

FIG. S1. An ARB maximum parsimony constraint tree including representative sequences from all bacterial phylotypes (indicated by "PT" in the reference number) recovered from our lichen samples as well as closely related sequences obtained from GenBank (accession are number indicated, and those from previous lichen-bacteria studies give the citation). The presence (in color) or absence (in gray) of each phylotype in our samples is indicated in the outer ring [moving from the inside (red) to the outside (blue) are the following lichen species: *Parmelia sulcata*, *Rhizoplaca chrysoleuca*, *Umbilicaria americana*, and *Umbilicaria phaea*). The tree is rooted with *Thermosulfidobacter takaii* (AB282756) from the Archaea (PT numbers with asterisks are found among the 15 most-dominant phylotypes per species, see Fig. 3; red branches = Alphaproteobacteria; scale bar = 10% sequence dissimilarity).

