



**Fig. 1.** Rooted Bayesian phylogenetic trees of SSU rRNA (A) and of LSU rRNA (B) (1048 and 2003 unambiguously aligned nucleic acid positions analysed, respectively). For clarity, only the subtrees corresponding to *Thermotogales* are shown (53 SSU and 20 LSU rRNA sequences). Full trees are available as Fig. S2. Numbers at nodes represent posterior probabilities (PP) inferred by MrBayes and bootstrap values (BV) inferred by TreeFinder. Only PP > 0.50 and BV > 50% are shown. Scale bars represent the average number of substitutions per site. *Thermotogales* sequences retrieved from mesothermic environments are shaded.