Supplemental Table S1

Primers for quantitative RT-PCR analysis

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| Gene name | Primer | Primer sequence (5’-3’) |
| ATP synthase gamma subunit | F | GAGGGCGACAACCTGTTC |
| R | GCTTACGGGTGGTCTTGG |
| ATP synthase F0 subunit 1 | F | TCGTTCCAACGTCGAGTTCG |
| R | TGAAAGCCTCAGCGATGGTC |
| ATP synthase beta subunit | F | GGACGGTCTCGTTCGTGG |
| R | GCTTGGCGTTGATGGGTC |
| putative ATPase | F | CGACTGTGGGCGTTGAGTTTGG |
| R | AGCCGATGAAGATGGCGATGAA |
| ATPase family AAA domain-containing protein 3A | F | CTGGCGTTCTCCATTGTTG |
| R | GTAAATTGCATTGGCTTCG |
| ATPase | F | GTTGAAGATGCGATTCCAGG |
| R | TGCTCACCGACTCAATAACC |
| ATP phosphoribosyltransferase | F | CATTATTGCGGAAAGCCAGAC |
| R | TCTCAAACTGCTTGAAATAGTCCC |
| cytochrome c oxidase subunit 2 | F | TCGGCATGTACGGCCTCAAGT |
| R | GCAGTCAGTGGCACGAGCAAT |
| long-chain-fatty-acid-CoA ligase | F | CGATCCTCCGCTACCTACTGA |
| R | GCGAGTGGGAGATACGAACAAT |
| acyl-CoA dehydrogenase, putative | F | AATACCTAATGGCTGAAA |
| R | TTATTTCTTGTACTCCTC |
| fumarate hydratase | F | GTGGGCACGGGACTCAATACG |
| R | CATGAGGGAGCAGGCGATGGT |
| malate dehydrogenase | F | TCGTGACCGACAAGGACTGGG |
| R | GCGGACATGGCACTGGAAAGC |
| triosephosphate isomerase | F | ACCAGAAGTTGCGGCAATGGA |
| R | CACAGAGCACTGCGGATGATAG |
| glucosylceramidase | F | CGAAGCTCAAGGCGGGTCAAG |
| R | AAGCCAAGCATGGTCTGGTACTGC |
| adenylosuccinate lyase | F | GAGAACATCTTGATGGCTTGCG |
| R | TCCACCTTGACACGCTTACCAG |
| aspartyl-tRNA synthetase | F | TTGTTGGTGGTAGCGTCCGTGAA |
| R | TTGTTGGTGGTAGCGTCCGTGAA |
| pleiotropic drug resistance protein | F | GGACCCGAAGAGCCCGAAAGA |
| R | CTTATCAGCACCCGACGACCC |
| ABC transporter-like protein | F | GATGCCGAACGAGAAGGTGG |
| R | TAGCTTGACGGGATGAGGT |
| elicitin | F | ACACCGAAACCCACGAAG |
| R | AGCCTTCTCAGCATGGTC |
| heat shock protein 90 | F | CCTCGCCGAGCTTCTCGA |
| R | GGTTATGTATTGCTCGTT |
| WS21 (40S ribosomal protein S3A) | F | GGAAAGAACAAACGCCTGAC |
| R | GTTGCGCTCCGAGAAGATA |
| UBC | F | GAAGCGGATCAACAAAGAGC |
| R | AAGCAGTGAGCAGATCGACA |