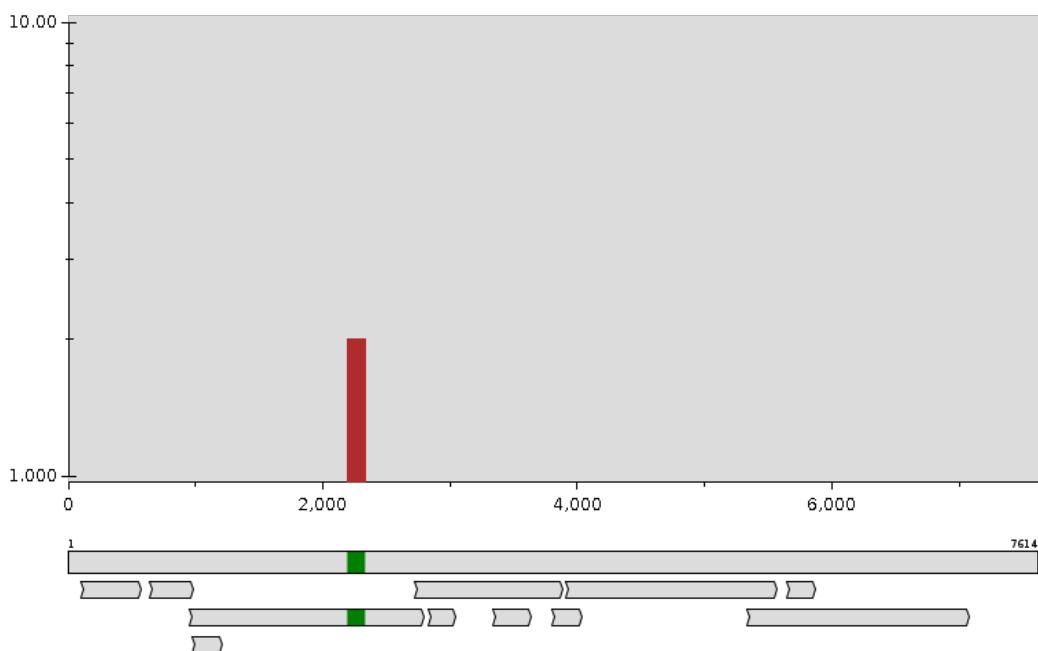


NGS Details (MG-6-RNASeq021-ZymoSeq): Nupapillomavirus 1

Assembly

Coverage Length	144 (1 contig(s))
Depth Of Coverage	1.9
Number Of Reads	2
Reads Per Million	0.02 rpm (after QC)
Ambiguities	0
Assembly Method	read mapping against reference + variant calling
Consensus Caller	Bcf Tools

Coverage Map



Assignment

Type	Nupapillomavirus 1 (Taxonomy ID: 334205)
Reference Genome	NC_001354.1
NT Identity (%)	100.0
AA Identity (%)	97.9167
Number Of Stop Codons	0
Number Of CDS	11

Alignment

Alignment Score	288.0 (NT) + 358.0 (AA) = 646.0
Concordance (%)	100.0

Genome Region

Sequence starts at position 2194 and ends at position 2337 relative to NC_001354.1 reference sequence.

Alignment Detailed Statistics

NT	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
	2194	2337	1.9%	288	100%	144 (100%)	144 (100%)	0/0	
Mutations:	<i>none</i>								
CDS									
ORF_E1	416	463	7.8%	358	94.0%	48 (100%)	47 (97.9%)	0/0/0/0	0
Proteins									
hypothetical protein (NP_040287.1)	416	463	7.8%	358	94.0%	48 (100%)	47 (97.9%)	0/0/0/0	0
Protein mutations:	<i>none</i>								
Codon mutations:	<i>none</i>								

*: Inserts / Deletes / Misaligned / Frameshifts

Analysis details

This analysis was performed with Pan-viral (2.14.6)