

## Figure S1 Nucleotide and amino acid alignments of MYB31 and MYB42

### S1a: MYB31 nucleotide sequence alignment

```
MYB31_ORF -----
MYB31_UTR -----ACAGCAGCAACAACAACAACAACCTCCACTGCCGCAACCCACCGAGAG
NM_001112479 GCATCGCACCTCACAGCAGCAGCAACAACAACAACCTCCACTGCCGCAACCCACCGAGAG
                *****

MYB31_ORF -----
MYB31_UTR GCGAGACCGGCGGCGGCAAAAAGGACGATACAAAAGCAGCCAGGGTTGCTGGCAACAGCGT
NM_001112479 GCGAGACCGGCGGCGGCAAAAAGGACGATACAAAAGCAGCCAGGGTTGCTGGCAACAGCGT
                *****

MYB31_ORF -----ATGGGGAGGTCGCCGTGCTGCGAGAAGGCGCACACCAACA
MYB31_UTR CGGTGCGCCCGCCGCTCGCCATGGGGAGGTCGCCGTGCTGCGAGAAGGCGCACACCAACA
NM_001112479 CGGTGCGCCCGCCGCTACGCCATGGGGAGGTCGCCGTGCTGCGAGAAGGCGCACACCAACA
                *****

MYB31_ORF AGGGCGCGTGGACCAAGGAGGAGGACGAGCGCCTGGTCGCGCACATCAGGGCGCACGGCG
MYB31_UTR AGGGCGCGTGGACCAAGGAGGAGGACGAGCGCCTGGTCGCGCACATCAGGGCGCACGGCG
NM_001112479 AGGGCGCGTGGACCAAGGAGGAGGACGAGCGCCTGGTCGCGCACATCAGGGCGCACGGCG
                *****

MYB31_ORF AGGGGTGCTGGCGCTCGCTGCCAAGGCCGCCGGCCTCCTGCGCTGCGGCAAGAGCTGCC
MYB31_UTR AGGGGTGCTGGCGCTCGCTGCCAAGGCCGCCGGCCTCCTGCGCTGCGGCAAGAGCTGCC
NM_001112479 AGGGGTGCTGGCGCTCGCTGCCAAGGCCGCCGGCCTCCTGCGCTGCGGCAAGAGCTGCC
                *****

MYB31_ORF GCCTCCGCTGGATCAACTACCTCCGCCCGACCTCAAGCGCGGCAACTTCACGGAGGAGG
MYB31_UTR GCCTCCGCTGGATCAACTACCTCCGCCCGACCTCAAGCGCGGCAACTTCACGGAGGAGG
NM_001112479 GCCTCCGCTGGATCAACTACCTCCGCCCGACCTCAAGCGCGGCAACTTCACGGAGGAGG
                *****

MYB31_ORF AGGACGAGCTCATCGTCAAGCTGCACAGCGTCTCGGCAACAAGTGGTCCCTGATCGCCG
MYB31_UTR AGGACGAGCTCATCGTCAAGCTGCACAGCGTCTCGGCAACAAGTGGTCCCTGATCGCCG
NM_001112479 AGGACGAGCTCATCGTCAAGCTGCACAGCGTCTCGGCAACAAGTGGTCCCTGATCGCCG
                *****

MYB31_ORF GAAGGCTGCCCGCAGGACGGACAACGAGATCAAGAACTACTGGAACACGCACATCCGGA
MYB31_UTR GAAGGCTGCCCGCAGGACGGACAACGAGATCAAGAACTACTGGAACACGCACATCCGGA
NM_001112479 GAAGGCTGCCCGCAGGACGGACAACGAGATCAAGAACTACTGGAACACGCACATCCGGA
                *****

MYB31_ORF GGAAGCTGCTGAGCAGGGGGATCGACCCGGTGACGCACCGCCGGTACGGAGCACCACG
MYB31_UTR GGAAGCTGCTGAGCAGGGGGATCGACCCGGTGACGCACCGCCGGTACGGAGCACCACG
NM_001112479 GGAAGCTGCTGAGCAGGGGGATCGACCCGGTGACGCACCGCCGGTACGGAGCACCACG
                *****

MYB31_ORF CGTCCAACATCACCATATCGTTGAGACGGAGGTGGCCGCCGCCGCCGCGTATGATAAGA
MYB31_UTR CGTCCAACATCACCATATCGTTGAGACGGAGGTGGCCGCCGCCGCCGCGTATGATAAGA
NM_001112479 CGTCCAACATCACCATATCGTTGAGACGGAGGTGGCCGCCGCCGCCGCGTATGATAAGA
                *****

MYB31_ORF AGGGCGCCGCTTCCGGCTGGAGGACGAGGAG-----CGCAACAAGGCGACGATGG
MYB31_UTR AGGGCGCCGCTTCCGGCTGGAGGACGAGGAG-----CGCAACAAGGCGACGATGG
NM_001112479 AGGGCGCCGCTTCCGGTGGAGGACGAGGAGGAGGAGGAGGAGGAGCGCAACAAGGCGACGATGG
                *****

MYB31_ORF TCGTCGGCCGCGACCGGCAGAGCCAGAGCCACAGCCACAGCCACCCCGCCGGCGAGTGGG
MYB31_UTR TCGTCGGCCGCGACCGGCAGAGCCAGAGCCACAGCCACAGCCACCCCGCCGGCGAGTGGG
NM_001112479 TCGTCGGCCGCGACCGGCAGAGCCAGAGCCACAGCCACAGCCACCCCGCCGGCGAGTGGG
                *****

MYB31_ORF GCCAGGGGAAGAGGCCGCTCAAGTGCCCCGACCTCAACCTGGACCTCTGCATCAGCCCGC
MYB31_UTR GCCAGGGGAAGAGGCCGCTCAAGTGCCCCGACCTCAACCTGGACCTCTGCATCAGCCCGC
NM_001112479 GCCAGGGGAAGAGGCCGCTCAAGTGCCCCGACCTCAACCTGGACCTCTGCATCAGCCCGC
                *****
```

MYB31\_ORF CGTGCCAGGAGGAGGAGGAGATGGAGGAGGCTGCGATGAGAGTGAGACCGGCGGTGAAGC  
 MYB31\_UTR CGTGCCAGGAGGAGGAGGAGATGGAGGAGGCTGCGATGAGAGTGAGACCGGCGGTGAAGC  
 NM\_001112479 CGTGCCAGGAGGAGGAGGAGATGGAGGAGGCTGCGATGAGAGTGAGACCGGCGGTGAAGC  
 \*\*\*\*\*

MYB31\_ORF GGGAGGCCGGGCTCTGCTTCGGCTGCAGCCTGGGGCTCCCCAGGACCGCGGACTGCAAGT  
 MYB31\_UTR GGGAGGCCGGGCTCTGCTTCGGCTGCAGCCTGGGGCTCCCCAGGACCGCGGACTGCAAGT  
 NM\_001112479 GGGAGGCCGGGCTCTGCTTCGGCTGCAGCCTGGGGCTCCCCAGGACCGCGGACTGCAAGT  
 \*\*\*\*\*

MYB31\_ORF GCAGCAGCAGCAGCTTCCTCGGGCTCAGGACCGCCATGCTCGACTTCAGAAGCCTCGAGA  
 MYB31\_UTR GCAGCAGCAGCAGCTTCCTCGGGCTCAGGACCGCCATGCTCGACTTCAGAAGCCTCGAGA  
 NM\_001112479 GCAGCAGCAGCAGCTTCCTCGGGCTCAGGACCGCCATGCTCGACTTCAGAAGCCTCGAGA  
 \*\*\*\*\*

MYB31\_ORF TGAAATGA-----  
 MYB31\_UTR TGAAATGAGCGCGCTTCTACCTCTCTGTGTAGCTTCTCCCCCGTCTCGTCTCGTTTTT  
 NM\_001112479 TGAAATGAGCGCGCTTCT-CCCTCTCTGTGTAGCTTCTCCCCCGTCTCGTCTCGTTTTT  
 \*\*\*\*\*

MYB31\_ORF -----  
 MYB31\_UTR GTTTTGCCACACCTCACATGGATGATGAATTGATGATACGTGGTTGGTTAGTTTTTCGT  
 NM\_001112479 GTTTTGCCACACCTCACATGGATGATGAATTGATGATACGTGGTTGGTTAGTTTTTCGT  
 \*\*\*\*\*

MYB31\_ORF -----  
 MYB31\_UTR AGGTGAAAAATACGCGATGGTGAGCGAGTGAAGAGAGATTTGTGCCCTGGGTCCCTCCT  
 NM\_001112479 AGGTGAAAAATACGCGATGGTGAGCGCGTGAAGAGAGATTTG-GCCCTGGGTCCCTCCT  
 \*\*\*\*\*

MYB31\_ORF -----  
 MYB31\_UTR CCCTGCTCTCTCGTGGTGCCCCATTGCGCCTCCTCTGTCCCCCTCTCTCTCTGTATC  
 NM\_001112479 CCGTGTCTCTCTCGTGGTGCCCCATTGCGCCTCCTCTGTCCCCCTCTCTCTCTGTATC  
 \*\* \*\*\*\*\*

MYB31\_ORF -----  
 MYB31\_UTR TCTGTAATCACCATCGCCA-----  
 NM\_001112479 TCTGTAATCACCATCGCCAAATGATCATGGGGGCAATATAATAATACATGCTGCTAA  
 \*\*\*\*\*

MYB31\_ORF -----  
 MYB31\_UTR -----  
 NM\_001112479 TGCTAT

## S1b: MYB31 amino acid sequence alignment

```
MYB31_ORF      MGRSPCCEKAHTNKGAWTKEEDERLVAHIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY
MYB31_UTR      MGRSPCCEKAHTNKGAWTKEEDERLVAHIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY
NM_001112479   MGRSPCCEKAHTNKGAWTKEEDERLVAHIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY
*****
```

```
MYB31_ORF      LRPDLKRGNFTEEEDELIVKLHSLVGNKWSLIAGRLPGRDTDNEIKNYWNTHIRKLLSRG
MYB31_UTR      LRPDLKRGNFTEEEDELIVKLHSLVGNKWSLIAGRLPGRDTDNEIKNYWNTHIRKLLSRG
NM_001112479   LRPDLKRGNFTEEEDELIVKLHSLVGNKWSLIAGRLPGRDTDNEIKNYWNTHIRKLLSRG
*****
```

```
MYB31_ORF      IDPVTHRVPTEHHSNITISFETEVA AAAARDKKGAVFRLEDEE---RNKATMVVGRDRQ
MYB31_UTR      IDPVTHRVPTEHHSNITISFETEVA AAAARDKKGAVFRLEDEE---RNKATMVVGRDRQ
NM_001112479   IDPVTHRVPTEHHSNITISFETEVA AAAARDKKGAVFRLEDEEEEEERNKATMVVGRDRQ
*****
```

```
MYB31_ORF      SQSHSHSPAGEWQGKRPLKCPDLNLDLCISPPCQEEEEEMEEAAMRVRPAVKREAGLCF
MYB31_UTR      SQSHSHSPAGEWQGKRPLKCPDLNLDLCISPPCQEEEEEMEEAAMRVRPAVKREAGLCF
NM_001112479   SQSHSHSPAGEWQGKRPLKCPDLNLDLCISPPCQEEEEEMEEAAMRVRPAVKREAGLCF
*****
```

```
MYB31_ORF      GCSLGLPRTADCKCSSSSFLGLRTAMLDFRSLEMK
MYB31_UTR      GCSLGLPRTADCKCSSSSFLGLRTAMLDFRSLEMK
NM_001112479   GCSLGLPRTADCKCSSSSFLGLRTAMLDFRSLEMK
*****
```

# S1c: MYB42 nucleotide sequence alignment

```
MYB42_ORF -----  
MYB42_UTR -----ACTCGCTGCCTTCTCAAATCCA  
NM_001112539 CGGGCGCAGGAATTCGGCACGAGGGGAAACCCGCGCCACTCGCTGCCTTCTCAAATCCA  
*****  
  
MYB42_ORF -----ATGGGGCGGTGCGCGTGC  
MYB42_UTR AACGCGAAGTAGCAACAAGCAAAGCCCAGATCGATAATACGATGGGGCGGTGCGCGTGC  
NM_001112539 AACGCGAAGTAGCAACAAGCAAAGCCCAGATCGATAATACGATGGGGCGGTGCGCGTGC  
*****  
  
MYB42_ORF TCGGAGAAGGCGCACACCAACAGGGGCGCGTGGACCAAGGAGGAGGACGAGCGGTGGT  
MYB42_UTR TCGGAGAAGGCGCACACCAACAGGGGCGCGTGGACCAAGGAGGAGGACGAGCGGTGGT  
NM_001112539 TCGGAGAAGGCGCACACCAACAGGGGCGCGTGGACCAAGGAGGAGGACGAGCGGTGGT  
*****  
  
MYB42_ORF GCCTACGTCCGCGCGCACGGCGAAGGGTGCCTGGCGCTCGCTGCCAGGGCGGCGGGCCTG  
MYB42_UTR GCCTACGTCCGCGCGCACGGCGAAGGGTGCCTGGCGCTCGCTGCCAGGGCGGCGGGCCTG  
NM_001112539 GCCTACGTCCGCGCGCACGGCGAAGGGTGCCTGGCGCTCGCTGCCAGGGCGGCGGGCCTG  
*****  
  
MYB42_ORF CTGCGCTGCGGCAAGAGCTGCCGCTGCGCTGGATCAACTACCTCCGCCCGGACCTCAAG  
MYB42_UTR CTGCGCTGCGGCAAGAGCTGCCGCTGCGCTGGATCAACTACCTCCGCCCGGACCTCAAG  
NM_001112539 CTGCGCTGCGGCAAGAGCTGCCGCTGCGCTGGATCAACTACCTCCGCCCGGACCTCAAG  
*****  
  
MYB42_ORF CGAGGCAACTTCACCGCCGACGAGGACGACCTCATCGTCAAGCTGCACAGCCTGCTCGGG  
MYB42_UTR CGCGGCAACTTCACCGCCGACGAGGACGACCTCATCGTCAAGCTGCACAGCCTGCTCGGG  
NM_001112539 CGAGGCAACTTCACCGCCGACGAGGACGACCTCATCGTCAAGCTGCACAGCCTGCTCGGG  
* * * * *  
  
MYB42_ORF AACAAAGTGGTTCGCTCATCGCCGCGCGCTCCCGGGGCGGACGGAACAACGAGATCAAGAAC  
MYB42_UTR AACAAAGTGGTTCGCTCATCGCCGCGCGCTCCCGGGGCGGACGGAACAACGAGATCAAGAAC  
NM_001112539 AACAAAGTGGTTCGCTCATCGCCGCGCGCTCCCGGGGCGGACGGAACAACGAGATCAAGAAC  
*****  
  
MYB42_ORF TACTGGAACACGCACATCCGGCGCAAGCTGCTGTGCAGCGGCATCGACCCCGTACGCGAC  
MYB42_UTR TACTGGAACACGCACATCCGGCGCAAGCTGCTGTGCAGCGGCATCGACCCCGTACGCGAC  
NM_001112539 TACTGGAACACGCACATCCGGCGCAAGCTGCTGTGGGCAGCGGCATCGACCCCGTACGCGAC  
*****  
  
MYB42_ORF CGCCGTGTCGCGGGTGGCGCCGCGACCACCATCTCGTTCCAGCCAGCCCCAACTCCGCC  
MYB42_UTR CGCCGTGTCGCGGGTGGCGCCGCGACCACCATCTCGTTCCAGCCAGCCCCAACTCCGCC  
NM_001112539 CGCCGTGTCGCGGGGCGCCGCGACCACCATCTCGTTCCAGCCAGCCCCAACTCCGCC  
*****  
  
MYB42_ORF GCCGCCGCCGCC--GCAGAAGCAGCAGCGCAGGCGCCGATCAAGGCCGAGGAGACGGCG  
MYB42_UTR GCCGCCGCCGCC--GCAGAAGCAGCAGCGCAGGCGCCGATCAAGGCCGAGGAGACGGCG  
NM_001112539 GCCGCCGCCGCCCGCCGAGAAACAGCAGCGCAGGCGCCGATCAAGGCCGAGGAGACGGCG  
*****  
  
MYB42_ORF GGCGTCAAGGCGCCAGGTGCCCTGACCTCAACCTGGACCTCTGCATCAGCCCGCGTGC  
MYB42_UTR GGCGTCAAGGCGCCAGGTGCCCTGACCTCAACCTGGACCTCTGCATCAGCCCGCGTGC  
NM_001112539 GGCGTCAAGGCGCCAGGTGCCCGACCTCAACCTGGACCTCTGCATCAGCCCGCGTGC  
* * * * *  
  
MYB42_ORF CAGCATGAGGACGACGGCGAGGAGGAGGACGAGGAGCTGGACCTCAAGCCCGCCTTCGTC  
MYB42_UTR CAGCATGAGGACGACGGCGAGGAGGAGGACGAGGAGCTGGACCTCAAGCCCGCCTTCGTC  
NM_001112539 CAGCATGAGGACGACGGCGAGGAGGAGGACGAGGAGCTGGACCTCAAGCCCGCCTTCGTC  
*****  
  
MYB42_ORF AAGCGGGAGGCGCTGCAGGCCGGCCACGGCCACGGCCACGGCCACGGCCCTCTGCCTCGGCTGCGGC  
MYB42_UTR AAGCGGGAGGCGCTGCAGGCCGGCCACGGCCACGGCCACGGCCACGGCCCTCTGCCTCGGCTGCGGC  
NM_001112539 AAGCGGGAGGCGCTGCAGGCCGGCCACGGCCACGGCCACGGCCACGGCCCTCTGCCTCGGCTGCGGC  
*****
```

MYB42\_ORF CTGGGCGGACAGAAGGGAGCGGCCGGGTGCAGCTGCAGCAACGGCCACCACCTTCCTGGGG  
MYB42\_UTR CTGGGCGGACAGAAGGGAGCGGCCGGGTGCAGCTGCAGCAACGGCCACCACCTTCCTGGGG  
NM\_001112539 CTGGGCGGACAGAAGGGAGCGGCCGGGTGCAGCTGCAGCAACGGCCACCACCTTCCTGGGG  
\*\*\*\*\*

MYB42\_ORF CTCAGGACCAGCGTGCTCGACTTCAGAGGCCTGGAGATGAAGTGA-----  
MYB42\_UTR CTCAGGACCAGCGTGCTCGACTTCAGAGGCCTGGAGATGAAGTGAACGAAACGAAGCCCA  
NM\_001112539 CTCAGGACCAGCGTGCTCGACTTCAGAGGCCTGGAGATGAAGTGAACGAAACGAAGCCCA  
\*\*\*\*\*

MYB42\_ORF -----  
MYB42\_UTR CACGTCCTTTCTTCTCC-----  
NM\_001112539 CACGTCCTTTCTTCTCCTTTTGTGTCGGTTGTAGTCTTGGCTTGTGGATTTGGATAGA  
\*\*\*\*\*

MYB42\_ORF -----  
MYB42\_UTR -----  
NM\_001112539 GCTAGTTGGTTACTAGTTGTTAGTTAGAAGATAGTGCAGGATGATCACTAGCTACTGGCT

MYB42\_ORF -----  
MYB42\_UTR -----  
NM\_001112539 ACCTCAACAGTACAGTAGCTGCTCCCTTCTCTCCATTCTATGTAAAAAAGAAACAAAA

MYB42\_ORF -----  
MYB42\_UTR -----  
NM\_001112539 TACTTATAAGGTGTTTGGGTTGAGAAATGAACTAGTCTATTATCTTTTC

## S1d: MYB42 amino acid sequence alignment

```
MYB42_ORF      MGRSPCCEKAHTNRGAWTKEEDERLVAYVRAHGEGCWRS LPRAAGLLRCGKSCRLRWINY
MYB42_UTR      MGRSPCCEKAHTNRGAWTKEEDERLVAYVRAHGEGCWRS LPRAAGLLRCGKSCRLRWINY
NM_001112539   MGRSPCCEKAHTNRGAWTKEEDERLVAYVRAHGEGCWRS LPRAAGLLRCGKSCRLRWINY
*****

MYB42_ORF      LRPDLKRGNF TAEDDDLIVKLHSL LGNKWSLIAARLPGR TDNEIKNYWNTHIRRKLLCSG
MYB42_UTR      LRPDLKRGNF TAEDDDLIVKLHSL LGNKWSLIAARLPGR TDNEIKNYWNTHIRRKLLCSG
NM_001112539   LRPDLKRGNF TAEDDDLIVKLHSL LGNKWSLIAARLPGR TDNEIKNYWNTHIRRKLLGSG
*****

MYB42_ORF      IDPVTHRRVAGGAATTISFQSPNSAAAAA-AEAAAQAPIKAEETAGVKAPRCPDLNLDL
MYB42_UTR      IDPVTHRRVAGGAATTISFQSPNSAAAAA-AEAAAQAPIKAEETAGVKAPRCPDLNLDL
NM_001112539   IDPVTHRRVAGGAATTISFQSPNSAAAAAETAQA PIKAEETA AVKAPRCPDLNLDL
*****

MYB42_ORF      CISPPCQHEDDGEEDDEELDLKPAFVKREALQAGHGHGHGLCLGCGLGGQKGAAGCSCSN
MYB42_UTR      CISPPCQHEDDGEEDDEELDLKPAFVKREALQAGHGHGHGLCLGCGLGGQKGAAGCSCSN
NM_001112539   CISPPCQHEDDGEEDDEELDLKPAFVKREALQAGHGHGHGLCLGCGLGGQKGAAGCSCSN
*****

MYB42_ORF      GHHFLGLRTSVLDFR GLEMK
MYB42_UTR      GHHFLGLRTSVLDFR GLEMK
NM_001112539   GHHFLGLRTSVLDFR GLEMK
*****
```