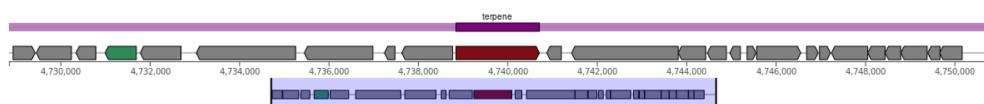
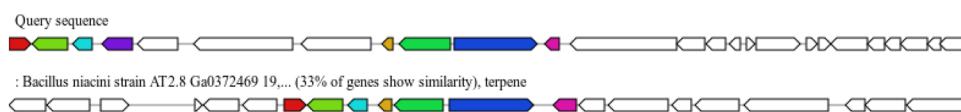


A**B****C**

Contig no./Locus tag	Identified protein
ctg1_4529	No significant similarity
ctg1_4530	Divergent polysaccharide deacetylase
ctg1_4531	Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
ctg1_4532	Response regulator receiver domain
ctg1_4533	PBP superfamily domain
ctg1_4534	Polyphosphate kinase N-terminal domain
ctg1_4535	Ppx/GppA phosphatase family
ctg1_4536	No significant similarity
ctg1_4537	Protein of unknown function (DUF2515)
ctg1_4538	Squalene-hopene cyclase N-terminal domain
ctg1_4539	Uracil DNA glycosylase superfamily
ctg1_4540	No significant similarity
ctg1_4541	Peptidase family M23
ctg1_4542	No significant similarity
ctg1_4543	No significant similarity
ctg1_4544	Helix-turn-helix
ctg1_4545	No significant similarity
ctg1_4546	No significant similarity
ctg1_4547	Spore germination GerPB
ctg1_4548	Glycosyl hydrolases family 25
ctg1_4549	No significant similarity
ctg1_4550	No significant similarity
ctg1_4551	No significant similarity
ctg1_4552	No significant similarity
ctg1_4553	Permuted papain-like amidase enzyme, YaeF/YiiX, C92 family

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.