

Additional file 2. Putative cis-acting regulatory elements identified in the *Mpc1* promoters. Promoter analysis was performed using New PLACE database. “+” – coding strand, “-” – template strand.

>promoter_TaMpc1-A2

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TTGAGAAAAATATTAATATTTAAAAATAAAAAATACATTTGTATTTTTATGATATTTTTTAAAAAAACCAACTGAAAATCGTAAAATTAGAGAC  
TTCGAGAAAAAACAAATTGACAACTGCAGGGAGCCGATGAAAGACAAAATGGGCCGCGCCATATTGTGAGCGCTTGGACAACGATCCATA  
GGACTTGTGCATAGAAAATTGGCTGCATCCGAGCTGCCGGCGATGTATGACGGCGAAGAACGCGCCGCTGTGCATCCCGATTTCATTGA  
ACACATTGGAGCTTTTCCTAGCCTTTTTGGTCCATCTACCTCTAGAGAGAAGTGTCGATCACGATGACCATGGCTGAGGGTGCTAAGCAGGT  
CCACGTAGACGCGCTACTGTACAATGCTTAACAGGTCCACGTAGACGCTCTGCTGTACACTGCTCAACGGGGCCACGTAGACGCGCCTA  
TGAATAAATACGGCTACAGCCCTGCTGCCACAGATGACAGACCCCCCCCCCCCCCTCTCTCTCTCTCTCTTAACACAATACACAC  
CGGAGATGAGGTGAGATAGAGAGGTTAGTTTCAGAGAAGAGGAAGGAAGATAGAGAGGGGAGAGA
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Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
GT1CONSENSUS	5 (+) GRWAAW		<u>S000198</u>
MYCCONSENSUSAT	33 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	33 (+) CANNTG		<u>S000407</u>
GATABOX	47 (+) GATA		<u>S000039</u>
MYB1AT	60 (+) WAACCA		<u>S000408</u>
MYCCONSENSUSAT	64 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	64 (+) CANNTG		<u>S000407</u>
MYB2CONSENSUSAT	64 (+) YAACKG		<u>S000409</u>
GT1CONSENSUS	69 (+) GRWAAW		<u>S000198</u>
GT1CONSENSUS	95 (+) GRWAAW		<u>S000198</u>
MYCCONSENSUSAT	103 (-) CANNTG		<u>S000407</u>
CAATBOX1	103 (+) CAAT		<u>S000028</u>
MYCCONSENSUSAT	103 (+) CANNTG		<u>S000407</u>
CAATBOX1	105 (-) CAAT		<u>S000028</u>
WRKY71OS	107 (+) TGAC		<u>S000447</u>
MYCCONSENSUSAT	110 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	110 (+) CANNTG		<u>S000407</u>
MYB2CONSENSUSAT	110 (+) YAACKG		<u>S000409</u>
DOFCOREZM	129 (+) AAAG		<u>S000265</u>
MYCCONSENSUSAT	134 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	134 (+) CANNTG		<u>S000407</u>
SORLIP2AT	139 (+) GGGCC		<u>S000483</u>
SORLIP2AT	144 (-) GGGCC		<u>S000483</u>
CAATBOX1	151 (-) CAAT		<u>S000028</u>
WRKY71OS	185 (-) TGAC		<u>S000447</u>
WRKY71OS	225 (+) TGAC		<u>S000447</u>
MYBCOREATCYCB1	237 (+) AACGG		<u>S000502</u>
CGCGBOXAT	242 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	242 (+) VCGCGB		<u>S000501</u>
CAATBOX1	263 (-) CAAT		<u>S000028</u>
MYCCONSENSUSAT	269 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	269 (+) CANNTG		<u>S000407</u>
DOFCOREZM	278 (-) AAAG		<u>S000265</u>
DOFCOREZM	288 (-) AAAG		<u>S000265</u>
CBFHV	318 (-) RYCGAC		<u>S000497</u>
WRKY71OS	329 (+) TGAC		<u>S000447</u>
CGCGBOXAT	365 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	365 (+) VCGCGB		<u>S000501</u>
CAATBOX1	378 (+) CAAT		<u>S000028</u>
MYBCORE	385 (-) CNGTTR		<u>S000176</u>
MYB2CONSENSUSAT	421 (+) YAACKG		<u>S000409</u>
SORLIP2AT	426 (+) GGGCC		<u>S000483</u>
BOXIIPCCHS	428 (-) ACGTGGC		<u>S000229</u>
SORLIP1AT	428 (+) GCCAC		<u>S000482</u>
CGCGBOXAT	437 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	437 (+) VCGCGB		<u>S000501</u>
MYCCONSENSUSAT	477 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	477 (+) CANNTG		<u>S000407</u>
WRKY71OS	481 (+) TGAC		<u>S000447</u>
CAATBOX1	525 (+) CAAT		<u>S000028</u>
GATABOX	549 (+) GATA		<u>S000039</u>
MYB1LEPR	558 (+) GTTAGTT		<u>S000443</u>
DOFCOREZM	570 (+) AAAG		<u>S000265</u>

>promoter_TaMpc1-B2

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ATCTGGTGGGAAGGAACCTTGCCATGCCTCTGAGGCCTCGAGCACCCGCAACTTCCGGGGAGTCGACTGGCAGCATGTCCCTCTTCTAA
TAGTAAATGTTTCGTGTTTCCCCCACCTAGACATACAAATGCAACGATTCTTAGGACTGTGCACAGAAATATGACATCAATCAAACCTG
CCGGCGAAGAAACGGCCGCGCTGCGCATCCCGATTTCATTGCACACATGGAGCTTTCCCTTGCCTTTTGTGCCATCCACCTCTAGAGAGAA
GTGTCGATCACGATAACCATGGCTGAGGGTGCTAAGCAGGTCCACGTAGACGCGCTATTGTACAATGCTAAACAGGTCCACGTAGCCGC
GCTGCTGTACAATGCTGAACGGGGCCACGTAGACGCGCTGATGTATATAAAATACGGCAACAATCCTGCCGCCACAGATGAGATGACAT
AGAGAGAGGTTGCCTCAGAAGAAAGAGGAAGATAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
WBOXATNPR1	4 (+) TTGAC		<u>S000390</u>
WRKY71OS	5 (+) TGAC		<u>S000447</u>
IBOX	23 (-) GATAAG		<u>S000124</u>
GATABOX	25 (-) GATA		<u>S000039</u>
CAATBOX1	28 (+) CAAT		<u>S000028</u>
DOFCOREZM	54 (-) AAAG		<u>S000265</u>
DOFCOREZM	69 (+) AAAG		<u>S000265</u>
MYCCONSENSUSAT	89 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	89 (+) CANNTG		<u>S000407</u>
CBFHV	151 (-) RYCGAC		<u>S000497</u>
CBFHV	151 (+) RYCGAC		<u>S000497</u>
E2FCONSENSUS	194 (+) WTTSSCSS		<u>S000476</u>
MYCCONSENSUSAT	214 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	214 (+) CANNTG		<u>S000407</u>
WRKY71OS	238 (-) TGAC		<u>S000447</u>
WRKY71OS	250 (+) TGAC		<u>S000447</u>
CAATBOX1	256 (+) CAAT		<u>S000028</u>
MYBCOREATCYCB1	278 (+) AACGG		<u>S000502</u>
CGCGBOXAT	283 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	283 (+) VCGCGB		<u>S000501</u>
CAATBOX1	304 (-) CAAT		<u>S000028</u>
MYCCONSENSUSAT	310 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	310 (+) CANNTG		<u>S000407</u>
DOFCOREZM	319 (-) AAAG		<u>S000265</u>
DOFCOREZM	329 (-) AAAG		<u>S000265</u>
CBFHV	359 (-) RYCGAC		<u>S000497</u>
GATABOX	368 (+) GATA		<u>S000039</u>
IBOXCORE	368 (+) GATAA		<u>S000199</u>
MYB1AT	370 (+) WAACCA		<u>S000408</u>
CGCGBOXAT	406 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	406 (+) VCGCGB		<u>S000501</u>
CAATBOX1	413 (-) CAAT		<u>S000028</u>
CAATBOX1	419 (+) CAAT		<u>S000028</u>
CGCGBOXAT	442 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	442 (+) VCGCGB		<u>S000501</u>
CAATBOX1	455 (+) CAAT		<u>S000028</u>
MYBCOREATCYCB1	463 (+) AACGG		<u>S000502</u>
SORLIP2AT	467 (+) GGGCC		<u>S000483</u>
BOXIIPCHS	469 (-) ACGTGGC		<u>S000229</u>
SORLIP1AT	469 (+) GCCAC		<u>S000482</u>
CGCGBOXAT	478 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	478 (+) VCGCGB		<u>S000501</u>
CAATBOX1	505 (+) CAAT		<u>S000028</u>
MYCCONSENSUSAT	520 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	520 (+) CANNTG		<u>S000407</u>
WRKY71OS	529 (+) TGAC		<u>S000447</u>
DOFCOREZM	556 (+) AAAG		<u>S000265</u>
GATABOX	565 (+) GATA		<u>S000039</u>
DOFCOREZM	570 (+) AAAG		<u>S000265</u>

>promoter_TaMpc1-D2

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TAGGACTTGTACAGAAATTTGGCTGCGTCAGGGCTGCCGGCGATATTATGACGGCGAAGAAACGGCCGCAGTACATCCCCGATTTAT
TGCACACATGGAGCTTTCATAGCCTTTTGCCCATCTACCTCTAGAGAGAAGTGTGATCACGATGACCATGGGTTGAGGGTGCTAAGC
AGGTCCACGTAGACGCGCTACTGTACAATGCTTAATAGGTCCACGTAGACGCTCTCCTGTACAACGCTGAACAGGGCCACGTAGACCCG
CTGCTGAATAAGTACGGCAACAACCTGCTGCCACAGATGACAGACCCCTCTACTCTCTCTCTCTCTCTAACAACAACACATACT
GGAGATGAGATGAGATAAGAGAGGTTAGTTTCAGAGAAAAGAGGAAGAGGAAGATAGAGAGGGAGAGA

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
MYCCONSENSUSAT	2 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	2 (+) CANNTG		<u>S000407</u>
GT1CONSENSUS	9 (+) GRWAAW		<u>S000198</u>
WRKY71OS	15 (+) TGAC		<u>S000447</u>
CGCGBOXAT	17 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	17 (+) VCGCGB		<u>S000501</u>
E2FCONSENSUS	19 (-) WTTSSCSS		<u>S000476</u>
CAATBOX1	23 (+) CAAT		<u>S000028</u>
GT1CONSENSUS	58 (+) GRWAAW		<u>S000198</u>
GT1CONSENSUS	59 (+) GRWAAW		<u>S000198</u>
MYCCONSENSUSAT	70 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	70 (+) CANNTG		<u>S000407</u>
GT1CONSENSUS	77 (+) GRWAAW		<u>S000198</u>
WRKY71OS	83 (+) TGAC		<u>S000447</u>
CGCGBOXAT	85 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	85 (+) VCGCGB		<u>S000501</u>
E2FCONSENSUS	87 (-) WTTSSCSS		<u>S000476</u>
CAATBOX1	91 (+) CAAT		<u>S000028</u>
WRKY71OS	122 (+) TGAC		<u>S000447</u>
MYCCONSENSUSAT	151 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	151 (+) CANNTG		<u>S000407</u>
WRKY71OS	187 (-) TGAC		<u>S000447</u>
WRKY71OS	206 (-) TGAC		<u>S000447</u>
GATABOX	221 (+) GATA		<u>S000039</u>
WRKY71OS	228 (+) TGAC		<u>S000447</u>
MYBCOREATCYCB1	240 (+) AACGG		<u>S000502</u>
CGCGBOXAT	245 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	245 (+) VCGCGB		<u>S000501</u>
CAATBOX1	266 (-) CAAT		<u>S000028</u>
MYCCONSENSUSAT	272 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	272 (+) CANNTG		<u>S000407</u>
DOFCOREZM	281 (-) AAAG		<u>S000265</u>
DOFCOREZM	291 (-) AAAG		<u>S000265</u>
E2FCONSENSUS	293 (+) WTTSSCSS		<u>S000476</u>
SORLIP2AT	296 (-) GGGCC		<u>S000483</u>
CBFHV	321 (-) RYCGAC		<u>S000497</u>
WRKY71OS	332 (+) TGAC		<u>S000447</u>
WBOXNTERF3	332 (+) TGACY		<u>S000457</u>
CGCGBOXAT	369 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	369 (+) VCGCGB		<u>S000501</u>
CAATBOX1	382 (+) CAAT		<u>S000028</u>
SORLIP2AT	430 (+) GGGCC		<u>S000483</u>
BOXIIPCCHS	432 (-) ACGTGGC		<u>S000229</u>
SORLIPIAT	432 (+) GCCAC		<u>S000482</u>
MYCCONSENSUSAT	481 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	481 (+) CANNTG		<u>S000407</u>
WRKY71OS	485 (+) TGAC		<u>S000447</u>
SORLIP5AT	498 (-) GAGTGAG		<u>S000486</u>
GATABOX	548 (+) GATA		<u>S000039</u>
IBOX	548 (+) GATAAG		<u>S000124</u>
MYB1LEPR	558 (+) GTTAGTT		<u>S000443</u>
DOFCOREZM	570 (+) AAAG		<u>S000265</u>
GATABOX	585 (+) GATA		<u>S000039</u>

>promoter_TaMpc1-D3

TGGTTTAGCTTTAGCCCTAGGCTTCGAGAAAATCCTGGCTCCGTCCTCTGTTTTACACGTTCCCTACTTTTCAACAATTTATAGATATTATG
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GTATATGTGTTATGTGTATATTGTGTATTGGGCCCGCCTCATAGTTCCTTATATAGTTGAGGTCGGTGACCCACCGTTGTACATCATAT
ATATGTGCCATGCACGAGAGCAATACATCGTGCAATCATAGTCTCATACTAGCGATCTGAAGCTTTACACCAGTTATAGGTTTTTC
TTCTCGACTTTGGACGGATATCATCATCGGTGCCGCCAGTGAGATGTATAGGCGGGGAACGGCGGTGCTGAACGTCGGTGTTCATG
CACAGATGGATCCTTTGCTAGCCGTTTGGTGTACCTAACTCGGACTTAGGTGTTGCTTGCGGTGACCACATGGTGTATTAATAAAGCAC
AACGGCCTTCTGCCACGGATCAAACACAGTACACACGGGCGAGTTGGGAAAAAGATAACGGGGAGG

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
MYB1AT	1 (-) WAACCA		<u>S000408</u>
DOFCOREZM	9 (-) AAAG		<u>S000265</u>
DOFCOREZM	64 (-) AAAG		<u>S000265</u>
CAATBOX1	72 (+) CAAT		<u>S000028</u>
GATABOX	81 (+) GATA		<u>S000039</u>
WRKY71OS	88 (+) TGAC		<u>S000447</u>
WBOXNTERF3	88 (+) TGACY		<u>S000457</u>
DOFCOREZM	93 (+) AAAG		<u>S000265</u>
WRKY71OS	110 (-) TGAC		<u>S000447</u>
MYCCONSENSUSAT	112 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	112 (+) CANNTG		<u>S000407</u>
DOFCOREZM	135 (-) AAAG		<u>S000265</u>
WRKY71OS	141 (-) TGAC		<u>S000447</u>
CGCGBOXAT	146 (-) VCGCGB		<u>S000501</u>
CGCGBOXAT	146 (+) VCGCGB		<u>S000501</u>
CAATBOX1	198 (-) CAAT		<u>S000028</u>
CAATBOX1	205 (-) CAAT		<u>S000028</u>
SORLIP2AT	208 (+) GGGCC		<u>S000483</u>
SORLIP2AT	209 (-) GGGCC		<u>S000483</u>
WRKY71OS	245 (+) TGAC		<u>S000447</u>
WBOXNTERF3	245 (+) TGACY		<u>S000457</u>
MYB2CONSENSUSAT	252 (-) YAACKG		<u>S000409</u>
CAATBOX1	289 (+) CAAT		<u>S000028</u>
CAATBOX1	301 (+) CAAT		<u>S000028</u>
DOFCOREZM	333 (-) AAAG		<u>S000265</u>
DOFCOREZM	365 (-) AAAG		<u>S000265</u>
MYBST1	373 (+) GGATA		<u>S000180</u>
GATABOX	374 (+) GATA		<u>S000039</u>
GATABOX	376 (-) GATA		<u>S000039</u>
MYBCOREATCYCB1	416 (+) AACGG		<u>S000502</u>
CAATBOX1	442 (-) CAAT		<u>S000028</u>
MYCCONSENSUSAT	448 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	448 (+) CANNTG		<u>S000407</u>
DOFCOREZM	458 (-) AAAG		<u>S000265</u>
MYBCOREATCYCB1	467 (-) AACGG		<u>S000502</u>
WRKY71OS	508 (+) TGAC		<u>S000447</u>
WBOXNTERF3	508 (+) TGACY		<u>S000457</u>
MYCCONSENSUSAT	512 (-) CANNTG		<u>S000407</u>
MYCCONSENSUSAT	512 (+) CANNTG		<u>S000407</u>
DOFCOREZM	528 (+) AAAG		<u>S000265</u>
MYB2CONSENSUSAT	534 (+) YAACKG		<u>S000409</u>
MYCCONSENSUSAT	575 (-) CANNTG		<u>S000407</u>
MYB2CONSENSUSAT	575 (-) YAACKG		<u>S000409</u>
MYCCONSENSUSAT	575 (+) CANNTG		<u>S000407</u>
GT1CONSENSUS	581 (+) GRWAAW		<u>S000198</u>
GT1CONSENSUS	582 (+) GRWAAW		<u>S000198</u>
DOFCOREZM	585 (+) AAAG		<u>S000265</u>
GATABOX	588 (+) GATA		<u>S000039</u>
IBOXCORE	588 (+) GATAA		<u>S000199</u>
MYB2CONSENSUSAT	590 (+) YAACKG		<u>S000409</u>

>promoter_TaMpc1-D4

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 GCACATAACCGGTTAGGTTGGCCCCGGTCTATGCCGACGACCGCCCTATGCCGACGGTCTCCGTAGGGGTATTTTCGAGCGGTCCCGACGG
 CCTCGTCTGTGCCGACGGCCCCGTGCGCATAGATGGATGTATGCTGACGGCTTTTTCTACGCTACGGCTGTCTTTGGCCGTGCGCATA
 GGCCCATCTATGCCGACGGGGGCCGTGCGCATAGAGAGGGCCGTGCGCGCAAGCAGTTATTCTGGTAGTGAAAAACGGCCGGCTGTTC
 ATTGCACAGATGGAGTCTTCTAGCCTTTTGATCCATCTAACTCTGAGATAAGTGTGCTCACGATGCCCGTGGGTTGAGGGTGCAAAG
 CATGTCCACGTAGACGCGCTACTGTACAATGATAACAGGTCCACGTTGACGCGCTGGTGAATAAATACGGCAACAACCCCGCTGCCCGC
 AGATGACAGACCCTCGCTCACTCGCTCTTAACACAACACCCACTGGAGAGAGAGAGAGAGAGA

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
GATABOX	30 (+)	GATA	S000039
DRERTCOREAT	35 (+)	RCCGAC	S000418
CGCGBOXAT	43 (-)	VCGCGB	S000501
CGCGBOXAT	43 (+)	VCGCGB	S000501
MYBCORE	46 (+)	CNGTTR	S000176
DRERTCOREAT	58 (-)	RCCGAC	S000418
WRKY71OS	78 (-)	TGAC	S000447
MYBCOREATCYCB1	82 (+)	AACGG	S000502
WRKY71OS	86 (-)	TGAC	S000447
MYBCORE	94 (-)	CNGTTR	S000176
MYBPZM	100 (-)	CCWACC	S000179
MYBPZM	104 (-)	CCWACC	S000179
SORLIP2AT	108 (-)	GGGCC	S000483
DRERTCOREAT	120 (+)	RCCGAC	S000418
CGCGBOXAT	128 (-)	VCGCGB	S000501
CGCGBOXAT	128 (+)	VCGCGB	S000501
DRERTCOREAT	138 (+)	RCCGAC	S000418
DRERTCOREAT	189 (+)	RCCGAC	S000418
SORLIP2AT	195 (-)	GGGCC	S000483
DRERTCOREAT	201 (-)	RCCGAC	S000418
WRKY71OS	223 (+)	TGAC	S000447
DOFCOREZM	229 (-)	AAAG	S000265
DRERTCOREAT	259 (-)	RCCGAC	S000418
SORLIP2AT	268 (-)	GGGCC	S000483
DRERTCOREAT	279 (+)	RCCGAC	S000418
SORLIP2AT	287 (+)	GGGCC	S000483
DRERTCOREAT	292 (-)	RCCGAC	S000418
DRERTCOREAT	310 (-)	RCCGAC	S000418
MYB2CONSENSUSAT	321 (-)	YAACKG	S000409
MYBCORE	321 (+)	CNGTTR	S000176
GT1CONSENSUS	337 (+)	GRWAAW	S000198
MYBCOREATCYCB1	341 (+)	AACGG	S000502
CGCGBOXAT	346 (-)	VCGCGB	S000501
CGCGBOXAT	346 (+)	VCGCGB	S000501
CAATBOX1	357 (-)	CAAT	S000028
MYCCONSUSAT	363 (-)	CANNTG	S000407
MYCCONSUSAT	363 (+)	CANNTG	S000407
DOFCOREZM	382 (-)	AAAG	S000265
GATABOX	404 (+)	GATA	S000039
IBOX	404 (+)	GATAAG	S000124
DOFCOREZM	442 (+)	AAAG	S000265
CGCGBOXAT	459 (-)	VCGCGB	S000501
CGCGBOXAT	459 (+)	VCGCGB	S000501
CAATBOX1	472 (+)	CAAT	S000028
GATABOX	476 (+)	GATA	S000039
IBOXCORE	476 (+)	GATAA	S000199
MYBCORE	478 (-)	CNGTTR	S000176
BP5OSWX	487 (-)	CAACGTG	S000436
WRKY71OS	492 (+)	TGAC	S000447
CGCGBOXAT	494 (-)	VCGCGB	S000501
CGCGBOXAT	494 (+)	VCGCGB	S000501
MYCCONSUSAT	534 (-)	CANNTG	S000407
MYCCONSUSAT	534 (+)	CANNTG	S000407
WRKY71OS	538 (+)	TGAC	S000447
SORLIP5AT	551 (-)	GAGTGAG	S000486

>promoter_HvMpc1-H2

ATGTTTGAATATAGTTACATGACACATAATTCCACAACGGGTGGGATGCTCCCTCCATGCTCACACACATCTGGGATGCCCCCTTCGG
TTTTGGGGGGTCCGGGTGCCTCGTGCTGACACAGGTGAGCCGTGAGCAAAGCTACGTGCTCTGGCTTCTTTGGACTCAAAGGGCAAC
GATCCTTTTCAGTTGTCAAAGAAATACGACATAGTACATCTCACCTGCCGGCGATCTTGACGGCGAAGAAATGGCCGCGCTGTTTAT
TGGACAAATGGAGCCTTCTAGCCTTTTGGTCCATCTAACTCTGAGATAAGTGTGCTCACGATGACTGTGGATTGAAGGTGCAAAGCA
GGTCCACGTAGACGCGCTATTGTACAATGCTAAACGGGTCCACGTAGACGCGCTAATGACTAAATACGGCAACAACCTGCTGCCCAA
GATGACGGACCCTCACTCTCTGCTCTCTAACACAACAACAACACACACCGGAGAAGA

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
BIHD1OS	20 (-) TGTC A		<u>S000498</u>
WRKY71OS	20 (+) TGAC		<u>S000447</u>
MYB2CONSENSUSAT	35 (+) YAACKG		<u>S000409</u>
MYCCONSUSAT	68 (-) CANNTG		<u>S000407</u>
MYCCONSUSAT	68 (+) CANNTG		<u>S000407</u>
BIHD1OS	116 (-) TGTC A		<u>S000498</u>
WRKY71OS	116 (+) TGAC		<u>S000447</u>
MYCCONSUSAT	121 (-) CANNTG		<u>S000407</u>
MYCCONSUSAT	121 (+) CANNTG		<u>S000407</u>
DOFCOREZM	139 (+) AAAG		<u>S000265</u>
DOFCOREZM	159 (-) AAAG		<u>S000265</u>
DOFCOREZM	169 (+) AAAG		<u>S000265</u>
DOFCOREZM	183 (-) AAAG		<u>S000265</u>
MYCCONSUSAT	188 (-) CANNTG		<u>S000407</u>
MYB2CONSENSUSAT	188 (-) YAACKG		<u>S000409</u>
MYCCONSUSAT	188 (+) CANNTG		<u>S000407</u>
BIHD1OS	192 (+) TGTC A		<u>S000498</u>
WRKY71OS	193 (-) TGAC		<u>S000447</u>
DOFCOREZM	197 (+) AAAG		<u>S000265</u>
MYCCONSUSAT	221 (-) CANNTG		<u>S000407</u>
MYCCONSUSAT	221 (+) CANNTG		<u>S000407</u>
CAATBOX1	266 (-) CAAT		<u>S000028</u>
MYCCONSUSAT	272 (-) CANNTG		<u>S000407</u>
MYCCONSUSAT	272 (+) CANNTG		<u>S000407</u>
DOFCOREZM	291 (-) AAAG		<u>S000265</u>
IBOX	313 (+) GATAAG		<u>S000124</u>
WBOXHVIS01	331 (+) TGACT		<u>S000442</u>
WRKY71OS	331 (+) TGAC		<u>S000447</u>
WBOXNTERF3	331 (+) TGACY		<u>S000457</u>
CAATBOX1	340 (-) CAAT		<u>S000028</u>
DOFCOREZM	351 (+) AAAG		<u>S000265</u>
OPAQUE2ZM22Z	359 (+) TCCACGTAGA		<u>S000017</u>
CAATBOX1	375 (-) CAAT		<u>S000028</u>
CAATBOX1	381 (+) CAAT		<u>S000028</u>
MYBCOREATCYCB1	389 (+) AACGG		<u>S000502</u>
OPAQUE2ZM22Z	395 (+) TCCACGTAGA		<u>S000017</u>
WBOXHVIS01	413 (+) TGACT		<u>S000442</u>
DOFCOREZM	443 (+) AAAG		<u>S000265</u>
WRKY71OS	448 (+) TGAC		<u>S000447</u>
SORLIP5AT	457 (-) GAGTGAG		<u>S000486</u>

>promoter_HvMpc1-H3

CCTCTTTTCTACTGGTGCCGGCCAGTTCGCGGGCAGAGGACGCGACCGTTTAAATTCGTTGCATGTCTACGATTCCTTTTTTTTTTATCG
TCAAATTAATTTCGTCTCGCCTTCCCTCTCGGGCGCCGACTGCACGGACCTGCTGCTATCGAGATAGGACGAGGAGGTTAGCCACGAGGGT
ATCTGAGACTGGGAGACGAACCACGCGTAGCAGCAGAGCACTAGCTCATGGCCCCGCGCATTCCATGCAACCGAGAGTCCAGGTCCTGCG
CCCCAACACGCTACGCCTGGAGGAGTCGCCACCGCTATCTTTCCAGACCAGGTGCGAGAGATCGTAGGGGGCCTAACGAGCTGAAGTAT
TGGATCCGGGTATATAAGACTTGGACGGATATCATCATTAGTGCAAGTGGAGATGTATAGGCGGGGAACGGCGGTGCTGGACGTCCGT
GTTTCATTACACGGATGGATCCTTGCTAGGCGTTTGGTGTACCTAATTCGGACTTAGGCGGTGCCACATGGTGTGTTAATAAAGCACAC
CGGCAACCTGCCACGGACCCAAACACAGCACACAGGCACTGGGGAAAAGAGATGAGATGGGGAGG

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
DOFCOREZM	4 (-) AAAG		S000265
CACTFTPPCA1	10 (+) YACT		S000449
MYBCOREATCYCB1	46 (-) AACGG		S000502
DOFCOREZM	75 (-) AAAG		S000265
GT1CONSENSUS	83 (-) GRWAAW		S000198
IBOXCORE	84 (-) GATAA		S000199
GATABOX	85 (-) GATA		S000039
WRKY71OS	89 (-) TGAC		S000447
GATABOX	144 (-) GATA		S000039
GATABOX	150 (+) GATA		S000039
SORLI1P1AT	168 (+) GCCAC		S000482
GATABOX	178 (-) GATA		S000039
CACTFTPPCA1	217 (+) YACT		S000449
SORLI2P2AT	228 (-) GGGCC		S000483
MYBCORE	245 (-) CNGTTR		S000176
SORLI1P1AT	295 (+) GCCAC		S000482
GATABOX	303 (-) GATA		S000039
DOFCOREZM	306 (-) AAAG		S000265
MYCCONSUSAT	316 (-) CANNTG		S000407
MYCCONSUSAT	316 (+) CANNTG		S000407
SORLI2P2AT	336 (+) GGGCC		S000483
CACTFTPPCA1	352 (-) YACT		S000449
CAATBOX1	355 (-) CAAT		S000028
MYBST1	383 (+) GGATA		S000180
GATABOX	384 (+) GATA		S000039
GATABOX	386 (-) GATA		S000039
CACTFTPPCA1	396 (-) YACT		S000449
MYCCONSUSAT	400 (-) CANNTG		S000407
MYCCONSUSAT	400 (+) CANNTG		S000407
CACTFTPPCA1	402 (-) YACT		S000449
MYBCOREATCYCB1	424 (+) AACGG		S000502
MYBPLANT	476 (-) MACCWAMC		S000167
MYCCONSUSAT	510 (-) CANNTG		S000407
MYCCONSUSAT	510 (+) CANNTG		S000407
DOFCOREZM	526 (+) AAAG		S000265
CACTFTPPCA1	575 (-) YACT		S000449
GT1CONSENSUS	580 (+) GRWAAW		S000198
DOFCOREZM	583 (+) AAAG		S000265