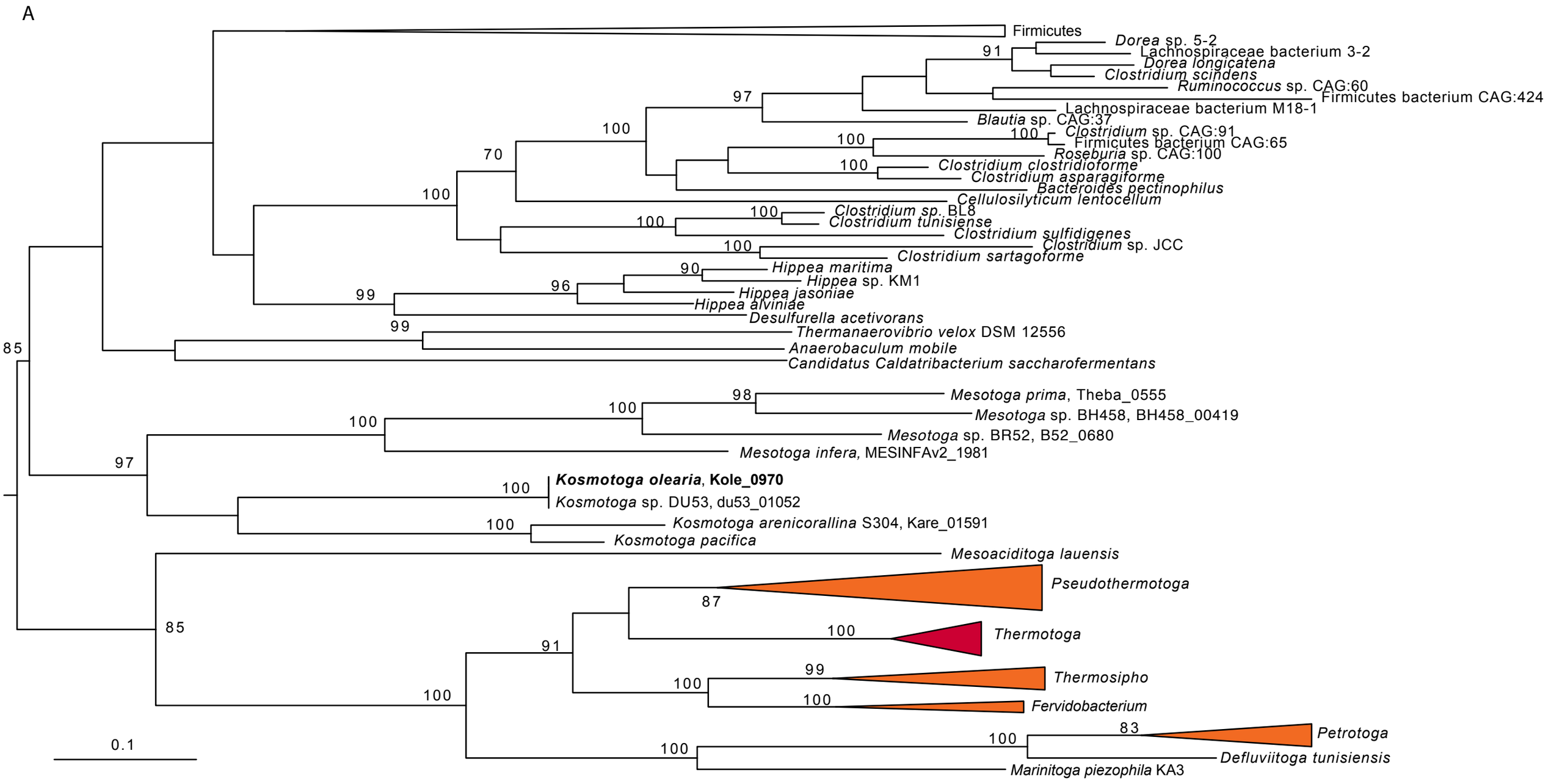
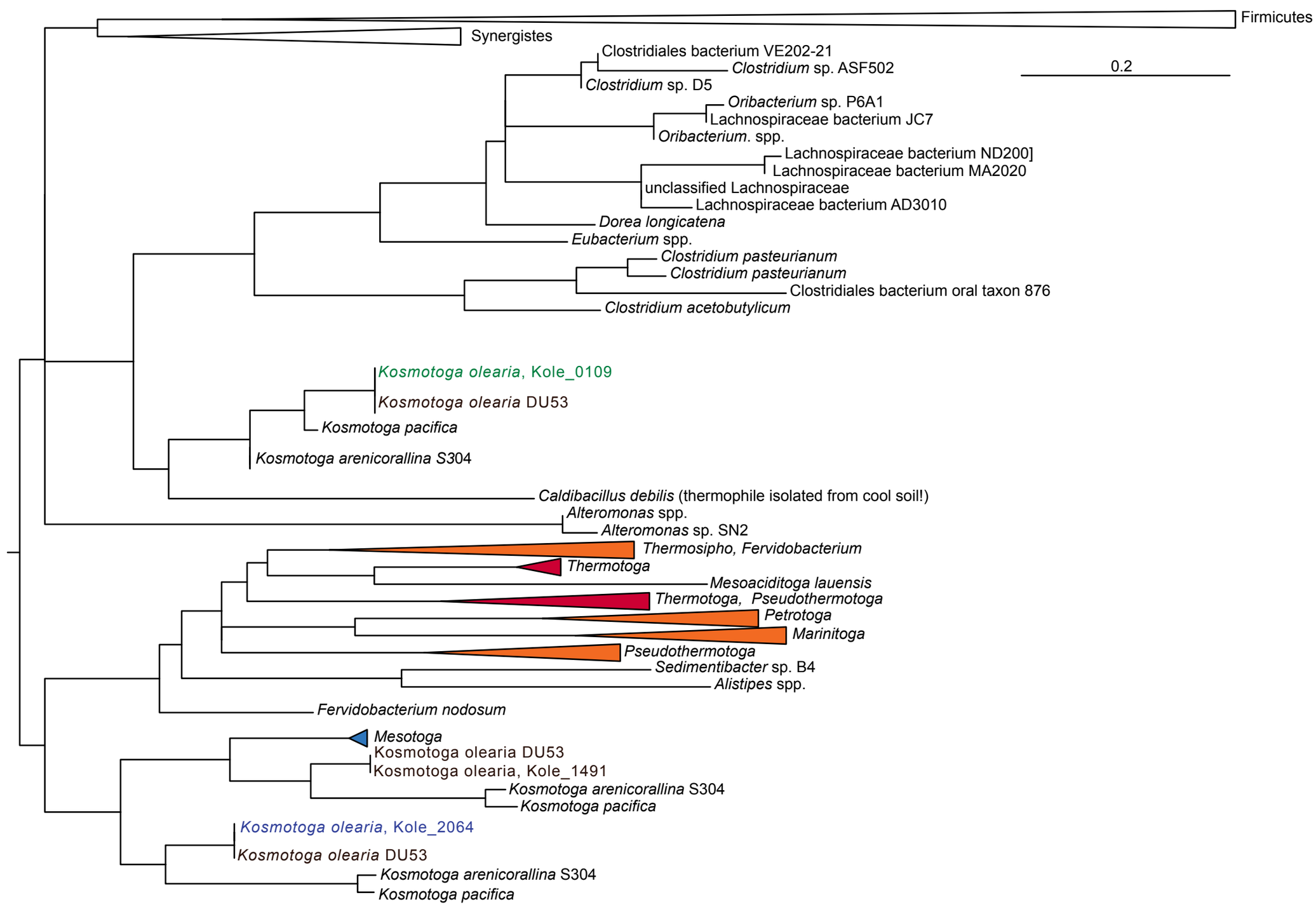
A


Firmicutes
Dorea sp. 5-2
Lachnospiraceae bacterium 3-2
Dorea longicatena
Clostridium scindens
Ruminococcus sp. CAG:60
Firmicutes bacterium CAG:424
Lachnospiraceae bacterium M18-1
Blautia sp. CAG:37
Clostridium sp. CAG:91
Firmicutes bacterium CAG:65
Roseburia sp. CAG:100
Clostridium clostridioforme
Clostridium asparagiforme
Bacteroides pectinophilus
Cellulosilyticum lentocellum
Clostridium sp. BL8
Clostridium tunisiense
Clostridium sulfidigenes
Clostridium sp. JCC
Clostridium sartagoforme
Hippea maritima
Hippea sp. KM1
Hippea jasoniae
Hippea alviniae
Desulfurella acetivorans
Thermanaerovibrio velox DSM 12556
Anaerobaculum mobile
Candidatus Caldatribacterium saccharofermentans
Mesotoga prima, Theba_0555
Mesotoga sp. BH458, BH458_00419
Mesotoga sp. BR52, B52_0680
Mesotoga infera, MESINFAv2_1981
Kosmotoga olearia, Kole_0970
Kosmotoga sp. DU53, du53_01052
Kosmotoga arenicorallina S304, Kare_01591
Kosmotoga pacifica
Mesoaciditoga lauensis
Pseudothermotoga
Thermotoga
Thermosipho
Fervidobacterium
Petrotoga
Defluviitoga tunisiensis
Marinitoga piezophila KA3
0.1

B


Firmicutes
Synergistes
Clostridiales bacterium VE202-21
Clostridium sp. ASF502
Clostridium sp. D5
0.2
Oribacterium sp. P6A1
Lachnospiraceae bacterium JC7
Oribacterium. spp.
Lachnospiraceae bacterium ND200]
Lachnospiraceae bacterium MA2020
unclassified Lachnospiraceae
Lachnospiraceae bacterium AD3010
Dorea longicatena
Eubacterium spp.
Clostridium pasteurianum
Clostridium pasteurianum
Clostridiales bacterium oral taxon 876
Clostridium acetobutylicum
Kosmotoga olearia, Kole_0109
Kosmotoga olearia DU53
Kosmotoga pacifica
Kosmotoga arenicorallina S304
Caldibacillus debilis (thermophile isolated from cool soil!)
Alteromonas spp.
Alteromonas sp. SN2
Thermosipho, Fervidobacterium
Thermotoga
Mesoaciditoga lauensis
Thermotoga, Pseudothermotoga
Petrotoga
Marinitoga
Pseudothermotoga
Sedimentibacter sp. B4
Alistipes spp.
Fervidobacterium nodosum
Mesotoga
Kosmotoga olearia DU53
Kosmotoga olearia, Kole_1491
Kosmotoga arenicorallina S304
Kosmotoga pacifica
Kosmotoga olearia, Kole_2064
Kosmotoga olearia DU53
Kosmotoga arenicorallina S304
Kosmotoga pacifica

C

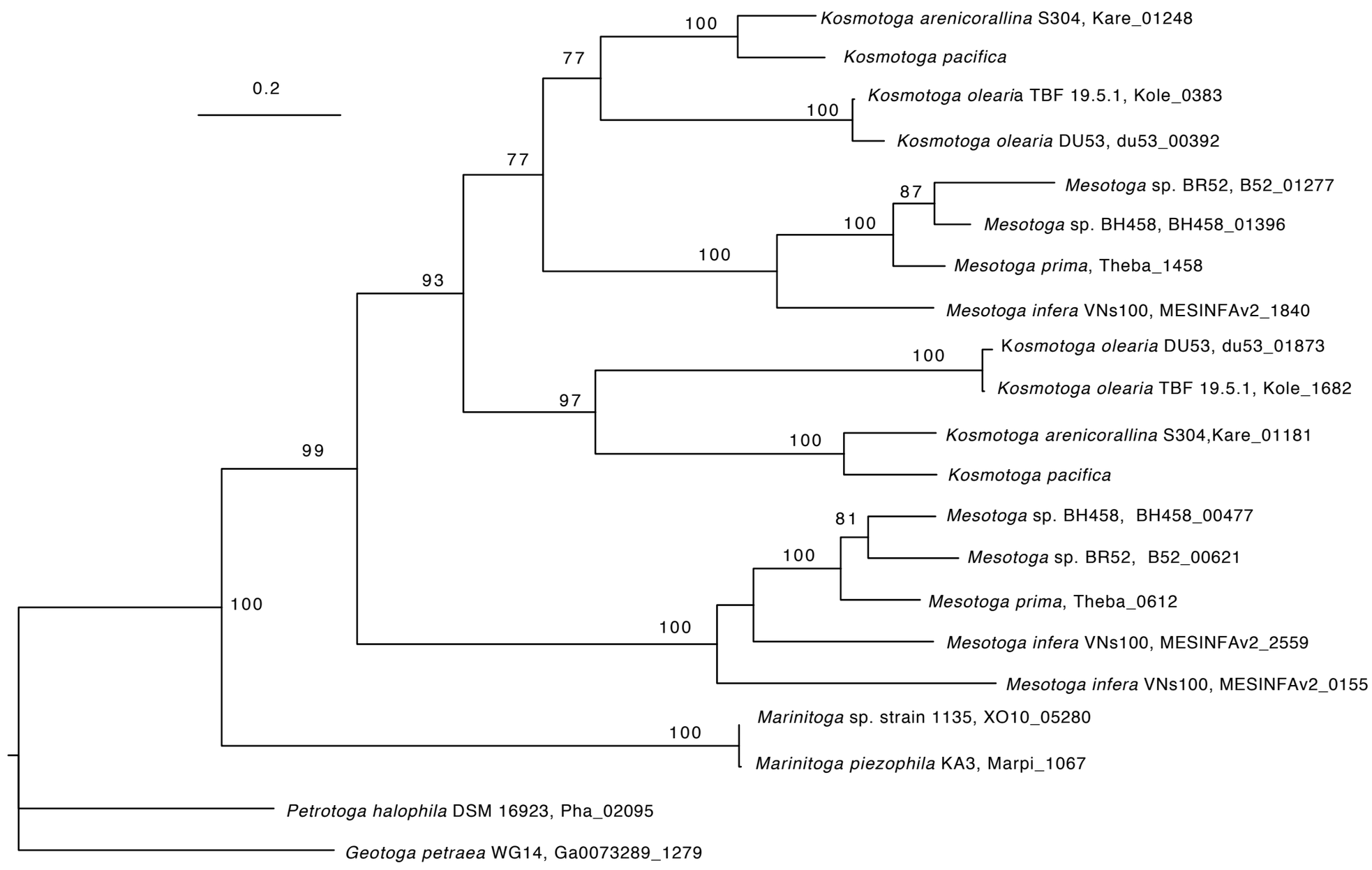

Kosmotoga arenicorallina S304, Kare_01248
Kosmotoga pacifica
0.2
Kosmotoga olearia TBF 19.5.1, Kole_0383
Kosmotoga olearia DU53, du53_00392
Mesotoga sp. BR52, B52_01277
Mesotoga sp. BH458, BH458_01396
Mesotoga prima, Theba_1458
Mesotoga infera VNs100, MESINFAv2_1840
Kosmotoga olearia DU53, du53_01873
Kosmotoga olearia TBF 19.5.1, Kole_1682
Kosmotoga arenicorallina S304,Kare_01181
Kosmotoga pacifica
Mesotoga sp. BH458, BH458_00477
Mesotoga sp. BR52, B52_00621
Mesotoga prima, Theba_0612
Mesotoga infera VNs100, MESINFAv2_2559
Mesotoga infera VNs100, MESINFAv2_0155
Marinitoga sp. strain 1135, XO10_05280
Marinitoga piezophila KA3, Marpi_1067
Petrotoga halophila DSM 16923, Pha_02095
Geotoga petraea WG14, Ga0073289_1279

FIG S6. Evolutionary histories of three temperature-responsive gene families. Panel A: Enoyl-(acyl-carrier-protein) reductase II (*fabK*, Kole_0970), a gene involved in fatty acid synthesis. Monophyletic Thermotogae genera are collapsed into triangles and color-coded according to their optimal growth temperature: hyperthermophiles are in red, thermophiles are in orange and mesophiles are in blue. Two clades containing Firmicutes are also collapsed. **Panel B:** Cold shock proteins (*Csp*) Kole_0109, Kole_1491, and Kole_2064. These proteins are short and highly conserved, resulting in poor bootstrap support for the branches in this tree (< 70%; values not shown). However, Kole_0109 and its homologs in other *Kosmotoga* spp. cluster outside the Thermotogae clade, suggesting that it was laterally acquired. Notably, in the *K. olearia* genome Kole_0109 is adjacent to two genes also predicted to have been laterally acquired (Kole_0110 and Kole_0111, see Dataset 1, Table 1). Therefore, we hypothesize that these three genes were likely acquired laterally from an unidentified bacterial lineage in a single event. **Panel C**: PpiC-type PPIases, Kole_1682 and Kole_0383. Only genes with > 30% amino acid sequence identity to the *K. olearia* homologs were included, since the remaining homologs could not be confidently aligned. The three trees were reconstructed using maximum likelihood method (WAG + Γ substitution model; shape parameter estimated; four rate categories) as implemented in RAxML (16) within Geneious v. 9.1.3. Bootstrapping analysis was performed with 100 replicates. Bootstrap support values below 70% are not shown.