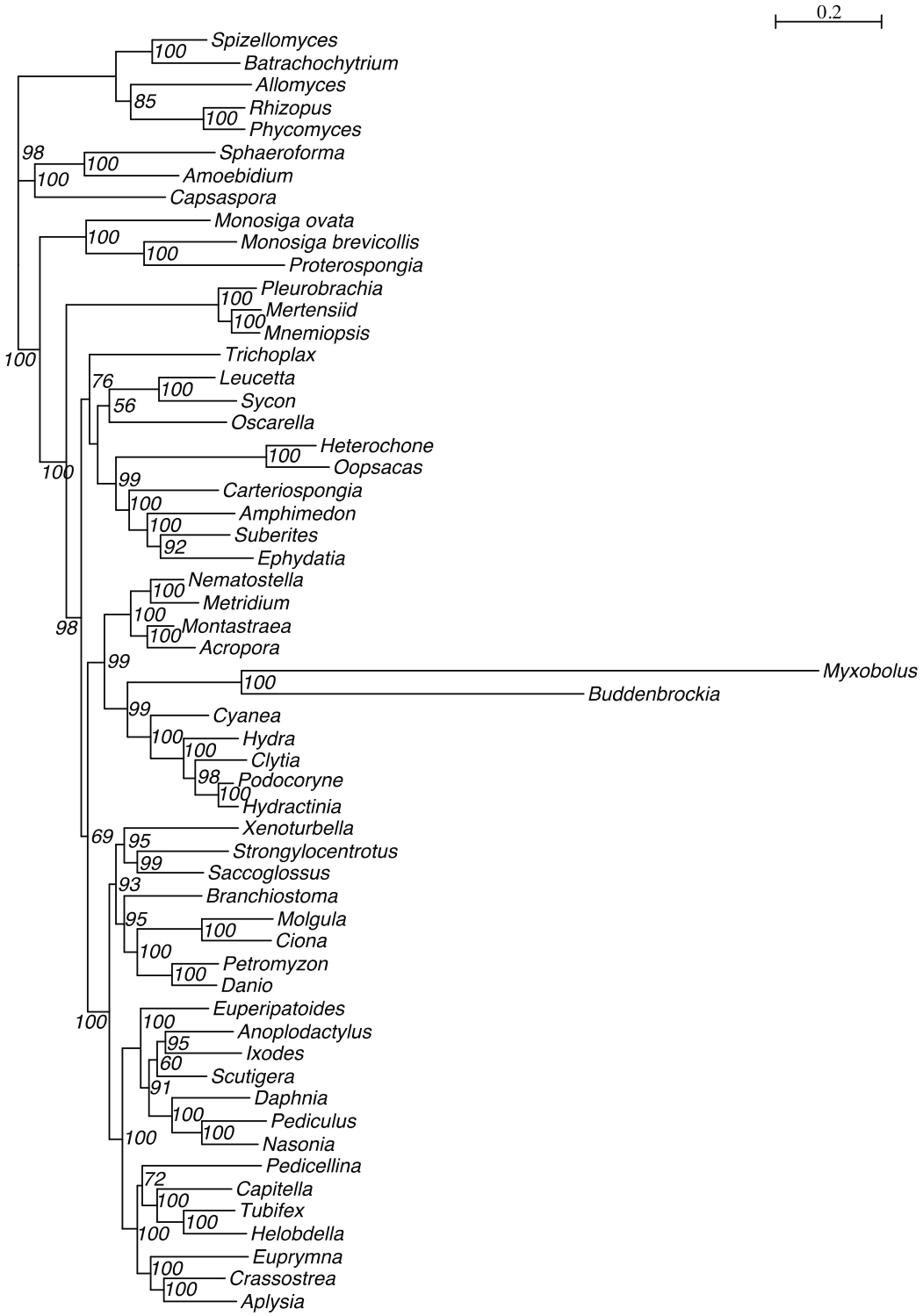Figure S6. Maximum likelihood tree calculated with the LG+G+F model based on 29,712 amino acid positions derived from 106 proteins (after excluding the 10% fastest evolving proteins and the 10% most heterogeneous proteins). Bootstrap values larger than 50% are shown to the right of the nodes.