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Α									
				CC 2: interleaved LAP					
			RiPP-like			-			
						$\rightarrow \leftarrow$			
3,980,000	3,982,000	3,984,000 3,986,0	0 3,988,000	3,990,000	3,992,000	3,994,000	3,996,000	3,998,000	4,000,000
В									
Query sequence					<b>_</b>	,			
: Cytobacillus eise	eniae strain FJ/	AT-2352 Sca (26% of	genes show simila	rity), LAP,bacte	riocin				
$\rightarrow \frown \frown \frown \frown$									$\longrightarrow$

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Contig no./Locus tag	Identified protein			
ctg1_3802	CorA-like Mg2+ transporter protein			
ctg1_3803	No significant similarity			
ctg1_3804	No significant similarity			
ctg1_3805	No significant similarity			
ctg1_3806	Cytochrome C oxidase subunit II, transmembrane domain			
ctg1_3807	Cytochrome C and Quinol oxidase polypeptide I			
ctg1_3808	Cytochrome c oxidase subunit III			
ctg1_3809	Prokaryotic Cytochrome C oxidase subunit IV			
ctg1_3810	No significant similarity			
ctg1_3811	No significant similarity			
ctg1_3812	B_an_ocin: bacteriocin, heterocycloanthracin/sonorensin family			
	ocin_ThiF_like: putative thiazole-containing bacteriocin			
ctg1_3813	maturation protein			
ctg1_3814	YcaO cyclodehydratase, ATP-ad Mg2+-binding			
ctg1_3815	Nitroreductase family			
ctg1_3816	Endonuclease/Exonuclease/phosphatase family			
ctg1_3817	Type I phosphodiesterase / nucleotide pyrophosphatase			
ctg1_3818	No significant similarity			
ctg1_3819	No significant similarity			
ctg1_3820	Spore germination protein gerPA/gerPF			
ctg1_3821	No significant similarity			
ctg1_3822	Cold-shock DNA-binding domain			
ctg1_3823	No significant similarity			
ctg1_3824	No significant similarity			
ctg1_3825	No significant similarity			
ctg1_3826	No significant similarity			
ctg1_3827	Spore germination GerPB			

**Supplementary Fig. 7.** Prediction of linear azo(in)e-containing peptide (LAP) and ribosomally synthesized and posttranslationally modified peptide (RiPP)-like in strain BRMEA1<sup>T</sup> 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.