*Supplementary Material*

# Overexpression of the MADS-box gene *SlMBP21* alters leaf morphology and affects reproductive development in tomato

**Appendix A.** Primers for PCR amplification and quantification. All the primers we used were designed by Primer premier 5.0 software.

| Primer names | Sequences (5' →3') |
| --- | --- |
| SlMBP21-F | AGAAAAATGGGAAGAGGAA |
| SlMBP21-R | GTTAACAAGCATCACTAATCTAAAC |
| TAGL1-F | ATGGTTTTTCCTATTAATCAGG |
| TAGL1-R | TGAAGATGAAGAGCCTTGA |
| NPT II -F | CTCAGAAGAACTCGTCAAGAAGG |
| NPT II -R | GACTGGGCACAACAGACAATC |
| SlMBP3-F | ATGATGATCTTGTGTATGGGAAGA |
| SlMBP3-R | CTACTGAAGTTCAAGGGACTTCTTG |
| TM6-Q-F | CTACAACCATTGCACCCCAAT |
| TM6-Q-R | CAGGAGAGACGTAGATCACGAGAA |
| TPI-Q-F | TCTGGGAGGAGACTATGGGATG |
| TPI-Q-R | TCAGACTGCTTGGCACTGATACTA |
| TM5-Q-F | CTTTGTGATGCTGAGGTTGCTC |
| TM5-Q-R | TTTCCAGTGCTTCTCGTGTTG |
| TAG1-Q-F | ATGAACTTGATGCCAGGGAGT |
| TAG1-Q-R | GGGGTTGGTCTTGTCTAGGGTA |
| SlMBP21-Q-F | AACCTTTCTTTCAACCTCTCCG |
| SlMBP21-Q-R | TCCATTAGAGCATCCACCCTG |
| qSlLA-Q-F | GAGTCTGATTCAATGGCATACACC |
| qSlLA-Q-R | GCAAACAGCAGCAATATGACAAG |
| qSlKNOX1-Q-F | AGATGTTTCCAAGGACCCAGAAC |
| qSlKNOX1-Q-R | CCGAACGGGAGCATTACCA |
| qSlKNOX2-Q-F | TTGTTGCGTAAGTACAGCGGT |
| qSlKNOX2-Q-R | CAGTTGTTTATTTGCTTCTGGTCC |
| qSlPHAN-Q-F | AGATTAGGAAAGTGGTGGGAAGT |
| qSlPHAN-Q-R | AGCCATAAGTAAACCTGGGACA |
| SlCRK1-Q-F | AAAGGGATTCTTCCTGATGGC |

| Primer names | Sequences (5' →3') |
| --- | --- |
| SlCRK1-Q-R | TCTCGGGTCCTTCTATGCTACA |
| SlPMEI-Q-F | AAACTCCTATCATTCCAAAACCC |
| SlPMEI-Q-R | CAATTGCATCTTCATACACCTCTT |
| LePRK3-Q-F | TGTCTGTCGTGGTGAAGAGGTT |
| LePRK3-Q-R | AGCTGAGCATGTGCTGTCCC |
| SlPRALF-Q-F | CTTCCTTCTTCAACGACCCTG |
| SlPRALF-Q-R | CATCGCCCTGTAACTAATGTGG |
| LAT52-Q-F | TAATGGAGACCACGAGAACGA |
| LAT52-Q-R | GGGAATAAACCCAACTCATCAAG |
| TAPG1-Q-F | TTGGAGTAAATGGGAAGAGGAA |
| TAPG1-Q-R | ATCACATGGAGTAGGCAATGGT |
| Cel2-Q-F | TTTTCACCAAACCCAAACCCA |
| Cel2-Q-R | TCTTGAAAATAGGGTCTGGCGTCT |
| PMEU1-Q-F | AAGAGTTAAATGGAAAGGGCACAA |
| PMEU1-Q-R | AAAGACCAAGAGAAAAAGGGAAGC |
| GOB-Q-F | CTGAACTTGACTGTATGTGGAGC |
| GOB-Q-R | GAACGTTTACAACAAAGTGACAAT |
| WUS-Q-F | TTTGGCTGCTCTTGAACTTACTCT |
| WUS-Q-R | ACATTACCATAAGGTCCAAATAGC |
| bl-Q-F | GGAAGATTTGATAGTTGTGTTG |
| bl-Q-R | CAAAAATAGAGCTACACAAAACC |
| ls-Q-F | TGTTTTCTACCTCCACCGCCT |
| ls-Q-R | ATGATTTGCTTCCTTCTCCGC |
| MC-Q-F | AAGTAGCAGAAGCAAGGAGGA |
| MC-Q-R | CAAGCGATTAGCAAAGAGTGA |
| J-Q-F | CTTGAAACTGGATTGAGCCG |
| J -Q-R | CTTCAGCCTGAGTAAGGTAGCC |
| SlEM1-Q-F | 5-AGAGGAGGTCAAACAAGAAGGG-3 |
| SlEM1-Q-R | 5-GTATTAGCATTACTGAGTCCGCC-3 |
| SlEM6-Q-F | 5-TGCTGAAGGTAGGAGCCGAG-3 |
| SlEM6-Q-R | 5-ACGCTCACCACCAGACTCATC-3 |
| SlSOM-Q-F | 5-GCCACGATTGGACGGATTG-3 |
| SlSOM-Q-R | 5-CCAACACTCAAACACCCCG -3 |

| Primer names | Sequences (5' →3') |
| --- | --- |
| SlABI3-Q-F | 5-TCACCGATTCGTCCTCTGTAA-3 |
| SlABI3-Q-R | 5-GTTTGATTATACGGAGGCACG-3 |
| SlABI5-Q-F | 5-GTAGAATGGGAAACGGTAGCG-3 |
| SlABI5-Q-R | 5-ATCCGACGACACGGGACTTAG-3 |
| SlCAC-Q-F | CGATGATGTTACTTTCCACCAATG |
| SlCAC-Q-R | GAGAAACCGAACACGCAATCC |
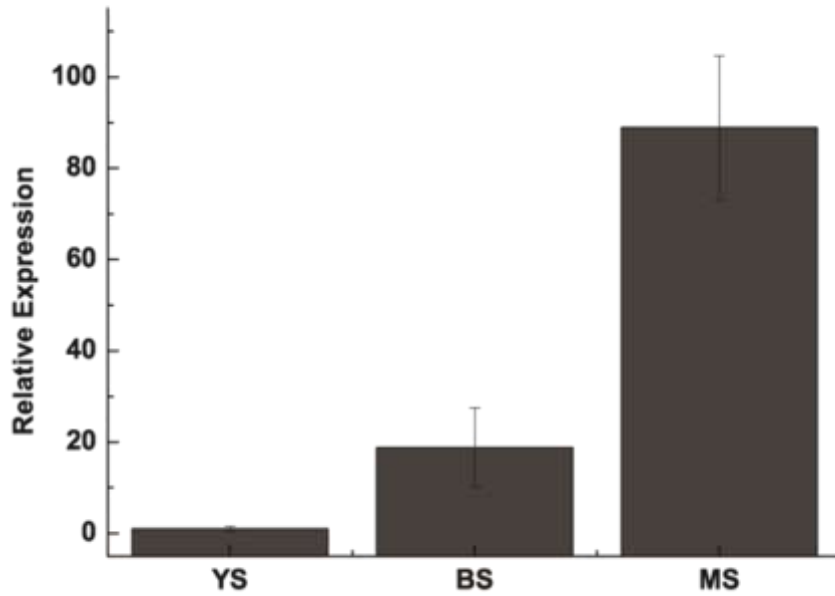
**Appendix B. *SlMBP21* gene expression pattern.** Expression profiles of the SlMBP21 gene in different seed samples of wild-type, including young seeds (YS); breaker seeds (BS) and mature seeds (MS).
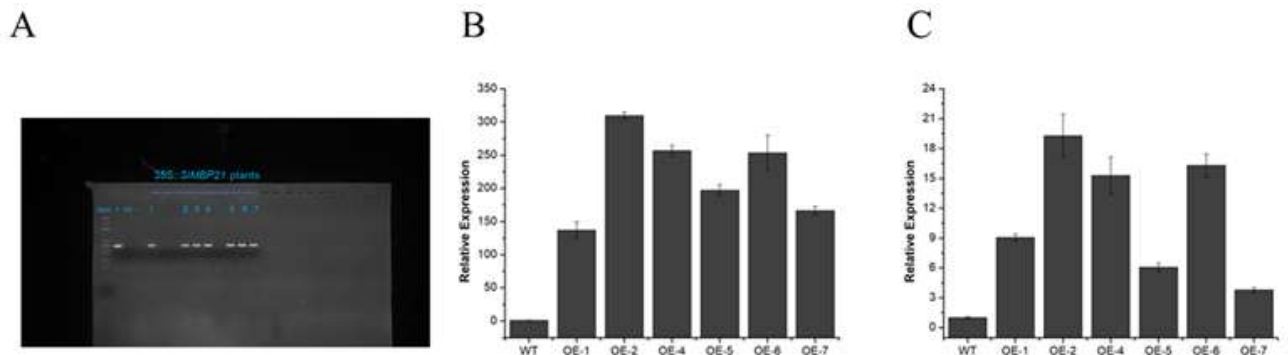


**Appendix C. Relative expression levels of *SlMBP21* in transgenic tomato lines. (A)** PCR analysis with the marker gene (NPT II) of the obtained transgenic plants Mark: BM5000 plus marker; 1-7: the obtained 35S::SlMBP21 transgenic plants. pBI121: positive control of transgenic; WT: negative control of transgenic; 一: dddH2O blank control. **(B)** qRT-PCR analysis of *SlMBP21* in leaf of 35S::SlMBP21 lines. **(C)** qRT-PCR analysis of *SlMBP21* in floral of 35S::SlMBP21 lines.

**Appendix D. pedicel AZ phenotype of 35S::*SlMBP21*.** (A) Inflorescence architecture of wild-type and 35S::*SlMBP21* lines. (B) Flower pedicel abscission was enhanced promotion by *SlMBP21* overexpression. (C) The abscission flowers with a small fruit.