

Figure S1. Maximum likelihood tree illustrating the phylogeny of *Hydnellum* and *Sarcodon* based on ITS sequence dataset. Branches are labeled with maximum likelihood bootstrap support greater than 50 % and Bayesian posterior probabilities greater than 0.95.

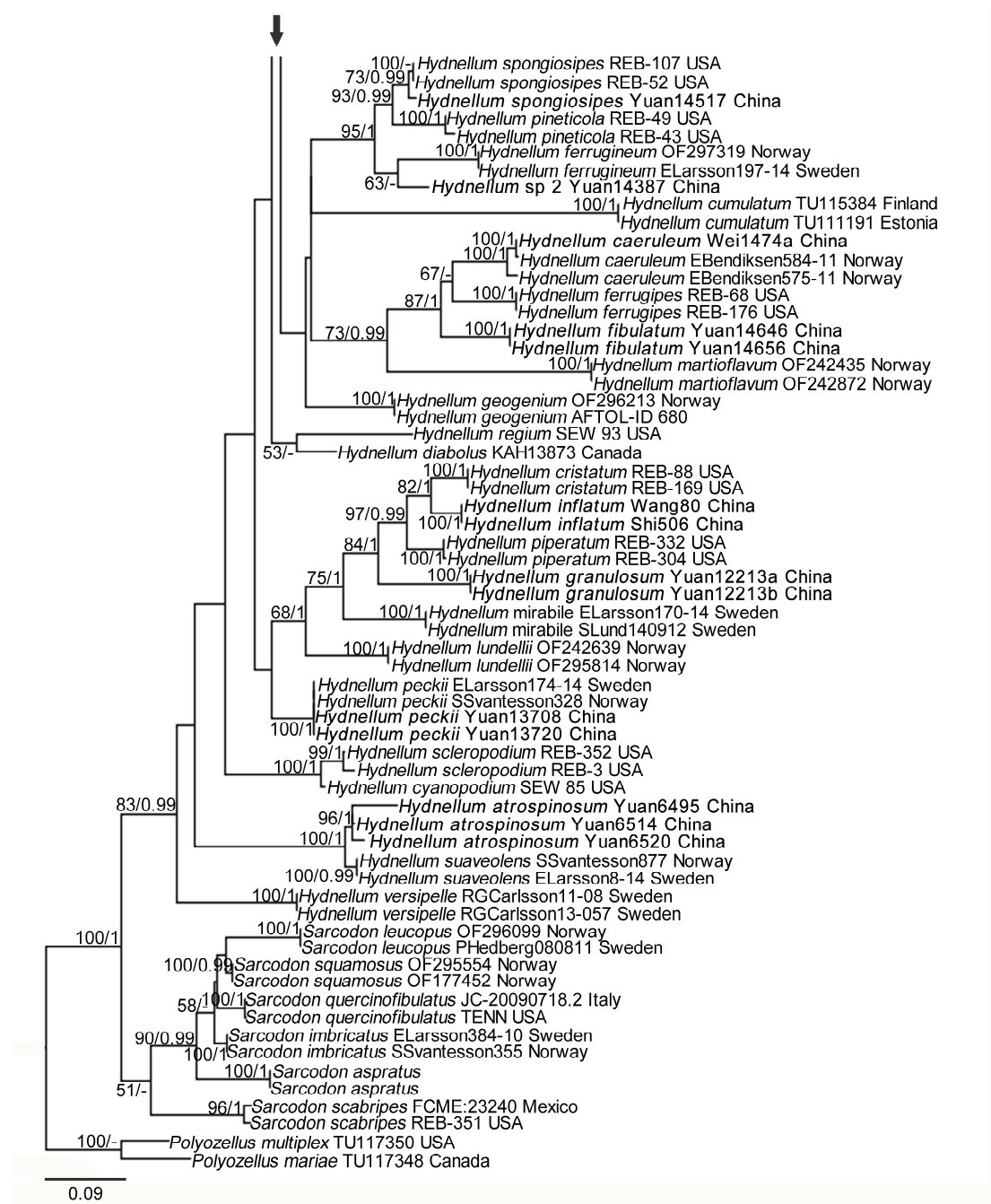


Figure S1. (continued)