FIGURE 1

(SEQ ID No.1)

MKRILGALLG LLSAQVCCVR GIQVEQSPPD LILQEGANST LRCNFSDSVN
NLQWFHQNPW GQLINLFYIP SGTKQNGRLS ATTVATERYS LLYISSSQTT
DSGVYF**CAVV ENNDMRFGAG TRLTVKP**NIQ NPDPAVYQLR DSKSSDKSVC
LFTDFDSQTN VSQSKDSDVY ITDK**C**VLDMR SMDFKSNSAV AWSNKSDFAC
ANAFNNSIIP EDTFFPSPES SCDVKLVEKS FETDTNLNFQ NLSVIGFRIL
LLKVAGFNLL MTLRLWSS

FIGURE 2

(SEQ ID No. 2)

MGCRLLCCAV LCLLGAVPID TEVTQTPKHL VMGMTNKKSL KCEQHMGHRA
MYWYKQKAKK PPELMFVYSY EKLSINESVP SRFSPECPNS SLLNLHLHAL
QPEDSALYLC ASS**PGRWYEQ YFGPGTRLTV T**EDLKNVFPP EVAVFEPSEA
EISHTQKATL VCLATGFYPD HVELSWWVNG KEVHSGV**C**TD PQPLKEQPAL
NDSRYCLSSR LRVSATFWQN PRNHFRCQVQ FYGLSENDEW TQDRAKPVTQ
IVSAEAWGRA DCGFTSESYQ QGVLSATILY EILLGKATLY AVLVSALVLM
AMVKRKDSRG

FIGURE 3

(SEQ ID No. 3)

MKRILGALLG LLSAQVCCVR GIQVEQSPPD LILQEGANST LRCNFSDSVN
NLQWFHQNPW GQLINLFYIP SGTKQNGRLS ATTVATERYS LLYISSSQTT
DSGVYFCAVV ENNDMRFGAG TRLTVKPNIQ NPDPAVYQLR DSKSSDKSVC
LFTDFDSQTN VSQSKDSDVY ITDKCVLDMR SMDFKSNSAV AWSNKSDFAC
ANAFNNSIIP EDTFFPSPES SCDVKLVEKS FETDTNLNFQ NLSVIGFRIL
LLKVAGFNLL MTLRLWSS**GS GATNFSLLKQ AGDVEENPGP** MGCRLLCCAV
LCLLGAVPID TEVTQTPKHL VMGMTNKKSL KCEQHMGHRA MYWYKQKAKK
PPELMFVYSY EKLSINESVP SRFSPECPNS SLLNLHLHAL QPEDSALYLC
ASSPGRWYEQ YFGPGTRLTV TEDLKNVFPP EVAVFEPSEA EISHTQKATL
VCLATGFYPD HVELSWWVNG KEVHSGVCTD PQPLKEQPAL NDSRYCLSSR
LRVSATFWQN PRNHFRCQVQ FYGLSENDEW TQDRAKPVTQ IVSAEAWGRA
DCGFTSESYQ QGVLSATILY EILLGKATLY AVLVSALVLM AMVKRKDSRG

FIGURE 4

(SEQ ID No. 4)

ATGAAGAGAATCCTGGGCGCCCTGCTGGGCCTGCTGTCCGCCCAGGTGTGCTGCGTG
CGGGGCATCCAGGTGGAGCAGAGCCCCCCTGACCTGATCCTGCAGGAAGGCGCCAAC
AGCACCCTGCGGTGCAACTTCAGCGACAGCGTGAACAACCTGCAGTGGTTCCACCAG
AACCCCTGGGGCCAGCTGATCAACCTGTTCTACATCCCCAGCGGCACCAAGCAGAAC
GGCAGACTGAGCGCCACCACCGTGGCCACCGAGCGGTACAGCCTGCTGTACATCAGC
AGCAGCCAGACCACCGACAGCGGCGTGTACTTCTG**CGCCGTGGTGGAGAACAACGAC**
ATGAGATTCGGAGCCGGCACCCGGCTGACCGTGAAGCCCAACATCCAGAACCCCGAC
CCCGCCGTGTACCAGCTGCGGGACAGCAAGAGCAGCGACAAGAGCGTGTGCCTGTTC
ACCGACTTCGACTCCCAGACCAACGTGTCCCAGAGCAAGGACTCCGACGTGTACATC
ACCGACAAGTGCGTGCTGGACATGCGGAGCATGGACTTCAAGAGCAACAGCGCCGTG
GCCTGGTCCAACAAGAGCGACTTCGCCTGCGCCAACGCCTTCAACAACAGCATCATC
CCCGAGGACACCTTTTTCCCCAGCCCCGAGAGCAGCTGCGACGTGAAACTGGTGGAG
AAGTCCTTCGAGACAGACACCAACCTGAACTTCCAGAACCTGAGCGTGATCGGCTTC
AGAATCCTGCTGCTGAAAGTGGCTGGATTCAACCTGCTGATGACCCTGCGGCTGTGG
AGCAGC

FIGURE 5

(SEQ ID No. 5)

ATGGGCTGCCGGCTGCTGTGCTGCGCCGTGCTGTGTCTGCTGGGCGCCGTGCCCATC
GACACCGAAGTGACCCAGACCCCCAAGCACCTGGTGATGGGCATGACCAACAAGAAA
AGCCTGAAGTGCGAGCAGCACATGGGCCACCGGGCCATGTACTGGTACAAGCAGAAG
GCCAAGAAACCCCCCGAGCTGATGTTCGTGTACAGCTACGAGAAGCTGTCCATCAAC
GAGAGCGTGCCCAGCAGATTCAGCCCTGAGTGCCCCAACTCCTCCCTGCTGAACCTG
CACCTGCATGCCCTGCAGCCCGAGGACAGCGCCCTGTACCTGTGCGCCAGCAGCC**CC**
GGCAGGTGGTACGAGCAGTACTTCGGCCCTGGCACCAGACTGACAGTGACCGAGGAC
CTGAAGAACGTGTTCCCCCCCGAGGTGGCCGTGTTCGAGCCCAGCGAGGCCGAGATC
AGCCACACCCAGAAAGCCACCCTGGTGTGCCTGGCCACCGGCTTCTACCCCGATCAC
GTGGAGCTGTCTTGGTGGGTGAACGGCAAAGAGGTGCACTCCGGCGTCTGCACCGAC
CCTCAGCCCCTGAAAGAGCAGCCCGCCCTGAACGACAGCCGGTACTGCCTGTCCTCC
CGGCTGAGAGTGTCTGCTACATTCTGGCAGAATCCCCGGAACCACTTCCGGTGCCAG
GTGCAGTTCTACGGCCTGAGCGAGAACGACGAGTGGACCCAGGACAGAGCCAAGCCC
GTGACCCAGATCGTGTCCGCCGAGGCCTGGGGCAGAGCCGACTGCGGCTTCACCAGC
GAGAGCTACCAGCAGGGCGTGCTGTCTGCCACCATCCTGTACGAGATCCTGCTGGGC
AAGGCCACCCTGTACGCCGTGCTGGTGTCCGCCCTGGTGCTGATGGCCATGGTGAAG
CGGAAGGACAGCAGAGGCTGA

FIGURE 6

(SEQ ID No. 6)

ATGAAGAGAATCCTGGGCGCCCTGCTGGGCCTGCTGTCCGCCCAGGTGTGCTGCGTG
CGGGGCATCCAGGTGGAGCAGAGCCCCCCTGACCTGATCCTGCAGGAAGGCGCCAAC
AGCACCCTGCGGTGCAACTTCAGCGACAGCGTGAACAACCTGCAGTGGTTCCACCAG
AACCCCTGGGGCCAGCTGATCAACCTGTTCTACATCCCCAGCGGCACCAAGCAGAAC
GGCAGACTGAGCGCCACCACCGTGGCCACCGAGCGGTACAGCCTGCTGTACATCAGC
AGCAGCCAGACCACCGACAGCGGCGTGTACTTCTGCGCCGTGGTGGAGAACAACGAC
ATGAGATTCGGAGCCGGCACCCGGCTGACCGTGAAGCCCAACATCCAGAACCCCGAC
CCCGCCGTGTACCAGCTGCGGGACAGCAAGAGCAGCGACAAGAGCGTGTGCCTGTTC
ACCGACTTCGACTCCCAGACCAACGTGTCCCAGAGCAAGGACTCCGACGTGTACATC
ACCGACAAGTGCGTGCTGGACATGCGGAGCATGGACTTCAAGAGCAACAGCGCCGTG
GCCTGGTCCAACAAGAGCGACTTCGCCTGCGCCAACGCCTTCAACAACAGCATCATC
CCCGAGGACACCTTTTTCCCCAGCCCCGAGAGCAGCTGCGACGTGAAACTGGTGGAG
AAGTCCTTCGAGACAGACACCAACCTGAACTTCCAGAACCTGAGCGTGATCGGCTTC
AGAATCCTGCTGCTGAAAGTGGCTGGATTCAACCTGCTGATGACCCTGCGGCTGTGG
AGCAGC**GGCAGCGGCGCCACCAACTTCAGCCTGCTGAAGCAGGCCGGCGACGTGGAG**
GAAAACCCTGGCCCCATGGGCTGCCGGCTGCTGTGCTGCGCCGTGCTGTGTCTGCTG
GGCGCCGTGCCCATCGACACCGAAGTGACCCAGACCCCCAAGCACCTGGTGATGGGC
ATGACCAACAAGAAAAGCCTGAAGTGCGAGCAGCACATGGGCCACCGGGCCATGTAC
TGGTACAAGCAGAAGGCCAAGAAACCCCCCGAGCTGATGTTCGTGTACAGCTACGAG
AAGCTGTCCATCAACGAGAGCGTGCCCAGCAGATTCAGCCCTGAGTGCCCCAACTCC
TCCCTGCTGAACCTGCACCTGCATGCCCTGCAGCCCGAGGACAGCGCCCTGTACCTG
TGCGCCAGCAGCCCCGGCAGGTGGTACGAGCAGTACTTCGGCCCTGGCACCAGACTG
ACAGTGACCGAGGACCTGAAGAACGTGTTCCCCCCCGAGGTGGCCGTGTTCGAGCCC
AGCGAGGCCGAGATCAGCCACACCCAGAAAGCCACCCTGGTGTGCCTGGCCACCGGC
TTCTACCCCGATCACGTGGAGCTGTCTTGGTGGGTGAACGGCAAAGAGGTGCACTCC
GGCGTCTGCACCGACCCTCAGCCCCTGAAAGAGCAGCCCGCCCTGAACGACAGCCGG
TACTGCCTGTCCTCCCGGCTGAGAGTGTCTGCTACATTCTGGCAGAATCCCCGGAAC
CACTTCCGGTGCCAGGTGCAGTTCTACGGCCTGAGCGAGAACGACGAGTGGACCCAG
GACAGAGCCAAGCCCGTGACCCAGATCGTGTCCGCCGAGGCCTGGGGCAGAGCCGAC
TGCGGCTTCACCAGCGAGAGCTACCAGCAGGGCGTGCTGTCTGCCACCATCCTGTAC
GAGATCCTGCTGGGCAAGGCCACCCTGTACGCCGTGCTGGTGTCCGCCCTGGTGCTG
ATGGCCATGGTGAAGCGGAAGGACAGCAGAGGCTGA

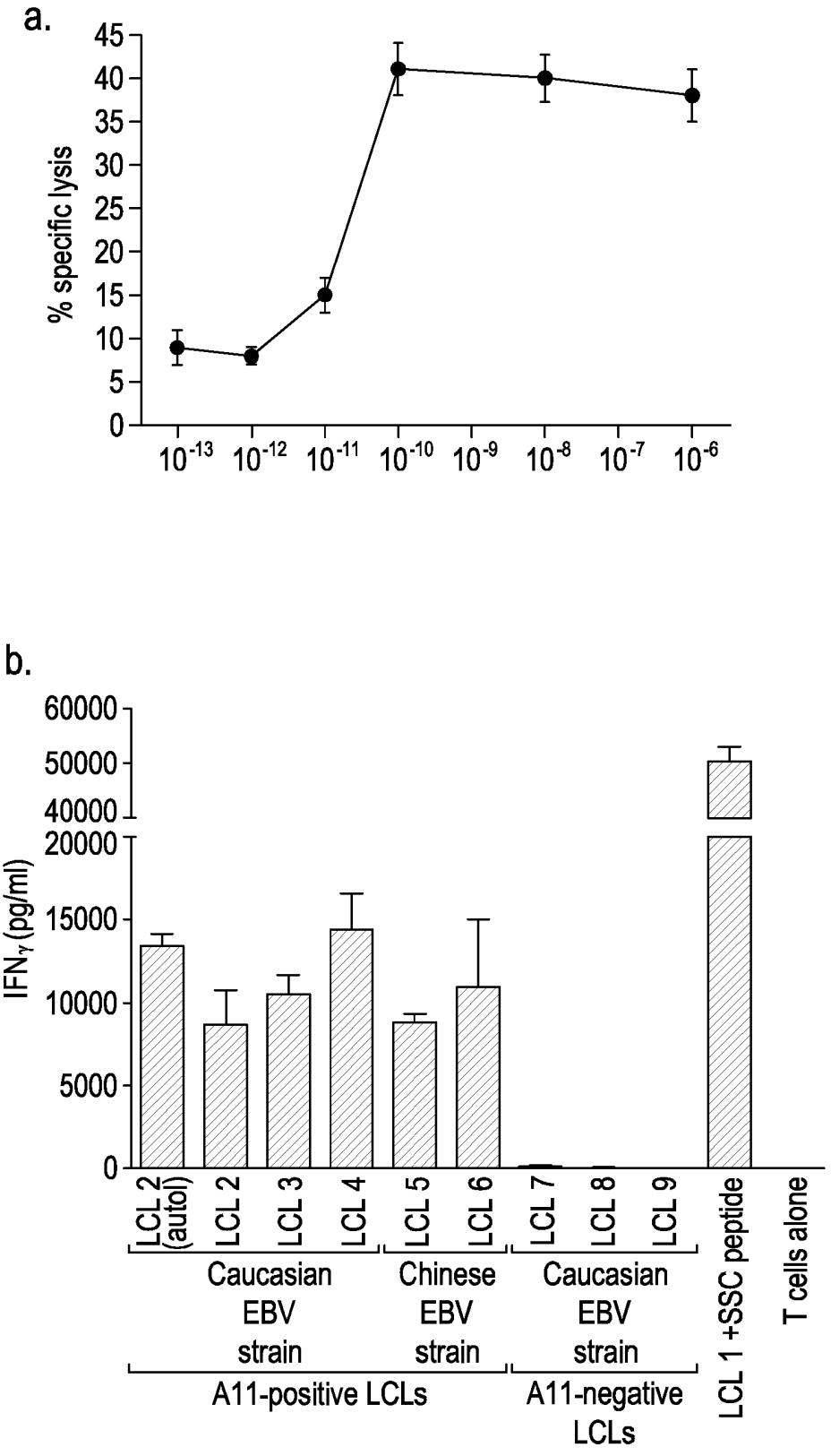

a.
% specific lysis
45
40
35
30
25
20
15
10
5
0
10-13
10-12
10-11
10-10
10-9
10-8
10-7
10-6
b.
IFNγ (pg/ml)
60000
50000
40000
20000
15000
10000
5000
0
LCL 2 (autol)
LCL 2
LCL 3
LCL 4
LCL 5
LCL 6
LCL 7
LCL 8
LCL 9
LCL 1 +SSC peptide
T cells alone
Caucasian EBV strain
Chinese EBV strain
Caucasian EBV strain
A11-positive LCLs
A11-negative LCLs

Figure 7

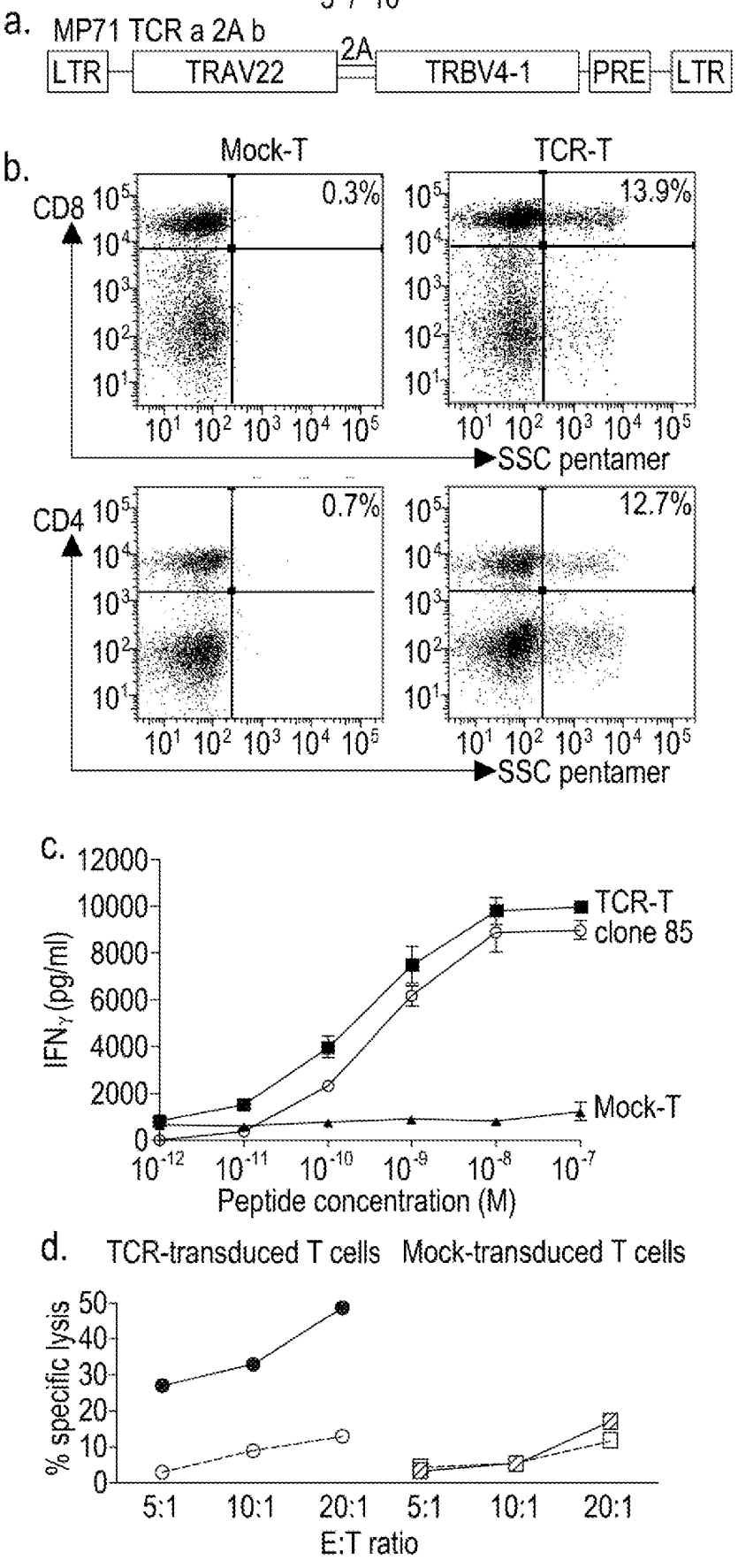

a.
MP71 TCR a 2A b
LTR
TRAV22
2A
TRBV4-1
PRE
LTR
b.
Mock-T
TCR-T
CD8
0.3%
13.9%
SSC pentamer
CD4
0.7%
12.7%
SSC pentamer
c.
IFNγ (pg/ml)
TCR-T
clone 85
Mock-T
Peptide concentration (M)
d.
TCR-transduced T cells
Mock-transduced T cells
% specific lysis
5:1
10:1
20:1
5:1
10:1
20:1
E:T ratio

Figure 8

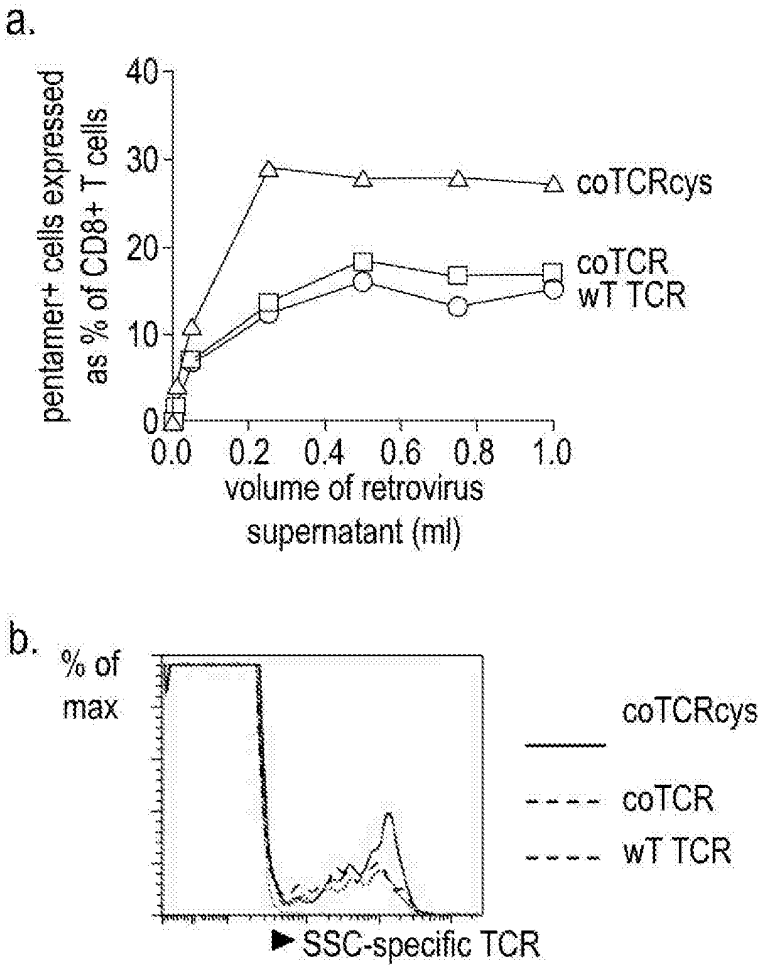

a.
pentamer+ cells expressed as % of CD8+ T cells
40
30
20
10
0
0.0
0.2
0.4
0.6
0.8
1.0
volume of retrovirus supernatant (ml)
coTCRcys
coTCR
wT TCR
b.
% of max
coTCRcys
coTCR
wT TCR
SSC-specific TCR
c.
IFNγ (pg/ml)
14000
12000
10000
8000
6000
4000
2000
0
WT TCR-T
coTCR-T
coTCRcys-T
Mock-T
10-12
10-11
10-10
10-9
10-8
10-7
10-6
Peptide conc (M)

Figure 9

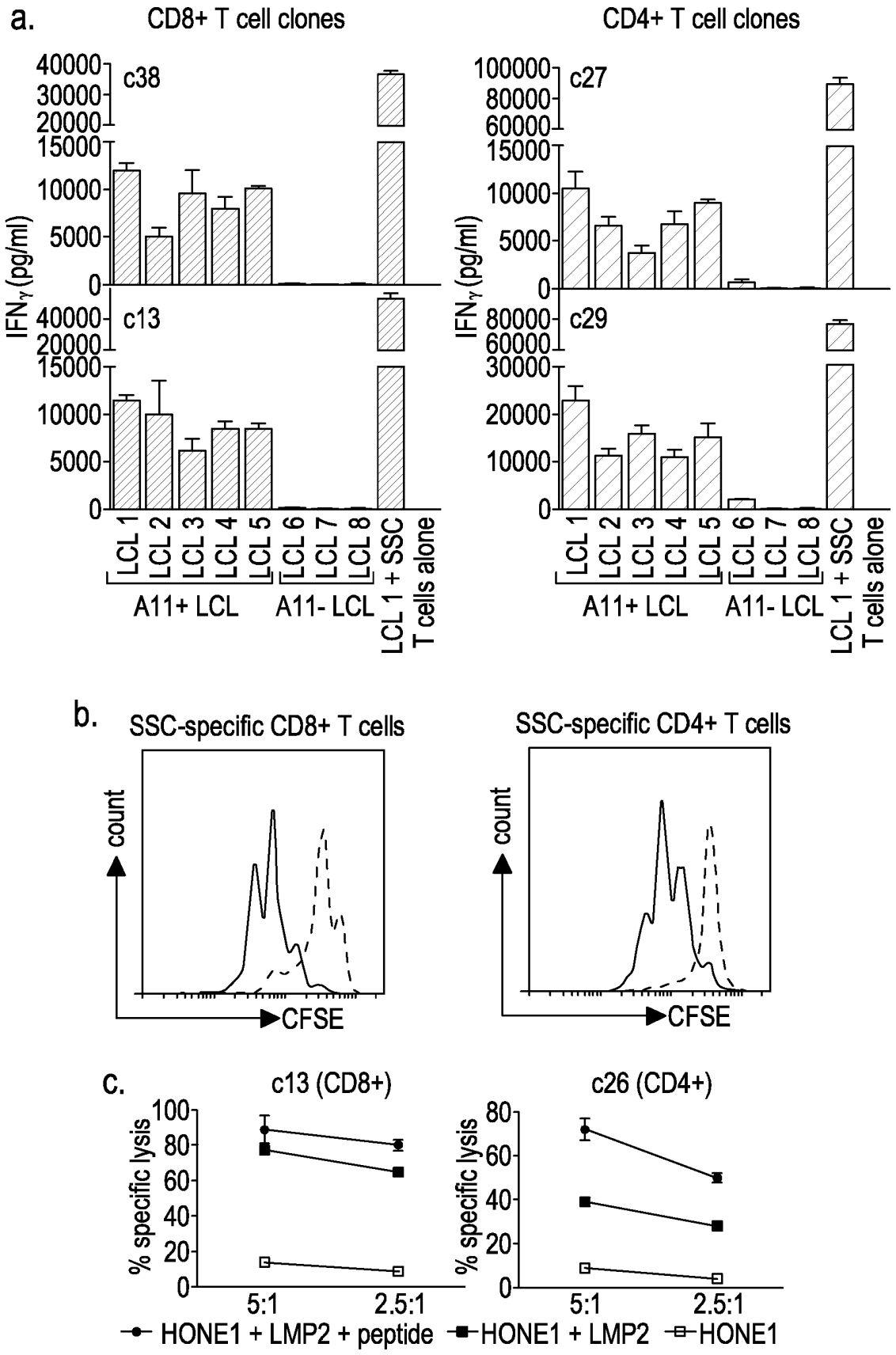

a.
CD8+ T cell clones
CD4+ T cell clones
c38
c13
c27
c29
IFNγ (pg/ml)
LCL 1
LCL 2
LCL 3
LCL 4
LCL 5
LCL 6
LCL 7
LCL 8
LCL 1 + SSC
T cells alone
A11+ LCL
A11- LCL
b.
SSC-specific CD8+ T cells
SSC-specific CD4+ T cells
count
CFSE
c.
c13 (CD8+)
c26 (CD4+)
% specific lysis
5:1
2.5:1
HONE1 + LMP2 + peptide
HONE1 + LMP2
HONE1

Figure 10

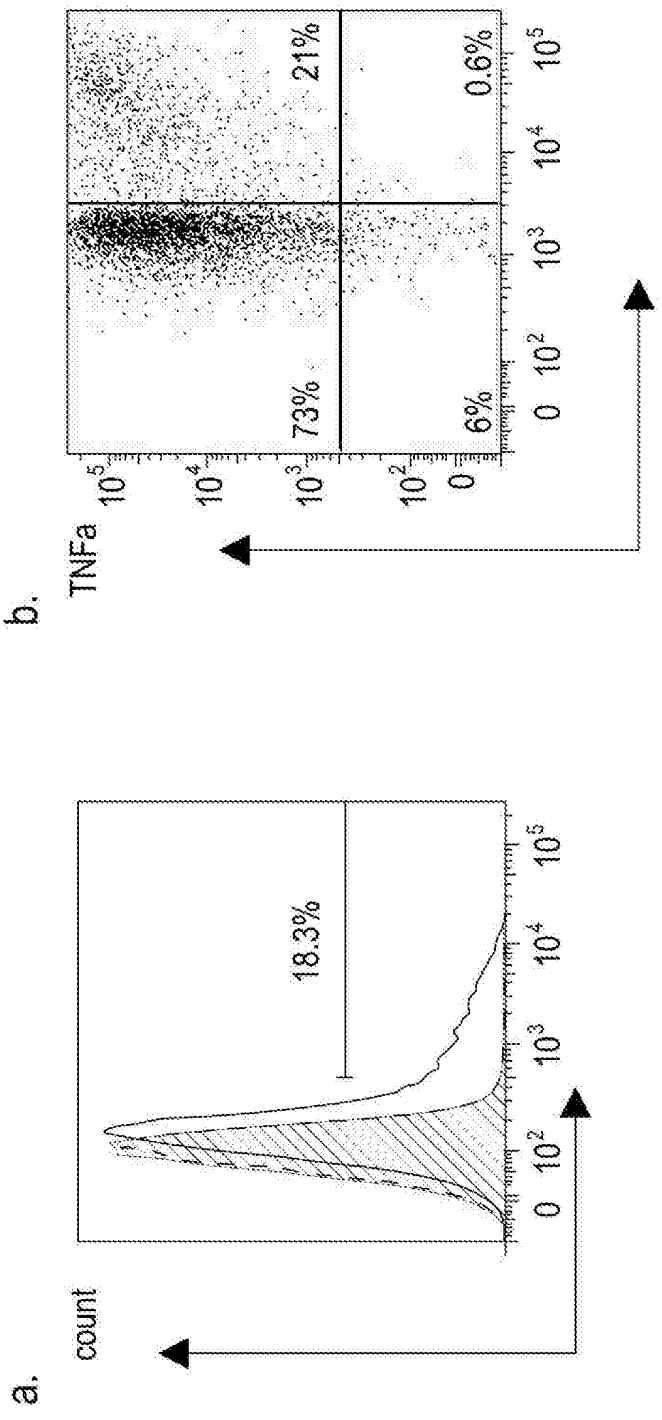
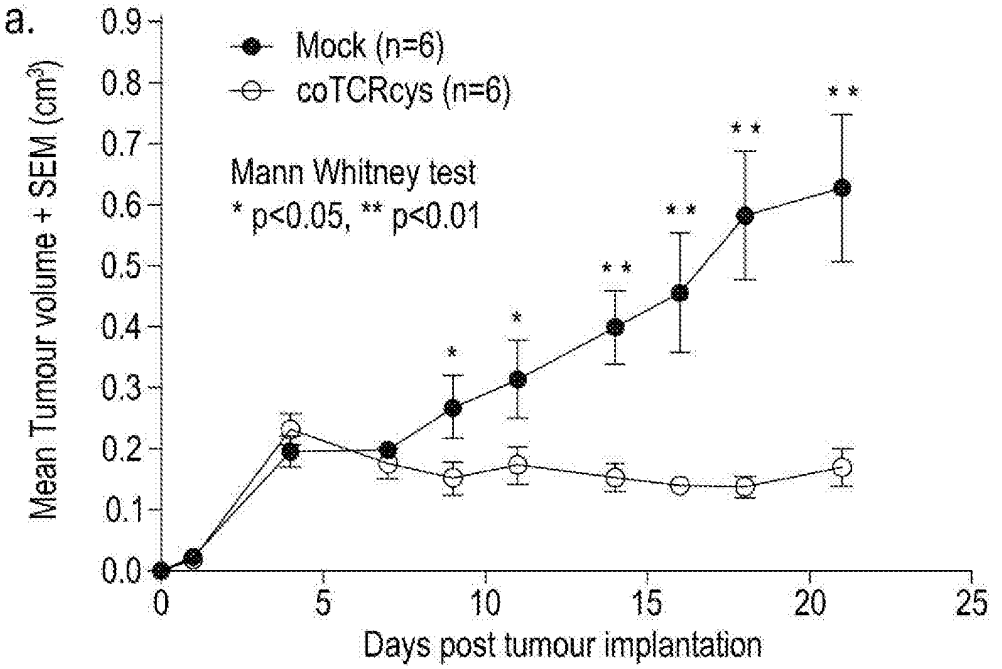


Figure 11


a.
Mean Tumour volume + SEM (cm³)
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Mock (n=6)
coTCRcys (n=6)
Mann Whitney test
* p<0.05, ** p<0.01
* *
* *
*
*
* *
0
5
10
15
20
25
Days post tumour implantation

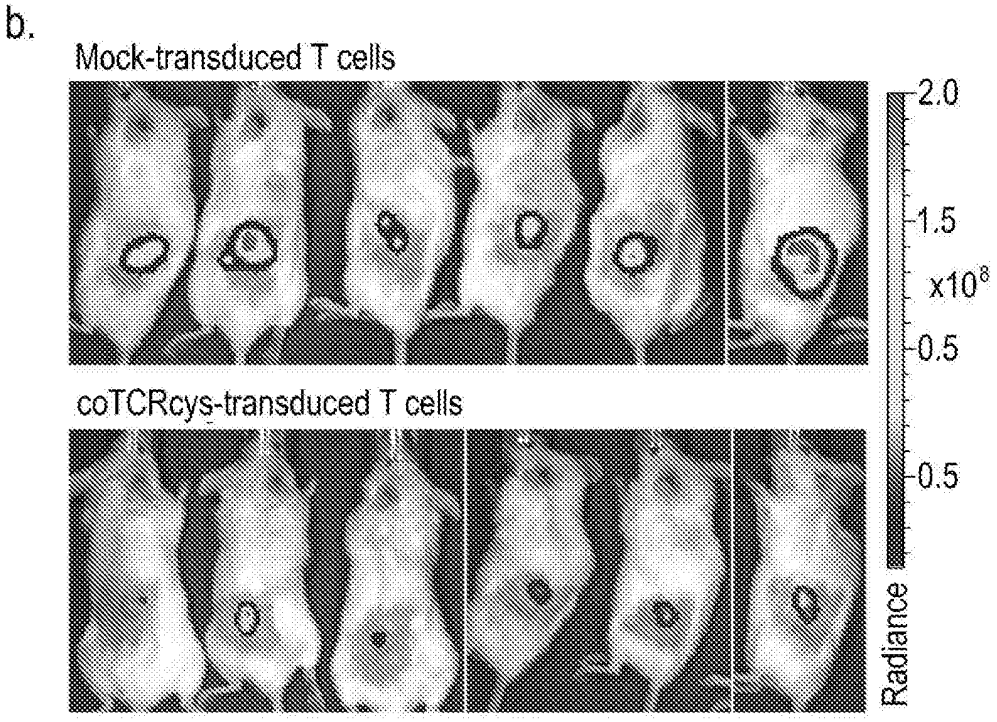

b.
Mock-transduced T cells
coTCRcys-transduced T cells
2.0
1.5
x10⁸
0.5
0.5
Radiance

Figure 12

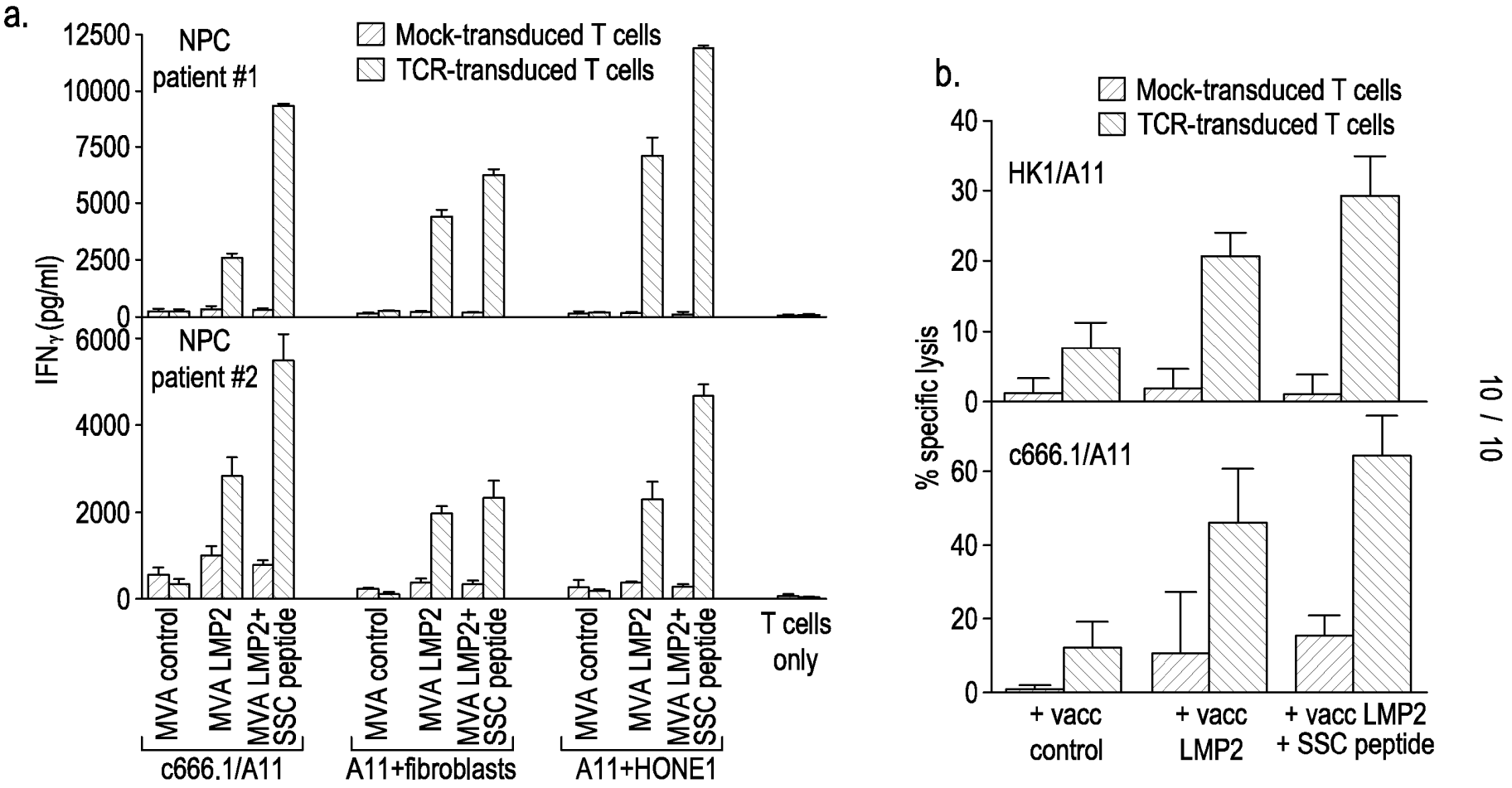

a.
NPC
patient #1
Mock-transduced T cells
TCR-transduced T cells
IFNγ (pg/ml)
12500
10000
7500
5000
2500
0
NPC
patient #2
6000
4000
2000
0
MVA control
MVA LMP2
MVA LMP2+ SSC peptide
T cells only
c666.1/A11
A11+fibroblasts
A11+HONE1
b.
Mock-transduced T cells
TCR-transduced T cells
HK1/A11
% specific lysis
40
30
20
10
0
c666.1/A11
60
40
20
0
+ vacc control
+ vacc LMP2
+ vacc LMP2 + SSC peptide

Figure 13