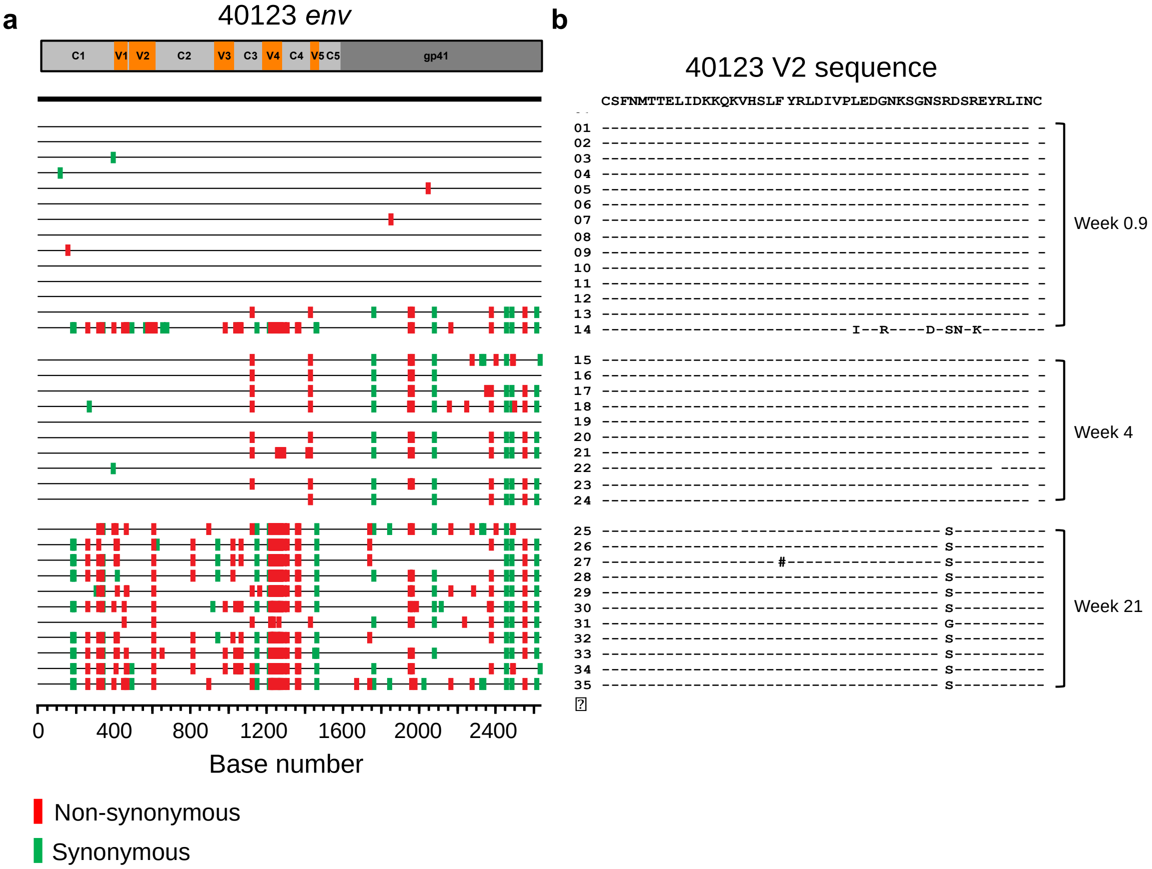


Figure S1. Longitudinal *env* and V2 sequences in participant 40123 at weeks 0.9, 4, and 21 post-infection. (**a**) Highlighter plot of HIV-1 *env* sequences from participant 40123 with changes from the consensus sequence (black line on the top represents the inferred T/F sequence at week 0) demarcated by red (synonymous) or green (non-synonymous) vertical markers. The V2 region is indicated by the vertical orange bar. (**b**) Sequence alignment of the HIV-1 Env V2 protein sequence from ~10 single-genome amplification (SGA) sequences for each time point. Sequence variation are indicated by the newer variant amino acid letter. The symbol "#" indicates frameshift mutation.

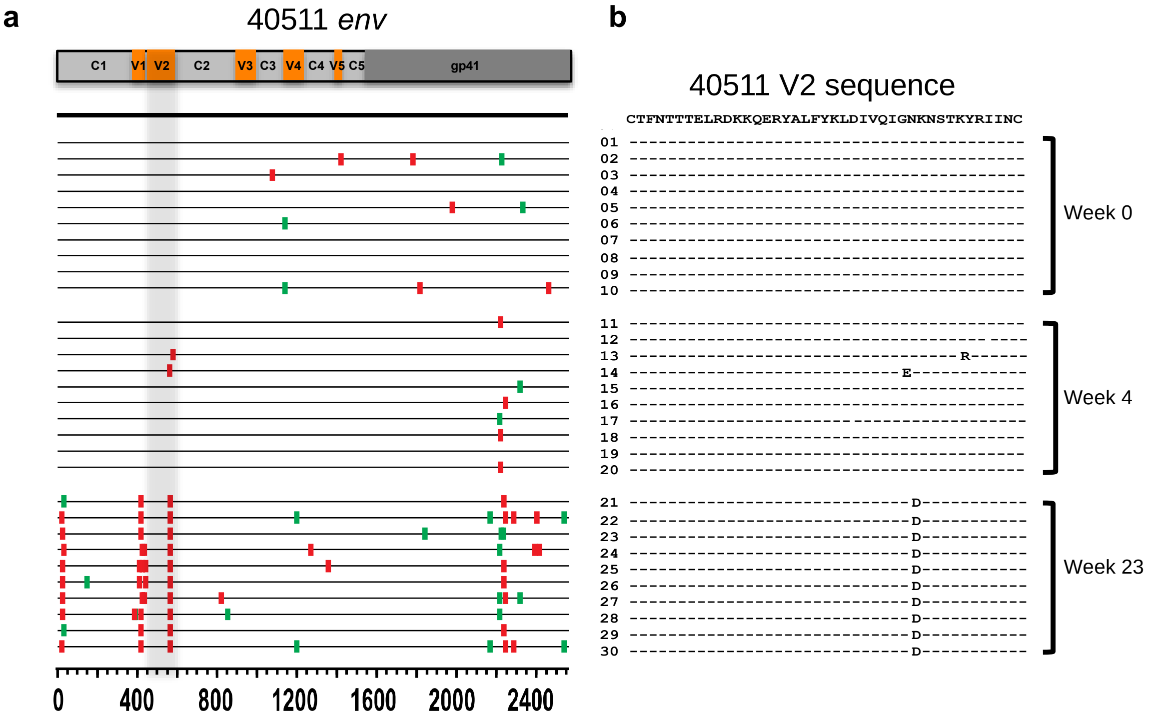


Figure S2. Longitudinal *env* and V2 sequences in participant 40511 at weeks 0, 4, and 23 post-infection. (**a**) Highlighter plot of HIV-1 *env* sequences from participant 40511 with changes demarcated by red (synonymous) or green (non-synonymous) vertical markers. The black line on the top represents the consensus sequence from week 0 (the inferred T/F sequence). The V2 region is indicated by the vertical orange bar. (**b**) Sequence alignment of the HIV-1 Env V2 protein sequence from ~10 single-genome amplification (SGA) sequences for each time point. Sequence variation is indicated by the newer variant amino acid letter.

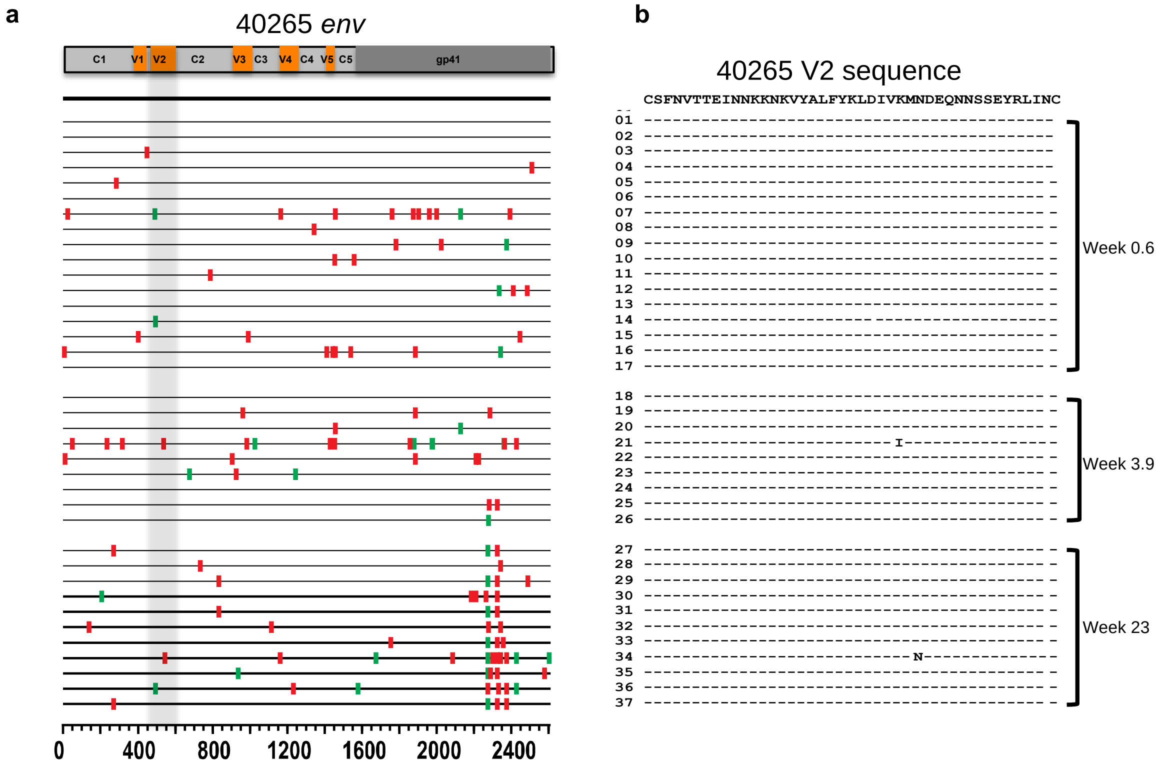
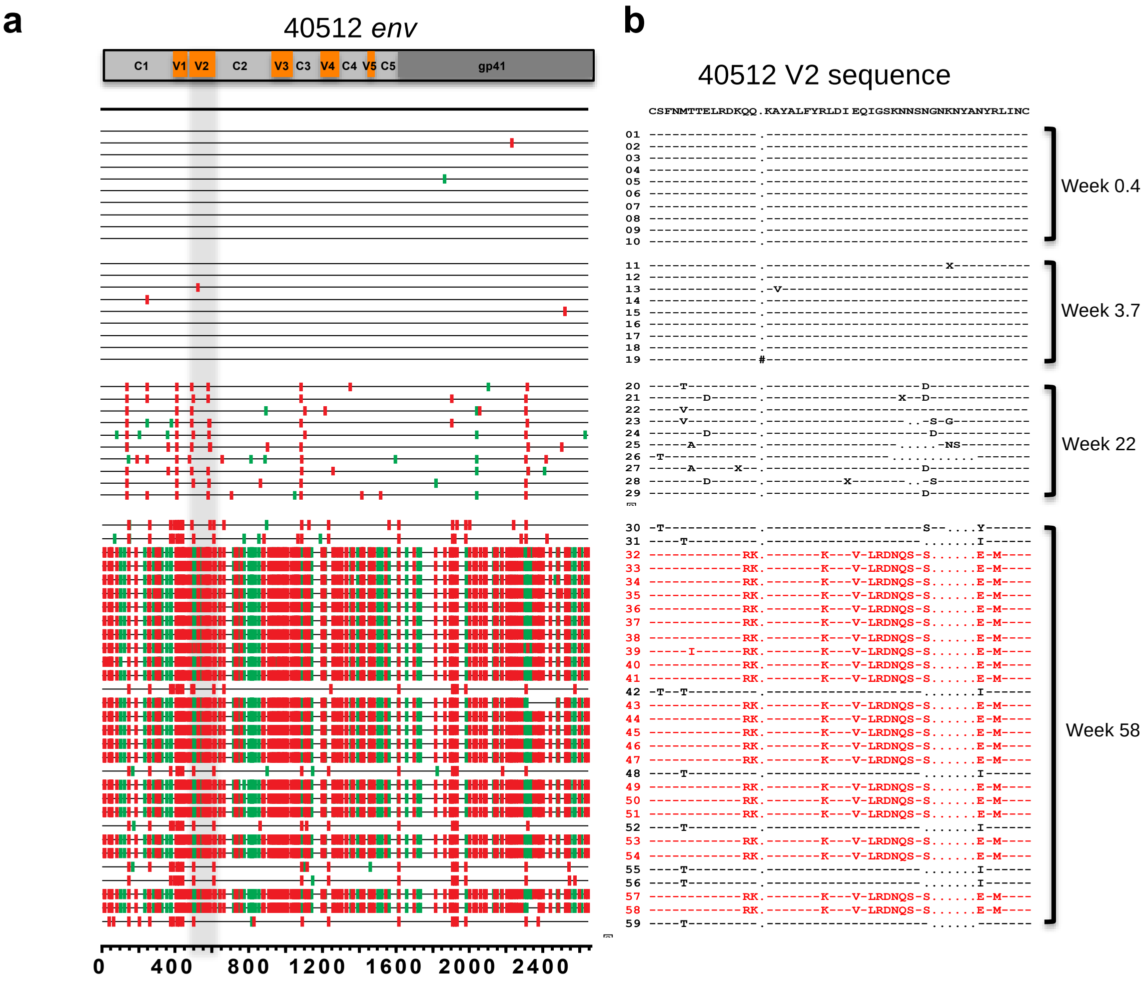


Figure S3. Longitudinal *env* and V2 sequences in participant 40265 at weeks 0.6, 3.9, and 23 post-infection. (**a**) Highlighter plot of HIV-1 *env* sequences from participant 40265 with changes from the consensus sequence (black line on the top represents the inferred T/F sequence at week 0) demarcated by red (synonymous) or green (non-synonymous) vertical markers. The V2 region is indicated by the vertical orange bar. (**b**) Sequence alignment of the HIV-1 Env V2 protein sequence from ~10 single-genome amplification (SGA) sequences for each time point. Sequence variation is indicated by the newer variant amino acid letter.



```
   CSFNMTTELRDKQQ.KAYALFYRLDI EQIGSKNNSNGNKNYANYRLINC
01 --------------.----------------------------------
02 --------------.----------------------------------
03 --------------.----------------------------------
04 --------------.----------------------------------
05 --------------.----------------------------------
06 --------------.----------------------------------
07 --------------.----------------------------------
08 --------------.----------------------------------
09 --------------.----------------------------------
10 --------------.----------------------------------

11 --------------.-----------------------X----------
12 --------------.----------------------------------
13 --------------.-V--------------------------------
14 --------------.----------------------------------
15 --------------.----------------------------------
16 --------------.----------------------------------
17 --------------.----------------------------------
18 --------------.----------------------------------
19 --------------#----------------------------------

20 ----T---------.---------------------D-------------
21 -------D------.------------------X--D-------------
22 ----V---------.----------------------------------
23 ----V---------.------------------..-S-G----------
24 -------D------.----------------------D------------
25 -----A--------.-----------------.....-NS---------
26 -T------------.----------------..........-------
27 -----A-----X--.---------------------D-------------
28 -------D------.-----------X-------..-S------------
29 --------------.---------------------D-------------

30 -T------------.---------------------S--....Y------
31 ----T---------.--------------------.......I------
32 ------------RK.--------K---V-LRDNQS-S......E-M----
33 ------------RK.--------K---V-LRDNQS-S......E-M----
34 ------------RK.--------K---V-LRDNQS-S......E-M----
35 ------------RK.--------K---V-LRDNQS-S......E-M----
36 ------------RK.--------K---V-LRDNQS-S......E-M----
37 ------------RK.--------K---V-LRDNQS-S......E-M----
38 ------------RK.--------K---V-LRDNQS-S......E-M----
39 -----I------RK.--------K---V-LRDNQS-S......E-M----
40 ------------RK.--------K---V-LRDNQS-S......E-M----
41 ------------RK.--------K---V-LRDNQS-S......E-M----
42 -T--T---------.--------------------.......I------
43 ------------RK.--------K---V-LRDNQS-S......E-M----
44 ------------RK.--------K---V-LRDNQS-S......E-M----
45 ------------RK.--------K---V-LRDNQS-S......E-M----
46 ------------RK.--------K---V-LRDNQS-S......E-M----
47 ------------RK.--------K---V-LRDNQS-S......E-M----
48 ----T---------.--------------------.......I------
49 ------------RK.--------K---V-LRDNQS-S......E-M----
50 ------------RK.--------K---V-LRDNQS-S......E-M----
51 ------------RK.--------K---V-LRDNQS-S......E-M----
52 ----T---------.--------------------.......I------
53 ------------RK.--------K---V-LRDNQS-S......E-M----
54 ------------RK.--------K---V-LRDNQS-S......E-M----
55 ----T---------.--------------------.......I------
56 ----T---------.--------------------.......I------
57 ------------RK.--------K---V-LRDNQS-S......E-M----
58 ------------RK.--------K---V-LRDNQS-S......E-M----
59 ----T---------.---------------------......-------
```

Figure S4. Longitudinal *env* and V2 sequences in participant 40512 at weeks 0.4, 3.7, 22 and 58 post-infection. (**a**) Highlighter plot of HIV-1 *env* sequences from participant 40512 with changes demarcated by red (synonymous) or green (non-synonymous) vertical markers. The black line on the top represents the consensus sequence from week 0 (i.e., the inferred T/F sequence). At week 58, a super-infecting strain was firstly detected and dominated the viral population. The V2 region is indicated by the vertical orange bar. (**b**) Sequence alignment of the HIV-1 Env V2 protein sequence from ~10 single-genome amplification (SGA) sequences for each time point. Sequence variation are indicated by the newer variant amino acid letter, and deletions are indicated by dots. The super-infecting viral lineage is highlighted in red. The symbol "#" indicates frameshift mutation and "x" indicates ambiguous codon.