CORRECTION

Correction: Recentrifuge: Robust comparative analysis and contamination removal for metagenomics

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Fig 6 is missing information due to a bug in the software used to rotate the vectorial figure generated by Recentrifuge's *retest* script. The author apologizes for missing this error. A corrected version is provided here.

Legend:
- *Zea mays* [just-control contaminant]
- *Homo sapiens* [critical contaminant]
- *Delftia acidovorans* SPH-1 [native]
- *Delftia acidovorans* [SPH-1 strain native]
- *Cutibacterium acnes* [severe contaminant]
- *Salmonella enterica* subs. enterica [native]
- *Salmonella enterica* [native]
- *Escherichia coli* [mild contaminant]
- *Methylobacterium radiotolerans* [native]
- *Methanosarcina mazei* [CROSSOVER contaminant]
- *Lactobacillus helveticus* [native]
- *Methanosarcina barkeri* [CROSSOVER contaminant]
- *Salmonella virus Stitch* [native]
- *Malassezia globosa* [other contaminant]
- *Salmonella bongori* [native]
- *Pan troglodytes* [mild contaminant]
- *Methanobacterium formicicum* DSM3637 [native]
- *M. formicicum* JCM 10132 [other cont.]
- *M. formicicum* [DSM3637 strain native]
- *Propionibacterium virus SKKY* [other cont.]
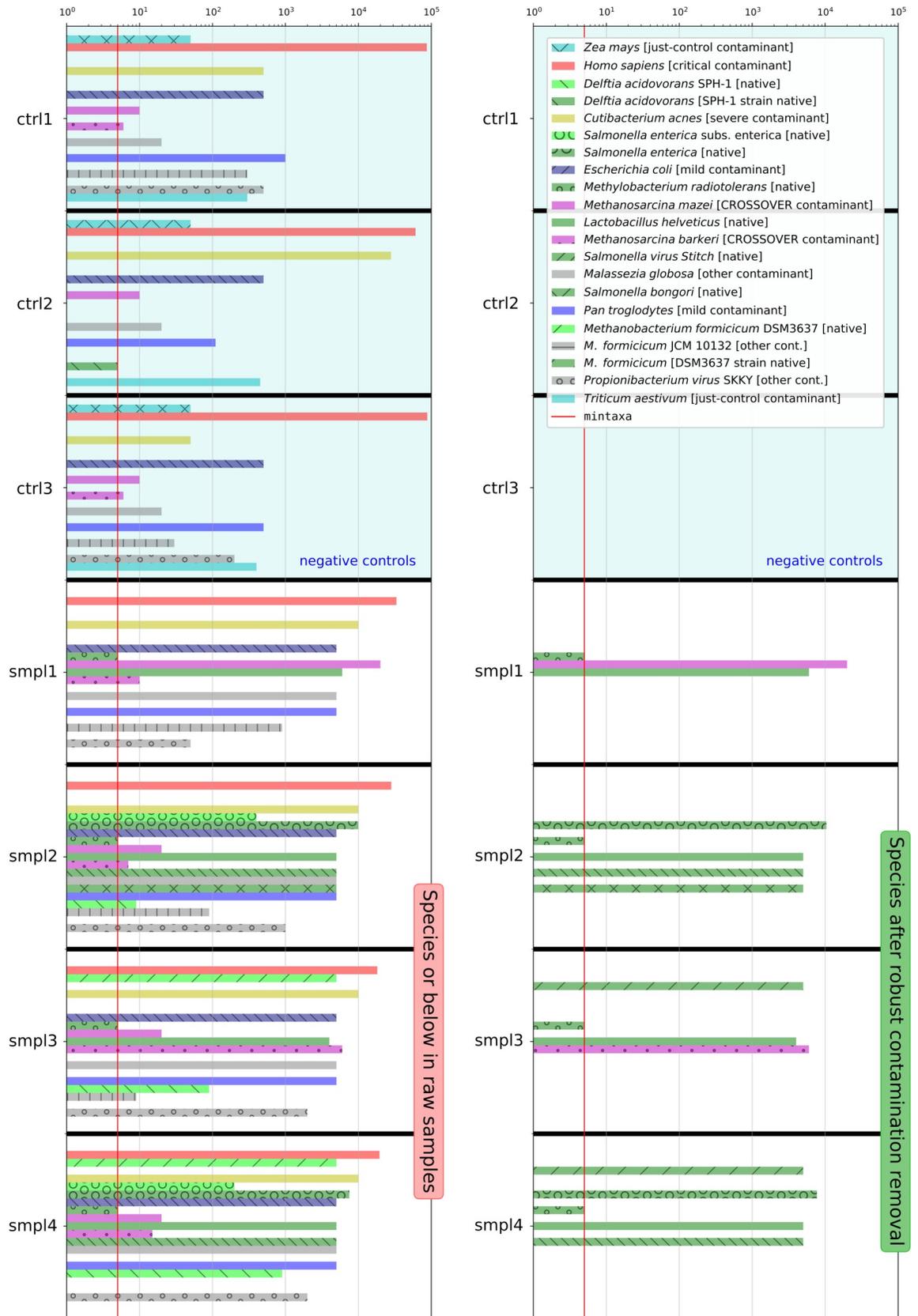- *Triticum aestivum* [just-control contaminant]
- mintaxa

Fig 6. Comparison of abundance histograms for some taxa (species or below) in the synthetic dataset before (raw samples) and after the robust contamination removal (`CTRL_species` samples). Data shown for samples `smpl1` to `smpl4` and the negative control samples (`ctrl1` to `ctrl3`), which were used by the contamination clearing process without modification. The legend of S13 Fig details the color code of the taxa. Here, the legend contains the name of each taxon followed by a note given in brackets; this remark is indicating either the type of contaminant, or which is the native strain of a species, or the native source for cross-contamination. Finally, the `mintaxa` level is drawn as a red line crossing all the samples.

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Reference

1. Martí JM (2019) Recentrifuge: Robust comparative analysis and contamination removal for metagenomics. PLoS Comput Biol 15(4): e1006967. https://doi.org/10.1371/journal.pcbi.1006967 PMID: 30958827