**Supplementary Table S1. Primers and characteristics of genes used in RT-PCR**.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene symbol | Gene name |  | Primer sequence (5’-3’) | Product length (bp) |
| *ACT* | Actin | ForwardReverse | AGTACTCTTCCAGCCGTCGCGCGCCGTGATCTCTTTGCTC | 182 |
| *COP1* | Constitutively photomorphogenic | ForwardReverse | ACAACCACCGCCACGAAAACGGCTGCAACAGGGACAATCG | 198 |
| *HY5* | Elongated hypocotyl 5 | ForwardReverse | GGAGGACTCCGGCTGAGAAATAGAACCACCGCTTCCCCTC | 243 |
| *PAL* | Phenylalanine ammonia-lyase | ForwardReverse | TCTACACGTACGCGGACGACTAGGTAGCACCGCCTTGAGC | 171 |
| *C4H* | Cinnamic acid 4-hydroxylase | ForwardReverse | CTGGCGCAAGATGAGGAGGATGGTCGCGGAGTCAGGATTC | 134 |
| *4CL* | 4-Coumarate-CoA ligase | ForwardReverse | TGTTCCGCCGCTTGTGATTGACACTGGTCCTGCCTCTGTC | 185 |
| *CHS* | Chalcone synthase | ForwardReverse | CTGCGGCCCAGACCATCTTAATCTTCTCCGCCTTGAGCCC | 250 |
| *CHI* | Chalcone isomerase | ForwardReverse | TTGCTCTCTCCCCTAACGGCCCCAGGAGACACACCCTTCT | 146 |
| *F3H* | Flavanone 3-hydroxylase | ForwardReverse | TCGCTCGAGACTTCTTCGCCAGCCAAACCCATCAGCCTCT | 242 |
| *FLS* | Flavonol synthase | ForwardReverse | CGTCGACCTAAGCAACCCCAGGAGTCTTCTGGCTTCGCGA | 193 |
| *F3’H* | Flavonoid 3'-Hydroxylase | ForwardReverse | GCGGTTCCTTTGGTTGTGCATCCACCGTGCAAGACCTAGC | 112 |
| *DFR* | Dihydroflavonol 4-reductase | ForwardReverse | AGCAGCTTGGGATTACGCGACCCTTGGCAGCAGCTTGTTC | 231 |
| *ANS* | Anthocyanidin synthase | ForwardReverse | TCAGACCGCTGTAACCACCGGGTCCCCGAGCTGTTGAAGT | 209 |
| *F5H* | Ferulate 5-hydroxylase | ForwardReverse | CGTCAGCGATAGAGTGGGCATCCACACGTCGGTCAAGTCC | 106 |
| *Lhcb1* | Light-harvesting complex Ⅱ chlorophyll a/b-binding protein gene | ForwardReverse | CCATCTGGCAGCCCATGGTA CAAGCATGGCCCATCTGCAG | 193 |
| *rbcL* | Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | ForwardReverse | ACTGCGGGTACATGCGAAGATGCATTGCACGGTGGATGTG | 167 |
| *rbcS* | Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit | ForwardReverse | CATTCCCAGTCACCCGCAAG GTGGCCACACCTACGAAACG | 249 |

Symbols, names, designed primer sequences, and product lengths (base pairs) indicated for selected genes searched by Blast among *Brassica napus* sequences in GenBank database.