CORRECTION

Correction to: Differences in gut microbiota associated with age, sex, and stool consistency in healthy Japanese subjects

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Published online: 6 September 2018
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Correction to: J Gastroenterol

<https://doi.org/10.1007/s00535-018-1488-5>

The authors would like to correct the errors in the publication of the original article. The correction details are given below for your reading.

The first sentence in the second paragraph beneath the heading “Microbiome analysis” in third page should be “The observed species, Chao1 and Shannon phylogenetic diversity indices were calculated by the R “phyloseq” package and were statistically analyzed using a Wilcoxon rank-sum test.”

The last two sentences in the first paragraph, in fifth page should be “In the younger group (20–39 years), the relative abundance of *Bifidobacterium* ($p < 0.01$) and *Ruminococcus* ($p < 0.05$) substantially increased in female subjects, and the relative abundance of *Escherichia* ($p < 0.05$) significantly increased in male subjects. In the middle age group (40–59 years), the relative abundance of *Prevotella* ($p < 0.05$) and *Megamonas* ($p < 0.05$)

increased in male subjects, and the relative abundance of *Ruminococcus* ($p < 0.01$) and *Oscillospira* ($p < 0.01$) significantly increased in female subjects. In the elderly group (60 years or older), the relative abundance of *Bacteroides* ($p < 0.01$) and *Turicibacter* ($p < 0.05$) increased in female subjects, and the relative abundance of *Prevotella* ($p < 0.01$), *Megasphaera* ($p < 0.05$) significantly increased in male subjects (Supplementary Fig. 4).”

The third sentence of the fourth paragraph, in seventh page should be “Characteristically, the genera *Prevotella* (middle age group and elderly group) and *Megamonas* (middle age group) were notably increased in male subjects, and the genera *Bifidobacterium* (younger group) was strikingly increased in female subjects”.

In addition, Figs. 4 and 8 were published incorrectly. The correct Figs. 4 and 8 are given in the following pages:

The original article can be found online at <https://doi.org/10.1007/s00535-018-1488-5>.

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Fig. 4 The relative abundance of gut microbiota in male and female subjects. The genera were significantly different between male and female subjects

(A) Male **(B) Female**

Fig. 8 Comparative analyses of the microbial community at the genus level for each stool consistency group. Genera were significantly different among each stool consistency group for male and

female subjects. Stool consistency was categorized into three groups: hard (BSS 1 or 2), intermediate (BSS 3 or 4), and loose (BSS 5 or 6)