

Supplementary Materials

**Stachyose attenuates DSS-induced colitis and is associated with elevated colonic
medium-chain fatty acids: an integrated multi-omics analysis**

Geunsoo Kim^{1,2,#}, Kaiwei Chen^{2,#}, Zhiyuan Xing³, Xiaoyu Wu¹, Haoyan Zhang¹, Yu
Fang¹, Zishuai Zhang¹, Ningning He^{2,*}, Shangyong Li^{2,*} and Fengjuan Zhang^{1,*}

¹ Department of Infectious Diseases, Affiliated Hospital of Qingdao University,
Qingdao, 266003, Shandong, China.

² School of Basic Medicine, Qingdao Medical College, Qingdao University, 266000,
Qingdao, China.

³ Department of Gastroenterology, Qingdao Central Hospital, University of Health
and Rehabilitation Sciences, 466000, Qingdao, China.

[#] These authors contributed equally

^{*} Corresponding author: Ningning He: heningning@qdu.edu.cn

Shangyong Li: lisy@qdu.edu.cn

Fengjuan Zhang: zhangfj66@163.com

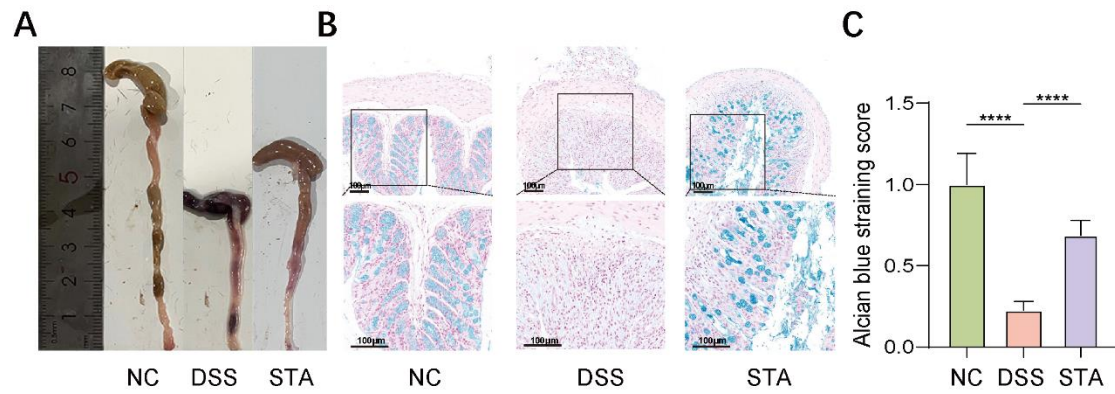


Figure 1S. STA alleviated the symptoms of DSS-induced colitis in mice. Length of colons (A). Representative colon sections and Alcian blue staining (B, C). Data are presented as mean $\pm$ SD. Statistical analysis was performed using one-way ANOVA with Tukey post hoc test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ and **** $p < 0.0001$.

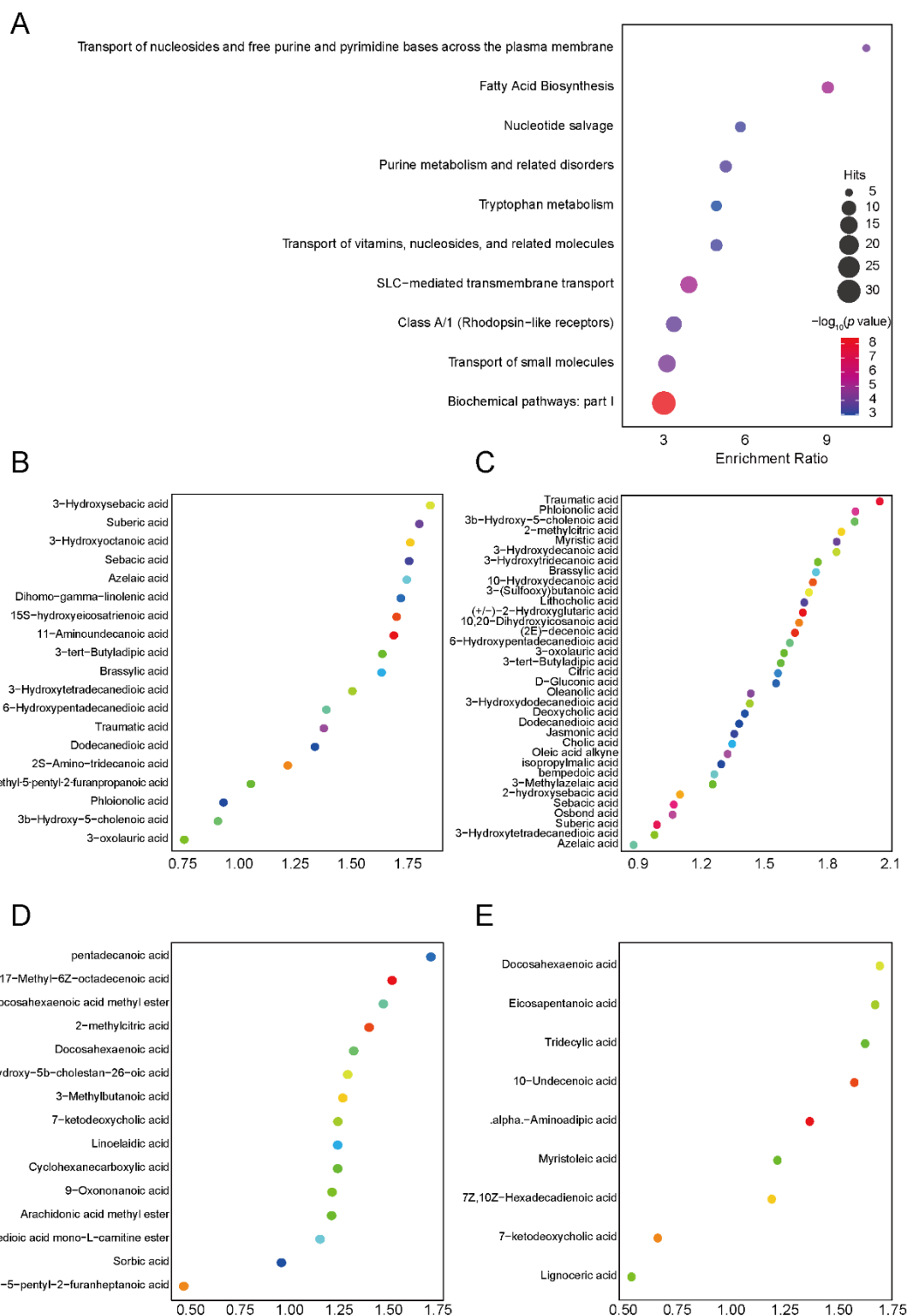
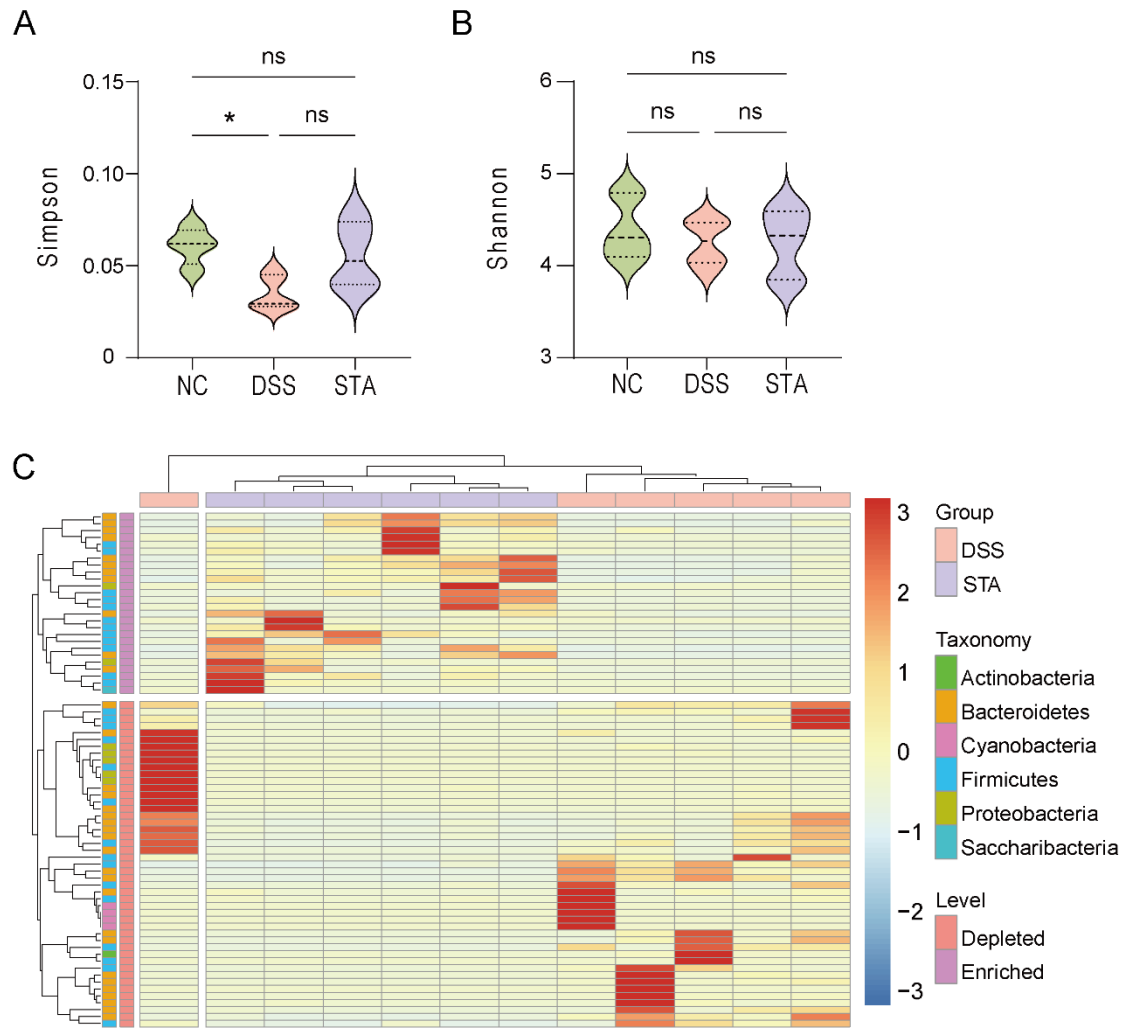


Figure 2S. STA impacts the metabolome of mice with DSS-induced UC. SMAPDB enrichment analysis of metabolic pathways ($VIP > 1$, $|\log_2FC| > 0.5$, $p < 0.05$, Wilcoxon rank-sum test) (A). VIP values of upregulated fatty acids fatty acid in positive ion (B) and negative ion modes (C). VIP values of downregulated fatty acids fatty acid in

29 positive ion (D) and negative ion modes (E).



31 **Figure 3S. STA modulated the gut microbiota composition of mice with DSS-**
32 **induced UC.** Alpha diversity indicated by the Simpson and Shannon index (A, B).
33 Phylum-level Heatmap in the DSS and STA groups (C). Data are presented as mean $\pm$
34 SD. Statistical analysis was performed using one-way ANOVA with Tukey post hoc
35 test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ and **** $p < 0.0001$.

36

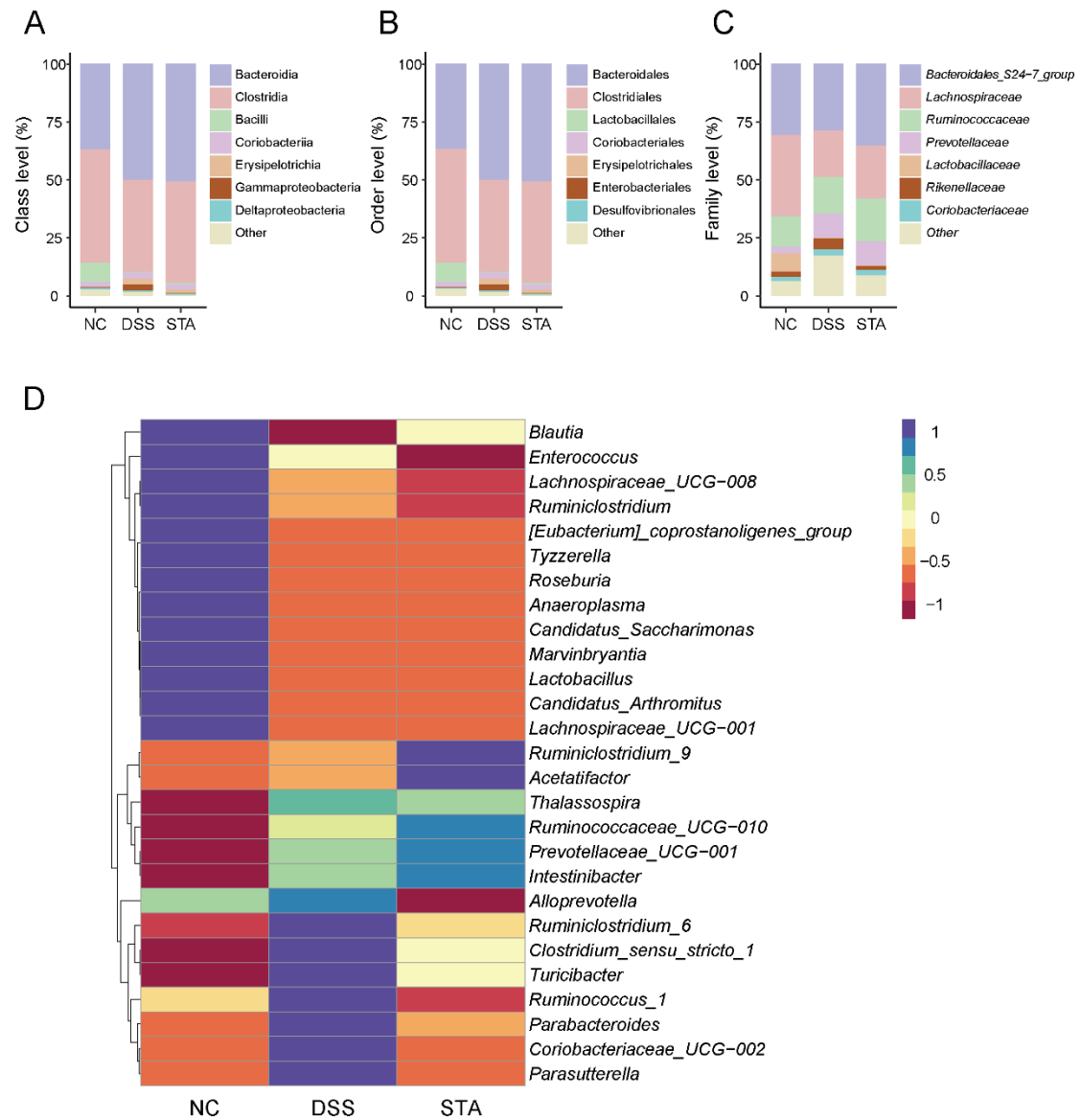


Figure 4S. STA modulated the gut microbiota composition of mice with DSS-induced UC. Overall structure of gut microbiota at Class (A), Order (B), and Family (C) levels. Genus-level Heatmap (D).