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Author Correction to: Association of Bacteroides acidifaciens relative abundance with high-fibre diet-associated radiosensitisation

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Following publication of the original article [1], it has been brought to the authors' attention that after 16S sequencing of the v1-8 region, the bacterium which we originally believed to be *F. prausnitzii* (a butyrate-producer) in our penultimate figure, Fig. 5k and Additional file 1: Figure S5B, was in fact *L. plantarum* (a lactate-producer). This does not affect the other data, especially the animal work, nor does it alter the final conclusions of this manuscript.

The correct Figs. 5 and S5 and their caption have been included below and the fully corrected version of Additional file 1 is attached to this Author Correction, and the original article [1] has been corrected.

The original article can be found online at https://doi.org/10.1186/s12915-020-00836-x.

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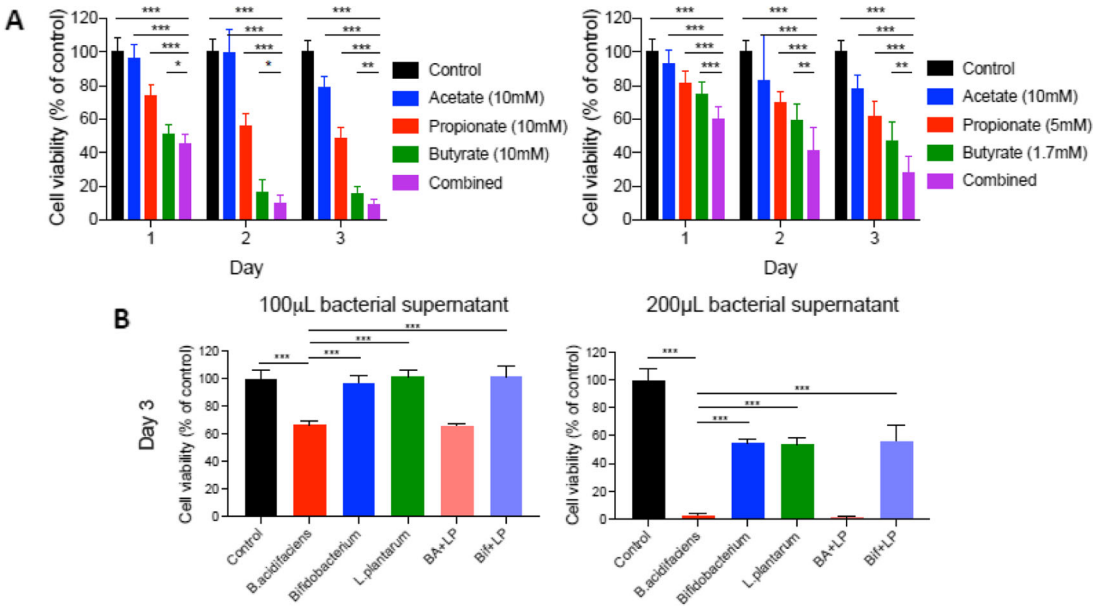

Figure S5. Cell survival analysis of RT112 bladder tumour cells treated with SCFAs and bacterial supernatants. (A) Inhibition of cell viability of RT112 cells single SCFA and combined SCFAs mixture in a time-dependent manner (N=3). The combined SCFAs denote the mixtures of 10 mM butyrate, 10 mM propionate, 10 mM butyrate for the left-hand graph and the mixtures of 10 mM butyrate, 5 mM propionate, 1.7 mM butyrate for the right-hand graph. (B) Reduced cell survival of RT112 cells by bacterial supernatants at day 3 (N=1). *BA+LP* denotes the cross-feeding of *B. acidifaciens* and *L. plantarum*, while *Bif+LP* denotes the cross-feeding of *Bifidobacterium* and *L. plantarum.* *P<0.05; **P<0.01; ***P<0.001.

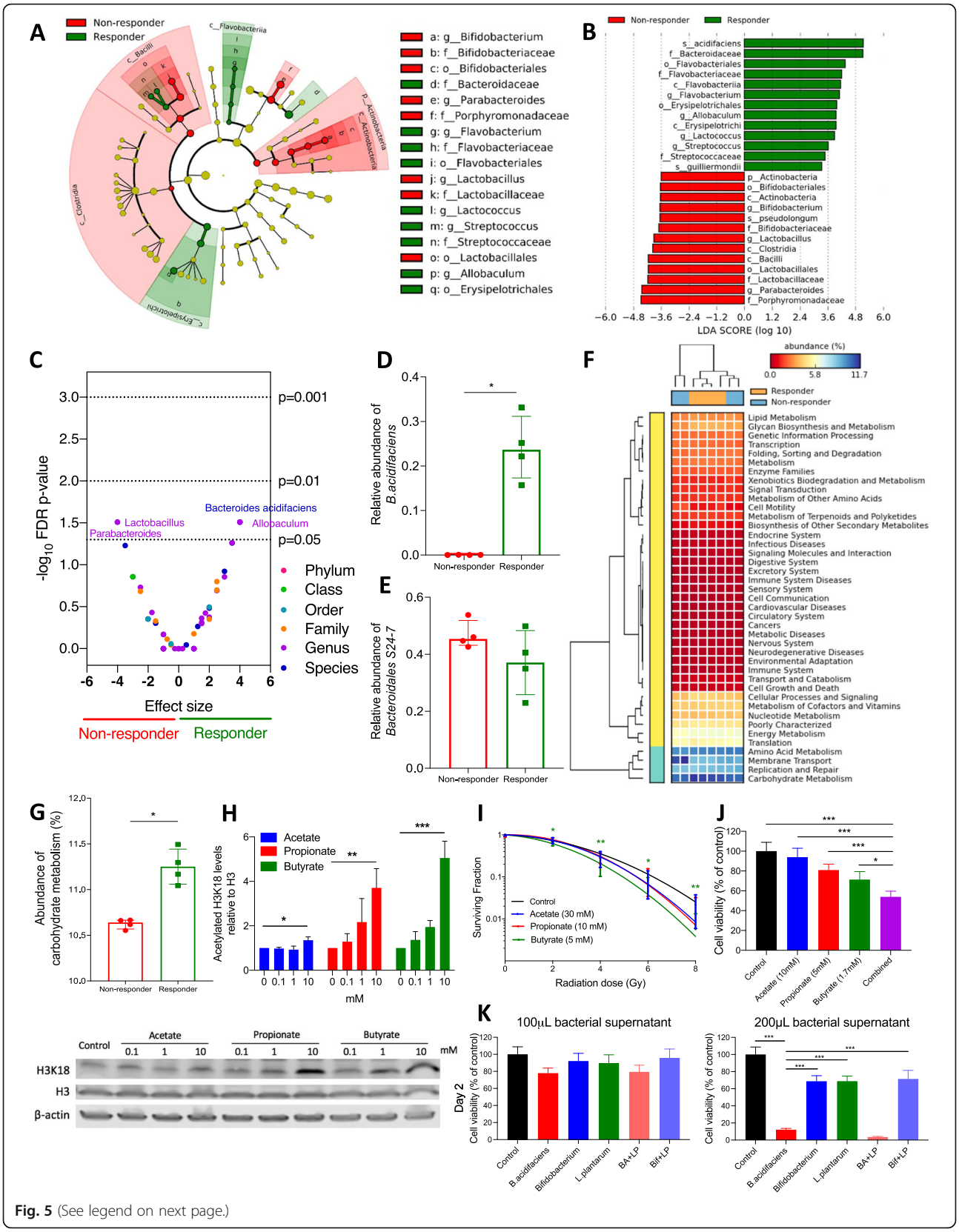

Fig. 5 (See legend on next page.)

(See figure on previous page.)
Fig. 5 Differences in composition of the gut microbiome between responders and non-responders. **a** Taxonomic cladogram from LEfSe showing differences among taxa between responders and non-responders in the soluble HF group. Dot size is proportional to the abundance of the taxon. **b** Linear discriminant analysis (LDA) scores computed for differentially abundant taxa in the microbiomes of responders (green) and non-responders (red). Length indicates the effect size associated with a taxon, $p = 0.05$ for the Kruskal-Wallis test. **c** Discrete false-discovery rate of different abundant taxa in responders and non-responders in the soluble HF group. Differential abundance within all taxonomic levels in responders versus non-responders by Mann-Whitney *U* test. Dots are overlapping between *Bacteroides acidifaciens* and *Allobaculum*, and between *Lactobacillus* and *Parabacteroides*. Relative abundance of **d** *B. acidifaciens* and **e** *Bacteroidales S24-7* and in responders and non-responders in the soluble HF group. **f**, **g** Metagenomic functional prediction by PICRUSt of the gut microbiome in responders ($n = 4$) and non-responders ($n = 4$) in the soluble HF group with reference to the KEGG database level 2. Columns represent mice (responders, orange; non-responders, blue), and rows represent enrichment of predicted KEGG pathways (red, low enrichment; yellow, medium enrichment; blue, high enrichment). **h** Western blot analysis of histone acetylation levels of RT112 cells treated with SCFAs ($N = 3$). **i** Linear quadratic survival curves of IC10-treated RT112 cells with receiving irradiation of 0–8 Gy ($N = 3$). **j** Cell survival analysis of RT112 cells treated with single SCFA and combined SCFAs mixture ($N = 3$). Combined (purple bar) denotes SCFA mixture of 10 mM acetate, 5 mM propionate, and 1.7 mM butyrate **k** Reduced cell survival of RT112 cells by bacterial supernatants at day 2 (N=1). *BA+LP* denotes the cross-feeding of *B. acidifaciens* and *L. plantarum*, while *Bif+LP* denotes the cross-feeding of *Bifidobacterium* and *L. plantarum*. *$p < 0.05$; **$p < 0.01$; ***$p < 0.001$

Furthermore, some sentences in the original article's main text need to be corrected. The affected text has been highlighted in **bold typeface**, and the original article [1] has been corrected.

Previous version

Results

To validate the anti-tumoural effects of *B. acidifaciens*, we treated the bladder tumour cells with bacterial supernatants of *B. acidifaciens* and its cross-feeding with ***F. prausnitzii***, and compared their effects with *Bifidobacterium* (acetate-producer) and ***F. prausnitzii* (butyrate-producer)**. Bacterial supernatants of *B. acidifaciens* and its cross-feeding with ***F. prausnitzii*** significantly increased cytotoxicity of bladder tumour cells compared to the other supernatants in day 2 (Figure 5K) and in day 3 (Additional file 1: Figure S5B).

Discussion

In this study, we revealed that bacterial supernatant from *B. acidifaciens* and its cross-feeding with ***F. prausnitzii*** caused significantly higher levels of cytotoxicity compared to the other supernatants (Figure 5K and Additional file 1: Figure S5B). This result supports our finding that *B. acidifaciens* may drive the radiosensitising effect. Moreover, *B. acidifaciens in vitro* has a greater effect on cell kill than ***F. prausnitzii* (butyrate-producer**; p<0.001), implying that metabolites other than **butyrate** may be involved in its effect.

Methods

All bacterial strains were obtained from DSMZ-German collection of microorganisms. Three strains of bacteria, namely *B. acidifaciens* (*BA*; DSM 15896), *Bifidobacterium animalis* (*Bif*; DSM10140), ***F. prausnitzii* (*FP*; DSM17677)**, and two cross-feeding combinations (***BA+FP*** and ***Bif+FP***) were cultured in Gifu Anaerobic Broth, Modified (GAM; Nissui Pharmaceutical, Japan).

Corrected version

Results

To validate the anti-tumoural effects of *B. acidifaciens*, we treated the bladder tumour cells with bacterial supernatants of *B. acidifaciens* and its cross-feeding with ***L. plantarum***, and compared their effects with *Bifidobacterium* (acetate-producer) and ***L. plantarum* (lactate-producer)**. Bacterial supernatants of *B. acidifaciens* and its cross-feeding with ***L. plantarum*** significantly increased cytotoxicity of bladder tumour cells compared to the other supernatants in day 2 (Figure 5K) and in day 3 (Additional file 1: Figure S5B).

Discussion

In this study, we revealed that bacterial supernatant from *B. acidifaciens* and its cross-feeding with ***L. plantarum*** caused significantly higher levels of cytotoxicity compared to the other supernatants (Figure 5K and Additional file 1: Figure S5B). This result supports our finding that *B. acidifaciens* may drive the radiosensitising effect. Moreover, *B. acidifaciens in vitro* has a greater effect on cell kill than ***L. plantarum* (lactate-producer**; p<0.001), implying that metabolites other than **lactate** may be involved in its effect.

Methods

All bacterial strains were obtained from DSMZ-German collection of microorganisms. Three strains of bacteria, namely *B. acidifaciens* (*BA*; DSM 15896), *Bifidobacterium animalis* (*Bif*; DSM10140), ***L. plantarum* (*LP*)**, and two cross-feeding combinations (***BA+LP*** and ***Bif+LP***) were cultured in Gifu Anaerobic Broth, Modified (GAM; Nissui Pharmaceutical, Japan).

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12915-021-01066-5.

Additional file 1: Figure S1. Similar bacterial components in the faecal and caecal microbiomes. **Figure S2.** Faecal butyrate levels and time taken for tumours to reach 50 mm^3. **Figure S3.** Differences in composition of the gut microbiome when tumours reached 350 mm^3. **Figure S4.** Individual mouse tumour growth curves. **Figure S5.** Cell survival analysis of RT112 bladder tumour cells treated with SCFAs and bacterial supernatants. **Figure S6.** Correlation of time to culling with *B. acidifaciens* or *Parabacteroides* genus abundance different groups. **Figure S7.** Effect of cage location of mice on relative abundance of *B.*

acidifaciens and *Parabacteroides* genus. **Table S1.** Rodent diets used in the study with varying levels of cellulose or inulin per 4000 kcal. **Table S2.** Details mouse diets, cages, *B. acidifaciens* relative abundance and time of culling.

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Reference

1. Then CK, Paillas S, Wang X, Hampson A, Kiltie AE. Association of Bacteroides acidifaciens relative abundance with high-fibre diet-associated radiosensitisation. BMC Biol. 2020;18(1):102 https://doi.org/10.1186/s12915-020-00836-x.