

S1 (table)

This supplementary information includes the data and corresponding citations presented in Box 1 Figure for the proportion of inactive cells in different systems.

Active cells were assessed using general eubacterial FISH (fluorescent *in situ* hybridization) probes or through the uptake and incorporation of CTC (5-cyano-2,3-ditolyl tetrazolium chloride). The total number of cells was determined using DAPI staining. The proportion of inactive cells was estimated as $[1 - (\text{active cell count} / \text{total cell count})]$.

System	Method	Percent Inactive
Activated sludge ¹	CTC	60
Activated sludge ²	FISH	11
Activated sludge ³	FISH	30
Activated sludge ⁴	FISH	38
Activated sludge ⁵	FISH	20
Human feces ⁶	FISH	30
Human feces ⁷	FISH	23
Human feces ⁸	FISH	3
Human feces ⁹	FISH	32
Lake ¹⁰	FISH	49
Lake ¹⁰	FISH	54
Lake ¹⁰	FISH	39
Lake ¹⁰	FISH	54
Lake ¹⁰	FISH	54
Lake ¹⁰	FISH	54
Lake ¹⁰	FISH	51
Lake ¹⁰	FISH	41
Lake ¹⁰	FISH	39
Lake ¹⁰	FISH	56
Lake ¹⁰	FISH	45
Lake ¹⁰	FISH	57
Lake ¹⁰	FISH	51
Lake ¹⁰	FISH	47
Lake ¹⁰	FISH	41
Lake ¹¹	FISH	23
Lake ¹¹	FISH	42
Lake ¹¹	FISH	37
Lake ¹¹	FISH	47
Lake ¹¹	FISH	39
Lake ¹¹	FISH	50
Lake ¹¹	FISH	57

Lake ¹¹	FISH	58
Lake ¹¹	FISH	50
Lake ¹¹	FISH	52
Lake ¹¹	FISH	39
Lake ¹¹	FISH	36
Lake ¹¹	FISH	23
Lake ¹¹	FISH	18
Lake ¹¹	FISH	55
Lake ¹¹	FISH	43
Lake ¹¹	FISH	48
Lake ¹¹	FISH	41
Lake ¹¹	FISH	60
Lake ¹¹	FISH	56
Lake ¹¹	FISH	56
Lake ¹¹	FISH	47
Lake ¹¹	FISH	56
Lake ¹¹	FISH	51
Lake ¹¹	FISH	35
Lake ¹¹	FISH	30
Lake ¹¹	FISH	22
Lake ¹¹	FISH	37
Lake ¹¹	FISH	45
Lake ¹¹	FISH	57
Lake ¹¹	FISH	42
Lake ¹¹	FISH	64
Lake ¹¹	FISH	74
Lake ¹¹	FISH	56
Lake ¹¹	FISH	41
Lake ¹¹	FISH	57
Lake ¹¹	FISH	35
Lake ¹¹	FISH	36
Lake ¹¹	FISH	41
Marine ¹²	FISH	74
Marine ¹⁰	FISH	58
Marine ¹⁰	FISH	4
Marine ¹⁰	FISH	15
Marine ¹⁰	FISH	43
Marine ¹⁰	FISH	39
Marine ¹⁰	FISH	28
Marine ¹³	FISH	12
Marine ¹³	FISH	28
Marine ¹³	FISH	45
Marine ¹³	FISH	12
Marine ¹³	FISH	20
Marine ¹³	FISH	35
Marine ¹³	FISH	20
Marine ¹³	FISH	19
Marine ¹³	FISH	30

Marine ¹³	FISH	12
Marine ¹³	FISH	15
Marine ¹⁴	FISH	30
Marine ¹⁴	FISH	25
Marine ¹⁴	FISH	38
Marine ¹⁴	FISH	78
Marine ¹⁴	FISH	22
Marine ¹⁴	FISH	47
Marine ¹⁴	FISH	64
Marine ¹⁰	FISH	28
Marine ¹⁰	FISH	36
Marine ¹⁰	FISH	38
Marine ¹⁰	FISH	34
Marine ¹⁰	FISH	61
Marine ¹⁵	FISH	41.1
Marine ¹⁵	FISH	28.6
Marine ¹⁵	FISH	39.7
Marine ¹⁵	FISH	68.8
Soil ¹⁶	CTC	96
Soil ¹⁷	CTC	72
Soil ¹⁸	CTC	75
Soil ¹⁹	CTC	96
Soil ²⁰	FISH	95
Soil ²¹	FISH	61

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Supplementary information S2 (box)

This supplementary information provides a brief description of the methods used for the metagenomic analyses presented in Box 2. Percent of genomes were calculated using *recA* recovery and gene length correction¹. Tblastx was used with *hipA*, *hipB*, *relE*, *relB*, *mazE*, *mazF*, *yafQ*, and *dinJ*, sequences from the *E. coli* K-12 genome accessed using <http://ecogene.org/> and the *RpfC* sequence from the *M. tuberculosis* H37Rv genome accessed with NCBI entrez. Metagenome matches to the above query sequences were reverse-blasted against NCBI's non-redundant protein sequences (nr) using blastx for quality control.

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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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