**MBD protein recognized flower control genes regulated by DNA methylation in** ***Chrysanthemum lavandulifolium***

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Supplementary Table 1-1. Primers for PCR analysis

|  |  |  |
| --- | --- | --- |
| **Gene** | **F -Primer sequence**  | **R -Primer Sequence** |
| *ClDFL* | CCGATTGTGATGAAGAAGTTGAAGG | AACGATACAGAGGTGTTCGCCAAAG |
| *ClGRAS* | ACAAACCAACCCTATTTCTTCCA | CATCATCACCCATAACCATCTCA |
| *ClWRKY12* | CACGAGTAATCATCAGCAGGTAT | GATCTGTTTCGAGAAGTGGTTGT |
| *ClWRKY21* | ATCCGATTGTGACGAAGAAGTTGAAGG | ACAACGATACAGAGGTGTTCGCCAAAG |
| *ClFT* | ATTACGGTTAGCCGCATCAAAGG | TTCCAGCGACAACAGGAGCACAG |
| *ClLsL* | GAGTAGATCAGAGCCCGGTTTCG | GCGTGTCCGTATTTCAAGTTCGC |
| *ClDOF* | TAGCGTTTGGTATTGAGTGCTGC | GGAGGTGGGATTGGGAGTGAGAA |
| *ClMET* | GGTGAGGTTTGGAATACTGGAGG | ATTTAGGGCGTTAGGATCAAGAG |
| *ClDELLA* | ATATGGCGTTGCCTGGAATGAAC | TGGACGACCAAGATGCTGGAGTT |
| *ClWRKY10* | ACCAAGTTACACGGTCTCCACTA | CAAACCTACGCAAGCAATCAATA |
| *ClWRKY12-2* | CCGATTGTGATGAAGAAGTTGAAGG | AACGATACAGAGGTGTTCGCCAAAG |
| *ClWRKY13* | TCCTTCCCTCTTATGACACCAAA | AAAGTGTTTCCACAAATAGCGTT |
| *ClWRKY14* | CACCCACCCAACTGCTTACTTTT | TTTCTGTACGCTTTCGAGACCTG |
| *ClWRKY15* | CAAGACCGTGATTTATTAGCATCT | TTGAACCTTACTGTACTAGCCTGAG |
| *ClWRKY17-1* | ATCCGATTGTGACGAAGAAGTTGAAGG | ACAACGATACAGAGGTGTTCGCCAAAG |
| *ClWRKY17-2* | AACAGATCCTCCACAACCACCAC | CGGACCTTCAACTTCTTCGTCAC |
| *ClWRKY17-3* | ATCCTCCACAACCACCACCATCC | AACGATACAGAGGTGTTCGCCAAAG |
| *ClWRKY17-4* | CCGTCGGAAAACGTAGTCGGAGC | AATCATCAAAATGGCAAAAGGCACA |
| *ClWRKY38* | GCATCATTCATCACGGCATTGTA | TGGAAGATGTTCTGTGGAGGGTC |
| *ClWRKY56* | AATTTGTCGGCTCGGTTGTGAGA | GACGGACCCTACTATGGTGATGG |
| *ClFCA* | TTGGAGAACCTAATAGCGACCAT | CTTCACATTTAGCATCCACGACA |
| *ClFLC* | CGGCGTAACGGACTGATGAAGAA | CGAAATGAAGCACGAATAAATGG |
| *ClGAI* | ACCAGCATTCACGCCTTTCCCTC | CTCTGACAAGCACCGGCCAGTTT |
| *ClCOL4* | GGGTTCCTATTGTTCCGTTTT | TAAGGCTATGCGATTGGTTC |
| *ClLs* | CACGAGTAATCATCAGCAGGTAT | GATCTGTTTCGAGAAGTGGTTGT |
| *ClROS1* | AGAAGAACAGTTTACTTTGGGAC | TCTAGCCATTAAAGGTCTAGGAG |
| *ClFRI* | TAAGTAGGCGTGGCAACAAAGGT | CAATGGTGTAGCAGCAGGGTATG |
| *ClDEMETER* | GACGTACCACCTATTTGTATTCG | ATGTTTATCGGAGGAGGTCTAAG |
| *ClCRY1b* | CAATAATGGCATAGCAGTTCG | TCAAATGACCCAAAAGAGGC |
| *ClPIE* | TAGTCCAACCCTGTCGCTTTGCT | GGACCTCATCTGATTGTTGTGCC |
| *ClFTL* | AACCTGTGGATGCCTATGTTTGG | AACCTGTGGATGCCTATGTTTGG |
| *CLCMT* | TCATCTCCGTCACAACCAACACC | TCGTCATCATCGTCCTCGCTATT |
| *ClLHY* | CAACGACACTATGTTCCGTAGAA | TGTAAGGTTTGAATCCCGTATGA |
| *ClDML* | ATAGCATCCCACCTTTGCTTCCA | AACGTCGGGCATCAACTTCTCAC |
| *ClACTIN* | TAAGAACGATAAG TGCCCACATAG | TTTTAGACATCAG CCATAACAGAGT |

Supplementary Table 1-2. Primer design results of MSP

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene** | **Type** | **Primer Sequence（5’-3’）** | **TM** | **Primer Sequence（5’-3’）** | **Amplified fragment length** |
| *ClWRKY12* | Methylation | 5' GTTAAACGTATCGGTTACGC 3' | Tm=58.12 | 5' ACGATAATTCCGTCGCTATA 3' | 130 bp |
| Unmethylation | 5' GTTAAATGTATTGGTTATGT 3' | Tm=48.02 | 5' ACAATAATTCCATCACTATA 3' |
| *ClWRKY17* | Methylation | 5' TTTAACGATTTATCGTTCGAC 3' | Tm=56.7 | 5' CTTCTTCGTCACAATCGAATA 3' | 100bp |
| Unmethylation | 5' ATATTTAATGATTTATTGTTTGAT 3' | Tm=51.93 | 5' AACTTCTTCATCACAATCAAATAA 3' |
| *ClWRKY21* | Methylation | 5' GAATCGATTCGAATCGAATC 3' | Tm=62.21 | 5' GATCTCGATTCGATTCGATT 3' | 173 bp |
| Unmethylation | 5' GAATTGATTTGAATTGAATT 3' | Tm=53.08 | 5' AATCTCAATTCAATTCAATT 3' |
| *ClFT* | Methylation | 5' TTGAGTCGTGTTTTTTGGTC 3' | Tm=59.04 | 5' TTAACCGTCCGATCTACTCC 3' | 110 bp |
| Unmethylation | 5' AAATTGAGTTGTGTTTTTTGGTT 3' | Tm=59.97 | 5' TTAACCATCCAATCTACTCCAAC 3' |
| *ClDFL* | Methylation | 5' TTGGATCGATCGATAAAATC 3' | Tm=59.09 | 5' CGATTTTTTAATCGAACCAA 3' | 123 bp |
| Unmethylation | 5' GATTGGATTGATTGATAAAATT 3' | Tm=55.9 | 5' CAATTTTTTAATCAAACCAAAC 3' |
| *ClMET* | Methylation | 5' AGTTCGTTTAGGTTCGGTTC 3' | Tm=58.44 | 5' AAACCAAATCGATTTTCGAT 3' | 124 bp |
| Unmethylation | 5' GAGTTTGTTTAGGTTTGGTTT 3' | Tm=56.25 | 5' TAAACCAAATCAATTTTCAAT 3' |

Note：In the Table Methylation and Unmethylation respectively represent primers designed according to the methylated and unmethylated states.