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Corrigendum: The effect of low-abundance OTU filtering methods on the reliability and variability of microbial composition assessed by 16S rRNA amplicon sequencing

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Error in Figure/Table

In the published article, there was an error in [Table 2](#) as published. Table 1 was incorrectly duplicated, while [Table 2](#) was omitted. The corrected [Table 2](#) and its caption The effect of filtering method on difference α -diversity metrics appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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TABLE 2 The effect of filtering method on different α -diversity metrics.

Filtering method	Observed OTUs Mean (SE)	Chao1 Mean (SE)	Shannon Mean (SE)	Inverse Simpson Mean (SE)
No filtering				
All OTUs included	266 (4.5)	380.9 (7.6)	3.243 (0.02)	13.289 (0.49)
Based on OTU abundance in whole dataset				
Filter OTUs with <0.1% abundance in dataset	65 (0.6)**	67.9 (0.7)**	2.922 (0.03)**	11.299 (0.38)*
Filter OTUs without >10 reads in at least one sample in dataset	189 (2.1)**	219.0 (2.6)**	3.218 (0.03)	13.196 (0.49)
Based on OTU abundance in individual sample				
Filter OTUs with one read	188 (2.7)**	188 (2.7)**	3.2 (0.03)	13.2 (0.5)
Filter OTUs with < 10 reads	106 (1.3)**	106 (1.3)**	3.164 (0.03)*	12.955 (0.48)
Based on OTU abundance in triplicate				
Filter OTUs without ≥ 10 reads in at least one of the three replicates	121 (1.4)**	121.4 (1.4)**	3.180 (0.03)	13.029 (0.48)
Filter OTUs if not present in all three replicates	169 (2.2)**	182.2 (2.6)**	3.206 (0.03)	13.141 (0.49)

* $p < 0.05$ vs All OTUs included, ** $p < 0.001$ vs All OTUs included.