

Supplement Material

Gene	Primer
16S rRNA	F:GGAGTACGGTCGCAAGATTA R: CTAGCGGATTCTCTCAATGTCAA
CagA	F:ATGCCGCCTTTTTCACAACC R:CTGCTTGAATGCGCCAAACT
IL-6	F:CACTGGTCTTTTGGAGTTTGAG R:GGACTTTTGTACTCATCTGCAC

Supplementary Table 1 Primer of 16S rRNA, CagA and IL-6. F indicates pre-primer, and R indicates pro-primer.

Name	Species	Percent identity	Gender	Age
LG-1	<i>Lactobacillus gasseri</i>	99.51%	Male	48
LG-2	<i>Lactobacillus gasseri</i>	98.61%	Female	33
LG-3	<i>Lactobacillus gasseri</i>	99.71%	Female	45
LG-4	<i>Lactobacillus gasseri</i>	99.71%	Female	51
LG-5	<i>Lactobacillus gasseri</i>	98.11%	Female	44
LG-6	<i>Lactobacillus gasseri</i>	99.71%	Male	56
LG-8	<i>Lactobacillus gasseri</i>	99.61%	Male	31
LPG-9	<i>Lactobacillus gasseri</i>	99.79%	Male	43
LO-1	<i>Lactobacillus oris</i>	99.50%	Female	34
LO-2	<i>Lactobacillus oris</i>	99.47%	Female	59
LV-1	<i>Lactobacillus vaginalis</i>	99.14%	Male	35

LP-1	<i>Lactobacillus plantarum</i>	97.12%	Male	56
------	--------------------------------	--------	------	----

Supplementary Table 2. Information of isolated *Lactobacillus* strains. A total of 12 *Lactobacillus* strains were isolated from the gastric mucosa of 12 healthy donors, consisting of 7 men and 5 women, with a median age of 44.6. None of them had *Helicobacter pylori* (*H. pylori*) infection. The percent identity represents the result of the blast with 16S rRNA sequencing.

LV-1	+	+	+	+	+	+	+	+	+
LRX-01	+	+	+	+	+	+	+	+	-

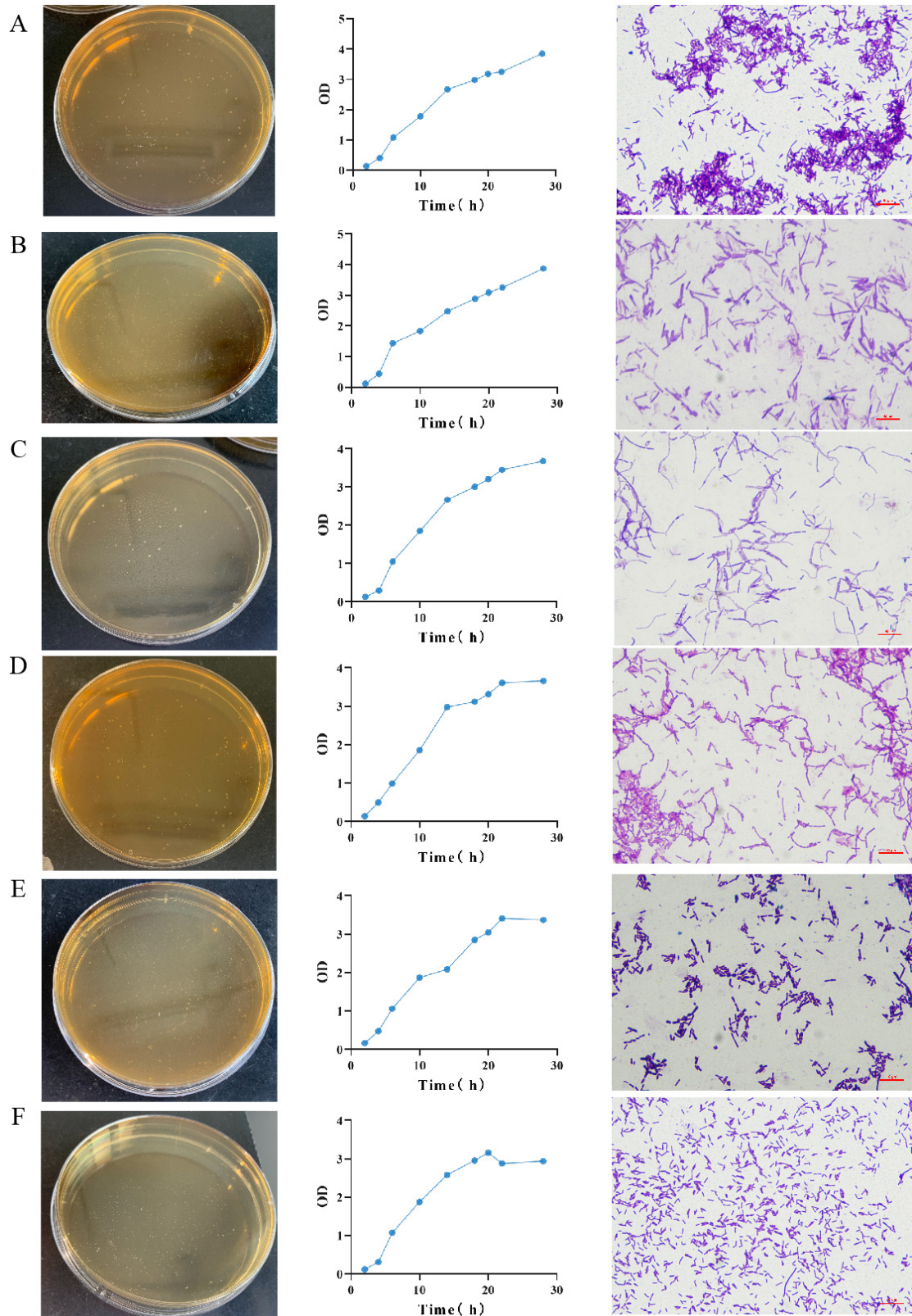
Supplementary Table 3 Results of sugar fermentation test of isolated *Lactobacillus* strains.

Blood index	Control	LPG-9	P value
White blood cell count($10^9/L$)	2.233 ± 1.004	3.667 ± 0.6888	0.3043
Lymphocytes ($10^9/L$)	1.433 ± 0.4096	2.4 ± 0.4702	0.1090
Red blood cell count ($10^{12}/L$)	8.997 ± 0.6067	9.170 ± 0.499	0.8071
Hemoglobin (g/L)	125 ± 10.15	93.75 ± 42.86	0.1062
Platelets ($10^9/L$)	232.3 ± 144.9	431.3 ± 104.6	0.6851

Supplementary Table 4 Routine blood indices analysis of mice in the acute animal toxicity experiment with LPG-9 (n=3).

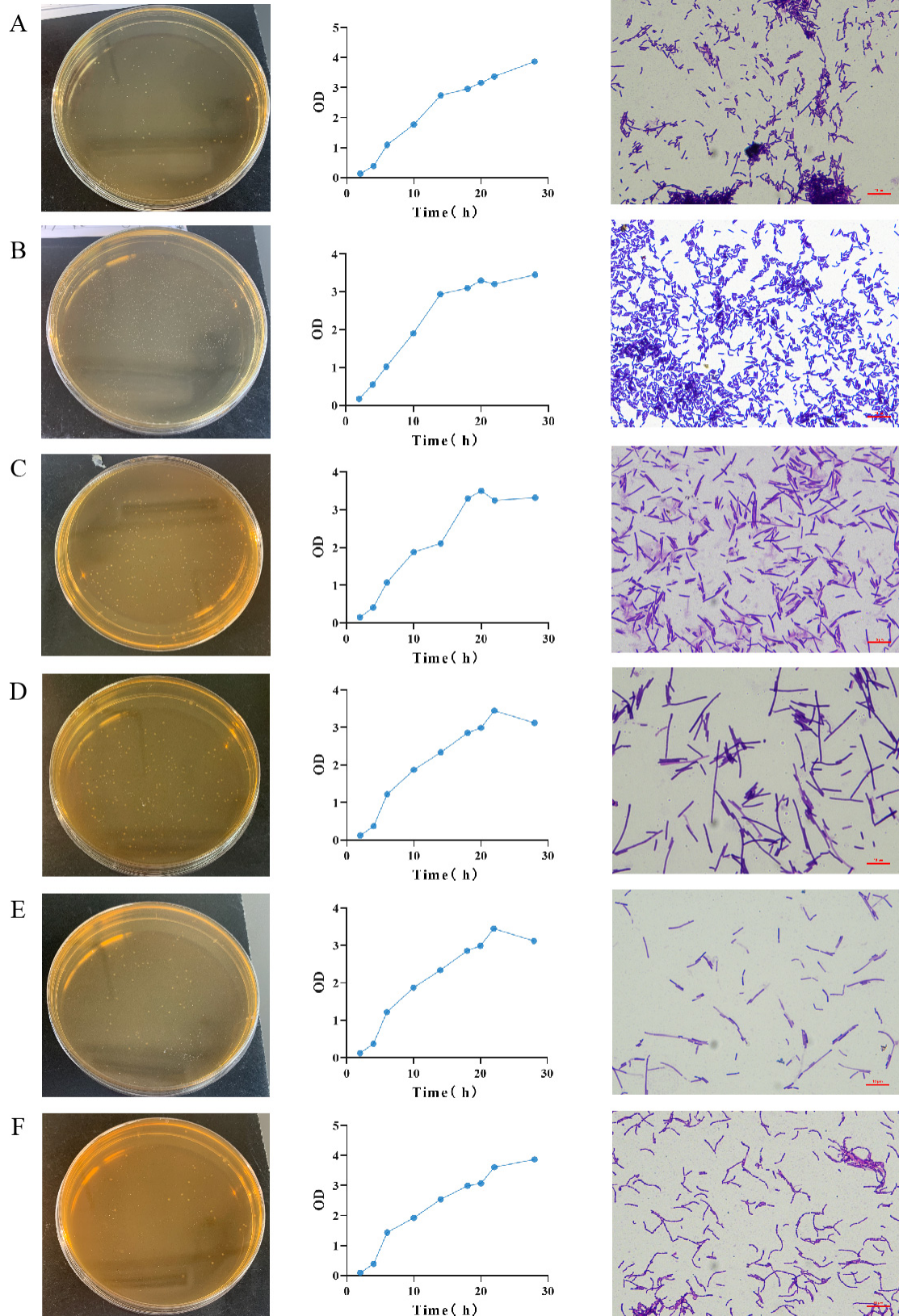
Attribute	Value
Genome size (bp)	1,974,286
Number of contigs	2
DNA G + C content (%)	34.91
Gene number	1,890
Total Gene size (bp)	1,773,453
Average Gene Length (bp)	938
Total repetitive sequence length (bp)	5,560
Repetitive sequence content (%)	0.28
rRNA	15
tRNA	55
CRISPR arrays	4
Prophage	4

Supplementary Table 5 General genome features of LPG-9.



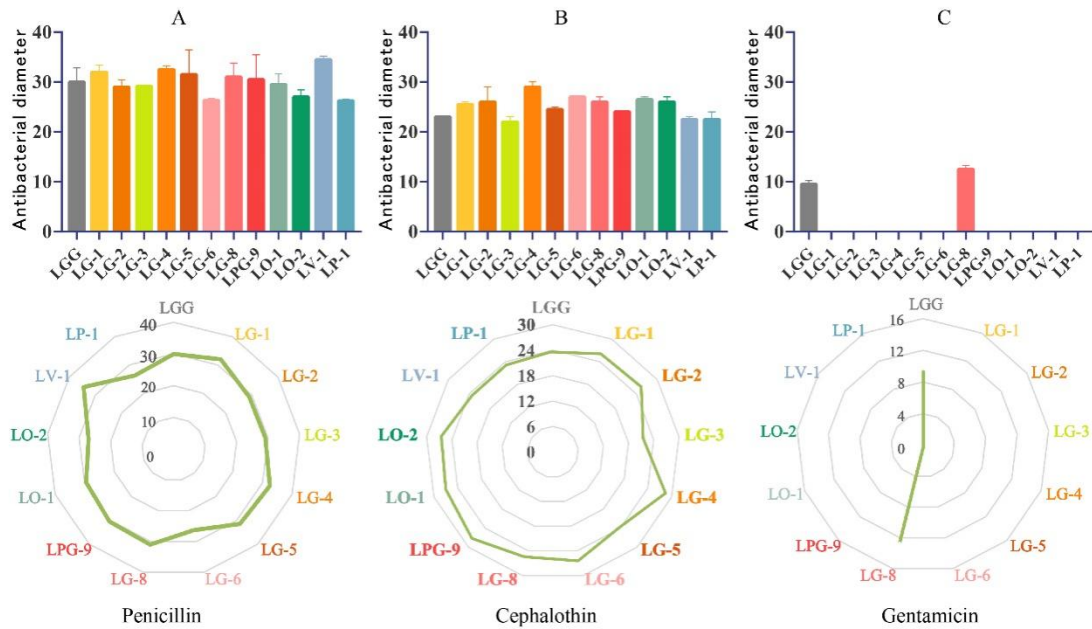
Supplementary Fig. 1. Identification process of human gastro-derived *Lactobacillus*. The results of colonial morphology, growth kinetics and Gram staining with *Lactobacillus* strains (A: LG-1; B:

LG-2; C: LG-3; D: LG-4; E: LG-5; F: LG-6).



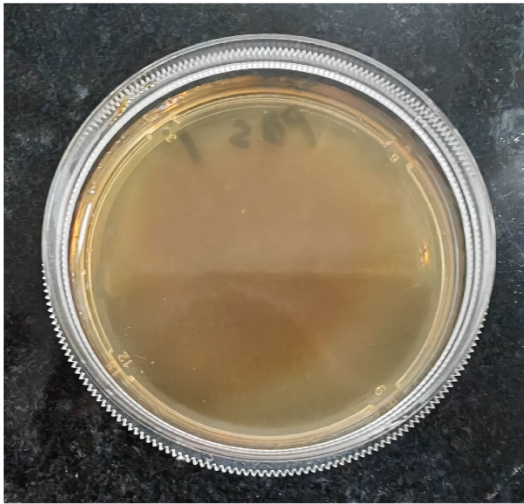
Supplementary Fig. 2. Identification process of human gastro-derived *Lactobacillus*. The results

of colonial morphology, growth kinetics and Gram staining with *Lactobacillus* strains (A: LG-8; B: LPG-9; C: LO-1; D: LO-2; E: LV-1; F: LP-1).

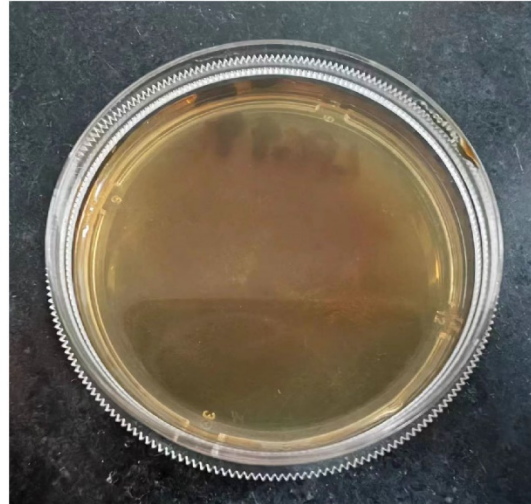


Supplementary Fig. 3. Antibiotic sensitivity. A: Penicillin; B: Cephalothin; C: Gentamicin. If the diameter of the inhibition zone was larger than the standard value (penicillin is more than 29mm, cephalosporin is more than 18mm, gentamicin is more than 15mm), the bacteria was considered sensitive to the drug, otherwise was resistant. All the 12 strains of isolated *Lactobacillus* and LGG tested in this study were sensitive to penicillin and cephalosporin.

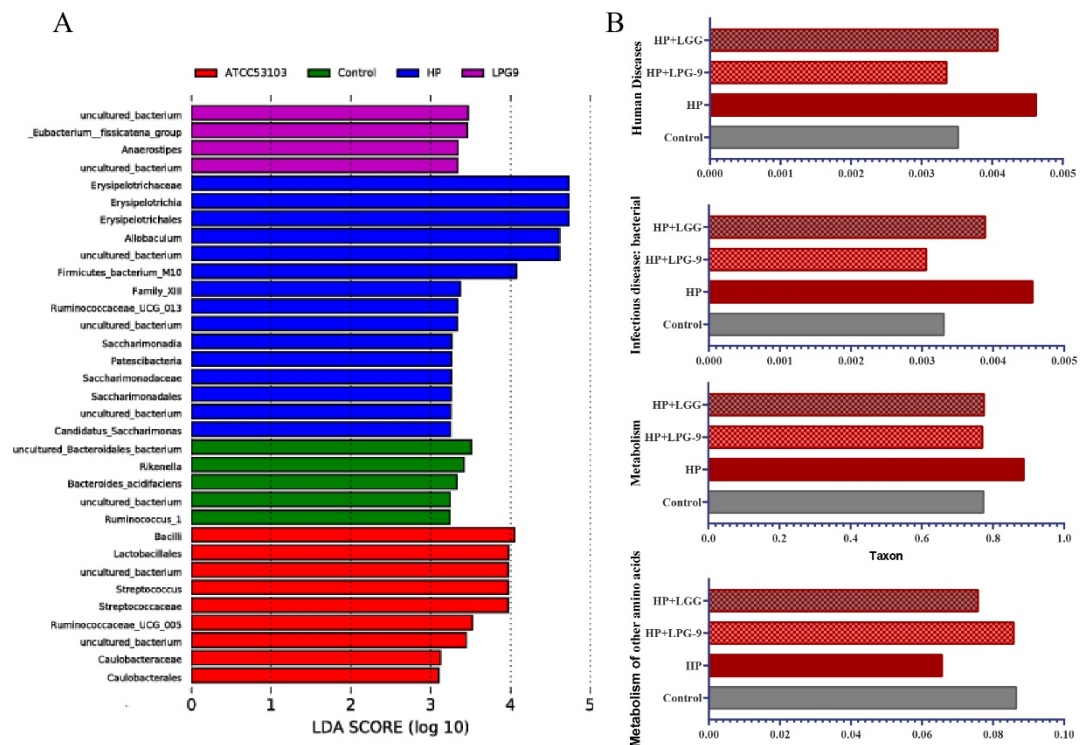
A



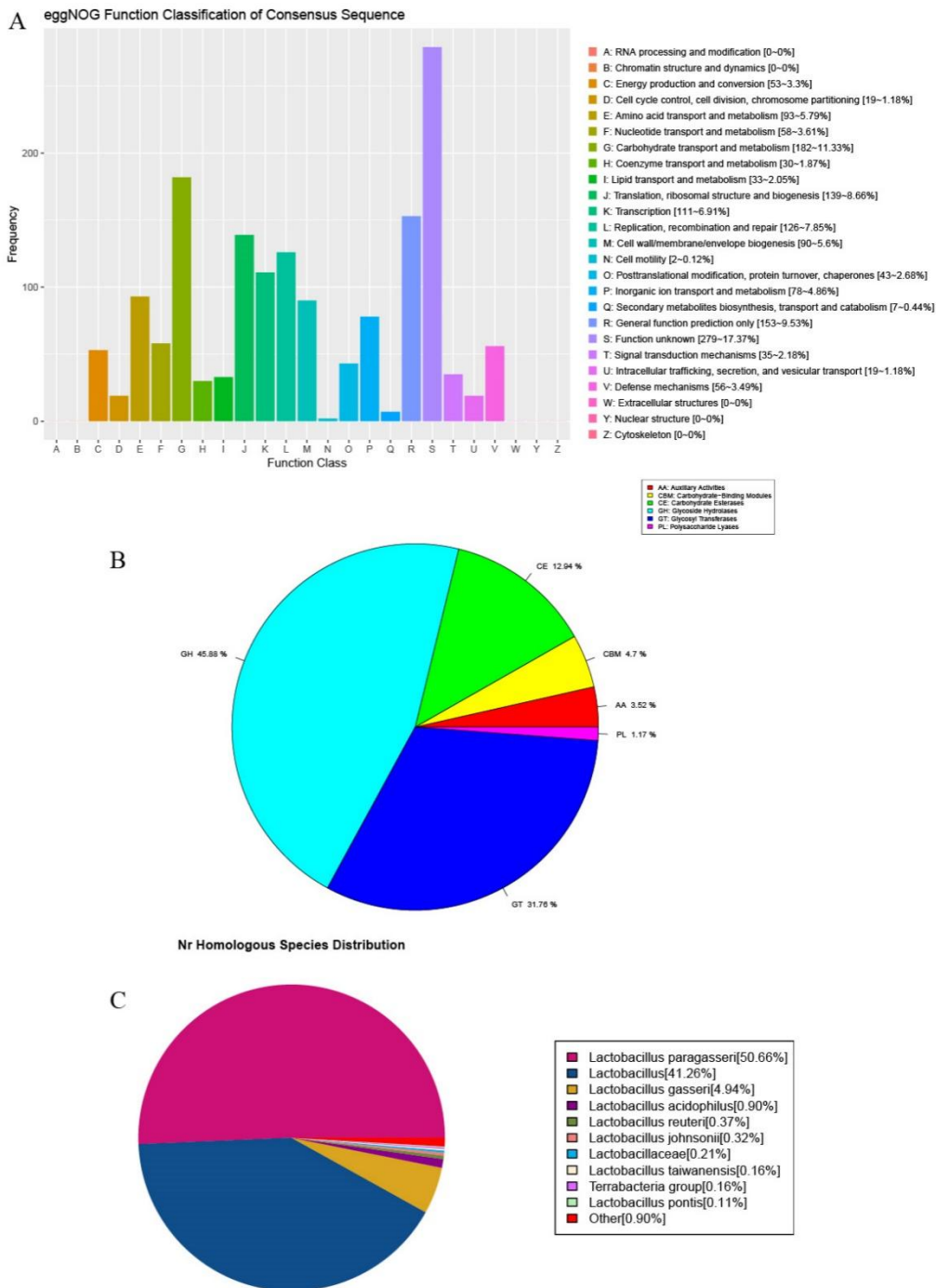
B



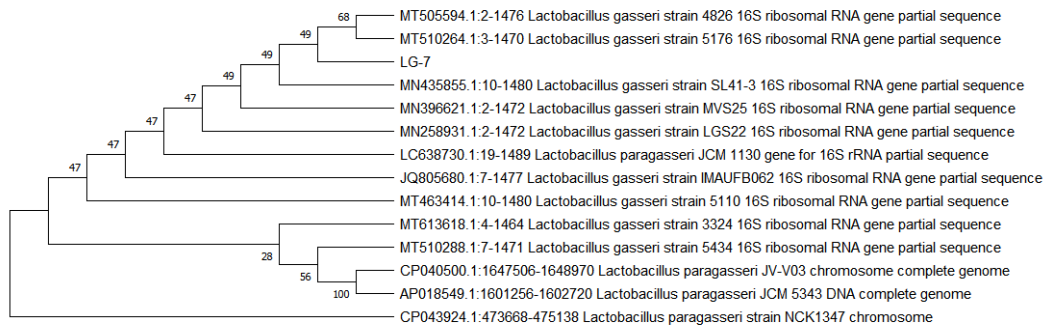
Supplementary Fig.4. Safety evaluation of LPG-9. The whole blood of C57 (n=3) was spread on MRS agar. No bacterial colony was found in control groups (A) or LPG-9 groups (B).



Supplementary Fig. 5. The homeostasis effect of gastric flora and whole genome sequencing with LPG-9. (A) LEfSe analysis of Gastric bacteria in mice. (B) Relative abundance levels of predicted gene functions related to KEGG pathways.



Supplementary Fig. 6. Whole genome sequencing with LPG-9. (A) Statistical map of functional classification of eggNOG functional genes. (B) Proportion plot of carbohydrate enzyme distribution. (C) Nr homologous species distribution. Different colors represent different species, reflecting the species distribution of the aligned sequences in the Nr database.



Supplementary Fig. 7. Phylogenomic analysis of LPG-9. Phylogenetic relationship between LPG-9 and other *L. gasseri* and *L. paragasseri* strains. Phylogenetic tree construction was based on the pairwise sequence similarities of the 16S rRNA sequences mined from the complete representative genome sequences and draft genome sequence of LPG-9. Minimum evolution phylogenetic dendrogram shows relationships of representative 16S rRNA gene sequences of LPG-9 among closely related species. Numbers at branch points depict bootstrap support based on this study.