

1 **Table S1.** Sample metadata.

Name	Type	Species	Depth (m)	Location	Coordinates	Country	Sampling Year	Sequencing Year	Sequencing technology
Aply16	Sponge Tissue	<i>Aplysina aerophoba</i>	10,25	Cala Montgo	N42°06'52.20", E3°10'06.52"	Spain	2014	2014	Hybrid Illumina Pacbio
Aply21	Sponge Tissue	<i>Aplysina aerophoba</i>	10,25	Cala Montgo	N42°06'52.20", E3°10'06.52"	Spain	2014	2014	Hybrid Illumina Pacbio
Aply22	Sponge Tissue	<i>Aplysina aerophoba</i>	10,25	Cala Montgo	N42°06'52.20", E3°10'06.52"	Spain	2014	2014	Hybrid Illumina Pacbio
Aply23	Sponge Tissue	<i>Aplysina aerophoba</i>	10,25	Cala Montgo	N42°06'52.20", E3°10'06.52"	Spain	2014	2014	Hybrid Illumina Pacbio
Pf4	Sponge Tissue	<i>Petrocia ficiformis</i>	5,5	Sfakia, Crete (Semi-dark zone)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
Pf5	Sponge Tissue	<i>Petrocia ficiformis</i>	5,5	Sfakia, Crete (Semi-dark zone)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
Pf6	Sponge Tissue	<i>Petrocia ficiformis</i>	5,5	Sfakia, Crete (Semi-dark zone)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
Pf7	Sponge Tissue	<i>Petrocia ficiformis</i>	5,5	Sfakia, Crete (Dark zone)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
Pf8	Sponge Tissue	<i>Petrocia ficiformis</i>	5,5	Sfakia, Crete (Dark zone)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
Pf9	Sponge Tissue	<i>Petrocia ficiformis</i>	5,5	Sfakia, Crete (Dark zone)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
Pf10	Sponge Tissue	<i>Petrocia ficiformis</i>	5,5	Sfakia, Crete (Entrance)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina

Pf11	Sponge Tissue	Petrocia ficiformis	5,5	Sfakia, Crete (Entrance)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
Pf12	Sponge Tissue	Petrocia ficiformis	5,5	Sfakia, Crete (Entrance)	N35°12'0.7", E24°7'09.8"	Greece	2018	2018	Illumina
gb1	Sponge Tissue	Geodia barretti	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb2_2	Sponge Tissue	Geodia barretti	150	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb4_2	Sponge Tissue	Geodia barretti	150	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb5_2	Sponge Tissue	Geodia barretti	150	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb6	Sponge Tissue	Geodia barretti	150	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb7	Sponge Tissue	Geodia barretti	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb8_2	Sponge Tissue	Geodia barretti	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb9	Sponge Tissue	Geodia barretti	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb10	Sponge Tissue	Geodia barretti	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb126	Sponge Tissue	Geodia barretti	1213	Davis Strait	N62°52'15.1", W58°37'34.32"	Canada	2015	2018	Illumina
gb278	Sponge Tissue	Geodia barretti	1335	Davis Strait	N61°53'36.13", W60°7'57.612"	Canada	2014	2018	Illumina
gb305	Sponge Tissue	Geodia barretti	1437	Davis Strait	N62°31'6.24", W59°58'13.872"	Canada	2014	2018	Illumina
gb1_f	Filtered Sea Water	N.a. Seawater Atl	150	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb2_f	Filtered Sea Water	N.a. Seawater Atl	150	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina

gb3_f	Filtered Sea Water	N.a. Seawater Atl	150	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb5_6_f	Filtered Sea Water	N.a. Seawater Atl	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb9_f	Filtered Sea Water	N.a. Seawater Atl	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
gb10_f	Filtered Sea Water	N.a. Seawater Atl	450	Scengsbukt-Korsfjord	N60°8'8", E5°6'42"	Norway	2017	2018	Illumina
sw_7	Filtered Sea Water	N.a. Seawater Med	10,25	Cala Montgo	N42°06'52.20", E3°10'06.52"	Spain	2014	2014	Illumina
sw_8	Filtered Sea Water	N.a. Seawater Med	10,25	Cala Montgo	N42°06'52.20", E3°10'06.52"	Spain	2014	2014	Illumina
sw_9	Filtered Sea Water	N.a. Seawater Med	10,25	Cala Montgo	N42°06'52.20", E3°10'06.52"	Spain	2014	2014	Illumina

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Table S2. Alpha and beta diversity statistical tests.

PERMANOVA Results	Taxonomy - based	GCF - based
Input	phyloFlash_compare.6.ntu_table.braycurtis	BiG_MAP.all_RPKM_NORM.braycurtis
test statistic name	pseudo-F	pseudo-F
sample size	35	35
number of groups	6	6
test statistic	55.7199	97.4049
p-value	0.001	0.002
number of permutations	999	1000

BGC-based alpha diversity scores				Taxonomy-based alpha diversity scores		
	Mean	Standard Deviation	Variance	Mean	Standard Deviation	Variance
All-Sponges	8.45	0.13	0.02	5.99	0.26	0.07

<i>G. barretti</i> NOR	8.36	0.07	0.01	5.71	0.08	0.01
<i>G. barretti</i> CAN	8.29	0.10	0.01	6.13	0.11	0.01
<i>P. ficiformis</i>	8.59	0.05	0.01	6.09	0.10	0.01
<i>A. aerophoba</i>	8.46	0.08	0.01	6.36	0.17	0.03
All-Seawater	6.94	0.74	0.56	6.96	0.16	0.03

BGC-based alpha diversity scores			Taxonomy-based alpha diversity scores		
	Kruskal-Wallis' H	pvalue	Kruskal-Wallis' H	pvalue	
All-Sponges	17.10	0.0007	19.97	0.0002	
<i>G. barretti</i> NOR & CAN	1.029	0.31	6.43	0.011	
<i>G. barretti</i> (NOR&CAN) & <i>A. aerophoba</i>	3.92	0.048	8.0	0.005	
<i>A. aerophoba</i> & <i>P. ficiformis</i>	4.67	0.031	5.36	0.021	
<i>G. barretti</i> (NOR&CAN) & <i>P. ficiformis</i>	12.33	0.0005	13.5	0.0002	

All-Sponges Coefficient of Determination = -18.64

All-Sponges Spearman r = -0.4159663865546219, pvalue = 0.013

5 **Table S3.** MAG assembly statistics.

Genome	Completeness	Contamination	Genome	Completeness	Contamination
gb2_2_bin.60	85.73	0.8	Pf11_bin.25	86.8	0.99
Pf4_bin.57	82.8	4.53	Aply16_bin.9	95.44	0.99
Pf7_bin.11	96.0	4.58	gb278_bin.73	91.55	0.0
Pf5_bin.33	79.62	0.83	gb278_bin.64	88.67	0.0
Pf12_bin.26	87.6	5.25	gb4_2_bin.32	93.95	0.0
gb5_6_f_bin.4	94.29	1.18	Pf8_bin.20	96.59	0.0
gb10_f_bin.41	90.26	1.71	Aply16_bin.3	96.59	0.0
gb_f_9_bin.4	90.26	0.0	Pf9_bin.30	94.61	0.0
gb5_6_f_bin.16	93.49	1.08	Pf10_bin.13	81.65	0.0
gb10_f_bin.38	94.76	4.82	Aply22_bin.4	86.69	0.0
Pf7_bin.57	92.57	0.04	Pf4_bin.24	95.73	1.71
Pf9_bin.46	93.73	0.68	gb1_bin.31	90.26	2.56
Pf5_bin.30	97.07	0.34	gb126_bin.75	89.46	1.71
gb5_6_f_bin.55	87.01	2.24	gb8_2_bin.30	93.07	0.0
Pf4_bin.22	89.08	0.0	gb126_bin.35	77.59	0.0
Pf5_bin.48	93.89	1.1	gb5_2_bin.68	92.02	0.0
gb305_bin.41	93.34	3.85	Pf10_bin.11	98.29	2.56
Pf10_bin.43	95.54	3.3	gb278_bin.39	90.12	2.28
gb5_6_f_bin.58	95.54	3.3	gb126_bin.36	76.84	0.43
gb10_f_bin.37	98.47	2.2	gb305_bin.7	90.46	7.26
Pf9_bin.12	92.12	1.1	gb7_bin.42	94.98	3.42
gb7_bin.51	95.54	2.2	gb7_bin.28	83.52	0.9
Pf8_bin.23	100.0	3.36	Pf8_bin.46	90.81	0.85
Pf9_bin.53	90.11	2.75	gb126_bin.28	80.79	6.03
gb4_2_bin.61	77.59	0.0	Pf5_bin.39	89.79	1.88
Pf11_bin.3	83.82	2.2	gb6_bin.52	84.62	0.85
gb305_bin.78	92.86	3.3	Pf4_bin.17	91.83	0.85
Aply22_bin.19	75.34	3.45	gb5_2_bin.9	93.59	2.56
Pf10_bin.2	97.8	3.3	Pf11_bin.39	93.16	1.03
gb8_2_bin.8	89.41	4.46	gb7_bin.52	81.39	1.07
gb305_bin.35	95.6	3.3	gb305_bin.22	75.86	0.0
gb3_2_bin.69	96.7	0.0	gb126_bin.47	80.89	1.76
Pf5_bin.5	97.74	1.1	gb305_bin.51	89.9	3.42
Pf9_bin.15	97.74	0.0	Pf5_bin.19	82.76	0.0
Pf12_bin.20	96.64	0.55	Pf7_bin.19	87.98	1.71
gb305_bin.13	95.6	0.3	Aply16_bin.4	79.33	1.93
Pf7_bin.67	97.8	0.3	gb126_bin.26	92.9	2.74
gb10_bin.62	93.34	1.1	gb126_bin.18	78.32	1.71
Pf7_bin.5	91.14	0.0	Pf5_bin.57	95.85	1.82
gb3_2_bin.44	82.13	2.26	gb8_2_bin.43	86.0	0.91
Pf7_bin.59	96.09	1.4	Aply22_bin.37	95.85	2.73
gb1_bin.4	86.16	2.2	gb5_2_bin.13	87.98	0.85
Aply21_bin.5	81.59	2.5	gb305_bin.19	94.34	1.28
gb_2_f_bin.4	83.52	0.0	Pf4_bin.21	93.16	3.42
Pf12_bin.35	96.58	1.64	gb5_2_bin.32	95.73	1.71
Pf7_bin.14	93.5	0.56	gb278_bin.63	93.16	2.56
Aply22_bin.9	94.92	1.13	Pf12_bin.44	82.82	1.73
Pf7_bin.31	93.48	1.98	Pf11_bin.13	96.59	1.68

gb278_bin.3	94.33	1.13	Aply16_bin.23	95.75	1.68
Pf4_bin.44	92.92	1.13	gb1_bin.7	93.22	0.84
Pf12_bin.28	98.39	0.54	gb5_2_bin.46	80.25	0.0
sw_9_bin.4	75.33	0.54	gb5_2_bin.36	91.55	2.52
sw_9_bin.11	92.03	3.76	gb278_bin.37	92.51	1.68
Aply22_bin.13	97.06	0.0	gb3_2_bin.16	91.34	3.36
sw_9_bin.14	84.93	1.75	Pf11_bin.31	93.23	3.36
sw_8_bin.5	95.06	1.53	gb5_6_f_bin.30	86.68	1.31
gb5_6_f_bin.25	93.55	2.66	gb10_f_bin.32	75.69	0.89
Pf7_bin.52	91.83	1.33	gb_1_f_bin.35	88.19	2.37
gb4_2_bin.25	84.45	5.49	Pf9_bin.23	84.67	0.0
gb3_2_bin.45	80.16	3.3	Pf12_bin.13	90.18	0.0
Pf8_bin.6	96.64	3.6	Pf6_bin.41	88.34	0.0
Pf5_bin.13	95.48	4.7	Pf5_bin.15	80.06	1.79
Pf5_bin.31	94.34	2.2	Aply22_bin.15	90.34	0.43
gb4_2_bin.48	79.06	0.0	sw_7_bin.3	94.82	0.58
Aply22_bin.11	97.58	2.25	gb_f_9_bin.8	99.53	0.94
gb4_2_bin.50	86.22	1.23	sw_7_bin.7	96.08	0.06
Pf8_bin.49	87.68	6.74	gb_f_9_bin.7	100.0	0.0
Pf10_bin.3	94.24	4.4	Aply23_bin.14	84.44	0.43
Pf12_bin.33	97.48	4.9	Pf4_bin.61	92.38	0.8
gb5_2_bin.34	77.82	2.25	gb305_bin.70	95.71	1.28
gb2_2_bin.46	76.66	1.1	gb5_6_f_bin.54	81.26	3.44
Pf9_bin.24	80.73	2.25	Aply22_bin.39	87.21	1.88
Pf5_bin.52	93.09	4.49	sw_9_bin.8	98.17	1.24
Aply23_bin.19	96.46	3.37	sw_9_bin.6	96.58	0.44
Pf9_bin.10	93.14	4.4	sw_7_bin.14	84.38	2.18
Pf5_bin.37	82.75	0.0	sw_7_bin.8	87.83	1.64
Pf5_bin.4	95.38	5.49	Aply16_bin.13	82.87	1.51
Aply16_bin.2	96.36	3.37	Pf9_bin.57	99.0	0.0
gb7_bin.5	84.35	2.2	Aply22_bin.45	92.74	0.5
Pf9_bin.14	97.42	4.49	gb278_bin.18	93.64	0.5
Pf11_bin.65	95.34	4.4	Pf7_bin.61	92.45	0.79
Pf4_bin.36	97.74	0.0	gb2_2_bin.49	88.09	0.03
Aply23_bin.13	97.15	0.0	Aply22_bin.44	75.74	2.17
gb126_bin.52	83.66	0.85	gb5_6_f_bin.61	88.59	1.27
Pf11_bin.32	90.02	1.28	gb305_bin.21	96.23	0.43
gb10_f_bin.14	78.82	1.3	gb8_2_bin.68	89.37	0.52
gb10_f_bin.44	99.15	2.23	Pf11_bin.50	96.96	0.43
gb305_bin.8	86.32	2.31	gb8_2_bin.1	95.02	0.17
Pf7_bin.64	98.29	2.14	Pf4_bin.37	94.43	0.5
Aply22_bin.36	92.31	2.14	sw_7_bin.10	99.0	0.03
Aply22_bin.5	83.05	2.99	Aply16_bin.21	95.38	0.0
gb8_2_bin.58	90.6	1.28	gb278_bin.34	94.54	0.0
Pf9_bin.45	94.44	1.28	Pf9_bin.40	94.42	0.84
Pf6_bin.60	96.58	1.28	Pf10_bin.9	96.1	0.0
Aply16_bin.8	80.12	3.5	gb5_2_bin.33	94.42	1.22
Aply23_bin.11	88.89	2.35	gb_f_9_bin.17	82.63	2.17
Pf9_bin.13	92.74	2.14	gb5_6_f_bin.31	80.99	1.22
Pf10_bin.8	95.73	1.28	gb_f_3_bin.30	89.02	0.61

gb5_6_f_bin.18	81.03	1.28	Pf4_bin.35	77.69	1.09
gb_f_9_bin.31	97.34	0.85	gb305_bin.15	80.29	3.43
gb10_f_bin.45	90.5	2.14	gb7_bin.36	75.56	1.61
Aply23_bin.8	96.15	1.28	gb305_bin.79	87.2	0.41
gb5_2_bin.28	92.99	1.28	Pf8_bin.36	78.45	3.3
Aply22_bin.47	88.89	1.28	gb278_bin.45	85.61	3.76
gb5_2_bin.63	93.16	1.28	Pf8_bin.5	86.0	5.11
gb5_2_bin.60	81.48	1.28	gb_1_f_bin.10	97.51	0.59
Pf7_bin.8	89.32	0.43	Pf9_bin.9	84.94	7.84
Aply22_bin.32	94.87	1.57	gb9_bin.59	79.71	1.99
Pf10_bin.10	92.12	0.0	Pf5_bin.16	90.23	1.72
gb126_bin.71	83.64	1.16	gb_f_9_bin.12	79.38	0.0
gb126_bin.20	81.36	0.91	gb_2_f_bin.27	78.37	0.33
Aply22_bin.17	97.27	1.82	gb_f_9_bin.10	82.9	0.45
gb5_6_f_bin.40	85.09	1.19	gb3_2_bin.25	83.26	0.0
gb126_bin.3	77.73	0.0	Pf5_bin.27	77.92	0.56
gb126_bin.13	84.92	2.1	Pf9_bin.7	85.8	1.48
Aply22_bin.41	90.91	0.91	Aply22_bin.18	84.26	1.11
gb305_bin.38	91.82	0.93	gb126_bin.66	84.13	2.21
gb6_bin.59	87.65	0.21	Pf7_bin.62	82.87	1.71
gb305_bin.52	82.01	0.0	Pf6_bin.10	81.8	0.91
gb305_bin.54	85.03	0.46	Pf11_bin.40	83.4	1.33
Pf4_bin.62	83.18	0.0	Pf6_bin.2	79.59	0.74
gb10_f_bin.34	75.02	1.43	Pf7_bin.23	85.49	1.54
Pf5_bin.43	94.39	0.99	gb3_2_bin.14	75.37	2.72
Pf12_bin.2	91.09	0.0	gb278_bin.58	85.73	0.31
gb10_f_bin.50	90.76	0.0	gb_1_f_bin.30	92.21	0.77
gb10_f_bin.10	78.62	6.16	sw_8_bin.2	100.0	0.84
Pf6_bin.31	91.75	0.99	sw_8_bin.15	98.42	0.67
gb5_2_bin.49	89.77	0.99	gb_f_3_bin.27	93.06	0.21
Aply22_bin.46	90.96	0.99	sw_8_bin.14	85.81	0.5
gb278_bin.5	86.8	2.64	gb5_6_f_bin.7	84.53	2.33
gb3_2_bin.67	83.99	0.0	gb278_bin.6	81.68	1.63
Pf6_bin.23	93.23	0.0	gb_f_3_bin.12	89.69	0.49
gb10_f_bin.46	77.05	1.98	Pf4_bin.53	91.42	1.11
gb5_2_bin.22	78.38	1.21	Pf10_bin.4	92.16	0.0
Pf5_bin.47	91.09	0.09	gb10_f_bin.30	79.99	1.73
Aply22_bin.34	94.22	0.99	gb126_bin.27	82.17	0.88
gb_f_9_bin.20	80.64	0.0	sw_9_bin.16	77.88	3.59
gb5_6_f_bin.38	78.07	3.19	sw_9_bin.13	93.17	0.0
gb5_6_f_bin.1	94.45	1.39	gb278_bin.54	83.43	0.2
Pf7_bin.1	83.83	0.0	gb278_bin.19	95.4	1.98
Pf4_bin.27	89.77	0.99	gb126_bin.31	78.67	1.98
gb7_bin.40	78.79	0.0	gb5_2_bin.7	87.29	0.99
gb5_2_bin.5	90.76	2.97	Pf10_bin.55	84.82	1.98
gb126_bin.73	89.71	1.32	gb1_bin.53	93.73	0.99
Pf9_bin.39	85.96	0.99	Pf9_bin.38	81.95	1.98
Aply23_bin.1	88.78	2.64	gb7_bin.12	88.78	3.16
Pf9_bin.5	95.51	0.99	gb7_bin.46	92.24	1.98
Aply22_bin.12	97.2	3.41	gb305_bin.80	94.72	0.44

Ap1y21_bin.3	95.51	0.99	Pf10_bin.14	75.17	0.5
Pf8_bin.4	96.7	0.0	Pf5_bin.25	95.71	0.0
Ap1y22_bin.16	90.76	1.98	gb8_2_bin.5	90.17	0.0
gb278_bin.49	80.27	0.0	gb5_2_bin.42	91.96	0.0
gb278_bin.16	82.64	9.11	gb3_2_bin.9	97.69	0.0
gb126_bin.45	75.74	8.03	gb126_bin.48	89.77	0.99
gb7_bin.2	79.67	0.0	gb278_bin.59	81.63	0.0
gb305_bin.37	87.1	0.0	gb1_bin.54	90.76	0.0
Pf7_bin.54	89.77	0.5	gb5_2_bin.54	86.8	0.0
gb126_bin.67	92.5	0.0	Pf7_bin.34	82.18	1.98

7 **Table S4.** SUP-like and swf-like GCF examples binned in MAGs, characterised by MAG distribution and phylum taxonomy.

SUP-like example			swf-like example		
GCF	Sponge species		GCF	Sponge species	
6130	Aplysina,Petrosia,Geodia		2399	Aplysina, Petrosia	
Encoding bin	Bin presence in host	Bin taxonomy	Encoding bin	Bin presence in host	Bin taxonomy
Pf4_bin.62	Petrosia	p__Chloroflexota	Aply22_bin.37	Aplysina	p__Nitrospirota
Pf7_bin.11	Petrosia	p__Spirochaetota	Pf7_bin.67	Aplysina, Petrosia	p__Latescibacterota
Pf9_bin.9	Petrosia	p__Proteobacteria	Pf10_bin.11	Petrosia	p__Acidobacteriota
Pf8_bin.5	Petrosia	p__Proteobacteria			
Pf6_bin.10	Petrosia	p__Proteobacteria	swf-like example		
Pf5_bin.39	Petrosia	p__Acidobacteriota	GCF	Sponge species	
Pf8_bin.46	Aplysina,Petrosia	p__Acidobacteriota	6055	Aplysina,Petrosia,Geodia	
gb5_2_bin.68	Geodia	p__Acidobacteriota	Encoding bin	Bin presence in host	Bin taxonomy
			gb10_bin.62	Geodia	p__Latescibacterota

8

9 **Table S5.** Ether Lipid A domain AdenylPred predictions, C1 and C2 refer to clades 1 and 2 as in Fig.5. Prediction probabilities are averaged within each clade.

Query	Predicted functional class (FC)	FC prediction probability	Predicted substrate specificity (SS)	SS prediction probability
C1 AMP_binding	Aryl-CoA ligase	0.48	cinnamate and succinylbenzoate derivatives	0.34
C2 AMP_binding	Long chain acyl-CoA synthetase	0.54	C13 through C17	0.45
BGC0000871_MXAN_1528_AMP-binding	Long chain acyl-CoA synthetase	0.67	C13 through C17	0.6

