**Table S3. Primers used in this study for *C. thyrsiflorus.***

|  |  |  |  |
| --- | --- | --- | --- |
| **gene\_id** | **gene** | **Fw** | **Rv** |
| c24602\_g1 | EF1A | TTCTTGGCAGCAGACTTGGT | TGACATGCGCCAGACAGTT |
| c26717\_g1 | NFR1 | ACAATCGAGGCGTTGACACA | TCGCTATTGCCACACGAACA |
| c37549\_g1 | NFR5 | CAGTGGGGCTTCCATTGTTG | AATCCGCCGGTCTTTCCATT |
| c39118\_g2 | EPR3 | TTCGCGGAGCTAAAGGTGTT | CATCTCCACAGGCATACCCC |
| c19475\_g1 | FLOT | GGCCGACGGAGAGTTCTATG | CCGAGAGCATCCAAAAGGGT |
| c27874\_g1 | VPY | AGAAGCGAACCAGCATGGAA | GGACAAGATCAGGACGGCTT |
| c38065\_g1 | LIN | CACCGGCCAGATTTTTGGTG | CGTGTTTCCCCTTTTCAGCC |
| c30458\_g1 | GS | GGGCGGCTCGTTACATTTTG | CACCCTGGATTGGCTTTGGA |
| c38184\_g1 | GOGAT | GCGTGCTGATAGAATTGGCG | CCATAAGGTTGACTCGCCGT |
| c20649\_g1 | NIR | GGCAATCCCTCTTGATGCCT | TTTTGCCTGTTTCCTCGGGT |
| c32191\_g1 | ASN1 | CGTGGACATGCTTGATGGGA | CAATAGCATCACGGGCAACG |
| c8699\_g1 | P5CS | CGTCATCGTCTTTTTCGCCG | AGACCGATCCATGTCCTCCA |
| c36839\_g1 | OAT | AAGCATTGGGTGGTGGAGTAA | GGTACTTCCATGCTCTCCAGG |
| c35880\_g1 | CPS | CTCGCAGATTAAGGCAAGATGG | CCAACAATGTCCCATGAACGAG |
| c37782\_g1 | ASSY | TTCTGGCCTATAGTGGTGGC | GCCAACATCAGCAGTAAAGCAA |
| c31877\_g1 | ARLY | TGATGCAGTGTCAGACCGAG | TCTGAAGCCCACAAAACCCA |
| c31424\_g1 | ARGH1 | ATGGAGGGTGGTTATGCTCG | TCTTTTGCCTTGTTCACGCC |
| c37501\_g1 | DUR3 | TCAGGTGGGCTTGTCTTTGG | TGAAGGTCGTGCAGCTATGG |
| c37737\_g2 | NAOAT | GAGTTCTGGGATTGCGGTGA | TTGCTGACATGGGTAAGCGT |
| c36428\_g1 | ARGJ | ATCACAGCCCCATGCTTGAC | AAGAAGGCTGGTGAGACCCA |
| c24096\_g1 | THIC | CATGGTTACGGGAGTGCTGA | TCCCCGCTGACAGTTTTCTT |
| c34246\_g1 | THI4 | TTCTATCCGTCTCCAGCCCA | GAGGGAGTCAAAGCGGACAT |
| c39174\_g2 | NUDT1 | CCTTGGGACAATCTTCCGTGT | TCAGCCTCAGCGATTACCAC |
| c35711\_g2 | ADCL | GCAGGAATGGATCGCTGAGA | CGACAGCATAAAGAGCCGGT |
| c4055\_g1 | GLB3 | TCTGGTGTGCTGTCCAATGC | GTCACCGTCCATTTCCCGTT |
| c17120\_g1 | HBP2 | GAAGAATGCTGGAGAGCTTGC | GCTCAGGAGGAACATCAGAGT |
| c33510\_g1 | SODC | TGCTAAGCTCATGTCCACCC | ACAAGCAGATTCCTCTCACCG |
| c19409\_g1 | SODM | TCCCACTAGGGTTTTCCTGC | CTGGTTTCGTCACCGACTCA |
| c19257\_g1 | PER42 | CATCCCAAAGCTCCTGTCCA | CCATGACTGTGCTGTCGAGT |
| c29022\_g1 | CATA | CGATGACACTGGGAATTGCG | GGCAATCAAAGGGTTGGCTG |
| c4825\_g1 | APX1 | ACCATTAAGCATCCCGCTGA | GAACTGCTCCTTGATGGGCT |
| c23716\_g1 | DHAR1 | CTGATGGGTCAGAACAGGCTT | AGTGACCTTCTCCCCAGCAA |
| c33792\_g1 | MDAR | GCAGCTAGGGAGTTTGCCA | TCATAAGGAGCCACCGCTTC |
| c11945\_g1 | GPX4 | CTCCACAACCTTCCCCTCTTT | CAGCTCCCCTTTACAAGTTCCT |
| c24098\_g1 | GPX6 | GGTGCATAGCGGTCAACAAC | GGTGGACTCTTTGGGGACAG |
| c25417\_g1 | GPX8 | GGTCAACGACTTTCCCGTCT | AAGTCTGGCAAATGGGGCAT |
| c31503\_g1 | RBS | CAACCACACCGCACAGTTTT | ACATAGCCGGACCCAGAAAC |
| c78883\_g1 | RBL | GCCAGAGAATTGGGAGTTCCT | CTCGGCAATAATGAGCCAAGC |
| c35348\_g1 | Ct12 | TGAAGGTGTCATTGTCGGGG | TTGGATGGCATACCGTGGTC |
| c29196\_g1 | CUCM1a | GAAAGCAATCACCAGCGACC | TCCCCAAAGCGAAAGATGGG |
| c34419\_g1 | CUCM1b | TTGTTGCCCCATTTTCAGCC | CCAAGCCGCAAGGATTTCAG |
| c33106\_g2 | AIR3 | GGGGTCATTTCACGCTGCTA | ATCCACGGGGCAAGATTTGT |
| c31672\_g1 | SUBL | ACGTCGCCAATGCAAGTCTA | GCAAACCTTGTAAGCGGCAA |
| c91758\_g1 | DEF1 | GCCTTTTGCACTCAGATGACG | ACAGCGATAAAGACGGCAGG |
| c90907\_g1 | DEF2 | GCTCCATAAGTTGCATACTCCCA | TGGTATGGGATTTGTTCGTGGT |