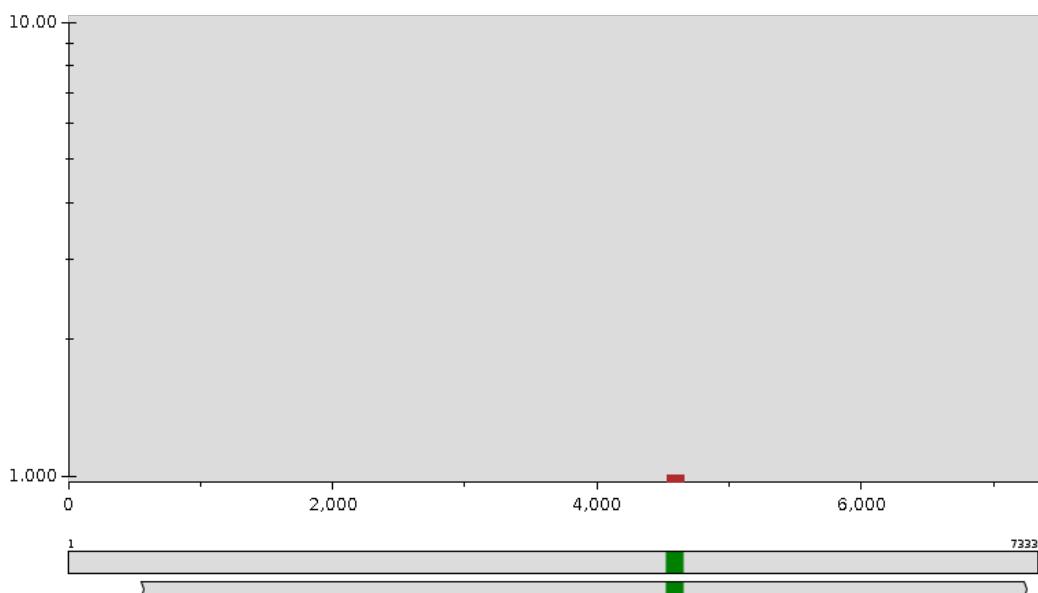


NGS Details (MG-12-RNASeq021-ZymoSeq): hepatovirus H2

Assembly

Coverage Length	134 (1 contig(s))
Depth Of Coverage	1.0
Number Of Reads	1
Reads Per Million	0.01 rpm (after QC)
Ambiguities	0
Assembly Method	de novo + reference guided assembly
Consensus Caller	Bcf Tools

Coverage Map



Assignment

Type	hepatovirus H2 (Taxonomy ID: 2766976)
Reference Genome	NC_028366.1
NT Identity (%)	78.3582
AA Identity (%)	80.0
Number Of Stop Codons	0
Number Of CDS	1

Alignment

Alignment Score	152.0 (NT) + 237.0 (AA) = 389.0
Concordance (%)	70.9854

Genome Region

Sequence starts at position 4527 and ends at position 4660 relative to NC_028366.1 reference sequence.

Alignment Detailed Statistics

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	4527	4660	1.8%	152	56.7%	134 (100%)	105 (78.4%)	0/0	
Mutations:									

CDS

AS012_gp1	1323	1367	2.0%	237	82.0%	45 (100%)	36 (80.0%)	0/0/0/0	0
Protein mutations:									
P1323S (4527C>T), S1326C (4537C>G), S1337A (4569T>G 4571A>T), S1347T (4600G>C), T1349A (4605A>G 4607T>C), S1353A (4617T>G), M1357L (4629A>C), R1365S (4655A>T)									
Codon mutations:									
CCT1323TCT (4527C>T), GAC1324GAT (4532C>T), CCT1325CCC (4535T>C), TCT1326TGT (4537C>G), ACT1329ACC (4547T>C), GTC1330GTT (4550C>T), GTT1332GTA (4556T>A), AAG1333AAA (4559G>A), GAG1334GAA (4562G>A), ATC1336ATT (4568C>T), TCA1337GCT (4569T>G 4571A>T), CTT1340CTC (4580T>C), CTA1341TTG (4581C>T) 4583A>G), TTC1342TTT (4586C>T), ATT1344ATA (4592T>A), GTT1346GTA (4598T>A), AGT1347ACT (4600G>C), CCA1348CCT (4604A>T), ACT1349GCC (4605A>G 4607T>C), TCT1353GCT (4617T>G), GTC1354GTT (4622C>T), ATG1357CTG (4629A>C), CTT1358TTG (4632C>T 4634T>G), GTT1360GTC (4640T>C), AGA1365AGT (4655A>T)									

Proteins

polyprotein (YP_009179216.1)	1323	1367	2.0%	237	82.0%	45 (100%)	36 (80.0%)	0/0/0/0	0
Protein mutations:									
P1323S (4527C>T), S1326C (4537C>G), S1337A (4569T>G 4571A>T), S1347T (4600G>C), T1349A (4605A>G 4607T>C), S1353A (4617T>G), M1357L (4629A>C), R1365S (4655A>T)									
Codon mutations:									
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*: Inserts / Deletes / Misaligned / Framehifts

Analysis details

This analysis was performed with Pan-viral (2.14.6)