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

Running Title: Symbiodiniaceae diversity in Red Sea *Porites*

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ACKNOWLEDGEMENTS

This research was undertaken in accordance with the policies and procedures of the King Abdullah University of Science and Technology (KAUST). Permissions relevant for KAUST to undertake the research have been obtained from the applicable governmental agencies in the Kingdom of Saudi Arabia. This project was supported by funding from KAUST (award # URF/1/1389-01-01, FCC/1/1973-07, and baseline research funds to C. R. Voolstra and M. L. Berumen).

The views expressed are purely those of the writers and may not in any circumstance be regarded as stating an official position of the European Commission.

We wish to thank the captain and crew of the MV Dream Master, the KAUST Coastal and Marine Resources Core Laboratory, and A. K. Gusti (KAUST) for fieldwork logistics in the Red Sea.

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

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

Methods

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

Results

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

Main conclusions

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

Keywords

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

INTRODUCTION

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

Symbiodiniaceae diversity in reef ecosystems is high and the specificity and variability of the associations that scleractinian-hosts form with these symbionts have proven to confer ecological advantages to corals under different ecological conditions (Berkelmans & van Oppen, 2006; LaJeunesse et al., 2010; Rosic et al., 2015; Hume et al., 2016). These associations influence the geographical zonation patterns of corals at large and small scales and provide the corals with different tolerance to light intensity (Baker, 2001) and temperature (Rowan & Knowlton, 1995; Glynn et al., 2001; Berkelmans & van Oppen, 2006). Indeed, different Symbiodiniaceae-host interactions impact the corals' susceptibility to bleaching events (for a definition of bleaching see van Oppen & Lough, 2018). The potential of corals to "shuffle" (*i.e.*, replacement of dominant population by a background resident population) or "switch" (*i.e.,* the exogenous uptake of a different population from the environment) their symbiont communities towards more tolerant ones could also play a major role towards ecological resilience of coral reefs (Baker et al., 2004; Sampayo et al., 2008; Kemp et al., 2014), yet this potential remains questionable, and the diversity of the symbiont communities associated with different hosts seems to be non-random (Rowan 1991; Trench 1988, 1992). Different patterns of host-symbiont associations have been documented in response to latitudinal, longitudinal, and environmental gradients, for various geographic locations and host taxa (Oliver & Palumbi, 2009; Huang et al., 2011; Keshavmurthy et al., 2014; Hume et al., 2015, 2016; Ziegler et al., 2015, Tonk et al., 2017). Nevertheless, our knowledge of the specificity and diversity of these associations is still poor, limiting our understanding of the ecological benefits that different associations provide (LaJeunesse et al., 2018).

Despite the lack of a single commonly accepted molecular marker for Symbiodiniaceae diversity typing, the Internal Transcribed Spacer II (ITS2) region is currently the most widely used barcode locus within the family (Hume et al., 2016, 2018; Smith et al., 2017). The multi-copy nature of this marker means that both intragenomic and intergenomic sequence variants may be present within any single coral Symbiodiniaceae sample. Distinguishing between these sequence variant sources is difficult and therefore the majority of commonly used analytical approaches aim to collapse the confounding intragenomic diversity (Arif et al., 2014; Cunning et al., 2017). However, the intragenomic diversity harboured within every Symbiodiniaceae genome may be taxonomically informative. Gel-based techniques have made use of this diversity to improve taxonomic resolution for more than 15 years (LaJeunesse, 2002). Most recently, the *SymPortal* analytical framework (symportal.org; github.com/SymPortal/SymPortal_framework; Hume et al., 2019) has been developed to make use of this intragenomic diversity for resolving genetic delineations using next generation sequencing (hereafter "NGS") ITS2 data. By leveraging the informative nature of Symbiodiniaceae intragenomic diversity, finer-scale resolutions of genetic delineations are now possible; these delineations far surpass what were previously achievable with the ITS2 marker (Smith et al., 2017; Thornhill et al., 2017; Hume et al., 2019).

As one of the hottest and most saline regions of the ocean, the Red Sea represents an ideal setting to explore Symbiodiniaceae diversity in a system where natural conditions are already exceeding the thresholds typical for Scleractinia persistence elsewhere in the world. Moreover, due to limited freshwater inflow, low circulatory exchange with the Indian Ocean, and high evaporation rates (~2m year^{-1}), the Red Sea displays extreme latitudinal environmental gradients (Trommer et al., 2009; Raitos et al., 2013). In particular, the sea surface temperature (SST) maxima ranges from 26°C (± 1.1°C) in the north to 31.3°C (± 1.1°C) in the south (Osman et al., 2018), the primary productivity increases from northern oligotrophic waters to southern nutrient rich waters (Raitos et al., 2013), and the salinity drops from 41 in the north to 36 in the south (Ngugi et al., 2012). Symbiodiniaceae diversity in the Red Sea has been recently evaluated from the widespread anthozoan host *Palythoa tuberculosa*, and clear biogeographical patterns of association were recovered along the Red Sea latitudinal gradients (Reimer et al., 2017).

The Red Sea is also recognized as a marine biodiversity hotspot, harbouring more than 2000 species of fish and 50 genera of corals (Briggs & Bowen, 2012; Berumen et al., 2013; DiBattista et al., 2016a, b). Hermatypic corals of the cosmopolitan genus *Porites* are among the most abundant, widespread, and diverse zooxanthellate scleractinians in the Red Sea (Sheppard & Sheppard, 1991). Up to 15 species of *Porites* have been reported from the region following traditional morphology-based classifications (Sheer & Pillai, 1983; Sheppard & Sheppard, 1991; Veron, 2000), however, species boundaries within the genus remain unresolved (Forsman et al., 2009, 2015, 2017; Prada et al., 2014; Dimond et al., 2017). Besides their role as fundamental reef builders, *Porites* corals are also among the most resistant corals to increasing water temperatures (LaJeunesse et al., 2003). During both the 2010 and the 2016 bleaching events, *Porites* was among the least affected coral genera in the Red Sea, with less than 40% of the resident population showing signs of bleaching (Furby et al., 2013; Monroe et al., 2018).

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

MATERIALS AND METHODS

Sampling and identification

A total of 80 *Porites* coral colonies were collected at seven coastal localities along the Saudi Arabian Red Sea between 2013 and 2016 (Fig. 1, Appendix S1 in Supporting Information). Logistical reasons prevented us from sampling all regions at the same time. Each coral colony was imaged in the field using a Canon G15 camera while SCUBA diving. A fragment of approximately 10cm^3 was sampled from each scleractinian colony using hammer and chisel. Once in the laboratory, a subsample of 1cm^3 was taken from each specimen and preserved in 99% ethanol for further molecular analyses. The rest of the coral was bleached in sodium hypochlorite for 48 hours to remove fresh tissue and was air dried for further morphological observations. Dried skeletons were imaged using a Canon G15 and were used for traditional morphology-based species identification.

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

Coral host DNA extraction and PCR amplification

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

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

Coral host phylogeny reconstructions

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

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

Symbiodiniaceae MiSeq sequencing library preparation

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

Symbiodiniaceae MiSeq data processing

Symbiodiniaceae NGS ITS2 data were analysed using the *SymPortal* framework (Hume et al., 2019) by submitting paired fastq.gz files directly to the framework. A standardized quality control (QC) of sequences was conducted as part of the submission. Briefly, the standard *SymPortal* QC is conducted using mothur 1.39.5 (Schloss et al., 2009), the BLAST+ suite of executables (Camacho et al., 2009), and minimum entropy decomposition (MED; Eren et al., 2015). The MED incorporated into the standard SymPortal QC pipeline uses an ‘M’ value cutoff meaning that MED nodes (a proxy for representative sequences) are identified down to a relative within sample, genus-partitioned abundance of 0.4% (i.e. 0.4% of the sequences for a given genus in a given sample; or four sequences if the sequencing is very shallow). As such, the ITS2 type profile predictions in the standard outputs of SymPortal should be viewed as being representative of the more abundant genotypes present in any given sample’s genus portioned collection genotypes (sequences are analysed on a genus partitioned basis within the SymPortal framework). Whilst the SymPortal approach of searching for genotypic representative sets of sequences can be applied to identify low abundance genotypes within samples (by searching for identified ITS2 type profiles in the pre-MED decomposition sequences that are also output by the SymPortal QC; providing that sequencing depth is adequate), this study concerned itself with only the standard output and thus the more abundant genotypes in the genus partition. This standard output contains two count tables: one provides sequence abundances listed by sample (see Appendix S3 in Supporting Information), and the second provides ITS2 type profile abundances listed by sample (see Appendix S3 in supporting Information). In the second count table, alongside the ITS2 type profile abundances, different hierarchical levels are given for each of the identified Symbiodiniaceae genotypes. Specifically, for this analysis, the clade (genus), majority ITS2 sequence (most abundant ITS2 sequence), and ITS2 type profile (representative of putative taxa) were used. The source code and detailed documentation of the logic underlying the SymPortal analysis are available from its GitHub repository (Hume 2019).

Environmental data

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

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

Statistical analyses

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

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

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

RESULTS

Traditional and molecular identification of *Porites*

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

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

Symbiodiniaceae community structure

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

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

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

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

Symbiodiniaceae biogeography across Red Sea gradients

The Red Sea environmental gradients correlated with the Symbiodiniaceae biogeographical patterns observed. Sequence data showed a shift from the genus *Cladocopium* to *Durusdinium* going from the north (Gulf of Aqaba and Duba) to the south (Farasan Islands) of the Red Sea, with corals in the central part of the Red Sea (Al Wajh, Yanbu, Thuwal, Farasan Banks) harbouring both *Cladocopium* and *Durusdinium* (Fig 1, 3). *Symbiodinium* appears mainly in the Farasan Islands at relative low abundance, and at very low abundance (never above 1%) in the rest of the localities. Similar biogeographical patterns highlighting a community break south of the Gulf of Aqaba have been previously found in different anthozoans symbiont communities. For example, similar patterns with Symbiodiniaceae community break at the entrance of the Gulf of Aqaba were also recorded by Reimer et al., (2017) for the Zoantharia *P. tuberculosa*. Nevertheless, although a different *Cladocopium* community was found outside the Gulf of Aqaba, this former work found *Cladocopium* from the Gulf of Aqaba to the Thuwal area, where *Durusdinium* also appeared. Sawall et al. (2014) found discontinuity in the symbiont communities associated with the coral *Pocillopora verrucosa* between the Gulf of Aqaba and the rest of the Red Sea. Similar to our findings, *P. verrucosa* colonies from the Gulf of Aqaba were characterized by the unique association with the genus *Cladocopium*, while only *Symbiodinium* was found in the remaining sites of the central and southern Red Sea. Similarly, Arrigoni et al. (2016) investigated the symbiont community of Red Sea *Stylophora.* All samples from the Gulf of Aqaba harboured *Cladocopium*, while outside coral host colonies also associated with *Symbiodinium*. This break has been proposed to be mainly driven by cooler temperature at the entrance of the Gulf of Aqaba and, in particular*,* has been proposed that *Cladocopium* might have colder water preference (Ulstrup et al., 2006, Sawall et al., 2014). However, whilst this cooler water preference hypothesis may be an effective explanation for individual Symbiodiniaceae taxa, it is important to note that this trend should not be extrapolated to include the whole of the genus *Cladocopium*, especially when exceptionally thermally tolerant members exist, *i.e. C. thermophilum.* (D'Angelo et al., 2015).

Genetic breaks have also been documented among populations between the central Red Sea and the Farasan Islands in the south. For example, genetic breaks have been reported in different fish populations, (Froukh & Kochzius, 2007; Nanninga et al., 2014; Saenz-Agudelo et al., 2015), sponges (Giles et al., 2015), and mussels (Shefer et al., 2004). From these studies, the genetic brakes matched with environmental transitions occurring around 16˚- 20˚ N in the Red Sea. In contrast to the rest of the Red Sea, the Farasan Islands region is a shallow reef system, characterized by less saline but warm, eutrophic, and turbid waters (Sheppard & Sheppard, 1991). Our data show a predominance of *Durusdinium* sequences in this environment, with high proportions of *D. trenchii* (D1-D4) expected. This distribution fits into theories that *D. trenchii* is a stress-resilient taxon within the Symbiodiniaceae, and thus found in association with warm and turbid environments or in response to stressful events (Baker, 2001; LaJeunesse et al., 2008). Recent studies showed association of *P. lutea, P. lobata,* and *P. harrisoni* with *C. thermophilum* symbionts in the southern Arabian Gulf where SST (36° C) and salinity (42) levels exceed the ones from the Red Sea (D'Angelo et al., 2015; Hume et al., 2016, 2018). D'Angelo et al. (2015) showed a community transition along the temperature and salinity gradient occurring between the southern Arabian Gulf and the Gulf of Oman: *C. thermophilum* was associated with 100% of *Porites* in the southern Arabian Gulf; in the transition zone between the Arabian Gulf and the Gulf of Oman *Porites* associated with *C. thermophilum* as well as C15 lineages and *D. trenchii*; finally, in the Gulf of Oman, where environmental conditions more resemble those present elsewhere in the tropical Indo-Pacific belt, *Porites* associated mainly with C15 lineages, as elsewhere in *Porites* hosts. In the Red Sea, we find a similar pattern. In the north and central Red Sea, *Porites* is found mainly in association with C15 radiation, the most common symbiont association within *Porites*. In the south, where the thermal stressors are higher (although not reaching levels as extreme as in the Arabian Gulf) *Porites* associates with the more resilient *D. trenchii*.

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

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

Host-symbiont specificity

By identifying previously overlooked Symbiodiniaceae ITS2 sequences, we were able to identify host-specific association patterns. Indeed, our data showed coupling between *Porites* genotypes (clade I to V) and Symbiodiniaceae ITS2 type profiles and the majority sequences that represent them. C15 radiation sequences were shared among four of the five genetic lineages of *Porites*, and made up the most of the ITS2 sequences in Clade I, II and V, confirming that the C15 radiation is commonly associated with *Porites* (LaJeunesse 2004; 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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Biosketch

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

Author contributions

T.I.T, R.A, M.L.B designed the study; T.I.T and F.B collected specimens; T.I.T performed molecular work and data analyses; B.C.C.H ran the *SymPortal* analysis; M.F performed 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, F.B, M.L.B.

TABLES

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).

		Symbiodiniaceae genus		**Symbiodiniaceae majority ITS2 sequences**		**Symbiodiniaceae ITS2 type profiles**	
	df	*F*	*p*	*F*	*p*	*F*	*p*
***Porites* molecular clade**	4	1.1427	0.307	1.7108	0.01	1.7959	0.001
Res	75						
CAP				48.75%		55%	
***Porites* 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	*F*	*p*	% var
Symbiodiniaceae genus	SST	20.289	0.001	20.64
	Chl- *a*	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- *a*	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- *a*	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.

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.

Figure 1

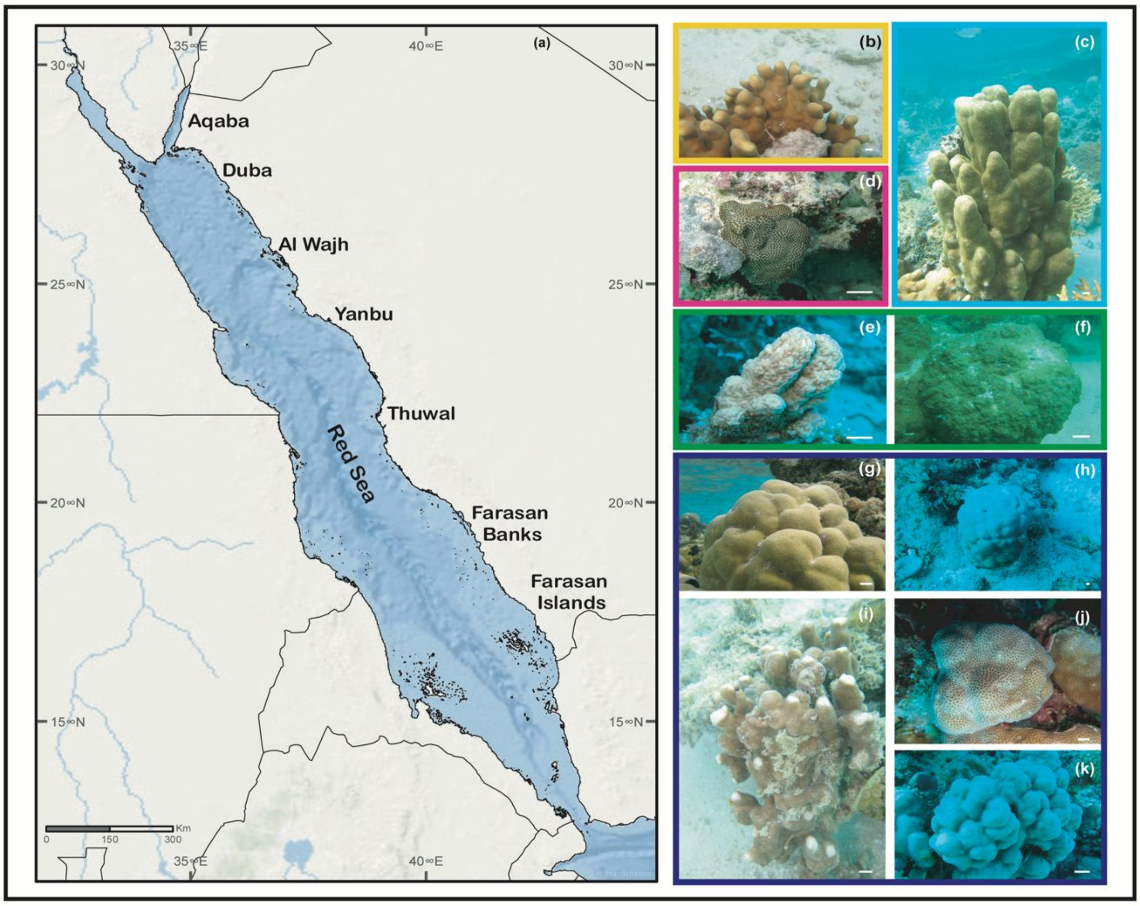


Figure 2

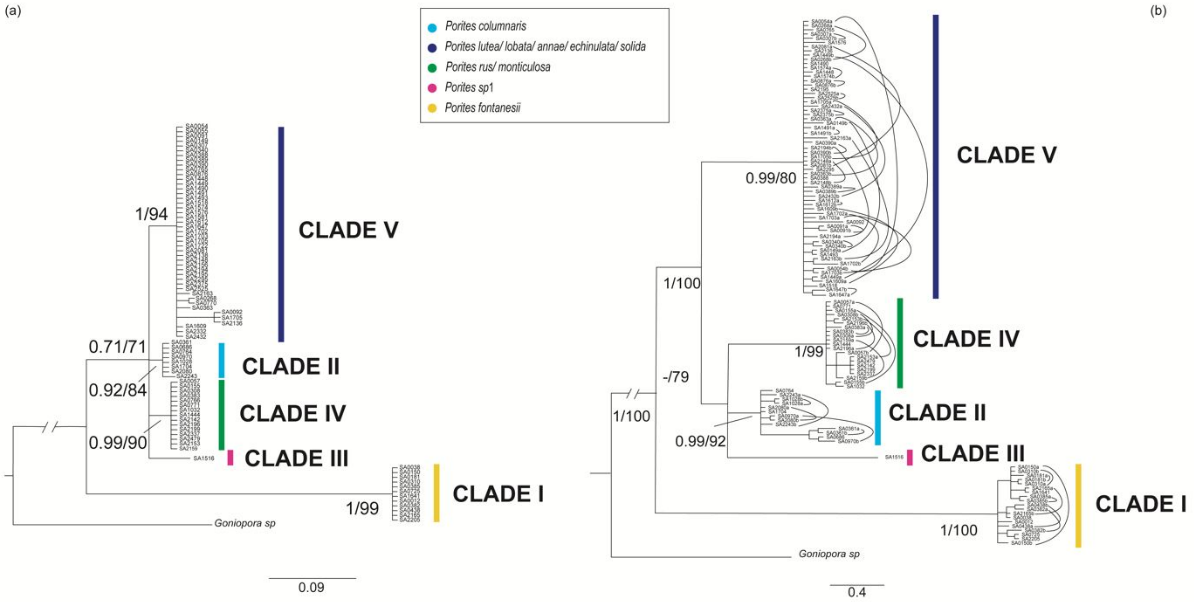
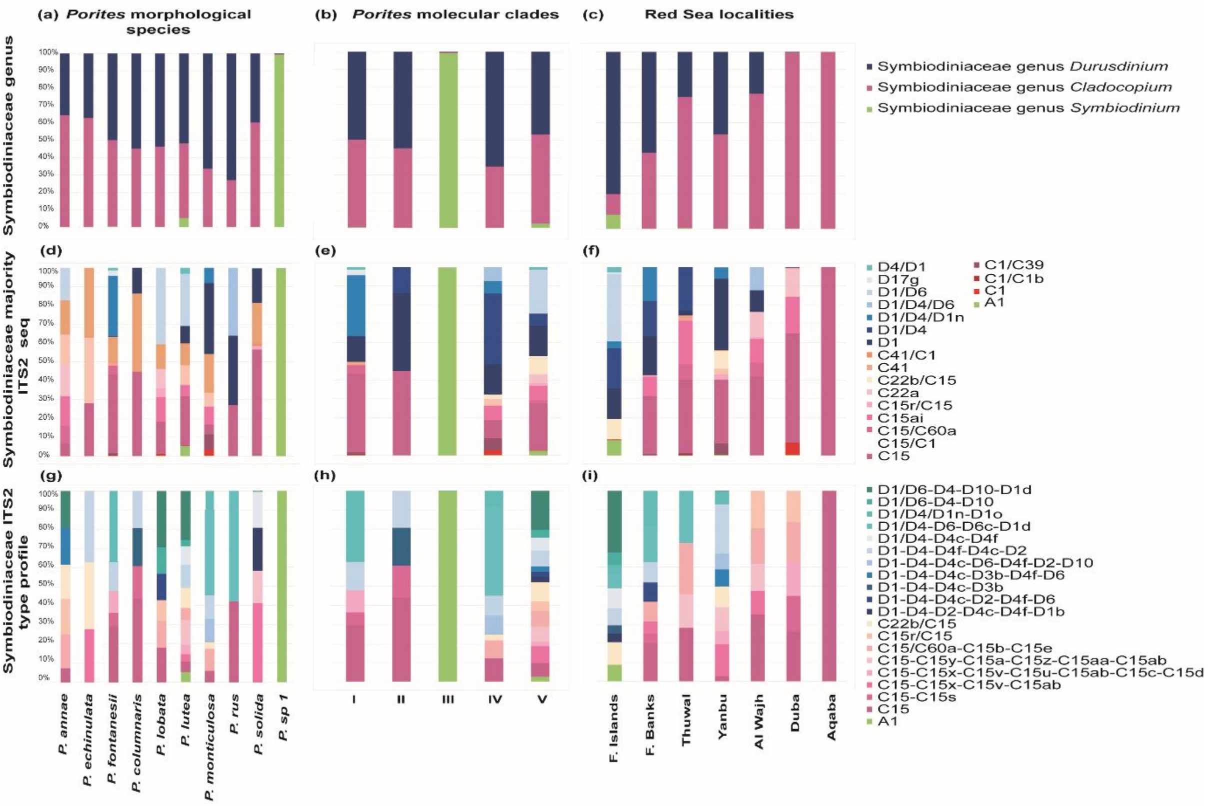


Figure 3



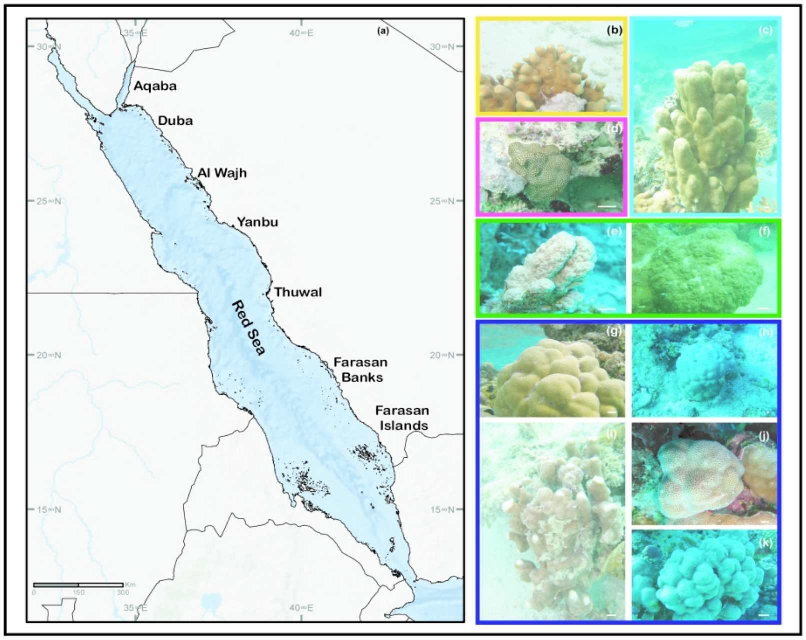
SUPPORTING INFORMATION

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

Appendix S4 Bi-plot CAP ordination of *Porites* (divided for location, molecular clades and morphological species) and Symbiodiniaceae clade (a-c), majority ITS2 sequence (d-f) and ITS2 type profiles (g-i) in relation with the four environmental variables studied.

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.



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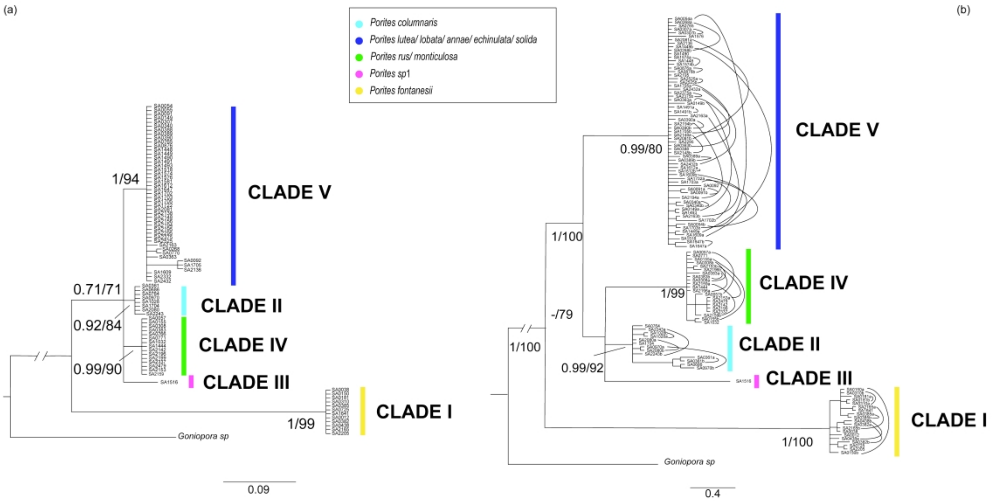

Figure 2 RAxML phylogeny reconstructions of Red Sea Porites at two molecular loci. (a) mitochondrial Control Region (b) nuclear Internal Transcribed Spaces region. Number on the branches represent support values corresponding to Bayesian posterior probabilities (>90%), ML bootstrap values (>70%). Goniopora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

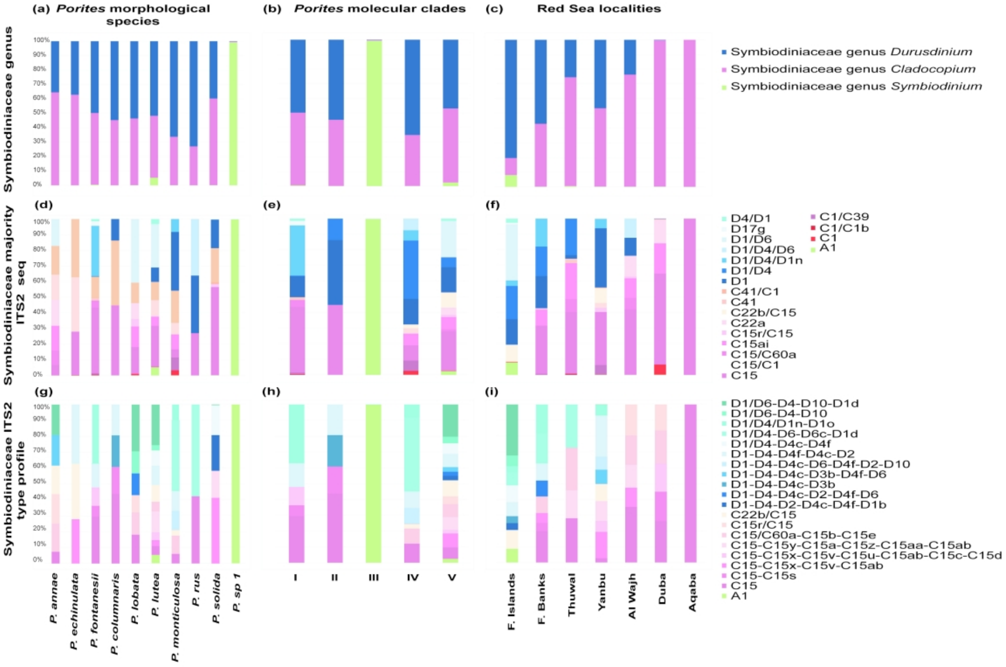

Figure 3 Stacked bar charts (100%) comparing Symbiodiniaceae diversity at the (a) (b) (c) genus level, (d) (e) (f) majority ITS2 sequence level (the 20 most abundant shown), (g) (h) (i) ITS2 type profile level (the 20 most abundant shown). For each of these three datasets, bar charts were plotted for 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	*Porites columnaris*	30/09/2013	Aqaba	28.264, 34.855	MK902958	MK881231 MK881232	II
SA1028	*Porites columnaris*	30/09/2013	Aqaba	28.264, 34.855	MK902959	MK881233 MK881234	II
SA1032	*Porites monticulosa*	30/09/2013	Aqaba	28.264, 34.855	MK902960	MK881235	IV
SA0725	*Porites fontanesii*	26/09/2013	Duba	27.998, 35.204	MK902951	MK881223	I
SA0764	*Porites columnaris*	27/09/2013	Duba	27.998, 35.204	MK902952	MK881183 MK881224	II
SA0765	*Porites lutea*	27/09/2013	Duba	27.998, 35.204	MK902953	MK881225	V
SA0766	*Porites monticulosa*	27/09/2013	Duba	27.998, 35.204	MK902954	MK881226	IV
SA0770	*Porites lobata*	27/09/2013	Duba	27.998, 35.204	MK902955	MK881227	V
SA0771	*Porites rus*	27/09/2013	Duba	27.998, 35.204	MK902956	MK881228	IV
SA0876	*Porites annae*	28/09/2013	Duba	27.998, 35.204	MK902957	MK881229 MK881230	V
SA0686	*Porites columnaris*	25/09/2013	Al Wajh	25.345, 36.891	MK902950	MK881222	II
SA2243	*Porites columnaris*	31/01/2016	Al Wajh	25.345, 36.891	MK902997	MK881290 MK881291	II
SA2295	*Porites lutea*	31/01/2016	Al Wajh	25.345, 36.891	MK902998	MK881292	V

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

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

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

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SUPPORTING INFORMATION

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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’-AGCAGACGCGGTGAAACTTA-3’) and zpCOX3r (5’-GCCCAAGTAACAGTACCCCC-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 Heathcare, 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’-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGGATCCATATGCTTAAGTTCAGCGGGT- 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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SUPPORTING INFORMATION

Environmental latitudinal gradients and host specificity shape Symbiodiniaceae

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

Appendix S3 SymPortal outputs and environmental data (DIVs proportions)

Samples	A1	A1c	A1a	A1k	A1l	C15
SA0012	0	0	0	0	0	0
SA0038	0	0	0	0	0	0.333
SA0054	0	0	0	0	0	0.629
SA0055	0	0	0	0	0	0.847
SA0057	0	0	0	0	0	0.006
SA0091	0	0	0	0	0	0
SA0092	0	0	0	0	0	0
SA0149	0	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

SA1032	0	0	0	0	0	0.451
SA1444	0	0	0	0	0	0
SA1448	0	0	0	0	0	0
SA1449	0.413	0	0	0	0	0.002
SA1490	0	0	0	0	0	0
SA1491	0.394	0.001	0.001	0.002	0	0.016
SA1493	0	0	0	0	0	0
SA1516	0.956	0	0	0	0	0.001
SA1518	0	0	0	0	0	0
SA1574	0	0	0	0	0	0
SA1576	0	0	0	0	0	0
SA1581	0.002	0	0	0	0	0.055
SA1609	0.002	0	0	0	0	0.001
SA1612	0	0	0	0	0	0
SA1641	0.003	0	0	0	0	0
SA1647	0	0	0	0	0	0
SA1702	0	0	0	0	0	0
SA1703	0	0	0	0	0	0.109
SA1704	0	0	0	0	0	0
SA1705	0	0	0	0	0	0
SA1722	0	0	0	0	0	0
SA2080	0	0	0	0	0	0
SA2081	0.002	0	0	0	0	0.487
SA2136	0	0	0	0	0	0.504
SA2138	0.005	0	0	0	0	0.368
SA2142	0	0	0	0	0	0
SA2148	0	0	0	0	0	0
SA2153	0	0	0	0	0	0
SA2156	0	0	0	0	0	0.51
SA2159	0	0	0	0	0	0
SA2163	0.001	0	0	0	0	0.517
SA2165	0	0	0	0	0	0.335
SA2194	0.003	0	0	0	0	0.287
SA2195	0	0	0	0	0	0.827
SA2196	0.006	0	0	0	0	0.226
SA2199	0	0	0	0	0	0.002
SA2205	0	0	0	0	0	0
SA2243	0.003	0.001	0	0	0	0.002
SA2295	0.004	0.001	0	0	0	0.805
SA2332	0	0	0	0	0	0.406
SA2337	0	0	0	0	0	0
SA2375	0	0	0	0	0	0.451
SA2432	0	0	0	0	0	0.186

SA2479	0	0	0	0	0	0.422
SA2525	0	0	0	0	0	0.545

distribution in Red Sea *Porites* corals

ncesca Benzoni, Zac H. Forsman, Michael L. Berumen

C22b	C1	C15ai	C22a	C15x	C15b	C15v
0	0.002	0	0	0	0	0
0	0.001	0	0	0.051	0	0
0	0	0	0	0	0.15	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
0	0	0.077	0	0.096	0	0.048
0	0.028	0	0	0	0	0
0	0.004	0	0	0	0	0
0	0	0	0	0.017	0	0.017
0.768	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	0.011	0	0	0	0	0
0	0	0	0	0	0	0
0	0.003	0	0	0	0	0
0	0.016	0	0	0.014	0	0.047
0	0	0	0	0	0	0
0	0.009	0	0	0.013	0	0.031
0	0	0	0	0.001	0.123	0
0	0	0	0	0.047	0	0.038
0	0.003	0	0	0.004	0	0.013
0	0.043	0	0	0.009	0	0.033
0	0	0	0	0	0	0
0	0.007	0	0	0.003	0	0
0	0	0	0	0	0	0
0	0	0	0	0.133	0	0.111
0	0.286	0	0	0	0	0
0	0.002	0	0	0.009	0	0.017
0	0	0	0	0.02	0	0.008
0	0.001	0	0	0	0.151	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0.001	0	0	0.012	0	0.005
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
0.002	0.002	0	0	0.001	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	0.002	0	0	0	0	0
0	0	0	0	0	0	0
0.791	0.001	0	0	0	0	0
0	0.022	0	0	0	0	0
0	0.001	0	0	0	0	0
0	0.004	0	0	0	0	0
0	0.004	0	0	0	0	0
0	0	0	0	0	0	0
0.606	0.002	0	0	0	0	0
0.002	0.002	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	0.028	0	0.03
0	0	0	0	0.093	0	0.028
0	0.018	0	0	0.04	0	0.03
0	0.366	0	0	0	0	0
0	0	0	0	0	0	0
0	0.002	0	0	0	0	0
0	0.003	0	0	0.08	0	0.028
0	0	0	0	0	0	0
0	0.001	0	0	0.008	0	0.03
0	0.006	0	0	0.126	0	0.081
0	0.001	0.318	0	0.067	0	0.045
0.047	0	0.012	0	0	0	0
0.046	0.002	0	0.378	0	0	0
0	0.001	0	0	0	0	0
0	0.006	0	0	0	0	0
0	0.002	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	0.077	0	0.066	0	0.035
0	0.289	0	0	0.007	0	0.009

0	0.003	0	0	0	0.28	0
0	0	0	0	0.059	0	0.016

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

0.001	0	0	0.017	0.004	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	0	0	0
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	0.001	0.043	0	0	0
0	0	0.008	0	0	0	0
0	0	0	0	0	0	0
0	0	0.002	0	0	0	0
0	0	0.003	0	0	0	0
0	0	0	0	0	0	0
0	0	0.001	0.036	0	0	0.001
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
0.039	0	0	0.047	0.009	0	0.014
0.02	0	0	0.034	0.011	0	0.005
0.012	0	0.006	0.018	0.013	0	0.02
0	0	0.129	0	0	0	0
0	0	0	0	0	0	0
0	0	0.001	0	0	0	0
0.014	0	0.001	0.004	0.012	0.004	0
0	0	0	0	0	0	0
0.035	0	0.001	0.049	0.009	0	0.025
0.053	0	0.002	0.02	0.007	0.038	0
0	0	0	0	0.008	0	0
0	0	0	0	0	0	0
0	0	0	0.038	0	0	0.018
0	0	0	0	0	0	0
0	0	0.002	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
0.008	0	0	0	0.015	0	0
0.002	0	0.013	0	0.033	0.015	0

0	0	0	0	0	0	0
0.019	0	0	0.031	0	0	0.012

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	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

0.001	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	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.04
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.024	0	0.032	0	0.001	0.033	0
0.016	0	0.019	0	0	0.031	0
0.006	0.061	0.025	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	0.006	0	0	0.063	0
0	0	0	0	0	0	0
0.019	0	0.035	0	0	0.028	0
0	0	0	0	0	0.061	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	0.045	0	0
0	0	0.002	0	0	0	0.006
0	0	0	0	0	0	0
0	0	0	0	0	0.01	0
0	0	0	0	0	0	0

0	0	0	0.032	0	0	0
0.03	0	0.025	0	0	0.016	0

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	0	0
0	0	0	0	0.001	0.001	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.005	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

0	0	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	0.001	0	0.001	0.001	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	0.001
0	0	0	0	0	0	0
0	0	0	0	0	0.001	0
0.001	0	0	0	0.002	0.007	0.003
0	0	0	0	0	0	0
0.001	0	0	0	0.001	0.001	0.001
0	0	0	0	0.001	0	0.001
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	0	0
0	0	0	0	0	0	0
0.004	0	0	0	0	0	0
0	0.03	0	0	0	0	0
0	0.009	0	0	0	0	0
0.001	0.021	0	0	0.003	0.032	0.001
0.005	0	0	0	0.104	0.118	0.002
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.008	0	0	0.004	0.001	0
0	0	0	0	0	0	0
0	0.033	0	0	0	0.001	0
0	0	0	0	0.002	0.002	0
0.002	0	0	0	0	0	0
0	0	0	0	0	0	0
0.001	0	0	0	0	0.001	0
0	0	0	0	0	0	0
0	0	0	0	0.001	0.001	0
0	0	0.026	0	0.001	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
0.003	0	0	0	0.012	0.003	0.001

0	0	0	0.12	0	0	0
0	0.024	0	0	0	0	0

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
0.007	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

0	0	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	0.001	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	0.001
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	0.001	0	0.002	0
0	0	0	0	0	0	0
0	0	0	0	0	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
0.019	0	0.004	0	0	0	0.001
0	0	0.004	0	0	0	0.007
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.002	0	0	0.007	0	0.002	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.035	0	0	0.001	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	0.004	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	0
0.007	0	0	0	0	0	0
0.002	0	0.002	0.015	0	0.012	0

0	0	0	0.002	0	0	0
0	0	0	0	0	0	0

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

0	0	0.001	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
0.005	0	0	0	0.002	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	0	0	0	0	0	0
0.001	0	0	0	0.002	0	0
0.001	0	0	0	0	0	0.001
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	0.002	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
0.014	0	0	0	0.001	0	0
0	0	0	0.003	0	0	0.005
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
0.001	0	0	0	0	0	0
0.001	0	0.002	0	0	0	0
0	0	0	0	0.001	0	0
0	0	0	0	0.003	0	0
0.001	0	0	0	0.003	0	0
0.001	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	0.001	0	0
0	0	0	0	0.5	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.031	0.003	0	0	0

0	0	0.002	0	0	0	0
0.001	0	0	0	0.001	0	0

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
0	0	0	0	0	0	0
0	0	0	0	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
0	0	0	0	0	0	0
0	0	0	0	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	0.003	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
0.005	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	0.001	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	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	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	0.006
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	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	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
0.001	0	0	0	0	0.001	0.001
0.004	0	0	0	0.006	0	0.008
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	0.001	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	0	0	0
0	0	0	0	0	0	0
0.001	0	0	0.01	0.001	0	0.001

0	0	0	0.001	0	0	0
0	0	0	0	0	0	0

C72a	C1ae	C15ac	C41b	C39c	C15m	C3az
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	0.002	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0	0	0	0
0	0	0	0.009	0	0.001	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	0	0	0	0	0
0	0.006	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.002	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0.002	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
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0.001	0	0	0
0	0.025	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
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0.001

0	0	0.002	0	0	0	0
0	0	0	0	0	0	0

C72c	C115	C3au	C72b	C41c	C72d	C163b
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0	0	0	0

C7	C50f	C39d	C1z	C3v	C39e	C1e
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	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	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	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	0

C15k	C39b	C1i	C91	C40	C29	C15.8
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	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	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	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	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0

C116g	C89	C3bl	D1	D4	D6	D17g
0	0	0	0.238	0.242	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.361	0.222	0.207	0
0	0	0	0.551	0.168	0.002	0
0	0	0	0.543	0.113	0.029	0
0	0	0	0	0	0	0
0	0	0	0.342	0.221	0	0
0	0	0	0.265	0.209	0.215	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.369	0.248	0.256	0
0	0	0	0.271	0.235	0.25	0
0	0	0	0.053	0.048	0	0.208
0	0	0	0.539	0.218	0	0
0	0	0	0.326	0.276	0.001	0
0	0	0	0.46	0.269	0	0
0	0	0	0.014	0.009	0	0
0	0	0	0.392	0.238	0.223	0
0	0	0	0.008	0.007	0.005	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.028	0.021	0	0
0	0	0	0.004	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	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	0.002	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	0.41	0.192	0.191	0
0	0	0	0.258	0.431	0	0
0	0	0	0.26	0.051	0.14	0
0	0	0	0.292	0.402	0	0
0	0	0	0.112	0.368	0.003	0
0	0	0	0.26	0.398	0	0
0	0	0	0.001	0	0	0
0	0	0	0.364	0.239	0.278	0
0	0	0	0.354	0.238	0.261	0
0	0	0	0.354	0.213	0.296	0
0	0	0	0.002	0.002	0.001	0
0	0	0	0.329	0.219	0.267	0
0	0	0	0.29	0.102	0.44	0
0	0	0	0.316	0.341	0.008	0
0	0	0	0.268	0.198	0.367	0
0	0	0	0.442	0.231	0.213	0
0	0	0	0.021	0.013	0.011	0
0	0	0	0.649	0.185	0	0
0	0	0	0.421	0.177	0	0
0	0	0	0.295	0.124	0.373	0
0	0	0	0.665	0.145	0	0
0	0	0	0.001	0.001	0.001	0
0	0	0	0	0	0	0
0	0	0	0.006	0.004	0.003	0
0	0.001	0	0.004	0.002	0	0
0	0	0	0.619	0.265	0.009	0
0	0	0	0.612	0.14	0.032	0
0	0	0	0	0	0	0
0	0	0	0.616	0.156	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.003	0.002	0.001	0
0	0	0	0	0	0	0
0	0	0	0.004	0.001	0	0
0	0	0	0.325	0.261	0.001	0
0	0	0	0.554	0.228	0	0
0	0	0	0.499	0.095	0.008	0
0	0	0	0	0	0	0
0	0	0	0.002	0.001	0	0
0	0	0	0.389	0.258	0.188	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0

D1n	D10	D2	D4c	D4f	D1o	D6c
0.274	0	0.007	0.004	0	0.091	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	0.021
0	0	0.041	0.042	0.098	0	0
0	0	0.006	0.02	0.139	0	0.003
0	0	0	0	0	0	0
0.095	0	0	0	0	0.025	0
0	0	0.001	0	0	0	0.051
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.028	0	0	0	0	0
0	0.003	0	0	0	0	0.04
0.059	0	0.001	0.001	0	0.003	0
0	0	0.014	0.067	0.068	0	0
0	0	0.171	0.071	0.002	0	0
0	0	0.047	0.07	0.028	0	0
0	0	0	0	0	0	0
0	0.002	0	0	0	0	0.017
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	0.003	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	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0.03
0	0	0	0.016	0.008	0	0
0	0.046	0	0.002	0	0	0.003
0.002	0	0	0.025	0.02	0	0
0	0	0	0.003	0	0	0
0.001	0	0	0.027	0.012	0	0
0	0	0	0	0	0	0
0	0.035	0	0	0	0	0
0	0.068	0	0	0	0	0.002
0	0.046	0	0	0	0	0
0	0	0	0	0	0	0
0	0.048	0	0	0	0	0
0	0.072	0	0	0	0	0
0.084	0.002	0.025	0.01	0	0.043	0
0	0.068	0	0	0	0	0
0	0.033	0	0	0	0	0
0	0.002	0	0	0	0	0
0	0	0	0.039	0.016	0	0
0	0	0.123	0.084	0.05	0	0
0	0.104	0	0	0	0	0
0	0	0.017	0.011	0.036	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
0.005	0	0.001	0.011	0.012	0	0.002
0	0.014	0.022	0.026	0.037	0	0.002
0	0	0	0	0	0	0
0	0	0.033	0.011	0.112	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.118	0	0.016	0.002	0	0.025	0
0	0	0.014	0.071	0.063	0	0
0	0	0.003	0.027	0.14	0	0.001
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.003	0	0	0	0	0.002
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0

D1d	D3b	D5	D9	D4d	D1h	D1m
0	0	0.001	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
0.026	0	0	0.001	0.001	0	0
0	0	0.003	0	0	0.038	0
0.004	0	0	0	0.003	0.016	0
0	0	0	0	0	0	0
0	0	0.005	0	0	0	0.005
0.034	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.022	0	0	0.007	0	0	0
0.033	0	0	0	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.038	0
0	0	0.005	0	0	0.039	0
0	0	0.005	0	0	0.064	0
0	0	0	0	0	0	0
0.02	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	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0.033	0	0	0	0.015	0	0
0	0	0	0	0	0.004	0
0.002	0	0	0.001	0.002	0	0
0	0	0	0	0	0.005	0
0.001	0	0	0	0	0	0
0	0	0	0	0	0.001	0
0	0	0	0	0	0	0
0.018	0	0	0.01	0	0	0
0.012	0	0	0.006	0.002	0	0
0.012	0	0	0.012	0.001	0	0
0	0	0	0	0	0	0
0	0	0	0.002	0	0	0
0.009	0	0	0.003	0	0	0
0	0	0.003	0	0	0.002	0
0.021	0	0	0.004	0	0	0
0.025	0	0	0.007	0	0	0
0.002	0	0	0	0	0	0
0	0.025	0	0	0	0.013	0
0	0	0	0	0	0.028	0
0.005	0	0	0.005	0	0	0
0	0	0.009	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
0	0.019	0	0	0.003	0.009	0
0.02	0.011	0.001	0	0.002	0.006	0
0	0	0	0	0	0	0
0	0	0.011	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	0.003	0	0	0	0.005
0	0	0	0	0	0.035	0
0	0	0	0	0.001	0.015	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.089	0	0	0	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0

D4a	D1c	D1l	D1p	D17	D1b	D2.2
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	0.001
0	0	0	0	0	0	0.001
0	0	0	0	0	0	0
0	0	0	0	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	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	0	0	0
0	0	0.002	0	0	0	0
0	0	0.002	0	0	0	0
0	0.002	0	0	0	0	0
0	0	0	0	0	0	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	0.023	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	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.002
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	0.003	0
0	0	0	0	0	0	0
0	0.002	0	0	0	0	0
0	0	0.003	0	0	0.025	0
0	0	0	0	0	0	0.002
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0.006	0	0	0
0.007	0.001	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	0.007	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

D1q	D1j	D4b	D1i	D1r	D2a	D1k
0	0	0	0	0	0	0
0	0	0	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	0.001	0	0	0.001	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	0.001	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	0.002	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	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
0.001	0	0	0	0.001	0	0
0	0	0	0	0	0.001	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
0.002	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
0.001	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	0.002	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	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	0.001	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	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0

D2b	D17e	D3a	D17c	D6b	D17d	D1t
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0

noName Clad	noName Clad	noName Clad	noName Clade D
0.003	0	0.002	0.128
0.002	0	0.498	0.001
0	0	0.12	0.002
0.002	0	0.132	0
0.004	0	0.003	0.142
0.001	0	0.001	0.045
0.003	0	0.001	0.116
0	0	0.352	0.001
0.004	0	0.017	0.199
0.002	0	0.004	0.206
0	0	0.139	0.001
0.003	0	0.128	0
0.001	0	0	0.07
0.002	0	0.001	0.162
0.001	0	0.001	0.583
0	0	0.012	0.015
0	0	0.002	0.103
0	0	0.002	0.047
0.005	0	0.333	0.003
0	0	0.001	0.105
0.003	0	0.292	0.001
0.001	0	0.096	0.001
0.001	0	0.183	0.001
0.001	0	0.401	0.007
0.002	0	0.465	0.001
0	0	0.174	0
0.003	0	0.497	0.001
0.003	0	0.182	0
0.001	0	0.209	0
0.002	0	0.669	0.001
0.001	0	0.267	0.001
0.001	0	0.088	0
0.001	0	0.13	0
0	0	0.323	0
0.002	0	0.132	0

0.001	0	0.498	0.001
0.001	0	0.001	0.102
0	0	0.002	0.28
0.005	0	0.004	0.054
0.001	0	0.001	0.252
0.003	0	0.022	0.056
0.002	0	0.002	0.294
0.033	0	0.003	0.001
0	0	0.001	0.056
0.001	0	0.001	0.047
0	0	0	0.063
0	0	0.096	0.001
0.001	0	0.013	0.047
0.001	0	0.01	0.057
0.001	0	0.002	0.148
0	0	0.001	0.06
0	0	0.002	0.042
0.001	0	0.136	0.004
0.002	0	0.001	0.06
0	0	0.002	0.086
0.001	0	0.001	0.089
0.002	0	0.001	0.104
0.001	0	0.219	0
0	0	0.227	0.001
0.002	0	0.242	0.002
0	0	0.203	0
0	0	0.003	0.021
0.003	0	0.001	0.056
0	0	0.245	0.001
0	0	0.001	0.049
0.001	0	0.205	0.002
0.002	0	0.221	0.003
0.001	0	0.257	0
0	0	0.11	0.001
0.003	0	0.269	0
0.001	0	0	0.238
0.002	0	0.004	0.014
0.005	0	0.013	0.147
0	0	0.142	0
0	0	0.082	0.004
0	0	0.002	0.067
0.001	0	0.33	0
0.003	0	0.341	0.001

0.002	0	0.133	0.001
0	0	0.218	0.001

Appendix S3 SymPortal outputs and environmental data (profiles proportions)

Sample ID	Molecular Cla	Morphologica	Locality	Site GPS (deg	CHL mean	CHL standard
Sample ID	Molecular Cla	Morphologica	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

SA1516	III	sp 1	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1518	V	annae	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1574	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1576	V	lobata	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1581	V	echinulata	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1609	V	lobata	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1612	V	lobata	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1641	I	fontanesii	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1647	V	lobata	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1702	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1703	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1704	II	columnaris	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1705	V	solida	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA1722	V	lutea	Farasan Islan	16.971, 41.11	1.29687286	0.81816606
SA2080	II	columnaris	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2081	V	lutea	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2136	V	solida	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2138	V	solida	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2142	IV	monticulosa	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2148	V	annae	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2153	IV	monticulosa	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2156	V	echinulata	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2159	IV	monticulosa	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2163	V	lutea	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2165	I	fontanesii	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2194	V	lobata	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2195	V	annae	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2196	IV	monticulosa	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2199	IV	monticulosa	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2205	I	fontanesii	Yanbu	24.101, 38.00	0.31583691	0.09140692
SA2243	II	columnaris	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA2295	V	lutea	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA2332	V	annae	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA2337	IV	rus	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA2375	V	lutea	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA2432	V	annae	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA2479	IV	monticulosa	Al Wajh	25.345, 36.89	0.21075491	0.08272508
SA2525	V	solida	Al Wajh	25.345, 36.89	0.21075491	0.08272508

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
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0.014
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
172.993778	60.653513	29.4634196	1.28347705	39.0019288	0.32380941	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.007
159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0
159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.006
159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0
159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0
159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.004
159.774729	38.8095105	28.3662303	1.9469936	39.5785363	0.03325393	0.005
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0.004
56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0.004
56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
56.9056799	20.7831098	26.8389518	2.28935736	40.2447814	0.02773799	0
52.3827691	26.9438428	24.7764459	2.26550846	40.5997183	0.07612554	0
52.3827691	26.9438428	24.7764459	2.26550846	40.5997183	0.07612554	0
52.3827691	26.9438428	24.7764459	2.26550846	40.5997183	0.07612554	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.411
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
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

279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.951
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.002
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.002
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0.003
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
279.7004	94.8237966	29.0013006	1.7462097	37.4063458	0.33564382	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.003
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.006
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.002
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.004
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0.007
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
94.7747001	30.3791847	28.183788	2.0563684	39.7164665	0.31807164	0
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0.005
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0.006
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0
61.295501	25.2413778	27.144424	2.28303022	40.1202975	0.01756859	0

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

0.004	0.002	0.951	0	0	0	0
0	0.932	0	0	0	0	0
0.005	0.929	0	0	0	0	0
0	0	0	0	0	0	0
0.843	0.005	0.002	0	0	0	0
0.051	0.861	0	0.002	0	0	0
0.013	0.909	0	0	0	0	0
0.009	0.778	0.003	0	0	0	0
0.01	0.918	0	0	0	0	0
0	0.941	0	0	0	0	0
0.713	0.048	0	0	0	0	0
0.005	0.896	0	0	0	0	0
0	0.878	0	0	0	0	0
0	0.9	0	0	0	0	0
0.005	0.872	0	0	0	0	0
0.646	0.003	0.003	0	0	0	0
0.65	0	0	0	0	0	0
0.551	0.015	0.006	0	0	0	0
0.724	0.007	0	0	0	0	0
0	0.933	0	0	0	0	0
0.003	0.879	0	0	0	0	0
0.676	0	0	0	0	0	0
0	0.926	0	0	0	0	0
0.676	0	0	0	0.002	0	0
0.731	0	0	0	0	0	0
0.605	0.006	0.004	0	0	0	0
0.872	0	0	0	0	0	0
0.649	0.005	0.007	0	0	0	0
0.004	0.725	0	0	0	0	0
0.011	0.928	0	0	0	0	0
0.03	0.773	0.005	0	0	0	0
0.803	0	0	0	0.006	0	0
0.901	0.003	0	0	0	0	0
0	0.833	0	0	0	0	0
0.634	0	0	0	0	0	0
0.5	0	0	0	0	0	0
0.85	0	0	0	0	0	0
0.664	0	0	0	0	0	0

majority ITS2 C1/C1b	majority ITS2 C1/C39	majority ITS2 C15	majority ITS2 C15h	majority ITS2 C1/C15	majority ITS2 C3/C3u	majority ITS2 C1
0	0	0	0	0	0	0.005
0.002	0	0.432	0	0	0	0
0	0	0	0	0	0	0
0	0	0.845	0	0	0	0
0	0	0.006	0	0	0	0
0	0	0	0.007	0	0	0
0	0	0	0	0	0	0
0	0	0.527	0	0	0	0
0	0.051	0	0	0	0	0
0	0	0	0	0.009	0	0
0	0	0.81	0	0	0	0
0.002	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.016	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0.004	0	0
0.022	0	0.182	0	0	0	0
0	0	0	0	0	0	0
0	0.02	0.389	0	0	0	0
0	0	0	0	0	0	0
0	0	0.59	0	0	0	0
0.004	0	0.361	0	0	0.001	0
0	0	0	0	0	0	0
0	0	0.813	0	0	0	0
0	0	0.449	0	0	0	0
0	0	0.77	0	0	0	0
0	0	0.732	0	0	0	0
0	0	0	0	0	0	0.283
0.002	0	0	0	0	0	0
0	0	0.625	0	0	0	0
0.001	0	0	0	0	0	0
0	0	0.554	0.015	0	0	0
0	0	0.605	0	0	0	0
0	0	0.447	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	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	0.005	0	0
0	0	0	0	0	0	0
0.002	0	0	0	0	0	0
0	0	0	0	0	0	0.051
0	0	0	0	0.002	0	0
0	0	0	0	0.009	0	0
0	0	0	0	0	0	0.01
0	0	0	0	0	0	0
0	0.005	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	0
0	0	0.646	0	0	0	0
0	0	0.65	0	0	0	0
0	0	0.44	0	0	0	0
0	0.724	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.004	0	0.672	0	0	0	0
0	0	0	0	0	0	0
0.001	0	0.675	0	0	0	0
0.008	0	0.723	0	0	0	0
0	0	0.285	0	0	0	0
0	0	0	0	0	0	0
0.002	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0.011	0	0
0	0	0	0.025	0	0	0
0	0	0.803	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.558	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.664	0	0	0	0

majority ITS2 C1/C72/C15/	majority ITS2 C1/C116/C15	majority ITS2 C3	majority ITS2 C21/C3	majority ITS2 C41/C1	majority ITS2 C15r/C15	majority ITS2 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	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	0.006	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	0.016	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.674	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	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

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	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	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.901	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

majority ITS2 C22b/C15	majority ITS2 C91f	majority ITS2 C3/C1/C41	majority ITS2 C116	majority ITS2 C72	majority ITS2 C15/C60a	majority ITS2 C41
0	0	0	0.001	0	0	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
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	0.111
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	0.859	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	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	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.841	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
0.708	0	0	0	0	0	0
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	0.06	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	0.004	0	0	0	0
0.872	0	0	0	0	0	0
0.271	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.85	0
0	0	0	0	0	0	0

majority ITS2 C15/C72/C1	majority ITS2 C15/C1	majority ITS2 C91e	majority ITS2 C15ai	majority ITS2 C22a	majority ITS2 D1	majority ITS2 D4/D1
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	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	0.848	0
0	0	0	0.077	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.101
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	0.025	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	0.057	0
0	0.326	0	0	0	0.008	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	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	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.482
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	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	0.007	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	0.896	0
0	0	0	0	0	0.878	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	0.007	0
0	0	0	0	0	0.933	0
0	0	0	0	0	0.879	0
0	0	0	0	0	0	0
0	0	0	0	0	0.926	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.316	0	0.006	0
0	0	0	0	0	0	0
0	0	0	0	0.376	0.005	0
0.004	0	0	0	0	0	0
0	0	0	0	0	0.928	0
0	0	0	0	0	0.773	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	0.076	0	0	0
0	0.5	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

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-
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	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	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	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

0	0.002	0	0	0	0.951	0
0	0.932	0	0	0	0	0
0	0.929	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.861	0	0	0	0	0
0	0.909	0	0	0	0	0
0	0	0	0.778	0	0.003	0
0	0.918	0	0	0	0	0
0	0.941	0	0	0	0	0
0	0.048	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0.9	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	0.015	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
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.725	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	0.833	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

type profile	type profile	type profile	type profile	type profile	type profile	type profile
A1-A1c-A1h-	A1-A1k-A1c-	A1-A1c-A1h-	A1/A1c-A1h	A1-A1f	A1/A1j-A1c-A	A1/A1k-A1g-
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	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	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.002	0	0	0	0	0	0
0	0	0	0.002	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0.006	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	0.002	0
0	0	0	0	0	0	0
0	0	0	0	0.004	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	0.006	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

type profile	type profile	type profile	type profile	type profile	type profile	type profile
A1-A1ad-A1z	A1-A1m	A1-A1k-A1c-A	A1k/A1-A1w	C1/C1b	C1/C39-C1b-C	C15
0	0	0	0	0	0	0
0	0	0	0	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.845
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	0.81
0	0	0	0	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0.016	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.007	0.022	0	0.182
0	0	0	0	0	0	0
0	0	0	0.006	0	0.02	0.389
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0.004	0.004	0	0.361
0	0	0	0.005	0	0	0
0	0	0	0	0	0	0.813
0	0	0	0	0	0	0.449
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	0.002	0	0
0	0	0	0	0	0	0.625
0	0	0	0	0.001	0	0
0	0	0	0	0	0	0.554
0	0	0	0	0	0	0.605
0	0	0	0	0	0	0.447
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.724	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	0.001	0	0
0	0	0	0	0.008	0	0
0	0	0	0	0	0	0.285
0	0	0	0	0	0	0
0	0	0	0	0.002	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.803
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

type profile	type profile	type profile	type profile	type profile	type profile	type profile
C15-C15y-C1	C15h-C15k	C1/C39-C1b-	C1/C15-C1b-	C3/C3u-C115	C1	C1/C72/C15/
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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
0.59	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	0.283	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	0.007
0	0	0	0	0	0	0
0	0	0	0	0	0	0.024
0	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	0	0	0	0	0
0	0	0	0.002	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	0.005	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	0	0
0.646	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.675	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.664	0	0	0	0	0	0

type profile C1/C116/C15	type profile C3-C3au	type profile C21/C3	type profile C15h	type profile C1/C15-C1b-	type profile C41/C1-C41b	type profile C15r/C15
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	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	0	0	0	0	0	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	0.016	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.674
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	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
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0.011	0	0
0.005	0	0	0.025	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.901
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

type profile	type profile	type profile	type profile	type profile	type profile	type profile
C1-C15-C1b-C	C40/C3	C22b/C15	C91f	C3/C1/C41-C	C15-C15x-C1	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	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
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.841	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
0.01	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.708	0	0	0	0
0	0	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	0.65	0
0	0	0	0.06	0	0.44	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	0.672	0
0	0	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	0.872	0	0	0	0
0	0	0.271	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.558	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

type profile	type profile	type profile	type profile	type profile	type profile	type profile
C3-C3au-C29	C72	C15/C60a-C1	C41	C15-C15s	C1/C15-C1b-	C15-C15x-C1
0	0	0	0	0	0	0
0	0	0	0	0.432	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
0.003	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	0.004	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	0.77	0	0
0	0	0	0	0	0	0.732
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.859	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	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	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.723
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.85	0	0	0	0
0	0	0	0	0	0	0

type profile C15/C72/C1-	type profile C1-C1b-C41-	type profile C15/C1-C15a	type profile C1/C15-C72-	type profile C91e	type profile C15ai	type profile C22a
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	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.077	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.326	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	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	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	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	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.316	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.376
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	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.076	0
0	0	0.5	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

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-D
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	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	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
0.057	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	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

0	0	0	0	0	0	0
0	0	0	0	0	0.932	0
0	0	0	0	0	0.929	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.909	0
0	0	0	0	0	0	0
0	0	0	0	0	0.918	0
0	0	0	0	0	0.941	0
0	0	0	0	0	0.048	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.9	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	0.015	0
0	0	0	0	0	0	0
0	0.933	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0.926
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	0.928
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

type profile D1/D4-D6-D6	type profile D1-D4-D4c-D	type profile D1/D4/D6	type profile D1/D4-D2-D4	type profile D1-D4-D6b-D	type profile D1-D4-D4c-D	type profile D1-D4-D4c-D
0	0	0	0	0	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	0.848	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.77	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0.824	0	0	0	0	0	0
0	0	0	0	0	0	0
0	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
0.888	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	0.008	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	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	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	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	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	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	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	0
0	0	0	0	0	0	0

type profile	type profile	type profile	type profile	type profile	type profile	type profile
D1-D4f-D4-D	D1-D4-D4c-D	D1/D4/D1n-D	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	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	0
0	0	0	0	0	0	0
0	0	0	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

0	0	0	0	0	0.002	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0.861	0
0	0	0	0	0	0	0
0	0	0.778	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	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	0.007	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0.879	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0.725	0	0	0	0
0	0	0	0	0	0	0
0.773	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0

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
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0.206
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	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	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0.878	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	0	0
0	0	0	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

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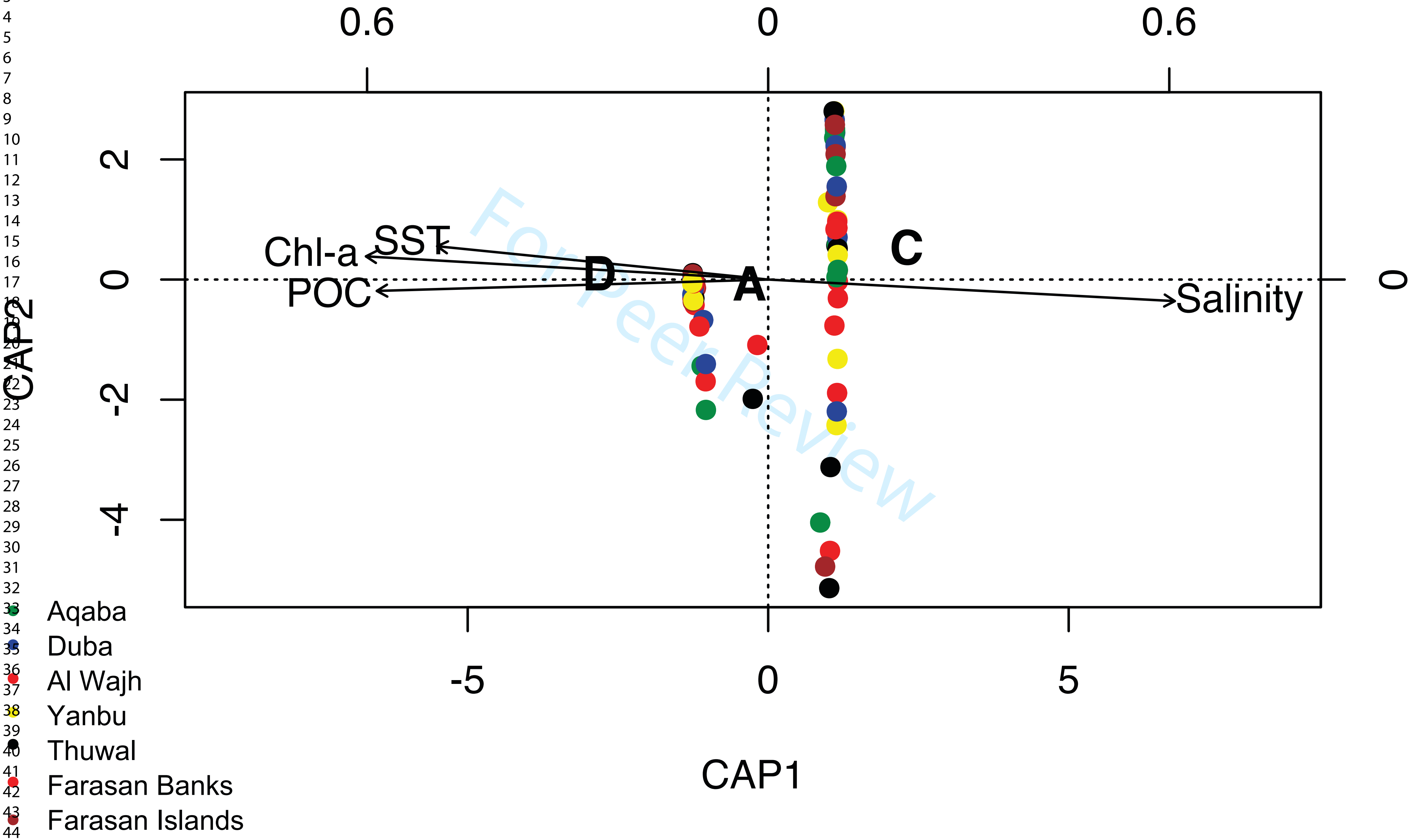
SUPPORTING INFORMATION

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

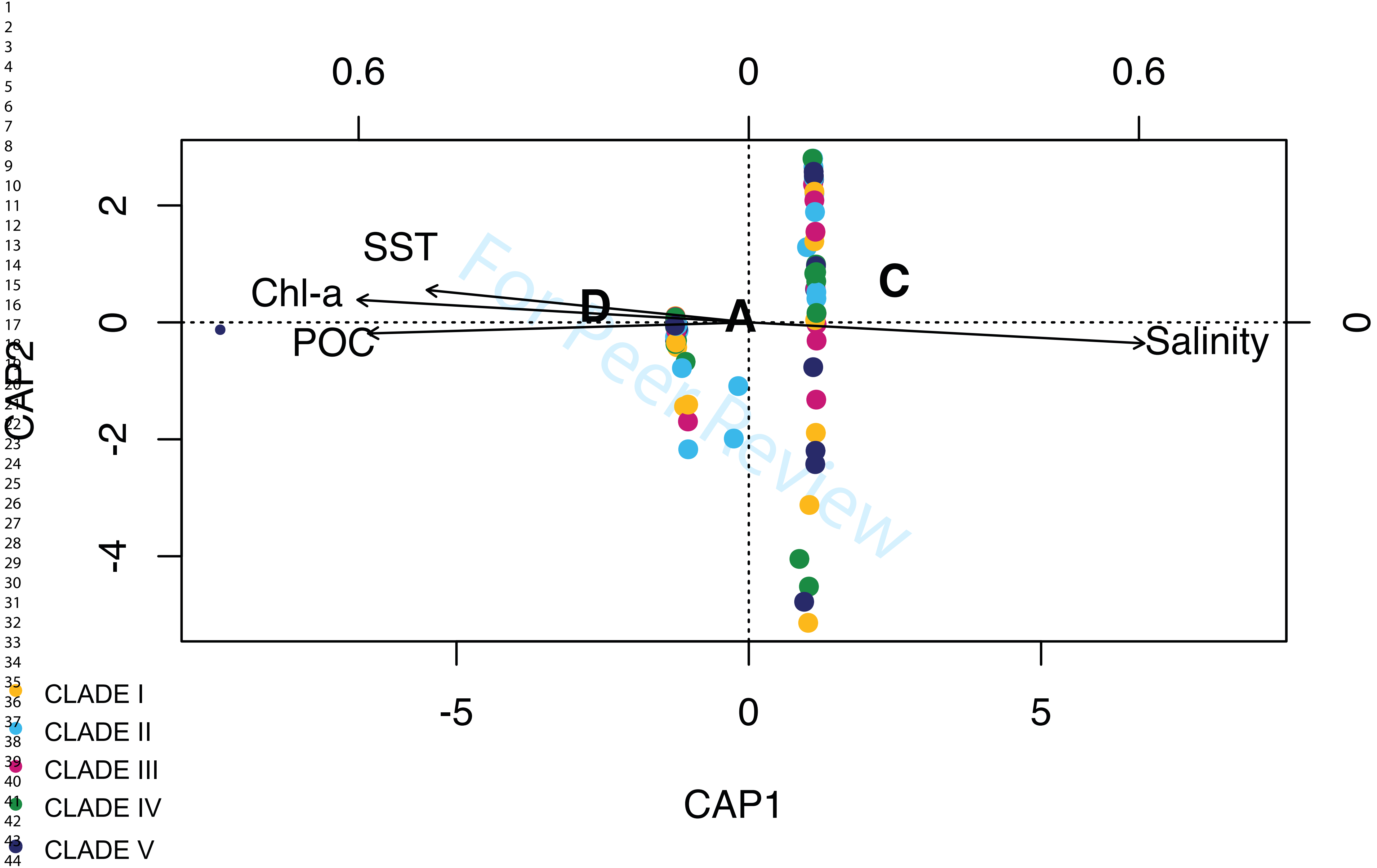
Tullia I. Terraneo, Marco Fusi, Benjamin C. C. Hume, Roberto Arrigoni, Christian R. Voolstra, Francesca Benzoni, Zac H. Forsman, Michael L. Berumen

Appendix S4 Bi-plot CAP ordination of *Porites* (divided for location, molecular clades and morphological species) and Symbiodiniaceae clade (a-c), majority ITS2 sequence (d-f) and ITS2 type profiles (g-i) in relation with the four environmental variables studied

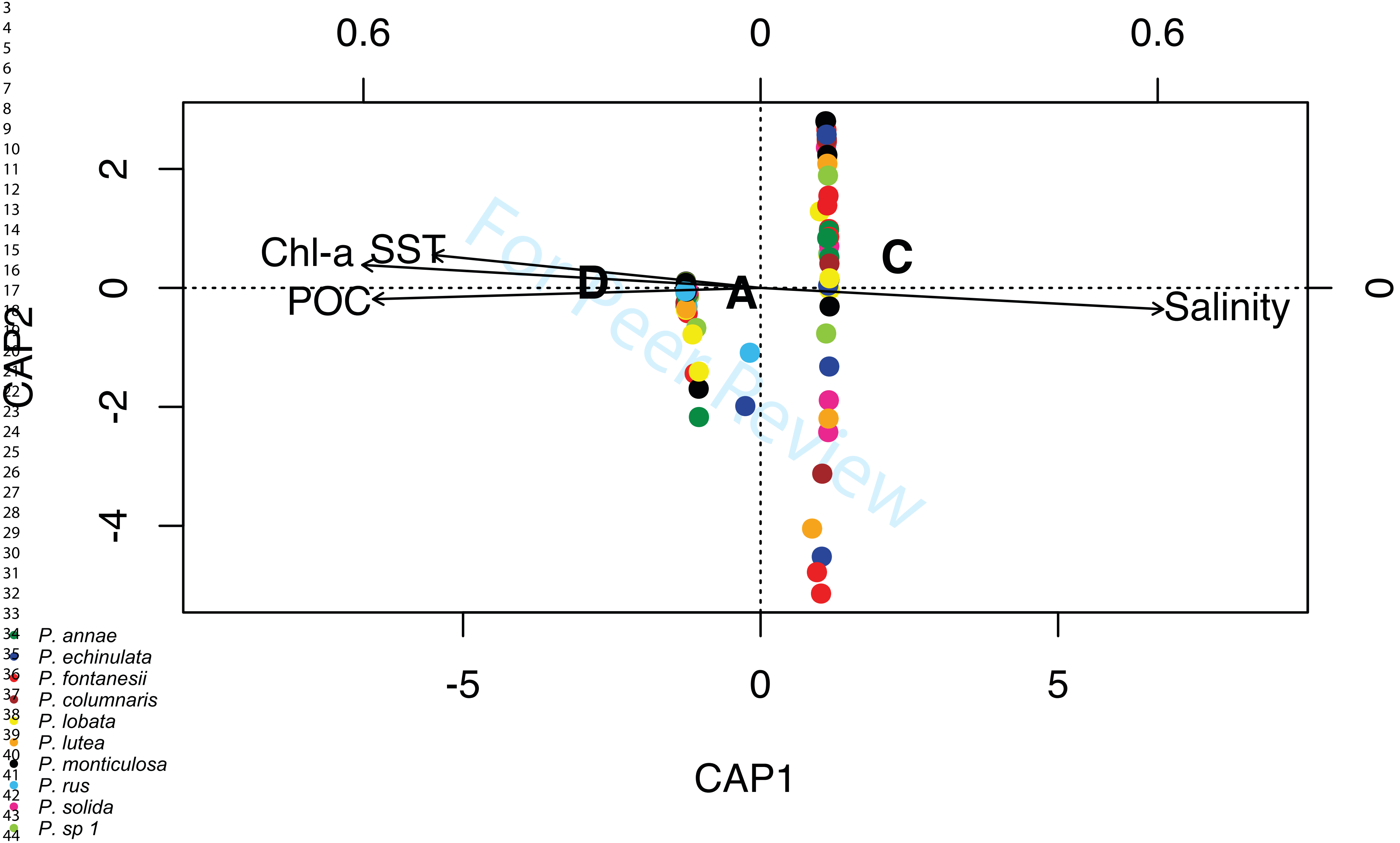
(a) Symbiodiniaceae clade - locality



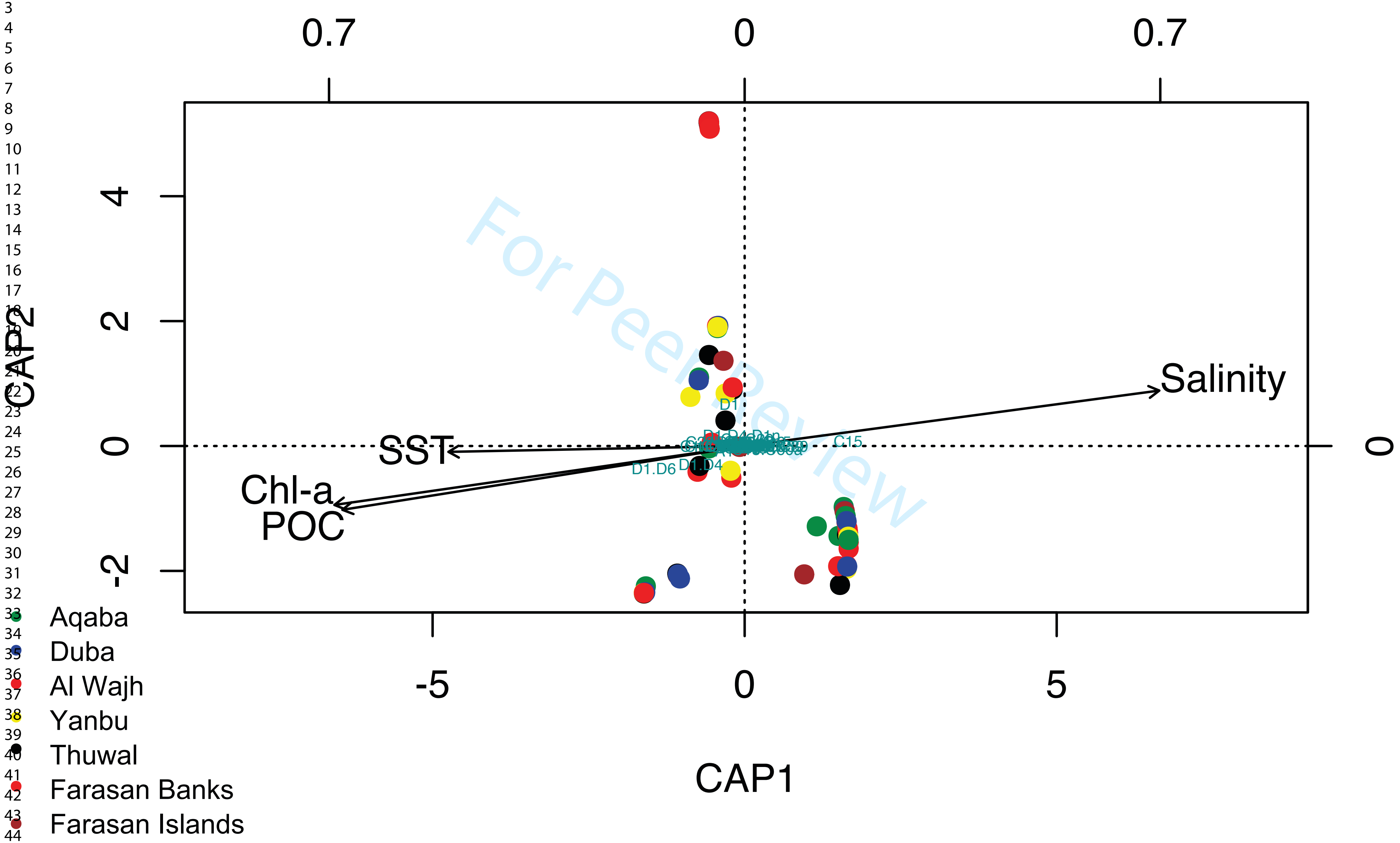
(b) Symbiodiniaceae clade - *Porites* molecular clade



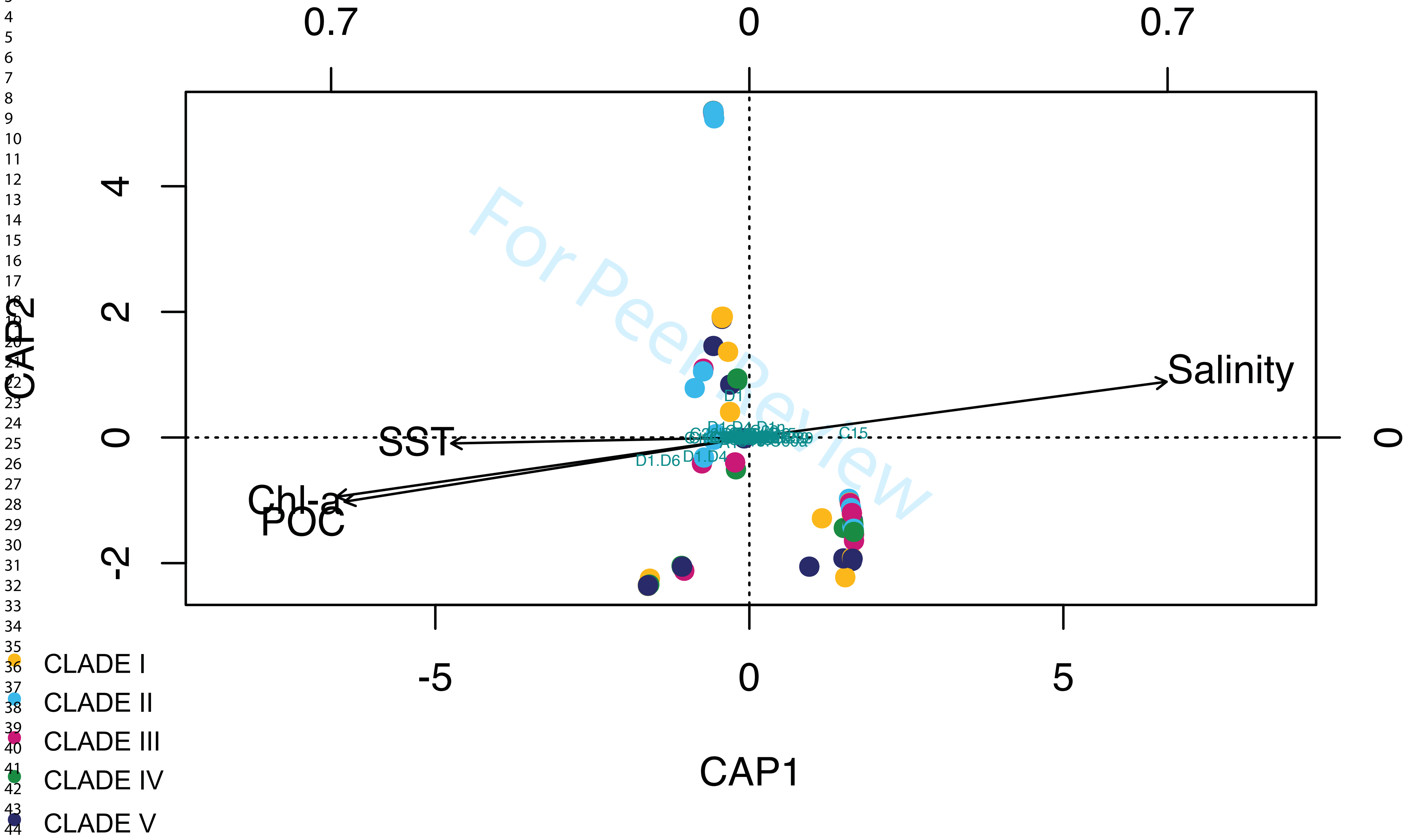
(c) Symbiodiniaceae clade - *Porites* morphological species



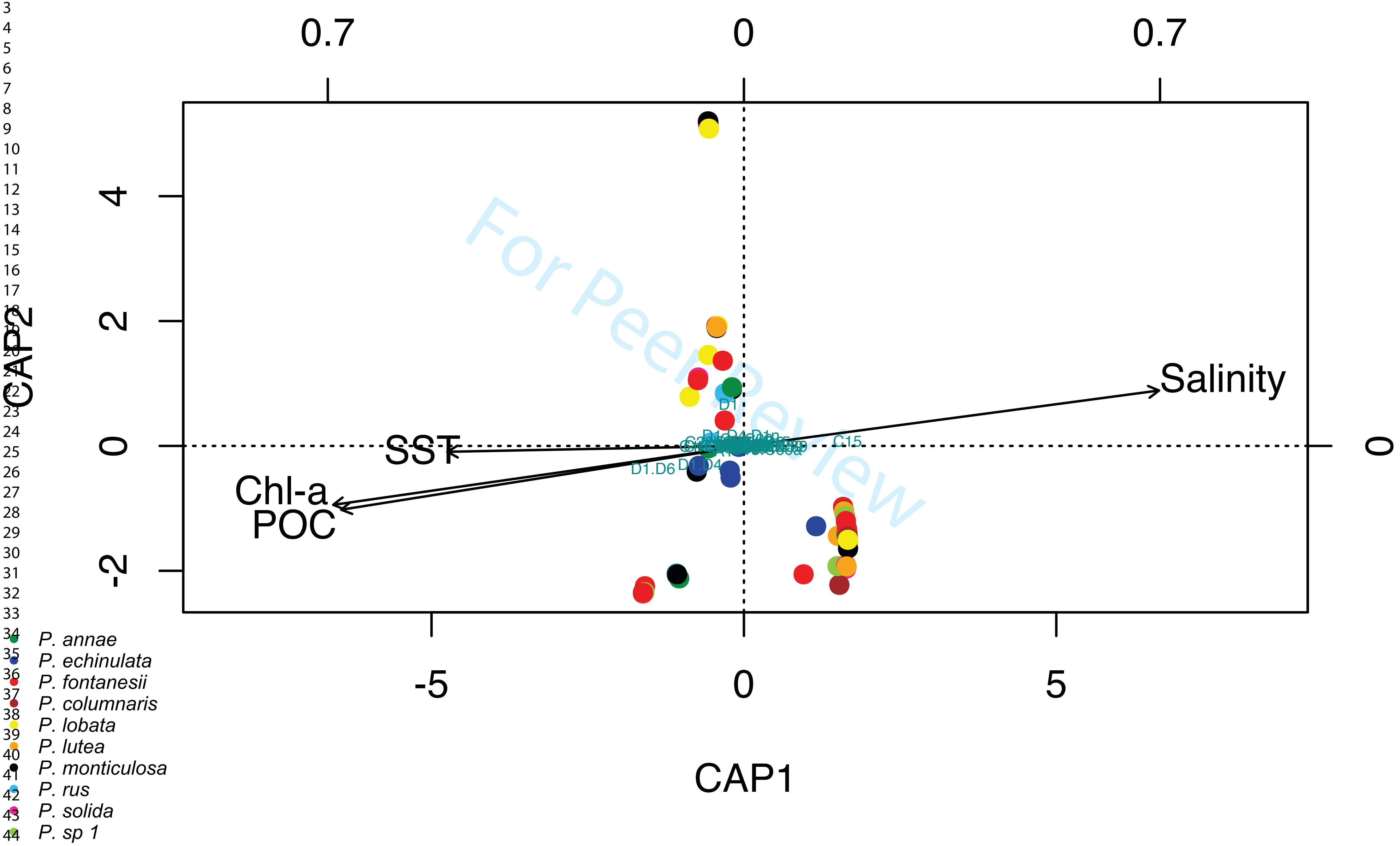
(d) Symbiodiniaceae majority ITS2 seq - locality



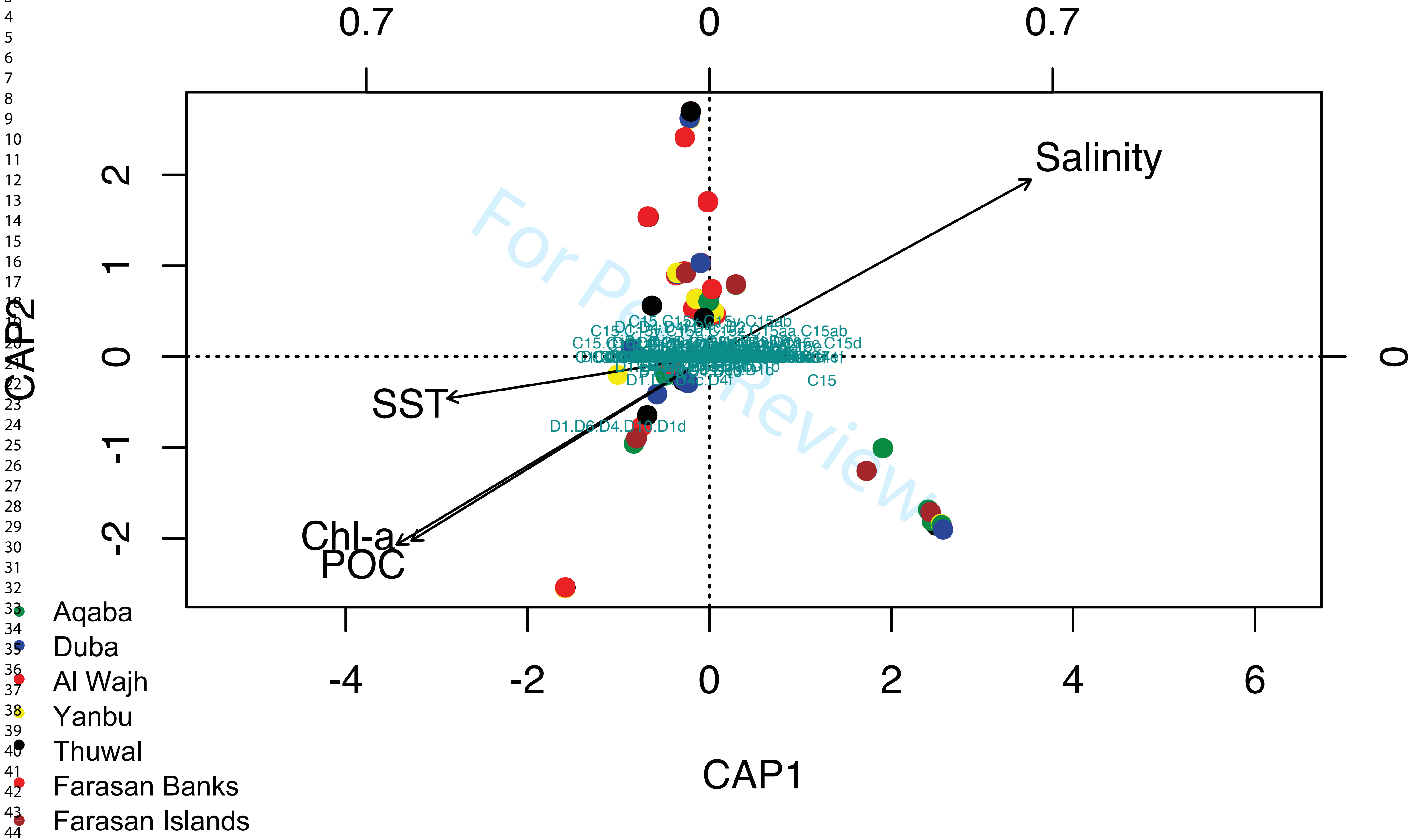
(e) Symbiodiniaceae majority ITS2 seq - *Porites* molecular clade



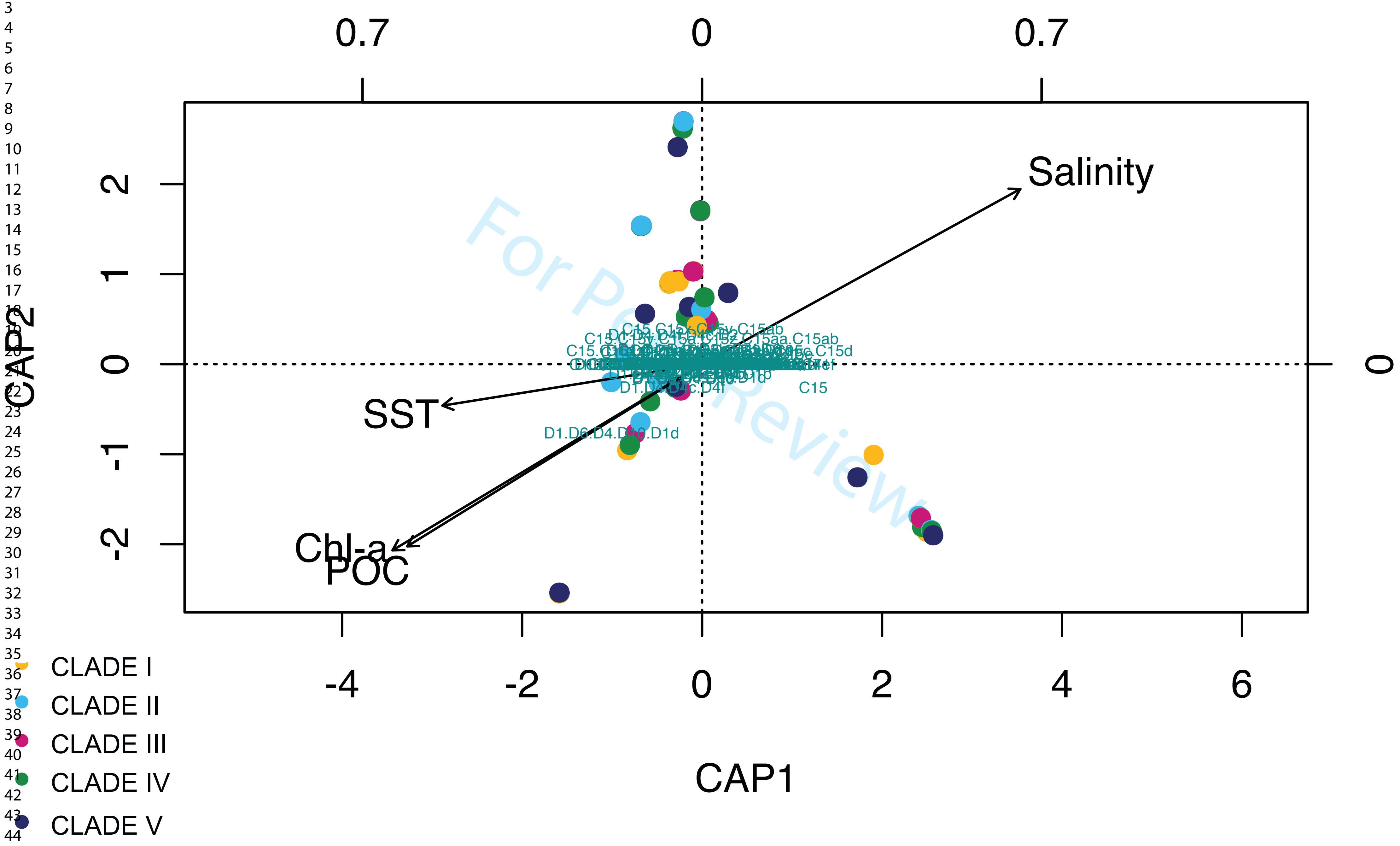
(f) Symbiodiniaceae majority ITS2 seq - *Porites* morphological species



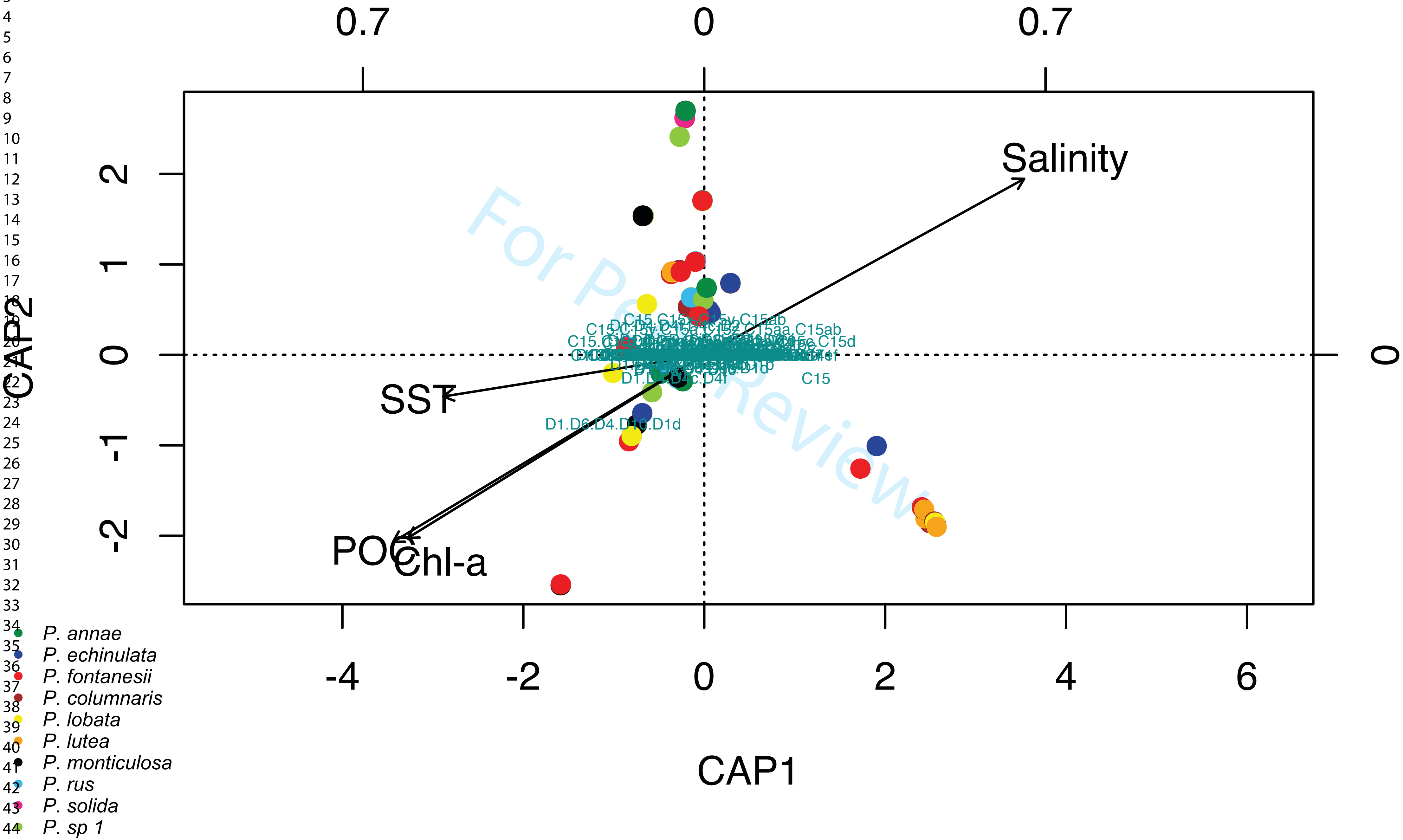
(g) Symbiodiniaceae ITS2 type profiles - locality



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



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



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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	*F*	*p*	*F*	*p*	*F*	*p*
Sampling Time	6	5.1843	0.001	2.3551	0.001	1.6933	0.001
Res	73						