

Table S5**Primers used in qPCR analysis.**

ID^(*)	Gene Product Name	Primers (5' - 3')	Amplicon (bp)	Efficiency (%)	Concentration (nM)
TERG_02214	zinc carboxypeptidase	FW: ACGAAGGCGTCGTCCTACT REV: AAAGCAACAAAGGCAAGAGC	121	101.89	800
TERG_07861	subtilase	FW: AACTATGACCGCTGGGATTG REV: CTTCTCCTGGAGGACGTTGA	138	101.72	700
TERG_06053	catalase (peroxisomal catalase)	FW: CTGAATCGCAACGTGAAAGA REV: CAAACATACGCGCTTGAAGA	118	95.42	700
TERG_08557	serine carboxypeptidase	FW: TGGACGGAGGCAAGTTTTAC REV: TGCAGGTGCTGGTGTCTAAG	114	100.03	700
TERG_02979	Delta(24(24(1)))-sterol reductase (Erg4)	FW: CCTTCCCTTGGTTTTACTTCG REV: TGTAGGGAACAGCCTTCTCG	126	102.07	600
TERG_03102	sterol 24-C-methyltransferase (Erg6)	FW: GGCTGACAAAGGGGACATAA REV: TGGTCACTCGAAGAGCACTG	98	101.35	800
TERG_01252	catalase (catalase A)	FW: CCACTGGTGATGCAGTCAAT REV: CACACCATAGCTCTCCACGA	107	100.45	800
TERG_01281	malate synthase	FW: CGCTGAGGGAAAGAGAGTTG REV: CAGCGAGCTGGTACTTGTG	107	102.92	600
TERG_00825	isocitrate lyase	FW: TATCCATCGTCTGGGAGAGC REV: GCTTAGCGTATGCCTTGGAA	107	108.63	700
TERG_01076	aconitase	FW: GGAATGCTTCCCCTTACCTT REV: GGTGGACACGGAGAGTCATT	121	91.35	800
TERG_01871	acetyl-CoA acetyltransferase	FW: CAGCAAGTTCACCACTGCTC REV: TGATCTCAAAGGCGTCAATG	92	100.55	600
TERG_03762	malate dehydrogenase	FW: GTTGACAGCCCCCTCTACAA REV: TGCTCGTACTCGGAGACCTT	116	96.77	700
TERG_04125	citrate synthase	FW: GCTACGTGTCTCAGCGTGAA REV: GTGTTCCGGTCAAGACACCAG	107	106.77	600

TERG_02198	CamK protein kinase	FW: CAAGGAATCCCAGAGCAAAG REV: GTAGAATTCGCACCGAAAGC	112	95.14	700
TERG_06573	calcineurin regulatory subunit B	FW: AGATGGCGGTGGTGACGTA REV: CGAACTGAAGGCCGATAACC	61	97.80	400
TERG_06392	calmodulin	FW: GGCCAGAACCCTTCGGAAT REV: TGTCGGCGTCAACCTCATT	58	107.50	400
TERG_08613	Multidrug resistance protein Mdr2	FW: TGACGAGGCTACATCAGCAC REV: GTCGGTGAGCAACAGCAATA	104	93.01	800
TERG_07801	ABC multidrug transporter Mdr4	FW: GGAAATTGAGCTTCGAGACG REV: TTCCAACGATAGCAGTGTGC	113	94.20	800
TERG_05742	DNA-dependent RNA polymerase II (rpb2)	FW: TGCAGGAGCTGGTGAAGA REV: GCTGGGAGGTACTGTTTGATCAA	59	94.99	300

(*) TERG: gene accession number at the *T. rubrum* genome database at the Broad Institute.