Supporting Information

Lin et al. 10.1073/pnas.1007246107

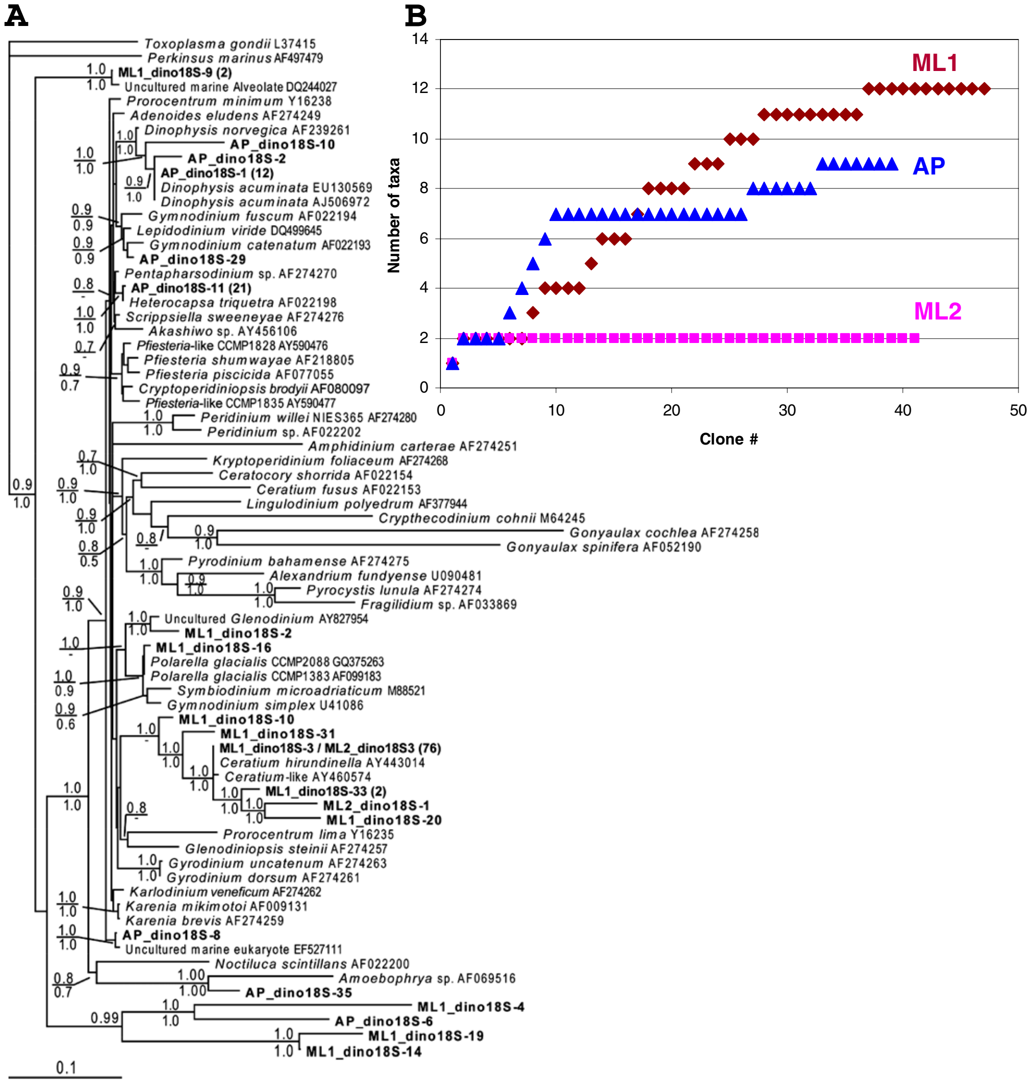


Fig. S1. Dinoflagellate diversity in the field samples analyzed in this study. (*A*) Phylogenetic analysis of the field-retrieved dinoflagellate 18S rDNA sequences (in bold) with documented sequences of dinoflagellates, *Perkinsus marinus*, and apicomplexans (as outgroup). Only unique clones from each sample were included in the analysis, with the number of clones identical to the one shown in the tree given in parentheses. Support of the nodes stemmed from maximum likelihood (ML)/Mr.Bayes analyses (MB). (*B*) Rarefaction curves of unique dinoflagellate taxa (based on 97% identity cutoff) detected from the sequenced 18S rDNA clone libraries. AP, Avery Point at Long Island Sound; ML1, Mirror Lake sample 1; ML2, Mirror Lake sample 2.

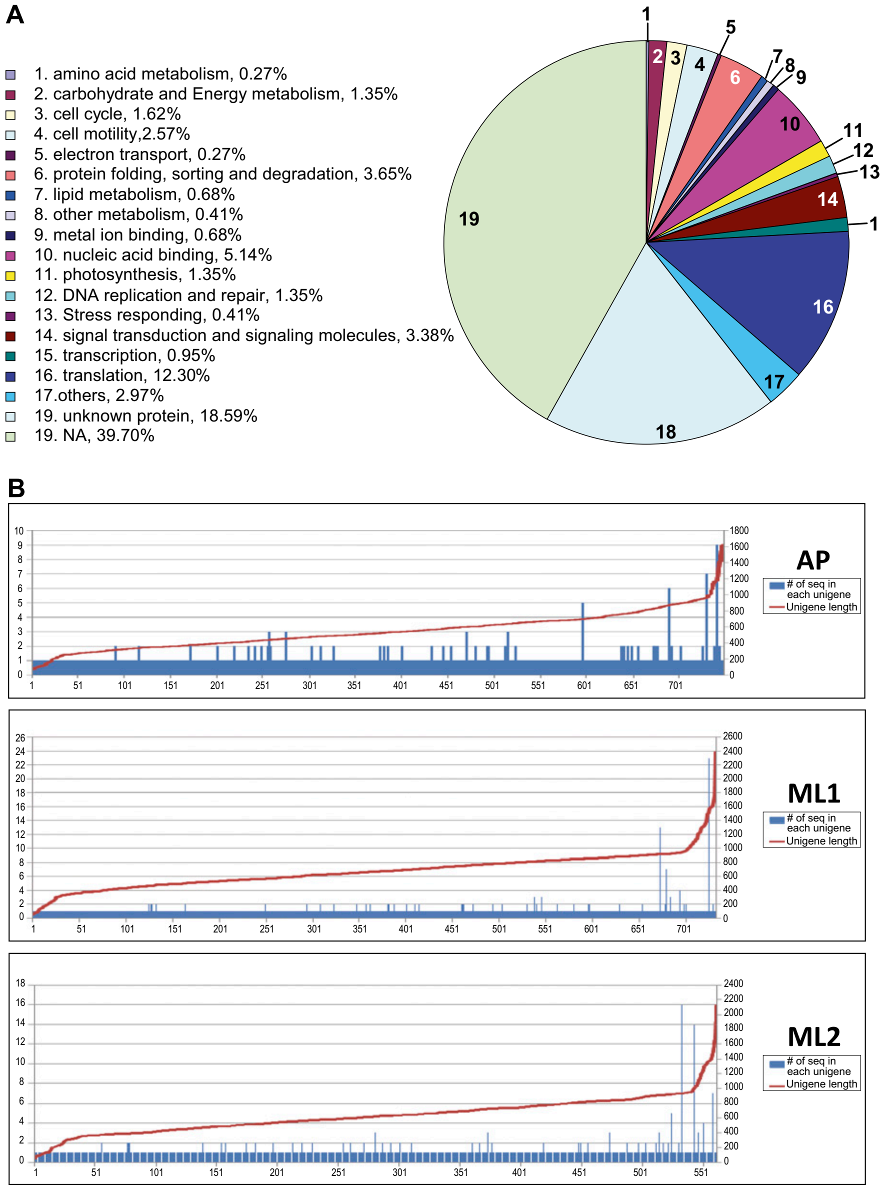


Fig. S2. (*A*) Diverse cellular processes represented in percentage of the cDNA libraries (e-cDNAs) from the Long Island Sound (AP) sample that had hits in GenBank. Each process is marked by a numeral in the chart; its name and percentage are indicated in the legend. (*B*) EST representation of each unigene from e-cDNA libraries. Note that the majority of genes were expressed at a homogeneous and low level (1–2 clones).

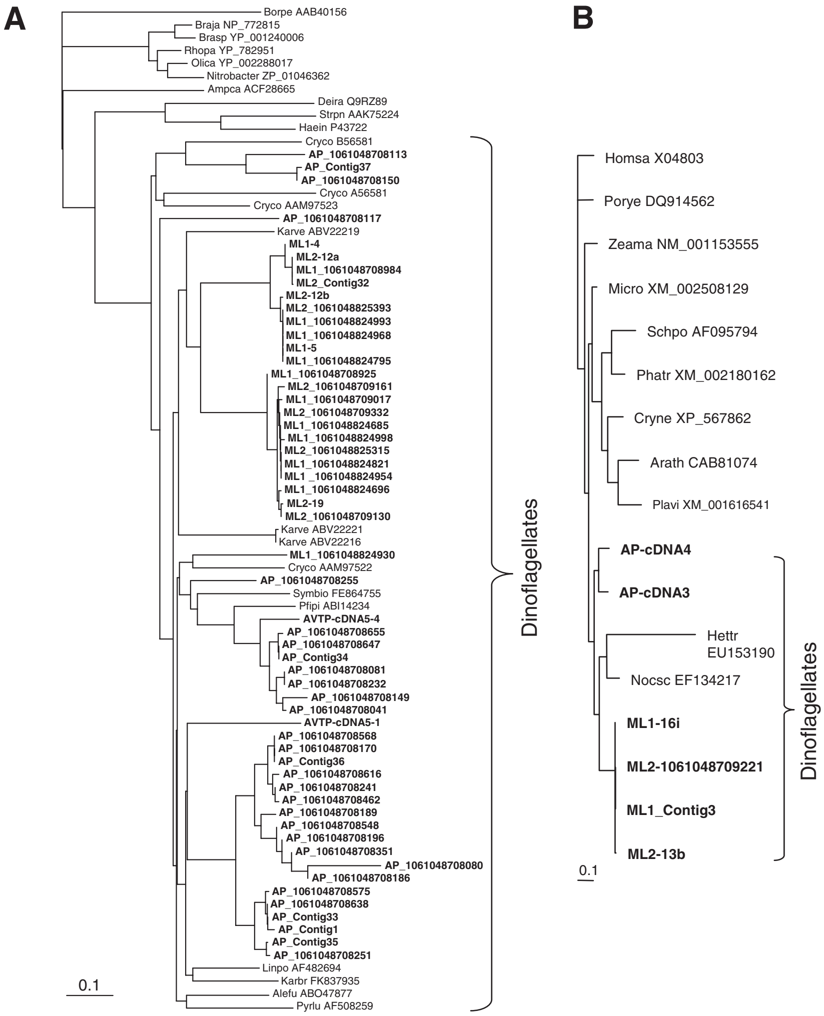


Fig. S3. (Continued)

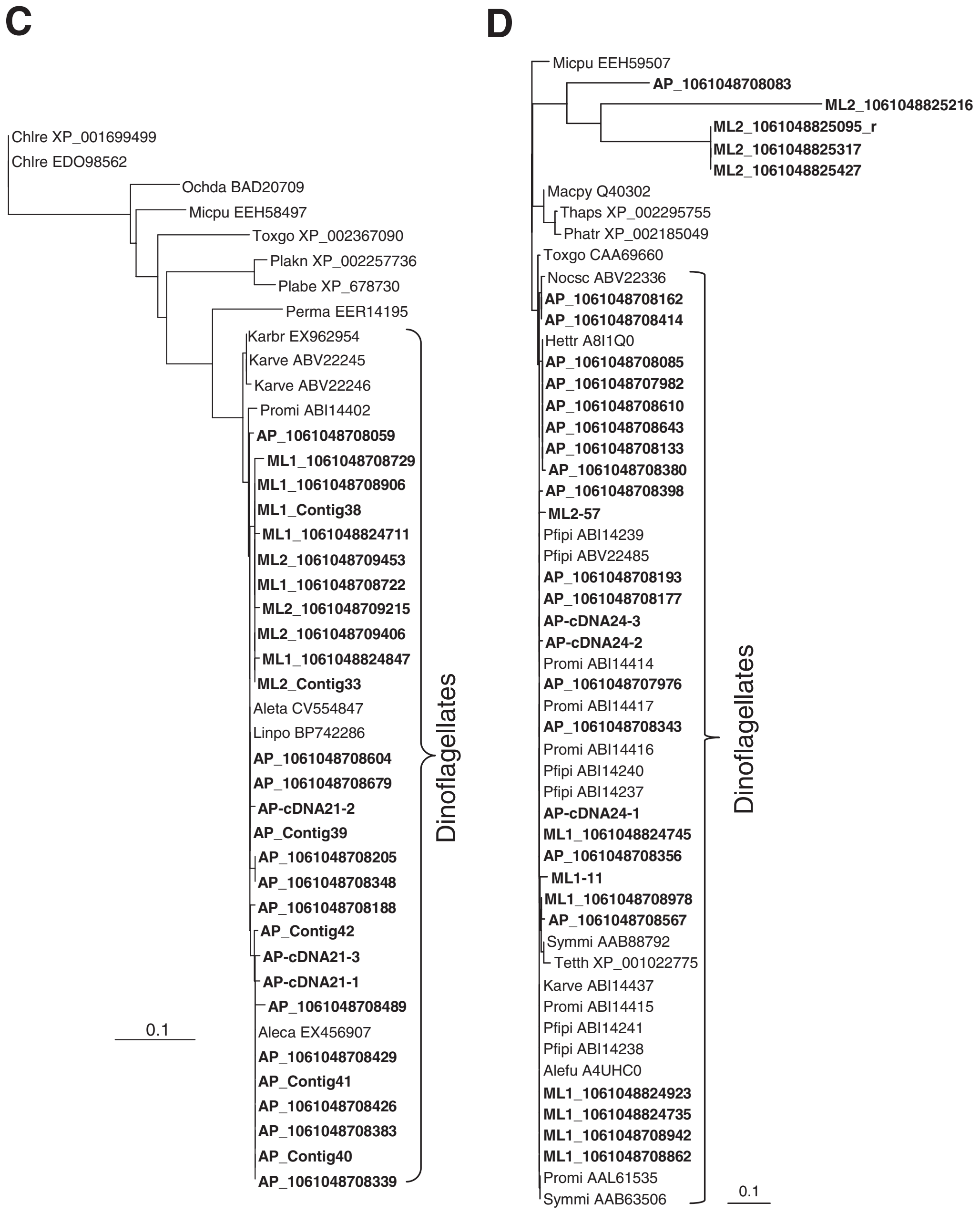


Fig. S3. (Continued)

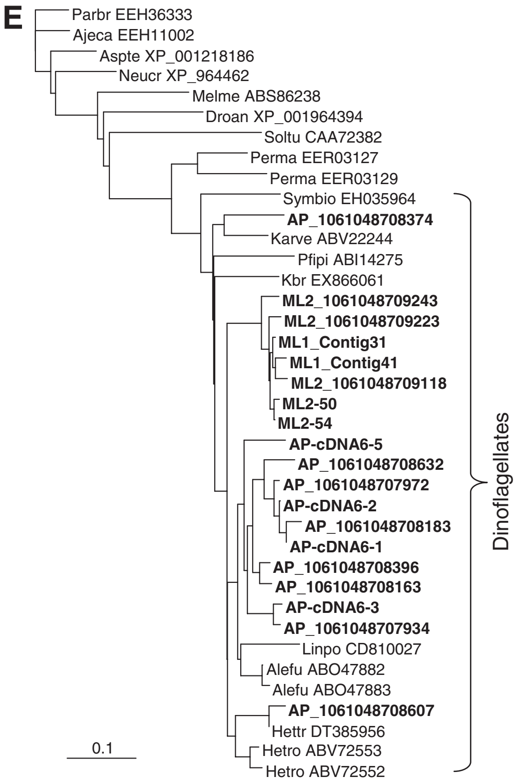


Fig. S3. Neighbor-joining (NJ) tree of the five most highly expressed common genes to show affiliation with documented dinoflagellates. Items in bold are from AP, ML1, and ML2. (*A*) Major basic nuclear protein. (*B*) Ubiquitin. (*C*) Centrin. (*D*) Calmodulin. (*E*) 14-3-3 protein.

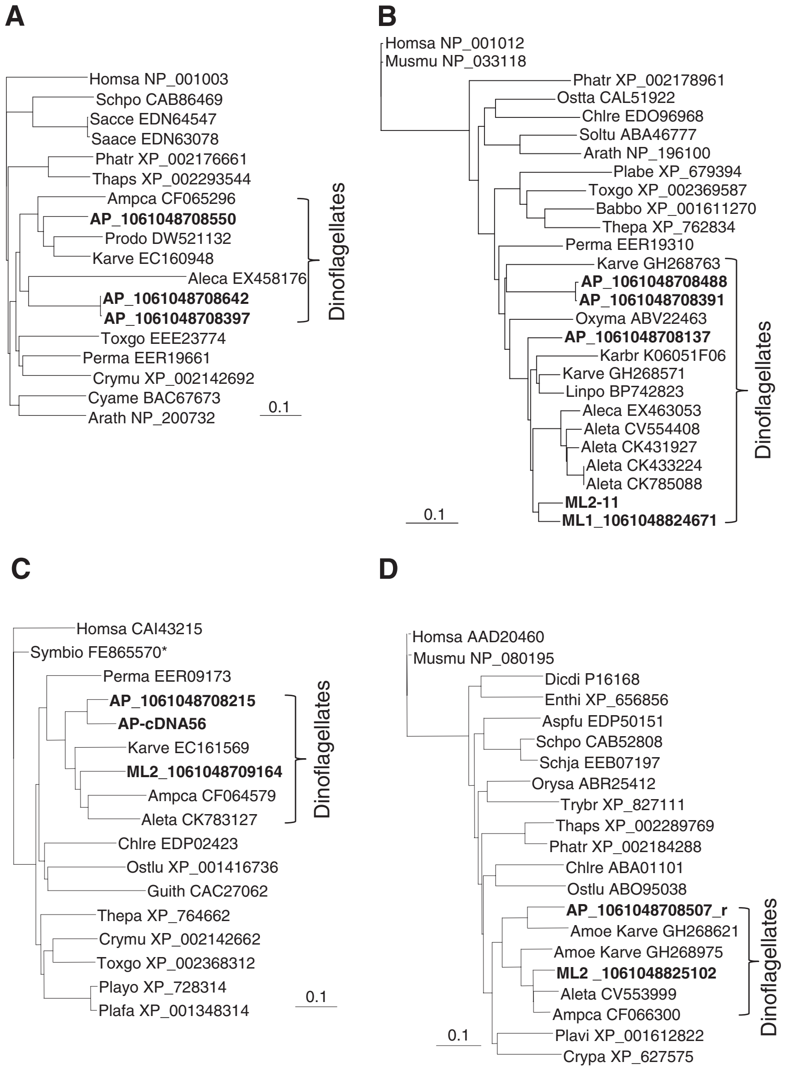


Fig. S4. NJ trees of example ribosomal proteins (RPs) found in this study to show affiliation of e-cDNAs (in bold) with dinoflagellates among other organisms. (*A*) 40S rpS8. (*B*) 40S rpS17. (*C*) 60S rpL10. Asterisks depict previously reported as sequence from dinoflagellate symbiont of coral (*Symbiodinium*) but possibly a sequence from coral contamination, which could be prevented by using dinoflagellate spliced-leader (DinoSL) primer. (*D*) 60S rpL11.

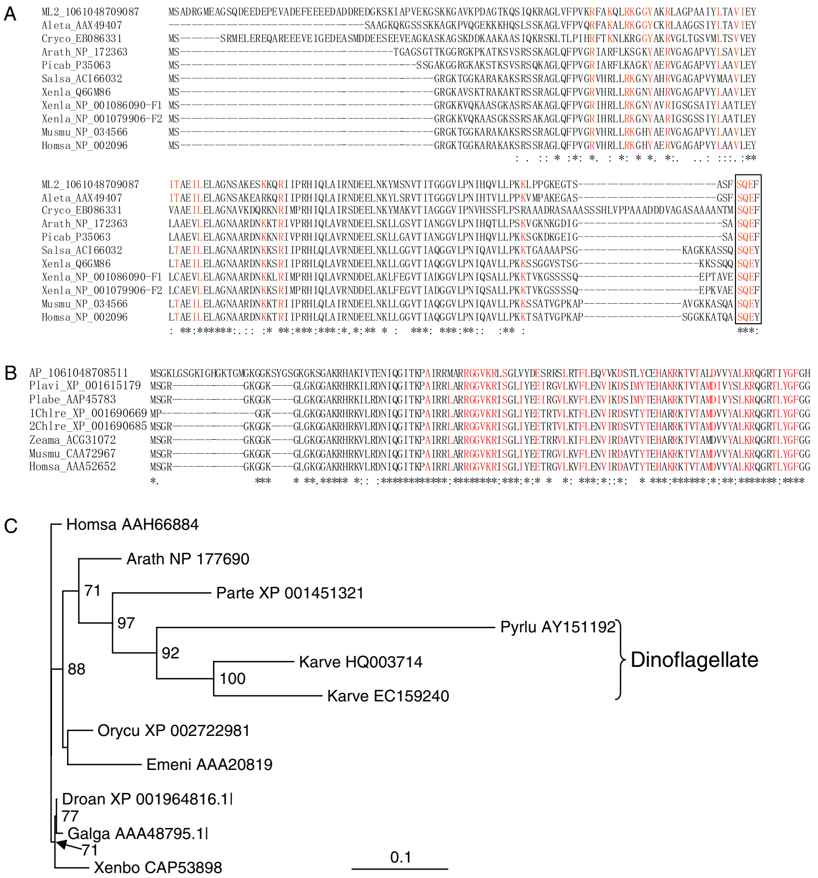
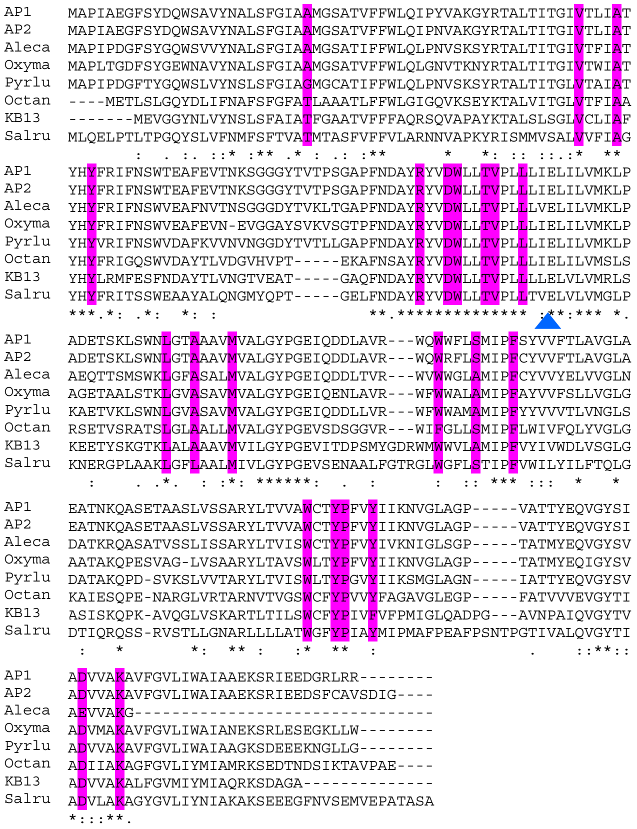


Fig. S5. Alignment and phylogenetic tree of field-retrieved and culture-based dinoflagellate histone sequences with homologs in other organisms. (*A*) Histone H2A.X from ML2 and *Alexandrium tamarense* (Aleta) and *Crypthecodinium cohnii* (Cryco) as well as other organisms. SQEF (boxed) at the C terminus is a signature motif of H2A.X. (*B*) Histone H4 from AP as well as other organisms. Asterisks depict identical residues; colons and semicolons indicate chemically similar residues. DNA binding sites are shown in red. (*C*) NJ tree of histone H3 from dinoflagellates and other organisms; the tree was rooted with human H3. Bootstrap values >50% are shown at nodes.



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AP1    MAPIAEGFSYDQWSAVYNALSFGIAAMGSATVFFWLQIPYVAKGYRTALTITGIVTLIAT
AP2    MAPIAEGFSYDQWSAVYNALSFGIAAMGSATVFFWLQIPNVAKGYRTALTITGIVTLIAT
Aleca  MAPIPDGFSYGQWSVVYNALSFGIAAMGSATIFFWLQLPNVSKSYRTALTITGIVTFIAT
Oxyma  MAPLTGDFSYGEWNAVYNALSFGIAAMGSATVFFWLQLGNVTKNYRTALTITGIVTWIAT
Pyrlu  MAPIPDGFTYGQWSLVYNSLSFGIAGMGCATIFFWLQLPNVSKSYRTALTITGLVTAIAT
Octan  ----METLSLGQYDLIFNAFSFGFATLAAATLFFWLGIGQVKSEYKTALVITGLVTFIAA
KB13   -------MEVGGYNLVYNSLSFAIATFGAATVFFFAQRSQVAPAYKTALSLSGLVCLIAF
Salru  MLQELPTLTPGQYSLVFNMFSFTVATMTASFVFFVLARNNVAPKYRISMMVSALVVFIAG
              :  . :. ::* :** .* : .: :**      *   *: :: ::.:*   **

AP1    YHYFRIFNSWTEAFEVTNKSGGGYTVTPSGAPFNDAYRYVDWLLTVPLLLIELILVMKLP
AP2    YHYFRIFNSWTEAFEVTNKSGGGYTVTPSGAPFNDAYRYVDWLLTVPLLLIELILVMKLP
Aleca  YHYFRIFNSWVEAFNVTNSGGGDYTVKLTGAPFNDAYRYVDWLLTVPLLLVELILVMKLP
Oxyma  YHYFRIFNSWVEAFEVN-EVGGAYSVKVSGTPFNDAYRYVDWLLTVPLLLIELILVMKLP
Pyrlu  YHYVRIFNSWVDAFKVVNVNGGDYTVTLLGAPFNDAYRYVDWLLTVPLLLIELILVMKLP
Octan  YHYFRIGQSWVDAYTLVDGVHVPT-----EKAFNSAYRYVDWLLTVPLLLIELILVMSLS
KB13   YHYLRMFESFNDAYTLVNGTVEAT-----GAQFNDAYRYVDWLLTVPLLLLELVLVMRLS
Salru  YHYFRITSSWEAAYALQNGMYQPT-----GELFNDAYRYVDWLLTVPLLTVELVLVMGLP
       ***.*: .*:  *: :                **.************** :**:*** *.

AP1    ADETSKLSWNLGTAAAVMVALGYPGEIQDDLAVR---WQWWFLSMIPFSYVVFTLAVGLA
AP2    ADETSKLSWNLGTAAAVMVALGYPGEIQDDLAVR---WQWRFLSMIPFCYVVFTLAVGLA
Aleca  AEQTTSMSWKLGFASALMVALGYPGEIQDDLTVR---WVWWGLAMIPFCYVVYELVVGLN
Oxyma  AGETAALSTKLGVASAVMVALGYPGEIQENLAVR---WFWWALAMIPFAYVVFSLLVGLG
Pyrlu  KAETVKLSWNLGVASAVMVALGYPGEIQDDLLVR---WFWWAMAMIPFYYVVVTLVNGLS
Octan  RSETVSRATSLGLAALLMVALGYPGEVSDSGGVR---WIFGLLSMIPFLWIVFQLYVGLG
KB13   KEETYSKGTKLALAAAVMVILGYPGEVITDPSMYGDRWMWWVLAMIPFVYIVWDLVSGLG
Salru  KNERGPLAAKLGFLAALMIVLGYPGEVSENAALFGTRGLWGFLSTIPFVWILYILFTQLG
         :    . .*.  : :*: ******:  .  :      :  :: *** :::  *   *

AP1    EATNKQASETAASLVSSARYLTVVAWCTYPFVYIIKNVGLAGP-----VATTYEQVGYSI
AP2    EATNKQASETAASLVSSARYLTVVAWCTYPFVYIIKNVGLAGP-----VATTYEQVGYSI
Aleca  DATKRQASATVSSLISSARYLTVISWCTYPFVYIVKNIGLSGP-----TATMYEQVGYSV
Oxyma  AATAKQPESVAG-LVSAARYLTAVSWLTYPFVYIIKNVGLAGP-----TATMYEQIGYSV
Pyrlu  DATAKQPD-SVKSLVVTARYLTVISWLTYPGVYIIKSMGLAGN-----IATTYEQVGYSV
Octan  KAIESQPE-NARGLVRTARNVTVGSWCFYPVVYFAGAVGLEGP-----FATVVVEVGYTI
KB13   ASISKQPK-AVQGLVSKARTLTILSWCFYPIVFVFPMIGLQADPG---AVNPAIQVGYTV
Salru  DTIQRQSS-RVSTLLGNARLLLLATWGFYPIAYMIPMAFPEAFPSNTPGTIVALQVGYTI
        :   *       *:  ** :   :*  **  :                .    ::**::

AP1    ADVVAKAVFGVLIWAIAAEKSRIEEDGRLRR--------
AP2    ADVVAKAVFGVLIWAIAAEKSRIEEDSFCAVSDIG----
Aleca  AEVVAKG--------------------------------
Oxyma  ADVMAKAVFGVLIWAIANEKSRLESEGKLLW--------
Pyrlu  ADVVAKAVFGVLIWAIAAGKSDEEEKNGLLG--------
Octan  ADIIAKAGFGVLIYMIAMRKSEDTNDSIKTAVPAE----
KB13   ADVVAKALFGVMIYMIAQRKSDAGA--------------
Salru  ADVLAKAGYGVLIYNIAKAKSEEEGFNVSEMVEPATASA
       *:::**.
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Fig. S6. Alignment of rhodopsin from dinoflagellates and bacteria. AP1, Avery Point clone AP-cDNA38 (GenBank accession number GU553957); AP2, AP_1061048708262 (GU554267); Aleca, *Alexandrium catenella* (EX456621); Oxyma, *Oxyrrhis marina* (ABV22432); Pyrlu, *Pyrocystis lunula* (AAO14677); Ocatan, *Octadecabacter antarcticus* (YP_002630106); KB13, beta proteobacterium KB13 (YP_002664979); Salru, *Salinibacter ruber* DSM 13855 (YP_445623). The pink highlight shows the 22 residues in the retinal-binding pocket, and the blue triangle points at the proton donor residue, which is glutamic acid (E) or aspartic acid (D) for ion pump rhodopsin and other residues in sensory rhodopsin (1).

1. Jung K-H (2007) The distinct signaling mechanisms of microbial sensory rhodopsins in Archaea, Eubacteria and Eukarya. *Photochem Photobiol* 83:63–69.

Table S1. DinoSL-containing sequences from CAMERA database that had matches to documented genes in GenBank database

Sequence name	Sequence description	Sequence length	Hit accession no.	*E* value	Similarity, %
JCVI_READ_1108839778669	DinoSL only, vector seq at 5′ end	974	AJ606472	$4.33e^{-37}$	98
JCVI_READ_2004228	Similar to *Heterocapsa arctica* spliced-leader (SL) RNA in SL-5S cluster	1014	FJ434749	$9.95e^{-14}$	91
JCVI_READ_1178274	*H. arctica* (SL)X kind	994	FJ434743	$9.75e^{-14}$	98
JCVI_READ_1222459	Dino SL-5S cluster, similar to Kbr but without U6	1014	FJ434801	$9.93e^{-52}$	94
JCVI_READ_2030933	DinoSL RNA	1000	XM_001868438	$8.60e^{-21}$	67
JCVI_READ_1920381	Kve SL RNA kind	1048	EF143079	$3.84e^{-19}$	98
JCVI_READ_2019721	SL followed by a small piece of 18S seq	927	EU793415	$3.37e^{-57}$	97
JCVI_READ_1306868	Dino RP s30 with SL	1046	EU153194	$1.52e^{-11}$	83
JCVI_READ_678516	Dino 28S-SL cluster	1051	EU795185	0	84
JCVI_READ_1095516037741	Two units of SL RNA, similar to Kve SL RNA	1013	EF143079	$2.85e^{-14}$	90
JCVI_READ_1095515504143	Kve SL RNA kind	959	EF143079	$9.39e^{-14}$	91
JCVI_READ_1092404076874	Dino 28S-SL cluster	1219	EU795185	0	84
JCVI_READ_1092405883731	Dino SL-5S cluster, without U6	1126	FJ434806	$7.97e^{-41}$	89
JCVI_READ_1105430289187	Dino5S-SL, without U6	1148	AY305326	$1.19e^{-38}$	89
JCVI_READ_1095516111160	Kve SL RNA kind, reverse	1022	EF143079	$2.87e^{-14}$	91
JCVI_READ_1092347070402	Dino 28S-SL cluster	1132	EU795185	0	81
JCVI_READ_1092351000339	DinoSL only, unknown	1145	GQ178071	$5.90e^{-11}$	92

Table S2. Base composition of the three e-cDNA libraries

		A	T	C	G	GC
ML1	Dino hit	0.2314 ± 0.0379	0.2233 ± 0.0236	0.2497 ± 0.0287	0.2994 ± 0.0195	0.5491 ± 0.0358
	No hit	0.2207 ± 0.0399	0.2239 ± 0.0325	0.2550 ± 0.0299	0.3081 ± 0.0293	0.5631 ± 0.0380
	Total	0.2242 ± 0.0366	0.2232 ± 0.0296	0.2531 ± 0.0283	0.3055 ± 0.0268	0.5586 ± 0.0381
ML2	Dino hit	0.2361 ± 0.0383	0.2224 ± 0.0255	0.2444 ± 0.0231	0.3013 ± 0.0200	0.5457 ± 0.0302
	No hit	0.2242 ± 0.0385	0.2207 ± 0.0377	0.2531 ± 0.0320	0.3079 ± 0.0284	0.5610 ± 0.0432
	Total	0.2288 ± 0.0365	0.2204 ± 0.0317	0.2517 ± 0.0283	0.3048 ± 0.0257	0.5566 ± 0.0389
LIS	Dino hit	0.2290 ± 0.0401	0.2008 ± 0.0360	0.2621 ± 0.0337	0.3132 ± 0.0332	0.5753 ± 0.0509
	No hit	0.2418 ± 0.0558	0.2241 ± 0.0478	0.2453 ± 0.0415	0.3112 ± 0.0434	0.5565 ± 0.0613
	Total	0.2373 ± 0.0457	0.2136 ± 0.0427	0.2540 ± 0.0371	0.3086 ± 0.0382	0.5625 ± 0.0558

Table S3. Twenty-two common genes with the five most highly expressed shaded

	ML1		ML2		AVPT	
Genes	contig	Total	contig	Total	contig	Total
ADP ribosylation factor	0	4	0	3	0	1
ATP synthase	0	3	0	6	0	4
Calmodulin	0	7	1(2)	7	0	19
Centrin/caltractin	1(2)	7	1(2)	6	4(8)	24
Mutant xylanase from *Streptomyces olivaceoviridis*	0	1	0	1	1(2)	4
Cyclophilin-like protein	0	2	1(3)	3	0	3
Cytochrome *c*	0	3	0	2	0	1
14-3-3	2(5)	5	0	5	0	15
Dynein light chain	0	2	0	6	0	5
Fumarate reductase	0	2	0	4	0	5
GST	1(2)	4	0	1	0	1
Major basic nuclear protein	0	14	1(2)	10	6(12)	44
Peptidyl-prolyl *cis-trans* isomerase fkbp-type	0	3	0	1	0	3
Peroxiredoxin	0	1	0	1	0	1
Fucoxanthin chlorophyll a/c-binding protein	2(6)	10	1(2)	2	0	1
Ribosomal protein: 40sRPS13	0	1	0	1	0	1
Ribosomal protein: 40sRPS17	0	3	0	3	0	3
Ribosomal protein: 60sRPL41	0	4	1(2)	5	2(2)	12
Small nuclear ribonucleoprotein	1(2)	8	0	1	0	3
Translation initiation factor 5a	0	1	1(2)	3	0	4
Ubiquitin family protein	2(20)	26	2(18)	30	0	7
NA_nseq contig93	0	1	0	1	0	1

The numbers of clones contributing to the contig are shown in parentheses.

Table S4. Cytoplasmic RPs identified in this study from DinoSL-based e-cDNAs and the largely unannotated dinoflagellate EST datasets (DinoEST) compared with homologs in general eukaryotes, humans, and *Plasmodium* (closest relative of dinoflagellates)

				ML and AP samples		DinoEST*		
Type	Eukaryotes	Humans	*Plasmodium falciparum*	Clone no.	BLASTX NR min. *E* value	Clone no.	TBLASTN min. *E* value	TBLASTN max. *E* value
40S	RPSA	RPSA	RPSA			6	$3.00e^{-75}$	$7.00e^{-13}$
	RPS2	RPS2	RPS2			4	$9.00e^{-76}$	$2.00e^{-11}$
	RPS3	RPS3	RPS3			5	$3.00e^{-96}$	$4.00e^{-20}$
	RPS3A	RPS3A	RPS3A	1	$4.29e^{-087}$	8	$2.00e^{-077}$	$5.00e^{-24}$
	RPS4	RPS4X	RPS4	2	$2.10e^{-103}$	15	$2.00e^{-096}$	$4.00e^{-27}$
		RPS4Y						
	RPS5	RPS5	RPS5	1	$1.02e^{-083}$	9	$2.00e^{-086}$	$2.00e^{-14}$
	RPS6	RPS6	RPS6	2	$1.24e^{-077}$	13	$7.00e^{-081}$	$2.00e^{-19}$
	RPS7	RPS7	RPS7	2	$1.81e^{-057}$	6	$2.00e^{-082}$	$6.00e^{-21}$
	RPS8	RPS8	RPS8	3	$9.97e^{-065}$	8	$2.00e^{-084}$	$2.00e^{-19}$
	RPS9	RPS9	RPS9	1	$1.31e^{-068}$	6	$4.00e^{-079}$	$5.00e^{-40}$
	RPS10	RPS10	RPS10	1	$1.52e^{-044}$	1	$3.00e^{-047}$	$3.00e^{-047}$
	RPS11	RPS11	RPS11	2	$1.55e^{-060}$	17	$2.00e^{-079}$	$9.00e^{-27}$
	RPS12	RPS12	RPS12	4	$6.81e^{-047}$	10	$7.00e^{-043}$	$2.00e^{-14}$
	RPS13	RPS13	RPS13	3	$1.58e^{-071}$	4	$4.00e^{-075}$	$1.00e^{-61}$
	RPS14	RPS14	RPS14			6	$6.00e^{-63}$	$1.00e^{-13}$
	RPS15	RPS15	RPS15	2	$3.23e^{-051}$	11	$1.00e^{-061}$	$1.00e^{-34}$
	RPS15A	RPS15A	RPS15A	1	$1.96e^{-052}$	4	$3.00e^{-057}$	$5.00e^{-35}$
	RPS16	RPS16	RPS16	2	$5.55e^{-056}$	1	$1.00e^{-047}$	$1.00e^{-047}$
	RPS17	RPS17	RPS17	5	$2.42e^{-050}$	10	$5.00e^{-043}$	$5.00e^{-28}$
	RPS18	RPS18	RPS18	1	$2.46e^{-050}$	7	$1.00e^{-066}$	$5.00e^{-15}$
	RPS19	RPS19	RPS19	1	$6.10e^{-041}$	6	$9.00e^{-046}$	$1.00e^{-18}$
	RPS20	RPS20	RPS20			11	$5.00e^{-47}$	$1.00e^{-18}$
	RPS21	RPS21	RPS21	5	$9.83e^{-033}$	1	$8.00e^{-033}$	$8.00e^{-033}$
	RPS23	RPS23	RPS23	5	$5.44e^{-068}$	12	$1.00e^{-075}$	$7.00e^{-19}$
	RPS24	RPS24	RPS24	1	$4.26e^{-044}$	6	$3.00e^{-045}$	$2.00e^{-33}$
	RPS25	RPS25	RPS25	2	$6.99e^{-043}$	18	$3.00e^{-045}$	$9.00e^{-19}$
	RPS26	RPS26	RPS26	2	$2.41e^{-039}$	6	$3.00e^{-040}$	$2.00e^{-26}$
	RPS27	RPS27	RPS27	5	$3.41e^{-035}$	6	$7.00e^{-040}$	$1.00e^{-18}$
	RPS27A	RPS27A	RPS27A			11	$3.00e^{-25}$	$4.00e^{-12}$
	RPS28	RPS28	RPS28	2	$4.46e^{-017}$	8	$4.00e^{-025}$	$6.00e^{-16}$
	RPS29	RPS29		2	$6.09e^{-014}$	4	$9.00e^{-014}$	$2.00e^{-11}$
	RPS30	RPS30	RPS30	4	$2.12e^{-027}$	2	$1.00e^{-019}$	$7.00e^{-14}$
60S	RPL3	RPL3	RPL3			17	$1.00e^{-103}$	$6.00e^{-16}$
	RPL4	RPL4	RPL4			5	$8.00e^{-92}$	$5.00e^{-40}$
	RPL5	RPL5	RPL5			11	$1.00e^{-89}$	$5.00e^{-28}$
	RPL6	RPL6		1	$2.24e^{-039}$	2	$2.00e^{-045}$	$2.00e^{-40}$
	RPL7	RPL7	RPL7			7	$9.00e^{-52}$	$3.00e^{-17}$
	RPL7A	RPL7A	RPL7A			12	$4.00e^{-71}$	$1.00e^{-21}$
	RPL8	RPL8	RPL8	1	$3.84e^{-053}$	6	$4.00e^{-054}$	$2.00e^{-26}$
	RPL9	RPL9	RPL9			6	$8.00e^{-55}$	$1.00e^{-38}$
	RPL10	RPL10	RPL10	3	$1.88e^{-084}$	5	$4.00e^{-088}$	$2.00e^{-46}$
	RPL10A	RPL10A	RPL10A			4	$6.00e^{-44}$	$9.00e^{-22}$
	RPL11	RPL11	RPL11	2	$1.79e^{-070}$	9	$5.00e^{-077}$	$5.00e^{-49}$
	RPL12	RPL12	RPL12	1	$8.10e^{-060}$	8	$9.00e^{-060}$	$3.00e^{-54}$
	RPL13	RPL13	RPL13			6	$4.00e^{-62}$	$2.00e^{-29}$
	RPL13A	RPL13A	RPL13A			7	$9.00e^{-59}$	$8.00e^{-14}$
	RPL14	RPL14	RPL14			6	$2.00e^{-26}$	$2.00e^{-12}$
	RPL15	RPL15	RPL15	2	$4.72e^{-080}$	3	$1.00e^{-054}$	$3.00e^{-32}$
	RPL17	RPL17	RPL17	1	$3.42e^{-48}$	6	$6.00e^{-63}$	$3.00e^{-28}$
	RPL18	RPL18	RPL18			4	$5.00e^{-48}$	$1.00e^{-39}$
	RPL18A	RPL18A	RPL18A			9	$7.00e^{-54}$	$6.00e^{-26}$
	RPL19	RPL19	RPL19			10	$1.00e^{-46}$	$3.00e^{-18}$
	RPL21	RPL21	RPL21	4	$1.00e^{-069}$	4	$2.00e^{-074}$	$9.00e^{-43}$
	RPL22	RPL22	RPL22	2	$2.65e^{-021}$	6	$3.00e^{-019}$	$8.00e^{-16}$
	RPL23	RPL23	RPL23	3	$9.76e^{-047}$	13	$3.00e^{-053}$	$3.00e^{-21}$
	RPL23A	RPL23A	RPL23A	3	$4.34e^{-041}$	3	$6.00e^{-039}$	$1.00e^{-16}$
	RPL24	RPL24	RPL24			9	$2.00e^{-22}$	$4.00e^{-10}$
	RPL26	RPL26	RPL26	2	$4.58e^{-055}$	12	$8.00e^{-058}$	$3.00e^{-34}$

Table S4. Cont.

				ML and AP samples		DinoEST*		
Type	Eukaryotes	Humans	*Plasmodium falciparum*	Clone no.	BLASTX NR min. *E* value	Clone no.	TBLASTN min. *E* value	TBLASTN max. *E* value
	RPL27	RPL27				4	$2.00e^{-24}$	$3.00e^{-11}$
	RPL27A	RPL27A	RPL27A	2	$4.84e^{-051}$	5	$3.00e^{-046}$	$2.00e^{-11}$
	RPL28	RPL28		2	$2.94e^{-008}$	3	$1.00e^{-027}$	$2.00e^{-23}$
	RPL29	RPL29	RPL29	3	$3.93e^{-013}$	2	$1.00e^{-004}$	$4.00e^{-03}$
	RPL30	RPL30	RPL30	2	$9.77e^{-040}$	3	$1.00e^{-049}$	$5.00e^{-38}$
	RPL31	RPL31	RPL31	3	$3.18e^{-037}$	5	$1.00e^{-036}$	$3.00e^{-16}$
	RPL32	RPL32	RPL32	1	$1.02e^{-055}$	4	$6.00e^{-058}$	$2.00e^{-32}$
	RPL34	RPL34	RPL34	3	$1.35e^{-034}$	11	$8.00e^{-043}$	$4.00e^{-32}$
	RPL35	RPL35	RPL35	1	$1.76e^{-041}$	9	$1.00e^{-051}$	$2.00e^{-30}$
	RPL35A	RPL35A	RPL35A	1	$5.88e^{-036}$	7	$3.00e^{-041}$	$2.00e^{-18}$
	RPL36	RPL36	RPL36	2	$2.06e^{-022}$	4	$4.00e^{-036}$	$1.00e^{-25}$
	RPL36A	RPL36A	RPL36A	2	$2.14e^{-043}$	9	$6.00e^{-026}$	$1.00e^{-06}$
	RPL37	RPL37	RPL37[‡] XM_002808716.1	1	$4.40e^{-025}$	1	$4.40e^{-025}$	$4.40e^{-025}$
	RPL37A	RPL37A	RPL37A	2	$2.70e^{-030}$	3	$9.00e^{-030}$	$1.00e^{-26}$
	RPL38	RPL38	RPL38	2	$1.22e^{-022}$	3	$3.00e^{-032}$	$5.00e^{-26}$
	RPL39	RPL39	RPL39	2	$3.51e^{-014}$	8	$4.00e^{-021}$	$4.00e^{-11}$
	RPL40	RPL40	RPL40			3	$1.00e^{-24}$	$1.00e^{-15}$
	RPL41	RPL41	RPL41	21	$1.40e^{-1}$	20	$4.00e^{-6}$	1.80E0
	RPLP0	RPLP0	RPLP0			6	$1.00e^{-65}$	$3.00e^{-10}$
	RPLP1	RPLP1	RPLP1	1	$2.74e^{-011}$	7	$1.00e^{-017}$	$6.00e^{-11}$
	RPLP2	RPLP2	RPLP2			4	$2.00e^{-16}$	$6.00e^{-11}$
	RPLP3[†]							
	ubiquitin-40S RP s27a fusion protein			1	$7.85e^{-024}$	8	$6.00e^{-042}$	$2.00e^{-22}$
	ubiquitin a-52 residue 60S RP L40 fusion product 1			4	$9.54e^{-064}$	2	$1.00e^{-069}$	$5.00e^{-68}$

Our analysis led to recognition (annotation) of the RPs in DinoEST; their GenBank accession numbers are listed below.* Yellow shading indicates using human RPs as query to TBLASTX against DinoEST. Red shading indicates using e-cDNA RPs as query to TBLASTX against DinoEST.

*GenBank accession numbers are shown below; for each RP, only the numbers of four sequences with the lowest *E* values are listed if there are more than four ESTs for that RP. **RPSA**: FE864067, EX461873, BP743535, FE864066; **RPS2**: EC162856, CK431500, EC152673, EC151729; **RPS3**: FE865686, EC160912, FE866030, CK784647; **RPS3A**: EX455617, CF066398, CF947809, EC156761; **RPS4**: CK786168, EC158151, EH036413, EH036412; **RPS5**: EX457652, EX463114, CK784712, GH268618; **RPS6**: GH269191, EC160198, DT386052, EC159409; **RPS7**: CK432698, CK783935, GH268589, BP743274; **RPS8**: EC160948, DW521132, GH268872, FE866078; **RPS9**: EC158991, EC156985, EC158218, BP742809; **RPS10**: CK783051; **RPS11**: DT385176, DT384597, EC154239, DT383171; **RPS12**: BP743751, CV554530, CK784123, CK432343; **RPS13**: CK782830, EC158941, CF948301, GH268607; **RPS14**: BP743861, CF947800, CK783890, CK431919; **RPS15**: CV554514, BP743080, CF947222, CK433056; **RPS15A**: EC156350, GH269011, CK431507, CF774661; **RPS16**: BP742940; **RPS17**: GH268571, GH268763, CK433224, CK785088; **RPS18**: BP743927, CK785635, CK432110, CK783557; **RPS19**: BP743382, EC162454, FK837667, FK838016; **RPS20**: GH269372, GH268829, EC156542, EC156167; **RPS21**: GH268630; **RPS23**: CF774669, CF774806, CF774847, CK433302; **RPS24**: CF947421, CF774746, EC151791, EC151847; **RPS25**: CK783795, EC163406, FK840398, FK851840; **RPS26**: EC152487, CK783891, GH268590, GH268581; **RPS27**: CK786492, GH268908, GH268622, CF067408; **RPS27A**: DT381620, FE537684, FE537685, DT380994; **RPS28**: GH269315, GH268787, GH269153, GH268848; **RPS29**: BP742738, GH268753, GH268762, GH268702; **RPS30**: CX769323, GH268588; **RPL3**: GH269008, EX956894, EX461586, EC160738; **RPL4**: EH037153, EX463676, EX457268, EX457915; **RPL5**: FE865567, CO061119, EX458933, EX459366; **RPL6**: CF948038, GH269328; **RPL7**: CF947136, EH037881, CF065757, EX974297; **RPL7A**: CO063265, FK838432, BP743582, DT383545; **RPL8**: DT386043, DT386057, DT385059, CO062061; **RPL9**: CO062246, GH268886, GH268796, CK784747; **RPL10**: EC161569, CF064579, CK783127, FE865570; **RPL10A**: BP742861, EX459988, CK785294, EC158490; **RPL11**: GH268621, GH268610, CV553999, GH268975; **RPL12**: BP742194, EX460551, EX461930, EX463061; **RPL13**: EH036222, EH036221, EH036220, GH268718; **RPL13A**: CF774794, EX457703, CV554811, GH269151; **RPL14**: EX458152, EC151394, GH268754, GH268701; **RPL15**: EH037984, CF751928, CX769720; **RPL17**: CF065070, EC159932, CK433848, GH268723; **RPL18**: CK784947, GH268606, GH268613, EC153742; **RPL18A**: FE538803, FE538804, CX769516, EC154473; **RPL19**: CF774731, GH268585, GH268599, CK784098; **RPL21**: EC154428, EX973439, CF948266, GH268694; **RPL22**: GH270475, GH268766, GH268625, GH268611; **RPL23**: CK432402, CF774850, CK785550, CF948359; **RPL23A**: FK848709, GH268600, DT383120; **RPL24**: CK433533, CK784248, GH268780, GH268865; **RPL26**: GH270489, GH269015, EX959412, EX959413; **RPL27**: CK785865, EC152973, CK786415, CF948032; **RPL27A**: EC154573, FE866413, CF774638, BP742244; **RPL28**: GH269020, CV554360, CK782502; **RPL29**: EC152546, BP742891; **RPL30**: CK784775, EC153975, GH268583; **RPL31**: EC153462, EC153222, CK432491, CK432500; **RPL32**: BP742874, CK433733, GH268656, GH268582; **RPL34**: CK783091, GH269113, GH268839, EX872312; **RPL35**: EX463411, EC152100, DT382207, DT381939; **RPL35A**: GH269005, EX962215;EX962216, CK433240; **RPL36**: DT383609, DT381630, DT381982, DT382489; **RPL36A**: GH268938, EC155427, EC150961, CK782483; **RPL37**: HQ110606; **RPL37A**: GH268817, CK782481, CK783858; **RPL38**: BP742980, DT382039, DT381465; **RPL39**: BP744199, GH268893, GH268604, GH268608; **RPL40**: CK784763, DT381149, DT380194; **RPL41**: GW795931, EX969058, GH269000, DQ864954; **RPLP0**: EX865562, EX865561, EX462251, GH269218; **RPLP1**: GH268619, BP742916, EX878504, CK433864; **RPLP2**: FE864820, CK433635, CF774573, CV554102; **ubiquitin-RPS27a fusion protein**: EC159986, GH268901, EC155299, GH269319; **ubiquitin-RPL40 fusion product**: BP744060, CV554507.

[†] Only documented in plants.

[‡] Not listed as existing in *Plasmodium falciparum* in the RP database (http://ribosome.med.miyazaki-u.ac.jp/) but is in GenBank.