FIG. 1:
PPV5B DNA Sequence

PPV5B_Reference:

```
gene            935..2024
               /label="Predicted replicase"
gene            2161..2860
               /label="Predicted gene of unknown function / ORF3"
gene            2861..5014
               /label="Predicted Capsid"
Sequence:
     GCTTCAAGTCTATTAATTTGCATAATTTATGCAAAGAGGAAGTTAACCTGATTGGTCAGTTTTTT
     GGCGGGAAGCAATTTGATTGGACGGGAACTCAAGTCCTAATTTGCATTGACGTGGACCAATCAGA
     ATTGAGTACATATTATATAAGGAGGCCGAAAAAGAGGAAGTTTGTCATTTGCGTTTTGGAGACCA
     TCGCGAGCAGAACTCCGTCGTTTTCGGCCTGTATTTGAAGATGGAAACCTACTGGACAGGTATTT
     GCAGACTTTTTCCTGATGTTTTAAAAATACCTGGTGTTTATGAAGGACGCTATATTTTTGAAGTT
     CCTGTTTCTACCAGAGACTTTATGAAATGGCCTGATATATTTCAAAATGAAAAAAATAATGAAAA
     CTGTGAGTCTGGCGCGGCGCCTGCGGCGCCGCGCGATGAAATTGACAGTAATCTAGTAACGGCTG
     TTAGACAAGGGGAGGCTCTATTTAGAGAGCTTCAAAAAGAACTTAGAAAATCCTGTAGATTAGGA
     GTAGATCCTGGCATTTTCATGCAATTGGAAAGAGTTGACTCAAAAGGTGGCTTACATTTGCATTG
     GTGTGTGTCTGTGTCCGCTGGTACCCCGCGAGATGTTTTAACTATATTCAAAAATACAGAAAAAA
     AAGTTTCATTATATTACTTTGGTGTTGAGGGACTTAGCTTTTTTGTGCCACACAAAAATAAACAC
     GGAGCATGGAAAAGCACAGATGAAGGGTTTATTTATAATTATTTGCTAAAAAAACTACCACTGAA
     AGAATGTCTTTATGCATGGACTACAATTGGAGGTACAATAGGTGAAGCCTGTTTAAATACAGAAA
     AAAGAAAAGAACTATTAGATAATAGACAAGATCCAGCAGTTATTGAAGAATTATCTGCTCCCATG
     TACAAATGTGCCACTGGAGAAAAAATGCTAGACATTGTACAGTGGTTGGTAGACAATAATATTTG
     TTCTGAATCCAGATGGGAGGGAAAAAATGCTCTAAGCTTATACTCATTCTTAGCCACACAAGCTG
     GAGGATATATGGCAAAACAATGCTTGAGAATCGCTCAGCAAAAATTACTAAAAGAAAAATCACTA
     GGGTTAACCTTAATGGATTTTAAAAACATGGATGCTTTAAGAGCTTTCCAACAAAGTGACATGGA
     GTGCTCATTCGATCATAACAGAATACATTACATTTTTGCAGCTAACAACTATGATCCTAAAATTG
     CTGCAGTTATAATGTTTCACTGGAGCATGAAACAAACGGGAAAAAGAAACTGTGTATGGTTTTAC
     GGTCCTGCTACAACAGGAAAAACAAATATTGCACAGGCAATCTGCCATAGCTCAGCTAATTATGG
     CAATGTTAACTGGAACAATCCAAATTTTCCTTTTCAAGATATTGTAGGAGCTCAGGTAGGGTGGT
     GGGAAGAAGGGAAAATGACAGGAGACATGGTAGAAGCTGCAAAAGCTTTGCTGGGGGGAACTGCT
     TTGCGCATCGACCGCAAATGTATGCAATCTGTTGAAGTCAACAGTCCACCGTTTATTATAACATC
     GAATGTGGACATGACCGTGGTTCAAGAAGGAAGTTTTGTAAGCTTTGAACACCAACAGCCGTTAG
     AGGACAGGATGATAAAATTTTCATTTAACCTGACACTACCTGGAAACTTTGGTCTGATTACAACT
     GAAGAAGTGAAATCTTTTTTCCGGATGGGTGCAAAACTTTCAGTTAAACCTGAAATCATGAATTG
     CCAAATTTTCAAAAGAGGACCTGCCAGCATCCGCCACCTAGTTCCTCTTGGAGAAATTCCTCCAC
     CAAAGGAGATGCATAAAAAACGACAGCCACTCTATTTGAGAGCTGAACCAGATGAAGAACAAGAA
     ACACCAGACGTCTTGGATCATTGGTTTGAAGAACCAAGTCAAAAAAGAAAGAAGACAGAAGACCC
     TGCAAACACGACACCTCCTGCGGCTTATGAGAATTTAGATGACAACTTTGAACCTGTTCCAGGTA
     AGAATTTTGCATTTATCATTTTTTAATGTTCCAAAACAATAGAGCAAACTGGTGATATGTGCATA
     ATTCTTACAGATAGCCAAGTGAACCTGATATTTGACGTGGTCTACGAAGAGACACCAGAGGTGGA
     CGAAGTGGAGGAACAATGAGCTTTAGTGGGTATTCTAAAAATCTCCCCCCGGGTTTAGAGGAAGT
     TACATTCCCATTTTGGGTTGATTTTTTGCTTGCCAGAATAGCTGATTTTATTAATTGGTGTGGGT
     ATTATAATATTAAATGTCCAGAAGCAGAAAAGGTATTTAGTATTGGACAATCTACACAGGTTTTA
     CTTAAATGGCCGGGTGCACAGGGAAAAGAAAACCGAGTTAAGAACTTTACCGAAGCTGCGTTTCC
```

FIG. 1 Cont.:

ATATATGAAAGTACCTGTGAGACCAGACAACATTGAATGGATTAAAATCCATGAGATGCTACATA
ATTATGATAGACAAATAACACCGCAGACAACTGAGAATGATTTACTTGCAGCTATCACTGCTGAC
TTCGATCAGAGAGAGATCATCCATCCAGTCACCGGCGAGAAATGGGTTTTCGGTAAGAAAACAGA
AGCTTTTGCTACTGATTTGGAAGAAGCCGTGGATGAAGAAGATCCTGATACAGAGAAAAAACAAC
CTACTGATAAAACACAAAGTAATAACAAGAAAGGGGAAATTGGTGAAAAGAAAGAAGAAGGTGAT
ACCCTTACGTCAAATGAGGAACATCACCAATCAAGAAAACTATTAGAACACGACTCAAGCGAAGA
ACAACCAGAAGAAGCTGGTCACCGAGAACAGAAAGAACTAGAAGACAATATTGAAGACATCAAAC
ATGGAGCGGGAGAAGACCAAACCGGAACCGGTATCAACTGGCCAGGACATCGCTACACAGGTCCT
GGAAATCCACTCCCTCACGGAGCTCCTCGCAATGAAATTGATCTCTCTGCTGCGAAACATGATAT
CAGGTACAAACAATATTCTCGATATGGTCACTGGCCATACATTTGGGCGCCATATATTGATAAAA
AAATGCAAGAAGATATTAGAGAGATAGTAAAAAAAGGTTTAGGATTAGAAGGTAAACTTTTAGGT
AACCTTATATCAGCTTTATGGCAAGCAAAATACAGATTAGGAGCCCCGATATATGAAATTTTAAA
AACAATTTTACCCCCGAAAAGTATGCCTACTAAAGAATCTGTAGAAAAACATTTACCAAAACCTT
TGCCCATTGATCCTCCACAGACATCCTTACCAGGTGCATCTCCTCCTCGAACTCCTGACTTGGGT
GGCGAGACTGGAATGAATGAAGAGCCTCCAGCAAAAAGAAGAATGACAGAAGACAGATGTGACAG
CACCACAAGGTGCGAAACATTGGACACACAATATGAGGATTCTAAAATGGCGGGAGGGGGTGGGG
GGGGAGGGAATCAACCTAAAAGTTCTTGGATTGGGGGGGCTTTCTTTACTGATACGACGGTTACT
ACTTATGGTACTAGAAGGTGTGTGCTTAGCTCTTTTCCGCATAACTACTGCACCACAGAGAGCGG
GGATCATATACCTAGCCTTGTTGTCTGTACTCCATGGTACTATTATGATCTTAACATTCTATCAG
CTCATTTCTCTCCCTCTGCTTGGCAAACGCTTTTAGAAGAGTATGATGCTTTTAAACCTTTAAAA
TTGGAAGTTAAAATTAAAGAGATAGTTGTTAAAGATGTTAATAATATGACAGGGAAACAATGCTG
TGACACAGTTTCTGACAATGCCATGGCTGCAGTGCTGTGTTTTGAGGATACACATTACGAGCTGC
CATATGTTTTGGGAGGGGGACAGCTAACAGTGCCTGGTCATCTTCCAGGACAAACTTATGAACTT
CCAAAATACTGCTATAGAACTGTGGGAAAACCGCATAGCGAGATGTGGTCACCTGTAGATGGTTC
CAAAAGAGCCCACTTAGACATGCCTTTTGTTCAGCCAACACAGAACACTGAGTTCTTTATTTTAG
AGAACAGACACTCTACCATCCTTCACACAGGCAATGAATTCTTTCAAACCTATGACTTTCCAGAT
TTACATTTTGAGCAGCTAACACAGTACATGTGGGACGCGAGGAGACTTGACAATCCAATGAAAGG
TCAAAGAATACAGGTTATGAAAAACAAACCTACAGAAAACAAAGATCAAATGTTTGGTATCAGAG
CTTCGAGTTACCTCGTTCCCTGGATTGTCAACTCTCTAAACAGACCTGCTATGTTTTTACAAGGA
GGAAGATTAAAAGACGGGGATTATTCCATTGTTGGGCCTGGGACCAGAGAACAGGCGACATACCA
CTACTTTAATGATACACCTGTCGTGGTTGAAAGAGATATTTACAAATTTACAACTAGTATGCTTA
AAAGAGAAACTCAACAGCCAGGACCGAGAACACAGGAAACAACGGTAAAAACACCTGATGGGACC
ATAATTATAACAACTAACAGTTTAGCGTATGGACAGGTGCCTGAAAACATTGATAACATACCGAG
TGATCACAAAGCCGCTTTCGGGGTTACAGGGTACAGGCTTGCTGTCGCTGAACAGAGAGGGTATA
GCACACCTGGAATGCCTTCTCATATAAGGGAGATATTATTGACAAAAACACCGAAACTATTAGAA
AAAGATCAGCAAGAAATCACATTTCCAAACTTTGAAGGGTCTGTCAGCGAAAAAACTTCCGCTAA
TCTAGAGTCTCAGATTTGGGCTTATATCCCTAACACTGATAACAAACATAACTGCGGAACGCCCC
CTTTATCTATATGGGGAATGGAAAATCCTCCACCTATGGTTTTTTTGAGGTTACTCCCTCAACTG
GGACCCCCTGAAAAATCCAGCTGTTCTGGAAGCAAACCTTCTAAAAAGTTCTTGAATCAGTACTG
CCAATTTTTACTGGAATATACTGTAACATGGGCTGTTGTGAGGCGAAAGAAACATACTCCGAGGT
GGAACCCTATGCCGGGGGTCACAATTCCAACTTATAACAACGATCCTGTGTACATCCTTGACCAA
AATGGATTTTATAAATTGCCAGAAACTGTTTGGACAGCAAAGCAACGTGTTAGAGCGCGAAGATA
ATAAAAAAAAATTTGAGAAAAAAAAAGTTACTTCCTCTTTTTTTTTGAATTTGAAAAGCGCCAGG
CCTCTCGCCGGTCGCCCCTGACGTCACATCCGCTTCCGGGTCAAAGGGCGGGGTCAAAGGTCAAA
GGTCTTCATACGTCATATCCGCTTCCGGGTCATGACC

Fig. 2:
PPV5B REPLICASE PROTEIN SEQUENCE

METYWTGICRLFPDVLKIPGVYEGRYIFEVPVSTRDFMKWPDIFQNEKNNENCESGAAPAAPRDEIDSNL
VTAVRQGEALFRELQKELRKSCRLGVDPGIFMQLERVDSKGGLHLHWCVSVSAGTPRDVLTIFKNTEKKV
SLYYFGVEGLSFFVPHKNKHGAWKSTDEGFIYNYLLKKLPLKECLYAWTTIGGTIGEACLNTEKRKELLD
NRQDPAVIEELSAPMYKCATGEKMLDIVQWLVDNNICSESRWEGKNALSLYSFLATQAGGYMAKQCLRIA
QQKLLKEKSLGLTLMDFKNMDALRAFQQSDMECSFDHNRIHYIFAANNYDPKIAAVIMFHWSMKQTGKRN
CVWFYGPATTGKTNIAQAICHSSANYGNVNWNNPNFPFQDIVGAQVGWWEEGKMTGDMVEAAKALLGGTA
LRIDRKCMQSVEVNSPPFIITSNVDMTVVQEGSFVSFEHQQPLEDRMIKFSFNLTLPGNFGLITTEEVKS
FFRMGAKLSVKPEIMNCQIFKRGPASIRHLVPLGEIPPPKEMHKKRQPLYLRAEPDEEQETPDVLDHWFE
EPSQKRKKTEDPANTTPPAAYENLDDNFEPVPGKNFAFIIF

Fig. 3:
PPV5B ORF3

MSFSGYSKNLPPGLEEVTFPFWVDFLLARIADFINWCGYYNIKCPEAEKVFSIGQSTQVLLKWPGAQGKE
NRVKNFTEAAFPYMKVPVRPDNIEWIKIHEMLHNYDRQITPQTTENDLLAAITADFDQREIIHPVTGEKW
VFGKKTEAFATDLEEAVDEEDPDTEKKQPTDKTQSNNKKGEIGEKKEEGDTLTSNEEHHQSRKLLEHDSS
EEQPEEAGHREQKELEDNIEDIK

Fig. 4:

PPV5B CAPSID PROTEIN SEQUENCE

MLHNYDRQITPQTTENDLLAAITADFDQREIIHPVTGEKWVFGKKTEAFATDLEEAVDEEDPDTEKKQPT
DKTQSNNKKGEIGEKKEEGDTLTSNEEHHQSRKLLEHDSSEEQPEEAGHREQKELEDNIEDIKHGAGEDQ
TGTGINWPGHRYTGPGNPLPHGAPRNEIDLSAAKHDIRYKQYSRYGHWPYIWAPYIDKKMQEDIREIVKK
GLGLEGKLLGNLISALWQAKYRLGAPIYEILKTILPPKSMPTKESVEKHLPKPLPIDPPQTSLPGASPPR
TPDLGGETGMNEEPPAKRRMTEDRCDSTTRCETLDTQYEDSKMAGGGGGGGNQPKSSWIGGAFFTDTTVT
TYGTRRCVLSSFPHNYCTTESGDHIPSLVVCTPWYYYDLNILSAHFSPSAWQTLLEEYDAFKPLKLEVKI
KEIVVKDVNNMTGKQCCDTVSDNAMAAVLCFEDTHYELPYVLGGGQLTVPGHLPGQTYELPKYCYRTVGK
PHSEMWSPVDGSKRAHLDMPFVQPTQNTEFFILENRHSTILHTGNEFFQTYDFPDLHFEQLTQYMWDARR
LDNPMKGQRIQVMKNKPTENKDQMFGIRASSYLVPWIVNSLNRPAMFLQGGRLKDGDYSIVGPGTREQAT
YHYFNDTPVVVERDIYKFTTSMLKRETQQPGPRTQETTVKTPDGTIIITTNSLAYGQVPENIDNIPSDHK
AAFGVTGYRLAVAEQRGYSTPGMPSHIREILLTKTPKLLEKDQQEITFPNFEGSVSEKTSANLESQIWAY
IPNTDNKHNCGTPPLSIWGMENPPPMVFLRLLPQLGPPEKSSCSGSKPSKKFLNQYCQFLLEYTVTWAVV
RRKKHTPRWNPMPGVTIPTYNNDPVYILDQNGFYKLPETVWTAKQRVRARR

Fig. 5

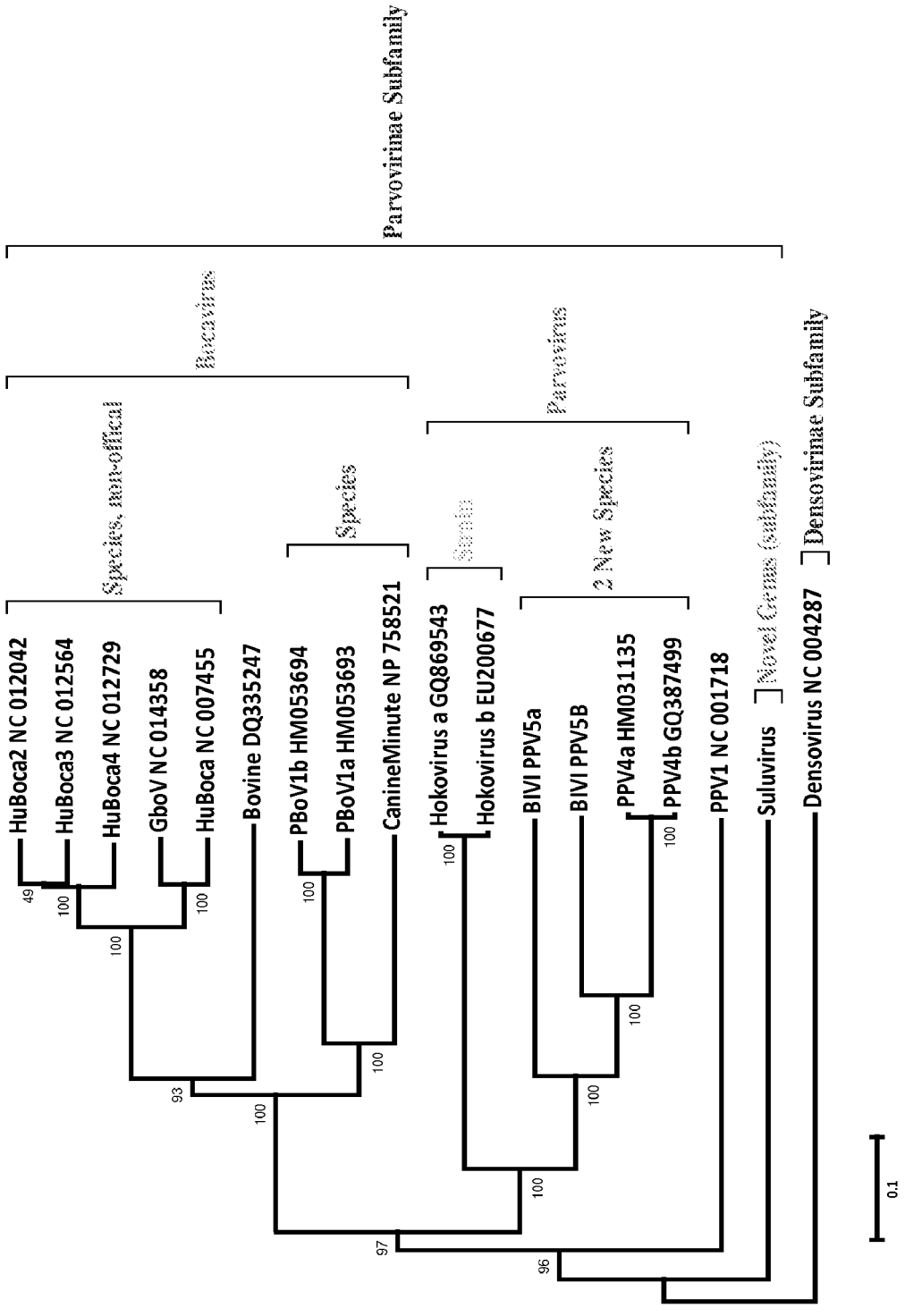
Pair-wise amino acid Identity comparisons

	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]	[10]	[11]	[12]	[13]	[14]	[15]	[16]
[1] Bovine		47.2%	52.3%	50.3%	50.5%	52.8%	52.8%	52.8%	52.6%	6.6%	22.7%	22.5%	20.7%	20.7%	**20.2%**	18.4%
[2] CanineMinute	43.3%		51.0%	60.2%	61.0%	50.5%	51.3%	50.5%	51.8%	7.4%	25.0%	24.7%	21.7%	21.7%	**21.4%**	18.1%
[3] GboV	43.7%	49.8%		50.0%	50.3%	91.3%	83.7%	83.7%	84.2%	6.6%	23.7%	23.7%	21.7%	21.7%	**22.5%**	17.6%
[4] PBoV1a	42.8%	53.5%	49.1%		93.9%	51.8%	50.5%	49.7%	51.5%	7.1%	24.0%	24.0%	20.9%	20.9%	**22.2%**	19.9%
[5] PBoV1b	43.3%	53.7%	49.5%	94.7%		51.8%	51.3%	49.7%	51.8%	7.9%	24.5%	24.5%	20.4%	20.4%	**22.5%**	20.2%
[6] HuBoca	44.2%	50.9%	93.3%	50.0%	50.7%		82.7%	82.7%	83.2%	6.9%	24.2%	24.2%	21.2%	21.2%	**22.5%**	17.9%
[7] HuBoca2	47.0%	50.5%	78.4%	50.0%	50.2%	80.5%		91.8%	91.1%	7.9%	23.5%	23.2%	20.9%	20.9%	**24.0%**	18.4%
[8] HuBoca3	44.7%	51.2%	92.6%	50.2%	50.5%	93.3%	80.0%		92.1%	8.7%	24.0%	23.7%	21.7%	21.7%	**23.0%**	18.6%
[9] HuBoca4	46.5%	50.2%	77.7%	50.0%	50.5%	80.2%	96.5%	79.3%		8.2%	23.5%	23.7%	21.4%	21.4%	**23.2%**	19.1%
[10] Densovirus	7.9%	7.0%	6.5%	7.7%	8.1%	6.5%	6.1%	6.7%	5.8%		7.7%	7.4%	8.4%	8.2%	**8.7%**	6.6%
[11] Hokovirus_a	20.5%	20.7%	20.5%	22.6%	22.3%	20.9%	20.2%	20.7%	20.5%	7.9%		99.5%	33.9%	34.2%	**32.9%**	17.6%
[12] Hokovirus_b	20.0%	20.9%	20.5%	22.6%	22.3%	20.9%	20.2%	20.7%	20.5%	8.1%	98.6%		33.9%	34.2%	**32.9%**	17.9%
[13] PPV4a	21.4%	21.2%	22.1%	22.1%	21.6%	22.8%	21.2%	22.8%	21.4%	6.3%	29.1%	29.1%		99.5%	**65.3%**	17.1%
[14] PPV4b	21.4%	21.2%	22.1%	22.1%	21.6%	22.8%	21.4%	22.8%	21.6%	6.3%	29.3%	29.3%	**22.1%**	**22.3%**	**65.6%**	**23.3%**
[15] BIVI_PPV5B	**21.4%**	**22.3%**	**23.0%**	**21.9%**	**21.9%**	**23.5%**	**21.9%**	**23.0%**	**21.9%**	**6.5%**	**29.1%**	**29.1%**	**90.5%**	**90.0%**		**18.4%**
[16] PPV1	18.6%	25.4%	23.3%	20.5%	21.2%	22.8%	26.1%	23.5%	25.1%	5.8%	16.5%	16.5%	18.4%	18.4%	**17.4%**	

Top = VP1/CAP amino acid identity

Bottom = REP amino acid identity

Fig. 6:
Phylogenetic analysis of VP1/CAP region of PPV5B



8/9

FIG. 7:

BLASTp results of PPV5B_Capsid vs. Total GenBank sequences.
Closest Match: Porcine Parvovirus 4 PPV4 -- GenBank Accession ID: AFM73881
Sequence Identities: 53% (367/690)
Sequence Homologies: 68% (468/690)

```
PPV5B  50   RYGHWPYIWAPYIDKKMQEDIREIVKKGLGLEGKLLGNLISALWQAKYRLGAPIYEILKT  109
            ++GHWP++WAP++D++M ++I++++K    L  KLL N I ALW+AK ++GAPIYEI+K
PPV4_  3    KHGHWPHLWAPFVDRQMSQEIQQVLKGSTKLSQKLLANFIIALWRAKEKIGAPIYEIVKG  62

PPV5B  110  ILPPKSMPTKESV-EKHLPKPLPIDPPQTSLPGASPPRTPDLGGETGMNEEPPAKRRMTE  168
            + P     T ES+     P P P   PQ     ASPP++P+   E  M+     K    E
PPV4_  63   VFPSVDKKTVESLLPHPDPIPAPPSSPQRGSKRASPPQSPNAHDEDTMSGHKRQKTMEVE  122

PPV5B  169  DRCDSTTRCETLDTQYEDSKMAGGGGGGGNQPKSSWIGGAFFTDTTVTTYGTRRCVLSSF  228
              CD +  C T +    D ++ G GGG  N+ K +W+GG  FTDT++ T+GTRRCVLS+F
PPV4_  123  SECDKSLLCPTQNAG-ADFELCGTGGGATNE-KGTWVGGTQFTDTSIRTFGTRRCVLSAF  180

PPV5B  229  PHNYCTTESGDHIPSLVVCTPWYYYDLNILSAHFSPSAWQTLLEEYDAFKPLKLEVKIKE  288
            P  YC+  SGD IPS++  TPWYYYDLNI+S HFSPSA+QTL+E+YDAF+P  L V +KE
PPV4_  181  PDTYCSMMSGDAIPSIIFNTPWYYYDLNIMSCHFSPSAFQTLIEDYDAFRPRSLTVHLKE  240

PPV5B  289  IVVKDVNNMTGKQCCDTVSDNAMAAVLCFEDTHYELPYVLGGGQLTVPGHLPGQTYELPK  348
            +V+KDV    G Q  + VSDN  A +L FED +YELPYVLGGGQ++VPGHLPGQ Y+LPK
PPV4_  241  LVIKDVCQQQGLQA-EQVSDNNSATLLAFEDVNYELPYVLGGGQVSVPGHLPGQPYQLPK  299

PPV5B  349  YCYRTVGKPHSEMWSPVDGSKRAHLDMPFVQP-------------TQNTEFFILENRHST  395
            Y YRTVGKP     S     +  H D     P              TQ+TEF+ILEN  +T
PPV4_  300  YSYRTVGKPDPN--SGFVPGRNTHPDQGPGHPKASKTIWYSQYLETQDTEFYILENHKAT  357

PPV5B  396  ILHTGNEFFQTYDFPDLHFEQLTQYMWDARRLDNPMKGQRIQVMKNKPTENKDQMFGIRA  455
            ILH+GN F Q Y+FPDL FEQLTQYMWDARR DNP+  QRIQVM     +   + F I+
PPV4_  358  ILHSGNTFSQNYNFPDLPFEQLTQYMWDARRQDNPLIDQRIQVMSRMYDDGPQKTFAIKV  417

PPV5B  456  SSYLVPWIVNSLNRPAMFLQGGRLKDGDYSIVGPGTREQATYHYFNDTPVVVERDIYKFT  515
            + Y+VP+ V S +RPAMFL GGR KDGDYSI GPG RE+ ++ Y+ND P ++ RD Y F+
PPV4_  418  NPYIVPFTVKSTSRPAMFLAGGRFKDGDYSITGPGDREKTSFRYYNDPPWIITRDTYLFS  477

PPV5B  516  TSMLKRETQQPGPRTQETTVKTPDGTIIITTNSLAYGQVPENIDNIPSDHKAAFGVTGYR  575
            + + K E +QPGPR  +T V+TPDGT+I+TTN+LAYG   E + NIP       GV  +R
PPV4_  478  SDLAKTEREQPGPRQGDTVVRTPDGTLIVTTNALAYGYTTEYLKNIPLLSSKYHGVENFR  537

PPV5B  576  LAVAEQRGYSTPGMPSHIREILLT-KTPKLL-------EKDQQEITFPNFEGSVSEKTSA  627
            LAV  +RGYS PG PSHIRE L   K P  +       E  ++EITFP++ GSV+EKT+A
PPV4_  538  LAVENERGYSMPGHPSHIRETLFRGKLPSEIRESTIKSEDQRKEITFPDYMGSVNEKTTA  597

PPV5B  628  NLESQIWAYIPNTDNKHNCGTPPLSIWGMENPPPMVFLRLLPQLGPPEKSSCSGSKPSKK  687
            NLESQIW+ IPNTD    C TPPLSIWGM+NPPPMVFLRLL Q+GPP +S+CSGS PS
PPV4_  598  NLESQIWSQIPNTDITEKCTTPPLSIWGMKNPPPMVFLRLLAQMGPPRRSACSGSIPSNT  657

PPV5B  688  FLNQYCQFLLEYTVTWAVVRRKKHTPRWNP  717
            +LNQYCQFLL Y + W V++R + T RWNP
PPV4_  658  YLNQYCQFLLTYEMEWDVIKRTRKTVRWNP  687
```

FIG. 8:

BLASTp results of PPV5B_REP gene vs. Total GenBank sequences.
Closest Match: Porcine Parvovirus 4 PPV4 -- GenBank Accession ID: ADF59557
Sequence Identities: 87% (517/597)
Sequence Homologies: 93% (555/597)

```
Query  1    METYWTGICRLFPDVLKIPGVYEGRYIFEVPVSTRDFMKWPDIFQNEKNNENCESGAAPA  60
            METYWTGICRLFPDVLKIPGVYEGRYIFEVP+STRD MKWPDIF NE N+EN +SGAAPA
Sbjct  1    METYWTGICRLFPDVLKIPGVYEGRYIFEVPISTRDCMKWPDIFGNENNSENQQSGAAPA  60

Query  61   APRDEIDSNLVTAVRQGEALFRELQKELRKSCRLGVDPGIFMQLERVDSKGGLHLHWCVS  120
            APR+ ++SNLV AVRQ EALFRELQKELRKSCRLGVDPGIFMQLE VDSKGGLHLHWCVS
Sbjct  61   APRENLNSNLVIAVRQAEALFRELQKELRKSCRLGVDPGIFMQLEEVDSKGGLHLHWCVS  120

Query  121  VSAGTPRDVLTIFKNTEKKVSLYYFGVEGLSFFVPHKNKHGAWKSTDEGFIYNYLLKKLP  180
            VSAGTPRDVLTIFKNTEKKVSLYYFGVEGLSFFVPHKNKHGAWKSTDEGFIYNYLLKKLP
Sbjct  121  VSAGTPRDVLTIFKNTEKKVSLYYFGVEGLSFFVPHKNKHGAWKSTDEGFIYNYLLKKLP  180

Query  181  LKECLYAWTTIGGTIGEACLNTEKRKELLDNRQDPAVIEELSAPMYKCATGEKMLDIVQW  240
            LKECLYAWTTIGG IG+ACLNT+KRKELLDNRQDPAVIEELSAPMYKCATGEKMLDIVQW
Sbjct  181  LKECLYAWTTIGGAIGDACLNTDKRKELLDNRQDPAVIEELSAPMYKCATGEKMLDIVQW  240

Query  241  LVDNNICSESRWEGKNALSLYSFLATQAGGYMAKQCLRIAQQKLLKEKSLGLTLMDFKNM  300
            LVDNNICSESRWE KNALSLYSFLATQAGGYMAKQCLRIAQQKLLKEK LGLTLM+FK+M
Sbjct  241  LVDNNICSESRWENKNALSLYSFLATQAGGYMAKQCLRIAQQKLLKEKPLGLTLMEFKDM  300

Query  301  DALRAFQQSDMECSFDHNRIHYIFAANNYDPKIAAVIMFHWSMKQTGKRNCVWFYGPATT  360
            +ALR FQQ + E +FD+NR+HYIFA NNYDPKIA+VIM+ WSMKQTGKRNCVWFYGPATT
Sbjct  301  NALRRFQQDEGEMTFDNNRMHYIFAINNYDPKIASVIMYFWSMKQTGKRNCVWFYGPATT  360

Query  361  GKTNIAQAICHSSANYGNVNWNNPNFPFQDIVGAQVGWWEEGKMTGDMVEAAKALLGGTA  420
            GKTN+AQAICHSSANYGNVNWNN NFPFQDIVGAQVGWWEEGKMTGDMVEAAKALLGGTA
Sbjct  361  GKTNMAQAICHSSANYGNVNWNNANFPFQDIVGAQVGWWEEGKMTGDMVEAAKALLGGTA  420

Query  421  LRIDRKCMQSVEVNSPPFIITSNVDMTVVQEGSFVSFEHQQPLEDRMIKFSFNLTLPGNF  480
            LRIDRKCMQS+EVNSPPF+ITSNVDMT+VQEGSFVSFEHQQPLEDRMIKFSFN+TLPGNF
Sbjct  421  LRIDRKCMQSIEVNSPPFLITSNVDMTIVQEGSFVSFEHQQPLEDRMIKFSFNMTLPGNF  480

Query  481  GLITTEEVKSFFRMGAKLSVKPEIMNCQIFKRGPASIRHLVPLGEIPPPKEMHKKRQPLY  540
            GLIT+EEVKSFFRMGAKL+ +P+IMNC IFK+GPASIRHLVP+GEIPPPKEM  KRQPLY
Sbjct  481  GLITSEEVKSFFRMGAKLAAQPDIMNCPIFKKGPASIRHLVPVGEIPPPKEMKHKRQPLY  540

Query  541  LRAEPDEEQETPDVLDHWFEE--PSQKRKKTEDPANTTPPAAYENLDDN-FEPVPGK  594
            +RAEPDE Q+ P+ LDHWFEE  P +K++KT++ A   P    E + +  F P PGK
Sbjct  541  MRAEPDEIQDNPEELDHWFEEEAPRKKKQKTKNTATKNPAETVEIITETEFIPAPGK  597
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