Supplementary Material for:

Multidomain ribosomal protein trees and the planctobacterial origin of neomura (eukaryotes, archaebacteria)

Thomas Cavalier-Smith and Ema E-Yung Chao

Figure S1. Site-heterogeneous PhyloBayes GTR-CAT (4 gamma rates) tree for 26 ribosomal proteins from 143 eukaryotes representing all the most divergent lineages.
Alignment of 4156 amino acids; the number included for each taxon is shown after the @. Support values are posterior probabilities. 105,136 trees were summed after removing the first 20% as burnin: maxdiff 0.29708. The tree is rooted between Eozoa and neokaryotes

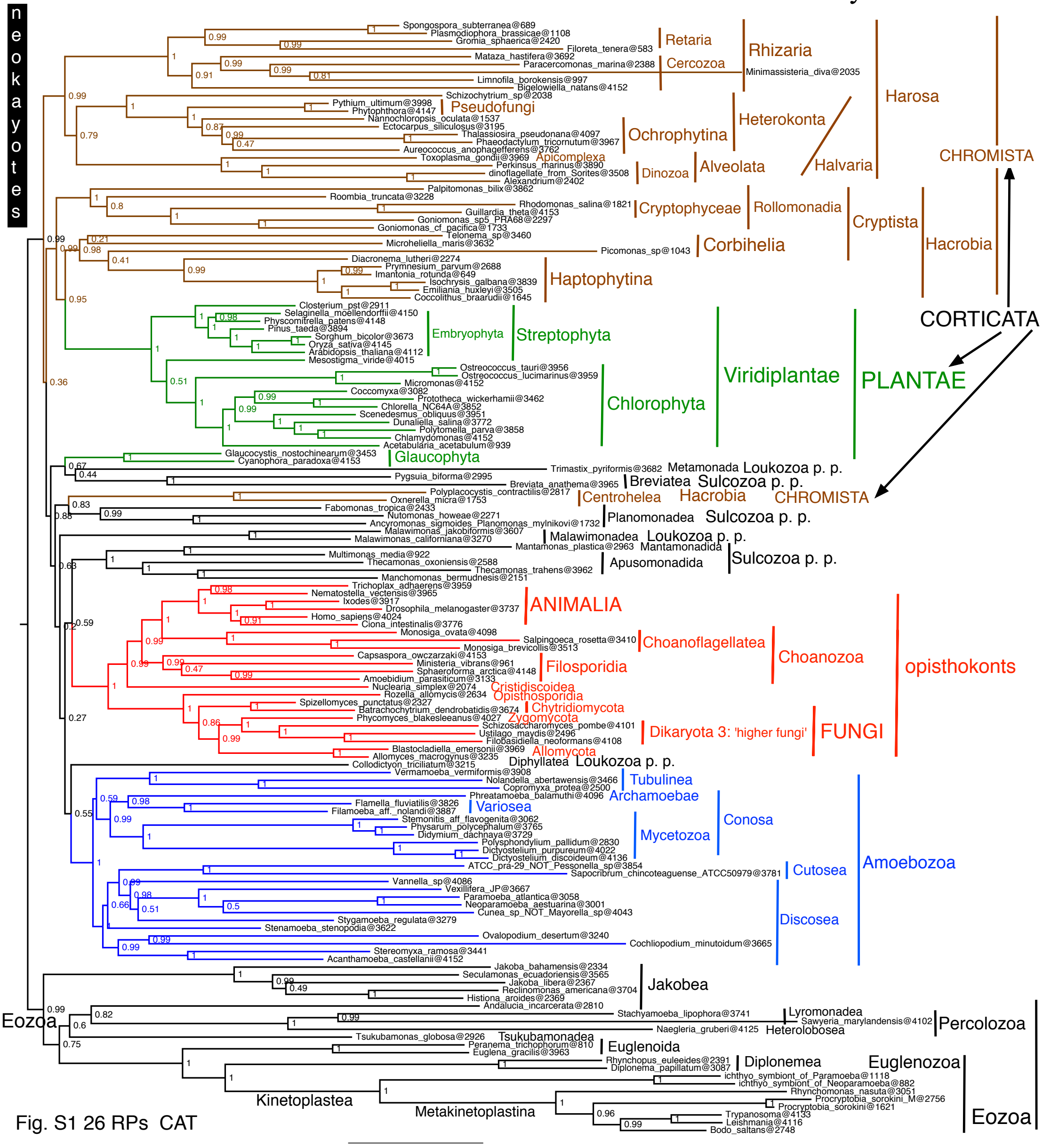


Fig. S1 26 RPs CAT

Fig. S2. Site-homogeneous RAxML PROTGAMMALGF (4 gamma rates) tree for 26 ribosomal proteins from 151 eukaryotes representing all the most divergent lineages.
Alignment of 4156 amino acids; the number included for each taxon is shown after the @. The tree is rooted between Eozoa and neokaryotes. Support values are percentages for 100 pseudoreplicates.

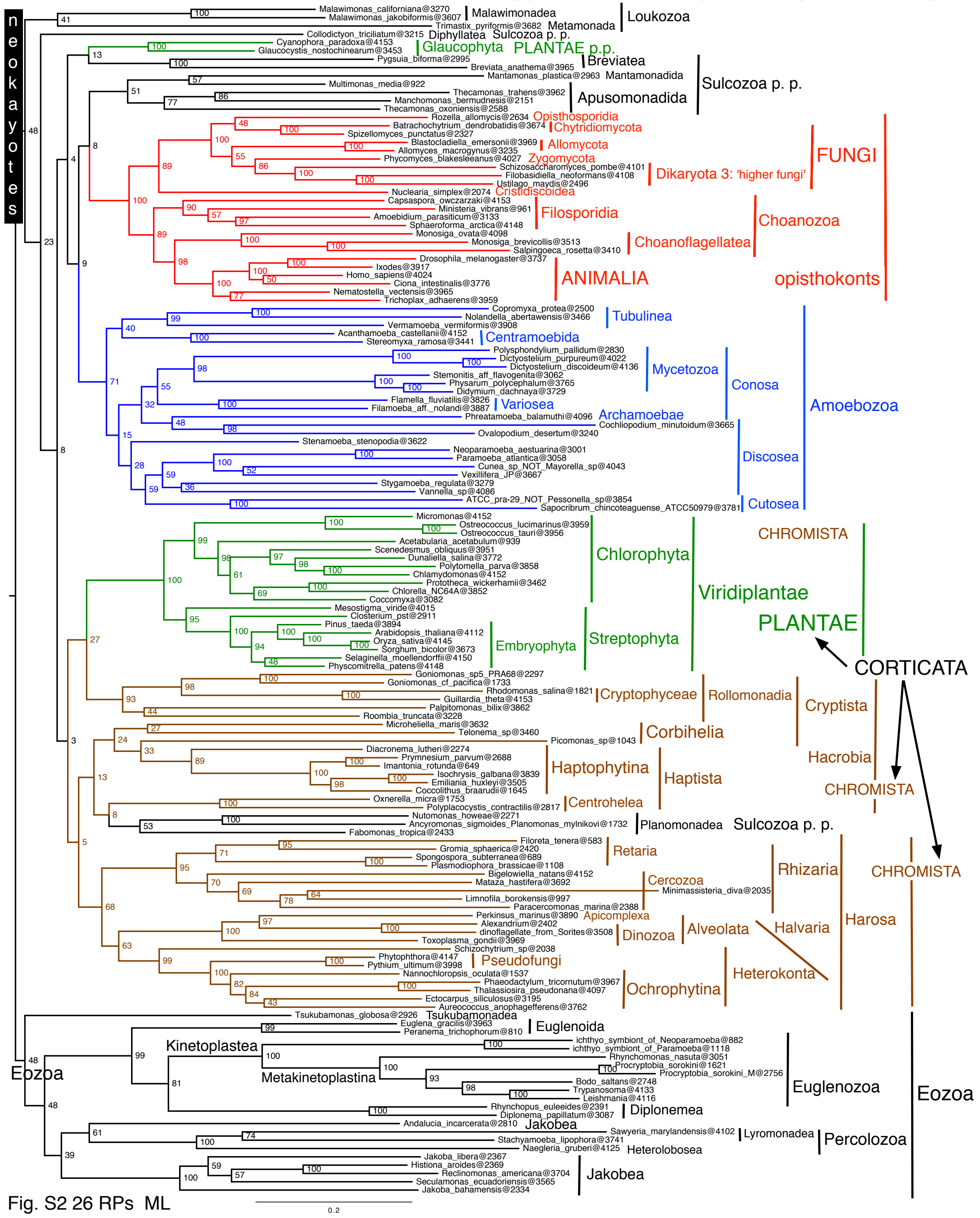
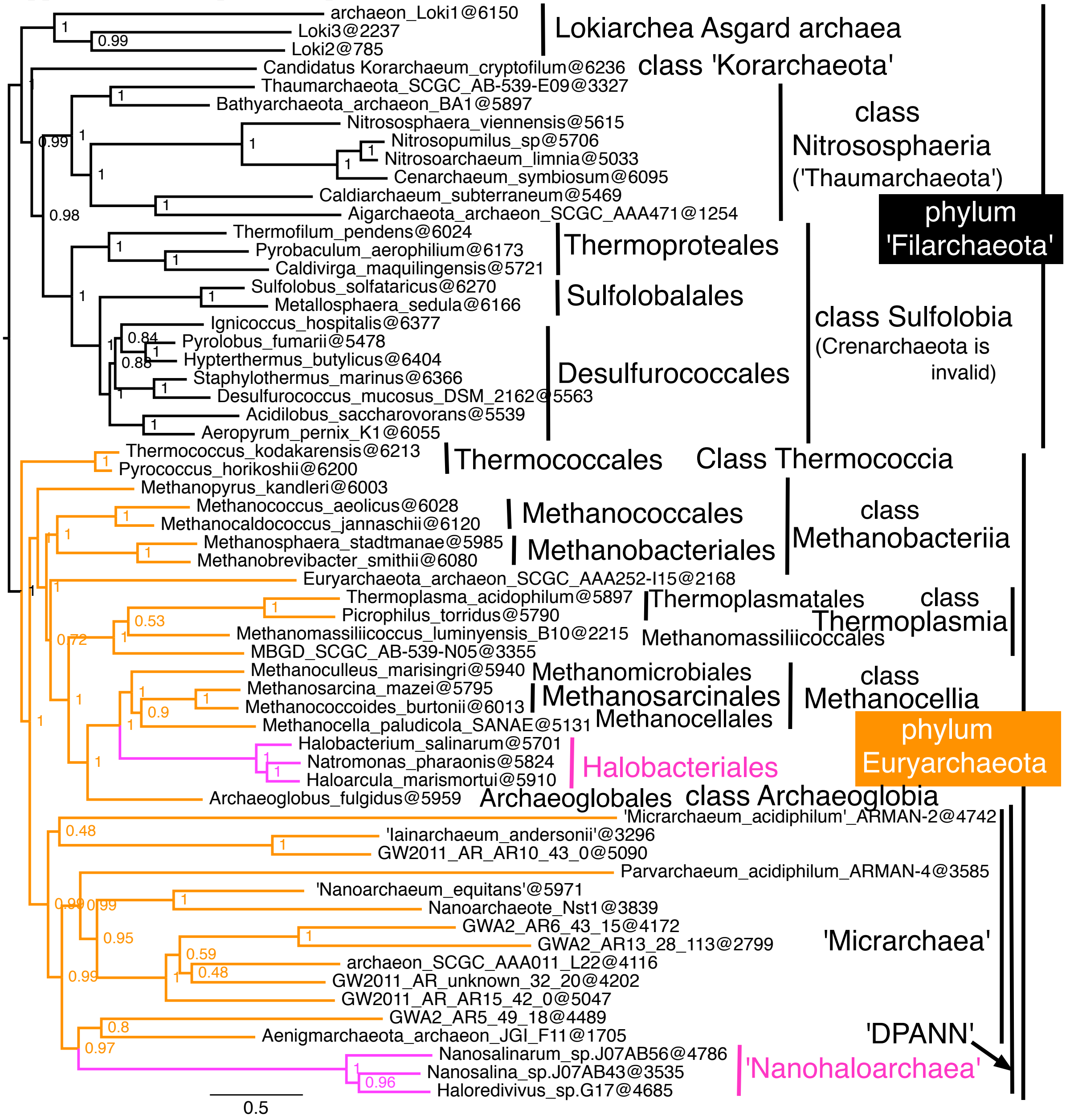


Fig. S2 26 RPs ML

Figure S3. Site-heterogeneous PhyloBayes GTR-CAT (4 gamma rates) tree for 51 ribosomal proteins from 60 archaebacteria representing all the most divergent lineages.
This is chain 2 which placed 'Nanohaloarchaea' in a different position from chain 1 (see Fig. 4). (49, 886 trees summed after removing 40% as burnin).
Support values are posterior probabilities.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Loki3@2237
Loki2@785
1
0.99
Lokiarchea Asgard archaea
Candidatus Korarchaeum_cryptofilum@6236
class 'Korarchaeota'
Thaumarchaeota_SCGC_AB-539-E09@3327
Bathyarchaeota_archaeon_BA1@5897
Nitrososphaera_viennensis@5615
Nitrosopumilus_sp@5706
Nitrosoarchaeum_limnia@5033
Cenarchaeum_symbiosum@6095
Caldiarchaeum_subterraneum@5469
Aigarchaeota_archaeon_SCGC_AAA471@1254
0.99
0.98
1
class
Nitrososphaeria
('Thaumarchaeota')
phylum
'Filarchaeota'
Thermofilum_pendens@6024
Pyrobaculum_aerophilium@6173
Caldivirga_maquilingensis@5721
Thermoproteales
Sulfolobus_solfataricus@6270
Metallosphaera_sedula@6166
Sulfolobales
Ignicoccus_hospitalis@6377
Pyrolobus_fumarii@5478
Hypterthermus_butylicus@6404
Staphylothermus_marinus@6366
Desulfurococcus_mucosus_DSM_2162@5563
Acidilobus_saccharovorans@5539
Aeropyrum_pernix_K1@6055
0.84
0.88
Desulfurococcales
class Sulfolobia
(Crenarchaeota is
invalid)
Thermococcus_kodakarensis@6213
Pyrococcus_horikoshii@6200
Thermococcales
Class Thermococcia
Methanopyrus_kandleri@6003
Methanococcus_aeolicus@6028
Methanocaldococcus_jannaschii@6120
Methanococcales
Methanosphaera_stadtmanae@5985
Methanobrevibacter_smithii@6080
Methanobacteriales
class
Methanobacteriia
Euryarchaeota_archaeon_SCGC_AAA252-I15@2168
Thermoplasma_acidophilum@5897
Picrophilus_torridus@5790
Thermoplasmatales
Methanomassiliicoccus_luminyensis_B10@2215
MBGD_SCGC_AB-539-N05@3355
Methanomassiliicoccales
class
Thermoplasmia
0.53
0.72
Methanoculleus_marisingri@5940
Methanosarcina_mazei@5795
Methanococcoides_burtonii@6013
Methanocella_paludicola_SANAE@5131
0.9
Methanomicrobiales
Methanosarcinales
Methanocellales
class
Methanocellia
phylum
Euryarchaeota
Halobacterium_salinarum@5701
Natromonas_pharaonis@5824
Haloarcula_marismortui@5910
Halobacteriales
Archaeoglobus_fulgidus@5959
Archaeoglobales
class Archaeoglobia
'Micrarchaeum_acidiphilum'_ARMAN-2@4742
'lainarchaeum_andersonii'@3296
GW2011_AR_AR10_43_0@5090
0.48
Parvarchaeum_acidiphilum_ARMAN-4@3585
'Nanoarchaeum_equitans'@5971
Nanoarchaeote_Nst1@3839
GWA2_AR6_43_15@4172
GWA2_AR13_28_113@2799
archaeon_SCGC_AAA011_L22@4116
GW2011_AR_unknown_32_20@4202
GW2011_AR_AR15_42_0@5047
0.99
0.99
0.95
0.59
0.48
0.99
'Micrarchaea'
GWA2_AR5_49_18@4489
Aenigmarchaeota_archaeon_JGI_F11@1705
0.8
0.97
'DPANN'
Nanosalinarum_sp.J07AB56@4786
Nanosalina_sp.J07AB43@3535
Haloredivivus_sp.G17@4685
0.96
'Nanohaloarchaea'
0.5

Figure S4. Site-heterogeneous PhyloBayes GTR-CAT (4 gamma rates) tree for 26 ribosomal proteins from 60 archaebacteria representing all the most divergent lineages. Support values are posterior probabilities. after removing 40% of the trees as burnin the remaining 55,580 trees from two chains were summed: maxdiff 0.0669948.

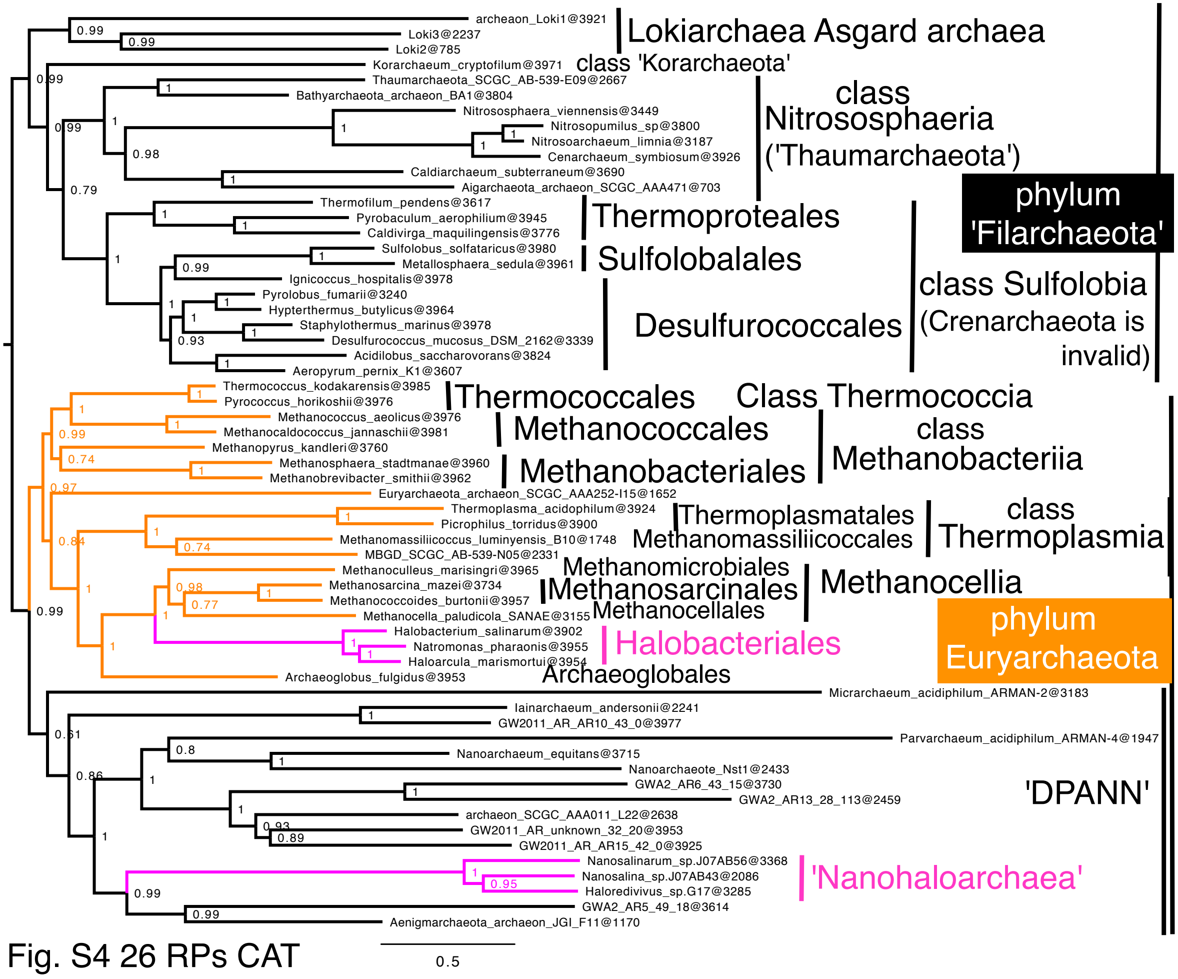
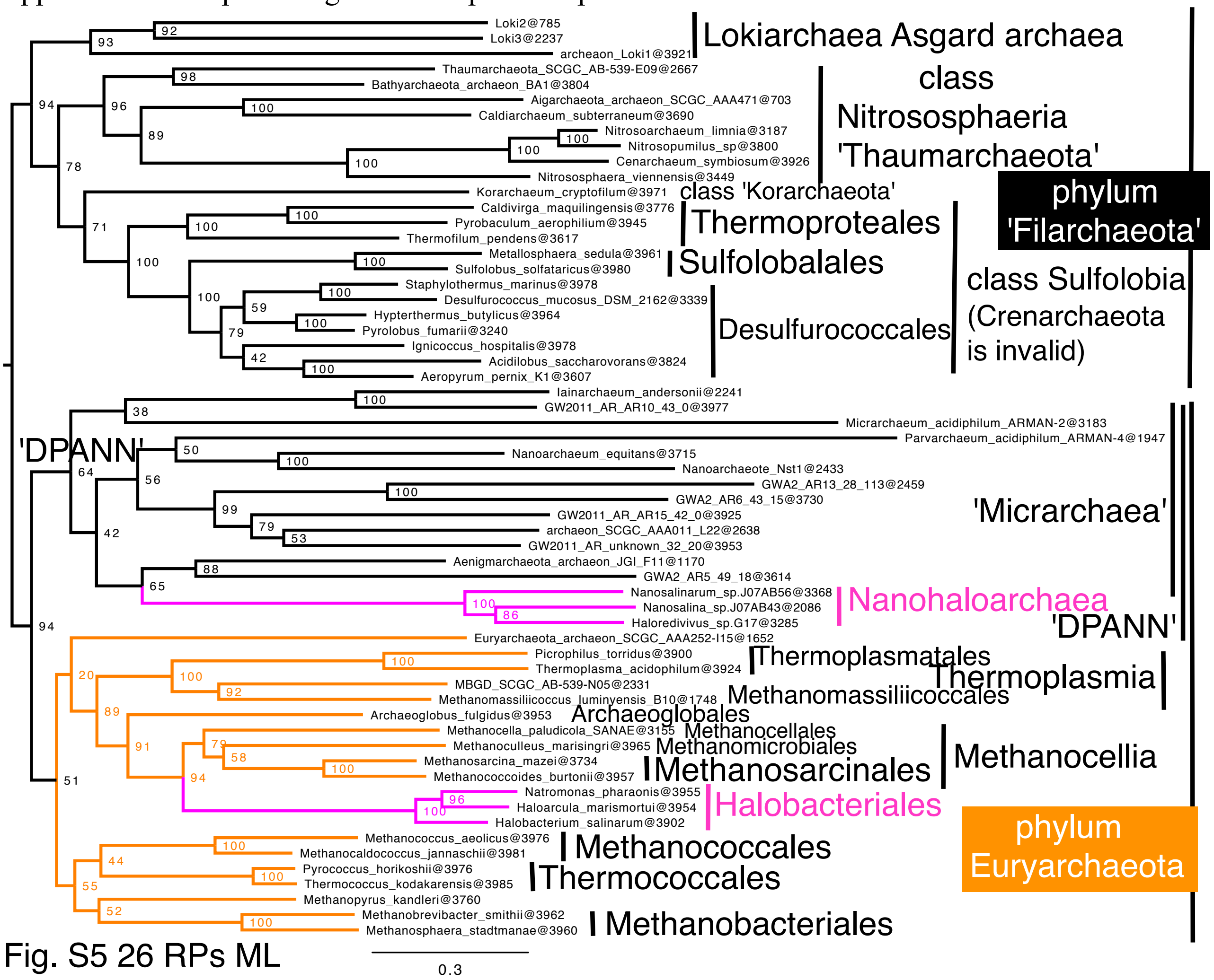

archeaon_Loki1@3921
Loki3@2237
Loki2@785
Lokiarchaea Asgard archaea
Korarchaeum_cryptofilum@3971
class 'Korarchaeota'
Thaumarchaeota_SCGC_AB-539-E09@2667
Bathyarchaeota_archaeon_BA1@3804
Nitrososphaera_viennensis@3449
Nitrosopumilus_sp@3800
Nitrosoarchaeum_limnia@3187
Cenarchaeum_symbiosum@3926
Caldiarchaeum_subterraneum@3690
Aigarchaeota_archaeon_SCGC_AAA471@703
class Nitrososphaeria ('Thaumarchaeota')
Thermofilum_pendens@3617
Pyrobaculum_aerophilium@3945
Caldivirga_maquilingensis@3776
Thermoproteales
Sulfolobus_solfataricus@3980
Metallosphaera_sedula@3961
Sulfolobalales
Ignicoccus_hospitalis@3978
Pyrolobus_fumarii@3240
Hypterthermus_butylicus@3964
Staphylothermus_marinus@3978
Desulfurococcus_mucosus_DSM_2162@3339
Acidilobus_saccharovorans@3824
Aeropyrum_pernix_K1@3607
Desulfurococcales
class Sulfolobia (Crenarchaeota is invalid)
phylum 'Filarchaeota'
Thermococcus_kodakarensis@3985
Pyrococcus_horikoshii@3976
Thermococcales
Class Thermococcia
Methanococcus_aeolicus@3976
Methanocaldococcus_jannaschii@3981
Methanococcales
Methanopyrus_kandleri@3760
Methanosphaera_stadtmanae@3960
Methanobrevibacter_smithii@3962
Methanobacteriales
class Methanobacteriia
Euryarchaeota_archaeon_SCGC_AAA252-I15@1652
Thermoplasma_acidophilum@3924
Picrophilus_torridus@3900
Thermoplasmatales
Methanomassiliicoccus_luminyensis_B10@1748
MBGD_SCGC_AB-539-N05@2331
Methanomassiliicoccales
class Thermoplasmia
Methanoculleus_marisingri@3965
Methanomicrobiales
Methanosarcina_mazei@3734
Methanococcoides_burtonii@3957
Methanosarcinales
Methanocella_paludicola_SANAE@3155
Methanocellales
Methanocellia
Halobacterium_salinarum@3902
Natromonas_pharaonis@3955
Haloarcula_marismortui@3954
Halobacteriales
Archaeoglobus_fulgidus@3953
Archaeoglobales
phylum Euryarchaeota
Micrarchaeum_acidiphilum_ARMAN-2@3183
Iainarchaeum_andersonii@2241
GW2011_AR_AR10_43_0@3977
Parvarchaeum_acidiphilum_ARMAN-4@1947
Nanoarchaeum_equitans@3715
Nanoarchaeote_Nst1@2433
GWA2_AR6_43_15@3730
GWA2_AR13_28_113@2459
archaeon_SCGC_AAA011_L22@2638
GW2011_AR_unknown_32_20@3953
GW2011_AR_AR15_42_0@3925
'DPANN'
Nanosalinarum_sp.J07AB56@3368
Nanosalina_sp.J07AB43@2086
Haloredivivus_sp.G17@3285
'Nanohaloarchaea'
GWA2_AR5_49_18@3614
Aenigmarchaeota_archaeon_JGI_F11@1170
Fig. S4 26 RPs CAT
0.5

Fig. S5. Site-homogeneous RAxML PROTGAMMALGF (4 gamma rates) tree for 26 ribosomal proteins from 60 archaebacteria representing all the most divergent lineages.

Support values are percentages for 100 pseudoreplicates.


Loki2@785
92
Loki3@2237
93
archeaon_Loki1@3921
Lokiarchaea Asgard archaea
94
Thaumarchaeota_SCGC_AB-539-E09@2667
98
Bathyarchaeota_archaeon_BA1@3804
96
Aigarchaeota_archaeon_SCGC_AAA471@703
100
Caldiarchaeum_subterraneum@3690
89
Nitrosoarchaeum_limnia@3187
100
Nitrosopumilus_sp@3800
100
Cenarchaeum_symbiosum@3926
100
Nitrososphaera_viennensis@3449
class
Nitrososphaeria
'Thaumarchaeota'
78
Korarchaeum_cryptofilum@3971
class 'Korarchaeota'
phylum
'Filarchaeota'
Caldivirga_maquilingensis@3776
100
Pyrobaculum_aerophilium@3945
71
100
Thermofilum_pendens@3617
Thermoproteales
Metallosphaera_sedula@3961
100
Sulfolobus_solfataricus@3980
100
Sulfolobalales
Staphylothermus_marinus@3978
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Desulfurococcus_mucosus_DSM_2162@3339
100
59
Hypterthermus_butylicus@3964
100
Pyrolobus_fumarii@3240
79
Ignicoccus_hospitalis@3978
42
Acidilobus_saccharovorans@3824
100
Aeropyrum_pernix_K1@3607
Desulfurococcales
class Sulfolobia
(Crenarchaeota
is invalid)
Iainarchaeum_andersonii@2241
100
GW2011_AR_AR10_43_0@3977
38
Micrarchaeum_acidiphilum_ARMAN-2@3183
'DPANN'
Parvarchaeum_acidiphilum_ARMAN-4@1947
50
64
Nanoarchaeum_equitans@3715
100
Nanoarchaeote_Nst1@2433
56
GWA2_AR13_28_113@2459
100
GWA2_AR6_43_15@3730
99
GW2011_AR_AR15_42_0@3925
'Micrarchaea'
79
archaeon_SCGC_AAA011_L22@2638
53
GW2011_AR_unknown_32_20@3953
42
Aenigmarchaeota_archaeon_JGI_F11@1170
88
GWA2_AR5_49_18@3614
65
Nanosalinarum_sp.J07AB56@3368
100
Nanosalina_sp.J07AB43@2086
86
Haloredivivus_sp.G17@3285
Nanohaloarchaea
'DPANN'
94
Euryarchaeota_archaeon_SCGC_AAA252-I15@1652
Picrophilus_torridus@3900
100
Thermoplasma_acidophilum@3924
Thermoplasmatales
20
100
Thermoplasmia
MBGD_SCGC_AB-539-N05@2331
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Methanomassiliicoccus_luminyensis_B10@1748
Methanomassiliicoccales
89
Archaeoglobus_fulgidus@3953
Archaeoglobales
Methanocella_paludicola_SANAE@3155
Methanocellales
91
79
Methanoculleus_marisingri@3965
Methanomicrobiales
58
Methanosarcina_mazei@3734
100
Methanococcoides_burtonii@3957
Methanosarcinales
Methanocellia
94
Natromonas_pharaonis@3955
96
Haloarcula_marismortui@3954
100
Halobacterium_salinarum@3902
Halobacteriales
51
phylum
Euryarchaeota
Methanococcus_aeolicus@3976
100
Methanocaldococcus_jannaschii@3981
Methanococcales
44
Pyrococcus_horikoshii@3976
100
Thermococcus_kodakarensis@3985
Thermococcales
55
Methanopyrus_kandleri@3760
52
Methanobrevibacter_smithii@3962
100
Methanosphaera_stadtmanae@3960
Methanobacteriales
0.3

Fig. S5 26 RPs ML

Figure S6. Site-homogeneous RAxML PROTGAMMALGF (4 gamma rates) tree for 26 ribosomal proteins from 151 eubacteria representing all the most divergent lineages. Support values are percentages for 100 pseudoreplicates.

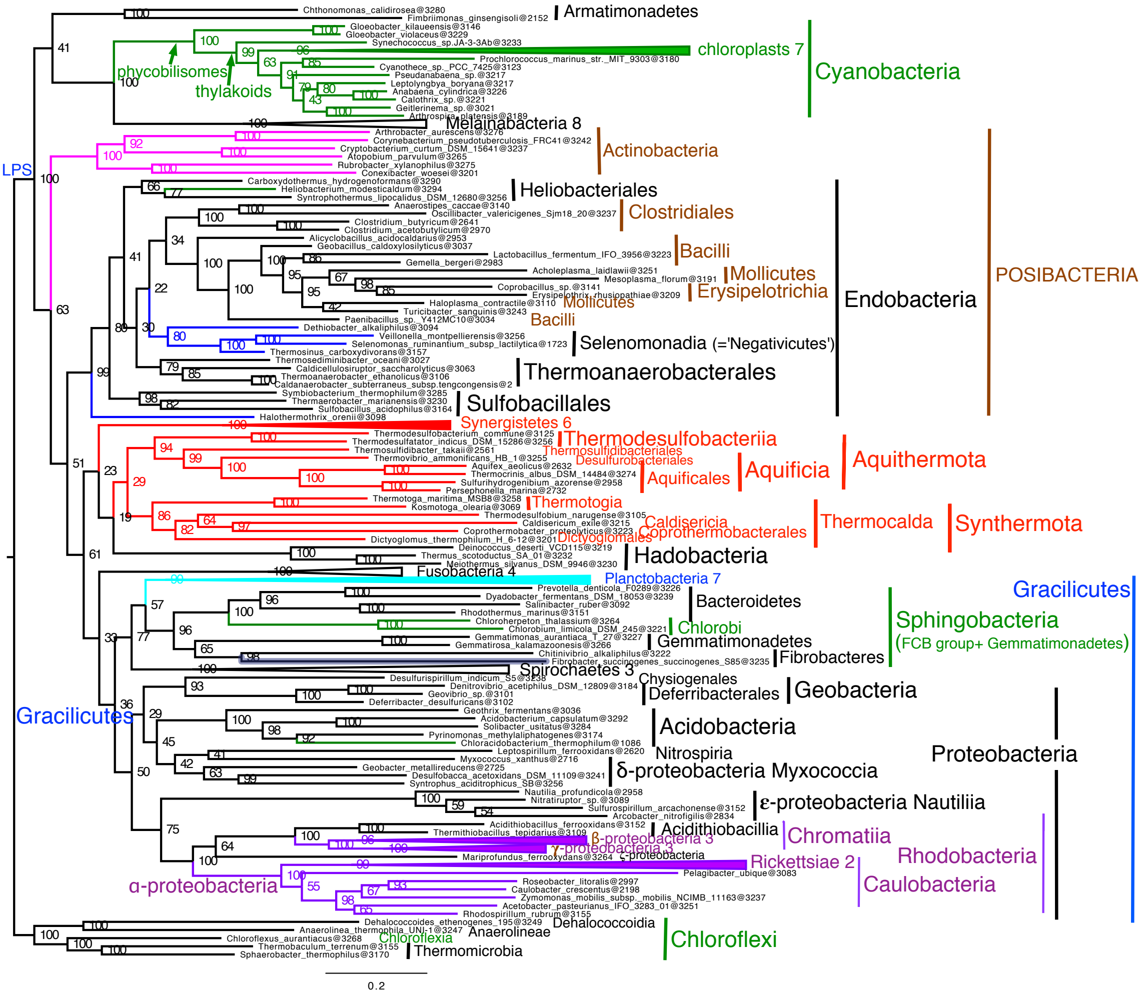
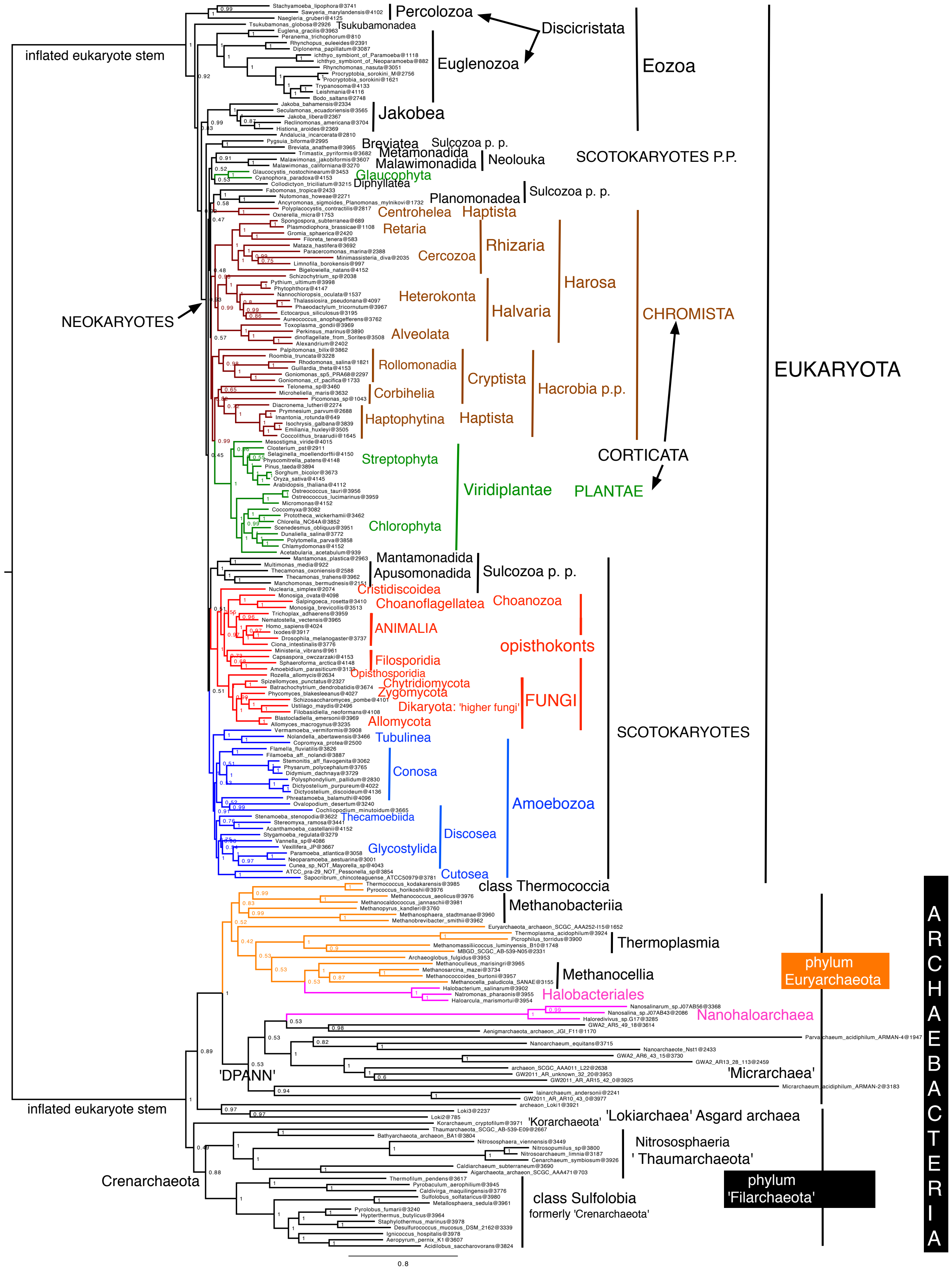

Chthonomonas_calidirosea@3280
Fimbriimonas_ginsengisoli@2152
Armatimonadetes
Gloeobacter_kilaueensis@3146
Gloeobacter_violaceus@3229
Synechococcus_sp.JA-3-3Ab@3233
chloroplasts 7
Prochlorococcus_marinus_str._MIT_9303@3180
Cyanothece_sp._PCC_7425@3123
Pseudanabaena_sp.@3217
Leptolyngbya_boryana@3217
Anabaena_cylindrica@3226
Calothrix_sp.@3221
Geitlerinema_sp.@3021
Arthrospira_platensis@3189
Cyanobacteria
phycobilisomes
thylakoids
Melainabacteria 8
Arthrobacter_aurescens@3276
Corynebacterium_pseudotuberculosis_FRC41@3242
Cryptobacterium_curtum_DSM_15641@3237
Atopobium_parvulum@3265
Rubrobacter_xylanophilus@3275
Conexibacter_woesei@3201
Actinobacteria
LPS
Carboxydothermus_hydrogenoformans@3290
Heliobacterium_modesticaldum@3294
Syntrophothermus_lipocalidus_DSM_12680@3256
Heliobacteriales
Anaerostipes_caccae@3140
Oscillibacter_valericigenes_Sjm18_20@3237
Clostridium_butyricum@2641
Clostridium_acetobutylicum@2970
Clostridiales
Alicyclobacillus_acidocaldarius@2953
Geobacillus_caldoxylosilyticus@3037
Lactobacillus_fermentum_IFO_3956@3223
Gemella_bergeri@2983
Bacilli
Acholeplasma_laidlawii@3251
Mesoplasma_florum@3191
Mollicutes
Coprobacillus_sp.@3141
Erysipelothrix_rhusiopathiae@3209
Erysipelotrichia
Haloplasma_contractile@3110
Mollicutes
Turicibacter_sanguinis@3243
Paenibacillus_sp._Y412MC10@3034
Bacilli
Dethiobacter_alkaliphilus@3094
Veillonella_montpellierensis@3256
Selenomonas_ruminantium_subsp_lactilytica@1723
Thermosinus_carboxydivorans@3157
Selenomonadia (='Negativicutes')
Thermosediminibacter_oceani@3027
Caldicellulosiruptor_saccharolyticus@3063
Thermoanaerobacter_ethanolicus@3106
Caldanaerobacter_subterraneus_subsp.tengcongensis@2
Thermoanaerobacterales
Symbiobacterium_thermophilum@3285
Thermaerobacter_marianensis@3230
Sulfobacillus_acidophilus@3164
Sulfobacillales
Halothermothrix_orenii@3098
Endobacteria
POSIBACTERIA
Synergistetes 6
Thermodesulfobacterium_commune@3125
Thermodesulfatator_indicus_DSM_15286@3256
Thermodesulfobacteriia
Thermosulfidibacter_takaii@2561
Thermosulfidibacteriales
Thermovibrio_ammonificans_HB_1@3255
Desulfurobacteriales
Aquifex_aeolicus@2632
Thermocrinis_albus_DSM_14484@3274
Sulfurihydrogenibium_azorense@2958
Persephonella_marina@2732
Aquificales
Aquificia
Aquithermota
Thermotoga_maritima_MSB8@3258
Kosmotoga_olearia@3069
Thermotogia
Thermodesulfobium_narugense@3105
Caldisericum_exile@3215
Caldisericia
Coprothermobacter_proteolyticus@3223
Coprothermobacterales
Dictyoglomus_thermophilum_H_6-12@3201
Dictyoglomales
Thermocalda
Synthermota
Deinococcus_deserti_VCD115@3219
Thermus_scotoductus_SA_01@3232
Meiothermus_silvanus_DSM_9946@3230
Hadobacteria
Fusobacteria 4
Planctobacteria 7
Prevotella_denticola_F0289@3226
Dyadobacter_fermentans_DSM_18053@3239
Salinibacter_ruber@3092
Rhodothermus_marinus@3151
Bacteroidetes
Chloroherpeton_thalassium@3264
Chlorobium_limicola_DSM_245@3221
Chlorobi
Gemmatimonas_aurantiaca_T_27@3227
Gemmatirosa_kalamazoonesis@3266
Gemmatimonadetes
Chitinivibrio_alkaliphilus@3222
Fibrobacter_succinogenes_succinogenes_S85@3235
Fibrobacteres
Spirochaetes 3
Gracilicutes
Sphingobacteria
(FCB group+ Gemmatimonadetes)
Desulfurispirillum_indicum_S5@3238
Chysiogenales
Denitrovibrio_acetiphilus_DSM_12809@3184
Geovibrio_sp.@3101
Deferribacter_desulfuricans@3102
Deferribacterales
Geobacteria
Geothrix_fermentans@3036
Acidobacterium_capsulatum@3292
Solibacter_usitatus@3284
Pyrinomonas_methylaliphatogenes@3174
Chloracidobacterium_thermophilum@1086
Acidobacteria
Leptospirillum_ferrooxidans@2620
Nitrospiria
Myxococcus_xanthus@2716
Geobacter_metallireducens@2725
Desulfobacca_acetoxidans_DSM_11109@3241
Syntrophus_aciditrophicus_SB@3256
δ-proteobacteria Myxococcia
Proteobacteria
Nautilia_profundicola@2958
Nitratiruptor_sp.@3089
Sulfurospirillum_arcachonense@3152
Arcobacter_nitrofigilis@2834
ε-proteobacteria Nautiliia
Acidithiobacillus_ferrooxidans@3152
Thermithiobacillus_tepidarius@3109
Acidithiobacillia
β-proteobacteria 3
γ-proteobacteria 3
Chromatiia
Mariprofundus_ferrooxydans@3264
ζ-proteobacteria
Rickettsiae 2
Pelagibacter_ubique@3083
Rhodobacteria
Roseobacter_litoralis@2997
Caulobacter_crescentus@2198
Zymomonas_mobilis_subsp._mobilis_NCIMB_11163@3237
Acetobacter_pasteurianus_IFO_3283_01@3251
Rhodospirillum_rubrum@3155
Caulobacteria
α-proteobacteria
Gracilicutes
Dehalococcoides_ethenogenes_195@3249
Dehalococcoidia
Anaerolinea_thermophila_UNI-1@3247
Anaerolineae
Chloroflexus_aurantiacus@3268
Chloroflexia
Thermobaculum_terrenum@3155
Sphaerobacter_thermophilus@3170
Thermomicrobia
Chloroflexi
0.2

Fig. S7. Site-heterogeneous PhyloBayes GTR-CAT (4 gamma rates) tree for 26 ribosomal proteins from 203 neomura representing all the most divergent lineages.
Support values are posterior probabilities.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Sawyeria_marylandensis@4102
Naegleria_gruberi@4125
Percolozoa
Tsukubamonas_globosa@2926
Tsukubamonadea
Discicristata
Euglena_gracilis@3963
Peranema_trichophorum@810
Rhynchopus_euleeides@2391
Diplonema_papillatum@3087
ichthyo_symbiont_of_Paramoeba@1118
ichthyo_symbiont_of_Neoparamoeba@882
Rhynchomonas_nasuta@3051
Procryptobia_sorokini_M@2756
Procryptobia_sorokini@1621
Trypanosoma@4133
Leishmania@4116
Bodo_saltans@2748
Euglenozoa
Eozoa
inflated eukaryote stem
Jakoba_bahamensis@2334
Seculamonas_ecuadoriensis@3565
Jakoba_libera@2367
Reclinomonas_americana@3704
Histiona_aroides@2369
Andalucia_incarcerata@2810
Jakobea
Pygsuia_biforma@2995
Breviata_anathema@3965
Breviatea
Sulcozoa p. p.
Trimastix_pyriformis@3682
Metamonadida
Malawimonas_jakobiformis@3607
Malawimonas_californiana@3270
Malawimonadida
Neolouka
SCOTOKARYOTES P.P.
Glaucocystis_nostochinearum@3453
Cyanophora_paradoxa@4153
Glaucophyta
Collodictyon_triciliatum@3215
Diphyllatea
Fabomonas_tropica@2433
Nutomonas_howeae@2271
Ancyromonas_sigmoides_Planomonas_mylnikovi@1732
Planomonadea
Sulcozoa p. p.
Polyplacocystis_contractilis@2817
Oxnerella_micra@1753
Centrohelea
Haptista
Spongospora_subterranea@689
Plasmodiophora_brassicae@1108
Gromia_sphaerica@2420
Filoreta_tenera@583
Retaria
Mataza_hastifera@3692
Paracercomonas_marina@2388
Minimassisteria_diva@2035
Limnofila_borokensis@997
Bigelowiella_natans@4152
Cercozoa
Rhizaria
Harosa
Schizochytrium_sp@2038
Pythium_ultimum@3998
Phytophthora@4147
Nannochloropsis_oculata@1537
Thalassiosira_pseudonana@4097
Phaeodactylum_tricornutum@3967
Ectocarpus_siliculosus@3195
Aureococcus_anophagefferens@3762
Heterokonta
Halvaria
NEOKARYOTES
CHROMISTA
Toxoplasma_gondii@3969
Perkinsus_marinus@3890
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Alexandrium@2402
Alveolata
Palpitomonas_bilix@3862
Roombia_truncata@3228
Rhodomonas_salina@1821
Guillardia_theta@4153
Goniomonas_sp5_PRA68@2297
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Rollomonadia
Cryptista
Telonema_sp@3460
Microheliella_maris@3632
Picomonas_sp@1043
Corbihelia
Hacrobia p.p.
EUKARYOTA
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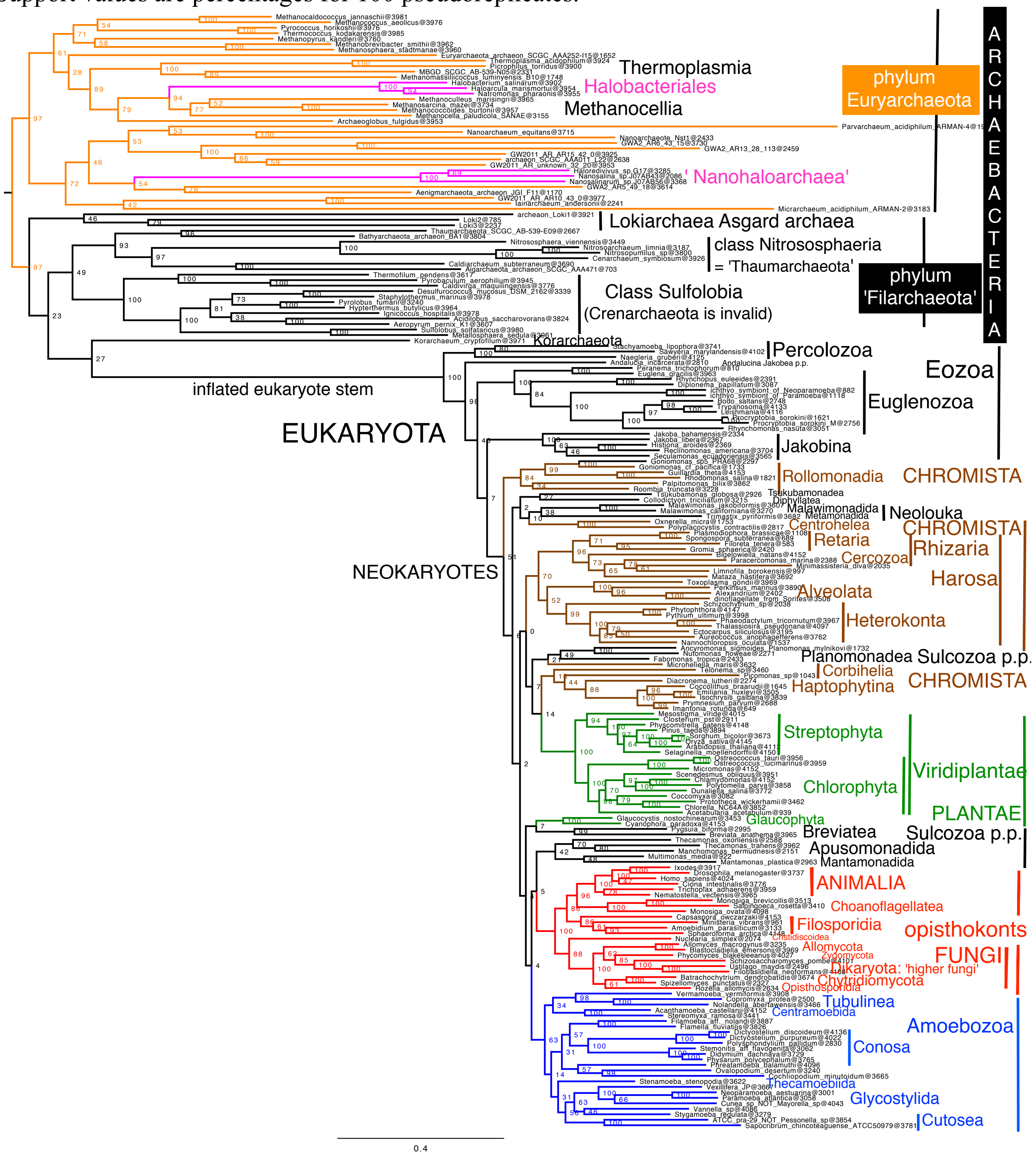
Prymnesium_parvum@2688
Imantonia_rotunda@649
Isochrysis_galbana@3839
Emiliania_huxleyi@3505
Coccolithus_braarudii@1645
Haptophytina
Haptista
CORTICATA
Mesostigma_viride@4015
Closterium_pst@2911
Selaginella_moellendorffii@4150
Physcomitrella_patens@4148
Pinus_taeda@3894
Sorghum_bicolor@3673
Oryza_sativa@4145
Arabidopsis_thaliana@4112
Streptophyta
Viridiplantae
PLANTAE
Ostreococcus_tauri@3956
Ostreococcus_lucimarinus@3959
Micromonas@4152
Coccomyxa@3082
Prototheca_wickerhamii@3462
Chlorella_NC64A@3852
Scenedesmus_obliquus@3951
Dunaliella_salina@3772
Polytomella_parva@3858
Chlamydomonas@4152
Acetabularia_acetabulum@939
Chlorophyta
Mantamonas_plastica@2963
Mantamonadida
Multimonas_media@922
Thecamonas_oxoniensis@2588
Thecamonas_trahens@3962
Manchomonas_bermudensis@2151
Apusomonadida
Sulcozoa p. p.
Nuclearia_simplex@2074
Cristidiscoidea
Monosiga_ovata@4098
Salpingoeca_rosetta@3410
Monosiga_brevicollis@3513
Choanoflagellatea
Choanozoa
Trichoplax_adhaerens@3959
Nematostella_vectensis@3965
Homo_sapiens@4024
Ixodes@3917
Drosophila_melanogaster@3737
Ciona_intestinalis@3776
ANIMALIA
opisthokonts
Ministeria_vibrans@961
Capsaspora_owczarzaki@4153
Sphaeroforma_arctica@4148
Amoebidium_parasiticum@3132
Filosporidia
Rozella_allomycis@2634
Opisthosporidia
Spizellomyces_punctatus@2327
Batrachochytrium_dendrobatidis@3674
Chytridiomycota
Phycomyces_blakesleeanus@4027
Zygomycota
Schizosaccharomyces_pombe@4101
Ustilago_maydis@2496
Filobasidiella_neoformans@4108
Dikaryota: 'higher fungi'
FUNGI
Blastocladiella_emersonii@3969
Allomyces_macrogynus@3235
Allomycota
SCOTOKARYOTES
Vermamoeba_vermiformis@3908
Nolandella_abertawensis@3466
Copromyxa_protea@2500
Tubulinea
Flamella_fluviatilis@3826
Filamoeba_aff_nolandi@3887
Stemonitis_aff_flavogenita@3062
Physarum_polycephalum@3765
Didymium_dachnaya@3729
Polysphondylium_pallidum@2830
Dictyostelium_purpureum@4022
Dictyostelium_discoideum@4136
Conosa
Amoebozoa
Phreatamoeba_balamuthi@4096
Ovalopodium_desertum@3240
Cochliopodium_minutoidum@3665
Stenamoeba_stenopodia@3622
Thecamoebida
Stereomyxa_ramosa@3441
Acanthamoeba_castellanii@4152
Stygamoeba_regulata@3279
Discosea
Vannella_sp@4086
Vexillifera_JP@3667
Paramoeba_atlantica@3058
Neoparamoeba_aestuarina@3001
Cunea_sp_NOT_Mayorella_sp@4043
Glycostylida
ATCC_pra-29_NOT_Pessonella_sp@3854
Sapocribrum_chincoteaguense_ATCC50979@3781
Cutosea
Thermococcus_kodakarensis@3985
Pyrococcus_horikoshii@3976
class Thermococcia
Methanococcus_aeolicus@3976
Methanocaldococcus_jannaschii@3981
Methanopyrus_kandleri@3760
Methanosphaera_stadtmanae@3960
Methanobrevibacter_smithii@3962
Methanobacteriia
Euryarchaeota_archaeon_SCGC_AAA252-I15@1652
Thermoplasma_acidophilum@3924
Picrophilus_torridus@3900
Methanomassiliicoccus_luminyensis_B10@1748
MBGD_SCGC_AB-539-N05@2331
Thermoplasmia
Archaeoglobus_fulgidus@3953
Methanoculleus_marisnigri@3965
Methanosarcina_mazei@3734
Methanococcoides_burtonii@3957
Methanocella_paludicola_SANAE@3155
Methanocellia
phylum
Euryarchaeota
Halobacterium_salinarum@3902
Natronomonas_pharaonis@3955
Haloarcula_marismortui@3954
Halobacteriales
Nanosalinarum_sp_J07AB56@3368
Nanosalina_sp_J07AB43@2086
Haloredivivus_sp_G17@3285
GWA2_AR5_49_18@3614
Nanohaloarchaea
Aenigmarchaeota_archaeon_JGI_F11@1170
Parvarchaeum_acidiphilum_ARMAN-4@1947
Nanoarchaeum_equitans@3715
Nanoarchaeote_Nst1@2433
GWA2_AR6_43_15@3730
GWA2_AR13_28_113@2459
archaeon_SCGC_AAA011_L22@2638
GW2011_AR_unknown_32_20@3953
GW2011_AR_AR15_42_0@3925
'DPANN'
'Micrarchaea'
Micrarchaeum_acidiphilum_ARMAN-2@3183
Iainarchaeum_andersonii@2241
GW2011_AR_AR10_43_0@3977
inflated eukaryote stem
archaeon_Loki1@3921
Loki3@2237
Loki2@785
'Lokiarchaea' Asgard archaea
Korarchaeum_cryptofilum@3971
'Korarchaeota'
Thaumarchaeota_SCGC_AB-539-E09@2667
Bathyarchaeota_archaeon_BA1@3804
Nitrososphaera_viennensis@3449
Nitrosopumilus_sp@3800
Nitrosoarchaeum_limnia@3187
Cenarchaeum_symbiosum@3926
Nitrososphaeria
' Thaumarchaeota'
Caldiarchaeum_subterraneum@3690
Aigarchaeota_archaeon_SCGC_AAA471@703
Crenarchaeota
Thermofilum_pendens@3617
Pyrobaculum_aerophilum@3945
Caldivirga_maquilingensis@3776
Sulfolobus_solfataricus@3980
Metallosphaera_sedula@3961
class Sulfolobia
formerly 'Crenarchaeota'
phylum
'Filarchaeota'
Pyrolobus_fumarii@3240
Hypterthermus_butylicus@3964
Staphylothermus_marinus@3978
Desulfurococcus_mucosus_DSM_2162@3339
Ignicoccus_hospitalis@3978
Aeropyrum_pernix_K1@3607
Acidilobus_saccharovorans@3824
ARCHAEBACTERIA
0.8

Figure S8. Site-homogeneous RAxML PROTGAMMALGF (4 gamma rates) tree for 26 ribosomal proteins from 203 neomura representing all the most divergent lineages. Support values are percentages for 100 pseudoreplicates.


ARCHAEBACTERIA
phylum Euryarchaeota
Thermoplasmia
Halobacteriales
Methanocellia
'Nanohaloarchaea'
Lokiarchaea Asgard archaea
class Nitrososphaeria = 'Thaumarchaeota'
phylum 'Filarchaeota'
Class Sulfolobia (Crenarchaeota is invalid)
Korarchaeota
Methanocaldococcus_jannaschii@3981
Methanococcus_aeolicus@3976
Pyrococcus_horikoshii@3978
Thermococcus_kodakarensis@3985
Methanopyrus_kandleri@3760
Methanobrevibacter_smithii@3962
Methanosphaera_stadtmanae@3960
Euryarchaeota_archaeon_SCGC_AAA252-I15@1652
Thermoplasma_acidophilum@3924
Picrophilus_torridus@3900
MBGD_SCGC_AB-539-N05@2331
Methanomassiliicoccus_luminyensis_B10@1748
Halobacterium_salinarum@3902
Haloarcula_marismortui@3954
Natronomas_pharaonis@3955
Methanoculleus_marisnigri@3965
Methanosarcina_mazei@3734
Methanococcoides_burtonii@3957
Methanocella_paludicola_SANAE@3155
Archaeoglobus_fulgidus@3953
Parvarchaeum_acidiphilum_ARMAN-4@1983
Nanoarchaeum_equitans@3715
Nanoarchaeote_Nst1@2433
GWA2_AR6_43_15@3730
GWA2_AR13_28_113@2459
GW2011_AR_AR15_42_0@3925
archaeon_SCGC_AAA011_L22@2638
GW2011_AR_unknown_32_20@3953
Halorediyivus_sp_G17@3285
Nanosalina_sp_J07AB43@2086
Nanosalinarum_sp_J07AB56@3368
GWA2_AR5_49_18@3614
Aenigmarchaeota_archaeon_JGI_F11@1170
GW2011_AR_AR10_43_0@3977
Iainarchaeum_andersonii@2241
Micrarchaeum_acidiphilum_ARMAN-2@3183
archaeon_Loki1@3921
Loki2@785
Loki3@2237
Thaumarchaeota_SCGC_AB-539-E09@2667
Bathyarchaeota_archaeon_BA1@3804
Nitrososphaera_viennensis@3449
Nitrosoarchaeum_limnia@3187
Nitrosopumilus_sp@3800
Cenarchaeum_symbiosum@3926
Caldiarchaeum_subterraneum@3690
Aigarchaeota_archaeon_SCGC_AAA471@703
Thermofilum_pendens@3617
Pyrobaculum_aerophilium@3945
Caldivirga_maquilingensis@3776
Desulfurococcus_mucosus_DSM_2162@3339
Staphylothermus_marinus@3978
Pyrolobus_fumarii@3240
Hypterthermus_butylicus@3964
Ignicoccus_hospitalis@3978
Acidilobus_saccharovorans@3824
Aeropyrum_pernix_K1@3607
Sulfolobus_solfataricus@3980
Metallosphaera_sedula@3961
Korarchaeum_cryptofilum@3971
inflated eukaryote stem
EUKARYOTA
NEOKARYOTES
Eozoa
Percolozoa
Euglenozoa
Jakobina
CHROMISTA
Rollomonadia
Neolouka
Malawimonadida
Metamonadida
Diphyllatea
Tsukubamonadea
Centrohelea
Retaria
Rhizaria
Cercozoa
Harosa
Alveolata
Heterokonta
Planomonadea
Sulcozoa p.p.
Corbihelia
Haptophytina
Streptophyta
Viridiplantae
Chlorophyta
PLANTAE
Glaucophyta
Breviatea
Apusomonadida
Mantamonadida
ANIMALIA
Choanoflagellatea
Filosporidia
opisthokonts
Cristidiscoidea
Allomycota
Zygomycota
FUNGI
Dikaryota: 'higher fungi'
Chytridiomycota
Opisthosporidia
Tubulinea
Centramoebida
Amoebozoa
Conosa
Thecamoebiida
Glycostylida
Cutosea
Stachyamoeba_lipophora@3741
Sawyeria_marylandensis@4102
Naegleria_gruberi@4125
Andalucia_incarcerata@2810
Andalucina Jakobea p.p.
Peranema_trichophorum@810
Euglena_gracilis@3963
Rhynchopus_euleeides@2391
Diplonema_papillatum@3087
ichthyo_symbiont_of_Neoparamoeba@882
ichthyo_symbiont_of_Paramoeba@1118
Bodo_saltans@2748
Trypanosoma@4133
Leishmania@4116
Procryptobia_sorokini@1621
Procryptobia_sorokini_M@2756
Rhynchomonas_nasuta@3051
Jakoba_bahamensis@2334
Jakoba_libera@2367
Histiona_aroides@2369
Reclinomonas_americana@3704
Seculamonas_ecuadoriensis@3565
Goniomonas_sp5_PRA68@2297
Goniomonas_cf_pacifica@1733
Guillardia_theta@4153
Rhodomonas_salina@1821
Palpitomonas_bilix@3862
Roombia_truncata@3228
Tsukubamonas_globosa@2926
Collodictyon_triciliatum@3215
Malawimonas_jakobiformis@3607
Malawimonas_californiana@3270
Trimastix_pyriformis@3682
Oxnerella_micra@1753
Polyplacocystis_contractilis@2817
Plasmodiophora_brassicae@1108
Spongospora_subterranea@689
Filoreta_tenera@583
Gromia_sphaerica@2420
Bigelowiella_natans@4152
Paracercomonas_marina@2388
Minimassisteria_diva@2035
Limnofila_borokensis@997
Mataza_hastifera@3692
Toxoplasma_gondii@3969
Perkinsus_marinus@3890
Alexandrium@2402
dinoflagellate_from_Sprites@3508
Schizochytrium_sp@2038
Phytophthora@4147
Pythium_ultimum@3998
Phaeodactylum_tricornutum@3967
Thalassiosira_pseudonana@4097
Ectocarpus_siliculosus@3195
Aureococcus_anophagefferens@3762
Nannochloropsis_oculata@1537
Ancyromonas_sigmoides_Planomonas_mylnikovi@1732
Nutomonas_howeae@2271
Fabomonas_tropica@2433
Microheliella_maris@3632
Telonema_sp@3460
Picomonas_sp@1043
Diacronema_lutheri@2274
Coccolithus_braarudii@1645
Emiliania_huxleyi@3505
Isochrysis_galbana@3839
Prymnesium_parvum@2688
Imantonia_rotunda@649
Mesostigma_viride@4015
Closterium_pst@2911
Physcomitrella_patens@4148
Pinus_taeda@3894
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Ostreococcus_lucimarinus@3959
Micromonas@4152
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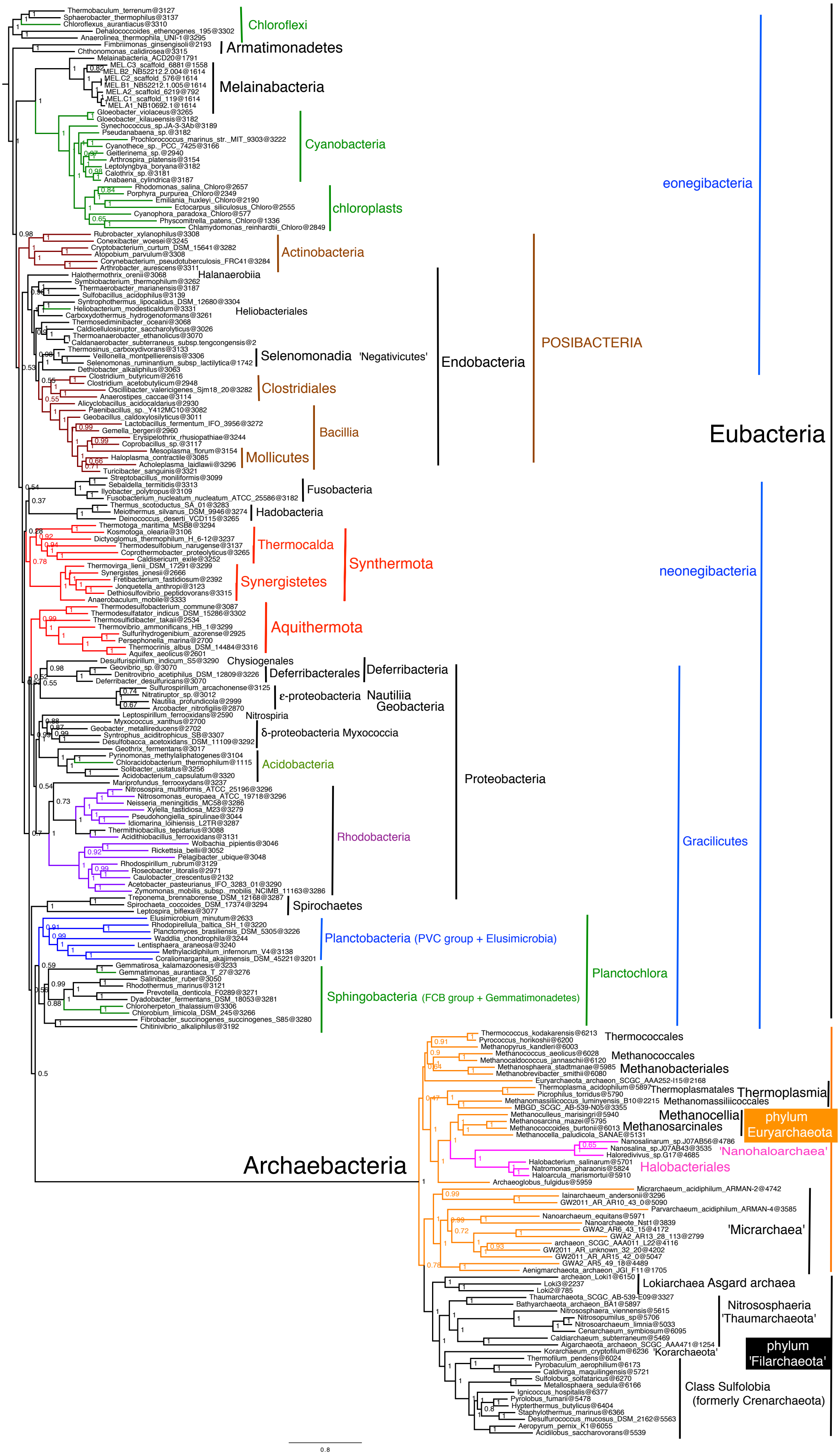
Chlamydomonas@4152
Polytomella_parva@3858
Dunaliella_salina@3772
Coccomyxa@3082
Prototheca_wickerhamii@3462
Chlorella_NC64A@3852
Acetabularia_acetabulum@939
Glaucocystis_nostochinearum@3453
Cyanophora_paradoxa@4153
Pygsuia_biforma@2995
Breviata_anathema@3965
Thecamonas_oxoniensis@2588
Thecamonas_trahens@3962
Manchomonas_bermudensis@2151
Multimonas_media@822
Mantamonas_plastica@2963
Ixodes@3917
Drosophila_melanogaster@3737
Homo_sapiens@4024
Ciona_intestinalis@3776
Trichoplax_adhaerens@3959
Nematostella_vectensis@3965
Monosiga_brevicollis@3513
Salpingoeca_rosetta@3410
Monosiga_ovata@4098
Capsaspora_owczarzaki@4153
Ministeria_vibrans@961
Amoebidium_parasiticum@3133
Sphaeroforma_arctica@4148
Nuclearia_simplex@2074
Allomyces_macrogynus@3235
Blastocladiella_emersonii@3969
Phycomyces_blakesleeanus@4027
Schizosaccharomyces_pombe@4101
Ustilago_maydis@2496
Filobasidiella_neoformans@4068
Batrachochytrium_dendrobatidis@3674
Spizellomyces_punctatus@2327
Rozella_allomycis@2634
Vermamoeba_vermiformis@3908
Copromyxa_protea@2500
Nolandella_abertawensis@3466
Acanthamoeba_castellanii@4152
Stereomyxa_ramosa@3441
Filamoeba_aff_nolandi@3887
Flamella_fluviatilis@3826
Dictyostelium_discoideum@4136
Dictyostelium_purpureum@4022
Polysphondylium_pallidum@2830
Stemonitis_aff_flavogenita@3062
Didymium_dachnaya@3729
Physarum_polycephalum@3765
Phreatamoeba_balamuthi@4096
Ovalopodium_desertum@3240
Cochliopodium_minutoidum@3665
Stenamoeba_stenopodia@3622
Vexillifera_JP@3667
Neoparamoeba_aestuarina@3001
Paramoeba_atlantica@3058
Cunea_sp_NOT_Mayorella_sp@4043
Vannella_sp@4086
Stygamoeba_regulata@3279
ATCC_pra-29_NOT_Pessonella_sp@3854
Sapocribrum_chincoteaguense_ATCC50979@3781
0.4

Fig. S9. Site-heterogeneous prokaryote PhyloBayes CAT-GTR tree for 51 ribosomal proteins from 60 archaebacteria and 26 ribosomal proteins from 151 eubacteria representing all the most divergent lineages, including chloroplasts. Support values are posterior probabilities. See next page: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Sphaerobacter_thermophilus@3137
Chloroflexus_aurantiacus@3310
Dehalococcoides_ethenogenes_195@3302
Anaerolinea_thermophila_UNI-1@3295
Fimbriimonas_ginsengisoli@2193
Chthonomonas_calidirosea@3315
Chloroflexi
Armatimonadetes
Melainabacteria_ACD20@1791
MEL.C3_scaffold_6881@1558
MEL.B2_NB52212.2.004@1614
MEL.C2_scaffold_576@1614
MEL.B1_NB52212.1.005@1614
MEL.A2_scaffold_6219@792
MEL.C1_scaffold_119@1614
MEL.A1_NB10692.1@1614
Melainabacteria
Gloeobacter_violaceus@3265
Gloeobacter_kilaueensis@3182
Synechococcus_sp.JA-3-3Ab@3189
Pseudanabaena_sp.@3182
Prochlorococcus_marinus_str._MIT_9303@3222
Cyanothece_sp._PCC_7425@3166
Geitlerinema_sp.@2940
Arthrospira_platensis@3154
Leptolyngbya_boryana@3182
Calothrix_sp.@3181
Anabaena_cylindrica@3187
Cyanobacteria
Rhodomonas_salina_Chloro@2657
Porphyra_purpurea_Chloro@2349
Emiliania_huxleyi_Chloro@2190
Ectocarpus_siliculosus_Chloro@2555
Cyanophora_paradoxa_Chloro@577
Physcomitrella_patens_Chloro@1336
Chlamydomonas_reinhardtii_Chloro@2849
chloroplasts
eonegibacteria
Rubrobacter_xylanophilus@3308
Conexibacter_woesei@3245
Cryptobacterium_curtum_DSM_15641@3282
Atopobium_parvulum@3308
Corynebacterium_pseudotuberculosis_FRC41@3284
Arthrobacter_aurescens@3311
Actinobacteria
Halothermothrix_orenii@3068
Halanaerobiia
Symbiobacterium_thermophilum@3262
Thermaerobacter_marianensis@3187
Sulfobacillus_acidophilus@3139
Syntrophothermus_lipocalidus_DSM_12680@3304
Heliobacterium_modesticaldum@3331
Carboxydothermus_hydrogenoformans@3261
Heliobacteriales
Thermosediminibacter_oceani@3068
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Thermoanaerobacter_ethanolicus@3070
Caldanaerobacter_subterraneus_subsp.tengcongensis@2
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Veillonella_montpellierensis@3306
Selenomonas_ruminantium_subsp_lactilytica@1742
Dethiobacter_alkaliphilus@3063
Selenomonadia
'Negativicutes'
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Clostridium_acetobutylicum@2948
Oscillibacter_valericigenes_Sjm18_20@3282
Anaerostipes_caccae@3114
Clostridiales
Alicyclobacillus_acidocaldarius@2930
Paenibacillus_sp._Y412MC10@3082
Geobacillus_caldoxylosilyticus@3011
Lactobacillus_fermentum_IFO_3956@3272
Gemella_bergeri@2960
Erysipelothrix_rhusiopathiae@3244
Coprobacillus_sp.@3117
Mesoplasma_florum@3154
Haloplasma_contractile@3085
Acholeplasma_laidlawii@3296
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Bacillia
Mollicutes
Endobacteria
POSIBACTERIA
Eubacteria
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Sebaldella_termitidis@3313
Ilyobacter_polytropus@3109
Fusobacterium_nucleatum_nucleatum_ATCC_25586@3182
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Coprothermobacter_proteolyticus@3265
Caldisericum_exile@3252
Thermocalda
Thermovirga_lienii_DSM_17291@3299
Synergistes_jonesii@2666
Fretibacterium_fastidiosum@2392
Jonquetella_anthropi@3123
Dethiosulfovibrio_peptidovorans@3315
Anaerobaculum_mobile@3333
Synergistetes
Synthermota
neonegibacteria
Thermodesulfobacterium_commune@3087
Thermodesulfatator_indicus_DSM_15286@3302
Thermosulfidibacter_takaii@2534
Thermovibrio_ammonificans_HB_1@3299
Sulfurihydrogenibium_azorense@2925
Persephonella_marina@2700
Thermocrinis_albus_DSM_14484@3316
Aquifex_aeolicus@2601
Aquithermota
Desulfurispirillum_indicum_S5@3290
Chrysiogenales
Geovibrio_sp.@3070
Denitrovibrio_acetiphilus_DSM_12809@3226
Deferribacter_desulfuricans@3070
Deferribacterales
Deferribacteria
Sulfurospirillum_arcachonense@3125
Nitratiruptor_sp.@3012
Nautilia_profundicola@2999
Arcobacter_nitrofigilis@2870
ε-proteobacteria
Nautiliia
Geobacteria
Leptospirillum_ferrooxidans@2590
Nitrospiria
Myxococcus_xanthus@2700
Geobacter_metallireducens@2702
Syntrophus_aciditrophicus_SB@3307
Desulfobacca_acetoxidans_DSM_11109@3292
δ-proteobacteria Myxococcia
Geothrix_fermentans@3017
Pyrinomonas_methylaliphatogenes@3104
Chloracidobacterium_thermophilum@1115
Solibacter_usitatus@3256
Acidobacterium_capsulatum@3320
Acidobacteria
Mariprofundus_ferrooxydans@3237
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Nitrosomonas_europaea_ATCC_19718@3296
Neisseria_meningitidis_MC58@3286
Xylella_fastidiosa_M23@3279
Pseudohongiella_spirulinae@3044
Idiomarina_loihiensis_L2TR@3287
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Acidithiobacillus_ferrooxidans@3131
Wolbachia_pipientis@3046
Rickettsia_bellii@3052
Pelagibacter_ubique@3048
Rhodospirillum_rubrum@3129
Roseobacter_litoralis@2971
Caulobacter_crescentus@2132
Acetobacter_pasteurianus_IFO_3283_01@3290
Zymomonas_mobilis_subsp._mobilis_NCIMB_11163@3286
Rhodobacteria
Proteobacteria
Treponema_brennaborense_DSM_12168@3287
Spirochaeta_coccoides_DSM_17374@3294
Leptospira_biflexa@3077
Spirochaetes
Gracilicutes
Elusimicrobium_minutum@2633
Rhodopirellula_baltica_SH_1@3220
Planctomyces_brasiliensis_DSM_5305@3226
Waddlia_chondrophila@3244
Lentisphaera_araneosa@3240
Methylacidiphilum_infernorum_V4@3138
Coraliomargarita_akajimensis_DSM_45221@3201
Planctobacteria (PVC group + Elusimicrobia)
Gemmatirosa_kalamazoonesis@3233
Gemmatimonas_aurantiaca_T_27@3276
Salinibacter_ruber@3050
Rhodothermus_marinus@3121
Prevotella_denticola_F0289@3271
Dyadobacter_fermentans_DSM_18053@3281
Chloroherpeton_thalassium@3306
Chlorobium_limicola_DSM_245@3266
Fibrobacter_succinogenes_succinogenes_S85@3280
Chitinivibrio_alkaliphilus@3192
Sphingobacteria (FCB group + Gemmatimonadetes)
Planctochlora
Thermococcus_kodakarensis@6213
Pyrococcus_horikoshii@6200
Methanopyrus_kandleri@6003
Thermococcales
Methanococcus_aeolicus@6028
Methanocaldococcus_jannaschii@6120
Methanococcales
Methanosphaera_stadtmanae@5985
Methanobrevibacter_smithii@6080
Methanobacteriales
Euryarchaeota_archaeon_SCGC_AAA252-I15@2168
Thermoplasma_acidophilum@5897
Thermoplasmatales
Picrophilus_torridus@5790
Thermoplasmia
Methanomassiliicoccus_luminyensis_B10@2215
Methanomassiliicoccales
MBGD_SCGC_AB-539-N05@3355
Methanoculleus_marisnigri@5940
Methanosarcina_mazei@5795
Methanococcoides_burtonii@6013
Methanocella_paludicola_SANAE@5131
Methanocellia
Methanosarcinales
phylum Euryarchaeota
Nanosalinarum_sp.J07AB56@4786
Nanosalina_sp.J07AB43@3535
Haloredivivus_sp.G17@4685
'Nanohaloarchaea'
Halobacterium_salinarum@5701
Natromonas_pharaonis@5824
Haloarcula_marismortui@5910
Halobacteriales
Archaeoglobus_fulgidus@5959
Archaebacteria
Micrarchaeum_acidiphilum_ARMAN-2@4742
Iainarchaeum_andersonii@3296
GW2011_AR_AR10_43_0@5090
Parvarchaeum_acidiphilum_ARMAN-4@3585
Nanoarchaeum_equitans@5971
Nanoarchaeote_Nst1@3839
GWA2_AR6_43_15@4172
GWA2_AR13_28_113@2799
archaeon_SCGC_AAA011_L22@4116
GW2011_AR_unknown_32_20@4202
GW2011_AR_AR15_42_0@5047
GWA2_AR5_49_18@4489
Aenigmarchaeota_archaeon_JGI_F11@1705
'Micrarchaea'
archaeon_Loki1@6150
Loki3@2237
Loki2@785
Lokiarchaea Asgard archaea
Thaumarchaeota_SCGC_AB-539-E09@3327
Bathyarchaeota_archaeon_BA1@5897
Nitrososphaera_viennensis@5615
Nitrosopumilus_sp@5706
Nitrosoarchaeum_limnia@5033
Cenarchaeum_symbiosum@6095
Caldiarchaeum_subterraneum@5469
Aigarchaeota_archaeon_SCGC_AAA471@1254
Nitrososphaeria
'Thaumarchaeota'
Korarchaeum_cryptofilum@6236
'Korarchaeota'
phylum 'Filarchaeota'
Thermofilum_pendens@6024
Pyrobaculum_aerophilum@6173
Caldivirga_maquilingensis@5721
Sulfolobus_solfataricus@6270
Metallosphaera_sedula@6166
Ignicoccus_hospitalis@6377
Pyrolobus_fumarii@5478
Hypterthermus_butylicus@6404
Staphylothermus_marinus@6366
Desulfurococcus_mucosus_DSM_2162@5563
Aeropyrum_pernix_K1@6055
Acidilobus_saccharovorans@5539
Class Sulfolobia
(formerly Crenarchaeota)
0.8

Fig. S9

Figure S10. Site-homogeneous prokaryote RAxML PROTGAMMALGF (4 gamma rates) tree for 26 ribosomal proteins from 60 archaebacteria and 151 eubacteria representing all the most divergent lineages.

Support values are percentages for 100 pseudoreplicates. See next page:

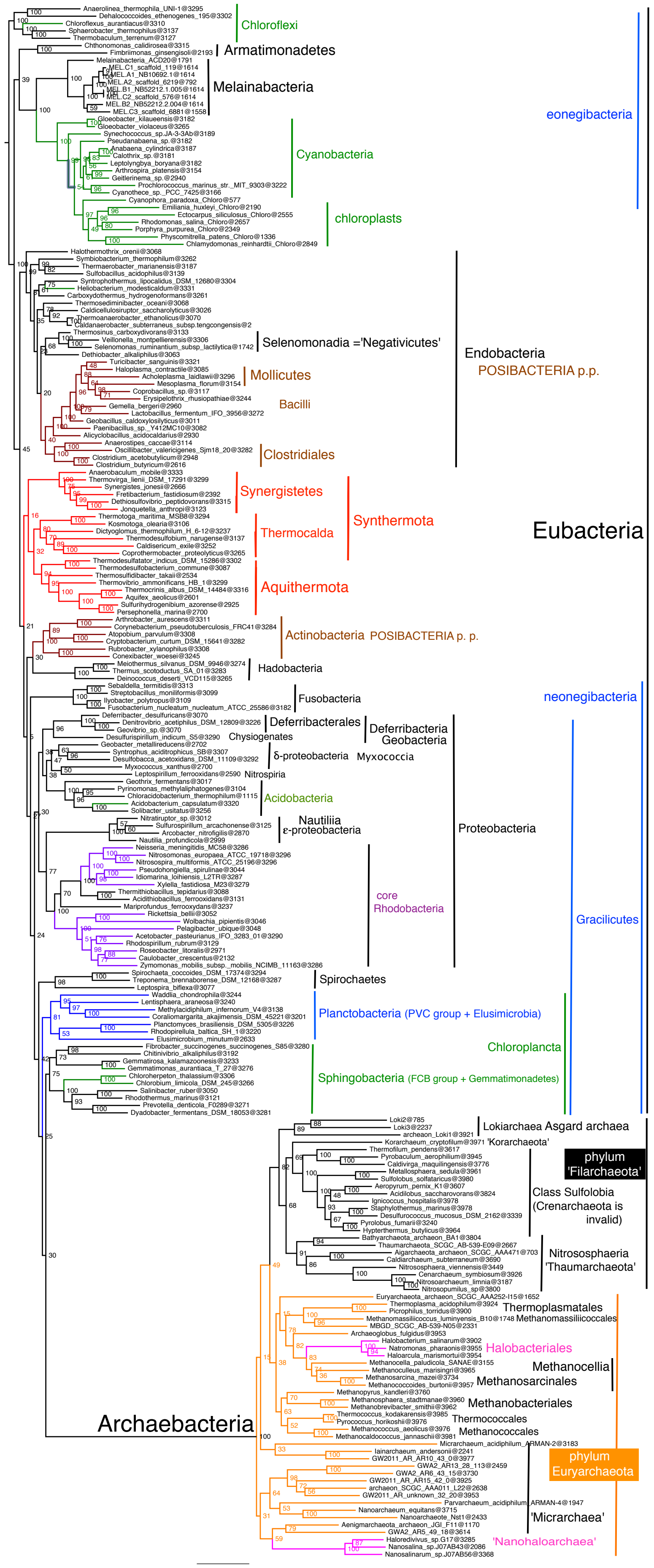
Chloroflexi
Armatimonadetes
Melainabacteria
Cyanobacteria
chloroplasts
eonegibacteria
Selenomonadia ='Negativicutes'
Endobacteria
POSIBACTERIA p.p.
Mollicutes
Bacilli
Clostridiales
Synergistetes
Synthermota
Thermocalda
Aquithermota
Eubacteria
Actinobacteria POSIBACTERIA p. p.
Hadobacteria
Fusobacteria
neonegibacteria
Deferribacterales
Deferribacteria
Geobacteria
Chysiogenates
δ-proteobacteria
Myxococcia
Nitrospiria
Acidobacteria
Nautiliia
ε-proteobacteria
Proteobacteria
core
Rhodobacteria
Gracilicutes
Spirochaetes
Planctobacteria (PVC group + Elusimicrobia)
Chloroplancta
Sphingobacteria (FCB group + Gemmatimonadetes)
Lokiarchaea Asgard archaea
'Korarchaeota'
phylum
'Filarchaeota'
Class Sulfolobia
(Crenarchaeota is
invalid)
Nitrososphaeria
'Thaumarchaeota'
Thermoplasmatales
Methanomassiliicoccales
Halobacteriales
Methanocellia
Methanosarcinales
Methanobacteriales
Thermococcales
Methanococcales
Archaebacteria
phylum
Euryarchaeota
'Micrarchaea'
'Nanohaloarchaea'
0.4

Fig. S10

Fig. S11. Site-heterogeneous 2-domain PhyloBayes CAT-GTR tree for 26 ribosomal proteins from 143 eukaryotes and 151 eubacteria representing all the most divergent lineages.
Support values are posterior probabilities. Consensus tree for two chains: 38,969 trees were summed after removing 40% as burnin. The chains converged on the same topology except for a few nodes with .5 or less support: Max diff 1. See next page:

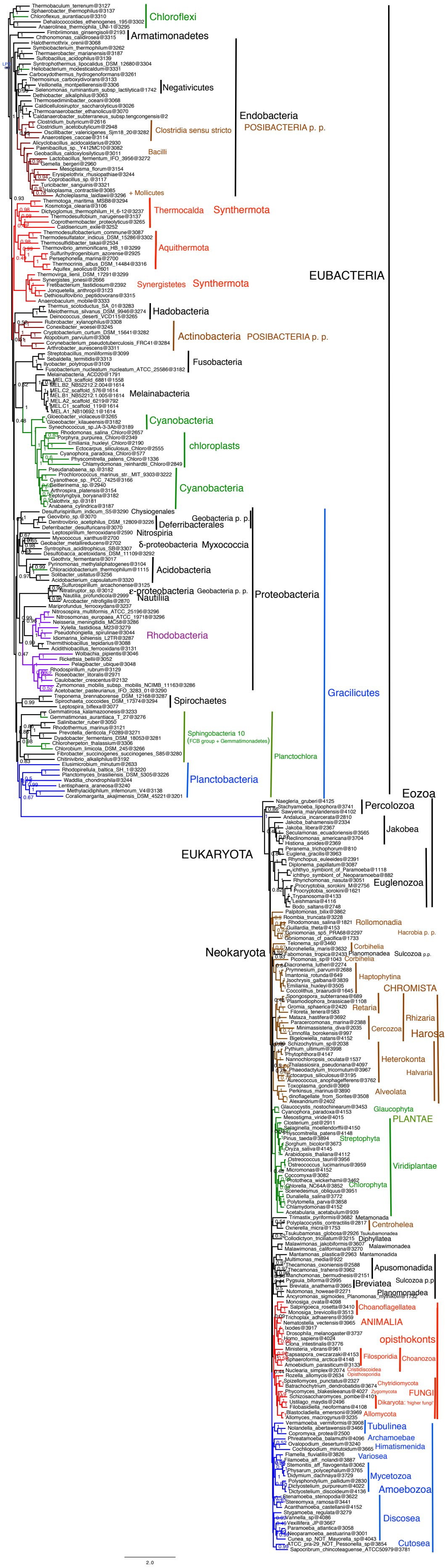
Chloroflexi
Armatimonadetes
Negativicutes
Endobacteria
POSIBACTERIA p. p.
Clostridia sensu stricto
Bacilli
+ Mollicutes
Thermocalda
Synthermota
Aquithermota
EUBACTERIA
Synergistetes
Synthermota
Hadobacteria
Actinobacteria
POSIBACTERIA p. p.
Fusobacteria
Melainabacteria
Cyanobacteria
chloroplasts
Cyanobacteria
Chrysiogenales
Geobacteria p. p.
Deferribacterales
Nitrospira
δ-proteobacteria
Myxococcia
Acidobacteria
ε-proteobacteria
Geobacteria p. p.
Nautilia
Proteobacteria
Rhodobacteria
Gracilicutes
Spirochaetes
Sphingobacteria 10
(FCB group + Gemmatimonadetes)
Planctochlora
Planctobacteria
Eozoa
Percolozoa
Jakobea
EUKARYOTA
Euglenozoa
Rollomonadia
Hacrobia p. p.
Corbihelia
Planomonadea
Sulcozoa p.p.
Corbihelia
Neokaryota
Haptophytina
CHROMISTA
Retaria
Rhizaria
Cercozoa
Harosa
Heterokonta
Halvaria
Alveolata
Glaucophyta
PLANTAE
Streptophyta
Viridiplantae
Chlorophyta
Metamonada
Centrohelea
Tsukubamonadea
Diphyllatea
Malawimonadea
Mantamonadida
Apusomonadida
Breviatea
Sulcozoa p.p
Planomonadea
Choanoflagellatea
ANIMALIA
opisthokonts
Filosporidia
Choanozoa
Cristidiscoidea
Opisthosporidia
Chytridiomycota
Zygomycota
FUNGI
Dikaryota: 'higher fungi'
Allomycota
Tubulinea
Archamoebae
Himatismenida
Variosea
Mycetozoa
Amoebozoa
Discosea
Cutosea
2.0

Figure S12. Site-homogeneous 2-domain RAxML PROTGAMMALGF (4 gamma rates) tree for 26 ribosomal proteins from 143 eukaryotes and 151 eubacteria eubacteria representing all the most divergent lineages.

Support values are percentages for 100 pseudoreplicates.

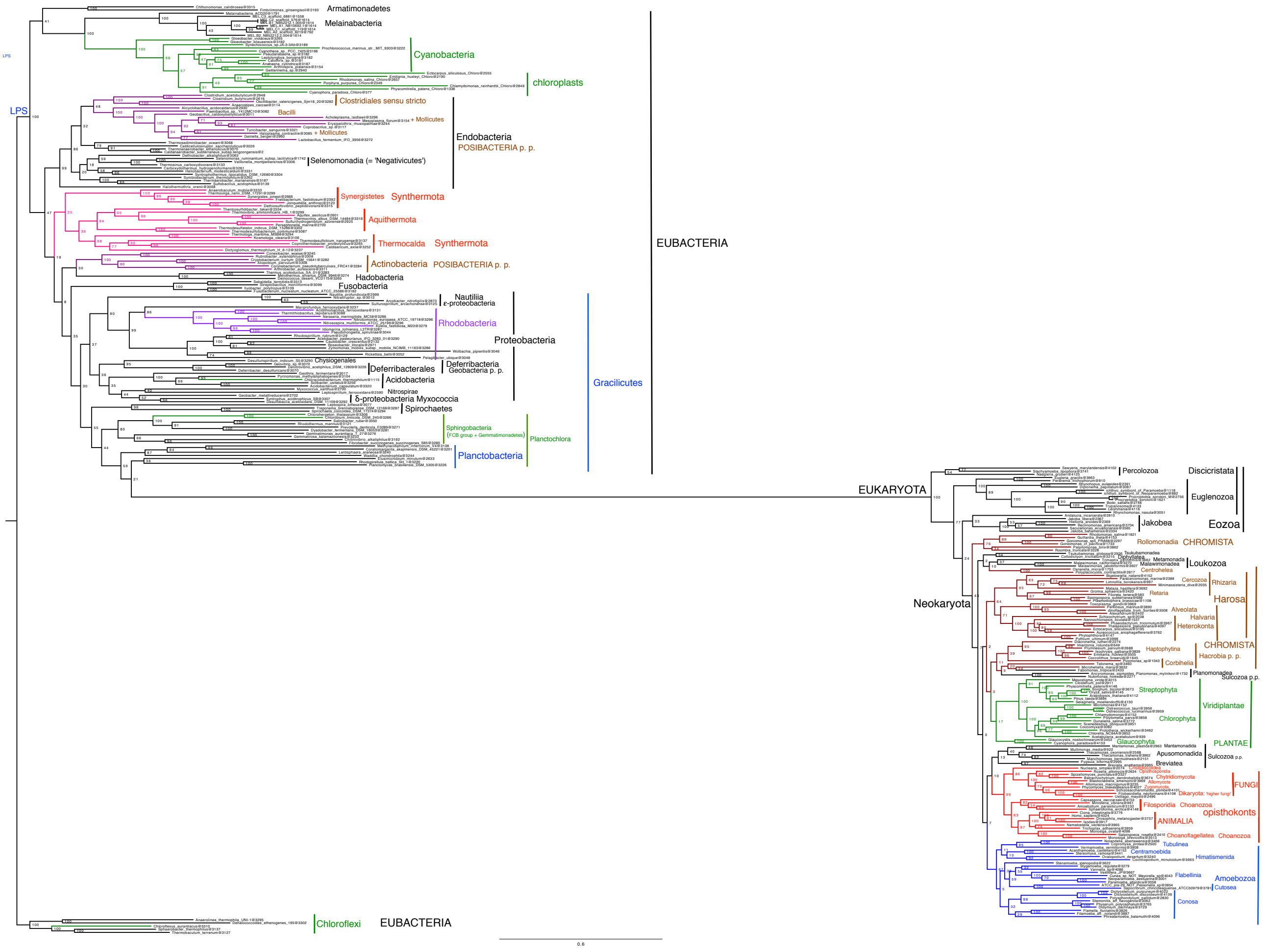

Fig. S13. Site-heterogeneous universal 3-domain PhyloBayes CAT-GTR tree for 26 ribosomal proteins from 143 eukaryotes, 60 archaebacteria, and 151 eubacteria representing all the most divergent lineages.

Support values are posterior probabilities. Two chains were summed (28,777 trees) after removing the first 40% pre-log-likelihood plateau trees as burnin; despite clear plateauing a few deep-branching topological differences (PP 0.5 or less only) remained between the two chains, making maxdiff 1. This consensus tree and chain 1 are the only trees that wrongly placed Thermodesulfobacteriaceae inside Proteobacteria, implying that in chain 1 PhyloBayes got stuck in the wrong topology and did not cope well with the large number of taxa. Chain 2 had maximum support for their being sisters of Aquificia, their usual position; the corresponding ML tree (Fig. S14) confirms this with 89% support. See next page:

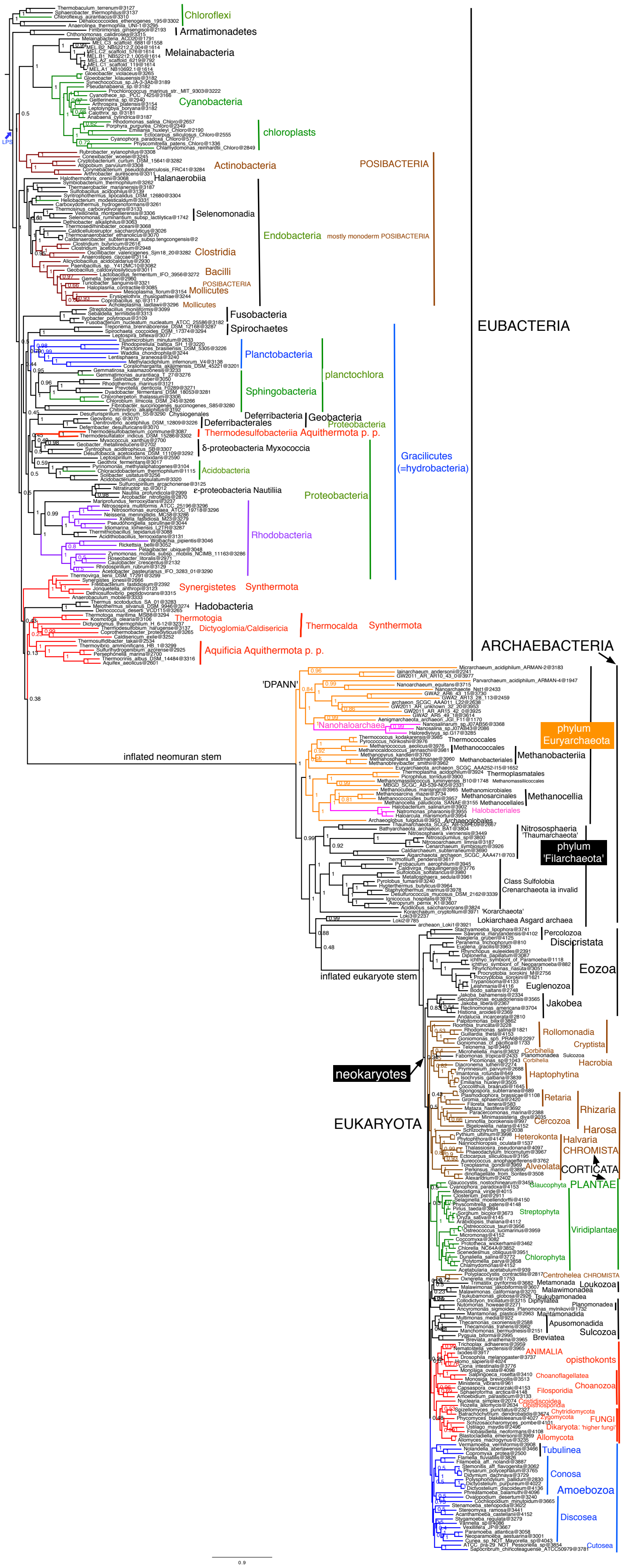
Chloroflexi
Armatimonadetes
Melainabacteria
Cyanobacteria
chloroplasts
LPS
Actinobacteria
POSIBACTERIA
Halanaerobiia
Selenomonadia
Endobacteria
mostly monoderm POSIBACTERIA
Clostridia
Bacilli
POSIBACTERIA
Mollicutes
Mollicutes
Fusobacteria
Spirochaetes
EUBACTERIA
Planctobacteria
planctochlora
Sphingobacteria
Deferribacteria
Geobacteria
Deferribacterales
Proteobacteria
Thermodesulfobacteriia Aquithermota p. p.
δ-proteobacteria Myxococcia
Gracilicutes
(=hydrobacteria)
Acidobacteria
ε-proteobacteria Nautiliia
Proteobacteria
Rhodobacteria
Synergistetes
Synthermota
Hadobacteria
Thermotogia
Dictyoglomia/Caldisericia
Thermocalda
Synthermota
Aquificia Aquithermota p. p.
ARCHAEBACTERIA
'DPANN'
'Nanohaloarchaea'
inflated neomuran stem
phylum
Euryarchaeota
Thermococcales
Methanococcales
Methanobacteriia
Methanobacteriales
Thermoplasmatales
Methanomicrobiales
Methanocellia
Methanosarcinales
Methanocellales
Halobacteriales
Archaeoglobales
Nitrososphaeria
'Thaumarchaeota'
phylum
'Filarchaeota'
Class Sulfolobia
Crenarchaeota ia invalid
'Korarchaeota'
Lokiarchaea Asgard archaea
Percolozoa
Discicristata
Eozoa
Euglenozoa
Jakobea
inflated eukaryote stem
Rollomonadia
Cryptista
Corbihelia
Sulcozoa
Hacrobia
Haptophytina
neokaryotes
Retaria
Rhizaria
Cercozoa
Harosa
EUKARYOTA
Heterokonta
Halvaria
CHROMISTA
Alveolata
CORTICATA
Glaucophyta
PLANTAE
Streptophyta
Viridiplantae
Chlorophyta
Centrohelea CHROMISTA
Metamonada
Loukozoa
Malawimonadea
Tsukubamonadea
Diphyllatea
Planomonadea
Mantamonadida
Apusomonadida
Sulcozoa
Breviatea
ANIMALIA
opisthokonts
Choanoflagellatea
Choanozoa
Filosporidia
Cristidiscoidea
Opisthosporidia
Chytridiomycota
Zygomycota
FUNGI
Dikaryota: 'higher fungi'
Allomycota
Tubulinea
Conosa
Amoebozoa
Discosea
Cutosea
0.9

Figure S14. Site-homogeneous universal 3-domain RAxML PROTGAMMALGF (4 gamma rates) tree for 26 ribosomal proteins from 143 eukaryotes, 60 archaebacteria, and 151 eubacteria representing all the most divergent lineages.
Support values are percentages for 100 pseudoreplicates. See next page:

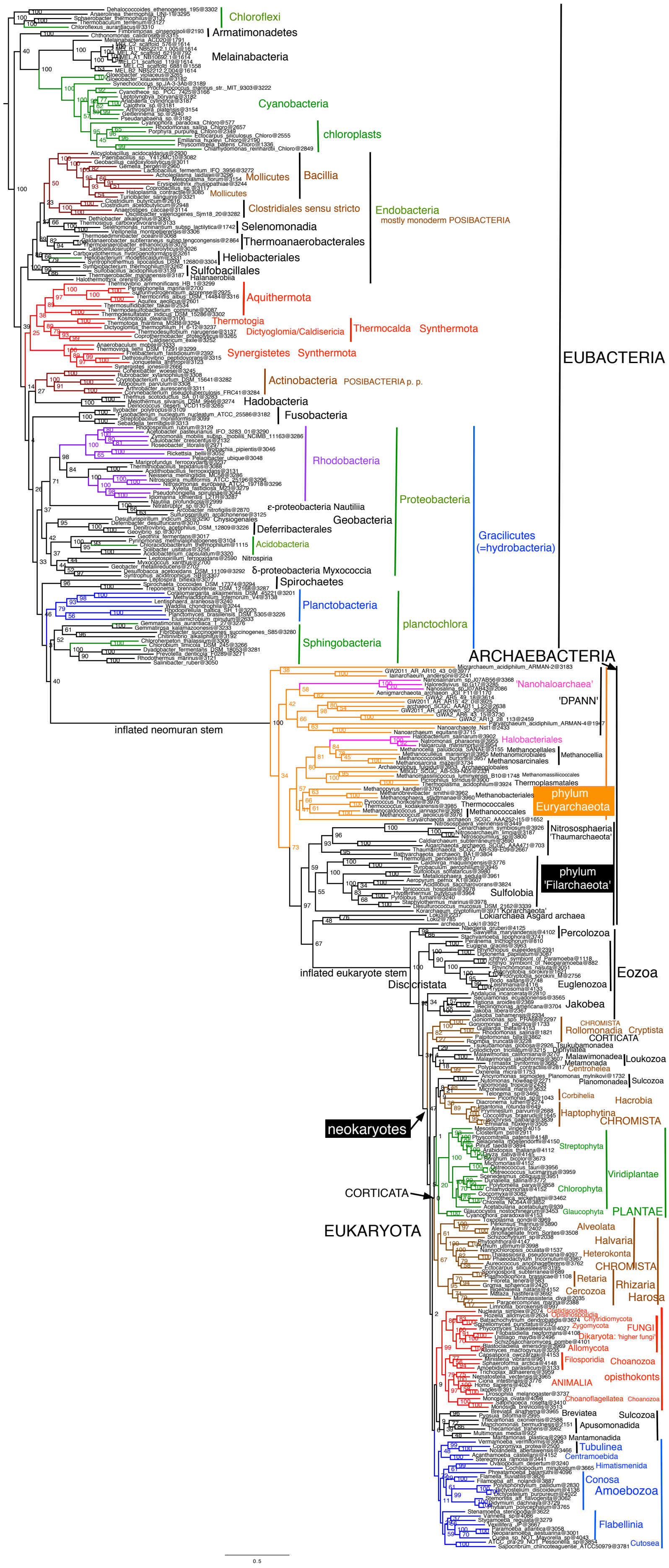
Chloroflexi
Armatimonadetes
Melainabacteria
Cyanobacteria
chloroplasts
Mollicutes
Bacilllia
Mollicutes
Clostridiales sensu stricto
Endobacteria
mostly monoderm POSIBACTERIA
Selenomonadia
Thermoanaerobacterales
Heliobacteriales
Sulfobacillales
Halanaerobiia
Aquithermota
Thermotogia
Dictyoglomia/Caldisericia
Thermocalda
Synthermota
Synergistetes
Synthermota
EUBACTERIA
Actinobacteria
POSIBACTERIA p. p.
Hadobacteria
Fusobacteria
Rhodobacteria
Proteobacteria
Gracilicutes
(=hydrobacteria)
ε-proteobacteria Nautiliia
Geobacteria
Deferribacterales
Acidobacteria
Nitrospiria
δ-proteobacteria Myxococcia
Spirochaetes
Planctobacteria
planctochlora
Sphingobacteria
ARCHAEBACTERIA
inflated neomuran stem
'Nanohaloarchaea'
'DPANN'
Halobacteriales
Methanocellales
Methanomicrobiales
Methanosarcinales
Methanocellia
Archaeoglobales
Methanomassiliicoccales
Thermoplasmatales
Methanobacteriales
phylum
Euryarchaeota
Thermococcales
Methanococcales
Nitrososphaeria
'Thaumarchaeota'
phylum
'Filarchaeota'
Sulfolobia
'Korarchaeota'
Lokiarchaea Asgard archaea
Percolozoa
inflated eukaryote stem
Discicristata
Euglenozoa
Eozoa
Jakobea
CHROMISTA
Rollomonadia
Cryptista
CORTICATA
Tsukubamonadea
Diphyllatea
Malawimonadea
Loukozoa
Metamonada
Centrohelea
Planomonadea
Sulcozoa
Corbihelia
Hacrobia
Haptophytina
CHROMISTA
neokaryotes
Streptophyta
Viridiplantae
CORTICATA
Chlorophyta
Glaucophyta
PLANTAE
EUKARYOTA
Alveolata
Halvaria
Heterokonta
CHROMISTA
Retaria
Rhizaria
Cercozoa
Harosa
Opisthosporidia
Chytridiomycota
Zygomycota
FUNGI
Dikaryota 'higher fungi'
Allomycota
Filosporidia
Choanozoa
opisthokonts
ANIMALIA
Choanoflagellatea
Choanozoa
Breviatea
Sulcozoa
Apusomonadida
Mantamonadida
Tubulinea
Centramoebida
Himatismenida
Conosa
Amoebozoa
Flabellinia
Cutosea
0.5

Fig. S15. Site-heterogeneous PhyloBayes CAT-GTR tree for 26 ribosomal proteins from 156 eubacteria representing all the most divergent lineages with cultivated repesentatives plus Melainabacteria, chloroplasts and 5 shorter-branch mitochondria.

Support values are posterior probabilities. Two chains were summed (40,782 trees) after removing 5725 pre-log-likelihood plateau trees as burnin; despite clear plateauing a few deep-branching topological differences (PP 0.5 or less only) remained between the two chains, making maxdiff 1. The corresponding ML tree placed mitochondria one node lower as sister to all α-proteobacteria. None grouped them with the long-branch rickettsias.

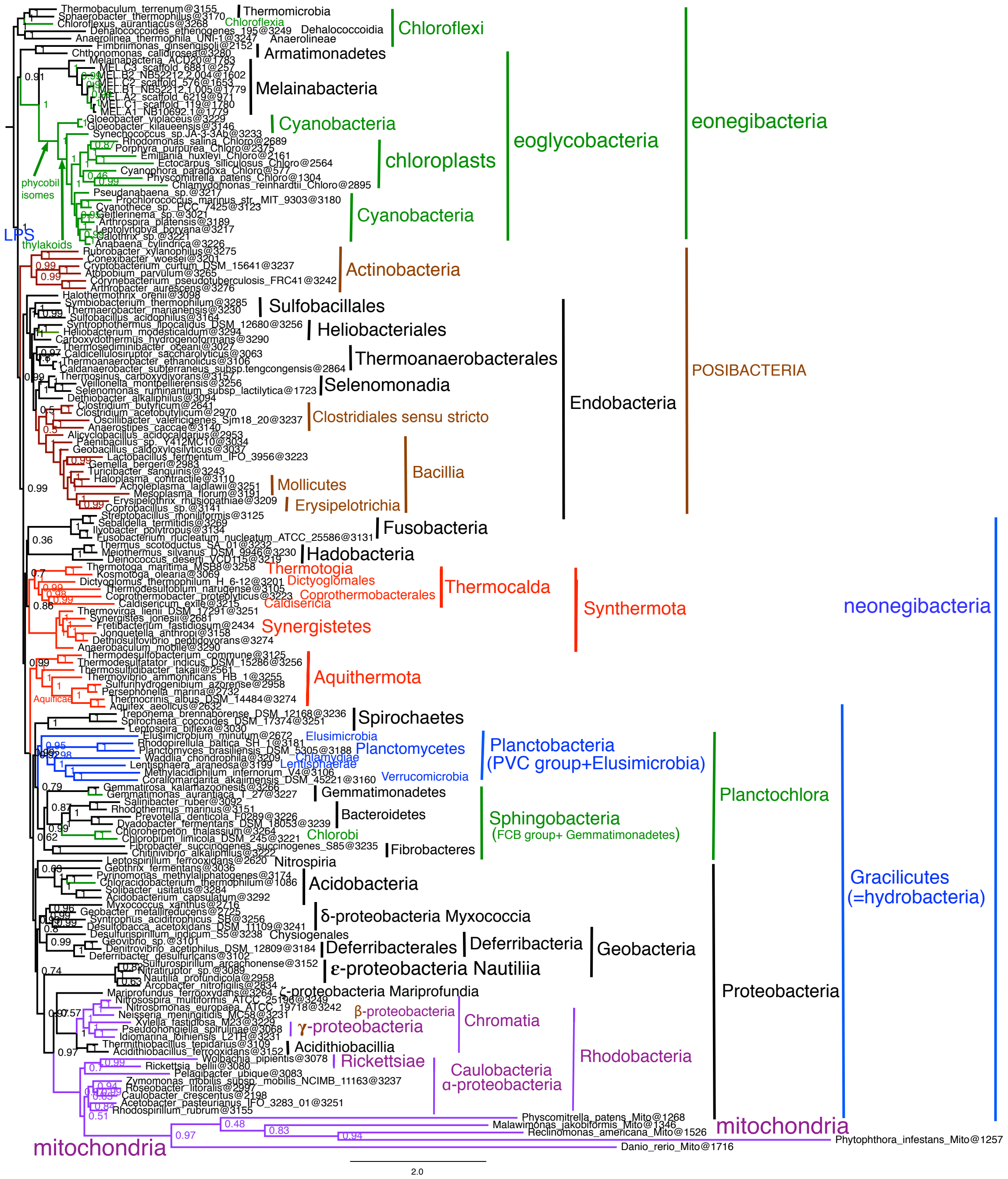
Thermobaculum_terrenum@3155
Sphaerobacter_thermophilus@3170
Chloroflexus_aurantiacus@3268
Dehalococcoides_ethenogenes_195@3249
Anaerolinea_thermophila_UNI-1@3247
Thermomicrobia
Chloroflexia
Dehalococcoidia
Anaerolineae
Chloroflexi
Fimbriimonas_ginsengisoli@2152
Chthonomonas_calidirosea@3280
Armatimonadetes
Melainabacteria_ACD20@1783
MEL.C3_scaffold_6881@257
MEL.B2_NB52212.2.004@1602
MEL.C2_scaffold_576@1653
MEL.B1_NB52212.1.005@1779
MEL.A2_scaffold_6219@971
MEL.C1_scaffold_119@1780
MEL.A1_NB10692.1@1779
Melainabacteria
Gloeobacter_violaceus@3229
Gloeobacter_kilaueensis@3146
Cyanobacteria
Synechococcus_sp.JA-3-3Ab@3233
Rhodomonas_salina_Chloro@2689
Porphyra_purpurea_Chloro@2375
Emiliania_huxleyi_Chloro@2161
Ectocarpus_siliculosus_Chloro@2564
Cyanophora_paradoxa_Chloro@577
Physcomitrella_patens_Chloro@1304
Chlamydomonas_reinhardtii_Chloro@2895
chloroplasts
Pseudanabaena_sp.@3217
Prochlorococcus_marinus_str._MIT_9303@3180
Cyanothece_sp._PCC_7425@3123
Geitlerinema_sp.@3021
Arthrospira_platensis@3189
Leptolyngbya_boryana@3217
Calothrix_sp.@3221
Anabaena_cylindrica@3226
Cyanobacteria
eoglycobacteria
eonegibacteria
phycobilisomes
LPS
thylakoids
0.91
Rubrobacter_xylanophilus@3275
Conexibacter_woesei@3201
Cryptobacterium_curtum_DSM_15641@3237
Atopobium_parvulum@3265
Corynebacterium_pseudotuberculosis_FRC41@3242
Arthrobacter_aurescens@3276
Actinobacteria
Halothermothrix_orenii@3098
Symbiobacterium_thermophilum@3285
Thermaerobacter_marianensis@3230
Sulfobacillus_acidophilus@3164
Sulfobacillales
Syntrophothermus_lipocalidus_DSM_12680@3256
Heliobacterium_modesticaldum@3294
Heliobacteriales
Carboxydothermus_hydrogenoformans@3290
Thermosediminibacter_oceani@3027
Caldicellulosiruptor_saccharolyticus@3063
Thermoanaerobacter_ethanolicus@3106
Caldanaerobacter_subterraneus_subsp.tengcongensis@2864
Thermoanaerobacterales
Thermosinus_carboxydivorans@3157
Veillonella_montpellierensis@3256
Selenomonas_ruminantium_subsp_lactilytica@1723
Selenomonadia
Dethiobacter_alkaliphilus@3094
Clostridium_butyricum@2641
Clostridium_acetobutylicum@2970
Oscillibacter_valericigenes_Sjm18_20@3237
Anaerostipes_caccae@3140
Clostridiales sensu stricto
Endobacteria
POSIBACTERIA
Alicyclobacillus_acidocaldarius@2953
Paenibacillus_sp._Y412MC10@3034
Geobacillus_caldoxylosilyticus@3037
Lactobacillus_fermentum_IFO_3956@3223
Gemella_bergeri@2983
Turicibacter_sanguinis@3243
Haloplasma_contractile@3110
Acholeplasma_laidlawii@3251
Mesoplasma_florum@3191
Mollicutes
Erysipelothrix_rhusiopathiae@3209
Coprobacillus_sp.@3141
Erysipelotrichia
Bacillia
0.99
Streptobacillus_moniliformis@3125
Sebaldella_termitidis@3269
Ilyobacter_polytropus@3134
Fusobacterium_nucleatum_nucleatum_ATCC_25586@3131
Fusobacteria
0.36
Thermus_scotoductus_SA_01@3232
Meiothermus_silvanus_DSM_9946@3230
Deinococcus_deserti_VCD115@3219
Hadobacteria
Thermotoga_maritima_MSB8@3258
Kosmotoga_olearia@3069
Thermotogia
Dictyoglomus_thermophilum_H_6-12@3201
Dictyoglomales
Thermodesulfobium_narugense@3105
Coprothermobacter_proteolyticus@3223
Coprothermobacterales
Caldisericum_exile@3215
Caldisericia
Thermocalda
0.86
Thermovirga_lienii_DSM_17291@3251
Synergistes_jonesii@2681
Fretibacterium_fastidiosum@2434
Jonquetella_anthropi@3158
Dethiosulfovibrio_peptidovorans@3274
Anaerobaculum_mobile@3290
Synergistetes
Synthermota
Thermodesulfobacterium_commune@3125
Thermodesulfatator_indicus_DSM_15286@3256
Thermosulfidibacter_takaii@2561
Thermovibrio_ammonificans_HB_1@3255
Sulfurihydrogenibium_azorense@2958
Persephonella_marina@2732
Thermocrinis_albus_DSM_14484@3274
Aquifex_aeolicus@2632
Aquificae
Aquithermota
neonegibacteria
Treponema_brennaborense_DSM_12168@3236
Spirochaeta_coccoides_DSM_17374@3251
Leptospira_biflexa@3030
Spirochaetes
Elusimicrobium_minutum@2672
Elusimicrobia
Rhodopirellula_baltica_SH_1@3181
Planctomyces_brasiliensis_DSM_5305@3188
Planctomycetes
Waddlia_chondrophila@3209
Chlamydiae
Lentisphaera_araneosa@3199
Lentisphaerae
Methylacidiphilum_infernorum_V4@3106
Coraliomargarita_akajimensis_DSM_45221@3160
Verrucomicrobia
Planctobacteria
(PVC group+Elusimicrobia)
Gemmatirosa_kalamazoonesis@3266
Gemmatimonas_aurantiaca_T_27@3227
Gemmatimonadetes
Salinibacter_ruber@3092
Rhodothermus_marinus@3151
Prevotella_denticola_F0289@3226
Dyadobacter_fermentans_DSM_18053@3239
Bacteroidetes
Chloroherpeton_thalassium@3264
Chlorobium_limicola_DSM_245@3221
Chlorobi
Fibrobacter_succinogenes_succinogenes_S85@3235
Chitinivibrio_alkaliphilus@3222
Fibrobacteres
Sphingobacteria
(FCB group+ Gemmatimonadetes)
Planctochlora
Leptospirillum_ferrooxidans@2620
Nitrospiria
Geothrix_fermentans@3036
Pyrinomonas_methylaliphatogenes@3174
Chloracidobacterium_thermophilum@1086
Solibacter_usitatus@3284
Acidobacterium_capsulatum@3292
Acidobacteria
Myxococcus_xanthus@2716
Geobacter_metallireducens@2725
Syntrophus_aciditrophicus_SB@3256
Desulfobacca_acetoxidans_DSM_11109@3241
δ-proteobacteria Myxococcia
Desulfurispirillum_indicum_S5@3238
Chysiogenales
Geovibrio_sp.@3101
Denitrovibrio_acetiphilus_DSM_12809@3184
Deferribacter_desulfuricans@3102
Deferribacterales
Deferribacteria
Geobacteria
Sulfurospirillum_arcachonense@3152
Nitratiruptor_sp.@3089
Nautilia_profundicola@2958
Arcobacter_nitrofigilis@2834
ε-proteobacteria Nautiliia
Mariprofundus_ferrooxydans@3264
ζ-proteobacteria Mariprofundia
Nitrosospira_multiformis_ATCC_25196@3249
Nitrosomonas_europaea_ATCC_19718@3242
Neisseria_meningitidis_MC58@3231
β-proteobacteria
Xylella_fastidiosa_M23@3229
Pseudohongiella_spirulinae@3068
Idiomarina_loihiensis_L2TR@3231
γ-proteobacteria
Chromatia
Thermithiobacillus_tepidarius@3109
Acidithiobacillus_ferrooxidans@3152
Acidithiobacillia
Wolbachia_pipientis@3078
Rickettsia_bellii@3080
Rickettsiae
Pelagibacter_ubique@3083
Zymomonas_mobilis_subsp._mobilis_NCIMB_11163@3237
Roseobacter_litoralis@2997
Caulobacter_crescentus@2198
Acetobacter_pasteurianus_IFO_3283_01@3251
Rhodospirillum_rubrum@3155
Caulobacteria
α-proteobacteria
Rhodobacteria
Proteobacteria
Gracilicutes
(=hydrobacteria)
Physcomitrella_patens_Mito@1268
Malawimonas_jakobiformis_Mito@1346
Reclinomonas_americana_Mito@1526
Phytophthora_infestans_Mito@1257
Danio_rerio_Mito@1716
mitochondria
mitochondria
0.48
0.83
0.94
0.97
2.0

Figure S16. Site-homogeneous RAxML-PROTGAMMALGF (4 gamma rates) tree of 305 prokaryotic structural maintenace of chromosome (SMC) proteins using 448 amino acid positions. See next page:

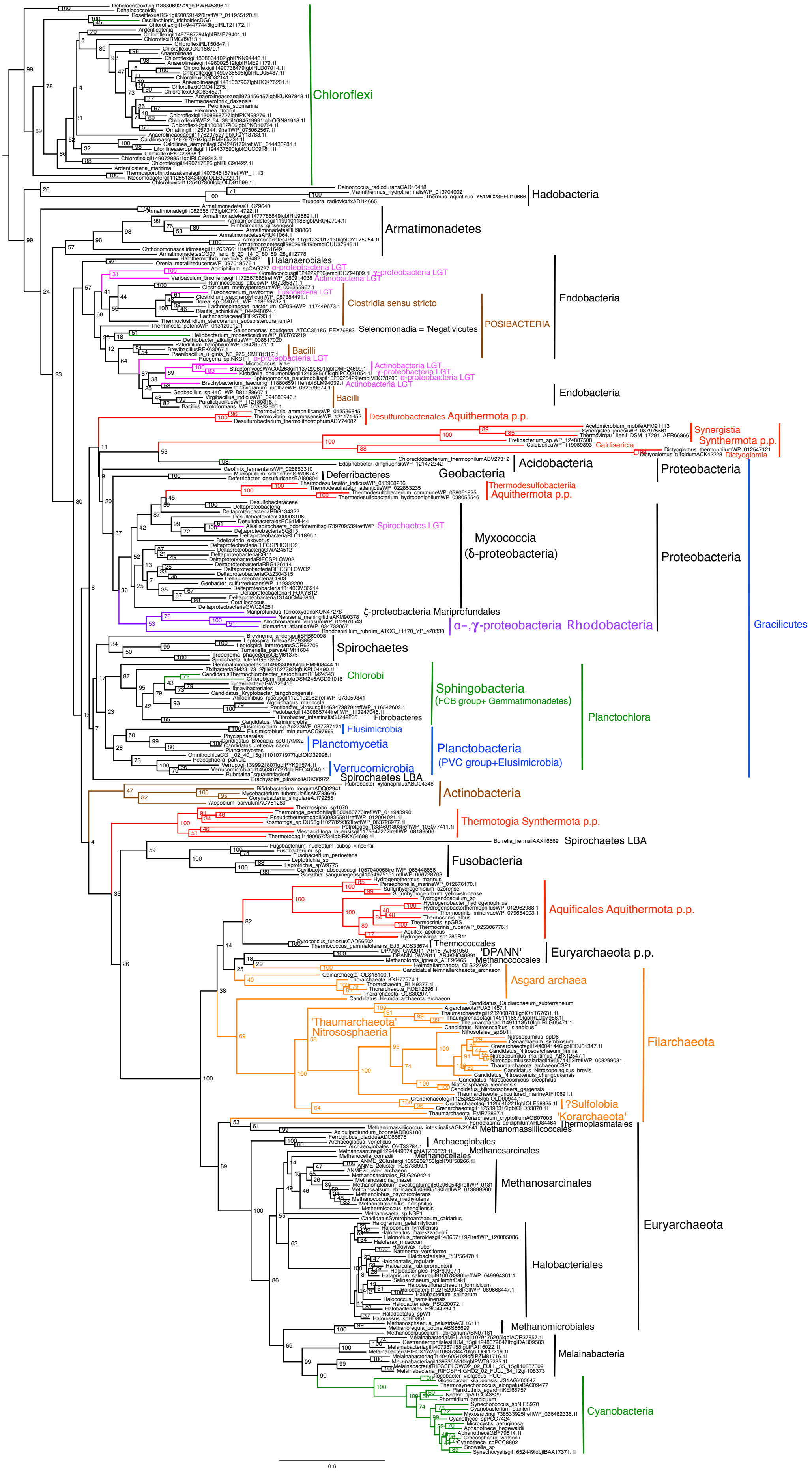
Chloroflexi
Hadobacteria
Armatimonadetes
Halanaerobiales
α-proteobacteria LGT
γ-proteobacteria LGT
Actinobacteria LGT
Fusobacteria LGT
Clostridia sensu stricto
Selenomonadia = 'Negativicutes
POSIBACTERIA
Endobacteria
Bacilli
Desulfurobacteriales Aquithermota p.p.
Synergistia
Synthermota p.p.
Caldisericia
Dictyoglomia
Acidobacteria
Geobacteria
Deferribacteres
Proteobacteria
Thermodesulfobacteriia
Aquithermota p.p.
Myxococcia
(δ-proteobacteria)
Spirochaetes LGT
ζ-proteobacteria Mariprofundales
α-,γ-proteobacteria Rhodobacteria
Gracilicutes
Spirochaetes
Chlorobi
Sphingobacteria
(FCB group+ Gemmatimonadetes)
Fibrobacteres
Planctochlora
Elusimicrobia
Planctomycetia
Planctobacteria
(PVC group+Elusimicrobia)
Verrucomicrobia
Spirochaetes LBA
Actinobacteria
Thermotogia Synthermota p.p.
Spirochaetes LBA
Fusobacteria
Aquificales Aquithermota p.p.
Thermococcales
'DPANN'
Euryarchaeota p.p.
Methanococcales
Asgard archaea
'Thaumarchaeota'
Nitrososphaeria
Filarchaeota
?Sulfolobia
'Korarchaeota'
Thermoplasmatales
Methanomassiliicoccales
Archaeoglobales
Methanosarcinales
Methanocellales
Methanosarcinales
Euryarchaeota
Halobacteriales
Methanomicrobiales
Melainabacteria
Cyanobacteria
0.6

Figure S16

Figure S17. Site-heterogeneous PhyloBayes CAT-GTR tree of 321 largely prokaryotic structural maintenace of chromosome (SMC) proteins using 448 amino acid positions. maxdiff 0.1246. Four of the five eukaryote sequences group weakly with a relatively short-branch arsgard seuce whereas the human sequence groups with a longer-branch lokiarchaeote sequence. Some other Asgard seunces have even longer branches and group weakly with *Korarchaeum* and strongly with an almiost ceratinly artefactual grouping of Sulfolobia. *Methanopyrus* and the Synthermote eubacterium *Coprothermobacter*, the longest branch on the whole tree.

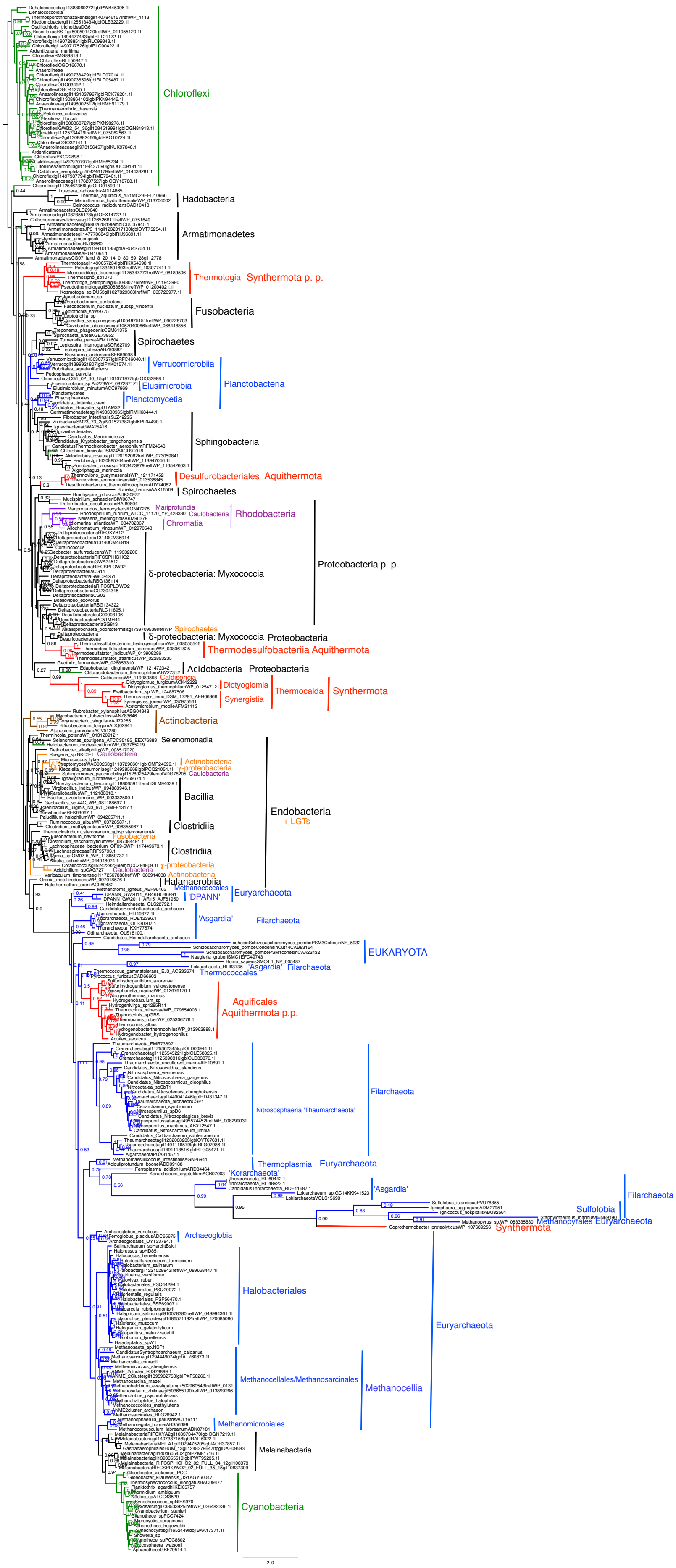
Chloroflexi
Hadobacteria
Armatimonadetes
Thermotogia Synthermota p. p.
Fusobacteria
Spirochaetes
Verrucomicrobiia
Elusimicrobia
Planctobacteria
Planctomycetia
Sphingobacteria
Desulfurobacteriales Aquithermota
Spirochaetes
Mariprofundia
Caulobacteria
Rhodobacteria
Chromatia
δ-proteobacteria: Myxococcia
Proteobacteria p. p.
Spirochaetes
δ-proteobacteria: Myxococcia Proteobacteria
Thermodesulfobacteriia Aquithermota
Acidobacteria Proteobacteria
Caldisericia
Dictyoglomia
Thermocalda
Synthermota
Synergistia
Actinobacteria
Selenomonadia
Caulobacteria
Actinobacteria
γ-proteobacteria
Caulobacteria
Bacillia
Endobacteria
+ LGTs
Clostridiia
Fusobacteria
Clostridiia
γ-proteobacteria
Caulobacteria
Actinobacteria
Halanaerobiia
Methanococcales
Euryarchaeota
'DPANN'
'Asgardia'
Filarchaeota
EUKARYOTA
'Asgardia' Filarchaeota
Thermococcales
Aquificales
Aquithermota p.p.
Filarchaeota
Nitrososphaeria 'Thaumarchaeota'
Thermoplasmia
Euryarchaeota
'Korarchaeota'
'Asgardia'
Filarchaeota
Sulfolobia
Methanopyrales Euryarchaeota
Synthermota
Archaeoglobia
Halobacteriales
Euryarchaeota
Methanocellales/Methanosarcinales
Methanocellia
Methanomicrobiales
Melainabacteria
Cyanobacteria
2.0

Figure S17

Ribosomal protein (RP) alignments in fasta format as a zip files
1. These 51 **.fasta files** comprise the regions for 51 RPs after trimming as used for our trees, including all trees shown directly on Figs 3-10 plus those by other methods whose support values are included on them and include over 414 taxa, some excluded from our final analyses.

To enable readers to identify those taxa for which our alignment database uses abbreviated names or interim names, we also include the SCAFOS taxonomy (OTU) file as a key to translate from them to the 354 final names on these trees:
OTU354Arch+Eub+Euk_NoAtrichosa_28July2016.txt

2. **SMC proteins.** 305 complete SMC sequences are in GenBank format (.gb) plus a mask (at the beginning of file) in which 1s mark the 448 included positions and 0s mark those excluded from our analyses.

Tree files in Newick format in a zip file with separate subfolders for each of the nine figures. These comprise all 22 trees used for Figs 3-10 and 12. Their titles indicate the method used (PoiPB means PhyloBayes Poisson; PB means PhyloBayes CAT-GTRGamma)