

Additional File 4: Additional Tables.

Table 1: Positive PCR amplification of cDNA using primers binding different regions of *ND3-ND4L-mtMutS* transcription units

Sr. No.	Primer Pair Forward/Reverse	Region	Length (bp)
1	M-6156/M-9137	Complete <i>mtMutS</i> /Start-Stop codons	2981
2	N4L-6071/M-8826	<i>ND4L-mtMutS</i>	2755
3	N3-5499/M-7199	<i>ND3-ND4L-mtMutS</i>	1700
4	N3-5499/M-6780	<i>ND3-ND4L-mtMutS</i>	1281
*	Primers	Sequence (5'---> 3')	
1	M-6156	ATGAATCAGATACCTATGC	
2	M-9137	TTACTCAGTTCCACTGTC	
3	N4L-6071	GCCATTATGGTAACTATTAC	
4	M-8826	CACTTCGGGATGGTAACTCC	
5	N3-5499	ACTACTTATCGTCAGCGGAAC	
6	M-7199	AGGCAATAAGTCCAATTGATATTCTGCTCG	
7	M-6780	TTAAGCCAACCCCGAGTCC	

Primer annotations as per *S. cf. cruciata* mitogenome (XXXX).

Table 2: qPCR primers used for quantification of alternative transcripts

No.	Gene	Nt. Position	Primer Sequences (5' to 3')	Amplicon Size (bp)
A. Reference gene primers				
1	<i>ACTB</i>	β -Actin*	for: CCAAGAGCTGTGTTCCCTTC rev: CTTTTGCTCTGGGCTTCGT	107
B. The <i>mtMutS</i> gene primers				
1	<i>mtMutS-A1</i>	6263-6381	for: GCATGAGCCCGATACTTCTAGT rev: ACGAAGCAACTTGTTCAATGG	118
2	<i>mtMutS-A2</i>	6263-6719	for: GCATGAGCCCGATACTTCTAGT rev: CCGGGTTACTTTGTCCCTGTCCG	456
3	<i>mtMutS-B1</i>	6655-6940	for: CAGCCATGAATGGGCATAG rev: TSGAGCAAAGCCACTCC	285
4	<i>mtMutS-B2</i>	6655-6780	for: CAGCCATGAATGGGCATAG rev: TTAAACCTACCCCGAGTCC	125
5	<i>mtMutS-C1</i>	9002-9083	for: GGTGCCAGTTTGTTC AAGC rev: ATGTCCTGGGGTTCTCTTCC	81
6	<i>mtMutS-C2</i>	9002-9137	for: GGTGCCAGTTTGTTC AAGC rev: TTA CTCAGTTCCACTGTC	135

* Gene name

Nucleotide positions as per *Sinularia cf. cruciata* mitogenome (Acc. No. XXXX)