Supplementary Materials

Table S1. Sequences used for tree construction

The number in column 1 denotes the sequences in the phylogenetic tree (Figure S1), column 2 is either GenBank or Uniprot ID, column 3 contains the species name, columns 4 and 5 give a short phylogenetic classification.

0	70984876	Aspergillus fumigatus Af293	Fungi	Dikarya
1	119498755	Neosartorya fischeri NRRL 181	Fungi	Dikarya
2	119183398	Coccidioides immitis RS	Fungi	Dikarya
3	303319805	Coccidioides posadasii C735 delta SOWgp	Fungi	Dikarya
4	302896042	Nectria haematococca mpVI 77-13-4	Fungi	Dikarya
5	169776569	Aspergillus oryzae RIB40	Fungi	Dikarya
6	134078485	Aspergillus niger	Fungi	Dikarya
7	317031638	Aspergillus niger CBS 513.88	Fungi	Dikarya
8	320034202	Coccidioides posadasii str. Silveira	Fungi	Dikarya
9	121718209	Aspergillus clavatus NRRL 1	Fungi	Dikarya
10	258570961	Uncinocarpus reesii 1704	Fungi	Dikarya
11	322703301	Metarhizium anisopliae ARSEF 23	Fungi	Dikarya
12	212535400	Penicillium marneffei ATCC 18224	Fungi	Dikarya
13	242792937	Talaromyces stipitatus ATCC 10500	Fungi	Dikarya
14	115432990	Aspergillus terreus NIH2624	Fungi	Dikarya
15	239612197	Ajellomyces dermatitidis ER-3	Fungi	Dikarya
16	261202318	Ajellomyces dermatitidis SLH14081	Fungi	Dikarya
17	54035096	Xenopus laevis	Metazoa	Chordata
18	67902532	Aspergillus nidulans FGSC A4	Fungi	Dikarya
19	289616376	Sordaria macrospora	Fungi	Dikarya
20	240277725	Ajellomyces capsulatus H143	Fungi	Dikarya
21	225557177	Ajellomyces capsulatus G186AR	Fungi	Dikarya
22	154285526	Ajellomyces capsulatus NAm1	Fungi	Dikarya
23	19115009	Schizosaccharomyces pombe 972h-	Fungi	Dikarya
24	171693061	Podospora anserina S mat+	Fungi	Dikarya
25	295666764	Paracoccidioides brasiliensis Pb01	Fungi	Dikarya
26	225683510	Paracoccidioides brasiliensis Pb03	Fungi	Dikarya
27	62857371	Xenopus (Silurana) tropicalis	Metazoa	Chordata
28	60688513	Xenopus (Silurana) tropicalis	Metazoa	Chordata
29	292623564	Danio rerio	Metazoa	Chordata
30	33989722	Danio rerio	Metazoa	Chordata
31	125842967	Danio rerio	Metazoa	Chordata
32	255949110	Penicillium chrysogenum Wisconsin 54-1255	Fungi	Dikarya
33	241701691	Ixodes scapularis	Metazoa	Arthropoda
34	148234435	Xenopus laevis	Metazoa	Chordata
39	47209292	Tetraodon nigroviridis	Metazoa	Chordata
40	311257098	Sus scrofa	Metazoa	Chordata
41	296231468	Callithrix jacchus	Metazoa	Chordata
42	55726200	Pongo abelii	Metazoa	Chordata
43	197102600	Pongo abelii	Metazoa	Chordata
44	7661532	Homo sapiens	Metazoa	Chordata
45	119603691	Homo sapiens	Metazoa	Chordata

46	119603692	Homo sapiens	Metazoa	Chordata
47	321457967	Daphnia pulex	Metazoa	Arthropoda
48	149699279	Equus caballus	Metazoa	Chordata
49	55644155	Pan troglodytes	Metazoa	Chordata
50	73957135	Canis familiaris	Metazoa	Chordata
51	296412406	Tuber melanosporum Mel28	Fungi	Dikarya
52	73957137	Canis familiaris	Metazoa	Chordata
53	296477903	Bos taurus	Metazoa	Chordata
54	94717663	Bos taurus	Metazoa	Chordata
55	34147121	Bos taurus	Metazoa	Chordata
58	189067249	Homo sapiens	Metazoa	Chordata
59	75075905	Macaca fascicularis	Metazoa	Chordata
60	109129054	Macaca mulatta	Metazoa	Chordata
61	118096647	Gallus gallus	Metazoa	Chordata
62	225719248	Caligus clemensi	Metazoa	Arthropoda
63	91083257	Tribolium castaneum	Metazoa	Arthropoda
64	301776556	Ailuropoda melanoleuca	Metazoa	Chordata
65	213407814	Schizosaccharomyces japonicus yFS275	Fungi	Dikarya
66	32822838	Mus musculus	Metazoa	Chordata
67	12862002	Mus musculus	Metazoa	Chordata
68	30794454	Mus musculus	Metazoa	Chordata
69	40018556	Rattus norvegicus	Metazoa	Chordata
70	110764915	Apis mellifera	Metazoa	Arthropoda
71	146104724	Leishmania infantum	Euglenozoa	Kinetoplastida
72	322503880	Leishmania donovani BPK282A1	Euglenozoa	Kinetoplastida
73	126305035	Monodelphis domestica	Metazoa	Chordata
74	198433412	Ciona intestinalis	Metazoa	Chordata
75	322491100	Leishmania mexicana MHOM/GT/2001/U1103	Euglenozoa	Kinetoplastida
76	268565835	Caenorhabditis briggsae	Metazoa	Nematoda
77	291243457	Saccoglossus kowalevskii	Metazoa	Hemichordata
78	260819118	Branchiostoma floridae	Metazoa	Chordata
79	157877550	Leishmania major strain Friedlin	Euglenozoa	Kinetoplastida
80	308473111	Caenorhabditis remanei	Metazoa	Nematoda
81	154346420	Leishmania braziliensis MHOM/BR/75/M2904	Euglenozoa	Kinetoplastida
82	17510345	Caenorhabditis elegans	Metazoa	Nematoda
83	74025168	Trypanosoma brucei TREU927	Euglenozoa	Kinetoplastida
84	261335104	Trypanosoma brucei gambiense DAL972	Euglenozoa	Kinetoplastida
85	312077128	Loa loa	Metazoa	Nematoda
86	45184963	Ashbya gossypii ATCC 10895	Fungi	Dikarya
87	240848549	Acyrthosiphon pisum	Metazoa	Arthropoda
88	195350607	Drosophila sechellia	Metazoa	Arthropoda
89	296808889	Arthroderma otae CBS 113480	Fungi	Dikarya
91	145348215	Ostreococcus lucimarinus CCE9901	Viridiplantae	Chlorophyta
92	157110629	Aedes aegypti	Metazoa	Arthropoda
93	170590151	Brugia malayi	Metazoa	Nematoda
94	221122438	Hydra magnipapillata	Metazoa	Cnidaria
95	195998205	Trichoplax adhaerens	Metazoa	Placozoa
96	325076475	Dictyostelium purpureum	Amoebozoa	Mycetozoa
97	145489175	Paramecium tetraurelia strain d4-2	Alveolata	Ciliophora
98	322828963	Trypanosoma cruzi	Euglenozoa	Kinetoplastida

99	71411734	Trypanosoma cruzi strain CL Brener	Euglenozoa	Kinetoplastida
102	67624613	Cryptosporidium hominis TU502	Alveolata	Apicomplexa
103	145496772	Paramecium tetraurelia strain d4-2	Alveolata	Ciliophora
104	323509051	Cryptosporidium parvum	Alveolata	Apicomplexa
105	66362738	Cryptosporidium parvum Iowa II	Alveolata	Apicomplexa
106	170054228	Culex quinquefasciatus	Metazoa	Arthropoda
107	303285400	Micromonas pusilla CCMP1545	Viridiplantae	Chlorophyta
108	158287629	Anopheles gambiae str. PEST	Metazoa	Arthropoda
109	71032433	Theileria parva strain Muguga	Alveolata	Apicomplexa
110	312372179	Anopheles darlingi	Metazoa	Arthropoda
111	84999362	Theileria annulata	Alveolata	Apicomplexa
112	156085886	Babesia bovis T2Bo	Alveolata	Apicomplexa
113	290996087	Naegleria gruberi	Heterolobosea	Schizopyrenida
114	157110627	Aedes aegypti	Metazoa	Arthropoda
115	195164379	Drosophila persimilis	Metazoa	Arthropoda
116	209879754	Cryptosporidium muris RN66	Alveolata	Apicomplexa
117	123470767	Trichomonas vaginalis G3	Parabasalia	Trichomonadida
118	56755379	Schistosoma japonicum	Metazoa	Platyhelminthes
119	256082921	Schistosoma mansoni	Metazoa	Platyhelminthes
120	68072593	Plasmodium berghei strain ANKA	Alveolata	Apicomplexa
121	308161294	Giardia lamblia P15	Diplomonadida	Hexamitidae
122	313234747	Oikopleura dioica	Metazoa	Chordata
123	294950547	Perkinsus marinus ATCC 50983	Alveolata	Perkinsea
124	303390591	Encephalitozoon intestinalis ATCC 50506	Fungi	Microsporidia
125	85014187	Encephalitozoon cuniculi GB-M1	Fungi	Microsporidia
127	269860783	Enterocytozoon bieneusi H348	Fungi	Microsporidia
276	14590587	Pyrococcus horikoshii OT3	Euryarchaeota	Thermococci
277	18977577	Pyrococcus furiosus DSM 3638	Euryarchaeota	Thermococci
278	14521536	Pyrococcus abyssi GE5	Euryarchaeota	Thermococci
279	240103243	Thermococcus gammatolerans EJ3	Euryarchaeota	Thermococci
280	242398719	Thermococcus sibiricus MM 739	Euryarchaeota	Thermococci
281	254171020	Thermococcus barophilus MP	Euryarchaeota	Thermococci
282	254173477	Thermococcus sp. AM4	Euryarchaeota	Thermococci
283	212224201	Thermococcus onnurineus NA1	Euryarchaeota	Thermococci
284	57640272	Thermococcus kodakarensis KOD1	Euryarchaeota	Thermococci
285	241905408	Methanocaldococcus infernus ME	Euryarchaeota	Methanococci
286	260569499	Ferroglobus placidus DSM 10642	Euryarchaeota	Archaeoglobi
287	126178224	Methanoculleus marisnigri JR1	Euryarchaeota	Methanomicrobia
288	15898992	Sulfolobus solfataricus P2	Crenarchaeota	Thermoprotei
289	154151932	Candidatus Methanoregula boonei 6A8	Euryarchaeota	Methanomicrobia
290	116753414	Methanosaeta thermophila PT	Euryarchaeota	Methanomicrobia
291	15679850	Methanothermobacter thermautotrophicus str. Delta H	Euryarchaeota	Methanobacteria
292	227826445	Sulfolobus islandicus M.14.25	Crenarchaeota	Thermoprotei
293	124027598	Hyperthermus butylicus DSM 5456	Crenarchaeota	Thermoprotei
294	227829054	Sulfolobus islandicus L.S.2.15	Crenarchaeota	Thermoprotei
295	229577852	Sulfolobus islandicus Y.G.57.14	Crenarchaeota	Thermoprotei
296	283849956	Aciduliprofundum boonei T469	Euryarchaeota	unclassified Euryarchaeota
297	118575223	Cenarchaeum symbiosum A	Thaumarchaeota	Cenarchaeales
298	256811158	Methanocaldococcus fervens AG86	Euryarchaeota	Methanococci
299	88602265	Methanospirillum hungatei JF-1	Euryarchaeota	Methanomicrobia
300	48477592	Picrophilus torridus DSM 9790	Euryarchaeota	Thermoplasmata

301	161527947	Nitrosopumilus maritimus SCM1	Thaumarchaeota	marine archaeal group 1
302	270496470	Methanocaldococcus sp. FS406-22	Euryarchaeota	Methanococci
303	219853252	Candidatus Methanosphaerula palustris E1-9c	Euryarchaeota	Methanomicrobia
304	257053743	Halorhabdus utahensis DSM 12940	Euryarchaeota	Halobacteria
305	163799818	Methanococcus voltae A3	Euryarchaeota	Methanococci
306	73670908	Methanosarcina barkeri str. Fusaro	Euryarchaeota	Methanomicrobia
307	91773751	Methanococcoides burtonii DSM 6242	Euryarchaeota	Methanomicrobia
308	15669666	Methanocaldococcus jannaschii DSM 2661	Euryarchaeota	Methanococci
309	261403030	Methanocaldococcus vulcanius M7	Euryarchaeota	Methanococci
310	254168358	Aciduliprofundum boonei T469	Euryarchaeota	unclassified Euryarchaeota
311	148642876	Methanobrevibacter smithii ATCC 35061	Euryarchaeota	Methanobacteria
312	167045231	uncultured marine crenarchaeote HF4000_APKG8O8	Thaumarchaeota	marine archaeal group 1
313	150400104	Methanococcus vannielii SB	Euryarchaeota	Methanococci
314	284164044	Haloterrigena turkmenica DSM 5511	Euryarchaeota	Halobacteria
315	147919544	uncultured methanogenic archaeon RC-I	Archaea	Euryarchaeota
316	284161308	Archaeoglobus profundus DSM 5631	Euryarchaeota	Archaeoglobi
317	156937454	Ignicoccus hospitalis KIN4/I	Crenarchaeota	Thermoprotei
318	84489829	Methanosphaera stadtmanae DSM 3091	Euryarchaeota	Methanobacteria
319	257387370	Halomicrobium mukohataei DSM 12286	Euryarchaeota	Halobacteria
320	126465626	Staphylothermus marinus F1	Crenarchaeota	Thermoprotei
321	55379766	Haloarcula marismortui ATCC 43049	Euryarchaeota	Halobacteria
322	11497997	Archaeoglobus fulgidus DSM 4304	Euryarchaeota	Archaeoglobi
323	257076419	Ferroplasma acidarmanus fer1	Euryarchaeota	Thermoplasmata
324	150403290	Methanococcus maripaludis C7	Euryarchaeota	Methanococci
325	45357937	Methanococcus maripaludis S2	Euryarchaeota	Methanococci
326	76803122	Natronomonas pharaonis DSM 2160	Euryarchaeota	Halobacteria
327	159904964	Methanococcus maripaludis C6	Euryarchaeota	Methanococci
328	110668963	Haloquadratum walsbyi DSM 16790	Euryarchaeota	Halobacteria
329	20089798	Methanosarcina acetivorans C2A	Euryarchaeota	Methanomicrobia
330	224819889	Natrialba magadii ATCC 43099	Euryarchaeota	Halobacteria
331	167044987	uncultured marine crenarchaeote HF4000_APKG8G2	Thaumarchaeota	marine archaeal group 1
332	134046328	Methanococcus maripaludis C5	Euryarchaeota	Methanococci
333	167044515	uncultured marine crenarchaeote HF4000_APKG6J21	Thaumarchaeota	marine archaeal group 1
334	124485596	Methanocorpusculum labreanum Z	Euryarchaeota	Methanomicrobia
335	146303522	Metallosphaera sedula DSM 5348	Crenarchaeota	Thermoprotei
336	227881179	Halogeometricum borinquense DSM 11551	Euryarchaeota	Halobacteria
337	254168268	Aciduliprofundum boonei T469	Euryarchaeota	unclassified Euryarchaeota
338	15922464	Sulfolobus tokodaii str. 7	Crenarchaeota	Thermoprotei
339	21228138	Methanosarcina mazei Go1	Euryarchaeota	Methanomicrobia
340	218884375	Desulfurococcus kamchatkensis 1221n	Crenarchaeota	Thermoprotei
341	150400747	Methanococcus aeolicus Nankai-3	Euryarchaeota	Methanococci
342	169236608	Halobacterium salinarum R1	Euryarchaeota	Halobacteria
343	13540951	Thermoplasma volcanium GSS1	Euryarchaeota	Thermoplasmata
344	16081221	Thermoplasma acidophilum DSM 1728	Euryarchaeota	Thermoplasmata
345	222480473	Halorubrum lacusprofundi ATCC 49239	Euryarchaeota	Halobacteria
346	70605879	Sulfolobus acidocaldarius DSM 639	Crenarchaeota	Thermoprotei

347	288561037	Methanobrevibacter ruminantium M1	Euryarchaeota	Methanobacteria
348	282163499	Methanocella paludicola SANAE	Euryarchaeota	Methanomicrobia
349	41615005	Nanoarchaeum equitans Kin4-M	Archaea	Nanoarchaeota
350	C1FFM3_9CHLO (C1FFM3)	Micromonas pusilla (strain CCMP1545)	Viridiplantae	Chlorophyta
351	A3A2E7_ORYSJ (A3A2E7)	Oryza sativa subsp. japonica	Viridiplantae	Streptophyta
352	A2X031_ORYSI (A2X031)	Oryza sativa subsp. indica	Viridiplantae	Streptophyta
353	B9RC94_RICCO (B9RC94)	Ricinus communis	Viridiplantae	Streptophyta
354	B6THX3_MAIZE (B6THX3)	Zea mays	Viridiplantae	Streptophyta
355	A5C6C5_VITVI (A5C6C5)	Vitis vinifera	Viridiplantae	Streptophyta
356	A2X031_ORYSI (A2X031)	Oryza sativa str. indica	Viridiplantae	Streptophyta
357	A4RZC6_OSTLU (A4RZC6)	Ostreococcus lucimarinus CCE9901	Viridiplantae	Chlorophyta
358	Q9FLL1_ARATH (Q9FLL1)	Arabidopsis thaliana	Viridiplantae	Streptophyta
359	A9SGD2_PHYPA (A9SGD2)	Phycomitrella patens	Viridiplantae	Streptophyta
360	Q016H5_OSTTA (Q016H5)	Ostreococcus tauri	Viridiplantae	Chlorophyta
361	B9GWG3_POPTR (B9GWG3)	Populus trichocarpa	Viridiplantae	Streptophyta
362	Q681U9_ARATH (Q681U9)	Arabidopsis thaliana	Viridiplantae	Streptophyta
363	C1N1X5_9CHLO (C1N1X5)	Micromonas pusilla (strain CCMP1545)	Viridiplantae	Chlorophyta
364	B6THD0_MAIZE (B6THD0)	Zea mays	Viridiplantae	Streptophyta
365	6324630	Saccharomyces cerevisiae S288c	Fungi	Dikarya

Table S2. Structures compared to PhNob1$_{PIN}$

PDB code	species	taxonomic group	Sequence similarity	Cα-RMSD (Å)	Aligned residues
1A76	*Methanococcus jannaschii*	Euryarchaeota	0.2222	2.06	54
1B43	*Pyrococcus furiosus*	Euryarchaeota	0.0598	2.13	31
1EXN	*Bacteriophage t5*	Virus	0.1282	2.63	29
1MC8	*Pyrococcus horikoshii*	Euryarchaeota	0.1282	2.15	37
1O4W	*Archaeoglobus fulgidus*	Euryarchaeota	0.3846	1.53	77
1RXV	*Archaeoglobus fulgidus*	Euryarchaeota	0.0940	2.28	36
1RXW	*Archaeoglobus fulgidus*	Euryarchaeota	0.1026	2.34	33
1TAQ	*Thermus aquaticus*	Deinoccus-Thermus	0.2906	1.84	65
1UT5	*Bacteriophage t5*	Virus	0.2137	2.36	47
1V8O	*Pyrobaculum aerophilum*	Crenarchaeota	0.2906	1.74	70
1V8P	*Pyrobaculum aerophilum*	Crenarchaeota	0.2821	1.69	68
1V96	*Pyrococcus horikoshii*	Euryarchaeota	0.2906	2.12	72
1W8I	*Archaeoglobus fulgidus*	Euryarchaeota	0.4103	2.40	87
1XO1	*Bacteriophage t5*	Virus	0.2479	1.96	62
1Y82	*Pyrococcus furiosus*	Euryarchaeota	0.2991	1.99	71
1YE5	*Pyrococcus horikoshii*	Euryarchaeota	0.3162	2.15	76
2BSQ	*Neisseria gonorrhoeae*	Proteobacteria	0.2991	1.73	75
2FE1	*Pyrobaculum aerophilum*	Crenarchaeota	0.3761	1.79	73
2H1C	*Neisseria gonorrhoeae*	Proteobacteria	0.2991	1.91	75
2IHN	*Bacteriophage t4*	Virus	0.1026	2.19	28

Supplementary Figures

Supplementary Figure S1. High resolution image of the phylogenetic tree shown in Figure 1A.

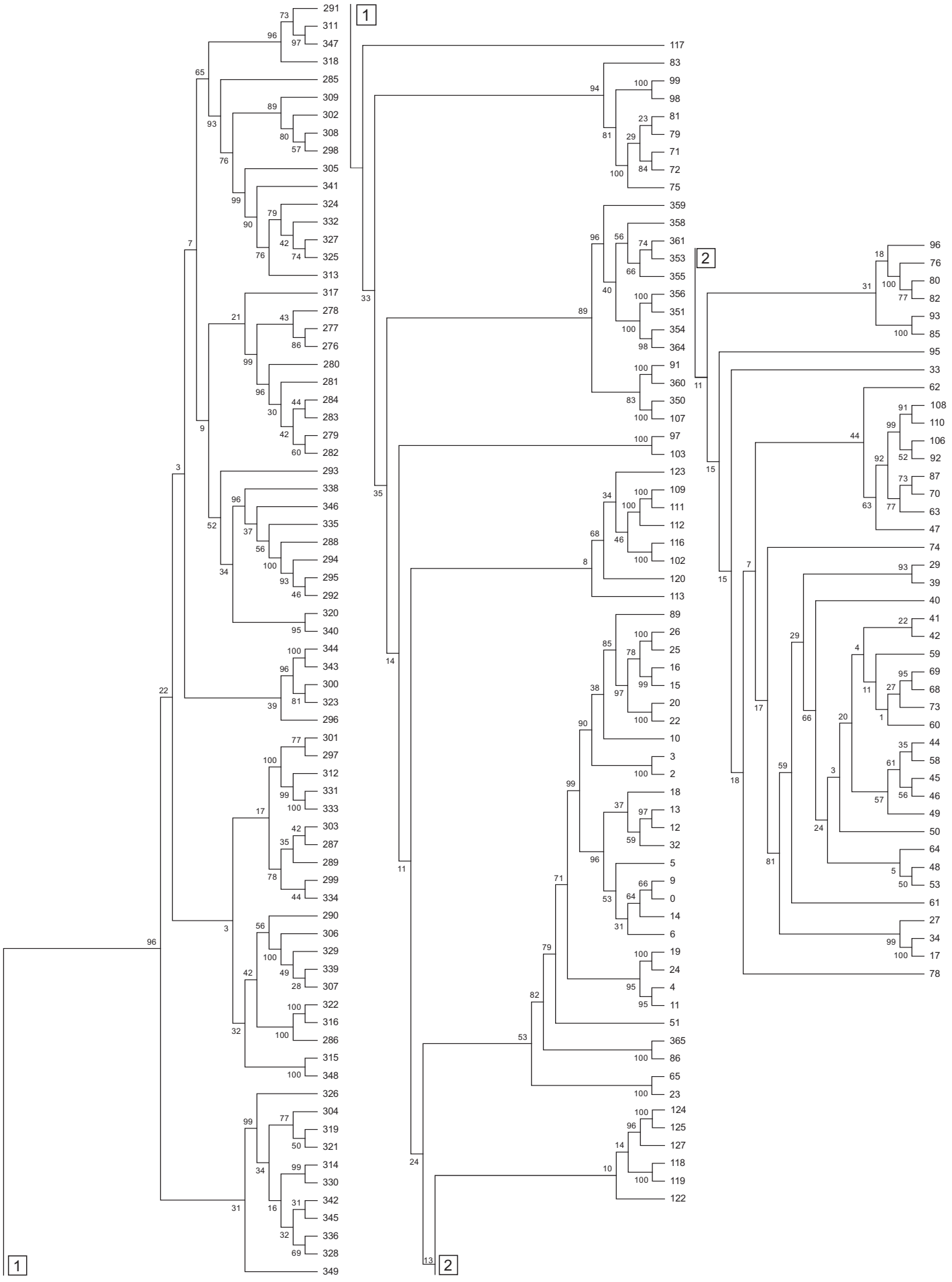
Supplementary Figure S2. Analysis of the conservation of the insertion between α5 and β4 and of the C-terminal extension in eukaryotic sequences.

Supplementary Figure S3. The cleavage is specific for the presence of PhNob1.

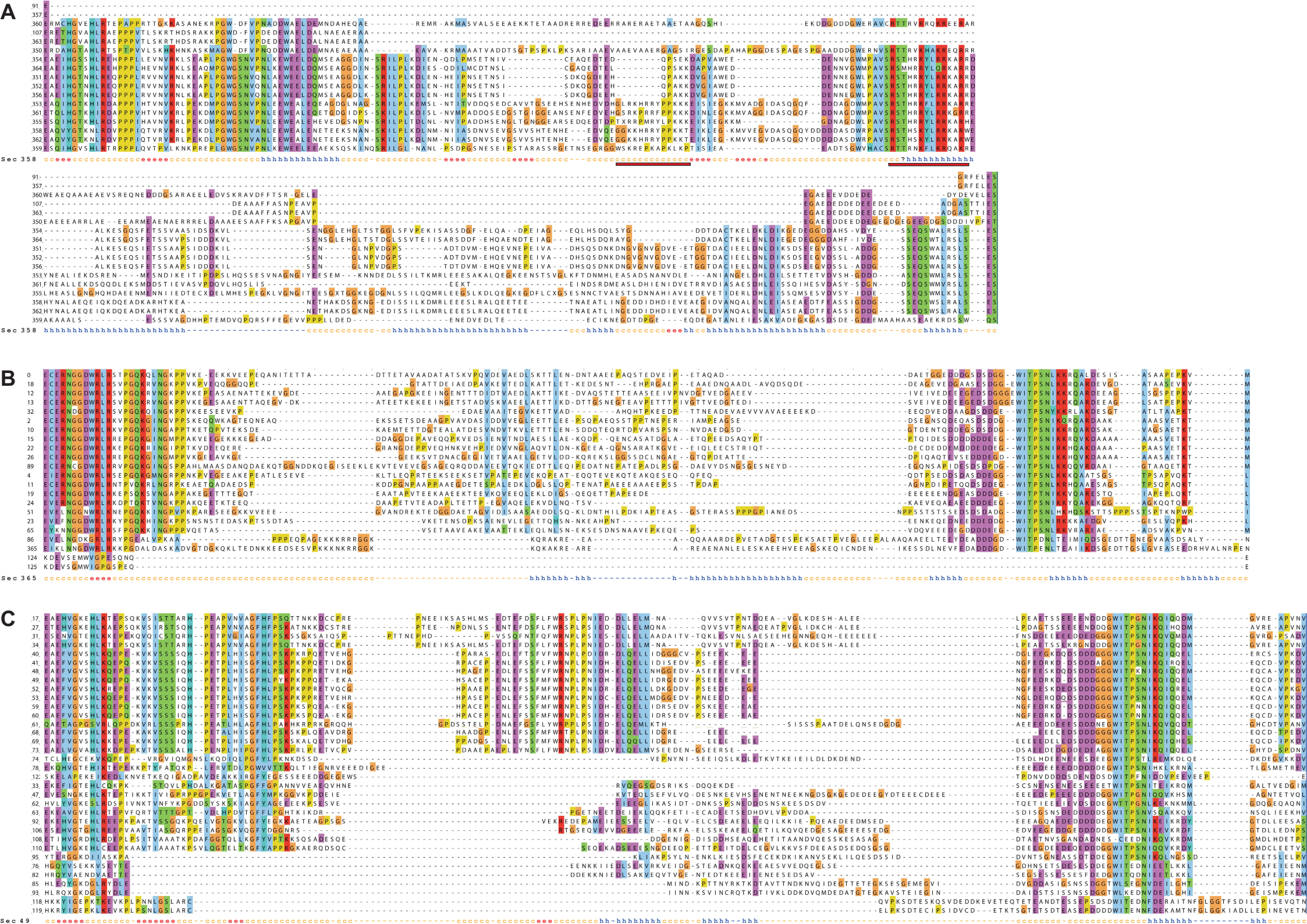
In vitro transcripts of sequences from the 3'-end of *P. horikoshii* 16S rRNA and part of the internal transcribed spacer 1 (ITS1) were 5'-labeled and subjected to different concentrations of recombinant PhNob1 or *E. coli* cell lysate with (right) or without (left) preincubation for 10 minutes at 75°C. Cleavage of RNAs was analyzed by denaturing SDS-PAGE followed by phosphorimaging. The arrow indicates the long (arrow 1) cleavage product.

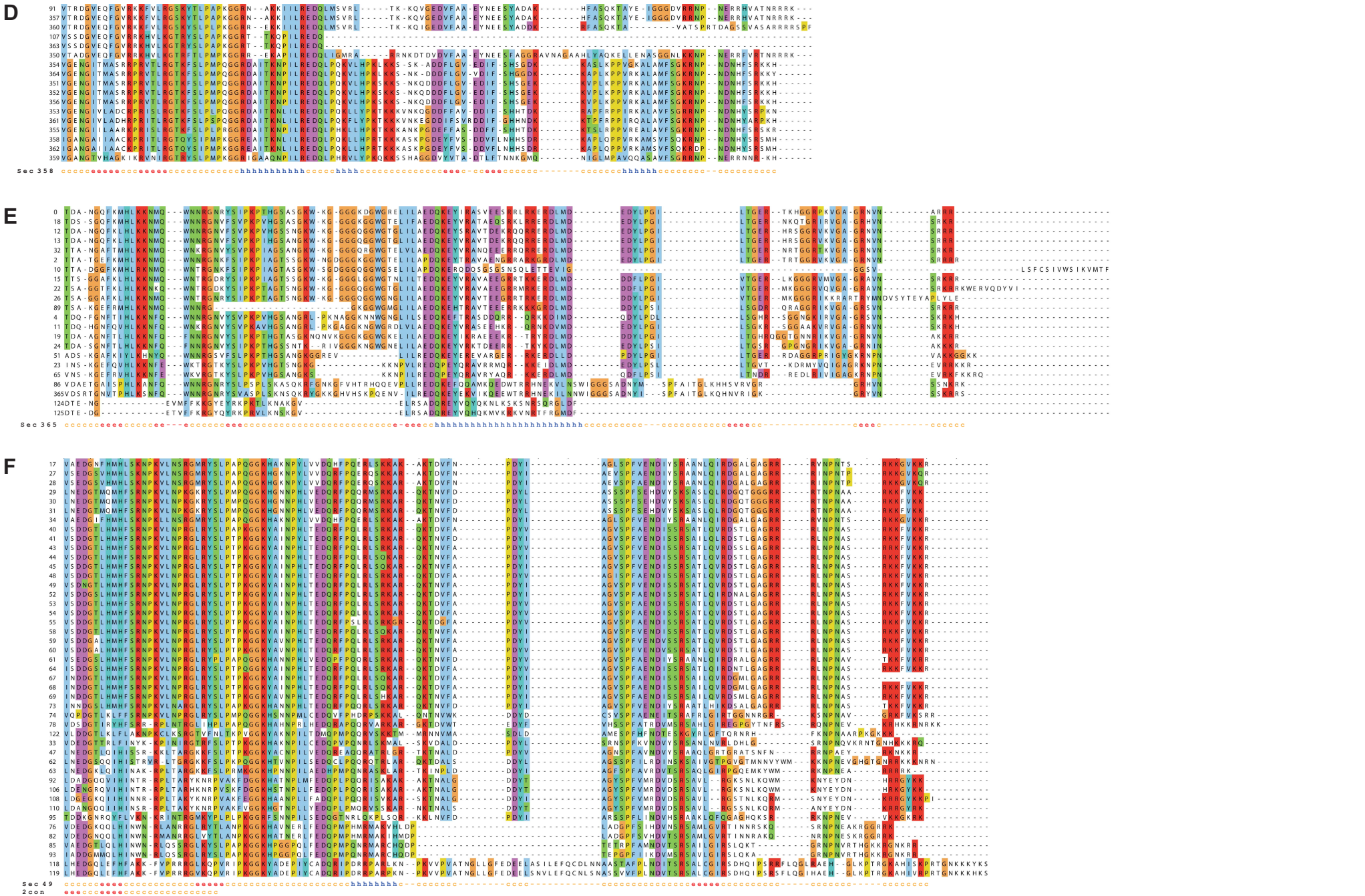
Supplementary Figure S4. Quantification of electrophoretic mobility shift analysis of substrate binding by PhNob1 and PhNob1$_{PIN}$.

The interaction between PhNob1 (A) or PhNob1$_{PIN}$ (B) and radioactively labeled PhNlong90 (long) or PhNlong23 (short) RNAs was analyzed (n≥3) as described in Figure 7C. Radioactivity of the shifted (bound) and non-shifted (free) RNA was quantified. Shown is the Hill plot of the observed values. The estimated K_D of the interactions of PhNob1 and PhNlong90 or PhNlong23 was calculated as 0.7±0.1 µM and 34±2 µM, respectively. The hill coefficients determined are 1.38±0.09 or 0.95±0.05, respectively. The estimated K_D of the interactions of PhNob1$_{PIN}$ and PhNlong90 or PhNlong23 was calculated as 5.5±0.3 µM and 64±5 µM, respectively. The hill coefficients determined are 1.1±0.1 or 1.01±0.07, respectively. Please note that saturation is reached only for the interaction of PhNob1 with PhNlong90.

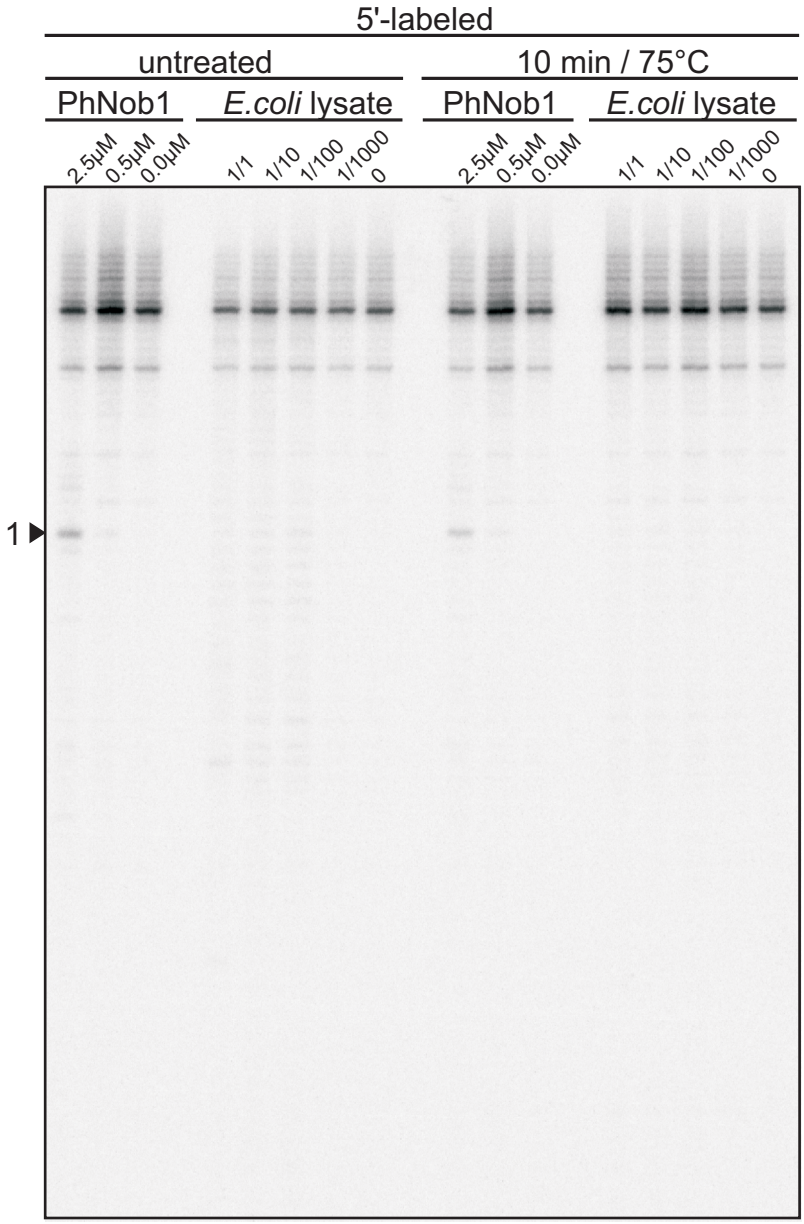


Supplementary Figure S1. High resolution image of the phylogenetic tree shown in Figure 1A.


A
B
C

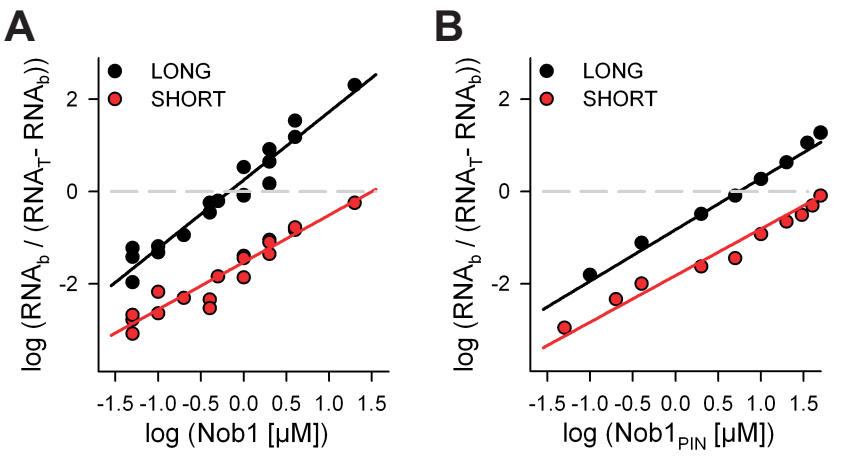


Supplementary Figure S2. Analysis of the conservation of the insertion between α5 and α4 and of the C-terminal extension in eukaryotic sequences. (A-F) The alignments of the sequences indicated on the left (supp. Table 1) were constructed as described for the phylogenetic analysis (Material and Methods) and presented with Jalview 2.6.1 (Waterhouse AM, Procter JB, Martin DM, Clamp M, Barton GJ. (2009) Jalview Version 2—a multiple sequence alignment editor and analysis workbench. *Bioinformatics.* 25: 1189-1191.) with coloring according to Clustalx (Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. ´(1997) The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res. 25: 4876-4882). The alignments of the intrinsic loop (A-C) or the C-terminal extension (D-F) of sequences found in various plant species (A, D), fungi (B.E) or metazoan (C,F). Underneath the result of the secondary structure prediction for the indicated sequences performed by consensus prediction (npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=npsa_sspred.html; Deleage, G., Blanchet, C., and Geourjon, C (1997) Protein structure prediction. Implications for the biologist. *Biochimie* 79:681-686) is shown. Here “e” stands for strand predicted and “h” for helix predicted. In F, the secondary structure of 2CON is indicated.



Supplementary Figure S3. The cleavage is specific for the presence of PhNob1.

In vitro transcripts of sequences from the 3'-end of *P. horikoshii* 16S rRNA and part of the internal transcribed spacer 1 (ITS1) were 5'-labeled and subjected to different concentrations of recombinant PhNob1 or *E. coli* cell lysate with (right) or without (left) preincubation for 10 minutes at 75°C. Cleavage of RNAs was analyzed by denaturing SDS-PAGE followed by phosphorimaging. The arrow indicates the long (arrow 1) cleavage product.



Supplementary Figure S4. Quantification of electrophoretic mobility shift analysis of substrate binding by PhNob1 and PhNob1$_{PIN}$.

The interaction between PhNob1 (A) or PhNob1$_{PIN}$ (B) and radioactively labeled PhNlong90 (long) or PhNlong23 (short) RNAs was analyzed (n≥3) as described in Figure 7C. Radioactivity of the shifted (bound) and non-shifted (free) RNA was quantified. Shown is the Hill plot of the observed values. The estimated K_D of the interactions of PhNob1 and PhNlong90 or PhNlong23 was calculated as 0.7±0.1 μM and 34±2 μM, respectively. The hill coefficients determined are 1.38±0.09 or 0.95±0.05, respectively. The estimated K_D of the interactions of PhNob1$_{PIN}$ and PhNlong90 or PhNlong23 was calculated as 5.5±0.3 μM and 64±5 μM, respectively. The hill coefficients determined are 1.1±0.1 or 1.01±0.07, respectively. Please note that saturation is reached only for the interaction of PhNob1 with PhNlong90.