

1 **Supplementary material**

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4 **Probing the fabric of the rare biosphere**

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11 Supplementary Figure 1. OTU accumulation curves of the Western English Channel sample
12 from Gibbons et al. (2013) (A) without singletons, as they analyzed it in the paper, and (B)
13 with the singletons they removed for their analysis. The black line is the Weibull cumulative
14 function fit ($R^2=0.99$) for both OTU accumulation curves. The Akaike's information criterion
15 (AIC) is indicated.

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35 Supplementary Table 1. The three mathematical functions that best fit the species
 36 accumulation curves and their goodness of fit. Coefficient of determination (R^2), residual
 37 sum of squares (RSS) and Akaike's information criterion (AIC) are shown. R^2 in percentage
 38 represents the model efficiency. The best fit corresponds to the highest R^2 and the lowest
 39 RSS and AIC, in this case found for the Weibull cumulative function. The parameters are
 40 indicated by letters a, b and c.

Function		Number of Parameters	Sample	R^2	RSS	AIC
Michaelis-Menten	(ax)/(b+x)	2	Surface	0.984	$5\,897 \times 10^2$	4\,979.17
			Bottom	0.989	$5\,325 \times 10^3$	6\,900.56
Rational	(a+bx)/(1+cx)	3	Surface	0.997	$1\,181 \times 10^2$	4\,174.13
			Bottom	0.997	$1\,139 \times 10^3$	6\,014.23
Weibull Cumulative	$a(1-\exp(-bx))^c$	3	Surface	0.999	2\,978	2\,326.46
			Bottom	0.999	6\,670	3\,053.40

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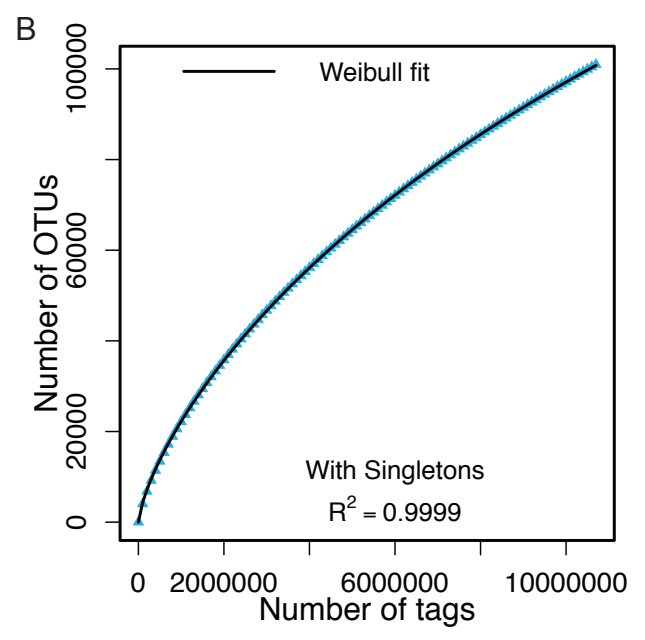
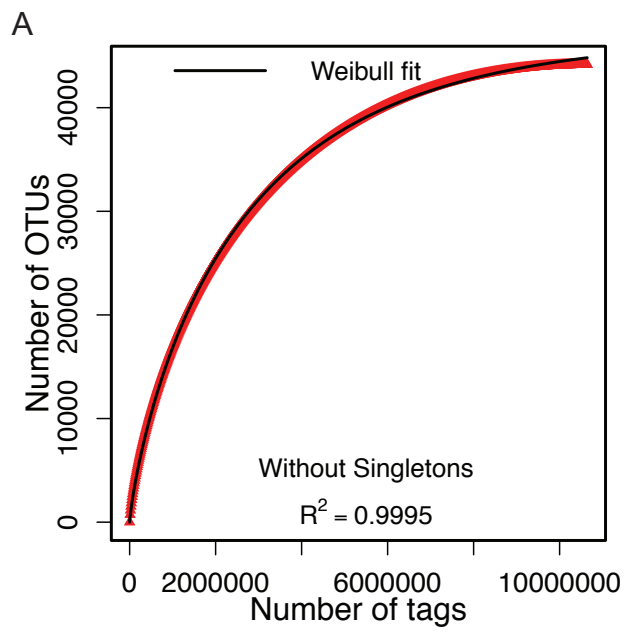
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44 Supplementary Table 2. Isolates not matching the tag sequences. Isolates' closest relative
 45 according to BLAST results, % of identity with the BLAST reference strain (identity
 46 BLAST), GenBank accession number of the BLAST reference strain and number of isolates
 47 of each taxa sequenced. *Actino* (*Actinobacteria*), *Bact* (*Bacteroidetes*), *Firm* (*Firmicutes*),
 48 *Alpha-P* (*Alpha-Proteobacteria*) and *Gamma-P* (*Gamma-Proteobacteria*).

Isolates' closest relative	Identity BLAST	GenBank accession number	Isolates number
<i>Microbacterium aquimaris</i> (Actino)	99.6 %	HQ009858	14
<i>Thalassospira</i> sp. (Alpha-P)	100 %	EU440837	12
<i>Fulvimarina pelagi</i> (Alpha-P)	96 %	HQ622550	8
<i>Alcanivorax</i> sp. (Gamma-P)	99.7 %	AB681671	6
<i>Devosia subaequoris</i> (Alpha-P)	100 %	JQ844475	5
<i>Alterierythrobacter</i> sp. (Alpha-P)	100 %	FM177586	4
<i>Alteromonas macleodii</i> (Gamma-P)	99.9 %	CP003917	4
<i>Erythrobacter</i> sp. (Alpha-P)	100 %	AB429073	3
<i>Brevundimonas</i> sp. (Alpha-P)	99.9 %	HQ830182	2
<i>Roseivirga spongicola</i> (Bact)	99.8 %	NR043531	2
<i>Devosia hwasunensis</i> (Alpha-P)	99 %	HQ697727	2
Rhizobiales family (Alpha-P)	96 %	HQ622550	2
<i>Arthrobacter oxydans</i> (Actino)	100 %	EU086823	1
<i>Emticicia</i> sp. (Bact)	100 %	JX426065	1
<i>Halomonas</i> sp. (Gamma-P)	100 %	HE586874	1
<i>Marinobacter hydrocarbonoclasticus</i> (Gamma-P)	100 %	JQ799097	1
<i>Nitratireductor</i> sp. (Alpha-P)	99.9 %	AM981316	1
<i>Nocardioides marinus</i> (Actino)	99.9 %	NR043787	1
<i>Pseudomonas</i> sp. (Gamma-P)	99.9 %	JN244973	1
<i>Sphingobium yanoikuyae</i> (Alpha-P)	99.9 %	DQ659593	1
<i>Thalassospira permensis</i> (Alpha-P)	99.9 %	FJ860275	1
<i>Alphaproteobacterium</i>	99.8 %	AY515421	1
<i>Martellella mediterranea</i> (Alpha-P)	99.8 %	EU440955	1
Uncultured <i>Nitratireductor</i> sp. (Alpha-P)	99.7 %	AM981316	1

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Supplementary Figure 1
Crespo et al.