

Patient	Total no. of Env SGA sequences	Mean genetic diversity (%)	Viral load (log10 copies/mL)	Time since MRCA (days)	Fiebig stage	Clinical stage of infection
FO	25	0.004	6.9	78	Fiebig IV	Acute infection
MP	26	0.001	7.0	12	Fiebig IV	Acute infection
CO	22	0.001	5.3	35	Fiebig VI	Acute infection
XE	20	0.004	6.7	68	Fiebig IV	Acute infection
PU	30	0.031	4.0			Chronic infection

**Supplemental Digital Content 1. Composition, diversity and time since MRCA of the *env* sequences derived from SGA and the characteristics of selected patients**