Supplemental Table 1

Table 1 Primer Sequences Used for qRT-PCR Analysis

	Forward Primer	**Reverse Primer**
URAT1	GCTACCAGAATCGGCACGCT	CACCGGGAAGTCCACAATCC
GLUT9	GAGATGCTCATTGTGGGACG	TCACTCCGAACAGGTATGGC
OAT1	CACAATGATTCGGCAGACGG	AGGTATGGAGGGGTAGAACTCG
OCT1	ACATCCATGTTGCTCTTTCG	TTGCTCCATTATCCTTACCG
ABCG2	GGCCTGGACAAAGTAGCAGA	GTTGTGGGCTCATCCAGGAA
TLR-4	GGAAGACAAAAGAAAGACAGCCC	TGGGGAGATTCTTGATCTGCT
MYD88	TCATGTTCTCCATACCCTTGGT	AAACTGCGAGTGGGGTCAG
NLRP3	GCAGCGATCAACAGGCGAGAC	TCCCAGCAAACCTATCCACTCCTC
OAT4	GCATAATACCGAGGGGCCAT	CCGTCTGCCGAATCATTGTG
Caspase1	CTTGGAGACATCCTGTCAGGG	AGTCACAACACCAGGCATATT
XOD	TAGAAGAAAGTTGGGGCTGTGCGG	AGGAGCAGATGGGGGTCAAGCAG
PNP	AGGCCCCAACTTTGAGACTG	ACAGTGCCTTGCGACGATAA
TNF-a	*GCCTCTTCTCATTCCTGCTTGTGG*	GTGGTTTGTGAGTGTGAGGGTCTG
IL-1b	*TCGCAGCAGCACATCAACAAGAG*	TGCTCATGTCCTCATCCTGGAAG
NFKB	*ATGGCAGACGATGATCCCTAC*	TGTTGACAGTGGTATTTCTGGTG
OCTN2	*CTTATTCCCATACGGGCGCT*	TTTCTGAGGCACCTGTCGTC
PRPS2	*ATGCCTAACATCGTGCTCTTC*	GATCTCGACACTGGTCTCCTG
Col1a1	*CCCTACTCAGCCGTCTGTGC*	GGGTTCGGGCTGATGTACC
Spp1	*TCACCATTCGGATGAGTCTG*	ACTTGTGGCTCTGATGTTCC
Timp1	*CAACTCGGACCTGGATGCTAA*	ACTCTTCACTGCGGTTCTGG
Cox-2	*CCCATTAGCAGCCAGTTGTC*	CAGGATGCAGTGCTGAGTTC
Occludin	*ACGGACCCTGACCACTATGA*	TCAGCAGCAGCCATGTACTC
Claudin-1	*AGCTGCCTGTTCCATGTACT*	CTCCCATTTGTCTGCTGCTC
Zo-1	*ACCCGAAACTGATGCTGTGGATAG*	AAATGGCCGGGCAGAACTTGTGTA
β-actin	*CAACTTGATGTATGAAGGCTTTGGT*	ACTTTTATTGGTCTCAAGTCAGTGTACAG

ABBREVIATIONS USED

UA, Uric acid; SUA, Serum uric acid; XOD, Xanthine Oxidase; SCFAs, Short-chain Fatty Acids; PO, Potassium oxonate; BUN, Blood urea nitrogen; CRE, Creatinine; ALT, Alanine aminotransferase; AST, Aspartate aminotransferase; H&E, Hematoxylin and eosin; PAS, Periodic acid-Schiff; OTU, Operational taxonomic units; UPGMA, Unweighted Pair Group Method with Arithmetic mean; PCoA, Principal coordinate analysis; URAT1, Urate transporter 1; GLUT9, Glucose transporter 9; OAT1, Organic anion transporter 1; OAT4, Organic anion transporter 4; OCTN2, Organic cation/carnitine transporter2; OCT1, Organic cation transporter 1; ABCG2, ATP-binding cassette superfamily G member 2; TLR4, Toll-like receptor 4; LPS, Lipopolysaccharide; PRPS, Phosphoribosyl pyrophosphate synthase; PNP, Purine nucleoside phosphorylase; NLRP3, Nucleotide-binding oligomerization domain-like receptor with a pyrin domain; TLR4, Toll-like receptor 4; MyD88, Myeloid differentiation factor 88; NF-κB, Nuclear factor kappa B

Microbiome sequencing and analysis.

For microbiome analysis, the raw data were processed to produce valid data after removing connectors and low-quality bases by implementing UNOISE in Vsearch (v2.6.0) and zero-radius Opera Tional Taxonomic Units (zOTU) were constructed. The SILVA ribosomal RNA database (138.1) was used as a reference for annotation. A follow-up analysis was performed using Qiime2 (https://docs.qiime2.org, combined with the R package vegan, ggpubr, ggplot, and Gplots). All samples were diluted to 40000 counts for alpha diversity index calculations and unweighted Unifrac principal coordinate analysis (PCoA) distance. Random forest was analyzed by R package "randomForest". And the other analysis were analyzed using the OmicStudio tools at (https://www.omicstudio.cn/tool;http://meta.bgi.com/). PICRUSt2(https://github.com /picrust/picrust2/wiki/Workflow) was used to predict the functional abundance of 16S rRNA genes.