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

Code assigned:	*2015.016aD*	(to be completed by ICTV officers)

Short title: One new species, *Sucra jujuba nucleopolyhedrovirus,* in the genus *Alphabaculovirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	1 ☒ 2 ☒ 3 ☐ 4 ☐ 5 ☐ 6 ☐ 7 ☐ 8 ☐ 9 ☐ 10 ☒

Author(s):

Xiaoping Liu, Feifei Yin, Zheng Zhu, Dianhai Hou, Jun Wang, Lei Zhang, Manli Wang, Hualin Wang, Zhihong Hu, Fei Deng*

Corresponding author with e-mail address:

Fei Deng (df@wh.iov.cn)

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:

ICTV has the following rule for distinguishing between names of virus isolates and names of species: Species names are entirely italicized, and names of virus isolates and genome sequences are entirely in regular type (e.g. no part is italicized). While historically baculovirologists have italicized the host genus and species in the names of virus isolates, this is no longer an accepted convention.

Please list the specific (representative) isolate of *Sucra jujuba nucleopolyhedrovirus* that was sequenced to produce GenBank accession no. KJ676450. A new taxonomy proposal template is present at the ICTV website that contains a space for listing the representative isolate.

Date first submitted to ICTV: June 15, 2015
Date of this revision (if different to above):   Sept 23, 2015

ICTV-EC comments and response of the proposer:

7/21/2015: Add tree construction method to Figure 1.
9/22/2015: The Figure 1 tree was replaced with a tree (with construction method indicated in the legend) showing that the new species of this proposal is different and distinct from the two other new *Alphabaculovirus* species discussed at EC47, *Chrysodeixis includens nucleopolyhedrovirus* and *Agrotis segetum nucleopolyhedrovirus B.*

MODULE 2: **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	*2015.016aD*	(assigned by ICTV officers)

To create 1 new species within:

		Fill in all that apply.
Genus:	*Alphabaculovirus*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Subfamily:		
Family:	*Baculoviridae*	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:		

Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
Sucra jujuba nucleopolyhedrovirus	Sucra jujuba nucleopolyhedrovirus isolate 473 (SujuNPV-473)	KJ676450

Reasons to justify the creation and assignment of the new species:
- Explain how the proposed species differ(s) from all existing species.
  - 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 9

The proposed species *Sucra jujuba nucleopolyhedrovirus* consists of a single virus Sucra jujuba nucleopolyhedrovirus (SujuNPV) and can be identified as a new species belonging to the *Alphabaculovirus* genus based on the following criteria of SujuNPV: host species of the insect order Lepidoptera; enveloped rod-shaped virions; double-stranded, circular DNA genome sized in 110-170 kb with a similar genome characteristic of other alphabaculoviruses; and phylogenetic relationships to other baculoviruses. Figure 1 shows the relationships of SujuNPV to viruses of other species in the *Baculoviridae*, based on the alignment of concatenated protein sequences of 37 core genes (Garavaglia et al., 2012).

Distinctions among species of the *Baculoviridae* have been based on host range, identity of nucleotide and predicted amino acid sequences, and gene order. A proposed species demarcation criterion published in 2006 is based on pairwise nucleotide distances estimated using the Kimura 2-parameter model of nucleotide substitution (Jehle et al, 2006). According to the criterion, if the pairwise nucleotide distances of two baculoviruses, calculated from alignments of partial *polh*, *lef8* and *lef9* genes and concatenated sequences of the three genes, are greater than 0.05 substitutions/site, the viruses are considered to be classified in different species.

SujuNPV was isolated from *Sucra jujuba* Chu (Lepidoptera: Geometridae), and is different from other baculoviruses. Phylogenetic relationships of SujuNPV to viruses of other species

(Figure 1) did not show a significant closest species, like the clade of AcMNPV and BmNPV. The branch length of SujuNPV to the closest relatives is comparable to the branch lengths of other recognized alphabaculovirus species. Pairwise Kimura 2-parameter nucleotide distances of SujuNPV with other baculoviruses are listed in Table 1 and 2. Distances estimated from alignments of individual *polh*, *lef8* and *lef9* and concatenated *polh-lef8-lef9* are reported. All of the distances for both the individual and the concatenated alignments are significant in excess of 0.05 substitutions/sites (Tables 1 and 2 in red). Distinctive genome features and gene order of the SujuNPV are detailed in the publication describing the genome of SujuNPV (Liu et al., 2014).

Finally, *Sucra jujuba nucleopolyhedrovirus* is also different and distinct from the two other *Alphabaculovirus* species proposed in 2015, *Chrysodeixis includens nucleopolyhedrovirus* and *Agrotis segetum nucleopolyhedrovirus B* (Figure 1).

additional material in support of this proposal

References:

Baculoviridae core genes and proposed species demarcation criterion

Jehle JA, 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 MJ, Miele SA, Iserte JA, Belaich MN, Ghiringhelli PD (2012) The ac53 , ac78 , ac101 and ac103 genes are newly discovered core genes in the family *Baculoviridae*. Journal of Virology 86: 12069-12079.

Sucra jujuba nucleopolyhedrovirus

Fan-Ren S (1986) Studies on the nuclear polyhedrosis virus disease of *Sucra jujuba* Chu. Virologica Sinica 1: 42-45.

Liu XP, Yin FF, Zhu Z, Hou DH, Wang J, Zhang L, Wang ML, Wang HL, Hu ZH, Deng F (2014) Genomic sequencing and analysis of Sucra jujuba nucleopolyhedrovirus. PLoS One 9(10): e110023.

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.
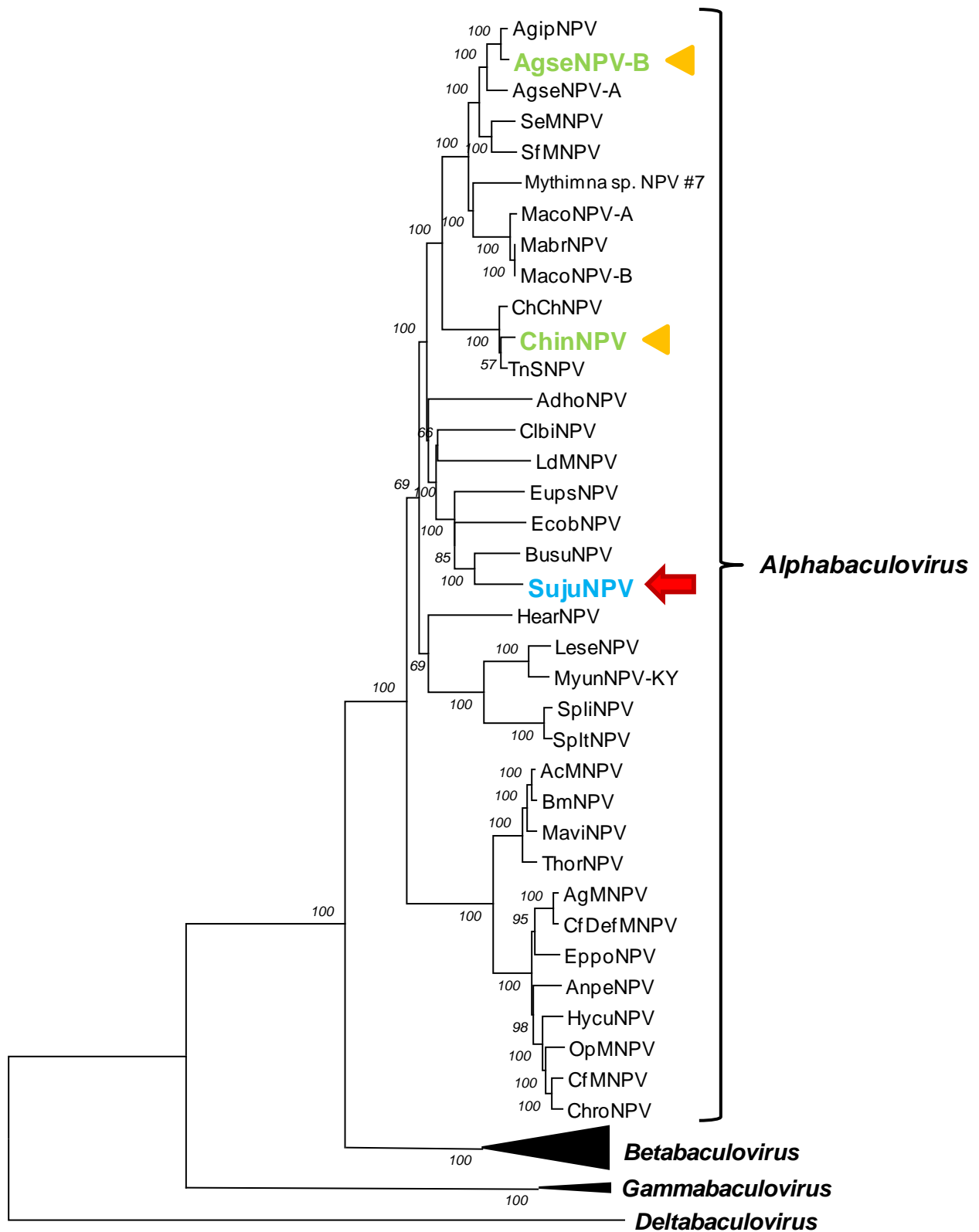
Figure 1. Relationships of baculovirus species and other isolates, inferred from the predicted amino acid sequences of baculovirus core genes. The phylogenetic tree was constructed from the concatenated alignments of 34 baculovirus core gene amino acid sequences using the minimum-evolution method using the James-Taylor-Thornton substitution model and a gamma parameter of 0.85 (estimated from the *dnapol* alignment). Bootstrap values are shown for each node. Clades

corresponding to the four genera of *Baculoviridae* are indicated. The proposed species is listed in blue font and denoted with a red arrow. Additional new *Alphabaculovirus* species discussed at EC47 are listed in green font and denoted with an orange arrowhead. *Alphabaculovirus* taxa include the reference isolates (abbreviations for the corresponding viruses are in brackets) for species *Adoxophyes honmai nucleopolyhedrovirus* (AdhoNPV), *Agrotis ipsilon multiple nucleopolyhedrovirus* (AgipNPV), *Agrotis segetum nucleopolyhedrovirus A* (AgseNPV-A), *Agrotis segetum nucleopolyhedrovirus B* (AgseNPV-B), *Antheraea pernyi nucleopolyhedrovirus* (AnpeNPV), *Anticarsia gemmatalis multiple nucleopolyhedrovirus* (AgMNPV), *Autographa californica multiple nucleopolyhedrovirus* (AcMNPV), *Bombyx mori nucleopolyhedrovirus* (BmNPV), *Buzura suppressaria nucleopolyhedrovirus* (BusuNPV), *Choristoneura fumiferana multiple nucleopolyhedrovirus* (CfMNPV), *Choristoneura fumiferana DEF multiple nucleopolyhedrovirus* (CfDEFNPV), *Chrysodeixis chalcites nucleopolyhedrovirus* (ChchNPV), *Chrysodeixis includens nucleopolyhedrovirus* (ChinNPV), *Clanis bilineata nucleopolyhedrovirus* (ClbiNPV), *Choristoneura rosaceana* nucleopolyhedrovirus (ChroNPV), *Ecotropis obliqua nucleopolyhedrovirus* (EcobNPV), *Epiphyas postvittana nucleopolyhedrovirus* (EppoNPV), *Euproctis pseudoconspersa nucleopolyhedrovirus* (EupsNPV), *Helicoverpa armigera nucleopolyhedrovirus* (HearNPV), *Hyphantria cunea nucleopolyhedrovirus* (HycuNPV), *Leucania separata nucleopolyhedrovirus* (LeseNPV), *Lymantria dispar multiple nucleopolyhedrovirus* (LdMNPV), *Mamestra configurata nucleopolyhedroviruses A* and *B* (MacoNPV-A and -B), *Maruca vitrata nucleopolyhedrovirus* (MaviNPV), *Spodoptera exigua multiple nucleopolyhedrovirus* (SeMNPV), *Spodoptera frugiperda multiple nucleopolyhedrovirus* (SfMNPV), *Spodoptera litura nucleopolyhedrovirus* (SpltNPV), and *Sucra jujuba nucleopolyhedrovirus* (SujuNPV), *Thysanoplusia orichalcea nucleopolyhedrovirus* (ThorNPV), and *Trichoplusia ni single nucleopolyhedrovirus* (TnSNPV), as well as isolates Mythimna spp. nucleopolyhedrovirus #7 (Mythimna sp. NPV #7) , and Mythimna unipuncta nucleopolyhedrovirus (MyunNPV-KY).

Table 1. Pairwise nucleotide distances calculated from partial *polh* and *lef8* sequences alignments*

lef8 \ polh	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1 AcMNPV		0.295	0.264	0.270	0.244	0.261	0.295	0.265	0.327	0.274	0.300	0.353	0.334	0.269	0.304	0.195	0.243	0.303	0.286	0.302	0.243	0.256	0.186
2 AdorNPV	0.509		0.276	0.336	0.234	0.349	0.239	0.304	0.301	0.256	0.329	0.281	0.310	0.270	0.326	0.251	0.289	0.259	0.267	0.298	0.271	0.350	0.262
3 AgseNPV	0.477	0.462		0.279	0.251	0.301	0.274	0.305	0.312	0.274	0.287	0.324	0.321	0.270	0.317	0.212	0.282	0.277	0.203	0.287	0.225	0.311	0.270
4 AnpeNPV	0.428	0.623	0.496		0.296	0.199	0.323	0.182	0.345	0.314	0.160	0.352	0.340	0.318	0.319	0.274	0.169	0.337	0.302	0.348	0.325	0.205	0.296
5 ApciNPV	0.479	0.380	0.445	0.623		0.332	0.201	0.302	0.300	0.220	0.301	0.278	0.276	0.228	0.374	0.234	0.280	0.201	0.246	0.269	0.202	0.288	0.221
6 BmNPV	0.028	0.500	0.475	0.434	0.473		0.356	0.224	0.330	0.317	0.210	0.348	0.353	0.340	0.318	0.300	0.211	0.317	0.306	0.380	0.334	0.155	0.304
7 BusuNPV	0.498	0.413	0.432	0.559	0.369	0.497		0.313	0.283	0.233	0.332	0.218	0.249	0.234	0.383	0.244	0.335	0.205	0.242	0.302	0.236	0.312	0.237
8 ChocNPV	0.408	0.582	0.472	0.246	0.594	0.407	0.540		0.320	0.287	0.167	0.328	0.324	0.296	0.329	0.260	0.140	0.306	0.300	0.314	0.280	0.218	0.287
9 ClbiNPV	0.491	0.434	0.459	0.553	0.423	0.489	0.446	0.566		0.319	0.356	0.276	0.272	0.260	0.380	0.279	0.330	0.271	0.304	0.348	0.294	0.364	0.272
10 EcobNPV	0.473	0.433	0.416	0.564	0.382	0.471	0.388	0.547	0.431		0.279	0.237	0.283	0.220	0.298	0.212	0.275	0.214	0.235	0.254	0.232	0.307	0.240
11 EppoNPV	0.393	0.521	0.518	0.301	0.518	0.394	0.517	0.291	0.536	0.515		0.341	0.337	0.303	0.326	0.295	0.156	0.312	0.294	0.315	0.309	0.181	0.339
12 EupsNPV	0.469	0.433	0.404	0.502	0.373	0.475	0.354	0.494	0.406	0.366	0.513		0.274	0.254	0.395	0.288	0.344	0.222	0.287	0.306	0.258	0.346	0.308
13 HearNPV-G4	0.487	0.431	0.407	0.565	0.410	0.486	0.417	0.531	0.443	0.426	0.527	0.403		0.287	0.393	0.310	0.328	0.252	0.293	0.308	0.308	0.345	0.292
14 HespNPV	0.484	0.467	0.457	0.572	0.394	0.487	0.399	0.550	0.444	0.397	0.528	0.341	0.448		0.345	0.229	0.313	0.212	0.259	0.256	0.232	0.322	0.258
15 LdMNPV	0.530	0.566	0.388	0.454	0.526	0.542	0.486	0.464	0.490	0.515	0.557	0.425	0.504	0.461		0.276	0.292	0.368	0.335	0.315	0.352	0.343	0.301
16 MacoNPV-A	0.476	0.439	0.319	0.575	0.446	0.474	0.445	0.553	0.456	0.433	0.551	0.438	0.421	0.448	0.471		0.255	0.228	0.207	0.293	0.213	0.318	0.219
17 OpMNPV	0.404	0.642	0.478	0.210	0.635	0.411	0.557	0.158	0.562	0.575	0.311	0.519	0.573	0.565	0.434	0.575		0.307	0.271	0.311	0.300	0.187	0.290
18 OrleNPV	0.468	0.463	0.414	0.521	0.368	0.463	0.379	0.505	0.435	0.369	0.519	0.335	0.419	0.371	0.421	0.443	0.520		0.248	0.326	0.216	0.324	0.253
19 SeMNPV	0.475	0.482	0.272	0.507	0.448	0.480	0.442	0.495	0.459	0.450	0.522	0.414	0.436	0.474	0.425	0.335	0.502	0.442		0.257	0.220	0.318	0.273
20 SpliNPV	0.491	0.527	0.452	0.552	0.498	0.495	0.516	0.552	0.508	0.495	0.562	0.473	0.472	0.528	0.431	0.483	0.553	0.489	0.459		0.287	0.362	0.284
21 SujuNPV	0.487	0.430	0.460	0.562	0.393	0.494	0.318	0.549	0.443	0.384	0.539	0.380	0.446	0.409	0.490	0.457	0.594	0.383	0.450	0.535		0.303	0.226
22 ThorNPV	0.178	0.499	0.479	0.417	0.470	0.179	0.486	0.400	0.514	0.463	0.383	0.453	0.491	0.491	0.530	0.501	0.404	0.467	0.482	0.500	0.487		0.292
22 TnNPV	0.499	0.451	0.408	0.577	0.432	0.491	0.430	0.554	0.447	0.440	0.522	0.455	0.421	0.491	0.500	0.399	0.576	0.462	0.419	0.501	0.457	0.477	

*The numbers of base substitutions per site between pairs of sequences are shown. Abbrevations of the taxa are as listed for Figure 1. Additional taxa include Adoxophyes orana nucleopolyhedrovirus (AdorNPV), Apocheima cinerarium nucleopolyhedrovirus (ApciNPV), Choristoneura occidentalis alphabaculovirus (ChocNPV), Hemileuca sp. nucleopolyhedrovirus (HespNPV) and Orgyia leucostigma nucleopolyhedrovirus (OrleNPV). Analyses were conducted using the Kimura 2-parameters model in MEGA 5.0. Pairwise distances for *lef8* (Table 1) and the concatenated *polh-lef8-lef9* (Table 2) sequences are listed below the diagonal lines, and *polh* (Table 1) and *lef9* (Table 2) distances are listed above the diagonal lines. Values for viruses in the proposed species are in red type.

Table 2. Pairwise nucleotide distances calculated from partial *lef9* and concatenated *polh-lef8-lef9* sequences alignments*

lef9 / polh-lef8-lef9	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1 AcMNPV		0.464	0.529	0.402	0.482	0.043	0.429	0.381	0.504	0.454	0.337	0.471	0.544	0.514	0.503	0.507	0.371	0.444	0.496	0.508	0.450	0.190	0.445
2 AdorNPV	0.453		0.462	0.541	0.400	0.455	0.402	0.516	0.418	0.399	0.477	0.419	0.447	0.450	0.496	0.429	0.525	0.397	0.475	0.504	0.414	0.448	0.431
3 AgseNPV	0.454	0.431		0.477	0.470	0.494	0.439	0.486	0.464	0.438	0.516	0.425	0.494	0.437	0.397	0.283	0.450	0.411	0.223	0.474	0.469	0.474	0.391
4 AnpeNPV	0.392	0.542	0.449		0.554	0.391	0.500	0.246	0.537	0.506	0.303	0.502	0.550	0.513	0.433	0.514	0.230	0.487	0.497	0.511	0.528	0.391	0.524
5 ApciNPV	0.440	0.367	0.419	0.543		0.468	0.370	0.555	0.409	0.351	0.484	0.368	0.459	0.355	0.520	0.440	0.527	0.347	0.465	0.484	0.365	0.461	0.422
6 BmNPV	0.064	0.455	0.451	0.380	0.449		0.420	0.378	0.496	0.421	0.336	0.449	0.469	0.476	0.481	0.475	0.364	0.435	0.489	0.476	0.430	0.184	0.438
7 BusuNPV	0.438	0.384	0.407	0.502	0.339	0.445		0.475	0.397	0.299	0.438	0.343	0.440	0.347	0.437	0.429	0.479	0.302	0.441	0.480	0.325	0.442	0.435
8 ChocNPV	0.376	0.512	0.445	0.234	0.534	0.366	0.482		0.547	0.491	0.281	0.481	0.527	0.516	0.422	0.491	0.174	0.473	0.490	0.487	0.520	0.366	0.540
9 ClbiNPV	0.470	0.415	0.434	0.509	0.401	0.466	0.399	0.517		0.407	0.523	0.421	0.446	0.450	0.479	0.444	0.532	0.416	0.473	0.450	0.419	0.504	0.403
10 EcobNPV	0.434	0.392	0.399	0.503	0.348	0.429	0.339	0.481	0.406		0.449	0.328	0.450	0.363	0.469	0.412	0.512	0.333	0.410	0.474	0.316	0.414	0.406
11 EppoNPV	0.360	0.478	0.477	0.278	0.467	0.344	0.464	0.266	0.501	0.453		0.470	0.494	0.500	0.525	0.489	0.285	0.449	0.511	0.523	0.441	0.338	0.494
12 EupsNPV	0.454	0.402	0.399	0.481	0.354	0.451	0.333	0.463	0.391	0.334	0.470		0.442	0.353	0.428	0.400	0.489	0.305	0.425	0.449	0.372	0.440	0.409
13 HearNPV-G4	0.473	0.415	0.417	0.523	0.402	0.458	0.395	0.492	0.395	0.410	0.484	0.398		0.477	0.475	0.442	0.509	0.456	0.457	0.424	0.422	0.439	0.418
14 HespNPV	0.457	0.428	0.418	0.512	0.357	0.462	0.354	0.502	0.414	0.349	0.484	0.333	0.428		0.429	0.443	0.499	0.355	0.415	0.468	0.370	0.485	0.429
15 LdMNPV	0.481	0.498	0.383	0.425	0.502	0.482	0.453	0.430	0.476	0.465	0.507	0.427	0.478	0.438		0.422	0.384	0.401	0.413	0.460	0.457	0.471	0.485
16 MacoNPV-A	0.438	0.406	0.291	0.499	0.409	0.445	0.405	0.481	0.419	0.389	0.486	0.404	0.409	0.412	0.426		0.463	0.427	0.299	0.453	0.418	0.466	0.360
17 OpMNPV	0.367	0.540	0.432	0.208	0.534	0.363	0.495	0.160	0.511	0.498	0.277	0.482	0.514	0.507	0.397	0.483		0.454	0.476	0.477	0.502	0.372	0.519
18 OrleNPV	0.430	0.405	0.387	0.484	0.328	0.428	0.322	0.463	0.396	0.333	0.461	0.309	0.396	0.337	0.409	0.399	0.463		0.411	0.445	0.351	0.439	0.416
19 SeMNPV	0.451	0.444	0.245	0.467	0.421	0.456	0.409	0.460	0.436	0.405	0.477	0.401	0.415	0.427	0.406	0.302	0.454	0.402		0.438	0.455	0.508	0.374
20 SpliNPV	0.456	0.467	0.429	0.494	0.455	0.462	0.461	0.480	0.466	0.444	0.501	0.438	0.431	0.458	0.411	0.445	0.479	0.447	0.417		0.475	0.507	0.454
21 SujuNPV	0.426	0.401	0.421	0.513	0.350	0.440	0.306	0.494	0.410	0.338	0.464	0.355	0.413	0.364	0.456	0.402	0.510	0.346	0.409	0.474		0.437	0.428
22 ThorNPV	0.193	0.456	0.449	0.372	0.438	0.177	0.441	0.358	0.482	0.419	0.333	0.434	0.451	0.462	0.477	0.459	0.357	0.435	0.466	0.474	0.434		0.441
22 TnNPV	0.424	0.411	0.380	0.506	0.389	0.443	0.391	0.503	0.401	0.397	0.482	0.419	0.400	0.437	0.464	0.356	0.507	0.413	0.380	0.447	0.405	0.433	

*See footnote of Table 1.