

Table S1: Operational taxonomic units (OTUs) associated with seagrass or microalgae chloroplasts, and the BLAST results.

OTU ID	Greengenes result	Sequence counts	Proportion of sequences	Top BLAST Result: Accession Number; Proportion Identity; Description	Alternative BLAST result: Accession Number; Proportion Identity; Description
Otu40	*	867	0.001	KX808295.1; 1; <i>Zostera noltei</i> 18S ribosomal RNA (rrn18) gene, complete sequence; mitochondrial	KX808392.1; 0.9951; <i>Zostera marina</i> voucher C2544 mitochondrion, complete genome
Otu16	*	2687	0.002	KX808295.1; 0.9378; <i>Zostera noltei</i> 18S ribosomal RNA (rrn18) gene, complete sequence; mitochondrial	KX808392.1; 0.933; <i>Zostera marina</i> voucher C2544 mitochondrion, complete genome
Otu11	Cyanobacteria Chloroplast	3628	0.002	HM485224.1; 1; Uncultured microorganism clone PK_Seq406_EDW_339 small subunit ribosomal RNA gene, partial sequence	
Otu92	Chloroplast	837	0.001	MF370229.1; 0.9631; <i>Zostera marina</i> chloroplast, complete genome	
Otu190	<i>Bacillariophyta</i>	2177	0.001	KT973350.1; 1; Uncultured prokaryote clone 2986479 16S ribosomal RNA gene, partial sequence	KP792487.1; 0.9975; <i>Bacillariophyta</i> sp. 867-32 small subunit ribosomal RNA gene, partial sequence; plastid
Otu15	<i>Bacillariophyta</i>	3291	0.002	JN232305.1; 0.9975; Uncultured diatom clone 1LM8-18 16S ribosomal RNA gene, partial sequence; plastid	EU542369.1; 0.9951; Uncultured phototrophic eukaryote clone SAV07H04 16S ribosomal RNA gene, partial sequence; plastid
Otu21	<i>Bacillariophyta</i>	8277	0.005	LC006286.1; 1; Uncultured cyanobacterium gene for 16S ribosomal RNA, partial sequence, clone: BZm-K31	KP792462.1; 0.9975; <i>Planoglabratella opercularis</i> isolate GO_m14-08 small subunit ribosomal RNA gene, partial sequence; plastid
Otu438	<i>Bacillariophyta</i>	9118	0.006	EU376247.1; 1; Uncultured bacterium clone sls1807 16S ribosomal RNA gene, partial sequence	EU580477.1; 0.9975; <i>Cymatopleura solea</i> clone D14 66 16S ribosomal RNA gene, partial sequence; chloroplast
Otu3	<i>Bacillariophyta</i>	17822	0.012	FM242434.1; 1; Uncultured diatom chloroplast partial 16S ribosomal RNA, clone 40 T12d+oil	FJ002196.1; 0.9926; <i>Melosira cf. octogona</i> isolate C122 16S ribosomal RNA gene, partial sequence; chloroplast
Otu2	<i>Bacillariophyta</i>	105622	0.070	HM018019.1; 0.9975; Uncultured bacterium clone Mar08_3 16S ribosomal RNA gene, partial sequence	KC246081.1; 0.9951; Uncultured cyanobacterium clone XSLA025 16S ribosomal RNA gene, partial sequence
Otu1	<i>Streptophyta</i>	1123249	0.743	MF370229.1; 1; <i>Zostera marina</i> chloroplast, complete genome	

Table S2: Alpha diversity indices across sites and salinity groups for bacterial and fungal communities. Values represent mean  $\pm$  SD (n = 5, sites; n = 5- 15, salinity group, n = 15, estuary classification).

Site	Bacteria		Fungi	
	Observed OTUs	Shannon Index	Observed OTUs	Shannon Index
Surrey River	62.0 $\pm$ 3.2 <sup>a</sup>	4.8 $\pm$ 0.21 <sup>ab</sup>	62.7 $\pm$ 10.8 <sup>a</sup>	4.6 $\pm$ 0.18 <sup>a</sup>
Fitzroy River	62.7 $\pm$ 8.2 <sup>a</sup>	4.4 $\pm$ 0.60 <sup>ab</sup>	41.9 $\pm$ 2.6 <sup>a</sup>	4.1 $\pm$ 0.32 <sup>a</sup>
Yambuk Inlet	77.6 $\pm$ 1.7 <sup>a</sup>	5.2 $\pm$ 0.12 <sup>a</sup>	58.2 $\pm$ 3.6 <sup>a</sup>	3.5 $\pm$ 0.23 <sup>a</sup>
Moyne River	80.4 $\pm$ 3.5 <sup>a</sup>	5.1 $\pm$ 0.37 <sup>ab</sup>	44.9 $\pm$ 11.0 <sup>a</sup>	1.8 $\pm$ 0.99 <sup>a</sup>
Curdies River	69.0 $\pm$ 5.3 <sup>a</sup>	4.6 $\pm$ 0.37 <sup>b</sup>	52.1 $\pm$ 11.0 <sup>a</sup>	3.0 $\pm$ 0.37 <sup>a</sup>
Sherbrook River	58.0 $\pm$ 2.8 <sup>a</sup>	4.7 $\pm$ 0.16 <sup>ab</sup>	52.8 $\pm$ 18.9 <sup>a</sup>	3.1 $\pm$ 0.93 <sup>a</sup>
<b>Salinity Group</b>				
Marine	80.4 $\pm$ 3.5 <sup>a</sup>	5.1 $\pm$ 0.37 <sup>a</sup>	44.9 $\pm$ 11.0 <sup>a</sup>	1.8 $\pm$ 0.99 <sup>a</sup>
Estuarine	67.8 $\pm$ 10.1 <sup>ab</sup>	5.0 $\pm$ 0.29 <sup>a</sup>	55.5 $\pm$ 13.9 <sup>a</sup>	3.3 $\pm$ 0.70 <sup>b</sup>
Fresh/Brackish	64.6 $\pm$ 6.7 <sup>b</sup>	4.6 $\pm$ 0.45 <sup>a</sup>	52.2 $\pm$ 12.4 <sup>a</sup>	3.9 $\pm$ 0.71 <sup>b</sup>
<b>Estuary Classification</b>				
Unimpacted	65.9 $\pm$ 8.9 <sup>a</sup>	4.9 $\pm$ 0.28 <sup>a</sup>	57.9 $\pm$ 13.4 <sup>a</sup>	3.7 $\pm$ 0.84 <sup>a</sup>
Impacted	70.7 $\pm$ 9.5 <sup>a</sup>	4.7 $\pm$ 0.54 <sup>a</sup>	46.3 $\pm$ 10.1 <sup>b</sup>	3.0 $\pm$ 1.1 <sup>a</sup>

Table S3: ANOVA tests for bacterial operational taxonomic units (OTUs) that were significantly different across sites (mean values shown in heat map). Classification of taxonomy is from Greengenes, with additional resolution from Silva v123 in parentheses.

Site	Test-Statistic	Bonferroni p-value	Surrey River	Fitzroy River	Yambuk	Moyne River	Curdies River	Sherbrook River	Taxonomy
Otu75	267.8133	1.70E-14	0.20	0.00	0.00	6.82	0.00	0.00	<i>p: Bacteroidetes, c: Flavobacteriia, o: Flavobacteriales, f: Flavobacteriaceae (g: Croceitalea)</i>
Otu31	243.4306	1.70E-14	0.00	0.00	0.00	7.88	0.00	0.00	<i>p: Proteobacteria (c: Gammaproteobacteria)</i>
Otu98	143.184	1.70E-14	0.20	0.00	0.00	6.27	0.34	0.00	<i>p: Proteobacteria, c: Deltaproteobacteria, o: Desulfobacterales (f: Desulfobulbaceae)</i>
Otu89	148.2928	1.70E-14	0.00	0.00	5.88	6.97	5.47	0.36	<i>p: Proteobacteria, c: Gammaproteobacteria (Silva – Proteobacteria)</i>
Otu87	202.2146	1.70E-14	6.74	0.00	0.00	0.16	0.00	0.00	<i>p: Proteobacteria, c: Gammaproteobacteria, o: Methylococcales</i>
Otu156	126.6387	3.40E-14	0.00	0.00	0.00	6.04	0.00	0.00	<i>p: Verrucomicrobia, c: Verrucomicrobiae, o: Verrucomicrobiales (Silva – Bacteria)</i>
Otu96	109.0997	1.70E-13	0.00	0.00	0.00	6.31	0.34	0.00	<i>p: Bacteroidetes, c: Flavobacteriia, o: Flavobacteriales, f: Flavobacteriaceae</i>
Otu60	88.27788	1.82E-12	0.00	0.00	0.00	6.13	0.00	0.00	<i>p: Proteobacteria, c: Gammaproteobacteria</i> <i>(o: Thiotrichales, f: Thiotrichaceae, g: Leucothrix)</i>
Otu100	88.21195	1.83E-12	0.00	0.00	0.65	6.83	0.00	0.00	<i>p: Verrucomicrobia, c: Verrucomicrobiae</i> <i>(o: Verrucomicrobiales, f: Verrucomicrobiaceae, g: Roseibacillus)</i>
Otu102	85.41009	2.65E-12	0.00	0.00	0.00	6.61	0.67	0.00	<i>p: Bacteroidetes, c: Flavobacteriia, o: Flavobacteriales, f: Flavobacteriaceae (g: Ornithobacterium)</i>
Otu101	83.37792	3.48E-12	0.20	0.00	0.00	5.63	0.00	0.00	<i>p: Bacteroidetes</i>
Otu161	72.7865	1.60E-11	0.00	0.00	5.07	5.25	7.09	0.67	<i>p: Proteobacteria, c: Gammaproteobacteria (c: Milano-WF1B-44)</i>
Otu5	67.84703	3.50E-11	12.08	10.54	8.79	0.62	9.19	10.20	<i>p: Proteobacteria, c: Betaproteobacteria, o: Methylophilales, f: Methylophilaceae</i> <i>p: Proteobacteria, c: Alphaproteobacteria, o: Caulobacteriales, f: Hyphomonadaceae (Silva – Proteobacteria)</i>
Otu94	67.66919	3.60E-11	0.00	0.00	0.00	7.04	0.53	0.00	<i>p: Verrucomicrobia, c: Verrucomicrobiae, o: Verrucomicrobiales (f: Rubritaleaceae, g: Rubritalea)</i>
Otu128	65.36027	5.29E-11	0.00	0.00	5.08	6.79	0.82	0.00	
Otu53	60.00062	1.36E-10	9.22	4.47	1.14	0.48	2.17	8.04	<i>p: Proteobacteria, c: Betaproteobacteria (o: Burkholderiales, f: Comamonadaceae)</i>
Otu1486	53.51935	4.76E-10	7.65	6.30	1.16	0.70	1.55	9.65	<i>p: Proteobacteria, c: Betaproteobacteria, o: Burkholderiales, f: Comamonadaceae</i> <i>p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacteriales, f: Rhodobacteraceae (g: Pseudorhodobacter)</i>
Otu8	52.51001	5.86E-10	10.67	9.46	4.64	2.55	3.66	9.47	
Otu110	50.30593	9.33E-10	7.45	1.09	0.00	0.00	0.00	1.03	<i>p: Proteobacteria (c: Betaproteobacteria, o: Hydrogenophilales, f: Hydrogenophilaceae)</i>
Otu18	47.5714	1.71E-09	9.81	8.39	1.61	0.62	2.98	8.85	<i>p: Proteobacteria, c: Betaproteobacteria (o: Burkholderiales, f: Comamonadaceae)</i> <i>p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacteriales, f: Rhodobacteraceae, g: Lokt anella (g: L_rosea)</i>
Otu4	47.1731	1.87E-09	2.96	7.08	10.39	11.41	10.58	9.27	
Otu129	46.2752	2.30E-09	0.30	0.49	5.59	5.27	7.46	1.73	<i>p: Proteobacteria, c: Gammaproteobacteria (o: Chromatiales, f: Ectothiorhodospiraceae)</i>
Otu63	45.57461	2.71E-09	8.51	5.95	1.35	0.00	0.53	5.78	<i>p: Proteobacteria, c: Betaproteobacteria (o: Burkholderiales, f: Comamonadaceae)</i>
Otu72	44.67469	3.35E-09	7.44	0.49	0.00	0.21	0.34	1.27	<i>p: Proteobacteria, c: Gammaproteobacteria (o: Methylococcales)</i>

Site	Test-Statistic	Bonferroni p-value	Surrey River	Fitzroy River	Yambuk	Moyne River	Curdies River	Sherbrook River	Taxonomy
Otu20	43.27946	4.71E-09	9.89	5.76	3.93	4.61	4.56	3.73	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Sphingomonadales,f:Erythrobacteraceae (g:Porphyrobacter,s:P_sanguineus)</i>
Otu157	42.68645	5.45E-09	0.00	0.00	4.96	6.41	3.70	0.00	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Xanthomonadales,f:JTB255_marine_benthic_group)</i>
Otu45	41.98155	6.51E-09	0.00	0.00	0.00	6.77	0.53	0.00	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Pibocella)</i>
Otu7	41.59387	7.18E-09	11.53	10.19	5.85	2.48	7.19	12.55	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales,f:Comamonadaceae (g:Hydrogenophaga)</i>
Otu58	41.20086	7.94E-09	0.43	0.00	0.00	6.89	3.13	0.00	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Xanthomonadales,f:JTB255_marine_benthic_group)</i>
Otu90	38.09396	1.82E-08	0.00	0.00	0.00	7.04	0.72	2.17	<i>p:Proteobacteria,c:Gammaproteobacteria,o:Gammaproteobacteria_incertae_sedis,g:Arenicella</i>
Otu99	36.61708	2.75E-08	2.56	5.61	7.93	8.51	7.43	8.18	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae (g:Sulfitobacter)</i>
Otu85	36.18943	3.11E-08	8.06	2.70	0.00	0.00	0.00	0.93	<i>p:Proteobacteria,c:Betaproteobacteria (o:Hydrogenophilales,f:Hydrogenophilaceae)</i>
Otu44	36.01323	3.27E-08	7.04	8.46	4.94	0.45	4.87	7.19	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae,g:Flavobacterium (s:F_ponti)</i>
Otu141	35.81053	3.47E-08	0.00	0.43	4.03	6.30	4.66	0.62	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Cellvibrionales,f:Haliaceae)</i>
Otu755	35.5121	3.78E-08	8.60	1.84	0.00	1.11	0.00	4.83	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae (p:Bacteroidetes,c:Sphingobacteriia,o:Sphingobacteriales,f:Saprosiraceae,g:Rubidimonas)</i>
Otu32	35.26577	4.07E-08	0.00	0.00	0.00	7.99	0.82	3.17	
Otu28	34.45914	5.17E-08	0.46	0.85	1.35	4.32	10.25	1.07	<i>p:Proteobacteria,c:Alphaproteobacteria</i>
Otu278	33.50671	6.91E-08	7.62	3.00	0.66	0.43	0.00	5.33	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales (f:Comamonadaceae)</i>
Otu495	33.00627	8.07E-08	6.75	2.06	3.95	0.00	3.98	6.67	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Sphingomonadales (f:Sphingomonadaceae)</i>
Otu138	31.51593	1.30E-07	3.50	7.03	7.13	1.42	7.31	2.74	<i>p:Proteobacteria,c:Gammaproteobacteria,o:Chromatiales (f:Chromatiaceae)</i>
Otu68	31.41355	1.34E-07	0.41	2.05	6.86	7.64	7.27	1.47	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Actibacter)</i>
Otu318	31.37973	1.36E-07	7.76	4.18	0.00	0.00	0.71	0.36	<i>p:Proteobacteria,c:Alphaproteobacteria</i>
Otu6	30.8014	1.64E-07	10.70	7.53	3.04	0.99	5.14	3.37	<i>(p:Bacteroidetes,c:Cytophagia,o:Cytophagales,f:Cytophagaceae)</i>
Otu57	30.22388	1.99E-07	0.00	0.00	7.71	3.51	7.43	0.00	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu114	30.10824	2.07E-07	7.70	3.48	1.45	0.64	1.19	9.42	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales</i>
Otu97	28.58937	3.49E-07	0.22	2.69	7.28	8.06	5.85	7.00	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu877	28.40659	3.72E-07	0.50	2.66	6.08	6.81	6.44	9.33	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>
Otu37	27.68756	4.82E-07	0.00	0.00	0.00	7.78	1.34	1.33	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu59	27.48206	5.19E-07	8.77	6.02	1.55	0.48	2.69	6.72	<i>d:Bacteria,p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales</i>
Otu131	27.04577	6.09E-07	6.69	1.18	0.00	0.00	1.01	0.36	<i>p:Bacteroidetes (c:Flavobacteriia,o:Flavobacteriales,f:NS9_marine_group)</i>

Site	Test-Statistic	Bonferroni p-value	Surrey River	Fitzroy River	Yambuk	Moyne River	Curdies River	Sherbrook River	Taxonomy
Otu83	26.6478	7.06E-07	0.31	5.17	6.55	5.77	6.77	3.17	<i>p:Proteobacteria,c:Alphaproteobacteria (o:Rhodobacterales,f:Rhodobacteraceae)</i>
Otu67	26.37644	7.82E-07	6.39	1.32	2.27	0.42	4.50	8.55	<i>p:Bacteroidetes,c:Flavobacteriia (o:Flavobacteriales,f:Cryomorphaceae)</i> <i>p:Proteobacteria,c:Gammaproteobacteria,o:Gammaproteobacteria_incertae_sedis,g:Marinicella</i>
Otu216	24.89709	1.38E-06	0.00	0.00	2.02	6.45	1.68	0.36	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu111	24.89436	1.39E-06	0.63	1.01	7.08	4.13	6.88	1.01	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales,f:Burkholderiales_incertae_sedis (f:Comamonadaceae)</i>
Otu160	24.83506	1.42E-06	7.37	5.80	1.31	0.00	3.23	5.77	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu109	24.42911	1.67E-06	1.41	5.30	6.54	7.05	6.53	2.02	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales,f:Burkholderiales_incertae_sedis (f:Comamonadaceae)</i>
Otu1949	24.32224	1.74E-06	5.04	1.70	0.00	0.49	0.53	7.68	<i>p:Bacteroidetes (c:Cytophagia,o:Cytophagales,f:Cytophagaceae,g:Leadbetterella)</i> <i>p:Proteobacteria,c:Gammaproteobacteria</i>
Otu261	24.15284	1.86E-06	6.68	1.12	0.00	0.36	2.02	5.11	<i>(o:Xanthomonadales,f:JTB255_marine_benthic_group)</i>
Otu66	23.49547	2.44E-06	0.00	0.66	3.79	7.24	6.45	1.95	<i>p:Bacteroidetes (c:Cytophagia,o:Cytophagales,f:Cytophagaceae)</i> <i>p:Proteobacteria,c:Gammaproteobacteria</i>
Otu79	23.38385	2.56E-06	7.23	2.86	0.00	0.00	0.00	2.28	<i>(o:Xanthomonadales,f:Xanthomonadaceae,g:Arenimonas)</i>
Otu88	23.08827	2.89E-06	5.56	5.37	4.07	0.75	5.56	6.53	<i>p:Proteobacteria,c:Gammaproteobacteria</i> <i>(o:Chromatiales,f:Granulosicoccaceae)</i>
Otu137	22.60809	3.55E-06	0.00	0.00	1.62	6.57	0.71	0.00	<i>(g:Granulosicoccus)</i>
Otu212	22.52335	3.68E-06	6.22	6.18	1.19	0.00	0.49	3.75	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales (f:Comamonadaceae)</i>
Otu166	22.30127	4.05E-06	1.04	3.33	5.75	5.74	5.93	0.36	<i>(p:Proteobacteria,c:Deltaproteobacteria,o:Myxococcales,f:Sandaracinaceae)</i>
Otu158	21.37328	6.08E-06	0.00	0.85	1.63	5.95	5.85	0.36	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Chromatiales,f:Ectothiorhodospiraceae)</i> <i>p:Proteobacteria,c:Betaproteobacteria,o:Methylophilales</i>
Otu489	21.18983	6.60E-06	5.42	5.09	7.29	2.40	4.88	5.28	<i>(f:Methylophilaceae,g:Methylotenera)</i> <i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae,g:Cellulophaga (s:C_tyrosinoxydans)</i>
Otu36	21.01482	7.15E-06	3.63	7.92	4.67	0.00	5.82	8.78	<i>p:Bacteroidetes</i> <i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu52	20.77448	7.97E-06	7.39	4.57	0.00	0.16	0.00	0.43	<i>(g:Winogradskyella)</i>
Otu106	20.67141	8.36E-06	0.00	0.00	0.00	6.21	1.16	0.71	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Caulobacteriales,f:Hyphomonadaceae</i>
Otu26	20.50353	9.03E-06	2.89	6.00	6.37	6.37	7.91	9.38	<i>p:Verrucomicrobia (c:OPB35_soil_group)</i>
Otu125	19.63151	1.36E-05	4.84	0.49	0.00	0.00	0.00	0.00	<i>p:Proteobacteria,c:Alphaproteobacteria</i>
Otu70	19.50459	1.44E-05	7.01	1.81	0.00	0.15	0.49	1.10	<i>p:Proteobacteria,c:Gammaproteobacteria</i>
Otu172	18.22639	2.71E-05	0.73	1.61	5.03	6.61	5.35	1.39	<i>(o:Xanthomonadales,f:JTB255_marine_benthic_group)</i> <i>p:Proteobacteria,c:Epsilonproteobacteria,o:Campylobacteriales,f:Helicobacteraceae,g:Sulfurovum</i>
Otu49	18.04144	2.98E-05	1.14	3.02	5.41	6.85	6.67	4.98	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>
Otu10	17.90817	3.19E-05	10.55	8.64	4.02	2.59	5.77	9.41	

Site	Test-Statistic	Bonferroni p-value	Surrey River	Fitzroy River	Yambuk	Moyne River	Curdies River	Sherbrook River	Taxonomy
Otu150	17.87246	3.25E-05	0.72	1.79	6.66	5.88	6.85	1.73	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Cellvibrionales,f:Haliaceae)</i>
Otu464	17.78169	3.40E-05	0.20	0.90	3.55	5.87	5.17	0.53	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Xanthomonadales,f:JTB255_marine_benthic_group)</i>
Otu81	17.00732	5.10E-05	0.00	0.00	0.00	4.39	0.00	0.00	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Thiotrichales,f:Thiotrichaceae,g:Cocleimonas)</i>
Otu107	16.59523	6.37E-05	0.00	0.70	5.09	7.14	4.54	2.60	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu39	16.59139	6.38E-05	7.07	2.39	1.44	1.92	2.65	9.29	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Cryomorpaceae</i>
Otu69	16.02982	8.69E-05	0.74	1.58	6.47	4.16	4.22	7.85	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Caulobacterales,f:Hyphomonadaceae (Silva – Alphaproteobacteria)</i>
Otu29	15.98279	8.92E-05	8.95	3.37	2.28	0.00	1.33	3.02	<i>p:Proteobacteria,c:Alphaproteobacteria (o:Sphingomonadales)</i>
Otu1107	15.66158	0.00010688	0.82	5.26	5.17	5.70	5.22	1.61	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Cellvibrionales,f:Haliaceae)</i>
Otu33	14.74369	0.0001818	8.98	4.40	1.74	0.70	2.40	6.90	<i>p:Proteobacteria,c:Alphaproteobacteria (o:Sphingomonadales)</i>
Otu22	14.56941	0.00020163	8.26	6.36	0.00	0.00	7.55	2.60	<i>(p:Bacteroidetes,c:Sphingobacteriia,o:Sphingobacteriales,f:Saprosiraceae)</i>
Otu43	14.39178	0.00022428	0.53	3.50	2.75	8.81	7.83	7.53	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Maribacter)</i>
Otu73	14.36027	0.00022857	0.31	5.35	6.56	7.21	6.97	7.53	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae,g:Sulfitobacter (s:S_sp._BSw21498)</i>
Otu55	14.2819	0.00023965	7.02	4.14	1.10	0.30	0.49	0.67	<i>p:Proteobacteria,c:Alphaproteobacteria (o:Rhodobacterales,f:Rhodobacteraceae)</i>
Otu64	13.81278	0.0003194	6.28	6.84	5.53	5.11	8.49	8.44	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>
Otu267	12.85357	0.0005874	1.25	4.08	6.18	6.74	4.21	1.82	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu228	12.47535	0.00075338	0.22	0.00	0.00	4.20	0.00	0.00	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Thiotrichales,f:Thiotrichaceae,g:Leucothrix)</i>
Otu74	12.45746	0.00076239	0.40	7.96	2.77	4.33	1.40	0.43	<i>p:Bacteroidetes (c:Sphingobacteriia,o:Sphingobacteriales,f:Saprosiraceae)</i>
Otu500	12.40392	0.00079009	0.34	0.00	0.00	5.13	0.34	0.00	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Thiotrichales,f:Thiotrichaceae,g:Leucothrix)</i>
Otu34	12.17673	0.00092029	0.00	0.00	3.10	7.01	4.58	0.00	<i>(p:Proteobacteria,c:Alphaproteobacteria,o:Sphingomonadales,f:SWB04)</i>
Otu9	12.13847	0.00094442	9.51	8.99	8.39	7.81	11.16	10.54	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>
Otu65	12.06827	0.00099049	5.69	0.96	0.65	0.00	0.34	0.67	<i>p:Proteobacteria,c:Betaproteobacteria (o:TRA3-20)</i>
Otu48	11.76614	0.00121843	5.02	4.47	1.92	0.00	0.00	1.01	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>
Otu95	10.71303	0.0025809	4.63	0.71	0.00	0.00	0.00	0.50	<i>p:Proteobacteria,c:Alphaproteobacteria (o:Parvularculales,f:Parvularculaceae,g:Parvularcula)</i>
Otu23	10.62774	0.00274832	8.19	5.29	8.90	4.89	10.24	8.84	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae (g:Marivita)</i>
Otu17	10.39782	0.00326093	8.57	2.84	1.14	2.31	3.05	1.76	<i>p:Proteobacteria,c:Alphaproteobacteria (o:Rhodobacterales,f:Rhodobacteraceae)</i>
Otu80	9.849815	0.00495043	1.00	4.03	5.82	4.00	2.44	8.09	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>

Site	Test-Statistic	Bonferroni p-value	Surrey River	Fitzroy River	Yambuk	Moyne River	Curdies River	Sherbrook River	Taxonomy
									(g:Maribacter)
Otu13	9.459105	0.0067259	8.86	6.42	4.70	5.04	4.55	5.09	p:Actinobacteria,c:Actinobacteria,o:Acidimicrobiales,f:Acidimicrobiaceae,g:Ilumatobacter (s:Ilumatobacter_nonamiensis_YM16-303)
Otu113	9.392313	0.00709314	5.98	2.01	1.38	0.00	0.71	4.37	p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Flavobacterium)
Otu1314	9.259378	0.00789018	4.79	5.94	6.34	3.26	5.49	6.25	p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae
Otu46	9.05751	0.00929148	5.26	8.77	4.10	5.71	6.60	2.51	p:Proteobacteria,c:Gammaproteobacteria
Otu42	8.91377	0.01045236	3.78	6.14	0.00	0.00	1.59	0.00	(p:Chloroflexi,c:Caldilineae,o:Caldilineales,f:Caldilineaceae)
Otu24	8.838857	0.01111871	0.00	0.00	2.39	8.08	2.55	2.90	p:Bacteroidetes (c:Flavobacteriia,o:Flavobacteriales,f:NS9_marine_group)
Otu572	8.437408	0.01556679	2.02	3.26	6.30	3.05	5.02	8.24	p:Proteobacteria,c:Alphaproteobacteria (o:Rhodobacterales,f:Rhodobacteraceae)
Otu41	8.109998	0.02062404	4.69	2.97	5.94	7.96	5.74	9.12	p:Proteobacteria,c:Alphaproteobacteria,o:Sphingomonadales,f:Erythrobacteraceae
Otu112	8.086592	0.02104815	0.00	0.66	2.60	6.76	2.55	3.23	p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Polaribacter)
Otu1004	8.079888	0.02117134	3.57	8.00	7.26	5.53	5.19	4.48	p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae,g:Phaeobacter (Silve - g:Pseudophaeobacter)
Otu134	8.012395	0.02245597	2.70	3.92	6.79	5.84	1.21	5.82	p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae
Otu1631	7.930002	0.02413941	2.54	6.73	5.70	4.36	5.62	3.02	p:Proteobacteria,c:Gammaproteobacteria (g:Candidatus_Thiobio)
Otu280	7.700016	0.02960238	0.41	5.44	5.56	6.93	3.94	2.41	p:Proteobacteria,c:Alphaproteobacteria (o:Rhizobiales,f:Phyllobacteriaceae,g:Pseudahrensia)
Otu19	7.626654	0.031615	9.05	2.89	4.06	1.90	2.55	3.96	p:Bacteroidetes (c:Cytophagia,o:Cytophagales,f:Cytophagaceae)
Otu50	7.48462	0.03594401	7.20	5.24	6.28	6.59	4.82	9.18	p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae
Otu858	7.396078	0.03896353	2.69	3.13	4.71	5.87	2.74	7.26	p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales
Otu383	7.266129	0.04390156	0.20	0.00	1.86	4.93	5.13	3.15	p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae (g:Octadecabacter,s:Octadecabacter_sp._SB1)
Otu84	7.256871	0.04427829	5.00	7.88	7.39	6.01	6.89	4.42	p:Actinobacteria,c:Actinobacteria,o:Acidimicrobiales,f:Acidimicrobiaceae,g:Ilumatobacter

Table S4: ANOVA tests for bacterial operational taxonomic units (OTUs) that were significantly different across salinity groups (mean values shown in heat map). Classification of taxonomy is from Greengenes, with additional resolution from Silva v123 in parentheses.

Salinity	Test-Statistic	Bonferroni p-value	Fresh/Brackish	Estuarine	Marine	Taxonomy
Otu102	207.2108	1.70E-14	0.22	0.00	6.61	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Aquibacter)</i>
Otu100	223.9302	1.70E-14	0.00	0.32	6.83	<i>p:Verrucomicrobia,c:Verrucomicrobiae (g:Roseibacillus)</i>
Otu96	290.6339	1.70E-14	0.11	0.00	6.31	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu98	381.2606	1.70E-14	0.18	0.00	6.27	<i>p:Proteobacteria,c:Deltaproteobacteria,o:Desulfobacterales (f:Desulfobulbaceae)</i>
Otu31	684.6485	1.70E-14	0.00	0.00	7.88	<i>p:Proteobacteria (c:Gammaproteobacteria)</i>
Otu156	356.1713	1.70E-14	0.00	0.00	6.04	<i>p:Verrucomicrobia,c:Verrucomicrobiae,o:Verrucomicrobiales (Silva - Unknown Bacteria)</i>
Otu60	248.2815	1.70E-14	0.00	0.00	6.13	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Thiotrichales,f:Thiotrichaceae,g:Leucothrix)</i>
Otu75	725.3394	1.70E-14	0.07	0.00	6.82	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae g:Croceitalea)</i>
Otu101	230.2909	1.70E-14	0.07	0.00	5.63	<i>p:Bacteroidetes</i>
Otu94	177.653	5.10E-14	0.18	0.00	7.04	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Caulobacteriales,f:Hyphomonadaceae (Silva - Proteobacteria)</i>
Otu45	112.4638	1.23E-11	0.18	0.00	6.77	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Pibocella)</i>
Otu5	94.91216	9.35E-11	10.60	9.50	0.62	<i>p:Proteobacteria,c:Betaproteobacteria,o:Methylophilales,f:Methylophilaceae</i>
Otu90	64.00102	8.68E-09	0.24	1.08	7.04	<i>p:Proteobacteria,c:Gammaproteobacteria,o:Gammaproteobacteria_incertae_sedis,g:Arenicella</i>
Otu37	58.83843	2.20E-08	0.45	0.67	7.78	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu32	49.36636	1.46E-07	0.27	1.58	7.99	<i>Bacteria (p:Bacteroidetes,c:Sphingobacteriia,o:Sphingobacteriales,f:Saprospiraceae,g:Rubidimonas)</i>
Otu137	48.95781	1.60E-07	0.24	0.81	6.57	<i>p:Proteobacteria,c:Gammaproteobacteria,o:Chromatiales,f:Granulosicoccaceae (g:Granulosicoccus)</i>
Otu106	47.92505	2.00E-07	0.39	0.35	6.21	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Winogradskyella)</i>
Otu81	47.83307	2.04E-07	0.00	0.00	4.39	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Thiotrichales,f:Thiotrichaceae,g:Cocleimonas)</i>
Otu58	43.74876	5.18E-07	1.19	0.00	6.89	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Xanthomonadales,f:JTB255_marine_benthic_group)</i>
Otu216	40.07995	1.27E-06	0.56	1.19	6.45	<i>p:Proteobacteria,c:Gammaproteobacteria,o:Gammaproteobacteria_incertae_sedis,g:Marinicella</i>
Otu228	34.81483	5.12E-06	0.07	0.00	4.20	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Thiotrichales,f:Thiotrichaceae,g:Leucothrix)</i>
Otu500	34.4339	5.70E-06	0.23	0.00	5.13	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Thiotrichales,f:Thiotrichaceae,g:Leucothrix)</i>
Otu88	32.8447	8.98E-06	5.50	5.30	0.75	<i>p:Proteobacteria,c:Gammaproteobacteria (o:Xanthomonadales,f:Xanthomonadaceae,g:Arenimonas)</i>
Otu22	30.92623	1.59E-05	7.39	1.30	0.00	<i>Unknown Bacteria (p:Bacteroidetes,c:Sphingobacteriia,o:Sphingobacteriales,f:Saprospiraceae)</i>
Otu44	29.13159	2.77E-05	6.79	6.07	0.45	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae,g:Flavobacterium (s:F_ponti)</i>
Otu489	27.51	4.68E-05	5.13	6.28	2.40	<i>p:Proteobacteria,c:Betaproteobacteria,o:Methylophilales (f:Methylophilaceae,g:Methylotenera)</i>
Otu128	26.18468	7.29E-05	0.27	2.54	6.79	<i>p:Verrucomicrobia,c:Verrucomicrobiae,o:Verrucomicrobiales (f:Rubritaleaceae,g:Rubritalea)</i>



Salinity	Test-Statistic	Bonferroni p-value	Fresh/Brackish	Estuarine	Marine	Taxonomy
Otu6	24.53299	0.00012943	7.79	3.20	0.99	<i>Bacteria (p:Bacteroidetes,c:Cytophagia,o:Cytophagales,f:Cytophagaceae)</i>
Otu69	21.48868	0.00039919	2.18	7.16	4.16	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Caulobacterales,f:Hyphomonadaceae (Silva – Alphaproteobacteria)</i>
Otu1314	19.65052	0.00082714	5.41	6.30	3.26	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>
Otu24	18.77582	0.00118674	0.85	2.64	8.08	<i>p:Bacteroidetes (c:Flavobacteriia,o:Flavobacteriales,f:NS9_marine_group)</i>
Otu97	17.64729	0.00191877	2.92	7.14	8.06	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu112	16.19758	0.00365143	1.07	2.91	6.76	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Polaribacter)</i>
Otu78	15.19753	0.00579825	0.42	1.06	4.87	<i>p:Proteobacteria,c:Gammaproteobacteria,o:Oceanospirillales,f:Oceanospirillaceae,g:Neptunomonas</i>
Otu36	15.14013	0.00595711	5.79	6.73	0.00	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae,g:Cellulophaga (s:C_tyrosinoydans)</i>
Otu80	14.49807	0.00809037	2.49	6.95	4.00	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae (g:Maribacter)</i>
Otu134	14.20743	0.00931423	2.61	6.31	5.84	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>
Otu7	13.54646	0.01290349	9.64	9.20	2.48	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales,f:Comamonadaceae (g:Hydrogenophaga)</i>
Otu495	13.37528	0.01405826	4.27	5.31	0.00	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Sphingomonadales (f:Sphingomonadaceae)</i>
Otu858	13.02356	0.01679454	2.86	5.98	5.87	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales</i>
Otu572	12.79593	0.01886693	3.43	7.27	3.05	<i>p:Proteobacteria,c:Alphaproteobacteria (o:Rhodobacterales,f:Rhodobacteraceae)</i>
Otu99	11.87508	0.03052797	5.20	8.06	8.51	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae (g:Sulfitobacter)</i>
Otu107	11.75949	0.03246883	1.75	3.85	7.14	<i>p:Bacteroidetes,c:Flavobacteriia,o:Flavobacteriales,f:Flavobacteriaceae</i>
Otu160	11.53466	0.03663391	5.46	3.54	0.00	<i>p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales,f:Comamonadaceae</i>
Otu877	11.45929	0.03815599	3.20	7.71	6.81	<i>p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>

Table S5: Core bacterial operational taxonomic units across all samples. Total number of sequences across all operational taxonomic units (OTUs) and samples was 276,285. Classification of taxonomy is from Greengenes, with additional resolution from Silva v123 in parentheses.

OTU	Taxonomy	sum across all samples
Otu4	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae,g:Loktanella (s: L_rosea)</i>	22337
Otu7	<i>d:Bacteria,p:Proteobacteria,c:Betaproteobacteria,o:Burkholderiales,f:Comamonadaceae (g:Hydrogenophaga)</i>	18732
Otu12	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	10961
Otu299	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	10462
Otu9	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	9672
Otu8	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae (g:Pseudorhodobacter)</i>	8114
Otu30	<i>d:Bacteria,p:Proteobacteria,c:Betaproteobacteria (o:Methylophilales,f:Methylophilaceae,g:Methylotenera)</i>	5142
Otu51	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria (o:Rhizobiales,f:Phyllobacteriaceae)</i>	3413
Otu20	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Sphingomonadales,f:Erythrobacteraceae (g:Porphyrobacter,s:P._sanguineus)</i>	3130
Otu99	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae (g:Sulfitobacter)</i>	2871
Otu13	<i>d:Bacteria,p:Actinobacteria,c:Actinobacteria,o:Acidimicrobiales,f:Acidimicrobiaceae,g:Ilumatobacter (s:I_nonamiensisYM16-303)</i>	2846
Otu50	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	2513
Otu26	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Caulobacterales,f:Hyphomonadaceae</i>	2332
Otu25	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Sphingomonadales (f:Erythrobacteraceae)</i>	2130
Otu123	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	1783
Otu64	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	1474
Otu84	<i>d:Bacteria,p:Actinobacteria,c:Actinobacteria,o:Acidimicrobiales,f:Acidimicrobiaceae,g:Ilumatobacter</i>	1236
Otu1004	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae,g:Phaeobacter (or Pseudophaeobacter)</i>	1023
Otu1314	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	452
Otu489	<i>d:Bacteria,p:Proteobacteria,c:Betaproteobacteria,o:Methylophilales (f:Methylophilaceae,g:Methylotenera)</i>	396
Otu10	<i>d:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhodobacterales,f:Rhodobacteraceae</i>	7986

OTU	Taxonomy	sum across all samples
Otu23	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales, f: Rhodobacteraceae (g: Marivita)</i>	4571
Otu115	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Sphingomonadales, f: Erythrobacteraceae (g: Erythrobacter)</i>	1417
Otu91	<i>d: Bacteria, p: Bacteroidetes, c: Flavobacteriia (o: Flavobacteriales, f: Cryomorphaceae, g: Fluviicola)</i>	1067
Otu143	<i>d: Bacteria, p: Actinobacteria, c: Actinobacteria, o: Acidimicrobiales, f: Acidimicrobiaceae, g: Ilumatobacter</i>	790
Otu5	<i>d: Bacteria, p: Proteobacteria, c: Betaproteobacteria, o: Methylophilales, f: Methylophilaceae</i>	16866
Otu41	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Sphingomonadales, f: Erythrobacteraceae</i>	2618
Otu46	<i>d: Bacteria, p: Proteobacteria, c: Gammaproteobacteria</i>	1138
Otu1266	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales, f: Rhodobacteraceae</i>	1113
Otu189	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales, f: Rhodobacteraceae</i>	897
Otu47	<i>d: Bacteria, p: Proteobacteria, c: Gammaproteobacteria, o: Chromatiales (f: Granulosicoccaceae, g: Granulosicoccus)</i>	845
Otu138	<i>d: Bacteria, p: Proteobacteria, c: Gammaproteobacteria, o: Chromatiales (f: Chromatiaceae)</i>	457
Otu88	<i>d: Bacteria, p: Proteobacteria, c: Gammaproteobacteria (o: Xanthomonadales, f: Xanthomonadaceae, g: Arenimonas)</i>	425
Otu1631	<i>d: Bacteria, p: Proteobacteria, c: Gammaproteobacteria (g: Candidatus_Thiobios)</i>	358
Otu54	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales, f: Rhodobacteraceae (g: Loktanella)</i>	1816
Otu49	<i>d: Bacteria, p: Proteobacteria, c: Epsilonproteobacteria, o: Campylobacterales, f: Helicobacteraceae, g: Sulfurovum</i>	1047
Otu109	<i>d: Bacteria, p: Bacteroidetes, c: Flavobacteriia, o: Flavobacteriales, f: Flavobacteriaceae (g: Robiginitalea)</i>	941
Otu572	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria (o: Rhodobacterales, f: Rhodobacteraceae)</i>	792
Otu858	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales</i>	728
Otu6	<i>d: Bacteria (p: Bacteroidetes, c: Cytophagia, o: Cytophagales, f: Cytophagaceae)</i>	8795
Otu44	<i>d: Bacteria, p: Bacteroidetes, c: Flavobacteriia, o: Flavobacteriales, f: Flavobacteriaceae, g: Flavobacterium (s: F_ponti)</i>	1392
Otu134	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales, f: Rhodobacteraceae</i>	601
Otu35	<i>d: Bacteria, p: Proteobacteria, c: Gammaproteobacteria, o: Chromatiales, f: Granulosicoccaceae (g: Granulosicoccus)</i>	2500
Otu877	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales, f: Rhodobacteraceae</i>	1671
Otu73	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales, f: Rhodobacteraceae, g: Sulfitobacter (s: S_sp._BSw21498)</i>	1603

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OTU	Taxonomy	sum across all samples
Otu350	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales</i>	1500
Otu93	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria, o: Rhodobacterales</i>	871
Otu267	<i>d: Bacteria, p: Bacteroidetes, c: Flavobacteriia, o: Flavobacteriales, f: Flavobacteriaceae</i>	760
Otu77	<i>d: Bacteria, p: Actinobacteria, c: Actinobacteria (c: Acidimicrobii, o: Acidimicrobiales, f: Sva0996_marine_group)</i>	558
Otu83	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria (o: Rhodobacterales, f: Rhodobacteraceae)</i>	547
Otu144	<i>d: Bacteria, p: Proteobacteria, c: Alphaproteobacteria (o: Sphingomonadales, f: Sphingomonadaceae, g: Sphingopyxis)</i>	543

Table S6: BLAST results of fungal operational taxonomic units (OTUs) that were significantly different across sites or salinity conditions or within the core microbiomes, but were unclassified in the UNITE database.

<u>OTU ID</u>	<u>UNITE result</u>	<u>Variable of Influence</u>	<u>Top Blast Result: Accession Number; Proportion Identity; Description</u>
Otu5	unknown	Site, Table S7	KC965494.1; 0.8498; Uncultured fungus clone 68_NA10_P31_H10 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence
Otu55	unknown	Site, Table S7	MF965343.1; 0.9831; Fungal sp. clone ITS1_OTU_110 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence
Otu57	unknown	Site, Table S7	MF555485.1; 0.9676; Uncultured <i>Acaulospora</i> clone OTU1 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence
Otu61	unknown	Site, Table S7	KU559644.1; 0.8857; Uncultured fungus clone 100_E_4046449 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence
Otu92	unknown	Site, Table S7	MK983654.1; 0.9467; Uncultured fungus clone Otu220 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence
Otu3	unknown	Salinity, Table S8	JX371114.1; 1; Uncultured fungus clone 035A16773 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence
Otu133	unknown	Salinity, Table S8	FR668924.1; 0.9828; <i>Ectocarpus fasciculatus</i> genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate S002 (virus)
Otu7	unknown	Core, Table S9	KC965494.1; 0.8128; Uncultured fungus clone 68_NA10_P31_H10 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

Table S7: ANOVA tests for fungal operational taxonomic units (OTUs) that were significantly different across sites (mean values shown in heat map).

Site	Test-Statistic	Bonferroni p-value	Surrey River	Fitzroy River	Yambuk	Moynes River	Curdies River	Sherbrook River	Taxonomy
Otu42	68.682386	2.73E-11	0.00	9.63	0.00	1.55	0.00	0.50	*
Otu16	59.853558	1.25E-10	0.77	0.38	11.93	1.21	1.10	0.17	*
Otu166	50.665949	7.74E-10	0.00	0.00	0.34	0.00	7.17	0.00	*
Otu64	50.112371	8.72E-10	8.47	0.00	1.00	0.76	0.32	0.50	p:Zygomycota
Otu100	46.937666	1.77E-09	3.99	8.42	0.00	0.00	7.53	10.16	*
Otu11	43.015147	4.50E-09	10.65	0.00	1.88	0.61	1.15	1.41	p:Ascomycota
Otu325	34.556189	4.50E-08	4.18	0.50	0.34	0.00	5.49	9.00	*
Otu3	32.173329	9.40E-08	1.64	2.75	2.86	18.13	4.27	0.89	*
Otu31	29.96211	1.95E-07	2.96	8.05	0.87	1.67	7.10	11.04	p:Basidiomycota
Otu67	29.955456	1.95E-07	0.04	0.25	9.79	3.82	0.27	0.00	*
Otu89	29.020152	2.69E-07	0.09	1.05	2.58	0.00	9.37	1.69	*
Otu75	25.469483	9.91E-07	0.00	0.15	0.15	9.57	0.00	0.00	p:Ascomycota,c:Dothideomycetes
Otu49	24.16661	1.66E-06	6.99	0.00	5.20	0.00	0.00	0.00	p:Ascomycota
Otu1902	23.846235	1.89E-06	1.63	5.41	0.00	0.00	6.27	8.79	*
Otu8	21.290781	5.65E-06	3.78	0.87	13.15	3.89	1.59	1.73	*
Otu30	20.206737	9.28E-06	0.00	0.00	10.28	2.17	0.74	1.56	*
Otu83	16.303683	6.69E-05	0.00	0.00	9.42	1.37	1.69	0.17	p:Ascomycota,c:Dothideomycetes
Otu2	15.822308	8.74E-05	9.70	10.90	3.17	5.46	3.53	14.36	p:Ascomycota,c:Leotiomycetes
Otu210	14.383294	0.0002019	6.90	0.00	0.66	0.00	0.00	0.00	p:Basidiomycota
Otu20	13.889026	0.0002728	0.92	4.22	1.41	1.49	0.00	11.52	*
Otu7	13.778037	0.0002922	7.41	7.06	13.28	3.70	2.14	1.87	*
Otu6	13.553848	0.0003361	5.83	9.06	13.35	4.22	3.59	3.61	p:Chytridiomycota
Otu93	12.928999	0.0005008	0.00	1.10	6.69	7.70	8.27	0.98	p:Basidiomycota
Otu2339	12.860841	0.0005235	0.83	1.51	9.53	2.17	1.70	0.00	p:Zygomycota
Otu82	12.859322	0.000524	6.66	0.00	1.02	0.00	0.00	0.00	p:Zygomycota

Site	Test-Statistic	Bonferroni p-value	Surrey River	Fitzroy River	Yambuk	Moyn River	Curdies River	Sherbrook River	Taxonomy
Otu151	12.615382	0.0006149	0.00	0.18	0.00	9.31	0.00	0.00	p:Ascomycota
Otu23	12.594046	0.0006236	1.83	1.69	11.56	6.35	3.06	2.05	p:Ascomycota,c:Sordariomycetes
Otu79	12.548493	0.0006426	6.41	0.00	0.00	0.76	0.00	0.40	p:Basidiomycota,c:Microbotryomycetes,o:Sporidiobolales,f:Sporidiobolales_fam_Incertae_sedis
Otu1	12.474011	0.0006752	6.28	8.43	10.93	16.36	14.10	9.65	p:Ascomycota,c:Sordariomycetes,o:Hypocreales
Otu90	12.024752	0.0009136	0.00	0.38	0.00	8.76	0.00	0.00	p:Ascomycota
Otu21	11.839703	0.001037	8.72	0.40	0.59	0.00	0.73	4.43	p:Basidiomycota,c:Microbotryomycetes,o:Sporidiobolales
Otu5	11.708934	0.0011351	3.02	1.27	9.65	4.30	13.39	5.86	*
Otu69	10.781458	0.0021979	0.00	0.15	1.10	0.00	0.00	8.03	p:Rozellomycota
Otu55	9.5061043	0.0058022	2.93	7.47	0.00	0.00	0.00	0.59	*
Otu61	9.1305303	0.0078402	1.41	0.00	10.16	3.63	2.33	1.64	*
Otu102	8.7916764	0.0103528	2.33	6.46	0.00	0.00	0.00	1.23	p:Chytridiomycota
Otu10	8.5317749	0.0128682	6.38	9.41	1.13	3.80	0.12	1.43	p:Ascomycota
Otu38	8.3215051	0.0153874	7.80	1.54	0.00	0.00	0.00	1.97	p:Basidiomycota,c:Microbotryomycetes,o:Sporidiobolales,f:Sporidiobolales_fam_Incertae_sedis,g: <i>Sporobolomyces</i>
Otu92	7.7477692	0.0254004	0.06	3.92	1.58	0.00	8.05	3.03	*
Otu48	7.2866526	0.0385738	0.00	8.51	6.15	1.16	1.83	0.57	p:Ascomycota
Otu103	7.1123205	0.0453401	7.07	0.06	0.31	0.00	1.13	3.67	p:Ascomycota,c:Leotiomycetes,o:Helotiales
Otu57	7.0895098	0.0463162	5.92	0.00	0.49	0.00	0.12	1.26	*

Table S8: ANOVA tests for fungal operational taxonomic units (OTUs) that were significantly different across salinity groups (mean values shown in heat map).

Salinity	Test-Statistic	Bonferroni p-value	Fresh	Brackish	Estuarine	Marine	
Otu3	75.16101	1.26E-09	2.886219	1.87501	18.1314	*	
Otu75	71.46996	2.24E-09	0.051247	0.075795	9.5703	p:Ascomycota,c:Dothideomycetes	
Otu151	35.444	3.85E-06	0.058444	0	9.3096	p:Ascomycota	
Otu90	33.64058	6.39E-06	0.126193	0	8.76436	p:Ascomycota	
Otu133	16.18901	0.003282	2.277801	2.863729	11.062	*	
Otu96	13.22702	0.013564	0.08246	0	6.874	p:Chytridiomycota	

Table S9: Core fungal operational taxonomic units across all samples. Total number of sequences across all operational taxonomic units (OTUs) and samples was 1,707,733.

OTU	Taxonomy	Sum across all samples
Otu1	p:Ascomycota,c:Sordariomycetes,o:Hypocreales	183617
Otu2	p:Ascomycota,c:Leotiomyces	138954
Otu4	p:Ascomycota,c:Sordariomycetes	100790
Otu6	p:Chytridiomycota	77961
Otu7	*	53239
Otu9	p:Ascomycota,c:Dothideomycetes,o:Pleosporales	36488
Otu22	p:Ascomycota,c:Leotiomyces	15346
Otu23	p:Ascomycota,c:Sordariomycetes	13537



Figure S1: Precipitation data from stations at the northernmost (Port Fairy) and southernmost (Port Campbell) regions of coastline studied. The grey box represents the time period of sampling in this study.

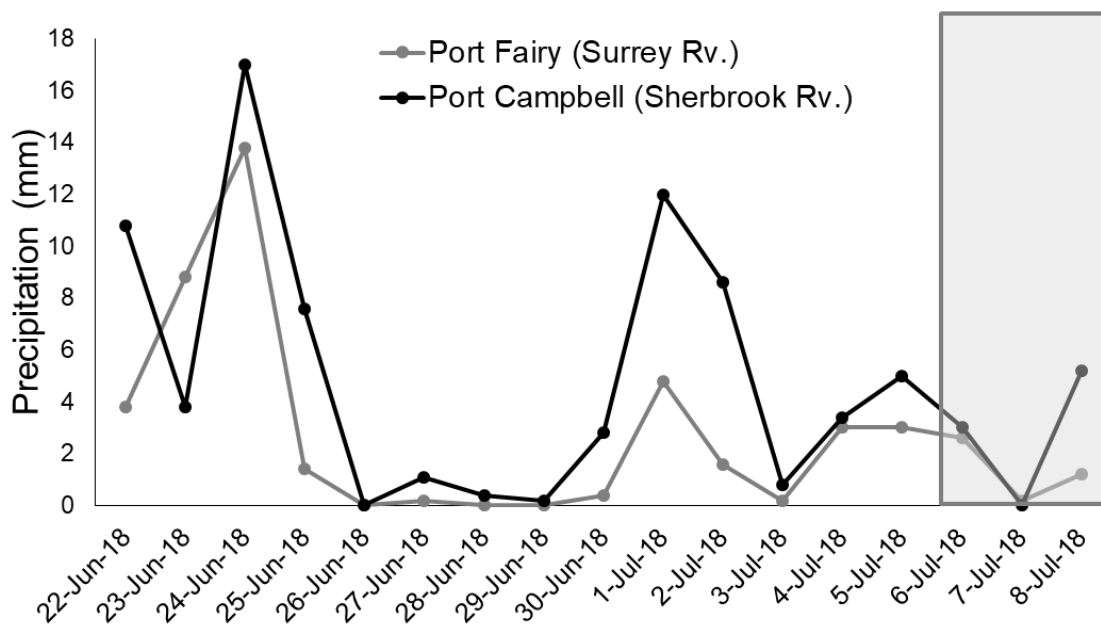


Figure S2: Rarefaction curves for (a) bacterial and (b) fungal amplicon datasets.

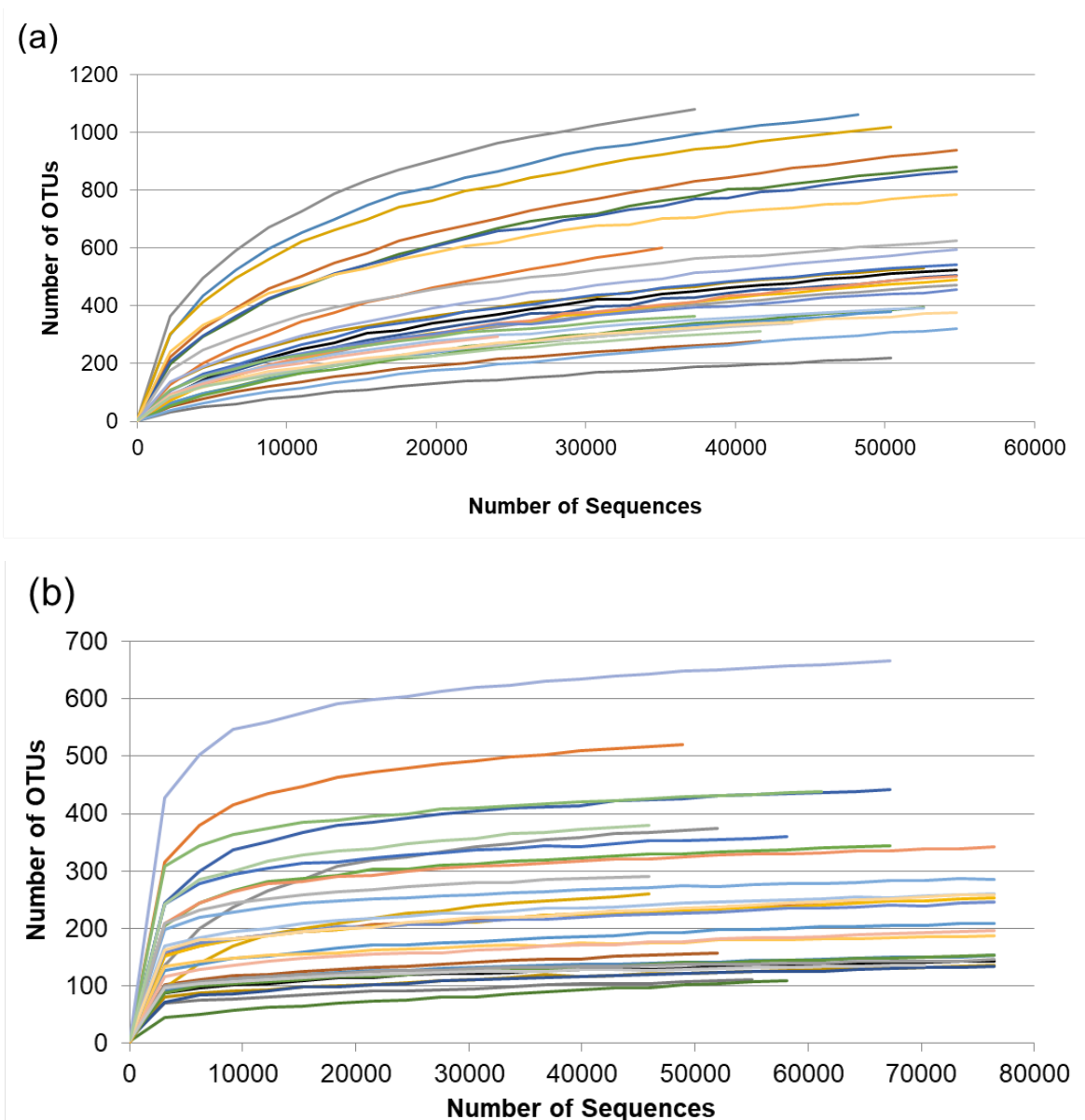
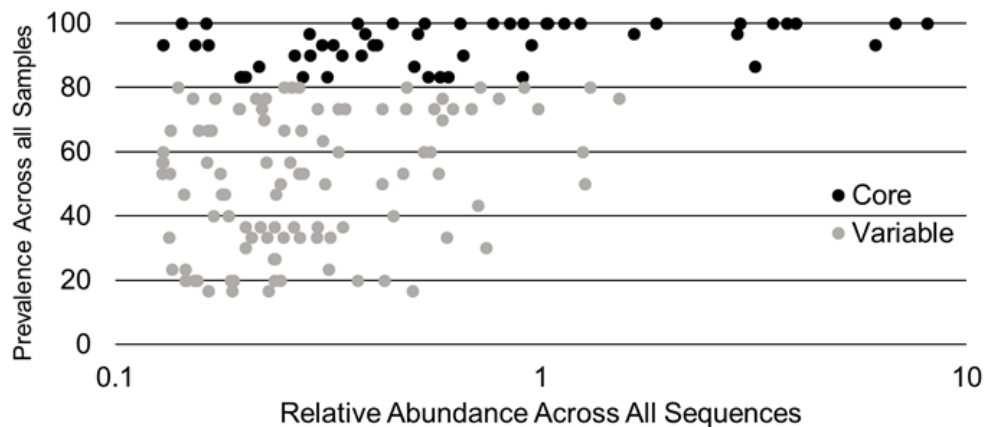


Figure S3: Scatterplots of core and variable microbiome operational taxonomic units (OTUs) for (a) bacterial and (b) fungal communities. OTU relative abundance across all sequences (log scale) was graphed against the OTU's prevalence across the samples. Prevalence >80% across all samples was defined as a core microbiome member, and prevalence >10% across all samples as a variable microbiome member.

(a) Bacterial OTUs



(b) Fungal OTUs

