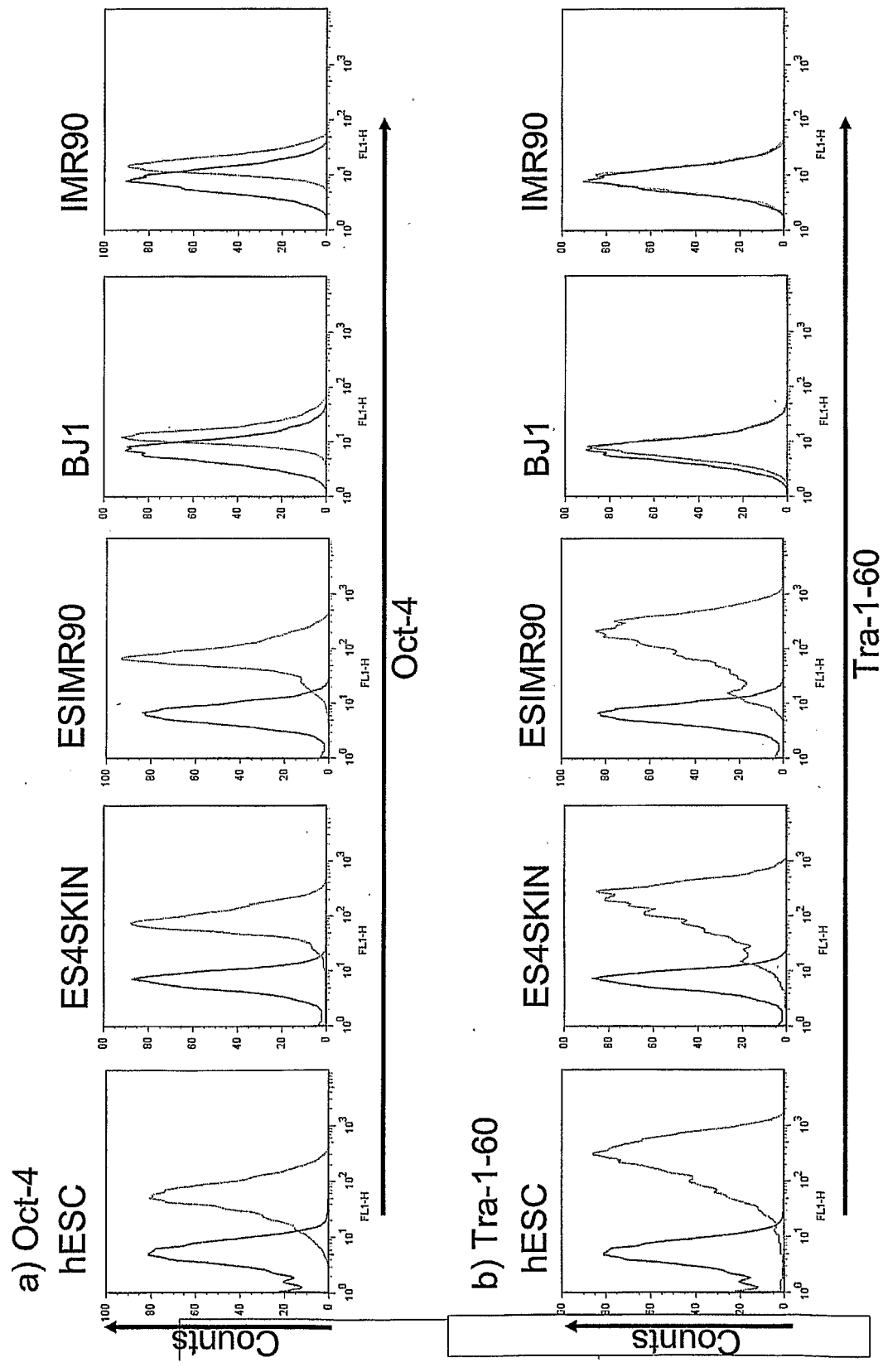

a) Oct-4
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
Counts
FL1-H
Oct-4
b) Tra-1-60
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
Counts
FL1-H
Tra-1-60

Figure 1

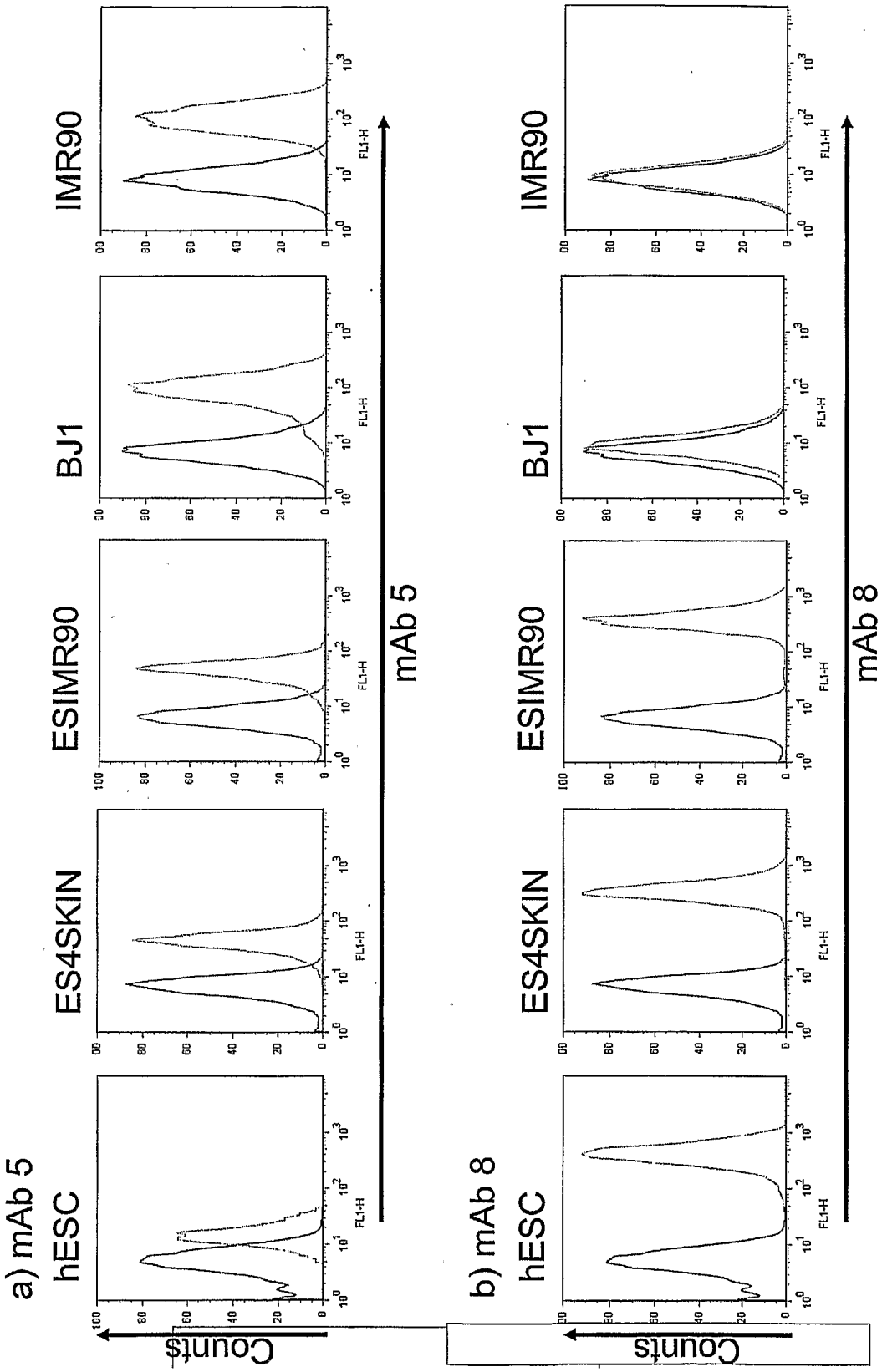

a) mAb 5
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
mAb 5
Counts
b) mAb 8
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
mAb 8
Counts
FL1-H

Figure 2

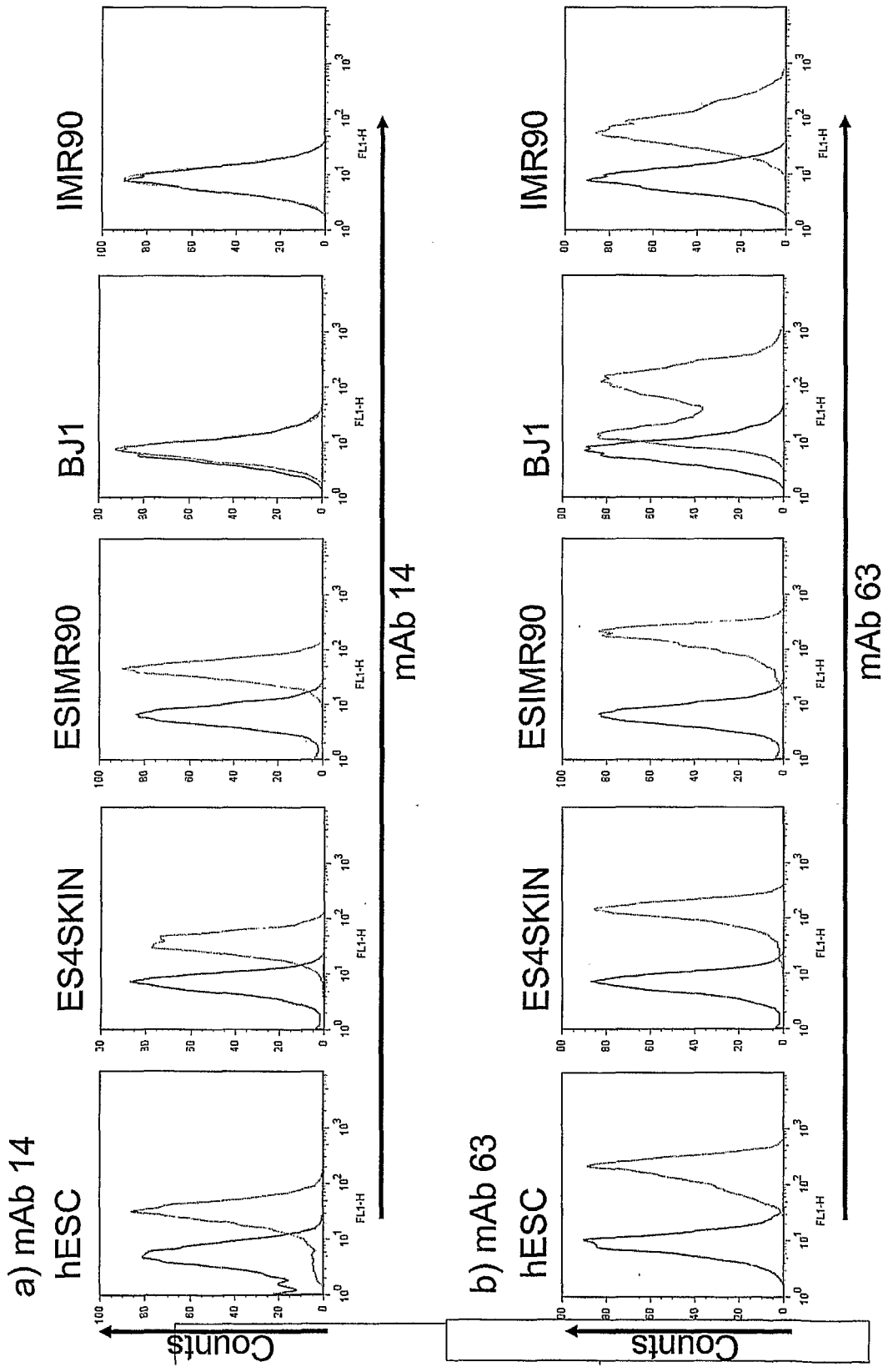

a) mAb 14
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
mAb 14
Counts
b) mAb 63
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
mAb 63
Counts
FL1-H

Figure 3

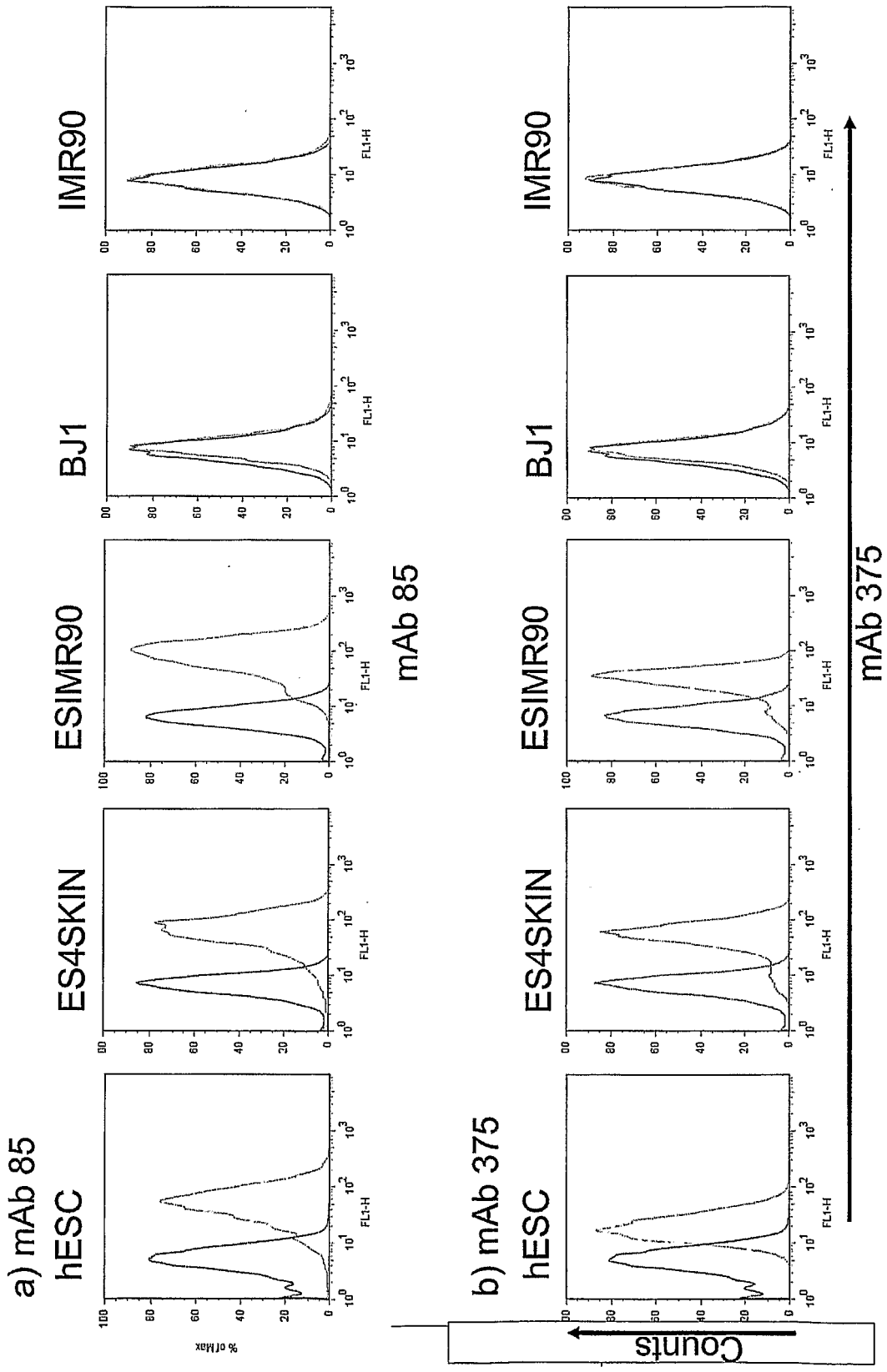

a) mAb 85
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
% of Max
FL1-H
mAb 85
b) mAb 375
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
Counts
FL1-H
mAb 375

Figure 4

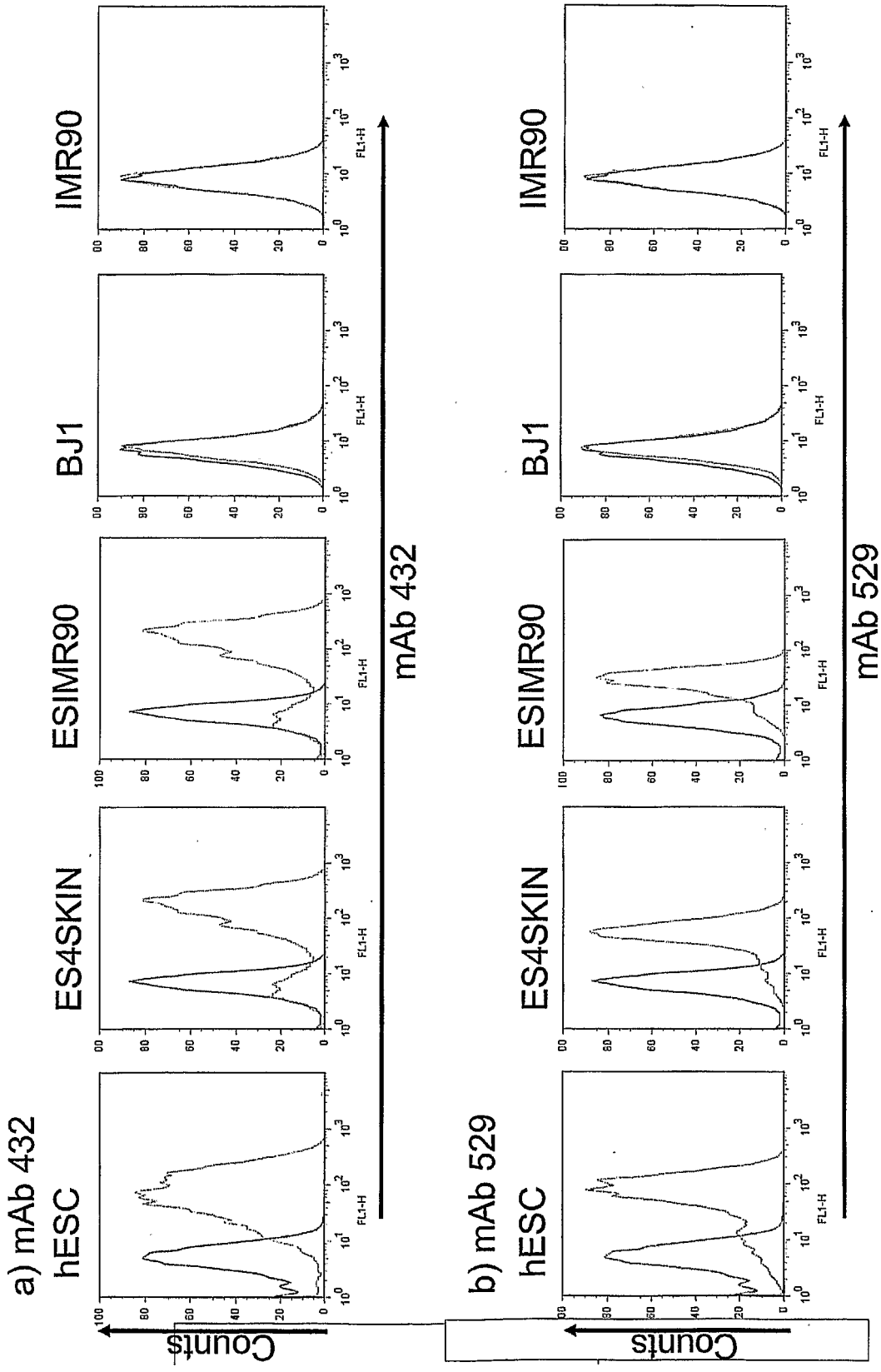

a) mAb 432
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
mAb 432
Counts
b) mAb 529
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
mAb 529
Counts
FL1-H

Figure 5

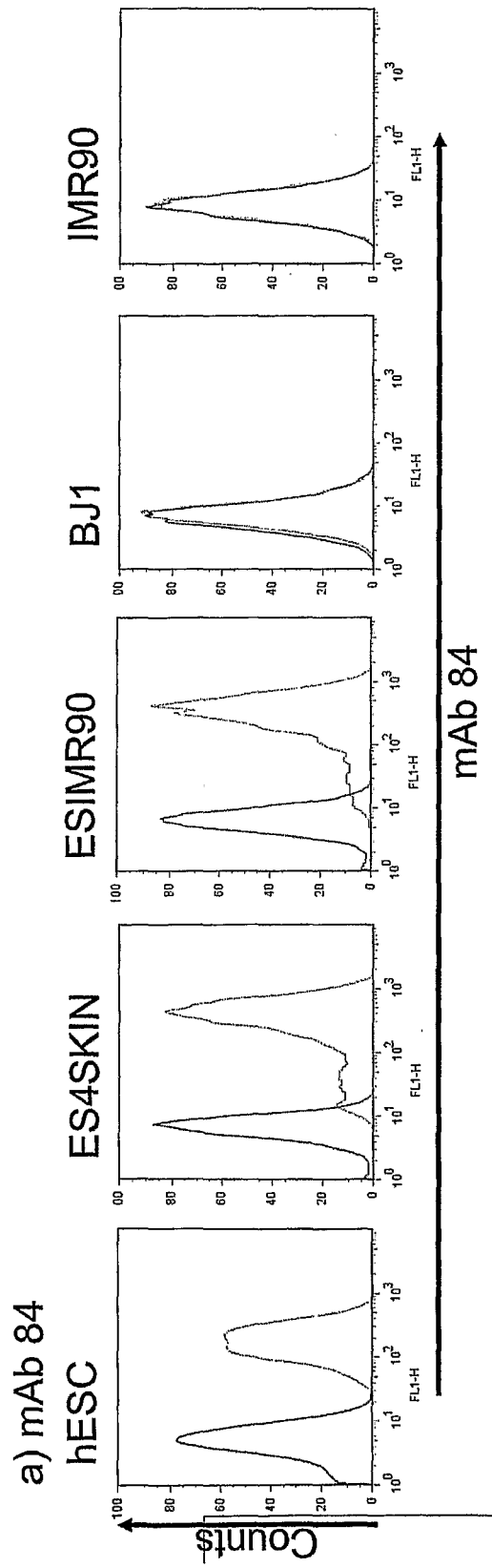


Figure 6

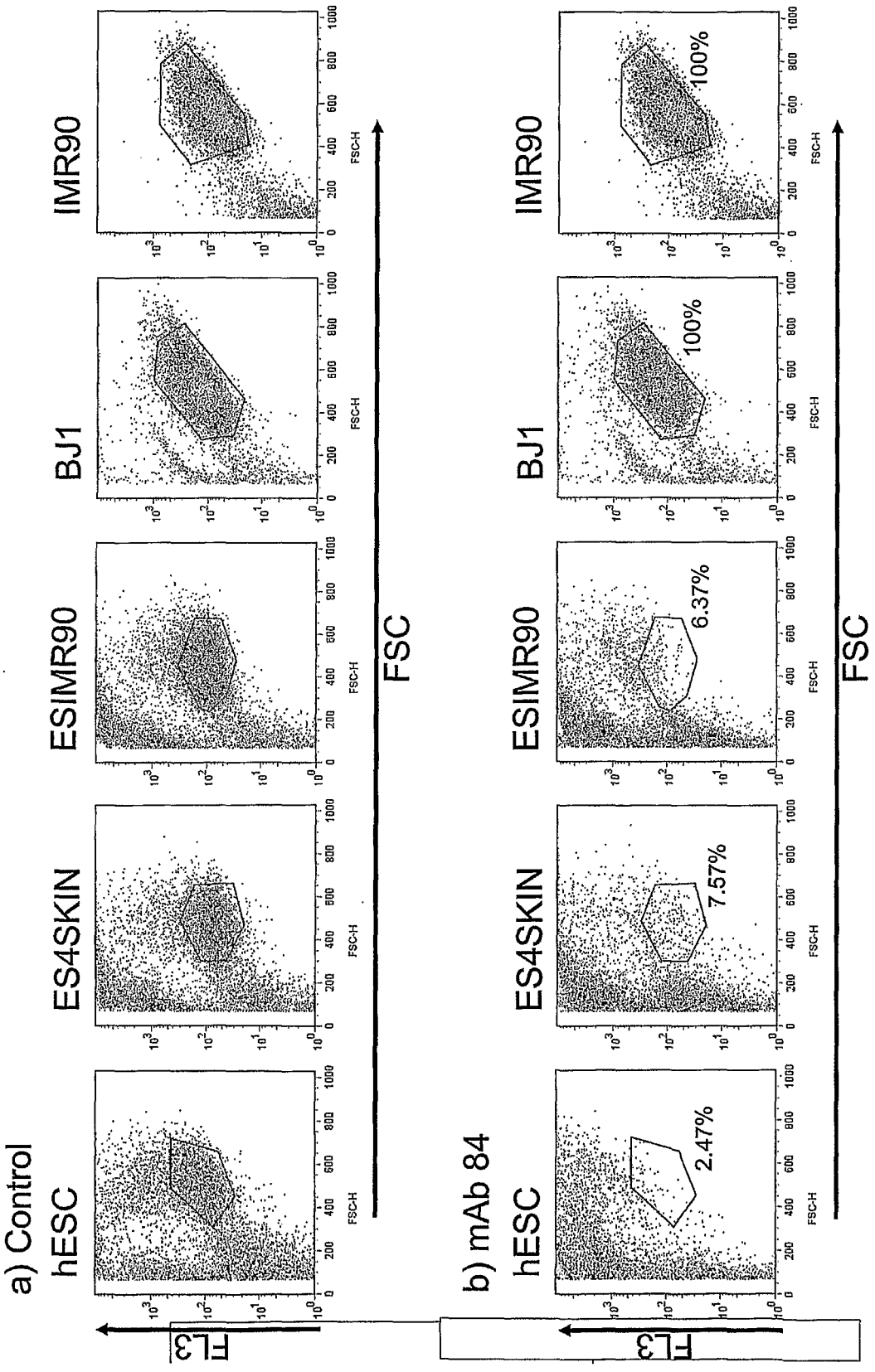

a) Control
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
b) mAb 84
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
2.47%
7.57%
6.37%
100%
100%
FL3
FSC
FSC-H

Figure 7

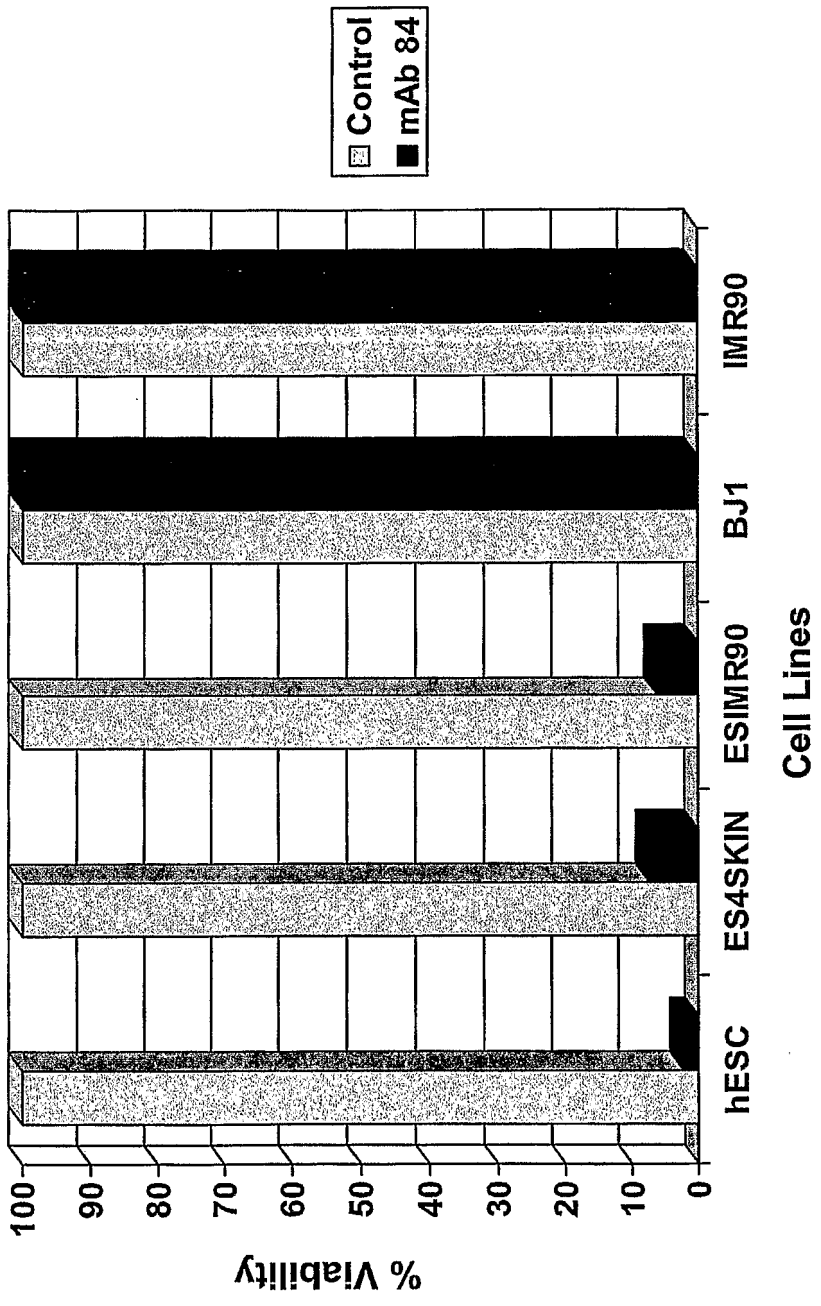

Control
mAb 84
% Viability
100
90
80
70
60
50
40
30
20
10
0
hESC
ES4SKIN
ESIMR90
BJ1
IMR90
Cell Lines

Figure 8

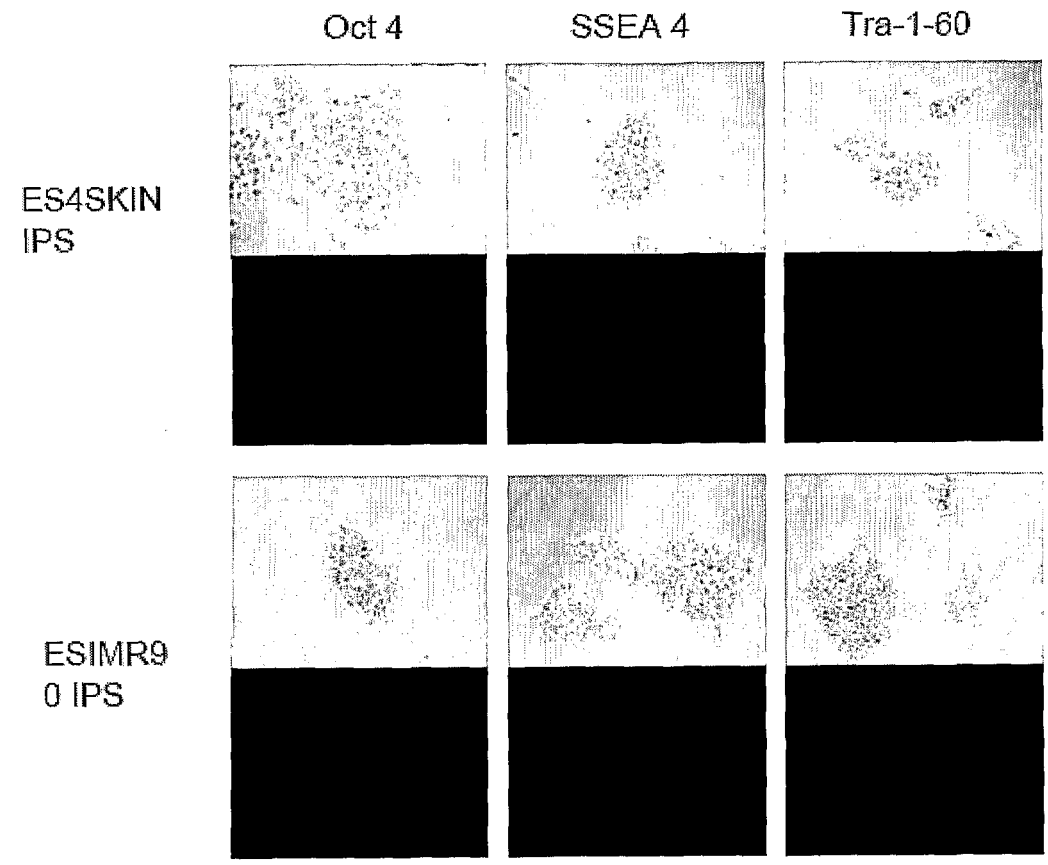

iPS Cells Express hESC-Pluripotent Markers
Oct 4
SSEA 4
Tra-1-60
ES4SKIN IPS
ESIMR90 IPS

Figure 9

Panel of hESC-specific mAbs Binds to iPS Cells

	HES-3 (hESC)	ES4SKIN (IPS)	ESIMR90 (IPS)	Foreskin	IMR90
mAb 84	✓	✓	✓	×	×
mAb 85	✓	✓	✓	×	×
mAb 5	✓	✓	✓	✓	✓
mAb 8	✓	✓	✓	×	×
mAb 14	✓	✓	✓	×	×
mAb 63	✓	✓	✓	✓	✓
mAb 95	✓	✓	✓	×	×
mAb 375	✓	✓	✓	×	×
mAb 432	✓	✓	✓	×	×
mAb 529	✓	✓	✓	×	×
OCT-4	✓	✓	✓	×	×
TRA-1-60	✓	✓	✓	×	×

Figure 10

```
  1  MRCALALSAL LLLLSTPPLL PSSPSPSPSP SPSQNATQTT TDSSNKTAPT
 51  PASSVTIMAT DTAQQSTVPT SKANEILASV KATTLGVSSD SPGTTTLAQQ
101  VSGPVNTTVA RGGGSGNPTT TIESPKSTKS ADTTTVATST ATAKPNTTSS
151  QNGAEDTTNS GGKSSHSVTT DLTSTKAEHL TTPHPTSPLS PRQPTLTHPV
201  ATPTSSGHDH LMKISSSSST VAIPGYTFTS PGMTTTLPSS VISQRTQQTS
251  SQMPASSTAP SSQETVQPTS PATALRTPTL PETMSSSPTA ASTTHRYPKT
301  PSPTVAHESN WAKCEDLETQ TQSEKQLVLN LTGNTLCAGG ASDEKLISLI
351  CRAVKATFNP AQDKCGIRLA SVPGSQTVVV KEITIHTKLP AKDVYERLKD
401  KWDELKEAGV SDMKLGDQGP PEEAEDRFSM PLIITIVCMA SFLLLVAALY
451  GCCHQRLSQR KDQQRLTEEL QTVENGYHDN PTLEVMETSS EMQEKKVVSL
501  NGELGDSWIV PLDNLTKDDL DEEEDTHL
```

SEQ ID NO: 1

Figure 11

```
      1  MRCALALSAL LLLLSTPPLL PSSPSPSPSP SQNATQTTTD SSNKTAPTPA SSVTIMATDT
61    AQQSTVPTSK ANEILASVKA TTLGVSSDSP GTTTLAQQVS GPVNTTVARG GGSGNPTTTI
121   ESPKSTKSAD TTTVATSTAT AKPNTTSSQN GAEDTTNSGG KSSHSVTTDL TSTKAEHLTT
181   PHPTSPLSPR QPTSTHPVAT PTSSGHDHLM KISSSSSTVA IPGYTFTSPG MTTTLLETVF
241   HHVSQAGLEL LTSGDLPTLA SQSAGITASS VISQRTQQTS SQMPASSTAP SSQETVQPTS
301   PATALRTPTL PETMSSSPTA ASTTHRYPKT PSPTVAHESN WAKCEDLETQ TQSEKQLVLN
361   LTGNTLCAGG ASDEKLISLI CRAVKATFNP AQDKCGIRLA SVPGSQTVVV KEITIHTKLP
421   AKDVYERLKD KWDELKEAGV SDMKLGDQGP PEEAEDRFSM PLIITIVCMA SFLLLVAALY
481   GCCHQRLSQR KDQQRLTEEL QTVENGYHDN PTLEVMETSS EMQEKKVVSL NGELGDSWIV
541   PLDNLTKDDL DEEEDTHL
      [O00592.2  GI:229462740; SEQ ID NO:2]
```

Figure 12

```
1     MRCALALSAL LLLLSTPPLL PSSPSPSPSP SPSQNATQTT TDSSNKTAPT PASSVTIMAT
61    DTAQQSTVPT SKANEILASV KATTLGVSSD SPGTTTLAQQ VSGPVNTTVA RGGSSGNPTT
121   TIESPKSTKS ADTTTVATST ATAKPNTTSS QNGAEDTTNS GGKSSHSVTT DLTSTKAEHL
181   TTPHPTSPLS PRQPTLTHPV ATPTSSGHDH LMKISSSSST VAIPGYTFTS PGMTTTLLET
241   VFHHVSQAGL ELLTSGDLPT LASQSAGITA SSVISQRTQQ TSSQMPASST APSSQETVQP
301   TSPATALRTP TLPETMSSSP TAASTTHRYP KTPSPTVAHE SNWAKCEDLE TQTQSEKQLV
361   LNLTGNTLCA GGASDEKLIS LICRAVKATF NPAQDKCGIR LASVPGSQTV VVKEITIHTK
421   LPAKDVYERL KDKWDELKEA GVSDMKLGDQ GPPEEAEDRF SMPLIITIVC MASFLLLVAA
481   LYGCCHQRLS QRKDQQRLTE ELQTVENGYH DNPTLEVMET SSEMQEKKVV SLNGELGDSW
541   IVPLDNLTKD DLDEEEDTHL
      [AAI43319.1  GI:219520307; SEQ ID NO: 3]
```

Figure 13

mAb 84 VL

The amino acids not underlined correspond to framework regions and underlined corresponds to CDRs.

```
1          ACGCCAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCCAACGCGTTGGGAG

61         CTCTCCCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATTGACATTGAGCTCACCCAG
1                                                    D  I  E  L  T  Q

121        TCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGC
7           S  P  A  I  M  S  A  S  P  G  E  K  V  T  M  T  C  S  A  S

181        TCAAGTGTAAATTACATGTACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAGACTCCTG
27          S  S  V  N  Y  M  Y  W  Y  Q  Q  K  P  G  S  S  P  R  L  L

241        ATTTATGACACATCCAACCTGGCTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGGTCT
47          I  Y  D  T  S  N  L  A  S  G  V  P  V  R  F  S  G  S  G  S

301        GGGACCTCTTACTCTCTCACAATCAGCCGAATGGAGGCTGAAGATGCTGCCACTTATTAC
67          G  T  S  Y  S  L  T  I  S  R  M  E  A  E  D  A  A  T  Y  Y

361        TGCCAGCAGTGGAGTAGTTACCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA
87          C  Q  Q  W  S  S  Y  P  Y  T  F  G  G  G  T  K  L  E  I  K

421        CGGAATCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAG
107         R

481        TGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGG
541        CGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGA
601        AGAGGCGCGCACCGATCGCCCTTCTCAACAGTTGCGCAGCCTGAATAGCGAATAGACGCG
661        CCCTGTAGCGGCGCATTATGCGCCGGCGGGGTGTGGTGGTTACGCGCAGCGTGACCGCTAC
721        ACTTGTCAGCGCCCTAGCGCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTC
781        GCCGGCTTGCTCGTCAGG
```

Based on V Base and Kabat Numbering
NOT UNDERLINED: Framework
underlined: CDR

Figure 14

mAb 84 VH

The amino acids not underlined correspond to framework regions and underlined corresponds to CDRs.

```
1          AGACGGCCAGTGAATTGTATACGACTCACTATAGGGCGAATTGGGCCCGACGTCGCATGCT

61         CCCGGCCGCCATGGCCGCGGGATTCAGGTGCAGCTGCAGCAGTCAGGAGGAGGCTTGGTG
1                                  Q  V  Q  L  Q  Q  S  G  G  G  L  V

121        CAACCTGGAGGATCCATGAAACTCTCCTGTGTTGCCTCTGGATTCACTTTCAGTAACTAC
13          Q  P  G  G  S  M  K  L  S  C  V  A  S  G  F  T  F  S  N  Y

181        TGGATGAACTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGCTTGCTGAAATTAGA
33          W  M  N  W  V  R  Q  S  P  E  K  G  L  E  W  V  A  E  I  R

241        TTGAAATCTAATAATTATGCAACACATTATGCGGAGTCTGTGAAAGGGAGGTTCACCATC
53          L  K  S  N  N  Y  A  T  H  Y  A  E  S  V  K  G  R  F  T  I

301        TCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAACTTAAGAGCTGAAGAC
73          S  R  D  D  S  K  S  S  V  Y  L  Q  M  N  N  L  R  A  E  D

361        ACTGGCATTTATTACTGTACGGGGGAGAGGGCCTGGGGCCAAGGGACCACGGTCACCGTC
93          T  G  I  Y  Y  C  T  G  E  R  A  W  G  Q  G  T  T  V  T  V

421        TCCTCAAATCACTAGTGCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGT
113         S  S

481        TGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCA
541        TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGA
601        AGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTG
661        CGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGC
721        CAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCGCTTCT
```

Based on V Base and Kabat Numbering
Not Underlined: Framework
Underlined: CDR

Figure 15

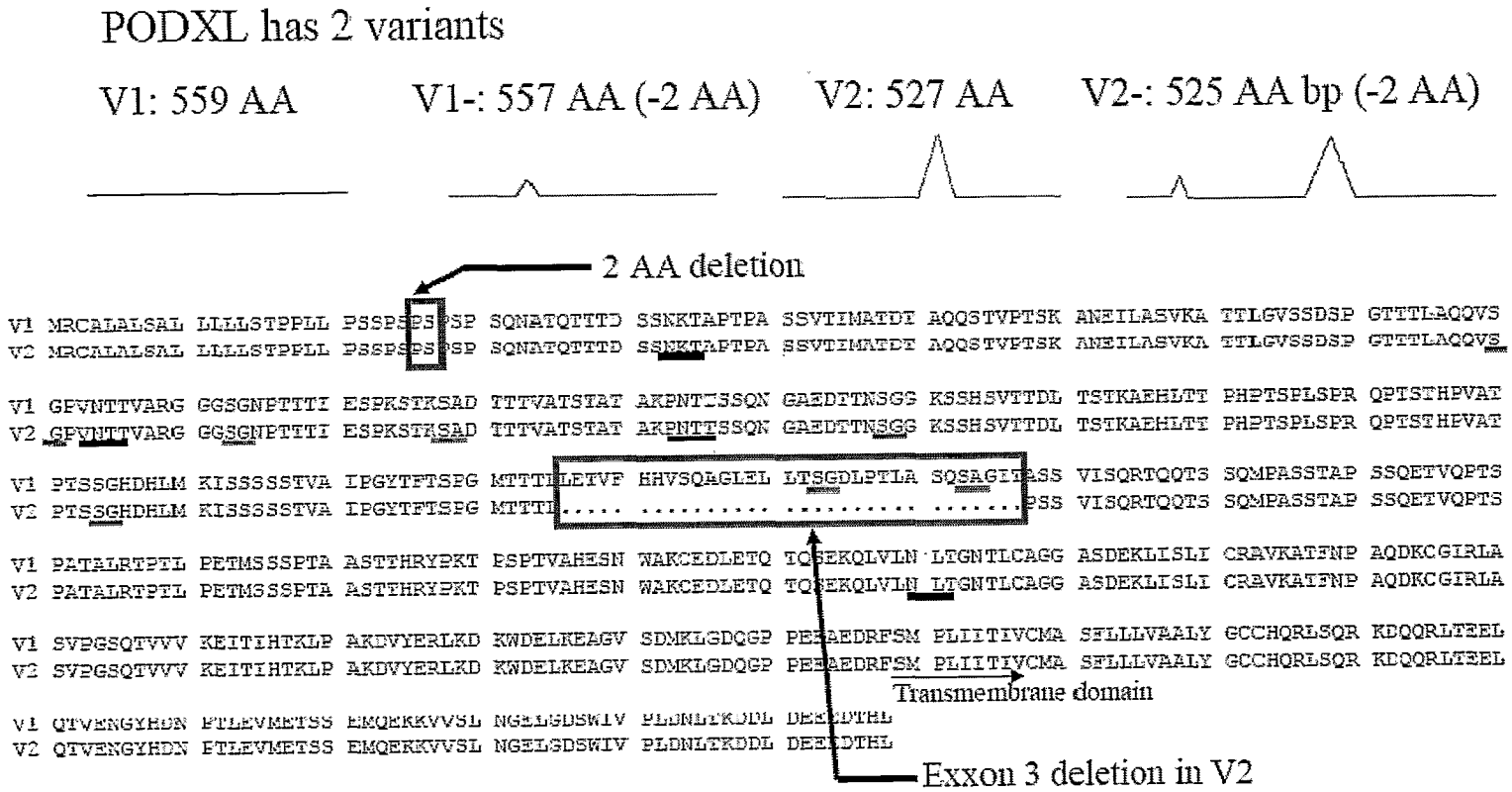

PODXL has 2 variants
V1: 559 AA
V1-: 557 AA (-2 AA)
V2: 527 AA
V2-: 525 AA bp (-2 AA)
2 AA deletion
V1 MRCALALSAL LLLLSTPPLL PSSPSPSPSP SQNATQTTTD SSKKTAPTPA SSVTIMATDT AQQSTVPTSK ANEILASVKA TTLGVSSDSP GTTTLAQQVS
V2 MRCALALSAL LLLLSTPPLL PSSPSPSPSP SQNATQTTTD SSKKTAPTPA SSVTIMATDT AQQSTVPTSK ANEILASVKA TTLGVSSDSP GTTTLAQQVS
V1 GPVNTTVARG GSSGNPTTTI ESPKSTKSAD TTTVATSTAT AKPNTTSSQN GAEDTTNSGG KSSHSVTTDL TSTKAEHLTT PHPTSPLSPR QPTSTHPVAT
V2 GPVNTTVARG GSSGNPTTTI ESPKSTKSAD TTTVATSTAT AKPNTTSSQN GAEDTTNSGG KSSHSVTTDL TSTKAEHLTT PHPTSPLSPR QPTSTHPVAT
V1 PTSSGHDHLM KISSSSSTVA IPGYTFTSPG MTTTLETVF HHVSQAGLEL LTSGDLPTLA SQSAGITGSS VISQRTQQTS SQMPASSTAP SSQETVQPTS
V2 PTSSGHDHLM KISSSSSTVA IPGYTFTSPG MTTTL..... ....PSS VISQRTQQTS SQMPASSTAP SSQETVQPTS
V1 PATALRTPTL PETMSSSPTA ASTTHRYPKT PSPTVAHESN WAKCEDLETQ TQPEKQLVLN LTGNTLCAGG ASDEKLISLI CRAVKATFNP AQDKCGIRLA
V2 PATALRTPTL PETMSSSPTA ASTTHRYPKT PSPTVAHESN WAKCEDLETQ TQPEKQLVLN LTGNTLCAGG ASDEKLISLI CRAVKATFNP AQDKCGIRLA
V1 SVPGSQTVVV KEITIHTKLP AKDVYERLKD KWDELKEAGV SDMKLGDQGP PEPAEDRFSM PLIITIVCMA SFLLLVAALY GCCHQRLSQR KDQQRLTEEL
V2 SVPGSQTVVV KEITIHTKLP AKDVYERLKD KWDELKEAGV SDMKLGDQGP PEPAEDRFSM PLIITIVCMA SFLLLVAALY GCCHQRLSQR KDQQRLTEEL
Transmembrane domain
V1 QTVENGYHDN PTLEVMETSS EMQEKKVVSL NGELGDSWIV PLDNLTKDDL DEEIDTHL
V2 QTVENGYHDN PTLEVMETSS EMQEKKVVSL NGELGDSWIV PLDNLTKDDL DEEIDTHL
Exxon 3 deletion in V2
4 N-linked glycosylation site
7 O-linked glycosylation site

Figure 16