

Characterization of Genomic, Physiological, and Probiotic Features *Lactiplantibacillus plantarum* JS21 Strain Isolated from of Traditional Fermented “Jiangshui”

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Figure S1. Location of phage on the JS21 genome (green marked regions: intact and the score >90, blue marked regions questionable and score between 70 and 90, the red-coloured regions: incomplete and the score <70)

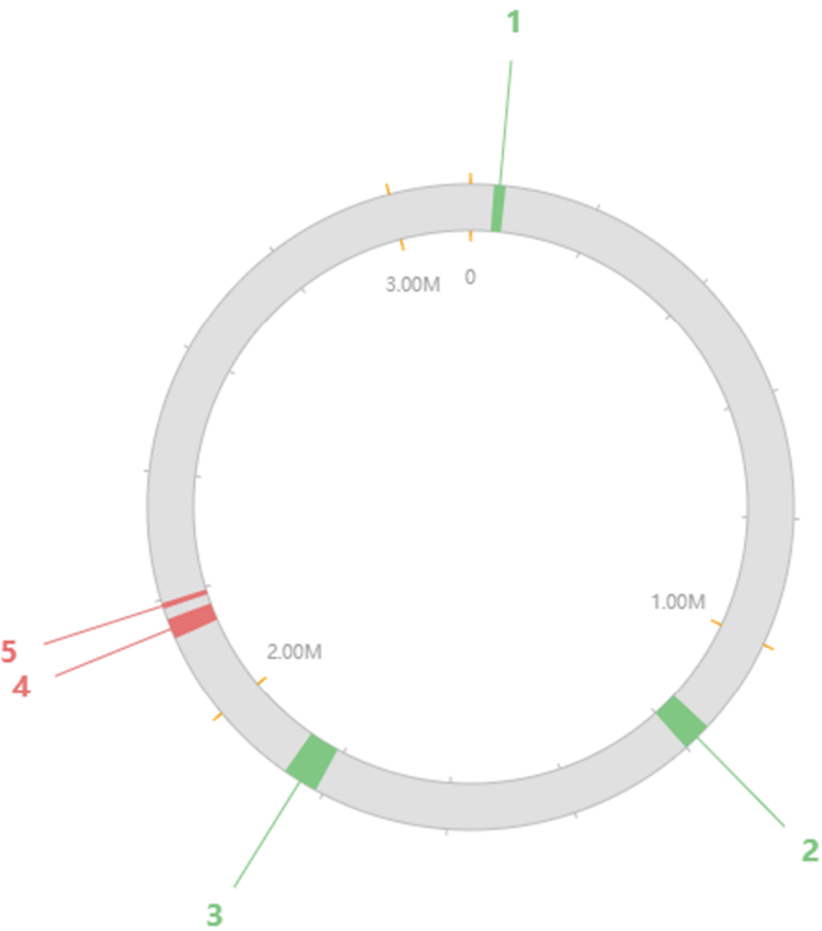
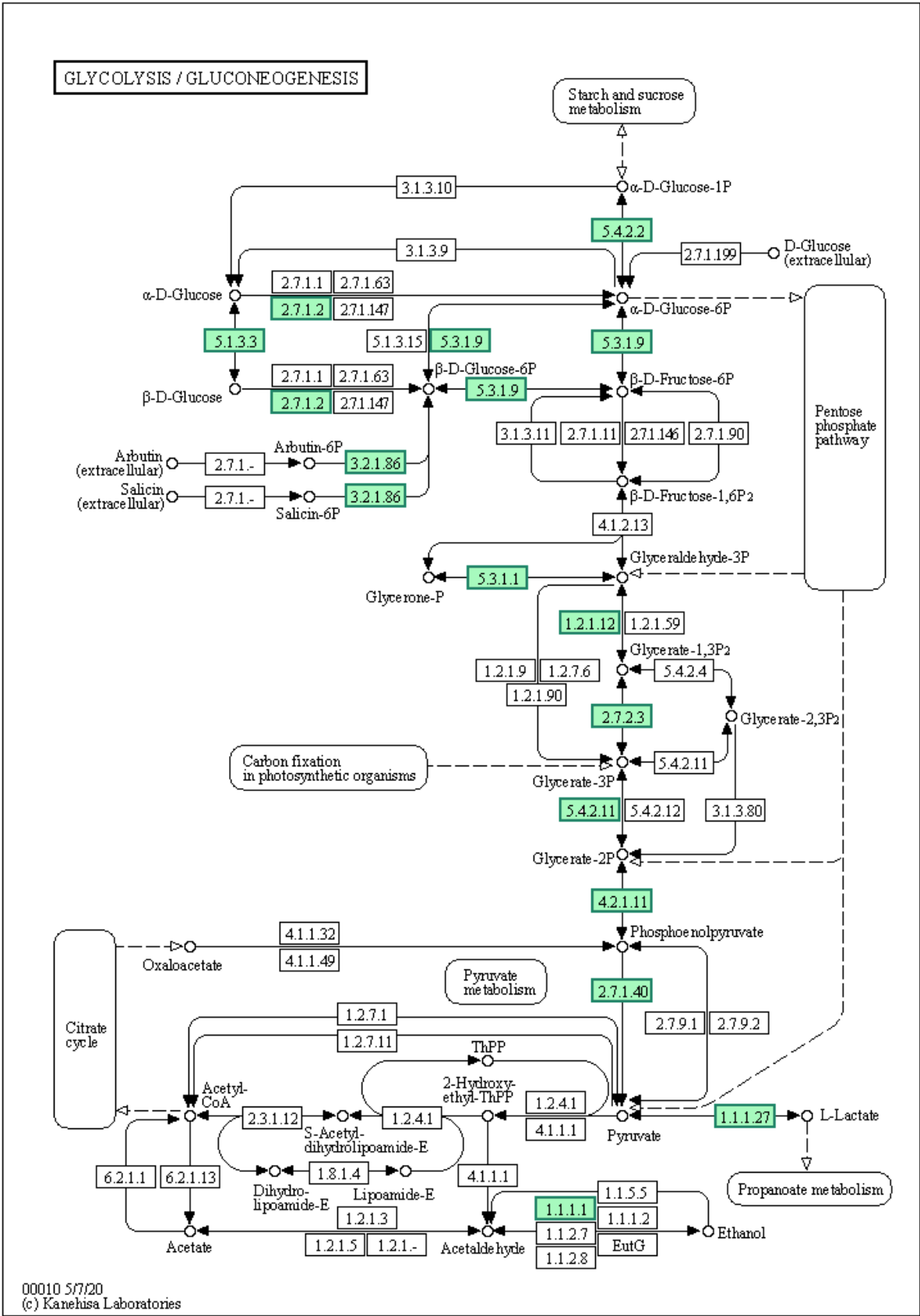


Figure S2. Annotated map of **glycolysis/gluconeogenesis** pathways in JS21 (Green coloured EC numbers indicate the presence of the pathway enzymes)



[illegible]

Figure S5. The ability of CFS to inhibit the growth of pathogenic bacteria. a- *Escherichia coli* ATCC 25922, b- *Escherichia coli* K88, c- *Staphylococcus aureus* CMCC 26003, d- *Listeria monocytogenes* CICC 21635.

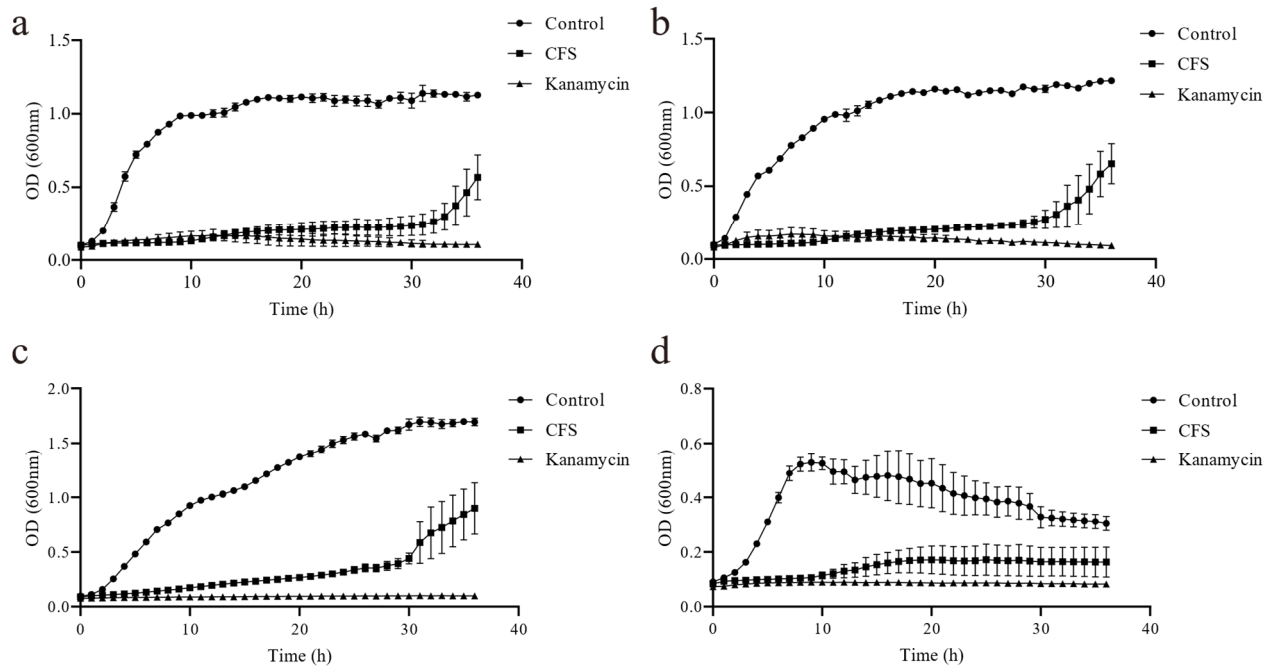


Figure S6. Growth curve(a) of JS21 versus acid production rate curve (b)

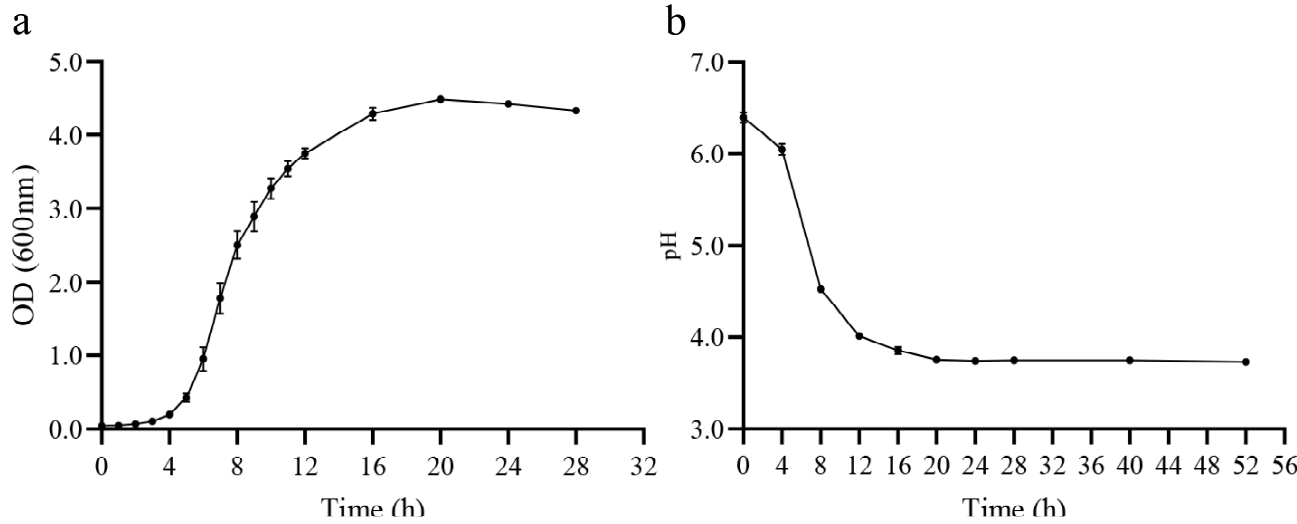


Table S1. The predicted prophage regions of *Lactiplantibacillus plantarum* strain JS21

Region	Length	Completeness	Score	Total Proteins	Region Position	Most Common Phage (Number of matching proteins)	GC %
1	18.1Kb	intact	100	25	36132-54235	PHAGE_Staphy_phiPV83_NC_002486(3)	42.15%
2	46Kb	intact	140	54	1154203-1200222	PHAGE_Lactob_Sha1_NC_019489(26)	40.70%
3	55.4Kb	intact	150	59	1812273-1867677	PHAGE_Lactob_Sha1_NC_019489(26)	40.65%
4	31.6Kb	incomplete	60	10	2137180-2168851	PHAGE_Paenib_Tripp_NC_028930(3)	43.31%
5	9.1Kb	incomplete	20	10	2186014-2195185	PHAGE_Strept_APCM01_NC_029030(1)	41.40%

Table S2. The first prophage (intact) region elements of *Lactiplantibacillus plantarum* JS21 (PHAGE_Staphy_phiPV83_NC_002486).

#	Locus	ORF Start	ORF Stop	Strand	Homolog/Ortholog Species	Homolog/Ortholog Protein	E-Value
1	PP_00028	36132	36581	Backward	Hypothetical protein	PP_00028, hypothetical protein, phage(gi100030), PHAGE_Lactob_PLE3_NC_031125	1.31E-17
2	PP_00029	36779	36979	Forward	Portal protein	PP_00029, portal protein, phage(gi100069), PHAGE_Vibrio_1.026.O._10N.222.49.C7_NC_049430	1.99E-08
3	PP_00030	37071	37295	Forward	Hypothetical protein	PP_00030, hypothetical	N/A
4	PP_00031	37513	38511	Forward	Transposase	PP_00031, putative transposase, phage(gi588498272), PHAGE_Staphy_StauST398_4_NC_023499	5.67E-63
5	<i>attL</i>	38584	38602	Forward	Attachment site(TATGATGGGCAGTCAGGGG)	<i>attL</i>	N/A
6	PP_00032	38879	40033	Backward	Integrase	PP_00032, integrase, phage(gi23097608),PROPHAGE_Oceano_HTE831	3.25E-86
7	PP_00033	40086	40652	Backward	Phage-like protein	PP_00033, putative transcriptional regulator, phage(gi446730276), PHAGE_Lactob_phiAQ113_NC_019782	4.25E-10
8	PP_00034	40969	41157	Forward	Phage-like protein	PP_00034, prophage Lp3 protein 4-like protein, phage(gi418489838), PHAGE_Lactob_Sha1_NC_019489	3.61E-08
9	PP_00035	41440	41658	Forward	Hypothetical protein	PP_00035, hypothetical	N/A
10	PP_00036	41655	42455	Forward	Hypothetical protein	PP_00036, hypothetical protein, phage(gi13095885), PHAGE_Lactoc_bIL310_NC_002669	7.03E-23
11	PP_00037	42455	43849	Forward	Tail protein	PP_00037, minor tail protein, phage(gi100055), PHAGE_Staphy_vB_SpsS_QT1_NC_048192	5.84E-77
12	PP_00038	43995	44474	Forward	Hypothetical protein	PP_00038, hypothetical	N/A
13	PP_00039	44489	44800	Forward	Hypothetical protein	PP_00039, hypothetical	N/A
14	PP_00040	44787	45128	Forward	Head protein	PP_00040, phage head-tail adaptor, phage(gi418489808), PHAGE_Lactob_Sha1_NC_019489	1.47E-14
15	PP_00041	45238	45510	Forward	Phage-like protein	PP_00041, phage endonuclease, phage(gi119443688), PHAGE_Staphy_Pv1108_NC_008689	1.19E-14
16	PP_00042	46414	46887	Forward	Phage-like protein	PP_00042, methyltransferase type 11, phage(gi100001), PHAGE_Gordon_Zirinka_NC_031097	2.34E-15
17	PP_00043	46884	48587	Forward	Hypothetical protein	PP_00043, hypothetical protein, phage(gi28876230), PHAGE_Strept_315.2_NC_004585	1.84E-132
18	PP_00044	48541	48741	Forward	Hypothetical protein	PP_00044, hypothetical	N/A
19	PP_00045	48742	49842	Forward	Portal protein	PP_00045, portal protein, phage(gi225626395), PHAGE_Enterо_EFAP_1_NC_012419	4.20E-49
20	PP_00046	49839	51374	Forward	Head protein	PP_00046, capsid protein, phage(gi9635171), PHAGE_Staphy_PVL_NC_002321	1.00E-44
21	PP_00047	51488	51757	Forward	Head protein	PP_00047, head-tail joining protein, phage(gi225626391), PHAGE_Enterо_EFAP_1_NC_012419	3.38E-08
22	PP_00048	51916	52284	Forward	Hypothetical protein	PP_00048, hypothetical	N/A
23	PP_00049	52408	52608	Forward	Portal protein	PP_00049, portal protein, phage(gi100069), PHAGE_Vibrio_1.026.O._10N.222.49.C7_NC_049430	7.45E-10
24	PP_00050	52695	52925	Forward	Hypothetical protein	PP_00050, hypothetical	N/A
25	PP_00051	52931	53044	Forward	Hypothetical protein	PP_00051, hypothetical	N/A
26	<i>attR</i>	53127	53145	Forward	Attachment site(TATGATGGGCAGTCAGGGG)	<i>attR</i>	N/A
27	PP_00052	53528	54235	Forward	Hypothetical protein	PP_00052, hypothetical protein, phage(gi100030), PHAGE_Altero_vB_AmeM_PT11_V22_NC_048847	3.00E-12

Table S3. The second prophage (intact) region elements of *Lactiplantibacillus plantarum* JS21 (PHAGE_Lactob_Sha1_NC_019489).

#	Locus	ORF Start	ORF Stop	Strand	Homolog/Ortholog Species	Homolog/Ortholog Protein	E-Value
1	PP_01075	1154203	1156470	Forward	Phage-like protein	PP_01075, ABC transporter, phage(gi371496158), PHAGE_Plankt_PaV_LD_NC_016564	4.26E-05
2	<i>attL</i>	1156982	1156998	Forward	Attachment site(AATTATGCCCCAGGCAG)	<i>attL</i>	N/A
3	PP_01076	1157115	1158251	Backward	Integrase	PP_01076, phage integrase, phage(gi418489824), PHAGE_Lactob_Sha1_NC_019489	0
4	PP_01077	1158655	1159170	Forward	Hypothetical protein	PP_01077, hypothetical protein, phage(gi100029), PHAGE_Pseudo_MD8_NC_031091	8.82E-07
5	PP_01078	1159471	1159647	Backward	Hypothetical protein	PP_01078, hypothetical	N/A
6	PP_01079	1159959	1161233	Backward	Hypothetical protein	PP_01079, hypothetical protein, phage(gi100036), PHAGE_Clostr_phiCDHM14_NC_048665	3.63E-28
7	PP_01080	1161290	1161697	Backward	Hypothetical protein	PP_01080, hypothetical protein, phage(gi100028), PHAGE_Lactob_PLE2_NC_031036	8.83E-39
8	PP_01081	1161690	1162022	Backward	Hypothetical protein	PP_01081, hypothetical protein, phage(gi100029), PHAGE_Lactob_PLE2_NC_031036	2.85E-37
9	PP_01082	1162280	1162501	Forward	Hypothetical protein	PP_01082, hypothetical	N/A
10	PP_01083	1162503	1163291	Forward	Phage-like protein	PP_01083, phage-related antirepressor, phage(gi418489833), PHAGE_Lactob_Sha1_NC_019489	1.07E-74
11	PP_01084	1163305	1163493	Forward	Phage-like protein	PP_01084, putative transcriptional regulator, phage(gi100045), PHAGE_Lactob_Lb_NC_047983	4.27E-06
12	PP_01085	1163490	1163891	Backward	Hypothetical protein	PP_01085, hypothetical	N/A
13	PP_01086	1164108	1164437	Forward	Hypothetical protein	PP_01086, hypothetical protein, phage(gi418489836), PHAGE_Lactob_Sha1_NC_019489	5.81E-72
14	PP_01087	1164527	1164781	Forward	Hypothetical protein	PP_01087, hypothetical	N/A
15	PP_01088	1164951	1165121	Forward	Hypothetical protein	PP_01088, hypothetical	N/A
16	PP_01089	1165121	1165981	Forward	Hypothetical protein	PP_01089, hypothetical protein, phage(gi971754947), PHAGE_Lactob_iLp1308_NC_028911	1.59E-48
17	PP_01090	1165982	1166644	Forward	Phage-like protein	PP_01090, phage nucleotide-binding protein, phage(gi418489844), PHAGE_Lactob_Sha1_NC_019489	9.83E-162
18	PP_01091	1166646	1167305	Forward	Hypothetical protein	PP_01091, hypothetical protein, phage(gi418489845), PHAGE_Lactob_Sha1_NC_019489	1.58E-156
19	PP_01092	1167352	1168044	Forward	Hypothetical protein	PP_01092, hypothetical protein, phage(gi418489846), PHAGE_Lactob_Sha1_NC_019489	2.96E-172
20	PP_01093	1168150	1168266	Forward	Hypothetical protein	PP_01093, hypothetical	N/A
21	PP_01094	1168273	1169022	Backward	Hypothetical protein	PP_01094, hypothetical protein, phage(gi418489416), PHAGE_Lactob_LF1_NC_019486	4.38E-42
22	PP_01095	1169090	1169896	Forward	Hypothetical protein	PP_01095, hypothetical protein, phage(gi238821328), PHAGE_Strept_PH10_NC_012756	9.65E-38
23	PP_01096	1169890	1170825	Forward	Phage-like protein	PP_01096, DNA replication protein, phage(gi971747669), PHAGE_Lactob_iA2_NC_028830	6.68E-55
24	PP_01097	1171121	1171429	Forward	Hypothetical protein	PP_01097, hypothetical protein, phage(gi418489790), PHAGE_Lactob_Sha1_NC_019489	1.10E-61
25	PP_01098	1171422	1171538	Forward	Hypothetical protein	PP_01098, hypothetical protein, phage(gi418489791), PHAGE_Lactob_Sha1_NC_019489	9.77E-09
26	PP_01099	1171773	1171886	Forward	Phage-like protein	PP_01099, LP1-like protein, phage(gi418489797), PHAGE_Lactob_Sha1_NC_019489	3.42E-16
27	PP_01100	1171867	1172292	Forward	Phage-like protein	PP_01100, phage transcriptional activator RinA, phage(gi418489798), PHAGE_Lactob_Sha1_NC_019489	1.10E-77
28	PP_01101	1172733	1172912	Forward	Hypothetical protein	PP_01101, hypothetical	N/A

29	PP_01102	1172917	1173870	Backward	Hypothetical protein	PP_01102, hypothetical	N/A
30	PP_01103	1174484	1174996	Forward	Hypothetical protein	PP_01103, hypothetical	N/A
31	PP_01104	1175491	1175949	Forward	Terminase	PP_01104, terminase small subunit, phage(gi422934327), PHAGE_Bacill_phIS3501_NC_019502	3.34E-22
32	PP_01105	1175936	1177726	Forward	Terminase	PP_01105, putative terminase large subunit, phage(gi418489114), PHAGE_Lactob_JCL1032_NC_019456	0
33	PP_01106	1177746	1178975	Forward	Portal protein	PP_01106, portal protein, phage(gi985759335), PHAGE_Bacter_Rani_NC_029084	1.85E-141
34	PP_01107	1178947	1179666	Forward	Protease	PP_01107, ATP-dependent Clp protease proteolytic subunit, phage(gi971740652), PHAGE_Paenib_HB10c2_NC_028758	1.16E-86
35	PP_01108	1179669	1180814	Forward	Head protein	PP_01108, major capsid protein, phage(gi971482315), PHAGE_Paenib_Harrison_NC_028746	5.95E-115
36	PP_01109	1180833	1180994	Forward	Hypothetical protein	PP_01109, hypothetical	N/A
37	PP_01110	1181047	1181391	Forward	Phage-like protein	PP_01110, phage protein DNA packaging protein, phage(gi418489807), PHAGE_Lactob_Sha1_NC_019489	2.59E-07
38	PP_01111	1181375	1181737	Forward	Head protein	PP_01111, phage head-tail adaptor, phage(gi418489808), PHAGE_Lactob_Sha1_NC_019489	1.30E-83
39	PP_01112	1181727	1182167	Forward	Head protein	PP_01112, phage head-tail joining protein, phage(gi418489809), PHAGE_Lactob_Sha1_NC_019489	1.04E-99
40	PP_01113	1182164	1182547	Forward	Hypothetical protein	PP_01113, hypothetical protein, phage(gi418489810), PHAGE_Lactob_Sha1_NC_019489	6.70E-84
41	PP_01114	1182548	1183186	Forward	Tail protein	PP_01114, major tail protein, phage(gi418489811), PHAGE_Lactob_Sha1_NC_019489	1.13E-144
42	PP_01116	1183213	1183329	Backward	Hypothetical protein	PP_01116, hypothetical	N/A
43	PP_01115	1183388	1183771	Forward	Hypothetical protein	PP_01115, hypothetical protein, phage(gi418489812), PHAGE_Lactob_Sha1_NC_019489	3.88E-85
44	PP_01117	1183768	1183959	Forward	Hypothetical protein	PP_01117, hypothetical protein, phage(gi418489813), PHAGE_Lactob_Sha1_NC_019489	3.71E-39
45	PP_01118	1183972	1189194	Forward	Tail protein	PP_01118, minor tail protein, phage(gi418489814), PHAGE_Lactob_Sha1_NC_019489	0
46	PP_01119	1189267	1191042	Forward	Phage-like protein	PP_01119, minor structural protein gp75-like protein, phage(gi418489815), PHAGE_Lactob_Sha1_NC_019489	0
47	PP_01120	1191108	1193522	Forward	Phage-like protein	PP_01120, minor structural protein gp89-like protein, phage(gi418489816), PHAGE_Lactob_Sha1_NC_019489	0
48	PP_01121	1193539	1195824	Forward	Hypothetical protein	PP_01121, hypothetical protein, phage(gi100085), PHAGE_Lactob_Satyr_NC_047918	0
49	PP_01122	1195802	1196053	Forward	Hypothetical protein	PP_01122, hypothetical protein, phage(gi418489818), PHAGE_Lactob_Sha1_NC_019489	1.68E-35
50	PP_01123	1196057	1196218	Forward	Hypothetical protein	PP_01123, hypothetical protein, phage(gi418489819), PHAGE_Lactob_Sha1_NC_019489	1.89E-25
51	PP_01124	1196202	1197299	Forward	Phage-like protein	PP_01124, prophage Lp2 protein 53-like protein, phage(gi418489820), PHAGE_Lactob_Sha1_NC_019489	3.98E-86
52	PP_01125	1197296	1197511	Forward	Hypothetical protein	PP_01125, hypothetical protein, phage(gi985757750), PHAGE_Lactob_LfeSau_NC_029068	6.53E-28
53	PP_01126	1197525	1198697	Forward	Phage-like protein	PP_01126, endolysin, phage(gi418489821), PHAGE_Lactob_Sha1_NC_019489	0
54	PP_01127	1198697	1198960	Forward	Phage-like protein	PP_01127, phage-related holin, phage(gi418489822), PHAGE_Lactob_Sha1_NC_019489	2.10E-55
55	PP_01128	1198973	1199503	Forward	Hypothetical protein	PP_01128, hypothetical protein, phage(gi418489823), PHAGE_Lactob_Sha1_NC_019489	1.22E-77
56	<i>attR</i>	1200222	1200238	Forward	Attachment site(AATTATGCCCCAGGCAG)	<i>attR</i>	N/A

Table S4. The third prophage (intact) region elements of *Lactiplantibacillus plantarum* JS21 (PHAGE_Lactob_Sha1_NC_019489).

#	Locus	ORF Start	ORF Stop	Strand	Homolog/Ortholog Species	Homolog/Ortholog Protein	E-Value
1	<i>attL</i>	1812273	1812284	Forward	Attachment site(AAACCAAAAAGC)	<i>attL</i>	N/A
2	PP_01770	1824504	1824878	Backward	Hypothetical protein	PP_01770, hypothetical protein, phage(gi100097), PHAGE_Lactob_Lenus_NC_047897	8.54E-46
3	PP_01771	1824891	1825154	Backward	Phage-like protein	PP_01771, phage-related holin, phage(gi418489822), PHAGE_Lactob_Sha1_NC_019489	7.74E-54
4	PP_01772	1825154	1826179	Backward	Phage-like protein	PP_01772, endolysin, phage(gi418489821), PHAGE_Lactob_Sha1_NC_019489	0
5	PP_01773	1826191	1826436	Backward	Hypothetical protein	PP_01773, hypothetical protein, phage(gi985757750), PHAGE_Lactob_LfeSau_NC_029068	1.89E-28
6	PP_01774	1826433	1827797	Backward	Phage-like protein	PP_01774, prophage Lp2 protein 53-like protein, phage(gi418489820), PHAGE_Lactob_Sha1_NC_019489	7.00E-78
7	PP_01775	1827781	1827942	Backward	Hypothetical protein	PP_01775, hypothetical protein, phage(gi418489819), PHAGE_Lactob_Sha1_NC_019489	3.05E-28
8	PP_01776	1827946	1828188	Backward	Hypothetical protein	PP_01776, hypothetical protein, phage(gi418489818), PHAGE_Lactob_Sha1_NC_019489	6.94E-41
9	PP_01777	1828181	1830976	Backward	Hypothetical protein	PP_01777, hypothetical protein, phage(gi100085), PHAGE_Lactob_Satyr_NC_047918	0
10	PP_01778	1830993	1833407	Backward	Phage-like protein	PP_01778, minor structural protein gp89-like protein, phage(gi418489816), PHAGE_Lactob_Sha1_NC_019489	0
11	PP_01779	1833473	1835245	Backward	Phage-like protein	PP_01779, minor structural protein gp75-like protein, phage(gi418489815), PHAGE_Lactob_Sha1_NC_019489	0
12	PP_01780	1835305	1840203	Backward	Tail protein	PP_01780, putative tail component protein, phage(gi29165636), PHAGE_Strept_DT1_NC_002072	0
13	PP_01781	1840235	1840426	Backward	Hypothetical protein	PP_01781, hypothetical protein, phage(gi418489813), PHAGE_Lactob_Sha1_NC_019489	3.26E-07
14	PP_01782	1840465	1840839	Backward	Hypothetical protein	PP_01782, hypothetical	N/A
15	PP_01783	1840914	1841567	Backward	Tail protein	PP_01783, putative major tail protein, phage(gi48697269), PHAGE_Lactob_phiAT3_NC_005893	2.59E-22
16	PP_01784	1841583	1841963	Backward	Tail protein	PP_01784, putative tail component, phage(gi48697268), PHAGE_Lactob_phiAT3_NC_005893	2.60E-16
17	PP_01785	1841963	1842370	Backward	Tail protein	PP_01785, putative tail component protein, phage(gi9632427), PHAGE_Strept_DT1_NC_002072	2.08E-35
18	PP_01786	1842373	1842720	Backward	Head protein	PP_01786, putative head-tail joining protein, phage(gi9632902), PHAGE_Strept_Sfi19_NC_000871	2.74E-16
19	PP_01787	1842710	1843042	Backward	Phage-like protein	PP_01787, phage protein DNA packaging protein, phage(gi418489807), PHAGE_Lactob_Sha1_NC_019489	4.77E-55
20	PP_01788	1843114	1844346	Backward	Head protein	PP_01788, HK97 family phage major capsid protein, phage(gi418489806), PHAGE_Lactob_Sha1_NC_019489	0
21	PP_01789	1844346	1845110	Backward	Protease	PP_01789, protease subunit of ATP-dependent Clp protease, phage(gi418489805), PHAGE_Lactob_Sha1_NC_019489	1.37E-170
22	PP_01790	1845088	1846251	Backward	Portal protein	PP_01790, phage portal protein, phage(gi418489804), PHAGE_Lactob_Sha1_NC_019489	0
23	PP_01791	1846254	1846448	Backward	Head protein	PP_01791, phage head-tail joining protein, phage(gi418489803), PHAGE_Lactob_Sha1_NC_019489	6.73E-35
24	PP_01792	1846438	1847805	Backward	Terminase	PP_01792, phage terminase-like protein large subunit, phage(gi418489802),	0

						PHAGE_Lactob_Sha1_NC_019489	
25	PP_01793	1847926	1849101	Forward	Transposase	PP_01793, transposase, phage(gi26246249), PROPHAGE_Escher_CFT073	2.25E-62
26	PP_01794	1849133	1849696	Backward	Terminase	PP_01794, phage terminase-like protein large subunit, phage(gi418489802), PHAGE_Lactob_Sha1_NC_019489	5.27E-104
27	PP_01795	1849706	1850161	Backward	Terminase	PP_01795, P27 family phage terminase small subunit, phage(gi418489801), PHAGE_Lactob_Sha1_NC_019489	2.19E-106
28	PP_01796	1850351	1850602	Backward	Hypothetical protein	PP_01796, hypothetical	N/A
29	PP_01797	1850620	1851036	Backward	Hypothetical protein	PP_01797, hypothetical	N/A
30	PP_01798	1851042	1851512	Backward	Phage-like protein	PP_01798, restriction endonuclease, phage(gi418489800), PHAGE_Lactob_Sha1_NC_019489	7.09E-103
31	PP_01799	1851523	1851693	Backward	Phage-like protein	PP_01799, HNH nuclease, phage(gi418489799), PHAGE_Lactob_Sha1_NC_019489	1.66E-32
32	PP_01800	1851865	1852803	Backward	Hypothetical protein	PP_01800, hypothetical	N/A
33	PP_01801	1853073	1853498	Backward	Phage-like protein	PP_01801, phage transcriptional activator RinA, phage(gi418489798), PHAGE_Lactob_Sha1_NC_019489	2.44E-86
34	PP_01802	1853479	1853649	Backward	Phage-like protein	PP_01802, LP1-like protein, phage(gi418489797), PHAGE_Lactob_Sha1_NC_019489	1.86E-27
35	PP_01803	1853642	1854118	Backward	Hypothetical protein	PP_01803, hypothetical protein, phage(gi100142), PHAGE_Lactob_Iacchus_NC_048084	2.20E-63
36	PP_01804	1854115	1854531	Backward	Head protein	PP_01804, capsid maturation protease, phage(gi100067), PHAGE_Lactob_Lpa804_NC_048134	2.80E-41
37	PP_01805	1854555	1854704	Backward	Hypothetical protein	PP_01805, hypothetical	N/A
38	PP_01806	1854750	1854863	Backward	Hypothetical protein	PP_01806, hypothetical protein, phage(gi418489791), PHAGE_Lactob_Sha1_NC_019489	3.19E-07
39	PP_01807	1854856	1855236	Backward	Phage-like protein	PP_01807, gp63, phage(gi16798850), PHAGE_Lister_A118_NC_003216	1.53E-35
40	PP_01808	1855233	1855733	Backward	Hypothetical protein	PP_01808, hypothetical protein, phage(gi23455787), PHAGE_Lactob_phig1e_NC_004305	1.19E-75
41	PP_01809	1855869	1856654	Backward	Phage-like protein	PP_01809, DNA replication protein, phage(gi418489789), PHAGE_Lactob_Sha1_NC_019489	2.69E-175
42	PP_01810	1856654	1857421	Backward	Fiber protein	PP_01810, tail fiber protein, phage(gi100052), PHAGE_Bacill_vB_BhaS_171_NC_030904	1.58E-50
43	PP_01811	1858047	1858220	Backward	Hypothetical protein	PP_01811, hypothetical protein, phage(gi418489841), PHAGE_Lactob_Sha1_NC_019489	5.78E-30
44	PP_01812	1858232	1858432	Backward	Hypothetical protein	PP_01812, hypothetical protein, phage(gi418489840), PHAGE_Lactob_Sha1_NC_019489	5.20E-36
45	PP_01813	1858435	1858683	Backward	Hypothetical protein	PP_01813, hypothetical protein, phage(gi418489839), PHAGE_Lactob_Sha1_NC_019489	8.76E-41
46	PP_01814	1859949	1860209	Backward	Hypothetical protein	PP_01814, hypothetical	N/A
47	PP_01815	1860267	1860488	Forward	Hypothetical protein	PP_01815, hypothetical	N/A
48	PP_01816	1860483	1860731	Backward	Hypothetical protein	PP_01816, hypothetical	N/A
49	PP_01817	1860745	1860954	Backward	Hypothetical protein	PP_01817, hypothetical protein, phage(gi9633008), PHAGE_Lactob_phiadh_NC_000896	9.80E-06
50	PP_01818	1860966	1861673	Backward	Phage-like protein	PP_01818, phage-related antirepressor, phage(gi418489833), PHAGE_Lactob_Sha1_NC_019489	1.43E-36
51	PP_01819	1861730	1861975	Forward	Hypothetical protein	PP_01819, hypothetical	N/A

52	PP_01820	1862264	1862479	Backward	Hypothetical protein	PP_01820, hypothetical	N/A
53	PP_01821	1862736	1863068	Forward	Hypothetical protein	PP_01821, hypothetical protein, phage(gi100029), PHAGE_Lactob_PLE2_NC_031036	7.11E-40
54	PP_01822	1863061	1863468	Forward	Hypothetical protein	PP_01822, hypothetical protein, phage(gi100028), PHAGE_Lactob_PLE2_NC_031036	6.39E-39
55	PP_01823	1863529	1864305	Forward	Hypothetical protein	PP_01823, hypothetical	N/A
56	PP_01824	1864317	1864517	Forward	Hypothetical protein	PP_01824, hypothetical protein, phage(gi418489829), PHAGE_Lactob_Sha1_NC_019489	4.61E-36
57	PP_01825	1864827	1865009	Forward	Hypothetical protein	PP_01825, hypothetical	N/A
58	PP_01826	1865199	1865513	Forward	Hypothetical protein	PP_01826, hypothetical	N/A
59	PP_01827	1865710	1866285	Backward	Hypothetical protein	PP_01827, hypothetical	N/A
60	<i>attR</i>	1866346	1866357	Forward	Attachment site(AAACCAAAAAGC)	<i>attR</i>	N/A
61	PP_01828	1866514	1867677	Forward	Integrase	PP_01828, phage integrase, phage(gi418489411), PHAGE_Lactob_LF1_NC_019486	5.03E-79

Table S5. The fourth prophage (incomplete) region elements of *Lactiplantibacillus plantarum* JS21 (PHAGE_Paenib_Tripp_NC_028930).

#	Locus	ORF Start	ORF Stop	Strand	Homolog/Ortholog Species	Homolog/Ortholog Protein	E-Value
1	<i>attL</i>	2137180	2137192	Forward	Attachment site(TTTGGAAAACAAA)	<i>attL</i>	N/A
2	PP_02105	2151081	2152970	Backward	Phage-like protein	PP_02105, ABC transporter, phage(gi9630145), PHAGE_Bacill_SPbeta_NC_001884	1.07E-30
3	PP_02106	2152970	2154700	Backward	Phage-like protein	PP_02106, ABC transporter, phage(gi9630145), PHAGE_Bacill_SPbeta_NC_001884	4.72E-18
4	PP_02107	2154954	2155814	Backward	Plate protein	PP_02107, putative baseplate hub protein, phage(gi100137), PHAGE_Escher_RCS47_NC_042128	3.77E-05
5	PP_02108	2155841	2156293	Backward	Hypothetical protein	PP_02108, hypothetical protein, phage(gi971746471), PHAGE_Staphy_StB20_like_NC_028821	9.01E-06
6	PP_02109	2156409	2156840	Backward	Transposase	PP_02109, transposase, phage(gi971756981), PHAGE_Paenib_Tripp_NC_028930	4.05E-27
7	PP_02110	2156813	2157184	Backward	Transposase	PP_02110, transposase, phage(gi971756982), PHAGE_Paenib_Tripp_NC_028930	4.19E-36
8	PP_02111	2157189	2157971	Forward	Phage-like protein	PP_02111, chromosome partitioning ATPase, phage(gi418489414), PHAGE_Lactob_LF1_NC_019486	8.72E-19
9	PP_02112	2158186	2158353	Forward	Hypothetical protein	PP_02112, hypothetical	N/A
10	PP_02113	2158353	2159060	Forward	Hypothetical protein	PP_02113, hypothetical	N/A
11	PP_02114	2159223	2160344	Forward	Integrase	PP_02114, putative integrase, phage(gi937456703), PHAGE_Lactob_LBR48_NC_027990	1.12E-52
12	<i>attR</i>	2168851	2168863	Forward	Attachment site(TTTGGAAAACAAA)	<i>attR</i>	N/A

Table S6. The fifth prophage (incomplete) region elements of *Lactiplantibacillus plantarum* JS21 (PHAGE_Strept_APCM01_NC_029030).

#	Locus	ORF Start	ORF Stop	Strand	Homolog/Ortholog Species	Homolog/Ortholog Protein	E-Value
1	<i>attL</i>	2186014	2186033	Forward	Attachment site(CTCGCCATCTCCATTATTGA)	<i>attL</i>	N/A
2	PP_02143	2188064	2188438	Backward	Hypothetical protein	PP_02143, hypothetical protein, phage(gi966201497), PHAGE_Strept_T12_NC_028700	1.94E-13
3	PP_02144	2188725	2190140	Backward	Hypothetical protein	PP_02144, hypothetical protein, phage(gi100019), PHAGE_Clostr_phiCT453A_NC_028991	1.64E-82
4	PP_02145	2190152	2190931	Backward	Hypothetical protein	PP_02145, hypothetical protein, phage(gi966198623), PHAGE_Strept_Str_PAP_1_NC_028666	1.85E-27
5	PP_02146	2190944	2191165	Backward	Hypothetical protein	PP_02146, hypothetical	N/A
6	PP_02147	2191158	2191580	Backward	Hypothetical protein	PP_02147, hypothetical	N/A
7	PP_02148	2191722	2191835	Backward	Hypothetical protein	PP_02148, hypothetical	N/A
8	PP_02149	2191893	2192159	Backward	Hypothetical protein	PP_02149, hypothetical	N/A
9	PP_02150	2192327	2193013	Backward	Phage-like protein	PP_02150, Orf3, phage(gi13095661), PHAGE_Lactoc_bIL311_NC_002670	4.99E-19
10	PP_02151	2193341	2193835	Forward	Phage-like protein	PP_02151, putative transcriptional regulator, phage(gi446730276), PHAGE_Lactob_phiAQ113_NC_019782	2.17E-19
11	PP_02152	2193885	2195051	Forward	Integrase	PP_02152, integrase, phage(gi23097608), PROPHAGE_Oceano_HTE831	2.64E-95
12	<i>attR</i>	2195185	2195204	Forward	Attachment site(CTCGCCATCTCCATTATTGA)	<i>attR</i>	N/A

Table S7. Horizontal gene transfer of prophage region proteins using ProteinBLAST

S/N	#	Locus	ORF Start	ORF Stop	Strand	Homolog/Ortholog Species	Protein BLAST	Accession	E-value
The first prophage (intact) region elements of <i>Lactiplantibacillus plantarum</i> strain JS21									
1	1	PP_00028	36132	36581	Backward	Hypothetical protein	pyridoxamine 5'-phosphate oxidase family protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_214334341.1	7E-103
2	4	PP_00031	37513	38511	Forward	Transposase	IS30 family transposase [<i>Lactiplantibacillus argenteratensis</i>]	MBT1142305.1	0.0
3	6	PP_00032	38879	40033	Backward	Integrase	site-specific integrase [<i>Lactiplantibacillus nangangensis</i>]	WP_137615032.1	0.0
4	7	PP_00033	40086	40652	Backward	Phage-like protein	helix-turn-helix domain-containing protein [<i>Lentilactobacillus buchneri</i>]	WP_172884887.1	5E-30
5	11	PP_00037	42455	43849	Forward	Tail protein	virulence-associated E family protein [<i>Levilactobacillus brevis</i>]	WP_087609387.1	0.0
6	19	PP_00045	48742	49842	Forward	Portal protein	phage portal protein [<i>Lactiplantibacillus nangangensis</i>]	WP_137615043.1	0.0
7	20	PP_00046	49839	51374	Forward	Head protein	phage major capsid protein [<i>Lactiplantibacillus nangangensis</i>]	WP_137615044.1	0.0
8	21	PP_00047	51488	51757	Forward	Head protein	head-tail connector protein [<i>Lactiplantibacillus xiangfangensis</i>]	WP_057705766.1	1e-56
9	22	PP_00048	51916	52284	Forward	Hypothetical protein	hypothetical protein [<i>Limosilactobacillus reuteri</i>]	WP_264508898.1	2e-78
10	23	PP_00049	52408	52608	Forward	Portal protein	cold-shock protein [<i>Limosilactobacillus reuteri</i>]	WP_169477496.1	3e-37
11	25	PP_00051	52931	53044	Forward	Hypothetical protein	TPA: hypothetical protein [<i>Caudoviricetes</i> sp.]	DAZ29239.1	5E-14
The second prophage (intact) region elements of <i>Lactiplantibacillus plantarum</i> strain JS21									
12	1	PP_01075	1154203	1156470	Forward	Phage-like protein	excinuclease ABC subunit UvrA [<i>Lactiplantibacillus argenteratensis</i>]	WP_225588668.1	0.00E+00
13	4	PP_01077	1158655	1159170	Forward	Hypothetical protein	DUF2335 domain-containing protein [<i>Levilactobacillus brevis</i>]	WP_015474456.1	1.00E-101
14	5	PP_01078	1159471	1159647	Backward	Hypothetical protein	exonuclease domain-containing protein [<i>Levilactobacillus fuyuanensis</i>]	WP_125700023.1	5.00E-120
15	11	PP_01084	1163305	1163493	Forward	Phage-like protein	hypothetical protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_285209501.1	3.00E-09
16	13	PP_01086	1164108	1164437	Forward	Hypothetical protein	DUF771 domain-containing protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_214334453.1	1.00E-73
17	14	PP_01087	1164527	1164781	Forward	Hypothetical protein	hypothetical protein LJA01_21400 [<i>Lactobacillus japonicus</i>]	GEK64237.1	3.00E-48
18	18	PP_01091	1166646	1167305	Forward	Hypothetical protein	DUF669 domain-containing protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_260354589.1	7.00E-155
19	19	PP_01092	1167352	1168044	Forward	Hypothetical protein	hypothetical protein LJA01_21460 [<i>Lactobacillus japonicus</i>]	GEK64243.1	4.00E-171
20	21	PP_01094	1168273	1169022	Backward	Hypothetical protein	DUF4393 domain-containing protein [<i>Lactobacillaceae</i>]	WP_187357782.1	2.00E-54
21	22	PP_01095	1169090	1169896	Forward	Hypothetical protein	phage replisome organizer N-terminal domain-containing protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_214417724.1	0.00E+00
22	23	PP_01096	1169890	1170825	Forward	Phage-like protein	ATP-binding protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_244975215.1	0.00E+00
23	24	PP_01097	1171121	1171429	Forward	Hypothetical protein	hypothetical protein [<i>Lactiplantibacillus fabifermentans</i>]	WP_033614079.1	2.00E-63
24	25	PP_01098	1171422	1171538	Forward	Hypothetical protein	hypothetical protein LJA01_21510 [<i>Lactobacillus japonicus</i>]	GEK64248.1	3.00E-14
25	26	PP_01099	1171773	1171886	Forward	Phage-like protein	hypothetical protein [<i>Lactiplantibacillus mudanjiangensis</i>]	WP_130846690.1	1.00E-14

26	27	PP_01100	1171867	1172292	Forward	Phage-like protein	transcriptional regulator [<i>Lactiplantibacillus argenteratensis</i>]	WP_253290706.1	4.00E-94
27	28	PP_01101	1172733	1172912	Forward	Hypothetical protein	hypothetical protein [<i>Weissella confusa</i>]	WP_199402017.1	2.00E-08
28	29	PP_01102	1172917	1173870	Backward	Hypothetical protein	hypothetical protein [<i>Weissella cibaria</i>]	WP_261721978.1	1.00E-95
29	31	PP_01104	1175491	1175949	Forward	Terminase	phage terminase small subunit P27 family [<i>Lactiplantibacillus mudanjiangensis</i>]	WP_130852332.1	1.00E-101
30	32	PP_01105	1175936	1177726	Forward	Terminase	terminase large subunit [<i>Levilactobacillus brevis</i>]	WP_069359847.1	0
31	33	PP_01106	1177746	1178975	Forward	Portal protein	phage portal protein [<i>Levilactobacillus brevis</i>]	WP_024526686.1	0.00E+00
32	34	PP_01107	1178947	1179666	Forward	Protease	Clp protease ClpP [<i>Levilactobacillus brevis</i>]	WP_060416649.1	8.00E-170
33	35	PP_01108	1179669	1180814	Forward	Head protein	phage major capsid protein [<i>Levilactobacillus brevis</i>]	WP_060416648.1	0.00E+00
34	37	PP_01110	1181047	1181391	Forward	Phage-like protein	head-tail connector protein [<i>Levilactobacillus brevis</i>]	WP_024526689.1	3.00E-70
35	40	PP_01113	1182164	1182547	Forward	Hypothetical protein	tail protein [<i>Lactobacillus</i> phage Sha1]	YP_007003562.1	4.00E-82
36	42	PP_01116	1183213	1183329	Backward	Hypothetical protein	TPA: hypothetical protein [<i>Siphoviridae</i> sp. ctk5O4]	DAF51228.1	0.019
37	43	PP_01115	1183388	1183771	Forward	Hypothetical protein	hypothetical protein F2048_23865 [<i>Bacteroides fragilis</i>]	KAA4797547.1	9.00E-83
38	44	PP_01117	1183768	1183959	Forward	Hypothetical protein	hypothetical protein [<i>Loigolactobacillus backii</i>]	WP_143452801.1	9.00E-22
39	51	PP_01124	1196202	1197299	Forward	Phage-like protein	collagen-like protein [<i>Pediococcus ethanolidurans</i>]	WP_216762492.1	0.00E+00
40	52	PP_01125	1197296	1197511	Forward	Hypothetical protein	hypothetical protein [<i>Levilactobacillus brevis</i>]	WP_216577569.1	6.00E-39
41	53	PP_01126	1197525	1198697	Forward	Phage-like protein	GH25 family lysozyme [<i>Lactiplantibacillus argenteratensis</i>]	WP_210696722.1	0.00E+00
42	55	PP_01128	1198973	1199503	Forward	Hypothetical protein	hypothetical protein [<i>Lactiplantibacillus fabifermentans</i>]	WP_056993534.1	1.00E-111
The third prophage (intact) region elements of <i>Lactiplantibacillus plantarum</i> strain JS21									
43	2	PP_01770	1824504	1824878)	Backward	Hypothetical protein	phage holin [<i>Lactiplantibacillus argenteratensis</i>]	WP_216491151.1	6.00E-74
44	5	PP_01773	1826191	1826436)	Backward	Hypothetical protein	hypothetical protein [<i>Lactiplantibacillus xiangfangensis</i>]	WP_057705566.1	1.00E-70
45	7	PP_01775	1827781	1827942)	Backward	Hypothetical protein	hypothetical protein [<i>Gluconobacter oxydans</i>]	WP_253441138.1	8.00E-48
46	9	PP_01777	1828181	1830976)	Backward	Hypothetical protein	phage tail protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_216491148.1	0.00E+00
47	12	PP_01780	1835305	1840203)	Backward	Tail protein	tape measure protein [<i>Lactobacillus japonicus</i>]	GEK64269.1	0.00E+00
48	14	PP_01782	1840465	1840839)	Backward	Hypothetical protein	phage tail assembly chaperone [<i>Lactiplantibacillus mudanjiangensis</i>]	WP_130851912.1	9.00E-80
49	17	PP_01785	1841963	1842370)	Backward	Tail protein	hypothetical protein LJA01_21670 [<i>Lactobacillus japonicus</i>]	GEK64264.1	4.00E-87
50	19	PP_01787	1842710	1843042)	Backward	Phage-like protein	head-tail connector protein [<i>Lactiplantibacillus mudanjiangensis</i>]	WP_130851908.1	3.00E-64
51	23	PP_01791	1846254	1846448)	Backward	Head protein	DUF1056 family protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_285209523.1	6.00E-34
52	24	PP_01792	1846438	1847805)	Backward	Terminase	terminase large subunit [<i>Pediococcus acidilactici</i>]	WP_159218408.1	0.00E+00
53	25	PP_01793	1847926	1849101	Forward	Transposase	IS256 family transposase [<i>Fructilactobacillus sanfranciscensis</i>]	WP_238979325.1	0.00E+00
54	26	PP_01794	1849133	1849696)	Backward	Terminase	terminase large subunit [<i>Bacteroides fragilis</i>]	KAA4797499.1	8.00E-123

55	29	PP_01797	1850620	1851036)	Backward	Hypothetical protein	hypothetical protein [<i>Levilactobacillus brevis</i>]	WP_060463300.1	1.00E-62
56	31	PP_01799	1851523	1851693)	Backward	Phage-like protein	hypothetical protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_214334474.1	2e-30
57	33	PP_01801	1853073	1853498)	Backward	Phage-like protein	RinA family transcriptional regulator [<i>Lactiplantibacillus fabifermentans</i> DSM 21115]	KRO24919.1	3e-89
58	36	PP_01804	1854115	1854531)	Backward	Head protein	YopX family protein [<i>Lactiplantibacillus argenteratensis</i>]	MBU5277831.1	2e-82
59	40	PP_01808	1855233	1855733)	Backward	Hypothetical protein	hypothetical protein [<i>Lentilactobacillus parabuchneri</i>]	WP_301521624.1	7e-94
60	41	PP_01809	1855869	1856654)	Backward	Phage-like protein	ATP-binding protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_216491080.1	0.0
61	46	PP_01814	1859949	1860209	Backward	Hypothetical protein	hypothetical protein DY78_GL000849 [<i>Lactiplantibacillus fabifermentans</i> DSM 21115]	KRO26535.1	2e-40
62	51	PP_01819	1861730	1861975	Forward	Hypothetical protein	hypothetical protein [<i>Limosilactobacillus reuteri</i>]	WP_143449772.1	8e-43
63	56	PP_01824	1864317	1864517	Forward	Hypothetical protein	capsule polysaccharide transpoter [<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>]	MBT9072018.1	4e-06
64	57	PP_01825	1864827	1865009	Forward	Hypothetical protein	hypothetical protein [<i>Lactiplantibacillus argenteratensis</i>]	WP_285209498.1	2e-32
The fourth prophage (incomplete) region elements of <i>Lactiplantibacillus plantarum</i> strain JS21									
65	2	PP_02105	2151081	2152970	Backward	Phage-like protein	Select seq dbj GEK64508.1 multidrug ABC transporter ATP-binding protein [<i>Lactobacillus japonicus</i>]	GEK64508.1	0.0
66	4	PP_02107	2154954	2155814	Backward	Plate protein	IS982 family transposase [<i>Levilactobacillus parabrevis</i>]	WP_260340338.1	0.0
67	6	PP_02109	2156409	2156840	Backward	Transposase	Transposase [<i>Levilactobacillus brevis</i> ATCC 367]	ABJ64411.1	2e-102
68	7	PP_02110	2156813	2157184	Backward	Transposase	Transposase [<i>Levilactobacillus brevis</i> ATCC 367]	ABJ64410.1	5e-84
69	8	PP_02111	2157189	2157971	Forward	Phage-like protein	ParA family protein [<i>Latilactobacillus curvatus</i>]	WP_221276490.1	2e-108
70	10	PP_02113	2158353	2159060	Forward	Hypothetical protein	Select seq ref WP_139960858.1 hypothetical protein [<i>Levilactobacillus brevis</i>]	WP_139960858.1	1e-67
The fifth prophage (incomplete) region elements of <i>Lactiplantibacillus plantarum</i> strain JS21									
71	8	PP_02149	2191893	2192159	Backward	Hypothetical protein	helix-turn-helix domain-containing protein [<i>Lactiplantibacillus mudanjiangensis</i>]	WP_130846642.1	2e-30

Table S8. The predicted transposases of the JS21 genome by using IS Finder

#	Sequences producing significant alignments	IS Family	Group	Origin	Score(bits)	E. value
1	ISP2	IS1182	IS427	<i>Lactobacillus plantarum</i>	3356	0
2	ISP1	ISL3		<i>Lactobacillus plantarum</i>	2809	0
3	IS1310	IS256		<i>Enterococcus hirae</i>	2216	0
4	ISLpl1	IS30		<i>Lactobacillus plantarum</i>	2028	0
5	ISPP1	IS30		<i>Pediococcus pentosaceus</i>	1925	0
6	ISLpl3	IS5	IS150	<i>Lactobacillus plantarum</i>	1643	0
7	ISLhe30	IS30		<i>Lactobacillus helveticus</i>	1473	0
8	ISLsa1	IS30		<i>Lactobacillus sakei</i>	1372	0
9	ISLpl2	IS3		<i>Lactobacillus plantarum</i>	61.9	0.000006
10	ISBame1	IS256		<i>Bacillus megaterium</i>	58	0.0001

TableS9. Match between antibiotic resistance gene search using KofamKOALA (KEGG Orthology) web servers and phenotypic antibiotic resistance results

Antibiotic group	Antibiotic	Inhibition zone diameter/status	Antibiotic Resistance Genes		
			KofamKOALA(ver. 2023-06-07, KEGG release 106.0)		
			Gene	Product	E-value
β-Lactams	Penicillin G (10U)	19.9 (S)	<i>pbp2A</i>	penicillin-binding protein 2A [EC:2.4.1.129 3.4.16.4]	2.70E-287
			<i>penP</i>	beta-lactamase class A [EC:3.5.2.6]	8.40E-51
	Ampicillin (10μg)	34.70 (S)	<i>abcA</i>	ATP-binding cassette, subfamily B, bacterial AbcA/BmrA [EC:7.6.2.2]	4.30E-204
			<i>oppA</i>	oligopeptide transport system substrate-binding protein	7.00E-141
	Amoxicillin (20μg)	34.29 (S)	<i>oppB</i>	oligopeptide transport system permease protein	6.20E-123
			<i>oppC</i>	oligopeptide transport system permease protein	1.70E-113
	Cefotaxime (30μg)	32.93 (S)	<i>oppD</i>	oligopeptide transport system ATP-binding protein	1.20E-197
			<i>oppF</i>	oligopeptide transport system ATP-binding protein	2.40E-161
Aminoglycosides	Kanamycin (30μg)	≤13(R)	-	-	-
	Gentamicin (10μg)	16.98 (S)	-	-	-
Macrolides	Erythromycin (15μg)	25.48 (S)	-	-	-
Tetracyclines	Tetracycline (30μg)	20.99 (S)	<i>tetM</i>	ribosomal protection tetracycline resistance protein	2.10E-276
	Minocycline (30μg)	24.00mm (S)	-	-	-
4-quinolones	Ciprofloxacin (5μg)	≤15 (R)	-	-	-
	Norfloxacin (10μg)	≤12 (R)	-	-	-
	Enrofloxacin (10μg)	14.18 (I)	-	-	-
Glycopeptides	Vancomycin (30μg)	≤14 (R)	<i>vanX</i>	zinc D-Ala-D-Ala dipeptidase [EC:3.4.13.22]	3.90E-61
			<i>vanY</i>	zinc D-Ala-D-Ala carboxypeptidase [EC:3.4.17.14]	2.60E-50
			<i>alr</i>	alanine racemase [EC:5.1.1.1]	3.30E-129
			<i>ddl</i>	D-alanine-D-alanine ligase [EC:6.3.2.4]	3.90E-109
			<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide-transferase [EC:2.7.8.13]	3.50E-119
			<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase [EC:6.3.2.10]	1.40E-147
			<i>murG</i>	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [EC:2.4.1.227]	2.10E-128
sulfa drugs	Sulffurazole (300μg)	≤12 (R)	-	-	-
Lincomycin	Lincomycin	Not tested	<i>lmrB</i>	MFS transporter, DHA2 family, lincomycin resistance protein	4.60E-139

Table S10. Horizontal gene transfer screenING for antibiotic resistance genes

Antibiotic	Gene	Protein BLAST result	Accession	Identity	E-Value
β-Lactams	<i>pbp2A</i>	PBP1A family penicillin-binding protein [<i>Lactiplantibacillus plantarum</i>]	QSE53449.1	99%	0.0
	<i>penP</i>	serine hydrolase [<i>Lactiplantibacillus plantarum</i>]	WP_011101017.1	100.00%	0.0
Tetracycline	<i>tetM</i>	TetM/TetW/TetO/TetS family tetracycline resistance ribosomal protection protein [<i>Lactiplantibacillus plantarum</i>]	WP_027822280.1	100.00%	0.0
Lincomycin	<i>lmrB</i>	DHA2 family efflux MFS transporter permease subunit [<i>Lactiplantibacillus plantarum</i>]	WP_015640444.1	100.00%	0.0
Vancomycin	<i>vanX</i>	M15 family metallopeptidase [<i>Lactiplantibacillus plantarum</i>]	WP_015825207.1	100.00%	3e-134
	<i>vanY</i>	M15 family metallopeptidase [<i>Lactiplantibacillus plantarum</i>]	WP_016511489.1	100.00%	3e-180
	<i>alr</i>	alanine racemase [<i>Lactiplantibacillus plantarum</i>]	GJI53677.1	100.00%	0.0
	<i>ddl</i>	D-alanine--D-alanine ligase [<i>Lactiplantibacillus plantarum</i> ZJ316]	AGE39858.1	99.73%	0.0
	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide-transferase [<i>Lactiplantibacillus plantarum</i>]	WP_003640859.1	100.00%	0.0
	<i>murF</i>	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase [<i>Lactiplantibacillus plantarum</i>]	WP_003643844.1	99.78%	0.0
	<i>murG</i>	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase [<i>Lactiplantibacillus plantarum</i>]	WP_003640857.1	100.00%	0.0
Efflux pumps	<i>efrB</i>	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	WP_111443160.1	99.84%	0.0
	<i>efrA</i>	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	WP_003641422.1	100.00%	0.0
	<i>mdlB</i>	Lipid A export ATP-binding/permease proteinMsbA [<i>Lactiplantibacillus plantarum</i>]	KZU11536.1	99.83%	0.0
	<i>mdlA</i>	ABC transporter transmembrane domain-containing protein [<i>Lactiplantibacillus plantarum</i>]	WP_016511510.1	100.00%	0.0
	<i>patB</i>	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	WP_249391052.1	99.83%	0.0
	<i>patA</i>	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	WP_027822837.1	100.00%	0.0
	<i>abcA</i>	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	WP_054519139.1	100.00%	0.0
	<i>oppA</i>	peptide ABC transporter substrate-binding protein [<i>Lactiplantibacillus plantarum</i>]	WP_072533228.1	99.81%	0.0
	<i>oppB</i>	ABC transporter permease [<i>Lactiplantibacillus plantarum</i>]	WP_072536085.1	99.68%	0.0
	<i>oppC</i>	ABC transporter permease [<i>Lactiplantibacillus plantarum</i>]	WP_259610052.1	99.71%	0.0
	<i>oppD</i>	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	WP_260390669.1	100.00%	0.0
	<i>oppF</i>	ATP-binding cassette domain-containing protein [<i>Lactiplantibacillus plantarum</i>]	WP_131072774.1	99%	0.0
	<i>blt</i>	tetracycline resistance MFS efflux pump [<i>Lactiplantibacillus plantarum</i>]	WP_003641027.1	100%	0.0
	<i>mdtG</i>	MFS transporter [<i>Lactiplantibacillus plantarum</i>]	WP_211758286.1	100%	0.0

Table S11. Carbohydrate metabolism genes annotated by KEGG orthology

Glycolysis / Gluconeogenesis				
#	Symbol	KEGG Entry	Definition	Copy Number
1	E1.1.1.1, <i>adh</i>	K00001	alcohol dehydrogenase [EC:1.1.1.1]	3
2	<i>adhE</i>	K04072	acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]	2
3	FBA, <i>fbaA</i>	K01624	fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	1
4	LDH, <i>ldh</i>	K00016	L-lactate dehydrogenase [EC:1.1.1.27]	6
5	E3.2.1.86B, <i>bglA</i>	K01223	6-phospho-beta-glucosidase [EC:3.2.1.86]	7
6	PGAM, <i>gpmA</i>	K01834	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	2
7	<i>pgm</i>	K01835	phosphoglucomutase [EC:5.4.2.2]	1
8	GAPDH, <i>gapA</i>	K00134	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [EC:1.2.1.12]	1
9	PGK, <i>pgk</i>	K00927	phosphoglycerate kinase [EC:2.7.2.3]	1
10	TPI, <i>tpiA</i>	K01803	triosephosphate isomerase (TIM) [EC:5.3.1.1]	1
11	ENO, <i>eno</i>	K01689	enolase [EC:4.2.1.11]	2
12	<i>galM</i>, GALM	K01785	aldose 1-epimerase [EC:5.1.3.3]	3
13	<i>crr</i>	K02777	sugar PTS system EIIA component [EC:2.7.1.-]	2
14	<i>glk</i>	K25026	glucokinase [EC:2.7.1.2]	1
15	PK, <i>pyk</i>	K00873	pyruvate kinase [EC:2.7.1.40]	1
16	<i>pfkA</i>, PFK	K00850	6-phosphofructokinase 1 [EC:2.7.1.11]	1
17	<i>pps</i> , <i>ppsA</i>	K01007	pyruvate, water dikinase [EC:2.7.9.2]	1
18	DLD, <i>lpd</i> , <i>pdhD</i>	K00382	dihydrolipoamide dehydrogenase [EC:1.8.1.4]	1
19	DLAT, <i>aceF</i> , <i>pdhC</i>	K00627	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	1
20	PDHB, <i>pdhB</i>	K00162	pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	1
21	PDHA, <i>pdhA</i>	K00161	pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	1
22	GPI, <i>pgi</i>	K01810	glucose-6-phosphate isomerase [EC:5.3.1.9]	1
23	E4.1.1.49, <i>pckA</i>	K01610	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	1
Citrate cycle (TCA cycle)				
#	Symbol	KEGG Entry	Definition	Copy Number
1	E4.2.1.2B, <i>fumC</i> , FH	K01679	fumarate hydratase, class II [EC:4.2.1.2]	1
2	PC, <i>pyc</i>	K01958	pyruvate carboxylase [EC:6.4.1.1]	1
3	DLD, <i>lpd</i> , <i>pdhD</i>	K00382	dihydrolipoamide dehydrogenase [EC:1.8.1.4]	1
4	DLAT, <i>aceF</i> , <i>pdhC</i>	K00627	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	1
5	PDHB, <i>pdhB</i>	K00162	pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	1
6	PDHA, <i>pdhA</i>	K00161	pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	1
7	E4.1.1.49, <i>pckA</i>	K01610	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	1
Pentose phosphate pathway				
#	Symbol	KEGG Entry	Definition	Copy Number
1	FBA, <i>fbaA</i>	K01624	fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	1
2	<i>rpiA</i>	K01807	ribose 5-phosphate isomerase A [EC:5.3.1.6]	2
3	PRPS, <i>prsA</i>	K00948	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	2
4	<i>eda</i>	K01625	2-dehydro-3-deoxyphosphogluconate aldolase / (4S)-4-hydroxy-2-oxoglutarate aldolase [EC:4.1.2.14 4.1.3.42]	1
5	<i>pgm</i>	K01835	phosphoglucomutase [EC:5.4.2.2]	1

6	E2.2.1.1, <i>tktA</i> , <i>tktB</i>	K00615	transketolase [EC:2.2.1.1]	1
7	<i>gntK</i>	K25031	gluconokinase [EC:2.7.1.12]	1
8	PGD, <i>gnd</i> , <i>gntZ</i>	K00033	6-phosphogluconate dehydrogenase [EC:1.1.1.44 1.1.1.343]	2
9	<i>rpe</i>, RPE	K01783	ribulose-phosphate 3-epimerase [EC:5.1.3.1]	1
10	<i>pfkA</i>, PFK	K00850	6-phosphofructokinase 1 [EC:2.7.1.11]	1
11	<i>pgl</i>	K07404	6-phosphogluconolactonase [EC:3.1.1.31]	1
12	<i>rbsK</i> , RBKS	K00852	ribokinase [EC:2.7.1.15]	2
13	GPI, <i>pgi</i>	K01810	glucose-6-phosphate isomerase [EC:5.3.1.9]	1
14	<i>xfp</i> , <i>xpk</i>	K01621	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase [EC:4.1.2.9 4.1.2.22]	1
15	G6PD, <i>zwf</i>	K00036	glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49 1.1.1.363]	1

Pentose and glucuronate interconversions

#	Symbol	KEGG Entry	Definition	Copy Number
1	UGP2, <i>galU</i>, <i>galF</i>	K00963	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	1
2	<i>rpe</i>, RPE	K01783	ribulose-phosphate 3-epimerase [EC:5.1.3.1]	1
3	<i>tarI</i>	K21030	D-ribitol-5-phosphate cytidylyltransferase [EC:2.7.7.40]	1
4	E1.1.1.137	K21680	ribulose-5-phosphate 2-dehydrogenase [EC:1.1.1.137]	1

Fructose and mannose metabolism

#	Symbol	KEGG Entry	Definition	Copy Number
1	DAK, TKFC	K00863	triose/dihydroxyacetone kinase / FAD-AMP lyase (cyclizing) [EC:2.7.1.28 2.7.1.29 4.6.1.15]	1
2	E2.7.1.4, <i>scrK</i>	K00847	fructokinase [EC:2.7.1.4]	2
3	<i>mtlA</i> , <i>cmtA</i>	K02800	mannitol PTS system EIICBA or EIICB component [EC:2.7.1.197]	1
4	<i>cmtB</i>	K02798	mannitol PTS system EIIA component [EC:2.7.1.197]	1
5	<i>mtlD</i>	K00009	mannitol-1-phosphate 5-dehydrogenase [EC:1.1.1.17]	1
6	FBA, <i>fbaA</i>	K01624	fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	1
7	<i>manX</i>	K02794	mannose PTS system EIIB component [EC:2.7.1.191]	1
8	<i>manY</i>	K02795	mannose PTS system EIIC component	1
9	<i>manZ</i>	K02796	mannose PTS system EIID component	1
10	<i>manXa</i>	K02793	mannose PTS system EIIA component [EC:2.7.1.191]	2
11	<i>fruAb</i>	K02769	fructose PTS system EIIB component [EC:2.7.1.202]	2
12	TPI, <i>tpiA</i>	K01803	triosephosphate isomerase (TIM) [EC:5.3.1.1]	1
13	<i>pfkA</i>, PFK	K00850	6-phosphofructokinase 1 [EC:2.7.1.11]	1
14	<i>fruK</i>	K00882	1-phosphofructokinase [EC:2.7.1.56]	1
15	<i>fruA</i>	K02770	fructose PTS system EIIBC or EIIC component [EC:2.7.1.202]	2
16	<i>srlB</i>	K02781	glucitol/sorbitol PTS system EIIA component [EC:2.7.1.198]	2
17	<i>manA</i> , MPI	K01809	mannose-6-phosphate isomerase [EC:5.3.1.8]	1
18	<i>fruB</i>	K02768	fructose PTS system EIIA component [EC:2.7.1.202]	1
19	<i>srlE</i>	K02782	glucitol/sorbitol PTS system EIIB component [EC:2.7.1.198]	1
20	<i>srlA</i>	K02783	glucitol/sorbitol PTS system EIIC component	1
21	<i>srlD</i>	K00068	sorbitol-6-phosphate 2-dehydrogenase [EC:1.1.1.140]	1

Galactose metabolism

#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>malZ</i>	K01187	alpha-glucosidase [EC:3.2.1.20]	1
2	E3.2.1.22B, <i>galA</i> , <i>rafA</i>	K07407	alpha-galactosidase [EC:3.2.1.22]	3

3	INV, <i>sacA</i>	K01193	beta-fructofuranosidase [EC:3.2.1.26]	1
4	IMA, <i>malL</i>	K01182	oligo-1,6-glucosidase [EC:3.2.1.10]	2
5	<i>galE</i> , GALE	K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]	3
6	UGP2, <i>galU</i> , <i>galF</i>	K00963	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	1
7	<i>pgm</i>	K01835	phosphoglucomutase [EC:5.4.2.2]	1
8	<i>galM</i> , GALM	K01785	aldose 1-epimerase [EC:5.1.3.3]	3
9	<i>glk</i>	K25026	glucokinase [EC:2.7.1.2]	1
10	<i>pfkA</i>, PFK	K00850	6-phosphofructokinase 1 [EC:2.7.1.11]	1
11	<i>agaF</i>	K02744	N-acetylgalactosamine PTS system EIIA component [EC:2.7.1.-]	1
12	<i>agaD</i>	K10986	galactosamine PTS system EIID component	1
13	<i>agaC</i>	K10985	galactosamine PTS system EIIC component	1
14	<i>agaB</i>	K10984	galactosamine PTS system EIIB component [EC:2.7.1.-]	1
15	<i>bgaB</i> , <i>lacA</i>	K12308	beta-galactosidase [EC:3.2.1.23]	2
16	<i>galT</i> , GALT	K00965	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]	1
17	<i>galK</i>	K00849	galactokinase [EC:2.7.1.6]	1
18	<i>lacZ</i>	K01190	beta-galactosidase [EC:3.2.1.23]	2
Ascorbate and aldarate metabolism				
#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>ulaC</i> , <i>sgaA</i>	K02821	ascorbate PTS system EIIA or EIIB component [EC:2.7.1.194]	1
2	<i>ulaB</i> , <i>sgaB</i>	K02822	ascorbate PTS system EIIB component [EC:2.7.1.194]	1
3	<i>ulaA</i> , <i>sgaT</i>	K03475	ascorbate PTS system EIIC component	1
Starch and sucrose metabolism				
#	Symbol	KEGG Entry	Definition	Copy Number
1	GBE1, <i>glgB</i>	K00700	1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	2
2	<i>glgC</i>	K00975	glucose-1-phosphate adenyltransferase [EC:2.7.7.27]	5
3	<i>glgA</i>	K00703	starch synthase [EC:2.4.1.21]	3
4	PYG, <i>glgP</i>	K00688	glycogen phosphorylase [EC:2.4.1.1]	3
5	<i>pgmB</i>	K01838	beta-phosphoglucomutase [EC:5.4.2.6]	2
6	<i>malZ</i>	K01187	alpha-glucosidase [EC:3.2.1.20]	1
7	AMY, <i>amyA</i> , <i>malS</i>	K01176	alpha-amylase [EC:3.2.1.1]	1
8	<i>mapA</i>	K00691	maltose phosphorylase [EC:2.4.1.8]	2
9	E2.7.1.4, <i>scrK</i>	K00847	fructokinase [EC:2.7.1.4]	2
10	<i>scrA</i> , <i>sacP</i> , <i>sacX</i> , <i>ptsS</i>	K02810	sucrose PTS system EIIBC or EIIBC component [EC:2.7.1.211]	2
11	INV, <i>sacA</i>	K01193	beta-fructofuranosidase [EC:3.2.1.26]	1
12	IMA, <i>malL</i>	K01182	oligo-1,6-glucosidase [EC:3.2.1.10]	2
13	<i>treC</i>	K01226	trehalose-6-phosphate hydrolase [EC:3.2.1.93]	1
14	<i>celB</i> , <i>chbC</i>	K02761	cellobiose PTS system EIIC component	12
15	E3.2.1.86B, <i>bglA</i>	K01223	6-phospho-beta-glucosidase [EC:3.2.1.86]	7
16	UGP2, <i>galU</i> , <i>galF</i>	K00963	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	1
17	<i>pgm</i>	K01835	phosphoglucomutase [EC:5.4.2.2]	1
18	<i>crr</i>	K02777	sugar PTS system EIIA component [EC:2.7.1.-]	2
19	<i>celC</i> , <i>chbA</i>	K02759	cellobiose PTS system EIIA component [EC:2.7.1.196 2.7.1.205]	3
20	<i>celA</i> , <i>chbB</i>	K02760	cellobiose PTS system EIIB component [EC:2.7.1.196 2.7.1.205]	4

21	<i>glk</i>	K25026	glucokinase [EC:2.7.1.2]	1
22	GPI, <i>pgi</i>	K01810	glucose-6-phosphate isomerase [EC:5.3.1.9]	1
23	<i>cd, ma, nplT</i>	K01208	cyclomaltodextrinase / maltogenic alpha-amylase / neopullulanase [EC:3.2.1.54 3.2.1.133 3.2.1.135]	1
Amino sugar and nucleotide sugar metabolism				
#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>glgC</i>	K00975	glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]	5
2	E2.7.1.4, <i>scrK</i>	K00847	fructokinase [EC:2.7.1.4]	2
3	<i>nagB</i> , GNPDA	K02564	glucosamine-6-phosphate deaminase [EC:3.5.99.6]	1
4	<i>glmU</i>	K04042	bifunctional UDP-N-acetylglucosamine pyrophosphorylase / glucosamine-1-phosphate N-acetyltransferase [EC:2.7.7.23 2.3.1.157]	1
5	<i>murA</i>	K00790	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [EC:2.5.1.7]	2
6	<i>nagA</i> , AMDHD2	K01443	N-acetylglucosamine-6-phosphate deacetylase [EC:3.5.1.25]	1
7	<i>manX</i>	K02794	mannose PTS system EIIB component [EC:2.7.1.191]	1
8	<i>manY</i>	K02795	mannose PTS system EIIC component	1
9	<i>manZ</i>	K02796	mannose PTS system EIID component	1
10	<i>manXa</i>	K02793	mannose PTS system EIIA component [EC:2.7.1.191]	2
11	<i>galE</i> , GALE	K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]	3
12	UGP2, <i>galU</i> , <i>galF</i>	K00963	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	1
13	<i>pgm</i>	K01835	phosphoglucomutase [EC:5.4.2.2]	1
14	<i>murB</i>	K00075	UDP-N-acetylmuramate dehydrogenase [EC:1.3.1.98]	1
15	<i>glmM</i>	K03431	phosphoglucosamine mutase [EC:5.4.2.10]	1
16	<i>glmS</i> , GFPT	K00820	glutamine---fructose-6-phosphate transaminase (isomerizing) [EC:2.6.1.16]	1
17	<i>mupP</i>	K22292	N-acetyl-D-muramate 6-phosphate phosphatase [EC:3.1.3.105]	1
18	<i>crr</i>	K02777	sugar PTS system EIIA component [EC:2.7.1.-]	2
19	<i>wecB</i>	K01791	UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14]	1
20	<i>glk</i>	K25026	glucokinase [EC:2.7.1.2]	1
21	<i>manA</i> , MPI	K01809	mannose-6-phosphate isomerase [EC:5.3.1.8]	1
22	GPI, <i>pgi</i>	K01810	glucose-6-phosphate isomerase [EC:5.3.1.9]	1
23	<i>nagE</i>	K02804	N-acetylglucosamine PTS system EIICBA or EIICB component [EC:2.7.1.193]	2
24	<i>galT</i> , GALT	K00965	UDPglucose--hexose-1-phosphate uridylyltransferase [EC:2.7.7.12]	1
25	<i>galK</i>	K00849	galactokinase [EC:2.7.1.6]	1
26	<i>murQ</i>	K07106	N-acetylmuramic acid 6-phosphate etherase [EC:4.2.1.126]	1
27	<i>nanE</i>	K01788	N-acylglucosamine-6-phosphate 2-epimerase [EC:5.1.3.9]	1
Pyruvate metabolism				
#	Symbol	KEGG Entry	Definition	Copy Number
1	E1.1.1.1, <i>adh</i>	K00001	alcohol dehydrogenase [EC:1.1.1.1]	3
2	<i>larA</i>	K22373	lactate racemase [EC:5.1.2.1]	1
3	<i>ackA</i>	K00925	acetate kinase [EC:2.7.2.1]	3
4	<i>adhE</i>	K04072	acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]	2
5	LDH, <i>ldh</i>	K00016	L-lactate dehydrogenase [EC:1.1.1.27]	6
6	<i>accB</i> , <i>bccP</i>	K02160	acetyl-CoA carboxylase biotin carboxyl carrier protein	3
7	<i>accC</i>	K01961	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]	2
8	<i>accD</i>	K01963	acetyl-CoA carboxylase carboxyl transferase subunit beta [EC:6.4.1.2 2.1.3.15]	2

9	<i>accA</i>	K01962	acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2 2.1.3.15]	2
10	<i>pta</i>	K00625	phosphate acetyltransferase [EC:2.3.1.8]	1
11	<i>spxB, poxL</i>	K00158	pyruvate oxidase [EC:1.2.3.3]	5
12	<i>ldhA</i>	K03778	D-lactate dehydrogenase [EC:1.1.1.28]	2
13	ME2, <i>sfcA, maeA</i>	K00027	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	1
14	E4.2.1.2B, <i>fumC</i> , FH	K01679	fumarate hydratase, class II [EC:4.2.1.2]	1
15	<i>mleA, mleS</i>	K22212	malolactic enzyme [EC:4.1.1.101]	1
16	<i>acyP</i>	K01512	acylphosphatase [EC:3.6.1.7]	1
17	PK, <i>pyk</i>	K00873	pyruvate kinase [EC:2.7.1.40]	1
18	<i>pps, ppsA</i>	K01007	pyruvate, water dikinase [EC:2.7.9.2]	1
19	PC, <i>pyc</i>	K01958	pyruvate carboxylase [EC:6.4.1.1]	1
20	DLD, <i>lpd, pdhD</i>	K00382	dihydrolipoamide dehydrogenase [EC:1.8.1.4]	1
21	DLAT, <i>aceF, pdhC</i>	K00627	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	1
22	PDHB, <i>pdhB</i>	K00162	pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	1
23	PDHA, <i>pdhA</i>	K00161	pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	1
24	E2.3.1.54, <i>pflD</i>	K00656	formate C-acetyltransferase [EC:2.3.1.54]	1
25	E4.1.1.49, <i>pckA</i>	K01610	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	1

Glyoxylate and dicarboxylate metabolism

#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>glcD</i>	K00104	glycolate oxidase [EC:1.1.3.15]	1
2	<i>gcvH</i> , GCSH	K02437	glycine cleavage system H protein	2
3	<i>eda</i>	K01625	2-dehydro-3-deoxyphosphogluconate aldolase / (4S)-4-hydroxy-2-oxoglutarate aldolase [EC:4.1.2.14 4.1.3.42]	1
4	<i>ttdB</i>	K03780	L(+)-tartrate dehydratase beta subunit [EC:4.2.1.32]	1
5	<i>ttdA</i>	K03779	L(+)-tartrate dehydratase alpha subunit [EC:4.2.1.32]	1
6	<i>glnA</i> , GLUL	K01915	glutamine synthetase [EC:6.3.1.2]	1
7	<i>gph</i>	K01091	phosphoglycolate phosphatase [EC:3.1.3.18]	1
8	DLD, <i>lpd, pdhD</i>	K00382	dihydrolipoamide dehydrogenase [EC:1.8.1.4]	1
9	<i>glyA</i> , SHMT	K00600	glycine hydroxymethyltransferase [EC:2.1.2.1]	1
10	<i>glxK, garK</i>	K00865	glycerate 2-kinase [EC:2.7.1.165]	1
11	<i>katE</i> , CAT, <i>catB, srpA</i>	K03781	catalase [EC:1.11.1.6]	1

Propanoate metabolism

#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>ackA</i>	K00925	acetate kinase [EC:2.7.2.1]	3
2	LDH, <i>ldh</i>	K00016	L-lactate dehydrogenase [EC:1.1.1.27]	6
3	<i>accB, bccP</i>	K02160	acetyl-CoA carboxylase biotin carboxyl carrier protein	3
4	<i>accC</i>	K01961	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]	2
5	<i>accD</i>	K01963	acetyl-CoA carboxylase carboxyl transferase subunit beta [EC:6.4.1.2 2.1.3.15]	2
6	<i>accA</i>	K01962	acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2 2.1.3.15]	2
7	<i>pta</i>	K00625	phosphate acetyltransferase [EC:2.3.1.8]	1
8	DLD, <i>lpd, pdhD</i>	K00382	dihydrolipoamide dehydrogenase [EC:1.8.1.4]	1
9	<i>dhaT</i>	K00086	1,3-propanediol dehydrogenase [EC:1.1.1.202]	1
10	E2.3.1.54, <i>pflD</i>	K00656	formate C-acetyltransferase [EC:2.3.1.54]	1

C5-Branched dibasic acid metabolism				
#	Symbol	KEGG Entry	Definition	Copy Number
1	E2.2.1.6L, <i>ilvB</i> , <i>ilvG</i> , <i>ilvI</i>	K01652	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	1
2	<i>alsD</i> , <i>budA</i> , <i>aldC</i>	K01575	acetolactate decarboxylase [EC:4.1.1.5]	1
Inositol phosphate metabolism				
#	Symbol	KEGG Entry	Definition	Copy Number
1	TPI, <i>tpiA</i>	K01803	triosephosphate isomerase (TIM) [EC:5.3.1.1]	1
2	E3.1.3.25, IMPA, <i>suhB</i>	K01092	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]	1
3	<i>iolU</i>	K22230	scyllo-inositol 2-dehydrogenase (NADP+) [EC:1.1.1.-]	3
4	<i>iolI</i>	K06606	2-keto-myo-inositol isomerase [EC:5.3.99.11]	2
5	<i>iolG</i>	K00010	myo-inositol 2-dehydrogenase / D-chiro-inositol 1-dehydrogenase [EC:1.1.1.18 1.1.1.369]	7
6	<i>iolE</i>	K03335	inosose dehydratase [EC:4.2.1.44]	1
Butanoate metabolism				
#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>adc</i>	K01574	acetoacetate decarboxylase [EC:4.1.1.4]	1
2	<i>adhE</i>	K04072	acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]	2
3	E2.2.1.6L, <i>ilvB</i> , <i>ilvG</i> , <i>ilvI</i>	K01652	acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	1
4	<i>alsD</i> , <i>budA</i> , <i>aldC</i>	K01575	acetolactate decarboxylase [EC:4.1.1.5]	1
5	HMGCS	K01641	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]	1
6	<i>gabD</i>	K00135	succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]	1
7	E2.3.1.54, <i>pflD</i>	K00656	formate C-acetyltransferase [EC:2.3.1.54]	1
8	E4.1.1.15, <i>gadB</i> , <i>gadA</i> , GAD	K01580	glutamate decarboxylase [EC:4.1.1.15]	1

Table S12. KEGG (BlastKOALA) orthology search results for ABC transporters

#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>oppA, mppA</i>	K15580	oligopeptide transport system substrate-binding protein	8
2	<i>cbiO</i>	K02006	cobalt/nickel transport system ATP-binding protein	2
3	<i>cbiM</i>	K02007	cobalt/nickel transport system permease protein	1
4	<i>ecfT</i>	K16785	energy-coupling factor transport system permease protein	3
5	<i>cycB, ganO, mdxE</i>	K15770	arabinogalactan oligomer / maltooligosaccharide transport system substrate-binding protein	1
6	<i>ganP, mdxF</i>	K15771	arabinogalactan oligomer / maltooligosaccharide transport system permease protein	1
7	<i>ganQ, mdxG</i>	K15772	arabinogalactan oligomer / maltooligosaccharide transport system permease protein	1
8	<i>msmX, msmK, malK, sugC, ggtA, msiK</i>	K10112	multiple sugar transport system ATP-binding protein [EC:7.5.2.-]	1
9	<i>msr, vmlR</i>	K18231	macrolide transport system ATP-binding/permease protein	1
10	<i>potD</i>	K11069	spermidine/putrescine transport system substrate-binding protein	1
11	<i>potC</i>	K11070	spermidine/putrescine transport system permease protein	1
12	<i>potB</i>	K11071	spermidine/putrescine transport system permease protein	1
13	<i>potA</i>	K11072	spermidine/putrescine transport system ATP-binding protein [EC:7.6.2.11]	1
14	<i>ytrB</i>	K16921	acetoin utilization transport system ATP-binding protein	2
15	<i>ytrC_D</i>	K16919	acetoin utilization transport system permease protein	1
16	<i>bioY</i>	K03523	biotin transport system substrate-specific component	1
17	<i>metQ</i>	K02073	D-methionine transport system substrate-binding protein	3
18	<i>metN</i>	K02071	D-methionine transport system ATP-binding protein	3
19	<i>metI</i>	K02072	D-methionine transport system permease protein	3
20	<i>tagG</i>	K09692	teichoic acid transport system permease protein	1
21	<i>tagH</i>	K09693	teichoic acid transport system ATP-binding protein [EC:7.5.2.4]	1
22	<i>opuC</i>	K05845	osmoprotectant transport system substrate-binding protein	2
23	<i>opuA</i>	K05847	osmoprotectant transport system ATP-binding protein [EC:7.6.2.9]	2
24	<i>blpA, lagD</i>	K20344	ATP-binding cassette, subfamily C, bacteriocin exporter	2
25	<i>phnE</i>	K02042	phosphonate transport system permease protein	2
26	<i>phnC</i>	K02041	phosphonate transport system ATP-binding protein [EC:7.3.2.2]	1
27	<i>phnD</i>	K02044	phosphonate transport system substrate-binding protein	1
28	<i>pstS</i>	K02040	phosphate transport system substrate-binding protein	2
29	<i>pstC</i>	K02037	phosphate transport system permease protein	1
30	<i>pstA</i>	K02038	phosphate transport system permease protein	1
31	<i>pstB</i>	K02036	phosphate transport system ATP-binding protein [EC:7.3.2.1]	2
32	<i>glnH</i>	K10036	glutamine transport system substrate-binding protein	2
33	<i>glnQ</i>	K10038	glutamine transport system ATP-binding protein [EC:7.4.2.1]	3
34	<i>peb1A, glnH</i>	K10039	aspartate/glutamate/glutamine transport system substrate-binding protein	1
35	<i>peb1B, glnP, glnM</i>	K10040	aspartate/glutamate/glutamine transport system permease protein	2
36	<i>ecfA1</i>	K16786	energy-coupling factor transport system ATP-binding protein [EC:7.-.-.]	1
37	<i>ecfA2</i>	K16787	energy-coupling factor transport system ATP-binding protein [EC:7.-.-.]	1
38	<i>mntA</i>	K19973	manganese transport system ATP-binding protein [EC:7.2.2.5]	1
39	<i>mntB</i>	K19976	manganese transport system permease protein	1
40	<i>mntC</i>	K19975	manganese transport system substrate-binding protein	1
41	<i>cydD</i>	K16013	ATP-binding cassette, subfamily C, bacterial CydD	1
42	<i>cydC</i>	K16012	ATP-binding cassette, subfamily C, bacterial CydC	1

43	<i>oppB</i>	K15581	oligopeptide transport system permease protein	2
44	<i>oppC</i>	K15582	oligopeptide transport system permease protein	2
45	<i>oppD</i>	K15583	oligopeptide transport system ATP-binding protein	2
46	<i>oppF</i>	K10823	oligopeptide transport system ATP-binding protein	2
47	<i>ugpC</i>	K05816	sn-glycerol 3-phosphate transport system ATP-binding protein [EC:7.6.2.10]	1
48	<i>ugpA</i>	K05814	sn-glycerol 3-phosphate transport system permease protein	1
49	<i>ugpE</i>	K05815	sn-glycerol 3-phosphate transport system permease protein	2
50	<i>ugpB</i>	K05813	sn-glycerol 3-phosphate transport system substrate-binding protein	1
51	<i>opuBD</i>	K05846	osmoprotectant transport system permease protein	2
52	<i>afuB, fbpB</i>	K02011	iron(III) transport system permease protein	1
53	<i>afuA, fbpA</i>	K02012	iron(III) transport system substrate-binding protein	1
54	<i>afuC, fbpC</i>	K02010	iron(III) transport system ATP-binding protein [EC:7.2.2.7]	1
55	<i>artR, artM</i>	K23060	arginine/lysine/histidine transport system ATP-binding protein [EC:7.4.2.1]	1
56	<i>artQ</i>	K17077	arginine/lysine/histidine transport system permease protein	1
57	<i>efrB, efrF</i>	K18888	ATP-binding cassette, subfamily B, multidrug efflux pump	1
58	<i>efrA, efrE</i>	K18887	ATP-binding cassette, subfamily B, multidrug efflux pump	1
59	<i>abcA, bmrA</i>	K18104	ATP-binding cassette, subfamily B, bacterial AbcA/BmrA [EC:7.6.2.2]	2
60	<i>mdlB, smdB</i>	K18890	ATP-binding cassette, subfamily B, multidrug efflux pump	1
61	<i>mdlA, smdA</i>	K18889	ATP-binding cassette, subfamily B, multidrug efflux pump	1
62	<i>livF</i>	K01996	branched-chain amino acid transport system ATP-binding protein	1
63	<i>livG</i>	K01995	branched-chain amino acid transport system ATP-binding protein	1
64	<i>livM</i>	K01998	branched-chain amino acid transport system permease protein	1
65	<i>livH</i>	K01997	branched-chain amino acid transport system permease protein	1
66	<i>livK</i>	K01999	branched-chain amino acid transport system substrate-binding protein	1
67	<i>patB, rscB, lmrC, satB</i>	K18892	ATP-binding cassette, subfamily B, multidrug efflux pump	1
68	<i>patA, rscA, lmrC, satA</i>	K18891	ATP-binding cassette, subfamily B, multidrug efflux pump	1
69	<i>tcyA, tcyJ, fliY</i>	K02424	L-cystine transport system substrate-binding protein	2
70	<i>tcyB, tcyL</i>	K10009	L-cystine transport system permease protein	1
71	<i>tcyC, tcyN</i>	K10010	L-cystine transport system ATP-binding protein [EC:7.4.2.1]	1
72	<i>rbsD</i>	K06726	D-ribose pyranase [EC:5.4.99.62]	1

Table S13. Phosphotransferase system (PTS) annotated by KEGG (BlastKOALA)

#	Symbol	KEGG Entry	Definition	Copy Number
1	<i>scrA, sacP, sacX, ptsS</i>	K02810	sucrose PTS system EIIBCA or EIIBC component [EC:2.7.1.211]	2
2	<i>mtlA, cmtA</i>	K02800	mannitol PTS system EIICBA or EIICB component [EC:2.7.1.197]	1
3	<i>cmtB</i>	K02798	mannitol PTS system EIIA component [EC:2.7.1.197]	1
4	<i>bglF, bglP</i>	K02757	beta-glucoside PTS system EIICBA component [EC:2.7.1.-]	5
5	<i>celB, chbC</i>	K02761	cellobiose PTS system EIIC component	12
6	<i>manX</i>	K02794	mannose PTS system EIIB component [EC:2.7.1.191]	1
7	<i>manY</i>	K02795	mannose PTS system EIIC component	1
8	<i>manZ</i>	K02796	mannose PTS system EIID component	1
9	<i>manXa</i>	K02793	mannose PTS system EIIA component [EC:2.7.1.191]	2
10	<i>fruAb</i>	K02769	fructose PTS system EIIB component [EC:2.7.1.202]	2
11	<i>ulaC, sgaA</i>	K02821	ascorbate PTS system EIIB component [EC:2.7.1.194]	1
12	<i>ulaB, sgaB</i>	K02822	ascorbate PTS system EIIB component [EC:2.7.1.194]	1
13	<i>ulaA, sgaT</i>	K03475	ascorbate PTS system EIIC component	1
14	<i>crr</i>	K02777	sugar PTS system EIIB component [EC:2.7.1.-]	2
15	<i>celC, chbA</i>	K02759	cellobiose PTS system EIIB component [EC:2.7.1.196 2.7.1.205]	3
16	<i>ptsH</i>	K02784	phosphocarrier protein HPr	1
17	<i>ptsI</i>	K08483	phosphoenolpyruvate-protein phosphotransferase (PTS system enzyme I) [EC:2.7.3.9]	1
18	<i>celA, chbB</i>	K02760	cellobiose PTS system EIIB component [EC:2.7.1.196 2.7.1.205]	4
19	<i>fruK</i>	K00882	1-phosphofructokinase [EC:2.7.1.56]	1
20	<i>fruA</i>	K02770	fructose PTS system EIIB or EIIC component [EC:2.7.1.202]	2
21	<i>srlB</i>	K02781	glucitol/sorbitol PTS system EIIB component [EC:2.7.1.198]	2
22	<i>nagE</i>	K02804	N-acetylglucosamine PTS system EIICBA or EIICB component [EC:2.7.1.193]	2
23	<i>agaF</i>	K02744	N-acetylgalactosamine PTS system EIIB component [EC:2.7.1.-]	1
24	<i>agaD</i>	K10986	galactosamine PTS system EIIB component	1
25	<i>agaC</i>	K10985	galactosamine PTS system EIIC component	1
26	<i>agaB</i>	K10984	galactosamine PTS system EIIB component [EC:2.7.1.-]	1
27	<i>fruB</i>	K02768	fructose PTS system EIIB component [EC:2.7.1.202]	1
28	<i>srlE</i>	K02782	glucitol/sorbitol PTS system EIIB component [EC:2.7.1.198]	1
29	<i>srlA</i>	K02783	glucitol/sorbitol PTS system EIIC component	1

Table S14. The predicted biosynthetic gene clusters of secondary metabolites.

Region	Length	Total Proteins	Type	Region Position	ClusterBlast
1	11.260Kb	13	RiPP-like	374,530 - 385,789	NZ_CP035143 (374689-386840), bacteriocin, 91% of genes show similarity
2	41.170Kb	38	T3PKS	1,792,491 - 1,833,660	NZ_CP028977 (1817876-1859046), T3PKS, 97% of genes show similarity
3	20.882Kb	21	terpene	2,844,604 - 2,865,485	NZ_CP015857 (2748148-2769030), terpene, 94% of genes show similarity
4	20.706Kb	19	cyclic-lactone-autoinducer	3,071,820 - 3,092,525	NZ_KB946320 (432500-458581), lanthipeptide, 13% of genes show similarity

Table S15. The RiPP-like region elements of *Lactiplantibacillus plantarum* JS21.

Gene	Start	Stop	Strand	Description	E-Value	Percent Identity	Accession
gene0357	375687	375858	+	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	4E-29	1	WP_027822766.1
gene0358	375912	377088	-	IS256 family transposase [<i>Lactiplantibacillus plantarum</i>]	0	0.9898	WP_310581100.1
gene0359	377181	377922	-	CPBP family intramembrane glutamic endopeptidase [<i>Lactiplantibacillus plantarum</i>]	7E-166	0.9917	WP_027821503.1
gene0360	378020	378179	-	two-peptide bacteriocin plantaricin EF subunit PlnF [<i>Lactiplantibacillus plantarum</i>]	5E-29	1	WP_027822764.1
gene0361	378203	378374	-	two-peptide bacteriocin plantaricin EF subunit PlnE [<i>Lactiplantibacillus plantarum</i>]	2E-30	0.9821	WP_102115620.1
gene0362 (<i>blpA</i>)	378639	379470	+	Transport/processing ATP-binding protein ComA [<i>Lactiplantibacillus plantarum</i>]	0	0.9819	OUS99406.1
gene0363 (<i>blpA</i>)	379529	380789	+	peptide cleavage/export ABC transporter [<i>Lactiplantibacillus plantarum</i>]	0	0.9976	WP_234521144.1
gene0364 (<i>blpB</i>)	380805	382182	+	HlyD family secretion protein [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_027821501.1
gene0365	382271	382961	+	CPBP family intramembrane glutamic endopeptidase [<i>Lactiplantibacillus plantarum</i>]	3E-163	0.9956	WP_053339246.1
gene0366	383028	383697	+	CPBP family intramembrane glutamic endopeptidase [<i>Lactiplantibacillus plantarum</i>]	6E-156	1	WP_027822761.1
gene0367	383783	384464	+	CPBP family intramembrane glutamic endopeptidase [<i>Lactiplantibacillus plantarum</i>]	5E-160	1	WP_027822760.1
gene0368	384557	385232	+	CPBP family intramembrane glutamic endopeptidase [<i>Lactiplantibacillus plantarum</i>]	7E-158	1	WP_027822759.1
gene0369(<i>higB-I</i>)	385379	385670	+	type II toxin-antitoxin system RelE/ParE family toxin [<i>Lactiplantibacillus plantarum</i>]	3E-65	1	WP_027822758.1

Table S16. The T3PKS region elements of *Lactiplantibacillus plantarum* JS21.

Gene	Start	Stop	Strand	Description	E-Value	Percent Identity	Accession
gene1731(<i>polC</i>)	1792817	1797131	-	DNA polymerase III subunit alpha [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_003640729.1
gene1732(<i>proS</i>)	1797624	1799334	-	proline-tRNA ligase [<i>Lactiplantibacillus plantarum</i>]	0	0.9982	WP_185936516.1
gene1733(<i>rseP</i>)	1799373	1800651	-	RIP metalloprotease RseP [<i>Lactiplantibacillus plantarum</i>]	0	0.9976	WP_172637917.1
gene1734 (<i>cdsA</i>)	1800688	1801474	-	phosphatidate cytidyltransferase [<i>Lactiplantibacillus plantarum</i>]	0	0.9962	WP_251335027.1
gene1735 (<i>uppS</i>)	1801489	1802269	-	isoprenyl transferase [<i>Lactiplantibacillus plantarum</i>]	0	0.9961	WP_045351394.1
gene1736 (<i>frr</i>)	1802388	1802952	-	ribosome recycling factor [<i>Lactiplantibacillus plantarum</i>]	1E-129	0.9947	WP_208664135.1
gene1737 (<i>pyrH</i>)	1802953	1803676	-	UMP kinase [<i>Lactiplantibacillus plantarum</i>]	1E-173	0.9958	WP_079111798.1
gene1738 (<i>tsf</i>)	1803875	1804754	-	translation elongation factor Ts [<i>Lactiplantibacillus plantarum</i>]	0	0.9966	WP_135517078.1
gene1739 (<i>rpsB</i>)	1804856	1805660	-	30S ribosomal protein S2 [<i>Lactiplantibacillus plantarum</i>]	0	0.9963	WP_259689552.1
gene1740	1805884	1806607	+	HAD family hydrolase [<i>Lactiplantibacillus plantarum</i>]	3E-175	0.9958	WP_160248452.1
gene1741 (<i>ldhA</i>)	1806896	1807895	-	D-2-hydroxyacid dehydrogenase [<i>Lactiplantibacillus plantarum</i>]	0	0.997	WP_142262829.1
gene1742	1807979	1808285	-	GIY-YIG nuclease family protein [<i>Lactiplantibacillus plantarum</i>]	1E-66	1	WP_003645628.1
gene1743	1808268	1809027	-	tRNA1(Val) (adenine(37)-N6)-methyltransferase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_003645629.1

gene1744 (<i>plsC</i>)	1809138	1809774	+	1-acylglycerol-3-phosphate O-acyltransferase [<i>Lactiplantibacillus plantarum</i> ST-III]	2E-153	1	ADN98865.1
gene1745	1809830	1810061	-	hypothetical protein LPST_C1650 [<i>Lactiplantibacillus plantarum</i> ST-III]	3E-48	1	ADN98866.1
gene1746	1810164	1810437	-	hypothetical protein Lp16_1605 [<i>Lactiplantibacillus plantarum</i> 16]	4E-56	1	AGO08290.1
gene1747 (<i>lexA</i>)	1810555	1811188	+	LexA repressor [<i>Lactiplantibacillus plantarum</i>]	1E-152	0.9952	MCG0732895.1
gene1748	1811811	1812441	+	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	2E-142	0.9904	WP_015825658.1
gene1749	1812490	1813660	-	hydroxymethylglutaryl-CoA synthase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_015380455.1
gene1750	1813695	1814088	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	3E-92	1	KZT97394.1
gene1751	1814251	1814644	+	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	5E-88	0.9923	WP_015380457.1
gene1752	1815089	1816031	+	glycosyltransferase family 2 protein [<i>Lactiplantibacillus plantarum</i>]	0	0.9968	MDN6215184.1
gene1753	1816730	1817303	-	helix-turn-helix domain containing protein [<i>Lactiplantibacillus plantarum</i>]	1E-135	0.9947	WP_031275254.1
gene1754 (<i>tagT_U_V</i>)	1817454	1818543	-	LCP family protein [<i>Lactiplantibacillus plantarum</i>]	0	1	MBS0953805.1
gene1755	1818581	1819013	-	putative transposase for insertion sequence element IS6501 [<i>Lactiplantibacillus plantarum</i>]	2E-102	1	OUT01805.1
gene1756	1818985	1819357	-	Transposase [<i>Lactiplantibacillus plantarum</i> ZJ316]	6E-85	1	AGE37926.1
gene1757	1819474	1820266	-	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	0	0.9962	WP_260187879.1
gene1758	1820284	1822027	-	ABC transporter permease subunit [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_016527118.1
gene1759 (<i>rodA</i>)	1822505	1823717	-	FtsW/RodA/SpoVE family cell cycle protein [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_003645640.1
gene1761	1824503	1824878	-	phage holin [<i>Lactiplantibacillus plantarum</i>]	8E-78	0.9839	WP_285298920.1
gene1762	1824890	1825154	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	2E-53	1	MCG0627622.1
gene1763	1825153	1826179	-	GH25 family lysozyme [<i>Lactiplantibacillus plantarum</i>]	0	0.9528	WP_172639632.1
gene1764	1826190	1826436	-	hypothetical protein [<i>Lactiplantibacillus paraplantarum</i>]	2E-44	0.9136	WP_056988443.1
gene1765	1826432	1827797	-	collagen-like protein [<i>Lactiplantibacillus plantarum</i>]	0	0.7362	WP_301667370.1
gene1766	1827780	1827942	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	8E-27	0.9811	WP_165836136.1
gene1767	1827945	1828188	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	3E-47	0.9875	WP_163627199.1
gene1768 (<i>sadA</i>)	1828180	1830976	-	phage tail protein [<i>Lactiplantibacillus plantarum</i>]	0	0.7575	WP_262339558.1
gene1769	1830992	1833407	-	phage tail spike protein [<i>Lactiplantibacillus plantarum</i>]	0	0.9478	WP_163627195.1

Table S17. The terpene region elements of *Lactiplantibacillus plantarum* JS21.

Gene	Start	Stop	Strand	Description	E-Value	Percent Identity	Accession
gene2784	2845125	2845353	-	PLDc N-terminal domain-containing protein [<i>Lactiplantibacillus plantarum</i>]	2E-46	0.9867	WP_074161759.1
gene2785	2845413	2846097	-	metallophosphoesterase [<i>Lactiplantibacillus plantarum</i>]	2E-167	1	WP_225914106.1
gene2786(<i>cpdA</i>)	2846093	2846261	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	2E-31	1	WP_225914107.1
gene2787	2846702	2847254	+	Acetyltransferase [<i>Lactiplantibacillus plantarum</i> subsp. <i>plantarum</i> P-8]	6E-133	0.9945	AGL65399.2
gene2788	2847525	2848524	-	IS30 family transposase [<i>Lactiplantibacillus plantarum</i>]	0	0.997	WP_247965010.1
gene2789(<i>lrgA</i>)	2848781	2849201	-	CidA/LrgA family protein [<i>Lactiplantibacillus plantarum</i>]	7E-90	0.9928	WP_063852339.1
gene2790(<i>lrgB</i>)	2849220	2849718	-	LrgB family protein [<i>Lactiplantibacillus plantarum</i>]	3E-107	0.9939	MCG5037381.1
gene2791(<i>lrgB</i>)	2849748	2849949	-	LrgB family protein [<i>Lactiplantibacillus plantarum</i>]	5E-37	1	WP_134795272.1
gene2792	2850123	2850999	-	DegV family protein [<i>Lactiplantibacillus plantarum</i> ZJ316]	0	1	AGE40626.1
gene2793	2851487	2851655	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	2E-31	1	WP_021357416.1

gene2794	2851822	2852521	+	zinc metalloproteinase [<i>Lactiplantibacillus plantarum</i>]	3E-165	0.9957	WP_057717055.1
gene2795	2853126	2854623	+	phytoene desaturase family protein [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_011102097.1
gene2796	2854603	2855485	+	phytoene/squalene synthase family protein [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_027822316.1
gene2797	2855846	2856788	+	alpha/beta hydrolase [<i>Lactiplantibacillus plantarum</i>]	0	0.9968	WP_168177697.1
gene2798	2856854	2857967	-	glycerate kinase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_054519129.1
gene2799	2858102	2859437	+	NAD(P)/FAD-dependent oxidoreductase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_027822314.1
gene2800	2859631	2859961	+	bacteriocin immunity protein [<i>Lactiplantibacillus plantarum</i>]	1E-72	1	WP_021357419.1
gene2801	2860183	2861482	-	adenylosuccinate lyase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_003645480.1
gene2802	2861798	2863088	+	adenylosuccinate synthase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_015381012.1
gene2803	2863130	2864108	+	GMP reductase [<i>Lactiplantibacillus plantarum</i> ZJ316]	0	1	AGE40638.1
gene2804	2864200	2865142	-	ABC transporter ATP-binding protein [<i>Lactiplantibacillus plantarum</i>]	0	0.9968	AYG28017.1

Table S18. The cyclic-lactone-autoinducer region elements of *Lactiplantibacillus plantarum* JS21.

Gene	Start	Stop	Strand	Description	E-Value	Percent Identity	Accession
gene3001	3072566	3073772	-	FAD-dependent oxidoreductase [<i>Lactiplantibacillus plantarum</i>]	0	0.9975	WP_301699601.1
gene3002	3074238	3074610	+	TIGR02328 family protein [<i>Lactiplantibacillus plantarum</i>]	6E-87	0.9919	WP_172637956.1
gene3003	3074805	3075354	-	folate family ECF transporter S component [<i>Lactiplantibacillus plantarum</i>]	6E-124	0.9945	WP_196241767.1
gene3004	3075483	3076482	+	IS30 family transposase [<i>Lactiplantibacillus plantarum</i>]	0	0.997	WP_247965010.1
gene3005	3076664	3076799	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	2E-20	1	WP_003642924.1
gene3006	3076815	3077061	-	GlsB/YeaQ/YmgE family stress response membrane protein [<i>Lactiplantibacillus plantarum</i>]	2E-44	1	WP_070085348.1
gene3007 (<i>katE</i>)	3077406	3078861	+	catalase [<i>Lactiplantibacillus plantarum</i> subsp. <i>plantarum</i> ATCC 14917 = JCM 1149 = CGMCC 1.2437]	0	0.9979	EFK28610.1
gene3008 (<i>spxA</i>)	3079018	3079456	-	Spx/MgsR family RNA polymerase-binding regulatory protein [<i>Lactiplantibacillus plantarum</i>]	2E-101	0.9931	WP_103420511.1
gene3009 (<i>agrA</i>)	3079811	3080555	-	LytTR family DNA-binding domain-containing protein [<i>Lactiplantibacillus plantarum</i>]	0	0.9919	WP_168786167.1
gene3010	3080547	3081810	-	GHKL domain-containing protein [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_054519202.1
gene3011	3081819	3081948	-	cyclic lactone autoinducer peptide [<i>Lactiplantibacillus</i>]	1E-21	1	WP_003643585.1
gene3012	3081928	3082525	-	accessory gene regulator AgrB [<i>Lactiplantibacillus plantarum</i>]	1E-134	0.9949	WP_241467921.1
gene3013 (<i>clpL</i>)	3082892	3085007	-	ATP-dependent Clp protease ATP-binding subunit [<i>Lactiplantibacillus plantarum</i>]	0	0.9972	WP_057137373.1
gene3014	3085397	3085631	-	hypothetical protein [<i>Lactiplantibacillus plantarum</i>]	6E-50	0.987	WP_169484439.1
gene3015 (<i>lctO</i>)	3086259	3087360	-	lactate oxidase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_102115675.1
gene3016	3087386	3089135	-	thiamine pyrophosphate-binding protein [<i>Lactiplantibacillus plantarum</i>]	0	0.9966	WP_108910153.1
gene3017	3089222	3089648	-	Rrf2 family transcriptional regulator [<i>Lactiplantibacillus plantarum</i>]	5E-99	0.9929	WP_123808678.1
gene3018 (<i>poxL</i>)	3089820	3091632	-	pyruvate oxidase [<i>Lactiplantibacillus plantarum</i>]	0	1	WP_003646223.1

gene3019	3092002	3092380	-	glucitol/sorbitol-specific PTS system IIA component	[<i>Lactiplantibacillus</i>	1E-84	1	BEI65651.1
(<i>srlB</i>)				<i>plantarum</i>]				

Table S19. Putative probiotic genes are found in the genome of *Lactiplantibacillus plantarum* JS21.

Gene ID	Gene Name	Strand	Start	End	KO ID	KO Description
Stress resistance genes						
gene2094	<i>atpC</i>	-	2128509	2128081	K02114	F-type H ⁺ -transporting ATPase subunit epsilon
gene2095	<i>atpD</i>	-	2129924	2128521	K02112	F-type H ⁺ /Na ⁺ -transporting ATPase subunit beta [EC:7.1.2.2 7.2.2.1]
gene2096	<i>atpG</i>	-	2130893	2129949	K02115	F-type H ⁺ -transporting ATPase subunit gamma
gene2097	<i>atpA</i>	-	2132443	2130923	K02111	F-type H ⁺ /Na ⁺ -transporting ATPase subunit alpha [EC:7.1.2.2 7.2.2.1]
gene2098	<i>atpH</i>	-	2133011	2132466	K02113	F-type H ⁺ -transporting ATPase subunit delta
gene2099	<i>atpF</i>	-	2133516	2133001	K02109	F-type H ⁺ -transporting ATPase subunit b
gene2100	<i>atpE</i>	-	2133782	2133570	K02110	F-type H ⁺ -transporting ATPase subunit c
gene2101	<i>atpB</i>	-	2134533	2133820	K02108	F-type H ⁺ -transporting ATPase subunit a
gene1587	<i>uup</i>	-	1641766	1639868	K15738	ABC transport system ATP-binding/permease protein
gene0566	-	-	591900	589918	K06158	ATP-binding cassette, subfamily F, member 3
gene0354	-	+	372316	373500	-	cation: proton antiporter
gene0651	<i>nhaK</i>	+	695509	697638	K24163	monovalent cation/hydrogen antiporter
gene0728	-	-	775397	773541	K03455	monovalent cation: H ⁺ antiporter-2, CPA2 family
gene2241	<i>nhaK</i>	+	2270261	2272264	K24163	monovalent cation/hydrogen antiporter
gene2293	<i>nhaK</i>	-	2321931	2320339	K24163	monovalent cation/hydrogen antiporter
gene2426	-	-	2468631	2467465	-	cation: proton antiporter
gene2691	<i>nhaK</i>	-	2747753	2746152	K24163	monovalent cation/hydrogen antiporter
gene2862	<i>nhaC</i>	-	2927387	2925963	K03315	Na ⁺ :H ⁺ antiporter, NhaC family
gene0123	-	-	130332	127594	-	MULTISPECIES: cation-transporting P-type ATPase
gene0945	<i>ctpE</i>	+	1011030	1013369	K12952	cation-transporting P-type ATPase E [EC:7.2.2.-]
gene1627	-	-	1689159	1686883	K01535	H ⁺ -transporting ATPase [EC:7.1.2.1]
gene2632	<i>copA</i>	-	2677369	2675444	K17686	P-type Cu ⁺ transporter [EC:7.2.2.8]
gene2855	-	+	2917466	2919310	-	MULTISPECIES: heavy metal translocating P-type ATPase
pWS05b0022	-	+	22708	25482	-	HAD-IC family P-type ATPase
DNA and protein protection and repair						
gene0618	<i>clpP</i>	-	650100	649510	K01358	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
gene0840	<i>clpC</i>	+	897938	900442	K03696	ATP-dependent Clp protease ATP-binding subunit ClpC
gene1000	<i>clpE</i>	-	1066996	1064930	K03697	ATP-dependent Clp protease ATP-binding subunit ClpE
gene1125	<i>clpP</i>	+	1178947	1179666	K01358	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
gene1613	<i>clpB</i>	-	1671411	1668808	K03695	ATP-dependent Clp protease ATP-binding subunit ClpB
gene1780	<i>clpP</i>	-	1845110	1844346	K01358	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
gene1865	<i>clpX</i>	-	1903396	1902131	K03544	ATP-dependent Clp protease ATP-binding subunit ClpX
gene3013	<i>clpL</i>	-	3085007	3082893	K04086	ATP-dependent Clp protease ATP-binding subunit ClpL
Exopolysaccharide biosynthesis responsible genes						
gene0228	<i>cysE</i>	-	244105	243563	K00640	serine O-acetyltransferase [EC:2.3.1.30]
gene0406	<i>glmU</i>	+	421185	422567	K04042	bifunctional UDP-N-acetylglucosamine pyrophosphorylase / glucosamine-1-phosphate N-acetyltransferase [EC:2.7.7.23 2.3.1.157]

gene0450	-	+	476535	478139	K03328	polysaccharide transporter, PST family
gene0555	<i>galE</i>	+	579356	580351	K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]
gene0572	<i>wecA</i>	+	598014	599111	K02851	UDP-GlcNAc:undecaprenyl-phosphate/decaprenyl-phosphate GlcNAc-1-phosphate transferase [EC:2.7.8.33 2.7.8.35]
gene0594	<i>galU</i>	+	620532	621452	K00963	UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]
gene0677	<i>licD</i>	-	725651	724842	K07271	lipopolysaccharide cholinephosphotransferase [EC:2.7.8.-]
gene0963	<i>wecB</i>	+	1029283	1030401	K01791	UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14]
gene1049	-	+	1122380	1124050	-	polysaccharide biosynthesis protein
gene1287	<i>pgaC</i>	-	1342525	1341212	K11936	poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
gene1440	-	+	1491247	1491852	K21713	lytic chitin monooxygenase [EC:1.14.99.53]
gene1843	-	-	1885579	1884575	-	polysaccharide biosynthesis C-terminal domain-containing protein
gene1852	<i>galE</i>	-	1892059	1891118	K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]
gene1855	<i>epsA</i>	-	1893757	1893560	K19420	protein tyrosine kinase modulator
gene1856	<i>epsA</i>	-	1894320	1893760	K19420	protein tyrosine kinase modulator
gene1887	<i>pgaC</i>	-	1927958	1926606	K11936	poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
gene2111	<i>manA</i>	-	2146653	2145688	K01809	mannose-6-phosphate isomerase [EC:5.3.1.8]
gene2327	<i>pgaC</i>	+	2362543	2363871	K11936	poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
gene2969	<i>galE</i>	-	3037290	3036286	K01784	UDP-glucose 4-epimerase [EC:5.1.3.2]
pWS03b0015	<i>epsA</i>	+	12532	13299	K19420	protein tyrosine kinase modulator
pWS03b0055	<i>epsA</i>	+	54095	54199	K19420	protein tyrosine kinase modulator
gene1854	<i>epsB</i>	-	1893542	1892835	K00903	protein-tyrosine kinase [EC:2.7.10.3]
pWS03b0016	<i>epsB</i>	+	13310	14038	K00903	protein-tyrosine kinase [EC:2.7.10.3]
Lipoteichoic acid (LTA) synthesis responsible genes						
gene1706	<i>dltD</i>	-	1767288	1766011	K03740	D-alanine transfer protein
gene1708	<i>dltB</i>	-	1768765	1767551	K03739	membrane protein involved in D-alanine export
Adhesion ability						
gene1524	-	-	1574724	1573018	-	fibronectin-binding domain-containing protein
gene0427	<i>srtA</i>	+	445842	446546	K07284	sortase A [EC:3.4.22.70]
Anti-pathogenic effect						
gene0609	<i>luxS</i>	+	638874	639350	K07173	S-ribosylhomocysteine lyase [EC:4.4.1.21]
Biofilm formation						
gene0018	<i>glgC</i>	+	23093	24232	K00975	glucose-1-phosphate adenyltransferase [EC:2.7.7.27]
gene0019	<i>glgC</i>	+	24229	25401	K00975	glucose-1-phosphate adenyltransferase [EC:2.7.7.27]
gene0020	<i>glgA</i>	+	25394	26833	K00703	starch synthase [EC:2.4.1.21]
gene0021	<i>glgP</i>	+	26853	29249	K00688	glycogen phosphorylase [EC:2.4.1.1]
gene0228	<i>cysE</i>	-	244105	243563	K00640	serine O-acetyltransferase [EC:2.3.1.30]
gene0609	<i>luxS</i>	+	638874	639350	K07173	S-ribosylhomocysteine lyase [EC:4.4.1.21]
gene0620	<i>rpoN</i>	+	651074	652411	K03092	RNA polymerase sigma-54 factor
gene0711	<i>crr</i>	+	758720	759211	K02777	sugar PTS system EIIA component [EC:2.7.1.-]
gene0963	<i>wecB</i>	+	1029283	1030401	K01791	UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing) [EC:5.1.3.14]
gene1287	<i>pgaC</i>	-	1342525	1341212	K11936	poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
gene1398	<i>trpE</i>	+	1453129	1454565	K01657	anthranilate synthase component I [EC:4.1.3.27]
gene1399	<i>trpG</i>	+	1454516	1455124	K01658	anthranilate synthase component II [EC:4.1.3.27]

gene1887	<i>pgaC</i>	-	1927958	1926606	K11936	poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
gene2327	<i>pgaC</i>	+	2362543	2363871	K11936	poly-beta-1,6-N-acetyl-D-glucosamine synthase [EC:2.4.1.-]
gene2575	<i>crr</i>	-	2625805	2625359	K02777	sugar PTS system EIIA component [EC:2.7.1.-]
gene2786	<i>cpdA</i>	-	2846261	2846094	K03651	3',5'-cyclic-AMP phosphodiesterase [EC:3.1.4.53]
pWS05 0001	<i>glgC</i>	+	3	392	K00975	glucose-1-phosphate adenyltransferase [EC:2.7.7.27]
pWS05 0002	<i>glgA</i>	+	389	1831	K00703	starch synthase [EC:2.4.1.21]
pWS05 0003	<i>glgP</i>	+	1838	4252	K00688	glycogen phosphorylase [EC:2.4.1.1]
pWS05 0035	<i>glgC</i>	+	38120	39268	K00975	glucose-1-phosphate adenyltransferase [EC:2.7.7.27]
pWS05 0036	<i>glgC</i>	+	39255	40424	K00975	glucose-1-phosphate adenyltransferase [EC:2.7.7.27]
pWS05 0037	<i>glgA</i>	+	40421	41863	K00703	starch synthase [EC:2.4.1.21]
pWS05 0038	<i>glgP</i>	+	41870	44284	K00688	glycogen phosphorylase [EC:2.4.1.1]

Table S20. The hydrophobicity, auto-aggregation, and co-aggregation of *Lactiplantibacillus plantarum* JS21

hydrophobicity	auto-aggregation	Co-aggregation			
		<i>E. coli</i> (ATCC 25922)	<i>E. coli</i> (K88)	<i>S. aureus</i> (CMCC 26003)	<i>L. monocytogenes</i> (CICC 21635)
60.04±0.96%	42.63±1.06%	31.69±0.51%	30.97±0.83%	44.92±0.30%	35.35±0.70%

Table S21. Tolerance of JS21 to simulated gastrointestinal fluids

Simulated gastric fluid(pH=2.0)			Simulated gastric fluid(pH3.0)		
Simulated Intestinal Fluid(pH=6.8)			Simulated Intestinal Fluid(pH=6.8)		
3h Survival rate (%)	3h Survival rate (%)	6h Survival rate (%)	3h Survival rate (%)	3h Survival rate (%)	6h Survival rate (%)
18.91%	173.72%	244.06%	143.75%	182.19%	205.48%

Table S22. JS21 Inhibition zone results of CFS against pathogens bacteria

Test Strain	Strain Code	Zone of Inhibition (±SD) (mm)			
		CFS	NC	Ampicillin	Kanamycin
<i>Escherichia coli</i>	ATCC 25922	16.35±0.04	0	11.17±0.07	19.85±0.04
<i>Escherichia coli</i>	K88	13.53±0.15	0	12.82±0.05	16.46±0.10
<i>Staphylococcus aureus</i>	CMCC 26003	16.78±0.11	0	31.72±0.14	17.43±0.03
<i>Listeria monocytogenes</i>	CICC 21635	14.80±0.08	0	10.8±0.04	18.51±0.04