

SUPPLEMENTARY MATERIAL

Acquisition of a bacterial RumA-like tRNA(uracil-54, C5)-methyltransferase by archaea through an ancient horizontal gene transfer

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PAB0719      . . . . .
PAB0760      . . . . .
RumA         . . . . .
Trm2         1  MTGSTEMVPPTMKHTVDNKRLSPLTDSGNRRTKKPKLRKYKAKKVETTSPMGVLEFEVNDLLKSQNLRSREQVLNDVTSI
RumB         . . . . .
TrmA         . . . . .

PAB0719      1  . . . . .MRGVIRKLNDDGFVGLK. . . . .GILVPFSAPGDEIIVERVERVKRRVASQWKLV
PAB0760      1  . . . . .MRGIIKGVSNDGLGVLG. . . . .EVLVPFAYPGDVEVISTRERFGRTIARDFKLV
RumA         1  . . . . .MAQFYSAKRRTTTRQIITVSVNDLDSFQGVARHNGKTLFIPGLLPQENAEVTVTEDKKQYARAKVVRRL
Trm2         81 LNDKSSTDGPIVLQYHREVKNVLEITSNGNGLALIDNPVETEKQVVIIPFGLPGDVNIKVFKTHPYVESDLLDVV
RumB         . . . . .
TrmA         . . . . .

PAB0719      51  RSSPLRVG. . . . .PRCKAFGKCGGCTLQHLNYDYQLEEFKRKKLK. . . . .RILGFEVEVVPSPK. . . . .IFGHRNRID
PAB0760      51  KSSPIRVP. . . . .GKCRYFGRCGGCLWQGLKYREQLKKEEIFK. . . . .RVTGVEAEIKGSPR. . . . .IWFFRNISN
RumA         71  SDSPERET. . . . .PRCPHFGVCGGQQQHASVDLQRSKSAALA. . . . .RLMKHEVSEVIADV. . . . .PWGYRRRAR
Trm2         161 EKSPMRRDDLIRDKYFGKSSGSQLEFLTYDDQLELKRKTIMNAYKFFAPRLVAEKLLPPFDTTVASPL. . . . .QFGYRTKIT
RumB         1  MQCALYDA. . . . .GRCRSQWIMQPIPEQLSAKTADLKN. . . . .LLADFPVEEWCAPVSGPEQGFRNKAK
TrmA         1  .MTPEHLP. . . . .TEQYEAQLAEKVVRLQSMMAP. . . . .FSDLVPEVFRSPVS. . . . .HYRMRAE

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PAB0719      113 LAITKDG. . . . .IGFRERGKWWIVDIDECPVFGKTSREAIERLKEFEEKISVWNIKKDEGFLRYMVLREGK
PAB0760      113 FIVTNG. . . . .IGFKEFGMPRTVVSVDECPVFSERTKLYIRAMKRFLRETGLNPWNKNGD. . . . .VHYLQVREGK
RumA         133 LSLNYLP. . . . .KTQQLMGFRKAGSSDIVDVKQCPILVPQLEALLPKVRACLG. . . . .SLQAMRHLGHVELVQATSGTLMI
Trm2         238 PHFDMPKRKQKELSVRFPLGFGQKRPQWRKDTLDIGHGSILDIDECVLATEVLNKGLTNERRKFEQEFKYKKGATIL
RumB         61  MVVSGSVEKP. . . . .LGMLHRDGT. . . . .PEDLCDCPLYPASFAPVFALKPFIARAGLTPYNVARKRGELKYILLTESQ
TrmA         50  FRIWHDGDD. . . . .LYHIFDQQTKS. . . . .RIRVDSFPAASELINQLMTAMIAGVRNPVLRHKLFQIDYLTTTLSNQAVVS

                *

PAB0719      182 FTEEVMVNFVTKE. . . . .GNLPDPTNYYDF.DSIYWSVNRSKSDVSYGDIERFWGKE.FIRERLDDVDYLIHPNSFF
PAB0760      180 FTGEEVMINVIAHIP. . . . .PSGREELTEAFGFADSVYWSLKRDKRDDPKGIPTLIKGNE. . . . .FIRESIEGLVYLIHPSTFFF
RumA         205 LRHTAPLSSADRE. . . . .KLECFSHSEGL. . . . .DLYLAPDSEILETVSGEMFWYDSN. . . . .GIRLTFSPRDFI
Trm2         318 LRENTTILDPSKPT. . . . .LEQLEEASRDENGDISYVEVEDKNNVRLAKTCVTNPRQ. . . . .IVTEYVDGYTFNFSAGEFF
RumB         132 SDGGMLREFVLRSDTKLAQLRKALPWLHELQLPQKVITYNIQVPHMAIMEGETEIYLTEQALAERFNDVPLWIRPQSFF
TrmA         122 LLYHKKLDDEWRQ. . . . .EAEALRDALRAQNLNVHLIGRATKTKIELDQYIDER. . . . .LPEVAG. . . . .KEMIYRQVENSET

PAB0719      252 QTNSYQAVNLVRKVSELVEGEK. . . . .ILDMYSCVGTFGIYLAKRGFNVKCFDSNEFAIEMARRVVEINNVDAEFE
PAB0760      253 QTNSYALPILLKAVESFAEGSK. . . . .VLDLYSCVGTFSLYLAKKGFEVTGVEVNEESVRVAKKSAEVNSLDVSFI
RumA         265 QVNAGVNQMVARALEWLDVEPE. . . . .VLDLFCCMGNFTLPLATQAASVVGVEGVPALVEKQQNARLNGLQNVTF
Trm2         391 QTNNSILPIVTKYVRDNLQAPAKGDDNKTKFLVDAYCGSGLFSICSSKGVDKVIGVEISADSVFAEKNAKANGVENCRF
RumB         212 QTNPAVASQLYATARDWVRQLP. . . . .VKHMWDLFCGVGFLHCATPDMQLTGIEIASEAIACAKQSAAELGLTRLQF
TrmA         190 QPNAAMNIQMLEWALDVTKGSG. . . . .DLELYCGNESLALARNFDRVLATEIAKPSVAAQYNIAANHIDNVQI

PAB0719      323 VASDREVSVKGFDT. . . . .VIVDPPRACLHPRLVKRLNREKPGVIVVVSCNPETFARDVK. . . . .
PAB0760      324 PGRAEDAKLKGYET. . . . .LIVDPPRKGLKD.FSKRIAKEGPENLIVVSCNPSKFVLDYRNYL. . . . .
RumA         339 YHENLEEDVTKQPWAKNG. . . . .FDKVLLDPARAGAAG.VMQIIKLEPIRIVVSCNPATLARDSEALL. . . . .
Trm2         471 IVGKAEKLFESIDTPSE. . . . .NTSVILDPPRKGCDELFLKQLAAYNPAKIIYVSCNVHSQARDVEYFLKET
RumB         286 QALDSTQFATAQDVP. . . . .ELVLVNPPRRGIGKPLCDYLSTMAPRFIIYSSCNAQTMAKDIRELP. . . . .
TrmA         263 IRMAAEEFTQAMNGVREFNRLQIDLKSYQCETIFVDPPRSGLDS.ETEKMVQAYP. RILYISCNPETLCKNLETLS. . . . .

PAB0719      378 . . . . .MLDYRIDEIVALDMFPHTPHVELVAKLV. . . . .
PAB0760      381 . . . . .SKAYKIEDAVLIDMFPHTPHVEAVVKLRRR. . . . .
RumA         403 . . . . .KAGYTARLAMLDMFPHTGHLSMVLFSRVK
Trm2         538 ENGSAHQIESIRGFDFPQTHVEVSCIMKRI. . . . .
RumB         348 . . . . .GFRIERVQLFDMFPHTAYEVLTLLVKQ. . . . .
TrmA         338 . . . . .QTHKVERLALFDQEPYTHHEMCGVLLTAK. . . . .

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Figure S1: Sequence alignment of four characterized RNA(uracil,C5)- methyltransferases and the two orthologous PAB0719 and PAB0760 proteins from *Pyrococcus abyssi*. The alignment was performed using CLUSTALW (Thompson et al., 1994) and the figure was made using ESPring (Gouet et al., 1999). The sequences composed of the conserved catalytic motifs and the S-AdoMet binding region are underlined in green. The catalytic cysteine is highlighted in blue. The four cysteines coordinating an iron-sulfur cluster in RumA (Lee et al., 2004) are indicated by blue stars.

Figure S2: Table showing the taxonomic distribution of the genes coding for the S-AdoMet-dependent RNA(uracil,C5)-methyltransferases (RumA,RumB,TrmA and Trm2) in 410 bacterial, archaeal and eukaryotic complete genomes. Asterisks indicate the presence and the number of putative genes detected the genome of each organism. The domain organization of the corresponding proteins is provided: TRAM indicated presence of a TRAM domain, the regular expressions including cysteines indicates the presence of motifs that may form a characteristic iron-sulfur cluster [4Fe-4S] and Mtase indicates the presence of a tRNA (uracil, C5)-methyltransferases.

Genomes	RumA				RumB				TrmA				Trm2				
	Nb copies	Domain organisation			Nb copies	Domain organisation			Nb copies	Domain organisation			Nb copies	Domain organisation			
		TRAM	Fe4S4	Mtase		TRAM	Fe4S4	Mtase		TRAM	Fe4S4	Mtase		TRAM	Fe4S4	Mtase	
<i>Polaromonas JS666</i>	*	TRAM	C-X(9)-C-X(2)-C	Mtase													
<i>Ralstonia eutropha_JMP134</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Ralstonia metallidurans_CH34</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Ralstonia solanacearum</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Rhodoferax ferrireducens_T118</i>	*	TRAM	C-X(9)-C-X(2)-C	Mtase													
<i>Thiobacillus denitrificans_ATCC_25259</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
Deltaproteobacteria																	
<i>Anaeromyxobacter dehalogenans_2CP_C</i>	*	TRAM	C-X(12)-C-X(2)-C	Mtase													
<i>Bdellovibrio bacteriovorus</i>	**	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Desulfotalea psychrophila_LSV54</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Desulfovibrio desulfuricans_G20</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Desulfovibrio vulgaris_Hildenborough</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Geobacter metallireducens_GS_15</i>	**	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Geobacter sulfurreducens</i>	**	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Lawsonia intracellularis_PHE_MN1_00</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Myxococcus xanthus_DK_1622</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Pelobacter carbinolicus</i>	**	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Syntrophus aciditrophicus_SB</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
Epsilonproteobacteria																	
<i>Campylobacter jejuni</i>									*	No motif		Mtase					
<i>Campylobacter jejuni_RM1221</i>									*	No motif		Mtase					
<i>Helicobacter acinonychis_Sheebea</i>																	
<i>Helicobacter hepaticus</i>									*	C-X(5,7)-C-X(2)-C		Mtase					
<i>Helicobacter pylori_26695</i>																	
<i>Helicobacter pylori_HPAG1</i>																	
<i>Helicobacter pylori_J99</i>																	
<i>Thiomicrospira denitrificans_ATCC_33889</i>									*	C-X(5,7)-C-X(2)-C		Mtase					
<i>Wolinella succinogenes</i>									*	C-X(5,7)-C-X(2)-C		Mtase					
Gammaproteobacteria																	
<i>Acinetobacter sp_ADP1</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Baumannia cicadellinicola_Homalodisca_c</i>																	
<i>Buchnera aphidicola str. APS</i>																	
<i>Buchnera aphidicola str. Bp</i>																	
<i>Buchnera aphidicola str. Sg</i>																	
<i>Candidatus Blochmannia floridae</i>																	
<i>Candidatus Blochmannia pennsylvanicus_B</i>																	
<i>Chromohalobacter salexigens_DSM_3043</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Colwellia psychrelythraea_34H</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Coxiella burnetii</i>																	
<i>Erwinia carotovora_atroseptica_SCR11043</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Escherichia coli_CFT073</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Escherichia coli_K12</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Escherichia coli_O157H7</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Escherichia coli_O157H7_EDL933</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Escherichia coli_UTI89</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Francisella tularensis_holarctica</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Francisella tularensis_tularensis</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Haemophilus ducreyi_35000HP</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Haemophilus influenzae</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Haemophilus influenzae_86_028NP</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Hahella chejuensis_KCTC_2396</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Idiomarina loihiensis_L2TR</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Legionella pneumophila_Lens</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Legionella pneumophila_Paris</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Legionella pneumophila_Philadelphia_1</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Mannheimia succiniciproducens_MBEL55E</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Methylococcus capsulatus_Bath</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Nitrosococcus oceani_ATCC_19707</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase													
<i>Pasteurella multocida</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Photobacterium profundum_SS9</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Photorhabdus luminescens</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase	*	C-X(5,7)-C-X(2)-C	Mtase	Mtase	*	No motif		Mtase					
<i>Pseudoalteromonas atlantica_T6c</i>									*	No motif		Mtase					
<i>Pseudoalteromonas haloplanktis_TAC125</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Pseudomonas aeruginosa</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Pseudomonas entomophila_L48</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Pseudomonas fluorescens_Pf_5</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Pseudomonas fluorescens_Pro_1</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Pseudomonas putida_KT2440</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					
<i>Pseudomonas syringae_phaseolicola_1448A</i>	*	TRAM	C-X(5,7)-C-X(2)-C	Mtase					*	No motif		Mtase					

Genomes

Eukaryotes

Alveolata

Cryptosporidium hominis
Cryptosporidium parvum
Toxoplasma gondii

Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium
Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporidiidae; Cryptosporidium
Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma

Plasmodium berghei

Alveolata; Apicomplexa; Haemosporida; Plasmodium

Plasmodium chabaudi

Alveolata; Apicomplexa; Haemosporida; Plasmodium

Plasmodium falciparum

Alveolata; Apicomplexa; Haemosporida; Plasmodium

Plasmodium yoelii

Alveolata; Apicomplexa; Haemosporida; Plasmodium

Diplomonadida

Giardia lamblia

Diplomonadida group; Diplomonadida; Hexamitidae; Giardiinae; Giardia

Euglenozoa

Leishmania major
Trypanosoma brucei
Trypanosoma cruzi

Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania; Leishmania; Leishmania major species complex
Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Trypanozoon
Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Trypanozoon

Fungi

Aspergillus nidulans
Aspergillus oryzae
Coccidioides immitis
Magnaporthe grisea
Neurospora crassa
Yarrowia lipolytica
Candida albicans
Candida glabrata
Debaryomyces hansenii
Ashbya gossypii
Kluyveromyces lactis
Saccharomyces cerevisiae
Schizosaccharomyces pombe
Cryptococcus neoformans
Ustilago maydis
Encephalitozoon cuniculi

Fungi/Metazoa group; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
Fungi/Metazoa group; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
Fungi/Metazoa group; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides
Fungi/Metazoa group; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe
Fungi/Metazoa group; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora
Fungi/Metazoa group; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia
Fungi/Metazoa group; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida
Fungi/Metazoa group; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida
Fungi/Metazoa group; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces
Fungi/Metazoa group; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Eremothecium
Fungi/Metazoa group; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces
Fungi/Metazoa group; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces
Fungi/Metazoa group; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces
Fungi/Metazoa group; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella
Fungi/Metazoa group; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago
Fungi/Metazoa group; Fungi; Microsporidia; Apansporoblastina; Unikaryonidae; Encephalitozoon

Metazoa

Danio rerio
Tetraodon nigroviridis
Mus musculus
Rattus norvegicus
Canis familiaris
Homo sapiens
Strongylocentrotus purpuratus
Drosophila melanogaster
Drosophila pseudoobscura
Anopheles gambiae
Aedes aegypti
Apis mellifera
Caenorhabditis elegans

Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Teleostei; Cyprinidae
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Teleostei; Tetraodontidae
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Gnathostomata; Tetrapoda; Mammalia; Theria; Eutheria; Murinae
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Gnathostomata; Tetrapoda; Mammalia; Theria; Eutheria; Murinae
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Gnathostomata; Tetrapoda; Mammalia; Theria; Eutheria; Carnivora; Canidae
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Gnathostomata; Tetrapoda; Mammalia; Theria; Eutheria; Primates; Hominidae; Homo
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Echinodermata; Strongylocentrotidae
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Arthropoda; Insecta; Diptera; Drosophila
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Arthropoda; Insecta; Diptera; Drosophila
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Arthropoda; Insecta; Diptera; Anopheles
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Arthropoda; Insecta; Diptera; Culicidae
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Coelomata; Protostomia; Arthropoda; Insecta; Hymenoptera
Fungi/Metazoa group; Metazoa; Eumetazoa; Bilateria; Pseudocoelomata; Nematoda; Chromadorea; Rhabdiida; Rhabditidae; Caenorhabditis

Conosa

Entamoeba histolytica
Dictyostelium discoideum

Entamoebidae; Entamoeba
Mycetozoa; Dictyostelida; Dictyostelium

Viriplantae

Ostreococcus tauri
Arabidopsis thaliana
Oryza sativa

Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales; Mamiellaceae; Ostreococcus
Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Brassicaceae
Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Liliopsida; Oryzaeae

Archaea

Crenarchaea

Aeropyrum pernix_K1
Cenarchaeum symbiosum
Pyrobaculum aerophilum_str_IM2
Sulfolobus acidocaldarius_DSM_639
Sulfolobus solfataricus

Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcaceae
Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae
Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae
Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae
Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae

Genomes

Sulfolobus tokodaii

Euryarchaea

Archaeoglobus fulgidus
*Haloarcula marismortui*_ATCC_43049
Halobacterium sp
Haloquadratum walsbyi
Methanobacterium thermoautotrophicum
*Methanococcoides burtonii*_DSM_6242
Methanococcus jannaschii
*Methanococcus maripaludis*_S2
Methanopyrus kandleri
Methanosarcina acetivorans
Methanosarcina barkeri_fusaro
Methanosarcina mazei
Methanosphaera stadtmanae
*Methanospirillum hungatei*_JF_1
Natronomonas pharaonis
*Picrophilus torridus*_DSM_9790
Pyrococcus abyssi
Pyrococcus furiosus
Pyrococcus horikoshii
*Thermococcus kodakaraensis*_KOD1
Thermoplasma acidophilum
Thermoplasma volcanium

Nanoarchaea

Nanoarchaeum equitans

Bacteria

Acidobacteria

Acidobacteria bacterium_Ellin345

Actinobacteria

Bifidobacterium longum
Corynebacterium diphtheriae
*Corynebacterium efficiens*_YS_314
*Corynebacterium glutamicum*_ATCC_13032_K
*Corynebacterium glutamicum*_ATCC_13032_K
*Corynebacterium jeikeium*_K411
Frankia CcI3
Leifsonia xyl_i_xyl_i_CTCBC
Mycobacterium avium
Mycobacterium bovis
Mycobacterium leprae
Mycobacterium MCS
*Mycobacterium tuberculosis*_CDC1551
*Mycobacterium tuberculosis*_H37Rv
*Nocardia farcinica*_IFM10152
*Propionibacterium acnes*_KPA171202
*Rubrobacter xylanophilus*_DSM_9941
Streptomyces avermitilis
Streptomyces coelicolor
*Thermobifida fusca*_YX
*Tropheryma whippelii*_TW08_27
*Tropheryma whippelii*_Twist

Aquificae

Aquifex aeolicus

Green non sulfur/Flavobacteria/Bacteroides:

*Bacteroides fragilis*_NCTC_9434
*Bacteroides fragilis*_YCH46
*Bacteroides thetaiotaomicron*_VPI_5482
*Chlorobium chlorochromatii*_CaD3
*Chlorobium tepidum*_TLS
*Pelodictyon luteolum*_DSM_273
*Porphyromonas gingivalis*_W83
*Salinibacter ruber*_DSM_13855

PVC group

Chlamydia muridarum
Chlamydia trachomatis
*Chlamydia trachomatis*_A_HAR_13

Taxonomic position

Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae

Euryarchaeota; Archaeoglobi; Archaeoglobales; Archaeoglobaceae
Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Haloarcula
Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Haloarcula
Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Haloquadra
Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae
Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae
Euryarchaeota; Methanococci; Methanococcales; Methanococcaceae
Euryarchaeota; Methanococci; Methanococcales; Methanococcaceae
Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae
Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae
Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae
Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae
Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae
Euryarchaeota; Methanomicrobia; Methanomicrobiales; Methanospirillaceae
Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Natronomonas
Euryarchaeota; Thermoplasmata; Thermoplasmatales; Picrophilaceae
Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae
Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae
Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae
Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae
Euryarchaeota; Thermoplasmata; Thermoplasmatales; Thermoplasmataceae
Euryarchaeota; Thermoplasmata; Thermoplasmatales; Thermoplasmataceae

Nanoarchaeota

Fibrobacteres/Acidobacteria group

Actinobacteria; Actinobacteria (class); Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Frankineae; Frankiaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Micrococcineae; Microbacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Streptosporangineae; Nocardiosaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae
Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae

Aquificae; Aquificae (class); Aquificales; Aquificaceae

Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Bacteroidaceae
Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Bacteroidaceae
Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Bacteroidaceae
Bacteroidetes/Chlorobi group; Chlorobi; Chlorobiales; Chlorobiaceae; Chlorobium/Pelodictyon group
Bacteroidetes/Chlorobi group; Chlorobi; Chlorobiales; Chlorobiaceae; Chlorobium/Pelodictyon group
Bacteroidetes/Chlorobi group; Chlorobi; Chlorobiales; Chlorobiaceae; Chlorobium/Pelodictyon group
Bacteroidetes/Chlorobi group; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Porphyromonadaceae
Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteria; Sphingobacteriales; Crenotrichaceae

Chlamydiae/Verrucomicrobia group; Chlamydiae; Chlamydiae (class); Chlamydiales; Chlamydiaceae
Chlamydiae/Verrucomicrobia group; Chlamydiae; Chlamydiae (class); Chlamydiales; Chlamydiaceae
Chlamydiae/Verrucomicrobia group; Chlamydiae; Chlamydiae (class); Chlamydiales; Chlamydiaceae

Genomes

Fusobacteria

Fusobacterium nucleatum

Alphaproteobacteria

Agrobacterium tumefaciens_C58_Cereon
Agrobacterium tumefaciens_C58_UWash
Anaplasma marginale_St_Maries
Anaplasma phagocytophilum_HZ
Bartonella henselae_Houston_1
Bartonella quintana_Toulouse
Bradyrhizobium japonicum
Brucella abortus_9_941
Brucella melitensis
Brucella melitensis_biovar_Abortus
Brucella suis_1330
Candidatus Pelagibacter_ubique_HTCC1062
Caulobacter crescentus
Ehrlichia canis_Jake
Ehrlichia chaffeensis_Arkansas
Ehrlichia ruminantium_Gardel
Ehrlichia ruminantium_str._Welgevonden
Ehrlichia ruminantium_Welgevonden
Erythrobacter litoralis_HTCC2594
Gluconobacter oxydans_621H
Jannaschia CCS1
Magnetospirillum magneticum_AMB_1
Mesorhizobium loti
Neorickettsia sennetsu_Miyayama
Nitrobacter hamburgensis_X14
Nitrobacter winogradskyi_Nb_255
Novosphingobium aromaticivorans_DSM_124
Rhizobium etli_CFN_42
Rhodobacter sphaeroides_2_4_1
Rhodopseudomonas palustris_BisB18
Rhodopseudomonas palustris_BisB5
Rhodopseudomonas palustris_CGA009
Rhodopseudomonas palustris_HaA2
Rhodospirillum rubrum_ATCC_11170
Rickettsia bellii_RML369_C
Rickettsia conorii
Rickettsia felis_URRWXCa2
Rickettsia prowazekii
Rickettsia typhi_wilmington
Silicibacter pomeroyi_DSS3
Silicibacter TM1040
Sinorhizobium melilot
Sphingopyxis alaskensis_RB2256
Wolbachia endosymbiont_of_Brugia_malayi
Wolbachia endosymbiont_of_Drosophila_mel
Zymomonas mobilis_ZM4

Betaproteobacteria

Azoarcus sp_EbN1
Bordetella bronchiseptica
Bordetella parapertussis
Bordetella pertussis
Burkholderia 383
Burkholderia cenocepacia_AU_1054
Burkholderia mallei_ATCC_23344
Burkholderia pseudomallei_1710b
Burkholderia pseudomallei_K96243
Burkholderia thailandensis_E264
Burkholderia xenovorans_LB400
Chromobacterium violaceum
Dechloromonas aromatica_RCB
Methylobacillus flagellatus_KT
Neisseria gonorrhoeae_FA_1090
Neisseria meningitidis_MC58
Neisseria meningitidis_Z2491
Nitrosomonas europaea
Nitrospira multiformis_ATCC_25196

Taxonomic position

Fusobacteria; *Fusobacteria* (class); *Fusobacterales*; *Fusobacteriaceae*

Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Rhizobiaceae*; *Rhizobium/Agrobacterium group*; *Agrobacterium*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Rhizobiaceae*; *Rhizobium/Agrobacterium group*; *Agrobacterium*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bartonellaceae*; *Bartonella*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bartonellaceae*; *Bartonella*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bradyrhizobiaceae*; *Bradyrhizobium*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Brucellaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Brucellaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Brucellaceae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *SAR11 cluster*
Proteobacteria; *Alphaproteobacteria*; *Caulobacterales*; *Caulobacteraceae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*; *Ehrlichia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*; *Ehrlichia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*; *Ehrlichia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*; *Ehrlichia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*; *Ehrlichia*
Proteobacteria; *Alphaproteobacteria*; *Sphingomonadales*; *Erythrobacteraceae*
Proteobacteria; *Alphaproteobacteria*; *Rhodospirillales*; *Acetobacteraceae*
Proteobacteria; *Alphaproteobacteria*; *Rhodobacteriales*; *Rhodobacteraceae*
Proteobacteria; *Alphaproteobacteria*; *Rhodospirillales*; *Rhodospirillaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Phyllobacteriaceae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bradyrhizobiaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bradyrhizobiaceae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Sphingomonadales*; *Sphingomonadaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Rhizobiaceae*; *Rhizobium/Agrobacterium group*
Proteobacteria; *Alphaproteobacteria*; *Rhodobacteriales*; *Rhodobacteraceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bradyrhizobiaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bradyrhizobiaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bradyrhizobiaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Bradyrhizobiaceae*
Proteobacteria; *Alphaproteobacteria*; *Rhodospirillales*; *Rhodospirillaceae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsiae*; *Rickettsia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsiae*; *Rickettsia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsiae*; *Rickettsia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsiae*; *Rickettsia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsiae*; *Rickettsia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsiae*; *Rickettsia*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Rickettsiae*; *Rickettsia*
Proteobacteria; *Alphaproteobacteria*; *Rhodobacteriales*; *Rhodobacteraceae*
Proteobacteria; *Alphaproteobacteria*; *Rhodobacteriales*; *Rhodobacteraceae*
Proteobacteria; *Alphaproteobacteria*; *Rhizobiales*; *Rhizobiaceae*; *Sinorhizobium/Ensifer group*
Proteobacteria; *Alphaproteobacteria*; *Sphingomonadales*; *Sphingomonadaceae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Wolbachiae*
Proteobacteria; *Alphaproteobacteria*; *Rickettsiales*; *Rickettsiaceae*; *Wolbachiae*
Proteobacteria; *Alphaproteobacteria*; *Sphingomonadales*; *Sphingomonadaceae*; *Zymomonas*

Proteobacteria; *Betaproteobacteria*; *Rhodocyclales*; *Rhodocyclaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Alcaligenaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Alcaligenaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Alcaligenaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Burkholderiales*; *Burkholderiaceae*
Proteobacteria; *Betaproteobacteria*; *Neisseriales*; *Neisseriaceae*; *Chromobacterium group*
Proteobacteria; *Betaproteobacteria*; *Rhodocyclales*; *Rhodocyclaceae*
Proteobacteria; *Betaproteobacteria*; *Methylophilales*; *Methylophilaceae*
Proteobacteria; *Betaproteobacteria*; *Neisseriales*; *Neisseriaceae*; *Neisseria*
Proteobacteria; *Betaproteobacteria*; *Neisseriales*; *Neisseriaceae*; *Neisseria*
Proteobacteria; *Betaproteobacteria*; *Neisseriales*; *Neisseriaceae*; *Neisseria*
Proteobacteria; *Betaproteobacteria*; *Nitrosomonadales*; *Nitrosomonadaceae*
Proteobacteria; *Betaproteobacteria*; *Nitrosomonadales*; *Nitrosomonadaceae*

Genomes

Pseudomonas syringae_pv_B728a
Pseudomonas syringae_tomato_DC3000
Psychrobacter arcticum_273_4
Psychrobacter cryohalolentis_K5
Saccharophagus degradans_2_40
Salmonella enterica_Choleraesuis
Salmonella enterica_Paratypi_ATCC_9150
Salmonella typhi
Salmonella typhi_Ty2
Salmonella typhimurium_LT2
Shewanella denitrificans_OS217
Shewanella oneidensis
Shigella boydii_Sb227
Shigella dysenteriae
Shigella flexneri_2a
Shigella flexneri_2a_2457T
Shigella sonnei_Ss046
Sodalis glossinidius_morsitans
Thiomicrospira crunogena_XCL_2
Vibrio cholerae
Vibrio fischeri_ES114
Vibrio parahaemolyticus
Vibrio vulnificus_CMCP6
Vibrio vulnificus_YJ016
Wigglesworthia brevipalpis
Xanthomonas axonopodis pv citri
Xanthomonas campestris str. ATCC 33913
Xanthomonas campestris_8004
Xanthomonas campestris_vesicatoria_851
Xanthomonas oryzae_KACC10331
Xanthomonas oryzae_MAFF_311018
Xylella fastidiosa
Xylella fastidiosa_Temecula1
Yersinia pestis_Antiqua
Yersinia pestis_biovvar_Mediaevails
Yersinia pestis_CO92
Yersinia pestis_KIM
Yersinia pestis_Nepal516
Yersinia pseudotuberculosis_IP32953

Spirochaetes

Borrelia burgdorferi
Borrelia garinii_PBI
Leptospira interrogans_serovar_Copenhagen
Leptospira interrogans_serovar_Lai
Treponema denticola_ATCC_35405
Treponema pallidum

Thermotogae

Thermotoga maritima

Taxonomic position

Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae
Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae
Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae
Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae
Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Saccharophagus
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae
Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Thiotrichales; Piscirickettsiaceae
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae
Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas
Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae
Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae

Spirochaetes; Spirochaetes (class); Spirochaetales; Spirochaetaceae
Spirochaetes; Spirochaetes (class); Spirochaetales; Spirochaetaceae
Spirochaetes; Spirochaetes (class); Spirochaetales; Leptospiraceae
Spirochaetes; Spirochaetes (class); Spirochaetales; Leptospiraceae
Spirochaetes; Spirochaetes (class); Spirochaetales; Spirochaetaceae
Spirochaetes; Spirochaetes (class); Spirochaetales; Spirochaetaceae

Thermotogae; Thermotogae (class); Thermotogales; Thermotogaceae

Figure S3: Maximum likelihood phylogeny of the 456 members of the S-AdoMet-dependent RNA(uracil,C5)-methyltransferases (RumA, RumB, TrmA and Trm2) detected in 410 complete genomes. 123 unambiguously aligned positions were kept for the phylogenetic analysis. The tree was computed using PHYML with a JTT model including a gamma correction (see Materials and Methods for more details). ML trees provide using other evolutionary models provide similar topologies (not shown). The type (RumA, RumB, TrmA, Trm2) and the domain organization of the corresponding proteins is provided (see Figure S2 for more details). Numbers at nodes represent bootstrap values computed by PHYML (see Materials and Methods). The scale bar represents the average number of substitutions per position. The tree was drawing with the treedyn software (Chevenet *et al.*, 2006).

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