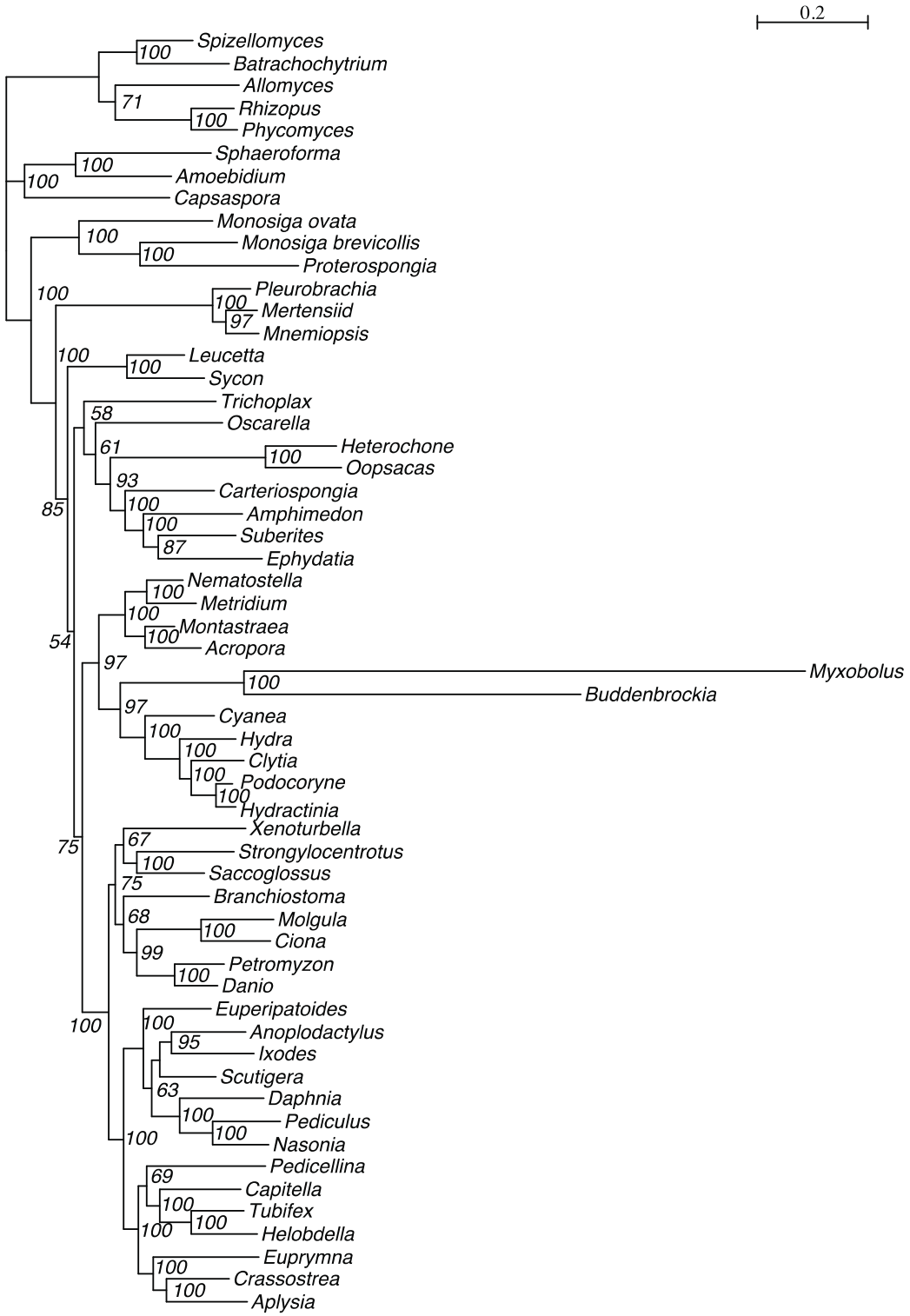Figure S2. Maximum likelihood tree calculated with the LG+G+F model based on 18,273 amino acid positions derived from 128 proteins (after excluding all positions for which no sequence information is available from myxozoans). Bootstrap values larger than 50% are shown to the right of the nodes.