Supplemental Material

More than 18,000 effectors in the *Legionella* genus genome provide multiple, independent combinations for replication in human cells

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Figure S9: The type IVB Dot/Icm secretion system is highly conserved whereas the Dot/Icm effectors are very diverse

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Figure S14: The capcity to replicate in human cells seems to have been acquired independently several times during the evolution.

Supplementary Material and Methods

Sequencing and assembly: Strains are listed in **Supplementary Table S1**. For strains sequenced in this study, DNA was extracted (Total DNA Extraction Kit, Sigma) and the *mip* gene was amplified and sequenced as described previously (1) to confirm species identification. *L. nagasikiensis*, *L. santicrucis* and *L. pneumophila* subespecies *fraserii*, were sequenced on an Illumina MiSeq. *L. bozemanii* 94163278 and *L. gormanii* 03/69 were sequenced on the Roche 454 GS-FLX platform with Titanium chemistry (paired-end reads, average insert size 8.9 kb). The reads, (average length of 215 bp), were assembled using Newbler 2.5.3 (Roche/454) into contigs with an average 26x read coverage. The remaining genomes were paired-end sequenced with the Illumina HiSeq (100 bases) and assembled using Velvet followed by an improvement pipeline (ref: PMID 28348874).

Sequence processing and annotation: The total size and GC content was calculated using "infoseq" (EMBOSS package(2). For completely sequenced genomes, plasmids were included in the calculation to avoid bias for those strains where plasmids were not defined. Genes were predicted using AMIGENE (http://www.genoscope.cns.fr/agc/tools/amigene/Form/form.php). For published genomes the published annotation was used. For functional annotation RAST (3) was used.

Pan/Core genome, orthologs and singletons: Orthologous gene reconstruction was done with PanOCT: amino acid percentage identity cutoff 30%, BLAST e-value cutoff 10^{-5}, and minimum percentage match length of subject and query 65% (**Supplementary Table S11**). An additional orthologous table with the same parameters incorporated two outgroups: *Coxiella burnettii* and *Rickettsiella grylli.* For comparisons we calculated orthologs groups also with OrthoMCL (4). In-house scripts were developed for calculating the pan-genome, core genome, unique genes and for the gene accumulation curve.

Phylogenetic reconstruction and evolutionary analysis: Phylogenetic reconstruction was carried out using all *Legionell*a species analyzed but with two outgroup species (*C. burnetii, R. grylli)* or without. Only genes belonging to the core genome with a minimum identity cut off of 50% were selected. Based on this criterion we obtained 707 genes (without outgroups) or 326 genes (with outgroups). The corresponding amino acid sequences were aligned using MUSCLE(5) yielding alignments of 277,694 and 132,336 amino acids, respectively.

Ambiguous regions were removed applying Gblocks (6) with less stringent conditions. The resulting alignments of 232,973 and 113,005 aa, respectively were used to reconstruct phylogenetic trees using RaXML with the model RaxML (PROTGAMMAWAG) (7). Statistical support for the nodes was obtained after 100 bootstrap replicates.

Evolutionary analysis of presence/absence of proteins containing eukaryotic motifs was performed using GLOOME (8) and stochastic mapping. We used a Mixture model that allows both gain and loss probabilities to be different and also a gain/loss ratio that can vary among sites. We chose 4 as the number of rate category, very high optimization level and allowed root frequencies to differ from stationary ones. The probability cutoff for accepting gain/loss events as valid was at least 0.5. For comparisons GLOOME using parsimony with default parameters (same penalty for gain and gene loss) was run.

Protein motifs were detected using the Pfam database (version 30.0) implemented in the Interpro database (version 5.20-59.0)(9). For small GTPase-like proteins detected with Pfam, a second run using NCBI domains to detect specific Rab or Ras or Rho hits was undertaken. Proteins similar to eukaryotic proteins were detected as follows: one *Legionella* protein from each orthologous group from the PanOCT output was selected as representative, which was blasted against the Uniprot eukaryote database. Only proteins blasting against eukaryotes with an e-value 10^{-4} or smaller, a minimum identity of 30% and coverage of at least 65% of the query protein were retained. These 6,809 proteins retained were then blasted against the Uniprot databases containing eukaryotes and prokaryotes. Results were filtered by e-value, coverage and identity as previously described with hits against bacterial genera often associated with amoeba not being taken into account: *Legionella, Fluoribacter, Tatlockia, Coxiella, Rickettsia, Chlamydia, Parachlamydia, Protochlamydia, Amoebophilus, Mycobacterium, Simkania, Waddlia* and *Piscichlamydia.* The *Legionella* proteins with the top hits against eukaryotic organisms or 90% of eukaryotic sequences among the first 25 hits were selected as putative eukaryotic-like proteins.

Phylogenetic analyses of Rab and eukaryotic-like proteins: For each orthologous group, one representative was used for Psiblast (NCBI non-redundant database, up to 500 hits). All significant blast results were recovered. For eukaryotic-like proteins, selected proteins were taken as query for Blastp (NCBI non-redundant database, up to 500 hits). Additionally, significant hits were searched by Blastp against only bacteria, amoeba, eukaryotes and archea. A possible redundancy was reduced using skipredundant (emboss package) and sequences of equal or higher than 90% identity were removed. The obtained proteins were aligned using

MUSCLE(5) and evaluated and cleaned with t-coffee (10). From resulting alignments phylogenetic trees were constructed using FastTree (11) and local support was calculated with the Shimodairea-Hasegawa test. Final editing was carried out with iTOL webtool (12).

Infection assays: THP-1 cell infections were carried out as described previously (13) at an MOI of 10. After 1h of incubation cells were treated with 100µg ml^{-1} gentamycin for 1h and washed with phosphate-buffered saline (PBS, Invitrogen) before incubation with serum-free medium. At 24, 48 and 72h THP-1 cells were lysed with PBS-0.1% TritonX-100. Replication was determined by counting colony-forming units (Cfu) on BCYE agar. Infections were carried out in duplicate or triplicate.

Statistical analysis: To define "replicating" and "non-replicating" species the CFUs obtained for each strain were compared to the *L. pneumophila* Paris reference strain at 24, 48 and 72h. Wilcoxon signed-rank test implemented in the R software was used for statistical significance.

Translocation assays: Selected genes were PCR-amplified, cloned in frame with the beta-lactamase (*blaM*) at the KpnI-XbaI sites of the plasmid pXDC61 (14). The resulting plasmids were electroporated into *L. pneumophila* or *L. longbeachae* strains. THP-1 cells were seeded in 96- well plates at 10^5 cells/well, quadruplicates per condition, and differentiated into adherent macrophage-like cells with 50 ng/ml PMA were infected with stationary-phase *L. pneumophila* and *L. longbeachae* carrying the different *blaM* fusions at MOI of 50 and centrifuged to synchronize the infection. 1h30 after infection cell monolayers were incubated with CCF4-AM (Life Technologies) and 0.1 M Probenecid, at room temperature for another 1h30. For flow cytometrymeasurements cells were washed with PBS and treated with Cell dissociation solution non-enzymatic (Sigma) for 30min at 37^{o}C before FACS analysis. Flow cytometry of a minimum of 10^5 events per sample was performed using a MACSQuant VYB system (Miltenyi Biotec), with excitation at 405 nm (violet) and emission collection with 525/50 (Green) and 450/50 (Blue) filters. Data were analyzed with FlowJo software (LLC). First, to eliminate cell debris, all events were gated using forward scatter (FSC) and side scatter (SSC). FACS gates for green and blue fluorescence were set using the analyzed data from uninfected cells without any treatment or loaded with CCF4-AM. For each strain, quadruplicate samples were analyzed in three independent experiments. For microplate reader translocation assays, Raw264.7 cells were infected for 1h with *L. pneumophila* wild type (*Lp*) or Δ*dotA (Lp*Δ*dotA)* expressing BlaM-effector fusions before adding the BlaM substrate CCF2-AM and translocation determined by measuring fluorescence emission of cleaved CCF2-AM (450 nm) product and substrate (520nm) using an excitation wavelength of 410 nm on a Fluostar Optima microplate reader. BlaM-LtpB was included as positive control and a BlaM-fusion of the *L. pneumophila* housekeeping gene *fabI* as background control.

Supplementary Figure Legends

Figure S1: Distribution of the genes predicted to encode for the biosynthesis of flagella among all *Legionella* species. The different *Legionella* species are represented in columns, the genes encoding for the flagella machinery are represented in rows. Blue squares, orthologous gene is present; yellow squares, orthologous gene is absent.

Figure S2: Phylogenetic analyses of the ergosterol, allinase and caleosin domain in *Legionella* suggest eukaryotic origin. Unrooted tree of *Legionella* **A)** ergosterol, **B)** allinase and **C)** caleosin domain proteins and their homologous recruited by Blastp constructed using likelihood. Local support values are represented on the corresponding branches (only local support of at least 0.7 are shown).

Figure S3: Presence/absence of proteins with small GTPase domains in the 80 *Legionella* strains analyzed in this study. Proteins in the same column are considered to be orthologous. On the top of the column the label of one selected protein belonging to the corresponding orthologous group is indicated. The colour of the square indicates the type of GTPases: blue (Rab domain), orange (Ras domain), pink (Rho domain), green (small GTPases without another specific domain). White squares represent absence of orthologous protein in the corresponding strain. F, F-box domain; U, U-box domain; A, Ankyrin motif.

Figure S4: **Alignment of Ras and Rab proteins of *Legionella* showing that the structural features of these eukaryotic domains are conserved.** Representatives of the different orthologous groups of *Legionella* Ras and Rab proteins were selected to represent the aminoacid sequence of the RabGTPase subfamily based on its HMM profile (Stenmarck and Olkkonen et al. 2001). RabF, Rab-specific residues; RabSF, subfamily-specific motifs; G, guanine-base-binding-motif; PM, phosphate/magnesium-binding motif.

Figure S5: Phylogenetic tree of selected small GTPases from different *Legionella* spp. The same color indicates proteins belonging to the same orthologous group. Proteins with an asterisk are the ones that have been selected for translocation assays.

Figure S6: Phylogenetic tree of sixteen Rab domain containing proteins identified in the genus *Legionella*. Homologues of the different Rab proteins of *Legionella* were recruited by blastp and used for phylogenetic reconstruction using likelihood (FastTree). Local support values are represented with numbers on the corresponding branches. The root of the tree was randomly chosen. The following proteins wre used to recruit homologues : A) *L. birminghamensis* protein Lbir2252; B) *L. gormanii* protein LgoA0634; C) *L. geestiana* protein Lges1860; D) *L. longbeachae* protein Llo2329; E) *L. maceachernii* protein Lma1540; F) *L. gratiana* protein Lgra3435 ; G) *L. massiliensis* protein LmasA1512; H) *L. massiliensis* protein LmasA3690; I) *L. quateirensis* protein Lqua0234; J) *L. quinlivanii* protein Lquin3026; K) *L. spiritensis* protein Lspi0161; L) *L. steigerwaltii* protein Lstei0814; M) *L. steigerwaltii* protein Lstei2185; N) *L. wadsworthii* protein Lwad3214; O) *L. waltersii* protein Lwal3261; P) *L. adelaidensis* protein Lade0491.

Figure S7: Phylogenetic analyses of the eukaryotic like protein LanA0735. Unrooted tree of LanA0735 and its homologues recruited by blastp constructed using likelihood. Local support values are represented on the corresponding branches (only local support of at least 0.7 are shown).

Figure S8: Ratio of gain *vs* loss events per branch for each of the 25 selected types of eukaryotic domains. In blue events that took place in internal branches and in red events that took place in terminal branches of the tree.

Figure S9: The type IVB Dot/Icm secretion system is highly conserved whereas the Dot/Icm effectors are very diverse. **A**) Dot/Icm secretion complex (modified from (15)). Proteins have been colored according to the percentage of the average aminoacid identity among the corresponding orthologous for each Dot/Icm component in the different strains analyzed (red for the most conserved ones to clear yellow for the less conserved ones). Green, IcmR as many *Legionella* species encode proteins with low or no-homology to IcmR from *L. pneumophila*. **B**) Conservation of validated Dot/Icm substrates of *L. pneumophila* strain Philadelphia in the different strains/species analyzed in this study. Blue, an orthologous substrate is present in the corresponding genome; yellow an orthologous protein is absent in the corresponding strain. Red square indicates the different *L. pneumophila* strains where the degree of conservation of the substrates is higher. Red arrows point to substrates that are present in all analyzed strains and that thus constitute the core effectors. **C)** Venn diagram showing the number of members of the different effector groups (ELP; eukaryotic-like protein; EM, protein with eukaryotic domains) and the number of orthologous proteins identified wiyhn all genomes sequenced. *Effectors predicted by the machine learning approach applied by Burstein and colleagues 2016. The summary of the differen orthologous proteins adds up to over 18 000 predicted substrates **D**) Growth accumulation curve representing how the total repertory of predicted effectors in the genus *Legionella* increases each time new genomes are sequenced.

Figure S10: FIR proteins and their predicted functional homologous in the 80 *Legionella* strains analyzed. Shared colour, shared homology due to either orthology or paralogy (based on OrthoMCL results, Table S9); white colour, absence of homologous gene.

Figure S11: Sequence alignment for the regions of FIR proteins that are predicted to interact with IcmQ. Predicted α helices based on JPred4 are indicated as yellow bars. The most hydrophobic residues according to this table are colored red and the most hydrophilic ones are colored blue.

Figure S12: The replication capacity of the different *Legionella* species in THP-1 cells at 24h and 48h. Replication of each strain at the time points 24h and 48h after infection of THP-1 cells is shown. Intracellular replication was determined by recording the number of colony-forming units (CFU) after plating on BCYE agar. *L. pneumophila* Paris was taken as representative of a replicating strain (blue box) and the *L. pneumophila* mutant Δ*dotA* was taking as a representative of non-replicating *Legionella* (red box). **A**) *Legionella* species replicating like or significantly better than *L. pneumophila* Paris at 24h. **B**) Species with no or significantly lower replication capacities than *L. pneumophila* Paris at 24h. **C**) *Legionella* species replicating like or significantly better than *L. pneumophila* Paris at 48h. **D**) Species with no or significantly lower replication capacities than *L. pneumophila* Paris at 48h.

Figure S13. Intracellular replication of 40 different *Legionella* species in THP-1 derived macrophages. *L. pneumophila* strain Paris wild type (wt) and its isogenic Δ*dotA* mutant were used as positive and negative controls, respectively. Intracellular replication for each strain was determined by recording the number of colony-forming units (CFU) through plating on BCYE agar aster 2, 24, 48 and 72 hours of infection. Results are expressed as Log10 ratio

CFU Tn/T0 and each point represents the mean ± standard deviation of two or three independent experiments. The error bars represent the standard deviation.

Figure S14: The capcity to replicate in human cells seems to have been acquired independently several times during the evolution. On the left the phylogeny of the genus *Legionella* established in this study. The first column provides the description of the strains as isolated form clinical cases (Clin) or from the environnement (Env) based on data from the literature. The second column provides information about the capacity of each strain to replicate in THP-1 cells based either on our experiments or on data from the literature.

Supplementary Table S1: *Legionella* strains analyzed in the present study

Species	strain	ATCC	DSMZ	CIP	Isol	Genome sequence	Acc. Number
L. adelaidensis	1762-AUS-E	49625	19888	103645	Env	This study	
L. anisa	WA-316-C3	35292	17627	103870	Cli	This study	
L. anisa	Linanisette				Cli	(17)	NZ_CANP01000001 /56
L. beliardensis	Wilkinson 1407-AL-H	700512	19152	106632	Env	This study	
L. birminghamensis	1407-AL-H	43702	19232	103871	Cli	This study	
L. bozemanii (bozemanae)	WIGA	33217	16523	103872	Cli	This study	
L. bozemanii (bozemanae)	94163278				?	This study	
L. brunensis	441-1	43878	19236	103874	Env	This study	
L. busanensis	BAA518			108685	Env	This study	
L. cherrii	ORW	35252	19213	103842	Env	This study	
L. cincinnatiensis	72-OH-0	43753	19233	103875	Cli	This study	
L. drancourtii (LLAP12)	LLAP12	50991			Env	(18)	NZ_ACUL02000000
L. drozanskii	LLAP1	700990	19890	107644	Env	This study	
L. dumoffii	NY23	33279	17625	103876	Cli	(19)	AGVU00000000
L. dumoffii	TexKL	33343			Cli	(19)	
L. erythra	SE-32A-C8	35303	17644	103843	Env	This study	
L. fairfieldensis	1725-Aus-E	49588		105266	Env	This study	
L. fallonii	LLAP10	700992	19889	107645	Env	(20)	PRJEB7322
L. feeleii	WO-44C	35072	17645	103877	Cli	This study	
L. geestiana	1308	49504		105569	Env	This study	
L. genomospecies	2055-AUS-E	51913		106678	Env	This study	
L. gormanii	LS-13	33297	16241	104724	Cli	This study	
L. gormanii	23801				?	This study	
L. gratiana	Lyon 8420412	49413		105267	Env	This study	
L. gresilensis	Greoux 11D13	700509		106631	Env	This study	
L. hackeliae	Lansing 2	35250	19214	103844	Cli	(20)	PRJEB7321
L. impletisoli	OA1-1		18493		Env	This study	
L. israelensis	Bercovier 4	43119	19235	103879	Env	This study	
L. jamestowniensis	JA-26-G1-E2	35298	19215	103845	Env	This study	
L. jordanis	Gorman BL-540	33623	19212	105268	Cli	This study	
L. lansingensis	1677-MI-H	49751	19556	103542	Cli	This study	
L. LIKE brunensis	W10-070				?	This study	
L. londiniensis	1477	49505		105269	Env	This study	
L. longbeachae	D-4968				Cli	(21)	GCA_000176095.1
L. longbeachae	NSW150				Cli	(22)	FN6501401
L. longbeachae	Long Beach 4	33462		103880T	Cli	(22)	
L. longbeachae	98072				?	(22)	
L. maceachernii	Gorman PX-1-G2-E2	35300	16642		Cli	This study	
L. massiliensis					Env	GCA_0007	GCA_000756695.1

						56695.1	
L. massilensis	LegA	24804	24804		Env	GCA_000756815.1	GCA_000756815.1
L. micdadei	Tatlock	33218	16640	103882	Cli	(20)	PRJEB7312
L. micdadei	02/42				Cli	(20)	SRP047311
L. moravica	316-86	43877	19234	103883	Env	This study	
L. nagasakiensis	JCM 15315	BAA-1557			Cli	This study	
L. nautarum	1224	49506		105270	Env	This study	
L. norrlandica	LEGN	BAA-2678			Env	No publication	
L. oakridgensis	Oak Ridge 10	33761		103884	Env	(23)	NZ_CP004006/7
L. oakridgensis	RV-2-2007				Env	(23)	GCA_000512715.1
L. osnabrueckensis	W05-934-2				?	This study	
L. parisiensis	PF-209C-C2	35299	19216	103847	Cli	This study	
L. pneumophila subsp. *pascullei*	Brown U8W	33737	7515	105570	Env	This study	
L. pneumophila	Paris			107629	Cli	(24)	CR628336
L. pneumophila	Lens			108286	Cli	(24)	C_006369
L. pneumophila	Philadelphia	33152	7513	103854T	Cli	(25)	NC_002942
L. pneumophila	Corby				Cli	(26)	NC_009494
L. pneumophila	Alcoy				Cli	(27)	CP001828
L. pneumophila	130b				Cli	(28)	FR687201
L. pneumophila	Lorraine			108729	Cli	(29)	FQ958210/2
L. pneumophila	HL06041035				Env	(29)	FQ958211
L. pneumophila	570-CO-H				Cli	(30)	CP003192
L. pneumophila	LPE509				Env	(31)	CP003885/6
L. pneumophila	Thunder Bay				Cli	(32)	CP003730
L. pneumophila subsp. *fraseri*	Los Angeles 1	33156		103858	Cli	This study	
L. pneumophila subsp. *fraseri*	Dallas 1E	33216		103859	Env	No publication	NZ_JFIK01000000
L. pneumophila subsp. *fraseri*	Lansing3	35251			Cli	No publication	NZ_JFIG01000000
L. quateirensis	Thacker 1335	49507		105271	Env	This study	
L. quinlivanii	1442-AUS-E	43830		105272	Env	This study	
L. rowbothamii	LLAP6	700991		107646	Env	This study	
L. rubrilucens	WA-270A-C2	35304	11884	103848	Env	This study	
L. sainthelensi	MSH-4	35248	19231	103885	Cli	This study	
L. santicrucis	SC-63-C7	352301	19325	103849	Env	This study	
L. shakespearei	CDC 214	49655	23087	103541	Env		NZ_AREN01000000
L. spiritensis	Bibb HSH-9	35249	19324	103850	Env	This study	
L. steigerwaltii	SC-18-C9	35302		103851	Env	This study	
L. taurinensis	Turin I	700508		106300	Env	This study	
L. tucsonensis	1087-AZ-H	49180	19246	105113	Cli	This study	
L. wadsworthii	81-716	33877		103886	Cli	This study	
L. waltersii	2074-AUS-E	51914		104965	Env	This study	
L. worsleiensis	95/83-1347	49508		105114	Env	This study	
L. yabuuchiae	OA1-2		18492	--	Env	This study	

Supplementary Table S2: Type IV secretion systems* predicted in the genomes analyzed

Species	strain	T4SS[&] typeF	T4SS[&] typeG	T4SS[&] typeI	T4SS[&] typeT
L. adelaidensis	1762-AUS-E	0	1	1	0
L. londiniensis	1477	0	1	1	0
L. yabuuchiae	OA1-2	0	1	1	0
L. impletisoli	OA1-1	1	0	1	1
L. oakridgensis	RV2-2007	2	1	1	1
L. oakridgensis	Oak Ridge 10	1	0	1	0
L. nagasakiensis	JCM 15315	0	0	0	2
L. LIKE brunensis	W10-070	0	0	1	1
L. jordanis	Gorman BL-540	0	2	1	0
L. lansingensis	1677-MI-H	0	0	1	0
L. jamestowniensis	JA-26-G1-E2	1	2	0	1
L. hackeliae	Lansing 2	1	1	0	0
L. brunensis	441-1	0	1	0	0
L. fairfieldensis	1725-Aus-E	0	2	1	0
L. massiliensis		1	1	1	0
L. massilensis	LegA	1	1	1	0
L. drozanskii	LLAP1	1	0	1	0
L. nautarum	1224	1	0	1	1
L. maceachernii	Gorman PX-1-G2-E2	1	2	1	0
L. micdadei	02-42	0	0	1	2
L. micdadei	Tatlock	0	1	1	1
L. feeleii	WO-44C	0	1	1	0
L. beliardensis	Wilkinson 1407-AL-H	1	2	1	0
L. gresilensis	Greoux 11D13	2	1	1	0
L. busanensis	BAA518	2	2	1	0
L. genomospecies	2055-AUS-E	0	1	1	1
L. quinlivanii	1442-AUS-E	1	0	1	1
L. birminghamensis	1407-AL-H	1	1	1	1
L. spiritensis	Bibb HSH-9	0	0	1	2
L. erythra	SE-32A-C8	2	1	1	1
L. rubrilucens	WA-270A-C2	1	2	1	1
L. taurinensis	Turin I	0	1	1	0
L. israelensis	Bercovier 4	0	1	1	1
L. rowbothamii	LLAP6	0	1	1	1
L. drancourtii (LLAP12)	LLAP12	0	3	1	2
L. gratiana	Lyon 8420412	*1*	1	1	1
L. sainthelensi	MSH-4	0	1	1	0
L. longbeachae	Long Beach 4	2	1	1	0
L. longbeachae	D-4968	1	1	1	1
L. longbeachae	NSW150	1	0	1	1
L. longbeachae	98072	1	0	1	0
L. cincinnatiensis	72-OH-0	2	1	1	0

L. santicrucis	SC-63-C7	3	3	1	1
L. dumoffii	TexKL	2	1	1	1
L. dumoffii	NY23	2	1	1	0
L. cherrii	ORW	0	0	1	1
L. steigerwaltii	SC-18-C9	2	0	1	0
L. wadsworthii	81-716	1	0	1	0
L. tucsonensis	1087-AZ-H	0	1	1	0
L. anisa	WA-316-C3	4	2	1	2
L. anisa	Linanisette	2	2	1	2
L. parisiensis	PF-209C-C2	1	1	1	1
L. bozemanii (bozemanae)	WIGA	1	0	1	0
L. bozemanii (bozemanae)	94163278	2	0	1	1
L. gormanii	03-69	2	1	1	1
L. gormanii	LS-13	0	0	1	1
L. fallonii	LLAP10	1	1	0	0
L. shakespearei	CDC 214	0	0	1	0
L. worsleiensis	95/83-1347	1	0	1	0
L. quateirensis	Thacker 1335	2	0	1	2
L. moravica	316-86	0	3	1	1
L. waltersii	2074-AUS-E	0	3	0	1
L. norrlandica	LEGN	0	1	1	1
L. pneumophila	Alcoy	0	1	0	2
L. pneumophila	Corby	0	2	0	2
L. pneumophila	Thunder Bay	1	2	0	0
L. pneumophila	570-CO-H	1	2	0	0
L. pneumophila	LPE509	1	1	0	2
L. pneumophila	Philadelphia	1	1	0	0
L. pneumophila	130b	0	2	0	1
L. pneumophila	Lens	1	1	0	0
L. pneumophila	Lorraine	1	1	0	1
L. pneumophila	Paris	1	2	0	0
L. pneumophila	HL06041035	0	2	0	0
L. pneumophila subsp. *fraseri*	Dallas 1E	1	1	0	0
L. pneumophila subsp. *fraseri*	Los Angeles 1	0	2	0	0
L. pneumophila subsp. *fraseri*	Lansing3	1	1	0	0
L. pneumophila subsp. *pascullei*	Brown U8W	0	1	0	1
L. geestiana	1308	0	1	0	2
L. osnabrueckensis	W0511934-2	1	1	0	1

* All T4SS except the Dot/Icm system

[&]The prediction was based on results by the program CONJscan-T4SSscan (https://galaxy.pasteur.fr/forms::CONJscan-T4SSscan)(16).

Supplementary Table S3: Eukaryotic like domains identified in the *Legionella* proteins analyzed

Interpro number	%Eukaryotic *	Motif name	*Legionella* proteins**
IPR020683	78.20	Ankyrin repeat-containing domain	1134
IPR000719	85.11	Protein kinase domain	519
IPR002110	78.68	Ankyrin repeat	292
IPR000883	94.63	Cytochrome c oxidase, subunit I	164
IPR001806	90.93	Small GTPase superfamily	157
IPR001810	99.38	F-box domain	155
IPR016174	80.45	Di-haem cytochrome, transmembrane	124
IPR001895	99.36	Guanine-nucleotide dissociation stimulator CDC25	105
IPR001128	75.16	Cytochrome P450	105
IPR000407	97.53	Nucleoside phosphatase GDA1/CD39	101
IPR025789	84.04	Histone methylation DOT1	92
IPR001214	90.05	SET domain	86
IPR005798	97,00	Cytochrome b/b6, C-terminal	80
IPR005797	96.79	Cytochrome b/b6, N-terminal	80
IPR008380	94.55	HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase	80
IPR011759	77.56	Cytochrome C oxidase subunit II, transmembrane domain	80
IPR003734	76.18	Protein of unknown function DUF155	80
IPR001611	82.86	Leucine-rich repeat	79
IPR015345	85.19	Cytokinin dehydrogenase 1, FAD/cytokinin binding domain	74
IPR020946	75.02	Flavin monooxygenase-like	70
IPR018108	99.85	Mitochondrial substrate/solute carrier	68
IPR003613	99.39	U box domain	63
IPR001938	97.90	Thaumatin	62
IPR000408	75.61	Regulator of chromosome condensation, RCC1	57
IPR004344	99.33	Tubulin-tyrosine ligase/Tubulin polyglutamylase	50
IPR001171	98.09	Ergosterol biosynthesis ERG4/ERG24	42
IPR001506	90.46	Peptidase M12A, astacin	42
IPR006603	79.94	PQ-loop repeat	42
IPR024518	94.34	Domain of unknown function DUF3421	41
IPR008758	90.40	Peptidase S28	40
IPR000504	95.22	RNA recognition motif domain	39
IPR004119	78.46	Protein of unknown function DUF227	39
IPR002680	88.29	Alternative oxidase	36
IPR000219	99.72	Dbl homology (DH) domain	33
IPR000198	99.15	Rho GTPase-activating protein domain	29
IPR001300	96.60	Peptidase C2, calpain, catalytic domain	29
IPR002909	77.51	IPT domain	28
IPR001245	99.36	Serine-threonine/tyrosine-protein kinase catalytic domain	26

IPR000904	98.92	Sec7 domain	26
IPR002553	99.95	Clathrin/coatomer adaptor, adaptin-like, N-terminal	25
IPR002885	98.48	Pentatricopeptide repeat	25
IPR025749	96.18	Sphingomyelin synthase-like domain	22
IPR000490	89.66	Glycoside hydrolase, family 17	21
IPR000980	99.76	SH2 domain	20
IPR000357	85.77	HEAT	20
IPR005492	98.89	Leucine-rich glioma-inactivated , EPTP repeat	19
IPR009772	97.24	D123	19
IPR022099	96.67	Protein of unknown function DUF3638	19
IPR003653	80.50	Peptidase C48, SUMO/Sentrin/Ubl1	18
IPR001388	99.13	Synaptobrevin	17
IPR001563	86.28	Peptidase S10, serine carboxypeptidase	17
IPR005200	83.64	Glycoside hydrolase, family 81	15
IPR008862	99.49	T-complex 11	14
IPR003323	97.54	Ovarian tumour, otubain	14
IPR013684	91.21	Mitochondrial Rho-like	14
IPR019012	93.82	RNA cap guanine-N2 methyltransferase	12
IPR000668	85.81	Peptidase C1A, papain C-terminal	12
IPR000863	76.04	Sulfotransferase domain	12
IPR007736	99.46	Caleosin	11
IPR009852	96.78	T-complex protein 10, C-terminal domain	11
IPR027796	94.95	OTT_1508-like deaminase	11
IPR000048	94.26	IQ motif, EF-hand binding site	11
IPR001548	80.86	Peptidase M2, peptidyl-dipeptidase A	10
IPR006948	100.00	Allinase, C-terminal	10
IPR001199	95.67	Cytochrome b5-like heme/steroid binding domain	9
IPR019400	93.17	Peptidase C65, otubain	9
IPR000626	99.39	Ubiquitin-like	8
IPR002128	96.48	NADH:ubiquinone/plastoquinone oxidoreductase, chloroplast chain 5, C-terminal	8
IPR005821	85.92	Ion transport domain	8
IPR006045	76.25	Cupin 1	8
IPR004886	99.84	Glucanosyltransferase	7
IPR004827	99.16	Basic-leucine zipper domain	7
IPR025733	98.88	Iron/zinc purple acid phosphatase-like C-terminal domain	7
IPR026003	80.29	HEAT repeat associated with sister chromatid cohesion protein	7
IPR001461	99.77	Aspartic peptidase	5
IPR006689	98.18	Small GTPase superfamily, ARF/SAR type	5
IPR013601	95.46	FAE1/Type III polyketide synthase-like protein	5
IPR001320	95.43	Ionotropic glutamate receptor	5
IPR000898	94.94	Indoleamine 2,3-dioxygenase	5
IPR001680	94.62	WD40 repeat	5

IPR000685	91.70	Ribulose bisphosphate carboxylase, large subunit, C-terminal	5
IPR008901	90.13	Ceramidase	5
IPR000260	87.00	NADH:ubiquinone oxidoreductase, chain 4, N-terminal	5
IPR003386	82.65	Lecithin:cholesterol/phospholipid:diacylglycerol acyltransferase	5
IPR013922	99.46	Cyclin PHO80-like	4
IPR013057	97.83	Amino acid transporter, transmembrane	4
IPR005150	97.65	Cellulose synthase	4
IPR012317	97.33	Poly(ADP-ribose) polymerase, catalytic domain	4
IPR009818	96.92	Ataxin-2, C-terminal	4
IPR013866	96.35	Sphingolipid delta4-desaturase, N-terminal	4
IPR023796	89.58	Serpin domain	4
IPR013112	79.82	FAD-binding 8	4
IPR013907	99.49	Sds3-like	3
IPR013098	98.45	Immunoglobulin I-set	3
IPR006202	98,40	Neurotransmitter-gated ion-channel ligand-binding	3
IPR017443	98.34	Ribulose bisphosphate carboxylase, large subunit, N-terminal	3
IPR013209	97.90	LNS2, Lipin/Ned1/Smp2	3
IPR018829	91.63	Domain of unknown function DUF2433	3
IPR010828	88.81	Alcohol acetyltransferase	3
IPR000768	84.42	NAD:arginine ADP-ribosyltransferase, ART	3
IPR015211	77.97	Peptidase M1, leukotriene A4 hydrolase, aminopeptidase C-terminal	3
IPR015374	75.10	Chs5p-Arf1p binding	3
IPR001356	99.93	Homeobox domain	2
IPR001767	99.40	Hedgehog protein, Hint domain	2
IPR001846	98.09	von Willebrand factor, type D domain	2
IPR026750	96.54	Protein N-terminal asparagine amidohydrolase	2
IPR008417	94.33	B-cell receptor-associated protein 29/31	2
IPR000242	90.71	Protein-tyrosine phosphatase, receptor/non-receptor type	2
IPR002126	84.74	Cadherin	2
IPR013515	81.88	Phytochrome, central region	2
IPR008496	100.00	Protein of unknown function DUF778	2
IPR012642	100.00	Transcription regulator Wos2-domain	2
IPR001040	99.96	Translation Initiation factor eIF- 4e	1
IPR003123	99.92	Vacuolar sorting protein 9	1
IPR004214	99.92	Conotoxin	1
IPR003151	99.77	PIK-related kinase, FAT	1
IPR018616	99.61	Guanylyl cyclase	1
IPR003690	99.49	Mitochodrial transcription termination factor-related	1
IPR014849	99.46	EKC/KEOPS complex, subunit Gon7	1
IPR007240	99.43	Autophagy-related protein 17	1
IPR007823	99.35	Methyltransferase-related	1

IPR006029	98.63	Neurotransmitter-gated ion-channel transmembrane domain	1
IPR010036	98.14	Magnesium-dependent phosphatase-1, eukaryotic/arcaheal type	1
IPR015034	97.18	Protein of unknown function DUF1917	1
IPR025799	96.57	Protein arginine N-methyltransferase	1
IPR004235	95.40	Scytalone dehydratase	1
IPR001330	94.41	Prenyltransferase/squalene oxidase	1
IPR009836	93.15	Protein of unknown function DUF1399	1
IPR001828	92.07	Extracellular ligand-binding receptor	1
IPR002182	88.23	NB-ARC	1
IPR017395	85.84	Chlorophyllase	1
IPR004201	84.02	CDC48, domain 2	1
IPR003338	81.25	CDC48, N-terminal subdomain	1
IPR002895	100.00	Paramecium surface antigen	1
IPR008606	100.00	Eukaryotic translation initiation factor 4E binding	1
IPR015367	100.00	Transcription factor CEP-1, DNA-binding domain	1
IPR027846	100.00	Protein of unknown function DUF4564	1

* The percentage indicates the occurrence of each selected domain in eukaryotic sequences according to the Interpro database. ** Indicates the number of proteins in the analyzed *Legionella* genomes that contain the selected domains.

Supplementary Table S4: Small GTPases domains detected in the genus *Legionella* as defined in the CDD ncbi domain database

Query	Hit type	PSSM-ID	From	To	E-Value	Bitscore	Accession	Short name	Incompl	Super-family
ACZGv1_12052	specific	206640	11	168	2.402e-46	153.381	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.402e-46	153.381	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	5.86619e-46	152.662	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	5.86619e-46	152.662	cl27030	Ras superfamily	-	-
	non-specific	306559	12	171	8.01284e-42	141.872	pfam00071	Ras	-	cl27030
	non-specific	178657	1	171	2.67464e-29	111.174	PLN03110	PLN03110	-	cl27030
	specific	224025	7	206	5.96626e-20	86.1679	COG1100	Gem1	-	cl27030
	non-specific	272973	12	166	1.16475e-14	70.0933	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	12	166	1.16475e-14	70.0933	cl27769	GTP_EFTU superfamily	-	-
ACZGv1_20575	specific	206648	16	157	1.66013e-07	48.2216	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	16	157	1.66013e-07	48.2216	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	235392	85	167	9.56755e-07	47.4127	PRK05291	trmE	N	cl26334
	superfamily	331155	85	167	9.56755e-07	47.4127	cl26334	MnmE_helical superfamily	N	-
	non-specific	315327	85	167	2.41831e-05	43.215	pfam12631	MnmE_helical	NC	cl26334
	non-specific	225171	85	162	0.00775603	35.7078	COG2262	HflX	N	cl25666
	superfamily	330487	85	162	0.00775603	35.7078	cl25666	HflX superfamily	N	-
ACZGv1_20687	non-specific	306559	19	164	1.53966e-44	149.191	pfam00071	Ras	-	cl27030
	superfamily	331851	19	164	1.53966e-44	149.191	cl27030	Ras superfamily	-	-
	non-specific	206661	13	171	2.38378e-41	141.312	cd01869	Rab1_Ypt1	-	cl21455
	superfamily	328724	13	171	2.38378e-41	141.312	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	19	169	1.16692e-35	126.083	smart00175	RAB	-	cl27030
	non-specific	178657	1	200	1.98578e-24	98.4622	PLN03110	PLN03110	-	cl27030
	specific	224025	19	179	1.47733e-16	76.9231	COG1100	Gem1	-	cl27030

	specific	312094	5	116	3.02945e-25	97.5761	pfam08477	Roc	-	cl21455
	non-specific	197555	4	157	1.10899e-23	94.8822	smart00175	RAB	-	cl27030
	superfamily	331851	4	157	1.10899e-23	94.8822	cl27030	Ras superfamily	-	-
	non-specific	178657	4	116	4.24252e-15	73.039	PLN03110	PLN03110	C	cl27030
	specific	224025	1	157	1.73196e-13	68.4487	COG1100	Gem1	-	cl27030
	non-specific	272973	4	152	1.07933e-12	64.7005	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	152	1.07933e-12	64.7005	cl27769	GTP_EFTU superfamily	-	-
Lade0491	specific	206640	9	158	2.04853e-31	114.861	cd00154	Rab	-	cl21455
	superfamily	328724	9	158	2.04853e-31	114.861	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	10	161	5.69634e-27	103.352	pfam00071	Ras	-	cl27030
	superfamily	331851	10	161	5.69634e-27	103.352	cl27030	Ras superfamily	-	-
	non-specific	197555	9	161	1.32022e-23	94.497	smart00175	RAB	-	cl27030
	specific	224025	7	178	1.511e-20	87.7087	COG1100	Gem1	-	cl27030
	non-specific	272973	8	151	5.02069e-16	73.9453	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	8	151	5.02069e-16	73.9453	cl27769	GTP_EFTU superfamily	-	-
	non-specific	215587	7	179	1.31048e-13	68.5435	PLN03118	PLN03118	-	cl27030
LanA0292	specific	206640	7	162	4.5342e-34	122.565	cd00154	Rab	-	cl21455
	superfamily	328724	7	162	4.5342e-34	122.565	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	7	167	2.21685e-32	118.379	smart00175	RAB	-	cl27030
	superfamily	331851	7	167	2.21685e-32	118.379	cl27030	Ras superfamily	-	-
	non-specific	306559	8	166	2.34837e-28	107.59	pfam00071	Ras	-	cl27030
	specific	224025	3	172	1.87668e-18	82.3159	COG1100	Gem1	-	cl27030
	non-specific	178657	7	160	8.09715e-18	80.743	PLN03110	PLN03110	C	cl27030
	non-specific	272973	7	160	2.5603e-13	66.6265	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	160	2.5603e-13	66.6265	cl27769	GTP_EFTU superfamily	-	-
LanA2294	specific	206640	11	168	2.22867e-50	163.781	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.22867e-50	163.781	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	2.30788e-46	153.433	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	2.30788e-46	153.433	cl27030	Ras superfamily	-	-
	non-specific	306559	12	171	4.14007e-42	142.643	pfam00071	Ras	-	cl27030

	non-specific	178655	11	171	1.08764e-25	101.171	PLN03108	PLN03108	C	cl27030
	specific	224025	7	187	6.91448e-19	83.0863	COG1100	Gem1	-	cl27030
	non-specific	272973	11	160	4.82167e-13	65.4709	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	160	4.82167e-13	65.4709	cl27769	GTP_EFTU superfamily	-	-
LanA2326	specific	206640	50	209	9.65799e-43	142.21	cd00154	Rab	-	cl21455
	superfamily	328724	50	209	9.65799e-43	142.21	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	51	208	9.41681e-37	126.85	pfam00071	Ras	-	cl27030
	superfamily	331851	51	208	9.41681e-37	126.85	cl27030	Ras superfamily	-	-
	non-specific	197555	50	209	1.84987e-33	118.379	smart00175	RAB	-	cl27030
	non-specific	178655	50	206	2.4349e-20	85.378	PLN03108	PLN03108	C	cl27030
	specific	224025	48	245	4.8699e-17	76.9231	COG1100	Gem1	-	cl27030
	non-specific	272973	50	204	4.66916e-12	62.0041	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	50	204	4.66916e-12	62.0041	cl27769	GTP_EFTU superfamily	-	-
LanA3056	specific	206640	13	168	2.2556e-42	142.98	cd00154	Rab	-	cl21455
	superfamily	328724	13	168	2.2556e-42	142.98	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	13	173	1.87572e-40	138.025	smart00175	RAB	-	cl27030
	superfamily	331851	13	173	1.87572e-40	138.025	cl27030	Ras superfamily	-	-
	non-specific	306559	14	173	2.26867e-40	138.02	pfam00071	Ras	-	cl27030
	non-specific	178657	1	173	3.67582e-30	113.1	PLN03110	PLN03110	-	cl27030
	specific	224025	9	189	4.72968e-21	88.8643	COG1100	Gem1	-	cl27030
	non-specific	272973	13	161	6.89894e-12	62.3893	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	13	161	6.89894e-12	62.3893	cl27769	GTP_EFTU superfamily	-	-
LanB0265	specific	206640	13	168	2.2556e-42	142.98	cd00154	Rab	-	cl21455
	superfamily	328724	13	168	2.2556e-42	142.98	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	13	173	1.87572e-40	138.025	smart00175	RAB	-	cl27030
	superfamily	331851	13	173	1.87572e-40	138.025	cl27030	Ras superfamily	-	-
	non-specific	306559	14	173	2.26867e-40	138.02	pfam00071	Ras	-	cl27030
	non-specific	178657	1	173	3.67582e-30	113.1	PLN03110	PLN03110	-	cl27030
	specific	224025	9	189	4.72968e-21	88.8643	COG1100	Gem1	-	cl27030
	non-specific	272973	13	161	6.89894e-12	62.3893	TIGR00231	small_GTP	-	cl27769

	superfamily	332590	13	161	6.89894e-12	62.3893	cl27769	GTP_EFTU superfamily	-	-
LanB0321	specific	206640	50	209	9.65799e-43	142.21	cd00154	Rab	-	cl21455
	superfamily	328724	50	209	9.65799e-43	142.21	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	51	208	9.41681e-37	126.85	pfam00071	Ras	-	cl27030
	superfamily	331851	51	208	9.41681e-37	126.85	cl27030	Ras superfamily	-	-
	non-specific	197555	50	209	1.84987e-33	118.379	smart00175	RAB	-	cl27030
	non-specific	178655	50	206	2.4349e-20	85.378	PLN03108	PLN03108	C	cl27030
	specific	224025	48	245	4.8699e-17	76.9231	COG1100	Gem1	-	cl27030
	non-specific	272973	50	204	4.66916e-12	62.0041	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	50	204	4.66916e-12	62.0041	cl27769	GTP_EFTU superfamily	-	-
LanB1276	specific	206640	7	162	4.5342e-34	122.565	cd00154	Rab	-	cl21455
	superfamily	328724	7	162	4.5342e-34	122.565	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	7	167	2.21685e-32	118.379	smart00175	RAB	-	cl27030
	superfamily	331851	7	167	2.21685e-32	118.379	cl27030	Ras superfamily	-	-
	non-specific	306559	8	166	2.34837e-28	107.59	pfam00071	Ras	-	cl27030
	specific	224025	3	172	1.87668e-18	82.3159	COG1100	Gem1	-	cl27030
	non-specific	178657	7	160	8.09715e-18	80.743	PLN03110	PLN03110	C	cl27030
	non-specific	272973	7	160	2.5603e-13	66.6265	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	160	2.5603e-13	66.6265	cl27769	GTP_EFTU superfamily	-	-
LanB2255	specific	206640	11	168	2.22867e-50	163.781	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.22867e-50	163.781	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	2.30788e-46	153.433	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	2.30788e-46	153.433	cl27030	Ras superfamily	-	-
	non-specific	306559	12	171	4.14007e-42	142.643	pfam00071	Ras	-	cl27030
	non-specific	178655	11	171	1.08764e-25	101.171	PLN03108	PLN03108	C	cl27030
	specific	224025	7	187	6.91448e-19	83.0863	COG1100	Gem1	-	cl27030
	non-specific	272973	11	160	4.82167e-13	65.4709	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	160	4.82167e-13	65.4709	cl27769	GTP_EFTU superfamily	-	-
Lbe0211	specific	224025	1	172	7.57463e-12	63.8263	COG1100	Gem1	-	cl27030
	superfamily	331851	1	172	7.57463e-12	63.8263	cl27030	Ras superfamily	-	-

	non-specific	306559	6	113	1.72817e-11	61.3656	pfam00071	Ras	C	cl27030
	non-specific	206641	5	161	4.95471e-10	57.5538	cd00157	Rho	-	cl21455
	superfamily	328724	5	161	4.95471e-10	57.5538	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197554	8	161	1.97806e-08	53.001	smart00174	RHO	-	cl27030
	non-specific	272973	4	113	3.86638e-06	46.2109	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	4	113	3.86638e-06	46.2109	cl27769	GTP_EFTU superfamily	C	-
Lbe0872	non-specific	206640	147	320	3.35816e-20	86.741	cd00154	Rab	-	cl21455
	superfamily	328724	147	320	3.35816e-20	86.741	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	151	313	1.59078e-13	67.914	pfam00071	Ras	-	cl27030
	superfamily	331851	151	313	1.59078e-13	67.914	cl27030	Ras superfamily	-	-
	non-specific	197555	147	313	1.20745e-09	56.7475	smart00175	RAB	-	cl27030
	non-specific	272973	148	318	3.18876e-06	46.5961	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	148	318	3.18876e-06	46.5961	cl27769	GTP_EFTU superfamily	-	-
	specific	224025	147	339	1.4221e-05	45.7219	COG1100	Gem1	-	cl27030
	non-specific	235392	223	318	0.00207388	40.0939	PRK05291	trmE	N	cl26334
	superfamily	331155	223	318	0.00207388	40.0939	cl26334	MnmE_helical superfamily	N	-
Lbir0344	non-specific	206640	701	854	2.21853e-15	74.4146	cd00154	Rab	-	cl21455
	superfamily	328724	701	854	2.21853e-15	74.4146	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	701	854	5.81696e-12	64.4472	pfam00071	Ras	-	cl27030
	superfamily	331851	701	854	5.81696e-12	64.4472	cl27030	Ras superfamily	-	-
	non-specific	197555	701	859	7.49066e-11	61.3699	smart00175	RAB	-	cl27030
	specific	224025	701	872	1.09404e-05	47.2627	COG1100	Gem1	-	cl27030
	non-specific	272973	701	849	3.53187e-05	44.6701	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	701	849	3.53187e-05	44.6701	cl27769	GTP_EFTU superfamily	-	-
	non-specific	215587	691	853	4.85968e-05	45.4315	PLN03118	PLN03118	-	cl27030
Lbir0398	specific	206648	14	168	1.69366e-07	50.1476	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	14	168	1.69366e-07	50.1476	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	234624	59	191	0.0010655	40.4159	PRK00089	era	NC	cl26333
	superfamily	331154	59	191	0.0010655	40.4159	cl26333	FeoB_N superfamily	NC	-
	non-specific	316621	270	329	0.00311408	36.342	pfam14110	DUF4282	C	cl16622

	superfamily	316621	270	329	0.00311408	36.342	cl16622	DUF4282 superfamily	C	-
Lbir1602	specific	206648	45	189	1.69444e-08	52.844	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	45	189	1.69444e-08	52.844	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	106	187	0.00033877	40.1839	smart00175	RAB	N	cl27030
	superfamily	331851	106	187	0.00033877	40.1839	cl27030	Ras superfamily	N	-
	specific	224025	38	223	0.00621197	37.2475	COG1100	Gem1	-	cl27030
Lbir1737	specific	206640	15	175	1.29041e-47	152.995	cd00154	Rab	-	cl21455
	superfamily	328724	15	175	1.29041e-47	152.995	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	16	177	5.21734e-44	143.798	pfam00071	Ras	-	cl27030
	superfamily	331851	16	177	5.21734e-44	143.798	cl27030	Ras superfamily	-	-
	non-specific	197555	16	175	1.39069e-37	127.624	smart00175	RAB	-	cl27030
	non-specific	178655	16	172	5.54946e-27	101.556	PLN03108	PLN03108	C	cl27030
	specific	224025	11	177	5.75084e-18	78.0787	COG1100	Gem1	-	cl27030
	non-specific	272973	16	170	1.70852e-13	65.0857	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	16	170	1.70852e-13	65.0857	cl27769	GTP_EFTU superfamily	-	-
Lbir2252	specific	206640	4	149	1.58779e-27	103.305	cd00154	Rab	-	cl21455
	superfamily	328724	4	149	1.58779e-27	103.305	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	4	149	3.33872e-20	84.0967	smart00175	RAB	-	cl27030
	superfamily	331851	4	149	3.33872e-20	84.0967	cl27030	Ras superfamily	-	-
	non-specific	306559	5	149	1.82057e-19	82.1664	pfam00071	Ras	-	cl27030
	specific	224025	1	116	9.10264e-16	73.8415	COG1100	Gem1	C	cl27030
	non-specific	272973	3	152	3.86047e-11	59.6929	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	3	152	3.86047e-11	59.6929	cl27769	GTP_EFTU superfamily	-	-
	non-specific	215587	2	149	4.77937e-08	51.9799	PLN03118	PLN03118	C	cl27030
Lbir3188	non-specific	206640	88	163	2.34981e-05	43.5987	cd00154	Rab	N	cl21455
	superfamily	328724	88	163	2.34981e-05	43.5987	cl21455	P-loop_NTPase superfamily	N	-
	non-specific	306559	113	161	0.0088704	35.9424	pfam00071	Ras	N	cl27030
	superfamily	331851	113	161	0.0088704	35.9424	cl27030	Ras superfamily	N	-
LboA1497	specific	206640	7	161	1.13152e-34	124.105	cd00154	Rab	-	cl21455
	superfamily	328724	7	161	1.13152e-34	124.105	cl21455	P-loop_NTPase superfamily	-	-

	non-specific	306559	8	164	1.49766e-27	105.278	pfam00071	Ras	-	cl27030
	superfamily	331851	8	164	1.49766e-27	105.278	cl27030	Ras superfamily	-	-
	non-specific	197555	7	161	7.08163e-27	103.742	smart00175	RAB	-	cl27030
	specific	224025	6	194	2.50024e-17	79.2343	COG1100	Gem1	-	cl27030
	non-specific	178657	7	159	4.81685e-16	75.7354	PLN03110	PLN03110	C	cl27030
	non-specific	272973	6	159	2.0884e-14	69.7081	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	6	159	2.0884e-14	69.7081	cl27769	GTP_EFTU superfamily	-	-
LboA2428	specific	206640	11	170	1.24534e-50	164.551	cd00154	Rab	-	cl21455
	superfamily	328724	11	170	1.24534e-50	164.551	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	173	2.06879e-46	153.818	smart00175	RAB	-	cl27030
	superfamily	331851	11	173	2.06879e-46	153.818	cl27030	Ras superfamily	-	-
	non-specific	306559	12	173	1.20451e-41	141.487	pfam00071	Ras	-	cl27030
	non-specific	178657	1	173	3.37259e-25	100.003	PLN03110	PLN03110	-	cl27030
	specific	224025	7	206	9.03354e-19	82.7011	COG1100	Gem1	-	cl27030
	non-specific	272973	11	161	2.16891e-12	63.9301	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	161	2.16891e-12	63.9301	cl27769	GTP_EFTU superfamily	-	-
LboA2457	specific	206640	30	189	4.03002e-46	149.914	cd00154	Rab	-	cl21455
	superfamily	328724	30	189	4.03002e-46	149.914	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	31	188	9.07757e-39	131.087	pfam00071	Ras	-	cl27030
	superfamily	331851	31	188	9.07757e-39	131.087	cl27030	Ras superfamily	-	-
	non-specific	197555	30	189	4.26421e-36	124.543	smart00175	RAB	-	cl27030
	non-specific	178655	30	186	1.48136e-23	93.4672	PLN03108	PLN03108	C	cl27030
	specific	224025	28	188	8.75179e-22	88.8643	COG1100	Gem1	-	cl27030
	non-specific	272973	30	184	3.24841e-15	70.0933	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	30	184	3.24841e-15	70.0933	cl27769	GTP_EFTU superfamily	-	-
LboB0786	non-specific	206640	13	64	1.25037e-10	53.999	cd00154	Rab	N	cl21455
	superfamily	328724	13	64	1.25037e-10	53.999	cl21455	P-loop_NTPase superfamily	N	-
	non-specific	306559	2	63	1.114e-09	51.7356	pfam00071	Ras	N	cl27030
	superfamily	331851	2	63	1.114e-09	51.7356	cl27030	Ras superfamily	N	-
	non-specific	197555	13	64	3.03073e-07	45.1915	smart00175	RAB	N	cl27030

	non-specific	178655	13	61	0.000110801	38.7688	PLN03108	PLN03108	NC	cl27030
LboB0787	non-specific	206640	30	117	6.58605e-26	94.445	cd00154	Rab	C	cl21455
	superfamily	328724	30	117	6.58605e-26	94.445	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	197555	30	116	4.36327e-20	79.8595	smart00175	RAB	C	cl27030
	superfamily	331851	30	116	4.36327e-20	79.8595	cl27030	Ras superfamily	C	-
	non-specific	306559	31	121	2.09821e-19	77.9292	pfam00071	Ras	C	cl27030
	specific	224025	29	114	9.74167e-15	66.9079	COG1100	Gem1	C	cl27030
	non-specific	215587	29	116	1.52593e-11	58.5283	PLN03118	PLN03118	C	cl27030
	non-specific	272973	30	111	1.46925e-07	46.9813	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	30	111	1.46925e-07	46.9813	cl27769	GTP_EFTU superfamily	C	-
LboB0816	specific	206640	11	170	4.27427e-51	165.707	cd00154	Rab	-	cl21455
	superfamily	328724	11	170	4.27427e-51	165.707	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	173	6.39482e-47	154.973	smart00175	RAB	-	cl27030
	superfamily	331851	11	173	6.39482e-47	154.973	cl27030	Ras superfamily	-	-
	non-specific	306559	12	173	3.46849e-42	143.028	pfam00071	Ras	-	cl27030
	non-specific	178657	1	173	3.06008e-26	103.085	PLN03110	PLN03110	-	cl27030
	specific	224025	7	206	5.78948e-19	83.4715	COG1100	Gem1	-	cl27030
	non-specific	272973	11	161	3.50251e-13	65.8561	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	161	3.50251e-13	65.8561	cl27769	GTP_EFTU superfamily	-	-
LboB2421	specific	206640	7	161	1.53852e-34	123.72	cd00154	Rab	-	cl21455
	superfamily	328724	7	161	1.53852e-34	123.72	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	8	164	7.62868e-27	103.352	pfam00071	Ras	-	cl27030
	superfamily	331851	8	164	7.62868e-27	103.352	cl27030	Ras superfamily	-	-
	non-specific	197555	7	161	2.71484e-26	102.201	smart00175	RAB	-	cl27030
	specific	224025	6	194	1.74601e-18	82.7011	COG1100	Gem1	-	cl27030
	non-specific	178657	7	159	1.26805e-16	77.2762	PLN03110	PLN03110	C	cl27030
	non-specific	272973	6	159	2.2163e-14	69.7081	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	6	159	2.2163e-14	69.7081	cl27769	GTP_EFTU superfamily	-	-
Lbru0408	non-specific	206640	9	171	3.5981e-16	74.7998	cd00154	Rab	-	cl21455
	superfamily	328724	9	171	3.5981e-16	74.7998	cl21455	P-loop_NTPase superfamily	-	-

	non-specific	312094	10	125	1.49917e-15	71.7677	pfam08477	Roc	-	cl21455
	specific	224025	4	187	3.67476e-12	64.5967	COG1100	Gem1	-	cl27030
	superfamily	331851	4	187	3.67476e-12	64.5967	cl27030	Ras superfamily	-	-
	non-specific	197555	9	159	4.71138e-12	63.2959	smart00175	RAB	-	cl27030
	non-specific	272973	8	166	1.00657e-08	53.5297	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	8	166	1.00657e-08	53.5297	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178655	9	194	1.6705e-07	51.0952	PLN03108	PLN03108	-	cl27030
Lbru1073	non-specific	206640	5	168	3.61815e-22	90.9782	cd00154	Rab	-	cl21455
	superfamily	328724	5	168	3.61815e-22	90.9782	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	5	121	6.05862e-14	67.1454	pfam08477	Roc	-	cl21455
	non-specific	197555	5	160	2.86201e-13	66.7627	smart00175	RAB	-	cl27030
	superfamily	331851	5	160	2.86201e-13	66.7627	cl27030	Ras superfamily	-	-
	specific	224025	1	160	2.21777e-12	65.3671	COG1100	Gem1	C	cl27030
	non-specific	237048	81	170	2.21717e-06	48.5281	PRK12299	obgE	N	cl25666
	superfamily	330487	81	170	2.21717e-06	48.5281	cl25666	HflX superfamily	N	-
	non-specific	274271	81	168	0.000439249	41.2533	TIGR02729	Obg_CgtA	N	cl25666
Lbru2537	specific	206640	11	167	3.83608e-30	112.549	cd00154	Rab	-	cl21455
	superfamily	328724	11	167	3.83608e-30	112.549	cl21455	P-loop_NTPase superfamily	-	-
	specific	312094	12	121	7.46952e-26	99.8873	pfam08477	Roc	-	cl21455
	specific	224025	6	197	4.95062e-22	92.7163	COG1100	Gem1	-	cl27030
	superfamily	331851	6	197	4.95062e-22	92.7163	cl27030	Ras superfamily	-	-
	non-specific	197555	11	179	2.49236e-21	89.1043	smart00175	RAB	-	cl27030
	non-specific	272973	10	155	5.92676e-14	68.5525	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	10	155	5.92676e-14	68.5525	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178657	12	188	1.13355e-13	69.187	PLN03110	PLN03110	-	cl27030
Lbu0304	non-specific	206640	4	170	1.7329e-08	52.8434	cd00154	Rab	-	cl21455
	superfamily	328724	4	170	1.7329e-08	52.8434	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	5	134	4.9932e-06	44.8038	pfam08477	Roc	-	cl21455
	non-specific	272973	4	177	6.37911e-05	42.7442	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	177	6.37911e-05	42.7442	cl27769	GTP_EFTU superfamily	-	-

	specific	224025	1	190	0.000232951	41.8699	COG1100	Gem1	C	cl27030
	superfamily	331851	1	190	0.000232951	41.8699	cl27030	Ras superfamily	C	-
Lbu2365	non-specific	206640	3	155	5.7303e-14	68.2514	cd00154	Rab	-	cl21455
	superfamily	328724	3	155	5.7303e-14	68.2514	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	4	117	2.75058e-11	59.4414	pfam08477	Roc	-	cl21455
	non-specific	128473	9	117	7.70798e-10	57.7139	smart00176	RAN	C	cl27030
	superfamily	331851	9	117	7.70798e-10	57.7139	cl27030	Ras superfamily	C	-
	non-specific	178620	4	117	3.5211e-09	55.913	PLN03071	PLN03071	C	cl27030
	specific	224025	2	212	1.49697e-07	51.1147	COG1100	Gem1	-	cl27030
	non-specific	272973	3	173	2.71854e-07	49.2925	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	3	173	2.71854e-07	49.2925	cl27769	GTP_EFTU superfamily	-	-
Lche0226	specific	206640	3	153	6.95755e-30	111.394	cd00154	Rab	-	cl21455
	superfamily	328724	3	153	6.95755e-30	111.394	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	4	155	1.07745e-22	92.1815	pfam00071	Ras	-	cl27030
	superfamily	331851	4	155	1.07745e-22	92.1815	cl27030	Ras superfamily	-	-
	non-specific	197555	3	150	5.37082e-20	84.8671	smart00175	RAB	-	cl27030
	non-specific	272973	3	155	3.08623e-14	69.3229	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	3	155	3.08623e-14	69.3229	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178657	3	153	3.38949e-11	61.8682	PLN03110	PLN03110	C	cl27030
	specific	224025	2	205	6.87715e-11	60.7447	COG1100	Gem1	-	cl27030
Lche1463	specific	206648	17	174	7.98537e-13	65.1703	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	17	174	7.98537e-13	65.1703	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	225138	4	174	3.50635e-09	55.5442	COG2229	Srp102	-	cl21455
	non-specific	287615	15	38	0.00170432	38.0208	pfam10662	PduV-EutP	C	cl21455
	specific	214640	12	142	0.0084353	36.1973	smart00382	AAA	-	cl28181
	superfamily	333001	12	142	0.0084353	36.1973	cl28181	AAA superfamily	-	-
Lche2249	non-specific	206640	62	149	3.58041e-08	52.4582	cd00154	Rab	N	cl21455
	superfamily	328724	62	149	3.58041e-08	52.4582	cl21455	P-loop_NTPase superfamily	N	-
	non-specific	197555	62	135	6.71771e-06	45.9619	smart00175	RAB	N	cl27030
	superfamily	331851	62	135	6.71771e-06	45.9619	cl27030	Ras superfamily	N	-

	non-specific	306559	62	135	7.82568e-06	45.5724	pfam00071	Ras	N	cl27030
Lche2737	specific	206640	11	170	6.01158e-53	170.329	cd00154	Rab	-	cl21455
	superfamily	328724	11	170	6.01158e-53	170.329	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	173	1.03361e-51	167.685	smart00175	RAB	-	cl27030
	superfamily	331851	11	173	1.03361e-51	167.685	cl27030	Ras superfamily	-	-
	non-specific	306559	12	173	3.25567e-50	163.443	pfam00071	Ras	-	cl27030
	non-specific	178657	1	177	3.15908e-36	129.278	PLN03110	PLN03110	-	cl27030
	specific	224025	7	186	2.5892e-23	95.4127	COG1100	Gem1	-	cl27030
	non-specific	272973	11	162	1.08857e-14	70.0933	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	162	1.08857e-14	70.0933	cl27769	GTP_EFTU superfamily	-	-
Lche2767	specific	206640	26	185	5.11451e-44	143.751	cd00154	Rab	-	cl21455
	superfamily	328724	26	185	5.11451e-44	143.751	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	26	185	3.10799e-36	124.157	smart00175	RAB	-	cl27030
	superfamily	331851	26	185	3.10799e-36	124.157	cl27030	Ras superfamily	-	-
	non-specific	306559	27	184	3.20922e-36	124.153	pfam00071	Ras	-	cl27030
	non-specific	178655	26	182	2.80897e-24	94.6228	PLN03108	PLN03108	C	cl27030
	specific	224025	24	184	5.83263e-17	75.7675	COG1100	Gem1	-	cl27030
	non-specific	272973	26	180	2.80453e-14	67.0117	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	26	180	2.80453e-14	67.0117	cl27769	GTP_EFTU superfamily	-	-
Lche3050	specific	206648	6	157	2.5916e-08	52.4588	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	6	157	2.5916e-08	52.4588	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	5	129	1.44356e-05	45.3367	COG1100	Gem1	C	cl27030
	superfamily	331851	5	129	1.44356e-05	45.3367	cl27030	Ras superfamily	C	-
	non-specific	235392	62	231	0.00557544	38.1679	PRK05291	trmE	N	cl26334
	superfamily	331155	62	231	0.00557544	38.1679	cl26334	MnmE_helical superfamily	N	-
	non-specific	197554	65	109	0.00805517	36.4374	smart00174	RHO	NC	cl27030
Lci1116	specific	206640	35	192	1.30368e-48	159.929	cd00154	Rab	-	cl21455
	superfamily	328724	35	192	1.30368e-48	159.929	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	35	195	1.15464e-46	155.359	smart00175	RAB	-	cl27030
	superfamily	331851	35	195	1.15464e-46	155.359	cl27030	Ras superfamily	-	-

	non-specific	306559	36	195	9.19089e-42	142.257	pfam00071	Ras	-	cl27030
	non-specific	178657	25	195	1.42155e-32	120.419	PLN03110	PLN03110	-	cl27030
	specific	224025	31	230	1.44899e-17	80.0047	COG1100	Gem1	-	cl27030
	non-specific	272973	36	190	3.52416e-13	66.2413	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	36	190	3.52416e-13	66.2413	cl27769	GTP_EFTU superfamily	-	-
Lci1233	specific	206640	17	170	9.6502e-27	103.305	cd00154	Rab	-	cl21455
	superfamily	328724	17	170	9.6502e-27	103.305	cl21455	P-loop_NTPase superfamily	-	-
	specific	312094	18	129	8.2454e-23	91.4129	pfam08477	Roc	-	cl21455
	non-specific	197555	17	170	1.6544e-17	78.3187	smart00175	RAB	-	cl27030
	superfamily	331851	17	170	1.6544e-17	78.3187	cl27030	Ras superfamily	-	-
	specific	224025	14	213	3.23227e-17	79.2343	COG1100	Gem1	-	cl27030
	non-specific	178657	17	129	1.95036e-11	62.6386	PLN03110	PLN03110	C	cl27030
	non-specific	272973	17	168	1.21222e-10	59.3077	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	17	168	1.21222e-10	59.3077	cl27769	GTP_EFTU superfamily	-	-
Ldra2229	specific	206640	10	165	2.85985e-52	168.403	cd00154	Rab	-	cl21455
	superfamily	328724	10	165	2.85985e-52	168.403	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	11	167	5.03949e-49	160.362	pfam00071	Ras	-	cl27030
	superfamily	331851	11	167	5.03949e-49	160.362	cl27030	Ras superfamily	-	-
	non-specific	197555	11	168	1.20896e-47	156.899	smart00175	RAB	-	cl27030
	non-specific	178655	11	168	9.82364e-28	106.564	PLN03108	PLN03108	C	cl27030
	specific	224025	10	195	3.24838e-23	94.6423	COG1100	Gem1	-	cl27030
	non-specific	272973	11	160	1.13771e-13	67.3969	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	160	1.13771e-13	67.3969	cl27769	GTP_EFTU superfamily	-	-
Ldra3848	non-specific	206640	4	159	4.98555e-20	85.2002	cd00154	Rab	-	cl21455
	superfamily	328724	4	159	4.98555e-20	85.2002	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	5	118	5.19987e-17	75.6197	pfam08477	Roc	-	cl21455
	non-specific	197555	4	155	1.72712e-16	75.6223	smart00175	RAB	-	cl27030
	superfamily	331851	4	155	1.72712e-16	75.6223	cl27030	Ras superfamily	-	-
	specific	224025	1	215	1.68928e-13	68.4487	COG1100	Gem1	-	cl27030
	non-specific	178655	4	118	1.63067e-10	59.5696	PLN03108	PLN03108	C	cl27030

	non-specific	272973	4	157	4.16998e-09	54.6853	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	157	4.16998e-09	54.6853	cl27769	GTP_EFTU superfamily	-	-
Ldro0084	non-specific	206640	13	174	3.60661e-16	74.7998	cd00154	Rab	-	cl21455
	superfamily	328724	13	174	3.60661e-16	74.7998	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	10	174	6.14121e-11	60.21	pfam00071	Ras	-	cl27030
	superfamily	331851	10	174	6.14121e-11	60.21	cl27030	Ras superfamily	-	-
	specific	224025	8	183	5.61444e-10	58.4335	COG1100	Gem1	-	cl27030
	non-specific	197555	13	174	6.55744e-10	57.1327	smart00175	RAB	-	cl27030
	non-specific	312736	296	344	0.00260817	37.2352	pfam09335	SNARE_assoc	C	cl00429
	superfamily	320969	296	344	0.00260817	37.2352	cl00429	SNARE_assoc superfamily	C	-
	non-specific	185444	51	172	0.0028739	38.1865	PTZ00099	PTZ00099	C	cl27030
Ldro2225	specific	224025	3	180	3.76605e-10	58.8187	COG1100	Gem1	-	cl27030
	superfamily	331851	3	180	3.76605e-10	58.8187	cl27030	Ras superfamily	-	-
	non-specific	312094	5	115	4.08677e-08	50.5818	pfam08477	Roc	-	cl21455
	superfamily	328724	5	115	4.08677e-08	50.5818	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	133330	3	125	2.42567e-07	50.0936	cd04130	Wrch_1	C	cl21455
	non-specific	197554	5	116	3.57475e-05	43.371	smart00174	RHO	C	cl27030
	non-specific	272973	2	122	8.1312e-05	42.359	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	2	122	8.1312e-05	42.359	cl27769	GTP_EFTU superfamily	C	-
	non-specific	237160	274	315	0.00527375	38.1933	PRK12652	PRK12652	NC	cl00807
	superfamily	321181	274	315	0.00527375	38.1933	cl00807	MNHE superfamily	NC	-
Ldro2226	specific	224025	3	195	7.35226e-09	54.9667	COG1100	Gem1	-	cl27030
	superfamily	331851	3	195	7.35226e-09	54.9667	cl27030	Ras superfamily	-	-
	non-specific	312094	5	111	8.73942e-08	49.8114	pfam08477	Roc	-	cl21455
	superfamily	328724	5	111	8.73942e-08	49.8114	cl21455	P-loop_NTPase superfamily	-	-
	specific	206648	6	121	8.57815e-07	48.2216	cd00882	Ras_like_GTPase	C	cl21455
	non-specific	197555	3	120	4.31262e-05	43.2655	smart00175	RAB	C	cl27030
	non-specific	237160	269	310	0.00358911	38.5785	PRK12652	PRK12652	NC	cl00807
	superfamily	321181	269	310	0.00358911	38.5785	cl00807	MNHE superfamily	NC	-
LduN230867	non-specific	206640	3	156	2.9466e-20	85.5854	cd00154	Rab	-	cl21455

	superfamily	328724	3	156	2.9466e-20	85.5854	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	4	151	8.12535e-13	65.2176	pfam00071	Ras	-	cl27030
	superfamily	331851	4	151	8.12535e-13	65.2176	cl27030	Ras superfamily	-	-
	non-specific	197555	3	157	9.03911e-13	65.2219	smart00175	RAB	-	cl27030
	non-specific	272973	2	154	1.11465e-11	62.0041	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	2	154	1.11465e-11	62.0041	cl27769	GTP_EFTU superfamily	-	-
	specific	224025	2	156	2.41654e-11	62.2855	COG1100	Gem1	-	cl27030
	non-specific	234624	70	157	1.57701e-10	60.8314	PRK00089	era	NC	cl26333
	superfamily	331154	70	157	1.57701e-10	60.8314	cl26333	FeoB_N superfamily	NC	-
LduN231401	non-specific	206640	14	167	1.24484e-10	59.0066	cd00154	Rab	-	cl21455
	superfamily	328724	14	167	1.24484e-10	59.0066	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	15	127	1.32884e-06	46.3446	pfam08477	Roc	-	cl21455
	non-specific	197555	14	142	0.000599944	39.7987	smart00175	RAB	C	cl27030
	superfamily	331851	14	142	0.000599944	39.7987	cl27030	Ras superfamily	C	-
	non-specific	225138	6	175	0.00425231	37.4398	COG2229	Srp102	-	cl21455
LduN233215	specific	206640	11	168	3.17604e-45	150.684	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	3.17604e-45	150.684	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	12	173	1.47732e-42	143.798	pfam00071	Ras	-	cl27030
	superfamily	331851	12	173	1.47732e-42	143.798	cl27030	Ras superfamily	-	-
	non-specific	197555	11	173	5.45836e-40	137.254	smart00175	RAB	-	cl27030
	non-specific	178655	7	173	5.42945e-31	115.424	PLN03108	PLN03108	C	cl27030
	specific	224025	7	173	1.93371e-16	76.5379	COG1100	Gem1	C	cl27030
	non-specific	272973	11	162	4.03944e-07	48.9073	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	162	4.03944e-07	48.9073	cl27769	GTP_EFTU superfamily	-	-
LduTex1150	non-specific	206640	14	167	1.24484e-10	59.0066	cd00154	Rab	-	cl21455
	superfamily	328724	14	167	1.24484e-10	59.0066	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	15	127	1.32884e-06	46.3446	pfam08477	Roc	-	cl21455
	non-specific	197555	14	142	0.000599944	39.7987	smart00175	RAB	C	cl27030
	superfamily	331851	14	142	0.000599944	39.7987	cl27030	Ras superfamily	C	-
	non-specific	225138	6	175	0.00425231	37.4398	COG2229	Srp102	-	cl21455

LduTex1682	non-specific	206640	3	156	2.28197e-20	85.9706	cd00154	Rab	-	cl21455
	superfamily	328724	3	156	2.28197e-20	85.9706	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	4	151	6.87365e-13	65.2176	pfam00071	Ras	-	cl27030
	superfamily	331851	4	151	6.87365e-13	65.2176	cl27030	Ras superfamily	-	-
	non-specific	197555	3	157	7.64762e-13	65.2219	smart00175	RAB	-	cl27030
	non-specific	272973	2	154	7.76353e-12	62.3893	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	2	154	7.76353e-12	62.3893	cl27769	GTP_EFTU superfamily	-	-
	specific	224025	2	156	1.95753e-11	62.6707	COG1100	Gem1	-	cl27030
	non-specific	234624	70	157	1.33402e-10	60.8314	PRK00089	era	NC	cl26333
	superfamily	331154	70	157	1.33402e-10	60.8314	cl26333	FeoB_N superfamily	NC	-
LduTex3173	specific	206640	11	168	3.17604e-45	150.684	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	3.17604e-45	150.684	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	12	173	1.47732e-42	143.798	pfam00071	Ras	-	cl27030
	superfamily	331851	12	173	1.47732e-42	143.798	cl27030	Ras superfamily	-	-
	non-specific	197555	11	173	5.45836e-40	137.254	smart00175	RAB	-	cl27030
	non-specific	178655	7	173	5.42945e-31	115.424	PLN03108	PLN03108	C	cl27030
	specific	224025	7	173	1.93371e-16	76.5379	COG1100	Gem1	C	cl27030
	non-specific	272973	11	162	4.03944e-07	48.9073	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	162	4.03944e-07	48.9073	cl27769	GTP_EFTU superfamily	-	-
Lery0478	specific	206648	12	144	1.85407e-12	62.0887	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	12	144	1.85407e-12	62.0887	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	11	167	9.41523e-06	44.5663	COG1100	Gem1	C	cl27030
	superfamily	331851	11	167	9.41523e-06	44.5663	cl27030	Ras superfamily	C	-
	non-specific	306901	4	28	0.00380867	37.1966	pfam00503	G-alpha	C	cl26635
	superfamily	331456	4	28	0.00380867	37.1966	cl26635	G-alpha superfamily	C	-
Lery1116	non-specific	234624	45	139	0.000296455	41.5715	PRK00089	era	NC	cl26333
	superfamily	331154	45	139	0.000296455	41.5715	cl26333	FeoB_N superfamily	NC	-
	specific	206648	42	139	0.000311234	40.5176	cd00882	Ras_like_GTPase	N	cl21455
	superfamily	328724	42	139	0.000311234	40.5176	cl21455	P-loop_NTPase superfamily	N	-
Lery2510	non-specific	206727	79	155	0.00226244	36.7034	cd04164	trmE	N	cl21455

	superfamily	328724	79	155	0.00226244	36.7034	cl21455	P-loop_NTPase superfamily	N	-
LFAv2_1192	specific	206648	16	158	6.32198e-07	46.6808	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	16	158	6.32198e-07	46.6808	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	235392	86	161	2.52434e-06	45.8719	PRK05291	trmE	N	cl26334
	superfamily	331155	86	161	2.52434e-06	45.8719	cl26334	MnmE_helical superfamily	N	-
	non-specific	315327	86	162	1.06541e-05	43.9854	pfam12631	MnmE_helical	NC	cl26334
	non-specific	223561	86	171	0.000347972	39.8506	COG0486	MnmE	N	cl26334
LFAv2_1711	non-specific	206640	4	165	2.82286e-17	77.8814	cd00154	Rab	-	cl21455
	superfamily	328724	4	165	2.82286e-17	77.8814	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	5	123	4.03261e-15	70.6122	pfam08477	Roc	-	cl21455
	specific	224025	1	123	1.28844e-12	66.1375	COG1100	Gem1	C	cl27030
	superfamily	331851	1	123	1.28844e-12	66.1375	cl27030	Ras superfamily	C	-
	non-specific	272973	3	163	8.30569e-10	56.9965	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	3	163	8.30569e-10	56.9965	cl27769	GTP_EFTU superfamily	-	-
	non-specific	197555	4	158	2.25248e-09	55.5919	smart00175	RAB	-	cl27030
	non-specific	234624	60	181	2.10039e-07	51.5867	PRK00089	era	C	cl26333
	superfamily	331154	60	181	2.10039e-07	51.5867	cl26333	FeoB_N superfamily	C	-
LFAv2_1897	non-specific	306559	12	171	4.62424e-39	134.553	pfam00071	Ras	-	cl27030
	superfamily	331851	12	171	4.62424e-39	134.553	cl27030	Ras superfamily	-	-
	specific	206640	11	168	2.51054e-38	132.58	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.51054e-38	132.58	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	1.88732e-37	130.321	smart00175	RAB	-	cl27030
	non-specific	178655	11	171	1.2069e-27	106.179	PLN03108	PLN03108	C	cl27030
	specific	224025	9	133	3.48832e-19	83.8567	COG1100	Gem1	C	cl27030
	non-specific	272973	11	163	4.83719e-14	68.1673	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	163	4.83719e-14	68.1673	cl27769	GTP_EFTU superfamily	-	-
LFAv2_2000	specific	206648	8	165	1.5902e-06	47.4512	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	8	165	1.5902e-06	47.4512	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	272973	8	169	0.000517358	40.0478	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	8	169	0.000517358	40.0478	cl27769	GTP_EFTU superfamily	-	-

Lfee1335	specific	206640	5	159	2.98368e-46	149.914	cd00154	Rab	-	cl21455
	superfamily	328724	5	159	2.98368e-46	149.914	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	5	159	2.47802e-38	129.935	smart00175	RAB	-	cl27030
	superfamily	331851	5	159	2.47802e-38	129.935	cl27030	Ras superfamily	-	-
	non-specific	306559	5	156	7.96819e-38	128.39	pfam00071	Ras	-	cl27030
	specific	224025	4	179	1.32943e-23	93.4867	COG1100	Gem1	-	cl27030
	non-specific	178655	6	179	6.77732e-22	88.8448	PLN03108	PLN03108	-	cl27030
	non-specific	272973	5	161	8.55207e-12	60.4633	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	5	161	8.55207e-12	60.4633	cl27769	GTP_EFTU superfamily	-	-
Lge0409	specific	206648	10	157	0.00504032	37.0508	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	10	157	0.00504032	37.0508	cl21455	P-loop_NTPase superfamily	-	-
Lge0493	specific	224025	11	220	3.76774e-15	72.3007	COG1100	Gem1	-	cl27030
	superfamily	331851	11	220	3.76774e-15	72.3007	cl27030	Ras superfamily	-	-
	non-specific	206640	14	161	1.43408e-13	66.3254	cd00154	Rab	-	cl21455
	superfamily	328724	14	161	1.43408e-13	66.3254	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	15	160	2.85354e-12	62.9064	pfam00071	Ras	-	cl27030
	non-specific	197555	14	176	2.56616e-10	57.5179	smart00175	RAB	-	cl27030
	non-specific	272973	14	133	4.86532e-07	48.1369	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	14	133	4.86532e-07	48.1369	cl27769	GTP_EFTU superfamily	C	-
	non-specific	178657	13	130	9.56858e-06	45.3047	PLN03110	PLN03110	C	cl27030
Lge0801	non-specific	206640	705	858	1.71822e-13	68.6366	cd00154	Rab	-	cl21455
	superfamily	328724	705	858	1.71822e-13	68.6366	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	705	858	1.7755e-12	65.988	pfam00071	Ras	-	cl27030
	superfamily	331851	705	858	1.7755e-12	65.988	cl27030	Ras superfamily	-	-
	non-specific	197555	705	863	2.44723e-10	59.8291	smart00175	RAB	-	cl27030
	non-specific	272973	705	853	0.000247021	42.359	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	705	853	0.000247021	42.359	cl27769	GTP_EFTU superfamily	-	-
	specific	224025	705	870	0.000270894	43.0255	COG1100	Gem1	-	cl27030
Lges1860	specific	206640	60	224	1.42081e-39	137.202	cd00154	Rab	-	cl21455
	superfamily	328724	60	224	1.42081e-39	137.202	cl21455	P-loop_NTPase superfamily	-	-

	non-specific	306559	61	229	1.56523e-34	124.153	pfam00071	Ras	-	cl27030
	superfamily	331851	61	229	1.56523e-34	124.153	cl27030	Ras superfamily	-	-
	non-specific	197555	60	229	1.08303e-33	121.846	smart00175	RAB	-	cl27030
	non-specific	178655	59	229	3.78096e-22	92.6968	PLN03108	PLN03108	-	cl27030
	specific	224025	60	258	9.61233e-21	88.8643	COG1100	Gem1	-	cl27030
	non-specific	272973	60	224	3.09947e-10	58.1521	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	60	224	3.09947e-10	58.1521	cl27769	GTP_EFTU superfamily	-	-
LgoA0634	specific	206640	7	159	3.33558e-35	125.261	cd00154	Rab	-	cl21455
	superfamily	328724	7	159	3.33558e-35	125.261	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	7	160	4.386e-30	112.216	smart00175	RAB	-	cl27030
	superfamily	331851	7	160	4.386e-30	112.216	cl27030	Ras superfamily	-	-
	non-specific	306559	8	157	4.55964e-29	109.516	pfam00071	Ras	-	cl27030
	specific	224025	6	189	7.34287e-21	88.8643	COG1100	Gem1	-	cl27030
	non-specific	178657	7	192	2.19704e-18	82.2838	PLN03110	PLN03110	-	cl27030
	non-specific	272973	7	157	8.55316e-18	78.9529	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	157	8.55316e-18	78.9529	cl27769	GTP_EFTU superfamily	-	-
LgoA0880	specific	206640	11	168	3.37441e-50	163.396	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	3.37441e-50	163.396	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	172	9.79435e-49	159.596	smart00175	RAB	-	cl27030
	superfamily	331851	11	172	9.79435e-49	159.596	cl27030	Ras superfamily	-	-
	non-specific	306559	12	172	7.36868e-44	147.265	pfam00071	Ras	-	cl27030
	non-specific	178657	5	176	1.35361e-29	111.944	PLN03110	PLN03110	-	cl27030
	specific	224025	7	187	6.53287e-17	77.6935	COG1100	Gem1	-	cl27030
	non-specific	272973	11	164	1.03032e-13	67.3969	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	164	1.03032e-13	67.3969	cl27769	GTP_EFTU superfamily	-	-
LgoA2567	non-specific	206640	256	417	7.12157e-23	94.0598	cd00154	Rab	-	cl21455
	superfamily	328724	256	417	7.12157e-23	94.0598	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	256	410	2.73817e-21	89.8703	pfam00071	Ras	-	cl27030
	superfamily	331851	256	410	2.73817e-21	89.8703	cl27030	Ras superfamily	-	-
	non-specific	197555	256	410	3.12068e-18	81.4003	smart00175	RAB	-	cl27030

	non-specific	240385	256	410	9.49401e-10	57.5663	PTZ00369	PTZ00369	-	cl27030
	specific	315592	200	238	0.000393237	37.8473	pfam12937	F-box-like	-	cl02535
	superfamily	321975	200	238	0.000393237	37.8473	cl02535	F-box superfamily	-	-
	specific	224025	333	423	0.00328072	38.7883	COG1100	Gem1	NC	cl27030
	non-specific	114219	29	195	0.0040106	39.3197	pfam05483	SCP-1	N	cl25732
	superfamily	330553	29	195	0.0040106	39.3197	cl25732	SMC_N superfamily	N	-
LgoA3158	specific	206648	24	182	2.94601e-12	64.0147	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	24	182	2.94601e-12	64.0147	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	307856	27	130	2.21302e-06	45.6865	pfam01926	MMR_HSR1	-	cl21455
	specific	224025	16	203	2.0291e-05	44.9515	COG1100	Gem1	-	cl27030
	superfamily	331851	16	203	2.0291e-05	44.9515	cl27030	Ras superfamily	-	-
LgoB0626	specific	206648	24	182	3.03285e-12	64.0147	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	24	182	3.03285e-12	64.0147	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	307856	27	130	2.12873e-06	46.0717	pfam01926	MMR_HSR1	-	cl21455
	specific	224025	16	215	2.39571e-05	44.9515	COG1100	Gem1	-	cl27030
	superfamily	331851	16	215	2.39571e-05	44.9515	cl27030	Ras superfamily	-	-
LgoB1531	specific	206640	7	159	4.92455e-34	122.179	cd00154	Rab	-	cl21455
	superfamily	328724	7	159	4.92455e-34	122.179	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	7	160	2.94149e-28	107.209	smart00175	RAB	-	cl27030
	superfamily	331851	7	160	2.94149e-28	107.209	cl27030	Ras superfamily	-	-
	non-specific	306559	8	157	3.2265e-27	104.508	pfam00071	Ras	-	cl27030
	specific	224025	6	159	1.52592e-18	82.7011	COG1100	Gem1	-	cl27030
	non-specific	272973	7	157	1.05718e-17	78.9529	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	157	1.05718e-17	78.9529	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178657	7	157	2.11804e-17	79.5874	PLN03110	PLN03110	C	cl27030
LgoB2964	non-specific	206640	256	417	1.88243e-23	95.6006	cd00154	Rab	-	cl21455
	superfamily	328724	256	417	1.88243e-23	95.6006	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	256	410	1.0447e-21	91.0259	pfam00071	Ras	-	cl27030
	superfamily	331851	256	410	1.0447e-21	91.0259	cl27030	Ras superfamily	-	-
	non-specific	197555	256	410	6.30305e-19	83.3263	smart00175	RAB	-	cl27030

	non-specific	178655	326	426	4.48169e-10	59.1844	PLN03108	PLN03108	N	cl27030
	specific	315592	200	238	0.000438206	37.4621	pfam12937	F-box-like	-	cl02535
	superfamily	321975	200	238	0.000438206	37.4621	cl02535	F-box superfamily	-	-
	specific	224025	333	423	0.00296795	38.7883	COG1100	Gem1	NC	cl27030
	non-specific	114219	29	195	0.00561456	38.9345	pfam05483	SCP-1	N	cl25732
	superfamily	330553	29	195	0.00561456	38.9345	cl25732	SMC_N superfamily	N	-
LgoB3164	specific	206640	11	168	2.80846e-50	163.396	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.80846e-50	163.396	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	172	8.33111e-49	159.981	smart00175	RAB	-	cl27030
	superfamily	331851	11	172	8.33111e-49	159.981	cl27030	Ras superfamily	-	-
	non-specific	306559	12	172	6.13778e-44	147.265	pfam00071	Ras	-	cl27030
	non-specific	178657	5	176	1.35361e-29	111.944	PLN03110	PLN03110	-	cl27030
	specific	224025	7	187	5.51049e-17	78.0787	COG1100	Gem1	-	cl27030
	non-specific	272973	11	164	8.78388e-14	67.7821	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	164	8.78388e-14	67.7821	cl27769	GTP_EFTU superfamily	-	-
Lgra1130	specific	206640	19	172	1.64258e-32	118.713	cd00154	Rab	-	cl21455
	superfamily	328724	19	172	1.64258e-32	118.713	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	19	173	9.4543e-28	106.053	smart00175	RAB	-	cl27030
	superfamily	331851	19	173	9.4543e-28	106.053	cl27030	Ras superfamily	-	-
	non-specific	306559	20	172	3.56007e-25	99.1151	pfam00071	Ras	-	cl27030
	specific	224025	16	215	1.14883e-18	83.0863	COG1100	Gem1	-	cl27030
	non-specific	178657	19	202	8.42855e-16	74.965	PLN03110	PLN03110	-	cl27030
	non-specific	272973	18	170	1.60048e-13	67.3969	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	18	170	1.60048e-13	67.3969	cl27769	GTP_EFTU superfamily	-	-
Lgra2032	specific	206640	11	168	1.32871e-50	164.551	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	1.32871e-50	164.551	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	5.4505e-49	160.366	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	5.4505e-49	160.366	cl27030	Ras superfamily	-	-
	non-specific	306559	12	171	7.24343e-47	154.969	pfam00071	Ras	-	cl27030
	non-specific	178657	1	171	3.16594e-33	121.574	PLN03110	PLN03110	-	cl27030

	specific	224025	7	201	2.48161e-21	90.0199	COG1100	Gem1	-	cl27030
	non-specific	272973	11	166	7.41358e-14	67.7821	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	166	7.41358e-14	67.7821	cl27769	GTP_EFTU superfamily	-	-
Lgra2891	specific	206640	47	185	9.34987e-32	115.631	cd00154	Rab	-	cl21455
	superfamily	328724	47	185	9.34987e-32	115.631	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	47	188	4.03607e-27	103.357	smart00175	RAB	-	cl27030
	superfamily	331851	47	188	4.03607e-27	103.357	cl27030	Ras superfamily	-	-
	non-specific	306559	47	188	1.28147e-25	99.5003	pfam00071	Ras	-	cl27030
	non-specific	178655	47	195	1.12823e-14	71.1256	PLN03108	PLN03108	-	cl27030
	specific	224025	46	197	1.049e-07	51.4999	COG1100	Gem1	-	cl27030
Lgra3435	specific	206640	74	228	1.75005e-27	104.075	cd00154	Rab	-	cl21455
	superfamily	328724	74	228	1.75005e-27	104.075	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	75	233	1.48355e-21	88.7148	pfam00071	Ras	-	cl27030
	superfamily	331851	75	233	1.48355e-21	88.7148	cl27030	Ras superfamily	-	-
	non-specific	197555	74	234	2.84789e-20	85.2523	smart00175	RAB	-	cl27030
	non-specific	215587	66	244	2.92035e-14	70.0843	PLN03118	PLN03118	-	cl27030
	specific	224025	74	263	5.80737e-10	58.0483	COG1100	Gem1	-	cl27030
	non-specific	272973	74	225	3.54133e-05	43.1294	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	74	225	3.54133e-05	43.1294	cl27769	GTP_EFTU superfamily	-	-
Lgra3465	non-specific	197554	600	765	9.39258e-61	202.458	smart00174	RHO	-	cl27030
	superfamily	331851	600	765	9.39258e-61	202.458	cl27030	Ras superfamily	-	-
	specific	206641	598	764	1.03186e-60	202.004	cd00157	Rho	-	cl21455
	superfamily	328724	598	764	1.03186e-60	202.004	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	598	765	1.53586e-45	159.977	pfam00071	Ras	-	cl27030
	specific	224025	597	771	1.04995e-30	120.065	COG1100	Gem1	-	cl27030
	non-specific	272973	597	713	1.96385e-17	80.1085	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	597	713	1.96385e-17	80.1085	cl27769	GTP_EFTU superfamily	C	-
	non-specific	178657	598	758	4.07364e-17	80.743	PLN03110	PLN03110	C	cl27030
	non-specific	319568	131	207	2.66464e-09	53.7883	cd16654	RING-Ubox_CHIP	-	cl17238
	superfamily	327409	131	207	2.66464e-09	53.7883	cl17238	RING_Ubox superfamily	-	-

	non-specific	319568	218	276	8.7909e-06	43.7731	cd16654	RING-Ubox_CHIP	-	cl17238
	superfamily	327409	218	276	8.7909e-06	43.7731	cl17238	RING_Ubox superfamily	-	-
	non-specific	128780	133	207	0.000133855	40.2961	smart00504	Ubox	-	cl17238
	non-specific	128780	229	272	0.000208327	39.9109	smart00504	Ubox	-	cl17238
	non-specific	252675	153	213	0.00231891	37.2904	pfam04564	U-box	-	cl17238
	non-specific	252675	220	275	0.00234181	37.2904	pfam04564	U-box	-	cl17238
Lgra3555	non-specific	206641	2	163	2.45935e-42	142.683	cd00157	Rho	-	cl21455
	superfamily	328724	2	163	2.45935e-42	142.683	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197554	3	167	2.1343e-41	140.441	smart00174	RHO	-	cl27030
	superfamily	331851	3	167	2.1343e-41	140.441	cl27030	Ras superfamily	-	-
	non-specific	306559	2	164	1.08335e-37	130.316	pfam00071	Ras	-	cl27030
	non-specific	272973	1	159	2.66521e-21	87.8125	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	1	159	2.66521e-21	87.8125	cl27769	GTP_EFTU superfamily	-	-
	specific	224025	1	195	2.56785e-18	81.1603	COG1100	Gem1	-	cl27030
	non-specific	215587	2	159	4.17716e-17	77.7883	PLN03118	PLN03118	-	cl27030
Lgre1002	non-specific	206640	10	168	1.53775e-12	64.7846	cd00154	Rab	-	cl21455
	superfamily	328724	10	168	1.53775e-12	64.7846	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	11	133	7.51197e-11	58.671	pfam08477	Roc	-	cl21455
	non-specific	197555	10	188	2.90886e-06	46.7323	smart00175	RAB	-	cl27030
	superfamily	331851	10	188	2.90886e-06	46.7323	cl27030	Ras superfamily	-	-
	non-specific	272973	9	157	7.56816e-06	45.4405	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	9	157	7.56816e-06	45.4405	cl27769	GTP_EFTU superfamily	-	-
	specific	224025	5	220	2.02351e-05	45.3367	COG1100	Gem1	-	cl27030
LHAv2_0998	non-specific	206640	33	179	1.37446e-17	78.6518	cd00154	Rab	-	cl21455
	superfamily	328724	33	179	1.37446e-17	78.6518	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	34	138	2.08161e-13	65.6046	pfam08477	Roc	-	cl21455
	non-specific	197555	33	178	2.49905e-13	66.7627	smart00175	RAB	-	cl27030
	superfamily	331851	33	178	2.49905e-13	66.7627	cl27030	Ras superfamily	-	-
	specific	224025	28	201	9.4958e-12	63.8263	COG1100	Gem1	-	cl27030
	non-specific	272973	33	179	1.05457e-07	50.8333	TIGR00231	small_GTP	-	cl27769

	superfamily	332590	33	179	1.05457e-07	50.8333	cl27769	GTP_EFTU superfamily	-	-
	non-specific	234624	96	185	2.36381e-07	51.2015	PRK00089	era	NC	cl26333
	superfamily	331154	96	185	2.36381e-07	51.2015	cl26333	FeoB_N superfamily	NC	-
LHAv2_1310	non-specific	312094	5	117	1.42795e-06	46.3446	pfam08477	Roc	-	cl21455
	superfamily	328724	5	117	1.42795e-06	46.3446	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	206736	5	191	3.11204e-05	44.6307	cd04173	Rnd2_Rho7	-	cl21455
	specific	224025	1	210	0.000671423	40.3291	COG1100	Gem1	-	cl27030
	superfamily	331851	1	210	0.000671423	40.3291	cl27030	Ras superfamily	-	-
	non-specific	311978	123	235	0.00124527	39.9053	pfam08317	Spc7	NC	cl25508
	superfamily	330329	123	235	0.00124527	39.9053	cl25508	Spc7 superfamily	NC	-
	non-specific	215587	4	118	0.00164752	39.2683	PLN03118	PLN03118	C	cl27030
LHAv2_2690	specific	312094	4	116	1.53288e-23	92.9537	pfam08477	Roc	-	cl21455
	superfamily	328724	4	116	1.53288e-23	92.9537	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	206640	3	151	2.07399e-20	85.9706	cd00154	Rab	-	cl21455
	non-specific	197555	3	117	3.85295e-18	79.8595	smart00175	RAB	C	cl27030
	superfamily	331851	3	117	3.85295e-18	79.8595	cl27030	Ras superfamily	C	-
	specific	224025	3	130	1.17293e-17	80.0047	COG1100	Gem1	C	cl27030
	non-specific	272973	2	117	4.92672e-11	60.0781	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	2	117	4.92672e-11	60.0781	cl27769	GTP_EFTU superfamily	C	-
	non-specific	178655	4	127	7.42882e-10	57.6436	PLN03108	PLN03108	C	cl27030
LHAv2_2691	non-specific	312094	4	56	2.47471e-08	45.5742	pfam08477	Roc	C	cl21455
	superfamily	328724	4	56	2.47471e-08	45.5742	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	206694	3	56	5.6277e-08	45.9435	cd04109	Rab28	C	cl21455
	non-specific	197555	3	56	1.19504e-05	39.4135	smart00175	RAB	C	cl27030
	superfamily	331851	3	56	1.19504e-05	39.4135	cl27030	Ras superfamily	C	-
	specific	224025	2	56	4.88905e-05	38.0179	COG1100	Gem1	C	cl27030
LHAv2_2693	non-specific	206640	3	152	1.35544e-21	89.0522	cd00154	Rab	-	cl21455
	superfamily	328724	3	152	1.35544e-21	89.0522	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	4	117	9.15186e-21	85.6349	pfam08477	Roc	-	cl21455
	non-specific	197555	3	118	8.59331e-19	81.7855	smart00175	RAB	C	cl27030

	superfamily	331851	3	118	8.59331e-19	81.7855	cl27030	Ras superfamily	C	-
	specific	224025	3	131	2.49361e-15	73.4563	COG1100	Gem1	C	cl27030
	non-specific	178657	4	178	3.32038e-07	49.9271	PLN03110	PLN03110	C	cl27030
	non-specific	272973	2	118	2.58507e-06	46.5961	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	2	118	2.58507e-06	46.5961	cl27769	GTP_EFTU superfamily	C	-
Lim1229	specific	206648	28	176	7.90757e-12	62.4739	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	28	176	7.90757e-12	62.4739	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	28	170	2.1947e-10	59.5891	COG1100	Gem1	C	cl27030
	superfamily	331851	28	170	2.1947e-10	59.5891	cl27030	Ras superfamily	C	-
	non-specific	197555	28	176	6.41078e-09	54.4363	smart00175	RAB	-	cl27030
	non-specific	272973	28	178	1.15807e-07	50.8333	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	28	178	1.15807e-07	50.8333	cl27769	GTP_EFTU superfamily	-	-
	non-specific	306559	36	176	8.79394e-07	48.2688	pfam00071	Ras	-	cl27030
	non-specific	235392	91	187	1.14972e-05	46.6423	PRK05291	trmE	N	cl26334
	superfamily	331155	91	187	1.14972e-05	46.6423	cl26334	MnmE_helical superfamily	N	-
	non-specific	226515	193	290	0.00341342	38.6908	COG4028	COG4028	NC	cl18759
	superfamily	226515	193	290	0.00341342	38.6908	cl18759	COG4028 superfamily	NC	-
Lja0129	specific	312094	4	114	4.53016e-25	96.8057	pfam08477	Roc	-	cl21455
	superfamily	328724	4	114	4.53016e-25	96.8057	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	206640	3	149	1.08941e-22	91.7486	cd00154	Rab	-	cl21455
	non-specific	197555	3	145	3.21894e-20	85.2523	smart00175	RAB	-	cl27030
	superfamily	331851	3	145	3.21894e-20	85.2523	cl27030	Ras superfamily	-	-
	specific	224025	3	114	6.88471e-15	72.3007	COG1100	Gem1	C	cl27030
	non-specific	178657	2	135	3.90572e-08	52.6235	PLN03110	PLN03110	C	cl27030
	non-specific	272973	4	114	7.16428e-08	50.8333	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	4	114	7.16428e-08	50.8333	cl27769	GTP_EFTU superfamily	C	-
Lja2306	non-specific	206640	4	156	1.45168e-24	97.1414	cd00154	Rab	-	cl21455
	superfamily	328724	4	156	1.45168e-24	97.1414	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	4	157	8.85908e-19	81.7855	smart00175	RAB	-	cl27030
	superfamily	331851	4	157	8.85908e-19	81.7855	cl27030	Ras superfamily	-	-

	non-specific	312094	5	112	5.67607e-18	77.9309	pfam08477	Roc	-	cl21455
	specific	224025	1	150	1.97486e-14	71.1451	COG1100	Gem1	C	cl27030
	non-specific	272973	4	159	2.24674e-09	55.4557	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	159	2.24674e-09	55.4557	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178655	4	151	3.06414e-07	49.9396	PLN03108	PLN03108	-	cl27030
Lja2501	non-specific	312094	5	119	3.19889e-09	54.0486	pfam08477	Roc	-	cl21455
	superfamily	328724	5	119	3.19889e-09	54.0486	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	206741	5	164	3.26345e-09	55.0347	cd09914	RocCOR	-	cl21455
	specific	224025	1	149	1.03924e-07	51.8851	COG1100	Gem1	C	cl27030
	superfamily	331851	1	149	1.03924e-07	51.8851	cl27030	Ras superfamily	C	-
	non-specific	197555	4	115	4.36269e-07	49.0435	smart00175	RAB	C	cl27030
	non-specific	178657	3	137	0.00265697	38.7563	PLN03110	PLN03110	C	cl27030
Lja2537	specific	206640	224	381	3.05919e-29	111.009	cd00154	Rab	-	cl21455
	superfamily	328724	224	381	3.05919e-29	111.009	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	226	374	1.62785e-27	106.434	pfam00071	Ras	-	cl27030
	superfamily	331851	226	374	1.62785e-27	106.434	cl27030	Ras superfamily	-	-
	non-specific	197555	226	381	9.93336e-24	96.423	smart00175	RAB	-	cl27030
	non-specific	240385	275	396	1.33472e-10	59.8775	PTZ00369	PTZ00369	N	cl27030
	specific	224025	220	381	1.50186e-05	45.7219	COG1100	Gem1	-	cl27030
	non-specific	272973	224	379	0.000138263	41.9738	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	224	379	0.000138263	41.9738	cl27769	GTP_EFTU superfamily	-	-
Ljor1196	specific	206648	23	178	2.43274e-09	55.5404	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	23	178	2.43274e-09	55.5404	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	22	138	3.28183e-07	47.8854	pfam08477	Roc	-	cl21455
	specific	224025	18	179	7.98308e-06	46.1071	COG1100	Gem1	C	cl27030
	superfamily	331851	18	179	7.98308e-06	46.1071	cl27030	Ras superfamily	C	-
	non-specific	235392	94	179	2.33533e-05	45.4867	PRK05291	trmE	N	cl26334
	superfamily	331155	94	179	2.33533e-05	45.4867	cl26334	MnmE_helical superfamily	N	-
	non-specific	197555	22	147	0.00862969	36.3319	smart00175	RAB	C	cl27030
Ljor2281	non-specific	206640	3	150	9.90944e-24	94.8302	cd00154	Rab	-	cl21455

	superfamily	328724	3	150	9.90944e-24	94.8302	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	3	159	2.20235e-17	77.5483	smart00175	RAB	-	cl27030
	superfamily	331851	3	159	2.20235e-17	77.5483	cl27030	Ras superfamily	-	-
	non-specific	306559	4	150	8.85048e-16	73.3068	pfam00071	Ras	-	cl27030
	specific	224025	2	182	1.11793e-13	68.8339	COG1100	Gem1	-	cl27030
	non-specific	178655	2	226	7.05166e-09	54.9472	PLN03108	PLN03108	-	cl27030
	non-specific	272973	2	151	8.62333e-06	45.0553	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	2	151	8.62333e-06	45.0553	cl27769	GTP_EFTU superfamily	-	-
Ljor2282	non-specific	206640	7	152	3.09448e-20	85.2002	cd00154	Rab	-	cl21455
	superfamily	328724	7	152	3.09448e-20	85.2002	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	8	118	2.00835e-18	79.0865	pfam08477	Roc	-	cl21455
	specific	224025	6	118	4.13827e-16	75.7675	COG1100	Gem1	C	cl27030
	superfamily	331851	6	118	4.13827e-16	75.7675	cl27030	Ras superfamily	C	-
	non-specific	197555	7	152	1.19941e-14	70.2295	smart00175	RAB	-	cl27030
	non-specific	272973	8	87	6.47443e-08	51.2185	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	8	87	6.47443e-08	51.2185	cl27769	GTP_EFTU superfamily	C	-
	non-specific	215587	7	121	2.16352e-05	44.6611	PLN03118	PLN03118	C	cl27030
Ljor2501	specific	224025	3	165	1.72146e-13	68.4487	COG1100	Gem1	C	cl27030
	superfamily	331851	3	165	1.72146e-13	68.4487	cl27030	Ras superfamily	C	-
	non-specific	206653	3	137	5.58032e-11	60.258	cd01860	Rab5_related	C	cl21455
	superfamily	328724	3	137	5.58032e-11	60.258	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	306559	3	139	7.01933e-10	56.7432	pfam00071	Ras	C	cl27030
	non-specific	197555	3	160	2.79055e-07	49.4287	smart00175	RAB	-	cl27030
	non-specific	185444	63	149	2.01283e-05	44.3497	PTZ00099	PTZ00099	C	cl27030
	non-specific	272973	61	134	0.00244733	37.7366	TIGR00231	small_GTP	NC	cl27769
	superfamily	332590	61	134	0.00244733	37.7366	cl27769	GTP_EFTU superfamily	NC	-
Ljor2641	non-specific	206640	18	174	7.91217e-16	73.6442	cd00154	Rab	-	cl21455
	superfamily	328724	18	174	7.91217e-16	73.6442	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	12	187	1.0558e-11	63.4411	COG1100	Gem1	-	cl27030
	superfamily	331851	12	187	1.0558e-11	63.4411	cl27030	Ras superfamily	-	-

	non-specific	306559	18	133	4.56674e-11	60.21	pfam00071	Ras	C	cl27030
	non-specific	197555	18	130	4.91379e-10	57.5179	smart00175	RAB	C	cl27030
	non-specific	272973	18	171	8.91204e-08	50.8333	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	18	171	8.91204e-08	50.8333	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178655	18	130	0.000147986	42.2356	PLN03108	PLN03108	C	cl27030
Llan0853	non-specific	206640	3	189	3.67618e-24	97.1414	cd00154	Rab	-	cl21455
	superfamily	328724	3	189	3.67618e-24	97.1414	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	4	125	3.67445e-21	87.5609	pfam08477	Roc	-	cl21455
	non-specific	197555	3	189	5.6179e-20	85.6375	smart00175	RAB	-	cl27030
	superfamily	331851	3	189	5.6179e-20	85.6375	cl27030	Ras superfamily	-	-
	specific	224025	2	218	1.19559e-19	86.5531	COG1100	Gem1	-	cl27030
	non-specific	178655	2	139	1.39352e-13	68.8144	PLN03108	PLN03108	C	cl27030
	non-specific	272973	2	127	1.19291e-08	53.5297	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	2	127	1.19291e-08	53.5297	cl27769	GTP_EFTU superfamily	C	-
	non-specific	310337	287	354	0.00642102	37.8363	pfam05661	DUF808	N	cl01002
	superfamily	321298	287	354	0.00642102	37.8363	cl01002	DUF808 superfamily	N	-
Llan0913	non-specific	206640	4	160	4.72668e-13	66.3254	cd00154	Rab	-	cl21455
	superfamily	328724	4	160	4.72668e-13	66.3254	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	5	116	5.88423e-12	61.7526	pfam08477	Roc	-	cl21455
	specific	224025	1	129	2.97296e-10	59.5891	COG1100	Gem1	C	cl27030
	superfamily	331851	1	129	2.97296e-10	59.5891	cl27030	Ras superfamily	C	-
	non-specific	197555	4	165	5.70385e-08	51.7399	smart00175	RAB	-	cl27030
	non-specific	178655	5	159	7.43901e-05	43.3912	PLN03108	PLN03108	C	cl27030
Llikebru0111	specific	206648	6	168	1.08111e-12	65.1703	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	6	168	1.08111e-12	65.1703	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	5	163	4.00799e-09	54.8172	pfam00071	Ras	-	cl27030
	superfamily	331851	5	163	4.00799e-09	54.8172	cl27030	Ras superfamily	-	-
	non-specific	197555	5	163	1.07174e-07	50.9695	smart00175	RAB	-	cl27030
	non-specific	235392	89	168	0.000111071	43.5607	PRK05291	trmE	N	cl26334
	superfamily	331155	89	168	0.000111071	43.5607	cl26334	MnmE_helical superfamily	N	-

	specific	224025	5	133	0.000154469	42.2551	COG1100	Gem1	C	cl27030
	non-specific	272973	4	168	0.000502257	40.0478	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	168	0.000502257	40.0478	cl27769	GTP_EFTU superfamily	-	-
Llikebru1058	non-specific	206640	15	168	2.83684e-11	60.1622	cd00154	Rab	-	cl21455
	superfamily	328724	15	168	2.83684e-11	60.1622	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	15	165	1.0718e-09	55.5876	pfam00071	Ras	-	cl27030
	superfamily	331851	15	165	1.0718e-09	55.5876	cl27030	Ras superfamily	-	-
	specific	224025	16	173	1.6169e-06	47.6479	COG1100	Gem1	C	cl27030
	non-specific	197466	24	165	3.21139e-06	46.014	smart00010	small_GTPase	-	cl27030
	non-specific	240385	24	165	5.23021e-06	45.6251	PTZ00369	PTZ00369	-	cl27030
	non-specific	272973	19	164	0.000372262	40.0478	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	19	164	0.000372262	40.0478	cl27769	GTP_EFTU superfamily	-	-
Llikebru1284	specific	206640	21	175	4.72418e-37	126.031	cd00154	Rab	-	cl21455
	superfamily	328724	21	175	4.72418e-37	126.031	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	21	177	8.47538e-37	125.694	pfam00071	Ras	-	cl27030
	superfamily	331851	21	177	8.47538e-37	125.694	cl27030	Ras superfamily	-	-
	non-specific	197555	21	177	7.46657e-34	117.994	smart00175	RAB	-	cl27030
	non-specific	178655	27	170	7.36569e-19	80.3704	PLN03108	PLN03108	C	cl27030
	specific	224025	18	199	1.72659e-13	66.1375	COG1100	Gem1	-	cl27030
	non-specific	272973	23	176	4.33648e-13	63.9301	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	23	176	4.33648e-13	63.9301	cl27769	GTP_EFTU superfamily	-	-
Llikebru2131	specific	224025	4	114	4.22433e-15	72.6859	COG1100	Gem1	C	cl27030
	superfamily	331851	4	114	4.22433e-15	72.6859	cl27030	Ras superfamily	C	-
	specific	206648	7	148	5.25482e-10	57.0811	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	7	148	5.25482e-10	57.0811	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	5	114	1.12851e-08	53.2764	pfam00071	Ras	C	cl27030
	non-specific	197555	4	114	4.0567e-07	49.0435	smart00175	RAB	C	cl27030
	non-specific	272973	4	115	0.000724653	39.2774	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	4	115	0.000724653	39.2774	cl27769	GTP_EFTU superfamily	C	-
	non-specific	178657	3	77	0.00108165	39.5267	PLN03110	PLN03110	C	cl27030

llo1716	specific	206640	4	157	1.05413e-29	111.009	cd00154	Rab	-	cl21455
	superfamily	328724	4	157	1.05413e-29	111.009	cl21455	P-loop_NTPase superfamily	-	-
	specific	312094	5	116	3.02945e-25	97.5761	pfam08477	Roc	-	cl21455
	non-specific	197555	4	157	1.10899e-23	94.8822	smart00175	RAB	-	cl27030
	superfamily	331851	4	157	1.10899e-23	94.8822	cl27030	Ras superfamily	-	-
	non-specific	178657	4	116	4.24252e-15	73.039	PLN03110	PLN03110	C	cl27030
	specific	224025	1	157	1.73196e-13	68.4487	COG1100	Gem1	-	cl27030
	non-specific	272973	4	152	1.07933e-12	64.7005	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	152	1.07933e-12	64.7005	cl27769	GTP_EFTU superfamily	-	-
llo2329	non-specific	306559	32	177	2.27213e-44	149.191	pfam00071	Ras	-	cl27030
	superfamily	331851	32	177	2.27213e-44	149.191	cl27030	Ras superfamily	-	-
	non-specific	206661	26	184	5.15244e-41	140.542	cd01869	Rab1_Ypt1	-	cl21455
	superfamily	328724	26	184	5.15244e-41	140.542	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	32	182	1.59852e-35	126.083	smart00175	RAB	-	cl27030
	non-specific	178657	14	213	2.25279e-24	98.4622	PLN03110	PLN03110	-	cl27030
	specific	224025	32	192	3.36742e-16	76.1527	COG1100	Gem1	-	cl27030
	non-specific	272973	30	174	1.68272e-07	50.0629	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	30	174	1.68272e-07	50.0629	cl27769	GTP_EFTU superfamily	-	-
llo2424	specific	206648	16	157	1.66013e-07	48.2216	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	16	157	1.66013e-07	48.2216	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	235392	85	167	9.56755e-07	47.4127	PRK05291	trmE	N	cl26334
	superfamily	331155	85	167	9.56755e-07	47.4127	cl26334	MnmE_helical superfamily	N	-
	non-specific	315327	85	167	2.41831e-05	43.215	pfam12631	MnmE_helical	NC	cl26334
	non-specific	225171	85	162	0.00775603	35.7078	COG2262	HflX	N	cl25666
	superfamily	330487	85	162	0.00775603	35.7078	cl25666	HflX superfamily	N	-
llo3288	specific	206640	11	168	2.402e-46	153.381	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.402e-46	153.381	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	5.86619e-46	152.662	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	5.86619e-46	152.662	cl27030	Ras superfamily	-	-
	non-specific	306559	12	171	8.01284e-42	141.872	pfam00071	Ras	-	cl27030

	non-specific	178657	1	171	2.67464e-29	111.174	PLN03110	PLN03110	-	cl27030
	specific	224025	7	206	5.96626e-20	86.1679	COG1100	Gem1	-	cl27030
	non-specific	272973	12	166	1.16475e-14	70.0933	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	12	166	1.16475e-14	70.0933	cl27769	GTP_EFTU superfamily	-	-
LIo981808	specific	206640	18	171	1.54906e-28	107.927	cd00154	Rab	-	cl21455
	superfamily	328724	18	171	1.54906e-28	107.927	cl21455	P-loop_NTPase superfamily	-	-
	specific	312094	19	130	8.99544e-25	96.8057	pfam08477	Roc	-	cl21455
	non-specific	197555	18	171	7.29243e-23	92.9563	smart00175	RAB	-	cl27030
	superfamily	331851	18	171	7.29243e-23	92.9563	cl27030	Ras superfamily	-	-
	non-specific	178657	18	130	1.06423e-14	71.8834	PLN03110	PLN03110	C	cl27030
	specific	224025	15	137	1.30622e-12	66.1375	COG1100	Gem1	C	cl27030
	non-specific	272973	18	166	2.91474e-12	63.9301	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	18	166	2.91474e-12	63.9301	cl27769	GTP_EFTU superfamily	-	-
LIo982467	non-specific	306559	32	177	1.61205e-44	149.576	pfam00071	Ras	-	cl27030
	superfamily	331851	32	177	1.61205e-44	149.576	cl27030	Ras superfamily	-	-
	non-specific	206661	26	184	4.02952e-41	140.927	cd01869	Rab1_Ypt1	-	cl21455
	superfamily	328724	26	184	4.02952e-41	140.927	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	32	182	1.37772e-35	126.469	smart00175	RAB	-	cl27030
	non-specific	178657	14	213	1.83064e-23	96.151	PLN03110	PLN03110	-	cl27030
	specific	224025	32	192	2.45358e-16	76.5379	COG1100	Gem1	-	cl27030
	non-specific	272973	30	174	1.21507e-07	50.4481	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	30	174	1.21507e-07	50.4481	cl27769	GTP_EFTU superfamily	-	-
LIo983459	specific	206640	11	168	2.4809e-46	153.381	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.4809e-46	153.381	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	5.9939e-46	152.662	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	5.9939e-46	152.662	cl27030	Ras superfamily	-	-
	non-specific	306559	12	171	9.93158e-42	141.487	pfam00071	Ras	-	cl27030
	non-specific	178657	1	171	2.67464e-29	111.174	PLN03110	PLN03110	-	cl27030
	specific	224025	7	206	8.2603e-20	85.7827	COG1100	Gem1	-	cl27030
	non-specific	272973	12	166	1.49647e-14	69.7081	TIGR00231	small_GTP	-	cl27769

	superfamily	332590	12	166	1.49647e-14	69.7081	cl27769	GTP_EFTU superfamily	-	-
LloAT1802	specific	206640	18	171	2.03632e-29	110.238	cd00154	Rab	-	cl21455
	superfamily	328724	18	171	2.03632e-29	110.238	cl21455	P-loop_NTPase superfamily	-	-
	specific	312094	19	130	4.92609e-25	97.1909	pfam08477	Roc	-	cl21455
	non-specific	197555	18	171	1.48173e-23	94.8822	smart00175	RAB	-	cl27030
	superfamily	331851	18	171	1.48173e-23	94.8822	cl27030	Ras superfamily	-	-
	non-specific	178657	18	130	4.41873e-15	73.039	PLN03110	PLN03110	C	cl27030
	specific	224025	15	171	3.84402e-13	67.6783	COG1100	Gem1	-	cl27030
	non-specific	272973	18	166	1.89659e-12	64.3153	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	18	166	1.89659e-12	64.3153	cl27769	GTP_EFTU superfamily	-	-
LloAT2494	non-specific	306559	32	177	2.27213e-44	149.191	pfam00071	Ras	-	cl27030
	superfamily	331851	32	177	2.27213e-44	149.191	cl27030	Ras superfamily	-	-
	non-specific	206661	26	184	5.15244e-41	140.542	cd01869	Rab1_Ypt1	-	cl21455
	superfamily	328724	26	184	5.15244e-41	140.542	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	32	182	1.59852e-35	126.083	smart00175	RAB	-	cl27030
	non-specific	178657	14	213	2.25279e-24	98.4622	PLN03110	PLN03110	-	cl27030
	specific	224025	32	192	3.36742e-16	76.1527	COG1100	Gem1	-	cl27030
	non-specific	272973	30	174	1.68272e-07	50.0629	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	30	174	1.68272e-07	50.0629	cl27769	GTP_EFTU superfamily	-	-
LloAT2599	specific	206648	16	157	1.66013e-07	48.2216	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	16	157	1.66013e-07	48.2216	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	235392	85	167	9.56755e-07	47.4127	PRK05291	trmE	N	cl26334
	superfamily	331155	85	167	9.56755e-07	47.4127	cl26334	MnmE_helical superfamily	N	-
	non-specific	315327	85	167	2.41831e-05	43.215	pfam12631	MnmE_helical	NC	cl26334
	non-specific	225171	85	162	0.00775603	35.7078	COG2262	HflX	N	cl25666
	superfamily	330487	85	162	0.00775603	35.7078	cl25666	HflX superfamily	N	-
LloAT3527	specific	206640	11	168	2.402e-46	153.381	cd00154	Rab	-	cl21455
	superfamily	328724	11	168	2.402e-46	153.381	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	5.86619e-46	152.662	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	5.86619e-46	152.662	cl27030	Ras superfamily	-	-

	non-specific	306559	12	171	8.01284e-42	141.872	pfam00071	Ras	-	cl27030
	non-specific	178657	1	171	2.67464e-29	111.174	PLN03110	PLN03110	-	cl27030
	specific	224025	7	206	5.96626e-20	86.1679	COG1100	Gem1	-	cl27030
	non-specific	272973	12	166	1.16475e-14	70.0933	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	12	166	1.16475e-14	70.0933	cl27769	GTP_EFTU superfamily	-	-
Llon1496	non-specific	206640	11	151	2.26648e-20	85.9706	cd00154	Rab	-	cl21455
	superfamily	328724	11	151	2.26648e-20	85.9706	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	11	168	2.97332e-14	70.7599	COG1100	Gem1	-	cl27030
	superfamily	331851	11	168	2.97332e-14	70.7599	cl27030	Ras superfamily	-	-
	non-specific	197555	11	151	2.63446e-13	66.7627	smart00175	RAB	-	cl27030
	non-specific	306559	11	151	1.06742e-12	64.8324	pfam00071	Ras	-	cl27030
	non-specific	272973	11	151	2.09905e-08	52.7593	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	151	2.09905e-08	52.7593	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178655	11	167	6.01636e-07	49.1692	PLN03108	PLN03108	-	cl27030
Lma0833	specific	224025	2	188	3.17094e-12	64.9819	COG1100	Gem1	-	cl27030
	superfamily	331851	2	188	3.17094e-12	64.9819	cl27030	Ras superfamily	-	-
	specific	206648	6	149	1.36547e-09	56.3107	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	6	149	1.36547e-09	56.3107	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	5	123	2.11033e-05	42.8778	pfam08477	Roc	-	cl21455
	non-specific	272973	2	124	0.00281869	37.7366	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	2	124	0.00281869	37.7366	cl27769	GTP_EFTU superfamily	C	-
Lma1004	non-specific	206640	10	154	1.43612e-21	89.4374	cd00154	Rab	-	cl21455
	superfamily	328724	10	154	1.43612e-21	89.4374	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	10	154	2.73132e-13	66.7627	smart00175	RAB	-	cl27030
	superfamily	331851	10	154	2.73132e-13	66.7627	cl27030	Ras superfamily	-	-
	non-specific	306559	10	154	4.78412e-11	60.21	pfam00071	Ras	-	cl27030
	specific	224025	1	155	6.22577e-08	52.2703	COG1100	Gem1	-	cl27030
	non-specific	272973	7	149	6.92597e-06	45.4405	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	149	6.92597e-06	45.4405	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178655	10	162	0.000420367	40.6948	PLN03108	PLN03108	-	cl27030

	non-specific	293602	181	297	0.00795228	37.6751	pfam16997	Wap1	NC	cl25249
	superfamily	293602	181	297	0.00795228	37.6751	cl25249	Wap1 superfamily	NC	-
Lma1540	specific	206640	3	161	2.56834e-35	124.105	cd00154	Rab	-	cl21455
	superfamily	328724	3	161	2.56834e-35	124.105	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	3	159	1.24636e-28	106.823	smart00175	RAB	-	cl27030
	superfamily	331851	3	159	1.24636e-28	106.823	cl27030	Ras superfamily	-	-
	non-specific	306559	14	162	1.15034e-24	96.4187	pfam00071	Ras	-	cl27030
	specific	224025	2	182	2.01581e-17	78.4639	COG1100	Gem1	-	cl27030
	non-specific	178655	9	151	7.27478e-14	68.4292	PLN03108	PLN03108	C	cl27030
LmasA0793	non-specific	312094	4	127	1.99942e-19	82.1681	pfam08477	Roc	-	cl21455
	superfamily	328724	4	127	1.99942e-19	82.1681	cl21455	P-loop_NTPase superfamily	-	-
	specific	206648	6	166	6.91556e-19	82.1191	cd00882	Ras_like_GTPase	-	cl21455
	non-specific	197555	3	169	1.35828e-14	70.2295	smart00175	RAB	-	cl27030
	superfamily	331851	3	169	1.35828e-14	70.2295	cl27030	Ras superfamily	-	-
	specific	224025	2	127	3.42079e-13	67.6783	COG1100	Gem1	C	cl27030
	non-specific	272973	2	166	4.44158e-13	65.8561	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	2	166	4.44158e-13	65.8561	cl27769	GTP_EFTU superfamily	-	-
	non-specific	215587	1	178	5.00329e-09	55.4467	PLN03118	PLN03118	-	cl27030
	non-specific	315327	70	210	0.00531192	37.8222	pfam12631	MnmE_helical	N	cl26334
	superfamily	331155	70	210	0.00531192	37.8222	cl26334	MnmE_helical superfamily	N	-
LmasA1290	non-specific	306559	15	159	1.66778e-08	50.9652	pfam00071	Ras	-	cl27030
	superfamily	331851	15	159	1.66778e-08	50.9652	cl27030	Ras superfamily	-	-
	specific	206648	16	156	2.59981e-08	50.1476	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	16	156	2.59981e-08	50.1476	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	235392	87	160	4.42854e-07	48.1831	PRK05291	trmE	N	cl26334
	superfamily	331155	87	160	4.42854e-07	48.1831	cl26334	MnmE_helical superfamily	N	-
	specific	224025	15	164	2.97773e-06	45.3367	COG1100	Gem1	C	cl27030
	non-specific	197555	87	160	0.00413498	35.9467	smart00175	RAB	N	cl27030
LmasA1512	non-specific	206661	691	850	7.41535e-54	184.069	cd01869	Rab1_Ypt1	-	cl21455
	superfamily	328724	691	850	7.41535e-54	184.069	cl21455	P-loop_NTPase superfamily	-	-

	specific	306559	692	851	4.67606e-53	181.933	pfam00071	Ras	-	cl27030
	superfamily	331851	692	851	4.67606e-53	181.933	cl27030	Ras superfamily	-	-
	non-specific	197555	691	853	2.36592e-49	171.537	smart00175	RAB	-	cl27030
	non-specific	178655	691	853	6.30955e-32	123.513	PLN03108	PLN03108	-	cl27030
	specific	224025	688	851	5.96497e-25	103.887	COG1100	Gem1	-	cl27030
	non-specific	272973	691	846	7.68012e-17	78.5677	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	691	846	7.68012e-17	78.5677	cl27769	GTP_EFTU superfamily	-	-
LmasA2084	specific	206648	9	156	1.56876e-15	72.8743	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	9	156	1.56876e-15	72.8743	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	2	188	9.49668e-10	57.6631	COG1100	Gem1	-	cl27030
	superfamily	331851	2	188	9.49668e-10	57.6631	cl27030	Ras superfamily	-	-
	non-specific	197555	10	157	1.18702e-09	56.3623	smart00175	RAB	-	cl27030
	non-specific	306524	9	157	3.71505e-08	52.2313	pfam00025	Arf	-	cl21455
	non-specific	272973	7	154	1.74185e-07	50.0629	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	154	1.74185e-07	50.0629	cl27769	GTP_EFTU superfamily	-	-
	non-specific	234624	7	155	0.0011708	40.0307	PRK00089	era	C	cl26333
	superfamily	331154	7	155	0.0011708	40.0307	cl26333	FeoB_N superfamily	C	-
LmasA2851	non-specific	312094	12	93	1.11575e-11	59.0562	pfam08477	Roc	C	cl21455
	superfamily	328724	12	93	1.11575e-11	59.0562	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	206640	11	83	4.15101e-11	58.6214	cd00154	Rab	C	cl21455
	non-specific	197555	11	86	4.65596e-11	58.2883	smart00175	RAB	C	cl27030
	superfamily	331851	11	86	4.65596e-11	58.2883	cl27030	Ras superfamily	C	-
	non-specific	215587	10	79	1.20517e-10	58.1431	PLN03118	PLN03118	C	cl27030
	specific	224025	9	83	0.00392929	36.8623	COG1100	Gem1	C	cl27030
	non-specific	272973	10	83	0.00901314	35.4254	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	10	83	0.00901314	35.4254	cl27769	GTP_EFTU superfamily	C	-
LmasA3184	non-specific	312094	9	115	7.05901e-15	69.8418	pfam08477	Roc	-	cl21455
	superfamily	328724	9	115	7.05901e-15	69.8418	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	206640	3	153	1.50785e-14	70.1774	cd00154	Rab	-	cl21455
	specific	224025	2	210	1.92852e-14	71.5303	COG1100	Gem1	-	cl27030

	superfamily	331851	2	210	1.92852e-14	71.5303	cl27030	Ras superfamily	-	-
	non-specific	215587	1	123	1.98824e-11	62.3803	PLN03118	PLN03118	C	cl27030
	non-specific	197555	12	139	1.59667e-09	55.9771	smart00175	RAB	-	cl27030
	non-specific	272973	2	153	2.93511e-08	52.3741	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	2	153	2.93511e-08	52.3741	cl27769	GTP_EFTU superfamily	-	-
LmasA3659	non-specific	206640	29	111	9.04954e-15	69.0218	cd00154	Rab	C	cl21455
	superfamily	328724	29	111	9.04954e-15	69.0218	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	312094	30	111	1.33125e-13	64.8342	pfam08477	Roc	C	cl21455
	non-specific	197555	29	111	4.11679e-13	64.8367	smart00175	RAB	C	cl27030
	superfamily	331851	29	111	4.11679e-13	64.8367	cl27030	Ras superfamily	C	-
	non-specific	215587	28	229	7.51779e-10	56.6023	PLN03118	PLN03118	-	cl27030
	superfamily	331851	28	229	7.51779e-10	56.6023	cl27030	Ras superfamily	-	-
	non-specific	178657	30	104	1.05351e-08	53.3939	PLN03110	PLN03110	C	cl27030
	specific	224025	27	110	5.89643e-06	45.3367	COG1100	Gem1	C	cl27030
LmasA3690	non-specific	197555	657	811	1.11751e-31	121.076	smart00175	RAB	-	cl27030
	superfamily	331851	657	811	1.11751e-31	121.076	cl27030	Ras superfamily	-	-
	specific	206640	657	815	8.91839e-31	118.327	cd00154	Rab	-	cl21455
	superfamily	328724	657	815	8.91839e-31	118.327	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	659	820	6.64335e-29	112.982	pfam00071	Ras	-	cl27030
	specific	238125	57	181	3.38114e-19	83.9722	cd00204	ANK	-	cl02529
	superfamily	321973	57	181	3.38114e-19	83.9722	cl02529	ANK superfamily	-	-
	non-specific	215587	647	811	3.21092e-16	78.1735	PLN03118	PLN03118	C	cl27030
	specific	224025	656	829	6.71955e-15	74.6119	COG1100	Gem1	-	cl27030
	specific	315466	67	152	1.31696e-12	63.9753	pfam12796	Ank_2	-	cl26073
	superfamily	330894	67	152	1.31696e-12	63.9753	cl26073	Ank_2 superfamily	-	-
	non-specific	272973	659	813	2.45867e-08	53.9149	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	659	813	2.45867e-08	53.9149	cl27769	GTP_EFTU superfamily	-	-
	specific	223738	23	118	1.13963e-06	50.5931	COG0666	ANKYR	N	cl26073
	non-specific	222939	61	163	1.2316e-05	48.3378	PHA02878	PHA02878	NC	cl26073
	specific	197603	62	91	0.000110941	39.8786	smart00248	ANK	-	cl02529

LmasA3771	non-specific	206713	15	115	5.91634e-07	48.042	cd04146	RERG_RasL11_like	N	cl21455
	superfamily	328724	15	115	5.91634e-07	48.042	cl21455	P-loop_NTPase superfamily	N	-
	non-specific	306559	49	120	5.21016e-05	42.1056	pfam00071	Ras	N	cl27030
	superfamily	331851	49	120	5.21016e-05	42.1056	cl27030	Ras superfamily	N	-
	non-specific	197554	51	112	0.00910944	35.667	smart00174	RHO	NC	cl27030
LmasB0793	non-specific	312094	4	127	1.99942e-19	82.1681	pfam08477	Roc	-	cl21455
	superfamily	328724	4	127	1.99942e-19	82.1681	cl21455	P-loop_NTPase superfamily	-	-
	specific	206648	6	166	6.91556e-19	82.1191	cd00882	Ras_like_GTPase	-	cl21455
	non-specific	197555	3	169	1.35828e-14	70.2295	smart00175	RAB	-	cl27030
	superfamily	331851	3	169	1.35828e-14	70.2295	cl27030	Ras superfamily	-	-
	specific	224025	2	127	3.42079e-13	67.6783	COG1100	Gem1	C	cl27030
	non-specific	272973	2	166	4.44158e-13	65.8561	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	2	166	4.44158e-13	65.8561	cl27769	GTP_EFTU superfamily	-	-
	non-specific	215587	1	178	5.00329e-09	55.4467	PLN03118	PLN03118	-	cl27030
	non-specific	315327	70	210	0.00531192	37.8222	pfam12631	MnmE_helical	N	cl26334
	superfamily	331155	70	210	0.00531192	37.8222	cl26334	MnmE_helical superfamily	N	-
LmasB1290	non-specific	306559	15	159	1.66778e-08	50.9652	pfam00071	Ras	-	cl27030
	superfamily	331851	15	159	1.66778e-08	50.9652	cl27030	Ras superfamily	-	-
	specific	206648	16	156	2.59981e-08	50.1476	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	16	156	2.59981e-08	50.1476	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	235392	87	160	4.42854e-07	48.1831	PRK05291	trmE	N	cl26334
	superfamily	331155	87	160	4.42854e-07	48.1831	cl26334	MnmE_helical superfamily	N	-
	specific	224025	15	164	2.97773e-06	45.3367	COG1100	Gem1	C	cl27030
	non-specific	197555	87	160	0.00413498	35.9467	smart00175	RAB	N	cl27030
LmasB1512	non-specific	206661	691	850	7.41535e-54	184.069	cd01869	Rab1_Ypt1	-	cl21455
	superfamily	328724	691	850	7.41535e-54	184.069	cl21455	P-loop_NTPase superfamily	-	-
	specific	306559	692	851	4.67606e-53	181.933	pfam00071	Ras	-	cl27030
	superfamily	331851	692	851	4.67606e-53	181.933	cl27030	Ras superfamily	-	-
	non-specific	197555	691	853	2.36592e-49	171.537	smart00175	RAB	-	cl27030
	non-specific	178655	691	853	6.30955e-32	123.513	PLN03108	PLN03108	-	cl27030

	specific	224025	688	851	5.96497e-25	103.887	COG1100	Gem1	-	cl27030
	non-specific	272973	691	846	7.68012e-17	78.5677	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	691	846	7.68012e-17	78.5677	cl27769	GTP_EFTU superfamily	-	-
LmasB2084	specific	206648	9	156	1.56876e-15	72.8743	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	9	156	1.56876e-15	72.8743	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	2	188	9.49668e-10	57.6631	COG1100	Gem1	-	cl27030
	superfamily	331851	2	188	9.49668e-10	57.6631	cl27030	Ras superfamily	-	-
	non-specific	197555	10	157	1.18702e-09	56.3623	smart00175	RAB	-	cl27030
	non-specific	306524	9	157	3.71505e-08	52.2313	pfam00025	Arf	-	cl21455
	non-specific	272973	7	154	1.74185e-07	50.0629	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	154	1.74185e-07	50.0629	cl27769	GTP_EFTU superfamily	-	-
	non-specific	234624	7	155	0.0011708	40.0307	PRK00089	era	C	cl26333
	superfamily	331154	7	155	0.0011708	40.0307	cl26333	FeoB_N superfamily	C	-
LmasB2851	non-specific	312094	12	93	1.11575e-11	59.0562	pfam08477	Roc	C	cl21455
	superfamily	328724	12	93	1.11575e-11	59.0562	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	206640	11	83	4.15101e-11	58.6214	cd00154	Rab	C	cl21455
	non-specific	197555	11	86	4.65596e-11	58.2883	smart00175	RAB	C	cl27030
	superfamily	331851	11	86	4.65596e-11	58.2883	cl27030	Ras superfamily	C	-
	non-specific	215587	10	79	1.20517e-10	58.1431	PLN03118	PLN03118	C	cl27030
	specific	224025	9	83	0.00392929	36.8623	COG1100	Gem1	C	cl27030
	non-specific	272973	10	83	0.00901314	35.4254	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	10	83	0.00901314	35.4254	cl27769	GTP_EFTU superfamily	C	-
LmasB3184	non-specific	312094	9	115	7.05901e-15	69.8418	pfam08477	Roc	-	cl21455
	superfamily	328724	9	115	7.05901e-15	69.8418	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	206640	3	153	1.50785e-14	70.1774	cd00154	Rab	-	cl21455
	specific	224025	2	210	1.92852e-14	71.5303	COG1100	Gem1	-	cl27030
	superfamily	331851	2	210	1.92852e-14	71.5303	cl27030	Ras superfamily	-	-
	non-specific	215587	1	123	1.98824e-11	62.3803	PLN03118	PLN03118	C	cl27030
	non-specific	197555	12	139	1.59667e-09	55.9771	smart00175	RAB	-	cl27030
	non-specific	272973	2	153	2.93511e-08	52.3741	TIGR00231	small_GTP	-	cl27769

	superfamily	332590	2	153	2.93511e-08	52.3741	cl27769	GTP_EFTU superfamily	-	-
LmasB3659	non-specific	206640	29	111	9.04954e-15	69.0218	cd00154	Rab	C	cl21455
	superfamily	328724	29	111	9.04954e-15	69.0218	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	312094	30	111	1.33125e-13	64.8342	pfam08477	Roc	C	cl21455
	non-specific	197555	29	111	4.11679e-13	64.8367	smart00175	RAB	C	cl27030
	superfamily	331851	29	111	4.11679e-13	64.8367	cl27030	Ras superfamily	C	-
	non-specific	215587	28	229	7.51779e-10	56.6023	PLN03118	PLN03118	-	cl27030
	superfamily	331851	28	229	7.51779e-10	56.6023	cl27030	Ras superfamily	-	-
	non-specific	178657	30	104	1.05351e-08	53.3939	PLN03110	PLN03110	C	cl27030
	specific	224025	27	110	5.89643e-06	45.3367	COG1100	Gem1	C	cl27030
LmasB3690	non-specific	197555	657	811	1.11751e-31	121.076	smart00175	RAB	-	cl27030
	superfamily	331851	657	811	1.11751e-31	121.076	cl27030	Ras superfamily	-	-
	specific	206640	657	815	8.91839e-31	118.327	cd00154	Rab	-	cl21455
	superfamily	328724	657	815	8.91839e-31	118.327	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	659	820	6.64335e-29	112.982	pfam00071	Ras	-	cl27030
	specific	238125	57	181	3.38114e-19	83.9722	cd00204	ANK	-	cl02529
	superfamily	321973	57	181	3.38114e-19	83.9722	cl02529	ANK superfamily	-	-
	non-specific	215587	647	811	3.21092e-16	78.1735	PLN03118	PLN03118	C	cl27030
	specific	224025	656	829	6.71955e-15	74.6119	COG1100	Gem1	-	cl27030
	specific	315466	67	152	1.31696e-12	63.9753	pfam12796	Ank_2	-	cl26073
	superfamily	330894	67	152	1.31696e-12	63.9753	cl26073	Ank_2 superfamily	-	-
	non-specific	272973	659	813	2.45867e-08	53.9149	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	659	813	2.45867e-08	53.9149	cl27769	GTP_EFTU superfamily	-	-
	specific	223738	23	118	1.13963e-06	50.5931	COG0666	ANKYR	N	cl26073
	non-specific	222939	61	163	1.2316e-05	48.3378	PHA02878	PHA02878	NC	cl26073
	specific	197603	62	91	0.000110941	39.8786	smart00248	ANK	-	cl02529
LmasB3771	non-specific	206713	15	115	5.91634e-07	48.042	cd04146	RERG_RasL11_like	N	cl21455
	superfamily	328724	15	115	5.91634e-07	48.042	cl21455	P-loop_NTPase superfamily	N	-
	non-specific	306559	49	120	5.21016e-05	42.1056	pfam00071	Ras	N	cl27030
	superfamily	331851	49	120	5.21016e-05	42.1056	cl27030	Ras superfamily	N	-

	non-specific	197554	51	112	0.00910944	35.667	smart00174	RHO	NC	cl27030
LmicB0409	non-specific	206640	10	154	1.86559e-22	91.7486	cd00154	Rab	-	cl21455
	superfamily	328724	10	154	1.86559e-22	91.7486	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	10	154	2.8399e-15	72.1555	smart00175	RAB	-	cl27030
	superfamily	331851	10	154	2.8399e-15	72.1555	cl27030	Ras superfamily	-	-
	specific	224025	8	155	7.48916e-11	60.7447	COG1100	Gem1	-	cl27030
	non-specific	306559	10	154	1.69333e-10	58.6692	pfam00071	Ras	-	cl27030
	non-specific	178655	10	165	3.61656e-08	53.0212	PLN03108	PLN03108	-	cl27030
	non-specific	272973	7	149	1.38181e-06	47.3665	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	149	1.38181e-06	47.3665	cl27769	GTP_EFTU superfamily	-	-
LmicB0828	non-specific	133330	78	146	1.83173e-06	47.012	cd04130	Wrch_1	NC	cl21455
	superfamily	328724	78	146	1.83173e-06	47.012	cl21455	P-loop_NTPase superfamily	NC	-
	non-specific	312094	78	135	0.000375935	39.0258	pfam08477	Roc	N	cl21455
	non-specific	197554	78	143	0.00377625	37.2078	smart00174	RHO	NC	cl27030
	superfamily	331851	78	143	0.00377625	37.2078	cl27030	Ras superfamily	NC	-
LMIv2_0854	non-specific	206640	10	154	1.44297e-22	92.1338	cd00154	Rab	-	cl21455
	superfamily	328724	10	154	1.44297e-22	92.1338	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	10	154	2.70227e-15	72.1555	smart00175	RAB	-	cl27030
	superfamily	331851	10	154	2.70227e-15	72.1555	cl27030	Ras superfamily	-	-
	specific	224025	8	155	6.25008e-11	61.1299	COG1100	Gem1	-	cl27030
	non-specific	306559	10	154	1.49293e-10	58.6692	pfam00071	Ras	-	cl27030
	non-specific	178655	10	165	3.61656e-08	53.0212	PLN03108	PLN03108	-	cl27030
	non-specific	272973	7	149	1.28033e-06	47.3665	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	149	1.28033e-06	47.3665	cl27769	GTP_EFTU superfamily	-	-
LMIv2_2158	non-specific	133330	78	146	2.43933e-06	47.012	cd04130	Wrch_1	NC	cl21455
	superfamily	328724	78	146	2.43933e-06	47.012	cl21455	P-loop_NTPase superfamily	NC	-
	non-specific	312094	78	135	0.000314262	39.7962	pfam08477	Roc	N	cl21455
	non-specific	197554	78	143	0.00398451	37.593	smart00174	RHO	NC	cl27030
	superfamily	331851	78	143	0.00398451	37.593	cl27030	Ras superfamily	NC	-
Lmo0615	non-specific	206640	70	230	1.47064e-13	67.8662	cd00154	Rab	-	cl21455

	superfamily	328724	70	230	1.47064e-13	67.8662	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	72	189	8.28966e-12	61.7526	pfam08477	Roc	-	cl21455
	non-specific	197555	66	219	7.9363e-08	51.3547	smart00175	RAB	-	cl27030
	superfamily	331851	66	219	7.9363e-08	51.3547	cl27030	Ras superfamily	-	-
	specific	224025	66	263	1.61891e-07	51.4999	COG1100	Gem1	-	cl27030
	non-specific	178655	65	224	5.21143e-07	49.9396	PLN03108	PLN03108	C	cl27030
	non-specific	311394	232	305	0.00273189	38.3649	pfam07426	Dynactin_p22	N	cl06456
	superfamily	311394	232	305	0.00273189	38.3649	cl06456	Dynactin_p22 superfamily	N	-
Lnau0521	specific	224025	17	205	3.74281e-10	59.2039	COG1100	Gem1	-	cl27030
	superfamily	331851	17	205	3.74281e-10	59.2039	cl27030	Ras superfamily	-	-
	specific	206648	20	182	6.52858e-08	51.3032	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	20	182	6.52858e-08	51.3032	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	19	130	2.48019e-07	48.6558	pfam08477	Roc	-	cl21455
	non-specific	197554	79	178	8.30234e-06	45.6822	smart00174	RHO	N	cl27030
	non-specific	272973	16	131	2.95239e-05	43.5145	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	16	131	2.95239e-05	43.5145	cl27769	GTP_EFTU superfamily	C	-
Lnau1544	non-specific	206640	8	174	2.1802e-18	80.963	cd00154	Rab	-	cl21455
	superfamily	328724	8	174	2.1802e-18	80.963	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	8	174	7.8199e-13	65.6028	pfam00071	Ras	-	cl27030
	superfamily	331851	8	174	7.8199e-13	65.6028	cl27030	Ras superfamily	-	-
	non-specific	197555	9	174	1.14832e-11	62.1403	smart00175	RAB	-	cl27030
	specific	224025	8	209	3.61659e-09	56.1223	COG1100	Gem1	-	cl27030
	non-specific	272973	7	169	0.00613417	36.9662	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	7	169	0.00613417	36.9662	cl27769	GTP_EFTU superfamily	-	-
Loas0638	non-specific	206641	54	174	4.22263e-33	116.875	cd00157	Rho	-	cl21455
	superfamily	328724	54	174	4.22263e-33	116.875	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197554	54	174	2.78069e-28	104.618	smart00174	RHO	-	cl27030
	superfamily	331851	54	174	2.78069e-28	104.618	cl27030	Ras superfamily	-	-
	non-specific	306559	57	195	8.27403e-17	74.0772	pfam00071	Ras	-	cl27030
	specific	224025	81	198	4.14171e-07	48.8035	COG1100	Gem1	N	cl27030

Loas2281	non-specific	206640	50	204	5.95605e-07	49.7618	cd00154	Rab	-	cl21455
	superfamily	328724	50	204	5.95605e-07	49.7618	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	50	207	1.78143e-05	45.5724	pfam00071	Ras	-	cl27030
	superfamily	331851	50	207	1.78143e-05	45.5724	cl27030	Ras superfamily	-	-
	non-specific	214541	111	196	0.000495147	41.3877	smart00173	RAS	N	cl27030
	non-specific	240385	45	178	0.00543166	38.6916	PTZ00369	PTZ00369	C	cl27030
Lpar0348	non-specific	206640	16	174	9.65526e-14	67.8662	cd00154	Rab	-	cl21455
	superfamily	328724	16	174	9.65526e-14	67.8662	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	16	134	2.49731e-06	45.5742	pfam08477	Roc	-	cl21455
	specific	224025	11	134	0.000366318	41.0995	COG1100	Gem1	C	cl27030
	superfamily	331851	11	134	0.000366318	41.0995	cl27030	Ras superfamily	C	-
Lpar0942	specific	206640	11	171	4.98086e-50	163.011	cd00154	Rab	-	cl21455
	superfamily	328724	11	171	4.98086e-50	163.011	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	174	3.55297e-45	150.736	smart00175	RAB	-	cl27030
	superfamily	331851	11	174	3.55297e-45	150.736	cl27030	Ras superfamily	-	-
	non-specific	306559	12	174	1.0389e-40	139.176	pfam00071	Ras	-	cl27030
	non-specific	178655	11	174	4.15461e-26	102.327	PLN03108	PLN03108	C	cl27030
	specific	224025	7	174	1.07697e-19	85.3975	COG1100	Gem1	-	cl27030
	non-specific	272973	11	162	1.4629e-11	61.6189	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	162	1.4629e-11	61.6189	cl27769	GTP_EFTU superfamily	-	-
Lpar0973	specific	206640	30	189	2.72624e-45	147.603	cd00154	Rab	-	cl21455
	superfamily	328724	30	189	2.72624e-45	147.603	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	31	188	1.07725e-41	138.791	pfam00071	Ras	-	cl27030
	superfamily	331851	31	188	1.07725e-41	138.791	cl27030	Ras superfamily	-	-
	non-specific	197555	30	189	2.88719e-39	132.632	smart00175	RAB	-	cl27030
	non-specific	178655	30	186	1.51986e-22	90.7708	PLN03108	PLN03108	C	cl27030
	specific	224025	28	215	1.46049e-19	83.0863	COG1100	Gem1	-	cl27030
	non-specific	272973	30	184	2.23505e-15	70.4785	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	30	184	2.23505e-15	70.4785	cl27769	GTP_EFTU superfamily	-	-
Lpar1023	non-specific	206640	248	409	5.96032e-23	94.445	cd00154	Rab	-	cl21455

	superfamily	328724	248	409	5.96032e-23	94.445	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	248	402	5.2202e-21	89.1	pfam00071	Ras	-	cl27030
	superfamily	331851	248	402	5.2202e-21	89.1	cl27030	Ras superfamily	-	-
	non-specific	197555	248	401	9.71041e-19	82.5559	smart00175	RAB	-	cl27030
	non-specific	178655	315	395	7.37273e-12	64.192	PLN03108	PLN03108	NC	cl27030
Lpar1509	specific	206640	7	161	1.30082e-35	126.417	cd00154	Rab	-	cl21455
	superfamily	328724	7	161	1.30082e-35	126.417	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	7	161	4.47575e-27	104.127	smart00175	RAB	-	cl27030
	superfamily	331851	7	161	4.47575e-27	104.127	cl27030	Ras superfamily	-	-
	non-specific	306559	8	164	3.63967e-26	101.812	pfam00071	Ras	-	cl27030
	specific	224025	6	194	1.50275e-18	82.7011	COG1100	Gem1	-	cl27030
	non-specific	272973	6	159	2.11565e-16	75.1009	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	6	159	2.11565e-16	75.1009	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178657	7	159	1.39635e-15	74.1946	PLN03110	PLN03110	C	cl27030
Lqua0234	specific	206640	358	524	4.18843e-45	156.077	cd00154	Rab	-	cl21455
	superfamily	328724	358	524	4.18843e-45	156.077	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	361	513	1.19847e-41	146.884	smart00175	RAB	-	cl27030
	superfamily	331851	361	513	1.19847e-41	146.884	cl27030	Ras superfamily	-	-
	non-specific	306559	358	524	4.26801e-39	139.946	pfam00071	Ras	-	cl27030
	non-specific	178655	355	513	3.96826e-28	111.572	PLN03108	PLN03108	C	cl27030
	specific	224025	353	472	2.24823e-22	95.4127	COG1100	Gem1	C	cl27030
	non-specific	272973	356	515	1.13457e-12	65.8561	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	356	515	1.13457e-12	65.8561	cl27769	GTP_EFTU superfamily	-	-
Lqua1848	non-specific	206640	22	170	2.09922e-14	70.1774	cd00154	Rab	-	cl21455
	superfamily	328724	22	170	2.09922e-14	70.1774	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	18	220	4.25792e-13	67.6783	COG1100	Gem1	-	cl27030
	superfamily	331851	18	220	4.25792e-13	67.6783	cl27030	Ras superfamily	-	-
	non-specific	312094	24	141	9.93353e-12	60.9822	pfam08477	Roc	-	cl21455
	non-specific	197555	18	170	1.33322e-10	59.4439	smart00175	RAB	-	cl27030
	non-specific	178655	17	209	3.87334e-06	47.2432	PLN03108	PLN03108	-	cl27030

	non-specific	272973	22	181	2.6817e-05	43.8997	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	22	181	2.6817e-05	43.8997	cl27769	GTP_EFTU superfamily	-	-
Lquin0486	specific	206648	710	861	5.08673e-17	79.0375	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	710	861	5.08673e-17	79.0375	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	708	861	3.9229e-15	73.692	pfam00071	Ras	-	cl27030
	superfamily	331851	708	861	3.9229e-15	73.692	cl27030	Ras superfamily	-	-
	non-specific	197555	708	861	1.53865e-11	63.2959	smart00175	RAB	-	cl27030
	specific	224025	708	862	1.93469e-07	52.6555	COG1100	Gem1	-	cl27030
	non-specific	272973	708	856	8.76304e-07	49.6777	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	708	856	8.76304e-07	49.6777	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178655	709	860	0.00441857	39.5392	PLN03108	PLN03108	C	cl27030
Lquin0849	specific	224025	11	126	2.4508e-14	69.9895	COG1100	Gem1	C	cl27030
	superfamily	331851	11	126	2.4508e-14	69.9895	cl27030	Ras superfamily	C	-
	non-specific	206640	14	161	3.64814e-14	67.8662	cd00154	Rab	-	cl21455
	superfamily	328724	14	161	3.64814e-14	67.8662	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	15	160	1.94848e-12	63.2916	pfam00071	Ras	-	cl27030
	non-specific	197555	14	176	5.12597e-10	56.7475	smart00175	RAB	-	cl27030
	non-specific	272973	14	127	2.75023e-07	48.9073	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	14	127	2.75023e-07	48.9073	cl27769	GTP_EFTU superfamily	C	-
	non-specific	178657	13	167	1.00262e-05	45.3047	PLN03110	PLN03110	C	cl27030
Lquin3026	specific	206640	16	175	2.26932e-35	125.261	cd00154	Rab	-	cl21455
	superfamily	328724	16	175	2.26932e-35	125.261	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	17	183	1.31223e-31	115.294	pfam00071	Ras	-	cl27030
	superfamily	331851	17	183	1.31223e-31	115.294	cl27030	Ras superfamily	-	-
	non-specific	197555	17	183	2.50355e-28	106.823	smart00175	RAB	-	cl27030
	non-specific	178655	17	175	3.98911e-18	80.7556	PLN03108	PLN03108	C	cl27030
	specific	224025	11	219	6.66529e-12	63.8263	COG1100	Gem1	-	cl27030
	non-specific	272973	17	172	3.41447e-07	48.9073	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	17	172	3.41447e-07	48.9073	cl27769	GTP_EFTU superfamily	-	-
Lrow0101	specific	206648	7	153	6.99587e-07	48.2216	cd00882	Ras_like_GTPase	-	cl21455

	superfamily	328724	7	153	6.99587e-07	48.2216	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	4	112	5.75398e-06	44.4186	pfam08477	Roc	-	cl21455
	specific	224025	2	157	1.47705e-05	45.3367	COG1100	Gem1	-	cl27030
	superfamily	331851	2	157	1.47705e-05	45.3367	cl27030	Ras superfamily	-	-
	non-specific	215587	4	67	7.43489e-05	43.1203	PLN03118	PLN03118	C	cl27030
	non-specific	197555	4	54	0.000240811	40.9543	smart00175	RAB	C	cl27030
Lrow0422	specific	206648	7	156	3.41034e-14	69.0223	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	7	156	3.41034e-14	69.0223	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	5	120	1.95207e-10	57.1302	pfam08477	Roc	-	cl21455
	non-specific	197555	4	150	2.12797e-08	52.5103	smart00175	RAB	-	cl27030
	superfamily	331851	4	150	2.12797e-08	52.5103	cl27030	Ras superfamily	-	-
	non-specific	178655	4	125	9.87121e-06	45.7024	PLN03108	PLN03108	C	cl27030
	non-specific	272973	4	152	4.41689e-05	43.1294	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	152	4.41689e-05	43.1294	cl27769	GTP_EFTU superfamily	-	-
	specific	224025	2	144	0.00104362	39.5587	COG1100	Gem1	C	cl27030
Lrow0424	specific	206648	24	164	2.10906e-16	75.1855	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	24	164	2.10906e-16	75.1855	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	24	123	1.25251e-09	54.819	pfam08477	Roc	-	cl21455
	specific	224025	12	129	3.3897e-07	50.3443	COG1100	Gem1	C	cl27030
	superfamily	331851	12	129	3.3897e-07	50.3443	cl27030	Ras superfamily	C	-
	non-specific	272973	15	132	1.31748e-06	47.3665	TIGR00231	small_GTP	C	cl27769
	superfamily	332590	15	132	1.31748e-06	47.3665	cl27769	GTP_EFTU superfamily	C	-
	non-specific	235392	80	164	0.000590832	41.2495	PRK05291	trmE	N	cl26334
	superfamily	331155	80	164	0.000590832	41.2495	cl26334	MnmE_helical superfamily	N	-
	non-specific	128473	22	124	0.00196446	38.8391	smart00176	RAN	C	cl27030
Lrow1057	non-specific	306559	16	175	1.46006e-36	128.005	pfam00071	Ras	-	cl27030
	superfamily	331851	16	175	1.46006e-36	128.005	cl27030	Ras superfamily	-	-
	specific	206640	15	172	9.88558e-36	125.646	cd00154	Rab	-	cl21455
	superfamily	328724	15	172	9.88558e-36	125.646	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	15	175	2.94338e-35	124.543	smart00175	RAB	-	cl27030

	non-specific	178655	14	175	1.32512e-22	92.6968	PLN03108	PLN03108	C	cl27030
	specific	224025	15	217	1.02534e-16	76.9231	COG1100	Gem1	-	cl27030
	non-specific	272973	15	167	1.45325e-10	58.5373	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	15	167	1.45325e-10	58.5373	cl27769	GTP_EFTU superfamily	-	-
Lrub0535	non-specific	206703	2	113	6.06376e-05	42.8054	cd04131	Rnd	C	cl21455
	superfamily	328724	2	113	6.06376e-05	42.8054	cl21455	P-loop_NTPase superfamily	C	-
	non-specific	272973	1	133	0.00273125	37.7366	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	1	133	0.00273125	37.7366	cl27769	GTP_EFTU superfamily	-	-
Lrub2218	non-specific	206640	44	177	0.00963462	35.1243	cd00154	Rab	-	cl21455
	superfamily	328724	44	177	0.00963462	35.1243	cl21455	P-loop_NTPase superfamily	-	-
Lsain0944	specific	206640	4	157	1.07096e-26	102.919	cd00154	Rab	-	cl21455
	superfamily	328724	4	157	1.07096e-26	102.919	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	4	157	1.22858e-22	92.1859	smart00175	RAB	-	cl27030
	superfamily	331851	4	157	1.22858e-22	92.1859	cl27030	Ras superfamily	-	-
	specific	312094	5	116	3.3612e-22	89.4869	pfam08477	Roc	-	cl21455
	specific	224025	1	186	5.9006e-17	78.0787	COG1100	Gem1	-	cl27030
	non-specific	178657	4	155	9.19718e-17	77.6614	PLN03110	PLN03110	C	cl27030
	non-specific	272973	4	155	7.69006e-14	68.1673	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	4	155	7.69006e-14	68.1673	cl27769	GTP_EFTU superfamily	-	-
	non-specific	316146	251	310	0.00203257	39.0834	pfam13593	SBF_like	NC	cl19217
	superfamily	327523	251	310	0.00203257	39.0834	cl19217	SBF superfamily	NC	-
Lsain1402	specific	206640	35	192	5.63133e-49	161.085	cd00154	Rab	-	cl21455
	superfamily	328724	35	192	5.63133e-49	161.085	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	35	195	2.44898e-46	154.203	smart00175	RAB	-	cl27030
	superfamily	331851	35	195	2.44898e-46	154.203	cl27030	Ras superfamily	-	-
	non-specific	306559	36	195	1.53871e-43	146.88	pfam00071	Ras	-	cl27030
	non-specific	178657	25	195	4.53587e-31	116.181	PLN03110	PLN03110	-	cl27030
	specific	224025	31	231	1.24012e-16	77.3083	COG1100	Gem1	-	cl27030
	non-specific	272973	35	188	5.89501e-15	71.2489	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	35	188	5.89501e-15	71.2489	cl27769	GTP_EFTU superfamily	-	-

Lsan1400	non-specific	306559	10	159	1.02477e-22	90.2555	pfam00071	Ras	-	cl27030
	superfamily	331851	10	159	1.02477e-22	90.2555	cl27030	Ras superfamily	-	-
	non-specific	206640	10	151	2.39306e-21	86.3558	cd00154	Rab	-	cl21455
	superfamily	328724	10	151	2.39306e-21	86.3558	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	10	165	7.64528e-21	85.2523	smart00175	RAB	-	cl27030
	non-specific	178657	10	122	1.31106e-08	53.0087	PLN03110	PLN03110	C	cl27030
	specific	224025	10	197	1.17418e-07	50.3443	COG1100	Gem1	-	cl27030
Lsan2168	specific	206640	8	161	6.44058e-25	98.297	cd00154	Rab	-	cl21455
	superfamily	328724	8	161	6.44058e-25	98.297	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	9	120	9.19843e-22	88.3313	pfam08477	Roc	-	cl21455
	non-specific	197555	8	161	9.43877e-19	81.7855	smart00175	RAB	-	cl27030
	superfamily	331851	8	161	9.43877e-19	81.7855	cl27030	Ras superfamily	-	-
	specific	224025	5	171	2.71443e-14	70.7599	COG1100	Gem1	-	cl27030
	non-specific	178657	8	120	5.18428e-12	64.1794	PLN03110	PLN03110	C	cl27030
	non-specific	272973	8	159	1.19648e-11	62.0041	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	8	159	1.19648e-11	62.0041	cl27769	GTP_EFTU superfamily	-	-
Lsan3135	specific	206640	35	192	1.16272e-45	152.225	cd00154	Rab	-	cl21455
	superfamily	328724	35	192	1.16272e-45	152.225	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	35	195	8.85022e-44	147.655	smart00175	RAB	-	cl27030
	superfamily	331851	35	195	8.85022e-44	147.655	cl27030	Ras superfamily	-	-
	non-specific	306559	36	195	1.66546e-40	139.176	pfam00071	Ras	-	cl27030
	non-specific	178657	25	203	3.06553e-29	111.559	PLN03110	PLN03110	-	cl27030
	specific	224025	31	230	2.65831e-16	76.5379	COG1100	Gem1	-	cl27030
	non-specific	272973	36	190	6.02001e-12	62.7745	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	36	190	6.02001e-12	62.7745	cl27769	GTP_EFTU superfamily	-	-
Lspi0161	specific	206640	339	495	2.93494e-38	139.128	cd00154	Rab	-	cl21455
	superfamily	328724	339	495	2.93494e-38	139.128	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	341	496	7.10829e-37	135.709	pfam00071	Ras	-	cl27030
	superfamily	331851	341	496	7.10829e-37	135.709	cl27030	Ras superfamily	-	-
	non-specific	197555	341	496	1.19158e-31	120.691	smart00175	RAB	-	cl27030

	specific	206640	567	716	5.49847e-30	115.631	cd00154	Rab	-	cl21455
	superfamily	328724	567	716	5.49847e-30	115.631	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	577	716	1.55115e-25	103.352	pfam00071	Ras	-	cl27030
	superfamily	331851	577	716	1.55115e-25	103.352	cl27030	Ras superfamily	-	-
	non-specific	197555	577	716	1.01576e-24	101.045	smart00175	RAB	-	cl27030
	non-specific	178655	342	510	5.8167e-20	88.8448	PLN03108	PLN03108	-	cl27030
	non-specific	178655	590	723	1.39242e-14	73.0516	PLN03108	PLN03108	-	cl27030
	specific	224025	337	510	1.46211e-11	64.5967	COG1100	Gem1	-	cl27030
	non-specific	272973	339	490	7.10405e-09	55.4557	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	339	490	7.10405e-09	55.4557	cl27769	GTP_EFTU superfamily	-	-
	non-specific	128780	48	95	1.68115e-05	42.6073	smart00504	Ubox	C	cl17238
	superfamily	327409	48	95	1.68115e-05	42.6073	cl17238	RING_Ubox superfamily	C	-
	non-specific	319569	49	91	2.38347e-05	41.8207	cd16655	RING-Ubox_WDSUB1_like	-	cl17238
	specific	224025	565	716	3.14186e-05	45.7219	COG1100	Gem1	-	cl27030
	non-specific	252675	47	112	0.000152335	40.372	pfam04564	U-box	-	cl17238
Lspi0220	non-specific	206660	52	208	3.41735e-52	169.663	cd01868	Rab11_like	-	cl21455
	superfamily	328724	52	208	3.41735e-52	169.663	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	55	209	3.99222e-52	169.611	smart00175	RAB	-	cl27030
	superfamily	331851	55	209	3.99222e-52	169.611	cl27030	Ras superfamily	-	-
	non-specific	306559	56	211	3.01688e-46	154.199	pfam00071	Ras	-	cl27030
	non-specific	178657	50	208	2.41188e-43	148.538	PLN03110	PLN03110	C	cl27030
	specific	224025	51	238	4.76399e-20	86.9383	COG1100	Gem1	-	cl27030
	non-specific	272973	55	204	5.67455e-18	79.7233	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	55	204	5.67455e-18	79.7233	cl27769	GTP_EFTU superfamily	-	-
Lspi2717	non-specific	206640	8	162	2.85849e-19	82.889	cd00154	Rab	-	cl21455
	superfamily	328724	8	162	2.85849e-19	82.889	cl21455	P-loop_NTPase superfamily	-	-
	specific	224025	5	191	1.50946e-15	74.2267	COG1100	Gem1	-	cl27030
	superfamily	331851	5	191	1.50946e-15	74.2267	cl27030	Ras superfamily	-	-
	non-specific	312094	10	88	7.41762e-13	64.0638	pfam08477	Roc	C	cl21455
	non-specific	272973	7	153	8.38687e-07	48.1369	TIGR00231	small_GTP	-	cl27769

	superfamily	332590	7	153	8.38687e-07	48.1369	cl27769	GTP_EFTU superfamily	-	-
	non-specific	197555	8	155	8.43106e-06	45.1915	smart00175	RAB	-	cl27030
	non-specific	178657	8	86	0.00134237	39.1415	PLN03110	PLN03110	C	cl27030
Lstei0182	specific	206640	3	155	5.61759e-28	106.386	cd00154	Rab	-	cl21455
	superfamily	328724	3	155	5.61759e-28	106.386	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	4	155	1.60416e-24	97.1891	pfam00071	Ras	-	cl27030
	superfamily	331851	4	155	1.60416e-24	97.1891	cl27030	Ras superfamily	-	-
	non-specific	197555	3	155	6.61186e-24	95.6526	smart00175	RAB	-	cl27030
	specific	224025	2	152	1.07013e-15	74.6119	COG1100	Gem1	C	cl27030
	non-specific	272973	3	157	4.15691e-15	71.6341	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	3	157	4.15691e-15	71.6341	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178655	3	152	2.5333e-12	64.9624	PLN03108	PLN03108	C	cl27030
Lstei0315	non-specific	206640	14	169	9.58607e-11	59.3918	cd00154	Rab	-	cl21455
	superfamily	328724	14	169	9.58607e-11	59.3918	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	15	129	4.11997e-05	42.1074	pfam08477	Roc	-	cl21455
	non-specific	197555	14	179	0.000340514	40.5691	smart00175	RAB	-	cl27030
	superfamily	331851	14	179	0.000340514	40.5691	cl27030	Ras superfamily	-	-
	specific	224025	10	129	0.000843643	39.9439	COG1100	Gem1	C	cl27030
	non-specific	312828	105	255	0.00740399	37.3894	pfam09455	Cas_DxTHG	N	cl21516
	superfamily	328768	105	255	0.00740399	37.3894	cl21516	Csx1_III-U superfamily	N	-
Lstei0784	specific	206640	11	171	4.02649e-49	160.699	cd00154	Rab	-	cl21455
	superfamily	328724	11	171	4.02649e-49	160.699	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	12	174	8.97959e-46	152.273	pfam00071	Ras	-	cl27030
	superfamily	331851	12	174	8.97959e-46	152.273	cl27030	Ras superfamily	-	-
	non-specific	197555	11	174	2.54888e-43	146.114	smart00175	RAB	-	cl27030
	non-specific	178655	7	174	8.29323e-31	115.038	PLN03108	PLN03108	C	cl27030
	specific	224025	7	187	4.56012e-19	83.8567	COG1100	Gem1	-	cl27030
	non-specific	272973	11	166	4.98422e-08	51.6037	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	166	4.98422e-08	51.6037	cl27769	GTP_EFTU superfamily	-	-
Lstei0814	specific	206640	24	183	1.48778e-46	150.684	cd00154	Rab	-	cl21455

	superfamily	328724	24	183	1.48778e-46	150.684	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	25	182	1.02109e-41	138.405	pfam00071	Ras	-	cl27030
	superfamily	331851	25	182	1.02109e-41	138.405	cl27030	Ras superfamily	-	-
	non-specific	197555	24	183	7.86365e-39	131.091	smart00175	RAB	-	cl27030
	non-specific	178655	24	178	5.09208e-26	99.6304	PLN03108	PLN03108	C	cl27030
	specific	224025	20	205	1.06268e-20	85.7827	COG1100	Gem1	-	cl27030
	non-specific	272973	24	179	9.84978e-17	73.9453	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	24	179	9.84978e-17	73.9453	cl27769	GTP_EFTU superfamily	-	-
Lstei2185	specific	206640	11	166	2.71098e-43	145.291	cd00154	Rab	-	cl21455
	superfamily	328724	11	166	2.71098e-43	145.291	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	171	3.57043e-40	137.639	smart00175	RAB	-	cl27030
	superfamily	331851	11	171	3.57043e-40	137.639	cl27030	Ras superfamily	-	-
	non-specific	306559	12	171	1.24984e-37	130.702	pfam00071	Ras	-	cl27030
	non-specific	178657	6	171	1.33604e-28	108.863	PLN03110	PLN03110	-	cl27030
	specific	224025	7	202	2.30724e-19	84.2419	COG1100	Gem1	-	cl27030
	non-specific	272973	11	159	2.79022e-07	49.2925	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	159	2.79022e-07	49.2925	cl27769	GTP_EFTU superfamily	-	-
Lstei2733	non-specific	206640	14	170	2.83615e-19	84.815	cd00154	Rab	-	cl21455
	superfamily	328724	14	170	2.83615e-19	84.815	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	291524	520	637	6.95075e-16	74.1132	pfam14860	DrrA_P4M	-	cl20758
	superfamily	291524	520	637	6.95075e-16	74.1132	cl20758	DrrA_P4M superfamily	-	-
	non-specific	306559	24	174	9.10853e-12	63.2916	pfam00071	Ras	-	cl27030
	superfamily	331851	24	174	9.10853e-12	63.2916	cl27030	Ras superfamily	-	-
	non-specific	197555	24	163	1.80955e-07	50.9695	smart00175	RAB	-	cl27030
	non-specific	225171	82	184	2.65178e-06	49.9602	COG2262	HflX	N	cl25666
	superfamily	330487	82	184	2.65178e-06	49.9602	cl25666	HflX superfamily	N	-
	non-specific	237177	308	462	1.41991e-05	47.8506	PRK12704	PRK12704	C	cl25602
	superfamily	330423	308	462	1.41991e-05	47.8506	cl25602	DUF3552 superfamily	C	-
	non-specific	129567	15	178	7.65951e-05	45.6345	TIGR00475	selB	C	cl27768
	superfamily	332589	15	178	7.65951e-05	45.6345	cl27768	SelB superfamily	C	-

	non-specific	235392	84	180	0.000491992	42.7903	PRK05291	trmE	N	cl26334
	superfamily	331155	84	180	0.000491992	42.7903	cl26334	MnmE_helical superfamily	N	-
Lstei3518	non-specific	206640	43	124	4.61271e-08	50.9174	cd00154	Rab	N	cl21455
	superfamily	328724	43	124	4.61271e-08	50.9174	cl21455	P-loop_NTPase superfamily	N	-
	non-specific	274669	61	143	1.47157e-05	45.1926	TIGR03596	GTPase_YlqF	C	cl26335
	superfamily	331156	61	143	1.47157e-05	45.1926	cl26335	RbgA superfamily	C	-
	non-specific	236570	61	167	0.000464844	40.5399	PRK09563	rbgA	C	cl26335
	non-specific	223447	73	204	0.00150761	39.5819	COG0370	FeoB	C	cl26333
	superfamily	331154	73	204	0.00150761	39.5819	cl26333	FeoB_N superfamily	C	-
	non-specific	225815	70	147	0.0038554	38.1491	COG3276	SelB	NC	cl27768
	superfamily	332589	70	147	0.0038554	38.1491	cl27768	SelB superfamily	NC	-
	non-specific	306559	43	130	0.0056064	36.3276	pfam00071	Ras	N	cl27030
	superfamily	331851	43	130	0.0056064	36.3276	cl27030	Ras superfamily	N	-
Ltau0427	specific	206648	1	141	0.00400619	37.0508	cd00882	Ras_like_GTPase	-	cl21455
	superfamily	328724	1	141	0.00400619	37.0508	cl21455	P-loop_NTPase superfamily	-	-
Ltuc0732	specific	206640	7	162	8.44031e-28	106.001	cd00154	Rab	-	cl21455
	superfamily	328724	7	162	8.44031e-28	106.001	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	7	162	5.22425e-25	98.7342	smart00175	RAB	-	cl27030
	superfamily	331851	7	162	5.22425e-25	98.7342	cl27030	Ras superfamily	-	-
	non-specific	306559	8	166	2.98398e-24	96.4187	pfam00071	Ras	-	cl27030
	specific	224025	3	172	5.1698e-16	75.7675	COG1100	Gem1	-	cl27030
	non-specific	272973	6	160	1.34955e-13	67.3969	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	6	160	1.34955e-13	67.3969	cl27769	GTP_EFTU superfamily	-	-
	non-specific	178657	7	160	1.50716e-13	68.4166	PLN03110	PLN03110	C	cl27030
Ltuc1844	specific	206640	13	168	6.80992e-38	131.424	cd00154	Rab	-	cl21455
	superfamily	328724	13	168	6.80992e-38	131.424	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	13	173	1.24458e-37	131.091	smart00175	RAB	-	cl27030
	superfamily	331851	13	173	1.24458e-37	131.091	cl27030	Ras superfamily	-	-
	non-specific	306559	14	173	6.8529e-35	123.768	pfam00071	Ras	-	cl27030
	non-specific	178657	1	180	7.60852e-30	112.329	PLN03110	PLN03110	-	cl27030

	specific	224025	9	201	4.49015e-19	83.4715	COG1100	Gem1	-	cl27030
	non-specific	272973	13	161	7.32532e-14	67.7821	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	13	161	7.32532e-14	67.7821	cl27769	GTP_EFTU superfamily	-	-
Ltuc2453	non-specific	206640	34	183	2.39317e-22	91.3634	cd00154	Rab	-	cl21455
	superfamily	328724	34	183	2.39317e-22	91.3634	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	34	178	2.5462e-15	72.1512	pfam00071	Ras	-	cl27030
	superfamily	331851	34	178	2.5462e-15	72.1512	cl27030	Ras superfamily	-	-
	non-specific	197555	34	178	2.227e-13	66.7627	smart00175	RAB	-	cl27030
	specific	224025	24	204	2.61736e-05	44.5663	COG1100	Gem1	-	cl27030
	non-specific	274720	27	196	3.79902e-05	44.6578	TIGR03680	eif2g_arch	C	cl27768
	superfamily	332589	27	196	3.79902e-05	44.6578	cl27768	SelB superfamily	C	-
	non-specific	235392	98	184	0.00015247	42.7903	PRK05291	trmE	N	cl26334
	superfamily	331155	98	184	0.00015247	42.7903	cl26334	MnmE_helical superfamily	N	-
Ltuc2903	specific	206640	11	170	8.54044e-50	162.24	cd00154	Rab	-	cl21455
	superfamily	328724	11	170	8.54044e-50	162.24	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	11	173	4.17677e-49	160.751	smart00175	RAB	-	cl27030
	superfamily	331851	11	173	4.17677e-49	160.751	cl27030	Ras superfamily	-	-
	non-specific	306559	12	173	7.08211e-42	141.872	pfam00071	Ras	-	cl27030
	non-specific	178655	11	173	1.2569e-29	111.572	PLN03108	PLN03108	C	cl27030
	specific	224025	7	206	3.68227e-20	86.5531	COG1100	Gem1	-	cl27030
	non-specific	272973	11	162	1.09756e-14	70.0933	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	11	162	1.09756e-14	70.0933	cl27769	GTP_EFTU superfamily	-	-
Lwad1230	non-specific	206640	3	156	4.05313e-17	77.111	cd00154	Rab	-	cl21455
	superfamily	328724	3	156	4.05313e-17	77.111	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	312094	4	115	7.20635e-12	61.3674	pfam08477	Roc	-	cl21455
	non-specific	197555	3	156	1.40863e-10	58.6735	smart00175	RAB	-	cl27030
	superfamily	331851	3	156	1.40863e-10	58.6735	cl27030	Ras superfamily	-	-
	specific	224025	2	190	1.58439e-08	54.1963	COG1100	Gem1	-	cl27030
	non-specific	235392	71	164	3.18493e-06	48.1831	PRK05291	trmE	N	cl26334
	superfamily	331155	71	164	3.18493e-06	48.1831	cl26334	MnmE_helical superfamily	N	-

	non-specific	272973	2	154	4.64644e-06	45.8257	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	2	154	4.64644e-06	45.8257	cl27769	GTP_EFTU superfamily	-	-
Lwad2065	specific	206640	22	180	1.44539e-51	167.248	cd00154	Rab	-	cl21455
	superfamily	328724	22	180	1.44539e-51	167.248	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	22	184	4.77193e-45	150.736	smart00175	RAB	-	cl27030
	superfamily	331851	22	184	4.77193e-45	150.736	cl27030	Ras superfamily	-	-
	non-specific	306559	23	184	1.28264e-43	146.88	pfam00071	Ras	-	cl27030
	non-specific	178657	16	188	6.3476e-30	113.1	PLN03110	PLN03110	-	cl27030
	specific	224025	18	200	8.13497e-17	77.6935	COG1100	Gem1	-	cl27030
	non-specific	272973	22	179	2.22529e-10	58.1521	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	22	179	2.22529e-10	58.1521	cl27769	GTP_EFTU superfamily	-	-
Lwad3214	specific	206640	238	405	2.82085e-25	100.608	cd00154	Rab	-	cl21455
	superfamily	328724	238	405	2.82085e-25	100.608	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	244	397	1.29276e-24	99.1151	pfam00071	Ras	-	cl27030
	superfamily	331851	244	397	1.29276e-24	99.1151	cl27030	Ras superfamily	-	-
	non-specific	197555	238	410	1.47524e-21	90.6451	smart00175	RAB	-	cl27030
	non-specific	178655	314	397	4.85928e-11	61.8808	PLN03108	PLN03108	NC	cl27030
	non-specific	272973	240	397	3.05158e-06	46.9813	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	240	397	3.05158e-06	46.9813	cl27769	GTP_EFTU superfamily	-	-
	specific	315592	192	230	6.86213e-06	42.4697	pfam12937	F-box-like	-	cl02535
	superfamily	321975	192	230	6.86213e-06	42.4697	cl02535	F-box superfamily	-	-
	specific	224025	234	424	0.000383319	41.4847	COG1100	Gem1	-	cl27030
	specific	197608	195	225	0.000725955	36.6458	smart00256	FBOX	C	cl02535
Lwal3261	specific	206640	22	171	2.87133e-30	108.312	cd00154	Rab	-	cl21455
	superfamily	328724	22	171	2.87133e-30	108.312	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	22	174	1.32477e-27	101.426	pfam00071	Ras	-	cl27030
	superfamily	331851	22	174	1.32477e-27	101.426	cl27030	Ras superfamily	-	-
	non-specific	197555	22	174	2.43584e-27	101.045	smart00175	RAB	-	cl27030
	non-specific	178655	20	187	6.22667e-14	66.8884	PLN03108	PLN03108	-	cl27030
	specific	224025	22	188	4.35696e-13	64.9819	COG1100	Gem1	-	cl27030

	non-specific	272973	20	166	0.000134437	40.433	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	20	166	0.000134437	40.433	cl27769	GTP_EFTU superfamily	-	-
Lwor1982	non-specific	306559	37	204	2.52246e-36	128.776	pfam00071	Ras	-	cl27030
	superfamily	331851	37	204	2.52246e-36	128.776	cl27030	Ras superfamily	-	-
	specific	206640	33	200	5.40182e-36	127.572	cd00154	Rab	-	cl21455
	superfamily	328724	33	200	5.40182e-36	127.572	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	197555	33	205	5.79259e-33	119.92	smart00175	RAB	-	cl27030
	non-specific	178655	29	205	6.09805e-16	75.3628	PLN03108	PLN03108	-	cl27030
	specific	224025	29	206	3.88678e-15	73.4563	COG1100	Gem1	-	cl27030
	non-specific	272973	33	197	4.56521e-08	51.6037	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	33	197	4.56521e-08	51.6037	cl27769	GTP_EFTU superfamily	-	-
	non-specific	281323	6	53	0.00384526	38.1847	pfam03308	ArgK	C	cl21455
	superfamily	328724	6	53	0.00384526	38.1847	cl21455	P-loop_NTPase superfamily	C	-
Lya1031	non-specific	206640	14	164	1.37372e-22	93.6746	cd00154	Rab	-	cl21455
	superfamily	328724	14	164	1.37372e-22	93.6746	cl21455	P-loop_NTPase superfamily	-	-
	non-specific	306559	14	164	1.00662e-17	79.8552	pfam00071	Ras	-	cl27030
	superfamily	331851	14	164	1.00662e-17	79.8552	cl27030	Ras superfamily	-	-
	non-specific	197555	14	164	3.92337e-17	78.3187	smart00175	RAB	-	cl27030
	specific	224025	6	164	2.00895e-10	60.3595	COG1100	Gem1	-	cl27030
	non-specific	178655	14	121	5.3416e-07	49.9396	PLN03108	PLN03108	C	cl27030
	non-specific	272973	17	162	1.08565e-05	45.4405	TIGR00231	small_GTP	-	cl27769
	superfamily	332590	17	162	1.08565e-05	45.4405	cl27769	GTP_EFTU superfamily	-	-
	non-specific	308683	342	398	0.00294546	39.3484	pfam03186	CobD_Cbib	C	cl00561
	superfamily	321043	342	398	0.00294546	39.3484	cl00561	CobD_Cbib superfamily	C	-

The hits reported in the table are defined according to the database used: top-ranking RPS-BLAST hit that meets or exceeds a domain-specific E-value threshold and represents a high confidence result = specific; hits that meet or exceed the RPS-BLAST threshold for statistical significance = non-specific and the domain cluster to which the specific and/or non-specific hits belongs = superfamily

Table S5: Eukaryotic like proteins detected in the *Legionella* genomes analyzed in this study

Protein label[1]	N[2]	Selection criteria[3]	Organism[4]	First eukaryotic blast hit annotation[4]	Acession number[5]	% Identity[6]
ACZG10723	1	2 first hsp are Euka	*Amphimedon queenslandica*	-	I1ENB1	30.34%
Lade1822	10	3 first hsp are Euka	*Aspergillus parasiticus*	FAD dependent oxidoreductase	A0A0F0IS82	46.59%
Lade1824	7	ratio Euka/Proka : 85.0 / 15.0	*Plasmodiophora brassicae*	-	A0A0G4IGX2	48.03%
Lade1989	9	ratio Euka/Proka : 87.5 / 12.5	*Fonticula alba*	-	A0A058Z2R2	30.65%
Lade2253	9	3 first hsp are Euka	*Parastrongyloides trichosuri*	-	A0A0N4ZLE8	87.10%
LanA0735	72	ratio Euka/Proka : 90.0 / 10.0	*Dictyostelium purpureum*	-	F1A5L6	44.38%
LanA1199	7	3 first hsp are Euka	*Ancylostoma ceylanicum*	Methyltransferase type 11 domain containing protein	A0A016VGN9	38.32%
LanA3229	2	3 first hsp are Euka	*Capsaspora owczarzaki*	-	A0A0D2WV05	32.08%
LanA3375	1	3 first hsp are Euka	*Dictyostelium lacteum*	Putative acyl-CoA dehydrogenase	A0A152A144	34.51%
LanA3786	20	ratio Euka/Proka : 90.0 / 10.0	*Polysphondylium pallidum*	-	D3B9U2	46.24%
LanB1993	2	3 first hsp are Euka	*Brachypodium distachyon*	-	I1GKX8	33.09%
Lbe0019	20	1 first hsp is Euka	*Acanthamoeba castellanii*	Eukaryotic family protein	L8HFQ5	35.25%
Lbe0340	1	2 first hsp are Euka	*Gonapodya prolifera*	-	A0A138ZX02	39.06%
Lbe0740	12	3 first hsp are Euka	*Callithrix jacchus*	DnaJ-like subfamily B member 3	F7F2J3	30.99%
Lbe0772	13	3 first hsp are Euka	*Perkinsus marinus*	Uridine phosphorylase, putative	C5KRK2	41.63%
Lbe1600	6	3 first hsp are Euka	*Ichthyophthirius multifiliis*	-	G0R1H7	33.52%
Lbe1645	1	3 first hsp are Euka	*Rhizophagus irregularis*	Skt5p	U9SN83	33.33%
Lbe1659	5	3 first hsp are Euka	*Rhizophagus irregularis*	Skt5p	A0A015JE96	34.68%
Lbe1728	4	ratio Euka/Proka : 81.25 / 18.75	*Physcomitrella patens*	-	A9TZI2	40.23%
Lbe1862	1	1 first hsp is Euka	*Rhizophagus irregularis*	Skt5p	A0A015JE96	31.58%
Lbe2177	15	ratio Euka/Proka : 80.0 / 20.0	*Sphaerobolus stellatus*	-	A0A0C9US25	32.30%
Lbe2282	6	3 first hsp are Euka	*Cladophialophora immunda*	-	A0A0D2C3Y5	49.57%
Lbe2299	1	3 first hsp are Euka	*Galdieria sulphuraria*	FBox-LRR protein	M2XRJ2	42.50%
Lbe2310	1	3 first hsp are Euka	*Capsaspora owczarzaki*	NOD3 protein	A0A0D2WSZ0	39.73%
Lbe2341	1	3 first hsp are Euka	*Chrysochromulina sp. CCMP291*	Surface antigen-like protein	A0A0M0KNG8	40.67%

Lbe2343	1	3 first hsp are Euka	*Emiliania huxleyi*	Adenylosuccinate synthetase	R1F4J9	34.80%
Lbe2344	1	3 first hsp are Euka	*Emiliania huxleyi*	-	R1DLW0	32.49%
Lbe2454	19	1 first hsp is Euka	*Botryosphaeria parva*	Putative endoglucanase ii protein	R1GLD6	30.51%
Lbe2456	1	ratio Euka/Proka : 90.0 / 10.0	*Emiliania huxleyi*	-	R1DGC4	40.70%
Lbir0552	1	3 first hsp are Euka	*Perkinsus marinus*	Chaperone protein DNAJ, putative	C5LFS5	30.97%
Lbir0715	4	ratio Euka/Proka : 90.0 / 10.0	*Penicillium brasilianum*	-	A0A0F7TRV6	55.38%
Lbir1228	3	3 first hsp are Euka	*Caenorhabditis briggsae*	Protein CBG20767	A8XYK4	30.21%
Lbir1251	6	3 first hsp are Euka	*Saprolegnia diclina*	-	T0RWI4	41.13%
Lbir1504	5	1 first hsp is Euka	*Stegodyphus mimosarum*	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	A0A087UUR9	37.45%
Lbir2190	1	ratio Euka/Proka : 85.0 / 15.0	*Talaromyces islandicus*	-	A0A0U1LI69	55.07%
Lbir2253	3	3 first hsp are Euka	*Fusarium langsethiae*	Glu leu phe val dehydrogenase family protein	A0A0M9EMS8	32.05%
Lbir2979	6	3 first hsp are Euka	*Stemphylium lycopersici*	Glycosyltransferase family 2 protein	A0A0L1HWJ1	30.60%
LboA0084	7	3 first hsp are Euka	*Candida parapsilosis*	-	G8BFF3	30.16%
LboA2873	1	3 first hsp are Euka	*Plasmodium falciparum*	Phage tail fiber repeat family protein	A0A0L1IDW5	47.56%
LboB2649	1	3 first hsp are Euka	*Plasmodium falciparum*	-	A0A0L7M116	45.83%
Lbru1260	1	3 first hsp are Euka	*Neolentinus lepideus*	-	A0A165SYS3	37.04%
Lbru1261	1	ratio Euka/Proka : 90.0 / 10.0	*Talaromyces marneffei*	-	B6Q2Y2	44.44%
Lbru1478	3	3 first hsp are Euka	*Naegleria gruberi*	-	D2V8Z2	39.85%
Lbru1758	3	2 first hsp are Euka	*Capsaspora owczarzaki*	LLRcontaining protein	A0A0D2WSZ0	31.65%
Lbru2096	12	3 first hsp are Euka	*Eimeria acervulina*	Trypsin, putative	U6GWD7	30.51%
Lbru2322	1	ratio Euka/Proka : 90.0 / 10.0	*Capsaspora owczarzaki*	-	A0A0D2WI15	30.00%
Lbru2342	8	ratio Euka/Proka : 90.0 / 10.0	*Aspergillus lentulus*	-	A0A0S7DG03	34.93%
Lbru3029	1	3 first hsp are Euka	*Naegleria gruberi*	-	D2W4W1	38.78%
Lbru3450	1	3 first hsp are Euka	*Chrysochromulina sp. CCMP291*	-	A0A0M0JZA7	43.57%
Lbu2390	1	3 first hsp are Euka	*Emiliania huxleyi*	-	R1EV16	43.75%
Lbu2846	2	ratio Euka/Proka : 95.0 / 5.0	*Pyrenochaeta sp. DS3sAY3a*	FAD-binding domain-containing protein	A0A178E9S5	34.95%
Lche1013	1	3 first hsp are Euka	*Globodera pallida*	-	A0A183CDG3	50.94%
Lche2319	3	1 first hsp is Euka	*Stylonychia lemnae*	-	A0A078AVP8	42.15%
Lche2728	1	3 first hsp are Euka	*Ostreococcus tauri*	SAICAR synthetase	A0A096PBL5	61.90%

Lci0457	3	3 first hsp are Euka	*Salpingoeca rosetta*	-	F2UPJ7	30.82%
Lci0897	12	ratio Euka/Proka : 95.0 / 5.0	*Brassica oleracea*	-	A0A0D3DHV8	33.44%
Lci2625	3	3 first hsp are Euka	*Aureobasidium pullulans*	Aldehyde reductase	A0A074XVJ7	34.56%
Lci3380	9	2 first hsp are Euka	*Serpula lacrymans*	-	F8Q8I7	30.00%
Lci3406	7	3 first hsp are Euka	*Tetrahymena thermophila*	Glycoside hydrolase family 45 protein	Q22C01	32.82%
Ldra0046	10	3 first hsp are Euka	*Gymnopus luxurians*	-	A0A0D0B9J6	48.09%
Ldra1192	11	3 first hsp are Euka	*Eucalyptus grandis*	Glutamate decarboxylase	A0A059AV55	50.93%
Ldra1891	1	1 first hsp is Euka	*Chrysochromulina sp. CCMP291*	-	A0A0M0JJJ8	32.33%
Ldra2081	1	1 first hsp is Euka	*Naegleria gruberi*	Leucine-rich repeat protein	D2W108	32.80%
Ldra2921	2	2 first hsp are Euka	*Sorghum bicolor*	-	A0A1B6Q4Z9	33.33%
Ldra3301	1	3 first hsp are Euka	*Diplodia seriata*	Putative glucoamylase i	A0A0G2E0P2	38.79%
Ldro0452	1	3 first hsp are Euka	*Trichomonas vaginalis*	Surface antigen BspA-like	A2DVL8	42.31%
Ldro0457	6	ratio Euka/Proka : 90.9 / 9.1	*Penicillium oxalicum*	-	S8ARP3	31.03%
Ldro2389	2	ratio Euka/Proka : 92.9 / 7.1	*Penicillium roqueforti*	-	W6QH56	38.49%
Ldro2472	1	3 first hsp are Euka	*Branchiostoma floridae*	-	C3YE87	38.26%
LduN233085	2	3 first hsp are Euka	*Acanthamoeba castellanii*	-	L8H1F6	35.23%
Lery0318	1	3 first hsp are Euka	*Triticum urartu*	Clade-C Terpene synthase, putative ent-copalyl diphosphate synthase 1, chloroplastic	T1NQ08	34.26%
Lery0465	3	ratio Euka/Proka : 94.4 / 5.6	*Ostreococcus lucimarinus*	-	A4RVY1	31.90%
Lfair0216	1	1 first hsp is Euka	*Salpingoeca rosetta*	-	F2U9A2	31.46%
Lfair0946	1	3 first hsp are Euka	*Echinococcus multilocularis*	DnaJ protein subfamily B 2	A0A068YAJ3	31.45%
Lfair1553	1	3 first hsp are Euka	*Ciona savignyi*	-	H2Z3Z9	46.51%
Lfair1778	1	1 first hsp is Euka	*Chrysochromulina sp. CCMP291*	-	A0A0M0JZA7	38.82%
Lfair2129	1	3 first hsp are Euka	*Leishmania braziliensis*	Hypothetical repeat protein	A4H7Q0	50.75%
Lfair2188	1	3 first hsp are Euka	*Pseudocercospora fijiensis*	-	N1QCJ6	33.33%
LFAv2_0557	1	3 first hsp are Euka	*Coccomyxa subellipsoidea*	Glycoside hydrolase	I0Z331	35.75%
LFAv2_1334	2	3 first hsp are Euka	*Trichinella sp. T6*	-	A0A0V0W3N9	47.55%
LFAv2_1881	1	3 first hsp are Euka	*Salpingoeca rosetta*	-	F2UJX0	33.02%

Lge1638	2	3 first hsp are Euka	*Capsaspora owczarzaki*	LLR containing protein	A0A0D2WSZ0	34.78%
Lge2437	1	ratio Euka/Proka : 85.0 / 15.0	*Solanum tuberosum*	-	M0ZWB1	63.04%
Lge2582	2	ratio Euka/Proka : 85.7 / 14.3	*Capsaspora owczarzaki*	-	A0A0D2UFC5	30.71%
Lges0487	1	2 first hsp are Euka	*Rhizophagus irregularis*	Ack1p	A0A015JL58	30.23%
Lges1836	2	ratio Euka/Proka : 90.0 / 10.0	*Musa acuminata*	-	M0TQA4	41.15%
LgoB0303	1	3 first hsp are Euka	*Cyanidioschyzon merolae*	Glycolate oxidase, peroxysomal	M1VAT1	57.69%
LgoB1635	1	3 first hsp are Euka	*Alligator mississippiensis*	26S proteasome non-ATPase regulatory subunit 10	A0A151NN67	30.29%
LgoB3790	1	1 first hsp is Euka	*Chrysochromulina sp. CCMP291*	Protein-tyrosine dual specificity domain protein	A0A0M0JXI1	32.08%
LgoB3932	1	3 first hsp are Euka	*Xenopus tropicalis*	-	A0A1B8Y5G5	41.44%
Lgra3222	8	3 first hsp are Euka	*Thecamonas trahens*	-	A0A0L0DKJ3	30.77%
Lgre2549	1	1 first hsp is Euka	*Phialophora attae*	Peptide deformylase	A0A0N1P1T9	47.22%
Lgre2588	1	3 first hsp are Euka	*Ciona savignyi*	-	H2YKI2	44.00%
Lgre3299	1	2 first hsp are Euka	*Gonapodya prolifera*	-	A0A138ZX02	38.50%
Lgre3406	1	3 first hsp are Euka	*Capsaspora owczarzaki*	-	A0A0D2X3N9	44.62%
Lgre3434	1	3 first hsp are Euka	*Tetrahymena thermophila*	Kinase domain protein	Q239Q8	36.27%
LHAv2_0826	1	3 first hsp are Euka	*Dictyostelium discoideum*	Predicted HD phosphohydrolase family protein	Q54GY3	40.00%
LHAv2_1055	2	3 first hsp are Euka	*Hebeloma cylindrosporum*	-	A0A0C3C641	58.82%
Lis0327	1	1 first hsp is Euka	*Myceliophthora thermophila*	-	G2QNU7	41.67%
Lis0768	1	2 first hsp are Euka	*Dictyostelium discoideum*	Hybrid signal transduction histidine kinase J	Q54YZ9	39.53%
Lis2217	2	3 first hsp are Euka	*Brugia timori*	Putative oxidoreductase	A0A0R3QW57	41.91%
Lis2218	2	ratio Euka/Proka : 95.0 / 5.0	*Pythium ultimum*	-	K3WR86	31.48%
Lis2789	1	ratio Euka/Proka : 80.0 / 20.0	*Rhizoctonia solani*	Phosphatidylcholine-hydrolyzing phospholipase C	A0A074RWD3	36.27%
Lis2901	4	1 first hsp is Euka	*Daphnia pulex*	-	E9HWS5	49.37%
Lis2956	13	3 first hsp are Euka	*Medicago truncatula*	-	G7LHI8	68.52%
Lis2997	1	3 first hsp are Euka	*Nematostella vectensis*	-	A7SID6	38.89%
Lja1163	1	3 first hsp are Euka	*Conidiobolus coronatus*	Carbohydrate esterase family 16 protein	A0A137NUQ3	36.52%
Llo981117	6	1 first hsp is Euka	*Neonectria ditissima*	-	A0A0P7BH29	31.10%
Llo981203	5	ratio Euka/Proka : 95.0 / 5.0	*Brassica napus*	BnaA02g03420D protein	A0A078D861	30.26%

Llo981314	4	3 first hsp are Euka	*Musa acuminata*	-	M0SNM2	32.86%
Llo981993	4	3 first hsp are Euka	*Metarhizium robertsii*	Peptide hydrolase	A0A0A1US54	39.69%
Llo981994	4	3 first hsp are Euka	*Trichosporon asahii*	Peptide hydrolase	K1VCD4	50.53%
Llo982493	1	2 first hsp are Euka	*Glycine soja*	Pentatricopeptide repeat-containing protein, mitochondrial	A0A0B2RBR6	34.69%
LloAT0689	3	1 first hsp is Euka	*Acanthamoeba castellanii*	Eukaryotic family protein	L8HFQ5	34.51%
Llon2243	1	3 first hsp are Euka	*Laccaria amethystina*	-	A0A0C9X1S9	30.50%
Lma0061	1	3 first hsp are Euka	*Heterocephalus glaber*	-	G5C4L0	32.84%
Lma1087	1	3 first hsp are Euka	*Amphimedon queenslandica*	-	I1E862	53.12%
Lma2959	4	1 first hsp is Euka	*Dictyostelium lacteum*	-	A0A151ZFY4	30.08%
LmasA0938	2	2 first hsp are Euka	*Eucalyptus grandis*	-	A0A059BDI1	30.43%
LmasA1109	3	2 first hsp are Euka	*Nematostella vectensis*	Leucine-rich repeat-containing protein 34	A7SML2	37.39%
LmasA2772	3	3 first hsp are Euka	*Sphaerulina musiva*	-	M3CKV8	30.80%
LmasA3802	2	ratio Euka/Proka : 80.0 / 20.0	*Triticum aestivum*	-	W5A8A8	37.86%
Lmo0476	2	3 first hsp are Euka	*Naegleria gruberi*	Eukaryotic family protein	D2VXH5	36.14%
Lna2633	1	3 first hsp are Euka	*Strongyloides papillosus*	Similar to Minor spike protein H acc. no. P03646	A0A0N5C599	100.00%
Lna2642	1	3 first hsp are Euka	*Chrysochromulina sp. CCMP291*	-	A0A0M0JE43	34.56%
Lno0580	1	ratio Euka/Proka : 80.0 / 20.0	*Musa acuminata*	-	M0RQC7	50.90%
LoakA0377	1	3 first hsp are Euka	*Medicago truncatula*	-	G7LHI8	70.37%
LoakA0667	1	3 first hsp are Euka	*Lucilia cuprina*	-	A0A0L0C8R3	39.13%
LoakA0772	2	3 first hsp are Euka	*Calocera viscosa*	-	A0A167JNM4	43.52%
LoakA1610	1	1 first hsp is Euka	*Chrysochromulina sp. CCMP291*	-	A0A0M0JJJ8	34.12%
LoakA2509	1	3 first hsp are Euka	*Medicago truncatula*	-	G7LHI8	70.37%
LoakA2834	1	ratio Euka/Proka : 80.0 / 20.0	*Rhizophagus irregularis*	Peptide hydrolase	U9UT29	43.48%
LoakB1951	1	3 first hsp are Euka	*Emmonsia crescens*	Saccharopine dehydrogenase [NAD(+), L-lysine-forming]	A0A0G2J7R7	37.76%
Loas1699	1	ratio Euka/Proka : 95.0 / 5.0	*Gallus gallus*	-	H9KZ13	31.10%
Loas2397	1	3 first hsp are Euka	*Tetranychus urticae*	-	T1KEY0	37.02%
Loas2810	1	3 first hsp are Euka	*Oxytricha trifallax*	-	J9EKJ8	47.89%
Loas2860	1	1 first hsp is Euka	*Canis lupus*	-	F1PNP2	37.58%

Lp130b1550	1	ratio Euka/Proka : 85.0 / 15.0	*Arthroderma gypseum*	Phosphatidylcholine-hydrolyzing phospholipase C	E5R3V7	32.89%
Lp570C1927	7	3 first hsp are Euka	*Chrysochromulina sp. CCMP291*	-	A0A0M0JNB0	31.50%
LpAlc2551	4	3 first hsp are Euka	*Brassica napus*	BnaC08g38470D protein	A0A078D0I7	41.38%
LpAlc3049	1	ratio Euka/Proka : 90.0 / 10.0	*Perkinsus marinus*	-	C5LIX6	54.30%
LpFRA0929	2	3 first hsp are Euka	*Physcomitrella patens*	-	A9U8F6	46.79%
LpFRA0930	1	3 first hsp are Euka	*Physcomitrella patens*	-	A9U8F6	50.00%
LpFRAC0736	1	3 first hsp are Euka	*Oreochromis niloticus*	-	I3K3J7	34.31%
LpFRAC1083	1	3 first hsp are Euka	*Salpingoeca rosetta*	Collagen type III alpha 1	F2UI75	56.59%
lpg0306	1	ratio Euka/Proka : 80.0 / 20.0	*Brugia timori*	-	A0A0R3RDH7	53.85%
lpg0573	1	ratio Euka/Proka : 80.0 / 20.0	*Brugia timori*	-	A0A0R3RDH7	53.85%
lpg2750	1	ratio Euka/Proka : 80.0 / 20.0	*Brugia timori*	-	A0A0R3RDH7	53.85%
lpl0592a	1	3 first hsp are Euka	*Aspergillus nomius*	-	A0A0L1ITU8	44.71%
lpl2493	2	1 first hsp is Euka	*Amphimedon queenslandica*	-	I1EU16	37.02%
LPOv2_3038	1	3 first hsp are Euka	*Beta vulgaris*	-	A0A0J7YMC9	75.44%
lpp0208	6	1 first hsp is Euka	*Vitis vinifera*	-	D7T2M7	30.42%
lpp0489	62	3 first hsp are Euka	*Spizellomyces punctatus*	-	A0A0L0HQ56	42.00%
lpp0517	80	3 first hsp are Euka	*Chrysochromulina sp. CCMP291*	-	A0A0M0JE43	34.57%
lpp0565	20	ratio Euka/Proka : 80.0 / 20.0	*Arthroderma gypseum*	Phosphatidylcholine-hydrolyzing phospholipase C	E5R3V7	35.10%
lpp0578	33	3 first hsp are Euka	*Nectria haematococca*	Phytanoyl-CoA dioxygenase domain-containing protein, putative	C7YR76	32.68%
lpp1120	49	3 first hsp are Euka	*Takifugu rubripes*	Lysosomal acid phosphatase	H2THN8	31.23%
lpp1145	28	3 first hsp are Euka	*Anolis carolinensis*	-	H9GI25	30.26%
lpp1157	40	ratio Euka/Proka : 95.0 / 5.0	*Solanum tuberosum*	-	M1CZC6	51.33%
lpp1192	77	3 first hsp are Euka	*Phaseolus vulgaris*	-	V7AMS5	40.69%
lpp1405	12	3 first hsp are Euka	*Pseudocohnilembus persalinus*	-	A0A0V0QNF5	42.68%
lpp1411	39	ratio Euka/Proka : 80.0 / 20.0	*Arthroderma gypseum*	Phosphatidylcholine-hydrolyzing phospholipase C	E5R3V7	33.88%
lpp1522	53	ratio Euka/Proka : 85.0 / 15.0	*Pythium ultimum*	-	K3WEM6	59.87%

lpp1644	65	3 first hsp are Euka	*Phytophthora parasitica*	Phosphoribosylamine-glycine ligase	W2YH10	57.30%
lpp1647	65	ratio Euka/Proka : 90.0 / 10.0	*Volvox carteri*	-	D8UJM7	62.09%
lpp1709	72	2 first hsp are Euka	*Thelazia callipaeda*	-	A0A0N5D1E5	30.47%
lpp2128	31	3 first hsp are Euka	*Astyanax mexicanus*	-	W5KB35	39.20%
lpp3022	80	ratio Euka/Proka : 90.0 / 10.0	*Phytophthora ramorum*	Cystathionine beta-synthase	H3G9B2	64.09%
Lqua0433	1	3 first hsp are Euka	*Botryosphaeria parva*	Putative ser thr protein phosphatase family protein	R1ERS2	46.77%
Lqua2316	1	3 first hsp are Euka	*Columba livia*	Glutamine-rich protein 2	R7VT40	38.57%
Lqua2379	1	3 first hsp are Euka	*Branchiostoma floridae*	-	C3ZUS6	34.62%
Lqua2577	1	3 first hsp are Euka	*Jatropha curcas*	-	A0A067KAT5	53.75%
Lqua2684	1	3 first hsp are Euka	*Penicillium rubens*	Pc21g03600 protein	B6HLH6	41.46%
Lquin0909	1	3 first hsp are Euka	*Strigamia maritima*	-	T1IW32	69.84%
Lquin1163	1	3 first hsp are Euka	*Strongyloides papillosus*	UMP-CMP kinase	A0A0N5BSX5	30.73%
Lquin1672	1	2 first hsp are Euka	*Saprolegnia parasitica*	-	A0A067CH58	30.19%
Lquin3025	1	ratio Euka/Proka : 90.0 / 10.0	*Phytophthora parasitica*	-	W2Y2U5	38.29%
Lquin3041	1	1 first hsp is Euka	*Glarea lozoyensis*	ALDH-like protein	S3E1F7	35.27%
Lrow1308	1	3 first hsp are Euka	*Dactylellina haptotyla*	-	S8C2R2	49.55%
Lrub0638	1	3 first hsp are Euka	*Hordeum vulgare*	Ent-copalyl diphosphate synthase 1, chloroplastic	M0XE17	39.00%
Lrub0759	1	3 first hsp are Euka	*Hymenolepis microstoma*	Dual specificity protein phosphatase 14	A0A068XAT5	39.81%
Lrub2305	1	ratio Euka/Proka : 85.0 / 15.0	*Talaromyces islandicus*	-	A0A0U1LKR4	57.45%
Lrub2306	3	3 first hsp are Euka	*Xenopus tropicalis*	-	A0A1B8XY96	42.28%
Lsain3451	1	3 first hsp are Euka	*Trichosporon asahii*	Peptide hydrolase	K1VCD4	39.01%
Lsan0032	1	3 first hsp are Euka	*Glarea lozoyensis*	DHS-like NAD/FAD-binding protein	S3CWH8	30.83%
Lsan1783	1	3 first hsp are Euka	*Entamoeba histolytica*	Vesicle-fusing ATPase putative	C4LYS4	32.43%
Lsan2473	1	3 first hsp are Euka	*Culex quinquefasciatus*	-	B0W8D6	61.79%
Lsan3225	1	ratio Euka/Proka : 80.0 / 20.0	*Dracunculus medinensis*	-	A0A0N4UBC6	35.22%
Lsan3934	1	3 first hsp are Euka	*Poecilia formosa*	-	A0A087YDD8	31.05%
LshaDSM1229	1	3 first hsp are Euka	*Acromyrmex echinatior*	Salivary glue protein Sgs-4	F4X351	40.35%
LshaDSM2723	1	ratio Euka/Proka : 85.0 / 15.0	*Trichomonas vaginalis*	Cytidyltransferase-related domain containing protein	A2FRN2	30.72%

LshaDSM2948	1	ratio Euka/Proka : 88.9 / 11.1	*Trichophyton interdigitale*	-	A0A059J360	36.84%
Lspi0963	1	3 first hsp are Euka	*Rhizophagus irregularis*	Ack1p	U9SN83	31.89%
Lspi2104	1	3 first hsp are Euka	*Rhizophagus irregularis*	Cdc15p	A0A015LMF8	31.91%
Lstei0649	1	3 first hsp are Euka	*Hypholoma sublateritium*	Peptide hydrolase	A0A0D2PHP7	35.65%
Lstei0663	1	3 first hsp are Euka	*Oryza sativa*	-	B8AZ42	43.62%
Ltau1785	1	1 first hsp is Euka	*Salpingoeca rosetta*	Glyoxalase/bleomycin resistance protein/dioxygenase	F2U941	31.90%
Lwad1781	1	3 first hsp are Euka	*Papilio xuthus*	-	A0A194PU65	44.04%
Lwad3230	1	3 first hsp are Euka	*Nematostella vectensis*	-	A7SL81	37.36%
Lwal0228	1	3 first hsp are Euka	*Conidiobolus coronatus*	-	A0A137NX20	38.04%
Lwal0984	1	3 first hsp are Euka	*Gonapodya prolifera*	ISP domain-containing protein	A0A139ASQ0	35.57%
Lwal1518	1	2 first hsp are Euka	*Pristionchus pacificus*	-	H3EDZ4	30.59%
Lwal1809	1	3 first hsp are Euka	*Pseudocohnilembus persalinus*	Kinase domain protein	A0A0V0QC22	32.72%
Lwal1928	1	3 first hsp are Euka	*Tetrahymena thermophila*	Serine/Threonine kinase domain protein	X1W3P2	33.27%
Lwal2580	1	ratio Euka/Proka : 85.0 / 15.0	*Pythium ultimum*	-	K3WEM6	44.81%
Lwal2592	1	3 first hsp are Euka	*Capsaspora owczarzaki*	-	A0A0D2WI15	38.22%
Lwor1242	1	3 first hsp are Euka	*Rhizophagus irregularis*	Skt5p	A0A015JE96	41.46%
Lwor1271	1	3 first hsp are Euka	*Naegleria gruberi*	-	D2W4W1	40.00%
Lya2270	1	3 first hsp are Euka	*Thalassiosira pseudonana*	Sphingosine-1-phosphate lyase 1	B8C894	39.58%
Lya2481	1	3 first hsp are Euka	*Chlamydomonas reinhardtii*	-	A8JHK1	31.65%

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[1] Protein label representing an orthologous group; [2] indicates the number of proteins contained in the corresponding orthologous group; [3] criteria for considering that the corresponding protein is an eukaryotic like protein; [4] organism of the first eukaryotic hit against the *Legionella* protein; [5] Annotation given for the first eukaryotic hit (hypothetical or unknown functions have not been taken into account; [6] corresponding accession number; [7] percentage of identity of this first hit with the respective *Legionella* protein.

Table S6. Aminoacid identity of the Dot/Icm components with respect to orthologous proteins in *L. pneumophila* Paris

	icmT	*icmS*	*icmR*	*icmQ*	*icmP* *dotM*	*icmO* *dotL*	*icm* *dotK*	*icmM* *dotJ*	*icmL* *dotI*	*icmK* *dotH*	*icmE* *dotG*	*icmG* *dotF*	*icmC* *dotE*	*icmD* *dotP*	*icmJ* *dotN*	*icmB* *dotO*	*icmF*	*icm* *dotU*	*dotV*	*lvgA*	*dotD*	*dotC*	*dotB*	*dotA*	*icmV*	*icmW*	*icmX*
*Lpp**	*0507*	*0508*	*0509*	*0510*	*0511*	*0512*	*0513*	*0514*	*0515*	*0516*	*0517*	*0518*	*0519*	*0520*	*0521*	*0522*	*0524*	*0525*	*0537*	*0590*	*2728*	*2729*	*2730*	*2740*	*2741*	*2742*	*2743*
Lade$	87%	82%		63%	70%	83%	56%	48%	84%	65%	53%	45%	66%	68%	80%	84%	56%	56%	49%	64%	78%	69%	89%	51%	60%	85%	39%
LanA		90%		69%	77%	88%	67%	61%	93%	72%	65%	51%	77%	82%	83%	86%	75%	73%	67%	64%	81%	80%	93%	51%	69%	90%	37%
LanB		90%		69%	77%	88%	67%	61%	93%	72%	73%	51%	77%	82%	83%	86%	75%	73%	67%	64%	81%	80%	93%	53%	69%	90%	37%
Lbe	81%	89%		49%	72%	85%	51%	52%	84%	85%	54%	41%	63%	66%	82%	83%	55%	57%	56%	59%	75%	70%	89%	48%	54%	81%	42%
Lbir		90%		62%	73%	85%	52%	49%	84%	70%	55%	42%	69%	75%	82%	86%	56%	59%	61%	61%	74%	72%	93%	54%	62%	84%	47%
LboA		90%		67%	77%	89%	68%	62%	93%	71%	74%	52%	77%	82%	83%	87%	75%	74%	71%	65%	81%	81%	93%	56%	69%	90%	39%
LboB		90%		66%	77%	89%	68%	62%	93%	71%	74%	53%	77%	81%	83%	87%	75%	74%	71%	65%	81%	80%	93%	56%	69%	90%	39%
Lbru	82%	87%		54%	73%	86%	65%	54%	85%	86%	58%	38%	64%	71%	83%	86%	56%	60%	61%	65%	77%	76%	92%	52%	57%	85%	40%
Lbu	82%	86%		49%	72%	84%	50%	54%	83%	82%	54%	38%	65%	66%	82%	83%	55%	57%	54%	61%	77%	71%	88%	48%	49%	81%	42%
Lche		89%		60%	77%	89%	67%		92%	71%	74%	52%	79%	79%	85%	87%	75%	74%	72%	63%	83%	77%	94%	55%	64%	90%	41%
Lci	84%	90%		68%	78%	88%	66%	56%	91%	71%	0%	54%	75%	79%	85%	87%	72%	72%	71%	60%	83%	80%	93%	47%	59%	91%	48%
Ldra	86%	90%		65%	79%	89%	65%		94%	74%	0%	54%	80%	81%	85%	88%	72%	75%	66%	68%	81%	81%	93%	58%	63%	90%	50%
Ldro	85%	85%		58%	73%	85%	55%	57%	86%	80%	62%	43%	70%	73%	82%	86%	56%	57%	55%	64%	84%	70%	93%	55%	62%	83%	43%
LduN23	82%	89%		65%	77%	89%	66%	67%	91%	72%	72%	51%	79%	79%	85%	87%	74%	73%	70%	65%	81%	80%	94%	55%	68%	89%	42%
LduTex	82%	89%		65%	77%	89%	66%	67%	91%	72%	0%	51%	79%	79%	85%	87%	74%	73%	70%	65%	81%	80%	94%	55%	68%	89%	42%
Lery	86%	87%		56%	74%	87%	62%	51%	75%	71%	65%	43%	69%	71%	83%	85%	54%	55%	51%	60%	83%	75%	94%	54%	64%	82%	44%
Lfair		87%		53%	72%	85%	61%		87%	86%	59%	47%	66%	73%	84%	86%	56%	57%	54%	67%	80%	75%	93%	50%	58%	82%	43%
LFAv2	87%	93%		72%	81%	89%	70%	67%	92%	77%	77%	59%	80%	75%	89%	88%	77%	79%	69%	67%	85%	83%	94%	57%	69%	93%	52%
Lfee	88%	90%		62%	73%	86%	59%		89%	83%	65%	45%	67%	76%	85%	88%	57%	59%	62%	59%	83%	75%	93%	53%	65%	82%	46%
Lge		90%		62%	71%	84%	54%	51%	84%	69%	56%	47%	68%	71%	81%	85%	56%	59%	61%	60%	74%	72%	93%	54%	60%	83%	45%
Lges	85%	79%		50%	67%	81%	55%	50%	84%	73%	49%	40%	57%	57%	75%	82%	48%	53%	47%	42%	74%	73%	88%	52%	52%	77%	43%
LgoA		89%		64%	76%	88%	68%	61%	94%	71%	71%	54%	76%	80%	84%	87%	74%	73%	70%	64%	83%	81%	94%	58%	66%	89%	41%
LgoB	82%	89%		64%	76%	88%	68%	61%	94%	71%	71%	54%	76%	80%	84%	87%	74%	73%	70%	64%	83%	81%	94%	58%	66%	89%	42%
Lgra	84%	88%		67%	79%	87%	63%	60%	92%	68%	0%	52%	76%	76%	85%	87%	73%	72%	72%	61%	83%	80%	94%	49%	61%	91%	47%
Lgre	85%	86%		51%	72%	84%	54%	53%	83%	82%	54%	39%	66%	66%	82%	83%	55%	58%	55%	62%	76%	70%	89%	48%	50%	82%	42%
LHAv2	87%	89%		61%	71%	85%	66%	57%	86%	87%	59%	41%	66%	71%	83%	86%	55%	60%	59%	65%	77%	74%	92%	0%	54%	84%	43%
Lim	88%	86%		61%	70%	84%	54%	51%	85%	69%	53%	40%	67%	65%	80%	83%	52%	57%	51%	58%	78%	73%	89%	51%	57%	80%	42%

Lis	78%	83%		60%	77%	86%	64%	51%	88%	73%	68%	41%	73%	70%	83%	85%	54%	60%	62%	62%	79%	70%	92%	55%	58%	83%	50%
Lja	83%	89%		57%	73%	86%	62%	56%	86%	87%	60%	39%	67%	72%	85%	87%	55%	59%	57%	63%	0%	76%	92%	53%	53%	83%	45%
Ljor	85%	85%		56%	72%	86%	63%	55%	86%	85%	64%	41%	68%	71%	84%	87%	55%	57%	55%	61%	76%	77%	92%	53%	57%	83%	43%
Llan	84%	87%		59%	72%	85%	63%	54%	87%	72%	64%	40%	66%	72%	87%	87%	56%	60%	54%	61%	74%	78%	90%	54%	54%	84%	45%
Llikebru	88%	88%		60%	73%	85%	60%	51%	85%	84%	63%	40%	69%	79%	85%	88%	56%	59%	55%	61%	79%	77%	92%	53%	56%	83%	42%
Llo98	83%	92%		69%	78%	87%	66%	59%	92%	72%	0%	53%	75%	80%	85%	87%	72%	71%	71%	60%	83%	79%	93%	51%	57%	92%	48%
LloAT	83%	92%		69%	78%	87%	66%	59%	92%	72%	0%	53%	75%	80%	85%	87%	72%	71%	71%	60%	83%	80%	93%	51%	57%	91%	47%
Llo D4968	83%	92%		69%	78%	87%	66%	59%	92%	86%	0%	53%	75%	80%	85%	87%	72%	71%	71%	60%	84%	80%	93%	51%	57%	91%	47%
Llon	85%	87%		62%	70%	82%	55%	47%	85%	70%	57%	45%	69%	67%	82%	83%	51%	51%	52%	63%	75%	73%	88%	54%	54%	83%	46%
LloNSW	83%	92%		69%	78%	87%	69%	59%	92%	72%	0%	53%	75%	80%	85%	87%	72%	71%	71%	60%	83%	80%	93%	51%	57%	91%	47%
Lma	88%	87%		58%	73%	86%	58%	55%	89%	78%	63%	48%	66%		86%	86%	57%	56%	53%	62%	83%	70%	93%	53%	59%	85%	43%
LmasB		86%		56%	73%	86%	56%	49%	84%	81%	64%	42%	62%	60%	84%	84%	57%	58%	56%	67%	81%	72%	92%	51%	55%	85%	40%
LmasA		86%		56%	73%	86%	56%	49%	84%	81%	64%	42%	62%	60%	84%	84%	57%	58%	56%	67%	81%	72%	92%	51%	55%	85%	40%
Lmic	86%	87%		57%	75%	85%	59%	56%	88%	76%	64%	46%	67%	68%	85%	86%	57%	57%	51%	62%	84%	70%	92%	52%	60%	85%	42%
LmicB		87%		57%	75%	85%	59%	56%	88%	76%	64%	46%	67%	68%	85%	86%	58%	57%	51%	62%	84%	70%	92%	52%	60%	85%	
Lmo	87%	90%		78%	82%	91%	73%		91%	77%	80%	62%	75%	77%	91%	89%	76%	84%	73%	73%	84%	88%	96%	63%	72%	93%	49%
Lna	85%	89%		69%	72%	85%	59%	43%	83%	73%	0%	45%	66%	63%	81%	83%	56%	56%	52%	66%	78%	73%	89%	51%	52%	81%	37%
Lnau	87%	87%		59%	74%	85%	54%	53%	87%	83%	63%	42%	69%	70%	82%	86%	57%	56%	56%	64%	85%	72%	94%	54%	60%	84%	42%
Lno	94%	96%	48%	86%	88%	94%	87%	74%	97%	81%	84%	79%	87%	85%	94%	94%	0%	90%	88%	79%	93%	95%	98%	72%	83%	97%	
LoakA	85%	88%		63%	70%	84%	56%	46%	83%	73%	59%	37%	66%	66%	83%	84%	56%	56%	54%	61%	79%	75%	89%	51%	52%	80%	36%
LoakB	85%	88%		63%	70%	84%	56%	46%	83%	73%	66%	46%	66%	66%	83%	84%	56%	56%	0%	61%	77%	75%	89%	51%	52%	80%	36%
Loas	83%	74%		54%	64%	77%	59%	33%	69%	70%	63%	37%	67%	66%	72%	80%	34%	36%	44%	54%	69%	69%	86%	52%	50%	71%	40%
Lp130b		100%	98%	99%	99%	100%	99%	95%	100%	99%	100%	99%	100%	99%	100%	100%	99%	100%	100%	99%	99%	86%	100%	99%	99%	100%	85%
Lp570C		100%	97%	99%	99%	100%	99%	97%	100%	99%	98%	99%	100%	99%	100%	100%	99%	100%	100%	96%	99%	100%	100%	86%	89%	99%	88%
LpAlc		100%	99%	99%	99%	100%	99%	96%	100%	99%	100%	99%	99%	98%	99%	100%	99%	100%	100%	99%	100%	100%	100%	91%	97%	99%	85%
Lpar		90%		69%	76%	88%	68%	63%	94%	71%	74%	51%	76%	82%	82%	86%	74%	73%	69%	63%	81%	80%	93%	56%	68%	90%	39%
LpCorby	100%	100%	99%	99%	99%	100%	99%	96%	100%	99%	100%	99%		98%	99%	100%	99%	100%	100%	99%	99%	100%	100%	90%	96%	99%	84%
LpFRA		100%	95%	96%	98%	99%	96%	95%	100%	95%	96%	93%	96%	98%	100%	99%	96%	97%	98%	98%	98%	99%	100%	84%	89%	99%	89%
LpFRA B		100%	95%	97%	98%	99%	96%	95%	100%	95%	97%	92%	96%	98%	100%	99%	96%	97%	98%	98%	98%	100%	99%	85%	91%	99%	86%

LpFRAC		100%	95%	97%	98%	99%	96%	95%	100%	95%	97%	93%	96%	98%	100%	99%	96%	97%	98%	98%	98%	99%	100%	84%	89%	99%	89%
LpLens	100%	100%	98%	99%	99%	100%	99%	95%	100%	99%	100%	98%	99%	99%	100%	100%	99%	100%	99%	99%	98%	100%	100%	86%	98%	100%	85%
LpLorr	100%	100%	99%	99%	99%	100%	99%	99%	100%	99%	100%	99%	100%	99%	100%	100%	99%	100%	100%	100%	100%	100%	100%	98%	99%	100%	85%
LpLPE		100%	97%	99%	99%	100%	99%	97%	100%	99%	98%	99%	100%	99%	100%	100%	99%	100%	100%	96%	99%	100%	100%	86%	89%	99%	88%
LpPAS		99%	95%	96%	98%	99%	97%	94%	100%	95%	97%	94%	97%	98%	99%	99%	96%	98%	97%	97%	98%	100%	100%	84%	89%	99%	89%
LpPhila	100%	100%	97%	99%	99%	100%	99%	97%	100%	99%	98%	99%	100%	99%	100%	100%	99%	100%	100%	96%	99%	100%	100%	86%	89%	99%	88%
LpThu		100%	97%	99%	99%	100%	99%	97%	100%	99%	98%	99%	100%	99%	100%	100%	99%	100%	100%	96%	99%	100%	100%	86%	89%	99%	88%
LPVv2	99%	99%	98%	99%	99%	99%	99%	97%	100%	99%	99%	99%	99%	99%	100%	100%	100%	100%	100%	100%	100%	100%	100%	99%	98%	100%	85%
Lqua	86%	92%		78%	82%	92%	74%	66%	92%	79%	81%	61%	76%	76%	91%	89%	77%	85%	76%	69%	86%	87%	95%	62%	74%	93%	51%
Lquin		90%		62%	72%	85%	54%	51%	84%	69%	56%	46%	69%	69%	81%	85%	56%	59%	61%	60%	74%	72%	93%	54%	60%	83%	47%
Lrow	85%	91%		65%	78%	88%	59%	66%	93%	71%	72%	47%	78%	79%	85%	87%	70%	71%	69%	70%	81%	80%	91%	56%	68%	91%	50%
Lrub	87%	88%		58%	74%	86%	61%	50%	75%	70%	65%	44%	68%	70%	84%	85%	54%	55%	52%	64%	84%	75%	94%	55%	66%	82%	44%
Lsain	83%	91%		68%	78%	87%	65%	57%	91%	70%	0%	53%	75%	80%	85%	87%	72%	72%	71%	60%	83%	80%	93%	51%	57%	91%	48%
Lsan	83%	92%		68%	78%	88%	66%	56%	92%	72%	0%	53%	75%	80%	85%	87%	72%	72%	72%	61%	83%	79%	93%	51%	57%	91%	47%
LshaDSM	88%	92%		82%	82%	90%	72%	64%	93%	80%	76%	61%	76%	80%	89%	89%	78%	83%	72%	73%	82%	85%	96%	64%	72%	93%	56%
Lspi	87%	89%		64%	72%	85%	53%	50%	80%	72%	63%	43%	65%	69%	85%	85%	55%	56%	55%	62%	81%	75%	92%	57%	58%	82%	41%
Lstei		89%		62%	75%	89%	66%	68%	93%	70%	75%	52%	79%	79%	85%	86%	75%	74%	71%	62%	82%	78%	94%	57%	67%	91%	40%
Ltau	87%	88%		57%	74%	86%	60%	50%	75%	70%	66%	44%	68%	70%	84%	85%	54%	54%	51%	65%	84%	75%	94%	55%	66%	82%	43%
Ltuc	85%	89%		68%	76%	88%	66%	64%	92%	73%	75%	53%	78%	82%	82%	86%	75%	72%	71%	61%	81%	81%	93%	54%	68%	90%	38%
Lwad		90%		63%	76%	88%	63%	67%	92%	71%	68%	46%	79%	80%	84%	86%	74%	73%	67%	67%	81%	81%	93%	0%	67%	90%	43%
Lwal	87%	92%		75%	84%	90%	75%	59%	91%	73%	77%	66%	77%	81%	87%	91%	75%	74%	71%	69%	86%	86%	92%	57%	69%	91%	43%
Lwor		88%		78%	81%	91%	71%	61%	92%	76%	79%	57%	76%	78%	90%	89%	76%	83%	71%	66%	84%	86%	95%	62%	66%	90%	49%
Lya	85%	87%		58%	71%	83%	51%	51%	85%	68%	54%	44%	67%	65%	81%	83%	52%	56%	51%	61%	75%	73%	89%	52%	55%	81%	43%

Blue indicates presence of an orthologous protein in the corresponding species, the darker the blue the higher the percentage of aminoacid identity. White means that there is an orthologous but the length or the percentage of identity regarding the orthologous from *L. pneumophila* Paris is under the cut-off established for the orthologous program used. Grey means that we detect a orthologous gene by blastn but the orthologous program used missed it. Black means absence of orthologous gene in the corresponding species. **lpp* are the gene identifiers for *L. pneumophila* strain Paris; *$* abbreviated name of the different *Legionella* species as specified in Table S1

Table S7: Distribution of seventeen highly conserved Dot/Icm secreted substrates

GENOMES		***vipF***	***ravC***	***cetLP1***	***-***	***-***	***-***	***-***	***ceg25***	***legA3/ankH/ankW***	***-***	***-***	***mavN***	***-***	***-***	***-***	***-***
Labels	***lpg0021***	***lpg0103***	***lpg0107***	***lpg0140***	***lpg0294***	***lpg0405***	***lpg1356***	***lpg1661***	***lpg1836***	***lpg2300***	***lpg2359***	***lpg2628***	***lpg2815***	***lpg2832***	***lpg2888***	***lpg2936***	***lpg3000***
L. adelaidensis	Lade0120	Lade0258	Lade0256	Lade0231	Lade0007	NA	Lade0943	Lade1699	Lade0588	Lade0699	Lade0795	NA	Lade1415	Lade1427	Lade0057	Lade2155	Lade0084
L. londinensis	Llon0485	Llon1628	Llon1626	Llon1596	Llon1711	Llon1839	Llon0620	NA	Llon0990	Llon0331	Llon1146	Llon0285	Llon0105	Llon0094	Llon1760	Llon0024	Llon0462
L. yabuuchiae	Lya2157	Lya1566	Lya1568	Lya1595	Lya2102	Lya1793	Lya1488	Lya1358	Lya1171	Lya0269	Lya0803	Lya0877	Lya0781	Lya0774	Lya1007	Lya0740	Lya0995
L. impletisoli	Lim1774	Lim1728	Lim1726	Lim1700	Lim2314	Lim1094	Lim0190	Lim0222	Lim0807	Lim1516	Lim1628	Lim1547	Lim1369	Lim1377	Lim1804	Lim1407	Lim1792
L. oakridgensis RV2-2007	LoakB0048	LoakB0105	LoakB0107	LoakB0146	LoakB0296	LoakB0423	LoakB1438	LoakB1357	LoakB2007	LoakB0808	LoakB0697	LoakB0769	LoakB2472	LoakB2481	LoakB2621	LoakB2512	LoakB2630
L. oakridgensis Oak Ridge 10	LoakA0077	LoakA0139	LoakA0142	LoakA0178	LoakA0370	LoakA0522	LoakA1666	LoakA1570	LoakA2296	LoakA0911	LoakA0777	LoakA0865	LoakA2839	LoakA2848/LoakB2849	LoakA3009	LoakA2885	LoakA3022
L. nagasakiensis	Lna1528	Lna2008	Lna2010	Lna2045	Lna2113	Lna1725	Lna0687	Lna0609	Lna0139	Lna0111	Lna0004	Lna0073	Lna0994	Lna1002	Lna1484	Lna1032	Lna1491
L. like brunensis	Llikebru0475	Llikebru2370	Llikebru2054	Llikebru0607	Llikebru1962	Llikebru1726	Llikebru2271	Llikebru1841	Llikebru0190	Llikebru0817	Llikebru2321	Llikebru2243	Llikebru0624	Llikebru0666	Llikebru2084	Llikebru0422	Llikebru0450
L. jordanis	Ljor0181	Ljor0067	Ljor0061	Ljor0027	Ljor2756	Ljor0479	Ljor1988	Ljor1122	Ljor0640	Ljor0604	Ljor2251	Ljor0708	Ljor0423	Ljor0386	Ljor0135	Ljor0296	Ljor0204
L. lansingensis	Llan0610	Llan0256	Llan0258	Llan0304	Llan0357	Llan0706	Llan2080	Llan1513	Llan2725	Llan1786	Llan0166	Llan0861	Llan1719	Llan1753	NA	Llan2522	Llan0588
L. jamestowniensis	Lja0661	Lja0802	Lja0804	Lja0852	Lja0892	Lja2122	Lja1659	Lja1782	Lja0127	Lja0168	Lja0368	Lja0056	Lja2055	Lja2007	Lja0763	Lja0582	Lja0633
L. hackeliae	LHAv2_0022	LHAv2_0223	LHAv2_0226	LHAv2_0268	LHAv2_0311	LHAv2_2963	LHAv2_1825	LHAv2_1510	LHAv2_0767	LHAv2_0726	LHAv2_0547	LHAv2_0847	LHAv2_3034	LHAv2_3080	LHAv2_0175	LHAv2_3209	LHAv2_3261
L. brunensis	Lbru1361	Lbru0140	Lbru0136	Lbru0093	Lbru0009	Lbru2928	Lbru0884	Lbru1537	Lbru2605	Lbru1623	Lbru2301	Lbru3291	Lbru2448	Lbru2417	Lbru0178	Lbru1233	Lbru1312
L. fairfieldensis	Lfair0234	Lfair1874	Lfair1871	Lfair1622	Lfair0178	Lfair0944	Lfair1684	Lfair1737	Lfair0747	Lfair1168	Lfair1274	Lfair0769	Lfair2370	Lfair0117	Lfair1905	Lfair1980	Lfair0217
L. massiliensis	LmasA0422	LmasA0559	LmasA0557	LmasA0616	NA	LmasA0175	LmasA2783	LmasA3553	LmasA1825	LmasA1990	LmasA1026	LmasA1295	LmasA0226	LmasA0251	LmasA0606	LmasA0469	LmasA0440
L. massiliensis LegA	LmasB0422	LmasB0559	LmasB0557	LmasB0616	NA	LmasB0175	LmasB2783	LmasB3553	LmasB1825	LmasB1990	LmasB1026	LmasB1295	LmasB0226	LmasB0251	LmasB0606	LmasB0469	LmasB0440
L. drozanskii	Ldro1241	Ldro1410	Ldro1414	Ldro1432	Ldro2913	Ldro0735	Ldro0986	Ldro1054	Ldro2438	Ldro0166	Ldro0006	Ldro0304	Ldro0791	Ldro0815	Ldro2722	Ldro1293	Ldro1266
L. nautarum	Lnau2381	Lnau2436	Lnau2440	Lnau2459	Lnau2891	Lnau1100	Lnau0153	Lnau0224	Lnau2977	Lnau1900	Lnau1626	Lnau1391	Lnau1035	Lnau2840	Lnau2207	Lnau2326	Lnau2353
L. maceachernii	Lma0224	Lma0452	Lma0449	Lma0431	Lma3074	Lma2334	Lma1421	Lma1496	Lma1093	Lma0711	Lma2083	Lma1135	Lma0016	Lma0043	Lma0113	Lma0288	Lma0249
L. micdadei RV2-2007	LmicB2635	LmicB2443	LmicB2440	LmicB2420	LmicB2327	LmicB2876	LmicB1204	LmicB1124	LmicB0503	LmicB2075	LmicB0302	LmicB0539	LmicB2820	LmicB2792	LmicB2722	LmicB2582	LmicB2614
L. micdadei Tatlock	LMIv2_0015	LMIv2_3006	LMIv2_3003	LMIv2_2983	LMIv2_2873	LMIv2_0264	LMIv2_1775	LMIv2_1856	LMIv2_0950	LMIv2_2612	LMIv2_0787	LMIv2_0985	LMIv2_0208	LMIv2_0179	LMIv2_0109	LMIv2_3139	LMIv2_3169
L. feeleii	Lfee0339	Lfee0213	Lfee0210	Lfee2067	Lfee3064	Lfee2121	Lfee0591	Lfee2480	Lfee1455	Lfee1629	Lfee2286	Lfee0148	Lfee0924	Lfee1032	NA	Lfee0279	Lfee0308
L. beliardensis	Lbe2206	Lbe1538	Lbe1540	Lbe1572	Lbe1630	Lbe2120	Lbe1827	Lbe0372	Lbe1061	Lbe1031	Lbe2592	Lbe1219	Lbe1502	Lbe1491	Lbe1368	Lbe1408	Lbe1388
L. gresilensis	Lgre1283	Lgre1346	Lgre1347	Lgre1382	Lgre1456	Lgre1902	Lgre0927	Lgre2800	Lgre1553	Lgre1583	Lgre0307	Lgre0473	Lgre1834	Lgre1818	Lgre1156	Lgre1206	Lgre1178

L. busanensis	Lbu1704	Lbu1761	Lbu1762	Lbu1792	Lbu3334	Lbu1396	Lbu0368	Lbu0629	Lbu2259	Lbu2290	Lbu2066	Lbu0841	Lbu1460	Lbu1476	Lbu1570	Lbu1631	Lbu1590
L. genomospecies	Lge1388	Lge1930	Lge1951	Lge1849	Lge3018	Lge1896	Lge2228	Lge1507	Lge3002	Lge3149	Lge1714	Lge2108	Lge1972	Lge1879	Lge2801	Lge3067	Lge1338
L. quinlivanii	Lquin1995	Lquin1111	Lquin1089	Lquin0684	Lquin2766	Lquin1145	Lquin0436	Lquin1681	Lquin0267	Lquin1879	Lquin2663	Lquin0151	Lquin0660	Lquin1162	Lquin1241	Lquin1273	Lquin1307
L. birminghamensis	Lbir1452	Lbir1011	Lbir1004	Lbir2042	Lbir2803	Lbir1053	Lbir1954	Lbir1523	Lbir0007	Lbir1888	Lbir1223	Lbir0118	Lbir2012	Lbir1074	Lbir0855	Lbir0885	Lbir1790
L. spiritensis	Lspi1416	Lspi1306	Lspi1298	Lspi1267	Lspi2978	Lspi0711	Lspi0243	Lspi2435	Lspi1993	Lspi2321	Lspi2467	Lspi2273	Lspi0656	Lspi0639	NA	Lspi0539	Lspi2948
L. erythra	Lery0969	Lery1353	Lery1362	Lery1399/Lery1400	Lery2130	Lery1795	Lery0403	Lery1481	Lery0732	Lery2768	Lery2375	Lery0139	Lery2565	Lery2238	Lery1326	Lery0899	Lery0944
L. rubrilucens	Lrub1678	Lrub1794	Lrub1805	Lrub1841	Lrub1506	Lrub2020	Lrub1286	Lrub2502	Lrub0296	Lrub0262	Lrub0108	Lrub0810	Lrub2073	Lrub2093	Lrub1767	Lrub1609	Lrub1654
L. taurinensis	Ltau1071	Ltau1191	Ltau1200	Ltau1238	Ltau2199	Ltau0895	Ltau0666	Ltau2007	Ltau0193	Ltau0157	Ltau0004	Ltau1339	Ltau0842	Ltau0823	Ltau1163	Ltau2100	Ltau1046
L. israelensis12	Lis1727	Lis1517	Lis1574	Lis2574	Lis1572	Lis0156	Lis1215	NA	Lis1132	Lis1848	Lis0793	Lis2018	Lis1904	Lis1040	Lis0489	Lis0192	Lis1176
L. rowbothamii	Lrow1191	Lrow1575	Lrow1576	Lrow1375	Lrow1425	Lrow2075	Lrow0558	Lrow0429	Lrow2607	Lrow3222	Lrow3267	Lrow0249	Lrow1644	Lrow1361	Lrow1346	Lrow1250	Lrow1165
L. drancourtii	Ldra0447	Ldra1030	Ldra1029	Ldra0996	Ldra2090	Ldra3282	Ldra0674	Ldra3800	Ldra1271	Ldra1597	Ldra1545	NA	Ldra3574	Ldra3517	Ldra3500	Ldra0409	Ldra0474
L. gratiana	Lgra2618	Lgra2065	Lgra2064	Lgra2005	Lgra3308	Lgra0743	Lgra1580	Lgra1155	Lgra0378	Lgra3021	Lgra0730	Lgra3107	Lgra1854	Lgra1818	Lgra1804	Lgra1707	Lgra2568
L. sainthelensi	Lsain3412	Lsain1427	Lsain1426	Lsain1373	Lsain3547	Lsain0177	Lsain0837	Lsain0915	Lsain2479	Lsain1722	Lsain0190	Lsain1981	Lsain0405	Lsain0364	Lsain0349	Lsain0280	Lsain1245
L. longbeachae Long Beach 4	LloAT0022	LloAT3552	LloAT3551	LloAT3499	LloAT0456	LloAT3041	LloAT1509	LloAT1776	LloAT1109	LloAT0582	LloAT3052	LloAT0806	LloAT0237	LloAT0196	LloAT0182	LloAT0060	LloAT3706
L. longbeachae D4968	ACZGv1_11837	ACZGv1_12026	ACZGv1_12027	ACZGv1_12082	ACZGv1_11390	ACZGv1_20110	ACZGv1_10213	ACZGv1_21344	ACZGv1_10638	ACZGv1_11266	ACZGv1_20099	ACZGv1_10947	ACZGv1_11617	ACZGv1_11659	ACZGv1_11673	ACZGv1_11799	ACZGv1_11890
L. longbeachae NSW150	llo0047	llo3312	llo3311	llo3260	llo0464	llo2845	llo1443	llo1691	llo1068	llo0584	llo2856	llo0787	llo0254	llo0214	llo0200	llo0081	llo3444
L. longbeachae 98072	Llo980024	Llo983484	Llo983483	Llo983431	Llo980450	Llo983036	Llo981490	Llo981781	Llo981102	Llo980578	Llo983047	Llo980817	Llo980231	Llo980196	Llo980182	Llo980060	Llo983625
L. cincinnatiensis	Lci0853	Lci1085	Lci1086	Lci3327	Lci2430	Lci3439	Lci0187	Lci1655	Lci0937	Lci2675	Lci2941	Lci2917	Lci1894	Lci1854	Lci2500	Lci1602	Lci0809
L. santicrucis	Lsan1166	Lsan3109	Lsan3110	Lsan3635	Lsan0788	Lsan0066	Lsan1098	Lsan3897	Lsan1677	Lsan0396	Lsan0055	Lsan2098	Lsan2295	Lsan3594	Lsan2760	Lsan1130	Lsan1209
L. dumoffii TexKL	LduTex0023	LduTex3196	LduTex3195	LduTex3145	LduTex2822	LduTex2707	LduTex1825	LduTex1660	LduTex1207	LduTex0590	LduTex0543	LduTex0914	LduTex0202	LduTex0153	LduTex0139	LduTex0060	LduTex3291
L. dumoffii NY23	LduN230023	LduN233239	LduN233238	LduN233186	LduN232883	LduN232622	LduN230726	LduN230889	LduN231343	LduN231869	LduN231916	LduN231648	LduN230200	LduN230152	LduN230138	LduN230058	LduN233343
L. cherrii	Lche2919	Lche2764	Lche2763	Lche2711	Lche2431	Lche2327	Lche0364	Lche0199	Lche1531	Lche2190	Lche2237	Lche1226	Lche2994	Lche2657	Lche2671	Lche0953	Lche2871
L. steigerwaltii	Lstei3111	Lstei0811	Lstei0810	Lstei3527	Lstei3451	Lstei2322	Lstei0047	Lstei0205	Lstei0383	Lstei3407	Lstei1651	Lstei1716	Lstei2513	Lstei1812	Lstei1827	Lstei3199	Lstei0929
L. wadsworthii	Lwad3260	Lwad2090	Lwad2089	Lwad2041	Lwad2587	Lwad1652	Lwad1362	Lwad1206	Lwad2311	Lwad0681	Lwad0724	Lwad2802	Lwad1885	Lwad1850	Lwad1836	Lwad1753	Lwad3065
L. tucsonensis	Ltuc3058	Ltuc2930	Ltuc2929	Ltuc2875	Ltuc1976	Ltuc1654	Ltuc0601	Ltuc0763	Ltuc1205	Ltuc2804	Ltuc2851	Ltuc0179	Ltuc2040	Ltuc2093	Ltuc2107	Ltuc2188	Ltuc3029
L. anisa awa-316-C3	LanB0709	LanB0318	LanB0317	LanB2865	LanB2798	LanB0095	LanB2384	LanB1300	LanB3906	LanB2807	LanB0183	LanB3591	LanB1049	LanB1142	LanB1128	LanB0673	LanB0740
L. anisa Linanisette	LanA0412	LanA2323	LanA2321	LanA2267	LanA3812	LanA2670	LanA0146	LanA2054	LanA3974	LanA3640	LanA3594	NA	LanA0582	LanA0547	LanA0532	LanA0448	LanA0381
L. parisiensis	Lpar1121	Lpar0969	Lpar0968	Lpar0915	Lpar2586	Lpar2116	Lpar1370	Lpar1532	Lpar0288	Lpar2920	Lpar2877	Lpar0725	Lpar1287	Lpar1252	Lpar1238	Lpar1155	Lpar1091

L. bozemanii WIGA	LboA2675	LboA2455	LboA2454	LboA2402	LboA3341	LboA0949	LboA1360	LboA1521	LboA0059	LboA2684	LboA2730	LboA0396	LboA1788	LboA1823	LboA1837	LboA2640	LboA2069
L. bozemanii 94163278	LboB0592	LboB0790	LboB0791	LboB0842	LboB1199	LboB1322	LboB2283	LboB2446	LboB2936	LboB0028	LboB0075	LboB3257	LboB0421	LboB0455	LboB0470	LboB0557	LboB0648
L. gormanii	LgoB3348	LgoB3192	LgoB3191	LgoB3112	LgoB2835	LgoB2712	LgoB1770	LgoB1559	LgoB1131	LgoB0432	LgoB0384	LgoB0796	LgoB3533	LgoB3489	LgoB3473	LgoB3389	LgoB3320
L. gormanii LS-13	LgoA0761	LgoA0908	LgoA0907	LgoA0832	LgoA1535	LgoA0104	LgoA0383	LgoA3073	LgoA0961	LgoA2883	LgoA1332	LgoA1288	LgoA1463	LgoA1505	LgoA2871	LgoA2637	LgoA0733
L. fallonii	LFAv2_0027	LFAv2_0162	LFAv2_0165	LFAv2_0200	LFAv2_0305	LFAv2_2711	LFAv2_1281	LFAv2_1679	LFAv2_1990	LFAv2_2306	LFAv2_3259	LFAv2_2574	LFAv2_3530	LFAv2_3562	LFAv2_3619	LFAv2_3709	LFAv2_3784
L. shakespearei	LshaDSM2968	LshaDSM0935	LshaDSM0939	LshaDSM0969	LshaDSM1059	LshaDSM2450	LshaDSM0485	LshaDSM1105	LshaDSM0193	LshaDSM2697	LshaDSM2023	LshaDSM1379	LshaDSM1531	LshaDSM1511	LshaDSM1275	LshaDSM1336	LshaDSM2279
L. worsleiensis	Lwor0817	Lwor0958	Lwor0963	Lwor0991	Lwor1033	Lwor2133	Lwor0227	Lwor0536	Lwor2355	Lwor1100	Lwor1044	Lwor0755	Lwor0455	Lwor0434	Lwor0372	Lwor0895	Lwor0838
L. quateirensis	Lqua0582	Lqua1864	Lqua1852	Lqua1816	Lqua1749	Lqua1640	Lqua1361	Lqua3377	Lqua0891	Lqua0318	Lqua0378	Lqua1994	Lqua0806	Lqua0790	Lqua0733	Lqua0683	Lqua0610
L. moravica	Lmo3232	Lmo0625	Lmo0619	Lmo0587	Lmo0497	Lmo2773	Lmo0077	Lmo2009	Lmo0442	Lmo1775	Lmo3095	Lmo0954	Lmo1402	Lmo1416	Lmo1542	Lmo1486	Lmo3295
L. waltersii	Lwal0138	Lwal0250	Lwal0252	Lwal0286	Lwal2886	Lwal0453	Lwal1212	Lwal0999	Lwal2291	Lwal3400	Lwal1566	Lwal1460	Lwal2719	Lwal1982	Lwal0012	Lwal0053	Lwal0108
L. norrlandica	Lno0955	Lno2009	Lno2012	Lno0467/Lno0468	Lno1814	Lno1902	Lno1315	Lno1128	Lno1195	Lno1390	Lno1790	Lno0273	Lno0196	Lno0181	NA	Lno0548	Lno0929/Lno0930
L. pneumophila Alcoy	LpAlc0021	LpAlc0118	LpAlc0122	LpAlc0159	LpAlc0365	LpAlc0472	LpAlc1467	LpAlc1782	LpAlc1971	LpAlc2435	LpAlc2499	LpAlc2823	LpAlc3018	LpAlc3036	LpAlc3097	LpAlc3166	LpAlc3248
L. pneumophila Corby	LPC_0022	LPC_0122	LPC_0126	LPC_0161	LPC_0373	LPC_2939	LPC_0770	LPC_1091	LPC_1280	LPC_1765	LPC_1828	LPC_0513	LPC_3101	LPC_3116	LPC_3174	LPC_3243	LPC_3316
L. pneumophila Thunder Bay	LpThu0022	LpThu0110	LpThu0114	LpThu0150	LpThu0309	LpThu0408	LpThu1406	LpThu1715	LpThu1896	LpThu2445	LpThu2508	LpThu2815	LpThu3003	LpThu3023	LpThu3082	LpThu3143	LpThu3213
L. pneumophila 570-CO-H	Lp570C0022	Lp570C0108	Lp570C0112	Lp570C0148	Lp570C0309	Lp570C0414	Lp570C1323	Lp570C1632	Lp570C1815	Lp570C2347	Lp570C2410	Lp570C2718	Lp570C2906	Lp570C2926	Lp570C2986	Lp570C3043	Lp570C3112
L. pneumophila LPE509	LpLPE3172	LpLPE3085	LpLPE3081	LpLPE3046	LpLPE2885	LpLPE2778	LpLPE1822	LpLPE1510	LpLPE1326	LpLPE0773	LpLPE0710	LpLPE0400	LpLPE0210	LpLPE0190	LpLPE0130	LpLPE0073	LpLPE0005
L. pneumophila Philadelphia	lpg0021	lpg0103	lpg0107	lpg0140	lpg0294	lpg0405	lpg1356	lpg1661	lpg1836	lpg2300	lpg2359	lpg2628	lpg2815	lpg2832	lpg2888	lpg2936	lpg3000
L. pneumophila 130b	Lp130b0022	Lp130b0105	Lp130b0109	Lp130b0144	Lp130b0411	Lp130b0518	Lp130b1437	Lp130b1771	Lp130b1949	Lp130b2559	Lp130b2626	Lp130b2958	Lp130b3157	Lp130b3177/Lp130b3178	Lp130b3243	Lp130b3311	Lp130b3373
L. pneumophila Lens	lpl0022	lpl0103	lpl0107	lpl0140	lpl0347	lpl0447	lpl1307	lpl1626	lpl1800	lpl2219	lpl2281	lpl2553	lpl2730	lpl2744	lpl2801	lpl2865	lpl2928
L. pneumophila Lorraine	LPOv2_0022	LPOv2_0111	LPOv2_0115	LPOv2_0153	LPOv2_0351	LPOv2_0465	LPOv2_1345	LPOv2_1696	LPOv2_1897	LPOv2_2371	LPOv2_2439	LPOv2_2904	LPOv2_3107	LPOv2_3127	LPOv2_3193	LPOv2_3261	LPOv2_3342
L. pneumophila Paris	lpp0021	lpp0117	lpp0121	lpp0155	lpp0372	lpp0471	lpp1310	lpp1632	lpp1799	lpp2248	lpp2308	lpp2681	lpp2867	lpp2889	lpp2947	lpp3004	lpp3072
L. pneumophila HL06041035	LPVv2_0025	LPVv2_0119	LPVv2_0123	LPVv2_0158	LPVv2_0389	LPVv2_0504	LPVv2_1469	LPVv2_1917	LPVv2_2108	LPVv2_2567	LPVv2_2633	LPVv2_2967	LPVv2_3168	LPVv2_3187	LPVv2_3246	LPVv2_3311	LPVv2_3388
L. pneumophila fraseri Dallas 1E	LpFRAB2690	LpFRAB2401	LpFRAB2405	LpFRAB2439	LpFRAB3039	LpFRAB1803	LpFRAB0138	LpFRAB0463	LpFRAB1319	LpFRAB0656	LpFRAB0718	LpFRAB2011	LpFRAB1578	LpFRAB1558	LpFRAB1500	LpFRAB1438	LpFRAB2662
L. pneumophila fraseri Los Angeles 1	LpFRA1679	LpFRA2130	LpFRA2134	LpFRA2168	LpFRA2876	LpFRA2306	LpFRA0193	LpFRA0518	LpFRA1216	LpFRA1546	LpFRA1609	LpFRA2493	LpFRA1041	LpFRA1022	LpFRA0965	LpFRA0902	LpFRA1707
L. pneumophila fraseri Lansing3	LpFRAC2182	LpFRAC1931	LpFRAC1935	LpFRAC1970	LpFRAC2858	LpFRAC0815	LpFRAC2572	LpFRAC1527	LpFRAC1358	LpFRAC0072	LpFRAC0009	LpFRAC1100	LpFRAC1272	LpFRAC1253	LpFRAC1194	LpFRAC2753	LpFRAC2210
L. pneumophila pascullei	LpPAS1745	LpPAS1656	LpPAS1652	LpPAS1618	LpPAS1436	LpPAS2677	LpPAS0242	LpPAS0576	LpPAS0750	LpPAS2315	LpPAS2378	LpPAS1207	LpPAS1399	LpPAS1416	LpPAS3023	LpPAS3076	LpPAS1770
L. geestiana	NA	Lges0377	Lges0321	Lges0292	NA	NA	Lges0005	Lges0876	NA	Lges1288	Lges1876	NA	Lges1017	Lges2240	Lges0346	Lges1633	Lges0445

L. osnabrueckensis	Loas2676	Loas2209	Loas2930	Loas1612	Loas2055	Loas2096	Loas0320	Loas0449	NA	Loas0978	Loas1180	Loas1127	Loas2090	Loas2160	NA	Loas1447	Loas2699

From more than 300 Dot/Icm *L. pneumophila* substrates, 17 are present in all or almost all analyzed species. In white: orthologous genes, in light blue: cases in which corresponding orthologous are two consecutive genes, and in yellow absence of significant orthologous gene.

Table S8: Comparison of the effector reperotoire among strains of the same *Legionella* species

Species	Number of strains	Common effectors
L .anisa	2	200/217 (92%)
L. bozemanii	2	186/218(85%)
L. dumoffii	2	179/184(97%)
L. gormanii	2	192/218(88%)
L. longbeachae	2	229/248(92%)
L. micdadei	2	135/148(91%)
L. oakridgensis	2	97/118(82%)
L. pneumophila	2	303/354(88%)
L. pneum. subs. fraserii	2	310/324(96%)
L. pneumophila	11	264/408 (65%)

Table S9. Number of Dot/Icm secreted proteins predicted in each strain analyzed

Species	**Strain**	**E1**	**E2**	**ELP**	**Etot**
L. adelaidensis	1762-AUS-E	38	57	12	93
L. londiniensis	1477	33	38	8	70
L. yabuuchiae	OA1-2	33	59	12	95
L. impletisoli	OA1-1	36	56	12	93
L. oakridgensis	RV2-2007	43	59	18	109
L. oakridgensis	Oak Ridge 10	38	56	22	106
L. nagasakiensis	JCM 15315	49	57	18	111
L. LIKE brunensis	W10-070	49	69	15	119
L. jordanis	Gorman BL-540	62	69	15	129
L. lansingensis	1677-MI-H	67	70	20	138
L. jamestowniensis	JA-26-G1-E2	69	97	28	164
L. hackeliae	Lansing 2	73	88	22	162
L. brunensis	441-1	75	96	32	183
L. fairfieldensis	1725-Aus-E	26	54	22	90
L. massiliensis		71	127	36	203
L. massilensis	LegA	71	127	36	203
L. drozanskii	LLAP1	47	103	30	162
L. nautarum	1224	46	107	24	162
L. maceachernii	Gorman PX-1-G2-E2	44	101	28	153
L. micdadei	févr-42	49	87	21	142
L. micdadei	Tatlock	48	88	18	141
L. feeleii	WO-44C	56	94	24	147
L. beliardensis	Wilkinson 1407-AL-H	60	87	42	163
L. gresilensis	Greoux 11D13	63	118	53	191
L. busanensis	BAA518	59	100	39	168
L. genomospecies	2055-AUS-E	51	74	33	141
L. quinlivanii	1442-AUS-E	51	79	38	149
L. birminghamensis	1407-AL-H	53	83	31	151
L. spiritensis	Bibb HSH-9	70	79	28	161
L. erythra	SE-32A-C8	66	87	27	150
L. rubrilucens	WA-270A-C2	71	80	28	155
L. taurinensis	Turin I	69	79	25	148
L. israelensis	Bercovier 4	51	76	22	137
L. rowbothamii	LLAP6	80	115	31	193
L. drancourtii (LLAP12)	LLAP12	74	99	29	173
L. gratiana	Lyon 8420412	112	98	37	212
L. sainthelensi	MSH-4	133	108	39	244
L. longbeachae	Long Beach 4	126	106	42	237
L. longbeachae	NSW150	126	109	45	240
L. longbeachae	98072	127	108	41	486
L. longbeachae	D-4968	128	108	44	-6

L. cincinnatiensis	72-OH-0	123	108	37	233
L. santicrucis	SC-63-C7	121	133	46	262
L. dumoffii	TexKL	90	90	24	182
L. dumoffii	NY23	90	89	24	181
L. cherrii	ORW	92	104	30	199
L. steigerwaltii	SC-18-C9	96	104	34	202
L. wadsworthii	81-716	95	86	28	188
L. tucsonensis	1087-AZ-H	91	77	25	171
L. anisa	WA-316-C3	99	112	26	210
L. anisa	Linanisette	97	110	26	207
L. parisiensis	PF-209C-C2	103	113	25	211
L. bozemanii (bozemanae)	WIGA	110	97	30	204
L. bozemanii (bozemanae)	94163278	109	92	31	200
L. gormanii	mars-69	101	104	27	208
L. gormanii	LS-13	101	103	23	202
L. fallonii	LLAP10	100	117	32	213
L. shakespearei	CDC 214	100	95	27	198
L. worsleiensis	95/83-1347	83	91	25	168
L. quateirensis	Thacker 1335	136	119	35	256
L. moravica	316-86	118	105	21	212
L. waltersii	2074-AUS-E	121	99	28	221
L. norrlandica	LEGN	98	63	17	160
L. pneumophila	Alcoy	261	78	26	321
L. pneumophila	Corby	261	80	25	322
L. pneumophila	Thunder Bay	296	77	25	345
L. pneumophila	570-CO-H	298	78	25	347
L. pneumophila	LPE509	299	77	24	347
L. pneumophila	Philadelphia	300	79	28	353
L. pneumophila	130b	265	85	27	330
L. pneumophila	Lens	246	79	30	308
L. pneumophila	Lorraine	269	81	30	331
L. pneumophila	Paris	268	89	25	335
L. pneumophila	HL06041035	275	83	27	335
L. pneumophila subsp. fraseri	Dallas 1E	255	79	23	315
L. pneumophila subsp. fraseri	Los Angeles 1	252	83	26	319
L. pneumophila subsp. fraseri	Lansing3	245	77	25	306
L. pneumophila subsp. pascullei	Brown U8W	267	84	25	328
L. geestiana	1308	35	61	12	89
L. osnabrueckensis	W0511934-2	51	70	25	127
	Total proteins	9110	7103	2196	16114

E1= effectors predicted by searching orthologs of effectors from *L. pneumophila* previously validated experimentally. E2=effectors predicted in the present study by searching proteins with eukaryotic motifs and their corresponding orthologous proteins. ELP= eukaryotic like proteins. E_{tot}= E1 + E2 + ELP removing duplicates.

Table S10. Replication capacity of the different *Legionella* species analyzed in this study and collection of literature data on *Legionella* replication

Species	Strain	ATCC	Isol	Clin.Fr.	THP1 (This study)			THP1 Summary	U937 cells	Mono Mac 6	Mouse macrophages	Guinea pig macrophages	A549	Guinea pigs
					24h	48h	72h							
L. adelaidensis	1762-AUS-E	49625	Env		-	-	-		N (17)					
L. anisa	WA-316-C3	35292	Clin	0,2	N	N	N	N		N (18)	N(19)	Y(19)		does not infect (20)
L. anisa	Linanisette		Clin		-	-	-							
L. beliardensis	Wilkinson 1407-AL-H	700512	Env		N	N	N	N						
L. birminghamensis	1407-AL-H	43702	Clin		Y	Y	Y	Y	Y(17); Y after 72h(21)	Y but at 72h	Y (19)	Y(19)		
L. bozemanii (bozemanae)	WIGA	33217	Clin	2,4	Y	Y	Y	Y	Y (17)	N (18)	Y (19)	Y (19)		Infects, does not kill (20)
L. bozemanii (bozemanae)	94163278		?		-	-	-							
L. brunensis	441-1	43878	Env		Y	N	N	Y at 24h	N (17)					
L. busanensis	BAA518		Env		N	N	N	N						
L. cherrii	ORW	35252	Env		N	N	N	N	N (17, 21)					
L. cincinnatiensis	72-OH-0	43753	Clin		N	N	N	N	N (17, 21)		N (19)	N (19)		
L. drancourtii	LLAP12	50991	Env		-	-	-							
L. drozanskii	LLAP1	700990	Env		-	-	-							
														Infects, does not

L. fairfieldensis	1725-Aus-E		Env		-	-	-							
L. fallonii	LLAP10	700992	Env		N	N	N	N (23)						
L. feeleii	WO-44C	35072	Clin	0,4	N	N	N	N	Y (17)		Y (19)	Y (19)		does not infect (20)
L. geestiana	1308	49504	Env		-	-	-							
L. genomospecies	2055-AUS-E	51913	Env		Y	N	N	Y at 24 h						
L. gormanii	LS-13	33297	Clin		Y	N	Y	Y	N (17)					
L. gormanii	03-69		?		-	-	-							
L. gratiana	Lyon 8420412	49413	Env		N	N	N	N	N (17, 21)					
L. gresilensis	Greoux 11D13	700509	Env		N	N	N	N						
L. hackeliae	Lansing 2	35250	Clin		N	N	N	N(23)	Y (17, 21)					infects and kills(20)
L. impletisoli	OA1-1		Env		-	-	-							
L. israelensis	Bercovier 4	43119	Env		N	N	N	N	N (17)					
L. jamestowniensis	JA-26-G1-E2	35298	Clin		Y	Y	Y	Y	Y (17)					
L. jordanis	Gorman BL-540	33623	Clin		Y	Y	Y	Y		N (18)	Y (19)	Y (19)		
L. lansingensis	1677-MI-H	49751	Clin		N	N	N	N			N (19)	Y (19)		
L. LIKE brunensis	W10-070		?		Y	Y	Y	Y						
L. londiniensis	1477	49505	Env		-	-	-		N (17)					
L. longbeachae	D-4968		Clin		-	-	-							
L. longbeachae	NSW150		Clin	3,9	Y	Y	Y	Y (24)						
L. longbeachae	Long Beach 4	33462	Clin		-	-	-		Y(17, 21); N(25)	N (18, 26)				does not infect (25)
L. longbeachae	98072		?		-	-	-							
L. maceachernii	Gorman PX-1-G2-E2	35300	Clin		N	N	Y	Y at 72h	Y (17, 21)		Y (19)	Y (19)		

L. massiliensis			Env		-	-	-							
L. massilensis	LegA	24804	Env		-	-	-							
L. micdadei	Tatlock	33218	Clin	0,60	N	Y	Y	Y 48h (23)		N (18, 26)	Y (19)	Y (19)		
L. micdadei	02-42		?		-	-	-	Y (27)					Y (27)	
L. moravica	316-86	43877	Env		-	-	-		N (17)					
L. nagasakiensis	JCM 15315	BAA-1557	Clin		N	N	Y	Y at 72h						
L. nautarum	1224	49506	Env		N	N	N	N						
L. norrlandica	LEGN	BAA-2678	Env		-	-	-							
L. oakridgensis	Oak Ridge 10	33761	Clin		Y	Y	N	Y 24-48h	Y (17, 28)	Y (18)	Y (19)	Y (19)		infects and kills(20)
L. oakridgensis	RV2-2007		Env		-	-	-		Y (28)					
L. osnabrueckensis	W0511934-2		?		-	-	-							
L. parisiensis	PF-209C-C2	35299	Clin		N	Y	Y	Y 48h	Y (17, 21)		Y (19)	Y (19)		
L. pneumophila subsp. *pascullei*	Brown U8W	33737	Env		Y	Y	Y	Y						
L. pneumophila	Paris		Clin	91,50	Y	Y	Y	Y						
L. pneumophila	Lens		Clin		-	-	-	Y	Y (29)					
L. pneumophila	Philadelphia	33152	Clin		-	-	-	Y (30)		Y (18, 26)	Y (19)	Y (19)		infects and kills(20)
L. pneumophila	Corby		Clin		-	-	-	Y (31)						infects and kills(25)
L. pneumophila	Alcoy		Clin		-	-	-							
L. pneumophila	130b		Clin		-	-	-	Y (27)	Y (32, 33)					
L. pneumophila	Lorraine		Clin		-	-	-							
L. pneumophila	HL06041035		Env		-	-	-							
L. pneumophila	570-CO-H		Clin		-	-	-							
L. pneumophila	LPE509		Env		-	-	-							

L. pneumophila	Thunder Bay		Clin		-	-	-						infects and kills(25)
L. pneumophila subsp. *fraseri*	Los Angeles 1	33156	Clin		N	N	N	N					infects and kills(25)
L. pneumophila subsp. *fraseri*	Dallas 1E	33216	Env		-	-	-						
L. pneumophila subsp. *fraseri*	Lansing3	35251	Clin		-	-	-						
L. quateirensis	Thacker 1335	49507	Env		-	-	-						
L. quinlivanii	1442-AUS-E	43830	Env		N	N	N	N	Y (17)				
L. rowbothamii	LLAP6	700991	Env		-	-	-						
L. rubrilucens	WA-270A-C2	35304	Clin		N	N	N	N	N (17)				
L. sainthelensi	MSH-4	35248	Clin		N	N	N	N	Y (17)		Y (19)	Y (19)	
L. santicrucis	SC-63-C7	352301	Env		-	-	-		Y (17); N (21)			Y (19)	
L. shakespearei	CDC 214	49655	Env		Y	Y	N						
L. spiritensis	Bibb HSH-9	35249	Env		N	N	N	N	N (17, 21)				
L. steigerwaltii	SC-18-C9	35302	Env		N	N	N	N	N (17)	N (18, 26)			
L. taurinensis	Turin I	700508	Env		Y	Y	Y	Y					
L. tucsonensis	1087-AZ-H	49180	Clin		Y	Y	Y	Y				N (19)	
L. wadsworthii	81-716	33877	Clin	0,2	N	N	N	N	N (17, 21)		N (19)	Y (19)	
L. waltersii	2074-AUS-E	51914	Env		-	-	-						
L. worsleiensis	95/83-1347	49508	Env		-	-	-						
L. yabuuchiae	OA1-2		Env		-	-	-						

For each species the capacity to replicate in THP1 cells was compared to the one of *L. pneumohila* strain Paris at time points: 24, 48 and 72h. Y, the species is replicating; N, the species either does not infect or the replication capacity is significantly lower than that of *L. pneumophila* strain Paris. The results of previous studies about infection and replication of particular species in different types of cells or animal models have been collected and are shown in the table. The 5th column shows the Clin frequency of the species most frequently found in clinical cases according to (34) and the 9th column that is boxed is the conclusion whetehr a sepcies can infect of not THP1 cells.

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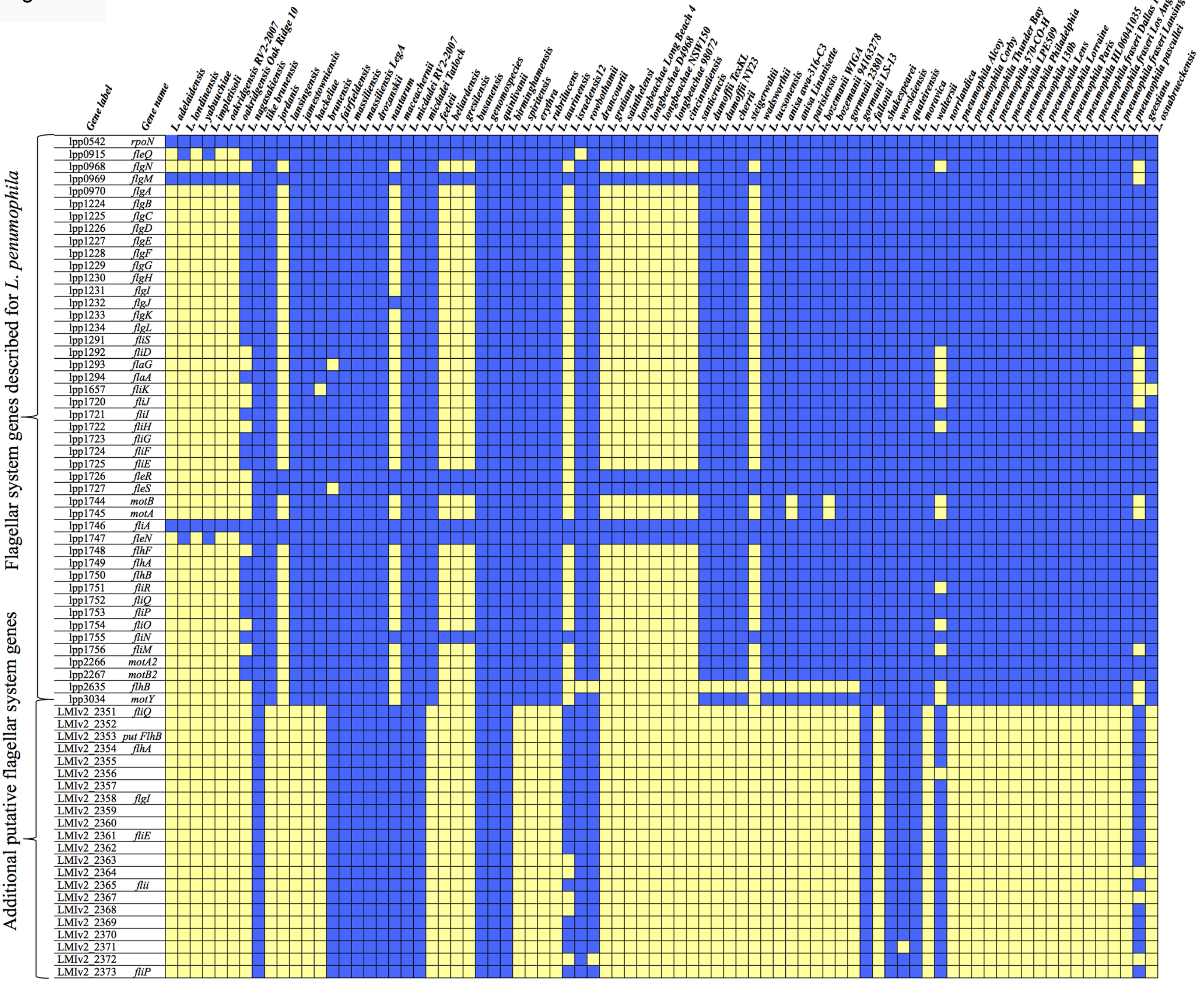
Figure S1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L. nagasakiensis
L. like brunensis
L. jordanis
L. lansingensis
L. jamestowniensis
L. hackeliae
L. brunensis
L. fairfieldensis
L. massiliensis
L. massiliensis LegA
L. drozanskii
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L. micdadei RV2-2007
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L. busanensis
L. genomospecies
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L. drancourtii
L. gratiana
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L. norrlandica
L. pneumophila Alcoy
L. pneumophila Corby
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L. pneumophila Philadelphia
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L. osnabrueckensis
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lpp1225 flgC
lpp1226 flgD
lpp1227 flgE
lpp1228 flgF
lpp1229 flgG
lpp1230 flgH
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Figure S2

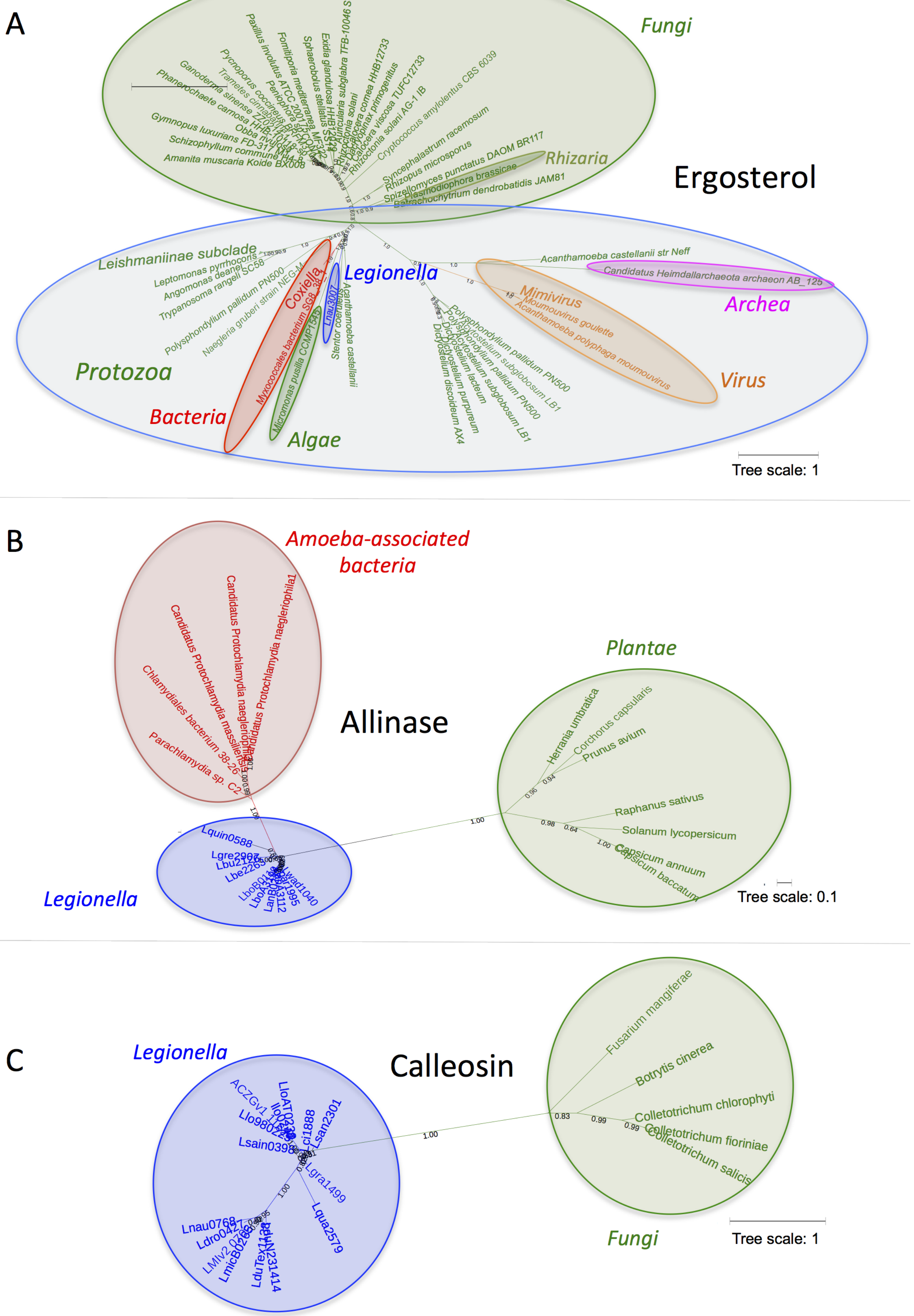
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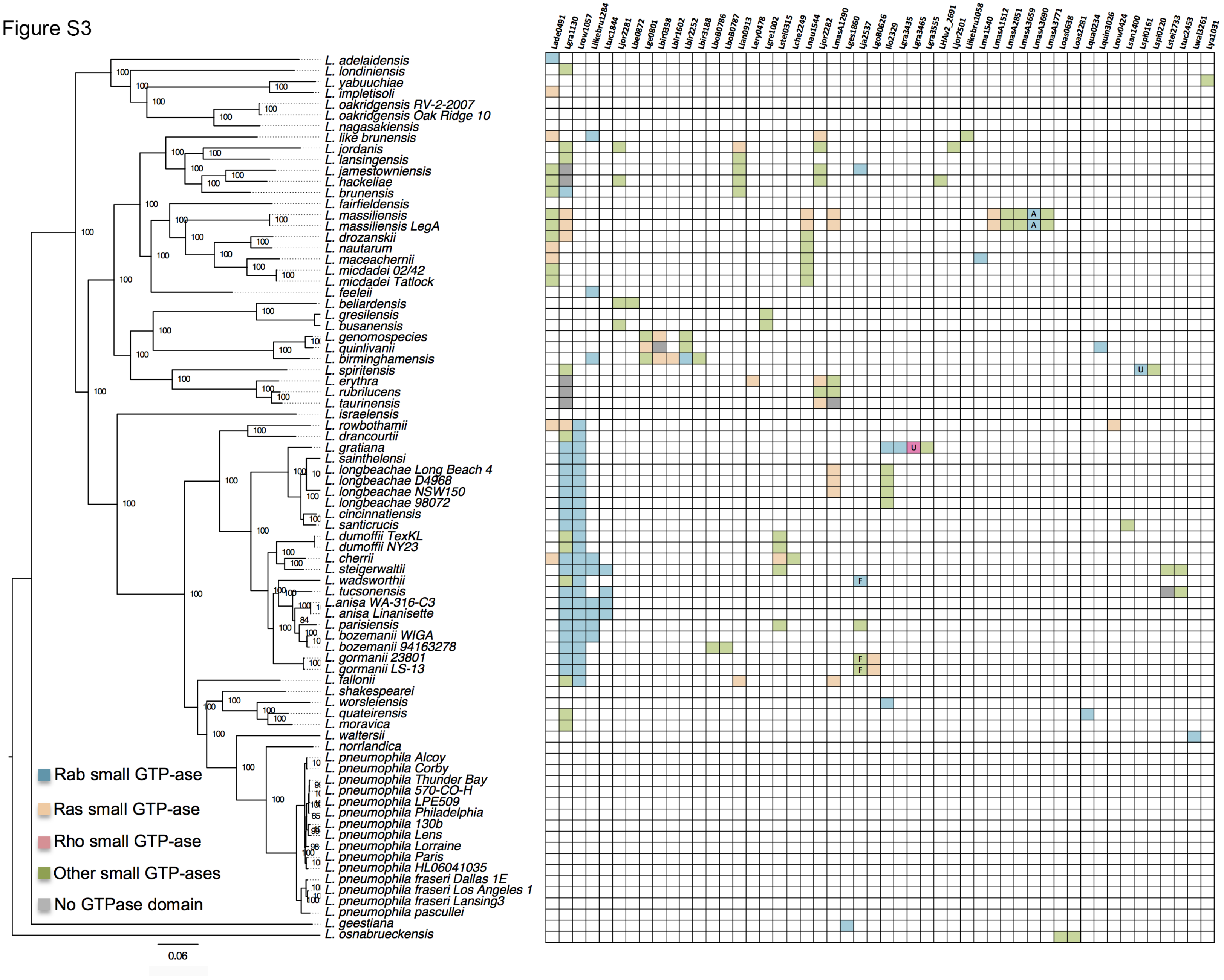
Figure S3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L. geestiana
L. osnabrueckensis
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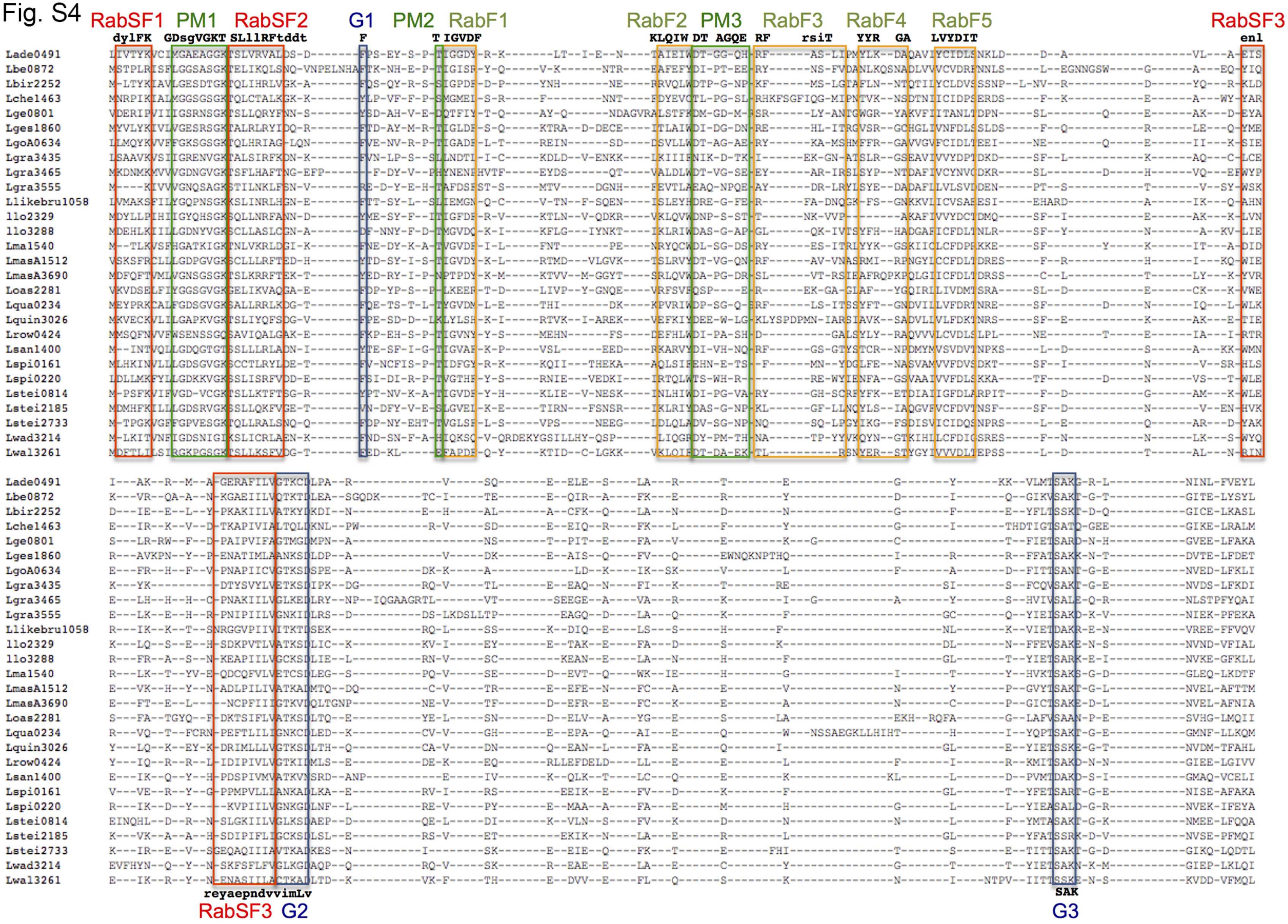
Fig. S4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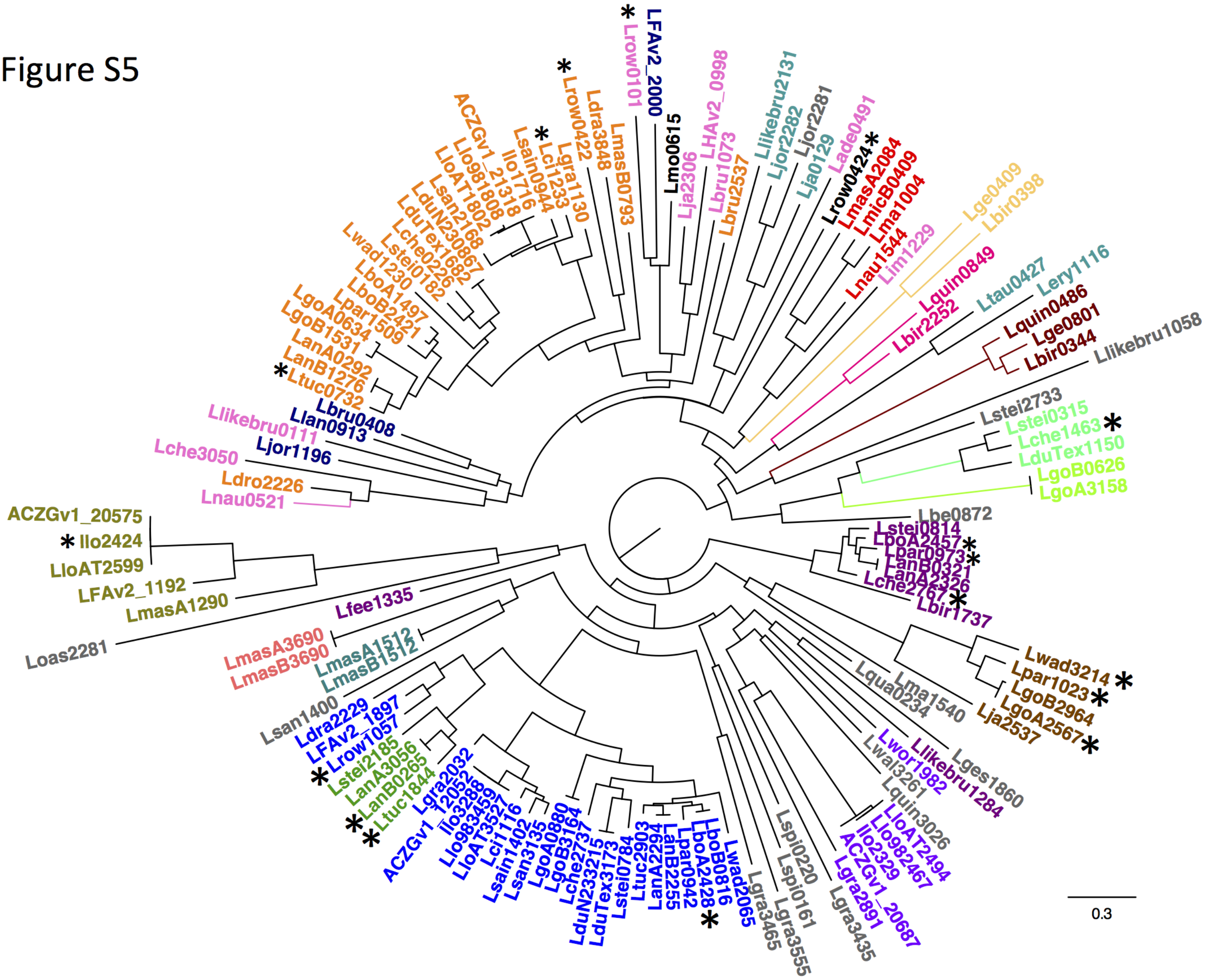
RabF1
RabF2
PM3
RabF3
RabF4
RabF5
RabSF3
dylFK
GDsgVGKT
SLllRFtddt
F
T
IGVDF
KLQIW
DT
AGQE
RF
rsiT
YYR
GA
LVYDIT
enl
reyaepndvvimLv
SAK
RabSF3
G2
G3

Figure S5


Loas2281
LmasA1290
LFAv2_1192
LloAT2599
* llo2424
ACZGv1_20575
Lnau0521
Ldro2226
Lche3050
Ljor1196
Llikebru0111
Llan0913
Lbru0408
*Ltuc0732
LanB1276
LanA0292
LgoB1531
LgoA0634
Lpar1509
LboB2421
LboA1497
Lwad1230
Lstei0182
Lche0226
LduTex1682
LduN2308867
Lsan2168
LloAT1802
Llo981808
ACZGv1_21318
llo1716
Lsain0944
*Lci1233
Lgra1130
*Lrow0422
Ldra3848
LmasB0793
*Lrow0101
LFAv2_2000
Lmo0615
Lja2306
LHAv2_0998
Lbru1073
Lbru2537
Llikebru2131
Ljor2282
Ljor2281
Lja0129
Lade0491
Lrow0424*
LmasA2084
LmicB0409
Lma1004
Lnau1544
Lim1229
Lge0409
Lbir0398
Lquin0849
Lbir2252
Ltau0427
Lery1116
Lquin0486
Lge0801
Lbir0344
Llikebru1058
Lstei2733
Lstei0315
Lche1463*
LduTex1150
LgoB0626
LgoA3158
Lbe0872
Lstei0814
LboA2457*
Lpar0973*
LanB0321
LanA2326
Lche2767*
Lbir1737
Lwad3214 *
Lpar1023*
LgoB2964
LgoA2567*
Lja2537
Lma1540
Lqua0234
Lges1860
Llikebru1284
Lwor1982
Lwal3261
Lquin3026
LloAT2494
Llo982467
llo2329
ACZGv1_20687
Lgra2891
Lgra3435
Lspi0220
Lspi0161
Lgra3555
Lgra3465
Lwad2065
LboB0816
LboA2428
*
Lpar0942
LanB2255
LanA2294
Ltuc2903
Lstei0784
LduTex3173
LduN233215
Lche2737
LgoB3164
LgoA0880
Lsan3135
Lsain1402
Lci1116
LloAT3527
Llo983459
llo3288
ACZGv1_12052
Lgra2032
*Ltuc1844
*LanB0265
LanA3056
*Lstei2185
Lrow1057
LFAv2_1897
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LmasA1512
LmasB3690
LmasA3690
Lfee1335
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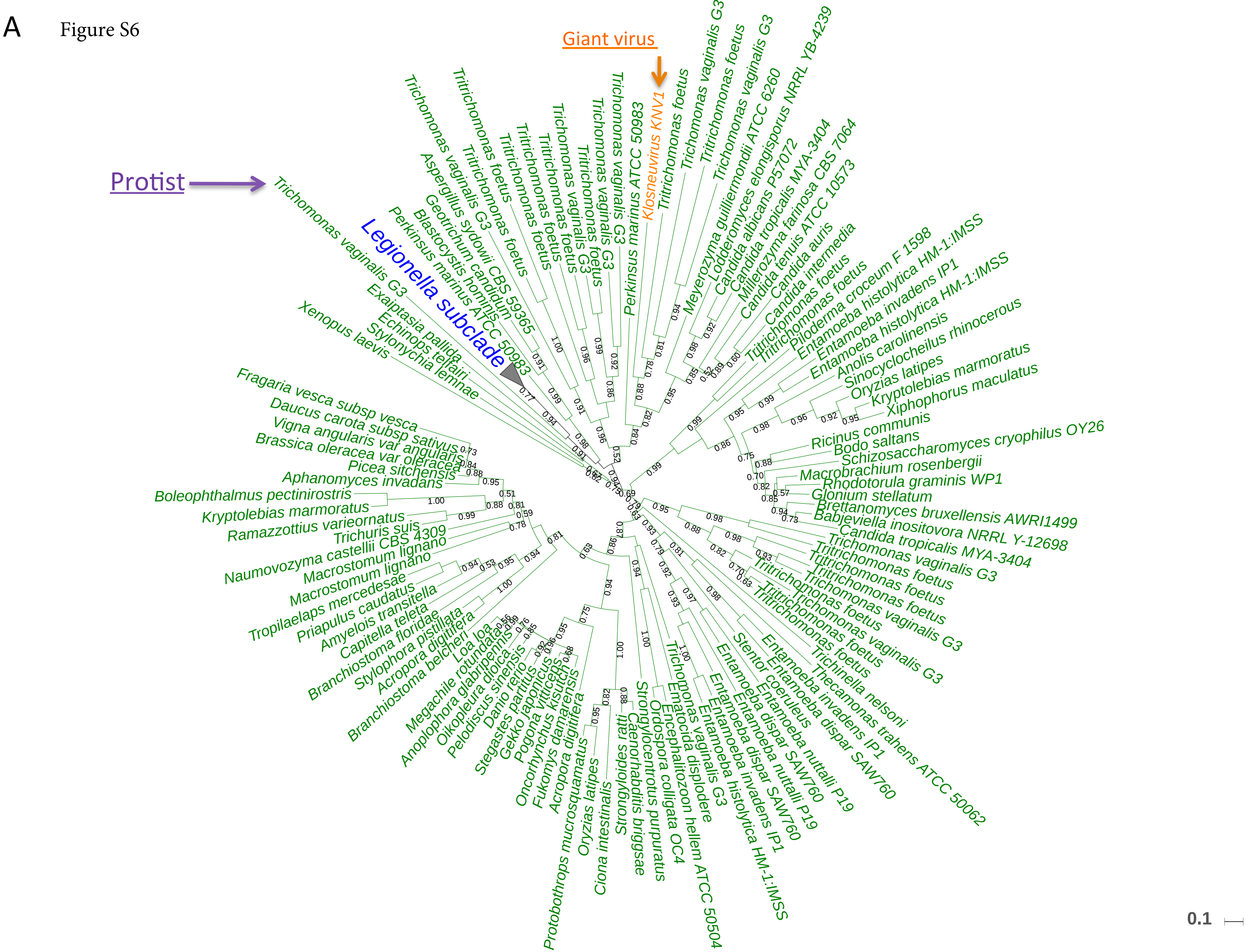
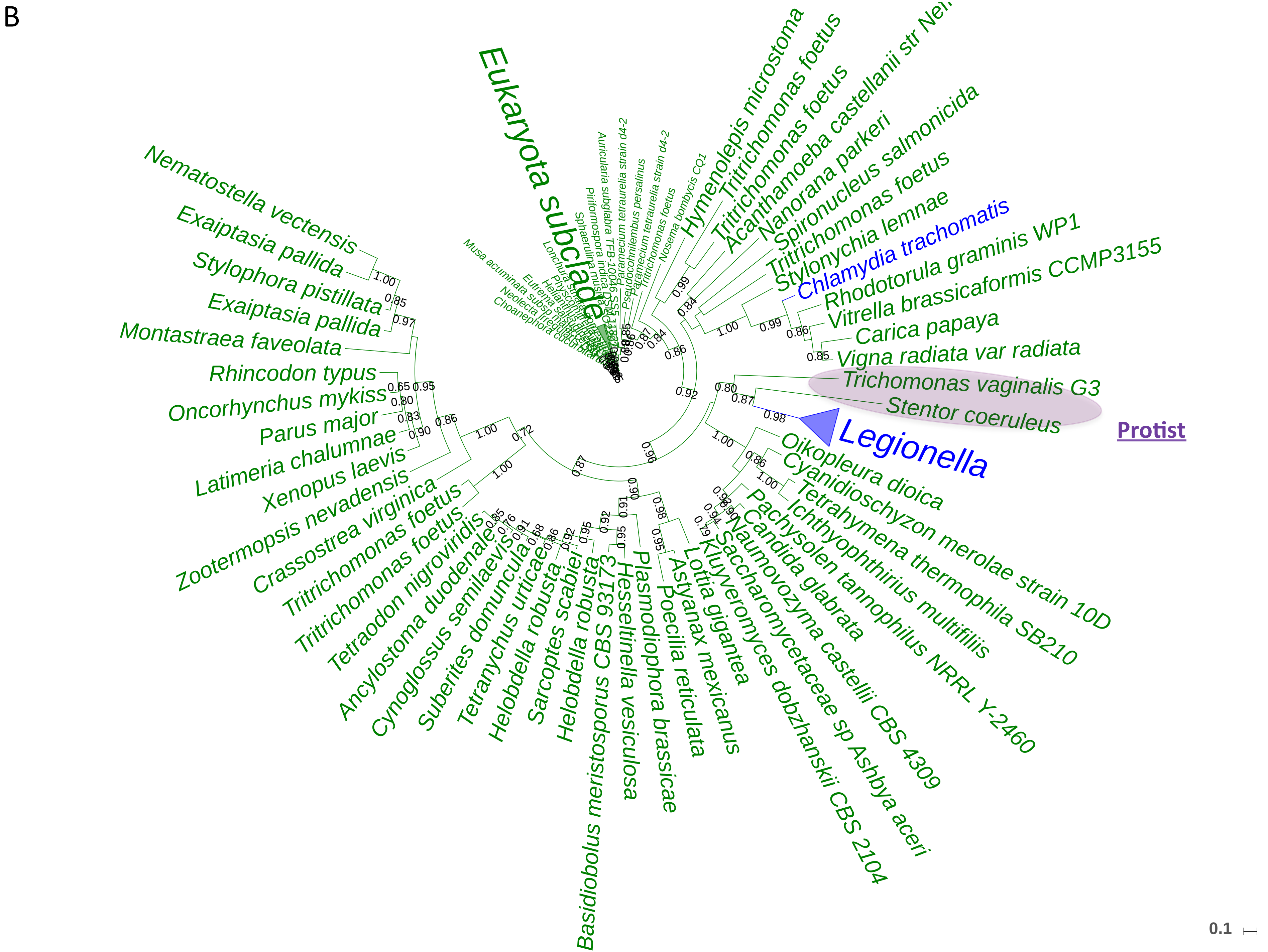
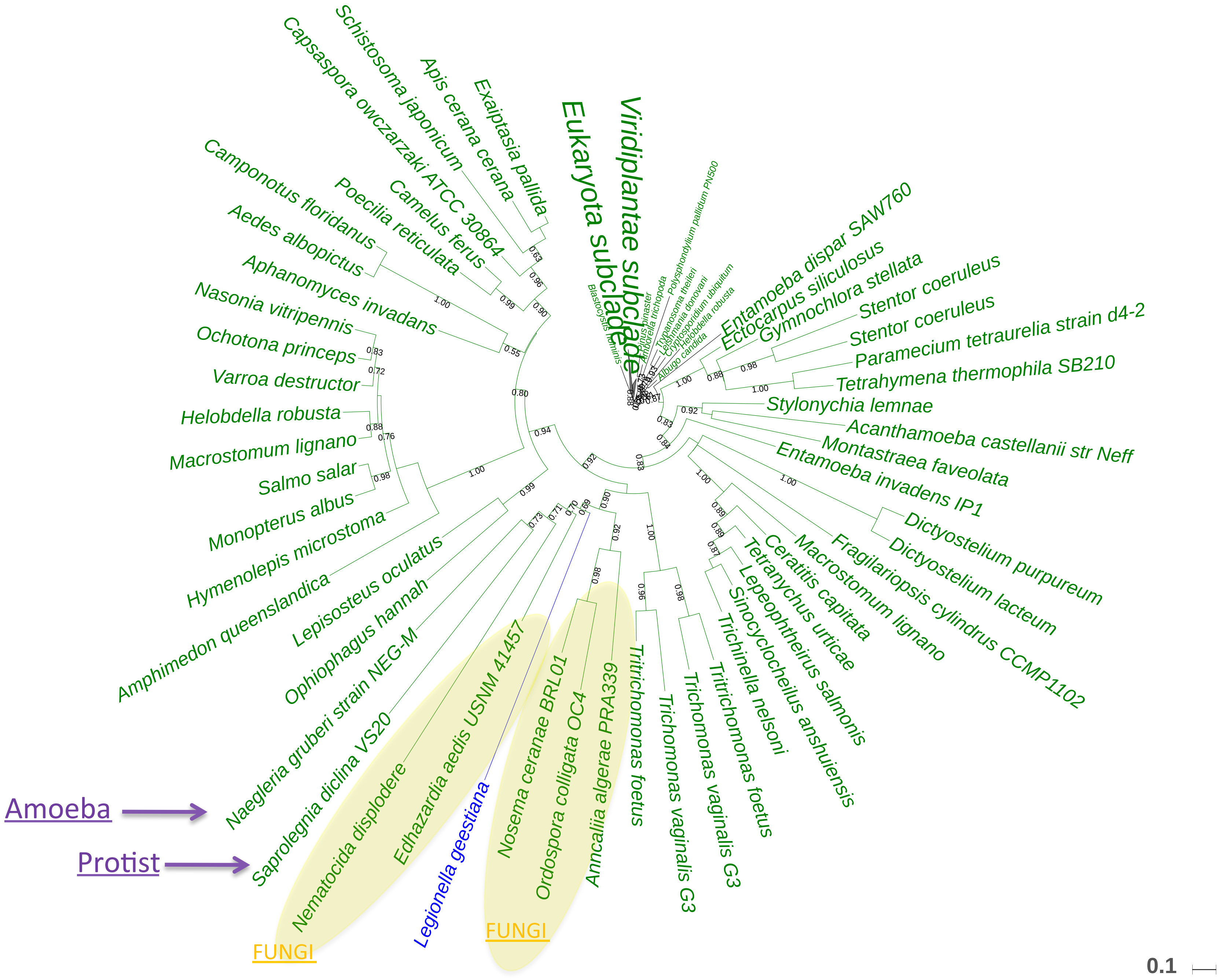
Figure S6


A
Protist
Giant virus
Legionella subclade
Trichomonas vaginalis G3
Exaiptasia pallida
Echinops telfairi
Stylonychia lemnae
Xenopus laevis
Perkinsus marinus ATCC 50983
Blastocystis hominis
Geotrichum candidum
Aspergillus sydowii CBS 59365
Trichomonas vaginalis G3
Tritrichomonas foetus
Tritrichomonas foetus
Tritrichomonas foetus
Tritrichomonas foetus
Tritrichomonas foetus
Trichomonas vaginalis G3
Tritrichomonas foetus
Trichomonas vaginalis G3
Trichomonas vaginalis ATCC 50983
Perkinsus marinus ATCC 50983
Klosneuvirus KNV1
Tritrichomonas foetus
Trichomonas vaginalis G3
Tritrichomonas foetus
Trichomonas vaginalis G3
Meyerozyma guilliermondii ATCC 6260
Lodderomyces elongisporus NRRL YB-4239
Candida albicans P57072
Candida tropicalis MYA-3404
Millerozyma farinosa CBS 7064
Candida tenuis ATCC 10573
Candida auris
Candida intermedia
Tritrichomonas foetus
Tritrichomonas foetus
Piloderma croceum F 1598
Entamoeba histolytica HM-1:IMSS
Entamoeba invadens IP1
Entamoeba histolytica HM-1:IMSS
Anolis carolinensis
Sinocyclocheilus rhinocerous
Oryzias latipes
Kryptolebias marmoratus
Xiphophorus maculatus
Ricinus communis
Bodo saltans
Schizosaccharomyces cryophilus OY26
Macrobrachium rosenbergii
Rhodotorula graminis WP1
Glonium stellatum
Brettanomyces bruxellensis AWRI1499
Babjeviella inositovora NRRL Y-12698
Candida tropicalis MYA-3404
Trichomonas vaginalis G3
Tritrichomonas foetus
Tritrichomonas foetus
Trichomonas foetus
Tritrichomonas foetus
Trichomonas vaginalis G3
Tritrichomonas foetus
Trichomonas vaginalis G3
Tritrichomonas foetus
Trichinella nelsoni
Thecamonas trahens ATCC 50062
Entamoeba invadens IP1
Entamoeba dispar SAW760
Entamoeba nuttalli P19
Stentor coeruleus
Entamoeba nuttalli P19
Entamoeba dispar SAW760
Entamoeba invadens IP1
Entamoeba histolytica HM-1:IMSS
Trichomonas vaginalis G3
Ematocida displodere
Encephalitozoon hellem ATCC 50504
Ordospora colligata OC4
Strongylocentrotus purpuratus
Caenorhabditis briggsae
Strongyloides ratti
Ciona intestinalis
Oryzias latipes
Protobothrops mucrosquamatus
Acropora digitifera
Fukomys damarensis
Oncorhynchus kisutch
Pogona vitticeps
Gekko japonicus
Stegastes partitus
Danio rerio
Pelodiscus sinensis
Oikopleura dioica
Anoplophora glabripennis
Megachile rotundata
Loa loa
Branchiostoma belcheri
Acropora digitifera
Stylophora pistillata
Branchiostoma floridae
Capitella teleta
Amyelois transitella
Priapulus caudatus
Tropilaelaps mercedesae
Macrostomum lignano
Macrostomum lignano
Naumovozyma castellii CBS 4309
Trichuris suis
Ramazzottius varieornatus
Kryptolebias marmoratus
Boleophthalmus pectinirostris
Aphanomyces invadans
Picea sitchensis
Brassica oleracea var oleracea
Vigna angularis var angularis
Daucus carota subsp sativus
Fragaria vesca subsp vesca
0.1


B
Eukaryota subclade
Musa acuminata subsp malaccensis
Choanephora cucurbitarum
Neolecta irregularis
Eutrema salsugineum
Helianthus annuus
Physcomitrella patens
Lonchura striata
Sphaerulina musiva
Piriformospora indica DSM 11827
Auricularia subglabra TFB-10046 SS5
Paramecium tetraurelia strain d4-2
Pseudocohnilembus persalinus
Paramecium tetraurelia strain d4-2
Tritrichomonas foetus
Nosema bombycis CQ1
Hymenolepis microstoma
Tritrichomonas foetus
Tritrichomonas foetus
Acanthamoeba castellanii str Neff
Nanorana parkeri
Spironucleus salmonicida
Tritrichomonas foetus
Stylonychia lemnae
Chlamydia trachomatis
Rhodotorula graminis WP1
Vitrella brassicaformis CCMP3155
Carica papaya
Vigna radiata var radiata
Trichomonas vaginalis G3
Stentor coeruleus
Protist
Legionella
Oikopleura dioica
Cyanidioschyzon merolae strain 10D
Tetrahymena thermophila SB210
Ichthyophthirius multifiliis
Pachysolen tannophilus NRRL Y-2460
Candida glabrata
Naumovozyma castellii CBS 4309
Saccharomycetaceae sp Ashbya aceri
Kluyveromyces dobzhanskii CBS 2104
Lottia gigantea
Astyanax mexicanus
Poecilia reticulata
Plasmodiophora brassicae
Hesseltinella vesiculosa
Basidiobolus meristosporus CBS 93173
Helobdella robusta
Sarcoptes scabiei
Helobdella robusta
Tetranychus urticae
Suberites domuncula
Cynoglossus semilaevis
Ancylostoma duodenale
Tetraodon nigroviridis
Tritrichomonas foetus
Tritrichomonas foetus
Crassostrea virginica
Zootermopsis nevadensis
Xenopus laevis
Latimeria chalumnae
Parus major
Oncorhynchus mykiss
Rhincodon typus
Montastraea faveolata
Exaiptasia pallida
Stylophora pistillata
Exaiptasia pallida
Nematostella vectensis
1.00
0.85
0.97
0.65
0.95
0.80
0.83
0.90
0.86
1.00
0.72
1.00
0.87
0.92
0.86
0.84
0.87
0.85
0.99
0.84
1.00
0.99
0.86
0.85
0.80
0.87
0.98
1.00
0.86
1.00
0.96
0.90
0.94
0.79
0.98
0.95
0.91
0.90
0.95
0.92
0.95
0.92
0.86
0.68
0.91
0.76
0.85
0.96
0.1

C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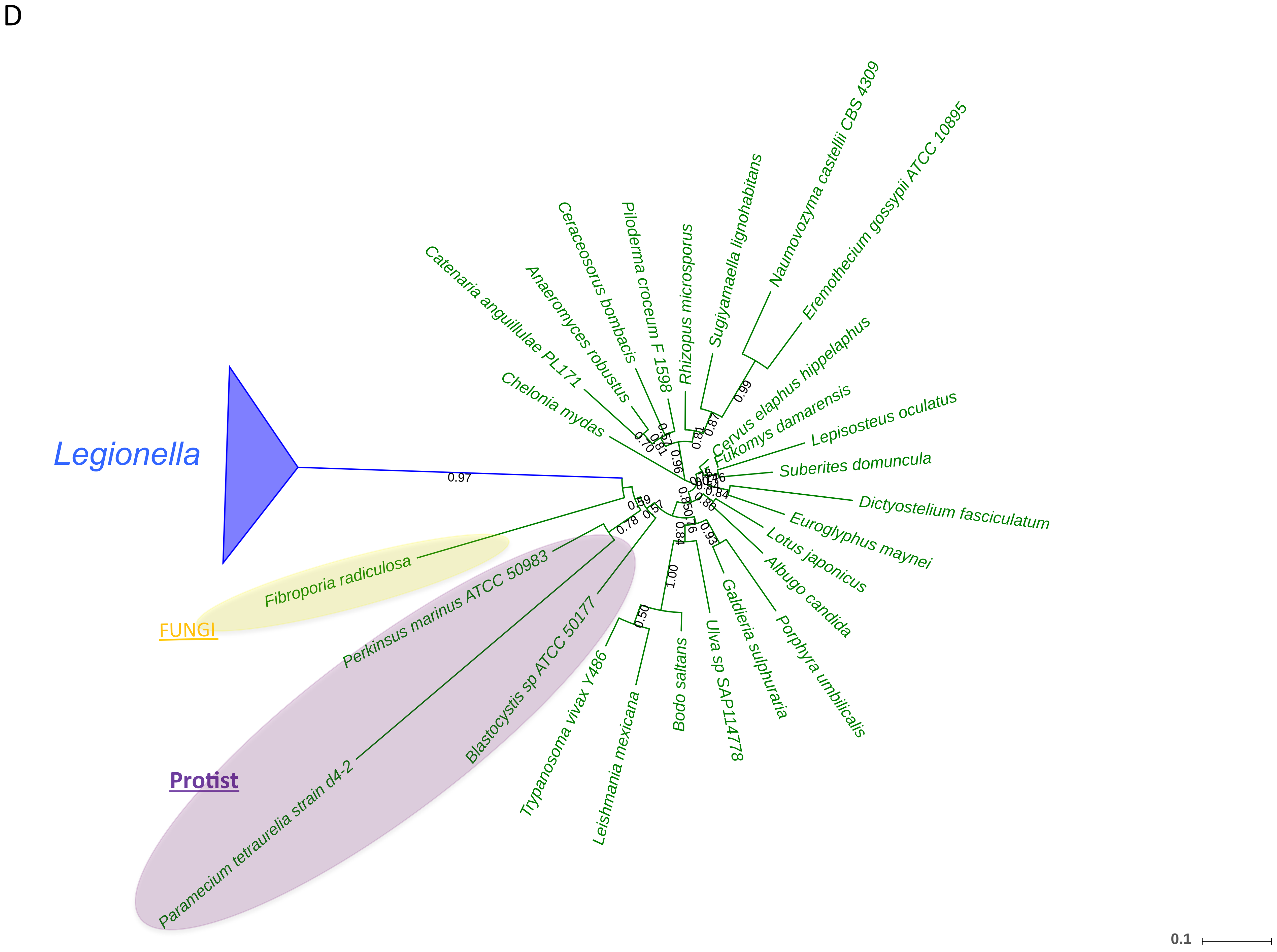
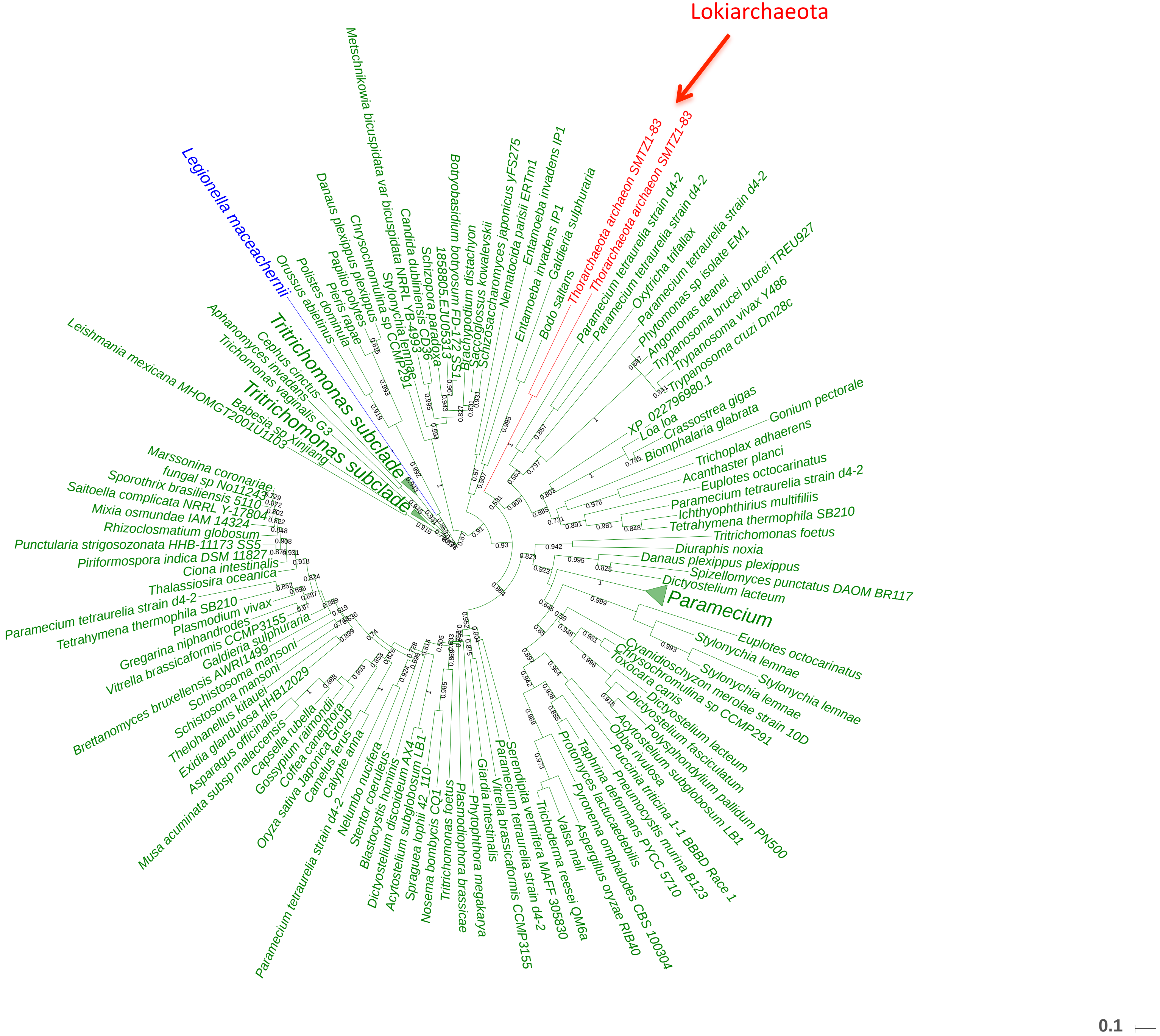
Viridiplantae subclade
Blastocystis hominis
Pinus pinaster
Amborella trichopoda
Polysphondylium pallidum PN500
Trypanosoma theileri
Leishmania donovani
Cryptosporidium ubiquitum
Helobdella robusta
Albugo candida
Entamoeba dispar SAW760
Ectocarpus siliculosus
Gymnochlora stellata
Stentor coeruleus
Stentor coeruleus
Paramecium tetraurelia strain d4-2
Tetrahymena thermophila SB210
Stylonychia lemnae
Acanthamoeba castellanii str Neff
Montastraea faveolata
Entamoeba invadens IP1
Dictyostelium purpureum
Dictyostelium lacteum
Fragilariopsis cylindrus CCMP1102
Macrostomum lignano
Ceratitis capitata
Tetranychus urticae
Lepeophtheirus salmonis
Sinocyclocheilus anshuiensis
Trichinella nelsoni
Tritrichomonas foetus
Trichomonas vaginalis G3
Trichomonas vaginalis G3
Tritrichomonas foetus
Anncaliia algerae PRA339
Ordospora colligata OC4
Nosema ceranae BRL01
Legionella geestiana
Edhazardia aedis USNM 41457
Nematocida displodere
Saprolegnia diclina VS20
Naegleria gruberi strain NEG-M
Ophiophagus hannah
Lepisosteus oculatus
Amphimedon queenslandica
Hymenolepis microstoma
Monopterus albus
Salmo salar
Macrostomum lignano
Helobdella robusta
Varroa destructor
Ochotona princeps
Nasonia vitripennis
Aphanomyces invadans
Aedes albopictus
Camponotus floridanus
Poecilia reticulata
Camelus ferus
Capsaspora owczarzaki ATCC 30864
Schistosoma japonicum
Apis cerana cerana
Exaiptasia pallida
Amoeba
Protist
FUNGI
FUNGI
0.1


D
Legionella
0.97
FUNGI
Protist
Catenaria anguillulae PL171
Anaeromyces robustus
Ceraceosorus bombacis
Piloderma croceum F 1598
Rhizopus microsporus
Sugiyamaella lignohabitans
Naumovozyma castellii CBS 4309
Eremothecium gossypii ATCC 10895
Chelonia mydas
Cervus elaphus hippelaphus
Fukomys damarensis
Lepisosteus oculatus
Suberites domuncula
Dictyostelium fasciculatum
Euroglyphus maynei
Lotus japonicus
Albugo candida
Porphyra umbilicalis
Galdieria sulphuraria
Ulva sp SAP14778
Bodo saltans
Leishmania mexicana
Trypanosoma vivax Y486
Blastocystis sp ATCC 50177
Paramecium tetraurelia strain d4-2
Perkinsus marinus ATCC 50983
Fibroporia radiculosa
0.99
0.87
0.81
0.57
0.81
0.70
0.96
0.76
0.84
0.80
0.85
0.76
0.84
0.93
1.00
0.50
0.59
0.57
0.78
0.1

E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Thorarchaeota archaeon SMTZ1-83
Thorarchaeota archaeon SMTZ1-83
Paramecium tetraurelia strain d4-2
Paramecium tetraurelia strain d4-2
Oxytricha trifallax
Paramecium tetraurelia strain d4-2
Phytomonas sp isolate EM1
Angomonas deanei
Trypanosoma brucei brucei TREU927
Trypanosoma vivax Y486
Trypanosoma cruzi Dm28c
XP_022796980.1
Loa loa
Crassostrea gigas
Biomphalaria glabrata
Gonium pectorale
Trichoplax adhaerens
Acanthaster planci
Euplotes octocarinatus
Paramecium tetraurelia strain d4-2
Ichthyophthirius multifiliis
Tetrahymena thermophila SB210
Tritrichomonas foetus
Diuraphis noxia
Danaus plexippus plexippus
Spizellomyces punctatus DAOM BR117
Dictyostelium lacteum
Paramecium
Euplotes octocarinatus
Stylonychia lemnae
Stylonychia lemnae
Stylonychia lemnae
Cyanidioschyzon merolae strain 10D
Chrysochromulina sp CCMP291
Toxocara canis
Dictyostelium lacteum
Dictyostelium fasciculatum
Polysphondylium pallidum PN500
Acytostelium subglobosum LB1
Obba rivulosa
Puccinia triticina 1-1 BBBD Race 1
Pneumocystis murina B123
Taphrina deformans PYCC 5710
Protomyces lactucaedebilis
Pyronema omphalodes CBS 100304
Aspergillus oryzae RIB40
Valsa mali
Trichoderma reesei QM6a
Serendipita vermifera MAFF 305830
Paramecium tetraurelia strain d4-2
Vitrella brassicaformis CCMP3155
Giardia intestinalis
Phytophthora megakarya
Plasmodiophora brassicae
Tritrichomonas foetus
Nosema bombycis CQ1
Spraguea lophii 42_110
Acytostelium subglobosum LB1
Dictyostelium discoideum AX4
Blastocystis hominis
Stentor coeruleus
Nelumbo nucifera
Paramecium tetraurelia strain d4-2
Calypte anna
Camelus ferus
Oryza sativa Japonica Group
Coffea canephora
Gossypium raimondii
Capsella rubella
Musa acuminata subsp malaccensis
Asparagus officinalis
Exidia glandulosa HHB12029
Thelohanellus kitauei
Schistosoma mansoni
Schistosoma mansoni
Brettanomyces bruxellensis AWRI1499
Galdieria sulphuraria
Vitrella brassicaformis CCMP3155
Gregarina niphandrodes
Plasmodium vivax
Tetrahymena thermophila SB210
Paramecium tetraurelia strain d4-2
Thalassiosira oceanica
Ciona intestinalis
Piriformospora indica DSM 11827
Punctularia strigosozonata HHB-11173 SS5
Rhizoclosmatium globosum
Mixia osmundae IAM 14324
Saitoella complicata NRRL Y-17804
Sporothrix brasiliensis 5110
fungal sp No11243
Marssonina coronariae
Leishmania mexicana MHOMGT2001U1103
Babesia sp Xinjiang
Tritrichomonas subclade
Trichomonas vaginalis G3
Aphanomyces invadans
Cephus cinctus
Tritrichomonas subclade
Orussus abietinus
Polistes dominula
Legionella maceachernii
Pieris rapae
Papilio polytes
Danaus plexippus plexippus
Chrysochromulina sp CCMP291
Metschnikowia bicuspidata var bicuspidata NRRL YB-4993
Stylonychia lemnae
Candida dubliniensis CD36
Schizopora paradoxa
1858805.EJU05313_SS1
Botryobasidium botryosum FD-172 SS1
Brachypodium distachyon
Saccoglossus kowalevskii
Schizosaccharomyces japonicus yFS275
Nematocida parisii ERTm1
Entamoeba invadens IP1
Entamoeba invadens IP1
Bodo saltans
Galdieria sulphuraria
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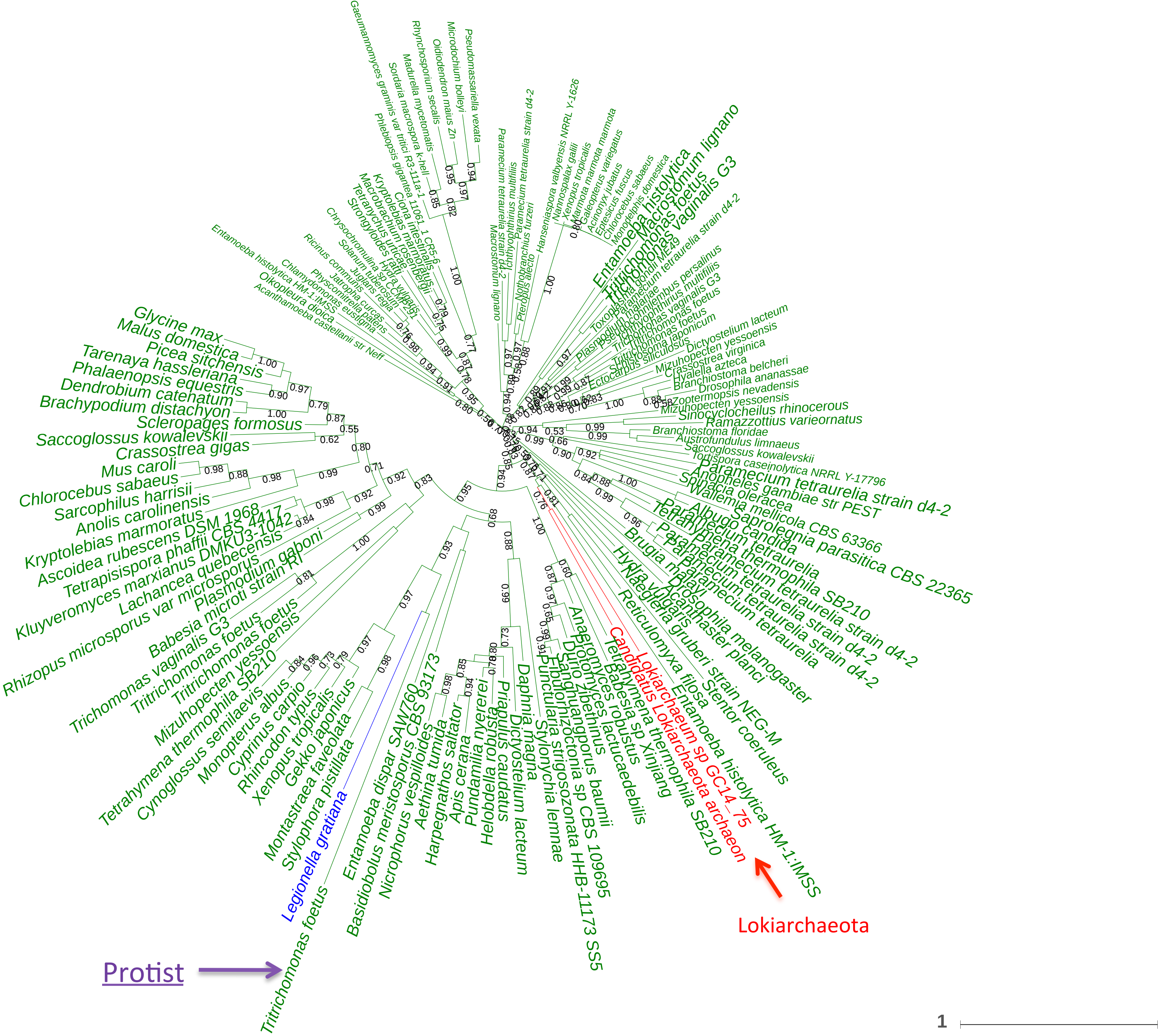
F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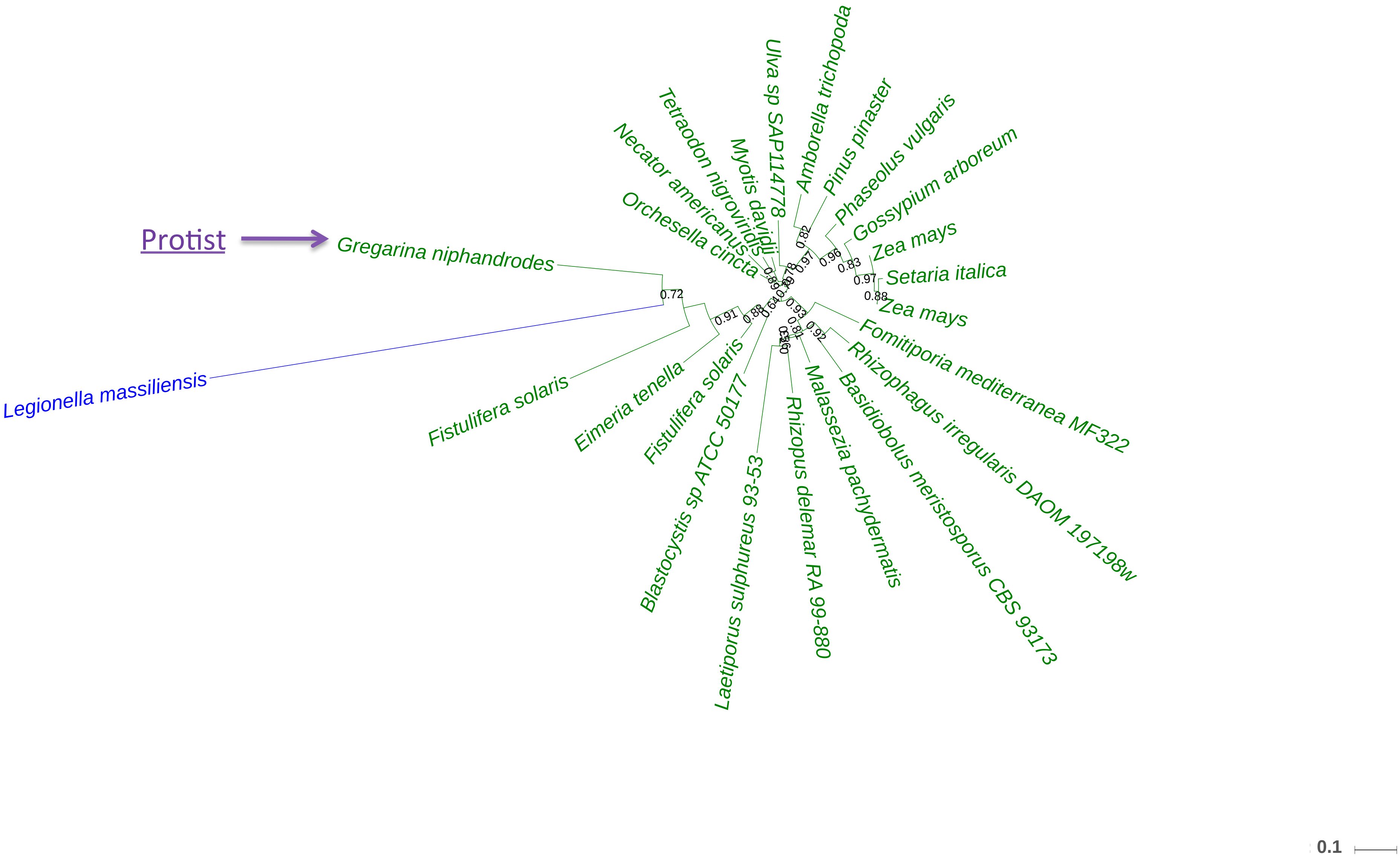
1
Legionella gratiana
Candidatus Lokiarchaeota archaeon
Lokiarchaeum sp GC14_75
Tritrichomonas foetus
Stylophora pistillata
Montastraea faveolata
Gekko japonicus
Xenopus tropicalis
Rhincodon typus
Cyprinus carpio
Monopterus albus
Cynoglossus semilaevis
Tetrahymena thermophila SB210
Mizuhopecten yessoensis
Tritrichomonas foetus
Trichomonas vaginalis G3
Babesia microti strain RI
Plasmodium gaboni
Rhizopus microsporus var microsporus
Lachancea quebecensis
Kluyveromyces marxianus DMKU3-1042
Tetrapisispora phaffii CBS 4417
Ascoidea rubescens DSM 1968
Kryptolebias marmoratus
Anolis carolinensis
Sarcophilus harrisii
Chlorocebus sabaeus
Mus caroli
Crassostrea gigas
Saccoglossus kowalevskii
Scleropages formosus
Brachypodium distachyon
Dendrobium catenatum
Phalaenopsis equestris
Tarenaya hassleriana
Picea sitchensis
Malus domestica
Glycine max
Acanthamoeba castellanii str Neff
Oikopleura dioica
Entamoeba histolytica HM-1:IMSS
Chlamydomonas eustigma
Physcomitrella patens
Ricinus communis
Jatropha curcas
Solanum tuberosum
Juglans regia
Chrysochromulina sp CCMP291
Hydra vulgaris
Strongyloides ratti
Tetranychus urticae
Macrobrachium rosenbergii
Kryptolebias marmoratus
Ciona intestinalis
Phlebiopsis gigantea 11061_1 CR5-6
Gaeumannomyces graminis var tritici R3-111a-1
Sordaria macrospora k-hell
Madurella mycetomatis
Rhynchosporium secalis
Oidiodendron maius Zn
Microdochium bolleyi
Pseudomassariella vexata
Macrostomum lignano
Paramecium tetraurelia strain d4-2
Ichthyophthirius multifiliis
Nothobranchius furzeri
Pteropus alecto
Paramecium tetraurelia strain d4-2
Hanseniaspora valbyensis NRRL Y-1626
Nannospalax galili
Xenopus tropicalis
Marmota marmota marmota
Galeopterus variegatus
Acinonyx jubatus
Eptesicus fuscus
Chlorocebus sabaeus
Monodelphis domestica
Entamoeba histolytica
Macrostomum lignano
Tritrichomonas foetus
Trichomonas vaginalis G3
Paramecium tetraurelia strain d4-2
Toxoplasma gondii ME49
Plasmodium malariae
Pseudocohnilembus persalinus
Ichthyophthirius multifiliis
Trichomonas vaginalis G3
Tritrichomonas foetus
Schistosoma japonicum
Ectocarpus siliculosus
Dictyostelium lacteum
Mizuhopecten yessoensis
Crassostrea virginica
Hyalella azteca
Branchiostoma belcheri
Drosophila ananassae
Zootermopsis nevadensis
Mizuhopecten yessoensis
Sinocyclocheilus rhinocerous
Ramazzottius varieornatus
Branchiostoma floridae
Austrofundulus limnaeus
Saccoglossus kowalevskii
Tortispora caseinolytica NRRL Y-17796
Paramecium tetraurelia strain d4-2
Anopheles gambiae str PEST
Spinacia oleracea
Wallemia mellicola CBS 63366
Saprolegnia parasitica CBS 22365
Albugo candida
Paramecium tetraurelia
Tetrahymena thermophila SB210
Paramecium tetraurelia strain d4-2
Paramecium tetraurelia strain d4-2
Paramecium tetraurelia strain d4-2
Paramecium tetraurelia
Drosophila melanogaster
Acanthaster planci
Brugia malayi
Naegleria gruberi strain NEG-M
Hydra vulgaris
Stentor coeruleus
Reticulomyxa filosa
Entamoeba histolytica HM-1:IMSS
Tetrahymena thermophila SB210
Babesia sp Xinjiang
Anaeromyces robustus
Protomyces lactucaedebilis
Durio zibethinus
Sanghuangporus baumii
Rhizoctonia sp CBS 109695
Tubulinosema ratisbonensis
Fibularhizoctonia sp CBS 109695
Punctularia strigosozonata HHB-11173 SS5
Stylonychia lemnae
Daphnia magna
Dictyostelium lacteum
Priapulus caudatus
Helobdella robusta
Pundamilia nyererei
Apis cerana
Harpegnathos saltator
Aethina tumida
Nicrophorus vespilloides
Basidiobolus meristosporus CBS 93173
Entamoeba dispar SAW760

G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Gregarina niphandrodes
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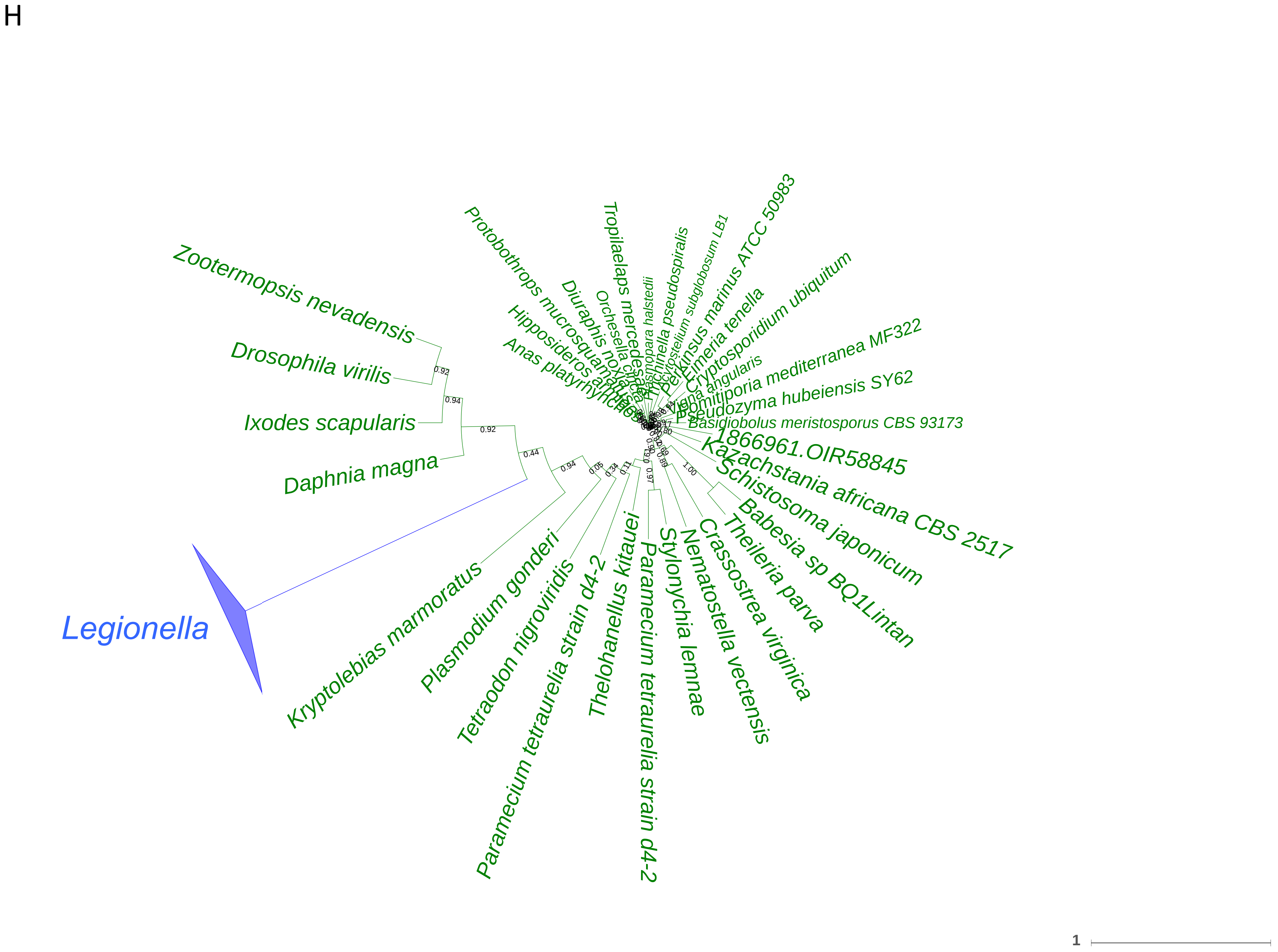
Fistulifera solaris
Eimeria tenella
Fistulifera solaris
Blastocystis sp ATCC 50177
Laetiporus sulphureus 93-53
Rhizopus delemar RA 99-880
Malassezia pachydermatis
Basidiobolus meristosporus CBS 93173
Rhizophagus irregularis DAOM 197198w
Fomitiporia mediterranea MF322
Zea mays
Setaria italica
Zea mays
Gossypium arboreum
Phaseolus vulgaris
Pinus pinaster
Amborella trichopoda
Ulva sp SAP114778
Myotis davidii
Tetraodon nigroviridis
Necator americanus
Orchesella cincta
0.72
0.91
0.88
0.64
0.89
0.78
0.97
0.82
0.96
0.83
0.97
0.88
0.93
0.81
0.92
0.1


H
Zootermopsis nevadensis
Drosophila virilis
Ixodes scapularis
Daphnia magna
Legionella
Kryptolebias marmoratus
Plasmodium gonderi
Tetraodon nigroviridis
Paramecium tetraurelia strain d4-2
Thelohanellus kitauei
Paramecium tetraurelia strain d4-2
Stylonychia lemnae
Nematostella vectensis
Crassostrea virginica
Theileria parva
Babesia sp BQ1Lintan
Schistosoma japonicum
Kazachstania africana CBS 2517
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Basidiobolus meristosporus CBS 93173
Pseudozyma hubeiensis SY62
Fomitiporia mediterranea MF322
Vigna angularis
Cryptosporidium ubiquitum
Eimeria tenella
Perkinsus marinus ATCC 50983
Acytostelium subglobosum LB1
Trachilinella pseudospiralis
Plasmopara halstedii
Tropilaelaps mercedesae
Orchesella cincta
Diuraphis noxia
Protobothrops mucrosquamatus
Hipposideros armiger
Anas platyrhynchos
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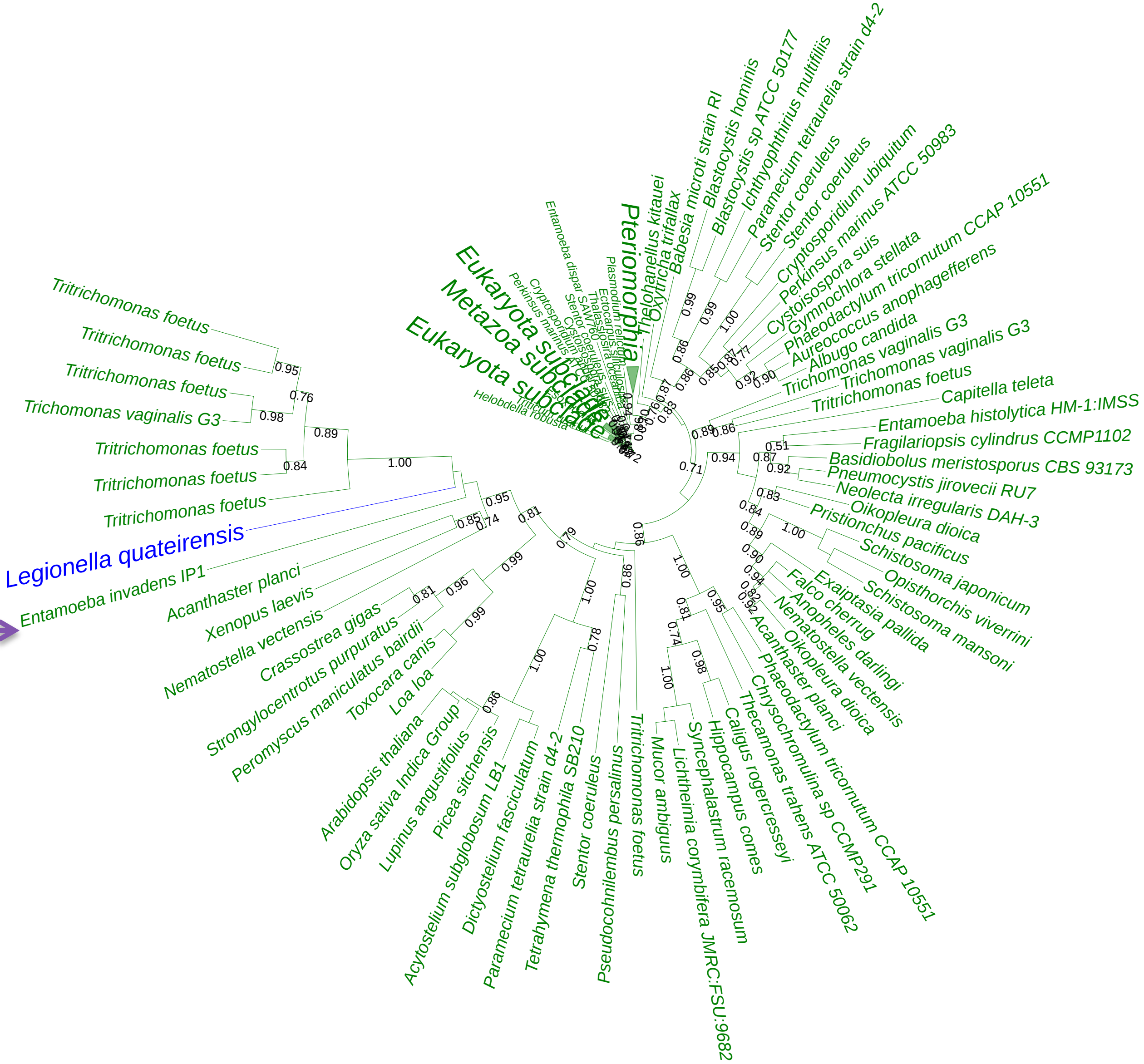
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Tritrichomonas foetus
Tritrichomonas foetus
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Tritrichomonas foetus
Tritrichomonas foetus
Legionella quateirensis
Entamoeba invadens IP1
Acanthaster planci
Xenopus laevis
Nematostella vectensis
Crassostrea gigas
Strongylocentrotus purpuratus
Peromyscus maniculatus bairdii
Toxocara canis
Loa loa
Arabidopsis thaliana
Oryza sativa Indica Group
Lupinus angustifolius
Picea sitchensis
Acytostelium subglobosum LB1
Dictyostelium fasciculatum
Paramecium tetraurelia strain d4-2
Tetrahymena thermophila SB210
Stentor coeruleus
Pseudocohnilembus persalinus
Tritrichomonas foetus
Mucor ambiguus
Lichtheimia corymbifera JMRC:FSU:9682
Syncephalastrum racemosum
Hippocampus comes
Caligus rogercresseyi
Thecamonas trahens ATCC 50062
Chrysochromulina sp CCMP291
Phaeodactylum tricornutum CCAP 10551
Acanthaster planci
Oikopleura dioica
Nematostella vectensis
Anopheles darlingi
Falco cherrug
Exaiptasia pallida
Schistosoma mansoni
Opisthorchis viverrini
Schistosoma japonicum
Pristionchus pacificus
Oikopleura dioica
Neolecta irregularis DAH-3
Pneumocystis jirovecii RU7
Basidiobolus meristosporus CBS 93173
Fragilariopsis cylindrus CCMP1102
Entamoeba histolytica HM-1:IMSS
Capitella teleta
Tritrichomonas foetus
Trichomonas vaginalis G3
Trichomonas vaginalis G3
Albugo candida
Aureococcus anophagefferens
Phaeodactylum tricornutum CCAP 10551
Gymnochlora stellata
Cystoisospora suis
Perkinsus marinus ATCC 50983
Cryptosporidium ubiquitum
Stentor coeruleus
Stentor coeruleus
Paramecium tetraurelia strain d4-2
Ichthyophthirius multifiliis
Blastocystis sp ATCC 50177
Blastocystis hominis
Babesia microti strain RI
Oxytricha trifallax
Thelohanellus kitauei
Pteriomorphia
Eukaryota subclade
Metazoa subclade
Eukaryota subclade
Entamoeba dispar SAW760
Perkinsus marinus
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0.99
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0.99
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0.86
0.86
1.00
0.81
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0.51
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0.90
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0.92
0.92
0.99
0.99
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0.92
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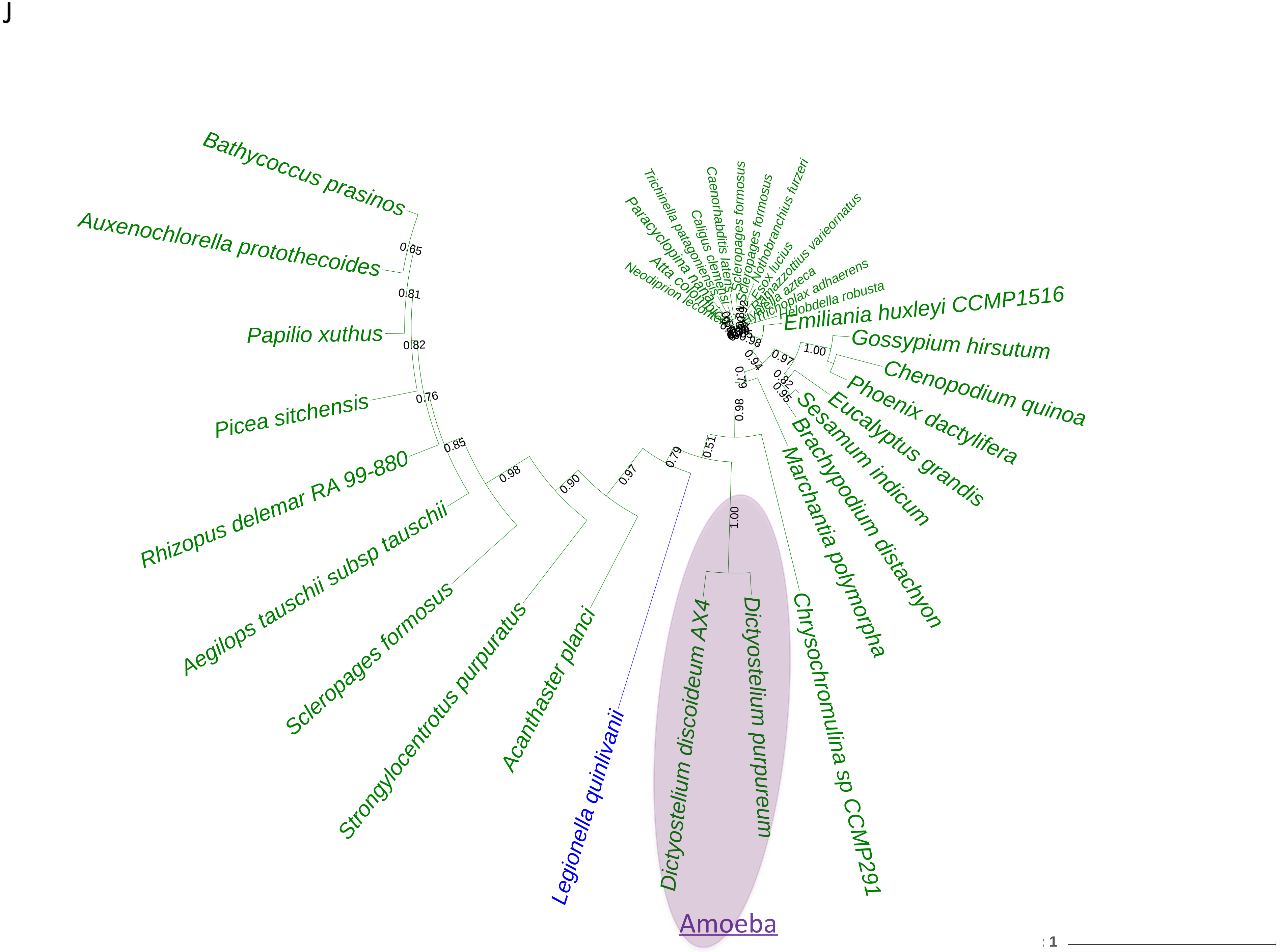
0.83

Amoeba

0.1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Picea sitchensis
Rhizopus delemar RA 99-880
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Scleropages formosus
Strongylocentrotus purpuratus
Acanthaster planci
Legionella quinlivanii
Dictyostelium discoideum AX4
Dictyostelium purpureum
Amoeba
Chrysochromulina sp CCMP291
Marchantia polymorpha
Brachypodium distachyon
Sesamum indicum
Eucalyptus grandis
Phoenix dactylifera
Chenopodium quinoa
Gossypium hirsutum
Emiliania huxleyi CCMP1516
Helobdella robusta
Trichoplax adhaerens
Hyalella azteca
Ramazzottius varieornatus
Esox lucius
Nothobranchius furzeri
Scleropages formosus
Scleropages formosus
Caenorhabditis latens
Caligus clemensi
Trichinella patagoniensis
Paracyclopina nana
Atta colombica
Neodiprion lecontei
0.65
0.81
0.82
0.76
0.85
0.98
0.90
0.97
0.79
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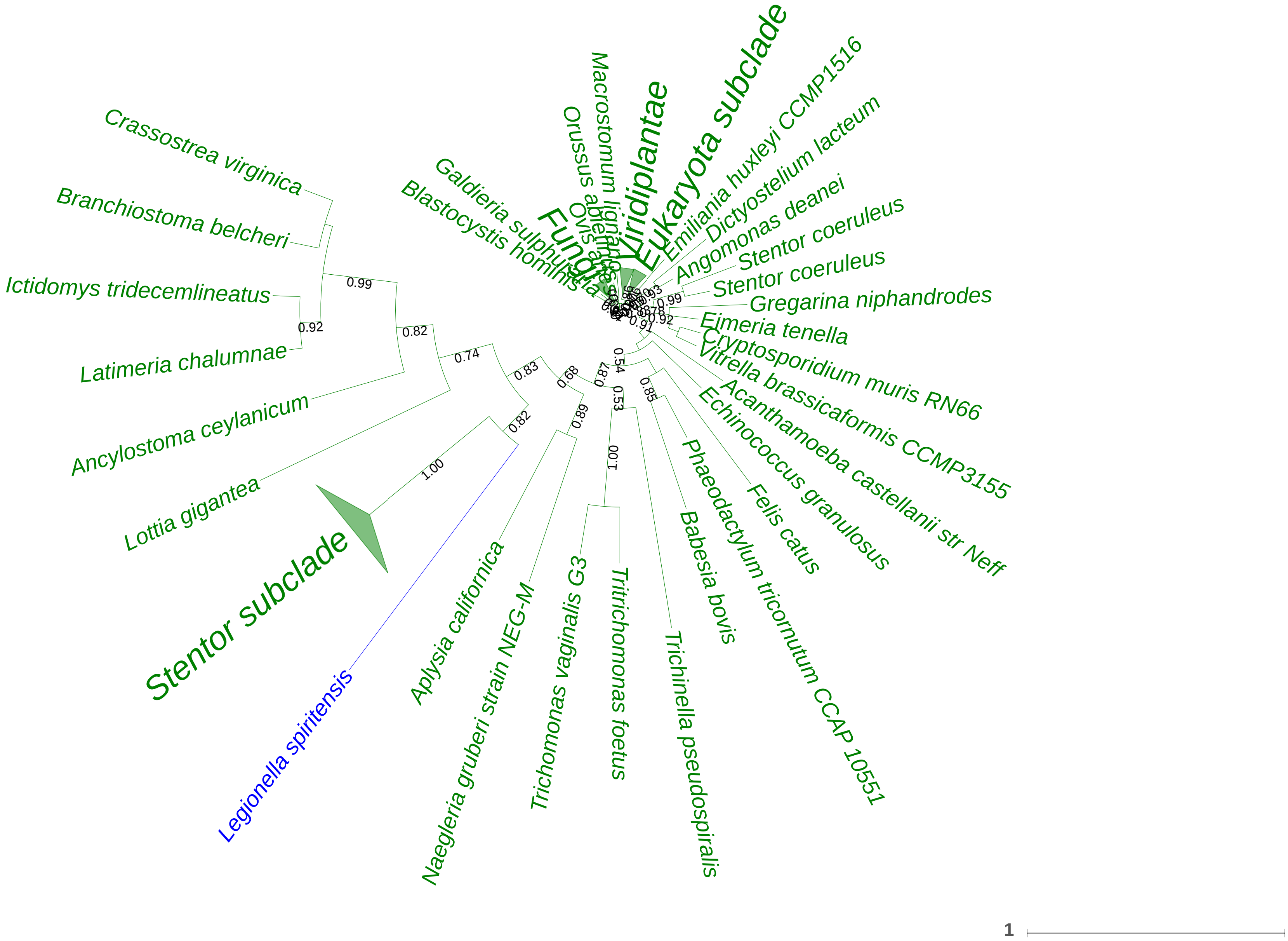
0.98
0.97
1.00
0.82
0.95
1.00
1

K Lspi0161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Latimeria chalumnae
Ancylostoma ceylanicum
Lottia gigantea
Stentor subclade
Legionella spiritensis
Aplysia californica
Naegleria gruberi strain NEG-M
Trichomonas vaginalis G3
Tritrichomonas foetus
Trichinella pseudospiralis
Babesia bovis
Phaeodactylum tricornutum CCAP 10551
Felis catus
Echinococcus granulosus
Acanthamoeba castellanii str Neff
Vitrella brassicaformis CCMP3155
Cryptosporidium muris RN66
Eimeria tenella
Gregarina niphandrodes
Stentor coeruleus
Stentor coeruleus
Angomonas deanei
Dictyostelium lacteum
Emiliania huxleyi CCMP1516
Eukaryota subclade
Viridiplantae
Macrostomum lignano
Orussus abietinus
Ovis aries
Fungi
Galdieria sulphuraria
Blastocystis hominis
0.99
0.92
0.82
0.74
0.83
0.68
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0.92
0.99
0.93
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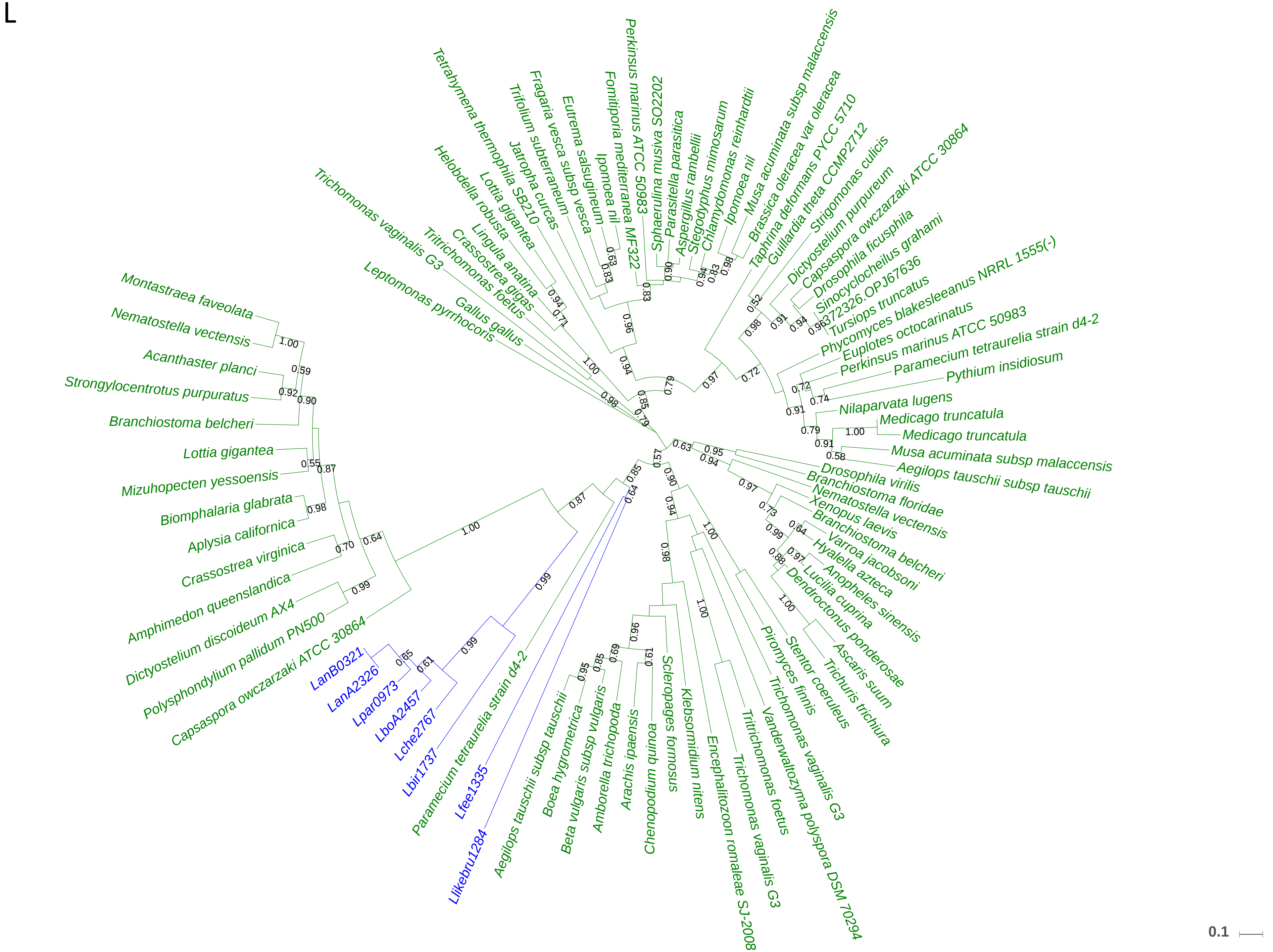
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Montastraea faveolata
Nematostella vectensis
Acanthaster planci
Strongylocentrotus purpuratus
Branchiostoma belcheri
Lottia gigantea
Mizuhopecten yessoensis
Biomphalaria glabrata
Aplysia californica
Crassostrea virginica
Amphimedon queenslandica
Dictyostelium discoideum AX4
Polysphondylium pallidum PN500
Capsaspora owczarzaki ATCC 30864
LanB0321
LanA2326
Lpar0973
LboA2457
Lche2767
Lbir1737
Lfee1335
Llikebru1284
Paramecium tetraurelia strain d4-2
Aegilops tauschii subsp tauschii
Boea hygrometrica
Beta vulgaris subsp vulgaris
Amborella trichopoda
Arachis ipaensis
Chenopodium quinoa
Scleropages formosus
Klebsormidium nitens
Encephalitozoon romaleae SJ-2008
Trichomonas vaginalis G3
Tritrichomonas foetus
Vanderwaltozyma polyspora DSM 70294
Trichomonas vaginalis G3
Piromyces finnis
Stentor coeruleus
Trichuris trichiura
Ascaris suum
Dendroctonus ponderosae
Lucilia cuprina
Anopheles sinensis
Hyalella azteca
Varroa jacobsoni
Branchiostoma belcheri
Xenopus laevis
Nematostella vectensis
Branchiostoma floridae
Drosophila virilis
Aegilops tauschii subsp tauschii
Musa acuminata subsp malaccensis
Medicago truncatula
Medicago truncatula
Nilaparvata lugens
Pythium insidiosum
Paramecium tetraurelia strain d4-2
Perkinsus marinus ATCC 50983
Euplotes octocarinatus
Phycomyces blakesleeanus NRRL 1555(-)
Tursiops truncatus
372326.OPJ67636
Sinocyclocheilus grahami
Drosophila ficusphila
Capsaspora owczarzaki ATCC 30864
Dictyostelium purpureum
Strigomonas culicis
Guillardia theta CCMP2712
Taphrina deformans PYCC 5710
Brassica oleracea var oleracea
Musa acuminata subsp malaccensis
Ipomoea nil
Chlamydomonas reinhardtii
Stegodyphus mimosarum
Aspergillus rambellii
Parasitella parasitica
Sphaerulina musiva SO2202
Perkinsus marinus ATCC 50983
Fomitiporia mediterranea MF322
Ipomoea nil
Eutrema salsugineum
Fragaria vesca subsp vesca
Trifolium subterraneum
Jatropha curcas
Tetrahymena thermophila SB210
Lottia gigantea
Helobdella robusta
Lingula anatina
Crassostrea gigas
Tritrichomonas foetus
Trichomonas vaginalis G3
Gallus gallus
Leptomonas pyrrhocoris
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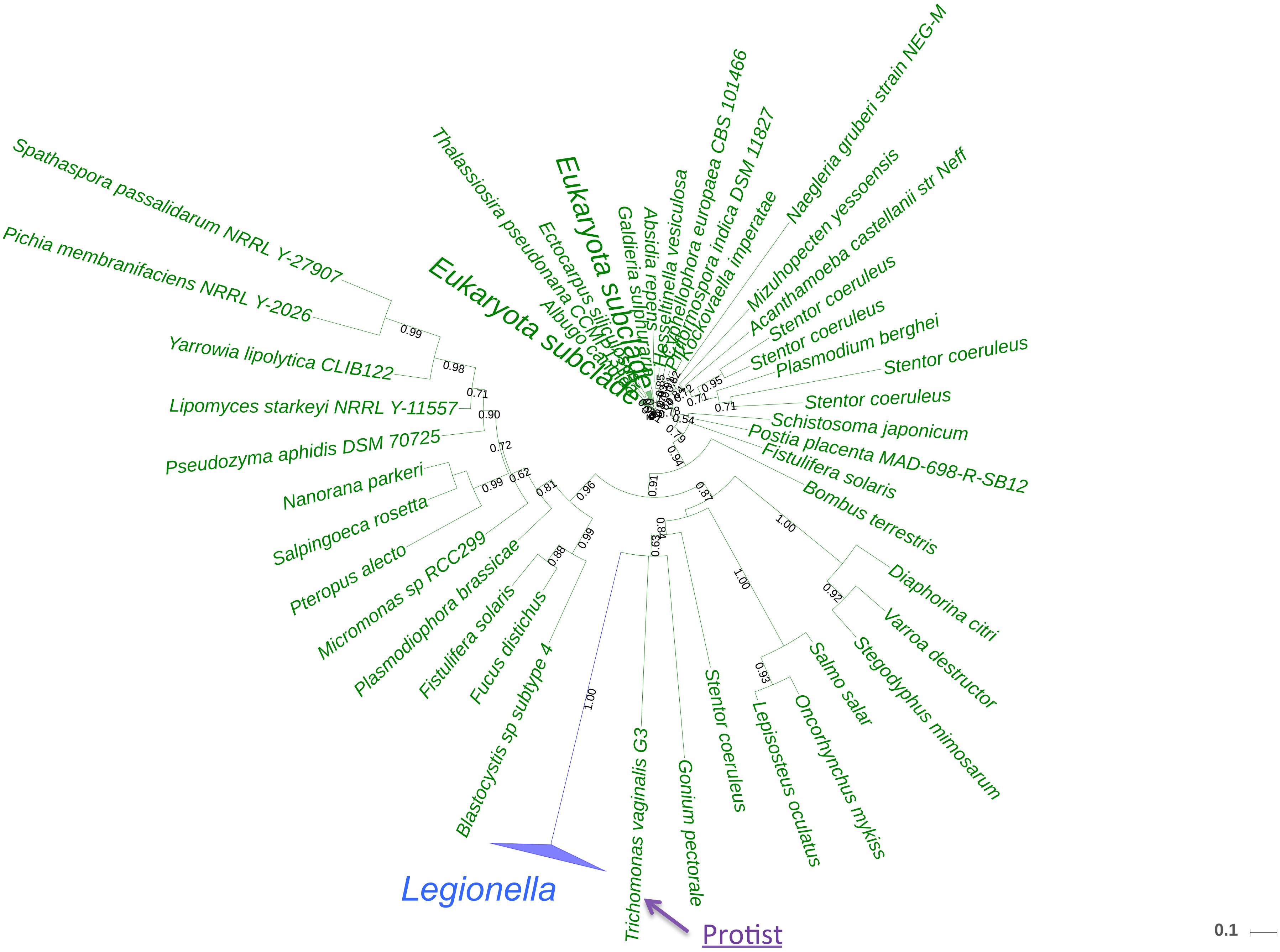
M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Pichia membranifaciens NRRL Y-2026
Yarrowia lipolytica CLIB122
Lipomyces starkeyi NRRL Y-11557
Pseudozyma aphidis DSM 70725
Nanorana parkeri
Salpingoeca rosetta
Pteropus alecto
Micromonas sp RCC299
Plasmodiophora brassicae
Fistulifera solaris
Fucus distichus
Blastocystis sp subtype 4
Legionella
Trichomonas vaginalis G3
Protist
Gonium pectorale
Stentor coeruleus
Lepisosteus oculatus
Oncorhynchus mykiss
Salmo salar
Stegodyphus mimosarum
Varroa destructor
Diaphorina citri
Bombus terrestris
Fistulifera solaris
Postia placenta MAD-698-R-SB12
Schistosoma japonicum
Stentor coeruleus
Stentor coeruleus
Plasmodium berghei
Stentor coeruleus
Stentor coeruleus
Acanthamoeba castellanii str Neff
Mizuhopecten yessoensis
Naegleria gruberi strain NEG-M
Kockovaella imperatae
Piriformospora indica DSM 11827
Cyphellophora europaea CBS 101466
Hesseltinella vesiculosa
Absidia repens
Galdieria sulphuraria
Eukaryota subclade
Ectocarpus siliculosus
Albugo candida
Thalassiosira pseudonana CCMP1335
Eukaryota subclade
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0.71
0.90
0.72
0.99
0.62
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0.96
0.88
0.99
1.00
0.61
0.63
0.84
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0.95
0.1

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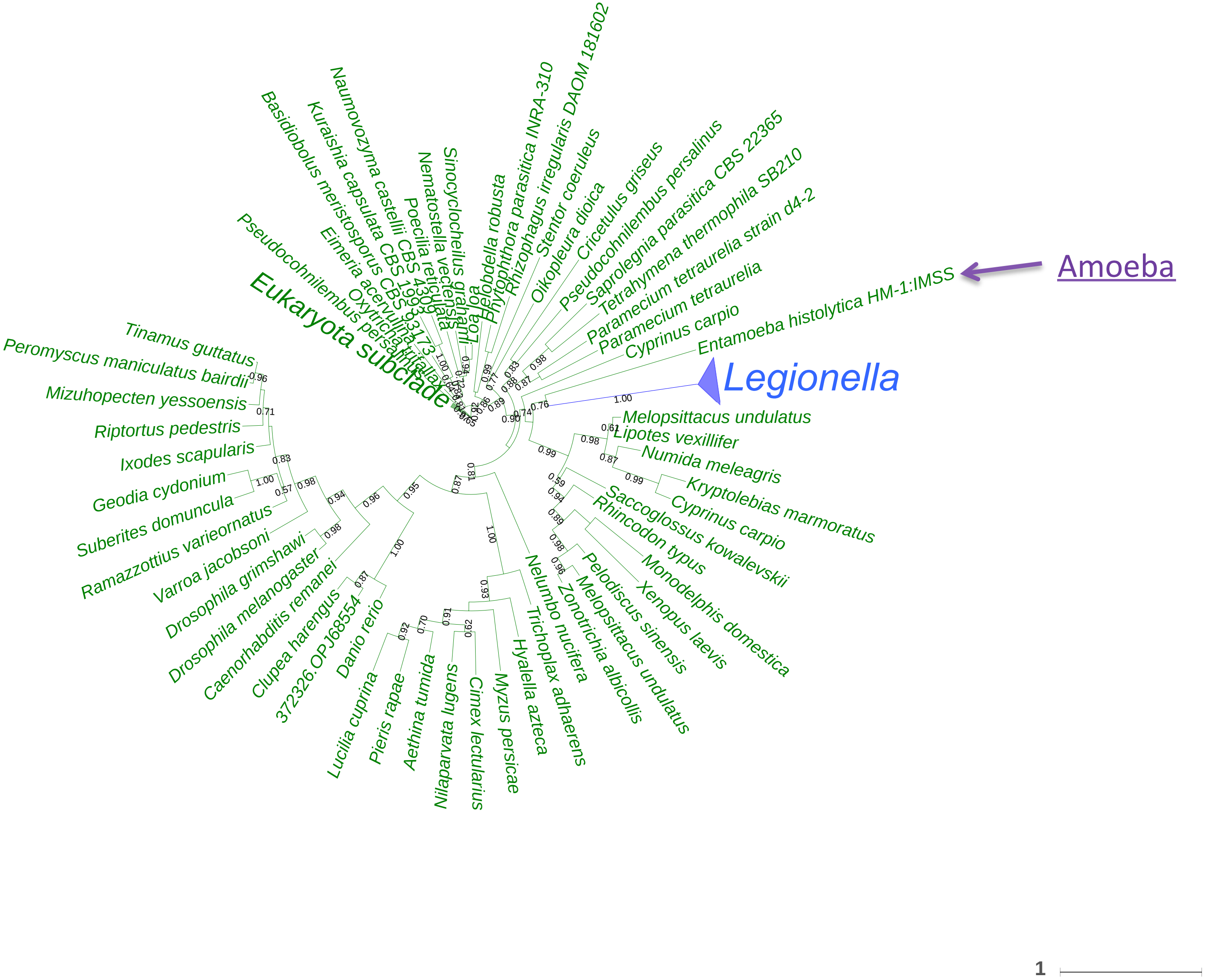
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Legionella
Eukaryota subclade
Entamoeba histolytica HM-1:IMSS
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Paramecium tetraurelia
Paramecium tetraurelia strain d4-2
Tetrahymena thermophila SB210
Saprolegnia parasitica CBS 22365
Pseudocohnilembus persalinus
Cricetulus griseus
Oikopleura dioica
Stentor coeruleus
Rhizophagus irregularis DAOM 181602
Phytophthora parasitica INRA-310
Helobdella robusta
Loa loa
Sinocyclocheilus grahami
Nematostella vectensis
Poecilia reticulata
Naumovozyma castellii CBS 4309
Kuraishia capsulata CBS 1993
Basidiobolus meristosporus CBS 931.73
Eimeria acervulina
Oxytricha trifallax
Pseudocohnilembus persalinus
Tinamus guttatus
Peromyscus maniculatus bairdii
Mizuhopecten yessoensis
Riptortus pedestris
Ixodes scapularis
Geodia cydonium
Suberites domuncula
Ramazzottius varieornatus
Varroa jacobsoni
Drosophila grimshawi
Drosophila melanogaster
Caenorhabditis remanei
Clupea harengus
372326.OPJ68554
Danio rerio
Lucilia cuprina
Pieris rapae
Aethina tumida
Nilaparvata lugens
Cimex lectularius
Myzus persicae
Hyalella azteca
Trichoplax adhaerens
Nelumbo nucifera
Zonotrichia albicollis
Melopsittacus undulatus
Pelodiscus sinensis
Xenopus laevis
Monodelphis domestica
Rhincodon typus
Saccoglossus kowalevskii
Cyprinus carpio
Kryptolebias marmoratus
Numida meleagris
Lipotes vexillifer
Melopsittacus undulatus
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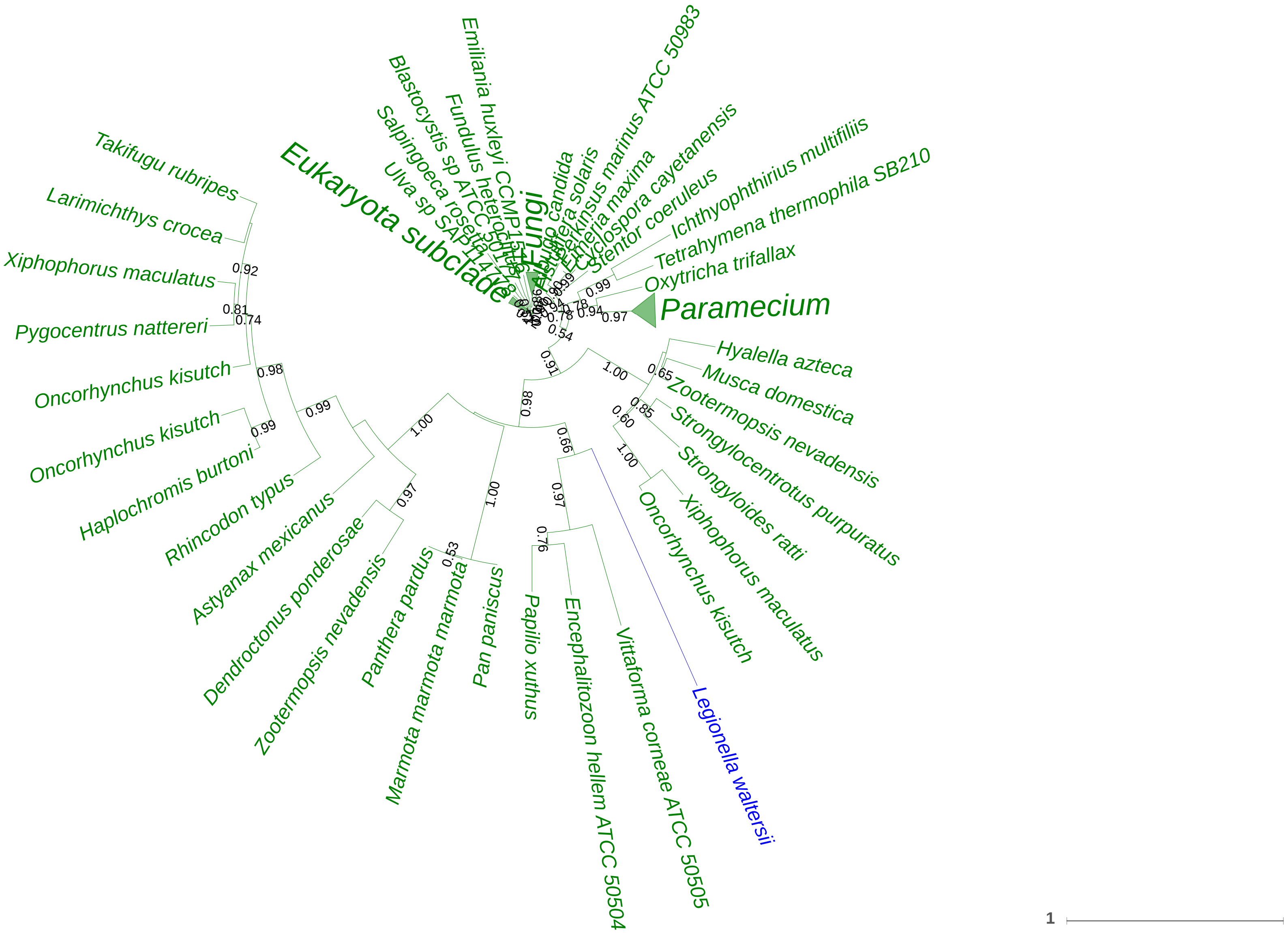
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Paramecium
Ulva sp SAP11.4
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Blastocystis sp ATCC 50177
Fundulus heteroclitus
Emiliania huxleyi CCMP1516
Albugo candida
Kipferlia solaris
Perkinsus marinus ATCC 50983
Eimeria maxima
Cyclospora cayetanensis
Stentor coeruleus
Ichthyophthirius multifiliis
Tetrahymena thermophila SB210
Oxytricha trifallax
Hyalella azteca
Musca domestica
Zootermopsis nevadensis
Strongylocentrotus purpuratus
Strongyloides ratti
Xiphophorus maculatus
Oncorhynchus kisutch
Legionella waltersii
Vittaforma corneae ATCC 50505
Encephalitozoon hellem ATCC 50504
Papilio xuthus
Pan paniscus
Marmota marmota marmota
Panthera pardus
Zootermopsis nevadensis
Dendroctonus ponderosae
Astyanax mexicanus
Rhincodon typus
Haplochromis burtoni
Oncorhynchus kisutch
Oncorhynchus kisutch
Pygocentrus nattereri
Xiphophorus maculatus
Larimichthys crocea
Takifugu rubripes
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0.97
0.53
1.00
0.98
0.91
0.54
0.78
0.94
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0.90
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1.00
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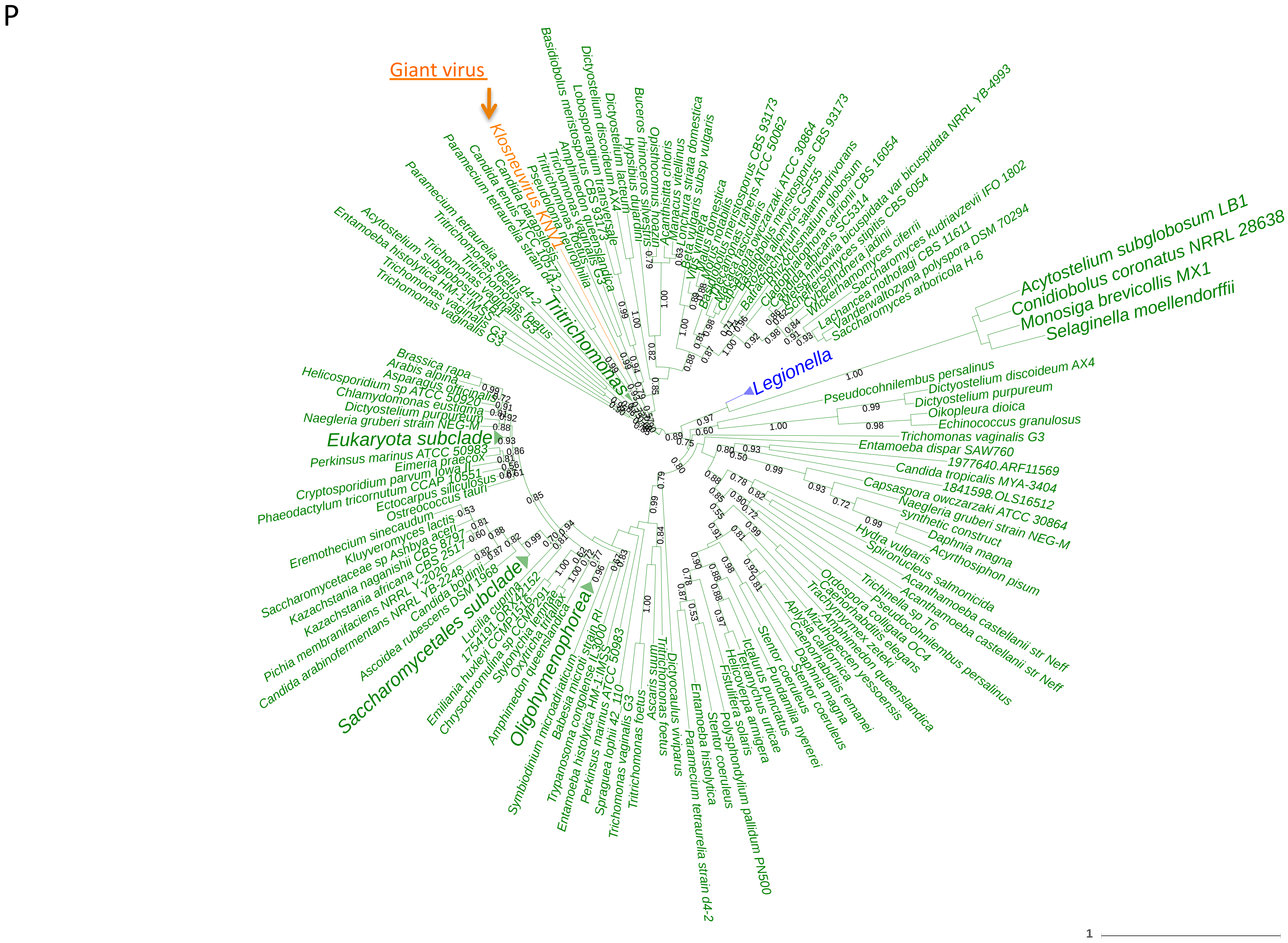
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Giant virus
Klosneuvirus KNV1
Legionella
Tritrichomonas
Eukaryota subclade
Saccharomycetales subclade
Oligohymenophorea
Acytostelium subglobosum LB1
Conidiobolus coronatus NRRL 28638
Monosiga brevicollis MX1
Selaginella moellendorffii
Pseudocohnilembus persalinus
Dictyostelium discoideum AX4
Dictyostelium purpureum
Oikopleura dioica
Echinococcus granulosus
Trichomonas vaginalis G3
Entamoeba dispar SAW760
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Candida tropicalis MYA-3404
1841598.OLS16512
Capsaspora owczarzaki ATCC 30864
Naegleria gruberi strain NEG-M
synthetic construct
Daphnia magna
Acyrthosiphon pisum
Hydra vulgaris
Spironucleus salmonicida
Trichinella sp T6
Acanthamoeba castellanii str Neff
Pseudocohnilembus persalinus
Ordospora colligata OC4
Caenorhabditis elegans
Trachymyrmex zeteki
Amphimedon queenslandica
Mizuhopecten yessoensis
Caenorhabditis remanei
Aplysia californica
Daphnia magna
Stentor coeruleus
Pundamilia nyererei
Ictalurus punctatus
Tetranychus urticae
Helicoverpa armigera
Fistulifera solaris
Polysphondylium pallidum PN500
Stentor coeruleus
Entamoeba histolytica
Paramecium tetraurelia strain d4-2
Dictyocaulus viviparus
Tritrichomonas foetus
Ascaris suum
Tritrichomonas foetus
Trichomonas vaginalis G3
Spraguea lophii 42_110
Perkinsus marinus ATCC 50983
Entamoeba histolytica HM-1:IMSS
Trypanosoma congolense IL3000
Babesia microti strain RI
Symbiodinium microadriaticum
Amphimedon queenslandica
Oxytricha trifallax
Stylonychia lemnae
Chrysochromulina sp CCMP291
Emiliania huxleyi CCMP1516
1754191.ORX42152
Lucilia cuprina
Ascoidea rubescens DSM 1968
Candida boidinii
Candida arabinofermentans NRRL YB-2248
Pichia membranifaciens NRRL Y-2026
Kazachstania africana CBS 2517
Kazachstania naganishii CBS 8797
Saccharomycetaceae sp Ashbya aceri
Kluyveromyces lactis
Eremothecium sinecaudum
Ostreococcus tauri
Ectocarpus siliculosus
Phaeodactylum tricornutum CCAP 10551
Cryptosporidium parvum Iowa II
Eimeria praecox
Perkinsus marinus ATCC 50983
Naegleria gruberi strain NEG-M
Dictyostelium purpureum
Chlamydomonas eustigma
Helicosporidium sp ATCC 50920
Asparagus officinalis
Arabis alpina
Brassica rapa
Trichomonas vaginalis G3
Trichomonas vaginalis G3
Entamoeba histolytica HM-1:IMSS
Acytostelium subglobosum LB1
Trichomonas vaginalis G3
Tritrichomonas foetus
Trichomonas foetus
Tritrichomonas foetus
Paramecium tetraurelia strain d4-2
Paramecium tetraurelia strain d4-2
Candida tenuis ATCC 10573
Candida parapsilosis
Pseudoloma neurophilia
Tritrichomonas foetus
Trichomonas vaginalis G3
Amphimedon queenslandica
Basidiobolus meristosporus CBS 93173
Lobosporangium transversale
Dictyostelium discoideum AX4
Dictyostelium lacteum
Hypsibius dujardini
Buceros rhinoceros silvestris
Opisthocomus hoazin
Acanthisitta chloris
Manacus vitellinus
Lonchura striata domestica
Beta vulgaris subsp vulgaris
Vitis vinifera
Malus domestica
Morus notabilis
Basidiobolus meristosporus CBS 93173
Monocercomonas trahens ATCC 50062
Capsaspora fasciculata
Basidiobolus owczarzaki ATCC 30864
Rozella allomycis CSF55
Batrachochytrium salamandrivorans
Basidiobolus meristosporus CBS 93173
Rhizoclosmatium globosum
Cladophialophora carrionii CBS 16054
Candida albicans SC5314
Metschnikowia bicuspidata var bicuspidata NRRL YB-4993
Scheffersomyces stipitis CBS 6054
Cyberlindnera jadinii
Wickerhamomyces ciferrii
Saccharomyces kudriavzevii IFO 1802
Lachancea nothofagi CBS 11611
Vanderwaltozyma polyspora DSM 70294
Saccharomyces arboricola H-6
1.00
0.99
0.98
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0.60
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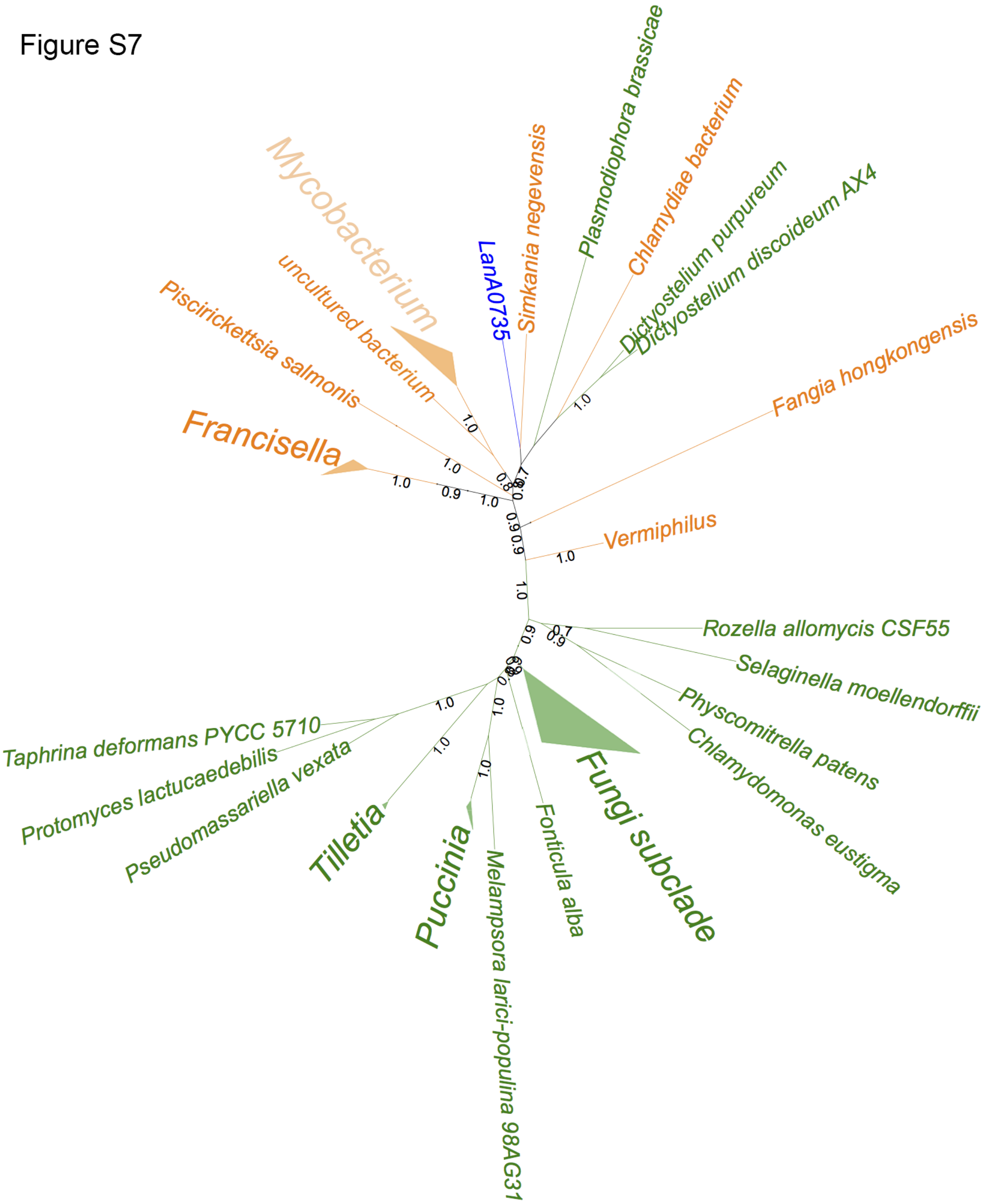
0.93
0.88
0.86
1

Figure S7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LanA0735
Simkania negevensis
Plasmodiophora brassicae
Chlamydiae bacterium
Dictyostelium purpureum
Dictyostelium discoideum AX4
Fangia hongkongensis
uncultured bacterium
Piscirickettsia salmonis
Francisella
Vermiphilus
Rozella allomycis CSF55
Selaginella moellendorffii
Physcomitrella patens
Chlamydomonas eustigma
Fungi subclade
Fonticula alba
Melampsora larici-populina 98AG31
Puccinia
Tilletia
Pseudomassariella vexata
Protomyces lactucaedebilis
Taphrina deformans PYCC 5710
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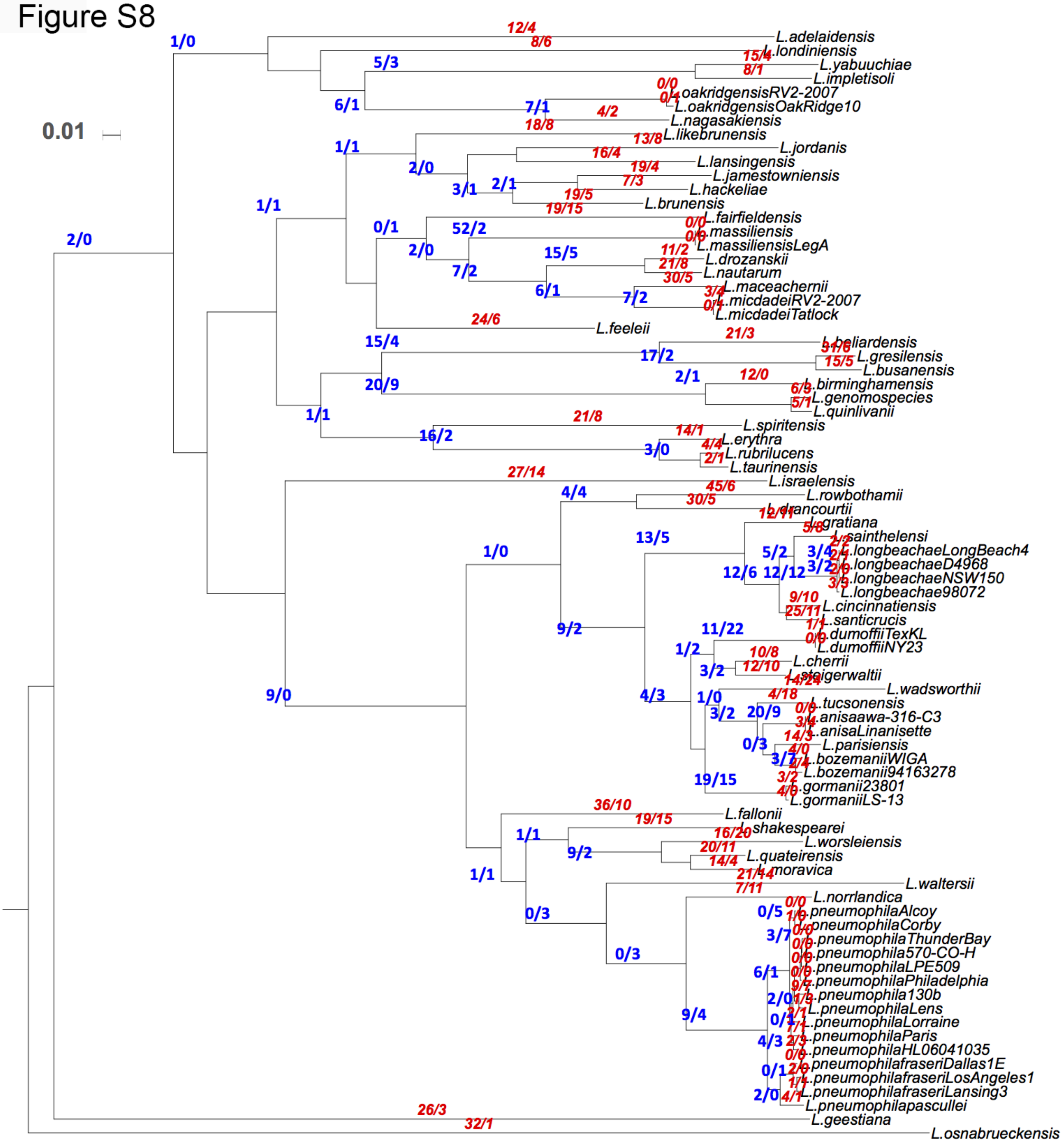
0.7

Figure S8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L.londiniensis
15/4
5/3
L.yabuuchiae
8/1
L.impletisoli
0/0
L.oakridgensisRV2-2007
0/4
6/1
L.oakridgensisOakRidge10
7/1
4/2
L.nagasakiensis
18/8
13/8
L.likebrunensis
1/1
L.jordanis
16/4
2/0
L.lansingensis
19/4
L.jamestowniensis
3/1
2/1
7/3
L.hackeliae
19/5
1/1
19/15
L.brunensis
0/1
0/0
L.fairfieldensis
52/2
0/0
L.massiliensis
2/0
L.massiliensisLegA
11/2
15/5
L.drozanskii
21/8
7/2
L.nautarum
30/5
6/1
L.maceachernii
3/4
7/2
L.micdadeiRV2-2007
0/1
L.micdadeiTatlock
24/6
L.feeleii
21/3
15/4
L.beliardensis
31/6
17/2
L.gresilensis
15/5
L.busanensis
2/1
12/0
20/9
L.birminghamensis
6/3
L.genomospecies
5/1
L.quinlivanii
1/1
21/8
L.spiritensis
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L.rowbothamii
30/5
L.drancourtii
12/11
L.gratiana
5/8
13/5
L.sainthelensi
2/2
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L.longbeachaeLongBeach4
5/2
3/4
2/1
L.longbeachaeD4968
12/6
12/12
3/2
2/0
L.longbeachaeNSW150
3/5
L.longbeachae98072
9/10
L.cincinnatiensis
25/11
11/22
L.santicrucis
1/1
9/2
L.dumoffiiTexKL
0/0
L.dumoffiiNY23
1/2
10/8
L.cherrii
3/2
12/10
L.steigerwaltii
14/24
4/18
L.wadsworthii
4/3
1/0
L.tucsonensis
0/0
3/2
20/9
L.anisaawa-316-C3
3/4
L.anisaLinanisette
14/3
9/0
L.parisiensis
0/3
4/0
3/7
L.bozemaniiWIGA
2/4
L.bozemanii94163278
3/2
19/15
L.gormanii23801
4/0
L.gormaniiLS-13
36/10
L.fallonii
19/15
1/1
L.shakespearei
16/20
9/2
L.worsleiensis
20/11
L.quateirensis
14/4
1/1
L.moravica
21/14
L.waltersii
7/11
L.norrlandica
0/0
0/3
0/5
L.pneumophilaAlcoy
1/0
L.pneumophilaCorby
0/0
3/7
L.pneumophilaThunderBay
0/0
0/3
L.pneumophila570-CO-H
0/0
L.pneumophilaLPE509
6/1
0/0
L.pneumophilaPhiladelphia
9/7
2/0
L.pneumophila130b
1/3
L.pneumophilaLens
2/1
9/4
0/1
L.pneumophilaLorraine
1/1
L.pneumophilaParis
4/3
2/3
L.pneumophilaHL06041035
0/0
L.pneumophilafraseriDallas1E
0/1
2/0
L.pneumophilafraseriLosAngeles1
1/1
L.pneumophilafraseriLansing3
2/0
4/1
L.pneumophilapascullei
26/3
L.geestiana
32/1
L.osnabrueckensis

Figure S9

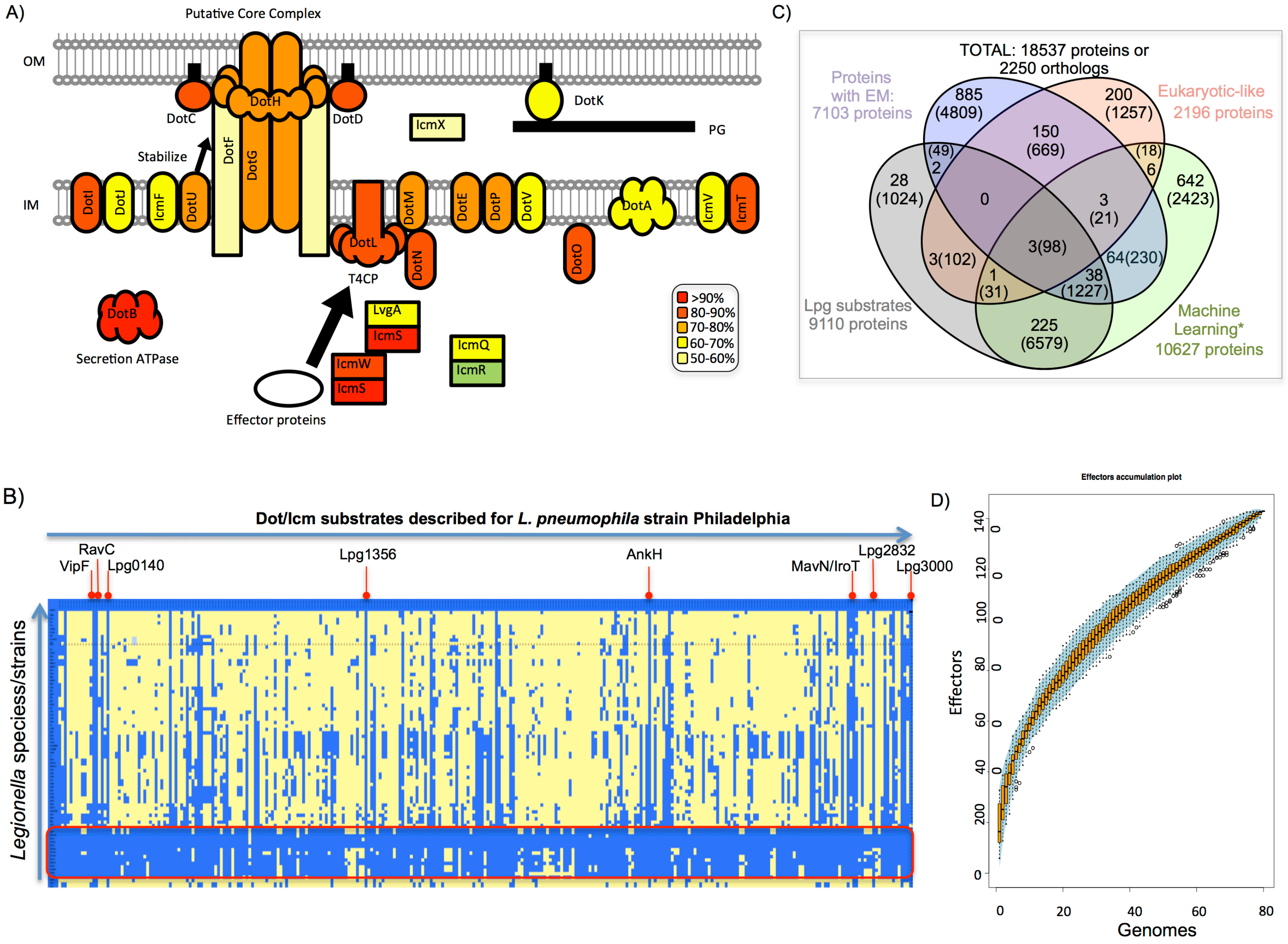
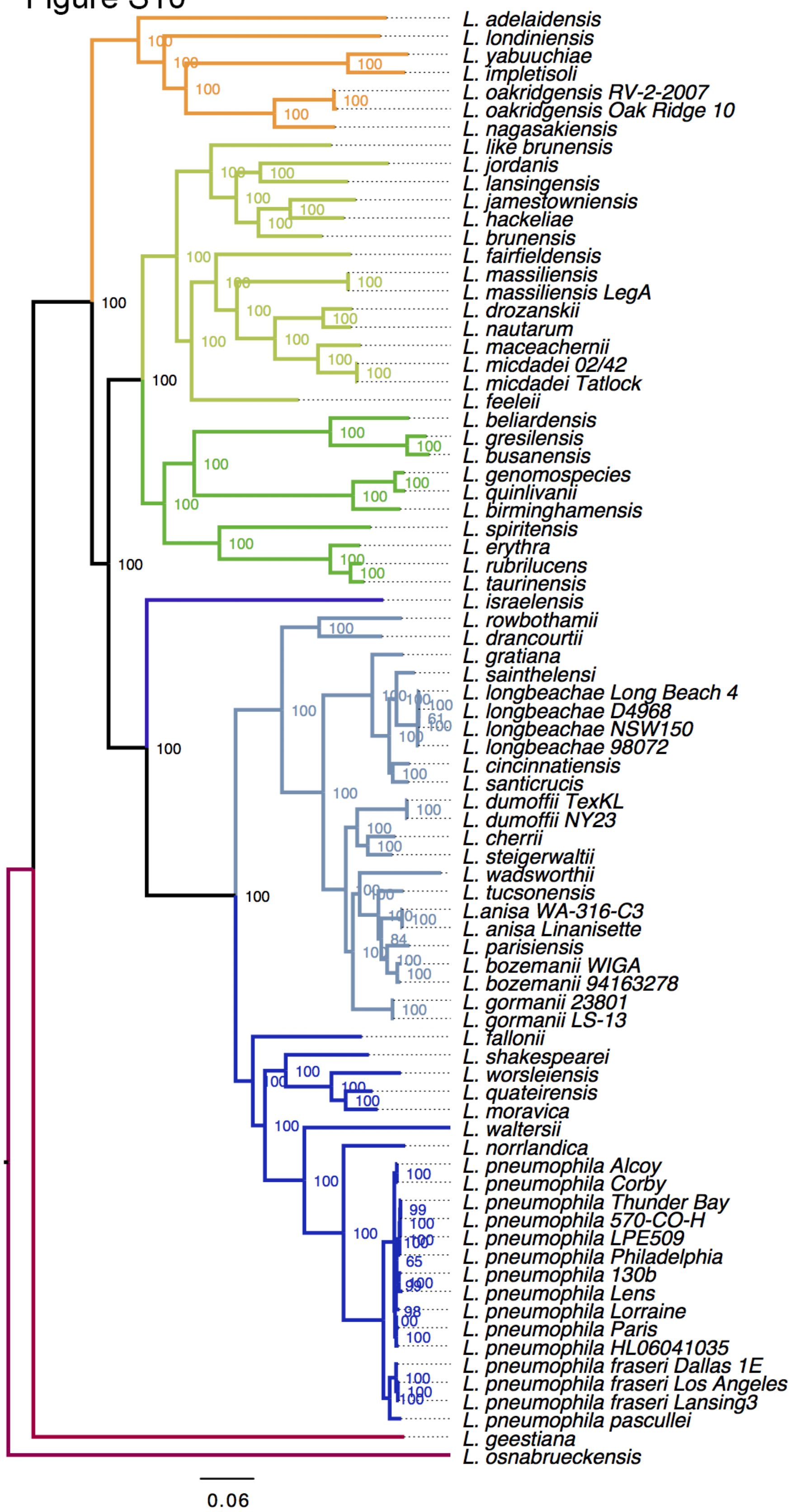

A)
Putative Core Complex
OM
DotC
DotH
DotD
IcmX
DotK
PG
Stabilize
DotF
DotG
IM
DotI
DotJ
IcmF
DotU
DotM
DotE
DotP
DotV
DotA
IcmV
IcmT
DotL
DotN
DotO
T4CP
DotB
Secretion ATPase
LvgA
IcmS
IcmW
IcmS
IcmQ
IcmR
Effector proteins
>90%
80-90%
70-80%
60-70%
50-60%
C)
TOTAL: 18537 proteins or
2250 orthologs
Proteins
with EM:
7103 proteins
Eukaryotic-like
2196 proteins
885
(4809)
200
(1257)
150
(669)
(49)
2
(18)
6
28
(1024)
0
3
(21)
642
(2423)
3(98)
3(102)
64(230)
1
(31)
38
(1227)
225
(6579)
Lpg substrates
9110 proteins
Machine
Learning*
10627 proteins
B)
Dot/Icm substrates described for L. pneumophila strain Philadelphia
RavC
VipF
Lpg0140
Lpg1356
AnkH
MavN/IroT
Lpg2832
Lpg3000
Legionella speciess/strains
D)
Effectors accumulation plot
Effectors
140 0
120 0
100 0
80 0
60 0
40 0
200
0
0
20
40
60
80
Genomes

Figure S10



Putative icmR genes	
Lad1472	
Llon2017	
Lya0191	
Lim1913	
LoakB2127	
LoakA2436	
Lna2432	
Llikebru0284	
Ljor1880	
Llan2226	
Lja1041	
LHAv2_2397	
Lbru1922	
Lfair1119	
LmasA1219	
LmasB1219	
Ldro0224	
Lnau1308	
Lma0769	Lma0770
LmicB2010	LmicB2009
LMIv2_2528	LMIv2_2527
Lfe1575	
Lbe2728	
Lgre0165	
Lbu1930	
Lge0164	
Lquin2160	
Lbir0469	
Lspi2212	
Lery0069	
Lrub0882	Lrub0883
Ltau1269	
Lis0610	Lis0611
Lrow2098	
Ldra3307	
Lgra0792	
Lsain0124	
LloAT2984	
ACZGv1_20168	
llo2793	
Llo982980	
Lcin2221	
Lsan0115	
LduTex2679	
LduN2322595	
Lche1896	
Lstei2286	
Lwad1623	
Ltuc1625	
LanB0124	
LanA2698	
Lpar2148	
LboA0982	
LboB1356	
LgoB2687	
LgoA0132	
LFAv2_2680	
LshaDSM2424	
Lwor2109	
Lqua1606	
Lmo2687	
Lwal0428	
Lno2514	
LpAlc0510	
LPC_2900	
LpThu0446	
Lp570C0452	
LpLPE2739	
lpg0443	
Lp130b0558	
lpl0485	
LPOv2_0509	
lpp0509	
LPVv2_0543	
LpFRAB1765	
LpFRA1871	
LpFRAC0853	
LpPAS2715	
Lges2285	
Loas0911	

Figure S11

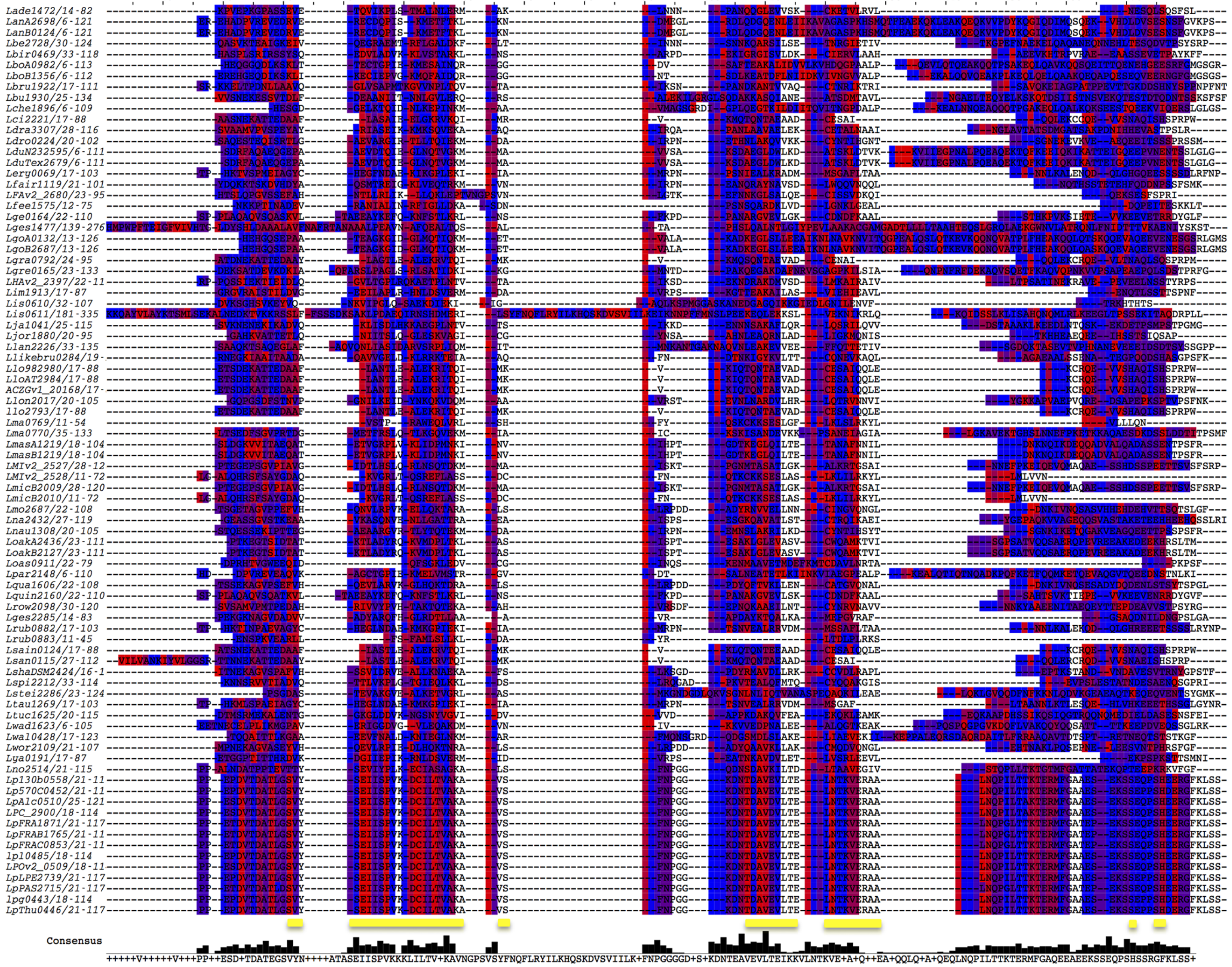

10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
Lade1472/14-82
LanA2698/6-121
LanB0124/6-121
Lbe2728/30-124
Lbir0469/33-118
LboA0982/6-113
LboB1356/6-112
Lbru1922/17-111
Lbu1930/25-134
Lche1896/6-109
Lci2221/17-88
Ldra3307/28-116
Ldro0224/20-102
LduN232595/6-111
LduTex2679/6-111
Lery0069/17-103
Lfair1119/21-101
LFAv2_2680/23-95
Lfee1575/12-75
Lge0164/22-110
Lges1477/139-276
LgoA0132/13-126
LgoB2687/13-126
Lgra0792/24-95
Lgre0165/23-133
LHAv2_2397/22-11
Lim1913/17-87
Lis0610/32-107
Lis0611/181-335
Lja1041/25-115
Ljor1880/20-95
Llan2226/33-135
Llikebru0284/19-
Llo982980/17-88
LloAT2984/17-88
ACZGv1_20168/17-
Llon2017/20-105
llo2793/17-88
Lma0769/11-54
Lma0770/35-133
LmasA1219/18-104
LmasB1219/18-104
LMIv2_2527/28-12
LMIv2_2528/11-72
LmicB2009/28-120
LmicB2010/11-72
Lmo2687/22-108
Lna2432/27-119
Lnau1308/20-105
LoakA2436/23-111
LoakB2127/23-111
Loas0911/22-79
Lpar2148/6-110
Lqua1606/22-108
Lquin2160/22-110
Lrow2098/30-120
Lges2285/14-83
Lrub0882/17-103
Lrub0883/11-45
Lsain0124/17-88
Lsan0115/27-112
LshaDSM2424/16-1
Lspi2212/33-114
Lstei2286/23-124
Ltau1269/17-103
Ltuc1625/20-115
Lwad1623/6-105
Lwal0428/17-123
Lwor2109/21-107
Lya0191/17-87
Lno2514/21-115
Lp130b0558/21-11
Lp570C0452/21-11
LpAlc0510/25-121
LPC_2900/18-114
LpFRA1871/21-117
LpFRAB1765/21-11
LpFRAC0853/21-11
lp10485/18-114
LPOv2_0509/18-11
LpLPE2739/21-117
LpPAS2715/21-117
lpg0443/18-114
LpThu0446/21-117
Consensus
+++++V+++++V+++PP++ESD+TDATEGSVYN++++ATASEIISPVKKKLILTV+KAVNGPSVSYFNQFLRYILKHQSKDVSVIILK+FNPGGGGD+S+KDNTEAVEVLTEIKKVLNTKVE+A+Q++EA+QQLQ+A+QEQLNQPILTTKTERMFGAQEEAEEKSSEQPSHSSRGFKLSS+

Figure S12

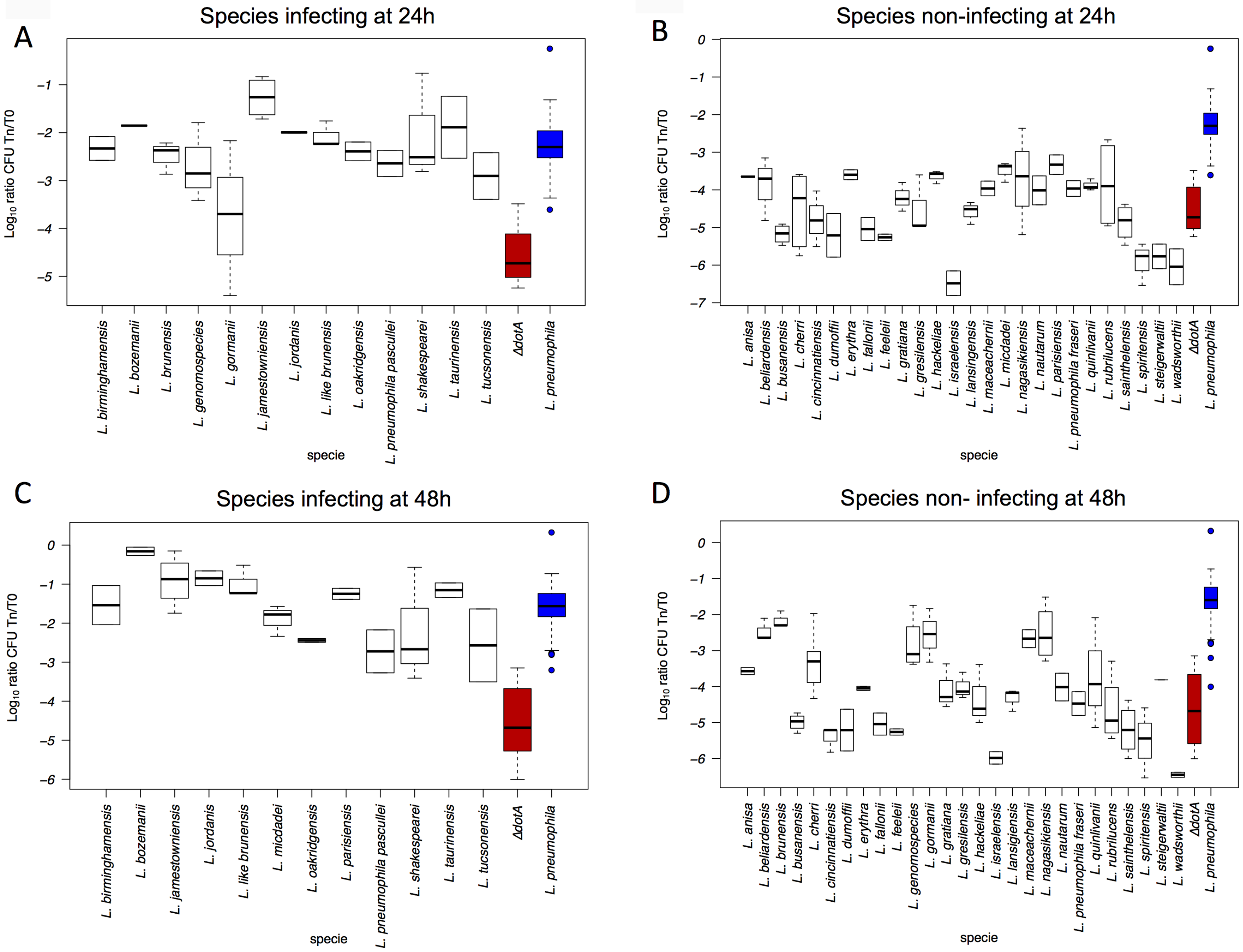
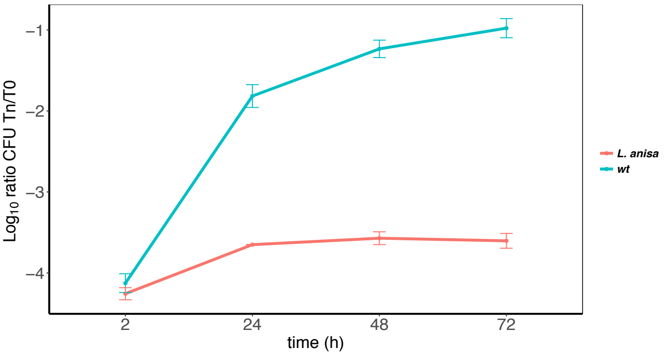
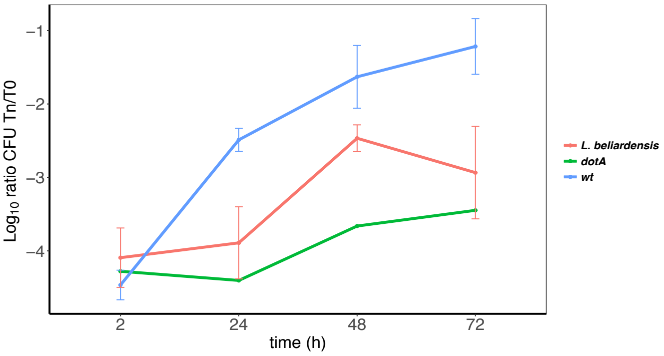

A
Species infecting at 24h
Log10 ratio CFU Tn/T0
−1
−2
−3
−4
−5
L. birminghamensis
L. bozemanii
L. brunensis
L. genomospecies
L. gormanii
L. jamestowniensis
L. jordanis
L. like brunensis
L. oakridgensis
L. pneumophila pascullei
L. shakespearei
L. taurinensis
L. tucsonensis
ΔdotA
L. pneumophila
specie
B
Species non-infecting at 24h
Log10 ratio CFU Tn/T0
0
−1
−2
−3
−4
−5
−6
−7
L. anisa
L. beliardensis
L. busanensis
L. cherri
L. cincinnatiensis
L. dumoffii
L. erythra
L. fallonii
L. feeleii
L. gratiana
L. gresilensis
L. hackeliae
L. israelensis
L. lansingensis
L. maceachernii
L. micdadei
L. nagasikiensis
L. nautarum
L. parisiensis
L. pneumophila fraseri
L. quinlivanii
L. rubrilucens
L. sainthelensis
L. spiritensis
L. steigerwaltii
L. wadsworthii
ΔdotA
L. pneumophila
specie
C
Species infecting at 48h
Log10 ratio CFU Tn/T0
0
−1
−2
−3
−4
−5
−6
L. birminghamensis
L. bozemanii
L. jamestowniensis
L. jordanis
L. like brunensis
L. micdadei
L. oakridgensis
L. parisiensis
L. pneumophila pascullei
L. shakespearei
L. taurinensis
L. tucsonensis
ΔdotA
L. pneumophila
specie
D
Species non- infecting at 48h
Log10 ratio CFU Tn/T0
0
−1
−2
−3
−4
−5
−6
L. anisa
L. beliardensis
L. brunensis
L. busanensis
L. cherri
L. cincinnatiensis
L. dumoffii
L. erythra
L. fallonii
L. feeleii
L. genomospecies
L. gormanii
L. gratiana
L. gresilensis
L. hackeliae
L. israelensis
L. lansigiensis
L. maceachernii
L. nagasikiensis
L. nautarum
L. pneumophila fraseri
L. quinlivanii
L. rubrilucens
L. sainthelensis
L. spiritensis
L. steigerwaltii
L. wadsworthii
ΔdotA
L. pneumophila
specie

Figure S13

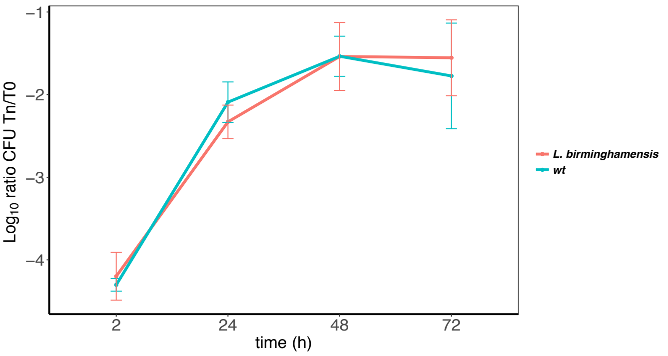
L. anisa



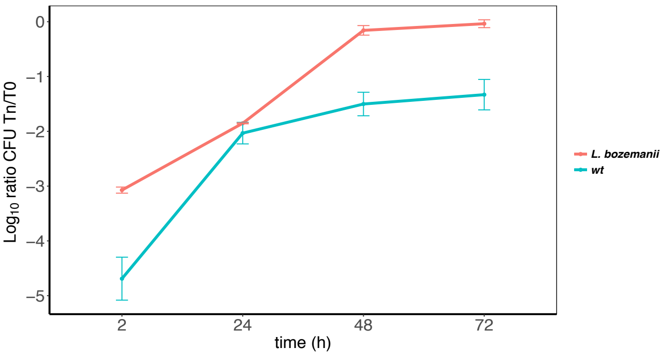
L. beliardensis



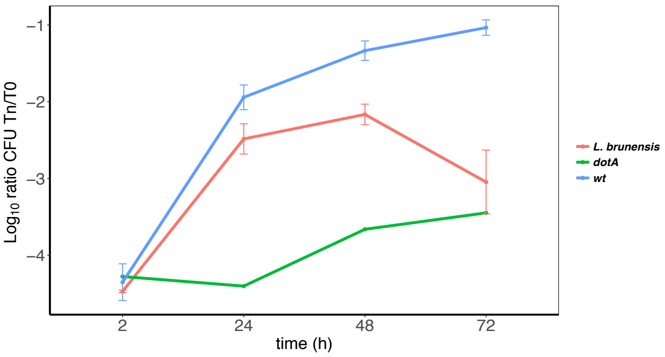
L. birminghamensis



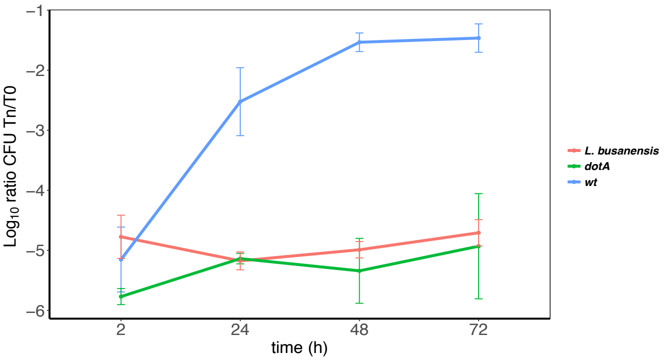
L. bozemanii



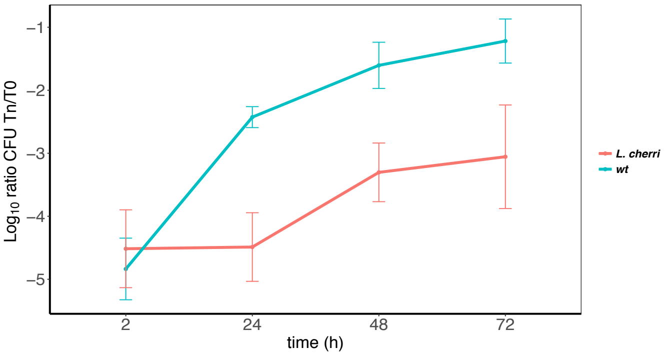
L. brunensis



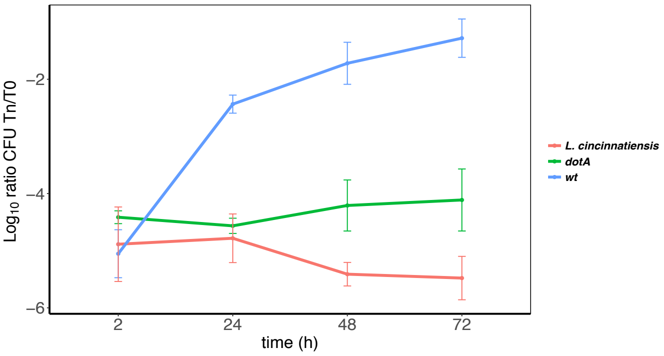
L. busanensis

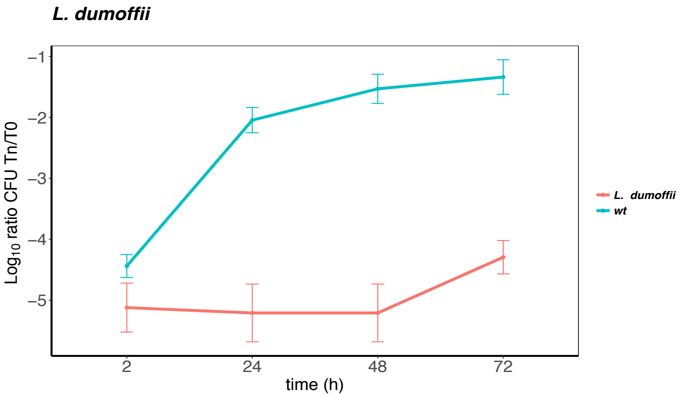


L. cherri

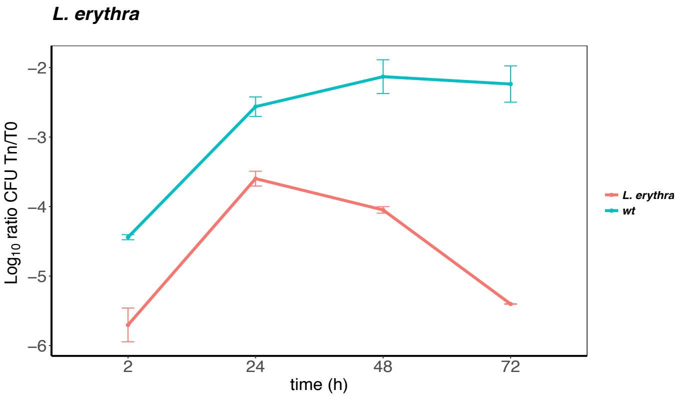


L. cincinnatiensis

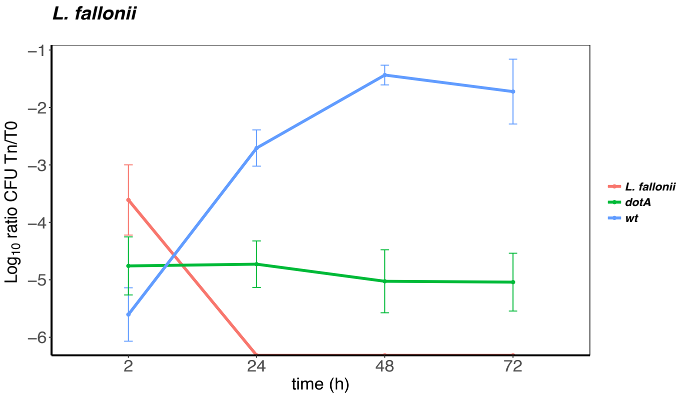




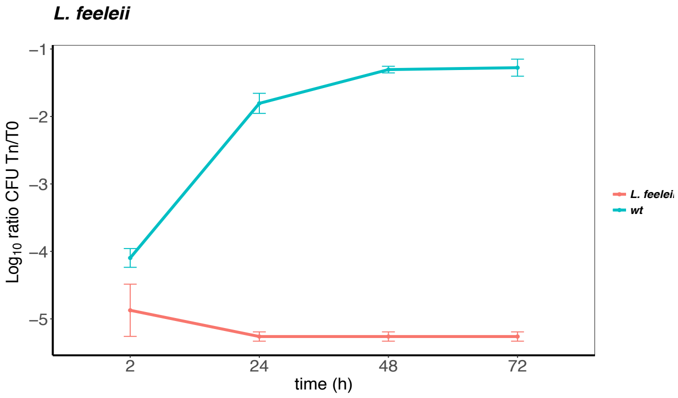
L. dumoffii



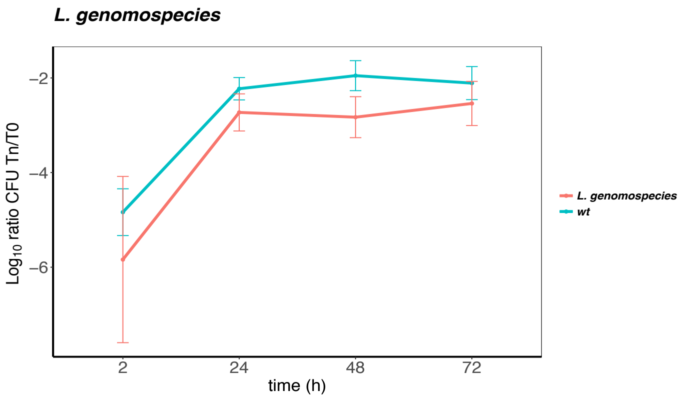
L. erythra



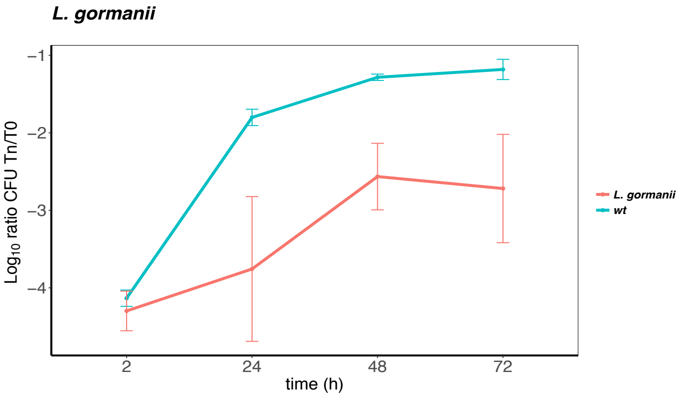
L. fallonii



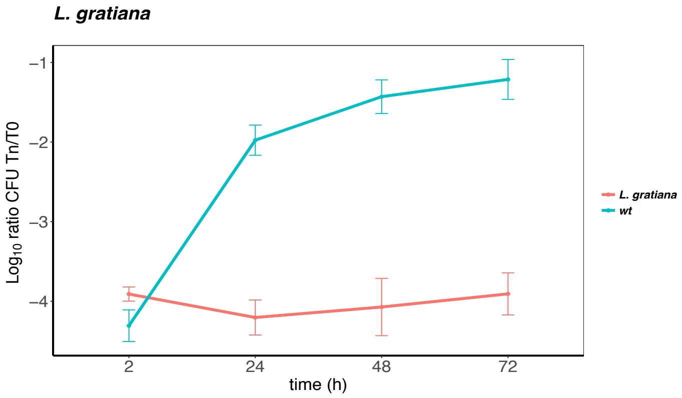
L. feeleii



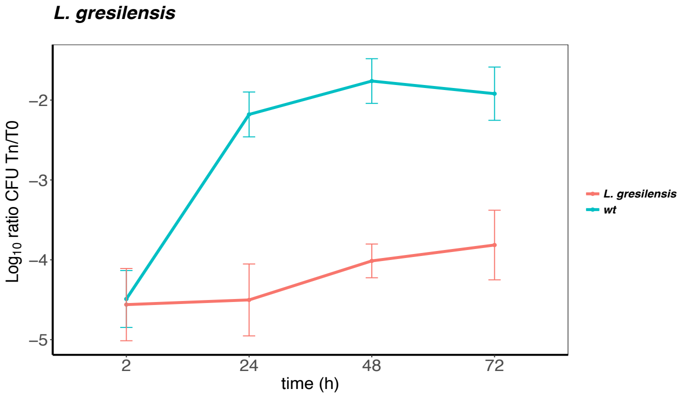
L. genomospecies



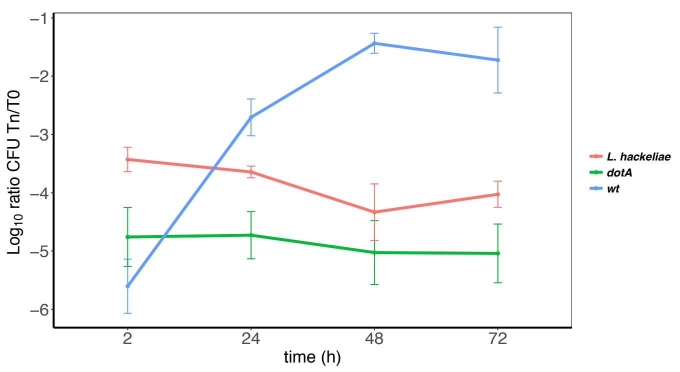
L. gormanii



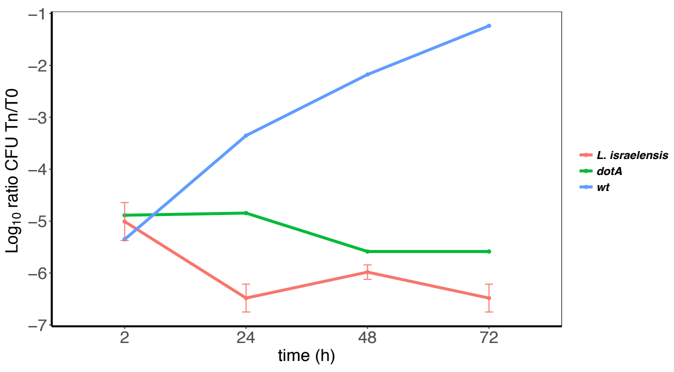
L. gratiana



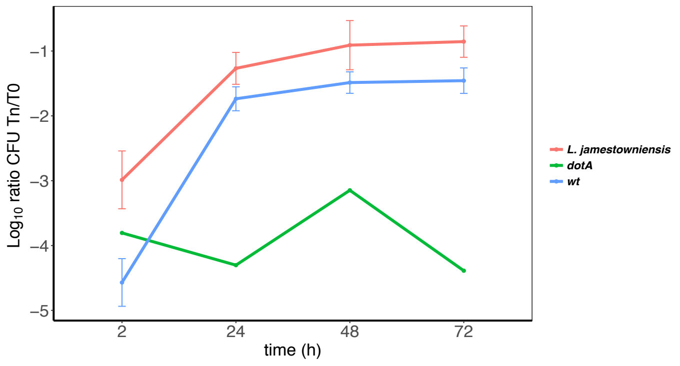
L. gresilensis



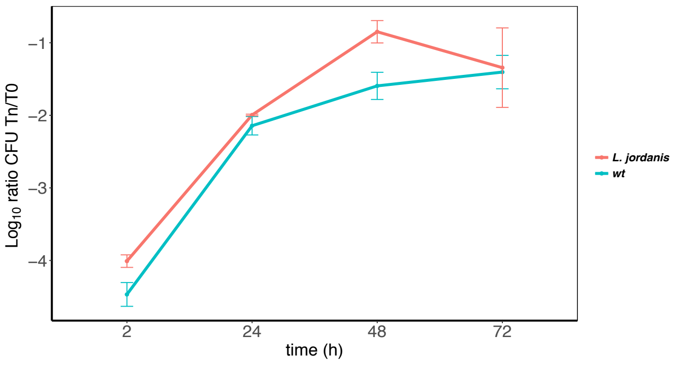
L. hackeliae



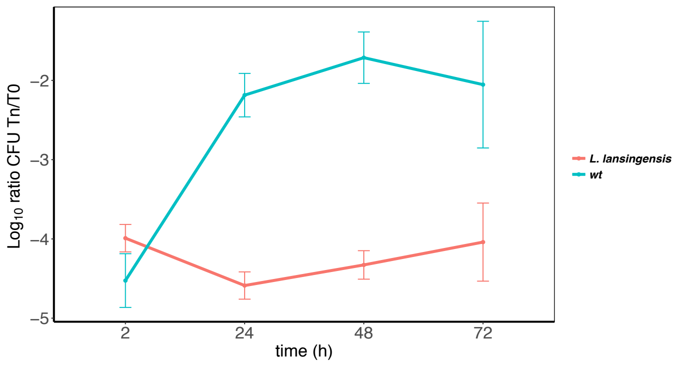
L. israelensis



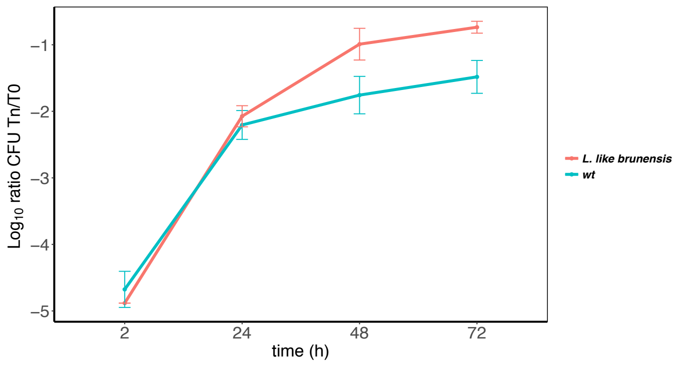
L. jamestowniensis



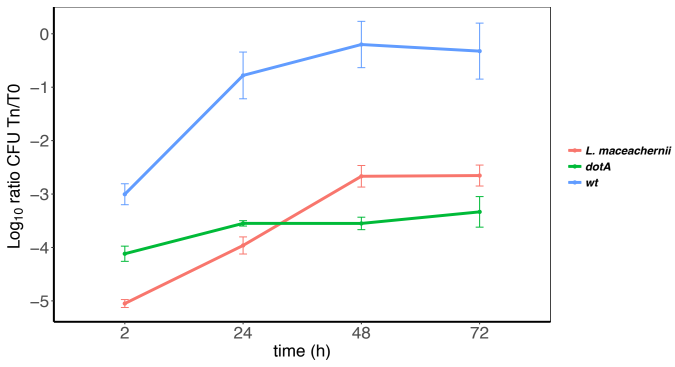
L. jordanis



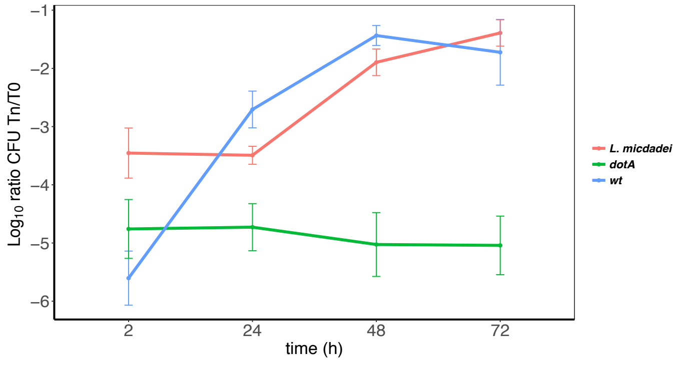
L. lansingensis



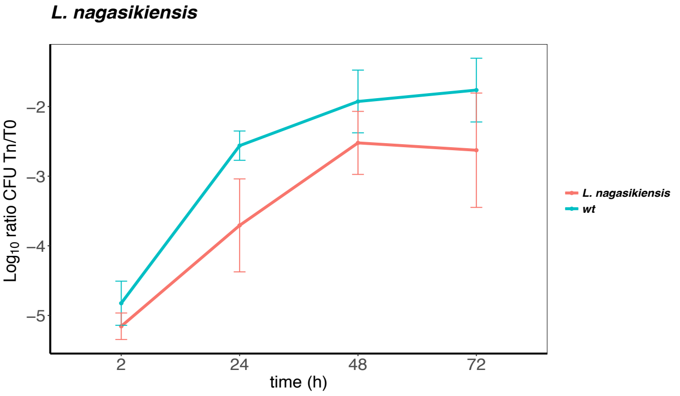
L. like brunensis



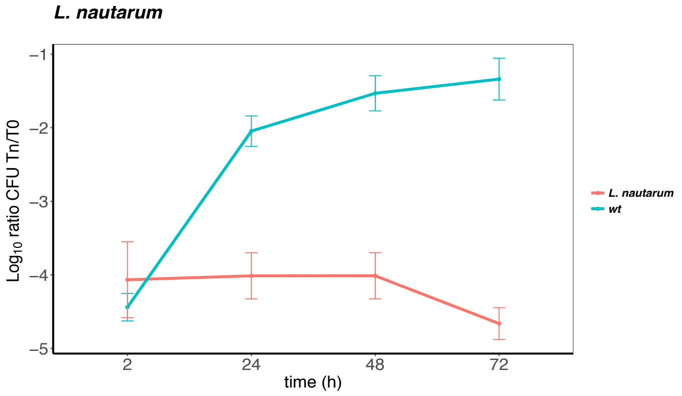
L. maceachernii



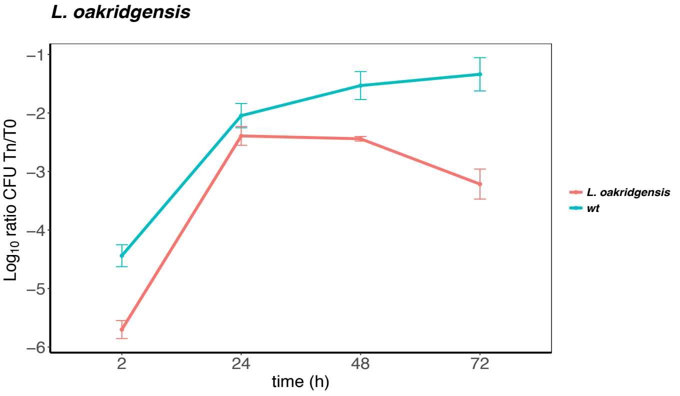
L. micdadei



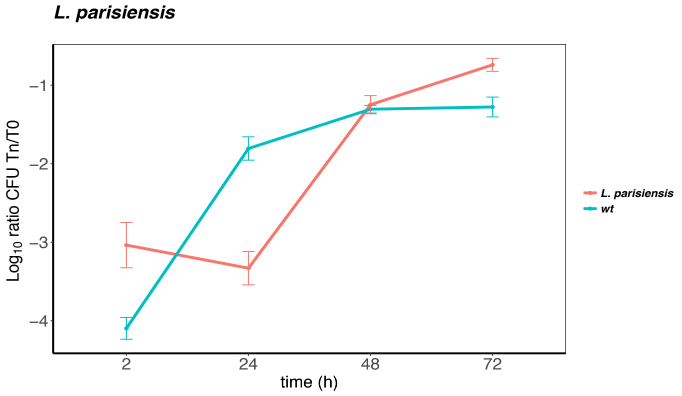
L. nagasikiensis



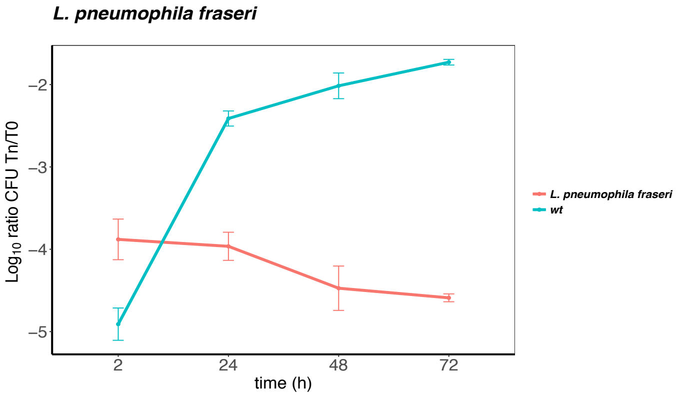
L. nautarum



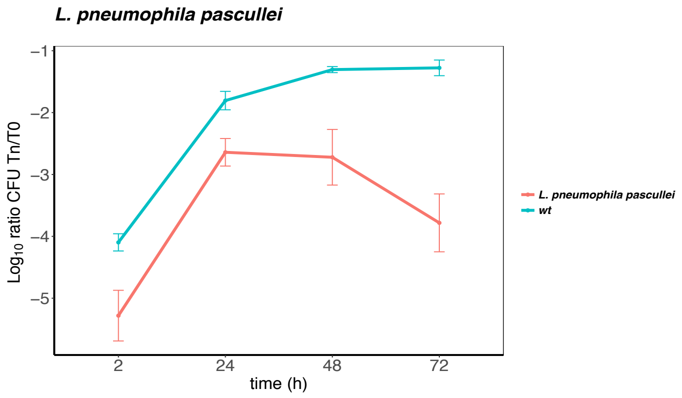
L. oakridgensis



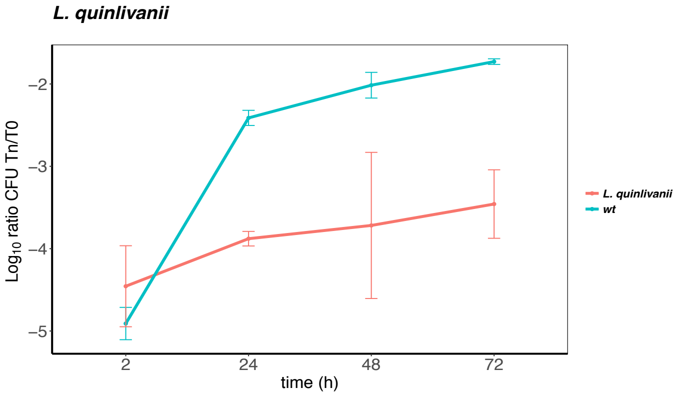
L. parisiensis



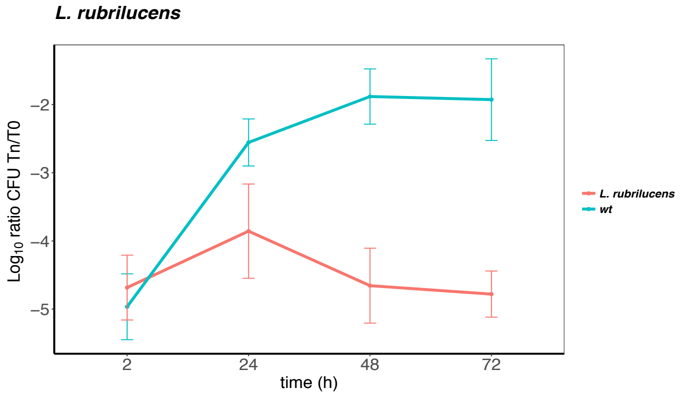
L. pneumophila fraseri



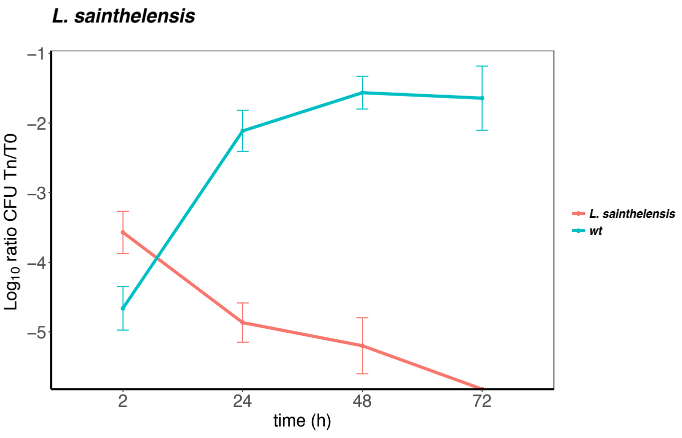
L. pneumophila pascullei

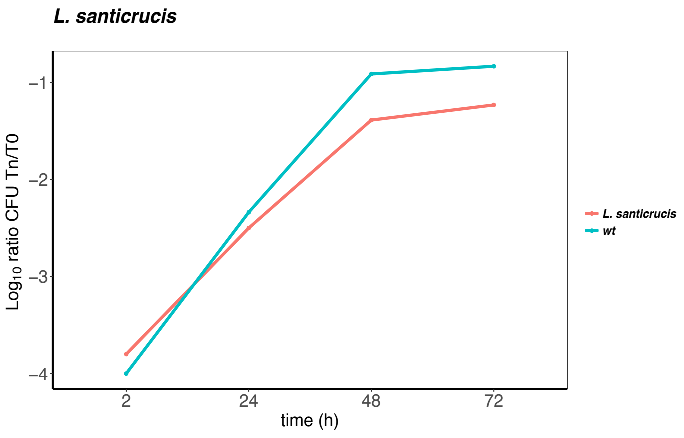


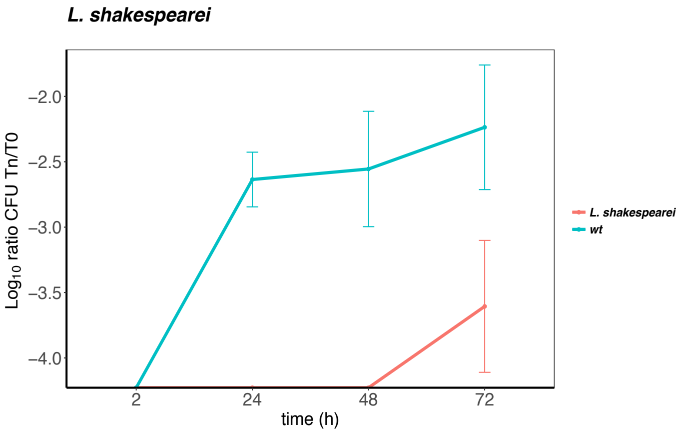
L. quinlivanii

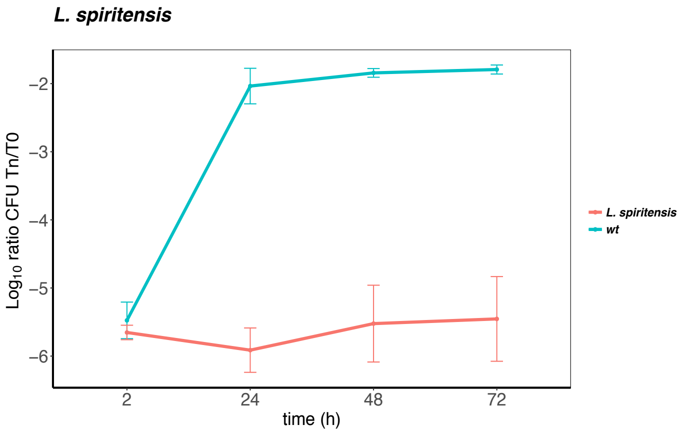


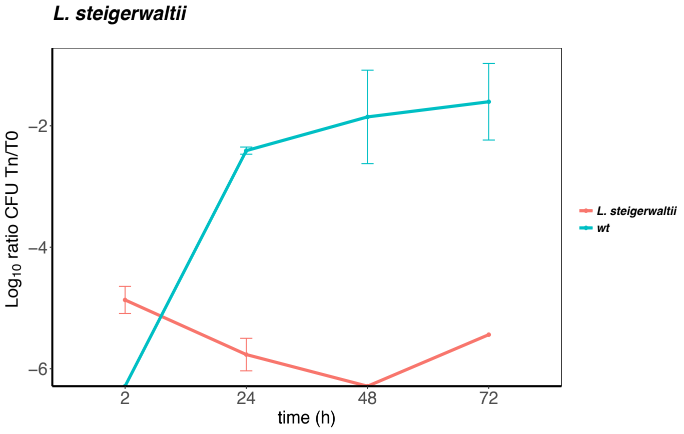
L. rubrilucens

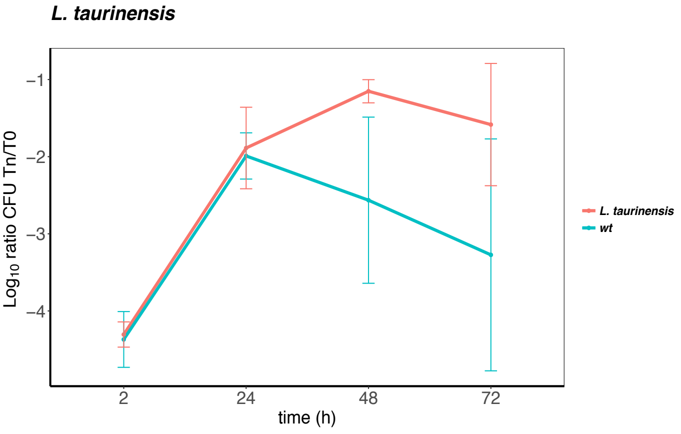

L. sainthelensis
Log$_{10}$ ratio CFU Tn/T0
−1
−2
−3
−4
−5
2
24
48
72
time (h)
L. sainthelensis
wt

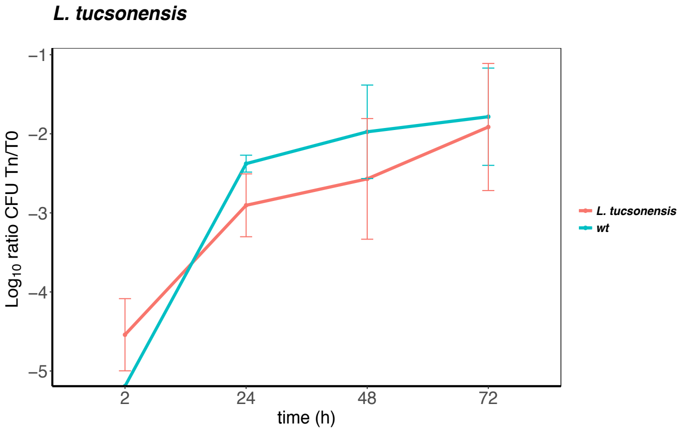

L. santicrucis
Log$_{10}$ ratio CFU Tn/T0
−1
−2
−3
−4
2
24
48
72
time (h)
L. santicrucis
wt


L. shakespearei
Log$_{10}$ ratio CFU Tn/T0
−2.0
−2.5
−3.0
−3.5
−4.0
2
24
48
72
time (h)
L. shakespearei
wt


L. spiritensis
Log$_{10}$ ratio CFU Tn/T0
−2
−3
−4
−5
−6
2
24
48
72
time (h)
L. spiritensis
wt


L. steigerwaltii
Log$_{10}$ ratio CFU Tn/T0
−2
−4
−6
2
24
48
72
time (h)
L. steigerwaltii
wt


L. taurinensis
Log$_{10}$ ratio CFU Tn/T0
−1
−2
−3
−4
2
24
48
72
time (h)
L. taurinensis
wt


L. tucsonensis
Log$_{10}$ ratio CFU Tn/T0
−1
−2
−3
−4
−5
2
24
48
72
time (h)
L. tucsonensis
wt

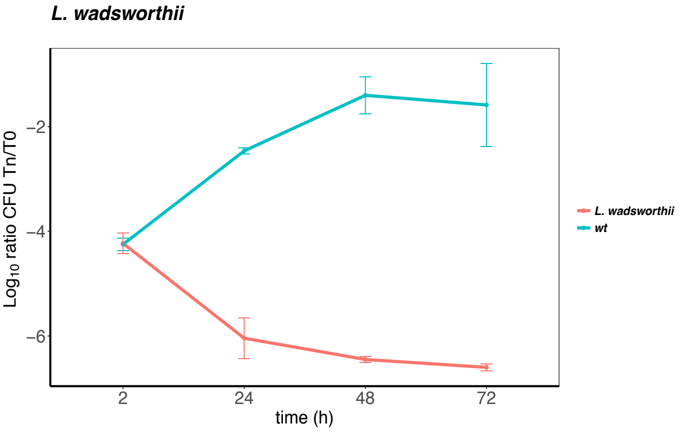
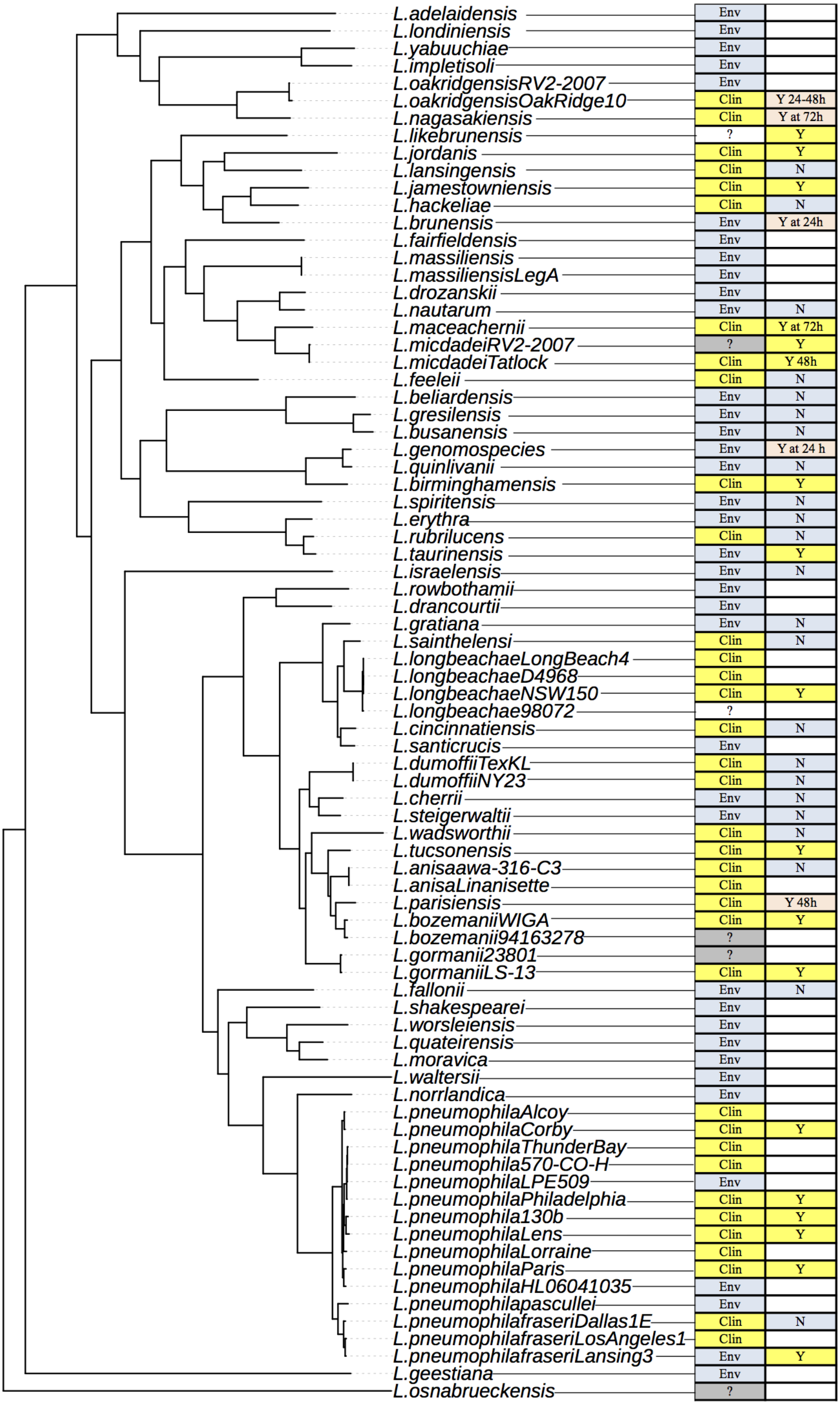

L. wadsworthii
Log$_{10}$ ratio CFU Tn/T0
−2
−4
−6
2
24
48
72
time (h)
L. wadsworthii
wt

Figure S14


L.adelaidensis Env
L.londiniensis Env
L.yabuuchiae Env
L.impletisoli Env
L.oakridgensisRV2-2007 Env
L.oakridgensisOakRidge10 Clin Y 24-48h
L.nagasakiensis Clin Y at 72h
L.likebrunensis ? Y
L.jordanis Clin Y
L.lansingensis Clin N
L.jamestowniensis Clin Y
L.hackeliae Clin N
L.brunensis Env Y at 24h
L.fairfieldensis Env
L.massiliensis Env
L.massiliensisLegA Env
L.drozanskii Env
L.nautarum Env N
L.maceachernii Clin Y at 72h
L.micdadeiRV2-2007 ? Y
L.micdadeiTatlock Clin Y 48h
L.feeleii Clin N
L.beliardensis Env N
L.gresilensis Env N
L.busanensis Env N
L.genomospecies Env Y at 24 h
L.quinlivanii Env N
L.birminghamensis Clin Y
L.spiritensis Env N
L.erythra Env N
L.rubrilucens Clin N
L.taurinensis Env Y
L.israelensis Env N
L.rowbothamii Env
L.drancourtii Env
L.gratiana Env N
L.sainthelensi Clin N
L.longbeachaeLongBeach4 Clin
L.longbeachaeD4968 Clin
L.longbeachaeNSW150 Clin Y
L.longbeachae98072 ?
L.cincinnatiensis Clin N
L.santicrucis Env
L.dumoffiiTexKL Clin N
L.dumoffiiNY23 Clin N
L.cherrii Env N
L.steigerwaltii Env N
L.wadsworthii Clin N
L.tucsonensis Clin Y
L.anisaawa-316-C3 Clin N
L.anisaLinanisette Clin
L.parisiensis Clin Y 48h
L.bozemaniiWIGA Clin Y
L.bozemanii94163278 ?
L.gormanii23801 ?
L.gormaniiLS-13 Clin Y
L.fallonii Env N
L.shakespearei Env
L.worsleiensis Env
L.quateirensis Env
L.moravica Env
L.waltersii Env
L.norrlandica Env
L.pneumophilaAlcoy Clin
L.pneumophilaCorby Clin Y
L.pneumophilaThunderBay Clin
L.pneumophila570-CO-H Clin
L.pneumophilaLPE509 Env
L.pneumophilaPhiladelphia Clin Y
L.pneumophila130b Clin Y
L.pneumophilaLens Clin Y
L.pneumophilaLorraine Clin
L.pneumophilaParis Clin Y
L.pneumophilaHL06041035 Env
L.pneumophilapascullei Env
L.pneumophilafraseriDallas1E Clin N
L.pneumophilafraseriLosAngeles1 Clin
L.pneumophilafraseriLansing3 Env Y
L.geestiana Env
L.osnabrueckensis ?