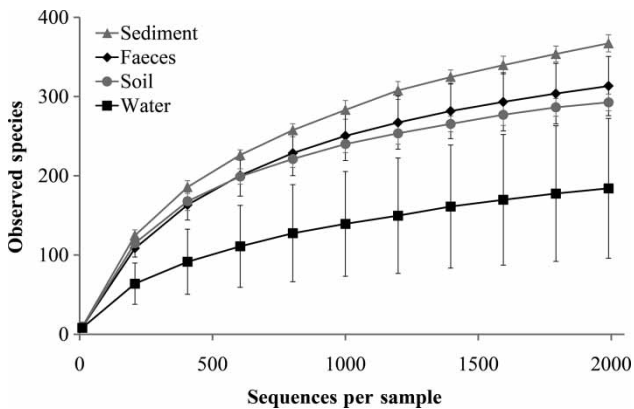


**Erratum: *Water Science and Technology* 72 (11), 1962–1972:  
Potential applications of next generation DNA sequencing of  
16S rRNA gene amplicons in microbial water quality  
monitoring, J. Vierheilig, D. Savio, R. E. Ley, R. L. Mach,  
A. H. Farnleitner and G. H. Reischer, doi: 10.2166/wst.2015.407**

The publisher regrets that due to an error in production, Figure 4 was incorrect in the online version of the above paper. We wish to apologise to the authors and to the readers for any inconvenience caused by this error. The correct version of Figure 4 is shown below:



**Figure 4** | Rarefaction analysis estimating average  $\alpha$ -diversity by counting the observed species in the samples of sediment ( $n = 2$ ), soil ( $n = 2$ ), faeces ( $n = 5$ ) and water ( $n = 9$ ). Error bars denote the standard deviation.

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