

Table S1. Most common sessile taxa (lowest taxonomic group identified), defined as presence most frequently detected, by root treatment. Numbers indicate the percentage of roots in each treatment that had that taxon present.

Phylum	Taxa	Natural	Scraped	Cut	Wood	PVC
Chordata	<i>Eudistoma olivaceum</i>	100	85	100	63	79
	<i>Pyuridae</i>	38	15	0	16	63
	<i>Styela</i> sp.	81	38	0	37	79
	<i>Pyura</i> sp.	69	23	0	21	26
Arthropoda	<i>Amphibalanus</i> spp.	75	77	33	79	100
Mollusca	<i>Brachidontes exustus</i> complex	44	23	17	37	58
	<i>Isognomon alatus</i>	69	54	83	26	53
	<i>Crassostrea rhizophorae</i>	88	85	67	79	84
	<i>Pinctada imbricata</i>	81	69	33	58	89
	<i>Ostrea stentina</i>	88	92	67	84	100
	<i>Dendostrea frons</i>	63	62	0	32	58
Rhodophyta	Turf algae	50	31	50	47	74
Porifera	<i>Tedania ignis</i>	69	23	83	47	68
	<i>Haliclona piscaderaensis</i>	56	38	17	53	58
	<i>Haliclona manglaris</i>	81	62	50	42	84
	<i>Mycale microsigmatosa</i>	50	69	33	63	89

Table S2. Most frequently detected mobile morphospecies (lowest taxa group able to be identified) by root treatment. Numbers indicate the percentage of roots in each treatment that had that morphospecies present.

Phylum	Morphospecies	Natural	Scraped	Cut	Wood	PVC
Annelida	Nereididae	94	85	50	63	100
	Terrebelidae	75	23	0	26	47
Arthropoda	Amphipoda	100	69	33	84	100
	<i>Cuapetes americanus</i>	100	85	50	58	89
	<i>Cirolana</i> spp.	75	38	17	53	74
	<i>Paracerceis</i> spp.	88	85	67	53	89
	Majoidea	75	46	0	32	47
	<i>Synalpheus apioceros</i>	81	31	33	37	63
Echinodermata	Xanthoidea	44	23	17	47	53
	Ophiuroidea	75	69	33	58	84
Mollusca	<i>Littoraria angulifera</i>	63	31	50	47	47

Table S3. Analysis of deviance results of generalized linear models examining bivalve and sponge biomass and richness response to the main effects of root treatment, site, the interaction of root treatment and site and initial root length as a covariate. Significant p-values ($p < 0.05$) are in bold.

Response variable	Explanatory variables	Chisquare	Df	P value
Sponge biomass	Treatment	2.219	4	0.696
	Site	9.790	1	0.002
	Initial root length	1.192	1	0.275
	Treatment x Site	7.317	4	0.120
Sponge richness	Treatment	15.690	4	0.003
	Site	0.057	1	0.057
	Initial root length	0.413	1	0.413
	Treatment x Site	0.573	4	0.573
Bivalve biomass	Treatment	15.541	4	0.004
	Site	0.037	1	0.849
	Initial root length	0.372	1	0.542
	Treatment x Site	1.977	4	0.740
Bivalve richness	Treatment	11.004	4	0.027
	Site	1.166	1	0.280
	Initial root length	0.382	1	0.536
	Treatment x Site	3.558	4	0.469

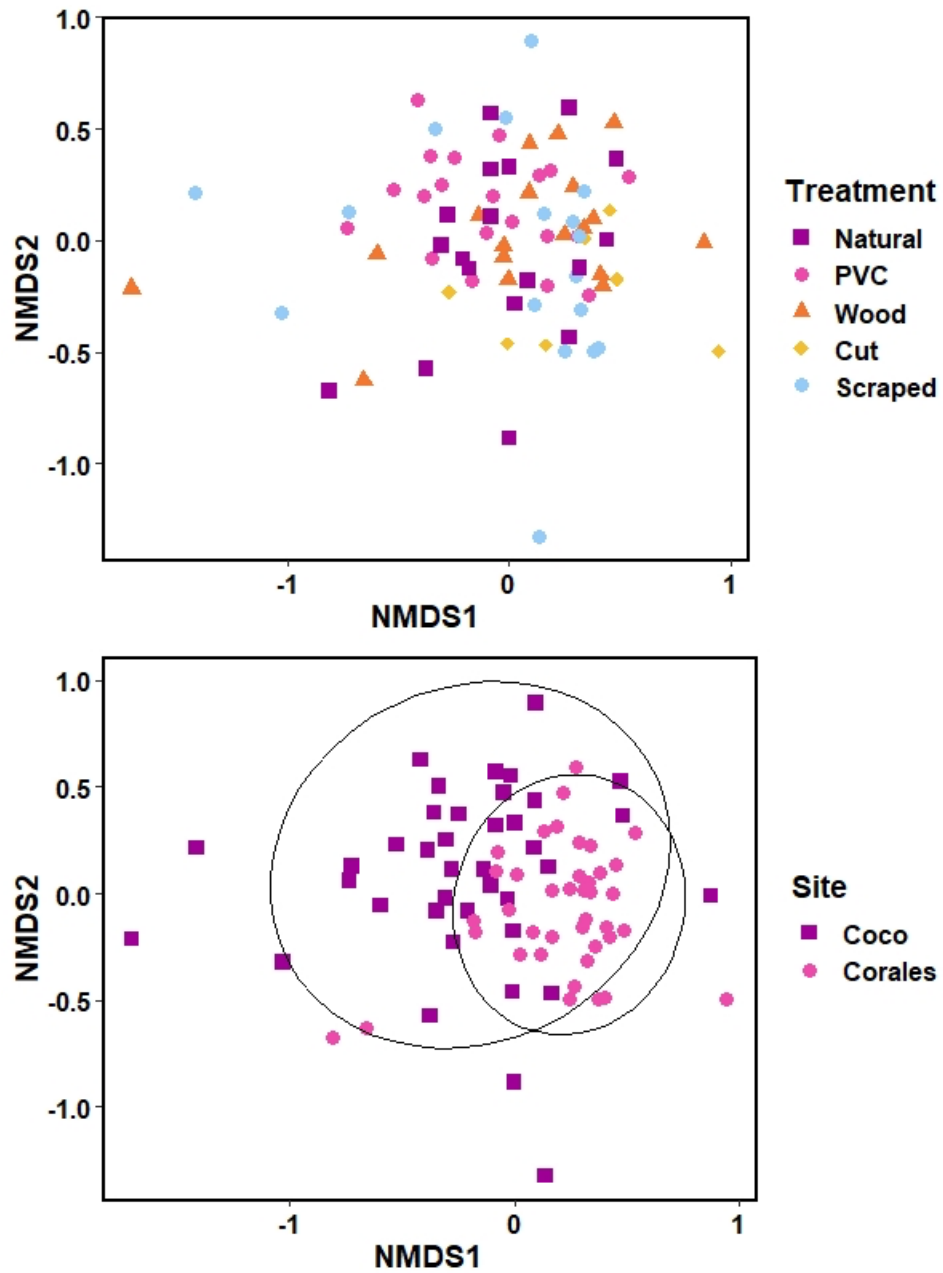


Figure S1. Non-metric Multi-dimensional Scaling (nMDS) plots of *in situ* percent cover community composition grouping by treatment and site.

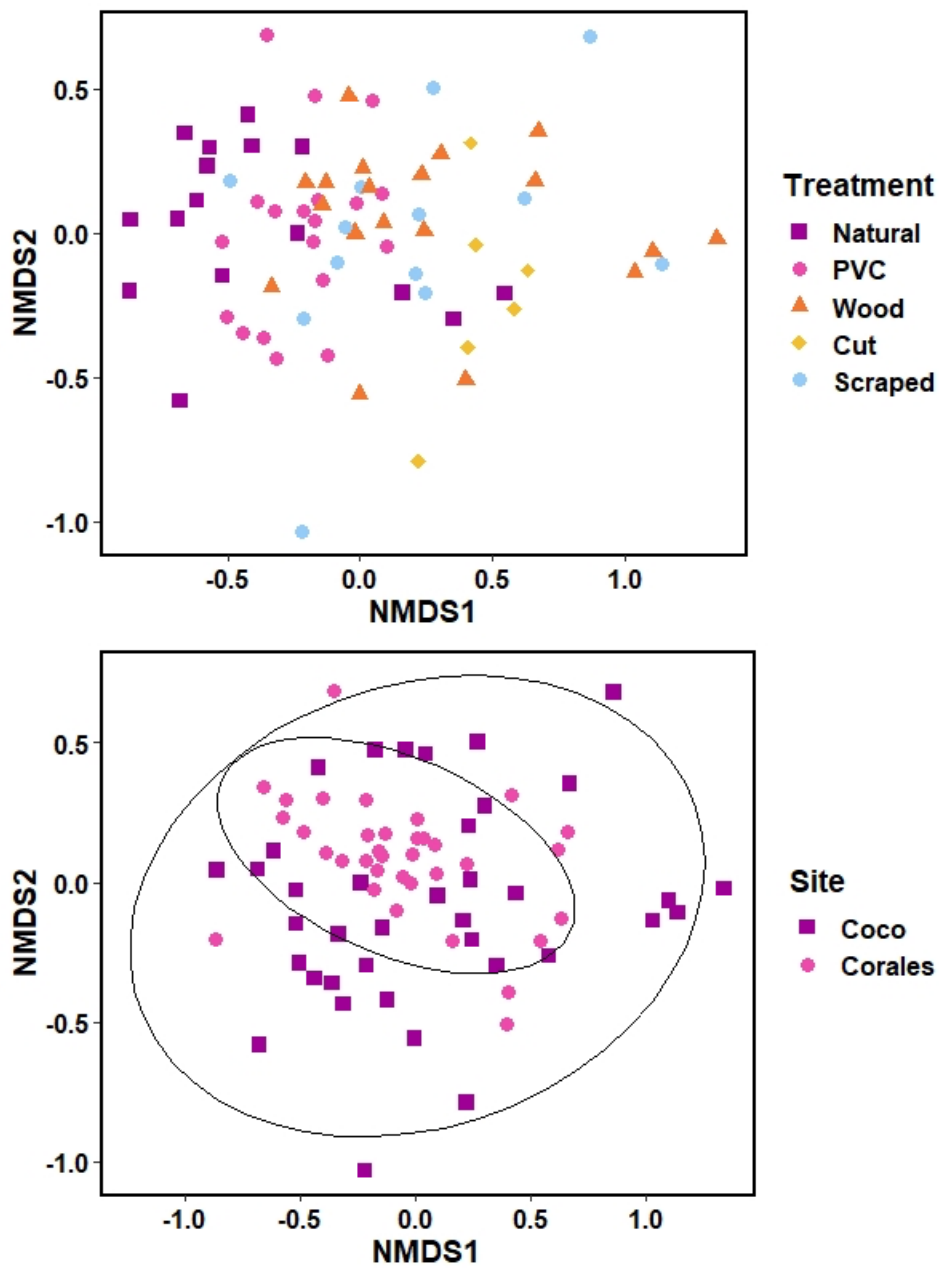


Figure S2. Non-metric Multi-dimensional Scaling (nMDS) plots of sessile community composition by biomass grouping by treatment and site.

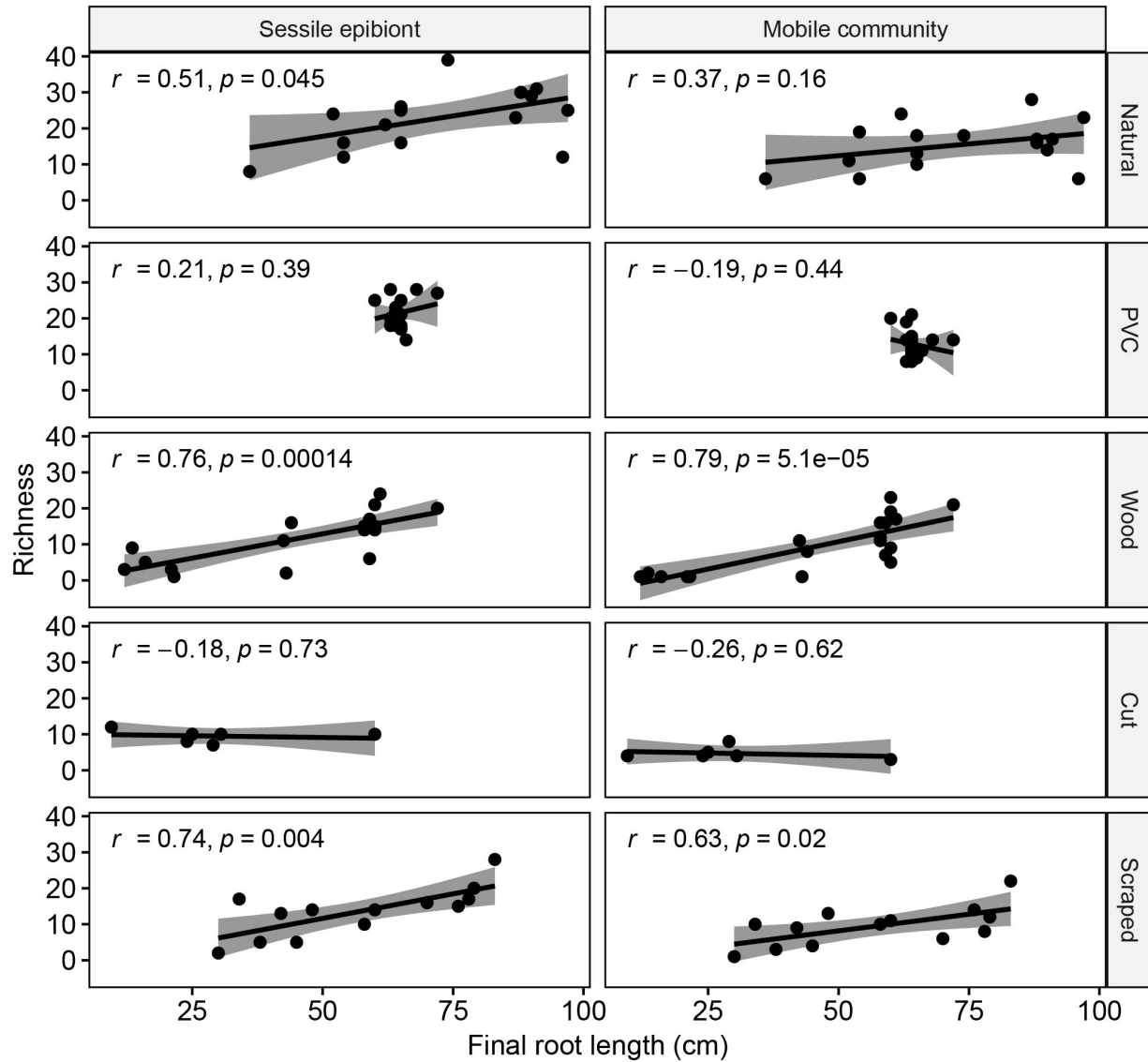


Figure S3. Linear regression plots with 95% confidence interval for sessile epibiont and mobile community species richness within each root treatment and correlation with final root length. r = Pearson's correlation coefficient.

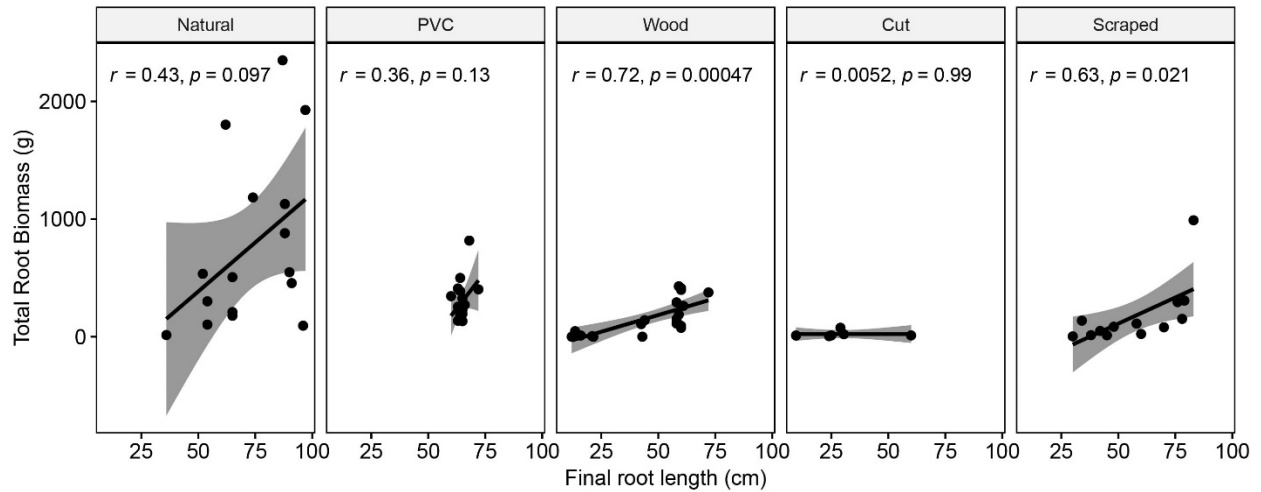


Figure S4. Linear regression plots with 95% confidence interval for total epibiont biomass within each root treatment and correlation with final root length. r = Pearson's correlation coefficient.

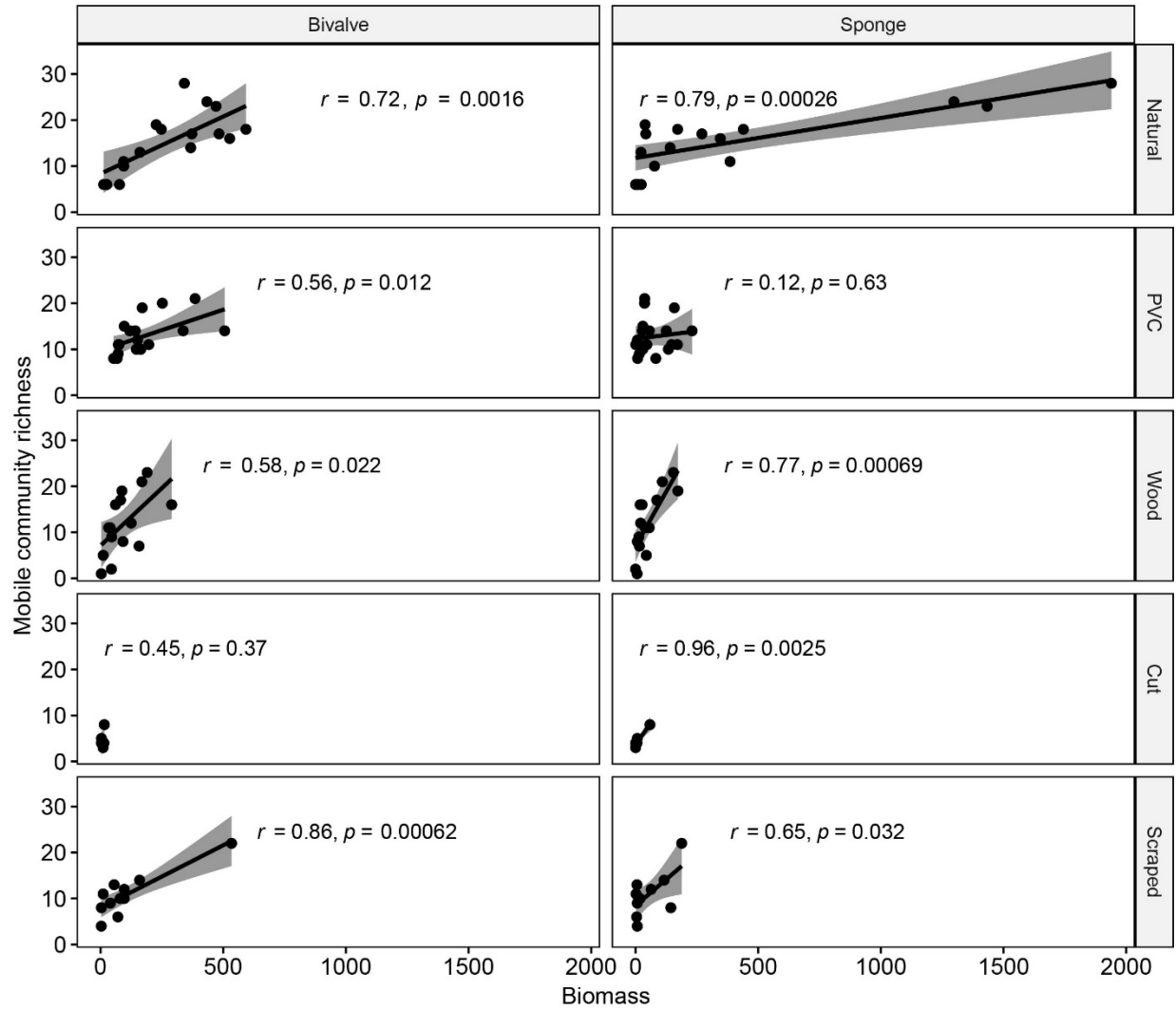


Figure S5. Linear regression plots with 95% confidence interval for mobile community richness within each root treatment and correlation with sponge and bivalve biomass. r = Pearson's correlation coefficient.