

S3 (table)

This supplementary information describes the acquisition and analysis of the z -value data presented in Fig. 3b of the manuscript. z -values for macroorganisms come from a large collection of data that were assembled by Drakare and colleagues¹. We used a total of 443 observations from the Drakare paper; for visual purposes, we eliminated 44 data points which had z -values that were negative or >1 . z -values for microorganisms ($n = 21$) came from the studies found in Table S3. We statistically compared the z -values for macroorganisms and microorganisms using a t-test on $\log_{10}$ transformed values to account for unequal variance.

Table S3

A collection of z -values for microorganisms from different systems.

Taxa/System	z -value
Salt marsh bacteria ²	0.0300
Soil bacteria ³	0.0300
Benthic ciliates ⁴	0.0430
Benthic diatoms ⁵	0.0660
Desert fungi ⁶	0.0740
Benthic ciliates ⁵	0.0770
Lake bacteria ⁷	0.1040
Aquatic Phytoplankton ⁸	0.1340
Sump tank bacteria ⁹	0.2700
Tree hole bacteria ¹⁰	0.2600
Soil bacteria ¹¹	0.4500
Soil fungi – ectomycorrhizal fungi ¹²	0.2000

Soil bacteria – functional gene sequences ¹²	0.0624
Soil bacteria – functional gene ¹²	0.0141
Soil bacteria – carbon degradation genes ¹²	0.0638
Soil bacteria – nitrification genes ¹²	0.0722
Soil bacteria – nitrogen reduction genes ¹²	0.0898
Soil bacteria – organic degradation genes ¹²	0.0850
Soil bacteria – metal reduction genes ¹²	0.0574
Soil fungi ¹²	0.0616
Soil archaea ¹²	0.0475
Soil bacteria ¹²	0.0748
Soil bacteria Gram-positive ¹²	0.0626
Soil bacteria Gram-negative ¹²	0.051
Soil bacteria α -Proteobacteria ¹²	0.0521
Soil bacteria β -Proteobacteria ¹²	0.0662
Soil bacteria δ -Proteobacteria ¹²	0.0519
Soil bacteria γ -Proteobacteria ¹²	0.0644

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