Supporting Information

S Methods

Methods 1

GDH preparations utilized for the present studies were obtained from *Klebsiellapneumonia* ATCC 25955. *K. pneumoniae* was kept at -20 °C at Zhejiang Gongshang University. The bacteria were harvested in the middle of the exponential growth phase, then inoculated into LB medium with a ratio of 5 mg dry wet weight of the bacteria/mL of the medium and cultivated again. After 18 h at 28 °C, the bacteria were harvested, washed and transferred into LB medium containing 5% (v/v) glucose and 10% (v/v) glycerol. The inoculation was incubated for 1 h at 25 degrees while the pH was kept between 5.5 and 6.5 to induce GDH production. The bacterial cells were broken in a Bead-Beater (BioSpec Products, USA) using glass beads with a diameter of 0.5 mm. A small amount of charcoal (Norit A) was added, and the preparation was centrifuged. The supernatant solution obtained was used as a crude GDH preparation for further studies. To decompose inner cobalamin, the crude eluents were placed under an UV light (9 W) (Leiman Co., Ltd., Shenzhen, China) with a light intensity of ca. 100 μmol/m^2/s. The GDH activity of the enzyme preparations was measured according to the method described by Luthi-Peng *et al.*.[1]

Method 2

E. coli DH5a was grown in LB medium. The cells (0.1 g) were re-suspended in 1 mL of potassium phosphate buffer (pH 7.0, 10 mmol/L) with 10% sucrose. Then, they were disrupted by a bead beater (BioSpec Products, USA) with 15 s strokes with 45 s intervals and8 cycles and then centrifuged at 5000× g for 20 min at 4 °C. The supernatant of the crude extract was placed under an UV light (9 W) (Leiman Co., Ltd., Shenzhen, China) with a light intensity of *ca.* 100 μmol/m^2/s. Activities of methionine synthase were measured by a methionine HPLC method according to that of Huang *et al.*.[2] Analysis of short-chain fatty acids in fresh faecal samples were handled and analysed as described by D'Hoe *et al.*.[3] Canonical correspondence analysis (CCA) was performed using Canoco for Windows v4.5 (Wageningen UR, Netherlands) to investigate the correlations between microbial genera and metabolites. All data were normalized by SPSS software to eliminate the influence of different dimensions before use in the CCA.

Reference

(1) Luthi-Peng, Q.; Dileme, F. B., Puhan, Z. Effect of glucose on glycerol bioconversion by Lactobacillus reuteri. *Appl. Microbiol. Biotechnol.* **2002**, 59, 289-296.

(2) Huang, L.; Zhang, J.; Hayakawa, T.; Tsuge H. Assays of methylenetetrahydrofolate

reductase and methionine synthase activities by monitoring 5-methyltetrahydrofolate and tetrahydrofolate using high-performance liquid chromatography with fluorescence detection. *Anal. Biochem.* **2001**, 299, 253-259.

(3) D'hoe, K.; Conterno, L.; Fava, F.; Falony, G.; Vieira-Silva, S.; Vermeiren, J.; Tuohy, K.; Raes, J. Prebiotic Wheat Bran Fractions Induce Specific Microbiota Changes. *Front. Microbiol.* **2018**, 9, 31.

S Figure Legends

S Fig. 1 The scheme for Induction of colitis and cobalamin treatment.

S Fig. 2 Schematic diagram of riboswitch-GFP construction.

S Fig. 3 Phylogenetic reconstruction of riboswitch from major bacteria.