



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**

<b>Code assigned:</b>	<b>2016.001aD</b>	(to be completed by ICTV officers)
<b>Short title:</b> One new species in the genus <i>Alphabaculovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )		
<b>Modules attached</b> (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"/>

**Author(s):**

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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* Study Group

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

Date first submitted to ICTV: July 13, 2016  
Date of this revision (if different to above): July 19, 2016

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

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MODULE 2: **NEW SPECIES**

Code	<b>2016.001aD</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<i>Alphabaculovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<i>Baculoviridae</i>	
Order:		
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Catopsilia pomona nucleopolyhedrovirus</i>	Catopsilia pomona nucleopolyhedrovirus isolate 416	KU565883

**Reasons to justify the creation and assignment of the new species:**

The proposed species *Catopsilia pomona nucleopolyhedrovirus* consists of isolates of *Catopsilia pomona nucleopolyhedrovirus* (CapoNPV) and can be identified as a new species belonging to genus *Alphabaculovirus* based on the following criteria: host species of the insect order Lepidoptera; enveloped rod-shaped virions; double-stranded, circular DNA genome similar in size to the genomes of other alphabaculoviruses; and phylogenetic relationships to other baculoviruses. Figure 1 shows the relationships of CapoNPV to viruses of other species in the *Baculoviridae*, based on the alignment of concatenated protein sequences of 37 core genes (Wang et al., 2016).

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 (Garavaglia et al., 2012).

CapoNPV was isolated from *Catopsilia pomona* (Lepidoptera: Pieridae), and is different from other baculoviruses. Phylogenetic relationships of CapoNPV to viruses of other species (Figure 1) did not show a significantly close relationship to another species, similar to the relationship between AcMNPV and BmNPV. The branch length of CapoNPV to the closest relatives is comparable to the branch lengths separating other recognized alphabaculovirus species. Pairwise Kimura 2-parameter nucleotide distances of CapoNPV with other baculoviruses are listed in Tables 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 significantly in excess of 0.05 substitutions/sites (Tables 1 and 2 in red). Distinctive genome features and the gene order of CapoNPV are detailed in the publication describing the genome of this isolate (Wang et al., 2016).

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.

Catopsilia pomona nucleopolyhedrovirus

Yang M, Lin Y, Liang S, Yuan A, Sun F (1993) Preliminary study on *Catopsilia pomona* NPV. *Forest Research*. 6(2): 228-230.  
Wang J, Zhu Z, Zhang L, Hou D, Wang M, Arif B, et al. (2016) Genome sequencing and analysis of *Catopsilia pomona* nucleopolyhedrovirus: A distinct species in Group I *Alphabaculovirus*. *PloS One*. 11(5): e0155134.

Figure 1. Relationships of viruses in the proposed baculovirus species and other baculoviruses. Phylogenetic tree was constructed based on the concatenated alignments of 37 core gene amino acid sequences by MEGA 6.0 with default parameters and 1000 randoms. Proposed species is marked in red, and the four genera of *Baculoviridae* are indicated. Virus taxa (abbreviations of corresponding virus names are in brackets after the species names) include *Rachiplusia ou* multiple nucleopolyhedrovirus (RoMNPV), *Plutella xylostella* nucleopolyhedrovirus (PlxyNPV), *Autographa californica* multiple nucleopolyhedrovirus (AcMNPV), *Bombyx mori* nucleopolyhedrovirus (BmNPV), *Bombyx mandarina* nucleopolyhedrovirus (BomaNPV), *Thysanoplusia orichalcea* nucleopolyhedrovirus (ThorNPV), *Catopsilia pomona* nucleopolyhedrovirus (CaponPV), *Choristoneura fumiferana* multiple nucleopolyhedrovirus (CfMNPV), *Choristoneura occidentalis* nucleopolyhedrovirus (ChocNPV), *Choristoneura murinana* nucleopolyhedrovirus (ChmuNPV), *Choristoneura rosaceana* nucleopolyhedrovirus (ChroNPV), *Orgyia pseudotsugata* multiple nucleopolyhedrovirus (OpMNPV), *Hyphantria cunea* nucleopolyhedrovirus (HycuNPV), *Antheraea pernyi* nucleopolyhedrovirus (AnpeNPV), *Philosamia cynthia ricini* nucleopolyhedrovirus (PhcyNPV), *Epiphyas postvittana* nucleopolyhedrovirus (EppoNPV), *Condylorrhiza vestigialis* multiple nucleopolyhedrovirus (CoveMNPV), *Anticarsia gemmatalis* nucleopolyhedrovirus (AngeNPV), *Choristoneura fumiferana* DEF multiple nucleopolyhedrovirus (CfDEFMNPV), *Lymantria dispar* multiple nucleopolyhedrovirus (LdMNPV), *Helicoverpa armigera* multiple nucleopolyhedrovirus (HearMNPV), *Spodoptera exigua* multiple nucleopolyhedrovirus (SeMNPV), *Xestia c-nigrum* granulovirus (XcGV), *Adoxophyes orana* granulovirus (AdorGV), *Cydia pomonella* granulovirus (CpGV), *Neodiprion abietis* nucleopolyhedrovirus (NeabNPV), *Neodiprion lecontei* nucleopolyhedrovirus (NeleNPV), *Neodiprion sertifer* nucleopolyhedrovirus (NeseNPV), *Culex nigripalpus* nucleopolyhedrovirus (CuniNPV).

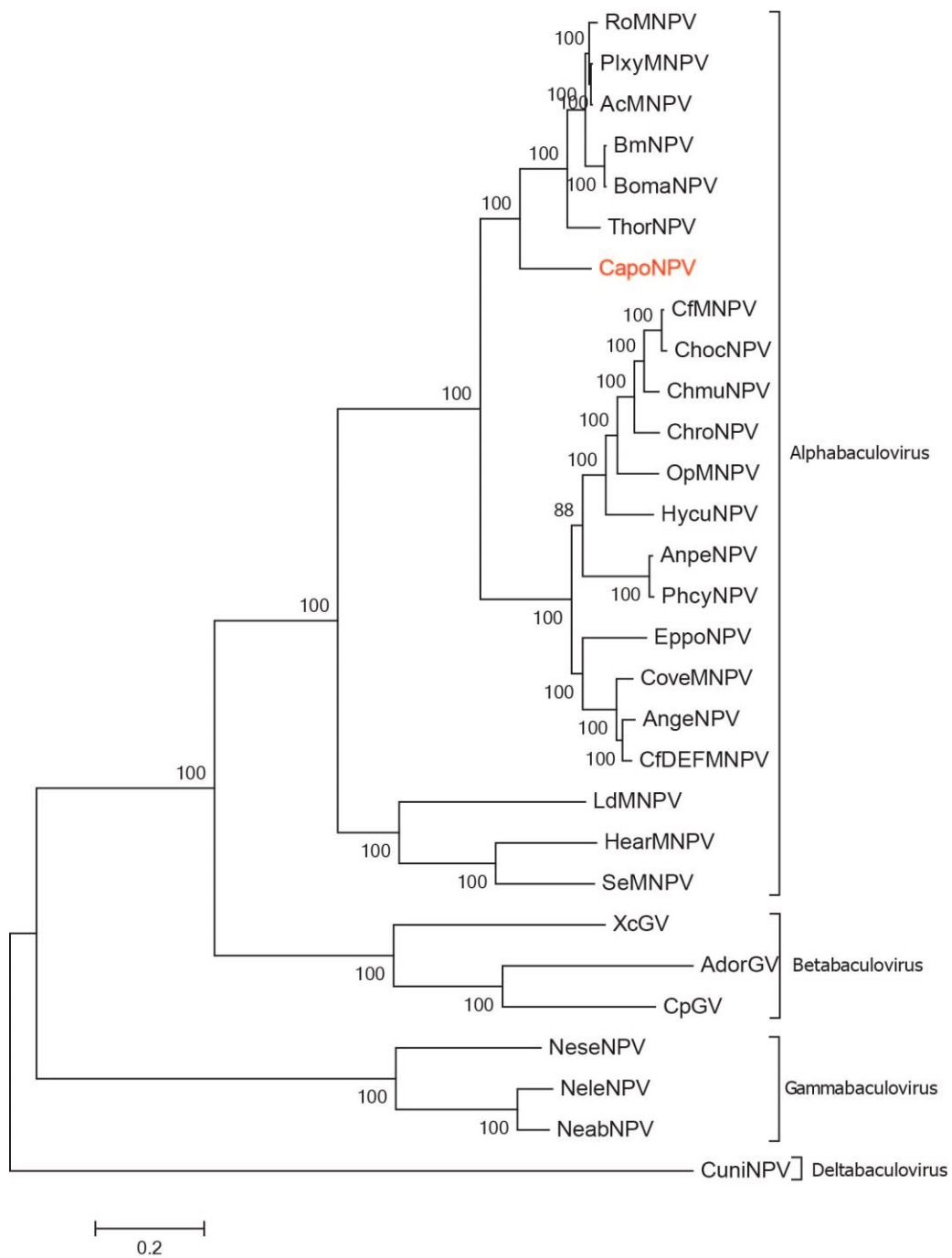


Table 1. Pairwise nucleotide distances calculated from partial *lef9* and *lef8* sequences alignments\*

<i>lef8</i> \ <i>lef9</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
1 PlxyMNPV		0.027	0.030	0.024	0.024	0.095	0.180	0.282	0.317	0.332	0.316	0.329	0.374	0.379	0.338	0.347	0.376	0.367	0.356	0.357	0.460	0.454	0.474	0.594	0.612	0.622	0.963	0.959	0.918
2 AcMNPV	0.006		0.006	0.042	0.041	0.111	0.188	0.269	0.325	0.345	0.322	0.330	0.389	0.392	0.350	0.359	0.387	0.384	0.368	0.369	0.485	0.465	0.475	0.589	0.632	0.622	0.965	0.953	0.917
3 RoMNPV	0.041	0.039		0.042	0.041	0.111	0.185	0.264	0.323	0.342	0.316	0.323	0.385	0.388	0.346	0.357	0.383	0.380	0.364	0.365	0.480	0.459	0.475	0.586	0.632	0.624	0.963	0.955	0.916
4 BmNPV	0.033	0.028	0.060		0.010	0.110	0.181	0.270	0.325	0.337	0.323	0.328	0.382	0.388	0.350	0.354	0.375	0.374	0.366	0.368	0.468	0.454	0.474	0.595	0.615	0.610	0.954	0.964	0.917
5 BomaNPV	0.033	0.028	0.059	0.007		0.108	0.182	0.269	0.321	0.333	0.316	0.327	0.380	0.386	0.346	0.360	0.379	0.375	0.370	0.372	0.468	0.444	0.471	0.587	0.613	0.613	0.946	0.954	0.920
6 MaviMNPV	0.098	0.095	0.115	0.106	0.107		0.193	0.274	0.325	0.340	0.327	0.329	0.386	0.387	0.347	0.351	0.379	0.379	0.361	0.364	0.473	0.458	0.490	0.571	0.621	0.638	0.956	0.973	0.948
7 ThorNPV	0.168	0.167	0.174	0.169	0.168	0.192		0.260	0.310	0.315	0.321	0.333	0.380	0.379	0.333	0.356	0.362	0.351	0.349	0.353	0.457	0.442	0.489	0.600	0.626	0.597	0.934	0.945	0.905
8 CapoNPV	0.271	0.270	0.273	0.268	0.270	0.273	0.274		0.348	0.358	0.345	0.363	0.408	0.410	0.351	0.355	0.352	0.356	0.351	0.354	0.446	0.424	0.464	0.583	0.585	0.606	0.920	0.917	0.921
9 AngeNPV	0.372	0.375	0.366	0.372	0.375	0.384	0.370	0.377		0.079	0.070	0.226	0.259	0.255	0.203	0.228	0.230	0.225	0.235	0.232	0.424	0.467	0.471	0.631	0.594	0.677	0.957	1.020	1.006
10 CfDEFMNPV	0.373	0.376	0.369	0.374	0.380	0.385	0.369	0.373	0.041		0.091	0.234	0.250	0.249	0.199	0.202	0.180	0.205	0.213	0.210	0.415	0.470	0.473	0.638	0.592	0.692	0.996	1.063	1.069
11 CoveMNPV	0.372	0.376	0.379	0.373	0.375	0.382	0.369	0.364	0.100	0.098		0.236	0.258	0.254	0.193	0.225	0.231	0.221	0.231	0.228	0.415	0.472	0.474	0.631	0.612	0.671	0.965	1.008	1.012
12 EppoNPV	0.377	0.377	0.370	0.374	0.379	0.386	0.366	0.379	0.234	0.230	0.230		0.299	0.301	0.251	0.278	0.262	0.293	0.270	0.271	0.509	0.476	0.492	0.588	0.641	0.662	0.947	0.966	0.959
13 AnpeNPV	0.414	0.413	0.415	0.417	0.421	0.427	0.398	0.402	0.256	0.245	0.268	0.284		0.013	0.233	0.226	0.244	0.238	0.244	0.240	0.421	0.484	0.478	0.659	0.624	0.733	1.096	1.137	1.149
14 PhcyNPV	0.417	0.415	0.417	0.424	0.427	0.430	0.399	0.405	0.257	0.248	0.274	0.290	0.018		0.239	0.229	0.254	0.235	0.249	0.245	0.422	0.495	0.480	0.650	0.616	0.744	1.086	1.129	1.145
15 HycuNPV	0.372	0.371	0.371	0.368	0.368	0.372	0.356	0.371	0.237	0.234	0.243	0.270	0.277	0.283		0.177	0.181	0.189	0.192	0.191	0.421	0.479	0.501	0.630	0.611	0.685	1.029	1.080	1.060
16 OpMNPV	0.388	0.389	0.399	0.396	0.399	0.420	0.389	0.404	0.257	0.243	0.272	0.293	0.199	0.200	0.193		0.155	0.163	0.174	0.173	0.369	0.468	0.465	0.670	0.608	0.713	1.156	1.182	1.172
17 ChroNPV	0.392	0.392	0.399	0.393	0.391	0.412	0.377	0.399	0.257	0.246	0.252	0.291	0.238	0.241	0.195	0.155		0.115	0.127	0.128	0.393	0.467	0.453	0.656	0.585	0.697	1.059	1.116	1.097
18 ChmuNPV	0.403	0.402	0.412	0.407	0.409	0.422	0.380	0.406	0.249	0.234	0.258	0.280	0.226	0.228	0.204	0.146	0.106		0.082	0.078	0.409	0.485	0.454	0.660	0.605	0.720	1.114	1.117	1.099
19 CfMNPV	0.394	0.393	0.398	0.390	0.393	0.414	0.383	0.392	0.263	0.248	0.275	0.280	0.240	0.241	0.206	0.152	0.122	0.076		0.005	0.418	0.488	0.473	0.671	0.632	0.716	1.075	1.109	1.065
20 ChocNPV	0.394	0.394	0.398	0.390	0.394	0.414	0.384	0.393	0.259	0.243	0.270	0.279	0.236	0.237	0.199	0.150	0.118	0.072	0.007		0.414	0.488	0.474	0.673	0.630	0.712	1.073	1.109	1.065
21 LdMNPV	0.493	0.490	0.510	0.505	0.507	0.517	0.491	0.492	0.512	0.505	0.540	0.529	0.427	0.423	0.488	0.408	0.461	0.443	0.444	0.444		0.434	0.418	0.703	0.574	0.699	1.181	1.104	1.150
22 HearMNPV	0.475	0.472	0.473	0.463	0.461	0.478	0.467	0.467	0.529	0.539	0.524	0.503	0.537	0.543	0.517	0.551	0.536	0.531	0.534	0.532	0.476		0.312	0.591	0.598	0.628	0.961	1.008	1.012
23 SeMNPV	0.457	0.455	0.455	0.460	0.462	0.478	0.466	0.452	0.519	0.513	0.530	0.495	0.478	0.483	0.477	0.480	0.488	0.491	0.479	0.474	0.406	0.324		0.633	0.591	0.698	1.060	1.081	1.081
24 XcGV	0.606	0.610	0.612	0.612	0.612	0.618	0.620	0.575	0.636	0.638	0.628	0.634	0.689	0.685	0.622	0.689	0.658	0.687	0.689	0.691	0.689	0.617	0.641		0.481	0.534	0.884	0.920	0.957
25 CpGV	0.616	0.612	0.626	0.608	0.611	0.645	0.624	0.586	0.628	0.628	0.647	0.643	0.617	0.623	0.629	0.606	0.615	0.626	0.617	0.615	0.576	0.607	0.569	0.512		0.461	1.036	1.037	1.030
26 AdorGV	0.609	0.608	0.603	0.605	0.608	0.613	0.613	0.562	0.663	0.674	0.652	0.649	0.734	0.741	0.642	0.732	0.714	0.712	0.725	0.718	0.739	0.631	0.637	0.487	0.465		0.929	0.918	0.942
27 NeseNPV	0.921	0.927	0.908	0.904	0.900	0.903	0.934	0.892	0.940	0.936	0.900	0.914	1.082	1.096	0.932	1.120	1.000	1.026	1.025	1.024	1.204	0.934	0.974	0.924	0.985	0.889		0.419	0.427
28 NeleNPV	0.930	0.935	0.916	0.931	0.923	0.936	0.950	0.909	1.005	1.022	0.993	0.964	1.119	1.139	1.011	1.140	1.045	1.082	1.083	1.084	1.157	0.945	1.006	0.919	1.002	0.893	0.369		0.127
29 NeabNPV	0.958	0.956	0.946	0.950	0.938	0.937	0.979	0.922	1.016	1.037	0.993	0.975	1.133	1.145	1.043	1.176	1.066	1.124	1.121	1.122	1.212	0.940	1.014	0.943	0.999	0.895	0.368	0.153	

\*The number of base substitutions per site between pairs of sequences are shown. Abbreviations of the taxa are as listed for Figure 1. Analyses were conducted using the Kimura 2-parameters model in MEGA 6.0. Pairwise distances for *lef8* (Table 1) and the concatenated *polh-lef8-lef9* (Table 2) sequences are listed below the diagonal lines, and *lef9* (Table 1) and *polh* (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 *polyhedrin* and concatenated *lef8-lef9-polh* sequences alignments\*

<i>lef8-lef9-polh</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
1 PlxyMNPV		0.001	0.233	0.263	0.263	0.251	0.257	0.263	0.293	0.279	0.266	0.300	0.270	0.268	0.273	0.242	0.259	0.254	0.265	0.266	0.323	0.218	0.289	0.596	0.534	0.587	0.731	0.674	0.705
2 AcMNPV	0.012		0.231	0.260	0.260	0.249	0.255	0.261	0.291	0.277	0.264	0.298	0.268	0.266	0.271	0.244	0.257	0.252	0.263	0.264	0.321	0.216	0.287	0.593	0.531	0.584	0.727	0.670	0.701
3 RoMNPV	0.065	0.056		0.082	0.082	0.120	0.145	0.232	0.217	0.203	0.199	0.202	0.187	0.189	0.205	0.211	0.202	0.232	0.207	0.209	0.346	0.297	0.330	0.589	0.548	0.582	0.673	0.662	0.695
4 BmNPV	0.063	0.066	0.057		0.000	0.109	0.158	0.231	0.226	0.200	0.207	0.212	0.199	0.201	0.221	0.209	0.220	0.252	0.223	0.225	0.326	0.286	0.305	0.589	0.553	0.585	0.706	0.688	0.696
5 BomaNPV	0.062	0.065	0.056	0.007		0.109	0.158	0.231	0.226	0.200	0.207	0.212	0.199	0.201	0.221	0.209	0.220	0.252	0.223	0.225	0.326	0.286	0.305	0.589	0.553	0.585	0.706	0.688	0.696
6 MaviMNPV	0.122	0.124	0.116	0.110	0.109		0.148	0.213	0.198	0.189	0.195	0.175	0.181	0.183	0.208	0.212	0.199	0.230	0.204	0.204	0.356	0.297	0.286	0.614	0.547	0.579	0.666	0.664	0.684
7 ThorNPV	0.185	0.188	0.173	0.171	0.171	0.186		0.205	0.198	0.186	0.193	0.183	0.205	0.203	0.193	0.185	0.211	0.222	0.219	0.218	0.345	0.295	0.317	0.581	0.537	0.573	0.698	0.698	0.704
8 CapoNPV	0.273	0.268	0.262	0.263	0.263	0.265	0.257		0.264	0.257	0.237	0.209	0.232	0.230	0.236	0.223	0.234	0.265	0.245	0.244	0.362	0.293	0.307	0.583	0.581	0.573	0.668	0.663	0.657
9 AngeNPV	0.341	0.345	0.327	0.333	0.333	0.334	0.321	0.347		0.082	0.103	0.169	0.161	0.159	0.189	0.186	0.189	0.195	0.193	0.193	0.347	0.291	0.300	0.576	0.534	0.588	0.673	0.674	0.732
10 CfDEFMNPV	0.344	0.350	0.331	0.333	0.334	0.338	0.320	0.347	0.059		0.047	0.141	0.152	0.150	0.164	0.166	0.180	0.198	0.187	0.187	0.320	0.275	0.299	0.550	0.508	0.558	0.733	0.705	0.721
11 CoveMNPV	0.337	0.341	0.327	0.329	0.328	0.334	0.323	0.334	0.090	0.087		0.150	0.156	0.155	0.170	0.160	0.170	0.186	0.181	0.177	0.337	0.294	0.328	0.547	0.497	0.532	0.713	0.673	0.701
12 EppoNPV	0.347	0.347	0.325	0.329	0.332	0.330	0.322	0.340	0.218	0.215	0.217		0.162	0.162	0.171	0.155	0.167	0.172	0.174	0.169	0.336	0.278	0.288	0.567	0.530	0.581	0.688	0.680	0.705
13 AnpeNPV	0.375	0.379	0.363	0.366	0.367	0.369	0.358	0.370	0.241	0.230	0.246	0.267		0.004	0.189	0.169	0.171	0.185	0.183	0.182	0.333	0.273	0.301	0.573	0.541	0.568	0.694	0.694	0.710
14 PhcyNPV	0.377	0.380	0.365	0.371	0.372	0.370	0.357	0.371	0.239	0.231	0.247	0.270	0.014		0.183	0.164	0.171	0.183	0.183	0.182	0.331	0.273	0.301	0.579	0.535	0.571	0.686	0.686	0.710
15 HycuNPV	0.344	0.347	0.334	0.337	0.336	0.337	0.321	0.339	0.217	0.210	0.214	0.245	0.246	0.249		0.149	0.174	0.183	0.188	0.188	0.335	0.273	0.291	0.591	0.515	0.593	0.681	0.699	0.722
16 OpMNPV	0.349	0.354	0.352	0.350	0.353	0.361	0.343	0.354	0.235	0.217	0.237	0.263	0.202	0.202	0.181		0.133	0.133	0.145	0.141	0.307	0.263	0.269	0.544	0.513	0.567	0.676	0.724	0.739
17 ChroNPV	0.363	0.366	0.357	0.356	0.356	0.363	0.343	0.353	0.236	0.213	0.230	0.258	0.227	0.232	0.187	0.152		0.120	0.015	0.014	0.341	0.266	0.293	0.567	0.550	0.599	0.686	0.683	0.711
18 ChmuNPV	0.364	0.369	0.368	0.368	0.370	0.374	0.342	0.363	0.230	0.217	0.233	0.262	0.221	0.220	0.196	0.149	0.110		0.124	0.119	0.328	0.275	0.322	0.556	0.525	0.568	0.690	0.697	0.722
19 CfMNPV	0.359	0.362	0.352	0.352	0.355	0.359	0.343	0.351	0.240	0.225	0.244	0.256	0.230	0.232	0.199	0.158	0.105	0.085		0.015	0.344	0.281	0.306	0.571	0.555	0.610	0.674	0.677	0.705
20 ChocNPV	0.359	0.363	0.352	0.353	0.356	0.360	0.344	0.351	0.237	0.222	0.240	0.255	0.226	0.228	0.195	0.156	0.102	0.081	0.007		0.342	0.281	0.301	0.562	0.550	0.598	0.678	0.678	0.705
21 LdMNPV	0.445	0.450	0.464	0.456	0.457	0.469	0.451	0.450	0.447	0.436	0.455	0.481	0.400	0.399	0.435	0.373	0.412	0.406	0.413	0.410		0.314	0.355	0.529	0.515	0.575	0.773	0.751	0.784
22 HearMNPV	0.420	0.422	0.438	0.430	0.426	0.440	0.429	0.420	0.464	0.466	0.464	0.452	0.470	0.476	0.460	0.468	0.463	0.468	0.472	0.470	0.429		0.209	0.584	0.555	0.574	0.708	0.706	0.696
23 SeMNPV	0.431	0.430	0.438	0.435	0.435	0.448	0.447	0.428	0.463	0.459	0.473	0.455	0.446	0.450	0.450	0.436	0.441	0.447	0.445	0.442	0.394	0.298		0.593	0.553	0.611	0.671	0.721	0.738
24 XcGV	0.599	0.600	0.601	0.604	0.601	0.603	0.607	0.582	0.624	0.624	0.617	0.611	0.660	0.656	0.619	0.658	0.642	0.658	0.664	0.664	0.665	0.603	0.627		0.258	0.274	0.835	0.910	0.877
25 CpGV	0.601	0.603	0.614	0.602	0.603	0.622	0.610	0.582	0.600	0.595	0.608	0.622	0.609	0.608	0.603	0.590	0.594	0.602	0.611	0.608	0.564	0.599	0.570	0.457		0.213	0.852	0.888	0.884
26 AdorGV	0.610	0.610	0.607	0.605	0.608	0.616	0.604	0.578	0.654	0.661	0.638	0.642	0.707	0.714	0.648	0.696	0.691	0.692	0.704	0.698	0.695	0.622	0.646	0.466	0.416		0.830	0.880	0.870
27 NeseNPV	0.901	0.905	0.883	0.881	0.877	0.874	0.887	0.856	0.901	0.929	0.896	0.894	1.015	1.015	0.926	1.051	0.968	0.996	0.984	0.984	1.108	0.894	0.931	0.914	0.976	0.889		0.216	0.212
28 NeleNPV	0.898	0.897	0.887	0.899	0.893	0.908	0.912	0.874	0.941	0.972	0.941	0.919	1.046	1.052	0.981	1.075	1.002	1.033	1.023	1.023	1.065	0.916	0.962	0.935	0.995	0.906	0.359		0.070
29 NeabNPV	0.907	0.902	0.893	0.896	0.891	0.903	0.913	0.876	0.959	0.990	0.948	0.930	1.067	1.070	0.995	1.093	1.015	1.052	1.037	1.037	1.111	0.919	0.972	0.943	0.992	0.912	0.358	0.131	

\*See footnote of Table 1.