

Environmental latitudinal gradients and host specificity shape Symbiodiniaceae distribution in Red Sea *Porites* corals

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Environmental latitudinal gradients and host specificity shape Symbiodiniaceae distribution in Red Sea *Porites* corals

Running Title: Symbiodiniaceae diversity in Red Sea *Porites*

Tullia I. Terraneo^{a,b*}, Marco Fusi^{a,c}, Benjamin C. C. Hume^a, Roberto Arrigoni^{a,d}, Christian R. Woolstra^{a,e}, Francesca Benzoni^f, Zac H. Forsman^g, Michael L. Berumen^a

^aRed Sea Research Center, Division of Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology, Thuwal 23955-6900, Saudi Arabia; ^bARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville 4811, QLD, Australia; ^cSchool of Applied Sciences, Edinburgh Napier University, Sighthill Court, Edinburgh EH11 4BN, UK; ^dEuropean Commission, Joint Research Centre, Directorate A - Strategy, Work Programme and Resources, Exploratory Research, Ispra 21027, Italy; ^eDepartment of Biology, University of Konstanz, Universitätsstraße 10, Konstanz 78457, Germany; ^fDepartment of Biotechnologies and Bioscience, University of Milano-Bicocca, Milan, 20126, Italy; ^gHawaii Institute of Marine Biology, Kaneohe 96744, HI, USA

*Tullia Isotta Terraneo, tulliaisotta.terraneo@kaust.edu.sa, Red Sea Research Center, Division of Biological and Environmental Science and Engineering, King Abdullah University of Science and Technology, Thuwal 23955-6900, Saudi Arabia; ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville 4811, QLD, Australia

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ABSTRACT

Aim

To assess the diversity of algal symbionts of the family Symbiodiniaceae associated with the coral genus *Porites* in the Red Sea, and to test for host-specificity and environmental variables driving biogeographical patterns of algal symbiont distribution.

Location

Saudi Arabian Red Sea

Taxon

49 Endosymbiotic dinoflagellates of the family Symbiodiniaceae in association with the reef-
50 building coral genus *Porites*.

51

52 **Methods**

53 Eighty *Porites* coral specimens were collected along the Saudi Arabian Red Sea coast. Species
54 boundaries were assessed morphologically and genetically (putative Control Region - mtCR;
55 ITS region – ITS). Community composition of symbiotic dinoflagellates of the family
56 Symbiodiniaceae was also assessed. Using the ITS2 marker with the *SymPortal* framework,
57 Symbiodiniaceae data at the genus, majority ITS2 sequence, and ITS2 type profile were used
58 to assess symbiont diversity and distribution patterns. These were analyzed in relation to coral
59 host diversity, geographic location, and environmental variables.

60

61 **Results**

62 Among the 80 *Porites* samples, 10 morphologies were identified. These corals were clustered
63 into five lineages (clades I to V) by each of the markers independently. Clades I, II, and III
64 each comprised of a single *Porites* morphology, while clades IV and V contained up to five
65 distinct morphologies. The diversity of Symbiodiniaceae associated with *Porites* was high and
66 latitudinal differentiation was observed. In particular, a shift from a *Cladocopium*- to a
67 *Durusdinium*-dominated community was found along the north-south gradient. Symbiont
68 diversity showed patterns of geographic-specific association at Symbiodiniaceae genus,
69 majority ITS2 sequence, and ITS2 type profile level. Specific associations with host-genotypes
70 (but not morphological species) were also recovered when considering Symbiodiniaceae
71 majority ITS2 sequence and ITS2 type profiles.

72

73 **Main conclusions**

74 This study provides the first large scale molecular characterization of Symbiodiniaceae
75 communities associated with *Porites* corals from the Saudi Arabian Red Sea. The use of
76 intragenomic diversity data enabled the resolution of host-symbiont specificity and
77 biogeographical patterns of distribution, previously unachievable with the ITS2 marker alone.
78 Finally, correlation among symbiont diversity and Red Sea environmental gradients was
79 documented.

80

81 **Keywords**

82 Latitudinal gradient, ITS2, next-generation sequencing, Scleractinia, symbiosis, *SymPortal*

83

84 **INTRODUCTION**

85

86 Shallow water tropical and subtropical corals rely on their association with microscopic
87 endosymbiotic dinoflagellates of the family Symbiodiniaceae. Providing the corals with up to
88 95% of their nutritional needs (Falkowski et al., 1984), these photosynthetic symbionts are
89 crucial for the growth and functioning of coral reefs (Hughes et al., 2017, 2018; Sampayo et
90 al., 2016).

91 Symbiodiniaceae diversity in reef ecosystems is high and the specificity and variability of the
92 associations that scleractinian-hosts form with these symbionts have proven to confer
93 ecological advantages to corals under different ecological conditions (Berkelmans & van
94 Oppen, 2006; LaJeunesse et al., 2010; Rosic et al., 2015; Hume et al., 2016). These associations
95 influence the geographical zonation patterns of corals at large and small scales and provide the
96 corals with different tolerance to light intensity (Baker, 2001) and temperature (Rowan &
97 Knowlton, 1995; Glynn et al., 2001; Berkelmans & van Oppen, 2006). Indeed, different
98 Symbiodiniaceae-host interactions impact the corals' susceptibility to bleaching events (for a

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3 99 definition of bleaching see van Oppen & Lough, 2018). The potential of corals to “shuffle”
4 100 (*i.e.*, replacement of dominant population by a background resident population) or “switch”
5 101 (*i.e.*, the exogenous uptake of a different population from the environment) their symbiont
6 102 communities towards more tolerant ones could also play a major role towards ecological
7 103 resilience of coral reefs (Baker et al., 2004; Sampayo et al., 2008; Kemp et al., 2014), yet this
8 104 potential remains questionable, and the diversity of the symbiont communities associated with
9 105 different hosts seems to be non-random (Rowan 1991; Trench 1988, 1992). Different patterns
10 106 of host-symbiont associations have been documented in response to latitudinal, longitudinal,
11 107 and environmental gradients, for various geographic locations and host taxa (Oliver & Palumbi,
12 108 2009; Huang et al., 2011; Keshavmurthy et al., 2014; Hume et al., 2015, 2016; Ziegler et al.,
13 109 2015, Tonk et al., 2017). Nevertheless, our knowledge of the specificity and diversity of these
14 110 associations is still poor, limiting our understanding of the ecological benefits that different
15 111 associations provide (LaJeunesse et al., 2018).

16 112 Despite the lack of a single commonly accepted molecular marker for Symbiodiniaceae
17 113 diversity typing, the Internal Transcribed Spacer II (ITS2) region is currently the most widely
18 114 used barcode locus within the family (Hume et al., 2016, 2018; Smith et al., 2017). The multi-
19 115 copy nature of this marker means that both intragenomic and intergenomic sequence variants
20 116 may be present within any single coral Symbiodiniaceae sample. Distinguishing between these
21 117 sequence variant sources is difficult and therefore the majority of commonly used analytical
22 118 approaches aim to collapse the confounding intragenomic diversity (Arif et al., 2014; Cunning
23 119 et al., 2017). However, the intragenomic diversity harboured within every Symbiodiniaceae
24 120 genome may be taxonomically informative. Gel-based techniques have made use of this
25 121 diversity to improve taxonomic resolution for more than 15 years (LaJeunesse, 2002). Most
26 122 recently, the *SymPortal* analytical framework (symportal.org;
27 123 github.com/SymPortal/SymPortal_framework; Hume et al., 2019) has been developed to make
28 124 use of this intragenomic diversity for resolving genetic delineations using next generation
29 125 sequencing (hereafter “NGS”) ITS2 data. By leveraging the informative nature of
30 126 Symbiodiniaceae intragenomic diversity, finer-scale resolutions of genetic delineations are
31 127 now possible; these delineations far surpass what were previously achievable with the ITS2
32 128 marker (Smith et al., 2017; Thornhill et al., 2017; Hume et al., 2019).

33 129 As one of the hottest and most saline regions of the ocean, the Red Sea represents an ideal
34 130 setting to explore Symbiodiniaceae diversity in a system where natural conditions are already
35 131 exceeding the thresholds typical for Scleractinia persistence elsewhere in the world. Moreover,
36 132 due to limited freshwater inflow, low circulatory exchange with the Indian Ocean, and high
37 133 evaporation rates ($\sim 2\text{m year}^{-1}$), the Red Sea displays extreme latitudinal environmental
38 134 gradients (Trommer et al., 2009; Raitos et al., 2013). In particular, the sea surface temperature
39 135 (SST) maxima ranges from $26^{\circ}\text{C} (\pm 1.1^{\circ}\text{C})$ in the north to $31.3^{\circ}\text{C} (\pm 1.1^{\circ}\text{C})$ in the south (Osman
40 136 et al., 2018), the primary productivity increases from northern oligotrophic waters to southern
41 137 nutrient rich waters (Raitos et al., 2013), and the salinity drops from 41 in the north to 36 in
42 138 the south (Ngugi et al., 2012). Symbiodiniaceae diversity in the Red Sea has been recently
43 139 evaluated from the widespread anthozoan host *Palythoa tuberculosa*, and clear
44 140 biogeographical patterns of association were recovered along the Red Sea latitudinal gradients
45 141 (Reimer et al., 2017).

46 142 The Red Sea is also recognized as a marine biodiversity hotspot, harbouring more than 2000
47 143 species of fish and 50 genera of corals (Briggs & Bowen, 2012; Berumen et al., 2013;
48 144 DiBattista et al., 2016a, b). Hermatypic corals of the cosmopolitan genus *Porites* are among
49 145 the most abundant, widespread, and diverse zooxanthellate scleractinians in the Red Sea
50 146 (Sheppard & Sheppard, 1991). Up to 15 species of *Porites* have been reported from the region
51 147 following traditional morphology-based classifications (Sheer & Pillai, 1983; Sheppard &
52 148 Sheppard, 1991; Veron, 2000), however, species boundaries within the genus remain

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3 149 unresolved (Forsman et al., 2009, 2015, 2017; Prada et al., 2014; Dimond et al., 2017). Besides
4 150 their role as fundamental reef builders, *Porites* corals are also among the most resistant corals
5 151 to increasing water temperatures (LaJeunesse et al., 2003). During both the 2010 and the 2016
6 152 bleaching events, *Porites* was among the least affected coral genera in the Red Sea, with less
7 153 than 40% of the resident population showing signs of bleaching (Furby et al., 2013; Monroe et
8 154 al., 2018).

9 155 In this work, we applied NGS to explore the diversity of the Symbiodiniaceae community
10 156 associated with *Porites* in the Saudi Arabian Red Sea along a 12° latitudinal gradient. We tested
11 157 for host-specificity as well as geographic and environmental variables driving biogeographical
12 158 patterns of algal symbiont distribution, with the aim of providing a better understanding of the
13 159 ecological resilience of Red Sea coral reefs.

16 160

17 161 MATERIALS AND METHODS

18 162

19 163 Sampling and identification

20 164 A total of 80 *Porites* coral colonies were collected at seven coastal localities along the Saudi
21 165 Arabian Red Sea between 2013 and 2016 (Fig. 1, Appendix S1 in Supporting Information).
22 166 Logistical reasons prevented us from sampling all regions at the same time. Each coral colony
23 167 was imaged in the field using a Canon G15 camera while SCUBA diving. A fragment of
24 168 approximately 10cm³ was sampled from each scleractinian colony using hammer and chisel.
25 169 Once in the laboratory, a subsample of 1cm³ was taken from each specimen and preserved in
26 170 99% ethanol for further molecular analyses. The rest of the coral was bleached in sodium
27 171 hypochlorite for 48 hours to remove fresh tissue and was air dried for further morphological
28 172 observations. Dried skeletons were imaged using a Canon G15 and were used for traditional
29 173 morphology-based species identification.

30 174 Specimens were identified based on skeletal morphology features of the corallum and corallites
31 175 following Sheer & Pillai (1983), Sheppard & Sheppard (1991), and Veron (2000) and are now
32 176 deposited at King Abdullah University of Science and Technology (KAUST – Saudi Arabia).

33 177

34 178 Coral host DNA extraction and PCR amplification

35 179 Genomic DNA was extracted from the coral samples using the DNeasy® Blood & Tissue Kit
36 180 (Qiagen Inc., Hilden, Germany). Extracted DNA was quantified with AccuBlue High
37 181 Sensitivity dsDNA quantitation kit (Biotium, Inc.) using a Qubit® fluorometer (ThermoFisher
38 182 Scientific, Inc, Wilmington, USA). Details on PCR amplifications and primers are provided in
39 183 Appendix S2 in Supporting Information.

40 184 Forward and reverse sequences were assembled and edited using Sequencher 5.3 (Gene Codes
41 185 Corp., Ann Arbor, USA). Nuclear sequences that showed intra-individual polymorphisms were
42 186 phased using Phase (Stephens et al., 2001; available online at [http://stephenslab.uchicago.edu/
43 187 software.html](http://stephenslab.uchicago.edu/software.html)) and SeqPHASE (Flot, 2010; available online at [http://seqphase.
44 188 mpg.de/seqphase/](http://seqphase.mpg.de/seqphase/)) when the alleles showed the same length, and using Champuru (Flot, 2007;
45 189 available online at [http://seqphase.mpg. de/champuru/](http://seqphase.mpg.de/champuru/)) when the two predominant alleles were
46 190 of different lengths. Alignments were performed using the E-INS-i option in MAFFT 7.130b
47 191 (Kato & Standley, 2013) and manually checked using BioEdit 7.2.5 (Hall, 1999). All the
48 192 produced sequences are deposited at GenBank (see Appendix S1 in Supporting Information),
49 193 and alignments are available upon request to the corresponding author.

50 194

51 195 Coral host phylogeny reconstructions

52 196 For each marker, the best fit substitution model was calculated using PartitionFinder 1.1.1
53 197 (Lanfear et al., 2012) with unlinked branch lengths, the greedy search algorithm for nucleotide
54 198 sequence, and a partitioning scheme comparison was performed using the corrected Akaike

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3 199 Information Criterion (AIC) and the Bayesian Information Criterion (BIC). For the mtCR,
4 200 PartitionFinder selected the evolutionary model GTR+I, while for the ITS region the GTR+I+G
5 201 was the most suitable model. Phylogenetic relationships were reconstructed under two different
6 202 criteria: Bayesian inference (BI) using MrBayes 3.2.6 (Ronquist et al., 2012) and Maximum
7 203 Likelihood (ML) using RAxML 2 (Stamatakis, 2014). The CIPRES server (Miller et al., 2012)
8 204 was used to run both the BI and ML analyses. BI runs were performed using four Markov
9 205 Chain Monte Carlo (MCMC) chains for 10 million generations, saving one tree every 100
10 206 generations. The tree searches were stopped when all parameters reached stationarity for
11 207 effective sampling size and unimodal posterior distribution using Tracer 1.6 (Rambaut et al.,
12 208 2014). The first 25% trees sampled were discarded as burn-in following indications by Tracer.
13 209 ML topologies were obtained under the default parameters shown on the CIPRES server with
14 210 a multiparametric bootstrap analyses of 1,000 bootstrap replicates.
15 211

18 212 **Symbiodiniaceae MiSeq sequencing library preparation**

19 213 Symbiodiniaceae types were characterized using PCR amplification of the ITS2 region (ITS2)
20 214 for the Illumina MiSeq platform in the KAUST Bioscience Core Laboratory (Thuwal, Saudi
21 215 Arabia). Details on PCR amplifications, library preparation, and sequencing are provided in
22 216 Appendix S2 in Supporting Information.
23 217

25 218 **Symbiodiniaceae MiSeq data processing**

26 219 Symbiodiniaceae NGS ITS2 data were analysed using the *SymPortal* framework (Hume et al.,
27 220 2019) by submitting paired fastq.gz files directly to the framework. A standardized quality
28 221 control (QC) of sequences was conducted as part of the submission. Briefly, the standard
29 222 *SymPortal* QC is conducted using mothur 1.39.5 (Schloss et al., 2009), the BLAST+ suite of
30 223 executables (Camacho et al., 2009), and minimum entropy decomposition (MED; Eren et al.,
31 224 2015). The MED incorporated into the standard *SymPortal* QC pipeline uses an 'M' value
32 225 cutoff meaning that MED nodes (a proxy for representative sequences) are identified down to
33 226 a relative within sample, genus-partitioned abundance of 0.4% (i.e. 0.4% of the sequences for
34 227 a given genus in a given sample; or four sequences if the sequencing is very shallow). As such,
35 228 the ITS2 type profile predictions in the standard outputs of *SymPortal* should be viewed as
36 229 being representative of the more abundant genotypes present in any given sample's genus
37 230 partitioned collection genotypes (sequences are analysed on a genus partitioned basis within the
38 231 *SymPortal* framework). Whilst the *SymPortal* approach of searching for genotypic
39 232 representative sets of sequences can be applied to identify low abundance genotypes within
40 233 samples (by searching for identified ITS2 type profiles in the pre-MED decomposition
41 234 sequences that are also output by the *SymPortal* QC; providing that sequencing depth is
42 235 adequate), this study concerned itself with only the standard output and thus the more abundant
43 236 genotypes in the genus partition. This standard output contains two count tables: one provides
44 237 sequence abundances listed by sample (see Appendix S3 in Supporting Information), and the
45 238 second provides ITS2 type profile abundances listed by sample (see Appendix S3 in supporting
46 239 Information). In the second count table, alongside the ITS2 type profile abundances, different
47 240 hierarchical levels are given for each of the identified Symbiodiniaceae genotypes.
48 241 Specifically, for this analysis, the clade (genus), majority ITS2 sequence (most abundant ITS2
49 242 sequence), and ITS2 type profile (representative of putative taxa) were used. The source code
50 243 and detailed documentation of the logic underlying the *SymPortal* analysis are available from
51 244 its GitHub repository (Hume 2019).
52 245
53 246

58 247 **Environmental data**

59 248 A total of four environmental variables were considered in this study, namely chlorophyll-*a*

249 (Chl-*a*), sea surface temperature (SST), particulate organic carbon (POC), and salinity. The
250 first three variables were gathered for each of the seven sampling localities of the Red Sea from
251 2010 to 2017 from the National Aeronautic and Space Administration (NASA) Giovanni
252 website (Acker & Leptoukh, 2007), developed and maintained by the NASA Goddard Earth
253 Sciences Data and Information Services Center (<https://giovanni.gsfc.nasa.gov/giovanni/>). In
254 particular, monthly average Chl-*a*, SST, and POC data were derived from 4 km resolution data
255 from the Moderate Resolution Imaging Spectroradiometer (MODIS) Aqua database. For each
256 sampling location, annual averages were then calculated. Following Reimer et al., 2017,
257 salinity for each sampling site was gathered from March 2010 (winter) data in Ngugi et al.,
258 (2012), as representative salinity occurring at each site. All environmental data are listed in
259 Appendix S3 in Supporting Information.

260

261 **Statistical analyses**

262 Statistical analyses were performed using PRIMER 6.1.15 (Primer-E, Plymouth, UK) with the
263 add-on PERMANOVA+ package (Anderson et al., 2008). Permutational multivariate analysis
264 of the variance (PERMANOVA) was performed on Bray-Curtis distance matrices to test for
265 significant differences in Symbiodiniaceae community composition along the Red Sea
266 latitudinal gradient, and to test for morphological and molecular host-specificity with *Porites*
267 corals. In particular, the three Symbiodiniaceae input datasets (genus level, ITS2 majority
268 sequence, ITS2 type profile) were tested for compositional differences for three biodiversity
269 metrics: Red Sea locality (seven levels: Gulf of Aqaba, Duba, Al Wajh, Yanbu, Thuwal,
270 Farasan Banks, Farasan Islands), *Porites* molecular clade (five levels: clades I, II, III, IV, V),
271 and *Porites* morphological species (10 levels: *P. annae*, *P. echinulata*, *P. fontanesii*, *P.*
272 *columnaris*, *P. lobata*, *P. lutea*, *P. monticulosa*, *P. rus*, *P. solida*, *P. sp1*). The factors were
273 fixed and orthogonal. Moreover, given that some Symbiodiniaceae communities may change
274 over time the three Symbiodiniaceae input datasets (genus level, ITS2 majority sequence, ITS2
275 type profile) were tested for sampling time (March 2013, September 2013, October 2014,
276 November 2015, December 2015, January 2016, February 2016). The factors were fixed and
277 orthogonal. Prior to running the PERMANOVA, we verified the homogeneity of the
278 dispersions of the categorical variables using PERMDISP. We chose PERMANOVA to test
279 for differences among the levels of our explanatory variables, as it can cope with the uneven
280 sample size of *Porites* at each studied location (Anderson et al., 2008).

281 Canonical Analysis of Principal coordinates (CAP) for each single factor was performed as a
282 validation, effectively testing how well CAP can correctly re-allocate the samples to their
283 respective groups (Anderson & Willis, 2003).

284 A marginal test in distance-based linear modelling (DistLM) was used to explore the
285 correlation between Symbiodiniaceae diversity (genus level, majority ITS2 sequence, ITS2
286 type profile) and the four environmental variables (salinity, Chl-*a*, DOM, and SST) (Anderson
287 et al., 2008). A Bray-Curtis dissimilarity matrix was built with the inclusion of a dummy
288 variable (+1) to accommodate for zeros in the biological data. Bi-plots of the CAP ordination
289 with Bray-Curtis distance were computed using R and the package “vegan” (Oksanen et al.,
290 2013) to visualize the relationship between environmental variables (*i.e.*, Chl-*a*, SST, POC,
291 and salinity) and each biodiversity metrics (*i.e.*, locality, *Porites* molecular clade, *Porites*
292 morphological species) and Symbiodiniaceae at the genus level, ITS2 majority sequence, and
293 ITS2 type profiles.

294

295 **RESULTS**

296

297 **Traditional and molecular identification of *Porites***

298 Among the 80 *Porites* colonies collected, a total of nine nominal species were identified based
 299 on morphological characters: *Porites annae*, *P. echinulata*, *P. fontanesii*, *P. columnaris*, *P.*
 300 *lobata*, *P. lutea*, *P. monticulosa*, *P. rus*, and *P. solida*. One sample did not match any of the
 301 existing original descriptions of *Porites* species in the literature and, therefore, was referred to
 302 as *Porites* sp1.

303 Sequence data for the mtCR and ITS region were obtained from all 80 analysed samples (see
 304 Appendix S1 in Supporting Information). One sequence of *Goniopora* sp. was added to the
 305 two datasets and used as outgroup in both the reconstructions following Kitano et al. (2014).
 306 The mtCR sequence alignment consisted of 1,292 bp, with 68 polymorphic and 31 parsimony
 307 informative sites. The ITS alignment encompassed 795 bp with 103 variable sites, 88 of which
 308 were parsimony informative. BI and ML tree topologies obtained from the two regions were
 309 largely congruent, recovering five highly-supported molecular clades in our samples (Clades I
 310 to V) (Fig. 2). Three clades were comprised of a single morphospecies, and their monophyly
 311 was highly supported: clade I included all *P. fontanesii* material, clade II grouped *P.*
 312 *columnaris*, and clade III was comprised solely of a sample from *P.* sp1. Conversely, clades
 313 IV and V grouped more than one morphospecies of *Porites*. Namely, clade IV included *P. rus*
 314 and *P. monticulosa*, while clade V comprised five different morphologies of *Porites*, i.e., *P.*
 315 *annae*, *P. echinulata*, *P. lobata*, *P. lutea*, and *P. solida*.

317 Symbiodiniaceae community structure

318 A total of 8,159,993 sequences were generated using Illumina MiSeq. After filtering, 5,506,746
 319 sequences were analysed with the *SymPortal* framework, and 156 Symbiodiniaceae-defining
 320 ITS2 intra-genomic variants were recorded within our 80 *Porites* samples. A total of 77 ITS2
 321 type profiles were recovered that were represented by 38 distinct ITS2 sequences found to be
 322 the most abundant in any one of the ITS2 type profiles (see Appendix S3 in Supporting
 323 Information). Symbiodiniaceae community composition at the genus level, the majority ITS2
 324 sequence level (most abundant ITS2 sequence for a given ITS2 type profile), and the ITS2 type
 325 profile level was visualized using stacked bar charts to compare the relative abundance for
 326 three factors, namely, locality, *Porites* molecular clade, and *Porites* morphological species
 327 (Fig. 3).

328 Overall, the most abundant genus of Symbiodiniaceae associated with *Porites* in the Red Sea
 329 was *Durusdinium* (51%), followed by *Cladocopium* (46%); only 3% of the sequences belonged
 330 to the genus *Symbiodinium* (Fig. 3). PERMANOVA analysis identified a significant
 331 geographical structure in the Symbiodiniaceae genera distribution along the latitudinal gradient
 332 of the Saudi Arabian Red Sea ($F_{6, 73} = 6.42$, $p = 0.001$, Table 1), with the cross-validation
 333 analysis re-assigning 42.5% of the sequences to the correct geographic location (Table 1). In
 334 particular, in the northern Red Sea (i.e. Gulf of Aqaba and Duba), *Porites* colonies exclusively
 335 harboured *Cladocopium*. From north to south, the Symbiodiniaceae community shifted
 336 gradually from *Cladocopium* dominated towards *Durusdinium* dominated. Indeed,
 337 *Durusdinium* represented 80% of the community in the southern Red Sea (i.e., Farasan
 338 Islands). Finally, the genus *Symbiodinium* appeared below 1% in the northern (Duba, Al Wajh,
 339 Yanbu) and central (Thuwal, Farasan Banks) Red Sea, while in the Farasan Islands represented
 340 8% of the symbiont community (Fig. 3). No significant correlations between Symbiodiniaceae
 341 genera and *Porites* morphological species ($F_{11, 68} = 0.73$, $p = 0.74$) or *Porites* molecular
 342 lineages ($F_{4, 75} = 1.14$, $p = 0.30$ - Table 1) were recorded.

343 The majority of ITS2 sequences for a given ITS2 type profile was C15 (accounting for 28% of
 344 the entire majority ITS2 sequences), followed by D1 (18% of the total diversity) (Fig. 3). A
 345 significant latitudinal structure of Symbiodiniaceae community emerged by analysing the
 346 distribution of the majority ITS2 sequence for the ITS2 type profiles predicted ($F_{6, 73} = 2.27$, p
 347 = 0.001 - cross-validation analysis reassigned 38.75% of the majority ITS2 sequences to the

correct location – Table 1). In the north, from the Gulf of Aqaba to Al Wajh, the C15 sequence was the most abundant majority ITS2 sequence, contributing to the entire diversity in the Gulf of Aqaba (100%) and to more than 40% of the diversity in Duba (58%) as well as in Al Wajh (42%). In Yanbu, D1 (34%) and C15 (38%) were the most abundant majority ITS2 sequences, while in Thuwal C15 was the most abundant majority ITS2 sequence (39%) together with D1 or D4 (23%) and C15 or C60a (23%). Similarly, in the Farasan Banks C15, D1, and D4 sequences were the most abundant majority ITS2 sequences (31%, 21%, and 19%, respectively). Finally, in the Farasan Islands, D1 or D6 and D1 or D4 sequences mostly contributed to the majority ITS2 sequences of the community (36% and 21% respectively) (Fig. 3). Symbiodiniaceae host specificity was recovered when considering the majority of ITS2 sequences in relation to *Porites* molecular clade ($F_{4,75} = 1.71, p = 0.01$; cross-validation reassigned 48.75% of the majority ITS2 sequences to correct *Porites* molecular clade – Table 1). In *Porites* clades I, II, III, and IV, the majority ITS2 sequences of the ITS2 types profiles was represented by one or two sequences. In particular, in clade I: C15 sequence (42%) and D1 or D4 or D1n (32%); clade II: C15 sequence (45%) and D1 sequence (41%); clade III: A1 sequence (100%). clade IV: D1 or D4 (37%) and D1 (16%). Finally, in *Porites* clade V, three sequences of Symbiodiniaceae made up more than 50% of the diversity: C15 (25%), D1 or D6, and D1 (Fig. 3). No correlation between *Porites* morphological species and Symbiodiniaceae ITS2 majority was identified ($F_{11,68} = 1.19, p = 0.1$ – Table 2).

A total of 77 Symbiodiniaceae ITS2 type profiles were recovered by the *SymPortal* analytical framework, distributed as follows: 38 type profiles belonged to the genus *Cladocopium*, 26 to *Durusdinium*, and 13 to *Symbiodinium* (see Appendix S3 in Supporting Information). Locality, *Porites* molecular clade, and *Porites* morphological species correlated with the Symbiodiniaceae type profiles recovered ($F_{6,73} = 1.49, p = 0.0004$; $F_{4,75} = 1.79, p = 0.001$; $F_{11,68} = 1.31, p = 0.006$, respectively – Fig. 3), but the cross-validation analyses only reassigned correctly ITS2 type profiles to the geographic location (42.5%), and the *Porites* molecular clade (55%), while only 10% of them were regrouped into correct morphological species (Table 1).

Finally, the PERMANOVA analysis identified a significant effect of the sampling time on the Symbiodiniaceae genera ($F_{6,73} = 5.18, p = 0.001$), majority of ITS2 sequence ($F_{6,73} = 2.35, p = 0.001$), and ITS2 type profiles ($F_{6,73} = 1.63, p = 0.001$) in the Saudi Arabian Red Sea (see Appendix S5 in Supporting Information).

Symbiodiniaceae diversity in relation to environmental variables

DistLM showed that the four environmental variables included in the analyses (*i.e.* salinity, Chl-*a*, POC, and SST) were statistically significantly explaining the variation of Symbiodiniaceae diversity at the Symbiodiniaceae genus level, majority ITS2 sequences, and the ITS2 type profile ($P \leq 0.002$, Table 2, Appendix S4 in Supporting Information). Interestingly, in all the datasets analysed, salinity was the most influential variable, which alone explained 31.3%, 10.9%, and 4.9% of the entire variability (Symbiodiniaceae genus, majority ITS2 sequence, and ITS2 type profile, respectively), followed by Chl-*a*, POC, and SST at all the levels (Table 2, Appendix S4 in Supporting Information).

DISCUSSION

Porites morpho-molecular diversity

Porites is one of the most speciose zooxanthellate coral genera in the world, accounting for over 160 described species, 62 of which are currently recognized as valid (WoRMS, 2018). Almost a quarter of these have been previously recorded in sympatry in the Red Sea (Sheer &

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3 398 Pillai, 1983; Sheppard & Sheppard, 1991; Veron, 2000), rendering the region a biodiversity
4 399 hotspot for *Porites* corals. In our study, we characterized 10 Red Sea *Porites* morphospecies at
5 400 two molecular loci. Only three out of the 10 morphospecies proved to be monophyletic (*i.e.* *P.*
6 401 *fontanesii*, *P. columnaris*, and *P. sp1*) and showed concordant morpho-molecular species
7 402 boundaries. The remaining seven species (*P. annae*, *P. echinulata*, *P. lobata*, *P. lutea*, *P.*
8 403 *solida*, *P. monticulosa*, and *P. rus*) clustered into two evolutionary lineages (clades IV and V).
9 404 Our molecular data demonstrate that the identification of *Porites* species based exclusively on
10 405 morphological features does not match with the molecular lineages occurring in the Red Sea,
11 406 at least based on the markers used herein (Fig. 2). As such, a deep gap in our understanding of
12 407 species boundaries and evolutionary relationships in the genus is confirmed (Forsman et al.,
13 408 2009, 2015, 2017). The use of a multi-disciplinary taxonomic approach has proven useful to
14 409 fill this gap for several coral genera (Benzoni et al., 2010; Schmidt-Roach et al., 2014; Kitahara
15 410 et al., 2016). Indeed, recent studies showed that coupling multi-locus molecular evidence with
16 411 new morphological evidence (*e.g.*, micromorphology and microstructure), reproductive
17 412 biology data, and symbiosis insights could provide us with a new understanding of Scleractinia
18 413 systematics and evolution.
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23 415 **Symbiodiniaceae biogeography across Red Sea gradients**

24 416 The Red Sea environmental gradients correlated with the Symbiodiniaceae biogeographical
25 417 patterns observed. Sequence data showed a shift from the genus *Cladocopium* to *Durusdinium*
26 418 going from the north (Gulf of Aqaba and Duba) to the south (Farasan Islands) of the Red Sea,
27 419 with corals in the central part of the Red Sea (Al Wajh, Yanbu, Thuwal, Farasan Banks)
28 420 harbouring both *Cladocopium* and *Durusdinium* (Fig 1, 3). *Symbiodinium* appears mainly in
29 421 the Farasan Islands at relative low abundance, and at very low abundance (never above 1%) in
30 422 the rest of the localities. Similar biogeographical patterns highlighting a community break
31 423 south of the Gulf of Aqaba have been previously found in different anthozoans symbiont
32 424 communities. For example, similar patterns with Symbiodiniaceae community break at the
33 425 entrance of the Gulf of Aqaba were also recorded by Reimer et al., (2017) for the Zoantharia
34 426 *P. tuberculosa*. Nevertheless, although a different *Cladocopium* community was found outside
35 427 the Gulf of Aqaba, this former work found *Cladocopium* from the Gulf of Aqaba to the Thuwal
36 428 area, where *Durusdinium* also appeared. Sawall et al. (2014) found discontinuity in the
37 429 symbiont communities associated with the coral *Pocillopora verrucosa* between the Gulf of
38 430 Aqaba and the rest of the Red Sea. Similar to our findings, *P. verrucosa* colonies from the Gulf
39 431 of Aqaba were characterized by the unique association with the genus *Cladocopium*, while
40 432 only *Symbiodinium* was found in the remaining sites of the central and southern Red Sea.
41 433 Similarly, Arrigoni et al. (2016) investigated the symbiont community of Red Sea *Stylophora*.
42 434 All samples from the Gulf of Aqaba harboured *Cladocopium*, while outside coral host colonies
43 435 also associated with *Symbiodinium*. This break has been proposed to be mainly driven by cooler
44 436 temperature at the entrance of the Gulf of Aqaba and, in particular, has been proposed that
45 437 *Cladocopium* might have colder water preference (Ulstrup et al., 2006, Sawall et al., 2014).
46 438 However, whilst this cooler water preference hypothesis may be an effective explanation for
47 439 individual Symbiodiniaceae taxa, it is important to note that this trend should not be
48 440 extrapolated to include the whole of the genus *Cladocopium*, especially when exceptionally
49 441 thermally tolerant members exist, *i.e.* *C. thermophilum*. (D'Angelo et al., 2015).
50 442 Genetic breaks have also been documented among populations between the central Red Sea
51 443 and the Farasan Islands in the south. For example, genetic breaks have been reported in
52 444 different fish populations, (Froukh & Kochzius, 2007; Nanninga et al., 2014; Saenz-Agudelo
53 445 et al., 2015), sponges (Giles et al., 2015), and mussels (Shefer et al., 2004). From these studies,
54 446 the genetic brakes matched with environmental transitions occurring around 16° - 20° N in the
55 447 Red Sea. In contrast to the rest of the Red Sea, the Farasan Islands region is a shallow reef
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3 448 system, characterized by less saline but warm, eutrophic, and turbid waters (Sheppard &
4 449 Sheppard, 1991). Our data show a predominance of *Durusdinium* sequences in this
5 450 environment, with high proportions of *D. trenchii* (D1-D4) expected. This distribution fits into
6 451 theories that *D. trenchii* is a stress-resilient taxon within the Symbiodiniaceae, and thus found
7 452 in association with warm and turbid environments or in response to stressful events (Baker,
8 453 2001; LaJeunesse et al., 2008). Recent studies showed association of *P. lutea*, *P. lobata*, and
9 454 *P. harrisoni* with *C. thermophilum* symbionts in the southern Arabian Gulf where SST (36° C)
10 455 and salinity (42) levels exceed the ones from the Red Sea (D'Angelo et al., 2015; Hume et al.,
11 456 2016, 2018). D'Angelo et al. (2015) showed a community transition along the temperature and
12 457 salinity gradient occurring between the southern Arabian Gulf and the Gulf of Oman: *C.*
13 458 *thermophilum* was associated with 100% of *Porites* in the southern Arabian Gulf; in the
14 459 transition zone between the Arabian Gulf and the Gulf of Oman *Porites* associated with *C.*
15 460 *thermophilum* as well as C15 lineages and *D. trenchii*; finally, in the Gulf of Oman, where
16 461 environmental conditions more resemble those present elsewhere in the tropical Indo-Pacific
17 462 belt, *Porites* associated mainly with C15 lineages, as elsewhere in *Porites* hosts. In the Red
18 463 Sea, we find a similar pattern. In the north and central Red Sea, *Porites* is found mainly in
19 464 association with C15 radiation, the most common symbiont association within *Porites*. In the
20 465 south, where the thermal stressors are higher (although not reaching levels as extreme as in the
21 466 Arabian Gulf) *Porites* associates with the more resilient *D. trenchii*.

22 467 Among the environmental variables tested, salinity resulted as partitioning the most variation
23 468 in the Symbiodiniaceae community distribution along the Red Sea latitudinal gradient. This
24 469 result was expected since in the Red Sea salinity changes linearly along the north-south
25 470 latitudinal gradient. Published datasets show that salinity in the Red Sea is relatively stable
26 471 among years (Roik et al., 2016), nevertheless oscillation in salinity can occur seasonally during
27 472 the year as result of evaporation rates, precipitations, and mixing of low saline surface inflow
28 473 from Gulf of Aden (Sofianos et al., 2002; Eshel & Heavens, 2007). Monitoring physio-
29 474 chemical variables for three reefs in the central Red Sea across two years, Roik et al., (2016)
30 475 show that although salinity oscillations occur seasonally (up to 1.43), they are smaller in
31 476 comparison to other reef systems affected by riverine and precipitation inputs, such as on
32 477 inshore reefs in the Great Barrier Reef, where salinity can fluctuate from 5 to 10 (Roik et al.,
33 478 2016). Comparing Ngugi et al., (2012) salinity dataset, with annual mean salinity data from the
34 479 World Ocean Atlas 2018 available at <https://www.nodc.noaa.gov/OC5/woa18/> (Conkright et
35 480 al., 2001; Zeng et al., in prep) the salinity trend along the north-south latitudinal gradient in the
36 481 Red Sea appeared stable, so we decided to include salinity in our analyses.

37 482 The residual variance not partitioned to the environmental factors tested in this study would
38 483 suggest that other sources of variation not considered in the present study might be involved in
39 484 explaining the dataset's variability across the gradient. For example, bathymetric distribution
40 485 has been shown to influence symbiotic association (Frade et al., 2008; Bongaerts et al., 2013,
41 486 2015). We thus suggest the incorporation of additional variables in future work.

487 488 489 **Host-symbiont specificity**

490 By identifying previously overlooked Symbiodiniaceae ITS2 sequences, we were able to
491 identify host-specific association patterns. Indeed, our data showed coupling between *Porites*
492 genotypes (clade I to V) and Symbiodiniaceae ITS2 type profiles and the majority sequences
493 that represent them. C15 radiation sequences were shared among four of the five genetic
494 lineages of *Porites*, and made up the most of the ITS2 sequences in Clade I, II and V,
495 confirming that the C15 radiation is commonly associated with *Porites* (LaJeunesse 2004;
496 Franklin et al., 2012; Keshavmurthy et al., 2014). Nevertheless, association is not exclusive in

our data and might vary depending on the host and the environment. Clade III was mainly associated with A1 sequences, although small sample size prevents us from drawing any firm conclusion about this association.

No specific pattern of association among morphologically-described nominal species of *Porites* and Symbiodiniaceae was recovered. This is an informative result in an era of coral taxonomic revolution, supporting the evidence that coral skeletal morphology alone can lead to misleading classifications. Evolutionary relationships in corals are being revised at every taxonomic level by combining genomic evidence with other lines of evidence. Our results highlighted that such evidence can come from detailed analyses of the associated symbiont community, a trait that has been so far only considered in a limited number of studies.

CONCLUSIONS

This study provides an overview of Symbiodiniaceae diversity associated with *Porites* corals in the Saudi Arabian Red Sea, one of the hottest and most saline environments in the world. This study was able to define zooxanthellae diversity at a new level through the use of an analytical approach leveraging the taxonomically-informative intragenomic sequence diversity harboured in every Symbiodiniaceae genome. Even if *Porites* clades inherently harboured a certain degree of variability at each location due to sample size and clade distribution, biogeographical patterns of symbiont distribution could be distinguished along 2000 km of Red Sea coast, and a correlation among symbiont diversity and Red Sea environmental gradients was found.

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42 880 43 881 **Biosketch**

44 882 Using a suite of different approaches, from modern molecular techniques to fine-scale
45 883 morphology and patterns of reproduction, T.I.T aims to provide a better understanding of corals
46 884 taxonomy and evolution.

47 885 48 886 **Author contributions**

49 887 T.I.T, R.A, M.L.B designed the study; T.I.T and F.B collected specimens; T.I.T performed
50 888 molecular work and data analyses; B.C.C.H ran the *SymPortal* analysis; M.F performed
51 889 statistical analyses; T.I.T wrote the paper with comments by B.C.C.H, C.R.V, R.A, M.F, Z.H.F,
52 890 F.B, M.L.B.

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892 **TABLES**

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894 **Table 1** PERMANOVA results calculated for three biodiversity metrics (Red Sea locality, *Porites* molecular clade, and *Porites* morphological species) for the datasets Symbiodiniaceae genus, Symbiodiniaceae majority ITS2 sequences, and Symbiodiniaceae ITS2 type profile. df = degrees of freedom. Res = Residual degree of freedom. CAP = Cross validation of the PERMANOVA results testing how well CAP routine can correctly re-allocate the samples to their respective groups (Anderson & Willis, 2003).

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		Symbiodiniaceae genus		Symbiodiniaceae majority ITS2 sequences		Symbiodiniaceae ITS2 type profiles	
	df	<i>F</i>	<i>p</i>	<i>F</i>	<i>p</i>	<i>F</i>	<i>p</i>
<i>Porites</i> molecular clade	4	1.1427	0.307	1.7108	0.01	1.7959	0.001
Res	75						
CAP				48.75%		55%	
<i>Porites</i> morphological species	11	0.7351	0.74	1.1925	0.108	1.3184	0.006
Res	68						
CAP						10%	
Red Sea locality	6	6.4268	0.001	2.2736	0.001	1.4954	0.004
Res	73						
CAP		42.5%		38.75%		42.5%	

Table 2 Marginal test results of the DistLM analyses for each of three datasets (Symbiodiniaceae genus, Symbiodiniaceae majority ITS2 sequence, and Symbiodiniaceae ITS2 type profile) against the environmental factors SST, Chl- *a*, POC, and Salinity. SS = Sum of squares; %var = percent of variance explained by each predictor variable.

	Environmental factor	<i>F</i>	<i>p</i>	% var
Symbiodiniaceae genus	SST	20.289	0.001	20.64
	Chl- <i>a</i>	34.536	0.001	30.68
	POC	35.656	0.001	29.18
	Salinity	35.656	0.001	31.37
Symbiodiniaceae majority ITS2 sequence	SST	5.3512	0.001	6.42
	Chl- <i>a</i>	9.3287	0.001	10.68
	POC	8.8295	0.001	10.16
	Salinity	9.639	0.001	10.99
Symbiodiniaceae ITS2 type profile	SST	2.5913	0.002	3.22
	Chl- <i>a</i>	3.8551	0.001	4.71
	POC	3.6152	0.001	4.43
	Salinity	4.0011	0.001	4.88

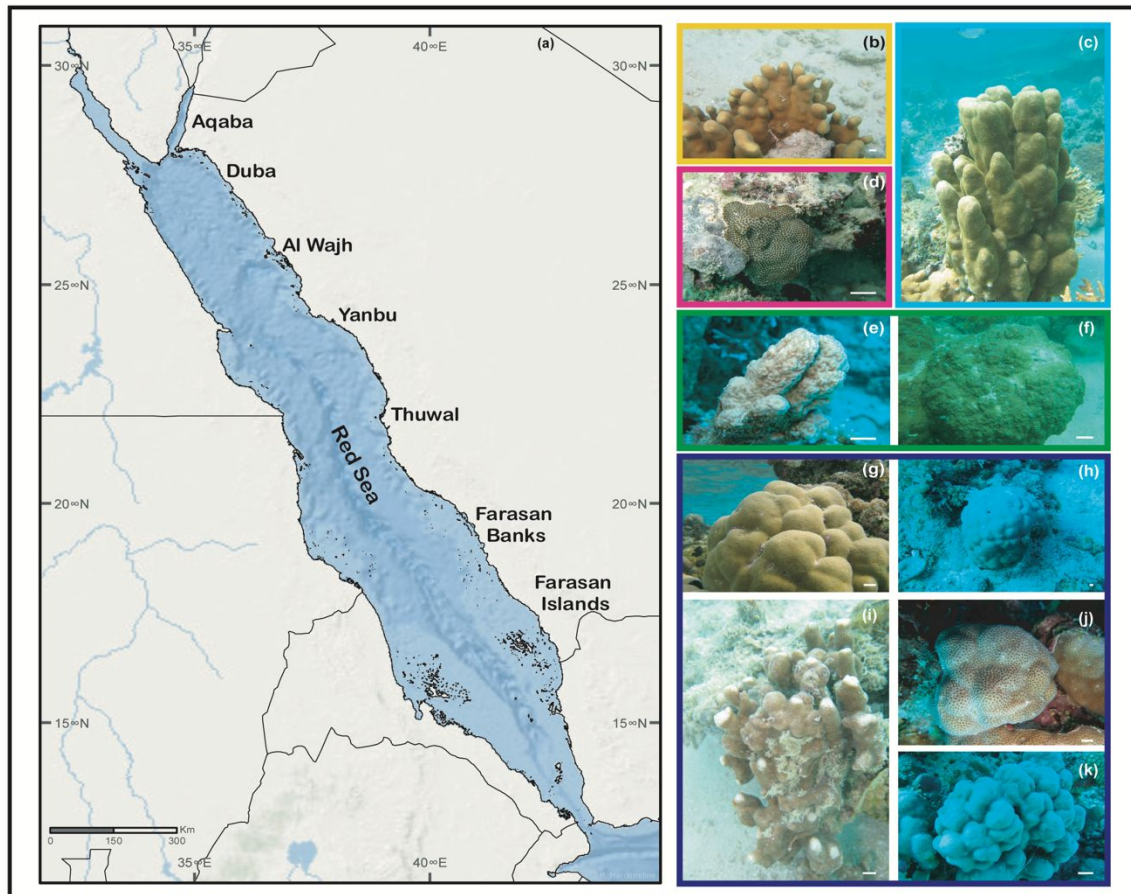
FIGURES

Figure 1 Sampling location and specimen collection overview (a) Red Sea map with sampling localities. (b) to (j) *Porites* morphologies encountered among our 80 collected samples. (b) *Porites fontanesii*, (c) *Porites columnaris*, (d) *Porites* sp1, (e) *Porites rus*, (f) *Porites monticulosa*, (g) *Porites lutea*, (h) *Porites lobata*, (i) *Porites annae*, (j) *Porites echinulata*, (k) *Porites solida*.

Figure 2 RAxML phylogeny reconstructions of Red Sea *Porites* at two molecular loci. (a) mitochondrial Control Region (b) nuclear Internal Transcribed Spaces region. Number on the branches represent support values corresponding to Bayesian posterior probabilities (>90%), ML bootstrap values (>70%). *Goniopora* was selected as outgroup in both the analyses. In (b) black curved lines connect the two sequences of heterozygotes individuals.

922 **Figure 3** Stacked bar charts (100%) comparing Symbiodiniaceae diversity at the (a) (b) (c)
 923 genus level, (d) (e) (f) majority ITS2 sequence level (the 20 most abundant shown), (g) (h) (i)
 924 ITS2 type profile level (the 20 most abundant shown). For each of these three datasets, bar
 925 charts were plotted for three different factors: (a) (d) (g) *Porites* morphological species, (b) (e)
 926 (h) *Porites* molecular clade, (c) (f) (j) Red Sea localities.

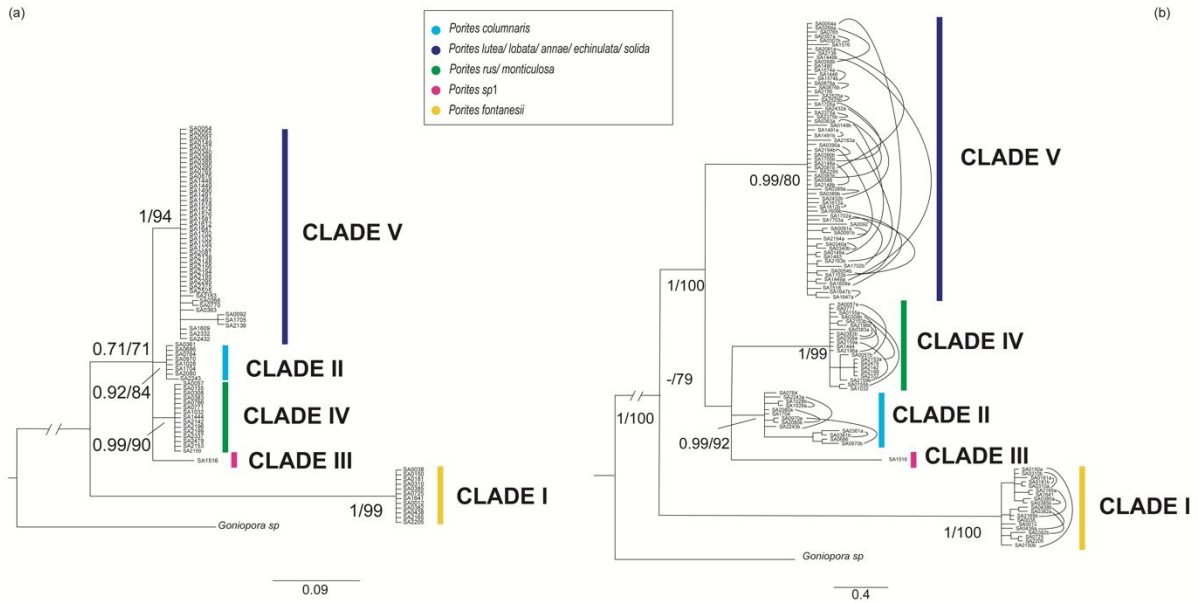
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928 **Figure 1**

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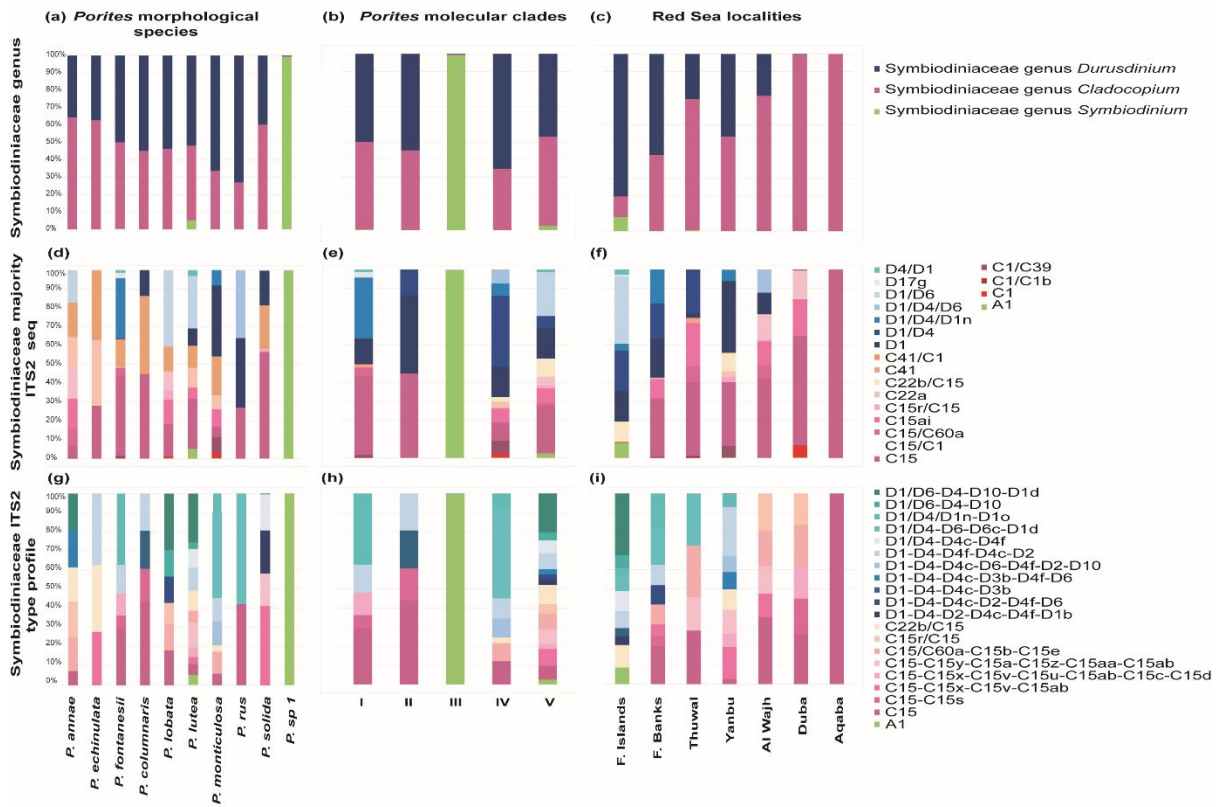
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931 **Figure 2**



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Figure 3



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SUPPORTING INFORMATION

Additional supporting Information may be found in the online version of this article.

Appendix S1 List of samples and relative collection and sequence data

Appendix S2 Details on molecular protocols

Appendix S3 *SymPortal* outputs and environmental data

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3 942 **Appendix S4** Bi-plot CAP ordination of *Porites* (divided for location, molecular clades and
4 943 morphological species) and Symbiodiniaceae clade (a-c), majority ITS2 sequence (d-f) and
5 944 ITS2 type profiles (g-i) in relation with the four environmental variables studied.
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7 946 **Appendix S5** PERMANOVA results calculated for the time of sampling (expressed as
8 947 month/year) for the datasets Symbiodiniaceae genus, Symbiodiniaceae majority ITS2
9 948 sequences, and Symbiodiniaceae ITS2 type profile. df = degrees of freedom.
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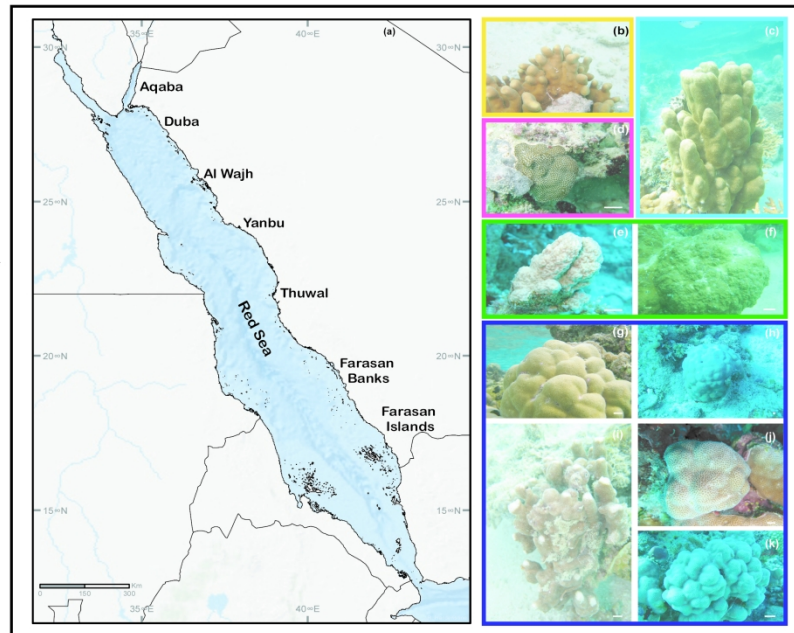


Figure 1 Sampling location and specimen collection overview (a) Red Sea map with sampling localities. (b) to (j) *Porites* morphologies encountered among our 80 collected samples. (b) *Porites fontanesii*, (c) *Porites columnaris*, (d) *Porites* sp1, (e) *Porites rus*, (f) *Porites monticulosa*, (g) *Porites lutea*, (h) *Porites lobata*, (i) *Porites annae*, (j) *Porites echinulata*, (k) *Porites solida*.

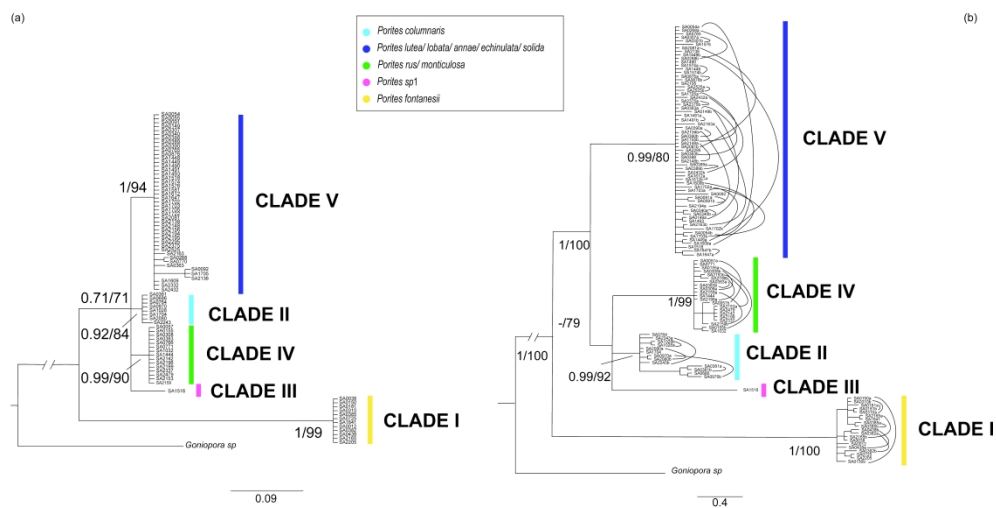


Figure 2 RAxML phylogeny reconstructions of Red Sea *Porites* at two molecular loci. (a) mitochondrial Control Region (b) nuclear Internal Transcribed Spaces region. Number on the branches represent support values corresponding to Bayesian posterior probabilities (>90%), ML bootstrap values (>70%). *Goniopora* was selected as outgroup in both the analyses. In (b) black curved lines connect the two sequences of heterozygotes individuals.

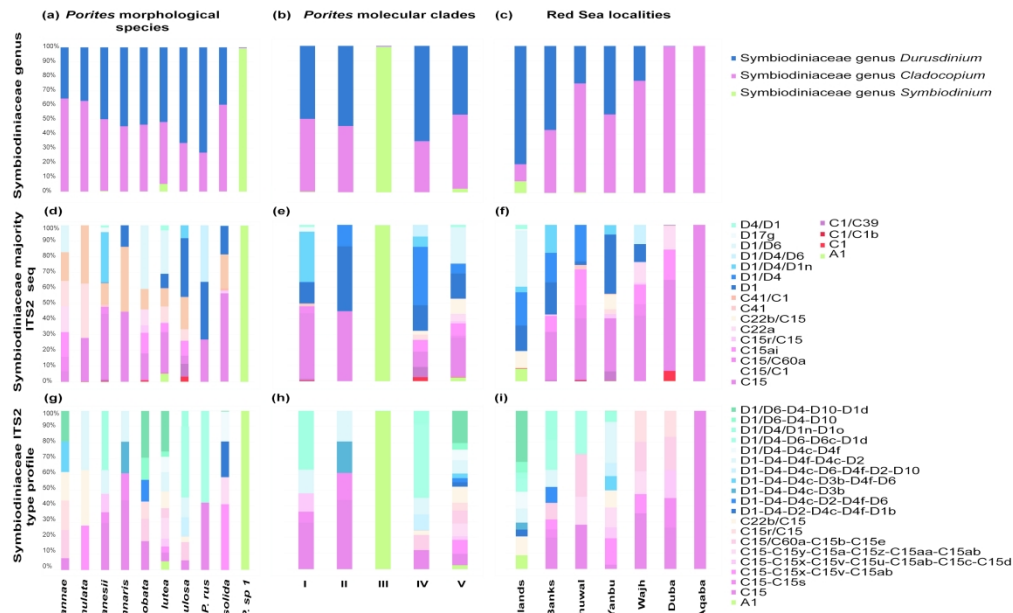


Figure 3 Stacked bar charts (100%) comparing Symbiodiniaceae diversity at the (a) (b) (c) genus level, (d) (e) (f) majority ITS2 sequence level (the 20 most abundant shown), (g) (h) (i) ITS2 type profile level (the 20 most abundant shown). For each of these three datasets, bar charts were plotted for three different factors: (a) (d) (g) *Porites* morphological species, (b) (e) (h) *Porites* molecular clade, (c) (f) (j) Red Sea localities.

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SUPPORTING INFORMATION

Environmental latitudinal gradients and host specificity shape Symbiodiniaceae distribution in Red Sea *Porites* corals

Tullia I. Terraneo, Marco Fusi, Benjamin C. C. Hume, Roberto Arrigoni, Christian R. Voolstra, Francesca Benzoni, Zac H. Forsman, Michael L. Berumen

Appendix S1 List of coral specimens examined in the study. For each sample, voucher code, morphological identified species, sampling locality, and GenBank accession numbers at each analysed locus are listed. SA stands for Saudi Arabian Red Sea, where the samples were collected.

Voucher code	Species	Date	Locality	Site GPS (degrees)	mtCR	ITS region	Molecular Clade
SA0970	<i>Porites columnaris</i>	30/09/2013	Aqaba	28.264, 34.855	MK902958	MK881231 MK881232	II
SA1028	<i>Porites columnaris</i>	30/09/2013	Aqaba	28.264, 34.855	MK902959	MK881233 MK881234	II
SA1032	<i>Porites monticulosa</i>	30/09/2013	Aqaba	28.264, 34.855	MK902960	MK881235	IV
SA0725	<i>Porites fontanesii</i>	26/09/2013	Duba	27.998, 35.204	MK902951	MK881223	I
SA0764	<i>Porites columnaris</i>	27/09/2013	Duba	27.998, 35.204	MK902952	MK881183 MK881224	II
SA0765	<i>Porites lutea</i>	27/09/2013	Duba	27.998, 35.204	MK902953	MK881225	V
SA0766	<i>Porites monticulosa</i>	27/09/2013	Duba	27.998, 35.204	MK902954	MK881226	IV
SA0770	<i>Porites lobata</i>	27/09/2013	Duba	27.998, 35.204	MK902955	MK881227	V
SA0771	<i>Porites rus</i>	27/09/2013	Duba	27.998, 35.204	MK902956	MK881228	IV
SA0876	<i>Porites annae</i>	28/09/2013	Duba	27.998, 35.204	MK902957	MK881229 MK881230	V
SA0686	<i>Porites columnaris</i>	25/09/2013	Al Wajh	25.345, 36.891	MK902950	MK881222	II
SA2243	<i>Porites columnaris</i>	31/01/2016	Al Wajh	25.345, 36.891	MK902997	MK881290 MK881291	II
SA2295	<i>Porites lutea</i>	31/01/2016	Al Wajh	25.345, 36.891	MK902998	MK881292	V

SA2332	<i>Porites annae</i>	01/02/2016	Al Wajh	25.345, 36.891	MK902999	MK881293	V
SA2337	<i>Porites rus</i>	01/02/2016	Al Wajh	25.345, 36.891	MK903000	MK881294	IV
SA2375	<i>Porites lutea</i>	02/02/2016	Al Wajh	25.345, 36.891	MK903001	MK881295 MK881296	V
SA2432	<i>Porites annae</i>	02/02/2016	Al Wajh	25.345, 36.891	MK903002	MK881297 MK881298	V
SA2479	<i>Porites monticulosa</i>	04/02/2016	Al Wajh	25.345, 36.891	MK903003	MK881299	IV
SA2525	<i>Porites solida</i>	04/02/2016	Al Wajh	25.345, 36.891	MK903004	MK881300 MK881301	V
SA2080	<i>Porites columnaris</i>	30/11/2015	Yanbu	24.101, 38.009	MK902981	MK881265 MK881266	II
SA2081	<i>Porites lutea</i>	30/11/2015	Yanbu	24.101, 38.009	MK902982	MK881267 MK881268	V
SA2136	<i>Porites solida</i>	30/11/2015	Yanbu	24.101, 38.009	MK902983	MK881269	V
SA2138	<i>Porites solida</i>	30/11/2015	Yanbu	24.101, 38.009	MK902984	MK881270	V
SA2142	<i>Porites monticulosa</i>	30/11/2015	Yanbu	24.101, 38.009	MK902985	MK881271	IV
SA2148	<i>Porites annae</i>	01/12/2015	Yanbu	24.101, 38.009	MK902986	MK881272 MK881273	V
SA2153	<i>Porites monticulosa</i>	01/12/2015	Yanbu	24.101, 38.009	MK902987	MK881274 MK881275	IV
SA2156	<i>Porites echinulata</i>	01/12/2015	Yanbu	24.101, 38.009	MK902988	MK881276	V
SA2159	<i>Porites monticulosa</i>	01/12/2015	Yanbu	24.101, 38.009	MK902989	MK881277 MK881278	IV

SA2163	<i>Porites lutea</i>	01/12/2015	Yanbu	24.101, 38.009	MK902990	MK881279 MK881280	V
SA2165	<i>Porites fontanesii</i>	01/12/2015	Yanbu	24.101, 38.009	MK902991	MK881281 MK881282	I
SA2194	<i>Porites lobata</i>	01/12/2015	Yanbu	24.101, 38.009	MK902992	MK881283 MK881284	V
SA2195	<i>Porites annae</i>	01/12/2015	Yanbu	24.101, 38.009	MK902993	MK881285	V
SA2196	<i>Porites monticulosa</i>	01/12/2015	Yanbu	24.101, 38.009	MK902994	MK881286 MK881287	IV
SA2199	<i>Porites monticulosa</i>	01/12/2015	Yanbu	24.101, 38.009	MK902995	MK881288	IV
SA2205	<i>Porites fontanesii</i>	01/12/2015	Yanbu	24.101, 38.009	MK902996	MK881289	I
SA0382	<i>Porites fontanesii</i>	16/03/2013	Thuwal	22.607, 38.918	MK902943	MK881209 MK881210	I
SA0383	<i>Porites monticulosa</i>	16/03/2013	Thuwal	22.607, 38.918	MK902944	MK881211 MK881212	IV
SA0385	<i>Porites fontanesii</i>	16/03/2013	Thuwal	22.607, 38.918	MK902945	MK881213 MK881214	I
SA0388	<i>Porites lutea</i>	16/03/2013	Thuwal	22.607, 38.918	MK902946	MK881215	V
SA0389	<i>Porites lutea</i>	16/03/2013	Thuwal	22.607, 38.918	MK902947	MK881216 MK881217	V
SA0390	<i>Porites annae</i>	16/03/2013	Thuwal	22.607, 38.918	MK902948	MK881218 MK881219	V
SA0438	<i>Porites fontanesii</i>	18/03/2013	Thuwal	22.607, 38.918	MK902949	MK881220 MK881221	I
SA0012	<i>Porites fontanesii</i>	03/03/2013	Farasan Banks	18.281, 41.445	MK902925	MK881177	I
SA0038	<i>Porites fontanesii</i>	04/03/2013	Farasan Banks	18.281, 41.445	MK902926	MK881178	I
SA0054	<i>Porites lobata</i>	04/03/2013	Farasan Banks	18.281, 41.445	MK902927	MK881179 MK881180	V
SA0055	<i>Porites lobata</i>	04/03/2013	Farasan Banks	18.281, 41.445	MK902928	MK881181	V
SA0057	<i>Porites monticulosa</i>	04/03/2013	Farasan Banks	18.281, 41.445	MK902929	MK881182 MK881302	IV
SA0091	<i>Porites echinulata</i>	05/03/2013	Farasan Banks	18.281, 41.445	MK902930	MK881184 MK881185	V
SA0092	<i>Porites lobata</i>	05/03/2013	Farasan Banks	18.281, 41.445	MK902931	MK881186	V
SA0149	<i>Porites solida</i>	06/03/2013	Farasan Banks	18.281, 41.445	MK902932	MK881187 MK881188	V
SA0150	<i>Porites fontanesii</i>	06/03/2013	Farasan Banks	18.281, 41.445	MK902933	MK881189 MK881190	I

SA0155	<i>Porites monticulosa</i>	06/03/2013	Farasan Banks	18.281, 41.445	MK902934	MK881191 MK881192	IV
SA0181	<i>Porites fontanesii</i>	06/03/2013	Farasan Banks	18.281, 41.445	MK902935	MK881193 MK881194	I
SA0268	<i>Porites lutea</i>	09/03/2013	Farasan Banks	18.281, 41.445	MK902936	MK881195 MK881196	V
SA0307	<i>Porites lutea</i>	09/03/2013	Farasan Banks	18.281, 41.445	MK902937	MK881197 MK881198	V
SA0308	<i>Porites monticulosa</i>	09/03/2013	Farasan Banks	18.281, 41.445	MK902938	MK881199 MK881200	IV
SA0310	<i>Porites fontanesii</i>	09/03/2013	Farasan Banks	18.281, 41.445	MK902939	MK881201 MK881202	I
SA0340	<i>Porites lutea</i>	10/03/2013	Farasan Banks	18.281, 41.445	MK902940	MK881203 MK881204	V
SA0361	<i>Porites columnaris</i>	11/03/2013	Farasan Banks	18.281, 41.445	MK902941	MK881205 MK881206	II
SA0363	<i>Porites lutea</i>	11/03/2013	Farasan Banks	18.281, 41.445	MK902942	MK881207 MK881208	V
SA1444	<i>Porites rus</i>	21/10/2014	Farasan Islands	16.971, 41.113	MK902961	MK881236	IV
SA1448	<i>Porites lutea</i>	21/10/2014	Farasan Islands	16.971, 41.113	MK902962	MK881237	V
SA1449	<i>Porites lutea</i>	21/10/2014	Farasan Islands	16.971, 41.113	MK902963	MK881238 MK881239	V
SA1490	<i>Porites solida</i>	22/10/2014	Farasan Islands	16.971, 41.113	MK902964	MK881240	V
SA1491	<i>Porites lutea</i>	22/10/2014	Farasan Islands	16.971, 41.113	MK902966	MK881241 MK881242	V
SA1493	<i>Porites lutea</i>	22/10/2014	Farasan Islands	16.971, 41.113	MK902967	MK881243	V
SA1516	<i>Porites</i> sp1	22/10/2014	Farasan Islands	16.971, 41.113	MK902968	MK881244	III
SA1518	<i>Porites annae</i>	22/10/2014	Farasan Islands	16.971, 41.113	MK902969	MK881245	V
SA1574	<i>Porites lutea</i>	23/10/2014	Farasan Islands	16.971, 41.113	MK902965	MK881246 MK881247	V
SA1576	<i>Porites lobata</i>	23/10/2014	Farasan Islands	16.971, 41.113	MK902970	MK881248	V
SA1581	<i>Porites echinulata</i>	23/10/2014	Farasan Islands	16.971, 41.113	MK902971	MK881249	V
SA1609	<i>Porites lobata</i>	23/10/2014	Farasan Islands	16.971, 41.113	MK902972	MK881250 MK881251	V
SA1612	<i>Porites lobata</i>	23/10/2014	Farasan Islands	16.971, 41.113	MK902973	MK881252 MK881253	V
SA1641	<i>Porites fontanesii</i>	24/10/2014	Farasan Islands	16.971, 41.113	MK902974	MK881254	I
SA1647	<i>Porites lobata</i>	24/10/2014	Farasan Islands	16.971, 41.113	MK902975	MK881255 MK881256	V
SA1702	<i>Porites lutea</i>	24/10/2014	Farasan Islands	16.971, 41.113	MK902976	MK881257 MK881258	V
SA1703	<i>Porites lutea</i>	24/10/2014	Farasan Islands	16.971, 41.113	MK902977	MK881259 MK881260	V
SA1704	<i>Porites columnaris</i>	24/10/2014	Farasan Islands	16.971, 41.113	MK902978	MK881261	II
SA1705	<i>Porites solida</i>	24/10/2014	Farasan Islands	16.971, 41.113	MK902979	MK881262 MK881263	V
SA1722	<i>Porites lutea</i>	25/10/2014	Farasan Islands	16.971, 41.113	MK902980	MK881264	V

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SUPPORTING INFORMATION

Environmental latitudinal gradients and host specificity shape Symbiodiniaceae distribution in Red Sea *Porites* corals

Tullia I. Terraneo, Marco Fusi, Benjamin C. C. Hume, Roberto Arrigoni, Christian R. Woolstra, Francesca Benzoni, Zac H. Forsman, Michael L. Berumen

Appendix S2 Details on molecular methods**Coral host DNA extraction and PCR amplification**

For the coral host, two loci were amplified via PCR: the putative mitochondrial control region (mtCR) and the ribosomal ITS region (ITS). The mtCR was amplified using the primers zpsRNAf (5'-AGCAGACGCGGTGAACTTA-3') and zpCOX3r (5'-GCCAAGTAACAGTACCC-3') newly designed in this study. The ITS region was amplified using primers ITSz1 (5'-TAAAAGTCGTAACAAGGTTTCCGTA-3') and ITSz2 (5'-CCT CCG CTT ATT GAT ATG CTT AAA T-3') (Forsman et al., 2009). All amplifications were conducted in a 15 µl volume, composed of 0.2 µM of each primer, 1X Multiplex PCR Master Mix (Qiagen Inc., Hilden, Germany), and <1 ng DNA. All PCR products were purified by adding 1.5 µl Illustra ExoStar (GE Healthcare, Buckinghamshire, UK), and incubating at 37° C for 60 min, followed by 85 ° C for 15 min, and directly sequenced in both forward and reverse directions using an ABI 3730xl DNA Analyzer (Applied Biosystems, Carlsbad, USA).

Symbiodiniaceae MiSeq sequencing library preparation

The primer sequences were (overhang adapter sequences underlined): 5'-TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAATTGCAGAACTCCGTG-3' (ITSintfor2) and 5'-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGATCCATATGCTTAAGTTTCAGCGGGT-3' (ITS2-reverse) (LaJeunesse, 2002). PCRs were run in triplicate per sample with 12.5 µl of Qiagen Multiplex PCR Kit (Qiagen, Hilden, Germany), 0.1 µM primers, 30 ng DNA, in a total volume of 25 µl. The following PCR conditions were used: 15 min at 94 °C, followed by 27 cycles of 94 °C for 30 s, 51 °C for 30 s, 72 °C for 30 s, and a final extension step of 10 min at 72 °C. PCR products were run on a 1 % agarose gel stained with 1x SYBR Safe (Invitrogen, Carlsbad, CA) to visualize successful amplification. The triplicate PCRs of each sample were pooled and cleaned with Agencourt AMPure XP magnetic bead system (Beckman Coulter, Brea, CA, USA). Nextera XT indexing and sequencing adapters were added via PCR (8 cycles) following the manufacturer's instructions. Samples were normalized and pooled using SequalPrep Normalization Plate Kit (ThermoFisher Scientific, Waltham, MA, USA). The samples were then quantified on Aligent BioAnalyzer 2100 (Agilent Technologies, Santa Clara, CA, USA) and qPCR (ThermoFisher Scientific, Waltham, MA, USA) to check library size and concentration. Libraries were sequenced using the Illumina MiSeq platform (Illumina, San Diego, CA, USA) and kit reagents v3 (2 x 300bp pair ended reads) at KAUST Core Lab (Thuwal, Saudi Arabia), following the manufacturer's protocol.

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Environmental latitudinal gradients and host specificity shape Symbiodiniaceae

Tullia I. Terraneo, Marco Fusi, Benjamin C. C. Hume, Roberto Arrigoni, Christian R. Voolstra, Frar

Appendix S3 SymPortal outputs and environmental data (DIVs proportions)

Samples	A1	A1c	A1a	A1k	A1l	C15
SA0012		0	0	0	0	0
SA0038		0	0	0	0	0.333
SA0054		0	0	0	0	0.629
SA0055		0	0	0	0	0.847
SA0057		0	0	0	0	0.006
SA0091		0	0	0	0	0
SA0092		0	0	0	0	0
SA0149		0	0	0	0	0.38
SA0150	0.013	0	0	0	0.001	0
SA0155	0	0	0	0	0	0
SA0181	0	0	0	0	0	0.814
SA0268	0	0	0	0	0	0.075
SA0307	0	0	0	0	0	0
SA0308	0	0	0	0	0	0
SA0310	0	0	0	0	0	0
SA0340	0	0	0	0	0	0
SA0361	0	0	0	0	0	0
SA0363	0	0	0	0	0	0
SA0382	0.007	0	0	0	0	0.185
SA0383	0	0	0	0	0	0
SA0385	0.006	0	0	0	0	0.393
SA0388	0	0	0	0	0	0.33
SA0389	0	0	0	0	0	0.457
SA0390	0.004	0	0	0	0	0.365
SA0438	0.005	0	0	0	0	0.19
SA0686	0	0	0	0	0	0.816
SA0725	0	0	0	0	0	0.454
SA0764	0	0	0	0	0	0.764
SA0765	0	0	0	0	0	0.275
SA0766	0.004	0	0	0	0	0.001
SA0770	0.004	0	0	0	0	0.211
SA0771	0	0	0	0	0	0.63
SA0876	0	0	0	0	0	0.643
SA0970	0	0	0	0	0	0.558
SA1028	0	0	0	0	0	0.608

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3	SA1032	0	0	0	0	0	0.451
4	SA1444	0	0	0	0	0	0
5	SA1448	0	0	0	0	0	0
6	SA1448	0	0	0	0	0	0
7	SA1449	0.413	0	0	0	0	0.002
8	SA1490	0	0	0	0	0	0
9	SA1491	0.394	0.001	0.001	0.002	0	0.016
10	SA1493	0	0	0	0	0	0
11	SA1516	0.956	0	0	0	0	0.001
12	SA1518	0	0	0	0	0	0
13	SA1518	0	0	0	0	0	0
14	SA1574	0	0	0	0	0	0
15	SA1574	0	0	0	0	0	0
16	SA1576	0	0	0	0	0	0
17	SA1576	0	0	0	0	0	0
18	SA1581	0.002	0	0	0	0	0.055
19	SA1609	0.002	0	0	0	0	0.001
20	SA1612	0	0	0	0	0	0
21	SA1641	0.003	0	0	0	0	0
22	SA1641	0.003	0	0	0	0	0
23	SA1647	0	0	0	0	0	0
24	SA1702	0	0	0	0	0	0
25	SA1702	0	0	0	0	0	0
26	SA1703	0	0	0	0	0	0.109
27	SA1704	0	0	0	0	0	0
28	SA1705	0	0	0	0	0	0
29	SA1705	0	0	0	0	0	0
30	SA1722	0	0	0	0	0	0
31	SA2080	0	0	0	0	0	0
32	SA2081	0.002	0	0	0	0	0.487
33	SA2081	0.002	0	0	0	0	0.487
34	SA2136	0	0	0	0	0	0.504
35	SA2138	0.005	0	0	0	0	0.368
36	SA2142	0	0	0	0	0	0
37	SA2142	0	0	0	0	0	0
38	SA2148	0	0	0	0	0	0
39	SA2153	0	0	0	0	0	0
40	SA2156	0	0	0	0	0	0.51
41	SA2156	0	0	0	0	0	0.51
42	SA2159	0	0	0	0	0	0
43	SA2163	0.001	0	0	0	0	0.517
44	SA2165	0	0	0	0	0	0.335
45	SA2165	0	0	0	0	0	0.335
46	SA2194	0.003	0	0	0	0	0.287
47	SA2195	0	0	0	0	0	0.827
48	SA2196	0.006	0	0	0	0	0.226
49	SA2196	0.006	0	0	0	0	0.226
50	SA2199	0	0	0	0	0	0.002
51	SA2205	0	0	0	0	0	0
52	SA2243	0.003	0.001	0	0	0	0.002
53	SA2243	0.003	0.001	0	0	0	0.002
54	SA2295	0.004	0.001	0	0	0	0.805
55	SA2332	0	0	0	0	0	0.406
56	SA2337	0	0	0	0	0	0
57	SA2337	0	0	0	0	0	0
58	SA2375	0	0	0	0	0	0.451
59	SA2432	0	0	0	0	0	0.186
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3	SA2479	0	0	0	0	0	0.422
4	SA2525	0	0	0	0	0	0.545
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6 **distribution in Red Sea *Porites* corals**

7 ncesca Benzoni, Zac H. Forsman, Michael L. Berumen
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13	C22b	C1	C15ai	C22a	C15x	C15b	C15v
14		0	0.002	0	0	0	0
15		0	0.001	0	0	0.051	0
16		0	0	0	0	0	0
17		0	0	0	0	0.15	0
18		0	0	0.014	0	0	0
19		0	0	0	0	0	0
20		0	0	0	0	0	0
21		0	0	0	0	0	0
22		0	0	0	0	0	0
23		0	0	0	0	0	0
24		0	0	0.077	0	0.096	0.048
25		0	0.028	0	0	0	0
26		0	0.004	0	0	0	0
27		0	0	0	0	0.017	0.017
28		0	0	0	0	0	0
29	0.768	0.001	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0.011	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0.003	0	0	0	0	0
38	0	0.016	0	0	0.014	0	0.047
39	0	0	0	0	0	0	0
40	0	0.009	0	0	0.013	0	0.031
41	0	0	0	0	0.001	0.123	0
42	0	0	0	0	0.047	0	0.038
43	0	0	0	0	0.004	0	0.013
44	0	0.003	0	0	0.009	0	0.033
45	0	0.043	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0.007	0	0	0.003	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0.133	0	0.111
50	0	0	0	0	0	0	0
51	0	0.286	0	0	0	0	0
52	0	0.002	0	0	0.009	0	0.017
53	0	0	0	0	0.02	0	0.008
54	0	0.001	0	0	0	0.151	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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3		0.001	0	0	0.012	0	0.005
4		0	0	0	0	0	0
5		0	0	0	0	0	0
6		0	0	0	0	0	0
7		0.003	0	0	0	0	0
8		0	0	0	0	0	0
9		0	0	0	0	0	0
10	0.002	0.002	0	0	0.001	0	0
11		0	0	0	0	0	0
12		0.001	0	0	0	0	0
13		0	0	0	0	0	0
14		0	0	0	0	0	0
15		0.002	0	0	0	0	0
16		0	0	0	0	0	0
17		0	0	0	0	0	0
18	0.791	0.001	0	0	0	0	0
19		0.022	0	0	0	0	0
20		0.001	0	0	0	0	0
21		0.004	0	0	0	0	0
22		0.004	0	0	0	0	0
23		0	0	0	0	0	0
24		0	0	0	0	0	0
25		0	0	0	0	0	0
26	0.606	0.002	0	0	0	0	0
27	0.002	0.002	0	0	0	0	0
28		0	0	0	0	0	0
29		0	0	0	0	0	0
30		0	0	0	0	0	0
31		0.001	0	0	0	0	0
32		0	0	0	0.028	0	0.03
33		0	0	0	0.093	0	0.028
34		0	0	0	0.04	0	0.03
35		0.018	0	0	0	0	0
36		0.366	0	0	0	0	0
37		0	0	0	0	0	0
38		0.002	0	0	0	0	0
39		0.003	0	0	0.08	0	0.028
40		0	0	0	0	0	0
41		0.001	0	0	0.008	0	0.03
42		0.006	0	0	0.126	0	0.081
43		0.001	0.318	0	0.067	0	0.045
44	0.047	0	0.012	0	0	0	0
45	0.046	0.002	0	0.378	0	0	0
46		0.001	0	0	0	0	0
47		0.006	0	0	0	0	0
48		0.002	0	0	0	0	0
49		0	0	0	0	0	0
50		0	0	0	0.001	0	0
51		0	0	0	0	0	0
52		0	0	0	0	0	0
53		0	0	0	0	0	0
54		0	0	0	0.001	0	0
55		0	0	0	0	0	0
56		0	0.077	0	0.066	0	0.035
57		0	0	0	0.007	0	0.009
58		0.289	0	0	0	0	0
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0	0.003	0	0	0	0.28	0
0	0	0	0	0.059	0	0.016

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	C15u	C116	C1b	C15a	C15ah	C15c	C15w	
		0	0.001	0.001	0	0	0	0
	0.004		0	0.001	0	0	0.005	0
	0		0	0	0	0	0	0
	0		0	0	0	0	0	0.005
	0		0	0	0	0	0	0
	0		0	0	0	0	0	0
	0		0	0	0	0	0	0
	0.015		0	0	0	0.015	0	0
	0		0	0.012	0	0	0	0
	0		0	0.002	0	0	0	0
	0.001		0	0	0	0.007	0	0
	0		0	0.001	0.008	0	0	0.007
	0		0	0	0	0	0	0
	0		0	0	0	0	0	0
	0		0	0	0	0	0	0
	0		0	0.005	0	0	0	0
	0		0	0	0	0	0	0
	0		0	0	0	0	0	0
	0.046		0	0.006	0	0.089	0.071	0
	0		0	0	0	0	0	0
	0.056		0	0.004	0	0.133	0	0
	0		0	0	0	0	0	0
	0.114		0	0	0.032	0.008	0	0.013
	0.012		0	0.001	0	0.092	0.015	0
	0.025		0	0.017	0	0.099	0.012	0
	0		0	0	0	0	0	0
	0.008		0	0.002	0	0	0	0
	0		0	0	0	0	0	0
	0.074		0	0	0.037	0.006	0.052	0
	0		0	0.001	0	0	0	0
	0.002		0	0	0.001	0	0	0
	0.006		0	0	0.109	0.003	0	0
	0		0	0.001	0	0	0	0
	0		0	0	0	0	0	0
	0		0	0	0	0	0	0

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3	0.001	0	0	0.017	0.004	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0.001	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0.001	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0.001	0.043	0	0	0
19	0	0	0.008	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0.002	0	0	0	0
22	0	0	0.003	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0.001	0.036	0	0	0.001
26	0	0	0.001	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0.039	0	0	0.047	0.009	0	0.014
33	0.02	0	0	0.034	0.011	0	0.005
34	0.012	0	0.006	0.018	0.013	0	0.02
35	0	0	0.129	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0.001	0	0	0	0
39	0.014	0	0.001	0.004	0.012	0.004	0
40	0	0	0	0	0	0	0
41	0.035	0	0.001	0.049	0.009	0	0.025
42	0.053	0	0.002	0.02	0.007	0.038	0
43	0	0	0	0	0.008	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0.038	0	0	0.018
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0.002	0	0	0	0
49	0	0	0.001	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0.008	0	0	0	0.015	0	0
58	0.002	0	0.013	0	0.033	0.015	0
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3	0	0	0	0	0	0	0
4	0.019	0	0	0.031	0	0	0.012
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C15y	C91f	C15z	C15e	C15g	C15ab	C15s	
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0.103
	0	0	0	0.043	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0.007	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.004	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.015	0	0	0	0
	0	0	0	0.043	0	0	0
	0.034	0	0.028	0	0	0.013	0
	0	0.001	0.001	0	0	0	0
	0	0	0.001	0	0	0	0
	0	0	0	0	0	0.005	0.003
	0	0.001	0	0	0	0	0
	0	0	0	0	0.041	0	0.008
	0	0	0.003	0	0	0.049	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0.001	0
	0.001	0	0	0	0	0.132	0
	0	0	0	0.027	0	0	0
	0	0	0	0	0.103	0	0
	0	0	0	0	0.255	0	0

1							
2							
3	0.001	0	0	0	0	0.007	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0.002	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0.004	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0.04
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0.024	0	0.032	0	0.001	0.033	0
33	0.016	0	0.019	0	0	0.031	0
34	0.006	0.061	0.025	0	0	0.007	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0.006	0	0	0.063	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0.019	0	0.035	0	0	0.028	0
44	0	0	0	0	0	0.061	0
45	0	0	0	0	0	0.001	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0.045	0	0
55	0	0	0.002	0	0	0	0.006
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0.01	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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2							
3	0	0	0	0.032	0	0	0
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5	0.03	0	0.025	0	0	0.016	0
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C3	C15aa	C15h	C60a	C39	C41	C41a	
	0	0	0	0	0	0	0.001
	0	0	0	0	0	0	0
	0	0	0	0.055	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.007	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0.002	0	0	0	0.005	0.003	0.001
	0	0	0	0	0.001	0.001	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0.001	0.001	0
	0	0	0	0	0	0	0
	0	0	0	0	0.005	0.113	0
	0	0	0	0	0	0	0
	0.001	0	0	0	0.003	0.004	0
	0	0	0	0.404	0	0.001	0
	0	0.031	0	0	0	0	0
	0.001	0	0	0	0.001	0.001	0
	0.001	0	0	0	0.007	0.008	0.019
	0	0	0	0	0	0	0
	0	0	0	0	0.002	0.008	0
	0	0	0	0	0	0	0
	0	0.005	0	0	0	0	0
	0.017	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0.042	0	0	0
	0	0	0.014	0	0	0	0
	0	0	0.001	0	0	0	0

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3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0.001	0	0
8	0	0	0	0	0	0	0
9	0	0	0.001	0	0.001	0.001	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0.001	0
12	0	0	0	0	0	0	0.001
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0.001
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0.001
17	0	0	0	0	0	0.001	0
18	0.001	0	0	0	0.002	0.007	0.003
19	0	0	0	0	0	0	0
20	0.001	0	0	0	0.001	0.001	0.001
21	0	0	0	0	0.001	0	0.001
22	0	0	0	0	0	0	0
23	0	0	0	0	0.001	0.001	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0.001	0.001	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0.004	0	0	0	0	0	0
31	0	0.03	0	0	0	0	0
32	0	0.009	0	0	0	0	0
33	0.001	0.021	0	0	0.003	0.032	0.001
34	0.005	0	0	0	0.104	0.118	0.002
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0.008	0	0	0.004	0.001	0
38	0	0	0	0	0	0	0
39	0	0.033	0	0	0	0.001	0
40	0	0	0	0	0.002	0.002	0
41	0.002	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0.001	0	0	0	0	0.001	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0.001	0.001	0
46	0	0	0.026	0	0.001	0	0
47	0	0	0.001	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0.003	0	0	0	0.012	0.003	0.001
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4	0	0	0	0.12	0	0	0
5	0	0.024	0	0	0	0	0
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	C15d	C1c	C41f	C93a	C1g	C15i	C1af	
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0.007	0	0	0	0	0	0
		0	0	0.001	0	0.013	0	0
		0	0	0.001	0	0.002	0	0
		0.002	0	0	0	0	0.001	0
		0	0	0	0	0.001	0.001	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0.007	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0.005	0	0.001	0.001
		0	0	0	0	0	0	0
		0.01	0	0	0	0	0.001	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0.002	0	0	0.002	0	0.002	0
		0	0	0.008	0.009	0	0.004	0.001
		0	0	0	0	0	0	0
		0	0	0	0.006	0	0.002	0
		0	0	0	0	0	0	0
		0.045	0	0	0	0	0	0
		0	0.014	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0.001	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0

1							
2							
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0.006	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0.001	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0.005	0	0	0	0.001
20	0	0	0	0	0	0	0
21	0	0	0.001	0	0	0	0
22	0	0	0.001	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0.001	0	0.002	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0.001	0	0	0	0	0	0
35	0.019	0	0.004	0	0	0	0.001
36	0	0	0.004	0	0	0	0.007
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0.002	0	0	0.007	0	0.002	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0.035	0	0	0.001	0	0.001	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0.004	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0.007	0	0	0	0	0	0
58	0.002	0	0.002	0.015	0	0.012	0
59							
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0	0	0	0.002	0	0	0
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C72	C91e	C93b	C1a	C15r	C15j	C39a	
	0	0	0	0	0	0	0
	0	0	0.001	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.001	0	0	0	0
	0	0	0.001	0	0.006	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.001	0.001	0	0	0
	0	0	0	0	0	0	0
	0	0	0.001	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0.011	0	0.001	0	0	0	0
	0	0	0.007	0.001	0	0	0.001
	0	0	0	0	0	0	0
	0	0	0.003	0	0.001	0	0
	0	0	0	0	0.001	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0.002	0	0	0	0.47	0	0
	0	0	0	0	0.001	0	0
	0	0	0.001	0	0.001	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0

1							
2							
3	0	0	0.001	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0.001	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0.005	0	0	0	0.002	0	0
11	0.001	0	0	0	0	0	0
12	0.001	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0.001	0	0	0	0.002	0	0
19	0.001	0	0	0	0	0	0.001
20	0	0.007	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0.002	0	0.007	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0.014	0	0	0	0.001	0	0
36	0	0	0	0.003	0	0	0.005
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0.003	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0.001	0	0	0	0	0	0
44	0.001	0	0.002	0	0	0	0
45	0	0	0	0	0.001	0	0
46	0	0	0	0	0.003	0	0
47	0	0	0	0	0.003	0	0
48	0.001	0	0	0	0.003	0	0
49	0.001	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0.006	0
53	0	0	0	0	0.001	0	0
54	0	0	0	0	0.5	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0.031	0.003	0	0	0
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3	0	0	0.002	0	0	0	0
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5	0.001	0	0	0	0.001	0	0
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C1f	C116d	C66	C3u	C1n	C21	C41e	
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
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	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0.001
	0	0	0	0	0	0	0.001
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
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	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0.001
	0	0	0	0.003	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0.005	0	0	0.004	0.001	0	0.004
	0	0	0	0	0	0	0
	0	0	0	0.003	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.004	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0.001	0	0	0
	0	0	0	0	0	0	0
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3		0	0	0	0	0	0
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5		0	0	0	0	0	0
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7		0	0	0	0	0	0
8		0	0	0	0	0	0
9		0	0	0	0	0	0
10		0	0	0	0	0	0
11		0	0	0	0	0	0
12		0	0	0	0	0	0
13		0	0	0	0	0	0
14		0	0	0	0	0	0
15		0	0	0	0	0	0
16		0	0	0	0	0	0
17		0	0	0	0	0	0
18		0	0	0	0	0	0
19	0.005	0	0	0	0	0	0.006
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0.001
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0.001	0	0	0
34	0	0	0	0	0	0.001	0.001
35	0.001	0	0	0	0	0	0.008
36	0.004	0	0	0	0.006	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0.003	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0.001	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0.001	0	0	0.01	0.001	0	0.001
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4	0	0	0	0.001	0	0	0	0
5	0	0	0	0	0	0	0	0
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	C72a	C1ae	C15ac	C41b	C39c	C15m	C3az	
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14		0	0.001	0	0	0	0	0
15		0	0	0	0	0	0	0
16		0	0	0	0	0	0	0
17		0	0	0	0	0	0	0
18		0	0	0	0	0	0	0
19		0	0	0	0	0	0	0
20		0	0	0	0	0	0	0
21		0	0	0	0	0	0	0
22		0	0	0	0	0	0	0
23		0	0	0	0	0	0	0
24		0	0	0	0	0	0	0
25		0	0.002	0	0	0	0	0
26		0	0	0	0	0	0	0
27		0	0	0	0	0	0	0
28		0	0	0	0	0	0	0
29		0	0	0	0	0	0	0
30		0	0	0	0	0	0	0
31		0	0	0	0	0	0	0
32		0	0	0	0	0	0	0
33		0	0	0	0	0	0	0
34		0	0.001	0	0	0	0	0
35		0	0	0	0	0	0	0
36		0	0	0	0	0	0	0
37		0	0	0	0	0	0	0
38		0	0	0	0.009	0	0.001	0
39		0	0	0	0	0	0	0
40		0	0	0	0	0	0.001	0
41		0	0	0	0	0	0	0
42		0	0	0	0	0	0	0
43		0	0	0	0	0	0	0
44		0	0	0	0	0	0	0
45		0	0	0	0	0	0	0
46		0	0.006	0	0	0	0	0
47		0	0	0	0	0	0	0
48		0	0	0	0	0	0	0
49		0	0	0	0.002	0	0	0
50		0	0	0	0	0	0	0
51		0	0	0	0	0	0	0
52		0	0	0	0	0	0	0
53		0	0	0	0	0	0	0
54		0	0	0	0	0	0	0
55		0	0	0	0	0	0	0
56		0	0	0	0	0	0	0
57		0	0	0	0	0	0	0
58		0	0	0	0	0	0	0
59		0	0	0	0	0	0	0
60		0	0	0	0	0	0	0

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3	0	0	0	0	0	0	0
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9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0.004	0	0.002	0	0	0
20	0	0	0	0	0	0	0
21	0	0.001	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
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25	0	0	0	0	0	0	0
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32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0.001	0	0.001	0	0	0
36	0	0.025	0	0	0	0	0.001
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
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49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0.001	0	0	0	0	0.001
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3			0.002				
4	0	0		0	0	0	0
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	C72c	C115	C3au	C72b	C41c	C72d	C163b	
14		0	0	0	0	0	0	0
15		0	0	0	0	0	0	0
16		0	0	0	0	0	0	0
17		0	0	0	0	0	0	0
18		0	0	0	0	0	0	0
19		0	0	0	0	0	0	0
20		0	0	0	0	0	0	0
21		0	0	0	0	0	0	0
22		0	0	0	0	0	0	0
23		0	0	0	0	0	0	0
24		0	0	0	0	0	0	0
25		0	0	0	0	0	0	0
26		0	0	0	0	0	0	0
27		0	0	0	0	0	0	0
28		0	0	0	0	0	0	0
29		0	0	0	0	0	0	0
30		0	0	0	0	0	0	0
31		0	0	0	0	0	0	0
32		0	0	0	0	0	0	0
33		0	0	0	0	0	0	0
34		0	0	0	0	0	0	0
35		0	0	0	0	0	0	0
36		0	0	0	0	0	0	0
37		0	0	0	0	0	0	0
38		0	0	0.001	0	0	0	0
39		0	0	0	0	0	0	0
40		0	0	0	0	0	0	0
41		0	0	0	0	0	0	0
42		0	0	0	0	0	0	0
43		0	0	0	0	0	0	0
44		0	0	0	0	0	0	0
45		0	0	0	0	0	0	0
46		0	0	0	0	0	0	0
47		0	0	0	0	0	0	0
48		0	0	0	0	0	0	0
49		0	0	0	0	0	0	0
50		0	0	0	0	0	0	0
51		0	0	0	0	0	0	0
52		0	0	0	0	0	0	0
53		0	0	0	0	0	0	0
54		0	0	0	0	0	0	0
55		0	0	0	0	0	0	0
56		0	0	0	0	0	0	0
57		0	0	0	0	0	0	0
58		0	0	0	0	0	0	0
59		0	0	0	0	0	0	0

For Peer Review

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3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
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30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
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35	0	0	0	0	0	0	0
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40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
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51	0	0	0	0	0	0	0
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57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0.001	0	0	0	0	0
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35	0.001	0	0	0	0	0	0
36	0	0	0	0	0.002	0	0
37	0	0	0	0	0	0	0
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39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
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57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0.001	0	0
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	C15k	C39b	C1i	C91	C40	C29	C15.8	
		0	0	0	0	0	0	0
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		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0.001	0	0	0
		0	0	0	0	0	0	0
		0	0	0	0	0	0	0
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		0	0	0	0	0	0	0
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		0	0	0	0	0	0	0
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		0	0	0	0	0	0	0
	0.001		0	0	0	0	0	0
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3	0	0	0	0	0	0	0
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47	0	0	0	0	0	0	0
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57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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For Peer Review

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	C116g	C89	C3bl	D1	D4	D6	D17g	
13								
14		0	0	0	0.238	0.242	0	0
15		0	0	0	0	0	0	0
16		0	0	0	0	0	0	0
17		0	0	0	0	0	0	0
18		0	0	0	0	0	0	0
19		0	0	0	0.361	0.222	0.207	0
20		0	0	0	0.551	0.168	0.002	0
21		0	0	0	0.543	0.113	0.029	0
22		0	0	0	0	0	0	0
23		0	0	0	0	0	0	0
24		0	0	0	0.342	0.221	0	0
25		0	0	0	0.265	0.209	0.215	0
26		0	0	0	0	0	0	0
27		0	0	0	0	0	0	0
28		0	0	0	0	0	0	0
29		0	0	0	0.369	0.248	0.256	0
30		0	0	0	0.271	0.235	0.25	0
31		0	0	0	0.053	0.048	0	0.208
32		0	0	0	0.539	0.218	0	0
33		0	0	0	0.326	0.276	0.001	0
34		0	0	0	0.46	0.269	0	0
35		0	0	0	0.014	0.009	0	0
36		0	0	0	0.392	0.238	0.223	0
37		0	0	0	0.008	0.007	0.005	0
38		0	0	0	0	0	0	0
39		0	0	0	0	0	0	0
40		0	0	0	0	0	0	0
41		0	0	0	0	0	0	0
42		0	0	0	0.028	0.021	0	0
43		0	0	0	0.004	0.002	0	0
44		0	0	0	0	0	0	0
45		0	0	0	0	0	0	0
46		0	0	0	0	0	0	0
47		0	0	0	0	0	0	0
48		0	0	0	0	0	0	0
49		0	0	0	0	0	0	0
50		0	0	0	0	0	0	0
51		0	0	0	0	0	0	0
52		0	0	0	0	0	0	0
53		0	0	0	0	0	0	0
54		0	0	0	0.006	0.002	0.001	0
55		0	0	0	0	0	0	0
56		0	0	0	0	0	0	0
57		0	0	0	0	0	0	0
58		0	0	0	0	0	0	0
59		0	0	0	0	0	0	0
60		0	0	0	0	0	0	0

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2							
3	0	0	0	0	0	0	0
4	0	0	0	0.41	0.192	0.191	0
5	0	0	0	0.258	0.431	0	0
6	0	0	0	0.26	0.051	0.14	0
7	0	0	0	0.292	0.402	0	0
8	0	0	0	0.112	0.368	0.003	0
9	0	0	0	0.26	0.398	0	0
10	0	0	0	0.001	0	0	0
11	0	0	0	0.364	0.239	0.278	0
12	0	0	0	0.354	0.238	0.261	0
13	0	0	0	0.354	0.213	0.296	0
14	0	0	0	0.002	0.002	0.001	0
15	0	0	0	0.329	0.219	0.267	0
16	0	0	0	0.29	0.102	0.44	0
17	0	0	0	0.316	0.341	0.008	0
18	0	0	0	0.268	0.198	0.367	0
19	0	0	0	0.442	0.231	0.213	0
20	0	0	0	0.021	0.013	0.011	0
21	0	0	0	0.649	0.185	0	0
22	0	0	0	0.421	0.177	0	0
23	0	0	0	0.295	0.124	0.373	0
24	0	0	0	0.665	0.145	0	0
25	0	0	0	0.001	0.001	0.001	0
26	0	0	0	0	0	0	0
27	0	0	0	0.006	0.004	0.003	0
28	0	0.001	0	0.004	0.002	0	0
29	0	0	0	0.619	0.265	0.009	0
30	0	0	0	0.612	0.14	0.032	0
31	0	0	0	0	0	0	0
32	0	0	0	0.616	0.156	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0.003	0.002	0.001	0
36	0	0	0	0	0	0	0
37	0	0	0	0.004	0.001	0	0
38	0	0	0	0.325	0.261	0.001	0
39	0	0	0	0.554	0.228	0	0
40	0	0	0	0.499	0.095	0.008	0
41	0	0	0	0	0	0	0
42	0	0	0	0.002	0.001	0	0
43	0	0	0	0.389	0.258	0.188	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0.002	0.001	0	0
47	0	0	0	0.389	0.258	0.188	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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3	0	0	0	0	0	0	0
4	0	0.003	0	0	0	0	0.03
5	0	0	0	0.016	0.008	0	0
6	0	0.046	0	0.002	0	0	0.003
7	0.002	0	0	0.025	0.02	0	0
8	0	0	0	0.003	0	0	0
9	0.001	0	0	0.027	0.012	0	0
10	0	0	0	0	0	0	0
11	0	0.035	0	0	0	0	0
12	0	0.068	0	0	0	0	0.002
13	0	0.046	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0.048	0	0	0	0	0
16	0	0.072	0	0	0	0	0
17	0.084	0.002	0.025	0.01	0	0.043	0
18	0	0.068	0	0	0	0	0
19	0	0.033	0	0	0	0	0
20	0	0.002	0	0	0	0	0
21	0	0	0	0.039	0.016	0	0
22	0	0	0.123	0.084	0.05	0	0
23	0	0.104	0	0	0	0	0
24	0	0	0.017	0.011	0.036	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0.001	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0.005	0	0.001	0.011	0.012	0	0.002
30	0	0.014	0.022	0.026	0.037	0	0.002
31	0	0	0	0	0	0	0
32	0	0	0.033	0.011	0.112	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0.005	0	0.001	0.011	0.012	0	0.002
39	0	0.014	0.022	0.026	0.037	0	0.002
40	0	0	0	0	0	0	0
41	0	0	0.033	0.011	0.112	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0.118	0	0.016	0.002	0	0.025	0
50	0	0	0.014	0.071	0.063	0	0
51	0	0	0.003	0.027	0.14	0	0.001
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0.003	0	0	0	0	0.002
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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3	0	0	0	0	0	0	0
4	0.033	0	0	0	0.015	0	0
5	0	0	0	0	0	0.004	0
6	0.002	0	0	0.001	0.002	0	0
7	0	0	0	0	0	0.005	0
8	0.001	0	0	0	0	0	0
9	0	0	0	0	0	0.001	0
10	0	0	0	0	0	0	0
11	0.018	0	0	0.01	0	0	0
12	0.012	0	0	0.006	0.002	0	0
13	0.012	0	0	0.012	0.001	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0.002	0	0	0
16	0.009	0	0	0.003	0	0	0
17	0	0	0.003	0	0	0.002	0
18	0.021	0	0	0.004	0	0	0
19	0.025	0	0	0.007	0	0	0
20	0.002	0	0	0	0	0	0
21	0	0.025	0	0	0	0.013	0
22	0	0	0	0	0	0.028	0
23	0.005	0	0	0.005	0	0	0
24	0	0	0.009	0	0	0.004	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0.019	0	0	0.003	0.009	0
32	0.02	0.011	0.001	0	0.002	0.006	0
33	0	0	0	0	0	0	0
34	0	0	0.011	0	0	0.009	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0.003	0	0	0	0.005
42	0	0	0	0	0	0.035	0
43	0	0	0	0	0.001	0.015	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0.003	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0.089	0	0	0	0.002	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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3	0	0	0	0	0	0	0
4	0	0	0	0	0	0.023	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0.001
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
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12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
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18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0.002
20	0	0	0	0	0	0	0.001
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0.003	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0.002	0	0	0	0	0
28	0	0	0.003	0	0	0.025	0
29	0	0	0	0	0	0	0.002
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0.015	0	0.006	0	0	0
39	0.007	0.001	0	0	0	0	0.003
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0.007	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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	D1q	D1j	D4b	D1i	D1r	D2a	D1k	
14		0	0	0	0	0	0	0
15		0	0	0	0	0	0	0
16		0	0	0	0	0	0	0
17		0	0	0	0	0	0	0
18		0	0	0	0	0	0	0
19		0	0	0	0	0	0.001	0
20		0	0	0.001	0	0	0.001	0
21		0.004	0	0	0	0	0	0
22		0	0	0	0	0	0	0
23		0	0	0	0	0	0	0
24		0	0	0	0	0	0	0
25		0	0	0	0	0	0	0
26		0	0	0	0	0	0.001	0
27		0	0	0	0	0	0	0
28		0	0	0	0	0	0	0
29		0	0	0	0	0	0	0
30		0	0	0	0	0	0	0
31		0	0	0	0	0	0.002	0
32		0	0	0	0	0	0	0
33		0	0	0	0	0	0	0
34		0	0	0	0	0	0	0
35		0	0	0	0	0	0	0
36		0	0	0	0	0	0	0
37		0	0	0	0	0	0	0
38		0	0	0	0	0	0	0
39		0	0	0	0	0	0	0
40		0	0	0	0	0	0	0
41		0	0	0	0	0	0	0
42		0	0	0	0	0	0	0
43		0	0	0	0	0	0	0
44		0	0	0	0	0	0	0
45		0	0	0	0	0	0	0
46		0	0	0	0	0	0	0
47		0	0	0	0	0	0	0
48		0	0	0	0	0	0	0
49		0	0	0	0	0	0	0
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51		0	0	0	0	0	0	0
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55		0	0	0	0	0	0	0
56		0	0	0	0	0	0	0
57		0	0	0	0	0	0	0
58		0	0	0	0	0	0	0
59		0	0	0	0	0	0	0
60		0	0	0	0	0	0	0

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3	0	0	0	0	0	0	0
4	0	0	0	0	0	0.001	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0.001	0	0	0	0.001	0	0
8	0	0	0	0	0	0.001	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0.001	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0.002	0	0	0	0	0	0
16	0.001	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0.001	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0.002	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0.001	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0.001	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0
53	0	0	0	0	0	0	0
54	0	0	0	0	0	0	0
55	0	0	0	0	0	0	0
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57	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0
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3	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0
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8	0	0	0	0	0	0	0	0
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10	0	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0
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20	0	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0
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25	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0
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29	0	0	0	0	0	0	0	0
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39	0	0	0	0	0	0	0	0
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41	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0
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44	0	0	0	0	0	0	0	0
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48	0	0	0	0	0	0	0	0
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50	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0
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54	0	0	0	0	0	0	0	0
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56	0	0	0	0	0	0	0	0
57	0	0	0	0	0	0	0	0
58	0	0	0	0	0	0	0	0
59	0	0	0	0	0	0	0	0
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14	0.003	0	0.002	0.128
15	0.002	0	0.498	0.001
16	0	0	0.12	0.002
17	0.002	0	0.132	0
18	0.004	0	0.003	0.142
19	0.001	0	0.001	0.045
20	0.003	0	0.001	0.116
21	0	0	0.352	0.001
22	0.004	0	0.017	0.199
23	0.002	0	0.004	0.206
24	0	0	0.139	0.001
25	0.003	0	0.128	0
26	0.001	0	0	0.07
27	0.002	0	0.001	0.162
28	0.001	0	0.001	0.583
29	0	0	0.012	0.015
30	0	0	0.002	0.103
31	0	0	0.002	0.047
32	0.005	0	0.333	0.003
33	0	0	0.001	0.105
34	0.003	0	0.292	0.001
35	0.001	0	0.096	0.001
36	0.001	0	0.183	0.001
37	0.001	0	0.401	0.007
38	0.002	0	0.465	0.001
39	0	0	0.174	0
40	0.003	0	0.497	0.001
41	0.003	0	0.182	0
42	0.001	0	0.209	0
43	0.002	0	0.669	0.001
44	0.001	0	0.267	0.001
45	0.001	0	0.088	0
46	0.001	0	0.13	0
47	0	0	0.323	0
48	0.002	0	0.132	0

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3	0.001	0	0.498	0.001
4	0.001	0	0.001	0.102
5	0.001	0	0.001	0.102
6	0	0	0.002	0.28
7	0.005	0	0.004	0.054
8	0.001	0	0.001	0.252
9	0.001	0	0.001	0.252
10	0.003	0	0.022	0.056
11	0.002	0	0.002	0.294
12	0.033	0	0.003	0.001
13	0.033	0	0.003	0.001
14	0	0	0.001	0.056
15	0.001	0	0.001	0.047
16	0.001	0	0.001	0.047
17	0	0	0	0.063
18	0	0	0.096	0.001
19	0.001	0	0.013	0.047
20	0.001	0	0.01	0.057
21	0.001	0	0.01	0.057
22	0.001	0	0.002	0.148
23	0	0	0.001	0.06
24	0	0	0.002	0.042
25	0	0	0.002	0.042
26	0.001	0	0.136	0.004
27	0.002	0	0.001	0.06
28	0	0	0.002	0.086
29	0	0	0.002	0.086
30	0.001	0	0.001	0.089
31	0.002	0	0.001	0.104
32	0.001	0	0.219	0
33	0.001	0	0.219	0
34	0	0	0.227	0.001
35	0.002	0	0.242	0.002
36	0	0	0.203	0
37	0	0	0.203	0
38	0	0	0.003	0.021
39	0.003	0	0.001	0.056
40	0	0	0.245	0.001
41	0	0	0.245	0.001
42	0	0	0.001	0.049
43	0.001	0	0.205	0.002
44	0.002	0	0.221	0.003
45	0.002	0	0.221	0.003
46	0.001	0	0.257	0
47	0	0	0.11	0.001
48	0.003	0	0.269	0
49	0.001	0	0	0.238
50	0.001	0	0	0.238
51	0.002	0	0.004	0.014
52	0.005	0	0.013	0.147
53	0	0	0.142	0
54	0	0	0.142	0
55	0	0	0.082	0.004
56	0	0	0.002	0.067
57	0.001	0	0.33	0
58	0.001	0	0.33	0
59	0.003	0	0.341	0.001
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3	0.002	0	0.133	0.001
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5	0	0	0.218	0.001
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For Peer Review

Appendix S3 SymPortal outputs and environmental data (profiles proportions)

Sample ID	Molecular Cl	Morphologic	Locality	Site GPS (deg	CHL mean	CHL standard
Sample ID	Molecular Cl	Morphologic	Locality	Site GPS (deg	CHL mean	CHL standard
SA0012	I	fontanesii	Farasan Bank	18.281, 41.44	0.66831068	0.19747577
SA0038	I	fontanesii	Farasan Bank	18.281, 41.4	0.66831068	0.19747577
SA0054	V	lobata	Farasan Bank	18.281, 41.4	0.66831068	0.19747577
SA0055	V	lobata	Farasan Bank	18.281, 41.4	0.66831068	0.19747577
SA0057	IV	monticulosa	Farasan Bank	18.281, 41.4	0.66831068	0.19747577
SA0091	V	echinulata	Farasan Bank	18.281, 41.4	0.66831068	0.19747577
SA0092	V	lobata	Farasan Bank	18.281, 41.4	0.66831068	0.19747577
SA0149	V	solida	Farasan Bank	18.281, 41.44	0.66831068	0.19747577
SA0150	I	fontanesii	Farasan Bank	18.281, 41.44	0.66831068	0.19747577
SA0155	IV	monticulosa	Farasan Bank	18.281, 41.44	0.66831068	0.19747577
SA0181	I	fontanesii	Farasan Bank	18.281, 41.44	0.66831068	0.19747577
SA0268	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA0307	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA0308	IV	monticulosa	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA0310	I	fontanesii	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA0340	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA0361	II	columnaris	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA0363	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA0382	I	fontanesii	Thuwal	22.607, 38.91	0.34640953	0.11105539
SA0383	IV	monticulosa	Thuwal	22.607, 38.91	0.34640953	0.11105539
SA0385	I	fontanesii	Thuwal	22.607, 38.91	0.34640953	0.11105539
SA0388	V	lutea	Thuwal	22.607, 38.91	0.34640953	0.11105539
SA0389	V	lutea	Thuwal	22.607, 38.91	0.34640953	0.11105539
SA0390	V	annae	Thuwal	22.607, 38.91	0.34640953	0.11105539
SA0438	I	fontanesii	Thuwal	22.607, 38.91	0.34640953	0.11105539
SA0686	II	columnaris	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA0725	I	fontanesii	Duba	27.998, 35.2	(0.19101191	0.06271219
SA0764	II	columnaris	Duba	27.998, 35.2	(0.19101191	0.06271219
SA0765	V	lutea	Duba	27.998, 35.2	(0.19101191	0.06271219
SA0766	IV	monticulosa	Duba	27.998, 35.2	(0.19101191	0.06271219
SA0770	V	lobata	Duba	27.998, 35.2	(0.19101191	0.06271219
SA0771	IV	rus	Duba	27.998, 35.2	(0.19101191	0.06271219
SA0876	V	annae	Duba	27.998, 35.2	(0.19101191	0.06271219
SA0970	II	columnaris	Aqaba	28.264, 34.8	0.1859509	0.10520139
SA1028	II	columnaris	Aqaba	28.264, 34.85	0.1859509	0.10520139
SA1032	IV	monticulosa	Aqaba	28.264, 34.85	0.1859509	0.10520139
SA1444	IV	rus	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1448	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1449	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1490	V	solida	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1491	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1493	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606

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2	SA1516	III	sp 1	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
3	SA1518	V	annae	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
4	SA1574	V	lutea	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
5							
6	SA1576	V	lobata	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
7	SA1581	V	echinulata	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
8	SA1609	V	lobata	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
9							
10	SA1612	V	lobata	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
11	SA1641	I	fontanesii	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
12	SA1647	V	lobata	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
13							
14	SA1702	V	lutea	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
15	SA1703	V	lutea	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
16	SA1704	II	columnaris	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
17	SA1705	V	solida	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
18	SA1722	V	lutea	Farasan Islan	(16.971, 41.11	1.29687286	0.81816606
19							
20	SA2080	II	columnaris	Yanbu	24.101, 38.000	0.31583691	0.09140692
21							
22	SA2081	V	lutea	Yanbu	24.101, 38.000	0.31583691	0.09140692
23	SA2136	V	solida	Yanbu	24.101, 38.000	0.31583691	0.09140692
24	SA2138	V	solida	Yanbu	24.101, 38.000	0.31583691	0.09140692
25							
26	SA2142	IV	monticulosa	Yanbu	24.101, 38.000	0.31583691	0.09140692
27	SA2148	V	annae	Yanbu	24.101, 38.000	0.31583691	0.09140692
28	SA2153	IV	monticulosa	Yanbu	24.101, 38.000	0.31583691	0.09140692
29							
30	SA2156	V	echinulata	Yanbu	24.101, 38.000	0.31583691	0.09140692
31	SA2159	IV	monticulosa	Yanbu	24.101, 38.000	0.31583691	0.09140692
32	SA2163	V	lutea	Yanbu	24.101, 38.000	0.31583691	0.09140692
33							
34	SA2165	I	fontanesii	Yanbu	24.101, 38.000	0.31583691	0.09140692
35	SA2194	V	lobata	Yanbu	24.101, 38.000	0.31583691	0.09140692
36	SA2195	V	annae	Yanbu	24.101, 38.000	0.31583691	0.09140692
37	SA2196	IV	monticulosa	Yanbu	24.101, 38.000	0.31583691	0.09140692
38							
39	SA2199	IV	monticulosa	Yanbu	24.101, 38.000	0.31583691	0.09140692
40	SA2205	I	fontanesii	Yanbu	24.101, 38.000	0.31583691	0.09140692
41							
42	SA2243	II	columnaris	Al Wajh	25.345, 36.890	0.21075491	0.08272508
43	SA2295	V	lutea	Al Wajh	25.345, 36.890	0.21075491	0.08272508
44	SA2332	V	annae	Al Wajh	25.345, 36.890	0.21075491	0.08272508
45	SA2337	IV	rus	Al Wajh	25.345, 36.890	0.21075491	0.08272508
46							
47	SA2375	V	lutea	Al Wajh	25.345, 36.890	0.21075491	0.08272508
48	SA2432	V	annae	Al Wajh	25.345, 36.890	0.21075491	0.08272508
49	SA2479	IV	monticulosa	Al Wajh	25.345, 36.890	0.21075491	0.08272508
50							
51	SA2525	V	solida	Al Wajh	25.345, 36.890	0.21075491	0.08272508
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	POC mean	POC standard	SST mean	SST standard	Salinity mean	Salinity stand	clade
	POC mean	POC standard	SST mean	SST standard	Salinity mean	Salinity stand	A
1							
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6							
7	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
8	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
9							
10	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
11	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
12	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
13							
14	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
15	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
16	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
17							
18	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0.014
19	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
20	172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
21							
22	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
23	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
24	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
25							
26	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
27	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
28	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
29							
30	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
31	159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.007
32	159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0
33							
34	159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.006
35	159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0
36	159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0
37	159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.004
38	159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.005
39							
40	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
41	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
42							
43	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
44	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
45	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0.004
46	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0.004
47	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
48	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
49	56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
50							
51	52.3827691	26.9438428	24.7764459	2.26550846	40.5997183	0.07612554	0
52	52.3827691	26.9438428	24.7764459	2.26550846	40.5997183	0.07612554	0
53	52.3827691	26.9438428	24.7764459	2.26550846	40.5997183	0.07612554	0
54							
55	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
56	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
57	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.411
58	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
59	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
60	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.393
	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0

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2	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.951
3	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
4	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
5	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
6	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
7	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.002
8	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.002
9	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
10	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
11	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.003
12	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
13	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
14	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
15	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
16	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
17	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
18	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
19	279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
20	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
21	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.003
22	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
23	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.006
24	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
25	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
26	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
27	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
28	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
29	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
30	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
31	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
32	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.002
33	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
34	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.004
35	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
36	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.007
37	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
38	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
39	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
40	94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
41	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0.005
42	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0.006
43	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
44	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
45	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
46	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
47	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
48	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
49	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
50	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
51	61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
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clade	clade	majority ITS2	majority ITS2	majority ITS2	majority ITS2	majority ITS2
C	D	A1	A1/A1c	A1/A1j	A1/A1k	A1k/A1
0.006	0.841	0	0	0	0	0
0.434	0	0	0	0	0	0
0.872	0	0	0	0	0	0
0.845	0	0	0	0	0	0
0.006	0.833	0	0	0	0	0
0.007	0.896	0	0	0	0	0
0	0.848	0	0	0	0	0
0.604	0	0	0	0	0	0
0.054	0.678	0	0	0	0.014	0
0.009	0.77	0	0	0	0	0
0.81	0	0	0	0	0	0
0.841	0	0	0	0	0	0
0	0.919	0	0	0	0	0
0	0.824	0	0	0	0	0
0	0.307	0	0	0	0	0
0.016	0.904	0	0	0	0	0
0	0.84	0	0	0	0	0
0.004	0.872	0	0	0	0	0
0.321	0.025	0	0	0	0	0.007
0	0.888	0	0	0	0	0
0.409	0.021	0	0	0	0	0.006
0.894	0	0	0	0	0	0
0.59	0	0	0	0	0	0
0.366	0.057	0	0	0	0	0.004
0.326	0.008	0	0	0	0	0.005
0.813	0	0	0	0	0	0
0.465	0	0	0	0	0	0
0.77	0	0	0	0	0	0
0.732	0	0	0	0	0	0
0.283	0	0.004	0	0	0	0
0.676	0.009	0.004	0	0	0	0
0.625	0	0	0	0	0	0
0.86	0	0	0	0	0	0
0.569	0	0	0	0	0	0
0.605	0	0	0	0	0	0
0.447	0	0	0	0	0	0
0	0.851	0	0	0	0	0
0	0.711	0	0	0	0	0
0.007	0.493	0.411	0	0	0	0
0	0.736	0	0	0	0	0
0.024	0.482	0.393	0	0	0	0
0.001	0.695	0	0	0	0	0

1							
2	0.004	0.002	0.951	0	0	0	0
3	0	0.932	0	0	0	0	0
4	0.005	0.929	0	0	0	0	0
5							
6	0	0	0	0	0	0	0
7	0.843	0.005	0.002	0	0	0	0
8	0.051	0.861	0	0.002	0	0	0
9							
10	0.013	0.909	0	0	0	0	0
11	0.009	0.778	0.003	0	0	0	0
12	0.01	0.918	0	0	0	0	0
13							
14	0	0.941	0	0	0	0	0
15	0.713	0.048	0	0	0	0	0
16	0.005	0.896	0	0	0	0	0
17							
18	0	0.878	0	0	0	0	0
19	0	0.9	0	0	0	0	0
20	0.005	0.872	0	0	0	0	0
21							
22	0.646	0.003	0.003	0	0	0	0
23	0.65	0	0	0	0	0	0
24	0.551	0.015	0.006	0	0	0	0
25							
26	0.724	0.007	0	0	0	0	0
27	0	0.933	0	0	0	0	0
28	0.003	0.879	0	0	0	0	0
29							
30	0.676	0	0	0	0	0	0
31	0	0.926	0	0	0	0	0
32	0.676	0	0	0	0.002	0	0
33							
34	0.731	0	0	0	0	0	0
35	0.605	0.006	0.004	0	0	0	0
36	0.872	0	0	0	0	0	0
37							
38	0.649	0.005	0.007	0	0	0	0
39	0.004	0.725	0	0	0	0	0
40	0.011	0.928	0	0	0	0	0
41							
42	0.03	0.773	0.005	0	0	0	0
43	0.803	0	0	0	0.006	0	0
44	0.901	0.003	0	0	0	0	0
45							
46	0	0.833	0	0	0	0	0
47	0.634	0	0	0	0	0	0
48	0.5	0	0	0	0	0	0
49	0.85	0	0	0	0	0	0
50							
51	0.664	0	0	0	0	0	0
52							
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1							
2	0	0	0	0	0.004	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0.005	0	0
5							
6	0	0	0	0	0	0	0
7	0.002	0	0	0	0	0	0
8	0	0	0	0	0	0	0.051
9							
10	0	0	0	0	0.002	0	0
11	0	0	0	0	0.009	0	0
12	0	0	0	0	0	0	0.01
13							
14	0	0	0	0	0	0	0
15	0	0.005	0	0	0	0	0
16	0	0	0	0	0.005	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0.646	0	0	0	0
22	0	0	0.65	0	0	0	0
23	0	0	0.44	0	0	0	0
24							
25	0	0.724	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0.004	0	0.672	0	0	0	0
30	0	0	0	0	0	0	0
31	0.001	0	0.675	0	0	0	0
32	0.008	0	0.723	0	0	0	0
33	0	0	0.285	0	0	0	0
34	0	0	0	0	0	0	0
35	0.002	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0.011	0	0
38	0	0	0	0.025	0	0	0
39	0	0	0.803	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0.558	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0.558	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0.664	0	0	0	0
51							
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majority ITS2	majority ITS2	majority ITS2	majority ITS2	majority ITS2	majority ITS2	majority ITS2
C1/C72/C15/(C1/C116/C15,C3	C21/C3	C41/C1	C15r/C15	C40/C3		
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.003	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.006	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.007	0.007	0	0	0	0	0
0	0	0	0	0	0	0
0.024	0.024	0	0	0	0	0
0	0	0	0	0	0	0

For Peer Review

0.674

0.016

1							
2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0.051	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0.901	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52							
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1							
2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0.841	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0.004	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0.708	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0.005	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0.06	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0.003	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0.004	0	0	0	0
36	0.872	0	0	0	0	0	0
37	0.271	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0.85	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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1							
2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0.005	0
8	0	0	0	0	0	0	0
9	0	0	0.007	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0.896	0
17	0	0	0	0	0	0.878	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0.872	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0.007	0
26	0	0	0	0	0	0.933	0
27	0	0	0	0	0	0.879	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0.926	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0.316	0	0.006	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0.376	0.005	0
38	0.004	0	0	0	0	0	0
39	0	0	0	0	0	0.928	0
40	0	0	0	0	0	0.773	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0.003	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0.076	0	0	0
47	0	0.5	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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majority ITS2	majority ITS2	majority ITS2	majority ITS2	majority ITS2	type profile	type profile
D1/D4	D1/D6	D1/D4/D6	D1/D4/D1n	D17g	A1	A1-A1c-A1h-A
0	0	0	0.841	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.833	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.678	0	0	0
0.77	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.919	0	0	0	0	0
0.824	0	0	0	0	0	0
0	0	0	0	0.206	0	0
0	0	0	0	0	0	0
0.84	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.888	0	0	0	0	0	0
0.021	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.851	0	0	0	0	0	0
0.711	0	0	0	0	0	0
0	0.493	0	0	0	0.411	0
0.736	0	0	0	0	0	0
0	0	0	0	0	0.393	0
0.695	0	0	0	0	0	0

1							
2	0	0.002	0	0	0	0.951	0
3	0	0.932	0	0	0	0	0
4	0	0.929	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0.861	0	0	0	0	0
9	0	0.909	0	0	0	0	0
10	0	0	0	0.778	0	0.003	0
11	0	0.918	0	0	0	0	0
12	0	0.941	0	0	0	0	0
13	0	0.048	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0.9	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0.003	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0.015	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0.725	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0.005
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0.833	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
52							
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1							
2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0.002	0	0	0	0	0	0
8	0	0	0	0.002	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0.003	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0.006	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0.002	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0.004	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0.007	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0.006	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0.002	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
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21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0.724	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0.004	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0.001	0	0
33	0	0	0	0	0.008	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0.285
36	0	0	0	0	0	0	0
37	0	0	0	0	0.002	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0.803
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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type profile	type profile	type profile	type profile	type profile	type profile	type profile
C15-C15y-C15k	C15h-C15k	C1/C39-C1b-C1/C15-C1b-C1/C15-C1b-C1/C3/C3u-C115 C1	C1/C39-C1b-C1/C15-C1b-C1/C15-C1b-C1/C3/C3u-C115 C1	C1/C39-C1b-C1/C15-C1b-C1/C15-C1b-C1/C3/C3u-C115 C1	C1/C39-C1b-C1/C15-C1b-C1/C15-C1b-C1/C3/C3u-C115 C1	C1/C72/C15-C1/C72/C15-C1/C72/C15-C1/C72/C15-C1/C72/C15-C1/C72/C15-C1/C72/C15-C1/C72/C15-C1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.051	0	0	0	0
0	0	0	0.009	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.59	0	0	0	0	0	0
0	0	0	0	0.001	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.283	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.015	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.007
0	0	0	0	0	0	0
0	0	0	0	0	0	0.024
0	0	0	0	0	0	0

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2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0.005	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0.002	0	0	0
11	0	0	0	0.009	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0.005	0	0	0	0
16	0	0	0	0.005	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0.646	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0.675	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0.664	0	0	0	0	0	0
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2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0.051	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0.011	0	0
41	0.005	0	0	0.025	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0.901
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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	type profile	type profile	type profile	type profile	type profile	type profile	type profile
	C1-C15-C1b-CC40/C3	C22b/C15	C91f	C3/C1/C41-C	C15-C15x-C15	C116	
	0	0	0	0	0	0	0.001
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0.527	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.839	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0

For Peer Review

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2	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0
7	0	0	0.841	0	0	0	0	0
8	0	0	0	0	0	0	0	0
9	0	0	0	0.004	0	0	0	0
10	0	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0	0
12	0.01	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0
15	0	0	0.708	0	0	0	0	0
16	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0	0
20	0	0	0	0	0.005	0	0	0
21	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0.65	0	0
24	0	0	0	0.06	0	0.44	0	0
25	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0
28	0	0	0	0	0.003	0	0	0
29	0	0	0	0	0	0.672	0	0
30	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0	0
35	0	0	0	0	0.004	0	0	0
36	0	0	0.872	0	0	0	0	0
37	0	0	0.271	0	0	0	0	0
38	0	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0
47	0	0	0	0	0	0.558	0	0
48	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0
52								
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type profile	type profile	type profile	type profile	type profile	type profile	type profile
C3-C3au-C29	C72	C15/C60a-C15	C41	C15-C15s	C1/C15-C1b-C15-C15x-C15	C15
0	0	0	0	0	0	0
0	0	0	0	0	0.432	0
0	0	0.872	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.003	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.004	0
0	0	0	0.111	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.894	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.001	0	0	0	0	0

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2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0.723
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0.85	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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	type profile C15/C72/C1-	type profile C1-C1b-C41-CC	type profile C15/C1-C15a	type profile C1/C15-C72-(C91e	type profile C15ai	type profile C22a
7	0	0.005	0	0	0	0
8	0	0	0	0	0	0
9	0	0	0	0	0	0
10	0	0	0	0	0	0
11	0	0	0	0	0	0
12	0	0	0	0	0	0
13	0	0	0	0	0	0
14	0	0	0	0	0	0
15	0	0	0	0	0	0
16	0	0	0	0	0	0.077
17	0	0	0	0	0	0
18	0	0	0	0	0	0
19	0	0	0	0	0	0
20	0	0	0	0	0	0
21	0	0	0	0	0	0
22	0	0	0	0	0	0
23	0	0	0	0	0	0
24	0	0	0	0	0	0
25	0	0	0	0	0	0
26	0	0	0	0	0	0
27	0	0	0	0	0	0
28	0	0	0	0	0	0
29	0	0	0	0	0	0
30	0	0	0	0	0	0
31	0	0	0	0	0	0
32	0	0	0	0	0	0
33	0	0	0	0	0	0
34	0	0	0	0	0	0
35	0	0	0	0	0	0
36	0	0	0	0	0	0
37	0	0	0	0	0	0
38	0	0	0	0	0	0
39	0	0	0.326	0	0	0
40	0	0	0	0	0	0
41	0	0	0	0	0	0
42	0	0	0	0	0	0
43	0	0	0	0	0	0
44	0	0	0	0	0	0
45	0	0	0	0	0	0
46	0	0	0	0	0	0
47	0	0	0	0	0	0
48	0	0	0	0	0	0
49	0	0	0	0	0	0
50	0	0	0	0	0	0
51	0	0	0	0	0	0
52	0	0	0	0	0	0
53	0	0	0	0	0	0
54	0	0	0	0	0	0
55	0	0	0	0	0	0
56	0	0	0	0	0	0
57	0	0	0	0	0	0
58	0	0	0	0	0	0
59	0	0	0	0	0	0
60	0	0	0	0	0	0

For Peer Review

1							
2	0	0	0	0.004	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0.051	0	0	0	0	0
9	0	0	0	0	0.007	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0.316	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0.376
38	0.004	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0.076	0
48	0	0	0.5	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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type profile	type profile	type profile	type profile	type profile	type profile	type profile
D1-D4-D4c-D	D1-D4-D4c-D	D1-D4-D6-D4	D4/D1-D4c	D1/D4-D4c-D	D1/D6-D4-D1	D1-D4-D4f-D4
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.896
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.919	0
0	0	0	0	0	0	0
0	0	0	0.101	0	0	0
0	0	0	0	0	0	0.904
0	0	0	0	0	0	0
0	0	0	0	0	0	0.872
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.057	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.009	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0.711	0	0
0	0	0	0	0	0	0
0	0	0	0	0.736	0	0
0	0	0	0.482	0	0	0
0	0	0	0	0.695	0	0

1							
2	0	0	0	0	0	0	0
3	0	0	0	0	0	0.932	0
4	0	0	0	0	0	0.929	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0.909	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0.918	0
13	0	0	0	0	0	0.941	0
14	0	0	0	0	0	0.048	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0.9	0
20	0	0	0	0	0	0	0.872
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0.015	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0.933	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0.926
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0.006	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0.928
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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2	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0.896
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0.005	0
39	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0
41	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0.833	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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	type profile	type profile	type profile	type profile	type profile	type profile	type profile
	D1-D4f-D4-D2	D1-D4-D4c-D	D1/D4/D1n-DD	D1/D6-D4-D1	D1-D4-D4c-D	D1/D6-D4-D1	D1-D4-D4c-D
	0	0	0.841	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0.678	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0.025
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0.493	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0
	0	0	0	0	0	0	0

1							
2	0	0	0	0	0	0.002	0
3	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0
8	0	0	0	0	0	0.861	0
9	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0
11	0	0	0.778	0	0	0	0
12	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0
18	0	0	0	0	0	0	0
19	0	0	0	0	0	0	0
20	0	0	0	0	0	0	0
21	0	0	0	0	0	0	0
22	0	0	0	0.003	0	0	0
23	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0
26	0	0.007	0	0	0	0	0
27	0	0	0	0	0	0	0
28	0	0	0	0	0.879	0	0
29	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0
32	0	0	0	0	0	0	0
33	0	0	0	0	0	0	0
34	0	0	0	0	0	0	0
35	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0
37	0	0	0	0	0	0	0
38	0	0	0	0	0	0	0
39	0	0	0.725	0	0	0	0
40	0	0	0	0	0	0	0
41	0.773	0	0	0	0	0	0
42	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0
47	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0
50	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0
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	type profile	type profile	type profile	type profile	type profile
	D1-D4-D6-D4	D1-D4-D4c-D	D1-D4-D6-D4	D1-D4-D2-D4	D17g
7	0	0	0	0	0
8	0	0	0	0	0
9	0	0	0	0	0
10	0	0	0	0	0
11	0	0	0	0	0
12	0	0	0	0	0
13	0	0	0	0	0
14	0	0	0	0	0
15	0	0	0	0	0
16	0	0	0	0	0
17	0	0	0	0	0
18	0	0	0	0	0
19	0	0	0	0	0
20	0	0	0	0	0
21	0	0	0	0	0
22	0	0	0	0	0
23	0	0	0	0	0
24	0	0	0	0	0
25	0	0	0	0	0
26	0	0	0	0	0.206
27	0	0	0	0	0
28	0	0	0	0	0
29	0	0	0	0	0
30	0	0	0	0	0
31	0	0	0	0	0
32	0	0	0	0	0
33	0	0	0	0	0
34	0	0	0	0	0
35	0	0	0	0	0
36	0	0	0	0	0
37	0	0	0	0	0
38	0	0	0	0	0
39	0	0	0	0	0
40	0	0	0	0	0
41	0	0	0	0	0
42	0	0	0	0	0
43	0	0	0	0	0
44	0	0	0	0	0
45	0	0	0	0	0
46	0	0	0	0	0
47	0	0	0	0	0
48	0	0	0	0	0
49	0	0	0	0	0
50	0	0	0	0	0
51	0	0	0	0	0
52	0	0	0	0	0
53	0	0	0	0	0
54	0	0	0	0	0
55	0	0	0	0	0
56	0	0	0	0	0
57	0	0	0	0	0
58	0	0	0	0	0
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14	0	0	0	0	0
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5 SUPPORTING INFORMATION
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8 **Environmental latitudinal gradients and host specificity shape**
9 **Symbiodiniaceae distribution in Red Sea *Porites* corals**
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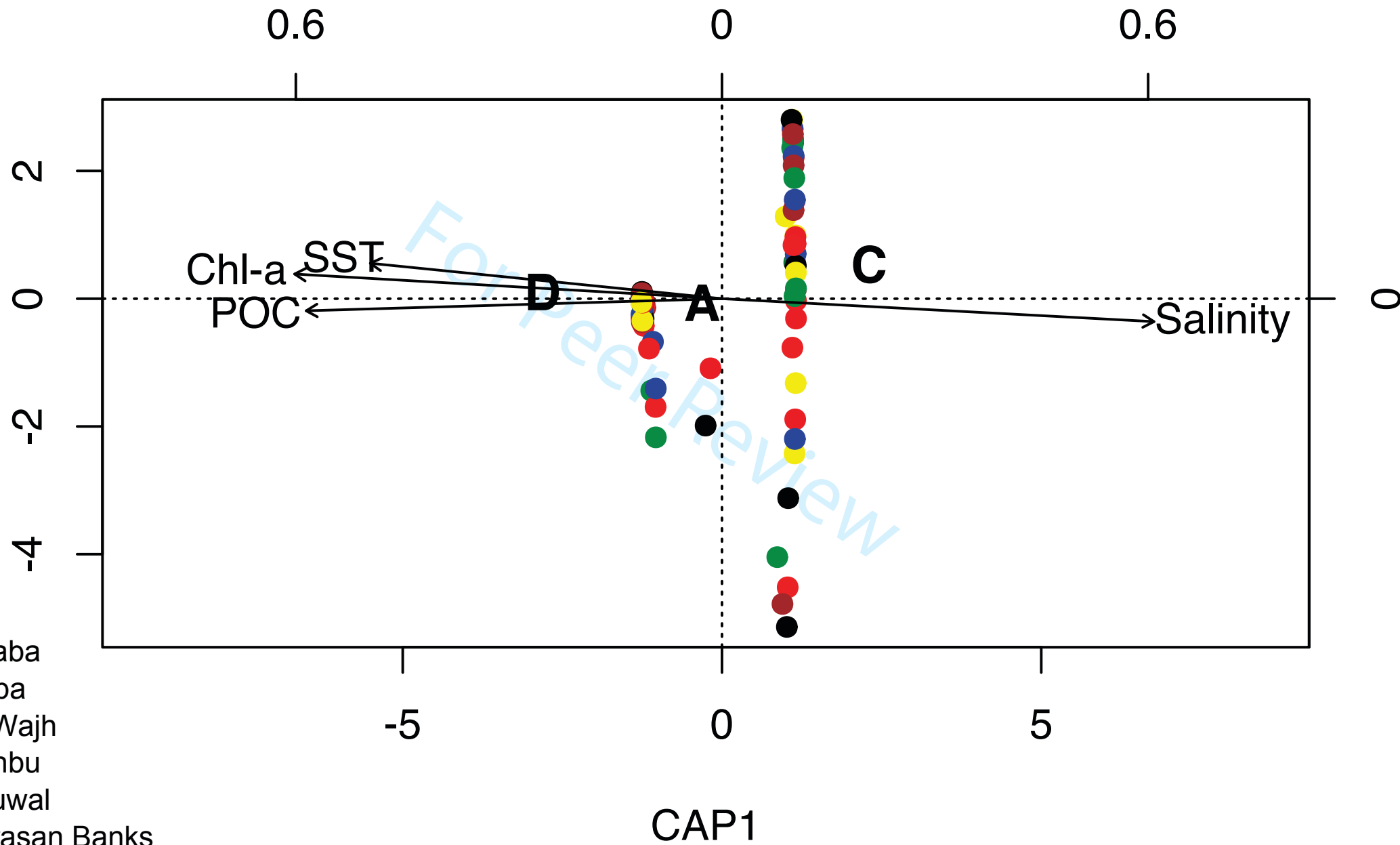
11 Tullia I. Terraneo, Marco Fusi, Benjamin C. C. Hume, Roberto Arrigoni, Christian R.
12 Voolstra, Francesca Benzoni, Zac H. Forsman, Michael L. Berumen
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16 **Appendix S4** Bi-plot CAP ordination of *Porites* (divided for location, molecular clades and
17 morphological species) and Symbiodiniaceae clade (a-c), majority ITS2 sequence (d-f) and
18 ITS2 type profiles (g-i) in relation with the four environmental variables studied
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(a) Symbiodiniaceae clade - locality

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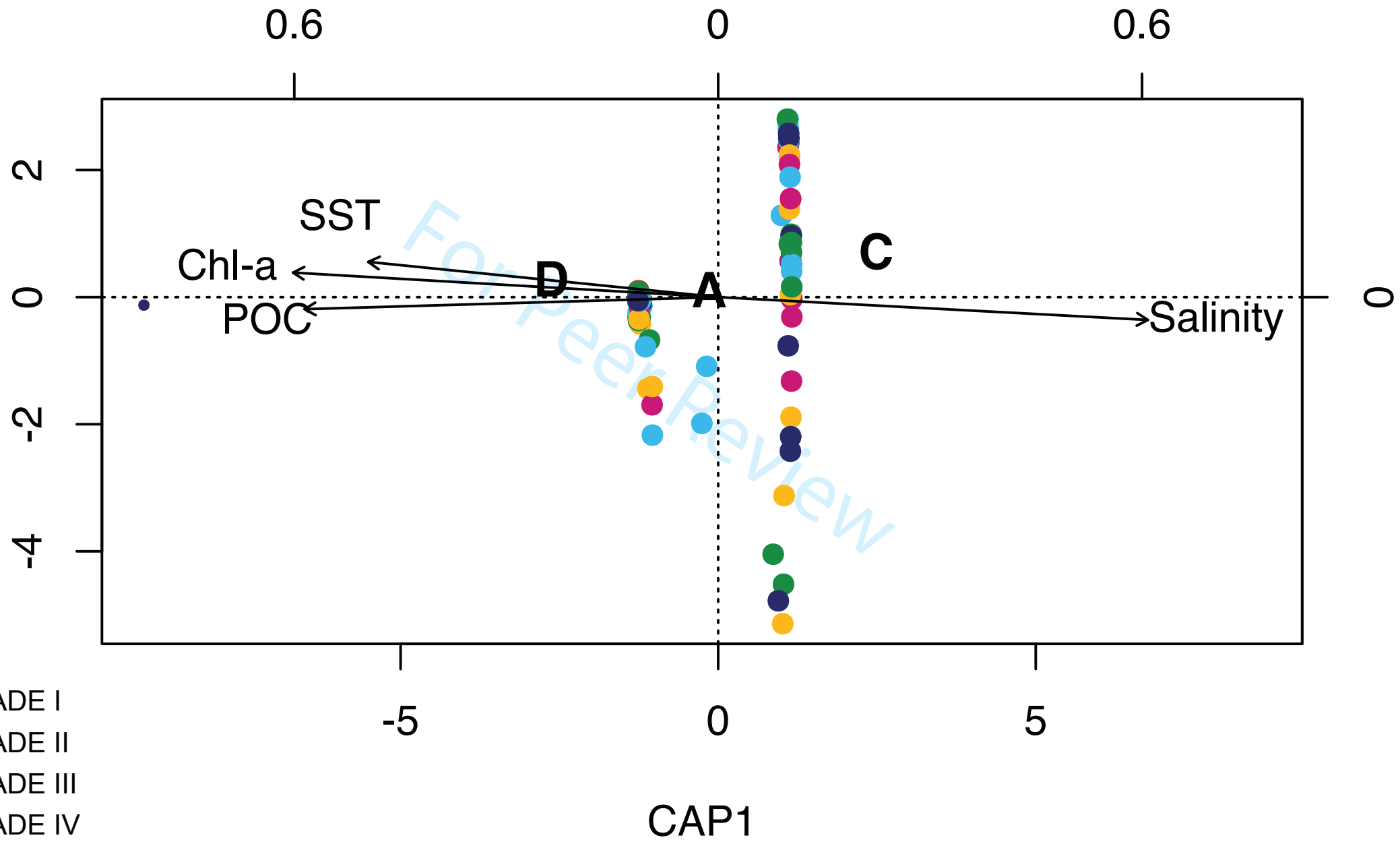


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- 33 Aqaba
- 34 Duba
- 35 Al Wajh
- 36 Yanbu
- 37 Thuwal
- 38 Farasan Banks
- 39 Farasan Islands

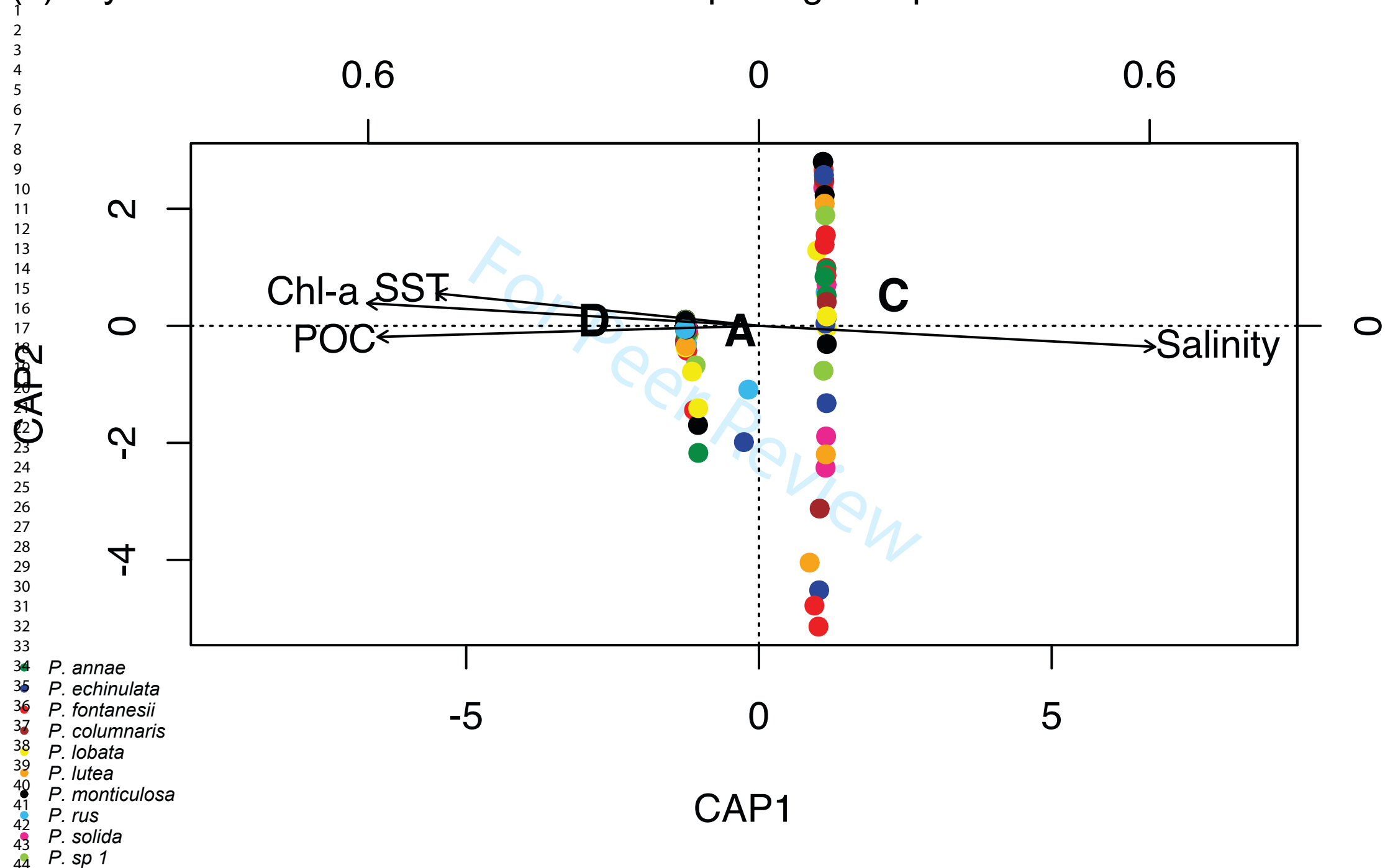
(b) Symbiodiniaceae clade - *Porites* molecular clade

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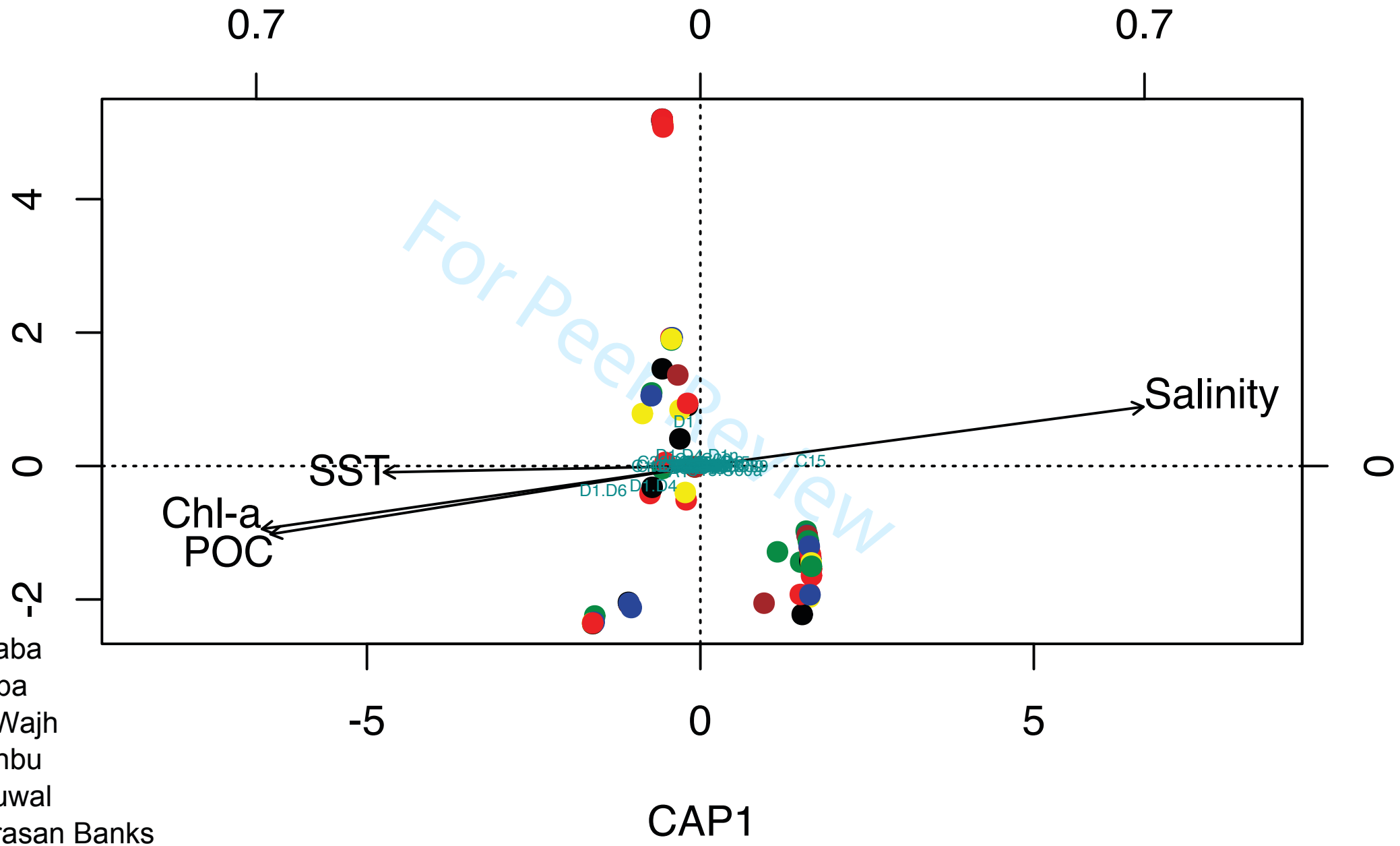
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- 35 CLADE I
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- 43 CLADE V
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(c) Symbiodiniaceae clade - *Porites* morphological species

(d) Symbiodiniaceae majority ITS2 seq - locality

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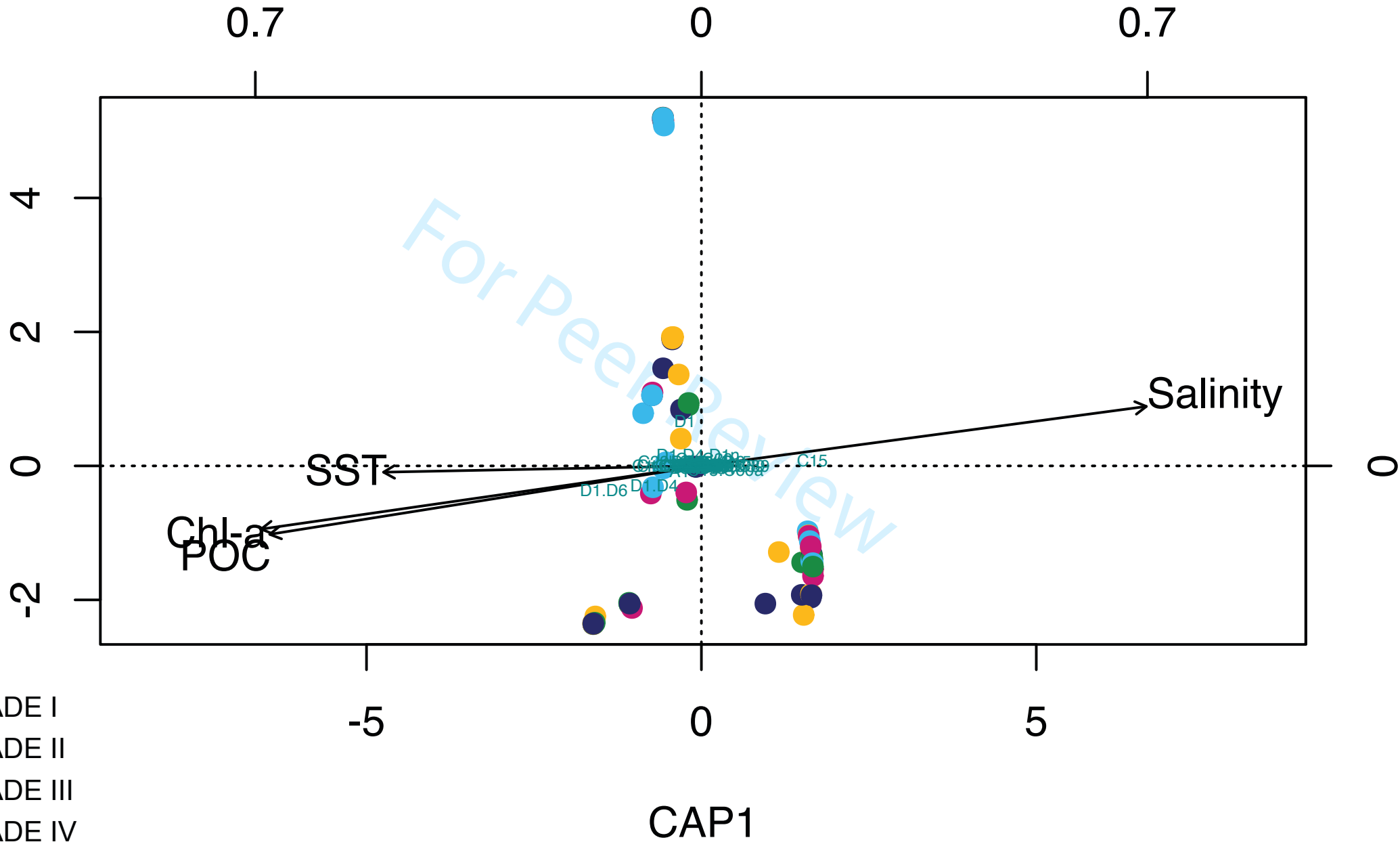


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- 33 Aqaba
- 34 Duba
- 35 Al Wajh
- 36 Yanbu
- 37 Thuwal
- 38 Farasan Banks
- 39 Farasan Islands

(e) Symbiodiniaceae majority ITS2 seq - *Porites* molecular clade

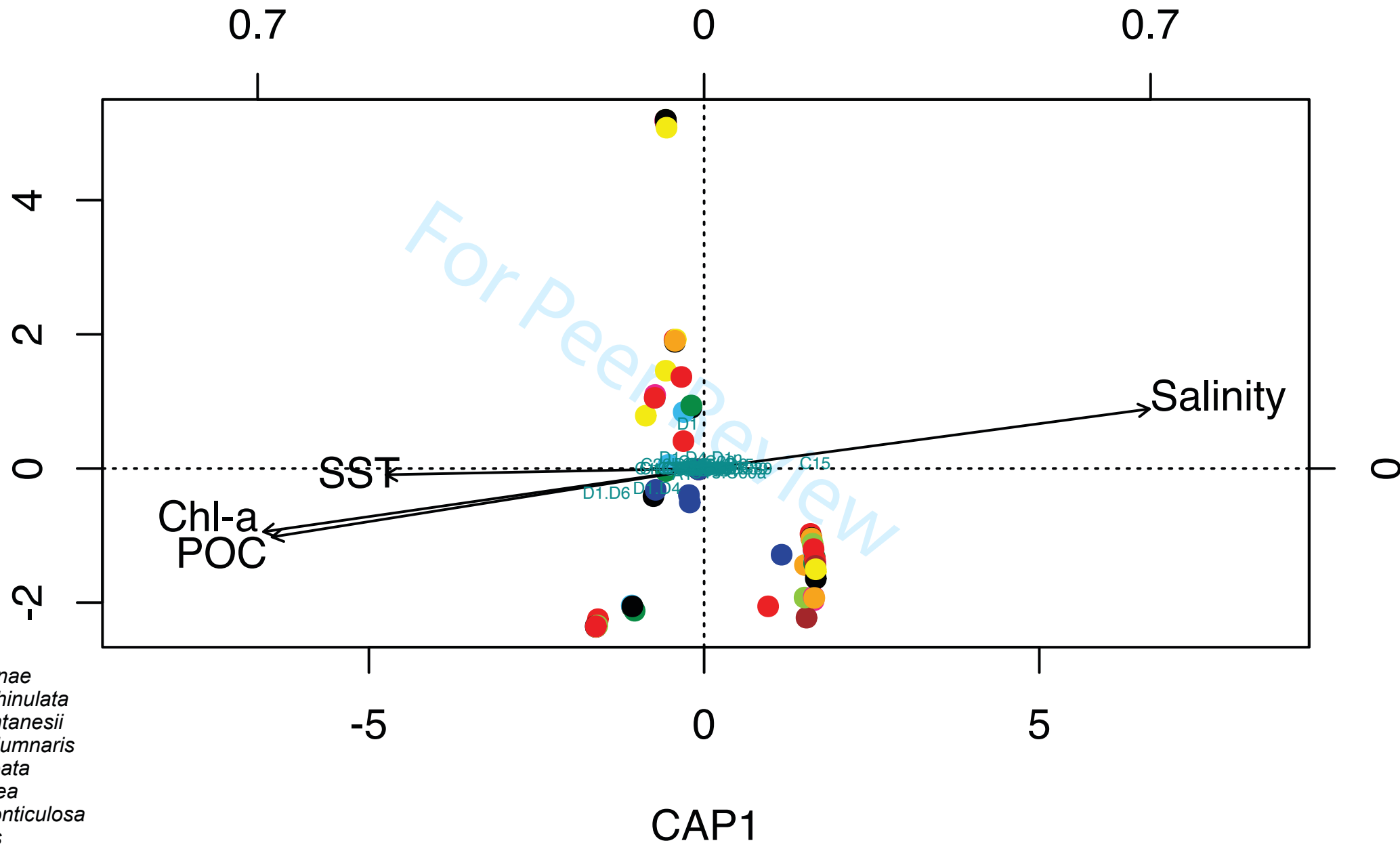
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- 35 CLADE I
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- 39 CLADE V

(f) Symbiodiniaceae majority ITS2 seq - *Porites* morphological species

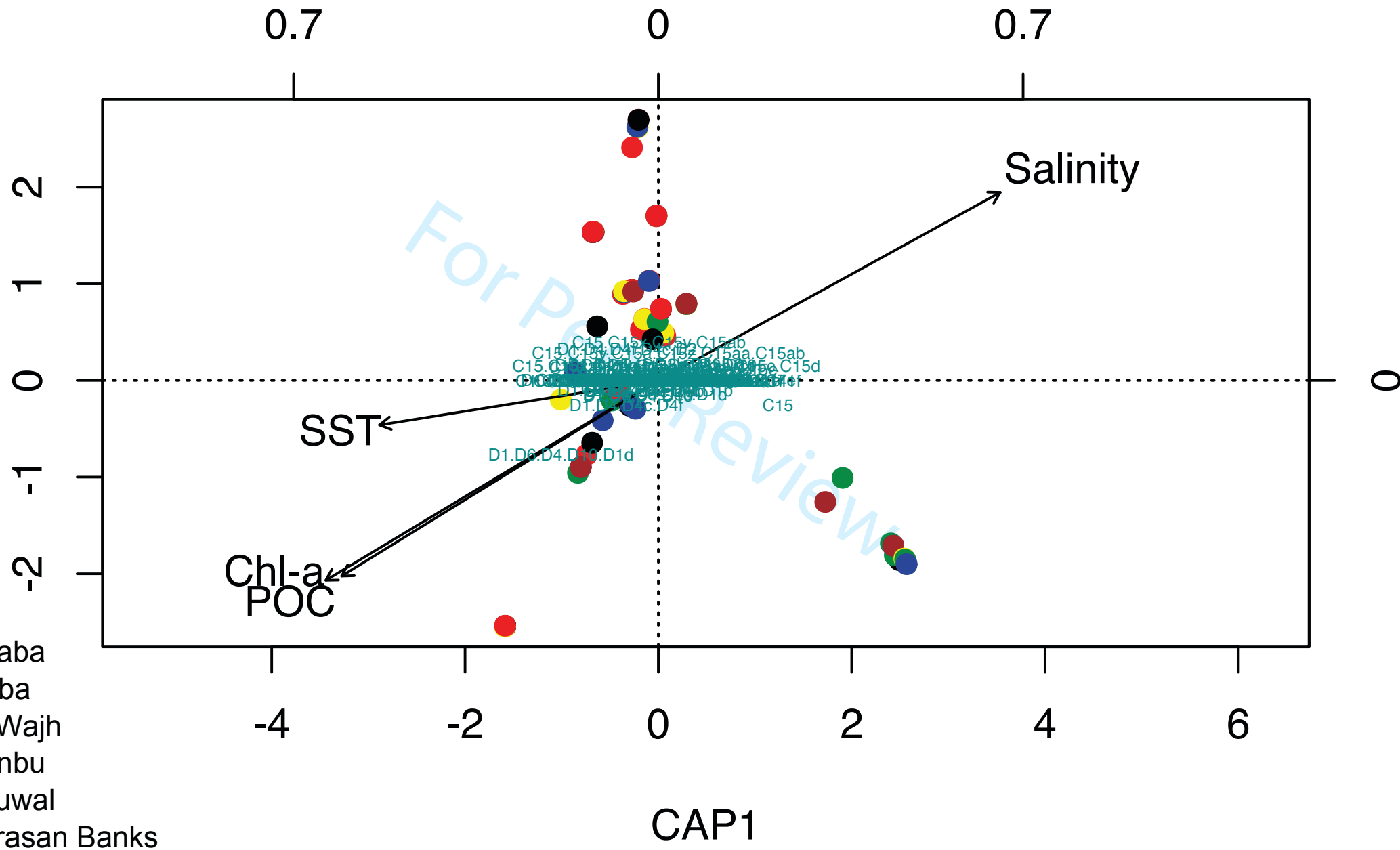
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- 34 *P. annae*
- 35 *P. echinulata*
- 36 *P. fontanesii*
- 37 *P. columnaris*
- 38 *P. lobata*
- 39 *P. lutea*
- 40 *P. monticulosa*
- 41 *P. rus*
- 42 *P. solida*
- 43 *P. sp 1*

(g) Symbiodiniaceae ITS2 type profiles - locality

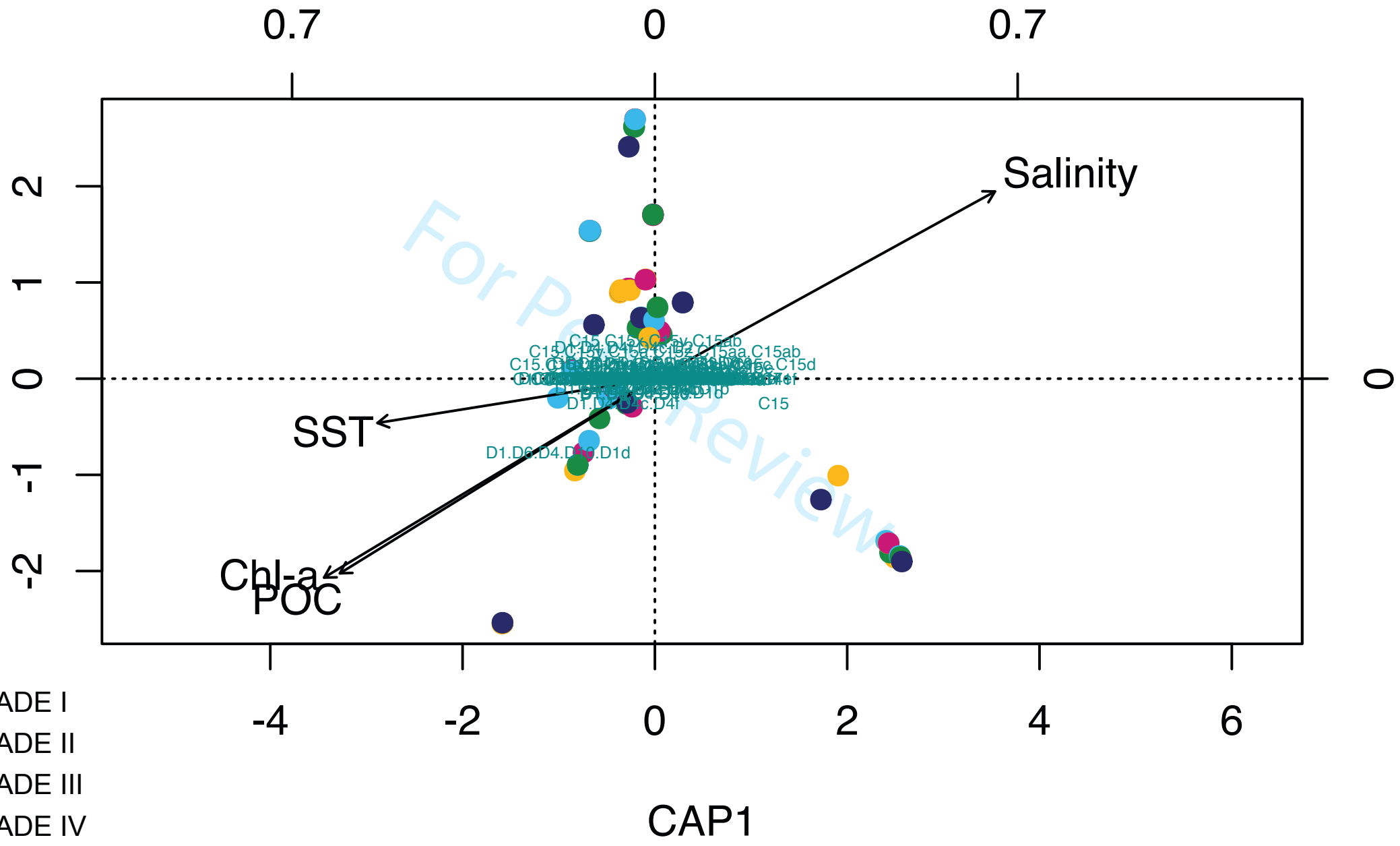
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- Aqaba
- Duba
- Al Wajh
- Yanbu
- Thuwal
- Farasan Banks
- Farasan Islands

(h) Symbiodiniaceae ITS2 type profile - *Porites* molecular clade

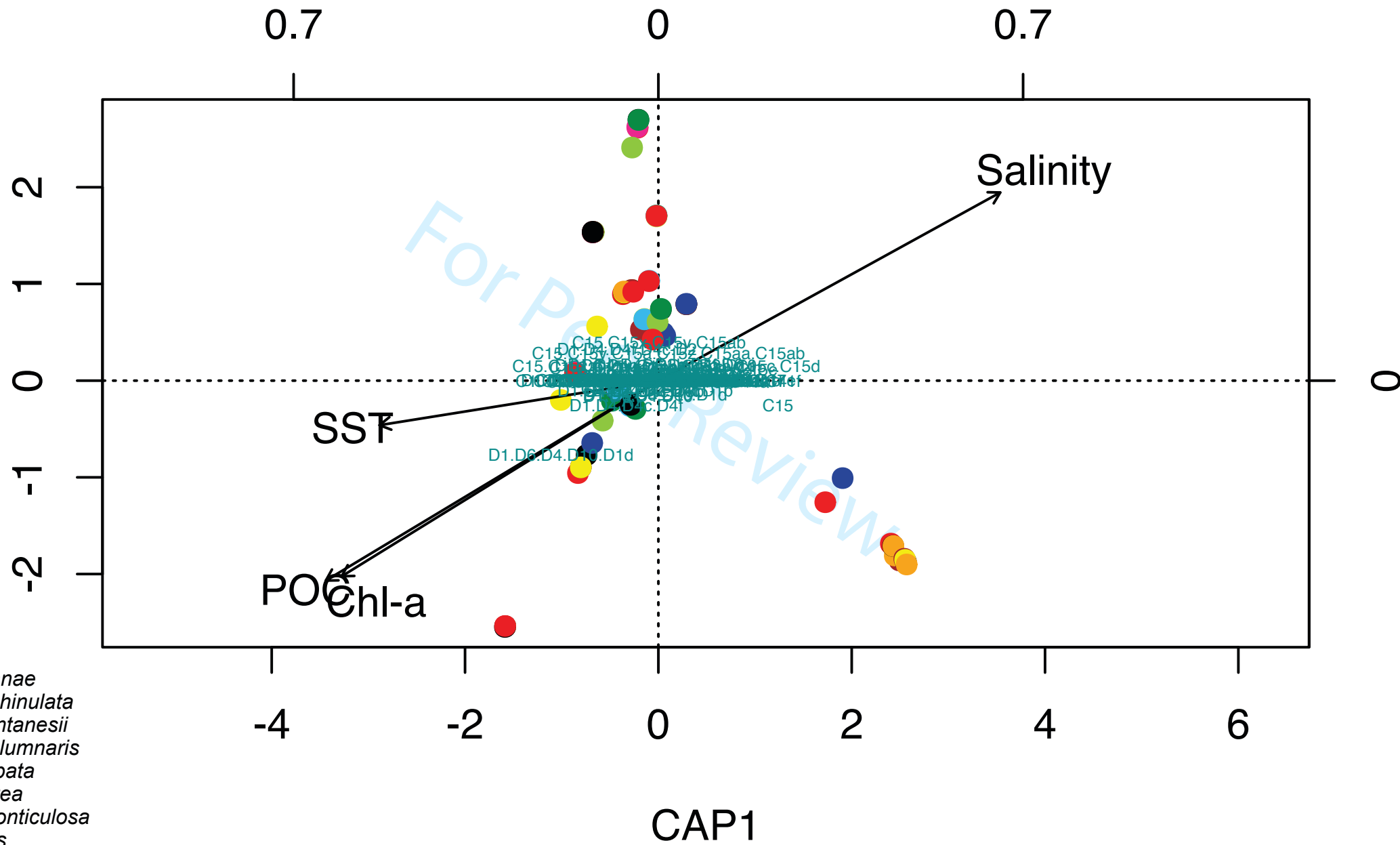
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(i) Symbiodiniaceae ITS2 type profiles - *Porites* morphological species

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SUPPORTING INFORMATION

Environmental latitudinal gradients and host specificity shape Symbiodiniaceae distribution in Red Sea *Porites* corals

Tullia I. Terraneo, Marco Fusi, Benjamin C. C. Hume, Roberto Arrigoni, Christian R. Voolstra, Francesca Benzoni, Zac H. Forsman, Michael L. Berumen

Appendix S5 PERMANOVA results calculated for the time of sampling (expressed as month/year) for the datasets Symbiodiniaceae genus, Symbiodiniaceae majority ITS2 sequences, and Symbiodiniaceae ITS2 type profile. df = degrees of freedom.

	Symbiodiniaceae genus			Symbiodiniaceae majority ITS2 sequences		Symbiodiniaceae ITS2 type profiles	
	df	<i>F</i>	<i>p</i>	<i>F</i>	<i>p</i>	<i>F</i>	<i>p</i>
<i>Sampling Time</i>	6	5.1843	0.001	2.3551	0.001	1.6933	0.001
Res	73						