Fig. 1A

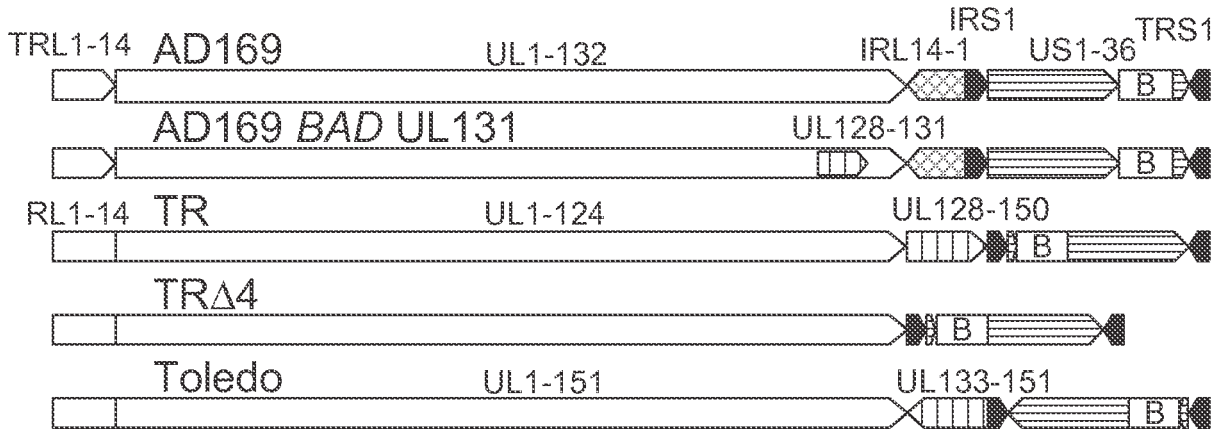

TRL1-14
AD169
UL1-132
IRS1
IRL14-1
US1-36
TRS1
B
AD169 BAD UL131
UL128-131
RL1-14
TR
UL1-124
UL128-150
TRΔ4
Toledo
UL1-151
UL133-151

Fig. 1B

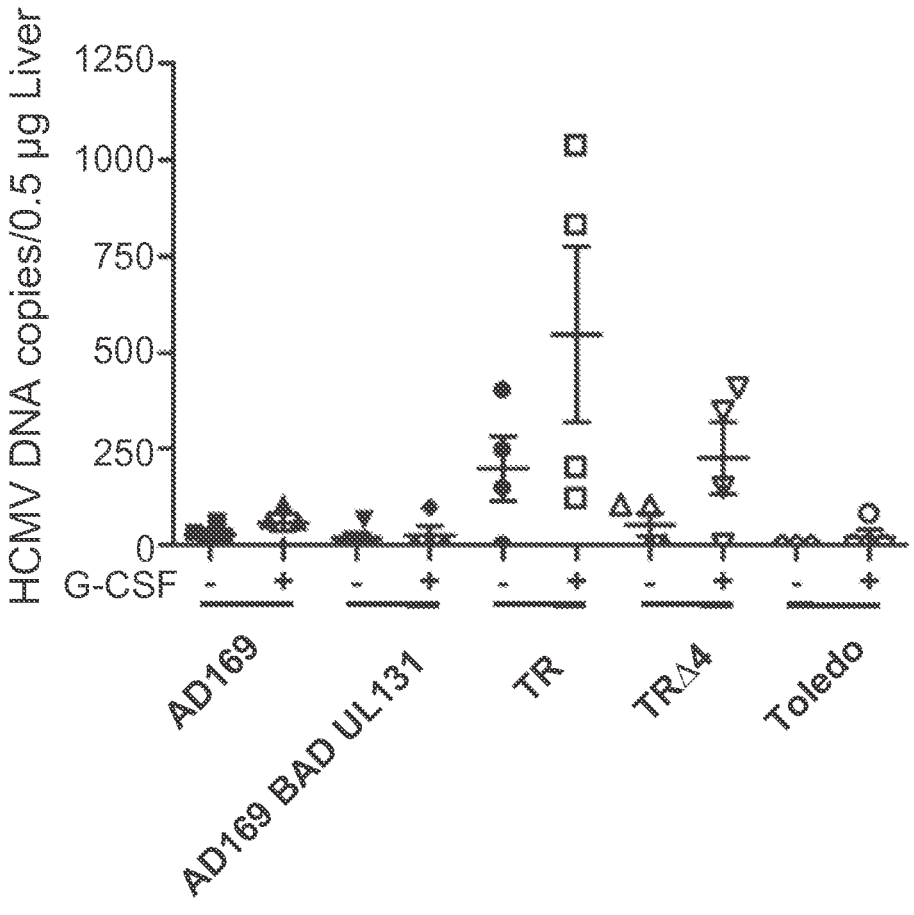

HCMV DNA copies/0.5 µg Liver
1250
1000
750
500
250
0
G-CSF
AD169
AD169 BAD UL131
TR
TRΔ4
Toledo

Fig. 2


Viral ORFs
Repeat
UL97 from HCMV AD169
US2 - US7 from HCMV AD169

Fig. 3

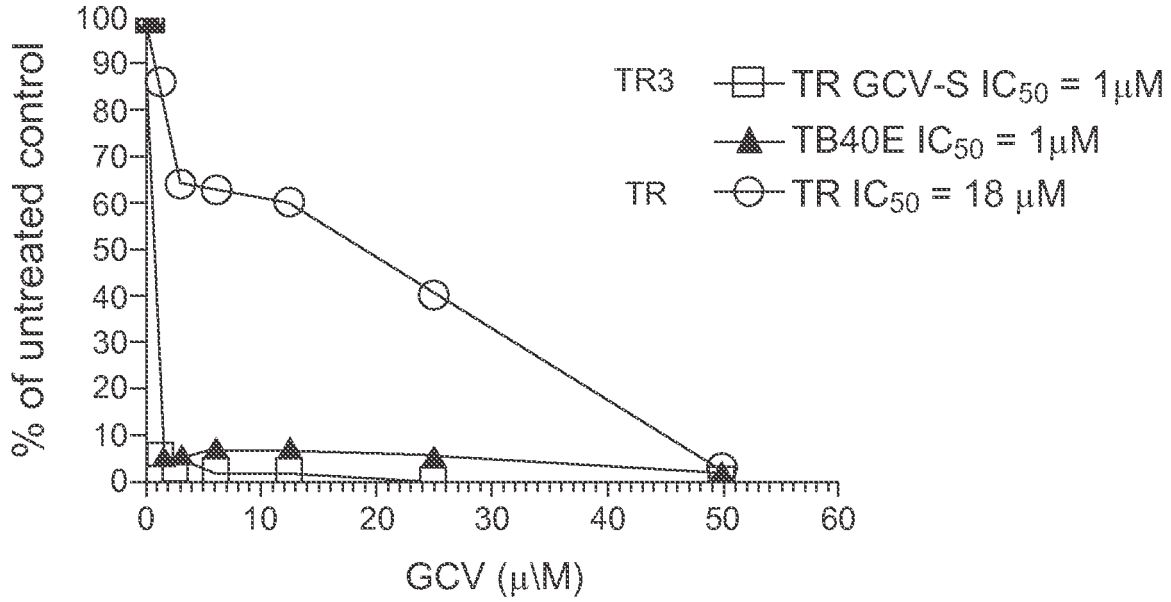

% of untreated control
100
90
80
70
60
50
40
30
20
10
0
0
10
20
30
40
50
60
GCV (μ\M)
TR3
TR GCV-S IC50 = 1μM
TB40E IC50 = 1μM
TR
TR IC50 = 18 μM

Fig. 4A

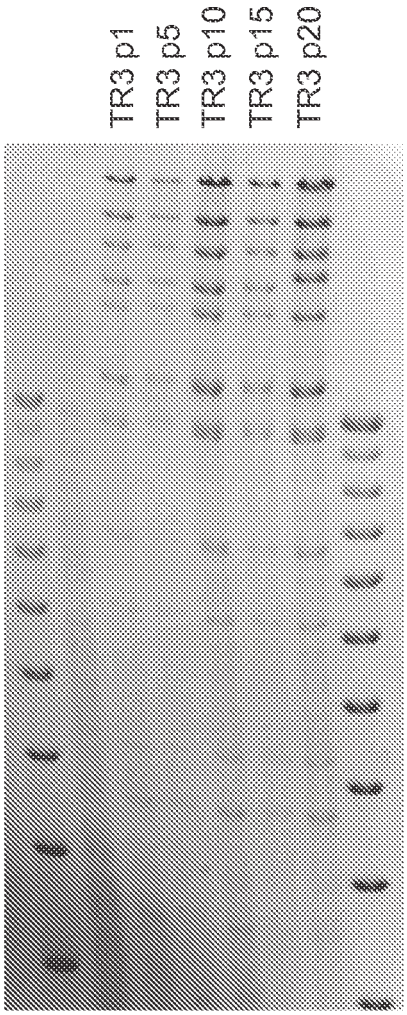


Fig. 4B

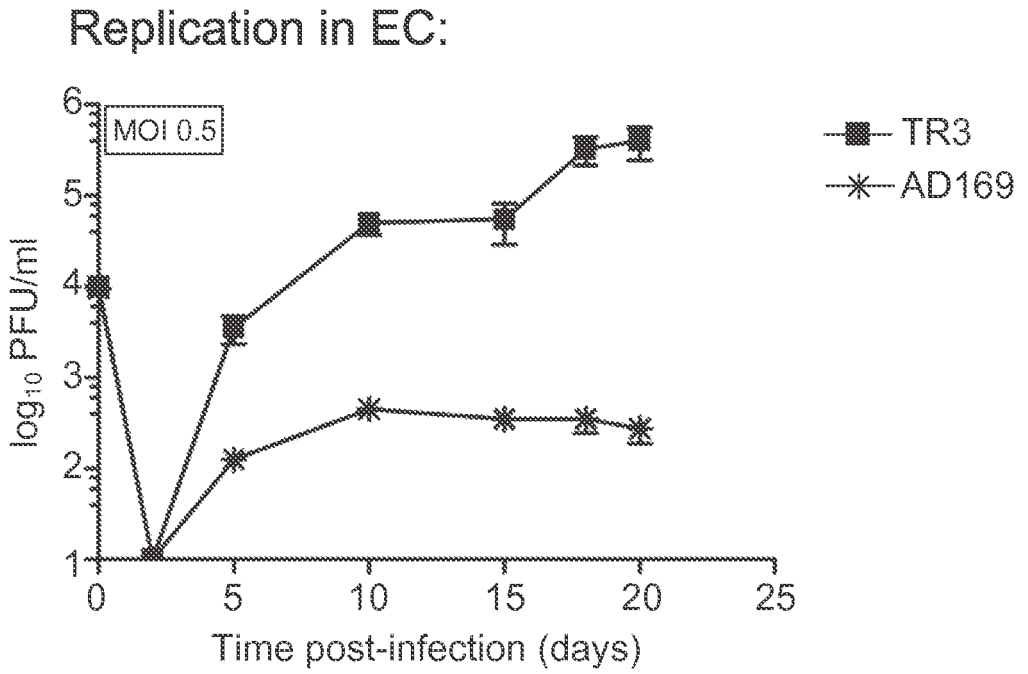

Replication in EC:
MOI 0.5
TR3
AD169
log10 PFU/ml
Time post-infection (days)
0
5
10
15
20
25
1
2
3
4
5
6

Fig. 5

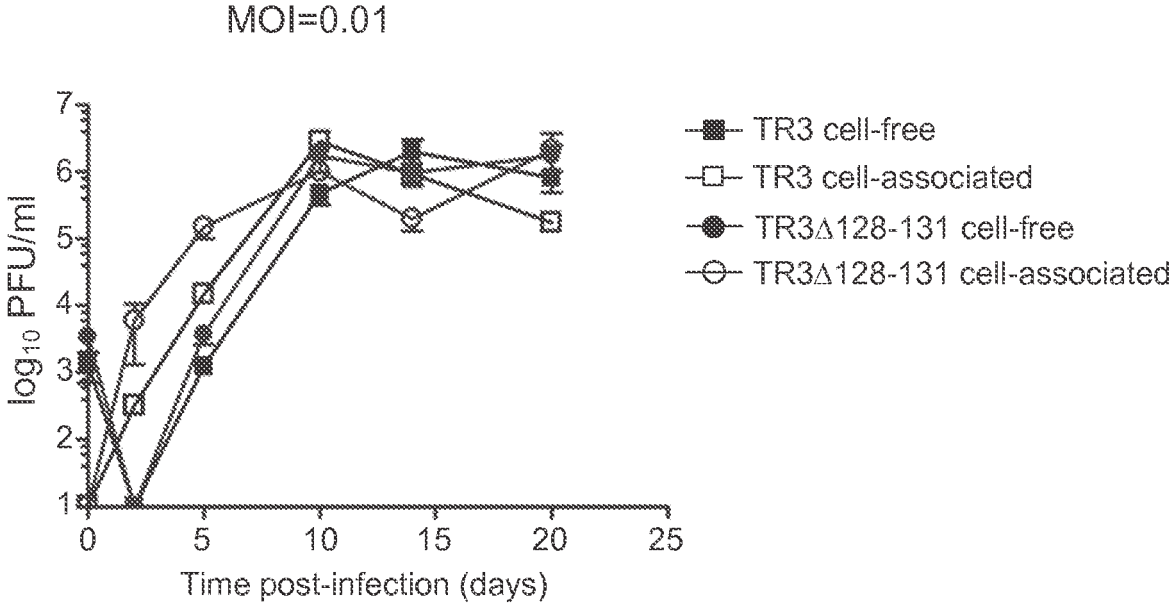

MOI=0.01
TR3 cell-free
TR3 cell-associated
TR3Δ128-131 cell-free
TR3Δ128-131 cell-associated
log10 PFU/ml
Time post-infection (days)
0
5
10
15
20
25
1
2
3
4
5
6
7

Fig. 6A

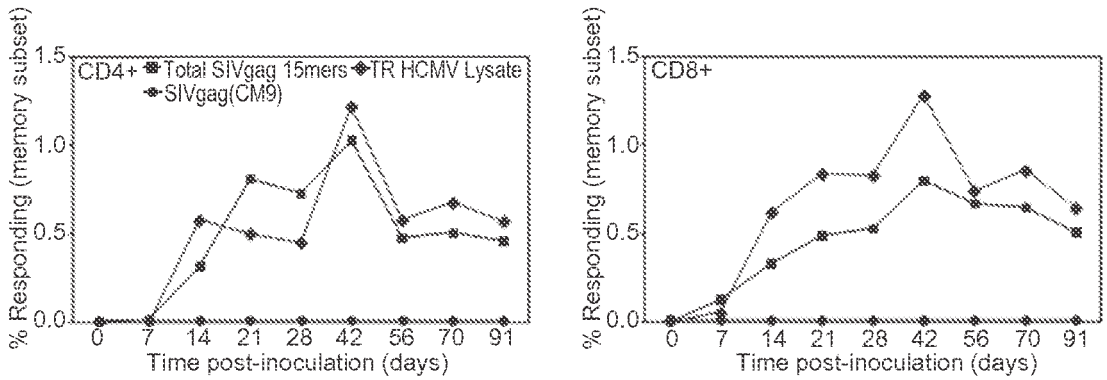


Fig. 6B

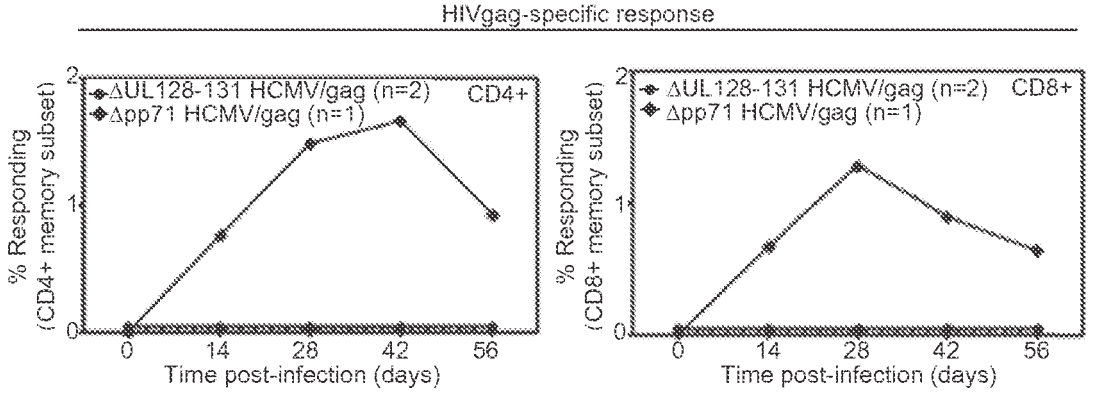


Fig. 7A

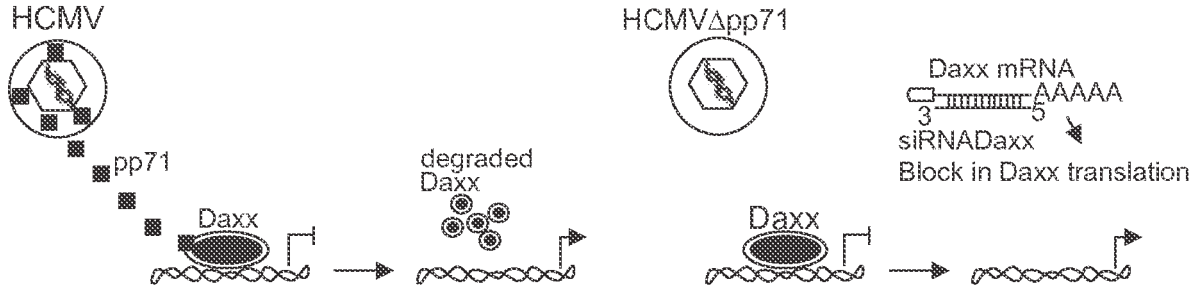


Fig. 7B

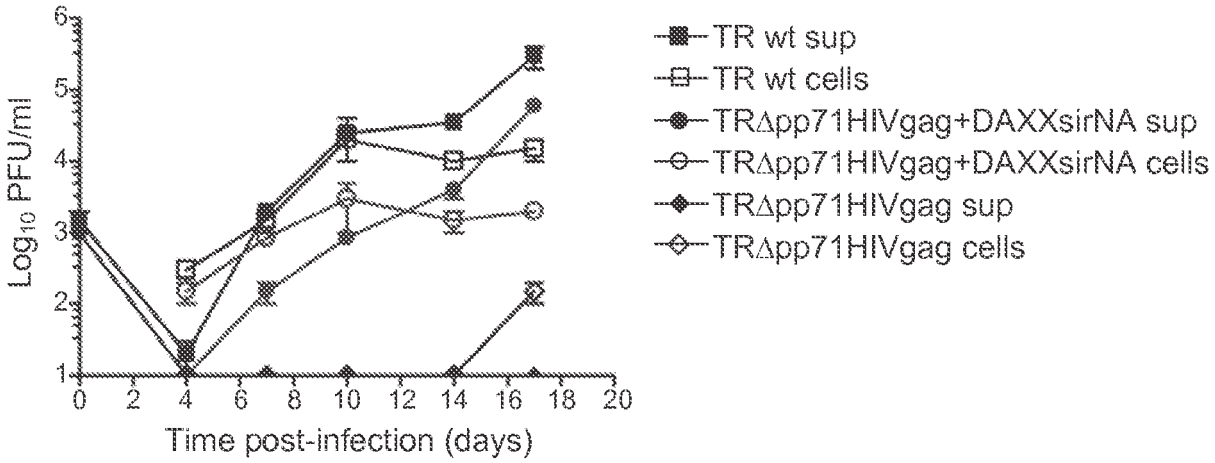

Log10 PFU/ml
Time post-infection (days)
TR wt sup
TR wt cells
TRΔpp71HIVgag+DAXXsirNA sup
TRΔpp71HIVgag+DAXXsirNA cells
TRΔpp71HIVgag sup
TRΔpp71HIVgag cells

Fig. 8A

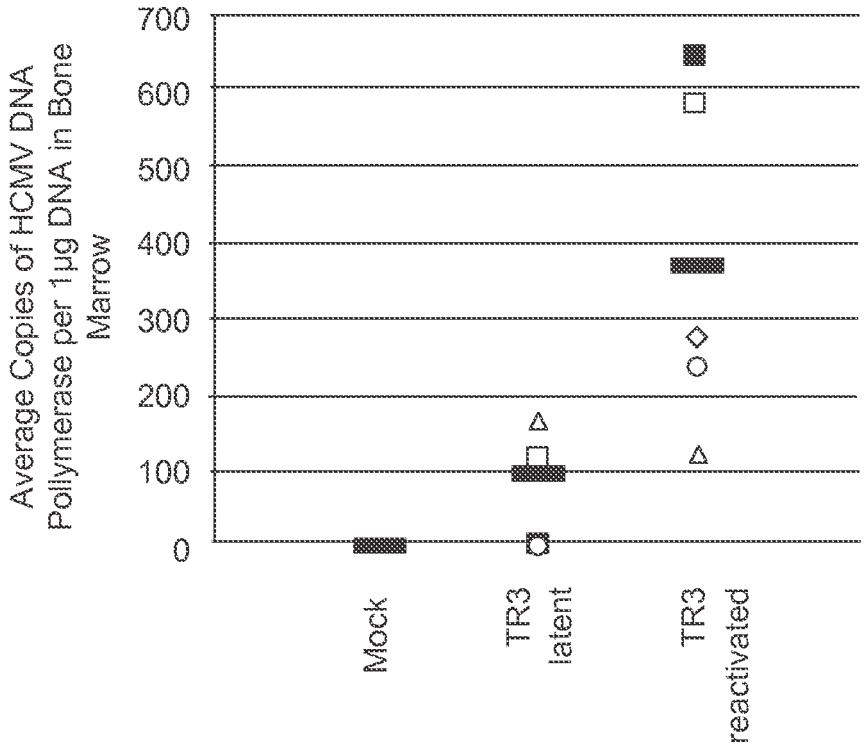

Average Copies of HCMV DNA Polymerase per 1µg DNA in Bone Marrow
Mock
TR3 latent
TR3 reactivated

Fig. 8B

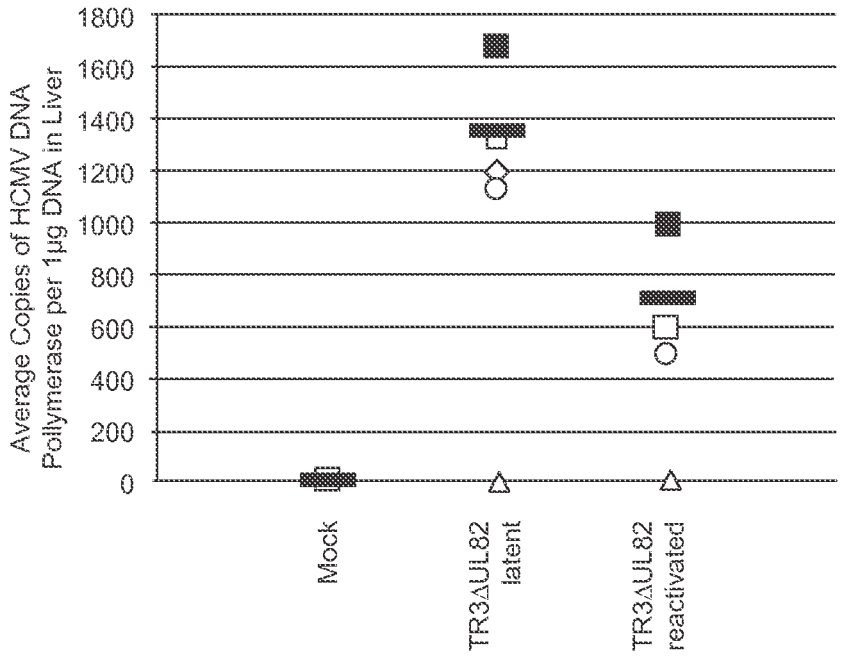

Average Copies of HCMV DNA Pollymerase per 1µg DNA in Liver
1800
1600
1400
1200
1000
800
600
400
200
0
Mock
TR3ΔUL82 latent
TR3ΔUL82 reactivated

Fig. 9

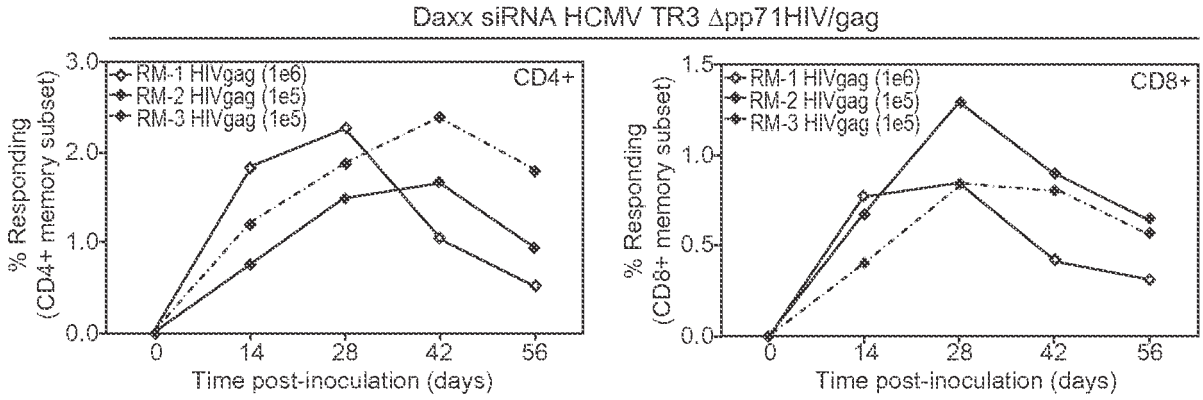

Daxx siRNA HCMV TR3 Δpp71HIV/gag
% Responding (CD4+ memory subset)
RM-1 HIVgag (1e6)
RM-2 HIVgag (1e5)
RM-3 HIVgag (1e5)
CD4+
3.0
2.0
1.0
0.0
0
14
28
42
56
Time post-inoculation (days)
% Responding (CD8+ memory subset)
CD8+
1.5
1.0
0.5
0.0

Fig. 10A

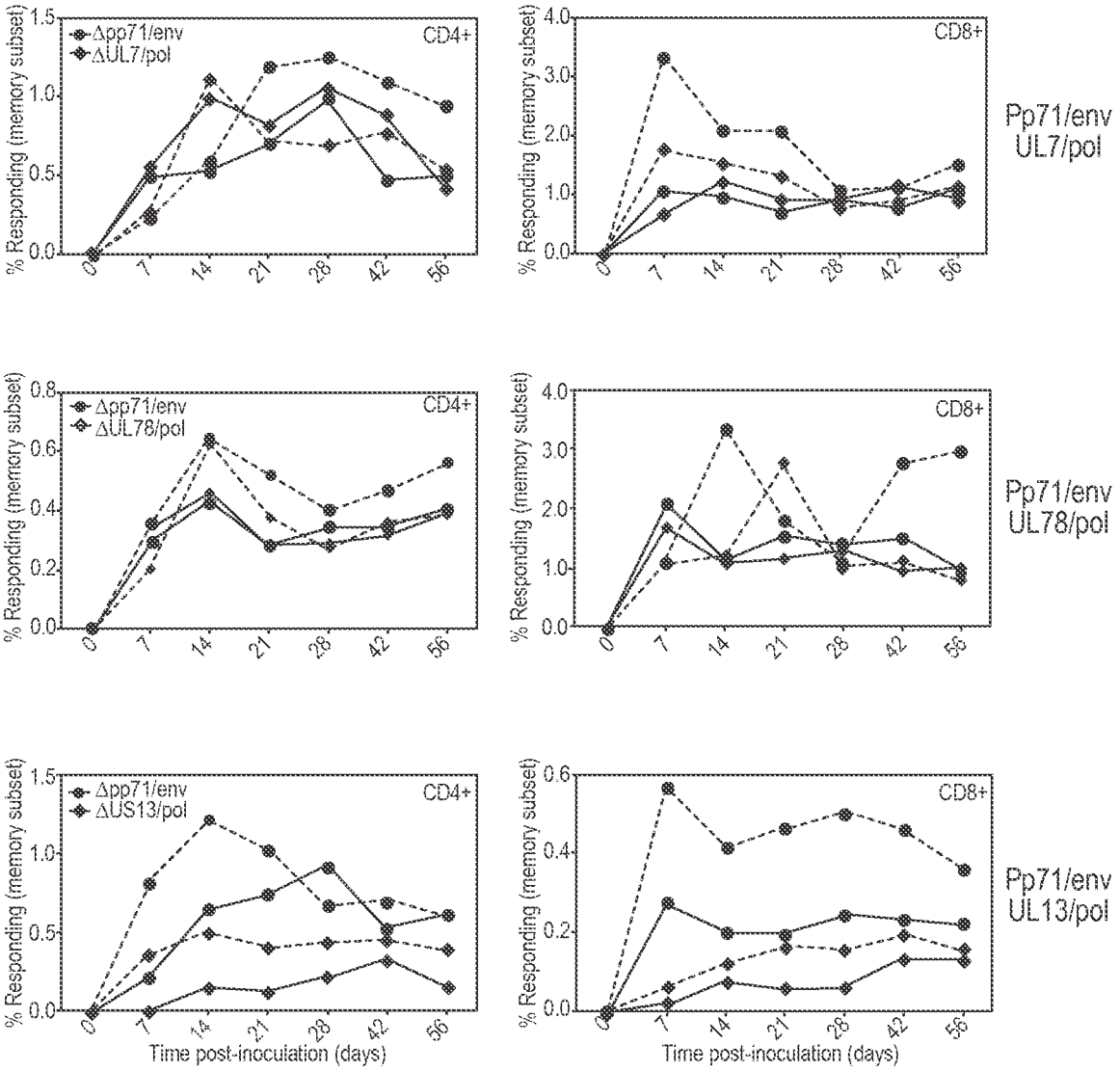

Δpp71/env
ΔUL7/pol
CD4+
% Responding (memory subset)
CD8+
Pp71/env
UL7/pol
ΔUL78/pol
Pp71/env
UL78/pol
ΔUS13/pol
Pp71/env
UL13/pol
Time post-inoculation (days)
0
7
14
21
28
42
56

Fig. 10B

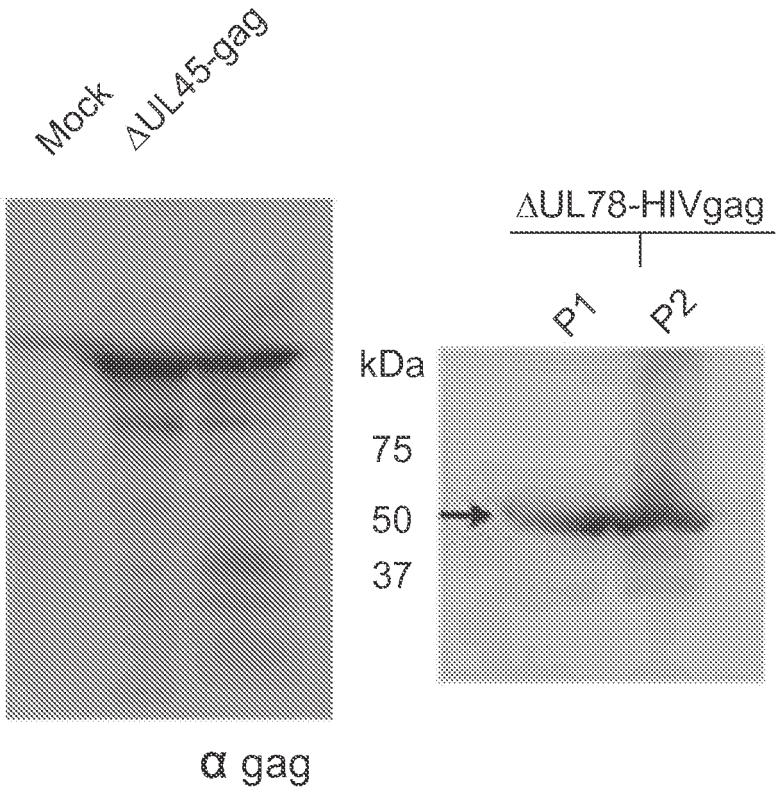


Fig. 11

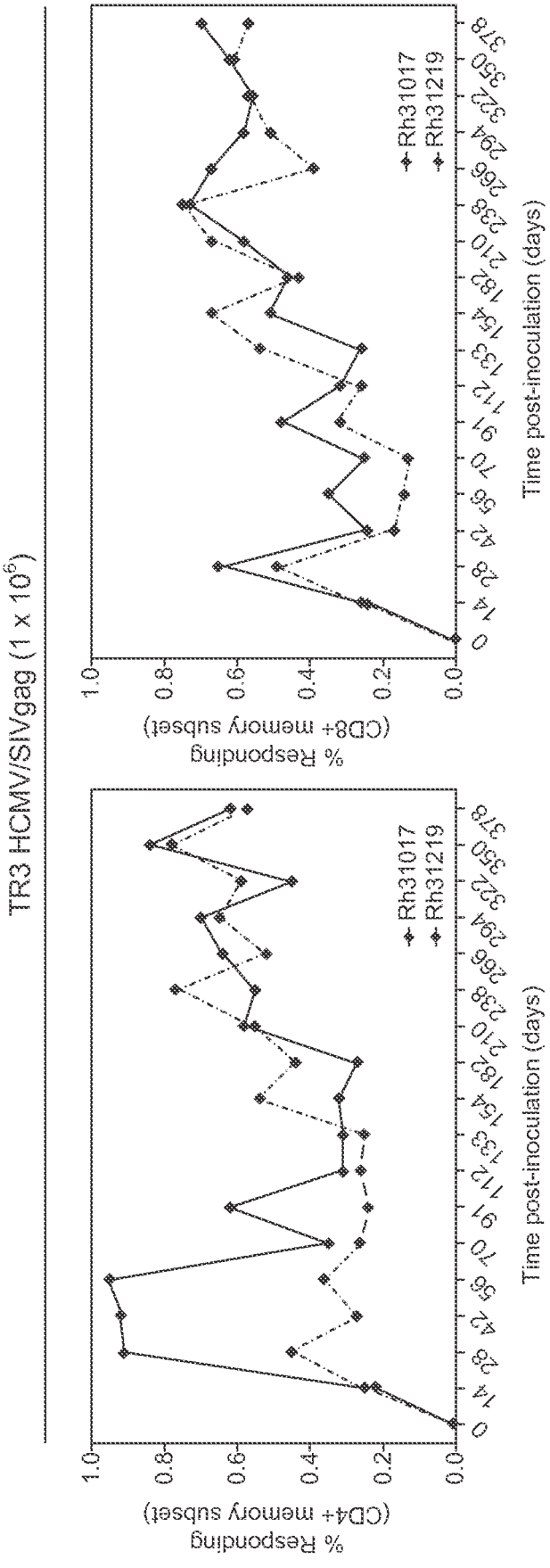

TR3 HCMV/SIVgag (1 x 10^6)
% Responding (CD4+ memory subset)
% Responding (CD8+ memory subset)
Time post-inoculation (days)
Rh31017
Rh31219
0.0
0.2
0.4
0.6
0.8
1.0
0
14
28
42
56
70
91
112
133
154
182
210
238
266
294
321
350
378

Fig. 12

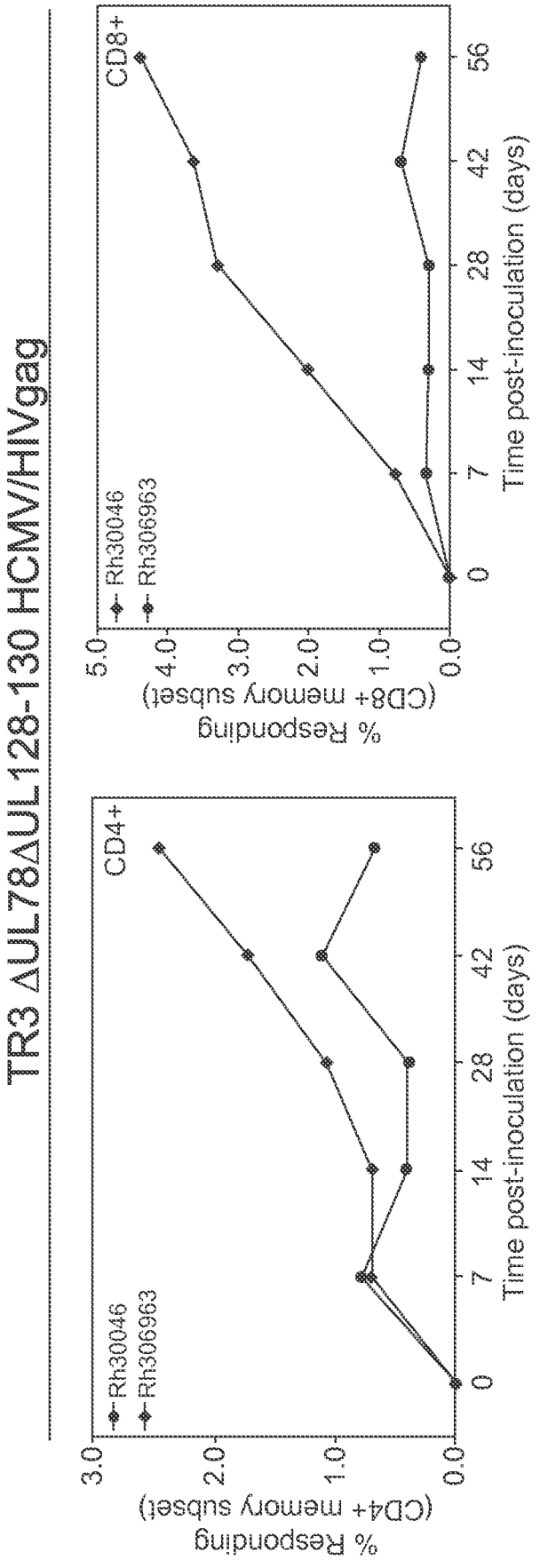

TR3 ΔUL78ΔUL128-130 HCMV/HIVgag
CD4+
CD8+
Rh30046
Rh306963
% Responding (CD4+ memory subset)
% Responding (CD8+ memory subset)
Time post-inoculation (days)
0.0
1.0
2.0
3.0
4.0
5.0
0
7
14
28
42
56

Fig. 13

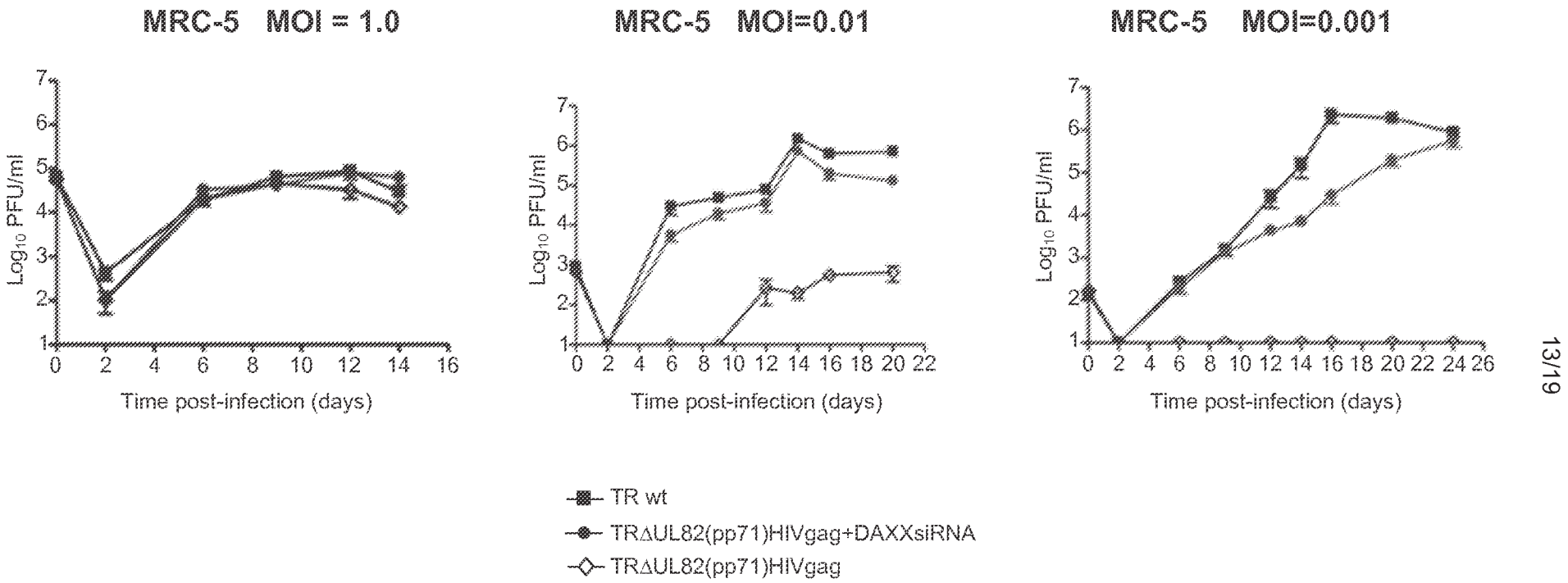

MRC-5 MOI = 1.0
MRC-5 MOI=0.01
MRC-5 MOI=0.001
Log10 PFU/ml
Time post-infection (days)
TR wt
TRΔUL82(pp71)HIVgag+DAXXsiRNA
TRΔUL82(pp71)HIVgag

Fig. 14

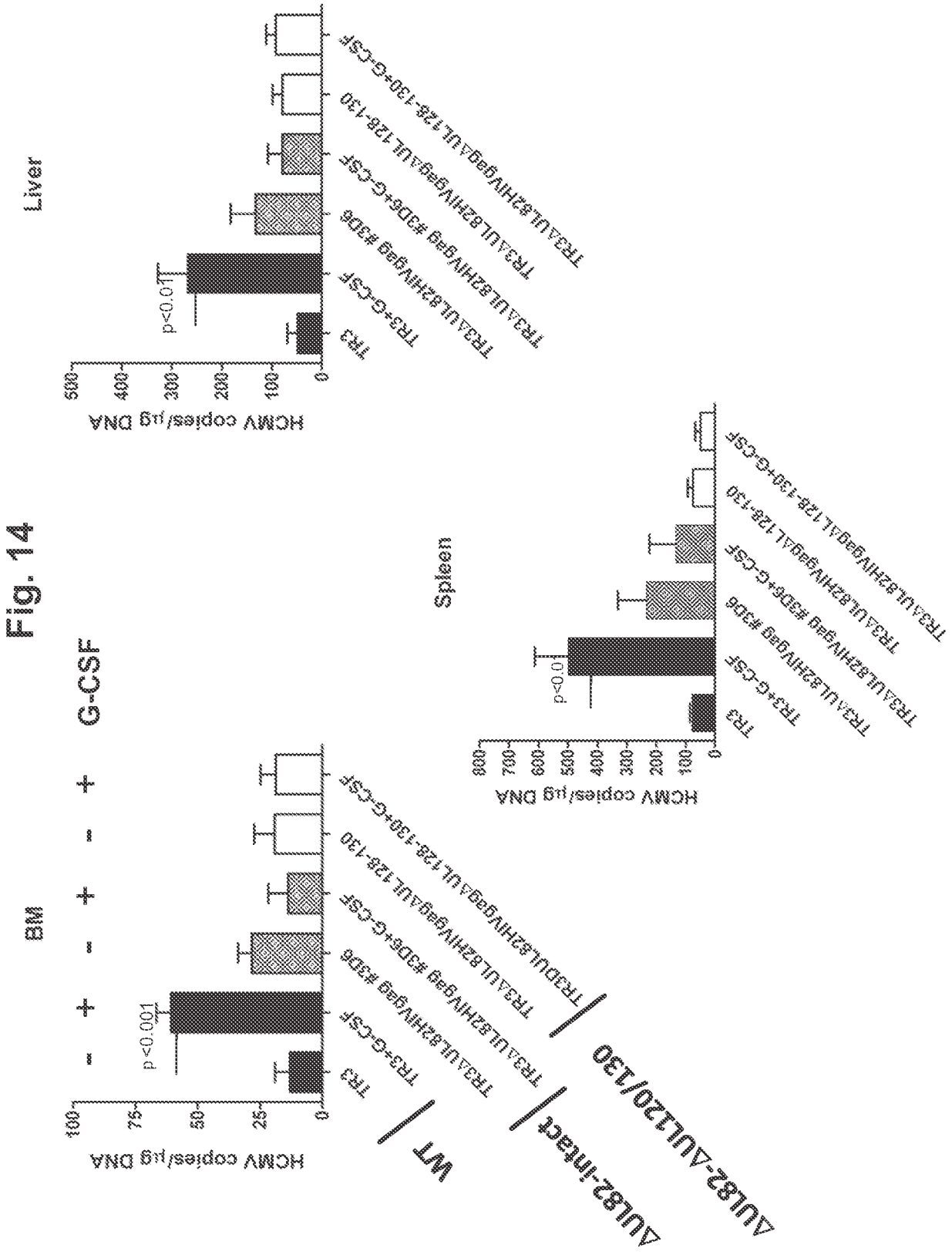
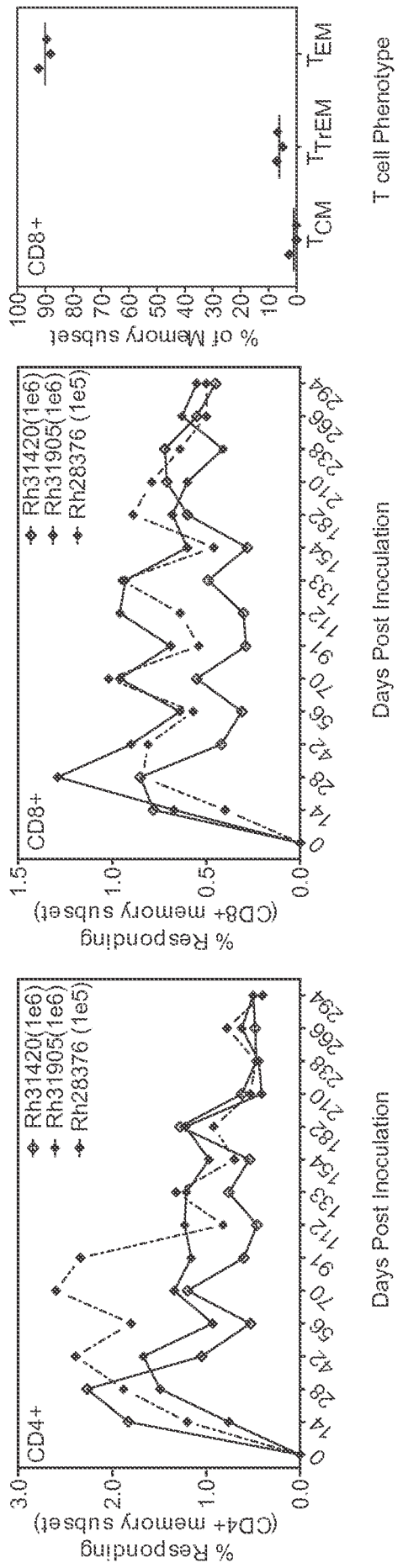

BM
G-CSF
Liver
Spleen
HCMV copies/µg DNA
p<0.001
p<0.01
p<0.0
TR3
TR3+G-CSF
TR3ΔUL82HIVgag #3D6
TR3ΔUL82HIVgag #3D6+G-CSF
TR3ΔUL82HIVgagΔUL128-130
TR3ΔUL82HIVgagΔUL128-130+G-CSF
WT
ΔUL82-intact
ΔUL82-ΔUL120/130

Fig. 15



ΔUL82 TR-HCMV/HIVgag

Fig. 16

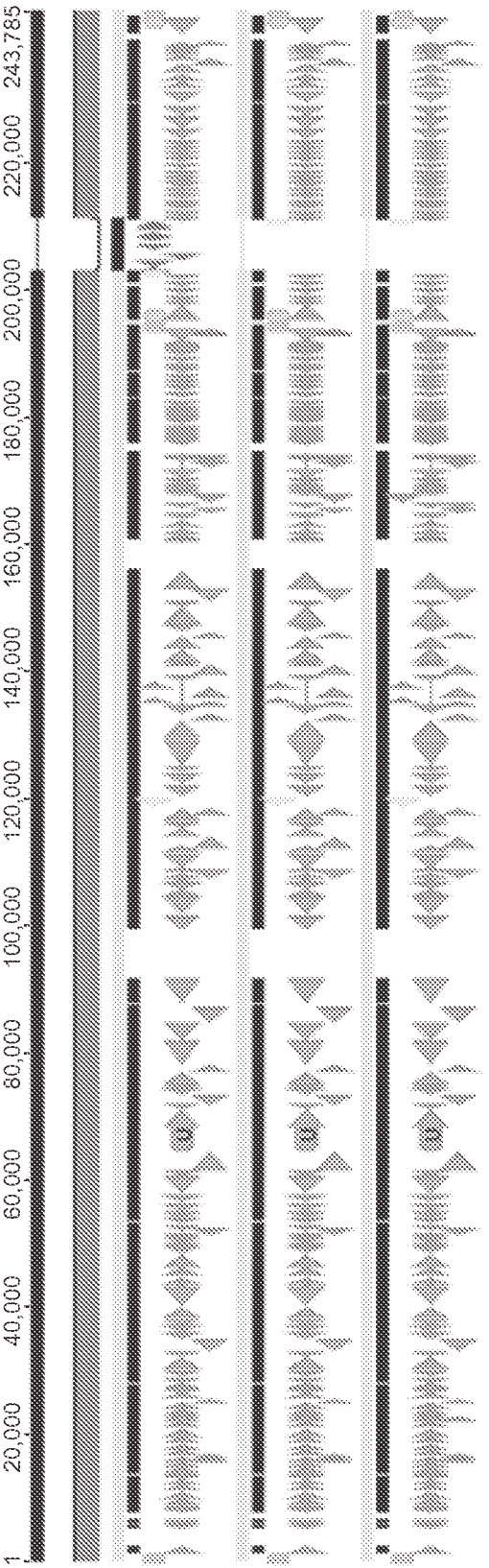
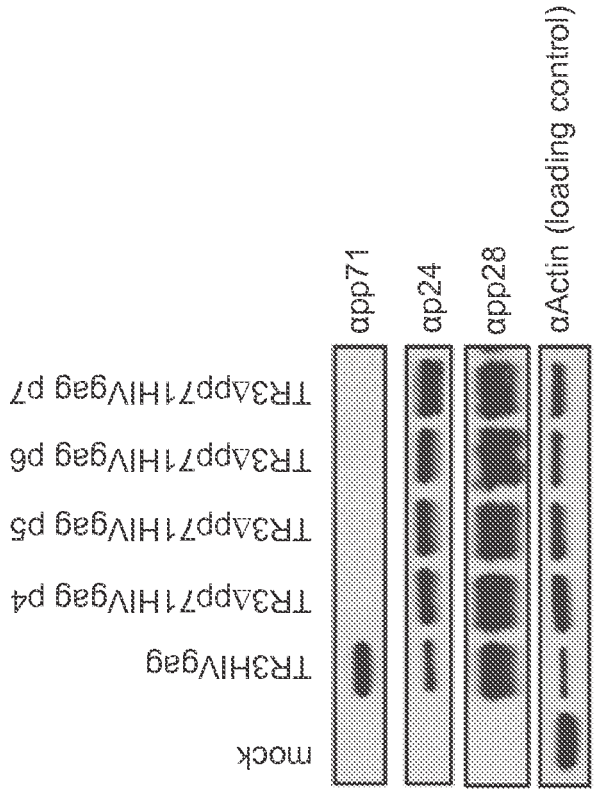

Consensus
Identity
HCMV TR3.1 ΔUL82 HIV-GAG (BAC)
HCMV TR3.1 ΔUL82 HIV-GAG (virus, p5)
HCMV TR3.1 ΔUL82 HIV-GAG (virus, p9)
1
20,000
40,000
60,000
80,000
100,000
120,000
140,000
160,000
180,000
200,000
220,000
243,785

Fig. 17A



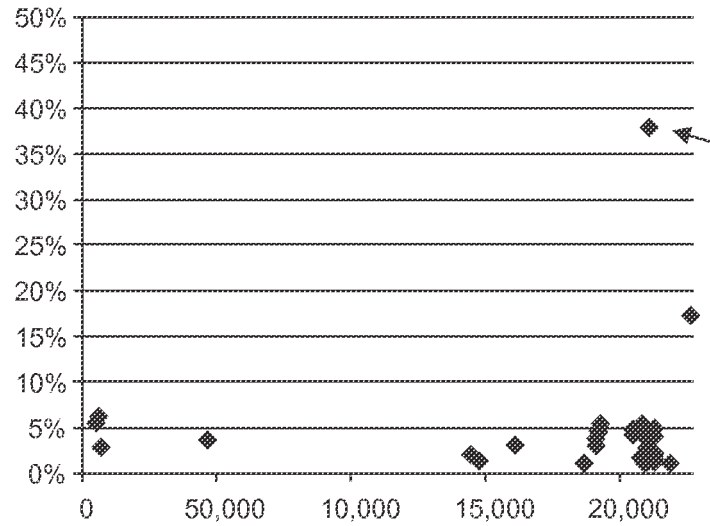
ΔUL82-HCMV-TR3/HIVgag

Fig. 17B

```
HIVgag          MAARASILSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELDRFALNPSLLETTEGCQQI 60
#3D6 p4         MAARASILSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELDRFALNPSLLETTEGCQQI 60
#3D6 p5         MAARASILSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELDRFALNPSLLETTEGCQQI 60
#3D6 p6         MAARASILSGGKLDAWEKIRLRPGGKKKYRLKHLVWASRELDRFALNPSLLETTEGCQQI 60
                ************************************************************

HIVgag          MNQLQPAVKTGTEEIKSLFNTVATLYCVHQRIDVKDTKEALDKIEEIQNKSKQKTQQAAA 120
#3D6 p4         MNQLQPAVKTGTEEIKSLFNTVATLYCVHQRIDVKDTKEALDKIEEIQNKSKQKTQQAAA 120
#3D6 p5         MNQLQPAVKTGTEEIKSLFNTVATLYCVHQRIDVKDTKEALDKIEEIQNKSKQKTQQAAA 120
#3D6 p6         MNQLQPAVKTGTEEIKSLFNTVATLYCVHQRIDVKDTKEALDKIEEIQNKSKQKTQQAAA 120
                ************************************************************

HIVgag          DTGDSSKVSQNYPIIQNAQGQMIHQNLSPRTLNAWVKVIEEKAFSPEVIPMFSALSEGAT 180
#3D6 p4         DTGDSSKVSQNYPIIQNAQGQMIHQNLSPRTLNAWVKVIEEKAFSPEVIPMFSALSEGAT 180
#3D6 p5         DTGDSSKVSQNYPIIQNAQGQMIHQNLSPRTLNAWVKVIEEKAFSPEVIPMFSALSEGAT 180
#3D6 p6         DTGDSSKVSQNYPIIQNAQGQMIHQNLSPRTLNAWVKVIEEKAFSPEVIPMFSALSEGAT 180
                ************************************************************

HIVgag          PQDLNVMLNIVGGHQAAMQMLKDTINEEAAEWDRLHPVQAGPIPPGQIREPRGSDIAGTT 240
#3D6 p4         PQDLNVMLNIVGGHQAAMQMLKDTINEEAAEWDRLHPVQAGPIPPGQIREPRGSDIAGTT 240
#3D6 p5         PQDLNVMLNIVGGHQAAMQMLKDTINEEAAEWDRLHPVQAGPIPPGQIREPRGSDIAGTT 240
#3D6 p6         PQDLNVMLNIVGGHQAAMQMLKDTINEEAAEWDRLHPVQAGPIPPGQIREPRGSDIAGTT 240
                ************************************************************

HIVgag          STPQEQLQWMTGNPPIPVGNIYKRWIILGLNKIVRMYSPVSILDIKQGPKEPFRDYVDRF 300
#3D6 p4         STPQEQLQWMTGNPPIPVGNIYKRWIILGLNKIVRMYSPVSILDIKQGPKEPFRDYVDRF 300
#3D6 p5         STPQEQLQWMTGNPPIPVGNIYKRWIILGLNKIVRMYSPVSILDIKQGPKEPFRDYVDRF 300
#3D6 p6         STPQEQLQWMTGNPPIPVGNIYKRWIILGLNKIVRMYSPVSILDIKQGPKEPFRDYVDRF 300
                ************************************************************

HIVgag          FKALRAEQATQDVKGWMTETLLVQNANPDCKSILKALGSGATLEEMMTACQGVGGPGHKA 360
#3D6 p4         FKALRAEQATQDVKGWMTETLLVQNANPDCKSILKALGSGATLEEMMTACQGVGGPGHKA 360
#3D6 p5         FKALRAEQATQDVKGWMTETLLVQNANPDCKSILKALGSGATLEEMMTACQGVGGPGHKA 360
#3D6 p6         FKALRAEQATQDVKGWMTETLLVQNANPDCKSILKALGSGATLEEMMTACQGVGGPGHKA 360
                ************************************************************

HIVgag          RVLAEAMSQAQQTNIMMQRGNFRGQKRIKCFNCGKEGHLARNCRAPRKKGCWKCGKEGHQ 420
#3D6 p4         RVLAEAMSQAQQTNIMMQRGNFRGQKRIKCFNCGKEGHLARNCRAPRKKGCWKCGKEGHQ 420
#3D6 p5         RVLAEAMSQAQQTNIMMQRGNFRGQKRIKCFNCGKEGHLARNCRAPRKKGCWKCGKEGHQ 420
#3D6 p6         RVLAEAMSQAQQTNIMMQRGNFRGQKRIKCFNCGKEGHLARNCRAPRKKGCWKCGKEGHQ 420
                ************************************************************

HIVgag          MKDCTERQANFLGKIWPSSKGRPGNFPQSRPEPTAPPAELFGMGEGIASLPKQEQKDREQ 480
#3D6 p4         MKDCTERQANFLGKIWPSSKGRPGNFPQSRPEPTAPPAELFGMGEGIASLPKQEQKDREQ 480
#3D6 p5         MKDCTERQANFLGKIWPSSKGRPGNFPQSRPEPTAPPAELFGMGEGIASLPKQEQKDREQ 480
#3D6 p6         MKDCTERQANFLGKIWPSSKGRPGNFPQSRPEPTAPPAELFGMGEGIASLPKQEQKDREQ 480
                ************************************************************

HIVgag          VPPLVSLKSLFGNDPLSQ 498
#3D6 p4         VPPLVSLKSLFGNDPLSQ 498
#3D6 p5         VPPLVSLKSLFGNDPLSQ 498
#3D6 p6         VPPLVSLKSLFGNDPLSQ 498
                ******************!
```

Fig. 18

Next generation sequencing of RhCMV 68-1.2 SIV-gag ΔUL36 viral DNA



Premature Stop codon due to
G → T substitution in SIV gag
in 37.9% of the population