

DHPV NS2 Amino acid sequence alignment

01 : JN082231-South Korea-Genotype I  
 02 : MT980830-Madagascar-Genotype I  
 03 : DQ002873-Thailand-Genotype II  
 04 : FJ410797-India-Genotype II  
 05 : DQ458781-Australia-Genotype III  
 06 : OQ857567-South Korea-Genotype IV-In this study  
 07 : OQ857568-South Korea-Genotype V-In this study

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01-MASKGEYFFTPRDLVNFVNTLLCHKISAIAMKMLTMKETEFLREVWIPYIQGFQTAHDLGV-----DKCGAAGSEYKVFLEDEKFMDFVTSFRRSVFISYGDKWREDDVSYFMADVFW
02-MACKGEYFFTPKDLVNFVNTLLCHKISAIAMKMLAMEEKEFLRAVWLPYIQGFQTAHELGVDT----DKCGAVGDDFQEVFDERKFDMSFRRSVFISYGQWRHKPSNFMADVFW
03-MASKGDYFFTPRDLVNFVNTLLCHKINAIAMKMLTMKEEDFLSQVWLPYIQGFQTAHDLGRDS----DKCGAAGDEFQEVFLDERKFDMSFRRSVFISYGDEWRHRSSEHFMADVFW
04-MASKGDYFFSTPKDLVNFVNTLLCHKISAIAMKMLTMKEDFLRDVWLPYIQGFQTAHDLGR-----DECGAAGDDFQEVFFDAQEFIDMSFRRSVFISYGDKWRDDSSYFMADEFW
05-----MSSFRRSVFISYGDEWRTGSECFMADVFW
06-MASKGE--YFFTHRNLVKVFVCTLLSHKISNIGVRMLTMDLEEF LGAVWLPYIRGFQTAHELGTTEE----DECGAAGSDYTKVFFDEEKFKNFITARRSVFISYGEWKRDIKYFRGDVFW
07-MSSKGEYFFTHRNLVKVFVCTLLGHKLSNIGIKMLTMDVEEFLGAVWLPYIRGFQTAHELGIEEEEEDDECGAAGSDYTRVFFDEEKFKDFITARRSVFISYGDKWKTVDVKCFRGDVFW

01-SDQLRQFWMIMFGECHFVNMSPCRKRLYIEMLPYYLAKMTTENRHLVEWEYMNPCPNTHVRRNKMTGMNFCQGVVIDNEYPDNQMGVCYNIDEHPLPGGIRWSGTNEYRTGYVHVNVKVKW
02-SDQLRQFWMIMFGECHFVNMAFCKRMYIDMLPYYLAKMTTENRHLIEWELMNPCKPTHVRRNEMTGMNFCSSGVVIDNEYPNQMGVCYNIDEHPLPGGIRWSSCNEYRTGYVHVNVKVKW
03-SDNLRQFWMIMFGECHFVNMSPCRKRLYVDMLPYYLAKMTTENRHLIEWEYMNPCPATHVRRNKMTGMNFCSSQGVVIDNEYPDNQMGVCYNIDEHPLPGGIRWSGNTNEYRTGYVHVNVKVKW
04-SDNLRQFWMIMFGECHFVNMSPCRKRLYVDMLPYYLAKMTTENRHLIEWEYMNPCPATHVRRNKMTGMNFCSSQGVVIDNEYPDNQMGVCYNIDEHPLPGGIRWSGNTNEYRTGYVHVNVKVKW
05-SDNLRQFWMIMFGECHFVDMSPCKRIYISMLPYYLAKMTTENRHLIEWEYMTFPCPSTHERRNKMTGMNFCSSQGVVIDNEYPDNQMGVCYNIDEHPLPGGIRWSGTTECSTRYVHVNVKVKW
06-SDDLWMFWYIMILGECHFVQLK-YSRVLIEMLPYYLAKMTSENGDKINWEYMRPIPEWDMYENKMEGIHF CRTGVVIDTEYPNQGLGLYNVDEHPLPGGIRWNKNTGKDDYVHVNVKVKW
07-SEELWMFWYIMILGECHFVQLK-YNRVVCVPMPLPYYLAKVTTENRDKIKWEHVIPIPESDVYENTAEGIHFCKAGVVIDTEYPSNQLGLYNVDEHPLPGGIRWAKKTGKDDYVHVNVKQW

01-LGVADKISDMEETSSDEEVPSSQEKYMKS-KEKKEQOKT-EKKEDEPANKRRKFSLTNTVLEKQKMELEKFFRMEEEPINIKLYDLEEGKEHHVHEAIRIDGSNSKFAKKKDEQGNVMD
02-LKVTDKVSDMEETSSDEEVPSSQEKYMKS-KEKKEQSKT-EKKEDEPASKRRKFSLSNTILEKQKLELGKFFRMEDEPINIKLYELEEGKERHVHEAIRIDSSNSKFAKKKDEQGNVMD
03-LGVTDKVSDMEETSSDEEVPSSQEKYMKS-KEKKEQPKTSEKKEDEPANKRRKFSLSNTVLEKQKMELEKFFRMEEEPINIKLYDLEEGKEHHVHEAIRIDGSNSKFAKKKDEHGNVMD
04-LGVTDKVSDMEETSSDEEVPSSQEKYMKS-KEKKEQOKTAEKKEDEPASKRRKFSLTNTVLEKQKMELEKFFRMEEEPINIKLYELEEGKEHHVHEAIRIDSSNSKFAKKKDEQGNVLD
05-LGVADKISDMEETSSDEEVPSSQEKYMKG-KDKRDQOKT-EKKEDEPPKKTFFSLSNTVLEKQKLELGKFFRMEEEPINIKLYELEEGKEHHVHEAIRIDGSNSKFAKKKDEQGNVLD
06-LTITDKVSEMEDTS-DEEVPSSQEKYMKMDKNKKEQLKE--KGEQPNKRRKLNLSNMALEKQKMELEGRFFRMEEEPINIKLNELEEGREYHVHEAVRVNSNSKFAKKKDEHGNMDD
07-LTITDKVSEMEDTS-DEEVPSSQEKYMKMEKKKTEQOK--KGEQ-QPNKRRKLNLSNMALEKQKMELEGRFFRMEEEPINIKLNELEEGREYHVHEAVRVNSNSKFAKKKDEHGNMDD

01-FKVIIVCDGNNLYGFFANTQLNKLFNKWHGTTKYSMKPEHNSILKVSQISEVRNGKMCIVKMGINDDVKCFAR*
02-FKVIACDGENNLYGFFANTQLNKLFNKWHGTTKYSMKPEHNSILKVSQISEVRNGKMCIVKMGINDDVKCFAR*
03-FKVIIVCDGNNLYGFFANTQLNKLFNKWHSTTKYSMKPEHNSILKVSQISEVRNGKMCIVKMGINDDVKCFAR*
04-FKVIIVCDGNNLYGFFANTQLNKLFNKWHGTTKYSMKPEHNSILKVSQISEVRNGKMCIVKMGINDDVKCFAR*
05-FKVIIVCDGNNLYGFFANTQLNKLFNKWHSTTKYSMKPEHNSILKVSQISEVRNGKMCIVKMGINDDVKCFAR*
06-FKVIICDGENNLYGFFANTQLNKLFNKWHSTTKYSMKPEHNSILKVSQISEVRNGKMCIVKMGINDDVKCFAR*
07-FKVIICDGENNLYGFFANTQLNKLFNKWHSTTKYSMKPEHNSILKVSQISEVRNGKMCIVKMGINDDVKCFAR*
    
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Fig. S1. DHPV NS2 amino acid sequence alignment data. Sequence alignment was processed by Clustal W (BioEdit).

## DHPV NS1 Amino acid sequence alignment

- 01 : AY008257-South Korea-Genotype I
- 02 : MT980830-Madagascar-Genotype I
- 03 : KR492913-China-Genotype I
- 04 : KR492914-Asian-Genotype I
- 05 : JN082231-South Korea-Genotype I
- 06 : KR492912-China-Genotype I
- 07 : DQ002873-Thailand-Genotype II
- 08 : FJ410797-India-Genotype II
- 09 : DQ458781-Australia-Genotype III
- 10 : OQ857567-South Korea-Genotype IV-In this study
- 11 : OQ857568-South Korea-Genotype V-In this study

01-MFCQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNWNNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDDCKDSANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHE  
02-MFHQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHVRCNDECKDSANKVCKDIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHE  
03-MFHQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHVRCNDECKDSANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHE  
04-MFYQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHVRCNDECKDSANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHE  
05-MFCQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNWNNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDDCKDSANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHE  
06-MFCQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNWNNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDDCKDSANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHE  
07-MFRQVMKLRKREGILDHNPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDNCKDSANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHD  
08-MFCQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDDCKDSANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHD  
09-MFCQVMKLRKREGMVDHNPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDNCKDLANKVCKNIYGPLHILLESVNEENWSKSSSRVLFVFRGYEKILQHE  
10-MFCQVMKLRREGIVDHNPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDNCKDAANKVCKNIYGPLHILLESVNDNWSKCSKRVLFVFRGYEKILQHE  
11-MFCQVMKLRREGIVEHSPLVTFYSGIIVKFEHWNKDNVSKVRKFLYKFAQWLYKECTYIHNI SAAVHDRCKDNCKDAANKVCKNIYGPLHILLESVNEENWSKCSKRVLFVFRGYEKILQHE

01-NQQWLEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSNEELLSKLVKMKDTQERDDLYEKACQFKRDKNAARKIENSTAKTLDGADN-DNIRLSSSRVLFVFRGYEKILQHE  
02-HKQLWEDLGLQKTSPPSSMSLWDGEMFRWYMFDRDKYAKVHGTYYYSSNGEFLSKLVKMKDTQERDDLYEKACQFKKDKNTARKIENSTAKTLDGVDN-DNIRLSSSRVLFVFRGYEKILQHE  
03-HKQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSNGEFLSKLVKMKDTQERDDLYEKACQFKKDKNTARKIENSTAKTLDGVDN-DNIRLSSSRVLFVFRGYEKILQHE  
04-HKQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSNGEFLSKLVKMKDTQERDDLYEKACQFKKDKNTARKIENSTAKTLDGVDN-ENIRLSSSRVLFVFRGYEKILQHE  
05-NKQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSNEELLSKLVKMKDTQERDDLYEKACQFKRDKNAARKIENSTAKTLDGADN-DNIRLSSSRVLFVFRGYEKILQHE  
06-NQQWLEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSNEELLSKLVKMKDTQERDDLYEKACQFKRDKNAARKIENSTAKTLDGADN-DNIRLSSSRVLFVFRGYEKILQHE  
07-NKQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYASVHGTYYYSSDAEFLNKLKMKDTQERDDLYEKACQFKRDRNTARKIENSTAKTLDGGENNDNIRLSSSRVLFVFRGYEKILQHE  
08-NKQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSNEEFLKLIEMKDTQERDDLYEKACQFKRDKNAARKIENSTAKTLDGGEN-ENIRLSSSRVLFVFRGYEKILQHE  
09-NRQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSDQFLKLIEMKDTQERDDLYEKACQFKRDRNTARKIENSTAKTLDGGENNDNIRLSSSRVLFVFRGYEKILQHE  
10-NKQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYAKVHGTYYYSSDQFLKLIEMKDTQERDDLYEKACQFKRDRNTARKIENSTAKTLDGVDN-DNIRLSSSRVLFVFRGYEKILQHE  
11-NKQLWEDLGLQKTSPPSSMSLWDGEMFKWYMFDRDKYARVHGTYYYSSDQFLKLIEMKDTQERDDLYEKACQFKRDRNTARKIENSTAKTLDGVDN-DNIRLSSSRVLFVFRGYEKILQHE

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Fig. S2. DHPV NS1 amino acid sequence alignment data. Sequence alignment was processed by Clustal W (BioEdit).

01-LVKHKCYTIQDFKMMQRNEDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLIGQSRQICIDGAYMMFNIIENMKVE  
 02-LIKHKCYTIRDFKMMQKNEDEIWNVNYMYDIQNLKVMIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLTGQSRQICIDGTYMMFKIIQNMKVE  
 03-LIKHKCYTIQDFKMMQKNEDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLIGQSRQICIDGAYMMFKIIQNMKVE  
 04-LIKHKCYTIQDFKMMQRNEDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLIGQSRQICIDGAYMMFKIIQNMKVE  
 05-LVKHKCYTIQDFKMMQRNEDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLIGQSRQICIDGAYMMFNIIENMKVE  
 06-LVKHKCYTIQDFKMMQRNEDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLIGQSRQICIDGAYMMFNIIENMKVE  
 07-LVKHKCYTIQDFKMMQRSDDDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLVGQSRQICIDGAYMMFKIIENMKVE  
 08-LRKHKCYTIQDFKMMQRNDEIWNVNYMYEIQNLKVKIEKLNIMEYSLQQADYIEGNPWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLIGQTKQICIDGAYMMFKIIENMRVE  
 09-LVKHKCYTIQDFKMMQRSDDDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGEDLWNTNSAYMRTVVKRGTDRYYWYIQRHISNRASLIGQSRQICIDGAYMMFKIIENMRVE  
 10-LVKHKCYTIQDFKMMQREDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGDDIWNTNSAYMRTVVKRGTDRYYWYIHRHIANRASLIGQNRQICIDGAYMVFKIIENMRVE  
 11-LIKHKCYTIQDFKMMQREDEIWNVNYMYDIQNLKVKIEKLNIMEYSLQQADYIEGNTWIGDDIWNTNSAYMRTVVKRGTDRYYWYIHRHIANRASLIGQNRQICIDGAYMVFKIIENMRVE

01-SRPKTIPIISKNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEALTGLVNTAIMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 02-SRPKTIPIVSNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEALAGLVNTAIMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 03-SRPKTIPIVSNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEALTGLVNTAIMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 04-SRPKTIPIVSNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEALTGLVNTAIMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 05-SRPKTIPIISKNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEALTGLVNTAIMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 06-SRPKTIPIISKNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEALTGLVNTAIMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 07-SRPKTIPIVSNKTVQWIQDFMDIIGHNLPKINCMMLYGNSNSGKTQLIEALTGLINTAIMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 08-SRPKTIPIISKNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEALTGLVNTAVMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 09-SRPKTIPIISKNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIDALTLVNTAVMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 10-SRPSTIPVISQNKTVQWIQDFMDIIGHNLPKINCMMLYGNSNSGKTQLIEVLTGLINTAVMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF  
 11-SRPSTIPVISQNKTVQWIQDFMDIMHGNLPKINCMMLYGNSNSGKTQLIEVLTGLVNTAVMTNVGDGGTFHFSNITEMSTIVVGNETKIRTQTEQWKGLCGGENVTMPMKYKEHKTHMF

01-RKPVFLTNQHHPLVDISHYDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYMNRDPDKKFKIGFFNKLYDALFENS\*  
 02-RKPVFLTNQHHPLVDISHYDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYMNRDPDRKFKIGFFNKLYDALFESS\*  
 03-RKPVFLTNQHHPLVDISHYDDRRAIENRSFMYKVELGSEAVNSHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYMNRDPDRKFKIGFFNKLYDALFESS\*  
 04-RKPVFLTNQHHPLVDISHYDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYMNRDPDRKFKIGFFTKLYDALFENS\*  
 05-RKPVFLTNQHHPLVDISHYDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYMNRDPDKKFKIGFFNKLYDALFENS\*  
 06-RKPVFLTNQHHPLVDISHYDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYMNRDPDKKFKIGFFNKLYDALFENS\*  
 07-RKPVFLTNQHHPLVEISNYDDRRAIENRCFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFILACMQYVHTNYMNRDPDRKFKIGFFNKLYDMLFEDS\*  
 08-RKPVFLTNQHHPLVEISNYDDRRAIENRCFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFILACMQYVHTNYMNRDPDRKFKIGFFNKLYDMLFEDS\*  
 09-RKPVFLTNQHHPLVDISHYDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYMNRDPDRKFKIGFFNKLYDMLFENN\*  
 10-RKPVFLTNQHHPLVEIKHHDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYRDRPDRSFNLRFFNKLYDALFAEG\*  
 11-RKPVFLTNQHHPLVEIKHHDDRRAIENRSFMYKVELGSEAVNAHIKFPNRMIPIRKNPELTQFVLASMQYVHTNYRDRPDRSFNLRFFNKLYDTLFAED\*

Fig. S2. (continued)

### DHPV VP Amino acid sequence alignment

- 01 : AY008257-South Korea-Genotype I
- 02 : MT980830-Madagascar-Genotype I
- 03 : KR492913-China-Genotype I
- 04 : KR492914-Asian-Genotype I
- 05 : JN082231-South Korea-Genotype I
- 06 : KR492912-China-Genotype I
- 07 : DQ002873-Thailand-Genotype II
- 08 : FJ410797-India-Genotype II
- 09 : EU617324-India-Genotype II
- 10 : DQ458781-Australia-Genotype III
- 11 : EU346369-New Caledonia-Genotype III
- 12 : KR492907-Egypt-Genotype III
- 13 : OL753005-Taiwan-Genotype IV
- 14 : OQ857567-South Korea-Genotype IV-In this study
- 15 : OQ857568-South Korea-Genotype V-In this study

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01-MSPTRKGGNYFASKHFQSKRKNKLGKVKDLLASKKRERK-FKGGKNTLSEEPSTSGWKDPVQRFPALQEERNTFAGLLAIEAAPDQRQLGRDSNNQLALVQRDTRVAVRQSTNRREAL
02-MSPTRKGGNYFASKHFQSKRKNKLGKVKDLLASKKKERK-FKGGKNTLSEEPSTSGWQDPVRRRFPALQEERNTFAGLLAIEAAPDQRQLGRDNNNQLALVQRDTRVAVRQSTNRREAL
03-MSPTRKGGNYFASKHFQSKRKNKLGKVKDLLASKKKERK-FKGGKNTLSEEPSTSGWQDPVRRRFPALQEERNTFAGLLAIEAAPDQRQLGRDNNNQLALVQRDTRVAVRQSTNRREAL
04-MSPTRKGGNYFASKHFQSKRKNKLGKVKDLLASKKKERR-FKGGKNTLDEQPSTSGWKDPVQRFPALQEERNFSFAGLLAIEAAPDQRQLGRDSNNQLALVQRDTRVAVRQSTNRREAL
05-MSPTRKGGNYFASKHFQSKRKNKLGKVKDLLASKKKERK-FKGGKNTLSEEPSTSGWKDPVQRFPALQEERNTFAGLLAIEAAPDQRQLGRDSNNQLALVQRDTRVAVRQSTNRREAL
06-MSPTRKGGNYFASKHFQSKRKNKLGKVKDLLASKKRERK-FKGGKNTLSEEPSTSGWKDPVQRFPALQEERNTFAGLLAIEAAPDQRQLGRDSNNQLALVQRDTRVAVRQSTNRREAL
07-MSPTRKGGNYFASKHFQSKRKNKLARVKDLLASKKKERR-FKGGKNTLSEEPSTSEWNPVQRFPALQEERNTFAGLLAIEAAPDQRQLGRDNNNQLALVQRDTRVAVRQSTNRGEAL
08-MSPTRRGGNYFASKHFQSKRKNKLAKVKDLLASKKRERR-FKGGKNTLSEEPSTSEWNPVQRFPALQEERNTFAGLLAIEAAPDQRQLGRDNNNQLALVQRDTRVAVRQSTNRGEAL
09-MSPTRRGGNYFASKHFQSKRKNKLAKVKDLLASKKRERR-FKGGKNTLSEEPSTSEWNPVQRFPALQEERNTFAGLLAIEAAPDQRQLGRDNNNQLALVQRDTRVAVRQSTNRGEAL
10-MSPTRRGGNYFASKHFQSKRKNKLQVRKDLLASKKKDRK-FKGGKNTLSEEPSTSGWRDPVQRFPALQEERNTFAGLLAIEAAPDQRQLGRDSNNQLALVQRDTRVAVRQSTNRREAL
11-MPPTRKGGNYFASKHFQTKRKS KLQVRKFLSKRKRDRR-FKGGKNTLSEEPSTSGWRDPVQRFPALQEERNTSAGLLAIEAAPDQRQLGRDSNNQLALVQRDTRVAVRQSTNRREAL
12-MPPTRKGGNYFASKHFQTKRKS KLQVRKFLSKRKRDRR-FKGGKNTLSEEPSTSGWRDPVQRFPALQEERNTSAGLLAIEAAPDQRQLGRDSNNQLALVQRDTRVAVRQSTNRREAL
13-MPPTKSTGNFYASKRFQ-ELKKKVKAIKKTVSFKAKDKKAKGKQTLGEE PSTSAWRDPVRERFPELTQEDRNNFAGILAEAAPDQRQLGRDSNNLALVQRSTRALVRHTEENRADAV
14-MPPTKSTGNFYASKRFQ-ELKKKVKAIKKTVSFKAKDKKAKGKQTLGEE PSTSAWRDPVRERFPELTQEDRNNFAGILAEAAPDQRQLGRDSNNLALVQRSTRALVRHTEENRADAV
15-MPPTRTKGNFYASKRFQ-EIKNQVKAIKNKVSEFKAKDKK-SKGGKHTLGEEPSTSGWRDPVRERFPELTQEDRNNFAGILAEAAPDQRQLGRDSNNQLALVQRSTRALVRHTEENRADAV
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(continued on next page)

Fig. S3. DHPV VP amino acid sequence alignment data. Sequence alignment was processed by Clustal W (BioEdit).

01-EVVRAANQAIRSGGERLAEIVQYASGFSDESTIVEVRQEDRIQRDIFQEEGQNLIAIEIALEGPSSVTQQFDQEKTPAVKRALELTQEEQLERIENAKKYIEEVIEETNREFESEVRQ  
02-EVVKAANQAIRSGGDRLAELVQAYASGFSDESTIVEITQGNRIQKIDIFQEEAQNLIAIEIALEGPSSVTQQFDQEKTPAVKRALELTQEEQLERIENAKKYIEEVIEETNQEELANQERQ  
03-EVVKAANQAIRSGGDRLAELVQAYASGFSDESTIVEITQENRIQKIDIFQEEAQNLIAIEIALEGPSSVTQQFDQEKTPAVKRALELTQEEQLERIENAKKYIEEVIEETNQEELANQERQ  
04-EVVRTANQAIRSGGERLAEIVQYASGFTDSTEIVEVRQESRVQKIDIFQEEGQNLIAIEIALEGPSSVTQQFDQEKTPAVKRALELTQEEQLERIENAKKYIEEVIEETNQEELANQERQ  
05-EVVRAANQAIRSGGERLAEIVQYASGFSDESTIVEVRQEDRIQRDIFQEEGQNLIAIEIALEGPSSVTQQFDQEKTPAVKRALELTQEEQLERIENAKKYIEEVIEETNREFESEVRQ  
06-EVVRAANQAIRSGGERLAEIVQYASGFSDESTIVEVRQEDRIQRDIFQEEGQNLIAIEIALEGPSSVTQQFDQEKTPAVKRALELTQEEQLERIENAKKYIEEVIEETNREFESEVRQ  
07-EVVRAANEAIRSGGDRLAELVQAYASGFSDESTIVEVRQEDRVQRDIFQEEGQNLIAIEIALQEPSSVAQQLDQERTPAVKRALELTQEEQLERIENAKKYIEEVIEETNQEELQEQERQ  
08-EVVRAANEAIRSGGDRLAELVRYASGFSDESTIVEVRQEDRVQRDIFQEEGQNLIAIEIALQEPSSVALQLDQERTPAVKRALELTQEEQLERIENAKKYIEEVIEETNQEELQEQERQ  
09-EVVRAANEAIRSGGDRLAELVRYASGFSDESTIVEVRQEDRVQRDIFQEEGQNLIAIEIALQEPSSVALQLDQERTPAVKRALELTQEEQLERIENAKKYIEEVIEETNQEELQEQERQ  
10-EVVRTANEAIRSGGDRLELVQAYASGFSDESTIVEVTRQEDRVQRDIFQEEGQNLIAIEIALEGPSSVTQQFDQERTLAVKRALELTQEEQLERIENAKKYIEEVIEETNRELATQERQ  
11-EVVRAANEAIRSGGDRLELVQAYASGFSDESTIVEVTRQEDRVQRDIFQEEGQNLIAIEIALEGPSSVTQQFDQERTLAVKRALELTQEEQLERIENAKKYIEEVIEETNRELATEERQ  
12-EVVRAANEAIRSGGDRLELVQAYASGFSDESTIVEVTRQEDRVQRDIFQEEGQNLIAIEIALEGPSSVTQQFDQERTLAVKRALELTQEEQLERIENAKKYIEEVIEETNRELATEERQ  
13-DLVRTATTAIRGGDILSELVQAFASGFTDHTQIVDLRQETRVQNDIFQEEGQNLIAIQLALEAPSTVAVQFDQERTPAVKRALDLTVYEEQAARTENAKRIIQEVIDETDRQLA-----  
14-DLVRTATTAIRGGDILSELVQAFASGFTDHTQIVDLRQETRVQNDIFQEEGQNLIAIQLALEAPSTVAVQFDQERTPAVKRALDLTVYEEQAARTENAKRIIQEVIDETDRQLA-----  
15-DLVRTASAAIRGGDILTELVQAFASGFTDHTQVVDLRQETRVQNDIFQEEGQNLIAIQLALEAPSAVASRFQDERTPAIKRALELTAYEEQAARTENAKRIIQEVIDETDRQLA-----

01-ETSAAEEDTMASAAPTPMEETSEPGVTAAPHQKSAA-GGGGGGGSGGETAGYGKNTNDAFQRHRNQPIDLKHIGDNVYVAQRVYKVEAECKLIHDKLTWS-ATADNPFVRRMLGNESSN  
02-ETSAAEEDTMASAAPTPMEETSEPGVTAAPHQSSAS-GGGGGGGSGGETAGYGKNTNDAFQRHRNSPIDLKHIGDNVYVAQRVYKVEAECKLVNDKLTWS-TTNDNAFTRRLGLEKDHT  
03-ETSAAEEDTMASAAPTPMEETSEPGVTAAPHQSSAA-GSGGGGGSGGETAGYGKNTNDAFQRHRNKPIDLKHIGDNVYVAQRVYKVEAECKLVHDKLTWS-ATSDNAYTRRLMGLEKDHD  
04-ETSAAEEDTMSTAAPTMEETSEPGVTAAPHQRAAS-GSGGGGGSGGETAGYGKNTNDAFQRHRNKPIDLKHIGDNVYVAQRVYKVEAECKLVNDKLVWS-ETEDSGYVRRMLGNESSN  
05-ETSAAEEDTMASAAPTPMEETSEPGVTAAPHQKSAA-GGGGGGGSGGETAGYGKNTNDAFQRHRNQPIDLKHIGDNVYVAQRVYKVEAECKLINDKLTWS-ATADNPFVRRMLGNASSN  
06-ETSAAEEDTMASAAPTPMEETSEPGVTAAPHQKSAA-GGGGGGGSGGETAGYGKNTNDAFQRHRNQPIDLKHIGDNVYVAQRVYKVEAECKLIHDKLTWS-ATADNPFVRRMLGNESSN  
07-EVSAAAEDTMNTEAPVPMETSESGATAAPQORAAA-GGGGSGGG--GESAGYGRNPSDSFQRHRNKPVDLKHIGDNVYVAQRVYKVEAECKLVGDKLSWS-NTTNSKYLRRLLGINGNSN  
08-EVSAAEADTMNTEAPVPMETSESGATAAPQORAAA-GGGGSGGG--GESAGYGRNPSDSFQRHRNKPIDLKHIGDNVYVAQRVYKVEAECKLVGDKLSWSPSTSNTKFIRRLGINGNSN  
09-EVSAAEADTMNTEAPVPMETSESGATAAPQORAAA-GGGGSGGG--GESAGYGRNPSDSFQRHRNKPIDLKHIGDNVYVAQRVYKVEAECKLVGDKLSWSPSTSNTKFIRRLGINGNSN  
10-DISAAAEDTMNSAAPTMEETSEPGTTAAPQQLSAA-GGGGGGGG-GGETAGYGRNTGSAFQRHRNKPIDLKHIGDNVYVAQRVYKVEAECKLVNKLWQ-ATEDNPFTRRLMGLSSASN  
11-DISAAAEDTMNSAAPTMEETSEPGTTAAPQQLSAS-GGGGGGGG-GGETAGYGRNTSSAFQRHRNKPIDLKHIGDNVYVAQRVYKVEAECKLVYNKLTWN-TTEDNPFTRRLMGLSSASN  
12-DISAAAEDTMNSAAPTMEETSEPGTTAAPQQLSAS-GGGGGGGG-GGETAGYGRNTSSAFQRHRNKPIDLKHIGDNVYVAQRVYKVEAECKLVYNKLTWN-TTEDNPFTRRLMGLSSASN  
13-----IEDTMSTEAPVPMETSENGAAAAPQORAAAGGGGGGGG--SGGESAGYGRNPSDAFQRHRNKPIDLKHIGNNVYSQRVYKVEAECKLVDDRLTWT-NTDDSTNIRRLMGRGDYN  
14-----IEDTMSTEAPVPMETSENGAAAAPQORAAAGGGGGGGGSGGESAGYGRNPSDAFQRHRNKPIDLKHIGNNVYSQRVYKVEAECKLVDDRLTWT-NTGDTTDIRRLMGRGDYN  
15-----LEDTMSTEAPVPMETIENGATAAPHQRAAGSGGGGGGGSGGESAGYGRNPSDAFQRHRNKPVDLKHIGNNVYSQRVYKVEAECKLVGDRLSWS-ETSDTTDVRRLMGTSGNYG

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Fig. S3. (continued)

01-SGDIKYSFNALLHGSIGLGNLALSNIYINAWGIDNMAKSEDSWAIATRGKMNHLQAFEMIPQMGETIVGYTSAPVQFGKLLGHIIYPPDPKGEEKIKVANHSNGQEYRIFDGAIDGYTLD  
02-QTGTKFSFKAPLNGSIGLGNLALGNINAWGLDNIKSEDSWAIATRGKMNHLQAFEMIPQLQGETVI GYTSAPVQFGKLLGHVYYPDPKGEEERLKVANNNDGREFKAFDGAIDGYKLD  
03-QGAIKFSYKSI LNGSITMGNLALGNINAWGIDNIAKSEDSWAIATRGKMNHLQAFEMIPQMGETTVGYTSAPVQFGKLLGHVYYPDPKGEEKIKVANSNDNGREVKVF DGALEGYKLD  
04-QGDIKYSFNALLHGSIGLGNLALSNIYINAWGLDNIKSEDSWAIATRGKMNHLQAFEMIPQMGETITIGYTSAPVQFGKLLGHVYYPDPKGEEKIKVANNNSNGKEYKIFDGAIDGLTLD  
05-SGDIKYSFNALLHGSIGLGNLALGNINAWGIDNMAKSEDSRAIISTRGKMNHLQAFEMIPQMGETITIMGYTSAPVQFGKLLGHIIYYPDPKGEEKIKVANNSDGQEYKIFDGAIDNGYPLD  
06-SGDIKYSFNALLHGSIGLGNLALSNIYINAWGIDNMAKSEDSWAIATRGKMNHLQAFEMIPQMGETIVGYTSAPVQFGKLLGHIIYYPDPKGEEKIKVANHSNGQEYRIFDGAIDGYTLD  
07-SGDIKHSFYTQLSGSIGLGNLALGNINAWGMDNISKSEDSWAIATRGKMNHLQAFEMVPOYQGETTVGYTSAPLQFGKLLGHVYYPDPKGEEERIKIASKADAKE SKMFKDAMAGYLLD  
08-TGDIKHGFSASLPGSIGLGNLALGNINAWGMDNISKSEDSWAIATRGKMNHLQAFEMVPOYQGETIVGYTSAPLQFGKLLGHVYYPDPKEEERIKISSKADGQEAKMFKDAMSRMYLD  
09-TGDIKHGFSASLPGSIGLGNLALGNINAWGMDNISKSEDSWAIATRGKMNHLQAFEMVPOYQGETIVGYTSAPLQFGKLLGHVYYPDPKEEERIKISSKADGQEAKMFKDAMSRMYLD  
10-QGNFKYSFKSILGGSVCLGNLNLNSNIYINAWGIDNIAKSEDSWAILCTRGMNHLQAFEMIPQLQGETVI GYTSAPVQFGKLLGHIIYYPDPKGEEETIKVAGI GNGKESQVFEQAQEGYLM  
11-QGDFKYSFKSILGGSINMGNLNLNLCNIYINAWGIDNIAKSEDSWAILCTRGMNHLQAFEMIPQLQGETTVGYTSAPVQFCKLLGHIIYYPDPKGEEETIKVAGIANGKESQAFNGAKEGYLM  
12-QGDFKYSFKSILGGSINMGNLNLNLCNIYINAWGIDNIAKSEDSWAILCTRGMNHLQAFEMIPQLQGETTVGYTSAPVQFCKLLGHIIYYPDPKGEEETIKVAGIANGKESQAFNGAKEGYLM  
13-DVDTKFNYKAKLAGSIQMGNLELGNYSI SAWGLDHIKSEDSWAIATRGKMNHLQAFEMVPLNGETVIGYNSVPVQFGKLLGHIIYYPDPKGNEQLKVACSGDGKEGNTFKGAIDGLVLD  
14-DVDTKFNYKAKLAGSIQMGNLELGNYSI SAWGLDHIKSEDSWAIATRGKMNHLQAFEMVPLNGETVIGYNSVPVQFGKLLGHIIYYPDPKGNEQLKVACSGDGKEGNTFKGAIDGLVLD  
15-TFDPKFNYNAKLSGSIQMGNLELGNYSI SAWGLDHIKSEDSWAIATRGKMNHLQAFEMVPLNGETVIGYNSVPVQFGKLLGHIIYYPDPKGNEQLKIACFRNGKEGNTFHRARDGLMLD

01-DDMNQKKITADQHHVFMFTDLRDA PMISEVTAYLNTDNPAQINGIGIEHQGFDM SNDANTALIGVMPSNCIRKRKEIQSGMDNVVLWSMQSNRLIDKRFWTPEGWSLKS VNGMANDRIDM  
02-DDMTQTKITTDQHKVVFVFTDLRDS PMMSYVTAYLNSDNPPQINGIGMEHQGYDVAGGENTSFI GLMPSNCIRKRKEIQSGMDNVVLWSMKS NRLLIDKRFWTPEGWSNKS ANGMANDRVEL  
03-DDMNQKKITADQHHVFMFTDLRDA PMISEVAAYLNTANPQQINGIGMEHQGYDVAGGENTSFI GVTPSNCIERRKEIQSGMDNVVLWSMKS NRLLIDKRFWTPEGWSNKS ANGMANDRVEL  
04-DDMNQKKITADQHHVFMFTDLRDA PMMSAVTAYLNTDTPAQINGIGIEHQGFDMTSDPNTALIGVMPSNCIQKRKEIQSGMDNVVLWSMKS NRLLIDKRFWTPEGWSH KSMNGMANDRVDI  
05-DDMNQKKITADQHHVFMFTDLRDA PMISKVTAYLNTDNPPQINGIGIEHQGFDM SNDANTALIGVMPSNCIRKRKEIQSGMDNVVLWSMQSNRLIDKRFWTPEGWSLKS VNGMANDRIDM  
06-DDMNQKKITADQHHVFMFTDLRDA PMISEVTAYLNTDNPAQINGIGIEHQGFDM SNDANTALIGVMPSNCIRKRKEIQSGMDNVVLWSMQSNRLIDKRFWTPEGWSLKS VNGMANDRIDM  
07-DDMNQTKVTS EHNHVFVFTDLRDS PVI SEVAAYQTND EPPKINGIGIEYQGFNL TSDTNAALIGLMPSNCISKRKEIQSGMDNVVLWSMKS NRLLIDKRFWKPEGWTKKSMNGMAKDKVNI  
08-DDMNQTKITA EHNHVFVFTDLRDS PMISEIAAYQTND EPPKINGIGIEYQGFNL TSDTNAALIGLMPSNCISKRKEIQSGMDNVVLWSMKS NRLLIDKRFWKPDGWT KSTNGMARDKIDT  
09-DDMNQTKITA EHNHVFVFTDLRDS PMISEIAAYQTND EPPKINGIGIEYQGFNL TSDTNAALIGLMPSNCISKRKEIQSGMDNVVLWSMKS NRLLIDKRFWKPDGWT KSTNGMARDKIDT  
10-DDMSQKITSEAHVPYMF TDLRDA PMISEVTAYLDSTNPTRISSVGEHQGFDMTNDANTALIGVTPSNCIQRKEIQSGMDVVIWSMKS NRLLIDKRFWKPEGWSKSLNGMANNRIDI  
11-DDMSQKITSE EHSVCMFTDLRDA PMISEVTAYLAVPDQDRHSIGIEHQGFDMTNDANTALIGVTPSNCMQRRKEIQSGMDVVIWSMKS NRLLIDKRFWRPEGWSNKS LNGMANNRVDI  
12-DDMSQKITSE EHSVCMFTDLRDA PMISEVTAYLAVPDQDRHSIGIEHQGFDMTNDANTALIGVTPSNCMQRRKEIQSGMDVVIWSMKS NRLLIDKRFWRPEGWSNKS LNGMANNRVDI  
13-DDMTQOKITTDHVVYVFTDLRDA PMMSRTAIYED-DGYVNIKGLGIEHQGFDMTSEAGTALIGVMPSRCISKRKEIQSGMDNIVLWAMKS NRLLIDKRFWTPEGWSKSVNGMAQDRLDI  
14-DDMTQOKITTDHVVYVFTDLRDA PMMSRTAIYED-DGYVNIKGLGIEHQGFDMTSEAGTALIGVMPSRCISKRKEIQSGMDNIVLWAMKS NRLLIDKRFWTPEGWSKSVNGMAQDRLDI  
15-DDMTQOKVTAADYVYVFTDLRSAPMISR TGIYED-AGYTTIKGLGIEHQGFDMTEEAGTALIGVMPSRCISKRKEIQSGMDNVVLWAMKS NRLLIDKRFWTPEGWSKSVNGMAPDRLDV

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Fig. S3. (continued)

01-**P**SE**G**AA**I**F**D**EA**H**V**T**R**T**S**N**YA**E**WA**R**NE**I**Y**S**AD**T**SD**N**AF**G**PS**N**T**G**AF**A**Q**K**Y**N**VS**N**Q**Y**AT**N**I**F**F**M**PA**H**T**Q**R**G**A**I**Q**D**IV**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**RS**V**Y**N**D**F**Y**H**IN**A**R**A**V**V**P**T**V**Y**DE**Y**K**D**R**T**F  
 02-**P**SE**G**AP**I**F**D**EA**H**V**T**R**T**SD**Y**A**E**WA**R**NE**I**F**Y**D**G**T**S**Y**S**E**F**AP**G**NN**G**AF**V**Q**K**Y**N**I**G**N**Q**Y**A**T**N**V**F**F**M**PA**H**T**Q**R**G**A**I**Q**D**IV**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**R**H**V**Y**N**D**F**Y**H**V**NA**K**AV**V**P**V**Y**D**N**Y**ID**R**P**Y**  
 03-**P**SE**G**AP**I**F**D**EA**H**V**T**R**T**SD**Y**A**E**WA**R**NE**I**F**Y**D**G**T**S**Y**S**E**F**AP**G**NN**G**AF**V**Q**K**Y**N**I**G**N**Q**Y**A**T**N**V**F**F**M**PA**H**T**Q**R**G**A**I**Q**D**IV**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**R**H**V**Y**N**D**F**Y**H**V**NA**K**AV**V**P**V**Y**D**N**Y**ID**R**P**Y**  
 04-**P**IE**G**DA**I**F**D**EA**H**V**T**R**T**SP**Y**A**E**WA**R**NE**I**F**Y**S**A**D**V**SD**N**AY**A**P**G**NP**G**A**F**T**Q**K**Y**N**I**G**N**Q**Y**A**T**S**I**F**F**M**P**Y**A**H**T**Q**R**G**A**I**Q**D**I**V**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**R**H**V**Y**N**D**F**H**H**V**NA**K**AV**T**P**I**V**Y**DE**Y**K**A**R**T**Y  
 05-**P**SE**G**AP**I**F**D**EA**H**V**T**R**T**SD**Y**A**E**WA**R**NE**I**Y**S**AD**T**SD**N**AF**G**PS**N**T**G**AF**A**Q**K**Y**N**VS**N**Q**Y**AT**N**I**F**F**M**PA**H**T**Q**R**G**A**I**Q**D**IV**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**RS**V**Y**N**D**F**Y**H**IN**A**R**A**V**V**P**T**V**Y**DE**Y**K**D**R**T**F  
 06-**P**SE**G**AA**I**F**D**EA**H**V**T**R**T**S**N**YA**E**WA**R**NE**I**Y**S**AD**T**SD**N**AF**G**PS**N**T**G**AF**A**Q**K**Y**N**VS**N**Q**Y**AT**N**I**F**F**M**PA**H**T**Q**R**G**A**I**Q**D**IV**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**RS**V**Y**N**D**F**Y**H**IN**A**R**A**V**V**P**T**V**Y**DE**Y**K**D**R**T**F  
 07-**T**PT**T**Y**D**I**Y**EE**A**H**V**T**R**T**D**Y**A**E**W**A**R**NE**I**F**Y**D**A**NT**S**Y**G**SV**G**PS**D**IG**N**F**V**Q**K**Y**N**LS**D**Q**Y**A**T**D**I**F**F**M**P**Y**V**H**T**Q**R**G**I**I**Q**D**I**V**I**N**F**DL**T**M**Q**IM**V**K**R**I**P**R**Q**V**Y**N**D**F**Y**H**I**N**T**R**A**M**N**P**V**K**Y**D**S**A**V**E**R**S**F**  
 08-**P**P**A**NY**D**I**Y**Q**E**A**H**V**T**R**T**A**E**Y**A**E**W**A**R**TE**I**F**Y**D**A**GT**S**Y**G**SV**G**PS**D**NG**Y**F**I**Q**K**Y**N**L**W**G**Q**Y**A**T**S**I**F**F**M**Y**V**H**T**R**R**G**I**I**Q**D**I**I**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**R**H**V**Y**N**D**F**Y**H**I**N**T**R**A**M**H**P**V**K**Y**D**S**A**I**D**R**T**F**  
 09-**P**P**A**NY**D**I**Y**Q**E**A**H**V**T**R**T**A**E**Y**A**E**W**A**R**TE**I**F**Y**D**A**GT**S**Y**G**SV**G**PS**D**NG**Y**F**I**Q**K**Y**N**L**W**G**Q**Y**A**T**S**I**F**F**M**Y**V**H**T**R**R**G**I**I**Q**D**I**I**I**N**F**DL**T**L**Q**IM**V**K**R**I**P**R**H**V**Y**N**D**F**Y**H**I**N**T**R**A**M**H**P**V**K**Y**D**S**A**I**D**R**T**F**  
 10-**P**A**E**G**A**P**I**Y**E**D**A**Y**V**C**R**T**S**D**Y**A**G**W**A**R**T**E**V**F**Y**D**A**N**T**E**Y**S**E**F**A**P**G**NT**G**A**F**T**Q**K**Y**N**S**N**Q**Y**A**T**C**I**F**F**M**Y**A**H**T**Q**R**G**A**I**Q**D**I**V**I**N**F**DL**T**L**Q**IM**V**K**R**I**A**R**H**V**Y**N**D**F**Y**H**V**N**T**K**A**A**H**P**V**V**Y**E**K**F**E**E**R**S**F**  
 11-**P**A**E**G**A**P**I**Y**E**D**A**Y**V**C**R**T**S**G**Y**A**E**W**A**R**T**E**V**F**Y**D**A**N**T**E**Y**S**E**F**A**P**G**NT**G**A**F**T**Q**K**Y**N**S**N**Q**Y**A**T**C**I**F**F**M**Y**A**H**T**Q**R**G**A**I**Q**D**I**V**I**N**F**DL**T**L**Q**IM**V**K**R**I**A**R**H**V**Y**N**D**F**Y**H**I**N**T**G**G**V**H**P**V**V**Y**T**K**F**E**E**R**S**F**  
 12-**P**A**E**G**A**P**I**Y**E**D**A**Y**V**C**R**T**S**G**Y**A**E**W**A**R**T**E**V**F**Y**D**A**N**T**E**Y**S**E**F**A**P**G**NT**G**A**F**T**Q**K**Y**N**S**N**Q**Y**A**T**C**I**F**F**M**Y**A**H**T**Q**R**G**A**I**Q**D**I**V**I**N**F**DL**T**L**Q**IM**V**K**R**I**A**R**H**V**Y**N**D**F**Y**H**I**N**T**G**G**V**H**P**V**V**Y**T**K**F**E**E**R**S**F**  
 13-**P**SE**D**KE**I**Y**A**E**A**H**V**T**R**T**S**N**Y**A**E**WA**R**NE**A**H**F**D**A**TE**R**ND**A**FT**P**AN**E**G**K**F**T**TK**Y**N**I**S**N**Q**Y**A**T**Q**I**F**F**M**P**Y**V**H**T**Q**R**G**A**V**Q**D**I**V**V**N**F**DL**T**L**Q**IM**I**KK**I**P**R**T**V**Y**N**D**F**Y**H**IN**A**R**A**Y**T**W**H**E**Y**T**S**T**A**R**T**Y  
 14-**P**TR**D**KE**I**Y**A**E**A**H**V**T**R**T**S**N**Y**A**E**WA**R**NE**A**H**F**D**A**TE**R**ND**A**FT**P**AN**E**G**K**F**T**TK**Y**N**I**S**N**Q**Y**A**T**Q**I**F**F**M**P**Y**V**H**T**Q**R**G**A**V**Q**D**I**V**V**N**F**DL**T**L**Q**IM**I**KK**I**P**R**T**V**Y**N**D**F**Y**H**IN**A**R**A**Y**T**W**H**E**Y**N**S**T**D**T**R**T**Y**  
 15-**A**R-**D**K**A**I**Y**A**E**A**H**V**T**R**T**S**E**Y**A**E**W**A**R**NE**A**H**Y**D**A**T**S**G**D**D**V**F**A**P**G**NE**G**KL**T**TK**Y**N**S**N**Q**Y**A**T**Q**I**F**F**M**Y**V**H**T**Q**R**G**A**V**Q**D**I**V**V**N**F**DL**T**L**Q**IM**V**RR**I**P**R**T**V**Y**N**D**F**Y**H**I**N**I**R**A**M**T**L**H**E**Y**T**D**V**S**N**R**T**F

01-**G**AT**E**I**S**H**R**G**K**N**I**H**V**N**I**T**G**H**G**S**K**Y**S**D**R**G**Q**V**S**R**I**G**A**T**K**K**N**F**A**T**R**A**Y**G**Q**K**Q**L**L**L**N**E**G**I**T**R**R**K**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**E**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**Q**K**K**K**K**Y**K**T**N**V\*  
 02-**T**G**N**Q**I**S**H**R**A**K**N**L**H**I**N**M**S**G**T**H**G**S**K**Y**A**D**R**G**Q**I**T**R**K**G**A**T**M**K**D**F**G**K**R**P**Y**G**Q**R**T**I**L**L**N**E**G**I**P**T**R**R**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**E**P**P**P**Q**P**Q**L**Q**K**E**K**K**K**P**K**T**N**V**\*  
 03-**T**G**A**Q**I**S**H**R**A**Q**N**L**H**I**N**M**T**G**T**H**G**S**K**Y**A**D**R**G**Q**I**S**R**K**G**A**T**M**K**D**F**G**K**R**P**Y**G**Q**R**T**I**L**L**N**E**G**I**P**T**R**R**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**E**P**P**P**Q**P**Q**L**Q**K**K**K**K**P**K**T**N**V\*  
 04-**G**A**Q**Q**I**K**N**R**A**Q**N**L**H**I**N**M**T**G**T**H**G**S**K**Y**S**D**R**G**Q**A**S**N**K**R**A**V**K**K**N**S**A**T**R**A**Y**A**Q**R**L**L**L**L**N**E**G**I**T**R**R**T**T**R**S**S**A**A**A**A**E**D**D**I**P**E**D**C**G**D**F**L**E**T**S**E**M**R**P**P**P**Q**P**L**Q**K**K**K**K**Y**R**T**D**V\*  
 05-**G**AT**E**I**S**H**R**G**K**N**I**H**V**N**I**T**G**H**G**S**K**Y**S**D**R**G**Q**V**S**R**I**G**A**T**K**K**N**F**A**T**R**A**Y**G**Q**K**Q**L**L**L**N**E**G**I**T**R**R**K**T**R-**S**S**A**A**A**E**D**D**I**P**D**D**C**E**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**Q**K**K**K**K**Y**K**T**N**V\*  
 06-**G**AT**E**I**S**H**R**G**K**N**I**H**V**N**I**T**G**H**G**S**K**Y**S**D**R**G**Q**V**S**R**I**G**A**T**K**K**N**F**A**T**R**A**Y**G**Q**K**Q**L**L**L**N**E**G**I**T**R**R**K**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**E**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**Q**K**K**K**K**Y**K**T**N**V\*  
 07-**G**Y**D**E**I**Y**A**R**S**I**K**I**H**E**N**I**S**G**T**H**G**S**K**Y**A**D**R**G**P**I**S**H**E**A**T**K**R**N**S**Y**Q**R**A**Y**A**Q**R**R**I**L**D**Q**G**V**S**K**M**K**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**D**P**P**P**Q**P**Q**L**P**K**K**K**K**Y**R**V**N**V\*  
 08-**G**Y**D**E**I**Y**A**R**S**I**N**I**H**E**H**M**S**G**T**H**G**S**K**Y**A**E**R**G**P**I**S**H**E**A**T**K**K**N**S**D**S**R**K**Y**A**Q**R**R**L**L**D**Q**G**V**S**R**M**K**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**P**K**K**K**K**Y**R**T**V**M\*  
 09-**G**Y**D**E**I**Y**A**R**S**I**N**I**H**E**H**M**S**G**T**H**G**S**K**Y**A**E**R**G**P**I**S**H**E**A**T**K**K**N**S**D**S**R**K**Y**A**Q**R**R**L**L**D**Q**G**V**S**R**M**K**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**P**K**K**K**K**Y**R**T**V**M\*  
 10-**G**A**D**N**I**K**H**R**A**H**N**I**H**V**N**M**S**G**T**H**G**S**K**Y**S**D**R**G**Q**V**S**R**K**K**A**I**K**A**D**H**D**K**R**P**Y**G**Q**R**R**I**M**V**E**E**S**P**V**R**R**T**R**-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**P**K**K**K**K**Y**R**T**V**M\*  
 11-**G**D**D**N**I**K**H**R**A**H**N**I**H**V**N**M**S**G**T**H**G**S**K**Y**A**D**R**G**Q**V**S**R**K**K**A**I**K**A**D**R**D**K**R**P**C**G**Q**R**R**L**M**I**E**V**G**A**G**P**M**R**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**P**K**K**K**K**Y**R**T**N**V\*  
 12-**G**D**D**N**I**K**H**R**A**H**N**I**H**V**N**M**S**G**T**H**G**S**K**Y**A**D**R**G**Q**V**S**R**K**K**A**I**K**A**D**R**D**K**R**P**C**G**Q**R**R**L**M**I**E**V**G**A**G**P**M**R**T**R-**S**S**A**A**A**E**D**D**I**P**E**D**C**D**D**F**L**E**T**S**E**M**E**S**P**P**Q**P**Q**L**P**K**K**K**K**Y**R**T**N**V\*  
 13-**G**V**G**D**I**R**S**R**A**R**N**I**H**Q**D**I**T**G**T**H**G**S**K**Y**S**D**R**G**P**I**K**D**G**S**T**M**K**I**H**P**E**R**A**Y**G**Q**K**R**I**F**L**D**K**G**I**S**K**R**T**R**S**K**T**A**A**A**D**D**D**I**P**D**D**C**D**D**F**L**E**T**S**E**M**R**M**P**P**Q**P**L**S**K**K**K**K**P**K**E\*--  
 14-**G**V**G**D**I**R**N**R**A**T**N**I**H**Q**D**I**T**G**T**H**G**S**K**Y**S**D**R**G**P**I**K**D**G**S**T**M**Q**I**H**P**E**R**A**Y**G**Q**K**R**I**F**L**D**K**G**I**S**K**R**T**R**S**K**T**A**A**A**D**D**D**I**P**D**D**C**D**D**F**L**E**T**S**E**M**R**M**P**P**Q**P**L**S**K**K**K**K**P**K**E\*--  
 15-**G**V**A**D**I**R**S**R**A**T**N**I**H**H**D**V**S**G**T**H**G**S**R**Y**A**D**R**G**P**I**S**H**K**G**S**T**M**K**S**H**S**R**V**Y**G**Q**K**R**I**L**L**D**K**G**I**S**R**M**T**R**S**R**T**A**A**A**D**D**D**I**P**D**D**C**D**D**F**L**E**T**S**E**I**E**M**P**P**Q**P**Q**S**Q**K**K**K**K**S**K**E**\*--

Fig. S3. (continued)

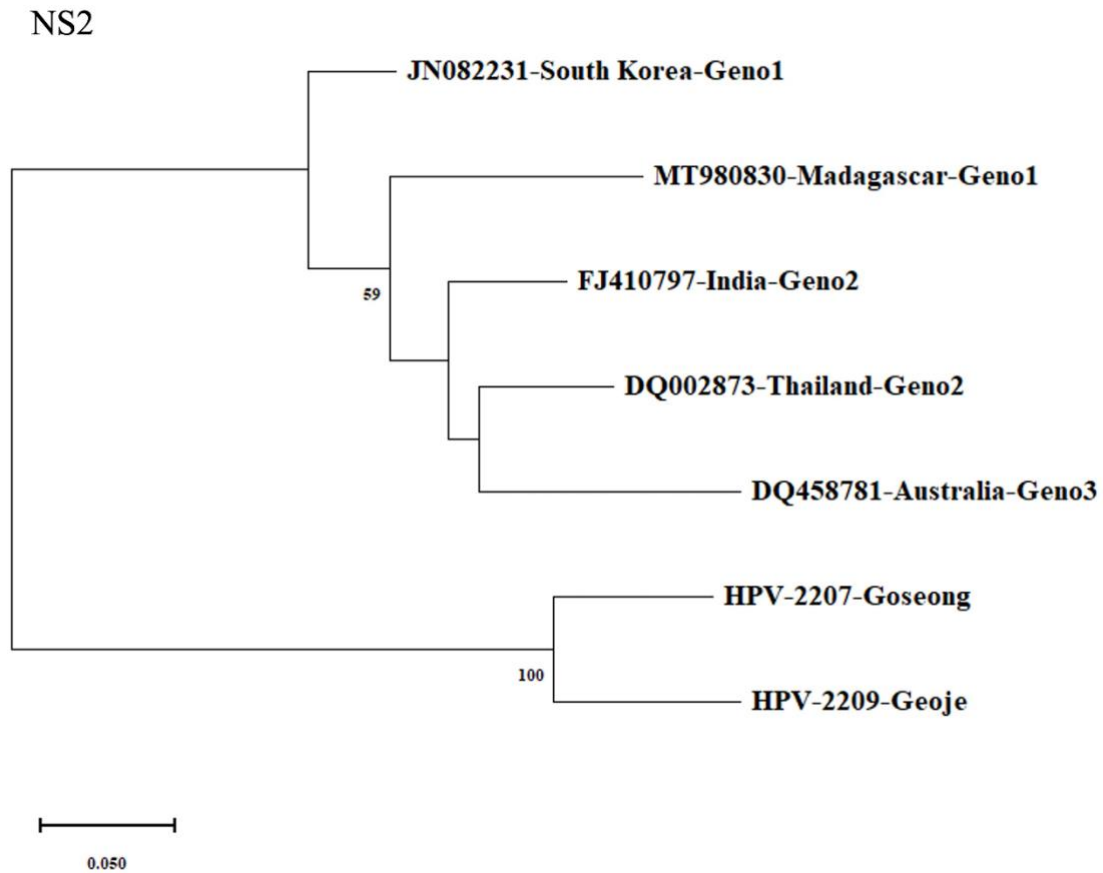


Fig. S4. Phylogenetic tree based on DHPV NS2 amino acid sequence. The tree was constructed by Maximum likelihood with 1000 bootstrap (MEGA11).



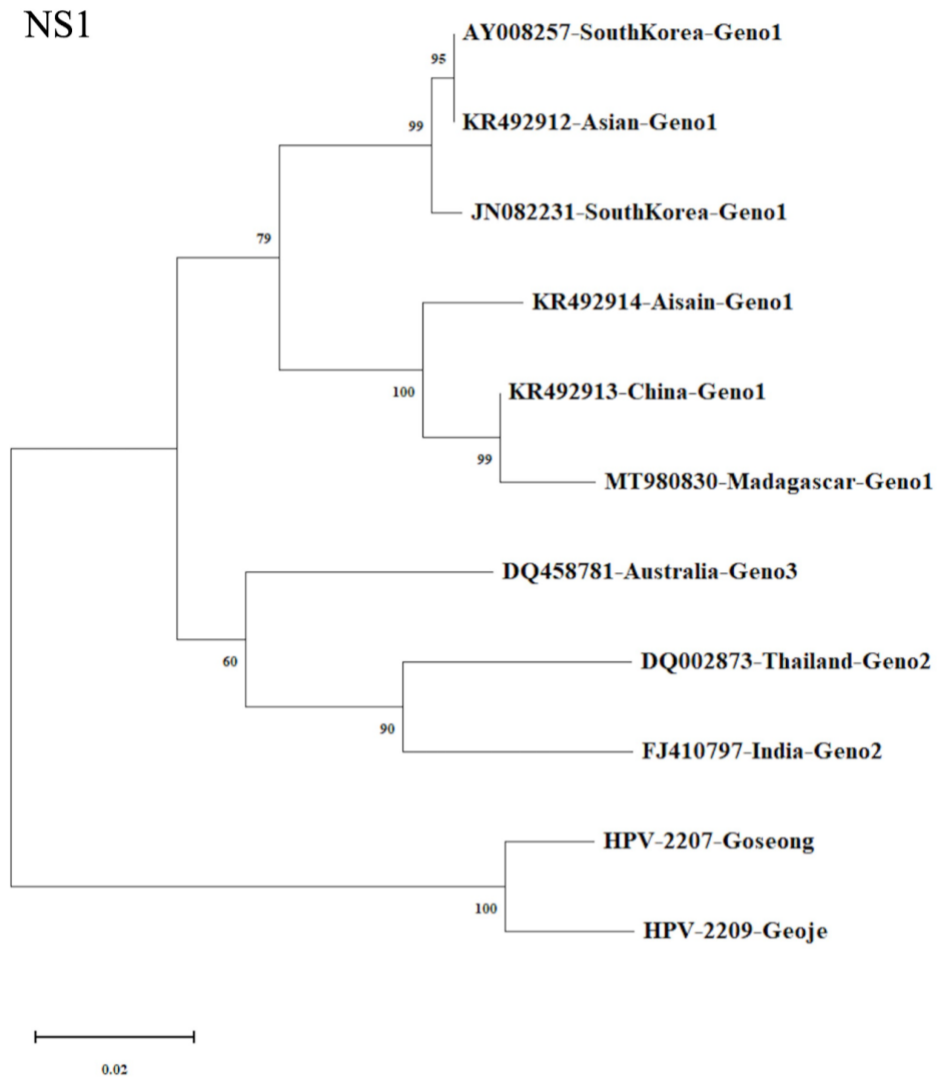


Fig. S5. Phylogenetic tree based on DHPV NS1 amino acid sequence. The tree was constructed by Maximum likelihood with 1000 bootstrap (MEGA11).