

Supplementary Materials

Table S1. Symbiodiniaceae nucleotide databases.

Species	Type	Reference
<i>Symbiodinium minutum</i>	Gene models	[1]
<i>Symbiodinium kawagutii</i>	Gene models	[2]
<i>Symbiodinium microadriaticum</i>	Gene models	[3]
<i>Symbiodinium microadriaticum</i>	Genome	[3]
<i>Symbiodinium aenigmaticum</i>	Transcriptome	[4]
<i>Symbiodinium minutum</i>	Transcriptome	[4]
<i>Symbiodinium pseudominutum</i>	Transcriptome	[4]
<i>Symbiodinium psymphilum</i>	Transcriptome	[4]

1. Shoguchi, E.; Tanaka, M.; Shinzato, C.; Kawashima, T.; Satoh, N. A genome-wide survey of photoreceptor and circadian genes in the coral, *Acropora digitifera*. *Gene* **2013**, *515*, 426-431.
2. Lin, S.; Cheng, S.; Song, B.; Zhong, X.; Lin, X.; Li, W.; et al. The *Symbiodinium kawagutii* genome illuminates dinoflagellate gene expression and coral symbiosis. *Science*, **2015**, *350*, 691-694.
3. Aranda, M.; Li, Y.; Liew, Y.J.; Baumgarten, S.; Simakov, O.; Wilson, M.C.; et al. Genomes of coral dinoflagellate symbionts highlight evolutionary adaptations conducive to a symbiotic lifestyle. *Sci. Rep.* **2016**, *6*, 1-15.
4. Parkinson, J.E.; Baumgarten, S.; Michell, C.T.; Baums, I.B.; LaJeunesse, T.C.; Voolstra, C.R. Gene expression variation resolves species and individual strains among coral-associated dinoflagellates within the genus *Symbiodinium*. *Genome Biol. Evol.* **2016**, *8*, 665-680.

Table S2. RT-qPCR Mastermix used for determining gene expression and efficiency.

Reagent	Volume per reaction (μl)	
	Gene expression	Gene efficiency
SsoAdvanced™ Inhibitor-Tolerant SYBR Green		
Supermix	10	5.2
Forward primer 10 μM	0.4	0.2

Reverse primer 10 μ M	0.4	0.2
cDNA template	1	1
Nuclease-free H ₂ O	3.2	3.4
Total reaction mix volume	14	10

Table S3. Coverage percentage of each coral genus in the two sites and in the whole study area.

Coral genus	Coverage (%)		
	Total area	Pulau Hantu	Kusu Island
<i>Pectinia</i>	10.93	13.34	8.20
<i>Dipsastraea</i>	9.18	7.97	10.55
<i>Merulina</i>	7.90	10.40	5.08
<i>Pachyseris</i>	5.14	4.33	6.05
<i>Goniopora</i>	5.05	8.32	1.37
<i>Platygyra</i>	4.96	4.16	5.86
<i>Favites</i>	4.78	2.77	7.03
<i>Galaxea</i>	4.59	4.51	4.69
<i>Heliopora</i>	4.22	0.35	8.59
<i>Goniastrea</i>	3.67	4.68	2.54
<i>Porites</i>	3.58	2.77	4.49
<i>Lobophyllia</i>	3.40	2.60	4.30
<i>Montipora</i>	3.40	1.04	6.05
<i>Turbinaria</i>	3.21	1.91	4.69
<i>Pavona</i>	2.66	4.33	0.78
<i>Cyphastrea</i>	2.48	4.51	0.20
<i>Echinopora</i>	2.48	3.64	1.17
<i>Fungia</i>	2.02	2.77	1.17
<i>Podabacia</i>	1.93	2.77	0.98
<i>Oxypora</i>	1.56	1.39	1.76
<i>Diploastrea</i>	1.29	0.87	1.76
<i>Lithophyllon</i>	1.19	1.56	0.78
<i>Hydnophora</i>	1.10	0.69	1.56
<i>Astreopora</i>	0.92	1.56	0.20
<i>Fimbriaphyllia</i>	0.92	1.39	0.39
<i>Herpolitha</i>	0.92	1.73	0.00
<i>Leptoria</i>	0.92	0.52	1.37
<i>Acropora</i>	0.83	0.17	1.56

<i>Ctenactis</i>	0.83	0.87	0.78
<i>Plerogyra</i>	0.83	1.21	0.39
<i>Coscinaraea</i>	0.73	0.35	1.17
<i>Mycedium</i>	0.73	0.00	1.56
<i>Pocillopora</i>	0.55	0.00	1.17
<i>Bernardpora</i>	0.28	0.35	0.20
<i>Psammocora</i>	0.28	0.00	0.59
<i>Acanthastrea</i>	0.18	0.00	0.39
<i>Echinophyllia</i>	0.18	0.17	0.20
<i>Danafungia</i>	0.09	0.00	0.20
<i>Leptastrea</i>	0.09	0.00	0.20

Table S4. Gene efficiency (E) for each analyzed gene (SD: standard deviation).

Gene	E	E minus SD	E plus SD	Intercept
<i>C-type lectin</i>	2.02	1.94	2.11	27.6
<i>C3</i>	2.12	2.07	2.22	30.0
<i>Hsp70</i>	2.04	2.16	2.16	30.4
<i>Actin</i>	2.20	2.1	2.36	29.1

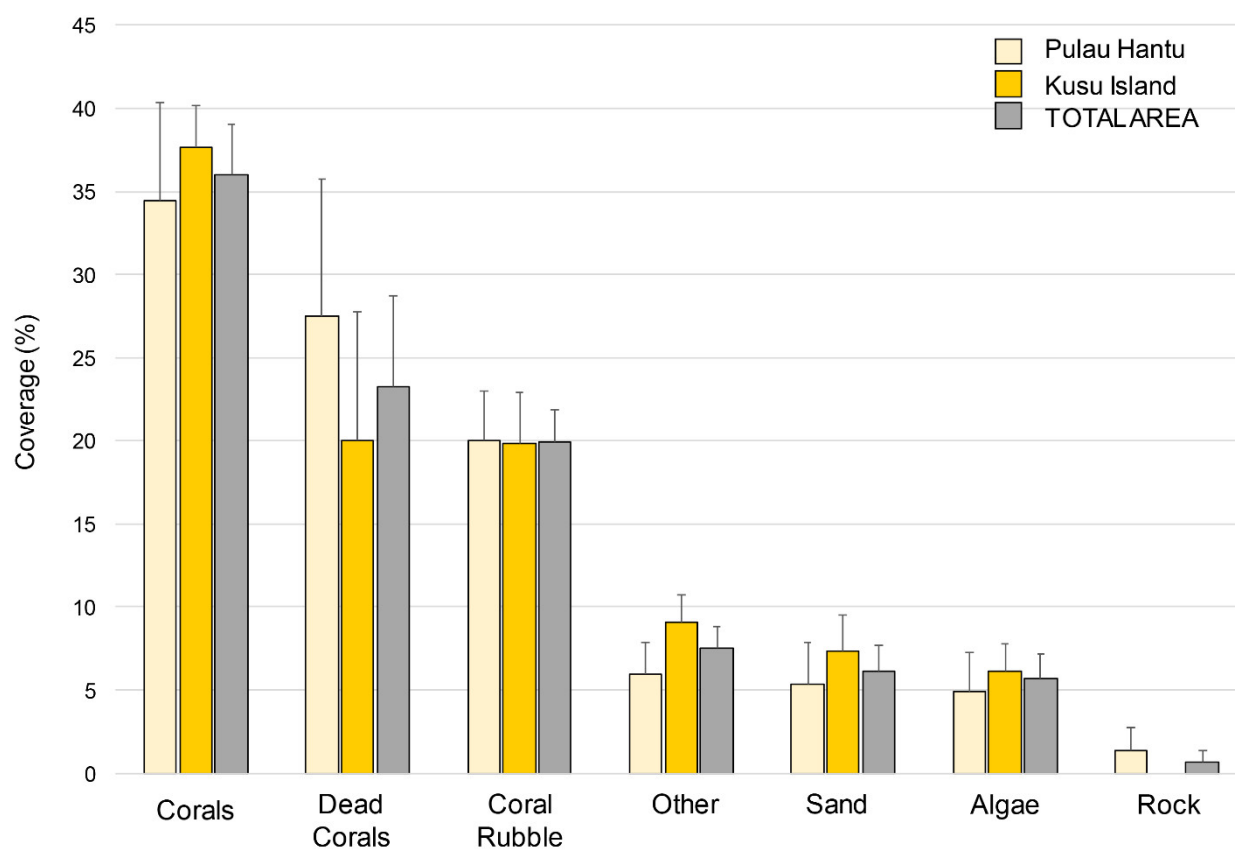


Figure S1. Coverage percentage of the different benthic categories in the two sites analyzed and in the whole study area. Data are expressed as the mean \pm SEM.

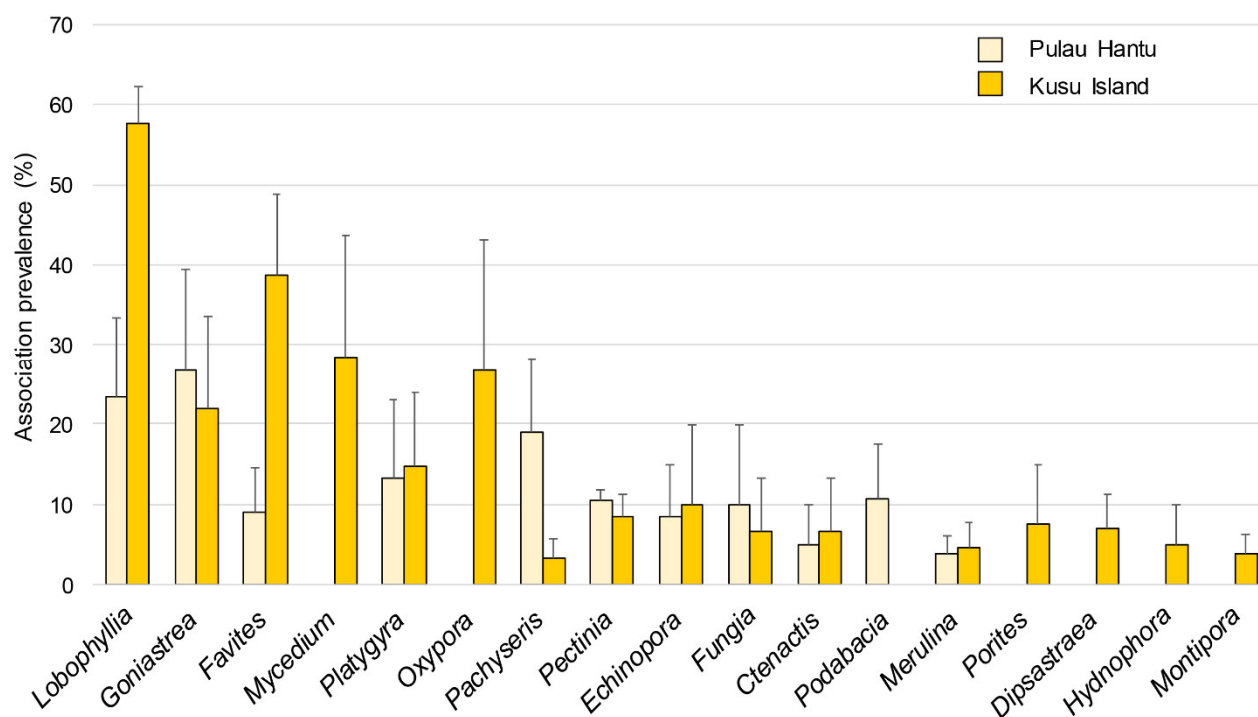


Figure S2. Prevalence (%) of *Waminoa* sp.-corals association by coral genus in the two sites. Data are expressed as the mean \pm SEM.