



Supplementary Fig. 8. Prediction of terpene BGCs in strain BRMEA1^T using anti-SMASH. (A) Detection of secondary metabolite regions using “relaxed” strictness. (B) Comparative analysis of type I polyketide synthase metabolite clusterblast against the National Center for Biotechnology Information (NCBI) database. (C) Pfam-based gene ontology (GO) term annotation gene. Rows highlighted in dark pink denote core biosynthetic genes; rows highlighted in light pink show additional biosynthetic genes.