Supplementary material

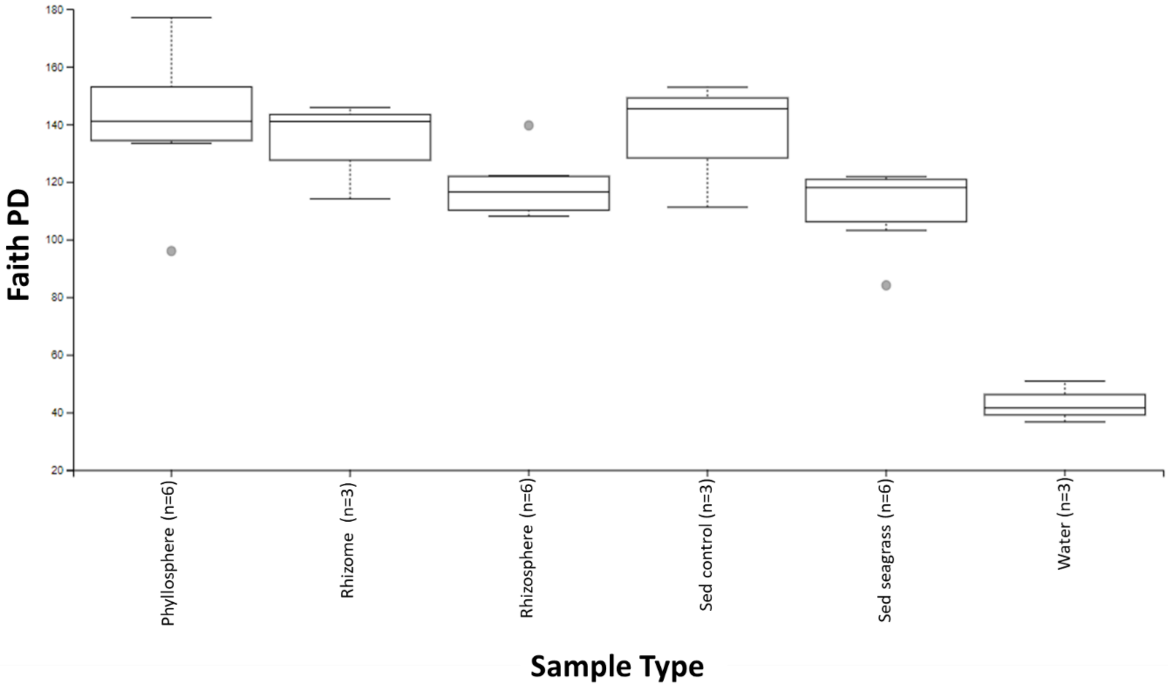


Figure S1. Boxplots of alpha diversity based on phylogenetic diversity (Faith's PD). Table S1 shows associated information.

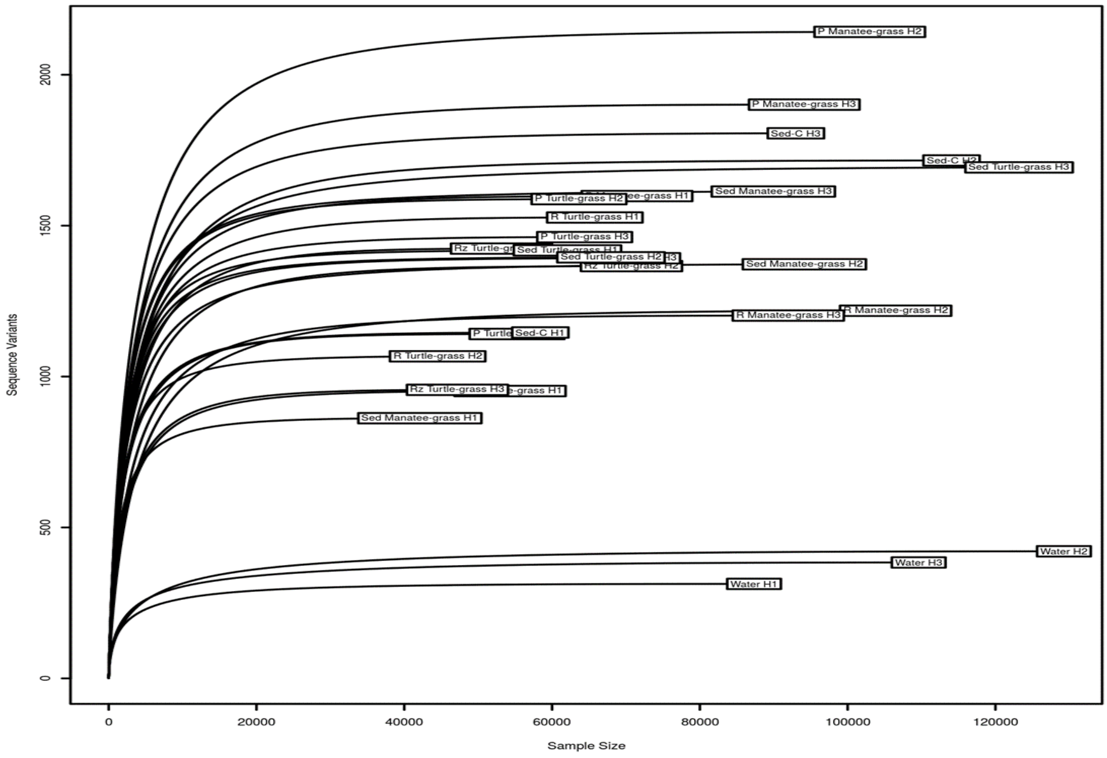


Figure S2. Rarefaction curve analysis of the sequences variants of all samples.

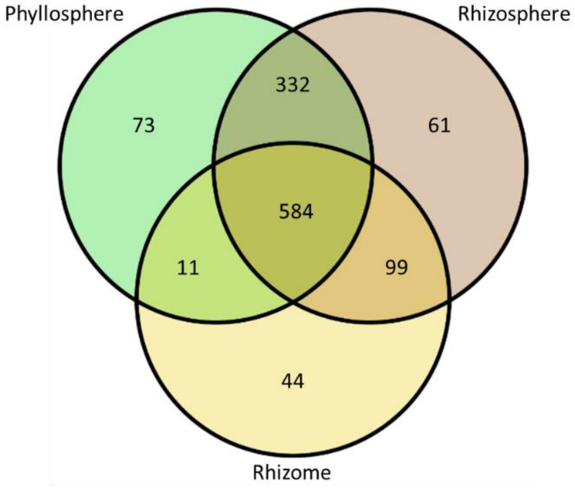


Figure S3. Venn diagram comparing the most common SVs that comprise more than 0.01% of the total SVs unique to or shared among the phyllospheres and rhizospheres of both species and the turtle grass rhizomes.

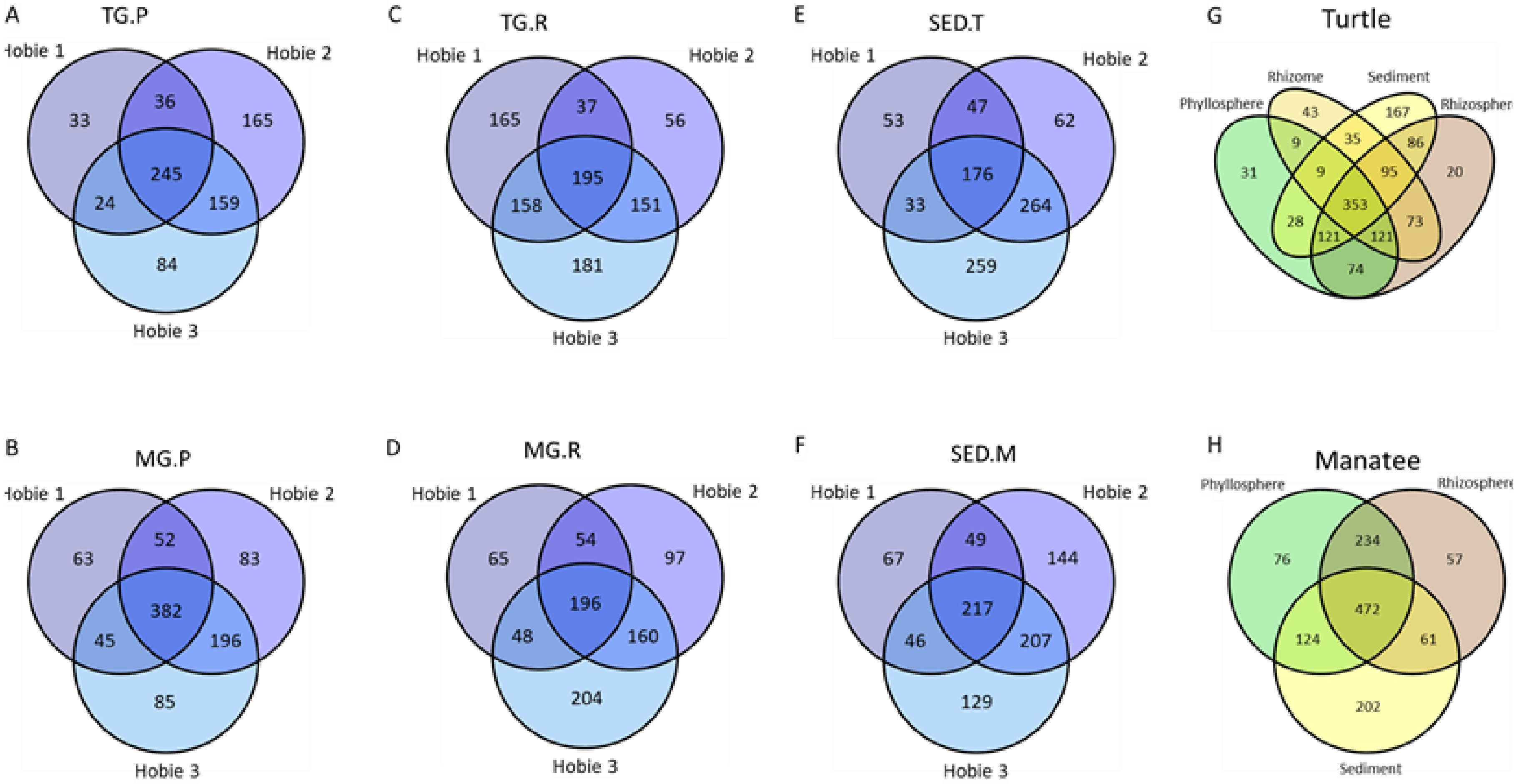


Figure S4. Venn diagrams comparing the most common SVs that comprise more than 0.01% of the total SVs unique to or shared among the three sampling sites, Hobie 1, Hobie 2 and Hobie 3, from (a) turtle grass leaves, (b) manatee grass leaves, (c) turtle grass roots, (d) manatee grass roots, (e) turtle grass sediment, (f) manatee grass sediment; comparison of the common SVs of the different plant segments of (g) turtle grass and (h) manatee grass.

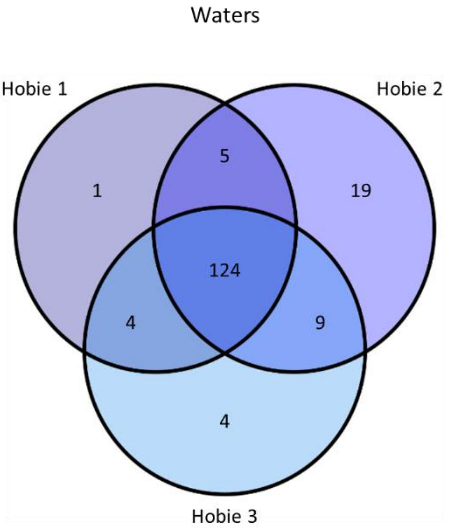


Figure S5. Venn diagram comparing the most common SVs that comprise more than 0.01% of the total SVs unique to or shared among the seawater samples from each sampling site, Hobie 1, Hobie 2 and Hobie 3.

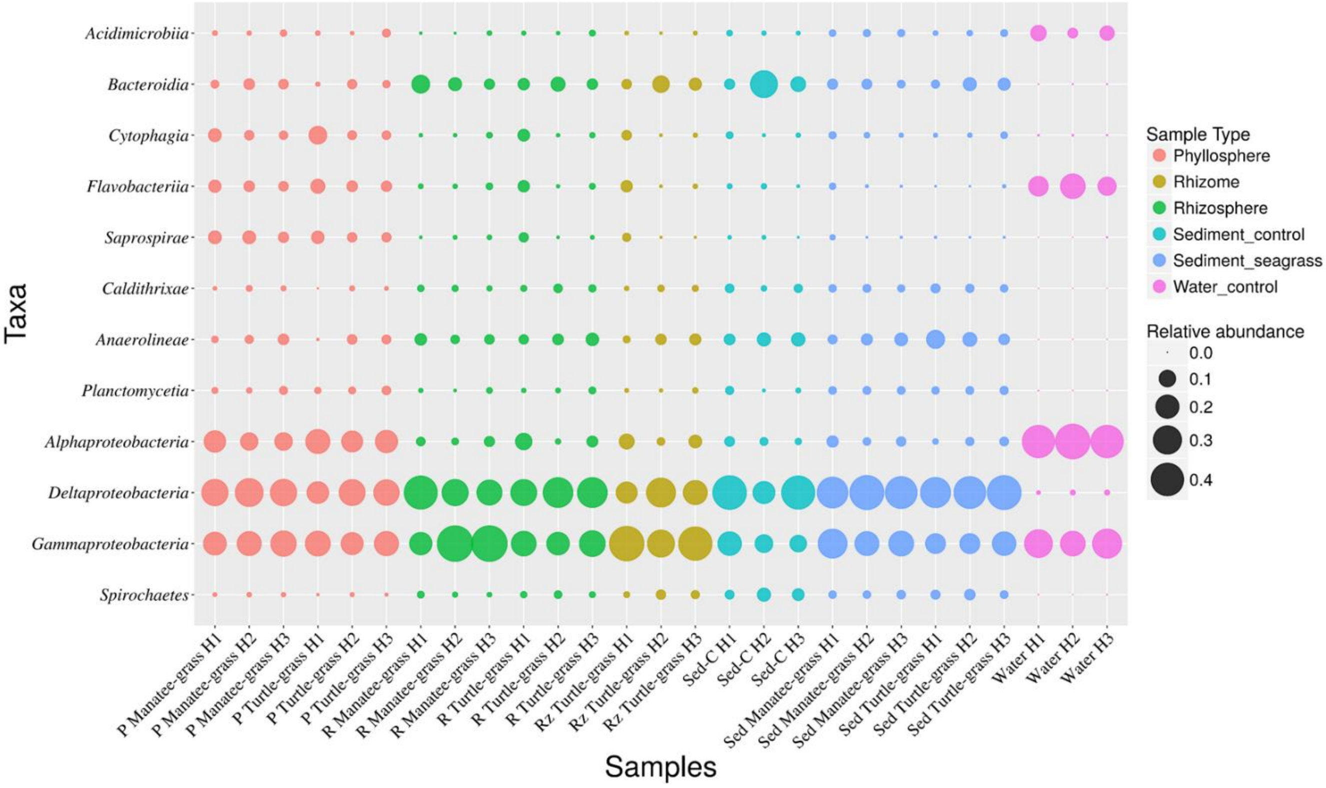


Figure S6. Relative abundance of the classes comprising more than 1% of the bacterial sequences in each sample. Taxa are classified to the lowest rank possible according the classifier. (H1: Hobie 1; H2: Hobie 2; H3: Hobie 3; P: phyllosphere; R: roots; Rz: rhizome; C: control; Sed: sediment)

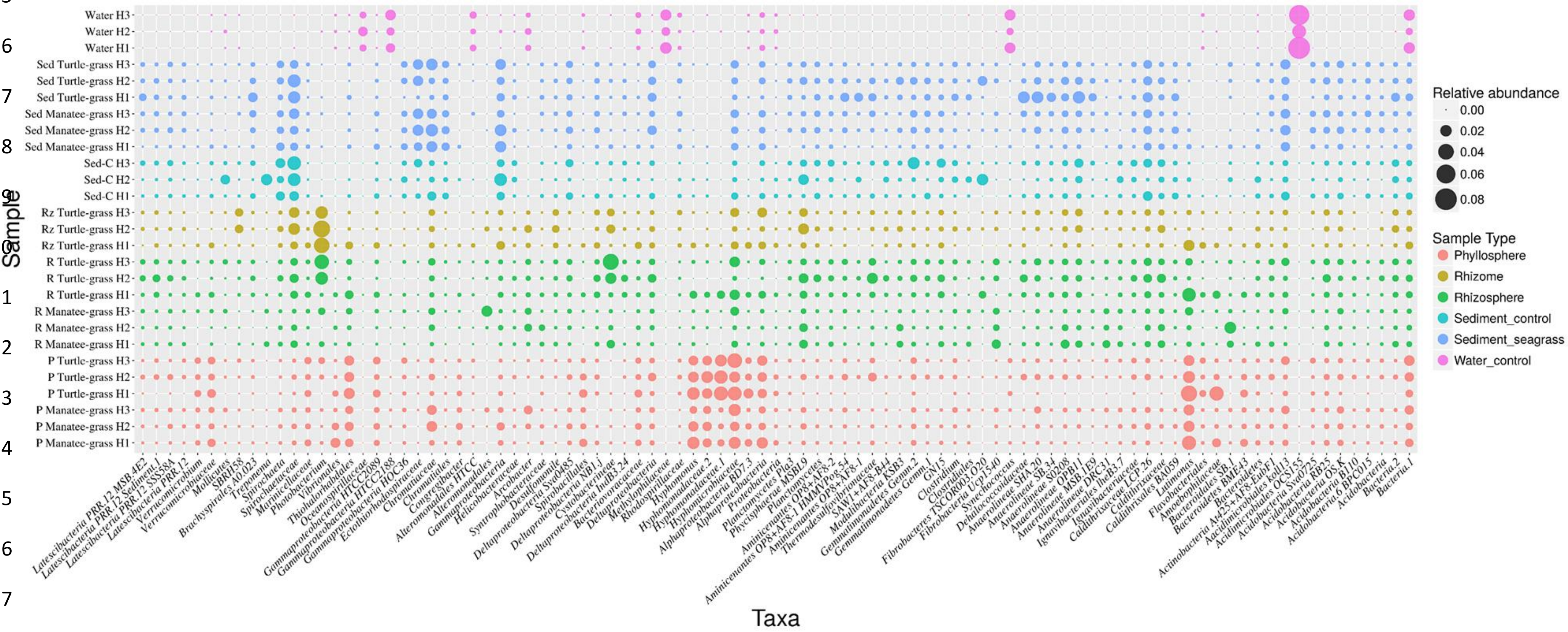


Figure S7. Relative abundance of the genera comprising between 0.1% and 1% of the bacterial sequences in each sample. Taxa are classified to the lowest rank possible according the classifier. (H1: Hobie 1; H2: Hobie 2; H3: Hobie 3; P: phyllosphere; R: roots; Rz: rhizome; C: control; Sed: sediment).

Table S1. Pairwise analysis of sample types. (Kruskal Wallis one-way ANOVA test using Faith PD alpha diversity; q-values are adjusted *p*-values with a Benjamin & Hochberg correction).

Group 1	Group 2	H	*p*-value	q-value
Phyllosphere (n=6)	Water_control (n=3)	5.40	0.02	0.10
Rhizosphere (n=6)	Water_control (n=3)	5.40	0.02	0.10
Sediment_seagrass (n=6)	Water_control (n=3)	5.40	0.02	0.10
Phyllosphere (n=6)	Sediment_seagrass (n=6)	4.33	0.04	0.12
Rhizome (n=3)	Water_control (n=3)	3.86	0.05	0.12
Sediment_control (n=3)	Water_control (n=3)	3.86	0.05	0.12
Phyllosphere (n=6)	Rhizosphere (n=6)	2.56	0.11	0.23
Rhizome (n=3)	Rhizosphere (n=6)	2.40	0.12	0.23
Rhizome (n=3)	Sediment_seagrass (n=6)	1.67	0.20	0.27
Rhizosphere (n=6)	Sediment_control (n=3)	1.67	0.20	0.27
Sediment_control (n=3)	Sediment_seagrass (n=6)	1.67	0.20	0.27
Rhizosphere (n=6)	Sediment_seagrass (n=6)	0.64	0.42	0.53
Phyllosphere (n=6)	Rhizome (n=3)	0.07	0.80	0.89
Rhizome (n=3)	Sediment_control (n=3)	0.05	0.83	0.89
Phyllosphere (n=6)	Sediment_control (n=3)	0.00	1.00	1.00

Table S2. Pairwise analysis of seagrass species and the sediment controls. (Kruskal Wallis one-way ANOVA test using Faith PD alpha diversity; q-values are adjusted *p*-values with a Benjamin & Hochberg correction).

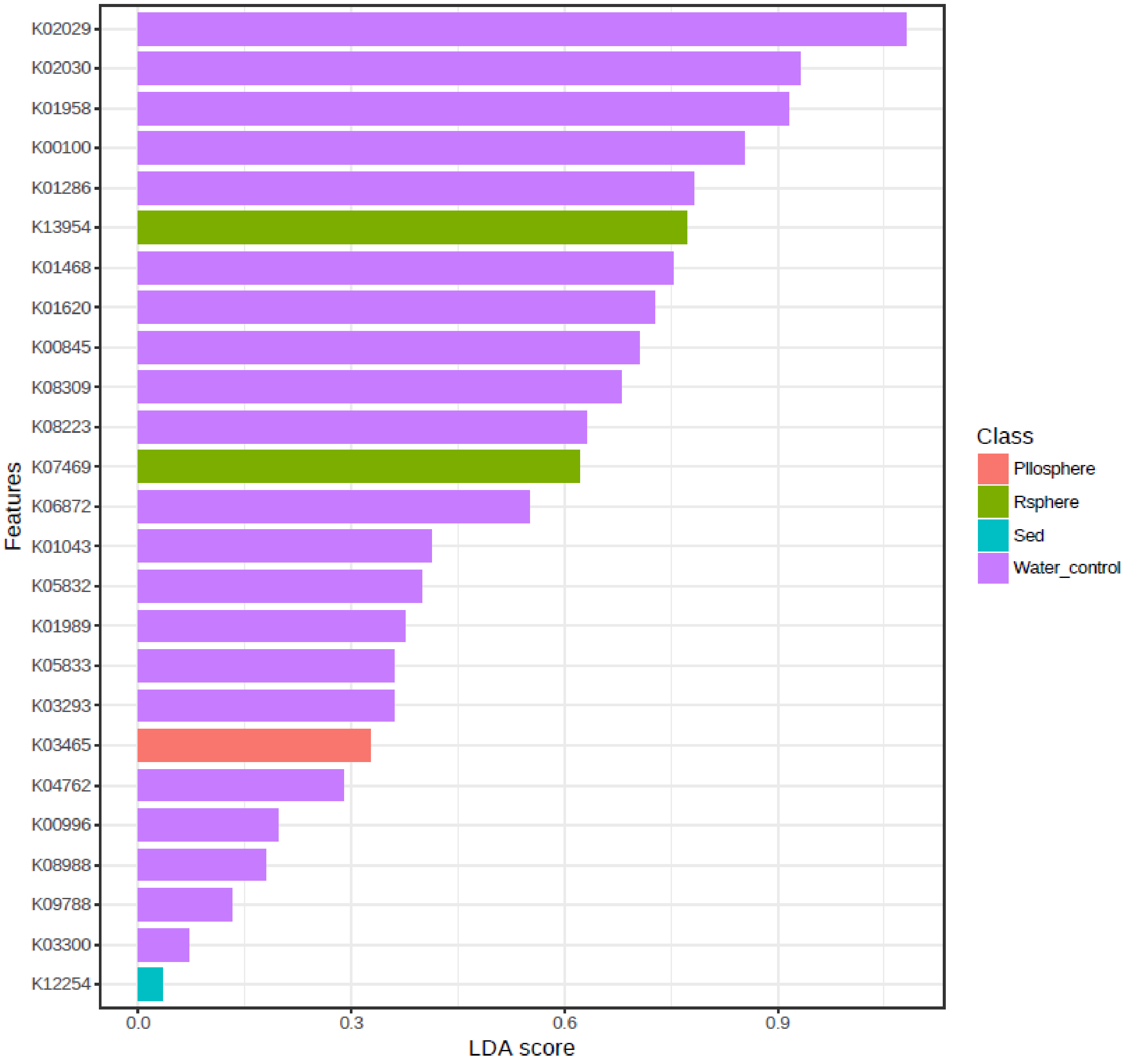
Group 1	Group 2	H	*p*-value	q-value
Turtle-grass (n=12)	Water (n=3)	6.75	0.01	0.04
Manatee-grass (n=9)	Water (n=3)	6.23	0.01	0.04
Sediment-control (n=3)	Water (n=3)	3.86	0.05	0.10
Sediment-control (n=3)	Turtle-grass (n=12)	1.02	0.31	0.47
Manatee-grass (n=9)	Sediment-control (n=3)	0.42	0.52	0.62
Manatee-grass (n=9)	Turtle-grass (n=12)	0.13	0.72	0.72

Table S3. Linear discriminant analysis effect size (LEfSe) of the most significant genes from the predictive metagenome of the microbial communities in each sample type.

KEGG ID	Function	P-values	Leaves	Roots	Rhizome	Sediment	Sed-control	Water-control	LDA score
K00845	glk; glucokinase	0.000179	8.035619	7.087147	6.626892	5.293922	6.077895	**13.428250**	0.705000
K03293	amino acid transporter, AAT family	0.000261	4.032242	3.587944	2.892067	2.321494	2.528329	**4.896308**	0.359000
K08309	soluble lytic murein transglycosylase	0.000268	10.126992	8.282040	7.727601	6.392645	6.988584	**13.932479**	0.679000
K02029	polar amino acid transport system permease protein	0.000273	27.067871	23.448377	20.051279	15.072857	15.227962	**36.912017**	1.080000
K01620	threonine aldolase	0.000283	3.829168	3.222452	3.238572	2.618063	2.638476	**11.277951**	0.727000
K02030	polar amino acid transport system substrate-binding protein	0.000299	19.309256	17.148610	13.604587	10.791966	11.096586	**25.894535**	0.932000
K01043	undetermined	0.000302	2.678694	1.648248	1.849810	1.217936	1.245954	**4.381189**	0.412000
K00100	butanol dehydrogenase	0.000368	16.678017	13.816362	10.830087	8.915192	9.597759	**21.165478**	0.853000
K08988	putative membrane protein	0.000395	1.333794	1.091106	0.742233	0.593760	0.596058	**1.615858**	0.179000
K05832	putative ABC transport system permease protein	0.000396	2.235991	1.561794	1.317041	0.888840	0.970719	**3.902992**	0.399000
K09788	2-methylaconitate isomerase	0.000396	0.755371	0.555600	0.579104	1.017602	0.751385	**1.262323**	0.131000
K04762	ribosome-associated heat shock protein Hsp15	0.000414	2.310915	2.116422	2.090539	1.657719	1.634073	**3.530218**	0.290000
K12254	NAD-dependent aldehyde dehydrogenase	0.000423	0.061807	0.046703	0.048555	**0.203810**	0.128794	0.134089	0.032800
K05833	putative ABC transport system ATP-binding protein	0.000431	1.942048	1.371242	1.157186	0.783497	0.850242	**3.361091**	0.360000
K01286	D-alanyl-D-alanine carboxypeptidase	0.000443	5.345353	4.177256	4.875712	2.888388	3.071168	**12.998411**	0.782000
K01989	putative ABC transport system substrate-binding protein	0.000444	2.713635	2.105066	1.672137	1.299262	1.371952	**4.053225**	0.376000
K08223	MFS transporter, FSR family, fosmidomycin resistance protein	0.000448	4.363350	3.724128	2.508803	2.124171	2.773647	**8.659608**	0.630000
K13954	alcohol dehydrogenase	0.000463	8.636313	**10.133672**	5.055904	4.592823	5.183233	0.283153	0.773000
K01468	hutI, AMDHD1; imidazolonepropionase	0.000465	3.607803	3.002708	2.574716	1.983094	2.276904	**11.299563**	0.753000
K01958	pyruvate carboxylase	0.000468	6.439184	4.465530	4.102776	2.713849	3.366694	**17.151255**	0.915000
K00996	undecaprenyl-phosphate galactose phosphotransferase	0.000477	1.110619	0.929308	0.823463	0.749728	0.824593	**1.896633**	0.197000

K03465	thymidylate synthase	0.000481	**2.813805**	2.442937	1.300913	1.006531	1.121770	0.574566	0.326000
K07469	aldehyde oxidoreductase	0.000490	5.524032	**6.362508**	3.105294	2.685889	3.010574	0.021235	0.620000
K06872	uncharacterized protein	0.000496	4.338583	3.957716	4.016613	2.796843	3.440344	**7.892967**	0.550000
K03300	citrate-Mg2+:H+ or citrate-Ca2+:H+ symporter, CitMHS family	0.000496	0.249924	0.205953	0.173305	0.449186	0.340620	**0.524211**	0.070200
K03535	MFS transporter, ACS family, glucarate transporter	0.000519	0.404577	0.402211	0.466396	**0.656721**	0.584688	0.211186	0.087300
K09972	amino acid transport system ATP-binding protein	0.000520	2.488648	2.142252	1.691467	1.387480	1.510278	**4.723289**	0.426000
K12506	ispDF	0.000535	4.426295	2.879025	2.350607	1.485751	1.446237	**7.703686**	0.616000
K07670	two-component system, OmpR family, response regulator MtrA	0.000538	0.184034	0.235983	0.139221	0.140758	**0.241005**	0.113645	0.026800
K12263	cytochrome c551	0.000540	0.000000	0.000000	0.006443	0.000000	0.000000	**0.221783**	0.045700

7 **Figure S8**. Linear discriminant analysis (LDA) scores of the top 25 most significant features from the
8 predictive metagenome of the microbial communities in each sample type. Features are described as
9 genes under the KEGG ID column on Table S3.



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