



Figure S1. Effects of *L. paracasei* subsp. *paracasei* DSM 27449 on glucose tolerance and serum lipid profile in letrozole-induced PCOS-like rats. (A) Fasting blood glucose and (B) fasting insulin levels in the rats. (C) The homeostasis model assessment of insulin resistance (HOMA-IR) index was calculated using the formula: [fasting glucose levels (mmol/L)] * [fasting insulin (mIU/mL)]/22.5. (D) Blood glucose levels from oral glucose tolerance test (OGTT). (E) The area under the curve (AUC) of blood glucose levels was calculated. The levels of (F) triglyceride, (G) total cholesterol, (H) high-density lipoprotein (HDL)-cholesterol, and (I) low-density lipoprotein (LDL)-cholesterol. N = 6–7 per group, * $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$ compared with the control group; # $p < 0.05$ compared with the letrozole group.

Figure S2. Differential microbiome composition of fecal specimens from control, letrozole, Diane-35, and DSM 27449 groups. **(A)** Bar plot and **(B)** cladogram of linear discriminant analysis effect size analysis showed the effect size for a particular taxon in a certain group. Only the taxa with linear discriminant analysis (LDA) scores >2 are displayed.

Table S1. Summary of 16S rRNA sequencing data quality

Sample name	% GC	Sequence length (bp)	Total sequences	Unique tags	No. of OTUs	Good's coverage
Control-1	55	1,484	34800	29608	23020	0.998
Control-2	55	1,483	44300	37270	28749	0.999
Control-3	55	1,489	29000	23044	17615	0.997
Control-4	54	1,480	31100	25758	19091	0.997
Control-5	55	1,489	33200	28300	22728	0.998
Control-6	55	1,490	30400	25374	19930	0.998
Control-7	55	1,481	38500	30798	22488	0.998
Control-8	55	1,486	41600	34672	27322	0.998
Letrozole-1	54	1,494	43200	32362	23119	0.998
Letrozole-2	54	1,490	50800	37186	25779	0.999
Letrozole-3	54	1,490	31800	23787	17280	0.998
Letrozole-4	55	1,493	36800	27687	19989	0.998
Letrozole-5	55	1,485	33700	28685	22708	0.998
Letrozole-6	55	1,487	35700	31029	24849	0.998
Letrozole-7	55	1,496	41100	30632	22151	0.998
Letrozole-8	55	1,480	40700	34262	26614	0.998
Diane-35-1	55	1,501	42000	31346	22709	0.998
Diane-35-2	56	1,484	48500	40511	30615	0.999
Diane-35-3	54	1,503	29200	21397	15788	0.998
Diane-35-4	55	1,486	30900	26945	21293	0.998
Diane-35-5	55	1,483	29100	24329	18737	0.998
Diane-35-6	55	1,477	26600	20837	14282	0.997
Diane-35-7	55	1,487	36700	29232	21869	0.997
Diane-35-8	55	1,486	43600	36349	28495	0.998
DSM 27449-1	55	1,488	37500	30132	23077	0.998
DSM 27449-2	55	1,485	44000	36703	27701	0.998
DSM 27449-3	55	1,478	29100	23668	17775	0.998
DSM 27449-4	54	1,493	28500	21813	16063	0.996
DSM 27449-5	54	1,497	36500	27780	18333	0.998
DSM 27449-6	55	1,489	31600	25899	20555	0.998
DSM 27449-7	55	1,477	34800	29490	23715	0.997
DSM 27449-8	55	1,488	41500	34528	26616	0.999

Data sources are provided by Genomics BioSci & Tech Co., New Taipei City, Taiwan. The sequencing depth was sufficient, as indicated by the Good's coverage value exceeding 0.99.

Table S2. MicroRNA stem-loop reverse transcribed primer and sequence of primers and probes for miR-Q probe qPCR Assay

Assay Name	5'- labeled	Sequence	3'- labeled
rno-miR-30a-5p reverse transcribed primer		GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTG GATACGACCTTCCA	
rno-miR-30a-5p-F	----	CGCGTGTAACATCCTCGAC	----
rno-miR-30a-5p-R	----	AGTGCAGGGTCCGAGGTATT	----
rno-miR-30a-5p-P	FAM	ACGACCTTCCAGTCG	MGB
rno-miR-324-3p reverse transcribed primer		GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTG GATACGACCCAGCA	
rno-miR-324-3p-F	----	ATATCCACTGCCCCAGGTGC	----
rno-miR-324-3p-R	----	AGTGCAGGGTCCGAGGTATT	----
rno-miR-324-3p-P	FAM	ACGACCCAGCAGCA	MGB
rno-miR-93-5p reverse transcribed primer		GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTG GATACGACCTACCT	
rno-miR-93-5p-F	----	CGCAAAGTGCTGTTCGTGC	----
rno-miR-93-5p-R	----	AGTGCAGGGTCCGAGGTATT	----
rno-miR-93-5p-P	FAM	ATACGACCTACCTGC	MGB
rno-miR-223-3p reverse transcribed primer		GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTG GATACGACGGGGTA	
rno-miR-223-3p-F	----	GCGCGTGTCTAGTTTGTCAAA	----
rno-miR-223-3p-R	----	AGTGCAGGGTCCGAGGTATT	----
rno-miR-223-3p-P	FAM	ATACGACGGGGTATT	MGB
rno-miR-320-3p reverse transcribed primer		GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTG GATACGACTCGCCC	
rno-miR-320-3p -F	----	GCGAAAAGCTGGGTTGAGA	----
rno-miR-320-3p-R	----	AGTGCAGGGTCCGAGGTATT	----
rno-miR-320-3p-P	FAM	ACGACTCGCCCTC	MGB
rno-miR-146a-5p reverse transcribed primer		GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTG GATACGACAACCCA	
rno-miR-146a-5p-F	----	CGCGTGAGAACTGAATTCCA	----
rno-miR-146a-5p-R	----	AGTGCAGGGTCCGAGGTATT	----
rno-miR-146a-5p-P	FAM	ACGACAACCCATG	MGB
U6 snRNA reverse transcribed primer		ATGGAACGCTTCACGAATTTG	
U6 snRNA-F	----	CTCGCTTCGGCAGCACATAT	----

U6 snRNA-R	----	ATGGAACGCTTCACGAATTTG	----
U6 snRNA-P	FAM	ACGATACAGAGAAGAT	MGB
cel-miR-39-3p reverse transcribed primer		GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTG GATACGACCAAGCT	
cel-miR-39-3p-F	----	CGCGTCACCGGGTGTAAG	----
cel-miR-39-3p-R	----	AGTGCAGGGTCCGAGGTATT	----
cel-miR-39-3p-P	FAM	ACGACCAAGCTGATTTACAC	MGB

FAM, Fluorescein amidites; MGB, minor groove binder. Data sources are provided by Topgen Biotech, Kaohsiung City, Taiwan.