

Analysis of HIV-1 envelope evolution suggests antibody-mediated selection of common epitopes among Chinese former plasma donors from a narrow-source outbreak

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1 SUPPLEMENTARY INFORMATION

2 Supplementary Figures

Figure S1A

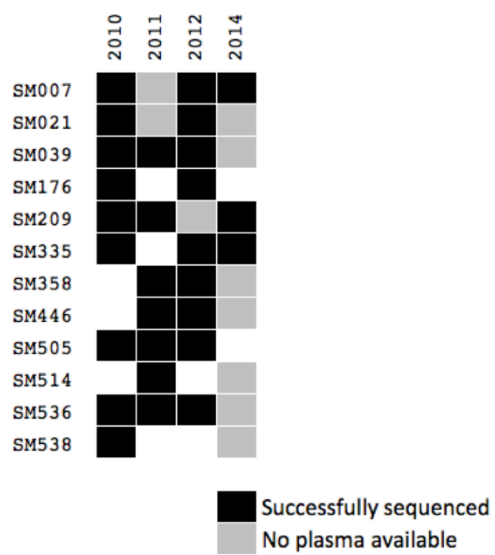
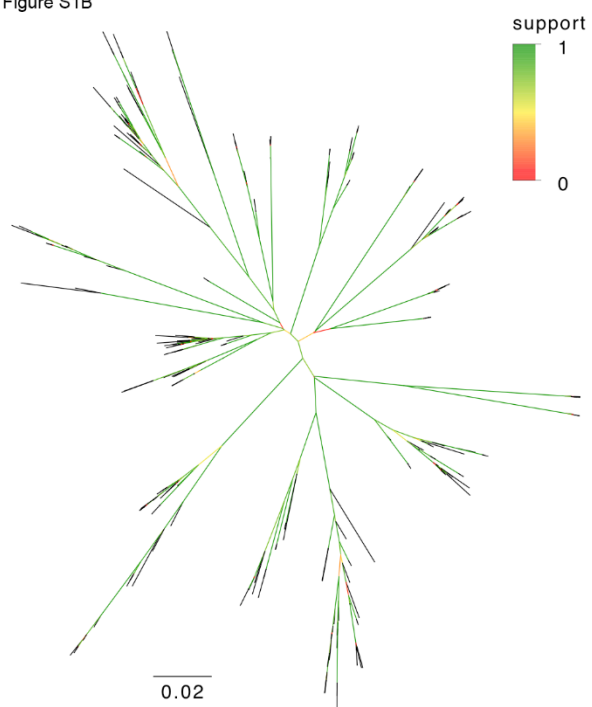


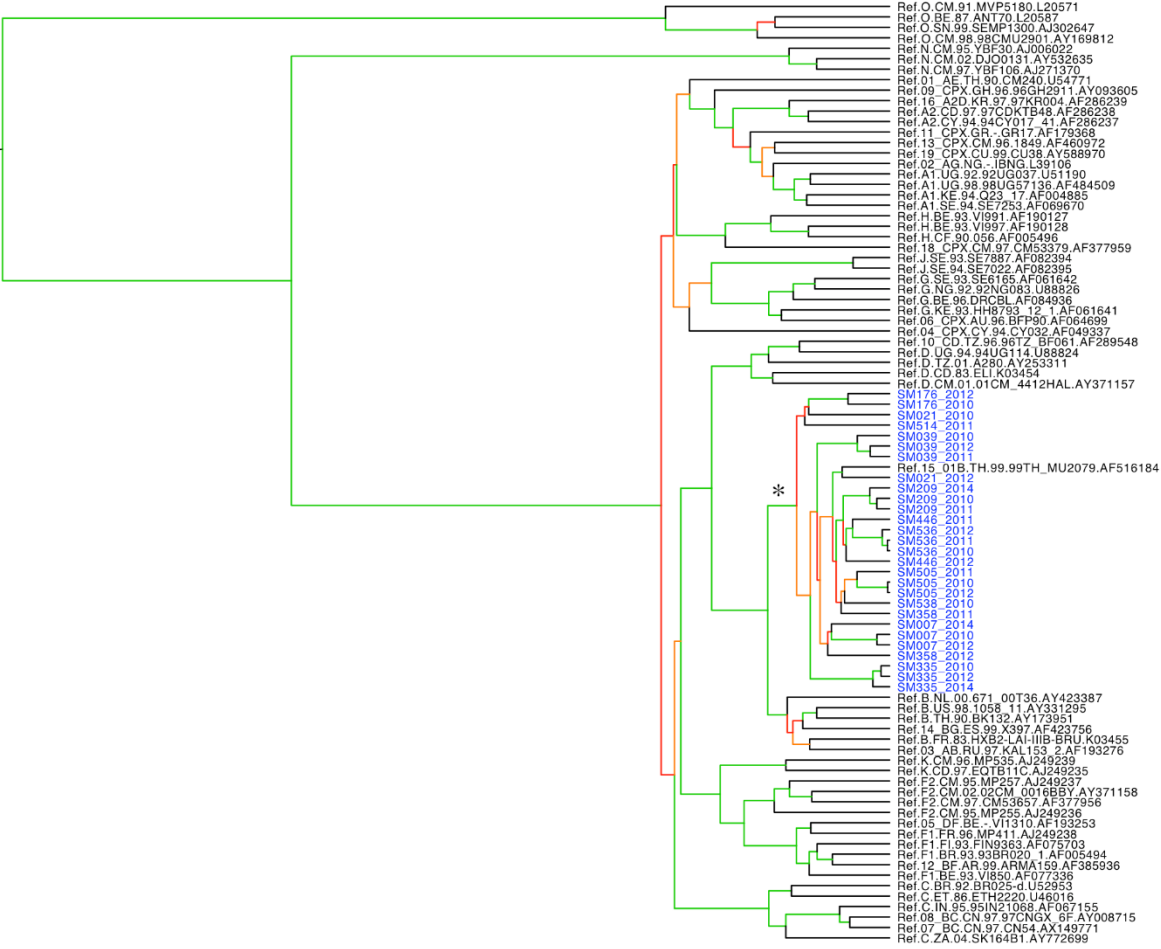
Figure S1B



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Figure S1C



1 **Supplementary Figure legends**

2 **Figure S1. Cohort characterisation. A)** PCR sequencing success for the samples available.

3 Successfully sequenced samples are shown in black, and failed samples are shown in white.

4 Samples shown in grey were unavailable. **B)** Maximum likelihood phylogenetic tree of

5 sequences obtained. Branch support is indicated by colour, as defined by the internal key. The

6 star-like shape of the phylogeny with short internal branches supports the narrow-source origin

7 of the cohort.

8

9 **Figure S2. Subtyping.** Phylogenetic subtyping of SM cohort viral sequences represented as a

10 midpoint-routed maximum clade credibility (MCC) tree of inpatient consensus sequences

11 (blue) aligned to the 2005 LANL *gp120* reference dataset (black). Branch support: ≥ 0.95

12 green; ≥ 0.75 orange; < 0.75 red. Support for the node associating all SM cohort sequences

13 with CRF 15-01B (marked with an asterisk) is 1.

1 **Supplementary Tables**

2 **Table S1. Primers used in the amplification and sequencing of the HIV-1 *env* gp120 fragment.**

Name	Sequence	Target	Corresponding to HIV-1 HXB2 (K03455)
FPD_Env_OF	AAAGAGCAGAAGACAGTGGCAATG	HIV-1 gp120	HXB2 6204-6227
FPD_ENV_OR	AGCCTCCTACTAYCATTATGAAT	HIV-1 gp120	HXB2 8276-8298
FPD_ENV_IF	CGGCTGGTTTTGCGATTCTA	HIV-1 gp120	HXB2 6883-6902
FPD_ENV_IR	TATTTATATAATTCACCTTCTCCA	HIV-1 gp120	HXB2 7659-7681
M13F	GTAAAACGACGGCCAG	pCR®4-TOPO	355-370
M13R	CAGGAAACAGCTATGAC	pCR®4-TOPO	205-221

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