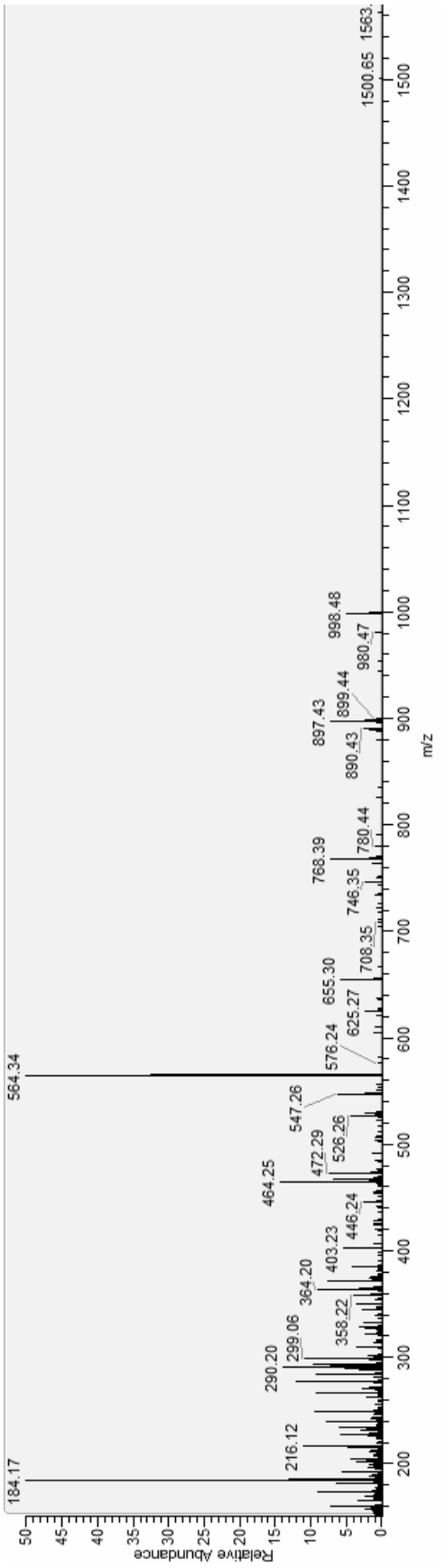

Relative Abundance
m/z
184.17
216.12
290.20
299.06
358.22
364.20
403.23
446.24
464.25
472.29
526.26
547.26
564.34
576.24
625.27
655.30
708.35
746.35
768.39
780.44
890.43
897.43
899.44
980.47
998.48
1500.65
1563.

FIG. 1

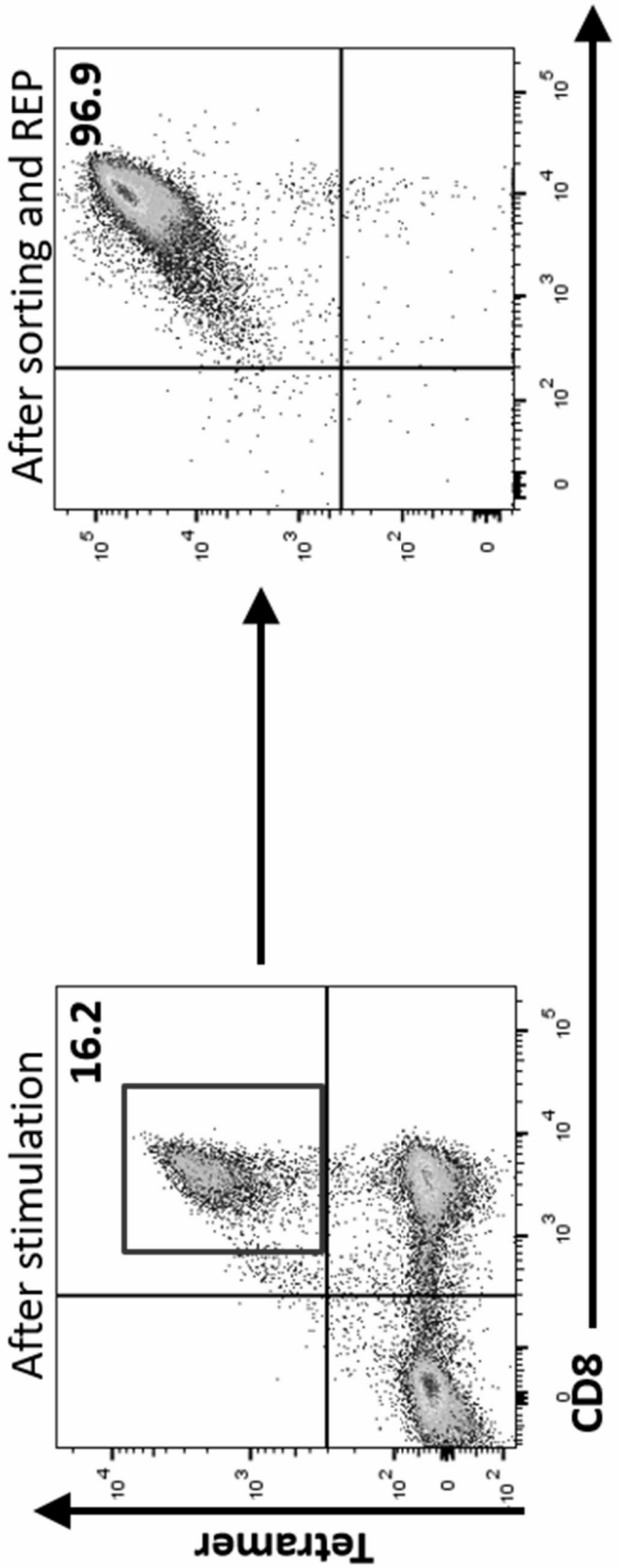

After stimulation
16.2
After sorting and REP
96.9
Tetramer
CD8

FIG. 2

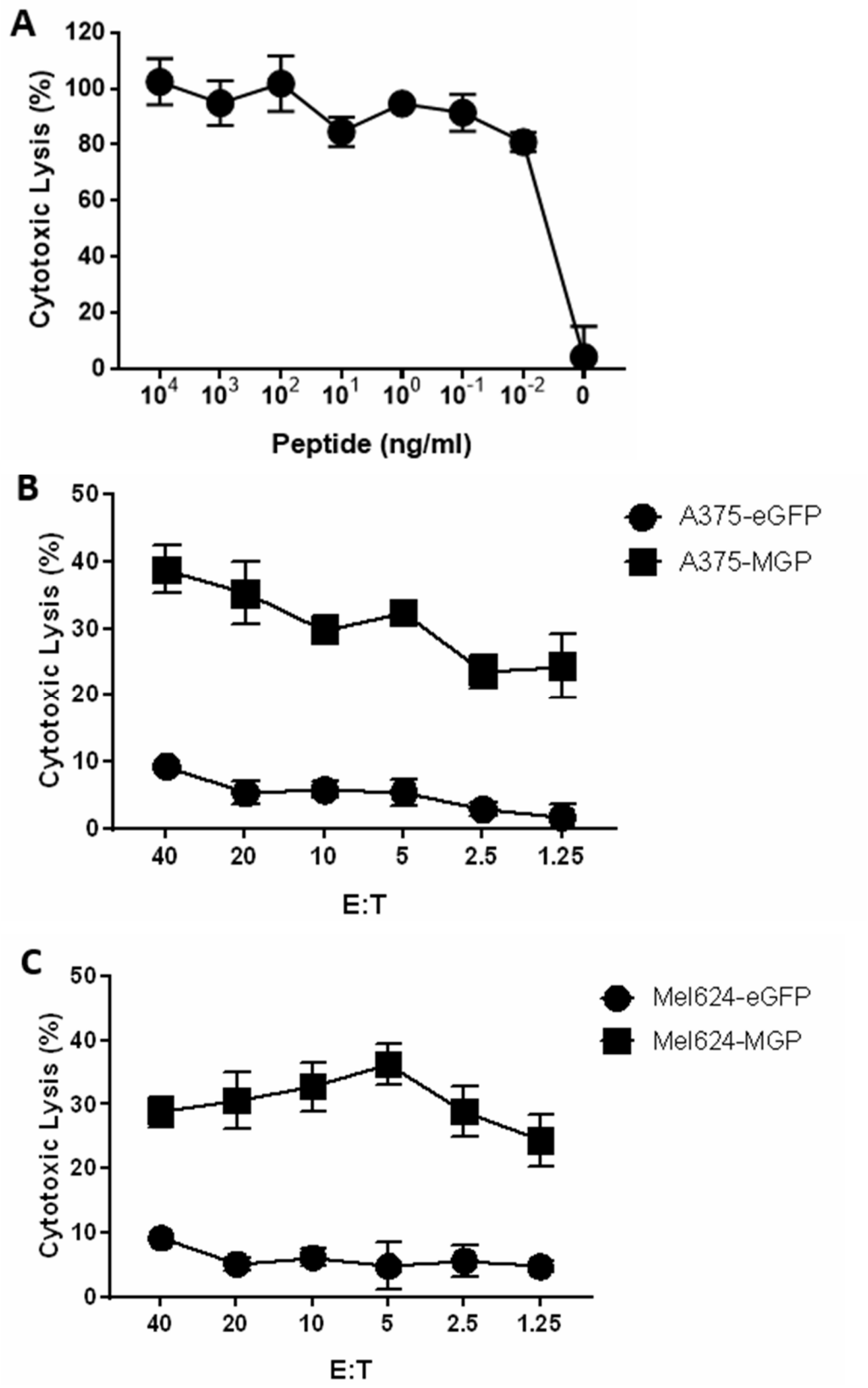

A
Cytotoxic Lysis (%)
120
100
80
60
40
20
0
10^4 10^3 10^2 10^1 10^0 10^-1 10^-2 0
Peptide (ng/ml)
B
Cytotoxic Lysis (%)
50
40
30
20
10
0
40 20 10 5 2.5 1.25
E:T
A375-eGFP
A375-MGP
C
Cytotoxic Lysis (%)
50
40
30
20
10
0
40 20 10 5 2.5 1.25
E:T
Mel624-eGFP
Mel624-MGP

FIG. 3A-C

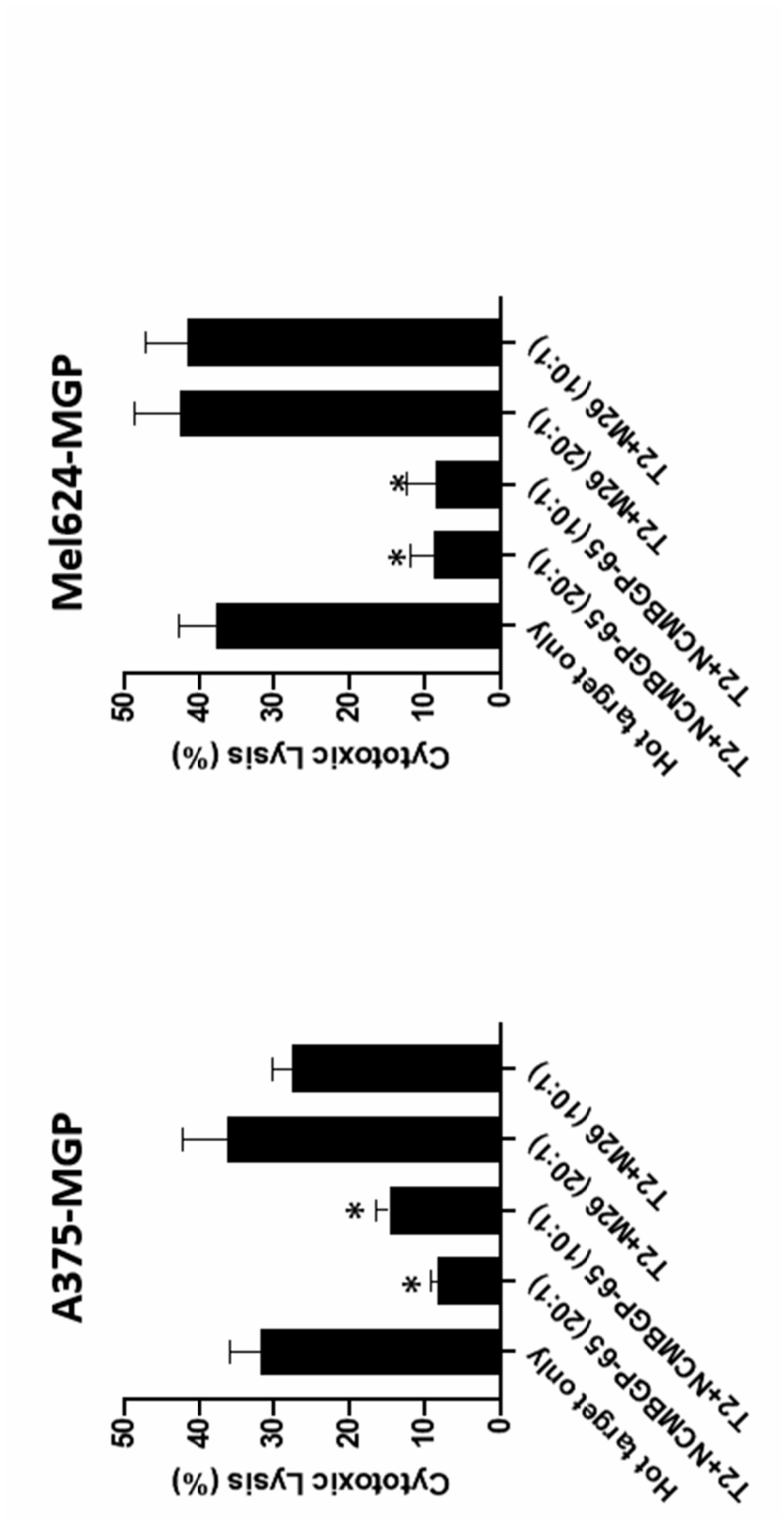

Mel624-MGP
Cytotoxic Lysis (%)
0
10
20
30
40
50
Hot target only
T2+NCMBGP-65 (20:1)
T2+NCMBGP-65 (10:1)
T2+M26 (20:1)
T2+M26 (10:1)
*
*
A375-MGP
Cytotoxic Lysis (%)
0
10
20
30
40
50
Hot target only
T2+NCMBGP-65 (20:1)
T2+NCMBGP-65 (10:1)
T2+M26 (20:1)
T2+M26 (10:1)
*
*

FIG. 4

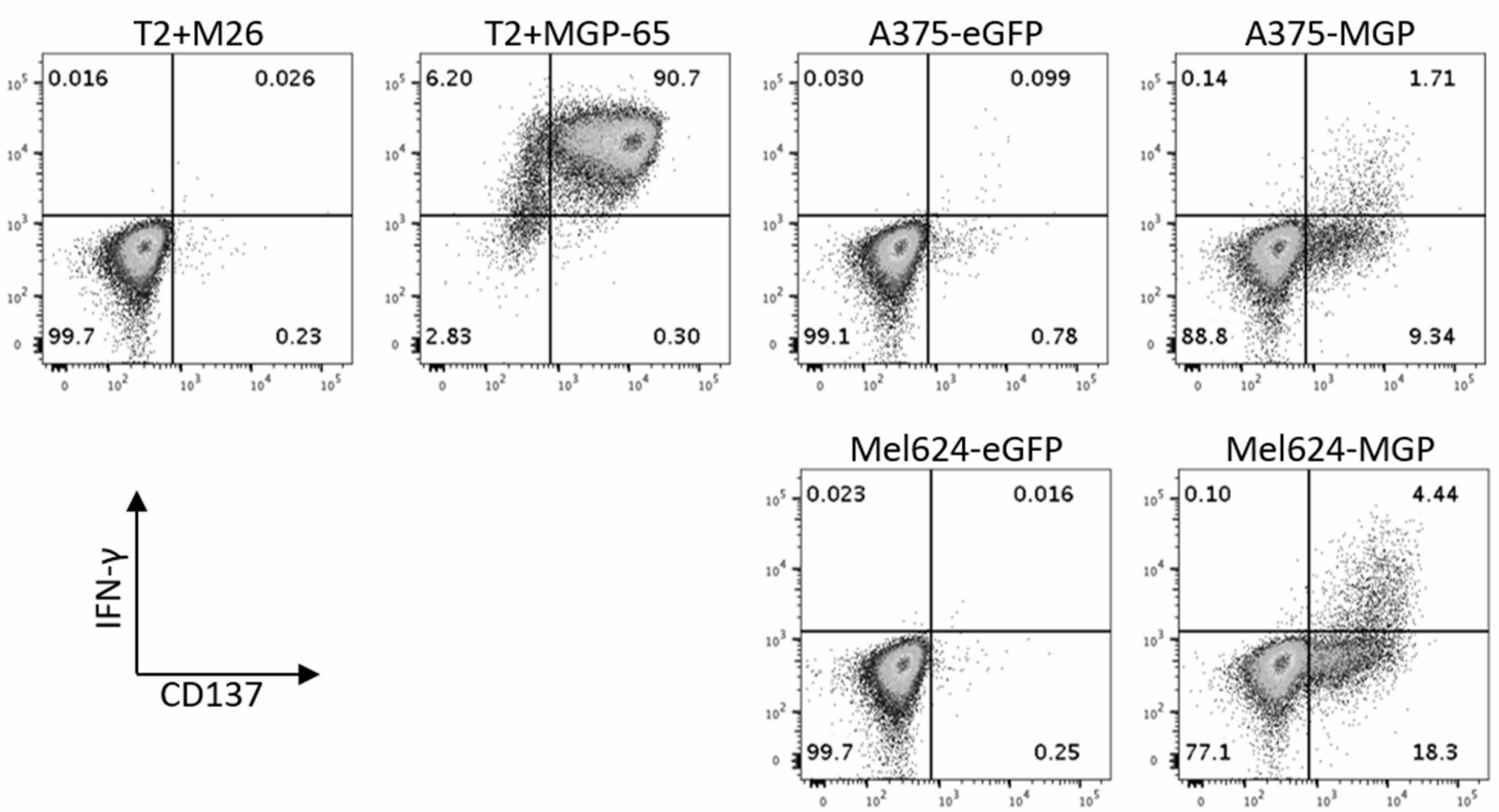

T2+M26
0.016
0.026
99.7
0.23
T2+MGP-65
6.20
90.7
2.83
0.30
A375-eGFP
0.030
0.099
99.1
0.78
A375-MGP
0.14
1.71
88.8
9.34
Mel624-eGFP
0.023
0.016
99.7
0.25
Mel624-MGP
0.10
4.44
77.1
18.3
IFN-γ
CD137

FIG. 5

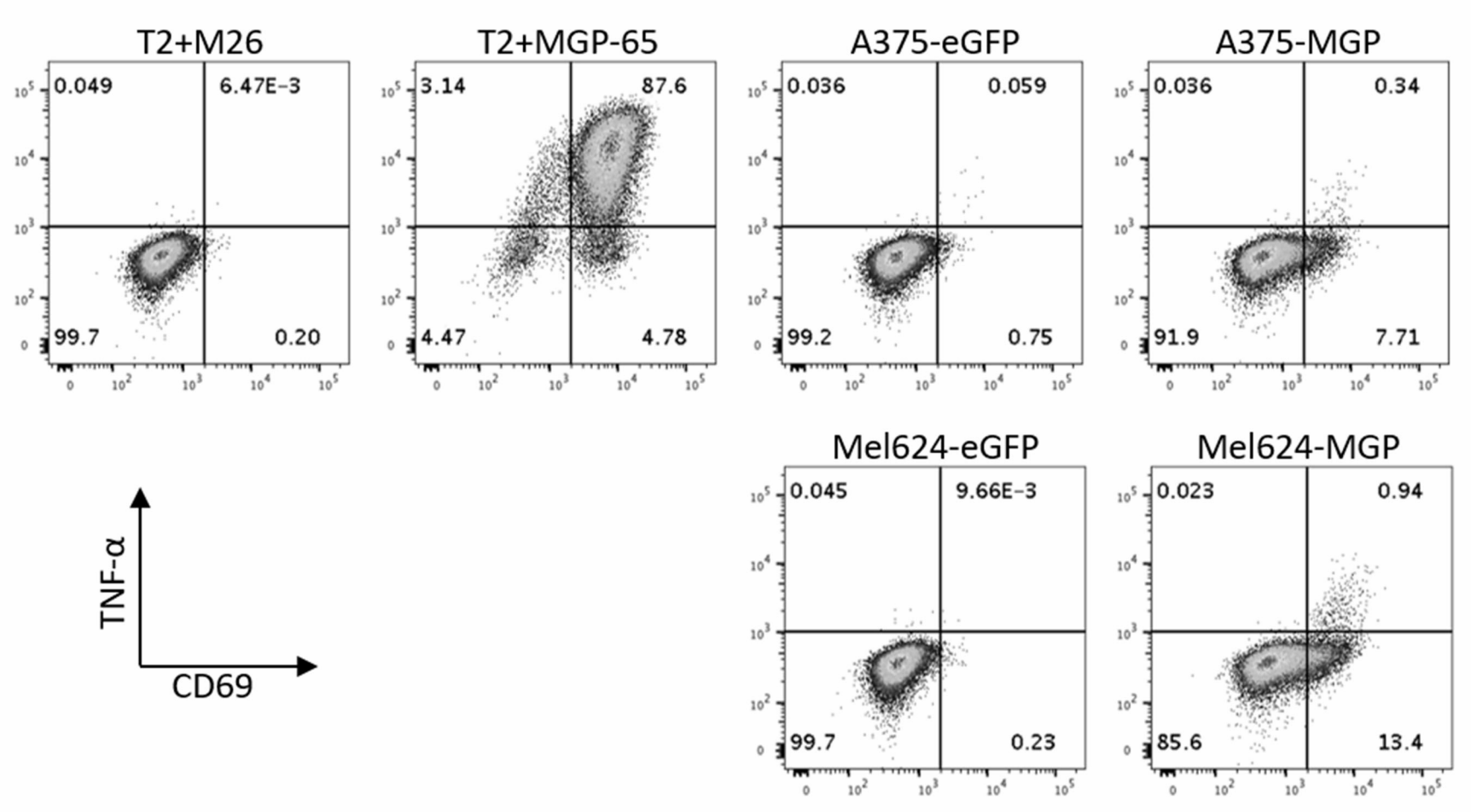


FIG. 5 Continued

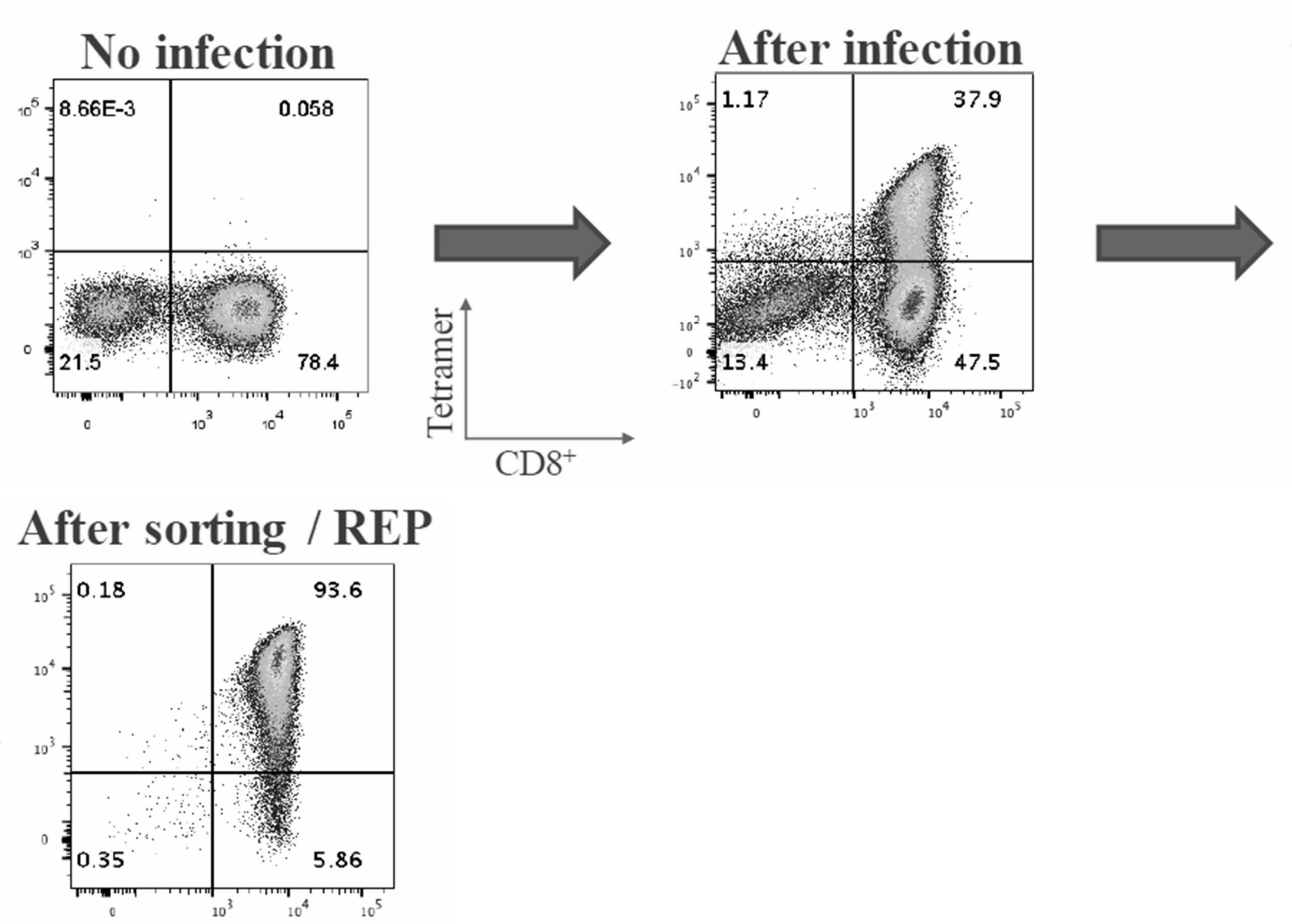

No infection
8.66E-3
0.058
21.5
78.4
Tetramer
CD8+
After infection
1.17
37.9
13.4
47.5
After sorting / REP
0.18
93.6
0.35
5.86

FIG. 6

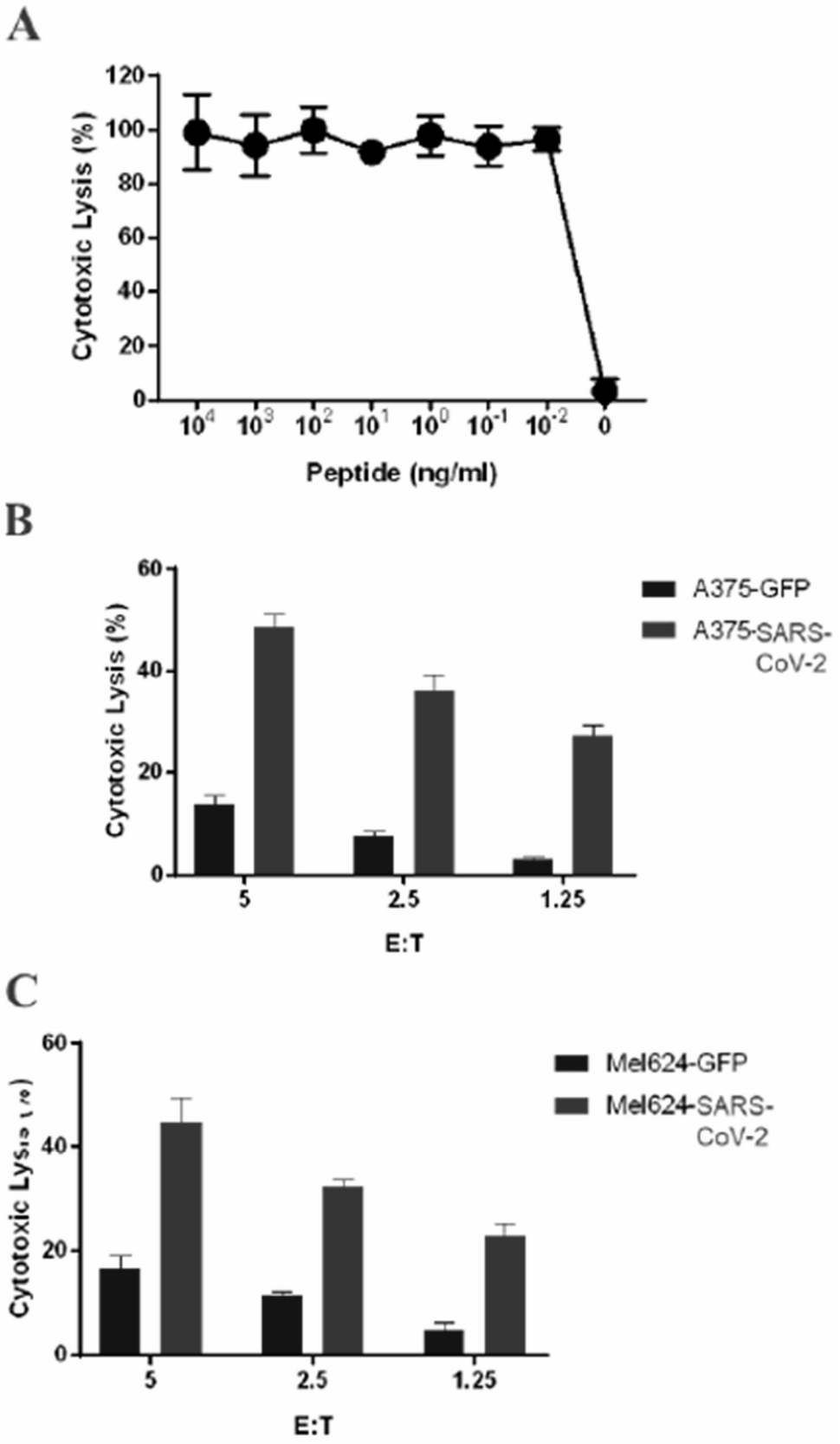

A
120
100
80
60
40
20
0
Cytotoxic Lysis (%)
10^4 10^3 10^2 10^1 10^0 10^-1 10^-2 0
Peptide (ng/ml)
B
60
40
20
0
Cytotoxic Lysis (%)
A375-GFP
A375-SARS-CoV-2
5
2.5
1.25
E:T
C
60
40
20
0
Mel624-GFP
Mel624-SARS-CoV-2
5
2.5
1.25
E:T

FIG. 7A-C

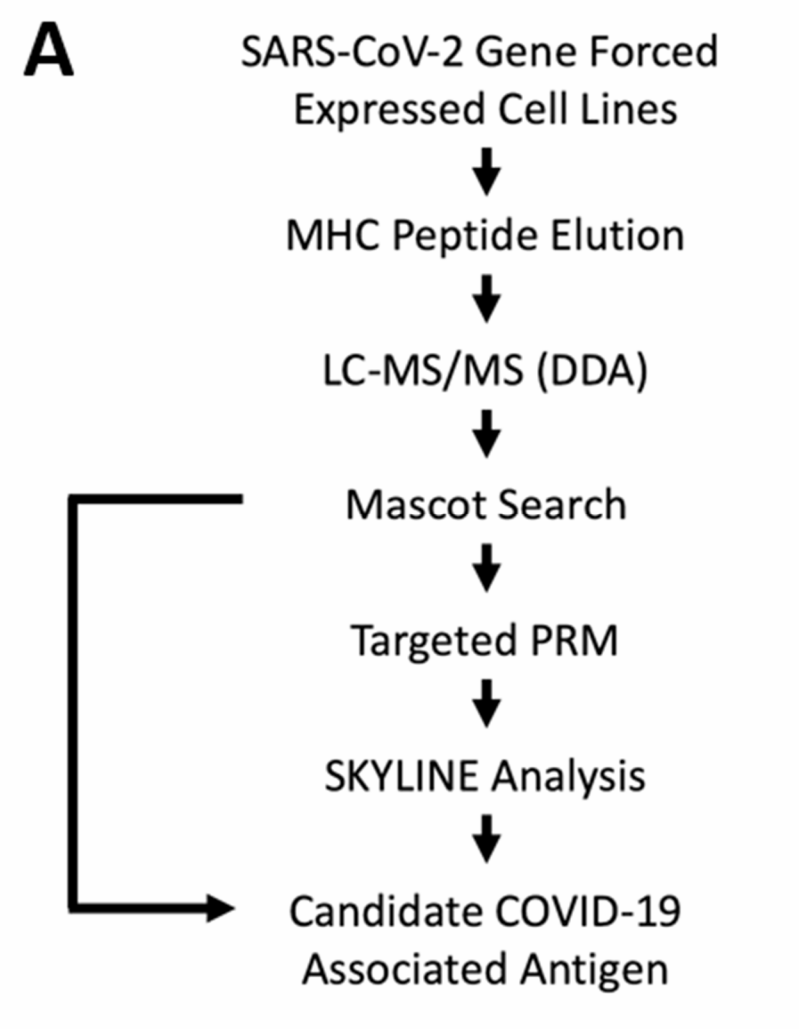

A
SARS-CoV-2 Gene Forced Expressed Cell Lines
MHC Peptide Elution
LC-MS/MS (DDA)
Mascot Search
Targeted PRM
SKYLINE Analysis
Candidate COVID-19 Associated Antigen

FIG. 8A

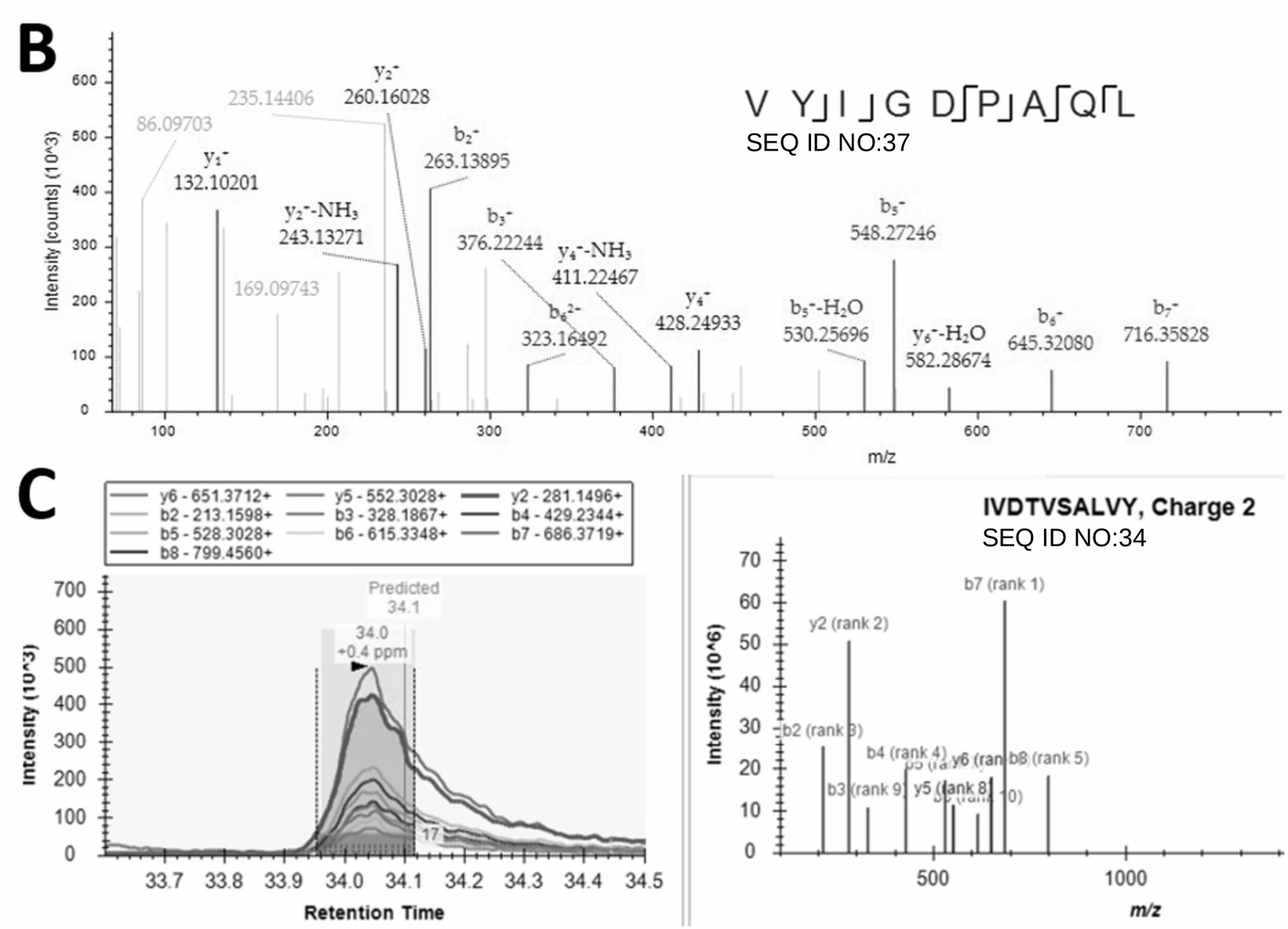

B
V YJI JG DSPJASQRL
SEQ ID NO:37
Intensity [counts] (10^3)
m/z
86.09703
235.14406
y2- 260.16028
b2- 263.13895
y1- 132.10201
y2*-NH3 243.13271
b3- 376.22244
y4*-NH3 411.22467
169.09743
b6 2- 323.16492
y4- 428.24933
b5- 548.27246
b5*-H2O 530.25696
y6*-H2O 582.28674
b6- 645.32080
b7- 716.35828
C
y6 - 651.3712+
y5 - 552.3028+
y2 - 281.1496+
b2 - 213.1598+
b3 - 328.1867+
b4 - 429.2344+
b5 - 528.3028+
b6 - 615.3348+
b7 - 686.3719+
b8 - 799.4560+
Predicted
34.1
34.0
+0.4 ppm
Intensity (10^3)
Retention Time
IVDTVSALVY, Charge 2
SEQ ID NO:34
Intensity (10^6)
b7 (rank 1)
y2 (rank 2)
b2 (rank 3)
b4 (rank 4)
b8 (rank 5)
b3 (rank 9)
y5 (rank 8)
m/z

FIG. 8B-C

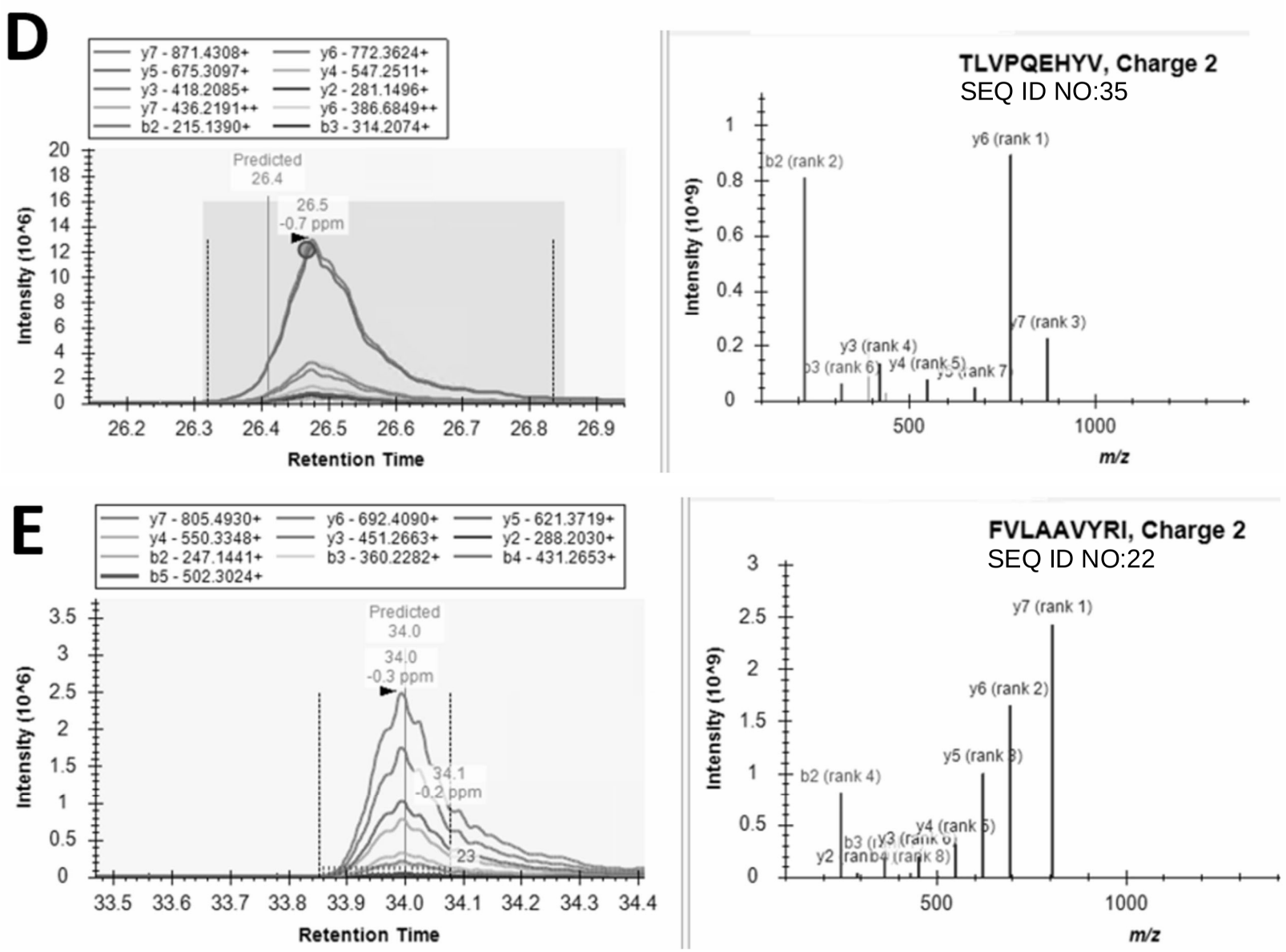

D
y7 - 871.4308+
y6 - 772.3624+
y5 - 675.3097+
y4 - 547.2511+
y3 - 418.2085+
y2 - 281.1496+
y7 - 436.2191++
y6 - 386.6849++
b2 - 215.1390+
b3 - 314.2074+
Predicted
26.4
26.5
-0.7 ppm
Intensity (10^6)
Retention Time
TLVPQEHYV, Charge 2
SEQ ID NO:35
b2 (rank 2)
y6 (rank 1)
y7 (rank 3)
y3 (rank 4)
y4 (rank 5)
Intensity (10^9)
m/z
E
y7 - 805.4930+
y6 - 692.4090+
y5 - 621.3719+
y4 - 550.3348+
y3 - 451.2663+
y2 - 288.2030+
b2 - 247.1441+
b3 - 360.2282+
b4 - 431.2653+
b5 - 502.3024+
Predicted
34.0
34.0
-0.3 ppm
34.1
-0.2 ppm
Intensity (10^6)
Retention Time
FVLAAVYRI, Charge 2
SEQ ID NO:22
y7 (rank 1)
y6 (rank 2)
y5 (rank 3)
b2 (rank 4)
y4 (rank 5)
Intensity (10^9)
m/z

FIG. 8D-E

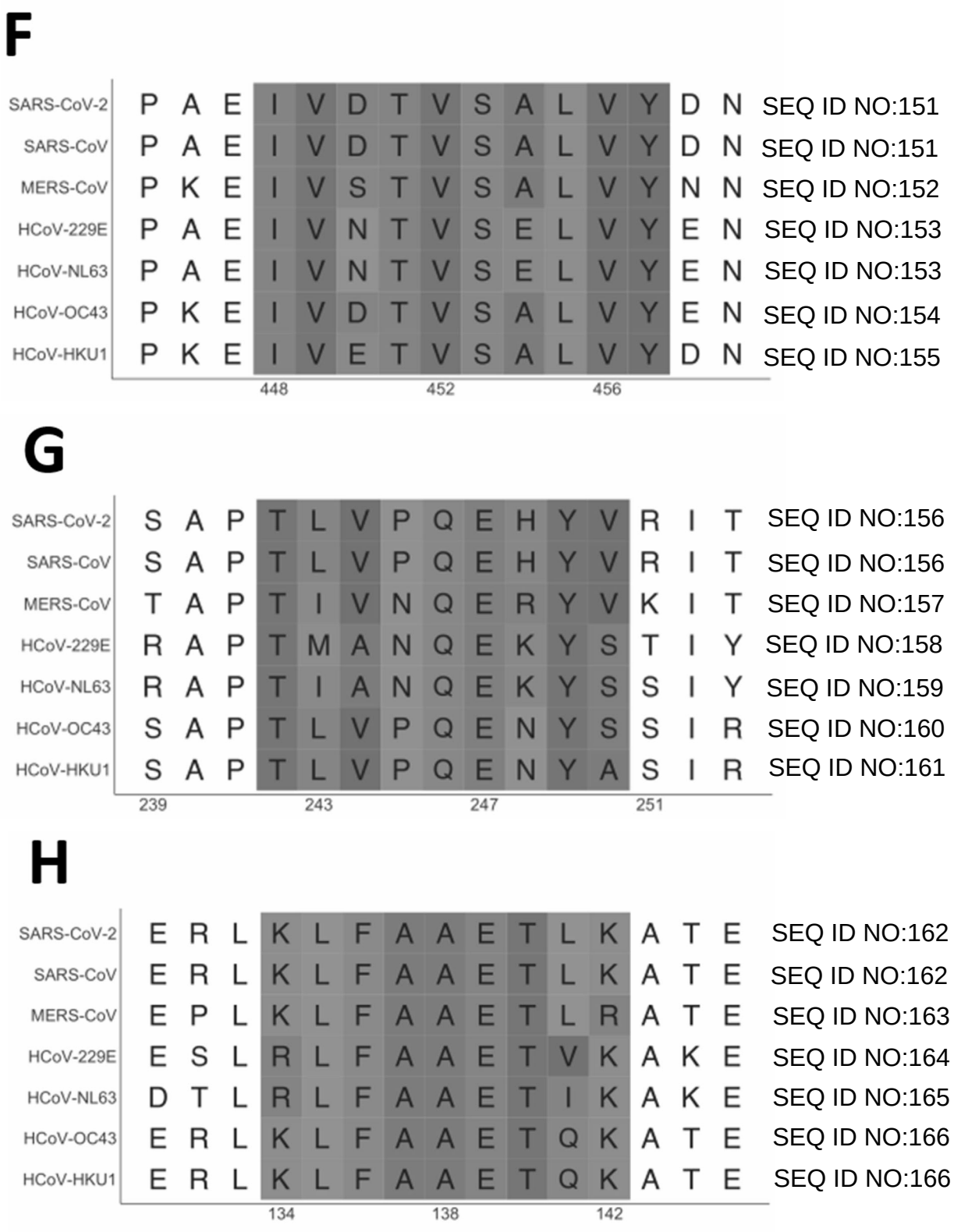

F
SARS-CoV-2 P A E I V D T V S A L V Y D N SEQ ID NO:151
SARS-CoV P A E I V D T V S A L V Y D N SEQ ID NO:151
MERS-CoV P K E I V S T V S A L V Y N N SEQ ID NO:152
HCoV-229E P A E I V N T V S E L V Y E N SEQ ID NO:153
HCoV-NL63 P A E I V N T V S E L V Y E N SEQ ID NO:153
HCoV-OC43 P K E I V D T V S A L V Y E N SEQ ID NO:154
HCoV-HKU1 P K E I V E T V S A L V Y D N SEQ ID NO:155
448
452
456
G
SARS-CoV-2 S A P T L V P Q E H Y V R I T SEQ ID NO:156
SARS-CoV S A P T L V P Q E H Y V R I T SEQ ID NO:156
MERS-CoV T A P T I V N Q E R Y V K I T SEQ ID NO:157
HCoV-229E R A P T M A N Q E K Y S T I Y SEQ ID NO:158
HCoV-NL63 R A P T I A N Q E K Y S S I Y SEQ ID NO:159
HCoV-OC43 S A P T L V P Q E N Y S S I R SEQ ID NO:160
HCoV-HKU1 S A P T L V P Q E N Y A S I R SEQ ID NO:161
239
243
247
251
H
SARS-CoV-2 E R L K L F A A E T L K A T E SEQ ID NO:162
SARS-CoV E R L K L F A A E T L K A T E SEQ ID NO:162
MERS-CoV E P L K L F A A E T L R A T E SEQ ID NO:163
HCoV-229E E S L R L F A A E T V K A K E SEQ ID NO:164
HCoV-NL63 D T L R L F A A E T I K A K E SEQ ID NO:165
HCoV-OC43 E R L K L F A A E T Q K A T E SEQ ID NO:166
HCoV-HKU1 E R L K L F A A E T Q K A T E SEQ ID NO:166
134
138
142

FIG. 8F-H

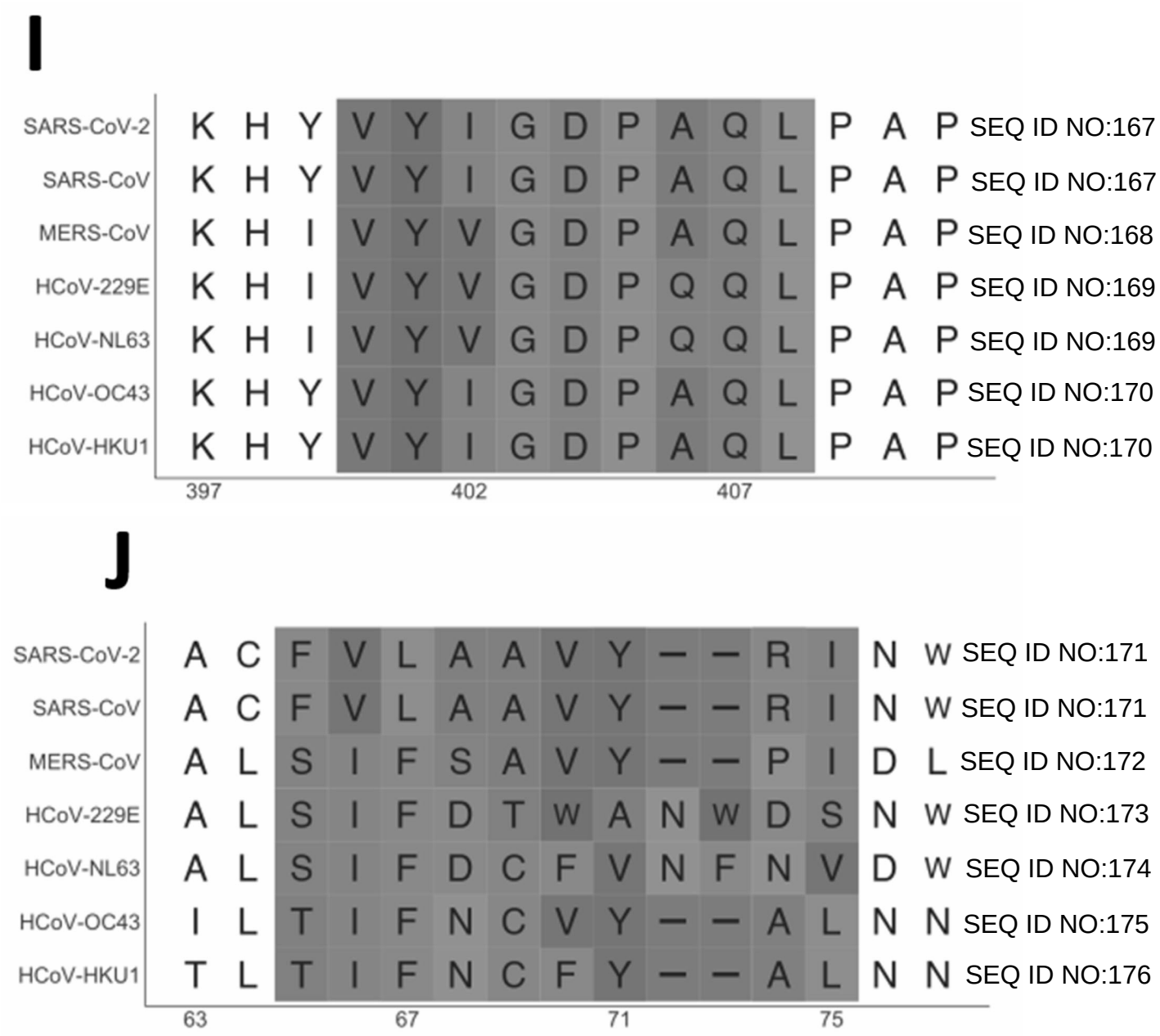

I
SARS-CoV-2 K H Y V Y I G D P A Q L P A P SEQ ID NO:167
SARS-CoV K H Y V Y I G D P A Q L P A P SEQ ID NO:167
MERS-CoV K H I V Y V G D P A Q L P A P SEQ ID NO:168
HCoV-229E K H I V Y V G D P Q Q L P A P SEQ ID NO:169
HCoV-NL63 K H I V Y V G D P Q Q L P A P SEQ ID NO:169
HCoV-OC43 K H Y V Y I G D P A Q L P A P SEQ ID NO:170
HCoV-HKU1 K H Y V Y I G D P A Q L P A P SEQ ID NO:170
397
402
407
J
SARS-CoV-2 A C F V L A A V Y — — R I N W SEQ ID NO:171
SARS-CoV A C F V L A A V Y — — R I N W SEQ ID NO:171
MERS-CoV A L S I F S A V Y — — P I D L SEQ ID NO:172
HCoV-229E A L S I F D T W A N W D S N W SEQ ID NO:173
HCoV-NL63 A L S I F D C F V N F N V D W SEQ ID NO:174
HCoV-OC43 I L T I F N C V Y — — A L N N SEQ ID NO:175
HCoV-HKU1 T L T I F N C F Y — — A L N N SEQ ID NO:176
63
67
71
75

FIG. 8I-J

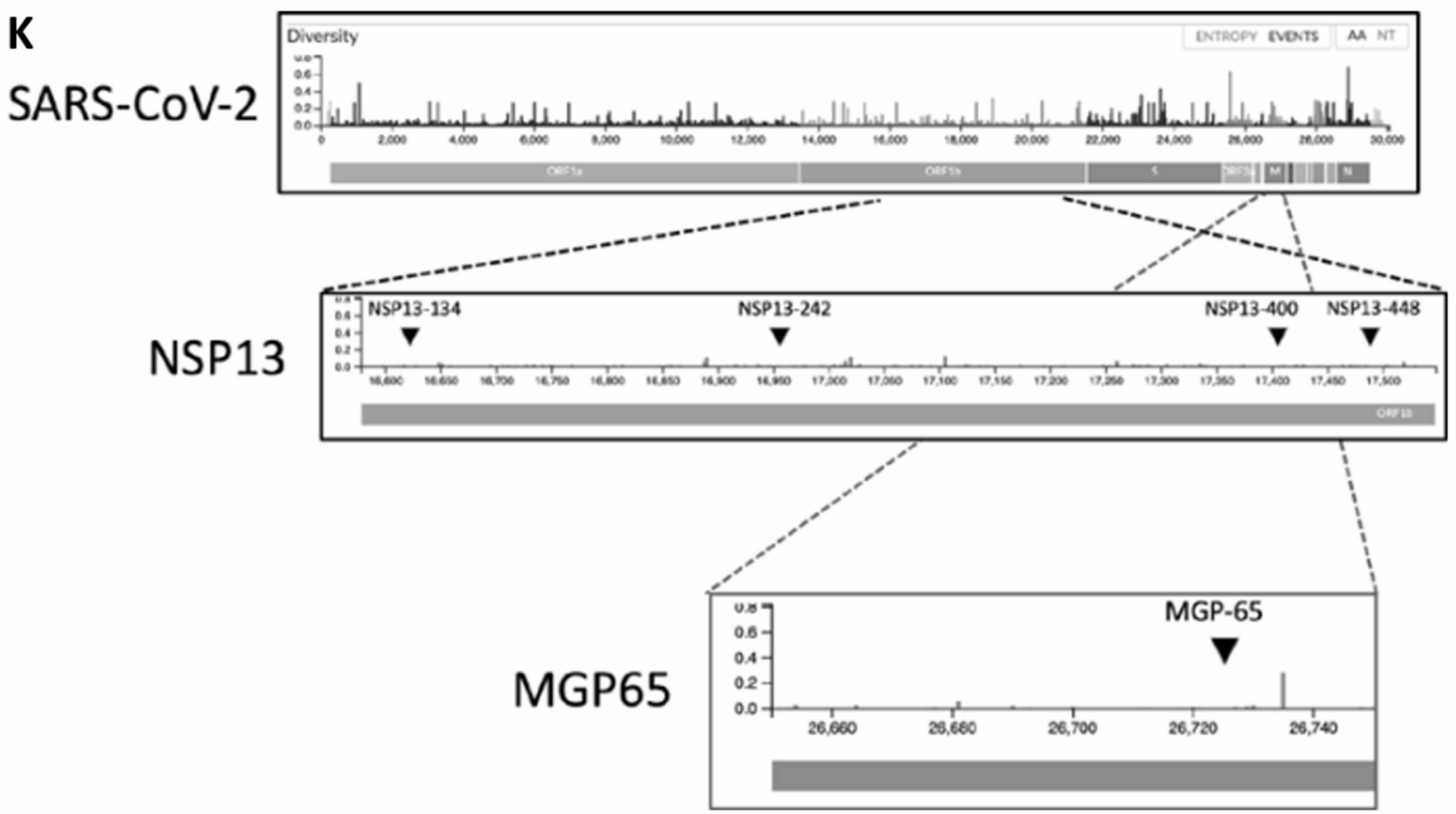

K
SARS-CoV-2
Diversity
ENTROPY EVENTS
AA NT
NSP13
NSP13-134
NSP13-242
NSP13-400
NSP13-448
MGP65
MGP-65

FIG. 8K

L

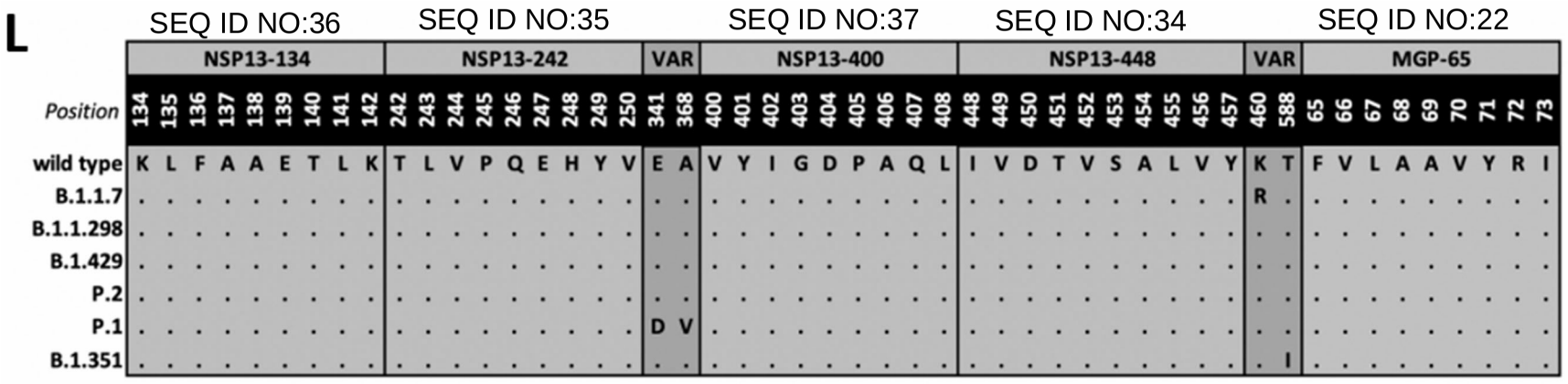

SEQ ID NO:36
SEQ ID NO:35
SEQ ID NO:37
SEQ ID NO:34
SEQ ID NO:22
NSP13-134
NSP13-242
VAR
NSP13-400
NSP13-448
VAR
MGP-65
Position
134 135 136 137 138 139 140 141 142
242 243 244 245 246 247 248 249 250
341 368
400 401 402 403 404 405 406 407 408
448 449 450 451 452 453 454 455 456 457
460 588
65 66 67 68 69 70 71 72 73
wild type K L F A A E T L K T L V P Q E H Y V E A V Y I G D P A Q L I V D T V S A L V Y K T F V L A A V Y R I
B.1.1.7 R
B.1.1.298
B.1.429
P.2
P.1 D V
B.1.351 I

FIG. 8L

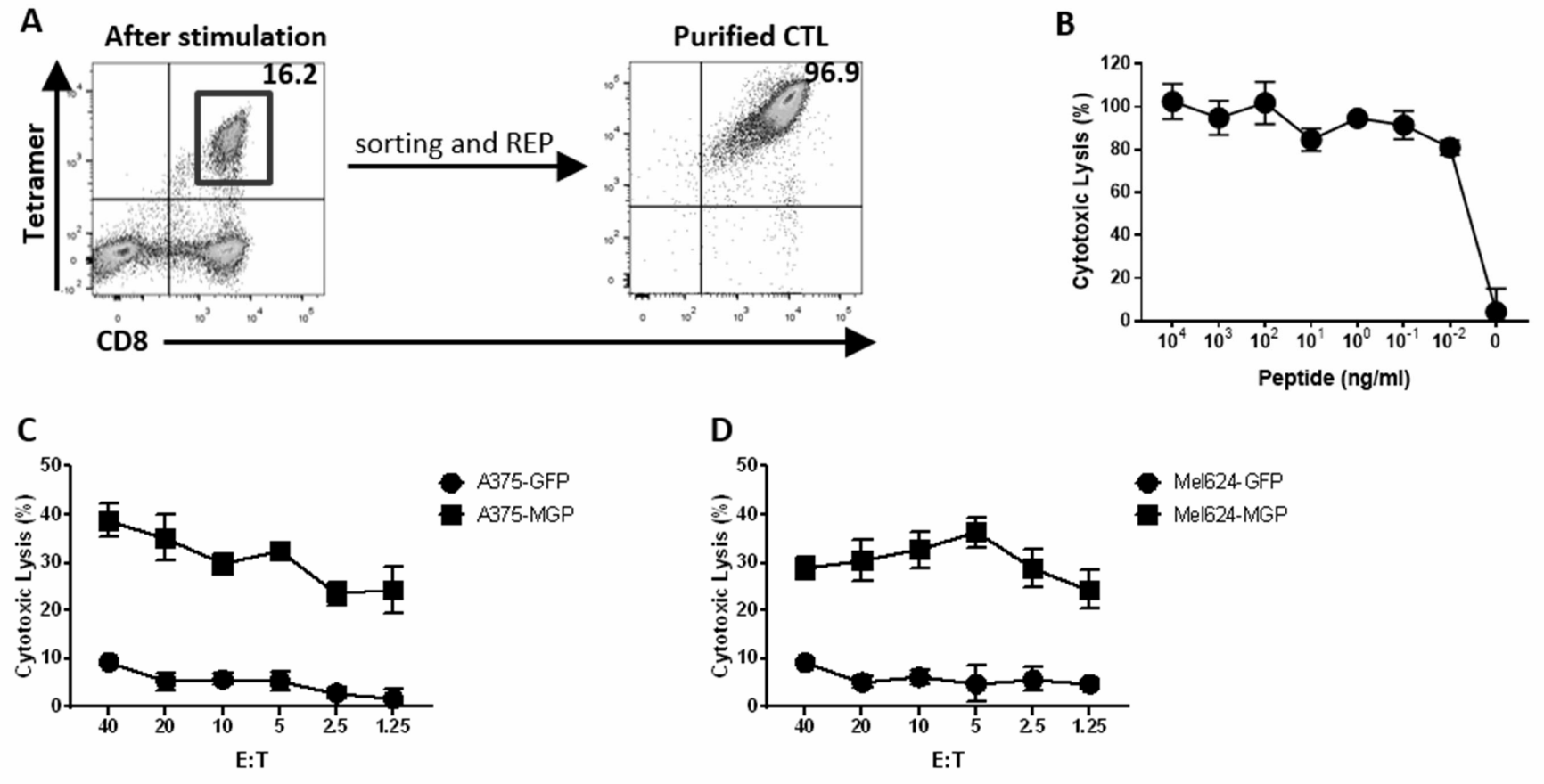

A
After stimulation
16.2
Purified CTL
96.9
sorting and REP
Tetramer
CD8
B
Cytotoxic Lysis (%)
Peptide (ng/ml)
C
A375-GFP
A375-MGP
Cytotoxic Lysis (%)
E:T
D
Mel624-GFP
Mel624-MGP
Cytotoxic Lysis (%)
E:T

FIG. 9A-D

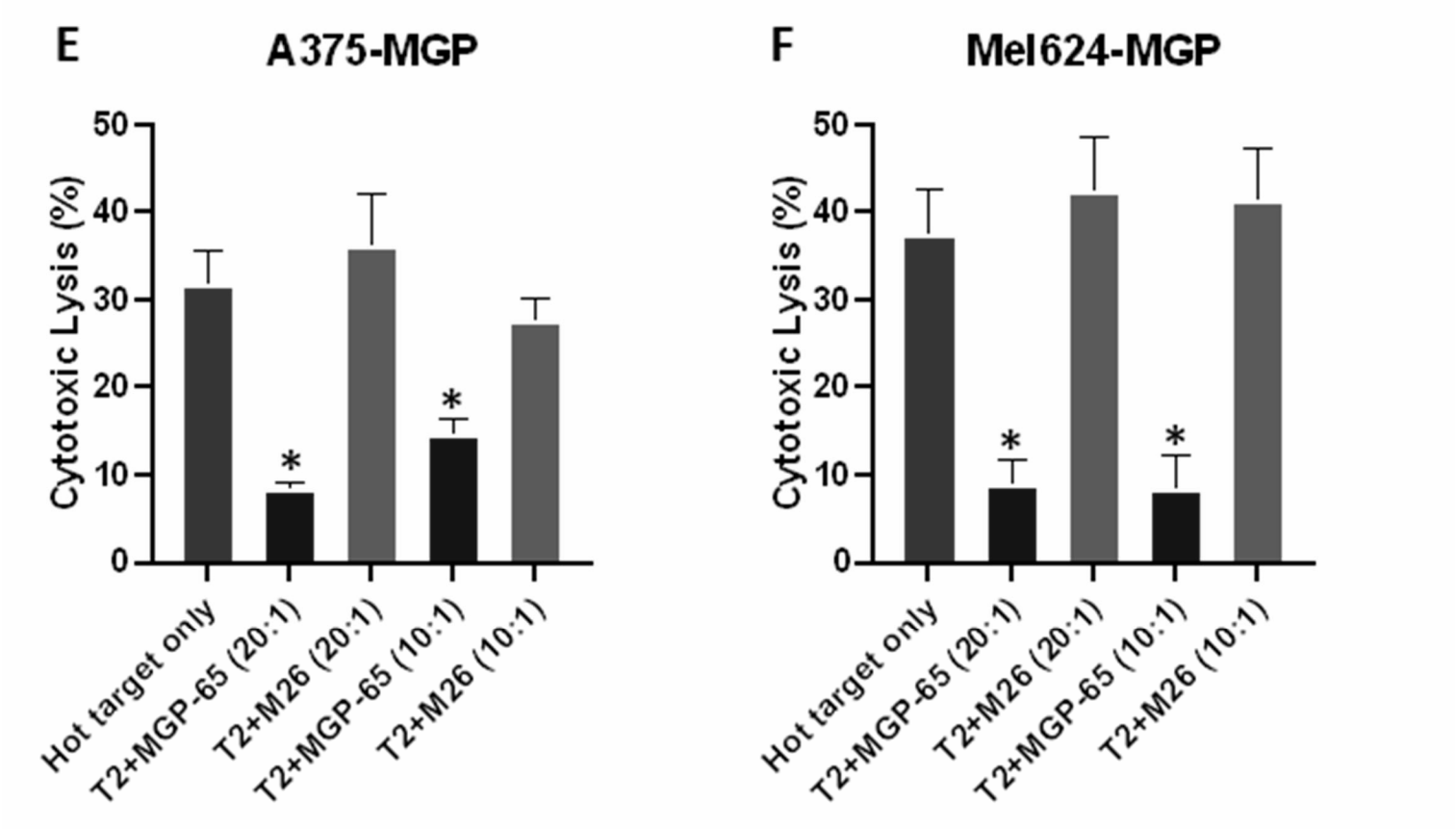

E
A375-MGP
Cytotoxic Lysis (%)
50
40
30
20
10
0
*
*
Hot target only
T2+MGP-65 (20:1)
T2+M26 (20:1)
T2+MGP-65 (10:1)
T2+M26 (10:1)
F
Mel624-MGP
Cytotoxic Lysis (%)
50
40
30
20
10
0
*
*
Hot target only
T2+MGP-65 (20:1)
T2+M26 (20:1)
T2+MGP-65 (10:1)
T2+M26 (10:1)

FIG. 9E-F

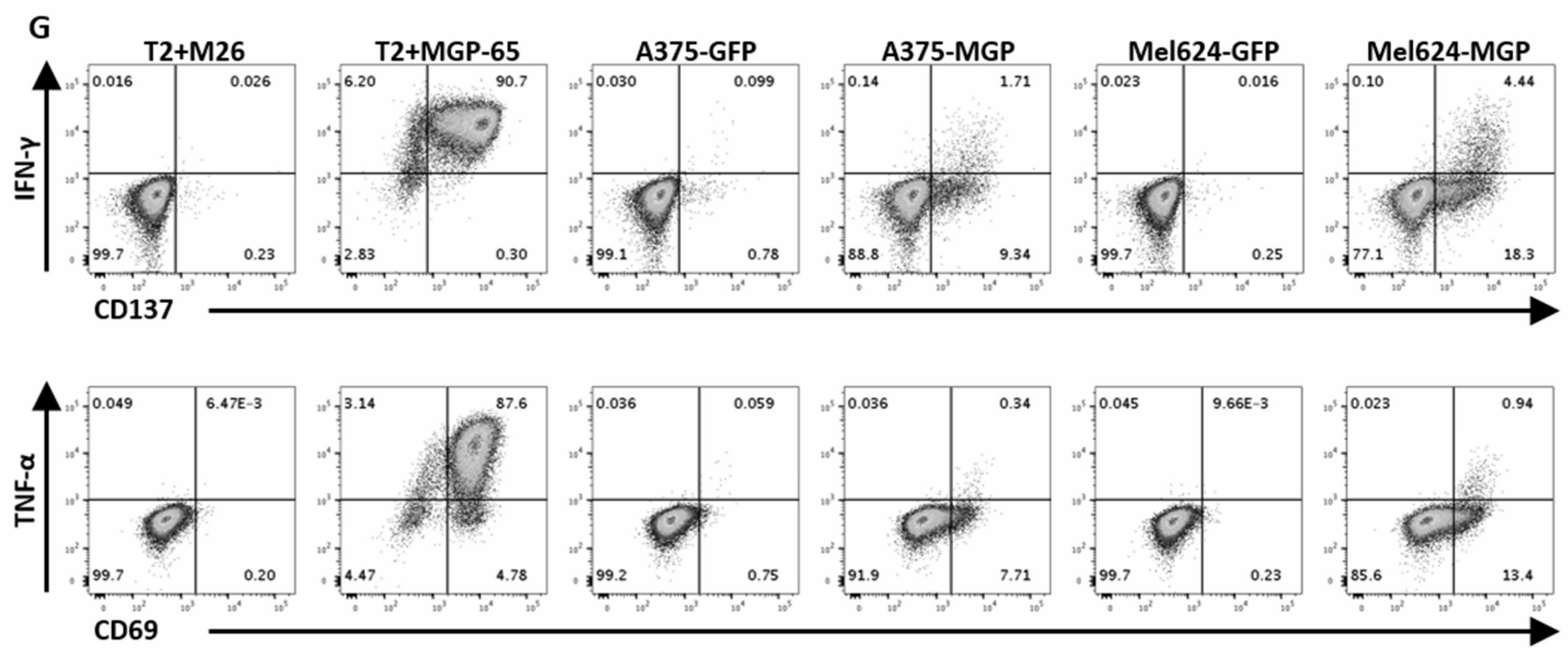

G
T2+M26
T2+MGP-65
A375-GFP
A375-MGP
Mel624-GFP
Mel624-MGP
IFN-γ
CD137
0.016
0.026
99.7
0.23
6.20
90.7
2.83
0.30
0.030
0.099
99.1
0.78
0.14
1.71
88.8
9.34
0.023
0.016
99.7
0.25
0.10
4.44
77.1
18.3
TNF-α
CD69
0.049
6.47E-3
99.7
0.20
3.14
87.6
4.47
4.78
0.036
0.059
99.2
0.75
0.036
0.34
91.9
7.71
0.045
9.66E-3
99.7
0.23
0.023
0.94
85.6
13.4

FIG. 9G

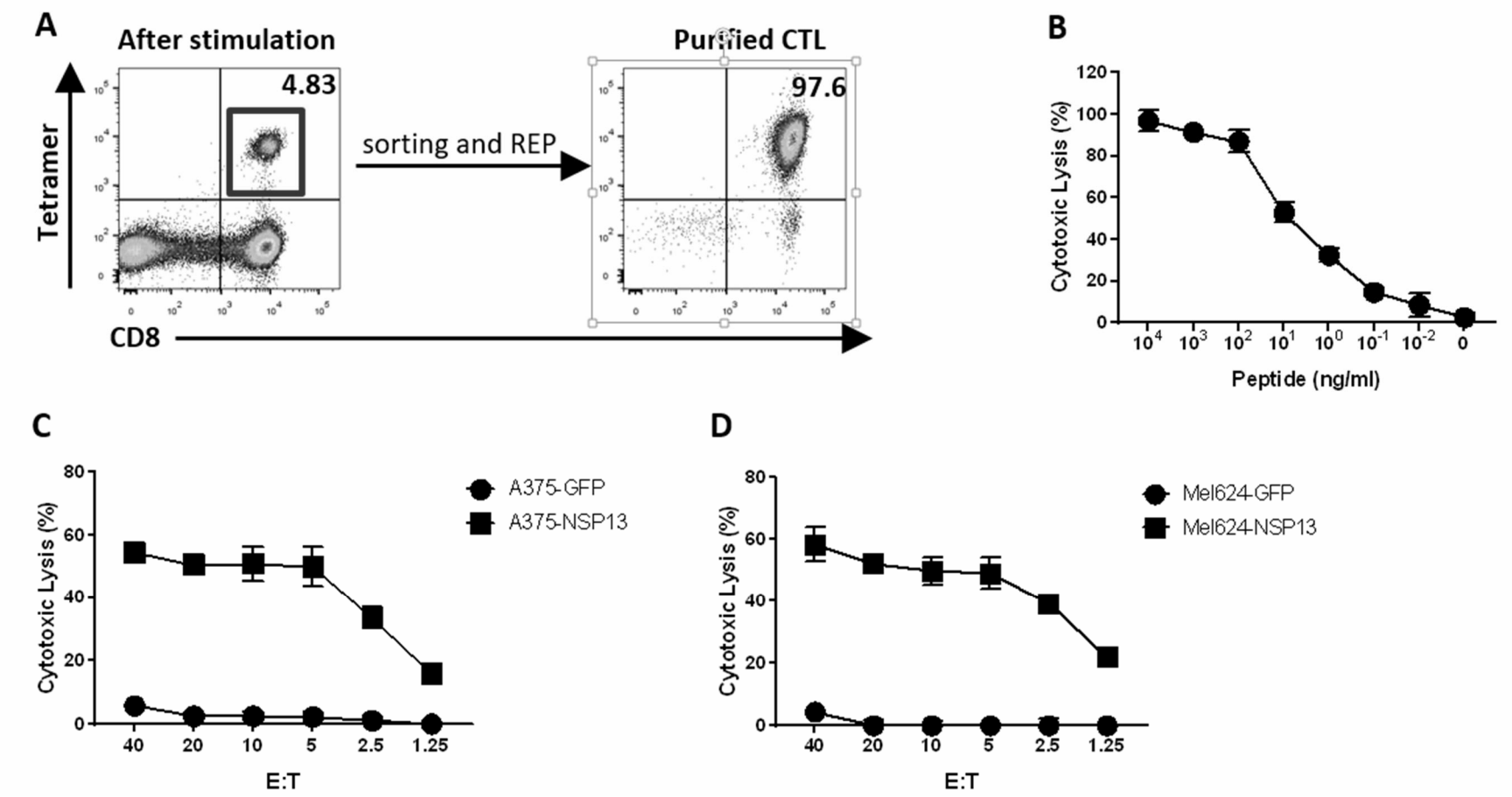

A
After stimulation
4.83
Tetramer
CD8
sorting and REP
Purified CTL
97.6
B
Cytotoxic Lysis (%)
Peptide (ng/ml)
C
Cytotoxic Lysis (%)
A375-GFP
A375-NSP13
E:T
D
Cytotoxic Lysis (%)
Mel624-GFP
Mel624-NSP13
E:T

FIG. 10A-D

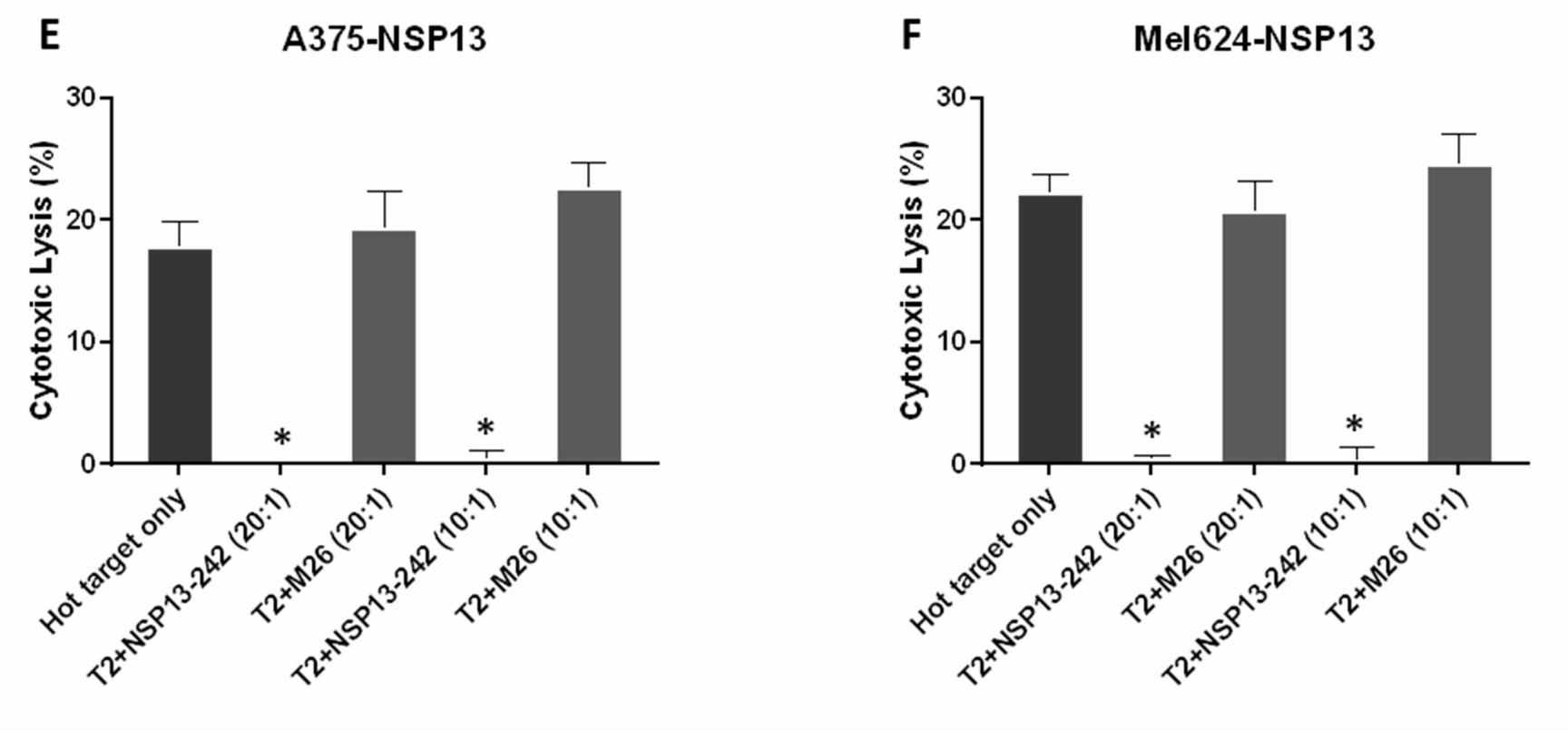

E
A375-NSP13
Cytotoxic Lysis (%)
30
20
10
0
*
*
Hot target only
T2+NSP13-242 (20:1)
T2+M26 (20:1)
T2+NSP13-242 (10:1)
T2+M26 (10:1)
F
Mel624-NSP13
Cytotoxic Lysis (%)
30
20
10
0
*
*
Hot target only
T2+NSP13-242 (20:1)
T2+M26 (20:1)
T2+NSP13-242 (10:1)
T2+M26 (10:1)

FIG. 10E-F

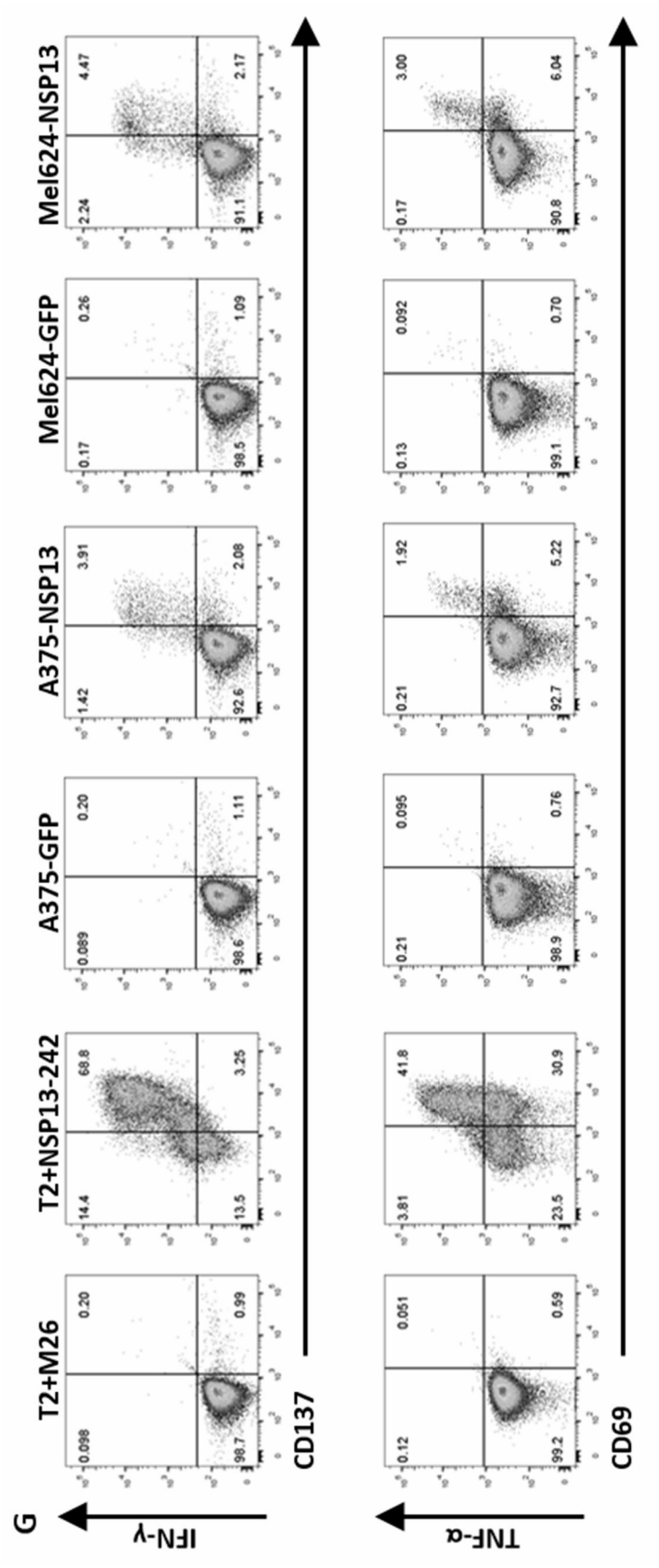

G
IFN-γ
TNF-α
CD137
CD69
T2+M26
T2+NSP13-242
A375-GFP
A375-NSP13
Mel624-GFP
Mel624-NSP13
0.098
0.20
98.7
0.99
0.12
0.051
99.2
0.59
14.4
68.8
13.5
3.25
3.81
41.8
23.5
30.9
0.089
0.20
98.6
1.11
0.21
0.095
98.9
0.76
1.42
3.91
92.6
2.08
0.21
1.92
92.7
5.22
0.17
0.26
98.5
1.09
0.13
0.092
99.1
0.70
2.24
4.47
91.1
2.17
0.17
3.00
90.8
6.04

FIG. 10G

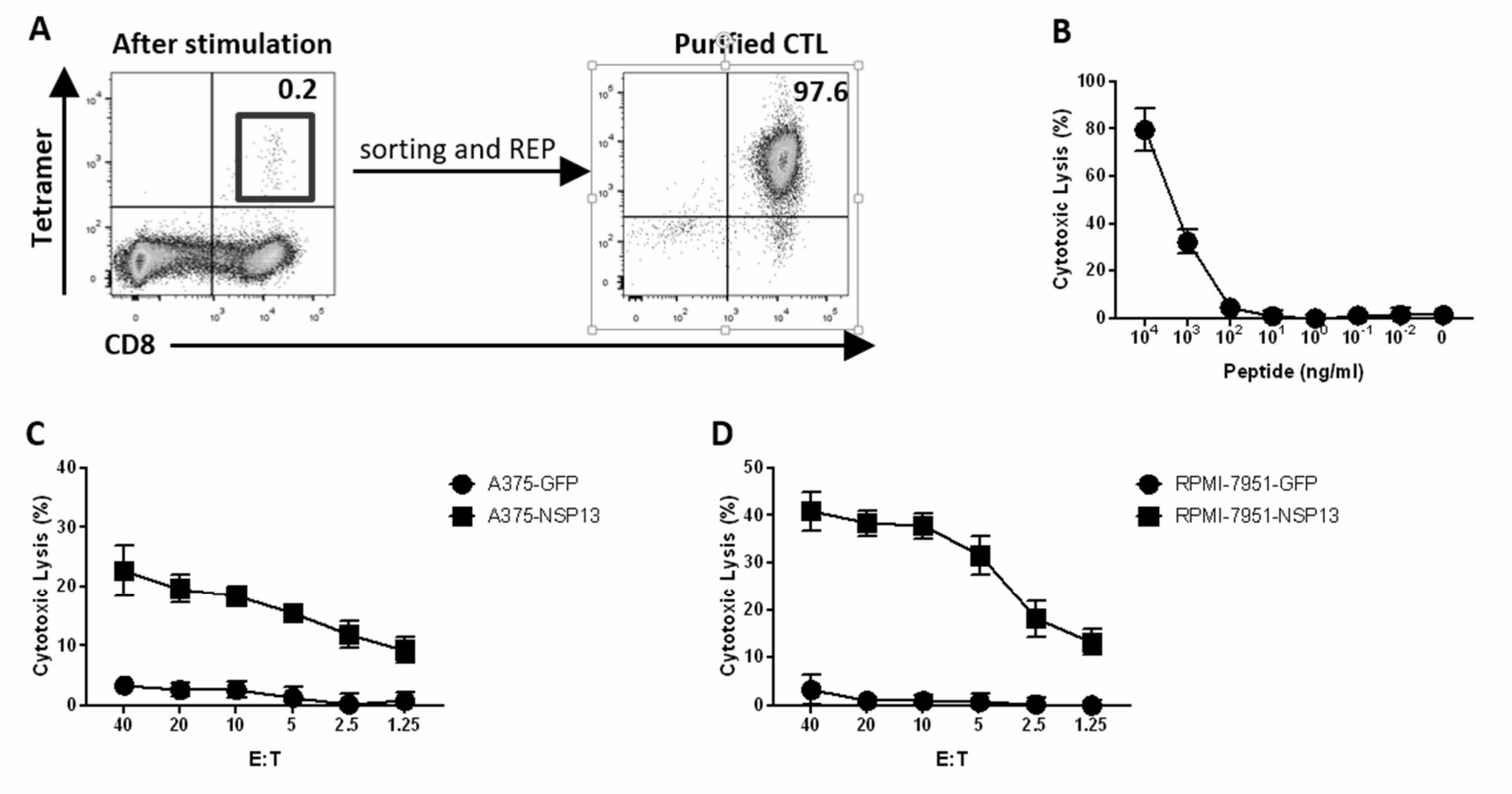

A
After stimulation
0.2
Tetramer
CD8
sorting and REP
Purified CTL
97.6
B
Cytotoxic Lysis (%)
Peptide (ng/ml)
C
A375-GFP
A375-NSP13
Cytotoxic Lysis (%)
E:T
D
RPMI-7951-GFP
RPMI-7951-NSP13
Cytotoxic Lysis (%)
E:T

FIG. 11A-D

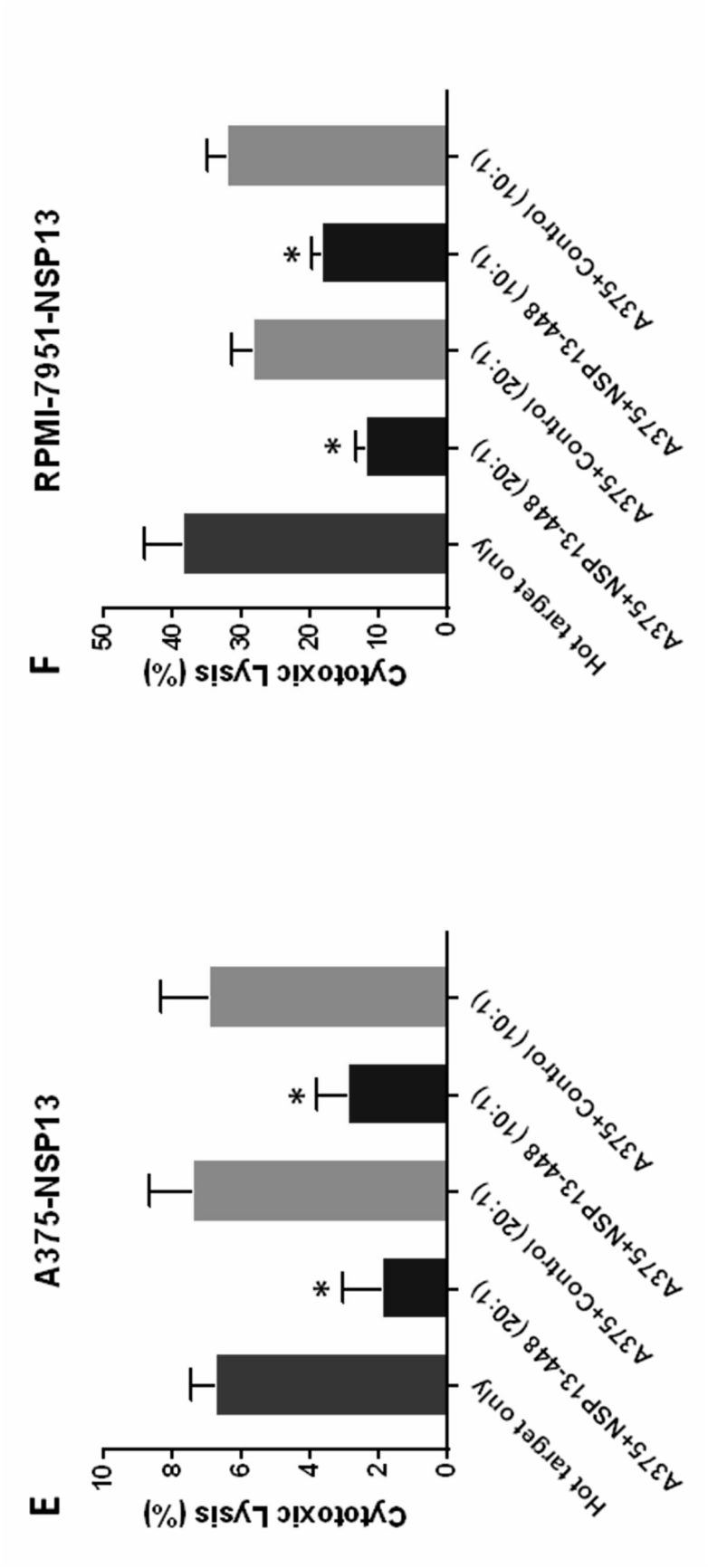

E
A375-NSP13
Cytotoxic Lysis (%)
0
2
4
6
8
10
Hot target only
A375+NSP13-448 (20:1)
A375+Control (20:1)
A375+NSP13-448 (10:1)
A375+Control (10:1)
*
*
F
RPMI-7951-NSP13
Cytotoxic Lysis (%)
0
10
20
30
40
50
Hot target only
A375+NSP13-448 (20:1)
A375+Control (20:1)
A375+NSP13-448 (10:1)
A375+Control (10:1)
*
*

FIG. 11E-F

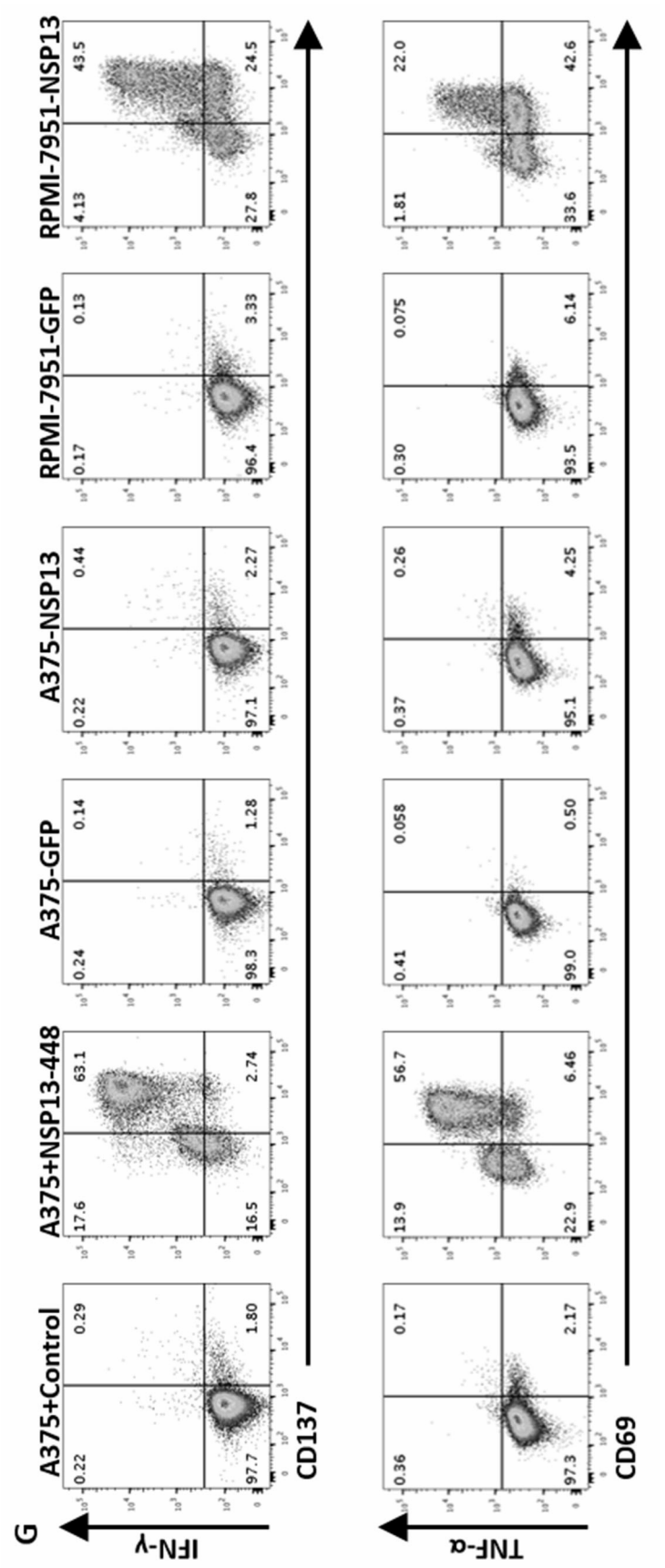

G
A375+Control
A375+NSP13-448
A375-GFP
A375-NSP13
RPMI-7951-GFP
RPMI-7951-NSP13
IFN-γ
CD137
TNF-α
CD69
0.22
0.29
97.7
1.80
17.6
63.1
16.5
2.74
0.24
0.14
98.3
1.28
0.22
0.44
97.1
2.27
0.17
0.13
96.4
3.33
4.13
43.5
27.8
24.5
0.36
0.17
97.3
2.17
13.9
56.7
22.9
6.46
0.41
0.058
99.0
0.50
0.37
0.26
95.1
4.25
0.30
0.075
93.5
6.14
1.81
22.0
33.6
42.6

FIG. 11G

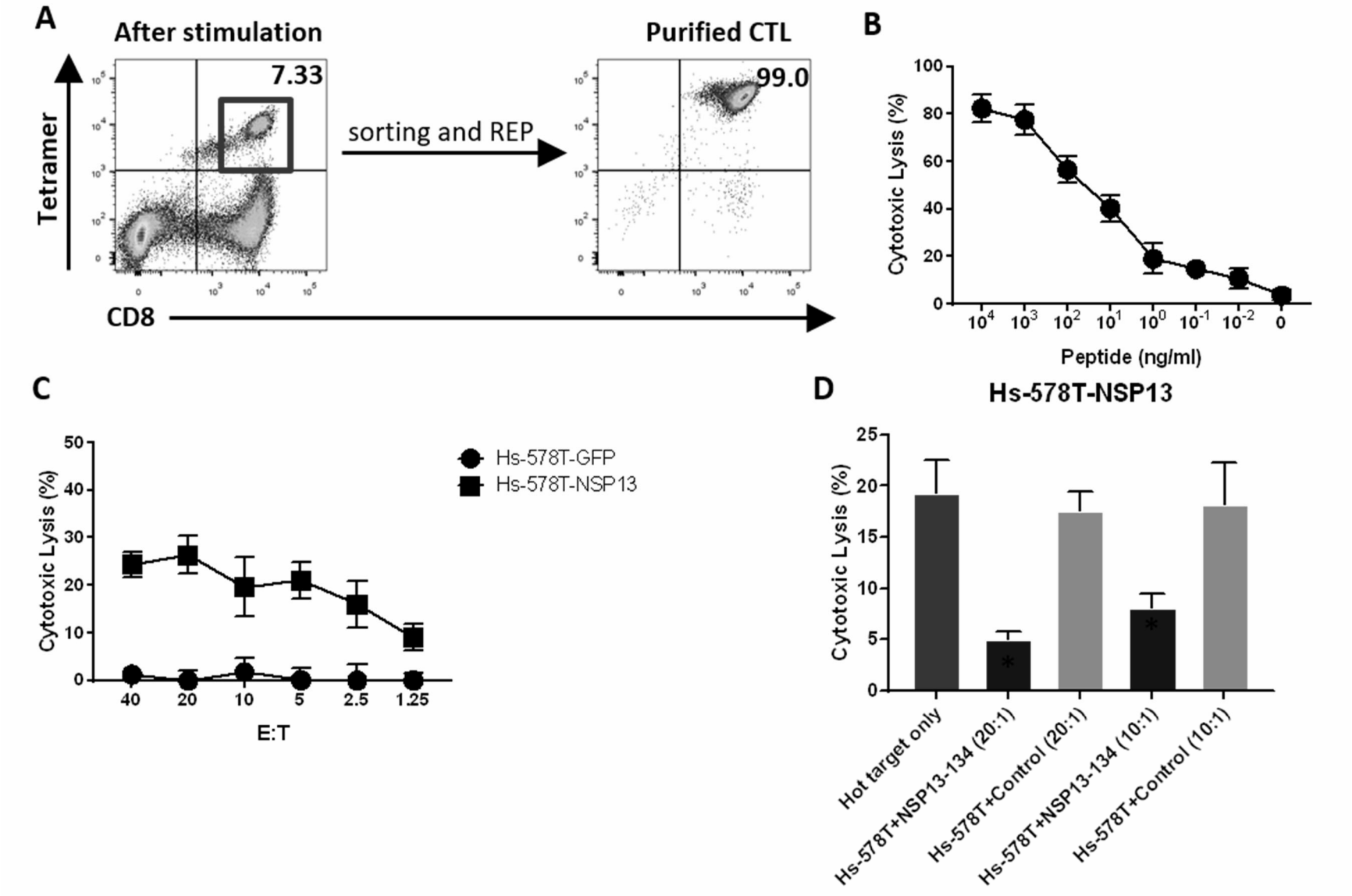

A
After stimulation
Purified CTL
7.33
99.0
sorting and REP
Tetramer
CD8
B
Cytotoxic Lysis (%)
Peptide (ng/ml)
C
Hs-578T-GFP
Hs-578T-NSP13
Cytotoxic Lysis (%)
E:T
D
Hs-578T-NSP13
Cytotoxic Lysis (%)
Hot target only
Hs-578T+NSP13-134 (20:1)
Hs-578T+Control (20:1)
Hs-578T+NSP13-134 (10:1)
Hs-578T+Control (10:1)

FIG. 12A-D

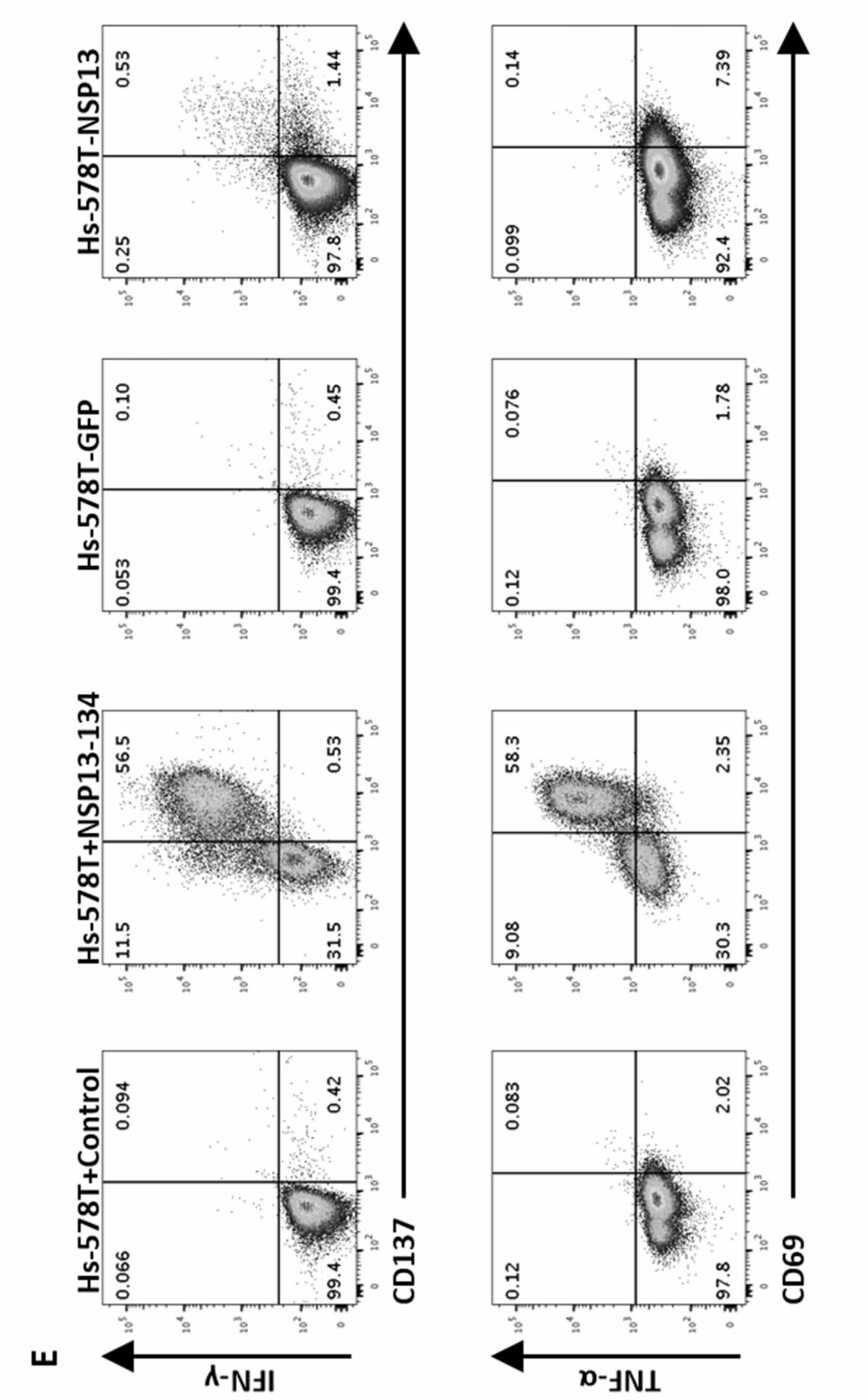

E
Hs-578T+Control
Hs-578T+NSP13-134
Hs-578T-GFP
Hs-578T-NSP13
IFN-γ
CD137
TNF-α
CD69
0.066
0.094
99.4
0.42
11.5
56.5
31.5
0.53
0.053
0.10
99.4
0.45
0.25
0.53
97.8
1.44
0.12
0.083
97.8
2.02
9.08
58.3
30.3
2.35
0.12
0.076
98.0
1.78
0.099
0.14
92.4
7.39

FIG. 12E

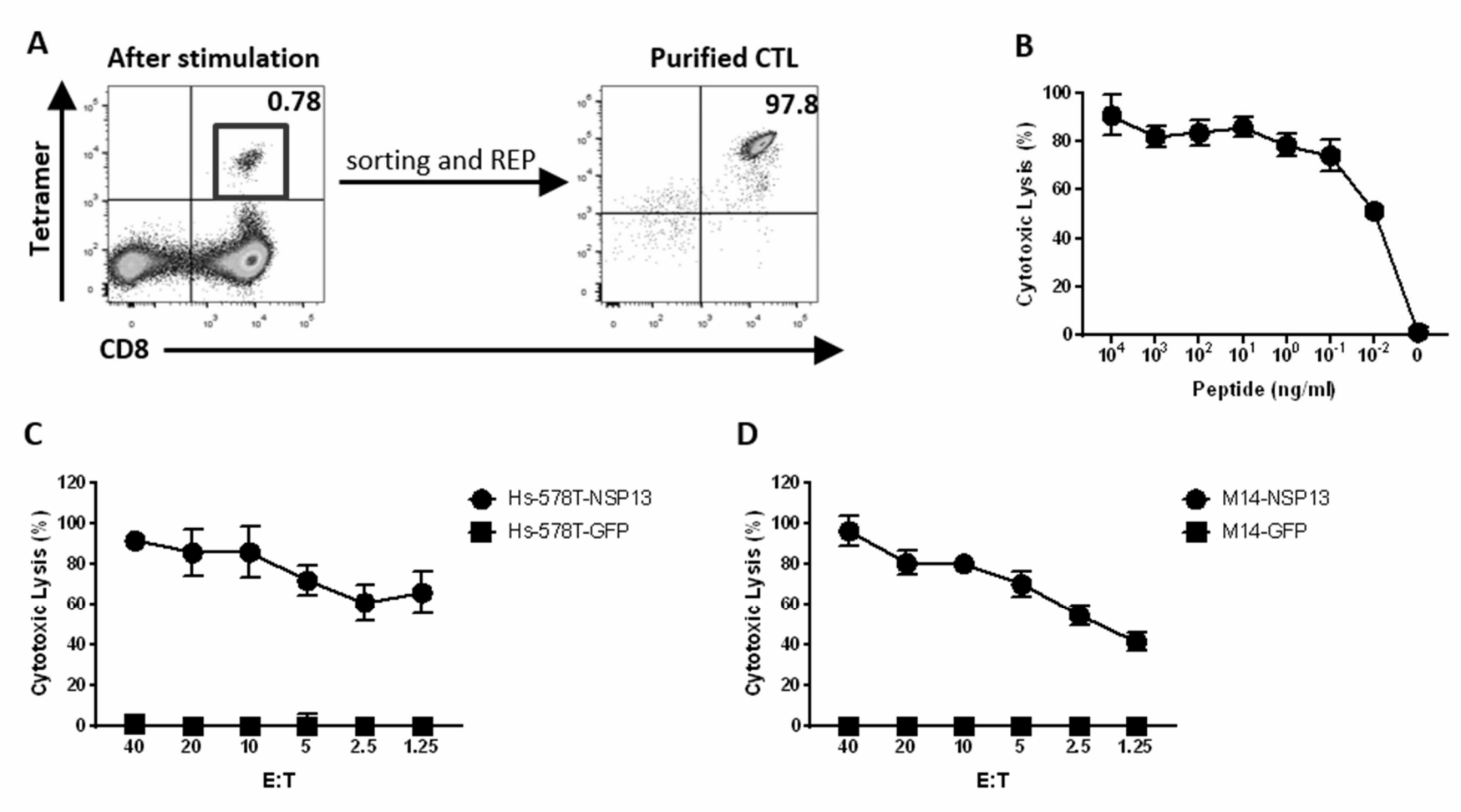

A
After stimulation
Purified CTL
0.78
97.8
sorting and REP
Tetramer
CD8
B
Cytotoxic Lysis (%)
Peptide (ng/ml)
C
Hs-578T-NSP13
Hs-578T-GFP
Cytotoxic Lysis (%)
E:T
D
M14-NSP13
M14-GFP
Cytotoxic Lysis (%)
E:T

FIG. 13A-D

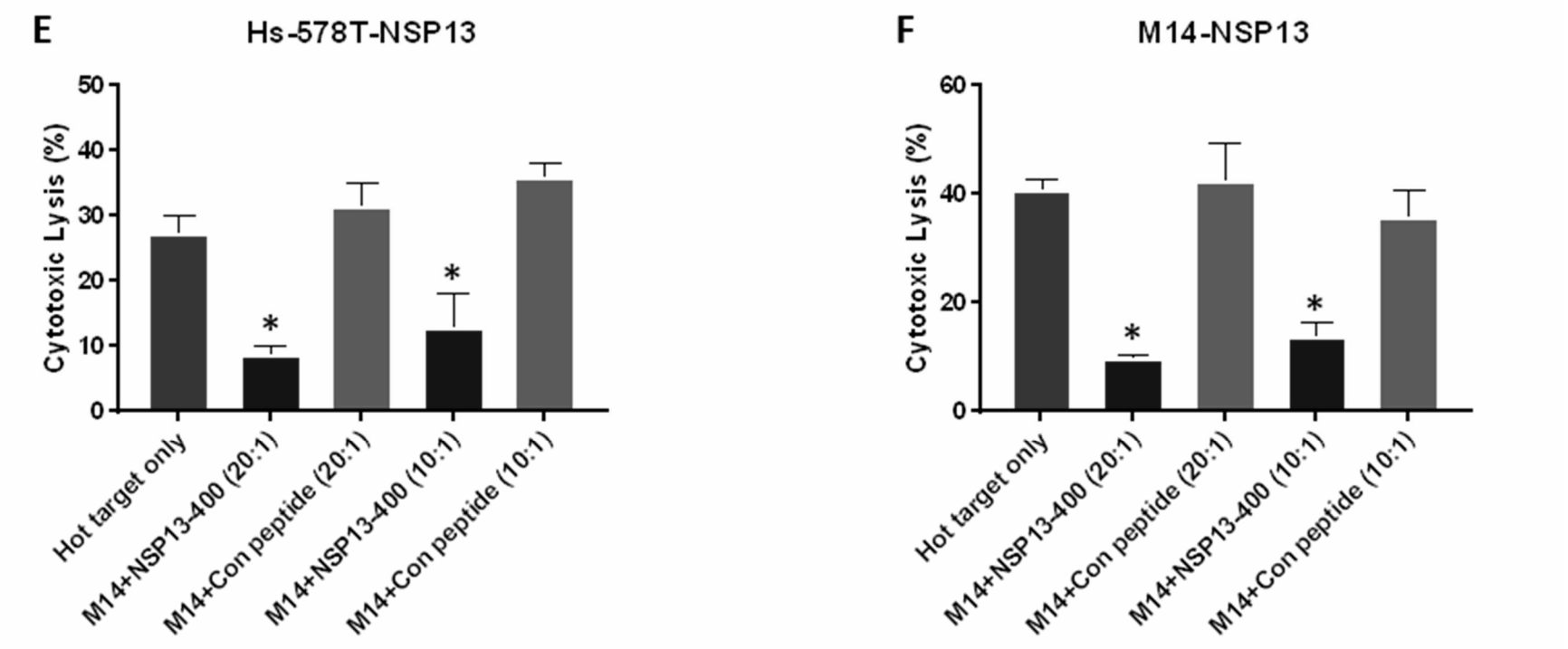

E
Hs-578T-NSP13
Cytotoxic Lysis (%)
50
40
30
20
10
0
*
*
Hot target only
M14+NSP13-400 (20:1)
M14+Con peptide (20:1)
M14+NSP13-400 (10:1)
M14+Con peptide (10:1)
F
M14-NSP13
Cytotoxic Lysis (%)
60
40
20
0
*
*
Hot target only
M14+NSP13-400 (20:1)
M14+Con peptide (20:1)
M14+NSP13-400 (10:1)
M14+Con peptide (10:1)

FIG. 13E-F

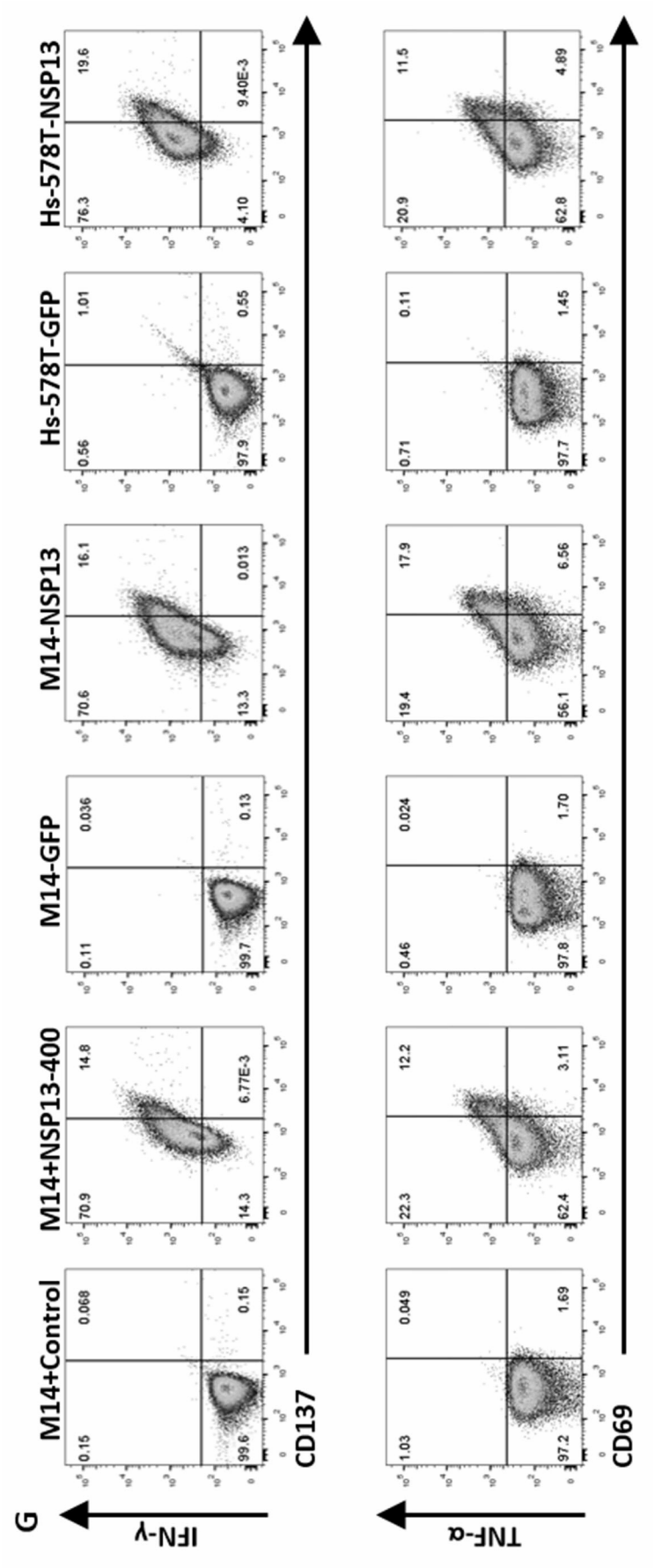

G
IFN-γ
TNF-α
CD137
CD69
M14+Control
M14+NSP13-400
M14-GFP
M14-NSP13
Hs-578T-GFP
Hs-578T-NSP13
0.15
0.068
99.6
0.15
70.9
14.8
14.3
6.77E-3
0.11
0.036
99.7
0.13
70.6
16.1
13.3
0.013
0.56
1.01
97.9
0.55
76.3
19.6
4.10
9.40E-3
1.03
0.049
97.2
1.69
22.3
12.2
62.4
3.11
0.46
0.024
97.8
1.70
19.4
17.9
56.1
6.56
0.71
0.11
97.7
1.45
20.9
11.5
62.8
4.89

FIG. 13G

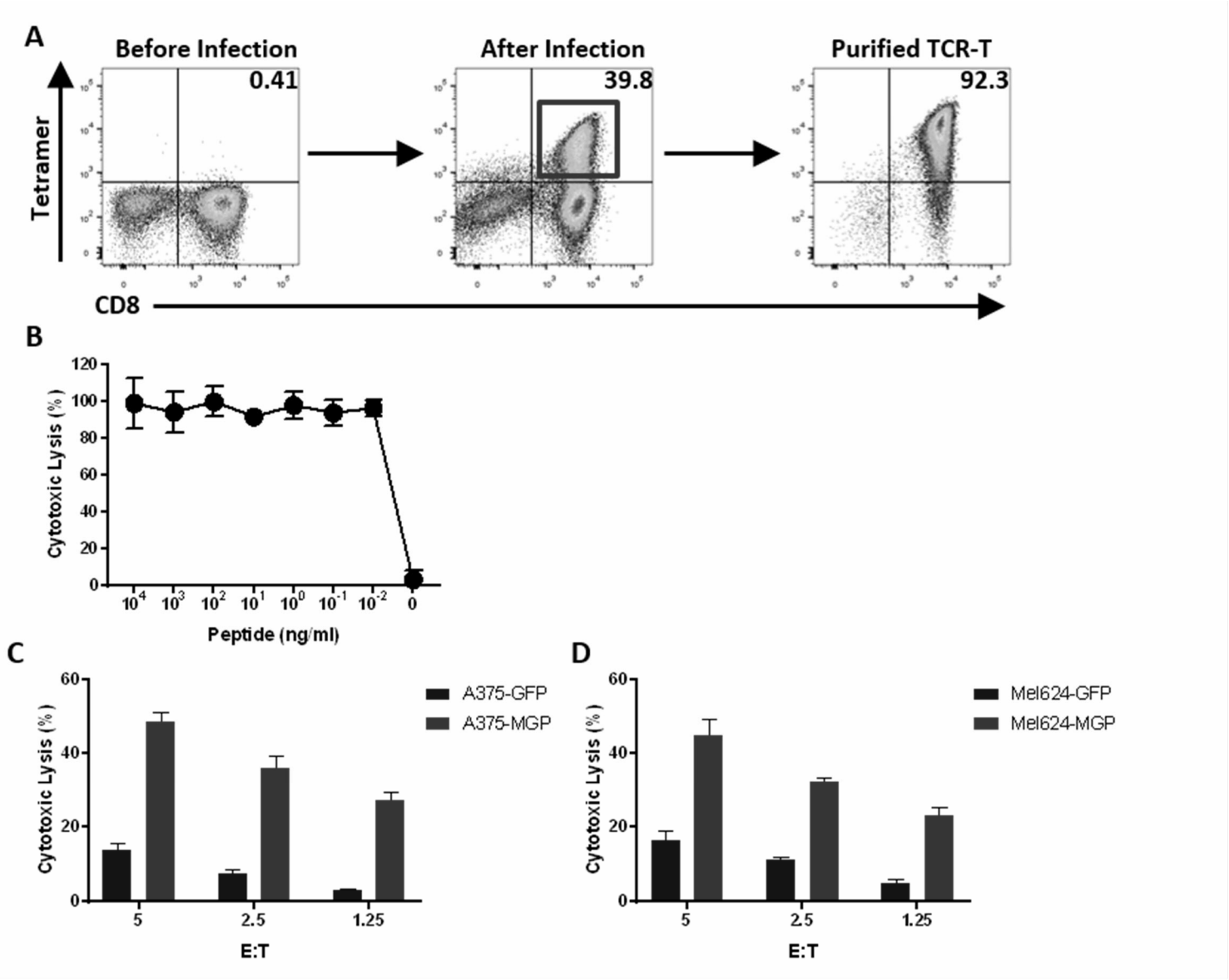

A
Before Infection
After Infection
Purified TCR-T
0.41
39.8
92.3
Tetramer
CD8
B
Cytotoxic Lysis (%)
Peptide (ng/ml)
C
A375-GFP
A375-MGP
Cytotoxic Lysis (%)
E:T
D
Mel624-GFP
Mel624-MGP
Cytotoxic Lysis (%)
E:T

FIG. 14A-D

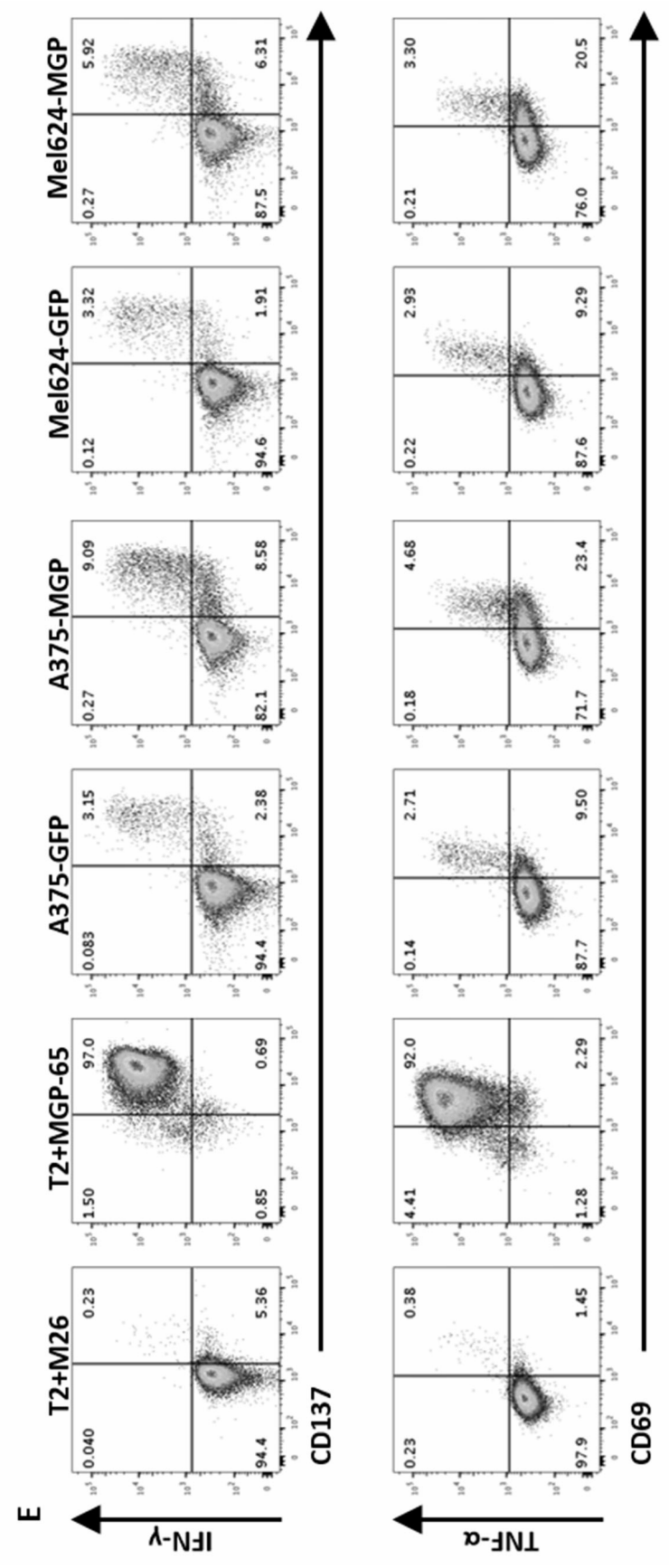

E
IFN-γ
CD137
TNF-α
CD69
T2+M26
T2+MGP-65
A375-GFP
A375-MGP
Mel624-GFP
Mel624-MGP
0.040
0.23
94.4
5.36
1.50
97.0
0.85
0.69
0.083
3.15
94.4
2.38
0.27
9.09
82.1
8.58
0.12
3.32
94.6
1.91
0.27
5.92
87.5
6.31
0.23
0.38
97.9
1.45
4.41
92.0
1.28
2.29
0.14
2.71
87.7
9.50
0.18
4.68
71.7
23.4
0.22
2.93
87.6
9.29
0.21
3.30
76.0
20.5

FIG. 14E

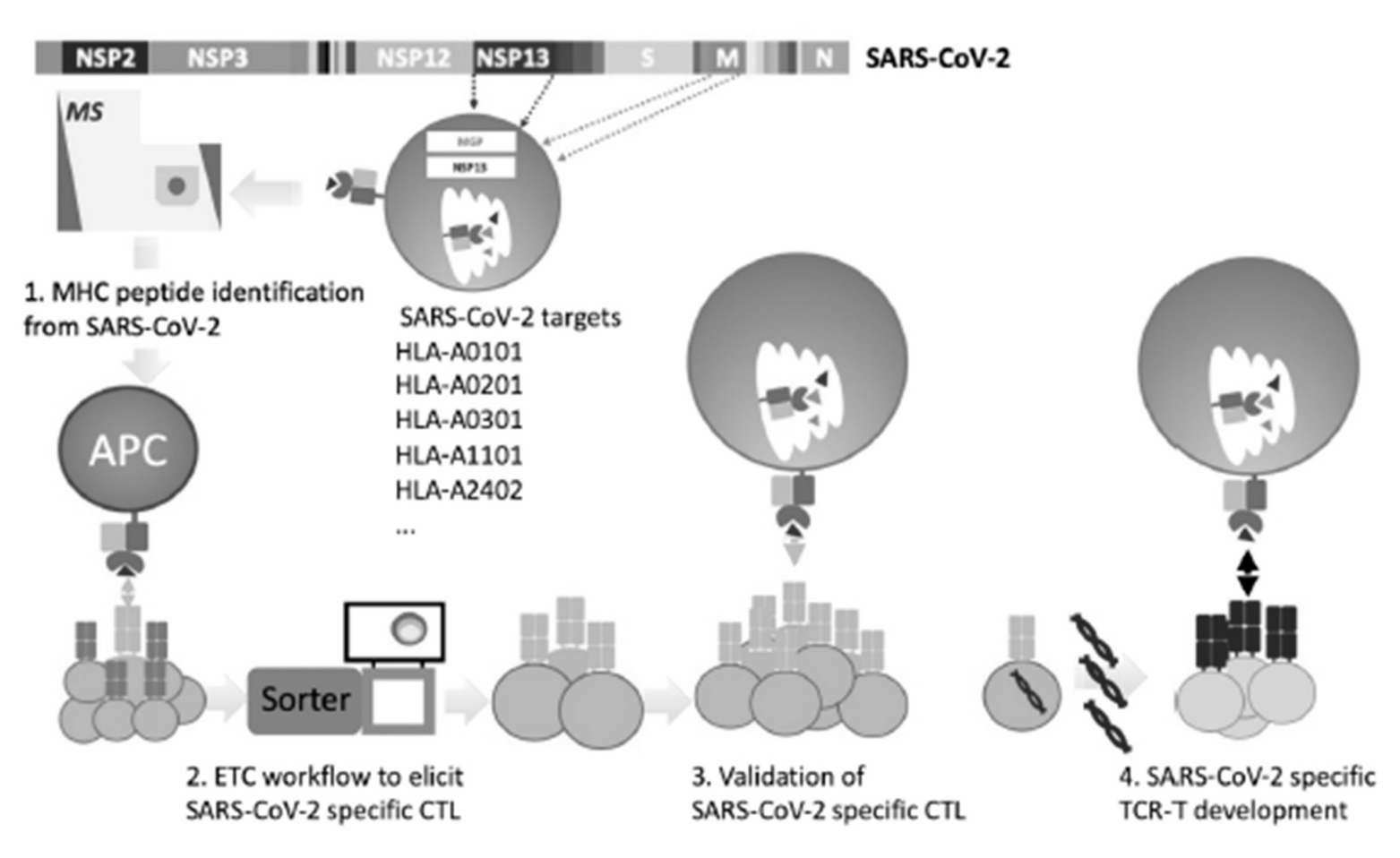

NSP2
NSP3
NSP12
NSP13
S
M
N
SARS-CoV-2
MS
1. MHC peptide identification from SARS-CoV-2
APC
SARS-CoV-2 targets
HLA-A0101
HLA-A0201
HLA-A0301
HLA-A1101
HLA-A2402
...
Sorter
2. ETC workflow to elicit SARS-CoV-2 specific CTL
3. Validation of SARS-CoV-2 specific CTL
4. SARS-CoV-2 specific TCR-T development

FIG. 15

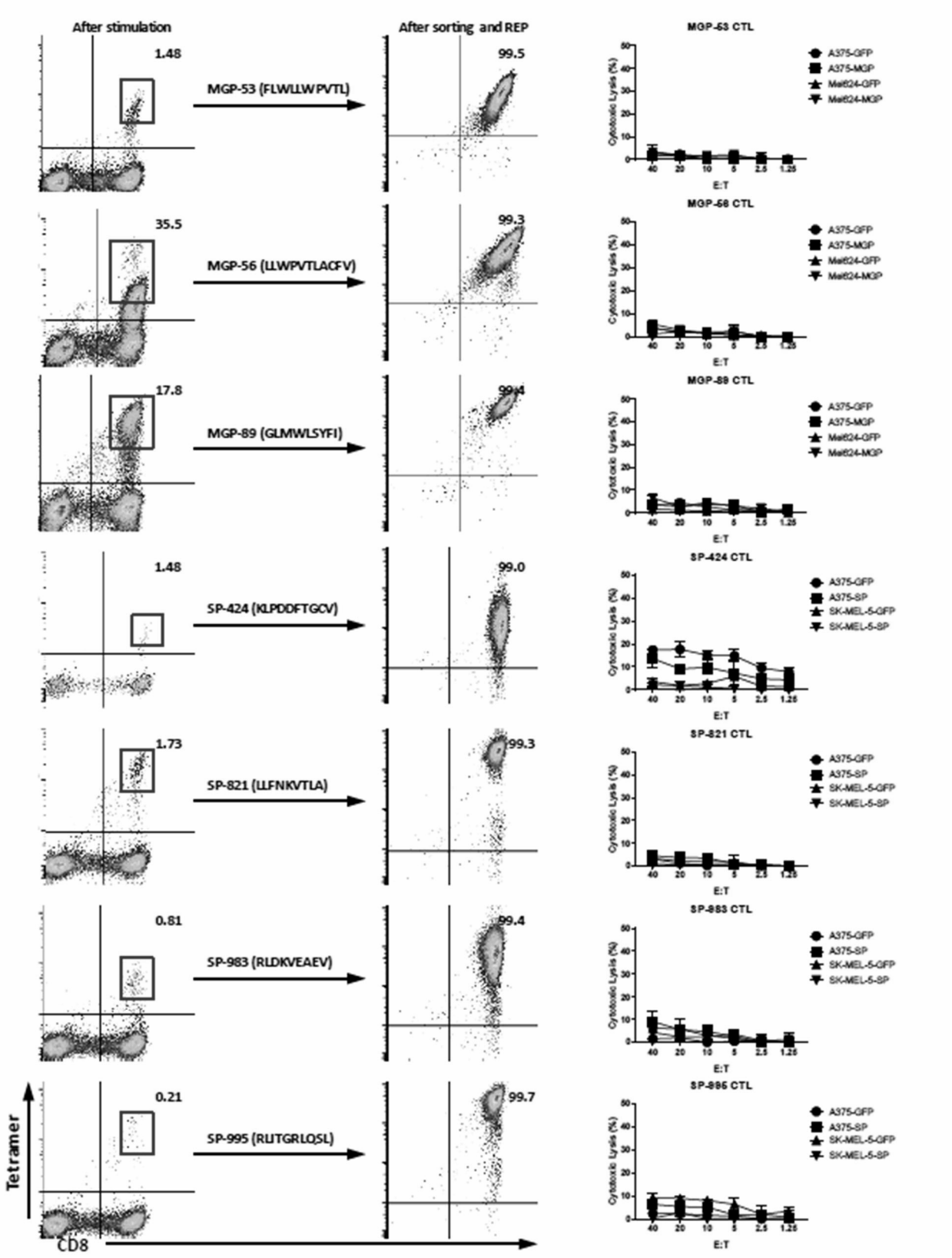

After stimulation
After sorting and REP
1.48
MGP-53 (FLWLLWPVTL)
99.5
MGP-53 CTL
35.5
MGP-56 (LLWPVTLACFV)
99.3
MGP-56 CTL
17.8
MGP-89 (GLMWLSYFI)
99.4
MGP-89 CTL
1.48
SP-424 (KLPDDFTGCV)
99.0
SP-424 CTL
1.73
SP-821 (LLFNKVTLA)
99.3
SP-821 CTL
0.81
SP-983 (RLDKVEAEV)
99.4
SP-983 CTL
0.21
SP-995 (RLITGRLQSL)
99.7
SP-995 CTL
Tetramer
CD8
A375-GFP
A375-MGP
Mel624-GFP
Mel624-MGP
A375-SP
SK-MEL-5-GFP
SK-MEL-5-SP
Cytotoxic Lysis (%)
E:T
40
20
10
5
2.5
1.25

FIG. 16

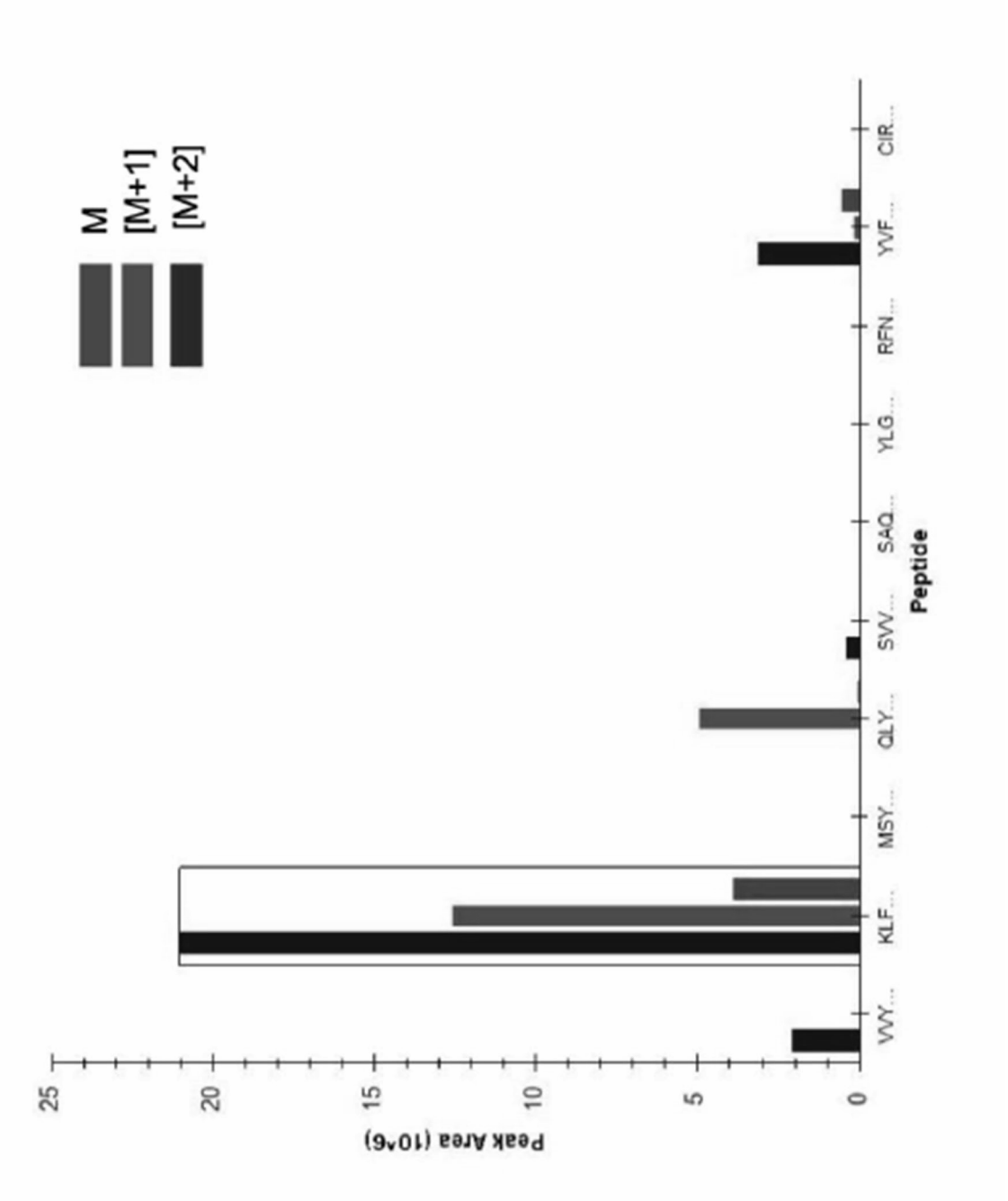

M
[M+1]
[M+2]
Peak Area (10^6)
0
5
10
15
20
25
VVY...
KLF...
MSY...
QLY...
SVV...
SAQ...
YLG...
RFN...
YVF...
CIR...
Peptide

FIG. 17

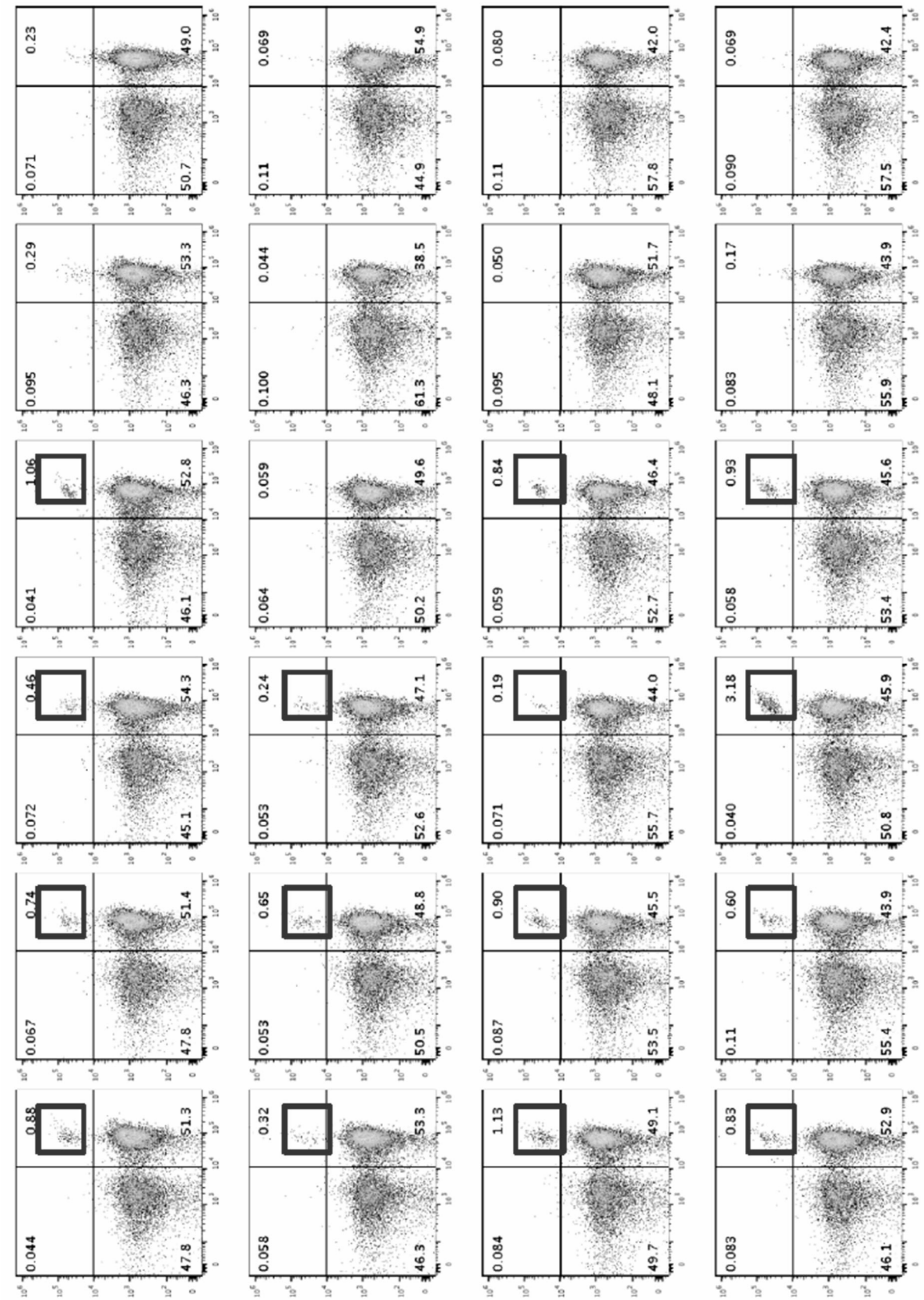

0.044
0.88
47.8
51.3
0.067
0.74
47.8
51.4
0.072
0.46
45.1
54.3
0.041
1.06
46.1
52.8
0.095
0.29
46.3
53.3
0.071
0.23
50.7
49.0
0.058
0.32
46.3
53.3
0.053
0.65
50.5
48.8
0.053
0.24
52.6
47.1
0.064
0.059
50.2
49.6
0.100
0.044
61.3
38.5
0.11
0.069
44.9
54.9
0.084
1.13
49.7
49.1
0.087
0.90
53.5
45.5
0.071
0.19
55.7
44.0
0.059
0.84
52.7
46.4
0.095
0.050
48.1
51.7
0.11
0.080
57.8
42.0
0.083
0.83
46.1
52.9
0.11
0.60
55.4
43.9
0.040
3.18
50.8
45.9
0.058
0.93
53.4
45.6
0.083
0.17
55.9
43.9
0.090
0.069
57.5
42.4

FIG. 18

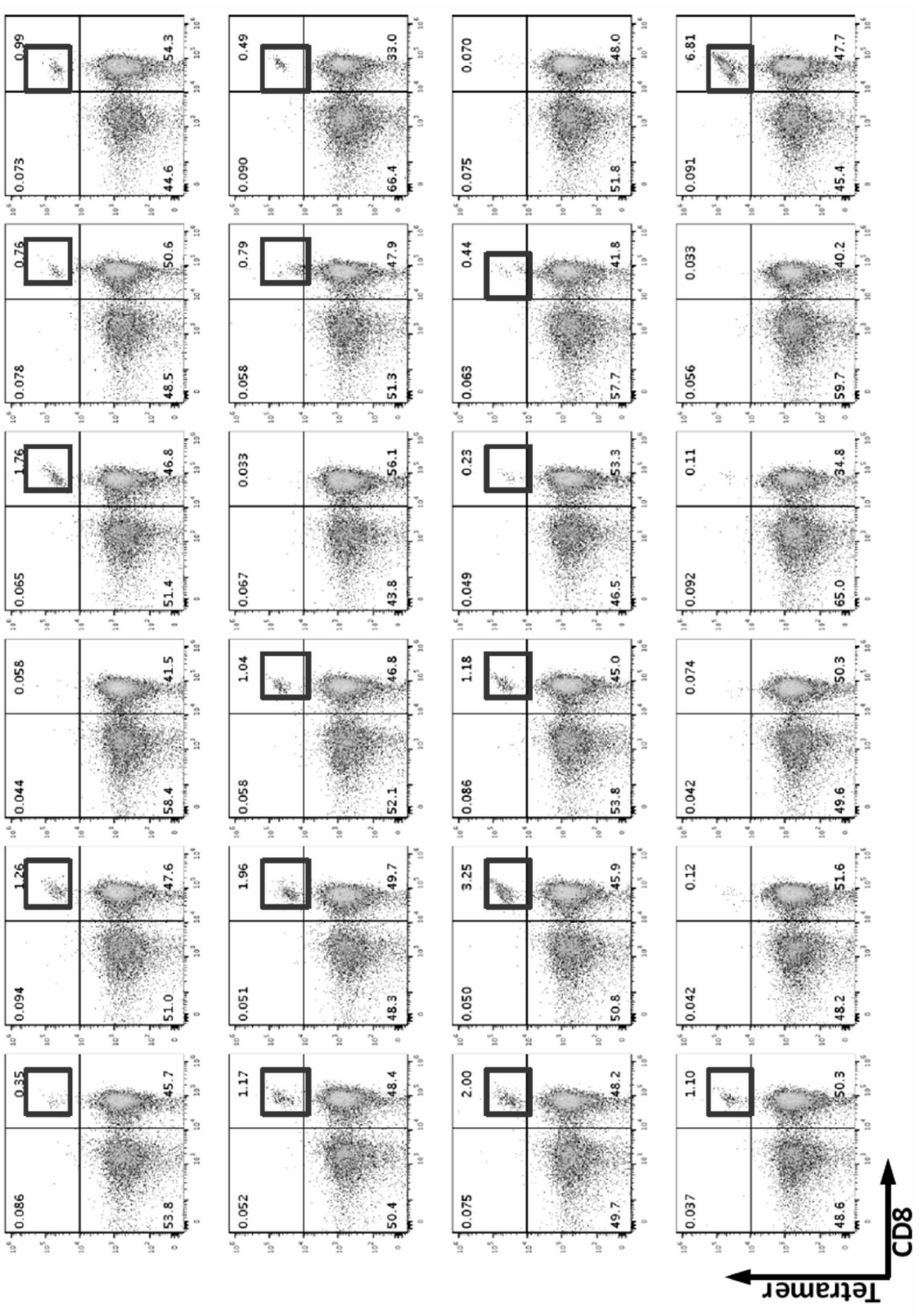


FIG. 18 Continued

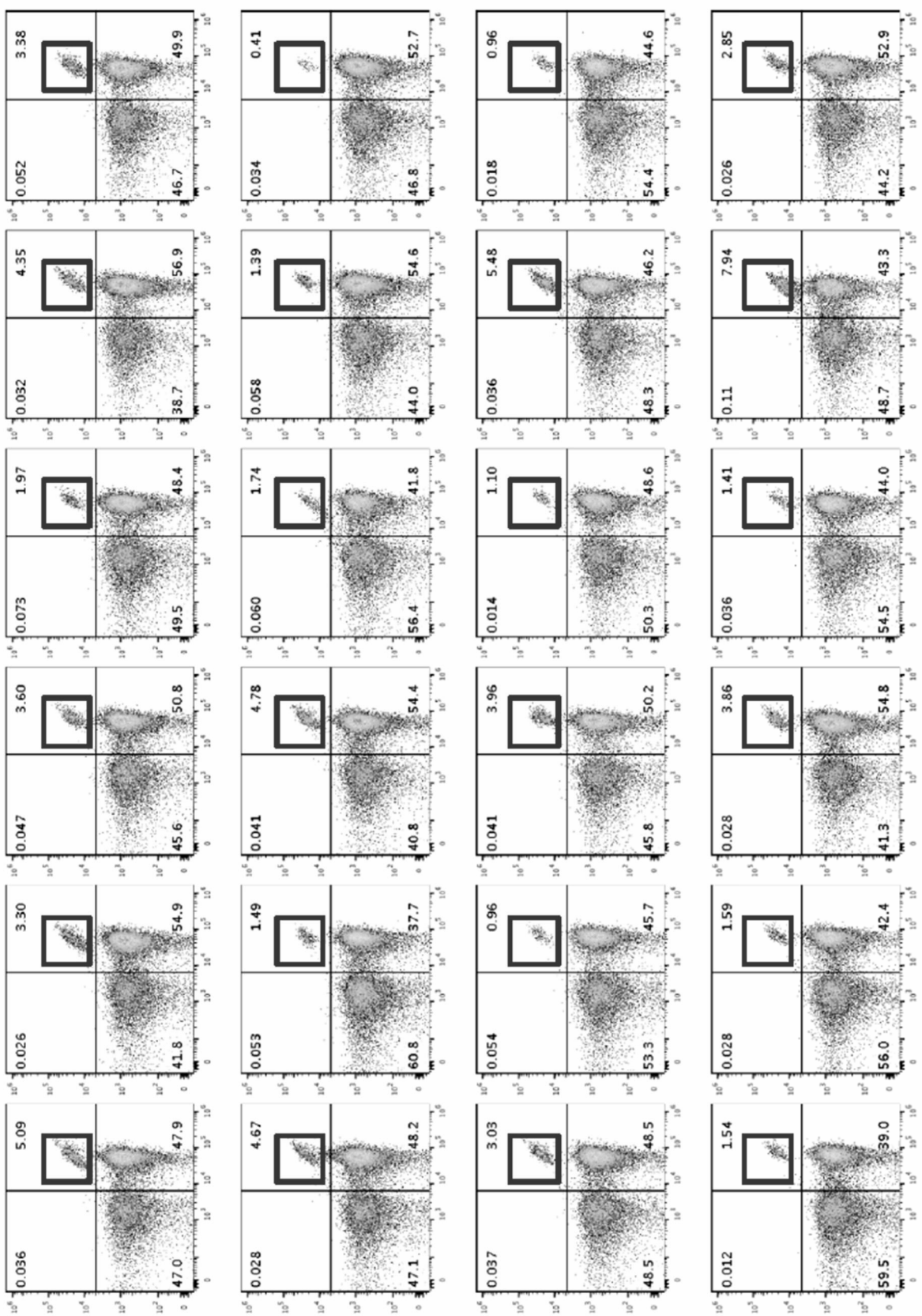

0.036
5.09
47.0
47.9
0.026
3.30
41.8
54.9
0.047
3.60
45.6
50.8
0.073
1.97
49.5
48.4
0.032
4.35
38.7
56.9
0.052
3.38
46.7
49.9
0.028
4.67
47.1
48.2
0.053
1.49
60.8
37.7
0.041
4.78
40.8
54.4
0.060
1.74
56.4
41.8
0.058
1.39
44.0
54.6
0.034
0.41
46.8
52.7
0.037
3.03
48.5
48.5
0.054
0.96
53.3
45.7
0.041
3.96
45.8
50.2
0.014
1.10
50.3
48.6
0.036
5.48
48.3
46.2
0.018
0.96
54.4
44.6
0.012
1.54
59.5
39.0
0.028
1.59
56.0
42.4
0.028
3.86
41.3
54.8
0.036
1.41
54.5
44.0
0.11
7.94
48.7
43.3
0.026
2.85
44.2
52.9

FIG. 19

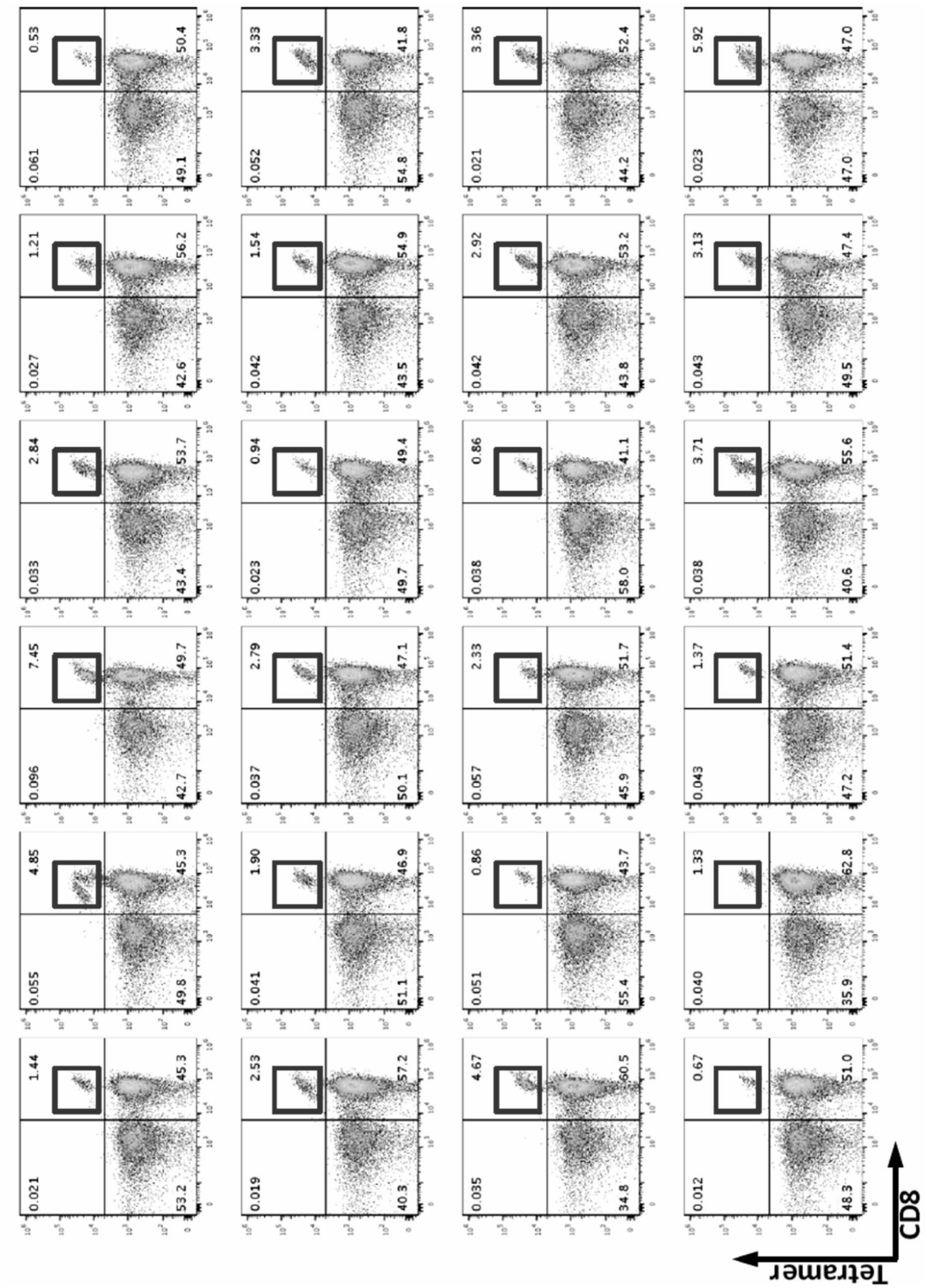


FIG. 19 Continued

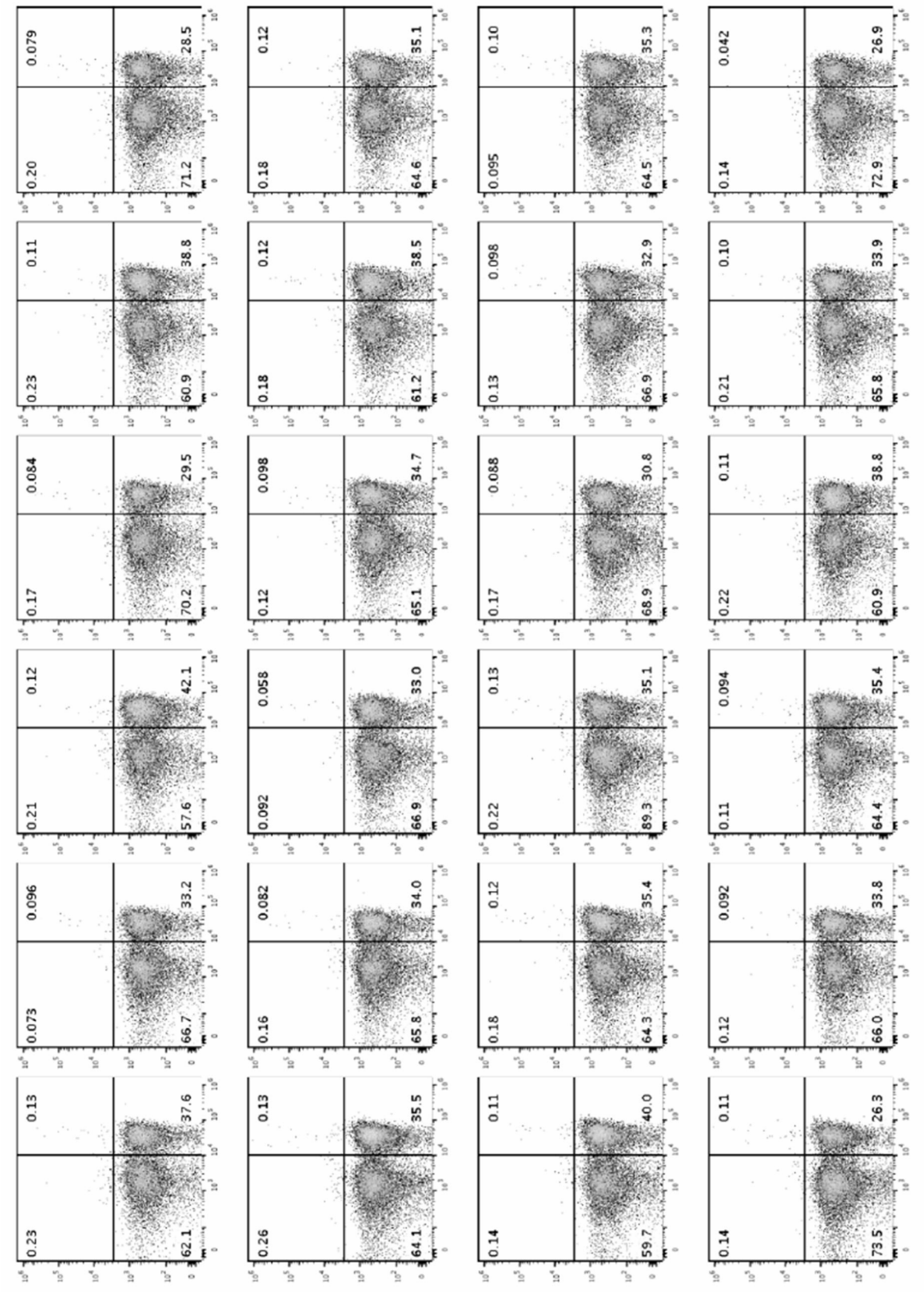

0.23 0.13 62.1 37.6
0.073 0.096 66.7 33.2
0.21 0.12 57.6 42.1
0.17 0.084 70.2 29.5
0.23 0.11 60.9 38.8
0.20 0.079 71.2 28.5
0.26 0.13 64.1 35.5
0.16 0.082 65.8 34.0
0.092 0.058 66.9 33.0
0.12 0.098 65.1 34.7
0.18 0.12 61.2 38.5
0.18 0.12 64.6 35.1
0.14 0.11 59.7 40.0
0.18 0.12 64.3 35.4
0.22 0.13 89.3 35.1
0.17 0.088 68.9 30.8
0.13 0.098 66.9 32.9
0.095 0.10 64.5 35.3
0.12 0.092 66.0 33.8
0.11 0.094 64.4 35.4
0.22 0.11 60.9 38.8
0.21 0.10 65.8 33.9
0.14 0.042 72.9 26.9
0.14 0.11 73.5 26.3

FIG. 20

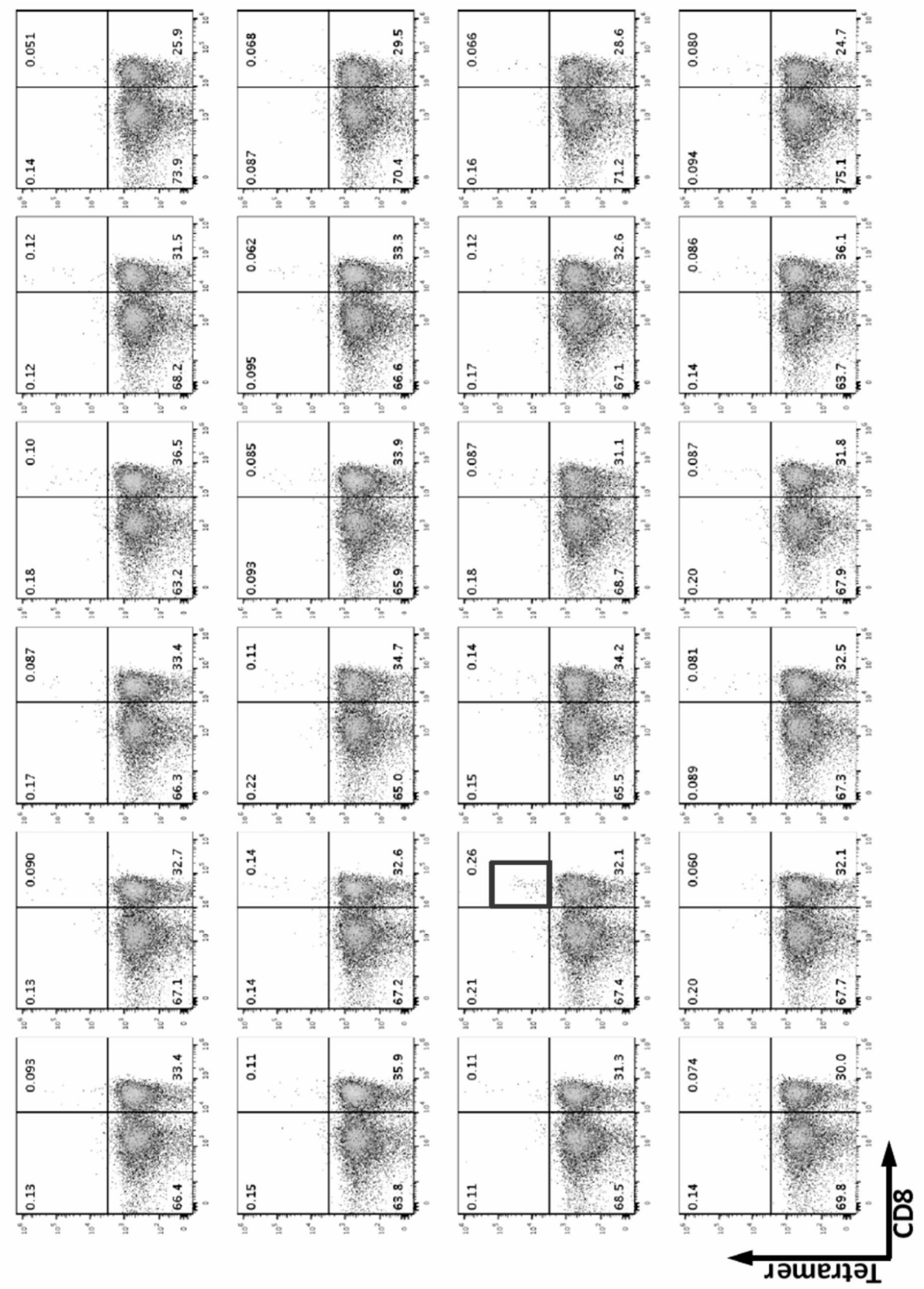


FIG. 20 Continued

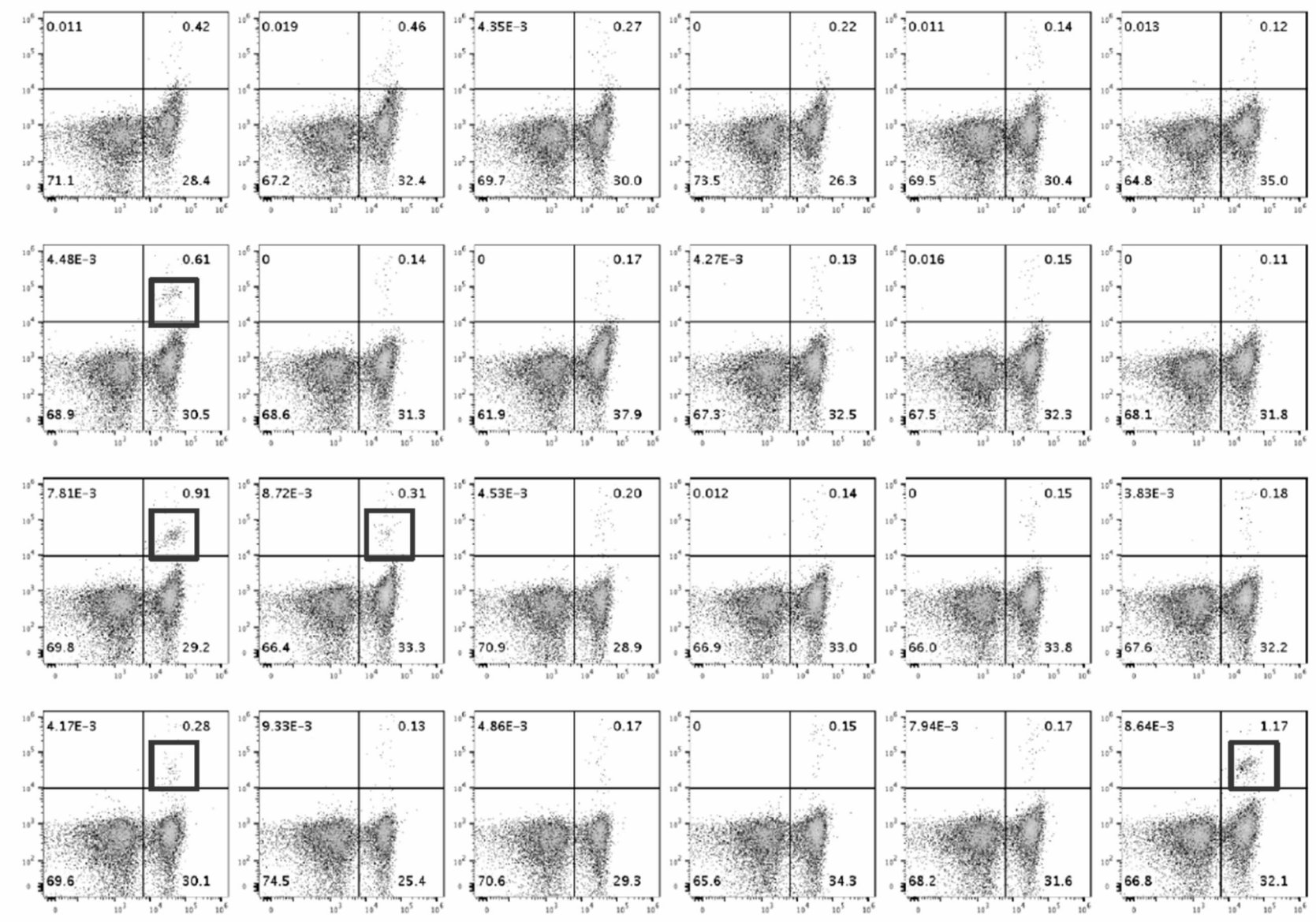

0.011
0.42
71.1
28.4
0.019
0.46
67.2
32.4
4.35E-3
0.27
69.7
30.0
0
0.22
73.5
26.3
0.011
0.14
69.5
30.4
0.013
0.12
64.8
35.0
4.48E-3
0.61
68.9
30.5
0
0.14
68.6
31.3
0
0.17
61.9
37.9
4.27E-3
0.13
67.3
32.5
0.016
0.15
67.5
32.3
0
0.11
68.1
31.8
7.81E-3
0.91
69.8
29.2
8.72E-3
0.31
66.4
33.3
4.53E-3
0.20
70.9
28.9
0.012
0.14
66.9
33.0
0
0.15
66.0
33.8
3.83E-3
0.18
67.6
32.2
4.17E-3
0.28
69.6
30.1
9.33E-3
0.13
74.5
25.4
4.86E-3
0.17
70.6
29.3
0
0.15
65.6
34.3
7.94E-3
0.17
68.2
31.6
8.64E-3
1.17
66.8
32.1

FIG. 21

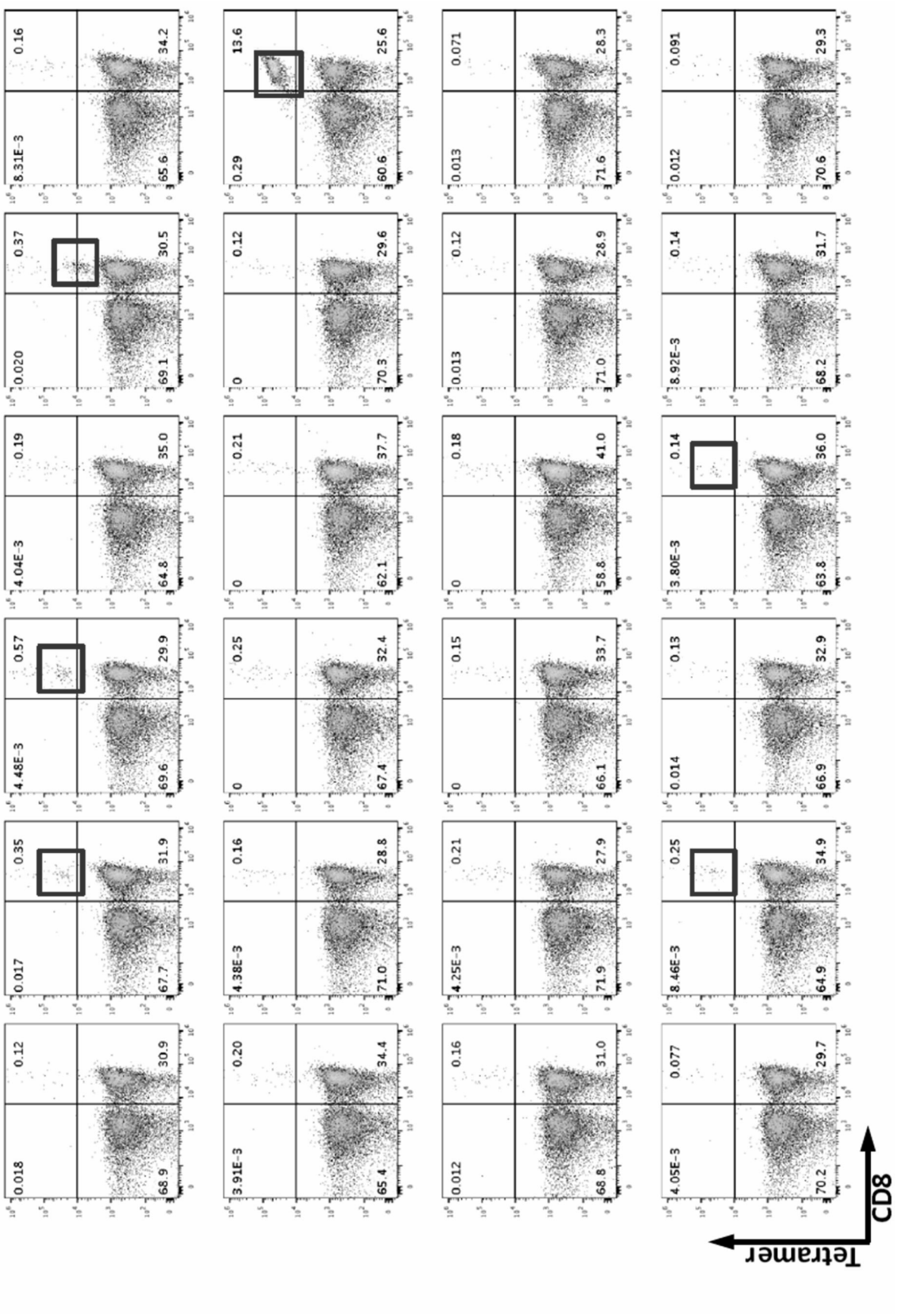


FIG. 21 Continued

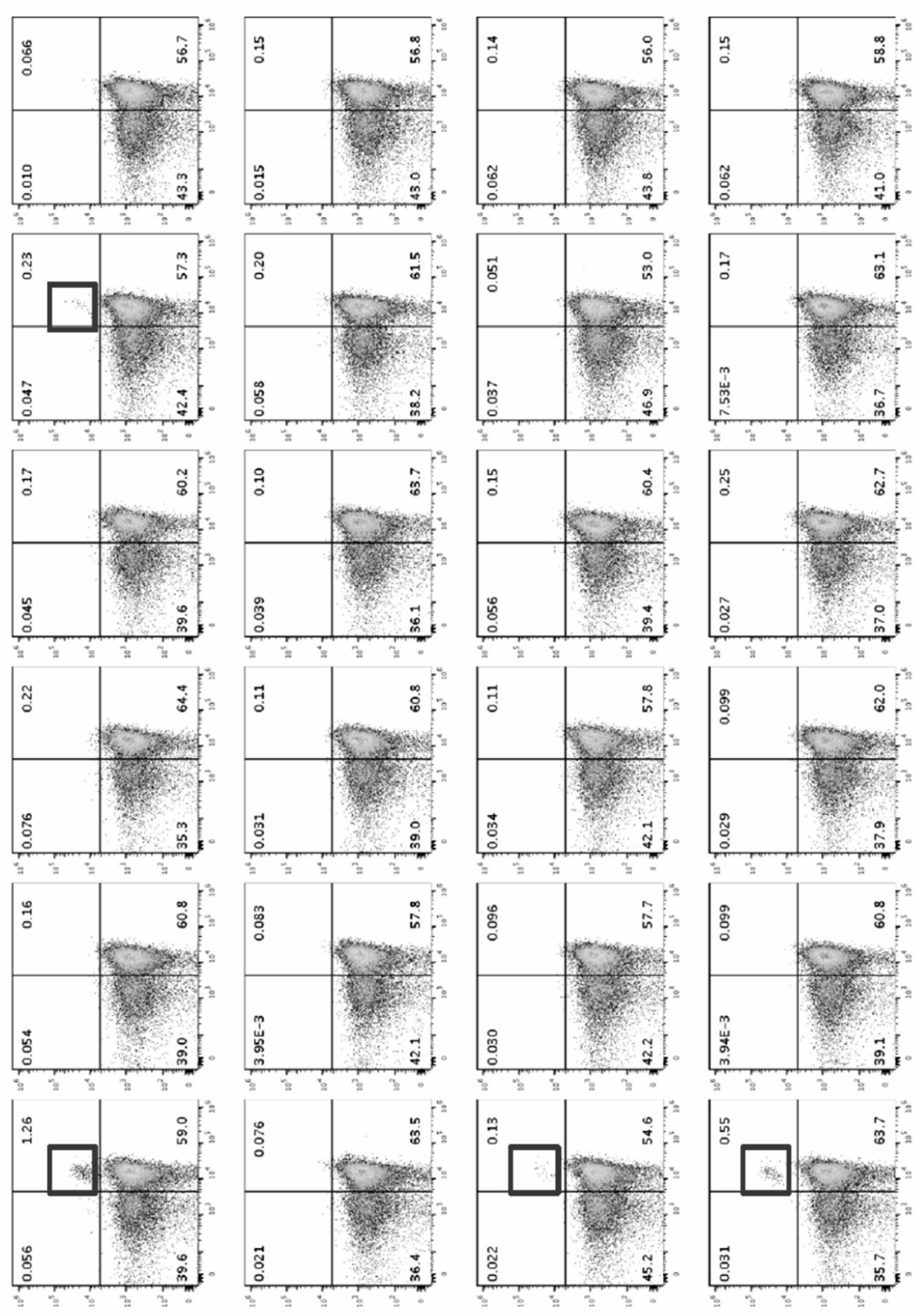

0.056
1.26
39.6
59.0
35.7
0.031
0.55
63.7
0.054
0.16
39.0
60.8
3.94E-3
0.099
39.1
60.8
0.076
0.22
35.3
64.4
0.030
0.096
42.2
57.7
0.034
0.11
37.9
62.0
0.045
0.17
39.6
60.2
0.029
0.099
42.1
57.8
0.039
0.10
36.1
63.7
0.056
0.15
39.4
60.4
0.027
0.25
37.0
62.7
0.047
0.23
42.4
57.3
0.037
0.051
46.9
53.0
0.058
0.20
38.2
61.5
0.037
0.14
43.8
56.0
7.53E-3
0.17
36.7
63.1
0.010
0.066
43.3
56.7
0.015
0.15
43.0
56.8
0.062
0.14
43.8
56.0
0.062
0.15
41.0
58.8
0.021
0.076
36.4
63.5
3.95E-3
0.083
42.1
57.8
0.031
0.11
39.0
60.8
0.022
0.13
45.2
54.6
0.030
0.096
42.2
57.7
0.034
0.11
42.1
57.8
0.039
0.10
36.1
63.7
0.056
0.15
39.4
60.4
0.027
0.25
37.0
62.7
0.058
0.20
38.2
61.5
0.037
0.14
43.8
56.0
7.53E-3
0.17
36.7
63.1
0.015
0.15
43.0
56.8
0.062
0.14
43.8
56.0
0.062
0.15
41.0
58.8

FIG. 22

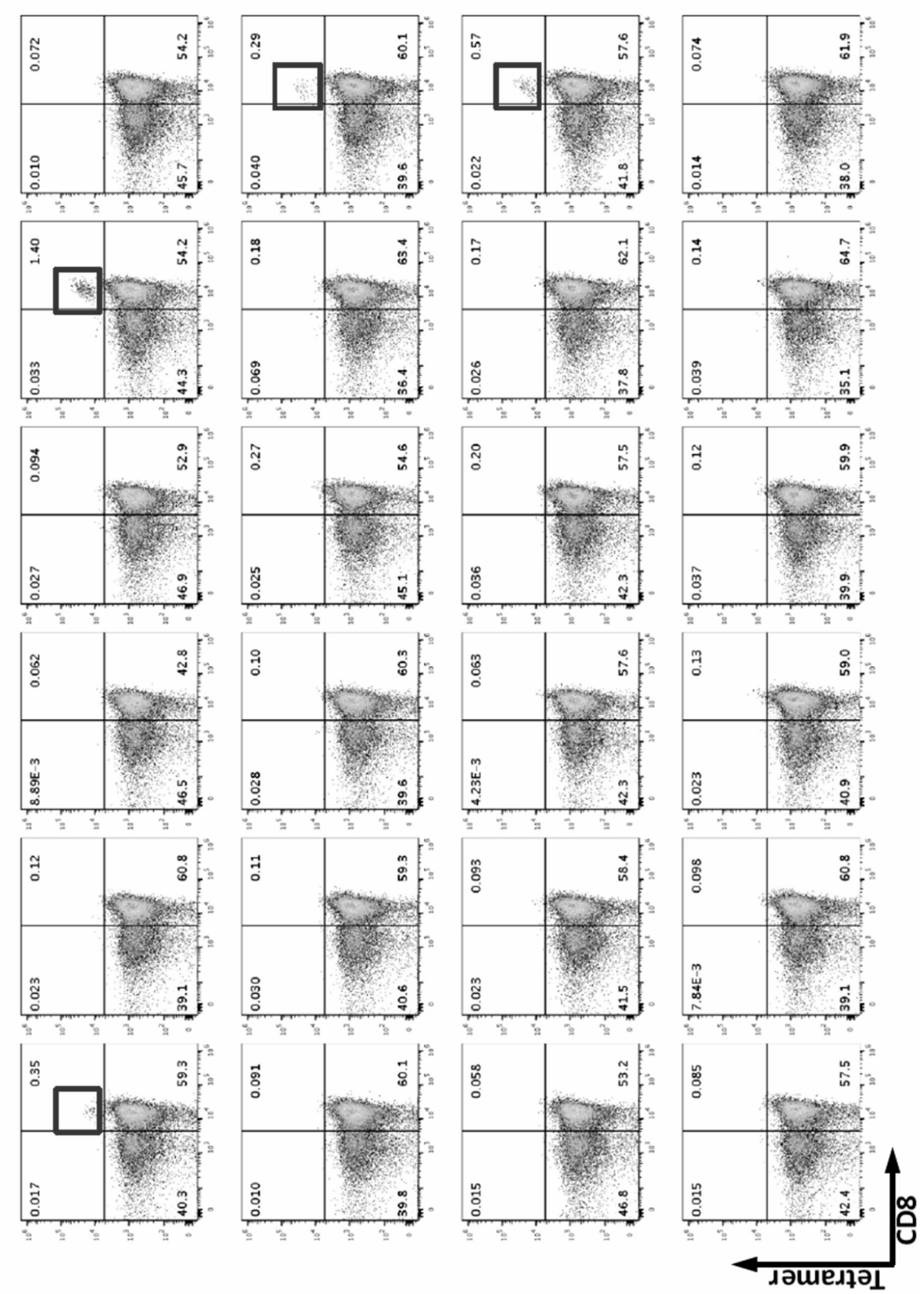


FIG. 22 Continued

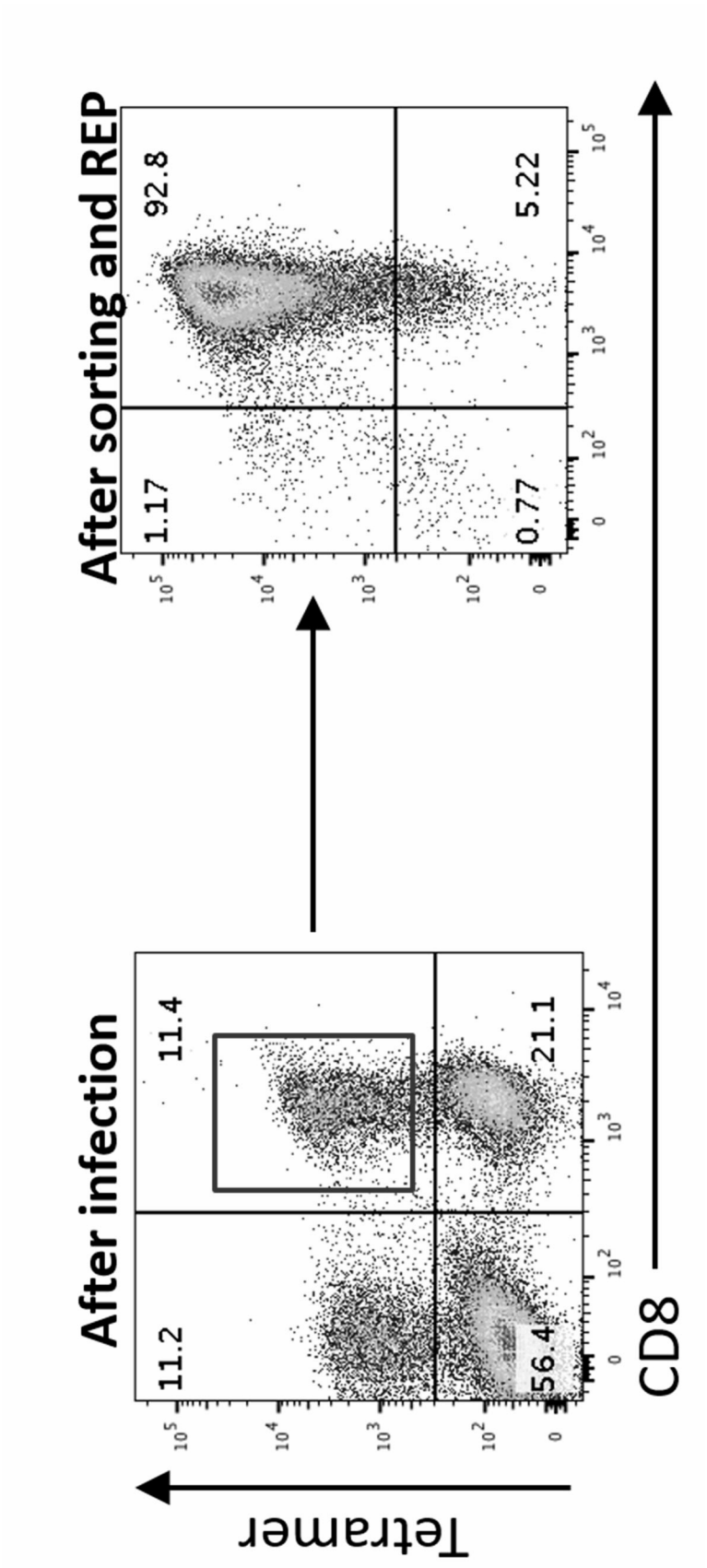

After infection
11.2
11.4
56.4
21.1
After sorting and REP
1.17
92.8
0.77
5.22
Tetramer
CD8

FIG. 23

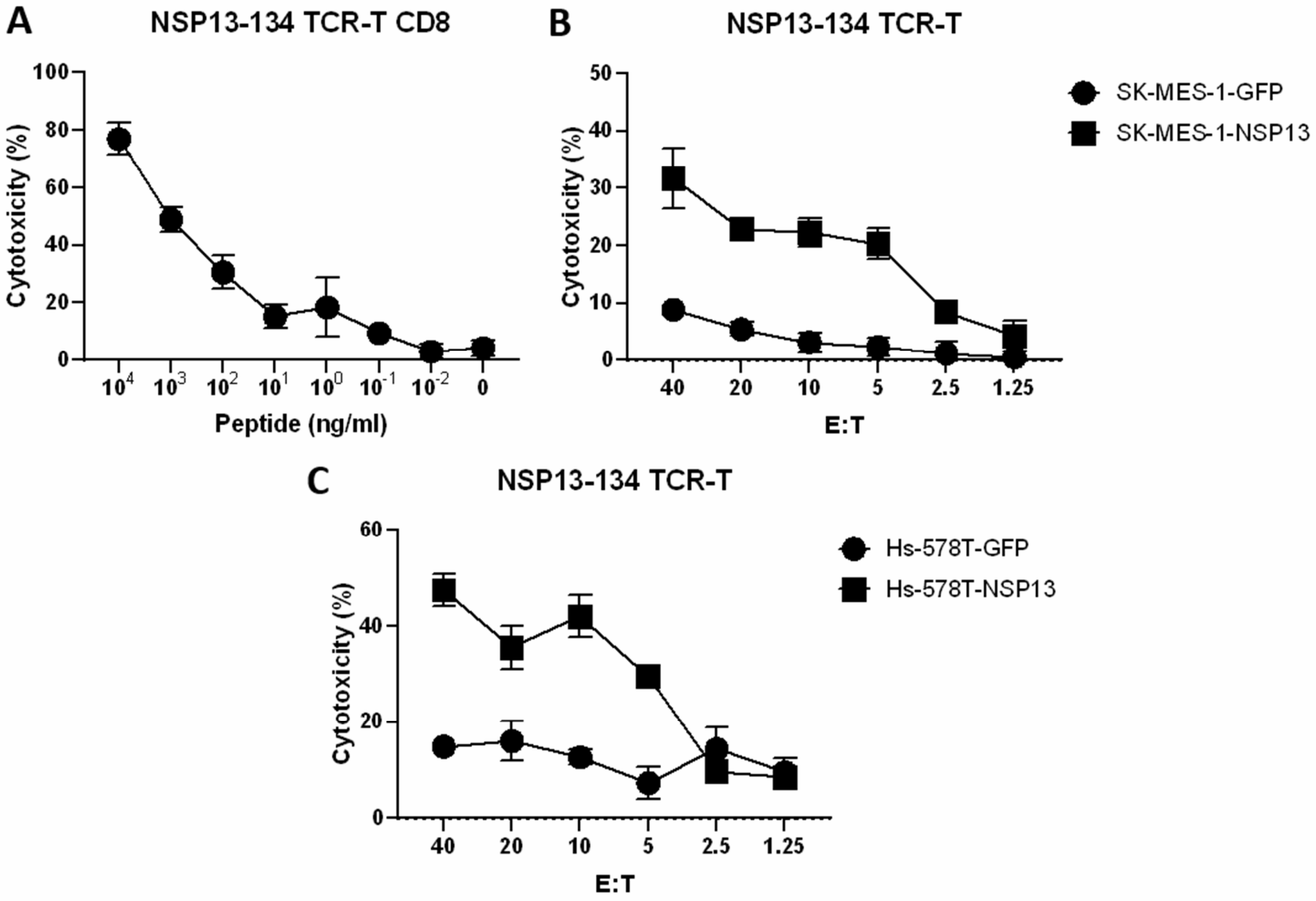

A
NSP13-134 TCR-T CD8
Cytotoxicity (%)
100
80
60
40
20
0
10^4 10^3 10^2 10^1 10^0 10^-1 10^-2 0
Peptide (ng/ml)
B
NSP13-134 TCR-T
Cytotoxicity (%)
50
40
30
20
10
0
40 20 10 5 2.5 1.25
E:T
SK-MES-1-GFP
SK-MES-1-NSP13
C
NSP13-134 TCR-T
Cytotoxicity (%)
60
40
20
0
40 20 10 5 2.5 1.25
E:T
Hs-578T-GFP
Hs-578T-NSP13

FIG. 24A-C

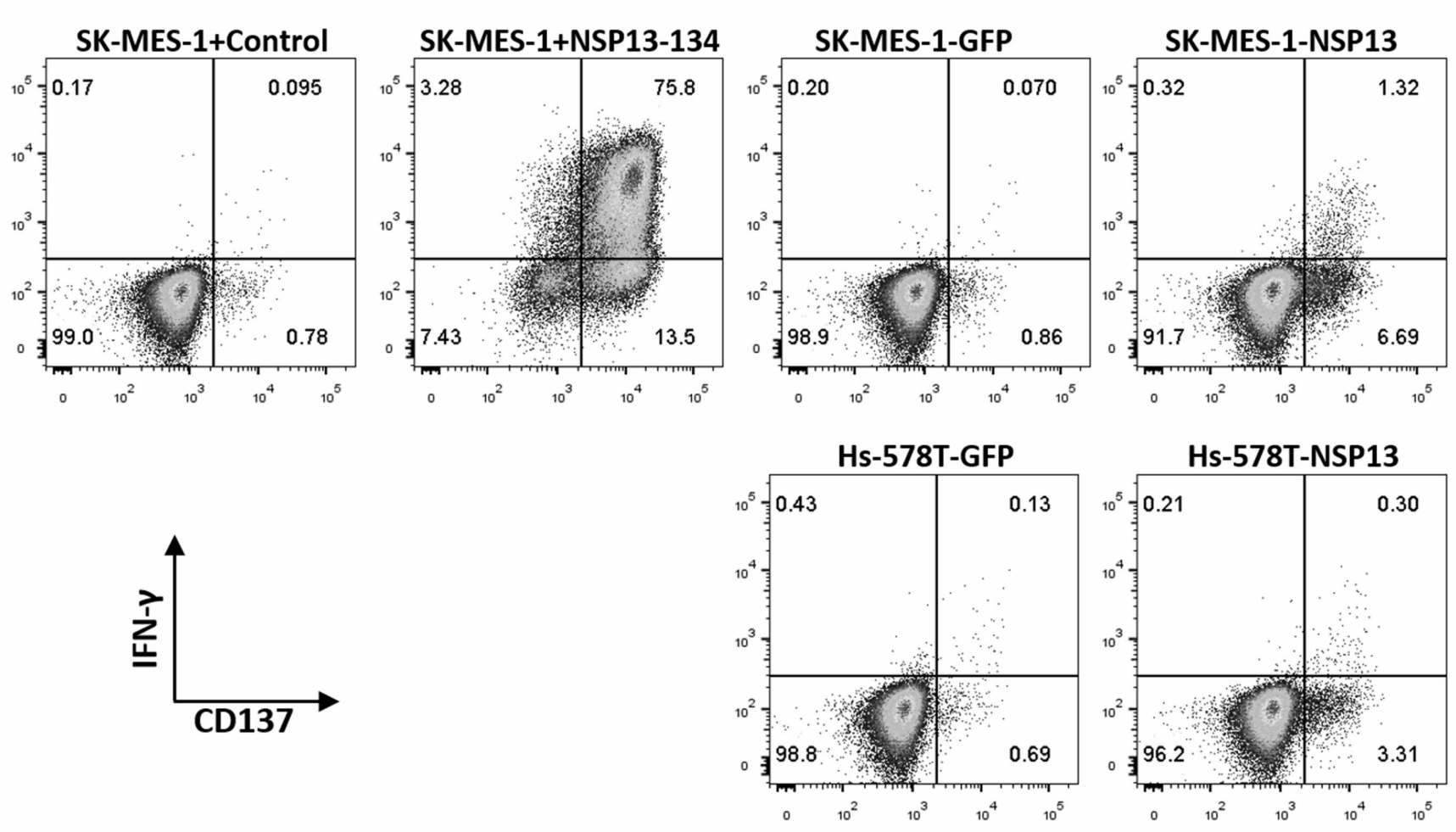

SK-MES-1+Control
0.17
0.095
99.0
0.78
SK-MES-1+NSP13-134
3.28
75.8
7.43
13.5
SK-MES-1-GFP
0.20
0.070
98.9
0.86
SK-MES-1-NSP13
0.32
1.32
91.7
6.69
Hs-578T-GFP
0.43
0.13
98.8
0.69
Hs-578T-NSP13
0.21
0.30
96.2
3.31
IFN-γ
CD137

FIG. 25

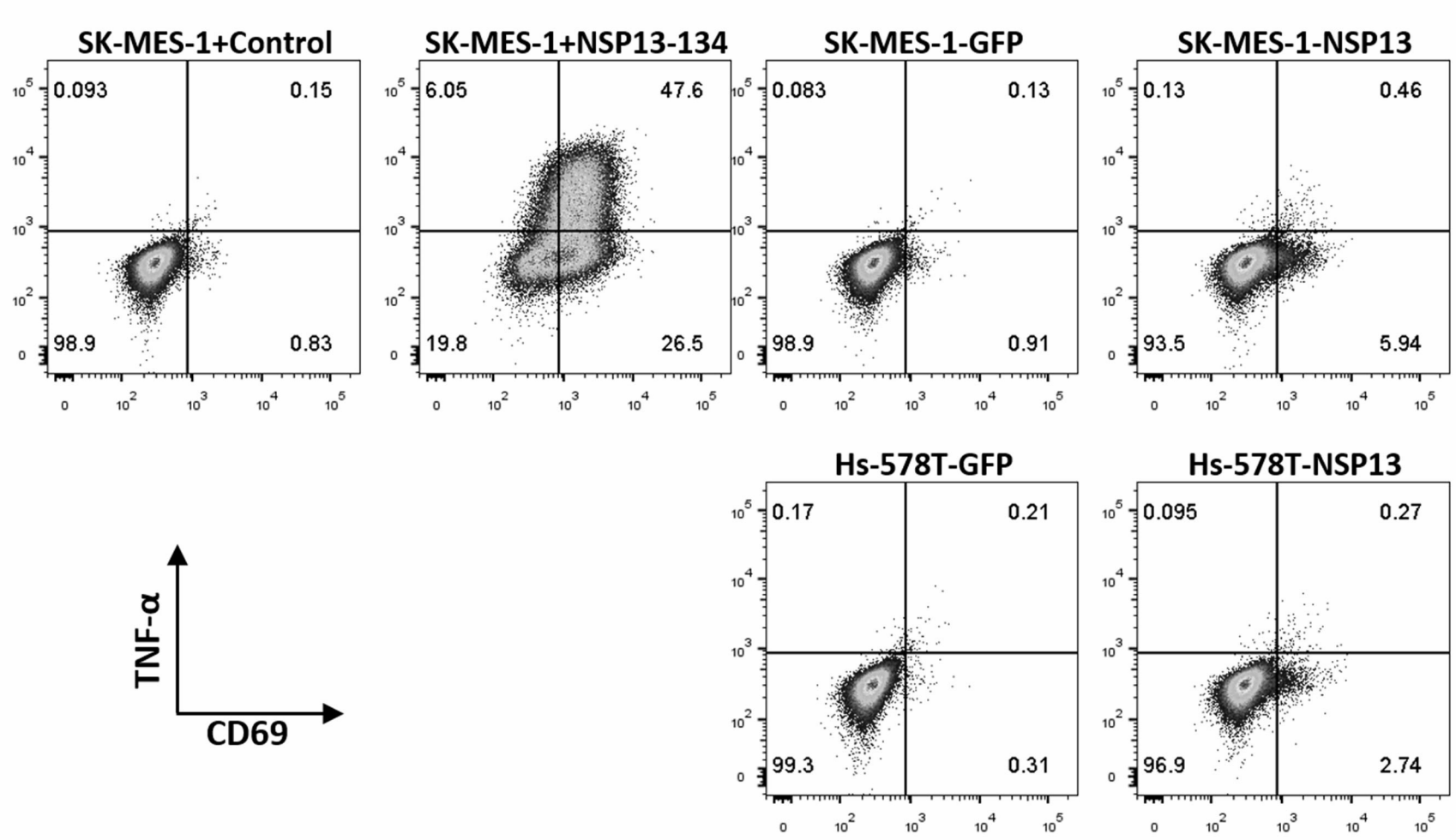


FIG. 25 (continued)

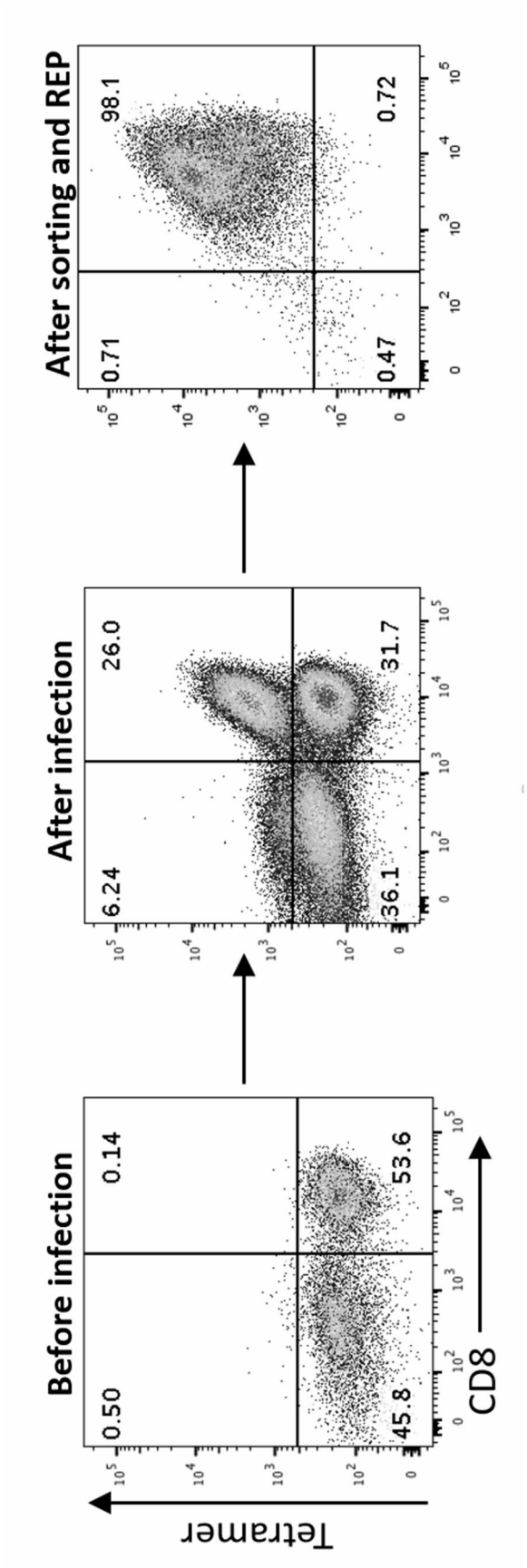

Before infection
0.50
0.14
45.8
53.6
Tetramer
CD8
After infection
6.24
26.0
36.1
31.7
After sorting and REP
0.71
98.1
0.47
0.72

FIG. 26

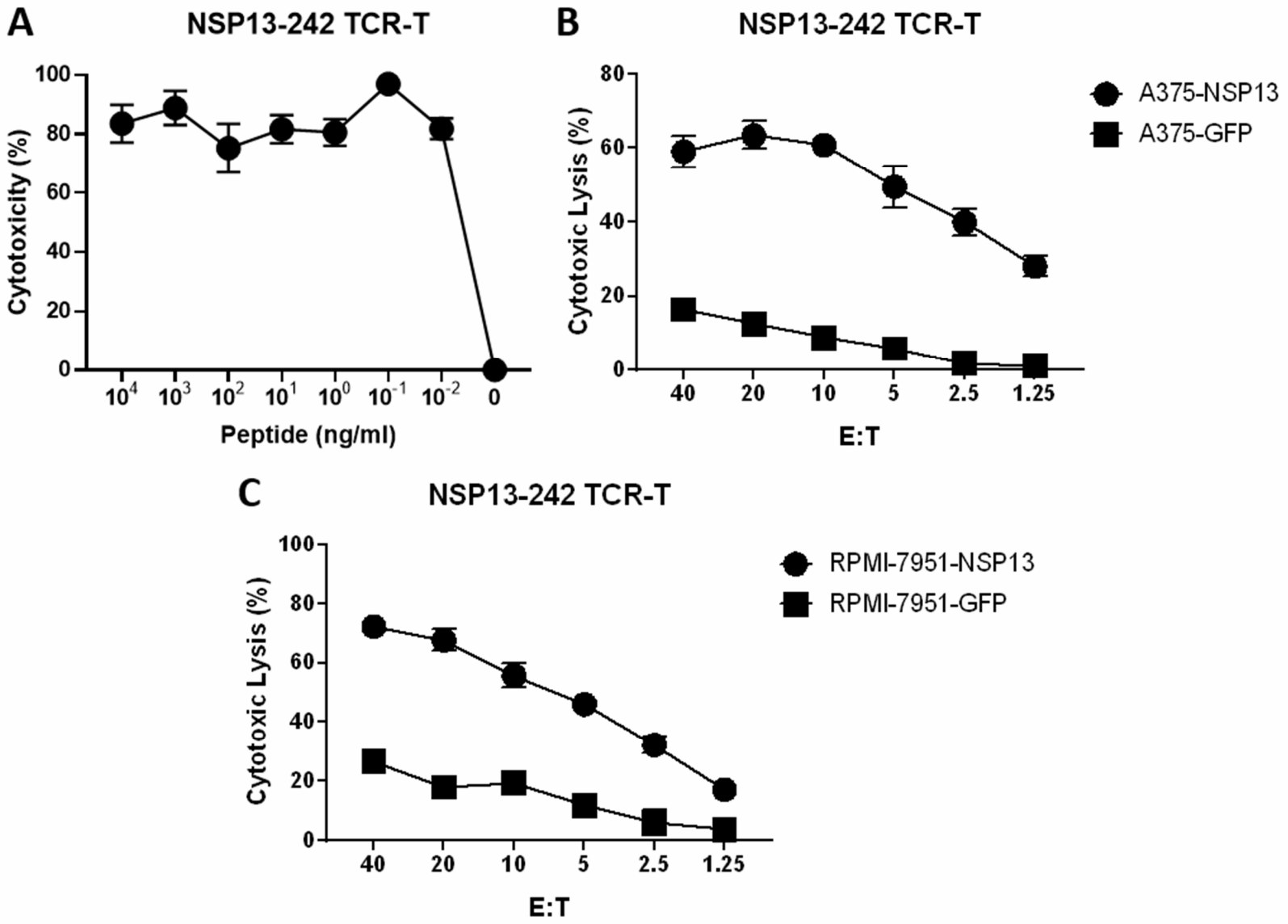

A
NSP13-242 TCR-T
Cytotoxicity (%)
100
80
60
40
20
0
10^4 10^3 10^2 10^1 10^0 10^{-1} 10^{-2} 0
Peptide (ng/ml)
B
NSP13-242 TCR-T
Cytotoxic Lysis (%)
80
60
40
20
0
40 20 10 5 2.5 1.25
E:T
A375-NSP13
A375-GFP
C
NSP13-242 TCR-T
Cytotoxic Lysis (%)
100
80
60
40
20
0
40 20 10 5 2.5 1.25
E:T
RPMI-7951-NSP13
RPMI-7951-GFP

FIG. 27A-C

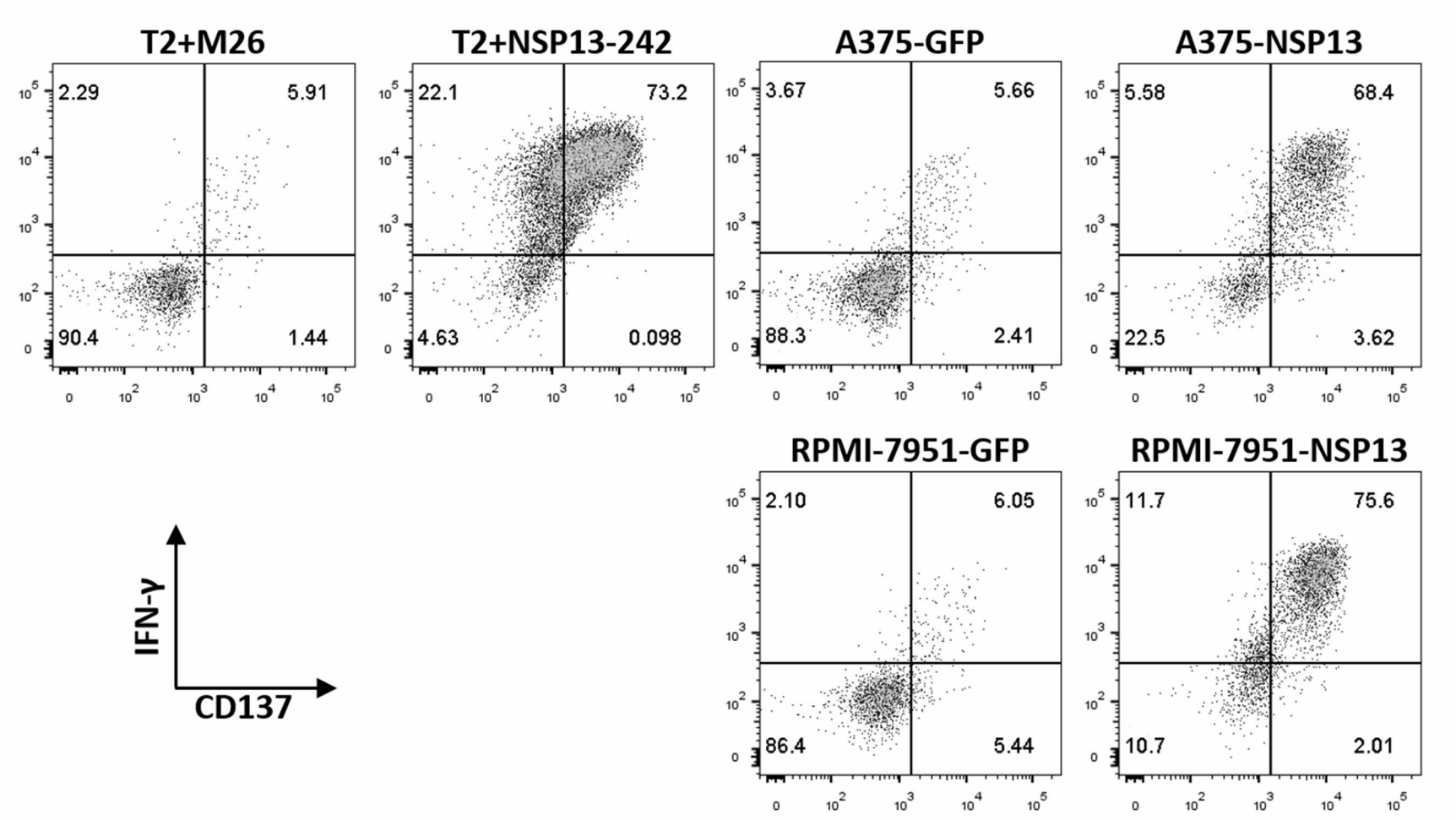

T2+M26
2.29
5.91
90.4
1.44
T2+NSP13-242
22.1
73.2
4.63
0.098
A375-GFP
3.67
5.66
88.3
2.41
A375-NSP13
5.58
68.4
22.5
3.62
RPMI-7951-GFP
2.10
6.05
86.4
5.44
RPMI-7951-NSP13
11.7
75.6
10.7
2.01
IFN-γ
CD137

FIG. 28

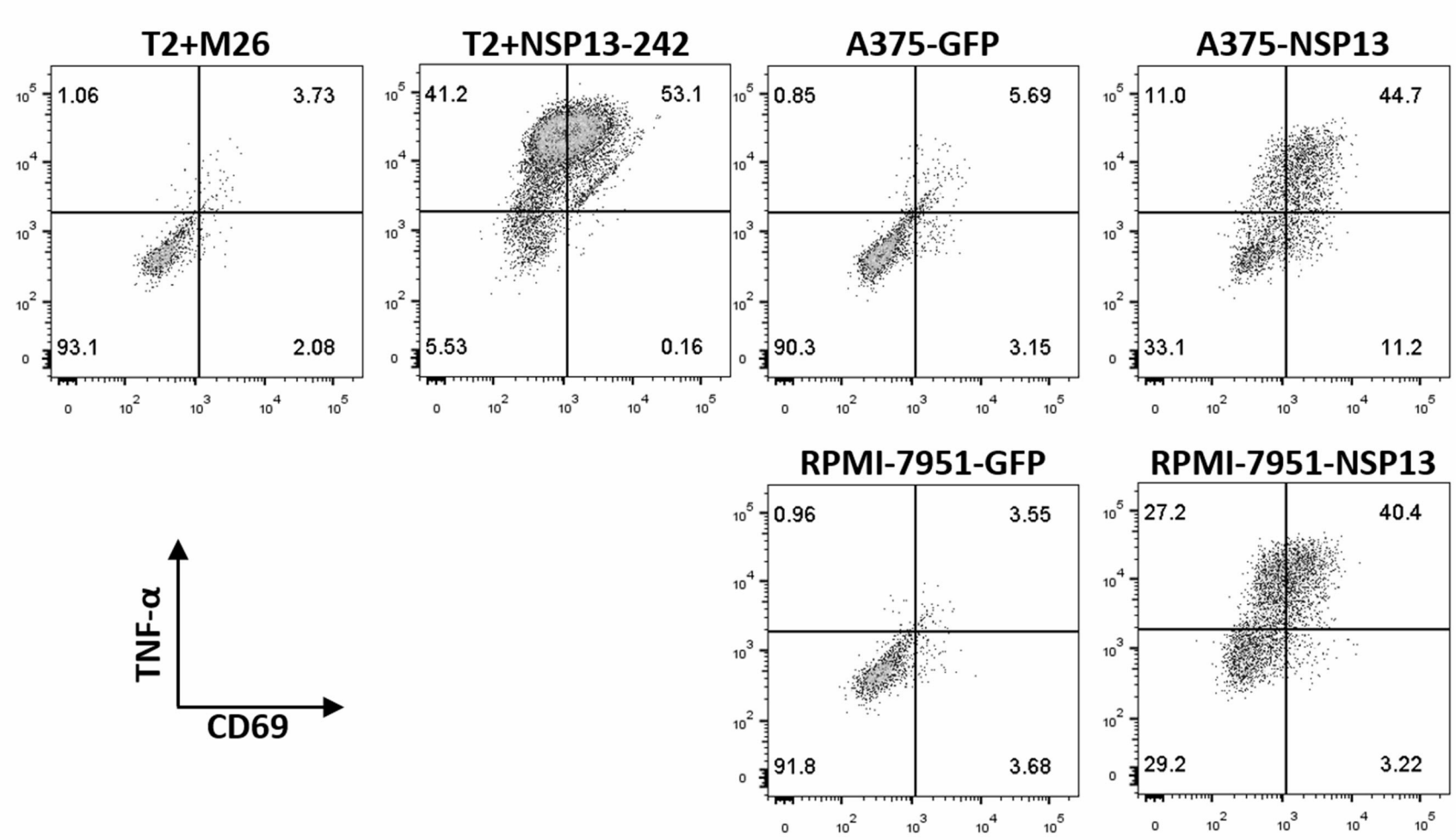


FIG. 28 (Continued)

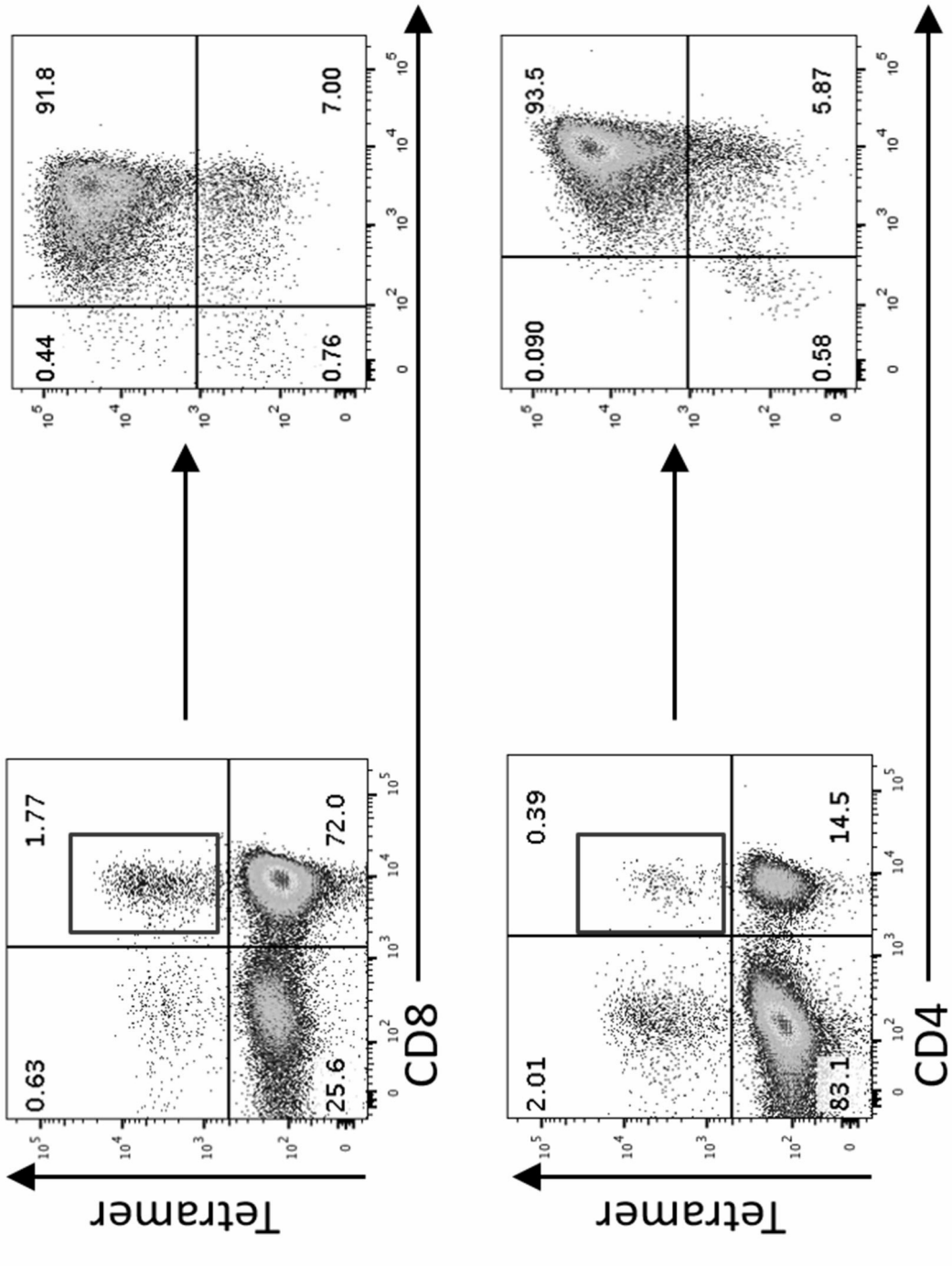

Tetramer
CD8
0.63
1.77
25.6
72.0
0.44
91.8
0.76
7.00
Tetramer
CD4
2.01
0.39
83.1
14.5
0.090
93.5
0.58
5.87

FIG. 29

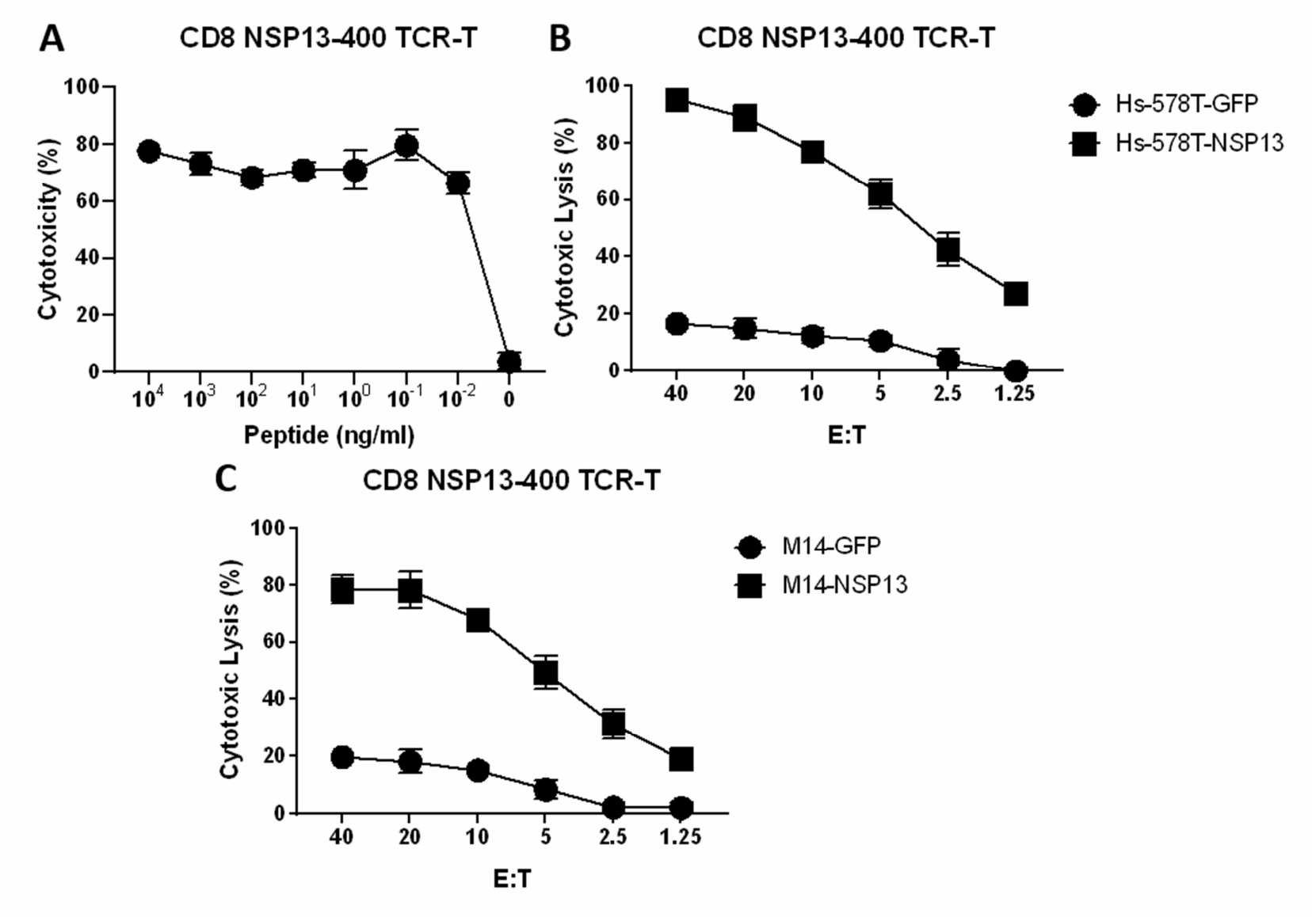

A
CD8 NSP13-400 TCR-T
Cytotoxicity (%)
100
80
60
40
20
0
10^4 10^3 10^2 10^1 10^0 10^-1 10^-2 0
Peptide (ng/ml)
B
CD8 NSP13-400 TCR-T
Cytotoxic Lysis (%)
100
80
60
40
20
0
40 20 10 5 2.5 1.25
E:T
Hs-578T-GFP
Hs-578T-NSP13
C
CD8 NSP13-400 TCR-T
Cytotoxic Lysis (%)
100
80
60
40
20
0
40 20 10 5 2.5 1.25
E:T
M14-GFP
M14-NSP13

FIG. 30A-C

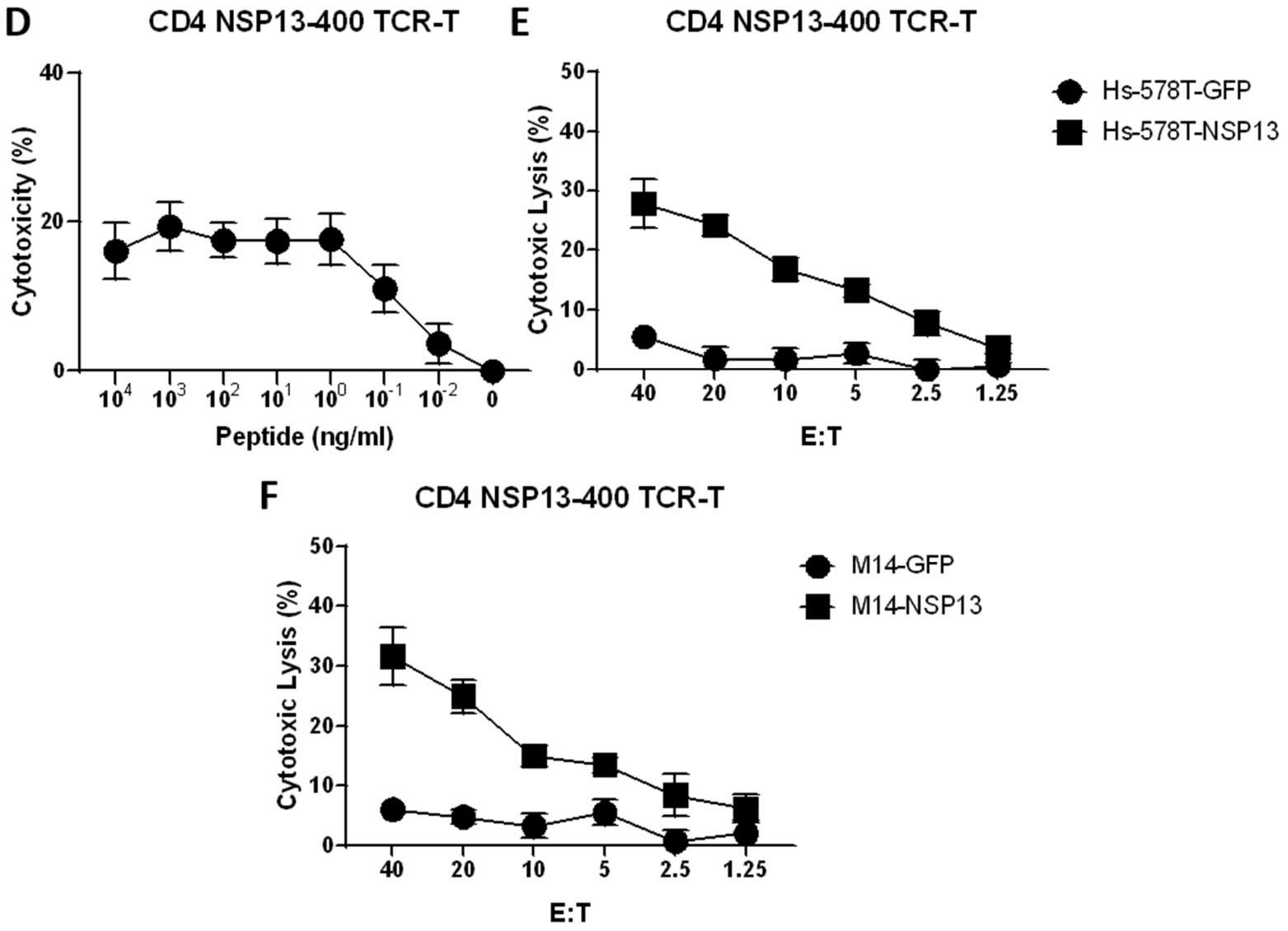

D
CD4 NSP13-400 TCR-T
Cytotoxicity (%)
40
20
0
10^4 10^3 10^2 10^1 10^0 10^{-1} 10^{-2} 0
Peptide (ng/ml)
E
CD4 NSP13-400 TCR-T
Cytotoxic Lysis (%)
50
40
30
20
10
0
40 20 10 5 2.5 1.25
E:T
Hs-578T-GFP
Hs-578T-NSP13
F
CD4 NSP13-400 TCR-T
Cytotoxic Lysis (%)
50
40
30
20
10
0
40 20 10 5 2.5 1.25
E:T
M14-GFP
M14-NSP13

FIG. 30D-F

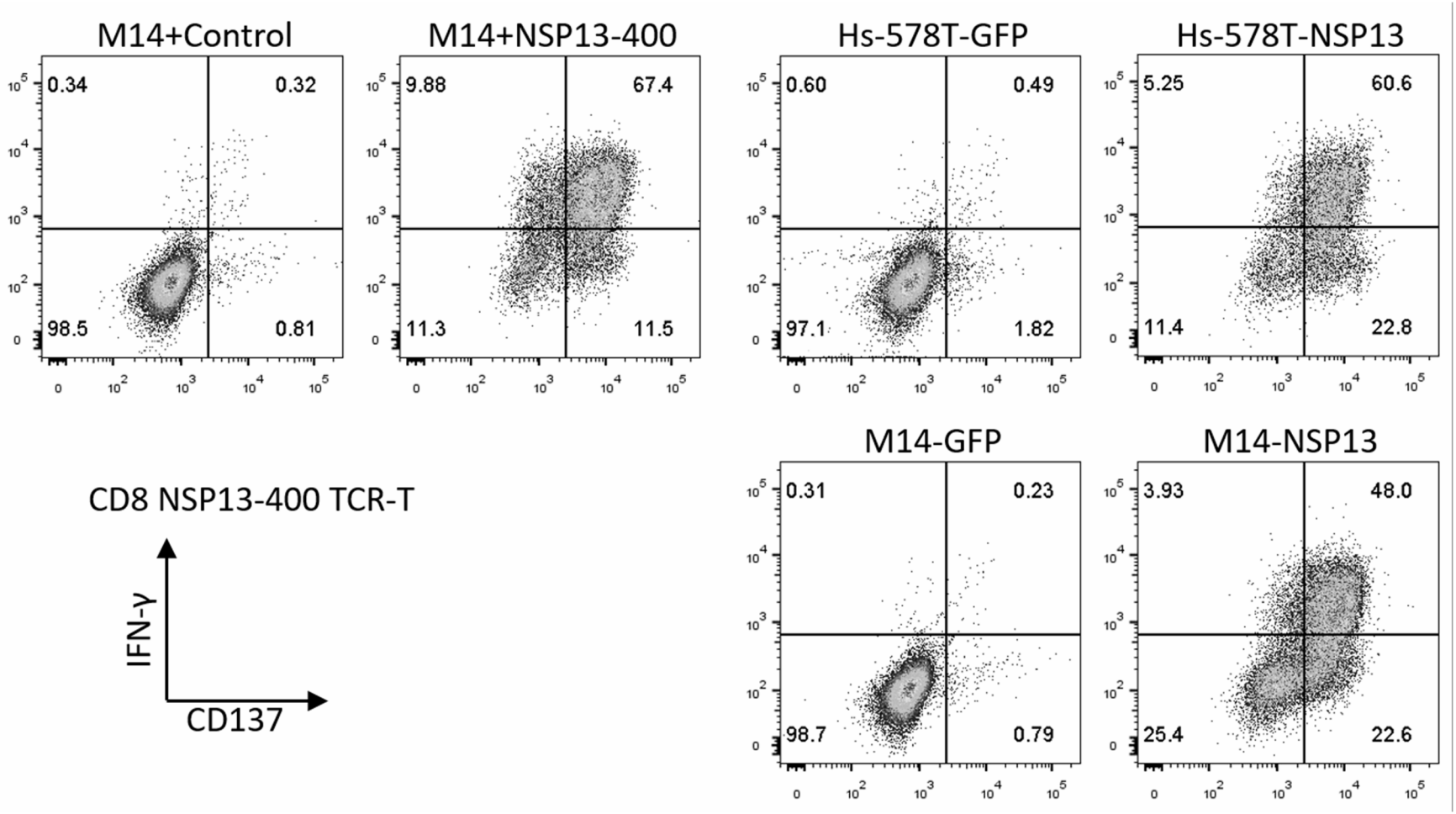

M14+Control
0.34
0.32
98.5
0.81
M14+NSP13-400
9.88
67.4
11.3
11.5
Hs-578T-GFP
0.60
0.49
97.1
1.82
Hs-578T-NSP13
5.25
60.6
11.4
22.8
M14-GFP
0.31
0.23
98.7
0.79
M14-NSP13
3.93
48.0
25.4
22.6
CD8 NSP13-400 TCR-T
IFN-γ
CD137

FIG. 31

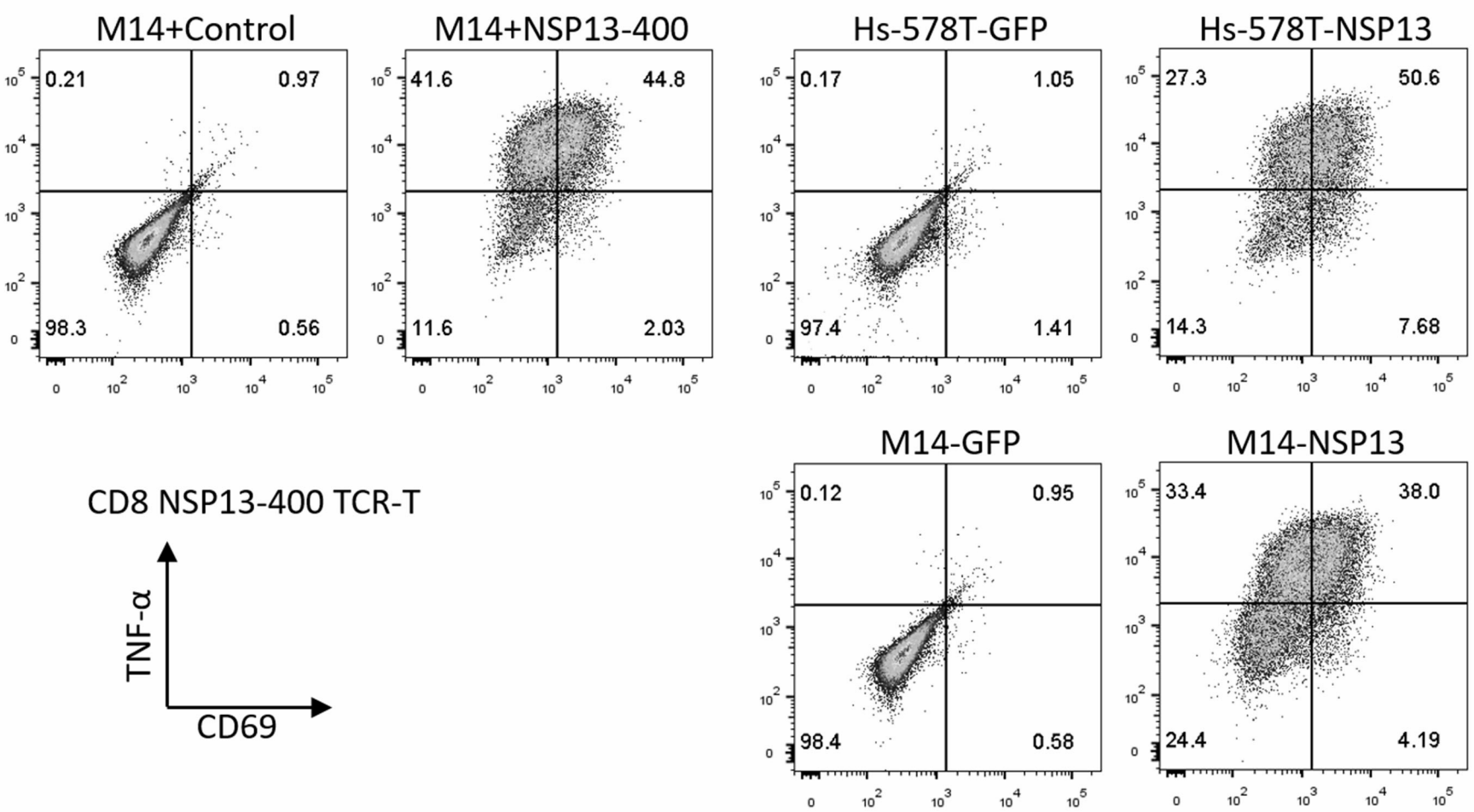


FIG. 31 (continued)

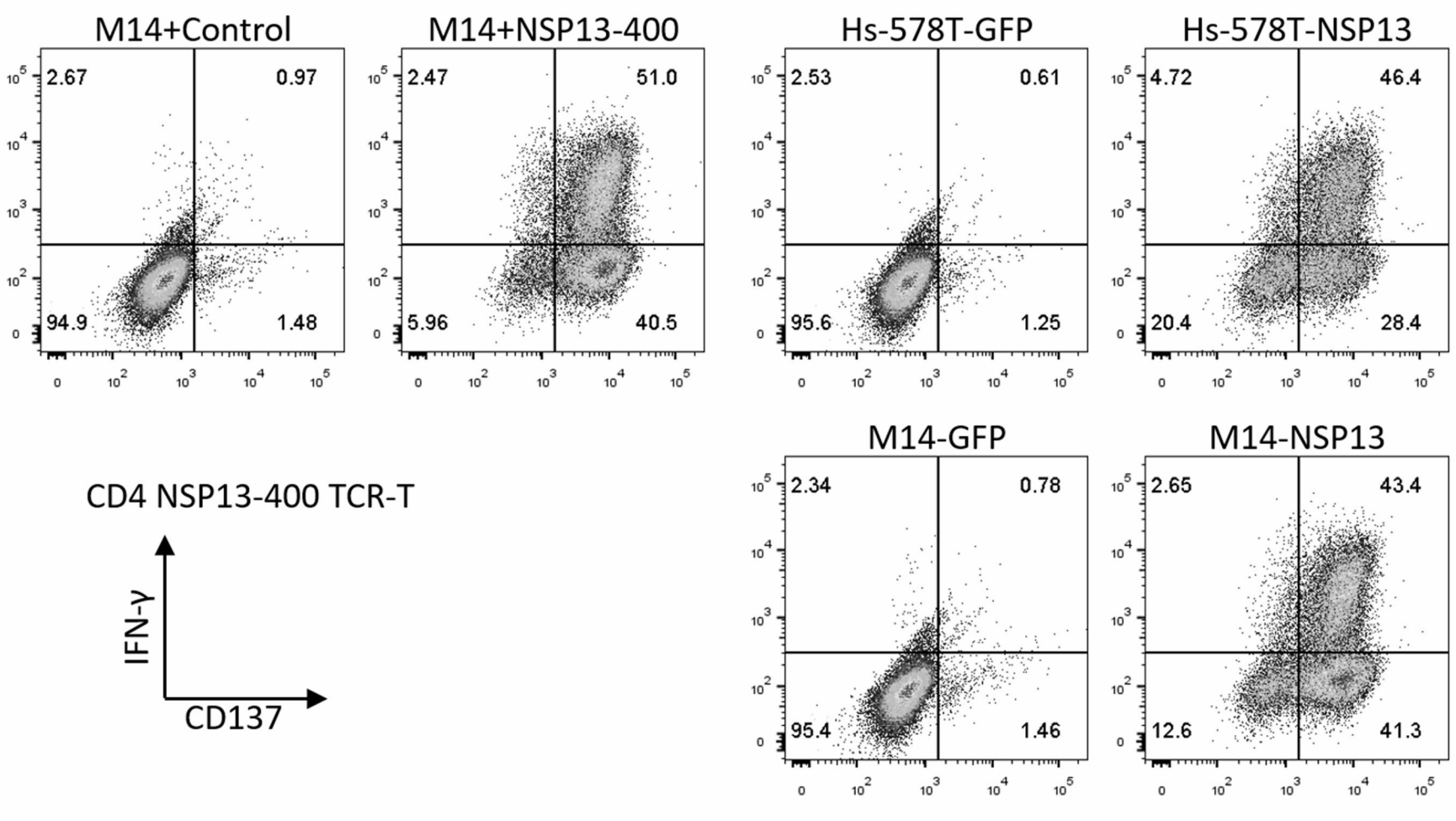


FIG. 31 (continued)

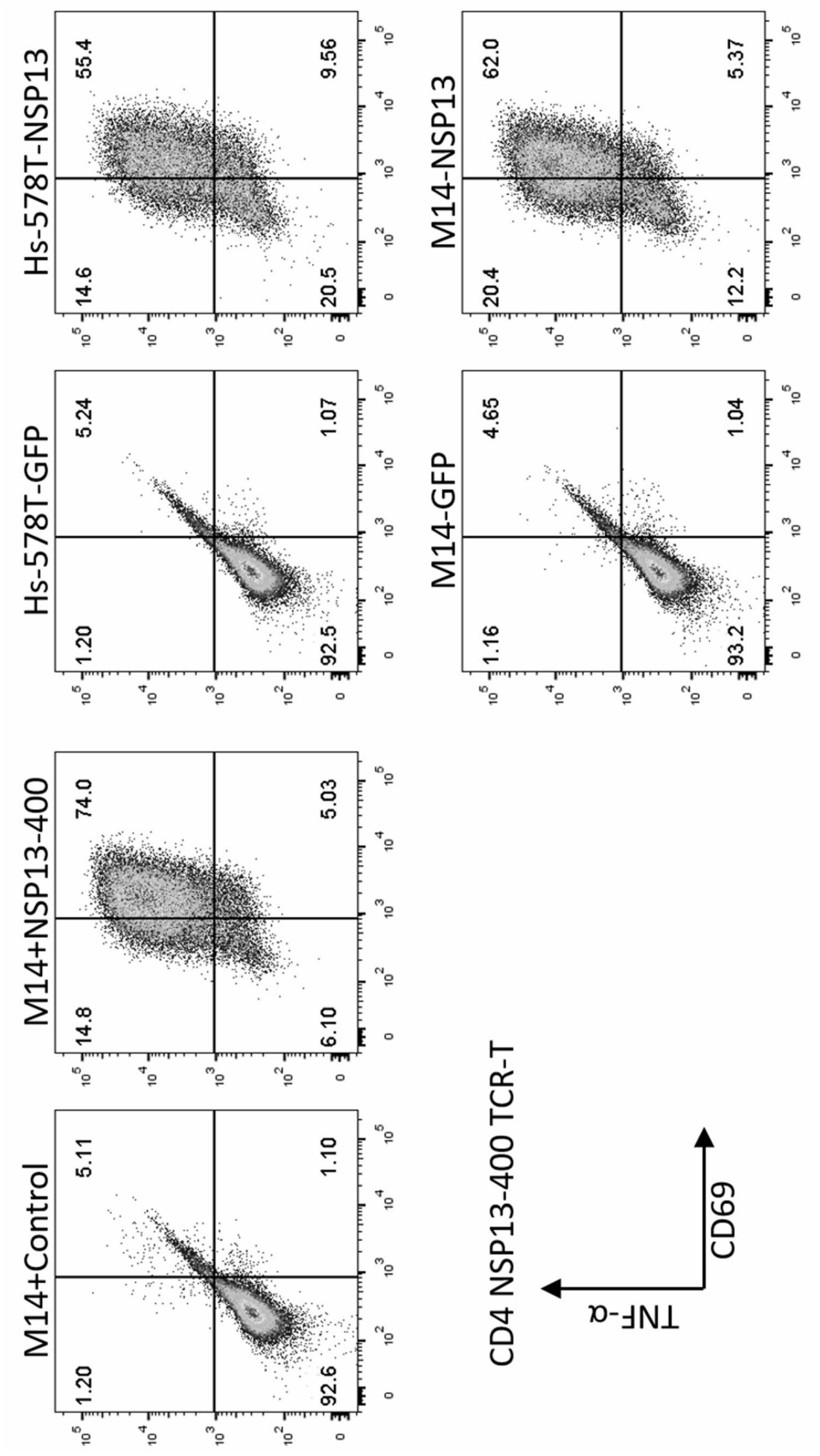


FIG. 31 (continued)

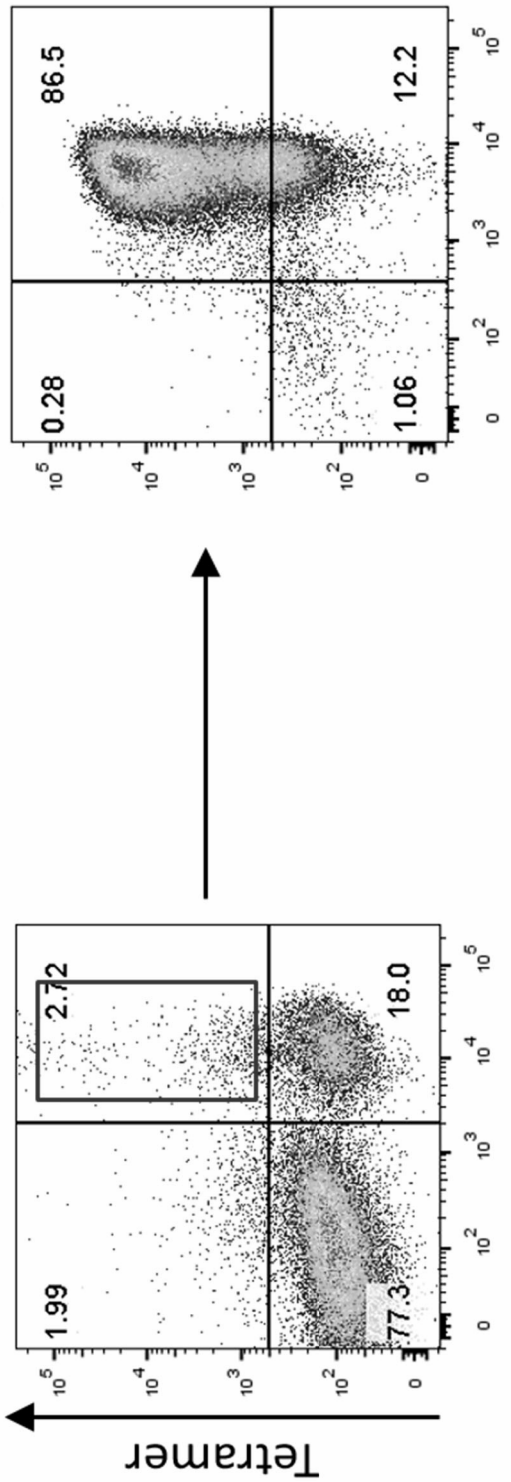

After infection
Tetramer
1.99
2.72
77.3
18.0
After sorting and REP
0.28
86.5
1.06
12.2

FIG. 32

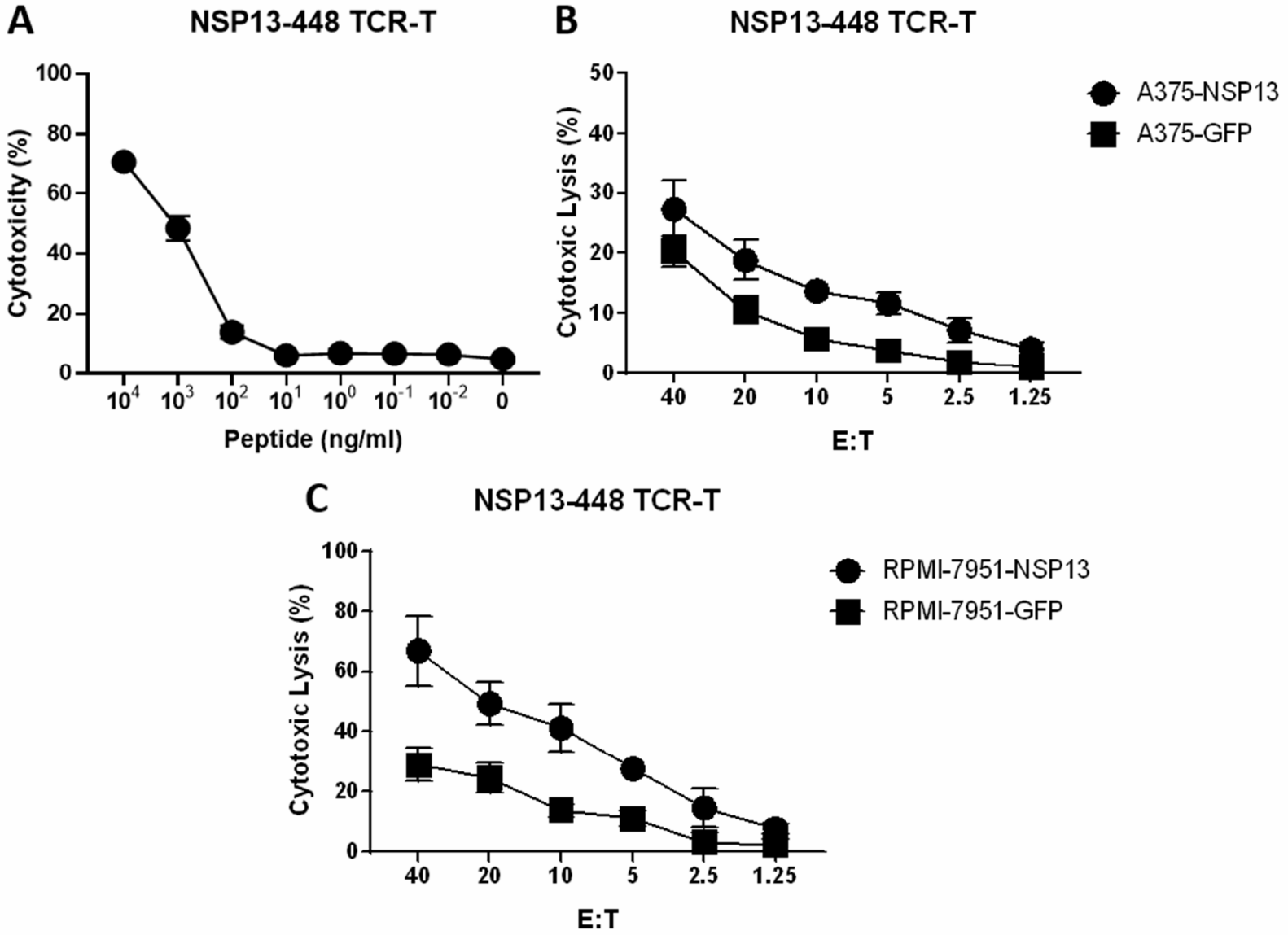

A
NSP13-448 TCR-T
Cytotoxicity (%)
100
80
60
40
20
0
10^4 10^3 10^2 10^1 10^0 10^{-1} 10^{-2} 0
Peptide (ng/ml)
B
NSP13-448 TCR-T
Cytotoxic Lysis (%)
50
40
30
20
10
0
40 20 10 5 2.5 1.25
E:T
A375-NSP13
A375-GFP
C
NSP13-448 TCR-T
Cytotoxic Lysis (%)
100
80
60
40
20
0
40 20 10 5 2.5 1.25
E:T
RPMI-7951-NSP13
RPMI-7951-GFP

FIG. 33A-C

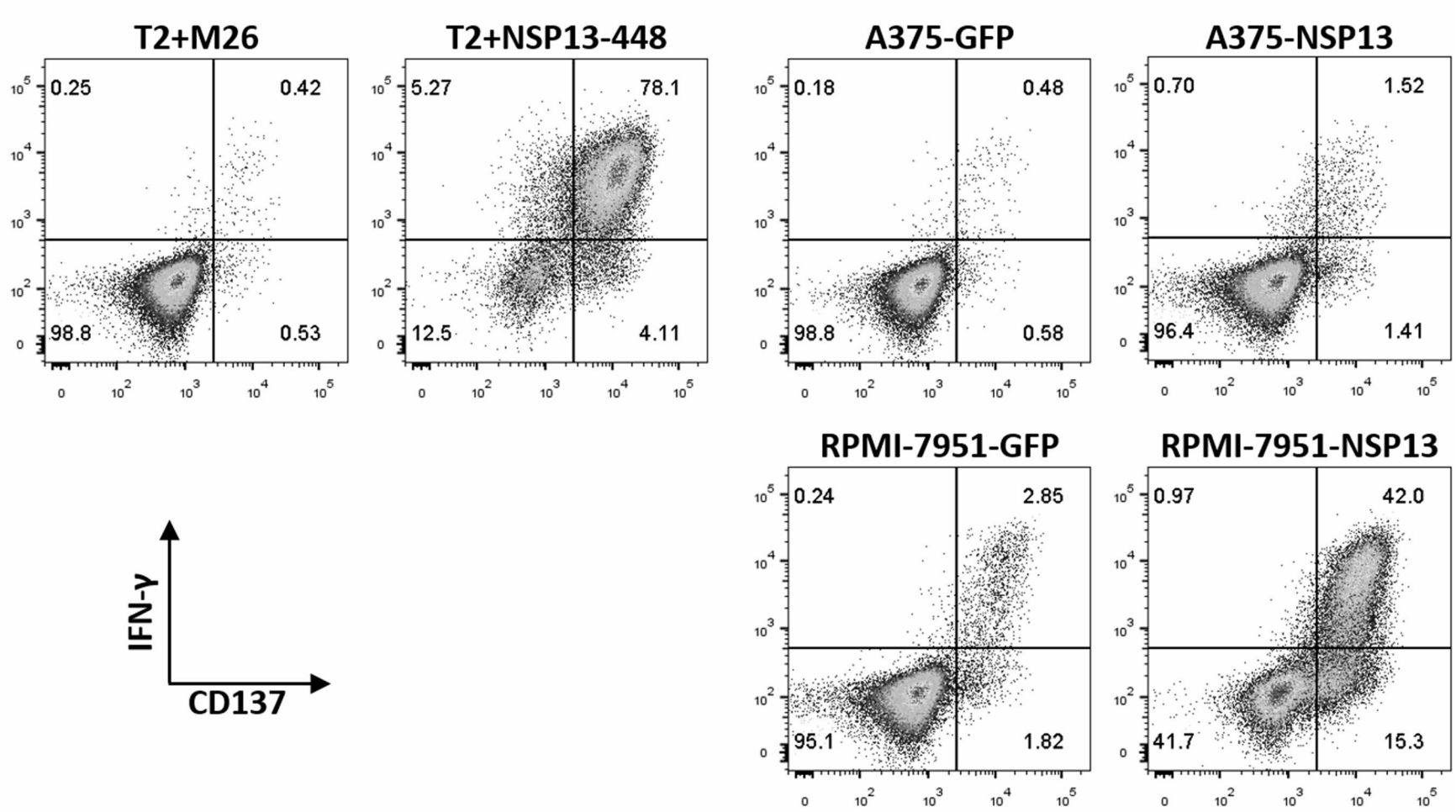

T2+M26
0.25
0.42
98.8
0.53
T2+NSP13-448
5.27
78.1
12.5
4.11
A375-GFP
0.18
0.48
98.8
0.58
A375-NSP13
0.70
1.52
96.4
1.41
RPMI-7951-GFP
0.24
2.85
95.1
1.82
RPMI-7951-NSP13
0.97
42.0
41.7
15.3
IFN-γ
CD137

FIG. 34

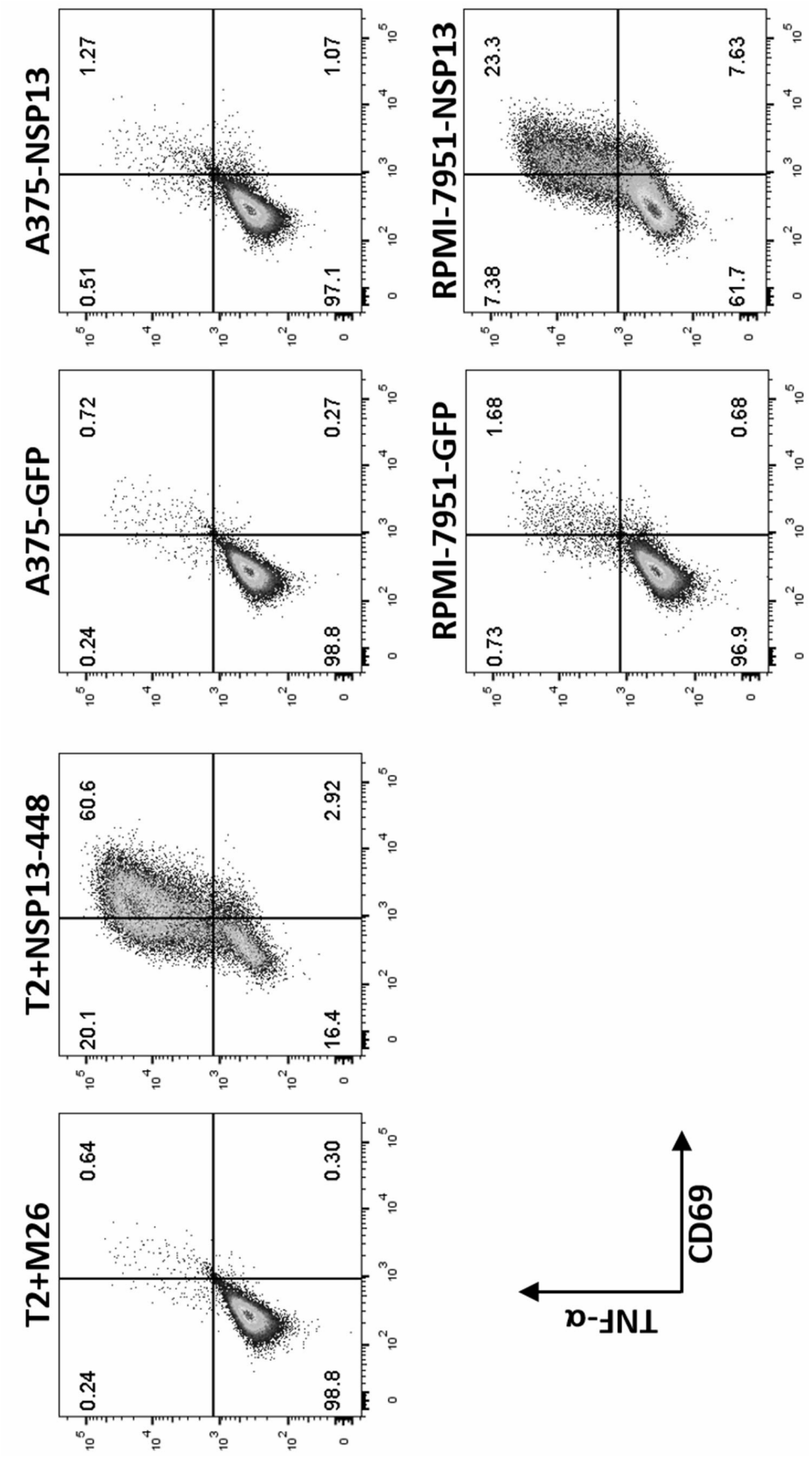


FIG. 34 (continued)