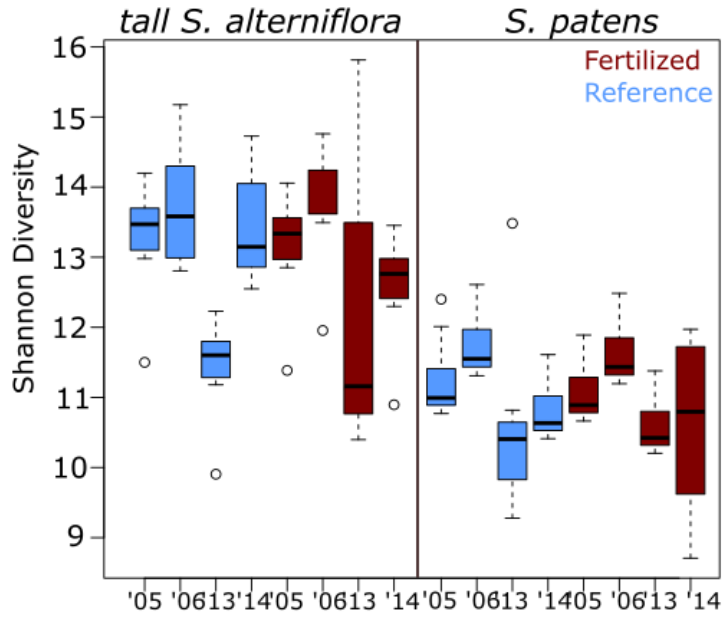


1 **Supplementary Information**

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4 **Supplementary Fig. 1. Nutrient enrichment did not alter diversity of the total microbial**

5 **community.** Box plots of average Shannon Diversity in the total community as assed by the 16S rRNA

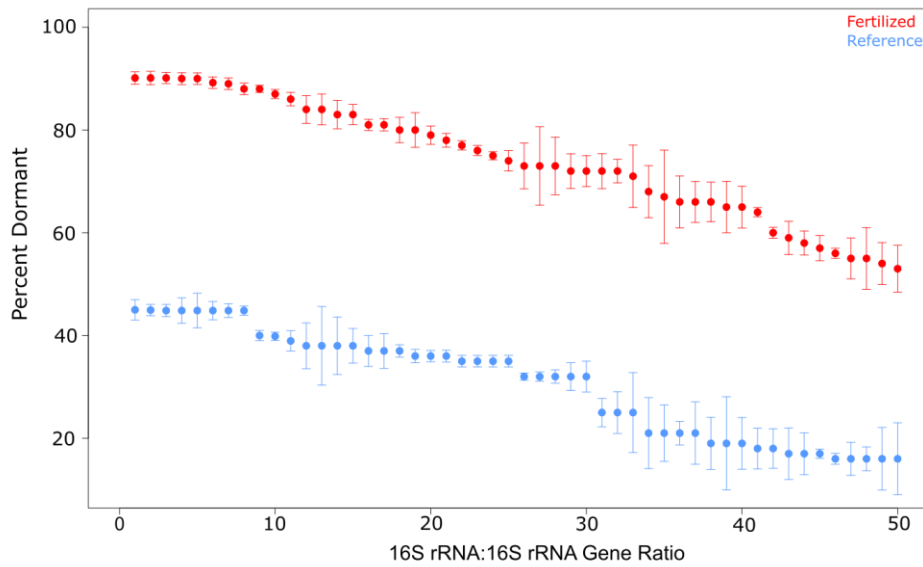
6 gene. Boxes are 25th and 75th quantiles with the medians in bold of samples collected each year from

7 reference marshes (blue) and fertilized marshes (red). Although the total diversity of bacteria in *S. patens*

8 is lower than that of *S. alterniflora*, there is no difference in diversity as a result of fertilization, in sharp

9 contrast with what was observed in the diversity of the active portion of the community.

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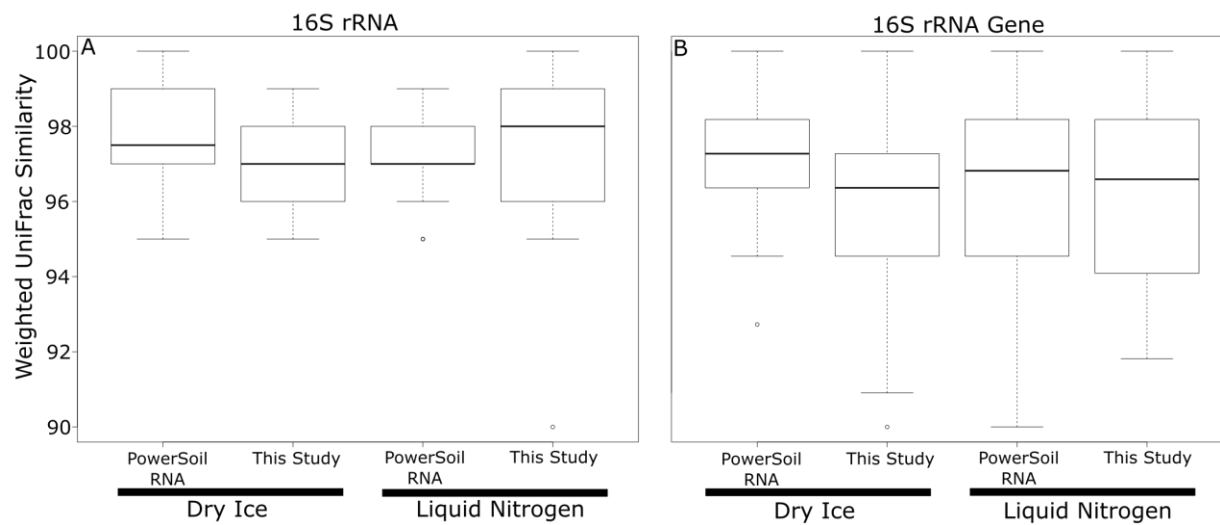
12 **Supplementary Fig. 2. Regardless of how dormancy is defined, nutrient enriched marshes have**
 13 **consistently higher dormancy than reference marshes.** Percent dormant taxa assessed by the ratio of
 14 16S rRNA to the 16S rRNA gene. Data were generated by increasing the ratio required for a taxon to be
 15 considered active from greater than 1 to 50. At all ratios, fertilized creeks had significantly higher
 16 dormant taxa than reference sediments, as assessed by a one-way ANOVA.

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22 **Supplementary Fig. 3. Comparison of nucleic acid preservation and extraction methods.** Weighted

23 UniFrac similarity comparing community similarity for 16S rRNA (A) and the 16S rRNA gene (B) for

24 different extraction methods and sample preservation techniques.

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27 **Supplementary Table 1. Significantly different microbial taxa.** Taxonomic information of the
28 32 significantly different (between fertilized and reference samples) OTUs present at least 100
29 times from figure 3 as determined by BLASTn. Bonferroni corrected p-values are significant at
30 <0.001 as determined by a Kruskal-Wallis test.

	Phylum	Class	Order	Family	Bonferroni <i>P</i>
OTU1	Proteobacteria	Deltaproteobacteria	Desulfobacterales	NA	1.25E-14
OTU2	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	NA	6.51E-10
OTU3	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	NA	1.15E-02
OTU4	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	Phormidiaceae	1.68E-15
OTU5	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	8.90E-13
OTU6	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	4.87E-05
OTU7	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	NA	7.80E-11
OTU8	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	NA	3.34E-03
OTU9	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	1.02E-06
OTU10	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	1.50E-02
OTU11	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	2.23E-09
OTU12	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	Phormidiaceae	2.47E-13
OTU13	Cyanobacteria	Oscillatoriophycideae	Oscillatoriales	NA	2.80E-14
OTU14	Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfobacteraceae	4.26E-09

OTU15	Cyanobacteria	Oscillatoriothycidae	Oscillatoriales	NA	4.14E-10
OTU16	Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	7.03E-11
OTU17	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	1.67E-09
OTU18	Cyanobacteria	Oscillatoriothycidae	Oscillatoriales	NA	1.28E-02
OTU19	Cyanobacteria	Oscillatoriothycidae	Oscillatoriales	NA	7.71E-14
OTU20	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	2.75E-06
OTU21	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	5.19E-09
OTU22	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	1.21E-08
OTU23	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	2.11E-05
OTU24	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	2.40E-06
OTU25	Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	1.73E-15
OTU26	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	8.47E-06
OTU27	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	7.47E-19
OTU28	Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	8.93E-17
OTU29	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	3.46E-12
OTU30	Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	7.18E-14
OTU31	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	7.79E-03
OTU32	Proteobacteria	Deltaproteobacteria	Desulfarculales	Desulfarculaceae	1.26E-02

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