Supplemental Information

Auxin's origin: do PILS hold the key?

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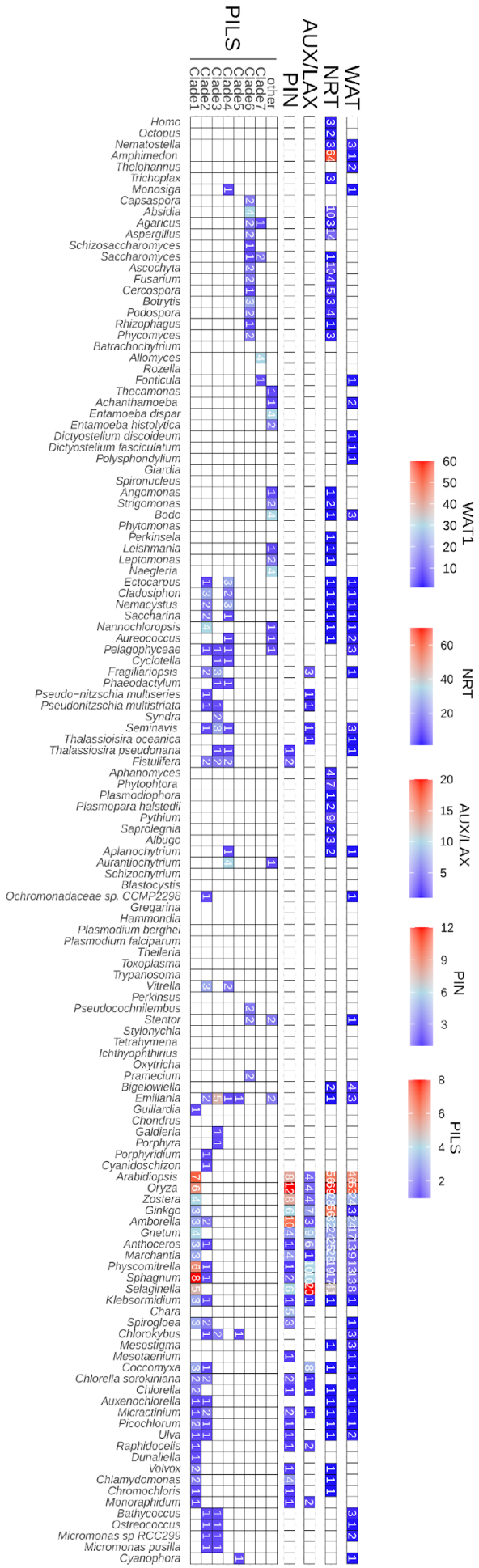
Inventory of supplementary items

Figure S1, related to Key Figure 1. Detailed version of the transporter family presence of Key Figure 1.
Figure S2, related to Figure 2 and 3. Overview of screening of reviewed references and databases.
Table S1, related to Key Figure 1. List with genomes included, url and/or bibliographic reference.
Table S2, related to Figure 2. List of identifiers of bacterial COG0679 genes included.
Table S3, related to Figure 2. Identifiers of PIN and PILS hits together with their relation to COG0679 or other EggNOG v5.0 orthology groups.
Table S4, related to Figure 2-3. Phylogenetic trees represented in newick format and with identifiers.

Figure S1, related to Key Figure 1. Expanded version of the heatmap of figure 1 including number of hits per PILS included reviewed genome. PILS transporters can be found in almost all major groups of the eukaryotes and have been ordered in different clades (see Figure 2A). The heatmap depicts the number of found homologs per clade. Above, color legends for the heatmap.



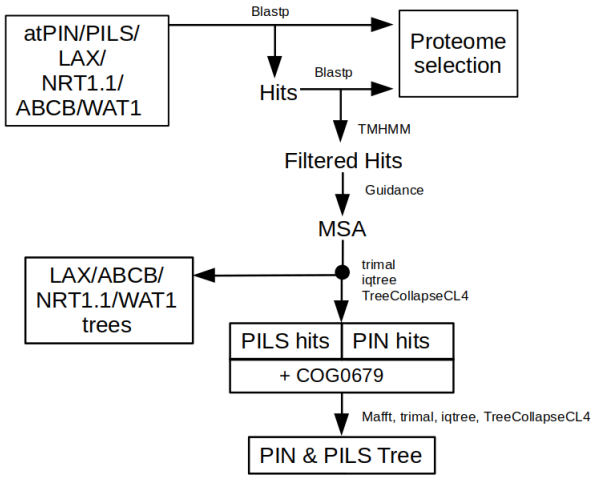


Figure S2, related to Figure 2 and 3. Schematic representation of the identification of putative transporter homologs and phylogenetic analysis. *Arabidopsis* transporters were used as query (blastp -evalue 10E10, version 2.2.29+) and resulting hits were blasted back to the same genome selection (including *Arabidopsis*) (Table S1). Resulting hits where filtered based on number of transmembrane domains using the TMHMM online tool (http://www.cbs.dtu.dk/services/TMHMM/): min. 5, max. 12 domains (PIN, PILS, LAX, ABCB hits), min. 8 and max. 13 (NRT hits) and min. 10 and max. 13 (WAT1 hits). Alignments were produced using Guidance v2.0.2 [S1] implementing MAFFT with seqCutoff option 0.4 and 0.5 progressively. Resulting multiple sequence alignment were aligned using iqtree (v1.6.7) (-st AA -m MFP -bb 1000 -alrt 1000 -bnni -nt AUTO) and TreeCollapseCL4.jar (http://emmahodcroft.com/TreeCollapseCL.html). PILS and PIN putative homologs identified were realigned together with a random subselection of COG0679 bacterial proteins and three putative PIN homologs according to literature MdcF, MleP, MJ1031 (Table S2) using Mafft [S2].

Table S1, related to Key Figure 1. Genomes selected from large Eukaryotic clades, included in this screen. The first column denotes the species, genus (or strain name). Asterisks denote which genomes were included for a smaller genome selection for ABCBs. The second column denotes the source database. Third column denotes the associated reference if available.

Taxon	Source	Ref.
Anthoceros angustus	https://datadryad.org/stash/dataset/doi:10.5061/dryad.msbcc2ftv	[S3]
Pythium ultimum	https://protists.ensembl.org/Pythium_ultimum/Info/Index	[S4]
Raphidocelis subcapitata NIES-35	https://www.ncbi.nlm.nih.gov/Traces/wgs/BDRX01?display=contigs	[S5]
Rhizophagus	https://genome.jgi.doe.gov/Gloin1/Gloin1.home.html	[S6]
Rozella allomycis	https://mycocosm.jgi.doe.gov/Rozal1_1/Rozal1_1.home.html	[S7]
Saccharina japonica	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S8]
*Saccharomyces cerevisiae v64**	http://sgd-archive.yeastgenome.org/sequence/S288C_reference/genome_releases/	[S9]
Saprolegnia parasitica CBS 223.65	https://phycocosm.jgi.doe.gov/Sappar1/Sappar1.home.html	[S10]
Schizosaccharomyces	https://www.pombase.org/downloads/protein-datasets	[S11]
Selaginella moellendorffii v1.0	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S12]
Seminavis	https://bioinformatics.psb.ugent.be/orcae/overview/Semro	[S13]
Sphagnum	https://phytozome-next.jgi.doe.gov/info/Sfallax_v1_1	[S14]
Mesotaenium	https://figshare.com/articles/dataset/Genomes_of_subaerial_Zygnematophyceae_provide_insights_into_land_plant_evolution/9911876/1	[S15]
Spirogloea	https://figshare.com/articles/dataset/Genomes_of_subaerial_Zygnematophyceae_provide_insights_into_land_plant_evolution/9911876/1	[S15]
Spironucleus	https://protists.ensembl.org/Spironucleus_salmonicida_gca_000497125/Info/Index	[S16]
Stentor coereuleus	https://protists.ensembl.org/Stentor_coeruleus_gca_001970955/Info/Index	[S17]
Stylonychia	http://stylo.ciliate.org/index.php/home/downloads	[S18]
Syndra	http://www.lin.irk.ru/sacus/index.php?r=site/page&view=downloads&lang=en	[S19]
Tetrahymena thermophila SB210	https://www.ncbi.nlm.nih.gov/genome/?term=txid5911[orgn]	[S20]
Thalassiosira oceanica CCMP1005	https://phycocosm.jgi.doe.gov/Thaoce1	[S21]
*Thalassiosira pseudonana**	https://mycocosm.jgi.doe.gov/Thaps3/Thaps3.info.html	[S22]
Theileria annulata	https://www.ncbi.nlm.nih.gov/genome/?term=txid5874[orgn]	[S23]
Thelohanellus kitauei	https://metazoa.ensembl.org/Thelohanellus_kitauei/Info/Index	[S24]
Toxoplasma gondii	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S25]
Trichoplax adhaerens	https://metazoa.ensembl.org/Trichoplax_adhaerens/Info/Index	[S26]
Trypanosoma brucei	https://protists.ensembl.org/Trypanosoma_brucei/Info/Index	[S27]
*Ulva mutabilis**	https://bioinformatics.psb.ugent.be/orcae/overview/Ulvmu	[S28]
Vitrella brassicaformis CCMP3155	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S29]
Volvox carteri	https://phycocosm.jgi.doe.gov/Volca2_1/Volca2_1.home.html	[S30]
*Arabidopsis**	https://www.arabidopsis.org/download_files/Proteins/TAIR10_protein_lists/TAIR10_pep_20101214	[S31]
Zostera marina	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Zmarina	[S32]
Ascochyta	https://mycocosm.jgi.doe.gov/Ascra1/Ascra1.home.html	[S33]
Aspergillus	https://fungi.ensembl.org/Aspergillus_oryzae/Info/Index	[S34]
Aurantiochytrium limacinum	https://genome.jgi.doe.gov/portal/Aurli1/Aurli1.download.html	[S35]
Aureococcus	https://phycocosm.jgi.doe.gov/Auran1/Auran1.home.html	[S36]
Auxenochlorella protothecoides	https://phycocosm.jgi.doe.gov/Auxeprot1/Auxeprot1.home.html	[S37]
Bathycoccus	https://bioinformatics.psb.ugent.be/gdb/bathycoccus/	[S38]
Bigelowiella	https://phycocosm.jgi.doe.gov/Bigna1/Bigna1.home.html	[S39]
Guillardia	https://phycocosm.jgi.doe.gov/Guith1/Guith1.home.html	[S39]
Blastocystis	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S40]
Bodo	ftp://ftp.sanger.ac.uk/pub/pathogens/Bodo/saltans	[S41]
Botrytis	http://fungi.ensembl.org/Botrytis_cinerea/Info/Index	[S42]
Capsaspora	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S43]
Cercospora beticola	https://bioinformatics.psb.ugent.be/gdb/cercospora/	[S44]
*Chara**	https://plants.ensembl.org/Chara_braunii/Info/Index	[S45]
*Chlamydomona**	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii	[S46]
*Chlorella**	https://phycocosm.jgi.doe.gov/ChlNC64A_1/ChlNC64A_1.home.html	[S47]
Achanthamoeba	https://protists.ensembl.org/Acanthamoeba_castellanii_str_neff_gca_000313135/Info/Index	[S48]
Chlorella sorokiniana	ftp://ftp.ncbi.nlm.nih.gov/genomes/genbank/plant/Chlorella_sorokiniana/latest_assembly_versions/GCA_002245835.2_Chlorella_sorokiniana_2.0	[S49]
Micractinium conductrix	https://www.ncbi.nlm.nih.gov/genome/56073	[S49]
Chlorokybus	https://phycocosm.jgi.doe.gov/Chlat1/Chlat1.home.html	[S50]
Mesostigma	https://www.ncbi.nlm.nih.gov/genome/?term=RHPH00000000	[S50]
*Chondrus**	https://plants.ensembl.org/Chondrus_crispus/Info/Index	[S51]
Chromochloris zofingiensis	https://phycocosm.jgi.doe.gov/Chrzof1	[S52]

Cladosiphon	https://marinegenomics.oist.jp/algae/viewer/download?project_id=53	[S53]
Coccomyxa	https://phycocosm.jgi.doe.gov/Coc_C169_1	[S54]
*Cyanidoschizon**	https://plants.ensembl.org/Cyanidioschyzon_merolae/Info/Index	[S55]
Galdieria	https://www.ncbi.nlm.nih.gov/assembly/GCF_000341285.1/	[S55]
Cyanophora	https://phycocosm.jgi.doe.gov/Cyapar1/Cyapar1.home.html	[S56]
Cyclotella	https://bioinformatics.psb.ugent.be/plaza/versions/plaza_diatoms_01/organism/view/Cyclotella%2Bcryptica	[S57]
Dictyostelium	https://www.ncbi.nlm.nih.gov/assembly/GCF_000004695.1/	[S58]
Agaricus	https://mycocosm.jgi.doe.gov/Agabi_varbur_1/Agabi_varbur_1.home.html	[S59]
Dictyostelium	https://www.ncbi.nlm.nih.gov/genome/?term=txid261658[Organism:exp]	[S60]
Polysphondylium	http://genomes.dictybase.org/pallidum	[S60]
Dunaliella	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S61]
*Ectocarpus**	https://bioinformatics.psb.ugent.be/orcae/overview/EctsiV2	[S62]
*Emiliania**	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S63]
Entamoeba histolytica	https://www.ncbi.nlm.nih.gov/genome/27?genome_assembly_id=22614	[S64]
Fistulifera	ncbi.nlm.nih.gov/genome/?term=txid1519565[Organism:noexp]	[S65]
Fragiliariopsis cylindricus	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S66]
Fusarium graminearum	https://fungi.ensembl.org/Fusarium_graminearum/Info/Index	[S67]
Albugo candida	https://rsat01.biologie.ens.fr/rsa-tools/data/genomes/Albugo_candida.ASM107853v1.34/genome/	[S68]
Giardia	https://www.ncbi.nlm.nih.gov/genome/?term=txid5741[Organism:exp]	[S69]
Ginkgo	https://plantcyc.org/content/ginkgocyc-1.0	[S70]
Gnetum	https://datadryad.org/stash/dataset/doi:10.5061/dryad.0vm37	[S71]
*Homo**	https://www.ncbi.nlm.nih.gov/assembly/GCF_000001405.39	[S72]
Ichthyophthirius	https://protists.ensembl.org/Ichthyophthirius_multifiliis_gca_000220395/Info/Index	[S73]
*Klebsormidium**	http://www.plantmorphogenesis.bio.titech.ac.jp/~algae_genome_project/klebsormidium/	[S74]
Leishmania	https://www.ncbi.nlm.nih.gov/assembly/GCF_000002845.2/	[S75]
Leptomonas	https://www.ncbi.nlm.nih.gov/assembly/GCF_001293395.1/	[S76]
*Marchantia**	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Mpolymorpha	[S77]
Micromonas pusilla	https://phycocosm.jgi.doe.gov/MicpuC3v2/MicpuC3v2.home.html	[S78]
Micromonas sp RCC299	https://phycocosm.jgi.doe.gov/MicpuN3v2/MicpuN3v2.home.html	[S78]
Monoraphidum neglectum	https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=Monneg1	[S79]
Monosiga	https://mycocosm.jgi.doe.gov/Monbr1/Monbr1.home.html	[S80]
Amborella	http://plants.ensembl.org/Amborella_trichopoda/Info/Index	[S81]
Naegleria	https://phycocosm.jgi.doe.gov/Naegr1/Naegr1.home.html	[S82]
Nemacystus decipiens Onna-1	https://phycocosm.jgi.doe.gov/Nemde1/Nemde1.home.html	[S83]
Nematostella	https://www.ncbi.nlm.nih.gov/assembly/GCF_000209225.1/	[S84]
Octopus	ftp://ftp.ensemblgenomes.org/pub/release-39/	[S85]
*Oryza**	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Osativa	[S86]
*Ostreococcus tauri RCC4221 v3.0**	https://bioinformatics.psb.ugent.be/orcae/overview/OsttaV2	[S87]
Oxytricha trifallax JRB310	https://phycocosm.jgi.doe.gov/Oxytri1	[S88]
Amphimedon	https://metazoa.ensembl.org/Amphimedon_queenslandica/Info/Index	[S89]
Perkinsela sp ccap 1560	https://protists.ensembl.org/Perkinsela_sp_ccap_1560_4_gca_001235845/Info/Index	[S90]
*Phaeodactylum tricornutum CCAP 1055/1 v2.0**	https://phycocosm.jgi.doe.gov/Phatr2	[S91]
Phycomyces	https://mycocosm.jgi.doe.gov/Phybl2/Phybl2.home.html	[S92]
*Physcomitrella patens**	https://phytozome.jgi.doe.gov/pz/portal.html#!	[S93]
Phytomonas	https://www.ncbi.nlm.nih.gov/assembly/GCA_000582765.1/	[S94]
Phytophthora infestans T30-4	https://www.ncbi.nlm.nih.gov/assembly/GCF_000142945.1/	[S95]
Picochlorum costavermella	https://bioinformatics.psb.ugent.be/orcae/overview/RCC4223	[S96]
Plasmodiophora	https://protists.ensembl.org/Plasmodiophora_brassicae_gca_001049375/Info/Index	[S97]
Plasmodium berghei	https://protists.ensembl.org/Plasmodium_berghei/Info/Index	[S98]
Plasmodium falciparum	https://protists.ensembl.org/Plasmodium_falciparum/Info/Index	[S99]
Plasmopara halstedii	https://protists.ensembl.org/Plasmopara_halstedii_gca_900000015/Info/Index	[S100]
Podospora anserina	https://www.ncbi.nlm.nih.gov/assembly/GCF_000226545.1/	[S101]
*Porphyra**	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Pumbilicalis_er	[S102]
*Porphyridium**	http://cyanophora.rutgers.edu/porphyridium/	[S103]
Paramecium tetraurelia	https://protists.ensembl.org/Paramecium_tetraurelia/Info/Index	[S104]
Pseudocochnilembus	https://protists.ensembl.org/Pseudocohnilembus_persalinus_gca_001447515/Info/Index	[S105]
Pseudonitzschia multistriata	https://protists.ensembl.org/Pseudonitzschia_multistriata/Info/Index	[S106]
Absidia glauca	https://www.ncbi.nlm.nih.gov/genome/?term=txid4829	N/A
Allomyces	https://mycocosm.jgi.doe.gov/Allma1/Allma1.home.html	N/A
Angomonas	https://protists.ensembl.org/Angomonas_deanei_gca_000442575/Info/Index	N/A
Aphanomyces	https://protists.ensembl.org/Aphanomyces_astaci_gca_003546765/Info/Index	N/A
Aplanochytrium kerguelense	https://genome.jgi.doe.gov/Aplke1/Aplke1.home.html	N/A

Batrachochytrium	https://mycocosm.jgi.doe.gov/Batde5/Batde5.home.html	N/A
Entamoeba dispar	https://www.ncbi.nlm.nih.gov/genome/372?genome_assembly_id=28745	N/A
Fonticula	https://protists.ensembl.org/Fonticula_alba_gca_000388065/Info/Index	N/A
Gregarina	https://www.ncbi.nlm.nih.gov/genome/?term=txid110365[Organism:noexp]	N/A
Hammondia	https://www.ncbi.nlm.nih.gov/assembly/GCA_000258005.2	N/A
Nannochloropsis salina CCMP1776	https://phycocosm.jgi.doe.gov/Nangad1	N/A
Ochromonadaceae sp. CCMP2298	https://phycocosm.jgi.doe.gov/Ochro2298_1	N/A
Pelagophyceae sp. CCMP2097 v1.0	https://phycocosm.jgi.doe.gov/Pelago2097_1	N/A
Perkinsus marinus	https://protists.ensembl.org/Perkinsus_marinus_atcc_50983_gca_000006405/Info/Index	N/A
*Pseudo-nitzschia multiseries CLN-47**	https://phycocosm.jgi.doe.gov/Psemu1	N/A
Schizochytrium aggregatum ATCC 28209	https://phycocosm.jgi.doe.gov/Schag1	N/A
Strigomonas	https://www.ncbi.nlm.nih.gov/genome/?term=txid28005[Organism:noexp]	N/A
Thecamonas trahens	https://protists.ensembl.org/Thecamonas_trahens_atcc_50062_gca_000142905/Info/Index	N/A

Table S2, related to Figure 2. Bacterial sequences included in the PIN-PILS tree. Identifiers of randomly selected bacterial representatives from COG0679 gene family acquired from EggNOG v5.0 (http://eggnog5.embl.de/#/app/home) and Uniprot identifiers of three bacterial putative PIN homologs MleP, MdcF and MJ1031.

EggNOG species code	EggNOG ortholog identifier	Species
I. COG0679 genes		
1002672	SAR11G3_00568	*Candidatus Pelagibacter sp. IMCC9063*
1042876	PPS_2852	*Pseudomonas putida S16*
1048834	TC41_0227	*Alicyclobacillus acidocaldarius subsp. acidocaldarius Tc-4-1*
1064535	MELS_1415	*Megasphaera elsdenii DSM 20460*
160492	XF1514	*Xylella fastidiosa 9a5c*
167879	CPS_0767	*Colwellia psychrerythraea 34H*
190486	XAC0191	*Xanthomonas axonopodis pv. citri str. 306*
198628	Dda3937_00369	*Dickeya dadantii 3937*
205922	Pfl01_0831	*Pseudomonas fluorescens Pf0-1*
207954	MED92_06118	*Neptuniibacter caesariensis*
223926	VP1094	*Vibrio parahaemolyticus RIMD 2210633*
244592	SADFL11_2112	*Labrenzia alexandrii DFL-11*
266834	SMc00317	*Sinorhizobium meliloti 1021*
269796	Rru_A0290	*Rhodospirillum rubrum ATCC 11170*
273068	TTE0420	*Thermoanaerobacter tengcongensis MB4*
283643	XP_776050	*Cryptococcus neoformans var. neoformans B 3501A*
289376	THEYE_A0723	*Thermodesulfovibrio yellowstonii DSM 11347*
293614	A1C_03325	*Rickettsia akari str. Hartford*
293826	Amet_0711	*Alkaliphilus metalliredigens QYMF*
314264	ROS217_15460	*Roseovarius sp. 217*
314271	RB2654_15641	*Maritimibacter alkaliphilus HTCC2654*
314608	KT99_17231	*Shewanella benthica KT99*
315456	RF_0679	*Rickettsia felis URRWXCal2*
319795	Dgeo_1082	*Deinococcus geothermalis DSM 11300*
321955	BlinB_010200012487	*Brevibacterium linens BL2*
334413	FMG_1541	*Finegoldia magna ATCC 29328*
338969	Rfer_2655	*Rhodoferax ferrireducens T118*
349521	HCH_06644	*Hahella chejuensis KCTC 2396*
379731	PST_0140	*Pseudomonas stutzeri A1501*
391596	PBAL39_00757	*Pedobacter sp. BAL39*
391597	LMED105_02975	*Limnobacter sp. MED105*
393305	YE0246	*Yersinia enterocolitica subsp. enterocolitica 8081*
395492	Rleg2_1641	*Rhizobium leguminosarum bv. trifolii WSM2304*
395495	Lcho_0325	*Leptothrix cholodnii SP-6*
396588	Tgr7_2040	*Thioalkalivibrio sulfidophilus HL-EbGr7*
403833	Pmob_0540	*Petrotoga mobilis SJ95*
40559	EDN28342	*Botryotinia fuckeliana*
411474	COPEUT_02003	*Coprococcus eutactus ATCC 27759*
420662	Mpe_A2024	*Methylibium petroleiphilum PM1*
439493	PB7211_489	*Candidatus Pelagibacter sp. HTCC7211*
439497	RR11_599	*Ruegeria sp. R11*

446470	Snas_2483	*Stackebrandtia nassauensis DSM 44728*
453591	Igni_1095	*Ignicoccus hospitalis KIN4/I*
4538	ORGLA01G0289900	*Oryza glaberrima*
4577	GRMZM2G112598_P01	*Zea mays*
460265	Mnod_6839	*Methylobacterium nodulans ORS 2060*
469382	Hbor_25260	*Halogeometricum borinquense DSM 11551*
469616	FMAG_00057	*Fusobacterium mortiferum ATCC 9817*
470145	BACCOP_00030	*Bacteroides coprocola DSM 17136*
471881	PROPEN_03934	*Proteus penneri ATCC 35198*
483218	BACPEC_03084	*Bacteroides pectinophilus ATCC 43243*
491952	Mar181_0736	*Marinomonas posidonica IVIA-Po-181*
521460	Athe_1433	*Caldicellulosiruptor bescii DSM 6725*
525318	HMPREF0497_2861	*Lactobacillus buchneri ATCC 11577*
52598	EE36_06333	*Sulfitobacter sp. EE-36*
553219	CAMSH0001_0463	*Campylobacter showae RM3277*
555779	Dthio_PD3840	*Desulfonatronospira thiodismutans ASO3-1*
556268	OFAG_00709	*Oxalobacter formigenes HOxBLS*
563040	Saut_0306	*Sulfurimonas autotrophica DSM 16294*
565653	EGBG_00675	*Enterococcus gallinarum EG2*
565664	EFXG_00544	*Enterococcus faecium C68*
572544	Ilyop_0121	*Ilyobacter polytropus DSM 2926*
575606	HMPREF0525_00848	*Lactobacillus jensenii 27-2-CHN*
575788	VS_II1418	*Vibrio splendidus LGP32*
578458	XP_003036603	*Schizophyllum commune H4 8*
590409	Dd586_2852	*Dickeya dadantii Ech586*
596154	Alide2_4040	*Alicycliphilus denitrificans K601*
610130	Closa_1229	*Clostridium saccharolyticum WM1*
622312	ROSEINA2194_02889	*Roseburia inulinivorans DSM 16841*
638300	HMPREF0198_2207	*Cardiobacterium hominis ATCC 15826*
638302	HMPREF0908_1184	*Selenomonas flueggei ATCC 43531*
640512	BC1003_4811	*Burkholderia sp. CCGE1003*
643562	Daes_0673	*Desulfovibrio aespoeensis Aspo-2*
649754	HMPREF0281_00921	*Corynebacterium ammoniagenes DSM 20306*
652103	Rpdx1_2837	*Rhodopseudomonas palustris DX-1*
657314	CK5_00400	*Ruminococcus obeum A2-162*
658655	HMPREF0988_02644	*Lachnospiraceae bacterium 1_4_56FAA*
666684	AfiDRAFT_2886	*Afipia sp. 1NLS2*
712938	LC40_1023	*Lactobacillus fermentum CECT 5716*
717774	Marme_1450	*Marinomonas mediterranea MMB-1*
717962	CC1_06600	*Coprococcus catus GD/7*
718252	FP2_28820	*Faecalibacterium prausnitzii L2-6*
742740	HMPREF9474_03343	*Clostridium symbiosum WAL-14163*
743718	Isova_0984	*Isoptericola variabilis 225*
745277	Rahaq2_0255	*Rahnella aquatilis CIP 78.65 = ATCC 33071*
756067	MicvaDRAFT_3814	*Microcoleus vaginatus FGP-2*
757424	Hsero_4764	*Herbaspirillum seropedicae SmR1*
759362	KVU_1975	*Ketogulonigenium vulgarum WSH-001*
761193	Runsl_0993	*Runella slithyformis DSM 19594*
768066	HELO_3965	*Halomonas elongata DSM 2581*
864563	HMPREF9166_2243	*Selenomonas sp. oral taxon 149 str. 67H29BP*

864565	HMPREF0379_0583	*Eubacterium yurii subsp. margaretiae ATCC 43715*
873447	SPB_1095	*Streptococcus parauberis NCFD 2020*
903510	vfu_A01279	*Vibrio furnissii NCTC 11218*
904306	HMPREF9192_0499	*Streptococcus vestibularis F0396*
936140	LfarK3_010100000515	*Lactobacillus farciminis KCTC 3681*
941770	LfruK3_010100002189	*Lactobacillus fructivorans KCTC 3543*
941770	LfruK3_010100006753	*Lactobacillus fructivorans KCTC 3543*
187272	Mlg_0636	*Alkalilimnicola ehrlichii MLHE-1*
II. Additional Sequences		
UniprotKB	**Gene (Organism)**	**Submitted name**
Q48797_OENOE	MleP [Oenococcus oeni (Leuconostoc oenos]	AEC family transporter/Malate permease/Putative Malate permease (MleP)
Y1031_METJA	MJ1031 [*Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440)]*	Uncharacterized transporter MJ1031
B5XRA2_KLEP3	MdcF [*Klebsiella pneumoniae (strain 342)]*	Malonate transporter MdcF

Table S3, related to Figure 2. Identifiers of PIN and PILS hits. Annotation using the online tool eggNOG-mapper (http://eggnog-mapper.embl.de/) using default settings [S107] of (I) putative PILS orthologs, (II) putative PIN orthologs and (III) 3 additional bacterial sequences: MleP (*Oenoccoccus oeni, Q48797_OENOE),* MdcF (*Klebsiella pneumoniae, B5XRA2, KLEP3)* and MJ1031 (*Methanococcus jannaschii*, Y1031_METJA). PILS orthologs (I) and the MleP, MdcF, are almost all predicted to be part of the EGGNOG Orthology groups (eggNOG_OGs, 2nd column) COG0679, including all Arabidopsis PILS, SPAC5D6.04 (AEL1) (I - red bold identifiers) and additional bacterial PIN like sequences (III), but not the PIN proteins.

query	Orthology mapping by eggNOG-mapper
I. Putative PILS orthologs	
PILS_Klebsormidium_kfl00099_0040_v1.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Klebsormidium_kfl00379_0030_v1.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Amborella_ERN17141	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Athaliana_AT2G17500.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta,3HSK3@3699|Brassicales
PILS_Athaliana_AT5G65980.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta,3HSK3@3699|Brassicales
PILS_Oryza_LOC_Os09g38210.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Oryza_LOC_Os09g38130.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta,3KQS8@4447|Liliopsida,3IE3H@38820|Poales
PILS_Zostera_Zosma49g00270.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Zostera_Zosma49g00280.1	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Gnetum_TnS000029377t12	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta,44PDC@71274|asterids
PILS_Gnetum_TnS000029377t13	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta,44PDC@71274|asterids
PILS_Gnetum_TnS000029377t14	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Gnetum_TnS000364231t08	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Athaliana_AT1G76530.1	COG0679@1|root,KOG2722@2759|Eukaryota,37QQQ@33090|Viridiplantae
PILS_Athaliana_AT1G76520.1	COG0679@1|root,KOG2722@2759|Eukaryota,37QQQ@33090|Viridiplantae,3GEXC@35493|Streptophyta,3HYQ1@3699|Brassicales
PILS_Athaliana_AT1G20925.1	COG0679@1|root,KOG2722@2759|Eukaryota,37QQQ@33090|Viridiplantae,3GEXC@35493|Streptophyta,3HYQ1@3699|Brassicales
PILS_Oryza_LOC_Os09g31478.1	COG0679@1|root,KOG2722@2759|Eukaryota,37QQQ@33090|Viridiplantae,3G78D@35493|Streptophyta,3KVSY@4447|Liliopsida,3I9R4@38820|Poales
PILS_AANG007573	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Marchantia_Mapoly0055s0125.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Physco_Pp3c7_11130V3.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Sphfalx05G009500.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Selaginella_115659	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Selaginella_117190	COG0679@1|root,KOG2722@2759|Eukaryota,37RGC@33090|Viridiplantae,3GCCN@35493|Streptophyta
PILS_Spirogloea_SM000197S05462	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Spirogloea_SM000051S17517	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta,3KNZ2@4447|Liliopsida,3I2C2@38820|Poales
PILS_Spirogloea_SM000103S09500	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta,3KNZ2@4447|Liliopsida,3I2C2@38820|Poales
PILS_Amborella_ERN00068	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Athaliana_AT1G71090.1	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta,3HXRH@3699|Brassicales
PILS_Oryza_LOC_Os08g09190.1	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta,3KNZ2@4447|Liliopsida,3I2C2@38820|Poales

PILS_Zostera_Zosma100g00060.1	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta,3KNZ2@4447|Liliopsida
PILS_Ginkobiloba_Gb_18659	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Gnetum_TnS000117101t07	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Gnetum_TnS000781647t01	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_AANG013543	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Physco_Pp3c22_21270V3.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Physco_Pp3c19_9720V3.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Sphfalx02G101700.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Sphfalx05G078800.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Selaginella_230605	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Marchantia_Mapoly0092s0043.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta
PILS_Amborella_ERN04282	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Athaliana_AT5G01990.1	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta,3HRXW@3699|Brassicales
PILS_Oryza_LOC_Os01g60230.3	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta,3KMGK@4447|Liliopsida,3I7VQ@38820|Poales
PILS_Oryza_LOC_Os05g40330.1	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta,3KMGK@4447|Liliopsida,3I7VQ@38820|Poales
PILS_Zostera_Zosma74g00300.1	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta,3KMGK@4447|Liliopsida
PILS_Ginkobiloba_Gb_31809	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta,4JF9M@91835|fabids
PILS_Ginkobiloba_Gb_24378	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Gnetum_TnS000018517t03	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Marchantia_Mapoly0134s0020.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Physco_Pp3c15_15840V3.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Physco_Pp3c15_19690V3.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Physco_Pp3c9_19600V3.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Sphfalx05G144100.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Sphfalx01G026000.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Sphfalx01G175300.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Sphfalx02G169400.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Sphfalx07G040800.1.p	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Selaginella_269010	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Selaginella_73552	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_AANG003487	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Klebsormidium_kfl00936_0010_v1.1	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Mesotaenium_ME000056S08403	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Spirogloea_SM000182S03949	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Spirogloea_SM000015S01290	COG0494@1|root,KOG2937@2759|Eukaryota,37NSB@33090|Viridiplantae,3G9I7@35493|Streptophyta
PILS_Spirogloea_SM000128S26228	COG0494@1|root,KOG2937@2759|Eukaryota,37NSB@33090|Viridiplantae,3G9I7@35493|Streptophyta
PILS_Mesotaenium_ME001390S00745	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae,3GBSI@35493|Streptophyta
PILS_Csubellipsoidea_38931	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34N83@3041|Chlorophyta
PILS_Auxenochlorella_XP_011402241.	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae

1	
PILS_ChlorellaSoro_PRW58159.1	29GN1@1|root,2RPUA@2759|Eukaryota,37VVM@33090|Viridiplantae,34HXU@3041|Chlorophyta
PILS_Chlamydomonas_Cre13.g564850.t1.1	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae
PILS_Volvox_jgi|Volca1|98930|fgenesh4_pg.C_scaffold_79000036	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae
PILS_Monoraphidium_jgi|Monneg1|11198|XM_014047829.1	COG0679@1|root,KOG2722@2759|Eukaryota,37M69@33090|Viridiplantae
PILS_Chlamydomonas_Cre16.g680200.t1.1	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34MTE@3041|Chlorophyta
PILS_Volvox_jgi|Volca1|104342|estExt_fgenesh4_pg.C_140220	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34MTE@3041|Chlorophyta
PILS_Chlorella_jgi|ChlNC64A_1|133407|IGS.gm_1_00543	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34MTE@3041|Chlorophyta
PILS_Csubellipsoidea_67572	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34MTE@3041|Chlorophyta
PILS_Csubellipsoidea_67574	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34MTE@3041|Chlorophyta
PILS_Guillardia_jgi|Guith1|111838|au.55_g12940	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Capsaspora_KJE93354	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta
PILS_Capsaspora_KJE94713	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta
PILS_Allomyces_KNE59237	COG0679@1|root,2QU6H@2759|Eukaryota,39H9B@33154|Opisthokonta,3NY4I@4751|Fungi
PILS_Allomyces_KNE58048	COG0679@1|root,2QU6H@2759|Eukaryota,39H9B@33154|Opisthokonta,3NY4I@4751|Fungi
PILS_Allomyces_KNE71529	COG0679@1|root,KOG2722@2759|Eukaryota,39PFJ@33154|Opisthokonta,3Q5SN@4751|Fungi
PILS_Allomyces_KNE57700	COG0679@1|root,KOG2722@2759|Eukaryota,39PFJ@33154|Opisthokonta,3Q5SN@4751|Fungi
PILS_Aureococcus_EGB12673	28JC1@1|root,2QRQZ@2759|Eukaryota
PILS_MicromonasCCMP1545_39353	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34N83@3041|Chlorophyta
PILS_Micromonas_96967	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34N83@3041|Chlorophyta
PILS_Emiliania_EOD08017	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Emiliania_EOD16028	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Cyclotella_g9016.t1	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Thalassiosira_jgi|Thaps3|7134|fgenesh1_pg.C_chr_7000517	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Fistulifera_GAX19290.1	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Fistulifera_GAX10915.1	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Seminavis_Sro518_g158840.1	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Phaeodactylum_jgi|Phatr2|45789|estExt_fgenesh1_pg.C_chr_80105	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Synedra_sac|12104	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Synedra_sac|17824	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Fragiliaropsis_jgi|Fracy1|223799|fgenesh2_pm.1_#_671	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Fragiliaropsis_jgi|Fracy1|257643|fgenesh2_pg.98_#_7	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Pseudonitzchia_multistriata_VEU40983	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Fragiliaropsis_jgi|Fracy1|206533|estExt_Genewise1Plus.C_30320	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_Seminavis_Sro1650_g288720.1	2FJQ5@1|root,2TM5R@2759|Eukaryota,2XCKA@2836|Bacillariophyta
PILS_SAM00224	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,1GVC5@112252|Fungi incertae sedis
PILS_Absidia_SAL95228	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,1GVC5@112252|Fungi incertae sedis
PILS_SAM08242	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,1GVC5@112252|Fungi incertae sedis
PILS_Phycomyces_OAD75472	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,1GVC5@112252|Fungi incertae sedis
PILS_SAM00012	COG0679@1|root,KOG3430@1|root,KOG2722@2759|Eukaryota,KOG3430@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,1GVC5@112252|Fungi incertae sedis
PILS_Phycomyces_OAD80371	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,1GVC5@112252|Fungi incertae sedis
PILS_Agaricus_EKM75343	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3UYY3@5204|Basidiomycota,2255M@155619|Agaricomycetes,3W6EC@5338|Agaricales
PILS_Ascochyta_KZM20306	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,2013I@147541|Dothideomycetes,4KGVB@92860|Pleosporales

PILS_Aspergillus_BAE56068	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,20B0T@147545|Eurotiomycetes,3S504@5042|Eurotiales
PILS_Botrytis_Bcin09p06910.1	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,20XBH@147548|Leotiomycetes
PILS_Podospora_CAP67642	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,214UV@147550|Sordariomycetes,3U4ZP@5139|Sordariales
PILS_Fusarium_FGRAMPH1_01T10577	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,214UV@147550|Sordariomycetes,3TDTV@5125|Hypocreales,1FNYG@110618|Nectriaceae
PILS_Cercospora_CBET3_02731-RA	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,2013I@147541|Dothideomycetes,3MGQ7@451867|Dothideomycetidae
PILS_Saccharomyces_YBR287W	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,3RRRP@4891|Saccharomycetes,3RYCH@4893|Saccharomycetaceae
PILS_Schizosaccharomyces_SPAC5D6.04:pep (AEL1)	COG0679@1|root,KOG2722@2759|Eukaryota,38EXJ@33154|Opisthokonta,3NUHS@4751|Fungi,3QKKD@4890|Ascomycota,3MDMH@451866|Taphrinomycotina
PILS_Rhizophagus_ESA23930	COG0679@1|root,KOG2722@2759|Eukaryota,39WJ5@33154|Opisthokonta,3NW4H@4751|Fungi
PILS_Bathycoccus_Bathy04g02680	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34N83@3041|Chlorophyta
PILS_Ostreococcus_Ot07g03120	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,34N83@3041|Chlorophyta
PILS_Cyanidoschizon_gnl|CMER|CMF138C	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Klebsormidium_kfl00172_0010_v1.1	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Spirogloea_SM000051S17547	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Spirogloea_SM000103S09479	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Sphfalx18G034000.1.p	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Physco_Pp3c17_24070V3.1.p	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Csubellipsoidea_60162	2CYRC@1|root,2S5VV@2759|Eukaryota,37VR8@33090|Viridiplantae,34KYK@3041|Chlorophyta
PILS_Micractinium_PSC67915.1	COG0488@1|root,KOG0062@2759|Eukaryota,37Z0S@33090|Viridiplantae,34KB1@3041|Chlorophyta
PILS_ChlorellaSoro_PRW60648.1	COG0036@1|root,KOG3111@2759|Eukaryota,37HKX@33090|Viridiplantae,34HMW@3041|Chlorophyta
PILS_Emiliania_EOD27484	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Emiliania_EOD21281	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_MicromonasCCMP1545_70242	2CYRC@1|root,2S5VV@2759|Eukaryota,37VR8@33090|Viridiplantae,34KYK@3041|Chlorophyta
PILS_Micromonas_63792	2CYRC@1|root,2S5VV@2759|Eukaryota,37VR8@33090|Viridiplantae,34KYK@3041|Chlorophyta
PILS_Amborella_ERN00008	2CYRC@1|root,2S5VV@2759|Eukaryota,37VR8@33090|Viridiplantae,3GYSI@35493|Streptophyta
PILS_Amborella_ERN05442	2CYRC@1|root,2S5VV@2759|Eukaryota,37VR8@33090|Viridiplantae,3GYSI@35493|Streptophyta
PILS_Bathycoccus_Bathy04g04620	2CYRC@1|root,2S5VV@2759|Eukaryota,37VR8@33090|Viridiplantae,34KYK@3041|Chlorophyta
PILS_Ostreococcus_Ot14g00650	2CYRC@1|root,2S5VV@2759|Eukaryota,37VR8@33090|Viridiplantae,34KYK@3041|Chlorophyta
PILS_Ectocarpus_Ec-15_004200	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Cladosiphon_Cok_S_s227_14826.t2	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Cladosiphon_Cok_S_s227_14826.t1	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Nemacystus_g11065.t1	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Saccharina_SJ00905	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Emiliania_EOD09217	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Emiliania_EOD04670	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Nannochloropsis_EWM26539	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta,3HXRH@3699|Brassicales
PILS_Nannochloropsis_EWM26540	COG0679@1|root,KOG2722@2759|Eukaryota,37HNS@33090|Viridiplantae,3GERD@35493|Streptophyta,3HXRH@3699|Brassicales
PILS_Galdieria_EME29360	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Thecamonas_KNC52281	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Aureococcus_EGB10400	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Emiliania_EOD30775	2E8NN@1|root,2SF47@2759|Eukaryota
PILS_Emiliania_EOD32892	2E8NN@1|root,2SF47@2759|Eukaryota
PILS_Agaricus_EKM77880	COG0679@1|root,KOG2722@2759|Eukaryota,39WJ5@33154|Opisthokonta,3NW4H@4751|Fungi,3V1G2@5204|Basidiomycota,225C7@155619|Agaricomycetes
PILS_Ascochyta_KZM23850	COG0679@1|root,KOG2722@2759|Eukaryota,39WJ5@33154|Opisthokonta,3NW4H@4751|Fungi,3QMUW@4890|Ascomycota,20BVA@147545|Eurotiomycetes,3MRXI@451870|Chaetothyriomycetidae
PILS_Fusarium_FGRAMPH1_01T12863	COG0679@1|root,KOG2722@2759|Eukaryota,39WJ5@33154|Opisthokonta,3NW4H@4751|Fungi,3QMUW@4890|Ascomycota,216A0@147550|Sordariomycetes,3TVYW@5125|Hypocreales,1FRTH@110618|Nectriaceae
PILS_Botrytis_Bcin11p01560.1	COG0679@1|root,KOG2722@2759|Eukaryota,39WJ5@33154|Opisthokonta,3NW4H@4751|Fungi,3QMUW@4890|Ascomycota
PILS_Aspergillus_BAE61412	COG0679@1|root,KOG2722@2759|Eukaryota,39WJ5@33154|Opisthokonta,3NW4H@4751|Fungi,3QMUW@4890|Ascomycota,20BVA@147545|Eurotiomycetes,3SDZ8@5042|Eurotiales

PILS_Botrytis_Bcin01p07400.1	COG0679@1|root,KOG2722@2759|Eukaryota,394XR@33154|Opisthokonta,3P0ZM@4751|Fungi,3RJFS@4890|Ascomycota
PILS_Podospora_CAP70196	COG0679@1|root,KOG2722@2759|Eukaryota,39WJ5@33154|Opisthokonta,3NW4H@4751|Fungi,3QMUW@4890|Ascomycota,216A0@147550|Sordariomycetes,3U8WY@5139|Sordariales
PILS_Paramecium_CAK87763	COG0679@1|root,KOG2722@2759|Eukaryota,3ZEZA@5878|Ciliophora
PILS_Paramecium_CAK76199	COG0679@1|root,KOG2722@2759|Eukaryota,3ZEZA@5878|Ciliophora
PILS_Paramecium_CAK87764	COG0679@1|root,KOG2722@2759|Eukaryota,3ZEZA@5878|Ciliophora
PILS_Entamoeba_EDR26241	COG0679@1|root,KOG2722@2759|Eukaryota,3XCEU@554915|Amoebozoa
PILS_EntamoebaHisto_rna_EHI_048980-1	COG0679@1|root,KOG2722@2759|Eukaryota,3XCEU@554915|Amoebozoa
PILS_Entamoeba_EDR28640	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Entamoeba_EDR21521	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Ectocarpus_Ec-01_003100	2E8NN@1|root,2SF47@2759|Eukaryota
PILS_Ectocarpus_Ec-01_003110	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Cladosiphon_Cok_S_s022_5637.t1	2E8NN@1|root,2SF47@2759|Eukaryota
PILS_Nemacystus_g14742.t1	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Cladosiphon_Cok_S_s022_5636.t1	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Nemacystus_g14743.t2	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Nemacystus_g14743.t1	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Saccharina_SJ05885	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Ectocarpus_Ec-01_003090	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Cyclotella_g23984.t1	29PC8@1|root,2RWPW@2759|Eukaryota,2XDXZ@2836|Bacillariophyta
PILS_Thalassiosira_jgi|Thaps3|1855|fgenesh1_pg.C_chr_1000989	29PC8@1|root,2RWPW@2759|Eukaryota,2XDXZ@2836|Bacillariophyta
PILS_Fistulifera_GAX11742.1	29PC8@1|root,2RWPW@2759|Eukaryota,2XDXZ@2836|Bacillariophyta
PILS_Fistulifera_GAX20810.1	29PC8@1|root,2RWPW@2759|Eukaryota,2XDXZ@2836|Bacillariophyta
PILS_Seminavis_Sro4_g003580.1	29PC8@1|root,2RWPW@2759|Eukaryota,2XDXZ@2836|Bacillariophyta
PILS_Phaeodactylum_jgi|Phatr2|46330|estExt_fgenesh1_pg.C_chr_90376	29PC8@1|root,2RWPW@2759|Eukaryota,2XDXZ@2836|Bacillariophyta
PILS_Angomonas_EPY29695	COG0679@1|root,KOG2722@2759|Eukaryota,3XSZJ@5653|Kinetoplastida
PILS_Strigomonas_EPY29613	COG0679@1|root,KOG2722@2759|Eukaryota,3XSZJ@5653|Kinetoplastida
PILS_Strigomonas_EPY35166	COG0679@1|root,KOG2722@2759|Eukaryota,3XSZJ@5653|Kinetoplastida
PILS_Strigomonas_EPY19136	COG0679@1|root,KOG2722@2759|Eukaryota,3XSZJ@5653|Kinetoplastida
PILS_Leishmania_CAM38259	COG0679@1|root,KOG2722@2759|Eukaryota,3XSZJ@5653|Kinetoplastida
PILS_Leptomonas_KPA82730	COG0679@1|root,KOG2722@2759|Eukaryota,3XSZJ@5653|Kinetoplastida
PILS_Leptomonas_KPA82731	COG0679@1|root,KOG2722@2759|Eukaryota,3XSZJ@5653|Kinetoplastida
PILS_Naegleria_jgi|Naegr1|71014|fgeneshNG_pg.scaffold_43000161	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Naegleria_jgi|Naegr1|75883|fgeneshNG_pg.scaffold_86000050	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Naegleria_jgi|Naegr1|79226|estExt_fgeneshNG_pg.C_160049	COG0679@1|root,KOG2722@2759|Eukaryota
PILS_Agaricus_EKM77471	COG0679@1|root,2QU6H@2759|Eukaryota,39H9B@33154|Opisthokonta,3NY4I@4751|Fungi,3V455@5204|Basidiomycota,225DV@155619|Agaricomycetes,3W5V2@5338|Agaricales
PILS_Saccharomyces_YNL095C	COG0679@1|root,2QU6H@2759|Eukaryota,39H9B@33154|Opisthokonta,3NY4I@4751|Fungi,3QMTD@4890|Ascomycota,3RRSJ@4891|Saccharomycetes,3RZW7@4893|Saccharomycetaceae
PILS_Saccharomyces_YOR092W	COG0679@1|root,2QU6H@2759|Eukaryota,39H9B@33154|Opisthokonta,3NY4I@4751|Fungi,3QMTD@4890|Ascomycota,3RRSJ@4891|Saccharomycetes,3RZW7@4893|Saccharomycetaceae
PILS_Entamoeba_EDR24988	COG0679@1|root,KOG2722@2759|Eukaryota,3X9R9@554915|Amoebozoa
PILS_EntamoebaHisto_rna_EHI_195130-1	COG0679@1|root,KOG2722@2759|Eukaryota,3X9R9@554915|Amoebozoa
II. Putative PIN orthologs	
PIN_Klebsormidium_kfl00071_0010_v1.1	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3KY9F@4447|Liliopsida,3IABS@38820|Poales
PIN_Amborella_ERN07440	28J8N@1|root,2QV64@2759|Eukaryota,37IVN@33090|Viridiplantae,3GB79@35493|Streptophyta
PIN_Amborella_ERM99121	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta
PIN_Amborella_ERN11331	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Ginkobiloba_Gb_29191	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Ginkobiloba_Gb_02144	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Ginkobiloba_Gb_06199	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta

PIN_Ginkobiloba_Gb_37787	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta
PIN_Gnetum_TnS000252569t03	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Oryza_LOC_Os11g04190.1	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta,3K VRP@4447|Liliopsida,3IE76@38820|Poales
PIN_Amborella_ERM94122	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta
PIN_Athaliana_AT1G73590.1	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3H MWK@3699|Brassicales
PIN_Oryza_LOC_Os02g50960.1	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3K Y9F@4447|Liliopsida,3IABS@38820|Poales
PIN_Oryza_LOC_Os06g12610.1	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3K Y9F@4447|Liliopsida,3IFMQ@38820|Poales
PIN_Zostera_Zosma111g00450.1	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,44 CMY@71274|asterids
PIN_Zostera_Zosma137g00190.1	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,44 CMY@71274|asterids
PIN_Zostera_Zosma62g00250.1	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta,4J D5Z@91835|fabids
PIN_Athaliana_AT1G70940.1	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Athaliana_AT1G23080.1	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Athaliana_AT2G01420.1	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta,3H W9K@3699|Brassicales
PIN_Oryza_LOC_Os01g51780.1	28J8N@1|root,2QS5F@2759|Eukaryota,37KCH@33090|Viridiplantae,3GF58@35493|Streptophyta,3KX AG@4447|Liliopsida,3I8ZY@38820|Poales
PIN_Marchantia_Mapoly0089s0050.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Selaginella_102666	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta
PIN_Selaginella_234325	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta
PIN_Selaginella_99301	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Amborella_ERN14532	28J8N@1|root,2QS5F@2759|Eukaryota,37KCH@33090|Viridiplantae,3GF58@35493|Streptophyta
PIN_Amborella_ERN14533	28J8N@1|root,2QS5F@2759|Eukaryota,37KCH@33090|Viridiplantae,3GF58@35493|Streptophyta
PIN_Athaliana_AT5G57090.1	28J8N@1|root,2QV64@2759|Eukaryota,37IVN@33090|Viridiplantae,3GB79@35493|Streptophyta,3HN B7@3699|Brassicales
PIN_Oryza_LOC_Os06g44970.1	28J8N@1|root,2QV64@2759|Eukaryota,37IVN@33090|Viridiplantae,3GB79@35493|Streptophyta,3KU 2Z@4447|Liliopsida,3I9U4@38820|Poales
PIN_Zostera_Zosma10g01540.1	28J8N@1|root,2QV64@2759|Eukaryota,37IVN@33090|Viridiplantae,3GB79@35493|Streptophyta,3KU 2Z@4447|Liliopsida,3I9U4@38820|Poales
PIN_Gnetum_TnS000894841t01	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta,4JIG 0@91835|fabids
PIN_Gnetum_TnS000586077t02	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta,4JIG 0@91835|fabids
PIN_AANG008386	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Amborella_ERN10025	28J8N@1|root,2QU8F@2759|Eukaryota,37S7B@33090|Viridiplantae,3GD0K@35493|Streptophyta
PIN_Ginkobiloba_Gb_23207	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta,4J D5Z@91835|fabids
PIN_Ginkobiloba_Gb_03217	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta
PIN_Physco_Pp3c24_2970V3.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Physco_Pp3c23_10200V3.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Physco_Pp3c10_24880V3.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Sphfalx01G042100.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Sphfalx01G156500.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Sphfalx02G136600.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Sphfalx16G039900.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Sphfalx19G033400.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta
PIN_Oryza_LOC_Os05g50140.2	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta,3M2 1G@4447|Liliopsida,3IEVZ@38820|Poales
PIN_Athaliana_AT5G15100.1	28J8N@1|root,2QS5F@2759|Eukaryota,37KCH@33090|Viridiplantae,3GF58@35493|Streptophyta,3H N9N@3699|Brassicales
PIN_Zostera_Zosma31g00470.1	28J8N@1|root,2QS5F@2759|Eukaryota,37KCH@33090|Viridiplantae,3GF58@35493|Streptophyta,3KX AG@4447|Liliopsida
PIN_Selaginella_231064	28J8N@1|root,2S7RE@2759|Eukaryota
PIN_Selaginella_268490	28J8N@1|root,2S7RE@2759|Eukaryota
PIN_Selaginella_119024	28J8N@1|root,2S7RE@2759|Eukaryota
PIN_Amborella_ERN14538	28J8N@1|root,2QS5F@2759|Eukaryota,37KCH@33090|Viridiplantae,3GF58@35493|Streptophyta
PIN_Athaliana_AT1G77110.1	28J8N@1|root,2QVQM@2759|Eukaryota,37MZF@33090|Viridiplantae,3GFB3@35493|Streptophyta,3H XRD@3699|Brassicales
PIN_Zostera_Zosma34g00750.1	28J8N@1|root,2QVQM@2759|Eukaryota,37MZF@33090|Viridiplantae,3GFB3@35493|Streptophyta
PIN_Gnetum_TnS000824613t01	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta,4J D5Z@91835|fabids
PIN_Amborella_ERN10021	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta
PIN_Athaliana_AT5G16530.1	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,3H

	R2I@3699|Brassicales
PIN_Oryza_LOC_Os01g69070.1	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,3KQ9D@4447|Liliopsida,3IB09@38820|Poales
PIN_Zostera_Zosma74g00880.1	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,4JFHW@91835|fabids
PIN_Zostera_Zosma74g00860.1	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,4JFHW@91835|fabids
PIN_Oryza_LOC_Os09g32770.1	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,3M30R@4447|Liliopsida,3I2BP@38820|Poales
PIN_Oryza_LOC_Os08g41720.1	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,3M5YT@4447|Liliopsida,3I2EY@38820|Poales
PIN_Oryza_LOC_Os01g45550.1	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta,3KY91@4447|Liliopsida,3I96M@38820|Poales
PIN_Oryza_LOC_Os01g58860.1	28J8N@1|root,2RFRD@2759|Eukaryota,37RUJ@33090|Viridiplantae,3GFB0@35493|Streptophyta,3KYUY@4447|Liliopsida,3I3EI@38820|Poales
PIN_Amborella_ERN14535	28J8N@1|root,2QS5F@2759|Eukaryota,37KCH@33090|Viridiplantae,3GF58@35493|Streptophyta
PIN_Mesotaenium_ME000389S06793	28J8N@1|root,2QS61@2759|Eukaryota,37QRD@33090|Viridiplantae,3GDA5@35493|Streptophyta,3KVRP@4447|Liliopsida,3IE76@38820|Poales
PIN_Spirogloea_SM000203S06137	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3KY9F@4447|Liliopsida
PIN_Spirogloea_SM000326S12431	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3KY9F@4447|Liliopsida
PIN_Spirogloea_SM000025S08435	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3KY9F@4447|Liliopsida
PIN_Sphfalx01G097600.1.p	28J8N@1|root,2QU8F@2759|Eukaryota,37S7B@33090|Viridiplantae,3GD0K@35493|Streptophyta
PIN_Sphfalx01G090900.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta,3M21G@4447|Liliopsida,3IEVZ@38820|Poales
PIN_Physco_Pp3c14_8850V3.1.p	28J8N@1|root,2QU8F@2759|Eukaryota,37S7B@33090|Viridiplantae,3GD0K@35493|Streptophyta
PIN_Marchantia_Mapoly0027s0108.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37IC4@33090|Viridiplantae,3G8Z9@35493|Streptophyta,3KY91@4447|Liliopsida,3I96M@38820|Poales
PIN_Marchantia_Mapoly0027s0111.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,3KY9F@4447|Liliopsida,3IFMQ@38820|Poales
PIN_Marchantia_Mapoly0053s0108.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta
PIN_Marchantia_Mapoly0027s0112.1.p	28J8N@1|root,2QRM7@2759|Eukaryota,37JUJ@33090|Viridiplantae,3GFSN@35493|Streptophyta,4JDBD@91835|fabids
PIN_Oryza_LOC_Os11g02950.1	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,3KQ9D@4447|Liliopsida,3IB09@38820|Poales
PIN_Chara_g29961	28J8N@1|root,2QV64@2759|Eukaryota,37IVN@33090|Viridiplantae,3GB79@35493|Streptophyta
PIN_Chara_g29962	28J8N@1|root,2QS1X@2759|Eukaryota,37HEN@33090|Viridiplantae,3GCG1@35493|Streptophyta,44J2F@71274|asterids
PIN_Chlorella_jgi|ChINC64A_1|137056|IGS.gm_18_00162	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_Micractinium_PSC76620.1	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_Micractinium_PSC76619.1	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_ChlorellaSoro_PRW59649.1	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_ChlorellaSoro_PRW59648.1	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_Picochlorum_NSC_01644	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_Chlamydomonas_Cre10.g448100.t1.2	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_Raphidocelis_GBF97510.1	2CV6T@1|root,2RRER@2759|Eukaryota,38478@33090|Viridiplantae,34NSV@3041|Chlorophyta
PIN_Volvox_jgi|Volca1|88990|fgenesh4_pg.C_scaffold_11000013	2CPYT@1|root,2R38C@2759|Eukaryota,3847W@33090|Viridiplantae,34NVS@3041|Chlorophyta
PIN_Chlamydomonas_Cre17.g710050.t1.1	COG0515@1|root,KOG0192@2759|Eukaryota
PIN_Fistulifera_GAX25221.1	28J8N@1|root,2S7RE@2759|Eukaryota
PIN_Fistulifera_GAX16927.1	28J8N@1|root,2S7RE@2759|Eukaryota
PIN_Thalassiosira_jgi|Thaps3|12050|fgenesh1_pg.C_chr_23000078	28J8N@1|root,2S7RE@2759|Eukaryota
III. Additional sequences	
Q48797_OENOE	COG0679@1|root,COG0679@2|Bacteria,1UY4N@1239|Firmicutes,4HDX5@91061|Bacilli,4AYC9@81850|Leuconostocaceae
Y1031_METJA	COG0679@1|root,arCOG04756@2157|Archaea,2XU4B@28890|Euryarchaeota,23Q5Q@183939|Methanococci
B5XRA2_KLEP3	COG0679@1|root,COG0679@2|Bacteria,1PINE@1224|Proteobacteria,1RS3Z@1236|Gammaproteobacteria

Table S4, related to Figure 2-3. Phylogenetic trees and identifiers represented in newick format. Identifiers are species_identifier except for PIN and PILS sets: PIN_<species>_<identifier> or PILS_<species>_<identifier>.

Content tree	**Related figure**	**Repository**
PILS,PIN and bacterial_COG0679 tree	Figure 2.	10.6084/m9.figshare.15124038
ABCB transporters	Figure 3. ABCB	10.6084/m9.figshare.15124050
AUX/LAX transporters	Figure 3. AUX1/LAX	10.6084/m9.figshare.15124032
NRT1.1 like transporters	Figure 3. SLC15A3-5 (NRT1.1)	10.6084/m9.figshare.15124035
WAT1 like transporters	Figure 3. WAT1	10.6084/m9.figshare.15124047

Supplemental References

S1 Sela, I. *et al.* (2015) GUIDANCE2: Accurate detection of unreliable alignment regions accounting for the uncertainty of multiple parameters. *Nucleic Acids Res.* 43, W7–W14

S2 Katoh, K. and Standley, D.M. (2013) MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. *Mol. Biol. Evol.* 30, 772–780

S3 Zhang, J. *et al.* (2020) The hornwort genome and early land plant evolution. *Nat. Plants* 6, 107–118

S4 Lévesque, C.A. *et al.* (2010) Genome sequence of the necrotrophic plant pathogen *Pythium ultimum* reveals original pathogenicity mechanisms and effector repertoire. *Genome Biol.* 11, R73

S5 Suzuki, S. *et al.* (2018) *Raphidocelis subcapitata* (=*Pseudokirchneriella subcapitata*) provides an insight into genome evolution and environmental adaptations in the Sphaeropleales. *Sci. Rep.* 8, 1–13

S6 Chen, E.C.H. *et al.* (2018) High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*. *New Phytol.* 220, 1161–1171

S7 Ahrendt, S.R. *et al.* (2018) Leveraging single-cell genomics to expand the fungal tree of life. *Nat. Microbiol.* 3, 1417–1428

S8 Ye, N. *et al.* (2015) *Saccharina* genomes provide novel insight into kelp biology. *Nat. Commun.* 6, 6986

S9 Cherry, J.M. *et al.* (2012) *Saccharomyces* Genome Database: The genomics resource of budding yeast. *Nucleic Acids Res.* 40, 700–705

S10 Jiang, R.H.Y. *et al.* (2013) Distinctive expansion of potential virulence genes in the genome of the oomycete fish pathogen *Saprolegnia parasitica*. *PLoS Genet.* 9,

S11 Wood, V. *et al.* (2003) The genome sequence of *Schizosaccharomyces pombe*. *Nature* 421, 94

S12 Banks, J.A. *et al.* (2011) The *Selaginella* genome identifies genetic changes associated with the evolution of vascular plants. *Science.* 332, 960–963

S13 Osuna-Cruz, C.M. *et al.* (2020) The *Seminavis robusta* genome provides insights into the evolutionary adaptations of benthic diatoms. *Nat. Commun.* 11,

S14 Shaw, A.J. *et al.* (2016) *The* Sphagnum *Genome Project. A new model for ecological and evolutionary genomics.*, 78Elsevier Ltd.

S15 Cheng, S. *et al.* (2019) Genomes of Subaerial Zygnematophyceae Provide Insights into Land Plant Evolution. *Cell* 179, 1057-1067.e14

S16 Xu, F. *et al.* (2014) The Genome of Spironucleus salmonicida Highlights a Fish Pathogen Adapted to Fluctuating Environments. *PLoS Genet.* 10,

S17 Slabodnick, M.M. *et al.* (2017) The Macronuclear Genome of Stentor coeruleus Reveals Tiny Introns in a Giant Cell. *Curr. Biol.* 27, 569–575

S18 Aeschlimann, S.H. *et al.* (2014) The draft assembly of the radically organized stylonychia lemnae macronuclear genome. *Genome Biol. Evol.* 6, 1707–1723

S19 Galachyants, Y.P. *et al.* (2015) Sequencing of the complete genome of an araphid pennate diatom Synedra acus subsp. radians from Lake Baikal. *Dokl. Biochem. Biophys.* 461, 84–88

S20 Eisen, J.A. *et al.* (2006) Macronuclear genome sequence of the ciliate Tetrahymena thermophila, a model eukaryote. *PLoS Biol.* 4, 1620–1642

S21 Lommer, M. *et al.* (2012) Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. *Genome Biol.* 13, R66

S22 Armbrust, E. V. (2004) The Genome of the Diatom Thalassiosira Pseudonana: Ecology, Evolution, and Metabolism. *Science (80-.).* 306, 79–86

S23 Pain, A. *et al.* (2005) Genome of the Host-Cell Transforming Parasite Theileria annulata Compared with T. parva. *Science (80-.*

). 309, 131–133

S24 Yang, Y. *et al.* (2014) The genome of the myxosporean Thelohanellus kitauei shows adaptation sto nutrient acquisition within its fish host. *Genome Biol. Evol.* 6, 3182–3198

S25 Kissinger, J.C. *et al.* (2003) ToxoDB: Accessing the Toxoplasma gondii genome. *Nucleic Acids Res.* 31, 234–236

S26 Srivastava, M. *et al.* (2008) The Trichoplax genome and the nature of placozoans. *Nature* 454, 955–960

S27 Berriman, M. *et al.* (2005) The genome of the African trypanosome Trypanosoma brucei. *Science* 309, 416—422

S28 De Clerck, O. *et al.* (2018) Insights into the evolution of Multicellularity from the Sea Lettuce Genome. *Curr. Biol.* 0, 1–13

S29 Woo, Y.H. *et al.* (2015) Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. *Elife* 4, 1–41

S30 Prochnik, S.E. *et al.* (2010) Genomic analysis of organismal complexity in the multicellular green alga Volvox carteri. *Science (80-.).* 329, 223–226

S31 Berardini, T.Z. *et al.* (2015) The arabidopsis information resource: Making and mining the "gold standard" annotated reference plant genome. *Genesis* 53, 474–485

S32 Olsen, J.L. *et al.* (2016) The genome of the seagrass *Zostera marina* reveals angiosperm adaptation to the sea. *Nature* 530, 331–335

S33 Verma, S. *et al.* (2016) Draft genome sequencing and secretome analysis of fungal phytopathogen *Ascochyta rabiei* provides insight into the necrotrophic effector repertoire. *Sci. Rep.* 6, 1–14

S34 Machida, M. *et al.* (2005) Genome sequencing and analysis of *Aspergillus oryzae*. *Nature* 438, 1157–1161

S35 Collier, J. (2009) , Comparative genome sequencing of four Labyrinthulomycete species to provide new insights into their biosynthetic pathways and role in global carbon cycling. .

S36 Gobler, C.J. *et al.* (2011) Niche of harmful alga *Aureococcus anophagefferens* revealed through ecogenomics. *Proc. Natl. Acad. Sci. U. S. A.* 108, 4352–4357

S37 Gao, C. *et al.* (2014) Oil accumulation mechanisms of the oleaginous microalga *Chlorella protothecoides* revealed through its genome, transcriptomes, and proteomes. *BMC Genomics* 15, 1–14

S38 Moreau, H. *et al.* (2012) Gene functionalities and genome structure in *Bathycoccus prasinos* reflect cellular specializations at the base of the green lineage. *Genome Biol.* 13, R74

S39 Curtis, B.A. *et al.* (2012) Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. *Nature* 492, 59–65

S40 Denoeud, F. *et al.* (2011) Genome sequence of the stramenopile *Blastocystis*, a human anaerobic parasite. *Genome Biol.* 12, R29

S41 Jackson, A.P. *et al.* (2008) Insights into the genome sequence of a free-living kinetoplastid: *Bodo saltans* (kinetoplastida: Euglenozoa). *BMC Genomics* 9, 1–11

S42 Amselem, J. *et al.* (2011) Genomic analysis of the necrotrophic fungal pathogens *Sclerotinia sclerotiorum* and *Botrytis cinerea*. *PLoS Genet.* 7,

S43 Suga, H. *et al.* (2013) The *Capsaspora* genome reveals a complex unicellular prehistory of animals. *Nat. Commun.* 4, 1–9

S44 Vaghefi, N. *et al.* (2017) De novo genome assembly of *Cercospora beticola* for microsatellite marker development and validation. *Fungal Ecol.* 26, 125–134

S45 Nishiyama, T. *et al.* (2018) The *Chara* Genome: Secondary complexity and implications for plant terrestrialization. *Cell* 174, 448-464.e24

S46 Merchant, S.S. *et al.* (2007) The *Chlamydomonas* genome reveals the evolution of key animal and plant functions. *Science* 318, 245–50

S47 Blanc, G. *et al.* (2010) The *Chlorella variabilis* NC64A genome reveals adaptation to photosymbiosis, coevolution with viruses, and cryptic sex. *Plant Cell* 22, 2943–2955

S48 Clarke, M. *et al.* (2013) Genome of *Acanthamoeba castellanii* highlights extensive lateral gene transfer and early evolution of

tyrosine kinase signaling. *Genome Biol.* 14,

S49 Arriola, M.B. *et al.* (2018) Genome sequences of *Chlorella sorokiniana* UTEX 1602 and *Micractinium conductrix* SAG 241.80: implications to maltose excretion by a green alga. *Plant J.* 93, 566–586

S50 Wang, S. *et al.* (2020) Genomes of early-diverging streptophyte algae shed light on plant terrestrialization. *Nat. Plants* 6, 95–106

S51 Collén, J. *et al.* (2013) Genome structure and metabolic features in the red seaweed *Chondrus crispus* shed light on evolution of the Archaeplastida. *Proc. Natl. Acad. Sci. U. S. A.* 110, 5247–52

S52 Roth, M.S. *et al.* (2017) Chromosome-level genome assembly and transcriptome of the green alga Chromochloris zofingiensis illuminates astaxanthin production. *Proc. Natl. Acad. Sci. U. S. A.* 114, E4296–E4305

S53 Nishitsuji, K. *et al.* (2016) A draft genome of the brown alga*, Cladosiphon okamuranus*, S-strain : a platform for future studies of 'mozuku' biology. *DNA Res.* 23, 561–570

S54 Blanc, G. *et al.* (2012) The genome of the polar eukaryotic microalga *Coccomyxa subellipsoidea* reveals traits of cold adaptation. *Genome Biol.* 13, R39

S55 Rossoni, A.W. *et al.* (2019) The genomes of polyextremophilic cyanidiales contain 1% horizontally transferred genes with diverse adaptive functions. *Elife* 8, 1–57

S56 Price, D.C. *et al.* (2019) Analysis of an improved *Cyanophora paradoxa* genome assembly. *DNA Res.* 26, 287–299

S57 Traller, J.C. *et al.* (2016) Genome and methylome of the oleaginous diatom *Cyclotella cryptica* reveal genetic flexibility toward a high lipid phenotype. *Biotechnol. Biofuels* 9, 1–20

S58 Eichinger, L. *et al.* (2005) The genome of the social amoeba *Dictyostelium discoideum*. *Nature* 435, 43–57

S59 Morin, E. *et al.* (2012) Genome sequence of the button mushroom *Agaricus bisporus* reveals mechanisms governing adaptation to a humic-rich ecological niche. *Proc. Natl. Acad. Sci. U. S. A.* 109, 17501–17506

S60 Heidel, A.J. *et al.* (2011) Phylogeny-wide analysis of social amoeba genomes highlights ancient origins for complex intercellular communication. *Genome Res.* 21, 1882–1891

S61 Polle, J.E.W. *et al.* (2017) Draft nuclear genome sequence of the halophilic and beta-carotene-accumulating green alga *Dunaliella salina* strain CCAP19/18. *Genome Announc.* 5, 17–19

S62 Cormier, A. *et al.* (2017) Re-annotation, improved large-scale assembly and establishment of a catalogue of noncoding loci for the genome of the model brown alga *Ectocarpus*. *New Phytol.* 214, 219–232

S63 Read, B.A. *et al.* (2013) Pan genome of the phytoplankton Emiliania underpins its global distribution. *Nature* 499, 209–213

S64 Lorenzi, H.A. *et al.* (2010) New assembly, reannotation and analysis of the *Entamoeba histolytica* genome reveal new genomic features and protein content information. *PLoS Negl. Trop. Dis.* 4,

S65 Tanaka, T. *et al.* (2015) Oil accumulation by the oleaginous diatom *Fistulifera solaris* as revealed by the genome and transcriptome. *Plant Cell* 27, 162–176

S66 Mock, T. *et al.* (2017) Evolutionary genomics of the cold-adapted diatom *Fragilariopsis cylindrus*. *Nature* 541, 536–540

S67 King, R. *et al.* (2015) The completed genome sequence of the pathogenic ascomycete fungus *Fusarium graminearum*. *BMC Genomics* 16, 1–21

S68 Links, M.G. *et al.* (2011) De novo sequence assembly of *Albugo candida* reveals a small genome relative to other biotrophic oomycetes. *BMC Genomics* 12, 503

S69 Morrison, H.G. *et al.* (2007) Genomic minimalism in the early diverging intestinal parasite *Giardia lamblia*. *Science* 317, 1921–1926

S70 Guan, R. *et al.* (2016) Draft genome of the living fossil *Ginkgo biloba*. *Gigascience* 5,

S71 Wan, T. *et al.* (2018) A genome for gnetophytes and early evolution of seed plants. *Nat. Plants* 4, 82–89

S72 Lander, E.S. *et al.* (2001) Initial sequencing and analysis of the human genome. *Nature* 412, 565–566

S73 Coyne, R.S. *et al.* (2011) Comparative genomics of the pathogenic ciliate *Ichthyophthirius multifiliis*, its free-living relatives and

a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. *Genome Biol.* 12, R100

S74 Hori, K. *et al.* (2014) *Klebsormidium flaccidum* genome reveals primary factors for plant terrestrial adaptation. *Nat. Commun.* 5, 3978

S75 la Fuente, S. *et al.* (2018) Complete and de novo assembly of the *Leishmania braziliensis* (M2904) genome. *Mem. Inst. Oswaldo Cruz* 114,

S76 Flegontov, P. *et al.* (2016) Genome of *Leptomonas pyrrhocoris*: A high-quality reference for monoxenous trypanosomatids and new insights into evolution of *Leishmania*. *Sci. Rep.* 6, 1–12

S77 Bowman, J.L. *et al.* (2017) Insights into land plant evolution garnered from the *Marchantia polymorpha* Genome. *Cell* 171, 287-304.e15

S78 Worden, A.Z. *et al.* (2009) Green evolution and dynamic adaptations revealed by genomes of the marine picoeukaryotes Micromonas. *Science.* 324, 268–272

S79 Bogen, C. *et al.* (2013) Reconstruction of the lipid metabolism for the microalga *Monoraphidium neglectum* from its genome sequence reveals characteristics suitable for biofuel production. *BMC Genomics* 14,

S80 King, N. *et al.* (2008) The genome of the choanoflagellate *Monosiga brevicollis* and the origin of metazoans. *Nature* 451, 783–788

S81 DePamphilis, C.W. *et al.* (2013) The *Amborella* genome and the evolution of flowering plants. *Science (80-.).* 342,

S82 Fritz-Laylin, L.K. *et al.* (2010) The Genome of *Naegleria gruberi* Illuminates Early Eukaryotic Versatility. *Cell* 140, 631–642

S83 Nishitsuji, K. *et al.* (2019) Draft genome of the brown alga, *Nemacystus decipiens*, Onna-1 strain: Fusion of genes involved in the sulfated fucan biosynthesis pathway. *Sci. Rep.* 9, 1–11

S84 Putnam, N.H. *et al.* (2007) Sea anemone genome reveals ancestral eumetazoan gene repertoire and genomic organization. *Science.* 317, 86–94

S85 Albertin, C.B. *et al.* (2015) The octopus genome and the evolution of cephalopod neural and morphological novelties. *Nature* 524, 220–224

S86 Ouyang, S. *et al.* (2007) The TIGR rice genome annotation resource: improvements and new features. *Nucleic Acids Res.* 35, 8–11

S87 Blanc-Mathieu, R. *et al.* (2014) An improved genome of the model marine alga Ostreococcus tauri unfolds by assessing Illumina de novo assemblies. *BMC Genomics* 15,

S88 Swart, E.C. *et al.* (2013) The *Oxytricha trifallax* macronuclear genome: A complex eukaryotic genome with 16,000 tiny chromosomes. *PLoS Biol.* 11,

S89 Srivastava, M. *et al.* (2010) The *Amphimedon queenslandica* genome and the evolution of animal complexity. *Nature* 466, 720–726

S90 Tanifuji, G. *et al.* (2017) Genome sequencing reveals metabolic and cellular interdependence in an amoeba-kinetoplastid symbiosis. *Sci. Rep.* 7, 1–13

S91 Bowler, C. *et al.* (2008) The *Phaeodactylum* genome reveals the evolutionary history of diatom genomes. *Nature* 456, 239–44

S92 Corrochano, L.M. *et al.* (2016) Expansion of signal Transduction Pathways in Fungi by Extensive Genome Duplication. *Curr. Biol.* 26, 1577–1584

S93 Rensing, S. a *et al.* (2008) The *Physcomitrella* genome reveals evolutionary insights into the conquest of land by plants. *Science.* 319, 64–9

S94 Porcel, B.M. *et al.* (2014) The streamlined genome of *Phytomonas spp*. relative to human pathogenic kinetoplastids reveals a parasite tailored for plants. *PLoS Genet.* 10,

S95 Haas, B.J. *et al.* (2009) Genome sequence and analysis of the Irish potato famine pathogen *Phytophthora infestans*. *Nature* 461, 393–398

S96 Krasovec, M. *et al.* (2018) Genome analyses of the microalga *Picochlorum* provide insights into the evolution of thermotolerance in the green lineage. *Genome Biol. Evol.* 10, 2347–2365

S97 Schwelm, A. *et al.* (2015) The *Plasmodiophora brassicae* genome reveals insights in its life cycle and ancestry of chitin synthases. *Sci. Rep.* 5, 1–12

S98 Hall, N. *et al.* (2005) A comprehensive survey of the *Plasmodium* life cycle by genomic, transcriptomic, and proteomic analyses. *Science* 307, 82—86

S99 Gardner, M.J. *et al.* (2002) Genome sequence of the human malaria parasite *Plasmodium falciparum*. *Nature* 419, 498—511

S100 Sharma, R. *et al.* (2015) Genome analyses of the sunflower pathogen *Plasmopara halstedii* provide insights into effector evolution in downy mildews and *Phytophthora*. *BMC Genomics* 16,

S101 Espagne, E. *et al.* (2008) The genome sequence of the model ascomycete fungus *Podospora anserina*. *Genome Biol.* 9,

S102 Blouin, N.A. *et al.* (2011) *Porphyra*: A marine crop shaped by stress. *Trends Plant Sci.* 16, 29–37

S103 Bhattacharya, D. *et al.* (2013) Genome of the red alga *Porphyridium purpureum*. *Nat. Commun.* 4, 1941

S104 Aury, J.-M. *et al.* (2006) Global trends of whole-genome duplications revealed by the ciliate *Paramecium tetraurelia*. *Nature* 444, 171—178

S105 Wei, W. *et al.* (2018) *Pseudocohnilembus persalinus* genome database - The first genome database of facultative scuticociliatosis pathogenS. *BMC Genomics* 19, 1–6

S106 Basu, S. *et al.* (2017) Finding a partner in the ocean: molecular and evolutionary bases of the response to sexual cues in a planktonic diatom. *New Phytol.* 215, 140–156

S107 Huerta-Cepas, J. *et al.* (2019) EggNOG 5.0: A hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. *Nucleic Acids Res.* 47, D309–D314