

Additional file 2 Real-time qPCR primers and expression estimation results. Transcript abundance levels via qPCR-based estimates and RNA-sequencing were collected on genotype III6D grown in the field in 2009. The samples were taken at 60 hours before floral opening on the 1st and 25th of September, respectively. The significance of the correlation was based on a *t*-test.

| Gene name | Primer pair (forward/reverse, 5'→3') | Estimate by qPCR (copies/pg cDNA) | Standard error | Estimate by normalized read number | Pearson correlation coefficient | P-value |
|--------------|--|--|-------------------|--|------------------------------------|---------|
| <i>CHS-D</i> | atggtgaccgtcgaggaggtc/ gtcgggcttagctgggacg | 1062.5 | 90.4 | 19196 | 0.774 | <0.05 |
| <i>CHI</i> | atgtctgcgccgccc/ ggctgcagttattagacgacgaccg | 537.4 | 75.8 | 10046 | | |
| <i>F3H</i> | atgacgacgggtcaacctta/ cgcatatatactttgtgactttactgca | 214.7 | 8.5 | 14241 | | |
| <i>F3'H</i> | atggctaccttaacctta/ cgctgcagttaattgagagtatagagat | 92.5 | 1.8 | 10924 | | |
| <i>DFR-B</i> | atggggacgggtaatacctctcttc/ gcgctgcagcttctcaagcttttaa | 344.1 | 8.5 | 7866 | | |
| <i>ANS</i> | atgctgtctactattactgcaactgttc/ tataagcttctaatttgattgatgatcatcatc | 422.7 | 27.9 | 17694 | | |
| <i>3GT</i> | atgggcagttcagagtgcc/ gcgctgcagaattccagcttatca | 1150.8 | 11.5 | 77241 | | |
| <i>MYB1</i> | tatggatccatcgtaattctctgcaag/ tatctcgagttaaatggttgtgtctaaaag | 14.1 | 1.9 | 2716 | | |
| <i>bHLH2</i> | gatggatccatggcggaaaccctg/ ggactcgagctaaaactgaggaattatrcatg | 1.0 | 0.1 | 4153 | | |
| <i>WDR1</i> | caaagatggtgaactcaac/ catctccttacacttttagc | 3.3 | 0.2 | 1251 | | |