

Table S2. 3'-anchored sequences for *CesA* gene family transcripts

| | 3'-anchored consensus sequence | Read # | % Match |
|---------------------|---|---------------|----------------|
| CesA6a | CGGAGGCTGCGGCAACCTTGTGCAGTTCGGCCACGAATATACTAGGGAAGATCGCGACCAA TCAATCAATCGATGACCGAGTTCAATTGTTCAAAG | 26 | 100 (93) |
| CesA6b ^a | CGGATCGACCCTTTCTTGCGAAGGATGATGGTCCCCTGTTGGAGGAGTGTGGTCTGGATTG CAACTAGGAGGTGAGCAGTGGACCTTCCCCTNAGTGTGTGG | 9 | 97 (104) |
| CesA8 | CGGGATCTCGAACGCGATCAACAACGGGTACGAGTCGTGGGGCCCCCTGTTCCGGGAAGCTC TTCTTCGCCTTCTGGGTGATCGTCCACCTGTACCCGTTCCCTCAAGGGTCTGGGTGGGG | 8 | 100 (113) |
| CesA10 | CGGACGCCACCATCGTCGTGCTCTGGTCCATCCTCTCGCTCCATCTTCTCGCTCGTCTG GGTCAGGATCGACCCGTTTATCCCGAAGGCCAAGGGCCCCAT | 2 | 100 (104) |
| CesA4a | CGGATACCCAGACGTGTGGCATCAACTGCTAGGGAAGTGAAGGTTTGTACTTTGTAGAAAC GGAGGAATACCACGTGCCATCTGTTGTCTGTTAAGTTATATAT | 5 | 100 (106) |
| CesA4b ^b | CGGATACCCAGACGTGTGGCATCAACTGCTAGGGAAGTGAAGGTTTGTACTTTGTAGAAAC GGAGGAATACCACGTGCCATCTGTTGTCTGTTAAGTTATATA | 2 | 95 (107) |
| CesA4c ^c | CGGGGTGTTGGTGTATTTGATGCATCAACTGATTACAACATGGAAGATGCCTTATTGTGAGTT CCAACACCCTCTCAGCTCACTCAATTTG | 2 | 100 (57) |
| CesA9 | CGGATACTCGAACGTGTGGCATCAACTGCTAGGGAGGTGAAGGTTTGTAGAACAGAGAGAT ACCACGAATGTGCCGCTGCCACAAATTGCTGTAAAG | 10 | 100 (98) |
| CesA5 | CGGGTCACTGGCCCTGATATCGCGAAATGTGGCATCAACTGCTAGGATGAGCTGAATATAGT TAAAGAGTGAAGTAGACGCATTGTGG | 27 | 96 (88) |
| CesA2 | CGGTGCTGCTGCAGACAATCATGGAGCCTTTCTACCTTGCTTGTAGTGTGGCCAGCAGCGT AAATTGTGAATTCTGCTTATTTTTTTAG | 14 | 100 (78) |
| CesA1 | CGGTGCTGCTGCGGACTAAGAATCACGGAGCCTTTCTACCTTCCATGTAGCGCCAGCCAGCA GCGTAAGATGTGTAATTTTGAAGTTTTGTATGTC | 18 | 97 (96) |
| CesA3 ^d | CGGCACAATCATGATCTACCCCTTCGTGAAATACCAGAGGTTAGGCAAGACTTTTCTTGGTA GGTGCGAAGATGTGTCGTTAAGTTCACTCTACTGCTAGTTTGGGGG | 17 | 100 (100) |

^a*CesA6b* reads are located upstream of the *CesA6a* consensus tag, consistent with a transcript containing a restriction site polymorphism. However, absence of the downstream *Msp1* site was not independently confirmed. ^b*CesA4b* contains 3 indel polymorphisms in comparison to *CesA4a* and all 3 are represented in both reads. ^c*CesA4c* aligns with a different genomic assembly than *CesA4a* and *CesA4b*. The *CesA4c* sequence contained part of an adjacent intron (highlighted in grey) identified in the MAGI4_30120 sequence. ^d*CesA3* aligns to a partial fragment and thus is not represented in the alignment.