

Table S1. Forward (F) and reverse (R) primers for real-time PCR.

Gene	Symbol	Acc. No.	Primer sequences (5' → 3')
Carnitine palmitoyltransferase 1A	CPT1A	JQ308822	F:GTGCCTTCGTTTCGTTCCATGATC
			R:TGATGCTTATCTGCTGCCTGTTTG
Enoyl-CoA hydratase	ECH	JQ308826	F:GCCCAAGAAGCCAAGCAATCAG
			R:CTTTAGCCATAGCAGAGACCAGTTTG
Hydroxyacyl-CoA dehydrogenase	HADH	JQ308829	F:GAACCTCAGCAACAAGCCAAGAG
			R:CTAAGAGGCGGTTGACAATGAATCC
Citrate synthase	CS	JX975229	F:TCCAGGAGGTGACGAGCC
			R:GTGACCAGCAGCCAGAAGAG
NADH-ubiquinone oxidoreductase chain 2	ND2	KC217558	F:TAGGTTGAATGACCATCGTA
			R:GGCTAAGGAGTTGAGGTT
NADH-ubiquinone oxidoreductase chain 5	ND5	KC217559	F:CCTAAACGCCTGAGCCCTGG
			R:GCTGTAAACGAGGTGGCTAGAAGG
Cytochrome c oxidase subunit I	COXI	KC217652	F:GTCCTACTTCTTCTGTCCCTTCCTGTTCT
			R:AGGTTTCGGTCTGTAAGGAGCATTGTAATC
Cytochrome c oxidase subunit II	COXII	KC217653	F:ACTGCCTACACAGGACCTTGCC
			R:GTCTGCTTCCAGGAGACGGAATTGT
Uncoupling protein 1	UCP1	FJ710211	F:GCACACTACCCAACATCACAAG
			R:CGCCGAACGCAGAAACAAAG
Uncoupling protein 2	UCP2	JQ859959	F:CGGCGGCGTCCTCAGTTG
			R:AAGCAAGTGGTCCCTCTTTGGTCAT
Proliferator-activated receptor gamma coactivator 1 alpha	PGC1 α	JX975264	F:CGTGGGACAGGTGTAACCAGGACTC
			R:ACCAACCAAGGCAGCACACTCTAATTCT
Proliferator-activated receptor gamma coactivator 1 beta	PGC1 β	JX975265	F:TCAGAGGAAGAGGCGGAT
			R:GACACAGGTGGAGGATGG
Hypoxia inducible factor-1 alpha	HIF-1 α	JQ308830	F:CAGATGAGCCTCTAACTTGTGGAC
			R:TTAGCAAGAATGGTGGCAAGATGAG
Catalase	CAT	JQ308823	F:TGGTCGAGA ACTTGAAGGCTGTC
			R:AGGACGCAGAAATGGCAGAGG

Glutathione peroxidase 4	GPX4	AM977818	F:TGCGTCTGATAGGGTCCACTGTC
			R:GTCTGCCAGTCCTCTGTCCGG
Glutathione reductase	GR	AJ937873	F:TGTTTCAGCCACCCACCCATCGG
			R:GCGTGATACATCGGAGTGAATGAAGTCTTG
Peroxiredoxin 3	PRDX3	GQ252681	F:ATCAACACCCCACGCAAGACTG
			R:ACCGTTTGGATCAATGAGGAACAGACC
Peroxiredoxin 5	PRDX5	GQ252683	F:GAGCACGGAACAGATGGCAAGG
			R:TCCACATTGATCTTCTTCACGACTCC
Superoxide dismutase [Mn]	Mn-SOD/SOD2	JQ308833	F:CCTGACCTGACCTACGACTATGG
			R:AGTGCCTCCTGATATTTCTCCTCTG
Glucose-regulated protein, 170 kDa	GRP-170	JQ308821	F:CAGAGGAGGCAGACAGCAAGAC
			R:TTCTCAGACTCAGCATTTCAGATTTC
Glucose-regulated protein, 94 kDa	GRP-94	JQ308820	F:AAGGCACAGGCTTACCAGACAG
			R:CTTCAGCATCATCGCCGACTTTC
70 kDa heat shock protein, mitochondrial	mtHsp70/GRP-75/Mortalin	DQ524993	F:TCCGGTGTGGATCTGACCAAAGAC
			R:TGTTTAGGCCCCAGAAGCATCCATG
Aryl hydrocarbon receptor 1	AHR1	EU254480	F:CCTGGGACTGAACGCCGAAG
			R:GCTAAGTGTGGGATGTGGTTGG
Cytochrome P450 1A1	CYP1A1	AF011223	F:GCATCAACGACCGCTTCAACGC
			R:CCTACAACCTTCTCATCCGACATCTGG
Growth hormone receptor I	GHR-I	AF438176	F:ACCTGTCAGCCACCACATGA
			R:TCGTGCAGATCTGGGTCGTA
Growth hormone receptor II	GHR-II	AY573601	F:GAGTGAACCCGGCCTGACAG
			R:GCGGTGGTATCTGATTCATGGT
Insulin-like growth factor-I	IGF-I	AY996779	F:TGTCTAGCGCTCTTTCCTTTCA
			R:AGAGGGTGTGGCTACAGGAGATAC
Insulin-like growth factor-II	IGF-II	AY996778	F:TGGGATCGTAGAGGAGTGTTGT
			R:CTGTAGAGAGGTGGCCGACA
β -Actin	ACTB	X89920	F:TCCTGCGGAATCCATGAGA
			R:GACGTCGCACTTCATGATGCT

Table S5. Cardiac changes in the relative mRNA expression levels of genes in seabream under dietary treatments subjected to hypoxia followed by normoxia (Recovery). Data are represented as mean \pm standard error mean. The sample size for each experimental group is specified between parenthesis. Different superscript letters indicate significant differences between dietary treatments ($P < 0.05$, one-way ANOVA, followed by Holm-Sidak test). The mean values obtained for ActbmRNA expression (used as HKG) in Control, *Gracilaria* and *Ulva* groups were 22.93 ± 0.15 , 23.39 ± 0.19 and 23.24 ± 0.12 Ct, respectively.

Biological process	Symbol	Control (5)	<i>Gracilaria</i> (7)	<i>Ulva</i> (6)	P-value
Oxidative metabolism	CPT1A ^a	1.33 \pm 0.17	1.73 \pm 0.30	0.95 \pm 0.13	0.12
	ECH^a	1.02 \pm 0.11^a	0.43 \pm 0.11^b	0.61 \pm 0.09^b	<0.01
	HADH ^a	2.09 \pm 0.16	1.68 \pm 0.34	1.97 \pm 0.34	0.61
	CS ^a	3.74 \pm 0.22	2.52 \pm 0.23	2.86 \pm 0.40	0.44
	ND2 ^b	47.81 \pm 5.41	40.90 \pm 5.18	53.51 \pm 4.28	0.13
	ND5 ^b	20.61 \pm 1.38	19.62 \pm 3.67	22.75 \pm 3.12	0.76
	COXI ^b	132.59 \pm 13.54	125.28 \pm 23.25	148.37 \pm 20.27	0.71
	COXII ^b	36.09 \pm 3.50	31.55 \pm 6.29	45.38 \pm 7.56	0.29
	UCP2 ^c	1.96 \pm 0.29	1.24 \pm 0.11	1.51 \pm 0.32	0.23
	PGC1 α ^d	1.33 \pm 0.19	1.08 \pm 0.17	1.07 \pm 0.08	0.44
	PGC1 β ^d	0.45 \pm 0.02	0.40 \pm 0.05	0.44 \pm 0.05	0.66
HIF-1α^d	3.34 \pm 0.57^a	1.98 \pm 0.33^b	2.93 \pm 0.54^{ab}	0.04	
Antioxidant defence	CAT	0.61 \pm 0.06	0.53 \pm 0.09	0.48 \pm 0.04	0.43
	GPX4	0.02 \pm 0.00	0.03 \pm 0.01	0.04 \pm 0.01	0.46
	GR	0.26 \pm 0.01	0.20 \pm 0.02	0.22 \pm 0.02	0.15
	PRDX3	0.76 \pm 0.05^a	0.28 \pm 0.05^b	0.45 \pm 0.08^b	<0.01
	PRDX5	1.55 \pm 0.14^a	0.81 \pm 0.16^b	1.26 \pm 0.20^{ab}	0.03
	Mn-SOD	1.21 \pm 0.07	0.97 \pm 0.24	1.20 \pm 0.20	0.63
Molecular chaperones	GRP-170	1.01 \pm 0.15	1.24 \pm 0.12	1.05 \pm 0.19	0.58
	GRP-94	0.61 \pm 0.09^a	0.43 \pm 0.04^b	0.39 \pm 0.04^b	0.04
	GRP-75	1.02 \pm 0.17^a	0.65 \pm 0.09^b	0.63 \pm 0.06^b	0.01
Xenobiotic metabolism	AHR1	0.11 \pm 0.01	0.13 \pm 0.01	0.12 \pm 0.01	0.47
	CYP1A1	1.77 \pm 0.41	0.92 \pm 0.34	1.48 \pm 0.37	0.32
GH/IGF axis	GHR-I	0.16 \pm 0.02	0.15 \pm 0.04	0.14 \pm 0.02	0.90
	GHR-II	0.74 \pm 0.13	0.85 \pm 0.20	1.11 \pm 0.28	0.54
	IGF-I	0.00 \pm 0.00	0.01 \pm 0.00	0.01 \pm 0.01	0.59
	IGF-II	1.08 \pm 0.10	1.73 \pm 0.15	1.08 \pm 0.09	0.83

Superscripts in gene symbols indicate the sub-biological process involved in each case: a, β -oxidation/Krebs cycle; b, OXPHOS; c, Mitochondrial respiration uncoupling; d, Transcription factor.