

**Supplemental Table 5. Insertion frequencies at Ebola polynucleotide regions**

Genome coordinates*	mRNA Thp1 @24hpi Random shear		mRNA Thp1 @24hpi (amplicon) Amplicon		mRNA in Vero @24hpi Random shear		vRNA Vero @ 24hpi Amplicon		vRNA Vero @ 1hpi Amplicon		Plasmid amplicon Amplicon		Pol II derived Amplicon Amplicon	
	Polynucleotide	%**	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%	Polynucleotide	%
<b>EBOV GP (virus/plasmid 7A) 6918-6924</b>	AAAAAA	0.25%	AAAAAA	0.14%	AAAAAA	0.50%	AAAAAA	0.25%	AAAAAA	0.32%	AAAAAA	0.03%	AAAAAA	0.27%
	AAAAAAA	67.92%	AAAAAAA	69.78%	AAAAAAA	71.65%	AAAAAAA	82.87%	AAAAAAA	97.55%	AAAAAAA	99.76%	AAAAAAA	98.71%
	AAAAAAA	28.04%	AAAAAAA	27.39%	AAAAAAA	25.90%	AAAAAAA	15.50%	AAAAAAA	1.76%	AAAAAAA	0.00%	AAAAAAA	0.79%
	AAAAAAA	1.91%	AAAAAAA	1.40%	AAAAAAA	1.26%	AAAAAAA	0.74%	AAAAAAA	0.05%	AAAAAAA	0.00%	AAAAAAA	0.01%
	AAAAAAA	1.73%	AAAAAAA	1.17%	AAAAAAA		AAAAAAA	0.48%	AAAAAAA	0.01%				
<b>Total reads</b>	<b>6078</b>	<b>99.84%</b>	<b>8631084</b>	<b>99.88%</b>	<b>8273</b>	<b>99.31%</b>	<b>4687772</b>	<b>99.84%</b>	<b>4933361</b>	<b>99.68%</b>	<b>336069</b>	<b>99.80%</b>	<b>629236</b>	<b>99.78%</b>
<b>EBOV GP (plasmid 8A) 6918-6925</b>											AAAAAA	0.00%	AAAAAA	0.06%
											AAAAAAA	0.82%	AAAAAAA	0.85%
											AAAAAAA	98.38%	AAAAAAA	95.99%
											AAAAAAA	0.47%	AAAAAAA	2.81%
<b>Total reads</b>										<b>566972</b>	<b>99.68%</b>	<b>579535</b>	<b>99.70%</b>	
<b>EBOV GP 6378-6383</b>	AAAAA	0.21%			AAAAA	0.18%	AAAAA	0.12%	AAAAA	0.09%	AAAAA	0.08%	AAAAA	0.14%
	AAAAAA	95.03%			AAAAAA	96.70%	AAAAAA	98.65%	AAAAAA	98.09%	AAAAAA	99.64%	AAAAAA	99.16%
	AAAAAAA	4.30%			AAAAAAA	2.87%	AAAAAAA	1.08%	AAAAAAA	1.72%	AAAAAAA	0.02%	AAAAAAA	0.59%
	AAAAAAA	0.26%			AAAAAAA	0.09%	AAAAAAA	0.04%	AAAAAAA	0.01%	AAAAAAA	0.00%	AAAAAAA	0.00%
<b>Total reads</b>	<b>3841</b>	<b>99.79%</b>			<b>11358</b>	<b>99.84%</b>	<b>914320</b>	<b>99.89%</b>	<b>5591149</b>	<b>99.91%</b>	<b>460245</b>	<b>99.74%</b>	<b>1357538</b>	<b>99.89%</b>
<b>EBOV VP30 8767-8772</b>	AAAAA	0.19%			AAAAA	0.22%	AAAAA	0.20%	AAAAA	0.18%	AAAAA	0.05%	AAAAA	0.13%
	AAAAAA	96.99%			AAAAAA	98.85%	AAAAAA	98.86%	AAAAAA	98.94%	AAAAAA	99.63%	AAAAAA	99.61%
	AAAAAAA	2.53%			AAAAAAA	0.81%	AAAAAAA	0.81%	AAAAAAA	0.72%	AAAAAAA	0.06%	AAAAAAA	0.12%
<b>Total reads</b>	<b>2091</b>	<b>99.71%</b>			<b>4079</b>	<b>99.88%</b>	<b>123615</b>	<b>99.87%</b>	<b>1384440</b>	<b>99.83%</b>	<b>735306</b>	<b>99.74%</b>	<b>180058</b>	<b>99.87%</b>
<b>EBOV NP 850-855</b>	AAAAA	0.06%			AAAAA	0.09%	AAAAA	0.10%	AAAAA	0.05%	AAAAA	0.01%	AAAAA	0.11%
	AAAAAA	98.47%			AAAAAA	99.30%	AAAAAA	99.45%	AAAAAA	99.36%	AAAAAA	99.92%	AAAAAA	99.57%
	AAAAAAA	1.27%			AAAAAAA	0.48%	AAAAAAA	0.33%	AAAAAAA	0.52%	AAAAAAA	0.01%	AAAAAAA	0.24%
<b>Total reads</b>	<b>11588</b>	<b>99.81%</b>			<b>10728</b>	<b>99.86%</b>	<b>1497497</b>	<b>99.89%</b>	<b>2415959</b>	<b>99.92%</b>	<b>874663</b>	<b>99.94%</b>	<b>369576</b>	<b>99.92%</b>
<b>EBOV NP 1288-1293</b>	AAAAA	0.04%			AAAAA	0.15%	AAAAA	0.07%	AAAAA	0.06%	AAAAA	0.00%		
	AAAAAA	98.50%			AAAAAA	98.91%	AAAAAA	98.78%	AAAAAA	99.32%	AAAAAA	99.93%		
	AAAAAAA	1.39%			AAAAAAA	0.88%	AAAAAAA	1.07%	AAAAAAA	0.54%	AAAAAAA	0.00%		
<b>Total reads</b>	<b>2598</b>	<b>99.92%</b>			<b>6670</b>	<b>99.94%</b>	<b>1888297</b>	<b>99.92%</b>	<b>76513</b>	<b>99.92%</b>	<b>550404</b>	<b>99.93%</b>		
<b>EBOV L 12146-12151</b>	UUUUUU	94.48%			UUUUUU	97.39%	UUUUUU	94.38%	UUUUUU	94.09%	UUUUUU	99.58%		
	UUUUUUU	5.34%			UUUUUUU	2.30%	UUUUUUU	5.37%	UUUUUUU	5.67%	UUUUUUU	0.03%		
	UUUUUUUU	0.00%			UUUUUUUU	0.00%	UUUUUUUU	0.15%	UUUUUUUU	0.15%	UUUUUUUU	0.00%		
<b>Total reads</b>	<b>562</b>	<b>99.82%</b>			<b>1305</b>	<b>99.69%</b>	<b>5252884</b>	<b>99.89%</b>	<b>6455486</b>	<b>99.90%</b>	<b>1402798</b>	<b>99.61%</b>		
<b>EBOV L 17521-17526</b>	UUUUUU	92.46%			UUUUUU	94.08%	UUUUUU	99.07%	UUUUUU	99.26%	UUUUUU	99.92%		
	UUUUUUU	7.30%			UUUUUUU	5.49%	UUUUUUU	0.73%	UUUUUUU	0.49%	UUUUUUU	0.00%		
	UUUUUUUU	0.00%			UUUUUUUU	0.09%	UUUUUUUU	0.02%	UUUUUUUU	0.00%	UUUUUUUU	0.00%		
<b>Total reads</b>	<b>411</b>	<b>99.76%</b>			<b>1166</b>	<b>99.66%</b>	<b>585199</b>	<b>99.82%</b>	<b>100263</b>	<b>99.76%</b>	<b>2610377</b>	<b>99.93%</b>		

\*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