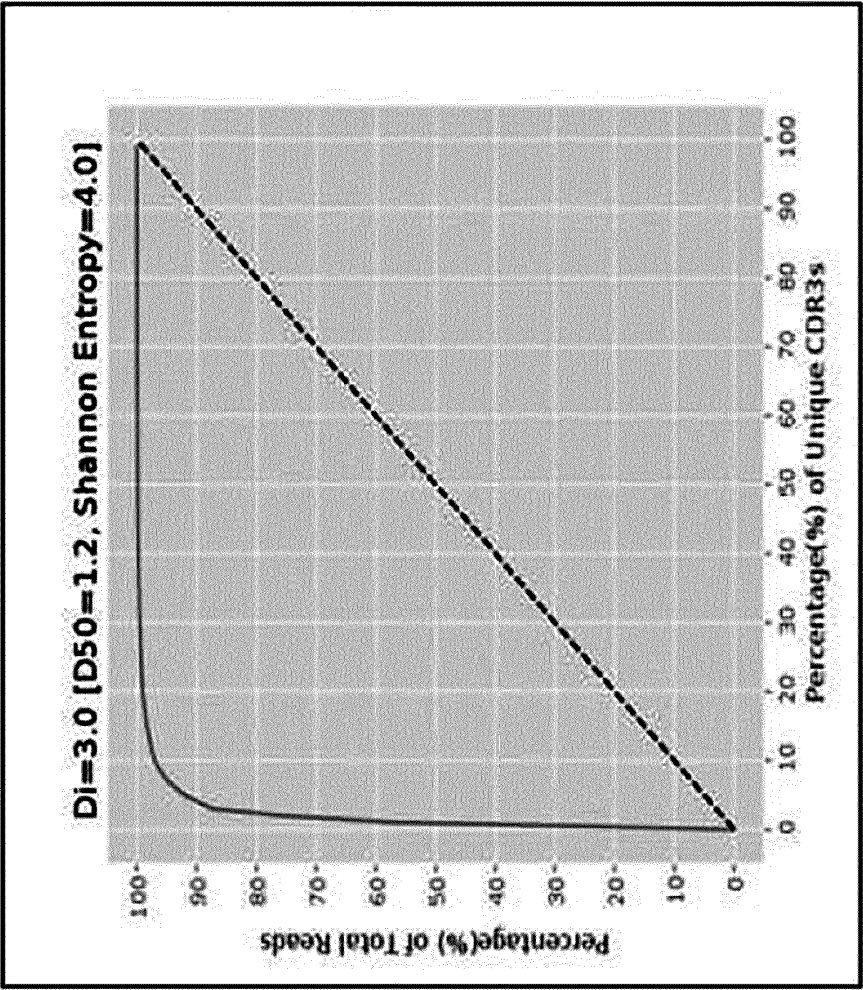
TRA CSFE high



Assessment of TCR repertoire clonotype in CH2811hG1 stimulated T cells

Fig. 13B

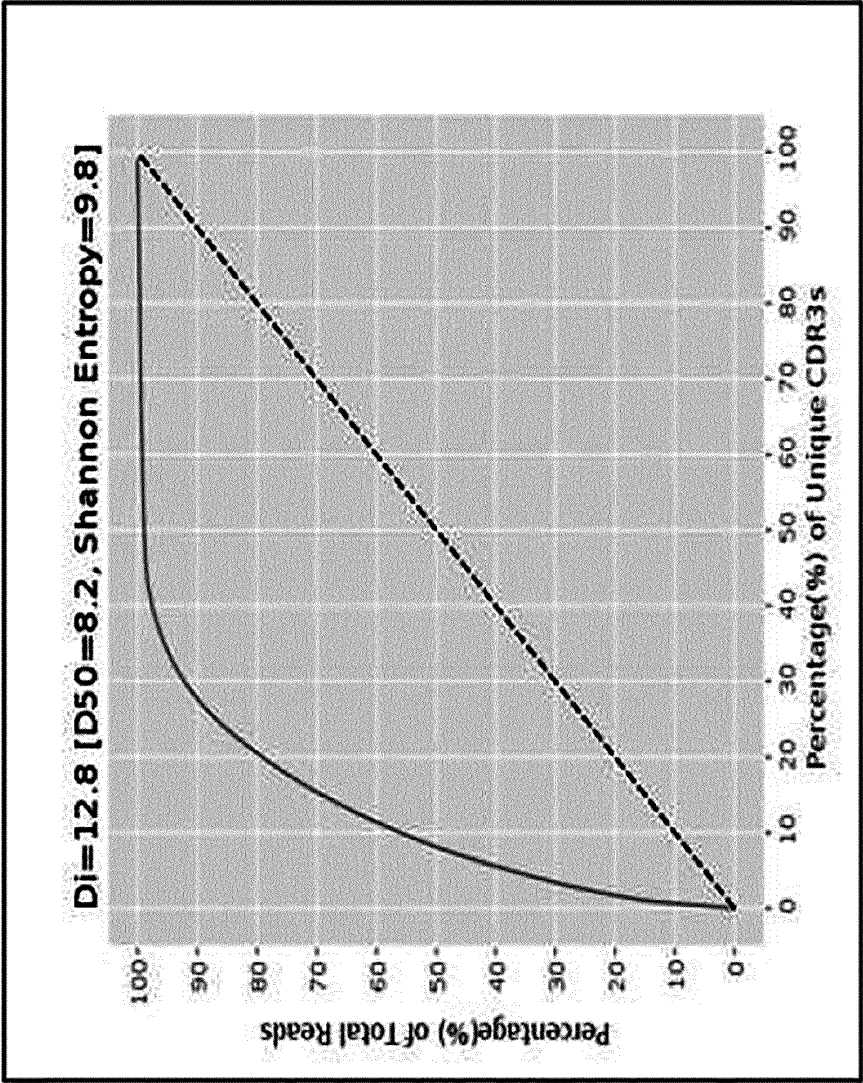
TRA CSFE low



Assessment of TCR  
repertoire clonotype  
in CH2811hG1  
stimulated T cells

Fig. 13C

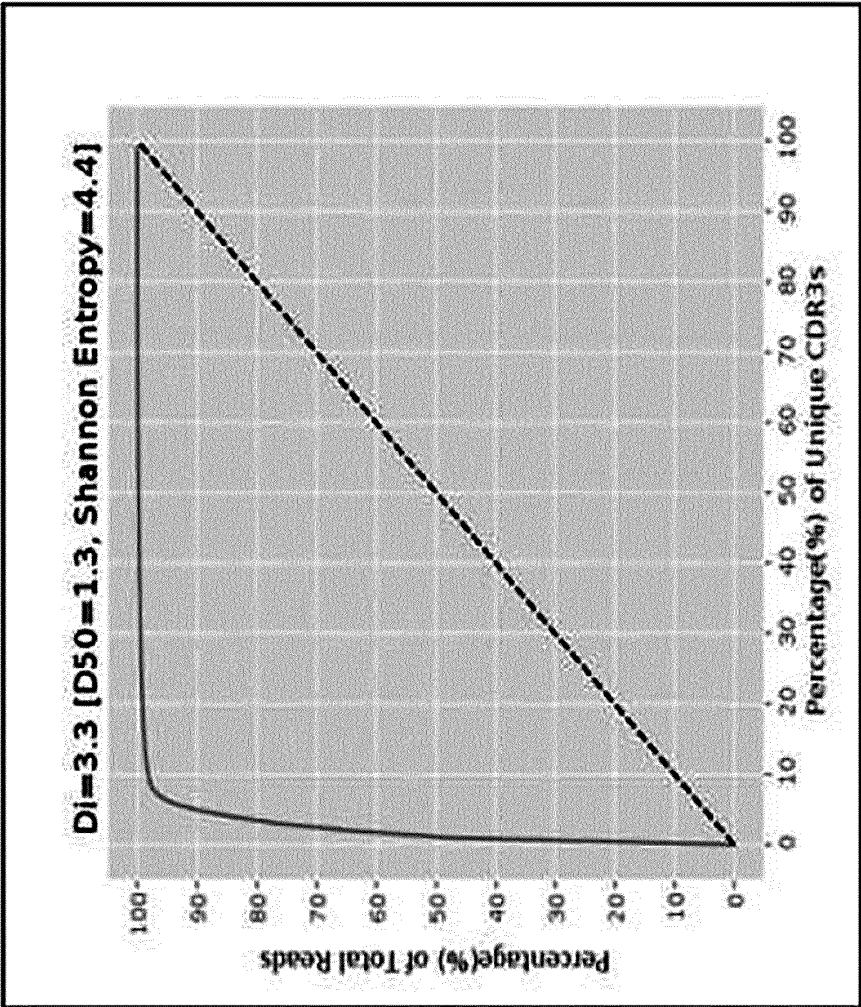
TRB CSFE high



Assessment of TCR  
repertoire clonotype  
in CH2811hG1  
stimulated T cells

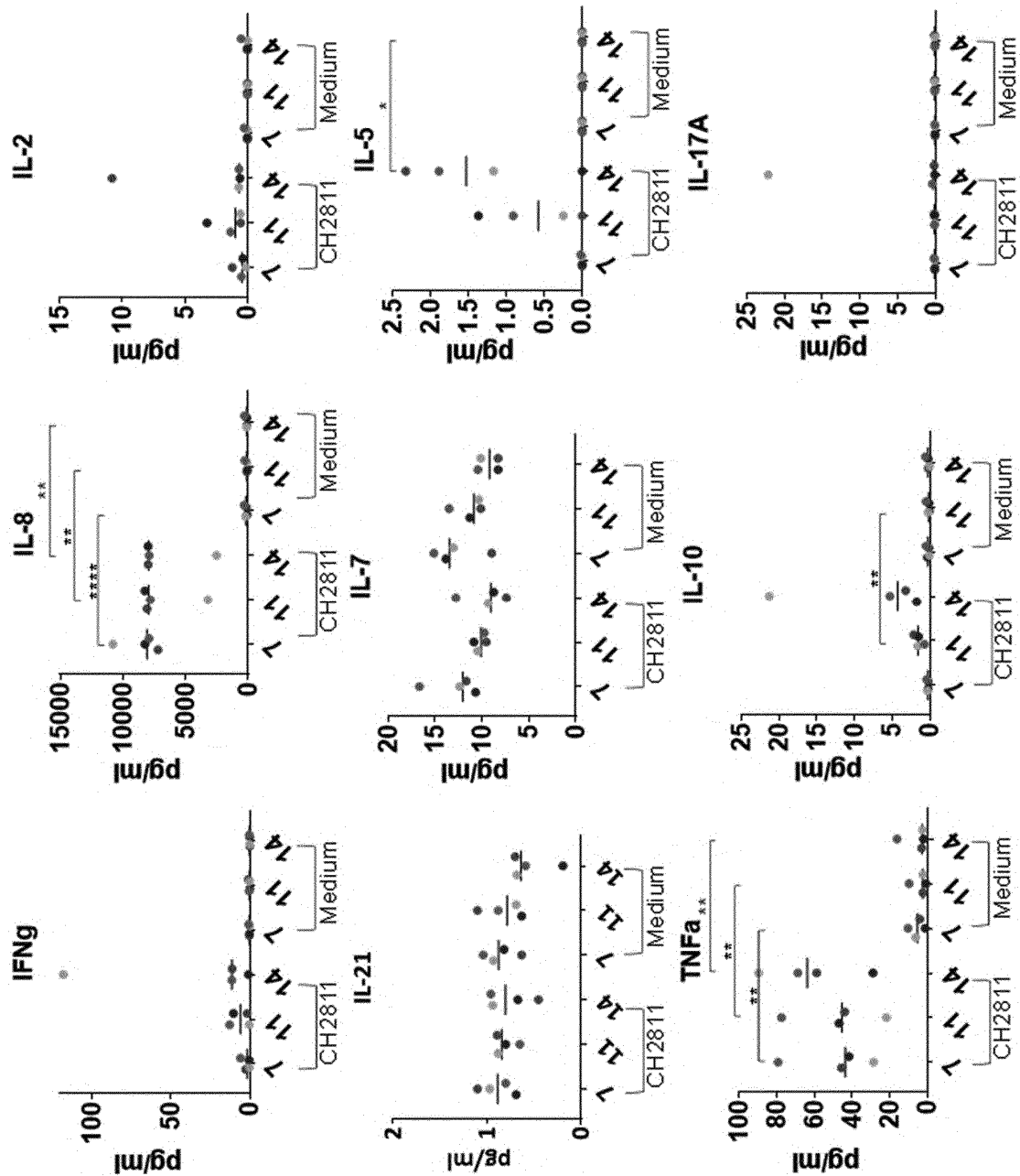
Fig. 13D

TRB CSFE low



Assessment of TCR repertoire clonotype in CH2811hG1 stimulated T cells

Fig. 13E



Dynamics of individual  
cytokine/chemokine  
responses

Fig. 14

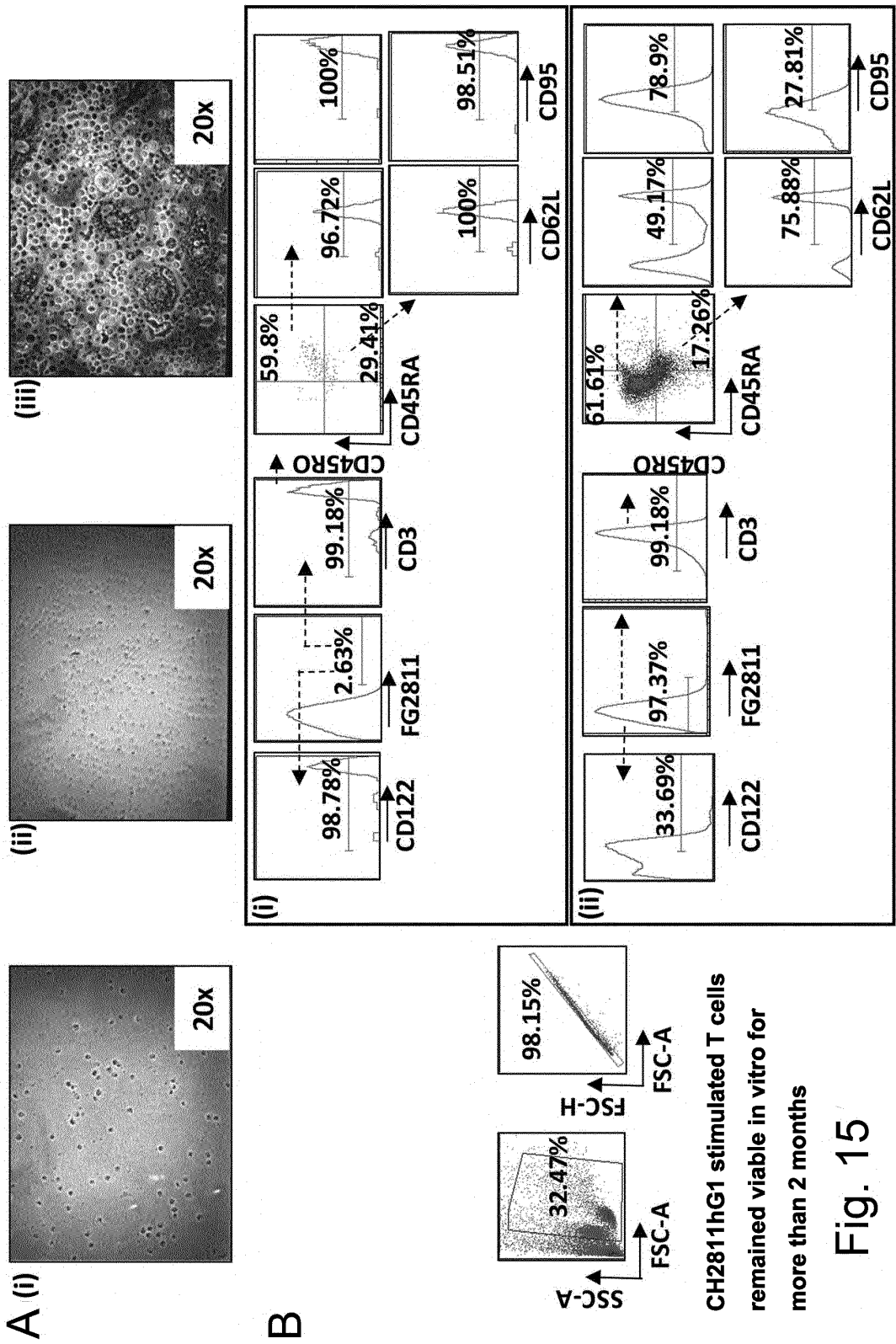
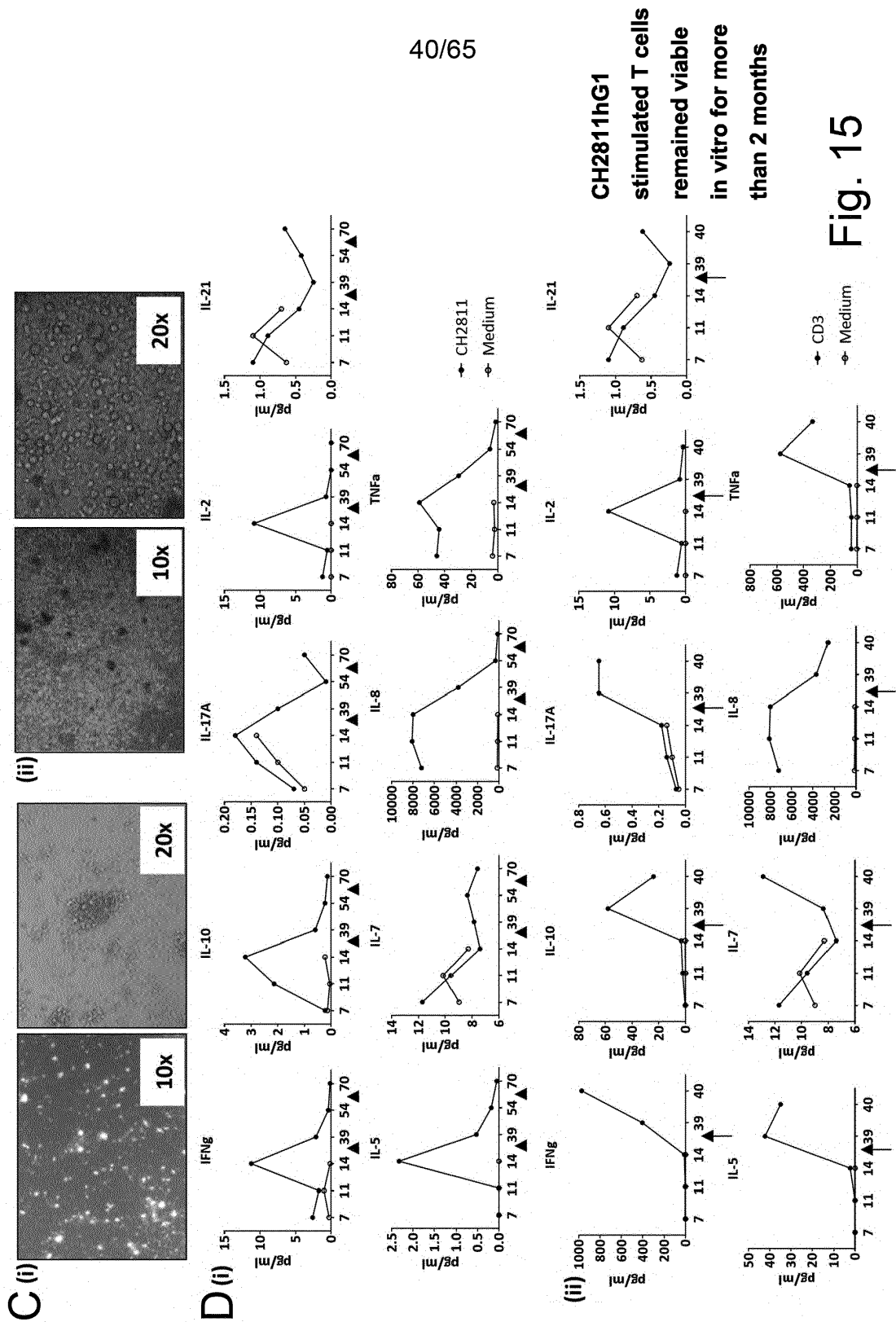
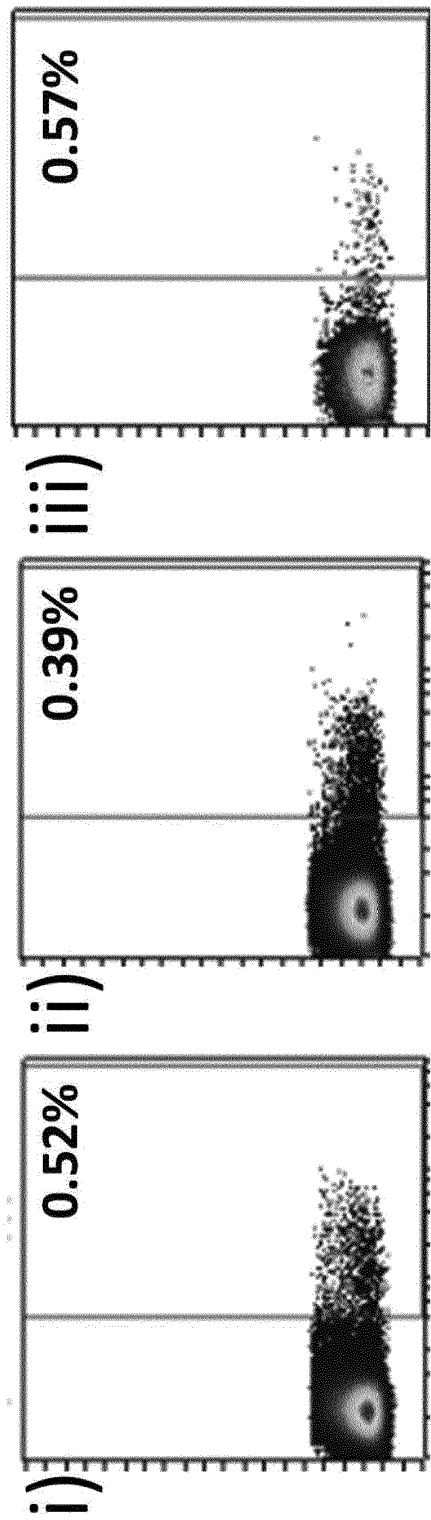


Fig. 15





**Fig. 16**  
**Expression of SSEA-4 on mouse immune cells**

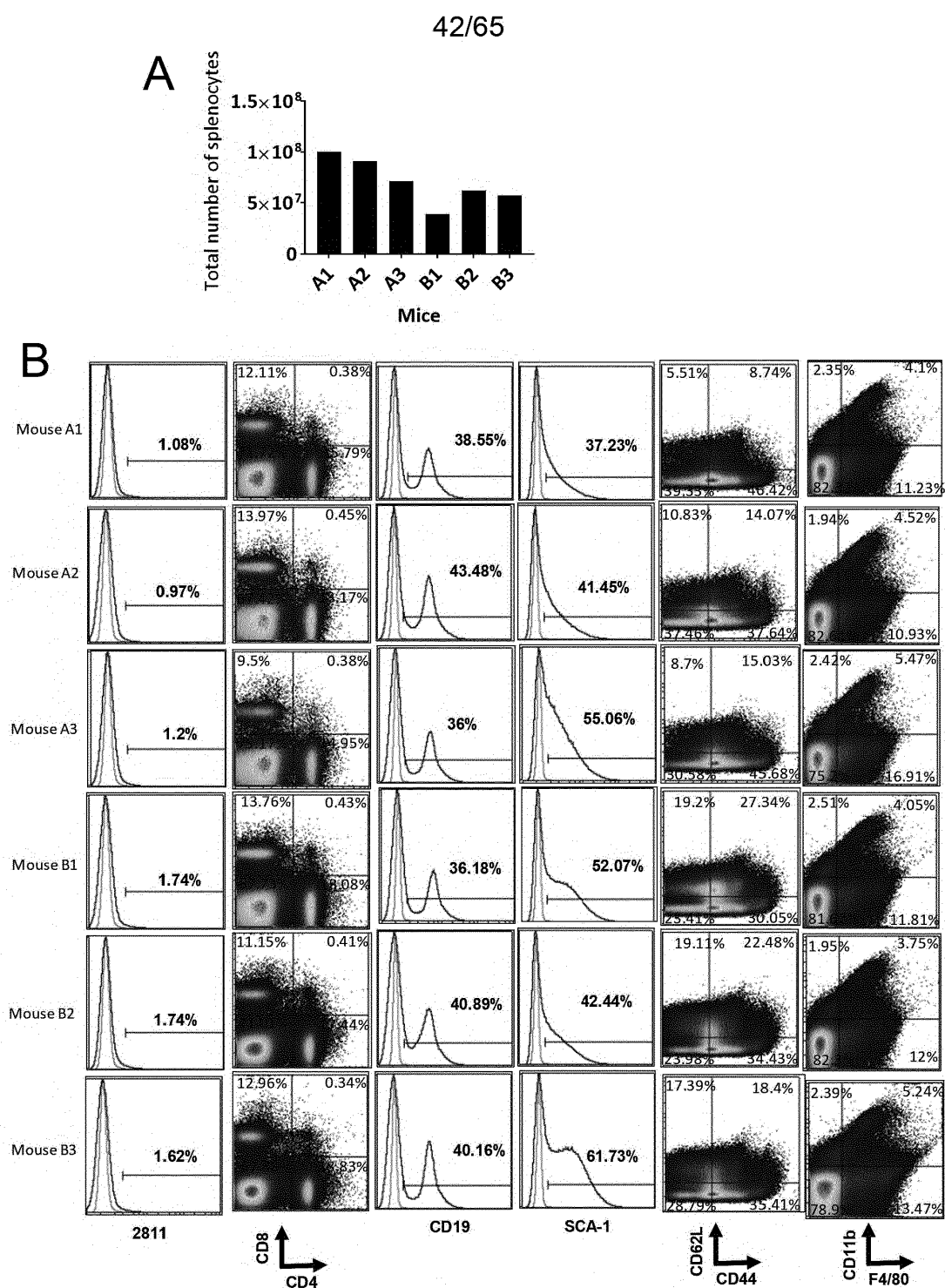


Fig. 17

FG2811mG1 induced phenotypic TSCM cells in C57/B6 mice

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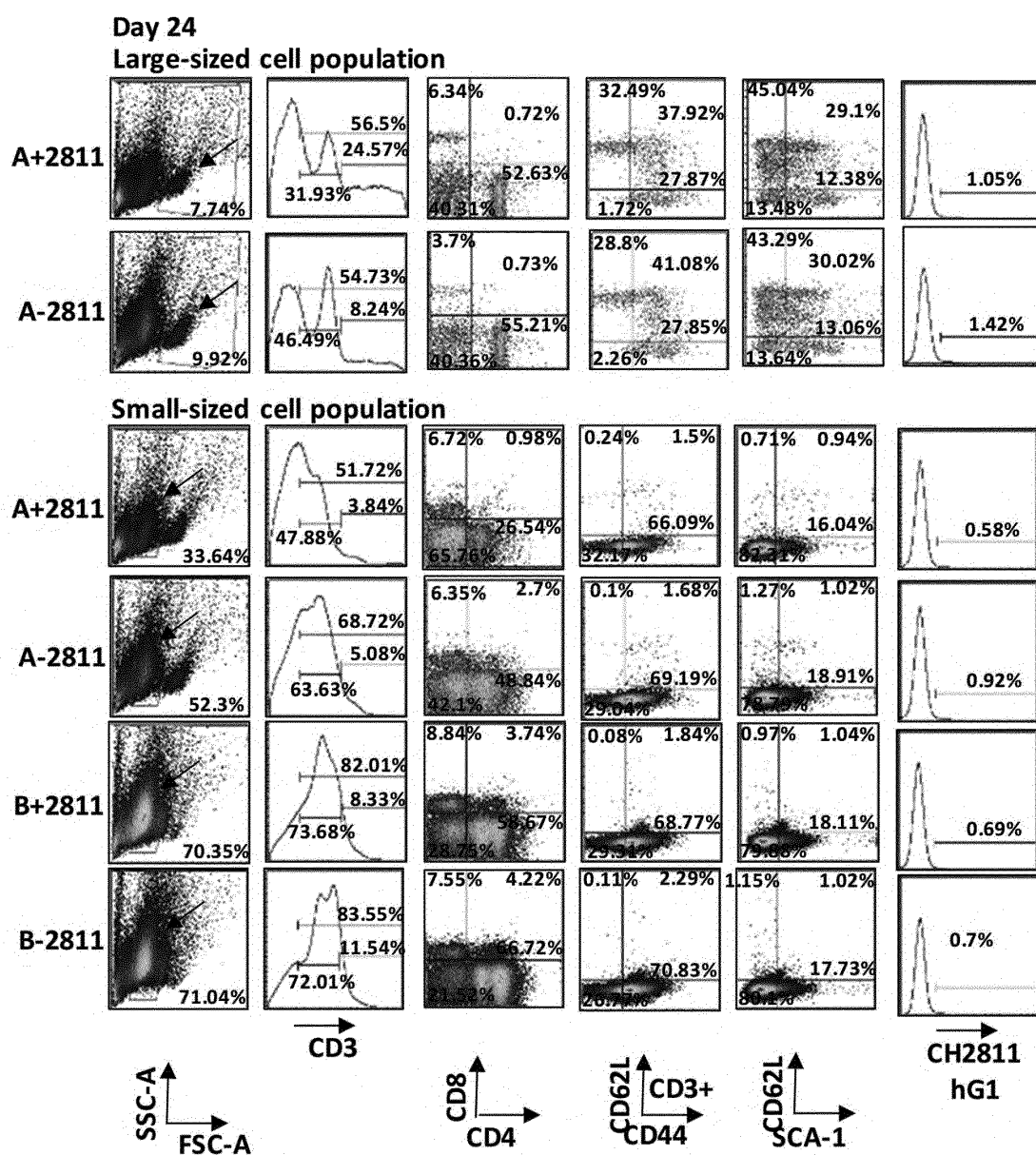


Fig. 17C

FG2811mG1 induced phenotypic TSCM cells in C57/B6 mice

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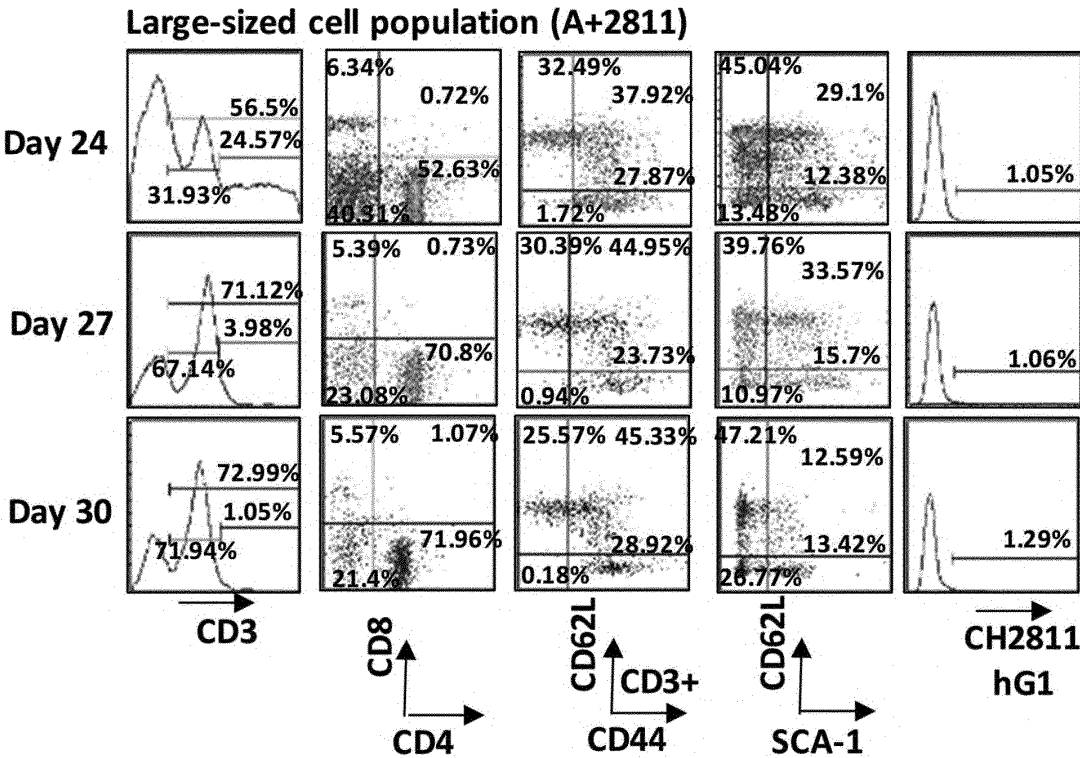


Fig. 17D

FG2811mG1 induced phenotypic TSCM cells in C57/B6 mice

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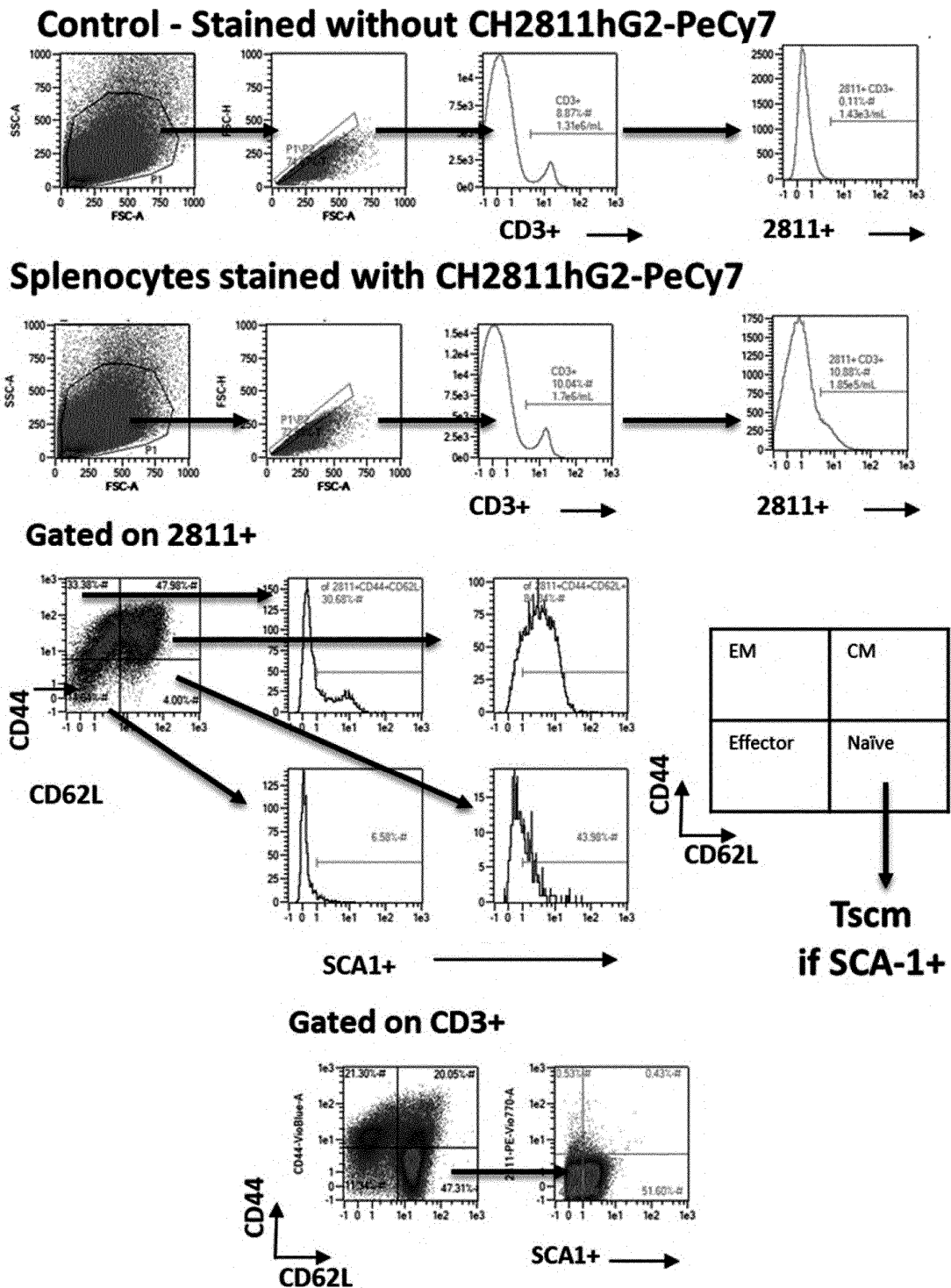


Fig. 18A

Direct ex vivo phenotyping Tscm cells from HHDII and HHDII/DP4 mice

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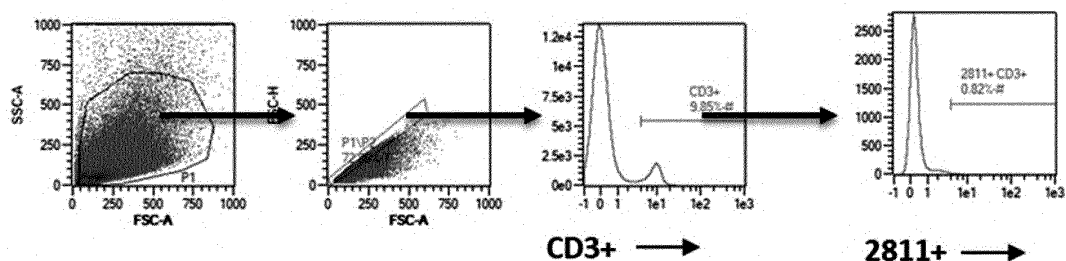
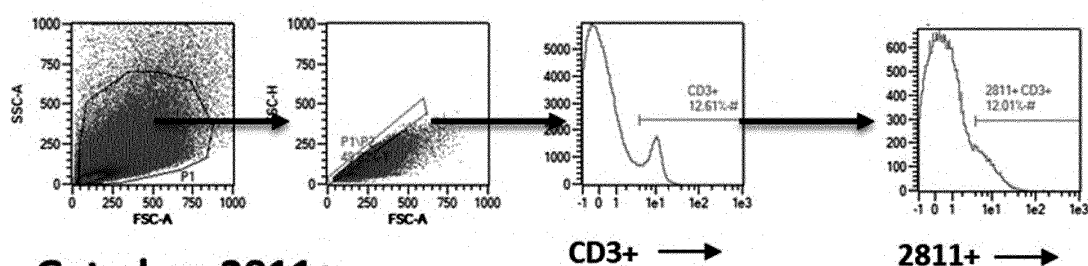
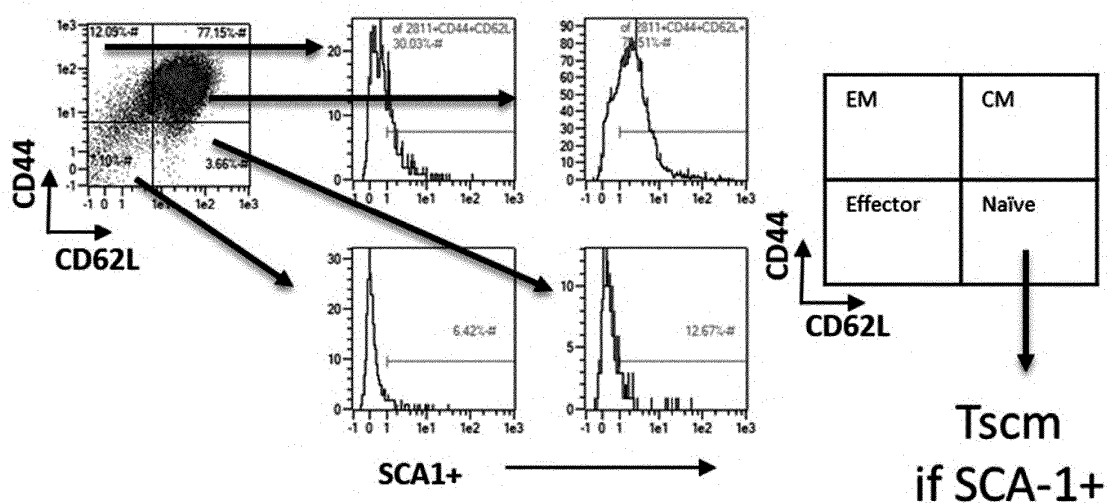
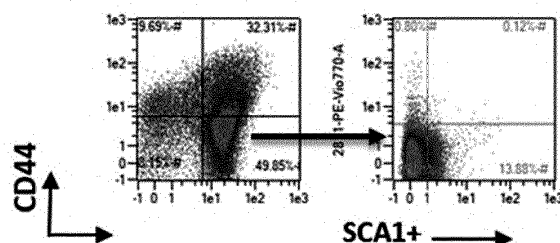
| Cells                   | % CD3 | Number of CD3+ (x10 <sup>6</sup> /mL) | %2811+ of CD3+ cells | Number of 2811+ cells (x10 <sup>5</sup> /mL) | % Tscm of CD3+ | %2811+ of Tscm |
|-------------------------|-------|---------------------------------------|----------------------|----------------------------------------------|----------------|----------------|
| Splenocytes (unstained) | 8.87  | 1.31                                  | 0.11                 | ND                                           | 25.26          | 0.03           |
| Splenocytes             | 10.04 | 1.7                                   | 10.88                | 1.85                                         | 24.61          | 0.78           |

| Cells       | %CD44+ CD62L- of 2811+ | %CD44+ CD62L- of 2811+ | %SCA1+ of CD44+ CD62L- of 2811+ | %CD44+ CD62L- of CD3+ | %CD44+ CD62L+ of CD3+ |
|-------------|------------------------|------------------------|---------------------------------|-----------------------|-----------------------|
| Splenocytes | 33.38                  | 47.98                  | 30.68                           | 21.30                 | 20.05                 |

Fig. 18B

Direct ex vivo phenotyping Tscm cells from HHDII and HHDII/DP4 mice

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**Control - Stained without CH2811hG2-PeCy7****Splenocytes stained with CH2811hG2-PeCy7****Gated on 2811+****Gated on CD3+**

Direct ex vivo  
phenotyping Tscm  
cells from HDDII  
and HDDII/DP4 mice

**Fig. 18C**

| Cells                   | % CD3 | Number of CD3+ (x10 <sup>6</sup> /mL) | %2811+ of CD3+ cells | Number of 2811+ cells (x10 <sup>5</sup> /mL) | % Tscm of CD3+ | %2811+ of Tscm |
|-------------------------|-------|---------------------------------------|----------------------|----------------------------------------------|----------------|----------------|
| Splenocytes (unstained) | 9.85  | 1.29                                  | 0.82                 | 0.106                                        | 9.30           | 0.09           |
| Splenocytes             | 12.61 | 0.759                                 | 12.01                | 0.911                                        | 6.98           | 0.80           |

| Cells       | %CD44+ CD62L- of 2811+ | %CD44+ CD62L+ of 2811+ | %SCA1+ of CD44+ CD62L- of 2811+ | %SCA1+ of CD44+ CD62L+ of 2811+ | %CD44+ CD62L- of CD3+ | %CD44+ CD62L+ of CD3+ |
|-------------|------------------------|------------------------|---------------------------------|---------------------------------|-----------------------|-----------------------|
| Splenocytes | 12.09                  | 77.15                  | 30.03                           | 75.51                           | 9.69                  | 32.31                 |

Fig. 18D

Direct ex vivo  
phenotyping Tscm  
cells from HHDI  
and HHDI/DP4 mice

| Cells                   | % CD4+ T cells | % CD8 T cells | %2811+ of CD4+ cells | %2811+ of CD8+ cells |
|-------------------------|----------------|---------------|----------------------|----------------------|
| Splenocytes (unstained) | 14.31          | 0.59          | 0.12                 | 2.50                 |
| Splenocytes             | 14.30          | 0.50          | 9.47                 | 10.14                |

| Cells       | %CD44+ CD62L- of 2811+ CD4+ | %CD44+ CD62L+ of 2811+ CD4+ | %CD44+ CD62L- of 2811+ CD8+ | %Tim3 of 2811+ CD4+ | %Tim3 of 2811+ CD8+ |
|-------------|-----------------------------|-----------------------------|-----------------------------|---------------------|---------------------|
| Splenocytes | 13.71                       | 80.82                       | 9.51                        | 0.42                | 0.34                |

Fig. 18E

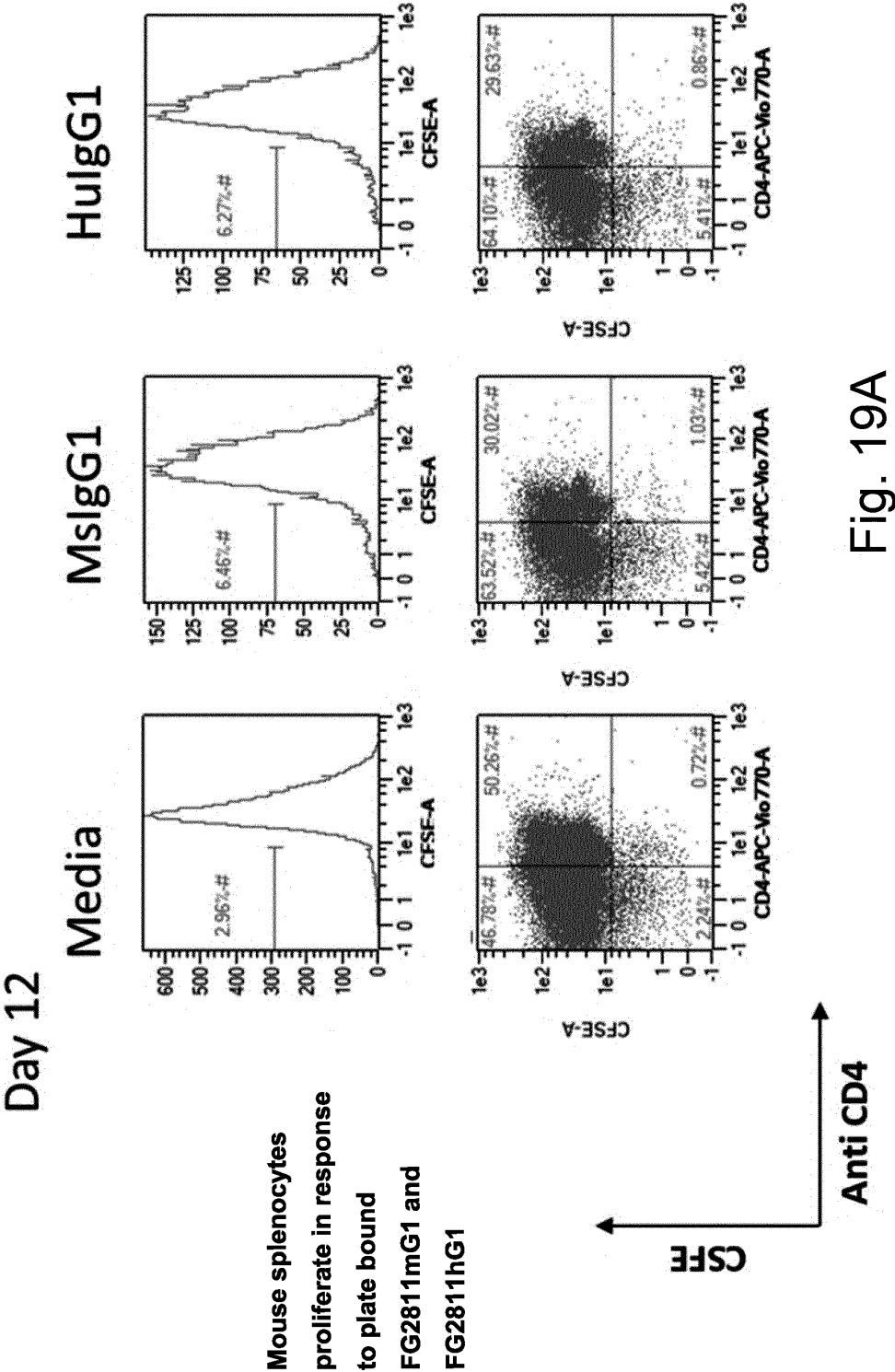
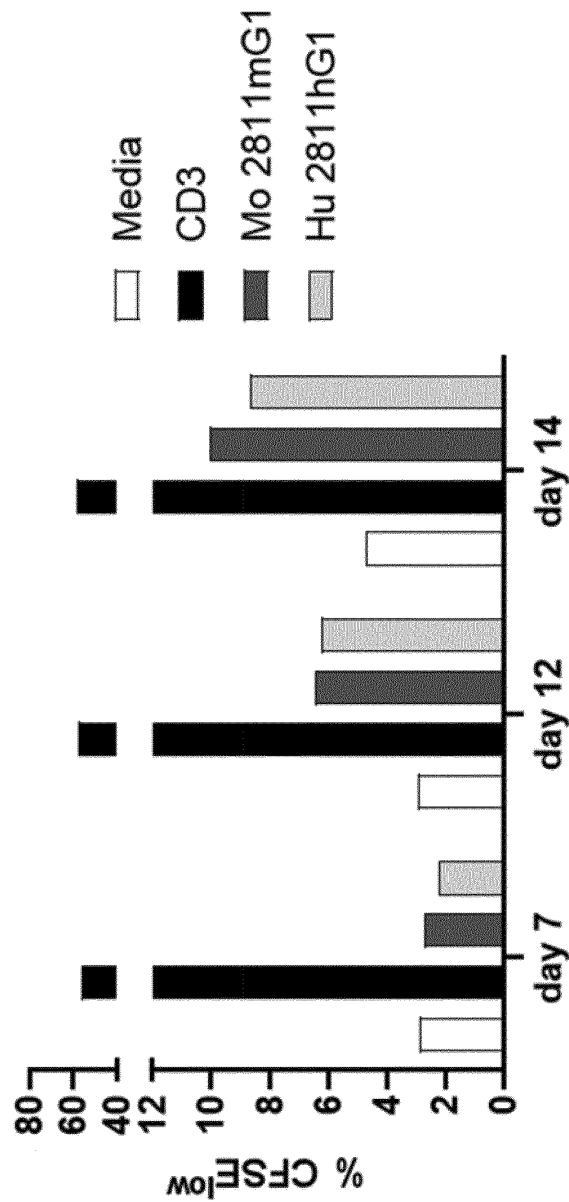


Fig. 19A



Mouse splenocytes proliferate in response to plate bound FG2811mG1 and FG2811hG1

Fig. 19B

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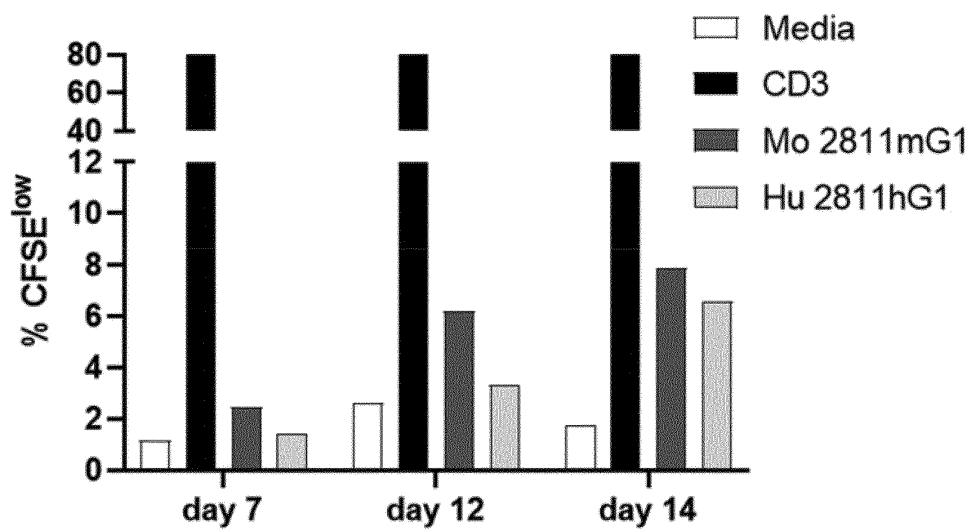


Fig. 19C

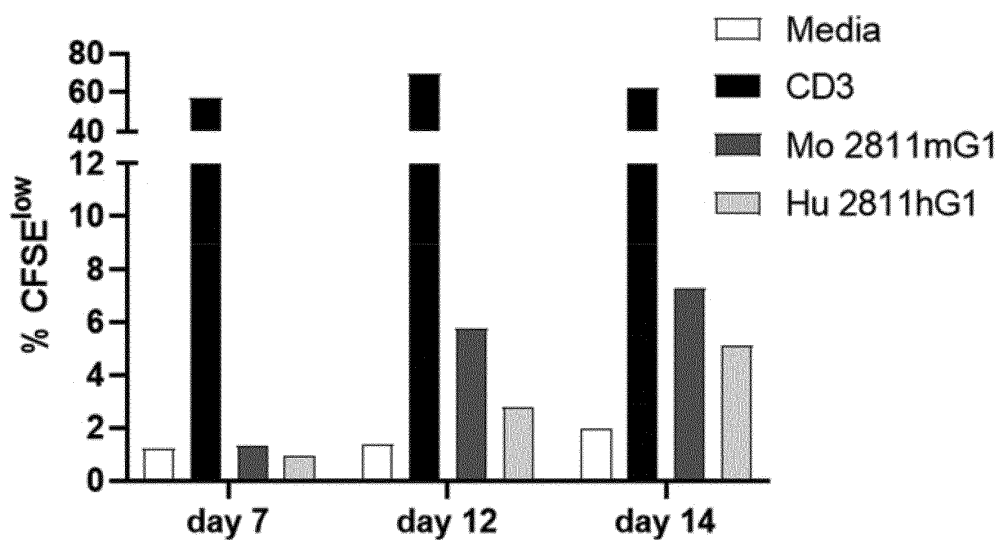


Fig. 19D

**Mouse splenocytes proliferate in response to plate  
bound FG2811mG1 and FG2811hG1**

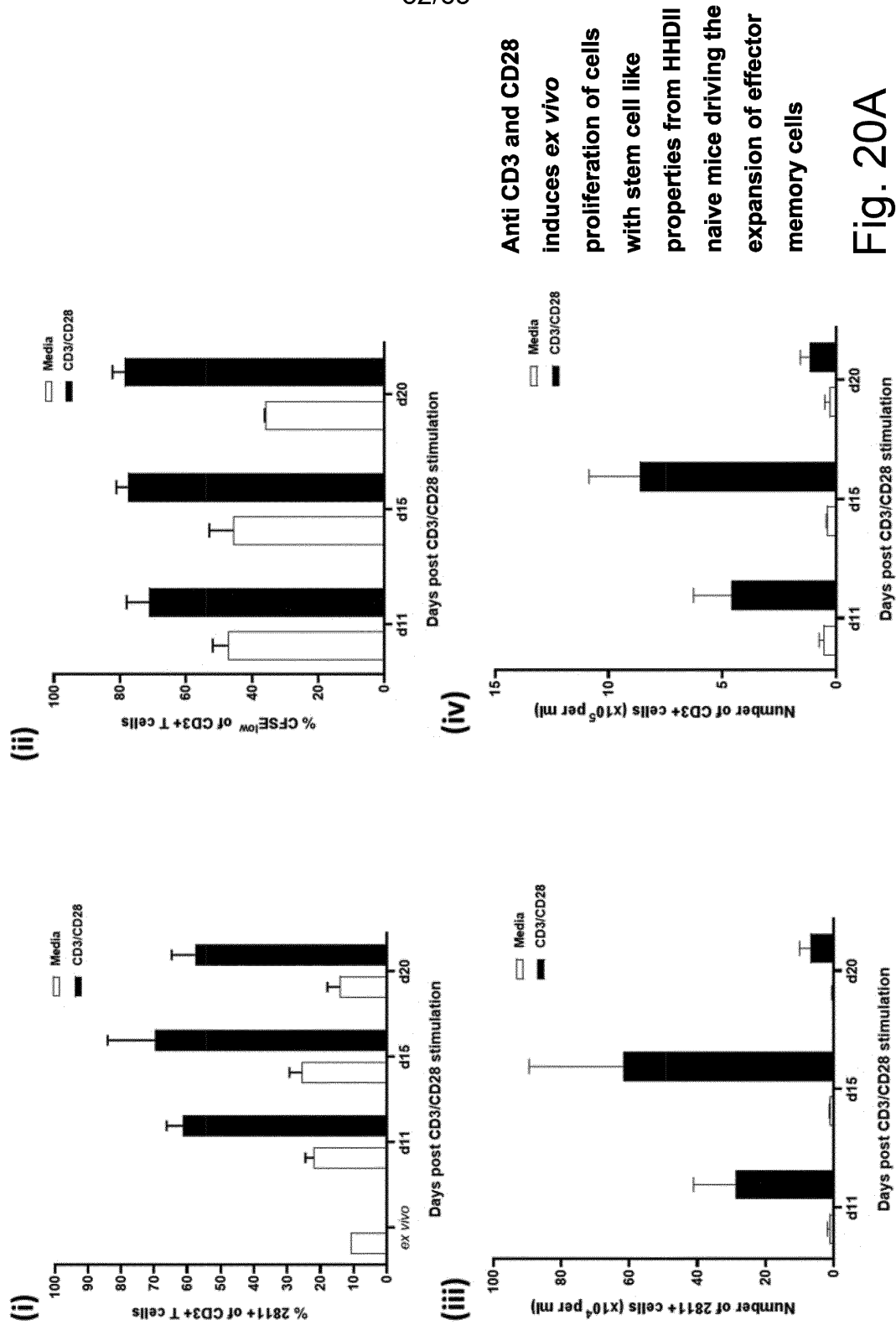


Fig. 20A

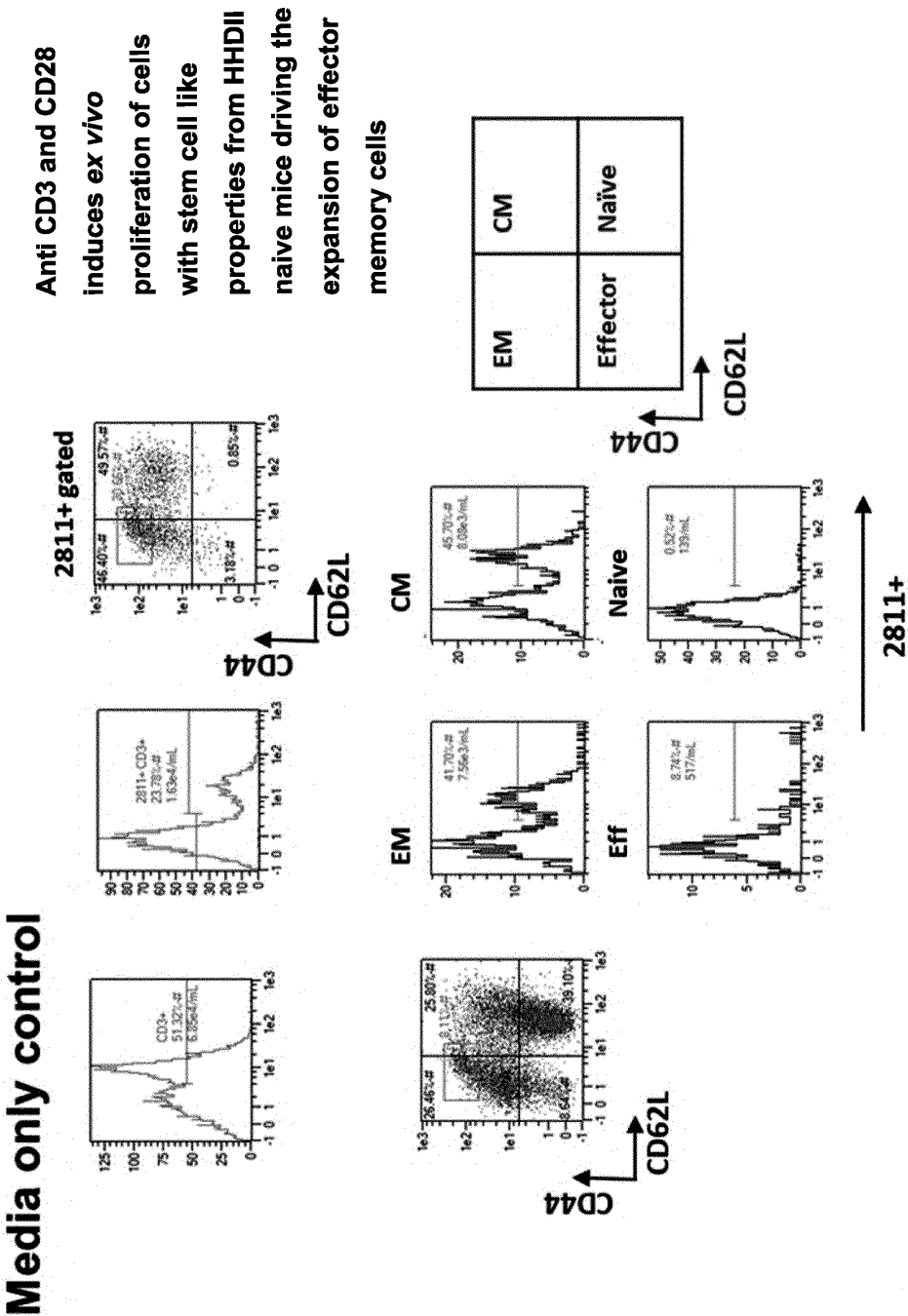
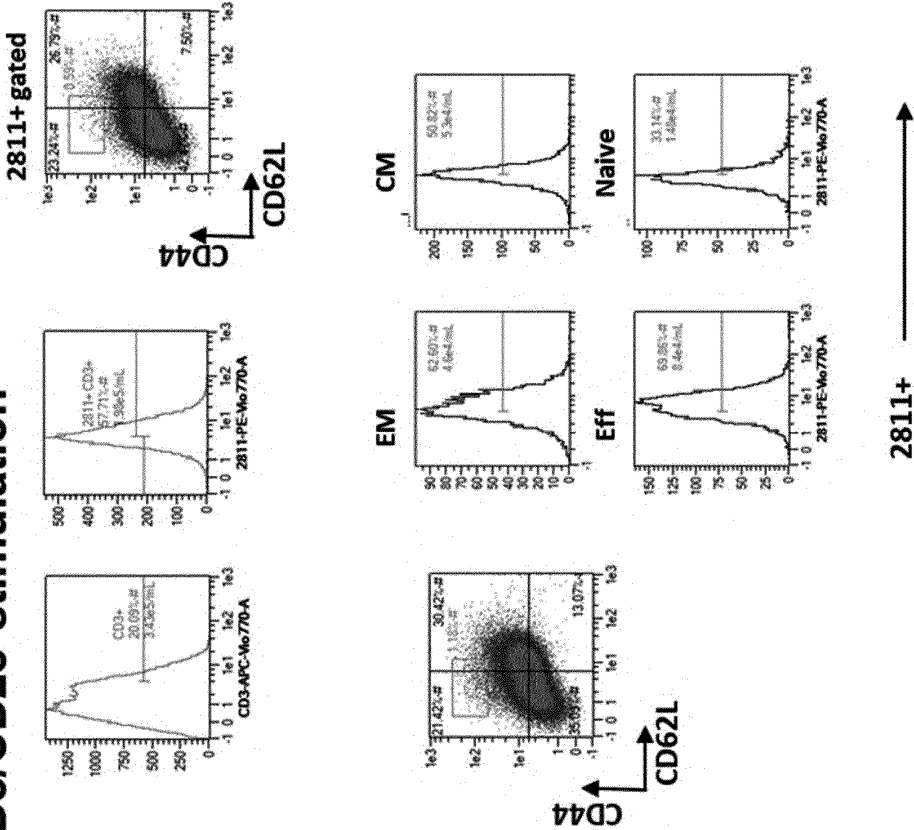


Fig. 20B

CD3/CD28 stimulation



Anti CD3 and CD28  
induces *ex vivo*  
proliferation of cells  
with stem cell like  
properties from HHDII  
naive mice driving the  
expansion of effector  
memory cells

Fig. 20B  
(continued)

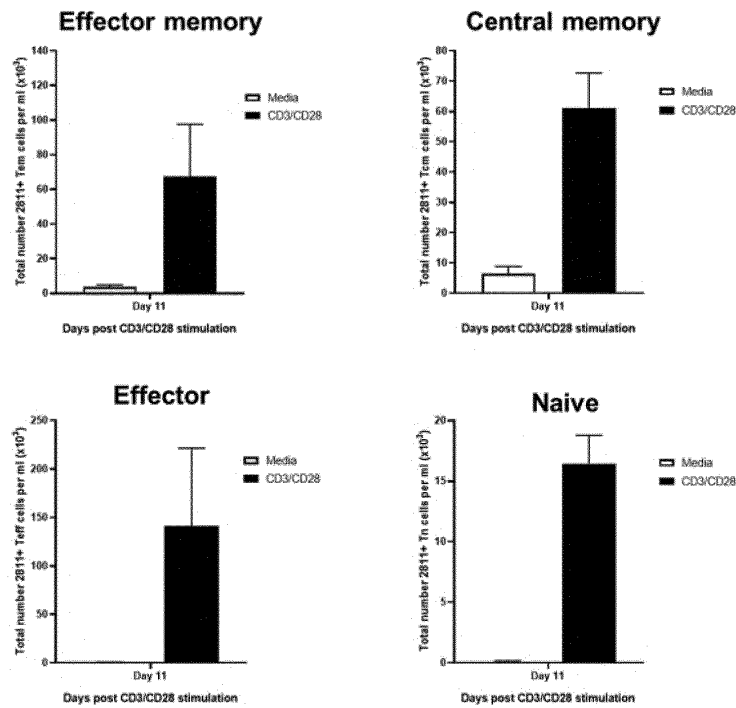
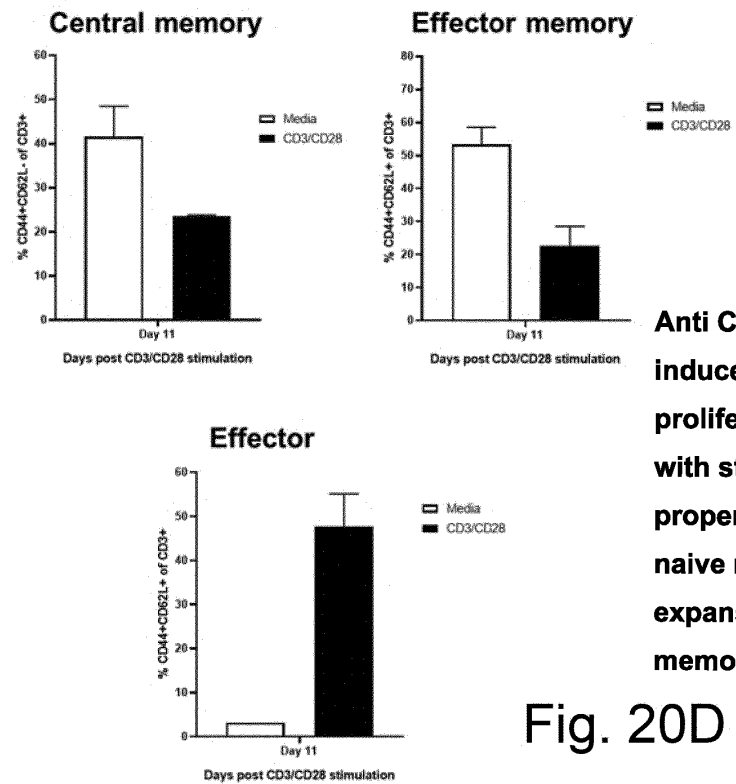


Fig. 20C



**Anti CD3 and CD28 induces *ex vivo* proliferation of cells with stem cell like properties from HHDII naive mice driving the expansion of effector memory cells**

Fig. 20D

Human 2811hG2 and  
Mouse 2811mG1  
induces ex vivo  
proliferation of cells  
with stem cell like  
properties from HHDI/  
DP4 naive mice driving  
the expansion of  
effector memory cells

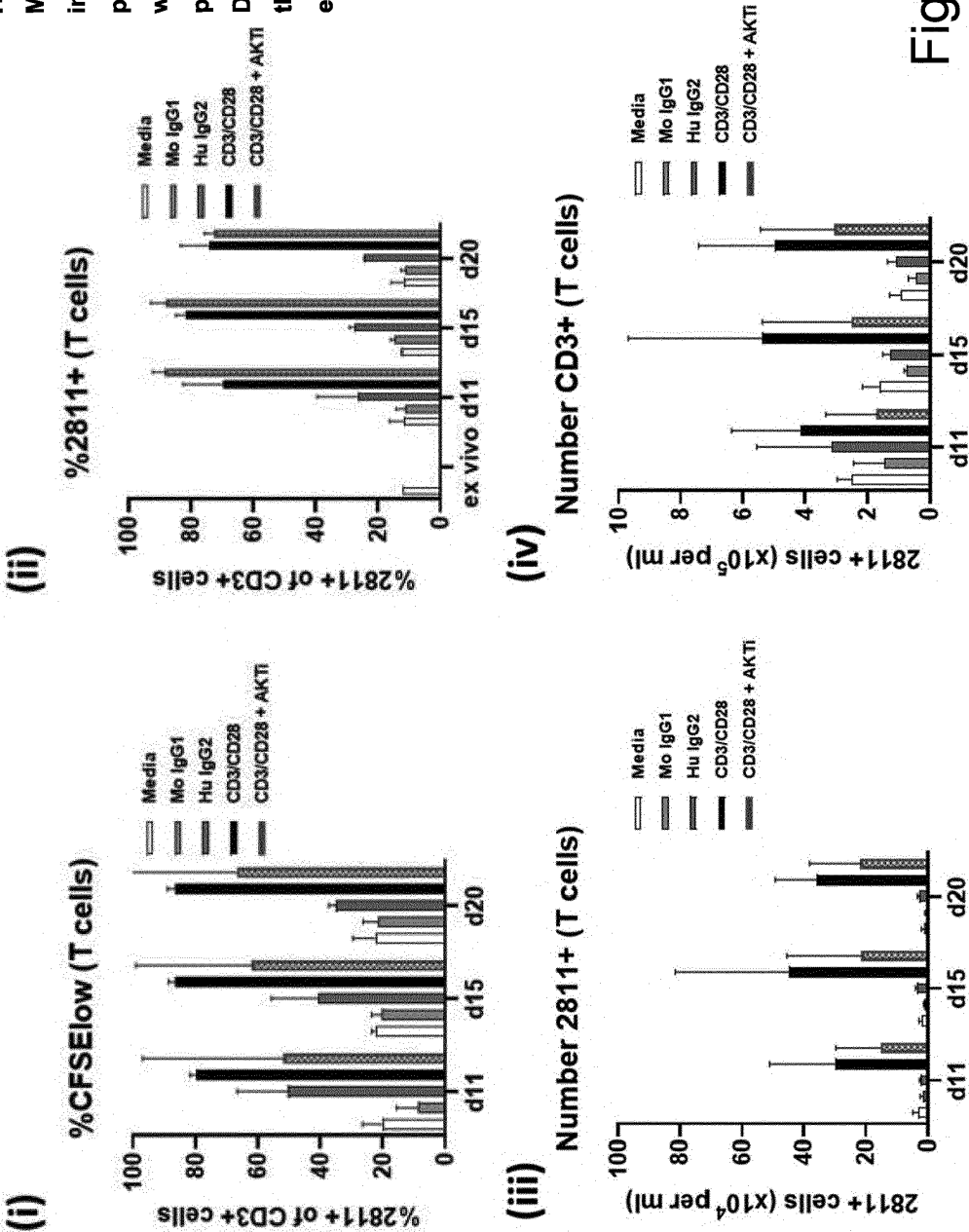
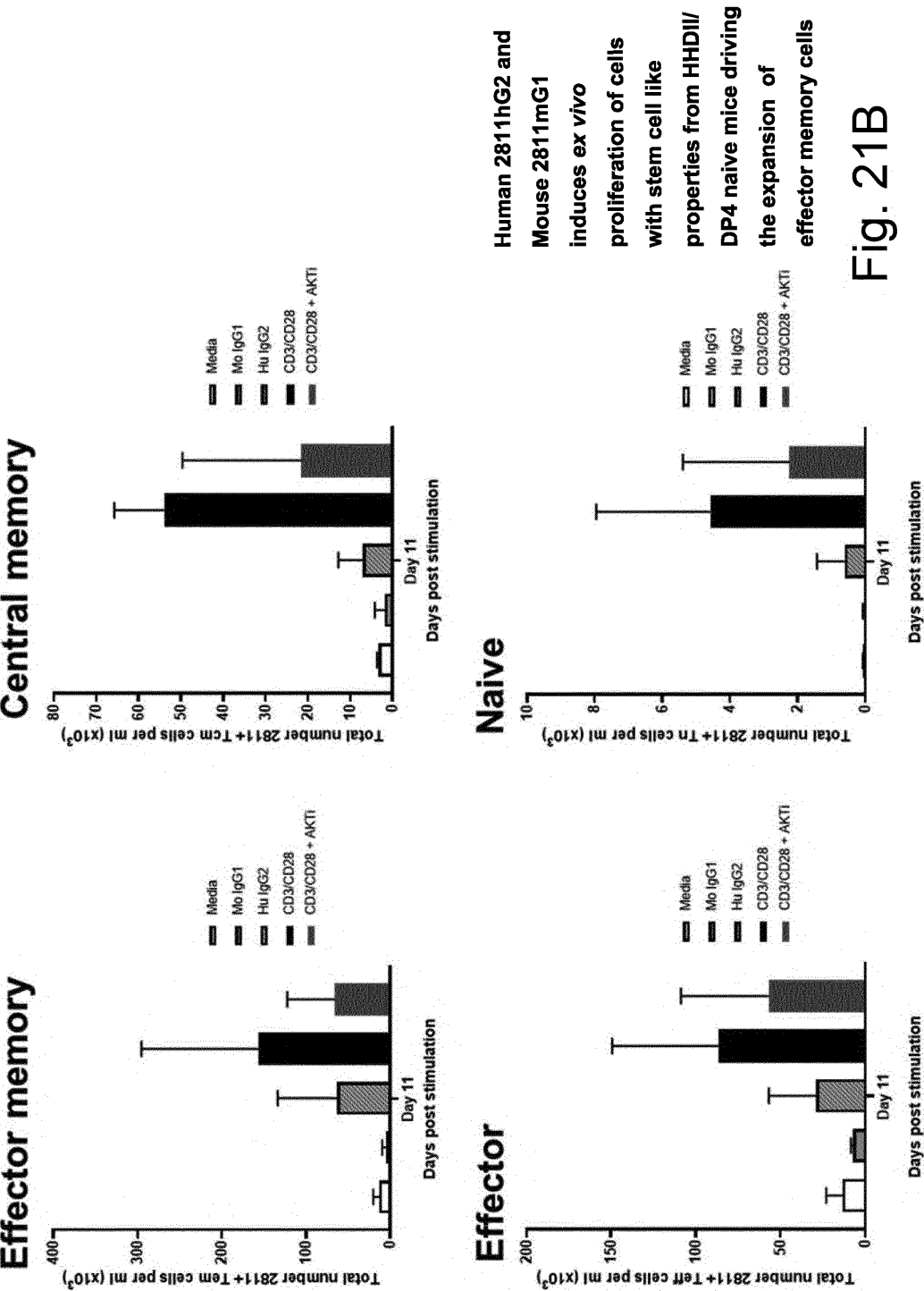
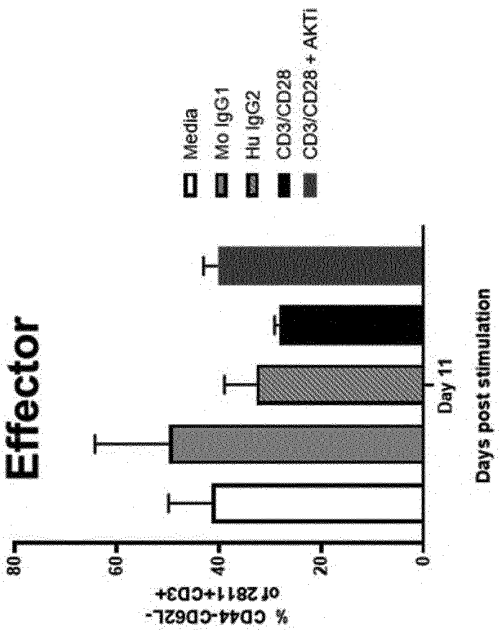
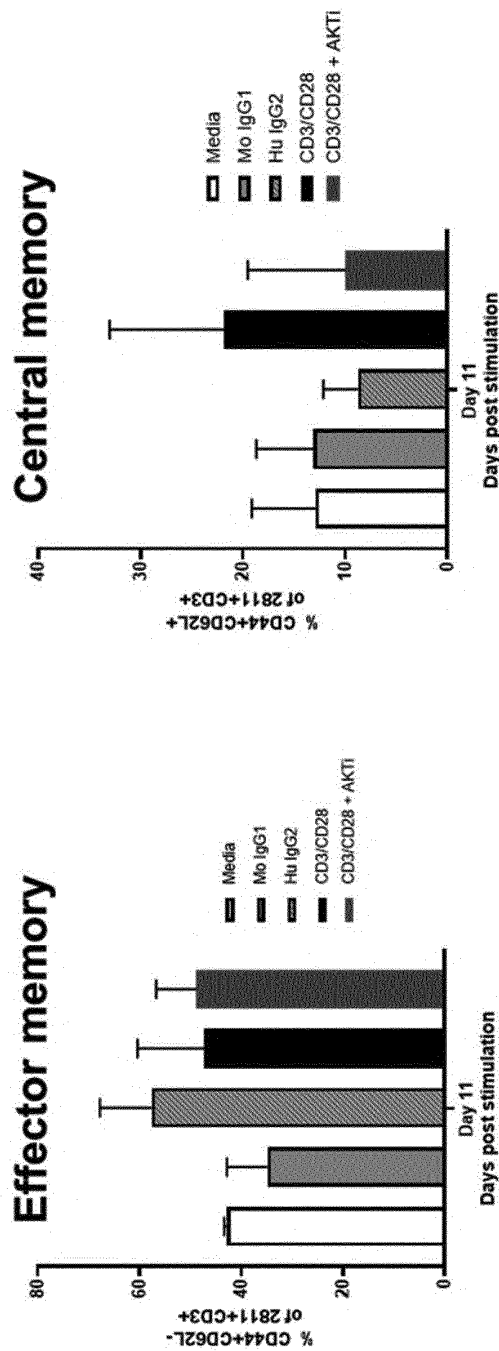


Fig. 21A



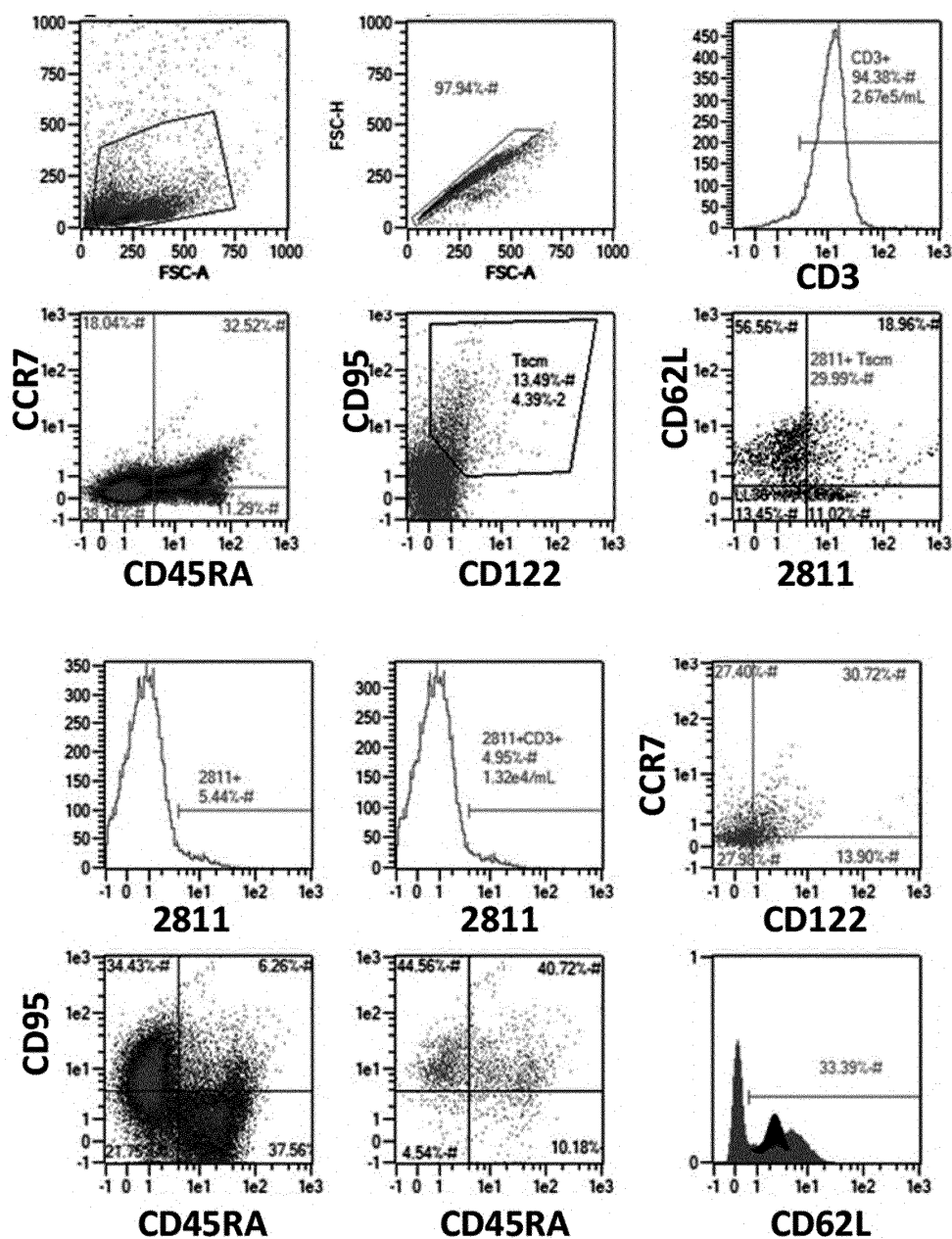


Human 2811hG2 and  
Mouse 2811mG1  
induces ex vivo  
proliferation of cells  
with stem cell like  
properties from HHDII/  
DP4 naive mice driving  
the expansion of  
effector memory cells

Fig. 21C

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## Media control day 20



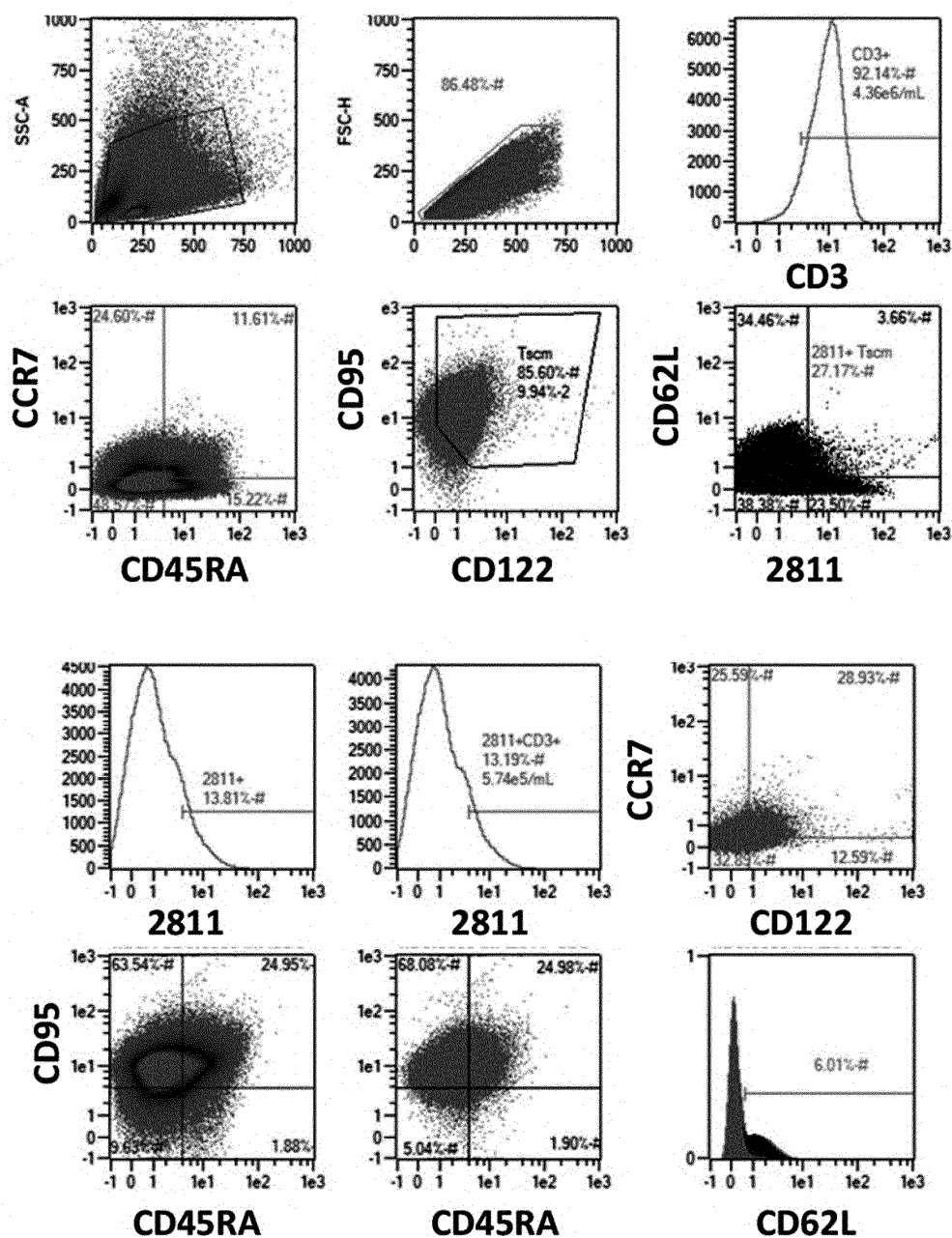
Anti CD3 and CD28 induces *ex vivo*  
proliferation of 2811+ cells isolated  
from healthy donors

Fig. 22A

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## CD3/CD28 stimulation day 20



Anti CD3 and CD28 induces *ex vivo* proliferation of 2811+ cells isolated from healthy donors

Fig. 22A  
(continued)

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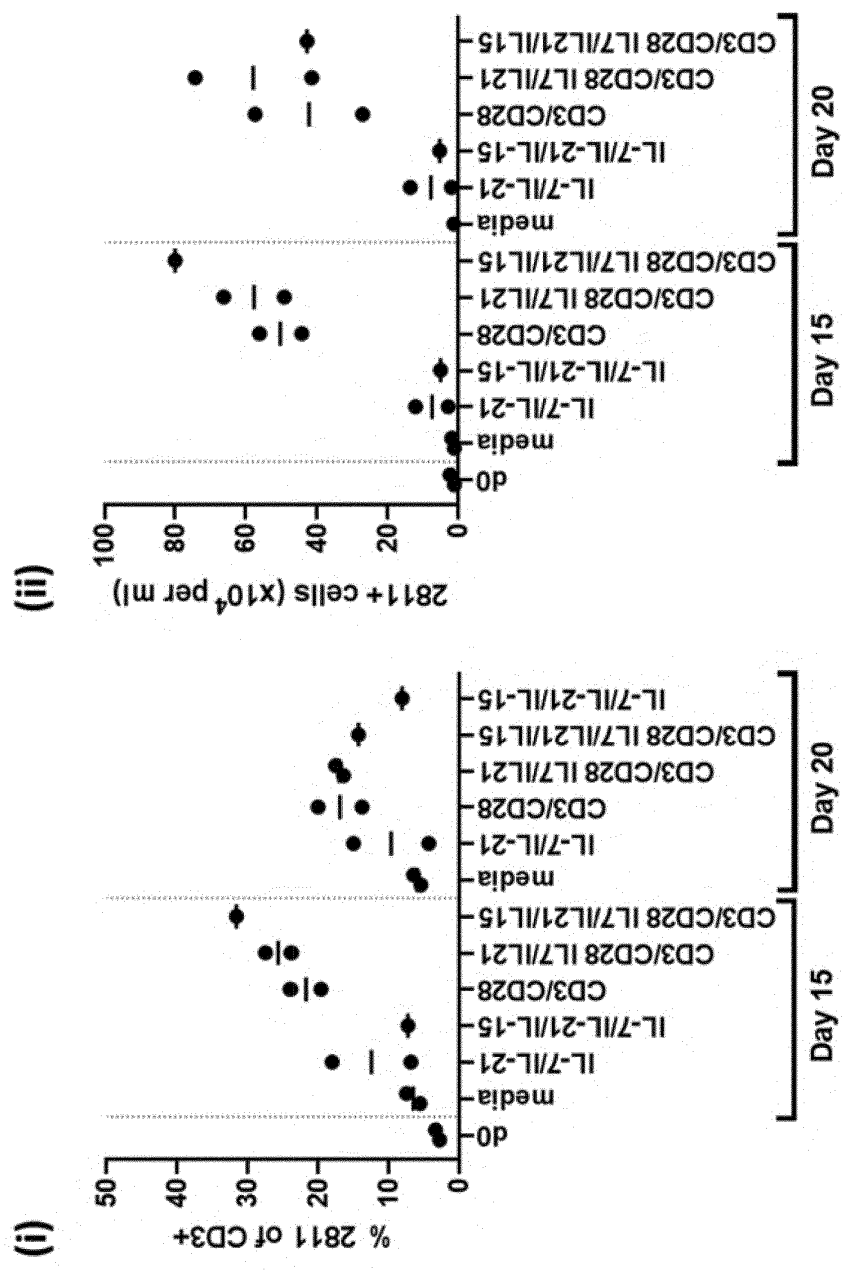


Fig. 22B

Anti CD3 and CD28 induces ex vivo proliferation of 2811+ cells isolated from healthy donors

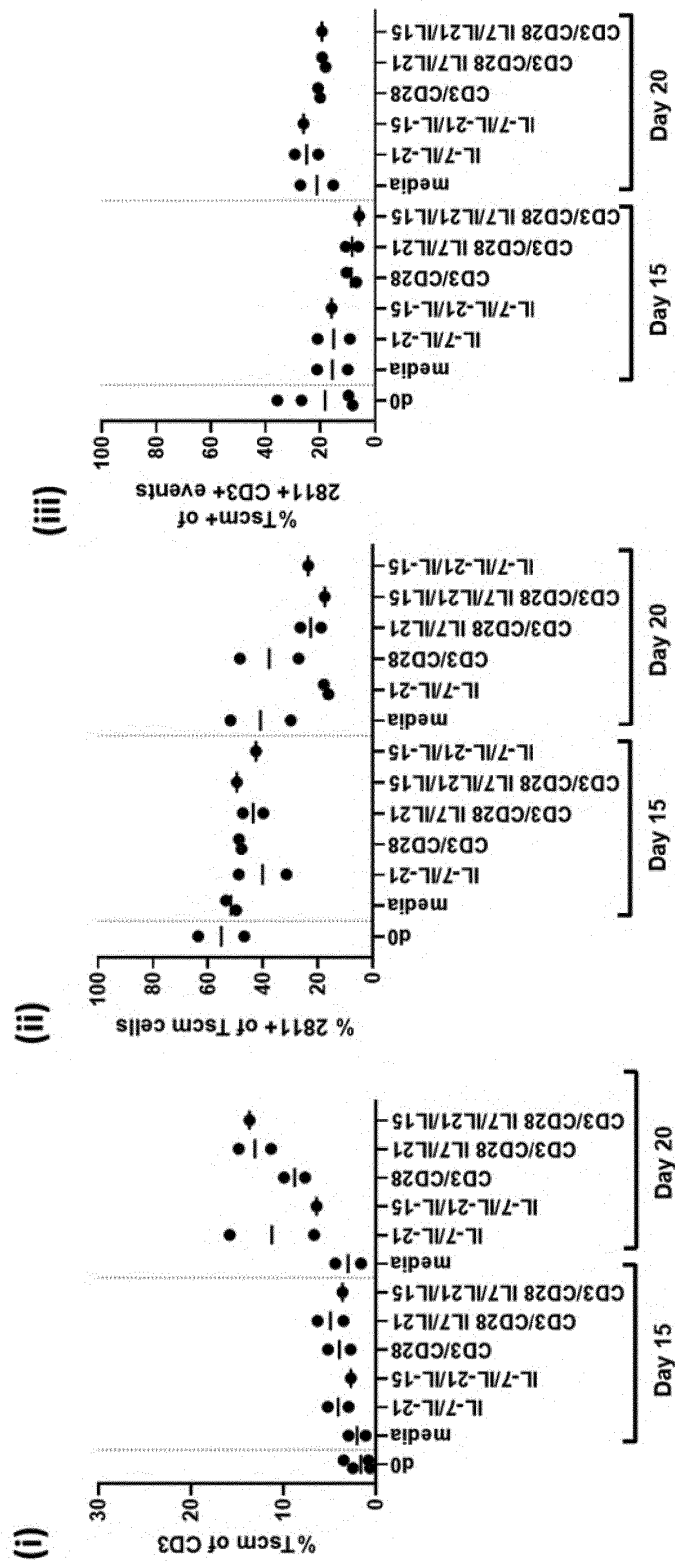
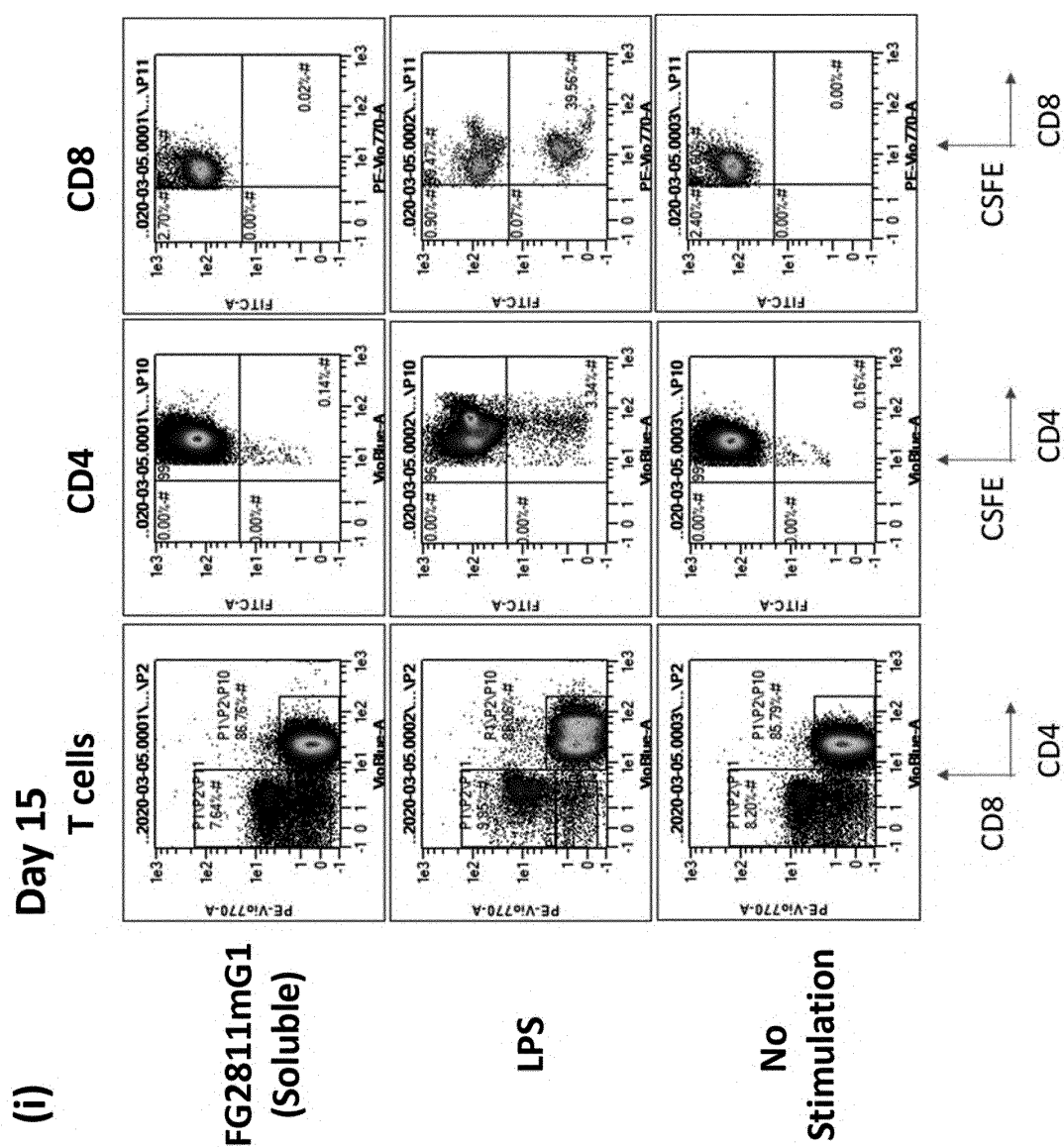
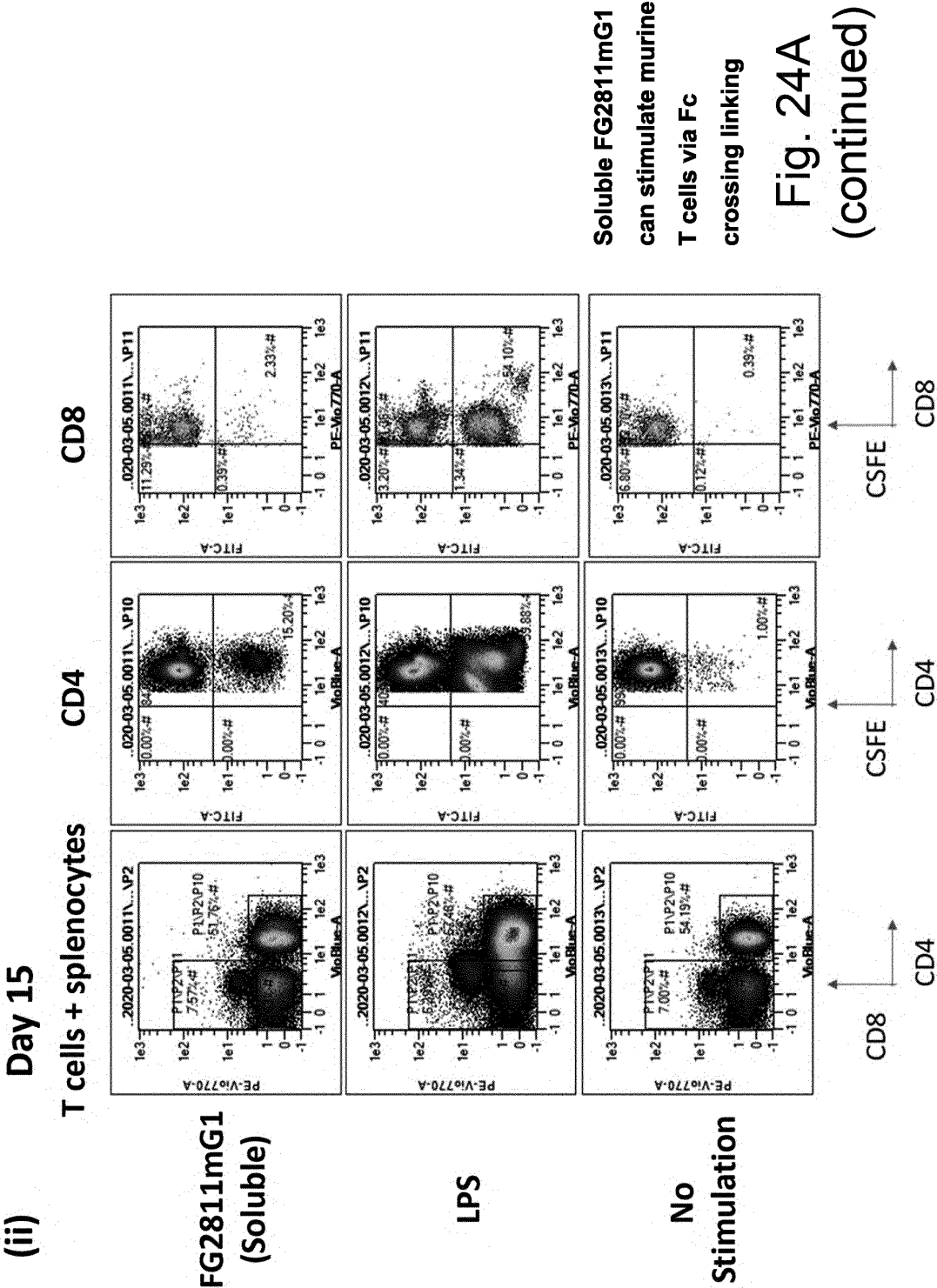


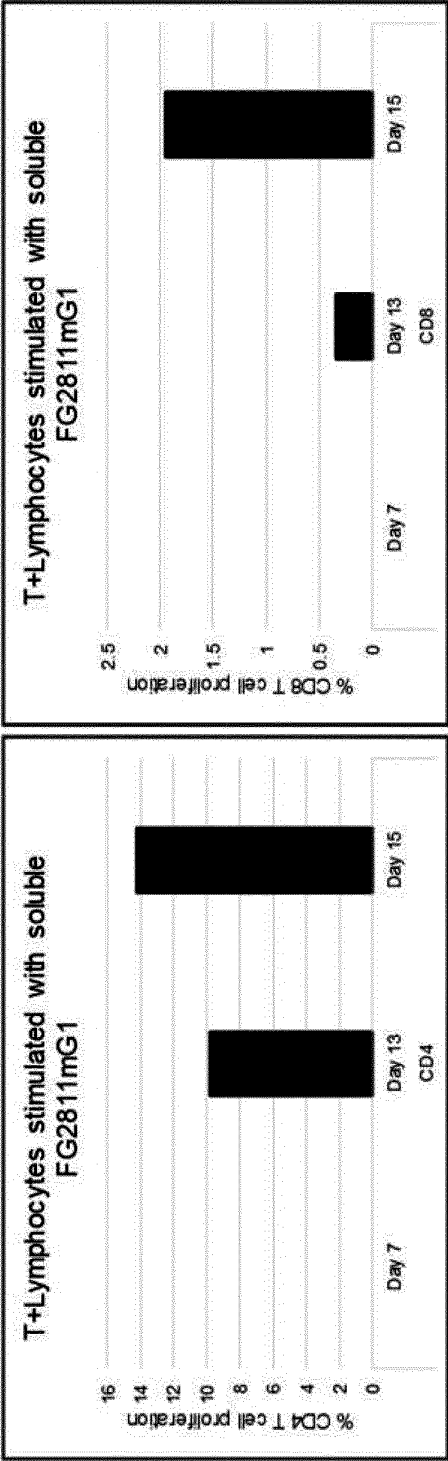
Fig. 23

The frequency of Tscm cells is increased following stimulation with anti CD3/CD28

**Fig. 24A**







Soluble FG2811mG1  
can stimulate murine  
T cells via Fc  
crossing linking

**Fig. 24B**