Supplemental information

Table S2: Allometric equations used to estimate *S. alterniflora* biomass by plant phenotype according to Wieski and Pennings (2014)

***S. alterniflora* phenotype**	**Equation**
Tall	$\ln(biomass) = -6.095 + 1.760 * \ln(height)$
Medium and short	$\ln(biomass) = -6.934 + 1.973 * \ln(height)$

Biomass: Shoot dry mass (g)

Height: Shoot height (cm)

Table S3: Extracellular enzyme substrates employed in the study identified by Chemical Abstracts Service (CAS) and Enzyme Commission (EC) designations.

Exoenzyme	**Substrate name**	**CAS number**	**EC number**
β-Glucosidase	4-Methyllumbelliferyl β-D-glucopyranoside	18997-57-4	3.2.1.21
β-1,4-N-acetylglucosaminidase (chitinase)	4-Methyllumbelliferyl N-acetyl-β-D-glucosaminide	37067-30-4	3.2.1.14
Phosphatase	4-Methyllumbelliferyl phosphate	3368-04-5	3.1.3.2 / 3.1.3.1

Table S4: PCR amplification conditions employed in the study.

Reaction	**Primer set**	**Initial Denaturat.**	**Denaturat.**	**PNAs annealing**	**Primers annealing**	**Extension**	**Final extension**
1st PCR	515F/806R[1]	2m, 95°C	94°C, 45s	78°C, 10s	50°C, 60s	72°C, 60s	10m, 72°C
			x28				
2nd PCR	Fluidigm 10-base barcodes	5m, 95°C	94°C, 30s	-	60°C, 30s	72°C, 30s	5m, 72°C
			x8				
qPCR	515F/806R[1]	2m, 95°C	94°C, 45s	78°C, 10s	50°C, 60s	72°C, 90s	-
			x40				

[1]Caporaso et al. (2011)

Fig. S1. Satellite images of study areas: (a) Sapelo Island GCE-6 site, and (b) Skidaway Island SERF site.

Fig. S2. Site ecological characterization. Boxplots of leaf N concentration, density of crab burrows, marsh periwinkle snail density, sediment redox potential (Eh), sediment pH, and porewater salinity grouped by *S. alterniflora* phenotype.

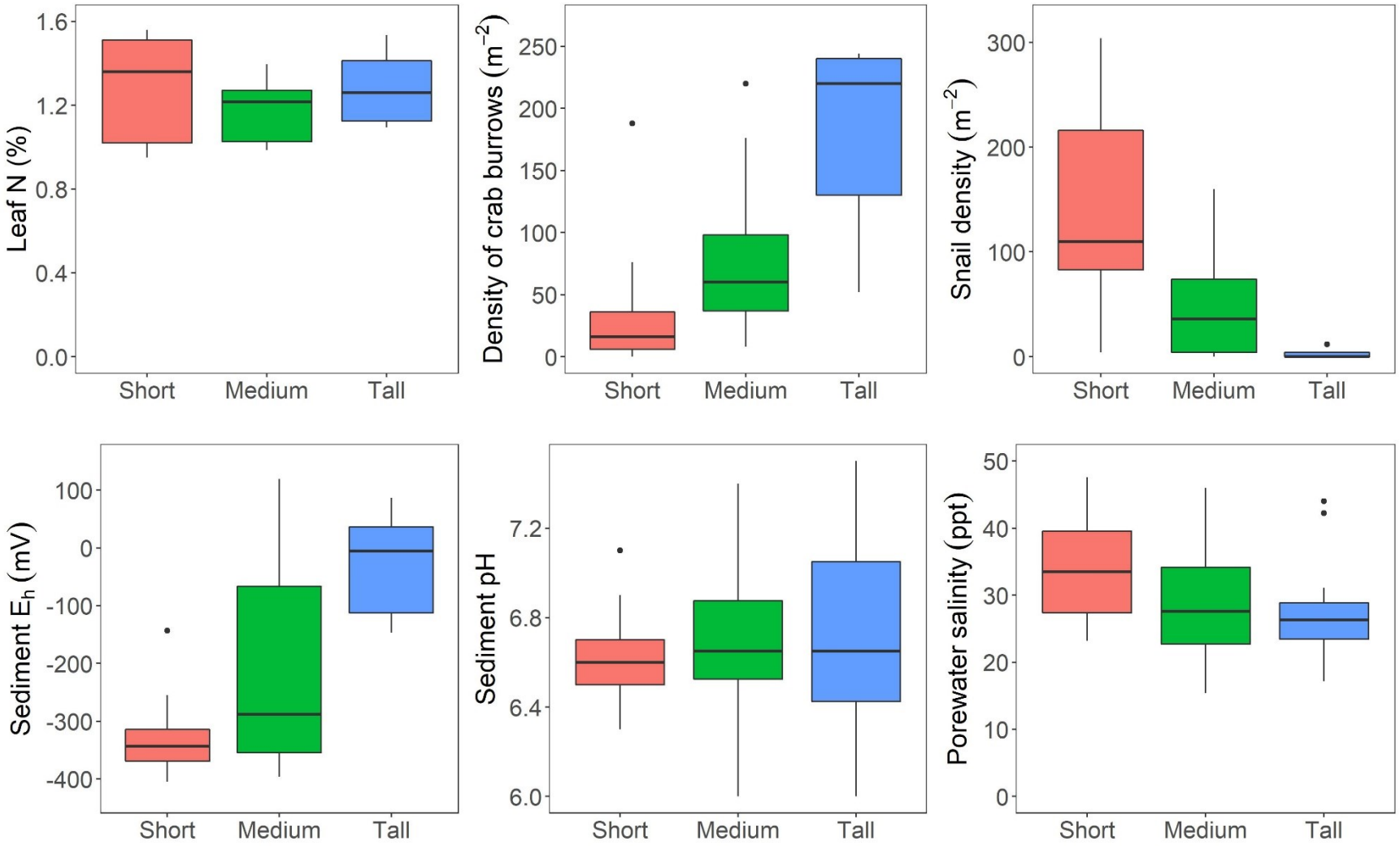

Fig. S3. Porewater chemistry characterization by *S. alterniflora* phenotype. Boxplots of ammonium, nitrate, phosphate, total sulfides, Fe(II), and Fe(III) porewater concentration per *S. alterniflora* phenotype.

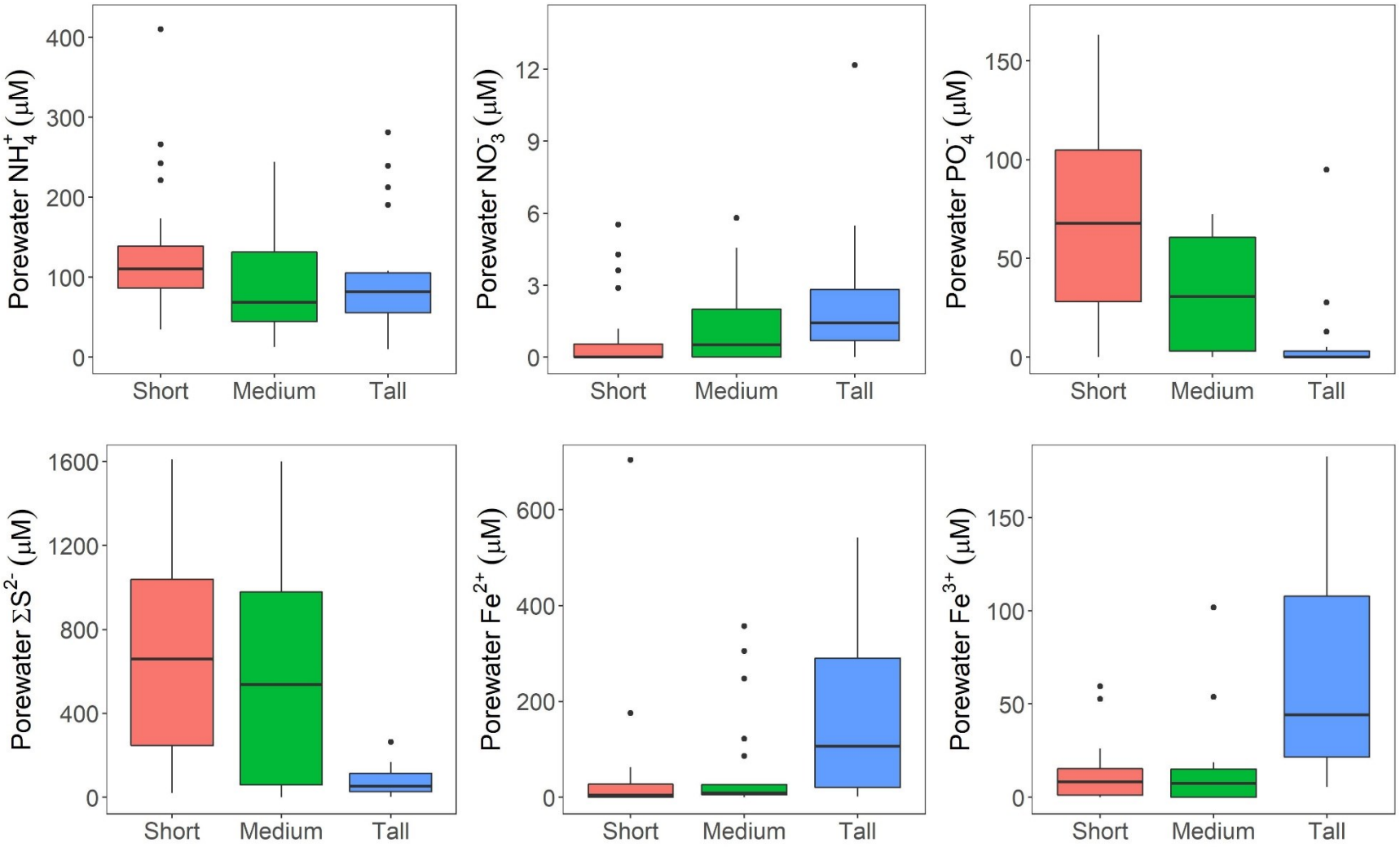

Fig. S4. C and N isotopic natural abundance by *S. alterniflora* phenotype. Boxplots of leaf $\delta^{15}N$, sediment $\delta^{15}N$, difference between leaf and sediment $\delta^{15}N$ ($\Delta^{15}N$), leaf $\delta^{13}C$, sediment $\delta^{13}C$, and difference between leaf and sediment $\delta^{13}C$ ($\Delta^{13}C$).

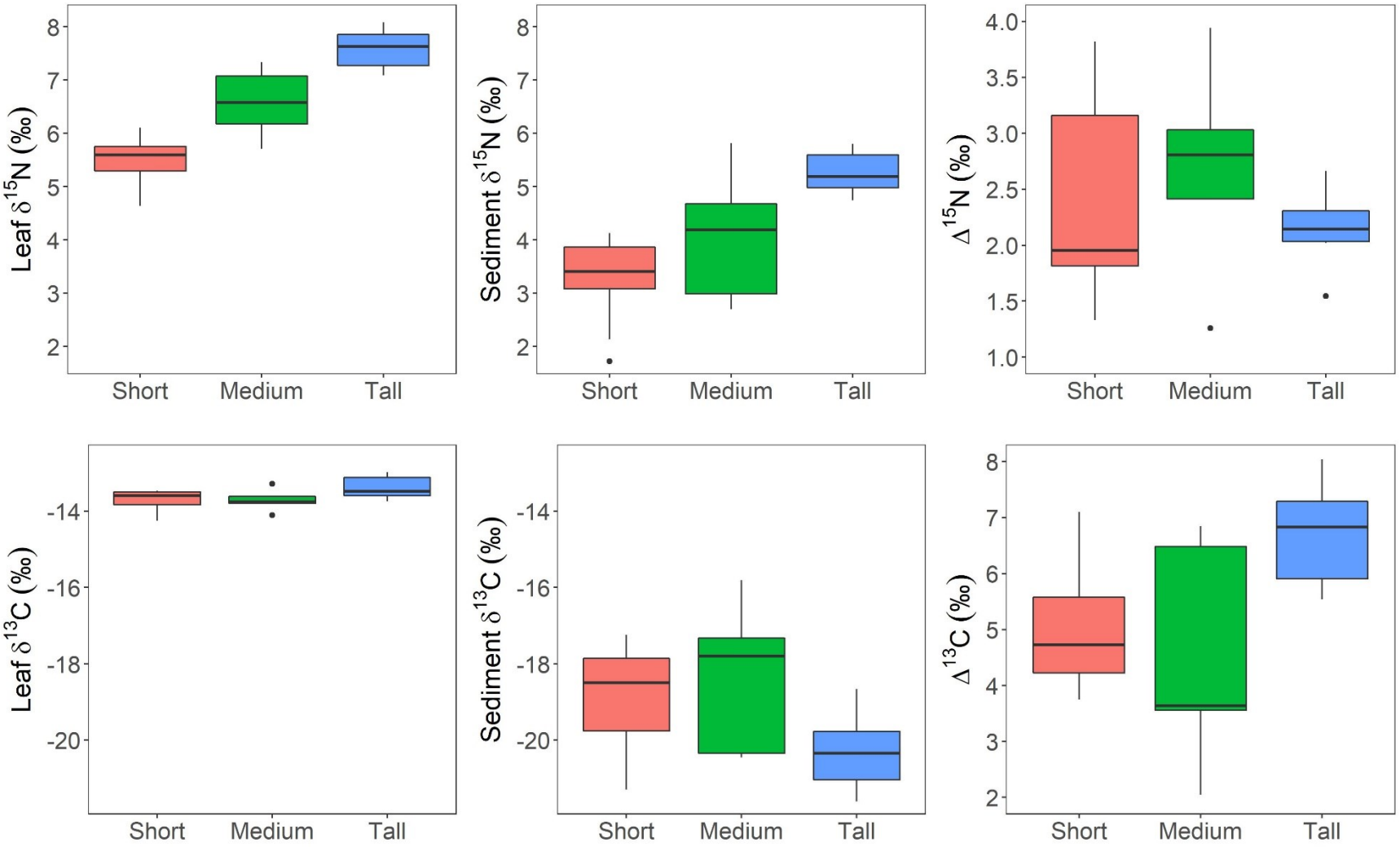

Fig. S5. Nearest taxon index (NTI) (a), and β-nearest taxon index (βNTI) (b) density plots per microbiome compartment. Dashed lines in -2 and, 2, represents interpretation thresholds. Continuous line represents median value according to index and microbiome compartment.

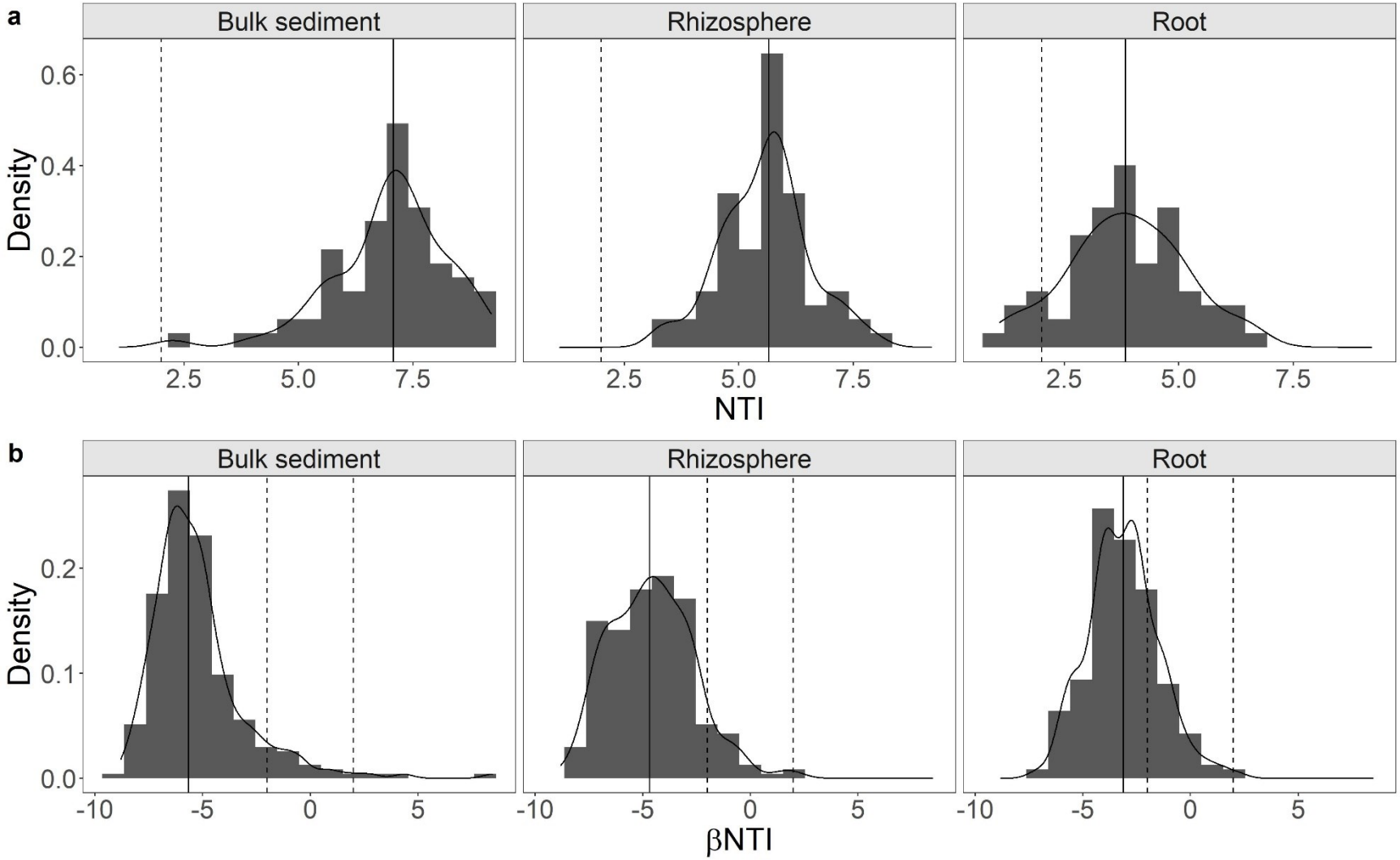

Fig. S6. Prokaryotic relative abundance partitioned at the phylum level according to microbiome compartment and *S. alterniflora* phenotype.

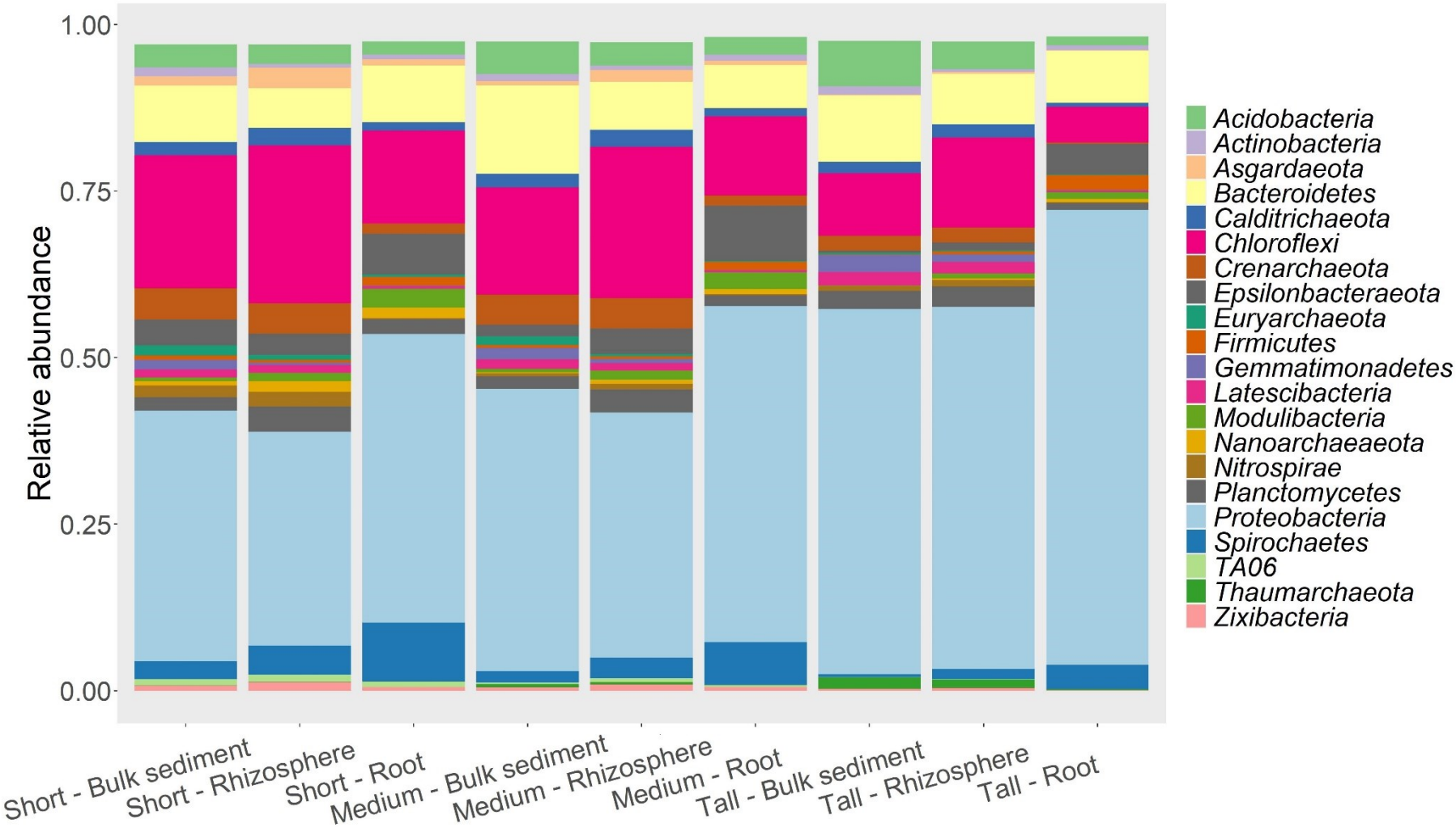

Fig. S7. Prokaryotic genera significantly enriched in the root in comparison to the bulk sediment compartments (a), and tall compared to short *S. alterniflora* phenotype (b) as assessed by DESeq2. Values represent the following: Yellow: Aerobic/facultative-anaerobic chemoheterotrophy, Green: N fixation, White: C fixation, Red: Nitrification, Blue: S oxidation, Black: S reduction, Brown: Methylotrophy, Purple: Metal reduction

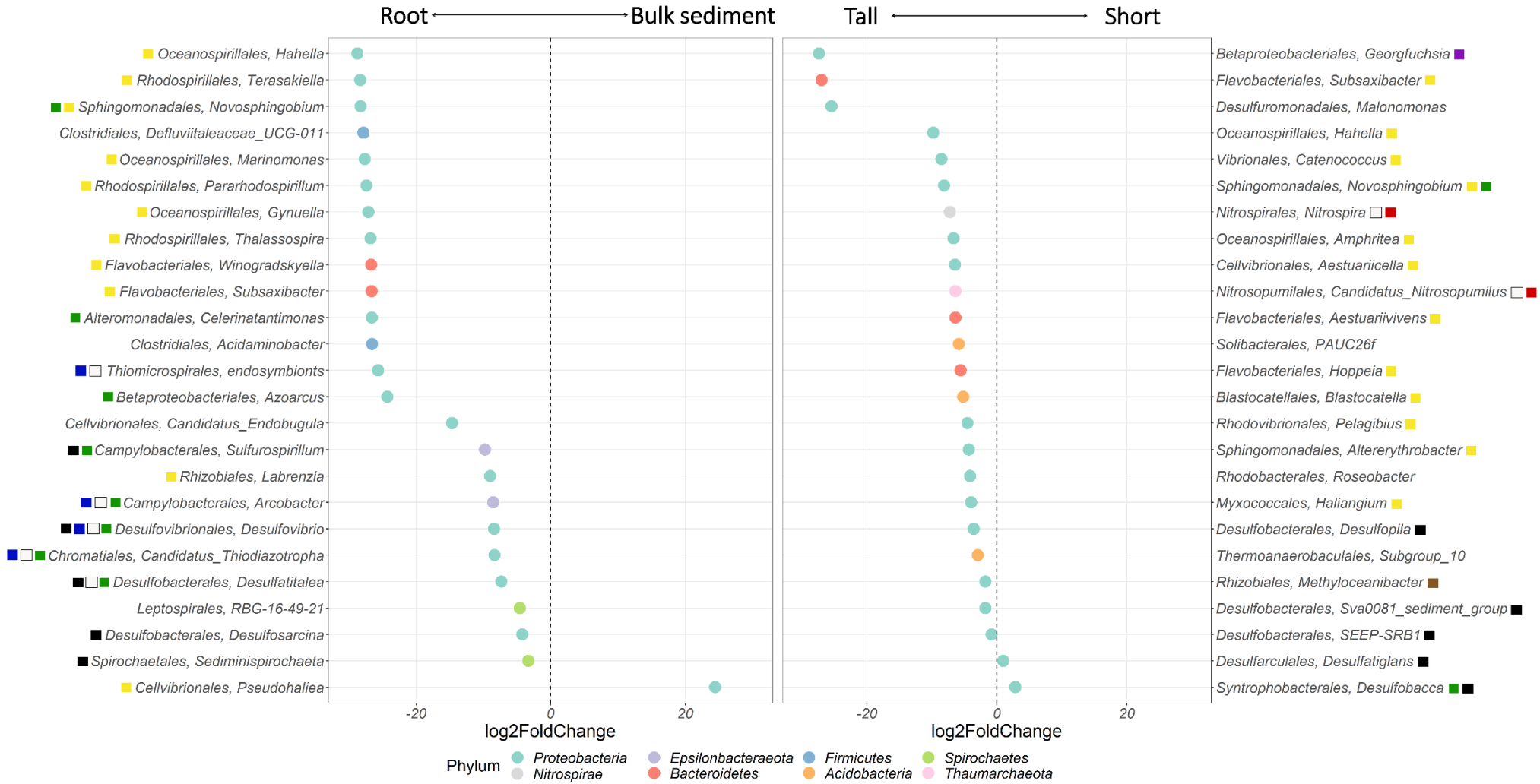

Fig. S8. Analysis of the core microbiome by accumulated richness and relative abundance with species prevalence cutoff thresholds at 10% intervals from 0% to 100% ASVs prevalence cutoffs.