

Supplemental Table 4. Marburg virus quasispecies

12 hpi Vero									
Genome position*	Designation	A	C	G	T	Change	% of minor variant	Type of change	Amino acid
2590	NP 3'-UTR	0	39	0	580	T/C	6%	3'-UTR +398**	
2598	NP 3'-UTR	0	36	0	554	T/C	6%	3'-UTR +406	
2640	NP 3'-UTR	0	39	0	439	T/C	8%	3'-UTR +448	
2643	NP 3'-UTR	0	40	0	440	T/C	8%	3'-UTR +451	
2663	NP 3'-UTR	0	40	0	457	T/C	8%	3'-UTR +471	
2834	NP 3'-UTR	78	0	27	0	A/G	26%	3'-UTR +642	
2836	NP 3'-UTR	0	11	0	39	T/C	22%	3'-UTR +644	
3400	VP35 ORF	660	0	0	76	A/T	10%	subst_NONSYNONYMOUS[TTA:L TTt:F c]***	152
4283	VP35 3'-UTR	0	27	0	243	T/C	10%	3'-UTR +348	
24 hpi Vero									
Genome position*	Designation	A	C	G	T	Change	% of minor variant	Type of change	Amino acid
2590	NP 3'-UTR	0	687	0	8164	T/C	8%	3'-UTR +398	
2598	NP 3'-UTR	1	674	0	7755	T/C	8%	3'-UTR +406	
2640	NP 3'-UTR	0	704	1	5946	T/C	11%	3'-UTR +448	
2643	NP 3'-UTR	1	699	1	5968	T/C	10%	3'-UTR +451	
2663	NP 3'-UTR	0	800	1	6101	T/C	12%	3'-UTR +471	
2724	NP 3'-UTR	1	926	0	8981	T/C	9%	3'-UTR +532	
2822	NP 3'-UTR	0	566	0	5349	T/C	10%	3'-UTR +630	
2824	NP 3'-UTR	2	568	1	5080	T/C	10%	3'-UTR +632	
2834	NP 3'-UTR	947	0	224	0	A/G	19%	3'-UTR +642	
2836	NP 3'-UTR	0	108	0	350	T/C	24%	3'-UTR +644	
3400	VP35 ORF	9126	6	6	2038	A/T	18%	subst_NONSYNONYMOUS[TTA:L TTt:F c]	152
4283	VP35 3'-UTR	1	346	0	3801	T/C	8%	3'-UTR +348	
24 hpi Thp1									
Genome position*	Designation	A	C	G	T	Change	% of minor variant	Type of change	Amino acid
2590	NP 3'-UTR	0	173	0	1745	T/C	9%	3'-UTR +398	
2598	NP 3'-UTR	0	165	0	1627	T/C	9%	3'-UTR +406	
2640	NP 3'-UTR	0	141	0	779	T/C	15%	3'-UTR +448	
2643	NP 3'-UTR	0	140	0	799	T/C	15%	3'-UTR +451	
2663	NP 3'-UTR	0	169	0	863	T/C	16%	3'-UTR +471	
2724	NP 3'-UTR	0	174	1	1076	T/C	14%	3'-UTR +532	
2836	NP 3'-UTR	0	9	0	17	T/C	35%	3'-UTR +644	
3400	VP35 ORF	3212	2	0	676	A/T	17%	subst_NONSYNONYMOUS[TTA:L TTt:F c]	152
4283	VP35 3'-UTR	0	63	0	314	T/C	17%	3'-UTR +348	
8433	GP 3'-UTR	2265	0	103	0	A/G	4%	3'-UTR +446	

*MAIN gij91177679|gb|DQ447653.1| Lake Victoria marburgvirus - Angola2005 strain Ang1379c, complete genome:

** UTR type of change example; "3-UTR +398". A change present in the 3'-UTR of the Designated gene 398 nucleotides from the stop codon.

***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.