

## Erratum to: Evaluating next-generation sequencing for direct clinical diagnostics in diarrhoeal disease

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Originally published article contains error.  
Figures 1, 2 and 3 of the original article were published with missing dots. The correct figures are shown below.

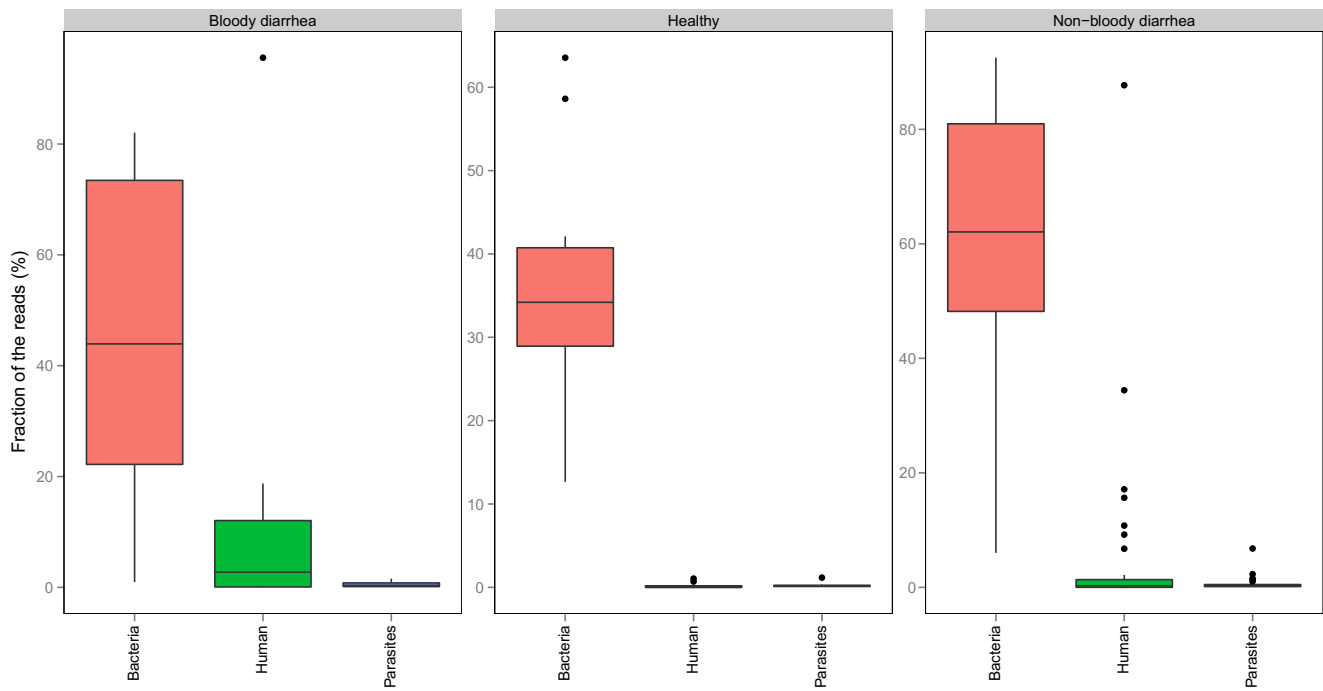
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The online version of the original article can be found at <http://dx.doi.org/10.1007/s10096-017-2947-2>

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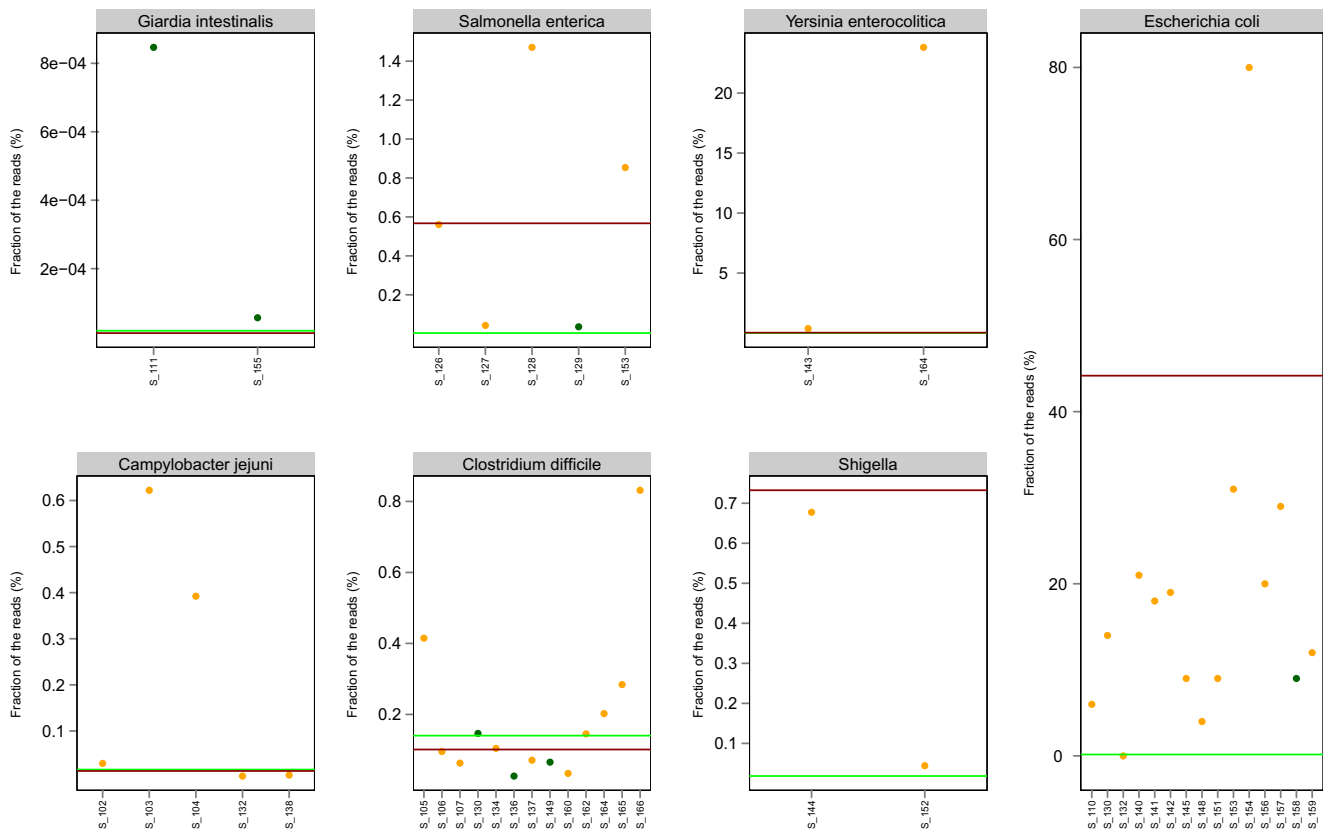
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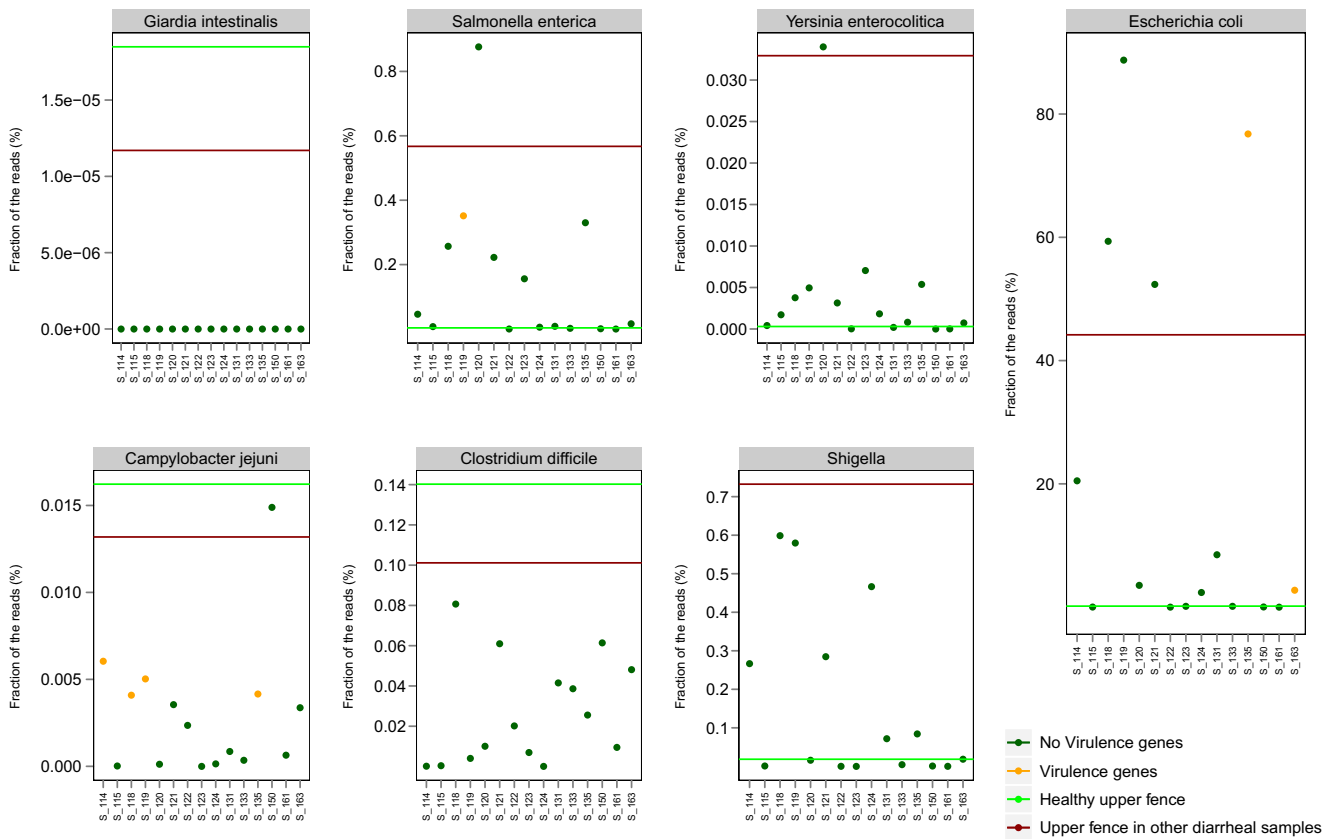
**Fig. 1** Abundance of bacterial, parasitic and human DNA among faecal samples. For each group of samples, healthy, patients with bloody diarrhoea and patients with non-bloody diarrhoea (or unknown), the

fraction of reads mapping to bacteria, parasites and human reference genomes is shown. The abundance is normalised according to the total number of reads in each specific sample



**Fig. 2** Relative abundance of pathogens in samples negative by conventional diagnostics. For samples that were either negative or virus-positive by conventional diagnostics, the fraction of reads mapping to each pathogen (*Giardia*, *Salmonella*, *Y. enterocolitica*, *E. coli*, *C. jejuni*, *C. difficile* and *Shigella*) was plotted. The orange dots

indicate the presence of pathogen-specific virulence genes, while the green dots indicate the absence. The upper fence (Q<sub>3</sub> + 1.5 × IQR) of the relative abundance for healthy controls and for the diarrhoea samples where the particular pathogen was not detected by conventional methods are shown



**Fig. 3** Relative abundance of pathogens in samples positive by conventional diagnostics. For each pathogen (*Giardia*, *Salmonella*, *Y. enterocolitica*, *E. coli*, *C. jejuni*, *C. difficile* and *Shigella*), the fraction of reads mapping to the pathogen is plotted for all samples positive by conventional diagnostic methods. The orange dots indicate the presence

of pathogen-specific virulence genes as determined by NGS analysis, while the green dots indicate the absence. The upper fence ( $Q_3 + 1.5 \times IQR$ ) of the relative abundance for the healthy controls and for the diarrhoea samples where the particular pathogen was not detected by conventional methods are shown