Supplementary Materials

Molecular composition shifts in saltmarsh root decay reveal soil recovery, not carbon stocks

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Table S1: Average elevation of the plots at each site relative to Mean Higher High Water (MHHW).

Site Name	Distance from MHHW (m)
Grazed 1 (G1)	+0.0205
Grazed 2 (G2)	-0.2624
Grazed 3 (G3)	-0.22
Restored 1 (R1)	+0.0079
Restored 2 (R2)	+0.0621
Restored 3 (R3)	+0.0377
Restored 4 (R4)	-0.1119
Natural Reference 1 (NR1)	+0.0492
Natural Reference 2 (NR2)	+0.0135

Table S2: Soil strength at two depths in grazed, restored and reference *Salicornia*-dominant saltmarsh ecosystems. Values represent means and standard error.

kPA	Grazed	Restored	Reference
10 cm depth	124.4 ± 8.0	53.5 ± 3.7	44.7 ± 5.9
20 cm depth	157.2 ± 8.4	73.7 ± 6.8	57.1 ± 5.8

Table S3: Decay rates of tea and *Salicornia quinqueflora* root litter. Decay rates are calculated using a single exponential decay equation using proportion mass (k), proportion carbon (k_C) or proportion nitrogen (k_N) remaining over time. Decay rate units are % d^{-1}. Values represent means and standard error.

Litter Type	Rehabilitation category	Decay rate, k	Carbon decay rate, k_C	Nitrogen decay rate, k_N
Salicornia roots	Grazed	0.635 ± 0.0705	0.556 ± 0.0538	0.379 ± 0.039
	Restored	0.591 ± 0.0477	0.501 ± 0.0119	0.429 ± 0.0195
	Reference	0.517 ± 0.0741	0.441 ± 0.0424	0.358 ± 0.0558
Green tea	Grazed	1.391 ± 0.269		
	Restored	1.418 ± 0.30		
	Reference	1.325 ± 0.153		
Rooibos tea	Grazed	0.181 ± 0.0203		
	Restored	0.166 ± 0.0056		
	Reference	0.163 ± 0.0183		

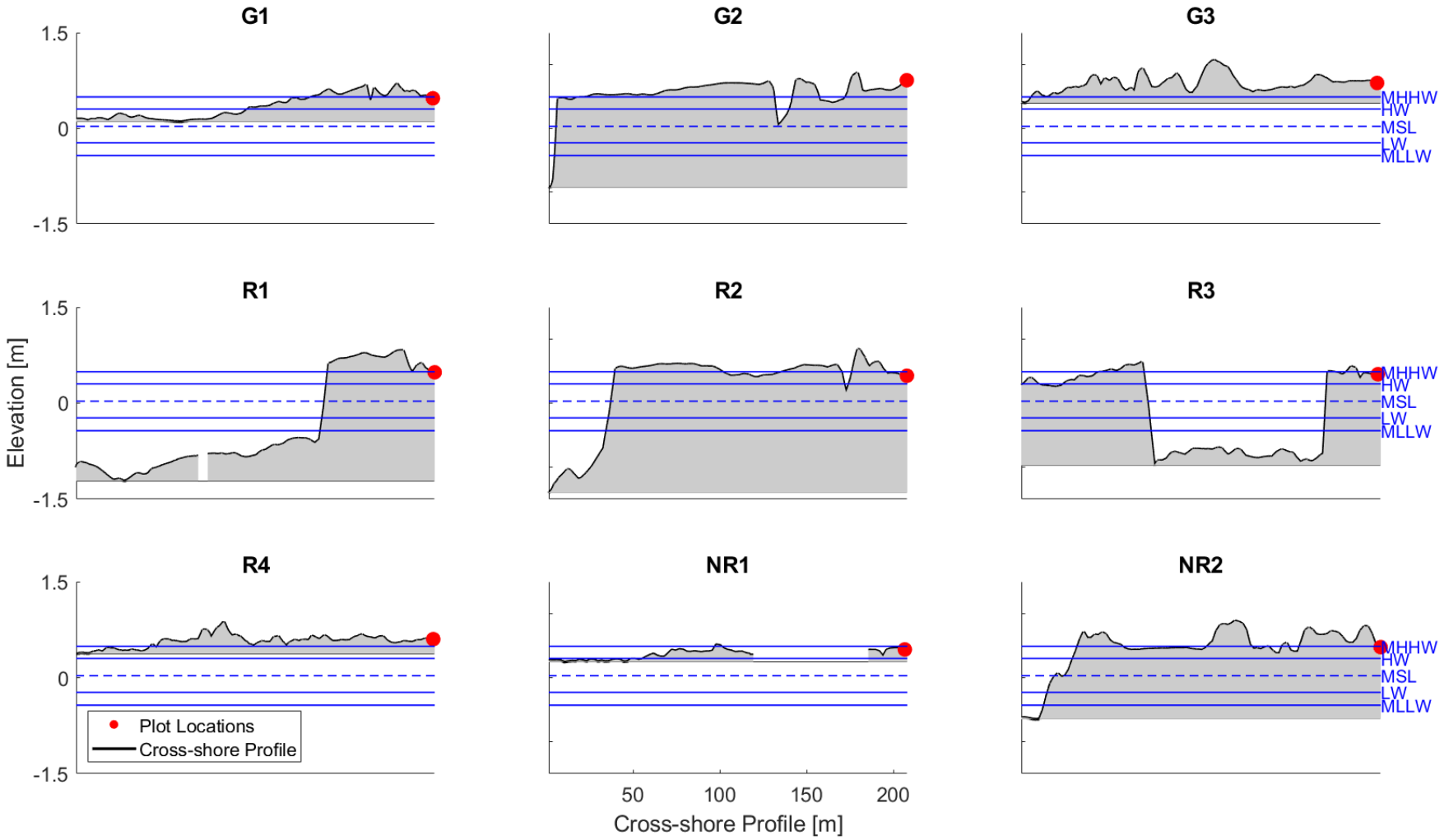

Figure S1: Cross-section of site elevation. G = Grazed site category, R = Restored site category, NR = Natural Reference site category, MHHW = Mean Higher High Water, HW = High Water, MSL = Mean Sea Level, LW = Low Water, and MLLW = Mean Lower Low Water.

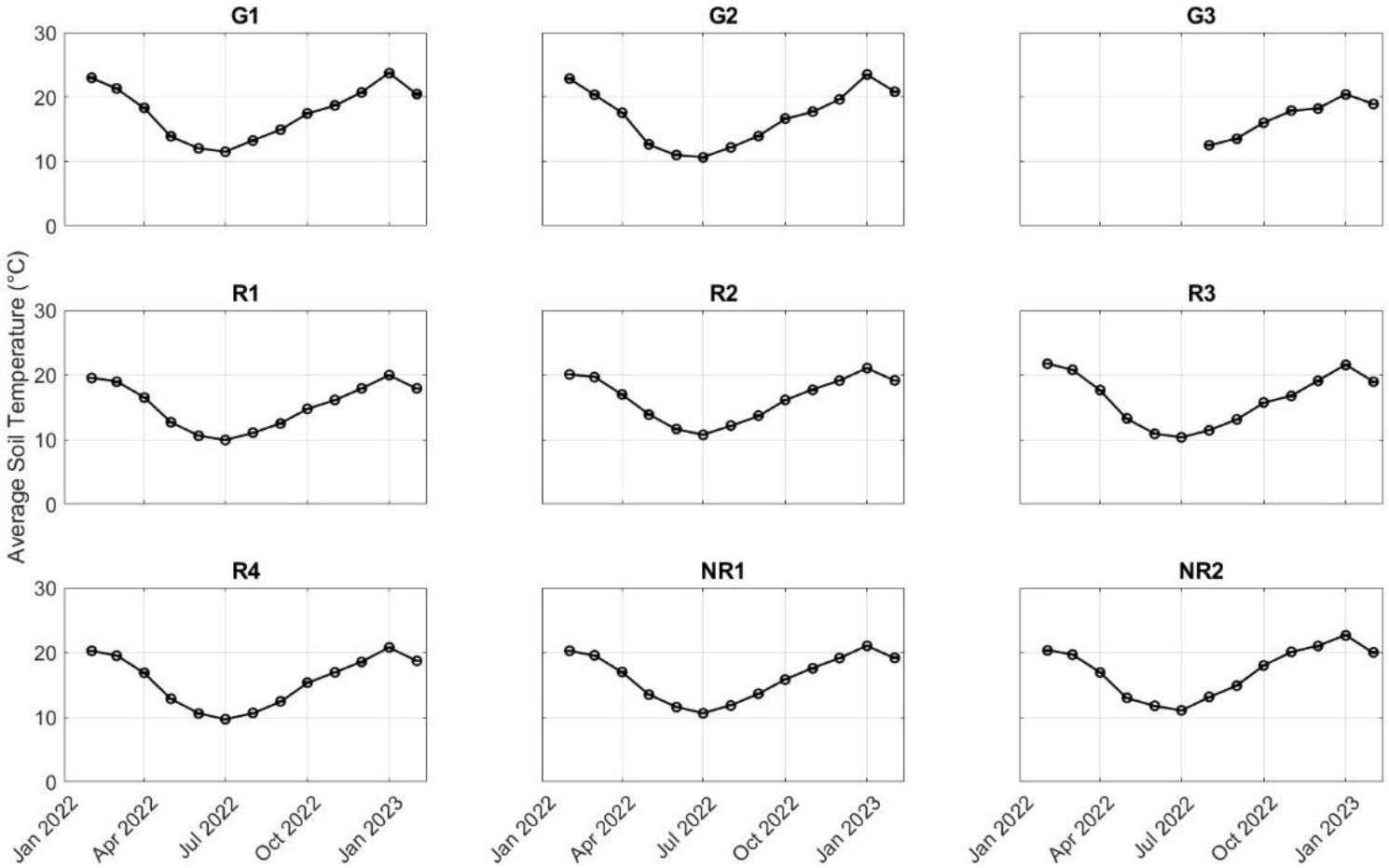

Figure S2: Monthly soil temperature time series for each site. Note that for site G3, there were logger fails resulting in lost temperature data for the first 6 months. G = Grazed, R = Restored and NR = Natural Reference. Points represent monthly means and standard deviation.

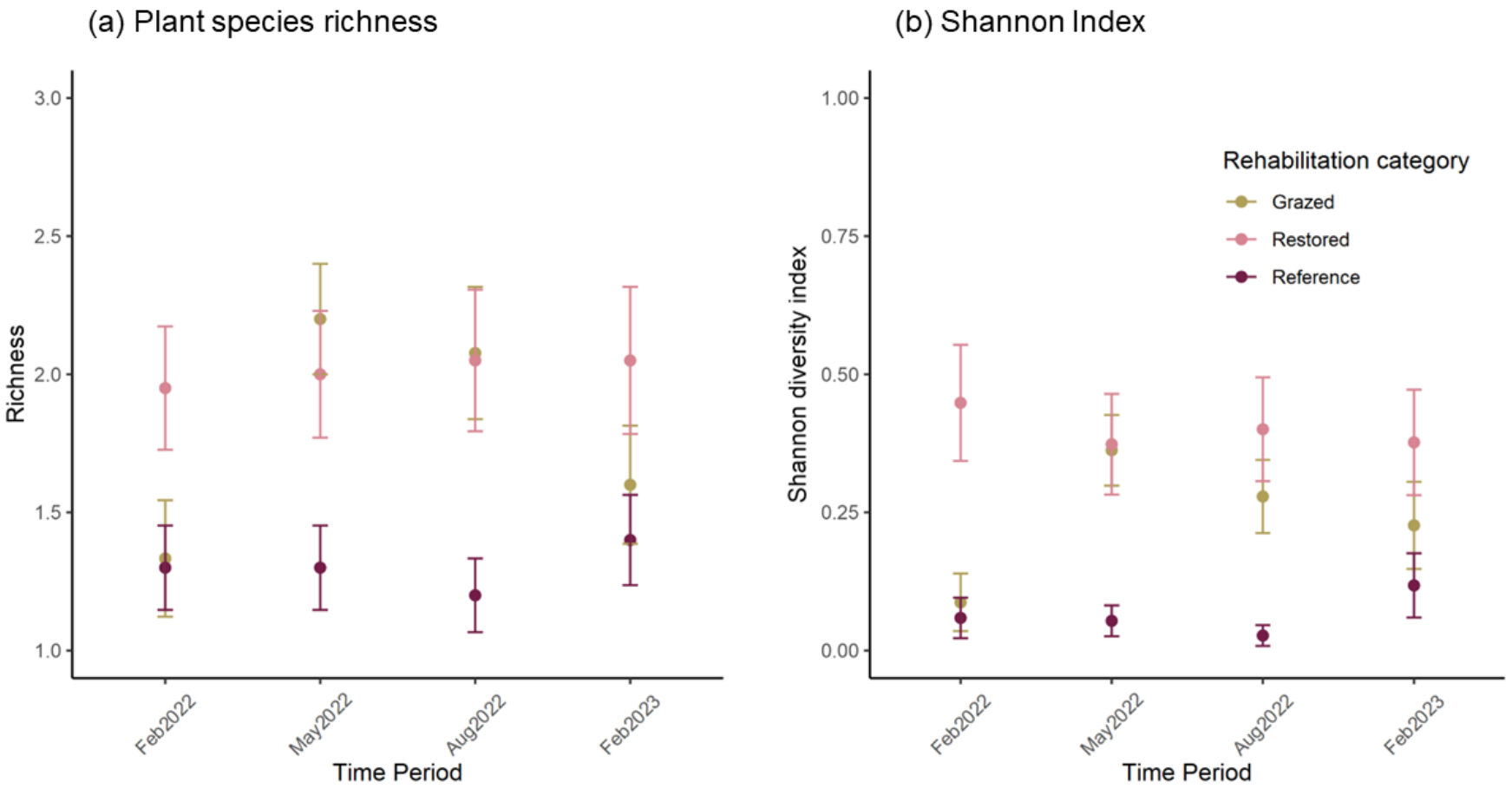

Figure S3: Vegetation alpha diversity metrics of saltmarsh plots at Grazed, Restored and Natural Reference sites. (a) Species richness. (b) Shannon Index. Vegetation surveys were taken of the experimental plots at initial, 3 month, 6 month and 12 month sampling periods. Values represent mean and standard error.

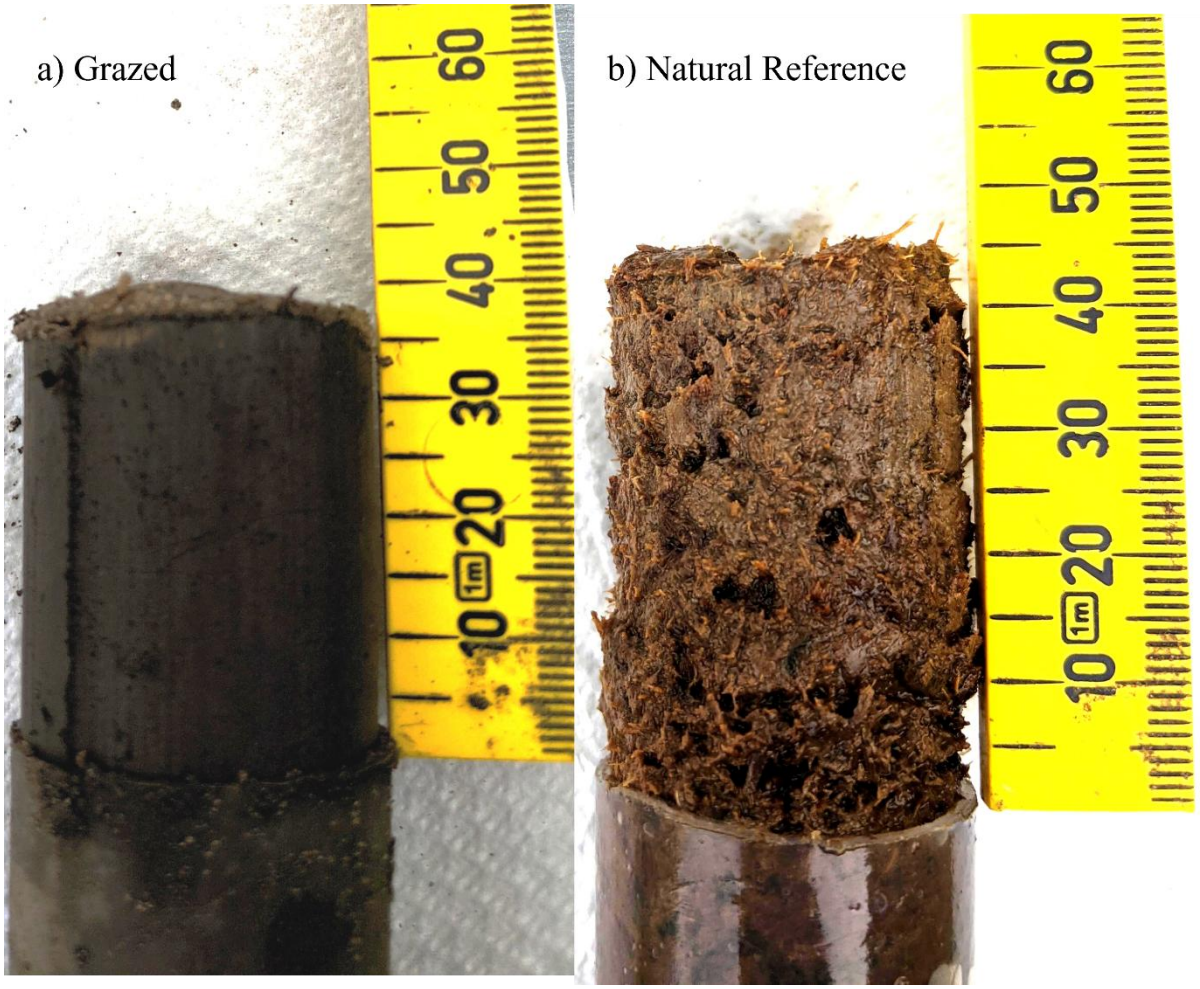

Figure S4: Soil cores demonstrating visible differences between Grazed and Restored belowground soil structure. (a) Shows the compaction and lack of roots at Grazed sites (b) shows peatier soil and presence of roots at Natural Reference sites.

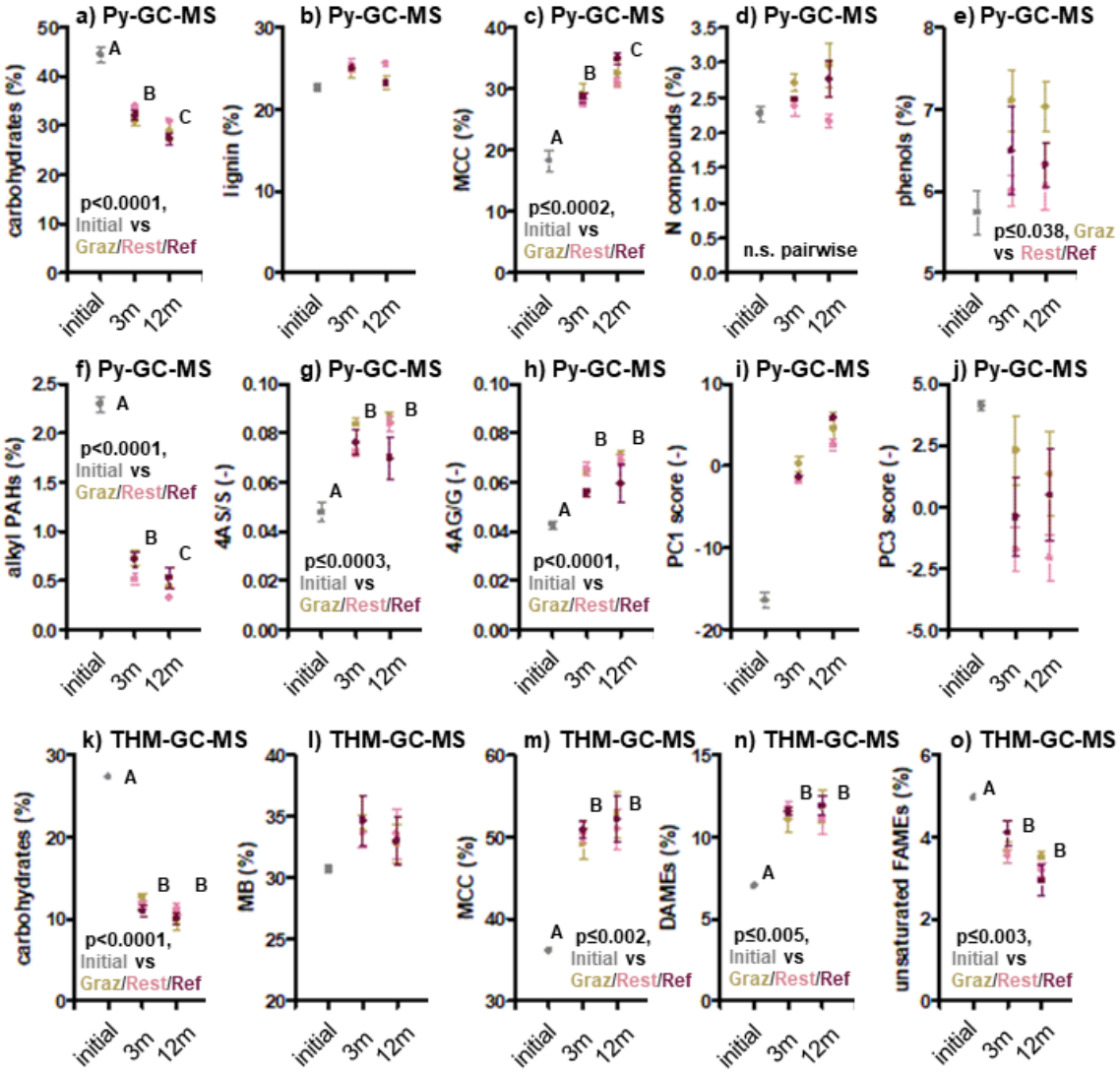

Figure S5: Molecular shifts of *Salicornia* roots with decay using Py-GC-MS and THM-GC-MS. (a-h) Molecular groups derived from pyrolysis gas chromatography mass spectrometry (Py-GC-MS). (i-j) Principal components 1 and 3 scores from Py-GC-MS molecular groups. (k-o) Molecular groups derived from thermally assisted hydrolysis and methylation gas chromatography mass spectrometry (THM-GC-MS). Decaying root materials were analysed for two sites in each rehabilitation category at initial, 3-month and 12-month time points. Capital letters indicate post hoc differences for significant shifts in a compound over time. Significant differences in rehabilitation categories are indicated as text in each panel. MCC = methylene chain compounds; PAH = polycyclic aromatic hydrocarbons; 4AS/S = syringyl-type lignin product; 4AG/G = guaiacyl- type lignin product; MB = methoxybenzenes; DAMEs = diacid methyl esters; FAMEs = fatty acid methyl esters. Values represent means and standard error.