Table S1. Longitudinal sequence analysis of virus isolated from individual R880F

Epitope	Day12[a]	Day73[b]		Day157[b]		Day241[b]		Day323[b]	
Gag 17-34	EKIRLRPGGKKKYRMKHL	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Gag 85-95	LYCVHQRIEVK	----------- --W--------	90% 10%	----------- -------M---	67% 33%	-----------	100%	----------- -------M---	86% 14%
Gag 140-157	GQMIHQPLSPRTLNAWVK	------------------	100%	------------------	100%	------------------ ------S-----------	83% 17%	------------------	100%
Pol 417-434	GKLNWASQIYPGIKVKQL	------------------	100%	------------------ -----------R------ --------------I---	33.3% 33.3% 33.3%	-------------Q---- --------------I--- ---K---------QI---	66% 17% 17%	-------------Q---- ------G------Q---- -------------QI---	72% 14% 14%
Pol 425-442	IYPGIKVKQLCKLLRGTK	------------------	100%	------------------ ---R-------------- ------I-----------	33.3% 33.3% 33.3%	-----Q------------ ------I----------- -----QI-----------	66% 17% 17%	-----Q------------ -----QI-----------	86% 14%
Pol 817-826	LKLAGRWPVK	----------	100%	----------	100%	----------	100%	----------	100%
Pol 969-986	NSDIKVVPRRKAKIIRDY	------------------ -----I------------	90% 10%	------------------	100%	------------------ -----I------------ --E--------V------	60% 20% 20%	------------------	100%
Pol 977-994	RRKAKIIRDYGKQMAGDD	------------------	100%	------------------	100%	------------------ ---V--------------	80% 20%	------------------	100%
Pol 985-1002	DYGKQMAGDDCVAGRQDE	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Env 350-368	GEYFKNKTITFNSSSGGD	------------------	100%	------------------	100%	------------------ ----R-------------	91% 9%	----R------------- ------------------	60% 40%
Env 815-823	VDTIAIAVA	--------- ------T--	80% 20%	-N------- --------- -N----T-- -E------- ---T-----	46% 33% 7% 7% 7%	—N------- --------- ------T-- ------V--	45% 27% 18% 9%	N-------- ------T--	73% 27%
Rev 11-21	ELLRAIRIIKI	-----------	100%	---K------- -----------	67% 33%	---K------- -----------	82% 18%	---K-------	100%
Vif 25-42	VKHHMYVSKRAKRWFYRH	------------------	100%	------------------ ---Q--------------	67% 33%	------------------ -----H------------ ------A-----------	75% 17% 8%	--------R--------- -----H------------ ------I----------- ------------------	64% 18% 9% 9%
Nef 177-194	EREVLKWKFDSRLALKHL	-------R---------- ----------C-------	90% 10%	-------R----------	100%	-------R---------- ----------CH-F----	91% 9%	-------R---------- -------R-----F----	56% 44%

[a] Epitope Amino acid sequence in the autologous virus at the earliest timepoint available for analysis (10 days post-Fiebig I/II)

[b] The proportion of viral genomes sequenced that retained the founder virus epitope sequence (indicated by dashes) or the mutant versions thereof at the indicated time-points (days post-Fiebig I/II)