



Supplementary Figure 2 – Condensed maximum likelihood tree based on an alignment of SSU rRNA gene sequences. Major lineages are collapsed and labeled as in Figure 1, with well-defined lineages named using italic font and lineages lacking an isolated representative named in regular font and highlighted with red dots. Bootstrap support values are indicated by circles on nodes – black for support of 85% and above, grey for support from 50% to 84%. The full SSU rRNA gene tree is available in newick format as Supplementary Dataset 4.