



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2016.004aD	(to be completed by ICTV officers)
Short title: Four new species in the genus <i>Alphabaculovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/> 2 <input checked="" type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/>	

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

Baculoviridae/Nudiviridae Study Group

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: July 15, 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2016.004aD	(assigned by ICTV officers)
To create 4 new species within:		
Genus:	<i>Alphabaculovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ (new) ” after its proposed name. • If no genus is specified, enter “ unassigned ” in the genus box.
Subfamily:		
Family:	<i>Baculoviridae</i>	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Choristoneura murinana nucleopolyhedrovirus</i>	Choristoneura murinana alphabaculovirus Darmstadt	KF894742
<i>Lambdina fiscellaria nucleopolyhedrovirus</i>	Lambdina fiscellaria nucleopolyhedrovirus GR15	KP752043
<i>Lymantria xyliina nucleopolyhedrovirus</i>	Lymantria xyliina multiple nucleopolyhedrovirus-5	GQ202541
<i>Orgyia leucostigma nucleopolyhedrovirus</i>	Orgyia leucostigma nucleopolyhedrovirus CFS-77	EU309041

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ◦ If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria. ◦ If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria. • Further material in support of this proposal may be presented in the Appendix, Module 11
<p>Isolates of the above proposed species can be identified as belonging to the genus <i>Alphabaculovirus</i> of family <i>Baculoviridae</i> on the basis of three or more of the following criteria:</p> <ul style="list-style-type: none"> • host species of the insect order Lepidoptera; • circular double-stranded DNA genome ranging in size from 110 – 170 kbp with a gene content characteristic of other alphabaculoviruses; • relationships to other baculoviruses as inferred by molecular phylogeny; • occlusion bodies formed within the nucleus with a characteristic shape and size (polyhedral or tetrahedral, 0.15 to 15 µm in diameter); • rod-shaped virions consisting of nucleocapsids enveloped singly or in bunches, with multiple virions embedded in each occlusion body. <p>Figure 1 shows the relationships of representative isolates of the proposed species to representative isolates of other recognized species in the genus <i>Alphabaculovirus</i> (Table 1), as</p>

well as a selection of representative isolates for the other three genera of *Baculoviridae* (*Betabaculovirus*, *Gammabaculovirus*, and *Deltabaculovirus*), determined from the concatenated alignment of the predicted amino acid sequences of 37 baculovirus core genes (Garavaglia et al., 2012). The tree shows that all four representatives of the proposed *Alphabaculovirus* species group with other alphabaculoviruses.

Distinctions among species of the *Baculoviridae* have been based on host range, DNA restriction endonuclease fragment patterns, and comparisons of nucleotide and predicted amino acid sequences from various genes. In addition, species demarcation criteria for baculoviruses have been proposed that rely upon pairwise nucleotide distances estimated with the Kimura-2-parameter substitution model from partial sequences of three conserved baculovirus genes: *lef-8* and *lef-9* (encoding viral RNA polymerase subunits), and *polh* (encoding the viral occlusion body matrix protein) (Jehle et al., 2006). If nucleotide distances between two viruses are less than 0.015 substitutions/site, the two baculoviruses are considered to be the same species. If nucleotide distances between two viruses are greater than 0.05 substitutions/site, the viruses are considered to be different species. If the nucleotide distances lie between 0.015 and 0.050 substitutions/site, additional characteristics of the two viruses (*i.e.* host range) must be considered to make a decision about their taxonomic status. The proposed criterion was originally based on an alignment of sequences from 117 separate baculovirus isolates and the phylogeny inferred from this alignment. Researchers have applied this criterion to other isolates to identify many new baculovirus species and variants of currently recognized species.

Pairwise nucleotide distances for *lef-8*, *lef-9*, and *polh* are shown in Tables 2 and 3. The distances between the sequences of the proposed species' representative isolates and other alphabaculovirus isolates are >0.05 substitutions/site for each locus, indicating that the isolates under consideration are representatives of new, previously unrecognized species and not variants of members of currently existing species.

References:

Baculoviridae core genes, Alphabaculovirus characteristics, and proposed species demarcation criterion

Jehle, J.A., Lange, M., Wang, H., Hu, Z., Wang, Y., Hauschild, R., 2006. Molecular identification and phylogenetic analysis of baculoviruses from Lepidoptera. *Virology* 346, 180-193.

Garavaglia, M.J., Miele, S.A., Iserte, J.A., Belaich, M.N., Ghiringhelli, P.D., 2012. The ac53, ac78, ac101, and ac103 genes are newly discovered core genes in the family *Baculoviridae*. *J Virol* 86, 12069-12079.

Herniou, E.A., Arif, B.M., Becnel, J.J., Blissard, G.W., Bonning, B., Harrison, R.L., Jehle, J.A., Theilmann, D.A., Vlcek, J.M., 2011. *Baculoviridae*, in: King, A.M.Q., Adams, M.J., Carstens, E.B., Lefkowitz, E.J. (Eds.), *Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses*. Elsevier, Oxford, pp. 163-174.

Choristoneura murinana nucleopolyhedrovirus

Naser, W.L., Harvey, J.P., Huger, A.M., Huber, J., 1987. *Choristoneura murinana* nuclear polyhedrosis virus: comparative biochemical and biological examination of replication *in vivo* and *in vitro*. *J Gen Virol* 68, 1251-1260.

Rohrmann, G.F., Erlandson, M.A., Theilmann, D.A., 2014. Genome sequence of an alphabaculovirus isolated from *Choristoneura murinana*. *Genome Announc* 2, e01135-13.

Lambdina fiscellaria nucleopolyhedrovirus

Levin, D.B., Laitinen, A.M., Clarke, T., Lucarotti, C.J., Morin, B., Otvos, I.S., 1997. Characterization of nuclear polyhedrosis viruses from three subspecies of *Lambdina fiscellaria*. *J Invertebr Pathol* 69, 125-134.

Rohrmann, G.F., Erlandson, M.A., Theilmann, D.A., 2015. Genome sequence of an alphabaculovirus isolated from the oak looper, *Lambdina fiscellaria*, contains a putative 2-kilobase-pair transposable element encoding a transposase and a FLYWCH domain-containing protein. *Genome Announc* 3, e00186-15.

Lymantria xyliana multiple nucleopolyhedrovirus

Wu, C.Y., Wang, C.H., 2005. Characterization and polyhedrin gene cloning of *Lymantria xyliana* multiple nucleopolyhedrovirus. *J Invertebr Pathol* 88, 238-246.

Nai, Y.S., Wu, C.Y., Wang, T.C., Chen, Y.R., Lau, W.H., Lo, C.F., Tsai, M.F., Wang, C.H., 2010. Genomic sequencing and analyses of *Lymantria xyliana* multiple nucleopolyhedrovirus. *BMC Genomics* 11, 116.

Orgyia leucostigma nucleopolyhedrovirus

van Frankenhuyzen, K., Ebling P., Thurston G., Lucarotti, C., Royama T., Goscott, R., Georgeson, E., Silver, J., 2002. Incidence and impact of *Entomophaga aulicae* (Zygomycetes: Entomophthorales) and a nucleopolyhedrovirus in an outbreak of the whitemarked tussock moth (Lepidoptera: Lymantriidae). *Can Entomol* 134, 825-845.

Thumbi, D.K., Eveleigh, R.J., Lucarotti, C.J., Lapointe, R., Graham, R.I., Pavlik, L., Lauzon, H.A.M., Arif, B.M., 2011. Complete sequence, analysis and organization of the *Orgyia leucostigma* nucleopolyhedrovirus genome. *Viruses* 3, 2301-2327.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1. Alphabaculovirus isolates used in core gene phylogeny and pairwise distance estimation. Isolates for newly proposed species are indicated in bold type.

Isolate	Species	Accession no.	Abbreviation
Adoxophyes honmai nucleopolyhedrovirus ADN001	<i>Adoxophyes honmai nucleopolyhedrovirus</i>	AP006270	AdhoNPV-ADN001
Agrotis ipsilon multiple nucleopolyhedrovirus Illinois	<i>Agrotis ipsilon multiple nucleopolyhedrovirus</i>	EU839994	AgipMNPV-Illinois
Agrotis segetum nucleopolyhedrovirus A	<i>Agrotis segetum nucleopolyhedrovirus A</i>	DQ123841	AgseNPV-A
Agrotis segetum nucleopolyhedrovirus B	<i>Agrotis segetum nucleopolyhedrovirus B</i>	KM102981	AgseNPV-B
Antheraea pernyi nucleopolyhedrovirus Liaoning	<i>Antheraea pernyi nucleopolyhedrovirus</i>	DQ486030	AnpeNPV-Liaoning
Anticarsia gemmatalis multiple nucleopolyhedrovirus 2D	<i>Anticarsia gemmatalis multiple nucleopolyhedrovirus</i>	DQ813662	AgMNPV-2D
Autographa californica multiple nucleopolyhedrovirus C6	<i>Autographa californica multiple nucleopolyhedrovirus</i>	L22858	AcMNPV-C6
Bombyx mori nucleopolyhedrovirus T3	<i>Bombyx mori nucleopolyhedrovirus</i>	L33180	BmNPV-T3
Buzura suppressaria nucleopolyhedrovirus Hubei	<i>Buzura suppressaria nucleopolyhedrovirus</i>	KF611977	BusuNPV-Hubei
Choristoneura fumiferana DEF multiple nucleopolyhedrovirus	<i>Choristoneura fumiferana DEF multiple nucleopolyhedrovirus</i>	AY327402	CfDEFNPV
Choristoneura fumiferana multiple nucleopolyhedrovirus Ireland	<i>Choristoneura fumiferana multiple nucleopolyhedrovirus</i>	AF512031	CfMNPV-Ireland
Choristoneura rosaceana nucleopolyhedrovirus NB1	<i>Choristoneura rosaceana nucleopolyhedrovirus</i>	KC961304	ChroNPV-NB1
Chrysodeixis chalcites nucleopolyhedrovirus	<i>Chrysodeixis chalcites nucleopolyhedrovirus</i>	AY864330	ChchNPV
Choristoneura murinana alphabaculovirus Darmstadt	<i>Choristoneura murinana nucleopolyhedrovirus</i>	KF894742	ChmuNPV-Darmstadt
Clanis bilineata nucleopolyhedrovirus DZ1	<i>Clanis bilineata nucleopolyhedrovirus</i>	DQ504428	ClbiNPV-DZ1
Dasychira pudibunda nucleopolyhedrovirus ML1	<i>Orgyia pseudotsugata multiple nucleopolyhedrovirus</i>	KP747440	DapuNPV-ML1
Ectropis obliqua nucleopolyhedrovirus A1	<i>Ectropis obliqua nucleopolyhedrovirus</i>	DQ837165	EcobNPV-A1
Epiphyas postvittana nucleopolyhedrovirus	<i>Epiphyas postvittana nucleopolyhedrovirus</i>	AY043265	EppoNPV
Euproctis pseudoconspersa nucleopolyhedrovirus Hangzhou	<i>Euproctis pseudoconspersa nucleopolyhedrovirus</i>	FJ227128	EupsNPV-Hangzhou
Helicoverpa armigera nucleopolyhedrovirus G4	<i>Helicoverpa armigera nucleopolyhedrovirus</i>	AF271059	HearNPV-G4
Hyphantria cunea nucleopolyhedrovirus N9	<i>Hyphantria cunea nucleopolyhedrovirus</i>	AP009046	HycuNPV-N9
Lambdina fiscellaria nucleopolyhedrovirus GR15	<i>Lambdina fiscellaria nucleopolyhedrovirus</i>	KP752043	LafiNPV-GR15
Leucania separata nucleopolyhedrovirus AH1	<i>Leucania separata nucleopolyhedrovirus</i>	AY394490	LeseNPV-AH1
Lymantria dispar multiple nucleopolyhedrovirus 5-6	<i>Lymantria dispar multiple nucleopolyhedrovirus</i>	AF081810	LdMNPV 5-6
Lymantria xyliina multiple nucleopolyhedrovirus-5	<i>Lymantria xyliina nucleopolyhedrovirus</i>	GQ202541	LyxyMNPV-5

Table 1, continued.

Isolate	Species	Accession no.	Abbreviation
Mamestra brassicae multiple nucleopolyhedrovirus K1	<i>Mamestra brassicae multiple nucleopolyhedrovirus</i>	JQ798165	MabrNPV-K1
Mamestra configurata nucleopolyhedrovirus A 90/2	<i>Mamestra configurata nucleopolyhedrovirus A</i>	U59461	MacoNPV-A 90/2
Mamestra configurata nucleopolyhedrovirus B 96B	<i>Mamestra configurata nucleopolyhedrovirus B</i>	AY126275	MacoNPV-B 96B
Maruca vitrata nucleopolyhedrovirus Taiwan	<i>Maruca vitrata nucleopolyhedrovirus</i>	EF125867	MaviNPV-Taiwan
Orgyia leucostigma nucleopolyhedrovirus CFS-77	<i>Orgyia leucostigma nucleopolyhedrovirus</i>	EU309041	OrleNPV-CFS77
Orgyia pseudotsugata multiple nucleopolyhedrovirus	<i>Orgyia pseudotsugata multiple nucleopolyhedrovirus</i>	U75930	OpMNPV
Pseudoplusia includens single nucleopolyhedrovirus-IE	<i>Chrysodeixis includens nucleopolyhedrovirus</i>	KJ631622	PsinNPV-IE
Spodoptera exigua multiple nucleopolyhedrovirus US1	<i>Spodoptera exigua multiple nucleopolyhedrovirus</i>	AF169823	SeMNPV-US1
Spodoptera frugiperda multiple nucleopolyhedrovirus 3AP2	<i>Spodoptera frugiperda multiple nucleopolyhedrovirus</i>	EF035042	SfMNPV-3AP2
Spodoptera littoralis nucleopolyhedrovirus AN1956	<i>Spodoptera littoralis nucleopolyhedrovirus</i>	JX454574	SpliNPV-AN1956
Spodoptera litura nucleopolyhedrovirus G2	<i>Spodoptera litura nucleopolyhedrovirus</i>	AF325155	SpltNPV-G2
Sucra jujuba nucleopolyhedrovirus 473	<i>Sucra jujuba nucleopolyhedrovirus</i>	KJ676450	SujuNPV-473
Thysanoplusia orichalcea nucleopolyhedrovirus P1	<i>Thysanoplusia orichalcea nucleopolyhedrovirus</i>	JX467702	ThorNPV-P1
Trichoplusia ni single nucleopolyhedrovirus Canada	<i>Trichoplusia ni single nucleopolyhedrovirus</i>	DQ017380	TnSNPV-Canada

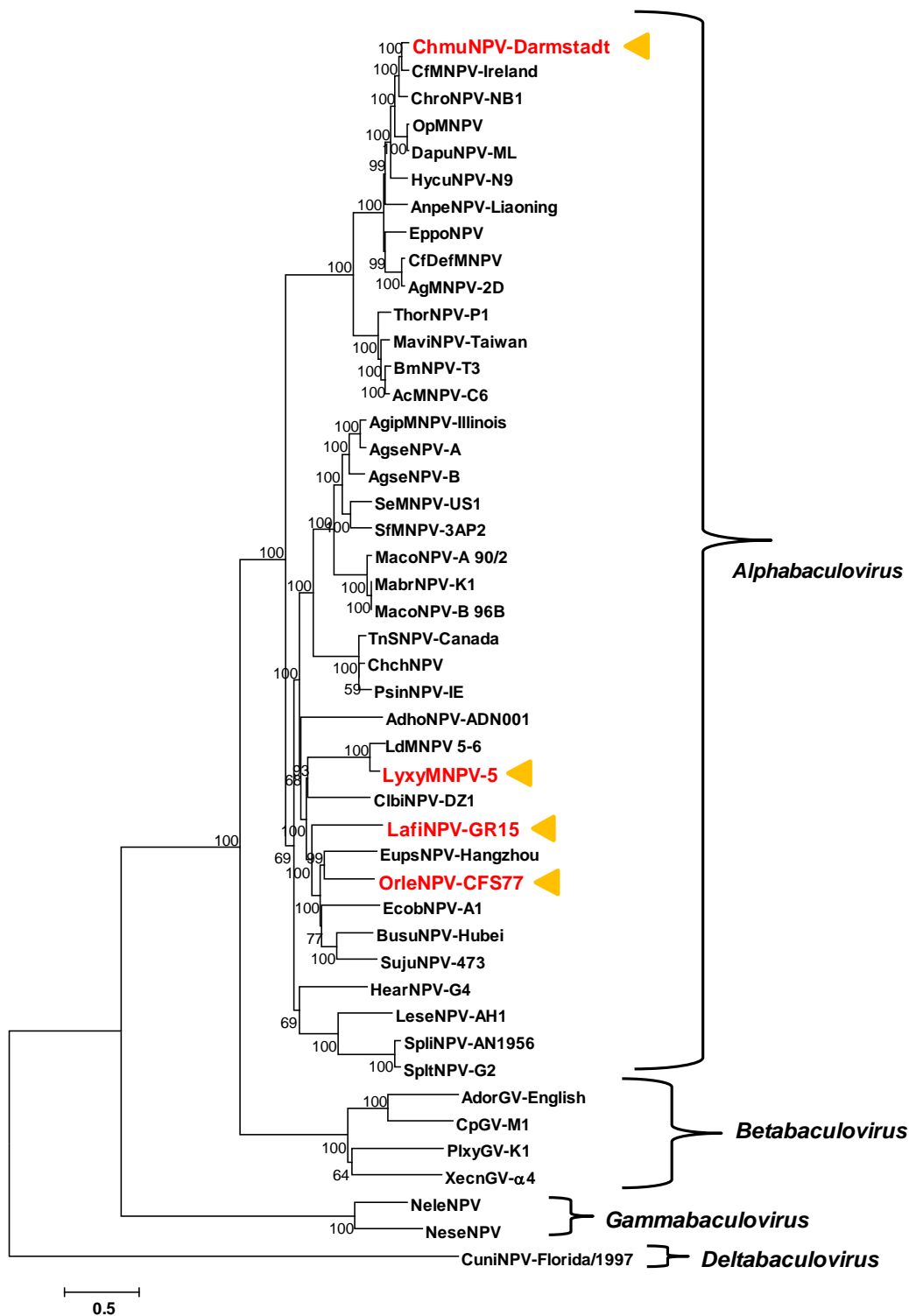


Figure 1. Relationships of alphabaculovirus isolates (Table 1) and other baculovirus isolates, inferred from the predicted amino acid sequences of baculovirus core genes. The phylogenetic tree was constructed from the concatenated alignments of 37 baculovirus core gene amino acid sequences using the minimum-evolution method using the James-Taylor-Thornton substitution model. Bootstrap values are shown for each node. Clades corresponding to the four genera of *Baculoviridae* are indicated. Representative isolates of the proposed species are listed in red font and denoted with a yellow arrow. In addition to alphabaculoviruses listed in Table 1, taxa from the other baculovirus genera are included in the analysis, including *Adoxophyes orana* granulovirus English (AdorGV-English), *Cydia pomonella* granulovirus M1 (CpGV-M1), *Culex nigripalpus* nucleopolyhedrovirus Florida/1997 (CuniNPV-Florida/1997), *Neodiprion lecontei* nucleopolyhedrovirus (NeleNPV), *Neodiprion sertifer* nucleopolyhedrovirus (NeseNPV), *Plutella xylostella* granulovirus K1 (PlxyGV-K1), and *Xestia c-nigrum* granulovirus α 4 (XecnGV- α 4).

Table 2. Pairwise nucleotide distances calculated from partial *lef-8* and *lef-9* sequence alignments*

<i>lef-9</i>		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39
<i>lef-8</i>	1. AchNPNV-ADN001		0.475	0.395	0.408	0.629	0.656	0.579	0.511	0.505	0.621	0.670	0.607	0.379	0.693	0.722	0.616	0.473	0.598	0.449	0.452	0.666	0.416	0.483	0.567	0.691	0.537	0.363	0.337	0.549	0.427	0.632	0.517	0.401	0.441	0.582	0.635	0.527	0.545	0.462
	2. AggMNPV-Illinois	0.975		0.195	0.051	0.260	0.457	0.533	0.471	0.529	0.481	0.421	0.401	0.410	0.410	0.790	0.333	0.399	0.538	0.461	0.576	0.439	0.352	0.352	0.241	0.388	0.307	0.258	0.307	0.489	0.466	0.342	0.403	0.288	0.261	0.412	0.481	0.494	0.571	0.247
	3. AggsNPV-A	1.026	0.314		0.202	0.428	0.489	0.500	0.441	0.509	0.501	0.407	0.419	0.479	0.447	0.668	0.388	0.437	0.603	0.463	0.671	0.410	0.363	0.416	0.308	0.363	0.284	0.271	0.284	0.497	0.406	0.378	0.409	0.248	0.235	0.449	0.579	0.510	0.446	0.466
	4. AggsNPV-B	0.822	1.04	0.365		0.398	0.491	0.591	0.522	0.502	0.518	0.452	0.420	0.441	0.399	0.790	0.361	0.420	0.567	0.448	0.578	0.407	0.360	0.392	0.378	0.452	0.312	0.280	0.312	0.489	0.479	0.371	0.411	0.268	0.235	0.435	0.521	0.498	0.529	0.395
	5. AnpeNPV-Liaoning	0.975	0.740	0.852	0.744		0.212	0.364	0.346	0.676	0.192	0.139	0.133	0.529	0.150	0.902	0.138	0.500	0.296	0.576	0.636	0.175	0.415	0.478	0.405	0.405	0.470	0.426	0.470	0.369	0.513	0.132	0.553	0.491	0.451	0.559	0.659	0.771	0.318	0.537
	6. AgMNPV-ZD	0.894	0.811	0.906	0.801	0.377		0.250	0.235	0.606	0.024	0.179	0.165	0.456	0.178	1.096	0.192	0.525	0.172	0.586	0.579	0.170	0.417	0.608	0.496	0.561	0.491	0.479	0.491	0.291	0.479	0.185	0.478	0.501	0.488	0.599	0.765	0.644	0.289	0.511
	7. AchMNPV-C8	0.857	0.947	0.990	0.896	0.896	0.897		0.832	0.544	0.251	0.332	0.330	0.461	0.362	1.082	0.330	0.505	0.287	0.607	0.618	0.373	0.511	0.591	0.482	0.520	0.458	0.520	0.458	0.134	0.463	0.320	0.441	0.473	0.518	0.683	0.704	0.524	0.238	0.458
	8. BmNPV-T3	0.864	0.976	1.021	0.913	0.983	0.719	0.038		0.555	0.235	0.334	0.312	0.427	0.363	0.979	0.294	0.603	0.559	0.589	0.354	0.460	0.538	0.479	0.489	0.428	0.471	0.426	0.135	0.473	0.285	0.439	0.448	0.447	0.648	0.542	0.487	0.208	0.446	
	9. BusuNPV-Hubei	0.764	0.891	0.957	0.803	1.067	0.743	0.814	0.830		0.604	0.626	0.623	0.529	0.613	0.658	0.673	0.220	0.888	0.371	0.532	0.573	0.338	0.626	0.527	0.582	0.521	0.468	0.521	0.516	0.269	0.656	0.479	0.481	0.535	0.585	0.622	0.357	0.543	0.539
	10. CIDEFNPV	0.823	0.862	0.948	0.825	0.344	0.042	0.682	0.702	0.751		0.160	0.159	0.502	0.171	1.106	0.172	0.512	0.165	0.588	0.576	0.171	0.426	0.579	0.485	0.522	0.479	0.467	0.479	0.330	0.467	0.186	0.502	0.525	0.511	0.641	0.781	0.630	0.281	0.575
	11. ChMNPV-Ireland	0.858	0.780	0.792	0.673	0.378	0.379	0.698	0.735	0.916	0.358		0.061	0.600	0.022	1.071	1.07	0.525	0.251	0.571	0.692	0.140	0.461	0.529	0.416	0.436	0.556	0.479	0.556	0.409	0.493	1.102	0.600	0.470	0.481	0.613	0.629	0.659	0.338	0.606
	12. ChroNPV-NB1	0.840	0.823	0.832	0.846	0.378	0.380	0.716	0.753	0.857	0.357	0.195		0.481	0.102	1.056	0.091	0.850	0.258	0.493	0.641	0.111	0.448	0.457	0.386	0.460	0.505	0.469	0.505	0.394	0.457	0.088	0.490	0.406	0.470	0.547	0.646	0.743	0.307	0.477
	13. ChchNPV	0.862	0.943	0.923	0.847	1.028	0.888	0.975	0.953	0.724	0.865	0.894	0.963		0.559	0.717	0.568	0.479	0.616	0.414	0.346	0.531	0.441	0.408	0.527	0.648	0.375	0.410	0.375	0.449	0.451	0.554	0.099	0.328	0.359	0.423	0.535	0.753	0.494	0.079
	14. ChrmNPV-Darmstadt	0.902	0.759	0.804	0.764	0.328	0.367	0.735	0.790	0.881	0.334	0.094	0.157	0.620		0.960	0.118	0.512	0.250	0.573	0.597	0.133	0.463	0.505	0.395	0.446	0.531	0.493	0.531	0.394	0.404	1.112	0.541	0.493	0.479	0.514	0.630	0.627	0.298	0.551
	15. ChbNPV-DZ1	0.715	0.855	0.981	0.740	0.171	0.889	0.872	0.917	0.635	0.910	0.970	0.939	0.689	0.916		0.972	0.751	1.116	0.227	0.644	0.908	0.661	0.531	0.837	0.809	0.809	0.719	0.809	0.959	0.872	0.946	0.717	0.747	0.712	0.669	0.953	0.769	1.010	0.727
	16. DapuNPV-ML1	1.015	0.745	0.767	0.802	0.275	0.342	0.818	0.844	0.945	0.319	0.221	0.222	0.975	0.913	0.922		0.561	0.262	0.554	0.690	0.089	0.416	0.415	0.386	0.469	0.528	0.458	0.528	0.501	0.004	0.579	0.457	0.468	0.572	0.613	0.781	0.342	0.581	
	17. EcobNPV-A1	0.646	0.702	0.710	0.688	0.900	0.779	0.778	0.835	0.580	0.762	0.812	0.809	0.730	0.637	0.661	0.853		0.536	0.367	0.507	0.586	0.270	0.437	0.418	0.431	0.446	0.391	0.446	0.601	0.225	0.574	0.394	0.437	0.385	0.524	0.564	0.285	0.500	0.431
	18. EppoNPV	0.772	0.999	0.998	0.929	0.420	0.325	0.655	0.697	0.835	0.311	0.431	0.400	0.973	0.430	0.897	0.448	0.803		0.642	0.513	0.274	0.539	0.680	0.588	0.591	0.482	0.571	0.482	0.341	0.488	0.270	0.591	0.659	0.541	0.801	0.818	0.560	0.295	0.595
	19. EupsNPV-Hangzhou	0.749	0.842	0.844	0.825	0.973	0.756	0.817	0.832	0.507	0.794	0.795	0.747	0.787	0.796	0.585	0.858	0.538	0.840		0.513	0.551	0.364	0.520	0.513	0.622	0.466	0.453	0.466	0.520	0.708	0.588	0.430	0.397	0.435	0.505	0.581	0.565	0.482	0.481
	20. HsaiNPV-G4	0.683	0.745	0.822	0.717	0.998	0.894	0.926	0.944	0.855	0.876	0.890	0.814	0.785	0.842	0.898	0.847	0.557	0.777	0.600		0.607	0.500	0.462	0.589	0.626	0.385	0.425	0.395	0.546	0.573	0.719	0.442	0.489	0.513	0.485	0.456	0.589	0.547	0.390
	21. HycuNPV-N9	0.894	0.847	0.895	0.868	0.457	0.348	0.761	0.784	0.782	0.329	0.279	0.282	0.923	0.288	0.925	0.272	0.730	0.423	0.799	0.577		0.456	0.549	0.415	0.469	0.538	0.511	0.538	0.352	0.537	0.083	0.554	0.481	0.461	0.598	0.686	0.630	0.296	0.565
	22. LatNPV-GR15	0.960	0.959	1.072	0.918	1.199	1.008	1.067	0.756	0.965	0.964	1.039	0.888	0.973	0.824	1.032	0.806	1.150	0.739	0.687	0.951		0.360	0.391	0.414	0.374	0.338	0.374	0.494	0.327	0.426	0.411	0.360	0.428	0.418	0.464	0.430	0.446	0.441	
	23. LesaNPV-AH1	1.008	0.525	0.551	0.604	0.776	0.833	0.828	0.921	1.020	0.918	0.849	0.856	0.820	0.790	1.032	0.741	0.873	0.881	0.914	0.678	0.981	0.914		0.396	0.470	0.429	0.378	0.429	0.637	0.518	0.405	0.464	0.382	0.436	0.299	0.326	0.648	0.629	0.382
	24. LdmNPV-5-6	1.019	0.551	0.660	0.678	0.713	0.838	1.039	1.072	0.739	0.816	0.739	0.827	0.706	0.688	0.741	0.647	0.769	1.001	0.564	0.776	0.840	0.789	0.631		0.075	0.431	0.378	0.431	0.431	0.406	0.376	0.473	0.344	0.406	0.452	0.475	0.497	0.475	0.451
	25. LyxNPV-F5	0.975	0.544	0.691	0.677	0.746	0.791	0.934	0.985	0.882	0.765	0.745	0.844	0.714	0.738	0.684	0.681	0.680	0.959	0.530	0.715	0.808	0.744	0.607	0.696		0.433	0.390	0.433	0.479	0.503	0.457	0.530	0.473	0.500	0.497	0.507	0.461	0.544	0.538
	26. MabNPV-K1	0.829	0.576	0.610	0.601	1.000	1.019	1.036	0.970	0.812	1.006	0.992	0.946	0.868	0.969	0.860	1.033	0.972	0.977	0.878	0.917	0.953	1.019	0.742	0.732	0.768		0.059	0.000	0.449	0.497	0.515	0.334	0.344	0.265	0.462	0.480	0.388	0.430	0.375
	27. MacoNPV-A 90/2	0.980	0.581	0.587	0.587	0.939	0.970	0.895	0.883	0.945	0.992	0.939	0.947	0.872	0.903	0.901	0.998	0.926	0.939	0.876	0.832	0.988	0.680	0.712	0.742	0.095		0.059	0.461	0.471	0.445	0.347	0.313	0.255	0.430	0.427	0.411	0.485	0.382	
	28. MacoNPV-B 96/8	1.032	0.559	0.598	0.596	1.022	1.009	0.998	0.962	0.805	0.998	0.994	0.957	0.844	0.971	0.853																								