

**Figure S1** Neutralization resistance of pseudovirus bearing the CNE6 Env to the polyclonal plasma samples from P08 (A) and P11 (B).

**Figure S2** Alignment of a total of 137 full-length envelope sequences from the sequential plasma samples of P08 (A) and P11 (B) over the course of natural infection. Dates of sampling are indicated on the left. Dots represent identical residues, while dashes represent gaps introduced to preserve the alignment. Asterisks indicate the premature stops. Signal peptide, hypervariable (V1, V2, V3, V4, and V5) and conserved (C1, C2, C3, C4, C5) regions, Loop D, CD4-binding loop in gp120, fusion peptide (FP), amino- and carboxy-terminal heptad repeat (NHR and CHR) sequences, immunodominant region (ID), membrane-proximal external region (MPER) and transmembrane domain (TM) in gp41 are highlighted along the sequences.

**Figure S3** Standard ELISA assay to measure the binding of sequential plasma samples from P08 and P11 (A, C) and selected mAbs (B, D) to soluble gp120 captured from the original (P08 and P11) and chimeric viruses (P08/CNE6 and P11/CNE6).

**Figure S4** Infectivity of chimeric viruses (P08/CNE6 and P11/CNE6) compared with the parental ones from P08 (A) and P11 (B) as well as control CNE6.

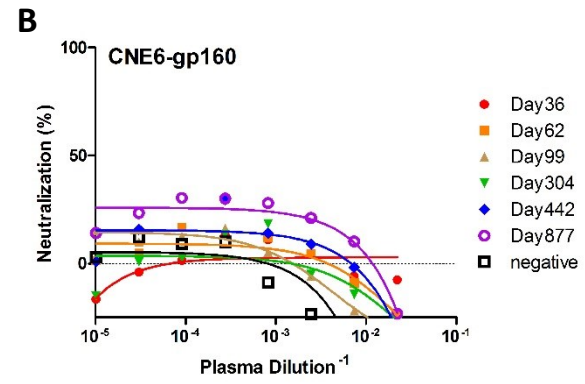
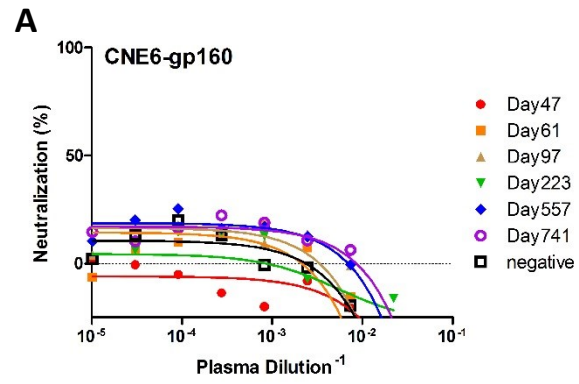
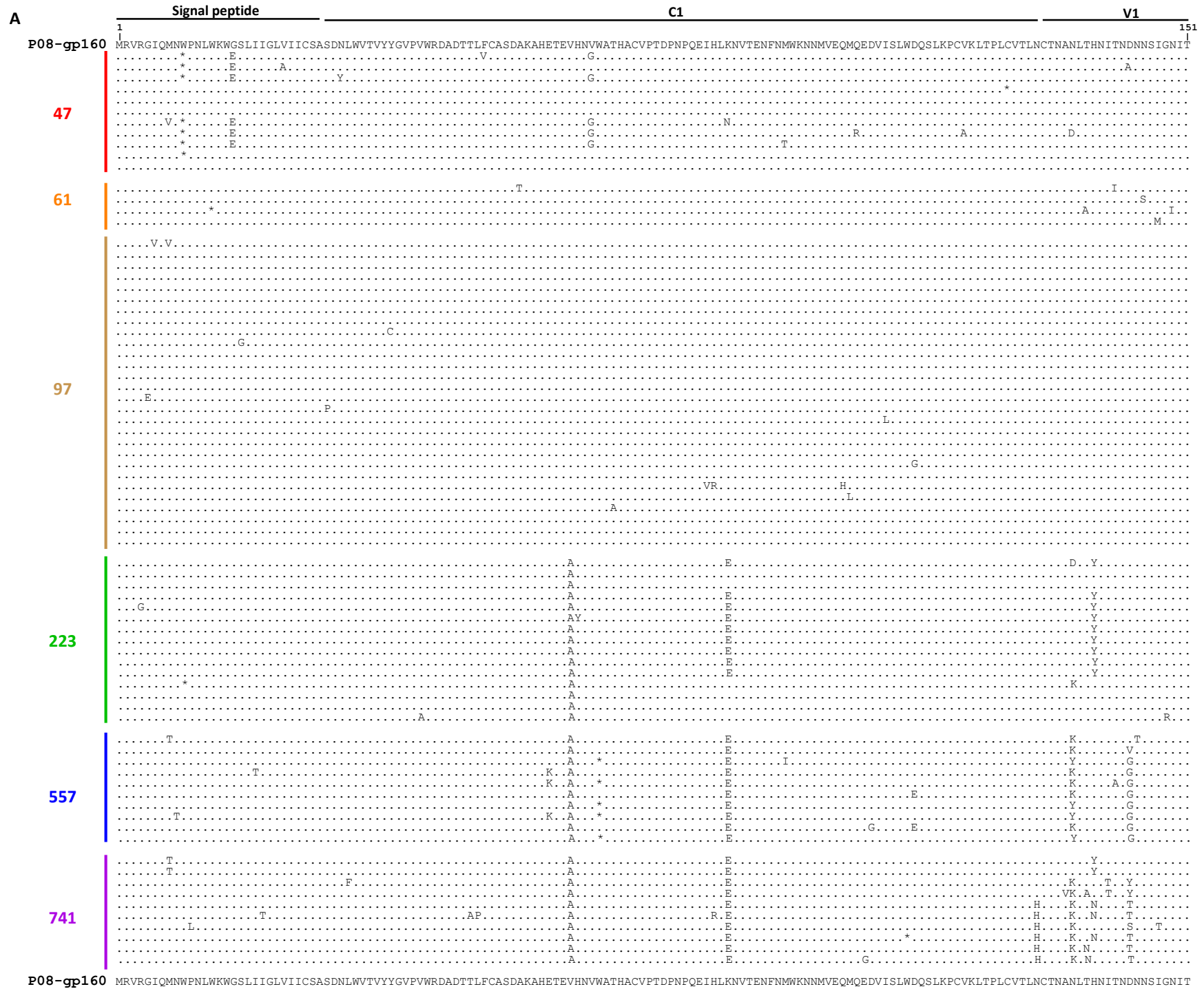


Figure S1



**Figure S2**

P08-gp160 DEVKNCTFNMTEIRGKLGKLVYALFSTLDIVHMGNDSEYRLISCNTSVIKQACPKISFDPIPIHYCAPAGYVILKCNDRKFNKGTGPKKNVSTVQCTHGKIPVSTQLLLNGSLAEEGIIINSENLTNNAKTIIVHLNKSVKINCTRPSN

47 T M L S R  
RE RE E  
P RE D

61 P S

97 S V D  
S E S  
T E  
R

223 P \*  
E E  
E E  
E E  
E E  
E E

557 I V E  
F.D. K.I. KE  
K. K.I. KE  
K. S. K.I. KE  
V F.D. --- E  
F.D. --- E  
I V A E

741 M  
M  
F.D. N  
F.D. E V  
A A I E V  
A A I E  
A P I E  
A A I E  
A A I V  
A A I V E

P08-gp160 DEVKNCTFNMTEIRGKLGKLVYALFSTLDIVHMGNDSEYRLISCNTSVIKQACPKISFDPIPIHYCAPAGYVILKCNDRKFNKGTGPKKNVSTVQCTHGKIPVSTQLLLNGSLAEEGIIINSENLTNNAKTIIVHLNKSVKINCTRPSN



P08-gp160

NATNET--FRPGGGNIKDNWRSELYKYKVVQLEPLGIAPTRARRRVVDREKRAVIGITMIFGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQORMLQLTVWGIKQLQARVLAVERYLKDQRFLLGLWGCSGKIICTTNVP

47

61

97

223

557

741

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.....*.....P.....
E.E.....E.....A.....
.....V.....T.....K.....*.....
.....K.....K.....G.....*.....
.....L.....A.....
.....C.....G.....
.....A.....N.....
.....E.....EF.....
V.....L.....Q.....A.....A.....I.....
.....K.....K.....K.....K.....P.....
V.....E.....K.....E.....E.....
.....R.....
V...ET.....K.....Q.....A.....R.....
I.....M.....K.....E.....Q.....A.....R.....
I.....K.....E.....K.....E.....
V...ET.....K.....G.....Q.....A.....W.....G.....
V...ET.....K.....Q.....A.....
V...ET.....K.....Q.....A.....G.....
V...ET.....K.....Q.....A.....

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P08-gp160

NATNET--FRPGGGNIKDNWRSELYKYKVVQLEPLGIAPTRARRRVVDREKRAVIGITMIFGFLGAAGSTMGAASITLTVQARQLLSGIVQQQSNLLRAIEAQORMLQLTVWGIKQLQARVLAVERYLKDQRFLLGLWGCSGKIICTTNVP

CHR MPER TM

610

759

P08-gp160

WNSTWSNKSYYEIIWDMNTWIQWEKEISNYTDQIYSLLETESQNQQEKNKDLLELDKASLWNNWFSITNWLWYIKIFIMIVGGIIGLRIFAVLSIVNRVRQGYSPSLQTPHHPDRPEGIEEGEGEQGRNRSVRLVSGFLALAWDD

47

.....G.....H.....A.....G.....P.....
\* S . \* N . . . . . M . . . . . H . . . . . T . . . . .
.....D.....P.....P.....
\* . \* N . . . . . \* . . . . . \* . . . . . T . . . . .

61

.....R.....A.....H.....G G.....
.....H.....G.....

97

.....H.....R.....D \*.....S.....D.....
.....R.....S.....D.....
.....A.....G.....C.....
.....R N.....
.....R.....R.....R.....R.....

223

.....K.....L.....F Q.....H.....
.....K.....E.....O.....
.....K.....E.....O.....
.....K.....L.....O.....
.....K.....L.....F.....O.....
.....K.....L.....O.....
.....K.....L.....G.....S.....
.....K.....L.....
.....K.....E H.....S.....S.....
.....A.....E.....
.....A.....E.....
.....K.....E.....

557

.....G.....A.....D.....D.....LF.....M.....
.....S.....L D A.....K.....LF.....
.....S.....D A.....N.....LF.....
.....G.....D A.....N.....LF.....K.....
.....G.....D A.....N.....LF.....K.....
.....S.....L D A.....K.....LF.....
.....G.....D A.....N.....LF.....K.....
.....G.....EL G.....N.....LF.....K.....
.....G.....D.....D.....LF.....

741

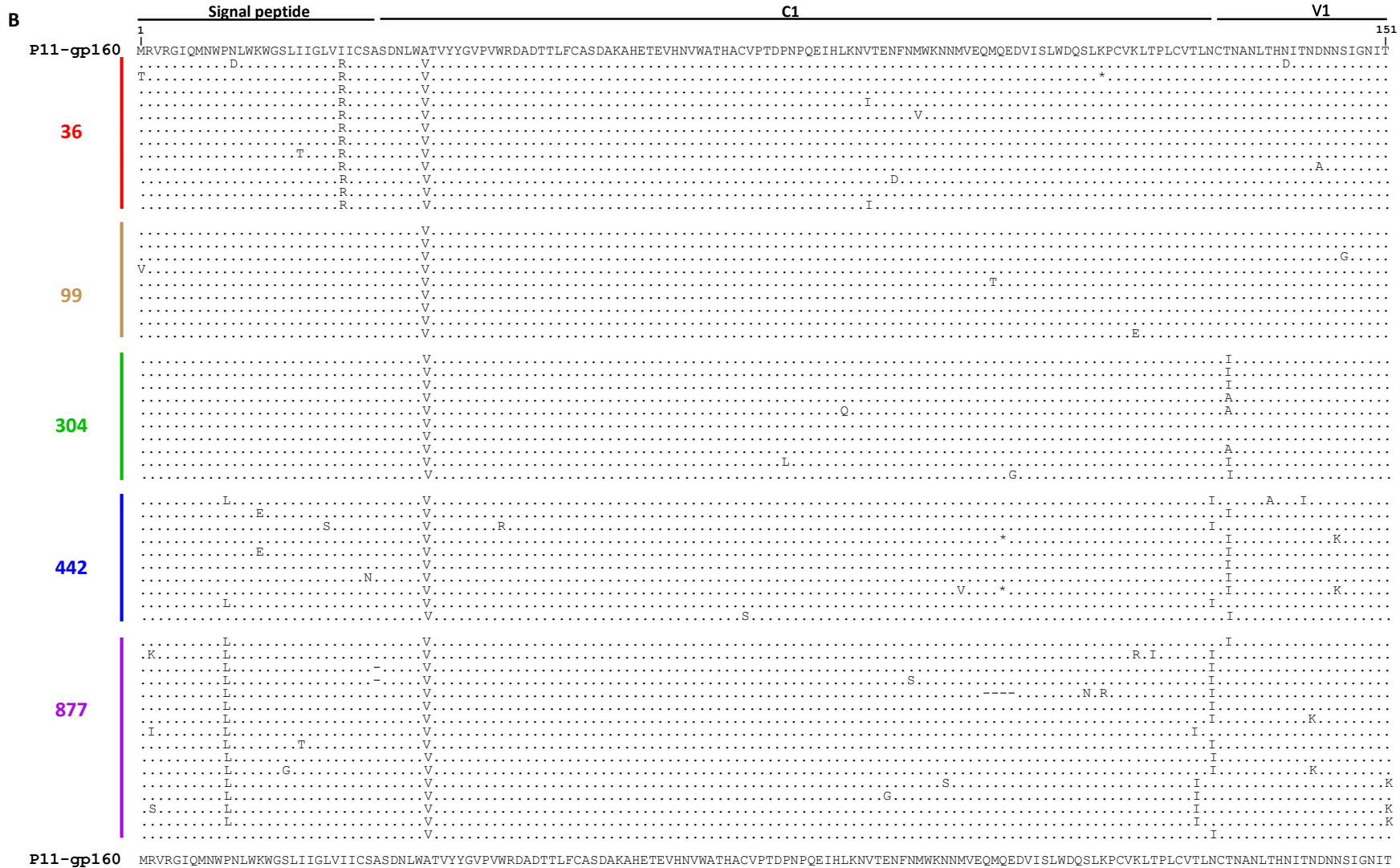
.....K.....L.....F Q.....
.....DK.....G.....N.....D A.....R.....D.....K.....LF R.....
.....K.....D A.....R.....D.....D.....LF.....
.....E.....D A.....T.....D.....K.....LF.....
.....G.....E.....L D A.....R.....D.....K.....LF.....G.....
.....E.....D.....D.....D.....FF.....
.....G.....L.....D.....D.....F Q.....
.....G.....E.....L D A.....T.....N.....L.....LF.....

P08-gp160

WNSTWSNKSYYEIIWDMNTWIQWEKEISNYTDQIYSLLETESQNQQEKNKDLLELDKASLWNNWFSITNWLWYIKIFIMIVGGIIGLRIFAVLSIVNRVRQGYSPSLQTPHHPDRPEGIEEGEGEQGRNRSVRLVSGFLALAWDD







**Figure S2**

	V2	C2	Loop D
	152		301
<b>P11-gp160</b>	DEVKNCIFNMTTEIRGKLQKVYALFSTLDIVHMGNDSEYRLISCNTSVIKQACPKISFDPIPIHYCAPAGYVILKCNDRKFKNGTGPCKNVSTVQCTHGIRKPVVSTQLLNGSLAEEGIIISSENLTNNAKTIIVHLNKSVKINCTRPSN		
<b>36</b>	.....P..... .....R.....Y..... .....S.....G.....S..... .....R.....Y.....		
<b>99</b>	.....A.....I..... .....D.....A..... .....VR.....		
<b>304</b>	.....R.....L.....*.....A.....R..... .....D.....A..... .....D.....A..... .....D.....D.....I.....D..... .....D.....R.....S.....		
<b>442</b>	.....M.....N.....F..... .....A.....R.....E.....R..... .....C.....R.....A..... .....A.....I..... .....R.....		
<b>877</b>	.....R.....I.....*.....G.....D.....M.....F..... .....M.....R.....I.....D.....F..... .....K.....R.....P.....ID.....F..... .....R.....R.....I.....D.....F..... .....Q.....R.....R.....V.....R..... .....S.....D.....F..... .....L.....D.....F..... .....L.....D.....F..... .....Q.....V.....---.....D.....F..... .....S.....T.....D.....F..... .....S.....D.....F..... .....S.....A.....D.....F..... .....S.....D.....F..... .....S.....G.....I.....D.....F.....		
<b>P11-gp160</b>	DEVKNCIFNMTTEIRGKLQKVYALFSTLDIVHMGNDSEYRLISCNTSVIKQACPKISFDPIPIHYCAPAGYVILKCNDRKFKNGTGPCKNVSTVQCTHGIRKPVVSTQLLNGSLAEEGIIISSENLTNNAKTIIVHLNKSVKINCTRPSN		

	V3	C3 CD4 binding loop	V4	C4
	302			459
<b>P11-gp160</b>	NTRTSIRIGPGQMFYRTGDIIGDIRKAYCEINGTEWNETLNQVTEKLLKHFNKTIIFQPPSGGDLETTTHHFNCRGEFFYCNTTKLFNSKELNAT-----IILPCRIKQIVNMWQGVGQAMYPISGIINCSINITGILLTRDGG			
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<b>P11-gp160</b>	NTRTSIRIGPGQMFYRTGDIIGDIRKAYCEINGTEWNETLNQVTEKLLKHFNKTIIFQPPSGGDLETTTHHFNCRGEFFYCNTTKLFNSKELNAT-----IILPCRIKQIVNMWQGVGQAMYPISGIINCSINITGILLTRDGG			

**P11-gp160** ISNATNET--FRPGGNIKDNWRSELYKYKVVQLEPLGIAPTRARRRVVDREKRAVGIGTMIFGFLGAAGSTMGAASITLTVQARQLLSGIVQQSNLLRAIEAQQRMLQLTVWGIKQLQARVLAVERYLKDQRFGLWGCSGKIICTTN

**36** .....T.....T.....R.....M.....N.....V.....A.....

**99** .....\*.....E.R.I.....S.....V.....E.R.I.....E.R.I.....A.....E.R.I.....S.....A.....E.R.I.....E.R.I.....E.R.I.....E.R.I.....E.R.I.....E.R.I.....E.R.I.....

**304** .....A.....K.....S.....A.....P.....C.....M.....\*.....

**442** .....I.....A.....A.....S.....K.....A.....A.....A.....A.....A.....L.....T.....S.....A.....A.....A.....

**877** .....V.D.....S.....I.....I.....A.....E.....V.D.....G.....I.....I.....A.....A.....A.....A.....P.....A.....K.....V.D.....A.....A.....A.....A.....A.....I.....I.....I.....I.....A.....Y.....AET.....I.....A.....A.....ET.....I.....A.....P.....A.....V.....ET.....I.....N.....A.....ET.....E.....I.....A.....ET.....I.....A.....

**P11-gp160** ISNATNET--FRPGGNIKDNWRSELYKYKVVQLEPLGIAPTRARRRVVDREKRAVGIGTMIFGFLGAAGSTMGAASITLTVQARQLLSGIVQQSNLLRAIEAQQRMLQLTVWGIKQLQARVLAVERYLKDQRFGLWGCSGKIICTTN



P11-gp160

DDLRSCLCFSYRRLRDFILIATRVELLGGKLRGWEGLKYLGNLLYWGQELKTSAISLLNAIAITTAEWTDREVIEVAQLAWRALLHIPRRIRQGFERALL

36

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.....*.....
.....G.....L.....
.....*.....

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99

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.....T.....D.....
.....T.G.....P.....D.....
.....T.R.....R.....D.....
.....T.....R.....D.....
.....T.....D.....
.....T.....D.....
.....R.....D.....

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304

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.....L.....
.....S.....
.....T.....P.....
.....G.....

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442

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.....G.....

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877

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.....R.....R.....
.....N.....F.....
.....K.....F.....
.....N.T.....F.....
.....R.....R.....F.....
.....P.....

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P11-gp160

DDLRSCLCFSYRRLRDFILIATRVELLGGKLRGWEGLKYLGNLLYWGQELKTSAISLLNAIAITTAEWTDREVIEVAQLAWRALLHIPRRIRQGFERALL

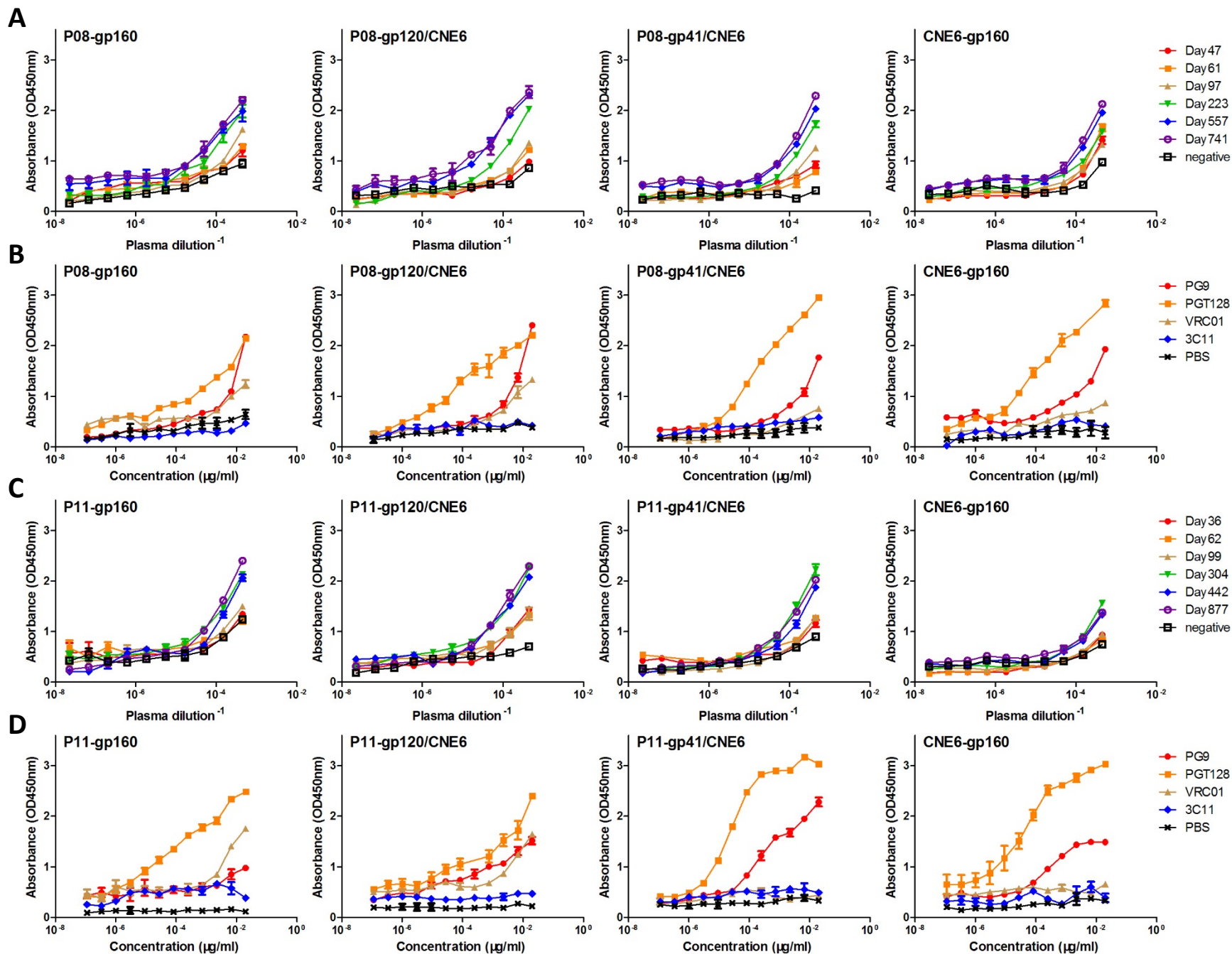
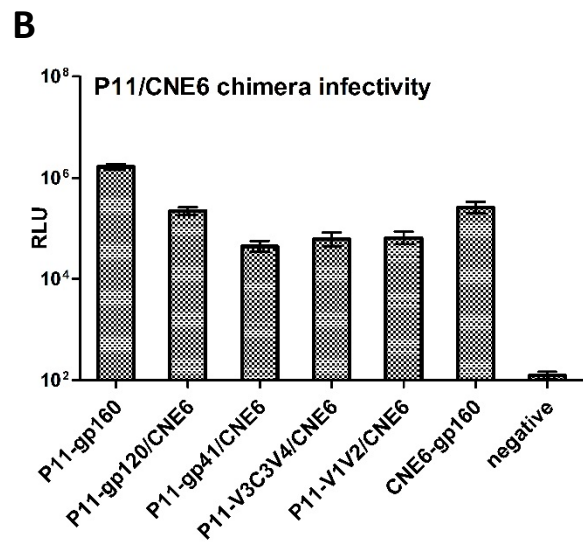
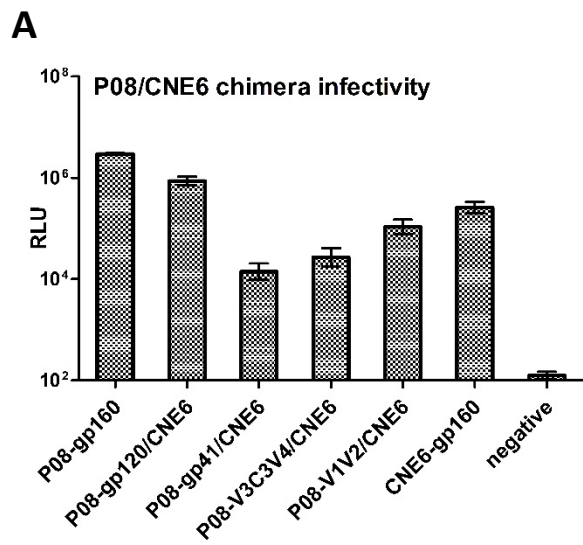


Figure S3



**Figure S4**