

Supplemental Table 3. Ebola virus quasiespecies

12 hpi Vero									
Genome position*	Designation	A	C	G	T	Change	% of minor variant	Type of change	Amino acid
1974	NP ORF	0	3546	0	856	C/T	19%	subst_NONSYNONYMOUS[TcG:S TtG:L U]**	502
3618	VP35 ORF	836	0	2654	1	G/A	24%	subst_NONSYNONYMOUS[GCC:A aCC:T c]	164
5219	VP40 ORF	0	564	0	1660	T/C	25%	subst_synonymous[TTT:F TTc:F c]	247
7213	GP ORF	2	2040	0	133	C/T	6%	subst_NONSYNONYMOUS[CCG:P CtG:L U]	392
7668	GP ORF	0	1831	0	587	C/T	24%	subst_NONSYNONYMOUS[TAG: cAG:Q U]	544
7691	GP ORF	832	0	1272	0	G/A	40%	subst_synonymous[AAG:K AAa:K c]	551
7706	GP ORF	100	0	2176	0	G/A	4%	subst_synonymous[GTG:V GTa:V c]	556
10866	VP24 ORF	483	0	158	0	A/G	25%	subst_synonymous[GGA:G GGg:G c]	174
24 hpi Vero									
Genome position	Designation	A	C	G	T	Change	% of minor variant	Type of change	Amino acid
1974	NP ORF	5	14182	5	3549	C/T	20%	subst_NONSYNONYMOUS[TcG:S TtG:L U]	502
3618	VP35 ORF	4339	2	13126	2	G/A	25%	subst_NONSYNONYMOUS[GCC:A aCC:T c]	164
5219	VP40 ORF	1	6034	1	16690	T/C	27%	subst_synonymous[TTT:F TTc:F c]	247
7213	GP ORF	3	26121	2	1600	C/T	6%	subst_NONSYNONYMOUS[CCG:P CtG:L U]	392
7668	GP ORF	3	22322	6	7661	C/T	26%	subst_NONSYNONYMOUS[TAG: cAG:Q U]	544
7691	GP ORF	10777	2	15988	4	G/A	40%	subst_synonymous[AAG:K AAa:K c]	551
7706	GP ORF	1300	3	27939	1	G/A	4%	subst_synonymous[GTG:V GTa:V c]	556
10866	VP24 ORF	4375	1	1397	0	A/G	24%	subst_synonymous[GGA:G GGg:G c]	174
12 hpi Thp1									
Genome position	Designation	A	C	G	T	Change	% of minor variant	Type of change	Amino acid
1974	NP ORF	0	878	1	188	C/T	18%	subst_NONSYNONYMOUS[TcG:S TtG:L U]	502
3618	VP35 ORF	145	0	452	0	G/A	24%	subst_NONSYNONYMOUS[GCC:A aCC:T c]	164
5219	VP40 ORF	0	153	0	406	T/C	27%	subst_synonymous[TTT:F TTc:F c]	247
7213	GP ORF	0	1299	1	85	C/T	6%	subst_NONSYNONYMOUS[CCG:P CtG:L U]	392
7668	GP ORF	0	391	0	119	C/T	23%	subst_NONSYNONYMOUS[TAG: cAG:Q U]	544
7691	GP ORF	168	0	254	0	G/A	40%	subst_synonymous[AAG:K AAa:K c]	551
10866	VP24 ORF	123	0	27	0	A/G	18%	subst_synonymous[GGA:G GGg:G c]	174
24 hpi Thp1									
Genome position	Designation	A	C	G	T	Change	% of minor variant	Type of change	Amino acid
1974	NP ORF	0	9385	3	2131	C/T	18%	subst_NONSYNONYMOUS[TcG:S TtG:L U]	502
3618	VP35 ORF	1776	0	5977	0	G/A	23%	subst_NONSYNONYMOUS[GCC:A aCC:T c]	164
5219	VP40 ORF	0	2242	1	7187	T/C	24%	subst_synonymous[TTT:F TTc:F c]	247
7213	GP ORF	5	32325	16	1937	C/T	6%	subst_NONSYNONYMOUS[CCG:P CtG:L U]	392
7668	GP ORF	0	8288	0	2810	C/T	25%	subst_NONSYNONYMOUS[TAG: cAG:Q U]	544
7691	GP ORF	3430	3	5992	2	G/A	36%	subst_synonymous[AAG:K AAa:K c]	551
7706	GP ORF	493	1	9929	1	G/A	5%	subst_synonymous[GTG:V GTa:V c]	556
10866	VP24 ORF	2127	0	640	1	A/G	23%	subst_synonymous[GGA:G GGg:G c]	174

*MAIN gi|10313991|ref|NC_002549.1| Ebola virus - Mayinga, Zaire, 1976 strain Mayinga:

**ORF type of change example; "subst_NONSYNONYMOUS[GAG:E GAt:D c]" the substitution is nonsynonymous where the codon of the reference strain GAG (codes for E=glutamic acid) is changed to GAT (codes for D=aspartic acid) and the lower case c indicates this is a conservative substitution.