

Supplemental Table 6. Insertion frequencies at Marburg-Ang polynucleotide regions

Genome coordinates*	mRNA Thp1 @24hpi Random shear		mRNA in Vero @24hpi Random shear		vRNA Vero @ 24hpi Amplicon		vRNA Vero @ 1hpi Amplicon		Plasmid amplicon Amplicon		Adrenal Gland Amplicon		Axillary LN Amplicon		Liver Amplicon		Mesenteric LN Amplicon	
	Polynucleotide*	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%
MARV NP 816-821	AAAAA	0.00%	AAAAA	0.05%	AAAAA	0.09%	AAAAA	0.07%	AAAAA	0.01%	AAAAA	0.08%	AAAAA	0.08%	AAAAA	0.06%	AAAAA	0.08%
	AAAAAA	91.89%	AAAAAA	87.06%	AAAAAA	98.41%	AAAAAA	98.65%	AAAAAA	99.81%	AAAAAA	99.00%	AAAAAA	98.83%	AAAAAA	98.08%	AAAAAA	99.04%
	AAAAAAA	7.88%	AAAAAAA	11.73%	AAAAAAA	1.36%	AAAAAAA	1.12%	AAAAAAA	0.01%	AAAAAAA	0.79%	AAAAAAA	0.92%	AAAAAAA	1.72%	AAAAAAA	0.73%
Total reads	1714	99.77%	5635	98.85%	28137	99.86%	459109	99.84%	666303	99.83%	9412642	99.87%	24815	99.84%	101814	99.86%	540854	99.85%
MARV L 17809-17815	AAAAA	0.00%	AAAAA	0.06%	AAAAA	0.09%	AAAAA	0.02%	AAAAA	0.15%								
	AAAAAA	80.09%	AAAAAA	80.58%	AAAAAA	98.86%	AAAAAA	99.06%	AAAAAA	99.91%	AAAAAA	97.07%						
	AAAAAAA	19.44%	AAAAAAA	16.54%	AAAAAAA	1.00%	AAAAAAA	0.80%	AAAAAAA	0.00%	AAAAAAA	2.70%						
Total reads	216	99.54%	659	97.12%	11578	99.92%	34649	99.95%	632418	99.92%	24815	99.92%						

*Only sequencing reads with perfect matches to the reference sequence 10 nucleotides to each side of the indicated homopolymer region were examined

**Percent reflects the number of total reads with the indicated homopolymer region. The total number of reads does not add up to 100% because the remaining fraction includes reads which have a nucleotide within this region different than the nucleotide within the homopolymer