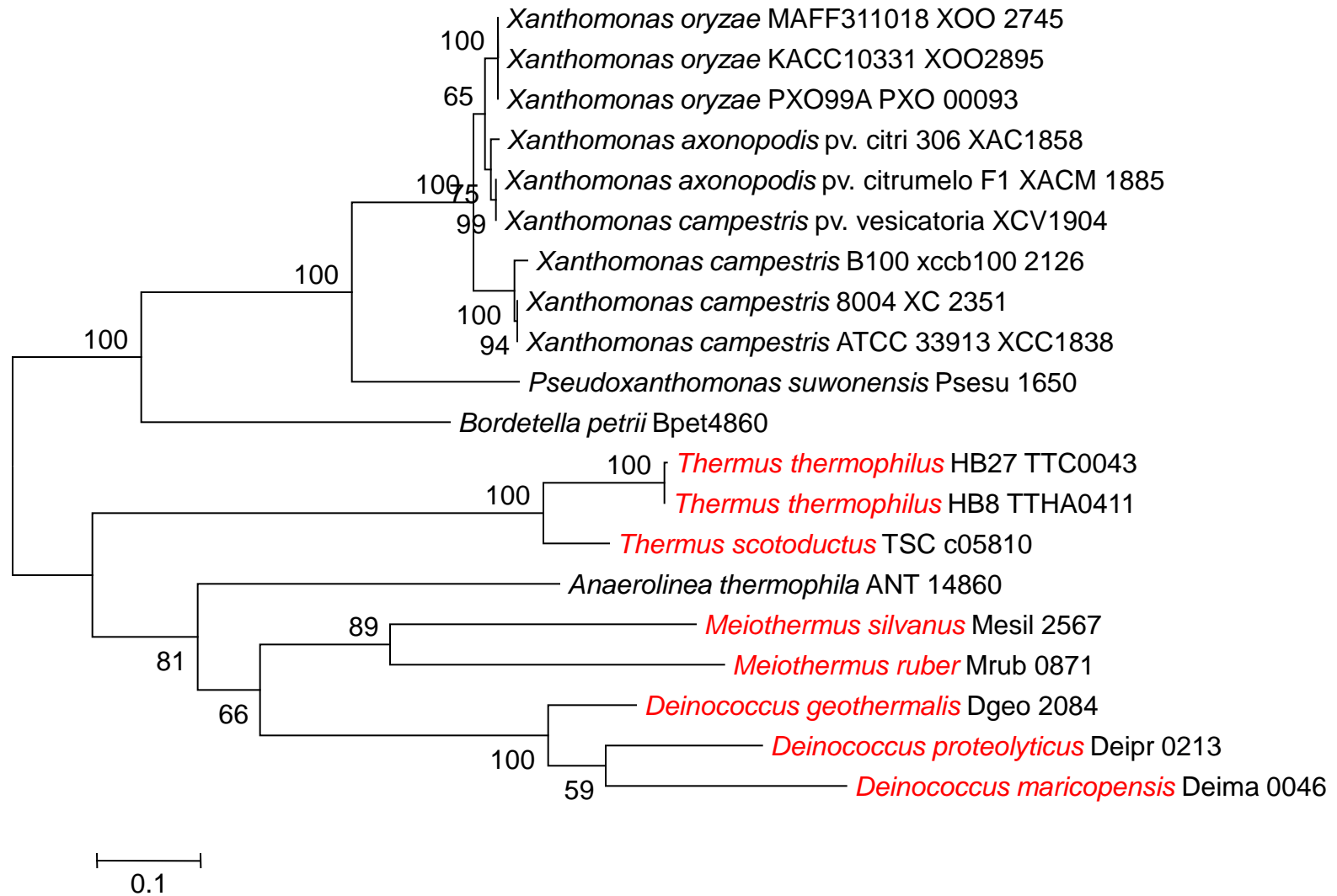


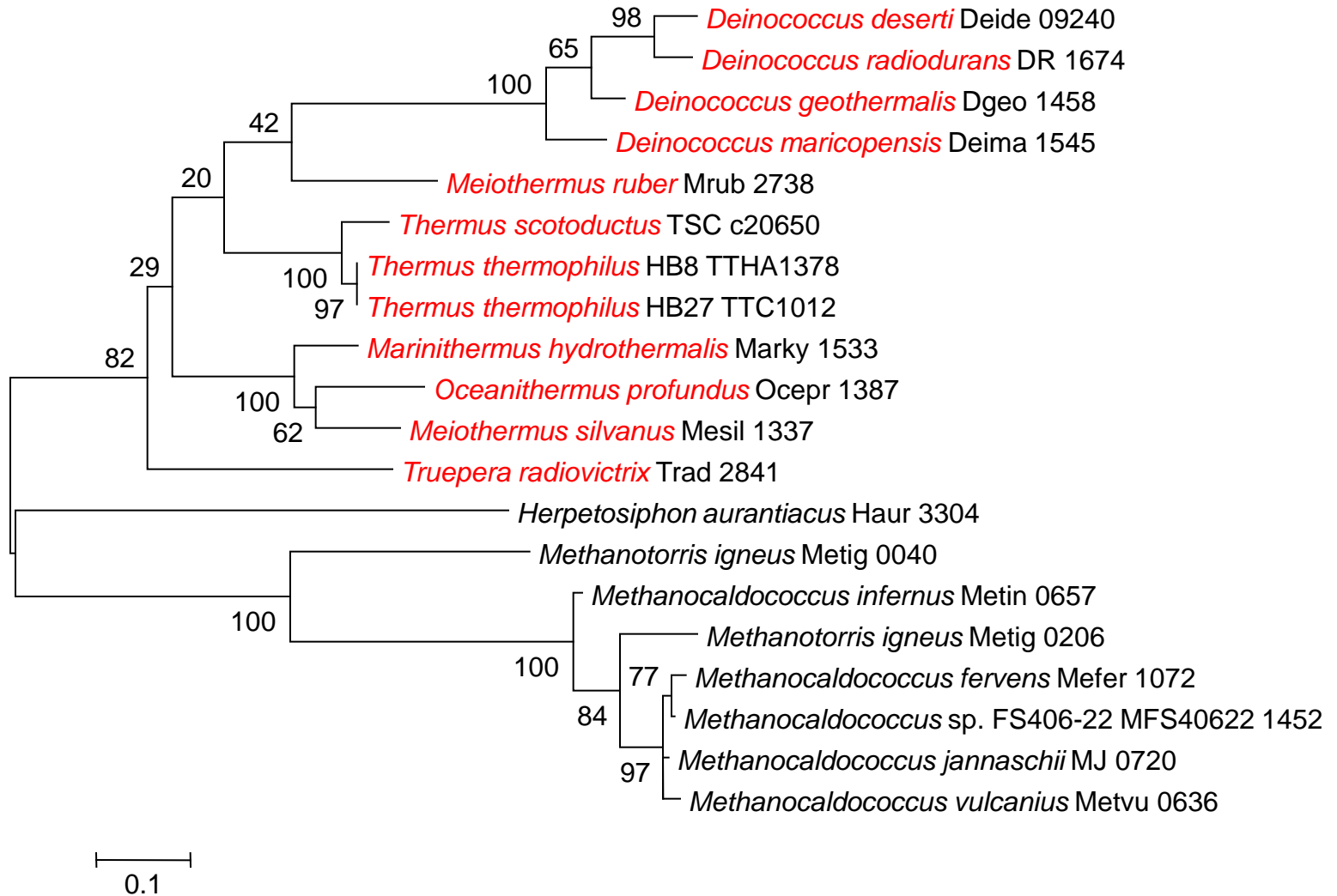
Supplementary Figures S1-S10.

We analyzed the distribution of each of the following 10 enzymes related to lysine biosynthesis through the AAA pathway in the *Deinococcus-Thermus* phylum: α -aminoadipate aminotransferase, homoisocitrate dehydrogenase, LysW- γ -L-lysine aminotransferase, LysW- γ -L-lysine hydrolase, LysW- γ -L- α -aminoadipate kinase, LysW- γ -L- α -aminoadipyl-6-phosphate reductase, α -aminoadipate-LysW ligase LysX, LysU, LysT, and homocitrate synthase. Homologous genes were selected on the basis of BLASTp search results by using each *T. thermophilus* enzyme for lysine biosynthesis through the AAA pathway and each *D. proteolyticus* enzyme for lysine biosynthesis through the DAP pathway. Multiple alignments were obtained using 20 amino acid sequences, with the highest to the 20th highest score by the BLASTp result. Maximum-likelihood trees were constructed using MEGA software version 5. The WAG model was used as the amino acid substitution model. The nearest neighbor interchange was used for the maximum-likelihood heuristic method. The γ -distributed rate was considered, and the number of discrete γ categories was 3. Bootstrap analysis was performed with 100 replicates. Red indicates bacteria belonging to the *Deinococcus-Thermus* phylum.

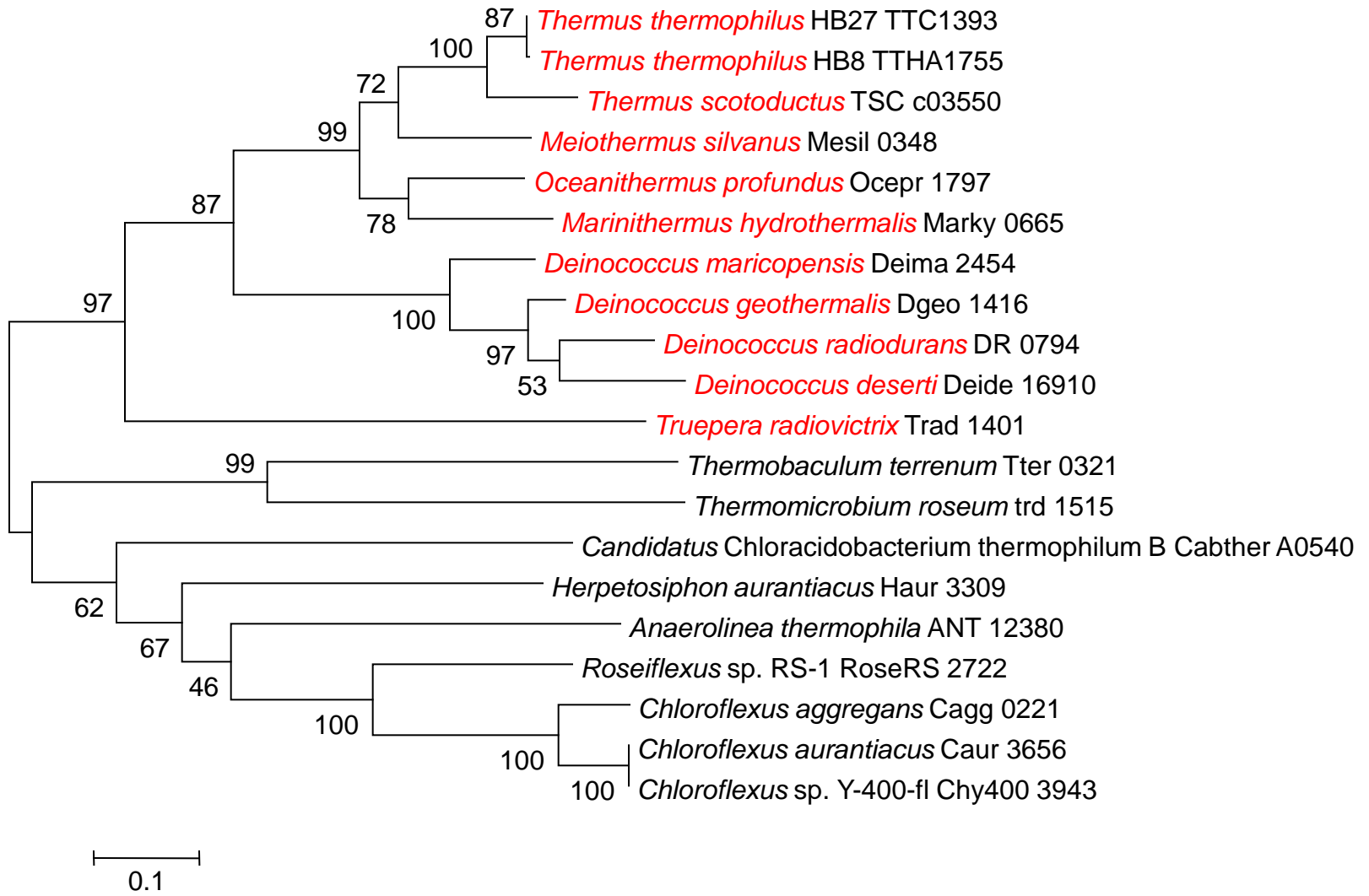
α -aminoadipate aminotransferase and the related proteins



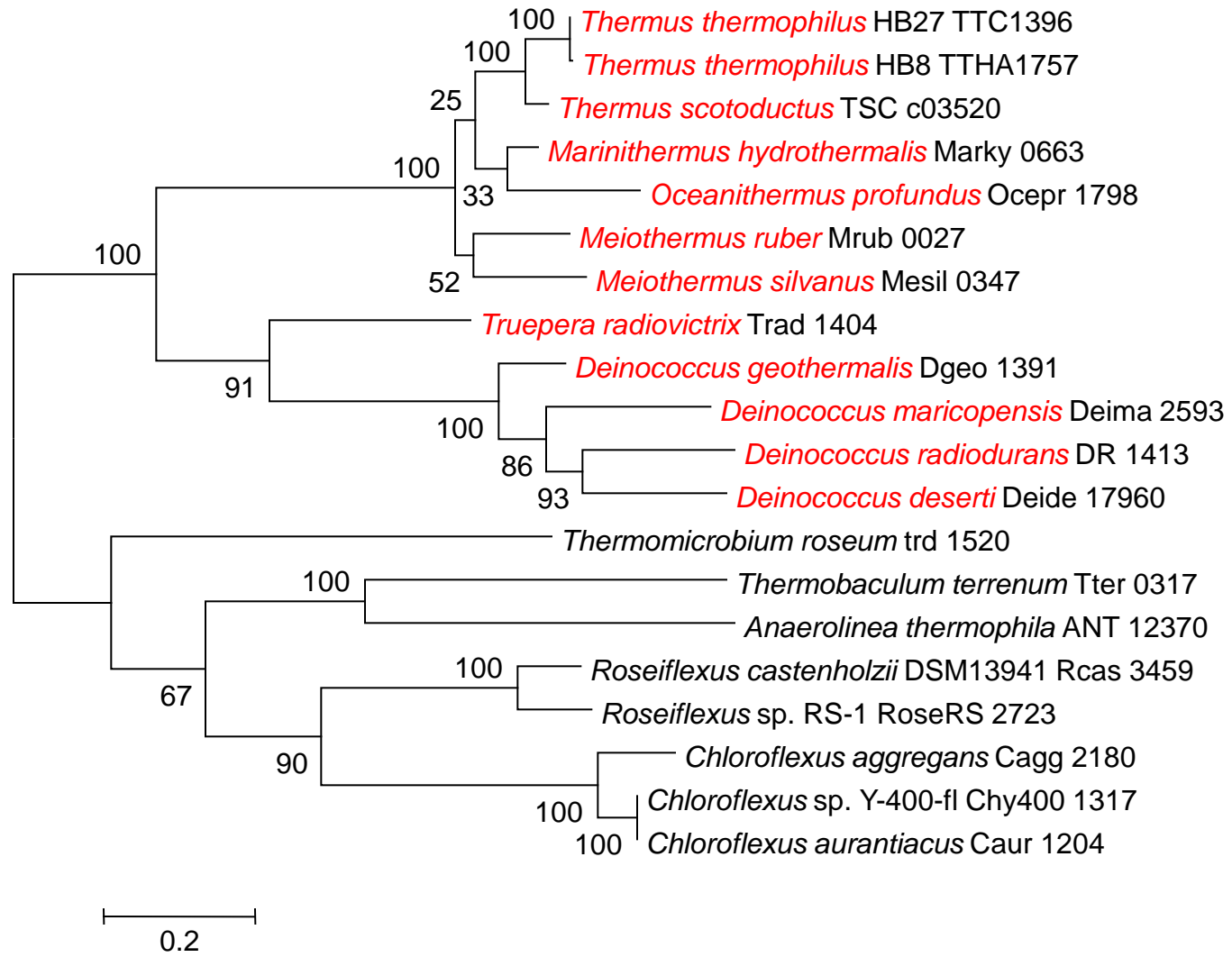
Homoisocitrate dehydrogenase and the related proteins



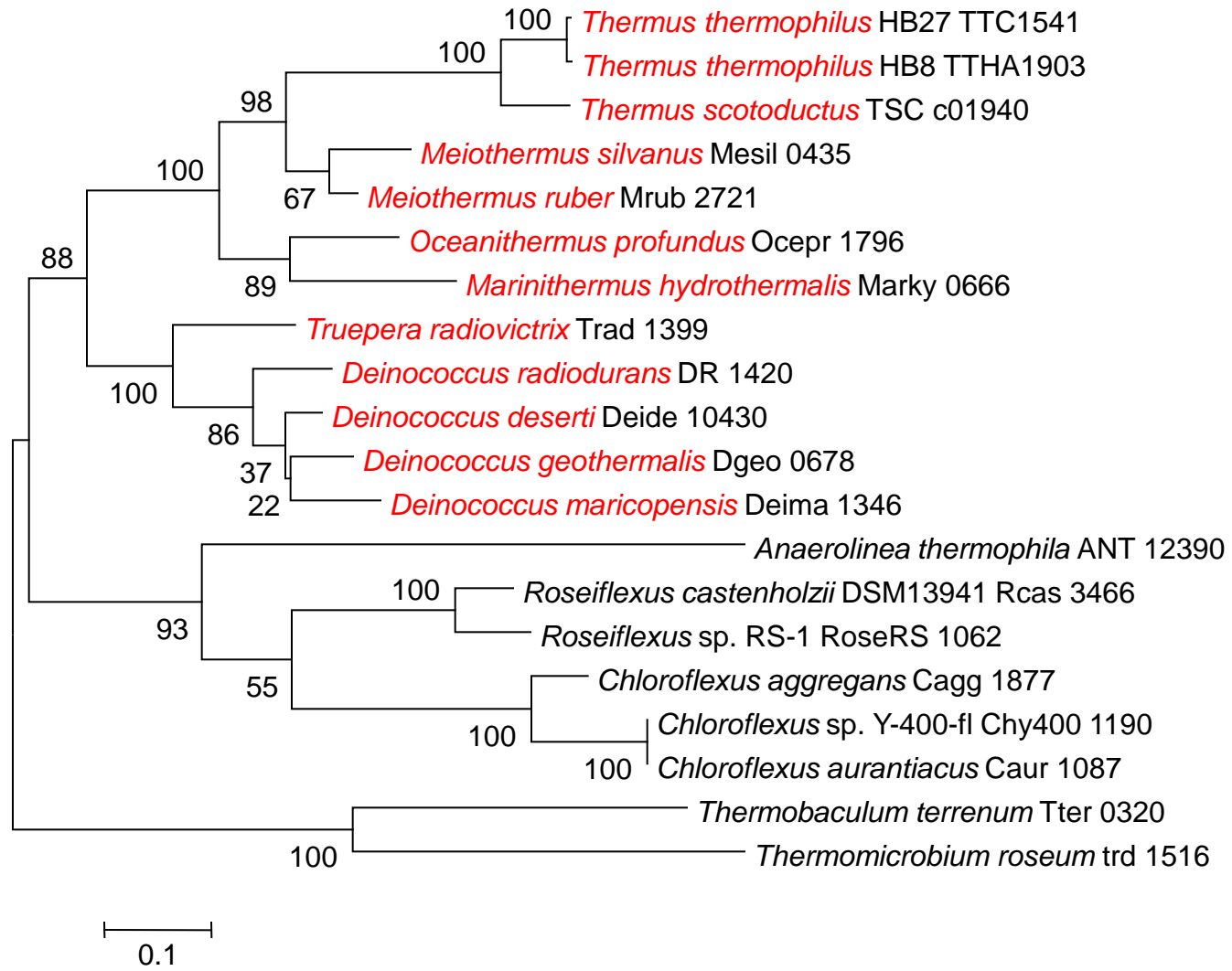
LysW- γ -L-lysine aminotransferase and the related proteins



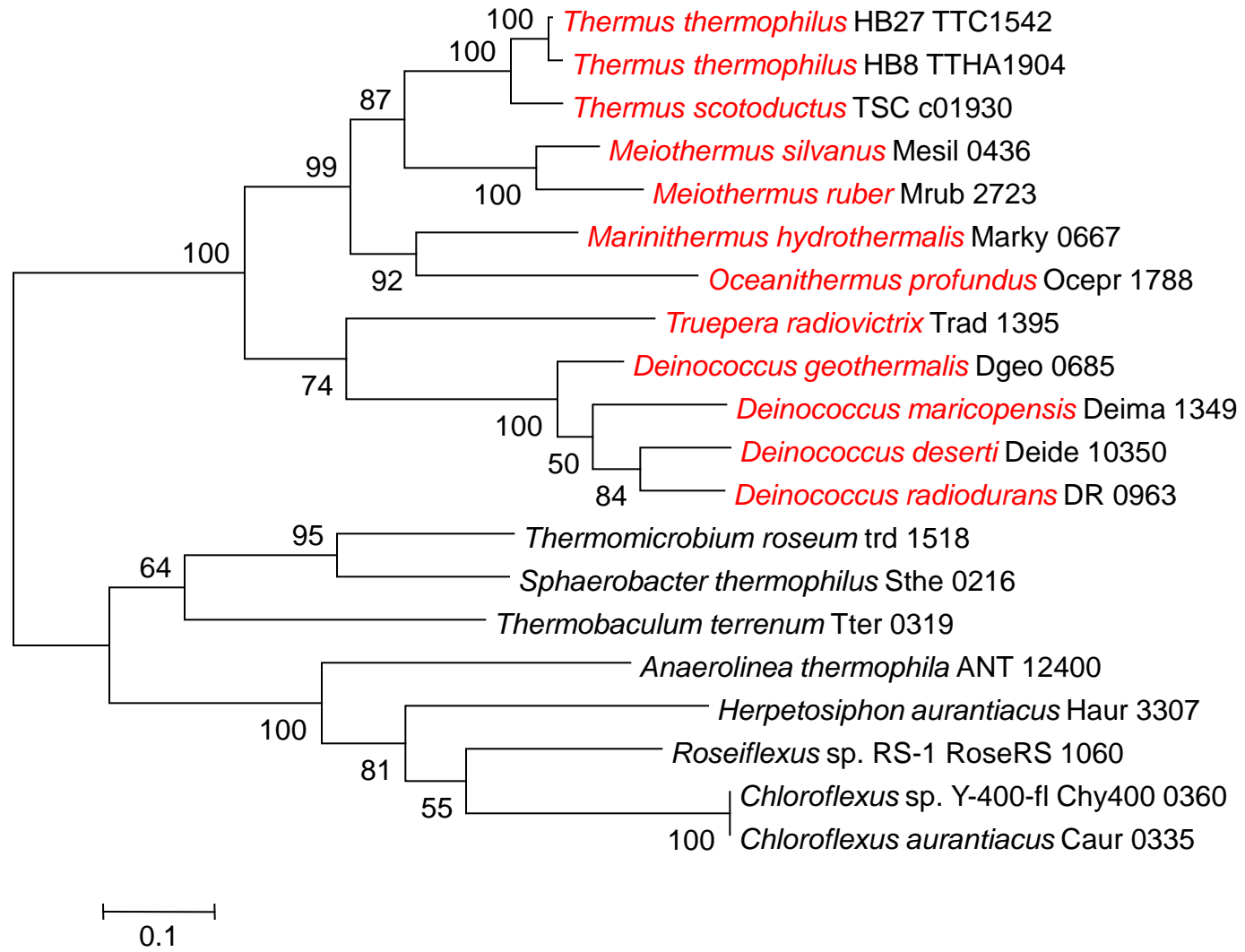
LysW- γ -L-lysine hydrolase and the related proteins



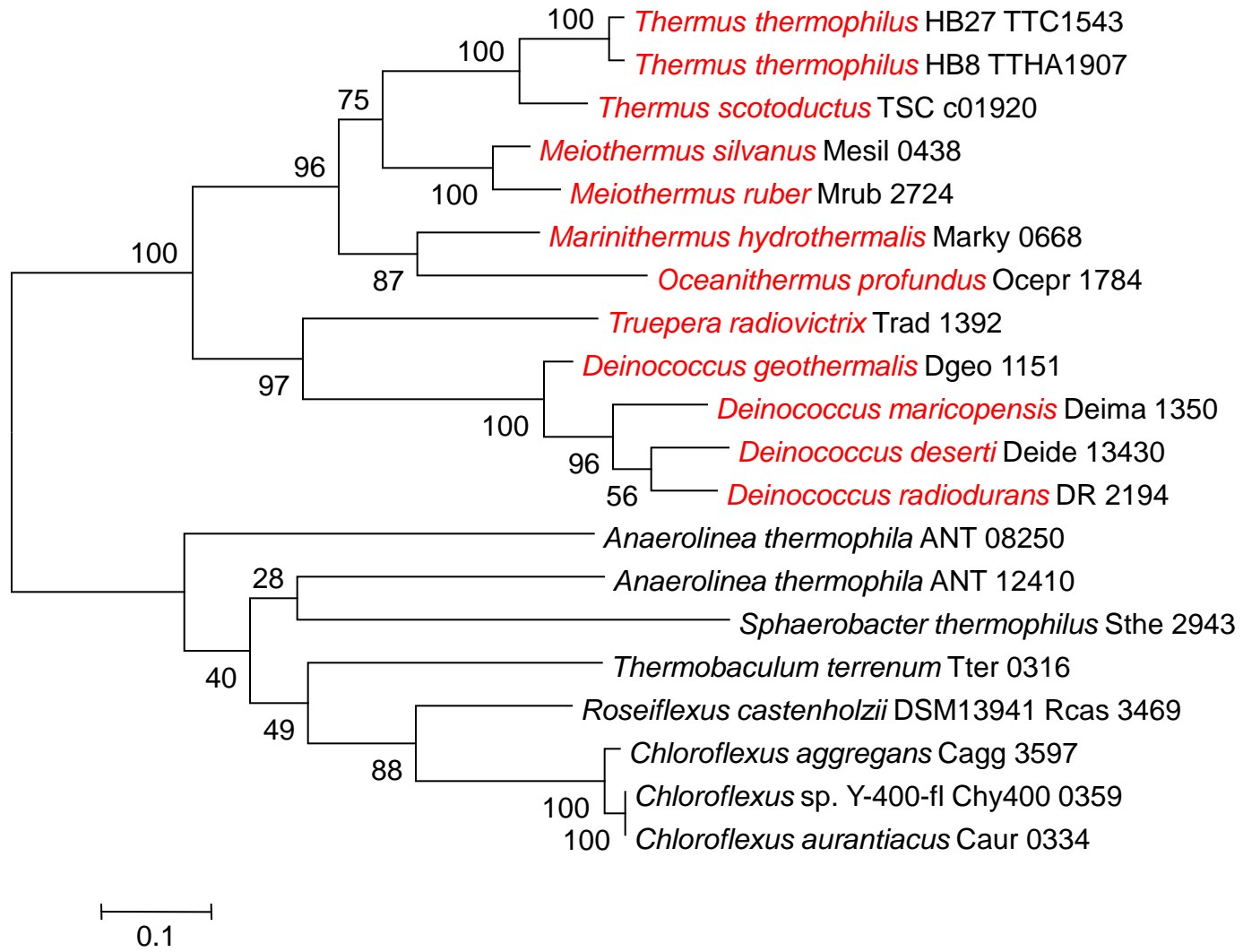
LysW- γ -L- α -aminoadipate kinase and the related proteins



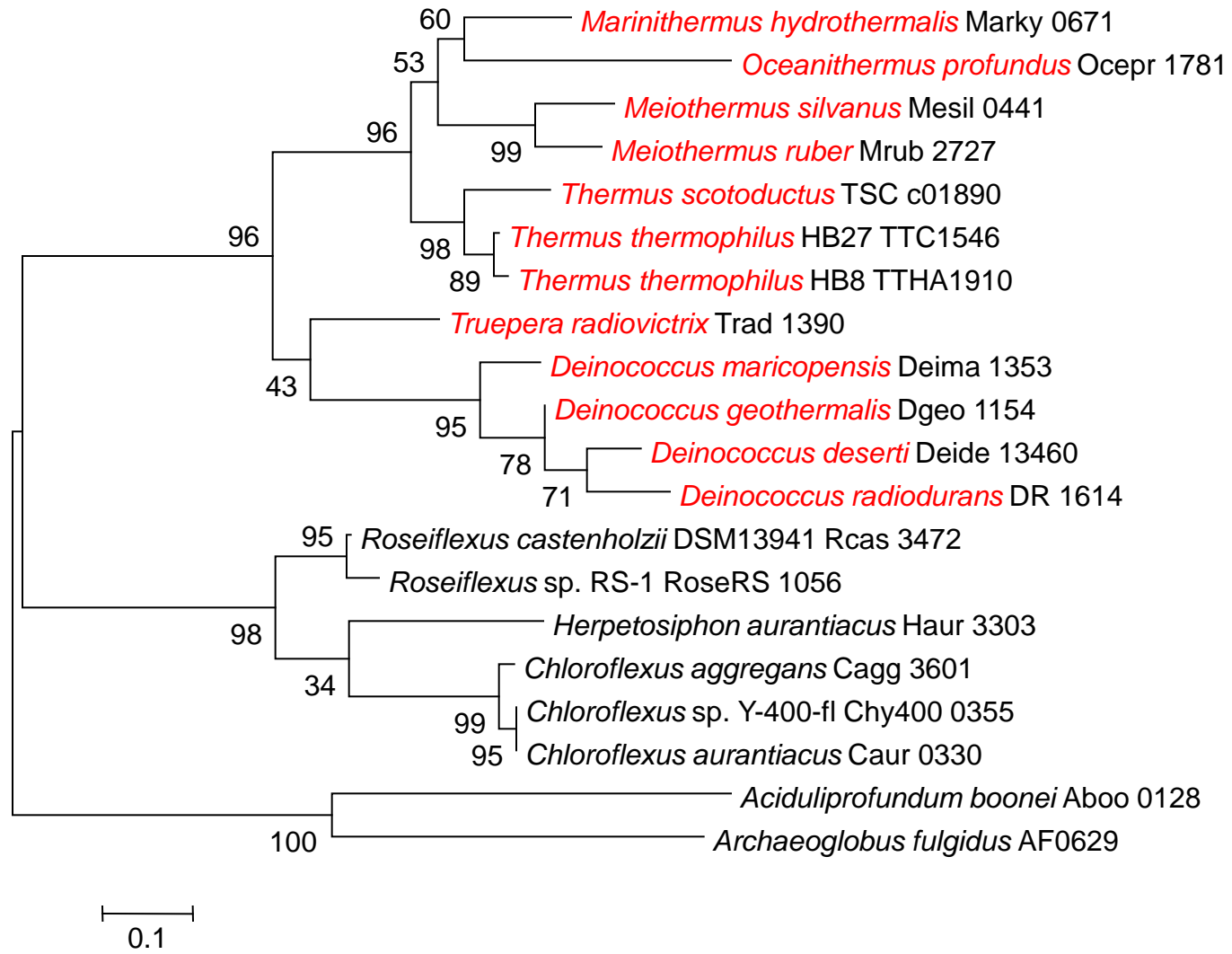
LysW- γ -L- α -aminoadipyl-6-phosphate reductase and the related proteins



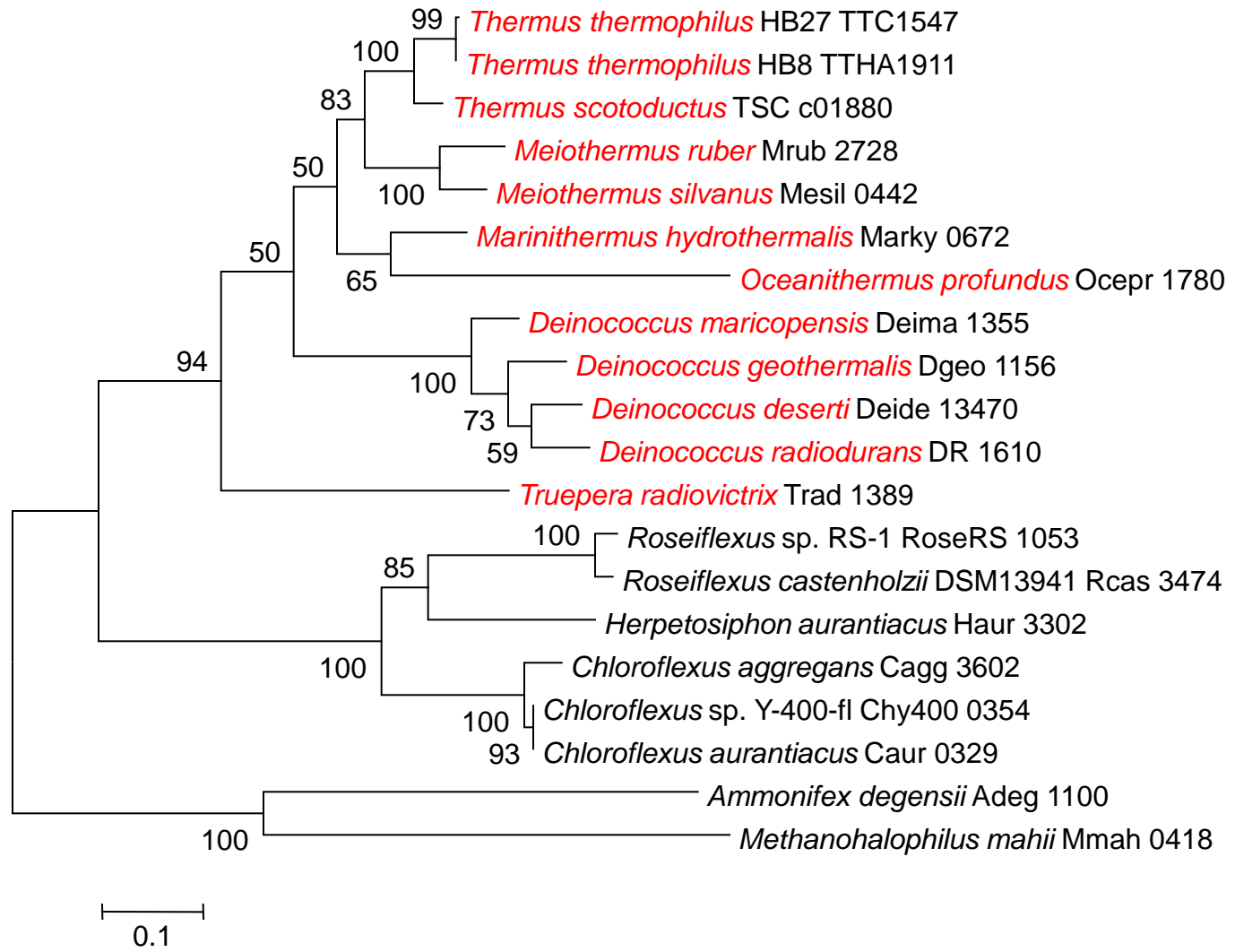
α -aminoadipate-LysW ligase LysX and the related proteins



LysU and the related proteins



LysT and the related proteins



Homocitrate synthase and the related proteins

