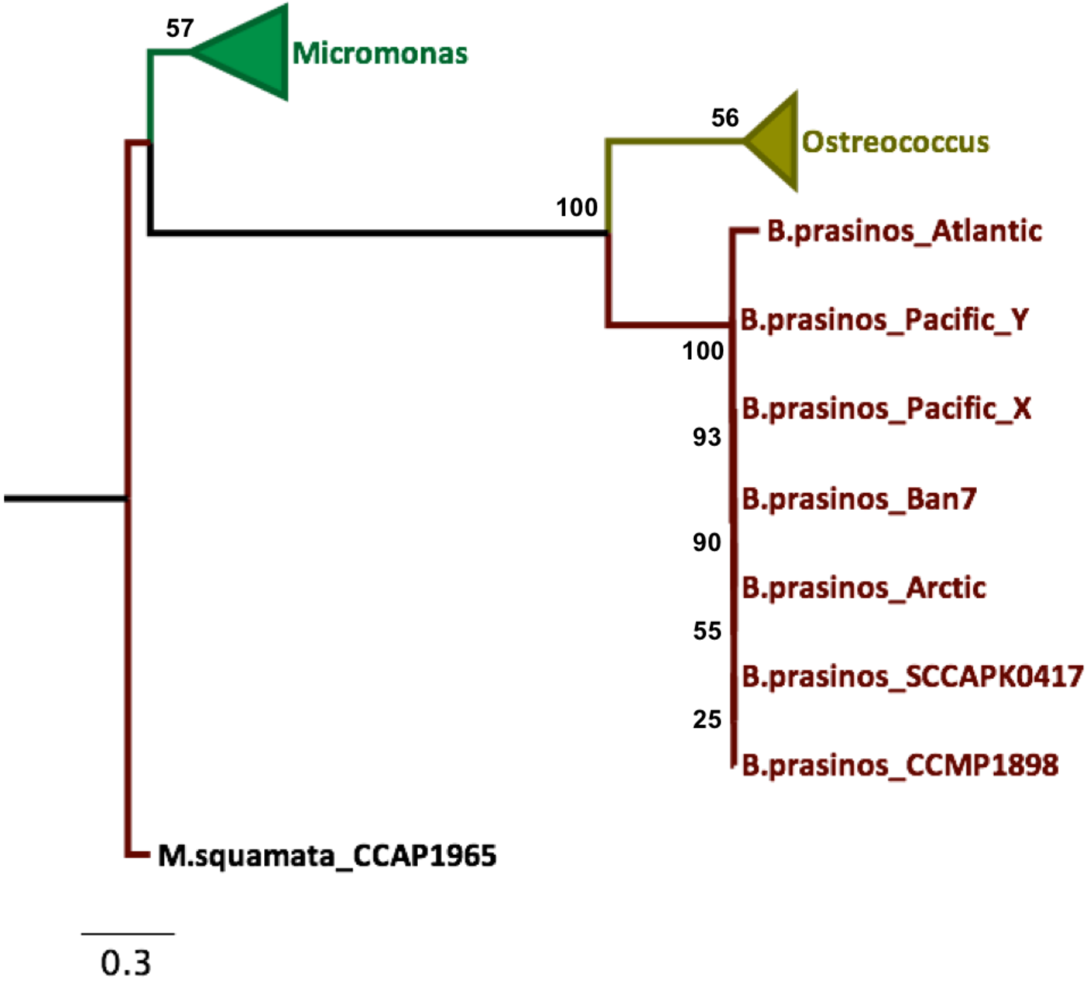

Figure S2: *Bathycoccus* phylogeny based on ITS2 rRNA genes. ML reconstruction using model GTR+G based on a multiple sequence alignment of 221 nucleotide positions. (Bootstrap replicate =100). Sequences from *B. prasinos*_Atlantic corresponds to a sorted population collected in the SE Atlantic open ocean (AFUW00000000.1); *B. prasinos*_Pacific_X et Y from a sorted population collected in Pacific coastal Chilean upwelling zone (CAFX01000001.1, CAFY01000001.1); *B.prasinos*_Ban7 from a cultured strain originally isolated from near Banyules, Mediterranean; *B. prasinos*_Arctic from this study; *B. prasinos*_SCCAPK0417 and *B. prasinos*_CCMP1898 was isolated from Italian Mediterranean coast (FN562453.1,FN562453.1). All 18S rRNA genes had ca. 100% similarity.