

10.1071/FP20356_AC

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Supplementary Material: *Functional Plant Biology*

Supplementary Material

MYB59* transcription factor behaves differently in metalicolous and non-metallicolous populations of *Arabidopsis halleri

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***A. thaliana* Col-0**

***A. halleri* I16**



***A. halleri* I29**

***A. halleri* PL22**

Fig. S1. Three-week-old plants of *Arabidopsis thaliana* ecotype Columbia (Col-0) and *Arabidopsis halleri* populations I16, I29 and PL22.

AtMYB59_genomic AGAGAGAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AhMYB59_genomic AGAGAAAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AtMYB59.1 AGAGAGAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AhMYB59.1 AGAGAAAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AtMYB59.2 AGAGAGAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AhMYB59.2 AGAGAAAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AtMYB59.3 AGAGAGAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AhMYB59.3 AGAGAAAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AtMYB59.4 -----ATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AhMYB59.5 AGAGAAAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA
AhMYB59.6 AGAGAAAGAGATGAACTTGTGCAAGAAGAATACCGTAAAGGACCGTGGACAGAACAGGA

AtMYB59_genomic GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AhMYB59_genomic GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AtMYB59.1 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AhMYB59.1 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AtMYB59.2 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AhMYB59.2 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AtMYB59.3 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AhMYB59.3 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AtMYB59.4 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AhMYB59.5 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC
AhMYB59.6 GGACATCCTCTTGGTCAACTTTGTCCACTTGTTCGGAGATCGAAGATGGGATTTTGTAGC

AtMYB59_genomic GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAATAGGTATAGGTTTGTTTTGG
AhMYB59_genomic GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAATAGGTATAGGTTTGTTTTGG
AtMYB59.1 GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAATAGGTATAGGTTTGTTTTGG
AhMYB59.1 GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAATAGGTATAGGTTTGTTTTGG
AtMYB59.2 GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAAT-----
AhMYB59.2 GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAAT-----
AtMYB59.3 GAAAGTTTC-----
AhMYB59.3 GAAAGTTTC-----
AtMYB59.4 GAAAGTTTC-----
AhMYB59.5 GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAATAGGTATAGGTTTGTTTTGG
AhMYB59.6 GAAAGTTTCAGGTTTGAAGGTGGAGGGAGAAACATAAGAATAGGTATAGGTTTGTTTTGG

AtMYB59_genomic AAAAATGGGCGGTCTTTGGAAAGGACCTTCCATTTAAAGAAATGACCTGGTTTTGGCTGT
AhMYB59_genomic AAAAATGGGCGGTCTTTGGAAAGGACCTTCCATTTAAAGAAATGACCTGGTTTTGGCTGT
AtMYB59.1 AAAAATGGGCGGTCTTTGGAAAGGACCTTCCATTTAAAGAAATGACCTGGTTTTGGCTGT
AhMYB59.1 AAAAATGGGCGGTCTTTGGAAAGGACCTTCCATTTAAAGAAATGACCTGGTTTTGGCTGT
AtMYB59.2 -----
AhMYB59.2 -----
AtMYB59.3 -----
AhMYB59.3 -----
AtMYB59.4 -----
AhMYB59.5 AAAAATGGGCGGTCTTTGGAAAGGACCTTCCATTTAAAGAAATGACCTGGTTTTGGCTGT
AhMYB59.6 AAAAATGGGCGGTCTTTGGAAAGGACCTTCCATTTAAAGAAATGACCTGGTTTTGGCTGT

AtMYB59_genomic AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AhMYB59_genomic AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AtMYB59.1 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AhMYB59.1 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AtMYB59.2 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AhMYB59.2 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AtMYB59.3 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AhMYB59.3 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AtMYB59.4 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AhMYB59.5 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG
AhMYB59.6 AGGTTTAAACAGAACAGGAAAGAGTTGCAGGTTAAGGTGGGTTAATTACCTGCATCCTGG

AtMYB59_genomic TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AhMYB59_genomic TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AtMYB59.1 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AhMYB59.1 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AtMYB59.2 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AhMYB59.2 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AtMYB59.3 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AhMYB59.3 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA
AtMYB59.4 TCTCAAACGTG-----
AhMYB59.5 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTTTAGTCCTTGAGCTTCACGCCAA

AhMYB59.6 TCTCAAACGTGGTAAGATGACTCCACAAGAAGAGCGTCTAGTCCTTGAGCTTCACGCCAA

AtMYB59_genomic ATGGGGAAACAGGTCAGAAGAATCTTCAAGAAACAGAGAAACCCCTAAAAATGTTTTTTTT
AhMYB59_genomic ATGGGGAAACAGGTCAGAATAATTTTTTCACGAAACAGAGAAACCCCTAAAAACGTTTTGAAT
AtMYB59.1 ATGGGGAAA-----
AhMYB59.1 ATGGGGAAA-----
AtMYB59.2 ATGGGGAAA-----
AhMYB59.2 ATGGGGAAA-----
AtMYB59.3 ATGGGGAAA-----
AhMYB59.3 ATGGGGAAA-----
AtMYB59.4 -----
AhMYB59.5 ATGGGGAAACAGGTCAGAATAATTTTTTCACGAAACAGAGAAACCCCTAAAAACGTTTTGAAT
AhMYB59.6 ATGGGGAAA-----

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AhMYB59_genomic CCTCTTTCC-----TTTTTTGTTTCTTGTATGAACTTTTGGATATTTTCATATGCAGA
AtMYB59.1 -----CAGG
AhMYB59.1 -----CAGA
AtMYB59.2 -----CAGG
AhMYB59.2 -----CAGA
AtMYB59.3 -----CAGG
AhMYB59.3 -----CAGA
AtMYB59.4 -----CAGG
AhMYB59.5 CCTCTTTCC-----TTTTTTGTTTCTTGCATGAACTTTTGGATATTTTCATATGCAGA
AhMYB59.6 -----

AtMYB59_genomic TGGTCAAAAATTGCCCGGAAATTACCGGGGAGAACAGATAATGAGATAAAGAAGCTACTGG
AhMYB59_genomic TGGTCAAAAATCGCCCGTAAATTGCCGGGAAGAACGGATAACGAGATAAAGAATTACTGG
AtMYB59.1 TGGTCAAAAATTGCCCGGAAATTACCGGGGAGAACAGATAATGAGATAAAGAAGCTACTGG
AhMYB59.1 TGGTCAAAAATCGCCCGTAAATTGCCGGGAAGAACGGATAACGAGATAAAGAATTACTGG
AtMYB59.2 TGGTCAAAAATTGCCCGGAAATTACCGGGGAGAACAGATAATGAGATAAAGAAGCTACTGG
AhMYB59.2 TGGTCAAAAATCGCCCGTAAATTGCCGGGAAGAACGGATAACGAGATAAAGAATTACTGG
AtMYB59.3 TGGTCAAAAATTGCCCGGAAATTACCGGGGAGAACAGATAATGAGATAAAGAAGCTACTGG
AhMYB59.3 TGGTCAAAAATCGCCCGTAAATTGCCGGGAAGAACGGATAACGAGATAAAGAATTACTGG
AtMYB59.4 TGGTCAAAAATCGCCCGTAAATTGCCGGGAAGAACGGATAACGAGATAAAGAATTACTGG
AhMYB59.5 TGGTCAAAAATCGCCCGTAAATTGCCGGGAAGAACGGATAACGAGATAAAGAATTACTGG
AhMYB59.6 -----

AtMYB59_genomic AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCTACTTCTTCA
AhMYB59_genomic AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCAACCTTCTTCA
AtMYB59.1 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCTACTTCTTCA
AhMYB59.1 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCAACCTTCTTCA
AtMYB59.2 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCTACTTCTTCA
AhMYB59.2 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCAACCTTCTTCA
AtMYB59.3 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCTACTTCTTCA
AhMYB59.3 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCAACCTTCTTCA
AtMYB59.4 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCTACTTCTTCA
AhMYB59.5 AGGACTCATATGAGGAAGAAGGCTCAAGAGAAGAAGCGACCTATGTCTCCAACCTTCTTCA
AhMYB59.6 -----

AtMYB59_genomic TCTTCAAACGTGCTCATCATCTATGACCACTACTACTAGTCAAGACACTGGAGGCTCC
AhMYB59_genomic TCTTCAAACGTGCTCATCATCTATGACCACTACTACTACTCAGGACACTGGCGGCTCC
AtMYB59.1 TCTTCAAACGTGCTCATCATCTATGACCACTACTACTAGTCAAGACACTGGAGGCTCC
AhMYB59.1 TCTTCAAACGTGCTCATCATCTATGACCACTACTACTACTCAGGACACTGGCGGCTCC
AtMYB59.2 TCTTCAAACGTGCTCATCATCTATGACCACTACTACTAGTCAAGACACTGGAGGCTCC
AhMYB59.2 TCTTCAAACGTGCTCATCATCTATGACCACTACTACTACTCAGGACACTGGCGGCTCC
AtMYB59.3 TCTTCAAACGTGCTCATCATCTATGACCACTACTACTAGTCAAGACACTGGAGGCTCC
AhMYB59.3 TCTTCAAACGTGCTCATCATCTATGACCACTACTACTACTCAGGACACTGGCGGCTCC
AtMYB59.4 -----
AhMYB59.5 TCTTCAAACGTGCTCATCATCTATGACCACTACTACTACTCAGGACACTGGCGGCTCC
AhMYB59.6 -----

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AtMYB59.1 AACGGGAAAATGAATCAAGAATGCGAAGACGGGTACTACTCCATGGATGACATATGGAGA
AhMYB59.1 AATGGGAAAATGAATCAAGAATGCGAAGACGGATATTACTCGATGGATGACATATGGAGA
AtMYB59.2 AACGGGAAAATGAATCAAGAATGCGAAGACGGGTACTACTCCATGGATGACATATGGAGA
AhMYB59.2 AATGGGAAAATGAATCAAGAATGCGAAGACGGATATTACTCGATGGATGACATATGGAGA
AtMYB59.3 AACGGGAAAATGAATCAAGAATGCGAAGACGGGTACTACTCCATGGATGACATATGGAGA
AhMYB59.3 AATGGGAAAATGAATCAAGAATGCGAAGACGGATATTACTCGATGGATGACATATGGAGA
AtMYB59.4 -----
AhMYB59.5 AATGGGAAAATGAATCAAGAATGCGAAGACGGATATTACTCGATGGATGACATATGGAGA
AhMYB59.6 AATGGGAAAATGAATCAAGAATGCGAAGACGGATATTACTCGATGGATGACATATGGAGA

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AhMYB59_genomic GAGATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACATCTACTACTCAGAG
AtMYB59.1 GAGATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACAACACTACTACTCAGAG
AhMYB59.1 GACATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACATCTACTACTCAGAG
AtMYB59.2 GAGATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACAACACTACTACTCAGAG
AhMYB59.2 GACATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACATCTACTACTCAGAG
AtMYB59.3 GAGATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACAACACTACTACTCAGAG
AhMYB59.3 GACATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACATCTACTACTCAGAG
AtMYB59.4 -----
AhMYB59.5 GACATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACATCTACTACTCAGAG
AhMYB59.6 GAGATTGATCAGTCTGGAGCAAACGTTATTAACCGGTAAAAGACATCTACTACTCAGAG

AtMYB59_genomic CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
AhMYB59_genomic CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
AtMYB59.1 CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
AhMYB59.1 CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
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AhMYB59.2 CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
AtMYB59.3 CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
AhMYB59.3 CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
AtMYB59.4 -----
AhMYB59.5 CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA
AhMYB59.6 CAAAGCTGTACTTGAATTTCCCTCCTCTGGCTTCTCCAACATGGGAAAGTTCCTTGGAA

AtMYB59_genomic TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
AhMYB59_genomic TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
AtMYB59.1 TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
AhMYB59.1 TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
AtMYB59.2 TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
AhMYB59.2 TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
AtMYB59.3 TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
AhMYB59.3 TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
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AhMYB59.6 TCTATATGGAACATGGATGCAGATGAAAGTAAGATGTCTTCTTTTGCTATTGATCAGTTT
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AhMYB59_genomic CCTCTAAGTTTGAACATGGTAGATCATCGTGGTCGTCTTATAAGTCTAGGATTTGATT
AtMYB59.1 CCTCTAAGTTTGAACATGGTA-----GTGGTCGCCTTAG---TCTAGGATTTGATT
AhMYB59.1 CCTCTAAGTTTGAACATGGTAGATCATCGTGGTCGTCTTATAAGTCTAGGATTTGATT
AtMYB59.2 CCTCTAAGTTTGAACATGGTA-----GTGGTCGCCTTAG---TCTAGGATTTGATT
AhMYB59.2 CCTCTAAGTTTGAACATGGTAGATCATCGTGGTCGTCTTATAAGTCTAGGATTTGATT
AtMYB59.3 CCTCTAAGTTTGAACATGGTA-----GTGGTCGCCTTAG---TCTAGGATTTGATT
AhMYB59.3 CCTCTAAGTTTGAACATGGTAGATCATCGTGGTCGTCTTATAAGTCTAGGATTTGATT
AtMYB59.4 CCTCTAAGTTTGAACATGGTA-----GTGGTCGCCTTAG---TCTAGGATTTGATT
AhMYB59.5 CCTCTAAGTTTGAACATGGTAGATCATCGTGGTCGTCTTATAAGTCTAGGATTTGATT
AhMYB59.6 CCTCTAAGTTTGAACATGGTAGATCATCGTGGTCGTCTTATAAGTCTAGGATTTGATT
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AtMYB59_genomic CATTTGGAAATGTTTATATGTGCAGC--ATATATATGTTATCAAACGACGACTGTAGTAGT
AhMYB59_genomic CATTTGGAAATGTTTATATGTGCAGC--ATATATATGTTATCAA---ACGACTGTAGTAGT
AtMYB59.1 CATTTGGAAATGTTTATATGTGCAGC--ATATATATGTTATCAAACGACGACTGTAGTAGT
AhMYB59.1 CATTTGGAAATGTTTATATGTGCAGCATATATATATATTATCAA---ACGACTGTAGTAGT
AtMYB59.2 CATTTGGAAATGTTTATATGTGCAGC--ATATATATGTTATCAAACGACGACTGTAGTAGT
AhMYB59.2 CATTTGGAAATGTTTATATGTGCAGCATATATATATATTATCAA---ACGACTGTAGTAGT
AtMYB59.3 CATTTGGAAATGTTTATATGTGCAGC--ATATATATGTTATCAAACGACGACTGTAGTAGT
AhMYB59.3 CATTTGGAAATGTTTATATGTGCAGCATATATATATATTATCAA---ACGACTGTAGTAGT
AtMYB59.4 CATTTGGAAATGTTTATATGTGCAGCATATATATATATTATCAA---ACGACTGTAGTAGT
AhMYB59.5 CATTTGGAAATGTTTATATGTGCAGCATATATATATATTATCAA---ACGACTGTAGTAGT
AhMYB59.6 CATTTGGAAATGTTTATATGTGCAGCATATATATATATTATCAA---ACGACTGTAGTAGT

AtMYB59_genomic TTCCATGACTTACATCA---AAAATCACCACCCACTGTACTAATCTCATAAGTAG---T
AhMYB59_genomic TTCCATGACTTACATCAG---AAAAAATAATCCACTGTACTAATCTCATAAGTAGCAT
AtMYB59.1 TTCCATGACTTACATCA---AAAATCACCACCCACTGTACTAATCTCATAAGTAG---T
AhMYB59.1 TTCCATGACTTACATCAG---AAAAAATAATCCACTGTACTAATCTCATAAGTAGCAT
AtMYB59.2 TTCCATGACTTACATCA---AAAATCACCACCCACTGTACTAATCTCATAAGTAG---T
AhMYB59.2 TTCCATGACTTACATCAGAAAATAAATAATCCACTGTACTAATCTCATAAGTAGCAT
AtMYB59.3 TTCCATGACTTACATCA---AAAATCACCACCCACTGTACTAATCTCATAAGTAG---T
AhMYB59.3 TTCCATGACTTACATCAGAAAATAAATAATCCACTGTACTAATCTCATAAGTAGCAT
AtMYB59.4 TTCCATGACTTACATCA---AAAATCACCACCCACTGTACTAATCTCATAAGTAG---T
AhMYB59.4 TTCCATGACTTACATCAGAAAATAAATAATCCACTGTACTAATCTCATAAGTAGCAT
AtMYB59.5 TTCCATGACTTACATCAGAAAATAAATAATCCACTGTACTAATCTCATAAGTAGCAT
AhMYB59.6 TTCCATGACTTACATCAGAAAATAAATAATCCACTGTACTAATCTCATAAGTAGCAT

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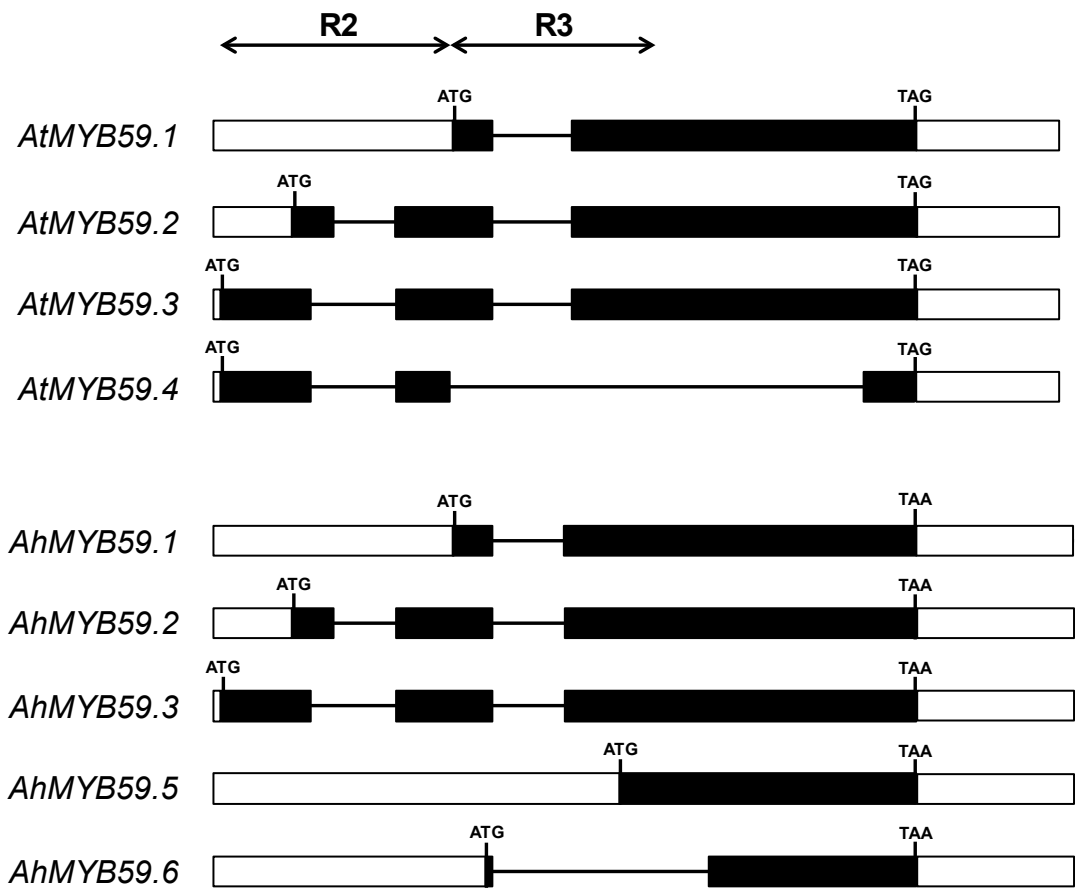
AhMYB59.6 TTTCCATGACTTACATCAG-AAAAAAAAAATCCACTGCTACTAATCTCATATGTAGTCAT

AtMYB59_genomic CATCATCTTATGCCTTTGTT-----TAGTTTGTAGAGTGAGTGAAAAGA
AhMYB59_genomic CATCATCCTATGCCTTTGTTTCCCTCAAATATGTTATAGTTTGTAGAGCGAGTGAAAAGA
AtMYB59.1 CATCATCTTATGCCTTTGTT-----TAGTTTGTAGAGTGAGTGAAAAGA
AhMYB59.1 CATCATCATATGCCTTTGTTTCCCTCAAATATGT--TAGTTTGTAGAGCGAGTG-AAAGA
AtMYB59.2 CATCATCTTATGCCTTTGTT-----TAGTTTGTAGAGTGAGTGAAAAGA
AhMYB59.2 CATCATCCTATGCCTTTGTTTCCCTCAAATATGT--TAGTTTGTAGAGCGAGTG-AAAGA
AtMYB59.3 CATCATCTTATGCCTTTGTT-----TAGTTTGTAGAGTGAGTGAAAAGA
AhMYB59.3 CATCATCCTATGCCTTTGTTTCCCTCAAATATGT--TAGTTTGTAGAGCGAGTG-AAAGA
AtMYB59.4 -----
AhMYB59.5 CATCATCCTATGCCTTTGTTTCCCTCAAATATGT--TAGTTTGTAGAGCGAGTG-AAAGA
AhMYB59.6 CATCATCCTATGCCTTTGTTTCCCTCAAATATGT--TAGTTTGTAGAGCGAGTGAAAAGA

AtMYB59_genomic TGTGTAATACAAGTCAGAACT
AhMYB59_genomic TGTGTAATACAAGTCAGAACT
AhMYB59.1 TGTGTAATACAAGTCAGAACT
AtMYB59.1 TGTGTAATACAAGTCAGAACT
AtMYB59.2 TGTGTAATACAAGTCAGAACT
AhMYB59.2 TGTGTAATACAAGTCAGAACT
AtMYB59.3 TGTGTAATACAAGTCAGAACT
AhMYB59.3 TGTGTAATACAAGTCAGAACT
AtMYB59.4 -----
AhMYB59.5 TGTGTAATACAAGTCAGAACT
AhMYB59.6 TGTGTAATACAAGTCAGAACT

Fig. S2. Alignment of *Arabidopsis thaliana* and *Arabidopsis halleri* MYB59 nucleotide sequences, obtained by the Clustal Omega software (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Predicted start codons are highlighted in green (*MYB59.1*), blue (*MYB59.2*), yellow (*MYB59.3* and *MYB59.4*) and grey (*AhMYB59.5* and *AhMYB59.5*). Stop codon is highlighted in red.

A



B

AtMYB59.1 -----
0
AhMYB59.1 -----
0
AtMYB59.2 -----MGFCSSESFRFEGGGRNIRI **GLNRTGKSCRLRWVN**
35
AhMYB59.2 -----MGFCSSESFRFEGGGRNIRI **GLNRTGKSCRLRWVN**
35
AtMYB59.3 MKLV **QEEYRKGPWTEQEDILLVNFVHLFGDRRWDF** ---- **VAKVSGLNRTGKSCRLRWVN**
56
AhMYB59.3 MKLV **QEEYRKGPWTEQEDILLVNFVHLFGDRRWDF** ---- **VAKVSGLNRTGKSCRLRWVN**
56
AtMYB59.4 MKLV **QEEYRKGPWTEQEDILLVNFVHLFGDRRWDF** ---- **VAKVSGLNRTGKSCRLRWVN**
56
AhMYB59.5 -----
0
AhMYB59.6 -----
0

AtMYB59.1 -----MTPQEERLVLELHAKWGNRWSKIARKLPGRTDNEIKNYWRTHMRKKAQEK
50
AhMYB59.1 -----MTPQEERLVLELHAKWGNRWSKIARKLPGRTDNEIKNYWRTHMRKKAQEK
50
AtMYB59.2 **YL**HPGLKRGKMT**PQEERLVLELHAKWGNRWSKIARKLPGRTDNEIKNYWRTHMRKKAQEK**
94
AhMYB59.2 **YL**HPGLKRGKMT**PQEERLVLELHAKWGNRWSKIARKLPGRTDNEIKNYWRTHMRKKAQEK**
94
AtMYB59.3 **YL**HPGLKRGKMT**PQEERLVLELHAKWGNRWSKIARKLPGRTDNEIKNYWRTHMRKKAQEK**
115
AhMYB59.3 **YL**HPGLKRGKMT**PQEERLVLELHAKWGNRWSKIARKLPGRTDNEIKNYWRTHMRKKAQEK**
115
AtMYB59.4 **YL**HPGLKRGK-----
65
AhMYB59.5 -----MRKKAQEK
8
AhMYB59.6 -----
0

AtMYB59.1 KRPMSPSSSSNCCSSSMTTTT**S**QDTGGSNGKMNQECEDGYYSMDDIWREIDQSGANVIK
110
AhMYB59.1 KRPMSPSSSSNCCSSSMTTTT**T**QDTGGSNGKMNQECEDGYYSMDDIWR**D**IDQSGANVIK
110
AtMYB59.2 KRPMSPSSSSNCCSSSMTTTT**S**QDTGGSNGKMNQECEDGYYSMDDIWREIDQSGANVIK
154
AhMYB59.2 KRPMSPSSSSNCCSSSMTTTT**T**QDTGGSNGKMNQECEDGYYSMDDIWR**D**IDQSGANVIK
154
AtMYB59.3 KRPMSPSSSSNCCSSSMTTTT**S**QDTGGSNGKMNQECEDGYYSMDDIWREIDQSGANVIK
175
AhMYB59.3 KRPMSPSSSSNCCSSSMTTTT**T**QDTGGSNGKMNQECEDGYYSMDDIWR**D**IDQSGANVIK
175
AtMYB59.4 -----
65
AhMYB59.5 KRPMSPSSSSNCCSSSMTTTT**T**QDTGGSNGKMNQECEDGYYSMDDIWR**D**IDQSGANVIK
68
AhMYB59.6 -----MGKMNQECEDGYYSMDDIWREIDQSGANVIK
31

AtMYB59.1	PVKDNYYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHGSRL
170	
AhMYB59.1	PVKD I YYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHG RSSW
170	
AtMYB59.2	PVKDNYYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHGSRL
214	
AhMYB59.2	PVKD I YYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHG RSSW
214	
AtMYB59.3	PVKDNYYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHGSRL
235	
AhMYB59.3	PVKD I YYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHG RSSW
235	
AtMYB59.4	-----MSSFAIDQFPLSFEHGSRL
85	
AhMYB59.5	PVKD I YYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHG RSSW
128	
AhMYB59.6	LVKD I YYSEQSCYLNFPPLASPTWESSLESIWMDADESKMSSFAIDQFPLSFEHG RSSW
91	
AtMYB59.1	--- 170
AhMYB59.1	SSL 173
AtMYB59.2	--- 214
AhMYB59.2	SSL 217
AtMYB59.3	--- 235
AhMYB59.3	SSL 238
AtMYB59.4	--- 85
AhMYB59.5	SSL 131
AhMYB59.6	SSL 94

Fig. S3. Comparison of *Arabidopsis thaliana* and *Arabidopsis halleri* MYB59 proteins. **(A)** Schematic representation of the different isoforms of the MYB59 transcription factor; blocks and lines indicate exons and introns, respectively. Black blocks are coding sequences, whereas white blocks are untranslated regions. R2 and R3 mark the position of R repeats for DNA binding. **(B)** Alignment of *A. thaliana* and *A. halleri* MYB59 proteins, obtained by the Clustal Omega software (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Differences in amino acidic sequences are marked with red characters. R2 and R3 MYB domains are highlighted in blue and grey, respectively; DNA-binding domains are underlined. The position of functional domains was determined by comparison with the Prosite database (<https://prosite.expasy.org/prosite.html>).

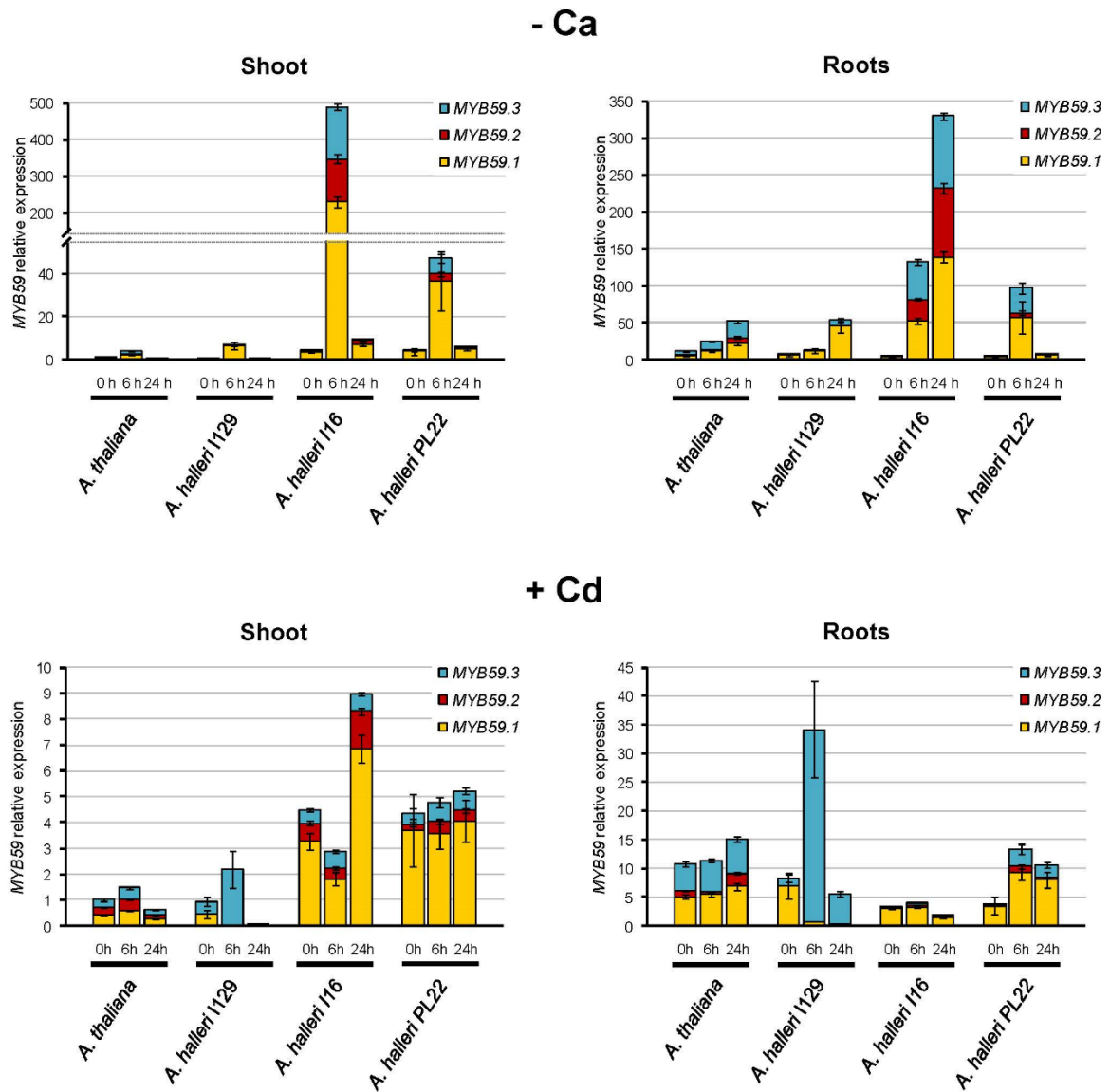


Fig. S4. Expression of *MYB59* splicing isoforms in *Arabidopsis thaliana* and *Arabidopsis halleri* upon Ca deficiency and Cd treatment.

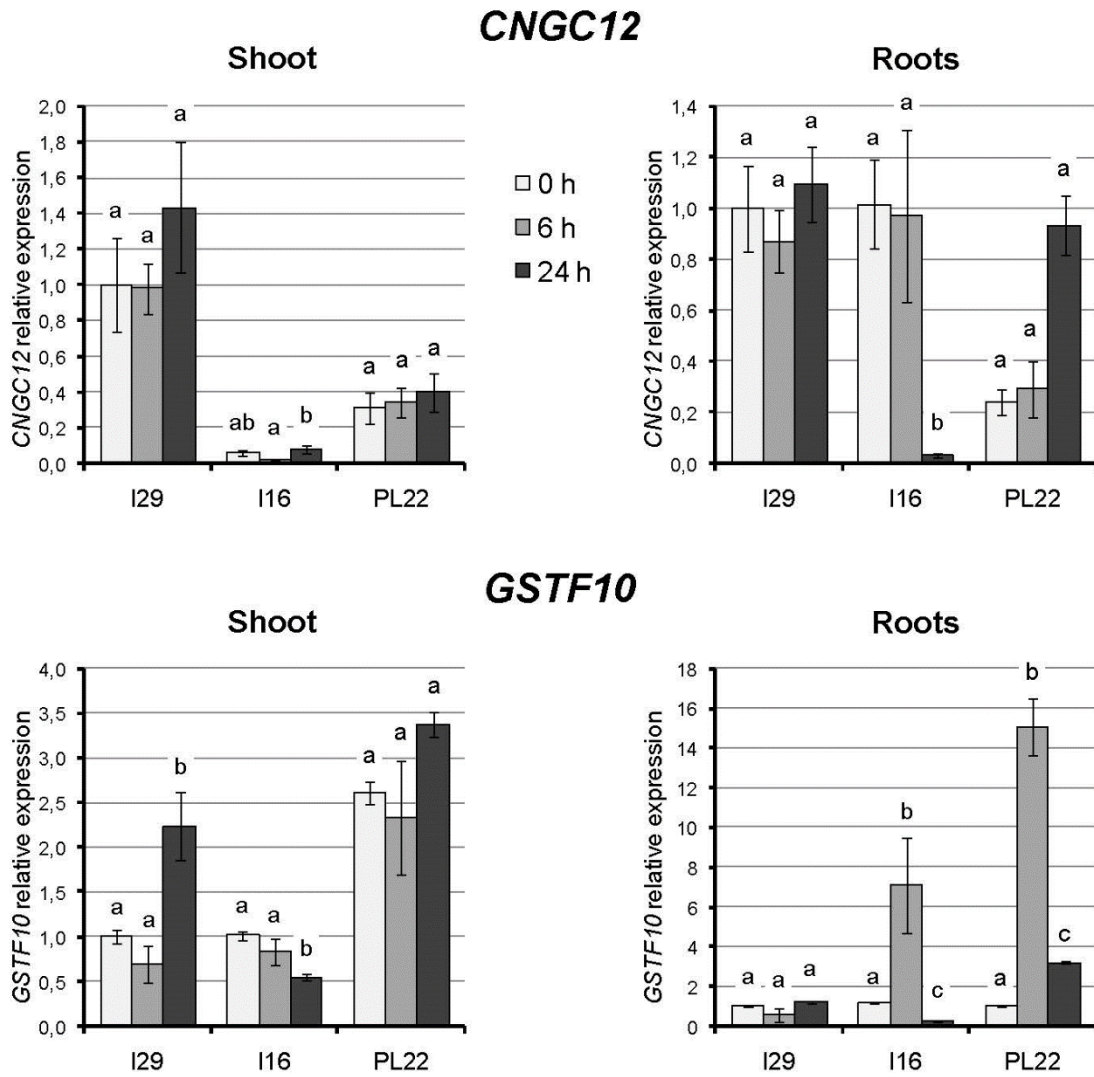


Fig. S5. Expression levels of *CNGC12* and *GSTF10* in leaves and roots of *Arabidopsis halleri* plants under Cd treatment.