

**Figure S8 Alignment of the promoter sequences of MYB25-like.**

*cis*-acting regulatory elements are underlined and color-coded. MYB binding sites: blue; elements involved in light responsiveness: red; gibberellin-responsive element: black; elements involved in MeJA-responsiveness: green; elements involved in salicylic acid responsiveness: orange. Bases 1-421 of P\_Pima S-7\_At and P\_Sicala 40\_At were aligned to chromosome Ca5 of *G. arboreum* rather than chromosome Ca9, on which the A2 genome *MYB25-like* (Cotton-A-06163) was located. Differences between P\_Pima S-7\_Dt and P\_Sicala 40\_Dt as well as P\_TM-1\_Dt are highlighted in yellow and boxed, including three SNPs (one in a putative light responsive element located within the core promoter region and another in a MYB-domain binding site), two small indel (1-bp deletion or insertion), and two deletions that contain two putative light responsive elements.

P_A2	--TGAGATACCAATTTTGGGCGTCGCGAGGGTG--CTAATAACTTCTCGCGGTAAC	56
P_PimaS-7_At	TTTGAAGGGATTTTGTGTTTGTCTCATTTTTCAATCTTTGTAAAAATCCCCCCTTACAT	60
P_Sicala40_At	TTTGAAGGGATTTTGTGTTTGTCTCATTTTTCAATCTTTGTAAAAATCCCCCCTTACAT	60
P_TM-1_At	TTTGAAGGGATTTTGTGTTTGTCTCATTTTTCAATCTTTGTAAAAATCCCCCCTTACAT	60
P_D5	---AAGGAAAAAAAAAAG-----GAAATCTAAACAAAACAATTTTAA	40
P_PimaS-7 Dt	-----AGGGAAAAAAAAAG-----GAAATCAAACAAAACAATTTTAA	38
P_Sicala40 Dt	-----AGGGAAAAAAAAAG-----GAAATCAAACAAAACAATTTTAA	38
P_TM-1 Dt	-----AGGGAAAAAAAAAG-----GAAATCAAACAAAACAATTTTAA	38
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P_A2	ACTCCCGAACCCCAATTTTCTCTGGACTTTCACGTAGACCTAAAT--TTAGCCTTCTT	113
P_PimaS-7 At	GATTTTGAATGGCTTTTATAGC-CATCTTTTACATGATTTTCTATTATTTCTTTTCTA	119
P_Sicala40 At	GATTTTGAATGGCTTTTATAGC-CATCTTTTACATGATTTTCTATTATTTCTTTTCTA	119
P_TM-1_At	GATTTTGAATGGCTTTTATAGC-CATCTTTTACATGATTTTCTATTATTTCTTTTCTA	119
P_D5	GATGTAATAATGTCTTTTTTGTGCTACTTTTTTTTTATAAATAATTTTATTATGATGTTATA	100
P_PimaS-7 Dt	GATGTAATAATGTCTTTTTTGTGCTACTTTTTTTTTATAAATAATTTTATTATGATGTTATA	98
P_Sicala40 Dt	GATGTAATAATGTCTTTTTTGTGCTACTTTTTTTTTATAAATAATTTTATTATGATGTTATA	98
P_TM-1 Dt	GATGTAATAATGTCTTTTTTGTGCTACTTTTTTTTTATAAATAATTTTATTATGATGTTATA	98
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P_A2	TTTGTFT-----TAAATAATTTTATTAGGTGTCGATCACAACATAA-----	157
P_PimaS-7 At	TTTTGTAGGTGGTGGTGGTAGACAATGGATA TCAAAAATGGG-----AGAAAAATGGGG	174
P_Sicala40 At	TTTTGTAGGTGGTGGTGGTAGACAATGGATA TCAAAAATGGG-----AGAAAAATTTT-	173
P_TM-1 At	TTTTGTAGGTGGTGGTGGTAGACAATGGATA TCAAAAATGGG-----AGAAAAATTTT-	173
P_D5	ATTGTA-AAACTTTTATTATGAACAATCACCTTTGCATATTCTATCCAAACAAAATAAATA	159
P_PimaS-7 Dt	ATTGTTAAACTTTTATTATGAACAATCACCTTTGCATATTCTATCCAAACAAAATAAATA	158
P_Sicala40 Dt	ATTGTTAAACTTTTATTATGAACAATCACCTTTGCATATTCTATCCAAACAAAATAAATA	158
P_TM-1 Dt	ATTGTTAAACTTTTATTATGAACAATCACCTTTGCATATTCTATCCAAACAAAATAAATA	158
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P_A2	AAA-AGGATCGGTGGCGAC-----TCCTTTGTAAATAAAAATCGAAAGTTT	202
P_PimaS-7 At	CAAGTGGGAAAGTGGCTAG--GTGGCTAGGGTTTCTTGGTTT-----TTT	217
P_Sicala40 At	-----	173
P_TM-1 At	-----	173
P_D5	AAATTACTTAATTTTCTTTTCTTCTACTACTTTTTAGTGTTTAAATAAGATAATAAATAT	219
P_PimaS-7 Dt	AAATTACTTAATTTTCTTTTCTTCTACTACTTTTTAGTGTTTAAATAAGATAATAAATAT	218
P_Sicala40 Dt	AAATTACTTAATTTTCTTTTCTTCTACTACTTTTTAGTGTTTAAATAAGATAATAAATAT	218
P_TM-1 Dt	AAATTACTTAATTTTCTTTTCTTCTACTACTTTTTAGTGTTTAAATAAGATAATAAATAT	218
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P_A2	GTTTTCAAATGT---TTAATAAATCGCCACAATTAGCGACCAAGCAAAAACAAAATTTT	259
P_PimaS-7 At	TTTTGGGGTTAGTTTTTTTTTTTTTTTTTTTTTTTTTGGGTT-TAGGTTTTTGGGGGAGGCTT	276
P_Sicala40_At	-----TCTTTTTTTTTTATTTTTTTGGGT-TAGGTTTTTGGGGGAGGCTT	216
P_TM-1_At	-----TCTTTTTTTTTTATTTTTTTGGGT-TAGGTTTTTGGGGGAGGCTT	216
P_D5	TATTTACTTTCTTTTTCTTTGCTTTCCTATCTTTAATT-CAAACAT-A-----	266
P_PimaS-7 Dt	TATTTACTTTATTTTTCTTTGCTTTCCTATCTTTAATT-CAAACAT-AGTAGAGGTGTT	276
P_Sicala40 Dt	TATTTACTTTATTTTTCTTTGCTTTCCTATCTTTAATT-CACACAT-AGTAGAGGTGTT	276
P_TM-1 Dt	TATTTACTTTATTTTTCTTTGCTTTCCTATCTTTAATT-CACACAT-AGTAGA-----	270
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P_A2	TTTACGTCG--CTACAA--GAACATTTAAATATTTT-----GC	293
P_PimaS-7_At	AATGGGCTTTTGAATG-----GGTTAATATTTGGGTTTGTAAATGGGTTTGGGTAGA	330
P_Sicala40_At	AATGGGCTTTTGAATG-----GGTTAATATTTGGGTTTGTAAATGGGTTTGGGTAGA	270
P_TM-1_At	AATGGGCTTTTGAATG-----GGTTAATATTTGGGTTTGTAAATGGGTTTGGGTAGA	270
P_D5	-----	266
P_PimaS-7 Dt	TATGGGTTGGGCGGCTC-----	293
P_Sicala40 Dt	TATGGGTTGGGCGGCTCGGCCCTGCTTTCCTATCTTTAATTCAAACAT----AGTAGAGG	332
P_TM-1 Dt	-----	272

P_A2	TATTTATATATTTAAAAACAATAAAAAATCATTTTAACTCAATAAATTTATAATTTGAT	353
P_PimaS-7_At	TGTAATGGGTCA-----TGGGTTAAGGGTTTTAGTGGGTTTTGAGGTTTGGTGGGT	384
P_Sicala40_At	TGTAATGGGTCA-----TGGGTTAAGGGTTTTAGTGGGTTTTGAGGTTTGGTGGGT	324
P_TM-1_At	TGTAATGGGTCA-----TGGGTTAAGGGTTTTAGTGGGTTTTGAGGTTTGGTGGGT	324
P_D5	-----	266
P_PimaS-7_Dt	-----GGCCCGGCC <b>CAATAC</b> CCGCGCGAAATATGGAAGGATTT	332
P_Sicala40_Dt	TGTTTATGGGTGGGGCGGCTGGCCCGGCC <b>CAACAG</b> CCGCGCGAAATATGGAAGGTT	391
P_TM-1_Dt	TGTTTATGGGTGGGGCGGCTGGCCCGGCC <b>CAACAG</b> CCGCGCGAAATATGGAAGGTT	331
P_A2	ATCTTTTTATTACAACCTCGTTAT-----AATTTTTTTTACTCTATCCTTT	399
P_PimaS-7_At	TTGATATAATGGGCCCGGGCAATTTGGGCTTCTACAGAGTATCTCTTGCTT-----	436
P_Sicala40_At	TTGATATAATCGGGCCCGGGCAATTTGGGCTTCTACAGAGTATCTCTTGCTT-----	376
P_TM-1_At	TTGATATAATCGGGCCCGGGCAATTTGGGCTTCTACAGAGTATCTCTTGCTT-----	376
P_D5	-----	266
P_PimaS-7_Dt	TGGATAAAAAATATAGGCCCGAAAT-----	356
P_Sicala40_Dt	TGGATAAAAAATATAGGCCCGAAATATGGGCTCGGGCACCACCTTTTTTGCCTGAGCCCGG	451
P_TM-1_Dt	TGGATAAAAAATATAGGCCCGAAATATGGGCTCGGGCACCACCTTTTTTGCCTGAGCCCGG	391
P_A2	ATCATAAATATCAAAATGAGTATCTCTTGCTTTCCTTGAAAAGTTAAATTTTTTATTAT	459
P_PimaS-7_At	---TCCTTGAAAAGT-----TAAAT-----TTTTTATTAT	464
P_Sicala40_At	---TCCTTGAAAAGT-----TAAAT-----TTTTTATTAT	404
P_TM-1_At	---TCCTTGAAAAGT-----TAAAT-----TTTTTATTAT	404
P_D5	-----	266
P_PimaS-7_Dt	-----ATGGGCTCGGGCACCACCTTTTTTTG	381
P_Sicala40_Dt	C-CCGGCCCGATATAA-----TACATATATTTGGGCTCGGGCACCACCTTTTTTTG	500
P_TM-1_Dt	-----	391
P_A2	CCCGATTCAAGAGAAGTTAAAGAAAGGAAAAAGAAAATCAAACAAAACAACCTTTTAAAG	519
P_PimaS-7_At	CCCGATTCAAGAGAAGTTAAAGAAAGGAAAAAGAAAATCAAACAAAACAACCTTTTAAAG	524
P_Sicala40_At	CCCGATTCAAGAGAAGTTAAAGAAAGGAAAAAGAAAATCAAACAAAACAACCTTTTAAAG	464
P_TM-1_At	CCCGATTCAAGAGAAGTTAAAGAAAGGAAAAAGAAAATCAAACAAAACAACCTTTTAAAG	464
P_D5	-----	266
P_PimaS-7_Dt	CCCGAGCCCGCCCGCCCGATATA--ATAAATATATTTATTTTTTAAATTTTTTTAAT	439
P_Sicala40_Dt	CCCGAGCCCGCCCGCCCGATATA--ATAAATATATTTATTTTTTAAATTTTTTTAAT	558
P_TM-1_Dt	-----CCCGCCCGATATA--ATAAATATATTTATTTTTTAAATTTTTTTAAT	438
P_A2	TGTATAATGTCTTTTTT-----GTCAAC	542
P_PimaS-7_At	TGTATAATGTCT-----TTTT-----TGICAA	546
P_Sicala40_At	TGTATAATGTCT-----TTTT-----TGICAA	486
P_TM-1_At	TGTATAATGTCT-----TTTT-----TGICAA	486
P_D5	-----	266
P_PimaS-7_Dt	TTTAAATATTTTTTAAATACTTTTTTATTATTTTTTAAATTTTTTAAATTTTTTAAATA	499
P_Sicala40_Dt	TTTAAATATTTTTTAAATACTTTTTTATTATTTTTTAAATTTTTTAAATTTTTTAAATA	618
P_TM-1_Dt	TTTAAATATTTTTTAAATACTTTTTTATTATTTTTTAAATTTTTTAAATTTTTTAAATA	498
P_A2	TTTTTTTTTTTTTATAAATAATTTTATGATGACGTTATAATTGTAAAACCTTATTATGA	602
P_PimaS-7_At	CTTT--TT--TTTTATAAATAATTTTATGATGACGTTATAATTGTAAAACCTTATTATGA	602
P_Sicala40_At	CTTT--TTTTTTTTTATAAATAATTTTATGATGACGTTATAATTGTAAAACCTTATTATGA	544
P_TM-1_At	CTTT--TTTTTTTTTATAAATAATTTTATGATGACGTTATAATTGTAAAACCTTATTATGA	544
P_D5	-----	266
P_PimaS-7_Dt	CTTTTTTTAATTTTTTAAATAAATTTTGGTATT--TATTAATAAATGGGCCGAGTCCG <b>AG</b>	557
P_Sicala40_Dt	CTTTTTTTAATTTTTTAAATAAATTTTGGTATT--TATTAATAAATGGGCCGAGTCCG <b>GG</b>	676
P_TM-1_Dt	CTTTTTTTAATTTTTTAAATAAATTTTGGTATT--TATTAATAAATGGGCCGAGTCCG <b>GS</b>	556
P_A2	ACAATCATTTCCTTTGCATATCTATCCAAACAAAAT-AAATAAATAAATACTTAATTTTCT	661
P_PimaS-7_At	ACAATCATTTCCTTTGCATATCTATCCAAACA-AAATAAATAAATACTTAATTTTCT	661
P_Sicala40_At	ACAATCATTTCCTTTGCATATCTATCCAAACA-AAATAAATAAATACTTAATTTTCT	603
P_TM-1_At	ACAATCATTTCCTTTGCATATCTATCCAAACA-AAATAAATAAATACTTAATTTTCT	603
P_D5	-----	266
P_PimaS-7_Dt	CCAGGCCTGGGCTTATGCTTTTTTCCCGGGCCGGGCTGGGCAAAATTTTAGGCCCATAT	617
P_Sicala40_Dt	CCAGGCCTGGGCTTATGCTTTTTTCCCGGGCCGGGCTGGGCAAAATTTTAGGCCCATAT	736
P_TM-1_Dt	CCAGGCCTGGGCTTATGCTTTTTTCCCGGGCCGGGCTGGGCAAAATTTTAGGCCCATAT	616

MYB binding site differs between Pima S-7 and Sicala 40

P\_A2 TTTC-----CTTCACTAATTTTTAGTGTTTAAA----- 689  
P\_PimaS-7\_At TTTC-----CTTCACTAATTTTTAGTGTTTAAAATAAGA 694  
P\_Sicala40\_At TTTC-----CTTCACTAATTTTTAGTGTTTAAAATAAGA 636  
P\_TM-1\_At TTTC-----CTTCACTAATTTTTAGTGTTTAAAATAAGA 636  
P\_D5 ----- 266  
P\_PimaS-7\_Dt TTTGGGCCGGGCCGGGGCCAGGACCGGGCCAAATTTTATGGGCCGGGCCA 676  
P\_Sicala40\_Dt TTTGGGCCGGGCCGGGGCCAGGACTCGGGCCAAATTTTATGGGCCGGGCCA 796  
P\_TM-1\_Dt TTTGGGCCGGGCCGGGGCCAGGACTCGGGCCAAATTTTATGGGCCGGGCCA 676

P\_A2 -----TAAGATAATAAATATTTTTACTTTCTTTTTCTTTGCTTTCCTA 734  
P\_PimaS-7\_At T-----AATAAATATTTACTTTCTTTTTCTTTGCTTTCCTA 734  
P\_Sicala40\_At T-----AATAAATATTTACTTTCTTTTTCTTTGCTTTCCTA 676  
P\_TM-1\_At T-----AATAAATATTTACTTTCTTTTTCTTTGCTTTCCTA 676  
P\_D5 ----- 266  
P\_PimaS-7\_Dt AACCCAGCCCGGCCCGGGCCAAACCCAGCCCGGCCGCGCCGAACCCGGCCCGGCCATG 736  
P\_Sicala40\_Dt AACCCAGCCCGGCCCGGGCCAAACCCAGCCCGGCCGCGCCGAACCCGGCCCGGCCATG 856  
P\_TM-1\_Dt AACCCAGCCCGGCCCGGGCCAAACCCAGCCCGGCCGCGCCGAACCCGGCCCGGCCATG 736

P\_A2 TCTTTAATTCAAACATAGTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 794  
P\_PimaS-7\_At TCTTTAATTCAAACATAGTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 794  
P\_Sicala40\_At TCTTTAATTCAAACATAGTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 736  
P\_TM-1\_At TCTTTAATTCAAACATAGTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 736  
P\_D5 -----GTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 309  
P\_PimaS-7\_Dt AGCACCTCTAAACATAGTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 796  
P\_Sicala40\_Dt AGCACCTCTAAACATAGTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 916  
P\_TM-1\_Dt AGCACCTCTAAACATAGTGTAGAAAAGAAAATTAATTTCTTAAAGAAGGGTATAATGG 796  
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P\_A2 TCATATAGGCTTATGCAATATTTATTAACACTGTAAGCCTATAAAACGCAGTTATATATC 854  
P\_PimaS-7\_At TCATATAGGCTTATGCAATATTTATTAACACTGTAAGCCTATAAAACGCAGTTATATATC 854  
P\_Sicala40\_At TCATATAGGCTTATGCAATATTTATTAACACTGTAAGCCTATAAAACGCAGTTATATATC 796  
P\_TM-1\_At TCATATAGGCTTATGCAATATTTATTAACACTGTAAGCCTATAAAACGCAGTTATATATC 796  
P\_D5 TCATATAGGCTTAAAGTAATATTTAT-TACACTGTAAGCCTATAAAACGCAGTTATATATC 368  
P\_PimaS-7\_Dt TCATATAGGCTTAAAGTAATATTTAT-TAGACTGTAAGCCTATAAAACGCAGTTATATATC 855  
P\_Sicala40\_Dt TCATATAGGCTTAAAGTAATATTTAT-TAGACTGTAAGCCTATAAAACGCAGTTATATATC 975  
P\_TM-1\_Dt TCATATAGGCTTAAAGTAATATTTAT-TAGACTGTAAGCCTATAAAACGCAGTTATATATC 855  
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P\_A2 TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 914  
P\_PimaS-7\_At TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 914  
P\_Sicala40\_At TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 856  
P\_TM-1\_At TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 856  
P\_D5 TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 428  
P\_PimaS-7\_Dt TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 915  
P\_Sicala40\_Dt TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 1035  
P\_TM-1\_Dt TACTTTAAATTAACCAACTCTACCCACATTTTCGTTGCTTTCAACTGCGTATAATCTCTC 915  
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P\_A2 TTTCCTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 974  
P\_PimaS-7\_At TTTCCTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 974  
P\_Sicala40\_At TTTCCTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 916  
P\_TM-1\_At TTTCCTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 916  
P\_D5 ---TCTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 484  
P\_PimaS-7\_Dt T--CTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 973  
P\_Sicala40\_Dt T--CTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 1093  
P\_TM-1\_Dt T--CTATCATCTCTTTATCATTGTCTGTTTTCAAATTAAGGAACCAAATTCATTGAGG 973  
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P\_A2 ATTCGGCCTGGCTTGA-TTCAAAGAACATG 1003  
P\_PimaS-7\_At ATTCGGCCTGGCTTGA-TTCAAAGAACATG 1003  
P\_Sicala40\_At ATTCGGCCTGGCTTGA-TTCAAAGAACATG 945  
P\_TM-1\_At ATTCGGCCTGGCTTGA-TTCAAAGAACATG 945  
P\_D5 ATTCGGCCTGGCTTGACTTCAAAGAACATG 514  
P\_PimaS-7\_Dt ATTCGGCCTGGCTTGACTTCAAAGAACATG 1003  
P\_Sicala40\_Dt ATTCGGCCTGGCTTGACTTCAAAGAACATG 1123  
P\_TM-1\_Dt ATTCGGCCTGGCTTGACTTCAAAGAACATG 1003  
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MYB binding site differs between At and Dt