

Supplementary Table S1. Sampling sites and coordinates

<i>Locations</i>	<i>Reef</i>	<i>Ns</i>	<i>Nt</i>	<i>Nseq</i>	<i>Coordinates</i>		<i>Depth</i>
MAQNA	R1	30	67	67	28° 31' 34.20"	34° 48' 14.30"	3-5
	R2	37			28° 25' 36.48"	34° 45' 06.17"	3-7m
AL-WAJH	R1	59	113	113	26° 11' 15.05"	36° 20' 57.21"	1-3m
	R2	2			26° 09' 59.80"	36° 23' 32.20"	3m
	R3	24			26° 14' 28.3"	36° 26' 25.3"	5-10m
	R4	28			26° 11' 06.2"	36° 22' 58.9"	3-7m
YANBU	R1	28	118	118	23° 56' 50.70"	38° 10' 31.80"	6-10
	R2	16			23° 54' 58.92"	38° 09' 00.63"	6-10
	R3	28			23° 57' 19.20"	38° 12' 16.00"	3-5m
	R4	29			23° 54' 41.4"	38° 09' 08.4"	3-7m
	R5	17			-----	-----	2-10m
KAUST	R1	42	135	135	22° 19' 09"	38° 51' 16"	1-7m
	R2	46			22° 04' 02"	38° 46' 09"	2-8m
	R3	47			22° 30' 48"	38° 55' 17"	2-10m
JEDDAH	R1	30	70	64	21° 45' 11.40"	38° 57' 45.09"	1-3m
	R2	20			21° 46' 06.3"	38° 57' 47.07"	2-5m
	R3	20			21° 41' 23.26"	39° 00' 49.05"	N/A
DOGA	R1	29	88	88	19° 38' 06.40"	40° 34' 31.30"	3-5m
	R2	29			19° 36' 50.50"	40° 38' 17.50"	3-5m
	R3	30			19° 39' 56.49"	40° 37' 21.59"	3-5m
FARASAN	R1	30	134	131	16° 34' 45.50"	42° 08' 57.50"	4-5m
	R2	30			16° 34' 44.38"	42° 14' 11.47"	3-5m
	R3	20			16° 31' 30.65"	42° 01' 57.11"	3-4m
	R4	30			16° 31' 38.5"	42° 01' 54.09"	3-6m
	R5	24			-----	-----	1-5m
Total			725	716			

Ns = Total number of samples per reef; Nt = Total number of samples per region; Nseq = Total number of sequences obtained for the mtORF gene

Supplementary Table S2. Primers and their respective references

Nuclear loci	Reference	Primer name	sequence (5'-3')
ITS1	Flot et al. 2011	F18S1	CGATYGAAYGGTTTAGTGAGGC
ITS1	Flot et al. 2011	ITScl-3	CATTTGCGTTCAAAGATTCG
ITS2	LaJeunesse 2007	ITSrev_LaJ	GGG ATC CAT ATG CTT AAG TTC AGCGGG T
ITS2	LaJeunesse 2007	Scler5.8SbF_LaJ	GAA GAA CGC AGCCAA CTG CGA
<i>hsp70</i>	Schmidt-Roach et al. 2013	HSP70A-F	CCTGGTTCAATCCGACAGA
<i>hsp70</i>	Schmidt-Roach et al. 2014	HSP70A-R	TGTTTCAGCTGTTTTCTTCG
<i>PMCA</i>	Zoccola et al. 2004	PMCA_R1	AGGTGGCAGGATGCCACATTT
<i>PMCA</i>	Zoccola et al. 2005	PMCA_R2	GGGCCACACTTCATCAAACCTT
<i>PMCA</i>	Zoccola et al. 2006	PMCA_R3	ATTGCGCCCCACATAACAGC
<i>PMCA</i>	Zoccola et al. 2007	PMCA_F1	TTGCTTTCAAATGTGGCATCC
<i>PMCA</i>	Zoccola et al. 2008	PMCA_F2	GTAAAGCTGTTATGTGGGGG
Mitochondrial loci			
<i>ORF</i>	Flot et al. 2011	FATP6.1	TTTGGGSATTCGTTTAGCAG
<i>ORF</i>	Flot et al. 2011	RORF	SCCAATATGTAAACASCATGTCA
CR	Flot et al. 2011	FNAD5.2deg	GCCYAGRGGTGTGTTCAT
CR	Flot et al. 2011	RCOI3deg	CGCAGAAAGCTCBARTCGTA
12S	This study	Ser_12s_F	TGTCTTTGGCGAACATGGGT
12S	This study	Ser_12s_R	AGGCCAAACGACTCCAAGTT
12S	This study	Ser_12s_IntF1	GGGGGATTGTGCCTTTTCCT
12S	This study	Ser_12s_IntF2	GCTTGAGTAGTACGGTCGCA
16S	This study	Sty_16s_F	GTGCCGGGTTTATATAACCGGT
16S	This study	Sty_16s_R	AAAGGCCAACCCTTCTCAC
16S	This study	Sty_16s_IntR_2	AATCCCCGCTCCTCTTTCTC
16S	This study	Sty_16s_IntR_3	GGCTGGTTCCAAGCCTACAT
<i>cox1</i>	This study	Sty_COXI_F	TTTTTGGTGGAGGTGCTGGT
<i>Cox1</i>	This study	Sty_COXI_R	TGACCACCACAAGCACAACCT

Supplementary Table S3. Polymorphic sites per gene

Locus	ALL REGIONS					RED SEA				
	Nseq	size (bp)	Polymorphic sites	Indels	Parsimony informative sites	Nseq	size (bp)	Polymorphic sites	Indels	Parsimony informative sites
nDNA genes										
ITS1	75	416	69	94	54	44	388	33	31	16
ITS2	56	329	90	22	68	42	300	44	3	26
<i>PMCA</i>	86	956	107	65	100	50	953	26	11	18
<i>hsp70</i>	738	732	119	2	70	646	732	91	2	33
mtDNA genes										
<i>mtORF (Clade 1 + 2)</i>	827	545	108	99	107	716	536	102	63	102
<i>mtORF (Clade 1)</i>	461	884	48	291	40	353	914	10	255	9
<i>mtORF (Clade 2)</i>	366	943	22	207	21	361	943	22	207	21
CR	401	757	68	461	65	325	620	3	146	3
12S	72	1381	33	0	33	50	1381	6	0	5
16S	61	1393	7	0	7	43	1393	1	0	1
<i>cox1</i>	147	538	19	0	12	110	538	0	0	0