

Table S1. General genome features of *L. plantarum* YY-112

	112_chr	112_plasmid1	112_plasmid2
Sequence length (bp)	3,346,642	72,756	22,510
G+C content (%)	44.53	39.51	36.2
ORF number	3174	83	27
ORF total length (bp)	2808279	54693	18060
ORF density (genes per kb)	0.948	1.141	1.199
Longest ORF length (bp)	9810	2190	1845
ORF average length (bp)	884.78	658.95	668.89
Intergenic region length (bp)	538363	18063	4450
ORF/Genome (%)	83.91	75.17	80.23
rRNA	16	0	0
tRNA	69	0	0
ncRNA	158	2	0

ORF total length: the number of bases occupied by ORF; ORF density: gene coding density (the number of genes present per 1kb base); ORF / Genome (coding percentage): ratio of total ORF length to genome length.

Table S2. Distribution of virulence factors in *L. plantarum* YY-112

VFDB name	ORF name	Related genes	Product	VF category
VF0244	chr_646	hasC [Streptococcus pyogenes M1 GAS]	UTP--glucose-1-phosphate uridylyltransferase	Immune modulation; Antiphagocytosis
VF0074	chr_669	clpP [Listeria monocytogenes EGD-e]	ATP-dependent Clp protease proteolytic subunit	Stress survival
VF0361	chr_996	cpsI [Enterococcus faecalis V583]	UDP-galactopyranose mutase	Immune modulation; Antiphagocytosis
VF0323	chr_996	glf [Campylobacter jejuni subsp. jejuni NCTC 11168]	UDP-galactopyranose mutase	Immune modulation; Antiphagocytosis
VF0361	chr_1040	cpsI [Enterococcus faecalis V583]	UDP-galactopyranose mutase	Immune modulation; Antiphagocytosis
VF0073	chr_1085	clpE [Listeria monocytogenes EGD-e]	ATP-dependent protease	Stress survival
VF0361	chr_1799	cpsA [Enterococcus faecalis V583]	undecaprenyl diphosphate synthase	Immune modulation; Antiphagocytosis
VF0350	chr_3052	bsh [Listeria monocytogenes EGD-e]	bile salt hydrolase	Stress survival
VF0274	plasmid1_64	cpsF [Streptococcus agalactiae 2603V/R]	polysaccharide biosynthesis protein CpsF	Immune modulation; Antiphagocytosis

Table S3. Distribution of CAZymes in *L. plantarum* YY-112

Class	Family	Gene
Glycoside Hydrolases	GH13	chr_152, chr_157, chr_166, chr_169, chr_18, chr_2041, chr_228, chr_23, chr_2369, chr_2764, chr_3134
	GH1	chr_2388, chr_2389, chr_2596, chr_2695, chr_3039, chr_3042, chr_3043, chr_3122, chr_389, chr_773
	GH25	chr_1215, chr_1559, chr_2116, chr_2417, chr_2663, chr_2795, chr_577, chr_583, chr_980 chr_2249, chr_2251, chr_3106, chr_3107,
	GH109	chr_3109, chr_3111, chr_693, chr_962, chr_983; plasmid1_33
	GH65	chr_1526, chr_159, chr_26, chr_3046
	GH73	chr_2276, chr_2710, chr_963
	GH78	chr_3001, chr_3003
	GH2; GH20; GH31; GH32; GH36; GH38; GH42; GH85; GH92; GH125	chr_3012; chr_3138; chr_3050; chr_164; chr_3014; chr_3124; chr_2999; chr_160; chr_3127; chr_3125
Glycosyl Transferases	GT2	chr_1004, chr_1018, chr_1038, chr_1039, chr_1267, chr_1352, chr_1613, chr_1816, chr_1840, chr_1880, chr_2333, chr_234, chr_2393, chr_365, plasmid1_51, plasmid1_72 chr_1002, chr_1015, chr_1016, chr_1089,
	GT4	chr_1090, chr_1109, chr_1116, chr_1118, chr_1842, chr_1843, chr_2112, chr_2286, chr_2445, chr_2446
	GT28	chr_1922, plasmid1_65
	GT51	chr_1244, chr_1545
	GT5; GT14; GT26; GT32; GT35	chr_21; chr_2115; chr_481; plasmid1_66; chr_22
Carbohydrate Esterases	CE1	chr_1553, chr_2267, chr_2288, chr_2546, chr_2937, chr_3033, chr_729
	CE10	chr_2524, chr_835, chr_854
	CE2; CE3; CE4; CE9; CE12	chr_2972; chr_1642; chr_2094; chr_479; chr_578
	AA6	chr_211, chr_2475, chr_2482, chr_828
Auxiliary Activities	AA3	chr_1253, chr_330, chr_944
	AA1-3; AA4; AA10	chr_317; chr_254; chr_1501

Carbohydrate- Binding Modules	CBM50	chr_1657, chr_1897, chr_2447, chr_2448, chr_2599, chr_2600, chr_265, chr_266, chr_2962
	CBM22; CBM40	chr_1209; chr_2588
Polysaccharide Lyases	PL3_1	chr_2762

Table S4. Genomic characterization of strain YY-112, selected *L. plantarum* and *L. pentosus*

Organism	Sample Name	Strain	CDS No.	Chromosome Size (Mb)	G+C content of chromosome (%)
<i>L. pentosus</i>	YY-112	YY-112	3343	3.346642	44.53
	GCF_002211885.1	SLC13	3154	3.52051	46.49
	GCF_003627295.1	ZFM222	3273	3.564857	46.40
	GCF_003627375.1	ZFM94	3252	3.564833	46.40
	GCF_003641185.1	DSM 20314	3272	3.622107	46.41
	GCF_016804305.1	MS031	3402	3.805124	46.07
	GCF_022701335.1	KZ0310	3469	3.873381	46.00
	GCF_025398935.1	Jan-68	3148	3.482151	46.53
	GCF_026222675.1	OHF 23	3212	3.622037	46.41
	GCF_004028315.1	13_3	3087	2.991504	44.85
<i>L. plantarum</i>	GCF_004028335.1	12_3	3235	3.213344	44.61
	GCF_004101505.1	SRCM103357	3307	3.277486	44.60
	GCF_004101545.1	SRCM103361	3077	3.163668	44.71
	GCF_019076805.1	XJ25	2919	3.169974	44.69
	GCF_019399915.1	41P	3075	3.210905	44.64
	GCF_019425695.1	DW12	2942	3.217574	44.63
	GCF_029637825.1	SPC-SNU-72-1	3116	3.129268	44.72

Organism: species name; Sample Name: sample name; Strain: strain number; CDS No.: number of CDS; Chromosome Size (Mb): size of chromosome; GC content of chromosome (%): GC content of chromosome.

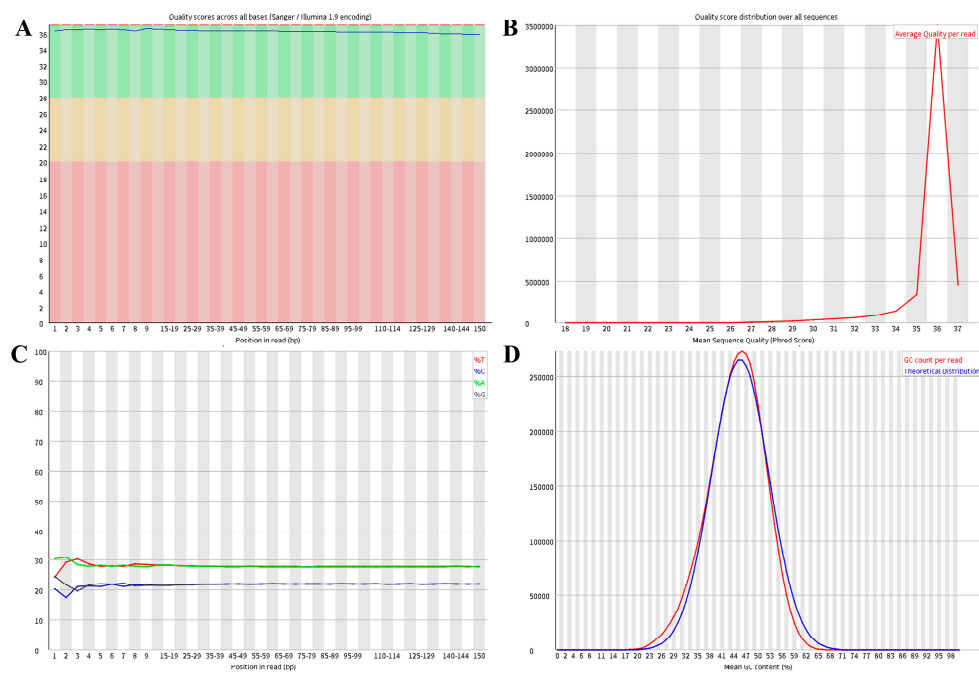


Figure S1. Quality control chart of partial next-generation sequencing data. (A) Per base sequence quality; (B) Per sequence quality scores; (C) Per base sequence content; (D) Per sequence GC content, the blue line is the theoretical distribution, whereas the red line is the sample distribution.

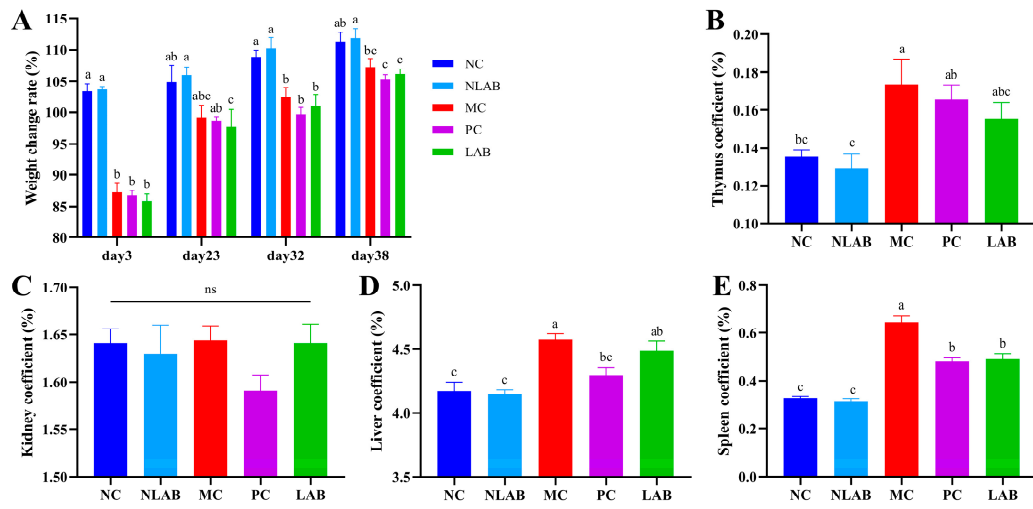


Figure S2. Effects of *L. plantarum* YY-112 on BW and organ coefficients. (A) BW; (B) Thymus coefficient; (C) Kidney coefficient; (D) Liver coefficient; (E) Spleen coefficient. NC, normal saline; NLAB, 1.0×10^9 CFU/mL *L. plantarum* YY-112; MC, normal saline; PC, 40 mg/kg LMS; LAB, 1.0×10^9 CFU/mL *L. plantarum* YY-112.