

S1 Table. Oligonucleotide primers used for RT-qPCR analysis

Protein name ¹	Gene ID ²	Upper (U) primer (5'-3')	Lower (L) primer (5'-3')	Tm U - L (C°)	Product (bp)
14-3-3 protein homolog	<i>C1_03220C</i>	CACCAACCCATCCAATCAG	AATCAGCAACAGCATCATCG	62.2-62.2	126
40S ribosomal protein S0	<i>C3_05370C*</i>	TGTTATTAGCTGCCAACGTCC	CAGCAGCAATGATTCTGGC	62.3-63.0	153
40S ribosomal protein S7-A	<i>C3_01490W</i>	TCAAGCTTTCGTTGATTTGG	GGTGGTGGAACGAAAACAG	61.2-61.4	129
60S acidic ribosomal protein P0	<i>C7_00990W</i>	TCCGAAGCTACCTTGTTGAAC	GATGGATGATGGGAAGACTTG	60.5-58.5	103
60S ribosomal protein L20	<i>C4_01520C</i>	GTTGGTGCTGTTGAAACCATG	CTCTGTGTGGTAATGGGAATTTC	61.6-61.8	169
Adenylosuccinate synthetase	<i>C1_09640W</i>	TTGGTTGAAGGTGCTAATGC	ATGGTTCTTGGAGGAATACCC	61.0-61.3	122
ATP-dependent RNA helicase eIF4A	<i>C1_01350C</i>	ACCGCTACCTTTACCATTCTG	ACCACCAATAGAAGCATGGAC	61.6-61.2	165
Cys-Gly metallodipeptidase DUG1	<i>C5_04300C</i>	GATATGGTTGCTCCTTTGACTG	ATGAAAGGGATGGGAATCTC	60.9-60.1	155
Deoxyhypusine hydroxylase	<i>C2_07290W</i>	CGAAGCTCTTGGTGCTCTTG	GCTTTTTCTGAGTTTTCCAGTG	63.6-63.5	138
D-lactate dehydrogenase	<i>C3_03040W</i>	CGGTGACTTCCCATTCTATG	ATTTGAGCCTCATCTTGTGC	60.3-60.2	144
Elongation factor 1-beta	<i>C4_04480C**</i>	ATGGTACTACTGCCACTCAAGC	CAGTGAATGAAGCAATGTGGT	60.6-61.2	102
Elongation factor 2	<i>C2_03100W**</i>	ACAAGATGGTTGCTTTCCTATTG	TTGGCAGCGGAAATAATACC	61.6-62.1	154
Elongation factor 3	<i>C5_01580C</i>	GATCACAATTGGGTCCAAGG	AGCAGCGGCAATCTTGTTAC	62.5-62.6	105
Guanylate kinase	<i>C5_03790W</i>	CATCTGCCAATAGACCAATCG	TGGTTTTCTGGTGGTGGTTTG	62.7-61.8	128
Heat shock protein SSA1	<i>C1_13480W</i>	CATTAGTGGTGCTTATGGTGC	ACTTCTTCAACAGTTGGTCCA	59.5-60.0	164

Inosine triphosphate pyrophosphatase	<i>C5_03860W</i>	GACTCCTCCTCCTCCTCATC	CAATGACTTTAGCAGCAGCTTG	60.2-62.3	148
Isocitrate dehydrogenase [NAD] subunit 1 (mitochondrial)	<i>C1_09630W**</i>	CGTTATTGCTCAAAAGAAGACTCC	CTTGACCAGCACCATCACC	60.1-62.7	125
Peptidyl-prolyl cis-trans isomerase	<i>C2_02320C</i>	TGCTTCAAGGTGGTGATTTTG	GGACCAGCATTGGCCATAG	63.3-63.8	139
Peptidyl-prolyl cis-trans isomerase	<i>C3_06360C</i>	CAATCGCATTGATTGCTTC	ACAACCGTGCCAAAGAGAC	60.2-61.1	170
Peroxiredoxin TSA1	<i>C3_06180C</i>	AAATTTGCCGAAAAGGATGC	TCTGGACAAGGAGTGGTTGG	62.2-61.6	150
Protein phosphatase Z1	<i>CR_06420W</i>	TCACAACAACGTCCACAACCA	GACAACGGTGAACCTGGC	62.9-61.1	173
Protein URE2	<i>C2_04710C</i>	GGTGAATGTTTATTATGGTCG	CTTTCTACAGCACTTGGTACTGG	60.1-60.2	152
Rad23p	<i>C2_01850W</i>	AACAACCACAACCAGCAGC	ATGCGGCTCTTAATGCAGC	62.2-63.7	129
Ribosomal 60S subunit protein L9B	<i>C3_02470C</i>	CCCAGAAGGTGTCACTGTTG	GCAGCAACGTGTTTTCTGTC	61.5-61.9	165
Transketolase 1	<i>C1_08320W</i>	TTCACCTTCGACCAACAATC	GCACCAAATCTGTTCAAACC	60.9-60.4	141
Ubiquitin-activating enzyme E1	<i>C3_06500W</i>	CAGGTGAAGAACCATTGAGC	GGCAAACCTTGACATAATCGC	60.7-60.5	113
Actin 1	<i>C1_13700W</i>	GTTGCTCCAGAAGAACATCC	ACCATCACCAGAATCCAAAAC	59.7-61.0	192

Based on ¹<http://www.uniprot.org/> and ² <http://www.candidagenome.org/>.

* The primers are flanking an intron in the gene.

**The upper primer is spanning an exon-intron boundary in the gene.

C1_13700W was used as an internal control in all experiments.