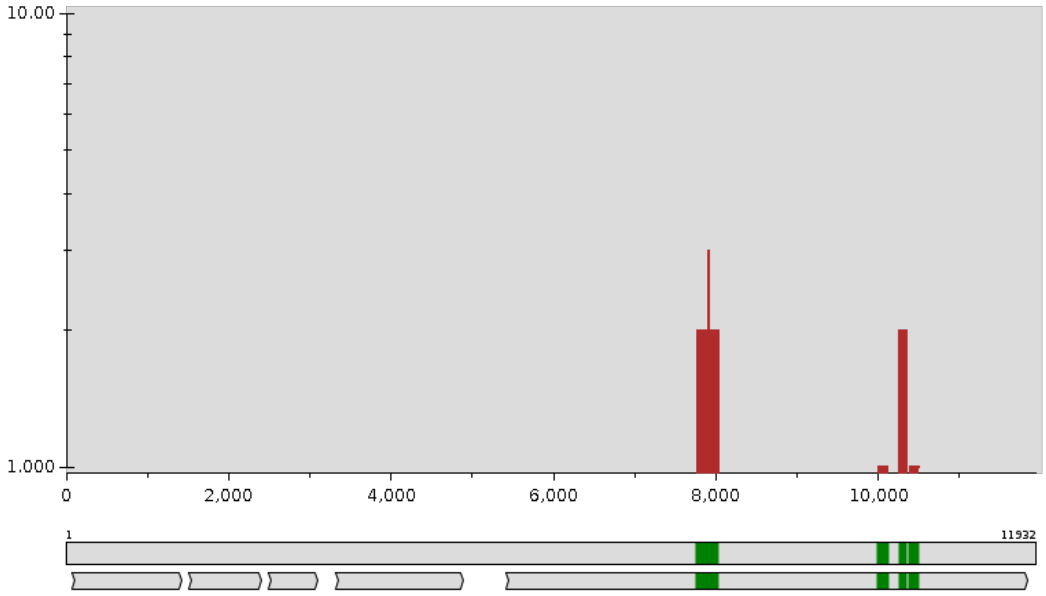
NGS Details (MG-4-RNASeq021-ZymoSeq): Lyssavirus rabies

Assembly

Coverage Length	670 (4 contig(s))
Depth Of Coverage	1.5
Number Of Reads	8
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 (%)	82.2388
AA Identity (%)	91.0314
Number Of Stop Codons	0
Number Of CDS	5

Alignment

Alignment Score	864.0 (NT) + 1406.0 (AA) = 2270.0
Concordance (%)	79.7891

Alignment Method	Global, seeded, nucleotide + amino acids (AGA)

Genome Region

Sequence starts at position 7751 and ends at position 10504 relative to NC_001542.1 reference sequence.

Alignment Detailed Statistics

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**7751**	**10504**	**5.6%**	**864**	**64.5%**	**670 (100%)**	**551 (82.2%)**	**0/0**	
Mutations:	7754A>G, 7775T>C, 7778C>T, 7796A>G, 7802T>C, 7803T>C, 7809A>C, 7820A>C, 7826G>A, 7847C>T, 7859C>T, 7860G>A, 7865T>C, 7874A>G, 7886C>T, 7901G>A, 7907G>A, 7916C>T, 7919G>C, 7920C>T, 7922A>G, 7925A>T, 7949G>A, 7955A>G, 7967T>C, 7971C>T, 7973G>A, 7976C>T, 7982A>T, 7985A>T, 7988G>A, 7991A>T, 7994C>A, 7997T>C, 8000C>T, 8009A>G, 8018A>T, 8022T>C, 8024A>G, 8030A>C, 9989C>A, 9993C>T, 9995A>G, 10001C>A, 10004T>C, 10019T>C, 10020G>T, 10022C>T, 10025A>G, 10034C>T, 10037A>G, 10040C>T, 10043C>T, 10046T>C, 10055G>A, 10065C>T, 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, 10122T>A, 10256T>G, 10259A>G, 10262C>T, 10266A>G, 10267C>T, 10268T>A, 10272G>T, 10273A>G, 10277C>T, 10285A>G, 10291A>G, 10293G>A, 10298C>A, 10301T>C, 10304G>A, 10306T>C, 10307A>C, 10310A>G, 10337A>G, 10349C>T, 10352T>A, 10375T>C, 10379G>C, 10385T>G, 10391A>C, 10394G>A, 10395G>A, 10397C>T, 10405A>G, 10406G>A, 10410T>C, 10412C>T, 10415G>A, 10421T>A, 10427C>T, 10430G>A, 10434T>C, 10448G>A, 10457C>A, 10460T>G, 10463T>C, 10469T>C, 10475T>C, 10478G>A, 10480C>A, 10487A>G, 10502T>G							

CDS

RABVgp5	779	1696	10.4%	1406	91.5%	223 (100%)	203 (91.0%)	0/0/0/0	0
Protein mutations:	V815I (7860G>A), A1535S (10020G>T 10022C>T), R1556K (10084G>A), N1557S (10087A>G 10088C>T), S1561G (10098A>G), D1564T (10107G>A 10108A>C 10109T>C), L1569M (10122T>A), T1617V (10266A>G 10267C>T 10268T>A), D1619C (10272G>T 10273A>G), N1623S (10285A>G), K1625R (10291A>G), V1626M (10293G>A), V1630A (10306T>C 10307A>C), V1653A (10375T>C), A1660T (10395G>A 10397C>T), K1663R (10405A>G 10406G>A), F1665L (10410T>C 10412C>T), P1688H (10480C>A)								
Codon mutations:	AAA779AAG (7754A>G), TAT786TAC (7775T>C), GAC787GAT (7778C>T), AAA793AAG (7796A>G), CCT795CCC (7802T>C), TTG796CTG (7803T>C), AGA798CGA (7809A>C), ATA801ATC (7820A>C), GTG803GTA (7826G>A), GCC810GCT (7847C>T), TGC814TGT (7859C>T), GTC815ATC (7860G>A), TCT816TCC (7865T>C), CAA819CAG (7874A>G), CTC823CTT (7886C>T), TCG828TCA (7901G>A), GTG830GTA (7907G>A), AAC833AAT (7916C>T), GCG834GCC (7919G>C), CTA835TTG (7920C>T 7922A>G), ACA836ACT (7925A>T), TTG844TTA (7949G>A), AAA846AAG (7955A>G), GAT850GAC (7967T>C), CTG852TTA (7971C>T 7973G>A), CTC853CTT (7976C>T), TCA855TCT (7982A>T), GTA856GTT (7985A>T), CAG857CAA (7988G>A), GCA858GCT (7991A>T), GTC859GTA (7994C>A), TTT860TTC (7997T>C), CAC861CAT (8000C>T), CTA864CTG (8009A>G), CCA867CCT (8018A>T), TTA869CTG (8022T>C 8024A>G), GGA871GGC (8030A>C), GAC1524..A (9989C>A), CTA1526TTG (9993C>T 9995A>G), ATC1528ATA (10001C>A), TTT1529TTC (10004T>C), AGT1534AGC (10019T>C), GCC1535TCT (10020G>T 10022C>T), AAA1536AAG (10025A>G), TAC1539TAT (10034C>T), CTA1540CTG (10037A>G), ACC1541ACT (10040C>T), CTC1542CTT (10043C>T), ATT1543ATC (10046T>C), CAG1546CAA (10055G>A), CTA1550TTG (10065C>T 10067A>G), CTC1551CTT (10070C>T), AGG1553AGA (10076G>A), GTT1554GTC (10079T>C), AGA1556AAA (10084G>A), AAC1557AGT (10087A>G 10088C>T), CTA1558CTC (10091A>C), TCT1559TCC (10094T>C), AAG1560AAA (10097G>A), AGT1561GGT (10098A>G), GAT1564ACC (10107G>A 10108A>C 10109T>C), CTG1566TTG (10113C>T), TTG1569ATG (10122T>A), GCT1613GCG (10256T>G), AGA1614AGG (10259A>G), ACC1615ACT (10262C>T), ACT1617GTA (10266A>G 10267C>T 10268T>A), GAT1619TGT (10272G>T 10273A>G), TAC1620TAT (10277C>T), AAC1623AGC (10285A>G), AAG1625AGG (10291A>G), GTG1626ATG (10293G>A), TCC1627TCA (10298C>A), CGT1628CGC (10301T>C), AAG1629AAA (10304G>A), GTA1630GCC (10306T>C 10307A>C), GGA1631GGG (10310A>G), CAA1640CAG (10337A>G), GTC1644GTT (10349C>T), TCT1645TCA (10352T>A), GTC1653GCC (10375T>C), TCG1654TCC (10379G>C), CTT1656CTG (10385T>G), ATA1658ATC (10391A>C), AGG1659AGA (10394G>A), GCC1660ACT (10395G>A 10397C>T), AAG1663AGA (10405A>G 10406G>A), TTC1665CTT (10410T>C 10412C>T), CAG1666CAA (10415G>A), CCT1668CCA (10421T>A), ATC1670ATT (10427C>T), TCG1671TCA (10430G>A), TTG1673CTG (10434T>C), CAG1677CAA (10448G>A), ACC1680ACA (10457C>A), GGT1681GGG (10460T>G), GCT1682GCC (10463T>C), TAT1684TAC (10469T>C), CTT1686CTC (10475T>C), AAG1687AAA (10478G>A), CCT1688CAT (10480C>A), CTA1690CTG (10487A>G), GTT1695GTG (10502T>G)								

Proteins

L protein (NP_056797.1)	779	1696	10.4%	1406	91.5%	223 (100%)	203 (91.0%)	0/0/0/0	0
Protein mutations:	V815I (7860G>A), A1535S (10020G>T 10022C>T), R1556K (10084G>A), N1557S (10087A>G 10088C>T), S1561G (10098A>G), D1564T (10107G>A 10108A>C 10109T>C), L1569M (10122T>A), T1617V (10266A>G 10267C>T 10268T>A), D1619C (10272G>T 10273A>G), N1623S (10285A>G), K1625R (10291A>G), V1626M (10293G>A), V1630A (10306T>C 10307A>C), V1653A (10375T>C), A1660T (10395G>A 10397C>T), K1663R (10405A>G 10406G>A), F1665L (10410T>C 10412C>T), P1688H (10480C>A)								
Codon mutations:	AAA779AAG (7754A>G), TAT786TAC (7775T>C), GAC787GAT (7778C>T), AAA793AAG (7796A>G), CCT795CCC (7802T>C), TTG796CTG (7803T>C), AGA798CGA (7809A>C), ATA801ATC (7820A>C), GTG803GTA (7826G>A), GCC810GCT (7847C>T), TGC814TGT (7859C>T), GTC815ATC (7860G>A), TCT816TCC (7865T>C), CAA819CAG (7874A>G), CTC823CTT (7886C>T), TCG828TCA (7901G>A), GTG830GTA (7907G>A), AAC833AAT (7916C>T), GCG834GCC (7919G>C), CTA835TTG (7920C>T 7922A>G), ACA836ACT (7925A>T), TTG844TTA (7949G>A), AAA846AAG (7955A>G), GAT850GAC (7967T>C), CTG852TTA (7971C>T 7973G>A), CTC853CTT (7976C>T), TCA855TCT (7982A>T), GTA856GTT (7985A>T), CAG857CAA (7988G>A), GCA858GCT (7991A>T), GTC859GTA (7994C>A), TTT860TTC (7997T>C), CAC861CAT (8000C>T), CTA864CTG (8009A>G), CCA867CCT (8018A>T), TTA869CTG (8022T>C 8024A>G), GGA871GGC (8030A>C), GAC1524..A (9989C>A), CTA1526TTG (9993C>T 9995A>G), ATC1528ATA (10001C>A), TTT1529TTC (10004T>C), AGT1534AGC (10019T>C), GCC1535TCT (10020G>T 10022C>T), AAA1536AAG (10025A>G), TAC1539TAT (10034C>T), CTA1540CTG (10037A>G), ACC1541ACT (10040C>T), CTC1542CTT (10043C>T), ATT1543ATC (10046T>C), CAG1546CAA (10055G>A), CTA1550TTG (10065C>T 10067A>G), CTC1551CTT (10070C>T), AGG1553AGA (10076G>A), GTT1554GTC (10079T>C), AGA1556AAA (10084G>A), AAC1557AGT (10087A>G 10088C>T), CTA1558CTC (10091A>C), TCT1559TCC (10094T>C), AAG1560AAA (10097G>A), AGT1561GGT (10098A>G), GAT1564ACC (10107G>A 10108A>C 10109T>C), CTG1566TTG (10113C>T), TTG1569ATG (10122T>A), GCT1613GCG (10256T>G), AGA1614AGG (10259A>G), ACC1615ACT (10262C>T), ACT1617GTA (10266A>G 10267C>T 10268T>A), GAT1619TGT (10272G>T 10273A>G), TAC1620TAT (10277C>T), AAC1623AGC (10285A>G), AAG1625AGG (10291A>G), GTG1626ATG (10293G>A), TCC1627TCA (10298C>A), CGT1628CGC (10301T>C), AAG1629AAA (10304G>A), GTA1630GCC (10306T>C 10307A>C), GGA1631GGG (10310A>G), CAA1640CAG (10337A>G), GTC1644GTT (10349C>T), TCT1645TCA (10352T>A), GTC1653GCC (10375T>C), TCG1654TCC (10379G>C), CTT1656CTG (10385T>G), ATA1658ATC (10391A>C), AGG1659AGA (10394G>A), GCC1660ACT (10395G>A 10397C>T), AAG1663AGA (10405A>G 10406G>A), TTC1665CTT (10410T>C 10412C>T), CAG1666CAA (10415G>A), CCT1668CCA (10421T>A), ATC1670ATT (10427C>T), TCG1671TCA (10430G>A), TTG1673CTG (10434T>C), CAG1677CAA (10448G>A), ACC1680ACA (10457C>A), GGT1681GGG (10460T>G), GCT1682GCC (10463T>C), TAT1684TAC (10469T>C), CTT1686CTC (10475T>C), AAG1687AAA (10478G>A), CCT1688CAT (10480C>A), CTA1690CTG (10487A>G), GTT1695GTG (10502T>G)								

*: Inserts / Deletes / Misaligned / Frameshifts

Analysis details

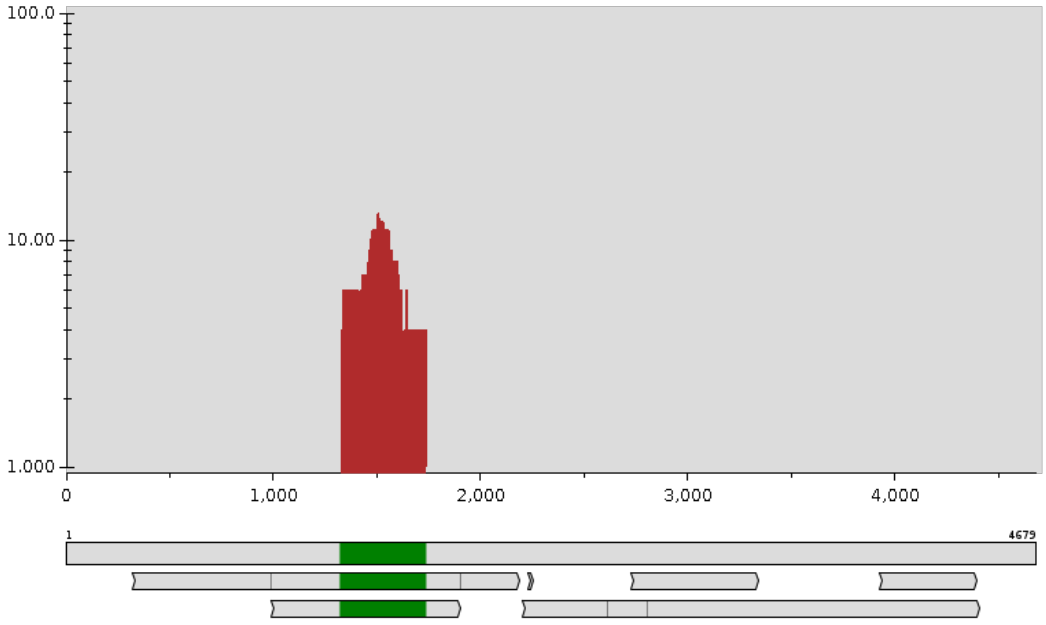
This analysis was performed with Pan-viral (2.14.6)

NGS Details (MG-4-RNASeq021-ZymoSeq): adeno-associated virus 2

Assembly

Coverage Length	415 (1 contig(s))
Depth Of Coverage	6.7
Number Of Reads	23
Reads Per Million	0.23 rpm (after QC)
Ambiguities	0
Assembly Method	de novo + reference guided assembly
Consensus Caller	Bcf Tools

Coverage Map



Assignment

Type	adeno-associated virus 2 (Taxonomy ID: 10804)
Reference Genome	NC_001401.2
NT Identity (%)	63.9024
AA Identity (%)	63.5036
Number Of Stop Codons	0
Number Of CDS	9

Alignment

Alignment Score	196.0 (NT) + 1732.0 (AA) = 1928.0
Concordance (%)	52.1376

Alignment Method	Global, seeded, nucleotide + amino acids (AGA)

Genome Region

Sequence starts at position 1324 and ends at position 1738 relative to NC_001401.2 reference sequence.

Alignment Detailed Statistics

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**1324**	**1738**	**8.9%**	**196**	**24.9%**	**410 (98.8%)**	**262 (63.1%)**	**0/5**	
Mutations:	1324C>G, 1326G>T, 1331T>A, 1338A>G, 1340G>A, 1341A>G, 1342C>A, 1350G>A, 1352G>A, 1357C>A, 1358C>T, 1361A>T, 1366A>G, 1367C>T, 1368A>G, 1372T>G, 1376C>T, 1382C>T, 1385G>C, 1388C>T, 1390T>G, 1391A>T, 1400C>A, 1405A>G, 1406G>A, 1407A>G, 1418C>T, 1421C>T, 1430C>G, 1436G>A, 1437A>G, 1438T>A, 1442G>A, 1445C>T, 1460G>T, 1469C>T, 1470G>A, 1471C>A, 1472C>T, 1475G>A, 1478C>T, 1487G>T, 1490C>G, 1499T>A, 1500C>T, 1502C>G, 1506G>A, 1508A>G, 1509A>T, 1510G>C, 1511C>T, 1512A>G, 1513A>C, 1514G>C, 1515G>A, 1517G>C, 1519G>A, 1520C>G, 1523G>T, 1526C>T, 1529G>A, 1534G>A, 1535C>T, 1538G>A, 1539T>G, 1540C>T, 1541C>A, 1544G>T, 1546C>T, 1547C>A, 1549A>C, 1550G>A, 1551A>G, 1552T>C, 1556C>A, 1559G>C, 1562T>A, 1565C>T, 1568G>A, 1572G>A, 1574C>A, 1578delT, 1579C>T, 1580C>G, 1583C>G, 1586C>T, 1587_1589delAAC, 1595C>T, 1596G>T, 1598C>A, 1601G>A, 1602A>G, 1604T>A, 1606A>G, 1607C>T, 1610G>C, 1614T>A, 1615C>G, 1616A>C, 1620delA, 1621C>G, 1625C>T, 1628A>G, 1632C>A, 1635C>G, 1640G>T, 1641T>C, 1643G>T, 1644C>G, 1646A>G, 1649C>G, 1650C>A, 1652G>A, 1658C>T, 1659A>C, 1660A>T, 1661A>G, 1664T>G, 1665G>A, 1666A>G, 1667A>G, 1668C>T, 1670C>T, 1672C>A, 1673C>T, 1674C>A, 1675G>T, 1676C>A, 1677C>A, 1678G>A, 1679T>A, 1680C>T, 1683G>C, 1685T>G, 1688T>A, 1691C>T, 1697G>A, 1703C>A, 1704A>T, 1706C>T, 1709G>A, 1710C>T, 1711A>G, 1716G>A, 1718C>T, 1720A>T, 1721A>G, 1724C>A, 1730C>T, 1732G>A, 1733G>C							

CDS

AAV2gp01	336	473	25.7%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A336S (1326G>T), K340E (1338A>G 1340G>A), T341D (1341A>G 1342C>A), A344T (1350G>A 1352G>A), A346D (1357C>A 1358C>T), H349R (1366A>G 1367C>T), T350A (1368A>G), V351G (1372T>G), V357G (1390T>G 1391A>T), E362G (1405A>G 1406G>A), N363D (1407A>G), M373E (1437A>G 1438T>A), A384N (1470G>A 1471C>A 1472C>T), G396R (1506G>A 1508A>G), K398A (1512A>G 1513A>C 1514G>C), V399I (1515G>A 1517G>C), R400Q (1519G>A 1520C>G), C405Y (1534G>A 1535C>T), S407V (1539T>G 1540C>T 1541C>A), A409V (1546C>T 1547C>A), Q410P (1549A>C 1550G>A), I411A (1551A>G 1552T>C), D412E (1556C>A), V418I (1572G>A 1574C>A), N421K (1583C>G), N423del (1587_1589delAAC), A426S (1596G>T 1598C>A), I428V (1602A>G 1604T>A), D429G (1606A>G 1607C>T), Q438K (1632C>A), Q439E (1635C>G), Q442E (1644C>G 1646A>G), D443E (1649C>G), K447L (1659A>C 1660A>T 1661A>G), F448L (1664T>G), E449R (1665G>A 1666A>G 1667A>G), L450F (1668C>T 1670C>T), T451N (1672C>A 1673C>T), R452I (1674C>A 1675G>T 1676C>A), R453K (1677C>A 1678G>A 1679T>A), D455Q (1683G>C 1685T>G), H456Q (1688T>A), T462S (1704A>T 1706C>T), Q464W (1710C>T 1711A>G), V466I (1716G>A 1718C>T), K467M (1720A>T 1721A>G), D468E (1724C>A), R471H (1732G>A 1733G>C)								
Codon mutations:	CCT335.GT (1324C>G), GCA336TCA (1326G>T), ACT337ACA (1331T>A), AAG340GAA (1338A>G 1340G>A), ACC341GAC (1341A>G 1342C>A), GCG344ACA (1350G>A 1352G>A), GCC346GAT (1357C>A 1358C>T), ATA347ATT (1361A>T), CAC349CGT (1366A>G 1367C>T), ACT350GCT (1368A>G), GTG351GGG (1372T>G), CCC352CCT (1376C>T), TAC354TAT (1382C>T), GGG355GGC (1385G>C), TGC356TGT (1388C>T), GTA357GGT (1390T>G 1391A>T), ACC360ACA (1400C>A), GAG362GGA (1405A>G 1406G>A), AAC363GAC (1407A>G), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GTC370GTG (1430C>G), AAG372AAA (1436G>A), ATG373GAG (1437A>G 1438T>A), GTG374GTA (1442G>A), ATC375ATT (1445C>T), GGG380GGT (1460G>T), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), AAG385AAA (1475G>A), GTC386GTT (1478C>T), TCG389TCT (1487G>T), GCC390GCG (1490C>G), ATT393ATA (1499T>A), CTC394TTG (1500C>T 1502C>G), GGA396AGG (1506G>A 1508A>G), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GCC (1512A>G 1513A>C 1514G>C), GTG399ATC (1515G>A 1517G>C), CGC400CAG (1519G>A 1520C>G), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TAT (1534G>A 1535C>T), AAG406AAA (1538G>A), TCC407GTA (1539T>G 1540C>T 1541C>A), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CCA (1549A>C 1550G>A), ATA411GCA (1551A>G 1552T>C), GAC412GAA (1556C>A), CCG413CCC (1559G>C), ACT414ACA (1562T>A), CCC415CCT (1565C>T), GTG416GTA (1568G>A), GTC418ATA (1572G>A 1574C>A), TCC420-TG (1578delT 1579C>T 1580C>G), AAC421AAG (1583C>G), ACC422ACT (1586C>T), AAC423del (1587_1589delAAC), TGC425TGT (1595C>T), GCC426TCA (1596G>T 1598C>A), GTG427GTA (1601G>A), ATT428GTA (1602A>G 1604T>A), GAC429GGT (1606A>G 1607C>T), GGG430GGC (1610G>C), TCA432AGC (1614T>A 1615C>G 1616A>C), ACC434-GC (1620delA 1621C>G), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAG438AAG (1632C>A), CAG439GAG (1635C>G), CCG440CCT (1640G>T), TTG441CTT (1641T>C 1643G>T), CAA442GAG (1644C>G 1646A>G), GAC443GAG (1649C>G), CGG444AGA (1650C>A 1652G>A), TTC446TTT (1658C>T), AAA447CTG (1659A>C 1660A>T 1661A>G), TTT448TTG (1664T>G), GAA449AGG (1665G>A 1666A>G 1667A>G), CTC450TTT (1668C>T 1670C>T), ACC451AAT (1672C>A 1673C>T), CGC452ATA (1674C>A 1675G>T 1676C>A), CGT453AAA (1677C>A 1678G>A 1679T>A), CTG454TTG (1680C>T), GAT455CAG (1683G>C 1685T>G), CAT456CAA (1688T>A), GAC457GAT (1691C>T), GGG459GGA (1697G>A), GTC461GTA (1703C>A), ACC462TCT (1704A>T 1706C>T), AAG463AAA (1709G>A), CAG464TGG (1710C>T 1711A>G), GTC466ATT (1716G>A 1718C>T), AAA467ATG (1720A>T 1721A>G), GAC468GAA (1724C>A), TTC470TTT (1730C>T), CGG471CAC (1732G>A 1733G>C)								
AAV2gp02	336	473	22.2%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A336S (1326G>T), K340E (1338A>G 1340G>A), T341D (1341A>G 1342C>A), A344T (1350G>A 1352G>A), A346D (1357C>A 1358C>T), H349R (1366A>G 1367C>T), T350A (1368A>G), V351G (1372T>G), V357G (1390T>G 1391A>T), E362G (1405A>G 1406G>A), N363D (1407A>G), M373E (1437A>G 1438T>A), A384N (1470G>A 1471C>A 1472C>T), G396R (1506G>A 1508A>G), K398A (1512A>G 1513A>C 1514G>C), V399I (1515G>A 1517G>C), R400Q (1519G>A 1520C>G), C405Y (1534G>A 1535C>T), S407V (1539T>G 1540C>T 1541C>A), A409V (1546C>T 1547C>A), Q410P (1549A>C 1550G>A), I411A (1551A>G 1552T>C), D412E (1556C>A), V418I (1572G>A 1574C>A), N421K (1583C>G), N423del (1587_1589delAAC), A426S (1596G>T 1598C>A), I428V (1602A>G 1604T>A), D429G (1606A>G 1607C>T), Q438K (1632C>A), Q439E (1635C>G), Q442E (1644C>G 1646A>G), D443E (1649C>G), K447L (1659A>C 1660A>T 1661A>G), F448L (1664T>G), E449R (1665G>A 1666A>G 1667A>G), L450F (1668C>T 1670C>T), T451N (1672C>A 1673C>T), R452I (1674C>A 1675G>T 1676C>A), R453K (1677C>A 1678G>A 1679T>A), D455Q (1683G>C 1685T>G), H456Q (1688T>A), T462S (1704A>T 1706C>T), Q464W (1710C>T 1711A>G), V466I (1716G>A 1718C>T), K467M (1720A>T 1721A>G), D468E (1724C>A), R471H (1732G>A 1733G>C)								
Codon mutations:	CCT335.GT (1324C>G), GCA336TCA (1326G>T), ACT337ACA (1331T>A), AAG340GAA (1338A>G 1340G>A), ACC341GAC (1341A>G 1342C>A), GCG344ACA (1350G>A 1352G>A), GCC346GAT (1357C>A 1358C>T), ATA347ATT (1361A>T), CAC349CGT (1366A>G 1367C>T), ACT350GCT (1368A>G), GTG351GGG (1372T>G), CCC352CCT (1376C>T), TAC354TAT (1382C>T), GGG355GGC (1385G>C), TGC356TGT (1388C>T), GTA357GGT (1390T>G 1391A>T), ACC360ACA (1400C>A), GAG362GGA (1405A>G 1406G>A), AAC363GAC (1407A>G), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GTC370GTG (1430C>G), AAG372AAA (1436G>A), ATG373GAG (1437A>G 1438T>A), GTG374GTA (1442G>A), ATC375ATT (1445C>T), GGG380GGT (1460G>T), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), AAG385AAA (1475G>A), GTC386GTT (1478C>T), TCG389TCT (1487G>T), GCC390GCG (1490C>G), ATT393ATA (1499T>A), CTC394TTG (1500C>T 1502C>G), GGA396AGG (1506G>A 1508A>G), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GCC (1512A>G 1513A>C 1514G>C), GTG399ATC (1515G>A 1517G>C), CGC400CAG (1519G>A 1520C>G), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TAT (1534G>A 1535C>T), AAG406AAA (1538G>A), TCC407GTA (1539T>G 1540C>T 1541C>A), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CCA (1549A>C 1550G>A), ATA411GCA (1551A>G 1552T>C), GAC412GAA (1556C>A), CCG413CCC (1559G>C), ACT414ACA (1562T>A), CCC415CCT (1565C>T), GTG416GTA (1568G>A), GTC418ATA (1572G>A 1574C>A), TCC420-TG (1578delT 1579C>T 1580C>G), AAC421AAG (1583C>G), ACC422ACT (1586C>T), AAC423del (1587_1589delAAC), TGC425TGT (1595C>T), GCC426TCA (1596G>T 1598C>A), GTG427GTA (1601G>A), ATT428GTA (1602A>G 1604T>A), GAC429GGT (1606A>G 1607C>T), GGG430GGC (1610G>C), TCA432AGC (1614T>A 1615C>G 1616A>C), ACC434-GC (1620delA 1621C>G), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAG438AAG (1632C>A), CAG439GAG (1635C>G), CCG440CCT (1640G>T), TTG441CTT (1641T>C 1643G>T), CAA442GAG (1644C>G 1646A>G), GAC443GAG (1649C>G), CGG444AGA (1650C>A 1652G>A), TTC446TTT (1658C>T), AAA447CTG (1659A>C 1660A>T 1661A>G), TTT448TTG (1664T>G), GAA449AGG (1665G>A 1666A>G 1667A>G), CTC450TTT (1668C>T 1670C>T), ACC451AAT (1672C>A 1673C>T), CGC452ATA (1674C>A 1675G>T 1676C>A), CGT453AAA (1677C>A 1678G>A 1679T>A), CTG454TTG (1680C>T), GAT455CAG (1683G>C 1685T>G), CAT456CAA (1688T>A), GAC457GAT (1691C>T), GGG459GGA (1697G>A), GTC461GTA (1703C>A), ACC462TCT (1704A>T 1706C>T), AAG463AAA (1709G>A), CAG464TGG (1710C>T 1711A>G), GTC466ATT (1716G>A 1718C>T), AAA467ATG (1720A>T 1721A>G), GAC468GAA (1724C>A), TTC470TTT (1730C>T), CGG471CAC (1732G>A 1733G>C)								
AAV2gp03	112	249	44.1%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A112S (1326G>T), K116E (1338A>G 1340G>A), T117D (1341A>G 1342C>A), A120T (1350G>A 1352G>A), A122D (1357C>A 1358C>T), H125R (1366A>G 1367C>T), T126A (1368A>G), V127G (1372T>G), V133G (1390T>G 1391A>T), E138G (1405A>G 1406G>A), N139D (1407A>G), M149E (1437A>G 1438T>A), A160N (1470G>A 1471C>A 1472C>T), G172R (1506G>A 1508A>G), K174A (1512A>G 1513A>C 1514G>C), V175I (1515G>A 1517G>C), R176Q (1519G>A 1520C>G), C181Y (1534G>A 1535C>T), S183V (1539T>G 1540C>T 1541C>A), A185V (1546C>T 1547C>A), Q186P (1549A>C 1550G>A), I187A (1551A>G 1552T>C), D188E (1556C>A), V194I (1572G>A 1574C>A), N197K (1583C>G), N199del (1587_1589delAAC), A202S (1596G>T 1598C>A), I204V (1602A>G 1604T>A), D205G (1606A>G 1607C>T), Q214K (1632C>A), Q215E (1635C>G), Q218E (1644C>G 1646A>G), D219E (1649C>G), K223L (1659A>C 1660A>T 1661A>G), F224L (1664T>G), E225R (1665G>A 1666A>G 1667A>G), L226F (1668C>T 1670C>T), T227N (1672C>A 1673C>T), R228I (1674C>A 1675G>T 1676C>A), R229K (1677C>A 1678G>A 1679T>A), D231Q (1683G>C 1685T>G), H232Q (1688T>A), T238S (1704A>T 1706C>T), Q240W (1710C>T 1711A>G), V242I (1716G>A 1718C>T), K243M (1720A>T 1721A>G), D244E (1724C>A), R247H (1732G>A 1733G>C)								
Codon mutations:	CCT111.GT (1324C>G), GCA112TCA (1326G>T), ACT113ACA (1331T>A), AAG116GAA (1338A>G 1340G>A), ACC117GAC (1341A>G 1342C>A), GCG120ACA (1350G>A 1352G>A), GCC122GAT (1357C>A 1358C>T), ATA123ATT (1361A>T), CAC125CGT (1366A>G 1367C>T), ACT126GCT (1368A>G), GTG127GGG (1372T>G), CCC128CCT (1376C>T), TAC130TAT (1382C>T), GGG131GGC (1385G>C), TGC132TGT (1388C>T), GTA133GGT (1390T>G 1391A>T), ACC136ACA (1400C>A), GAG138GGA (1405A>G 1406G>A), AAC139GAC (1407A>G), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GTC146GTG (1430C>G), AAG148AAA (1436G>A), ATG149GAG (1437A>G 1438T>A), GTG150GTA (1442G>A), ATC151ATT (1445C>T), GGG156GGT (1460G>T), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), AAG161AAA (1475G>A), GTC162GTT (1478C>T), TCG165TCT (1487G>T), GCC166GCG (1490C>G), ATT169ATA (1499T>A), CTC170TTG (1500C>T 1502C>G), GGA172AGG (1506G>A 1508A>G), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GCC (1512A>G 1513A>C 1514G>C), GTG175ATC (1515G>A 1517G>C), CGC176CAG (1519G>A 1520C>G), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TAT (1534G>A 1535C>T), AAG182AAA (1538G>A), TCC183GTA (1539T>G 1540C>T 1541C>A), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CCA (1549A>C 1550G>A), ATA187GCA (1551A>G 1552T>C), GAC188GAA (1556C>A), CCG189CCC (1559G>C), ACT190ACA (1562T>A), CCC191CCT (1565C>T), GTG192GTA (1568G>A), GTC194ATA (1572G>A 1574C>A), TCC196-TG (1578delT 1579C>T 1580C>G), AAC197AAG (1583C>G), ACC198ACT (1586C>T), AAC199del (1587_1589delAAC), TGC201TGT (1595C>T), GCC202TCA (1596G>T 1598C>A), GTG203GTA (1601G>A), ATT204GTA (1602A>G 1604T>A), GAC205GGT (1606A>G 1607C>T), GGG206GGC (1610G>C), TCA208AGC (1614T>A 1615C>G 1616A>C), ACC210-GC (1620delA 1621C>G), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAG214AAG (1632C>A), CAG215GAG (1635C>G), CCG216CCT (1640G>T), TTG217CTT (1641T>C 1643G>T), CAA218GAG (1644C>G 1646A>G), GAC219GAG (1649C>G), CGG220AGA (1650C>A 1652G>A), TTC222TTT (1658C>T), AAA223CTG (1659A>C 1660A>T 1661A>G), TTT224TTG (1664T>G), GAA225AGG (1665G>A 1666A>G 1667A>G), CTC226TTT (1668C>T 1670C>T), ACC227AAT (1672C>A 1673C>T), CGC228ATA (1674C>A 1675G>T 1676C>A), CGT229AAA (1677C>A 1678G>A 1679T>A), CTG230TTG (1680C>T), GAT231CAG (1683G>C 1685T>G), CAT232CAA (1688T>A), GAC233GAT (1691C>T), GGG235GGA (1697G>A), GTC237GTA (1703C>A), ACC238TCT (1704A>T 1706C>T), AAG239AAA (1709G>A), CAG240TGG (1710C>T 1711A>G), GTC242ATT (1716G>A 1718C>T), AAA243ATG (1720A>T 1721A>G), GAC244GAA (1724C>A), TTC246TTT (1730C>T), CGG247CAC (1732G>A 1733G>C)								

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**1324**	**1738**	**8.9%**	**196**	**24.9%**	**410 (98.8%)**	**262 (63.1%)**	**0/5**	
AAV2gp04	112	249	34.7%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A112S (1326G>T), K116E (1338A>G 1340G>A), T117D (1341A>G 1342C>A), A120T (1350G>A 1352G>A), A122D (1357C>A 1358C>T), H125R (1366A>G 1367C>T), T126A (1368A>G), V127G (1372T>G), V133G (1390T>G 1391A>T), E138G (1405A>G 1406G>A), N139D (1407A>G), M149E (1437A>G 1438T>A), A160N (1470G>A 1471C>A 1472C>T), G172R (1506G>A 1508A>G), K174A (1512A>G 1513A>C 1514G>C), V175I (1515G>A 1517G>C), R176Q (1519G>A 1520C>G), C181Y (1534G>A 1535C>T), S183V (1539T>G 1540C>T 1541C>A), A185V (1546C>T 1547C>A), Q186P (1549A>C 1550G>A), I187A (1551A>G 1552T>C), D188E (1556C>A), V194I (1572G>A 1574C>A), N197K (1583C>G), N199del (1587_1589delAAC), A202S (1596G>T 1598C>A), I204V (1602A>G 1604T>A), D205G (1606A>G 1607C>T), Q214K (1632C>A), Q215E (1635C>G), Q218E (1644C>G 1646A>G), D219E (1649C>G), K223L (1659A>C 1660A>T 1661A>G), F224L (1664T>G), E225R (1665G>A 1666A>G 1667A>G), L226F (1668C>T 1670C>T), T227N (1672C>A 1673C>T), R228I (1674C>A 1675G>T 1676C>A), R229K (1677C>A 1678G>A 1679T>A), D231Q (1683G>C 1685T>G), H232Q (1688T>A), T238S (1704A>T 1706C>T), Q240W (1710C>T 1711A>G), V242I (1716G>A 1718C>T), K243M (1720A>T 1721A>G), D244E (1724C>A), R247H (1732G>A 1733G>C)								
Codon mutations:	CCT111.GT (1324C>G), GCA112TCA (1326G>T), ACT113ACA (1331T>A), AAG116GAA (1338A>G 1340G>A), ACC117GAC (1341A>G 1342C>A), GCG120ACA (1350G>A 1352G>A), GCC122GAT (1357C>A 1358C>T), ATA123ATT (1361A>T), CAC125CGT (1366A>G 1367C>T), ACT126GCT (1368A>G), GTG127GGG (1372T>G), CCC128CCT (1376C>T), TAC130TAT (1382C>T), GGG131GGC (1385G>C), TGC132TGT (1388C>T), GTA133GGT (1390T>G 1391A>T), ACC136ACA (1400C>A), GAG138GGA (1405A>G 1406G>A), AAC139GAC (1407A>G), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GTC146GTG (1430C>G), AAG148AAA (1436G>A), ATG149GAG (1437A>G 1438T>A), GTG150GTA (1442G>A), ATC151ATT (1445C>T), GGG156GGT (1460G>T), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), AAG161AAA (1475G>A), GTC162GTT (1478C>T), TCG165TCT (1487G>T), GCC166GCG (1490C>G), ATT169ATA (1499T>A), CTC170TTG (1500C>T 1502C>G), GGA172AGG (1506G>A 1508A>G), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GCC (1512A>G 1513A>C 1514G>C), GTG175ATC (1515G>A 1517G>C), CGC176CAG (1519G>A 1520C>G), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TAT (1534G>A 1535C>T), AAG182AAA (1538G>A), TCC183GTA (1539T>G 1540C>T 1541C>A), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CCA (1549A>C 1550G>A), ATA187GCA (1551A>G 1552T>C), GAC188GAA (1556C>A), CCG189CCC (1559G>C), ACT190ACA (1562T>A), CCC191CCT (1565C>T), GTG192GTA (1568G>A), GTC194ATA (1572G>A 1574C>A), TCC196-TG (1578delT 1579C>T 1580C>G), AAC197AAG (1583C>G), ACC198ACT (1586C>T), AAC199del (1587_1589delAAC), TGC201TGT (1595C>T), GCC202TCA (1596G>T 1598C>A), GTG203GTA (1601G>A), ATT204GTA (1602A>G 1604T>A), GAC205GGT (1606A>G 1607C>T), GGG206GGC (1610G>C), TCA208AGC (1614T>A 1615C>G 1616A>C), ACC210-GC (1620delA 1621C>G), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAG214AAG (1632C>A), CAG215GAG (1635C>G), CCG216CCT (1640G>T), TTG217CTT (1641T>C 1643G>T), CAA218GAG (1644C>G 1646A>G), GAC219GAG (1649C>G), CGG220AGA (1650C>A 1652G>A), TTC222TTT (1658C>T), AAA223CTG (1659A>C 1660A>T 1661A>G), TTT224TTG (1664T>G), GAA225AGG (1665G>A 1666A>G 1667A>G), CTC226TTT (1668C>T 1670C>T), ACC227AAT (1672C>A 1673C>T), CGC228ATA (1674C>A 1675G>T 1676C>A), CGT229AAA (1677C>A 1678G>A 1679T>A), CTG230TTG (1680C>T), GAT231CAG (1683G>C 1685T>G), CAT232CAA (1688T>A), GAC233GAT (1691C>T), GGG235GGA (1697G>A), GTC237GTA (1703C>A), ACC238TCT (1704A>T 1706C>T), AAG239AAA (1709G>A), CAG240TGG (1710C>T 1711A>G), GTC242ATT (1716G>A 1718C>T), AAA243ATG (1720A>T 1721A>G), GAC244GAA (1724C>A), TTC246TTT (1730C>T), CGG247CAC (1732G>A 1733G>C)								
Proteins									
Rep 68 protein (YP_680422.1)	336	473	25.7%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A336S (1326G>T), K340E (1338A>G 1340G>A), T341D (1341A>G 1342C>A), A344T (1350G>A 1352G>A), A346D (1357C>A 1358C>T), H349R (1366A>G 1367C>T), T350A (1368A>G), V351G (1372T>G), V357G (1390T>G 1391A>T), E362G (1405A>G 1406G>A), N363D (1407A>G), M373E (1437A>G 1438T>A), A384N (1470G>A 1471C>A 1472C>T), G396R (1506G>A 1508A>G), K398A (1512A>G 1513A>C 1514G>C), V399I (1515G>A 1517G>C), R400Q (1519G>A 1520C>G), C405Y (1534G>A 1535C>T), S407V (1539T>G 1540C>T 1541C>A), A409V (1546C>T 1547C>A), Q410P (1549A>C 1550G>A), I411A (1551A>G 1552T>C), D412E (1556C>A), V418I (1572G>A 1574C>A), N421K (1583C>G), N423del (1587_1589delAAC), A426S (1596G>T 1598C>A), I428V (1602A>G 1604T>A), D429G (1606A>G 1607C>T), Q438K (1632C>A), Q439E (1635C>G), Q442E (1644C>G 1646A>G), D443E (1649C>G), K447L (1659A>C 1660A>T 1661A>G), F448L (1664T>G), E449R (1665G>A 1666A>G 1667A>G), L450F (1668C>T 1670C>T), T451N (1672C>A 1673C>T), R452I (1674C>A 1675G>T 1676C>A), R453K (1677C>A 1678G>A 1679T>A), D455Q (1683G>C 1685T>G), H456Q (1688T>A), T462S (1704A>T 1706C>T), Q464W (1710C>T 1711A>G), V466I (1716G>A 1718C>T), K467M (1720A>T 1721A>G), D468E (1724C>A), R471H (1732G>A 1733G>C)								
Codon mutations:	CCT335.GT (1324C>G), GCA336TCA (1326G>T), ACT337ACA (1331T>A), AAG340GAA (1338A>G 1340G>A), ACC341GAC (1341A>G 1342C>A), GCG344ACA (1350G>A 1352G>A), GCC346GAT (1357C>A 1358C>T), ATA347ATT (1361A>T), CAC349CGT (1366A>G 1367C>T), ACT350GCT (1368A>G), GTG351GGG (1372T>G), CCC352CCT (1376C>T), TAC354TAT (1382C>T), GGG355GGC (1385G>C), TGC356TGT (1388C>T), GTA357GGT (1390T>G 1391A>T), ACC360ACA (1400C>A), GAG362GGA (1405A>G 1406G>A), AAC363GAC (1407A>G), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GTC370GTG (1430C>G), AAG372AAA (1436G>A), ATG373GAG (1437A>G 1438T>A), GTG374GTA (1442G>A), ATC375ATT (1445C>T), GGG380GGT (1460G>T), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), AAG385AAA (1475G>A), GTC386GTT (1478C>T), TCG389TCT (1487G>T), GCC390GCG (1490C>G), ATT393ATA (1499T>A), CTC394TTG (1500C>T 1502C>G), GGA396AGG (1506G>A 1508A>G), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GCC (1512A>G 1513A>C 1514G>C), GTG399ATC (1515G>A 1517G>C), CGC400CAG (1519G>A 1520C>G), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TAT (1534G>A 1535C>T), AAG406AAA (1538G>A), TCC407GTA (1539T>G 1540C>T 1541C>A), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CCA (1549A>C 1550G>A), ATA411GCA (1551A>G 1552T>C), GAC412GAA (1556C>A), CCG413CCC (1559G>C), ACT414ACA (1562T>A), CCC415CCT (1565C>T), GTG416GTA (1568G>A), GTC418ATA (1572G>A 1574C>A), TCC420-TG (1578delT 1579C>T 1580C>G), AAC421AAG (1583C>G), ACC422ACT (1586C>T), AAC423del (1587_1589delAAC), TGC425TGT (1595C>T), GCC426TCA (1596G>T 1598C>A), GTG427GTA (1601G>A), ATT428GTA (1602A>G 1604T>A), GAC429GGT (1606A>G 1607C>T), GGG430GGC (1610G>C), TCA432AGC (1614T>A 1615C>G 1616A>C), ACC434-GC (1620delA 1621C>G), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAG438AAG (1632C>A), CAG439GAG (1635C>G), CCG440CCT (1640G>T), TTG441CTT (1641T>C 1643G>T), CAA442GAG (1644C>G 1646A>G), GAC443GAG (1649C>G), CGG444AGA (1650C>A 1652G>A), TTC446TTT (1658C>T), AAA447CTG (1659A>C 1660A>T 1661A>G), TTT448TTG (1664T>G), GAA449AGG (1665G>A 1666A>G 1667A>G), CTC450TTT (1668C>T 1670C>T), ACC451AAT (1672C>A 1673C>T), CGC452ATA (1674C>A 1675G>T 1676C>A), CGT453AAA (1677C>A 1678G>A 1679T>A), CTG454TTG (1680C>T), GAT455CAG (1683G>C 1685T>G), CAT456CAA (1688T>A), GAC457GAT (1691C>T), GGG459GGA (1697G>A), GTC461GTA (1703C>A), ACC462TCT (1704A>T 1706C>T), AAG463AAA (1709G>A), CAG464TGG (1710C>T 1711A>G), GTC466ATT (1716G>A 1718C>T), AAA467ATG (1720A>T 1721A>G), GAC468GAA (1724C>A), TTC470TTT (1730C>T), CGG471CAC (1732G>A 1733G>C)								
Rep 78 protein (YP_680423.1)	336	473	22.2%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A336S (1326G>T), K340E (1338A>G 1340G>A), T341D (1341A>G 1342C>A), A344T (1350G>A 1352G>A), A346D (1357C>A 1358C>T), H349R (1366A>G 1367C>T), T350A (1368A>G), V351G (1372T>G), V357G (1390T>G 1391A>T), E362G (1405A>G 1406G>A), N363D (1407A>G), M373E (1437A>G 1438T>A), A384N (1470G>A 1471C>A 1472C>T), G396R (1506G>A 1508A>G), K398A (1512A>G 1513A>C 1514G>C), V399I (1515G>A 1517G>C), R400Q (1519G>A 1520C>G), C405Y (1534G>A 1535C>T), S407V (1539T>G 1540C>T 1541C>A), A409V (1546C>T 1547C>A), Q410P (1549A>C 1550G>A), I411A (1551A>G 1552T>C), D412E (1556C>A), V418I (1572G>A 1574C>A), N421K (1583C>G), N423del (1587_1589delAAC), A426S (1596G>T 1598C>A), I428V (1602A>G 1604T>A), D429G (1606A>G 1607C>T), Q438K (1632C>A), Q439E (1635C>G), Q442E (1644C>G 1646A>G), D443E (1649C>G), K447L (1659A>C 1660A>T 1661A>G), F448L (1664T>G), E449R (1665G>A 1666A>G 1667A>G), L450F (1668C>T 1670C>T), T451N (1672C>A 1673C>T), R452I (1674C>A 1675G>T 1676C>A), R453K (1677C>A 1678G>A 1679T>A), D455Q (1683G>C 1685T>G), H456Q (1688T>A), T462S (1704A>T 1706C>T), Q464W (1710C>T 1711A>G), V466I (1716G>A 1718C>T), K467M (1720A>T 1721A>G), D468E (1724C>A), R471H (1732G>A 1733G>C)								
Codon mutations:	CCT335.GT (1324C>G), GCA336TCA (1326G>T), ACT337ACA (1331T>A), AAG340GAA (1338A>G 1340G>A), ACC341GAC (1341A>G 1342C>A), GCG344ACA (1350G>A 1352G>A), GCC346GAT (1357C>A 1358C>T), ATA347ATT (1361A>T), CAC349CGT (1366A>G 1367C>T), ACT350GCT (1368A>G), GTG351GGG (1372T>G), CCC352CCT (1376C>T), TAC354TAT (1382C>T), GGG355GGC (1385G>C), TGC356TGT (1388C>T), GTA357GGT (1390T>G 1391A>T), ACC360ACA (1400C>A), GAG362GGA (1405A>G 1406G>A), AAC363GAC (1407A>G), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GTC370GTG (1430C>G), AAG372AAA (1436G>A), ATG373GAG (1437A>G 1438T>A), GTG374GTA (1442G>A), ATC375ATT (1445C>T), GGG380GGT (1460G>T), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), AAG385AAA (1475G>A), GTC386GTT (1478C>T), TCG389TCT (1487G>T), GCC390GCG (1490C>G), ATT393ATA (1499T>A), CTC394TTG (1500C>T 1502C>G), GGA396AGG (1506G>A 1508A>G), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GCC (1512A>G 1513A>C 1514G>C), GTG399ATC (1515G>A 1517G>C), CGC400CAG (1519G>A 1520C>G), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TAT (1534G>A 1535C>T), AAG406AAA (1538G>A), TCC407GTA (1539T>G 1540C>T 1541C>A), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CCA (1549A>C 1550G>A), ATA411GCA (1551A>G 1552T>C), GAC412GAA (1556C>A), CCG413CCC (1559G>C), ACT414ACA (1562T>A), CCC415CCT (1565C>T), GTG416GTA (1568G>A), GTC418ATA (1572G>A 1574C>A), TCC420-TG (1578delT 1579C>T 1580C>G), AAC421AAG (1583C>G), ACC422ACT (1586C>T), AAC423del (1587_1589delAAC), TGC425TGT (1595C>T), GCC426TCA (1596G>T 1598C>A), GTG427GTA (1601G>A), ATT428GTA (1602A>G 1604T>A), GAC429GGT (1606A>G 1607C>T), GGG430GGC (1610G>C), TCA432AGC (1614T>A 1615C>G 1616A>C), ACC434-GC (1620delA 1621C>G), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAG438AAG (1632C>A), CAG439GAG (1635C>G), CCG440CCT (1640G>T), TTG441CTT (1641T>C 1643G>T), CAA442GAG (1644C>G 1646A>G), GAC443GAG (1649C>G), CGG444AGA (1650C>A 1652G>A), TTC446TTT (1658C>T), AAA447CTG (1659A>C 1660A>T 1661A>G), TTT448TTG (1664T>G), GAA449AGG (1665G>A 1666A>G 1667A>G), CTC450TTT (1668C>T 1670C>T), ACC451AAT (1672C>A 1673C>T), CGC452ATA (1674C>A 1675G>T 1676C>A), CGT453AAA (1677C>A 1678G>A 1679T>A), CTG454TTG (1680C>T), GAT455CAG (1683G>C 1685T>G), CAT456CAA (1688T>A), GAC457GAT (1691C>T), GGG459GGA (1697G>A), GTC461GTA (1703C>A), ACC462TCT (1704A>T 1706C>T), AAG463AAA (1709G>A), CAG464TGG (1710C>T 1711A>G), GTC466ATT (1716G>A 1718C>T), AAA467ATG (1720A>T 1721A>G), GAC468GAA (1724C>A), TTC470TTT (1730C>T), CGG471CAC (1732G>A 1733G>C)								
Rep 40 protein (YP_680424.1)	112	249	44.1%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A112S (1326G>T), K116E (1338A>G 1340G>A), T117D (1341A>G 1342C>A), A120T (1350G>A 1352G>A), A122D (1357C>A 1358C>T), H125R (1366A>G 1367C>T), T126A (1368A>G), V127G (1372T>G), V133G (1390T>G 1391A>T), E138G (1405A>G 1406G>A), N139D (1407A>G), M149E (1437A>G 1438T>A), A160N (1470G>A 1471C>A 1472C>T), G172R (1506G>A 1508A>G), K174A (1512A>G 1513A>C 1514G>C), V175I (1515G>A 1517G>C), R176Q (1519G>A 1520C>G), C181Y (1534G>A 1535C>T), S183V (1539T>G 1540C>T 1541C>A), A185V (1546C>T 1547C>A), Q186P (1549A>C 1550G>A), I187A (1551A>G 1552T>C), D188E (1556C>A), V194I (1572G>A 1574C>A), N197K (1583C>G), N199del (1587_1589delAAC), A202S (1596G>T 1598C>A), I204V (1602A>G 1604T>A), D205G (1606A>G 1607C>T), Q214K (1632C>A), Q215E (1635C>G), Q218E (1644C>G 1646A>G), D219E (1649C>G), K223L (1659A>C 1660A>T 1661A>G), F224L (1664T>G), E225R (1665G>A 1666A>G 1667A>G), L226F (1668C>T 1670C>T), T227N (1672C>A 1673C>T), R228I (1674C>A 1675G>T 1676C>A), R229K (1677C>A 1678G>A 1679T>A), D231Q (1683G>C 1685T>G), H232Q (1688T>A), T238S (1704A>T 1706C>T), Q240W (1710C>T 1711A>G), V242I (1716G>A 1718C>T), K243M (1720A>T 1721A>G), D244E (1724C>A), R247H (1732G>A 1733G>C)								

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**1324**	**1738**	**8.9%**	**196**	**24.9%**	**410 (98.8%)**	**262 (63.1%)**	**0/5**	
Codon mutations:	CCT111.GT (1324C>G), GCA112TCA (1326G>T), ACT113ACA (1331T>A), AAG116GAA (1338A>G 1340G>A), ACC117GAC (1341A>G 1342C>A), GCG120ACA (1350G>A 1352G>A), GCC122GAT (1357C>A 1358C>T), ATA123ATT (1361A>T), CAC125CGT (1366A>G 1367C>T), ACT126GCT (1368A>G), GTG127GGG (1372T>G), CCC128CCT (1376C>T), TAC130TAT (1382C>T), GGG131GGC (1385G>C), TGC132TGT (1388C>T), GTA133GGT (1390T>G 1391A>T), ACC136ACA (1400C>A), GAG138GGA (1405A>G 1406G>A), AAC139GAC (1407A>G), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GTC146GTG (1430C>G), AAG148AAA (1436G>A), ATG149GAG (1437A>G 1438T>A), GTG150GTA (1442G>A), ATC151ATT (1445C>T), GGG156GGT (1460G>T), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), AAG161AAA (1475G>A), GTC162GTT (1478C>T), TCG165TCT (1487G>T), GCC166GCG (1490C>G), ATT169ATA (1499T>A), CTC170TTG (1500C>T 1502C>G), GGA172AGG (1506G>A 1508A>G), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GCC (1512A>G 1513A>C 1514G>C), GTG175ATC (1515G>A 1517G>C), CGC176CAG (1519G>A 1520C>G), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TAT (1534G>A 1535C>T), AAG182AAA (1538G>A), TCC183GTA (1539T>G 1540C>T 1541C>A), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CCA (1549A>C 1550G>A), ATA187GCA (1551A>G 1552T>C), GAC188GAA (1556C>A), CCG189CCC (1559G>C), ACT190ACA (1562T>A), CCC191CCT (1565C>T), GTG192GTA (1568G>A), GTC194ATA (1572G>A 1574C>A), TCC196-TG (1578delT 1579C>T 1580C>G), AAC197AAG (1583C>G), ACC198ACT (1586C>T), AAC199del (1587_1589delAAC), TGC201TGT (1595C>T), GCC202TCA (1596G>T 1598C>A), GTG203GTA (1601G>A), ATT204GTA (1602A>G 1604T>A), GAC205GGT (1606A>G 1607C>T), GGG206GGC (1610G>C), TCA208AGC (1614T>A 1615C>G 1616A>C), ACC210-GC (1620delA 1621C>G), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAG214AAG (1632C>A), CAG215GAG (1635C>G), CCG216CCT (1640G>T), TTG217CTT (1641T>C 1643G>T), CAA218GAG (1644C>G 1646A>G), GAC219GAG (1649C>G), CGG220AGA (1650C>A 1652G>A), TTC222TTT (1658C>T), AAA223CTG (1659A>C 1660A>T 1661A>G), TTT224TTG (1664T>G), GAA225AGG (1665G>A 1666A>G 1667A>G), CTC226TTT (1668C>T 1670C>T), ACC227AAT (1672C>A 1673C>T), CGC228ATA (1674C>A 1675G>T 1676C>A), CGT229AAA (1677C>A 1678G>A 1679T>A), CTG230TTG (1680C>T), GAT231CAG (1683G>C 1685T>G), CAT232CAA (1688T>A), GAC233GAT (1691C>T), GGG235GGA (1697G>A), GTC237GTA (1703C>A), ACC238TCT (1704A>T 1706C>T), AAG239AAA (1709G>A), CAG240TGG (1710C>T 1711A>G), GTC242ATT (1716G>A 1718C>T), AAA243ATG (1720A>T 1721A>G), GAC244GAA (1724C>A), TTC246TTT (1730C>T), CGG247CAC (1732G>A 1733G>C)								
Rep 52 protein (YP_680425.1)	112	249	34.7%	433	43.2%	137 (99.3%)	87 (63.0%)	0/1/2/2	0
Protein mutations:	A112S (1326G>T), K116E (1338A>G 1340G>A), T117D (1341A>G 1342C>A), A120T (1350G>A 1352G>A), A122D (1357C>A 1358C>T), H125R (1366A>G 1367C>T), T126A (1368A>G), V127G (1372T>G), V133G (1390T>G 1391A>T), E138G (1405A>G 1406G>A), N139D (1407A>G), M149E (1437A>G 1438T>A), A160N (1470G>A 1471C>A 1472C>T), G172R (1506G>A 1508A>G), K174A (1512A>G 1513A>C 1514G>C), V175I (1515G>A 1517G>C), R176Q (1519G>A 1520C>G), C181Y (1534G>A 1535C>T), S183V (1539T>G 1540C>T 1541C>A), A185V (1546C>T 1547C>A), Q186P (1549A>C 1550G>A), I187A (1551A>G 1552T>C), D188E (1556C>A), V194I (1572G>A 1574C>A), N197K (1583C>G), N199del (1587_1589delAAC), A202S (1596G>T 1598C>A), I204V (1602A>G 1604T>A), D205G (1606A>G 1607C>T), Q214K (1632C>A), Q215E (1635C>G), Q218E (1644C>G 1646A>G), D219E (1649C>G), K223L (1659A>C 1660A>T 1661A>G), F224L (1664T>G), E225R (1665G>A 1666A>G 1667A>G), L226F (1668C>T 1670C>T), T227N (1672C>A 1673C>T), R228I (1674C>A 1675G>T 1676C>A), R229K (1677C>A 1678G>A 1679T>A), D231Q (1683G>C 1685T>G), H232Q (1688T>A), T238S (1704A>T 1706C>T), Q240W (1710C>T 1711A>G), V242I (1716G>A 1718C>T), K243M (1720A>T 1721A>G), D244E (1724C>A), R247H (1732G>A 1733G>C)								
Codon mutations:	CCT111.GT (1324C>G), GCA112TCA (1326G>T), ACT113ACA (1331T>A), AAG116GAA (1338A>G 1340G>A), ACC117GAC (1341A>G 1342C>A), GCG120ACA (1350G>A 1352G>A), GCC122GAT (1357C>A 1358C>T), ATA123ATT (1361A>T), CAC125CGT (1366A>G 1367C>T), ACT126GCT (1368A>G), GTG127GGG (1372T>G), CCC128CCT (1376C>T), TAC130TAT (1382C>T), GGG131GGC (1385G>C), TGC132TGT (1388C>T), GTA133GGT (1390T>G 1391A>T), ACC136ACA (1400C>A), GAG138GGA (1405A>G 1406G>A), AAC139GAC (1407A>G), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GTC146GTG (1430C>G), AAG148AAA (1436G>A), ATG149GAG (1437A>G 1438T>A), GTG150GTA (1442G>A), ATC151ATT (1445C>T), GGG156GGT (1460G>T), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), AAG161AAA (1475G>A), GTC162GTT (1478C>T), TCG165TCT (1487G>T), GCC166GCG (1490C>G), ATT169ATA (1499T>A), CTC170TTG (1500C>T 1502C>G), GGA172AGG (1506G>A 1508A>G), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GCC (1512A>G 1513A>C 1514G>C), GTG175ATC (1515G>A 1517G>C), CGC176CAG (1519G>A 1520C>G), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TAT (1534G>A 1535C>T), AAG182AAA (1538G>A), TCC183GTA (1539T>G 1540C>T 1541C>A), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CCA (1549A>C 1550G>A), ATA187GCA (1551A>G 1552T>C), GAC188GAA (1556C>A), CCG189CCC (1559G>C), ACT190ACA (1562T>A), CCC191CCT (1565C>T), GTG192GTA (1568G>A), GTC194ATA (1572G>A 1574C>A), TCC196-TG (1578delT 1579C>T 1580C>G), AAC197AAG (1583C>G), ACC198ACT (1586C>T), AAC199del (1587_1589delAAC), TGC201TGT (1595C>T), GCC202TCA (1596G>T 1598C>A), GTG203GTA (1601G>A), ATT204GTA (1602A>G 1604T>A), GAC205GGT (1606A>G 1607C>T), GGG206GGC (1610G>C), TCA208AGC (1614T>A 1615C>G 1616A>C), ACC210-GC (1620delA 1621C>G), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAG214AAG (1632C>A), CAG215GAG (1635C>G), CCG216CCT (1640G>T), TTG217CTT (1641T>C 1643G>T), CAA218GAG (1644C>G 1646A>G), GAC219GAG (1649C>G), CGG220AGA (1650C>A 1652G>A), TTC222TTT (1658C>T), AAA223CTG (1659A>C 1660A>T 1661A>G), TTT224TTG (1664T>G), GAA225AGG (1665G>A 1666A>G 1667A>G), CTC226TTT (1668C>T 1670C>T), ACC227AAT (1672C>A 1673C>T), CGC228ATA (1674C>A 1675G>T 1676C>A), CGT229AAA (1677C>A 1678G>A 1679T>A), CTG230TTG (1680C>T), GAT231CAG (1683G>C 1685T>G), CAT232CAA (1688T>A), GAC233GAT (1691C>T), GGG235GGA (1697G>A), GTC237GTA (1703C>A), ACC238TCT (1704A>T 1706C>T), AAG239AAA (1709G>A), CAG240TGG (1710C>T 1711A>G), GTC242ATT (1716G>A 1718C>T), AAA243ATG (1720A>T 1721A>G), GAC244GAA (1724C>A), TTC246TTT (1730C>T), CGG247CAC (1732G>A 1733G>C)								

*: Inserts / Deletes / Misaligned / Frameshifts

Analysis details

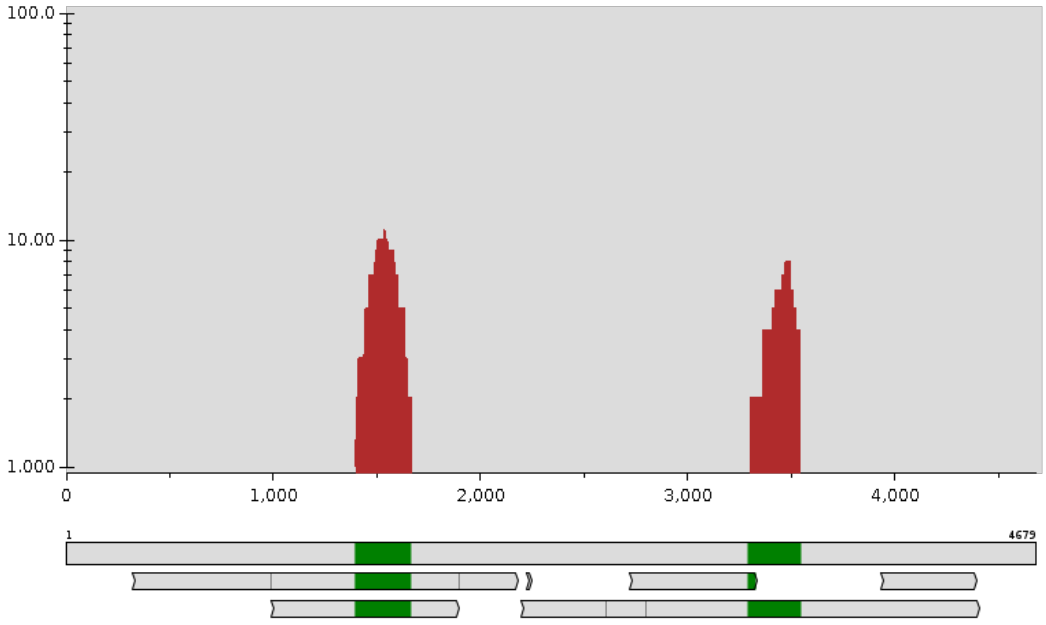
This analysis was performed with Pan-viral (2.14.6)

NGS Details (MG-4-RNASeq021-ZymoSeq): adeno-associated virus 2

Assembly

Coverage Length	514 (2 contig(s))
Depth Of Coverage	5.3
Number Of Reads	22
Reads Per Million	0.22 rpm (after QC)
Ambiguities	0
Assembly Method	de novo + reference guided assembly
Consensus Caller	Bcf Tools

Coverage Map



Assignment

Type	adeno-associated virus 2 (Taxonomy ID: 10804)
Reference Genome	NC_001401.2
NT Identity (%)	58.7452
AA Identity (%)	59.2126
Number Of Stop Codons	4
Number Of CDS	9

Alignment

Alignment Score	160.0 (NT) + 1522.0 (AA) = 1682.0
Concordance (%)	40.8225

Alignment Method	Global, seeded, nucleotide + amino acids (AGA)

Genome Region

Sequence starts at position 1397 and ends at position 3544 relative to NC_001401.2 reference sequence.

Alignment Detailed Statistics

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**1397**	**3544**	**11.0%**	**160**	**15.9%**	**512 (97.0%)**	**309 (58.5%)**	**14/2**	
Mutations:	1400C>T, 1403T>C, 1406G>A, 1415C>A, 1418C>T, 1421C>T, 1423A>G, 1430C>G, 1433C>T, 1436G>A, 1440G>A, 1442G>T, 1445C>T, 1454G>A, 1461A>C, 1463G>A, 1469C>T, 1470G>A, 1471C>A, 1472C>T, 1478C>A, 1481G>T, 1484G>A, 1487G>T, 1490C>T, 1502C>G, 1505A>G, 1508A>T, 1509A>T, 1510G>C, 1511C>T, 1512A>G, 1513A>G, 1514G>T, 1517G>A, 1518C>A, 1520C>A, 1523G>T, 1526C>T, 1529G>A, 1534G>C, 1535C>T, 1538G>A, 1539T>G, 1540C>G, 1544G>T, 1546C>T, 1547C>A, 1550G>A, 1553A>T, 1555A>C, 1556C>T, 1559G>C, 1560delA, 1565C>T, 1566G>A, 1568G>A, 1572G>A, 1574C>A, 1577C>T, 1578T>A, 1579C>G, 1580C>T, 1583C>T, 1585C>T, 1586C>G, 1589C>T, 1590delA, 1594G>A, 1595C>T, 1596G>A, 1597C>T, 1598C>G, 1601G>A, 1602A>G, 1604T>G, 1605G>A, 1607C>T, 1610G>C, 1613C>G, 1615C>G, 1617A>G, 1619G>T, 1620A>C, 1621C>T, 1622C>A, 1625C>T, 1628A>G, 1631C>T, 1632C>A, 1634G>A, 1635C>G, 1637G>A, 1640G>T, 1644C>G, 1645A>G, 1649C>A, 1650C>A, 1652G>A, 1656T>G, 1658C>T, 1660A>T, 1661A>G, 1665G>A, 1667A>G, 1668C>A, 1669T>G, 3309C>A, 3312C>T, 3314T>C, 3316G>C, 3321A>T, 3324G>A, 3330A>G, 3331T>G, 3333C>A, 3334C>A, 3335T>C, 3338C>T, 3339C>A, 3341T>A, 3342G>T, 3343A>T, 3345_3346insATTACCAT, 3348C>T, 3352A>G, 3354T>A, 3355C>A, 3357G>C, 3358G>A, 3360A>C, 3361G>A, 3365G>C, 3366A>C, 3366_3367insACTCCC, 3367C>A, 3369C>G, 3370T>G, 3372T>A, 3373T>G, 3375A>T, 3381C>T, 3385C>T, 3387G>A, 3390G>A, 3399T>A, 3400T>A, 3401C>G, 3402T>C, 3405G>A, 3411G>A, 3413G>A, 3414T>C, 3417C>A, 3420A>C, 3423C>T, 3424A>G, 3426C>T, 3428T>A, 3429T>C, 3431C>G, 3435C>T, 3436A>G, 3438C>A, 3441C>T, 3442A>C, 3443C>A, 3444T>C, 3452A>C, 3454G>T, 3456T>C, 3459T>A, 3464A>G, 3466A>T, 3467G>C, 3469A>T, 3473A>T, 3475G>A, 3476C>G, 3477T>C, 3483C>T, 3488G>A, 3489T>A, 3490C>A, 3491T>C, 3492G>C, 3493G>A, 3494A>C, 3497G>C, 3500T>G, 3501C>A, 3502A>T, 3503T>C, 3504G>T, 3511C>T, 3513C>A, 3514A>G, 3516C>T, 3519C>T, 3525C>T, 3528G>T, 3531T>C, 3533A>C, 3534C>T, 3537G>T, 3539G>A, 3542G>A								
CDS									
AAV2gp01	360	450	16.9%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D368G (1423A>G), V374I (1440G>A 1442G>T), K381Q (1461A>C 1463G>A), A384N (1470G>A 1471C>A 1472C>T), K398G (1512A>G 1513A>G 1514G>T), C405S (1534G>C 1535C>T), S407G (1539T>G 1540C>G), A409V (1546C>T 1547C>A), D412A (1555A>C 1556C>T), V416I (1566G>A 1568G>A), V418I (1572G>A 1574C>A), T422M (1585C>T 1586C>G), C425Y (1594G>A 1595C>T), A426M (1596G>A 1597C>T 1598C>G), I428V (1602A>G 1604T>G), D429N (1605G>A 1607C>T), N431K (1613C>G), S432* (1615C>G), T433A (1617A>G 1619G>T), T434L (1620A>C 1621C>T 1622C>A), Q438K (1632C>A 1634G>A), Q439E (1635C>G 1637G>A), Q442G (1644C>G 1645A>G), D443E (1649C>A), F446V (1656T>G 1658C>T), K447M (1660A>T 1661A>G), E449K (1665G>A 1667A>G)								
Codon mutations:	ACC360ACT (1400C>T), AAT361AAC (1403T>C), GAG362GAA (1406G>A), CCC365CCA (1415C>A), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GAC368GGC (1423A>G), GTC370GTG (1430C>G), GAC371GAT (1433C>T), AAG372AAA (1436G>A), GTG374ATT (1440G>A 1442G>T), ATC375ATT (1445C>T), GAG378GAA (1454G>A), AAG381CAA (1461A>C 1463G>A), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), GTC386GTA (1478C>A), GTG387GTT (1481G>T), GAG388GAA (1484G>A), TCG389TCT (1487G>T), GCC390GCT (1490C>T), CTC394CTG (1502C>G), GGA395GGG (1505A>G), GGA396GGT (1508A>T), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GGT (1512A>G 1513A>G 1514G>T), GTG399GTA (1517G>A), CGC400AGA (1518C>A 1520C>A), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TCT (1534G>C 1535C>T), AAG406AAA (1538G>A), TCC407GGC (1539T>G 1540C>G), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CAA (1550G>A), ATA411ATT (1553A>T), GAC412GCT (1555A>C 1556C>T), CCG413CCC (1559G>C), ACT414-CT (1560delA), CCC415CCT (1565C>T), GTG416ATA (1566G>A 1568G>A), GTC418ATA (1572G>A 1574C>A), ACC419ACT (1577C>T), TCC420AGT (1578T>A 1579C>G 1580C>T), AAC421AAT (1583C>T), ACC422ATG (1585C>T 1586C>G), AAC423AAT (1589C>T), ATG424-TG (1590delA), TGC425TAT (1594G>A 1595C>T), GCC426ATG (1596G>A 1597C>T 1598C>G), GTG427GTA (1601G>A), ATT428GTG (1602A>G 1604T>G), GAC429AAT (1605G>A 1607C>T), GGG430GGC (1610G>C), AAC431AAG (1613C>G), TCA432TGA (1615C>G), ACG433GCT (1617A>G 1619G>T), ACC434CTA (1620A>C 1621C>T 1622C>A), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAC437CAT (1631C>T), CAG438AAA (1632C>A 1634G>A), CAG439GAA (1635C>G 1637G>A), CCG440CCT (1640G>T), CAA442GGA (1644C>G 1645A>G), GAC443GAA (1649C>A), CGG444AGA (1650C>A 1652G>A), TTC446GTT (1656T>G 1658C>T), AAA447ATG (1660A>T 1661A>G), GAA449AAG (1665G>A 1667A>G), CTC450AG. (1668C>A 1669T>G)								
AAV2gp02	360	450	14.6%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D368G (1423A>G), V374I (1440G>A 1442G>T), K381Q (1461A>C 1463G>A), A384N (1470G>A 1471C>A 1472C>T), K398G (1512A>G 1513A>G 1514G>T), C405S (1534G>C 1535C>T), S407G (1539T>G 1540C>G), A409V (1546C>T 1547C>A), D412A (1555A>C 1556C>T), V416I (1566G>A 1568G>A), V418I (1572G>A 1574C>A), T422M (1585C>T 1586C>G), C425Y (1594G>A 1595C>T), A426M (1596G>A 1597C>T 1598C>G), I428V (1602A>G 1604T>G), D429N (1605G>A 1607C>T), N431K (1613C>G), S432* (1615C>G), T433A (1617A>G 1619G>T), T434L (1620A>C 1621C>T 1622C>A), Q438K (1632C>A 1634G>A), Q439E (1635C>G 1637G>A), Q442G (1644C>G 1645A>G), D443E (1649C>A), F446V (1656T>G 1658C>T), K447M (1660A>T 1661A>G), E449K (1665G>A 1667A>G)								
Codon mutations:	ACC360ACT (1400C>T), AAT361AAC (1403T>C), GAG362GAA (1406G>A), CCC365CCA (1415C>A), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GAC368GGC (1423A>G), GTC370GTG (1430C>G), GAC371GAT (1433C>T), AAG372AAA (1436G>A), GTG374ATT (1440G>A 1442G>T), ATC375ATT (1445C>T), GAG378GAA (1454G>A), AAG381CAA (1461A>C 1463G>A), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), GTC386GTA (1478C>A), GTG387GTT (1481G>T), GAG388GAA (1484G>A), TCG389TCT (1487G>T), GCC390GCT (1490C>T), CTC394CTG (1502C>G), GGA395GGG (1505A>G), GGA396GGT (1508A>T), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GGT (1512A>G 1513A>G 1514G>T), GTG399GTA (1517G>A), CGC400AGA (1518C>A 1520C>A), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TCT (1534G>C 1535C>T), AAG406AAA (1538G>A), TCC407GGC (1539T>G 1540C>G), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CAA (1550G>A), ATA411ATT (1553A>T), GAC412GCT (1555A>C 1556C>T), CCG413CCC (1559G>C), ACT414-CT (1560delA), CCC415CCT (1565C>T), GTG416ATA (1566G>A 1568G>A), GTC418ATA (1572G>A 1574C>A), ACC419ACT (1577C>T), TCC420AGT (1578T>A 1579C>G 1580C>T), AAC421AAT (1583C>T), ACC422ATG (1585C>T 1586C>G), AAC423AAT (1589C>T), ATG424-TG (1590delA), TGC425TAT (1594G>A 1595C>T), GCC426ATG (1596G>A 1597C>T 1598C>G), GTG427GTA (1601G>A), ATT428GTG (1602A>G 1604T>G), GAC429AAT (1605G>A 1607C>T), GGG430GGC (1610G>C), AAC431AAG (1613C>G), TCA432TGA (1615C>G), ACG433GCT (1617A>G 1619G>T), ACC434CTA (1620A>C 1621C>T 1622C>A), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAC437CAT (1631C>T), CAG438AAA (1632C>A 1634G>A), CAG439GAA (1635C>G 1637G>A), CCG440CCT (1640G>T), CAA442GGA (1644C>G 1645A>G), GAC443GAA (1649C>A), CGG444AGA (1650C>A 1652G>A), TTC446GTT (1656T>G 1658C>T), AAA447ATG (1660A>T 1661A>G), GAA449AAG (1665G>A 1667A>G), CTC450AG. (1668C>A 1669T>G)								
AAV2gp03	136	226	29.1%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D144G (1423A>G), V150I (1440G>A 1442G>T), K157Q (1461A>C 1463G>A), A160N (1470G>A 1471C>A 1472C>T), K174G (1512A>G 1513A>G 1514G>T), C181S (1534G>C 1535C>T), S183G (1539T>G 1540C>G), A185V (1546C>T 1547C>A), D188A (1555A>C 1556C>T), V192I (1566G>A 1568G>A), V194I (1572G>A 1574C>A), T198M (1585C>T 1586C>G), C201Y (1594G>A 1595C>T), A202M (1596G>A 1597C>T 1598C>G), I204V (1602A>G 1604T>G), D205N (1605G>A 1607C>T), N207K (1613C>G), S208* (1615C>G), T209A (1617A>G 1619G>T), T210L (1620A>C 1621C>T 1622C>A), Q214K (1632C>A 1634G>A), Q215E (1635C>G 1637G>A), Q218G (1644C>G 1645A>G), D219E (1649C>A), F222V (1656T>G 1658C>T), K223M (1660A>T 1661A>G), E225K (1665G>A 1667A>G)								
Codon mutations:	ACC136ACT (1400C>T), AAT137AAC (1403T>C), GAG138GAA (1406G>A), CCC141CCA (1415C>A), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GAC144GGC (1423A>G), GTC146GTG (1430C>G), GAC147GAT (1433C>T), AAG148AAA (1436G>A), GTG150ATT (1440G>A 1442G>T), ATC151ATT (1445C>T), GAG154GAA (1454G>A), AAG157CAA (1461A>C 1463G>A), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), GTC162GTA (1478C>A), GTG163GTT (1481G>T), GAG164GAA (1484G>A), TCG165TCT (1487G>T), GCC166GCT (1490C>T), CTC170CTG (1502C>G), GGA171GGG (1505A>G), GGA172GGT (1508A>T), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GGT (1512A>G 1513A>G 1514G>T), GTG175GTA (1517G>A), CGC176AGA (1518C>A 1520C>A), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TCT (1534G>C 1535C>T), AAG182AAA (1538G>A), TCC183GGC (1539T>G 1540C>G), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CAA (1550G>A), ATA187ATT (1553A>T), GAC188GCT (1555A>C 1556C>T), CCG189CCC (1559G>C), ACT190-CT (1560delA), CCC191CCT (1565C>T), GTG192ATA (1566G>A 1568G>A), GTC194ATA (1572G>A 1574C>A), ACC195ACT (1577C>T), TCC196AGT (1578T>A 1579C>G 1580C>T), AAC197AAT (1583C>T), ACC198ATG (1585C>T 1586C>G), AAC199AAT (1589C>T), ATG200-TG (1590delA), TGC201TAT (1594G>A 1595C>T), GCC202ATG (1596G>A 1597C>T 1598C>G), GTG203GTA (1601G>A), ATT204GTG (1602A>G 1604T>G), GAC205AAT (1605G>A 1607C>T), GGG206GGC (1610G>C), AAC207AAG (1613C>G), TCA208TGA (1615C>G), ACG209GCT (1617A>G 1619G>T), ACC210CTA (1620A>C 1621C>T 1622C>A), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAC213CAT (1631C>T), CAG214AAA (1632C>A 1634G>A), CAG215GAA (1635C>G 1637G>A), CCG216CCT (1640G>T), CAA218GGA (1644C>G 1645A>G), GAC219GAA (1649C>A), CGG220AGA (1650C>A 1652G>A), TTC222GTT (1656T>G 1658C>T), AAA223ATG (1660A>T 1661A>G), GAA225AAG (1665G>A 1667A>G), CTC226AG. (1668C>A 1669T>G)								
AAV2gp04	136	226	22.9%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D144G (1423A>G), V150I (1440G>A 1442G>T), K157Q (1461A>C 1463G>A), A160N (1470G>A 1471C>A 1472C>T), K174G (1512A>G 1513A>G 1514G>T), C181S (1534G>C 1535C>T), S183G (1539T>G 1540C>G), A185V (1546C>T 1547C>A), D188A (1555A>C 1556C>T), V192I (1566G>A 1568G>A), V194I (1572G>A 1574C>A), T198M (1585C>T 1586C>G), C201Y (1594G>A 1595C>T), A202M (1596G>A 1597C>T 1598C>G), I204V (1602A>G 1604T>G), D205N (1605G>A 1607C>T), N207K (1613C>G), S208* (1615C>G), T209A (1617A>G 1619G>T), T210L (1620A>C 1621C>T 1622C>A), Q214K (1632C>A 1634G>A), Q215E (1635C>G 1637G>A), Q218G (1644C>G 1645A>G), D219E (1649C>A), F222V (1656T>G 1658C>T), K223M (1660A>T 1661A>G), E225K (1665G>A 1667A>G)								

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**1397**	**3544**	**11.0%**	**160**	**15.9%**	**512 (97.0%)**	**309 (58.5%)**	**14/2**	
Codon mutations:	ACC136ACT (1400C>T), AAT137AAC (1403T>C), GAG138GAA (1406G>A), CCC141CCA (1415C>A), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GAC144GGC (1423A>G), GTC146GTG (1430C>G), GAC147GAT (1433C>T), AAG148AAA (1436G>A), GTG150ATT (1440G>A 1442G>T), ATC151ATT (1445C>T), GAG154GAA (1454G>A), AAG157CAA (1461A>C 1463G>A), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), GTC162GTA (1478C>A), GTG163GTT (1481G>T), GAG164GAA (1484G>A), TCG165TCT (1487G>T), GCC166GCT (1490C>T), CTC170CTG (1502C>G), GGA171GGG (1505A>G), GGA172GGT (1508A>T), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GGT (1512A>G 1513A>G 1514G>T), GTG175GTA (1517G>A), CGC176AGA (1518C>A 1520C>A), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TCT (1534G>C 1535C>T), AAG182AAA (1538G>A), TCC183GGC (1539T>G 1540C>G), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CAA (1550G>A), ATA187ATT (1553A>T), GAC188GCT (1555A>C 1556C>T), CCG189CCC (1559G>C), ACT190-CT (1560delA), CCC191CCT (1565C>T), GTG192ATA (1566G>A 1568G>A), GTC194ATA (1572G>A 1574C>A), ACC195ACT (1577C>T), TCC196AGT (1578T>A 1579C>G 1580C>T), AAC197AAT (1583C>T), ACC198ATG (1585C>T 1586C>G), AAC199AAT (1589C>T), ATG200-TG (1590delA), TGC201TAT (1594G>A 1595C>T), GCC202ATG (1596G>A 1597C>T 1598C>G), GTG203GTA (1601G>A), ATT204GTG (1602A>G 1604T>G), GAC205AAT (1605G>A 1607C>T), GGG206GGC (1610G>C), AAC207AAG (1613C>G), TCA208TGA (1615C>G), ACG209GCT (1617A>G 1619G>T), ACC210CTA (1620A>C 1621C>T 1622C>A), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAC213CAT (1631C>T), CAG214AAA (1632C>A 1634G>A), CAG215GAA (1635C>G 1637G>A), CCG216CCT (1640G>T), CAA218GGA (1644C>G 1645A>G), GAC219GAA (1649C>A), CGG220AGA (1650C>A 1652G>A), TTC222GTT (1656T>G 1658C>T), AAA223ATG (1660A>T 1661A>G), GAA225AAG (1665G>A 1667A>G), CTC226AG. (1668C>A 1669T>G)				
AAV2gp05	368	448	11.0%	217	37.1%	81 (94.2%)	43 (50.0%)	5/0/1/1	0
Protein mutations:	M371T (3314T>C), V372L (3316G>C), Y377E (3331T>G 3333C>A), L378T (3334C>A 3335T>C), T379I (3338C>T 3339C>A), L380H (3341T>A 3342G>T), N381Y (3343A>T), N381_N382insITX (3345_3346insATTACCAT), S384G (3352A>G 3354T>A), Q385N (3355C>A 3357G>C), A386T (3358G>A 3360A>C), V387I (3361G>A), G388A (3365G>C 3366A>C), G388_R389insTP (3366_3367insACTCCC), S390A (3370T>G 3372T>A), S391A (3373T>G 3375A>T), R404H (3413G>A 3414T>C), N408D (3424A>G 3426C>T), F409Y (3428T>A 3429T>C), T410S (3431C>G), S412G (3436A>G 3438C>A), T414H (3442A>C 3443C>A 3444T>C), D417A (3452A>C), V418F (3454G>T 3456T>C), H421R (3464A>G), S423C (3469A>T), Y424F (3473A>T), A425S (3475G>A 3476C>G 3477T>C), S429K (3488G>A 3489T>A), L430T (3490C>A 3491T>C 3492G>C), D431T (3493G>A 3494A>C), R432P (3497G>C), L433R (3500T>G 3501C>A), M434S (3502A>T 3503T>C 3504G>T), I438V (3514A>G 3516C>T), Y444S (3533A>C 3534C>T), L445F (3537G>T), S446N (3539G>A), R447K (3542G>A)				
Codon mutations:	GTC369GTA (3309C>A), TTC370TTT (3312C>T), ATG371ACG (3314T>C), GTG372CTG (3316G>C), CCA373CCT (3321A>T), CAG374CAA (3324G>A), GGA376GGG (3330A>G), TAC377GAA (3331T>G 3333C>A), CTC378ACC (3334C>A 3335T>C), ACC379ATA (3338C>T 3339C>A), CTG380CAT (3341T>A 3342G>T), AAC381TAC (3343A>T), AAC381_AAC382insATTACCAT- (3345_3346insATTACCAT), AAC382AAT (3348C>T), AGT384GGA (3352A>G 3354T>A), CAG385AAC (3355C>A 3357G>C), GCA386ACC (3358G>A 3360A>C), GTA387ATA (3361G>A), GGA388GCC (3365G>C 3366A>C), GGA388_CGC389insACTCCC (3366_3367insACTCCC), CGC389AGG (3367C>A 3369C>G), TCT390GCA (3370T>G 3372T>A), TCA391GCT (3373T>G 3375A>T), TAC393TAT (3381C>T), CTG395TTA (3385C>T 3387G>A), GAG396GAA (3390G>A), CCT399CCA (3399T>A), TCT400AGC (3400T>A 3401C>G 3402T>C), CAG401CAA (3405G>A), CTG403CTA (3411G>A), CGT404CAC (3413G>A 3414T>C), ACC405ACA (3417C>A), GGA406GGC (3420A>C), AAC407AAT (3423C>T), AAC408GAT (3424A>G 3426C>T), TTT409TAC (3428T>A 3429T>C), ACC410AGC (3431C>G), TTC411TTT (3435C>T), AGC412GGA (3436A>G 3438C>A), TAC413TAT (3441C>T), ACT414CAC (3442A>C 3443C>A 3444T>C), GAC417GCC (3452A>C), GTT418TTC (3454G>T 3456T>C), CCT419CCA (3459T>A), CAC421CGC (3464A>G), AGC422TCC (3466A>T 3467G>C), AGC423TGC (3469A>T), TAC424TTC (3473A>T), GCT425AGC (3475G>A 3476C>G 3477T>C), AGC427AGT (3483C>T), AGT429AAA (3488G>A 3489T>A), CTG430ACC (3490C>A 3491T>C 3492G>C), GAC431ACC (3493G>A 3494A>C), CGT432CCT (3497G>C), CTC433CGA (3500T>G 3501C>A), ATG434TCT (3502A>T 3503T>C 3504G>T), CTC437TTA (3511C>T 3513C>A), ATC438GTT (3514A>G 3516C>T), GAC439GAT (3519C>T), TAC441TAT (3525C>T), CTG442CTT (3528G>T), TAT443TAC (3531T>C), TAC444TCT (3533A>C 3534C>T), TTG445TTT (3537G>T), AGC446AAC (3539G>A), AGA447AAA (3542G>A)				
AAV2gp06_1	231	311	13.5%	217	37.1%	81 (94.2%)	43 (50.0%)	5/0/1/1	0
Protein mutations:	M234T (3314T>C), V235L (3316G>C), Y240E (3331T>G 3333C>A), L241T (3334C>A 3335T>C), T242I (3338C>T 3339C>A), L243H (3341T>A 3342G>T), N244Y (3343A>T), N244_N245insITX (3345_3346insATTACCAT), S247G (3352A>G 3354T>A), Q248N (3355C>A 3357G>C), A249T (3358G>A 3360A>C), V250I (3361G>A), G251A (3365G>C 3366A>C), G251_R252insTP (3366_3367insACTCCC), S253A (3370T>G 3372T>A), S254A (3373T>G 3375A>T), R267H (3413G>A 3414T>C), N271D (3424A>G 3426C>T), F272Y (3428T>A 3429T>C), T273S (3431C>G), S275G (3436A>G 3438C>A), T277H (3442A>C 3443C>A 3444T>C), D280A (3452A>C), V281F (3454G>T 3456T>C), H284R (3464A>G), S286C (3469A>T), Y287F (3473A>T), A288S (3475G>A 3476C>G 3477T>C), S292K (3488G>A 3489T>A), L293T (3490C>A 3491T>C 3492G>C), D294T (3493G>A 3494A>C), R295P (3497G>C), L296R (3500T>G 3501C>A), M297S (3502A>T 3503T>C 3504G>T), I301V (3514A>G 3516C>T), Y307S (3533A>C 3534C>T), L308F (3537G>T), S309N (3539G>A), R310K (3542G>A)				
Codon mutations:	GTC232GTA (3309C>A), TTC233TTT (3312C>T), ATG234ACG (3314T>C), GTG235CTG (3316G>C), CCA236CCT (3321A>T), CAG237CAA (3324G>A), GGA239GGG (3330A>G), TAC240GAA (3331T>G 3333C>A), CTC241ACC (3334C>A 3335T>C), ACC242ATA (3338C>T 3339C>A), CTG243CAT (3341T>A 3342G>T), AAC244TAC (3343A>T), AAC244_AAC245insATTACCAT- (3345_3346insATTACCAT), AAC245AAT (3348C>T), AGT247GGA (3352A>G 3354T>A), CAG248AAC (3355C>A 3357G>C), GCA249ACC (3358G>A 3360A>C), GTA250ATA (3361G>A), GGA251GCC (3365G>C 3366A>C), GGA251_CGC252insACTCCC (3366_3367insACTCCC), CGC252AGG (3367C>A 3369C>G), TCT253GCA (3370T>G 3372T>A), TCA254GCT (3373T>G 3375A>T), TAC256TAT (3381C>T), CTG258TTA (3385C>T 3387G>A), GAG259GAA (3390G>A), CCT262CCA (3399T>A), TCT263AGC (3400T>A 3401C>G 3402T>C), CAG264CAA (3405G>A), CTG266CTA (3411G>A), CGT267CAC (3413G>A 3414T>C), ACC268ACA (3417C>A), GGA269GGC (3420A>C), AAC270AAT (3423C>T), AAC271GAT (3424A>G 3426C>T), TTT272TAC (3428T>A 3429T>C), ACC273AGC (3431C>G), TTC274TTT (3435C>T), AGC275GGA (3436A>G 3438C>A), TAC276TAT (3441C>T), ACT277CAC (3442A>C 3443C>A 3444T>C), GAC280GCC (3452A>C), GTT281TTC (3454G>T 3456T>C), CCT282CCA (3459T>A), CAC284CGC (3464A>G), AGC285TCC (3466A>T 3467G>C), AGC286TGC (3469A>T), TAC287TTC (3473A>T), GCT288AGC (3475G>A 3476C>G 3477T>C), AGC290AGT (3483C>T), AGT292AAA (3488G>A 3489T>A), CTG293ACC (3490C>A 3491T>C 3492G>C), GAC294ACC (3493G>A 3494A>C), CGT295CCT (3497G>C), CTC296CGA (3500T>G 3501C>A), ATG297TCT (3502A>T 3503T>C 3504G>T), CTC300TTA (3511C>T 3513C>A), ATC301GTT (3514A>G 3516C>T), GAC302GAT (3519C>T), TAC304TAT (3525C>T), CTG305CTT (3528G>T), TAT306TAC (3531T>C), TAC307TCT (3533A>C 3534C>T), TTG308TTT (3537G>T), AGC309AAC (3539G>A), AGA310AAA (3542G>A)				
AAV2gp06_2	193	205	6.3%	11	9.8%	13 (100%)	3 (23.1%)	0/0/0/0	0
Protein mutations:	S194Y (3309C>A), S195L (3312C>T), W196R (3314T>C 3316G>C), H198L (3321A>T), S199N (3324G>A), D201G (3330A>G 3331T>G), T202K (3333C>A 3334C>A), S203P (3335T>C), P204Y (3338C>T 3339C>A), *205I (3341T>A 3342G>T 3343A>T)								
Codon mutations:	TCT194TAT (3309C>A), TCA195TTA (3312C>T), TGG196CGC (3314T>C 3316G>C), CAC198CTC (3321A>T), AGT199AAT (3324G>A), GAT201GGG (3330A>G 3331T>G), ACC202AAA (3333C>A 3334C>A), TCA203CCA (3335T>C), CCC204TAC (3338C>T 3339C>A), TGA205ATT (3341T>A 3342G>T 3343A>T)								
AAV2gp07	166	246	15.2%	217	37.1%	81 (94.2%)	43 (50.0%)	5/0/1/1	0
Protein mutations:	M169T (3314T>C), V170L (3316G>C), Y175E (3331T>G 3333C>A), L176T (3334C>A 3335T>C), T177I (3338C>T 3339C>A), L178H (3341T>A 3342G>T), N179Y (3343A>T), N179_N180insITX (3345_3346insATTACCAT), S182G (3352A>G 3354T>A), Q183N (3355C>A 3357G>C), A184T (3358G>A 3360A>C), V185I (3361G>A), G186A (3365G>C 3366A>C), G186_R187insTP (3366_3367insACTCCC), S188A (3370T>G 3372T>A), S189A (3373T>G 3375A>T), R202H (3413G>A 3414T>C), N206D (3424A>G 3426C>T), F207Y (3428T>A 3429T>C), T208S (3431C>G), S210G (3436A>G 3438C>A), T212H (3442A>C 3443C>A 3444T>C), D215A (3452A>C), V216F (3454G>T 3456T>C), H219R (3464A>G), S221C (3469A>T), Y222F (3473A>T), A223S (3475G>A 3476C>G 3477T>C), S227K (3488G>A 3489T>A), L228T (3490C>A 3491T>C 3492G>C), D229T (3493G>A 3494A>C), R230P (3497G>C), L231R (3500T>G 3501C>A), M232S (3502A>T 3503T>C 3504G>T), I236V (3514A>G 3516C>T), Y242S (3533A>C 3534C>T), L243F (3537G>T), S244N (3539G>A), R245K (3542G>A)				
Codon mutations:	GTC167GTA (3309C>A), TTC168TTT (3312C>T), ATG169ACG (3314T>C), GTG170CTG (3316G>C), CCA171CCT (3321A>T), CAG172CAA (3324G>A), GGA174GGG (3330A>G), TAC175GAA (3331T>G 3333C>A), CTC176ACC (3334C>A 3335T>C), ACC177ATA (3338C>T 3339C>A), CTG178CAT (3341T>A 3342G>T), AAC179TAC (3343A>T), AAC179_AAC180insATTACCAT- (3345_3346insATTACCAT), AAC180AAT (3348C>T), AGT182GGA (3352A>G 3354T>A), CAG183AAC (3355C>A 3357G>C), GCA184ACC (3358G>A 3360A>C), GTA185ATA (3361G>A), GGA186GCC (3365G>C 3366A>C), GGA186_CGC187insACTCCC (3366_3367insACTCCC), CGC187AGG (3367C>A 3369C>G), TCT188GCA (3370T>G 3372T>A), TCA189GCT (3373T>G 3375A>T), TAC191TAT (3381C>T), CTG193TTA (3385C>T 3387G>A), GAG194GAA (3390G>A), CCT197CCA (3399T>A), TCT198AGC (3400T>A 3401C>G 3402T>C), CAG199CAA (3405G>A), CTG201CTA (3411G>A), CGT202CAC (3413G>A 3414T>C), ACC203ACA (3417C>A), GGA204GGC (3420A>C), AAC205AAT (3423C>T), AAC206GAT (3424A>G 3426C>T), TTT207TAC (3428T>A 3429T>C), ACC208AGC (3431C>G), TTC209TTT (3435C>T), AGC210GGA (3436A>G 3438C>A), TAC211TAT (3441C>T), ACT212CAC (3442A>C 3443C>A 3444T>C), GAC215GCC (3452A>C), GTT216TTC (3454G>T 3456T>C), CCT217CCA (3459T>A), CAC219CGC (3464A>G), AGC220TCC (3466A>T 3467G>C), AGC221TGC (3469A>T), TAC222TTC (3473A>T), GCT223AGC (3475G>A 3476C>G 3477T>C), AGC225AGT (3483C>T), AGT227AAA (3488G>A 3489T>A), CTG228ACC (3490C>A 3491T>C 3492G>C), GAC229ACC (3493G>A 3494A>C), CGT230CCT (3497G>C), CTC231CGA (3500T>G 3501C>A), ATG232TCT (3502A>T 3503T>C 3504G>T), CTC235TTA (3511C>T 3513C>A), ATC236GTT (3514A>G 3516C>T), GAC237GAT (3519C>T), TAC239TAT (3525C>T), CTG240CTT (3528G>T), TAT241TAC (3531T>C), TAC242TCT (3533A>C 3534C>T), TTG243TTT (3537G>T), AGC244AAC (3539G>A), AGA245AAA (3542G>A)				
Proteins									
Rep 68 protein (YP_680422.1)	360	450	16.9%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D368G (1423A>G), V374I (1440G>A 1442G>T), K381Q (1461A>C 1463G>A), A384N (1470G>A 1471C>A 1472C>T), K398G (1512A>G 1513A>G 1514G>T), C405S (1534G>C 1535C>T), S407G (1539T>G 1540C>G), A409V (1546C>T 1547C>A), D412A (1555A>C 1556C>T), V416I (1566G>A 1568G>A), V418I (1572G>A 1574C>A), T422M (1585C>T 1586C>G), C425Y (1594G>A 1595C>T), A426M (1596G>A 1597C>T 1598C>G), I428V (1602A>G 1604T>G), D429N (1605G>A 1607C>T), N431K (1613C>G), S432* (1615C>G), T433A (1617A>G 1619G>T), T434L (1620A>C 1621C>T 1622C>A), Q438K (1632C>A 1634G>A), Q439E (1635C>G 1637G>A), Q442G (1644C>G 1645A>G), D443E (1649C>A), F446V (1656T>G 1658C>T), K447M (1660A>T 1661A>G), E449K (1665G>A 1667A>G)								

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**1397**	**3544**	**11.0%**	**160**	**15.9%**	**512 (97.0%)**	**309 (58.5%)**	**14/2**	
Codon mutations:	ACC360ACT (1400C>T), AAT361AAC (1403T>C), GAG362GAA (1406G>A), CCC365CCA (1415C>A), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GAC368GGC (1423A>G), GTC370GTG (1430C>G), GAC371GAT (1433C>T), AAG372AAA (1436G>A), GTG374ATT (1440G>A 1442G>T), ATC375ATT (1445C>T), GAG378GAA (1454G>A), AAG381CAA (1461A>C 1463G>A), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), GTC386GTA (1478C>A), GTG387GTT (1481G>T), GAG388GAA (1484G>A), TCG389TCT (1487G>T), GCC390GCT (1490C>T), CTC394CTG (1502C>G), GGA395GGG (1505A>G), GGA396GGT (1508A>T), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GGT (1512A>G 1513A>G 1514G>T), GTG399GTA (1517G>A), CGC400AGA (1518C>A 1520C>A), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TCT (1534G>C 1535C>T), AAG406AAA (1538G>A), TCC407GGC (1539T>G 1540C>G), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CAA (1550G>A), ATA411ATT (1553A>T), GAC412GCT (1555A>C 1556C>T), CCG413CCC (1559G>C), ACT414-CT (1560delA), CCC415CCT (1565C>T), GTG416ATA (1566G>A 1568G>A), GTC418ATA (1572G>A 1574C>A), ACC419ACT (1577C>T), TCC420AGT (1578T>A 1579C>G 1580C>T), AAC421AAT (1583C>T), ACC422ATG (1585C>T 1586C>G), AAC423AAT (1589C>T), ATG424-TG (1590delA), TGC425TAT (1594G>A 1595C>T), GCC426ATG (1596G>A 1597C>T 1598C>G), GTG427GTA (1601G>A), ATT428GTG (1602A>G 1604T>G), GAC429AAT (1605G>A 1607C>T), GGG430GGC (1610G>C), AAC431AAG (1613C>G), TCA432TGA (1615C>G), ACG433GCT (1617A>G 1619G>T), ACC434CTA (1620A>C 1621C>T 1622C>A), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAC437CAT (1631C>T), CAG438AAA (1632C>A 1634G>A), CAG439GAA (1635C>G 1637G>A), CCG440CCT (1640G>T), CAA442GGA (1644C>G 1645A>G), GAC443GAA (1649C>A), CGG444AGA (1650C>A 1652G>A), TTC446GTT (1656T>G 1658C>T), AAA447ATG (1660A>T 1661A>G), GAA449AAG (1665G>A 1667A>G), CTC450AG. (1668C>A 1669T>G)								
Rep 78 protein (YP_680423.1)	360	450	14.6%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D368G (1423A>G), V374I (1440G>A 1442G>T), K381Q (1461A>C 1463G>A), A384N (1470G>A 1471C>A 1472C>T), K398G (1512A>G 1513A>G 1514G>T), C405S (1534G>C 1535C>T), S407G (1539T>G 1540C>G), A409V (1546C>T 1547C>A), D412A (1555A>C 1556C>T), V416I (1566G>A 1568G>A), V418I (1572G>A 1574C>A), T422M (1585C>T 1586C>G), C425Y (1594G>A 1595C>T), A426M (1596G>A 1597C>T 1598C>G), I428V (1602A>G 1604T>G), D429N (1605G>A 1607C>T), N431K (1613C>G), S432* (1615C>G), T433A (1617A>G 1619G>T), T434L (1620A>C 1621C>T 1622C>A), Q438K (1632C>A 1634G>A), Q439E (1635C>G 1637G>A), Q442G (1644C>G 1645A>G), D443E (1649C>A), F446V (1656T>G 1658C>T), K447M (1660A>T 1661A>G), E449K (1665G>A 1667A>G)								
Codon mutations:	ACC360ACT (1400C>T), AAT361AAC (1403T>C), GAG362GAA (1406G>A), CCC365CCA (1415C>A), TTC366TTT (1418C>T), AAC367AAT (1421C>T), GAC368GGC (1423A>G), GTC370GTG (1430C>G), GAC371GAT (1433C>T), AAG372AAA (1436G>A), GTG374ATT (1440G>A 1442G>T), ATC375ATT (1445C>T), GAG378GAA (1454G>A), AAG381CAA (1461A>C 1463G>A), ACC383ACT (1469C>T), GCC384AAT (1470G>A 1471C>A 1472C>T), GTC386GTA (1478C>A), GTG387GTT (1481G>T), GAG388GAA (1484G>A), TCG389TCT (1487G>T), GCC390GCT (1490C>T), CTC394CTG (1502C>G), GGA395GGG (1505A>G), GGA396GGT (1508A>T), AGC397TCT (1509A>T 1510G>C 1511C>T), AAG398GGT (1512A>G 1513A>G 1514G>T), GTG399GTA (1517G>A), CGC400AGA (1518C>A 1520C>A), GTG401GTT (1523G>T), GAC402GAT (1526C>T), CAG403CAA (1529G>A), TGC405TCT (1534G>C 1535C>T), AAG406AAA (1538G>A), TCC407GGC (1539T>G 1540C>G), TCG408TCT (1544G>T), GCC409GTA (1546C>T 1547C>A), CAG410CAA (1550G>A), ATA411ATT (1553A>T), GAC412GCT (1555A>C 1556C>T), CCG413CCC (1559G>C), ACT414-CT (1560delA), CCC415CCT (1565C>T), GTG416ATA (1566G>A 1568G>A), GTC418ATA (1572G>A 1574C>A), ACC419ACT (1577C>T), TCC420AGT (1578T>A 1579C>G 1580C>T), AAC421AAT (1583C>T), ACC422ATG (1585C>T 1586C>G), AAC423AAT (1589C>T), ATG424-TG (1590delA), TGC425TAT (1594G>A 1595C>T), GCC426ATG (1596G>A 1597C>T 1598C>G), GTG427GTA (1601G>A), ATT428GTG (1602A>G 1604T>G), GAC429AAT (1605G>A 1607C>T), GGG430GGC (1610G>C), AAC431AAG (1613C>G), TCA432TGA (1615C>G), ACG433GCT (1617A>G 1619G>T), ACC434CTA (1620A>C 1621C>T 1622C>A), TTC435TTT (1625C>T), GAA436GAG (1628A>G), CAC437CAT (1631C>T), CAG438AAA (1632C>A 1634G>A), CAG439GAA (1635C>G 1637G>A), CCG440CCT (1640G>T), CAA442GGA (1644C>G 1645A>G), GAC443GAA (1649C>A), CGG444AGA (1650C>A 1652G>A), TTC446GTT (1656T>G 1658C>T), AAA447ATG (1660A>T 1661A>G), GAA449AAG (1665G>A 1667A>G), CTC450AG. (1668C>A 1669T>G)								
Rep 40 protein (YP_680424.1)	136	226	29.1%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D144G (1423A>G), V150I (1440G>A 1442G>T), K157Q (1461A>C 1463G>A), A160N (1470G>A 1471C>A 1472C>T), K174G (1512A>G 1513A>G 1514G>T), C181S (1534G>C 1535C>T), S183G (1539T>G 1540C>G), A185V (1546C>T 1547C>A), D188A (1555A>C 1556C>T), V192I (1566G>A 1568G>A), V194I (1572G>A 1574C>A), T198M (1585C>T 1586C>G), C201Y (1594G>A 1595C>T), A202M (1596G>A 1597C>T 1598C>G), I204V (1602A>G 1604T>G), D205N (1605G>A 1607C>T), N207K (1613C>G), S208* (1615C>G), T209A (1617A>G 1619G>T), T210L (1620A>C 1621C>T 1622C>A), Q214K (1632C>A 1634G>A), Q215E (1635C>G 1637G>A), Q218G (1644C>G 1645A>G), D219E (1649C>A), F222V (1656T>G 1658C>T), K223M (1660A>T 1661A>G), E225K (1665G>A 1667A>G)								
Codon mutations:	ACC136ACT (1400C>T), AAT137AAC (1403T>C), GAG138GAA (1406G>A), CCC141CCA (1415C>A), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GAC144GGC (1423A>G), GTC146GTG (1430C>G), GAC147GAT (1433C>T), AAG148AAA (1436G>A), GTG150ATT (1440G>A 1442G>T), ATC151ATT (1445C>T), GAG154GAA (1454G>A), AAG157CAA (1461A>C 1463G>A), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), GTC162GTA (1478C>A), GTG163GTT (1481G>T), GAG164GAA (1484G>A), TCG165TCT (1487G>T), GCC166GCT (1490C>T), CTC170CTG (1502C>G), GGA171GGG (1505A>G), GGA172GGT (1508A>T), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GGT (1512A>G 1513A>G 1514G>T), GTG175GTA (1517G>A), CGC176AGA (1518C>A 1520C>A), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TCT (1534G>C 1535C>T), AAG182AAA (1538G>A), TCC183GGC (1539T>G 1540C>G), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CAA (1550G>A), ATA187ATT (1553A>T), GAC188GCT (1555A>C 1556C>T), CCG189CCC (1559G>C), ACT190-CT (1560delA), CCC191CCT (1565C>T), GTG192ATA (1566G>A 1568G>A), GTC194ATA (1572G>A 1574C>A), ACC195ACT (1577C>T), TCC196AGT (1578T>A 1579C>G 1580C>T), AAC197AAT (1583C>T), ACC198ATG (1585C>T 1586C>G), AAC199AAT (1589C>T), ATG200-TG (1590delA), TGC201TAT (1594G>A 1595C>T), GCC202ATG (1596G>A 1597C>T 1598C>G), GTG203GTA (1601G>A), ATT204GTG (1602A>G 1604T>G), GAC205AAT (1605G>A 1607C>T), GGG206GGC (1610G>C), AAC207AAG (1613C>G), TCA208TGA (1615C>G), ACG209GCT (1617A>G 1619G>T), ACC210CTA (1620A>C 1621C>T 1622C>A), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAC213CAT (1631C>T), CAG214AAA (1632C>A 1634G>A), CAG215GAA (1635C>G 1637G>A), CCG216CCT (1640G>T), CAA218GGA (1644C>G 1645A>G), GAC219GAA (1649C>A), CGG220AGA (1650C>A 1652G>A), TTC222GTT (1656T>G 1658C>T), AAA223ATG (1660A>T 1661A>G), GAA225AAG (1665G>A 1667A>G), CTC226AG. (1668C>A 1669T>G)								
Rep 52 protein (YP_680425.1)	136	226	22.9%	215	32.2%	91 (100%)	61 (67.0%)	0/0/2/2	1
Protein mutations:	D144G (1423A>G), V150I (1440G>A 1442G>T), K157Q (1461A>C 1463G>A), A160N (1470G>A 1471C>A 1472C>T), K174G (1512A>G 1513A>G 1514G>T), C181S (1534G>C 1535C>T), S183G (1539T>G 1540C>G), A185V (1546C>T 1547C>A), D188A (1555A>C 1556C>T), V192I (1566G>A 1568G>A), V194I (1572G>A 1574C>A), T198M (1585C>T 1586C>G), C201Y (1594G>A 1595C>T), A202M (1596G>A 1597C>T 1598C>G), I204V (1602A>G 1604T>G), D205N (1605G>A 1607C>T), N207K (1613C>G), S208* (1615C>G), T209A (1617A>G 1619G>T), T210L (1620A>C 1621C>T 1622C>A), Q214K (1632C>A 1634G>A), Q215E (1635C>G 1637G>A), Q218G (1644C>G 1645A>G), D219E (1649C>A), F222V (1656T>G 1658C>T), K223M (1660A>T 1661A>G), E225K (1665G>A 1667A>G)								
Codon mutations:	ACC136ACT (1400C>T), AAT137AAC (1403T>C), GAG138GAA (1406G>A), CCC141CCA (1415C>A), TTC142TTT (1418C>T), AAC143AAT (1421C>T), GAC144GGC (1423A>G), GTC146GTG (1430C>G), GAC147GAT (1433C>T), AAG148AAA (1436G>A), GTG150ATT (1440G>A 1442G>T), ATC151ATT (1445C>T), GAG154GAA (1454G>A), AAG157CAA (1461A>C 1463G>A), ACC159ACT (1469C>T), GCC160AAT (1470G>A 1471C>A 1472C>T), GTC162GTA (1478C>A), GTG163GTT (1481G>T), GAG164GAA (1484G>A), TCG165TCT (1487G>T), GCC166GCT (1490C>T), CTC170CTG (1502C>G), GGA171GGG (1505A>G), GGA172GGT (1508A>T), AGC173TCT (1509A>T 1510G>C 1511C>T), AAG174GGT (1512A>G 1513A>G 1514G>T), GTG175GTA (1517G>A), CGC176AGA (1518C>A 1520C>A), GTG177GTT (1523G>T), GAC178GAT (1526C>T), CAG179CAA (1529G>A), TGC181TCT (1534G>C 1535C>T), AAG182AAA (1538G>A), TCC183GGC (1539T>G 1540C>G), TCG184TCT (1544G>T), GCC185GTA (1546C>T 1547C>A), CAG186CAA (1550G>A), ATA187ATT (1553A>T), GAC188GCT (1555A>C 1556C>T), CCG189CCC (1559G>C), ACT190-CT (1560delA), CCC191CCT (1565C>T), GTG192ATA (1566G>A 1568G>A), GTC194ATA (1572G>A 1574C>A), ACC195ACT (1577C>T), TCC196AGT (1578T>A 1579C>G 1580C>T), AAC197AAT (1583C>T), ACC198ATG (1585C>T 1586C>G), AAC199AAT (1589C>T), ATG200-TG (1590delA), TGC201TAT (1594G>A 1595C>T), GCC202ATG (1596G>A 1597C>T 1598C>G), GTG203GTA (1601G>A), ATT204GTG (1602A>G 1604T>G), GAC205AAT (1605G>A 1607C>T), GGG206GGC (1610G>C), AAC207AAG (1613C>G), TCA208TGA (1615C>G), ACG209GCT (1617A>G 1619G>T), ACC210CTA (1620A>C 1621C>T 1622C>A), TTC211TTT (1625C>T), GAA212GAG (1628A>G), CAC213CAT (1631C>T), CAG214AAA (1632C>A 1634G>A), CAG215GAA (1635C>G 1637G>A), CCG216CCT (1640G>T), CAA218GGA (1644C>G 1645A>G), GAC219GAA (1649C>A), CGG220AGA (1650C>A 1652G>A), TTC222GTT (1656T>G 1658C>T), AAA223ATG (1660A>T 1661A>G), GAA225AAG (1665G>A 1667A>G), CTC226AG. (1668C>A 1669T>G)								
major coat protein VP1 (YP_680426.1)	368	448	11.0%	217	37.1%	81 (94.2%)	43 (50.0%)	5/0/1/1	0
Protein mutations:	M371T (3314T>C), V372L (3316G>C), Y377E (3331T>G 3333C>A), L378T (3334C>A 3335T>C), T379I (3338C>T 3339C>A), L380H (3341T>A 3342G>T), N381Y (3343A>T), N381_N382insITX (3345_3346insATTACCAT), S384G (3352A>G 3354T>A), Q385N (3355C>A 3357G>C), A386T (3358G>A 3360A>C), V387I (3361G>A), G388A (3365G>C 3366A>C), G388_R389insTP (3366_3367insACTCCC), S390A (3370T>G 3372T>A), S391A (3373T>G 3375A>T), R404H (3413G>A 3414T>C), N408D (3424A>G 3426C>T), F409Y (3428T>A 3429T>C), T410S (3431C>G), S412G (3436A>G 3438C>A), T414H (3442A>C 3443C>A 3444T>C), D417A (3452A>C), V418F (3454G>T 3456T>C), H421R (3464A>G), S423C (3469A>T), Y424F (3473A>T), A425S (3475G>A 3476C>G 3477T>C), S429K (3488G>A 3489T>A), L430T (3490C>A 3491T>C 3492G>C), D431T (3493G>A 3494A>C), R432P (3497G>C), L433R (3500T>G 3501C>A), M434S (3502A>T 3503T>C 3504G>T), I438V (3514A>G 3516C>T), Y444S (3533A>C 3534C>T), L445F (3537G>T), S446N (3539G>A), R447K (3542G>A)								
Codon mutations:	GTC369GTA (3309C>A), TTC370TTT (3312C>T), ATG371ACG (3314T>C), GTG372CTG (3316G>C), CCA373CCT (3321A>T), CAG374CAA (3324G>A), GGA376GGG (3330A>G), TAC377GAA (3331T>G 3333C>A), CTC378ACC (3334C>A 3335T>C), ACC379ATA (3338C>T 3339C>A), CTG380CAT (3341T>A 3342G>T), AAC381TAC (3343A>T), AAC381_AAC382insATTACCAT- (3345_3346insATTACCAT), AAC382AAT (3348C>T), AGT384GGA (3352A>G 3354T>A), CAG385AAC (3355C>A 3357G>C), GCA386ACC (3358G>A 3360A>C), GTA387ATA (3361G>A), GGA388GCC (3365G>C 3366A>C), GGA388_CGC389insACTCCC (3366_3367insACTCCC), CGC389AGG (3367C>A 3369C>G), TCT390GCA (3370T>G 3372T>A), TCA391GCT (3373T>G 3375A>T), TAC393TAT (3381C>T), CTG395TTA (3385C>T 3387G>A), GAG396GAA (3390G>A), CCT399CCA (3399T>A), TCT400AGC (3400T>A 3401C>G 3402T>C), CAG401CAA (3405G>A), CTG403CTA (3411G>A), CGT404CAC (3413G>A 3414T>C), ACC405ACA (3417C>A), GGA406GGC (3420A>C), AAC407AAT (3423C>T), AAC408GAT (3424A>G 3426C>T), TTT409TAC (3428T>A 3429T>C), ACC410AGC (3431C>G), TTC411TTT (3435C>T), AGC412GGA (3436A>G 3438C>A), TAC413TAT (3441C>T), ACT414CAC (3442A>C 3443C>A 3444T>C), GAC417GCC (3452A>C), GTT418TTC (3454G>T 3456T>C), CCT419CCA (3459T>A), CAC421CGC (3464A>G), AGC422TCC (3466A>T 3467G>C), AGC423TGC (3469A>T), TAC424TTC (3473A>T), GCT425AGC (3475G>A 3476C>G 3477T>C), AGC427AGT (3483C>T), AGT429AAA (3488G>A 3489T>A), CTG430ACC (3490C>A 3491T>C 3492G>C), GAC431ACC (3493G>A 3494A>C), CGT432CCT (3497G>C), CTC433CGA (3500T>G 3501C>A), ATG434TCT (3502A>T 3503T>C 3504G>T), CTC437TTA (3511C>T 3513C>A), ATC438GTT (3514A>G 3516C>T), GAC439GAT (3519C>T), TAC441TAT (3525C>T), CTG442CTT (3528G>T), TAT443TAC (3531T>C), TAC444TCT (3533A>C 3534C>T), TTG445TTT (3537G>T), AGC446AAC (3539G>A), AGA447AAA (3542G>A)								

	Begin	End	Coverage	Score	Concordance	Matches	Identities	I/D/M/F*	Stop Codons
NT	**1397**	**3544**	**11.0%**	**160**	**15.9%**	**512 (97.0%)**	**309 (58.5%)**	**14/2**	
major coat protein VP2 (YP_680427.1)	231	311	13.5%	217	37.1%	81 (94.2%)	43 (50.0%)	5/0/1/1	0
Protein mutations:	M234T (3314T>C), V235L (3316G>C), Y240E (3331T>G 3333C>A), L241T (3334C>A 3335T>C), T242I (3338C>T 3339C>A), L243H (3341T>A 3342G>T), N244Y (3343A>T), N244_N245insITX (3345_3346insATTACCAT), S247G (3352A>G 3354T>A), Q248N (3355C>A 3357G>C), A249T (3358G>A 3360A>C), V250I (3361G>A), G251A (3365G>C 3366A>C), G251_R252insTP (3366_3367insACTCCC), S253A (3370T>G 3372T>A), S254A (3373T>G 3375A>T), R267H (3413G>A 3414T>C), N271D (3424A>G 3426C>T), F272Y (3428T>A 3429T>C), T273S (3431C>G), S275G (3436A>G 3438C>A), T277H (3442A>C 3443C>A 3444T>C), D280A (3452A>C), V281F (3454G>T 3456T>C), H284R (3464A>G), S286C (3469A>T), Y287F (3473A>T), A288S (3475G>A 3476C>G 3477T>C), S292K (3488G>A 3489T>A), L293T (3490C>A 3491T>C 3492G>C), D294T (3493G>A 3494A>C), R295P (3497G>C), L296R (3500T>G 3501C>A), M297S (3502A>T 3503T>C 3504G>T), I301V (3514A>G 3516C>T), Y307S (3533A>C 3534C>T), L308F (3537G>T), S309N (3539G>A), R310K (3542G>A)							
Codon mutations:	GTC232GTA (3309C>A), TTC233TTT (3312C>T), ATG234ACG (3314T>C), GTG235CTG (3316G>C), CCA236CCT (3321A>T), CAG237CAA (3324G>A), GGA239GGG (3330A>G), TAC240GAA (3331T>G 3333C>A), CTC241ACC (3334C>A 3335T>C), ACC242ATA (3338C>T 3339C>A), CTG243CAT (3341T>A 3342G>T), AAC244TAC (3343A>T), AAC244_AAC245insATTACCAT- (3345_3346insATTACCAT), AAC245AAT (3348C>T), AGT247GGA (3352A>G 3354T>A), CAG248AAC (3355C>A 3357G>C), GCA249ACC (3358G>A 3360A>C), GTA250ATA (3361G>A), GGA251GCC (3365G>C 3366A>C), GGA251_CGC252insACTCCC (3366_3367insACTCCC), CGC252AGG (3367C>A 3369C>G), TCT253GCA (3370T>G 3372T>A), TCA254GCT (3373T>G 3375A>T), TAC256TAT (3381C>T), CTG258TTA (3385C>T 3387G>A), GAG259GAA (3390G>A), CCT262CCA (3399T>A), TCT263AGC (3400T>A 3401C>G 3402T>C), CAG264CAA (3405G>A), CTG266CTA (3411G>A), CGT267CAC (3413G>A 3414T>C), ACC268ACA (3417C>A), GGA269GGC (3420A>C), AAC270AAT (3423C>T), AAC271GAT (3424A>G 3426C>T), TTT272TAC (3428T>A 3429T>C), ACC273AGC (3431C>G), TTC274TTT (3435C>T), AGC275GGA (3436A>G 3438C>A), TAC276TAT (3441C>T), ACT277CAC (3442A>C 3443C>A 3444T>C), GAC280GCC (3452A>C), GTT281TTC (3454G>T 3456T>C), CCT282CCA (3459T>A), CAC284CGC (3464A>G), AGC285TCC (3466A>T 3467G>C), AGC286TGC (3469A>T), TAC287TTC (3473A>T), GCT288AGC (3475G>A 3476C>G 3477T>C), AGC290AGT (3483C>T), AGT292AAA (3488G>A 3489T>A), CTG293ACC (3490C>A 3491T>C 3492G>C), GAC294ACC (3493G>A 3494A>C), CGT295CCT (3497G>C), CTC296CGA (3500T>G 3501C>A), ATG297TCT (3502A>T 3503T>C 3504G>T), CTC300TTA (3511C>T 3513C>A), ATC301GTT (3514A>G 3516C>T), GAC302GAT (3519C>T), TAC304TAT (3525C>T), CTG305CTT (3528G>T), TAT306TAC (3531T>C), TAC307TCT (3533A>C 3534C>T), TTG308TTT (3537G>T), AGC309AAC (3539G>A), AGA310AAA (3542G>A)							
assembly activating protein AAP (YP_004030758.1)	193	205	6.3%	11	9.8%	13 (100%)	3 (23.1%)	0/0/0/0	0
Protein mutations:	S194Y (3309C>A), S195L (3312C>T), W196R (3314T>C 3316G>C), H198L (3321A>T), S199N (3324G>A), D201G (3330A>G 3331T>G), T202K (3333C>A 3334C>A), S203P (3335T>C), P204Y (3338C>T 3339C>A), *205I (3341T>A 3342G>T 3343A>T)							
Codon mutations:	TCT194TAT (3309C>A), TCA195TTA (3312C>T), TGG196CGC (3314T>C 3316G>C), CAC198CTC (3321A>T), AGT199AAT (3324G>A), GAT201GGG (3330A>G 3331T>G), ACC202AAA (3333C>A 3334C>A), TCA203CCA (3335T>C), CCC204TAC (3338C>T 3339C>A), TGA205ATT (3341T>A 3342G>T 3343A>T)							
major coat protein VP3 (YP_680428.1)	166	246	15.2%	217	37.1%	81 (94.2%)	43 (50.0%)	5/0/1/1	0
Protein mutations:	M169T (3314T>C), V170L (3316G>C), Y175E (3331T>G 3333C>A), L176T (3334C>A 3335T>C), T177I (3338C>T 3339C>A), L178H (3341T>A 3342G>T), N179Y (3343A>T), N179_N180insITX (3345_3346insATTACCAT), S182G (3352A>G 3354T>A), Q183N (3355C>A 3357G>C), A184T (3358G>A 3360A>C), V185I (3361G>A), G186A (3365G>C 3366A>C), G186_R187insTP (3366_3367insACTCCC), S188A (3370T>G 3372T>A), S189A (3373T>G 3375A>T), R202H (3413G>A 3414T>C), N206D (3424A>G 3426C>T), F207Y (3428T>A 3429T>C), T208S (3431C>G), S210G (3436A>G 3438C>A), T212H (3442A>C 3443C>A 3444T>C), D215A (3452A>C), V216F (3454G>T 3456T>C), H219R (3464A>G), S221C (3469A>T), Y222F (3473A>T), A223S (3475G>A 3476C>G 3477T>C), S227K (3488G>A 3489T>A), L228T (3490C>A 3491T>C 3492G>C), D229T (3493G>A 3494A>C), R230P (3497G>C), L231R (3500T>G 3501C>A), M232S (3502A>T 3503T>C 3504G>T), I236V (3514A>G 3516C>T), Y242S (3533A>C 3534C>T), L243F (3537G>T), S244N (3539G>A), R245K (3542G>A)							
Codon mutations:	GTC167GTA (3309C>A), TTC168TTT (3312C>T), ATG169ACG (3314T>C), GTG170CTG (3316G>C), CCA171CCT (3321A>T), CAG172CAA (3324G>A), GGA174GGG (3330A>G), TAC175GAA (3331T>G 3333C>A), CTC176ACC (3334C>A 3335T>C), ACC177ATA (3338C>T 3339C>A), CTG178CAT (3341T>A 3342G>T), AAC179TAC (3343A>T), AAC179_AAC180insATTACCAT- (3345_3346insATTACCAT), AAC180AAT (3348C>T), AGT182GGA (3352A>G 3354T>A), CAG183AAC (3355C>A 3357G>C), GCA184ACC (3358G>A 3360A>C), GTA185ATA (3361G>A), GGA186GCC (3365G>C 3366A>C), GGA186_CGC187insACTCCC (3366_3367insACTCCC), CGC187AGG (3367C>A 3369C>G), TCT188GCA (3370T>G 3372T>A), TCA189GCT (3373T>G 3375A>T), TAC191TAT (3381C>T), CTG193TTA (3385C>T 3387G>A), GAG194GAA (3390G>A), CCT197CCA (3399T>A), TCT198AGC (3400T>A 3401C>G 3402T>C), CAG199CAA (3405G>A), CTG201CTA (3411G>A), CGT202CAC (3413G>A 3414T>C), ACC203ACA (3417C>A), GGA204GGC (3420A>C), AAC205AAT (3423C>T), AAC206GAT (3424A>G 3426C>T), TTT207TAC (3428T>A 3429T>C), ACC208AGC (3431C>G), TTC209TTT (3435C>T), AGC210GGA (3436A>G 3438C>A), TAC211TAT (3441C>T), ACT212CAC (3442A>C 3443C>A 3444T>C), GAC215GCC (3452A>C), GTT216TTC (3454G>T 3456T>C), CCT217CCA (3459T>A), CAC219CGC (3464A>G), AGC220TCC (3466A>T 3467G>C), AGC221TGC (3469A>T), TAC222TTC (3473A>T), GCT223AGC (3475G>A 3476C>G 3477T>C), AGC225AGT (3483C>T), AGT227AAA (3488G>A 3489T>A), CTG228ACC (3490C>A 3491T>C 3492G>C), GAC229ACC (3493G>A 3494A>C), CGT230CCT (3497G>C), CTC231CGA (3500T>G 3501C>A), ATG232TCT (3502A>T 3503T>C 3504G>T), CTC235TTA (3511C>T 3513C>A), ATC236GTT (3514A>G 3516C>T), GAC237GAT (3519C>T), TAC239TAT (3525C>T), CTG240CTT (3528G>T), TAT241TAC (3531T>C), TAC242TCT (3533A>C 3534C>T), TTG243TTT (3537G>T), AGC244AAC (3539G>A), AGA245AAA (3542G>A)							

*: Inserts / Deletes / Misaligned / Frameshifts

Analysis details

This analysis was performed with Pan-viral (2.14.6)