

**Table S1.** LFM medium composition. Yeast Nitrogen Base (Sigma-Aldrich, Merck KGaA, Darmstadt, GE) supplemented with:

Pyridoxal-5'-phosphate	40 mg/L
D-Glucose	20g/L
L-Cysteine	100 µM
L-Phenylalanine	100 µM
L-Histidine	100 µM
L-Glycine	100 µM
L-Glutamic acid	100 µM

**Table S2.** Antimicrobial activity at 37 °C by cell-free supernatant (CFS) from the five *Lp. plantarum* strains against different indicator bacteria. The data (mean ± SD; n = 3) are expressed as zone of inhibition-ZOI (mm). Different lowercase letters (a–c) in each row indicate significant differences ( $p < 0.05$ ).

Indicator bacteria	<i>Lp. plantarum</i> strains					
	LP 8	LP 25	LP 86	LP 95	LP 100	ATCC 14917
<i>P. aeruginosa</i> ATCC 27853	24.0 ± 3.0 <sup>a</sup>	21.0 ± 1.0 <sup>a</sup>	20.0 ± 2.0 <sup>a</sup>	19.0 ± 2.0 <sup>a</sup>	18.0 ± 3.0 <sup>a</sup>	20.0 ± 2.0 <sup>a</sup>
<i>E. coli</i> ATCC 11775	9.0 ± 3.0 <sup>a</sup>	0.0 ± 0.0 <sup>b</sup>	9.0 ± 2.0 <sup>a</sup>	9.0 ± 1.0 <sup>a</sup>	10.0 ± 1.0 <sup>a</sup>	7.0 ± 3.0 <sup>a</sup>
<i>P. mirabilis</i> ATCC 29906	8.0 ± 2.0 <sup>b</sup>	0.0 ± 0.0 <sup>c</sup>	13.0 ± 2.0 <sup>a</sup>	12.0 ± 3.0 <sup>a</sup>	14.0 ± 1.0 <sup>a</sup>	9.0 ± 3.0 <sup>a</sup>
<i>E. faecalis</i> ATCC 29212	8.0 ± 1.0 <sup>a</sup>	9.0 ± 1.0 <sup>a</sup>	7.0 ± 2.0 <sup>a</sup>	10.0 ± 1.0 <sup>a</sup>	9.0 ± 3.0 <sup>a</sup>	7.0 ± 2.0 <sup>a</sup>
<i>S. aureus</i> ATCC 29213	0.0 ± 0.0 <sup>c</sup>	0.0 ± 0.0 <sup>c</sup>	7.0 ± 1.0 <sup>a</sup>	8.0 ± 1.0 <sup>a</sup>	8.0 ± 2.0 <sup>a</sup>	4.0 ± 2.0 <sup>b</sup>

**Table S3.** GABA production (pmol GABA/µg BSA Eq.) from the five *Lp. plantarum* strains grown in LFM medium with and without L-glutamic acid (GLU). All values are expressed as mean ± standard deviation (n = 3). Different lowercase letters (a–d) in each row indicate significant differences ( $p < 0.05$ ).

GABA production of <i>Lp. plantarum</i> strains						
LFM medium	LP 8	LP 25	LP 86	LP 95	LP 100	ATCC 14917
without GLU	0.068±0.011 <sup>b</sup>	0.060±0.011 <sup>b</sup>	0.047±0.008 <sup>b</sup>	0.055±0.008 <sup>b</sup>	0.088±0.006 <sup>a</sup>	0.116±0.031 <sup>a</sup>
with GLU	0.781±0.055 <sup>c</sup>	0.345±0.026 <sup>d</sup>	1.004±0.063 <sup>c</sup>	2.227±0.118 <sup>a</sup>	1.350±0.111 <sup>b</sup>	1.204±0.134 <sup>b</sup>