

**Supporting Information**

Table S1. Outcome of PERMANOVA pairwise comparisons of the microbial community structure (square-root transformed relative abundances) and composition (presence/absence) for Condition (healthy *vs* bleached) at each site within three regions in each biogeographic province (BP).

			Closed-reference				Open-reference			
			Square-root		P/A		Square-root		P/A	
Significant pairwise comparisons			89 %		77 %		92 %		96 %	
BP	Region	Site	<i>t</i> <sub>1,8</sub>	<i>P</i>						
NSW	Crowdy	Me	2.9	<b>0.009</b>	1.5	<b>0.016</b>	3.2	<b>0.007</b>	2.5	<b>0.008</b>
		Di	3.6	<b>0.008</b>	2.4	<b>0.009</b>	3.6	<b>0.008</b>	3.8	<b>0.006</b>
		Cr	1.7	<b>0.009</b>	1.5	<b>0.015</b>	1.5	<b>0.007</b>	1.5	<b>0.009</b>
	Sydney	CB	2.3	<b>0.007</b>	1.3	<b>0.008</b>	2.7	<b>0.010</b>	2.2	<b>0.007</b>
		Ku	3.1	<b>0.008</b>	1.7	<b>0.015</b>	2.8	<b>0.008</b>	2.5	<b>0.008</b>
		LB	1.6	<b>0.023</b>	1.0	0.204	1.4	<b>0.031</b>	1.2	<b>0.034</b>
	Batemans	To	4.1	<b>0.008</b>	1.8	<b>0.008</b>	3.8	<b>0.009</b>	3.1	<b>0.008</b>
		Pr	3.0	<b>0.008</b>	1.8	<b>0.016</b>	2.6	<b>0.008</b>	2.2	<b>0.008</b>
		Mo	2.2	<b>0.009</b>	1.4	<b>0.025</b>	2.1	<b>0.009</b>	2.1	<b>0.008</b>
TAS	Bicheno	B7	1.8	<b>0.009</b>	1.3	<b>0.018</b>	2.3	<b>0.008</b>	2.1	<b>0.007</b>
		B8	6.0	<b>0.009</b>	4.6	<b>0.008</b>	3.6	<b>0.009</b>	3.0	<b>0.008</b>
		B9	4.3	<b>0.008</b>	1.7	<b>0.008</b>	3.5	<b>0.007</b>	2.7	<b>0.008</b>
	Fortescue	F4	3.2	<b>0.008</b>	1.7	<b>0.008</b>	3.0	<b>0.008</b>	2.5	<b>0.009</b>
		F5	2.8	<b>0.009</b>	1.1	0.147	2.5	<b>0.009</b>	2.1	<b>0.008</b>
		F6	1.5	<b>0.025</b>	1.0	0.48	1.6	<b>0.009</b>	1.3	<b>0.042</b>
	Southport	S1	1.2	0.148	1.1	0.244	1.4	0.072	1.3	<b>0.046</b>
		S2	2.7	<b>0.008</b>	1.3	<b>0.008</b>	2.7	<b>0.008</b>	2.1	<b>0.009</b>
		S3	2.5	<b>0.008</b>	1.3	<b>0.015</b>	2.3	<b>0.009</b>	1.7	<b>0.006</b>
WA	Jurien	J1	1.8	<b>0.007</b>	1.5	<b>0.008</b>	1.8	<b>0.007</b>	1.7	<b>0.009</b>
		J2	2.4	<b>0.008</b>	1.3	<b>0.015</b>	2.2	<b>0.007</b>	1.8	<b>0.008</b>
	Marmion	M1	2.3	<b>0.009</b>	1.5	<b>0.009</b>	2.2	<b>0.010</b>	2.0	<b>0.008</b>
		M2	2.8	<b>0.006</b>	1.4	<b>0.007</b>	2.3	<b>0.010</b>	2.0	<b>0.009</b>
		M3	3.4	<b>0.009</b>	2.0	<b>0.009</b>	2.9	<b>0.008</b>	2.4	<b>0.008</b>
	Hamelin	H1	1.5	0.065	1.2	0.063	1.6	<b>0.019</b>	1.4	<b>0.048</b>
		H2	1.1	0.264	1.0	0.295	1.2	0.193	1.2	0.163
		H3	2.7	<b>0.008</b>	1.7	<b>0.008</b>	2.3	<b>0.007</b>	1.9	<b>0.008</b>

Table S2. Estimates of components of variation (square-root) of all terms in the PERMANOVA model for microbial community structure (square-root transformed relative abundances) and composition (presence/absence) obtained through the closed- and open-reference protocols. Random effects in *italics*.

Terms	Closed-reference		Open-reference	
	Square-root	P/A	Square-root	P/A
Condition	16.26	6.82	19.81	19.81
Biogeographic				
province	9.11	6.04	13.92	13.92
Region	5.20	3.46	7.28	7.28
Co x BP	8.66	4.73	12.58	12.58
Co x Re	4.33	1.60	6.55	6.55
BP x Re	10.93	8.99	13.74	13.74
<i>Site(BP x Re)</i>	<i>11.84</i>	<i>8.99</i>	<i>14.05</i>	<i>14.05</i>
Co x BP x Re	4.07	3.09	7.95	7.95
<i>Co x Si(BP x Re)</i>	<i>11.72</i>	<i>8.24</i>	<i>16.41</i>	<i>16.41</i>
<i>Residual</i>	<i>21.39</i>	<i>22.06</i>	<i>30.87</i>	<i>30.87</i>

Table S3. DISTLM analyses of the relationships between microbial community structure (square-root transformed relative abundances) and composition (presence/absence) for (a) closed-reference or (b) open-reference OTUs on healthy or bleached kelp and all environmental variables independently or in combinations (Best) at all sites across Australia.\*

	Healthy (square-root)			Bleached (square-root)			Healthy (P/A)			Bleached (P/A)		
<b>a) Closed-reference</b>												
Variables	pseudo- $F_{1,24}$	$P$	$R^2$	pseudo- $F_{1,24}$	$P$	$R^2$	pseudo- $F_{1,24}$	$P$	$R^2$	pseudo- $F_{1,24}$	$P$	$R^2$
NH <sub>3</sub>	1.10	0.35	0.04	0.75	0.67	0.03	1.73	0.10	0.07	1.11	0.28	0.04
NO <sub>x</sub>	1.13	0.32	0.04	1.26	0.22	0.05	1.10	0.33	0.04	1.19	0.28	0.05
PO <sub>4</sub>	1.74	0.09	0.07	1.70	0.08	0.07	2.72	<b>0.02</b>	0.10	3.28	<b>0.00</b>	0.12
T	3.01	<b>0.00</b>	0.11	2.66	<b>0.00</b>	0.10	1.98	0.05	0.08	1.45	0.14	0.06
L	3.18	<b>0.00</b>	0.12	2.62	<b>0.00</b>	0.10	1.91	0.07	0.07	1.32	0.20	0.05
W	2.57	<b>0.01</b>	0.10	1.12	0.32	0.04	1.84	0.07	0.07	0.93	0.43	0.04
W <sub>m</sub>	1.49	0.16	0.06	1.21	0.27	0.05	1.21	0.26	0.05	1.24	0.26	0.05
	Best	AIC	$R^2$	Best	AIC	$R^2$	Best	AIC	$R^2$	Best	AIC	$R^2$
	<b>L, W, W<sub>m</sub></b>	162.94	0.27	<b>T</b>	154.84	0.10	<b>PO<sub>4</sub>, T, W</b>	151.05	0.24	<b>PO<sub>4</sub></b>	138.93	0.12
<b>b) Open-reference</b>												
Variables	pseudo- $F_{1,24}$	$P$	$R^2$	pseudo- $F_{1,24}$	$P$	$R^2$	pseudo- $F_{1,24}$	$P$	$R^2$	pseudo- $F_{1,24}$	$P$	$R^2$
NH <sub>3</sub>	0.80	0.63	0.03	0.98	0.46	0.04	0.73	0.67	0.03	1.06	0.37	0.04
NO <sub>x</sub>	1.89	<b>0.04</b>	0.07	1.64	0.05	0.06	1.64	0.11	0.06	1.61	0.08	0.06
PO <sub>4</sub>	1.11	0.33	0.04	1.29	0.18	0.05	1.13	0.30	0.04	1.45	0.13	0.06
T	4.84	<b>0.00</b>	0.17	3.51	<b>0.00</b>	0.13	3.63	<b>0.00</b>	0.13	3.66	<b>0.00</b>	0.13
L	4.39	<b>0.00</b>	0.15	3.24	<b>0.00</b>	0.12	3.56	<b>0.00</b>	0.13	3.40	<b>0.00</b>	0.12
W	3.71	<b>0.00</b>	0.13	1.37	0.14	0.05	4.52	<b>0.00</b>	0.16	1.30	0.19	0.05
W <sub>m</sub>	1.81	0.05	0.07	1.36	0.15	0.05	1.59	0.11	0.06	1.33	0.18	0.05
	Best	AIC	$R^2$	Best	AIC	$R^2$	Best	AIC	$R^2$	Best	AIC	$R^2$
	<b>T, W, W<sub>m</sub></b>	175.28	0.33	<b>T</b>	171.94	0.13	<b>T, W, W<sub>m</sub></b>	161.84	0.33	<b>T</b>	152.44	0.13

\* Sequential tests were done using the AIC selection criterion and a Best procedure. T<sub>m</sub> and Latitude (correlated with T;  $r=0.99$ ,  $r=-0.96$ , respectively) and L<sub>m</sub> (correlated with L,  $r=0.91$ ) were excluded from the analyses. All tests were done using 9,999 permutations of the raw data. T, temperature; L, light; W, wave motion. Resemblance measure for community data: distances among centroids based on Bray-Curtis matrices.

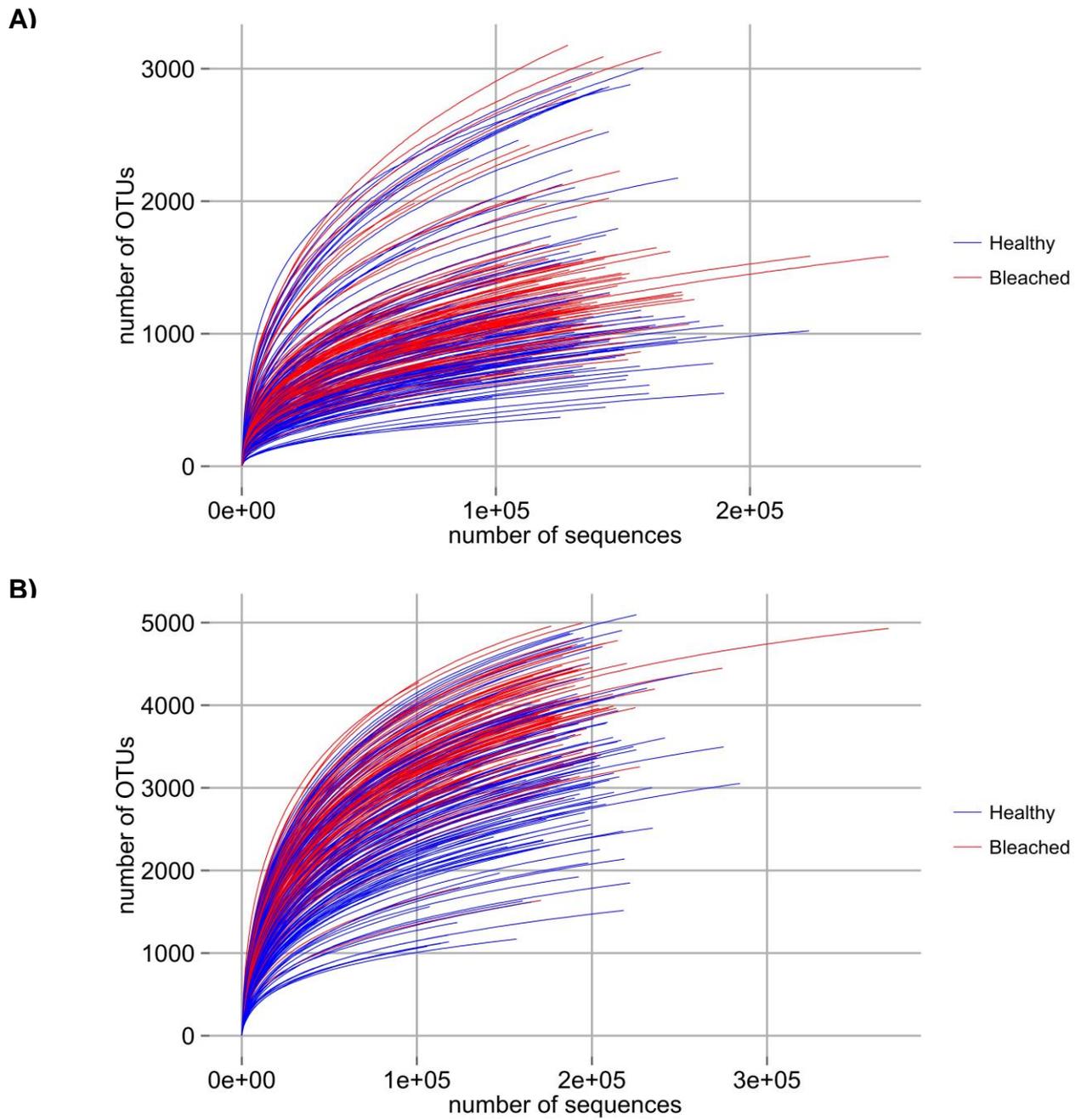


Fig. S1. Rarefaction curves for healthy (blue lines) and bleached kelp samples (red lines) for the (A) closed- and (B) open-reference protocols.

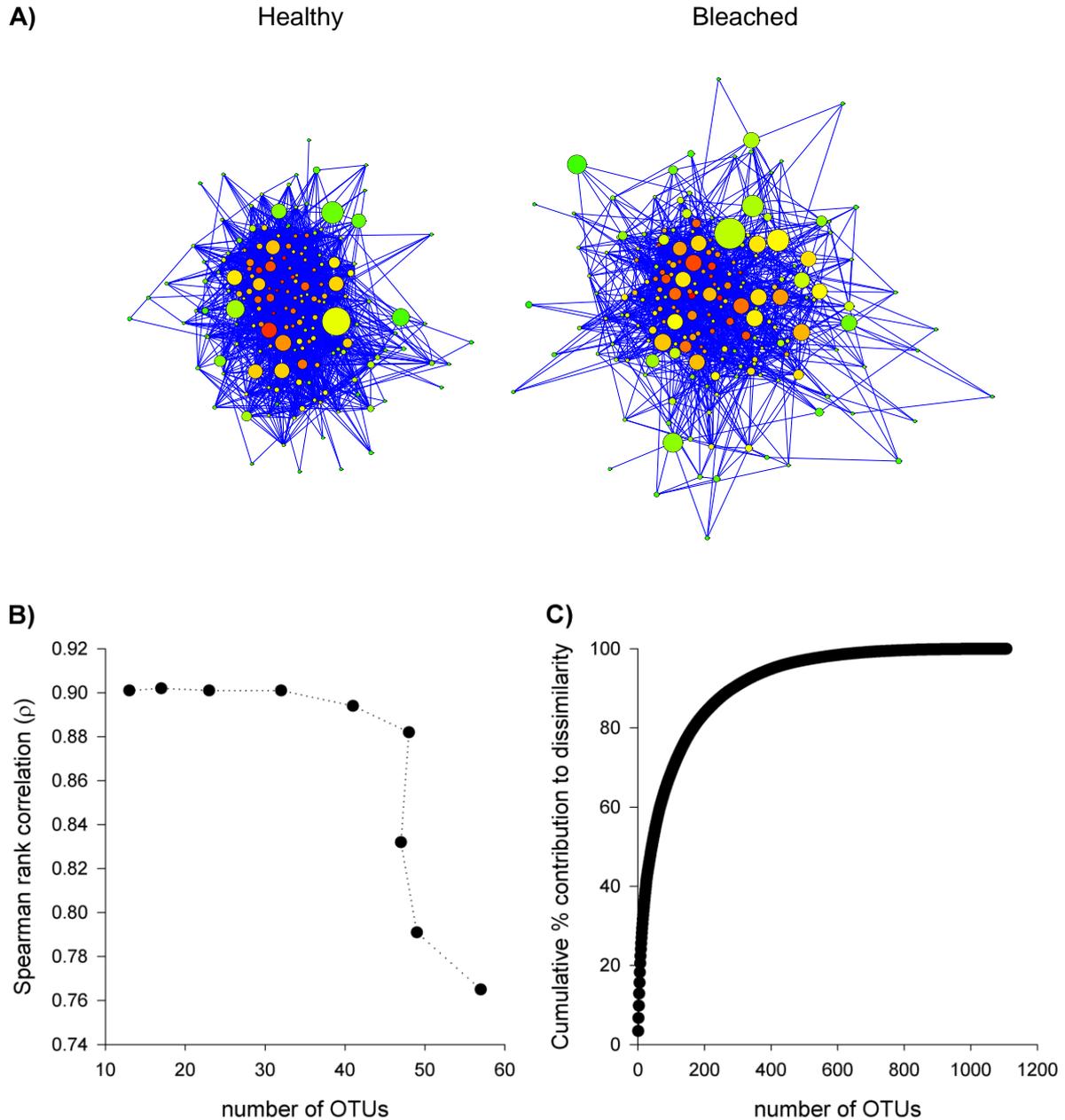


Fig. S2. Connectedness and structural redundancy in surface-associated bacterial communities on kelp. A) Networks of communities on healthy or bleached kelp, generated by uniting 3 replicate networks of each condition in each biogeographic province (see *Methods*). Nodes (OTUs) were coloured by the local clustering coefficient (ranging from green=less connected to red=highly connected) and sized by their average relative abundance. B) Relationship between the smallest subsets of OTUs obtained using the BVSTEP analyses and their corresponding Spearman rank correlation values for correlations between similarity matrices using these OTU subsets and the total OTU similarity matrix (see *Methods*). C) Relationship between the cumulative % contribution to the dissimilarity between healthy and bleached hosts and the number of OTUs obtained through the closed-reference protocol (SIMPER analysis on Bray-Curtis resemblance matrix of square-root transformed relative abundances; see *Methods*).

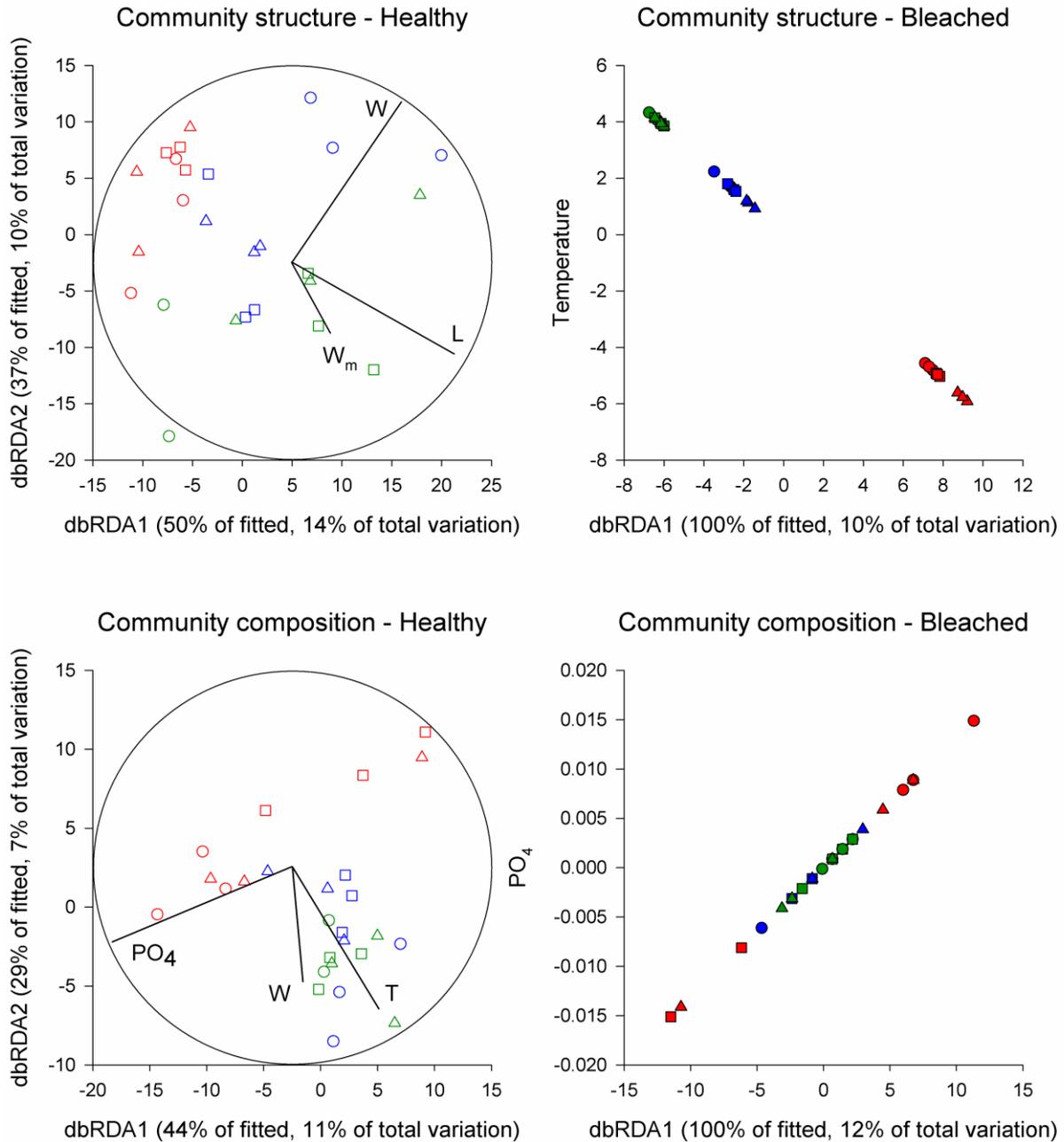


Fig. S3. Distance-based Redundancy Analyses of microbial community structure (square-root transformed relative abundances) and composition (presence/absence) on healthy or bleached kelp, independently, as explained by a subset of environmental variables selected from distance-based linear modelling (DISTLM analyses, Table S8; see *Methods*). Environmental variables: L (light intensity), W (wave motion), T (temperature). Vectors are multiple partial correlations. Direction of vectors coincides with direction of relationships; vector length indicates relationship strength, with the circle representing a correlation value of 1. Ordinations are based on distances among centroids for each site based on Bray-Curtis similarity measures of OTUs on healthy (empty symbols) or bleached (filled symbols) hosts at the three regions (North: circles, Centre: squares, South: triangles) sampled in each state (NSW: blue, TAS: red, WA: green) along the east and west coast of Australia (Table S1). OTUs were obtained through a closed-reference protocol (see *Methods*).

