



Supplementary materials

File S1: List of strains compared by the PATRIC Codon Trees service to construct the phylogenetic tree showed in Figure 2.

- 1) Geobacillus sp. 12AMOR1
- 2) Geobacillus kaustophilus HTA426
- 3) Geobacillus thermoleovorans CCB_US3_UF5
- 4) Geobacillus sp. Y412MC61
- 5) Geobacillus thermodenitrificans NG80-2
- 6) Geobacillus sp. LC300
- 7) Bacillus cytotoxicus NVH 391-98
- 8) Geobacillus thermoglucosidans TNO-09.020
- 9) Bacillus toyonensis BCT-7112
- 10) Bacillus thuringiensis 97-27
- 11) Bacillus cereus B4264
- 12) Bacillus cereus ATCC 4342
- 13) Bacillus cereus F837/76
- 14) Bacillus thuringiensis HD682
- 15) Bacillus cereus strain ISSFR-23F
- 16) Bacillus thuringiensis str. Al Hakam
- 17) Bacillus cereus ATCC 14579
- 18) Bacillus cereus strain JEM-2
- 19) Bacillus cereus strain ISSFR-3F
- 20) Bacillus cereus strain NJ-W
- 21) Bacillus cereus strain ISSFR-9F
- 22) Bacillus cereus ATCC 10987
- 23) Bacillus anthracis strain delta Sterne
- 24) Bacillus sp. JEM-1 strain JEM-1

- 25) *Bacillus* sp. S1-R4H1-FB strain S1-R4H1-FB
- 26) *Bacillus anthracis* A0157
- 27) *Bacillus mycoides* ATCC 6462
- 28) *Bacillus thuringiensis* BMB171
- 29) *Bacillus* sp. S2-R3J1-FB-BA1 strain S2-R3J1-FB-BA1
- 30) *Bacillus anthracis* strain Han
- 31) *Bacillus anthracis* strain Cvac02
- 32) *Bacillus cereus* Q1
- 33) *Bacillus anthracis* str. Ames
- 34) *Bacillus anthracis* strain 2000031021
- 35) *Bacillus anthracis* str. V770-NP-1R
- 36) *Bacillus anthracis* strain Smith 1013
- 37) *Bacillus* sp. S1-R1J2-FB strain S1-R1J2-FB
- 38) *Bacillus cereus* FM1
- 39) *Bacillus anthracis* PAK-1
- 40) *Bacillus cereus* 03BB102
- 41) *Bacillus* sp. ISSFR-25F strain ISSFR-25F
- 42) *Bacillus weihenstephanensis* strain WSBC 10204
- 43) *Bacillus cereus* strain FORC_013
- 44) *Bacillus cereus* biovar anthracis str. CI
- 45) *Bacillus cereus* 03BB87
- 46) *Bacillus* sp. S1-R2T1-FB strain S1-R2T1-FB
- 47) *Bacillus bombysepticus* str. Wang
- 48) *Bacillus anthracis* str. Sterne
- 49) *Bacillus anthracis* RA3
- 50) *Bacillus* sp. S1-R5C1-FB strain S1-R5C1-FB
- 51) *Bacillus cereus* AH187
- 52) *Bacillus anthracis* BA1015

- 53) *Bacillus anthracis* Ohio ACB
- 54) *Bacillus anthracis* str. Turkey32
- 55) *Bacillus cereus* 3a
- 56) *Bacillus anthracis* str. H9401
- 57) *Bacillus anthracis* K3
- 58) *Bacillus anthracis* Vollum 1B
- 59) *Bacillus anthracis* str. SVA11
- 60) *Bacillus cereus* D17
- 61) *Bacillus mycoides* strain 219298
- 62) *Bacillus anthracis* Pollino
- 63) *Bacillus weihenstephanensis* KBAB4
- 64) *Bacillus anthracis* 2002013094
- 65) *Bacillus cereus* G9842
- 66) *Bacillus anthracis* str. A16R
- 67) *Bacillus cereus* AH820
- 68) *Bacillus cereus* G9241
- 69) *Bacillus anthracis* strain BFV
- 70) *Bacillus thuringiensis* serovar kurstaki str. HD73
- 71) *Bacillus anthracis* strain A1144
- 72) *Bacillus anthracis* str. A0248
- 73) *Bacillus anthracis* 9080-G
- 74) *Bacillus cereus* E33L
- 75) *Bacillus anthracis* str. CDC 684
- 76) *Bacillus anthracis* 8903-G
- 77) *Bacillus anthracis* str. 'Ames Ancestor'
- 78) *Bacillus anthracis* 52-G
- 79) *Bacillus thuringiensis* strain YGD22-03
- 80) *Bacillus anthracis* str. A16

- 81) *Bacillus anthracis* strain Stendal
- 82) *Bacillus thuringiensis* serovar morrisoni strain BGSC
- 83) *Bacillus thuringiensis* strain YWC2-8
- 84) *Bacillus thuringiensis* strain HS18-1
- 85) *Bacillus thuringiensis* serovar galleriae HD-29
- 86) *Bacillus cereus* 03BB108
- 87) *Bacillus thuringiensis* serovar indiana strain HD521
- 88) *Bacillus thuringiensis* serovar kurstaki str. YBT-1520
- 89) *Bacillus thuringiensis* serovar kurstaki HD 1
- 90) *Bacillus thuringiensis* serovar kurstaki str. HD-1
- 91) *Bacillus thuringiensis* HD-789
- 92) *Bacillus thuringiensis* strain YC-10
- 93) *Bacillus thuringiensis* serovar thuringiensis str. IS5056
- 94) *Bacillus thuringiensis* serovar tolworthi
- 95) *Bacillus thuringiensis* Bt407
- 96) *Bacillus thuringiensis* HD1002

File S2: List of genes/proteins selected by the PATRIC Codon Trees service to produce Figure 2.

- 1) Excinuclease ABC subunit C
- 2) Oligoendopeptidase F
- 3) Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)
- 4) Dihydrolipoamide dehydrogenase of branched-chain alpha-keto acid dehydrogenase (EC 1.8.1.4)
- 5) tRNA-i(6)A37 methylthiotransferase (EC 2.8.4.3)
- 6) N-acetylglucosamine-1-phosphate uridyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)
- 7) Glycyl-tRNA synthetase (EC 6.1.1.14)
- 8) Dihydroorotase (EC 3.5.2.3)
- 9) 16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)
- 10) ADP-ribose pyrophosphatase of COG1058 family (EC 3.6.1.13) / Nicotinamide-nucleotide amidase (EC 3.5.1.42)
- 11) Dihydrofolate synthase (EC 6.3.2.12) @ Folylpolyglutamate synthase (EC 6.3.2.17)
- 12) Cystathionine gamma-synthase (EC 2.5.1.48) @ O-acetylhomoserine sulfhydrylase (EC 2.5.1.49)
- 13) GTP-binding protein YqeH, required for biogenesis of 30S ribosome subunit
- 14) Uncharacterized MFS-type transporter YfkF
- 15) N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)
- 16) Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)
- 17) Tetraprenyl-beta-curcumene synthase (EC 4.2.3.130)
- 18) Heat-inducible transcription repressor HrcA
- 19) ABC transporter, permease protein EscB
- 20) UPF0348 protein family
- 21) Ribosomal protein L11 methyltransferase
- 22) DNA polymerase III delta subunit (EC 2.7.7.7)
- 23) Dipicolinate synthase subunit A
- 24) Allergen V5/Tpx-1 related
- 25) Stage 0 sporulation protein YaaT
- 26) (2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10)
- 27) Uncharacterized membrane protein YkvI

- 28) UPF0701 protein YicC
- 29) Prephenate dehydratase (EC 4.2.1.51)
- 30) FIG00003568: ACT domain protein
- 31) 2',3'-cyclic-nucleotide 2'-phosphodiesterase, Bsub YmdB
- 32) Succinate dehydrogenase iron-sulfur protein (EC 1.3.5.1)
- 33) 16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)
- 34) NAD kinase (EC 2.7.1.23)
- 35) Chromosome (plasmid) partitioning protein ParB
- 36) 3'-to-5' oligoribonuclease A, Bacillus type
- 37) HesA/MoeB/ThiF family protein
- 38) Efflux ABC transporter, permease protein
- 39) FIG007013: polysaccharide deacetylase, putative
- 40) NAD kinase (EC 2.7.1.23) homolog
- 41) RNA polymerase sporulation specific sigma factor SigG
- 42) Late competence protein ComER, proline oxidase (EC 1.5.1.2)
- 43) 2,4-dienoyl-CoA reductase (EC 1.3.1.34)
- 44) Quorum-quenching lactonase YtnP
- 45) Ribonuclease III (EC 3.1.26.3)
- 46) Phosphatidylserine decarboxylase (EC 4.1.1.65)
- 47) Menaquinone-cytochrome C oxidoreductase, cytochrome C subunit
- 48) Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13)
- 49) Bis(5'-nucleosyl)-tetrphosphatase (asymmetrical) (EC 3.6.1.17)
- 50) Uracil phosphoribosyltransferase (EC 2.4.2.9)
- 51) Chromosome replication initiation protein DnaD
- 52) KtrCD potassium uptake system, peripheral membrane component KtrC
- 53) N-acetylglucosaminyl-L-malate N-acetyl hydrolase
- 54) Peptidoglycan-N-acetylmuramic acid deacetylase PdaA
- 55) Ribonuclease HII (EC 3.1.26.4)

- 56) Heptaprenylglyceryl phosphate synthase (EC 2.5.1.n9)
- 57) Stage IV sporulation protein FA (SpoIVFA)
- 58) Uncharacterized protein YjaZ
- 59) Endonuclease III (EC 4.2.99.18)
- 60) SSU ribosomal protein S4p (S9e) @ SSU ribosomal protein S4p (S9e), zinc-independent
- 61) Uracil-DNA glycosylase, family 1 (EC 3.2.2.27)
- 62) Uncharacterized membrane protein YjbE
- 63) Stage II sporulation protein related to metalloproteases (SpoIIQ)
- 64) Peptidyl-tRNA hydrolase (EC 3.1.1.29)
- 65) Acyl-CoA:1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
- 66) Cell division protein FtsQ
- 67) Uncharacterized protein YpeP
- 68) Acetyltransferase, GNAT family
- 69) KinB signaling pathway activation protein
- 70) Spore cortex biosynthesis protein
- 71) Transcription factor FapR
- 72) 16S rRNA (guanine(1207)-N(2))-methyltransferase (EC 2.1.1.172)
- 73) dCMP deaminase (EC 3.5.4.12) @ Late competence protein ComEB
- 74) Stage III sporulation protein AF
- 75) Transcriptional repressor for NAD biosynthesis in gram-positives
- 76) Outer spore coat protein CotE
- 77) DUF402 family nucleoside diphosphatase
- 78) NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.13)
- 79) Hydrolase (HAD superfamily), YqeK
- 80) UPF0234 protein Yitk
- 81) ATP synthase delta chain (EC 3.6.3.14)
- 82) Adenylate cyclase (EC 4.6.1.1)
- 83) Ribonucleotide reductase transcriptional regulator NrdR

- 84) 2H phosphoesterase superfamily protein Bsu1186 (yjcG)
- 85) Peptide-methionine (S)-S-oxide reductase MsrA (EC 1.8.4.11)
- 86) 16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)
- 87) Uncharacterized protein YpjA
- 88) Cell division initiation protein DivIVA
- 89) RNA binding protein, contains ribosomal protein S1 domain
- 90) Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly
- 91) Uncharacterized protein YisN
- 92) FIG001553: Hydrolase, HAD subfamily IIIA
- 93) Transamidase GatB domain protein
- 94) Menaquinone-cytochrome C reductase iron-sulfur subunit
- 95) Putative iron-sulfur cluster assembly scaffold protein for SUF system, SufE2
- 96) LSU ribosomal protein L10p (P0)
- 97) Ribose-5-phosphate isomerase B (EC 5.3.1.6)
- 98) Histidine triad (HIT) nucleotide-binding protein, similarity with At5g48545 and yeast YDL125C (HNT1)
- 99) D-aminoacyl-tRNA deacylase (EC 3.1.1.96)
- 100) Peroxide stress regulator PerR, FUR family

File S3: List of strains selected to construct the phylogenetic tree (PATRIC Codon Trees service) of the ISS strains, compared with the reference strains of the *Bacillus cereus* group, and showed in Figure 3.

- 1) *Bacillus cereus* strain ISSFR-23F
- 2) *Bacillus cereus* strain JEM-2
- 3) *Bacillus cereus* strain ISSFR-3F
- 4) *Bacillus cereus* strain ISSFR-9F
- 5) *Bacillus cereus* ATCC 14579
- 6) *Bacillus* sp. JEM-1 strain JEM-1
- 7) *Bacillus* sp. S1-R4H1-FB strain S1-R4H1-FB
- 8) *Bacillus* sp. S2-R3J1-FB-BA1 strain S2-R3J1-FB-BA1
- 9) *Bacillus anthracis* str. Ames
- 10) *Bacillus* sp. S1-R1J2-FB strain S1-R1J2-FB
- 11) *Bacillus* sp. ISSFR-25F strain ISSFR-25F
- 12) *Bacillus cereus* biovar anthracis str. CI
- 13) *Bacillus* sp. S1-R2T1-FB strain S1-R2T1-FB
- 14) *Bacillus* sp. S1-R5C1-FB strain S1-R5C1-FB
- 15) *Bacillus thuringiensis* serovar kurstaki str. HD-1

File S4: List of genes/proteins selected by the PATRIC Codon Trees service to produce Figure 3.


- 1) Sensor histidine kinase/response regulator
- 2) Acetoacetyl-CoA synthetase [leucine] (EC 6.2.1.16)
- 3) membrane-anchoring domain / Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
- 4) Two-component sensor kinase SA14-24
- 5) Oligoendopeptidase F
- 6) CoA-disulfide reductase (EC 1.8.1.14) / Polysulfide binding and transferase domain
- 7) Argininosuccinate lyase-like protein
- 8) Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98)
- 9) Endospore coat-associated protein YheD
- 10) Deoxyribodipyrimidine photolyase (EC 4.1.99.3)
- 11) Bis-ABC ATPase
- 12) DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)
- 13) ATP-dependent RNA helicase BA2475
- 14) Spore cortex-lytic enzyme, N-acetylglucosaminidase SleL
- 15) Two-component system YycFG regulatory protein YycH
- 16) Niacin transporter NiaP
- 17) Oxalate/formate antiporter
- 18) Ornithine aminotransferase (EC 2.6.1.13)
- 19) Flavohemoglobin / Nitric oxide dioxygenase (EC 1.14.12.17)
- 20) ABC transporter, permease protein EscB
- 21) Aminotransferase BA2899
- 22) putative membrane protein
- 23) Cystathionine gamma-lyase (EC 4.4.1.1) @ Homocysteine desulfhydrase (EC 4.4.1.2)
- 24) Branched-chain amino acid dehydrogenase [deaminating] (EC 1.4.1.9)(EC 1.4.1.23)
- 25) N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47)
- 26) Spore germination endopeptidase Gpr (EC 3.4.24.78)
- 27) Membrane metalloprotease

- 28) Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)
- 29) FIGfam013899: ABC transporter substrate-binding protein
- 30) Cystathionine gamma-synthase (EC 2.5.1.48) @ O-acetylhomoserine sulfhydrylase (EC 2.5.1.49)
- 31) Endospore coat-associated protein YutH
- 32) ABC transporter, permease protein
- 33) Oxidoreductase, Gfo/Idh/MocA family
- 34) Zinc ABC transporter, substrate-binding protein ZnuA
- 35) hypothetical protein
- 36) Oxidoreductase, aldo/keto reductase family
- 37) Transcriptional regulator in cluster with unspecified monosaccharide ABC transport system
- 38) Molybdenum cofactor biosynthesis enzyme and related Fe-S oxidoreductases
- 39) 3-Oxoadipate enol-lactonase, alpha/beta hydrolase fold family [EC:3.1.1.24]
- 40) Ser/Thr protein phosphatase family protein
- 41) Membrane protease family protein BA0301
- 42) Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)
- 43) Chromosome (plasmid) partitioning protein ParB
- 44) UPF0750 membrane protein YvjA
- 45) Quorum-quenching lactonase YtnP
- 46) Glycine betaine ABC transport system, permease protein OpuAB
- 47) RNA binding methyltransferase FtsJ like
- 48) NAD synthetase (EC 6.3.1.5)
- 49) Serine/threonine protein kinase
- 50) 2',3'-cyclic-nucleotide 2'-phosphodiesterase, Bsub YmdB
- 51) Uncharacterized membrane protein YkoY
- 52) RNA polymerase sporulation specific sigma factor SigG
- 53) Inositol-1-monophosphatase (EC 3.1.3.25)
- 54) 2,4-dienoyl-CoA reductase (EC 1.3.1.34)
- 55) Alkanesulfonate ABC transporter ATP-binding protein SsuB

- 56) Ribonuclease III (EC 3.1.26.3)
- 57) RNA polymerase sporulation specific sigma factor SigE
- 58) 16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)
- 59) 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase related protein BA2564
- 60) Uncharacterized protein YwmB
- 61) N-acetylglucosaminyl-L-malate N-acetyl hydrolase
- 62) ClpCP protease substrate adapter protein MecA
- 63) SAM-dependent methyltransferase Rv1498c
- 64) Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)
- 65) Substrate-specific component ThiT of thiamin ECF transporter
- 66) Uncharacterized membrane protein YtaF
- 67) Cell envelope stress response system LiaFSR, response regulator LiaR(VraR)
- 68) Redox-sensing transcriptional repressor Rex
- 69) DUF1054 superfamily protein
- 70) Phosphohydrolase (MutT/nudix family protein)
- 71) putative secreted protein
- 72) Hydrolase, haloacid dehalogenase-like family
- 73) Nucleoside 5-triphosphatase RdgB (dHATP, dITP, XTP-specific) (EC 3.6.1.66)
- 74) Conserved membrane protein in copper uptake, YcnI
- 75) Uncharacterized protein YhbD
- 76) hypothetical protein
- 77) Secreted and spore coat-associated protein 1, similar to biofilm matrix component TasA and to camelysin
- 78) putative lipoprotein
- 79) hypothetical protein
- 80) Possible caffeoyl-CoA O-methyltransferase (EC 2.1.1.104)
- 81) UPF0398 protein YpsA
- 82) Uncharacterized membrane protein YuaF
- 83) ATP synthase delta chain (EC 3.6.3.14)

- 84) Possible colicin V production protein
- 85) SAM-dependent methyltransferase
- 86) DUF402 family nucleoside diphosphatase
- 87) Putative metal-dependent hydrolase YfiT
- 88) ThiJ/PfpI family protein YhbO
- 89) tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207)
- 90) UPF0302 protein YpiB
- 91) Cyclic pyranopterin monophosphate synthase (EC 4.6.1.17)
- 92) Uncharacterized protein YpoC
- 93) Inosine/xanthosine triphosphatase
- 94) UPF0478 protein YtxG
- 95) UPF0756 membrane protein YtwI
- 96) hypothetical protein
- 97) Uncharacterized N-acetyltransferase BT9727_3663 (EC 2.3.1.-)
- 98) Uncharacterized membrane protein YqhR
- 99) DNA topology modulation protein FlaR
- 100) LSU ribosomal protein L9p

Table S1. Unique genetic variants, with a predicted high impact on protein product, of the ISS *Bacillus* strain/s compared with *B. anthracis* str. Ames; the data were extracted from the results presented in Figure 5 based on the PATRIC RAST Sequence-based Comparison tool.

Strain(s) name(s)  Copyright: © 2022 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).	Unique genetic variants of the strain/s compared with <i>B. anthracis</i> str. Ames	Unique variant with a predicted high impact on protein product	Gene product	Effect of the variant
Bacillus sp. ISSFR-23F	51	1	Ferrous iron transporter FeoB	Frameshift variant
Bacillus sp. ISSFR-9F	22	2	Efflux ABC transporter, ATP-binding protein	Start lost
			Uncharacterized protein YknW	Frameshift variant
Bacillus sp. JEM-1	51	1	Hypothetical protein	Start lost
Bacillus sp. S2-R3J1-FB-BA1	127	2	Hypothetical protein	Stop lost
			Hypothetical protein	Start lost
Bacillus sp. ISSFR-25F	287	4	Signal transduction histidine kinase CheA	Frameshift variant
			Hypothetical protein	Stop lost
			Hypothetical protein	Frameshift variant
			Hypothetical protein	Frameshift variant
Bacillus sp. S1-R2T1-FB	87	2	Hypothetical protein	Stop gained

			Hypothetical protein	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. ISSFR-9F	5	1	MBL-fold metallo-hydrolase superfamily	Start loss
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-1	15	1	Flagellin protein FlaA	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1	16	1	Nutrient germinant receptor inner membrane subunit A (GerKA/GerAA/GerBA)	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. ISSFR-9F, Bacillus sp. S2-R3J1-FB-BA1	3	1	Hypothetical protein	Start loss
Bacillus sp. ISSFR-23F, Bacillus sp. ISSFR-9F, Bacillus sp. S1-R2T1-FB	2	1	Efflux ABC transporter, permease protein	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1	6	1	Mobile element protein	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. JEM-1, Bacillus sp. S1-R4H1-FB	53	2	FMN reductase, NADPH-dependent	Stop gained
			Uncharacterized protein YknW	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1, Bacillus sp. S1-R4H1-FB	88	1	Hypothetical protein	Frameshift variant
Bacillus sp. S1-R4H1-FB, Bacillus sp. S2-R3J1-FB-BA1, Bacillus sp. S1-R1J2-FB, Bacillus sp. ISSFR-25, Bacillus sp. S1-R2T1-FB	1	1	Mobile element protein	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1,	58	2	Uncharacterized protein YpbB	Frameshift variant

Bacillus sp. S1-R4H1-FB, Bacillus sp. S1-R1J2-FB			Quaternary ammonium compound-resistance protein	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1, Bacillus sp. S1-R4H1-FB, Bacillus sp. S2-R3J1-FB-BA1, Bacillus sp. S1-R1J2-FB	53	2	Single-stranded DNA-binding protein UDP-N-acetylmuramoyl-dipeptide--2,6-diaminopimelate ligase (EC 6.3.2.13)	Stop gained Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1, Bacillus sp. S1-R4H1-FB, Bacillus sp. S1-R1J2-FB, Bacillus sp. S1-R2T1-FB	146	2	2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16) Wall-associated protein precursor	Stop gained Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. JEM-1, Bacillus sp. S1-R4H1-FB, Bacillus sp. S2-R3J1-FB-BA1, Bacillus sp. S1-R1J2-FB, Bacillus sp. S1-R2T1-FB	17	1	Hypothetical protein	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2, Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1, Bacillus sp. S1-R4H1-FB, Bacillus sp. S2-R3J1-FB-BA1, Bacillus sp. S1-R1J2-FB, Bacillus sp. S1-R2T1-FB	1047	17	Hypothetical protein Hypothetical protein MBL-fold metallo-hydrolase superfamily Hypothetical protein Hypothetical protein Hypothetical protein Hypothetical protein	Stop lost Frameshift variant Stop gained Stop lost Frameshift variant Frameshift variant Frameshift variant Start lost

			Hypothetical protein	Frameshift variant
			Hypothetical protein	Stop gained
			Putative membrane protein	Frameshift variant
			Hypothetical protein	Frameshift variant
			Hypothetical protein	Stop gained
			Phage protein	Stop lost
			Phage protein	Stop gained
			Putative membrane-spanning protein	Frameshift variant
			Hypothetical protein	Frameshift variant
Bacillus sp. ISSFR-23F, Bacillus sp. JEM-2,118 Bacillus sp. ISSFR-9F, Bacillus sp. JEM-1, Bacillus sp. S1-R4H1-FB, Bacillus sp. S1- R1J2-FB, Bacillus sp. ISSFR-25, Bacillus sp. S1-R2T1-FB		2	Hypothetical protein	Stop lost
			Hypothetical protein	Start lost

