

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2020.003M** |  |
| **Short title:** Create ten new species in the genus *Sigmavirus* (*Mononegavirales*: *Rhabdoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Rhabdoviridae* Study Group |

**ICTV study group comments and response of proposer**

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| Approved by all responding SG members (9 of 14). Minor comments and corrections suggested by the Study Group have mostly been implemented. |

**Authority to use the name of a living person**

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 19 December 2019 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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|  |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2020.003M.R.Sigmavirus\_10nsp.xlxs |

**Abstract**

|  |
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| **The genus *Sigmavirus* currently comprises seven species of viruses infecting flies (Diptera: Drosophilidae and Muscidae). We propose here the creation of 10 new species in the genus *Sigmavirus* to accommodate additional viruses infecting flies (Diptera) for which complete coding sequences are now available and which cluster phylogenetically with sigmaviruses based on complete L protein sequences. Each new member virus was detected by metagenomic sequence analysis. No virus isolates are available at this time.** |

**Text of proposal**

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| |  | | --- | | According to the current description (10th ICTV Report) viruses assigned to the genus *Sigmavirus* have the following distinguishing characteristics.  “Viruses assigned to the genus *Sigmavirus*form a distinct monophyletic group based on well-supported maximum-likelihood trees inferred from complete or partial L sequences. Sigmaviruses each infect a dipteran insect of single species in the families Drosophilidae or Muscidae in which they are transmitted only vertically; other dipterans also appear to harbour sigmaviruses. Sigmavirus genomes may feature an additional gene (*X*) located between the *P* and *M* genes, encoding a protein of unknown function.”  Here we propose the assignment of 10 new species in the genus to accommodate viruses infecting flies of various species within the families Drosophilidae, Muscidae, Tephritidae or Hippoboscidae, or other unidentified dipteran flies.  **The viruses**  Wuhan louse fly virus 9 (WhLFV-9) was detected in louse flies (Hippoboscidae) collected in Wuhan, China, in 2013 [1]. The near-complete genome sequence (11,370 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Hippoboscid sigmavirus* is proposed to accommodate this virus.  Wuhan louse fly virus 10 (WhLFV-10) was detected in louse flies (Hippoboscidae) collected in Wuhan, China, in 2013 [1]. The near-complete genome sequence (11,541 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Lousefly sigmavirus* is proposed to accommodate this virus.  Hubei dimarhabdovirus 1 (HbDRV-1) was detected in unidentified flies (Diptera) collected in Hubei Province, China, in 2013 [5]. The near-complete genome sequence (11,145 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Ying sigmavirus* is proposed to accommodate this virus.  Hubei diptera virus 9 (HbDV-9) was detected in unidentified flies (Diptera) collected in Hubei Province, China, in 2013 [5]. The near-complete genome sequence (13,000 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Hubei sigmavirus* is proposed to accommodate this virus.  Hubei diptera virus 10 (HbDV-10) was detected in unidentified flies (Diptera) collected in Hubei Province, China, in 2013 [5]. The near-complete genome sequence (13,161 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Myga sigmavirus* is proposed to accommodate this virus.  Ceratitis capitata sigmavirus (CCapSV) was detected in a laboratory strain of Mediterranean fruit flies (*Ceratitis capitata*) captured in Hawaii [2]. The near-complete genome sequence (12,583 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Capitata sigmavirus* is proposed to accommodate this virus.  Drosophila sturtevanti sigmavirus (DStuSV) was detected in fruit flies (*Drosophila sturtevanti*) collected in Spain, in 2009 [2]. The near-complete genome sequence (13,233 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Sturtevanti sigmavirus* is proposed to accommodate this virus.  Shayang fly virus 2 (SyFV-2) was detected in house flies (*Musca domestica*) collected in Shayang, China, in 2012 [1]. The near-complete genome sequence (12,291 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Shayang sigmavirus* is proposed to accommodate this virus.  Wuhan house fly virus 1 (WhHFV-1; strain SYY2-4) was detected in house flies (*Musca domestica*) collected in Wuhan, China, in 2013 [1]. The near-complete genome sequence (12,651 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. A second strain of the virus (SCM39215) was detected in house flies collected in Wuhan, China, in 2013 [5]. The near-complete genome sequence (12,665 nt) of the second strain has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Wuhan sigmavirus* is proposed to accommodate this virus.  Wuhan fly virus 2 (WhFV-2) was detected in house flies (*Musca domestica*) collected in Wuhan, China, in 2013 [1]. The near-complete genome sequence (12,247 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. The new species *Domestica sigmavirus* is proposed to accommodate this virus.  **Genome architecture**  Sigmavirus genomes typically contain the five canonical rhabdovirus structural protein genes (*N*, *P*, *M*, *G* and *L*) and an additional gene (*X*) located between the *P* gene and *M* gene. Seven of the viruses be assigned to new species conform with this genome organization (**Figure 1**), with an *X* gene encoding secreted proteins with the common predicted structural feature of an N-terminal signal peptide (**Figure 2**). However, three of the viruses (WhLFV-9, WhLFV-10 and HbDRV-1) lack an additional gene corresponding to the *X* gene.  **Phylogeny and sequence relationships**  Based on ML trees generated from complete L protein sequences, all new viruses to be assigned to the genus *Sigmavirus* form a well-supported monophyletic clade (BSP = 99%) with currently assigned sigmaviruses (**Figure 3**). Furthermore, WhLFV-9, WhLFV-10 and HbDRV-1 fall within a well-supported sub-clade (BSP = 100%) with DMelSV and CCapSV (which contain the *X* gene), indicating that these viruses appear to have lost the *X* gene. Amino acid sequence divergence in pair-wise alignments (p-distances) between viruses assigned to different species are >10% in the N proteins, >15% in the G proteins and >10% in the L protein (**Tables 1-3**). The two viruses identified as different samples of WhHFV-1 share amino acid sequence identities of 91.2% in the N gene, 85.5% in the G gene and 91.0% in the L gene.  **Other probable members of the genus**  Wuhan louse fly virus 8 (WhLFV-8) was detected in louse flies (Hippoboscidae) collected in Wuhan, China, in 2013 [1]. Only a partial genome sequence (6,653 nt) has been determined, including the complete L gene sequence.  Drosophila algonquin sigmavirus (DAlgSV) was detected in fruit flies (*Drosophila affinis* or *Drosophila athabasca*) collected in the USA, in 2010 [2]. Only a partial genome sequence (7,016 nt) has been determined, including the complete L gene sequence.  Drosophila montana sigmavirus (DMonSV) was detected in fruit flies (*Drosophila montana*) collected in Finland, in 2008 [2]. Only a partial L gene sequence (5,853 nt) has been determined.  Drosophila tristis sigmavirus (DTriSV) was detected in fruit flies (*Drosophila tristis*) collected in the United Kingdom, in 2011 [2]. Only a partial L gene sequence (5,347 nt) has been determined.  Scaptodrosophila deflexa sigmavirus (SDefSV) was detected in fruit flies (*Drosophila tristis*) collected in the United Kingdom, in 2011 [2]. Only partial L gene sequences (746 nt, 1,029 nt and 997 nt) have been determined.  The viruses have not been proposed to be assigned to species at this time as complete coding sequences are not available.  **Other related viruses**  Seven other rhabdoviruses that have been detected in insects appear to be related phylogenetically to the sigmaviruses based on the L protein sequences. However, as shown in **Figure 4**, the viruses form several clusters that fall outside the sigmavirus clade and bootstrap support linking them to sigmaviruses is poor (BSP = 36%).  Gata virus (GATV) and Orgi virus (ORGIV) were each isolated from Douglas-fir tussock moths (*Orgyia pseudotsugata*) collected in the USA in 2016 [3]. The near-complete genome sequences of GATV (11,238 nt) and ORGIV (11,308 nt) have been determined, including complete coding sequences but incomplete 3' and 5' termini.  Hubei dimarhabdovirus 2 (HbDRV-2) was detected in mealy plum aphids (*Hyalopterus pruni*) collected in Wuhan, China, in 2013 [5]. The near-complete genome sequence (11,332 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini.  Wuhan insect virus 7 (WhIV-7) was detected in unidentified dragonflies/damselflies (Odonata) collected in Hubei Province, China, in 2013 [1]. The near-complete genome sequence (11,165 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. Tetrastichus brontispae RNA virus 1 (TbRV-1) was detected in laboratory-reared wasps (*Tetrastichus brontispae*) in China, in 2017 [4]. The near-complete genome sequence (11,165 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini. Pararge aegeria rhabdovirus (PAeRV) was detected in a laboratory population of butterflies (*Pararge aegeria*) in Belgium, in 2013 [2]. The near-complete genome sequence (13,062 nt) of the virus has been determined, including complete coding sequences but incomplete 3' and 5' termini.  Hubei lepidoptera virus 2 (HbLV-2; strain LCM101902) was detected in insects (Lepidoptera) collected in Hubei Province, China, in 2013 [5]. The near-complete genome sequence (13,109 nt) has been determined, including complete coding sequences but incomplete 3' and 5' termini.  The classification of these viruses will be the subject of a separate taxonomic proposal.  **Species demarcation criteria**  Viruses assigned to different species within the genus *Sigmavirus*have one or both of the following characteristics: A) minimum amino acid sequence divergence of 10% in L; and B) occupy different ecological niches as evidenced by differences in hosts.  All proposed members of the new genus meet these demarcation criteria.  **Derivation of the species names**  *Hippoboscid sigmavirus* - derived from louse flies (family Hippoboscidae) in which the virus was detected.  *Lousefly sigmavirus* - derived from louse flies in which the virus was detected.  *Ying sigmavirus -* derived from unidentified flies (Chinese “ying” for fly) in which the virus was detected.  *Hubei sigmavirus* - derived from Hubei Province in China, the location of collection of unidentified flies in which the virus was detected.  *Myga sigmavirus* - derived from unidentified flies (Greek “mýga” for fly), in which the virus was detected.  *Capitata sigmavirus -* derived from fruit flies of the species *Ceratitis capitata*, in which the virus was detected.  *Sturtevanti sigmavirus -* derived from fruit flies of the species *Drosophila sturtevanti,* in which the virus was detected.  *Shayang sigmavirus -* derived from Shayang County in China, the location of collection of house flies in which the virus was detected.  *Wuhan sigmavirus -* derived from Wuhan city in China, the location of collection of house flies in which the virus was detected.  *Domestica sigmavirus -* derived from house flies of the species *Musca domestica*, in which the virus was detected. | |

**Supporting evidence**

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**Figure 1.** Sigmavirus genome organisations. Each genome contains long open reading frames (ORFs) in the N, P, M, G and L genes (open arrows) and most contain an ORF (X) encoding a protein with a predicted N-terminal signal peptide (shaded yellow).

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**Figure 2.** A Clustal X alignment of the sigmavirus X proteins. Predicted N-terminal signal peptides are shown. Cysteine residues are highlighted in black. Other relatively conserved residues are also highlighted.

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**Figure 3.** The evolutionary history was inferred from a Clustal W alignment of complete L protein sequences of 157 animal rhabdoviruses including all viruses currently assigned or recently proposed for assignment to genera, the viruses proposed here to be assigned to new species in the genus *Sigmavirus*. Phylogenetically informative sites were selected from the alignment using Gblocks resulting in 978 positions in the final dataset. The tree was inferred in MEGA7 by using the Maximum Likelihood method based on the Whelan and Goldman + Freq. model. The tree with the highest log likelihood (-118341.43) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node. Sigmaviruses already classified are shown in black font (bold) and viruses proposed here to be assigned to the genus are shown in blue font. Note that two samples of Wuhan house fly virus 1 are represented. Two viruses considered likely members of the genus but for which incomplete genome sequences are available are also shown (\*).



**Figure 4.** The evolutionary history was inferred from a Clustal W alignment of complete L protein sequences of 26 animal rhabdoviruses including all viruses currently assigned or proposed here to be assigned to new species in the genus *Sigmavirus* and seven other more distantly related viruses infecting detected in insects. To simplify the analysis, vesicular stomatitis Indiana virus (genus *Vesiculovirus*) was used as the outgroup. The tree was inferred in MEGA7 by using the Maximum Likelihood method based on the Whelan and Goldman + Freq. model. The tree with the highest log likelihood (-76591.43) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Bootstrap values (100 iterations) are shown for each node.

**Table 1.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sigmavirus N proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Viruses | WhLFV-9 | WhLFV-10 | DMelSV | HbDRV-1 | CCapSV | DImmSV | DObSV | DAnaSV | DStuSV | DAffSV | HbDV-9 | WhHFV-1a | WhHFV-1b | HbDV-10 | WhFV-2 | SyFV-2 |
| WhLFV-9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhLFV-10 | 51.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DMelSV | 35.9 | 35.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDRV-1 | 22.4 | 25.1 | 26.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CCapSV | 29.1 | 28.9 | 32.4 | 25.9 |  |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 20.4 | 20.6 | 21.1 | 17.8 | 22.9 |  |  |  |  |  |  |  |  |  |  |  |
| DObSV | 22.1 | 21.6 | 22.9 | 18.3 | 25.1 | 46.5 |  |  |  |  |  |  |  |  |  |  |
| DAnaSV | 22.9 | 20.1 | 20.9 | 20.4 | 20.4 | 23.4 | 23.6 |  |  |  |  |  |  |  |  |  |
| DStuSV | 22.4 | 22.4 | 21.4 | 20.6 | 22.1 | 19.8 | 22.9 | 25.6 |  |  |  |  |  |  |  |  |
| DAffSV | 23.1 | 22.4 | 21.1 | 20.9 | 23.1 | 20.1 | 25.1 | 25.9 | 46.5 |  |  |  |  |  |  |  |
| HbDV-9 | 22.6 | 25.9 | 24.1 | 20.1 | 25.6 | 25.1 | 24.1 | 24.9 | 25.6 | 26.4 |  |  |  |  |  |  |
| WhHFV-1a\* | 22.1 | 22.9 | 24.4 | 20.4 | 20.9 | 21.1 | 23.9 | 25.1 | 23.9 | 25.6 | 29.9 |  |  |  |  |  |
| WhHFV-1b\* | 22.1 | 23.1 | 24.1 | 20.1 | 20.1 | 20.6 | 21.6 | 24.6 | 23.6 | 26.1 | 30.2 | 91.2 |  |  |  |  |
| HbDV-10 | 23.6 | 22.4 | 24.4 | 20.6 | 23.4 | 21.4 | 22.1 | 26.1 | 27.1 | 28.6 | 30.7 | 29.4 | 29.6 |  |  |  |
| WhFV-2 | 26.1 | 24.6 | 23.6 | 19.1 | 23.6 | 22.6 | 21.9 | 29.9 | 28.9 | 28.9 | 32.4 | 29.1 | 29.1 | 36.4 |  |  |
| SyFV-2 | 25.6 | 24.6 | 24.1 | 19.3 | 23.1 | 22.6 | 21.6 | 30.2 | 27.9 | 28.6 | 32.7 | 29.6 | 29.4 | 35.9 | 84.4 |  |

\* WhHFV-1 accession numbers (a) KX884432 and (b) KM817648

**Table 2.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sigmavirus G proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Viruses | WhLFV-9 | WhLFV-10 | DMelSV | HbDRV-1 | CCapSV | DImmSV | DObSV | DAnaSV | DStuSV | DAffSV | HbDV-9 | WhHFV-1a | WhHFV-1b | HbDV-10 | WhFV-2 | SyFV-2 |
| WhLFV-9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhLFV-10 | 35.9 | #### |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DMelSV | 24.7 | 25.1 | #### |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDRV-1 | 24.5 | 24.0 | 29.0 | #### |  |  |  |  |  |  |  |  |  |  |  |  |
| CCapSV | 24.2 | 23.6 | 31.2 | 27.9 | #### |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 21.0 | 22.1 | 20.6 | 21.4 | 21.6 | ### |  |  |  |  |  |  |  |  |  |  |
| DObSV | 21.2 | 20.3 | 22.5 | 21.9 | 23.2 | 38.7 | #### |  |  |  |  |  |  |  |  |  |
| DAnaSV | 23.6 | 20.8 | 24.0 | 25.8 | 22.5 | 19.3 | 21.6 | #### |  |  |  |  |  |  |  |  |
| DStuSV | 22.9 | 24.7 | 23.8 | 22.1 | 23.6 | 21.9 | 24.9 | 20.3 | #### |  |  |  |  |  |  |  |
| DAffSV | 21.2 | 21.4 | 25.3 | 23.4 | 23.6 | 19.9 | 22.5 | 22.1 | 50.6 | ### |  |  |  |  |  |  |
| HbDV-9 | 21.9 | 23.4 | 21.4 | 24.0 | 21.4 | 20.1 | 19.5 | 21.6 | 25.3 | 23.6 | #### |  |  |  |  |  |
| WhHFV-1a\* | 23.8 | 21.6 | 24.9 | 24.9 | 24.5 | 24.5 | 23.8 | 25.1 | 24.5 | 23.2 | 23.2 | #### |  |  |  |  |
| WhHFV-1b\* | 24.0 | 22.7 | 24.9 | 24.9 | 25.3 | 26.2 | 23.2 | 25.5 | 25.1 | 24.7 | 24.0 | 85.5 | #### |  |  |  |
| HbDV-10 | 18.8 | 21.4 | 24.9 | 24.5 | 23.8 | 23.2 | 21.2 | 24.5 | 26.6 | 28.1 | 32.3 | 29.7 | 29.9 | #### |  |  |
| WhFV-2 | 20.8 | 21.4 | 22.9 | 22.7 | 23.8 | 22.5 | 23.2 | 22.3 | 26.6 | 27.5 | 27.7 | 27.7 | 27.1 | 39.6 | ### |  |
| SyFV-2 | 20.3 | 21.6 | 22.3 | 22.5 | 22.9 | 21.0 | 20.3 | 23.4 | 26.6 | 26.0 | 29.7 | 28.8 | 29.2 | 38.7 | 71.6 |  |

\* WhHFV-1 accession numbers (a) KX884432 and (b) KM817648

**Table 3.** Percentage amino acid sequence identities (p-distance) of a CLUSTAL W alignment of sigmavirus L proteins.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Viruses | WhLFV-8 | WhLFV-9 | WhLFV-10 | DMelSV | HbDRV-1 | CCapSV | DImmSV | DObSV | DAnaSV | DStuSV | DAffSV | DAlgSV | HbDV-9 | WhHFV-1a | WhHFV-1b | HbDV-10 | WhFV-2 | SyFV-2 |
| WhLFV-8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhLFV-9 | 78.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| WhLFV-10 | 70.0 | 69.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DMelSV | 52.0 | 53.2 | 52.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| HbDRV-1 | 52.5 | 52.6 | 52.3 | 50.5 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CCapSV | 52.4 | 52.0 | 51.8 | 49.7 | 49.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| DImmSV | 41.6 | 42.0 | 42.0 | 42.6 | 42.9 | 43.1 |  |  |  |  |  |  |  |  |  |  |  |  |
| DObSV | 42.9 | 42.4 | 42.9 | 42.5 | 42.2 | 42.6 | 57.2 |  |  |  |  |  |  |  |  |  |  |  |
| DAnaSV | 42.1 | 42.2 | 43.1 | 41.9 | 42.8 | 43.5 | 43.6 | 43.4 |  |  |  |  |  |  |  |  |  |  |
| DStuSV | 42.1 | 42.3 | 42.4 | 41.9 | 42.3 | 42.4 | 41.4 | 42.5 | 42.6 |  |  |  |  |  |  |  |  |  |
| DAffSV | 41.6 | 41.7 | 41.3 | 40.5 | 40.9 | 42.4 | 40.4 | 42.2 | 42.2 | 62.4 |  |  |  |  |  |  |  |  |
| DAlgSV | 42.1 | 42.5 | 41.5 | 40.7 | 41.8 | 42.3 | 40.9 | 42.4 | 42.0 | 61.8 | 87.5 |  |  |  |  |  |  |  |
| HbDV-9 | 44.1 | 43.0 | 43.8 | 43.8 | 43.7 | 44.6 | 44.7 | 45.3 | 45.1 | 43.4 | 42.7 | 42.9 |  |  |  |  |  |  |
| WhHFV-1a\* | 43.4 | 42.5 | 43.2 | 42.1 | 42.7 | 45.0 | 43.5 | 43.8 | 43.7 | 42.8 | 42.5 | 42.1 | 51.5 |  |  |  |  |  |
| WhHFV-1b\* | 43.5 | 42.7 | 43.2 | 41.9 | 42.7 | 44.8 | 43.8 | 42.6 | 43.6 | 42.4 | 42.3 | 42.2 | 52.0 | 91.0 |  |  |  |  |
| HbDV-10 | 44.4 | 44.2 | 44.2 | 44.5 | 44.5 | 46.5 | 43.5 | 44.3 | 47.1 | 44.8 | 45.1 | 45.1 | 54.2 | 54.1 | 53.4 |  |  |  |
| WhFV-2 | 43.1 | 42.8 | 43.8 | 42.9 | 44.2 | 45.3 | 43.7 | 45.1 | 45.3 | 43.7 | 43.4 | 43.0 | 51.9 | 52.6 | 52.5 | 54.1 |  |  |
| SyFV-2 | 43.7 | 43.5 | 43.8 | 43.2 | 44.7 | 45.5 | 44.4 | 44.8 | 45.6 | 43.1 | 42.7 | 42.6 | 51.7 | 52.6 | 52.2 | 54.9 | 83.7 |  |

\* WhHFV-1 accession numbers (a) KX884432 and (b) KM817648

**References**

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