

Appendix 1

Consensus sequence for CDV/FMR1 sample after Clustal Ω

ATATGCTGACATTCTCGTGGTACCTGCATGCGCTGTCATTAATCGATGATTTCGATATATGATAAATGAATCCTTGATGATATCACTG
 ATGATTCTGGCGAATATTATTCCGATGGAATGCTTCATCTAACTGGGGATATTCTTTTCGGCCTTAAACCATACATATCGGCTGAT
 GTGATCATGCTGATGGAATATGAATTGATTGCTCTGCTCAATACAATCATAAATGTGGGGATTAATAAAAATGGATGGGAATACTC
 TGCATTTCCACACAATCCCGAATGTAATACATATGATCCGGATTGTGGACCCATTAAAAATGGCACATGATATATGTCATCCTCA
 CATGGAATGGGGATATTTGCTGGATCGACAAATGGTGCAACCCAATCTGCACTCAATTCACTGGGGGATCATCATGGCCAATTGT

Consensus sequence for CDV/FMR2 sample after Clustal Ω

AAGATGCTGACAGTCTCGTGGTACCTGCAGGCGCTGTCAGTAATCGAGGATTCGAGAGAGGAGAAGGAAGCCTTGATGATAGCACT
 GAGGATTCTGGCGAAGATTCTTCCGAGGGAAATGCTTCATCTAACTGGGGATCTTCTTTTCGGCCTTAAACCAGACAGAGCGGCTGA
 TGTGAGCATGCTGATGGAAGAGGAATTGAGTGCTCTGCTCAAGACAAGCAGAAATGTGGGGATTAAGAAAAGGGATGGGAAGACT
 CTGCAGTTCCACACAATCCCGAAGGTAAGACAGAGGATCCGGAGTGTGGACCCATTAAAAAGGGCACAGGAGAGAGGTCAGCCTC
 ACATGGAATGGGGATAGTTGCTGGATCGACAAATGGTGCAACCCAATCTGCACTCAAGTCAACTGGGGGATCATCAGGGCCATGTT

Appendix 2

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	Canine morbillivirus Yanaka viral cRNA, complete genome	551	551	99%	8e-153	89.93%	LC338064.1
<input type="checkbox"/>	Canine distemper virus P gene for phosphoprotein, complete cds, strain:Yanaka	551	551	99%	8e-153	89.93%	AB028914.1
<input type="checkbox"/>	Canine distemper virus P gene for phosphoprotein, complete cds, strain:Jujo	545	545	99%	4e-151	89.70%	AB028916.1
<input type="checkbox"/>	Canine morbillivirus isolate CDV6_TH/2014, complete genome	540	540	99%	2e-149	89.46%	MH496779.1
<input type="checkbox"/>	Canine morbillivirus isolate CDV4_TH/2014, complete genome	540	540	99%	2e-149	89.46%	MH496775.1
<input type="checkbox"/>	Canine distemper virus isolate CDV_SY, complete genome	540	540	99%	2e-149	89.46%	KJ466106.1
<input type="checkbox"/>	Canine distemper virus strain HLJ1-06, complete genome	540	540	99%	2e-149	89.46%	JX681125.1
<input type="checkbox"/>	Canine distemper virus genes for phosphoprotein P, C protein, complete cds, strain: Th12	540	540	99%	2e-149	89.46%	AB755426.1
<input type="checkbox"/>	Canine distemper virus viral cRNA, nearly complete genome, strain: Ac961-H358	540	540	99%	2e-149	89.46%	AB753776.1
<input type="checkbox"/>	Canine distemper virus strain PS, complete genome	540	540	99%	2e-149	89.46%	JN896331.1

A: NIP from CDV/FMR1 sequence by BLAST program.

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

Alignments Download GenBank Graphics Distance tree of results

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/> Canine morbillivirus Yanaka viral cRNA, complete genome	774	774	99%	0.0	99.53%	LC338064.1
<input type="checkbox"/> Canine distemper virus P gene for phosphoprotein, complete cds, strain:Yanaka	774	774	99%	0.0	99.53%	AB028914.1
<input type="checkbox"/> Canine morbillivirus isolate CDV6 TH/2014, complete genome	763	763	99%	0.0	99.06%	MH496779.1
<input type="checkbox"/> Canine morbillivirus isolate CDV4 TH/2014, complete genome	763	763	99%	0.0	99.06%	MH496775.1
<input type="checkbox"/> Canine distemper virus isolate CDV SY, complete genome	763	763	99%	0.0	99.06%	KJ466106.1
<input type="checkbox"/> Canine distemper virus strain HLJ1-06, complete genome	763	763	99%	0.0	99.06%	JX681125.1
<input type="checkbox"/> Canine distemper virus genes for phosphoprotein P, C protein, complete cds, strain: Th12	763	763	99%	0.0	99.06%	AB755426.1
<input type="checkbox"/> Canine distemper virus viral cRNA, nearly complete genome, strain: Ac96I-H358	763	763	99%	0.0	99.06%	AB753776.1
<input type="checkbox"/> Canine distemper virus strain PS, complete genome	763	763	99%	0.0	99.06%	JN896331.1
<input type="checkbox"/> Canine distemper virus strain HLJ1-06, partial genome	763	763	99%	0.0	99.06%	HQ540293.1

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

Alignments Download GenBank Graphics Distance tree of results

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/> Canine morbillivirus Yanaka viral cRNA, complete genome	774	774	99%	0.0	99.53%	LC338064.1
<input type="checkbox"/> Canine distemper virus P gene for phosphoprotein, complete cds, strain:Yanaka	774	774	99%	0.0	99.53%	AB028914.1
<input type="checkbox"/> Canine morbillivirus isolate CDV6 TH/2014, complete genome	763	763	99%	0.0	99.06%	MH496779.1
<input type="checkbox"/> Canine morbillivirus isolate CDV4 TH/2014, complete genome	763	763	99%	0.0	99.06%	MH496775.1
<input type="checkbox"/> Canine distemper virus isolate CDV SY, complete genome	763	763	99%	0.0	99.06%	KJ466106.1
<input type="checkbox"/> Canine distemper virus strain HLJ1-06, complete genome	763	763	99%	0.0	99.06%	JX681125.1
<input type="checkbox"/> Canine distemper virus genes for phosphoprotein P, C protein, complete cds, strain: Th12	763	763	99%	0.0	99.06%	AB755426.1
<input type="checkbox"/> Canine distemper virus viral cRNA, nearly complete genome, strain: Ac96I-H358	763	763	99%	0.0	99.06%	AB753776.1
<input type="checkbox"/> Canine distemper virus strain PS, complete genome	763	763	99%	0.0	99.06%	JN896331.1
<input type="checkbox"/> Canine distemper virus strain HLJ1-06, partial genome	763	763	99%	0.0	99.06%	HQ540293.1

B: NIP from CDV/FMR2 sequence by BLAST.

