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Table S1. Genome information of the selected strains of *Lactiplantibacillus pentosus*.

Strains	Source	Genome size ¹ (Mb)	GC (%)	CDS (coding)(n)	Accession number ²
<i>L. pentosus</i> DSM20314	Type strain	3.62	46.4	3156	NZ_CP032757.1
<i>L. pentosus</i> BGM48	Olive fermentation	3.59	46.3	3152	NZ_CP016491.1
<i>L. pentosus</i> ZFM222	Fermented vegetables	3.56	46.4	3077	NZ_CP032654.1
<i>L. pentosus</i> ZFM94	Healthy Infant feces	3.56	46.4	3066	NZ_CP032659.1
<i>L. pentosus</i> SLC13	Mustard pickles	3.52	46.5	3027	NZ_CP022130.1
<i>L. pentosus</i> MS031	Pickle	3.58	46.5	3097	NZ_CP043671.1
<i>L. pentosus</i> KZ0310	Pickle	3.58	46.5	3095	NZ_CP044245.1
<i>L. pentosus</i> KCA1	Vagina of a healthy Nigerian woman	3.43	46.4	2964	NZ_CM001538.1

Note: ¹ chromosome sequence length; ² NCBI accession number (GenBank).

Table S2. EggNOG category distribution of functional annotation results of *Lactiplantibacillus pentosus* 68-1 chromosome.

COG categories	Categories function	ORF number	Percentage (%)
A	RNA processing and modification	0	0
B	Chromatin structure and dynamics	1	0.0321
C	Energy production and conversion	120	3.8536
D	Cell cycle control, cell division, chromosome partitioning	24	0.7707
E	Amino acid transport and metabolism	209	6.7116
F	Nucleotide transport and metabolism	84	2.6975
G	Carbohydrate transport and metabolism	273	8.7669
H	Coenzyme transport and metabolism	81	2.6012
I	Lipid transport and metabolism	64	2.0552
J	Translation, ribosomal structure and biogenesis	149	4.7848
K	Transcription	261	8.3815
L	Replication, recombination and repair	163	5.2344
M	Cell wall/membrane/envelope biogenesis	179	5.7482
N	Cell motility	0	0
O	Posttranslational modification, protein turnover, chaperones	68	2.1837
P	Inorganic ion transport and metabolism	137	4.3995
Q	Secondary metabolites biosynthesis, transport and catabolism	22	0.7065
R	General function prediction only	0	0
S	Function unknown	631	20.2633
T	Signal transduction mechanisms	81	2.6012
U	Intracellular trafficking, secretion, and vesicular transport	20	0.6423
V	Defense mechanisms	64	2.0552
W	Extracellular structures	0	0
Y	Nuclear structure	0	0
Z	Cytoskeleton	0	0
-	Not in eggNOG	483	15.5106
Total	-	3114	100

Table S3. Relatedness of the sequenced genomes of the *Lactiplantibacillus pentosus* 68-1 to those of reference strains

Strains	ANIb	ANIm	TETRA	GGDC ¹
68-1	100.00	100.00	1.00000	100.0
<i>L. pentosus</i> KZ0310	97.52	98.02	0.99903	81.5
<i>L. pentosus</i> MS031	97.52	98.02	0.99903	81.5
<i>L. pentosus</i> DSM20314	97.46	97.94	0.99897	80.9
<i>L. pentosus</i> ZFM222	97.41	97.96	0.99875	80.4
<i>L. pentosus</i> ZFM94	97.41	97.96	0.99875	80.4
<i>L. pentosus</i> SLC13	97.29	97.93	0.99847	80.0
<i>L. pentosus</i> BGM48	96.90	97.54	0.99839	77.6
<i>L. pentosus</i> KCA1	92.41	93.36	0.99757	50.4

Note: ¹ the GGDC results were based on the recommended formula 2.

Table S4. CAZy function classification of the selected *Lactiplantibacillus pentosus* strains

Strains	GT	PL	CE	AA	CBM	GH	total
<i>L. pentosus</i> 68-1	37	0	26	7	9	54	133
<i>L. pentosus</i> DSM20314	38	0	1	0	16	56	111
<i>L. pentosus</i> ZFM94	41	0	1	0	16	57	115
<i>L. pentosus</i> SLC13	35	2	2	0	15	60	114
<i>L. pentosus</i> BGM48	35	0	1	0	16	56	108
<i>L. pentosus</i> IG1	34	0	1	0	9	47	91
<i>L. pentosus</i> MP-10	33	0	1	0	6	52	92

Note: GT, glycosyltransferase; GH, glycoside hydrolase; AA, enzymes for auxiliary activities; CBM, carbohydrate binding module; CE, carbohydrate esterase; PL, polysaccharide lyase.

Table S5. Acid and bile stress-related genes in the genome of *Lactiplantibacillus pentosus* 68-1.

Gene ID	Gene name	Annotation
General stress response		
chr_1808	<i>dnaK</i>	Molecular chaperone DnaK
chr_1807	<i>dnaJ</i>	Molecular chaperone DnaJ
chr_1809	<i>grpE</i>	Molecular chaperone GrpE
chr_1810	<i>hrcA</i>	Heat-inducible transcriptional repressor HrcA
chr_659	<i>groES</i>	Chaperonin GroES
chr_660	<i>groEL</i>	Chaperonin GroEL
chr_118	<i>hsp20</i>	Hsp20/alpha crystallin family protein
chr_2861	<i>hsp20</i>	Hsp20/alpha crystallin family protein
chr_2327	<i>hsp20</i>	Hsp20/alpha crystallin family protein
chr_499	<i>hslO</i>	Hsp33 family molecular chaperone HslO
chr_1664	<i>hslU</i>	ATP-dependent protease ATPase subunit HslU
chr_498	<i>ftsH, hflB</i>	Cell division protease FtsH
chr_35	<i>degP, htrA</i>	Serine protease Do
chr_559	<i>clpP</i>	ATP-dependent Clp protease, protease subunit ClpP(EC:3.4.21.92)
chr_717	<i>clpP</i>	ATP-dependent Clp endopeptidase proteolytic subunit ClpP (EC:3.4.21.92)
chr_913	<i>clpC</i>	ATP-dependent Clp protease, protease subunit ClpC (EC:3.4.21.92)
chr_1148	<i>clpL</i>	ATP-dependent Clp protease, protease subunit ClpL (EC:3.4.21.92)
chr_1902	<i>clpX</i>	ATP-dependent Clp protease ATP-binding subunit ClpX
chr_1709	<i>clpB</i>	ATP-dependent chaperone ClpB
chr_1038	<i>cspA</i>	Cold shock protein
chr_28	<i>cspA</i>	Cold shock protein
chr_899	<i>cspC</i>	Cold shock protein
chr_844	<i>amaP</i>	Alkaline shock response membrane anchor protein
chr_846	<i>asp23</i>	Alkaline shock protein
chr_847	<i>asp23</i>	Alkaline shock protein
chr_1439	<i>gls24</i>	Alkaline shock protein
chr_819	<i>mutT</i>	8-oxo-dGTP diphosphatase, GrpB family protein
pH tolerance		
chr_2125	<i>atpC</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit epsilon
chr_2126	<i>atpD</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit beta
chr_2127	<i>atpG</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit gamma
chr_2128	<i>atpA</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit alpha

chr_2129	<i>atpH</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit delta
chr_2130	<i>atpF</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit b
chr_2131	<i>atpE</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit c
chr_2132	<i>atpB</i>	F-type H ⁺ /Na ⁺ -transporting ATPase subunit a
chr_170	<i>nhaC</i>	Na ⁺ /H ⁺ antiporter, NhaC family
chr_366	-	Na ⁺ /H ⁺ antiporter
chr_748	-	Na ⁺ /H ⁺ antiporter
chr_818	-	Na ⁺ /H ⁺ antiporter, CPA2 family
chr_2273	-	Na ⁺ /H ⁺ antiporter
chr_2331	-	Na ⁺ /H ⁺ antiporter
chr_2389	-	Na ⁺ /H ⁺ antiporter
chr_2465	-	Na ⁺ /H ⁺ antiporter
chr_2848	<i>nhaC</i> ;	Na ⁺ /H ⁺ antiporter, NhaC family
chr_3027	-	Na ⁺ /H ⁺ antiporter
chr_339	<i>ldh</i>	L-lactate dehydrogenase
chr_489	<i>ldh</i>	L-lactate dehydrogenase
chr_987	<i>mdh</i>	Malate dehydrogenase; L-lactate dehydrogenase
chr_1128	-	L-lactate dehydrogenase
chr_1839	<i>ldhA</i>	D-lactate dehydrogenase
chr_2114	-	L-lactate dehydrogenase
bile tolerance		
chr_55	-	Choloylglycine hydrolase family protein; bile salt hydrolase
chr_2245	-	Linear amide C-N hydrolase ; choloylglycine hydrolase
chr_2869	-	Choloylglycine hydrolase family protein ;bile salt hydrolase
chr_59	-	MFS transporter; multidrug-effluxtransporter
chr_71	<i>mepA</i> ;	MATE family efflux transporter
chr_814	<i>sugE</i> ;	SMR transporter, SugE
chr_2803	<i>ebrB</i>	SMR transporter, EbrB
chr_2804	-	SMR transporter, QacE family
chr_701	<i>blt</i> ;	MFS transporter, DHA1 family, multidrug resistance protein
chr_767	-	MFS transporter, DHA2 family
chr_895	-	MFS transporter; DHA2 family
chr_1113	-	MFS transporter
chr_1591	<i>yebQ</i> ;	MFS transporter, DHA2 family
chr_1736	-	MFS transporter, DHA2 family, EmrB/QacA subfamily
chr_2332	-	MFS transporter
chr_2470	<i>mdeA</i> ;	MFS transporter, DHA2 family

chr_2696	-	MFS transporter, DHA2 family
chr_2827	-	MFS transporter; multidrug transport protein, EmrB/QacA subfamily
chr_182	-	ABC transporter, subfamily C, bacterial;
chr_1682	<i>uup</i> ;	ABC transporter
chr_1765	<i>ytrB</i> ;	ABC transporter
chr_2149	<i>efrB</i> ;	ABC transporter , subfamily B
chr_2150	<i>efrA</i> ;	ABC transporter , subfamily B
chr_2167	-	ABC transporter, subfamily C, bacterial;
chr_2240	-	ABC transporter, subfamily C (CFTR/MRP), member 1;
chr_2386	-	ABC transporter
chr_2524	<i>mdlB, smdB</i> ;	ABC transporter,
chr_2525	<i>mdlA, smdA</i> ;	ABC transporter, subfamily B
chr_2585	<i>abcA, bmrA</i> ;	ABC transporter
chr_2640	<i>patA, rscA, lmrC, satA</i>	ABC transporter , subfamily B
chr_3080	<i>mdlA, smdA</i>	ABC transporter, subfamily B, bacterial AbcA/BmrA;
chr_3081	<i>mdlB, smdB</i> ;	ABC transporter, subfamily B, bacterial AbcA/BmrA;

Table S6. Adhesion-related genes in the genome of *Lactiplantibacillus pentosus* 68-1.

Gene ID	Gene name	Annotation
chr_1136	-	Muc BP domain-containing protein
chr_1481	-	Muc BP domain-containing protein
chr_2159	-	Muc BP domain-containing protein
chr_2252	-	Collagen-binding protein,
chr_186	-	Fibronectin-binding protein
chr_1622	-	Fibronectin-binding protein
chr_980	<i>psaA, scaA</i>	Manganese/zinc transport system substrate-binding protein
chr_2818	-	Manganese/zinc transport system substrate-binding protein
chr_1377	<i>pgaC, icaA</i>	Poly- β -1,6-N-acetyl-D-glucosamine synthase
chr_1424	<i>glnA</i>	Glutamine synthetase
chr_2172	<i>pgi</i>	Glucose-6-phosphate isomerase
chr_267	<i>gapA</i>	Glyceraldehyde 3-phosphate dehydrogenase (EC:1.2.1.12)
chr_722	<i>gapA</i>	Glyceraldehyde 3-phosphate dehydrogenase (EC:1.2.1.13)
chr_725	<i>eno</i>	Phosphopyruvate dydrolase;enolase (EC:4.2.1.11)
chr_1904	<i>tuf</i>	Elongation factor Tu,
chr_724	<i>tpiA</i>	Triosephosphate isomerase
chr_462	<i>srtA</i>	Sortase A (EC:3.4.22.70)
chr_723	<i>pgk</i>	Phosphoglycerate kinase
chr_817	<i>gpmB</i>	Probable phosphoglycerate mutase
chr_2431	<i>gpmB</i>	Probable phosphoglycerate mutase
chr_2706	<i>gpmA</i>	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
chr_660	<i>groEL</i>	Chaperonin GroEL
chr_659	<i>groES</i>	Chaperonin GroES
chr_1808	<i>dnaK</i>	Molecular chaperone DnaK
chr_1807	<i>dnaJ</i>	Molecular chaperone DnaJ

Table S7. Bacteriocin clusters predicted in *Lactiplantibacillus pentosus* 68-1 using BAGEL 4 (<http://bagel.molgenrug.nl/>).

AOI	Start	End	Class
Chr.0.AOI.01	3233207	3253507	159.2; Pediocin
Chr.0.AOI.02	408608	428956	171.2; Plantaricin_F

Table S8. The virulence factors in the genome of *Lactiplantibacillus pentosus* 68-1.

VFDB ID	Gene ID	VFDB name	VFDB name	Annotation
VFG000964			Hyaluronic	MULTISPECIES: UTP--glucose-1-phosphate
(gb NP_270109)	chr_684	VF0244	acid capsule	uridylyltransferase GalU;
VFG000077				MULTISPECIES: ATP-dependent Clp
(gb NP_465991)	chr_717	VF0074	ClpP	endopeptidase proteolytic subunit ClpP
VFG002182				
(gb NP_816133)	chr_1057	VF0361	Capsule	UDP-galactopyranose mutase
VFG001967				
(gb NP_282580)	chr_1057	VF0323	Capsule	UDP-galactopyranose mutase
VFG001347				UDP-N-acetylglucosamine--LPS
(gb NP_688179)	chr_1062	VF0274	Capsule	N-acetylglucosamine transferase
VFG002182				
(gb NP_816133)	chr_1105	VF0361	Capsule	UDP-galactopyranose mutase
VFG000080				ATP-dependent Clp protease,
(gb NP_464522)	chr_1148	VF0073	ClpL	ATP-binding subunit ClpL
				isoprenyl transferase; undecaprenyl
				pyrophosphate synthase (UPP
				synthase); ditrans,
VFG002190				Polycis-undecaprenyl-diphosphate
(gb NP_816141)	chr_1831	VF0361	Capsule	synthase;

Table S9. Antibiotic resistance genes in the genome of *Lactiplantibacillus pentosus* 68-1.

Gene ID	Location	Type	Gene name	Annotation	KEGG-ID
chr_466	517531-518919	vancomycin resistance	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	K01929
chr_470	521906-523033	vancomycin resistance	<i>alr</i>	Alanine racemase	K01775
chr_700	769387-769944	vancomycin resistance	<i>vanX</i>	Zinc D-Ala-D-Ala dipeptidase	K08641
chr_909	1011693-1012466	vancomycin resistance	<i>vanY</i>	Zinc D-Ala-D-Ala carboxypeptidase	K07260
chr_1971	2193481-2194578	vancomycin resistance	<i>murG</i>	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	K02563
chr_1973	2197095-2197955	vancomycin resistance	<i>mraY</i>	Phospho-N-acetylmuramoyl-pentapeptide-transferase	K01000
chr_2111	2352482-2353594	vancomycin resistance	<i>ddl</i>	D-alanine-D-alanine ligase	K01921
chr_175	198424-200085	β -Lactam resistance	<i>oppA</i> , <i>mppA</i>	Oligopeptide transport system substrate-binding protein	K15580
chr_176	200835-202496	β -Lactam resistance	<i>oppA</i> , <i>mppA</i>	Oligopeptide transport system substrate-binding protein	K15580
chr_391	434363-435853	β -Lactam resistance	<i>oppB</i>	Oligopeptide transport system permease protein	K15581
chr_392	435855-436793	β -Lactam resistance	<i>oppC</i>	Oligopeptide transport system permease protein	K15582
chr_393	436807-437895	β -Lactam resistance	<i>oppD</i>	Oligopeptide transport system ATP-binding protein	K15583
chr_394	437903-438823	β -Lactam resistance	<i>oppF</i>	Oligopeptide transport system ATP-binding protein	K10823
chr_437	481766-482593	β -Lactam resistance	<i>penP</i>	β -lactamase class A	K17836
chr_715	786856-788508	β -Lactam resistance	<i>oppA</i> , <i>mppA</i>	Oligopeptide transport system substrate-binding protein	K15580
chr_914	1020930-1021553	β -Lactam resistance	<i>nalD</i>	TetR/AcrR family transcriptional regulator, repressor of the <i>mexAB-oprM</i> multidrug resistance operon	K18135
chr_1140	1261008-1262654	β -Lactam resistance	<i>oppA</i> , <i>mppA</i>	Oligopeptide transport system substrate-binding protein	K15580

chr_1141	1262846-1263742	β -Lactam resistance	<i>oppB</i>	Oligopeptide transport system permease protein	K15581
chr_1142	1263746-1264780	β -Lactam resistance	<i>oppC</i>	Oligopeptide transport system permease protein	K15582
chr_1143	1264796-1265875	β -Lactam resistance	<i>oppD</i>	Oligopeptide transport system ATP-binding protein	K15583
chr_1144	1265882-1266847	β -Lactam resistance	<i>oppF</i>	Oligopeptide transport system ATP-binding protein	K10823
chr_1254	1421886-1424015	β -Lactam resistance	<i>pbp2A</i>	Penicillin-binding protein 2A	K12555
chr_1413	1598981-1601017	β -Lactam resistance	<i>pbp2B</i> , <i>penA</i>	Penicillin-binding protein 2B	K00687
chr_1584	1778260-1780566	β -Lactam resistance	<i>mrcA</i>	Penicillin-binding protein 1A	K05366
chr_2585	2884988-2886745	β -Lactam resistance	<i>abcA</i> , <i>bmrA</i>	ATP-binding cassette, subfamily B, bacterial AbcA/BmrA	K18104
chr_2788	3103723-3104688	β -Lactam resistance	<i>oppC</i>	Oligopeptide transport system permease protein	K15582
chr_2789	3104690-3106180	β -Lactam resistance	<i>oppB</i>	Oligopeptide transport system permease protein	K15581
chr_2790	3106283-3108250	β -Lactam resistance	<i>oppA</i> , <i>mppA</i>	Oligopeptide transport system substrate-binding protein	K15580
chr_2965	3300433-3302136	β -Lactam resistance	<i>nagZ</i>	β -N-acetylhexosaminidase	K01207
chr_35	46716-47978	CAMP resistance	<i>degP</i> , <i>htrA</i>	Serine protease Do	K04771
chr_625	687105-689708	CAMP resistance	<i>mprF</i> , <i>fmtC</i>	Phosphatidylglycerol lysyltransferase	K14205
chr_1248	1415836-1416072	CAMP resistance	<i>dltC</i>	D-alanine-poly (phosphoribitol) ligase subunit 2	K14188
chr_1787	2000156-2001004	CAMP resistance	<i>amiAB</i> , <i>C</i>	N-acetylmuramoyl-L-alanine amidase	K01448
chr_1801	2015245-2016522	CAMP resistance	<i>dltD</i>	D-alanine transfer protein	K03740
chr_1803	2016786-2018000	CAMP resistance	<i>dltB</i>	Membrane protein involved in D-alanine	K03739
chr_1804	2017997-2019523	CAMP resistance	<i>dltA</i>	D-alanine-poly (phosphoribitol) ligase subunit 1	K03367
chr_191	218234-219754	macrolide resistance	<i>msrA</i> , <i>vmlR</i>	Macrolide transport system ATP-binding/permease protein	K18231
chr_1616	1813578-1814246	phenicol resistance	<i>catA</i>	Chloramphenicol O-acetyltransferase type A	K19271

chr_2514	2798293-2798862	phenicol resistance	<i>catB</i>	Chloramphenicol O-acetyltransferase type B	K00638
chr_2639	2940150-2941820	fluoroquinolone resistance	<i>patB</i> , <i>rscB</i> , <i>lmrC</i> , <i>satB</i>	ATP-binding cassette, subfamily B	K18892
chr_2640	2941924-2943648	fluoroquinolone resistance	<i>pataA</i> , <i>rscA</i> , <i>lmrC</i> , <i>satA</i>	ATP-binding cassette, subfamily B	K18891
chr_71	84923-86251	multidrug resistance	<i>mepA</i>	Multidrug efflux pump	K18908
chr_701	770376-770768	multidrug resistance	<i>blt</i>	MFS transporter, DHA1 family	K08153
chr_1591	1784549-1785940	multidrug resistance	<i>yebQ</i>	MFS transporter, DHA2 family	K08169
chr_2149	2393929-2395815	multidrug resistance	<i>efrB</i>	ATP-binding cassette, subfamily B	K18888
chr_2150	2395815-2397545	multidrug resistance	<i>efrA</i>	ATP-binding cassette, subfamily B	K18887
chr_2239	2487157-2488887	multidrug resistance	<i>efrB</i>	ATP-binding cassette, subfamily B	K18888
chr_2470	2757441-2758925	multidrug resistance	<i>mdeA</i>	MFS transporter, DHA2 family	K18936
chr_2524	2807784-2809571	multidrug resistance	<i>mdlB</i> , <i>smdB</i>	ATP-binding cassette, subfamily B	K18890
chr_2525	2809571-2811322	multidrug resistance	<i>mdlA</i> , <i>smdA</i>	ATP-binding cassette, subfamily B	K18889
chr_2803	3122567-3122947	multidrug resistance	<i>ebrB</i>	Multidrug resistance protein EbrB	K11815
chr_2880	3204764-3205987	multidrug resistance	<i>mdtG</i>	MFS transporter, DHA1 family	K08161
chr_3080	3438308-3440065	multidrug resistance	<i>mdlA</i> , <i>smdA</i>	ATP-binding cassette, subfamily B,	K18889
chr_3081	3440094-3441848	multidrug resistance	<i>mdlB</i> , <i>smdB</i>	ATP-binding cassette, subfamily B	K18890

Table S10. Prophages predicted in *Lactiplantibacillus pentosus* 68-1 using PHASTER (<https://www.phaster.ca>).

Region	Region length	Completeness	Score	Total CDS	Region position	GC (%)	Most common phage
1 (chr)	44kb	Intact	130	57	595926-639955	41.00	PHAGE_Lactob_Sha1_NC_019489(18)
1 (plasmid 3)	24.1kb	Questionable	80	19	530-24700	41.02	PHAGE_Erwini_pEp_SNUABM_01_NC_048807(3)

Table S11. Genomic islands predicted in *Lactiplantibacillus pentosus* 68-1 using IslandViewer 4.

Island start	Island end	Length
295427	302887	7460
301719	306260	4541
596092	641079	44987
596092	606321	10229
610801	615613	4812
617466	628011	10545
678718	683402	4684
679244	684077	4833
795127	799663	4536
1021882	1029071	7189
1030342	1049100	18758
1175589	1182221	6632
1176250	1195017	18767
1473219	1480049	6830
2060800	2066116	5316
2071319	2076126	4807
2075836	2082981	7145
2332490	2339115	6625
2403802	2408618	4816
2861956	2866959	5003
3294231	3307826	13595
3345618	3352381	6763
3355993	3360377	4384
3405411	3411748	6337

Note: predicted by at least one method.

Table S12. Insertion elements (IS) predicted in *Lactiplantibacillus pentosus* 68-1 using ISfinder (<https://www-is.biotoul.fr>).

Sequences producing significant alignments	IS Family	Group	Origin	Score (bits)	E. value
ISP1	ISL3		<i>Lactiplantibacillus plantarum</i>	2531	0.0
ISLpl3	IS5	IS427	<i>Lactiplantibacillus plantarum</i>	1362	0.0
ISP2	IS1182		<i>Lactiplantibacillus plantarum</i>	63.9	2e-06
ISLho3	IS4	ISPepr1	<i>LPaucilactobacillus hokkaidonensis</i>	63.9	2e-06
ISLpl2	IS3	IS150	<i>Lactiplantibacillus plantarum</i>	56.0	4e-04
SLhe65	IS200/IS605	IS1341	<i>Lactobacillus helveticus</i>	54.0	0.002

Note: searching parameters: word size 11, E. value: 0.01, gap open existence:5 extension:2

Table S13. CPISPR/*cas* predicted in *Lactiplantibacillus pentosus* 68-1 using CRISPRCasFinder (<https://crisprcas.i2bc.paris-saclay.fr/>).

Element	CRISPR Id /Cas Type	Start	End	Spacer/ Gene	Repeat consensus/cas genes	Direction	Evidence Level
Cas cluster	CAS-TypeII A	118227	124359	4	cas9_TypeII, cas1_TypeII, cas2_TypeI-II-III, csn2_TypeIIA GTCTTGAATAGTA		
CRISPR	chr_1	124384	125079	10	GTCATATCAAAC AGGTTTAGAAC GGATCACCCCCG	+	4
CRISPR	chr_2	1293828	1294343	8	CATACGCGGGGA ACAG GGATCACCCCCGT	ND	4
CRISPR	chr_3	1546373	1546830	7	ATACACGGGGAA TAG	ND	4
Cas cluster	CAS-TypeIE	1549098	1556661	6	cas3_TypeI, cse1_TypeIE, cse2_TypeIE, cas7_TypeIE, cas5_TypeIE, cas6_TypeIE GTACTCCCCGTGT		
CRISPR	chr_4	1556831	1557224	6	ATACGGGGGTGA TCC	ND	4
CRISPR	chr_5	2814915	2815136	1	AAGTTGTTGCACA CCACTTACT	ND	1