

Table S1_file

Element	CRISPR ID/cas type	Start	End	Spacer Gene	Repeat consensus/cas gene	Direction	Evidence level
CRISPR	Contig_1_1	217705	217803	1	GAAGGATCAGAAACTGACAAAGA A	ND	1
CRISPR	Contig_7_1	118657	118809	1	CTTATACTGTTTTCTTAAAAGCCC TCTCAAATAAAAATCAAGAACAGT	ND	1
Cas cluster	cas	16200	17699	2	cas3_TypeI, cas3_TypeI	-	-
CRISPR	Contig_28_1	2042	2190	3	AAAGCGTGAAACTCACGAGTAAA	ND	1
CRIPSR	Contig_30_1	9330	9405	1	TTGATTTATGTCTTATGTTATAGG	ND	1

Table S2_file

Subject strain	dDDH value	ANI value	G+C content difference (in %)
<i>Peribacillus frigoritolerans</i> DSM 8801 ^T	86.5	97.0	0.1
<i>P. castrilensis</i> N3 ^T	79.2	96.7	0.2
<i>P. simplex</i> NBRC 15720 ^T	65.6	92.8	0.6
<i>P. butanolivorans</i> DSM 18926 ^T	33.6	84.1	2.5
<i>P. muralis</i> DSM 16288 ^T	32.9	84.1	0.5
<i>P. loiseleuriae</i> FJAT-27997 ^T	13.7	71.5	2.9
<i>P. psychrosaccharolyticus</i> ATCC 23296 ^T	13.8	70.2	1.6

Table S3_file

Function	Gene name	Gene Annotation
Transport	<i>LysE</i> <i>MFS</i> <i>ABC</i> <i>NAD</i> -	LysE family transporter. Major facilitator superfamily Amino acid ABC transporter substrate binding ABC transporter NAD(P)-dependent oxidoreductase Branched-chain amino acid ABC transporter permease
Transcriptional regulator	<i>AraC</i> <i>AsnC</i> <i>LysR</i> <i>TetR/AcrR</i> <i>IclR</i> <i>MerR</i> <i>DeoR</i> <i>PadR</i>	AraC family transcriptional regulator Lrp/AsnC family transcriptional regulator LysR family transcriptional regulator TetR/AcrR family transcriptional regulator IclR family transcriptional regulator MerR family transcriptional regulator DeoR family transcriptional regulator PadR family transcriptional regulator
Secretion and delivery system	<i>EssA</i> <i>EsaA</i> <i>tatA</i> - - - -	Type VII secretion protein Type VII secretion protein Protein secretion by the type II secretion system MATE family efflux transporter Multidrug resistance efflux transporter family protein HlyD family efflux transporter periplasmic adaptor subunit Efflux RND transporter permease subunit
Plant polymer degradation/modification	<i>TreC</i> - -	Alpha,alpha-phosphotrehalase M48 family metalloproteinase Alpha/beta hydrolase
Detoxification	- - -	2-dehydropantoate 2-reductase Glutathione-dependent formaldehyde dehydrogenase SDR family oxidoreductase
Redox potential maintenance	- - - -	Aldehyde dehydrogenase family protein Acryloyl-CoA reductase L-lactate dehydrogenase Carbonate dehydratase
Virulence and antibiotic factors	<i>LiaF</i> <i>BlaOXA</i> - -	Cell wall-active antibiotics response protein LiaF Class D beta-lactamase Antibiotic biosynthesis monooxygenase YihY/virulence factor BrkB family protein Conserved virulence factor C family protein
Others	<i>lysA</i> - -	Diaminopimelate decarboxylase Hypothetical protein 2-isopropylmalate synthase

Table S4_file

Biodegradation Function	Gene name	Gene annotation
nitroalkanes	-	nitronate monooxygenase
Organosulfonate	ssuD TauD/TfdA	alkanesulfonate monooxygenase taurine dioxygenase
Heavy metals	copZ CopC/CopD family protein arsC cbiQ mgtE gudD corA nikA	copper ion binding copper resistance arsenate reductase P-type cobalt transporter heavy metal translocating P-type ATPase magnesium transporter magnesium ion binding magnesium/cobalt transporter nickel ABC transporter
Tryptophan	kynA	tryptophan 2,3-dioxygenase
Aromatic compounds	- -	glyoxalase/bleomycin resistance/dioxygenase ring-cleaving dioxygenase