

Group	Number of OTU	Taxon Tags
Control	380±29	51146±5446
Model	490±25	57452±4764
RSH	569±34	61989±4980
RSM	546±32	56605±4095
RSL	525±38	61535±5253

Table S1: OTU analysis of fecal samples of mice in each group.

					Model	Ce-RS3		
NO.	Metabolites	m/z	RT	Formula	vs	vs	Related Pathway	
					Control	Model		
ESI+	1	L-Valine	118.0863	1.84	C ₅ H ₁₁ NO ₂	↓##	↑	Valine, Leucine and Isoleucine Degradation/Propanoate Metabolism
	2	Spermidine	146.1652	0.82	C ₇ H ₁₉ N ₃	↑##	↓*	Methionine Metabolism/Spermidine and Spermine Biosynthesis
	3	4-(2-Aminophenyl)-2,4-dioxobutanoic acid	208.0604	2.42	C ₁₀ H ₉ NO ₄	↓#	↓**	Tryptophan Metabolism
	4	Pantothenic acid	220.1179	2.14	C ₉ H ₁₇ NO ₅	↑##	↓*	Beta-Alanine Metabolism/Pantothenate and CoA biosynthesis
	5	Ricinoleic acid	299.2581	8.25	C ₁₈ H ₃₄ O ₃	↑##	↓*	Lipid metabolism/Fatty acid metabolism
	6	LysoPE(14:0/0:0)	426.2615	6.38	C ₁₉ H ₄₀ NO ₇ P	↓##	↑*	Glycerophospholipid metabolism
	7	Stearoylcarnitine	428.3734	7.77	C ₂₅ H ₄₉ NO ₄	↑##	↑	Mitochondrial Beta-Oxidation of Long Chain Saturated Fatty Acids
	8	LysoPE(16:0/0:0)	454.2928	7.42	C ₂₁ H ₄₄ NO ₇ P	↓##	↑	Phospholipid Biosynthesis/Glycerophospholipid metabolism

	9	LysoPC(14:0/0:0)	468.3085	7.96	C ₂₂ H ₄₆ NO ₇ P	↓##	↑*	Arachidonic Acid Metabolism/Glycerophospholipid metabolism
ESI-	1	Succinic acid	117.0193	1.38	C ₄ H ₆ O ₄	↑##	↓*	Arginine and Proline and Glutamate Metabolism
	2	Indole-3-carboxylic acid	160.0404	2.64	C ₉ H ₇ NO ₂	↓#	↑**	Tryptophan Metabolism
	3	3-Methyldioxyindole	162.0561	2.46	C ₉ H ₉ NO ₂	↓##	↑**	Tryptophan Metabolism
	4	Phenyllactic acid	165.0557	2.95	C ₉ H ₁₀ O ₃	↓##	↓**	Phenylalanine Metabolism
					Model	Ce-RS3		
NO.		Metabolites	m/z	RT	Formula	vs	vs	Related Pathway
					Control	Model		
	5	Kynurenic acid	188.0353	2.32	C ₁₀ H ₇ NO ₃	↓##	↓**	Tryptophan Metabolism
	6	Tryptophan	203.0826	2.33	C ₁₁ H ₁₂ N ₂ O ₂	↓#	↑*	Tryptophan Metabolism
	7	Palmitic acid	255.233	9.55	C ₁₆ H ₃₂ O ₂	↓##	↑**	Lipid metabolism/Fatty acid metabolism
	8	Ricinoleic acid	297.2435	7.47	C ₁₈ H ₃₄ O ₃	↑##	↓**	Lipid metabolism/Fatty acid metabolism

9	12-Hydroxystearic acid	299.2592	7.98	C ₁₈ H ₃₆ O ₃	↑##	↓*	Lipid metabolism/Fatty acid metabolism
10	Chenodeoxycholic acid	391.2854	6.30	C ₂₄ H ₄₀ O ₄	↑##	↓*	Bile acid biosynthesis
11	7-Ketodeoxycholic acid	405.2646	4.17	C ₂₄ H ₃₈ O ₅	↑##	↓**	Bile acid biosynthesis
12	Cholic acid	407.2803	4.89	C ₂₄ H ₄₀ O ₅	↑##	↑*	Bile acid biosynthesis
13	LysoPE(14:0/0:0)	424.247	6.34	C ₁₉ H ₄₀ NO ₇ P	↓##	↑*	Glycerophospholipid metabolism
14	LysoPE(15:0/0:0)	438.2625	6.70	C ₂₀ H ₄₂ NO ₇ P	↓##	↑	Glycerophospholipid metabolism
15	3-Sulfodeoxycholic acid	457.2232	4.23	C ₂₃ H ₃₈ O ₇ S	↑##	↑*	Bile acid biosynthesis
16	LysoPE(18:0/0:0)	480.3096	8.46	C ₂₃ H ₄₈ NO ₇ P	↓##	↑*	Glycerophospholipid metabolism
17	LysoPA(18:0/0:0)	483.2728	10.66	C ₂₁ H ₄₃ O ₇ P	↓##	↑*	Cardiolipin Biosynthesis/Glycerophospholipid metabolism

Table S2. Potential biomarker information. The up (↑) and down (↓) arrows represent the relative increasing or decreasing trend of the metabolites, “—” represents no relative differences between two group. # $p < 0.05$, ## $p < 0.01$ model versus the control group, * $p < 0.05$, ** $p < 0.01$, RS3 and Met versus the Model group.

Target genes	Forward primer	Reverse primer
ZO-1	5'- ACCCGAAACTGATGCTGTGGA TAG-3'	5'- AAATGGCCGGGCAGAACTTGT GTA-3'
Occludin	5'-ATGTCCGGCCGATGCTCTC- 3'	5'- TTTGGCTGCTCTTGGGTCTGTA T-3'
TNF- α	5'- TAGCCAGGAGGGAGAACAGA- 3'	5'- TTTTCTGGAGGGAGATGTGG-3'
IL-1 β	5'-TTGAAGAAGAGCCCATCCTC -3'	5'-CAGCTCATATGGGTCCGAC - 3'
IL-6	5'-CCGGAGAGGAGACTTCAC-3'	5'-TCCACGATTTCCCAGAGA-3'
IL-10	5'- GCTCTTACTGACTGGCATGAG - 3'	5'- CGCAGCTCTAGGAGCATGTG-3'

Table S3. Primers used in this study.

