

Erratum

In the article by Takahashi et al., entitled 'Reduced abundance of butyrate-producing bacteria species in the fecal microbial community in Crohn's disease' [Digestion 2016;93:59–65, DOI: 10.1159/000441768], the name sequence of the authors was corrected, missing underlining in table 1 was added, and an error in the legend of figure 1 was corrected.

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Table 1. Characteristics of patients and normal individuals enrolled in this study

	CD	Healthy subjects
Female/male	21/47 (<u>5/5</u>)	22/24 (<u>5/5</u>)
Age, years (mean)	35.3 (<u>30.5</u>)	40.0 (<u>35.5</u>)
Type of disease, n (%)		
Ileitis	27 (39.7)	–
Ileocolitis	33 (48.5)	–
Colitis	8 (11.8)	–
CDAI, mean (range)	90.1 (13.8–168)	–
Medications, n (%)		
5-ASA/SASP	54 (79.4)	–
Prednisolone	10 (14.7)	–
AZA/6MP	25 (36.8)	–
Biologics	51 (75.0)	–
Elemental diet	29 (42.6)	–
Period after the last biologics, days, mean (range)		
Infliximab (n = 35)	39.1 (1–58)	–
Adalimumab (n = 16)	13.7 (2–21)	–

Underline indicates the patients and normal subjects for 16S rRNA sequencing analysis. 5-ASA = 5-aminosalicylic acid; AZA = azathioprine; 6MP = 6-mercaptopurine.

Fig. 1. Results of 16S rRNA sequencing of fecal samples from CD patients (n = 10) and healthy controls (n = 10). **a** Average number of reads per sample. The average of 62,201 reads per CD sample was significantly lower than the average of 73,716 reads per control sample. ** p < 0.01. **b** Comparison of the fecal microbial community of CD patients and healthy controls at the phylum level. * p < 0.05. **c** Comparison of the fecal microbial community at the genus level. Heat map shows the distribution of relative abundance of genera at the genus level. The dendrogram was constructed by the Pearson's similarity coefficient analysis and the unweighted pair-group method.