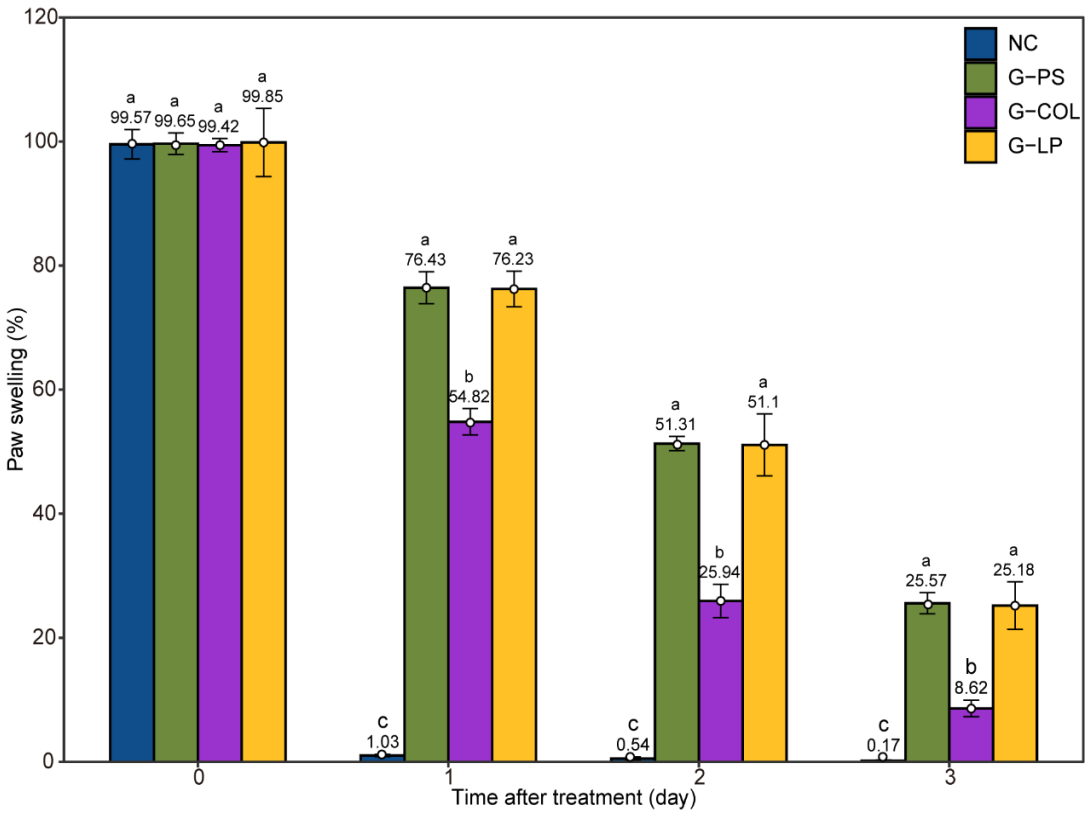
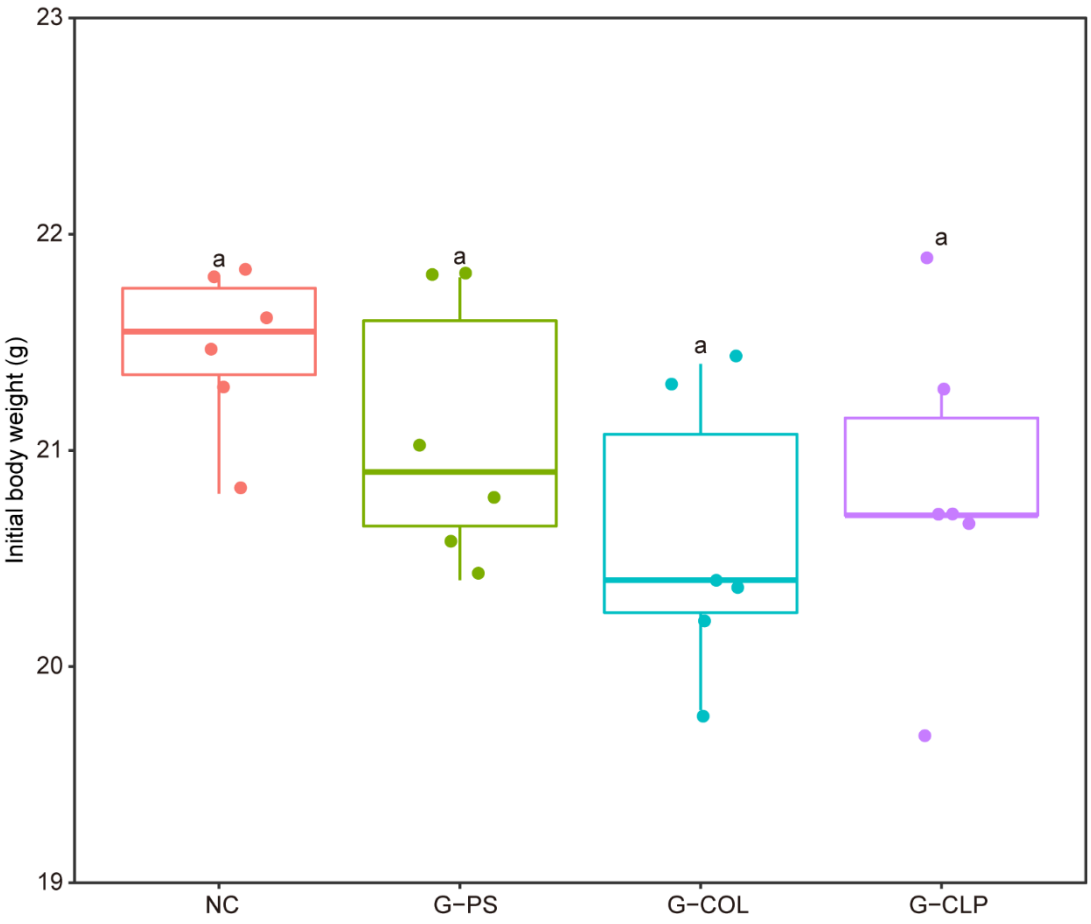
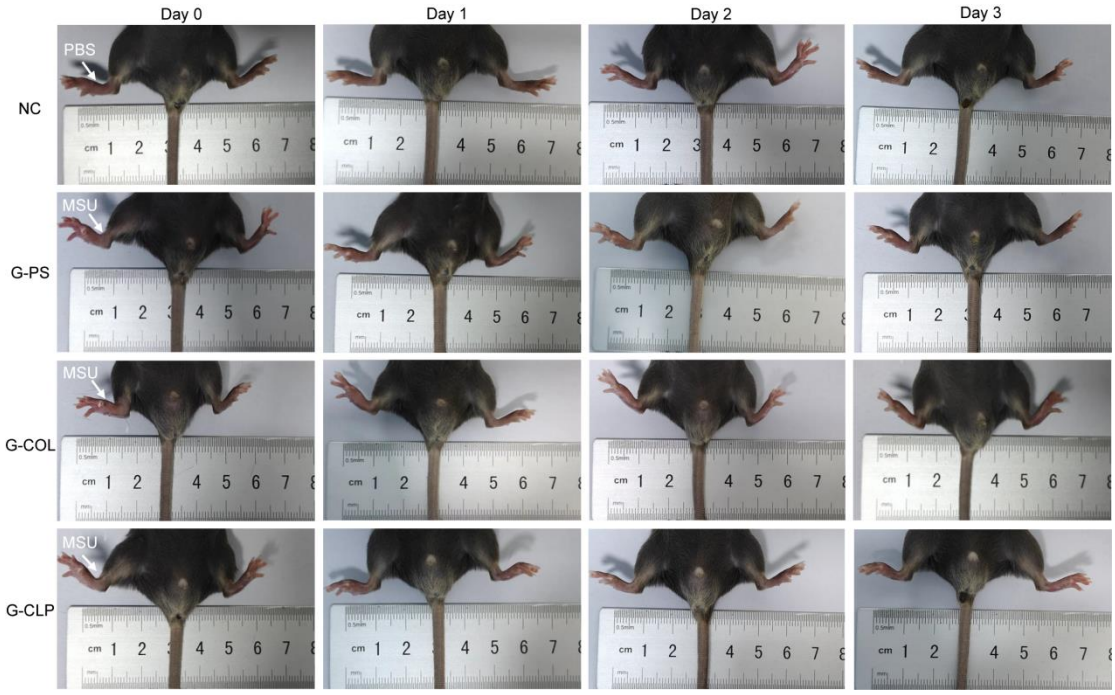


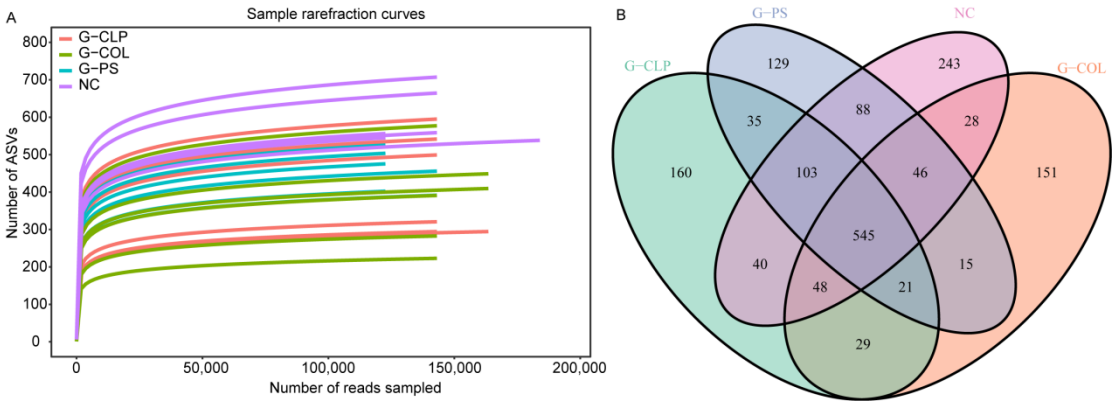
Supplementary Figure 1. Paw swelling at different time points after treatment. NC, normal control; G-PS, gout treated with physiological saline; G-COL; gout treated with COL; G-LP, gout treated with *Lactobacillus paracasei* GY-1. Different low-case letters indicate statistical difference at P <0.05, one-way ANOVA followed by Tukey's post hoc test (n = 6 in each group).



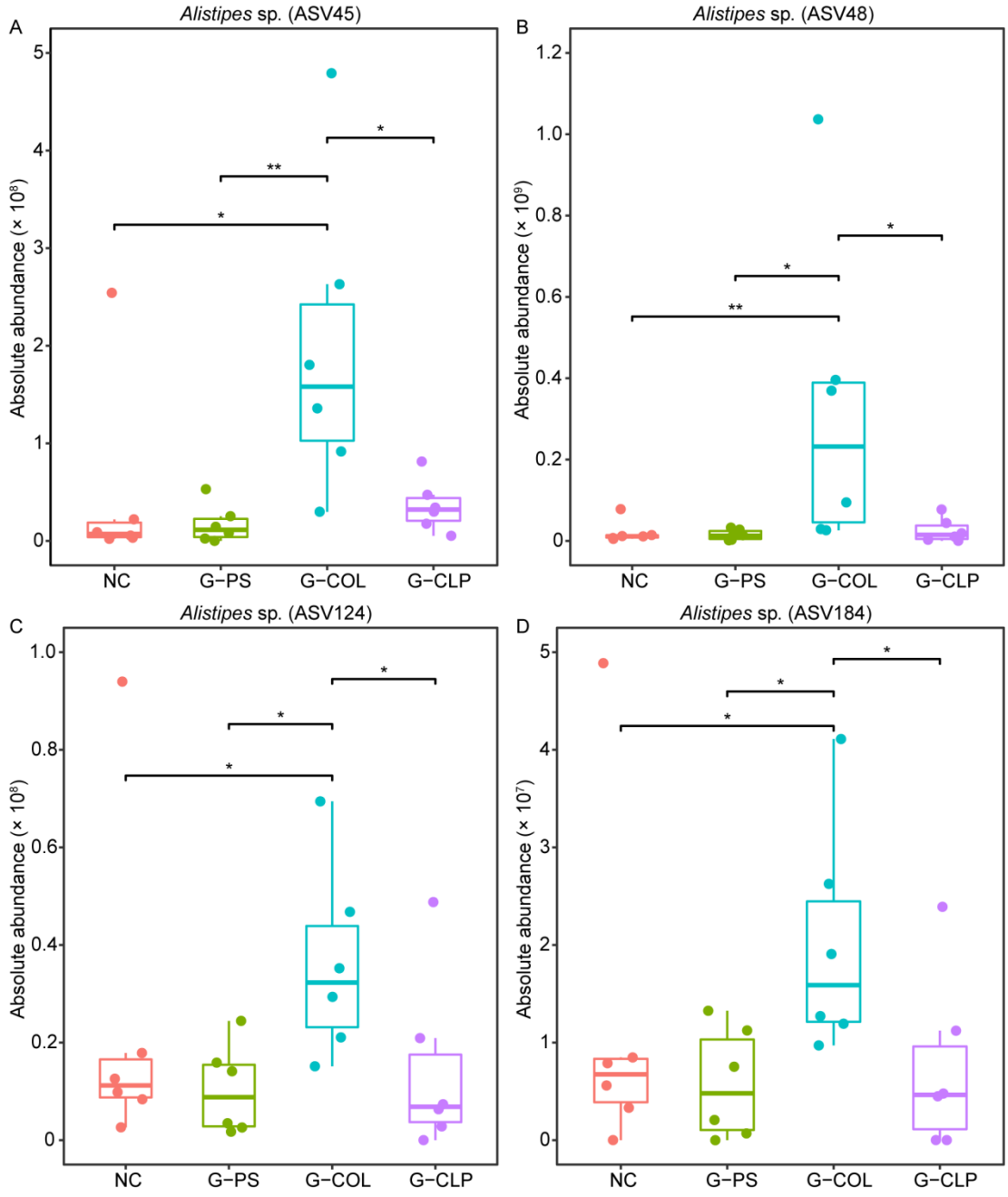
Supplementary Figure 2. Initial body weights for all the mice in the four groups. Different low-case letters indicate statistical difference at P <0.05, one-way ANOVA followed by Tukey's post hoc test (n = 6 in each group).



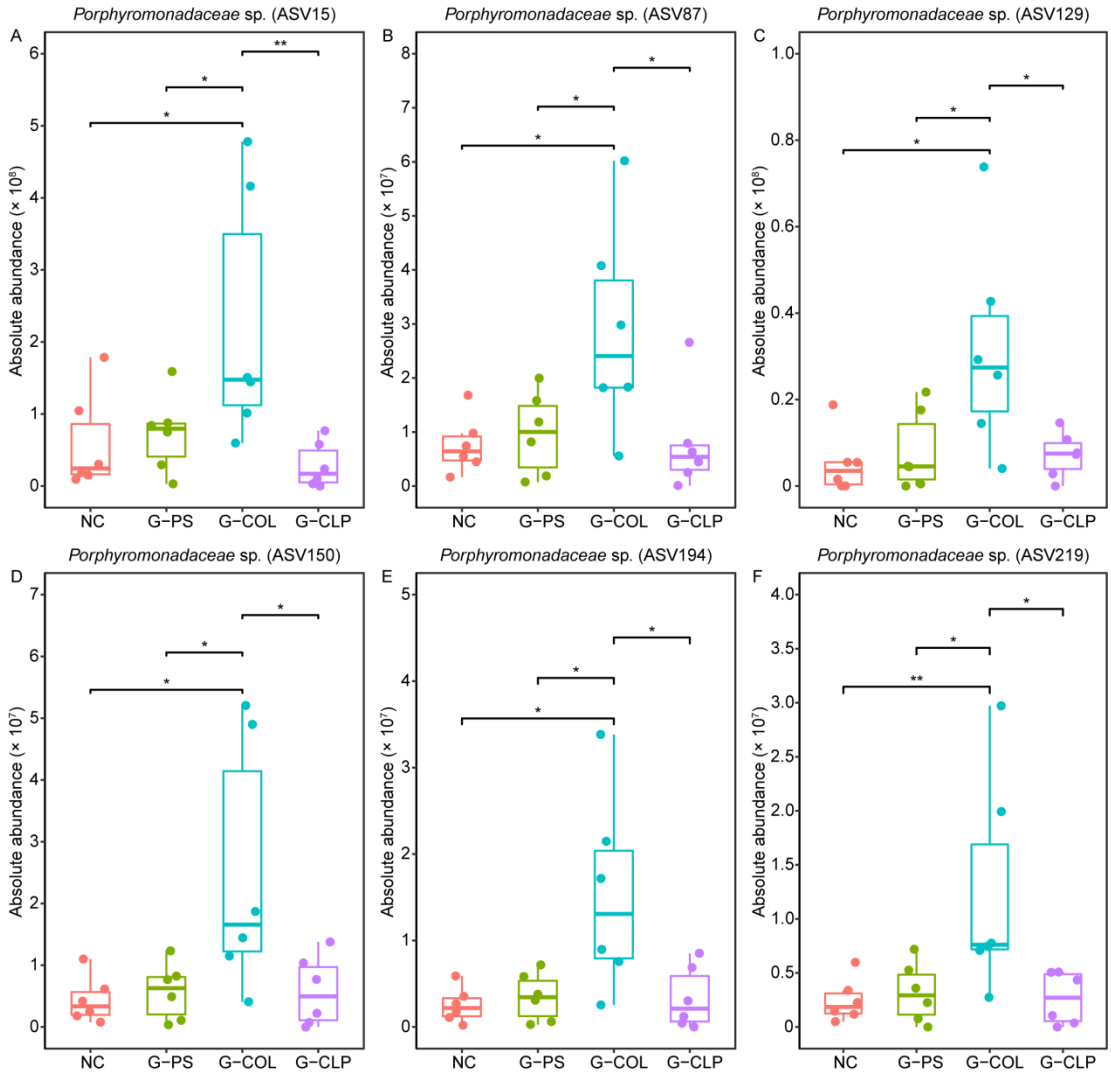
Supplementary Figure 3. Representative picture of paw swelling. Either MSU crystals or PBS was injected into the right hind paw on day 0.



Supplementary Figure 4. Sample rarefaction curves and Venn diagram for amplicon sequence variants (ASVs). A, Rarefaction curves for all samples. B, Venn diagram illustrating the unique and shared ASVs.



Supplementary Figure 5. Four *Alistipe* species responsible for toxicity mitigation. A, the absolute abundance of *Alistip* sp. (ASV45); B, the absolute abundance of *Alistip* sp. (ASV48); C, the absolute abundance of *Alistip* sp. (ASV124); D, the absolute abundance of *Alistip* sp. (ASV184). **P* <0.05, and ***P* <0.01, Wilcoxon rank sum test with continuity correction compared to the G-COL group.



Supplementary Figure 6. Six *Porphyromonadaceae* species responsible for toxicity mitigation. A, the absolute abundance of *Porphyromonadaceae* sp. (ASV15); B, the absolute abundance of *Porphyromonadaceae* sp. (ASV87); C, the absolute abundance of *Porphyromonadaceae* sp. (ASV129); D, the absolute abundance of *Porphyromonadaceae* sp. (ASV150); E, the absolute abundance of *Porphyromonadaceae* sp. (ASV194); F, the absolute abundance of *Porphyromonadaceae* sp. (ASV219). **P* <0.05, and ***P* <0.01, Wilcoxon rank sum test with continuity correction compared to the G-COL group.

Table S1. Primer list for quantitative Real-Time PCR amplification.

Gene	Forward primer	Reverse primer
GAPDH	5'-GCATCCACTGGTGCTGCC-3'	5'-TCATCATACTTGGCAGGTTTC-3'
Occludin	5'-ATGTCCGGCCGATGCTCTC-3'	5'-TTTGGCTGCTCTTGGGTCTGTAT-3'
Claudin-1	5′-GTTTGCAGAGACCCCATCAC-3′	5‘-AGAAGCCAGGATGAAACCCA-3’
Zo-1	5'-ACCCGAAACTGATGCTGTGGATAG-3'	5'-AAATGGCCGGGCAGAACTTGTGTA-3'

Table S2. The reads were obtained per sample

Sample ID	# Raw reads	# Remained reads	% of remained reads	Group
J1-1	224,813	203,120	90.35	G-CLP
J2-1	227,826	207,942	91.27	G-CLP
J3-1	224,058	197,636	88.21	G-CLP
J4-1	232,350	205,305	88.36	G-CLP
J5-1	227,570	204,106	89.69	G-CLP
J6-1	230,034	203,472	88.45	G-CLP
M1-1	216,653	192,173	88.7	G-PS
M2-1	218,073	193,578	88.77	G-PS
M3-1	230,479	206,889	89.76	G-PS
M4-1	226,853	202,059	89.07	G-PS
M5-1	230,802	205,001	88.82	G-PS
M6-1	221,574	193,938	87.53	G-PS
Q1-1	232,439	209,563	90.16	G-COL
Q2-1	221,379	199,418	90.08	G-COL
Q3-1	231,025	204,041	88.32	G-COL
Q4-1	221,766	196,262	88.5	G-COL
Q5-1	227,525	204,221	89.76	G-COL
Q6-1	218,671	193,030	88.27	NC
Z1-1	227,561	202,959	89.19	NC
Z2-1	232,893	207,797	89.22	NC
Z3-1	222,642	199,703	89.7	NC
Z4-1	224,028	198,469	88.59	NC
Z5-1	228,549	204,989	89.69	NC
Z6-1	228,110	202,891	88.94	NC