

Supplementary figure S1

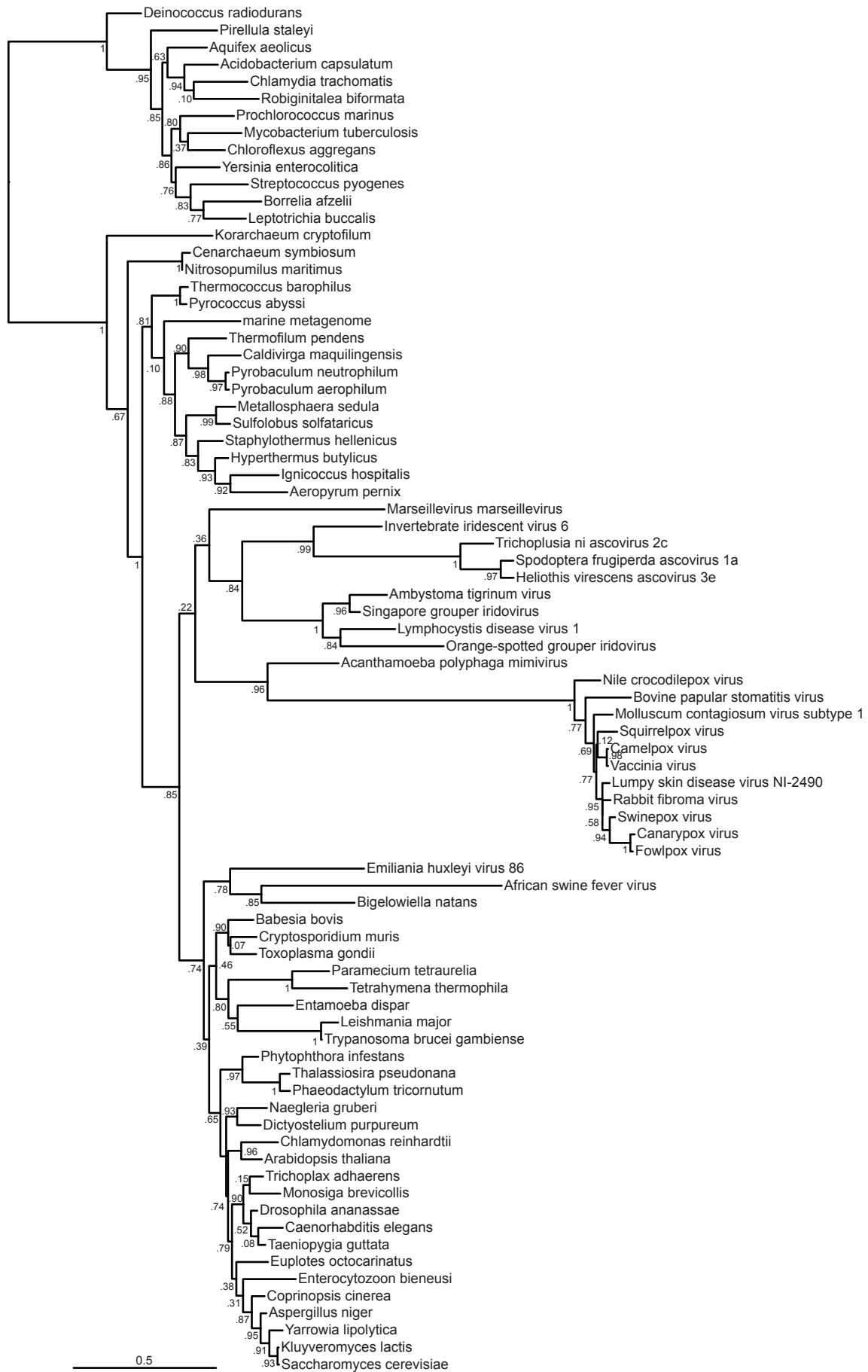


Figure S1. Phylogenetic tree of RNAP2 (80 sequences, 272 amino acid positions) reconstructed by approximated maximum likelihood and the JTT model. The tree is rooted on the bacteria. Numbers at branches are SH-like local support values. Bar represents 0.5 substitutions per site.

Supplementary figure S2



Figure S2. Phylogenetic tree of RNAP2 (80 sequences, 272 amino acid positions), including 3 random sequences. The tree is reconstructed by approximated maximum likelihood and the JTT model, and rooted on the bacteria. Numbers at branches are SH-like local support values. Bar represents 0.5 substitutions per site.