

Supplementary Materials for

Ingestion of *Lacticaseibacillus rhamnosus* Fmb14 prevents depression-like behavior and brain neural activity via the microbiota-gut-brain axis

Hongyuan Zhao¹, Xiaoyu Chen¹, Li Zhang³, Chao Tang¹, Fanqiang Meng¹,
Libang Zhou¹, Ping Zhu¹, Zhaoxin Lu^{1*}, Yingjian Lu^{2*}

*Corresponding author. Email: fmb@njau.edu.cn

Table 1. The abbreviations of regulated pathway of control to model group

Pathway	Description	logFC	P-value
PWY0-1338	polymyxin resistance	2.373	0.0006 07
PWY-7391	isoprene biosynthesis II (engineered)	2.166	0.0182 4
CODH-PWY	reductive acetyl coenzyme A pathway	1.719	0.0040 96
GLUCOSE1PMETAB-PWY	glucose and glucose-1-phosphate degradation	1.681	0.0044 88
SO4ASSIM-PWY	sulfate reduction I (assimilatory)	1.024	0.0018 05
PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	0.9987	0.0158
PWY-5863	superpathway of phylloquinol biosynthesis	0.9791	0.0167 8
PYRIDOXSYN-PWY	pyridoxal 5'-phosphate biosynthesis I	0.8841	0.0213 5
PWY0-1241	ADP-L-glycero-β-D-manno-heptose biosynthesis	0.8619	0.0208 9
PWY-7328	superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis	0.8474	0.0045 22
PWY0-845	superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	0.8103	0.0172 8
PWY-5345	superpathway of L-methionine biosynthesis (by sulfhydrylation)	0.783	0.0053 29
SULFATE-CYS-PWY	superpathway of sulfate assimilation	0.7508	0.0072

	and cysteine biosynthesis		19
PWY-7539	6-hydroxymethyl-dihydropterin diphosphate biosynthesis III (Chlamydia)	-0.6423	0.0216 9
SER-GLYSYN-PWY	superpathway of L-serine and glycine biosynthesis I	-0.657	0.0006 59
PYRIDNUCSAL-PWY	NAD salvage pathway I	-0.6619	0.0162
PWY-6182	superpathway of salicylate degradation	-0.6652	0.0060 97
P4-PWY	superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	-0.6674	0.0235 3
ANAEROFrucAT-PWY	homolactic fermentation	-0.6695	0.0054 61
PROTocatechuate-Ortho-Cleavage-PWY	protocatechuate degradation II (ortho-cleavage pathway)	-0.6933	0.0113 8
PWY0-781	aspartate superpathway	-0.6979	0.0204 8
ASPASN-PWY	superpathway of L-aspartate and L-asparagine biosynthesis	-0.6999	0.0153
PWY0-1586	peptidoglycan maturation (meso-diaminopimelate containing)	-0.7036	0.0041 41
TRPSYN-PWY	L-tryptophan biosynthesis	-0.7049	0.0123 9
DAPLYSINESYN-PWY	L-lysine biosynthesis I	-0.7128	0.0063 96
GLYCOGENSYNTH-PWY	glycogen biosynthesis I (from ADP-D-Glucose)	-0.7213	0.0055 79
P23-PWY	reductive TCA cycle I	-0.7653	0.0156 5
PWY-5180	toluene degradation I (aerobic) (via o-cresol)	-0.7707	0.0126 9
PWY-5182	toluene degradation II (aerobic) (via 4-methylcatechol)	-0.7707	0.0126 9
P221-PWY	octane oxidation	-0.7823	0.0246
PWY-7242	D-fructuronate degradation	-0.7948	0.0082 8
PWY-6317	galactose degradation I (Leloir pathway)	-0.7966	0.0102 8
PWY-5347	superpathway of L-methionine biosynthesis (transsulfuration)	-0.8039	0.0053 31
PENTOSE-P-PWY	pentose phosphate pathway	-0.8129	0.0072
MET-SAM-PWY	superpathway of S-adenosyl-L-methionine biosynthesis	-0.8157	0.0071 17

PWY-621	sucrose degradation III (sucrose invertase)	-0.8228	0.0046 16
PWY-6507	4-deoxy-L-threo-hex-4-enopyranuronate degradation	-0.8299	0.0222 1
HOMOSER-METSYN-PWY	L-methionine biosynthesis I	-0.833	0.0061 02
PWY-5028	L-histidine degradation II	-0.9112	0.0028 67
PWY-722	nicotinate degradation I	-0.9209	0.0089 18
P281-PWY	3-phenylpropanoate degradation	-0.9298	0.0086 74
GALACTUROCAT-PWY	D-galacturonate degradation I	-0.9513	0.0015 22
PWY-5505	L-glutamate and L-glutamine biosynthesis	-0.9629	0.0010 51
GALACT-GLUCUROCAT-PWY	superpathway of hexuronide and hexuronate degradation	-1.027	0.0002 5
GLUCUROCAT-PWY	superpathway of β-D-glucuronide and D-glucuronate degradation	-1.041	0.0002 58
PWY-6478	GDP-D-glycero-α-D-mannoheptose biosynthesis	-1.187	0.0121 4
PWY-5705	allantoin degradation to glyoxylate III	-1.379	0.0004 56
NAD-BIOSYNTHESIS-II	NAD salvage pathway II	-1.406	0.0063 17
PWY-6731	starch degradation III	-1.549	0.0013 32
P341-PWY	glycolysis V (Pyrococcus)	-1.896	0.0017 3

Table 2. The abbreviations of regulated pathway of control to H-treat group

Pathway	Description	logFC	P-value
METH-ACETATE-PWY	methanogenesis from acetate	3.419	2.51E-09
SUCSYN-PWY	sucrose biosynthesis I (from photosynthesis)	0.6402	0.000343
PWY-7347	sucrose biosynthesis III	0.2552	0.000347

Table 3. The abbreviations of regulated pathway of control to M-treat group

Pathway	Description	logFC	P-value
PWY-1361	benzoyl-CoA degradation I (aerobic)	3.093	6.07E-05

GLUCOSE1PMETAB-PWY	glucose and glucose-1-phosphate degradation	2.025	0.002773
PWY-6404	superpathway of mycolyl-arabinogalactan-peptidoglycan complex biosynthesis	1.415	1.43E-07
SO4ASSIM-PWY	sulfate reduction I (assimilatory)	1.128	0.000465
PYRIDOXSYN-PWY	pyridoxal 5'-phosphate biosynthesis I	1.069	0.00056
PWY-7328	superpathway of UDP-glucose-derived O-antigen building blocks biosynthesis	1.065	4.1E-06
PWY0-845	superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	1.064	1.99E-05
PWY-7254	TCA cycle VII (acetate-producers)	1.003	0.000152
PWY-5345	superpathway of L-methionine biosynthesis (by sulfhydrylation)	0.8744	0.002509
SULFATE-CYS-PWY	superpathway of sulfate assimilation and cysteine biosynthesis	0.7876	0.001119
PWY-5392	reductive TCA cycle II	0.5427	2.33E-06
PENTOSE-P-PWY	pentose phosphate pathway	-0.6776	0.001585
GLYCOCAT-PWY	glycogen degradation I (bacterial)	-0.7002	0.002792
SER-GLYSYN-PWY	superpathway of L-serine and glycine biosynthesis I	-0.7256	0.001903
MET-SAM-PWY	superpathway of S-adenosyl-L-methionine biosynthesis	-0.8179	0.00152
PWY-1541	superpathway of taurine degradation	-1.026	0.001825
GALACT-GLUCUROCAT-PWY	superpathway of hexuronide and hexuronate degradation	-1.221	0.001255
GLUCUROCAT-PWY	superpathway of β-D-glucuronide and D-glucuronate degradation	-1.236	0.000633
GALACTUROCAT-PWY	D-galacturonate degradation I	-1.241	0.002675
PWY-3661	glycine betaine degradation I	-2.841	0.000684

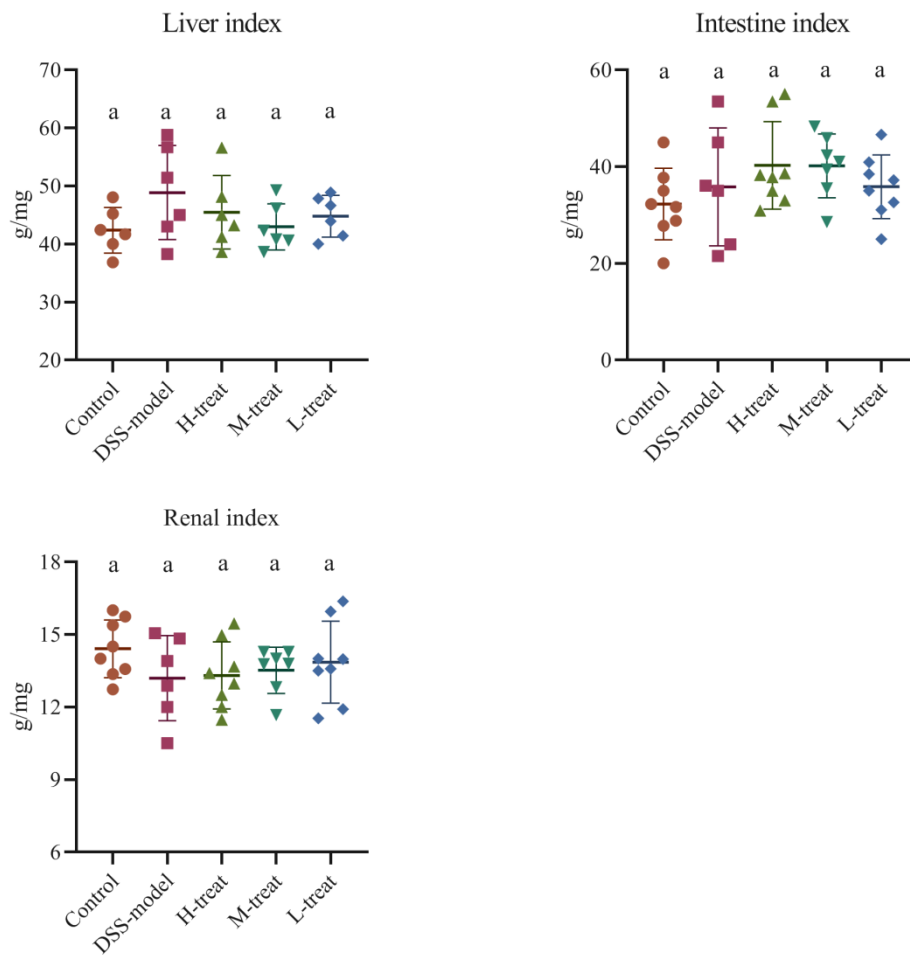


Figure 1. The effect of Fmb14 treatment on organ index of DSS-induced mice. The mean \pm SD ($n > 6$ per group) was represented by bars, different lowercase letters represent significant differences at $p < 0.05$, labels a to d represent lower to upper levels, respectively.

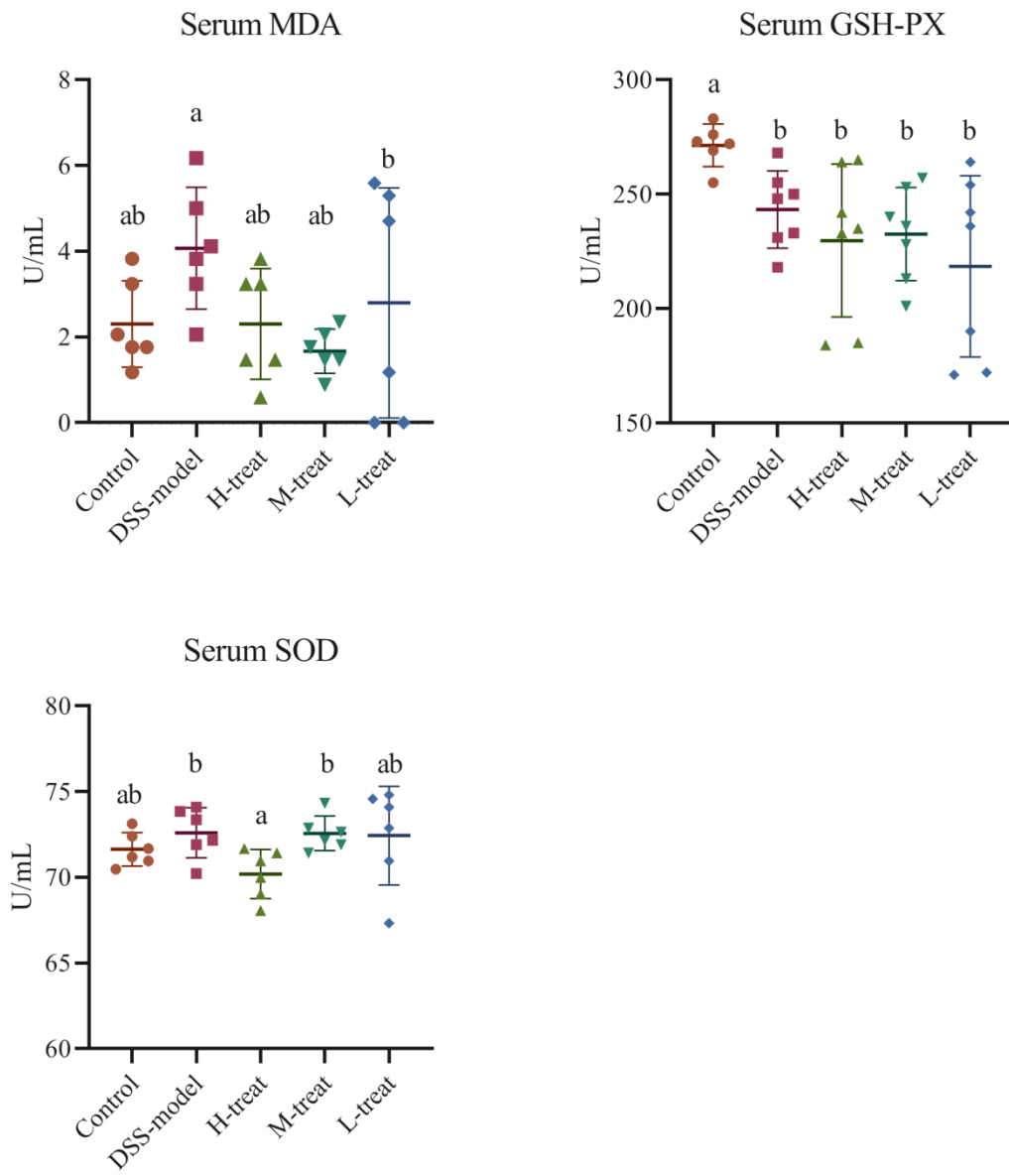


Figure 2. The effect of Fmb14 treatment on serum antioxidant of DSS-induced mice. The mean \pm SD ($n > 6$ per group) was represented by bars, different lowercase letters represent significant differences at $p < 0.05$, labels a to d represent lower to upper levels, respectively.

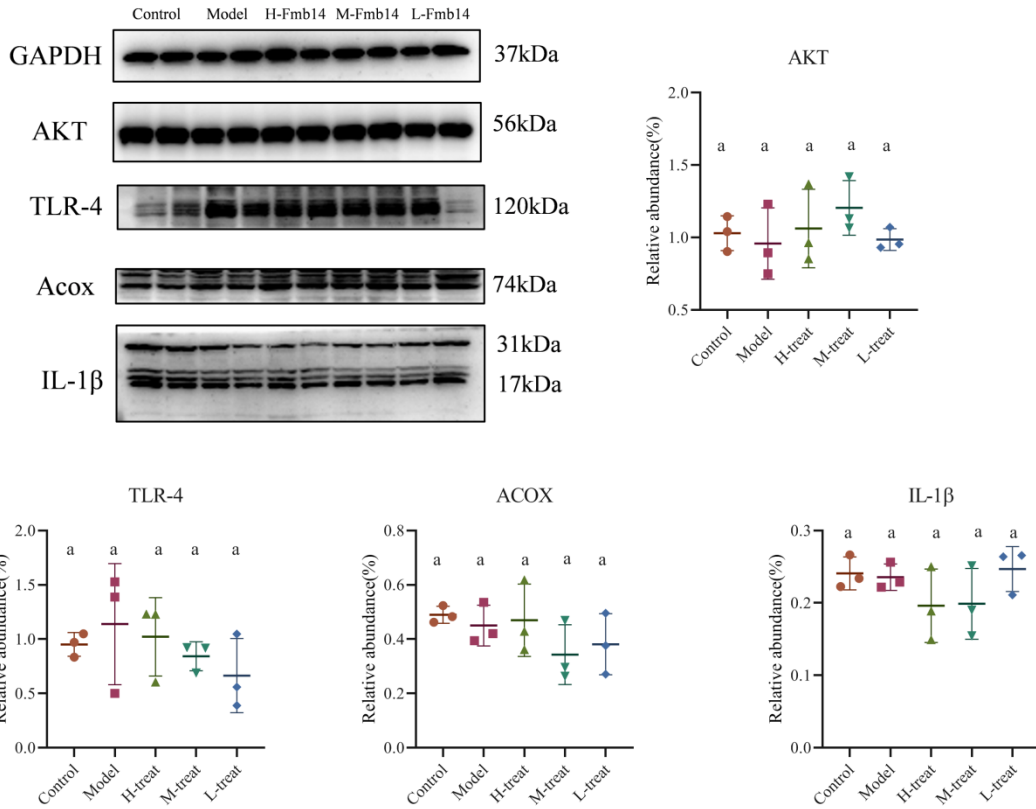


Figure 3. The effect of Fmb14 treatment on brain biomarkers of DSS-induced mice. The mean \pm SD (n >3 per group) was represented by bars, different lowercase letters represent significant differences at $p < 0.05$, labels a to d represent lower to upper levels, respectively.

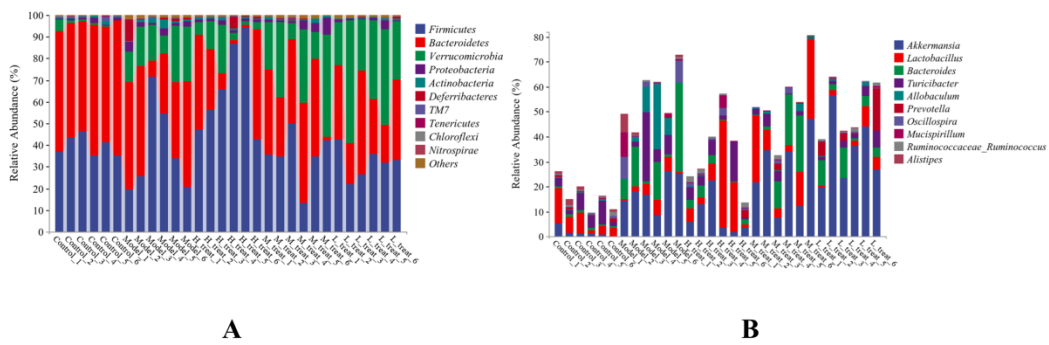


Figure 4. Effects of *L. rhamnosus* Fmb14 treatment on the microbial diversity of the gut microbiota in mice at Phylum(A) and Genus (B) levels.

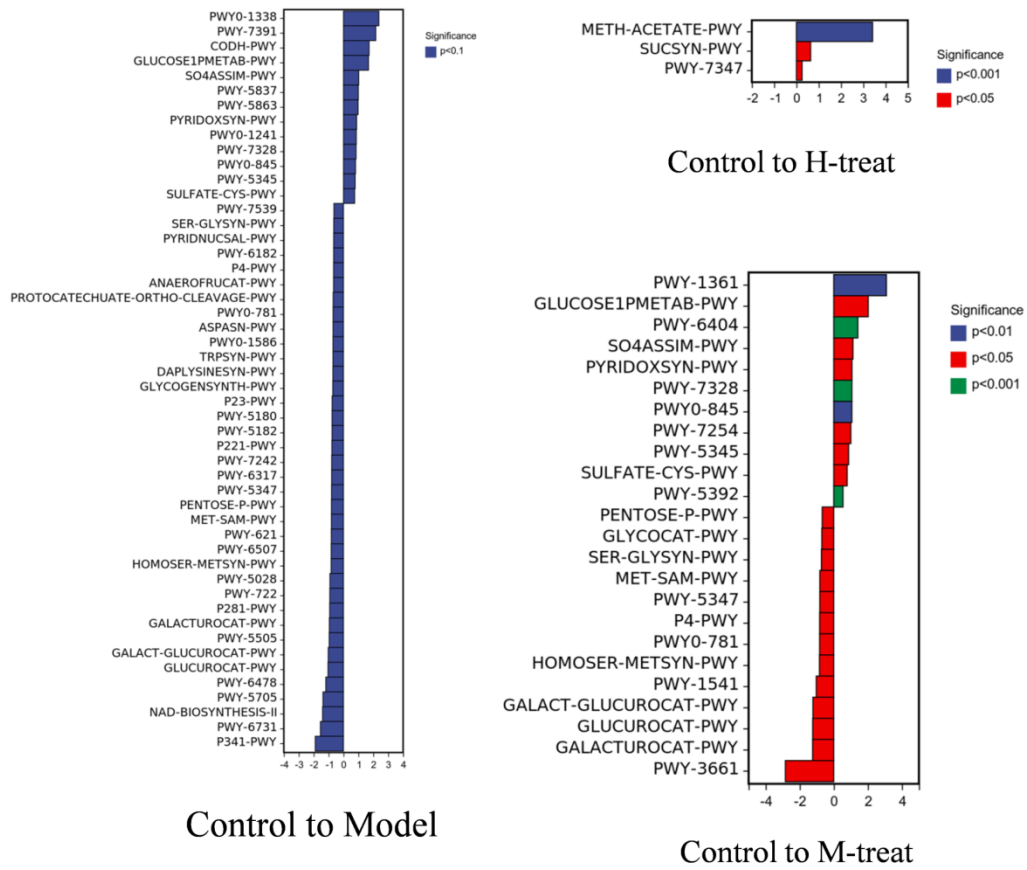


Figure 5. Effects of *L. rhamnosus* Fmb14 treatment on the metabolism pathways of the gut microbiota in mice.