



**Supplementary Fig. 9.** Prediction of type III polyketide synthase BGCs in strain BRMEA1<sup>T</sup> using the anti-SMASH. (A) Identification of secondary metabolite regions using a “relaxed” strictness. (B) Comparative analysis of type I polyketide synthase metabolite clusterblast against 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.