Supplementary Materials for

Rapid evolution in action: environmental filtering supports coral adaptation to a hot, acidic and deoxygenated extreme habitat

Carlos Leiva *et al.*

*Corresponding author. Email: cleivama@gmail.com

This PDF file includes:

Figs. S1 to S13
Captions for Table S1, S2 and S3

Other Supplementary Materials for this manuscript include the following:

Table S1, S2 and S3

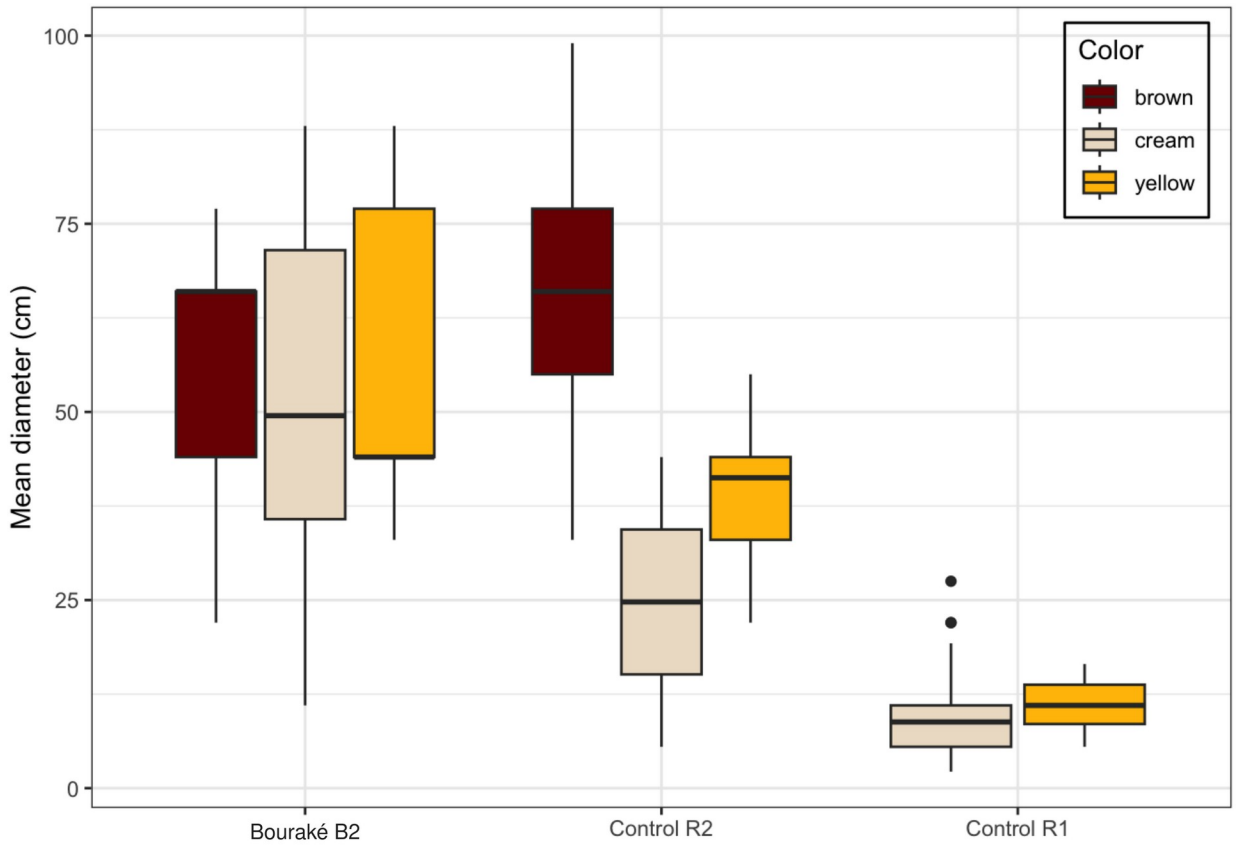

Fig. S1

Size distribution and color morph of *Acropora tenuis* colonies at three study sites.

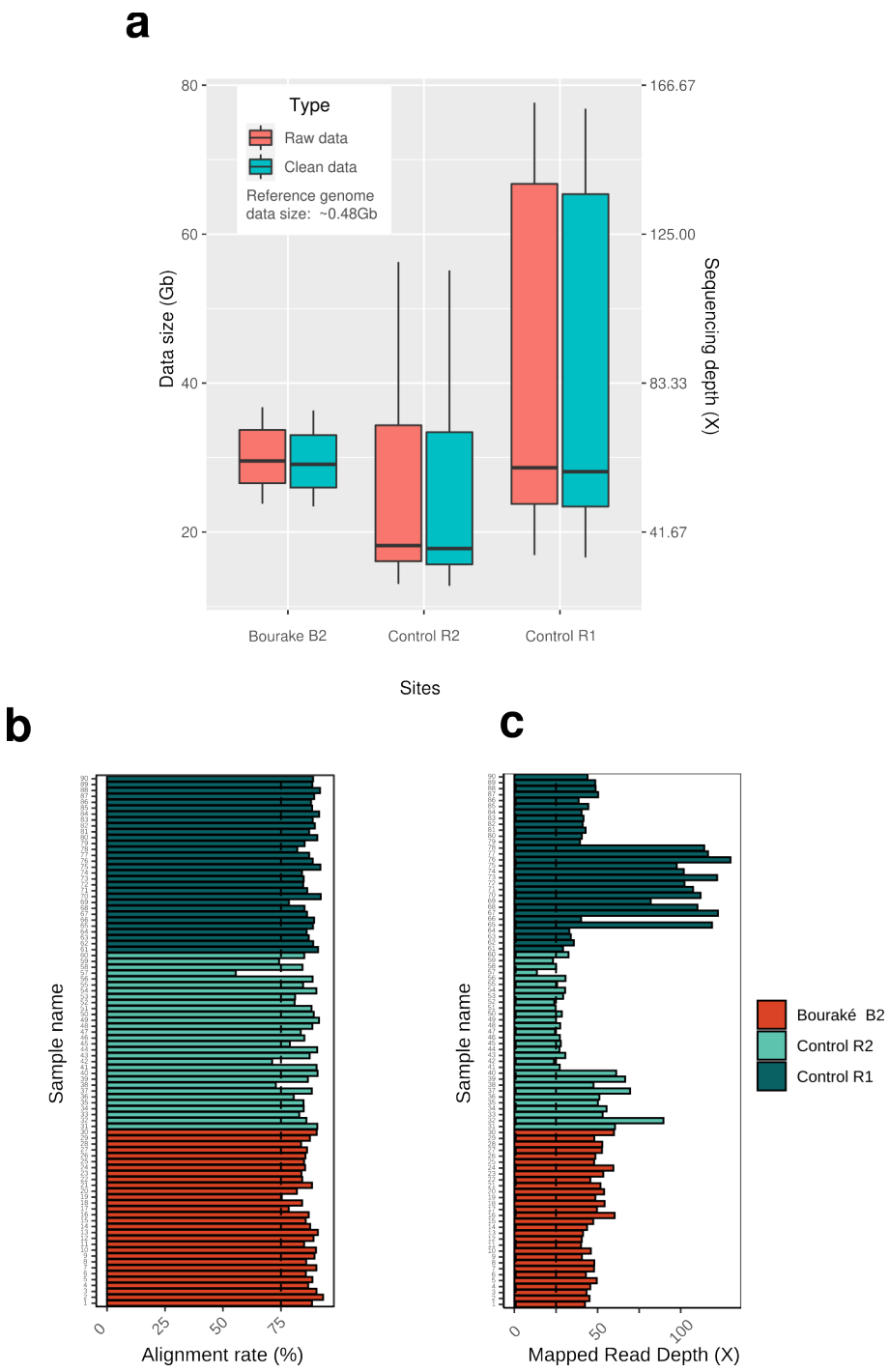

Fig. S2

a) Sequencing data size and sequencing depth for Acropora tenuis samples in this study. Boxplots show the median with hinges at the 25th and 75th percentile and whiskers extending 1.5 times the interquartile range. **b**) Alignment rate per sample. **c**) Read depth per sample.

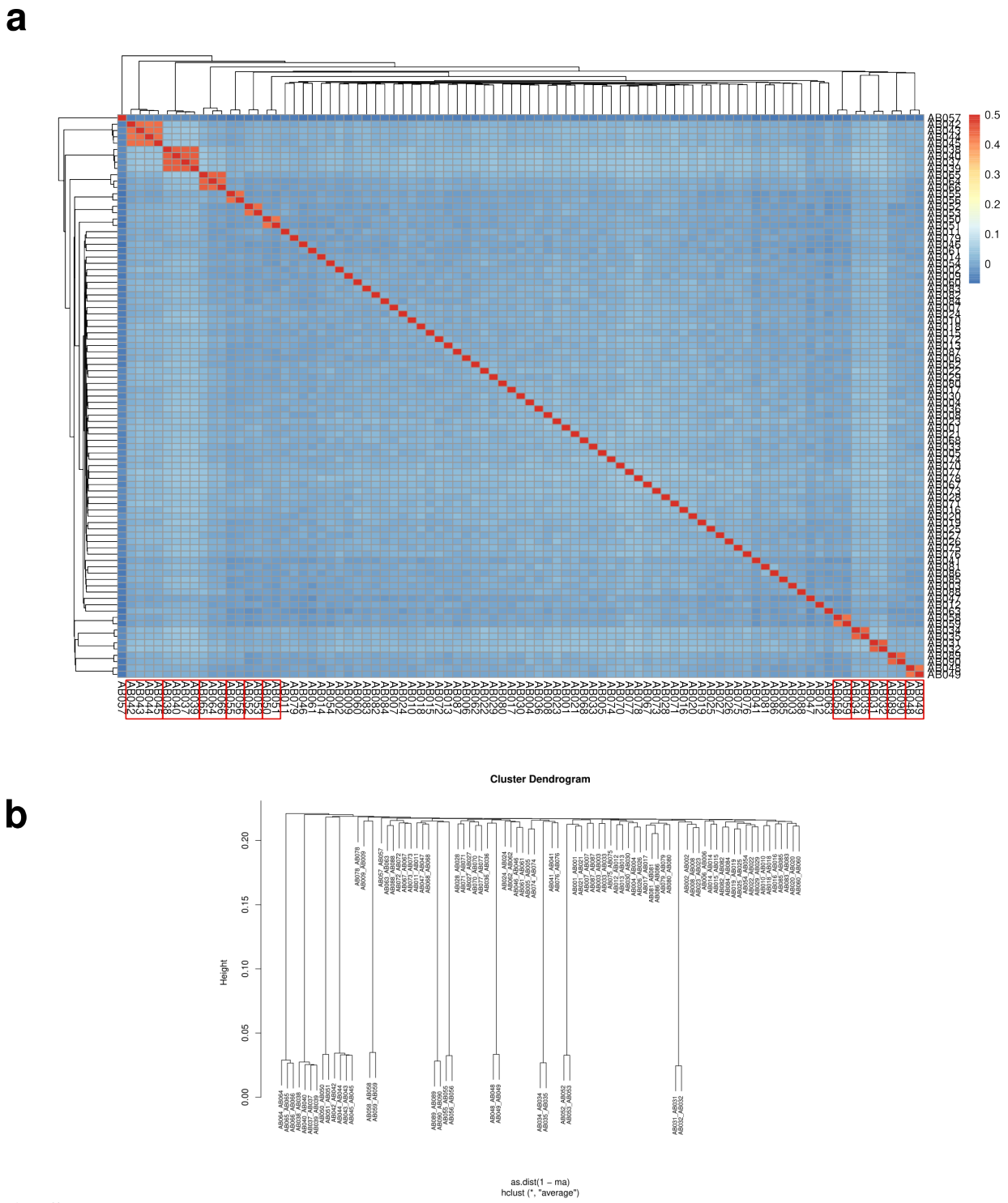

Fig. S3

Clone detection and symbiont profiles. a) Heatmap of the relatedness values among samples, obtained using VCFtools relatedness2 and plotted with ggplot2, showing the presence of 10 clone clusters (red squares). **b**) Identity-by-state (IBS) dendrogram calculated with SNPRelate, supporting the presence of 10 clone clusters due to their significantly low dissimilarity.

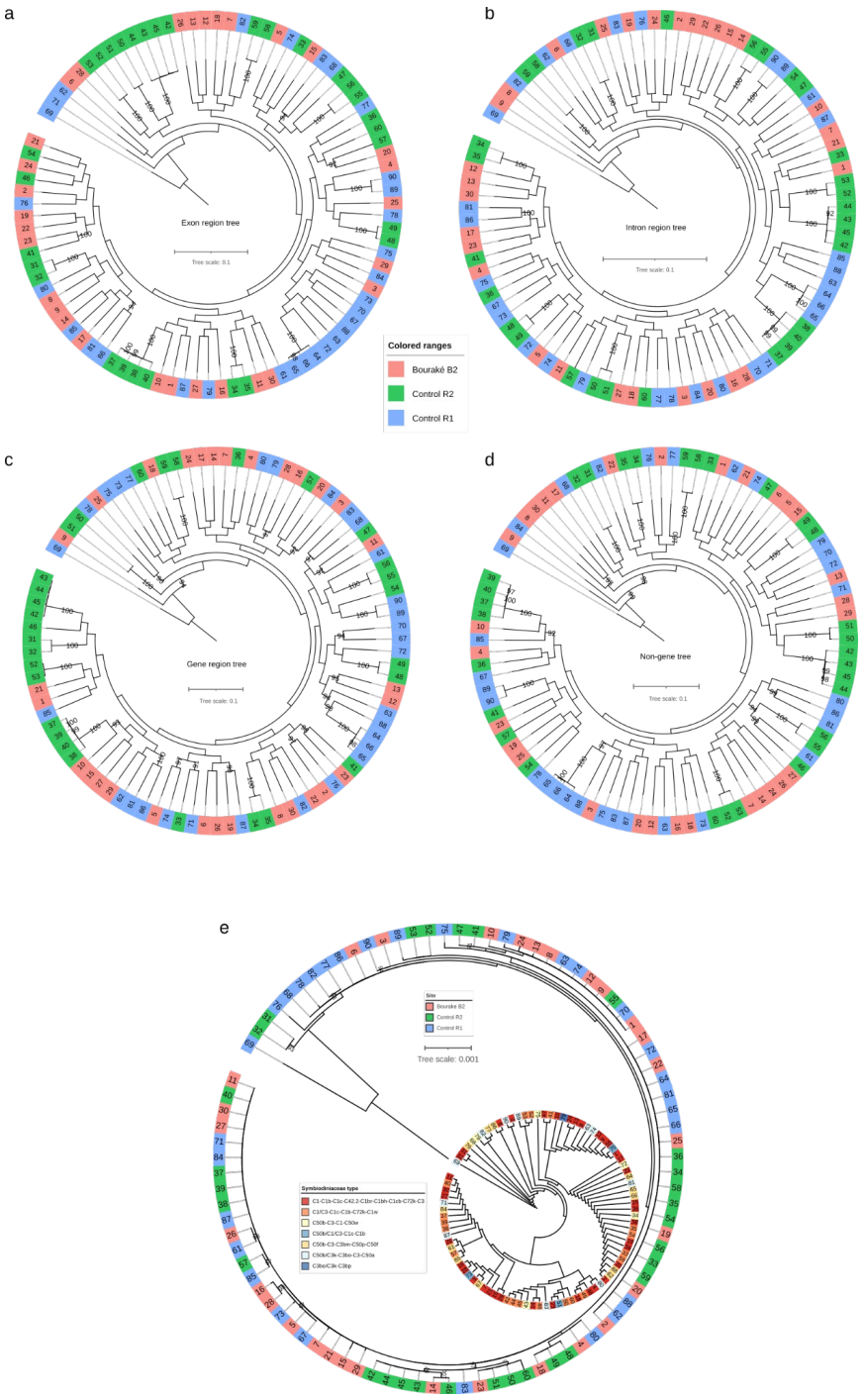

Fig. S4

Phylogenetic trees based on nuclear (a–d) and mitochondrial (e) SNPs inferred using IQtree. **a**) Exon region tree. **b**) Intron region tree. **c**) Gene region tree. **d**) Non-gene region tree. **e**) Mitochondrial phylogenetic trees, both showing the same tree, but the inner is colored by dominant symbiont type and the outer is colored by sampling site. All trees were rooted by the midpoint.

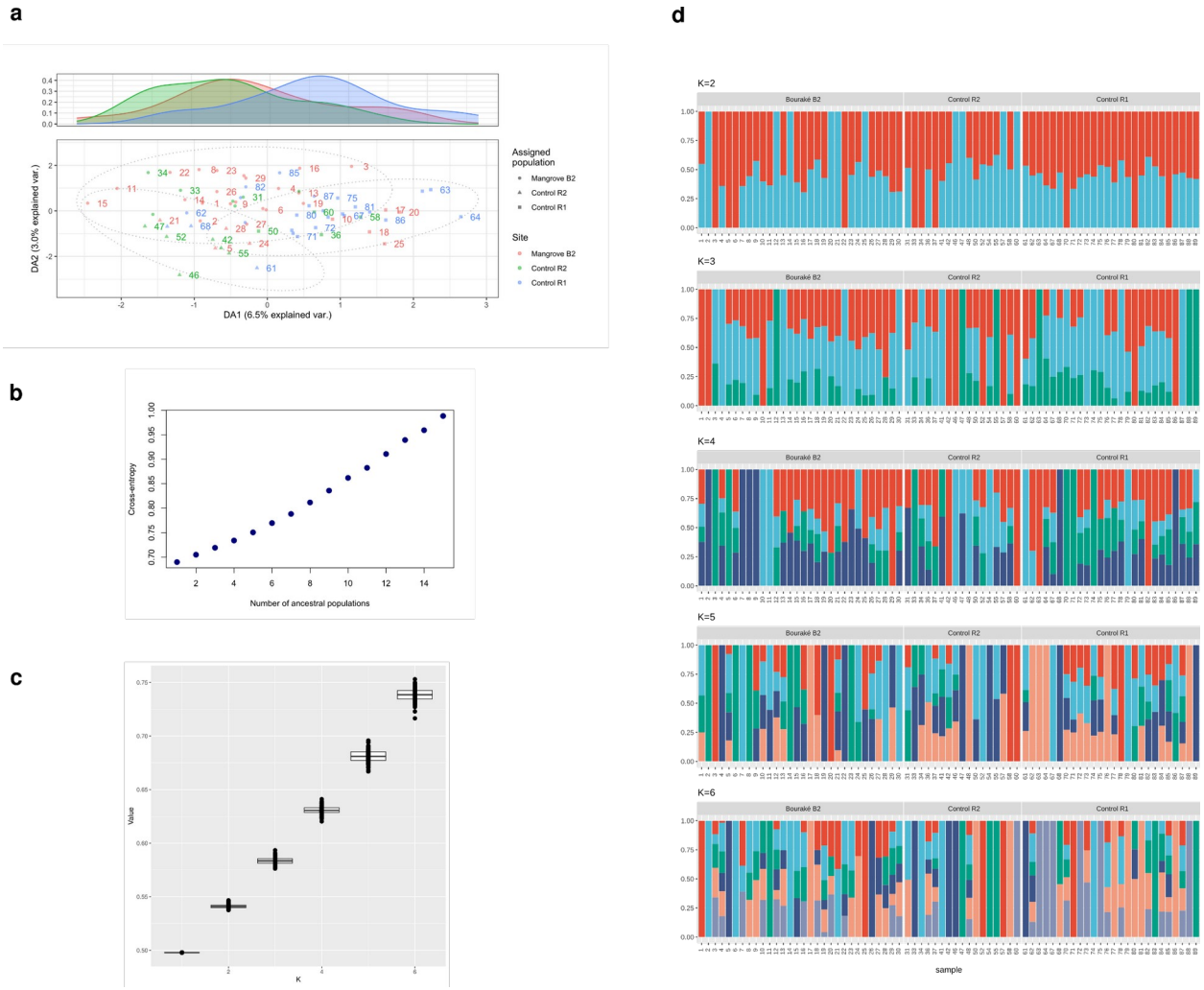

Fig. S5

Additional population genetic structure analyses. a) DAPC results grouping samples by sampling site. **b**) Cross-entropy of the different K values for the "snmf" analysis in LEA. **c**) Cross validation errors of the different K values for the ADMIXTURE analysis. **d**) ADMIXTURE results for K2–K6. All analyses support the lack of genome-wide population genetic structure in our samples.

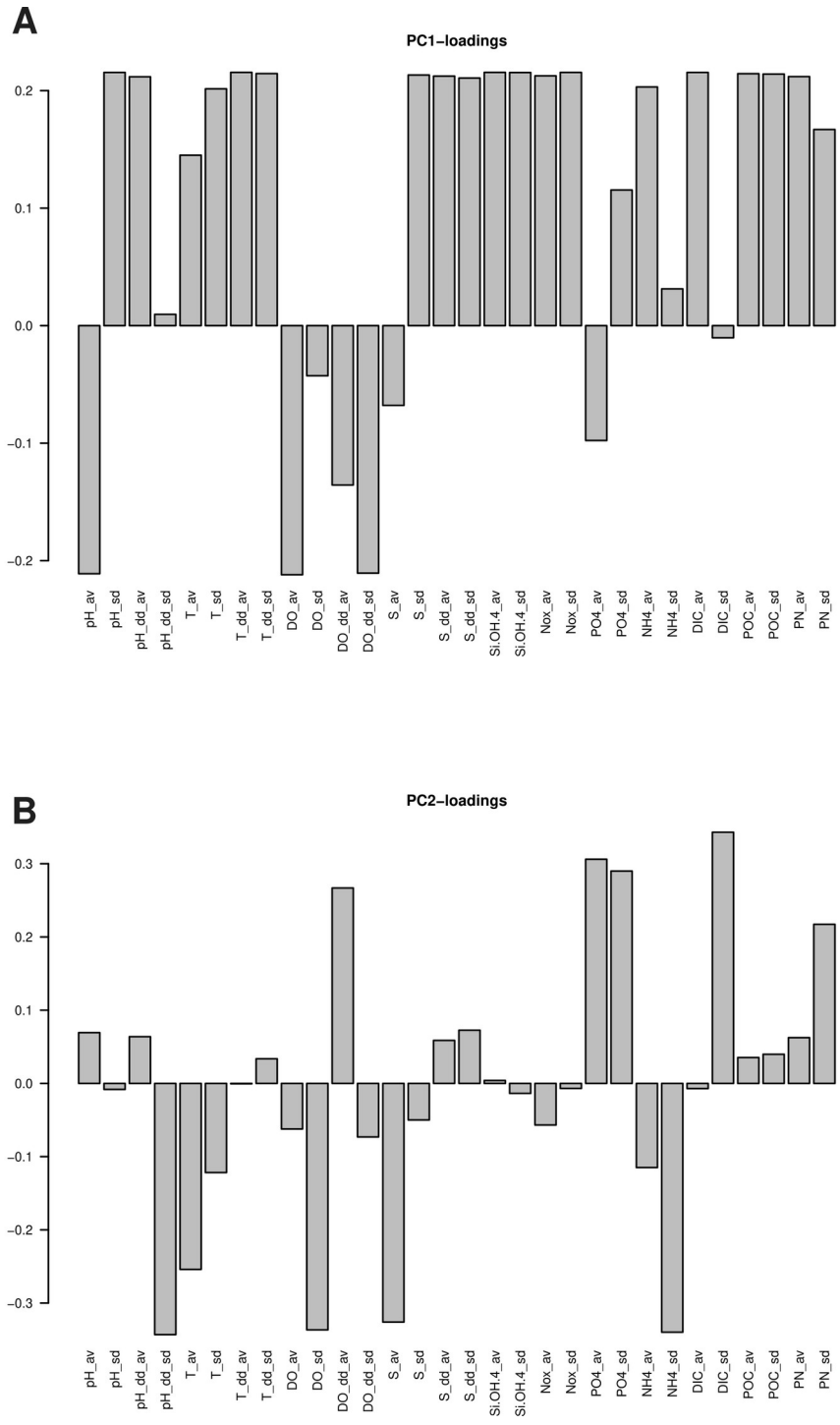

Fig. S6

PC loadings for ePC1 (A) and ePC2 (B)

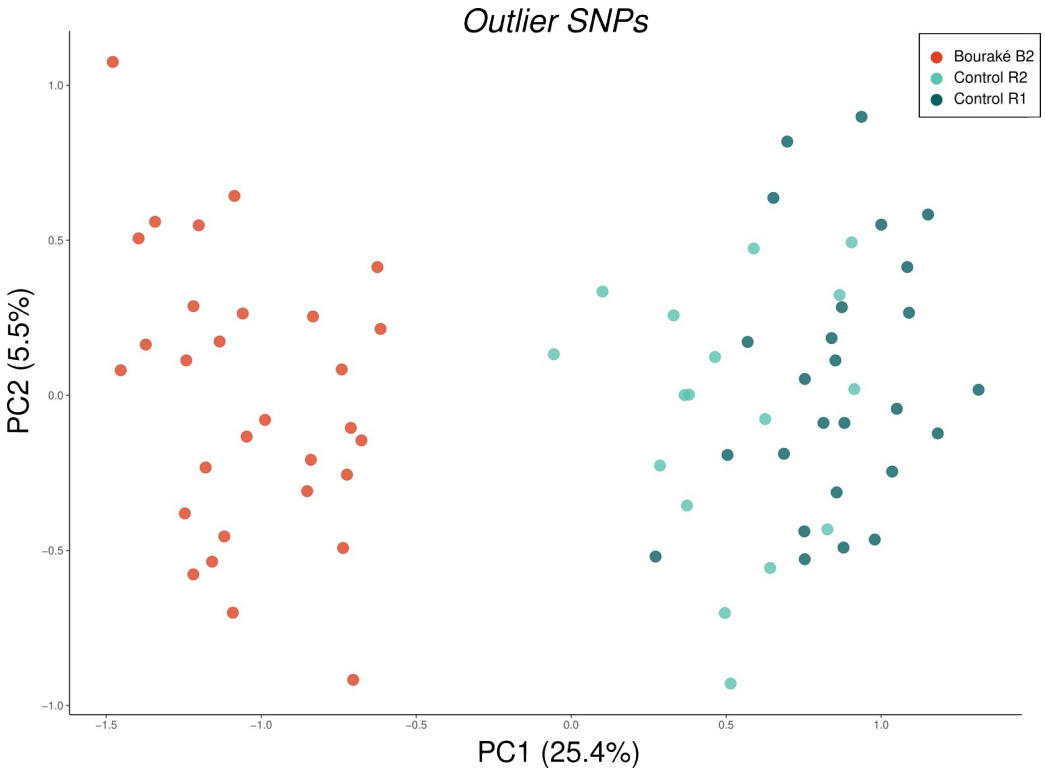

Fig. S7
PCA results using the 89 outlier SNPs associated with the environmental variables.

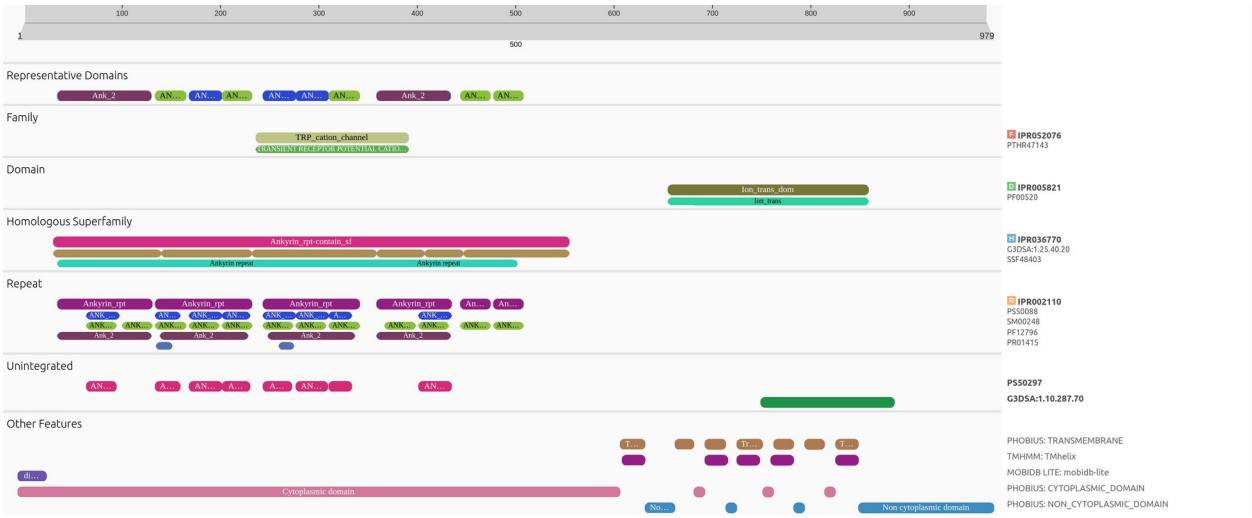

Fig. S8

InterProScan functional results for TRPA1.

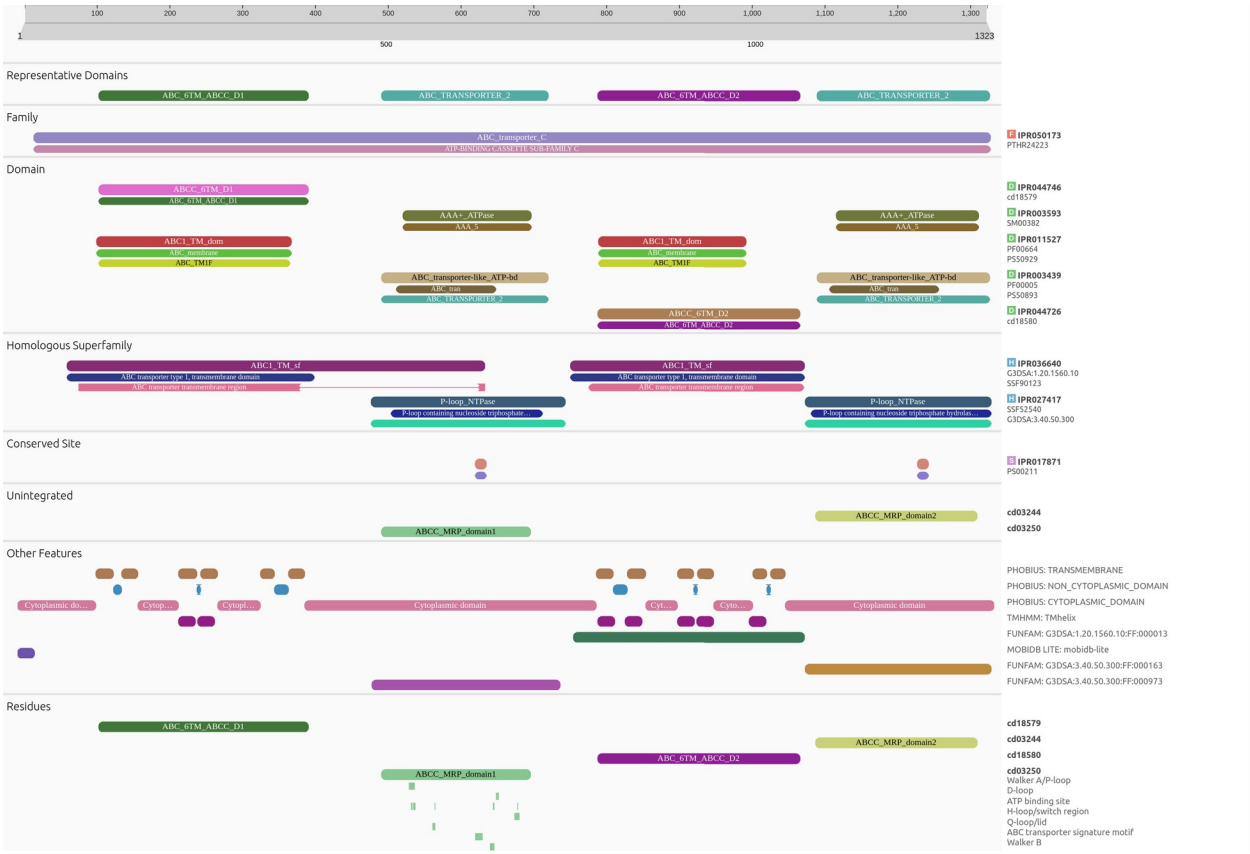

Fig. S9

InterProScan functional results for ABCC4.

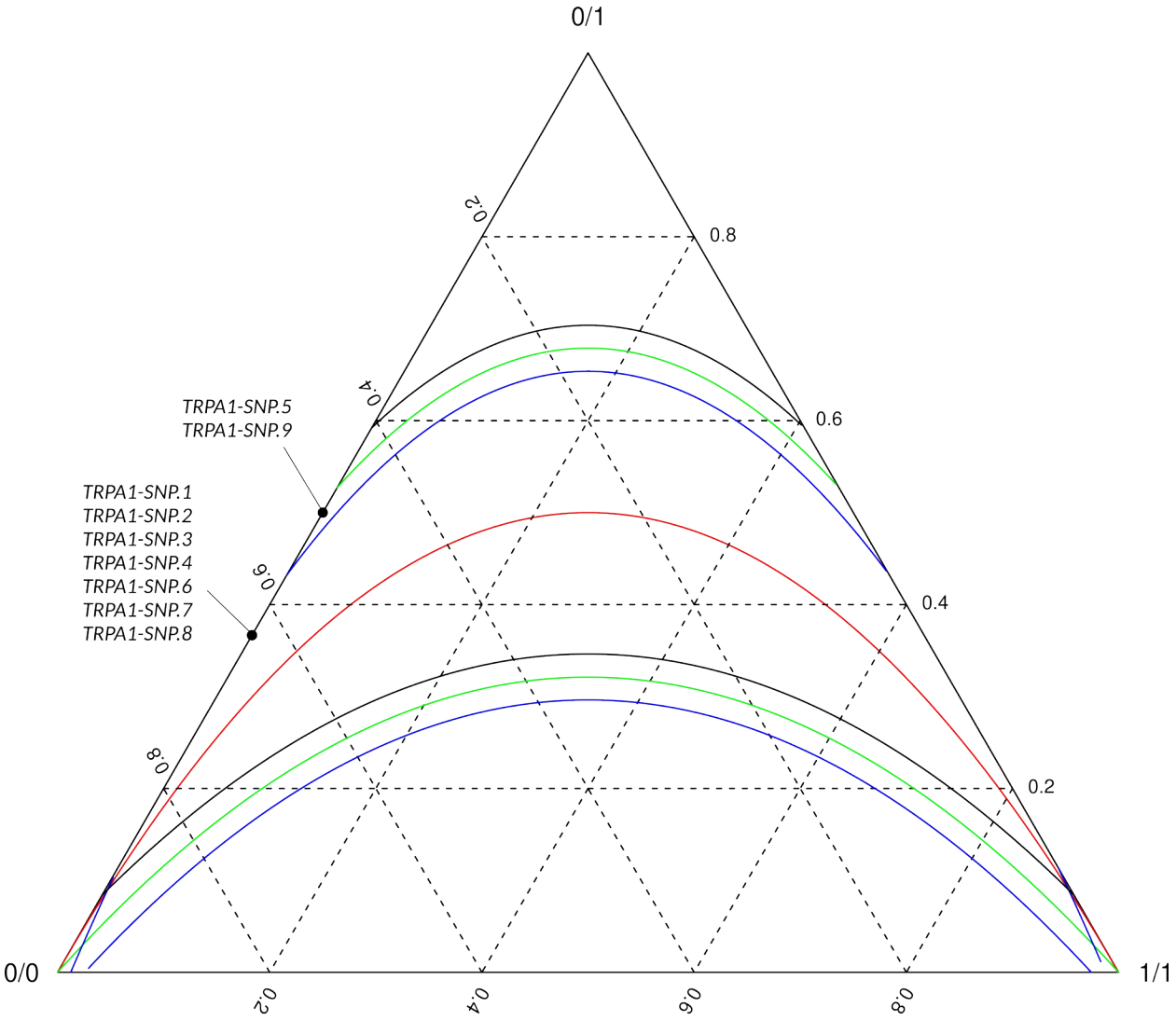

Fig. S10

Ternary plot showing the genotype frequencies of the nine SNPs with signals of environmental selection in the TRPA1 gene (black dots), relative to the expected genotype frequencies under Hardy-Weinberg Equilibrium (red parabola) and the different significance thresholds: the limits of the acceptance region for an ordinary chi-square test in green, the limits of the acceptance region for a chi-square test with continuity correction when D > 0 in blue, and the limits of the acceptance region for a chi-square test with continuity correction when D < 0 in black.

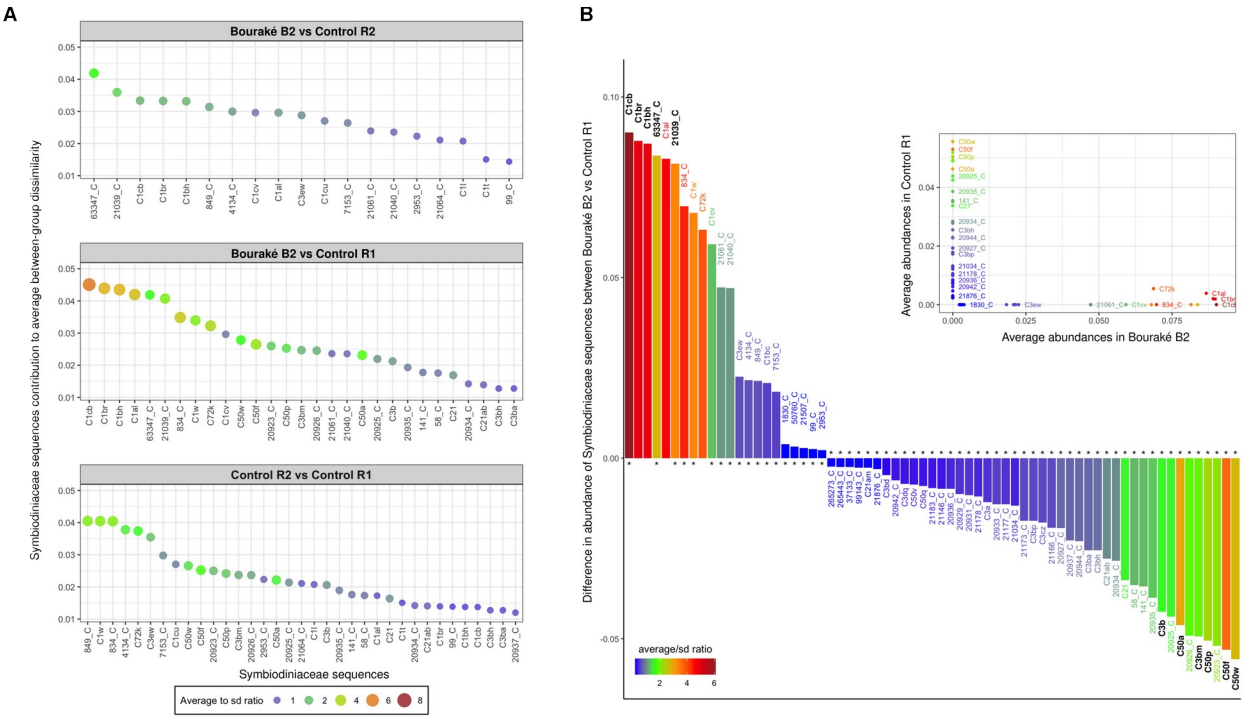

Fig. S11

(**A**) Symbiodiniaceae ITS2 sequences that drive differentiation of samples of Bouraké B2 from Control site R2 (top), Bouraké B2 from Control site R1 (middle) and Control site R1 from Control site R2 (bottom). The y-axis shows the contribution of each ITS2 sequence to the average between-group dissimilarity. The average to sd ratio is indicated by a color and size scale. (**B**) Difference in the abundance of Symbiodiniaceae ITS2 sequences between Bouraké B2 and Control site R1. Sequences that are unique to one or the other site are indicated with an asterisk and sequences mentioned in the main text are highlighted using bold black labels. Positive values represent Symbiodiniaceae sequences more abundant in Bouraké B2, while negative values represent Symbiodiniaceae sequences more abundant in Control C1. The inlet shows the abundances in Bouraké B2 and Control C1 for each sequence.

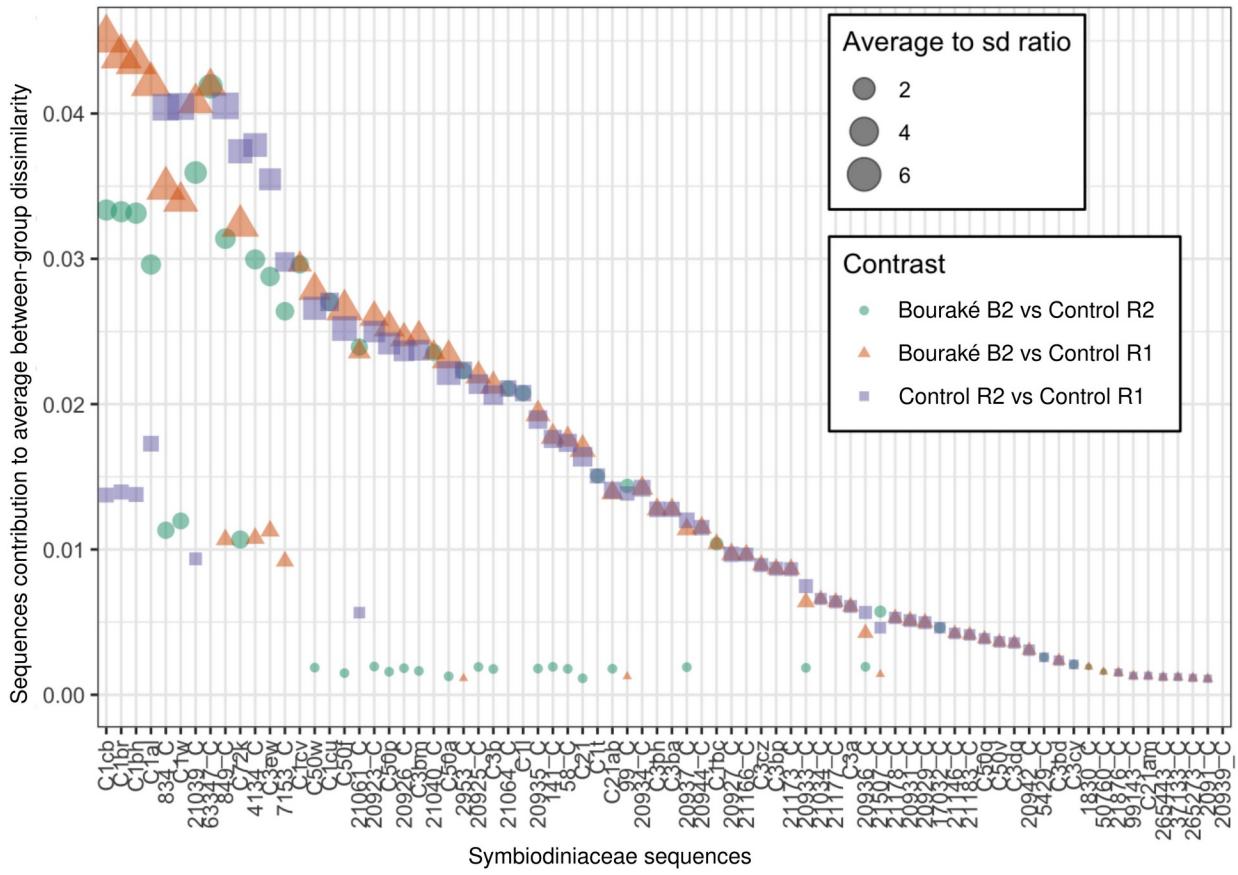

Fig. S12

Simper results showing the species contribution to average between-group dissimilarity for each Symbiodiniaceae species. This plot summarizes the simper results for the three between-group comparisons.

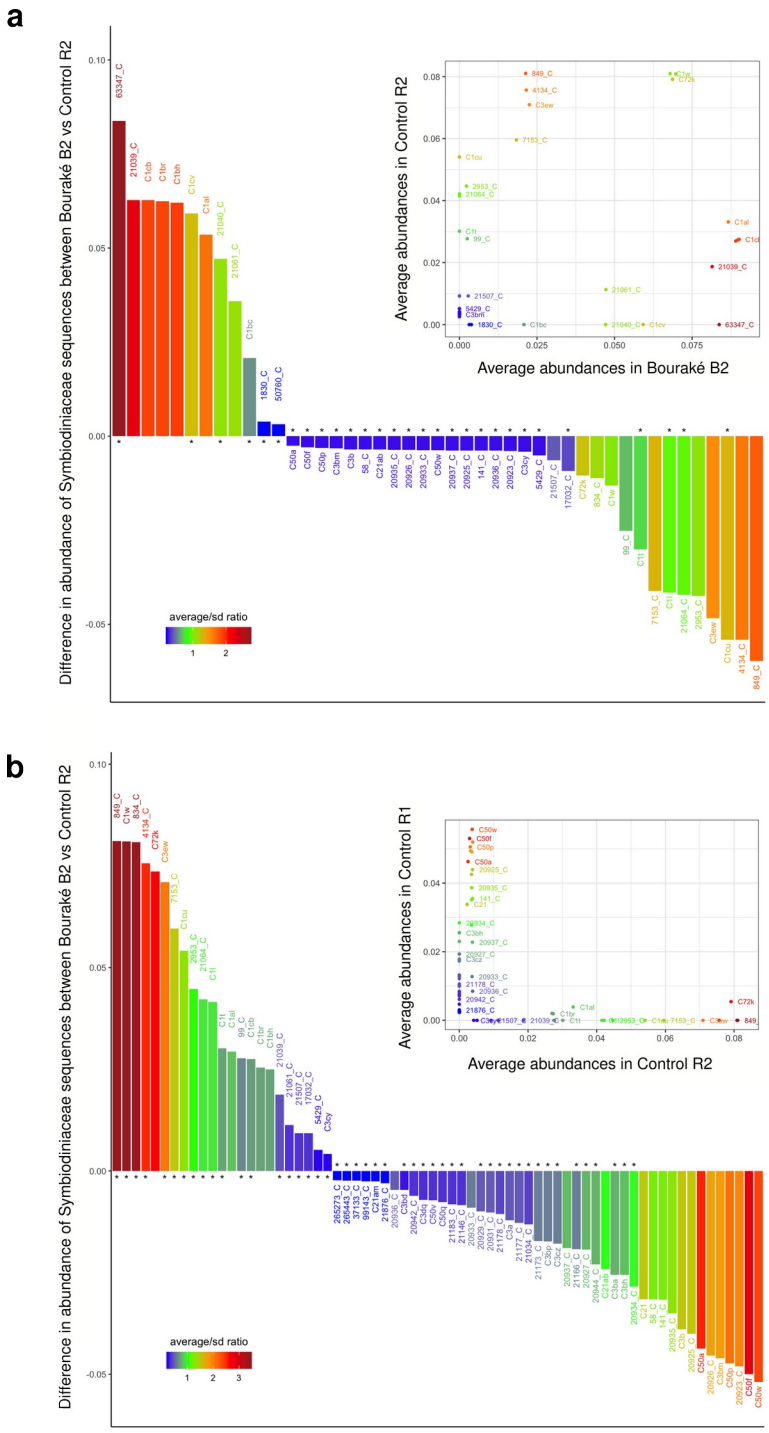

Fig. S13

Simper results showing the difference in the abundance of Symbiodiniaceae species between (**a**) Bouraké B2 and Control site R2 and (**b**) Control site R1 and Control site R2. Species that are unique to one or the other site are indicated with an asterisk.

Table S1 (separate file)

Environmental matrix used for the genotype-environment association analysis.

Table S2 (separate file)

Functional annotation results revealing the 57 genes affected by the 89 SNPs highly associated with Bouraké (snpEff output).

Table S3 (separate file)

Observed and expected (under HWE) genotype frequencies and the *p*-values of the two statistical significance tests performed.