

Supplementary Table S1. Primer abbreviation, GenBank accession numbers, full names, sequences, amplicon sizes and oligo efficiencies (E) are provided for the genes of interest in *P. tricornutum*.

GENES	GenBank Acc. N.	Gene Name on GenBank	Primer Forward	Primer Reverse	Amplicon Size	Efficiency
HSP40A	XM_002177988.1	chaperone, dnaj-like protein (HSP40A)	AGAAATGCGGATGAA AGTGC	GAAGTTTTTGGTCGCTT GCT	102 NT	2
HSP40C	XM_002179448.1	chaperone, dnaj-like protein (HSP40C)	CCAATAATTACCGCGC TTGT	GTTGCTCGTCCTCGTTT AGC	187 NT	2
HSP70_1	XM_002177261.1	predicted protein (Hsp70_1)	TCCCTACCCTTCATCA CAGC	ATTCGCGTCATACCTC CAAC	194 NT	2
HSP70A	XM_002177315.1	chaperone, dnaj-like protein (HSP40A)	TGCTATTGCGTATGGT CTCG	CGAAATCTTCTCCACC CAAA	161 NT	2
MDR	XM_002178678.1	small multidrug resistance protein	CTGGCTCAGTTCCACC AAAT	GACTTCGATTTTTGCCA AGC	187NT	2
CYP450	XM_002178794.1	cytochrome P450	CTCTACGCCATGCATC AAGA	GAGGTAGGGACCCAA GAAGG	159NT	2
GPX	XM_002180703.1	glutathione peroxidase	TAGCGTTCGAGTCCTTTT CGT	AATTTTGTGCGGCCTCT TCG	189 NT	2
GSH	XM_002186446.1	glutathione synthetase. GSH synthetase (gshB)	ATTGCCCTGGATCGCT TTGA	CGACTTGCCCCAGTTTT GTG	196 NT	2
GOX	XM_002178555.1	glycolate oxidase	ATTTTTCGGTTGTCCGA CTG	TTGGGTCCGTTGAATA GCTC	156 NT	2
APX	XM_002180836.1	l-ascorbate peroxidase	TGCAGTACCAGGATCC TTCC	TCCCTTGGAGATCAAA GCAG	161NT	2
SOD1	XM_002180461.1	precursor of mutase superoxide dismutase [Fe/Mn] (SOD1)	AGGTGCCCCATTCTTGA TTTG	TTGATGAGGTCGACAA GCTG	163 NT	2
SOD2	XM_002177217.1	mutase superoxide dismutase (SOD2)	F:CACCGCATAGCTTCA TCAGA	AGTTGGCAGCTCATGC TTCT	224 NT	2
TOC	XM_002181879.1	tocopherol cyclase (VTE1)	CTCAGTTCGCCAGTA AAGC	ATGCGGTACTTGTCCG TTTC	167 NT	2
MAD1	XM_002181572.1	mitotic spindle assembly checkpoint protein (Pt-MAD1)	TTTCGAAGGGTTGGTA GTGG	TTCAAGGGTACGGGAA ACAG	185NT	2
MAD2	XM_002181266.1	mitotic checkpoint protein with homology with MAD2	ACGAAAATGACCAGC CAAAC	CGAGCAAATCAAAAG TGCAA	156 NT	2
HYS	XM_002184494.1	histone deacetylase 1 isoform	TGGCCTTTACAAGGAG ATGG	AAAGACGGGACAATC AGTGG	181 NT	2
CASP	XM_002182516.1	metacaspase	TGAAGATGCGGGGTAT TCTC	CGTCATTATGGCATCC ACTG	189NT	2
SQD1	XM_002185932.1	UDP-sulfoquinovose synthase	TACGGAAGTACGGGTG GAGA	ACTTGGTGGCATGGTA GACG	118	2
SQD2	XM_002185240.1	sulfoquino- vosyldiacylglycerol synthase	AACTGACTCGCAACGGT GATT	TCCAGCATGGGCTTG ATGT	194	2
MGD1	XM_002181649.1	monogalactosyldiacylglycerol synthase	GGTACCACAGTGCAGTCTT TCAA	CTTCTTGCCGGGGA GATA	164	2
MGD2	XM_002186319.1	monogalactosyldiacylglycerol synthase	ACCATCGGCAACTTCG ACTT	TTGAGCGCCCCTTGAT TCTT	165	2
MGD3	XM_002176764.1	monogalactosyldiacylglycerol synthase	GAGTCCGCCGAGAGTT GAAA	TCATTACGACCGCAGA CCAC	166	2