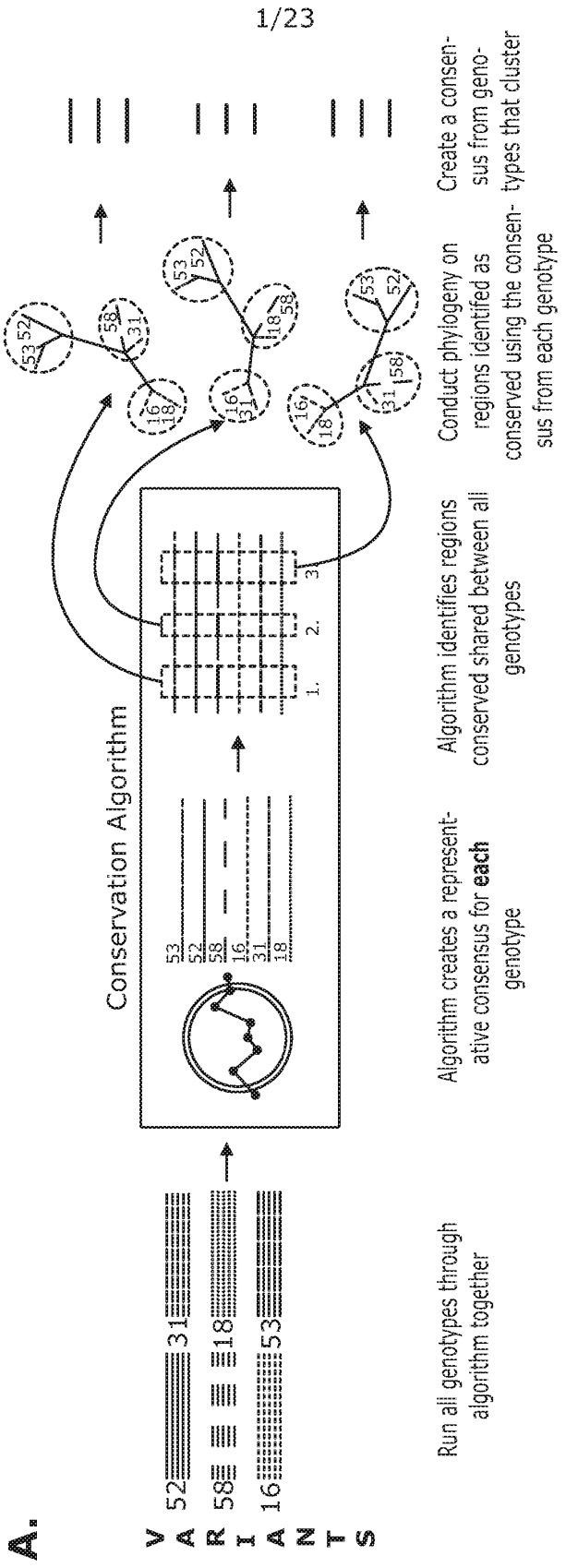

A.
VARIANTS
52
58
16
31
18
53
Run all genotypes through algorithm together
Conservation Algorithm
Algorithm creates a representative consensus for each genotype
Algorithm identifies regions conserved shared between all genotypes
Conduct phylogeny on regions identifed as conserved using the consensus from each genotype
Create a consensus from genotypes that cluster

Figure 1

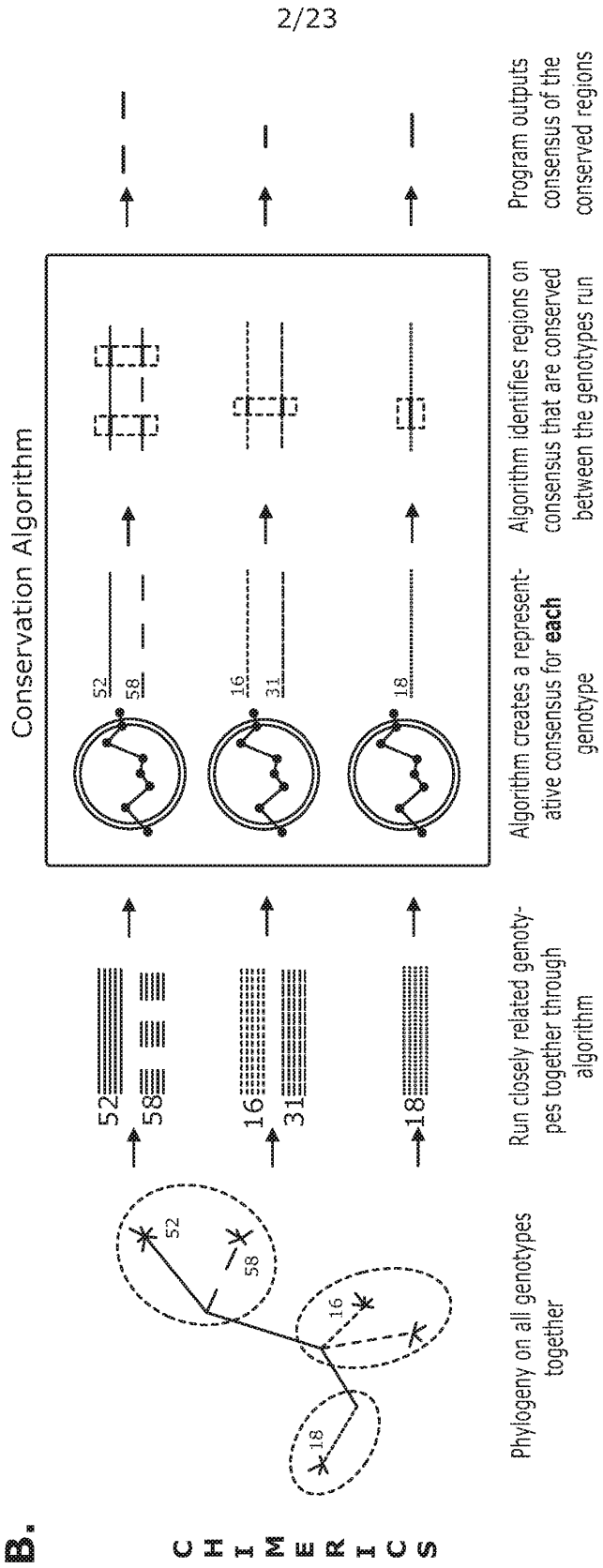


Figure 1 continued

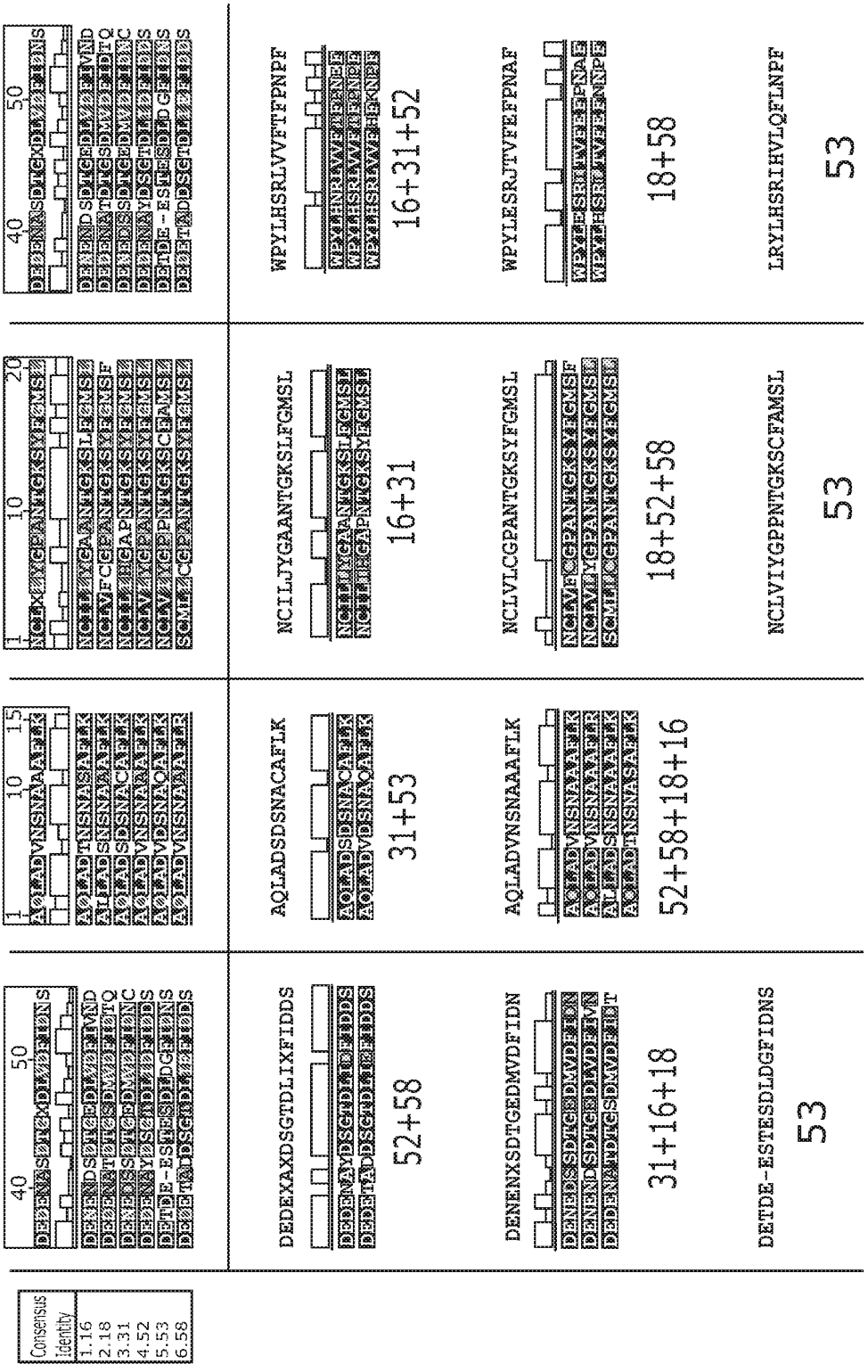

Conserved Region 1
Conserved Region 2
Conserved Region 3
Conserved Region 4
Consensus identity
1.16
2.18
3.31
4.52
5.53
6.58
DEDEXAXDSGTDLIXFIDDS
52+58
DENENXSDTGEDMVDFIDN
31+16+18
DETDE-ESTESDLDGFIDNS
53
AQLADSDSNACAFLK
31+53
AQLADVNSNAAAFLK
52+58+18+16
NCILJYGAANTGKSLFGMSL
16+31
NCLVLCGPANTGKSYFGMSL
18+52+58
NCLVIYGPPNTGKSCFAMSL
53
WPYLHSRLJVVFTFPNPF
16+31+52
WPYLESRJTVVFEFPNAF
18+58
LRYLHSRIHVLQFLNPF
53

Figure 2

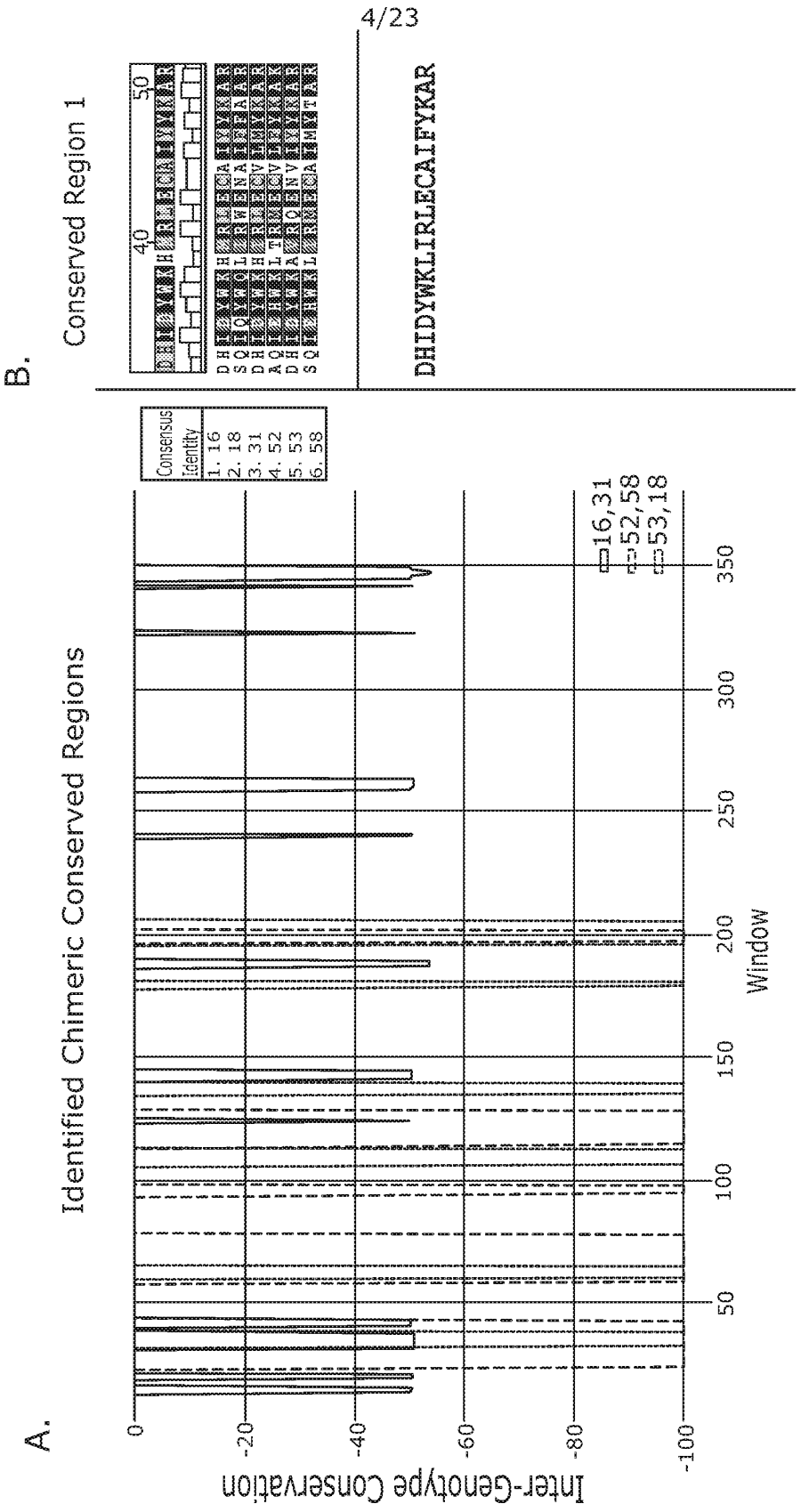

A.
Identified Chimeric Conserved Regions
Inter-Genotype Conservation
Window
0
-20
-40
-60
-80
-100
50
100
150
200
250
300
350
16,31
52,58
53,18
Consensus Identity
1. 16
2. 18
3. 31
4. 52
5. 53
6. 58
B.
Conserved Region 1
40
50
DHIDYWKLIRLECAIFYKAR

Figure 3

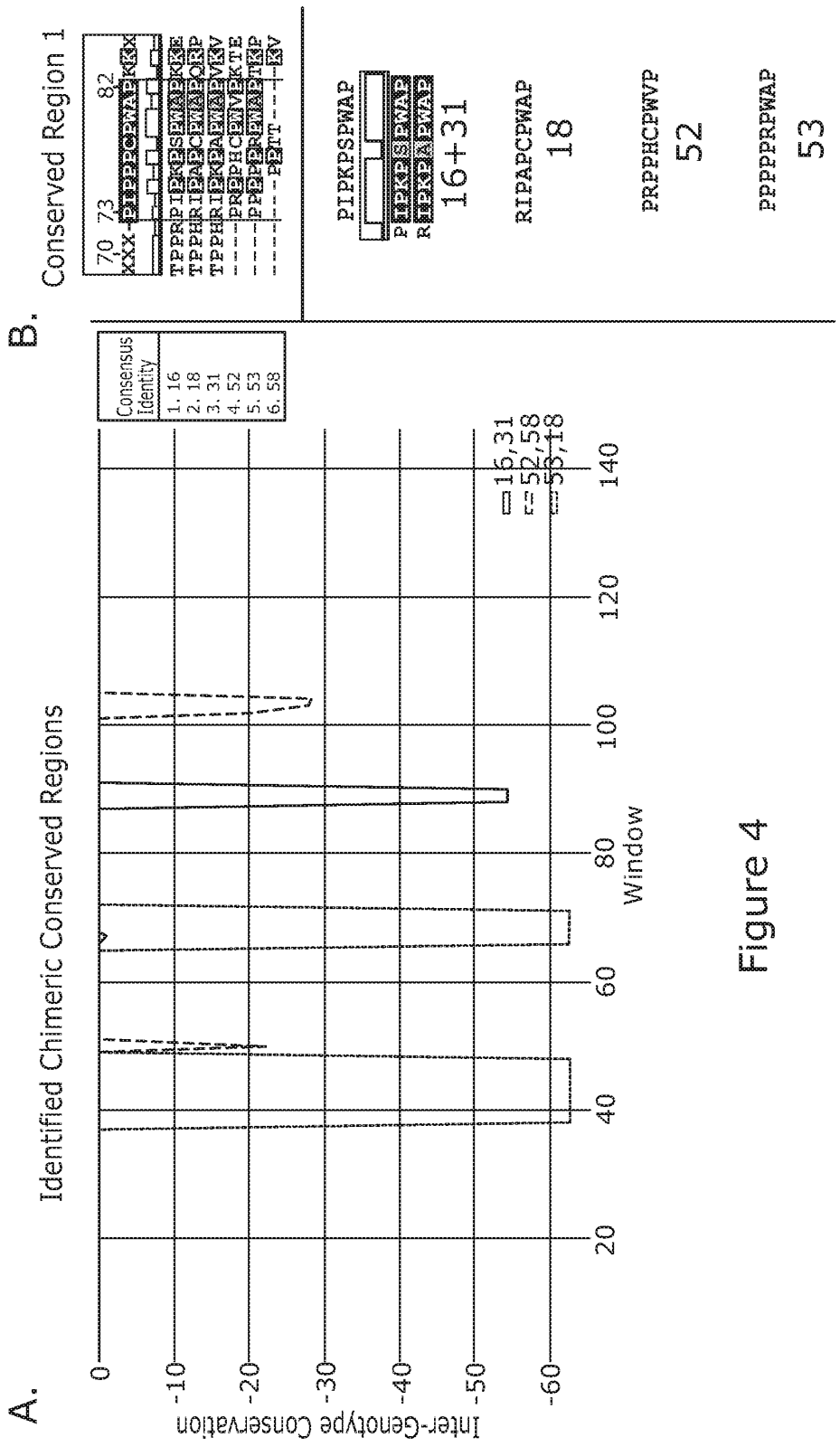

A.
Identified Chimeric Conserved Regions
Inter-Genotype Conservation
0
-10
-20
-30
-40
-50
-60
20
40
60
80
100
120
140
Window
16,31
52,58
53,18
Consensus Identity
1. 16
2. 18
3. 31
4. 52
5. 53
6. 58
B.
Conserved Region 1
70 73
82
PIPKPSPWAP
16+31
RIPAPCPWAP
18
PRPPHCPWVP
52
PPPPPRPWAP
53

Figure 4

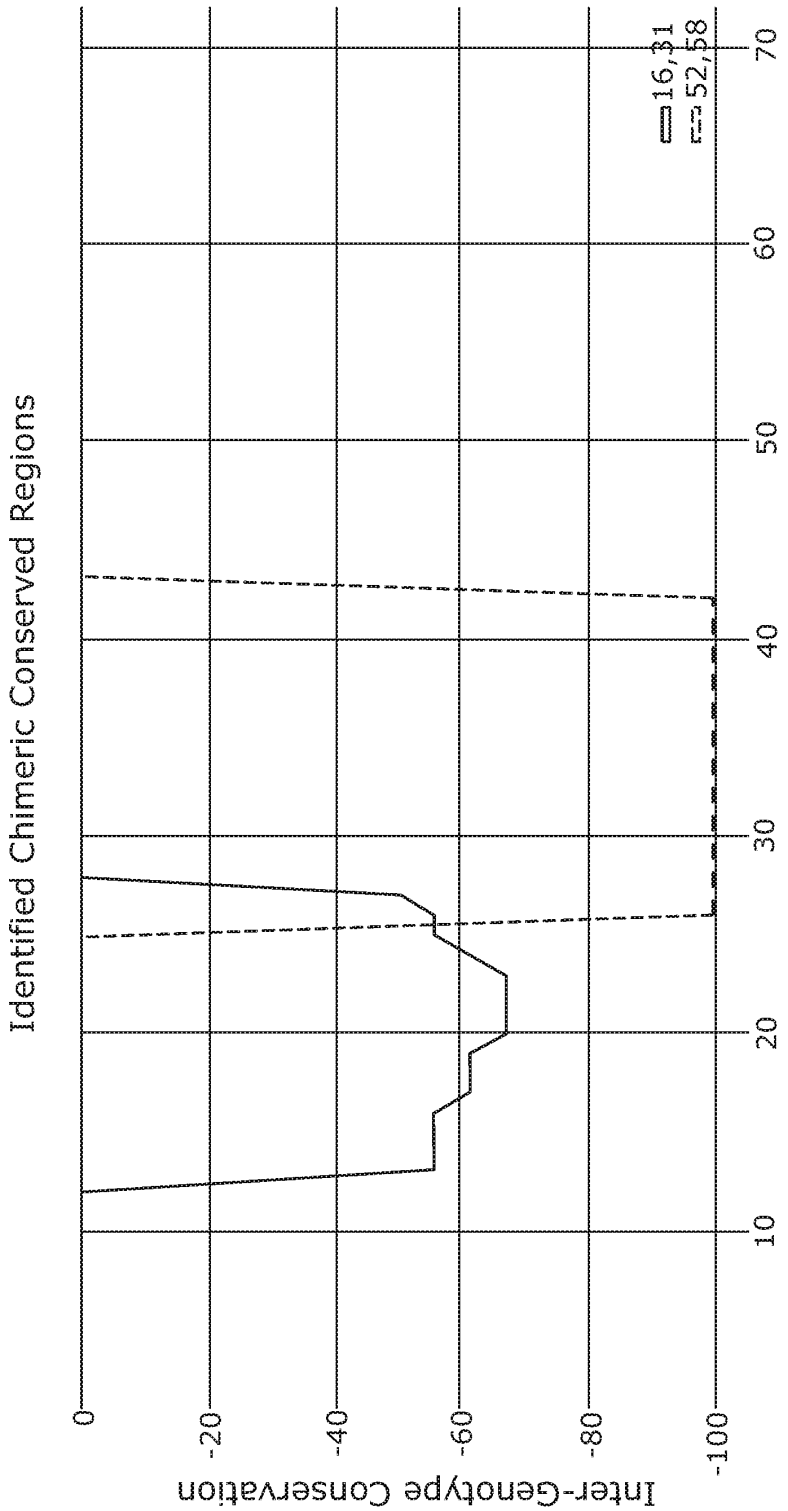

Identified Chimeric Conserved Regions
Inter-Genotype Conservation
0
-20
-40
-60
-80
-100
10
20
30
40
50
60
70
Window
16,31
52,58

Figure 5

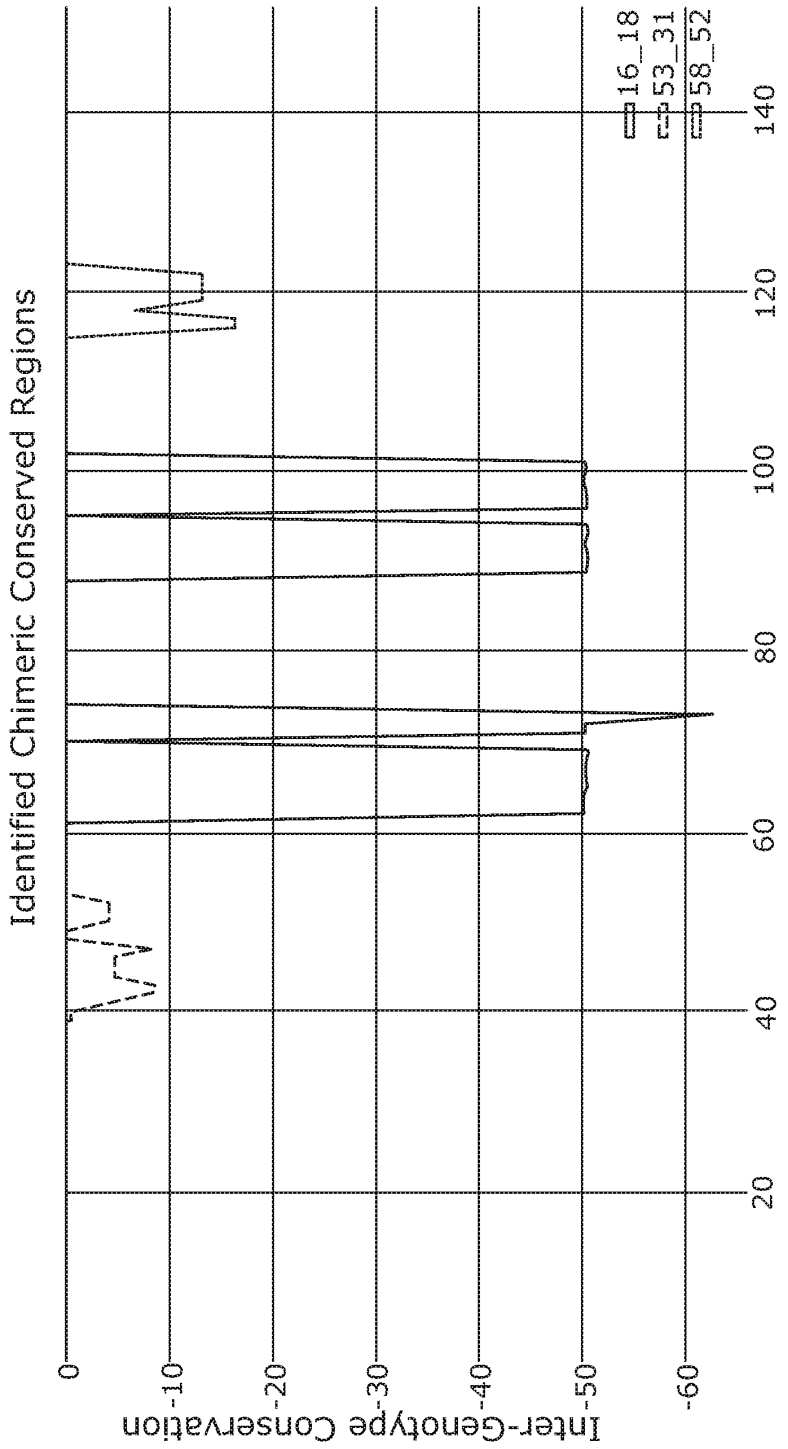

Identified Chimeric Conserved Regions
Inter-Genotype Conservation
0
-10
-20
-30
-40
-50
-60
20
40
60
80
100
120
140
Window
16_18
53_31
58_52

Figure 6

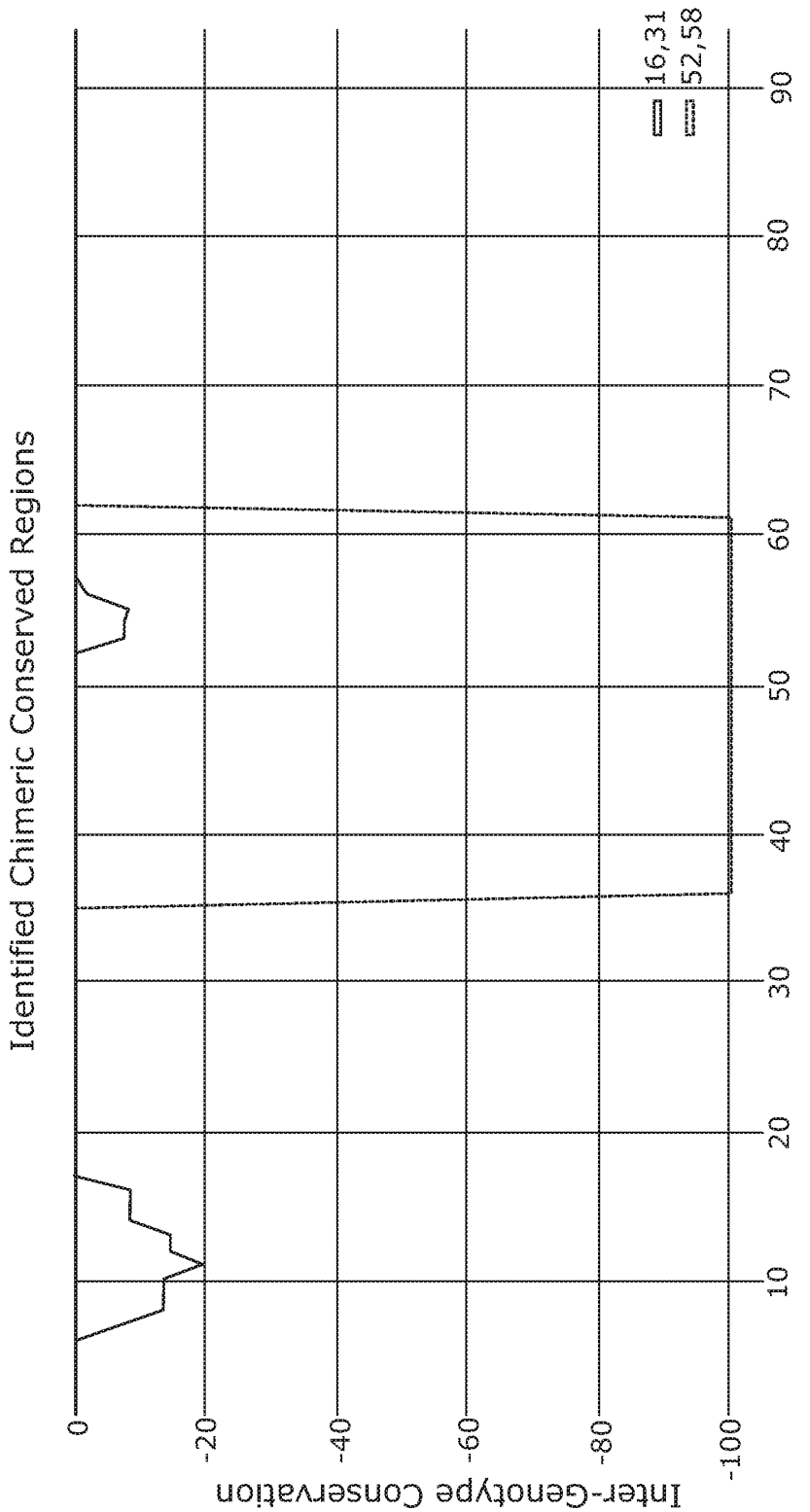

Identified Chimeric Conserved Regions
Inter-Genotype Conservation
0
-20
-40
-60
-80
-100
10
20
30
40
50
60
70
80
90
Window
16,31
52,58

Figure 7

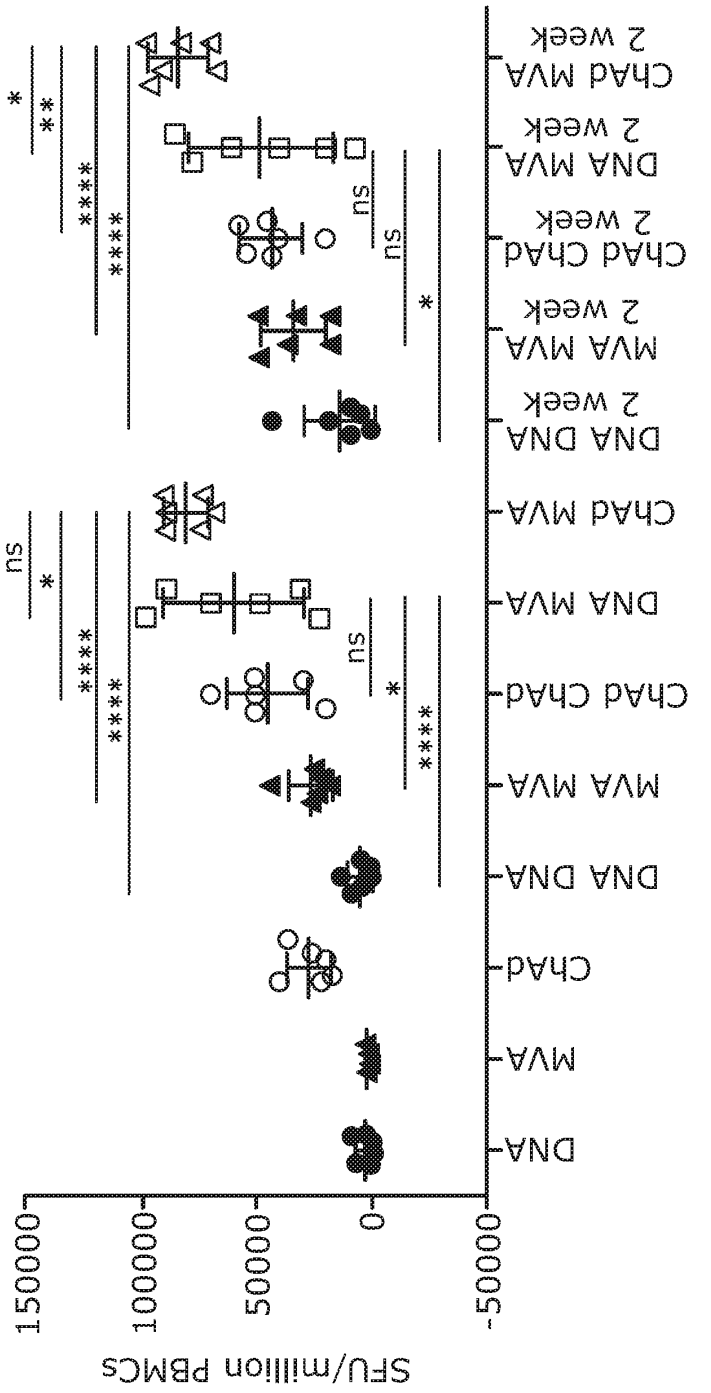

SFU/million PBMCs
150000
100000
50000
0
-50000
DNA
MVA
ChAd
DNA DNA
MVA MVA
ChAd ChAd
DNA MVA
ChAd MVA
DNA DNA 2 week
MVA MVA 2 week
ChAd ChAd 2 week
DNA MVA 2 week
ChAd MVA 2 week
ns
*
****
****
****
ns
*
****
ns
*
****
****
****
ns
*
**
*

Figure 8

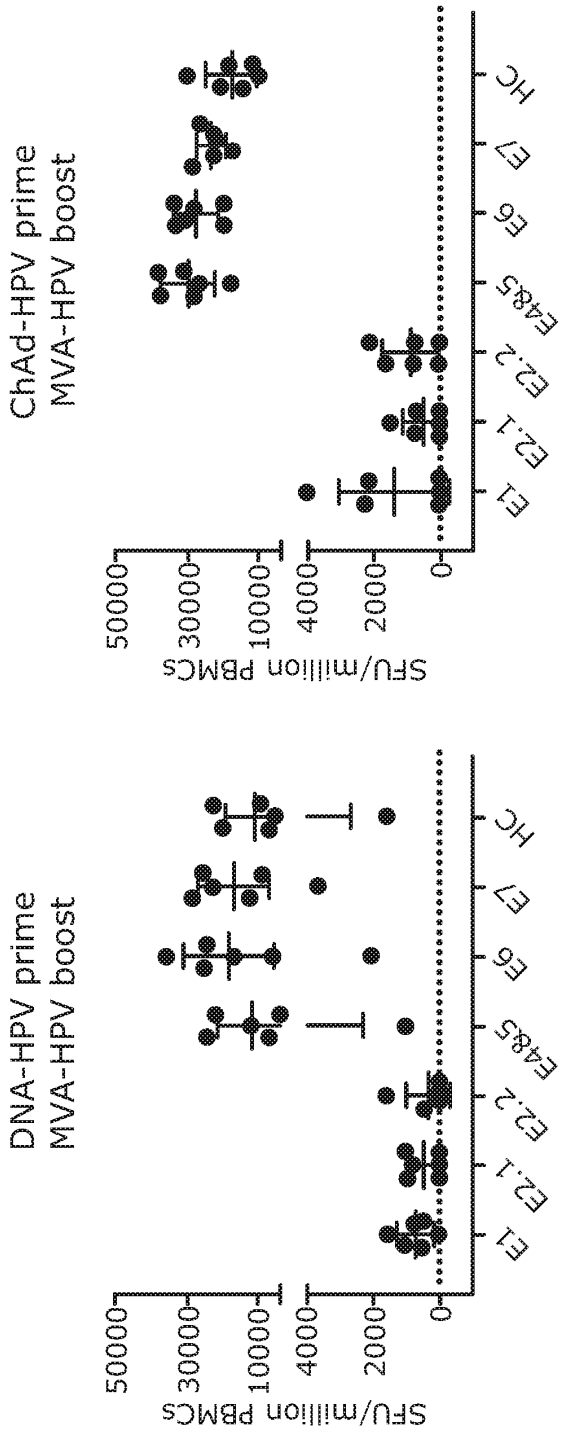

ChAd-HPV prime
MVA-HPV boost
DNA-HPV prime
MVA-HPV boost
SFU/million PBMCs
50000
30000
10000
4000
2000
0
E1
E2.1
E2.2
E4&5
E6
E7
HC

Figure 9

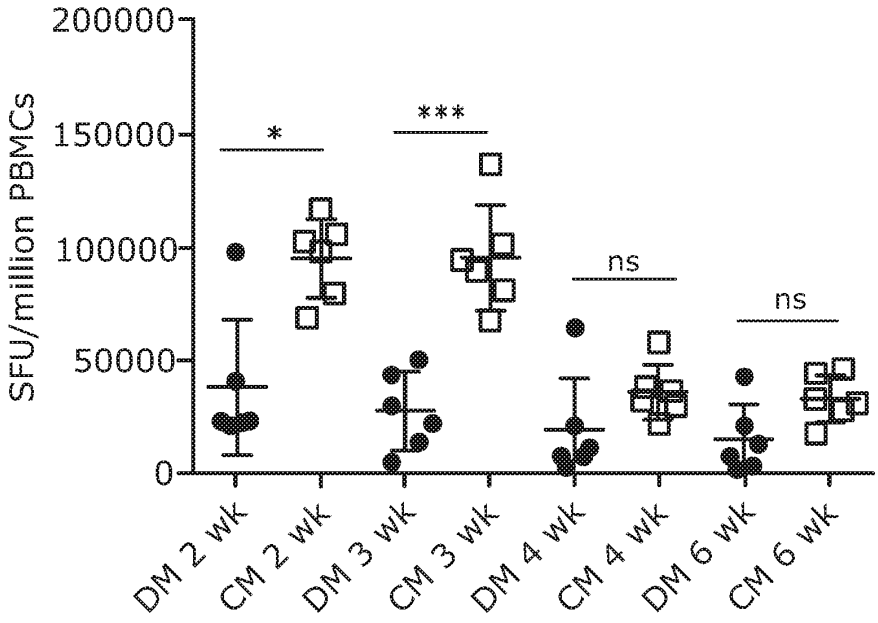

200000
150000
100000
50000
0
SFU/million PBMCs
*
***
ns
ns
DM 2 wk
CM 2 wk
DM 3 wk
CM 3 wk
DM 4 wk
CM 4 wk
DM 6 wk
CM 6 wk

Figure 10A

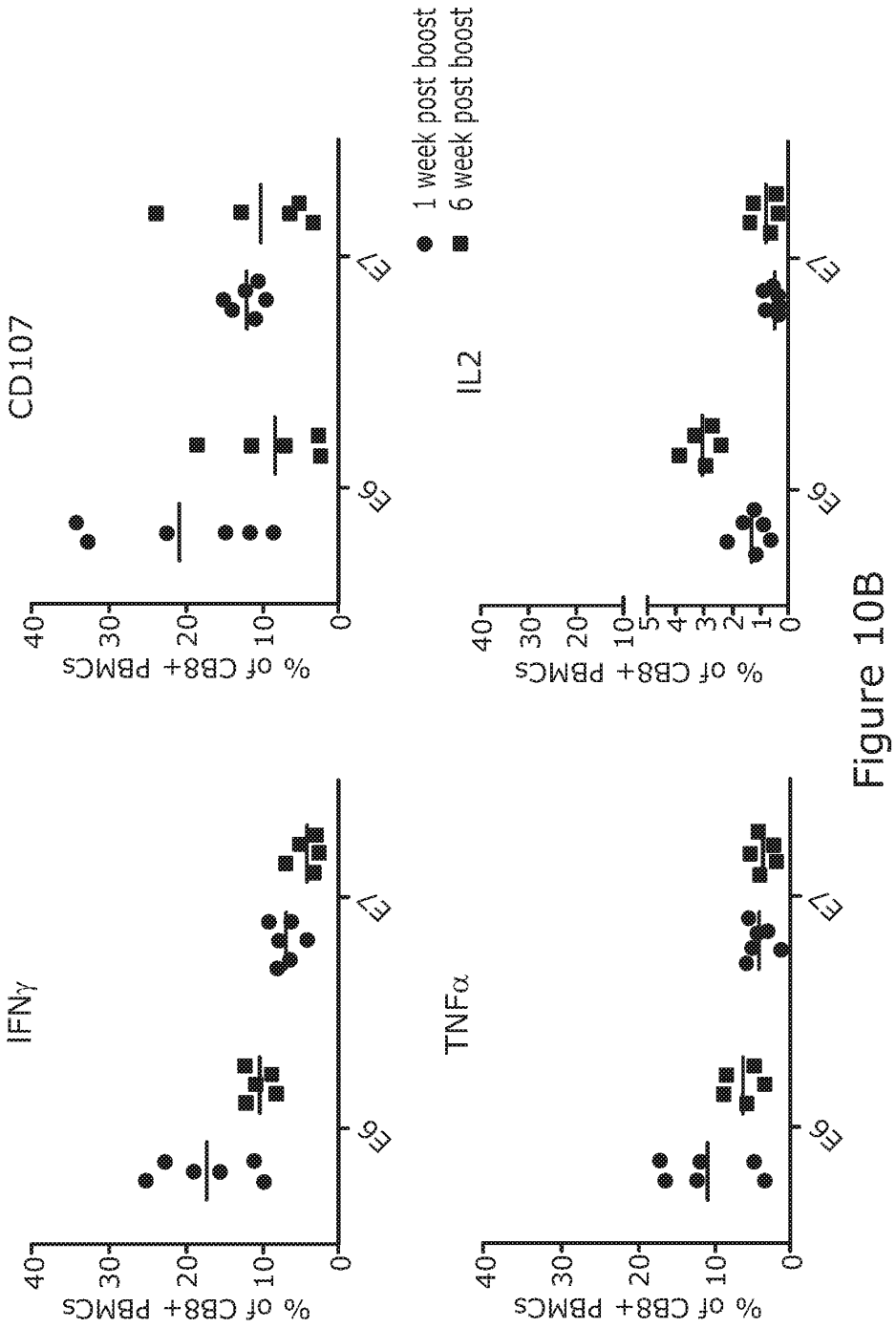

CD107
IL2
IFNγ
TNFα
% of CB8+ PBMCs
E6
E7
1 week post boost
6 week post boost

Figure 10B

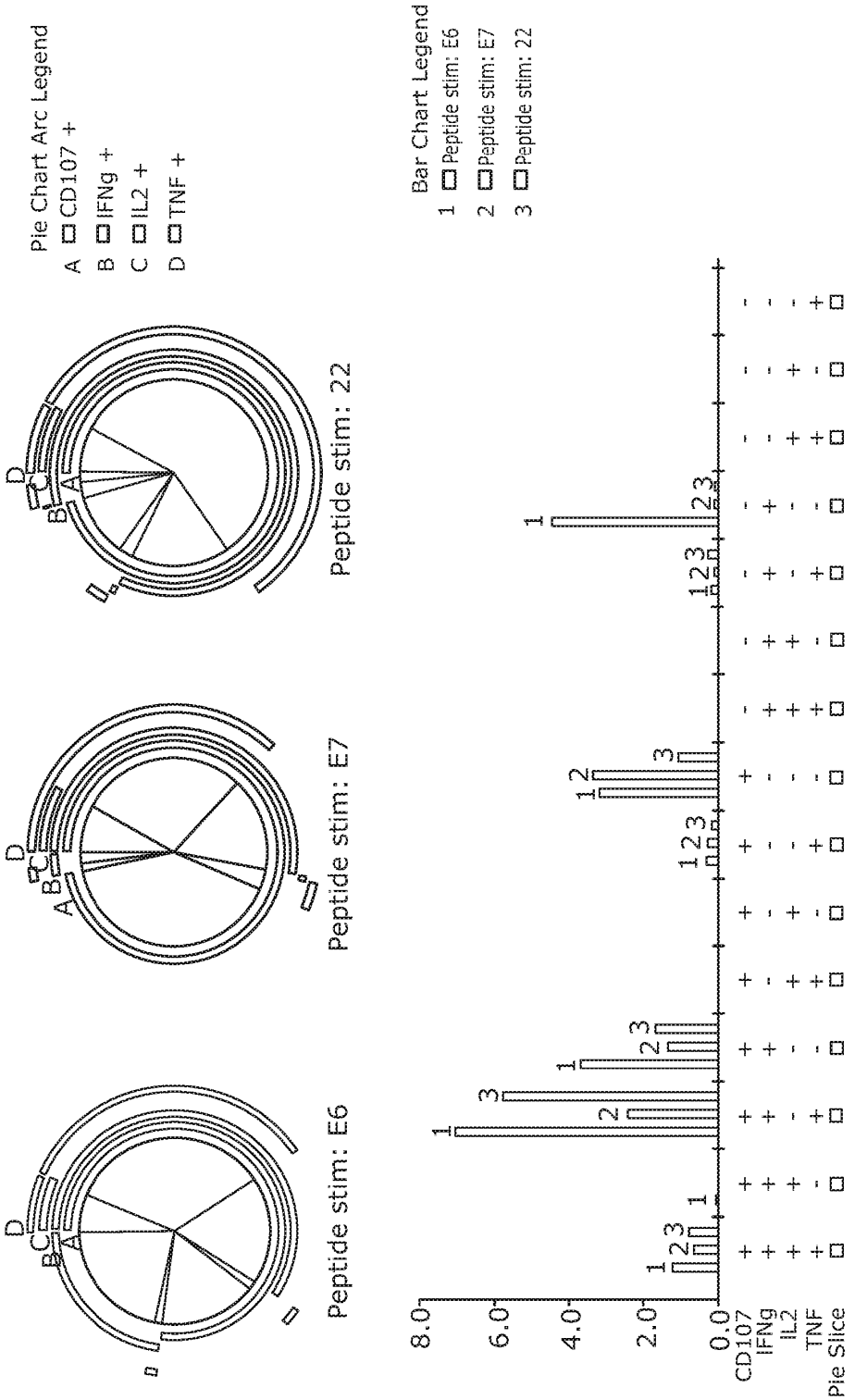

Pie Chart Arc Legend
A CD107 +
B IFNg +
C IL2 +
D TNF +
Peptide stim: E6
Peptide stim: E7
Peptide stim: 22
Bar Chart Legend
1 Peptide stim: E6
2 Peptide stim: E7
3 Peptide stim: 22
8.0
6.0
4.0
2.0
0.0
CD107
IFNg
IL2
TNF
Pie Slice

Figure 11

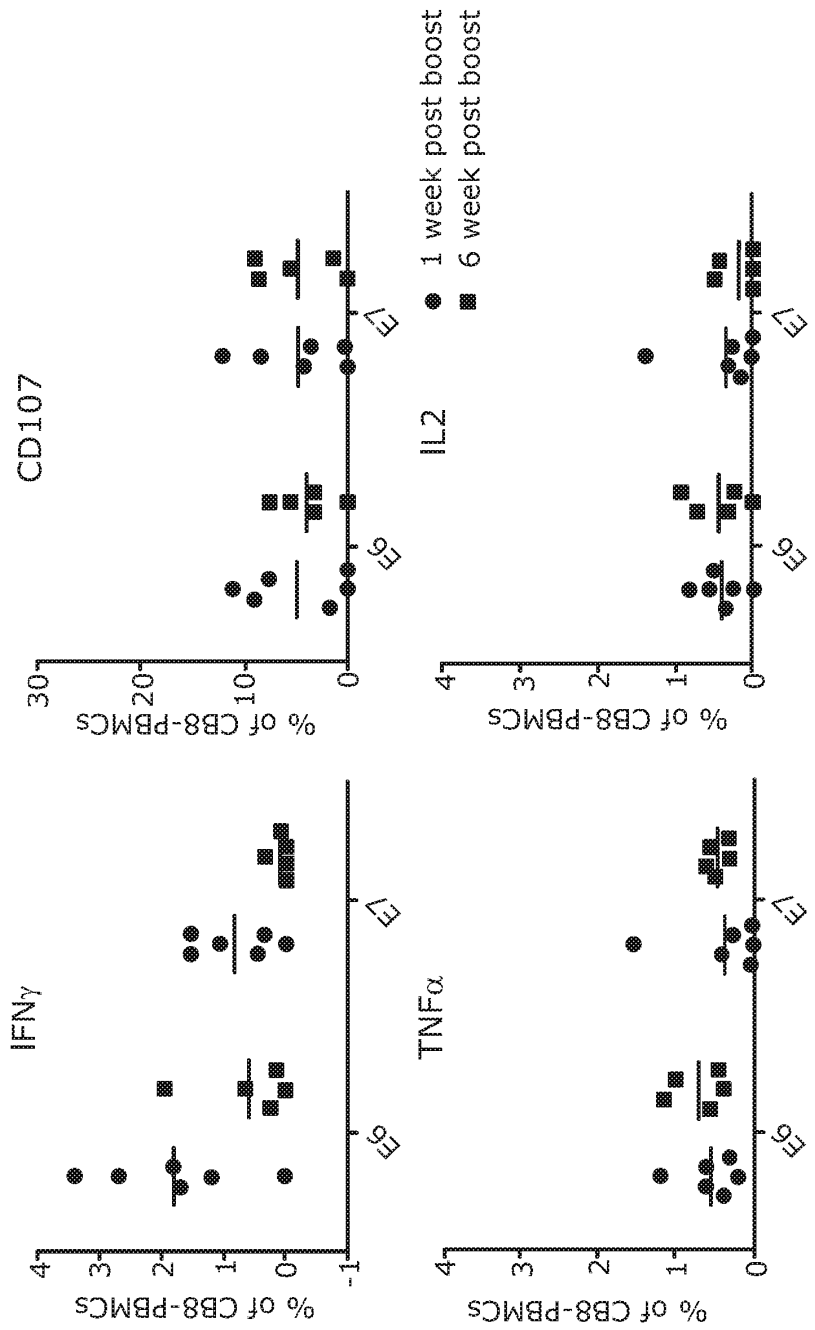

CD107
IL2
IFNγ
TNFα
% of CB8-PBMCs
1 week post boost
6 week post boost
E6
E7
0
10
20
30
1
2
3
4
-1

Figure 12

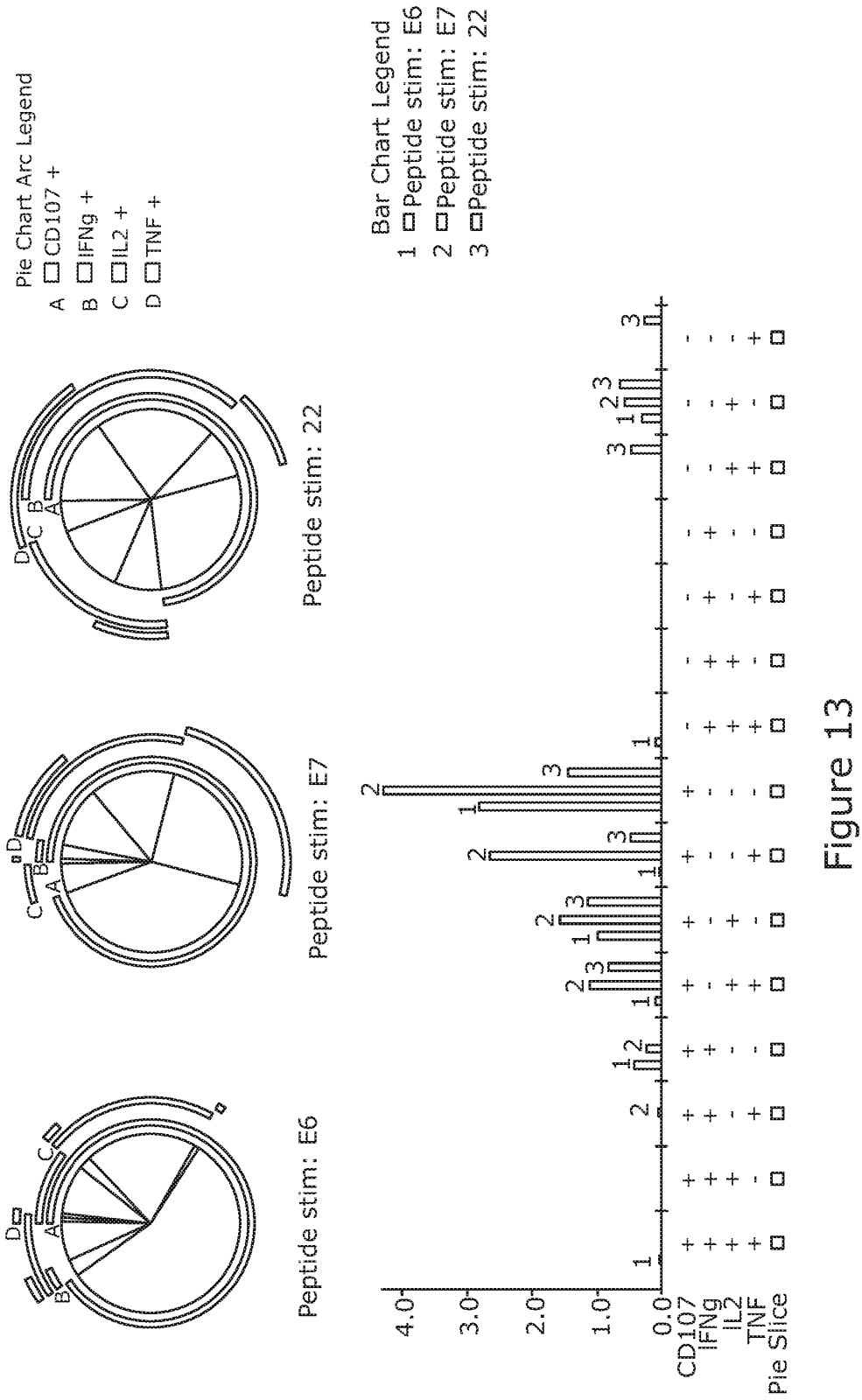

Pie Chart Arc Legend
A CD107 +
B IFNg +
C IL2 +
D TNF +
Bar Chart Legend
1 Peptide stim: E6
2 Peptide stim: E7
3 Peptide stim: 22
Peptide stim: E6
Peptide stim: E7
Peptide stim: 22
4.0
3.0
2.0
1.0
0.0
CD107
IFNg
IL2
TNF
Pie Slice

Figure 13

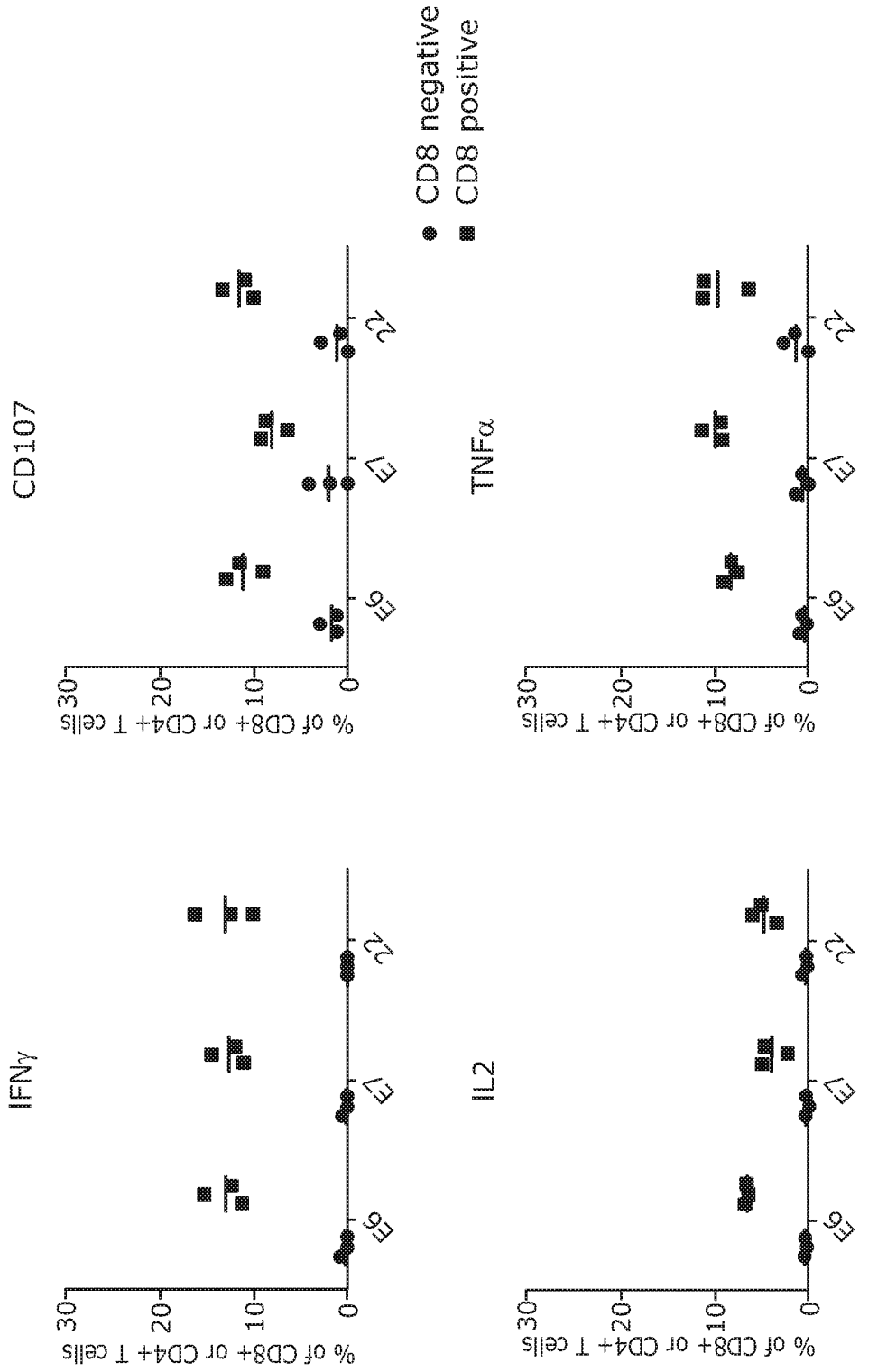

CD8 negative
CD8 positive
CD107
TNFα
IFNγ
IL2
% of CD8+ or CD4+ T cells
0
10
20
30
E6
E1
22

Figure 14

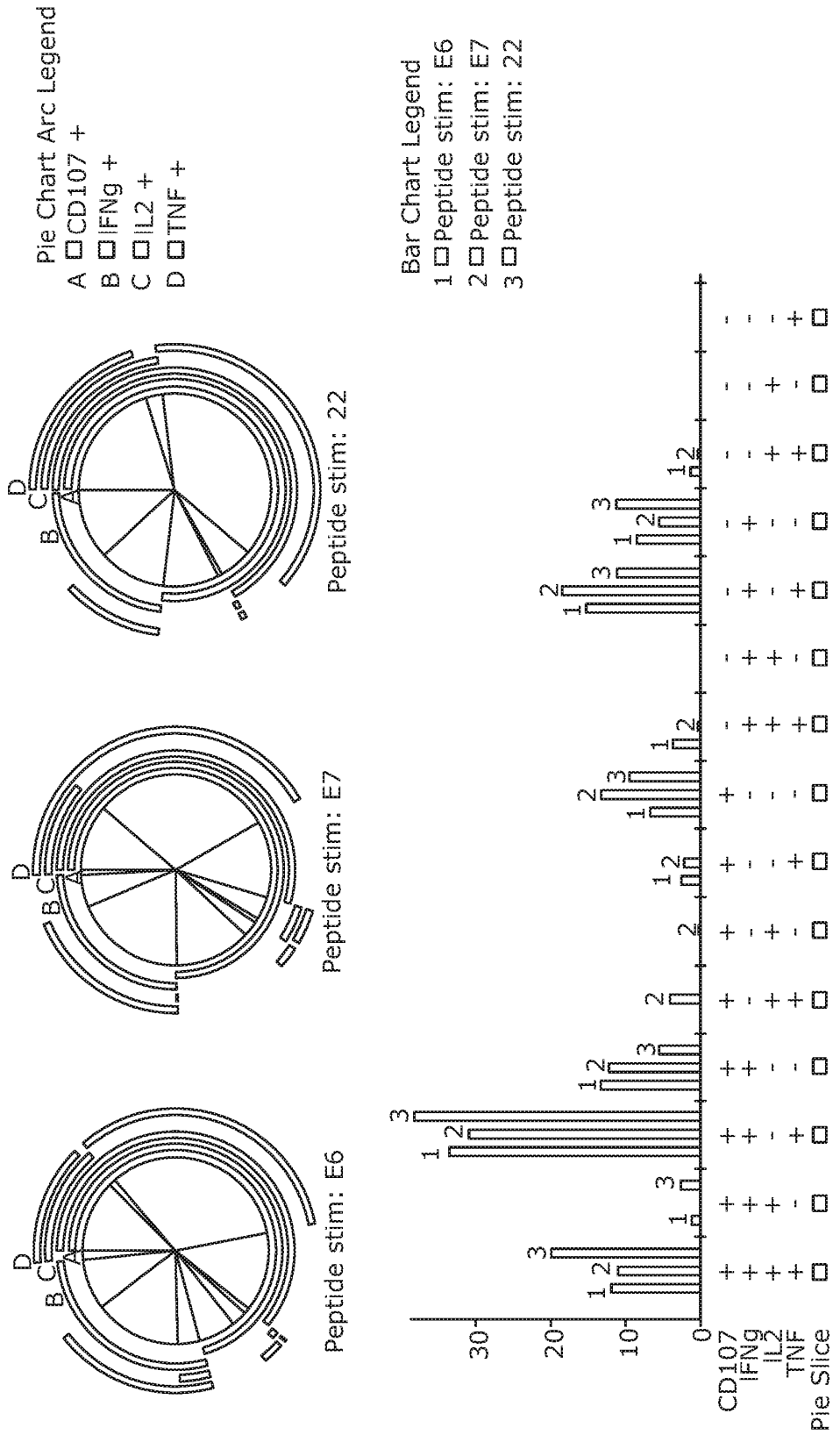

Pie Chart Arc Legend
A CD107 +
B IFNg +
C IL2 +
D TNF +
Bar Chart Legend
1 Peptide stim: E6
2 Peptide stim: E7
3 Peptide stim: 22
Peptide stim: E6
Peptide stim: E7
Peptide stim: 22
CD107
IFNg
IL2
TNF
Pie Slice
0
10
20
30

Figure 15

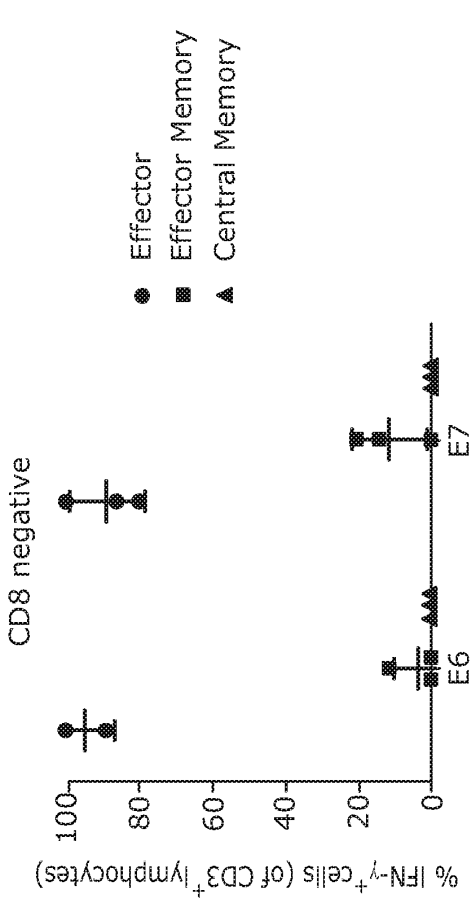


Figure 16

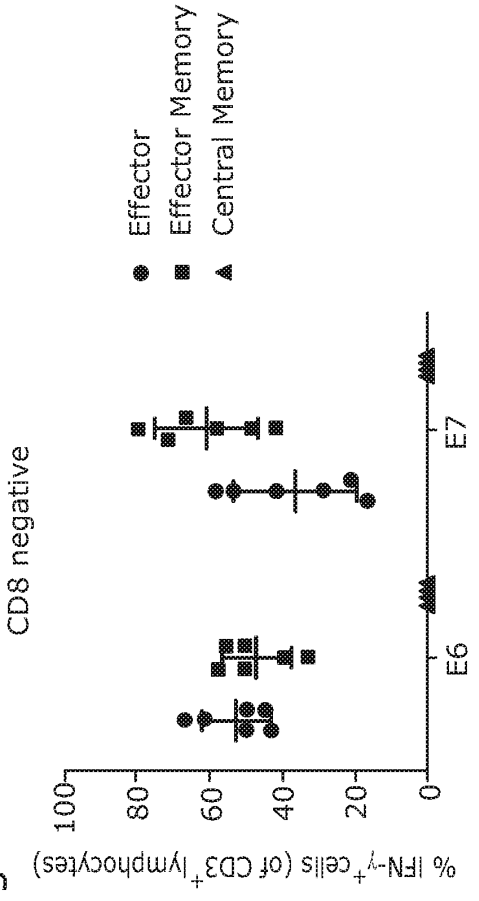
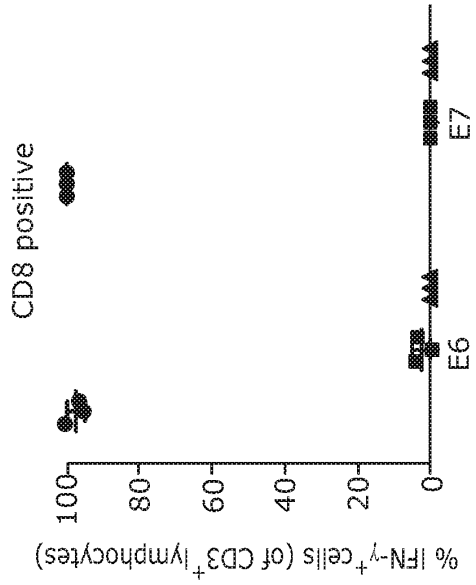
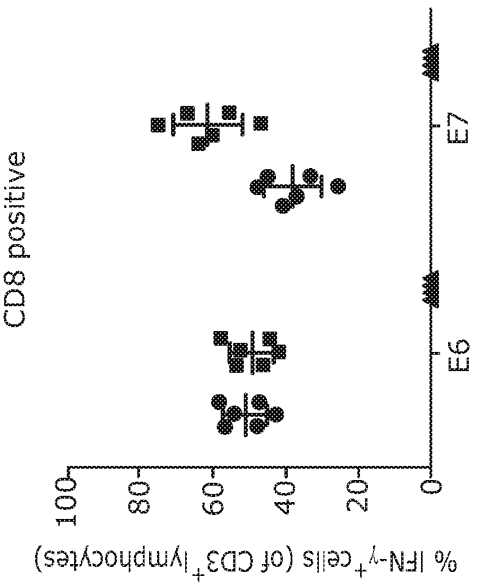


Figure 17





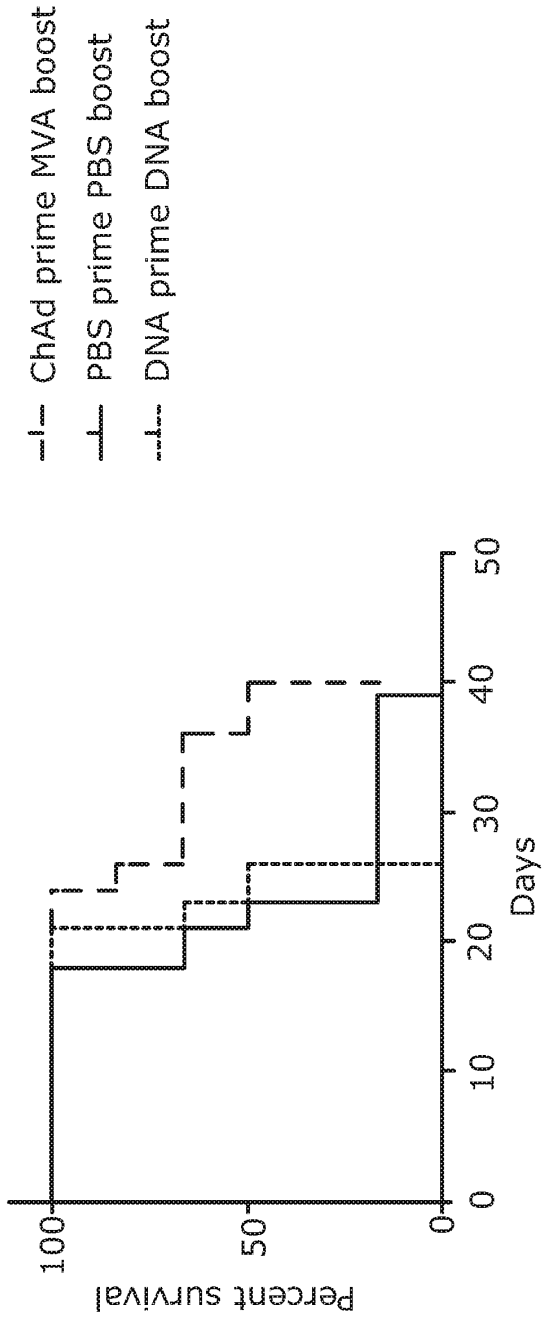


Figure 18

Median survival
PBS prime PBS boost: 22 days
DNA prime DNA boost: 24.5 days
ChAd Prime MVA boost: 38 days

p=0.02 (Log-rank(Mantel-Cox) test)

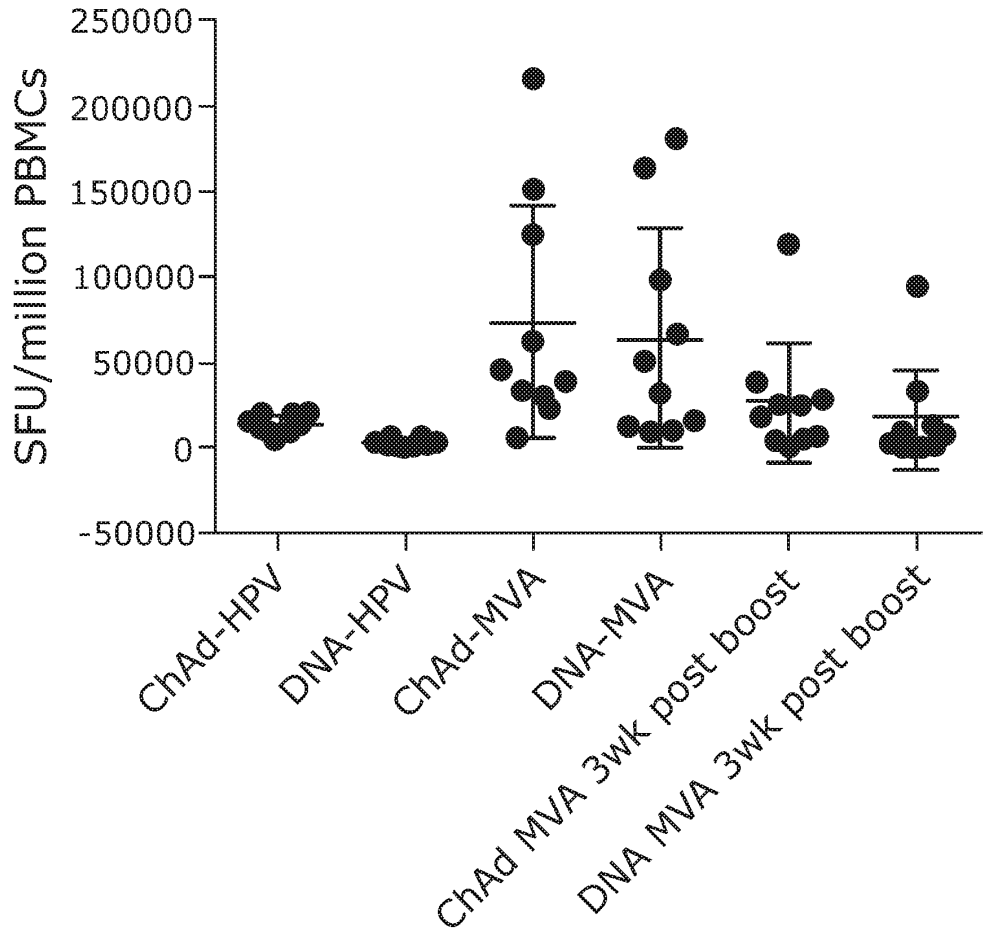

SFU/million PBMCs
250000
200000
150000
100000
50000
0
-50000
ChAd-HPV
DNA-HPV
ChAd-MVA
DNA-MVA
ChAd MVA 3wk post boost
DNA MVA 3wk post boost

Figure 19

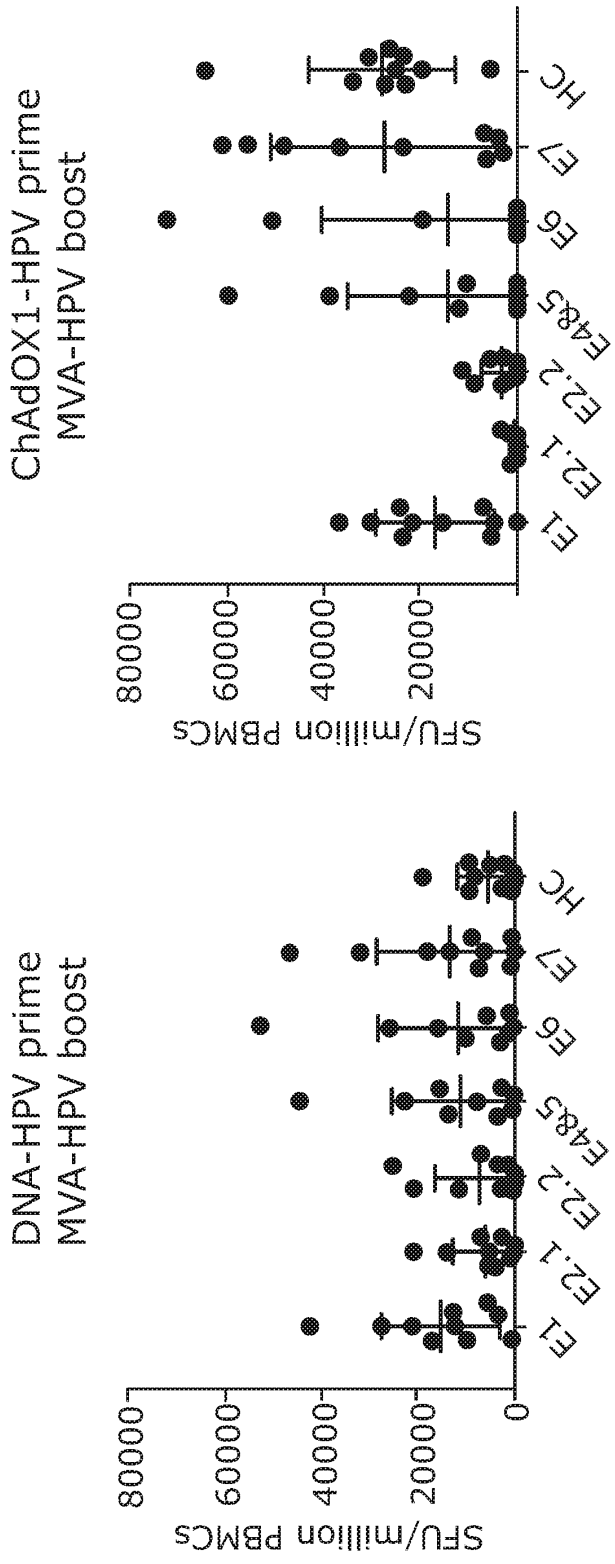
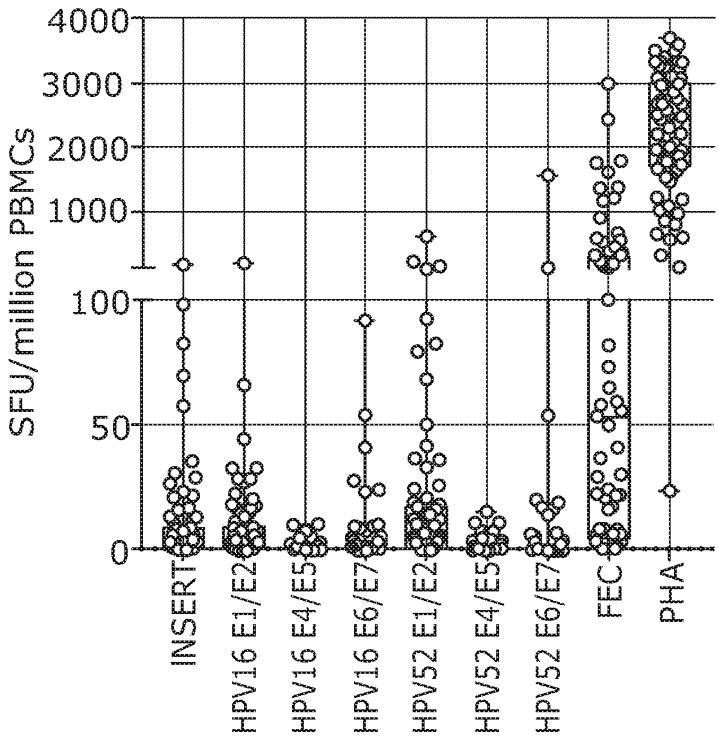
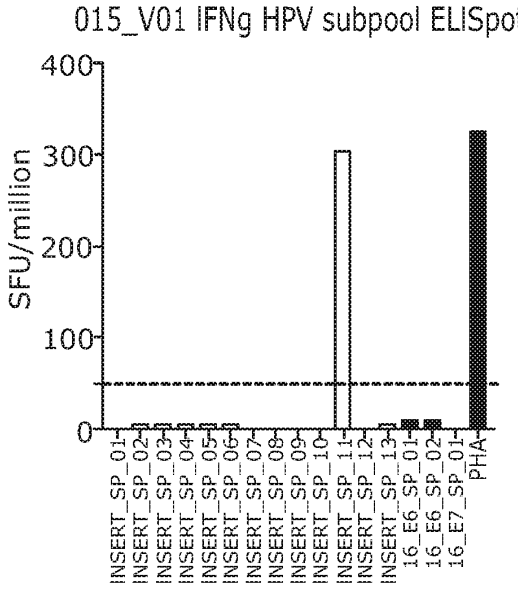

ChAdOX1-HPV prime
MVA-HPV boost
SFU/million PBMCs
80000
60000
40000
20000
E1
E2.1
E2.2
E4&5
E6
E7
HC
DNA-HPV prime
MVA-HPV boost
SFU/million PBMCs
80000
60000
40000
20000
0
E1
E2.1
E2.2
E4&5
E6
E7
HC

Figure 20


4000
3000
2000
1000
100
50
0
SFU/million PBMCs
INSERT
HPV16 E1/E2
HPV16 E4/E5
HPV16 E6/E7
HPV52 E1/E2
HPV52 E4/E5
HPV52 E6/E7
FEC
PHA


015_V01 IFNg HPV subpool ELISpot
400
300
200
100
0
SFU/million
INSERT_SP_01
INSERT_SP_02
INSERT_SP_03
INSERT_SP_04
INSERT_SP_05
INSERT_SP_06
INSERT_SP_07
INSERT_SP_08
INSERT_SP_09
INSERT_SP_10
INSERT_SP_11
INSERT_SP_12
INSERT_SP_13
16_E6_SP_01
16_E6_SP_02
16_E7_SP_01
PHA

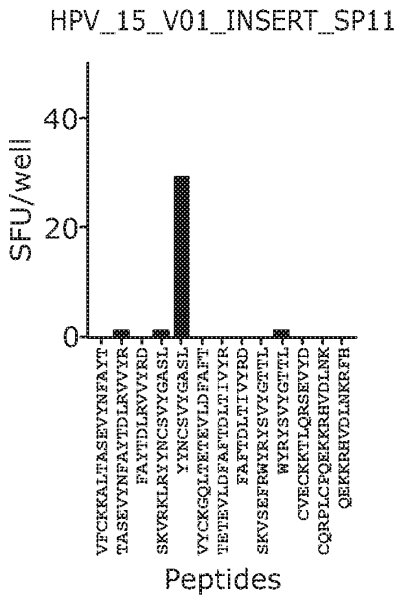

HPV_15_V01_INSERT_SP11
40
20
0
SFU/well
VFCKKALTASEVYNFAYT
TASEVYNFAYTDLRVVYR
FAYTDLRVVYRD
SKVRKLRYYNCSVYGASL
YYNCSVYGASL
VYCKGQLTETEVLDFAFT
TETEVLDFAFTDLTIVYR
FAFTDLTIVYRD
SKVSEFRWYRYSVYGETL
WYRYSVYGETL
CVECKKTLQRSEVYD
CQRPLCPQEKKRHVDLNK
QEKKRHVDLNKRFH
Peptides

Figure 21

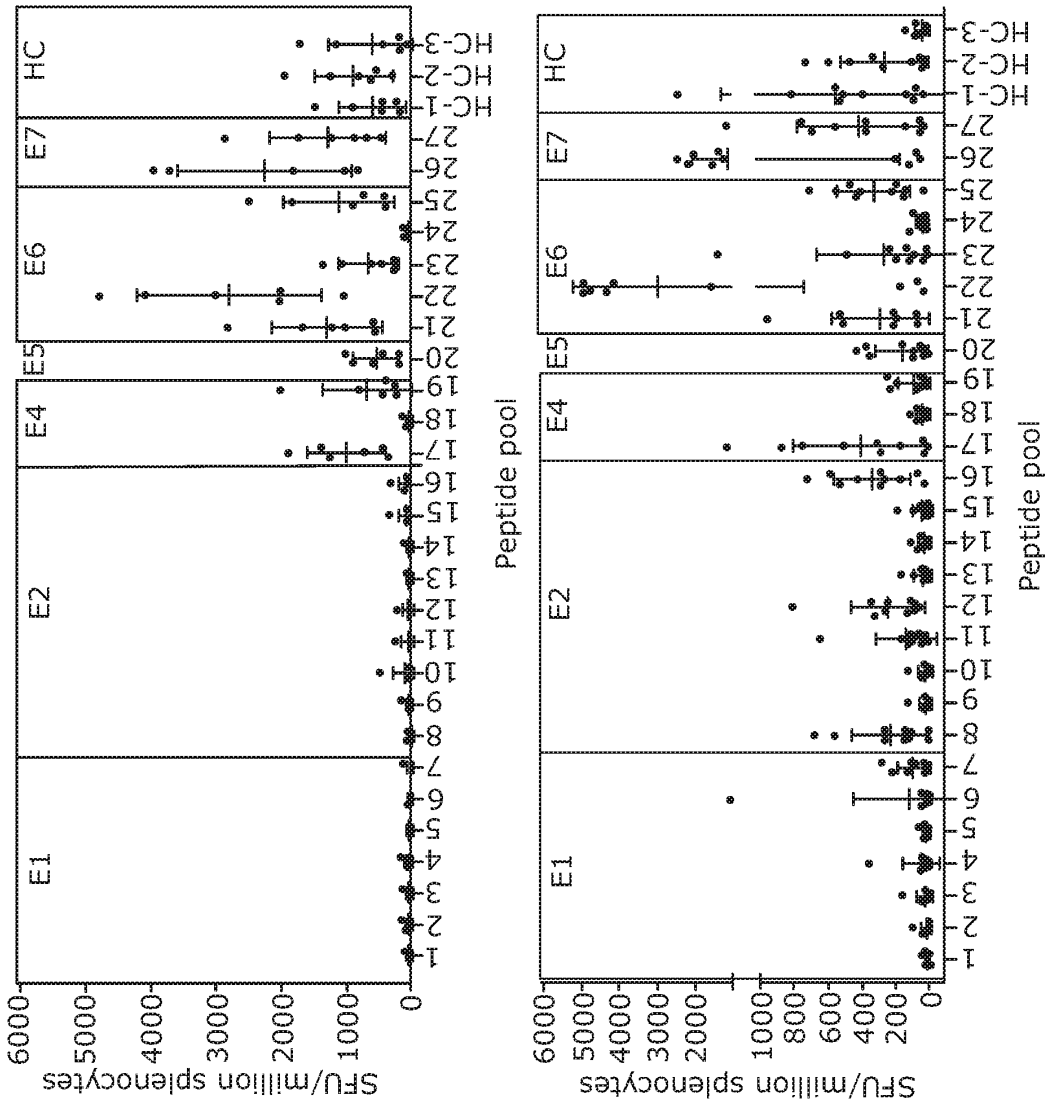

SFU/million splenocytes
Peptide pool
E1
E2
E4
E5
E6
E7
HC
SFU/million splenocytes
Peptide pool
E1
E2
E4
E5
E6
E7
HC

Figure 22