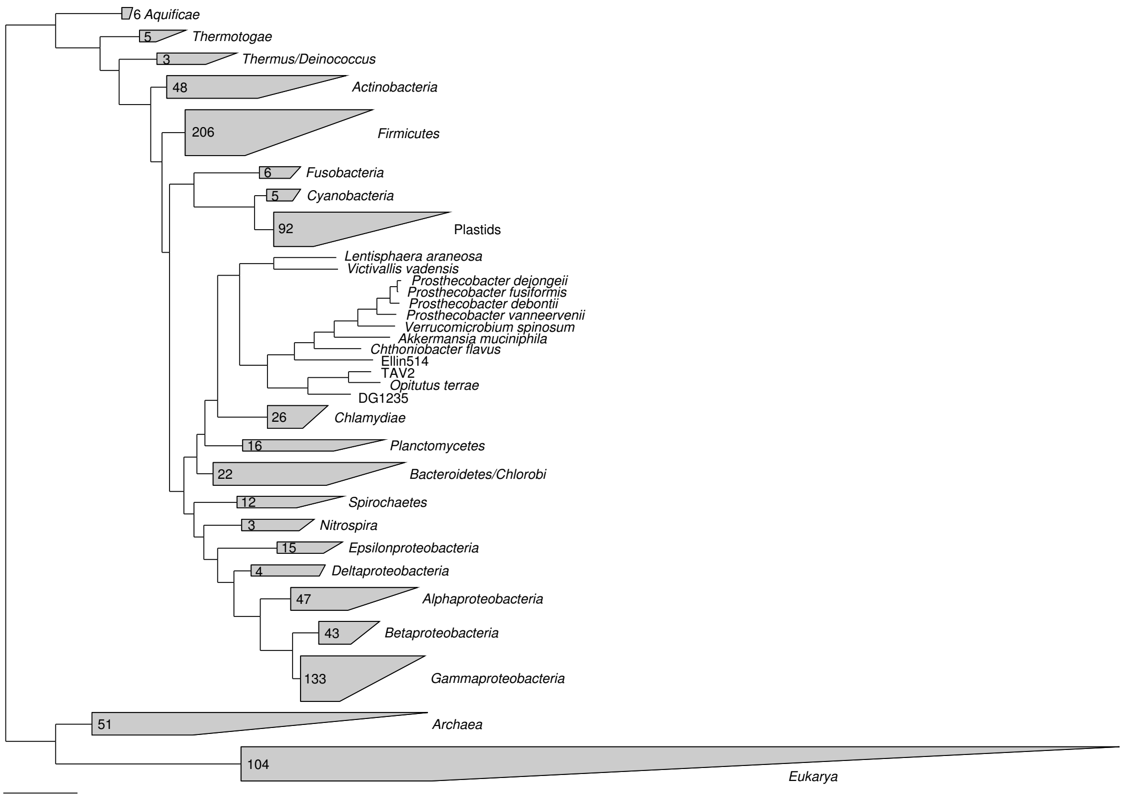
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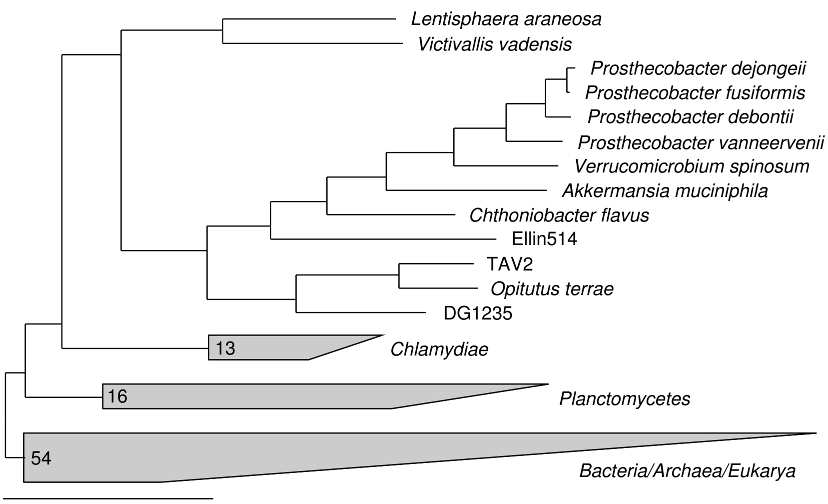
5 Thermotogae
3 Thermus/Deinococcus
48 Actinobacteria
206 Firmicutes
6 Fusobacteria
5 Cyanobacteria
92 Plastids
Lentisphaera araneosa
Victivallis vadensis
Prosthecobacter dejongeii
Prosthecobacter fusiformis
Prosthecobacter debontii
Prosthecobacter vanneervenii
Verrucomicrobium spinosum
Akkermansia muciniphila
Chthoniobacter flavus
Ellin514
TAV2
Opitutus terrae
DG1235
26 Chlamydiae
16 Planctomycetes
22 Bacteroidetes/Chlorobi
12 Spirochaetes
3 Nitrospira
15 Epsilonproteobacteria
4 Deltaproteobacteria
47 Alphaproteobacteria
43 Betaproteobacteria
133 Gammaproteobacteria
51 Archaea
104 Eukarya

(A)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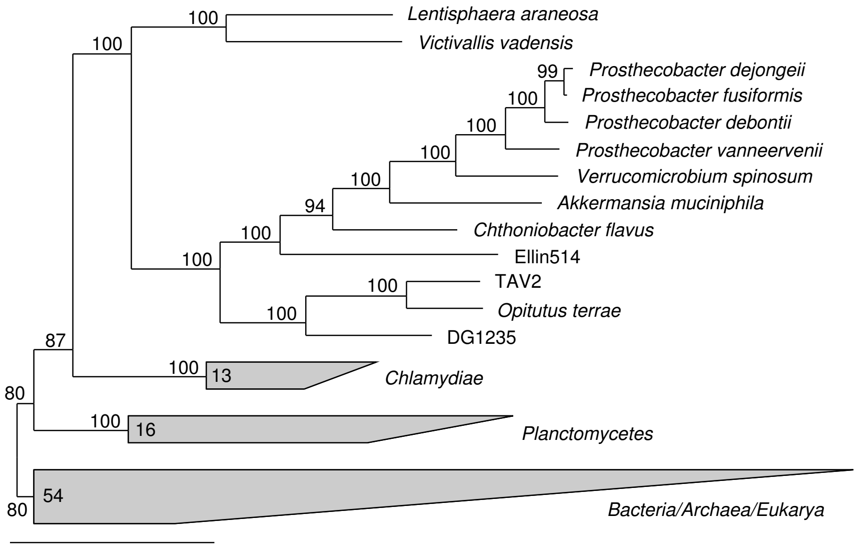
Verrucomicrobium spinosum
Akkermansia muciniphila
Chthoniobacter flavus
Ellin514
TAV2
Opitutus terrae
DG1235
13 Chlamydiae
16 Planctomycetes
54 Bacteria/Archaea/Eukarya

(B)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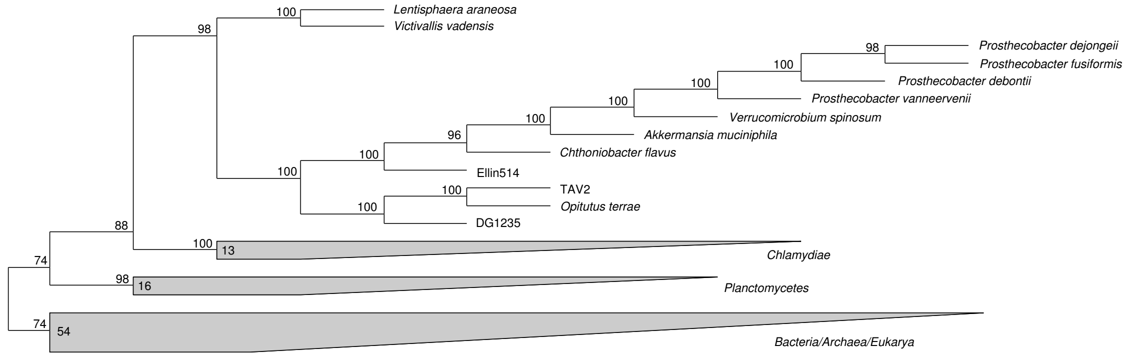
Prosthecobacter vanneervenii
100
Verrucomicrobium spinosum
94
Akkermansia muciniphila
100
Chthoniobacter flavus
100
Ellin514
100
TAV2
100
Opitutus terrae
DG1235
87
100
13
Chlamydiae
80
100
16
Planctomycetes
54
Bacteria/Archaea/Eukarya
80

(C)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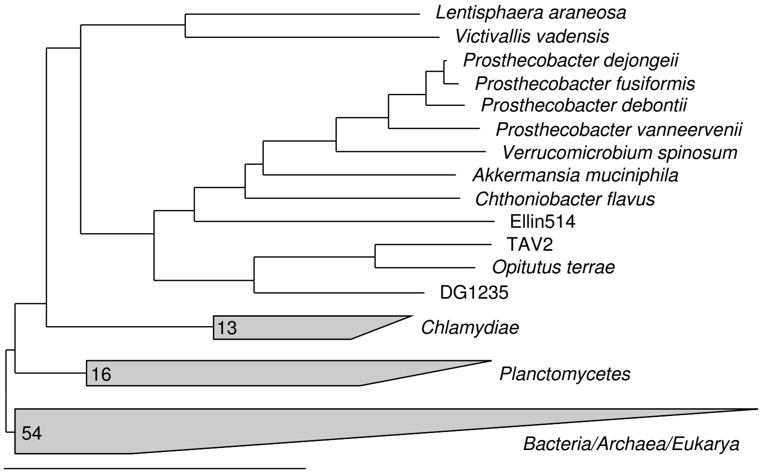
100
Prosthecobacter vanneervenii
100
Verrucomicrobium spinosum
96
Akkermansia muciniphila
100
Chthoniobacter flavus
100
Ellin514
100
TAV2
100
Opitutus terrae
DG1235
88
100
13
Chlamydiae
74
98
16
Planctomycetes
74
54
Bacteria/Archaea/Eukarya

(D)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Verrucomicrobium spinosum
Akkermansia muciniphila
Chthoniobacter flavus
Ellin514
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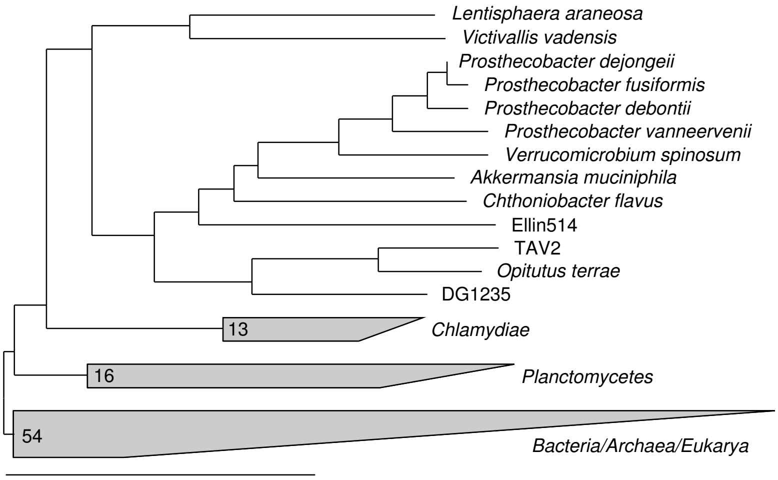
DG1235
13
Chlamydiae
16
Planctomycetes
54
Bacteria/Archaea/Eukarya

(E)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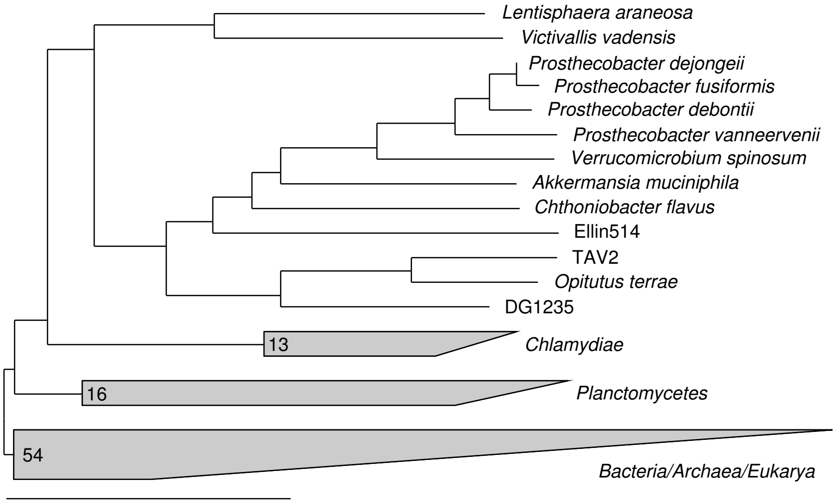
Verrucomicrobium spinosum
Akkermansia muciniphila
Chthoniobacter flavus
Ellin514
TAV2
Opitutus terrae
DG1235
13
Chlamydiae
16
Planctomycetes
54
Bacteria/Archaea/Eukarya

(F)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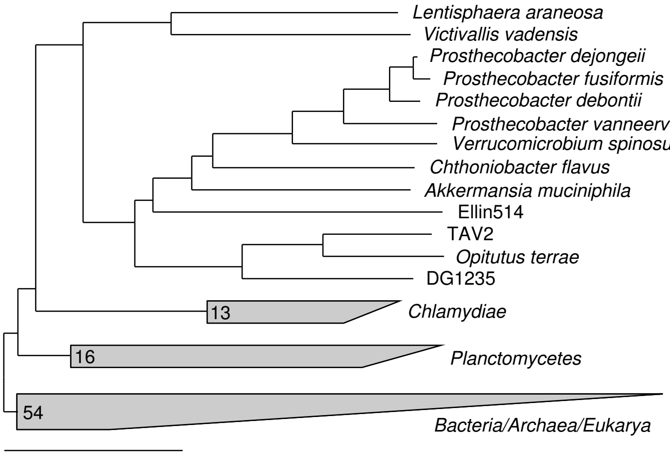
Akkermansia muciniphila
Chthoniobacter flavus
Ellin514
TAV2
Opitutus terrae
DG1235
13
Chlamydiae
16
Planctomycetes
54
Bacteria/Archaea/Eukarya

(G)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Victivallis vadensis
Prosthecobacter dejongeii
Prosthecobacter fusiformis
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Verrucomicrobium spinosum
Chthoniobacter flavus
Akkermansia muciniphila
Ellin514
TAV2
Opitutus terrae
DG1235
13
Chlamydiae
16
Planctomycetes
54
Bacteria/Archaea/Eukarya

(H)

Supplementary Material – Representative selection of 23S rRNA trees.

Phylogenetic 23S rRNA trees were produced using the treeing methods and minimum similarity filters listed below. Numbers in closed groups denote the number of included sequences. Numbers at nodes represent bootstrap values in percent. Bar represents 10% estimated evolutionary distance. Except for Panel A, the group of other *Bacteria* / *Archaea* / *Eukarya* was scaled down graphically.

(A) RAxML; 50%; same tree as Figure 4A with group *Bacteria/Archaea/Eukarya* opened

(B) AxML; 50%

(C) PHYML; 50%; 1000 bootstraps

(D) DNAPARS; 50%; 1000 bootstraps

(E) FITCH; 50%

(F) NEIGHBOR; 50%

(G) NEIGHBOR; 20%

(H) NEIGHBOR; 0%