

Table S1 Table of the *Cladocopium psbA<sup>ncr</sup>* lineages (*sensu* Noda et al. 2017) for each tagged colony for throughout the study. The specimens were collected in four different period of the study Jul16 (July 27, 2016), Jan17 (January 30, 2017), Aug17 (August 17, 2017), and Apr18 (April 9, 2018). Depth: D = Deep,  $\approx$  10 m; S = Shallow,  $\approx$  2 m; TPs = Tidal Pools, < 1.5 m. \* indicates colonies that switched during the period of study and the point of which the *Cladocopium* lineage switched. <sup>+</sup>Grey boxes represent colonies which died during the study. UN=Unresolved lineage.

Code	Location	Depth	SITE	Surveys			
				Jul16	Jan17	Aug17	Apr18
0D-1	0	D	0D	2	2	2	2
0D-2	0	D	0D	2	2	2	2
0D-3	0	D	0D	2	2	2	2
0D-4	0	D	<u>0D*</u>	2	2	2	<u>5*</u>
0D-5	0	D	0D	2	2	2	2
0S-1	0	S	<u>0S*</u>	2	UN	2	<u>1*</u>
0S-2	0	S	<u>0S*</u>	2	2	<u>1*</u>	1
0S-3	0	S	<u>0S*</u>	2	2	2	<u>1*</u>
0S-4	0	S	<u>0S*</u>	2	2	2	<u>1*</u>
0S-5	0	S	<u>0S*</u>	2	2	<u>1*</u>	1
TPs-1		TPs	TPs	UN	4	4	UN
TPs-2		TPs	<u>TPs*</u>	4	4	4	<u>1*</u>
TPs-3		TPs	<u>TPs*</u>	4	4	4	<u>1*</u>
TPs-4		TPs	TPs	4	4	4	4
TPs-5		TPs	TPs	4	4	UN	4
500D-1	500	D	500D	2	2	2	2
500D-2	500	D	<u>500D*</u>	2	<u>5*</u>	2	2
500D-3	500	D	500D	2	2	2	2
500D-4	500	D	<u>500D*</u>	2	<u>1*</u>	1	UN
500D-5	500	D	<u>500D*</u>	1	<u>2*</u>	2	2
500S-1	500	S	500S	1	1	1	1
500S-2	500	S	<u>500S*</u>	1	<u>3*</u>	<u>2*</u>	2
500S-3	500	S	500S	1	1	1	1
500S-4	500	S	500S	2	2	UN	UN
500S-5	500	S	<u>500S*</u>	2	<u>1*</u>	<u>2*</u>	<u>1*</u>
1000D-1	1000	D	1000D	2	2	2	2
1000D-2	1000	D	1000D	2	2	2	2
1000D-3	1000	D	1000D	2	2	2	2
1000D-4	1000	D	1000D	2	2	2	2
1000D-5	1000	D	1000D	2	2	2	2
1000S-1	1000	S	<u>1000S*</u>	2	<u>1*</u>	1	1
1000S-2 <sup>+</sup>	1000	S	1000S	2	-	-	-
1000S-3	1000	S	<u>1000S*</u>	2	2	2	<u>1*</u>
1000S-4 <sup>+</sup>	1000	S	1000S	1	-	-	-
1000S-5	1000	S	<u>1000S*</u>	2	<u>1*</u>	1	1

Table S2 **Table of the net mean genetic distances among the lineages of (a) forward and (b) reverse *psbA*<sup>ncr</sup>.**

(a) <i>psbA</i> <sup>ncr</sup> forward sequences				
	lineage 1	lineage 2		
lineage 2	0.099			
lineage 4	0.345	0.306		

(b) <i>psbA</i> <sup>ncr</sup> reverse sequences				
	lineage 1	lineage 2	lineage 3	lineage 4
lineage 2	0.007			
lineage 3	0.023	0.030		
lineage 4	0.070	0.078	0.054	
lineage 5	0.054	0.046	0.046	0.103

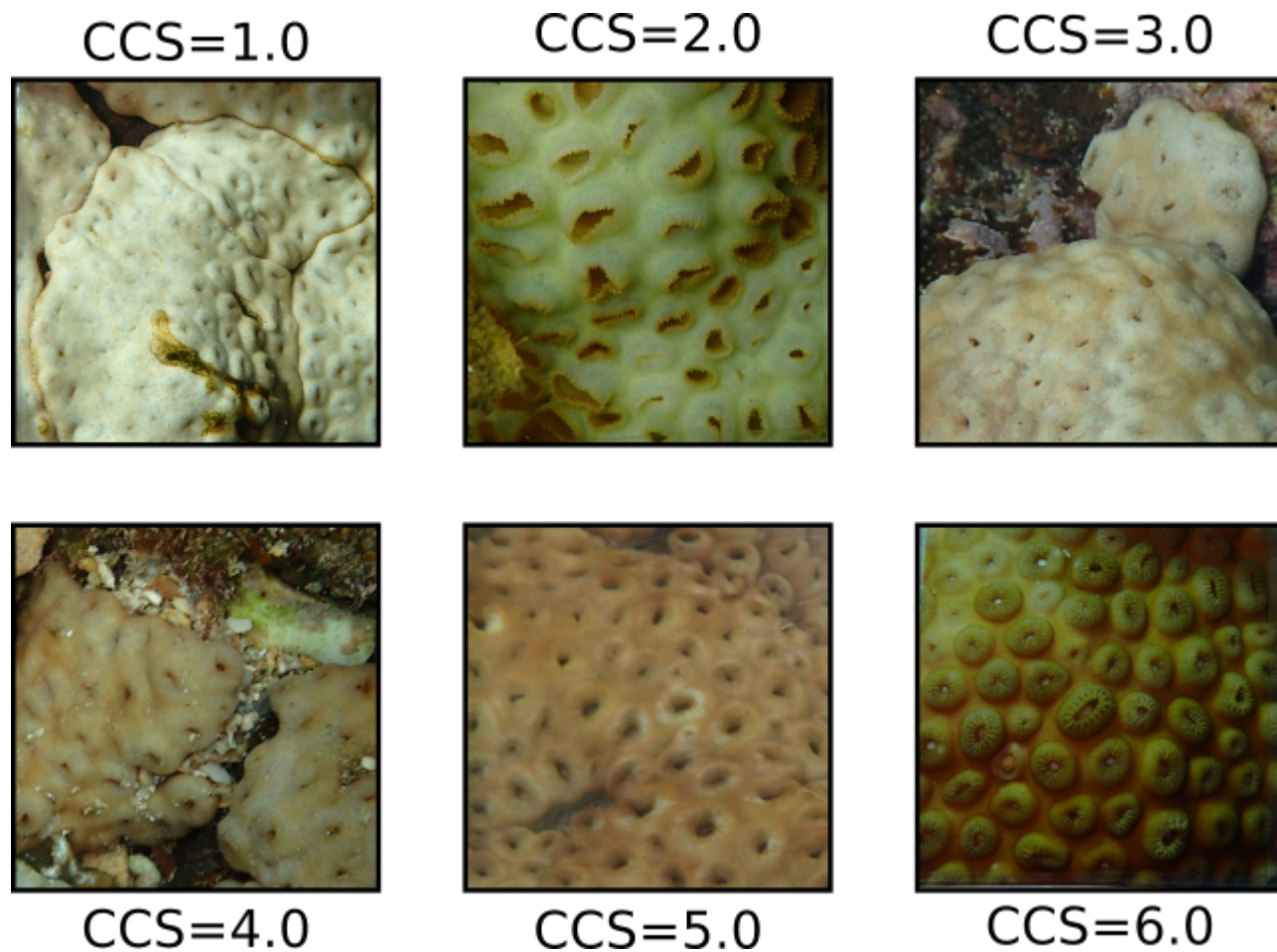


Figure S1 Example Coral Colour Scores (CCS) images of colonies of *Palythoa tuberculosa* from different survey periods at the coast of Mizugama, Okinawa, Japan. Colonies were photographed between 27 July 2016 to 9 April 2018 utilizing a Coral Colour Reference Card (Siebeck et al. 2006).

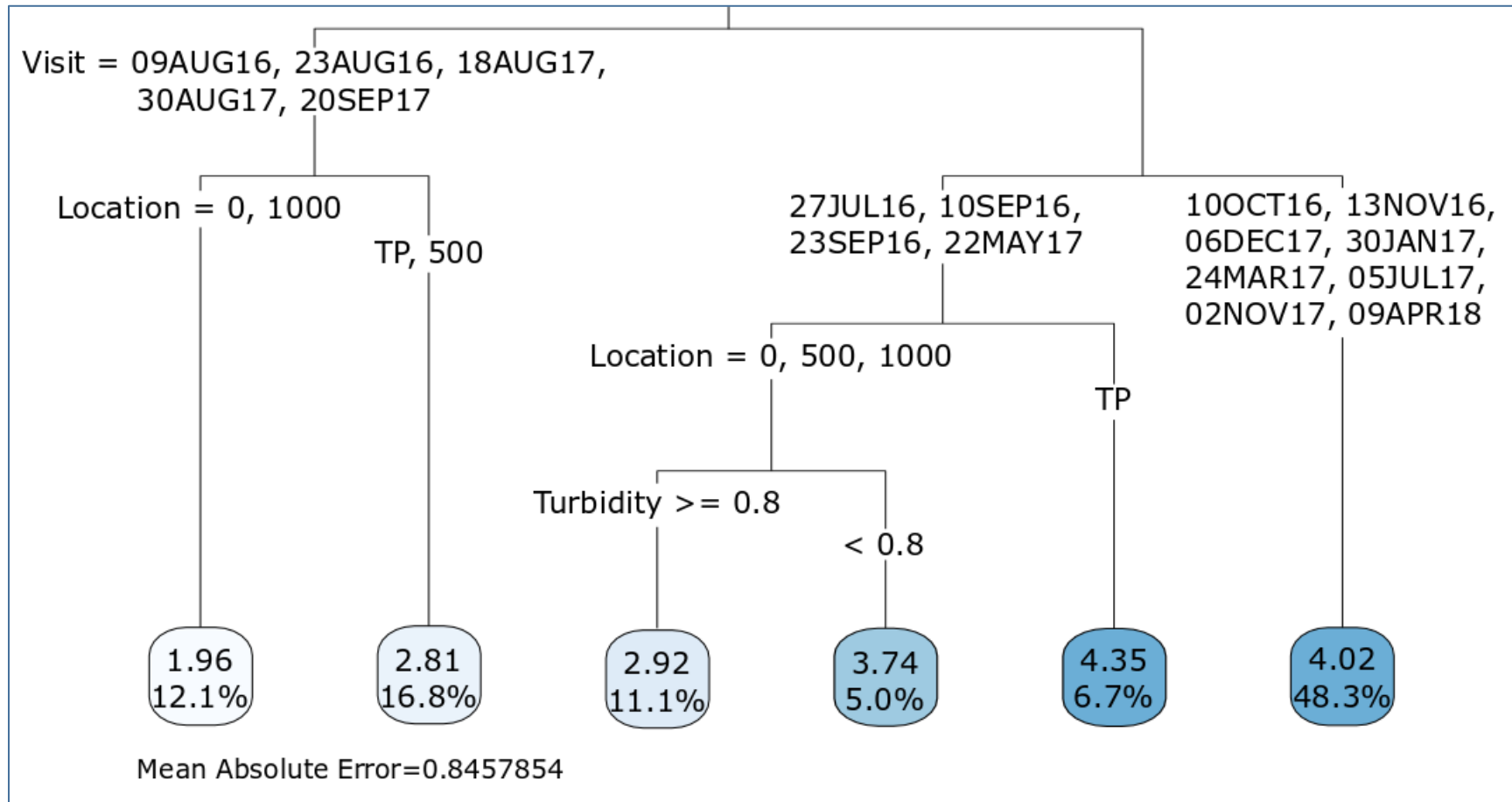


Figure S2 **Multivariate Regression Tree (MRT)** based on the **Colour Density Score (CDS)** of tagged shallow *Palythoa tuberculosa* colonies. The MRT decision tree is categorized based on factors such as surveys (a-q, refer to Table 1b), location (TPs, 0 m, 500 m, 1000 m) and water parameters (pH, turbidity, temperature, salinity, conductivity). The leaves of the MRT represent the mean CDS of tagged *P. tuberculosa* colonies. TPs= tidal pools. The dates are in DDMMYY format.

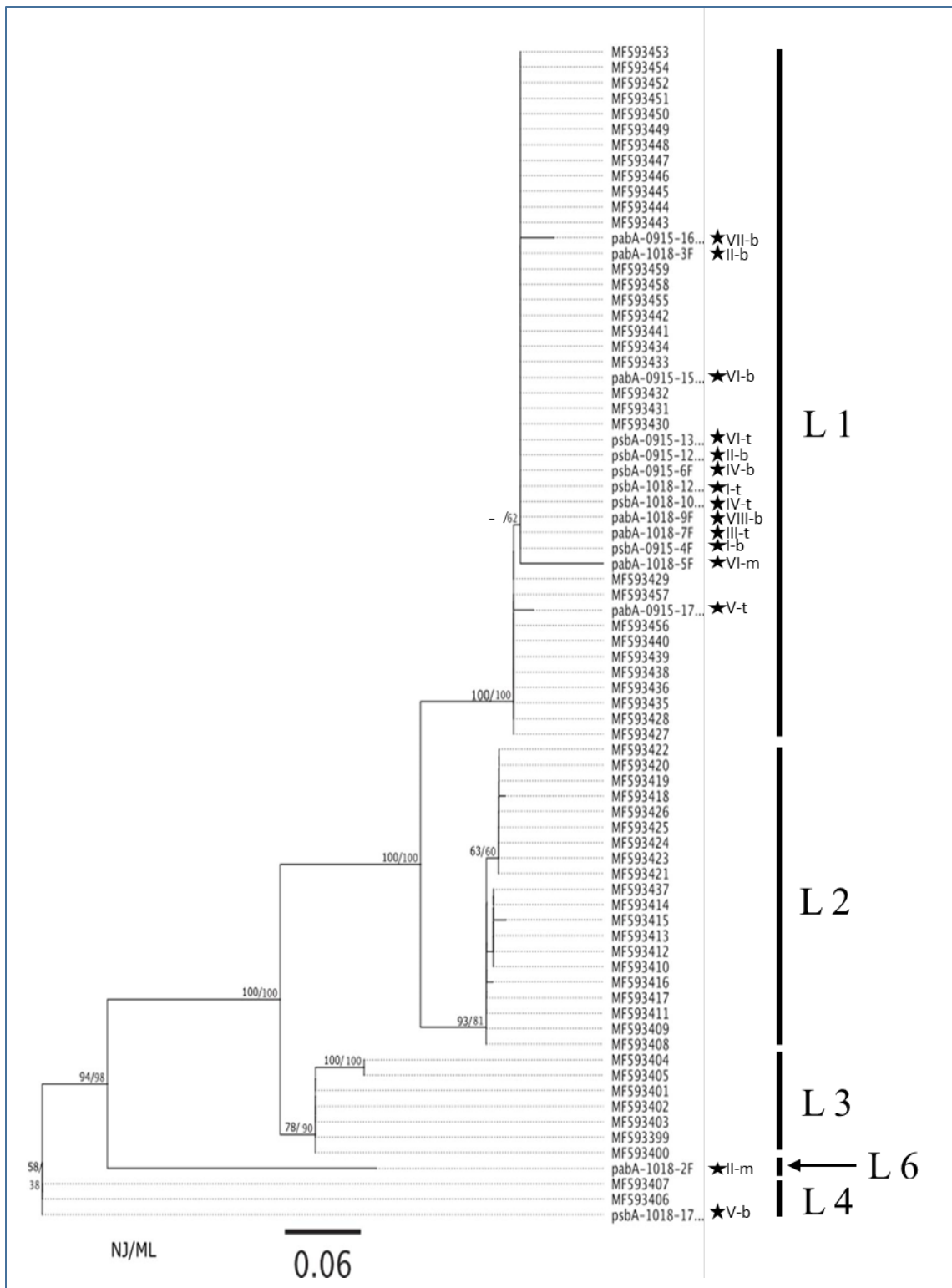


Figure S3 Phylogeny of *Cladocopium psbA<sup>ncr</sup>* lineages from *Palythoa tuberculosa* at Hija River mouth for the intracolony variation of Symbiodiniaceae. Maximum Likelihood (ML) tree of forward sequences of *Cladocopium* chloroplast psbA noncoding region (psbA<sup>ncr</sup>) with reference from Noda et al. (2017) of the same region. Values at the branches represent ML and neighbor joining (NJ). The colonies and the parts were represented based on Table 2