

Figure 1

Number of Positive Pools: 4x background

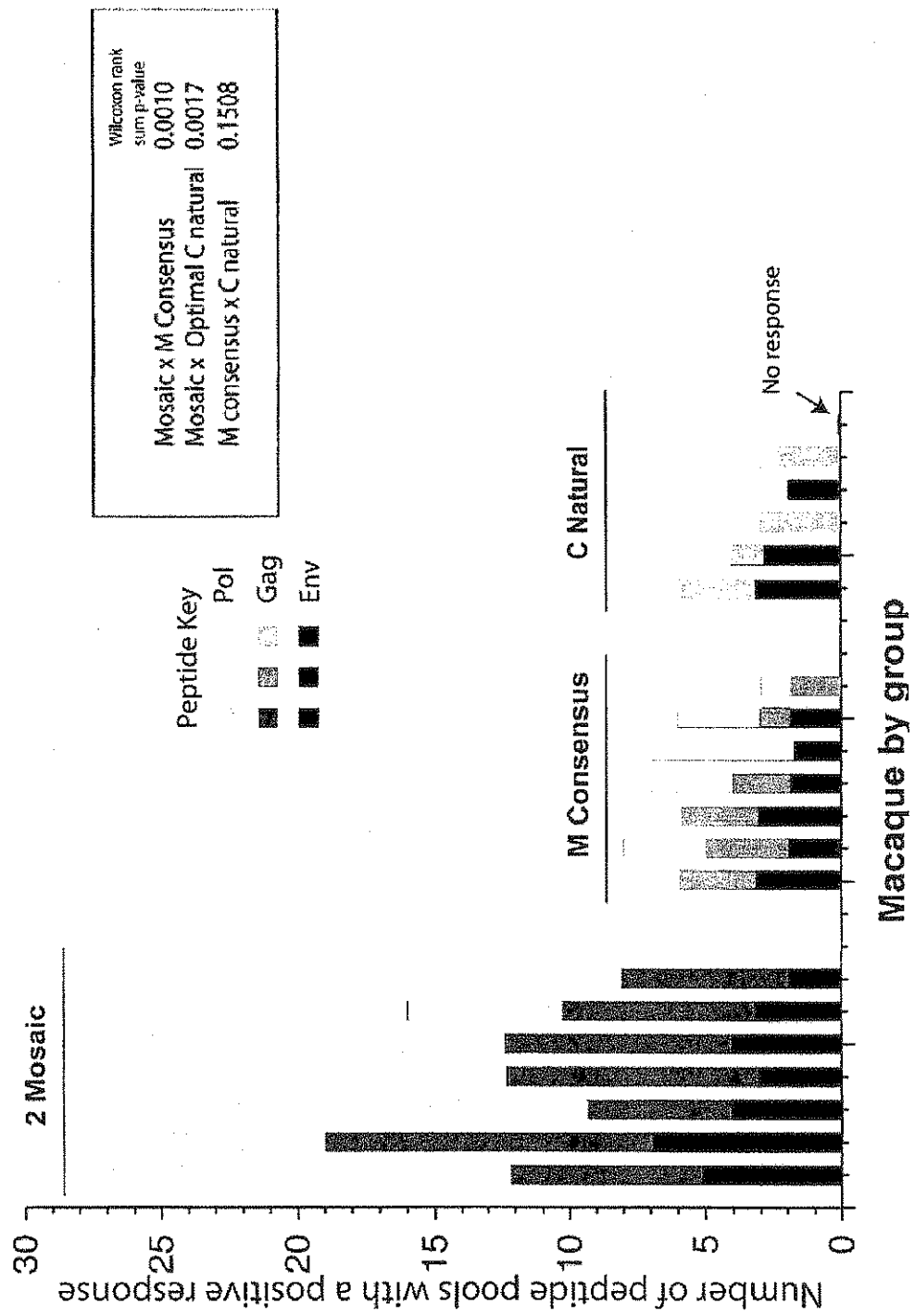
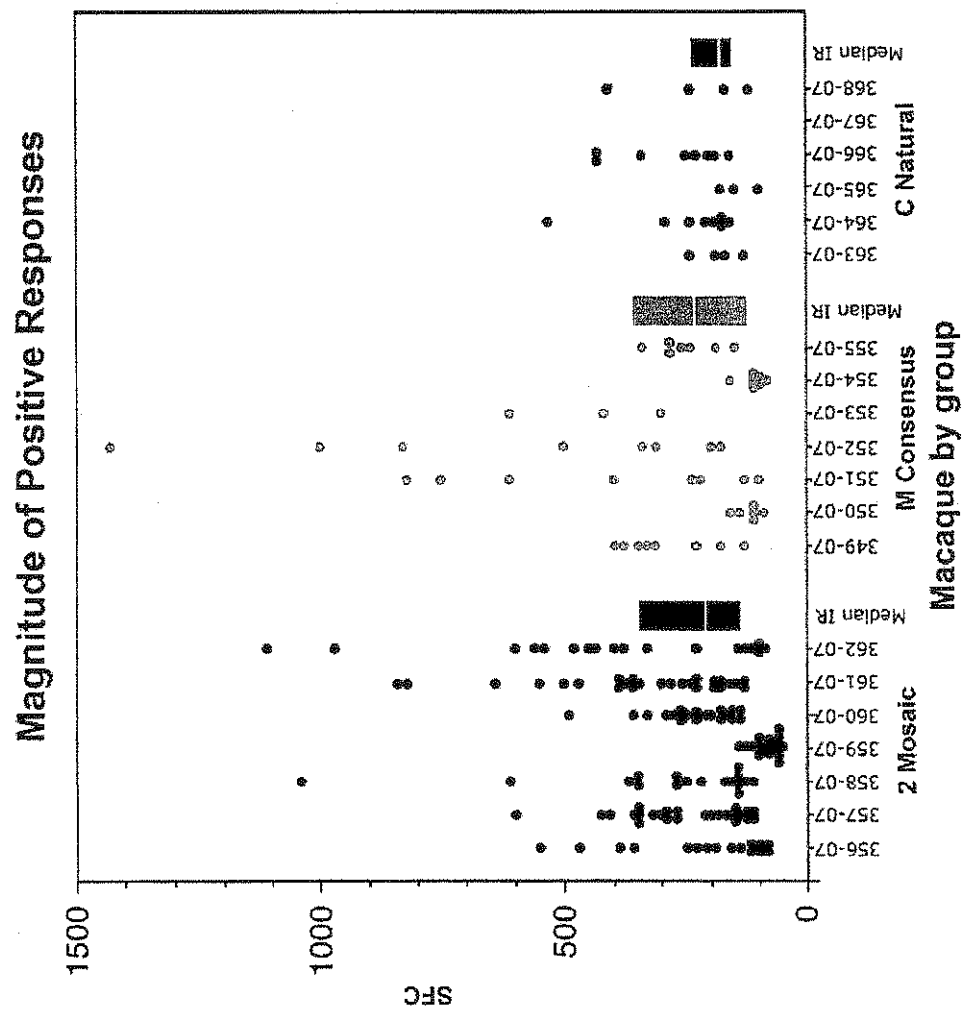


Figure 2



Mos x Con, $p = 0.56$
 Mos x C natural, $p = 0.95$
 Con x C natural, $p = 0.71$

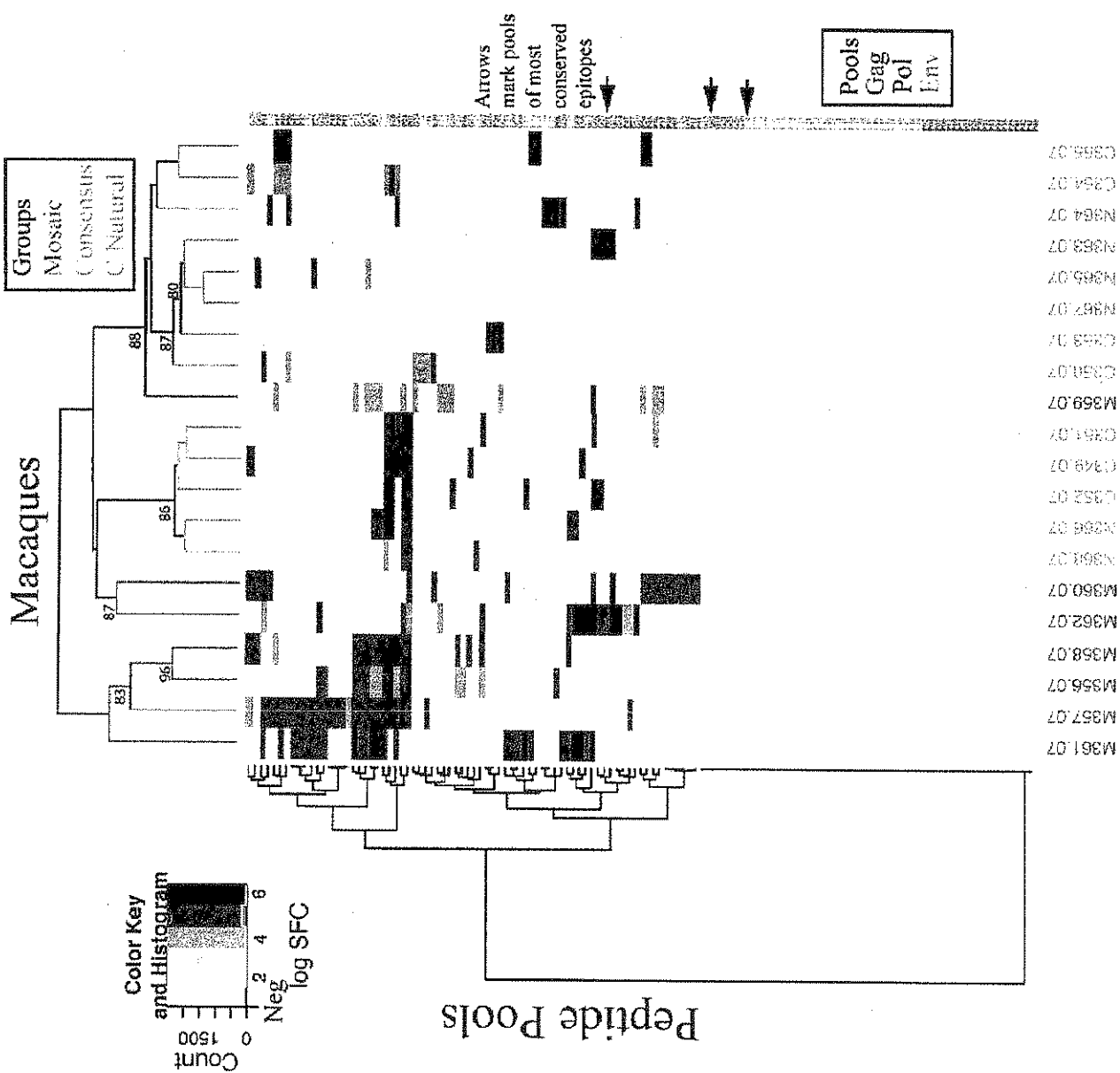


Figure 4
PTE and M group 9-mer coverage of different vaccine candidates

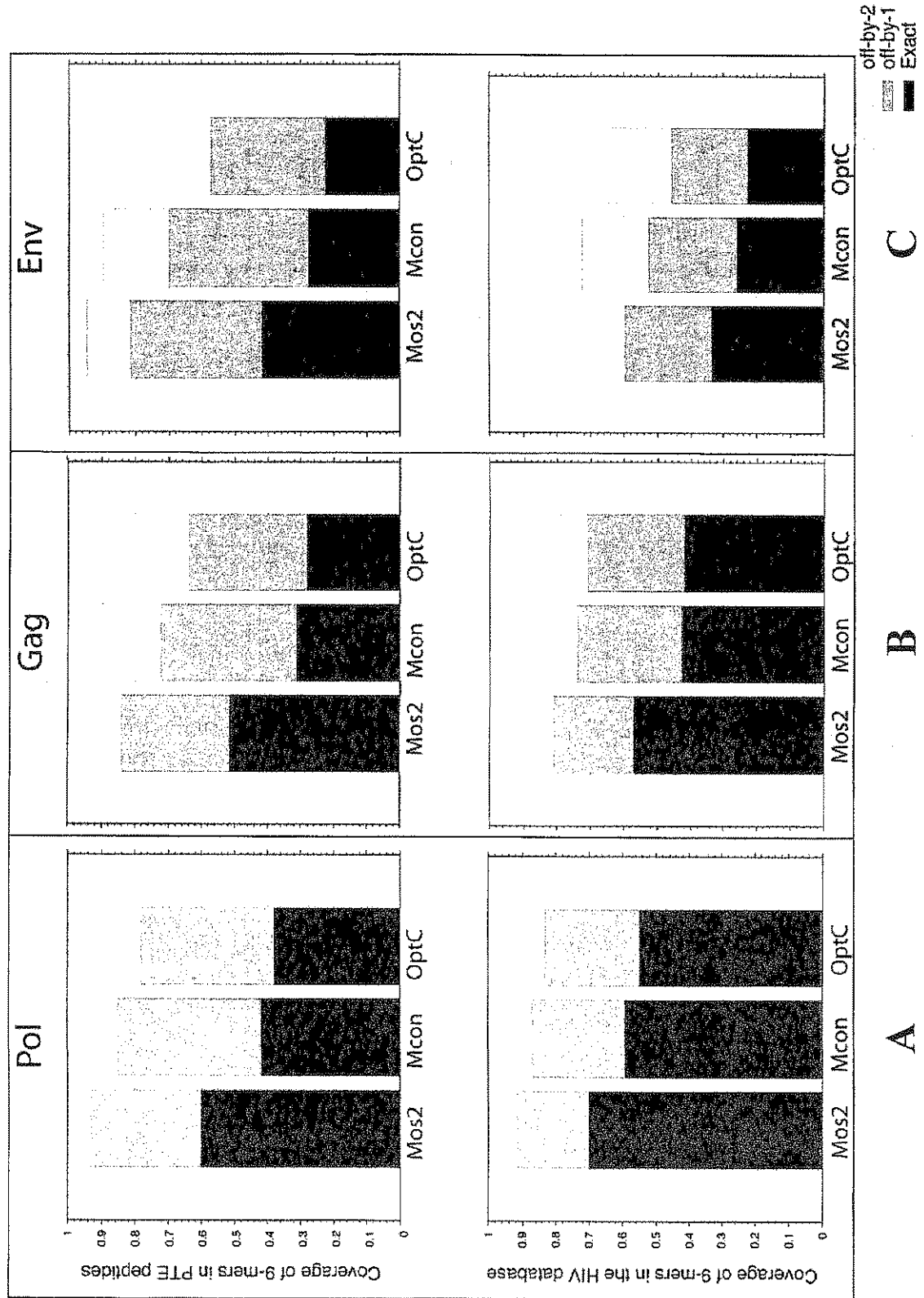


Figure 5

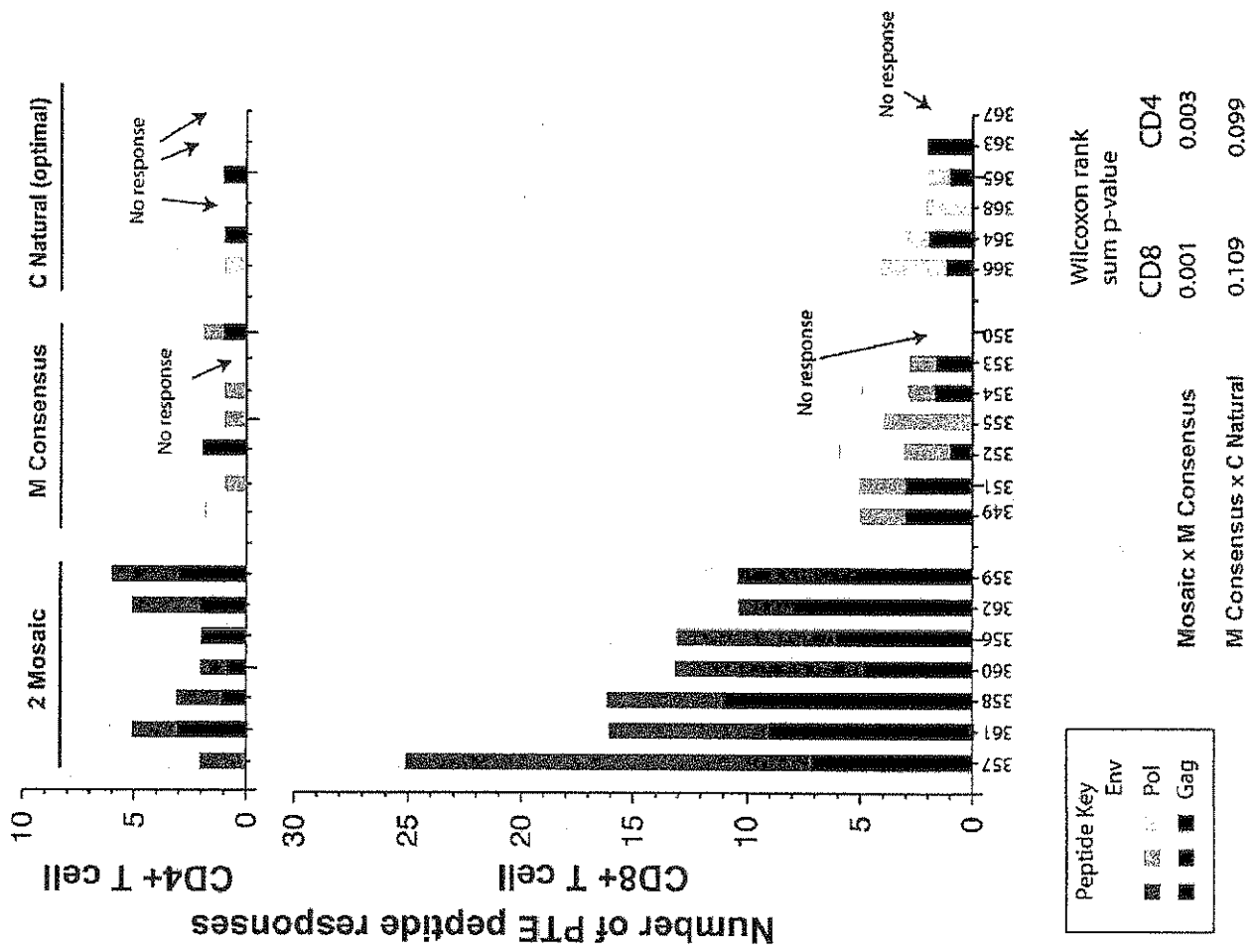


Figure 6

- CD8 T cells: median (range)
 - 2 Mosaic: 16 (12-29)
 - Mcon: 6 (0-7)
 - OptC: 3 (0-7)
- CD4 T cells:
 - 2 Mosaic: 4 (2-6)
 - Mcon: 1 (0-2)
 - OptC: 0.5 (0-2)

Figure 7

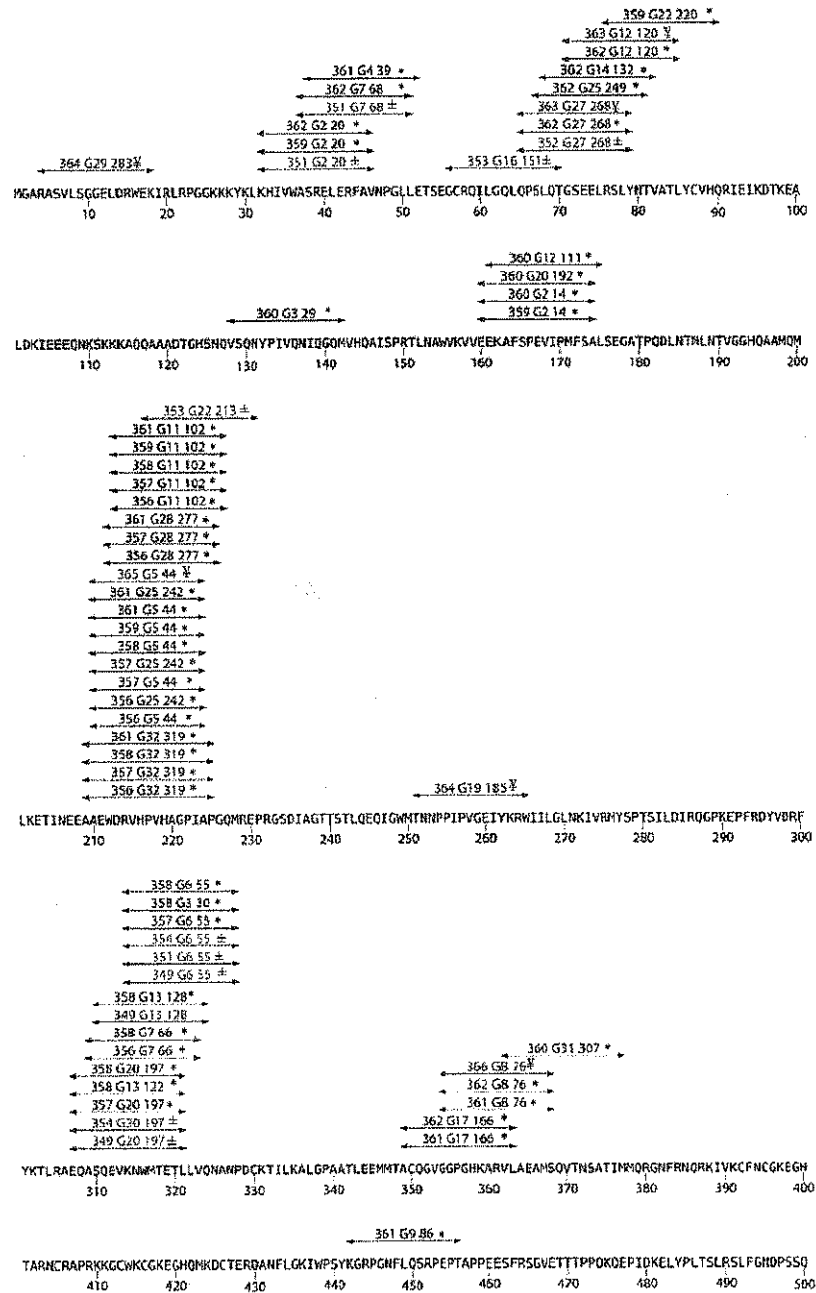


Figure 8

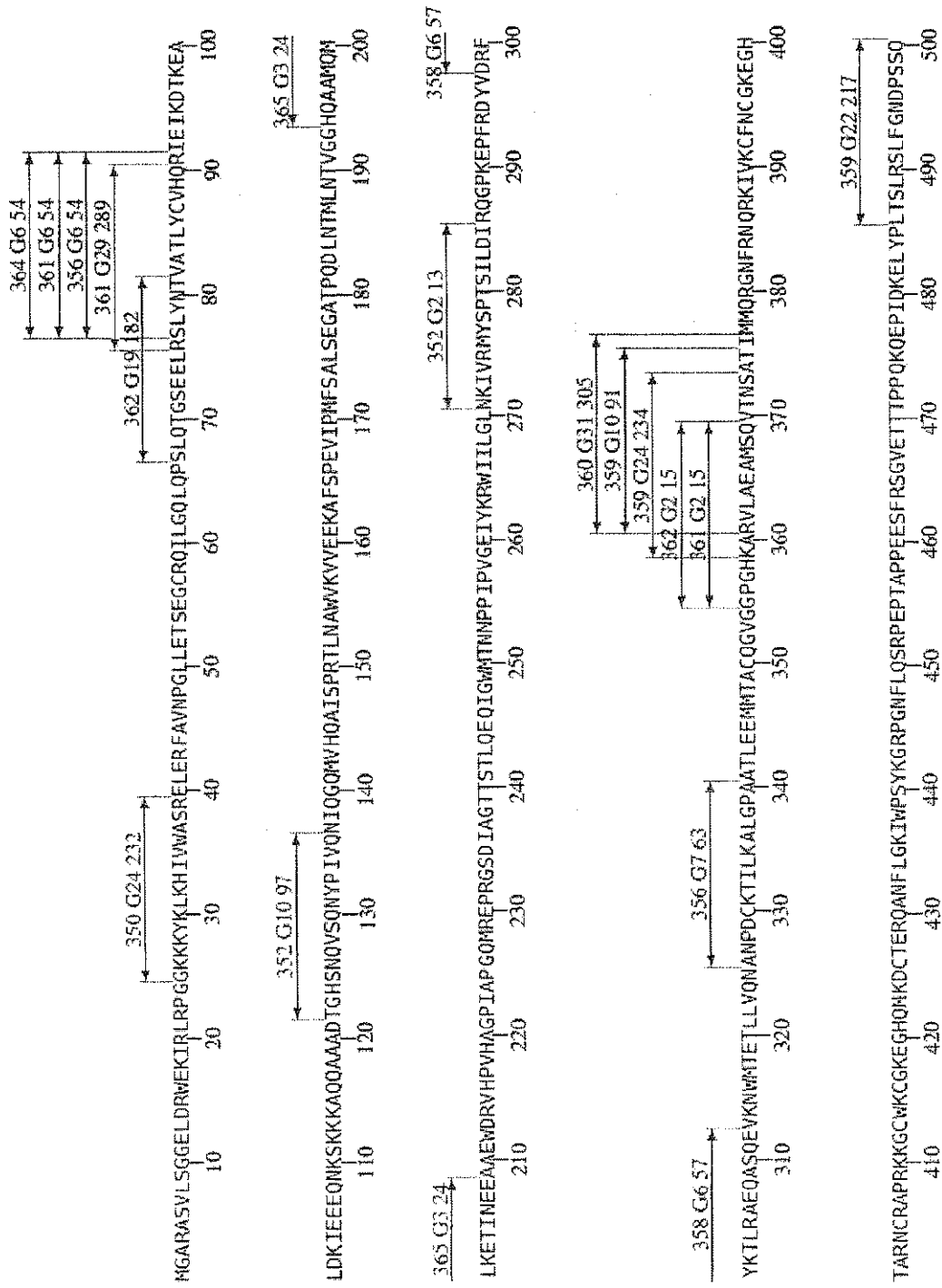


Figure 9

OptC 366-07:

5 CD8 responses:

OptC	IVQQQSNLLRAIEAQQ		
E54	VVQQQSNLLRAIEAQ	Env	548 562
E72	-VQQQNNLLRAIEAQH	Env	549 563

OptC	AVFIHNFKRKGGIGGY		
P22	AVFIHNFKRKGGIGG	Pol	894 908
P236	-VLIHNFKRKGGIGGY	Pol	895 909

OptC	MAICEEMEKEGKITK		
P224	TAICEEMEKEGKITK	Pol	190 204

OptC	CTHGKIPVVSITQLLL		
E15	CTHGKIPVVSITQLLL	Env	247 261

OptC	GGPSHKARVLAEMMS		
G76	GGPSHKARVLAEMMG	Gag	354 368

1 CD4 response:

OptC	LIQVQRDQAEHLKTA		
P86	LIQVQRDQAEHLKTA	Pol	876 890

Figure 10

Mos1	ICTTTPWNASWSNKSL	T...A
Mos2	ICTTAVPWNTSWSNKSQ	T...S
E334	ICTTTPWNASWSNR	A...A
E214	-CTTTPWNSSWSNKT	A...T
E158	--TTAVPWNASWSNKSL	
E290	--TTAVPWNTSWSNKSL	

Figure 11

8 CD8 responses:			5 CD4 responses:		
Mos1	EQLIKERVYLSWVPAHKGIG		Mos1	RSLYNTVATLYCVHQR	
Mos2	EQLIKKEKVYLAWPVPAHKGIG		Mos2	RSLENTVATLYCVHAE	76
P221	BELIKKEKVYLAWP	Pol	G289	KSLENTVATLYCVHA	90
P250	BELIKKEKVYLSWVP	Pol	G54	-SLYNTVATLYCVHQR	77
P316	-KLIERKDVYLSWVPA	Pol			91
P223	--LIKKERVYLSWVP	Pol	Mos1	YVTDGRGQKIVSLTE	
P169	-----EKVYLAWPVPAHKGIG	Pol	Mos2	YVTDGRGQKVVS LTD	
P83	-----EKVYLSWVPVPAHKGIG	Pol	P134	YVTDGRGQKVVS L TE	612
				626	
Mos1	CTHGIRPVVSTQLLL				
Mos2	CTHGIRPVVSTQLLL				
E15	CTHGIRPVVSTQLLL	Env	Mos1	CTTVPWNASWSNKS	
E47	CTHGIRPVVSTQLLL	Env	Mos2	CTTAVPWNISWSNKS	
			E53	CTTNVPWNSSWSNKS	604
Mos1	ICTTVPWNASWSNKS L			618	
Mos2	ICTTAVPWNISWSNKSQ				
E334	ICTTVPWNASWSNR	Env	Mos1	WWAGIQOEF GIPYNP	
E214	-CTTVPWNSSGNKT	Env	Mos2	WWAGIQOEF GIPYNP	
E158	--TTAVPWNASWSNKS L	Env	P135	WWAGIQOEF GIPYNP	846
E290	--TTAVPWNISWSNKS L	Env		860	
Mos1	ACQGVGCGFCHKARVLAEMS		Mos1	GFCHKARVLAEMSQ	
Mos2	ACQGVGCGF SHKARVLAEMS		Mos2	GFSSHKARVLAEMSQ	
G166	ACQEVGCGFCHKARVL	Gag	G15	GFCHKARVLAEMSQ	355
G76	-----GGF SHKARVLAEMG	Gag		369	
Mos1	AAEWDRVHPVHAGPIAPGQ				
Mos2	AAEWDRLHPVHAGFVAPGQ				
G319	AAE--DRLHPVHAGPI P	Gag			
G242	-ADWDRLHPVHAGPVA	Gag			
G44	-AEWDRLHPVHAGPIA	Gag			
G277	--WDRVHPVHAGPNPPG	Gag			
G102	----DRVHPVHAGPIPPGQ	Gag			
Mos1	HSNWRAMASDFNLPP				
Mos2	HSNWRAMASEFNLPP				
P93	HSNWRAMASDFNLPP	Pol			
Mos1	KGRPGNF LQNRPEPT				
Mos2	KGRPGNF LQSRPEPT				
G86	KGRPGNF LQNRPEPT	Gag			
Mos1	SRELERFAVNPGLLE				
Mos2	SRELERFALNPGLLE				
G39	SRELERFALNPGLLE	Gag			

Figure 12

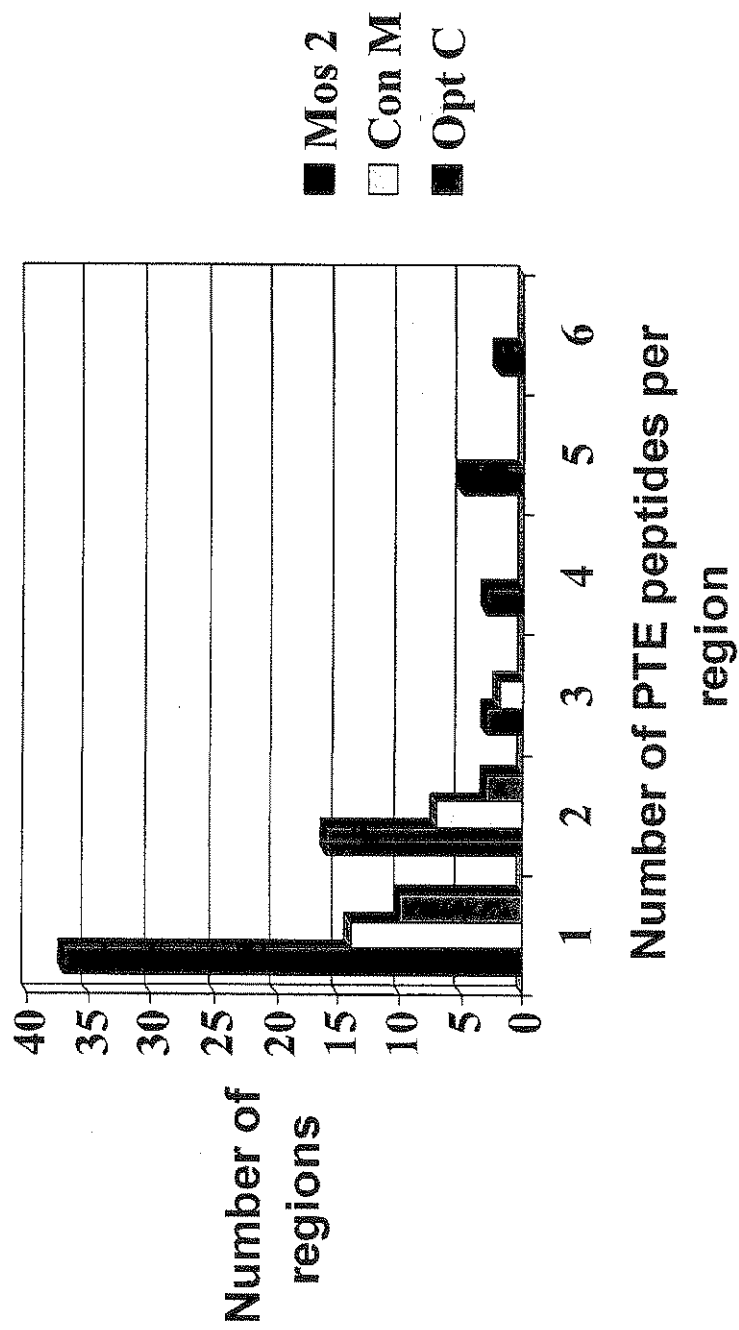


Figure 13

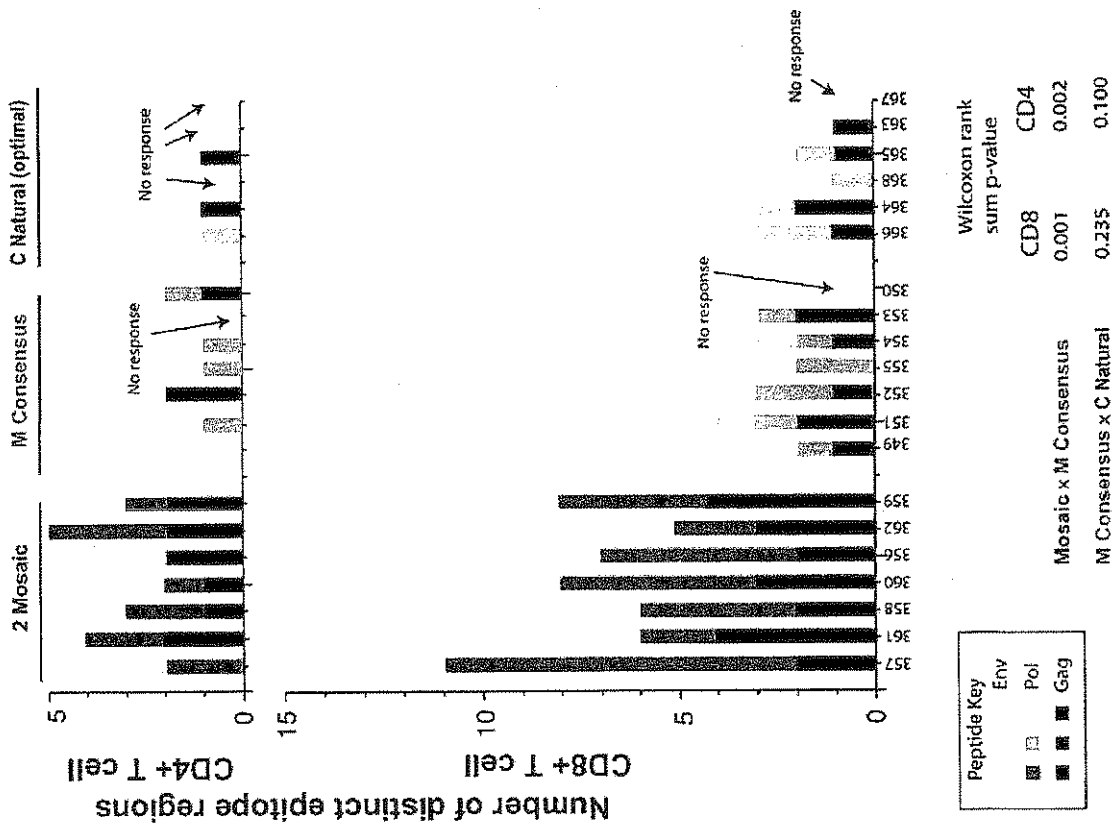
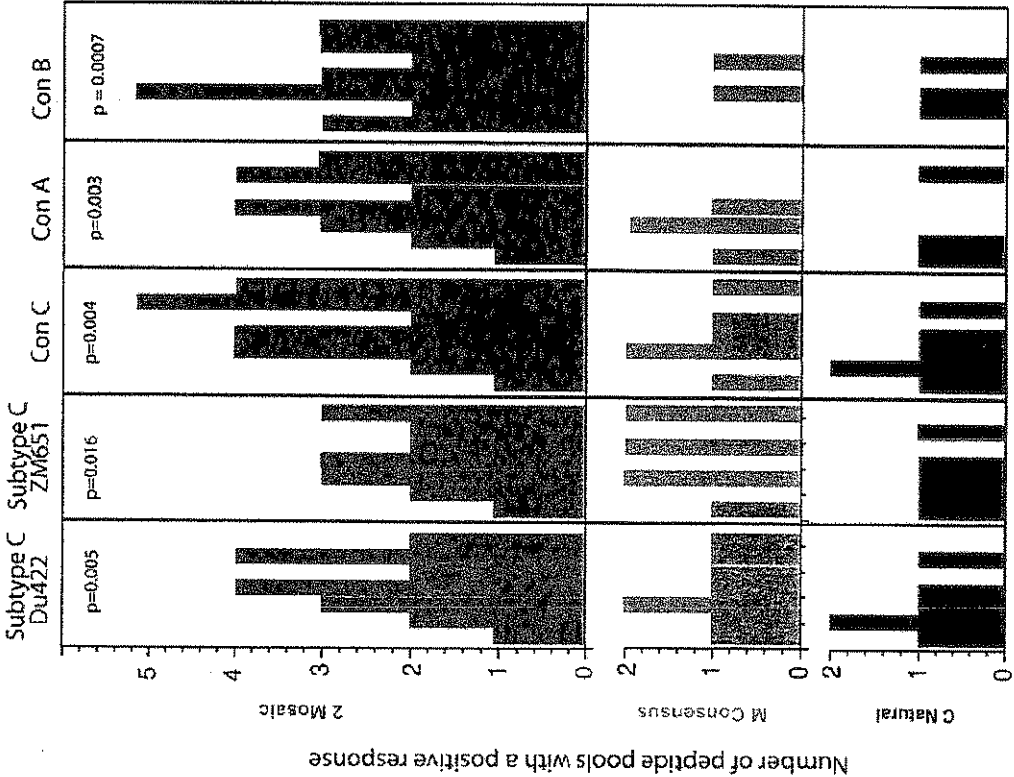


Figure 14

- CD8 T cells: median (range)
 - 2 Mosaic: 8 (7-14)
 - Mcon: 3 (0-6)
 - OptC: 1.5 (0-5)
- CD4 T cells:
 - 2 Mosaic: 3 (2-5)
 - Mcon: 1 (0-2)
 - OptC: 0.5 (0-2)

Figure 15

Testing responses in vaccine groups against
Positive Peptides Pools based on 5 different Gags



Each animal's responses to each of the sets of peptides
The p values are Wilcoxon rank tests, Mosaic x M con.
M con and C optimal natural were not significantly different.

Figure 16

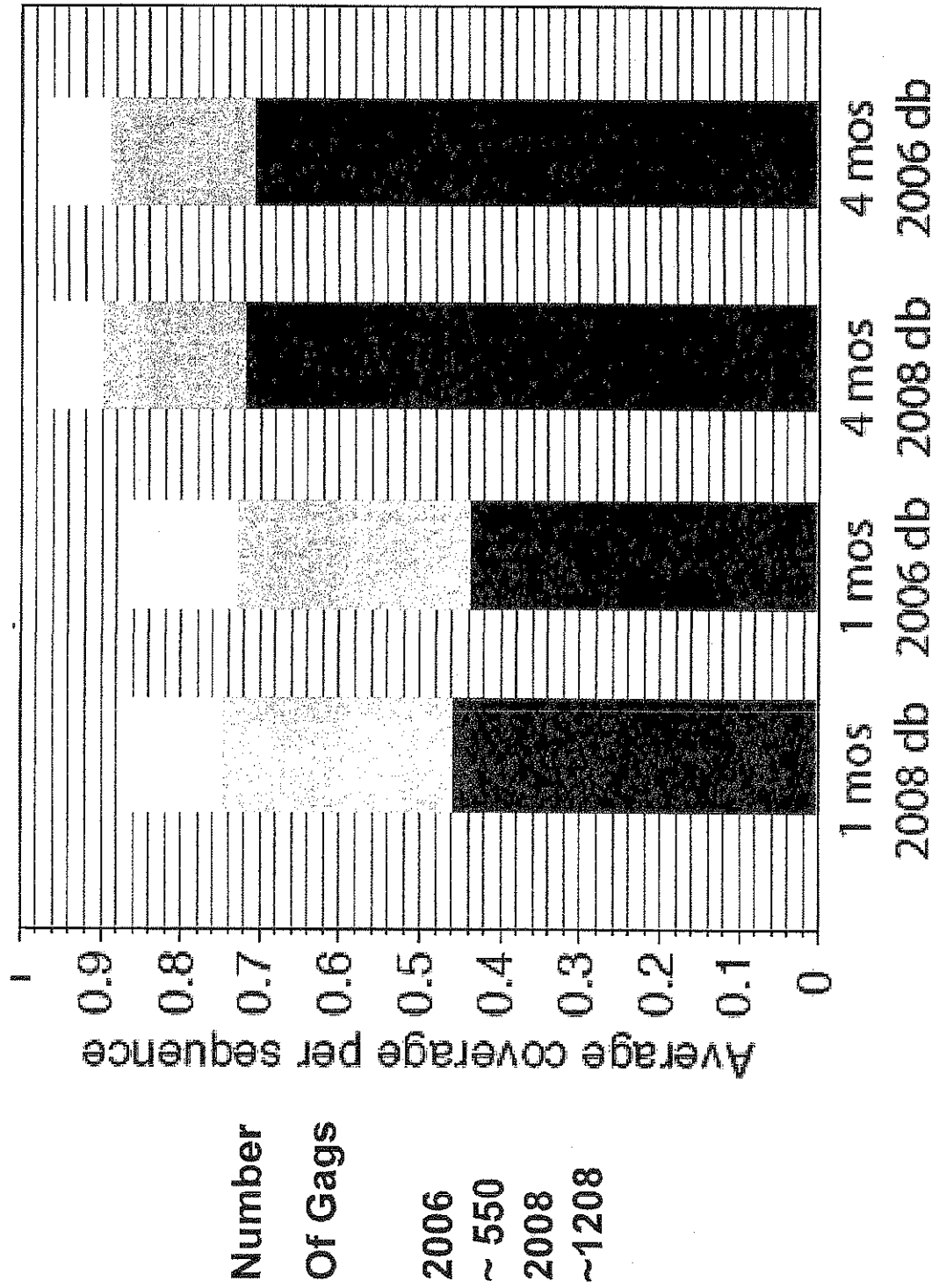
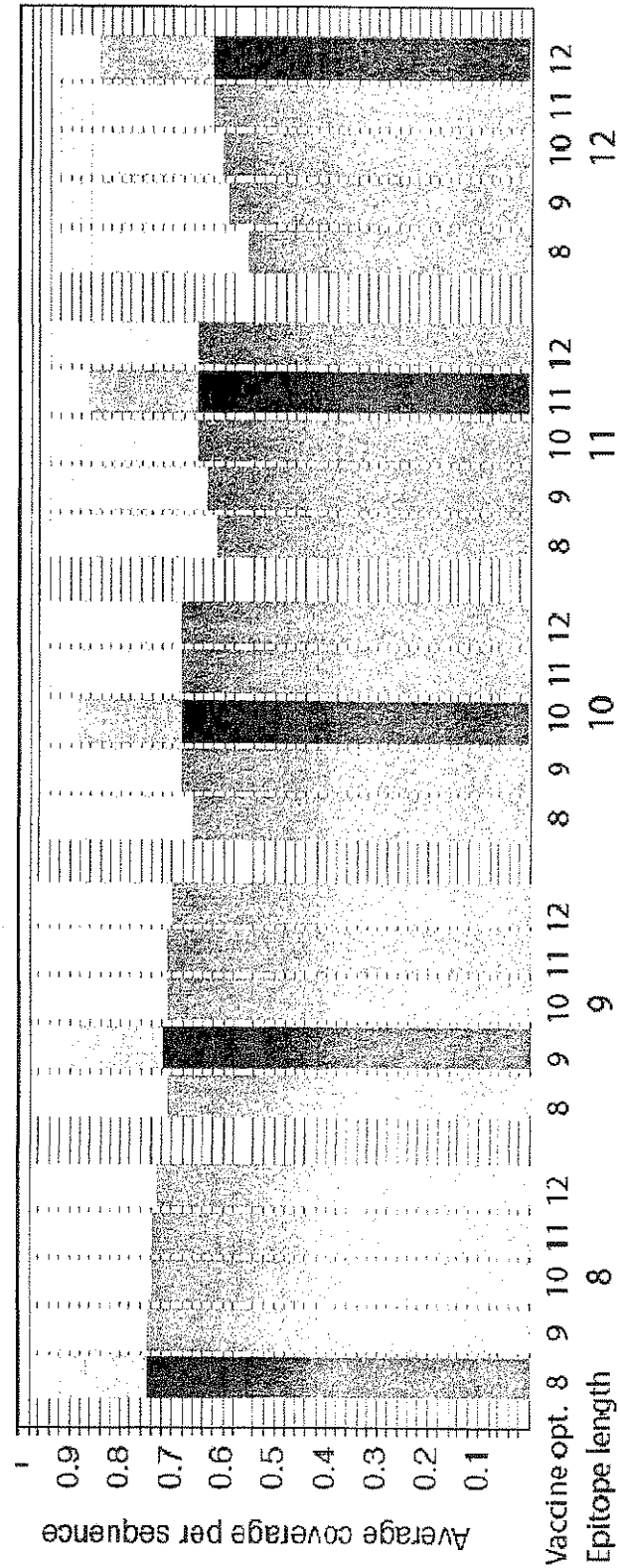


Figure 17



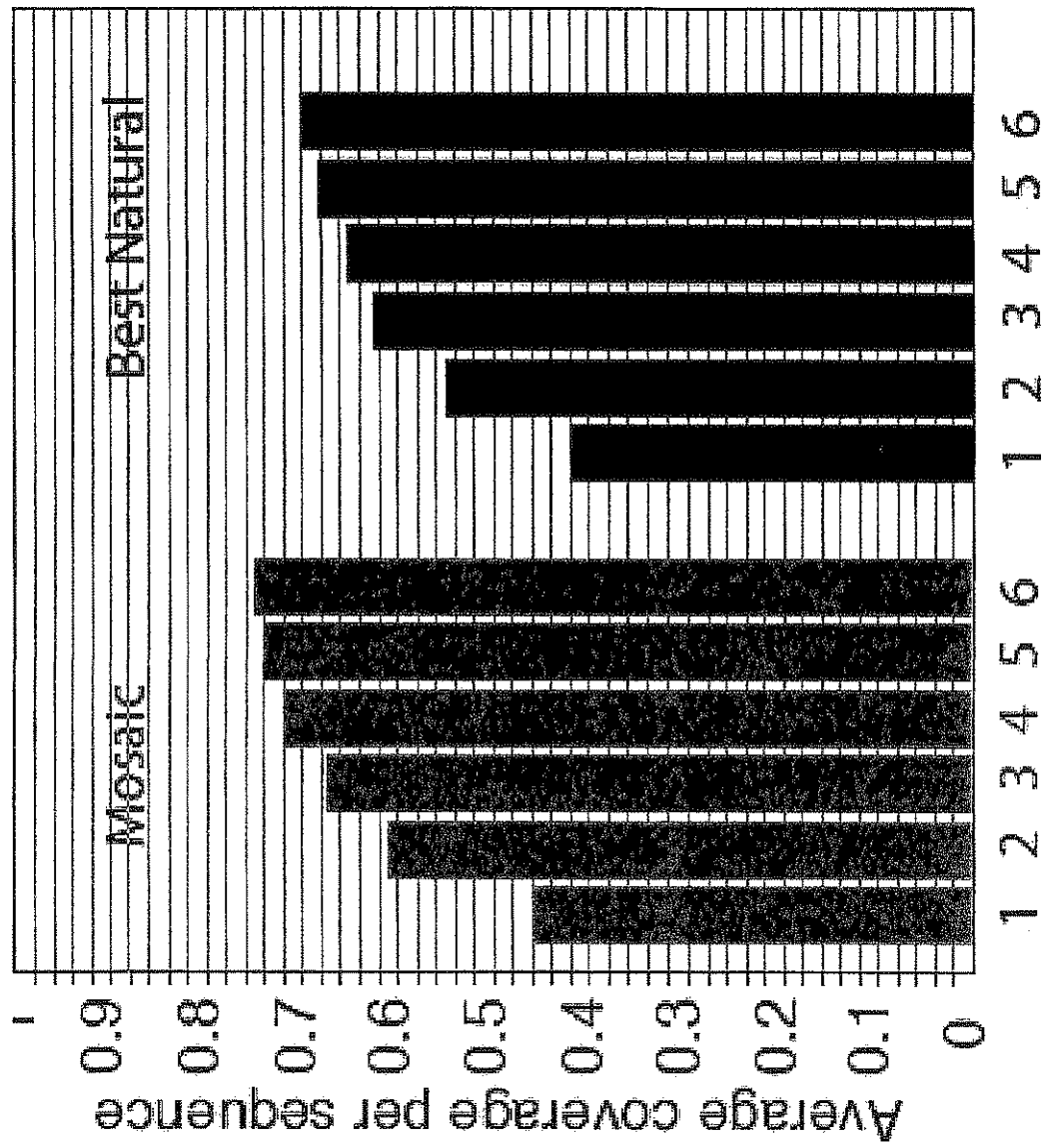


Figure 18

Figure 19

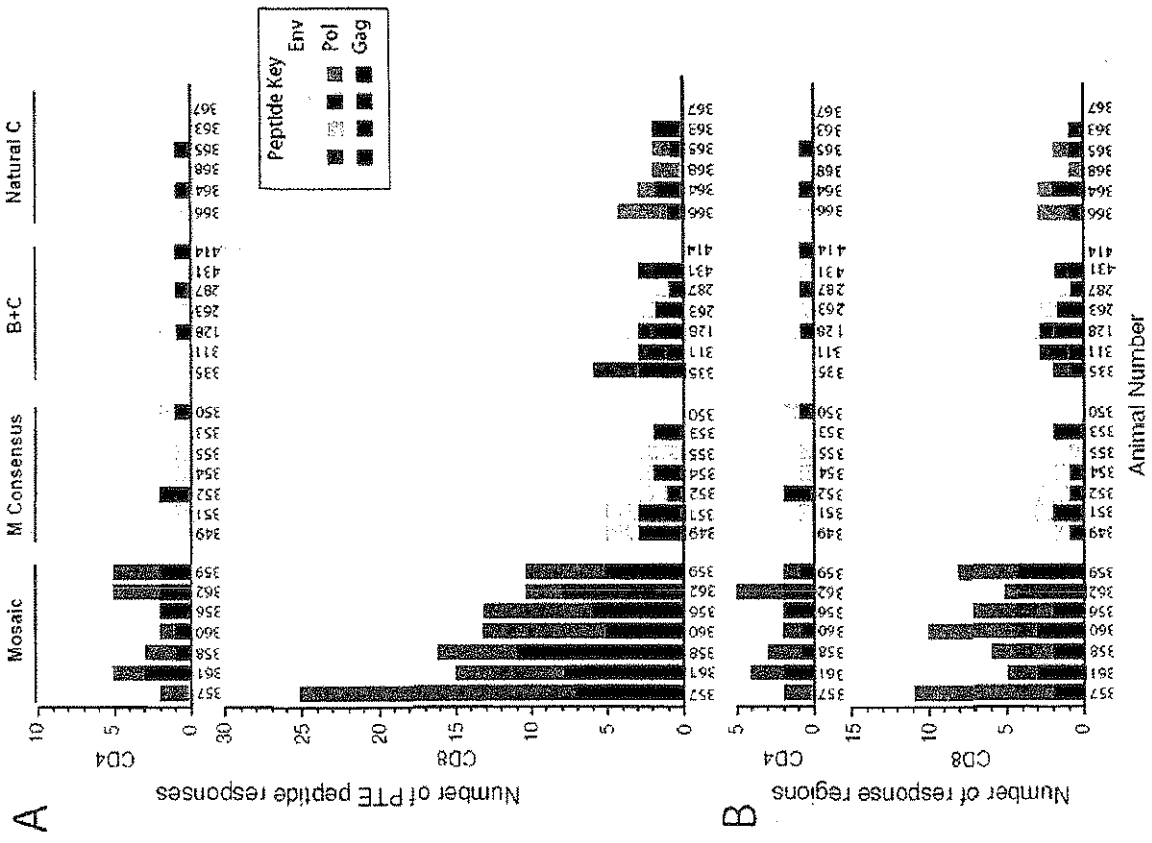
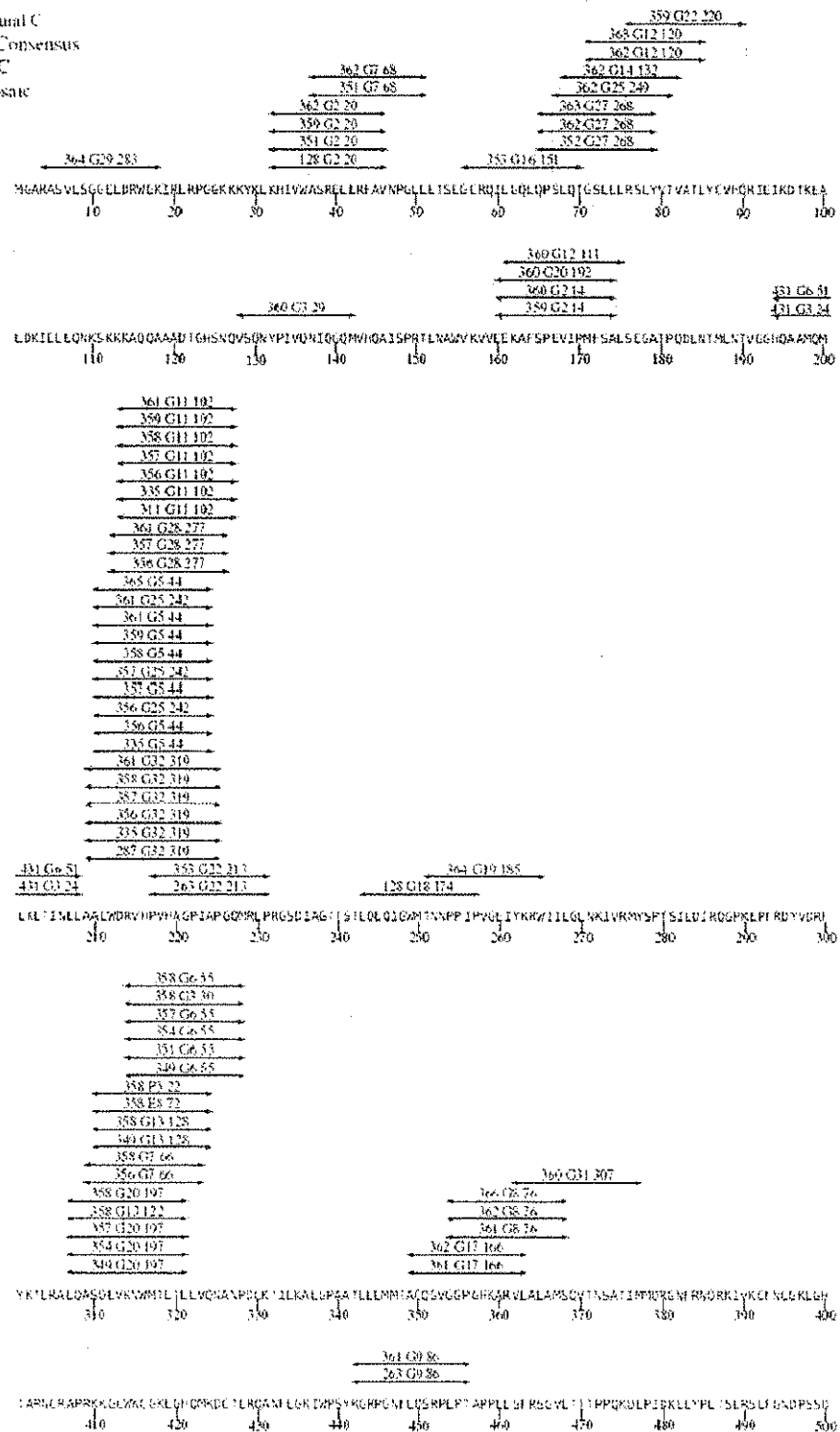


Figure 20A

CD8 Gag

Natural C
M Consensus
B+C
Mosaic



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Figure 20B

CD8 Pol

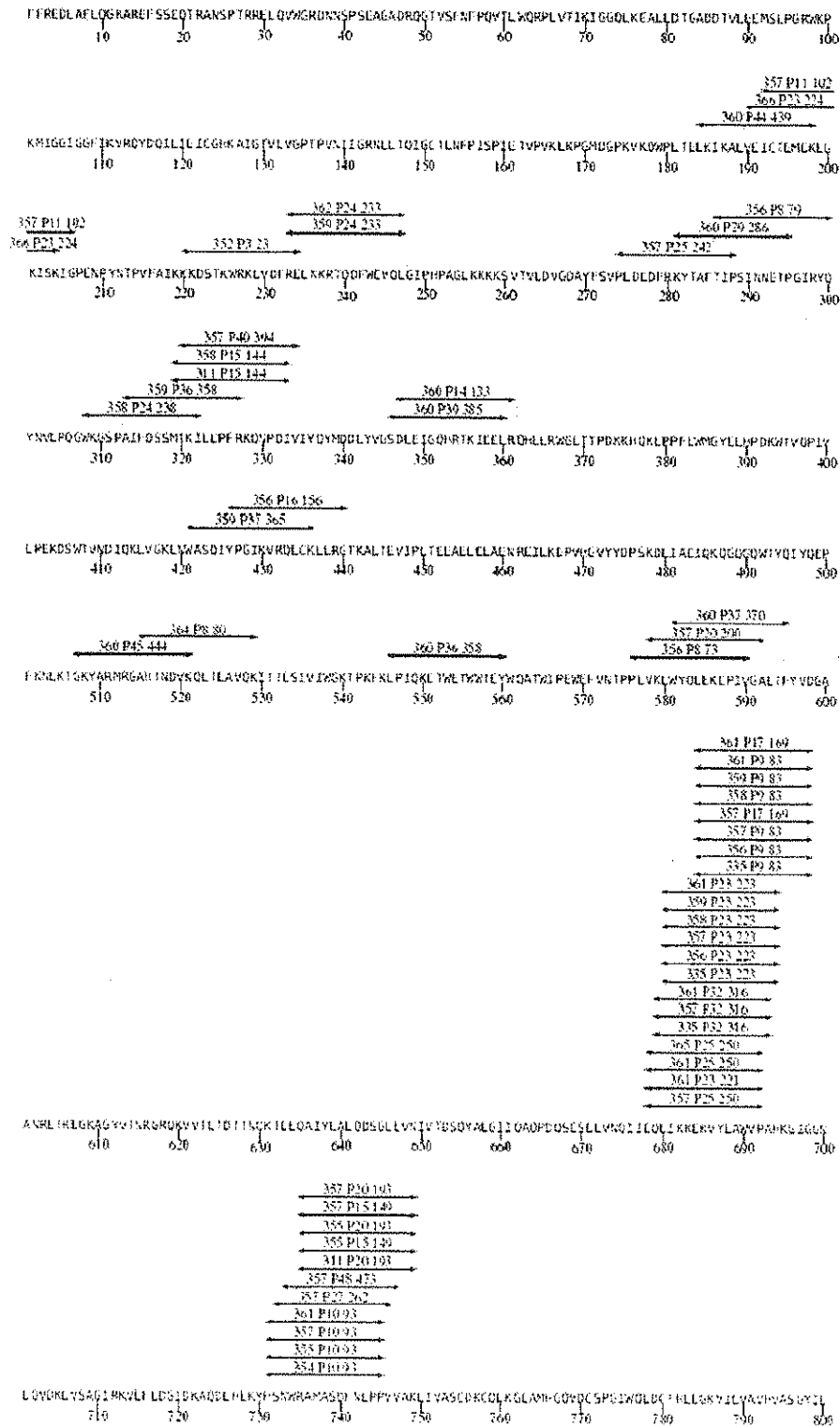


Figure 20B (con't)

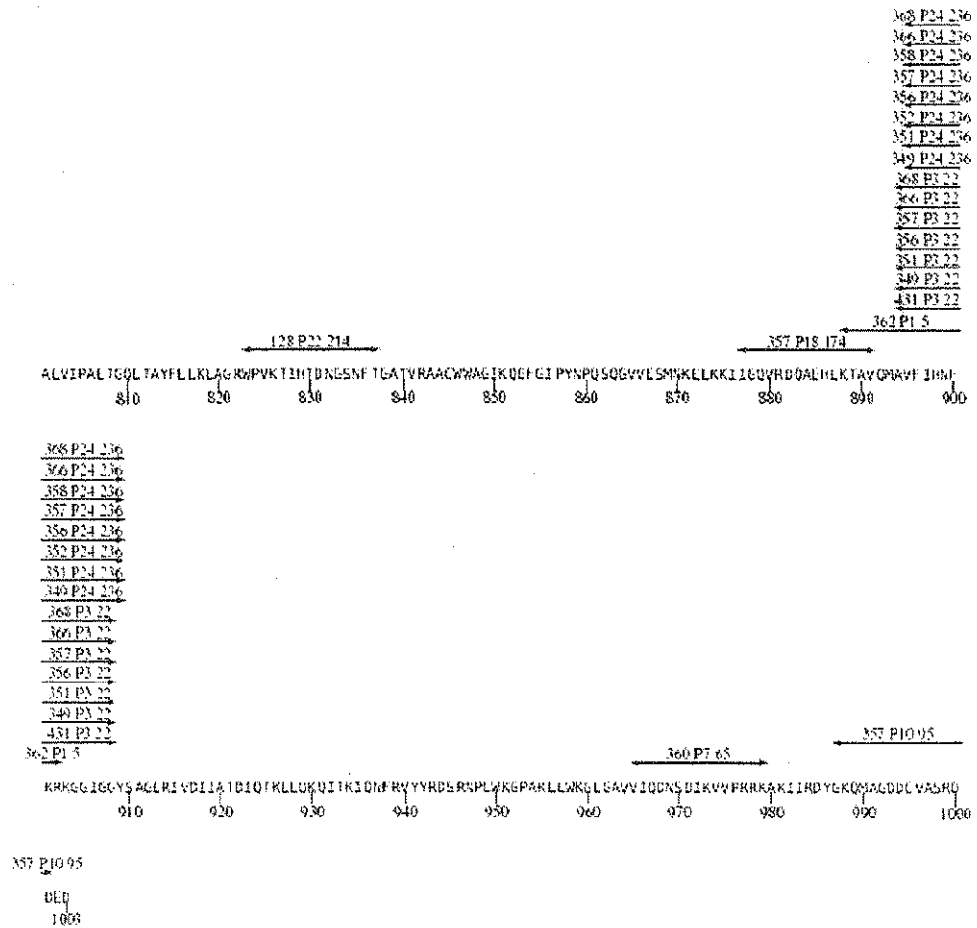


Figure 21A

CD4 Gag

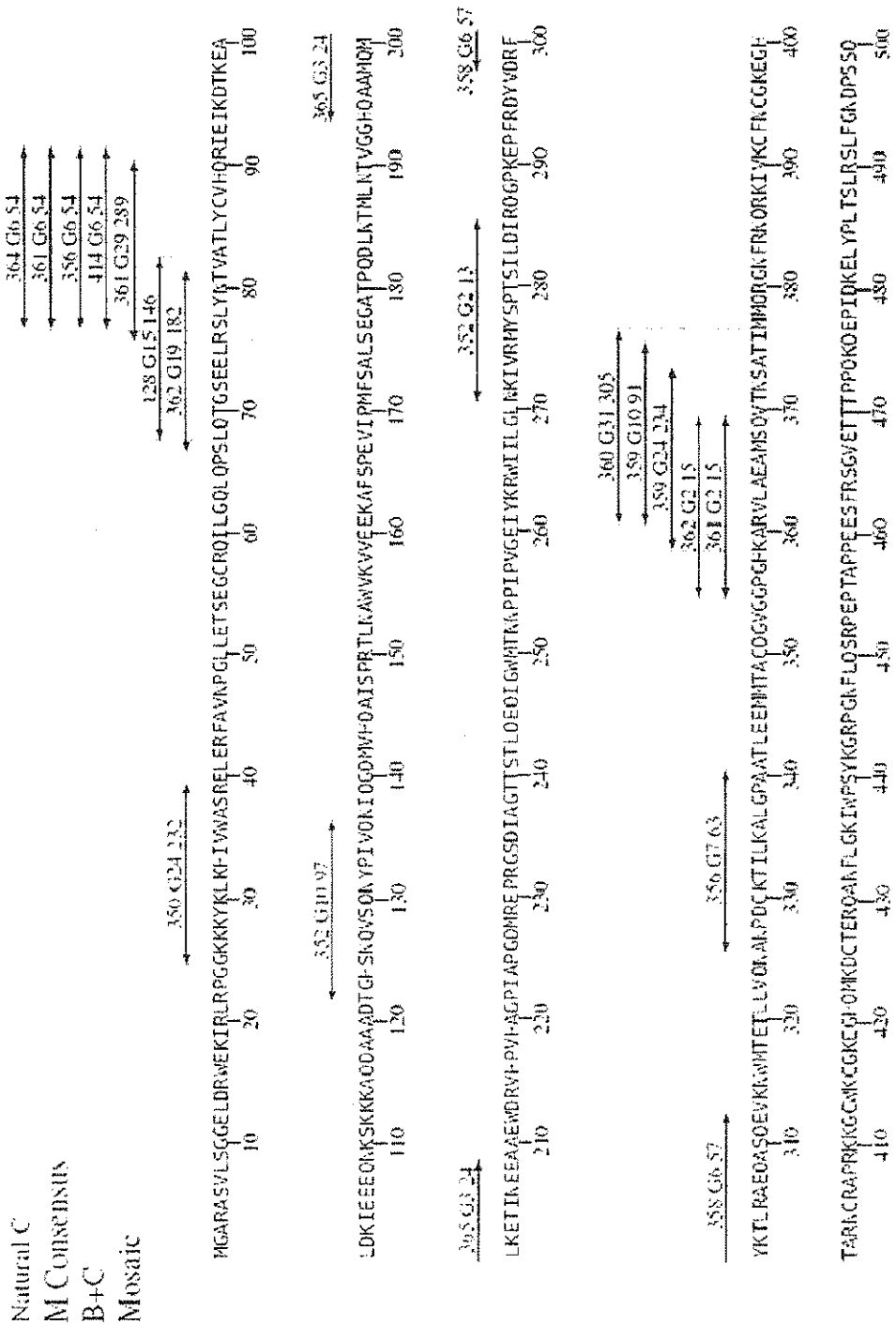


Figure 21B

CD4 Pol

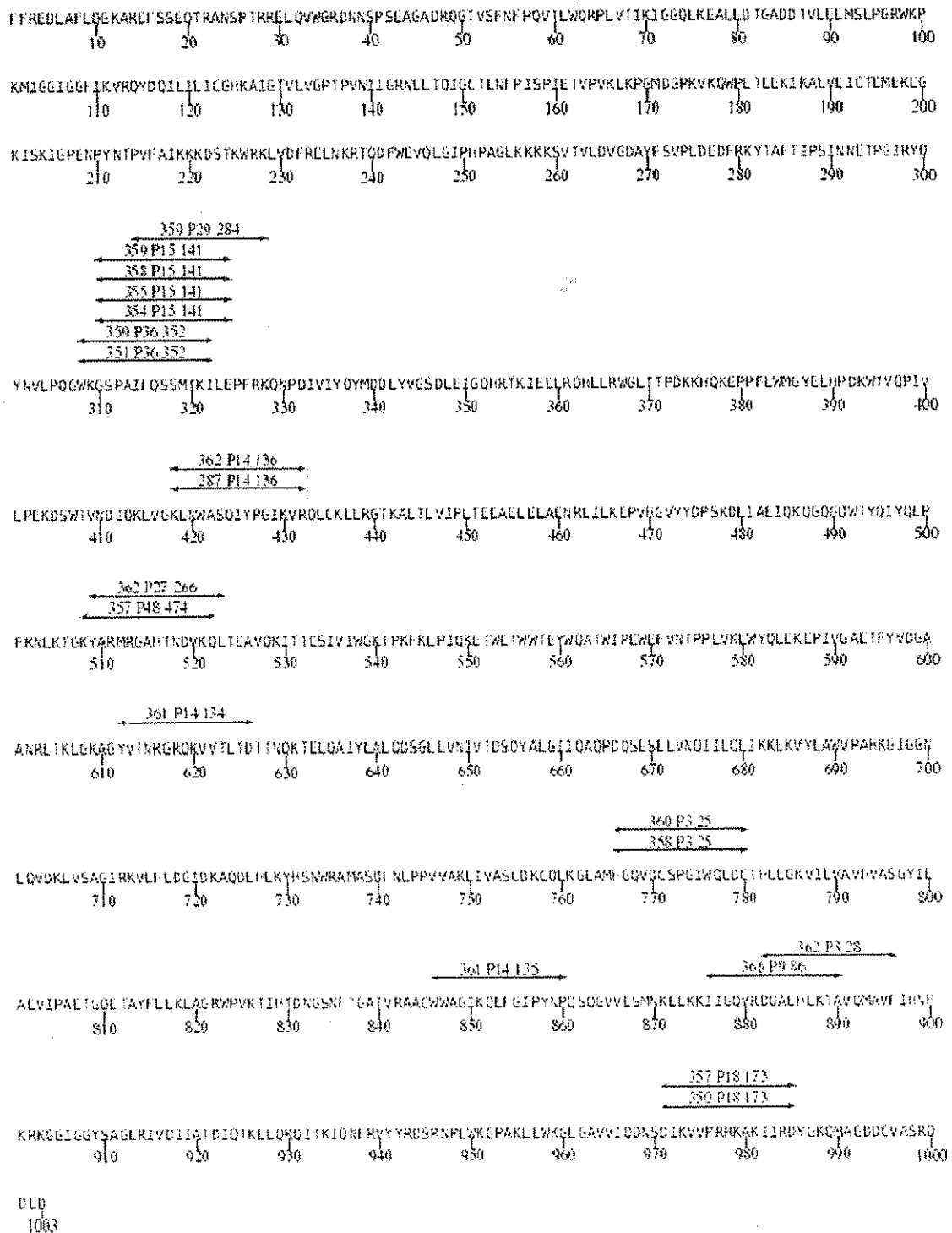


Figure 21C

CD4 Env

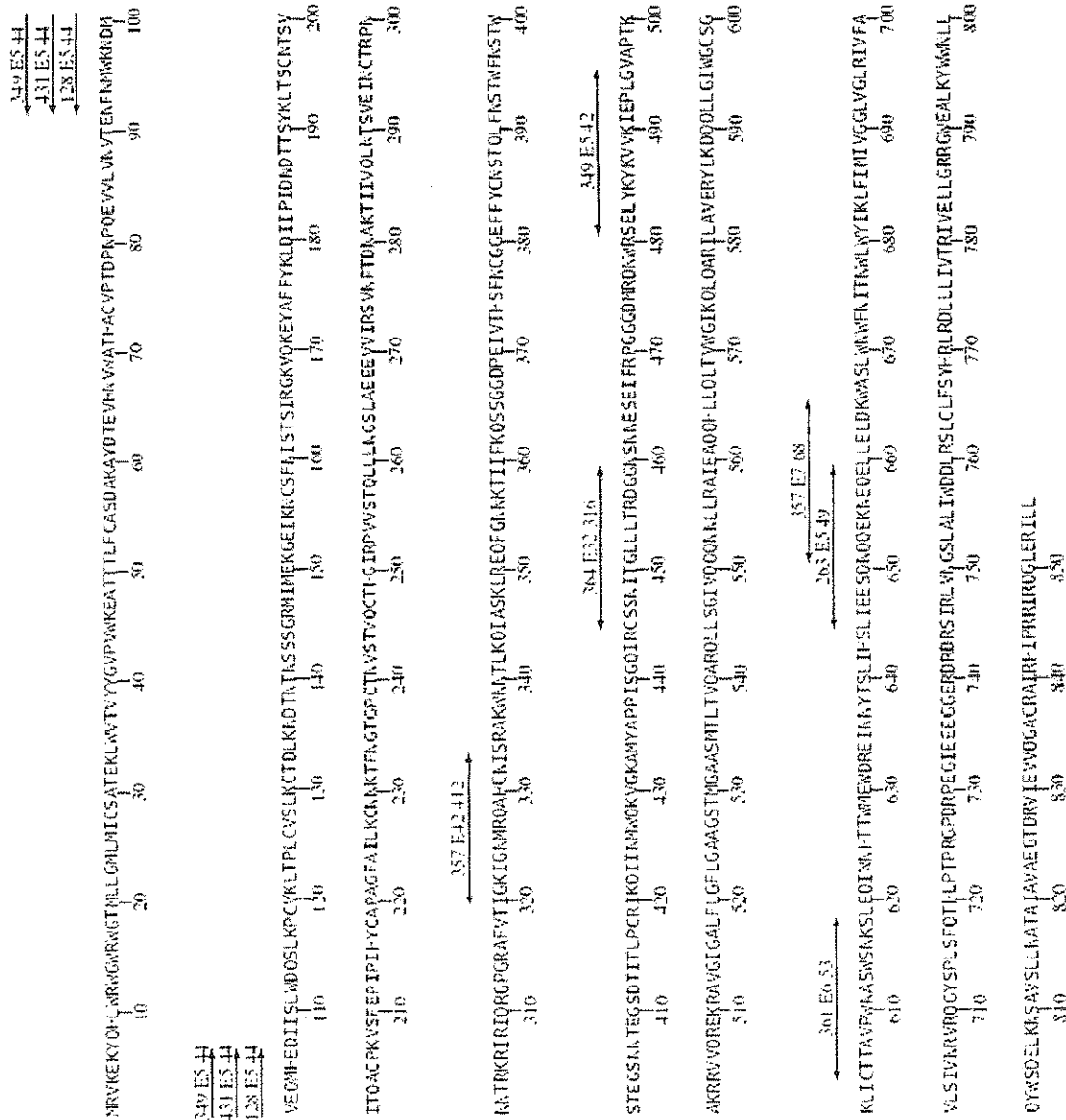


Figure 22

Reactive peptides and breadth and depth of responses: Clade B+C Vaccine

Clade B+C 287-95:

3 CD8 PTE+, 1 CD4 PTE+

2 CD8+ regions, 1 CD4+ region

Number of overlapping peptides per region: CD8: 1 2 CD4: 1

3 CD8 responses:

C AAEWDRLEHPVHAGPIA

B AAEWDRLEHPVHAGPIA

G319 AAE-DRLHPVHAGPIPGag 209 225

C EQMHEDIISLWDQSLK

B EQMHEDIISLWDQSLK

E286 EQMHEDIISLWDQSL Env 102 116

E282 HMHEDIISLWDESLK Env 103 117

1 CD4 response:

C KLNWASQIYSGIKVR

B KLNWASQIYPGIKVR

P136 KLNWASQIYAGIKVK Pol 416 432

Clade B+C 128-92:

5 CD8 PTE+, 2 CD4 PTE+

5 CD8+ regions, 2 CD4+ regions

Number of overlapping peptides per region: CD8: 1 1 1 1 1 CD4: 1 1

5 CD8 responses:

C KHLVWASRELERFAL

B KHLVWASRELERFAV

G20 KHLVWASRELERFAL Gag 32 46

C LQEQIAWMTNPPFVP

B LQEQIGWMTNPPPIF

G174 LAEQIAWMTSNPPPIF Gag 243 257

C QMHEDIISLWDQSLK

B QMHEDIISLWDQSLK

E282 HMHEDIISLWDESLK Env 103 117

C DIWDNMTWMQWDREI

B EIWDNMTWMEWEREI

E297 EIWNMTWMENEKEI Env 621 635

C WPKVIHTANGSNFT

B WPKTIHTANGSNFT

P214 WPKVVTHTDNGSNFT Pol 823 837

2 CD4 responses:

C AQTGTEELRSLYNTV

B LQTGSEELRSLYNTV

G146 LQTGSEELKSLNTV Gag 88 92

C YFNMWKNDMVDQMHE

B NFNMWKNNMVEQMHE

E344 NFNMWKNNMVEQMHE Env 92 106

Figure 22 (con't)

Clade B+C 263-00:

3 CD8 PTE+, 1 CD4 PTE+

3 CD8+ regions, 1 CD4+ region

Number of overlapping peptides per region: CD8: 1 1 1 CD4: 1

3 CD8 responses:

C	GRFGNFLQSRPEPT			
B	GRFGNFLQSRPEPT			
G86	GRFGNFLQNRPEPT	Gag	442	456

C	PVHAGPIAPGQMREP			
B	PVHAGPIAPGQMREP			
G213	PVQAGPIAPGQMREP	Gag	217	231

C	VQQQSNLLRAIEAQQ			
B	VQQQNNLLRAIEAQQ			
E72	VQQQNNLLRAIEAQH	Env	549	563

1 CD4 response:

C	LLEESQNQQEKNEKD			
B	LLEESQNQQEKNEQE			
E49	LLEESQNQQEKNEQD	Env	645	659

Clade B+C 311-00:

5 CD8 PTE+, 0 CD4 PTE+

5 CD8+ regions, 0 CD4+ region

Number of overlapping peptides per region: CD8: 1 1 1 1 1 CD4: 0

5 CD8 responses:

C	DRLHPVHAGPIAPGQ			
B	DRLHPVHAGPIAPGQ			
G102	DRVHPVHAGPIPPGQ	Gag	213	227

C	GDIIGDIRQAHCNIS			
B	GEIIGDIRQAHCNIS			
E64	GDIIGDIRQAHCNIS	Env	321	334

C	TGMLRNCQPWWIWGI			
B	KGIRKNYQHLWRWGT			
E459	KEIRKNYQHLWRWGT	Env	4	16

C	MTKILEPFRKNPEI			
B	MTKILEPFRKQNPDI			
P144	MTKILEPFRKQNPDI	Pol	319	323

C	RAMASEFNLPVVAK			
B	RAMASDFNLPVVAK			
P193	KAMASDFNLPPIVAK	Pol	735	749

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Figure 22 (con't)

Clade B+C 335-96:

6 CD8 PTE+, 0 CD4 PTE+

2 CD8+ regions, 0 CD4+ region

Number of overlapping peptides per region: CD8: 3 3 CD4: 0

6 CD8 responses:

C	AAEWDRLHPVHAGPIAPGQ			
B	AAEWDRLHPVHAGPIAPGQ			
G319	AAE-DRLHPVHAGPIP	Gag	209	225
G44	AEWDRLHPVHAGPIA	Gag	210	224
G102	DRVHPVHAGPIPPGQ	Gag	213	227

C	QLINKERVYLSWVPAHKGIG			
B	QLIKKEKVYLAWVPAHKGIG			
P316	KLIEKDKVYLSWVPA	Pol	679	693
P223	LIKERVYLSWVPAH	Pol	680	694
P83	EKVYLSWVPAHKGIG	Pol	684	698

Clade B+C 414-95:

0 CD8 PTE+, 1 CD4 PTE+

0 CD8+ regions, 1 CD4+ region

Number of overlapping peptides per region: CD8: 0 CD4: 1

1 CD4 responses:

C	SLYNTVATLYCVHAG			
B	SLYNTVATLYCVHQK			
G54	SLYNTVATLYCVHQK	Gag	77	91

Clade B+C 431-01:

3 CD8 PTE+, 1 CD4 PTE+

2 CD8+ regions, 1 CD4+ region

Number of overlapping peptides per region: CD8: 2 1 CD4: 1

3 CD8 responses:

C	HQAAMQMLKDTINEE			
B	HQAAMQMLKETINEE			
G24	HQAAMQMLKDTINEE	Gag	194	208
G51	HQAAMQMLKETINEE	Gag	194	208

C	AVFIHNFKRKGGIGG			
B	AVFIHNFKRKGGIGG			
P22	AVFIHNFKRKGGIGG	Pol	894	908

1 CD4 response:

C	YFNMWKNMVDQMHE			
B	NFNMWKNNMVEQMHE			
E44	NFNMWKNNMVEQMHE	Env	92	106

Figure 22 (con't)

Reactive peptides and breadth and depth of responses: M Consensus Vaccine

M consensus 349-07:

7 CD8 PTE-, 2 CD4 PTE+

3 CD8+ regions, 2 CD4+ regions

Number of overlapping peptides per region: CD8: 3 2 2 CD4: 1 1

3 CD8 responses:

Moon	EQATQDVKNWMTDTLLVQANAF			
G197	EQSTQEVKNWMTDTL	Gag	307	321
G128	---TQEVKNWMTDTLLIQ	Gag	310	324
G55	-----KNWMTDTLLVQANAF	Gag	314	323

Moon	IVQQQSNLLRAIEAQO			
E54	IVQQQSNLLRAIEAQ	Env	548	562
E72	-VQQQSNLLRAIEAQH	Env	549	563

Moon	AVFIHNEFKRKGIGGY			
P22	AVFIHNEFKRKGIGG	Pol	894	908
P236	-VLIHNEFKRKGIGGY	Pol	895	909

2 CD4 responses:

Moon	SELYKYKVVKIEPLG			
E40	SELYKYKVVKIEPLG	Env	481	495

Moon	NFNMWKNNMVEQMHE			
E44	NFNMWKNNMVEQMHE	Env	92	106

M consensus 350-07:

2 CD8 PTE-, 2 CD4 PTE+

3 CD8+ regions, 2 CD4+ regions

Number of overlapping peptides per region: CD8: none CD4: 1 1

2 CD4 responses:

Moon	GKKKYRLKHLVWASR			
G232	GKKKYRLKHLVWASR	Gag	25	39

Moon	DIKVVPRRKAKIIRD			
P173	DIKVVPRSKVKIIRD	Pol	971	985

M consensus 351-07:

7 CD8 PTE-, 1 CD4 PTE+

4 CD8+ regions, 1 CD4+ regions

Number of overlapping peptides per region: CD8: 2 2 2 1 CD4: 1

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4 CD8 responses:

Mcon	KHLVWASRELERFALNPGLL			
G20	KHLVWASRELERFAL	Gag	32	46
G68	-----ASRELERFAVNPGLL	Gag	37	5
Mcon	IVQQQSNLLRAIEAQQ			
E6	VVQQQSNLLRAIEAQ	Env	548	562
E8	-VQQQNNLLRAIEAQH	Env	549	563
Mcon	AVFIHNFKRKGGIGGY			
P22	AVFIHNFKRKGGIGG	Pol	894	908
P236	-VLIHNFKRKGGIGGY	Pol	895	909
Mcon	KNWMTDTLLVQNANP			
G55	KNWMTDTLLVQNANP	Gag	314	328

1 CD4 response:

Mcon	WKGSPAIFQSSMTKI			
P352	WKGSPAIFQASMTKI	Pol	308	322

M consensus 352-07:

6 CD8 PTE+, 2 CD4 PTE+

6 CD8+ regions, 2 CD4+ regions

Number of overlapping peptides per region: CD8: 1 1 1 1 1 1 CD4: 1

6 CD8 responses:

Mcon	QPALQTGSEELRSLY			
G268	LPALKTGSEELRSLY	Gag	65	79
Mcon	IVQQQSNLLRAIEAQ			
E54	VVQQQSNLLRAIEAQ	Env	548	562
Mcon	CSGKLICTTTVPWNS			
E73	CSGKLICTTAVPWNS	Env	598	612
Mcon	AKAYDTEVHNVWATH			
E215	AKAYEKEVENVWATH	Env	58	72
Mcon	KKDSTKWRKLVDFRE			
P23	KKDSTKWRKLVDFRE	Pol	220	234
Mcon	VFIHNFKRKGGIGGY			
P236	VLIHNFKRKGGIGGY	Pol	895	909

2 CD4 responses:

Mcon	NKIVRMYSFVSILDI			
G13	NKIVRMYSFVSILDI	Gag	271	285
Mcon	KGNSSKVSQNYPIVQ			
G97	TENSSQVSQNYPIVQ	Gag	102	136

Figure 22 (con't)

M consensus 353-07:

2 CD8 PTE+, 0 CD4 PTE+

2 CD8+ regions, 0 CD4+ regions

Number of overlapping peptides per region: CD8: 1 1 CD4: none

2 CD8 responses:

Moon GCKQIIGQLQFALQT

G151 GCRQILGQLQPSLQT Gag 56 70

Moon PVHAGPIPPGQMREP

G213 PVQAGPIAPGQMREP Gag 217 231

M consensus 354-07:

5 CD8 PTE+, 1 CD4 PTE+

3 CD8+ regions, 1 CD4+ regions

Number of overlapping peptides per region: CD8: 2 2 1 CD4: 1

3 CD8 responses:

Moon EQATQDVKNWMTDTLLVQNANF

G197 EQSTQEVKNWMTDTL Gag 307 321

G55 -----KNWMTDTLLVQNANF Gag 314 328

Moon IVQQQSNNLLRAIEAQQ

E54 VVQQQSNNLLRAIEAQ Env 548 562

E72 -VQQQNNLLRAIEAQH Env 549 563

Moon HSNWRAMASDFNLPP

P93 HSNWRAMASDFNLPP Pol 731 745

1 CD4 response:

Moon GSPAIFQSSMTKILE

P141 GSPAIFQSSMTKILD Pol 310 324

M consensus 355-07:

3 CD8 PTE+, 1 CD4 PTE-

2 CD8+ regions, 1 CD4- regions

Number of overlapping peptides per region: CD8: 1 3 CD4: 1

2 CD8 responses:

Moon IIGDIRQAHCNISGT

E325 ITGDIRQAHCNVRS Env 322 336

Moon SNWRAMASDFNLPPIVAK

P93 SNWRAMASDFNLPP Pol 731 745

P149 ---RTMASDFNLPPVAK Pol 735 749

P193 ---KAMASDFNLPPIVAK Pol 735 749

1 CD4 response:

Moon GSPAIFQSSMTKILE

P141 GSPAIFQSSMTKILD Pol 310 324

Figure 22^{33/51} (con't)

Reactive peptides and breadth and depth of responses: Mosaic Vaccine

Mosaic 356-07:

15 CD8 PTE+, 2 CD4 PTE+

8 CD8+ regions, 2 CD4+ regions

Number of overlapping peptides per region: CD8: 5 3 1 2 1 1 1 2 CD4: 1 1

8 CD8 responses:

Mos1	AAEWDRVHPVHAGPIAFGQ			
Mos2	AAEWDRLHPVHAGPVAFGQ			
G319	AAE-DRLEPVPVHAGPIF	Gag	209	225
G44	-AEWDRLHPVHAGPIA	Gag	210	224
G242	-AEWDRLHPVHAGPVA	Gag	210	224
G277	---WDRVHPVHAGPNPPG	Gag	212	226
G102	----DRVHPVHAGPIPPGQ	Gag	213	227

Mos1	IVQQQNNLLRAIEAQQ			
Mos2	IVQQQSNLLRAIEAQQ			
E54	VVQQQSNLLRAIEAQ	Env	549	562
E72	-VQQQNNLLRAIEAQH	Env	549	563
E191	-VQQQSNLLRAIEAQQ	Env	549	563

Mos1	ASQDVKNWMTETLLV			
Mos2	ATQDVKNWMTDTLLV			
G66	ASQEVKNWMTETLLI	Gag	309	323

Mos1	AVFIHNEFKRKGIGGY			
Mos2	AVFIHNEFKRKGIGGY			
P22	AVFIHNEFKRKGIGG	Pol	894	908
P236	-VLIHNEFKRKGIGGY	Pol	895	909

Mos1	PLVKLWYQLEKDPIA			
Mos2	PLVKLWYQLEKEPIV			
P73	PLVKLWYQLEKEPIV	Pol	576	590

Mos1	TIPSTNNETPGIRYQ			
Mos2	TIPSINNETPGIRYQ			
P79	TIPSINNETPGIRYQ	Pol	286	300

Mos1	YPGIKVRQLCKLLRG			
Mos2	YAGIKVRQLCKLLRG			
P156	YPGIKVRQLCKLLRG	Pol	426	440

Mos1	LIKKERVYLSWVPAHKGIG			
Mos2	LIKKERVYLSWVPAHKGIG			
P223	LIKKERVYLSWVPAH	Pol	680	694
P83	----EKVYLSWVPAHKGIG	Pol	684	698

2 CD4 responses:

Mos1	SLYNTVATLYCVHQR			
Mos2	SLFNTVATLYCVHAE			
G54	SLYNTVATLYCVHQR	Gag	77	91

Mos1	ANPDCKTILKALGPA			
Mos2	ANPDCKTILRALGPG			
G63	ANPDCKTILRALGPG	Gag	326	340

Figure 22 (con't)

Mosaic 357-07:

29 CD8 PTE+, 4 CD4 PTE+

14 CD8+ regions, 4 CD4+ regions

Number of overlapping peptides per region: CD8: 5 2 2 5 5 0 1 1 1 1 1 1 1 1 CD4: 1 1 1 1

14 CD8 responses:

Mos1	EQLIKKERVYLSWVPAHKGIG			
Mos2	EQLIKKERVYLSWVPAHKGIG			
P250	EPLIKKEKVYLSWVF	Pol	678	692
P316	-KLIKEDKVYLSWVPA	Pol	679	693
P223	--LIKKERVYLSWVPAH	Pol	680	694
P169	-----EKVYLSWVPAHKGIG	Pol	684	698
P93	-----EKVYLSWVPAHKGIG	Pol	684	698
Mos1	IVQQQNNLLRAIEAQQ			
Mos2	IVQQQSNLLRAIEAQQ			
E54	VVQQQSNLLRAIEAQQ	Env	549	562
E70	-VQQQNNLLRAIEAQH	Env	549	563
Mos1	BQASQDVKNWMTETLLVQNANP			
Mos2	BQATQDVKNWMTETLLVQNANP			
G197	EOSTQEVKNWMTDTL	Gag	307	321
G55	-----KNWMTETLLVQNANP	Gag	314	328
Mos1	HSNWRAMASDFNLPPVAK			
Mos2	HSNWRAMASEFNLPPIVAK			
P93	HSNWRAMASDFNLPP	Pol	731	745
P262	-SNWRAMASEFNLPP	Pol	732	746
F473	--NWRMTASDFNLPPVI	Pol	733	747
F149	----RTMASDFNLPPVAK	Pol	735	749
F193	----KAMASDFNLPPIVAK	Pol	735	749
Mos1	AEWDRVHPVHAGPIAPGQ			
Mos2	AEWDRLHPVHAGPVAPGQ			
G319	AEDRLHPVHAGPIP	Gag	209	225
G242	ADWDRLHPVHAGPVA	Gag	210	224
G44	AEDRLHPVHAGPIA	Gag	210	224
G277	--WDRVHPVHAGFPNPPG	Gag	210	226
G102	---DRVHPVHAGPIPPGQ	Gag	213	227
Mos1	AVFIHNFKRKGIGGY			
Mos2	AVFIHNFKRKGIGGY			
P22	AVFIHNFKRKGIGG	Pol	894	908
P236	-VLIHNFKRKGIGGY	Pol	895	909
Mos1	PLDEGFRKYTAFTIP			
Mos2	PLDEDFRKYTAFTIP			
P242	PLDESTRKYTAFTIP	Pol	274	288
Mos1	TRILEPFRKQNPPIV			
Mos2	TKILEPFRKQNPDIIV			
P394	TKILEPFRQNPPIV	Pol	320	334
Mos1	ICEEMEKEGKITKIG			
Mos2	ICTEMEKEGKISKIG			
P112	ICTEMEKEGKISKIG	Pol	292	296
Mos1	VKLWYQLEKDPVAGV			
Mos2	VKLWYQLEKEPIVGA			
P200	VKLWYQLEKDPVGA	Pol	573	590
Mos1	GDIIGDIRQAHCNIS			
Mos2	GDIIGDIRQAHCNLS			
E764	GDIIGDIRQAHCNIS	Env	321	334
Mos1	ICTTTVPWNASWSNK			
Mos2	ICTTAVPWNTWSNK			
E334	ICTTTVPWNASWSNR	Env	233	247

Figure 22 (con't)

X181	IGQVRDQAEHLKAV		
X182	IGQVRDQAEHLKAV		
E174	IFQVRQAEHLKAV	201	577 592
X181	GKQAGACDVAGRQD		
X182	GKQAGACDVAGRQD		
E185	GKQAGACDVAGRQD	201	587 601
4 CD4 responses:			
X181	KYAKRTAHTNDVKQ		
X182	KYAKRTAHTNDVKQ		
E174	KYAKRTAHTNDVKQ	201	502 522
X181	AGDIIGDIQAHCNL		
X182	TGDIIGDIQAHCNL		
E181	TGDIIGDIQAHCNL	EVV	300 333
X181	NOEKNEKDLALDS		
X182	NOEKNEKDLALDS		
E181	NOEKNEKDLALDS	EVV	251 285
X181	DIKVPKRVKIKD		
X182	DIKVPKRVKIKD		
E172	DIKVPKRVKIKD	201	271 295
Mosaic 358-07:			
19 CD8 P1E4, 3 CD4 E1E-			
7 CD8 regions, 3 CD4 regions			
Number of overlapping peptides per region: CD8: 14 - 1 1 1 CD4: 1 1 1			
7 CD8 responses:			
X181	LIRKERVYLSVPAHKG13		
X182	LIRKERVYLSVPAHKG13		
E182	LIRKERVYLSVPAH	201	280 294
E183	-----EYVLSVPAHKG13	201	284 298
X181	IVQGNILRAIERQCHH10L		
X182	IVQGNILRAIERQCHH10L		
E184	IVQGNILRAIERQ	EVV	546 560
E185	IVQGNILRAIERQ	EVV	549 563
E186	IVQGNILRAIERQ	EVV	549 563
E187	IVQGNILRAIERQ	EVV	554 568
X181	AVFIHNEKKGIGG1		
X182	AVFIHNEKKGIGG1		

Figure 22 (con't)

P222	AVFIHNKRGKGGIG	Pol	894	908
P236	-VLIHNKRGKGGIGY	Pol	895	909
Mos1	EQASQDVKNWMTETLLVQNANP			
Mos2	EQATQDVKNWMTETLLVQNANP			
G122	EQASQDVKNWMTETL	Gag	307	321
G197	EQSTQEVKNWMTETL	Gag	307	321
G66	--ASQEVKNWMTETLLI	Gag	309	323
G138	---IQVKNWMTETLLIQ	Gag	310	324
G30	-----KNWMTETLLVQNANP	Gag	314	328
G55	-----KNWMTETLLVQNANP	Gag	314	328
Mos1	AEDRVHFPVHAGPIAPGQ			
Mos2	AEDRRLHPVHAGPVAPGQ			
G319	AAEDRRLHPVHAGPIA	Gag	209	225
G44	AEDRRLHPVHAGPIA	Gag	210	224
G11	---DRVEHVPVHAGPIPPGQ	Gag	213	227
Mos1	WKGPSAIFQCSMTRI			
Mos2	WKGPSAIFQSSMTKI			
P238	WKGPSAIFQCSMTKI	Pol	308	322
Mos1	MTKILEPFRKRNPHI			
Mos2	MTKILEPFRKQNPDI			
P144	MTKILEPFRKQNPDI	Pol	319	333
3 CD4 responses:				
Mos1	GSPAIFQCSMTRI			
Mos2	GSPAIFQSSMTKI			
P141	GSPAIFQSSMTKILD	Pol	310	324
Mos1	HGQVDCSPGIWQLAC			
Mos2	HGQVDCSTGIWQLAC			
P25	HGQVDCSPGIWQLDC	Pol	766	780
Mos1	DRFYKILRAEQASQD			
Mos2	DRFYKILRAEQATQD			
G57	DRFYKILRAEQASQE	Gag	298	312
Mosaic 359-07:				
12 CD8 PTE+, 5 CD4 PTE+				
10 CD8+ regions, 2 CD4+ regions				
Number of overlapping peptides per region: CD8: 2 1				
10 CD8 responses:				
Mos1 LIKKREVLYLSWFAHKGIG				

Figure 22 (con't)

X081	LIRKERVYLANVPAHKGIS	Pol	680	694
F003	LIRKERVYLSWVPAH	Pol	684	698
F13	----EKVLSWVPAHKGIS			
X081	AEWDVHFVHAGPIRAGQ	Gay	214	224
X082	AEWDRHFVHAGVPAQ	Gay	218	227
G44	AENDRLHFVHAGPIA			
G100	---DRVHFVHAGPIEFAG			
X081	ALFQCSMTIRILEPFR	Pol	313	327
X082	ALFQSSMTKILERFR			
F359	ALFQSSMTIRILEPFR			
X081	ASQIYEGIKVRQOLCK	Pol	421	436
X082	ASQIYAGIKVRQOLCK			
F365	WSQIYAGIKVRQOLCK			
X081	RELKRTQDFWEVQOL	Pol	133	147
X082	RELKRTQDFWEVQOL			
F139	RELKRTQDFWEVQOL			
X081	LIRAIERQOHLQOLT	Env	555	569
X082	LIRAIERQOHLQOLT			
E007	LMALERQOHLQOLT			
X081	LICTTVFVNASWSN	Env	600	616
X082	LICTTAVFWNTSWSN			
E432	HICTTVFVNASWSN			
X081	KHIVWASRELERFAY	Gay	30	46
X082	KHIVWASRELERFAL			
G11	KHIVWASRELERFAL			
X081	RSINYTVATLYCVHQ	Gay	76	90
X082	RSINYTVATLYCVHA			
G123	RSINYTVATLYCVHQ			
X081	ERAFSPREVIFMESA	Gay	160	174
X082	ERAFSPREVIFMFTA			
G14	ERAFSPREVIFMESA			
2 CD4 responses:				
X081	WXSPALFQCSMTIRILEPFR	Pol	338	350
X082	WXSPALFQSSMTKILERFR	Pol	340	354
F350	WXSPALFQSSMTKILERFR			
P141	--GSPALFQSSMTKIL			

[illegible]

Accession	Peptide	Position	Score
X180	WYQLEKEPIVGAETP	Pol 561	595
P370	WYQLEKDFIAEAEIS		
X181	ENVTEFNMMKNNNV	Env 57	101
X182	ENVTEFNMMKNNNV		
P373	ENVTEFNMMKNNNV		
X183	VIQNSDIKVPERRK	Pol 365	979
X184	VIQNSDIKVPERRK		
P376	VIQNSDIKVPERRK		
X185	VSQNYPIVQNLIQGM	Gag 103	142
X186	VSQNYPIVQNLIQGM		
P379	VSQNYPIVQNLIQGM		
X187	VLAAMSQVTSNTIM	Gag 362	377
X188	VLAAMSQ-TNSTILM		
P382	VLAAMSQ-AQQTINM		
X189	RVLAEAMSQVTSNTAT	Pol 361	376
X190	RVLAEAMSQVTSNTIL		
P385	RVLAEAMSQVTSNTIL		
X191	CTHGIRPVVSTQILL	Env 347	361
X192	CTHGIRPVVSTQILL		
P388	CTHGIRPVVSTQILL		

1 CD8 P12+, 6 CD4 P12-
 2 CD3- regions, 5 CD4- regions
 Number of overlapping peptides

M68	--LIIKERVYLSWVPARKGIG
M69	-QLIKHEKVYLAWVPARKGIG
P000	ELIKKEKVILANP
P001	EALIKKEVYSKP
P010	-LEIKDEVYLSKPA
P009	--LIKERVYLSWPAP
P100	-----EKVYLAWVPARKGIG
P02	-----EKLVSWSVPARKGIG

YAS1 CTHGIRPVVSTQLLL
YAS2 CTHGIRPVVSTQLLL
E15 CTHGIRPVVSTQLLL

Figure 22 (con't)

E47	CIHGIREVSIQLLL	ENV	247	261
M081	ICTTVFNNASWSNKS			
M082	ICTTAVPNTSWSNKS			
E084	ICTTVFNNASWSNR	ENV	603	617
E014	ICTTVFNNASWSNKC	ENV	604	618
E106	ICTTAVFNNASWSNKS	ENV	605	619
E190	ICTTAVPNTSWSNKS	ENV	605	619
M081	ACQSYGGGPGHKARVLAEMS			
M180	ACQSYGGGPGSHKARVLAEMS			
G160	ACQSYGGGPGHKARVL	Gag	349	363
G176	-----GGFSGHKARVLAEMS	Gag	354	368
M081	AEEDRVHPVHAGPIAFGQ			
M080	AEEDRLHPVHAGPVAFGQ			
G019	AEEDRLHPVHAGPIF	Gag	209	225
G040	AEEDRLHPVHAGPIA	Gag	210	224
G44	AEEDRLHPVHAGPIA	Gag	210	224
G177	AEEDRVHPVHAGPIFPG	Gag	210	225
G100	AEEDRVHPVHAGPIFPG	Gag	210	226
M081	HSNWRAMASDENLPP			
M080	HSNWRAMASEFNLPP			
E90	HSNWRAMASDENLPP	Pol	731	745
M081	KGRPGNFLOSRPEPT			
M080	KGRPGNFLOSRPEPT			
G06	KGRPGNFLOSRPEPT	Gag	440	456
S CD4 responses:				
M081	RSLYNTVATLYCVHQR			
M080	RSLYNTVATLYCVHAE			
G019	RSLYNTVATLYCVHA	Gag	76	80
G04	RSLYNTVATLYCVHQR	Gag	77	91
M081	YVDRGRQKIVSLTE			
M080	YVDRGRQKIVSLTD			
E104	YVDRGRQKIVSLTE	Pol	610	626
M081	CTTVFNNASWSNKS			
M080	CTTAVPNTSWSNKS			
E53	CTTVFNNASWSNKS	ENV	604	616
M081	HWAGIQEFGIPYNP			
M080	HWAGIQEFGIPYNP			

Figure 22 (con't)

P135	WWAGIQQEFQIPYNP	Pol	846	860
Mos1	GPCHKARVLAERMSQ			
Mos2	GPCHKARVLAERMSQ			
G15	GPCHKARVLAERMSQ	Gag	355	369
Mosaic 362-07:				
13 CD8 PTE+, 5 CD4 PTE+				
7 CD8+ regions, 5 CD4+ regions				
Number of overlapping peptides per region: CD8: 2 2 4 2 1 1 1 CD4: 1 1 1 1 1				
7 CD8 responses:				
Mos1	CTHGIRPVVSTQILL			
Mos2	CTHGIRPVVSTQILL			
E15	CTHGIRPVVSTQILL	Env	247	261
E47	CTHGIRPVVSTQILL	Env	247	261
Mos1	KHIVWASRELERFAVNPGLL			
Mos2	KHIVWASRELERFALNPGLL			
G20	KHIVWASRELERFAL	Gag	32	46
G68	-----ASRELERFAVNPGLL	Gag	37	51
Mos1	QPSLQTGSEELRSLYNTVATL			
Mos2	QPALQTGTEELRSLENTVATL			
G268	CPALKTGSEELRSLY	Gag	65	79
G249	--ALQTGSEELRSLENT	Gag	67	81
G132	---LQTGTEELRSLENTV	Gag	68	82
G120	-----GSEELRSLYNTVATL	Gag	71	85
Mos1	ACQGVGGPGCHKARVLAERMS			
Mos2	ACQGVGGPGSHKARVLAERMS			
G166	ACQGVGGPGCHKARVL	Gag	349	363
G76	-----GGPSHKARVLAERMG	Gag	354	368
Mos1	RELNKRRTQDFWEVQL			
Mos2	RELNKRRTQDFWEVQL			
P233	RELNKRRTQDFWEVQL	Pol	233	247
Mos1	LLRAIEAQQHLLQLT			
Mos2	LLRAIEAQQHLLQLT			
E227	LLMAIEAQQHLLQLT	Env	555	569
Mos1	KTAVQMAVFTHNEKR			
Mos2	KTAVQMAVFTHNEKR			
P5	KTAVQMAVFTHNEKR	Pol	888	902

Figure 22 (con't)

5 CD4 responses:
X061 KLNWASQIYFGIKVR
X062 KLNWASQIYRGIKVR
E136 KLNWASQIYRGIKVR
P01 418 432

X061 YAKMTAHTNDVKQL
X062 YAKMTAHTNDVKQL
E136 YAKMTAHTNDVKQL
P01 509 523

X061 DQAEHLKTAVMQAVF
X062 DQAEHLKTAVMQAVF
E136 DQAEHLKTAVMQAVF
P01 662 696

X061 SLQTGSEELRSLYNT
X062 ALQTGSEELRSLYNT
E136 ALQTGSEELRSLYNT
GAG 67 81

X061 GFCHKARVLAERMSQ
X062 GFCHKARVLAERMSQ
G15 GFCHKARVLAERMSQ
GAG 355 369

Reactive peptides and breadth and depth of responses: Optimal Natural Clade C Vaccine

Natural Clade C 363-07:
2 CD8 FIE+, 3 CD4 FIE+
1 CD8- regions, 0 CD4+ regions
Number of overlapping peptides per region: CD8: 2 CD4: none

1 CD8 responses:
C QPALTGTSEELRSLYNTVAIL
G165 LPAKMTGSEELRSLY
G120 -----GSEELRSLYNTVAIL

Natural Clade C 364-07:
3 CD8 FIE+, 2 CD4 FIE+
3 CD8- regions, 2 CD4+ regions
Number of overlapping peptides per region: CD8: 1 1 1 1 1 CD4: 1 1

5 CD8 responses:
C ARTNDVKQLTEAVQK
E10 ARTNDVKQLTEAVQK P01 515 529

C GDIIGDIRQAHCHNIS
E84 EDIIGDIRQAHCHNIS ERV 321 334

Figure 22 (con't)

C	SEKSAVGIGAVELGF		
E11C	PERKAVGLAVELGF	Env	506 502
C	PASILGGCKLDWEK		
G133	SASLRSCKLDWEK	Gag	4 10
C	TNNPFVFGDIYKRW		
G135	ISNPFVFGDIYKRW	Gag	231 263
2 CD4 responses:			
C	CKSNITGLLITRDGG		
E310	CTSNITGLLITRDGG	Env	445 459
C	SLINTVATLYCVHAG		
G54	SLINTVATLYCVHQR	Gag	77 91
Natural Clade C 365-07:			
C	CD8 P1E+, 1 CD4 P1E+		
2 CD8+ regions, 1 CD4+ regions			
Number of overlapping peptides per region: CD8: 1 1 CD4: 1			
2 CD8 responses:			
C	EQLINKERVYLSWVP		
P053	EPLKKKERVYLSWVF	P01	678 690
C	AEMDRLHPVHAGPIA		
G44	AEMDRLHPVHAGPIA	Gag	210 224
1 CD4 response:			
C	HQAAQMQLKDTINEE		
G14	HQAAQMQLKDTINEE	Gag	194 208
Natural Clade C 366-07:			
C	CD8 P1E+, 1 CD4 P1E+		
4 CD8+ regions, 1 CD4+ regions			
Number of overlapping peptides per region: CD8: 2 1 1 1 CD4: 1			
4 CD8 responses:			
C	IVQQSNLLRAIEHQ		
E54	IVQQSNLLRAIEHQ	Env	549 562
E72	IVQQSNLLRAIEHQ	Env	549 563
C	AVFIHNPKKGGIGGY		
E44	AVFIHNPKKGGIGG	P01	394 908
E336	AVFIHNPKKGGIGGY	P01	393 909

Figure 22 (con't)

C	MAICEMEREKGIK	Pol	190	204
EC04	TAICEMEREKGIK			
C	GGPSHKARVLAAMS	Seq	354	368
GT6	GGPSHKARVLAAMG			
1 CD4 response:				
C	LIQVVRDQAEHLKTA	Pol	876	890
EC6	LIQVVRDQAEHLKTA			
Natural Clade C 367-07:				
C	CD8 FTE+, 0 CD4 FTE+			
C	CD8- regions, 0 CD4+ regions			
Number of overlapping peptides per region: none				
0 CD8 responses				
0 CD4 responses				
Natural Clade C 368-07:				
C	CD8 FTE+, 0 CD4 FTE+			
C	CD8- regions, 0 CD4+ regions			
Number of overlapping peptides per region: CD8: 0 CD4: 0				
1 CD8 response				
C	AVFIHNERKGGIGG	Pol	894	908
EC1	AVFIHNERKGGIGG			
EC36	-VLIHNERKGGIGG	Pol	893	909

Figure 23

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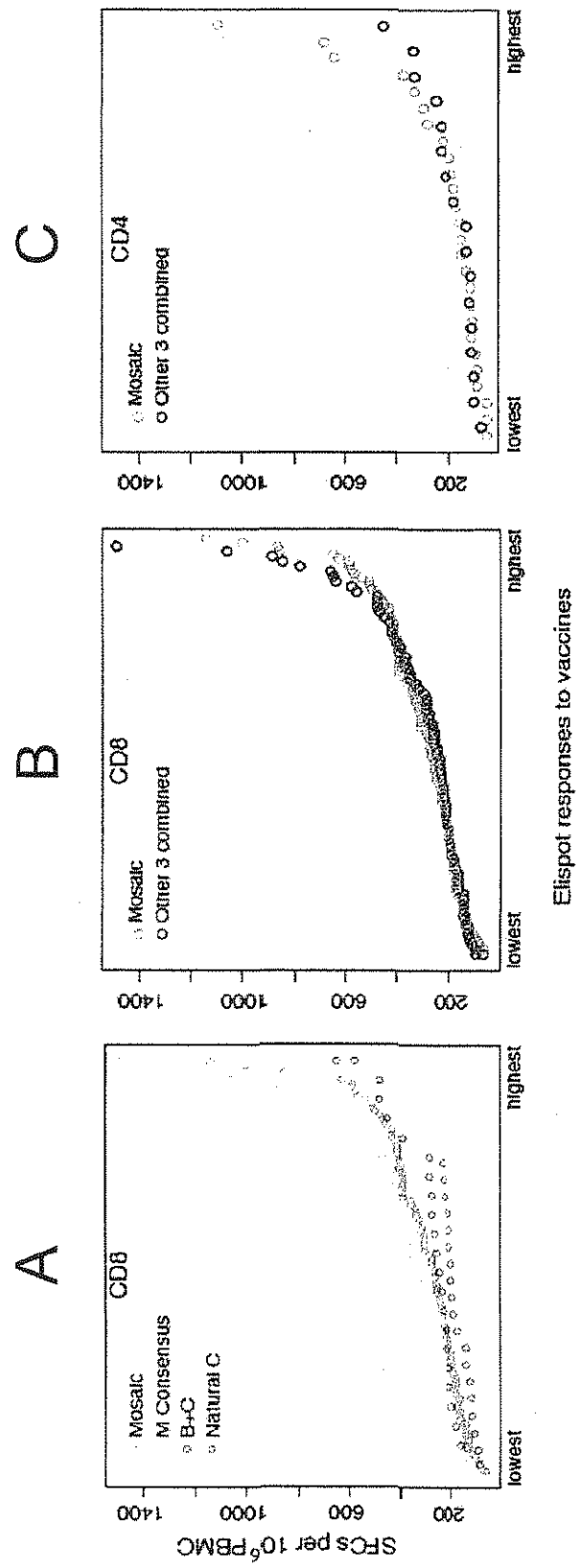


Figure 24

A

Monkey 366 (Natural C)

OptC IVQQQSNLLRAIERAQ
 E54 VVQQQSNLLRAIERAQ
 E72 -VVQQQSNLLRAIERAQ

OptC AVFIHNFPRKGGIGGY
 P22 AVFIHNFPRKGGIGG
 P236 -VLIHNFPRKGGIGGY

OptC MAICEEMEKEGKITK
 P224 TAICEEMEKEGKITK

OptC GGPSSHKARVLAEAMS
 G76 GGPSSHKARVLAEAMG

B

Monkey 361 (Mosaic)

Mos1 EQLIKKERVYLSWVPAHKGIG
 Mos2 EQLIKKERVYLSWVPAHKGIG
 P221 EELIKKERVYLSWVP
 P250 EPLIKKERVYLSWVP
 P316 -KLIKKDKVYLSWVPA
 P223 --LIKKERVYLSWVPAH
 P169 -----EKVYLSWVPAHKGIG
 P83 -----EKVYLSWVPAHKGIG

Mos1 CTHGIRPVVSTQLLL
 Mos2 CTHGIRPVVSTQLLL
 E15 CTHGIRPVVSTQLLL
 E47 CTHGIRPVVSTQLLL

Mos1 ICTTVPWNASWSNKSLL
 Mos2 ICTTAVPWNISWSNKSQ
 E334 ICTTVPWNASWSNR
 E214 -CTTVPWNSSWSNKT
 E158 --PTAVPWNASWSNKSLL
 E290 --TTAVPWNISWSNKSLL

Mos1 ACQGYGGPGGHKARVLAEAMS
 Mos2 ACQGYGGPGSHKARVLAEAMS
 G166 ACQEVGGPGGHKARVL
 G76 -----GGPSHKARVLAEAMG

Mos1 AEWDRLHPVHAGPIAPGQ
 Mos2 AEWDRLHPVHAGVPAGQ
 G319 AAE-DRLHPVHAGPIP
 G242 -ADWDRLHPVHAGVPA
 G44 -AEWDRLHPVHAGPIA
 G277 ---WDRVHPVHAGNPFG
 G102 ----DRVHPVHAGPIPPGQ

Mos1 HSNWRAMASDFNLPP
 Mos2 HSNWRAMASEFNLPP
 P93 HSNWRAMASDFNLPP

Mos1 KGRPGNFQNRPEPT
 Mos2 KGRPGNFQSRPEPT
 G86 KGRPGNFQNRPEPT

Figure 24 (con't)

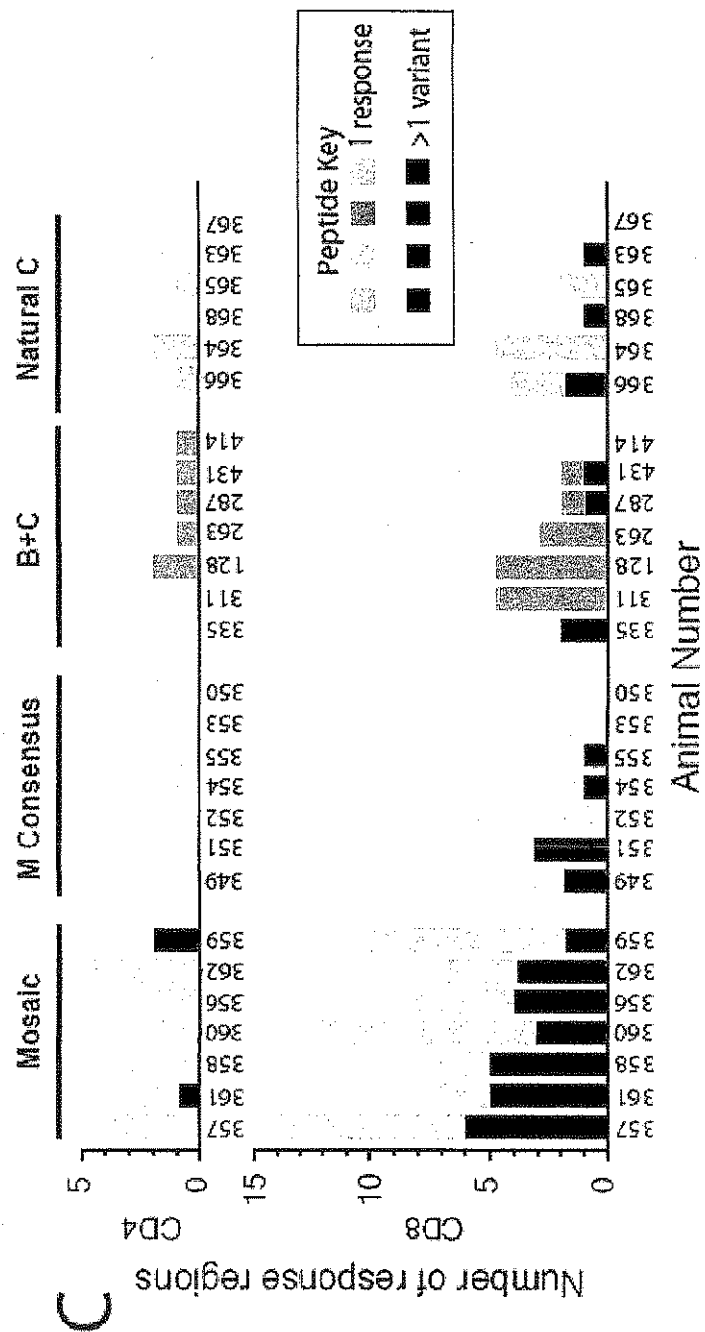


Figure 25

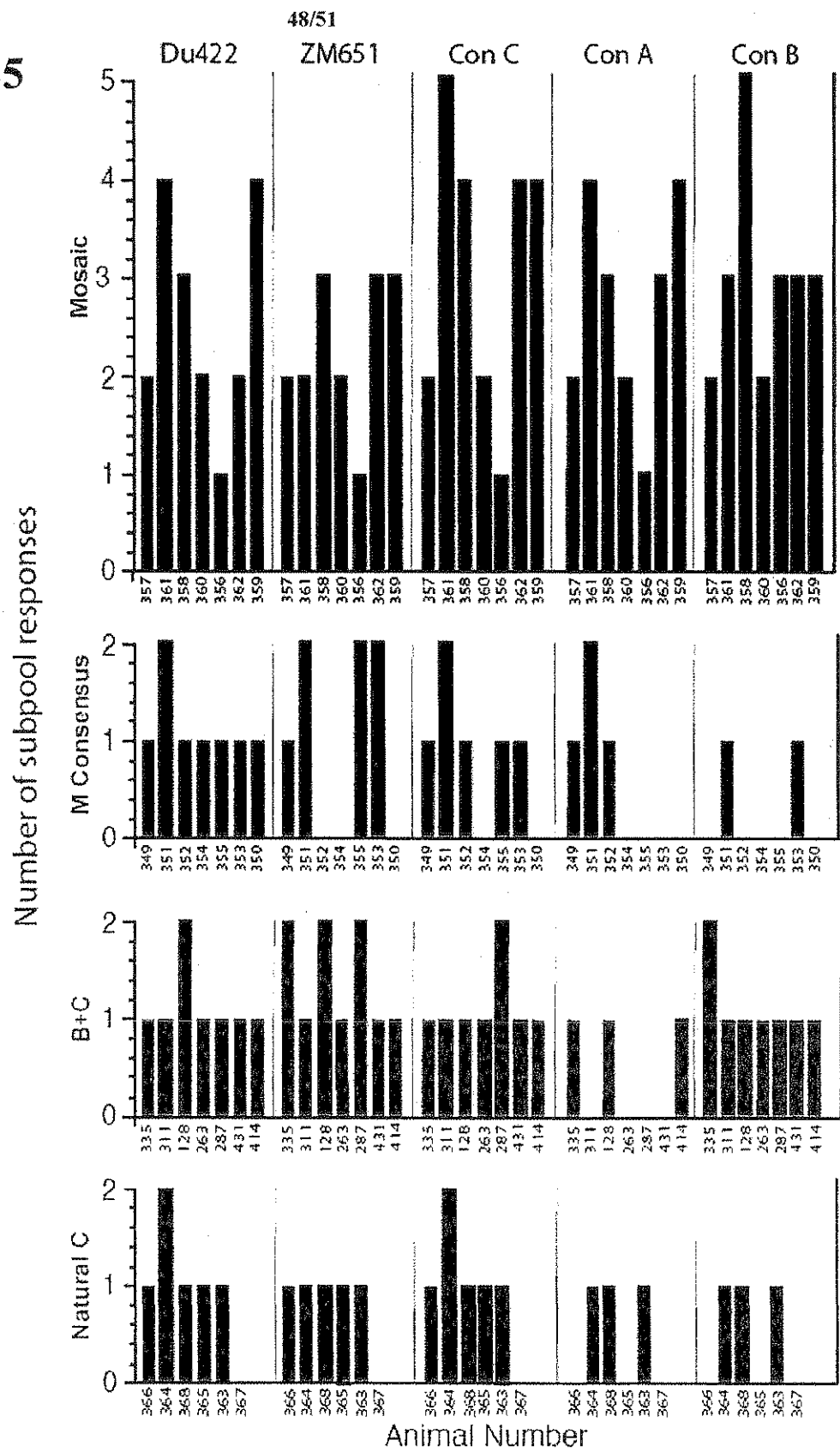


Figure 26

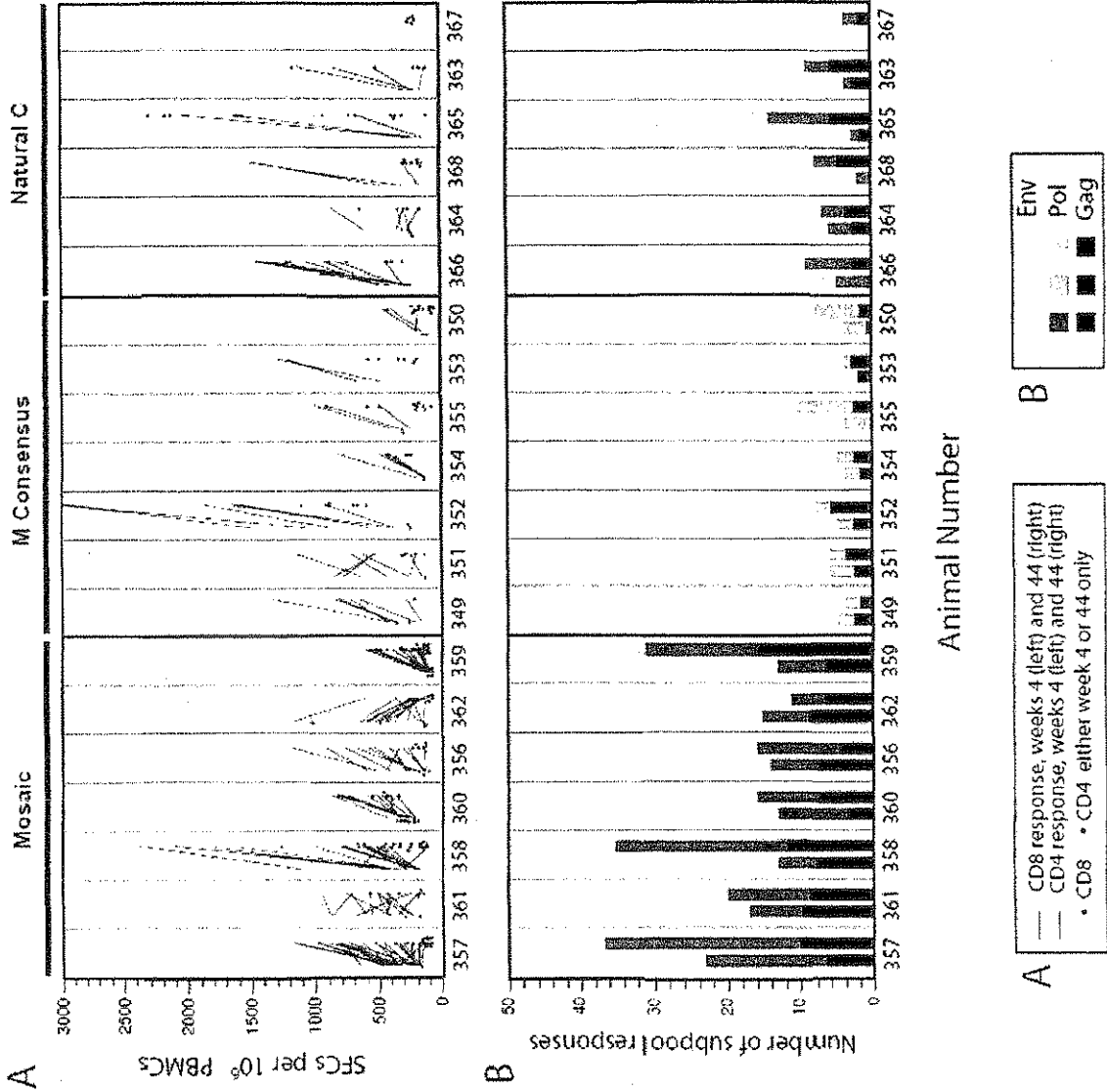
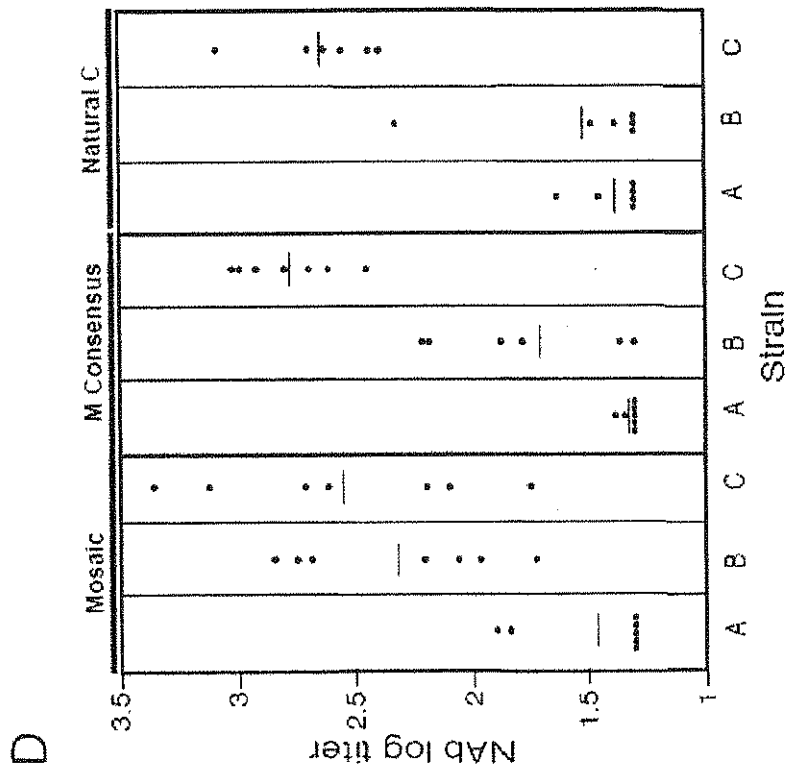
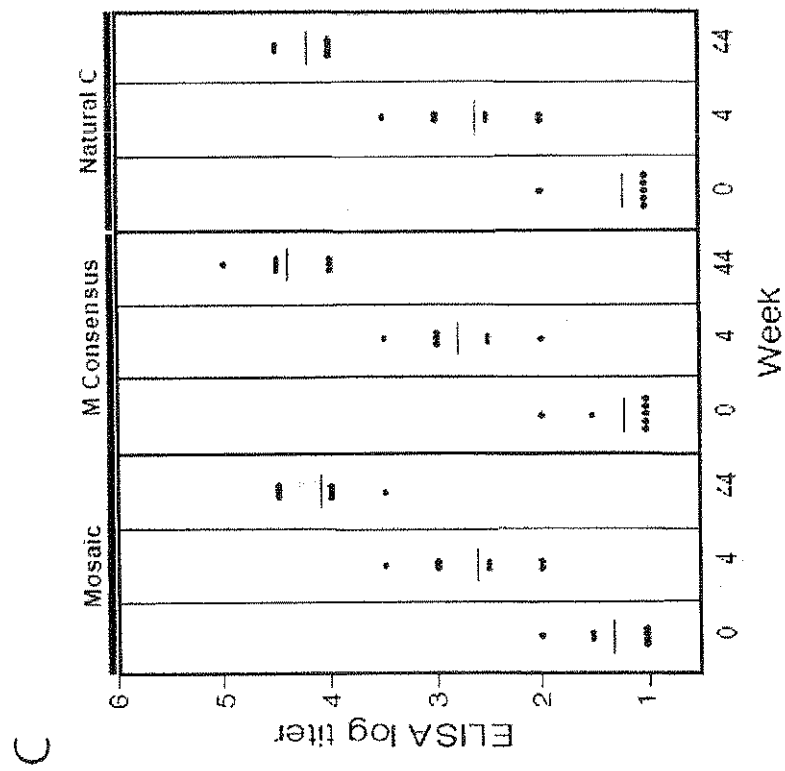


Figure 26 (con't)



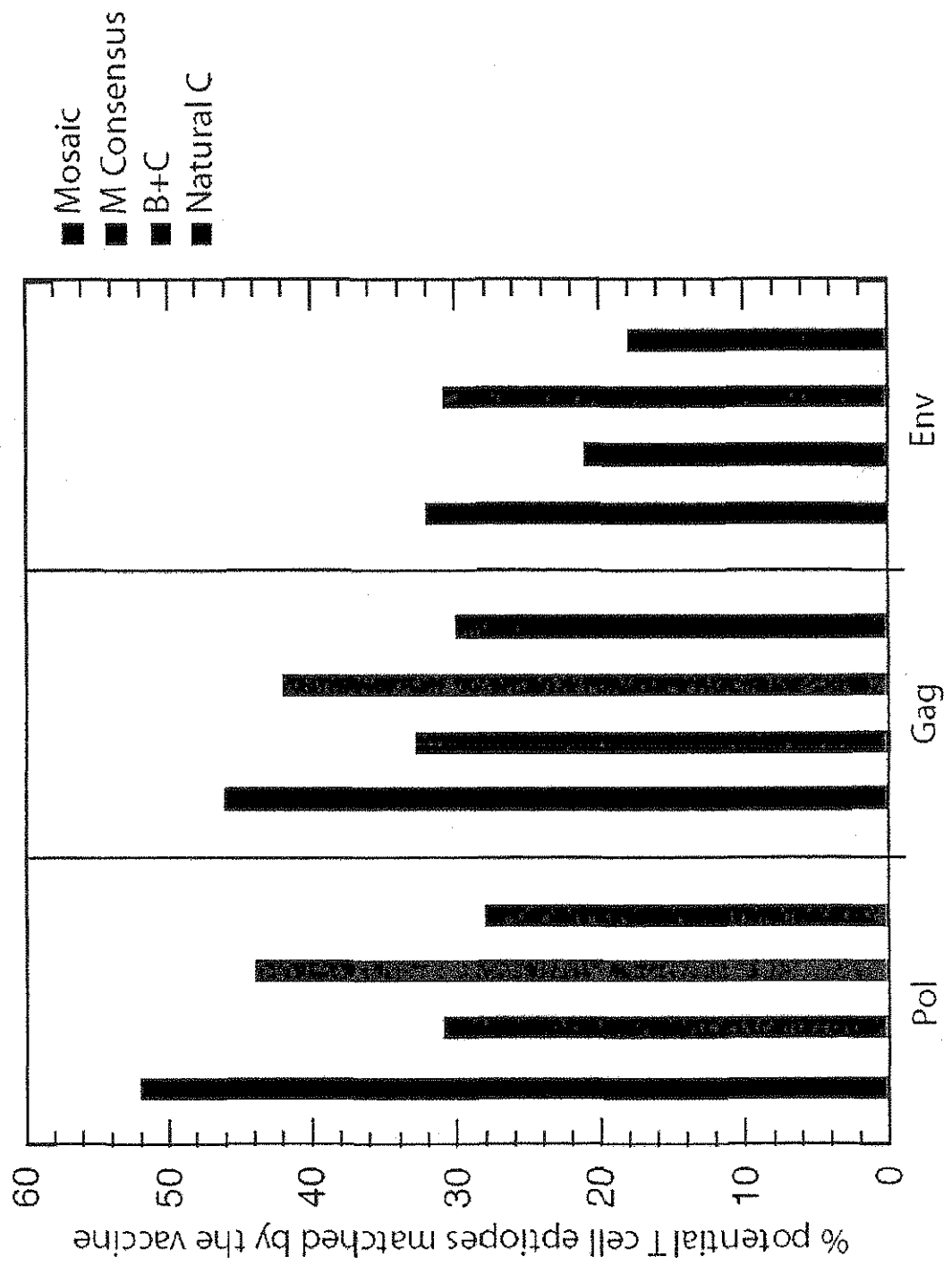


Figure 27