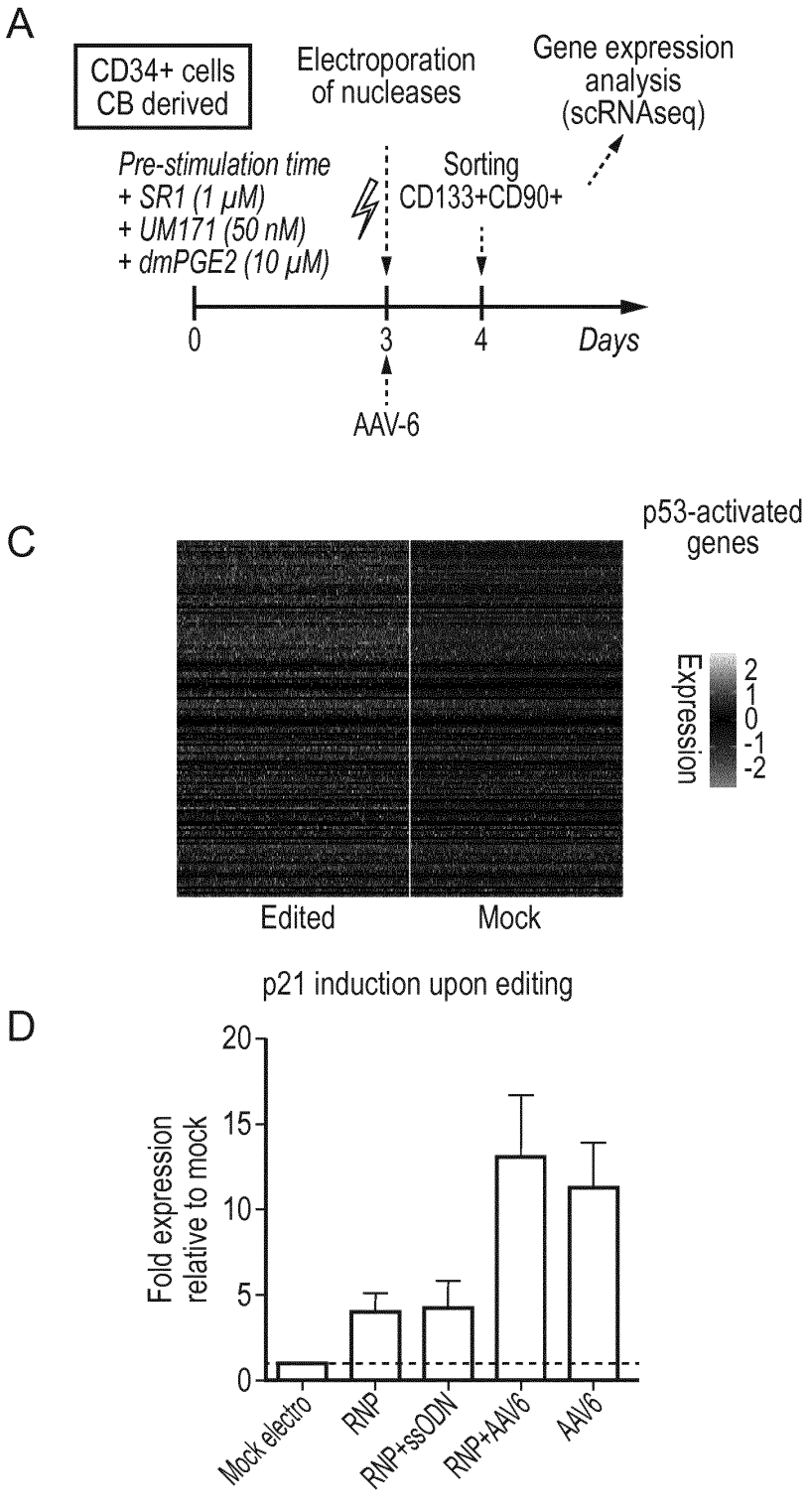

A
CD34+ cells
CB derived
Electroporation
of nucleases
Gene expression
analysis
(scRNAseq)
Pre-stimulation time
+ SR1 (1 µM)
+ UM171 (50 nM)
+ dmPGE2 (10 µM)
Sorting
CD133+CD90+
0
3
4
Days
AAV-6
C
p53-activated
genes
Expression
2
1
0
-1
-2
Edited
Mock
p21 induction upon editing
D
Fold expression
relative to mock
20
15
10
5
0
Mock electro
RNP
RNP+ssODN
RNP+AAV6
AAV6

FIG. 1

Reactome

Index	Name	P-value	Adjusted p-value	Z-score	Combined score
1	Transcriptional Regulation by TP53_ Homo sapiens_R-HSA-3700989	4.670e-12	1.378e-9	-2.31	60.15
2	TP53 Regulates Transcription of Cell Death Genes_Homo sapiens_R-HSA-5633008	2.828e-9	4.172e-7	-1.98	39.05
3	Generic Transcription Pathway_Homo sapiens_R-HSA-212436	0.000001411	0.0001387	-2.25	30.28
4	TP53 Regulates Transcription of Genes Involved in Cytochrome C Release_Homo sapiens_R-HSA-6803204	0.000002821	0.0002081	-1.84	23.45
5	TP53 Regulates Transcription of Cell Cycle Genes_Homo sapiens_R-HSA-6791312	0.000005688	0.0003356	-1.93	23.26
6	TNFs bind their physiological receptors_ Homo sapiens_R-HSA-5669034	0.0002777	0.01365	-2.19	17.95
7	Apoptosis_Homo sapiens_R-HSA-109581	0.001842	0.04180	-2.06	12.94
8	Programmed Cell Death_Homo sapiens_ R-HSA-5357801	0.001995	0.04186	-2.07	12.86
9	Gene Expression_Homo sapiens_R-HSA-74160	0.002469	0.04294	-2.04	12.23
10	CASP8 activity is inhibited_Homo sapiens_ R-HSA-5218900	0.001511	0.04180	-1.65	10.69

FIG. 1B

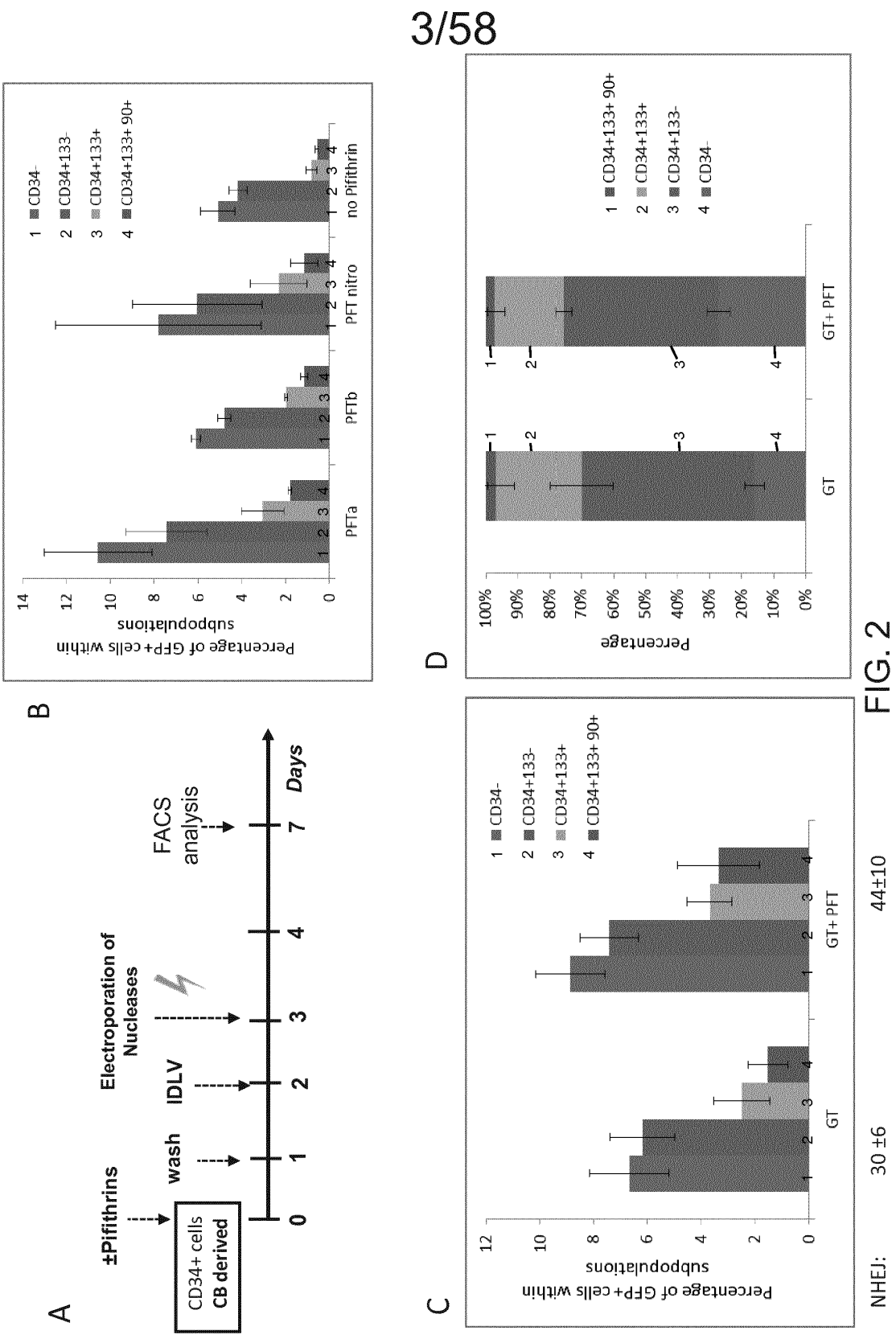

A
±Pifithrins
wash
IDLV
Electroporation of Nucleases
FACS analysis
CD34+ cells CB derived
0 1 2 3 4 7 Days
B
Percentage of GFP+ cells within subpopulations
1 CD34-
2 CD34+133-
3 CD34+133+
4 CD34+133+ 90+
PFTa
PFTb
PFT nitro
no Pifithrin
C
Percentage of GFP+ cells within subpopulations
GT
GT+ PFT
NHEJ: 30 ±6 44±10
D
Percentage
1 CD34+133+ 90+
2 CD34+133+
3 CD34+133-
4 CD34-
GT
GT+ PFT

FIG. 2

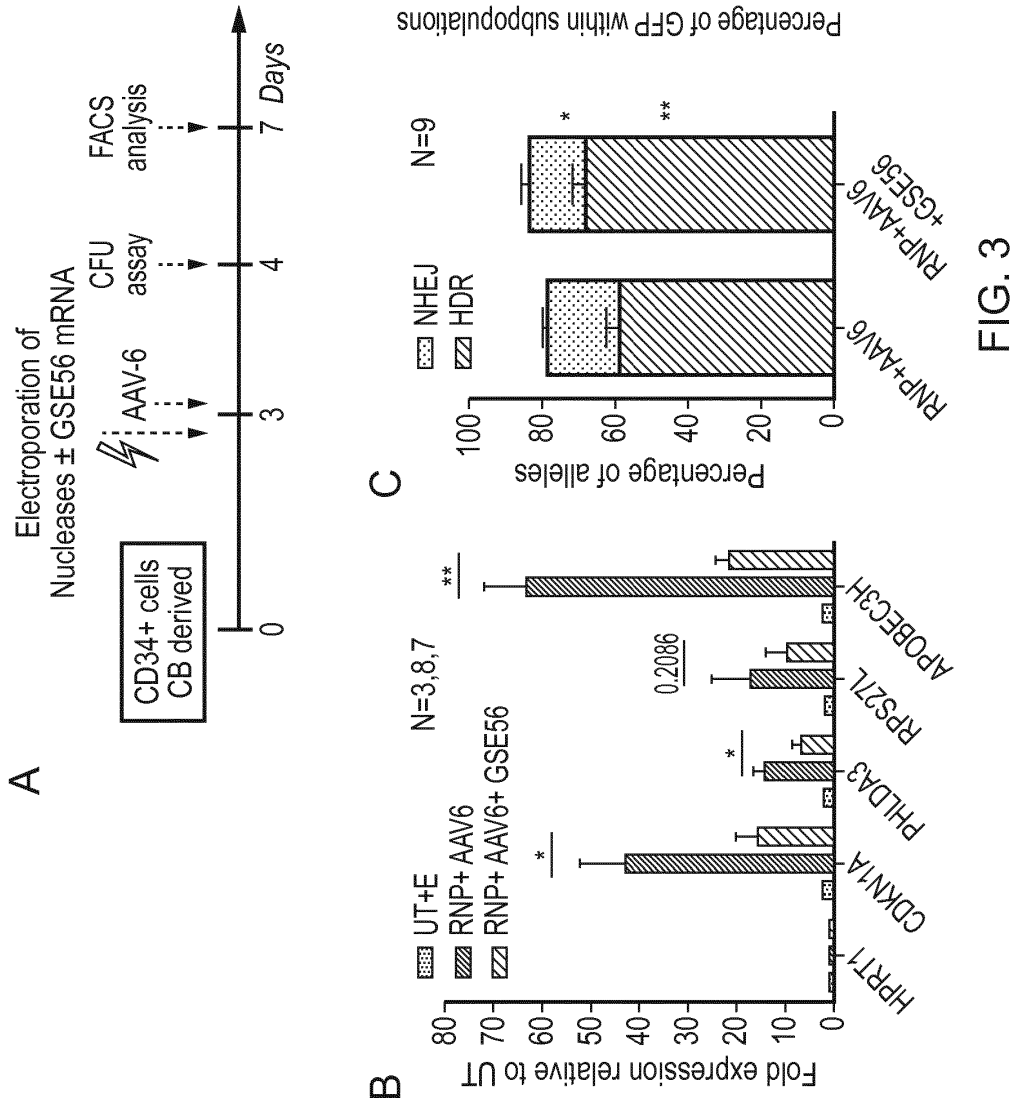

A
Electroporation of
Nucleases ± GSE56 mRNA
CD34+ cells
CB derived
AAV-6
CFU
assay
FACS
analysis
0
3
4
7 Days
B
UT+E
RNP+ AAV6
RNP+ AAV6+ GSE56
N=3,8,7
Fold expression relative to UT
HPRT1
CDKN1A
PHLDA3
RPS27L
APOBEC3H
0,2086
C
NHEJ
HDR
N=9
Percentage of alleles
RNP+AAV6
RNP+AAV6 +GSE56
1 CD34-
2 CD34+ CD133-
3 CD34+ CD133+
4 CD34+ CD133+ CD90+
N=15
Percentage of GFP within subpopulations

FIG. 3

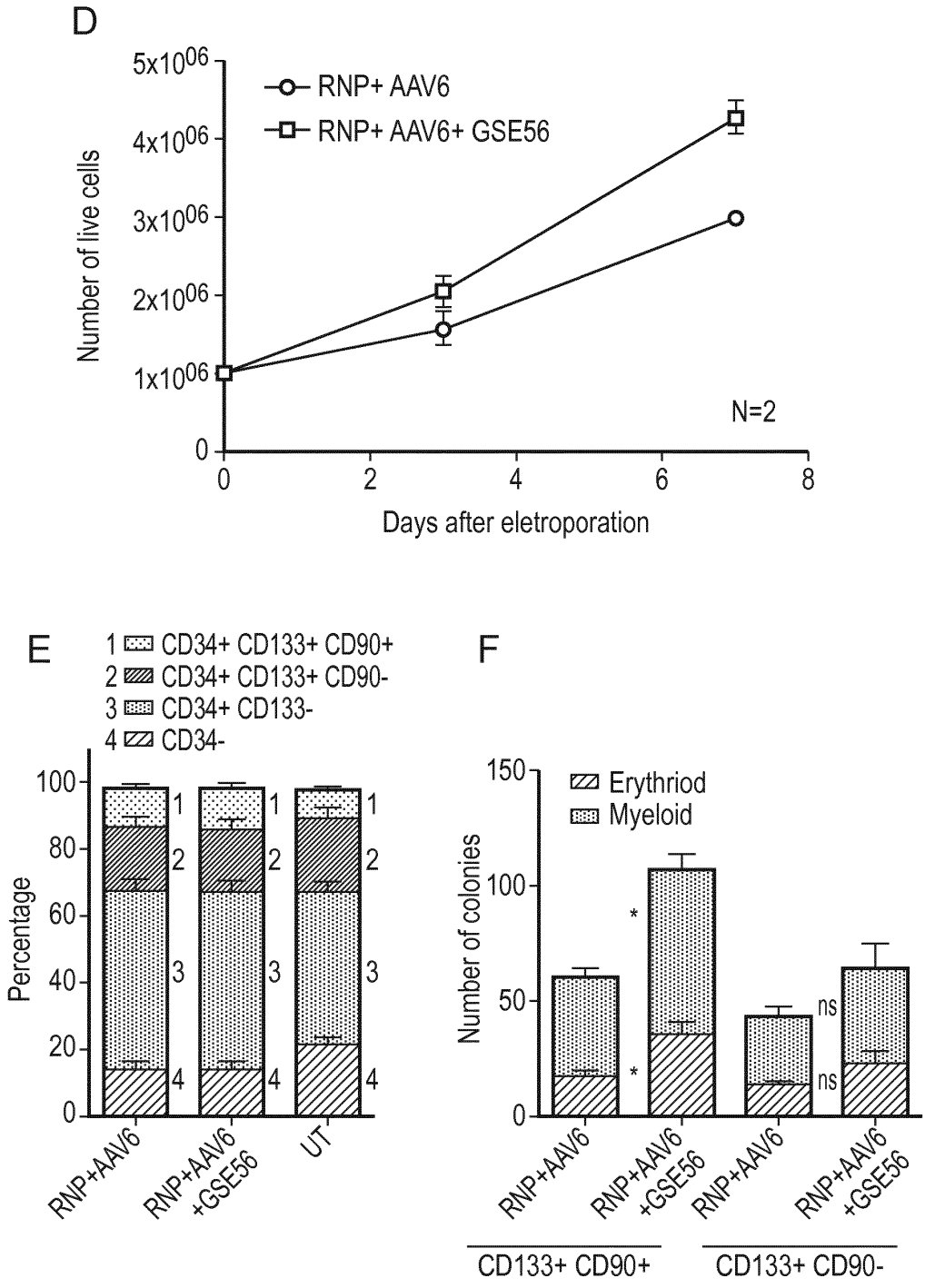


FIG. 3 (Continued)

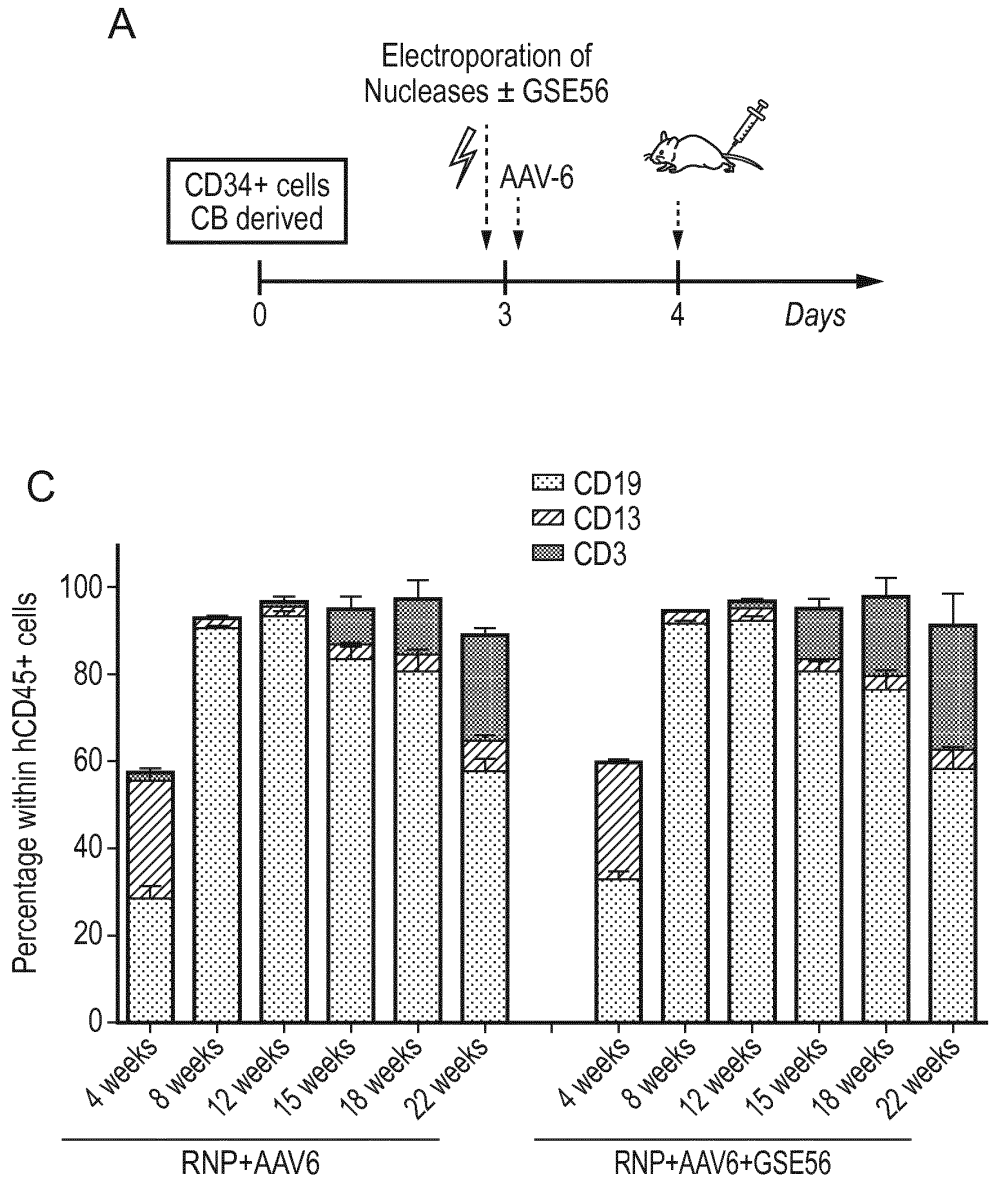

A
Electroporation of
Nucleases ± GSE56
AAV-6
CD34+ cells
CB derived
0
3
4
Days
C
CD19
CD13
CD3
Percentage within hCD45+ cells
100
80
60
40
20
0
4 weeks
8 weeks
12 weeks
15 weeks
18 weeks
22 weeks
RNP+AAV6
RNP+AAV6+GSE56

FIG. 4

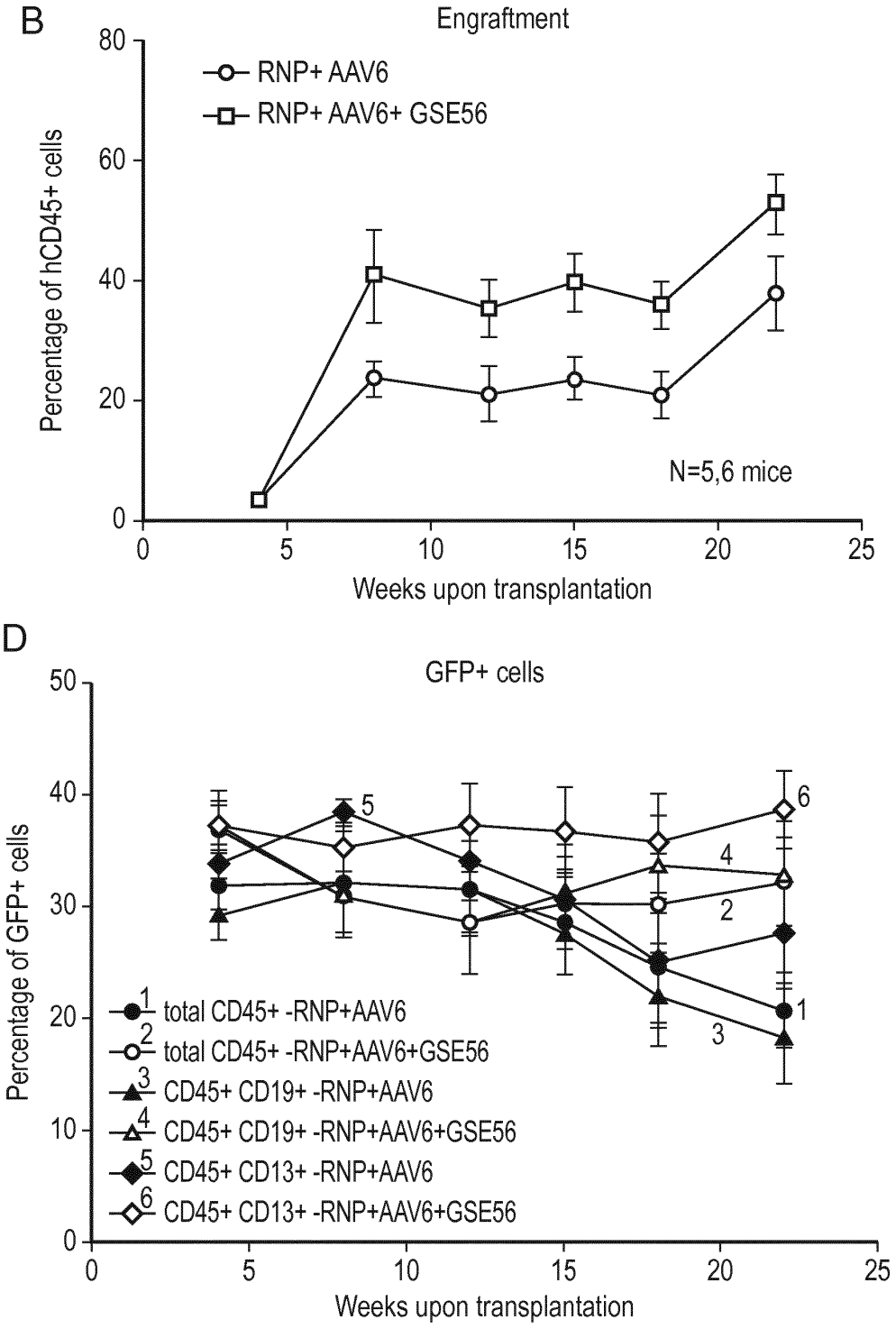


FIG. 4 (Continued)

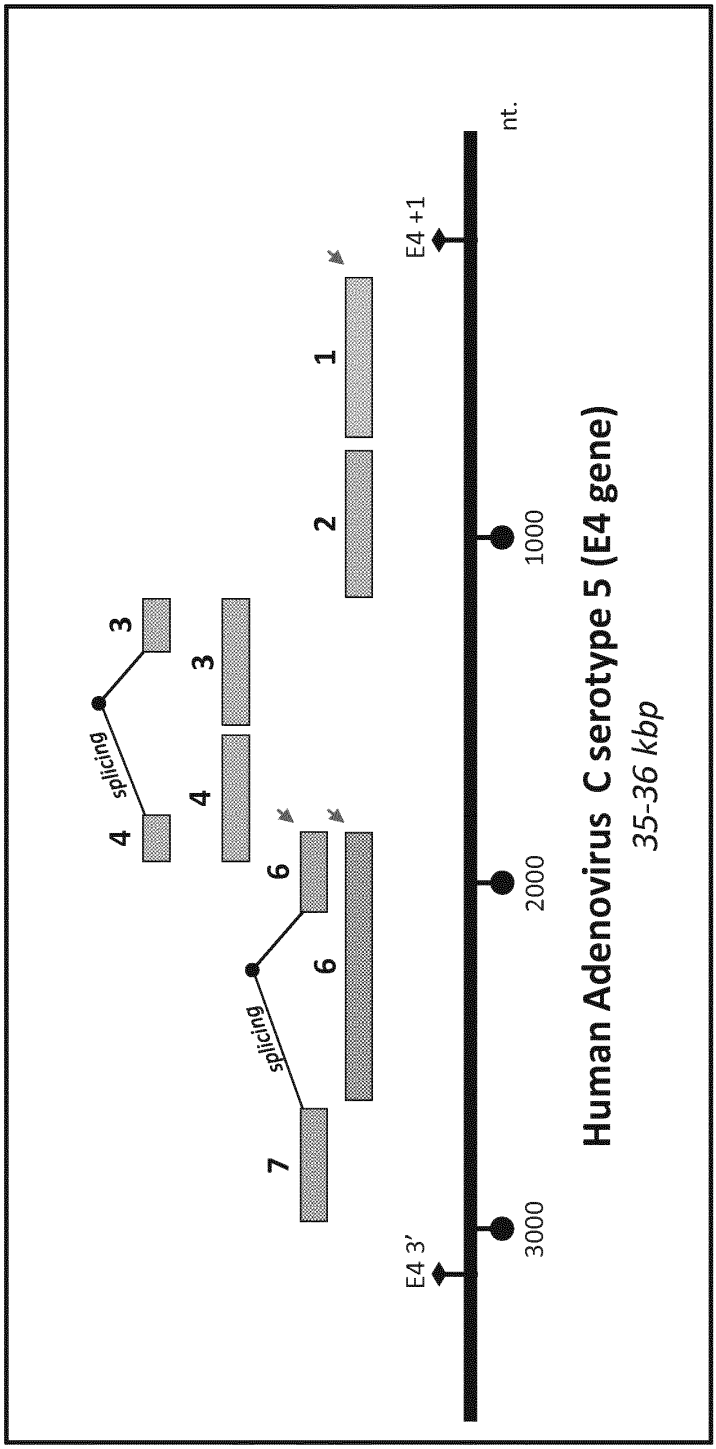

Human Adenovirus C serotype 5 (E4 gene)
35-36 kbp
E4 +1
E4 3'
nt.
1000
2000
3000
1
2
3
4
6
7
splicing
splicing

FIG. 5

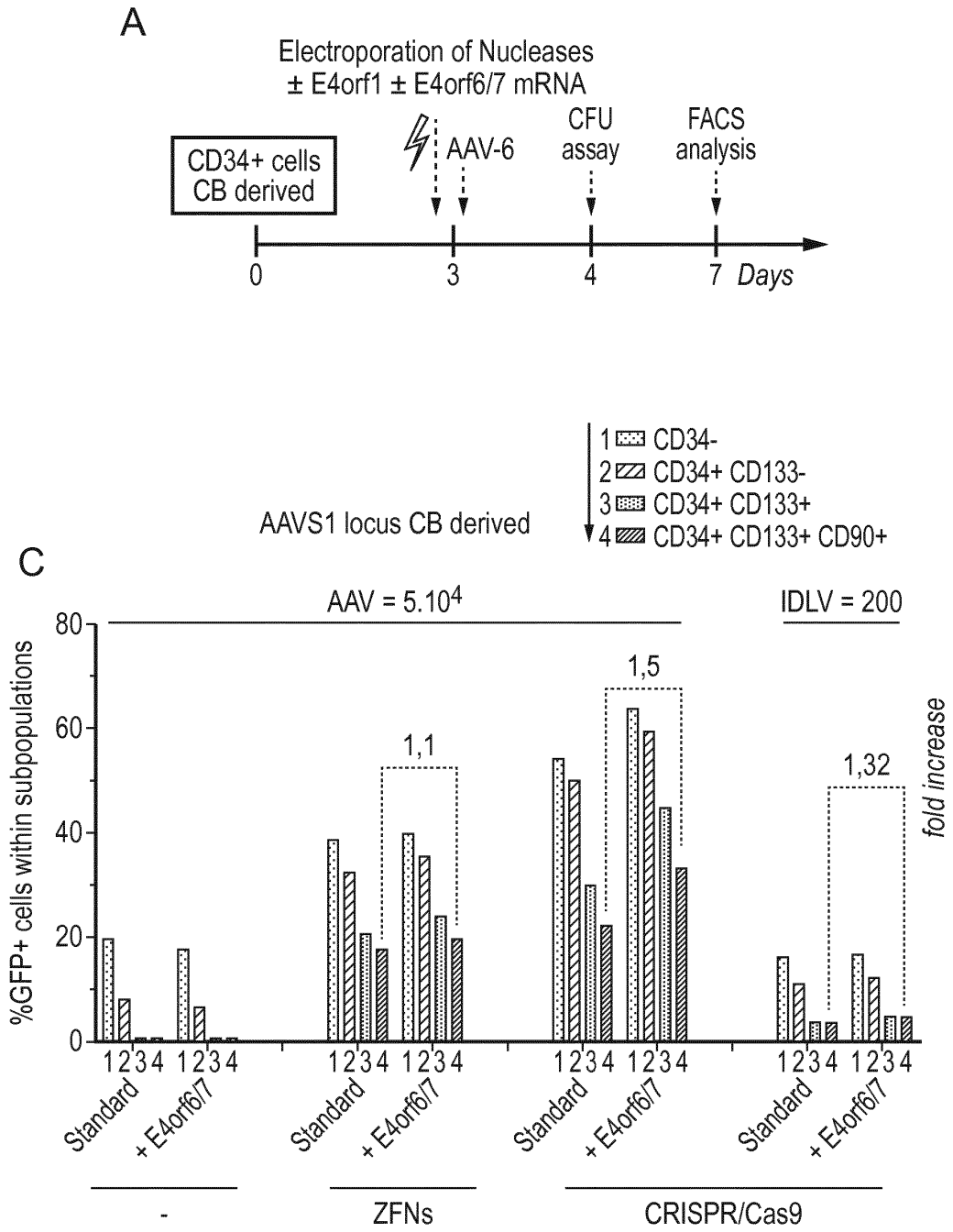

A
Electroporation of Nucleases
± E4orf1 ± E4orf6/7 mRNA
CD34+ cells
CB derived
AAV-6
CFU
assay
FACS
analysis
0
3
4
7 Days
AAVS1 locus CB derived
1 CD34-
2 CD34+ CD133-
3 CD34+ CD133+
4 CD34+ CD133+ CD90+
C
AAV = 5.10^4
IDLV = 200
%GFP+ cells within subpopulations
fold increase
1,1
1,5
1,32
Standard
+ E4orf6/7
-
ZFNs
CRISPR/Cas9

FIG. 6

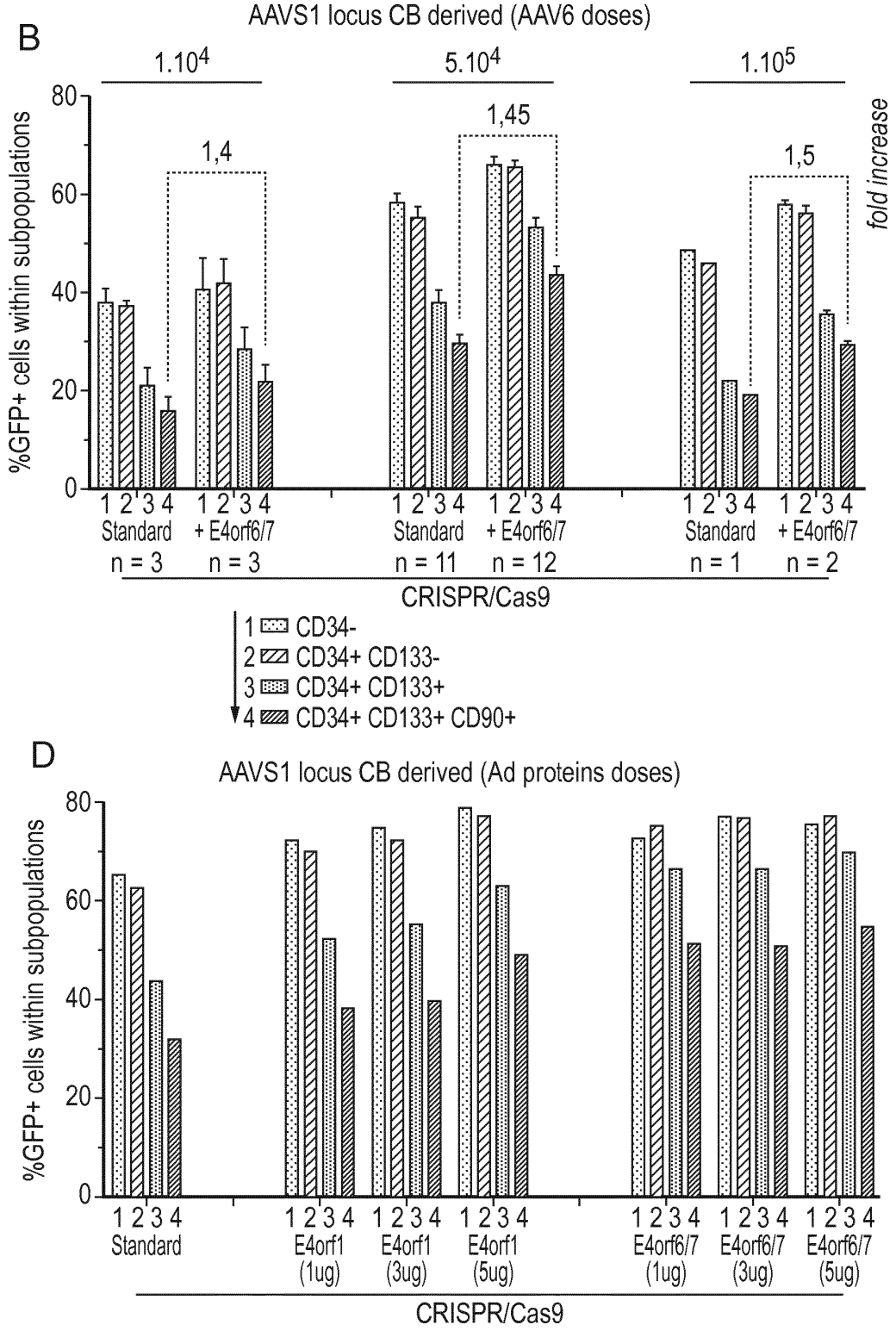
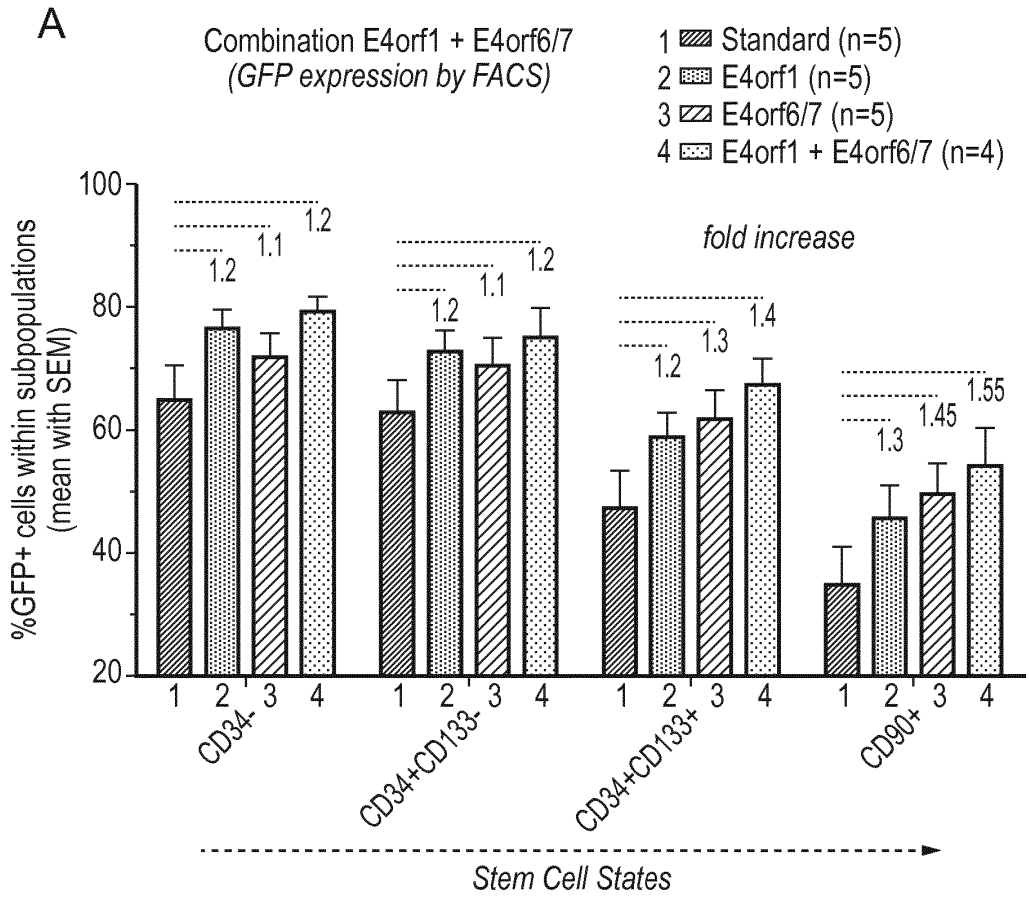


FIG. 6 (Continued)


A
Combination E4orf1 + E4orf6/7
(GFP expression by FACS)
1 Standard (n=5)
2 E4orf1 (n=5)
3 E4orf6/7 (n=5)
4 E4orf1 + E4orf6/7 (n=4)
%GFP+ cells within subpopulations
(mean with SEM)
100
80
60
40
20
fold increase
1.2
1.1
1.2
1.2
1.1
1.2
1.2
1.3
1.4
1.3
1.45
1.55
1 2 3 4
CD34-
CD34+CD133-
CD34+CD133+
CD90+
Stem Cell States

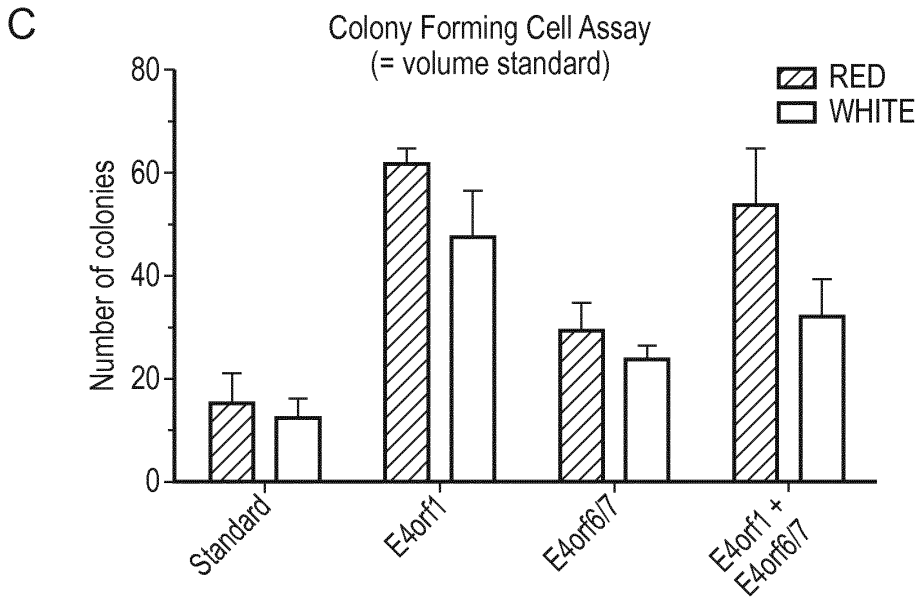

C
Colony Forming Cell Assay
(= volume standard)
RED
WHITE
Number of colonies
80
60
40
20
0
Standard
E4orf1
E4orf6/7
E4orf1 +
E4orf6/7

FIG. 7

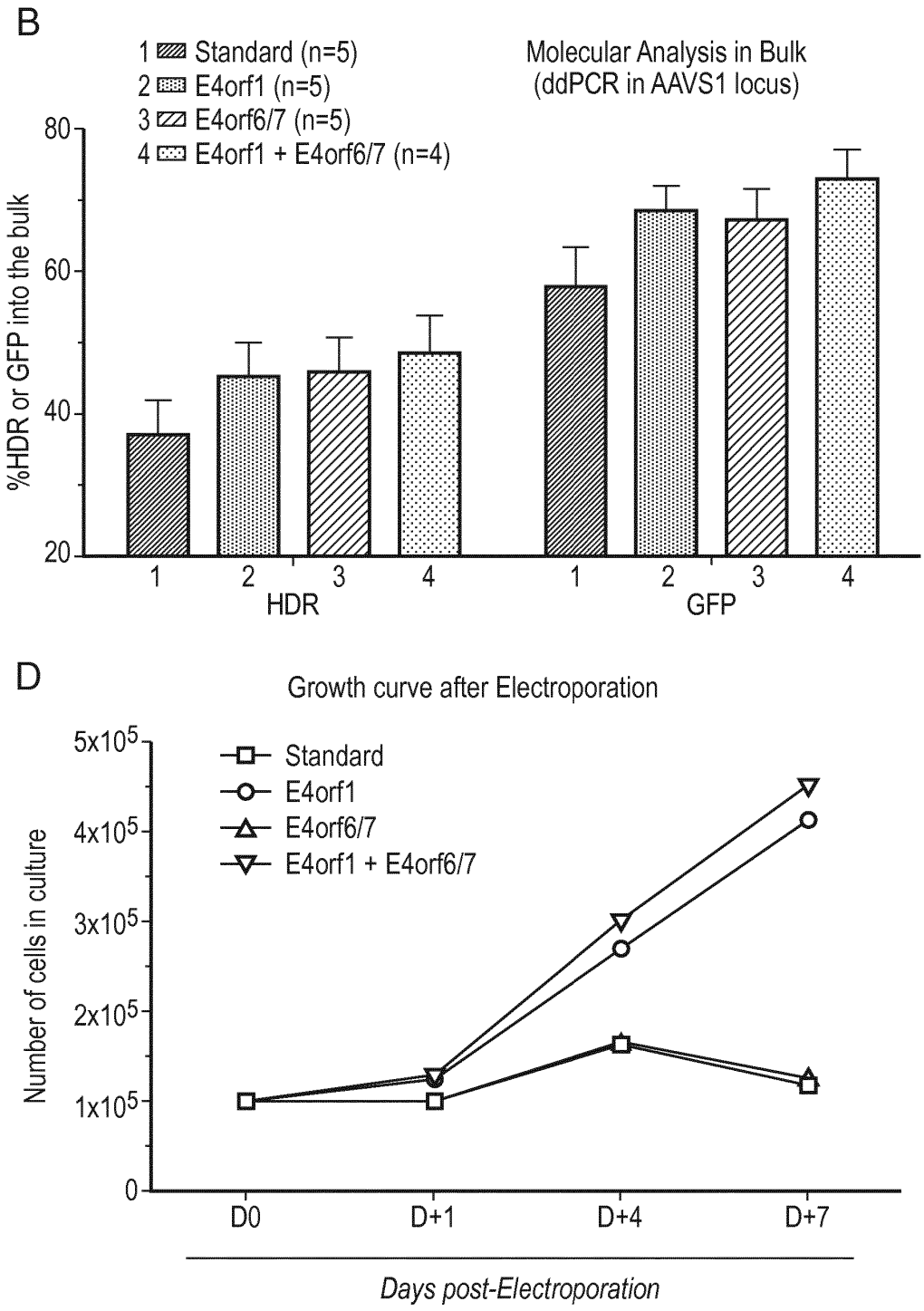
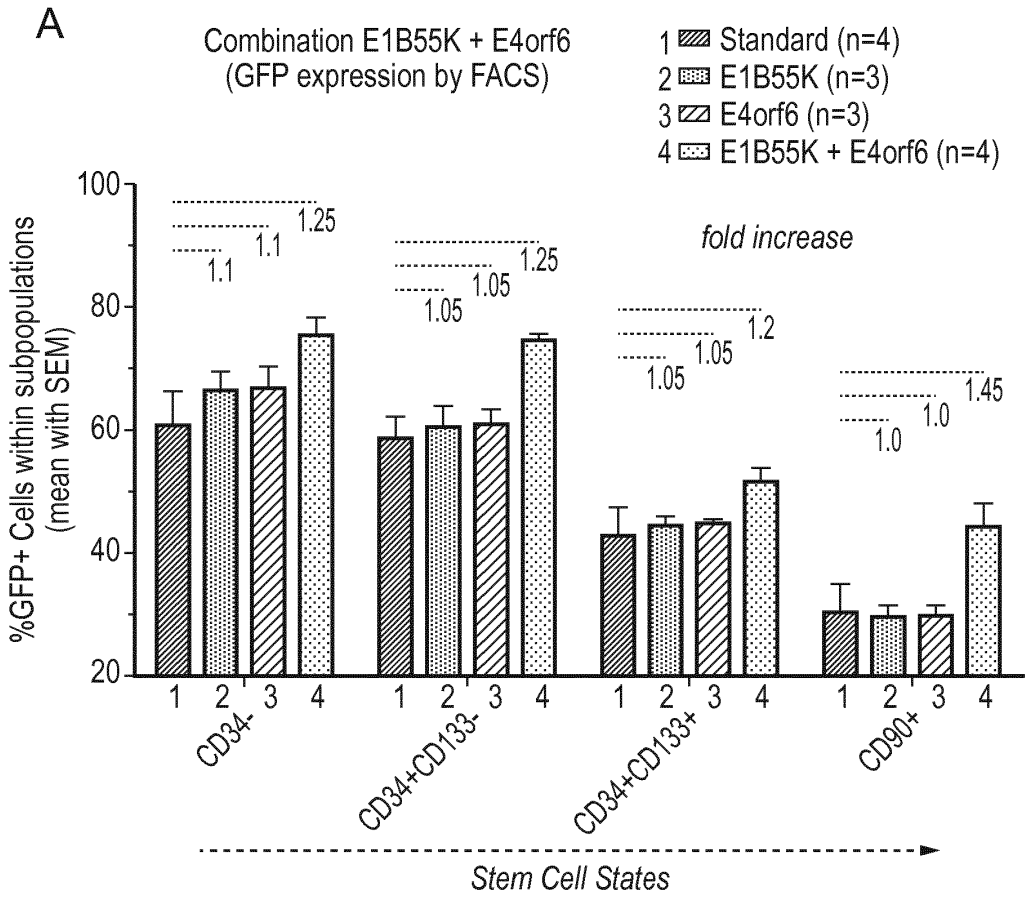


FIG. 7 (Continued)


A
Combination E1B55K + E4orf6
(GFP expression by FACS)
1 Standard (n=4)
2 E1B55K (n=3)
3 E4orf6 (n=3)
4 E1B55K + E4orf6 (n=4)
%GFP+ Cells within subpopulations
(mean with SEM)
fold increase
CD34-
CD34+CD133-
CD34+CD133+
CD90+
Stem Cell States

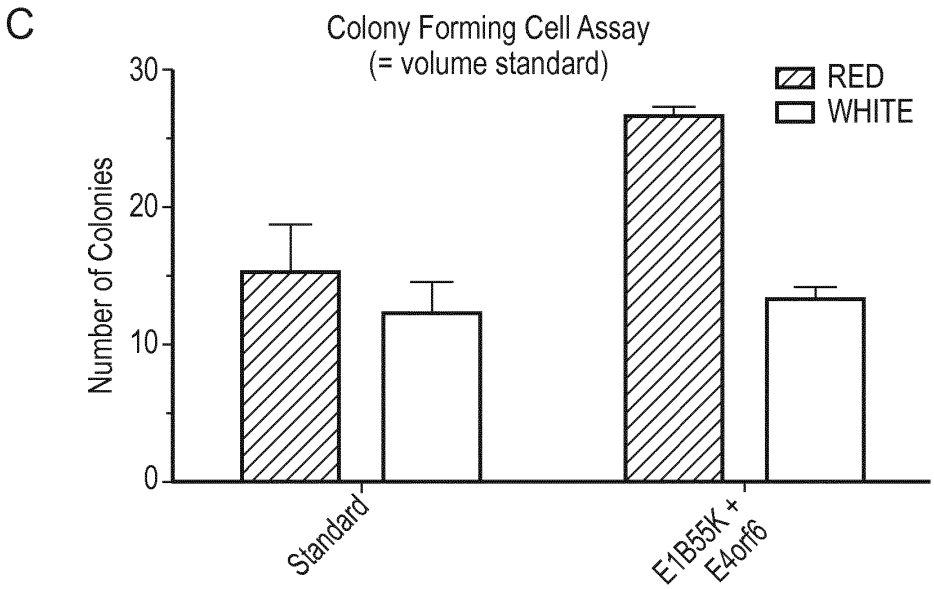

C
Colony Forming Cell Assay
(= volume standard)
RED
WHITE
Number of Colonies
Standard
E1B55K + E4orf6

FIG. 8

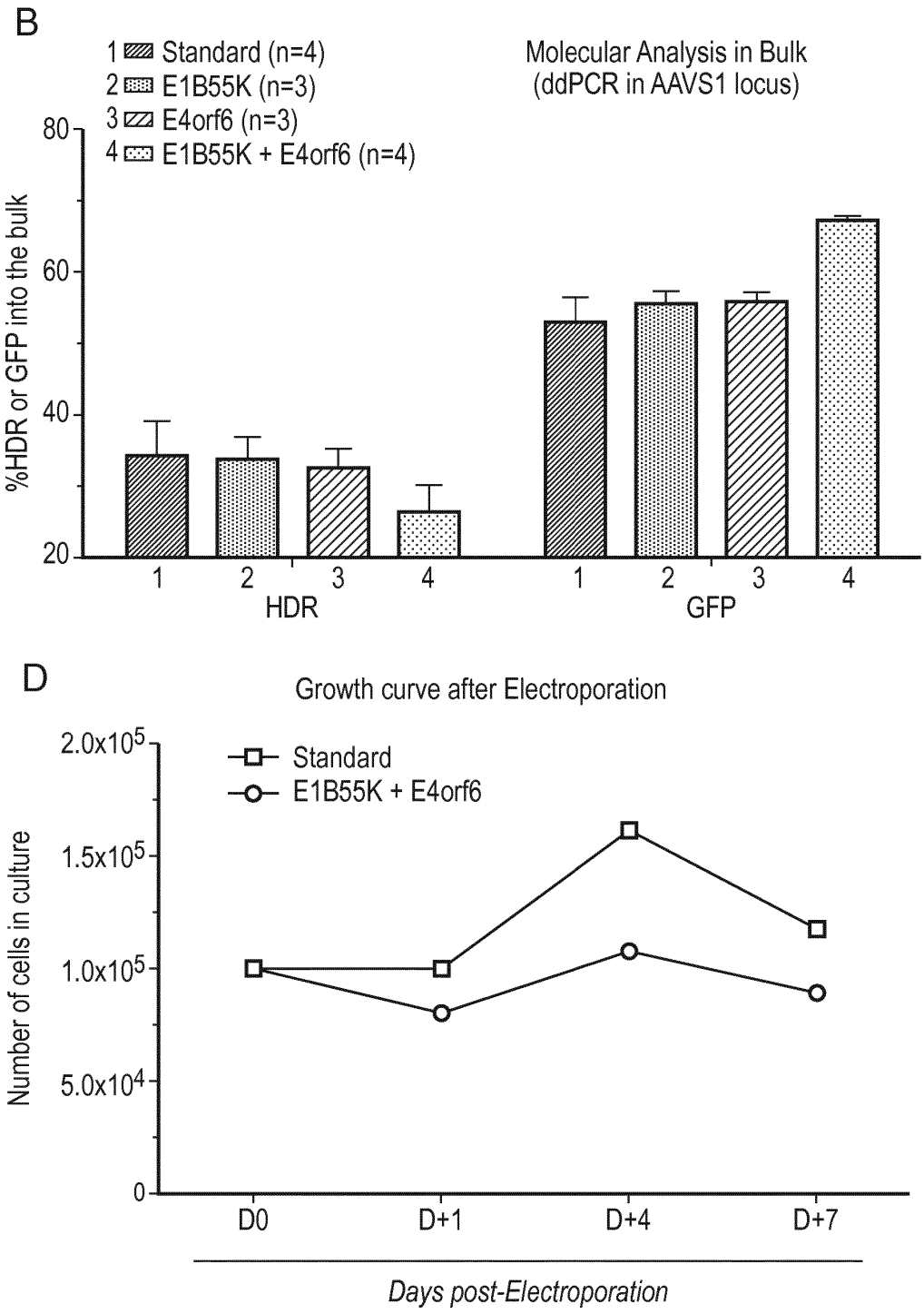
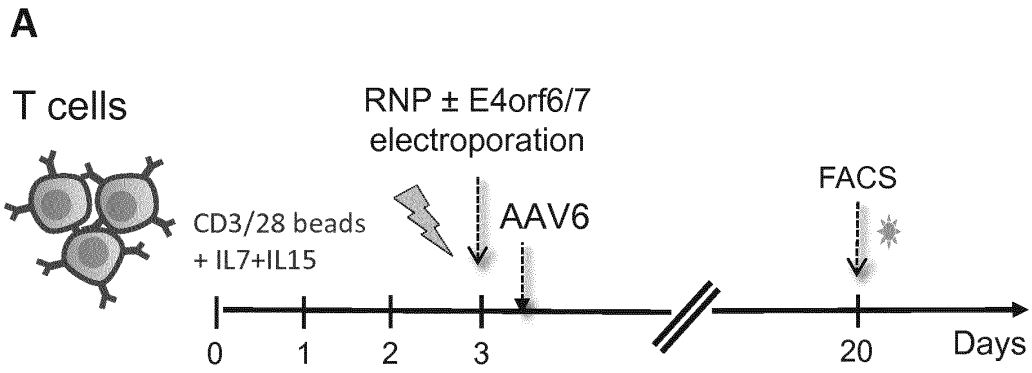


FIG. 8 (Continued)


A
T cells
RNP ± E4orf6/7
electroporation
CD3/28 beads
+ IL7+IL15
AAV6
FACS
0
1
2
3
20
Days

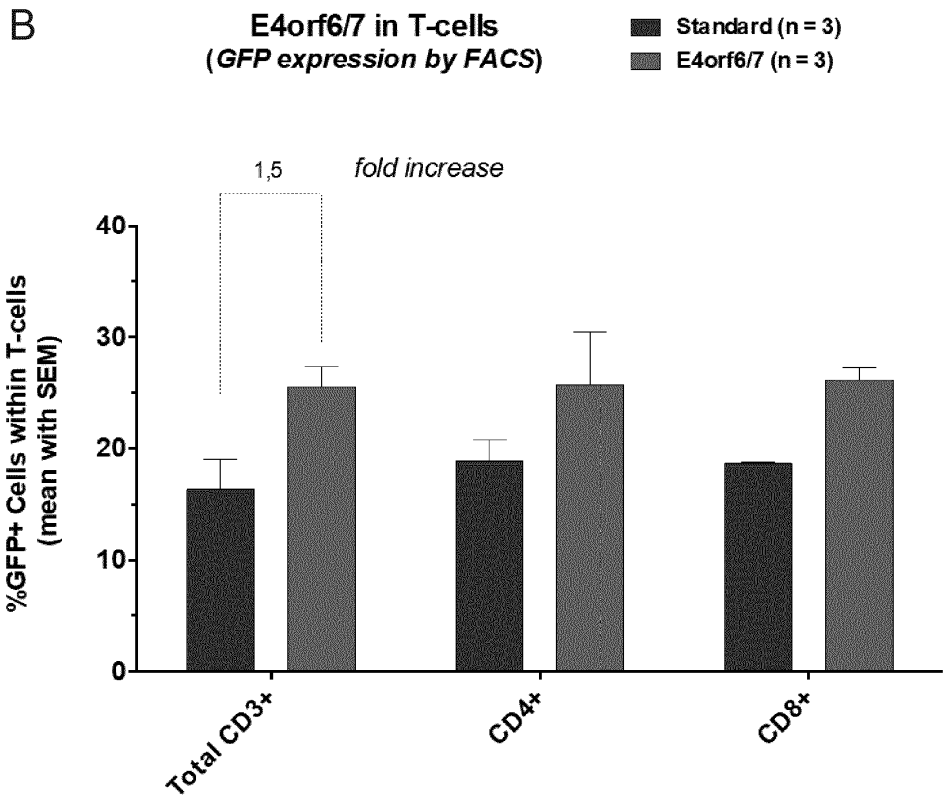

B
E4orf6/7 in T-cells
(GFP expression by FACS)
Standard (n = 3)
E4orf6/7 (n = 3)
1,5
fold increase
%GFP+ Cells within T-cells
(mean with SEM)
40
30
20
10
0
Total CD3+
CD4+
CD8+

FIG. 9

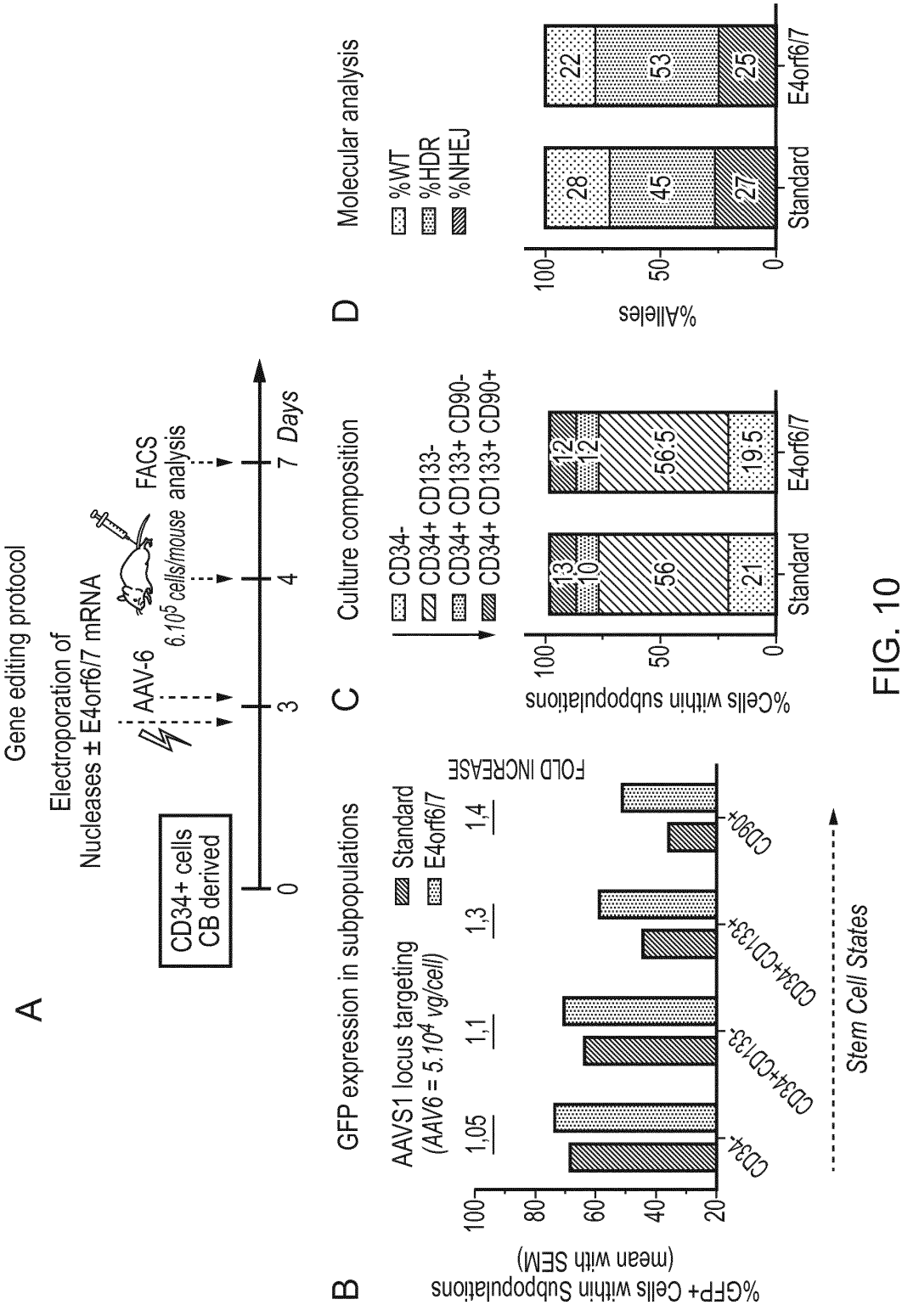

A
Gene editing protocol
Electroporation of
Nucleases ± E4orf6/7 mRNA
AAV-6
6.10^5 cells/mouse
FACS
analysis
CD34+ cells
CB derived
0
3
4
7 Days
B
GFP expression in subpopulations
AAVS1 locus targeting
(AAV6 = 5.10^4 vg/cell)
1,05
1,1
1,3
1,4
Standard
E4orf6/7
FOLD INCREASE
%GFP+ Cells within Subpopulations
(mean with SEM)
CD34-
CD34+CD133-
CD34+CD133+
CD90+
Stem Cell States
C
Culture composition
CD34-
CD34+ CD133-
CD34+ CD133+ CD90-
CD34+ CD133+ CD90+
%Cells within subpopulations
13
10
56
21
12
12
56.5
19.5
Standard
E4orf6/7
D
Molecular analysis
%WT
%HDR
%NHEJ
%Alleles
28
45
27
22
53
25
Standard
E4orf6/7

FIG. 10

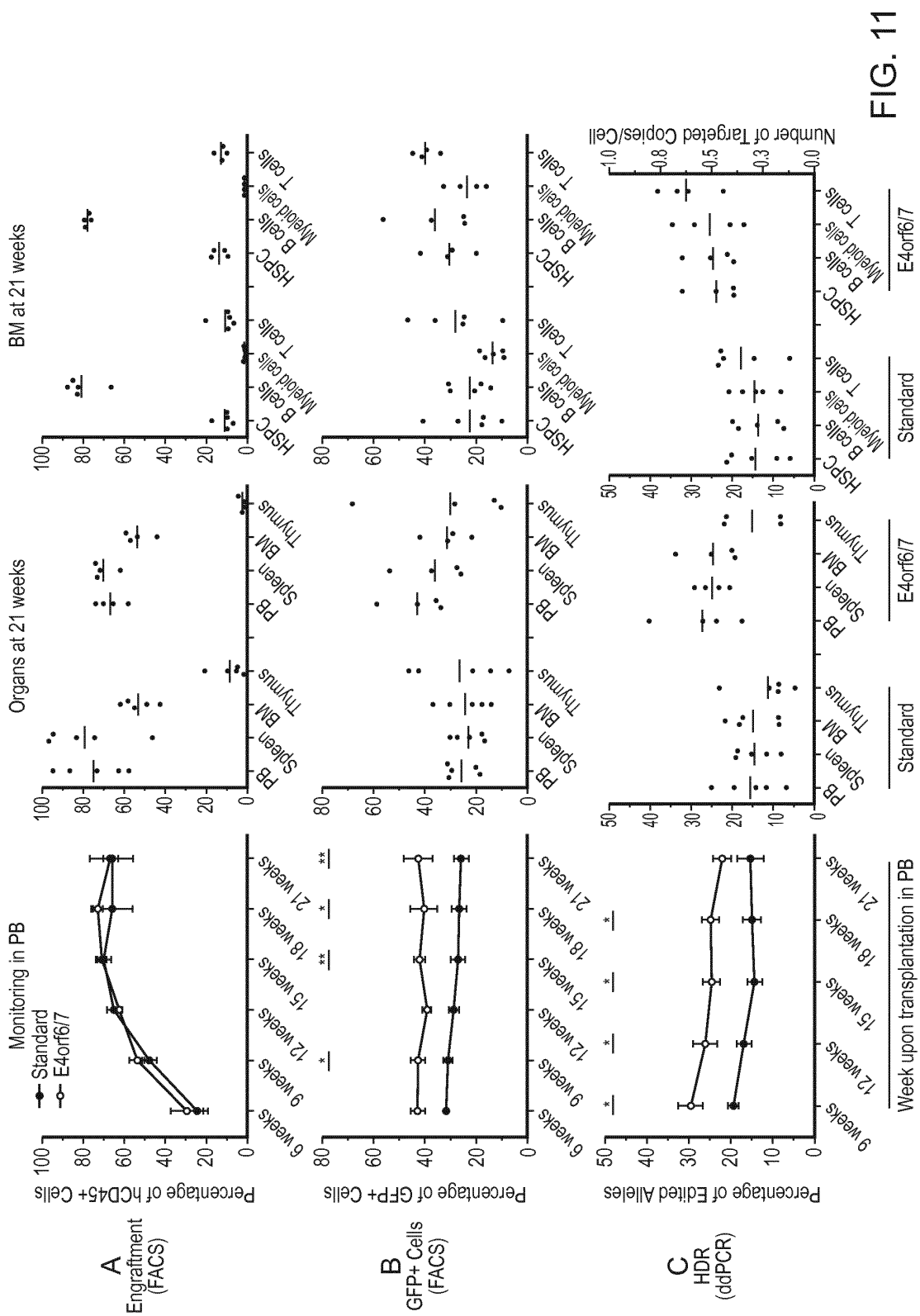

A
Engraftment (FACS)
Monitoring in PB
Standard
E4orf6/7
Percentage of hCD45+ Cells
6 weeks
9 weeks
12 weeks
15 weeks
18 weeks
21 weeks
Organs at 21 weeks
PB
Spleen
BM
Thymus
BM at 21 weeks
HSPC
B cells
Myeloid cells
T cells
B
GFP+ Cells (FACS)
Percentage of GFP+ Cells
C
HDR (ddPCR)
Percentage of Edited Alleles
Number of Targeted Copies/Cell
Week upon transplantation in PB
Standard
E4orf6/7

FIG. 11

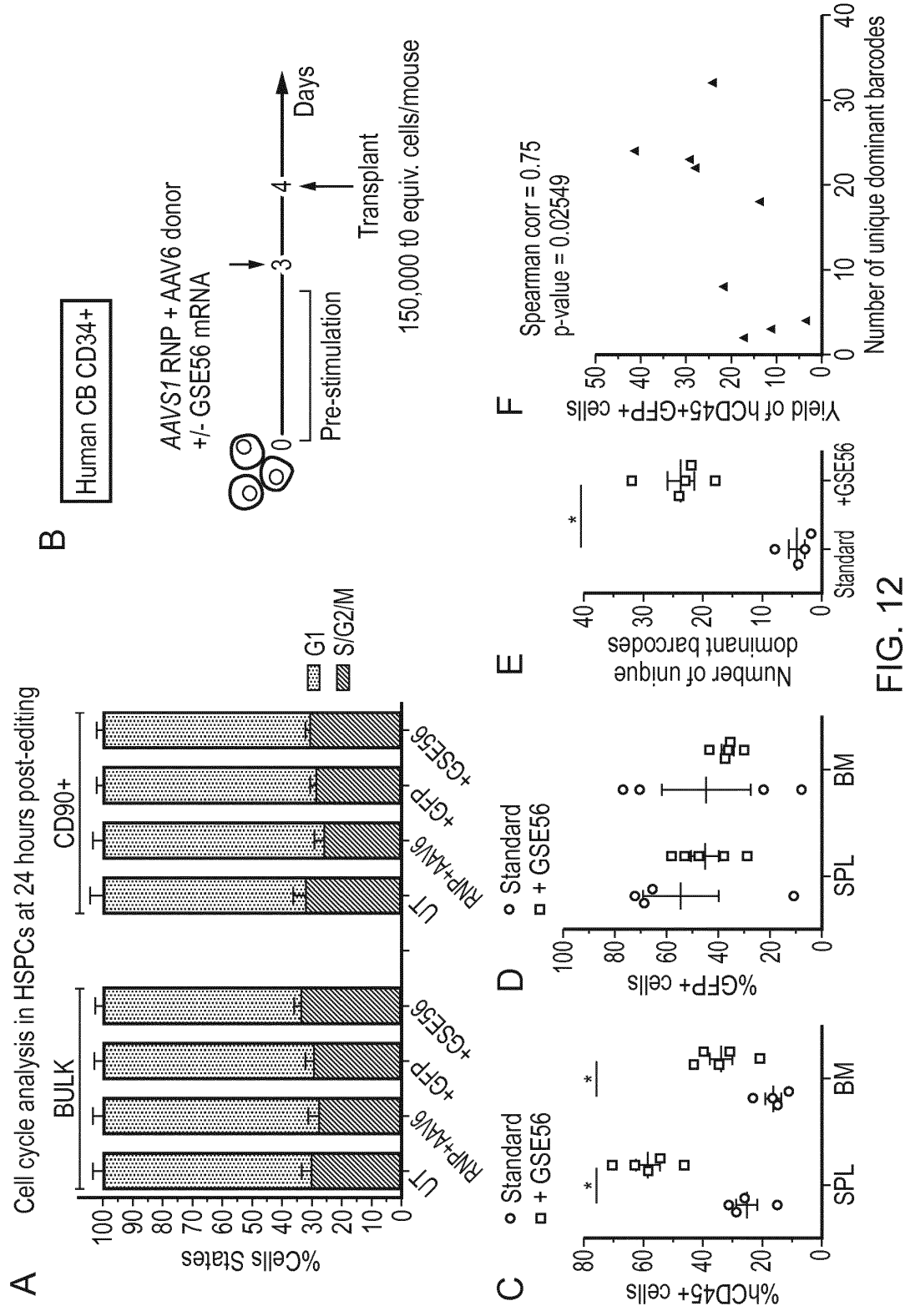

A
Cell cycle analysis in HSPCs at 24 hours post-editing
BULK
CD90+
%Cells States
G1
S/G2/M
UT
RNP+AAV6
+GFP
+GSE56
B
Human CB CD34+
AAVS1 RNP + AAV6 donor
+/- GSE56 mRNA
Pre-stimulation
Transplant
Days
150,000 t0 equiv. cells/mouse
C
Standard
+ GSE56
%hCD45+ cells
SPL
BM
D
%GFP+ cells
E
Number of unique dominant barcodes
Standard
+GSE56
F
Spearman corr = 0.75
p-value = 0.02549
Yield of hCD45+GFP+ cells
Number of unique dominant barcodes

FIG. 12

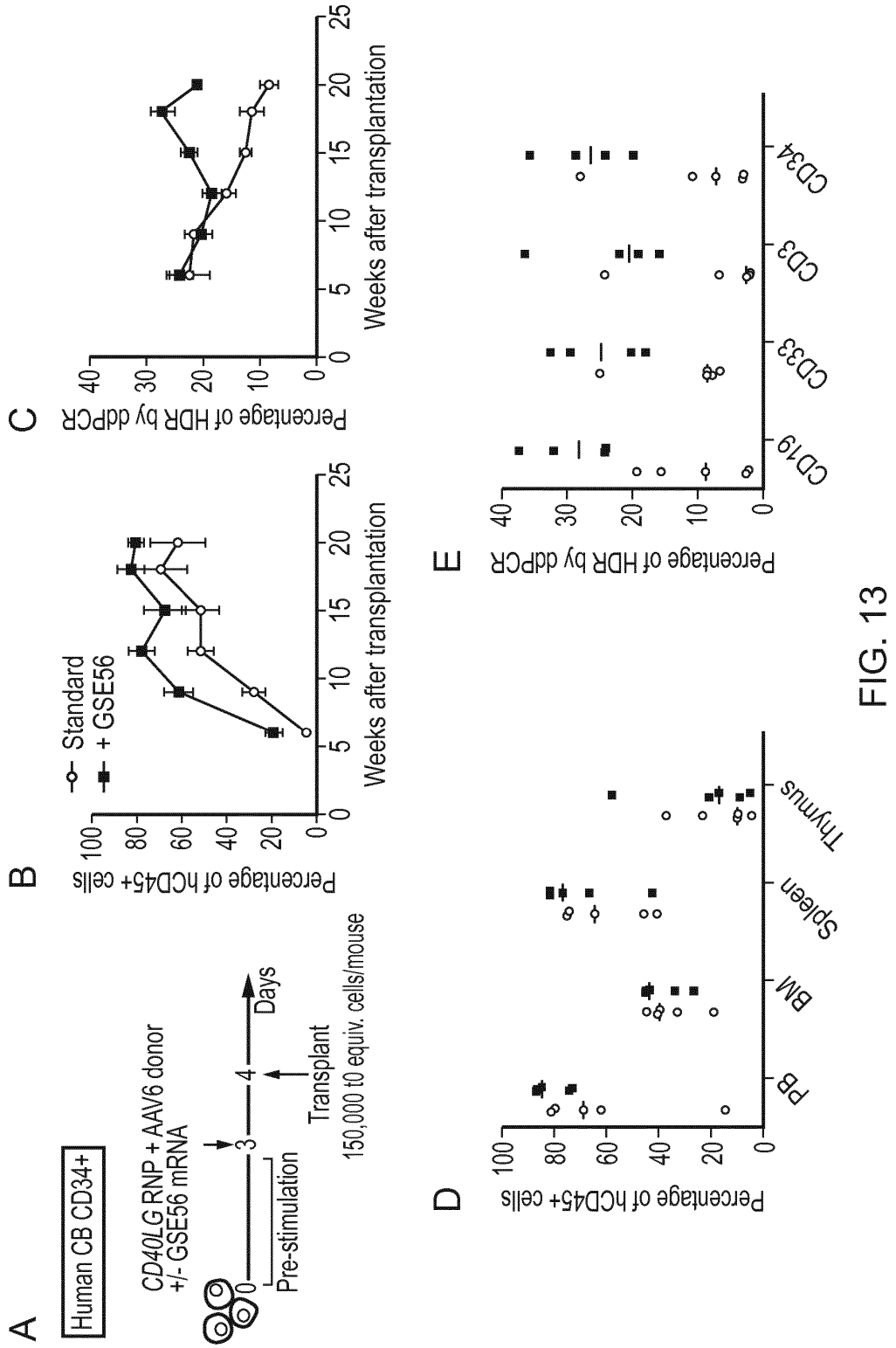
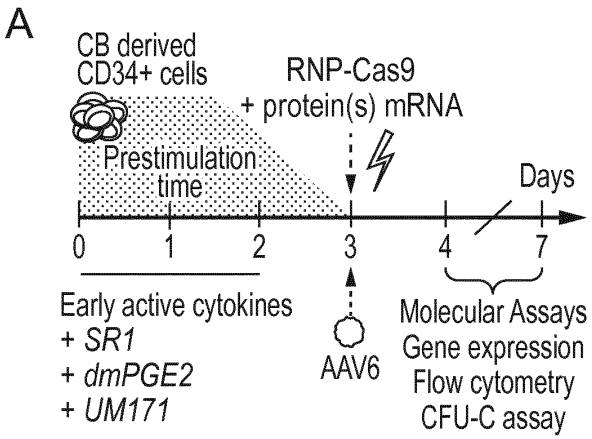

A
Human CB CD34+
CD40LG RNP + AAV6 donor
+/- GSE56 mRNA
0
3
4
Days
Pre-stimulation
Transplant
150,000 t0 equiv. cells/mouse
B
Standard
+ GSE56
Percentage of hCD45+ cells
Weeks after transplantation
C
Percentage of HDR by ddPCR
Weeks after transplantation
D
Percentage of hCD45+ cells
PB
BM
Spleen
Thymus
E
Percentage of HDR by ddPCR
CD19
CD33
CD3
CD34

FIG. 13


A
CB derived
CD34+ cells
RNP-Cas9
+ protein(s) mRNA
Prestimulation
time
Days
0
1
2
3
4
7
Early active cytokines
+ SR1
+ dmPGE2
+ UM171
AAV6
Molecular Assays
Gene expression
Flow cytometry
CFU-C assay

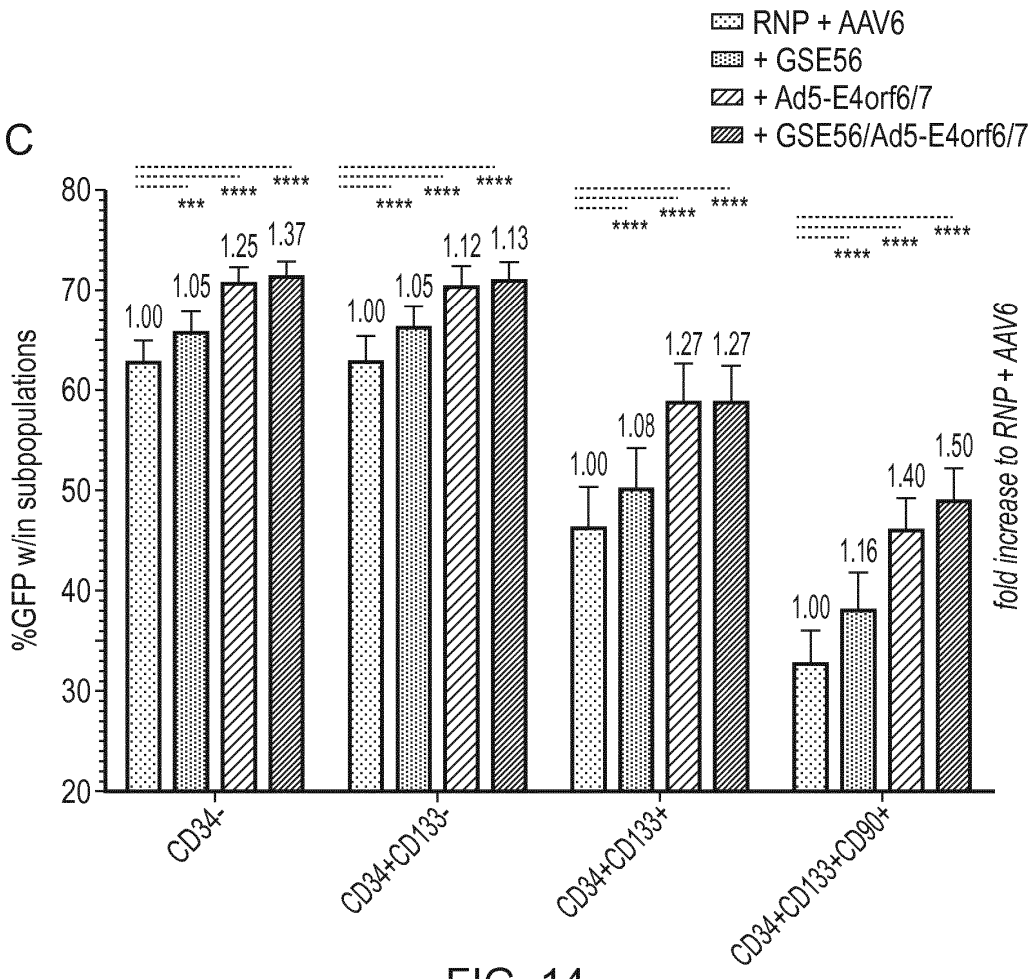
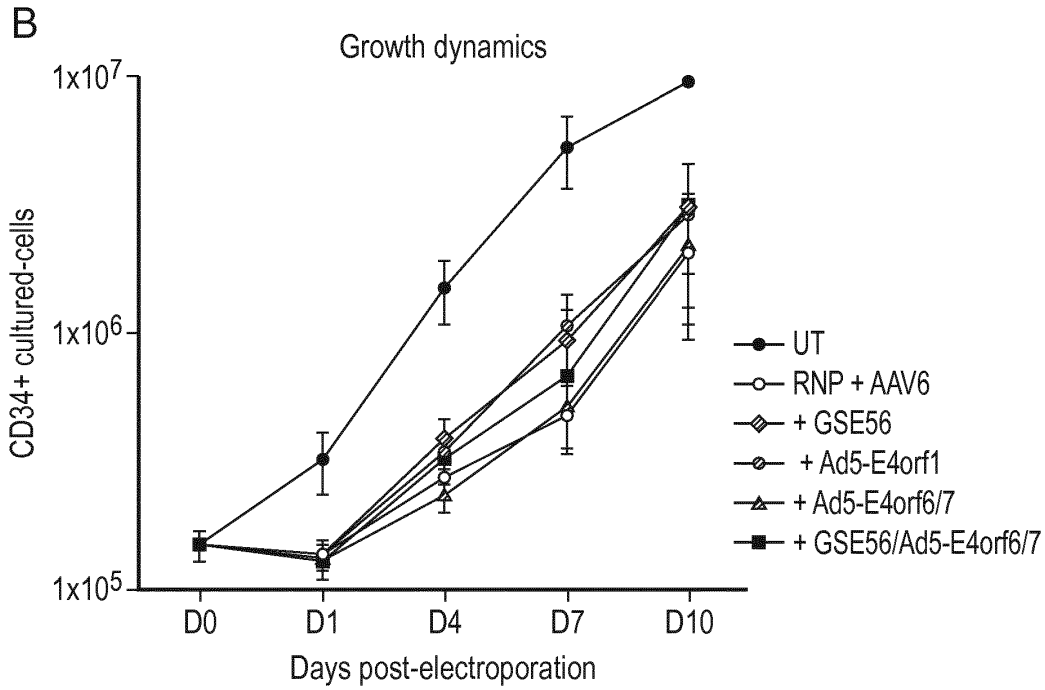

C
RNP + AAV6
+ GSE56
+ Ad5-E4orf6/7
+ GSE56/Ad5-E4orf6/7
%GFP w/in subpopulations
fold increase to RNP + AAV6
80
70
60
50
40
30
20
1.00
1.05
1.25
1.37
1.00
1.05
1.12
1.13
1.00
1.08
1.27
1.27
1.00
1.16
1.40
1.50
CD34-
CD34+CD133-
CD34+CD133+
CD34+CD133+CD90+

FIG. 14



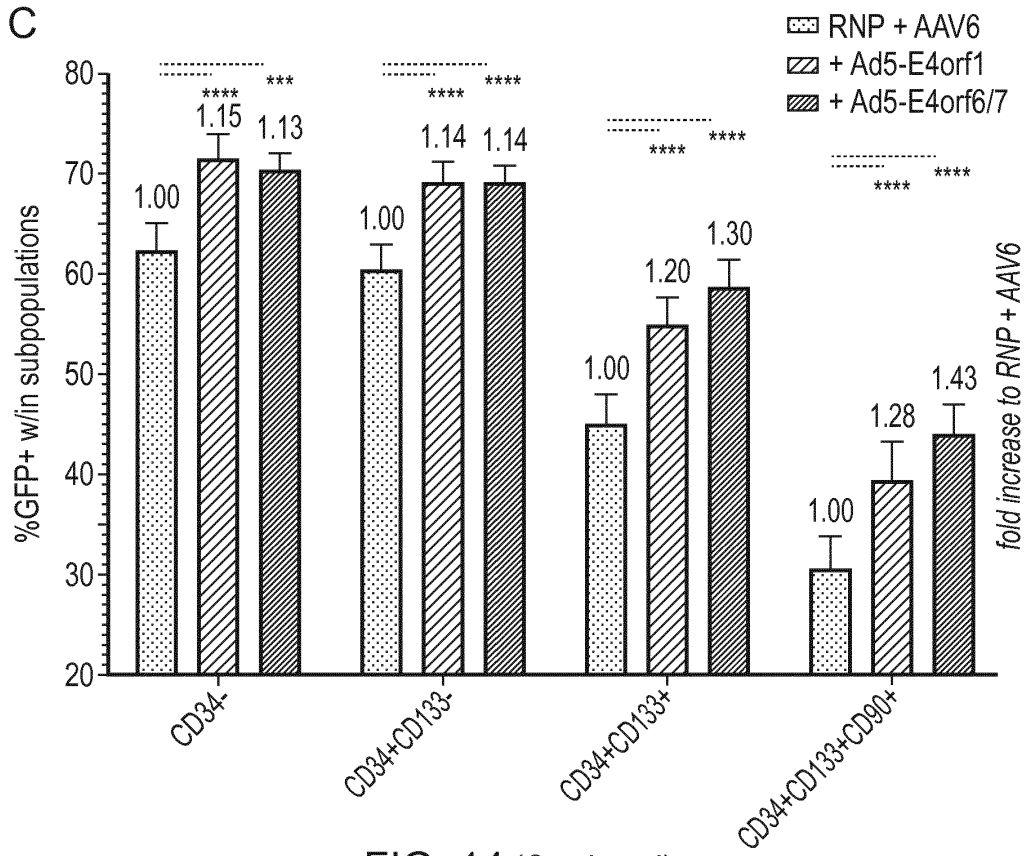


FIG. 14 (Continued)

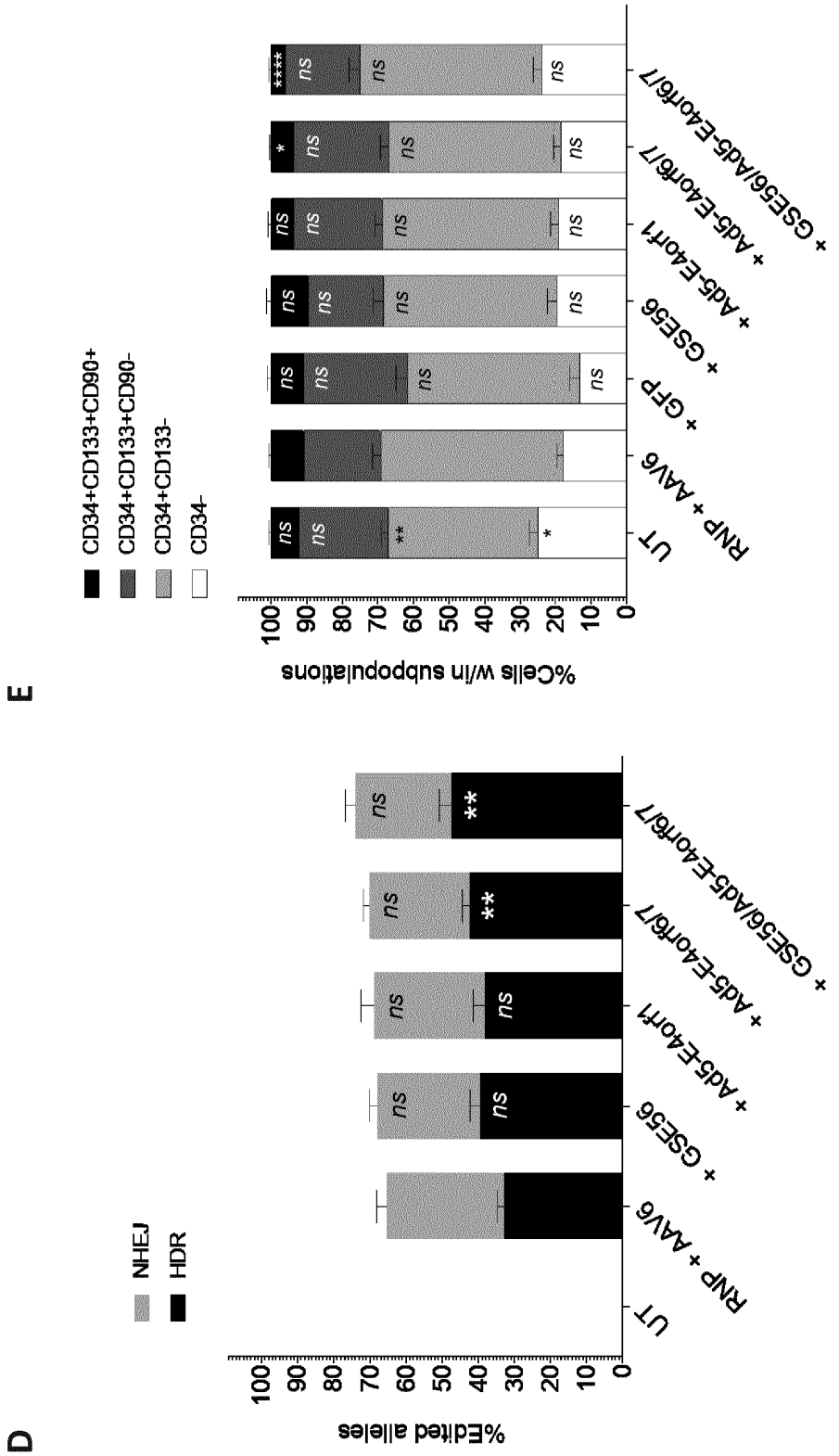


FIG. 14 (Continued)

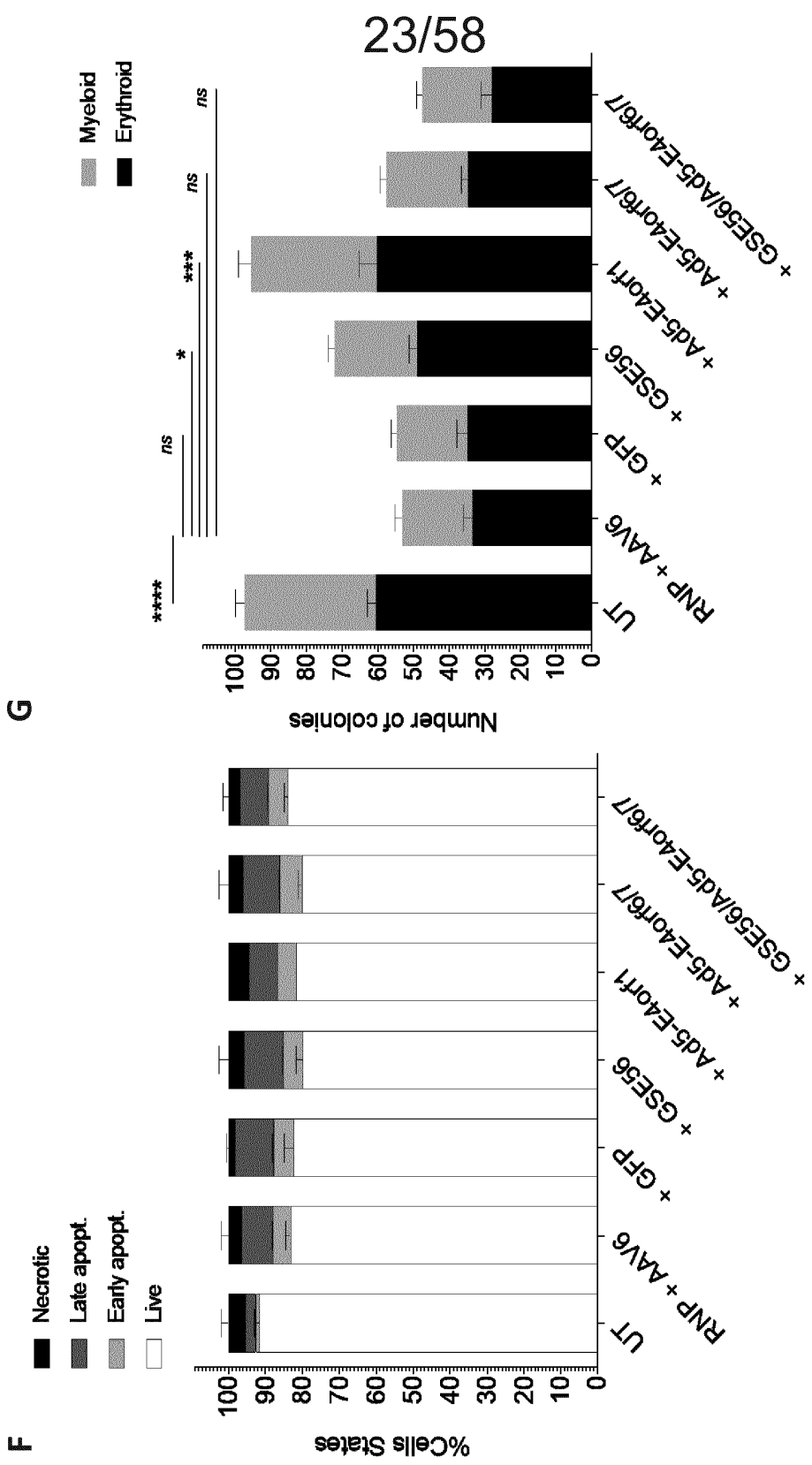


FIG. 14 (Continued)

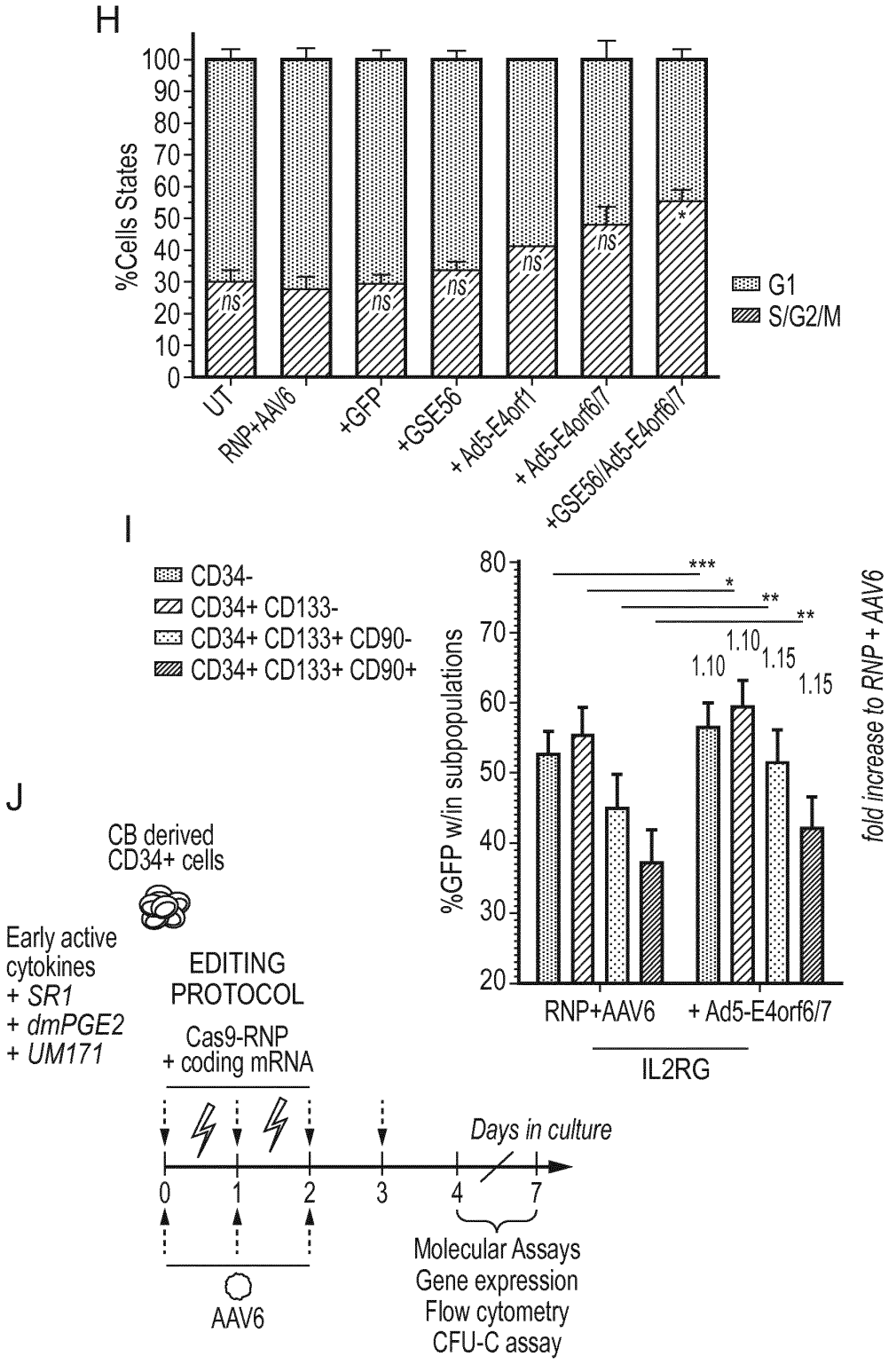


FIG. 14 (Continued)

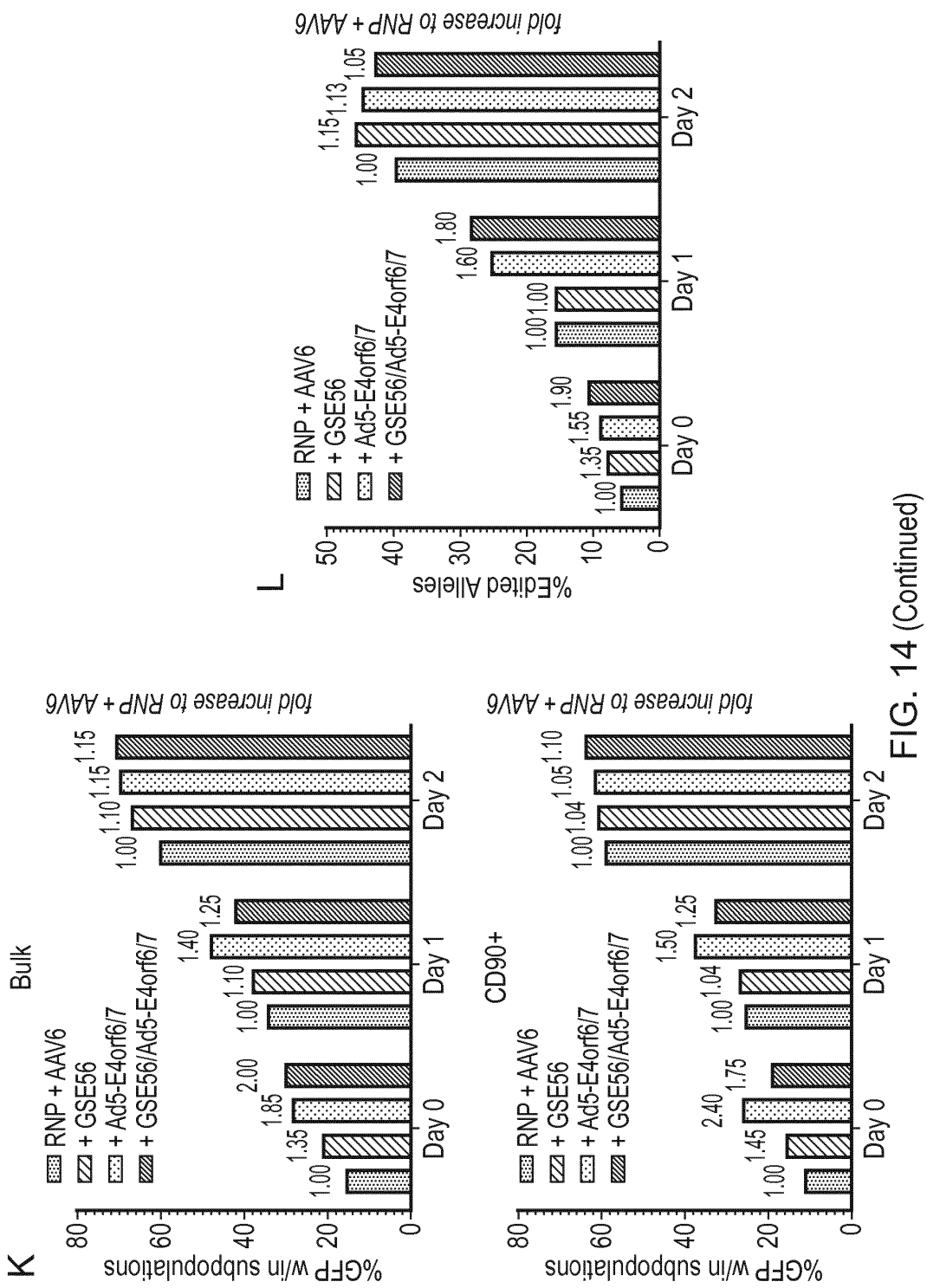


FIG. 14 (Continued)

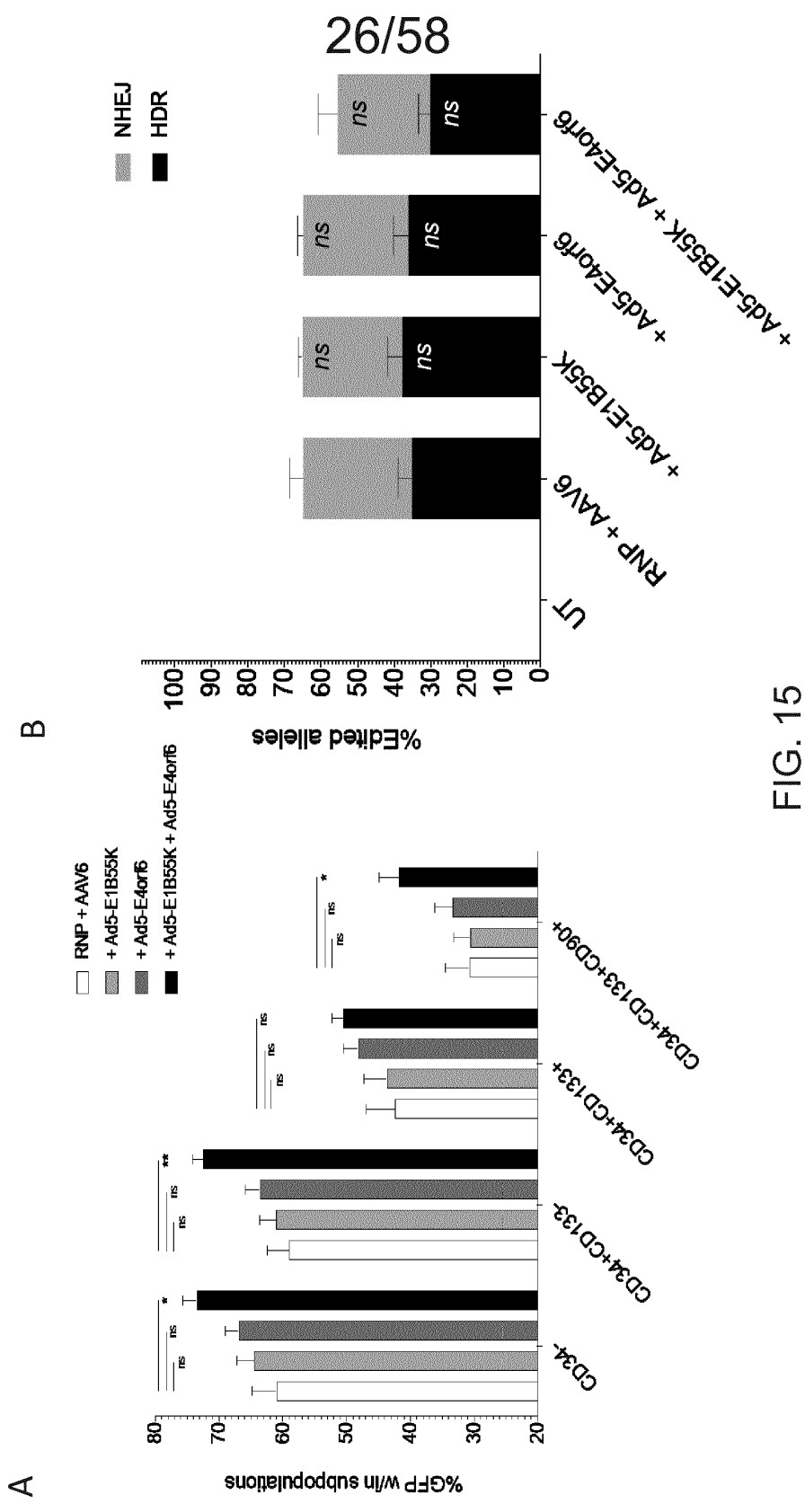

A
%GFP w/in subpopulations
CD34-
CD34+CD133-
CD34+CD133+
CD34+CD133+CD90+
RNP + AAV6
+ Ad5-E1B55K
+ Ad5-E4orf6
+ Ad5-E1B55K + Ad5-E4orf6
B
%Edited alleles
UT
RNP + AAV6
+ Ad5-E1B55K
+ Ad5-E4orf6
+ Ad5-E1B55K + Ad5-E4orf6
NHEJ
HDR
ns

FIG. 15

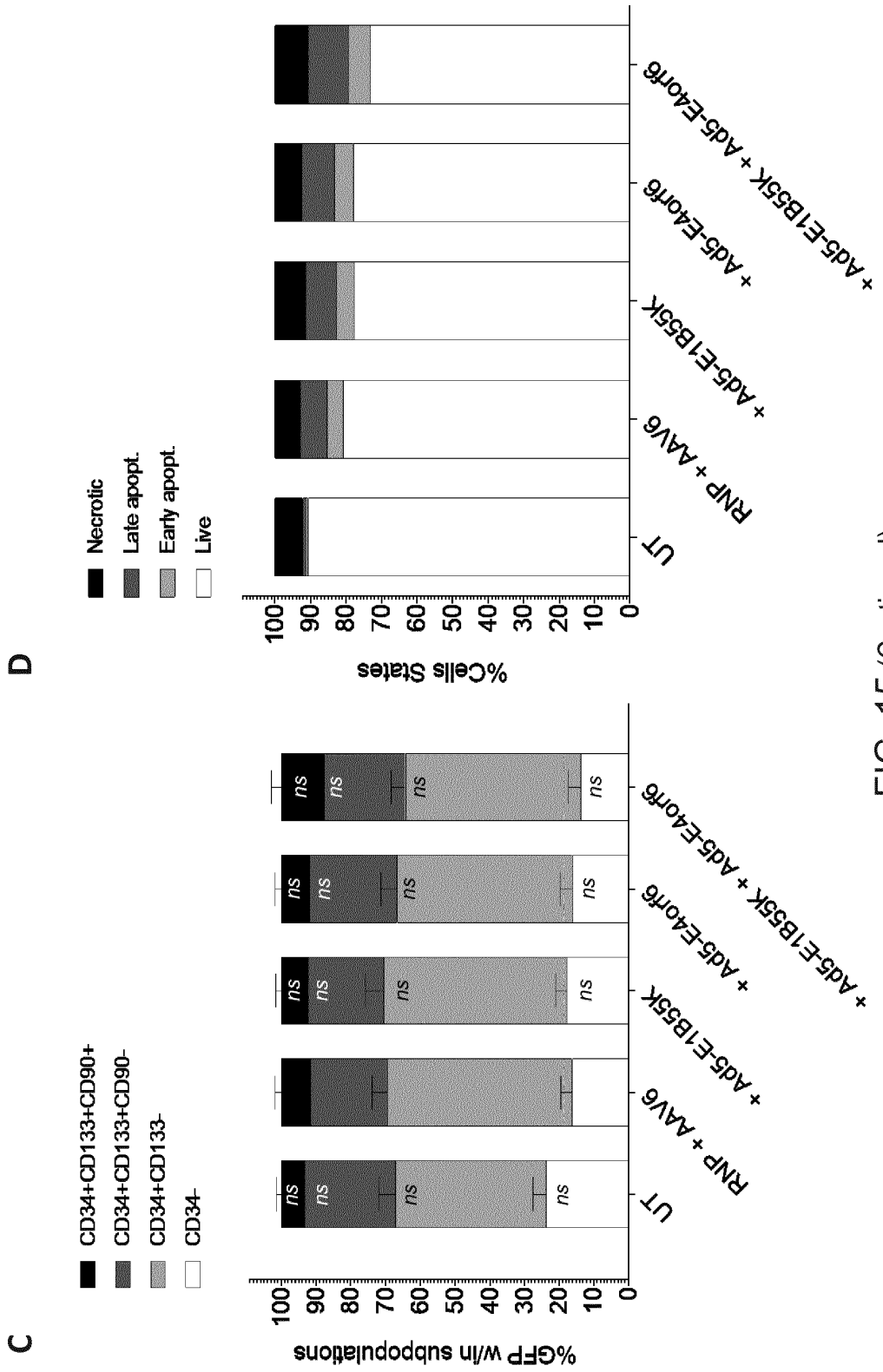


FIG. 15 (Continued)

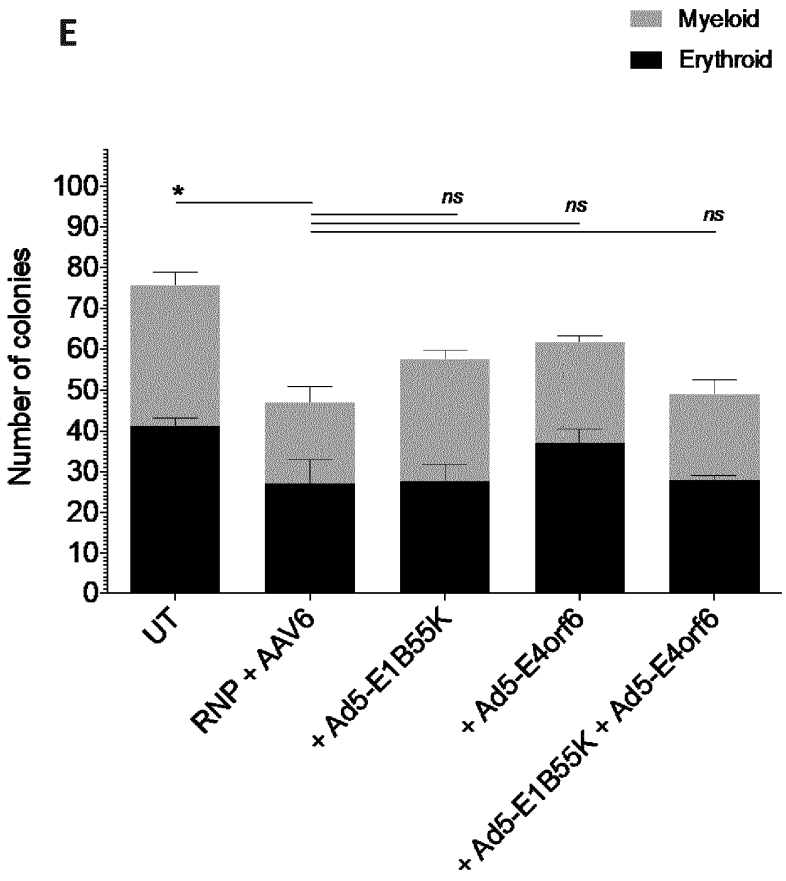


FIG. 15 (Continued)

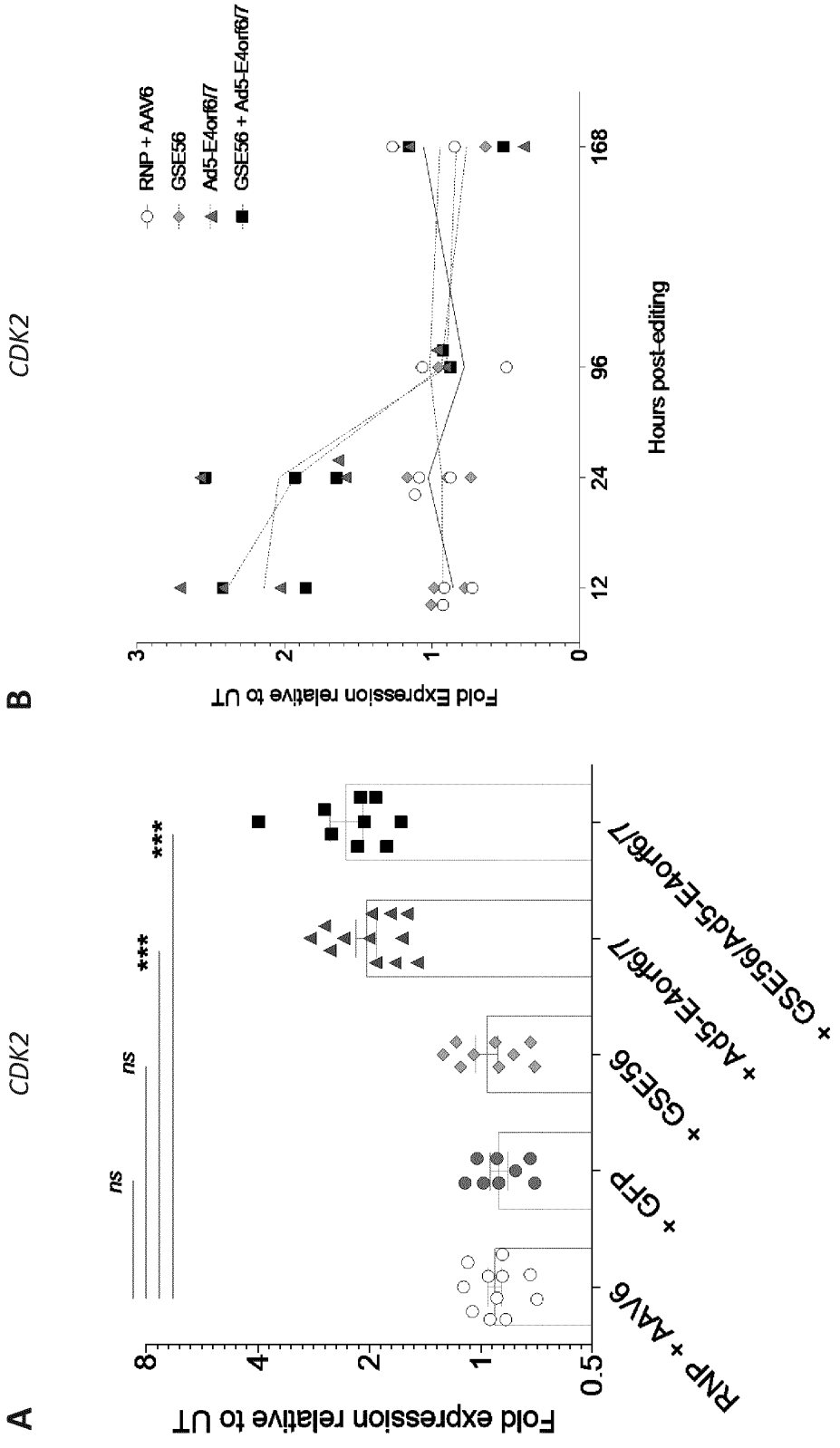

A
CDK2
Fold expression relative to UT
8
4
2
1
0.5
ns
ns
***
***
RNP + AAV6
+ GFP
+ GSE56
+ Ad5-E4orf6/7
+ GSE56/Ad5-E4orf6/7
B
CDK2
Fold Expression relative to UT
3
2
1
0
12
24
96
168
Hours post-editing
RNP + AAV6
GSE56
Ad5-E4orf6/7
GSE56 + Ad5-E4orf6/7

FIG. 16

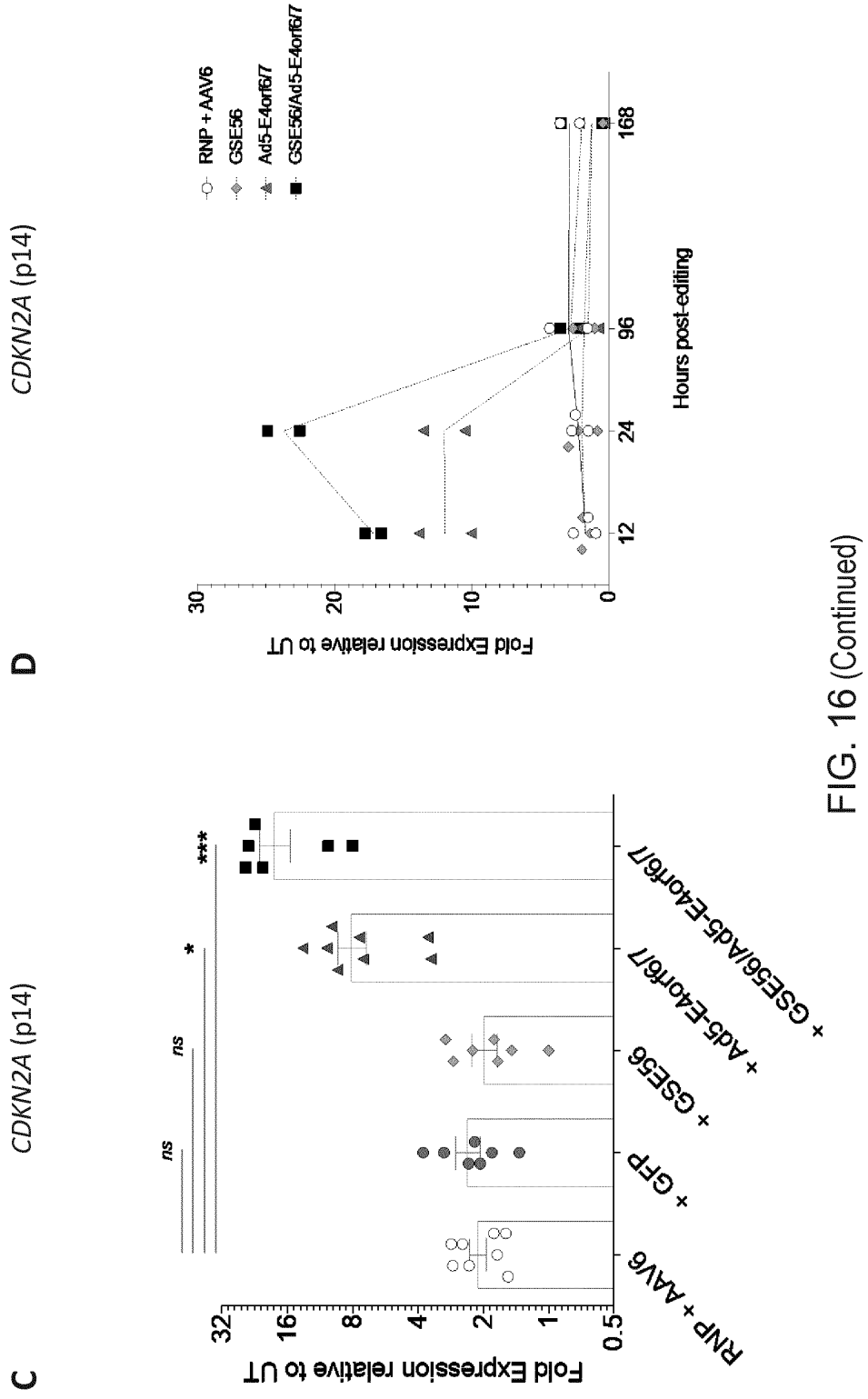


FIG. 16 (Continued)

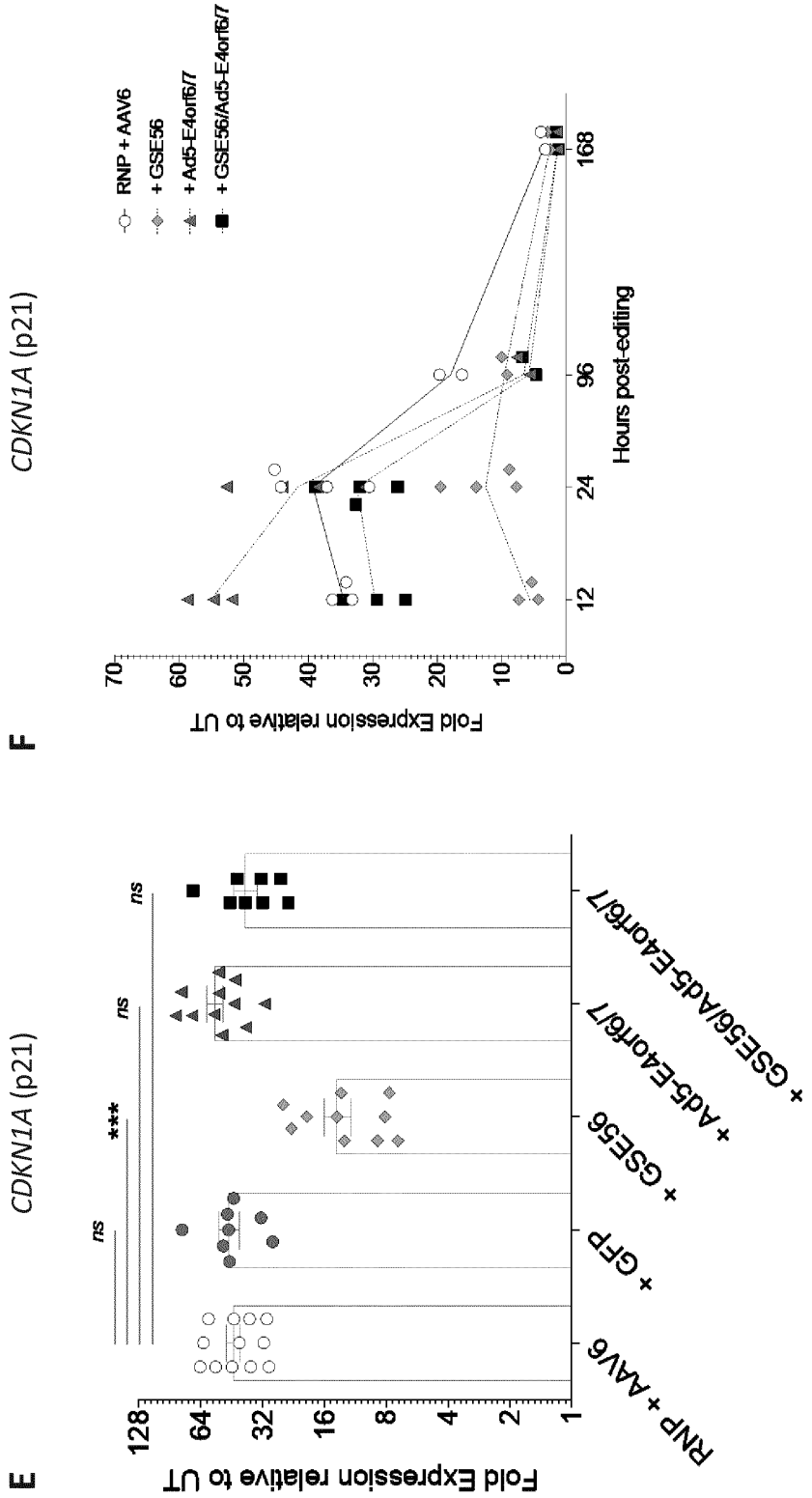


FIG. 16 (Continued)

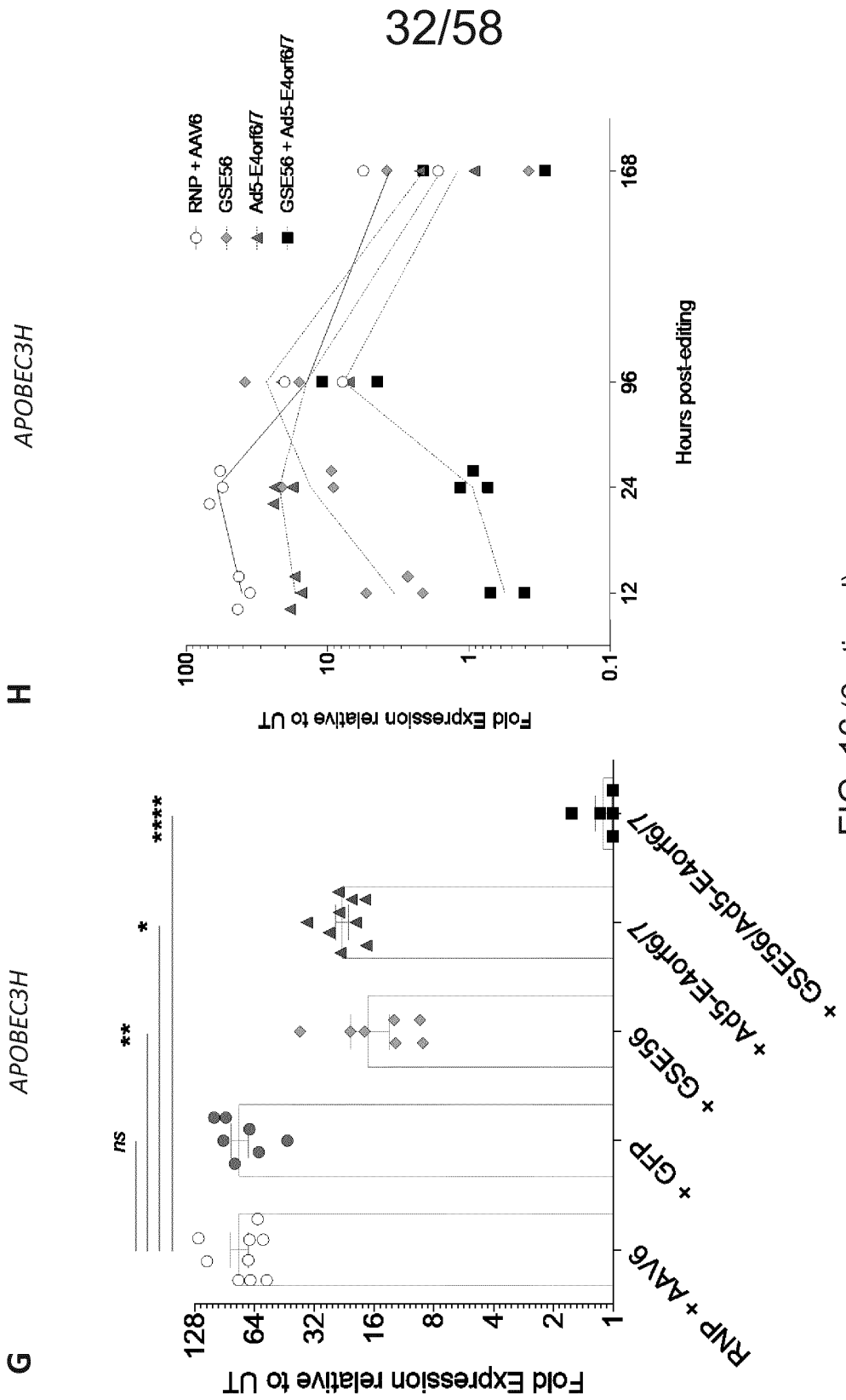


FIG. 16 (Continued)

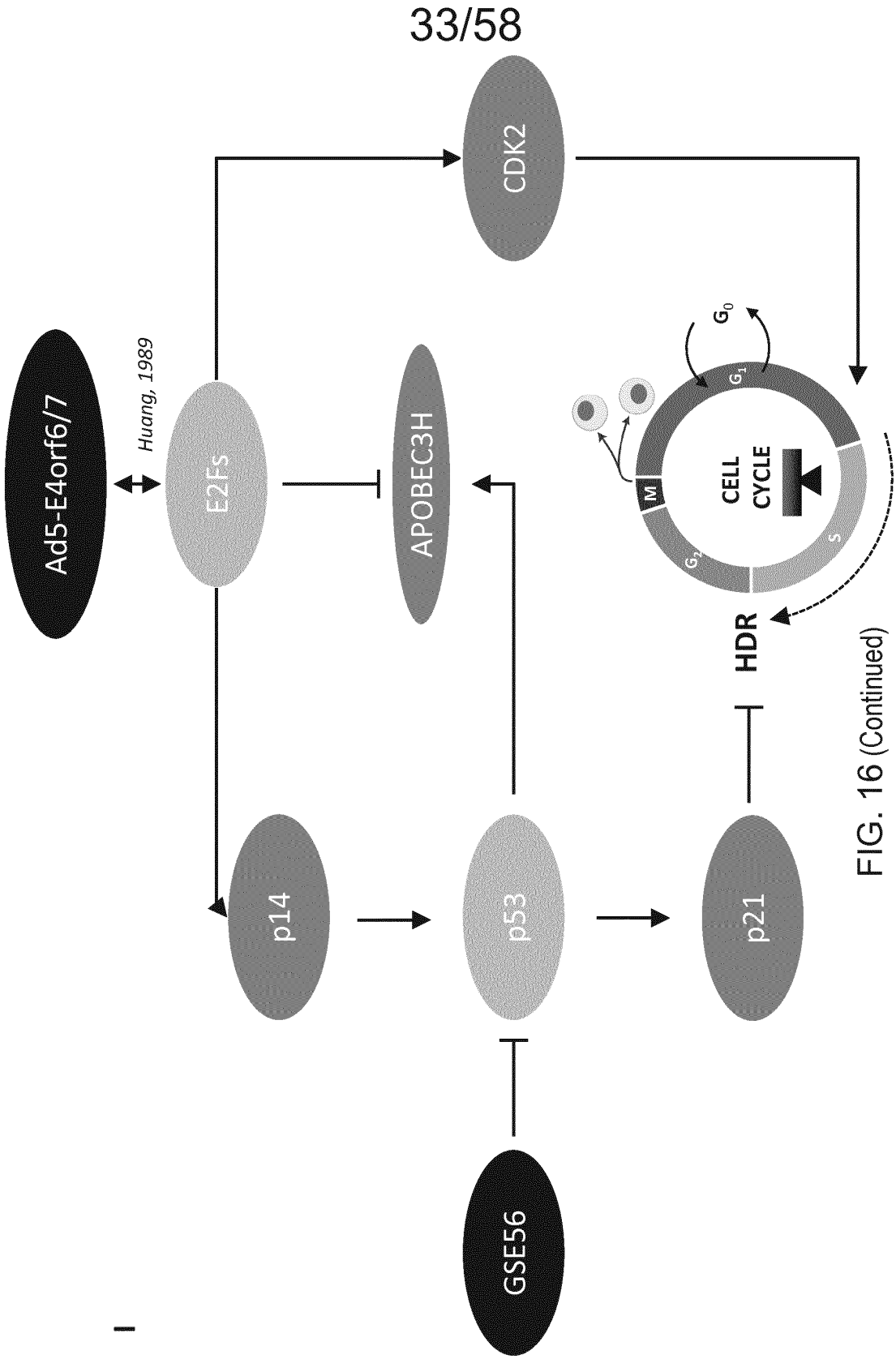


FIG. 16 (Continued)

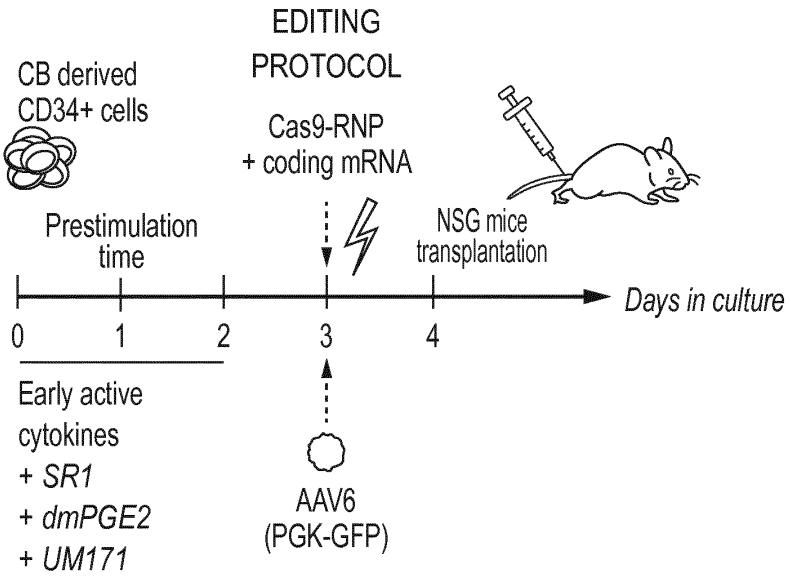

EDITING
PROTOCOL
CB derived
CD34+ cells
Cas9-RNP
+ coding mRNA
Prestimulation
time
NSG mice
transplantation
Days in culture
0
1
2
3
4
Early active
cytokines
+ SR1
+ dmPGE2
+ UM171
AAV6
(PGK-GFP)

FIG. 17A

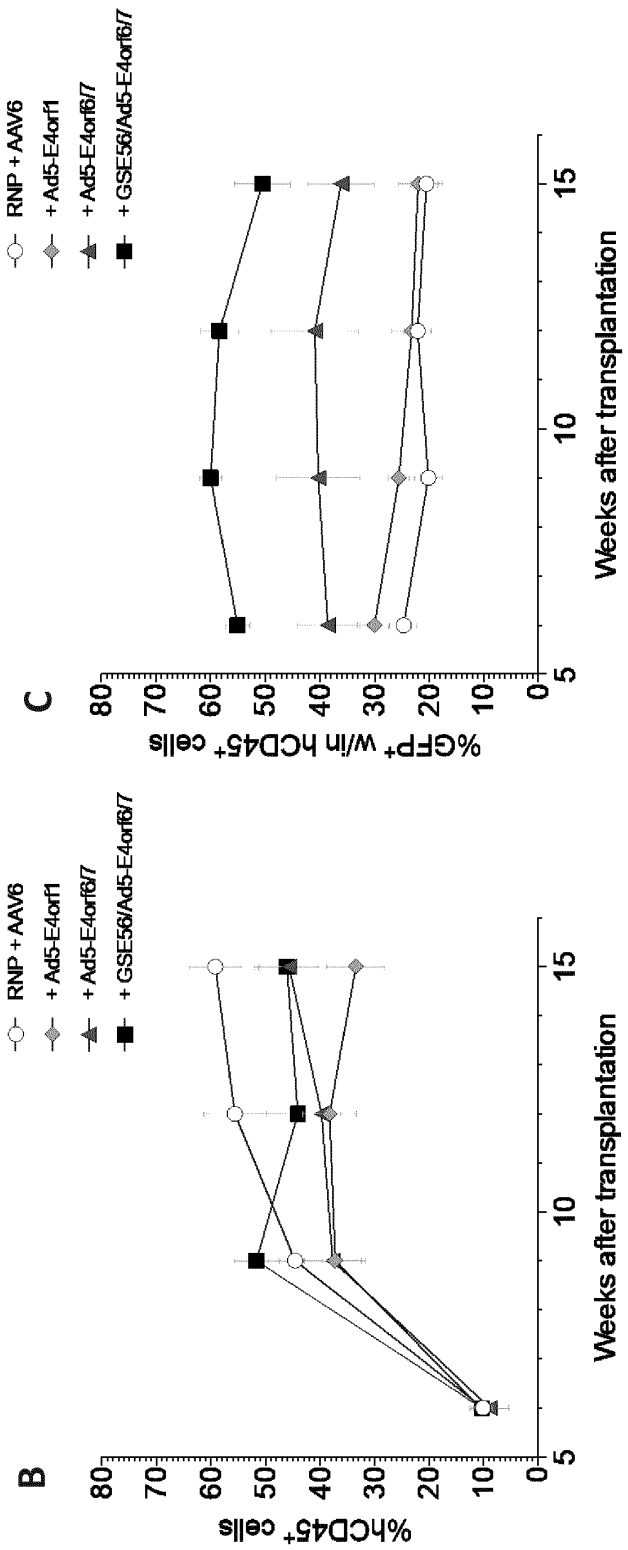


FIG. 17 (Continued)

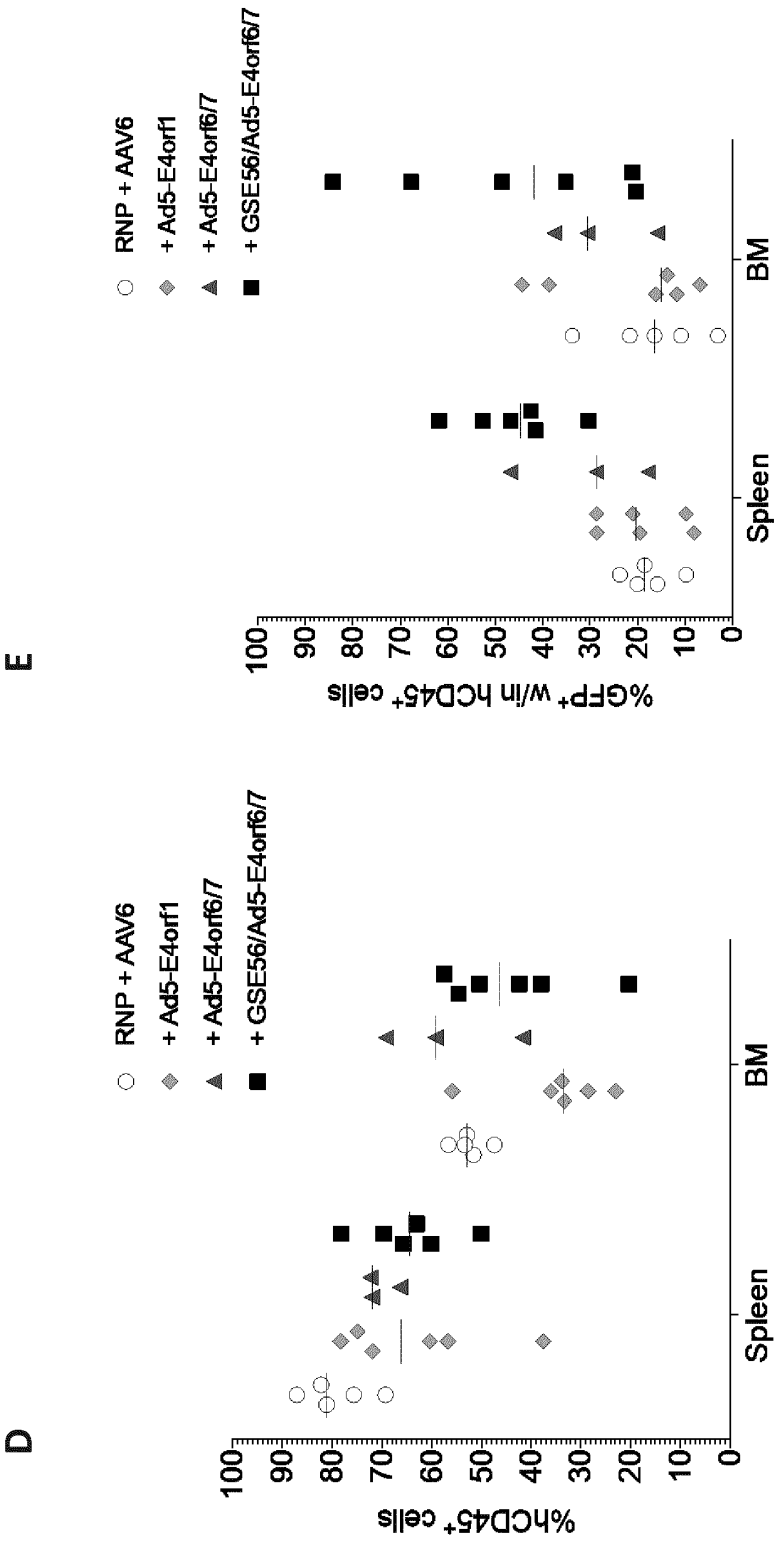


FIG. 17 (Continued)

F

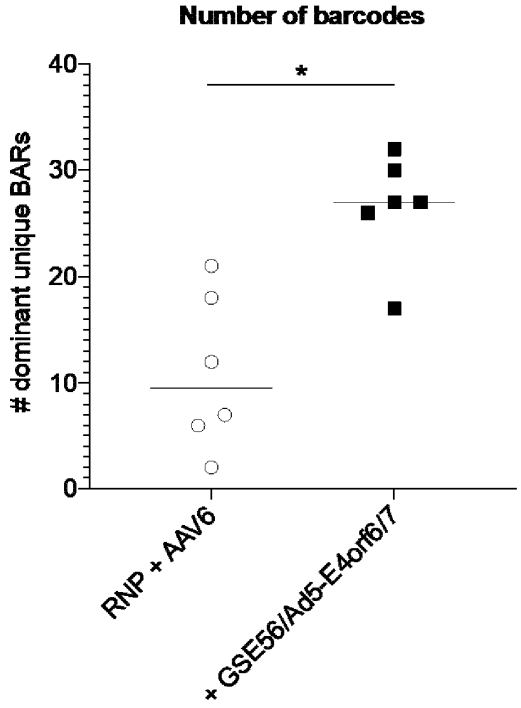


FIG. 17 (Continued)

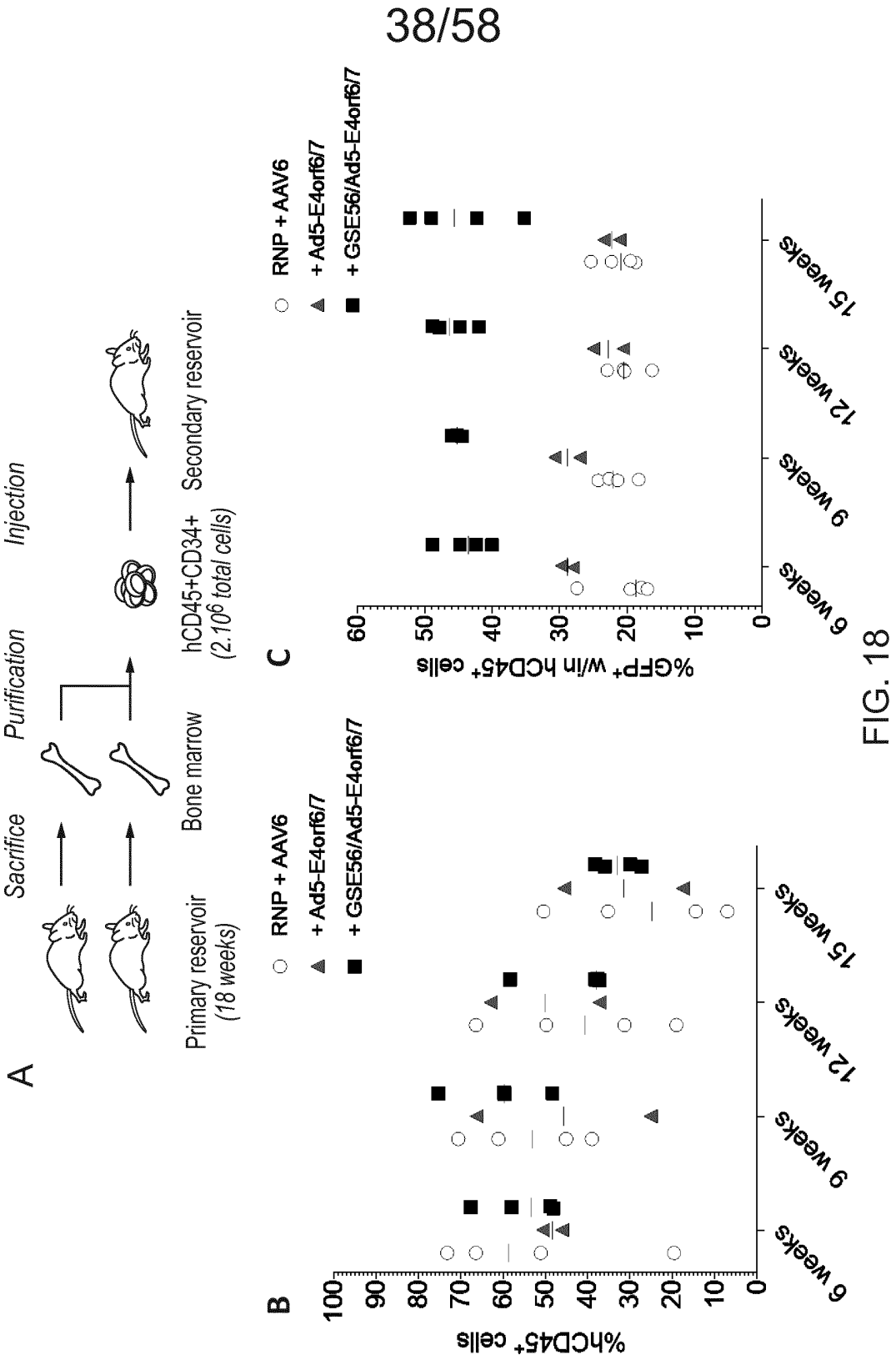

A
Sacrifice
Purification
Injection
Primary reservoir
(18 weeks)
Bone marrow
hCD45+CD34+
(2.10^6 total cells)
Secondary reservoir
B
%hCD45+ cells
RNP + AAV6
+ Ad5-E4orf6/7
+ GSE56/Ad5-E4orf6/7
6 weeks
9 weeks
12 weeks
15 weeks
C
%GFP+ w/in hCD45+ cells
RNP + AAV6
+ Ad5-E4orf6/7
+ GSE56/Ad5-E4orf6/7
6 weeks
9 weeks
12 weeks
15 weeks

FIG. 18

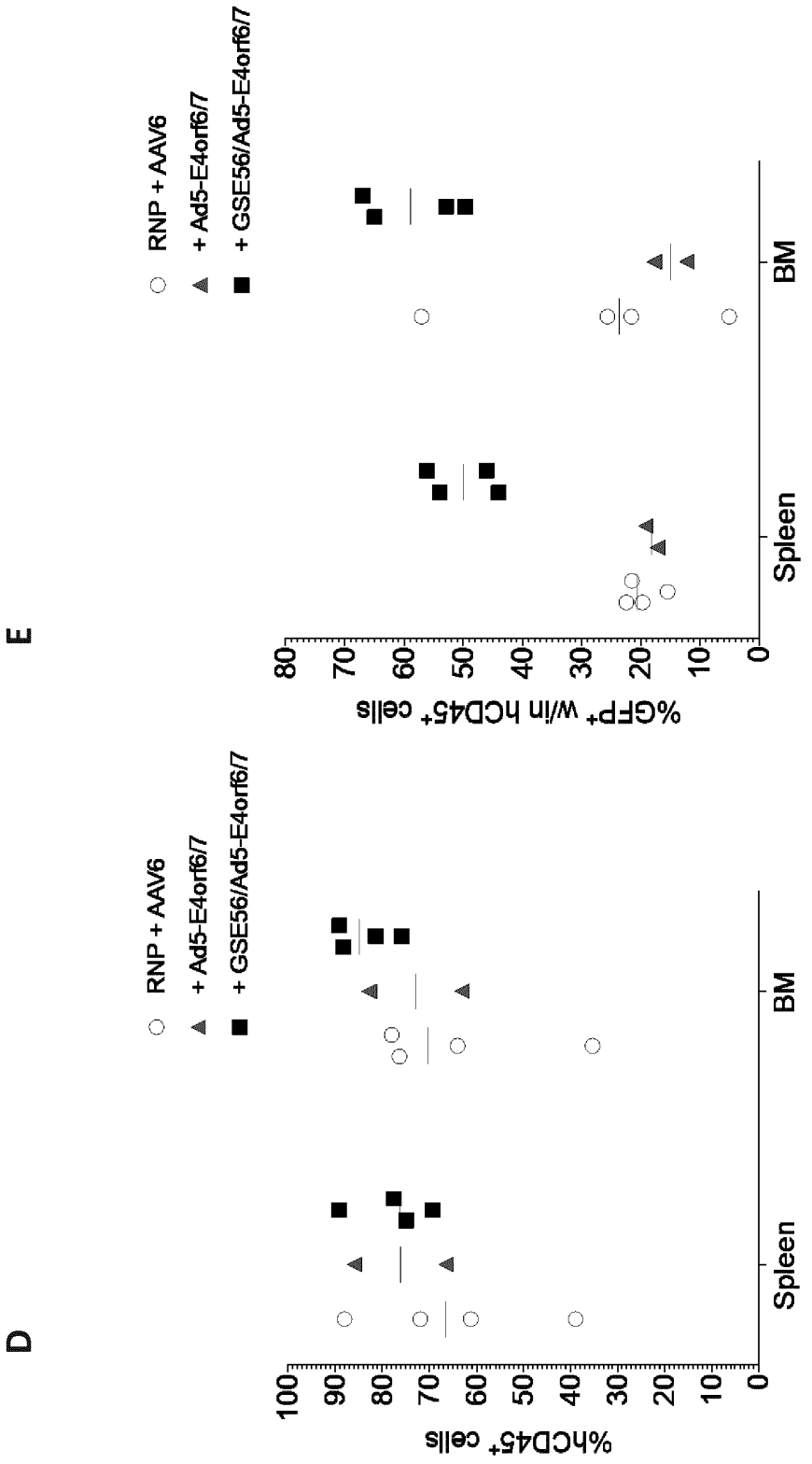


FIG. 18 (Continued)

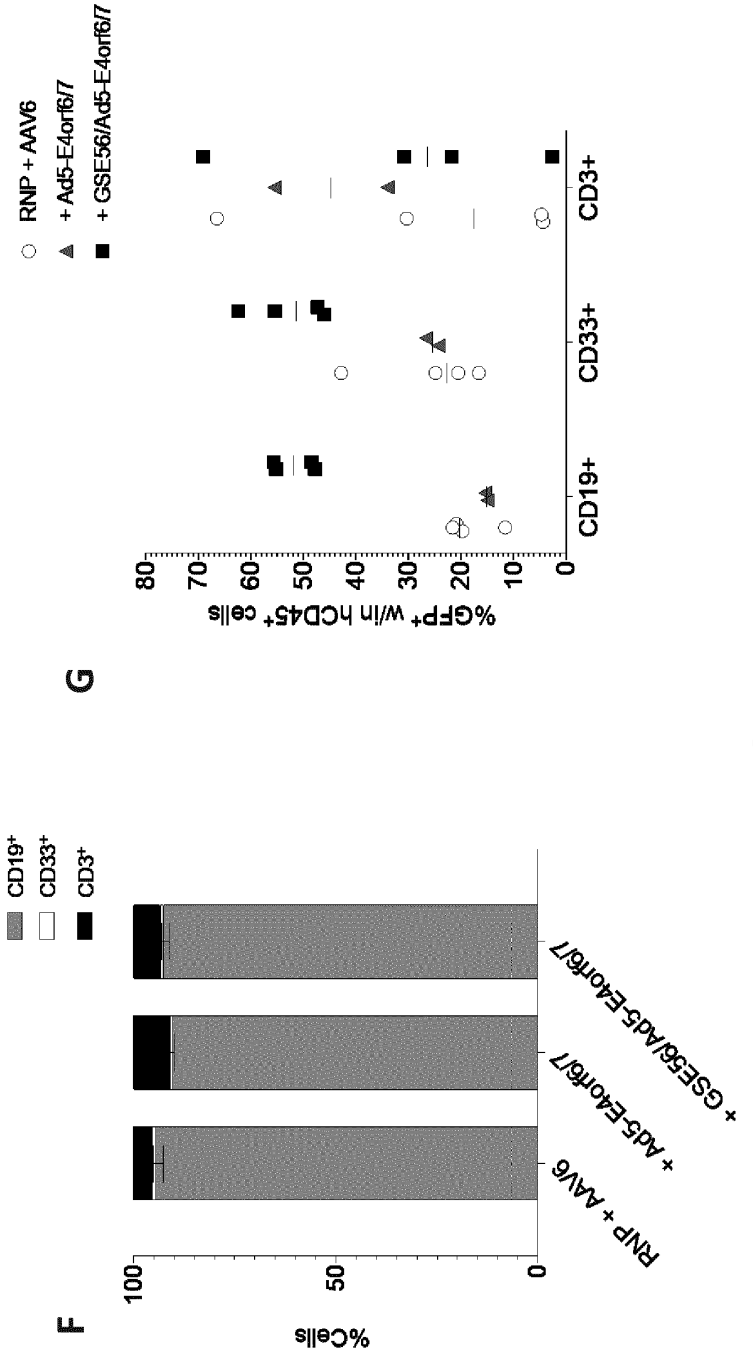


FIG. 18 (Continued)

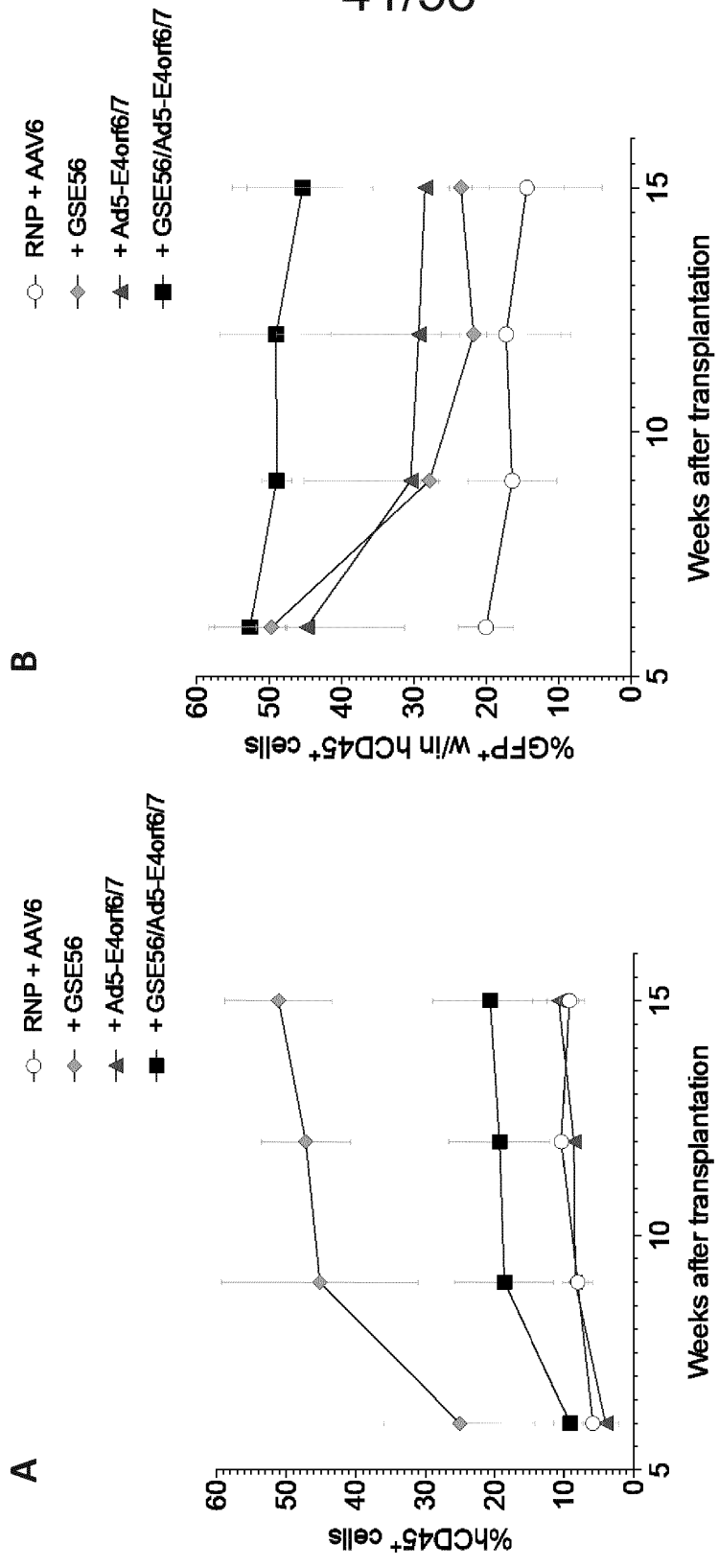

A
B
RNP + AAV6
+ GSE56
+ Ad5-E4orf6/7
+ GSE56/Ad5-E4orf6/7
%hCD45+ cells
%GFP+ w/in hCD45+ cells
Weeks after transplantation
0
10
20
30
40
50
60
5
10
15

FIG. 19

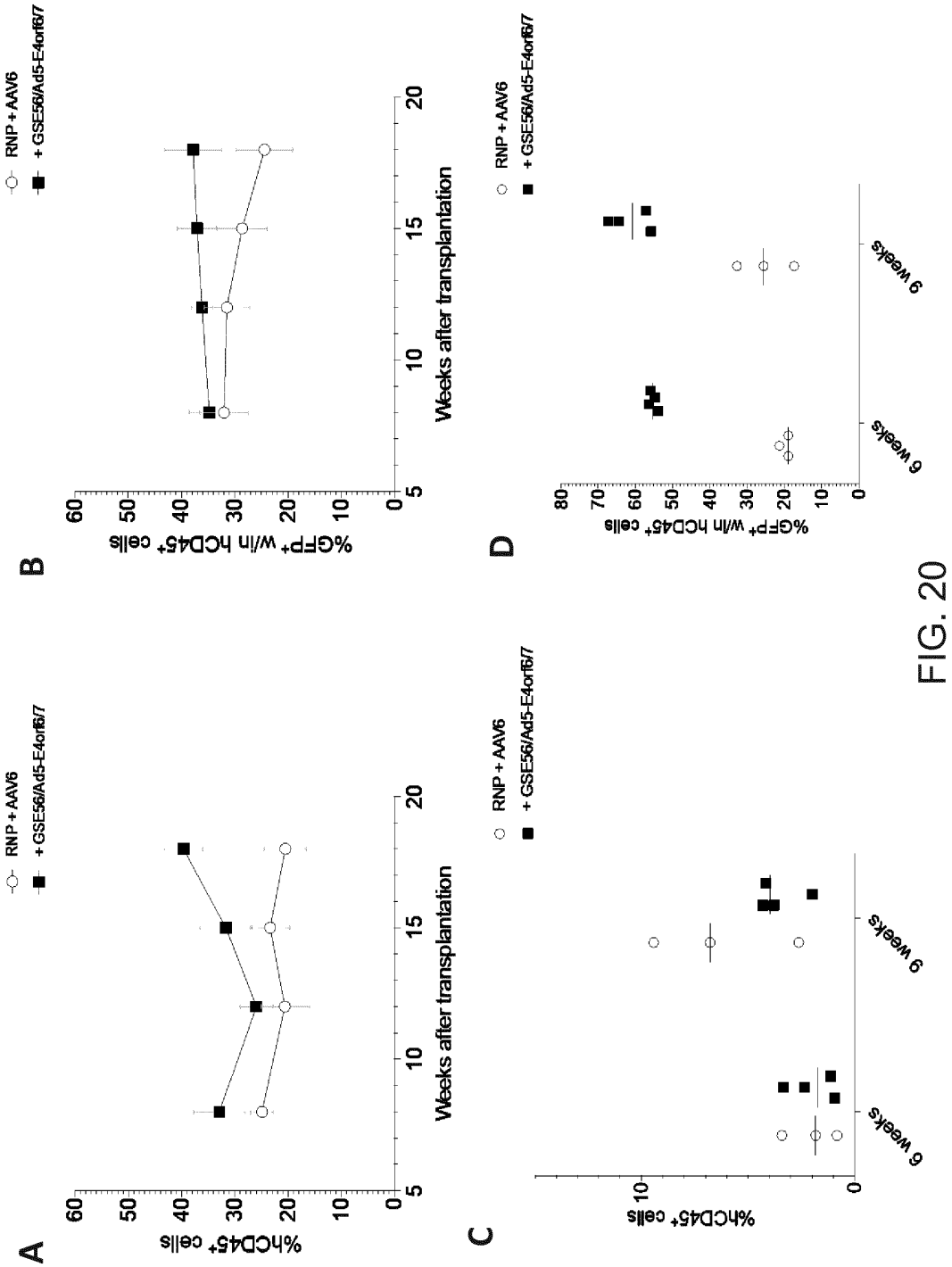

A
B
C
D
RNP + AAV6
+ GSE56/Ad5-E4orf6/7
%hCD45+ cells
%GFP+ w/in hCD45+ cells
Weeks after transplantation
6 weeks
9 weeks

FIG. 20

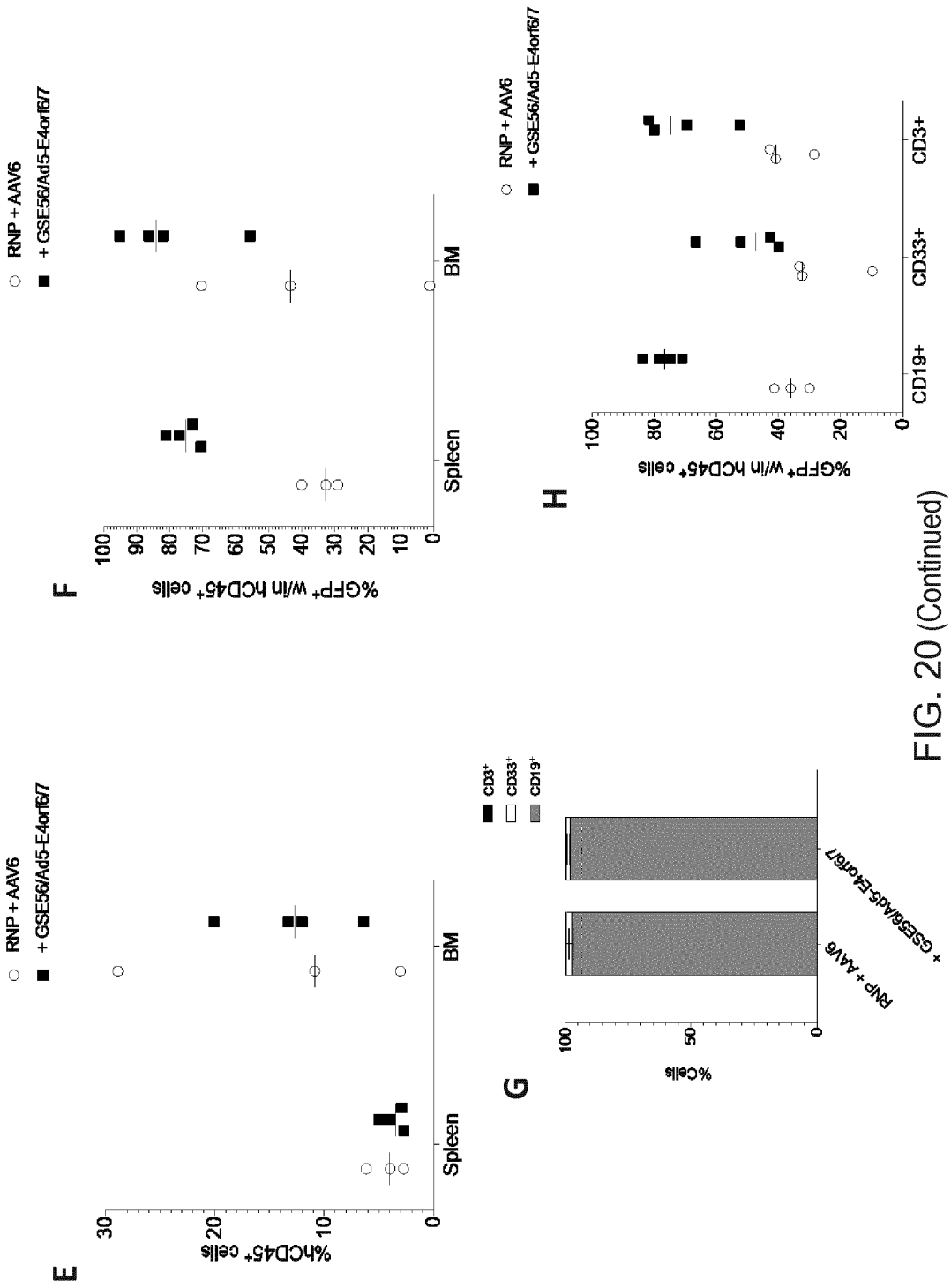


FIG. 20 (Continued)

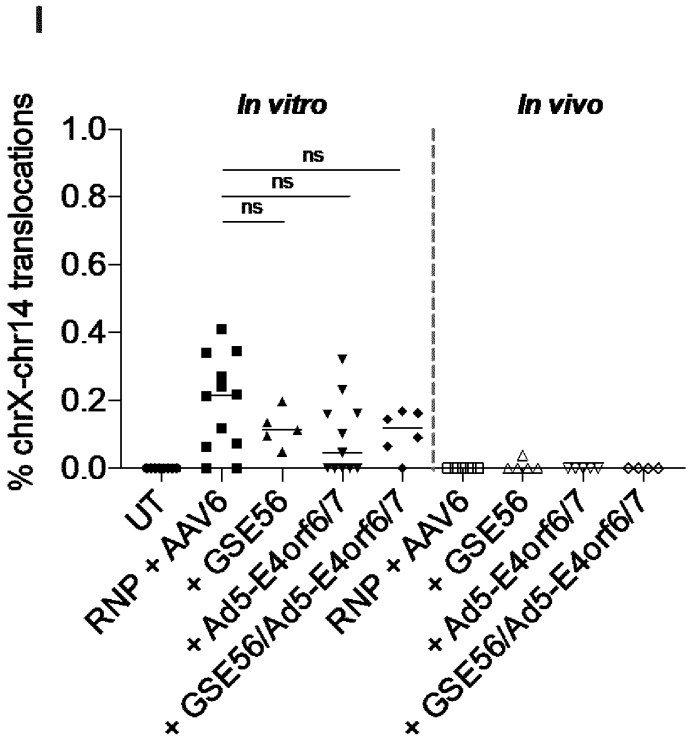


FIG. 20 (Continued)

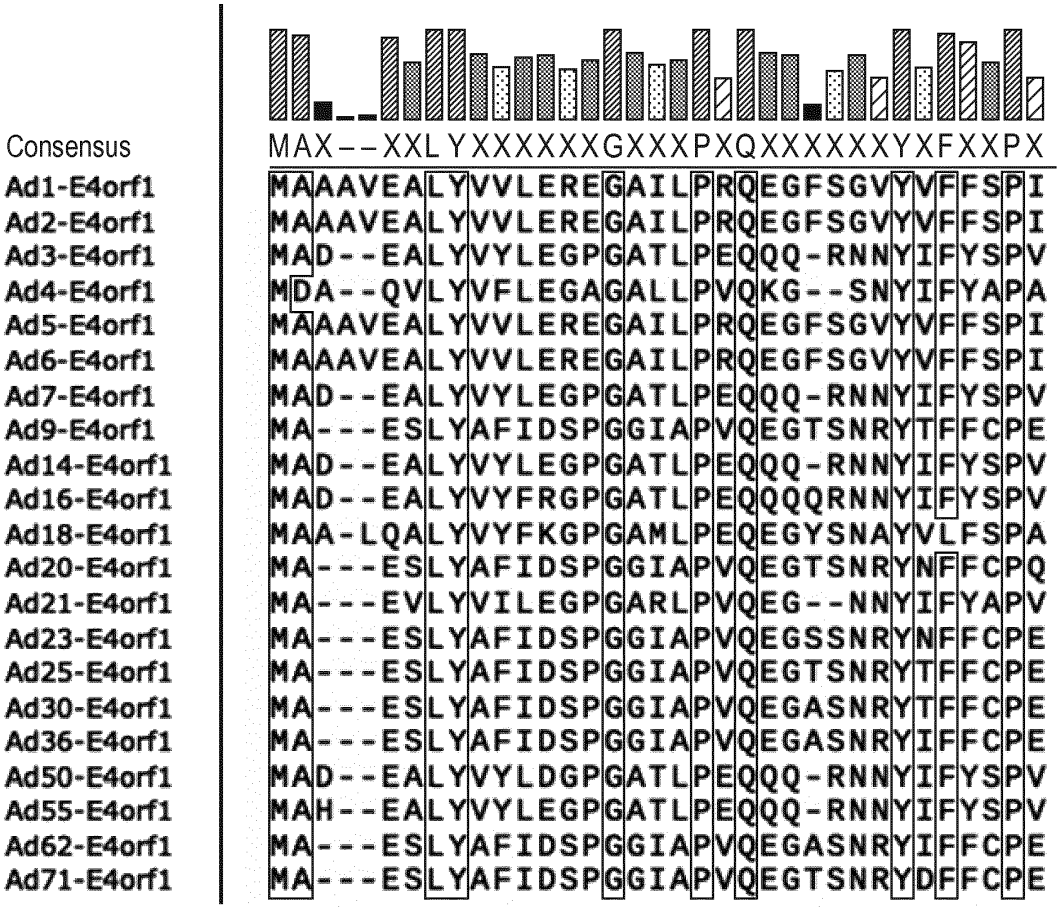

Consensus
MAX--XXLYXXXXXXGXXXPXQXXXXXXYXFXXPX
Ad1-E4orf1 MAAAVEALYVVLEREGAILPRQEGFSGVYVFFSPI
Ad2-E4orf1 MAAAVEALYVVLEREGAILPRQEGFSGVYVFFSPI
Ad3-E4orf1 MAD--EALYVYLEGPGATLPEQQQ-RNNYIFYSPV
Ad4-E4orf1 MDA--QVLYVFLEGAGALLPVQKG--SNYIFYAPA
Ad5-E4orf1 MAAAVEALYVVLEREGAILPRQEGFSGVYVFFSPI
Ad6-E4orf1 MAAAVEALYVVLEREGAILPRQEGFSGVYVFFSPI
Ad7-E4orf1 MAD--EALYVYLEGPGATLPEQQQ-RNNYIFYSPV
Ad9-E4orf1 MA---ESLYAFIDSPGGIAPVQEGTSNRYTFFCPE
Ad14-E4orf1 MAD--EALYVYLEGPGATLPEQQQ-RNNYIFYSPV
Ad16-E4orf1 MAD--EALYVYFRGPGATLPEQQQQRNNYIFYSPV
Ad18-E4orf1 MAA-LQALYVYFKGPGAMLPEQEGYSNAYVLFSPA
Ad20-E4orf1 MA---ESLYAFIDSPGGIAPVQEGTSNRYNFFCPQ
Ad21-E4orf1 MA---EVLYVILEGPGARLPVQEG--NNYIFYAPV
Ad23-E4orf1 MA---ESLYAFIDSPGGIAPVQEGSSNRYNFFCPE
Ad25-E4orf1 MA---ESLYAFIDSPGGIAPVQEGTSNRYTFFCPE
Ad30-E4orf1 MA---ESLYAFIDSPGGIAPVQEGASNRYTFFCPE
Ad36-E4orf1 MA---ESLYAFIDSPGGIAPVQEGASNRYIFFCPE
Ad50-E4orf1 MAD--EALYVYLDGPGATLPEQQQ-RNNYIFYSPV
Ad55-E4orf1 MAH--EALYVYLEGPGATLPEQQQ-RNNYIFYSPV
Ad62-E4orf1 MA---ESLYAFIDSPGGIAPVQEGASNRYIFFCPE
Ad71-E4orf1 MA---ESLYAFIDSPGGIAPVQEGTSNRYDFFCPE

FIG. 21A

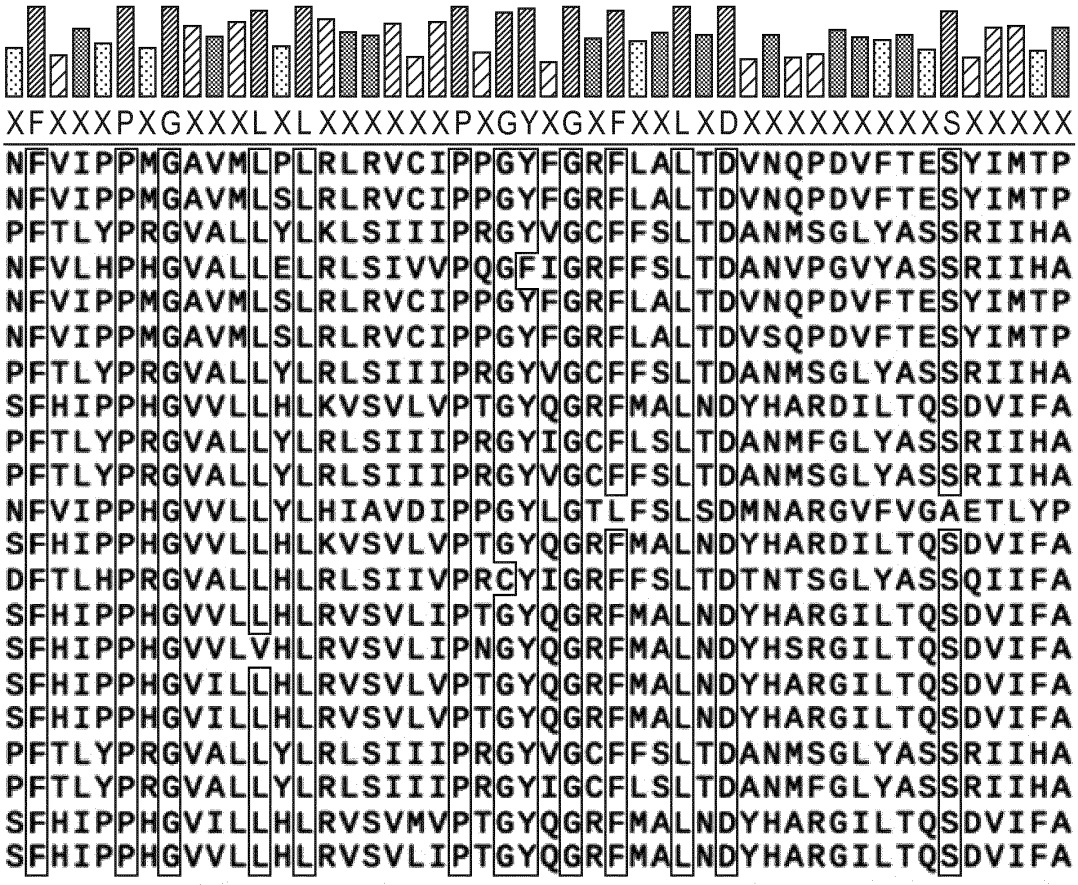


FIG. 21A (Continued)

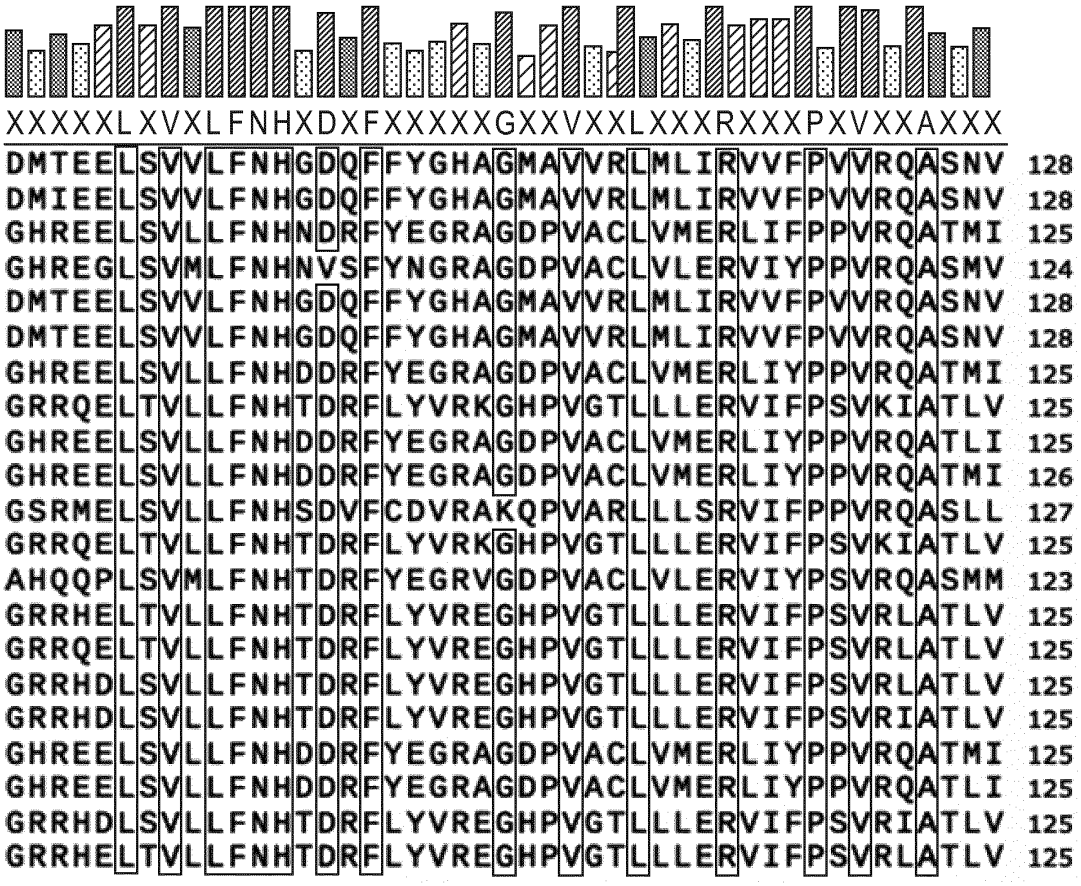


FIG. 21A (Continued)

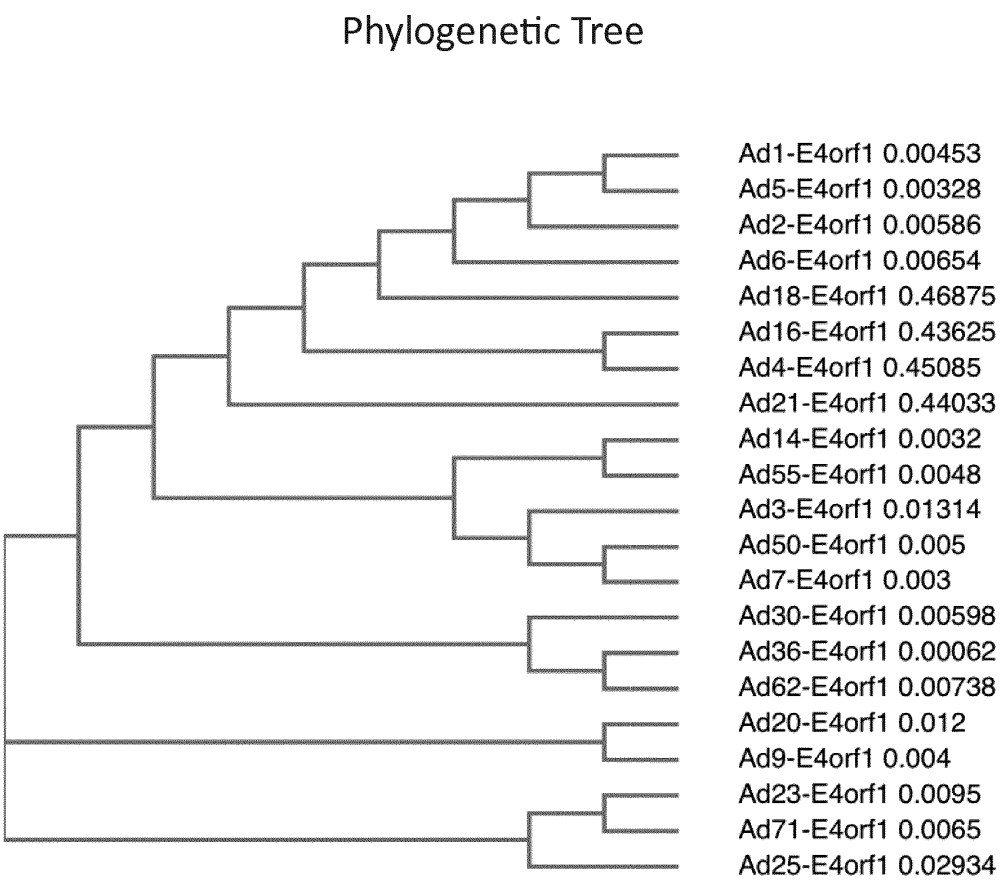

Phylogenetic Tree
Ad1-E4orf1 0.00453
Ad5-E4orf1 0.00328
Ad2-E4orf1 0.00586
Ad6-E4orf1 0.00654
Ad18-E4orf1 0.46875
Ad16-E4orf1 0.43625
Ad4-E4orf1 0.45085
Ad21-E4orf1 0.44033
Ad14-E4orf1 0.0032
Ad55-E4orf1 0.0048
Ad3-E4orf1 0.01314
Ad50-E4orf1 0.005
Ad7-E4orf1 0.003
Ad30-E4orf1 0.00598
Ad36-E4orf1 0.00062
Ad62-E4orf1 0.00738
Ad20-E4orf1 0.012
Ad9-E4orf1 0.004
Ad23-E4orf1 0.0095
Ad71-E4orf1 0.0065
Ad25-E4orf1 0.02934

FIG. 21B

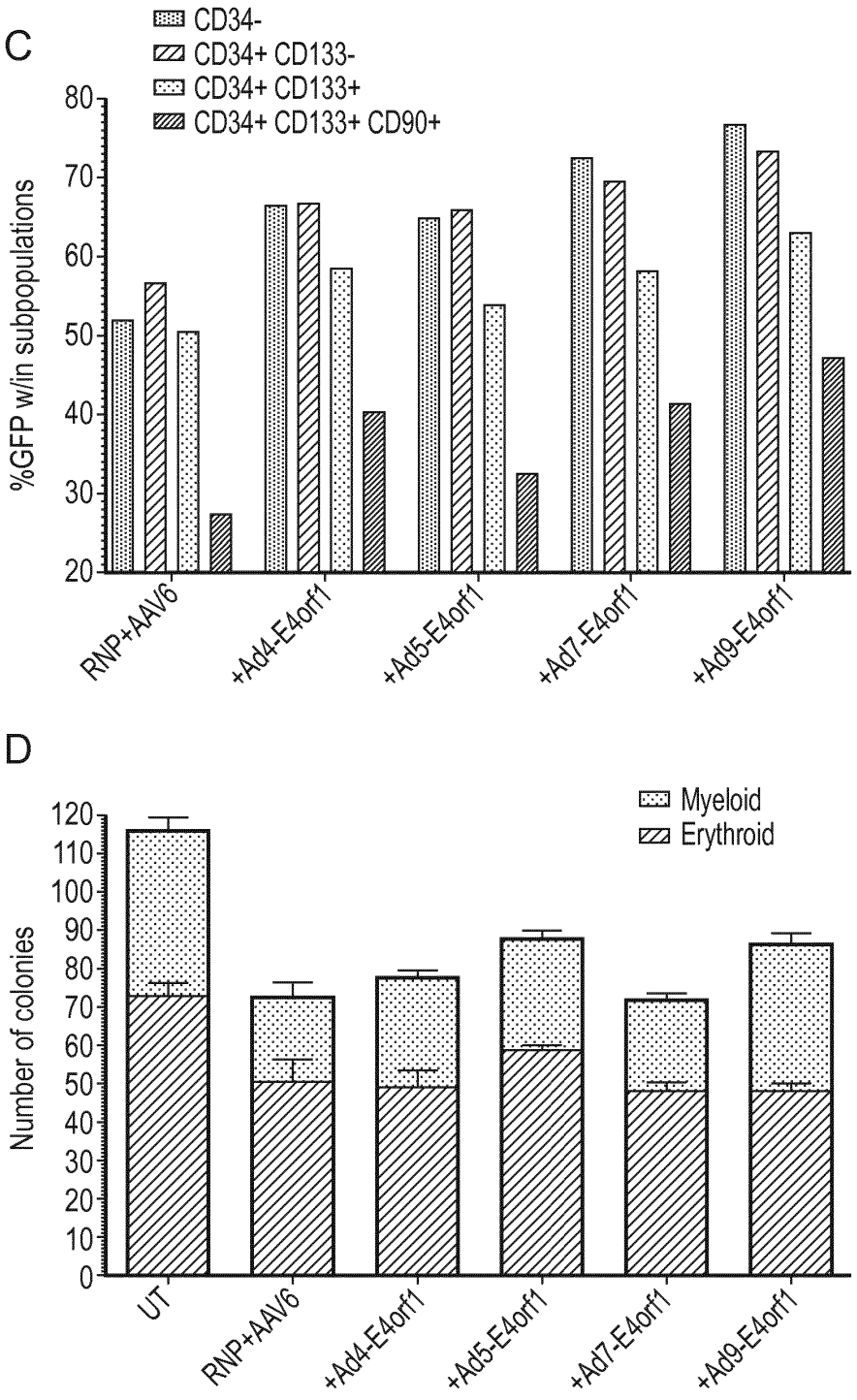


FIG. 21 (Continued)

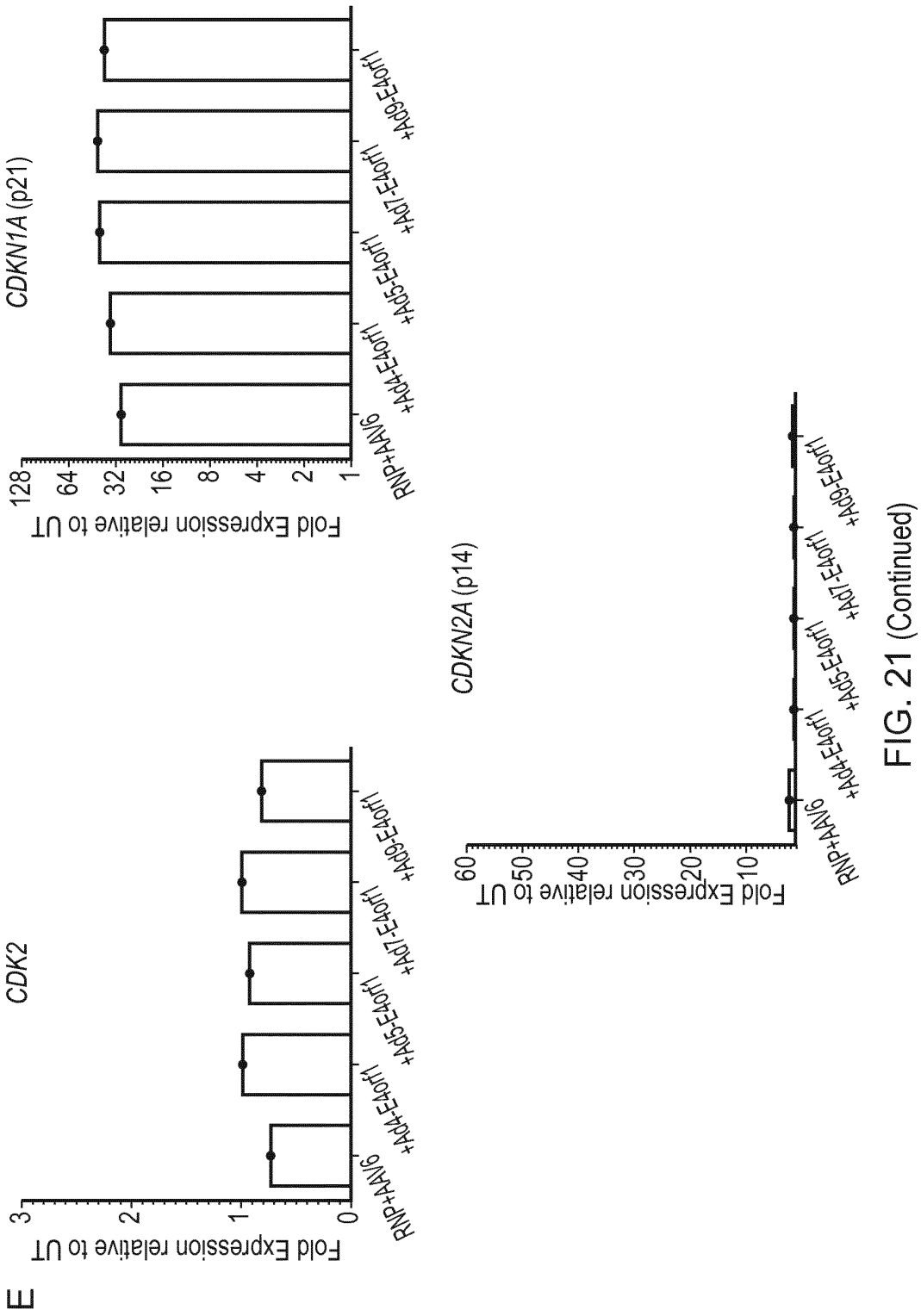


FIG. 21 (Continued)

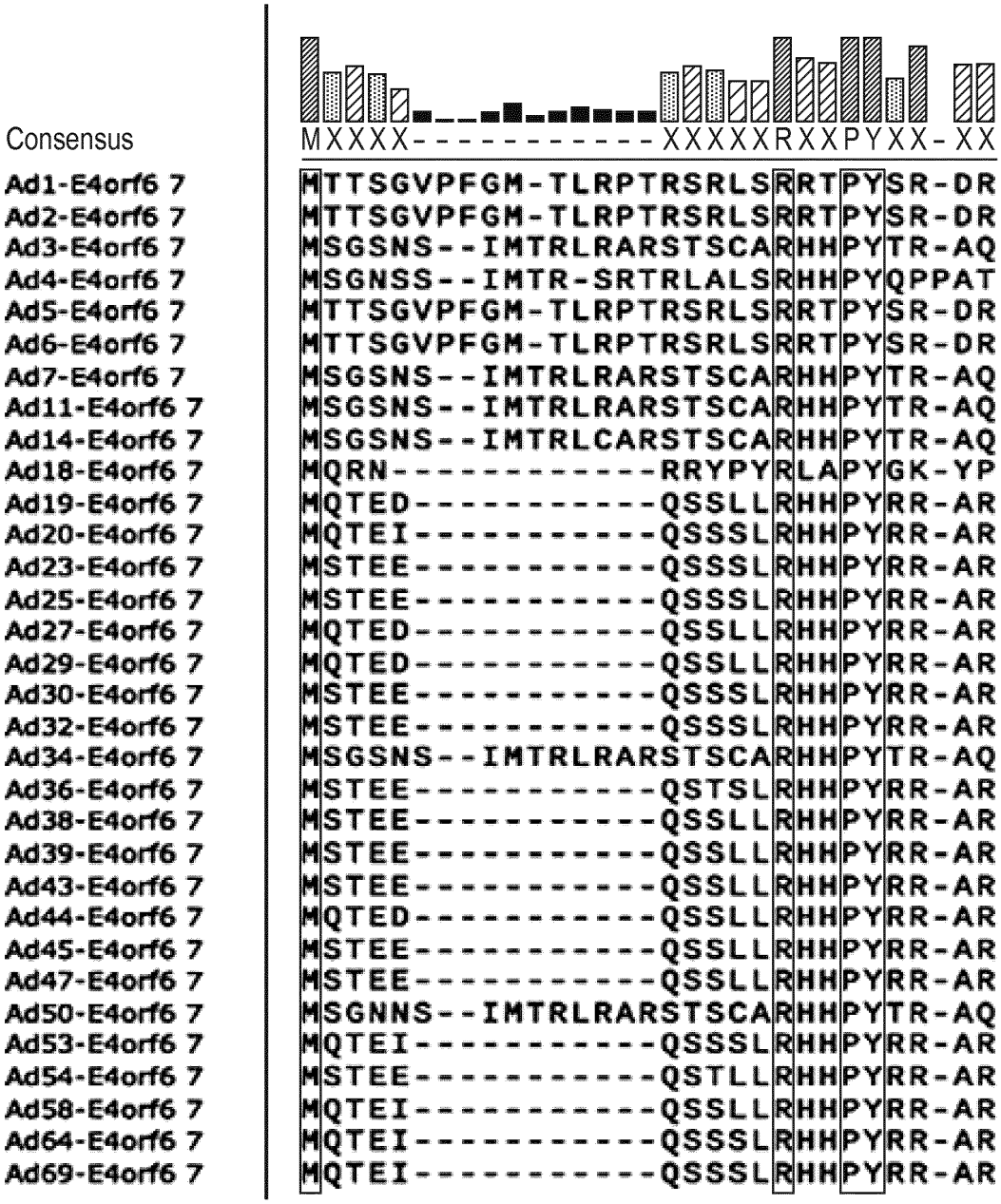

Consensus
MXXXX----------XXXXXRXXPYXX-XX
Ad1-E4orf6 7 MTTSGVPFGM-TLRPTRSRLSRRTPYSR-DR
Ad2-E4orf6 7 MTTSGVPFGM-TLRPTRSRLSRRTPYSR-DR
Ad3-E4orf6 7 MSGSNS--IMTRLRARSTSCARHHPYTR-AQ
Ad4-E4orf6 7 MSGNSS--IMTR-SRTRLALSRHHPYQPPAT
Ad5-E4orf6 7 MTTSGVPFGM-TLRPTRSRLSRRTPYSR-DR
Ad6-E4orf6 7 MTTSGVPFGM-TLRPTRSRLSRRTPYSR-DR
Ad7-E4orf6 7 MSGSNS--IMTRLRARSTSCARHHPYTR-AQ
Ad11-E4orf6 7 MSGSNS--IMTRLRARSTSCARHHPYTR-AQ
Ad14-E4orf6 7 MSGSNS--IMTRLCARSTSCARHHPYTR-AQ
Ad18-E4orf6 7 MQRN----------RRYPYRLAPYGK-YP
Ad19-E4orf6 7 MQTED----------QSSLLRHHPYRR-AR
Ad20-E4orf6 7 MQTEI----------QSSSLRHHPYRR-AR
Ad23-E4orf6 7 MSTEE----------QSSSLRHHPYRR-AR
Ad25-E4orf6 7 MSTEE----------QSSSLRHHPYRR-AR
Ad27-E4orf6 7 MQTED----------QSSLLRHHPYRR-AR
Ad29-E4orf6 7 MQTED----------QSSLLRHHPYRR-AR
Ad30-E4orf6 7 MSTEE----------QSSSLRHHPYRR-AR
Ad32-E4orf6 7 MSTEE----------QSSSLRHHPYRR-AR
Ad34-E4orf6 7 MSGSNS--IMTRLRARSTSCARHHPYTR-AQ
Ad36-E4orf6 7 MSTEE----------QSTSLRHHPYRR-AR
Ad38-E4orf6 7 MSTEE----------QSSLLRHHPYRR-AR
Ad39-E4orf6 7 MSTEE----------QSSLLRHHPYRR-AR
Ad43-E4orf6 7 MSTEE----------QSSLLRHHPYRR-AR
Ad44-E4orf6 7 MQTED----------QSSLLRHHPYRR-AR
Ad45-E4orf6 7 MSTEE----------QSSLLRHHPYRR-AR
Ad47-E4orf6 7 MSTEE----------QSSLLRHHPYRR-AR
Ad50-E4orf6 7 MSGNNS--IMTRLRARSTSCARHHPYTR-AQ
Ad53-E4orf6 7 MQTEI----------QSSSLRHHPYRR-AR
Ad54-E4orf6 7 MSTEE----------QSTLLRHHPYRR-AR
Ad58-E4orf6 7 MQTEI----------QSSLLRHHPYRR-AR
Ad64-E4orf6 7 MQTEI----------QSSSLRHHPYRR-AR
Ad69-E4orf6 7 MQTEI----------QSSSLRHHPYRR-AR

FIG. 22A

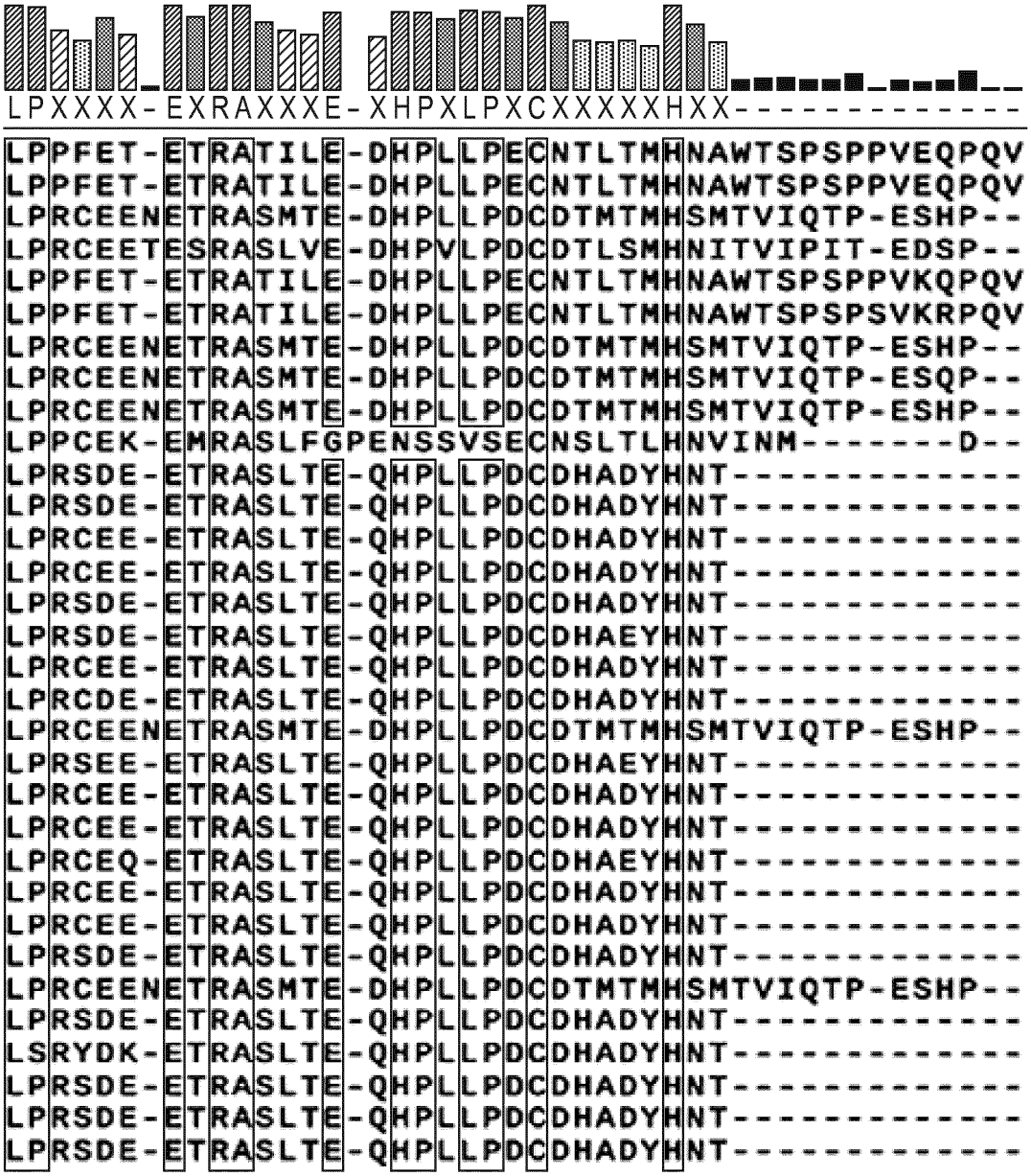


FIG. 22A (Continued)

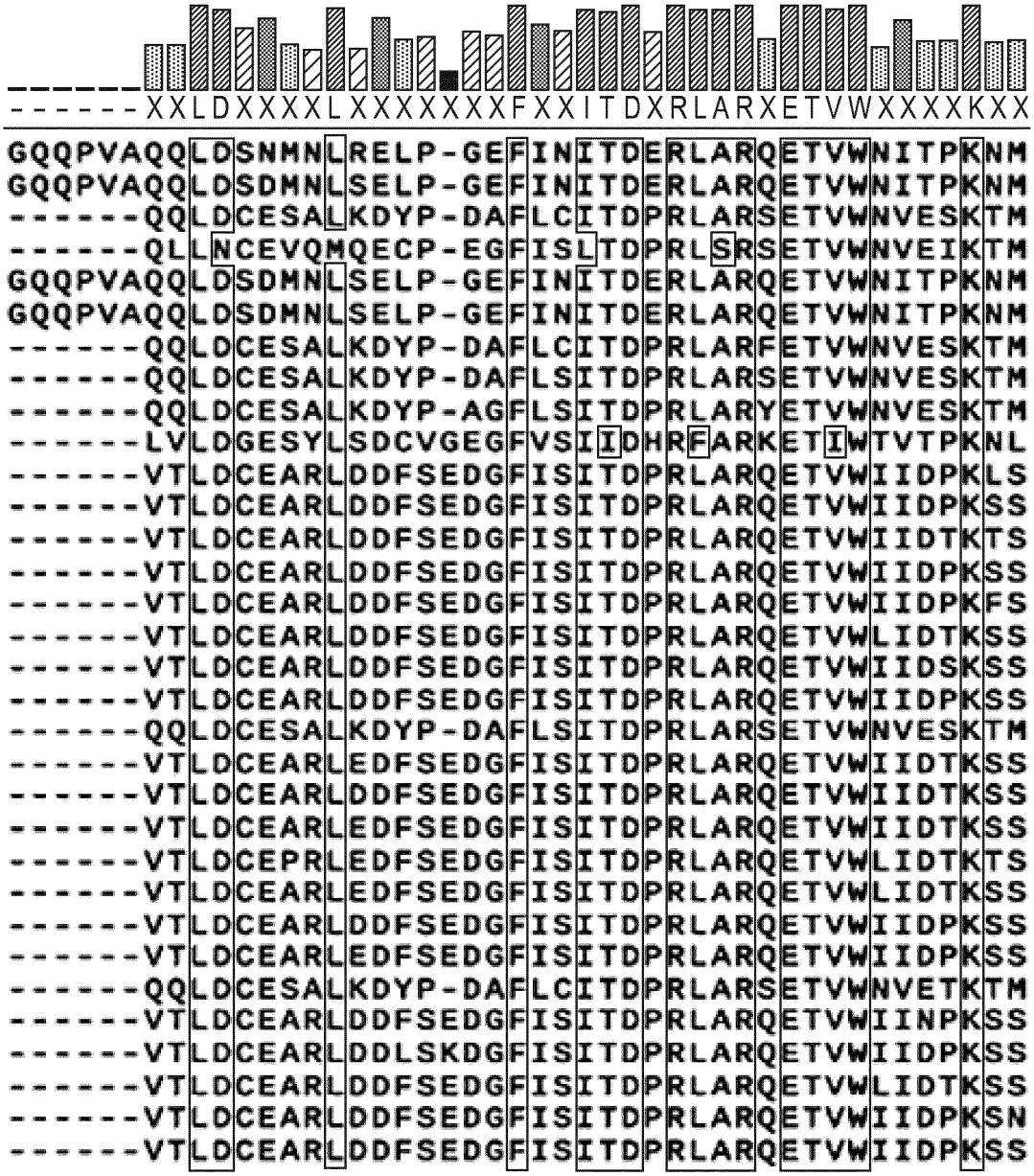
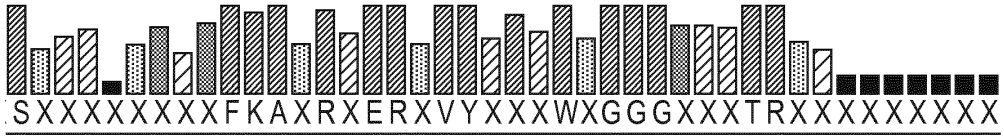


FIG. 22A (Continued)




```
SVTH-DMMLFKASRGERTVYSVCWEGGGRLNTRVL------- 150
SVTH-DMMLFKASRGERTVYSVCWEGGGRLNTRVL------- 150
SISN-GIQMFKAVRGERLVYSVKWEGGGKITTRIL------- 141
SITN-SIQMFKAVRGERIVYSMRWEGGGKITTRIL------- 141
SVTH-DMMLFKASRGERTVYSVCWEGGGRLNTRVL------- 150
SVTH-DMMLFKASRGERTVYSVCWEGGGRLNTRVL------- 150
SICN-GIQMFKAVRGERLVYSVKWEGGGKITTRIL------- 141
SISN-GIQMFKAVRGERLVYSVKWEGGGKITTRIL------- 141
SISN-GIQMFKAVRGERLVYSVKWEGGGKITTRSL------- 141
SRNM-HMQLFSAIKGERVVYKIKWEGGGSLTTRIV------- 126
SRTNQNIPLFKATRAERTVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNISLFKATRAERTVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNNNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNISLFKATRAERTVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SRANQNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDP 130
SRTNQNIFLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SISN-GIQMFKAVRGERLVYSVKWEGGGKITTRIL------- 141
SRTNQNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SRSNNNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDS 130
SRTNQNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNIPLFKATRAERTVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNIPLFKATRAERTVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNISLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNQNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SISN-GIQMFKAVRGERLVYSVKWEGGGKITTRIL------- 141
SRTNENFPLFKATRAERIVYTVKWAGGGRMCTRAGVKINKDT 130
SRTNENFPLFKATRTERIVYTVKWAGGGRMCTRAGVKINKDT 130
SRANQNIPLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
SRTNENISLFKATRAERTVYTVKWAGGGRLSTRAGVKINKDT 130
SRTNQNISLFKATRAERIVYTVKWAGGGRLTTRAGVKINKDT 130
```

FIG. 22A (Continued)

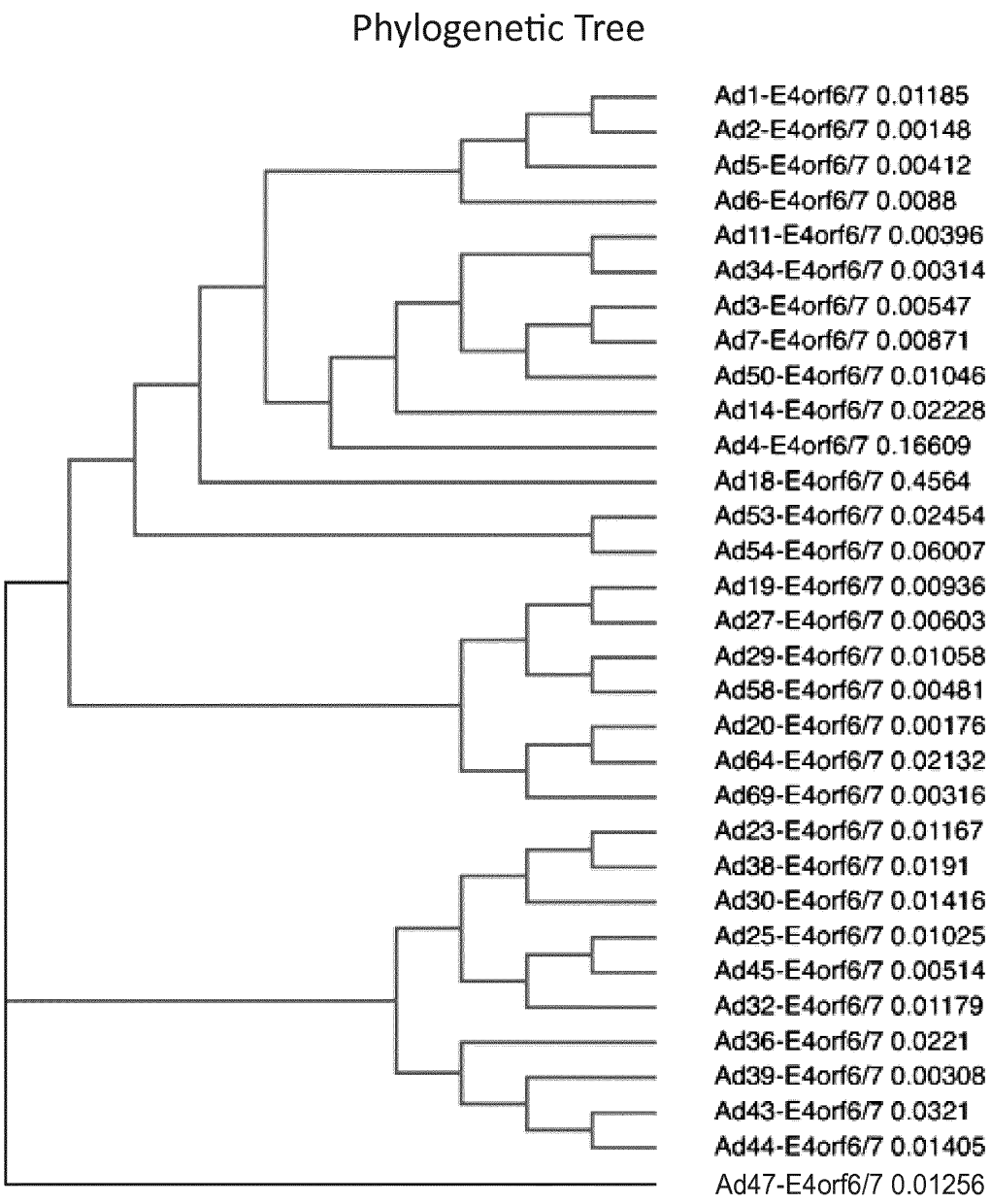

Phylogenetic Tree
Ad1-E4orf6/7 0.01185
Ad2-E4orf6/7 0.00148
Ad5-E4orf6/7 0.00412
Ad6-E4orf6/7 0.0088
Ad11-E4orf6/7 0.00396
Ad34-E4orf6/7 0.00314
Ad3-E4orf6/7 0.00547
Ad7-E4orf6/7 0.00871
Ad50-E4orf6/7 0.01046
Ad14-E4orf6/7 0.02228
Ad4-E4orf6/7 0.16609
Ad18-E4orf6/7 0.4564
Ad53-E4orf6/7 0.02454
Ad54-E4orf6/7 0.06007
Ad19-E4orf6/7 0.00936
Ad27-E4orf6/7 0.00603
Ad29-E4orf6/7 0.01058
Ad58-E4orf6/7 0.00481
Ad20-E4orf6/7 0.00176
Ad64-E4orf6/7 0.02132
Ad69-E4orf6/7 0.00316
Ad23-E4orf6/7 0.01167
Ad38-E4orf6/7 0.0191
Ad30-E4orf6/7 0.01416
Ad25-E4orf6/7 0.01025
Ad45-E4orf6/7 0.00514
Ad32-E4orf6/7 0.01179
Ad36-E4orf6/7 0.0221
Ad39-E4orf6/7 0.00308
Ad43-E4orf6/7 0.0321
Ad44-E4orf6/7 0.01405
Ad47-E4orf6/7 0.01256

FIG. 22B

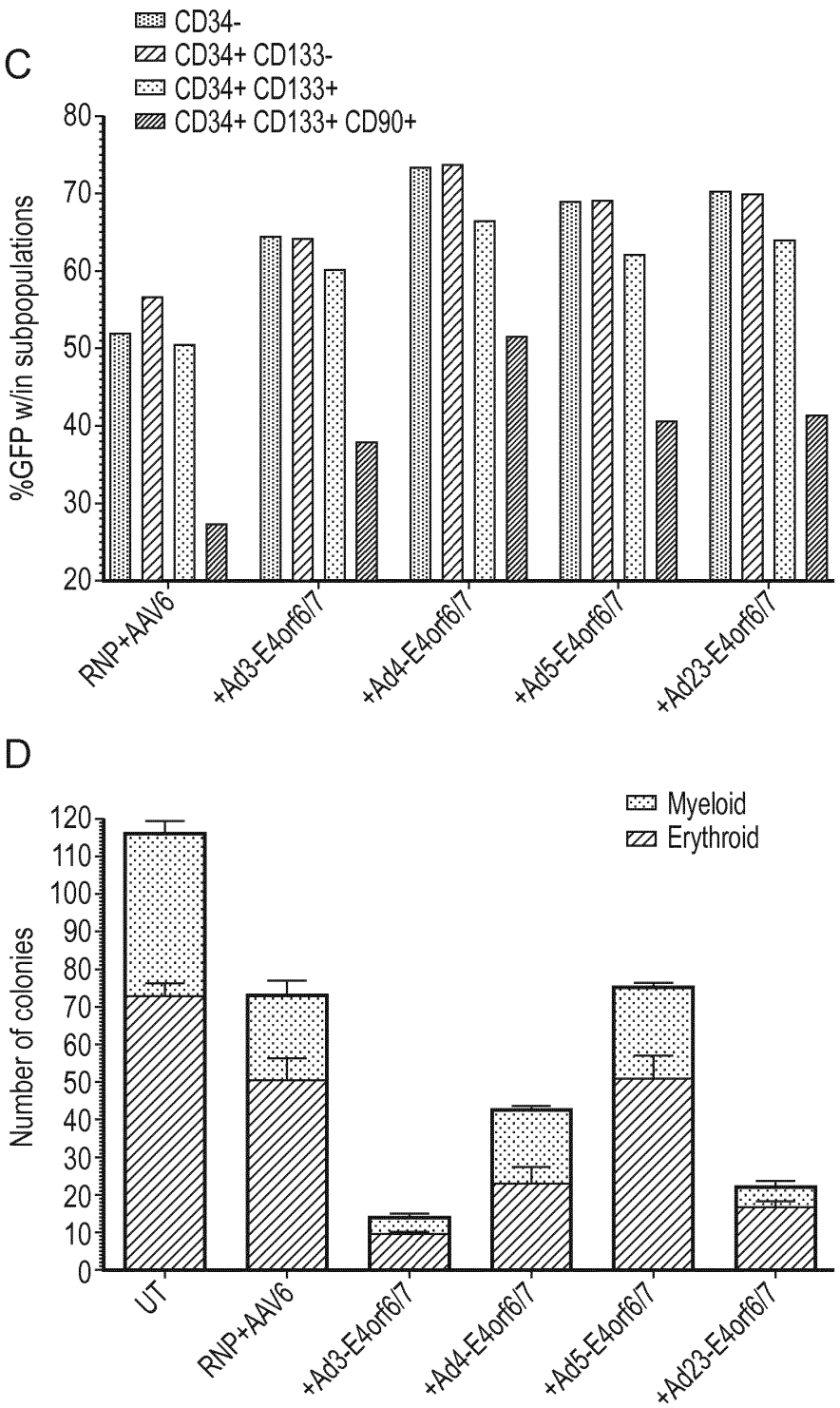


FIG. 22 (Continued)

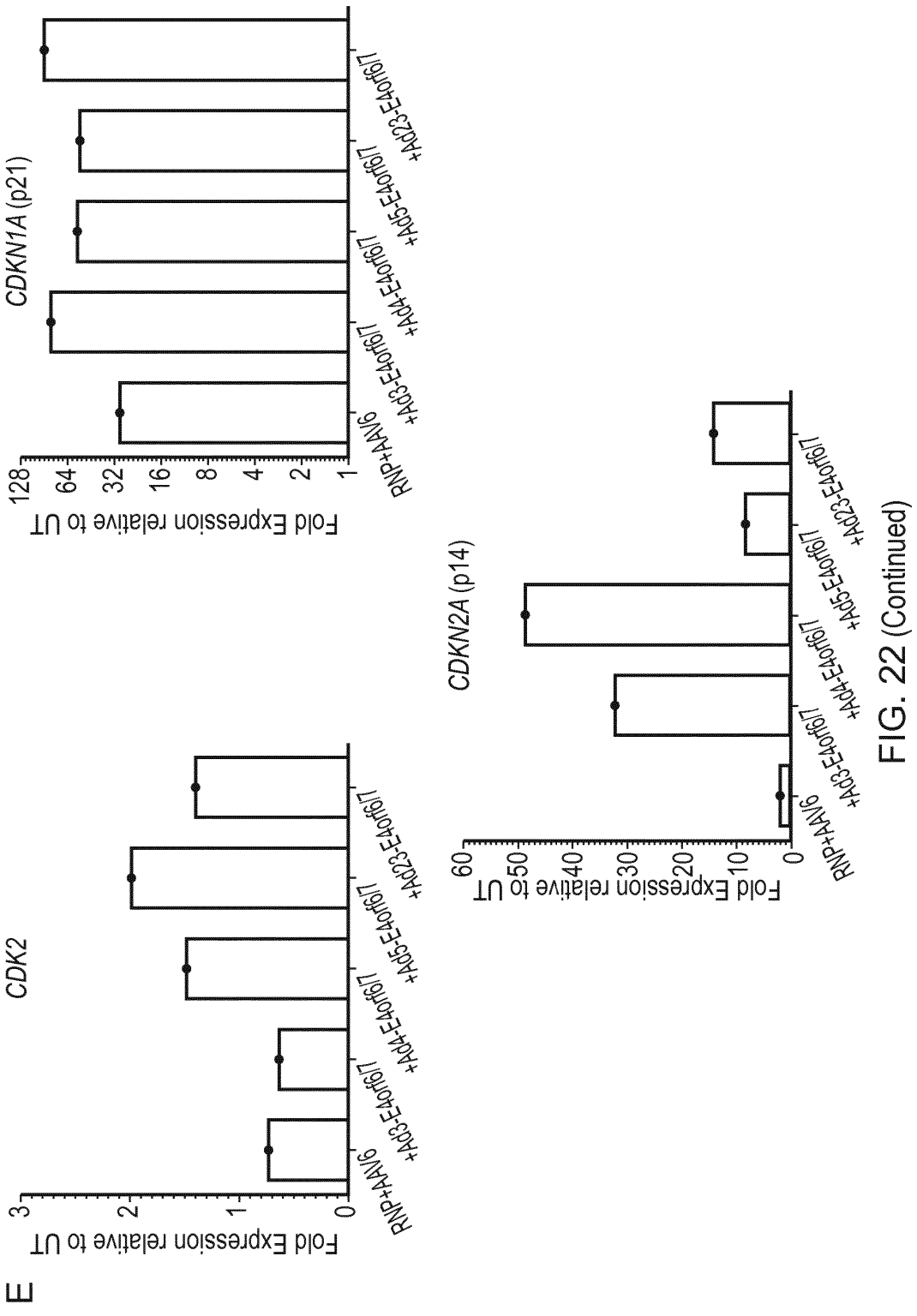


FIG. 22 (Continued)

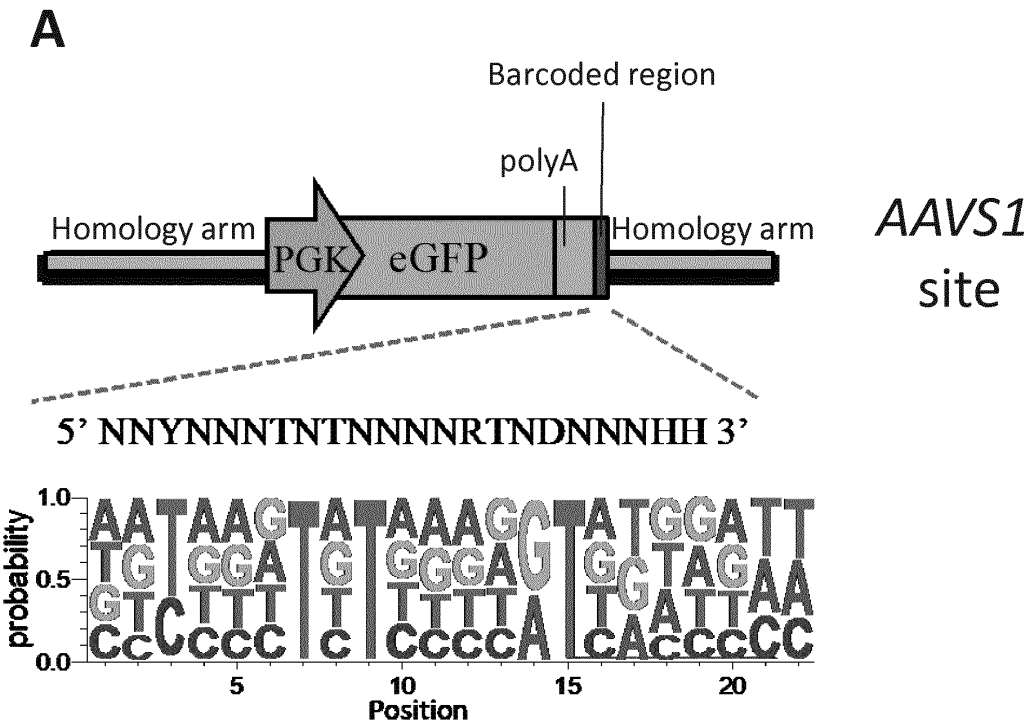

A
Barcoded region
polyA
Homology arm
PGK
eGFP
Homology arm
AAVS1
site
5' NNYNNNTNTNNNNRTNDNNNHH 3'
probability
1.0
0.5
0.0
5
10
15
20
Position

FIG. 23