2a) RecA

2b) SS-rRNA

Figure 2. Comparison of consensus trees for RecA and SS-rRNA.

Strict-rule consensus trees representing the phylogenetic patterns found in all trees generated by multiple methods for each molecule are shown. The RecA consensus (A) was generated from the PAUP, *protpars*, Fitch-Margoliash, De Soete and neighbor-joining trees (see Methods). The SS-rRNA consensus (B) was generated from the *dnapars*, Fitch-Margoliash, De Soete and neighbor-joining trees. Comparable species are aligned in the middle and species are ordered to minimize branch crossing (note two crossed branches in SS-rRNA tree). Consensus clades are shaded for each molecule.