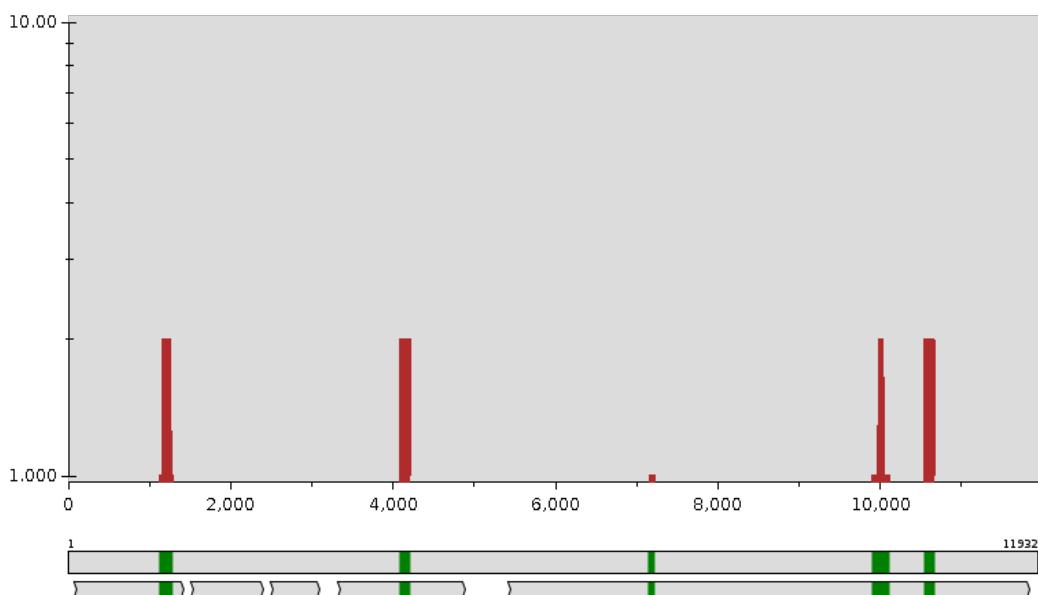


## NGS Details (MG-9-RNASeq021-ZymoSeq): Lyssavirus rabies

### Assembly

Coverage Length	769 (5 contig(s))
Depth Of Coverage	1.5
Number Of Reads	9
Reads Per Million	0.08 rpm (after QC)
Ambiguities	0
Assembly Method	de novo + reference guided assembly
Consensus Caller	Bcf Tools

### Coverage Map



### Assignment

Type	Lyssavirus rabies (Taxonomy ID: 11292)
Reference Genome	NC_001542.1
NT Identity (%)	82.1847
AA Identity (%)	89.4942
Number Of Stop Codons	0
Number Of CDS	5

### Alignment

Alignment Score	990.0 (NT) + 1578.0 (AA) = 2568.0
Concordance (%)	78.773

## Genome Region

Sequence starts at position 1123 and ends at position 10674 relative to NC\_001542.1 reference sequence.

## Alignment Detailed Statistics

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	1123	10674	6.4%	990	64.4%	769 (100%)	632 (82.2%)	0/0	
Mutations:	1123G>A, 1129G>A, 1132A>T, 1141A>G, 1144A>G, 1153A>G, 1156T>C, 1159G>A, 1171A>G, 1174A>G, 1177C>T, 1183G>A, 1190C>T, 1198G>A, 1199A>G, 1204C>G, 1205G>A, 1206T>C, 1210A>G, 1211C>A, 1221T>C, 1228T>A, 1234C>T, 1240C>T, 1243C>T, 1258A>C, 1270A>G, 1276G>A, 1282T>A, 1288T>C, 1291T>A, 1300A>G, 4091A>C, 4097C>T, 4098G>T, 4100G>A, 4103G>T, 4109A>C, 4113A>G, 4115T>C, 4118A>T, 4136C>G, 4138G>A, 4142G>A, 4152T>C, 4154G>A, 4157C>T, 4165G>A, 4178T>A, 4184C>T, 4187T>C, 4190T>C, 4193A>G, 7145C>T, 7160C>T, 7163G>A, 7164C>T, 7181C>T, 7190G>A, 7196T>C, 7199A>G, 7214G>A, 7216T>A, 7220C>T, 7226A>G, 9899T>A, 9904A>G, 9911C>T, 9920A>C, 9923C>T, 9932T>C, 9945C>T, 9947A>G, 9956G>A, 9964T>C, 9965A>G, 9968C>A, 9971G>A, 9974G>A, 9977T>A, 9980A>G, 9989C>A, 9993C>T, 9995A>G, 10001C>A, 10004T>C, 10019T>C, 10020G>A, 10022C>T, 10025A>G, 10034C>T, 10034G>A, 10043C>T, 10046T>C, 10055G>A, 10065G>T>A, 10067A>G, 10070C>T, 10076G>A, 10079T>C, 10084G>A, 10087A>G, 10088C>T, 10091A>C, 10094T>C, 10097G>A, 10098A>G, 10107G>A, 10108A>C, 10109T>C, 10113C>T, 10541G>T, 10553G>A, 10556A>G, 10559C>A, 10574A>G, 10585T>C, 10589G>A, 10595C>T, 10598T>C, 10601T>A, 10607G>A, 10616C>T, 10617C>T, 10625T>A, 10628C>A, 10631A>G, 10640A>G, 10641C>T, 10643G>A, 10646T>C, 10664G>C, 10667A>G, 10671A>G								

## CDS

RABVgp1	352	411	13.3%	359	89.3%	60 (100%)	54 (90.0%)	0/0/0/0	0
Protein mutations: T377A (1199A>G), D378E (1204C>G), V379T (1205G>A) 1206T>C 1207A>G), G397S (1259G>A), I410M (1300A>G)									
Codon mutations: GGG351..A (1123G>A), GGG353GGA (1129G>A), ACA354ACT (1132A>T), AGA357AGG (1141A>G), AGA358AGG (1144A>G), AGA361AGG (1153A>G), GAT362GAC (1156T>C), GAG363GAA (1159G>A), CAA367CAG (1171A>G), GAA368GAG (1174A>G), TAC369AT (1177C>T), CGC371GCA (1183G>A), CTG374TTG (1190C>T), AAG376AAA (1198G>A), ACT377GCT (1199A>G), GAC378GAG (1204C>G), GTG379ACG (1205G>A) 1206T>C 1207A>G), GCA380GCC (1210A>C), CTG381TTG (1211C>T), GAT384GAC (1222T>C), ACT386ACA (1228T>A), AAC388AAT (1234C>T), GAC390GAT (1240C>T), GAC391GAT (1243C>T), TCA396TCC (1258A>C), GGT397AGT (1259G>A), AGA400AGG (1270A>G), CGC402CCA (1276G>A), GCT404GCA (1282T>A), TAT406TAC (1288T>C), ACT407ACA (1291T>A), ATA410ATG (1300A>G)									
RABVgp4	255	299	8.6%	298	87.6%	45 (100%)	39 (86.7%)	0/0/0/0	0
Protein mutations: A261S (4098G>T 4100G>A), M262I (4103G>T), N266D (4113A>G 4115T>C), E267D (4118A>T), G274D (4138G>A), R283H (4165G>A)									
Codon mutations: ACA258ACC (4091A>C), GTC260GTT (4097C>T), GCG261TCA (4098G>T 4100G>A), ATG262ATT (4103G>T), ACA264ACC (4109A>C), AAT266GAC (4113A>G 4115T>C), GAA267GAT (4118A>T), CCC273CCG (4136C>G), GGT274GAT (4138G>A), CA275CCA (4142G>A), TTG279CTA (4152T>C 4154G>A), CAC280CAT (4157C>T), CGC283CAC (4165G>A), ATT287ATA (4178T>A), CAC289CAT (4184C>T), CTT290CTC (4187T>C), GTT291GTC (4190T>C), GTA292GTG (4193A>G)									
RABVgp5	576	1753	7.1%	921	89.8%	152 (100%)	137 (90.1%)	0/0/0/0	0
Protein mutations: V600D (7216T>A), K1496R (9904A>G), V1516A (9964T>C 9965A>G), D1524E (9989C>A), A1535S (10020G>T 10022C>T), R1556K (10084G>A), N1557S (10087A>G 10088C>T), S1561G (10098A>G), D1564T (10107G>A 10108A>C 10109T>C), L1723P (10585T>C), R1749S (10664G>C), N1752D (10671A>G)									
Codon mutations: ATC576ATT (7145C>T), GAC581GAT (7160C>T), GCG582GCA (7163G>A), CTG583TTG (7164C>T), AAC588AAT (7181C>T), AAG591AAA (7190G>A), TTT593TTC (7196T>C), AAA594AAC (7199A>G), AGG599AGA (7214G>A), GTC600GAC (7216T>A), ACC601ACT (7220C>T), CAA603CAG (7226A>G), ACT1494ACA (9899T>A), AAA1496AGA (9904A>G), GGC1498GGT (9911C>T), TCA1501TCC (9920A>C), ATC1502ATT (9923C>T), TAT1505TAC (9932T>C), CTA1501TTG (9945C>T 9947A>G), GAG1513GAA (9956G>A), GTC1516GCG (9964T>C 9965A>G), ATC1517ATA (9968C>A), ACG1518ACA (9971G>A), GCG1519GCA (9974G>A), TCT1520TCA (9977T>A), CCA1521CCG (9980A>G), GAC1524GAA (9989C>A), CTA1526TTG (9993C>T 9995A>G), ATC1528ATA (1001C>A), TTT1529TTC (10004T>C), AGT1534AGC (10019T>C), GCC1535TCT (10020G>T 10022C>T), AAA1536AAC (10025A>G), TAC1539TAT (10034C>T), CTAA1540CTG (10037A>C), ACC1541ACT (10040C>T), CTC1542CTT (10043C>T), ATT1543ATC (10046T>C), CAG1546CAA (10055G>A), CTA1550TTG (10065C>T 10067A>G), CTC1551CTT (10070C>T), AGG1553AAG (10076G>A), GTT1554GTC (10079T>C), AGA1556AAA (10084G>A), AAC1557AGT (10087A>C 10088C>T), CTAA1558CTC (10091A>C), TCT1559TCC (10094T>C), AAC1560AAA (10097G>A), AGT1561GGT (10098A>G), GAT1564ACC (10107G>A), 10108A>C 10109T>C), CTG1566TGT (10113C>T), GGG1708GGT (10541G>A), AGG1712AGA (10553G>A), GCA1713GCG (10556A>G), GTC1714GTA (10559C>A), CCA1719CG (10574A>G), CCT1723CCCT (10585T>C), GTG1724GTA (10589G>A), AAC1726AAT (10595C>T), AGT1727AGC (10598T>C), CTT1728CTA (10601T>A), GAG1730GAA (10607G>A), GAC1733GAT (10616C>T), CTG1734TTG (10617C>T), GCT1736GCA (10625T>A), TCC1737TCA (10628C>A), GGA1738GGG (10631A>G), CCA1741CCG (10640A>G), CTG1742TTA (10641C>T 10643G>A), CCT1743CCC (10646T>C), AGG1749AGC (10664G>C), GGA1750GGG (10667A>G), AAT1752GAT (10671A>G)									

## Proteins

nucleoprotein N (NP_056793.1)	352	411	13.3%	359	89.3%	60 (100%)	54 (90.0%)	0/0/0/0	0
Protein mutations: T377A (1199A>G), D378E (1204C>G), V379T (1205G>A) 1206T>C 1207A>G), G397S (1259G>A), I410M (1300A>G)									
Codon mutations: GGG351..A (1123G>A), GGG353GGA (1129G>A), ACA354ACT (1132A>T), AGA357AGG (1141A>G), AGA358AGG (1144A>G), AGA361AGG (1153A>G), GAT362GAC (1156T>C), GAG363GAA (1159G>A), CAA367CAG (1171A>G), GAA368GAG (1174A>G), TAC369AT (1177C>T), CGC371GCA (1183G>A), CTG374TTG (1190C>T), AAG376AAA (1198G>A), ACT377GCT (1199A>G), GAC378GAG (1204C>G), GTG379ACG (1205G>A) 1206T>C 1207A>G), GCA380GCC (1210A>C), CTG381TTG (1211C>T), GAT384GAC (1222T>C), ACT386ACA (1228T>A), AAC388AAT (1234C>T), GAC390GAT (1240C>T), GAC391GAT (1243C>T), TCA396TCC (1258A>C), GGT397AGT (1259G>A), AGA400AGG (1270A>G), CGC402CCA (1276G>A), GCT404GCA (1282T>A), TAT406TAC (1288T>C), ACT407ACA (1291T>A), ATA410ATG (1300A>G)									
transmembrane glycoprotein G (NP_056796.1)	255	299	8.6%	298	87.6%	45 (100%)	39 (86.7%)	0/0/0/0	0
Protein mutations: A261S (4098G>T 4100G>A), M262I (4103G>T), N266D (4113A>G 4115T>C), E267D (4118A>T), G274D (4138G>A), R283H (4165G>A)									
Codon mutations: ACA258ACC (4091A>C), GTC260GTT (4097C>T), GCG261TCA (4098G>T 4100G>A), ATG262ATT (4103G>T), ACA264ACC (4109A>C), AAT266GAC (4113A>G 4115T>C), GAA267GAT (4118A>T), CCC273CCG (4136C>G), GGT274GAT (4138G>A), CA275CCA (4142G>A), TTG279CTA (4152T>C 4154G>A), CAC280CAT (4157C>T), CGC283CAC (4165G>A), ATT287ATA (4178T>A), CAC289CAT (4184C>T), CTT290CTC (4187T>C), GTT291GTC (4190T>C), GTA292GTG (4193A>G)									
L protein (NP_056797.1)	576	1753	7.1%	921	89.8%	152 (100%)	137 (90.1%)	0/0/0/0	0
Protein mutations: V600D (7216T>A), K1496R (9904A>G), V1516A (9964T>C 9965A>G), D1524E (9989C>A), A1535S (10020G>T 10022C>T), R1556K (10084G>A), N1557S (10087A>G 10088C>T), S1561G (10098A>G), D1564T (10107G>A 10108A>C 10109T>C), L1723P (10585T>C), R1749S (10664G>C), N1752D (10671A>G)									
Codon mutations: ATC576ATT (7145C>T), GAC581GAT (7160C>T), GCG582GCA (7163G>A), CTG583TTG (7164C>T), AAC588AAT (7181C>T), AAG591AAA (7190G>A), TTT593TTC (7196T>C), AAA594AAC (7199A>G), AGG599AGA (7214G>A), GTC600GAC (7216T>A), ACC601ACT (7220C>T), CAA603CAG (7226A>G), ACT1494ACA (9899T>A), AAA1496AGA (9904A>G), GGC1498GGT (9911C>T), TCA1501TCC (9920A>C), ATC1502ATT (9923C>T), TAT1505TAC (9932T>C), CTA1501TTG (9945C>T 9947A>G), GAG1513GAA (9956G>A), GTC1516GCG (9964T>C 9965A>G), ATC1517ATA (9968C>A), ACG1518ACA (9971G>A), GCG1519GCA (9974G>A), TCT1520TCA (9977T>A), CCA1521CCG (9980A>G), GAC1524GAA (9989C>A), CTA1526TTG (9993C>T 9995A>G), ATC1528ATA (10001C>A), TTT1529TTC (10004T>C), AGT1534AGC (10019T>C), GCC1535TCT (10020G>T 10022C>T), AAA1536AAC (10025A>G), TCT1539TAT (10034C>T), CTAA1540CTG (10037A>C), ACC1541ACT (10040C>T), CTC1542CTT (10043C>T), ATT1543ATC (10046T>C), CAG1546CAA (10055G>A), CTA1550TTG (10065C>T 10067A>G), CTC1551CTT (10070C>T), AGG1553AAG (10076G>A), GTT1554GTC (10079T>C), AGA1556AAA (10084G>A), AAC1557AGT (10087A>C 10088C>T), CTAA1558CTC (10091A>C), TCT1559TCC (10094T>C), AAC1560AAA (10097G>A), AGT1561GGT (10098A>G), GAT1564ACC (10107G>A), 10108A>C 10109T>C), CTG1566TTG (10113C>T), GGG1708GGT (10541G>A), AGG1712AGA (10553G>A), GCA1713GCG (10556A>G), GTC1714GTA (10559C>A), CCA1719CG (10574A>G), CCT1723CCCT (10585T>C), GTG1724GTA (10589G>A), AAC1726AAT (10595C>T), AGT1727AGC (10598T>C), CTT1728CTA (10601T>A), GAG1730GAA (10607G>A), GAC1733GAT (10616C>T), CTG1734TTG (10617C>T), GCT1736GCA (10625T>A), TCC1737TCA (10628C>A), GGA1738GGG (10631A>G), CCA1741CCG (10640A>G), CTG1742TTA (10641C>T 10643G>A), CCT1743CCC (10646T>C), AGG1749AGC (10664G>C), GGA1750GGG (10667A>G), AAT1752GAT (10671A>G)									

\*: Inserts / Deletes / Misaligned / Frameshifts

## Analysis details



This analysis was performed with Pan-viral (2.14.6)