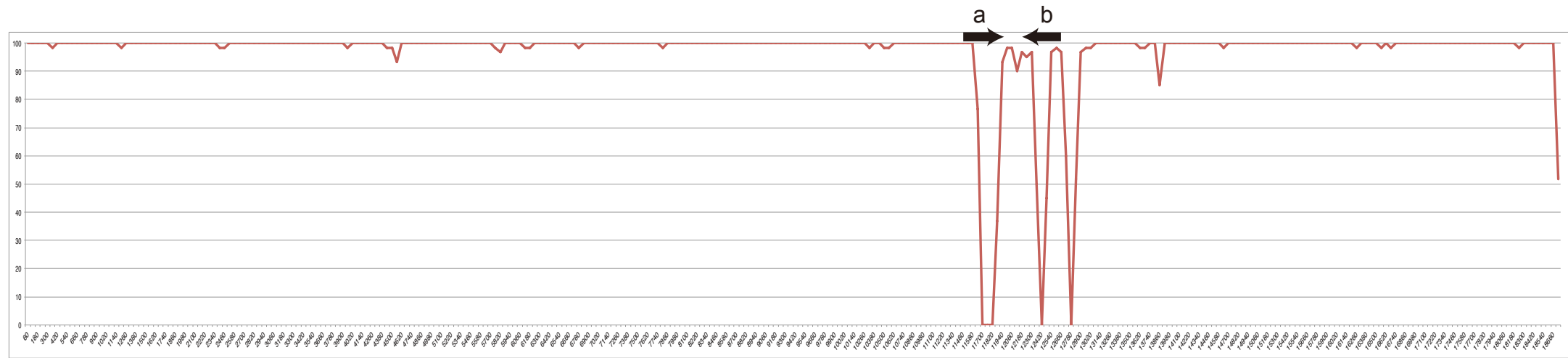


Supplementary Fig. 1

Frequencies of identical nucleotides in 60 bp sliding windows



a: RNS2 flanking region (300 bp)

b: GR flanking region (300 bp)

Supplementary Fig. 2

Table S 1. Shotgun sequencing data (HiSeq2500, 250 bp paied-end) of coral species used in this study

Colony IDs	Number of sequencing pairs	Total amount of basepair obtained	Length of mitochondrial genome assembled (bp)	Mapping rate of sequence data to the assembled mitochondrial genome (%)	Accession numbers of assembled mitochondria genome
car1	3367407	1796442737	18373	0.17	LC201813
car2	3149196	1685318759	18372	0.35	LC201814
acu	3878093	2112014606	18586	0.55	LC201815
aus	2876443	1546418599	18346	0.74	LC201816
cyt1	2959536	1607753259	18568	0.22	LC201817
cyt2	3681403	1999195740	18567	0.46	LC201818
cyt3	4273430	2330048749	18568	0.71	LC201819
ech1	3806346	2067711944	18480	0.16	LC201820
ech2	4343385	2317850689	18480	0.13	LC201821
ech3	3620618	1916997459	18480	0.21	LC201822
ech4	3801720	2002076650	18480	0.39	LC201823
ech5	4098787	2187935333	18480	0.21	LC201824
ech6	3616695	1962631349	18480	0.63	LC201825
ech7	3270030	1796697214	18482	0.26	LC201826
flo	3470418	1819438400	18365	0.47	LC201827
gra	3698134	1972553862	18479	0.62	LC201828
hya1	3620603	1906943573	18567	0.63	LC201829
hya2	3665653	1976242358	18567	0.35	LC201830
hya3	3592503	1972822254	18567	0.35	LC201831
hya4	3257839	1774658951	18568	0.33	LC201832
int	4152622	2272624556	18479	0.44	LC201833
sp	3525840	1944726206	18481	0.53	LC201834
sp1	4072885	2255450380	18368	0.22	LC201835
sp2	3513970	1941895056	18482	0.35	LC201836
sp3	3772572	2056091223	18368	0.41	LC201837
sp4	3176578	1753588443	18480	0.27	LC201838
sp5	2246499	1234378818	18482	0.17	LC201839
sp6	2377151	1307400928	18480	0.2	LC201840
sp7	1893803	1042472832	18367	0.29	LC201841
mic	1961295	1057435930	18479	0.52	LC201842
micD	2461567	1349712700	18481	0.25	LC201843
mur	2366241	1289180256	18480	0.57	LC201844
nas1	2875349	1576430860	18374	0.49	LC201845
nas2	3558273	1861092779	18484	0.4	LC201846
sel1	3575287	1929303103	18482	0.3	LC201847
sel2	3456066	1837574598	18480	0.47	LC201848
awi1	3683732	1997169293	18479	0.8	LC201849
awi2	3937101	2172887859	18479	0.7	LC201850
awi3	3883260	2127325278	18479	0.47	LC201851
awi4	3654174	2025305178	18479	0.46	LC201852
awi5	3851645	2130342123	18479	0.7	LC201853
awi6	4052097	2228809055	18479	0.66	LC201854
awi7	4399971	2406175346	18479	0.34	LC201855
ten1	3816691	2120452861	18342	0.68	LC201856
ten10	2375983	1292393914	18342	0.57	LC201857
ten11	3721532	2048716582	18343	1.01	LC201858
ten12	3758520	2041398504	18342	0.57	LC201859
ten13	4003353	2101282078	18342	0.66	LC201860
ten14	4269708	2329115318	18342	0.78	LC201861
ten15	4419011	2361477787	18343	0.78	LC201862
ten2	4022864	2200368866	18342	0.49	LC201863
ten3	2371259	1285509935	18342	0.57	LC201864
ten4	2722342	1499595814	18342	0.78	LC201865
ten5	3753338	2060306029	18342	0.83	LC201866
ten6	2516053	1355975681	18342	0.89	LC201867
ten7	2577141	1369986222	18342	0.54	LC201868
ten8	2889143	1521250287	18341	0.81	LC201869
ten9	2444329	1339643217	18342	0.67	LC201870

Abbreviations are the same as in Table 1.

Table S 2. Percent identity of mtCR sequences to the most similar sequence within the corals used in this study

mtCR types in the database	Percent identity	Most similar mtCR in the database
car1	99.76	car2
car2	99.76	car1
acu	89.16	micD
aus	97.44	ten12_ten13_ten1_ten2_ten3_ten7
cyt1	99.89	cyt2_cyt3_hya1_hya2_hya3_hya4
cyt2_cyt3_hya1_hya2_hya3_hya4	99.89	cyt1
ech1_ech2_ech5_ech6_mur_sel2	99.89	ech3_ech4
ech3_ech4	100.00	adi
ech7	99.89	ech3_ech4
flo	98.17	sp2_sp4
gra_int_awi1_awi2_awi3_awi4_awi5_awi6_awi7	99.68	cyt1
sp1_sp6	99.89	ech3_ech4
sp2_sp4	99.63	sp
sp3	99.89	sp1_sp6
sp5	99.89	ech7
sp7	99.89	sp5
sp	99.63	sp2_sp4
micD	98.61	cyt1
mic	99.25	ech3_ech4
nas1	88.45	nas2
nas2	99.89	ech3_ech4
sel1	99.89	ech3_ech4
ten10_ten11_ten14_ten15_ten4_ten5_ten8_ten9	99.88	ten6
ten12_ten13_ten1_ten2_ten3_ten7	99.88	ten6
ten6	99.88	ten10_ten11_ten14_ten15_ten4_ten5_ten8_ten9
adi	100.00	ech3_ech4

Abbreviations are the same as in Table 1 and IDs those mitochondrial DNA are identical are concatenated.

Table S3. Percent identities of 300 bp flanking the RNS2 primer compared to the most similar mtCR sequence in the corals used in this study

RNS2 types in the database used	Percent identity	Most similar RNS2 types
aus	97.00	ten
cyt_hya	99.00	flo_gra_int_awi
flo_gra_int_awi	99.00	cyt_hya
ten	97.00	aus
acu	85.03	micD
ech_adi_mur_sel_sp	99.67	sp1_sp2-4_sp6
sp1_sp2-4_sp6	99.67	ech_adi_mur_sel_sp
sp5_sp7	99.67	ech_adi_mur_sel_sp
car1	99.67	car2
car2	99.67	car1
nas2	99.67	ech_adi_mur_sel_sp
micD	98.33	cyt1
mic	99.33	ech_adi_mur_sel_sp
nas1	47.42	nas2
Abbreviations are the same as in Figure 3.		

Table S 4. Percent identities of 300 bp flanking the GR primer to the most similar mtCR sequence in the corals used in this study

GR types	Percent identity	Most similar GR type
ten6	99.67	ten12_ten13_ten1_ten2_ten3_ten7
cyt2_cyt3_hya1_hya2_hya3_hya4	99.67	nas_mic_ech_adi_sel_sp
nas_mic_ech_adi_sel_sp	99.67	cyt2_cyt3_hya1_hya2_hya3_hya4
sp2_sp4	99.67	flo
car2	99.67	car1
ech7	99.67	nas_mic_ech_adi_sel_sp
micD	99.00	cyt2_cyt3_hya1_hya2_hya3_hya4
ten12_ten13_ten1_ten2_ten3_ten7	99.67	ten6
sp7	99.67	ech7
aus	98.33	ten12_ten13_ten1_ten2_ten3_ten7
ten10_ten11_ten14_ten15_ten4_ten5_ten8_ten9	99.67	ten6
flo	99.67	sp2_sp4
car1	99.67	car2

Abbreviations are the same as in Table 1.

Table S 5. Weight in water and number of valid alignments of *Acropora* species used in this study

	<i>Acropora</i> species	Number of colonies	Weight in water (kg)	Number of valid alignment	Number of valid alignment per kg	Average number of read per kg
Tank1	<i>tenuis</i>	20	11.2	59487	5311.34	3389.98
	<i>echinata, digitifera, selago, nasta, muricata, Acropora</i> sp.	9	1.94	3873	1996.39	
	<i>hyacinthus, cytherea</i>	7	0.54	2038	3774.07	
	<i>acuminata</i>	1	0.07	23	328.57	
	<i>austera</i>	1	0.11	271	2463.64	
	<i>grandis, intermedia, florida</i>	3	0.38	1165	3065.79	
	<i>microphthalma</i>	1	0.1	938	9380.00	
	<i>carduus</i>	2	0.17	136	800.00	
Tank2	<i>echinata</i>	7	1.1	15909	14462.73	13492.34
	<i>awi</i>	7	1.3	3419	2630.00	
	<i>Acropora</i> sp.	7	1.4	32738	23384.29	

Acropora sp. is unidentified species similar to *A. echinata*