

Supplementary Materials

Dissecting of the AI-2/LuxS Mediated Growth Characteristics and Bacteriostatic Ability of *Lactiplantibacillus plantarum* SS-128 by Integration of Transcriptomics and Metabolomics

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Table S1. The mean inhibition zone diameter (mm) of CFS of *L. plantarum* against the *E. coli*, *S. baltica*, *S. aureus* and *A. johnsonii*.

Time (h)		<i>E. coli</i>	<i>S. aureus</i>	<i>S. baltica</i>	<i>A. johnsonii</i>
8	SS-128	9.67±0.07 ^e	9.79±0.11 ^c	10.41±0.08 ^c	9.24±0.13 ^c
	Δ LuxS/SS-128	9.08±0.02 ^f	9.84±0.08 ^c	10.12±0.14 ^f	9.19±0.06 ^c
14	SS-128	13.14±0.15 ^b	13.77±0.14 ^a	13.25±0.21 ^c	14.27±0.05 ^b
	Δ LuxS/SS-128	12.08±0.19 ^d	13.40±0.05 ^b	12.96±0.01 ^d	13.08±0.14 ^d
24	SS-128	13.95±0.03 ^a	13.68±0.12 ^a	16.41±0.03 ^a	14.74±0.06 ^a
	Δ LuxS/SS-128	12.63±0.04 ^c	13.56±0.14 ^a	15.18±0.08 ^b	13.86±0.01 ^c

Means (n=3) in the same column without a common superscript letter (a-f) are statistically different, $P < 0.05$.

Table S2. Comparison of statistical results and reference genome.

Sample	SS128-1	SS128-2	SS128-3	Δ luxS/SS128-1	Δ luxS/SS128-2	Δ luxS/SS128-3
Total_reads	6648096	8189065	8086430	8077747	7498249	7251646
Mapped_reads	6253360	7708836	7613056	7620400	7078502	6851383
Map_PCG_Sn	74%	67%	69%	65%	64%	68%
Map_PCG_At	2%	2%	2%	3%	2%	2%
Map_rRNA_Sn	0%	0%	0%	0%	0%	0%
Map_rRNA_At	0%	0%	0%	0%	0%	0%
Map_tRNA_Sn	0%	0%	0%	0%	0%	0%
Map_tRNA_At	0%	0%	0%	0%	0%	0%
Map_miRNA_Sn	17%	22%	21%	22%	24%	20%
Map_miRNA_At	0%	1%	0%	1%	1%	1%
Map_un_region	8%	8%	7%	9%	9%	9%

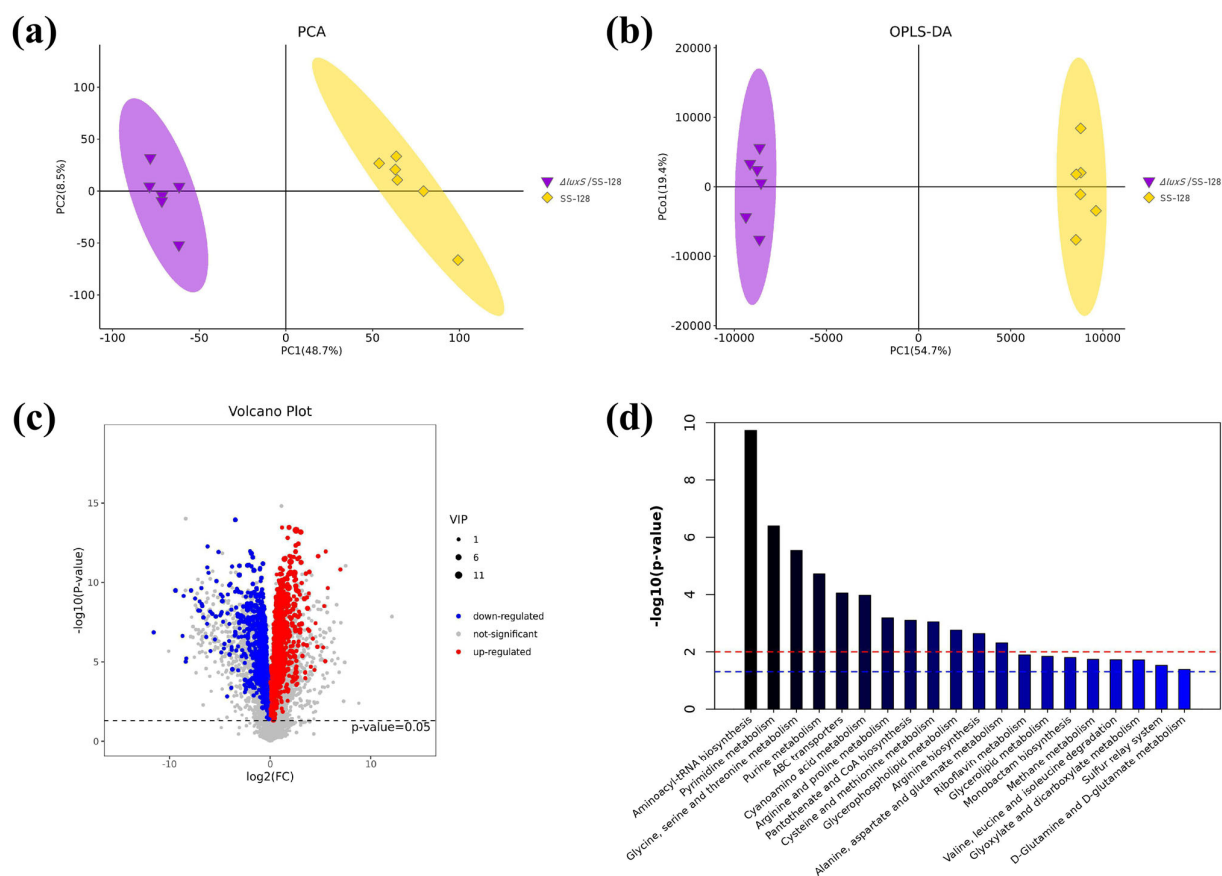


Figure S1. Changes in the metabolite contents compared the *luxS* mutant group with the control by LC-MS. The PCA (a), OPLS-DA (b), volcano plot (c) and metabolic pathway enrichment map-Top 20 (d) between $\Delta luxS/SS-128$ and SS-128 under the cut off of $P\text{-value} < 0.05$ ($\Delta luxS/SS-128$ vs SS-128). The red line and blue line in (d) indicate $P = 0.01$ and 0.05 , respectively.