Supplementary information

Supplementary Table S1. Composition of the experimental diets (%, w/w)

Ingredients	Control	EtOH	EtOH+L-RR	EtOH+M-RR	EtOH+H-RR
AIN93M diet	100	100	98	96	92
Red raspberry	-	-	2	4	8
Total	100	100	100	100	100

Supplementary Table S2. Estimated values of various nutrients of AIN93M standard feed

Ingredients	AIN93M
Energy	3601 Kcal/kg
Total calculated digestible energy from protein	14.1%
Total calculated digestible energy from lipids	10%
Water content	6.8%
Fat	4%
Carbohydrates	72.7%
Protein	12.5%
Ash	3.89%
Amino acid content	
Alanine	3.3g
Arginine	4.5g
Aspartic acid	8g
Glutamate	25.5g
Glycine	2.3g
Lysine	9.2g
Methionine	3.3g
Cystine	2.4g
Tryptophan	1.6g

Proline 14.3		
Serine	6.7g	
Histidine	3.3g	
Leucine	10.9g	
Isoleucine	5.9g	
Phenylalanine	6.2g	
Tyrosine	6.6g	
Threonine	4.7g	
Valine	7g	
Mineral content		
Calcium	5000ppm	
Phosphorus	3000ppm	
Potassium	3600ppm	
Sodium	1033ppm	
Magnesium	511ppm	
Iron	45ppm	
Zinc	35ppm	
Copper	6ppm	
Iodine	0.2ppm	
Chromium	lppm	
Inorganic Sulfur 300p		
Chlorine	1613ppm	
Vitamin content		
Vitamin A	4IU/g	
Vitamin D	1IU/g	
Vitamin E	0.075IU/g	
Vitamin K	0.86 ppm	
Thiamine, B1	5 ppm	
Riboflavin	6 ppm	
Viacin 30 ppm		
Pantothenic acid	15 ppm	
Vitamin B6	6 ppm	
Choline	1000 ppm	
Folic acid	2ppm	
Biotin	0.2ppm	
Vitamin B12	25ppb	

Product code: LAD3001M. http://www.trophic.cn

Method for the determination of red raspberry polyphenols composition

Red raspberry extract was analyzed by high-performance liquid chromatography (HPLC) based on targeted and untargeted method. The analytical conditions were as follows: HPLC column, shim-pack GISS C18 (pore size 1.9 μ m, length 2.1 × 100 mm); the solvent system was solvent A (aqueous 0.04% acetic acid) and solvent B (acetonitrile (0.04% acetic acid)). The gradient program was 0 min, 5% B; 12.0 min, 95% B; 13.2 min, 95% B; 13.3 min, 5% B; 15.0 min, 5% B, with a flow rate of 0.4 mL/min. The temperature was 40 °C and the injection volume was 2 μ L. Raspberry extract was performed in the Full-Scan mode by Q Exactive Focus Orbitrap LC-MS/MS (Thermo Scientific, USA) Using Compound Discoverer 3.3 software to analyze the raw data. The ESI source operation parameters were as follows: nebulizing gas flow, 3 L/min; heating gas flow, 10 L/min; interface temperature, 500 °C; DL temperature, 250 °C; heat block temperature, 400 °C; drying gas flow, 10 L/min.

Identification of compounds

The identification was carried out by comparison of the accurate m/z values, the retention time (RT), and the fragmentation patterns with those obtained from available standards analyzed in the same conditions. For high-quality (S/N>10) metabolic signals, we compared the MS2 spectral information of metabolic signals with the database by using Compound Discover 3.3 software and annotated these metabolic signals in batches. Then we identified metabolic signals that did not match the information in the database by querying the MS2 spectral data taken from the literature or to search the databases (e.g., METLIN, MassBank).

Supplementary Table S3. Primers used in this study

Gene name	Primer sequence	Gene ID/Reference	
ZO-1	F: CGGAACTATGACCATCGCCTAC	NM-001163574.1	
	R: CTTCGGGATGTTGTCTGGAGTC		
Occludin	F: TTCCACACTTGCTTGGGACAGA	NM-0088756.2	
	R: TCCGCCATAGCCATAGCCATAG		
Claudin-1	F: GGGCTGATCGCAATCTTTGTGT	NM-016674.4	
	R: CCACTAATGTCGCCAGACCTGA		
Claudin-4	F: GGCTGAGCGATGGCGTCTAT	NM-009903.2	
	R: CGATGTTGCTGCCGATGAAGG		
E-cadherin	F: GCCATCGCCTACACCATCGT	NM-009864.3	
	R: GCAGCCTGAACCACCAGAGT		
CD14	F: GAGCGTGTGCTTGGCTTGTT	1	
	R: CCGTAAGCCGCTTTAAGGACA		
TLR4	F: GCATGGATCAGAAACTCAGCAAA	1	
	R: CTCCACAGCCACCAGATTCTC		
NF-ĸB	F: GCTGCCAAAGAAGGACACGACA	NM_008689	
	R: GGCAGGCTATTGCTCATCACAG		
CYP 2E1	F: TGGGGAAACAGGGTAATGAG	2	
	R: CTGGCCTTTGGTCTTTTTGA	-	
β-actin	F: GGCTGTATTCCCTCCATCG	NM_007393.5	
	R: CCAGTTGGTAACAATGCCATG		

F, forward; R, reverse

Primers were designed using BLAST of NCBI (USA) and synthesized by TSINGKE Biotech Co., Ltd. (Wuhan, China).

Detection antibody	Company	Item No	Dilution
Detection antibody	Company		with TBST
Mouse monoclonal antibody	Wuhan Boster Biological	BM0627	1.500
β-actin (42KD)	Engineering Co., Ltd.	BW10027	1.300
Rabbit anti ZO-1 (240KD)	Boster	PB9234	1:1000
Rabbit anti Occludin (59KD)	Affinity	DF7504	1:2000
Mouse anti E-cadherin	Wuhan Sanying	Sanying	
(120KD)	Biotechnology Co., Ltd.	60335-1-1g	1:3000
Rabbit anti Claudin1(23KD)	Affiniy	AF0127	1:2000
Robbit onti Cloudin (22KD)	Wuhan Sanying	16105 1 AD	1:1000
Rabbit anti Claudii (22KD)	Biotechnology Co., Ltd.	10195-1-AF	
Rabbit anti MLC2 (19KD)	Wuhan Sanying		P 1.2000
Rubble und MEO2 (19RD)	Biotechnology Co., Ltd.	10700 1 711	1.2000
Mouse anti p-MLC2 (18KD)	CST	3675S	1:1000
Rabbit anti MLCK (211KD)	Affinity	AF5314	1:1000
Rabbit anti NFKB (65KD)	Invitrogen	PA5-17264	1:1000
Rabbit anti p-NFKB (60KD)	Affinity	AF2006	1:1000
HRP-labeled goat anti-mouse	Dester	BA1051	1:10000
secondary antibody	Boster		
HRP-labeled goat anti-rabbit	Boster	BA1054	1.10000
secondary antibody	DOSICI		1.10000

Supplementary Table S4. Antibodies and their dilution ratio used in this study



Supplementary Fig. 1. (A) Operational taxonomic unit (OTU) number in cecal samples of mice in the five groups after six weeks of treatment. (B) Venn diagram showing microbial common and unique features among mice from the five experimental groups.



Supplementary Fig. 2. Cecal content species network at genus level of mice in the five

experimental groups.

Circles represent species and the size of the circle corresponds to the abundance; The correlation between two species is represented by the edges, the thickness of the edge represents the strength of the correlation, and the color of the line: orange represents the positive correlation, while green represents green the negative correlation.

References:

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- Y. Ren, Y. Ding, F. Meng, L. Jiang, H. Li, J. Huang, P. Yu and Z. Qiu,
 Quantification of CYP2E1 in rat liver by UPLC-MS/MS-based targeted proteomics assay: a novel approach for enzyme activity assessment, *Anal. Bioanal. Chem.*, 2020, 412, 5409–5418.