

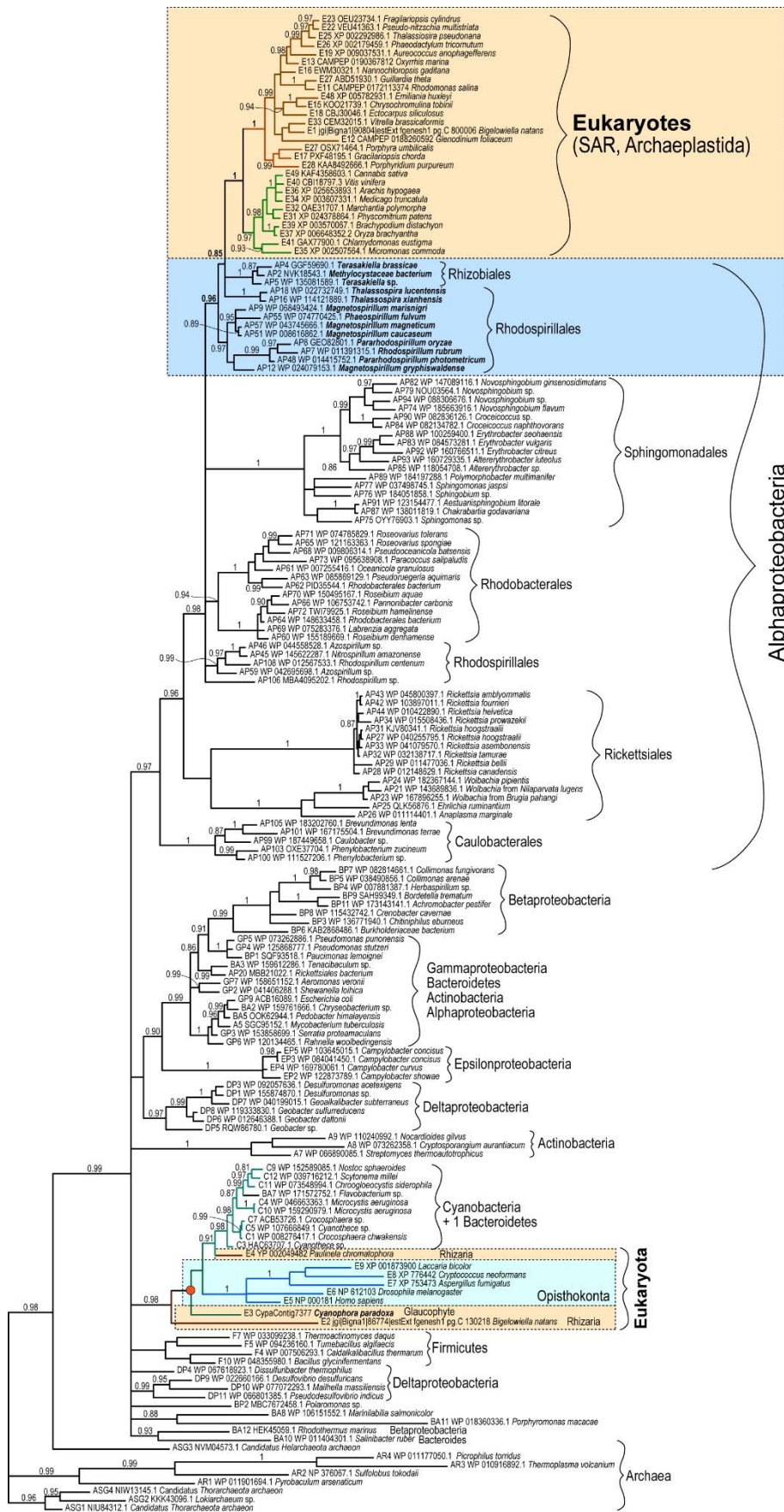
Supplementary material

Supplementary figure S1: Bayesian phylogenetic tree as inferred from amino acid sequences of PBGD. Numbers above branches indicate Bayesian posterior probabilities.

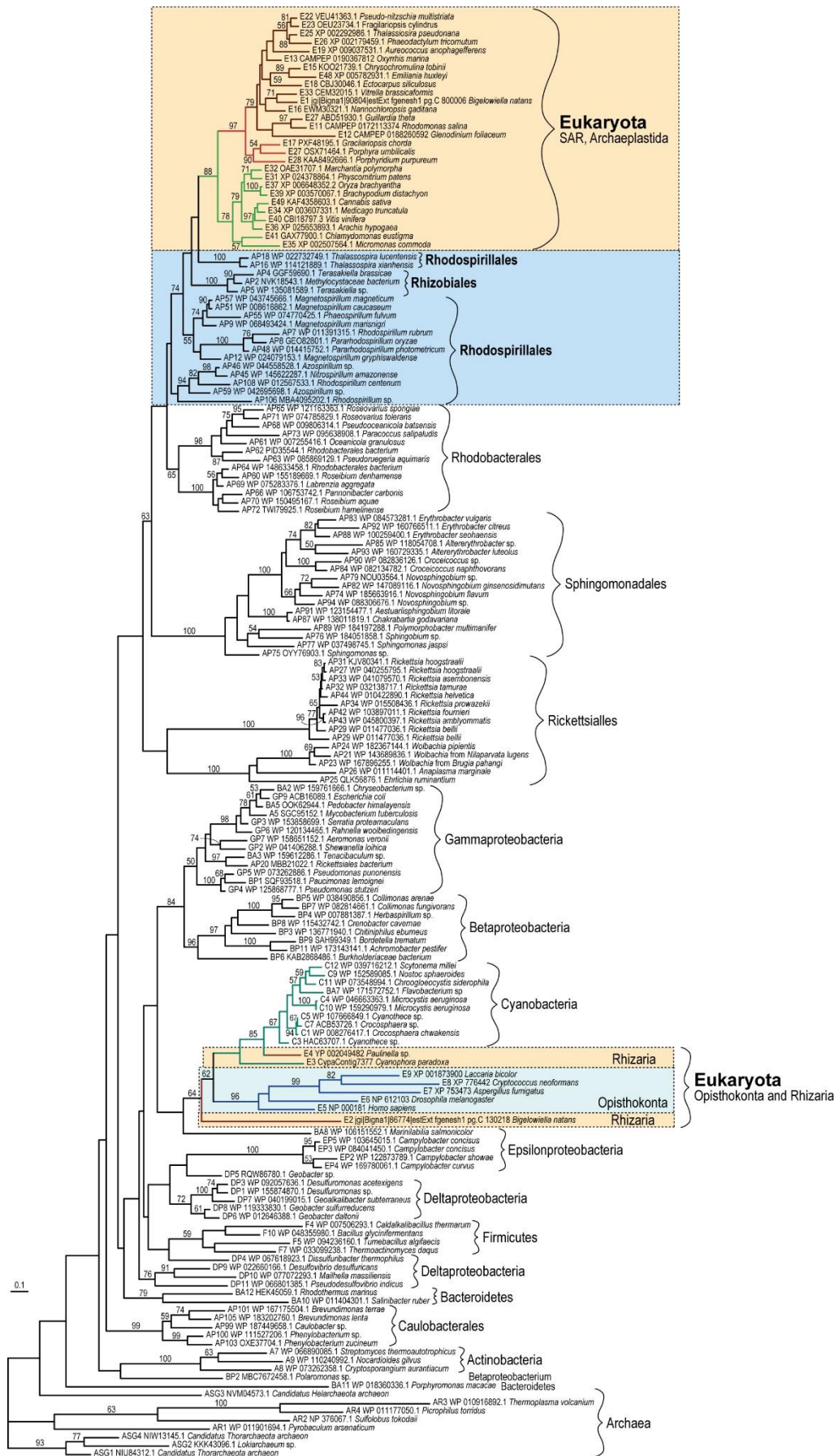
Supplementary figure S2: Maximum likelihood phylogenetic tree as inferred from amino acid sequences of PBGD. Numbers above branches indicate ML bootstrap support.

Dataset S1: Multiple alignment (fasta) of PBGD amino acid sequences used for the construction of phylogenetic trees.

Supplementary Figure 1:



Supplementary figure 2:



Supplementary file 1:

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>BA12_HEK45059.1_Rhodothermus_marinus
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