

Online Resource 2a Relative abundance of core ASVs within either, all samples, root samples only (*O. deceptionensis* and *O. 'mediterranea'*), or *O. deceptionensis* samples only (palp and tissue). ASVs are denoted first by their associated family and genus (NR SILVA), followed by their unique ASV number. ASV relative abundance values within each sample are based on a data set of 1551 filtered ASVs. DR: *O. deceptionensis*-roots, MR: *O. 'mediterranea'*-roots, DP: *O. deceptionensis*-palps

ASV	DR8	DR13	DR21	MR1	MR2	DP3	DP6	DP9	DP11	DP16
All Samples										
Burkholderiaceae;Burkholderiaceae_unclassified;1706	0.34	0.39	0.01	0.18	0.00	2.98	4.33	1.76	0.19	0.20
Propionibacteriaceae;Cutibacterium;2462	0.08	0.09	0.02	1.09	0.03	1.82	1.08	0.28	0.08	0.09
Mycoplasmataceae;Mycoplasma;4812	0.50	0.20	<0.01	0.02	0.02	0.50	1.67	0.87	0.43	0.06
Root Samples <i>O. deceptionensis</i> and <i>O. 'mediterranea'</i>										
uncultured;uncultured_ge;87	<0.01	0.21	0.13	2.28	0.03	-	-	-	-	-
Flavobacteriaceae;Lutibacter;127	0.03	0.01	0.08	0.03	0.05	-	-	-	-	-
Sulfurospirillaceae;Sulfurospirillum;140	3.66	0.03	0.36	18.9	0.08	-	-	-	-	-
Unknown_Family;Alkalimarinus;944	0.01	0.02	0.08	2.51	37.8	-	-	-	-	-
Arcobacteraceae;Arcobacter;1252	0.01	<0.01	<0.01	0.20	0.03	-	-	-	-	-
Marinifilaceae;Marinifilum;1380	0.14	0.01	0.36	0.24	0.01	-	-	-	-	-
Burkholderiaceae;Burkholderiaceae_unclassified;1706	0.34	0.39	0.01	0.18	<0.01	-	-	-	-	-
Bacteroidetes_VC2.1_Bac22_fa;Bacteroidetes_VC2.1_Bac22_ge;2204	0.18	0.03	0.24	0.01	1.44	-	-	-	-	-
Propionibacteriaceae;Cutibacterium;2462	0.08	0.09	0.02	1.09	0.03	-	-	-	-	-
Nitrosomonadaceae;Nitrosomonas;2707	0.01	0.08	0.01	<0.01	0.01	-	-	-	-	-
Mycoplasmataceae;Mycoplasma;4812	0.50	0.20	<0.01	0.02	0.02	-	-	-	-	-
Desulfobacteraceae;Desulfobacteraceae_unclassified;5540	0.01	<0.01	0.48	0.24	0.36	-	-	-	-	-
Colwelliaceae;Colwellia;5689	0.06	1.07	0.14	0.02	0.01	-	-	-	-	-
Rhizobiaceae;Cohaesibacter;5901	0.02	<0.01	<0.01	0.09	0.93	-	-	-	-	-
Root and Palp Samples <i>O. deceptionensis</i>										
Thiovulaceae;Sulfurimonas;510	0.06	<0.01	0.01	-	-	<0.01	0.03	0.01	<0.01	<0.01
Saccharospirillaceae;Oleispira;960	27.5	0.11	1.69	-	-	0.04	11.6	0.01	0.01	0.09
Kangiellaceae;uncultured;1445	<0.01	0.40	0.01	-	-	0.01	0.07	3.01	66.0	0.01
Burkholderiaceae;Ottowia;1548	0.13	0.23	<0.01	-	-	1.10	1.84	0.80	0.10	0.10
Burkholderiaceae;Burkholderiaceae_unclassified;1706	0.34	0.39	0.01	-	-	2.98	4.33	1.76	0.19	0.20
Terasakiellaceae;uncultured;2024	0.03	0.20	0.04	-	-	0.01	0.15	0.08	3.81	0.17
Moraxellaceae;Enhydrobacter;2258	0.05	0.12	<0.01	-	-	2.14	1.26	0.68	0.03	0.01
Rhizobiaceae;Lentilitoribacter;2384	0.02	0.78	0.62	-	-	0.01	0.11	<0.01	0.49	0.03
Propionibacteriaceae;Cutibacterium;2462	0.08	0.09	0.02	-	-	1.82	1.08	0.28	0.08	0.09
Nitrincolaceae;uncultured;2484	<0.01	0.10	0.08	-	-	<0.01	0.02	<0.01	0.01	<0.01
Pseudomonadaceae;Pseudomonas;2850	0.01	0.01	<0.01	-	-	0.03	0.17	0.04	0.02	0.01
Alteromonadaceae;Paraglaciecola;3944	0.12	0.14	0.09	-	-	0.01	0.41	0.01	0.01	<0.01
Weeksellaceae;Cloacibacterium;4745	0.03	0.04	<0.01	-	-	0.38	0.63	0.13	0.01	0.04
Mycoplasmataceae;Mycoplasma;4812	0.50	0.20	<0.01	-	-	0.50	1.67	0.87	0.43	0.06
Microbacteriaceae;Leucobacter;6196	0.03	0.01	<0.01	-	-	0.14	0.46	0.01	0.04	0.02
Mycoplasmataceae;Mycoplasma;6227	0.10	0.03	<0.01	-	-	0.10	0.37	0.27	0.10	0.01

Online Resource 2b Relative abundance of top ASVs. Showing relative abundance of ASVs with at least 5% and 3% total abundance within one of *O. deceptionensis*-roots, *O. deceptionensis*-palps or *O. 'mediterranea'* roots. ASVs are denoted by their associated family and genus (NR SILVA), followed by their unique ASV number

ASV	Relative abundance (%)		
	<i>O. deceptionensis</i>	<i>O. deceptionensis</i>	<i>O. 'mediterranea'</i>
Above 5%	Roots	Palps	Roots
Alphaproteobacteria_unclassified;4230	<0.01	13.3	-
Alphaproteobacteria_unclassified;4953	-	-	9.6
Arcobacteraceae;Arcobacter;6298	<0.1	5.0	-
Kangiellaceae;uncultured;1445	0.1	16.9	-
Nitrincolaceae;Profundimonas;1903	28.9	12.6	-
Nitrincolaceae;Profundimonas;5088	<0.1	<0.1	6.8
Saccharospirillaceae;Oleispira;960	9.1	1.7	-
Sulfurospirillaceae;Sulfurospirillum;140	1.3	<0.1	8.9
Thioglobaceae;SUP05_cluster;5513	<0.1	19.8	-
Unknown_Family;Alkalimarinus;944	<0.1	<0.1	21.3
Above 3%			
Desulfobacteraceae;Desulfobacter;4455	-	-	3.6
Desulfobacteraceae;Desulfobacterium;81	0.5	4.1	<0.01
Desulfobulbaceae;Desulforhopalus;1442	3.1	<0.1	-
Flavobacteriaceae_unclassified;3078	3.3	<0.01	-
Marinifilaceae;Marinifilum;568	3.1	<0.1	-
Moraxellaceae;Acinetobacter;2150	<0.1	4.3	0.5
Rhodobacteraceae_unclassified;518	-	-	4.7

Online Resource 2c Differentially abundant (DA) ASVs between either *Osedax* species or body tissue. Calculated using edgeR, where logFC: log fold-change, logCPM: log counts per million, PValue: for genes <0.01, FDR: Benjamini-Hochberg P-value adjustment

DA ASVs between <i>O. deceptionensis</i> and <i>O. 'mediterranea'</i> roots				
ASV	logFC	logCPM	PValue	FDR
Nitrincolaceae;Profundimonas;1903	-16.68	17.37	0.01	0.62
Alphaproteobacteria_unclassified;4953	15.23	15.33	0.00	0.62
Saccharospirillaceae;Oleispira;960	-15.16	15.84	0.01	0.62
Rhodobacteraceae_unclassified;518	14.02	14.12	0.00	0.62
Desulfobacteraceae;Desulfobacter;4455	13.80	13.90	0.00	0.62
Desulfobulbaceae;Desulforhopalus;1442	-13.60	14.29	0.02	0.76
Marinifilaceae;Marinifilum;568	-13.56	14.25	0.02	0.76
Flavobacteriaceae_unclassified;1383	13.49	13.59	0.00	0.62
Flavobacteriaceae_unclassified;3078	-13.48	14.16	0.02	0.76
Desulfobacteraceae;Desulfofrigus;131	13.29	13.40	0.00	0.62
Desulfobulbaceae_unclassified;5061	13.13	13.24	0.00	0.62
Halieaceae_unclassified;5140	13.09	13.19	0.00	0.62
Desulfobacteraceae;Desulfobacterium;4368	-13.06	13.75	0.03	0.78
Unknown_Family;Marinicella;4412	-13.02	13.71	0.03	0.78
Desulfobacteraceae;Desulfofrigus;4523	-12.92	13.60	0.03	0.78
Songiobacteraceae;BD1-7_clade;3986	12.88	12.98	0.00	0.62
Bacteria_unclassified;3965	12.80	12.90	0.00	0.62
Kiritimatiellaceae;R76-B128;610	12.47	12.57	0.01	0.62
Thiovulaceae;Sulfurimonas;4383	-12.19	12.88	0.04	0.79
DA ASVs between <i>O. deceptionensis</i> root and palp body tissues				
ASV	logFC	logCPM	PValue	FDR
Alphaproteobacteria_unclassified;4230	-13.27	16.70	0.00	0.38
Fusobacteriaceae;Psychrilyobacter;2221	11.84	12.04	0.00	0.35
Desulfobacteraceae;Desulfobacter;5262	11.60	11.80	0.00	0.35
Arcobacteraceae;Arcobacter;2715	-11.21	12.14	0.01	0.57
Thioglobaceae;SUP05_cluster;5513	-10.83	17.19	0.01	0.39
Desulfobulbaceae;Desulfotalea;768	10.71	10.93	0.00	0.38
Kangiellaceae;Aliikangiella;4529	10.41	10.64	0.00	0.38
Spirochaetaceae_unclassified;4300	9.80	10.05	0.00	0.38
Desulfobacteraceae;Desulfofrigus;4523	9.76	12.93	0.00	0.38
Sneathiellaceae;Sneathiella;4955	9.57	9.83	0.00	0.38
Acanthopleuribacteraceae;Acanthopleuribacter;557	9.42	9.69	0.00	0.38
Sulfurovaceae;Sulfurovum;449	9.38	9.65	0.00	0.38
Bacteroidia_unclassified;4420	9.30	9.58	0.00	0.38
Desulfobacteraceae;Desulfoconvexum;1596	9.27	12.00	0.00	0.38
MSBL8;MSBL8_ge;2565	9.23	9.51	0.01	0.38
Beggiatoaceae;Candidatus_Thiopilula;4310	9.22	9.50	0.01	0.38
Spirochaetaceae;Sediminispirochaeta;1642	9.17	9.46	0.01	0.38
Colwelliaceae;Colwellia;618	-9.05	10.03	0.05	0.69
Marinifilaceae;Marinifilum;6105	8.97	9.27	0.01	0.39
Songiobacteraceae_unclassified;3297	8.94	9.25	0.01	0.39
Desulfobacteraceae_unclassified;3064	8.90	11.44	0.00	0.38
Bacteroidetes_BD2-2;Bacteroidetes_BD2-2_ge;918	8.76	9.08	0.01	0.44
Desulfobacteraceae;Desulfobacterium;4368	8.59	13.08	0.00	0.38

Crocinitomicaceae;Fluviicola;4764	8.58	11.17	0.00	0.38
Alphaproteobacteria_unclassified;1560	-8.45	9.47	0.07	0.70
OM190_fa;OM190_ge;3871	8.39	8.75	0.01	0.57
Family_XI;Peptoniphilus;3753	-8.34	11.08	0.04	0.66
Desulfobulbaceae_unclassified;537	8.25	11.22	0.00	0.38
Saccharospirillaceae;Oleispira;2924	8.19	8.57	0.01	0.57
Methylophilaceae;Methylothermus;575	8.19	8.57	0.01	0.57
