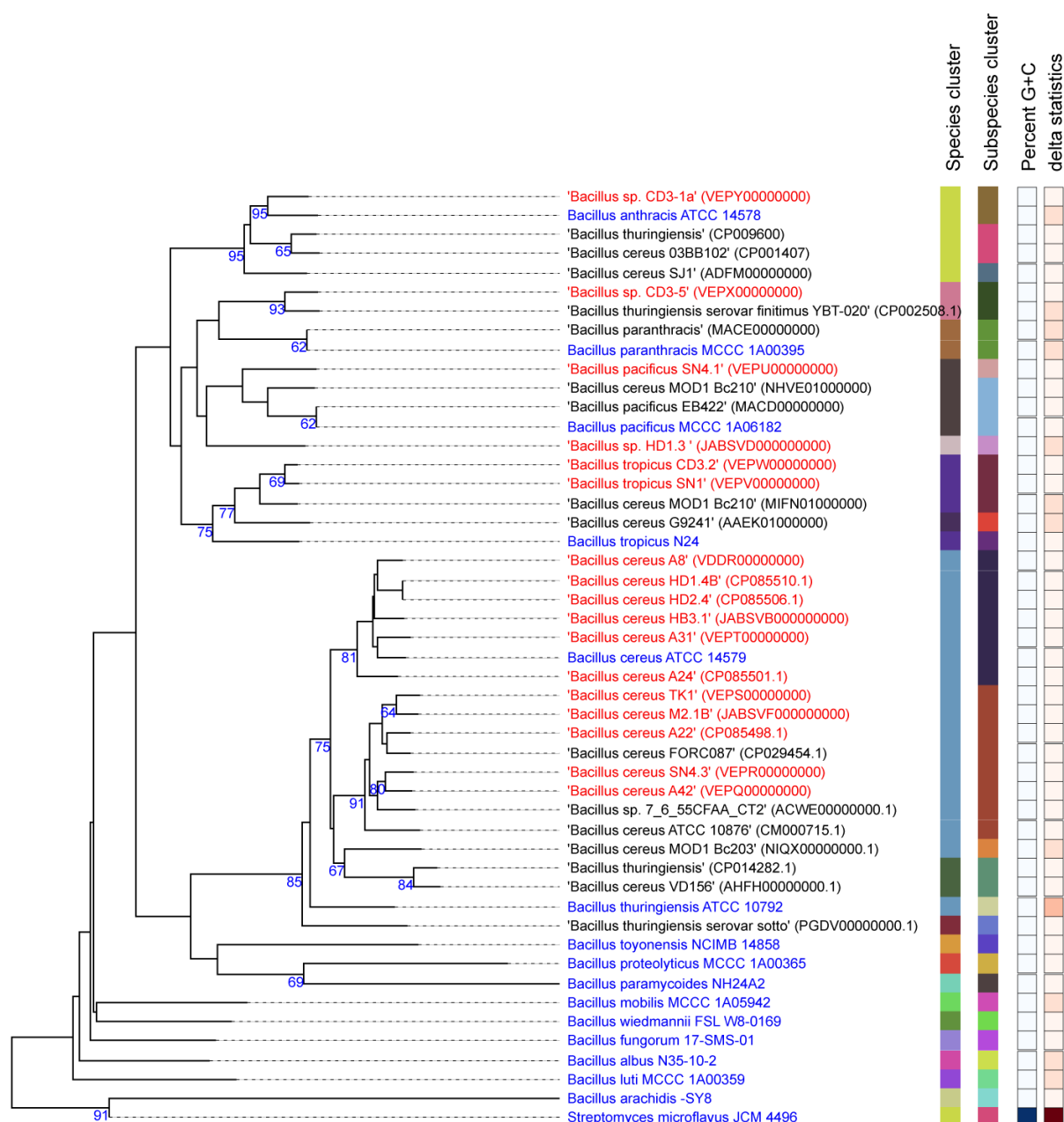
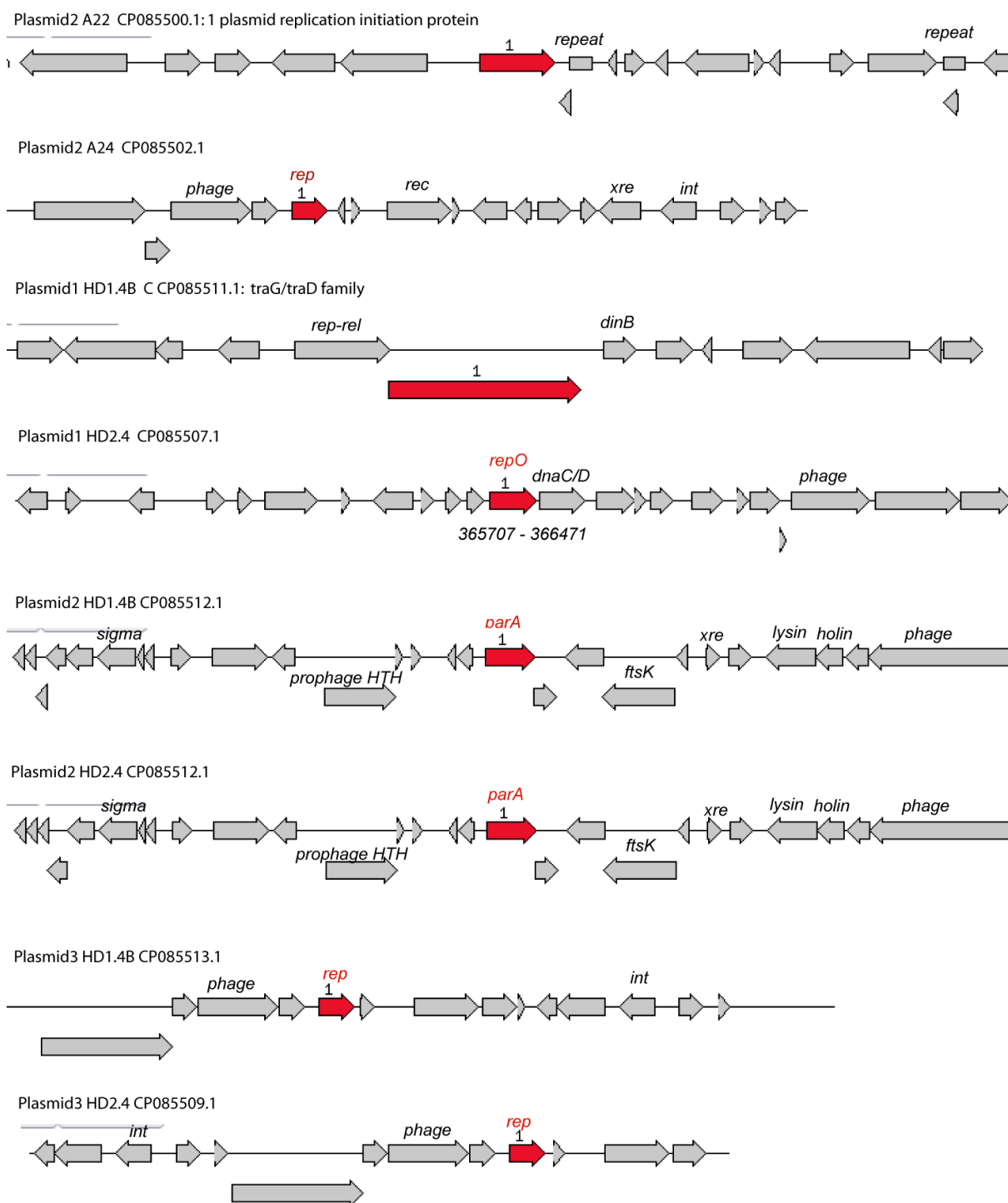


Suppl. Figure S1: Tree inferred with FastMe 2.1.6.1 from GBDP distances calculated from 16S rDNA gene sequences. The branch lengths are scaled in terms of GBDP distance formula d_5 . The numbers above branches are GBDP pseudo-bootstrap support values >60% from 100 replications, with an average branch support of 28.5%. The tree was rooted at the midpoint. The 17 Vietnamese crop plant isolates are indicated by red letters. Type strains are indicated by blue letters.

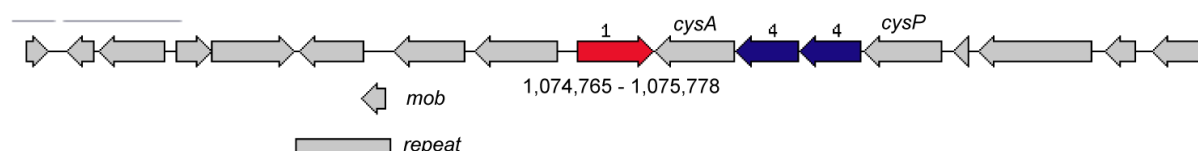


Suppl. Figure S2. GBDP tree (whole genome sequence based) inferred with FastMe 2.1.6.1 from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d_5 . The number above branches are GBDP pseudo-bootstrap support values > 60% from 100 replications, with an average branch support of 52.7%. The tree was rooted at the midpoint. The 17 Vietnamese crop plant isolates are indicated by red letters. Type strains are indicated by blue letters.

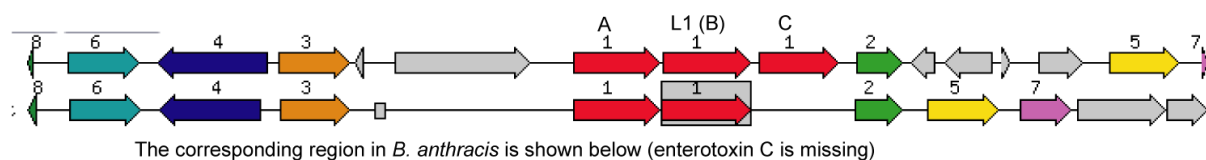


Suppl. Figure S4. Environment of the Rep protein genes in the plasmid sequences of A22, A24, HD1.4B, and HD2.4.

A22 chromosome CPo85498: Cytotoxin K (1) , 4, sulfate permeases



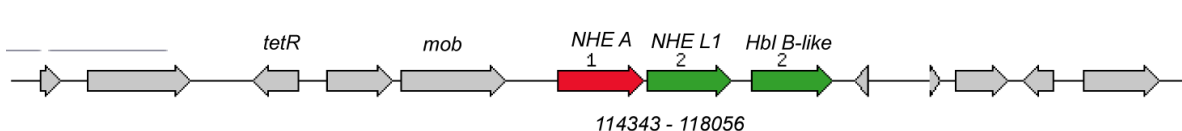
A22 chromosome CPo85498: Non-hemolytic enterotoxin 1,732,559 - 1,736,153



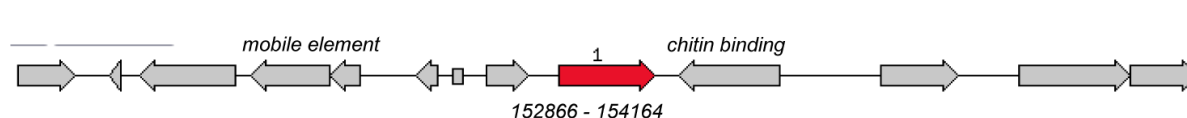
A22 chromosome CPo85498: Hemolytic endotoxin HBL 3,004,503 - 3,200,081



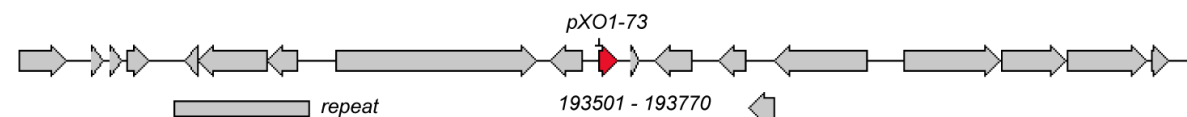
Plasmid1 HD2.4 CP085507.1: 1: non-hemolytic enterotoxin A 2: NHE lytic component L1 2: Hemolytic enterotoxin



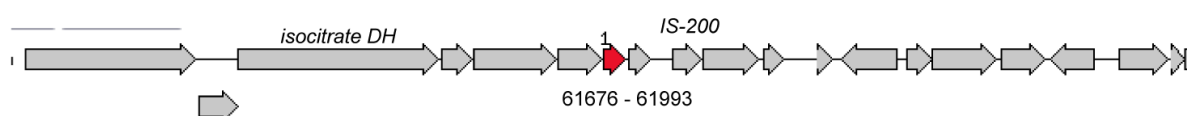
Plasmid1 HD2.4 CP085507.1: 1: Phosphatidylinositol-specific phospholipase C (EC 4.6.1.13)



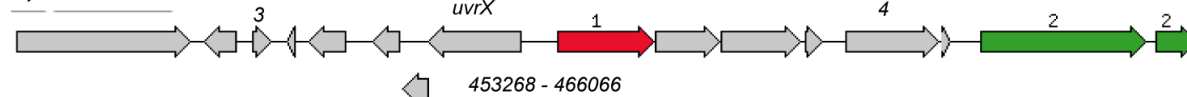
Plasmid1 HD2.4 CP085507.1: 1: pXO1-73 lysophospholipid acyltransferase



Plasmid 2 A22 CP085500.1: 1: pXO2-44

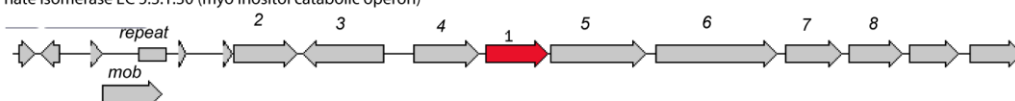


Plasmid1 A24 CP085502.1 : 1: hemolysin and related proteins containing CBS domains 2: chitin binding proteins, 3 pOX1-73, 4: glycosyl hydrolase

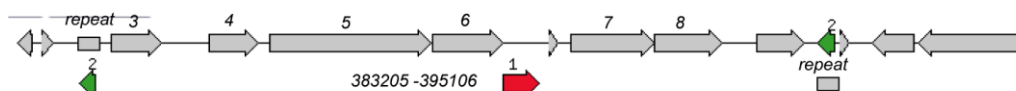


Suppl. Figure S5. Localization of virulence genes and gene clusters on chromosomes and plasmids of *B. cereus* isolates. The *cytK* gene and the NHE/HBL gene clusters were chromosomally localized. The complete set of NHE and HBL genes was chromosomally localized in all four completely sequenced strains (A22, A24, HD1.4B, HD2.4). The P1 plasmid sequences of HD1.4B and HD2.4 harbored genes with similarity to the NHE/HBL enterotoxin family.

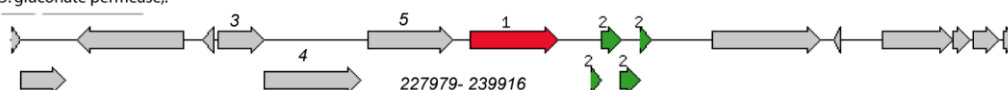
Plasmid1 A22 CP085499.1 : Myo-inositol catabolic operon: 1: 5-keto-2-deoxygluconokinase EC2.7.1.92, 2: transcriptional regulator IolR, 3: alpha-ketoglutarate permease, 4: myo-inositol-2-dehydrogenase, EC 1.1.1.18 (iolG) 5: malonate-semialdehyde dehydrogenase EC 1.2.1.18 (iolA), 6: 3D-trihydroxy,cyclohexane-1,2-dione hydrolase EC3.71.22, 7: inosose dehydratase EC 4.2.44,8: KDGP aldolase EC 4.1.2.29, 9: 5-deoxy-glucuronate isomerase EC 5.3.1.30 (myo inositol catabolic operon)



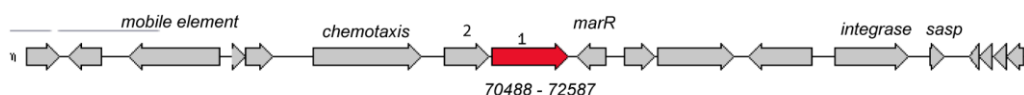
Plasmid1 A22 CP085499.1 : Anthrose biosynthetic operon: 1: O acetyl transferase, 2: hypothetical proteins, 3: SAM-dependent methyltransferase, 4: Enoyl CoA hydratase, 5: glycosyl transferase, 6: aminotransferase, 7: methyltransferase, 8: glycosyltransferase (anthrose biosynthesis)



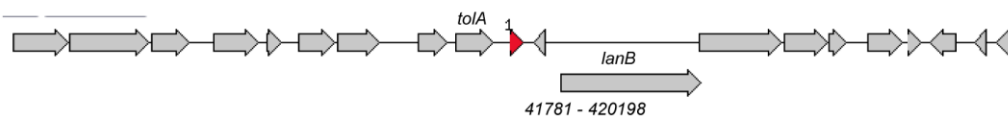
Plasmid1 A24 CP085502.1 : gluconate operon 1: phospho gluconate dehydrogenase, 2: conserved proteins, 3 repressor, 4 gluconokinase, 5: gluconate permease,.



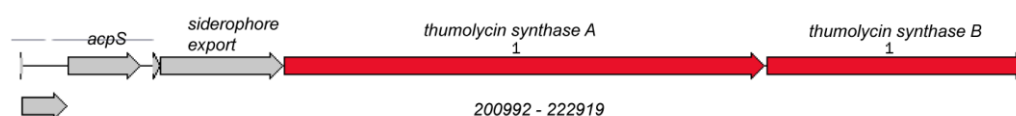
Plasmid1 HD2.4 CP085507.1: 1: pulcherriminic acid synthase (EC1.14.15.13), 2: Cyclodileucine synthase (EC2.3.2.22)



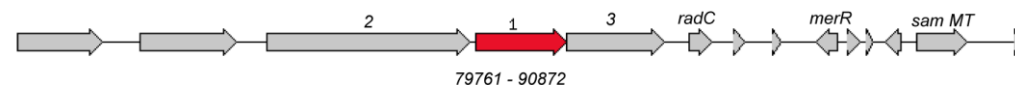
Plasmid1 HD2.4 CP085507.1: 1: bacteriocin cerein 7B precursor



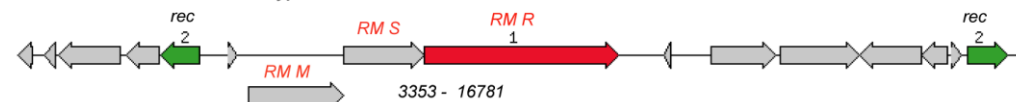
Plasmid1 HD2.4 CP085507.1: 1: Thumolycin synthase



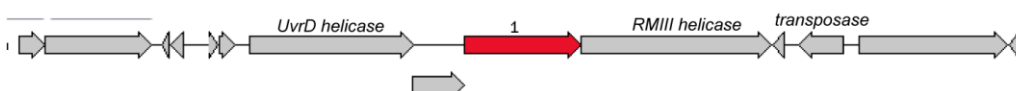
Plasmid1 A24 CP085502.1 : type 1 restriction modification system: 1: restriction subunit M (EC2.1.1.72), 2: restriction subunit R (EC3.1.21.3), 3 subunit S



Plasmid 2 A22 CP085500.1: 1: type I restriction modification subunit restriction



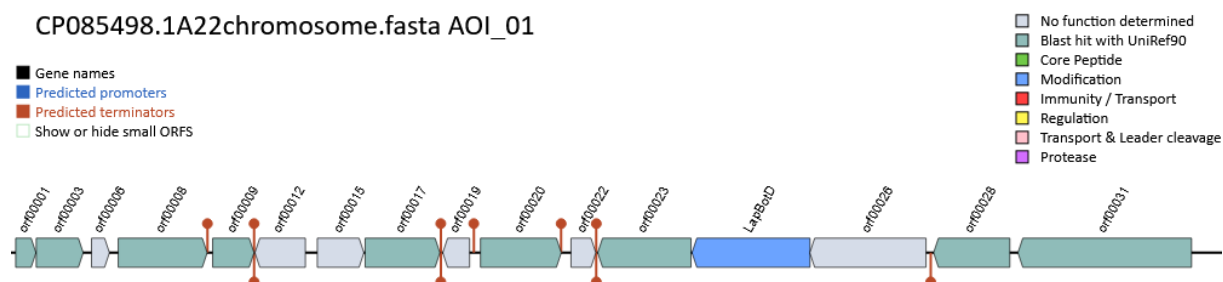
Plasmid1 HD1.4B CP085511.1: 1: type III restriction modification subunit methylation



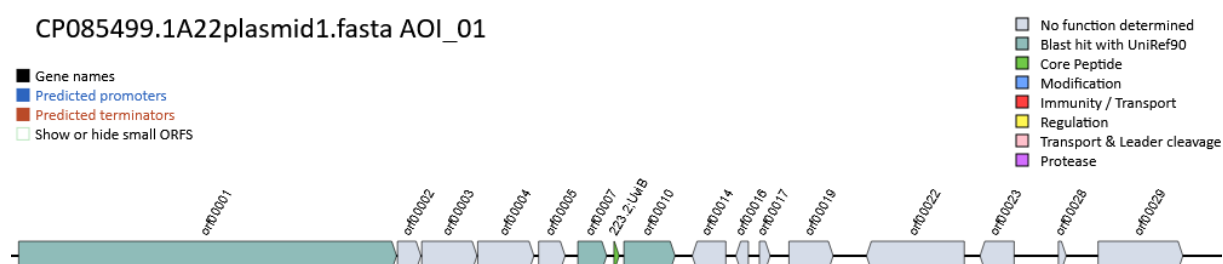
Suppl. Figure S6: Plasmid encoded catabolic operons, biosynthetic gene clusters (BGCs) and restriction/modification systems.



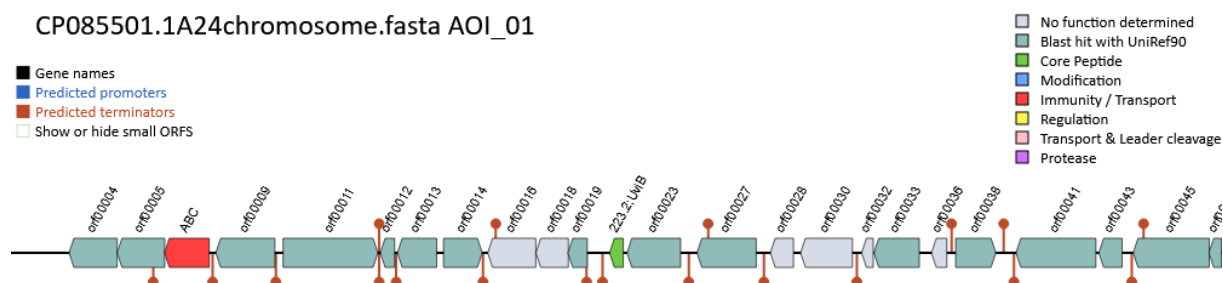
Suppl. Figure S7. BGCs in the *B. cereus* group isolates encoding NRPS/NRPK and other secondary metabolites



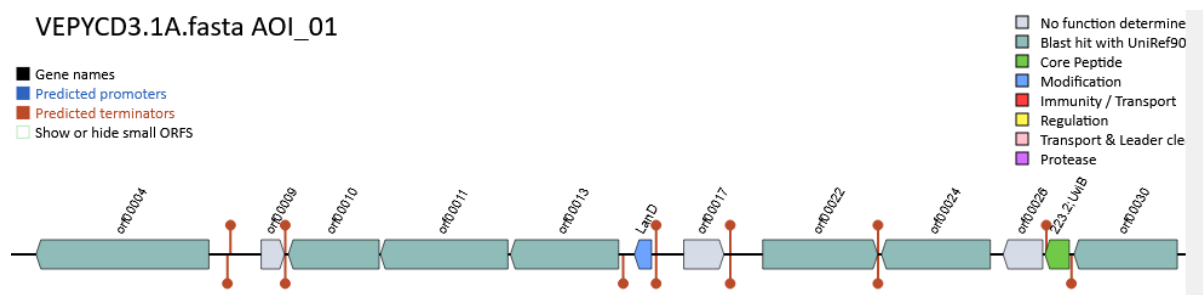
The LAPBotD gene cluster located within the A8 node 12, the A22 chromosome from 1,203,959 – 1,223,959, the A24 chromosome from 4,003,443-4,009,306.



UviB (223.2) located within the A22 chromosome from 350679– 350766. The UviB core peptide sequence is: MLFITQKKNEQCEEQYQAVIQKNQEVEIE



UviB (223.2) located within the A24 chromosome from 1,060,832-1081057. The UviB prepeptide sequence MEEQIFNSMIQQGAFALFVWMLFTTQKKNEQREEQYQKVIEKNQQVIEEQAKAFSSLSKDL SDVKKRILGNDDK is identical with *Bacillus thuringiensis* serovar israelensis ATCC35

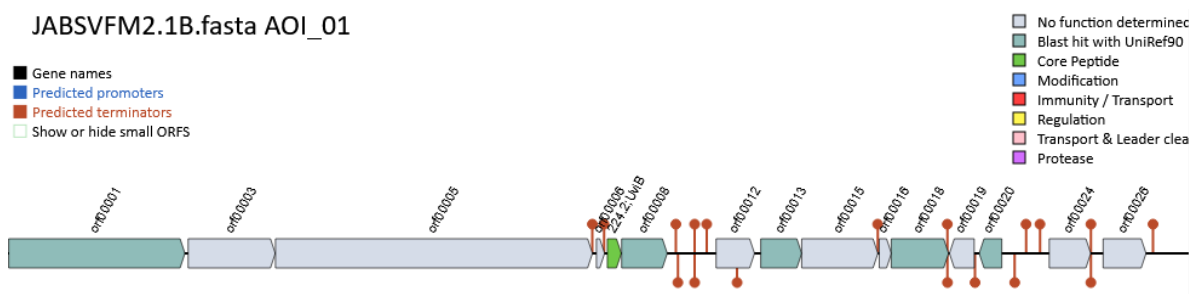


UviB (223.2)/LanD located in *Bacillus* sp. CD3.1A VEPY 12.1.

Query VKTVEEQIFNSMIQQGAF AALFVWMLFTTQKKNEQREAQYQAVIQKNQEVIEEQAKAFGSISKDVTEIKQQIFAD
+EEQIFNSMIQQGAF AALFVWMLFTTQKKNEQRE QYQ VI+KNQ+VIEEQAKAF S+SKD++++KQ+I +

UviB MEEQIFNSMIQQGAF AALFVWMLFTTQKKNEQREEQYQKVIEKNQVIEEQAKAFSSLSKDLSDVKQKILGNGDEK

JABSVFM2.1B.fasta AOI_01

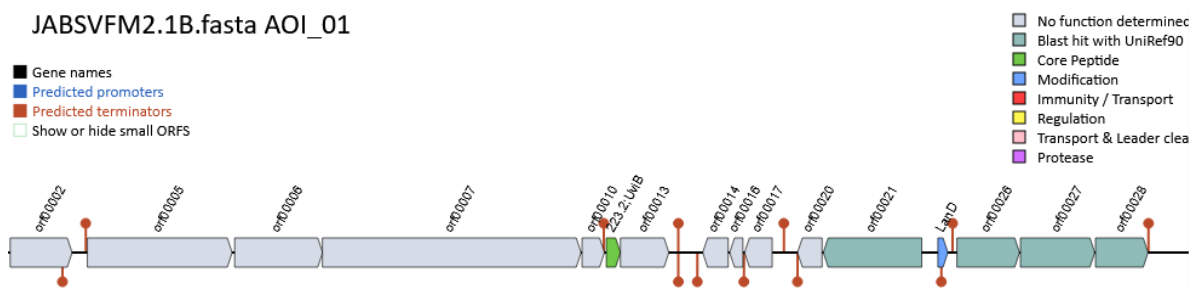


UviB (224.2) located within *B. cereus* M2.1B JABSVF 20. Weak similarity to *B. thuringiensis* sv *israelensis* ATCC35.

Query MLEQLAQVGLKEGIFALLFIWLLVDTKKESKEREDKLYNFLDGMKDEF SKLVHNYESLSSDVEDIKNDI
M EQ+ +++G FA LF+W+L T+K++++RE++ ++ +D +K + LS DV +IK I

UviB MEEQIFNSMIQQGAF AALFVWMLFTTQKKNEQREEQYQKVIEKNQDVITKQAEAFGDLSDVSEIKQKILGSGDVQ

JABSVFM2.1B.fasta AOI_01

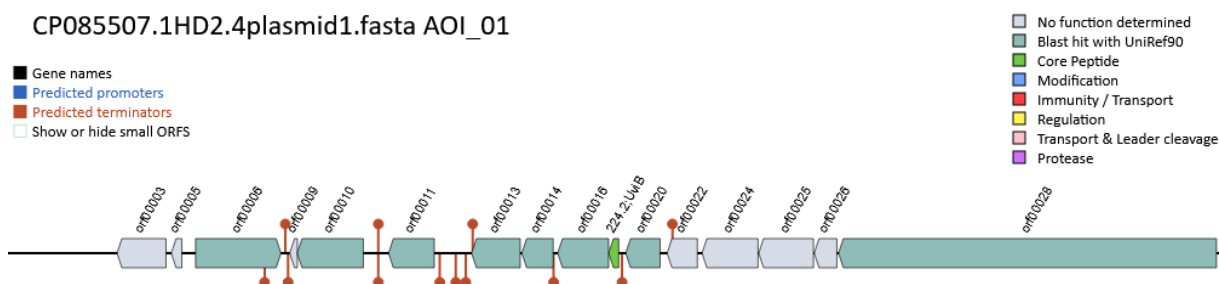


UviB (223.2) located within *B. cereus* M2.1B JABSVF 1. Similar to *B. thuringiensis* sv *israelensis* ATCC35.

Query MRTVEDAIFNSVIQQGAF AALFVWMLFTTQKKNEQREEKYQQVIDRNQQVIEEQAKAFGSISKDVTEIKQKLF-EGD
+E+ IFNS+IQQGAF AALFVWMLFTTQKKNEQREE+YQ+VI++NQQVIEEQAKAF S+SKD++++KQK+ GD

UviB MEEQIFNSMIQQGAF AALFVWMLFTTQKKNEQREEQYQKVIEKNQVIEEQAKAFSSLSKDLSDVKQKILGNGDEK

CP085507.1HD2.4plasmid1.fasta AOI_01

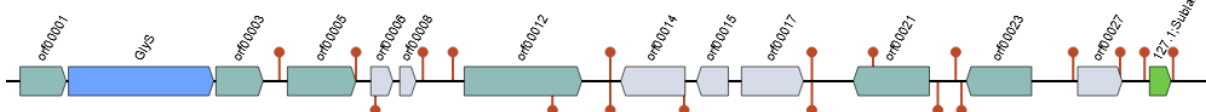


BhlA/UviB (224.2) holin like peptide [WP_098328186.1](#) in HD2.4 plasmid 1. Weak similarity with *Bacillus thuringiensis* serovar *israelensis* ATCC35

CP085503.1plasmid2.fasta AOI_01

■ Gene names
 ■ Predicted promoters
 ■ Predicted terminators
 □ Show or hide small ORFs

□ No function determined
 ■ Blast hit with UniRef90
 ■ Core Peptide
 ■ Modification
 ■ Immunity / Transport
 ■ Regulation
 ■ Transport & Leader cleavage
 ■ Protease



Query MKDLFKELKVEELDKHTGHGGMGWAQCAALLAQCSSGGRIGCGGTATQAYGQCNTYRKMC
 M+ LFKE+K+EEL+ G G+G AQCAAL QC+SGG IGC GG A C YR+ C
Sublancin_168 MEKLFKEVKLEELLENQKG-SGLGKAQCAALWLQCASGGTIGCGGGAV----ACQNYRQFCR

Bridges

Bridges

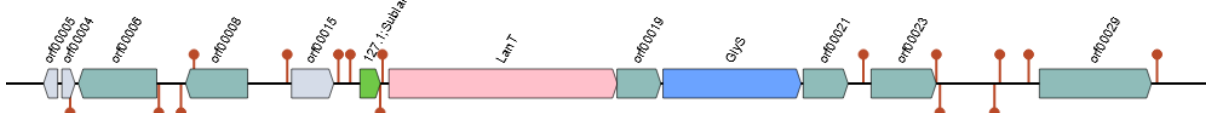
Sublancin 168 (ComC, subclass glyocin) [PF03047](#) in A24-plasmid 2 from 1,652-12,241.

GlyS: SP beta glycosyltransferase SunS.

CP085509.1HD2.4plasmid3.fasta AOI_01

■ Gene names
 ■ Predicted promoters
 ■ Predicted terminators
 □ Show or hide small ORFs

□ No function determined
 ■ Blast hit with UniRef90
 ■ Core Peptide
 ■ Modification
 ■ Immunity / Transport
 ■ Regulation
 ■ Transport & Leader cleavage
 ■ Protease



Sublancin 168 (ComC, subclass glyocin) [P68577](#)

/LanT in HD1.4B plasmid 3.

Query MKDLFKELKVEELDKHTGHGGMGWAQCAALLAQCSSGGRIGCGGTATQAYGQCNTYRKMC
 M+ LFKE+K+EEL+ G G+G AQCAAL QC+SGG IGC GG A C YR+ C
Sublancin_168 MEKLFKEVKLEELLENQKG-SGLGKAQCAALWLQCASGGTIGCGGGAV----ACQNYRQFCR

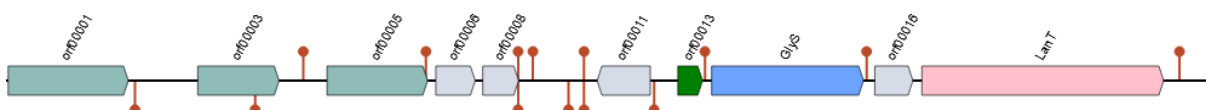
Bridges

Bridges

JABSVB01HB31.fasta AOI_01

■ Gene names
 ■ Predicted promoters
 ■ Predicted terminators
 □ Show or hide small ORFs

□ No function determined
 ■ Blast hit with UniRef90
 ■ Core Peptide
 ■ Modification
 ■ Immunity / Transport
 ■ Regulation
 ■ Transport & Leader cleavage
 ■ Protease

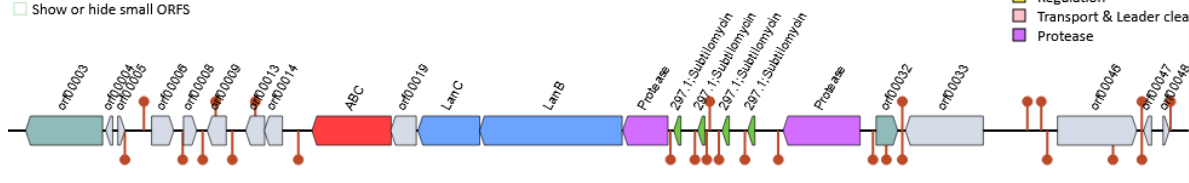


ComC/ GlyS/LanT gene cluster In HB3.1 29.1.

VEPRSN41.fasta AOI_01

■ Gene names
 ■ Predicted promoters
 ■ Predicted terminators
 □ Show or hide small ORFs

□ No function determined
 ■ Blast hit with UniRef90
 ■ Core Peptide
 ■ Modification
 ■ Immunity / Transport
 ■ Regulation
 ■ Transport & Leader cleavage
 ■ Protease



Subtilomycin (297.1)/LanB/LanC gene cluster in SN4-3 VEPR 27.1.

Query MNKELFDLDINKKMETPTMTAQWTIVKV---SKAVCKTGTCT-TSCSNC
 +FDLDINKKME+ +E++AQTW TI K S C+T TC C+ SCSNC

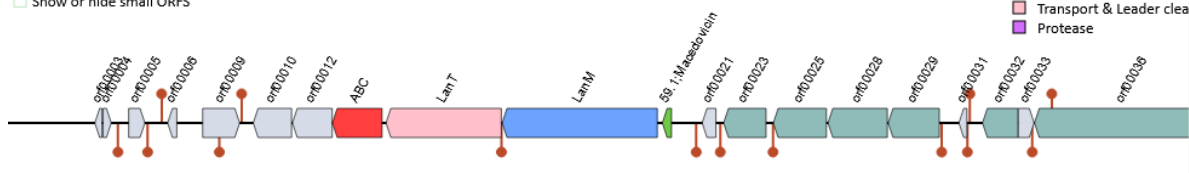
Subtilomycin MEKNNIFDLDINKKMESTSEVSAQTWATIGKTIVQSVKCRFTTCGCSLGS CSNCN

Subclass Lanthipeptide
 Organism Bacillus subtilis
 Literature [Reference](#)
 NCBI [JX912247.1](#)

VEPRSN41.fasta AOI_01

■ Gene names
 ■ Predicted promoters
 ■ Predicted terminators
 □ Show or hide small ORFs

□ No function determined
 ■ Blast hit with UniRef90
 ■ Core Peptide
 ■ Modification
 ■ Immunity / Transport
 ■ Regulation
 ■ Transport & Leader cleavage
 ■ Protease



Macedovicin (59.1)/LanM/LanT gene cluster in SN4-3 VEPR 6.2.

Query METEKYLQVVEDEEIEQLVGGVGPWETLTCDPGYKPYACITIAQTII--CKRC
 E + +++ V D+E+E L+GG GWI+TLTKDCP C AG I CK C

Macedovicin MMNATENQIFVETVSDQLEMLIGGADRGWIKTLTKDCPNVISSIC---AGTIITACKNCA

Bridges

Bridges

Bridges

Modifications MMNATENQIFVETVSDQLEMLIGGADRGWIK***L***KDCPNVISSIC---AGTIITACKNCA

Subclass Lanthipeptide B

Organism Streptococcus macedonicus ACA-DC198

Literature [Reference](#)

UniProt [H2A7G5](#)

propeptide 1 - 25

chain Lantibiotic macedovicin 26 - 58

modified residue 2,3-didehydrobutyrine 33

modified residue 2,3-didehydrobutyrine 35

disulfide bond 46 - 54

cross-link Beta-methyllanthionine (Thr-Cys) 33 - 38

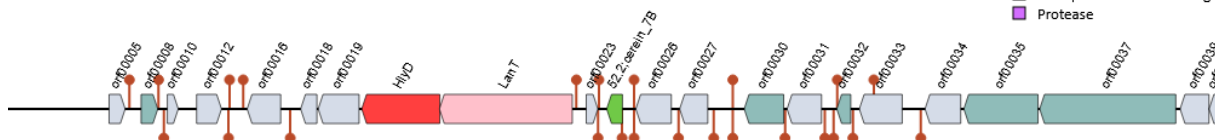
cross-link Beta-methyllanthionine (Thr-Cys) 35 - 57

The macedovicin peptide was found identical to bovicin HJ50 and thermophilin 1277.

CP085507.1HD2.4plasmid1.fasta AOI_02

■ Gene names
 ■ Predicted promoters
 ■ Predicted terminators
 □ Show or hide small ORFs

□ No function determined
 ■ Blast hit with UniRef90
 ■ Core Peptide
 ■ Modification
 ■ Immunity / Transport
 ■ Regulation
 ■ Transport & Leader cleavage
 ■ Protease

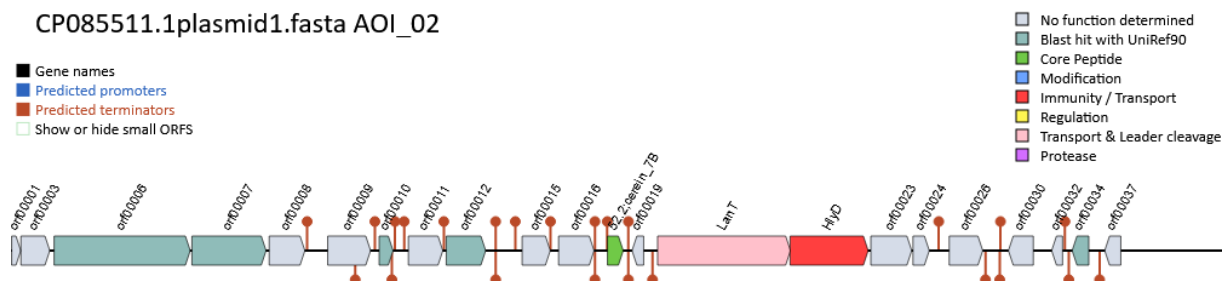


Cerein_7B (52.2) [Q2MDB2](#)

LanT gene cluster in HD2.4 plasmid 1 from 409,978-430,197

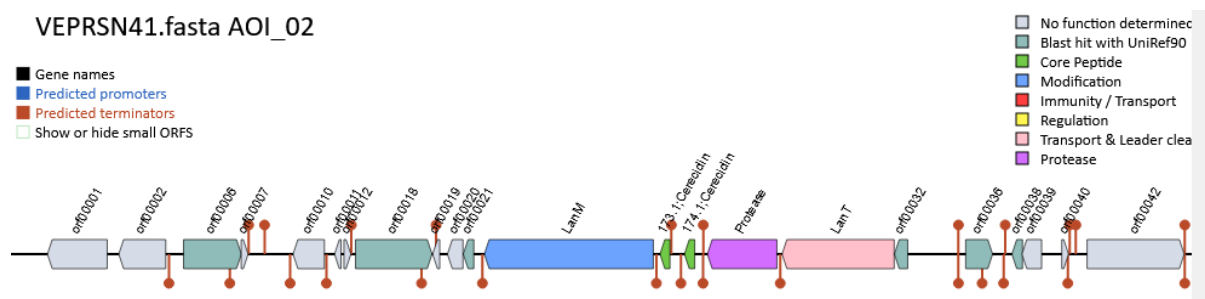
HlyD putative bacteriocin ABC transporter. Cerein_7B ComC; L_biotic_typeA, bacteriocin_IIC.

CP085511.1plasmid1.fasta AOI_02



Cerein_7B (subclass D) gene cluster in HD1.4B) plasmid1 from 270,830-291,049. Q2MDB2. Similar to B. cereus

VEPRSN41.fasta AOI_02



Cerecidin (173.1, 174.1) gene cluster in VEPR 6.1 SN4-3.

Query MNRNQVIEELAVNHPAGAKLVEVSREELTRVYGGGDVQAETTPMTPTLYLNGITIGLALSQSC

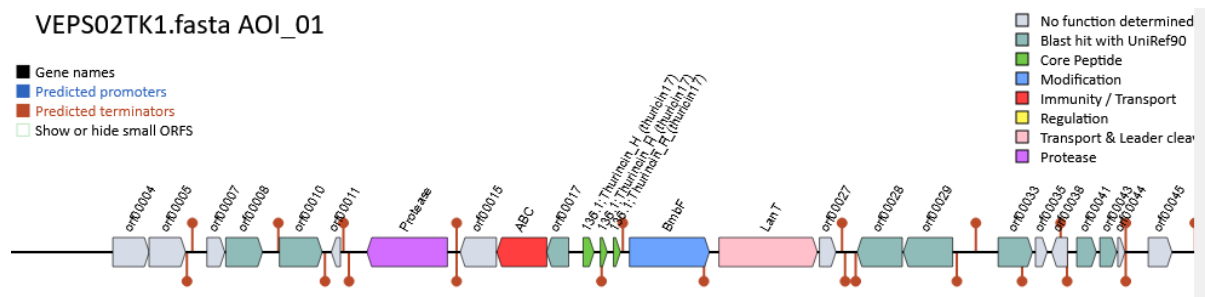
NHP+G L E+S EEL + G DVQ ETP+ G+ IG+ S + C

Cerecidin MSKGYKFTKEELVEAWKDPQVREKLKDLPNHPSGKALNELSEEELAEIQGASDVQPETTPLC-----VGVIIGITASIKICK

Subclass Lanthipeptide B

Organism *Bacillus cereus*Literature [Reference](#)NCBI [AHJ59543.1](#)

VEPS02TK1.fasta AOI_01



Sactipeptide Thurincin_H (thuricin 17)/BmbF/LanT gene cluster in M2.1B, JABSVF 11.1, TK1 VEPS 63.1

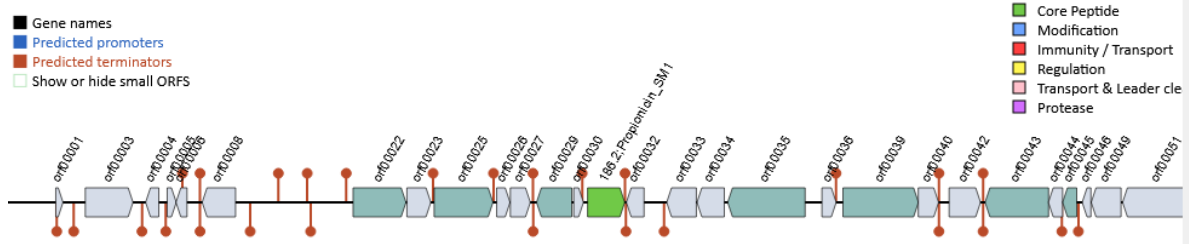
Query METPVVQPRDWT CWSCLVCAACSVELLNLTAAATGASTAS

METPVVQPRDWT CWSCLVCAACSVELLNLTAAATGASTAS

Thurincin_H (thuricin17) METPVVQPRDWT CWSCLVCAACSVELLNLTAAATGASTAS

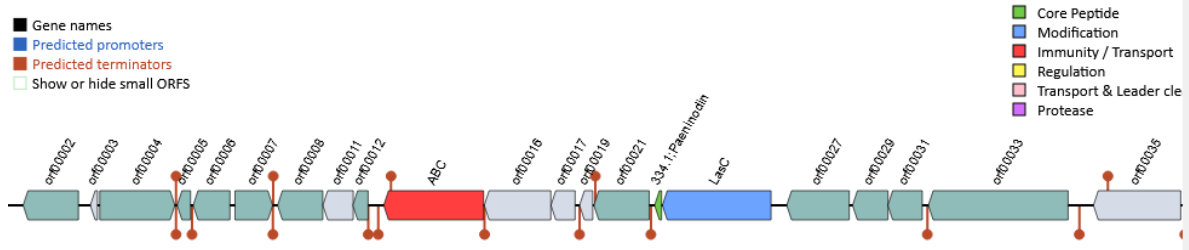
Subclass Sactipeptide
Organism *Bacillus thuringiensis*

VEPYCD3.1A.fasta AOI_01



Propionisin (186.2) in *Bacillus* sp. CD3.1A VEPY 16.1. Weak similarity to Propionisin Miescher S, Stierli MP, Teuber M, Meile L. Propionisin SM1, a bacteriocin from *Propionibacterium jensenii* DF1: isolation and characterization of the protein and its gene. *Syst Appl Microbiol.* 2000 Jun;23(2):174-84. doi: 10.1016/S0723-2020(00)80002-8. PMID: 10930068.

VEPYCD3.1A.fasta AOI_01

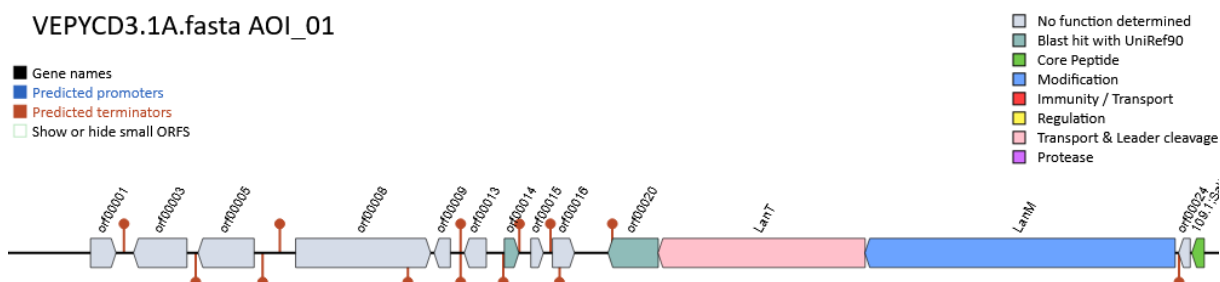


Suppl. Fig. S: Paeninodin (334.1) / LanC/ABC gene cluster in *Bacillus* sp. CD3.1A VEPY 1 and *B. pacificus* HD1,3

Query MKKDWTIPTLEVLDINMTMAGPGLKTPDAVQPDIDEVVHY
 AGPG TPDA QPD DE VHY
Paeninodin AGPGTSTPDAFQPDDEDVHYDS

Subclass Lasso peptide
Organism *Paenibacillus dendritiformis* C454

VEPYCD3.1A.fasta AOI_01

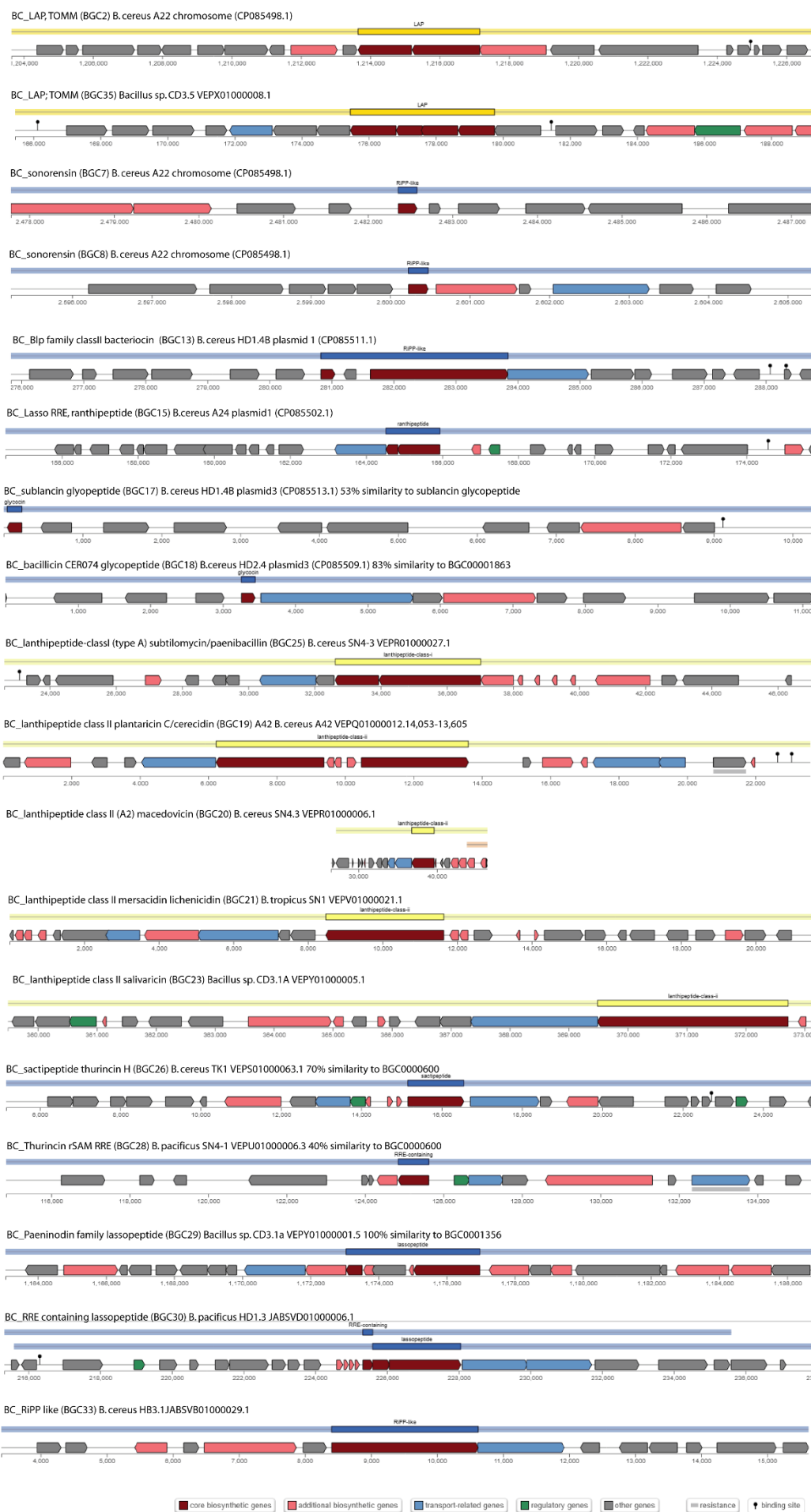


Salivaricin A (109.1)/LanT/ LanM gene cluster in *Bacillus* sp. CD3.1A VEPY 5.1

Query MEELKSVVMTVTDEELQE-AAGAAGCGWLCTVTDDCPNSVFVCC
 L +V+ V+++EL E A G G GW T+TDDCPNSVFVCC
SalivaricinA MERRMSFMKNSKILTNVIEEVSEKELMEVAGGKKGSGWFATITDDCPNSVFVCC

Subclass Lanthipeptide B
Organism *Streptococcus pyogenes* MGAS10394

Suppl. Figure S8. RiPP gene clusters detected by applying the BAGEL4 software (<http://bagel4.molgenrug.nl/>) in the Vietnamese *Bacillus cereus* group genomes.



Suppl. Figure S9: RiPP gene clusters detected by applying the antiSMASH version 6 software in the Vietnamese *Bacillus cereus* group genomes.