

**Table S1.** Results of parameters' comparisons by One Way ANOVA in the soil of *Petromarula pinnata*

Parameter		Sum of squares	df	Mean square	F	<i>p</i>
NAG	Between groups	5.322	2	2.661	43.606	0
	Within the groups	0.732	12	0.061		
	Total	6.054	14			
BG	Between groups	1.131	2	0.565	6.016	0.015
	Within the groups	1.128	12	0.094		
	Total	2.259	14			
pH	Between groups	1.89	2	0.945	13.272	0.001
	Within the groups	0.854	12	0.071		
	Total	2.744	14			

**Table S2.** Results of Tukey HSD parameters' comparisons in the soil of *Petromarula pinnata*

	Dependent variable		Standard deviation	<i>p</i>	Confidence intervals	
NAG	Lower	Intermediate	0.156	0.82	-0.511	0.322
		Higher	0.156	0*	-1.725	-0.891
	Intermediate	Lower	0.156	0.82	-0.322	0.511
		Higher	0.156	0*	-1.63	-0.797
	Higher	Lower	0.156	0*	0.891	1.725
		Intermediate	0.156	0*	0.797	1.63
BG	Lower	Intermediate	0.194	0.02*	0.1	1.135
		Higher	0.194	0.916	-0.439	0.595
	Intermediate	Lower	0.194	0.02*	-1.135	-0.1
		Higher	0.194	0.041*	-1.057	-0.022
	Higher	Lower	0.194	0.916	-0.595	0.439
		Intermediate	0.194	0.041*	0.022	1.057
pH	Lower	Intermediate	0.169	0.313	-0.708	0.192
		Higher	0.169	0.001	-1.298	-0.398
	Intermediate	Lower	0.169	0.313*	-0.192	0.708
		Higher	0.169	0.011*	-1.04	-0.14
	Higher	Lower	0.169	0.001*	0.398	1.298
		Intermediate	0.169	0.011*	0.14	1.04

\* The mean difference is statistically significant at 0.05.

**Table S3.** Raw counts of taxonomic units at the phylum and genus levels per altitudinal class (Lower: 45 m; Intermediate: 260 m; Higher: 450 m above sea level).

<b>Altitude</b>	45 m	45 m	45 m	260 m	260 m	260 m	450 m	450 m	450 m
<b>Phyla</b>									
Acidobacteriota	10 6	11 7	10 4	37	294	138	28	241	117
Actinobacteriota	38 40	31 49	43 98	220 0	488 9	514 2	682 7	543 4	662 9
Armatimonadota	7	12	17	6	18	21	16	44	29
Bacteroidota	13 38	17 54	15 19	597	179 7	107 6	238 9	340 5	239 0
Chloroflexi	16 2	24 7	35 7	73	915	712	220	705	660
Cyanobacteria	80	99	78	63	39	45	85	64	73
Firmicutes	11 10	12 01	20 43	60	166 7	135 4	119 6	246 6	244 9
Gemmatimonadota	11 3	77	98	20	171	82	26	220	177
Halobacterota	5	0	0	0	9	25	0	4	0
Latescibacterota	6	1	3	0	2	0	0	2	3
Methyloirabilota	5	3	6	0	6	7	0	15	10
Myxococcota	16 3	19 7	13 9	88	229	165	13	216	88
NB1_j	4	5	7	0	7	7	0	2	0
Nitrospirota	10	9	9	4	29	20	9	3	16
Not_Assigned	12	10	13	0	11	16	9	23	28
Others	3	0	2	0	11	5	2	6	7
Patescibacteria	56	58	57	41	167	72	282	170	329
Planctomycetota	2	1	0	6	1	1	0	0	0
Proteobacteria	51 31	53 80	62 53	288 2	105 10	783 7	633 2	612 6	697 6
Verrucomicrobiota	10	19	15	32	14	24	6	36	7
WS2	0	1	4	0	2	2	0	4	0
<b>Genera</b>									
Achromobacter	4	0	5	0	6	6	6	0	9
Acidibacter	40	72	42	0	153	73	0	37	26
Acidotherrnus	0	0	0	0	0	0	0	10	7
Acidovorax	62	59	61	0	105	56	187	0	9
Acinetobacter	12	29	41	0	28	3	27	14	19
Actinocorallia	2	2	9	0	0	0	6	17	7
Actinomadura	0	7	15	0	17	0	0	9	9
Actinomycetospora	8	0	7	0	0	0	9	14	0
Actinophytocola	0	0	5	0	7	0	0	9	3
Actinoplanes	4	5	5	8	20	15	0	0	0
Actinopolymorpha	4	4	0	0	9	4	0	6	6
Adhaeribacter	0	0	0	4	13	4	11	4	11
Aeromicrobium	22 1	14 1	18 1	46	105	124	349	350	441
Aeromonas	4	5	0	0	12	23	0	0	0
Agrococcus	10	0	0	12	0	14	24	7	15
Agromyces	15 8	13 7	15 1	76	263	248	258	169	213

Ahniella	0	8	4	5	16	9	0	0	0
Algoriphagus	20	17	17	52	18	12	24	31	52
Allorhizobium_Neorhizobium_Pararhizobium_Rhizobium	147	248	271	32	205	174	1164	220	337
Altererythrobacter	50	40	37	84	124	104	71	33	91
Amaricoccus	56	88	98	4	89	131	85	121	159
Ammoniphilus	27	19	29	0	41	20	22	39	33
Arachidicoccus	0	0	0	0	0	0	0	10	9
Arcticibacter	0	0	1	0	0	0	22	1	0
Arenibacter	0	0	0	0	8	0	0	4	6
Arenimonas	131	57	144	262	518	318	86	76	90
Aridibacter	0	6	4	0	10	7	0	0	3
Arthrobacter	32	45	49	0	19	38	56	52	62
Asticcacaulis	50	49	66	18	71	32	15	177	136
Bacillus	905	985	1608	53	1230	999	894	2091	2060
Bauldia	19	11	0	0	22	10	0	0	11
Bhargavaea	3	3	2	0	0	4	0	0	0
BIyi10	3	5	0	0	6	7	0	4	0
Blastococcus	11	42	67	31	15	72	92	78	72
Bosea	29	46	31	6	136	76	69	53	72
Brachybacterium	0	4	11	14	0	2	5	8	11
Bradyrhizobium	22	31	49	22	131	79	29	43	45
Brevundimonas	14	37	40	12	53	50	34	25	106
Bryobacter	27	0	14	10	32	19	0	26	10
Caenimonas	0	0	0	20	11	10	0	0	0
CandidatuAlysiosphaera	10	8	21	0	26	14	22	5	26
CandidatuChloroploca	5	0	7	0	0	5	2	0	7
CandidatuSolibacter	2	3	0	0	0	6	0	0	3
CandidatuUdaeobacter	0	2	0	0	0	0	0	11	4
Catellatospora	0	0	0	0	12	16	14	0	20
Caulobacter	95	133	133	89	103	104	149	135	149
Cellulomonas	26	15	30	0	14	0	50	43	51
Cellulosimicrobium	34	27	39	0	23	33	34	34	27
Cellvibrio	462	428	412	262	765	363	67	239	343
Chiayiivirga	6	5	5	47	19	8	7	0	0
Chitinophaga	3	17	23	2	20	27	12	49	38
Chryseobacterium	46	63	71	0	30	19	2	70	108
Chryseolinea	13	12	27	2	25	11	9	18	18
Citricoccus	13	18	27	0	29	26	13	28	24
CL500_29marinegroup	9	10	7	5	9	8	0	7	4
Clostridiumsensustrict1	7	13	12	0	45	30	10	22	14
Cohnella	0	0	0	0	12	6	9	0	0
Conexibacter	17	10	7	0	0	2	0	10	16
Craurococcus_Caldovatus	0	0	0	0	4	0	0	2	5
Crocinitomix	0	0	0	8	0	2	5	0	0
Cytophaga	0	0	0	0	0	0	0	19	27
Dactylosporangium	4	3	0	0	4	0	0	5	7
Devosia	190	155	198	163	399	319	391	305	410
Dokdonella	95	84	134	25	115	66	30	128	69

Domibacillus	7	0	9	0	0	13	12	0	13
Dongia	70	71	69	72	172	134	22	115	91
Dyadobacter	33	63	45	11	29	27	94	240	113
Edaphobaculum	0	9	7	0	30	18	1	13	3
Ellin6067	4	0	0	0	13	0	0	3	0
Emticia	10 5	10 7	77	14	85	40	17	41	56
Ensifer	40	61	92	0	140	187	92	53	73
Enterobacter	8	5	0	0	0	0	0	0	0
Exiguobacterium	12	17	18	0	0	0	38	4	6
Falsirhodobacter	1	0	5	0	8	0	8	0	5
Ferrovibrio	24	27	11	0	41	25	7	43	15
Ferruginibacter	37	88	57	0	58	24	9	72	34
FFCH7168	3	0	2	4	6	7	0	4	6
Fictibacillus	2	0	0	0	9	8	0	0	0
Fimbriimonas	5	11	14	4	8	9	14	36	27
Flavisolibacter	0	18	6	6	17	9	3	13	13
Flavitalea	0	0	5	6	10	22	9	9	11
Flavobacterium	53 8	73 4	56 1	245	374	171	706	204 3	975
Fluviicola	4	8	2	0	12	2	0	12	21
Gaiella	20	58	54	18	94	51	35	111	119
Geminicoccus	0	0	6	3	0	0	0	3	4
Gemmatimonas	15	6	16	0	5	0	2	20	6
Geodermatophilus	38	25	12	0	60	18	16	9	16
Georgenia	8	6	0	0	4	0	7	10	0
Glutamicibacter	50	55	25	19	26	30	288	0	103
Gracilibacillus	0	2	6	0	6	4	6	4	0
Haliangium	5	3	0	0	14	9	0	0	0
Haloactinopolyspora	7	0	0	0	10	0	0	0	0
Hassallia	0	7	4	7	43	29	0	4	0
Hermiiniimonas	6	4	0	0	0	0	0	22	25
Herpetosiphon	0	1	8	2	8	36	0	19	8
Hirschia	31	30	27	10	83	89	6	8	6
Hydrogenophaga	74	70	73	66	258	151	18	32	25
Hyphomicrobium	28	30	32	0	72	52	0	33	27
Iamia	68	63	76	84	101	73	43	70	107
Ilumatobacter	26	6	26	29	66	85	25	45	30
IMCC26207	5	0	0	0	7	10	0	0	0
Irregularibacter	0	3	2	0	8	0	2	0	0
IS_44	3	0	7	0	26	21	0	0	0
Isoptericola	17	0	0	18	0	0	0	0	0
Jatrophihabitans	0	0	0	0	0	3	0	10	5
Kaistia	0	1	5	0	12	9	0	3	5
Kocuria	17	13	27	0	24	17	39	30	38
Kribbella	5	5	6	8	7	12	16	11	12
Labrys	0	2	0	4	1	1	6	0	0
Lacibacter	4	3	0	16	12	6	16	0	0
Lacunisphaera	5	10	7	20	13	15	2	8	2
Lautropia	0	5	0	0	18	13	3	10	9
Lechevalieria	53	35	46	25	50	33	125	31	26
Legionella	3	0	5	0	3	6	2	0	0
Limibaculum	31	17	47	0	21	33	15	50	33
Limnobacter	33	15	24	0	0	0	4	2	6
Litorilinea	0	1	0	0	0	5	0	7	0

Longispora	5	4	7	0	23	18	0	1	1
Luteimonas	0	2	0	0	0	3	0	50	21
Luteitalea	0	2	9	0	14	0	0	0	0
Lysinibacillus	22	23	36	0	30	32	16	45	32
Lysobacter	24 5	16 7	27 1	144	469	301	116	104	105
Mariniflexile	4	3	9	30	6	4	0	21	10
Marmoricola	51	43	45	45	75	93	87	28	51
Massilia	15	36	4	0	0	15	26	3	0
Melghirimyces	0	0	0	0	0	0	0	4	9
Mesorhizobium	91	94	12 9	57	182	136	123	201	180
Methanobrevibacter	0	0	2	0	4	12	1	7	0
Methanoculleus	5	0	0	0	5	20	0	4	0
Methylobacillus	34	17	27	108	74	38	29	36	14
Methylobacter	2	4	1	0	6	0	0	0	0
Methyloceanibacter	0	3	0	0	17	10	0	4	0
Methylophilus	10	8	16	5	18	12	7	13	28
Methyлотenera	92	85	96	38	220	121	106	23	66
Microbacterium	55 1	40 6	67 5	172	577	633	816	531	597
Microlunatus	0	0	0	5	22	22	20	0	17
Micromonospora	9	27	7	0	22	15	0	21	34
Microvirga	58	67	56	8	104	69	78	85	130
MM2	7	9	5	12	8	0	33	9	11
MND1	11	10	12	0	29	20	5	0	0
Modestobacter	7	8	41	0	7	7	8	12	43
Mucilaginibacter	0	0	0	0	1	0	0	13	9
Mycobacterium	10 7	92	14 6	47	146	142	198	175	219
Nannocystis	0	7	14	0	35	41	7	17	11
Niastella	0	4	14	0	24	8	3	15	20
Nitrospira	5	4	0	0	0	8	0	5	0
Nitrospira	10	9	9	4	29	20	9	3	16
Nocardia	4	3	6	8	12	12	5	7	22
Nocardioides	69 5	47 9	78 4	644	123 3	136 0	183 7	874	127 6
Nonomuraea	11	10	0	0	9	10	13	0	29
Nordella	8	17	19	8	15	27	13	16	15
Not_Assigned	26 76	27 28	34 36	102 0	569 3	442 4	271 6	441 6	434 2
Novibacillus	4	4	12	0	13	4	0	0	3
Noviherbaspirillum	0	0	3	0	5	3	0	0	0
Novosphingobium	0	21	13	27	34	22	23	28	29
Oceanicella	0	0	0	0	0	5	0	8	0
Oceanobacillus	9	7	15	0	0	10	0	0	0
Ochrobactrum	0	0	9	0	5	0	10	0	7
Ohtaekwangia	16	13	13	0	49	16	6	33	14
Ornithinibacillus	0	0	11	0	13	7	0	0	0
Ornithinococcus	15	6	23	0	10	7	1	25	14
Ornithinimicrobium	0	0	18	0	6	0	5	26	3
Others	18	21	19	10	42	37	21	44	21
Oxalophagus	5	0	0	2	0	0	0	12	0
Paenarthrobacter	10 3	77	19 1	44	80	102	131	80	135

Paenibacillus	9	20	59	0	26	22	24	52	61
Paeniclostridium	0	5	7	0	17	9	4	8	0
Paenisporosarcina	5	0	0	0	12	0	0	5	0
Pajaroellobacter	1	0	0	0	0	0	0	0	9
Paracoccus	7	12	20	0	16	26	42	32	25
Parasegetibacter	0	2	0	4	5	0	0	2	1
Patulibacter	3	3	1	0	0	4	0	2	6
Paucisalibacillus	0	0	10	0	18	0	0	11	0
Pedobacter	40 7	45 7	43 2	93	350	332	133 9	406	647
Pedococcus_Phycococcus	17	0	10	0	0	0	10	0	14
Pedomicrobium	9	21	19	0	72	21	6	26	15
Phaselicystis	7	6	4	0	0	6	3	12	4
Phenylobacterium	61	28	52	41	77	44	16	64	29
Phyllobacterium	0	2	0	8	9	10	27	4	0
Pilimelia	0	0	0	0	14	7	0	0	0
Planococcus	48	37	11 2	0	21	24	114	69	86
Polaromonas	14	13	20	20	55	23	20	12	27
Pontibacter	0	0	0	8	5	0	6	8	4
Porphyrobacter	0	0	0	0	0	0	0	26	18
Promicromonospora	16	3	7	20	0	15	34	11	0
Pseudoflavitalea	0	0	4	9	24	2	0	0	0
Pseudolabrys	13	0	10	8	28	12	10	36	21
Pseudomonas	69	58	88	18	68	76	30	17	27
Pseudonocardia	25	15	23	0	21	19	10	35	59
Pseudorhodoferax	10	6	15	7	6	10	0	0	15
Pseudorhodoplanes	0	0	0	0	12	11	0	0	0
Pseudoxanthomonas	61	59	62	63	150	117	263	107	138
Psychrobacillus	2	5	7	0	0	0	0	13	9
Quadrisphaera	9	0	0	0	15	5	8	27	24
Ramlibacter	0	0	0	0	11	18	0	0	7
Rathayibacter	0	0	0	0	0	0	10	0	12
Reyranella	6	15	18	0	40	50	14	30	30
Rhabdanaerobium	0	0	1	0	5	0	2	0	5
Rheinheimera	5	12	18	13	5	0	4	0	20
Rhizobacter	0	8	0	0	0	0	6	9	0
Rhizobiumsphaerophysaegroup	54	10 1	82	0	54	53	62	174	96
Rhizocola	3	3	2	0	2	0	0	15	9
Rhodanobacter	0	0	0	0	0	0	3	88	79
Rhodobacter	0	4	8	0	0	5	0	0	0
Rhodococcus	24	27	34	9	23	64	41	33	100
Rhodocytophaga	0	0	0	16	22	13	9	0	4
Rhodomicrobium	0	3	13	0	12	7	3	13	5
Rhodoplanes	0	0	0	0	12	9	0	0	0
Romboutsia	7	13	0	0	45	22	5	18	22
Roseomonas	5	5	0	6	5	3	23	2	12
Rubellimicrobium	0	3	4	7	19	11	14	19	16
Rubrobacter	0	6	0	0	0	31	19	6	0
Rurimicrobium	0	0	2	0	7	4	0	5	0
Saccharomonospora	9	4	14	0	5	9	4	6	3
Sandaracinus	5	2	2	4	6	6	1	1	8
Sedimentibacter	0	0	0	0	7	3	0	0	0
Serratia	0	0	0	10	0	2	0	0	0





unidentifiedSolirubrobacteraceae	0	0	2	0	0	0	0	3	9
unidentifiedSteroidobacteraceae	0	6	0	0	0	2	2	0	8
unidentifiedVicinamibacterales	0	10	13	0	0	0	0	29	9
unidentifiedXanthobacteraceae	7	11	13	0	34	24	13	17	6
UTBCD1	0	3	0	2	8	0	0	4	0
Variovorax	39	29	23	6	58	60	110	22	67
Virgisporangium	6	0	7	0	9	0	4	6	0
Vitellibacter	6	13	10	0	0	0	5	18	7
Williamsia	0	0	0	0	0	0	4	0	7
Woeseia	0	1	0	0	7	0	5	4	0
YC_ZSS_LKJ147	4	6	2	6	0	2	0	5	5

**Table S4.** Analysis of variance (ANOVA) for the relative abundances of the top 10 phyla and genera.

\*\*\* p<0.001; \* p<0.05.

		<b>F-statistic</b>	<b>p-value</b>	<b>sig. level</b>
Top Phyla	Acidobacteriota	0.5372	0.6101	-
	Actinobacteriota	0.7671	0.505	-
	Bacteroidota	5.3769	0.04593	*
	Chloroflexi	0.6973	0.5342	-
	Firmicutes	2.121	0.201	-
	Gemmatimonadota	0.3015	0.7503	-
	Myxococcota	1.6544	0.2678	-
	Patescibacteria	9.771	0.01296	*
	Proteobacteria	33.1353	0.0005722	***
Top Genera	Bacillus	2.6039	0.1534	-
	Cellvibrio	7.4292	0.0238	*
	Flavobacterium	2.2761	0.1838	-
	Microbacterium	1.2184	0.3597	-
	Nocardioides	2.2073	0.1912	-
	Pedobacter	1.0694	0.4007	-
	Sphingobium	0.1525	0.8618	-
	Sphingomonas	0.8803	0.4621	-
	Streptomyces	0.9356	0.4429	-

**Table S5.** T-test of significance on the predicted functions according to the COG library for prokaryotic communities in the rhizosphere of *Petromarula pinnata* at three different altitudes in eastern Crete (\*\*p<0.01; \* p<0.05).

Function	Description	Relative abundances				p-value	Significance	Category	Code
		Intermediate	Higher						
		mean	stdev	mean	stdev				
COG1028	NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family	0.00421	0.00006	0.00409	0.00004	0.049	*	Lipid transport and metabolism	I
COG0673	Predicted dehydrogenase	0.00223	0.00003	0.00239	0.00004	0.005	**	General function	R
COG0625	Glutathione S-transferase	0.00193	0.00008	0.00159	0.00002	0.015	*	Posttranslational modification, protein turnover, chaperones	O
COG0683	ABC-type branched-chain amino acid transport system, periplasmic component	0.00184	0.00006	0.00163	0.00001	0.025	*	Amino acid transport and metabolism	E
COG1733	DNA-binding transcriptional regulator, HxIR family	0.00131	0.00011	0.00153	0.00007	0.046	*	Transcription	K
COG0715	ABC-type nitrate/sulfonate/bicarbonate transport system, periplasmic component	0.00153	0.00003	0.00146	0.00001	0.041	*	Transcription	K
COG0366	Glycosidase	0.00109	0.00002	0.00117	0.00002	0.012	*	Carbohydrate transport and metabolism	G
COG1473	Metal-dependent amidase/amino acylase/carboxypeptidase	0.00104	0.00003	0.00111	0.00002	0.033	*	General function	R
COG0776	Bacterial nucleoid DNA-binding protein	0.00104	0.00003	0.00095	0.00003	0.028	*	Replication, recombination and repair	L
COG0402	Cytosine/adenosine deaminase or related metal-dependent hydrolase	0.00100	0.00001	0.00092	0.00002	0.003	**	Nucleotide transport and metabolism	F

		Lower		Intermediate					
		mean	stdev	mean	stdev				
COG0204	1-acyl-sn-glycerol-3-phosphate acyltransferase	0.00117	0.00002	0.00122	0.00001	0.020	*	Lipid transport and metabolism	I
COG0842	ABC-type multidrug transport system, permease component	0.00104	0.00002	0.00108	0.00002	0.039	*	Defense mechanisms	V
COG0402	Cytosine/adeno sine deaminase or related metal-dependent hydrolase	0.00097	0.00001	0.00100	0.00001	0.025	*	Nucleotide transport and metabolism	F
		Lower		Higher					
		mean	stdev	mean	stdev				
COG0642	Signal transduction histidine kinase	0.00456	0.00011	0.00424	0.00004	0.026	*	Signal transduction mechanisms	T
COG0596	Pimeloyl-ACP methyl ester carboxylesterase	0.00457	0.00011	0.00432	0.00005	0.049	*	Coenzyme transport and metabolism	H
COG0745	DNA-binding response regulator, OmpR family, contains REC and winged-helix (wHTH) domain	0.00455	0.00010	0.00421	0.00003	0.023	*	Transcription	K
COG0451	Nucleoside-diphosphate-sugar epimerase	0.00427	0.00016	0.00389	0.00006	0.044	*	Cell wall/membrane/envelope biogenesis	M
COG0515	Serine/threonine protein kinase	0.00337	0.00027	0.00261	0.00011	0.025	*	Signal transduction mechanisms	T
COG1028	NAD(P)-dependent dehydrogenase , short-chain alcohol dehydrogenase family	0.00417	0.00003	0.00409	0.00004	0.050	*	Lipid transport and metabolism	I
COG1357	Uncharacterized protein YjbI, contains pentapeptide repeats	0.00283	0.00032	0.00185	0.00013	0.021	*	Function unknown	S
COG4636	Endonuclease, Uma2 family (restriction endonuclease fold)	0.00271	0.00033	0.00171	0.00014	0.021	*	General function	R
COG2814	Predicted arabinose	0.00327	0.00007	0.00350	0.00006	0.012	*	Carbohydrate transport	G

	efflux permease, MFS family							and metabolism	
COG1595	DNA-directed RNA polymerase specialized sigma subunit, sigma24 family	0.00290	0.00008	0.00329	0.00009	0.006	**	Transcription	K
COG1309	DNA-binding transcriptional regulator, AcrR family	0.00296	0.00009	0.00325	0.00005	0.017	*	Transcription	K
COG1012	Acyl-CoA reductase or other NAD-dependent aldehyde dehydrogenase	0.00251	0.00011	0.00286	0.00004	0.020	*	Energy production and conversion	C
COG0664	cAMP-binding domain of CRP or a regulatory subunit of cAMP-dependent protein kinases	0.00253	0.00012	0.00227	0.00005	0.046	*	Signal transduction mechanisms	T
COG1131	ABC-type multidrug transport system, ATPase component	0.00249	0.00006	0.00269	0.00008	0.026	*	Defense mechanisms	V
COG0589	Nucleotide-binding universal stress protein, UspA family	0.00237	0.00011	0.00205	0.00007	0.019	*	Signal transduction mechanisms	T
COG1960	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	0.00216	0.00013	0.00260	0.00007	0.015	*	Lipid transport and metabolism	I
COG1846	DNA-binding transcriptional regulator, MarR family	0.00211	0.00014	0.00258	0.00005	0.020	*	Transcription	K