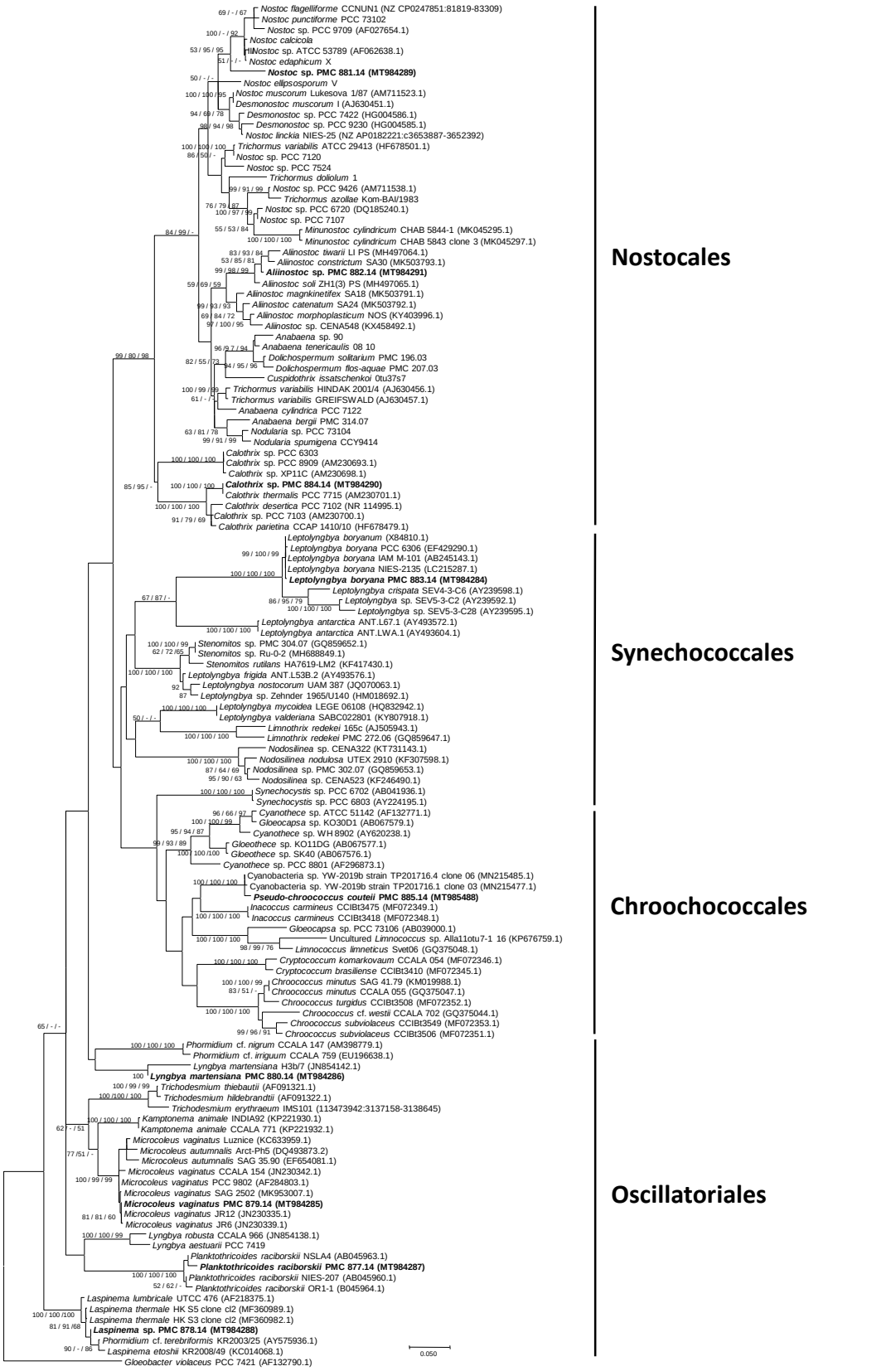

Figure S1. Consensus phylogenetic tree based on 16S rRNA gene sequences of representative cyanobacteria strains belonging to the orders Oscillatoriales, Nostocales, Chroococcales and Synechococcales, Balaruc-les-Bains strains (in bold) and one outgroup (*Gloeobacter violaceus*). Numbers above branches indicate bootstrap support (>50%) from 1000 replicates. Bootstrap values are given in the following order: neighbor joining/maximum likelihood/maximum parsimony.