

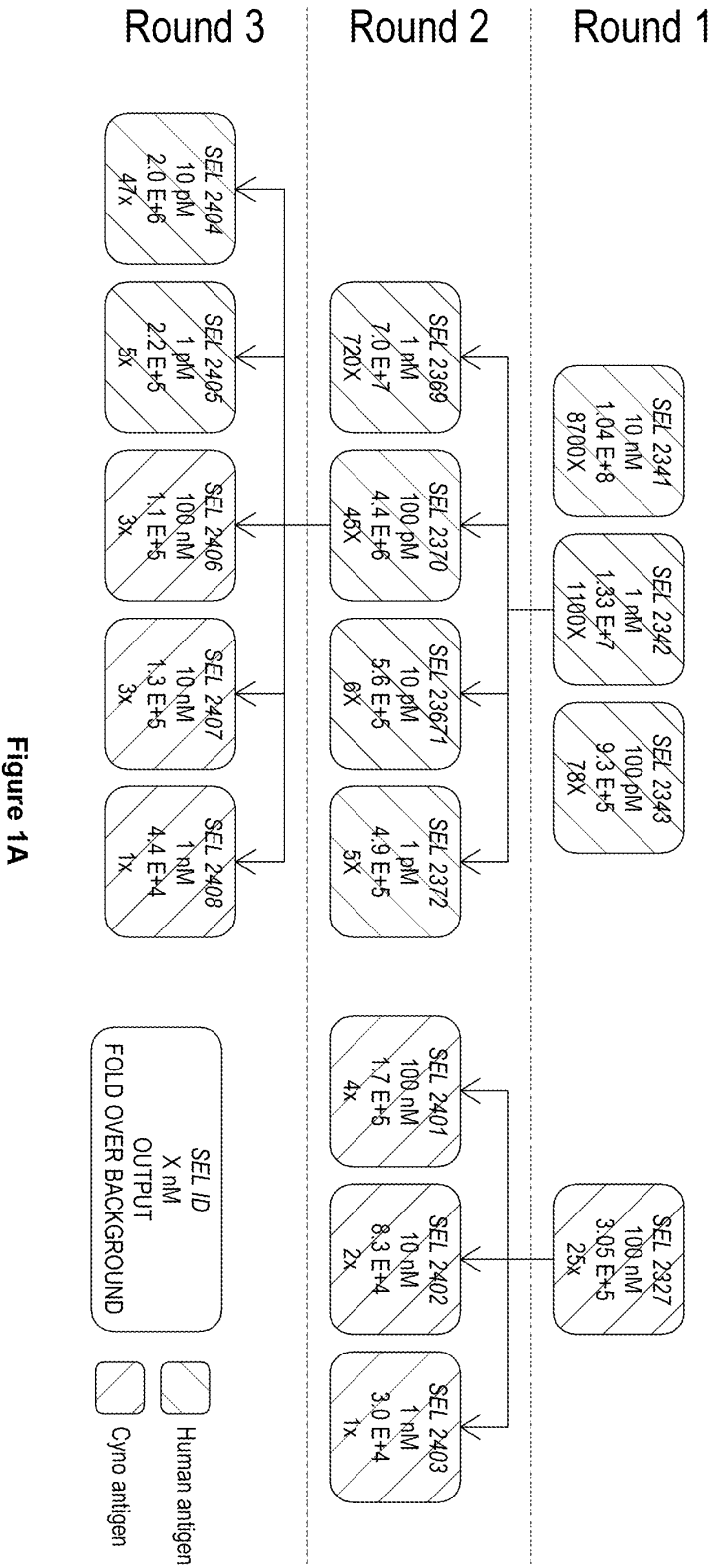


Figure 1A

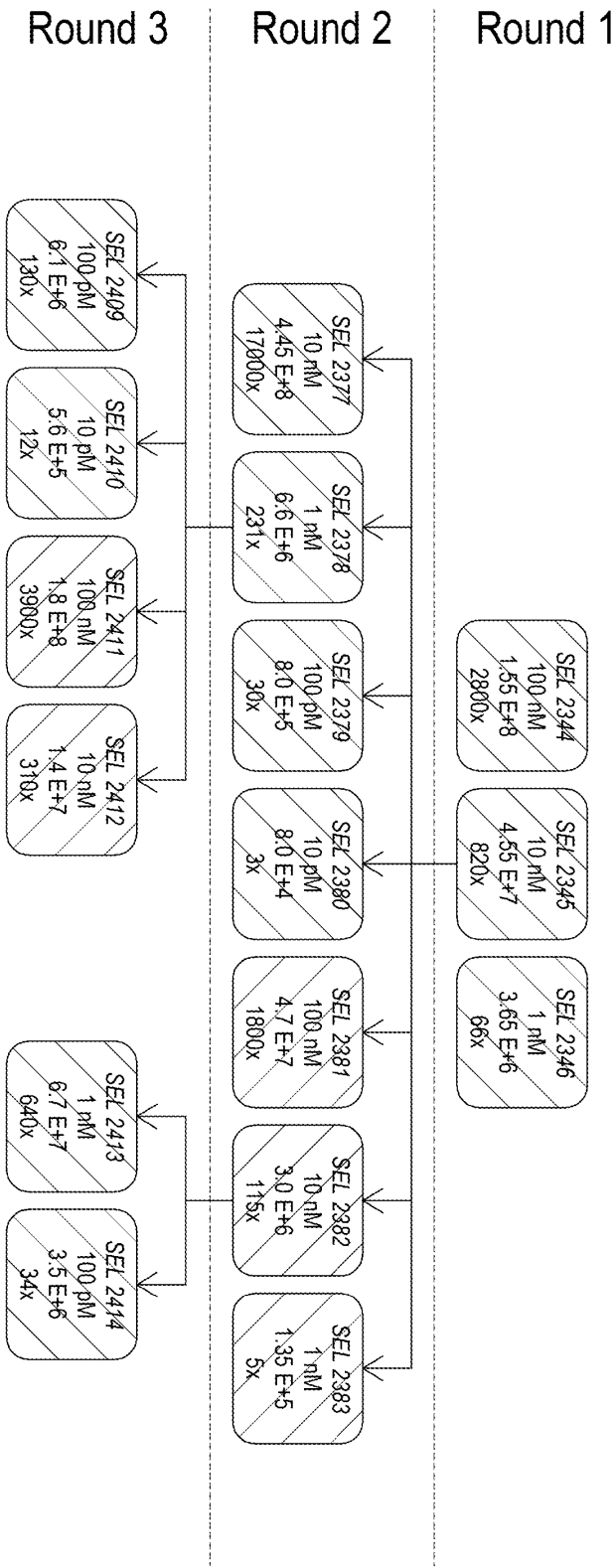


Figure 1B

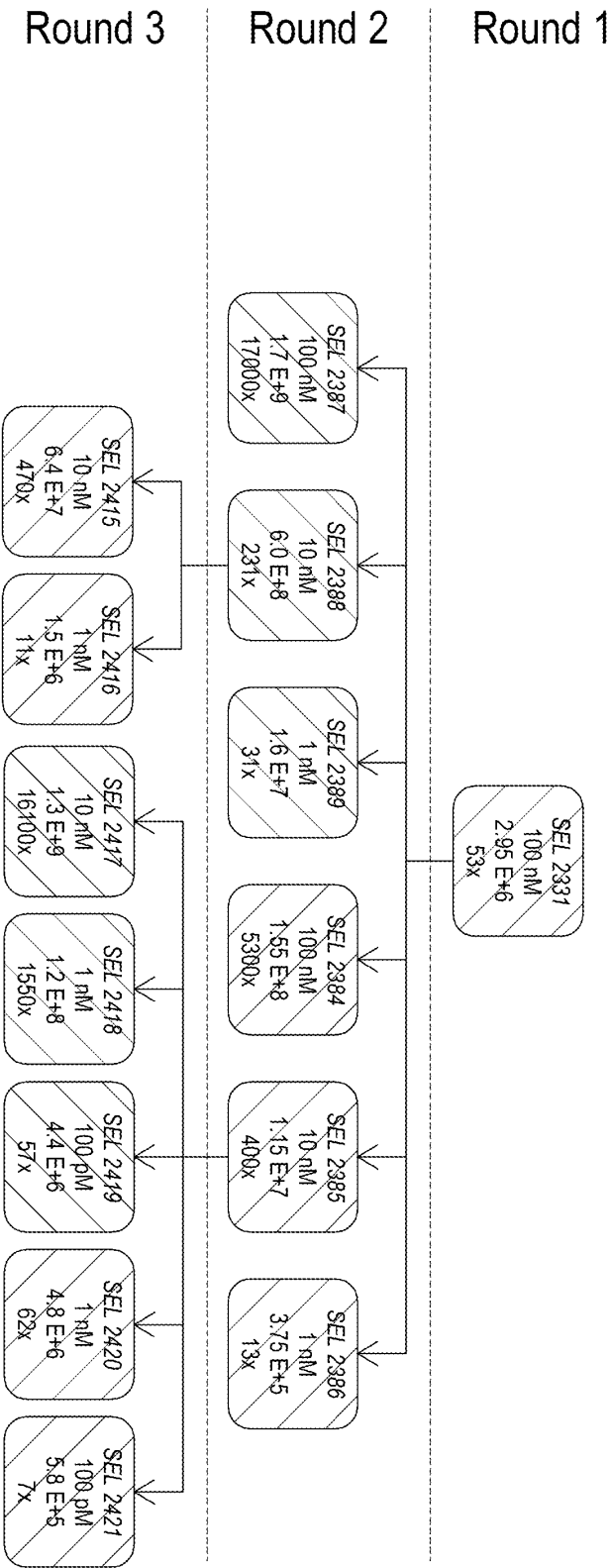


Figure 1C

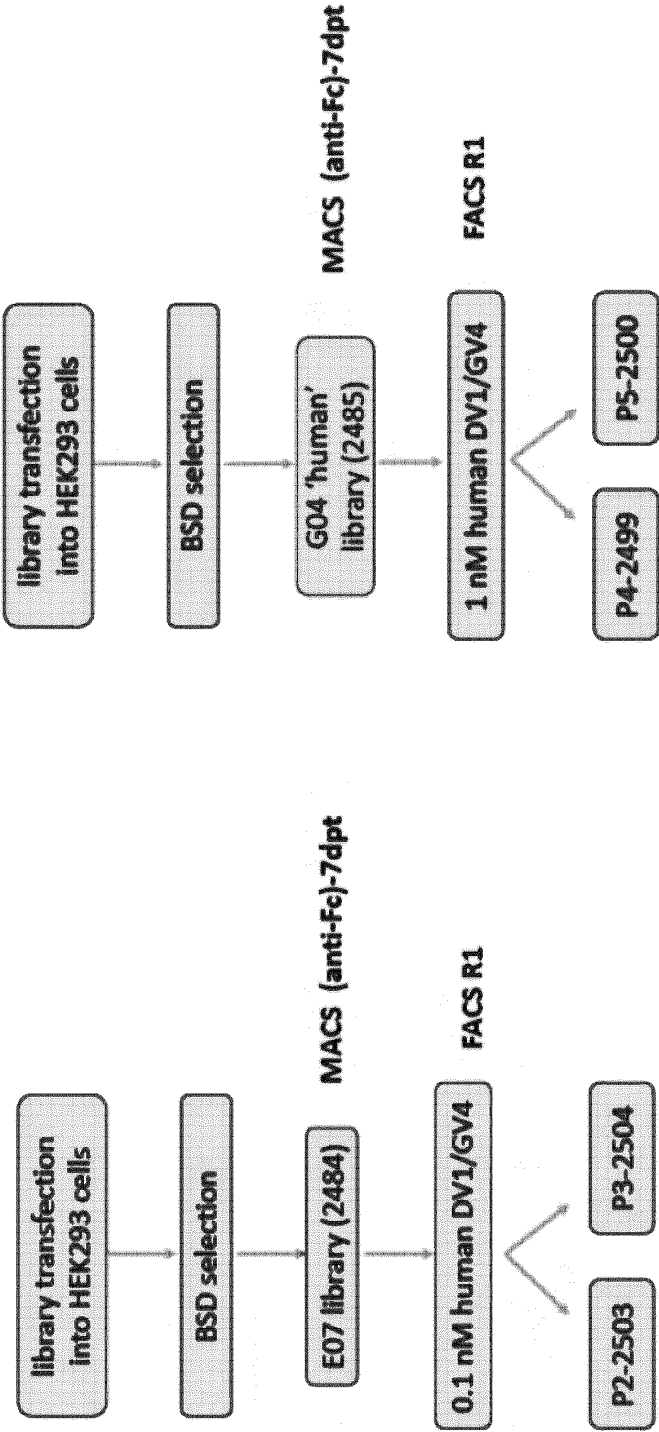


Figure 2A

Figure 2B

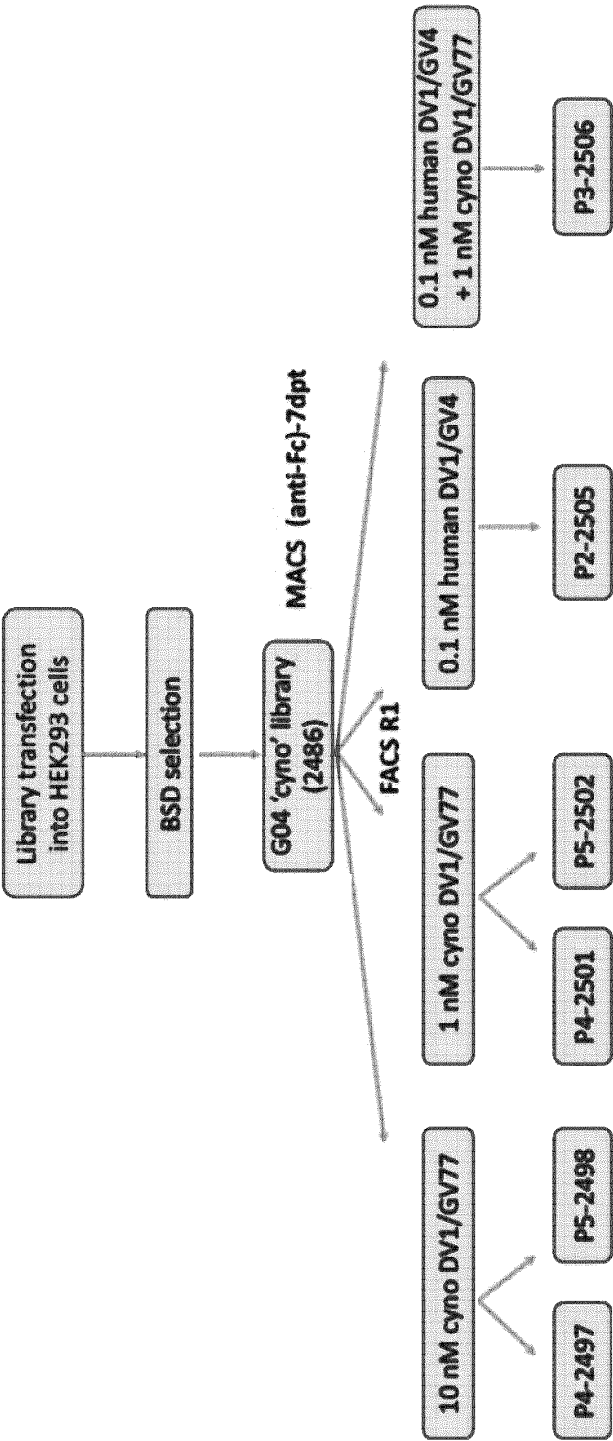


Figure 2C

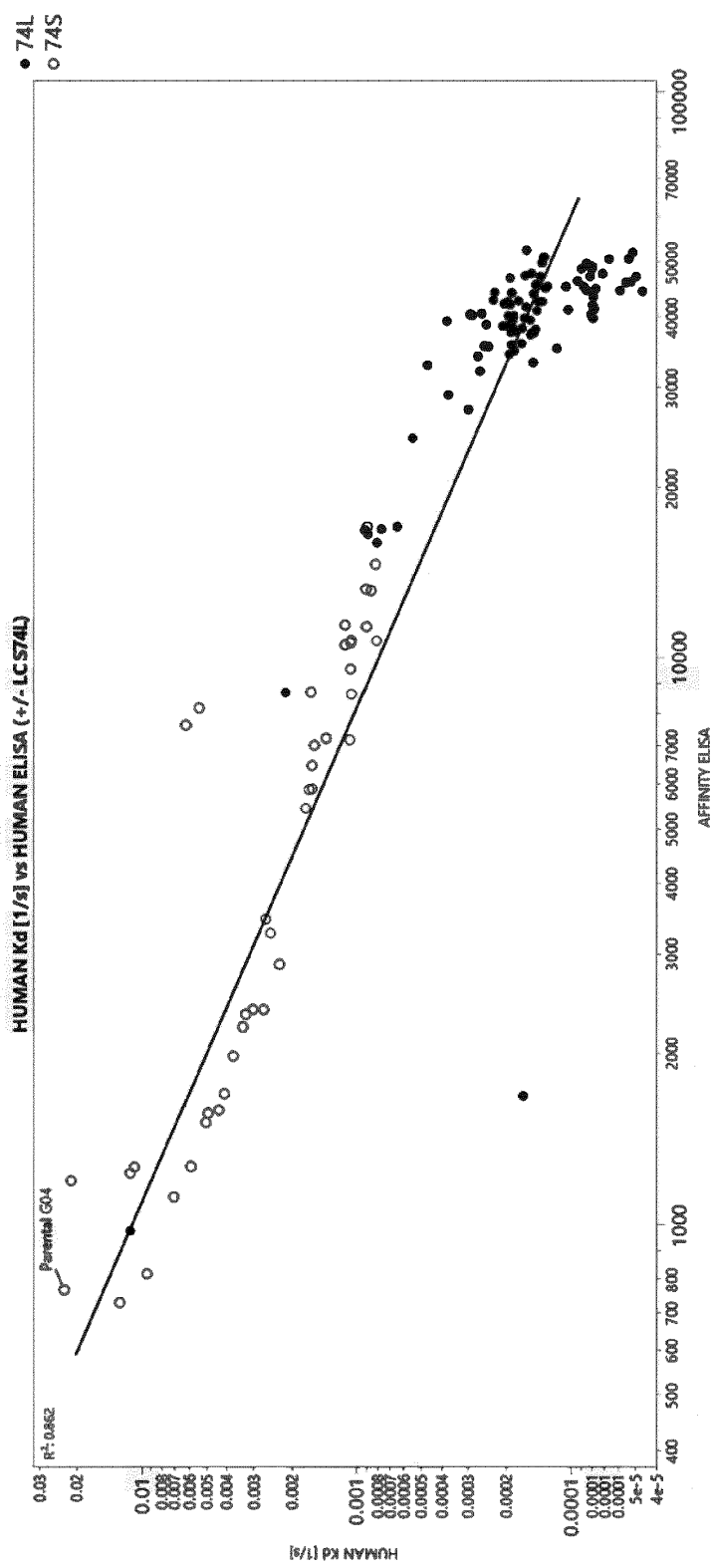


Figure 3A

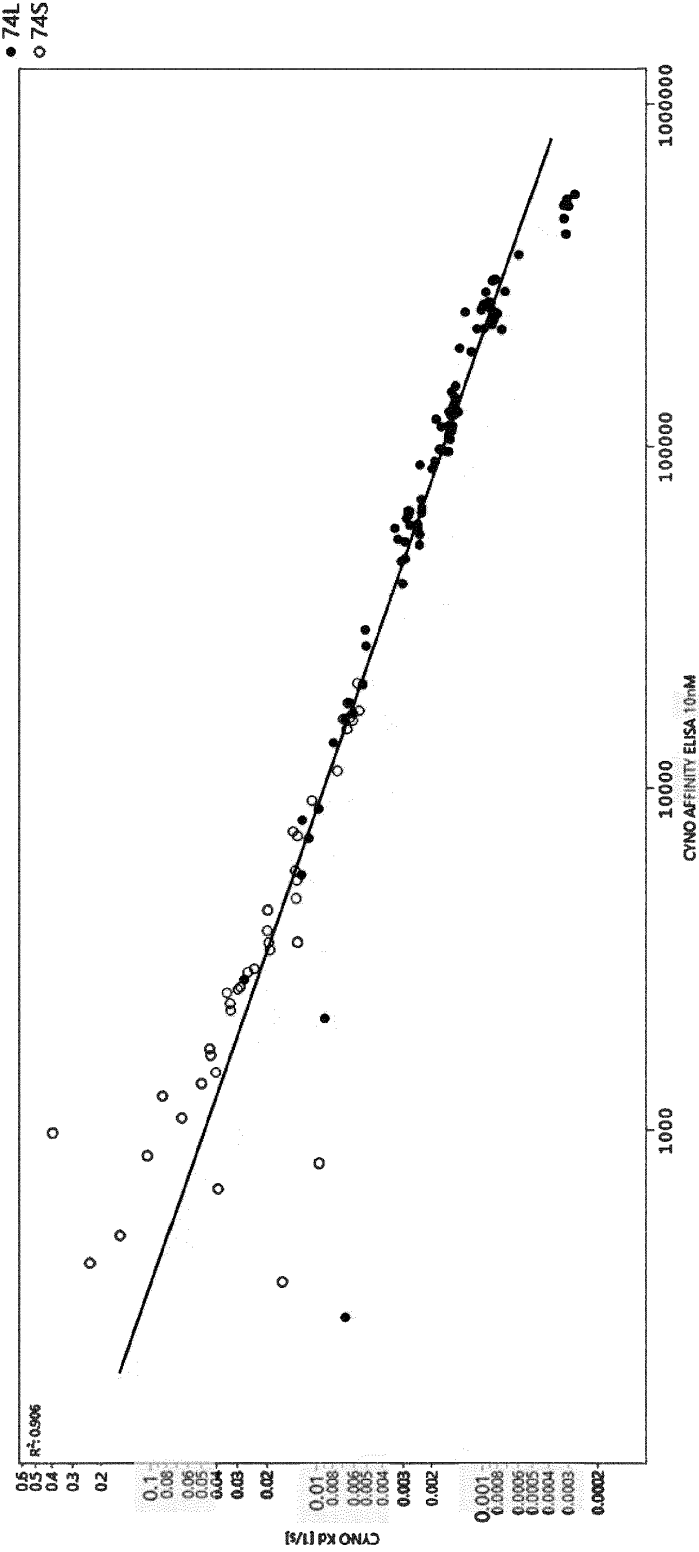


Figure 3B

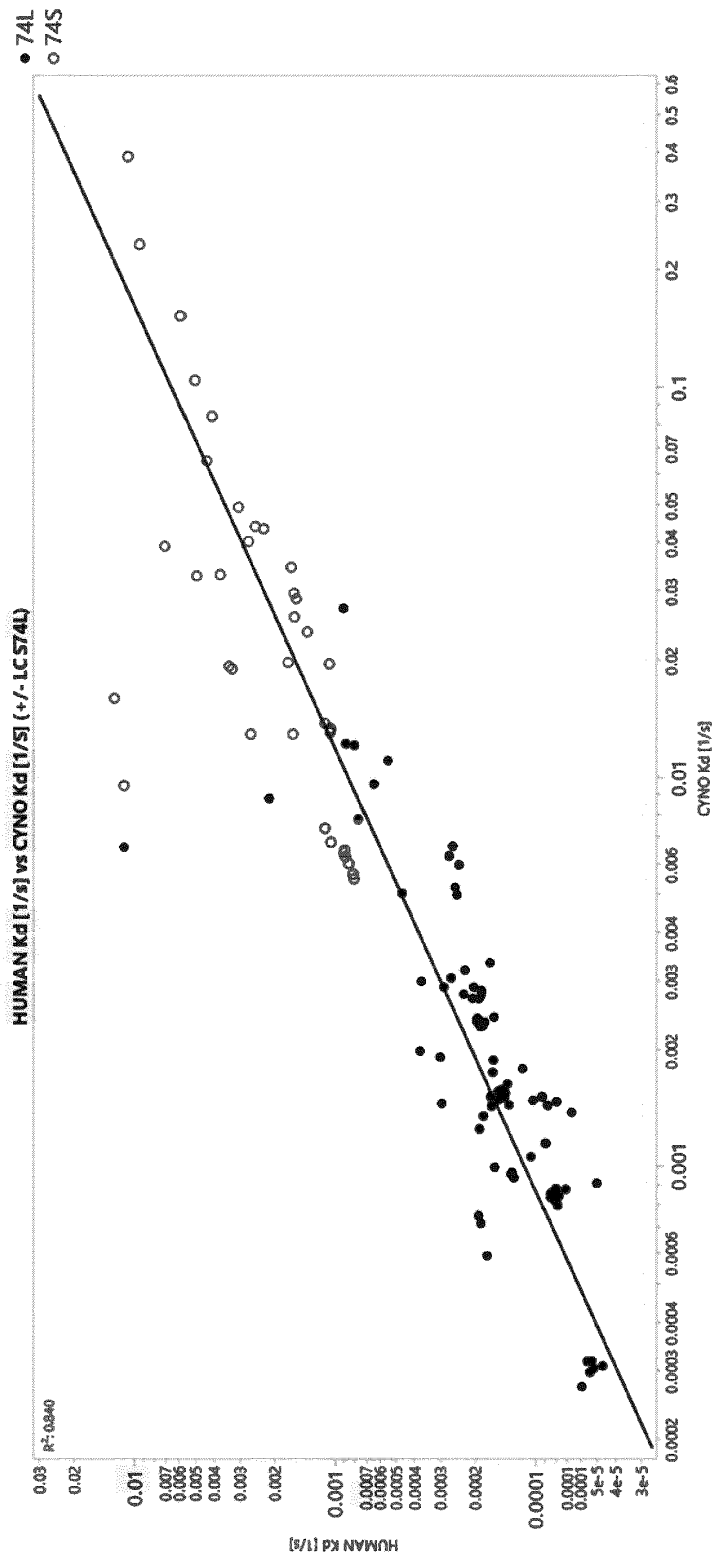


Figure 3C





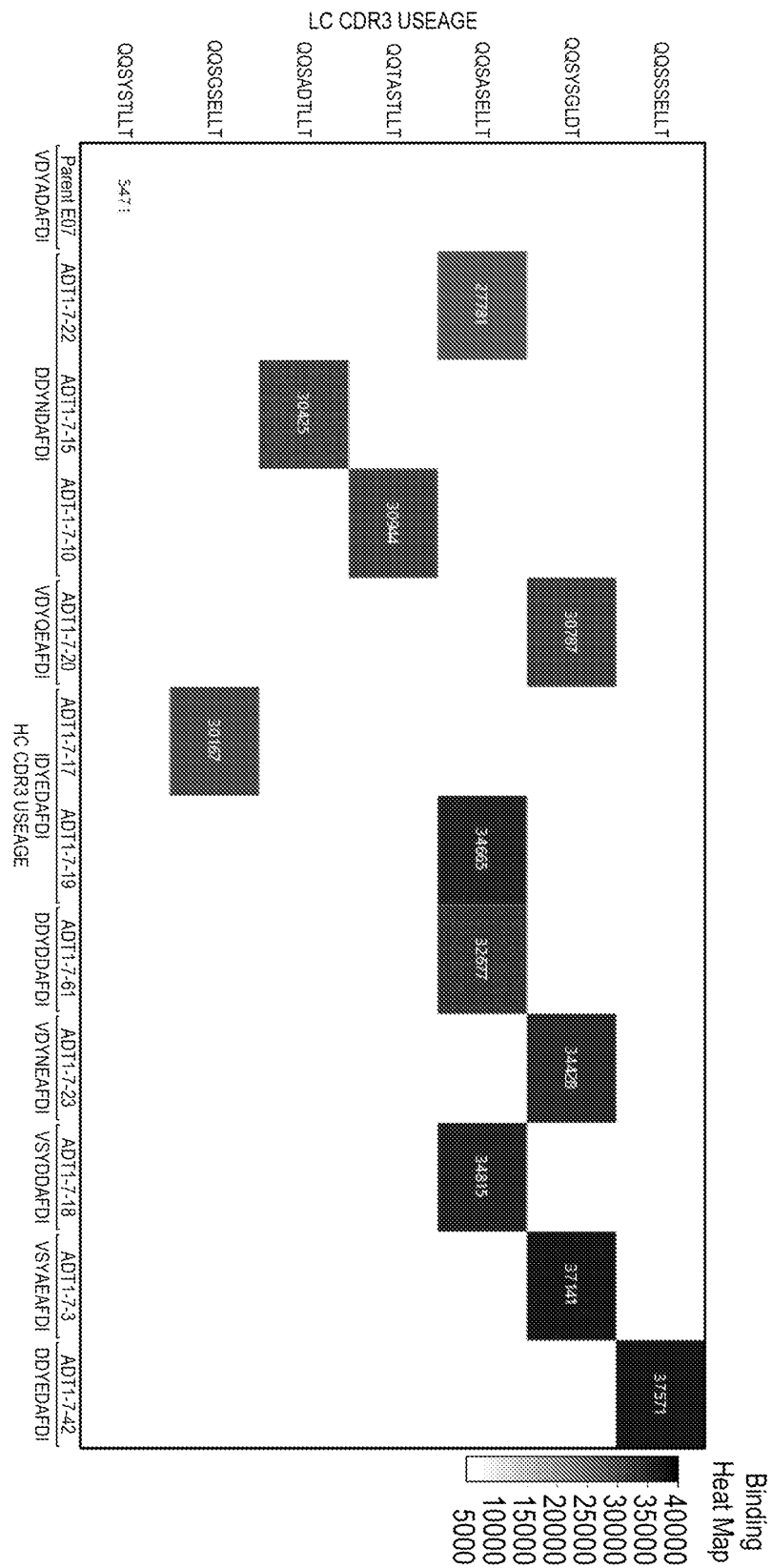
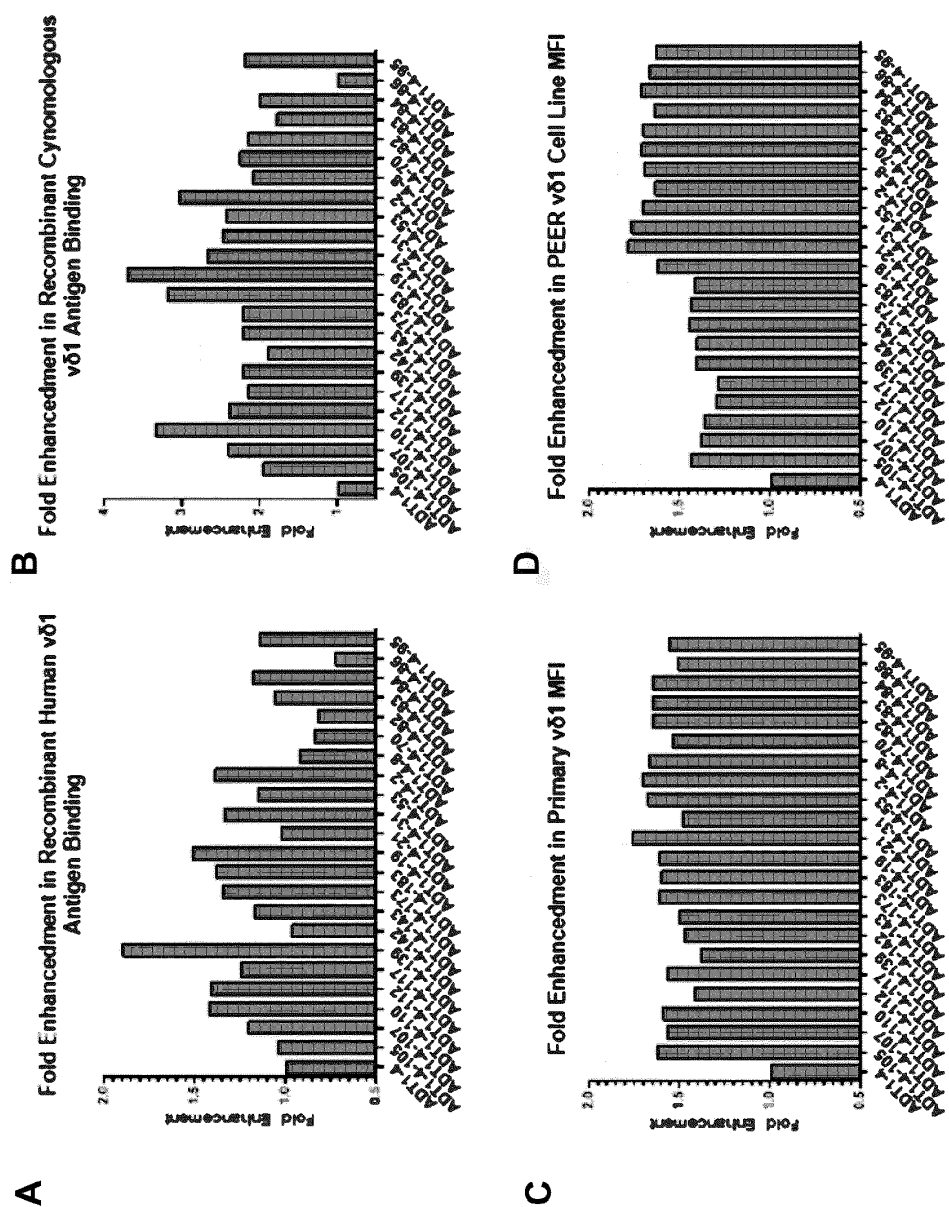


Figure 4C



## Figure 5

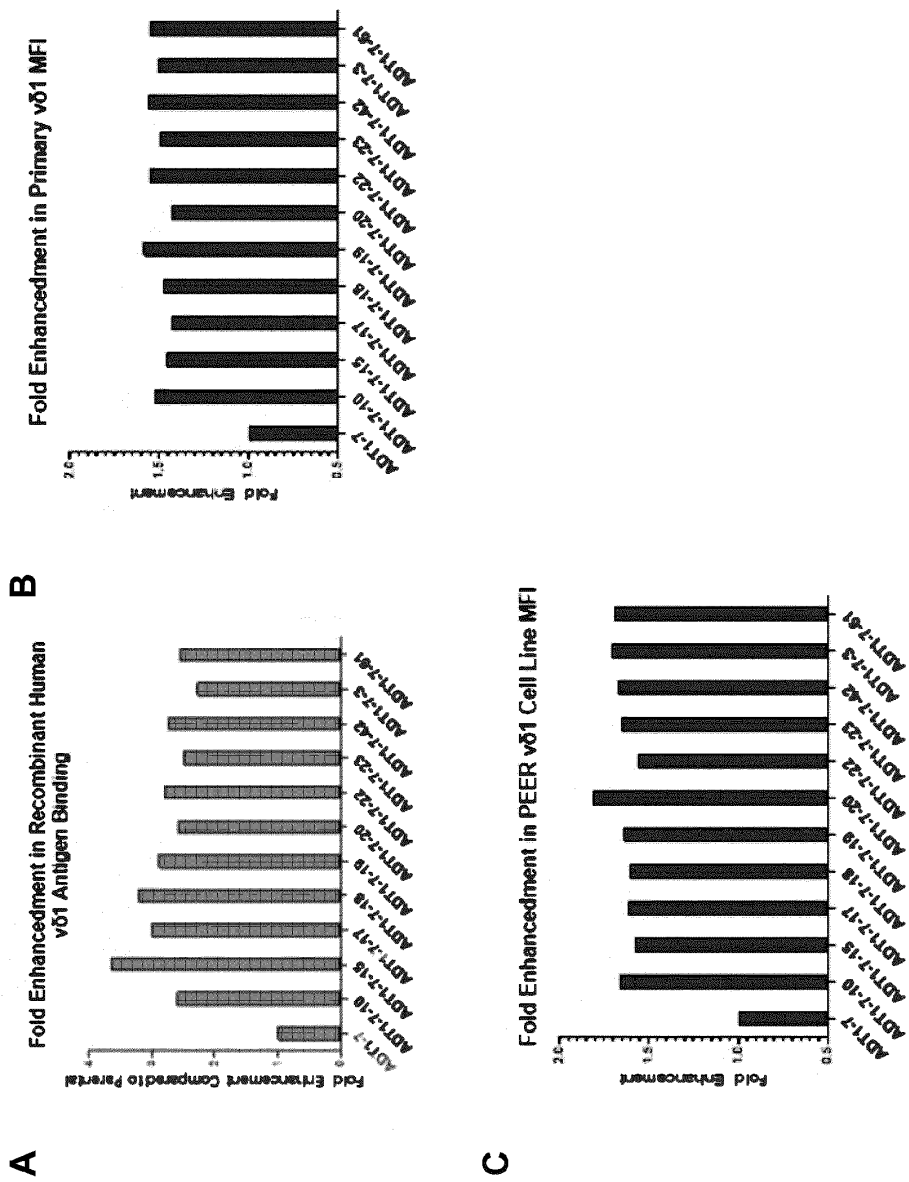


Figure 6

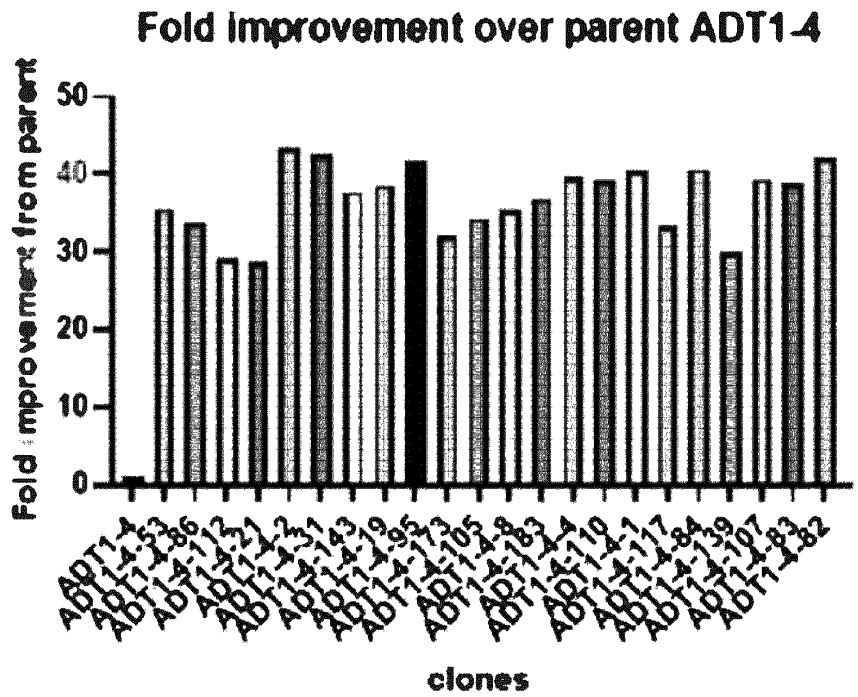


Figure 7A

**Fold improvement from parent ADT1-4 in binding to cyno antigen**

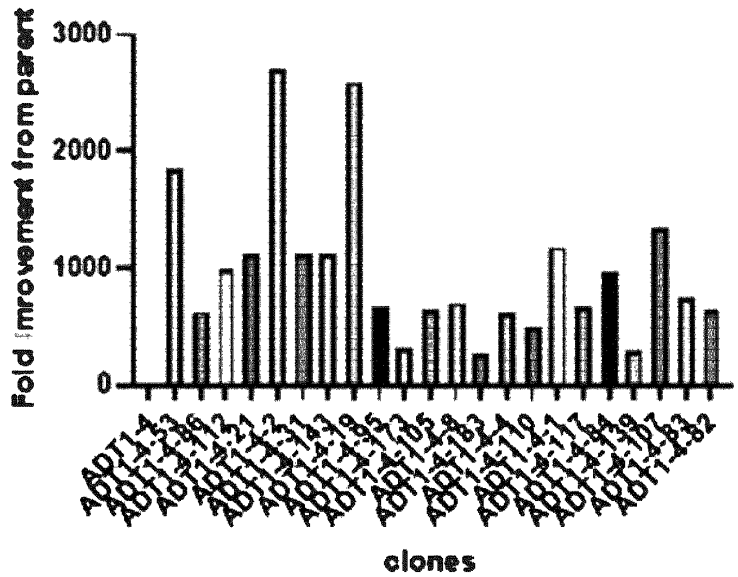
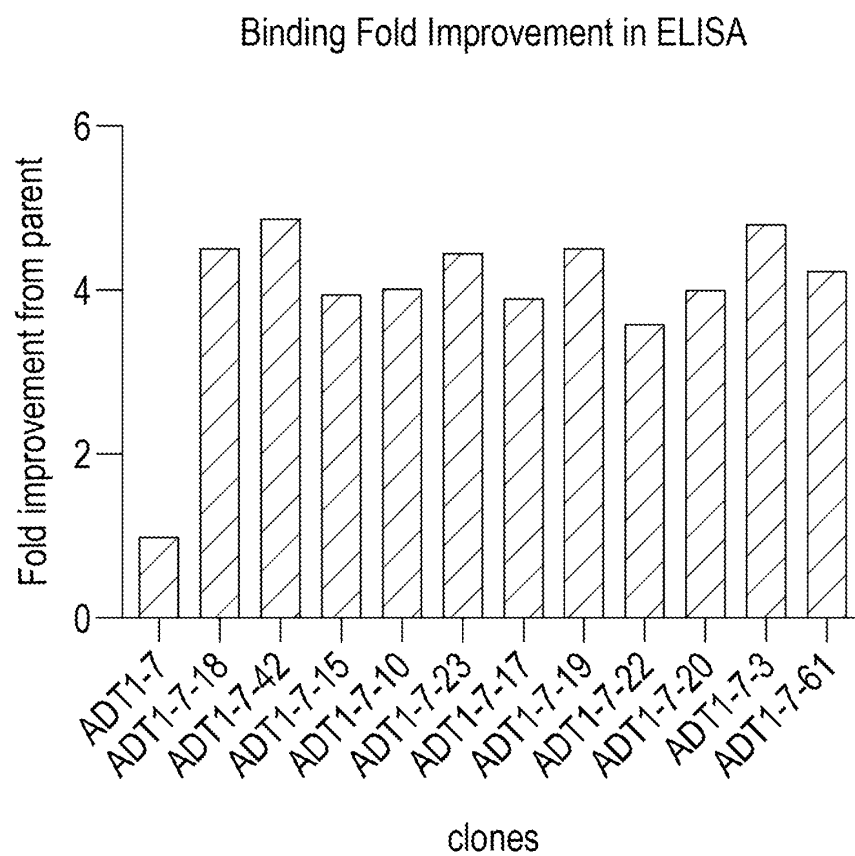


Figure 7B

**Figure 7C**

Human KD

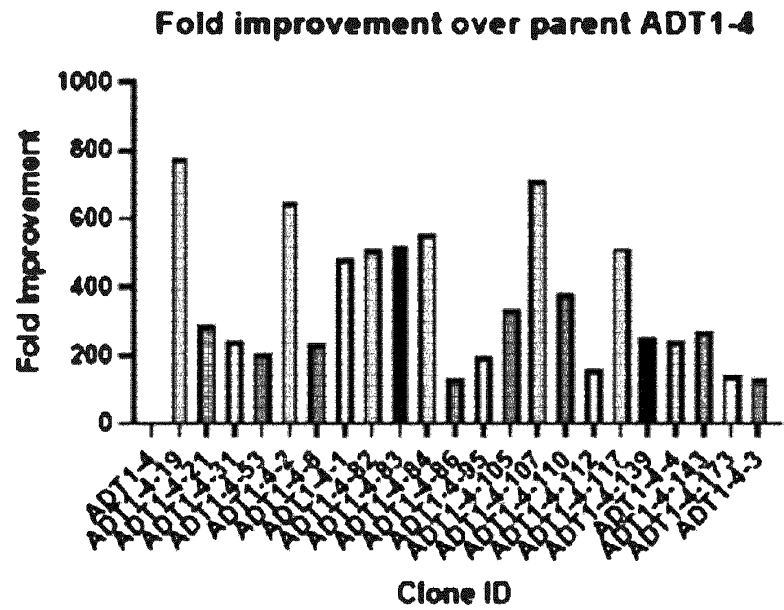


Figure 8A

Cyno KD

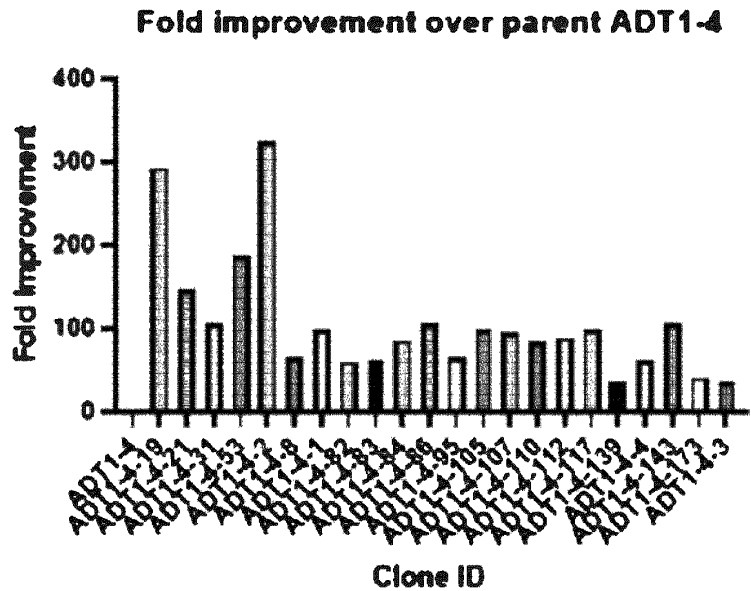


Figure 8B

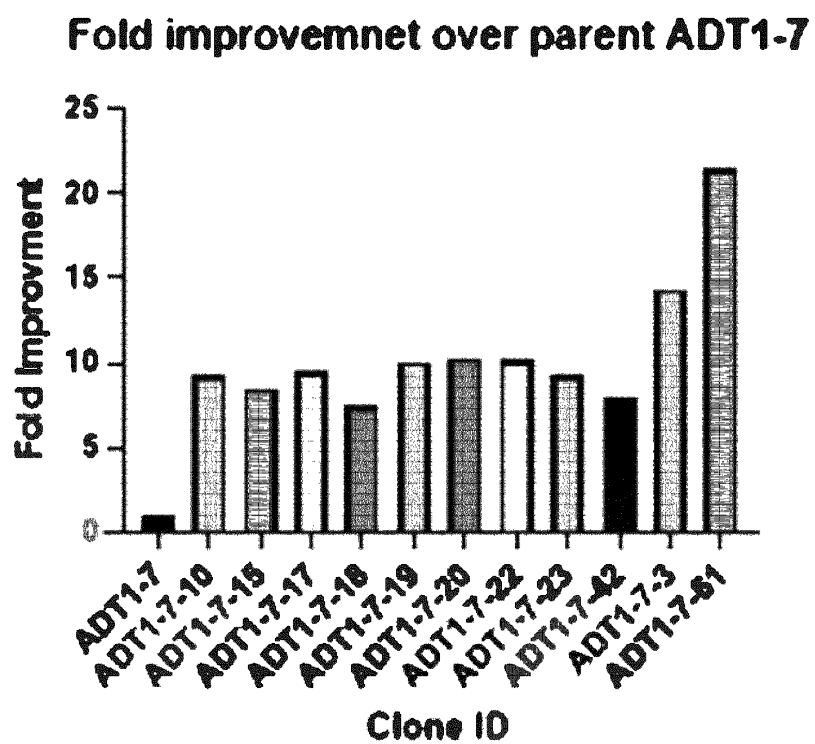


Figure 8C

Clones: ADT1-4-derived Analyte: human VD1

**A**

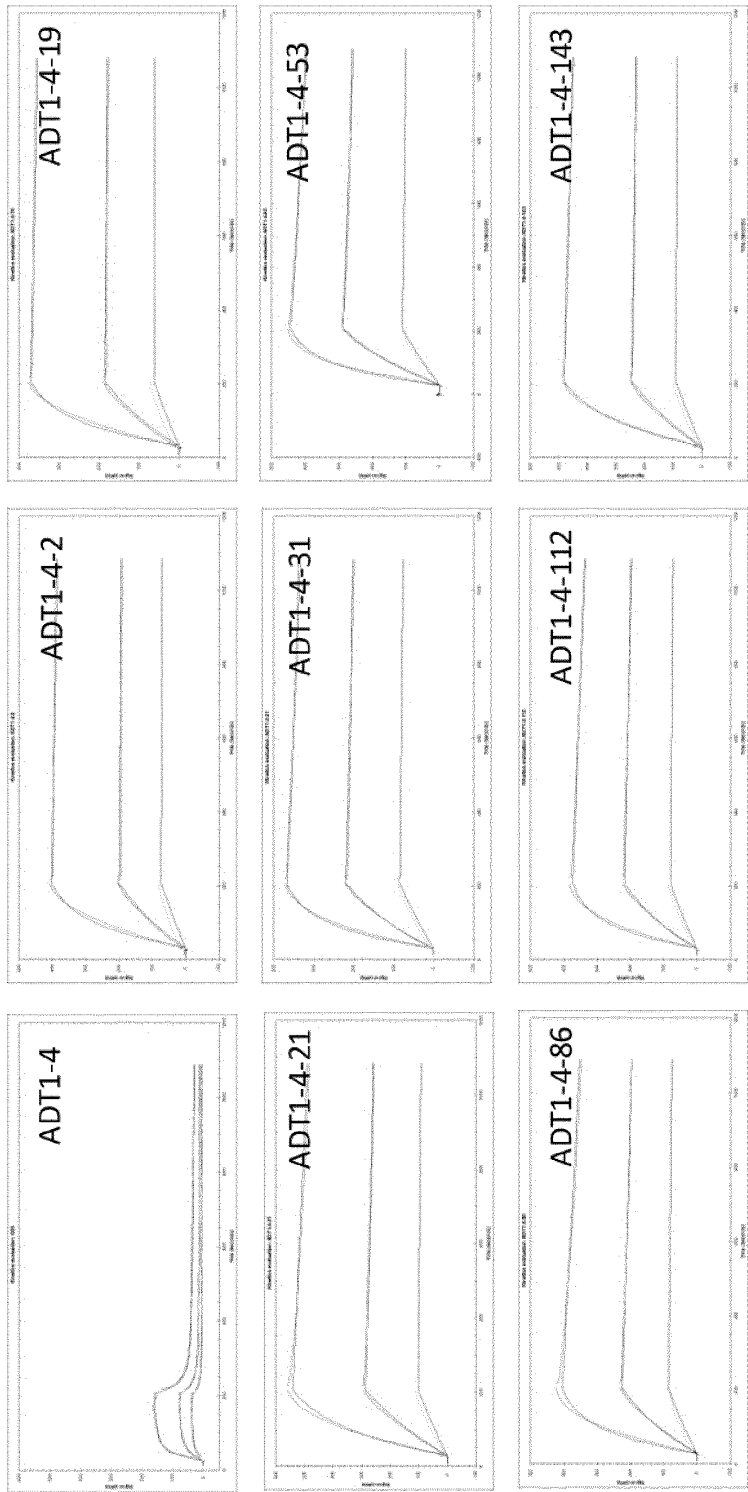


Figure 9A

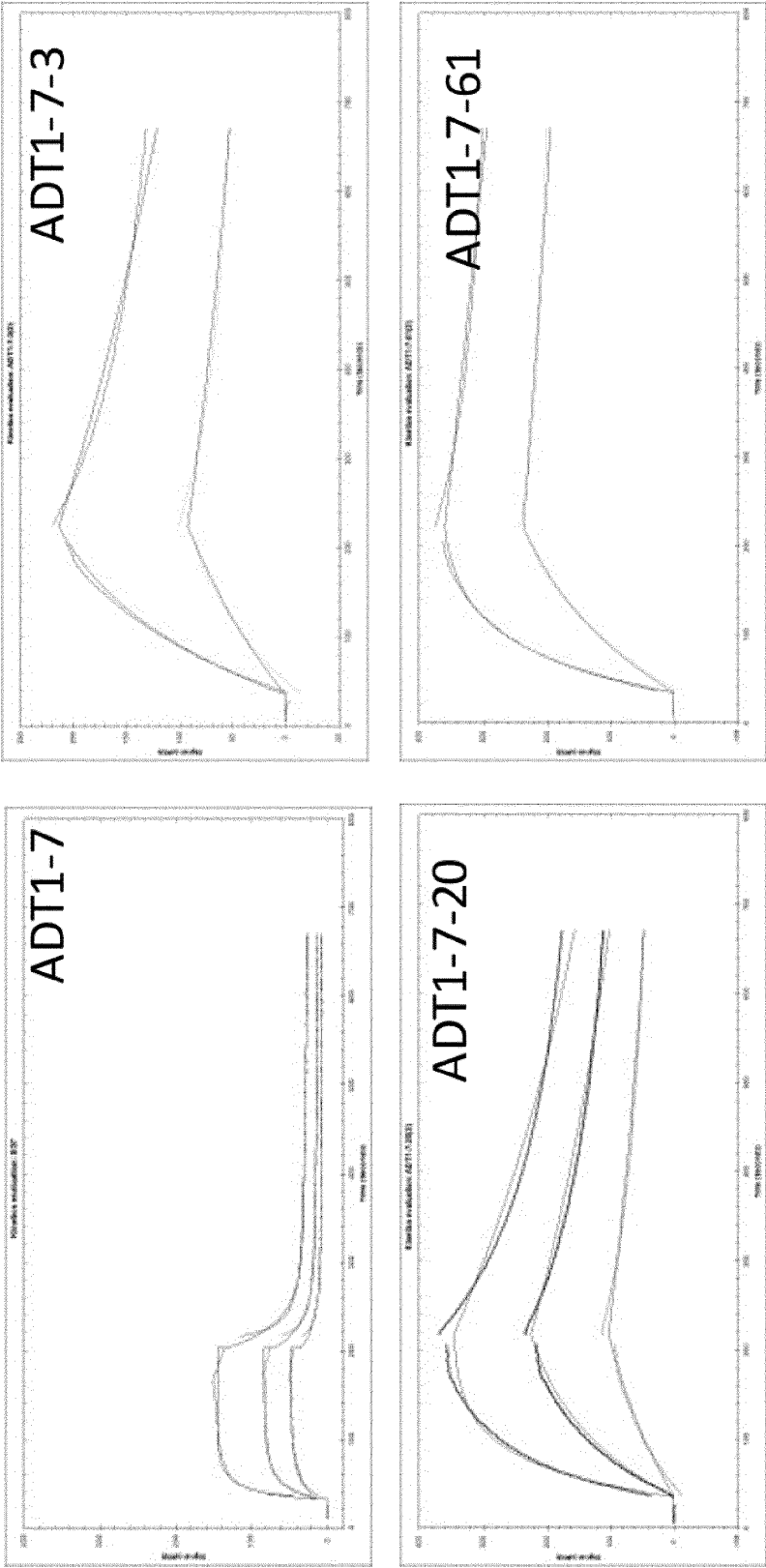


Figure 9B

| Clone     | Avg KD (M) | Fold-change |
|-----------|------------|-------------|
| ADT1-7    | 3.81E-08   | 1.00        |
| ADT1-7-3  | 3.78E-09   | 10.07       |
| ADT1-7-20 | 4.99E-09   | 7.63        |
| ADT1-7-61 | 1.04E-09   | 36.62       |

Figure 9D

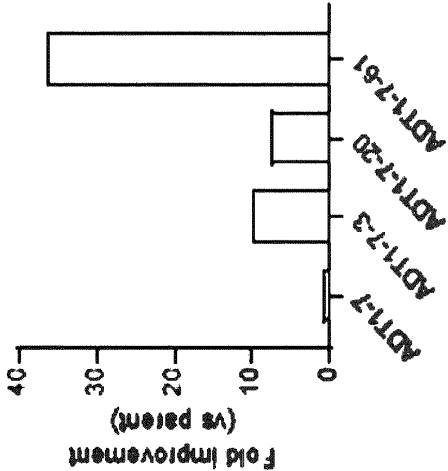


Figure 9F

| Clone      | Avg KD (M) | Fold-change |
|------------|------------|-------------|
| ADT1-4     | 1.49E-07   | 1.00        |
| ADT1-4-2   | 1.90E-10   | 784.21      |
| ADT1-4-19  | 1.77E-10   | 841.81      |
| ADT1-4-21  | 4.74E-10   | 314.35      |
| ADT1-4-31  | 4.42E-10   | 337.49      |
| ADT1-4-53  | 5.07E-10   | 294.18      |
| ADT1-4-86  | 7.16E-10   | 208.25      |
| ADT1-4-112 | 5.65E-10   | 263.95      |
| ADT1-4-143 | 4.24E-10   | 351.42      |

Figure 9C

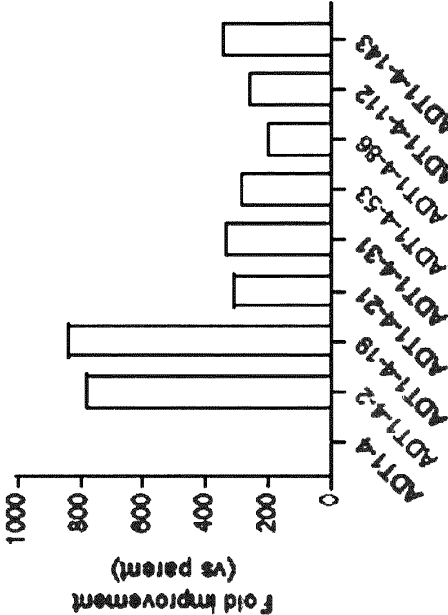


Figure 9E

| Clone      | Avg KD (M) |
|------------|------------|
| ADT1-4     | No binding |
| ADT1-4-2   | 1.92E-09   |
| ADT1-4-19  | 2.25E-09   |
| ADT1-4-21  | 4.38E-09   |
| ADT1-4-31  | 6.45E-09   |
| ADT1-4-53  | 4.01E-09   |
| ADT1-4-86  | 9.22E-09   |
| ADT1-4-112 | 8.27E-09   |
| ADT1-4-143 | 7.61E-09   |

B

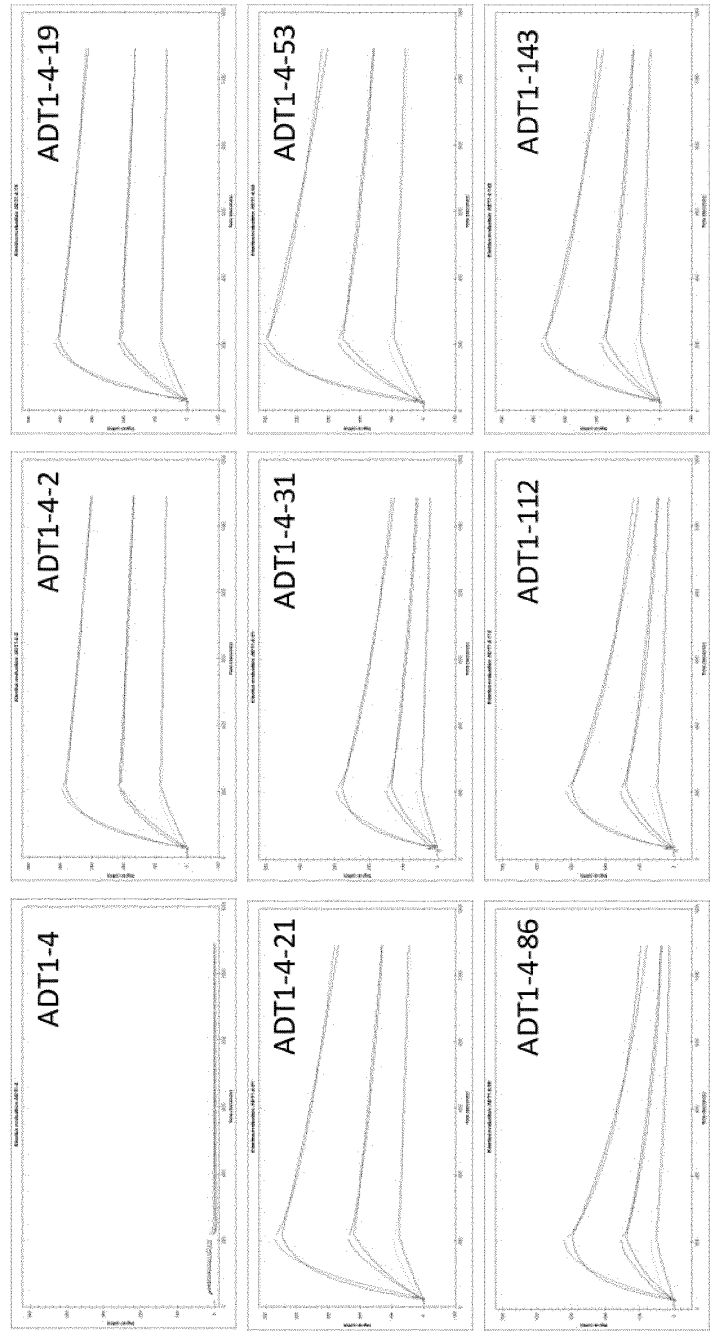


Figure 10

A

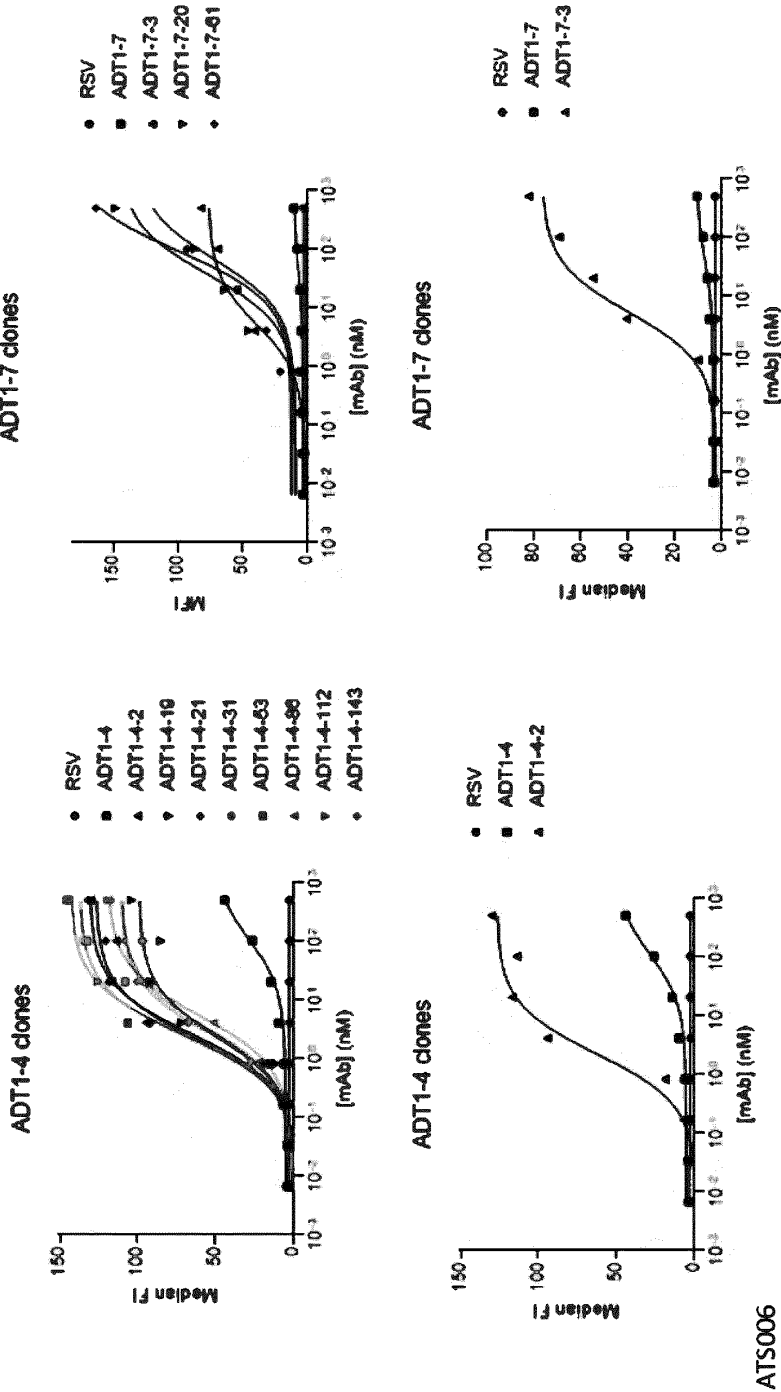


Figure 11A

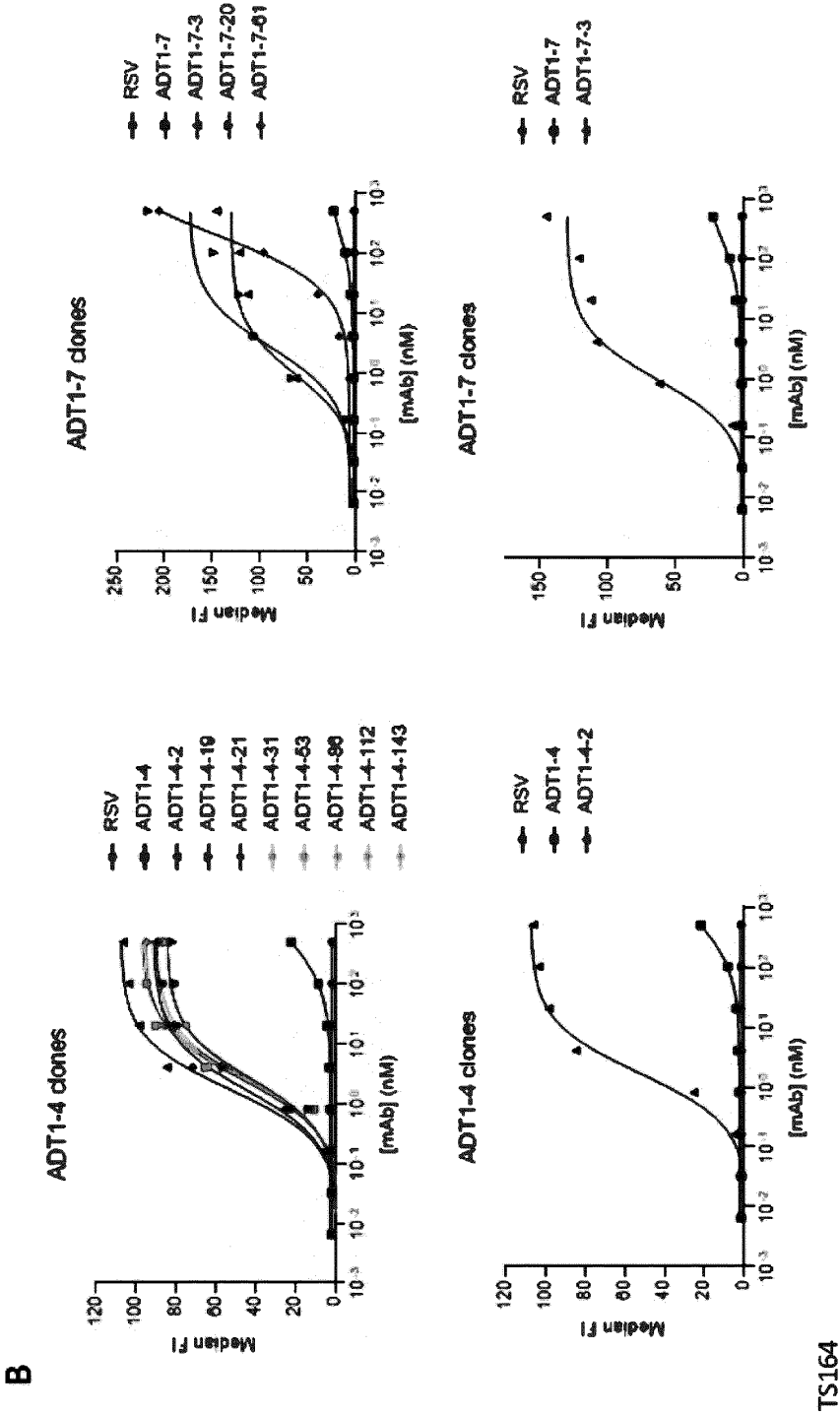


Figure 11B

|           | ATS006 |                       | TS164  |                       |
|-----------|--------|-----------------------|--------|-----------------------|
|           | IC50   | % improvement in IC50 | IC50   | % improvement in IC50 |
| ADT1-7    | >100   | 0.00                  | 225.6  | 0.00                  |
| ADT1-7-3  | 5.153  | N/A                   | 0.9517 | 23604.95              |
| ADT1-7-20 | 37.22  | N/A                   | 2.684  | 8305.37               |
| ADT1-7-61 | 93.01  | N/A                   | 195.7  | 15.28                 |

| mAb        | ATS006 |                       | TS164 |                       |
|------------|--------|-----------------------|-------|-----------------------|
|            | IC50   | % improvement in IC50 | IC50  | % improvement in IC50 |
| ADT1-4     | 107.7  | 0.00                  | 575.9 | 0.00                  |
| ADT1-4-2   | 2.164  | 4876.89               | 1.703 | 33716.79              |
| ADT1-4-19  | 2.375  | 4434.74               | 2.456 | 23348.70              |
| ADT1-4-21  | 2.536  | 4146.85               | 1.675 | 34282.09              |
| ADT1-4-31  | 3.33   | 3134.23               | 2.63  | 21797.34              |
| ADT1-4-53  | 2.228  | 4733.93               | 2.456 | 23348.70              |
| ADT1-4-86  | 5.357  | 1910.45               | 2.34  | 24511.11              |
| ADT1-4-112 | 2.621  | 4009.12               | 2.436 | 23541.22              |
| ADT1-4-143 | 2.819  | 3720.50               | 3.066 | 18683.43              |

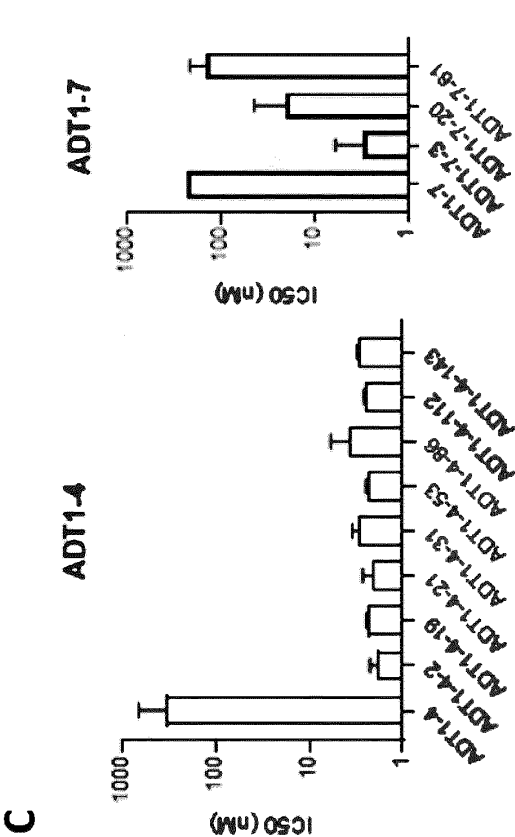


Figure 11C

| IC50 (nM)  |                     |                    |            |            |            |            |             |             |             |             |
|------------|---------------------|--------------------|------------|------------|------------|------------|-------------|-------------|-------------|-------------|
| mAb        | Donor 1<br>(ATS006) | Donor 2<br>(TS164) | HEK293T    | Raji       | CD8 (PBMC) | CD4 (PBMC) | CD56 (PBMC) | CD19 (PBMC) | CD14 (PBMC) | CD14 (PBMC) |
| ADT1-4     | 107.7               | 575.9              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-2   | 2.164               | 1.703              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-19  | 2.375               | 2.456              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-21  | 2.536               | 1.675              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-31  | 3.33                | 2.63               | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-53  | 2.228               | 2.456              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-86  | 5.357               | 2.34               | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-112 | 2.621               | 2.436              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-4-143 | 2.819               | 3.066              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |

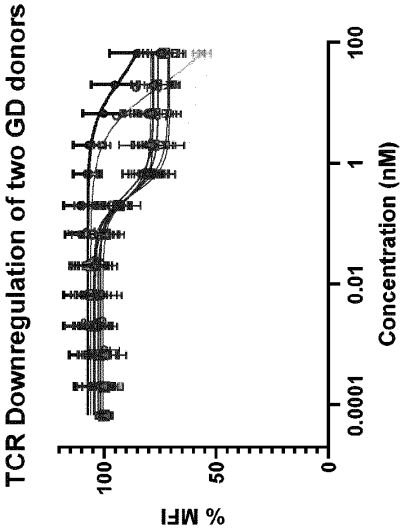
| IC50 (nM) |                     |                    |            |            |            |            |             |             |             |             |
|-----------|---------------------|--------------------|------------|------------|------------|------------|-------------|-------------|-------------|-------------|
| mAb       | Donor 1<br>(ATS006) | Donor 2<br>(TS164) | HEK293T    | Raji       | CD8 (PBMC) | CD4 (PBMC) | CD56 (PBMC) | CD19 (PBMC) | CD14 (PBMC) | CD14 (PBMC) |
| ADT1-7    | >100                | 225.6              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-7-3  | 5.153               | 0.9517             | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-7-20 | 37.22               | 2.684              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |
| ADT1-7-61 | 93.01               | 195.7              | No binding | No binding | No binding | No binding | No binding  | No binding  | No binding  | No binding  |

| IC50 (nM)         |                     |            |            |             |             |             |
|-------------------|---------------------|------------|------------|-------------|-------------|-------------|
| mAb               | Donor 1<br>(ATS006) | CD8 (PBMC) | CD4 (PBMC) | CD56 (PBMC) | CD19 (PBMC) | CD14 (PBMC) |
| OKT3              | 2.889               | 0.252      | 0.1906     | No binding  | No binding  | No binding  |
| RSV (IgG control) | No binding          | No binding | No binding | No binding  | No binding  | No binding  |

Figure 11D

- ADT1-4
- ADT1-4-1
- ADT1-4-2
- ADT1-4-6
- ADT1-4-19
- ADT1-4-21
- ADT1-4-31
- ADT1-4-53
- ADT1-4-86
- ADT1-4-112
- ADT1-4-138
- ADT1-4-143
- OKT3



- ADT1-7
- ADT1-7-3
- ADT1-7-20
- ADT1-7-61
- OKT3

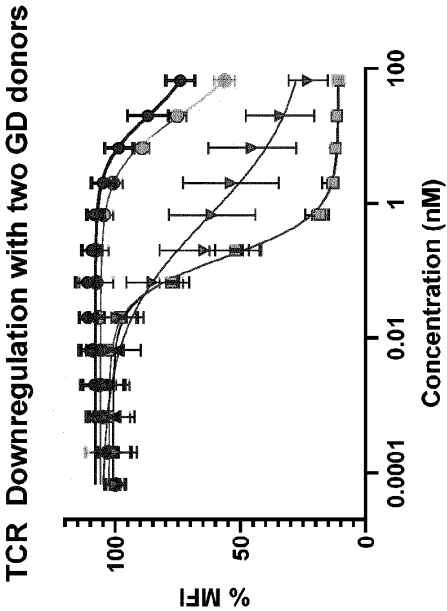


Figure 12

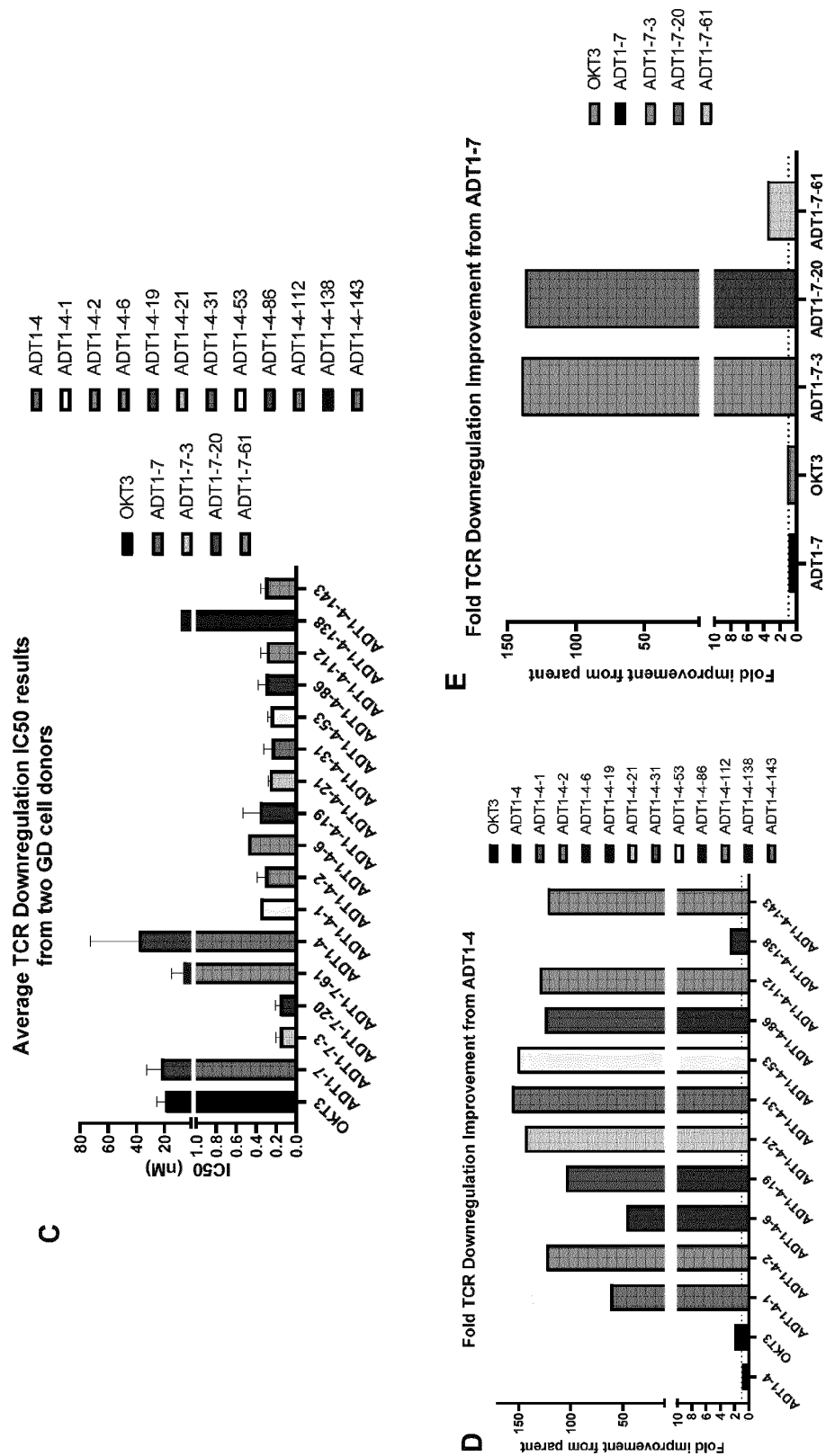


Figure 12 cont.

G

|            | IC50  | % improvement in IC50 |
|------------|-------|-----------------------|
| ADT1-4     | 38.28 | 100                   |
| OKT3       | 19.43 | 197                   |
| ADT1-4-2   | 0.31  | 12348                 |
| ADT1-4-31  | 0.24  | 15630                 |
| ADT1-4-21  | 0.27  | 14372                 |
| ADT1-4-86  | 0.31  | 12472                 |
| ADT1-4-143 | 0.31  | 12219                 |
| ADT1-4-19  | 0.37  | 10420                 |
| ADT1-4-53  | 0.25  | 15090                 |
| ADT1-4-112 | 0.30  | 12964                 |
| ADT1-4-1   | 0.36  | 6185                  |
| ADT1-4-6   | 0.48  | 4648                  |
| ADT1-4-138 | 8.38  | 266                   |

|            | IC50  | Fold improvement in IC50 |
|------------|-------|--------------------------|
| ADT1-4     | 38.28 | 1                        |
| OKT3       | 19.43 | 2                        |
| ADT1-4-1   | 0.36  | 62                       |
| ADT1-4-2   | 0.31  | 123                      |
| ADT1-4-6   | 0.48  | 46                       |
| ADT1-4-19  | 0.37  | 104                      |
| ADT1-4-21  | 0.27  | 144                      |
| ADT1-4-31  | 0.24  | 156                      |
| ADT1-4-53  | 0.25  | 151                      |
| ADT1-4-86  | 0.31  | 125                      |
| ADT1-4-112 | 0.30  | 130                      |
| ADT1-4-138 | 8.38  | 3                        |
| ADT1-4-143 | 0.31  | 122                      |

F

|           | IC50  | % improvement in IC50 |
|-----------|-------|-----------------------|
| ADT1-7    | 22.42 | 100                   |
| OKT3      | 19.43 | 115                   |
| ADT1-7-3  | 0.16  | 13968                 |
| ADT1-7-20 | 0.16  | 13697                 |
| ADT1-7-61 | 6.26  | 358                   |

|           | IC50  | Fold improvement in IC50 |
|-----------|-------|--------------------------|
| ADT1-7    | 22.42 | 1                        |
| OKT3      | 19.43 | 1                        |
| ADT1-7-3  | 0.16  | 140                      |
| ADT1-7-20 | 0.16  | 137                      |
| ADT1-7-61 | 6.26  | 4                        |

Figure 12 cont

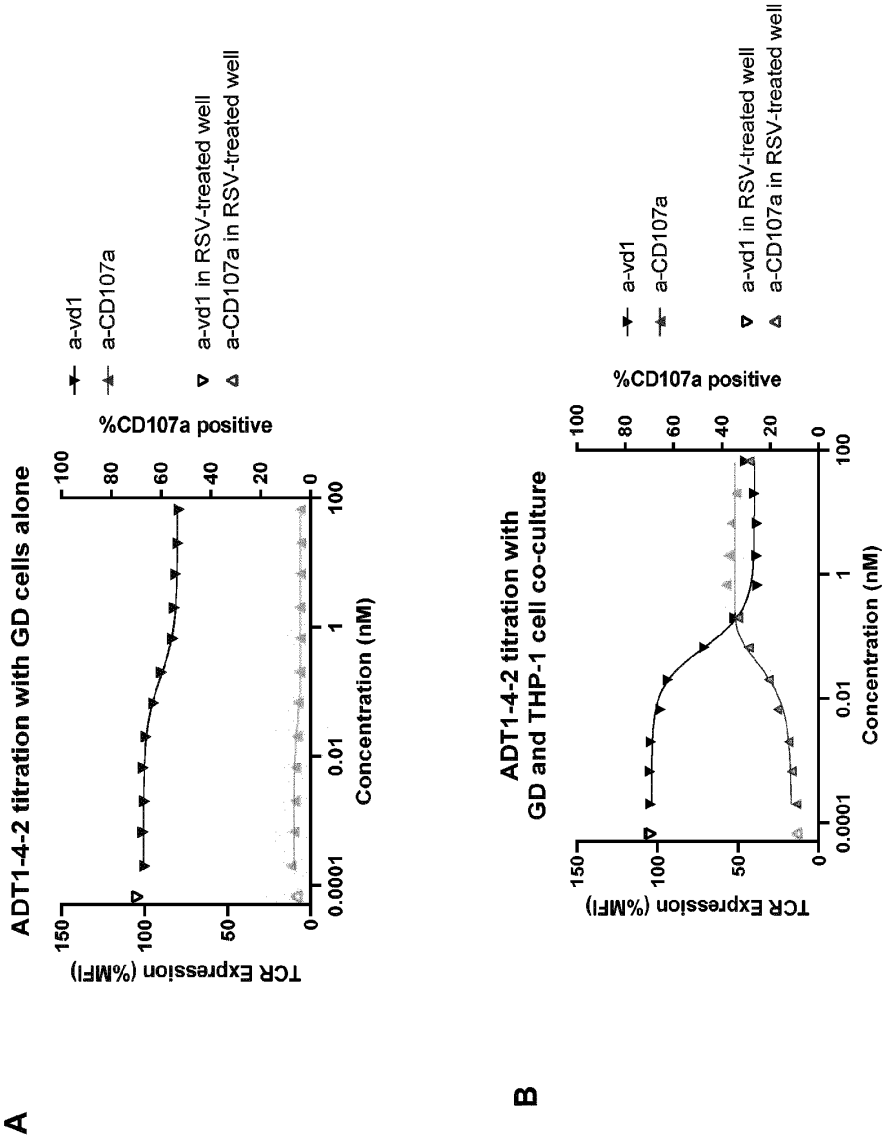
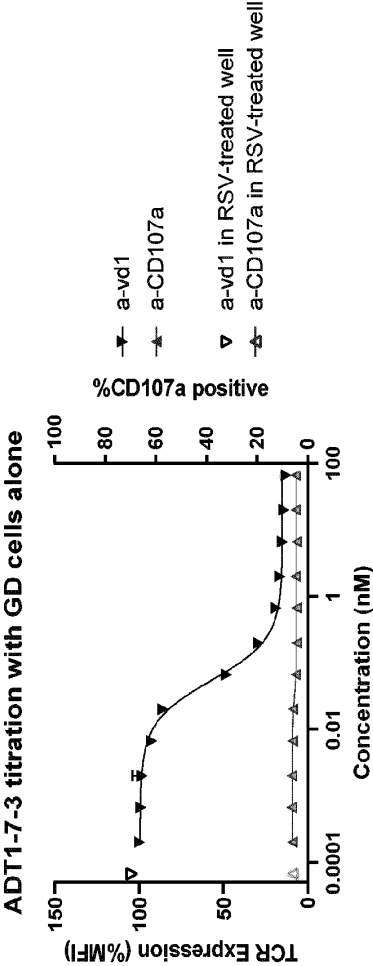


Figure 13

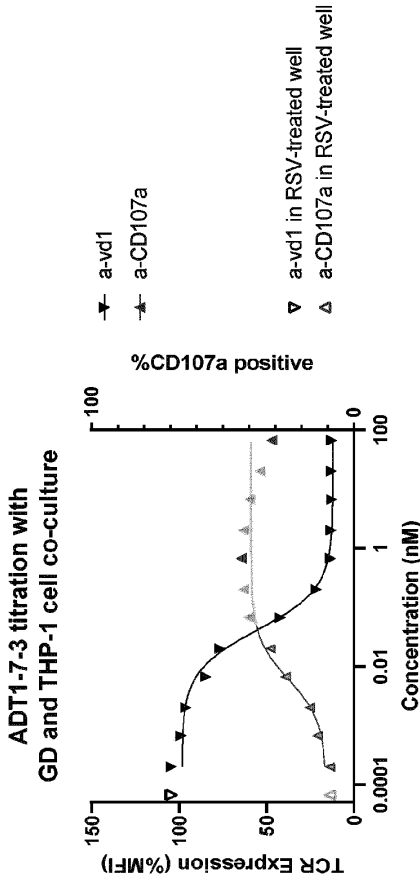
C



E

|          | % increase in CD107a positive cells |
|----------|-------------------------------------|
| ADT1-4-2 | 24.705                              |
| ADT1-7-3 | 26.7                                |

F



D

| Condition  | mAb      | % maximum increase in CD107a positive cells |
|------------|----------|---------------------------------------------|
| GD         | ADT1-4-2 | -3.73                                       |
| GD         | ADT1-7-3 | -1.28                                       |
| GD + THP-1 | ADT1-4-2 | 19.53                                       |
| GD + THP-1 | ADT1-7-3 | 22.3                                        |

Figures 13 cont.

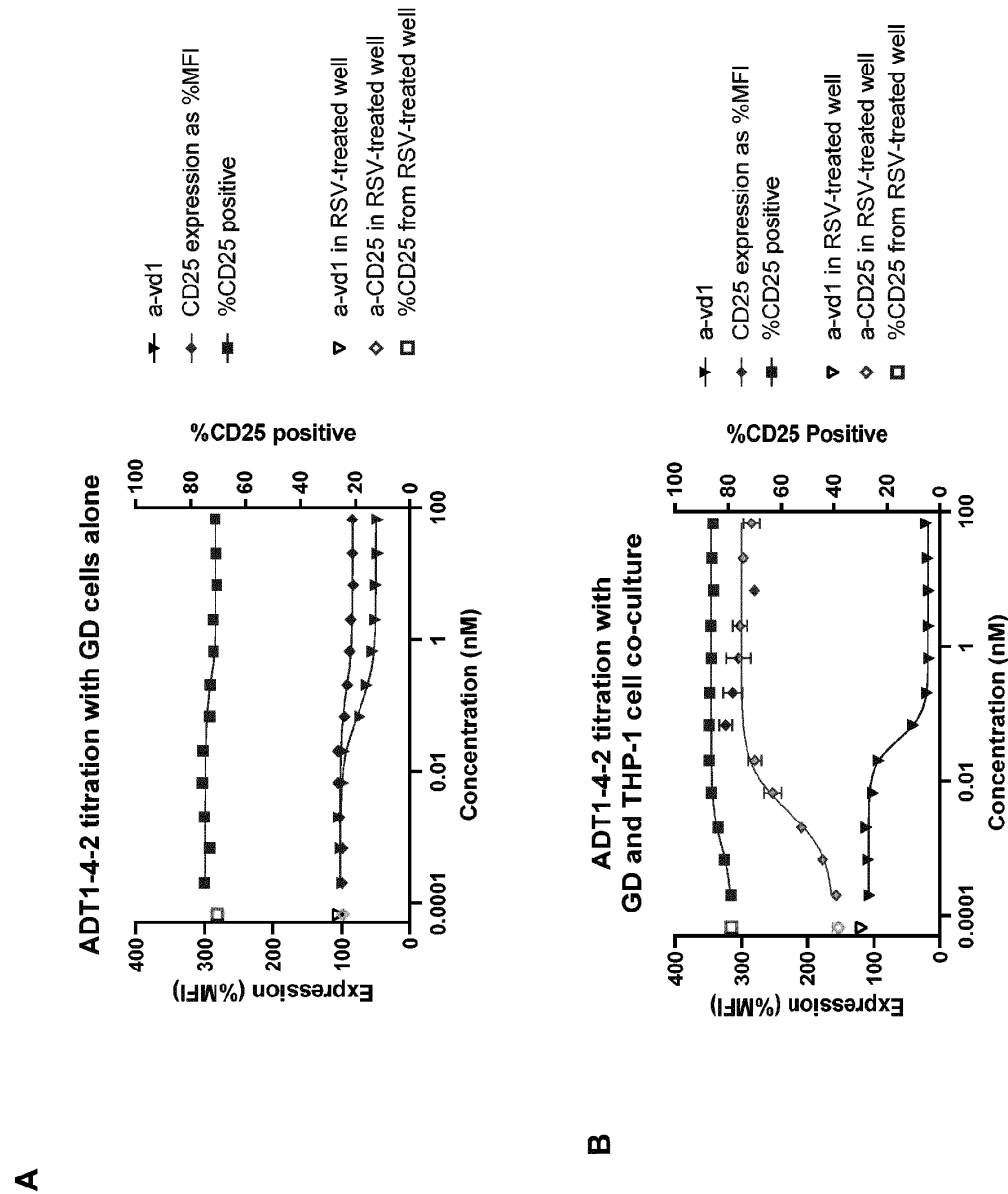
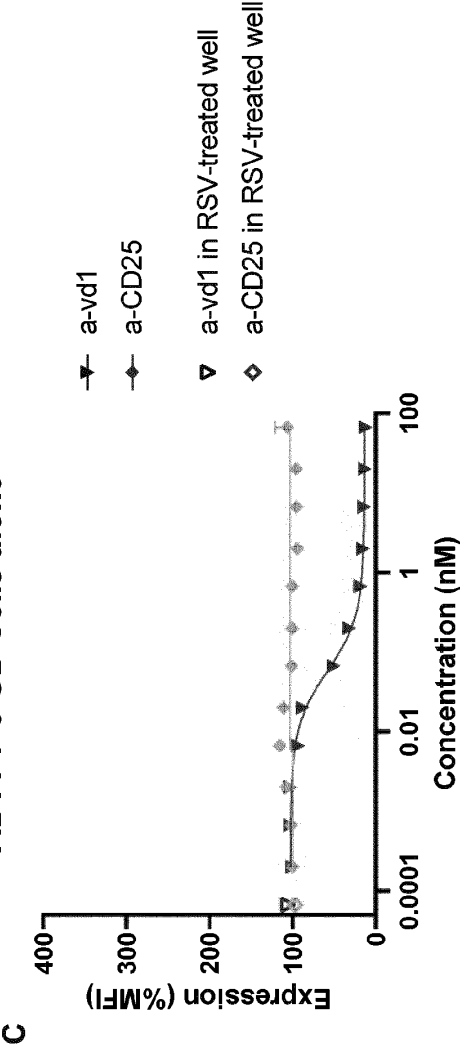


Figure 14

ADT1-7-3 GD Cells alone



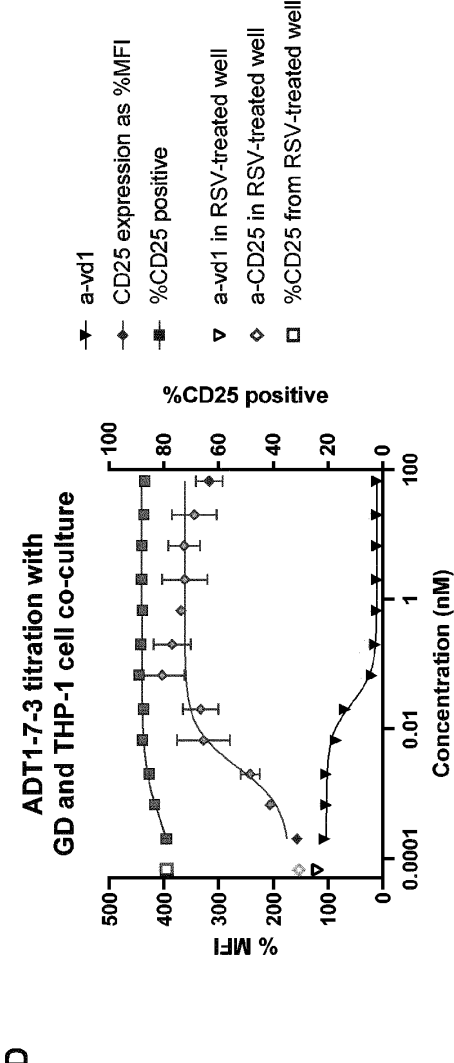
**E**

|          | % increase in CD25 expression |
|----------|-------------------------------|
| ADT1-4-2 | 170.1                         |
| ADT1-7-3 | 220.9                         |

**F**

| Condition  | mAb      | % maximum Increase in CD25 expression |
|------------|----------|---------------------------------------|
| GD         | ADT1-4-2 | -15.23                                |
| GD + THP-1 | ADT1-4-2 | 116.8                                 |
| GD         | ADT1-7-3 | 3.84                                  |
| GD + THP-1 | ADT1-7-3 | 162.2                                 |

ADT1-7-3 titration with GD and THP-1 cell co-culture



Figures 14 cont.

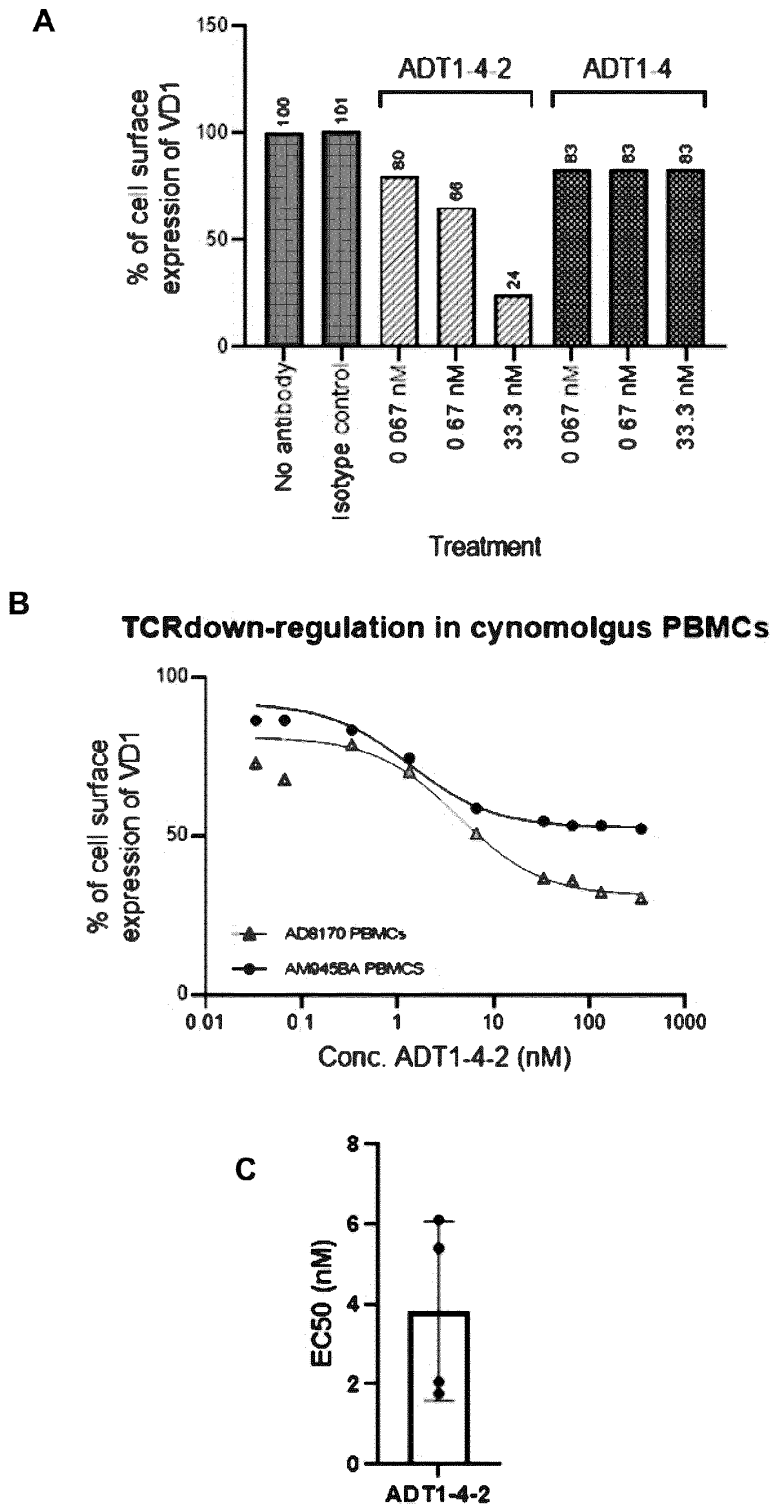


Figure 15

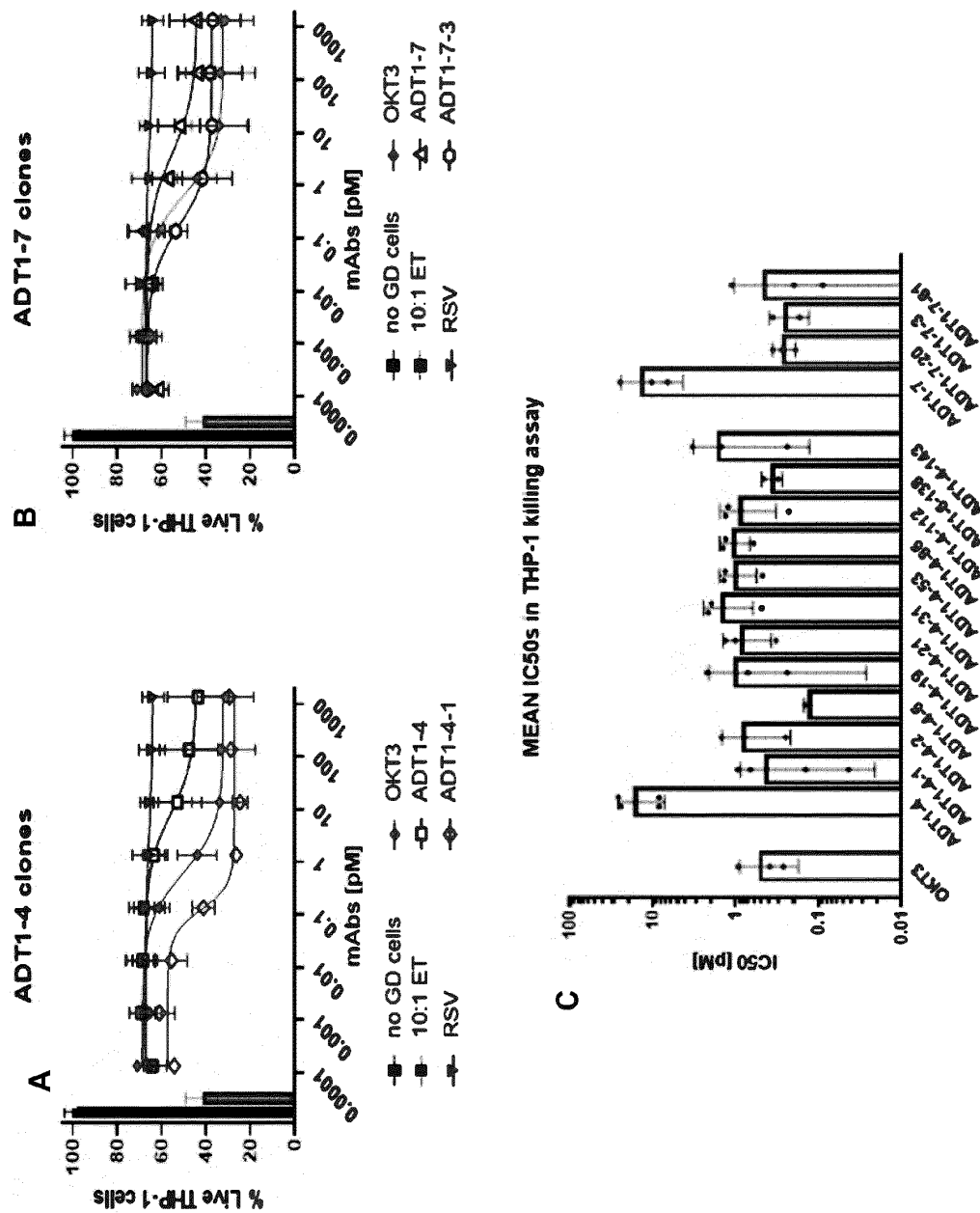


Figure 16

| Clone ID                   | THP-1 killing assay EC50<br>[pM] (average of ≥3 donors) | Standard<br>deviation | Fold<br>improvement | % improvement<br>over parent |
|----------------------------|---------------------------------------------------------|-----------------------|---------------------|------------------------------|
| OKT3 <sub>(anti CD3)</sub> | 3.53                                                    | 2.40                  |                     |                              |
| ADT1-4                     | 121.47                                                  | 136.80                | 1.0                 | 100%                         |
| ADT1-4-1                   | 3.00                                                    | 2.87                  | 40.5                | 4049%                        |
| ADT1-4-2                   | 6.33                                                    | 3.67                  | 19.2                | 1918%                        |
| ADT1-4-6                   | 0.93                                                    | 0.07                  | 130.1               | 13014%                       |
| ADT1-4-19                  | 8.33                                                    | 6.13                  | 14.6                | 1458%                        |
| ADT1-4-21                  | 6.13                                                    | 2.93                  | 19.8                | 1980%                        |
| ADT1-4-31                  | 10.93                                                   | 4.73                  | 11.1                | 1111%                        |
| ADT1-4-53                  | 7.40                                                    | 3.13                  | 16.4                | 1641%                        |
| ADT1-4-86                  | 7.60                                                    | 2.87                  | 16.0                | 1598%                        |
| ADT1-4-112                 | 6.47                                                    | 3.53                  | 18.8                | 1878%                        |
| ADT1-6-138                 | 2.53                                                    | 0.73                  | 47.9                | 4795%                        |
| ADT1-4-143                 | 13.07                                                   | 9.27                  | 9.3                 | 930%                         |
| ADT1-7                     | 65.20                                                   | 54.80                 | 1.0                 | 100%                         |
| ADT1-7-20                  | 1.87                                                    | 0.53                  | 34.9                | 3493%                        |
| ADT1-7-3                   | 1.33                                                    | 0.87                  | 48.9                | 4890%                        |
| ADT1-7-61                  | 3.60                                                    | 3.60                  | 18.1                | 1811%                        |

Figure 16 cont.

D

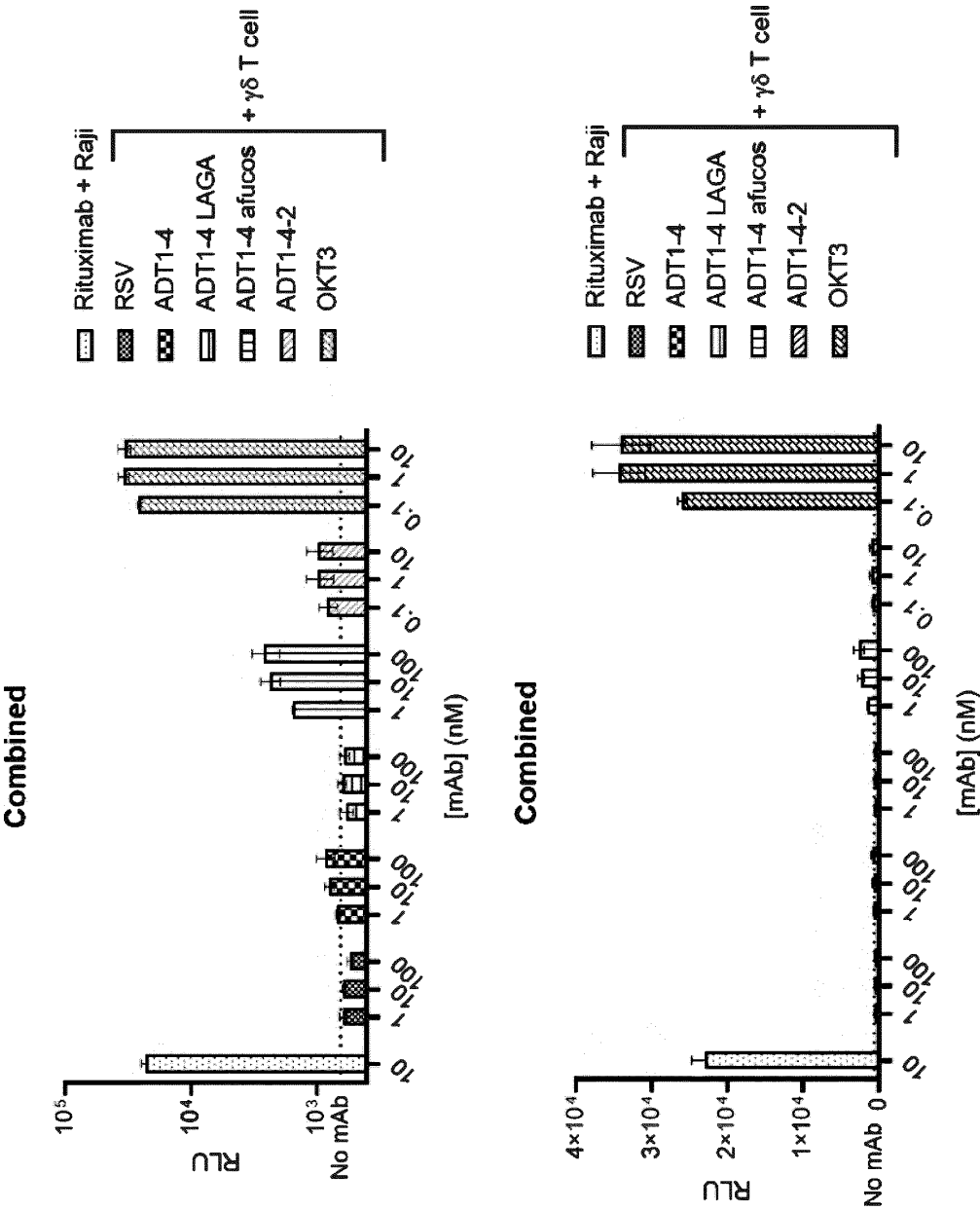


Figure 17

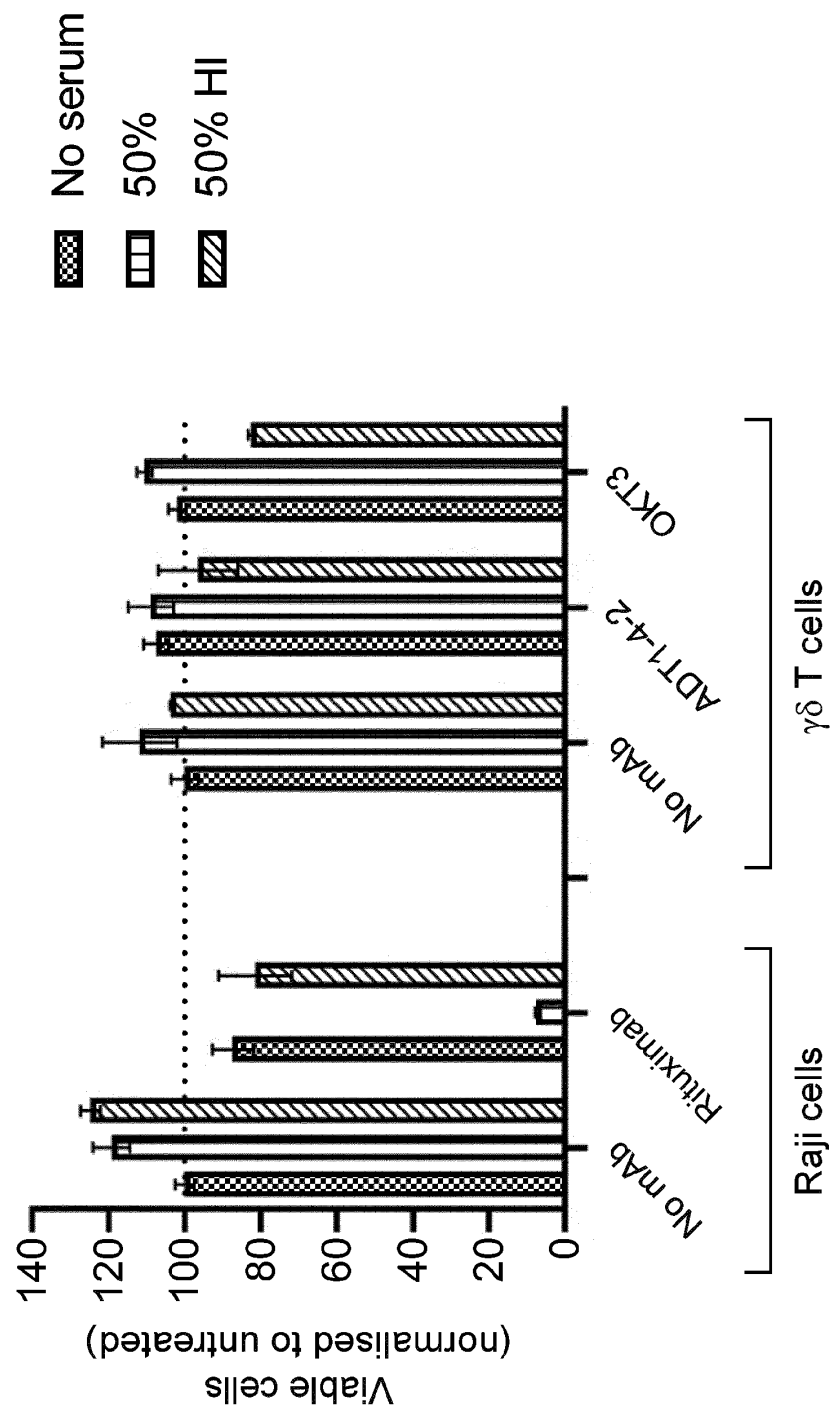


Figure 18

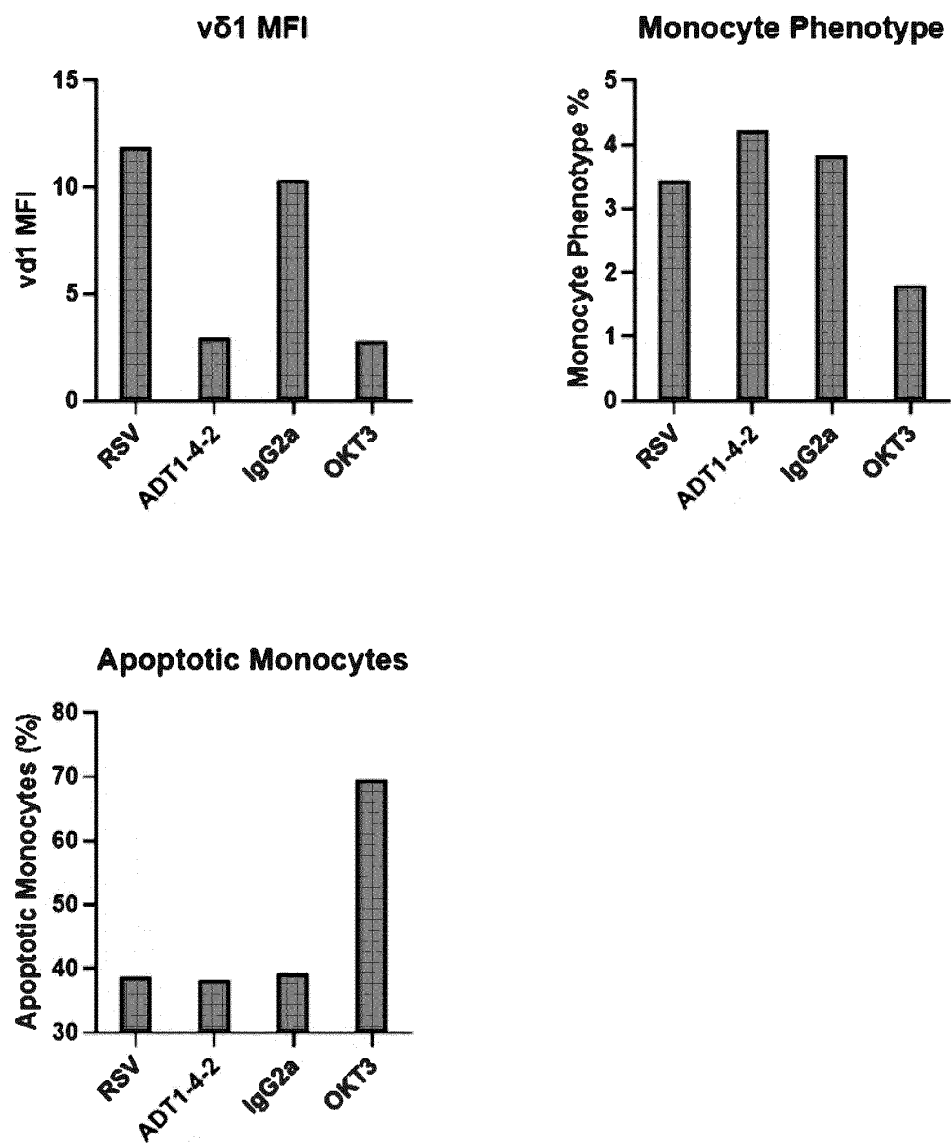


Figure 19

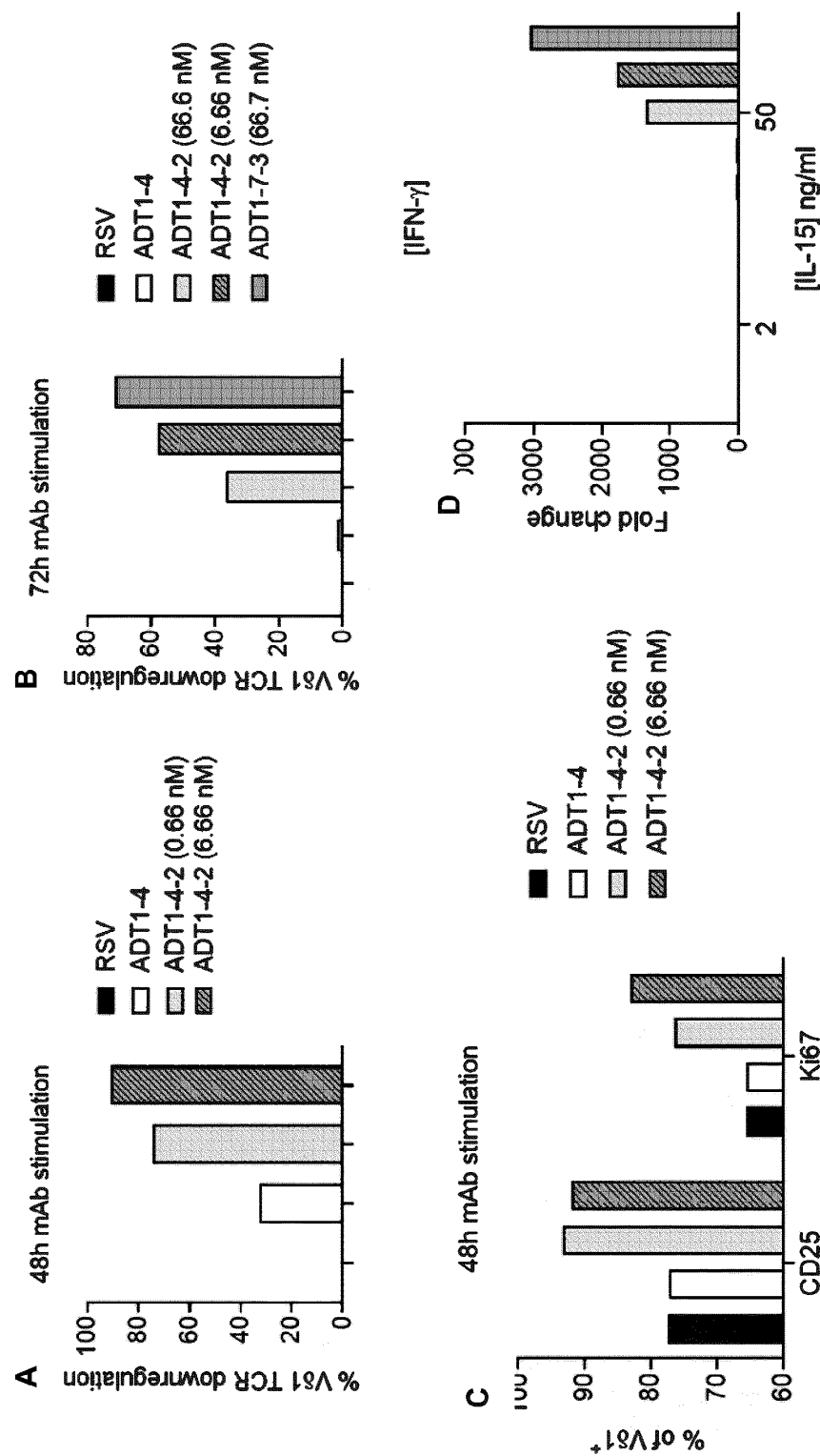


Figure 20

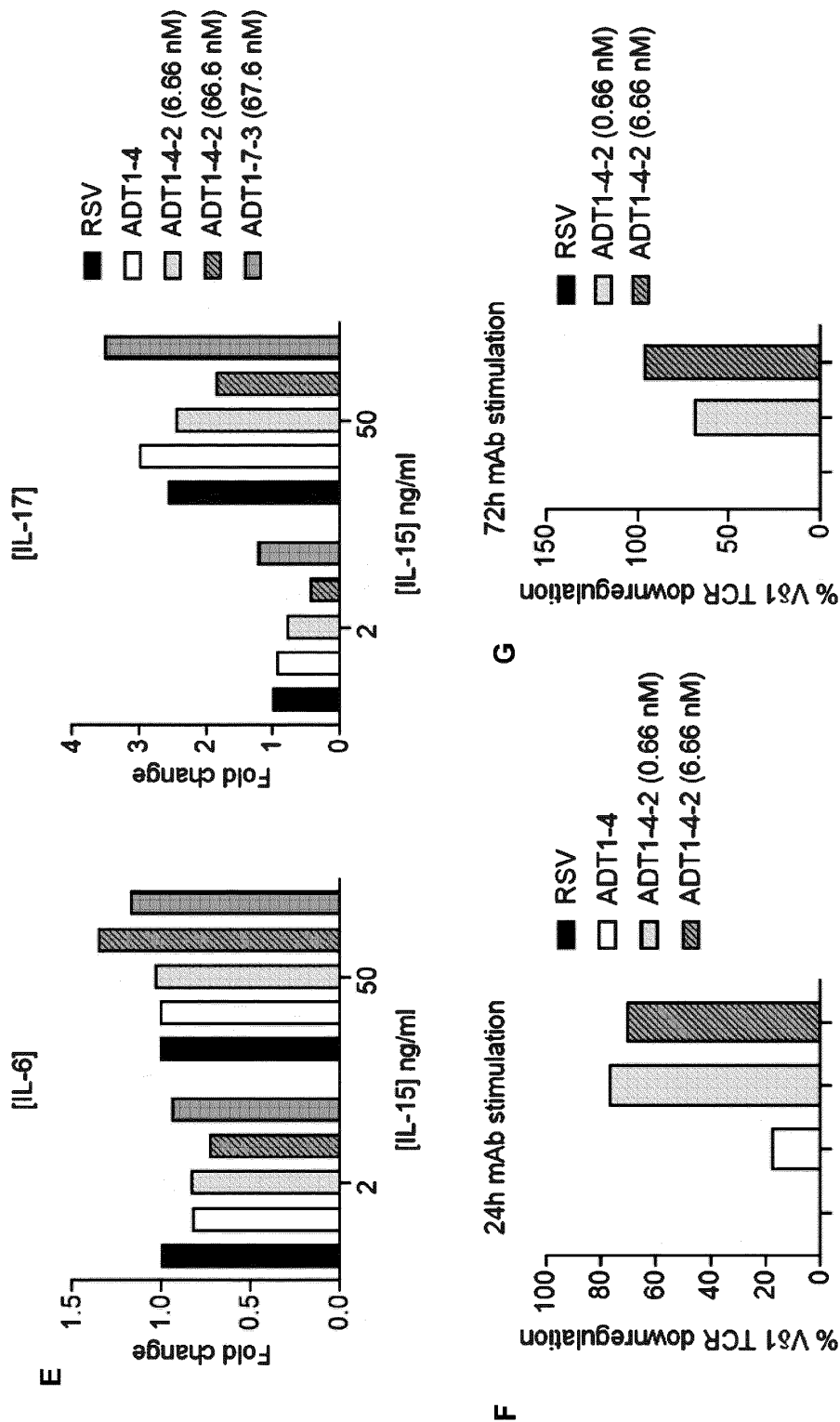


Figure 20 cont.

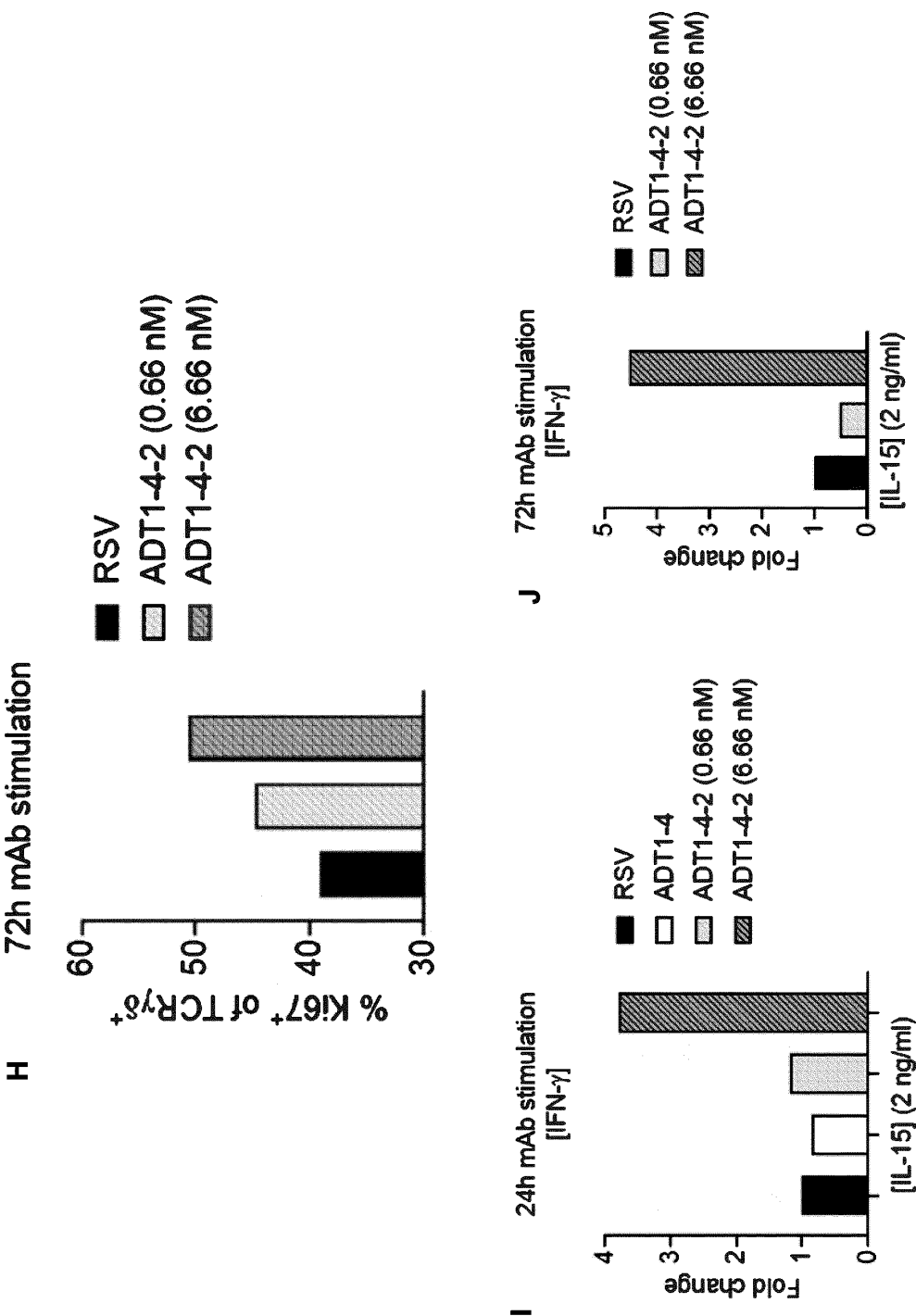


Figure 20 cont.

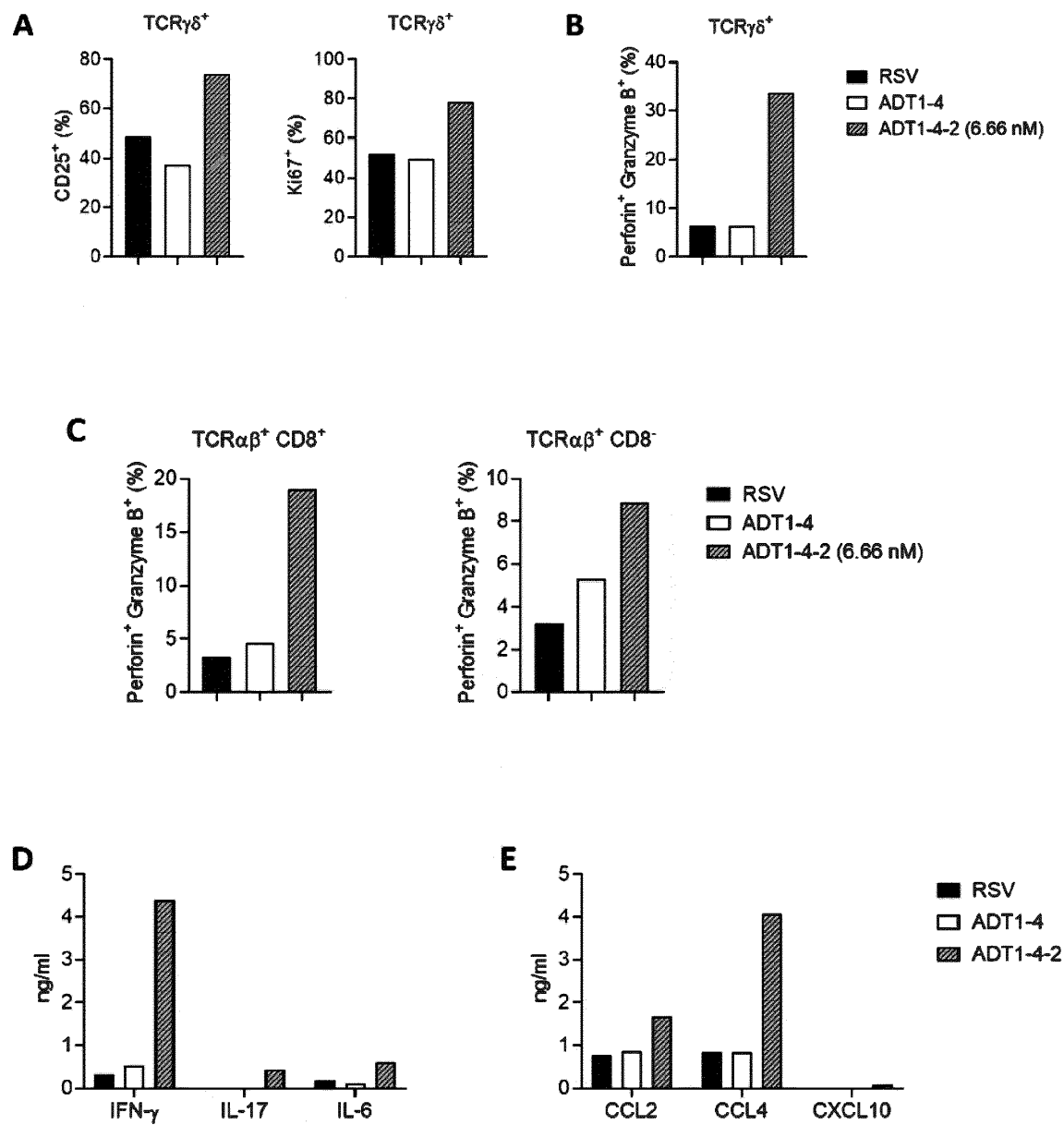


Figure 21

ADT1-4-105 2499\_01\_D07  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-107 2499\_01\_F07  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-110 2499\_02\_A02  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-112 2499\_02\_B04  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-117 2499\_02\_F12  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-19 2501\_01\_H01  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-21 2501\_02\_A05  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-31 2501\_02\_G09  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-139 2502\_01\_C07  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-4 2502\_01\_E01  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-143 2502\_01\_E05  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK  
 ADT1-4-53 2505\_02\_E12  
 DIQMTQSPALASVGDRVITTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESVPLRFSGSGSGTEFTLTATISSLQDDFATYYCQQRKYSTPQITFGQGRLEIK

Figure 22

ADT1-4-173 2505\_02\_G11  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-2 2506\_01\_B10  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-8 2506\_01\_B11  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-82 2506\_02\_B09  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-83 2506\_02\_B10  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-3 2506\_02\_C01  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-84 2506\_02\_C02  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-86 2506\_02\_C12  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-95 2506\_02\_H04  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-1 2501\_01\_C09  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-6 2506\_1\_B06  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK  
 ADT1-4-138 2502\_01\_B03  
 DIQMTQSPALASVGDRTTTCRASQDINDWLAWYQHKPGKAPKLLIYDASSLESGVPLRFSGSGGTEFTLTISLQDDFATYYCQOKYSAPQVTFGQGRLEIK

Figure 22 cont.

ADT1-4-105 2499\_01\_D07  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-107 2499\_01\_F07  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-110 2499\_02\_A02  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-112 2499\_02\_B04  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-117 2499\_02\_F12  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-119 2501\_01\_H01  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-21 2501\_02\_A05  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-31 2501\_02\_G09  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-139 2502\_01\_C07  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-4 2502\_01\_E01  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-143 2502\_01\_E05  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

ADT1-4-53 2505\_02\_E12  
EVQLQQSGPGLVKPSQTLSTLCAISGDSVSKSAANNWIRQSPSRGLEWLGETYRSKWSTDYAAASKSRITINPDTSKNQLSLQLNSVTPEDTAVYYCARTWVGADVWGQGLTVTVSS

Figure 23

ADT1-4-173 2505\_02\_G11  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWAGYPDVWGQGTLLVTVSS

ADT1-4-2 2506\_01\_B10  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYVDVWGQGTLLVTVSS

ADT1-4-8 2506\_01\_B11  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGTLLVTVSS

ADT1-4-82 2506\_02\_B09  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGTLLVTVSS

ADT1-4-83 2506\_02\_B10  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARSWVGYVDVWGQGTLLVTVSS

ADT1-4-3 2506\_02\_C01  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARSWVGYVDVWGQGTLLVTVSS

ADT1-4-84 2506\_02\_C02  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWADYVDVWGQGTLLVTVSS

ADT1-4-86 2506\_02\_C12  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGTLLVTVSS

ADT1-4-95 2506\_02\_H04  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWLGNVVDVWGQGTLLVTVSS

ADT1-4-1 2501\_01\_C09  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGTLLVTVSS

ADT1-4-6 2506\_1\_B06  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWVGYADVWGQGTLLVTVSS

ADT1-4-138 2502\_01\_B03  
 EVQLQSGPGLVKPSQTLSTCAISGDSVSSKSAANNWIRQSPSRGLEWLGRTYRSKWSTDYAASVKSRITINPDTSKNQLSLQNSVTPEDTAVYYCARTWADYVDVWGQGTLLVTVSS

Figure 23 cont.

ADT1-7-10 2503\_1\_C12  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQTASTLLTFGRGTKVEIK

ADT1-7-15 2503\_1\_F01  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSADTLLTFGRGTKVEIK

ADT1-7-17 2503\_1\_G05  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSGSELLTFGRGTKVEIK

ADT1-7-18 2503\_1\_G06  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSASELLTFGRGTKVEIK

ADT1-7-19 2503\_1\_G10  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSYSGLDTFGRGTKVEIK

ADT1-7-20 2503\_1\_H02  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSSSELLTFGRGTKVEIK

ADT1-7-22 2503\_2\_A02  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSASELLTFGRGTKVEIK

ADT1-7-23 2503\_2\_A07  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSYSGLDTFGRGTKVEIK

ADT1-7-42 2503\_2\_H06  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSSSELLTFGRGTKVEIK

ADT1-7-3 2504\_1\_A01  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSYSGLDTFGRGTKVEIK

ADT1-7-61 2504\_1\_F02  
DIQMTQSPSSLSASVGDRTTIACRAGQSSIGTYLNWYQOKPGKAPKLLIYVASSLQSGVPSRPSGSGSGTEFTLTISLQPEDFATYYCQQSASELLTFGRGTKVEIK

Figure 24

ADT1-7-10 2503 1\_C12  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**DDYNDADF**IMGQGTlIVTVSS

ADT1-7-15 2503 1\_F01  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**DDYNDADF**IMGQGTlIVTVSS

ADT1-7-17 2503 1\_G05  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**IDYEDADF**IMGQGTlIVTVSS

ADT1-7-18 2503 1\_G06  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**IDYEDADF**IMGQGTlIVTVSS

ADT1-7-19 2503 1\_G10  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**IDYEDADF**IMGQGTlIVTVSS

ADT1-7-20 2503 1\_H02  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**VDYQEA**FDIMGQGTlIVTVSS

ADT1-7-22 2503 2\_A02  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**DDYNDADF**IMGQGTlIVTVSS

ADT1-7-23 2503 2\_A07  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**VDYNEA**FDIMGQGTlIVTVSS

ADT1-7-42 2503 2\_H06  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**DDYEDADF**IMGQGTlIVTVSS

ADT1-7-3 2504 1\_A01  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**VSYAEAFD**IMGQGTlIVTVSS

ADT1-7-61 2504 1\_F02  
EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKLEWVS**YISSSGSTI**YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR**DDYDDADF**IMGQGTlIVTVSS

Figure 25

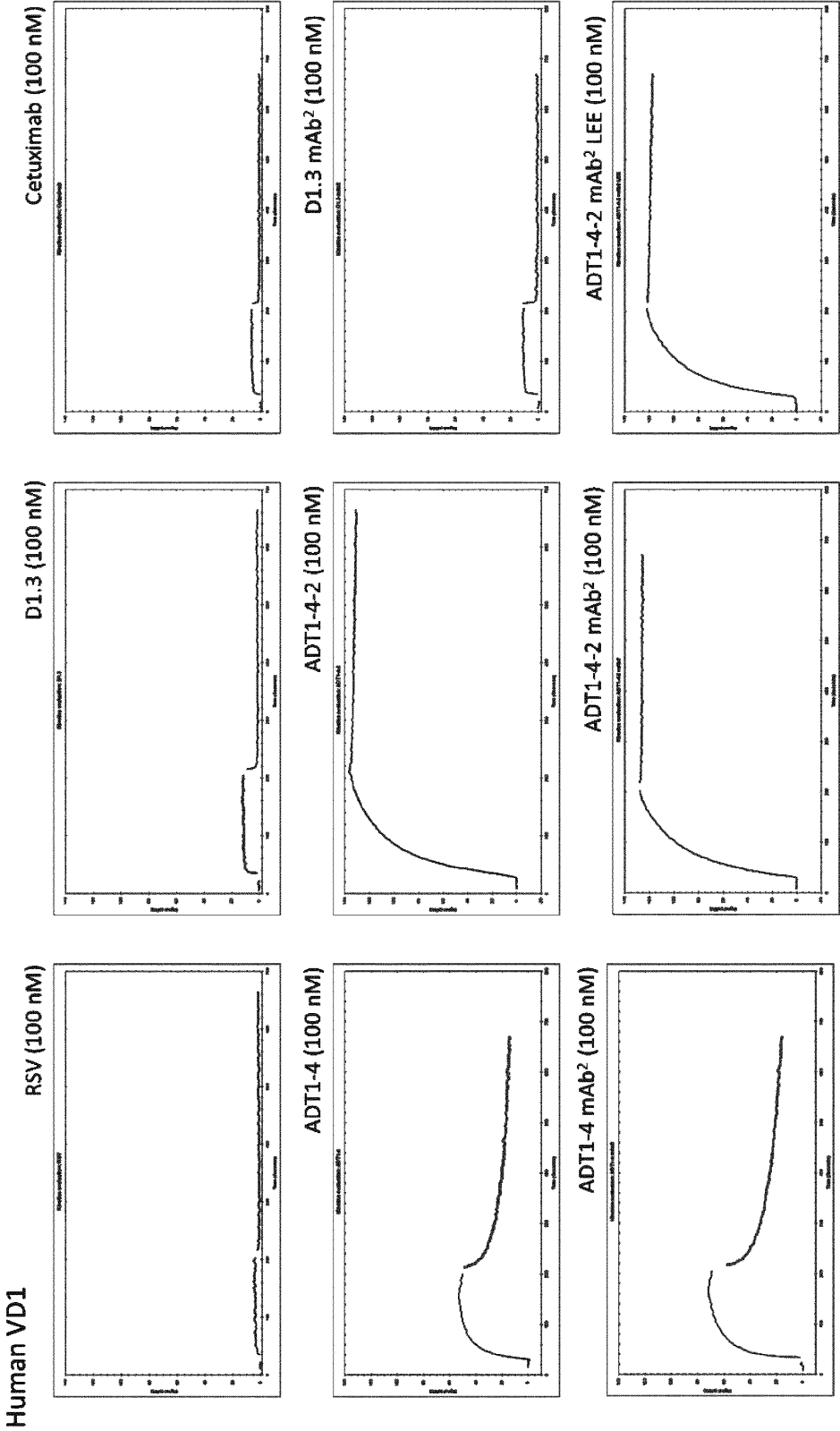
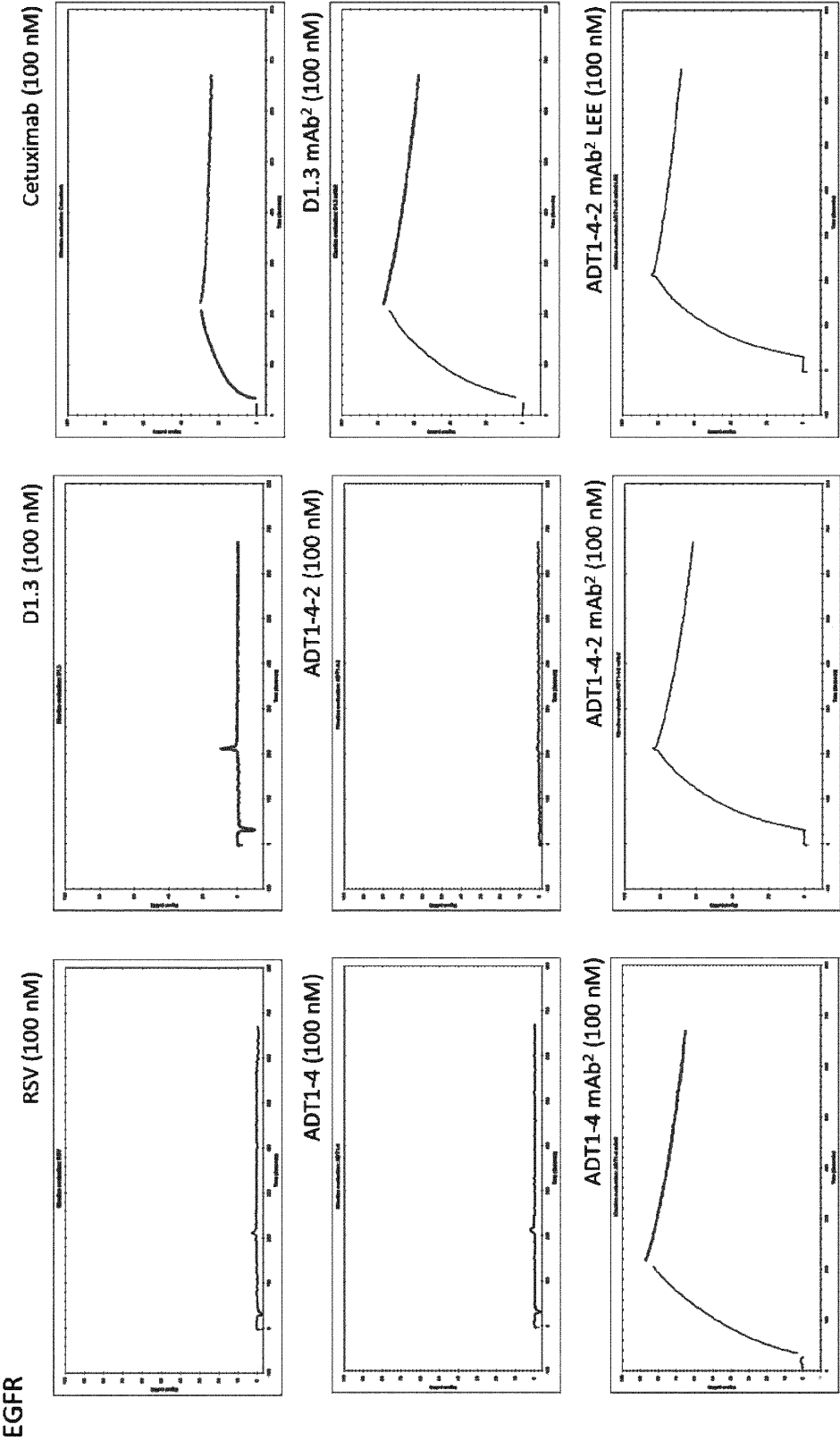


FIG 26A



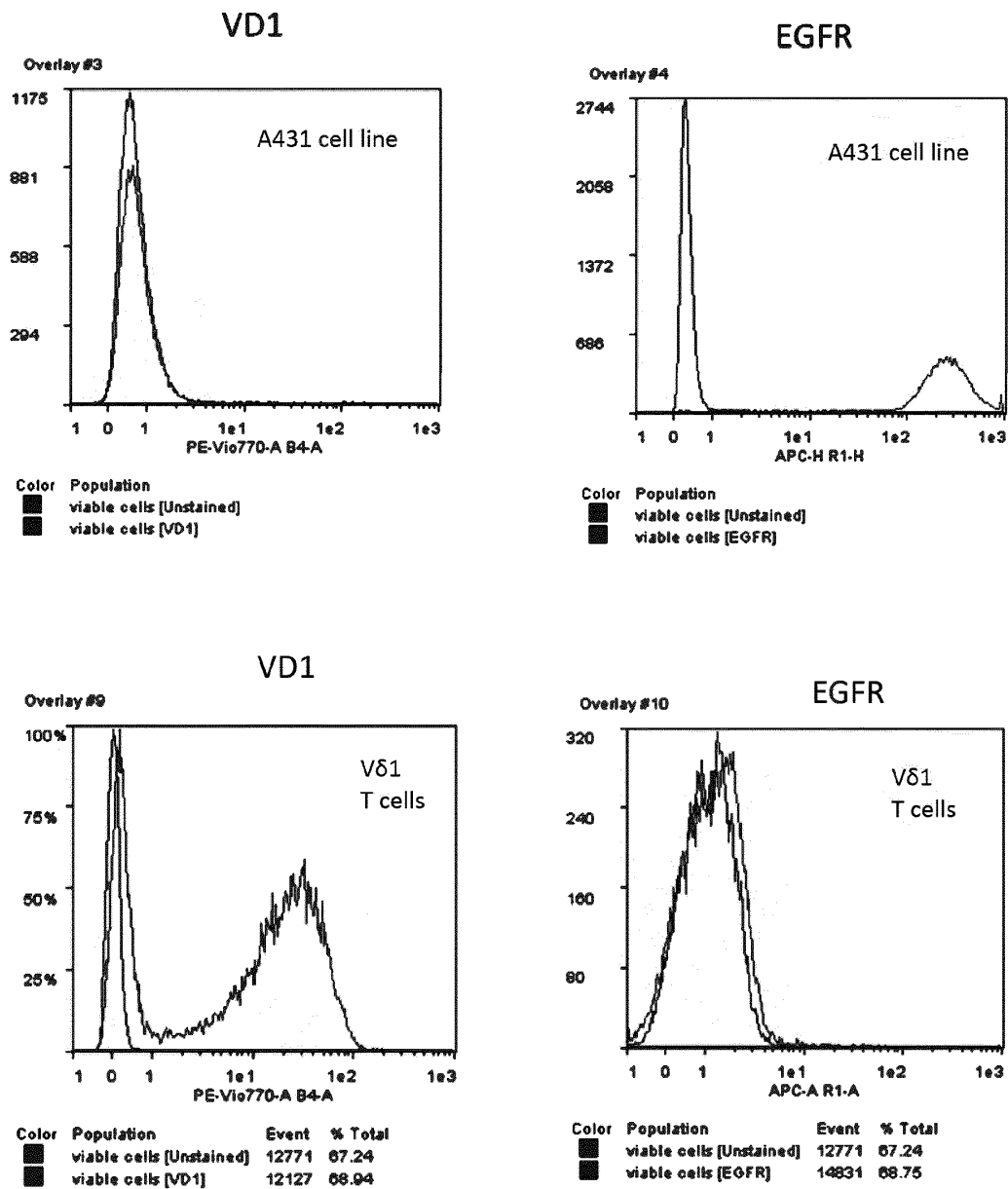


FIG 27A

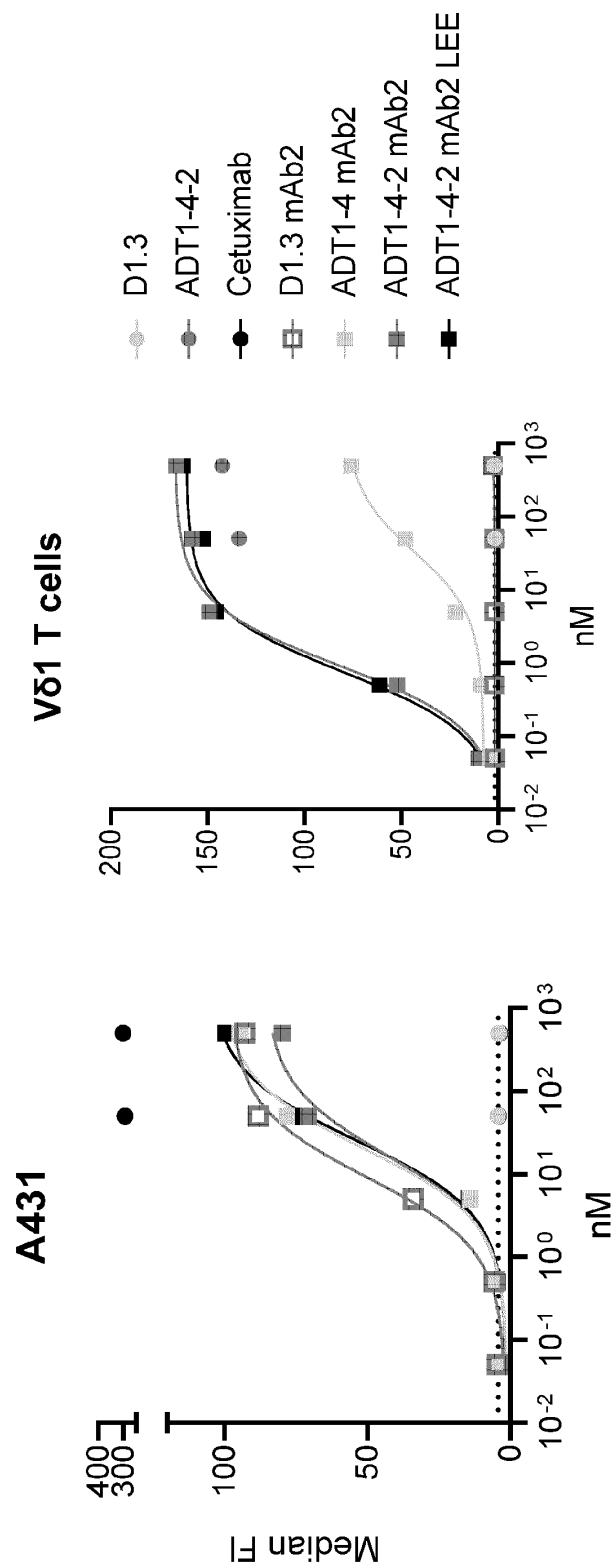


FIG 27B

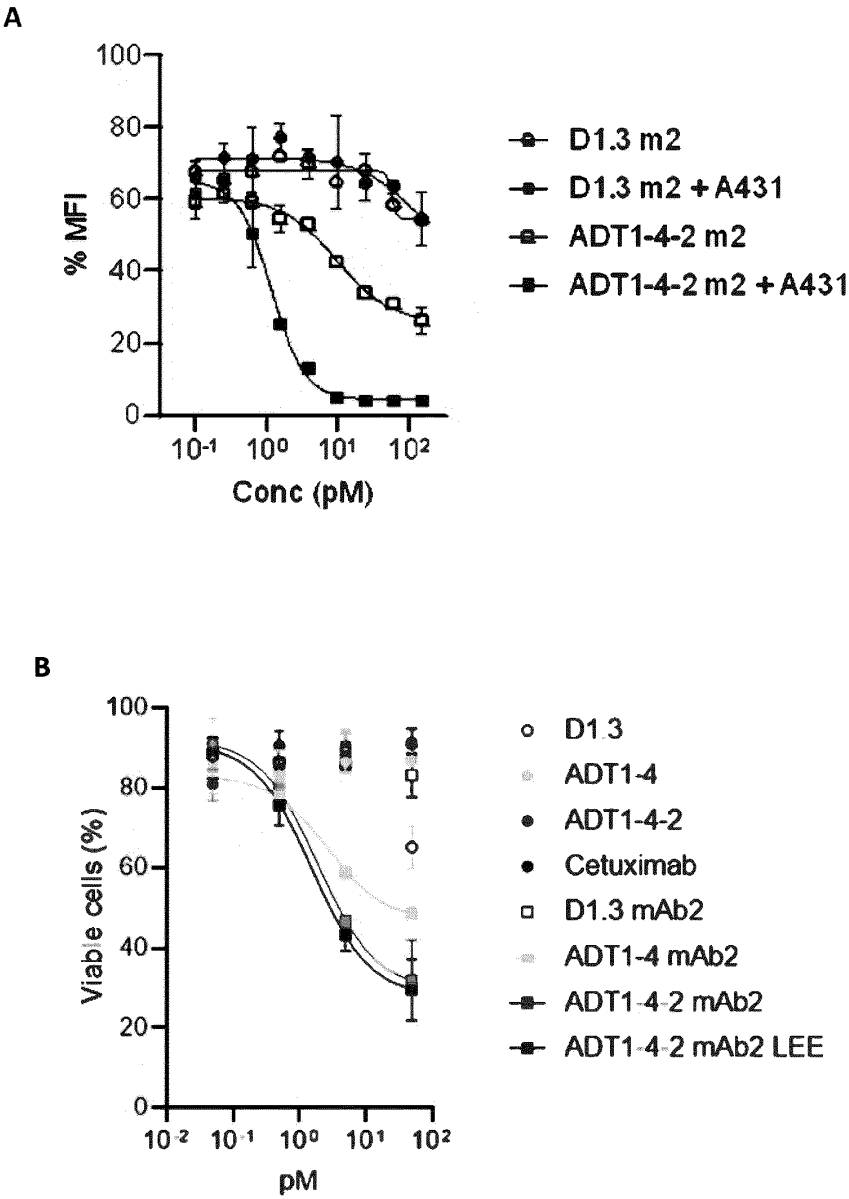


FIG 28

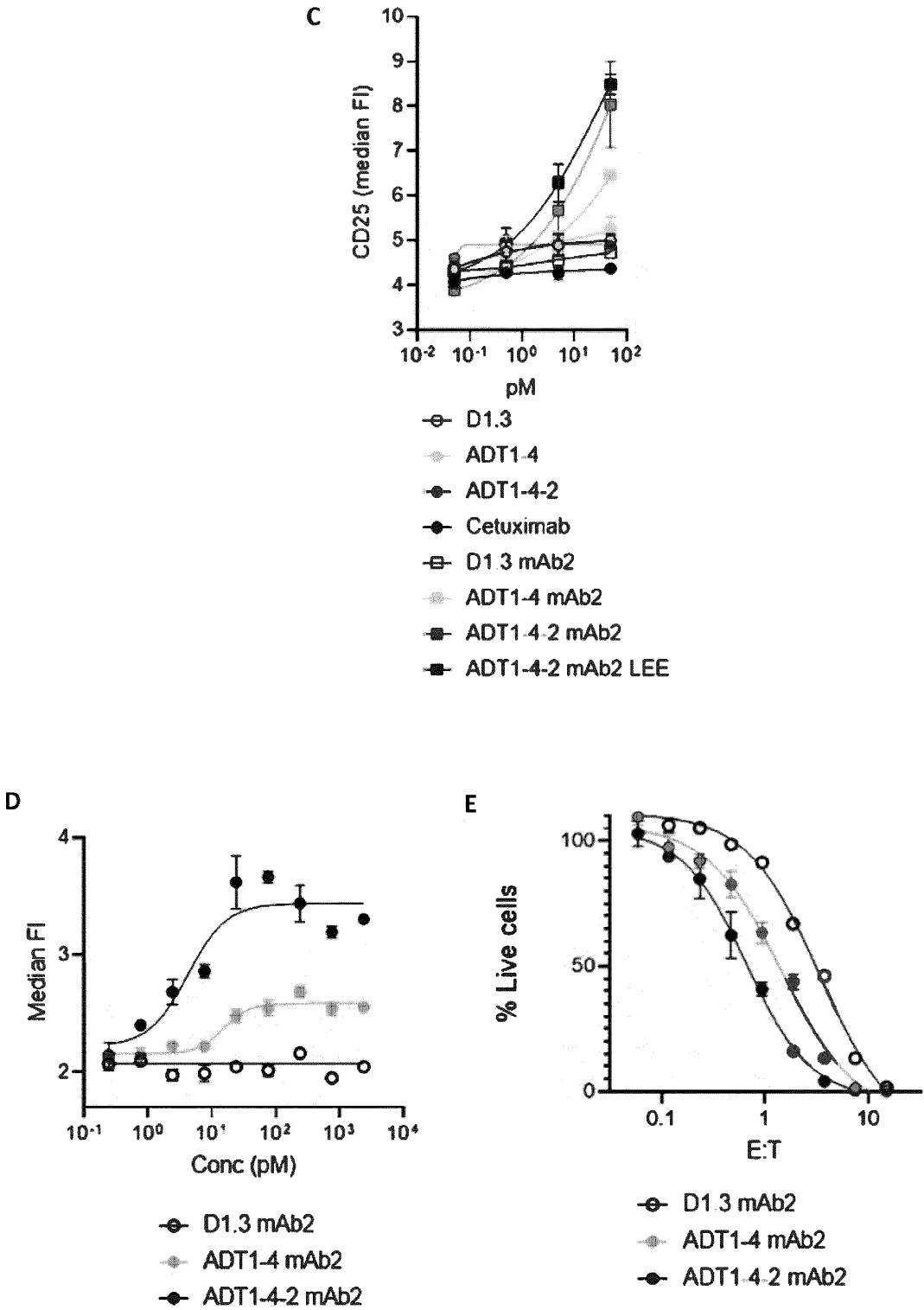


FIG 28 cont.

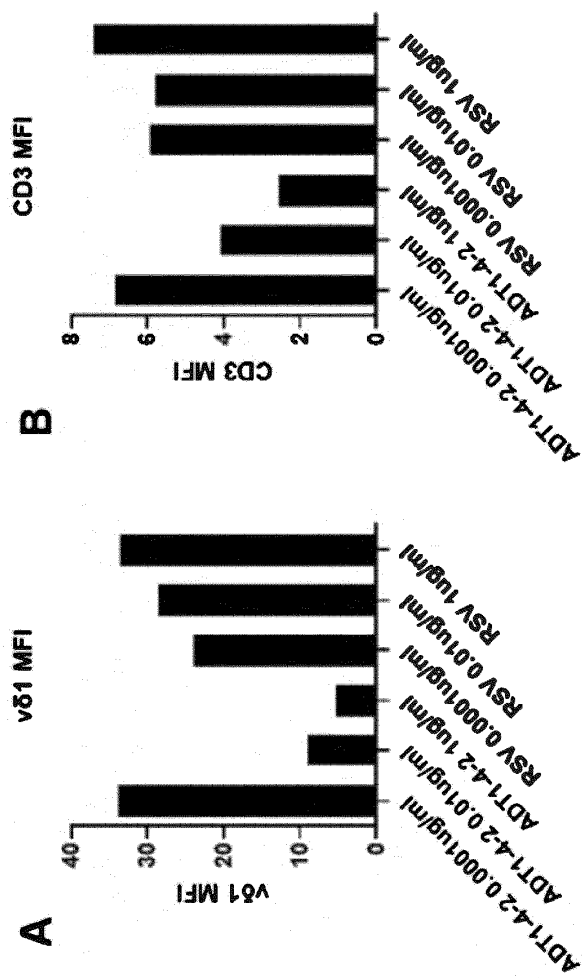


FIG 29

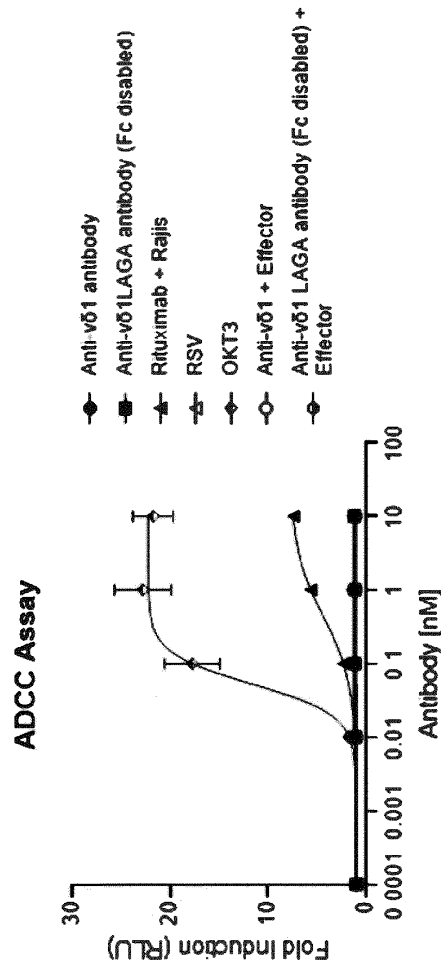


FIG 30

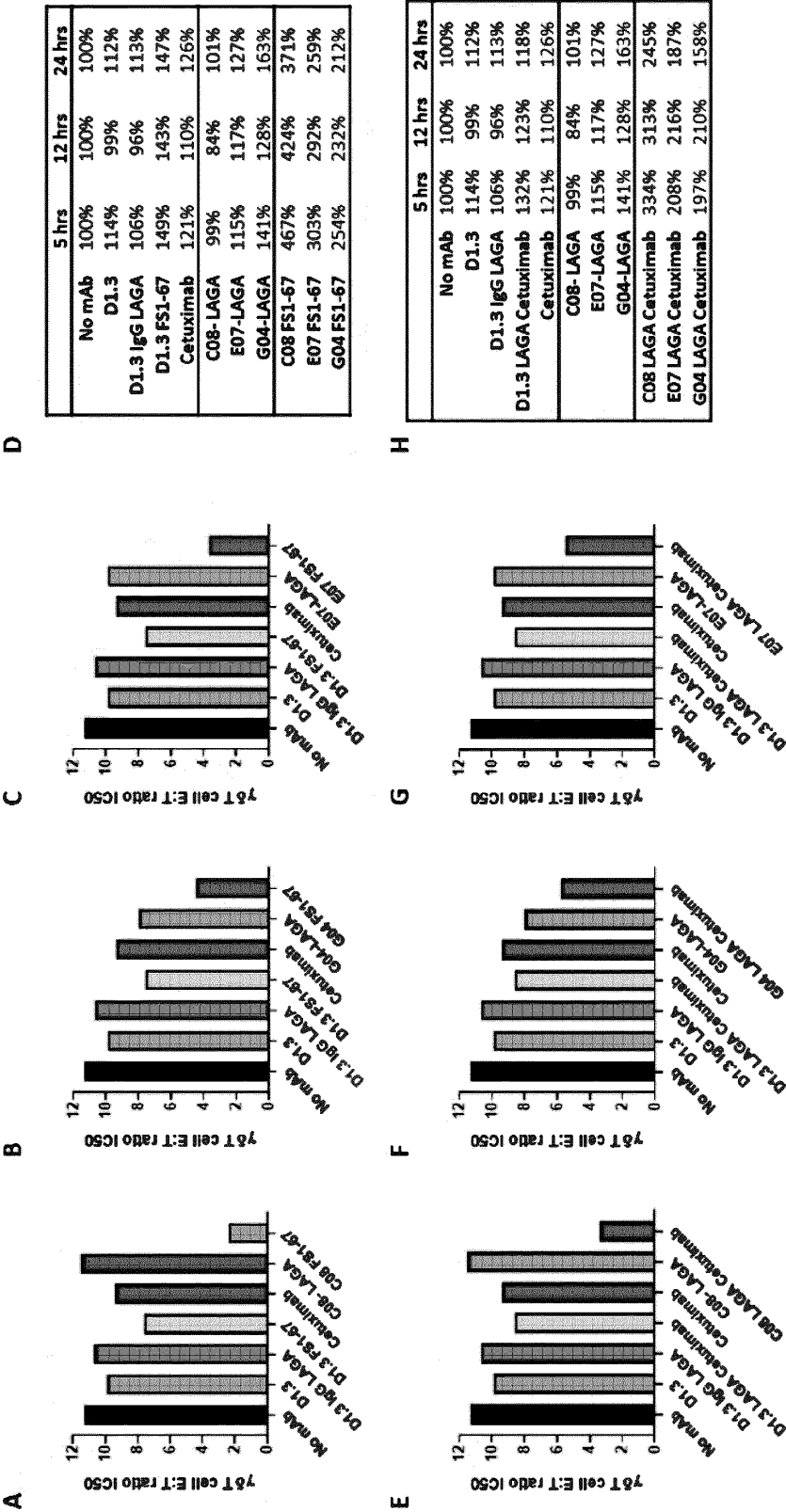


FIGURE 31

EGFR binding domains (IgG1 CH1-CH2-CH3)

FS1-67 (SEQ ID NO: 385)  
ASTKGPSVFPLAAPSSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTLIMISRTPEVTCV  
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDDEGPPVSLTCLVKGFFPSDIAVENEWESTYGFENNNYKTTTPVLDSDGSFFLY  
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE (SEQ ID NO: 392)  
ASTKGPSVFPLAAPSSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTLIMISRTPEVTCV  
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELEEGPVSLTCLVKGFFPSDIAVENEWESTYGFENNNYKTTTPVLDSDGSFFLY  
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE1 (SEQ ID NO: 509)  
ASTKGPSVFPLAAPSSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELAGAPSVFLFPPKPKDTLIMISRTPEVTCV  
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFFPSDIAVENEWESTYGFENNNYKTTTPVLDSDGSFFLY  
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE2 (SEQ ID NO: 521)  
ASTKGPSVFPLAAPSSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTLIMISRTPEVTCV  
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELEEGPVSLTCLVKGFFPSDIAVENEWSNGQFENNNYKTTTPVLDSDGSFFLY  
SKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

LEE3 (SEQ ID NO: 531)  
ASTKGPSVFPLAAPSSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTLIMISRTPEVTCV  
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELEEGPVSLTCLVKGFFPSDIAVENEWESTYGFENNNYKTTTPVLDSDGSFFLY  
SKLTVSYRWQQGNVFSCVMHEALHNHYTQKSLSLSPG

FS1-65 (SEQ ID NO: 540)  
ASTKGPSVFPLAAPSSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTLIMISRTPEVTCV  
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELDEGGPVSLTCLVKGFFPSDIAVENEWESTYGFENNNYKTTTPVLDSDGSFEL  
YSKLTVSYRWYKGNVFSCVMHEALHNHYTQKSLSLSPG

747 (SEQ ID NO: 551)  
ASTKGPSVFPLAAPSSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGGSPVFLFPPKPKDTLIMISRTPEVTCV  
VVDUSHEDEPKFNNWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDETESGPVSLTCLVKGFFPSDIAVENEWSKFGFENNNYKTTTPVLDSDGSFFLY  
SKLTVSNLRTWKGVFSCVMHEALHNHYTQKSLSLSPG

FIGURE 32

EGFR binding domains (IgG1 CH3 only, with EU numbering 341 through to 446 inclusive)

|        | 34                    | 35                                                               | 36                   | 37                   | 38                   | 39                   | 40                   | 41                   | 42                   | 43                   | 44                   |
|--------|-----------------------|------------------------------------------------------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|
|        | 123456789012345678901 | 23456789012345678901                                             | 23456789012345678901 | 23456789012345678901 | 23456789012345678901 | 23456789012345678901 | 23456789012345678901 | 23456789012345678901 | 23456789012345678901 | 23456789012345678901 | 23456789012345678901 |
| IgG1   | QPREPOVYTLPPSRDEITKN  | QVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |                      |
| FS1-67 | QPREPOVYTLPPSRDEITDKG | PVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVS            | YWRWYKGNVFC          | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |
| LEE    | QPREPOVYTLPPSRDEILEG  | PVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVS            | YWRWYKGNVFC          | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |
| LEE1   | QPREPOVYTLPPSRDEITKN  | QVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVS            | YWRWYKGNVFC          | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |
| LEE2   | QPREPOVYTLPPSRDEILEG  | PVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVS            | YWRWYKGNVFC          | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |
| LEE3   | QPREPOVYTLPPSRDEILEG  | PVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVS            | YWRWYKGNVFC          | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |
| 747    | QPREPOVYTLPPSRDEITKSG | PVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVS            | YWRWYKGNVFC          | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |
| FS1-65 | QPREPOVYTLPPSRDEITDKG | PVSLACIVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVS            | YWRWYKGNVFC          | SVMH                 | ALHNHYTQKSLSLSPG     |                      |                      |                      |                      |                      |                      |

|        | AB LOOP                        | CD LOOP           | EF LOOP                             |
|--------|--------------------------------|-------------------|-------------------------------------|
| FS1-67 | L358T.T359D.K360D.N361G.Q362P  | N384T.G385Y.Q386G | D413S.K414Y.S415W.Q418Y.Q419K       |
| LEE    | T359E.K360E.N361G.Q362P        | N384T.G385Y.Q386G | D413S.K414Y.S415W.Q418Y.Q419K       |
| LEE1   |                                | N384T.G385Y.Q386G | D413S.K414Y.S415W.Q418Y.Q419K       |
| LEE2   | T359E.K360E.N361G.Q362P        |                   | D413S.K414Y.S415W.Q418Y.Q419K       |
| LEE3   | T359E.K360E.N361G.Q362P        | N384T.G385Y.Q386G | D413S.K414Y.S415W                   |
| 747    | L358T.T359E.K360S.N361G.Q362P  | A378V             | D413S.K414N.S415L.Q418T.Q419K.N421H |
| FS1-65 | T359D.K360E.N361G.361-IG.Q362P | N384K.G385F.Q386G | D413S.K414Y.S415W.Q418V.Q419K       |

FIGURE 32 cont.

| Human CH3 numbering convention (with cross-reference to IGHG1*01 wild-type)                        |                                    |                                                                                |                                                                                   |                                                                                              |
|----------------------------------------------------------------------------------------------------|------------------------------------|--------------------------------------------------------------------------------|-----------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|
| CH3 Human Sequence IGHG1 amino acid translation J00228 (J00228 corresponds to the IGHG1*01 allele) | IMGT unique numbering for C-DOMAIN | IMGT CH3 exon numbering – see IMGT.Org (also for source of this adapted Table) | Eu numbering – see Edelman, G.M. et al., Proc. Natl. Acad. USA, 63, 78-85 (1969). | Kabat numbering – see Kabat, E.A. et al., NIH publication n° 91-3242, pp 662,680,689 (1991). |
| G                                                                                                  | 1.4                                | 1                                                                              | 341                                                                               | 361                                                                                          |
| Q                                                                                                  | 1.3                                | 2                                                                              | 342                                                                               | 363                                                                                          |
| P                                                                                                  | 1.2                                | 3                                                                              | 343                                                                               | 364                                                                                          |
| R                                                                                                  | 1.1                                | 4                                                                              | 344                                                                               | 365                                                                                          |
| E                                                                                                  | 1                                  | 5                                                                              | 345                                                                               | 366                                                                                          |
| P                                                                                                  | 2                                  | 6                                                                              | 346                                                                               | 367                                                                                          |
| Q                                                                                                  | 3                                  | 7                                                                              | 347                                                                               | 368                                                                                          |
| V                                                                                                  | 4                                  | 8                                                                              | 348                                                                               | 369                                                                                          |
| Y                                                                                                  | 5                                  | 9                                                                              | 349                                                                               | 370                                                                                          |
| T                                                                                                  | 6                                  | 10                                                                             | 350                                                                               | 371                                                                                          |
| L                                                                                                  | 7                                  | 11                                                                             | 351                                                                               | 372                                                                                          |
| P                                                                                                  | 8                                  | 12                                                                             | 352                                                                               | 373                                                                                          |
| P                                                                                                  | 9                                  | 13                                                                             | 353                                                                               | 374                                                                                          |
| S                                                                                                  | 10                                 | 14                                                                             | 354                                                                               | 375                                                                                          |
| R                                                                                                  | 11                                 | 15                                                                             | 355                                                                               | 376                                                                                          |
| D                                                                                                  | 12                                 | 16                                                                             | 356                                                                               | 377                                                                                          |
| E                                                                                                  | 13                                 | 17                                                                             | 357                                                                               | 378                                                                                          |
| L                                                                                                  | 14                                 | 18                                                                             | 358                                                                               | 381                                                                                          |
| T                                                                                                  | 15                                 | 19                                                                             | 359                                                                               | 382                                                                                          |
| K                                                                                                  | 16                                 | 20                                                                             | 360                                                                               | 383                                                                                          |
| N                                                                                                  | 17                                 | 21                                                                             | 361                                                                               | 384                                                                                          |
| (extra insert found in one example construct)                                                      | 17.1                               | 21.1                                                                           | 361.1                                                                             | 384.1                                                                                        |
| Q                                                                                                  | 18                                 | 22                                                                             | 362                                                                               | 385                                                                                          |
| V                                                                                                  | 19                                 | 23                                                                             | 363                                                                               | 386                                                                                          |
| S                                                                                                  | 20                                 | 24                                                                             | 364                                                                               | 387                                                                                          |
| L                                                                                                  | 21                                 | 25                                                                             | 365                                                                               | 388                                                                                          |
| T                                                                                                  | 22                                 | 26                                                                             | 366                                                                               | 389                                                                                          |
| C                                                                                                  | 23                                 | 27                                                                             | 367                                                                               | 390                                                                                          |
| L                                                                                                  | 24                                 | 28                                                                             | 368                                                                               | 391                                                                                          |
| V                                                                                                  | 25                                 | 29                                                                             | 369                                                                               | 392                                                                                          |
| K                                                                                                  | 26                                 | 30                                                                             | 370                                                                               | 393                                                                                          |
| G                                                                                                  | 27                                 | 31                                                                             | 371                                                                               | 394                                                                                          |
| F                                                                                                  | 28                                 | 32                                                                             | 372                                                                               | 395                                                                                          |
| Y                                                                                                  | 29                                 | 33                                                                             | 373                                                                               | 396                                                                                          |
| P                                                                                                  | 30                                 | 34                                                                             | 374                                                                               | 397                                                                                          |
| S                                                                                                  | 35                                 | 35                                                                             | 375                                                                               | 398                                                                                          |
| D                                                                                                  | 36                                 | 36                                                                             | 376                                                                               | 399                                                                                          |
| I                                                                                                  | 37                                 | 37                                                                             | 377                                                                               | 400                                                                                          |
| A                                                                                                  | 38                                 | 38                                                                             | 378                                                                               | 401                                                                                          |

FIGURE 33 cont.

|   |      |    |     |     |
|---|------|----|-----|-----|
| V | 39   | 39 | 379 | 402 |
| E | 40   | 40 | 380 | 405 |
| W | 41   | 41 | 381 | 406 |
| E | 42   | 42 | 382 | 407 |
| S | 43   | 43 | 383 | 408 |
| N | 44   | 44 | 384 | 410 |
| G | 45   | 45 | 385 | 411 |
| Q | 45.1 | 46 | 386 | 414 |
| P | 45.2 | 47 | 387 | 415 |
| E | 45.3 | 48 | 388 | 416 |
| N | 45.4 | 49 | 389 | 417 |
| N | 77   | 50 | 390 | 418 |
| Y | 78   | 51 | 391 | 419 |
| K | 79   | 52 | 392 | 420 |
| T | 80   | 53 | 393 | 421 |
| T | 81   | 54 | 394 | 422 |
| P | 82   | 55 | 395 | 423 |
| P | 83   | 56 | 396 | 424 |
| V | 84   | 57 | 397 | 425 |
| L | 84.1 | 58 | 398 | 426 |
| D | 84.2 | 59 | 399 | 427 |
| S | 84.3 | 60 | 400 | 428 |
| D | 84.4 | 61 | 401 | 430 |
| G | 85.4 | 62 | 402 | 433 |
| S | 85.3 | 63 | 403 | 434 |
| F | 85.2 | 64 | 404 | 435 |
| F | 85.1 | 65 | 405 | 436 |
| L | 85   | 66 | 406 | 437 |
| Y | 86   | 67 | 407 | 438 |
| S | 87   | 68 | 408 | 439 |
| K | 88   | 69 | 409 | 440 |
| L | 89   | 70 | 410 | 441 |
| T | 90   | 71 | 411 | 442 |
| V | 91   | 72 | 412 | 443 |
| D | 92   | 73 | 413 | 444 |
| K | 93   | 74 | 414 | 445 |
| S | 94   | 75 | 415 | 446 |
| R | 95   | 76 | 416 | 447 |
| W | 96   | 77 | 417 | 448 |
| Q | 97   | 78 | 418 | 449 |
| Q | 98   | 79 | 419 | 450 |
| G | 99   | 80 | 420 | 451 |
| N | 100  | 81 | 421 | 452 |
| V | 101  | 82 | 422 | 453 |
| F | 102  | 83 | 423 | 454 |
| S | 103  | 84 | 424 | 455 |

FIGURE 33 cont.

|   |     |         |     |     |
|---|-----|---------|-----|-----|
| C | 104 | 85      | 425 | 456 |
| S | 105 | 86      | 426 | 457 |
| V | 106 | 87      | 427 | 458 |
| M | 107 | 88      | 428 | 459 |
| H | 108 | 89      | 429 | 460 |
| E | 109 | 90      | 430 | 461 |
| A | 110 | 91      | 431 | 462 |
| L | 112 | 92      | 432 | 463 |
| H | 113 | 93      | 433 | 464 |
| N | 114 | 94      | 434 | 465 |
| H | 115 | 95      | 435 | 466 |
| Y | 116 | 96      | 436 | 467 |
| T | 117 | 97      | 437 | 468 |
| Q | 118 | 98      | 438 | 469 |
| K | 119 | 99      | 439 | 470 |
| S | 120 | 100     | 440 | 471 |
| L | 121 | 101     | 441 | 472 |
| S | 122 | 102     | 442 | 473 |
| L | 123 | 103     | 443 | 474 |
| S | 124 | 104     | 444 | 475 |
| P | 125 | 105     | 445 | 476 |
| G | 129 | CHS 106 | 446 | 477 |
| K | 130 | CHS 107 | 447 | 478 |

FIGURE 33 cont

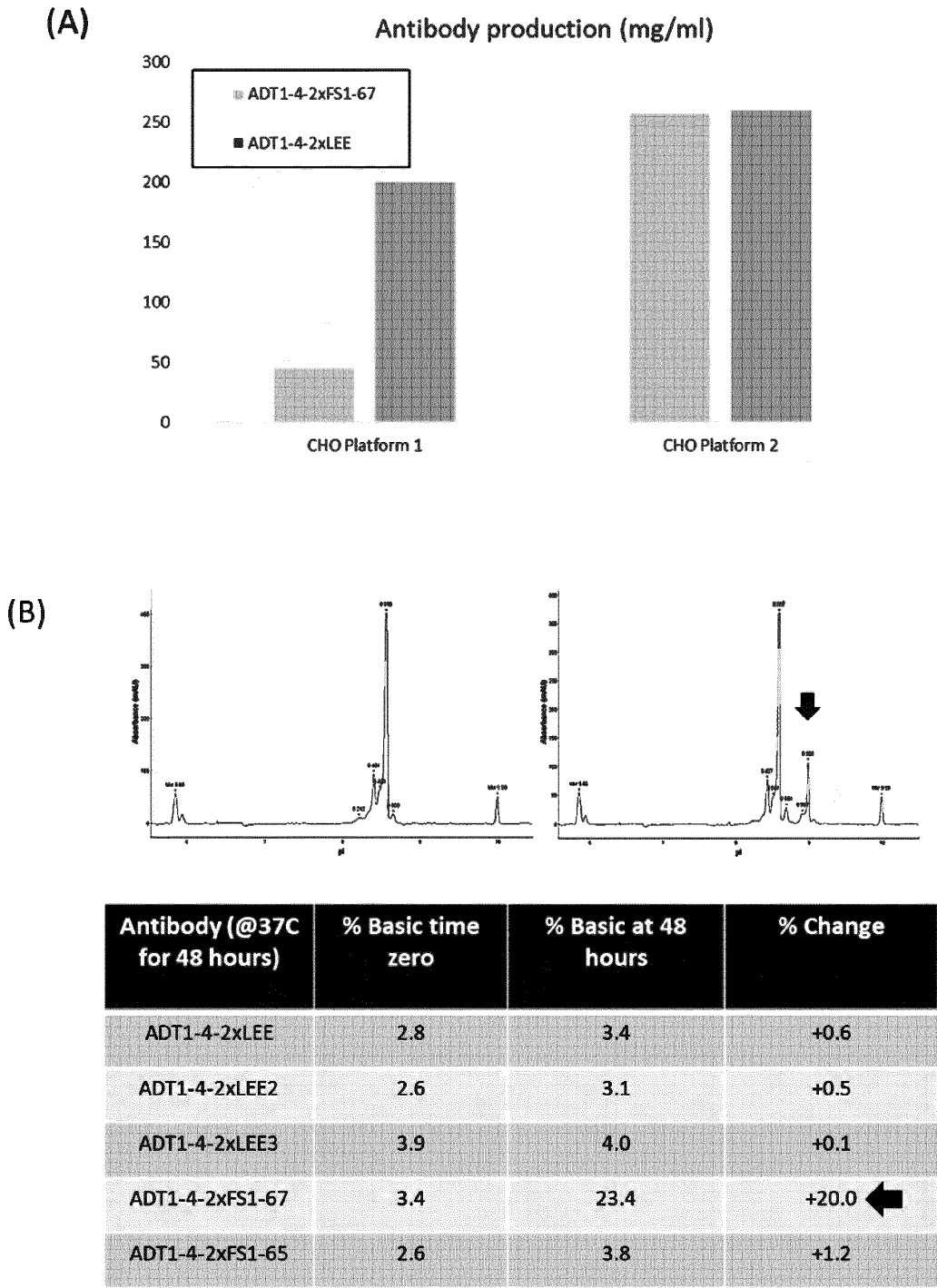
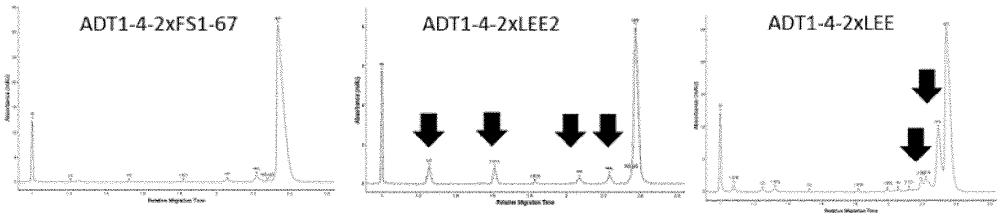


FIGURE 34

(C)

| Antibody        | Tm onset (°C) | Tagg onset (°C) | Delta(°C) |
|-----------------|---------------|-----------------|-----------|
| ADT1-4-2xLEE    | 63.8          | 63.8            | 0         |
| ADT1-4-2xLEE2   | 67.7          | 64.2            | -3.5      |
| ADT1-4-2xLEE3   | 67.8          | 64.4            | -3.4      |
| ADT1-4-2xFS1-67 | 68.9          | 65.7            | -3.2      |
| ADT1-4-2xFS1-65 | 74            | 57.6            | -16.4 ←   |

(D)



| Antibody @ 5mg/ml | % Monomer (time zero) | % Monomer (18 days, 37°C) | % change over 18-days |
|-------------------|-----------------------|---------------------------|-----------------------|
| ADT1-4-2xLEE      | 98.0                  | 60.6                      | -37.4                 |
| ADT1-4-2xLEE2     | 97.7                  | 74.0                      | -23.7                 |
| ADT1-4-2xLEE3     | 97.5                  | 68.3                      | -29.2                 |
| ADT1-4-2xFS1-67   | 95.6                  | 94.0                      | -1.6                  |
| ADT1-4-2xFS1-65   | 96.8                  | 72.7                      | -24.1                 |

(E)

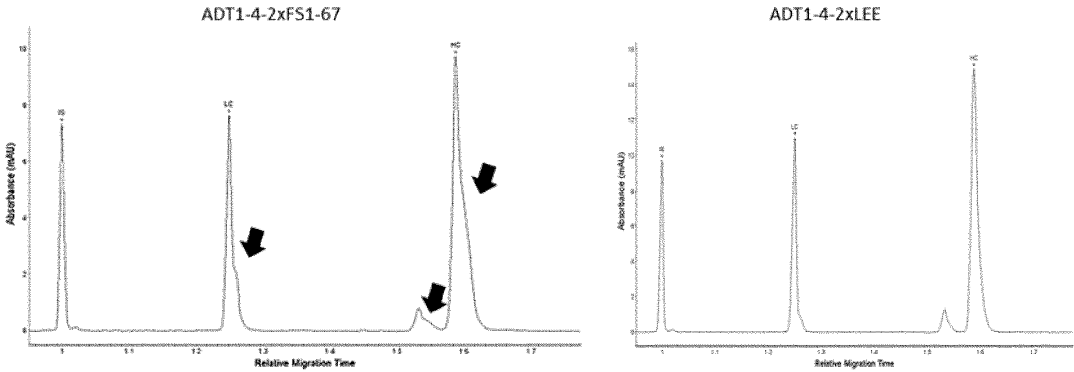


FIGURE 34 cont.  
64/84

(F)

| Antibody        | Yield | Stable Charge at 37C | Favorable Tm/Tagg delta | %Monomer 5mg/ml, 18d @ 37C (non-reduced) | Typical HC + LC profile at 5mg/ml 18 d @ 37C (reduced) | Total Score | AB loop modifications          | BC loop modifications     | EF loop modifications         | No. of changes (and % identity) relative to human CH3 sequence P343 to G446 (EU numbering) |
|-----------------|-------|----------------------|-------------------------|------------------------------------------|--------------------------------------------------------|-------------|--------------------------------|---------------------------|-------------------------------|--------------------------------------------------------------------------------------------|
| ADT1-4-2xLEE    | ++    | +++                  | +++                     | +                                        | ++                                                     | 11          | T359E.K360E.N361G.Q362P        | N384T.G385Y.Q386G         | D413S.K414Y.S415W.Q418Y.Q419K | 12 (88%)                                                                                   |
| ADT1-4-2xLEE2   | ++    | +++                  | ++                      | ++                                       | ++                                                     | 11          | T359E.K360E.N361G.Q362P        | No changes from wild-type | D413S.K414Y.S415W.Q418Y.Q419K | 9 (91%)                                                                                    |
| ADT1-4-2xLEE3   | ++    | +++                  | ++                      | ++                                       | ++                                                     | 11          | T359E.K360E.N361G.Q362P        | N384T.G385Y.Q386G         | D413S.K414Y.S415W             | 10 (90%)                                                                                   |
| ADT1-4-2xFS1-67 | +     | +                    | ++                      | +++                                      | -                                                      | 7           | L358T.T359D.K360D.N361G.Q362P  | N384T.G385Y.Q386G         | D413S.K414Y.S415W.Q418Y.Q419K | 13 (88%)                                                                                   |
| ADT1-4-2xFS1-65 | ++    | +++                  | -                       | ++                                       | ++                                                     | 9           | T359D.K360D.N361G.361.1G.Q362P | N384T.G385Y.Q386G         | D413S.K414Y.S415W.Q418Y.Q419K | 13 (88%)                                                                                   |

FIGURE 34 cont.

| Antibody          | EC50 (pM) | EC95 (pM) | MFI (at saturation) |
|-------------------|-----------|-----------|---------------------|
| EGFR control      | N/A       | N/A       | ~ 0.4950            |
| ADT1-4-2xADT3-2   | 275.9     | 2698      | 101.1               |
| ADT1-4-6xADT3-2   | 279.2     | 2766      | 87.56               |
| ADT1-4-138xADT3-2 | 208.8     | 2254      | 46.31               |

C)

| Antibody          | Affinity to Vδ1 (nM) |
|-------------------|----------------------|
| ADT1-4-2/ADT3-2   | 0.24                 |
| ADT1-4-6/ADT3-2   | 1.26                 |
| ADT1-4-138/ADT3-2 | 18.3                 |

Note: EGFR affinity similar for all  
Approx. 1 nM

B)

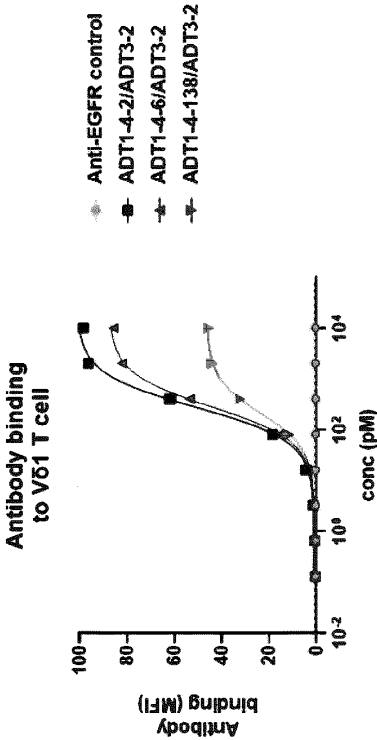


FIGURE 35

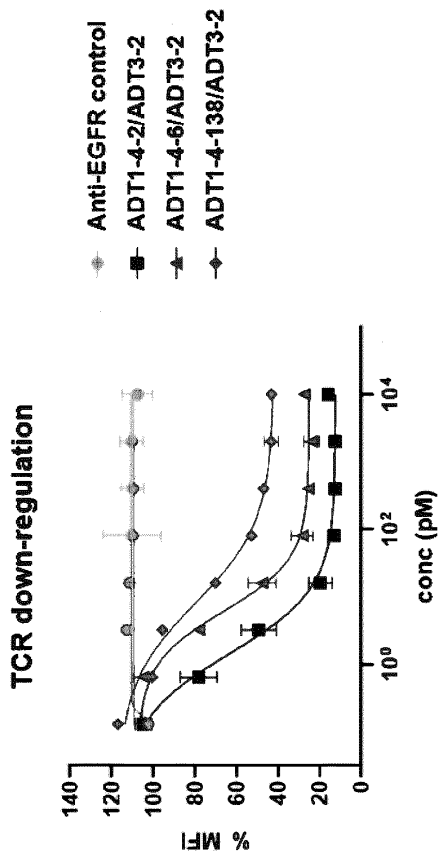
E)

| Antibody          | EC50 (pM) | EC95 (pM) | % change (at saturation) |
|-------------------|-----------|-----------|--------------------------|
| EGFR control      | N/A       | N/A       | -                        |
| ADT1-4-2xADT3-2   | 1.422     | 37.85     | 101.9                    |
| ADT1-4-6xADT3-2   | 6.056     | 83.63     | 81.94                    |
| ADT1-4-138xADT3-2 | 7.981     | 495.6     | 75.34                    |

G)

| Antibody          | % inc CD107a-pos (at saturation) |
|-------------------|----------------------------------|
| EGFR control      | -                                |
| ADT1-4-2xADT3-2   | 34.86                            |
| ADT1-4-6xADT3-2   | 28.09                            |
| ADT1-4-138xADT3-2 | 12.04                            |

D)



F)

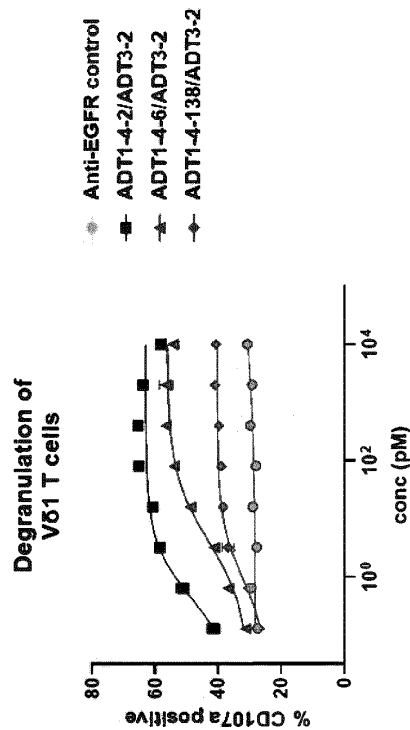


FIGURE 35 cont.

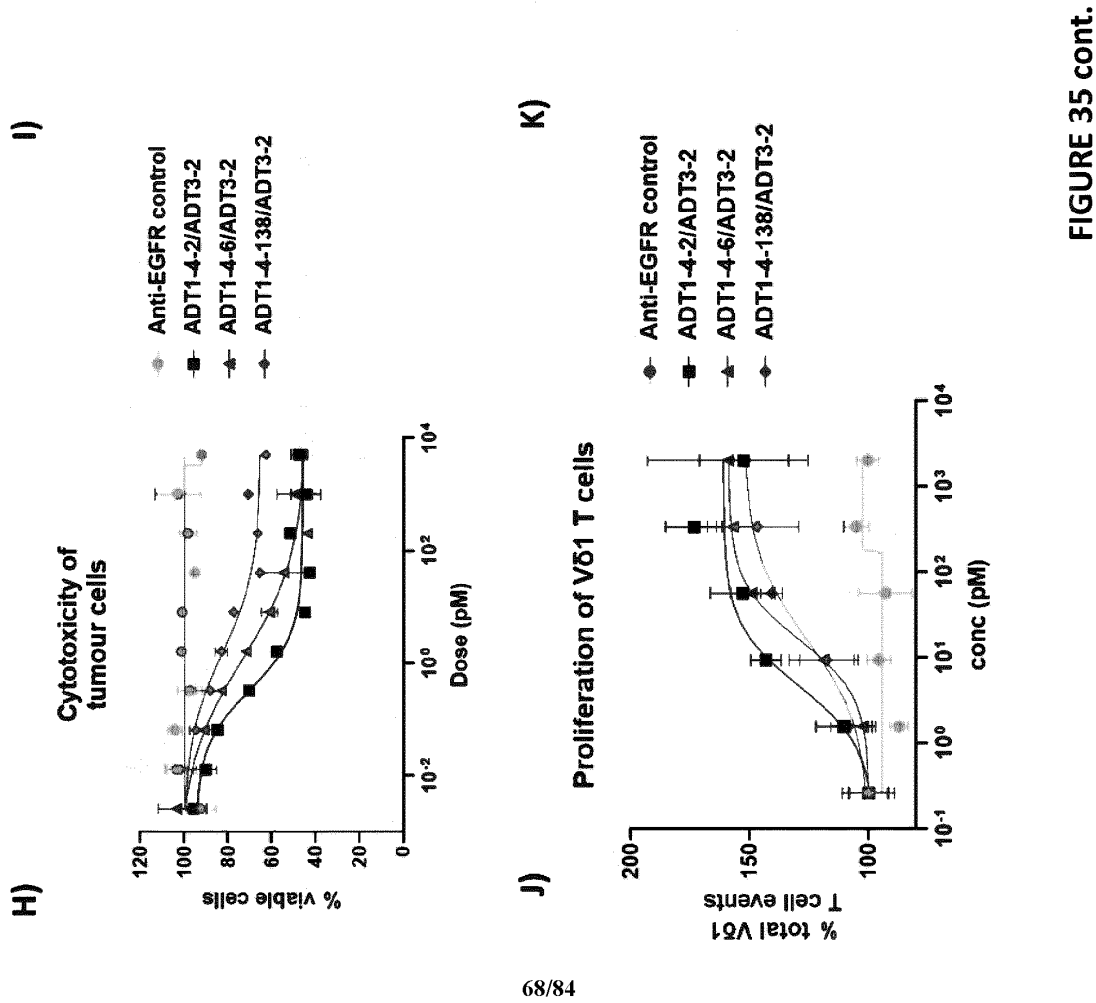
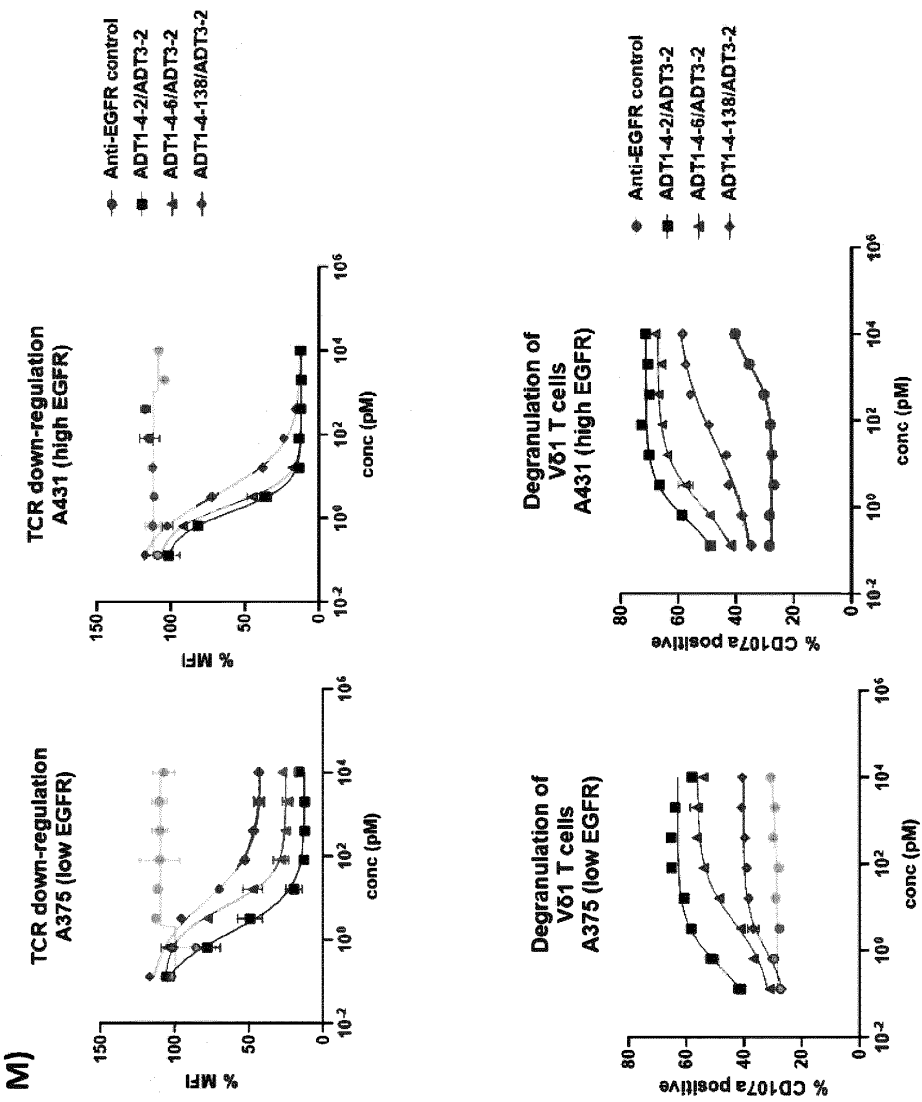


FIGURE 35 cont.

L)

| Technical effect conferred on primary tissue-derived V61+ by anti-V61 TCR antibodies of this invention | Is this effect further enhanced by increasing the affinity of the antibody to less than 10nM ? | Can the diminished effect conferred by lower affinity molecules be compensated for by increasing conc. 100-fold or more ? |
|--------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|
| Binding (MFI)                                                                                          | YES                                                                                            | NO                                                                                                                        |
| V61 TCR downregulation                                                                                 | YES                                                                                            | NO                                                                                                                        |
| CD107A upregulation                                                                                    | YES                                                                                            | NO                                                                                                                        |
| Cytotoxicity                                                                                           | YES                                                                                            | NO                                                                                                                        |
| Proliferation                                                                                          | YES                                                                                            | YES                                                                                                                       |

FIGURE 35 cont.



| Antibody          | A375 (lower EGFR) | A431 (high EGFR) |
|-------------------|-------------------|------------------|
| EGFR control      | -                 | -                |
| ADT1-4-2xADT3-2   | 101.9             | 99               |
| ADT1-4-6xADT3-2   | 81.94             | 99.15            |
| ADT1-4-138xADT3-2 | 75.34             | 98.73            |

| Antibody          | A375 (lower EGFR) | A431 (high EGFR) |
|-------------------|-------------------|------------------|
| EGFR control      | -                 | -                |
| ADT1-4-2xADT3-2   | 34.86             | 42.92            |
| ADT1-4-6xADT3-2   | 28.09             | 38.77            |
| ADT1-4-138xADT3-2 | 12.04             | 33.13            |

FIGURE 35 cont.

(A)

| Antibody        | Alias (if any)  | Affinity to EGFR (nM) | No of changes vs wild-type immunoglobulin sequence |         |         |
|-----------------|-----------------|-----------------------|----------------------------------------------------|---------|---------|
|                 |                 |                       | AB loop                                            | CD loop | EF loop |
| ADT1-4-2        | -               | -                     | 0                                                  | 0       | 0       |
| ADT1-4-2xADT3-1 | ADT1-4-2xFS1-67 | 1.37                  | 5                                                  | 3       | 5       |
| ADT1-4-2xADT3-2 | ADT1-4-2xLEE    | 1.49                  | 4                                                  | 3       | 5       |
| ADT1-4-2xADT3-3 | ADT1-4-2xFS1-65 | 1.35                  | 6                                                  | 3       | 5       |
| ADT1-4-2xADT3-4 | ADT1-4-2x747    | 2.35                  | 5(+1)                                              | 3       | 6       |
| ADT1-4-2xADT3-5 | ADT1-4-2xLEE1   | 142                   | 0                                                  | 3       | 5       |
| ADT1-4-2xADT3-6 | ADT1-4-2xLEE2   | 19.2                  | 4                                                  | 0       | 5       |
| ADT1-4-2xADT3-7 | ADT1-4-2xLEE3   | 8.63                  | 4                                                  | 3       | 3       |

(B)

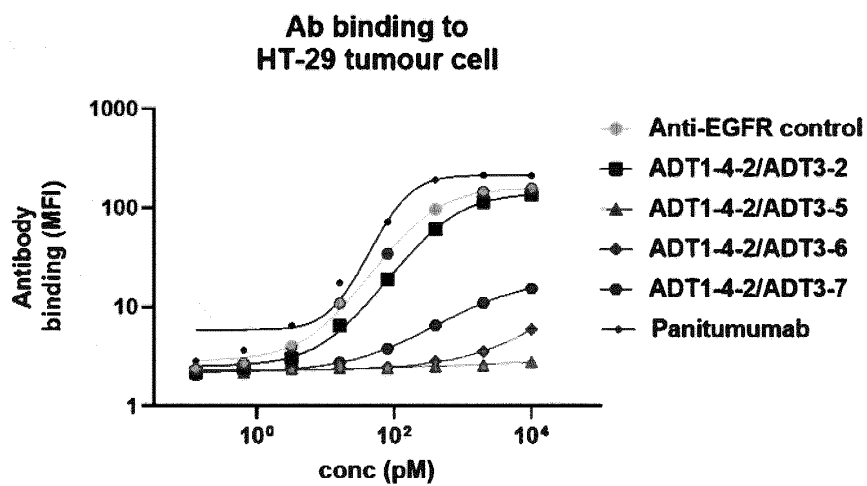


FIGURE 36

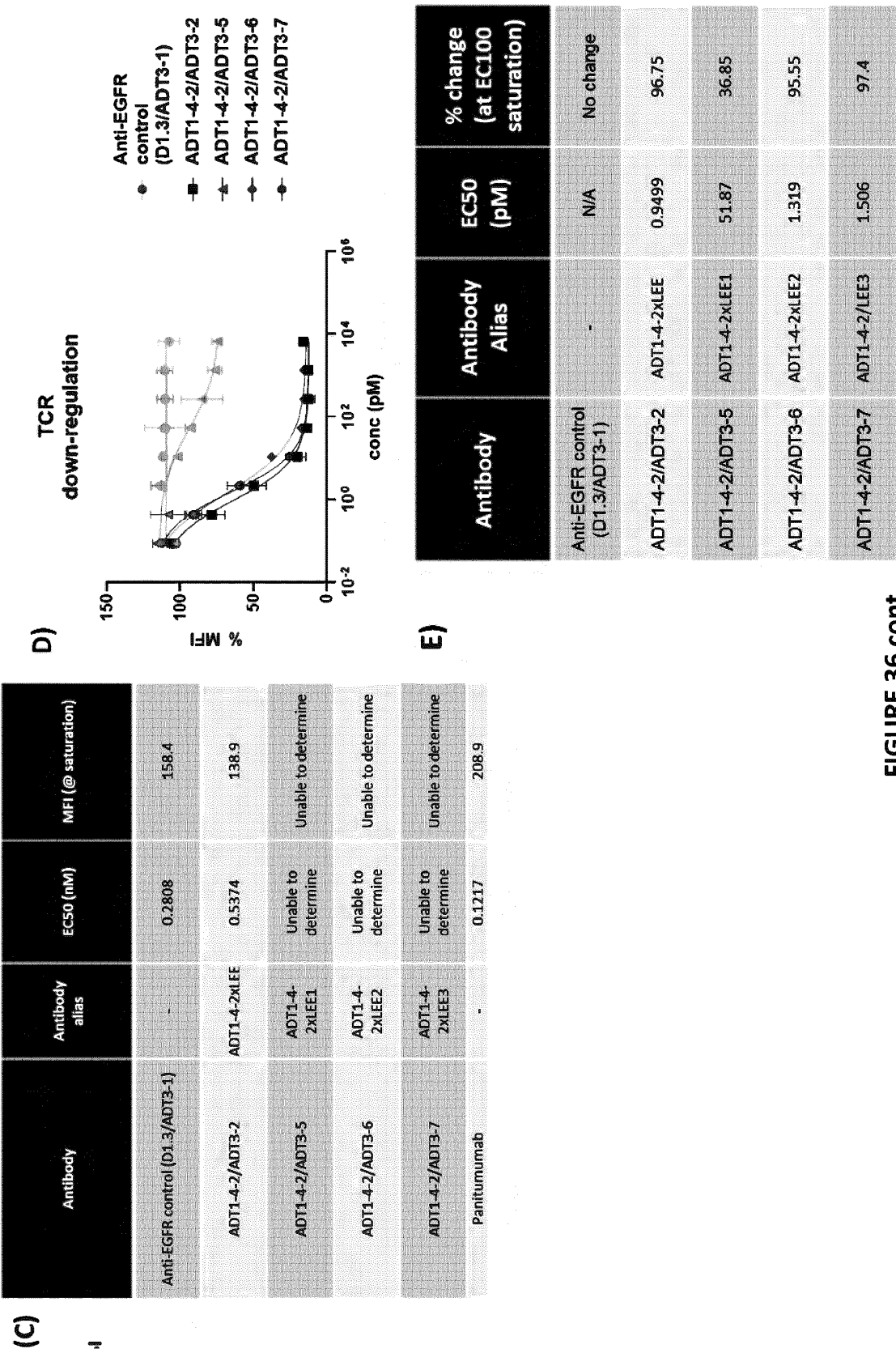
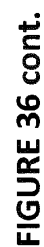
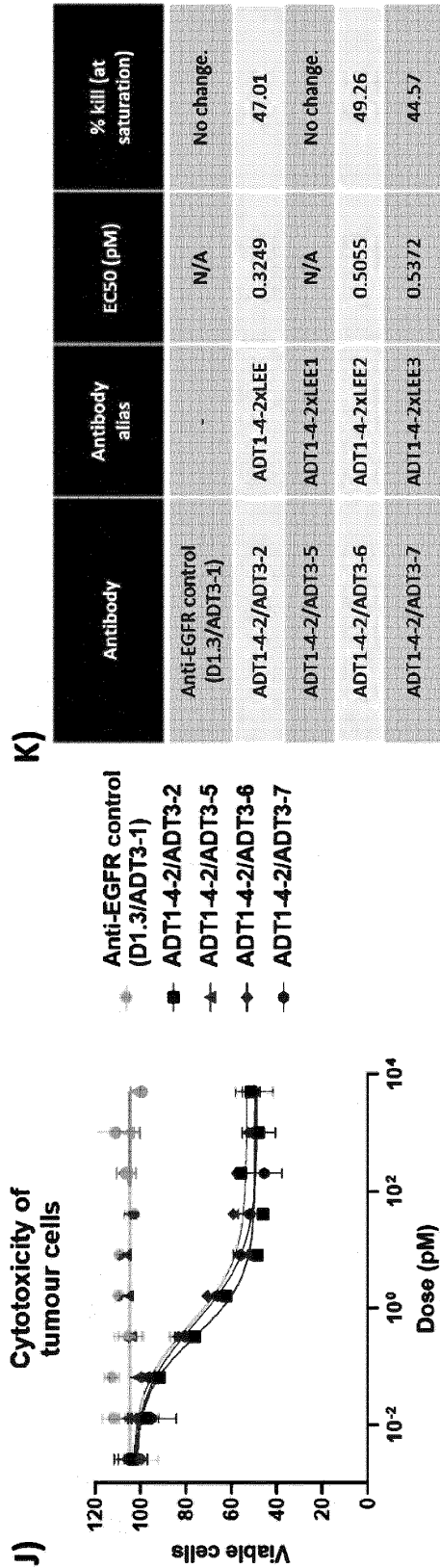


FIGURE 36 cont.





74/84

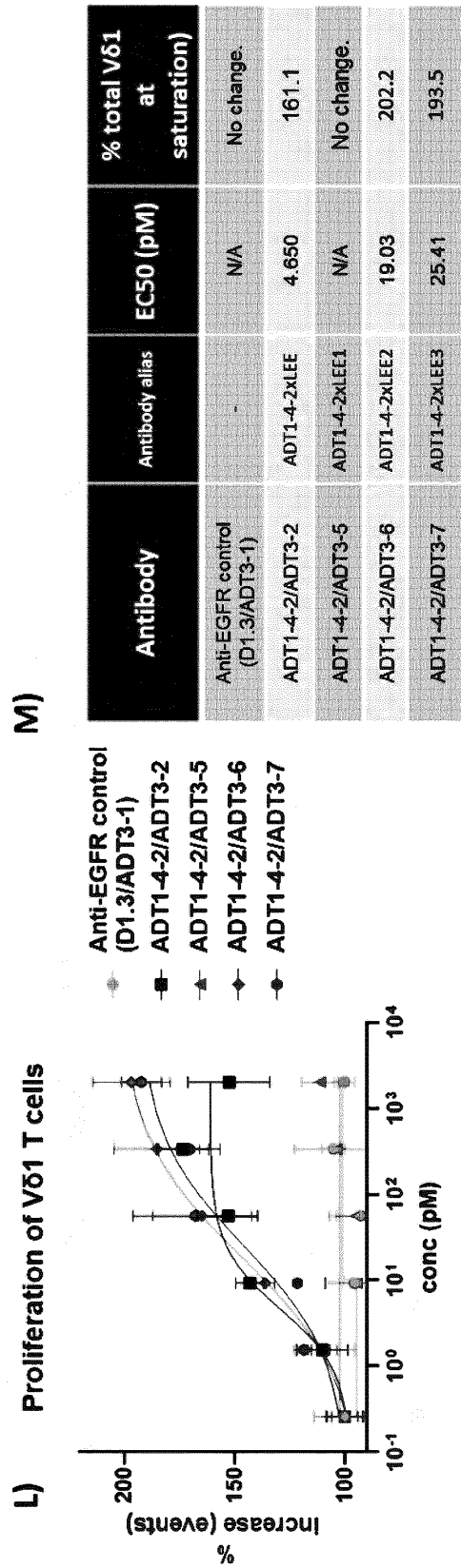


FIGURE 36 cont.

| Antibody                        | TCR Downregulation<br>% change (at saturation) |
|---------------------------------|------------------------------------------------|
|                                 | A375 (low EGFR)                                |
|                                 | A431 (high EGFR)                               |
| Anti-EGFR control (D1.3/ADT3-1) | No change                                      |
| ADT1-4-2/ADT3-2                 | 96.75                                          |
| ADT1-4-2/ADT3-5                 | 36.85                                          |
| ADT1-4-2/ADT3-6                 | 95.55                                          |
| ADT1-4-2/ADT3-7                 | 97.4                                           |

| Antibody                        | Degradation<br>% change (at saturation) |
|---------------------------------|-----------------------------------------|
|                                 | A375 (low EGFR)                         |
|                                 | A431 (high EGFR)                        |
| Anti-EGFR control (D1.3/ADT3-1) | No change                               |
| ADT1-4-2/ADT3-2                 | 36.53                                   |
| ADT1-4-2/ADT3-5                 | 7.37                                    |
| ADT1-4-2/ADT3-6                 | 33.54                                   |
| ADT1-4-2/ADT3-7                 | 33.53                                   |

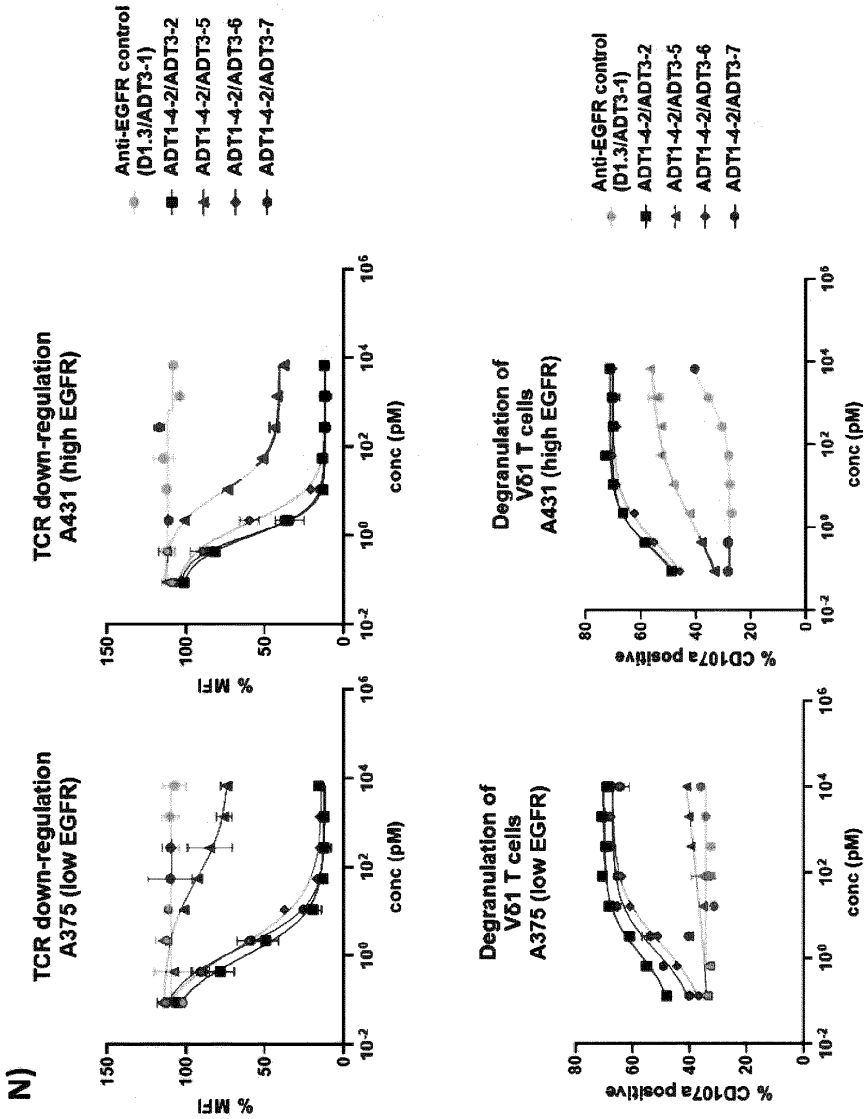


FIGURE 36 cont.

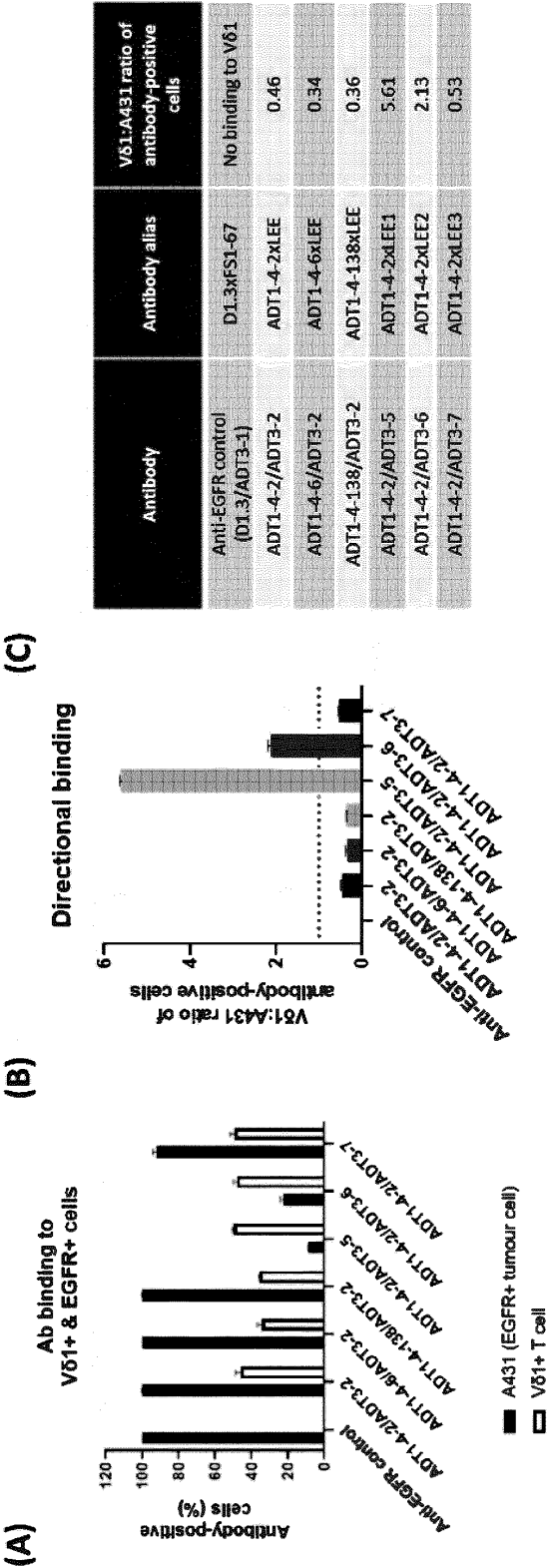


FIGURE 37



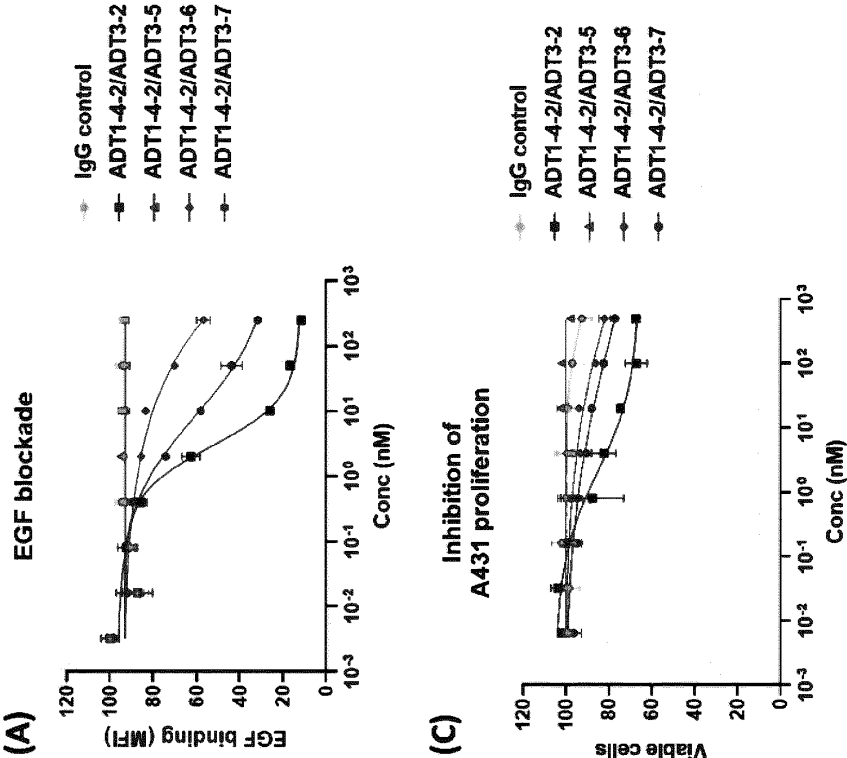
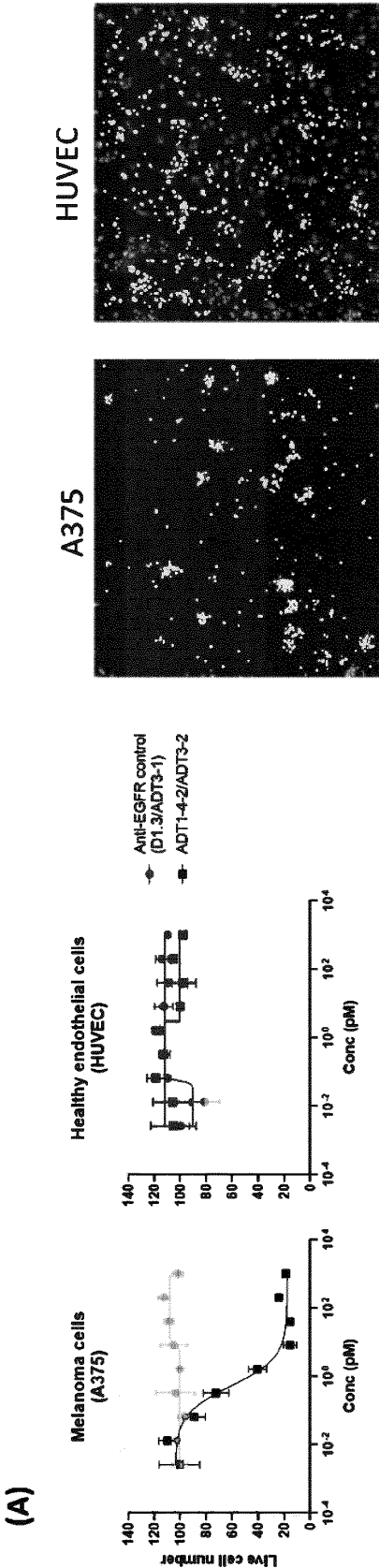


FIGURE 39



HUVEC

A375

(C)

| Antibody | EC50 (pM) | % kill (at saturation) |
|----------|-----------|------------------------|
| A375     | 0.5091    | 86.2                   |
| HUVEC    | N/A       | No change.             |

FIGURE 40

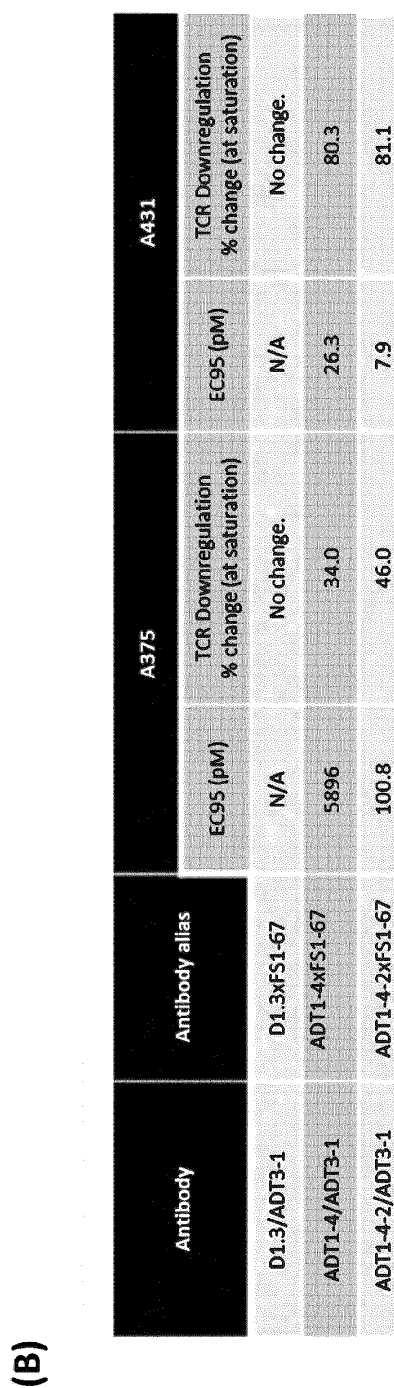
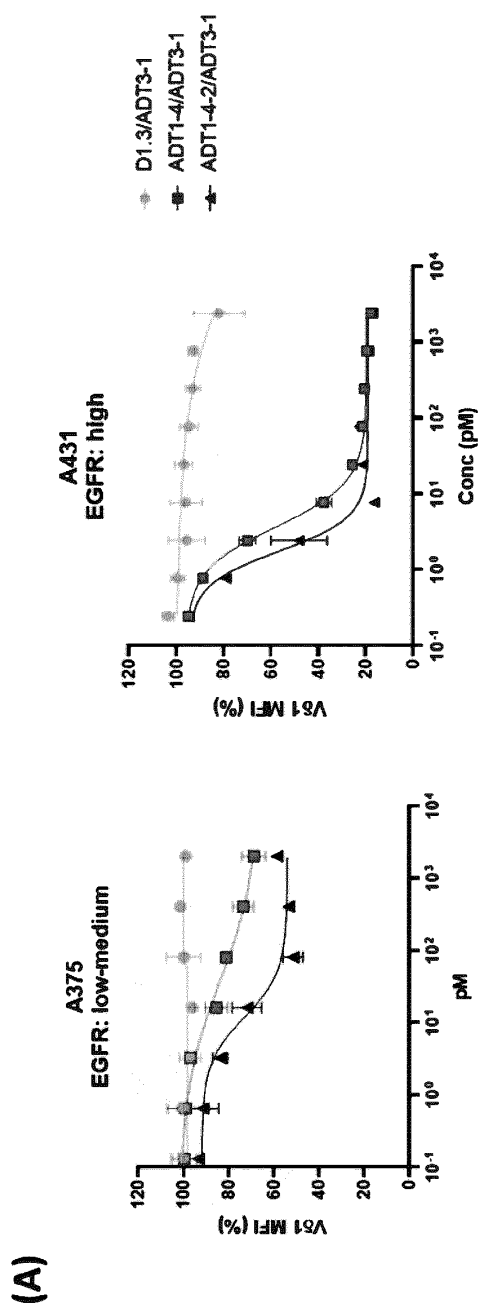


**FIGURE 41**

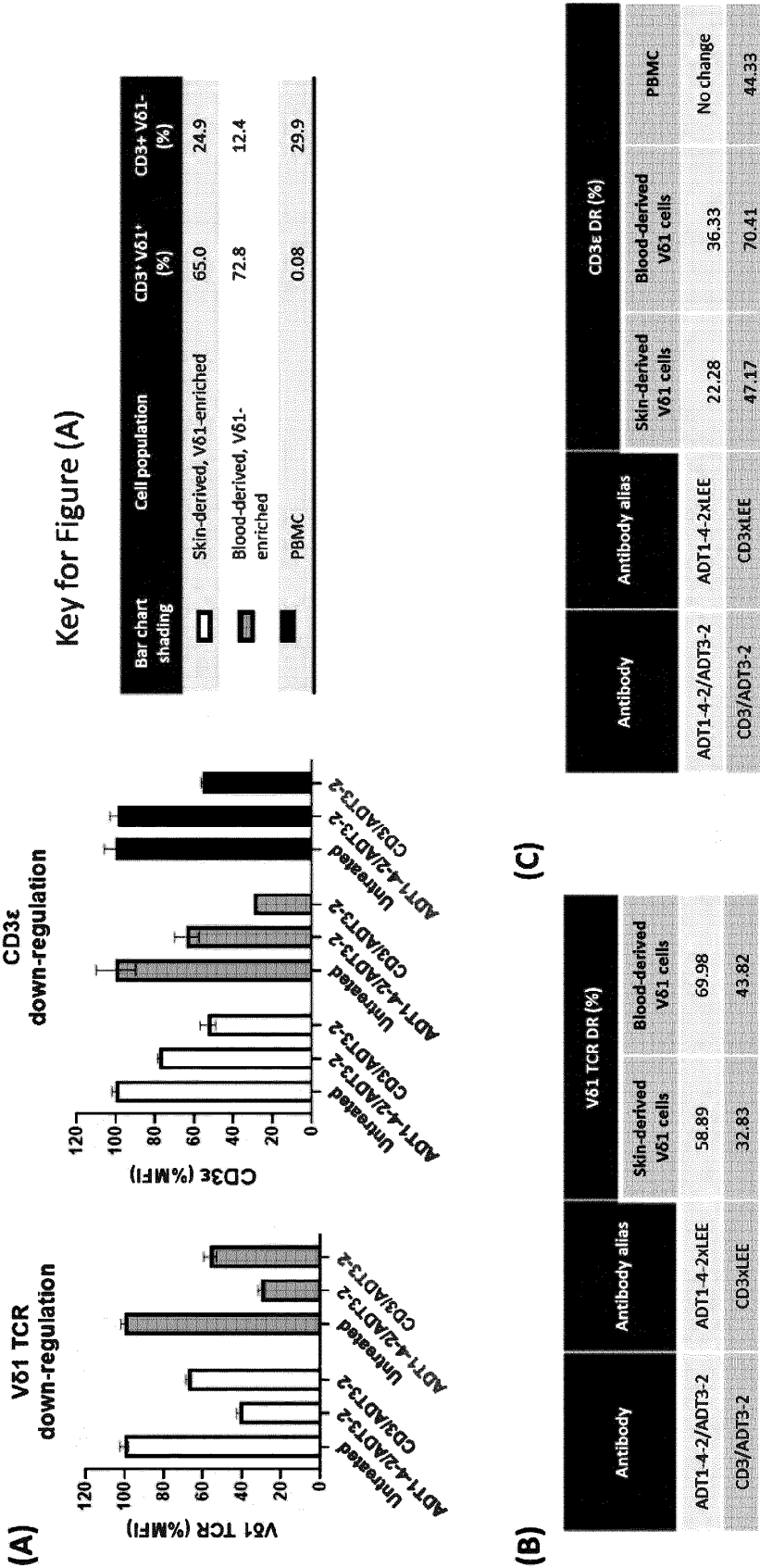
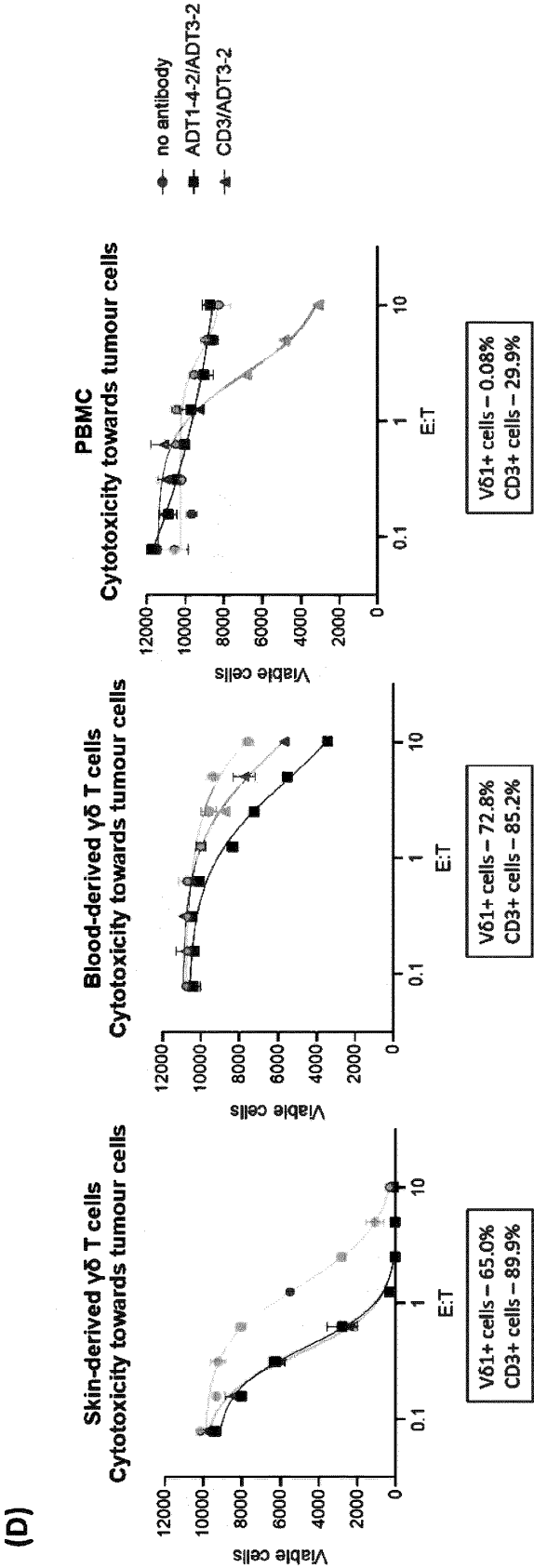


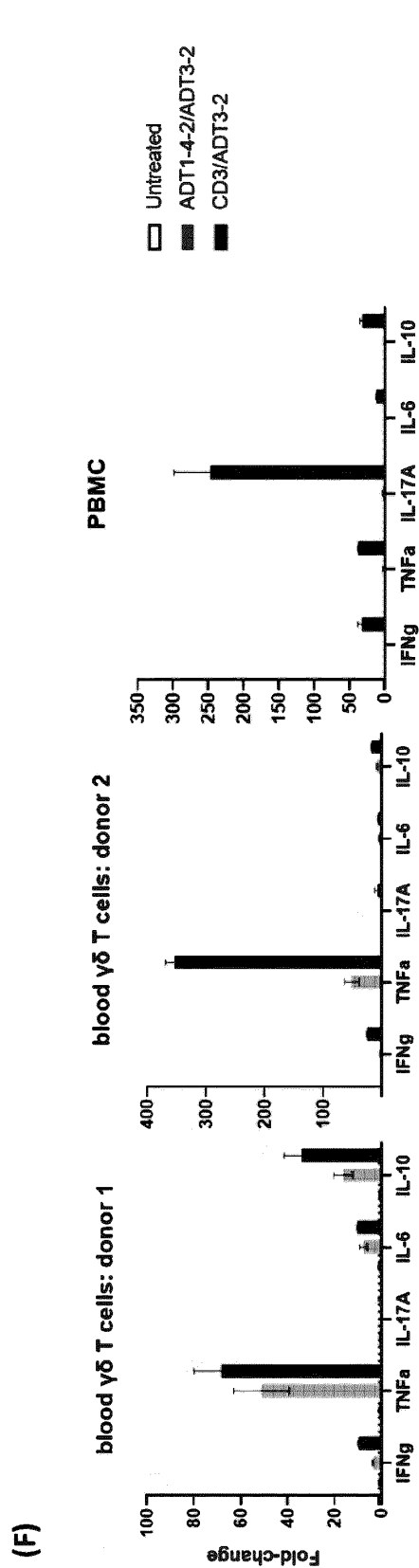
FIGURE 42



**(E)**

| Antibody        | Antibody alias | Targeted subset | Tumour cytotoxicity score           |                                      |      |
|-----------------|----------------|-----------------|-------------------------------------|--------------------------------------|------|
|                 |                |                 | Skin-derived $\gamma\delta$ T cells | Blood-derived $\gamma\delta$ T cells | PBMC |
| ADT1.4-2/ADT3-2 | ADT1.4-2xLEE   | V61+            | ++                                  | ++                                   | -    |
| CD3/ADT3-2      | CD3xLEE        | CD3+            | ++                                  | +                                    | ++   |

FIGURE 42 cont.



(G)

83/84

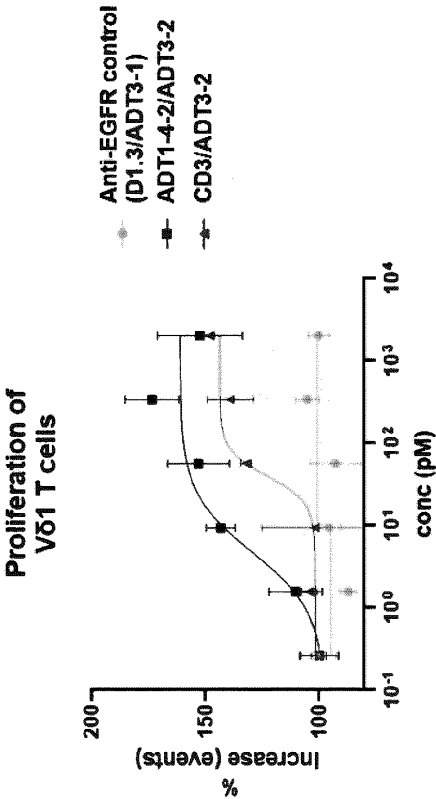
| Antibody        | Antibody alias | TNFα (fold-increase)   |                         |      |
|-----------------|----------------|------------------------|-------------------------|------|
|                 |                | Skin-derived Vβ1 cells | Blood-derived Vβ1 cells | PBMC |
| ADT1-4-2/ADT3-2 | ADT1-4-2xLEE   | 51.2                   | 52.0                    | 2.0  |
| CD3/ADT3-2      | CD3xLEE        | 68.4                   | 353.1                   | 38.1 |

| Antibody        | Antibody alias | IL-17A (fold-increase) |                         |       |
|-----------------|----------------|------------------------|-------------------------|-------|
|                 |                | Skin-derived Vβ1 cells | Blood-derived Vβ1 cells | PBMC  |
| ADT1-4-2/ADT3-2 | ADT1-4-2xLEE   | No increase.           | No increase.            | 2.8   |
| CD3/ADT3-2      | CD3xLEE        | No increase.           | 7                       | 247.5 |

FIGURE 42 cont.

(H)

(I)



| Antibody                        | Antibody alias | EC50 (pM) | % total Vδ1 at saturation |
|---------------------------------|----------------|-----------|---------------------------|
| Anti-EGFR control (D1.3/ADT3-1) | -              | N/A       | No change.                |
| ADT1-4-2/ADT3-2                 | ADT1-4-2xLEE   | 4.65      | 161.1                     |
| CD3/ADT3-2                      | CD3xLEE        | 38.98     | 143.7                     |

FIGURE 42 cont.