



# Correction for Tarallo et al., “Altered Fecal Small RNA Profiles in Colorectal Cancer Reflect Gut Microbiome Composition in Stool Samples”

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Volume 4, no. 5, e00289-19, 2019, <https://doi.org/10.1128/mSystems.00289-19>. The following text corrections are necessary.

Page 2, third line from the bottom, the paragraph should read: “At the phylum level, the abundances of *Proteobacteria* and *Verrucomicrobia* in adenoma patients were significantly different from those seen in the healthy group. In particular, *Verrucomicrobia* showed the lowest abundance, whereas *Proteobacteria* showed intermediate abundance in the adenoma group (see Table S1A). *Proteobacteria* was the most significantly abundant phylum in the carcinoma group compared with both the healthy and adenoma groups, while *Firmicutes* abundance significantly decreased from the healthy group to the carcinoma group (Fig. 1A; see also Table S1A).”

Page 5, Fig. 2 legend should read: “(A) Flow chart summarizing the analyses performed to identify and analyze the sRNA-Seq reads assigned to microbial genomes and bsRNAs. WMS, whole-metagenome sequencing. (B) Stacked bar plots reporting the relative abundances of bacterial phyla detected using whole-metagenome sequencing (top) and small RNA sequencing (sRNA-Seq; bottom) data, respectively. (C) Bar plot reporting the Pearson correlation coefficient ( $r$ ) computed from comparisons between metagenomic and sRNA-Seq data for each phylum. (D) Heat map representing the  $\log_{10}$  numbers of reads assigned to bsRNAs from the Bacteria Small RNA Database (BSRD). Only annotations that were significantly different (adjusted  $P$  value of  $<0.05$ ) between healthy, adenoma, and CRC groups are shown. *P.aeu*, *P. aeruginosa*. (E) Heat map reporting the  $\log_2$  ratios of relative abundances between bsRNAs and bacterial DNA profiles. Only ratios of bacterial species with median values greater than 1 are reported.”

Page 5, fourth line from the bottom, the text should read: “The most correlated bacterial phyla were *Spirochaetes* ( $r = 0.902$ ), *Proteobacteria* ( $r = 0.786$ ), and *Fusobacteria* ( $r = 0.646$ ) (Fig. 2C). At the species level, *Porphyromonas asaccharolytica* was characterized by the highest correlation ( $r = 0.999$ ; adjusted  $P$  value of  $<0.0001$ ), while *F. nucleatum* ( $r = 0.990$ ; adjusted  $P$  value of  $<0.0001$ ) and *E. coli* ( $r = 0.632$ ; adjusted  $P$  value of  $<0.0001$ ) were among the 15 most highly correlated species (see Table S4C).”

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Page 9, sixth line from the top, the text should read: "In our analyses, the *Firmicutes* abundances characterizing cancer samples were significantly different from those characterizing the healthy group. Interestingly, the *Verrucomicrobia* phylum, characterized by a significant decrease in abundance in the adenoma samples, may represent a potential candidate biomarker for precancer lesions."