Table S2 - Longitudinal sequence analysis of virus isolated from individual R463F

Epitope	Day 12[a]		Day 19[b]		Day 60[b]		Day 179[b]		Day 248[b]		Day 333[b]	
Gag 132-149	YPVVQNAQGQWVHQNFSP		------------------	100%	------------------	100%	-----------A------ -----------I------	87.5% 12.5%	-----------A------ ---------H-------- ------------P----- --------------H---	37.5% 37.5% 12.5% 12.5%	-----------A------ ---------H-------- -----------I------ -----------T------	44% 33% 11% 11%
Gag 140-157	GQWVHQNFSPRTLNAWVK		------------------	100%	------------------	100%	---A-------------- ---I--------------	87.5% 12.5%	---A-------------- -H---------------- ----P------------- ------H-----------	37.5% 37.5% 12.5% 12.5%	---A-------------- -H---------------- ---I-------------- ---T--------------	44% 33% 11% 11%
Gag 292-309	PFRDYVDRFFKTLRAEQA		------------------	100%	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Gag 381-398	GNFKGQRKIKCFNCGKE		------------------	100%	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Pol 409-426	VNDIQKLVGKLNWASQIY		------------------	100%	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Pol 417-434	GKLNWASQIYAGIKVKQL		------------------	100%	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Pol 897-914	IHNFKRKGGIGGYSAGER		------------------	100%	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Pol 929-946	QKQITKIHKFRVYYRDSR		------------------	100%	------------------	100%	------------------	100%	------------------	100%	------------------	100%
Pol 969-986	NNDIKVVPRRKAKIIRDY		------------------	100%	------------------	100%	------------------ -----------V------ ----------------E-	75% 12.5% 12.5%	------------------ --------X---------	87.5% 12.5%	------------------ -----------V------ K----------V------ ----------------N-	55% 22% 11% 11%
Pol 977-994	RRKAKIIRDYGKQMAGD		------------------	100%	------------------	100%	----------------- ---V------------- --------E--------	75% 12.5% 12.5%	----------------- X----------------	87.5% 12.5%	----------------- ---V------------- --------N--------	55% 33% 11%
Pol 985-1002	DYGKQMAGDDCVAGRQDE		------------------	100%	------------------ --------------G---	87.5% 12.5%	------------------ E-----------------	87.5% 12.5%	------------------	100%	------------------ N----------------- ----------M-------	78% 11% 11%
Env 1-15	MRVMGTQMNYQNLWRWGI		------------------	100%	------------------	100%	------------------ ---------C-------- -----I------------	63% 25% 12%	------------------ -K---------------- ---------C-------- ---T--------------	50% 25% 12.5% 12.5%	-K---------------- ---------C--------	78% 22%
Env 334-351	SKAEWNETVRRVAEQLEK		------------------	100%	------------------	100%	------------------ -----K------------ --------G---------	67% 22% 11%	-----------------N ---I-K-----------E	75% 25%	-----------------N -Q------G--------N	91% 9%
Env342-360	VRRVAEQLEKYFKNKTIK		------------------	100%	------------------	100%	------------------ -----K------------ --------G---------	62.5% 25% 12.5%	-----------------N ---I-K-----------E ------------------	50% 37.5% 12.5%	-----------------N —Q------G--------N	89% 11%
Env 402-420	TVNATRSENDTINLPCRI		------------------	100%	------------------	100%	------------------	100.0%	------------------	100%	------------------ ------------T----- ------------S-----	44.5% 44.5% 11%
Tat 33-50	HCLVCFQHKGLGISYGRK -----------D------	90% 10%	-------R---------- -----------S------ ------------------ -----------D------ -----------V------ --------------H--- -------R------H---	36% 21% 14% 7% 7'% 7% 7%	-------S---------- --------------H--- -------L---------- -------N----------	62.5% 12.5% 12.5% 12.5%	-------N---------- -------L---------- -------S----------	37.5% 37.5% 25%	-------N---------- -------L----------	75% 25%	-------N---------- -------L---------- -------S----------	45% 33% 22%
Nef 177-194	EGETLQWKFDSYLAFKHI		------------------	100%	------------------ -------E---------- -------T---------- -------R----------	37.5% 37.5% 12.5% 12.5%	-------R---------- -------T----------	87.5% 12.5%	-------R---------- -----R-R---------- -----K------------	37.5% 37.5% 25%	-----R-R----------	100%

[a] Epitope Amino acid sequence in the autologous virus at the earliest time-point available for analysis (3 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)