Table S1. Sequences of primers used for Q-PCR

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| Gene ID | Primer sequences  (5’–3’) | Product size (bp) | Annealing temperature (°C) |
| GME10808\_g | F: TTGCTCGGATGGGTGGATATTC  R: CTTCAAGAAGTTCATCGGTCGTC | 138 | 60.2 |
| GME4497\_g | F: CGCATATACAGTGTTATGGGAAAC  R: CGACTCTACTGTACTCTTCCCAC | 239 | 59.5 |
| GME2815\_g | F: GGGAGGTGTTGTAATTGAGATG  R: GGAACATCGTTACTCATCATCAGC | 126 | 59.0 |
| GME6224\_g | F: GAGAGACCCTGAGATTTACGCTG  R: TCAAATCGTGCTTGGCTGTTATC | 108 | 60.2 |
| GME11160\_g | F: TACCACCATCCACCCCAGCAGT  R: CCTCAGATTCCGATGCAGACACT | 198 | 62.1 |
| GME3484\_g | F: CAGTTCATTACGACGACCTTCAG  R: TCTACGAACTCCATAGCTTCCTC | 131 | 60.2 |
| GME11461\_g | F: CAGAAAAGGTGGTAGGGAGTAAG  R: AATCGACTAGGCCAGCTCTCTTG | 171 | 61.0 |
| GME9953\_g | F: CGCCGAATACCAGATGCAAATACC  R: CCTCCACATCTCCTATCTCATCC | 185 | 61.7 |
| GME11480\_g | F: CAGCGATTCTTTCCCTAGTTCAC  R: GCGAGACGTTGTTCAAATTATGC | 170 | 59.2 |
| GME2873\_g | F: TGGTCGGTCGGGTGCATATTC  R: ATCCAATCCCAGCTCATCTAATGC | 228 | 61.0 |
| GME10202\_g | F: CGTTGATGAAGAAGCGGCTAAGC  R: ATCACGGACCTTTTGCATGAACC | 203 | 60.9 |
| GME3132\_g | F: GTCTTCGGTCTGGCTGCTGATG  R: CGCATTCAAAAGGATCGGGTGTTC | 140 | 62.1 |
| GME10647\_g | F: CTTGATAGGGGAAGAGTAGTGC  R: CCTTCATGTCCTTCTCCCACTG | 187 | 60.9 |
| GME5148\_g | F: GGGTTCCACTGGTAAAGAAGTCG  R: ACCATCATTACGATACACAAGAAGC | 114 | 59.5 |
| GME11273\_g | F: GTCTTCCAACAAAAGGTCCAGG  R: TCGCTTCTTCTCTTCCAACTCG | 129 | 59.6 |
| GME9038\_g | F: TTAGGAGGTGCGACTGGTGGAT  R: TTCTTCCAAACACGCTGAATCACC | 212 | 61.5 |
| GME5859\_g | F: GAGTTTTTGGCGGACGTGTATG  R: CAATCTCCTTCCTGCCTTTACC | 118 | 59.2 |
| GME7934\_g | F: GGAAGAAACATCAAGCCAAGTGG  R: CATTCCCAGACCTCCACAACTC | 219 | 60.9 |
| GME9386\_g | F: CCGTCACACCAATCAACTCTATC  R: CAACCTTGTAGAAATCAATCCCTG | 165 | 59.2 |
| GME8711\_g | F: CTGGAAATGACCTGGCGTTATAC  R: TCTTGCTCACCCACATAAACACC | 205 | 60.2 |
| GME8678\_g | F: GCACATGCAAACTGGGAAATCG  R: GATCCTGGTGTATCTCCTGTCG | 155 | 60.2 |
| GME1797\_g | F: GATGATAGACTACGGCATGGATG  R: CACCCACCAATCTCCCAGTTAC | 144 | 61.0 |
| GME10493\_g | F: GGGACCCTTTGATGTTGTTCTCC  R: CCGTTCTATCCTCGCTGATTCC | 103 | 61.8 |
| GME9838\_g | F: CTGCTACTTCCGACTTGAGTGAC  R: CCTCCTCAATCTTGGGTCTATCC | 150 | 61.8 |
| GME9978\_g | F: ATACGAGGTTCTTGTTGGCGAC  R: ATGAATGCACCATCGAGTTTCTC | 198 | 59.2 |
| GME6807\_g | F: ACAAGTGCATCAAATTCCCCTG  R: TTCTTCTCCAGCCTTCCTCTTC | 156 | 59.2 |
| GME9454\_g | F: CCCGTAGCAGAGGAGAAGTTTG  R: CCAGTCGCATTTATCGTAGGTTCC | 141 | 61.5 |
| GME10889\_g | F: CCATCGACATCTGTGGGTATCC  R: TCAGACTCCTCATGCTCTCCTC | 172 | 61.5 |
| GME8409\_g | F: GAGATGACGCAAAGCCAAGACC  R: TCACCACACTTGTTGCCCGAC | 136 | 61.5 |
| GME7725\_g | F: AGTTGTGTGATGATGGCGGAG  R: TGAAAGCACCGTCCCTCTTACTC | 112 | 60.9 |
| GME8831\_g | F: CCAGCAGCATCAAGTGATCTAC  R: AATGTCTACTCTGCACCTGGATC | 176 | 59.6 |
| GME6006\_g | F: CATACAATGGCACTTCCGCTTG  R: CTTCTTCGTCCTCTTATGCTGTCC | 219 | 60.9 |
| GME1644\_g | F: CTTACTACCCACCTCCCGATTTC  R: TCTGTTCTCTCGACCAACTCCTC | 130 | 61.8 |
| GME4506\_g | F: GAAACCGCTTATCCCTGATGC  R: GATAATCCACCACTCCCACTTGC | 183 | 60.2 |
| GME4280\_g | F: TATGCTTCCACCTCCCCAACC  R: GGTAACCATGCGCTCTTCTTGC | 109 | 61.5 |
| GME1998\_g | F: ATCCCACCACCACTGTCGATTC  R: TATGATCCCCCTGAATACTGCG | 173 | 60.9 |
| GME1283\_g | F: GGATAGAGGAGATGATCTGGACG  R: TTCATAACCACCCCGACTAGCAC | 127 | 61.8 |
| GME3988\_g | F: CGAGATGAATACTATTGGCTCTGG  R: ACTCCGAATTGATACCCCTGCT | 179 | 59.6 |
| GAPDH | F: ATTGGCGTGGTGGTCGTAG  R: ACGGAAACATCAAGGGTAGGG | 142 | 59.6 |