

# Supplementary material for “Predicting functional capabilities of host-specific prokaryotic communities associated with Antarctic continental shelf sponges”

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## Section 1: Sponge barcoding and morphological taxonomy

For morphological taxonomic identification, the sponge samples stored in 70% EtOH were investigated by light microscopy at the Senckenberg Research Institute and Natural Museum. The photos taken of the complete sponges directly upon their collection were also used for identification. Skeletal elements (spicules) of the sponges were studied upon preparations following the generally accepted technique of dissolving soft tissue of fragments of sponge in nitric acid; the preparation procedure is described e.g. by Boury-Esnault and Rützler (Boury-Esnault and Rützler, 1997). The spicules were mounted on microscope slides and studied by light microscopy. For the identification relevant literature (Hentschel, 1914; Koltun, 1964; Plotkin and Janussen, 2008) and the World Porifera Database ([www.marinespecies.org/porifera/](http://www.marinespecies.org/porifera/)) were consulted. The sponge samples used for morphological identification are housed in the Senckenberg Nature Museum (Frankfurt am Main, Germany).

## Extraction, PCR and sequencing

DNA was extracted using Spin Columns (Machery-Nagel) following the manufacturer's protocol. Fragments of the mitochondrial cytochrome oxidase subunit 1 (standard barcoding fragment) and the C-Region of the large nuclear ribosomal subunit (28S) were amplified using the degenerated version of universal barcoding primers dgLCO1490 (GGT CAA CAA ATC ATA AAG AYA TYG G) with dgHCO2198 (TAA ACT TCAG GGT GAC CAA ARA AYC A) (Meyer and Paulay,

2005) and 28S-C2-fwd (GAA AAG AAC TTT GRA RAG AGA GT) with 28S-D2-rev (TCC GTG TTT CAA GAC GGG) (Chombard et al., 1998). These two markers are the current standards for sponge DNA barcoding and constitute the currently most used marker for sponge biodiversity assessments (Erpenbeck et al., 2008, 2016). The 15 µL PCR mix consisted of 2.5 µL 5x green GoTaq® PCR Buffer (Promega Corp, Madison, WI), 2µL 25mM MgCl<sub>2</sub> (Promega Corp, Madison, WI), 1 µL 10mM dNTPs, 1 µL BSA (100µg/ml), 0.5 µL each primer (5µM), 3.9 µL water, 0.1µL GoTaq® DNA polymerase (5u/µl) (Promega Corp, Madison, WI) and 1 µL DNA. Temperature profile comprised an initial denaturation phase of 94°C for 3 min followed by 35 cycles of 30 s denaturation at 94°C, 20 s annealing at 51°C, 60 s elongation at 72°C each and a final elongation at 72°C for 5 min. PCR products were purified with the freeze-squeeze method (Tautz and Renz, 1983) before cycle sequencing with the BigDye-Terminator Mix v3.1 (Applied Biosystems) following the manufacturer's protocol. Both strands of the template were sequenced on an ABI 3730 automated sequencer. Sequences were basecalled, trimmed and assembled in CodonCode Aligner v 3.7.1.1 ([www.codoncode.com](http://www.codoncode.com)). Sequences are deposited in NCBI Genbank under accession numbers MH371760 - MH371774.

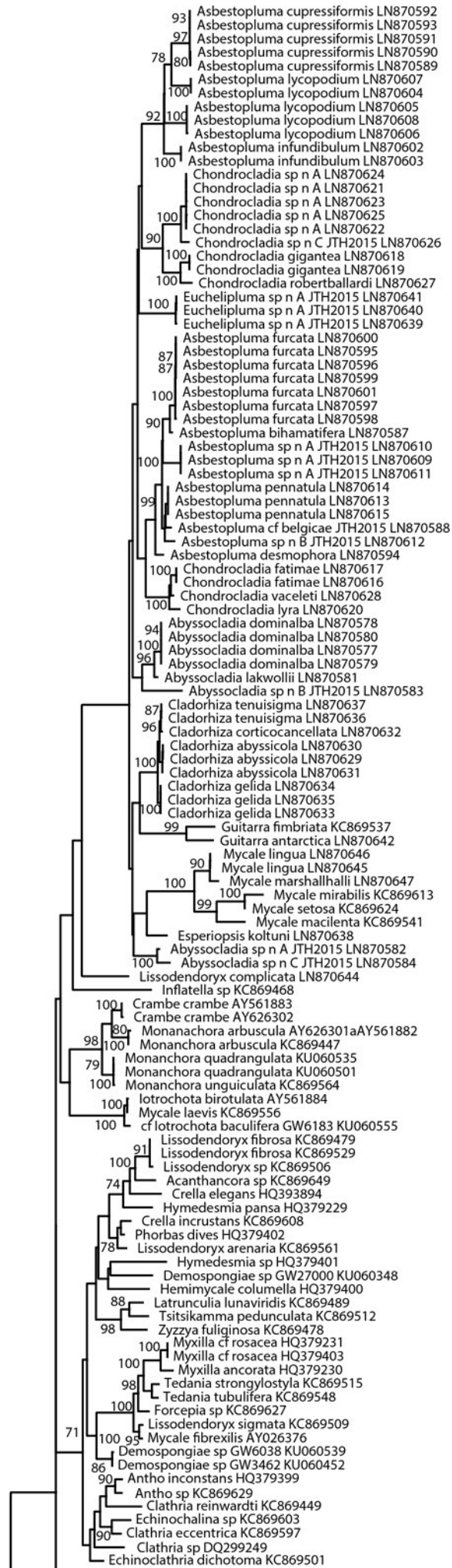
Phylogenetic analyses were performed after incorporation of all available 28S and CO1 respectively sequences as currently published in NCBI Genbank and the Sponge Genetree Server ([www.spongegenetrees.org](http://www.spongegenetrees.org)). Here, secondary structure information has been implemented where feasible as suggested earlier (Erpenbeck et al., 2007). Phylogenetic reconstructions were performed with RAxML 7.2.8 as implemented in GENEIOUS 8.1.6. (<http://www.geneious.com>) under the GTRCAT model and 100 rapid bootstrap replicates (Kearse et al., 2012).

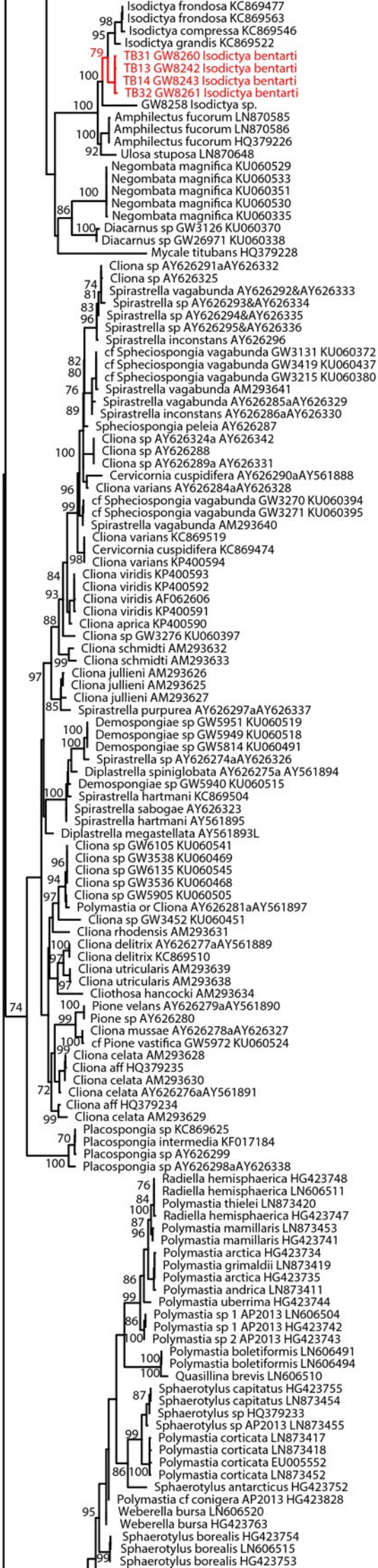
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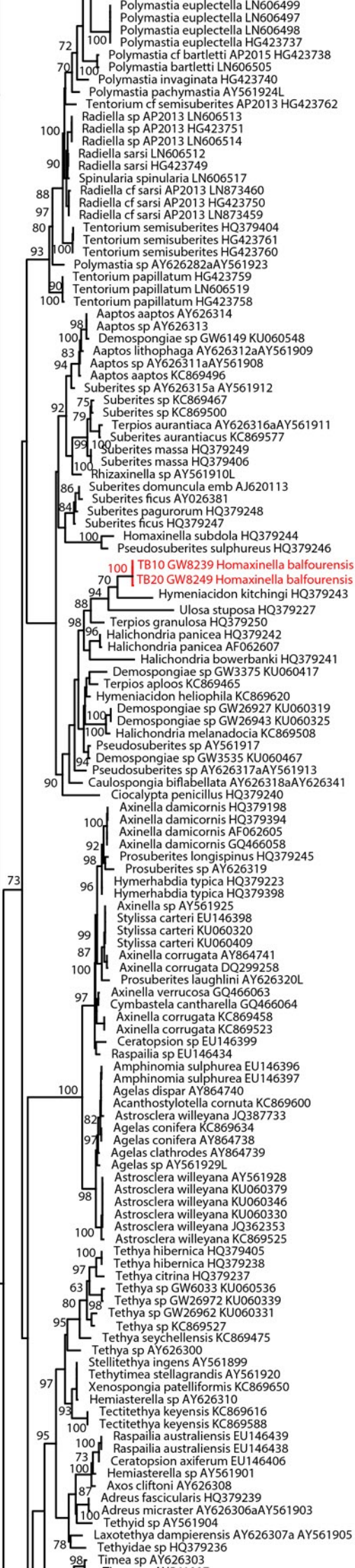
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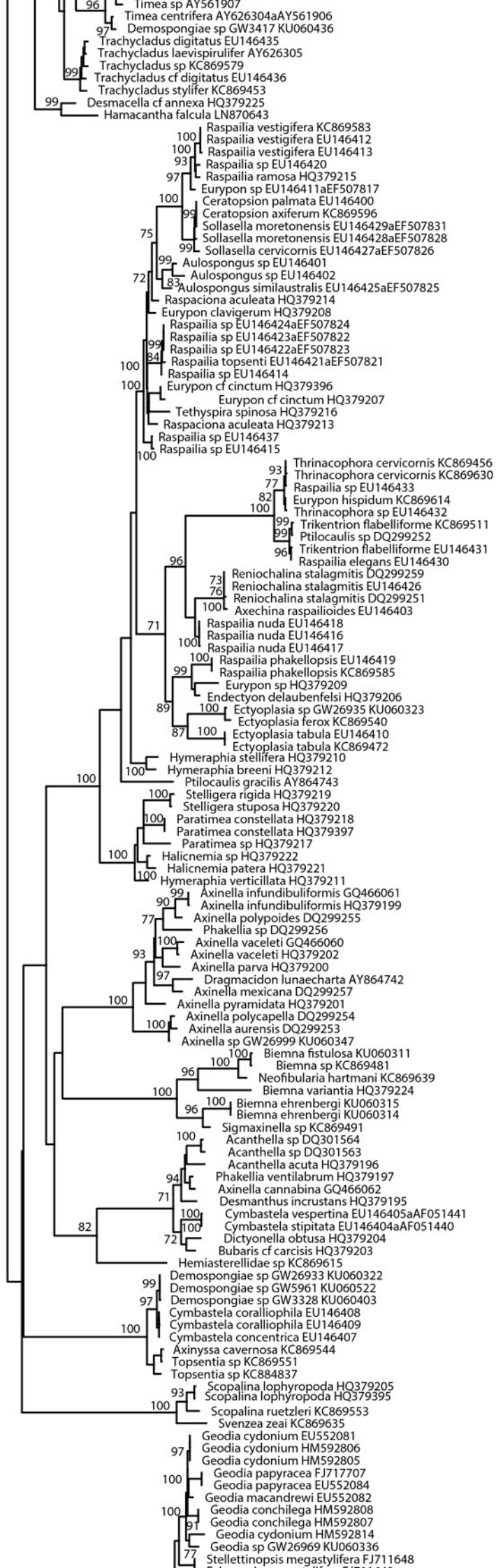
Section 2: Supplementary Figures and Tables

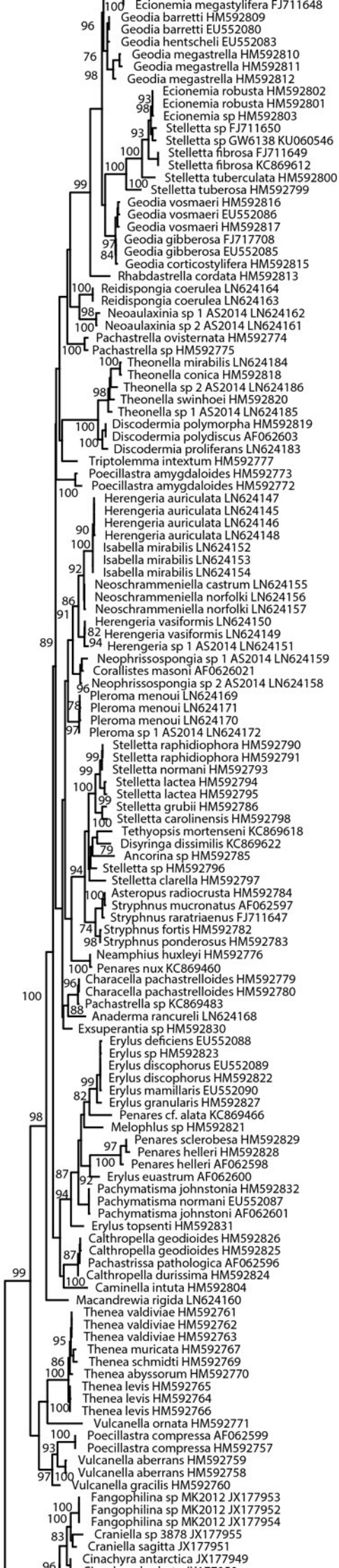


















**Supplementary Figure 1.** Maximum-likelihood phylogram based on the 28S C-Region obtained from different sponges with the target taxa in red. Numbers following the taxon names are NCBI GenBank accession numbers. Numbers on branches depict bootstrap support > 70. The scale bar depicts substitutions per site.

**Supplementary Table 1.** Senckenberg Collection Identifiers and sample IDs.

<b>SMF</b>	<b>Sample</b>
	11647 TB01
	11651 TB05
	11656 TB10
	11657 TB11
	11659 TB13
	11660 TB14
	11662 TB16
	11664 TB18
	11665 TB19
	11666 TB20
	11667 TB21
	11668 TB22
	11673 TB27
	11677 TB31
	11678 TB32

**Supplementary Table 2.** Phylum rank absolute abundance table.

<b>Taxon</b>	<b><i>Haliclona</i> sp.</b>	<b><i>Haliclona</i> sp.</b>	<b><i>Haliclona</i> sp. sum</b>	<b><i>A. leptoderma</i></b>	<b><i>A. leptoderma</i></b>
Proteobacteria	96	109	205	24	40
Bacteroidetes	37	47	84	9	8
Actinobacteria	7	4	11	12	10
Nitrospinae	1	4	5	2	3
Planctomycetes	2	3	5	0	0
Marinimicrobia_(SAR406_clade)	1	2	3	0	0
Firmicutes	1	5	6	2	0
Acidobacteria	1	0	1	1	0
Chloroflexi	1	0	1	0	5
Verrucomicrobia	1	0	1	0	0
Gemmatimonadetes	0	0	0	0	0
Spirochaetae	0	1	1	0	0
Nitrospirae	1	0	1	0	0
Euryarchaeota	0	0	0	0	0
Microgenomates	0	0	0	0	0
Cyanobacteria	0	0	0	0	0
Thaumarchaeota	0	0	0	0	1
SBR1093	0	0	0	0	1
Aminicenantes	0	0	0	0	0
Tenericutes	1	0	1	0	0
Gracilibacteria	0	0	0	0	0
Parcubacteria	0	0	0	0	0
Fusobacteria	0	0	0	0	0
PAUC34f	0	0	0	0	0
Fibrobacteres	0	0	0	0	0
Ignavibacteriae	0	0	0	0	0
Chlamydiae	0	0	0	0	0
Deferribacteres	0	0	0	0	0
Elusimicrobia	0	0	0	0	0
Lentisphaerae	0	0	0	0	0
TM6_(Dependentiae)	1	0	1	0	0

<i>A. leptoderma</i>	<i>A. leptoderma</i>	<i>A. leptoderma</i>	<i>A. leptoderma</i>	<i>A. leptoderma</i>	<i>A. leptoderma</i>	<i>A. leptoderma</i> sum	<i>H. balfourensis</i>	<i>H. balfourensis</i>
50	79	120	132	106		551	53	116
5	25	33	52	38		170	33	60
15	27	43	58	22		187	2	12
1	5	6	6	7		30	2	5
1	5	9	5	9		29	5	9
0	1	5	5	1		12	0	1
0	2	1	3	7		15	1	0
6	0	1	6	2		16	0	0
4	1	2	2	0		14	0	0
0	0	2	0	0		2	0	2
1	1	1	4	1		8	0	1
0	1	1	1	0		3	0	1
0	0	0	1	0		1	0	1
0	0	0	0	0		0	0	0
0	0	0	1	1		2	0	1
0	0	0	0	0		0	0	0
0	0	0	1	1		3	0	0
1	1	0	0	0		3	0	0
0	0	0	1	1		2	0	0
0	0	0	0	1		1	0	0
0	0	0	0	0		0	0	1
0	0	0	0	0		0	1	0
0	0	0	0	0		0	0	0
0	0	0	0	0		0	0	0
0	0	0	0	0		0	0	0
0	0	0	0	0		0	0	0
0	0	0	0	0		0	0	0
0	0	0	0	0		0	0	0
0	0	0	0	1		1	0	0
0	0	0	1	0		1	0	0
0	0	0	1	0		1	0	0
0	0	1	0	0		1	0	0
0	0	0	0	0		0	0	0

[illegible]



[illegible]

**Supplementary Table 3.** Kruskal-Wallis Sum Test and pairwise Dunn Test for the OTU richness, Phylogenetic diversity PD, and Inverse Simpson D-1 alpha-diversity indices. Kruskal-Wallis values are chi-squared  $\chi^2$ , degrees of freedom  $df$ , and  $p$  values. Dunn Test values are Z score, unadjusted  $p$  value, and Benjamini-Hochberg adjusted  $p$  values.

Kruskal-Wallis Rank Sum Test					
	$\chi^2$	$df$	$p$ -value		
OTU richness	3.60	4	0.462		
Dunn Test					
	Z	$p$ .unadj	$p$ .adj		
OTU richness	<i>A. leptoderma</i> - <i>Haliclona</i> sp.	-0.94	0.346	0.576	
	<i>A. leptoderma</i> - <i>H. balfourensis</i>	-0.31	0.753	0.753	
	<i>Haliclona</i> sp. - <i>H. balfourensis</i>	0.50	0.614	0.768	
	<i>A. leptoderma</i> - <i>I. bentarti</i>	1.21	0.228	0.759	
	<i>Haliclona</i> sp. - <i>I. bentarti</i>	1.75	0.081	0.809	
	<i>H. balfourensis</i> - <i>I. bentarti</i>	1.16	0.244	0.611	
	<i>A. leptoderma</i> - seawater	0.42	0.675	0.750	
	<i>Haliclona</i> sp. - seawater	1.25	0.211	1.000	
	<i>H. balfourensis</i> - seawater	0.59	0.554	0.792	
	<i>I. bentarti</i> - seawater	-0.96	0.335	0.670	
Kruskal-Wallis Rank Sum Test					
	$\chi^2$	$df$	$p$ -value		
Phylogenetic diversity PD	10.00	4	0.040		
Dunn Test					
	Z	$p$ .unadj	$p$ .adj		
Phylogenetic diversity PD	<i>A. leptoderma</i> - <i>Haliclona</i> sp.	-2.33	<b>0.020</b>	0.196	
	<i>A. leptoderma</i> - <i>H. balfourensis</i>	-2.18	<b>0.029</b>	0.098	
	<i>Haliclona</i> sp. - <i>H. balfourensis</i>	0.13	0.900	1.000	
	<i>A. leptoderma</i> - <i>I. bentarti</i>	-0.17	0.863	1.000	
	<i>Haliclona</i> sp. - <i>I. bentarti</i>	2.04	0.042	0.083	
	<i>H. balfourensis</i> - <i>I. bentarti</i>	1.89	0.059	0.098	
	<i>A. leptoderma</i> - seawater	-0.36	0.719	1.000	
	<i>Haliclona</i> sp. - seawater	2.23	<b>0.026</b>	0.130	
	<i>H. balfourensis</i> - seawater	2.06	<b>0.039</b>	0.098	
	<i>I. bentarti</i> - seawater	-0.11	0.913	0.913	
Kruskal-Wallis Rank Sum Test					
	$\chi^2$	$df$	$p$ -value		
Phylogenetic diversity PD	19.13	4	< 0.001		
Dunn Test					
	Z	$p$ .unadj	$p$ .adj		
Inverse Simpson D <sup>-1</sup>	<i>A. leptoderma</i> - <i>Haliclona</i> sp.	-3.11	<b>0.002</b>	<b>0.019</b>	
	<i>A. leptoderma</i> - <i>H. balfourensis</i>	-1.85	0.064	0.107	
	<i>Haliclona</i> sp. - <i>H. balfourensis</i>	1.01	0.313	0.392	
	<i>A. leptoderma</i> - <i>I. bentarti</i>	0.19	0.846	0.940	
	<i>Haliclona</i> sp. - <i>I. bentarti</i>	3.02	<b>0.003</b>	<b>0.008</b>	
	<i>H. balfourensis</i> - <i>I. bentarti</i>	1.85	0.064	0.127	
	<i>A. leptoderma</i> - seawater	-3.03	<b>0.002</b>	<b>0.012</b>	
	<i>Haliclona</i> sp. - seawater	1.37	0.169	0.242	
	<i>H. balfourensis</i> - seawater	0.05	0.956	0.956	
	<i>I. bentarti</i> - seawater	-2.71	<b>0.007</b>	<b>0.017</b>	

**Supplementary Table 4.** Full list of LEFSE significant predicted pathways with source (Environment), LDA effect size and *p* values.

KEGG Pathway	Environment	Effect size	p value
ko00524_Butirosin_and_neomycin_biosynthesis	<i>Antarctotetilla leptoderma</i>	2.026296592	0.003517133
ko04727_GABAergic_synapse	<i>Antarctotetilla leptoderma</i>	2.368294939	0.000116
ko00030_Pentose_phosphate_pathway	<i>Antarctotetilla leptoderma</i>	3.087554963	0.006533041
ko00643_Styrene_degradation	<i>Antarctotetilla leptoderma</i>	2.427082746	0.001787937
ko00500_Starch_and_sucrose_metabolism	<i>Antarctotetilla leptoderma</i>	3.936780033	0.000279778
ko04141_Protein_processing_in_endoplasmic_reticulum	<i>Antarctotetilla leptoderma</i>	2.537286149	0.000421527
ko03410_Base_excision_repair	<i>Antarctotetilla leptoderma</i>	2.813844487	0.000120536
ko00053_Ascorbate_and_aldarate_metabolism	<i>Antarctotetilla leptoderma</i>	2.728472589	0.000178883
ko04940_Type_1_diabetes_mellitus	<i>Antarctotetilla leptoderma</i>	2.283259258	0.000580683
ko00364_Fluorobenzoate_degradation	<i>Antarctotetilla leptoderma</i>	2.227002669	0.000900738
ko03040_Spliceosome	<i>Antarctotetilla leptoderma</i>	2.149156841	0.001492704
ko00785_Lipoic_acid_metabolism	<i>Antarctotetilla leptoderma</i>	2.625711975	0.001299006
ko00680_Methane_metabolism	<i>Antarctotetilla leptoderma</i>	3.342538625	0.000190814
ko00020_Citrate_cycle_TCA_cycle_	<i>Antarctotetilla leptoderma</i>	2.760652549	0.000359519
ko00521_Streptomycin_biosynthesis	<i>Antarctotetilla leptoderma</i>	2.828712451	0.000796835
ko00450_Selenocompound_metabolism	<i>Antarctotetilla leptoderma</i>	2.696802592	0.001981919
ko00473_D_Alanine_metabolism	<i>Antarctotetilla leptoderma</i>	3.062663226	0.000116
ko04122_Sulfur_relay_system	<i>Antarctotetilla leptoderma</i>	2.898743054	0.00180802
ko00281_Geraniol_degradation	<i>Antarctotetilla leptoderma</i>	2.708902593	0.009864855
ko00710_Carbon_fixation_in_photosynthetic_organisms	<i>Antarctotetilla leptoderma</i>	2.677981744	0.000465904
ko00561_Glycerolipid_metabolism	<i>Antarctotetilla leptoderma</i>	2.416077404	0.000963954
ko03030_DNA_replication	<i>Antarctotetilla leptoderma</i>	2.632737971	0.022911123
ko00010_Glycolysis_Gluconeogenesis	<i>Antarctotetilla leptoderma</i>	2.87397348	0.000136986
ko00750_Vitamin_B6_metabolism	<i>Antarctotetilla leptoderma</i>	2.963046844	0.000410997
ko00520_Amino_sugar_and_nucleotide_sugar_metabolism	<i>Antarctotetilla leptoderma</i>	3.476857892	0.000353711
ko00984_Steroid_degradation	<i>Antarctotetilla leptoderma</i>	2.453208353	0.01972158
ko01051_Biosynthesis_of_ansamycins	<i>Antarctotetilla leptoderma</i>	2.886861449	0.000168553
ko00280_Valine_leucine_and_isoleucine_degradation	<i>Antarctotetilla leptoderma</i>	3.179931392	0.000563026
ko01057_Biosynthesis_of_type_II_polyketide_products	<i>Antarctotetilla leptoderma</i>	2.002057698	0.0018523
ko03050_Proteasome	<i>Antarctotetilla leptoderma</i>	3.036367727	0.000364478
ko00640_Propanoate_metabolism	<i>Antarctotetilla leptoderma</i>	2.854646565	0.000511905
ko00040_Pentose_and_glucuronate_interconversions	<i>Antarctotetilla leptoderma</i>	3.186525613	0.001258255
ko03008_Ribosome_biogenesis_in_eukaryotes	<i>Antarctotetilla leptoderma</i>	2.402322839	0.000127943
ko00460_Cyanoamino_acid_metabolism	<i>Antarctotetilla leptoderma</i>	2.661995358	0.000173221
ko05134_Legionellosis	<i>Antarctotetilla leptoderma</i>	2.424431749	0.002297836
ko00562_Inositol_phosphate_metabolism	<i>Antarctotetilla leptoderma</i>	3.263219906	0.000192441
ko00760_Nicotinate_and_nicotinamide_metabolism	<i>Antarctotetilla leptoderma</i>	3.031396711	0.000501807
ko00909_Sesquiterpenoid_and_triterpenoid_biosynthesis	<i>Antarctotetilla leptoderma</i>	2.663602143	0.000301289
ko00940_Phenylpropanoid_biosynthesis	<i>Antarctotetilla leptoderma</i>	2.717343621	0.000174563
ko00730_Thiamine_metabolism	<i>Antarctotetilla leptoderma</i>	2.704988029	0.006508727
ko00603_Glycosphingolipid_biosynthesis_globo_series	<i>Antarctotetilla leptoderma</i>	2.160273521	0.0001905
ko03420_Nucleotide_excision_repair	<i>Antarctotetilla leptoderma</i>	3.188051829	0.000546932
ko02040_Flagellar_assembly	<i>Antarctotetilla leptoderma</i>	3.584550623	0.000173086
ko00410_beta_Alanine_metabolism	<i>Antarctotetilla leptoderma</i>	2.417113639	0.000312975
ko00900_Terpenoid_backbone_biosynthesis	<i>Antarctotetilla leptoderma</i>	3.074155697	0.003022969
ko00400_Phenylalanine_tyrosine_and_tryptophan_biosynthesis	<i>Antarctotetilla leptoderma</i>	3.061424715	0.004743337
ko05152_Tuberculosis	<i>Antarctotetilla leptoderma</i>	2.482032249	0.000116
ko00522_Biosynthesis_of_12_14_and_16_membered_macrolides	<i>Antarctotetilla leptoderma</i>	2.661641063	0.000292778
ko00930_Caprolactam_degradation	<i>Antarctotetilla leptoderma</i>	2.114480702	0.032275239
ko03440_Homologous_recombination	<i>Antarctotetilla leptoderma</i>	3.129670704	0.003769628
ko00604_Glycosphingolipid_biosynthesis_ganglio_series	<i>Antarctotetilla leptoderma</i>	2.169664954	0.000224197
ko00471_D_Glutamine_and_D_glutamate_metabolism	<i>Antarctotetilla leptoderma</i>	2.199155019	0.002233063
ko00860_Porphyrin_and_chlorophyll_metabolism	<i>Antarctotetilla leptoderma</i>	3.466949473	0.000627635
ko00430_Taurine_and_hypotaurine_metabolism	<i>Antarctotetilla leptoderma</i>	2.810257513	0.000446263
ko00550_Peptidoglycan_biosynthesis	<i>Antarctotetilla leptoderma</i>	3.270936398	0.001165532
ko00523_Polyketide_sugar_unit_biosynthesis	<i>Antarctotetilla leptoderma</i>	2.274977738	0.028746621

ko00300_Lysine_biosynthesis	<i>Haliclona</i> sp.	2.86052389	0.027310907
ko00260_Glycine_serine_and_threonine_metabolism	<i>Haliclona</i> sp.	3.747364997	0.00027944
ko00630_Glyoxylate_and_dicarboxylate_metabolism	<i>Haliclona</i> sp.	3.085845855	0.001171996
ko00770_Pantothenate_and_CoA_biosynthesis	<i>Haliclona</i> sp.	2.711675701	0.045908782
ko05204_Chemical_carcinogenesis	<i>Haliclona</i> sp.	2.40432607	0.000822784
ko00250_Alanine_aspartate_and_glutamate_metabolism	<i>Haliclona</i> sp.	2.828214501	0.044516295
ko00970_Aminoacyl_tRNA_biosynthesis	<i>Haliclona</i> sp.	3.584415398	0.022489798
ko00270_Cysteine_and_methionine_metabolism	<i>Haliclona</i> sp.	3.253026336	0.000520236
ko03010_Ribosome	<i>Haliclona</i> sp.	3.168961776	0.030870305
ko00624_Polycyclic_aromatic_hydrocarbon_degradation	<i>Haliclona</i> sp.	2.369783458	0.005563896
ko00670_One_carbon_pool_by_folate	<i>Haliclona</i> sp.	2.75265269	0.000383645
ko00980_Metabolism_of_xenobiotics_by_cytochrome_P450	<i>Haliclona</i> sp.	2.355986502	0.001792937
ko00740_Riboflavin_metabolism	<i>Haliclona</i> sp.	2.652672534	0.009691343
ko00401_Novobiocin_biosynthesis	<i>Haliclona</i> sp.	2.178585207	0.022086641
ko03060_Protein_export	<i>Haliclona</i> sp.	2.885210426	0.040943288
ko00564_Glycerophospholipid_metabolism	<i>Homaxinella balfourensis</i>	3.003268475	0.000425608
ko05132_Salmonella_infection	<i>Homaxinella balfourensis</i>	2.491957208	0.002840256
ko00540_Lipopolysaccharide_biosynthesis	<i>Homaxinella balfourensis</i>	3.629597595	0.000427332
ko04723_Retrograde_endocannabinoid_signaling	<i>Homaxinella balfourensis</i>	2.252818784	0.00050453
ko00920_Sulfur_metabolism	<i>Homaxinella balfourensis</i>	3.098075682	0.000141965
ko04626_Plant_pathogen_interaction	<i>Homaxinella balfourensis</i>	2.649251933	0.000635373
ko04910_Insulin_signaling_pathway	<i>Homaxinella balfourensis</i>	2.143449422	0.022665796
ko05142_Chagas_disease_American_trypanosomiasis	<i>Homaxinella balfourensis</i>	2.291773263	0.001156935
ko01053_Biosynthesis_of_siderophore_group_nonribosomal_peptides	<i>Homaxinella balfourensis</i>	2.840851031	0.001399349
ko00982_Drug_metabolism_cytochrome_P450	<i>Homaxinella balfourensis</i>	2.47399408	0.00130354
ko01040_Biosynthesis_of_unsaturated_fatty_acids	<i>Homaxinella balfourensis</i>	2.616280746	0.000933049
ko05143_African_trypanosomiasis	<i>Homaxinella balfourensis</i>	2.347319054	0.002623891
ko00253_Tetracycline_biosynthesis	<i>Homaxinella balfourensis</i>	2.342004552	0.001220219
ko00330_Arginine_and_proline_metabolism	<i>Homaxinella balfourensis</i>	3.364422005	0.000196637
ko05133_Pertussis	<i>Homaxinella balfourensis</i>	3.065374204	0.00160875
ko02060_Phosphotransferase_system_PTS	<i>Homaxinella balfourensis</i>	2.550769566	0.002610894
ko00590_Arachidonic_acid_metabolism	<i>Homaxinella balfourensis</i>	2.168267418	0.000516497
ko00910_Nitrogen_metabolism	<i>Isodictya bentarti</i>	3.665572405	0.000189923
ko03070_Bacterial_secretion_system	<i>Isodictya bentarti</i>	3.638523224	0.000572376
ko00130_Ubiquinone_and_other_terpenoid_quinone_biosynthesis	<i>Isodictya bentarti</i>	2.804189251	0.006634486
ko00623_Toluene_degradation	<i>Isodictya bentarti</i>	2.695007586	0.00020129
ko03450_Non_homologous_end_joining	<i>Isodictya bentarti</i>	2.289171511	0.000473656
ko00960_Tropane_piperidine_and_pyridine_alkaloid_biosynthesis	<i>Isodictya bentarti</i>	2.341289329	0.009034081
ko00622_Xylene_degradation	<i>Isodictya bentarti</i>	2.306673884	0.004988143
ko04112_Cell_cycle_Caulobacter	<i>Isodictya bentarti</i>	3.425101076	0.001570221
ko00620_Pyruvate_metabolism	<i>Isodictya bentarti</i>	2.71031394	0.000390309
ko00510_N_Glycan_biosynthesis	<i>Isodictya bentarti</i>	2.762894152	0.002481636
ko04113_Meiosis_yeast	<i>Isodictya bentarti</i>	2.524470781	0.000751958
ko00361_Chlorocyclohexane_and_chlorobenzene_degradation	<i>Isodictya bentarti</i>	2.206931264	0.013687931
ko00621_Dioxin_degradation	<i>Isodictya bentarti</i>	2.32250844	0.006697978
ko02030_Bacterial_chemotaxis	<i>Isodictya bentarti</i>	3.634426447	0.000229039
ko05111_Vibrio_cholerae_pathogenic_cycle	<i>Isodictya bentarti</i>	3.075435091	0.002128904
ko00650_Butanoate_metabolism	<i>Isodictya bentarti</i>	2.868720939	0.004770695
ko00625_Chloroalkane_and_chloroalkene_degradation	<i>Isodictya bentarti</i>	2.600628014	0.000802371
ko04722_Neurotrophin_signaling_pathway	<i>Isodictya bentarti</i>	2.181945431	0.000981373
ko03320_PPAR_signaling_pathway	<i>Isodictya bentarti</i>	2.304669513	0.005393114
ko04920_Adipocytokine_signaling_pathway	<i>Isodictya bentarti</i>	2.209654034	0.002107978
ko04146_Peroxisome	<i>Isodictya bentarti</i>	2.449335599	0.000657973
ko00190_Oxidative_phosphorylation	<i>Isodictya bentarti</i>	3.370133473	0.000340783
ko05120_Epithelial_cell_signaling_in_Helicobacter_pylori_infection	<i>Isodictya bentarti</i>	2.636187747	0.000338266
ko02020_Two_component_system	<i>Isodictya bentarti</i>	4.260189224	0.001585065
ko03013_RNA_transport	<i>Isodictya bentarti</i>	2.597651684	0.000328946
ko00071_Fatty_acid_metabolism	<i>Isodictya bentarti</i>	2.908408498	0.014666447
ko00626_Naphthalene_degradation	<i>Isodictya bentarti</i>	2.392729095	0.012995034

ko01054_Nonribosomal_peptide_structures	<i>Isodictya bentarti</i>	3.313356125	0.000511905
ko00642_Ethylbenzene_degradation	<i>Isodictya bentarti</i>	2.496560251	0.000714211
ko00791_Atrazine_degradation	<i>Isodictya bentarti</i>	2.334475324	0.002856058
ko04011_MAPK_signaling_pathway_yeast	seawater	2.156047255	0.000116
ko00351_DDT_degradation	seawater	2.162343221	0.000143278
ko04210_Apoptosis	seawater	2.413247128	0.000143614
ko00311_Penicillin_and_cephalosporin_biosynthesis	seawater	2.702087606	0.000218508
ko05010_Alzheimers_disease	seawater	2.41369667	0.00018417
ko04142_Lysosome	seawater	2.721643743	0.000344505
ko04621_NOD_like_receptor_signaling_pathway	seawater	2.277385225	0.000138218
ko00830_Retinol_metabolism	seawater	2.308615134	0.000160993
ko00340_Histidine_metabolism	seawater	3.175578038	0.000258335
ko00480_Glutathione_metabolism	seawater	3.186072653	0.000123882
ko00051_Fructose_and_mannose_metabolism	seawater	3.090419512	0.001463362
ko00061_Fatty_acid_biosynthesis	seawater	3.234571754	0.000208764
ko03018_RNA_degradation	seawater	3.520574981	0.000133671
ko00240_Pyrimidine_metabolism	seawater	3.426068422	0.000521354
ko00531_Glycosaminoglycan_degradation	seawater	2.564094391	0.000381241
ko00052_Galactose_metabolism	seawater	2.84091012	0.001248239
ko00790_Folate_biosynthesis	seawater	2.873159008	0.030684242
ko00600_Sphingolipid_metabolism	seawater	2.733493726	0.000282717
ko00720_Carbon_fixation_pathways_in_prokaryotes	seawater	2.727168216	0.01981089
ko04974_Protein_digestion_and_absorption	seawater	2.786952103	0.000145119
ko00591_Linoleic_acid_metabolism	seawater	2.644172126	0.000200733
ko00780_Biotin_metabolism	seawater	3.058539963	0.006555814
ko00230_Purine_metabolism	seawater	3.373670958	0.000318615
ko00072_Synthesis_and_degradation_of_ketone_bodies	seawater	2.070875304	0.00075913
ko00312_beta_Lactam_resistance	seawater	2.384678627	0.000324215
ko00360_Phenylalanine_metabolism	seawater	3.070936787	0.001124029
ko00983_Drug_metabolism_other_enzymes	seawater	2.426701581	0.000232674
ko00350_Tyrosine_metabolism	seawater	2.719568702	0.002922343
ko05150_Staphylococcus_aureus_infection	seawater	2.345876301	0.000205091
ko00380_Tryptophan_metabolism	seawater	3.011689625	0.000229039
ko05016_Huntingtons_disease	seawater	2.225191105	0.000425023
ko05340_Primary_immunodeficiency	seawater	2.124826667	0.000126957
ko05100_Bacterial_invasion_of_epithelial_cells	seawater	2.810492641	0.000805531
ko00363_Bisphenol_degradation	seawater	2.517148438	0.001189779
ko03430_Mismatch_repair	seawater	2.90405837	0.000265051
ko00140_Steroid_hormone_biosynthesis	seawater	2.462393505	0.000248673
ko00310_Lysine_degradation	seawater	2.967693221	0.000159339
ko00511_Other_glycan_degradation	seawater	2.867027068	0.000588806
ko02010_ABC_transporters	seawater	3.758107276	0.013936637
ko00633_Nitrotoluene_degradation	seawater	2.539710942	0.000272975
ko00440_Phosphonate_and_phosphinate_metabolism	seawater	2.665376505	0.000171591
ko00906_Carotenoid_biosynthesis	seawater	2.705035554	0.006521683