



Supplementary Fig. 7. Prediction of linear azo(in)e-containing peptide (LAP) and ribosomally synthesized and posttranslationally modified peptide (RiPP)-like in strain BRMEAT^T using anti-SMASH. (A) Identification of secondary metabolite regions using “relaxed” strictness. (B) Comparative analysis of TIPK metabolite cluster 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.