Additional file 8: Table S3. The primers used for q-PCR.

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| --- | --- | --- | --- | --- | --- |
| Gene ID | Description | Sequence Length | Product Length | Primer sequence | Tm |
| GSMUA\_Achr6T14620\_001 | Putative Peroxidase 52 | 795 | 128 | For: | GCACTCCGACCAGGAGCTGTTCAA | 63.4 |
| Rev: | AGAGGCTAATGTTGCCCATCTTCACCAT | 63.3 |
| GSMUA\_Achr10T14220\_001 | Peroxidase 4 | 870 | 299 | For: | TCCTGGACGACACACCGACGAT | 61.7 |
| Rev: | TGCGAACTTACTGATGAGACTGCTGAG | 61.7 |
| GSMUA\_Achr7T18420\_001 | 1-aminocyclopropane-1-carboxylate oxidase | 957 | 117 | For: | GTGGCTCAGACTGATGGCAACAG | 60.1 |
| Rev: | CTCCTTCTTCTCCTCCGCTTCCTT | 60.2 |
| GSMUA\_Achr6T00870\_001 | 1-aminocyclopropane-1-carboxylate oxidase | 882 | 199 | For: | AGGTCGTGAGCAATGGCGTCTA | 60.1 |
| Rev: | TTGTCTGAGAACTTGGTCTTGGTGTAG | 59.7 |
| GSMUA\_Achr4T11940\_001 | Luminal-binding protein 4 | 2169 | 172 | For: | TCTTGAGCGGAGAAGGTGGTGAA | 60 |
| Rev: | GTCTGCTGATCTTGGTAAGTCGTGAA | 59.8 |
| GSMUA\_Achr3T27250\_001 | Luminal-binding protein 5 | 1806 | 210 | For: | AAGGATTCCGAAGGTCCAACAACTCT | 60.9 |
| Rev: | GTCATCACTCCACCAACCGTCTCA | 60.9 |
| GSMUA\_Achr11T04480\_001 | S-norcoclaurine synthase 1 | 1071 | 222 | For: | TGAACGACGTTGAAGGACTCCATATCA | 61 |
| Rev: | GAGGACCAACCACCGCCGAATA | 60.6 |
| GSMUA\_Achr11T04520\_001 | Putative S-norcoclaurine synthase 1 | 1068 | 100 | For: | CCCGCTCAACCTCTCACTTTCAGA | 60.9 |
| Rev: | CCAGATTCGTCGCCATCACCTCT | 60.8 |
| GSMUA\_Achr11T04500\_001 | S-norcoclaurine synthase 1 | 1068 | 189 | For: | CGCTCTCATCGCTAACATCGGTGATA | 61.5 |
| Rev: | ACATACTTCGGCTTGCACTCCTTCA | 61.1 |
| GSMUA\_Achr7T26580\_001 | UDP-glucose 6-dehydrogenase | 393 | 114 | For: | TAGCATCTACGATCCTCAAGTGACAGTG | 61.1 |
| Rev: | GCATAATCCAGCTTCCTGAACTCATCC | 60.7 |
| GSMUA\_Achr1T17550\_001 | Catalase isozyme 2 | 339 | 176 | For: | CTGGCAAGCGTGAGAAGAATGTGATT | 61 |
| Rev: | CGACAGGAACGAGATCCAGATGCT | 60.8 |
| GSMUA\_Achr11T03210\_001 | Putative Ethylene-responsive transcription factor ERF024 | 519 | 125 | For: | GCCGCAACTGCTGGTGAACA | 59.8 |
| Rev: | ACGGATAGCTCCACCTCCACAG | 59.5 |
| GSMUA\_Achr11T15810\_001 | Ethylene-responsive transcription factor ERF071 | 600 | 191 | For: | AAGCAAGTCTCCGTCGCTCTCG | 60.9 |
| Rev: | ATCCCAATATTCCCTGTCACAACCTCAT | 61 |
| GSMUA\_Achr1T23990\_001 | putative MYB DNA-binding domain superfamily protein [Zea mays] | 993 | 264 | For: | ATCTGGACCTGCTCCGCCTCTT | 61.4 |
| Rev: | AGATACAAGTAGCTGTGCCACAACCT | 60.9 |
| GSMUA\_Achr1T10080\_001 | Putative Probable WRKY transcription factor 40 | 1008 | 135 | For: | GCACCACCAGCGACGATTCTTG | 60.7 |
| Rev: | GCCCATATTTCCTCCATTGATAGCCATC | 60.9 |
| GSMUA\_Achr6T05880\_001 | Putative WRKY transcription factor 6 | 1431 | 220 | For: | GGTCCTCGTGCCAAGACAGTTCA | 61.1 |
| Rev: | TTGCTCGGTGCTACTCGCTTCC | 61.2 |
| GSMUA\_Achr6T33100\_001 | Mitogen-activated protein kinase 5 | 1104 | 260 | For: | TTACGGCATCGTCTGTTCGGTGAT | 61 |
| Rev: | CTTGGTTGGAGCGGATTATATGGTGAAG | 61 |
| GSMUA\_Achr8T27900\_001 | Putative Acidic endochitinase SE2 | 654 | 150 | For: | ACGTGTGGGTGCAGTTCTACAACAA | 61.7 |
| Rev: | GCCGTAGTTGGACGCAGTCTTGAT | 61.7 |
| GSMUA\_Achr9T29630\_001 | Putative E3 ubiquitin-protein ligase PUB23 | 1857 | 222 | For: | AACTCTTCTCCGTCCCTCACTTCTC | 60.2 |
| Rev: | CCACCTCTTCGCCTCTTCCTCTT | 60.1 |
| GSMUA\_Achr7T03450\_001 | Polyphenol oxidase, chloroplastic | 1848 | 269 | For: | ACGACGAGAACGCCGACTTAGT | 60.1 |
| Rev: | TATCTCCTCCTCATCTTCCTTCTCCTTG | 60 |
| GSMUA\_Achr10T03730\_001  | Actin | 1134 | 66 | For: | TGGTATGGAAGCCGCTGGTA | 60.2 |
| Rev: | TCTGCTGGAATGTGCTGAGG | 60.4 |