



## Author Correction: Cross-kingdom synthetic microbiota supports tomato suppression of Fusarium wilt disease

Correction to: *Nature Communications*  
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The original version of this article contained errors in Fig. 4. The same image was inadvertently duplicated for panel f and panel g. Panel g has been replaced with a correct image. In addition, in panel i, the data points were misaligned with the trend line.

In addition, there was an error in the first paragraph of the Results section, which incorrectly read ‘The fungal and bacterial compositions ( $R = 0.6317$  for bacteria, and  $R = 0.8876$  for fungi,  $P < 0.001$  for both) of rhizosphere microbial communities clustered into distinct groups that corresponded well to the host biogeography, as determined by analysis of molecular variance (AMOVA) and multivariate analysis of variance (PERMANOVA)’.

The correct version replaces this sentence with ‘The fungal and bacterial compositions ( $R = 0.6317$  for bacteria, and  $R = 0.8876$  for fungi,  $P = 0.001$  for both) of rhizosphere microbial communities clustered into distinct groups that corresponded well to the host biogeography, as determined by analysis of molecular variance (ANOSIM) and multivariate analysis of variance (PERMANOVA)’.

The methods description for ANOSIM was mistakenly omitted from the Supplementary Information. The sentence ‘The differences in the community composition of different groups were also calculated using the analysis of similarities (ANOSIM) (nested “anosim” in vegan R package)<sup>73</sup>’ has now been included.

These errors have been corrected in both the PDF and HTML versions of the article.

### Additional information

**Supplementary information** The online version contains supplementary material available at <https://doi.org/10.1038/s41467-023-42557-z>.

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