

## Supplementary data legends

**Supplementary Table S1.** List of oligonucleotides used in this study.

**Supplementary Table S2.** Key attributes of *C. arietinum* WRKY domain-encoding genes. The *CaWRKY* gene family associated features are represented along with the locus ID of orthologues *WRKY* genes from *M. truncatula*. The *C. arietinum* (*Desi* variety 'ICC4958') matching ID from the annotated CDS v2.0 are also mentioned. The coordinates of *CaWRKYs* from start to stop codon on the assembled chromosomes (ASM33114v1) of variety 'CDC Frontier' are mentioned, except for the unplaced *CaWRKYs*. The 'WRKYGQK' variants are highlighted in red. The names of tandem-duplicated genes in a group are highlighted with bold-blue letters.

**Supplementary Table S3.** The WRKY domain (WD)-encoding genes of *M. truncatula* and their associated attributes. The CDS coordinates are shown for the largest transcript, when multiple transcript isoforms are known. The variants of the WD's heptad-peptide sequence 'WRKYGQK' are highlighted in red. The genes marked with (#) were corrected for intron-exon boundaries. The partial *MtWRKY* genes are also mentioned. The locus IDs of tandem-duplicated genes in a group are highlighted with bold-blue letters.

**Supplementary Fig. S1.** Position of 70 *Cicer arietinum* and 96 *Medicago truncatula* *WRKY* genes on assembled chromosomes. Eight assembled chromosomes are placed in pairs as per highest inter-legume synteny between them. The chickpea *CaWRKY* genes are represented by their name and *M. truncatula* *WRKYs* by locus ID (Mt4.0v1).

**Supplementary Fig. S2.** Maximum-likelihood based phylogeny of *C. arietinum* and *A. thaliana* WRKY domains. *CaWRKYs* and *AtWRKYs* are highlighted with a filled and open circle, respectively. The alignment was performed on MUSCLE and phylogeny was constructed using MEGA6.06. Bootstrap values were derived from 1000 iterations. The group names are indicated against deep branches.

**Supplementary Fig. S3.** The group based conservation in the WRKY domains of *C. arietinum* and *M. truncatula*. The multiple protein sequence alignment of WRKY domains was performed by MUSCLE and manually edited. The WebLogo was generated to demonstrate the conservation pattern. Arrow marked is the 'WRKYGQK' heptad sequence and the cysteine and histidine amino acids of zinc-fingers.

**Supplementary Fig. S4.** The motif analysis for CaWRKYs. The WRKYs are arranged as per their groups along with four unclassified WRKY proteins. The WRKY domain is highlighted by dotted red line above the motifs. The colored boxes represent 12 different motifs. The motifs were identified by MEME suite 4.11.1 using the width-criteria as 6 and 60 for minimum and maximum motif size, respectively.

**Supplementary Fig. S5.** The motif analysis for MtWRKYs. The WRKYs are arranged as per their groups along with seven unclassified WRKY proteins. The colored boxes represent 12 different motifs. The WRKY domain is highlighted by dotted red line above the motifs. The motifs were identified by MEME suite 4.11.1 using the width-criteria as 6 and 60 for minimum and maximum motif size, respectively.

**Supplementary Fig. S6.** The CaWRKY16, CaWRKY17, Medtr5g073620, Medtr5g074200 and GmWRP1 proteins share similar type of N-terminal transmembrane domain. A. The output of TMHMM Server v. 2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>) for the selected unique proteins of *C. arietinum* and *M. truncatula*. B. Multiple alignment representation of only the N-terminal transmembrane domain performed by ClustalX and represented by JalView.

**Supplementary Fig. S7.** The yeast based nuclear-import assay (NIA) was used to decipher the possibility of CaWRKY50 movement into the yeast nucleus. The rationale behind this was that *S. cerevisiae* cells lack WRKY proteins and thus the plant-specific interacting partners of WRKY proteins should also be absent. If CaWRKY50 fused protein activated reporter in the experiment then CaWRKY50 moves into yeast nucleus by itself. CaWRKY50 was fused downstream to the modified LexA protein (lacking nuclear localization signal). The *Agrobacterium* VirD2 served as positive control and VirE2 as negative control. The activation of *LacZ* reporter under LexA operator suggested that the CaWRKY50 is capable of moving into yeast cell nucleus.

**Supplementary Fig. S8.** A. Expression of *CaWRKY50* in vector control (BV) and different tobacco transgenic lines. B. DAB staining in leaves of wild type, vector control and transgenic lines. The hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) accumulation *in planta* was visualized by DAB (3,3'-Diaminobenzidine) staining. The tobacco leaves to be examined for H<sub>2</sub>O<sub>2</sub> were vacuum-infiltrated for 3 min with DAB-HCl solution (1 mg/ml, pH 3.8) and incubated in dark at room temperature for 1 hr. The leaves chlorophyll was removed by incubating in 96% boiling ethanol for 10 min. The image of the stained leaves was

acquired by a flat bed scanner (HP). Positive correlation between chlorotic symptoms and *CaWRKY50* expression pattern was observed.

**Supplementary Fig. S9.** Height attained by the transgenic tobacco plants measured at 20<sup>th</sup> week after seed germination. The bar graph shows results of height measurement (in cm) for the pBI121 vector control (BV) and *CaWRKY50* transgenic tobacco lines (B2, B3, P1, X1 and Y1) of T<sub>0</sub> and T<sub>1</sub> generations.

**Supplementary Fig. S10.** Genomic DNA methylation analysis of *CaWRKY16* sequences flanking the cleavage and polyadenylation sites of *CaWRKY16c* and *CaWRKY16d* transcript isoforms. The DNA methylation analysis of CG-, CHG- and CHH-types was performed using EpiTect<sup>®</sup> Bisulfite kit and data was analysed through kismeth online tool. The three differently colored bars show the percentage methylation of each type. A graph above the methylation data shows the %GC in the original DNA sequence region of 1671 bp. The *CaWRKY16* genomic and derived four transcripts structure are depicted below to show the region selected for DNA methylation analysis.

**Supplementary Fig. S11.** The maximum-likelihood based phylogenetic tree was generated for Exo70 proteins of *A. thaliana*, *C. arietinum*, *M. truncatula* and *G. max*, with 1000 bootstrap iterations. The multiple alignment of Exo70 proteins was performed using PROMALS3D multiple sequence and structure alignment server. The Exo70 proteins of *M. truncatula* and *G. max* are represented by locus identifiers; *Arabidopsis* by names and *C. arietinum* by gene symbol (LOCs) except CaWRKY16. The groups from Exo70A to Exo70J are marked by different colors. The partial Exo70 domains flank the WRKY domain in CaWRKY16 and Medtr5g073620 proteins.

**Supplementary Fig. S12.** *C. arietinum* mitogen activated protein kinase kinase kinase (CaMEKK; Gene ID:LOC101498916) failed to interact with CaWRKY50 and CaWRKY76 in split-ubiquitin based yeast-two hybrid assay. The bait and prey ORFs were cloned in bait (pGDHB1) and prey (pGPR3-N) destination vectors, modified from the pDHB1 and pPR3-N vectors of DUALhunter kit (Dualsystems Biotech AG, Switzerland). The generated clones were co-transformed in yeast strain NMY51 and selected on synthetic dropout (SD) media lacking Leu and Trp amino acids. These cells were suspended in 100  $\mu$ l of 0.9% NaCl and spot-inoculated on SD-Leu-Trp and SD-Leu-Trp-His-Ade selection media. After 3 days of incubation at 30°C, photographs were taken. The growth of yeast co-transformed with bait clone and bait expression verification clone (pAI-Alg5) showed that all bait clones were expressed in yeast cells. The blank pENTR/D-TOPO recombined bait (pGDHB1) and prey (pGPR3-N) vector clones, and DL2-Alg5 clones served as negative controls of protein-protein interaction in yeast.

**Supplementary Table S1.** List of oligonucleotides used for this study.

Name	Sequence <sup>#</sup>	Purpose
KT7EW1F	CATGCCATGGATATGCAATACAAAATGGAG	<i>CaWRKY50</i> in pGBKT7 vector at <i>NcoI</i> and <i>EcoRI</i>
KT7EW1R	CGGGATCCCAGTACGATTAGGAGAAAAAGCC	
W1ADR1	CGGGATCCAATGTCCGATTCTGAACAAG	Reverse primers (used with KT7EW1F) for activation domain deletions of <i>CaWRKY50</i> in pGBKT7 vector
W1ADR2	CGGGATCCGCTGCTCAAGAAGGAATC	
W1ADR3	CGGGATCCATTATCCGTTTTGACAGTCAAG	
W1ADF2	CATGCCATGGATCAGATAAGAGTGAGC	Forward primer (used with KT7EW1R) for activation domain deletion of <i>CaWRKY50</i> in pGBKT7 vector
W1pNIAF	CGGGATCCATATGCAATACAAAATGGAG	<i>CaWRKY50</i> in pNIA vector at <i>BamHI</i> and <i>PstI</i>
W1pNIAR	AAGTGCAGTCAAGTACGATTAGGAGAAAAAG	
OE2W1F	TCTAGATAGATACCAAGCACCAACATC	<i>CaWRKY50</i> in pBI121 at <i>XbaI</i> and <i>SacI</i>
OE2W1R1	GAGCTCCCTCACTATCATTGCTGATTC	
W1Y1HR	CGAGCTCCTGAATGAAGGAATTGGAAG	<i>CaWRKY50</i> promoter in pHIS2.1 vector at <i>EcoRI</i> and <i>SacI</i>
Pchn5F1	AATTCGGAACCTTGACCATCCGTTGACCTTAGGGCTGCAGGAGCT	W- box containing oligo-duplex cloned at <i>EcoRI</i> and <i>SacI</i> in pHIS2.1 vector
Pchn5R1	CCTGCAGCCCTAAGGTCAACGGATGGTCAAGTTCCG	
mPchn5F1	AATTCGGAACCTTGAACATCCGTTGAACTTAGGGCTGCAGGAGCT	mutated W- box containing oligo-duplex cloned at <i>EcoRI</i> and <i>SacI</i> in pHIS2.1 vector
mPchn5R1	CCTGCAGCCCTAAGTTCAACGGATGTTCAAGTTCCG	
CaM35SeqF	ATCGTTGAAGATGCCTCTGC	CaMV 35S promoter specific primer
NPTII-F	TGCTCGACGTTGTCACCTGAAG	<i>NptII</i> gene for pBI121 T-DNA confirmation in tobacco transgenic
NPTII-R	GTCAAGAAGGCGATAGAAGGC	
CaWRR1	AATGGGTTTTTGTCCATATTTTCTCC	5' RACE of selected <i>WRKY</i> genes
CaWRR2	GTTGTGGAACAACGAAACACAGTTG	
CaWRR3	TGCTACCAACATATGTTGTGAGAGC	
CaWRR4	TTGCTTCCGAACTAGACAATTAAGTC	
CaWRR5	GTAGTGAACCATTGAAATTAATGGATTAC	
NesCaWRR5	ATGAGTATTATTGTTTGGTACAAGAGATGAC	
CaWRR6	ATGAAGTATGATGTCATGATTGAGTAAGTTATG	
CaWRR7	GCAAGAATGTCCACCTACGTATTG	
CaWRR8	TGCTAATGAATTTCTTCTAGTTGGTTGTG	
CaWRR9	TCTCACATTGCATCCTTGTGTAGC	
NesCaWRR9	ACGAGATCCATTAGCAACATCATC	
CaWRR10	GTTGCTGCTGCTGATGTTGTATTTG	
CaWRR11	GTCACAAGAAAAGTGTCTCATTGGTATG	
CaWRR12	CATAAGTTGTTATCACATAGCTCGAGTCAT	
CaWRR13	GGTTGCGTCGCATCTTTCTTC	
CaWRR14	GTCGATGATTATGTGGTCCATTG	
CaWRR15	CAAATCTGGATTGCCAATGTC	
CaWRF1	GTGCAGCAAGAAAGCTTGTAGATAAAAAG	3' RACE of selected <i>WRKY</i> genes
CaWRF2	ATGCATAGGAAACGTTTACTATAGATAAC	
CaWRF3	GACATTCGCAATCCAAGATTTG	
CaWRF4	AGCTCCATTTCCAAGTGTACATTG	

CaMEKK1F	<u>TCCGCGGCCGCC</u> ATGAATCACTTACCTCGAATCTTC	CaMEKK (LOC101498916) cloning in pENTR/D-TOPO at <i>NotI</i> and <i>AscI</i> sites
CaMEKK1R	GTC <u>GCGCGCCC</u> ACCTCTTGTGAGAATATGTGGAG	
NtEF1F	TACAAGATTGGTGGTATTGGTACT	Tobacco <i>EF</i> gene primers for expression control
NtEF1R	GTTCTTGACGTTGAATCCAACAT	
WRKYRTF	GTCACTGAGCCACGTAAGTCAC	<i>CaWRKY50</i> expression in transgenic tobacco
WRKYRTR	GTCGGATTCTGAACAAGGCTTG	
GUSR	GACTTCGCGCTGATACCAGACG	pBI121 T-DNA confirmation in tobacco transgenic
CW6_155F	<u>TCCGCGGCCGCC</u> ATGCAATACAAAATGGAGAATG	<i>CaWRKY50</i> cloning in pENTR/D-TOPO at <i>NotI</i> and <i>AscI</i> sites
CW6_155R	GTCGCGCGCCC <u>CGGAGAAA</u> AGCCAAGATTATTG	
CWs1981_10F	<u>TCCGCGGCCGCC</u> ATGGAAGAGAACATGAAGTGTG	<i>CaWRKY76</i> cloning in pENTR/D-TOPO at <i>NotI</i> and <i>AscI</i> sites
CWs1981_10R	GTCGCGCGCCC <u>CACAAAGT</u> CTTGTGCGTTGA	
pBI121R2	TGCCAAATGTTTGAACGATC	NOS terminator reverse primer
CW2_1251F	<u>TCCGCGGCCGCC</u> ATGACACCAATCTCATCCAAATTTG	<i>CaWRKY16d</i> isoform in pENTR/D-TOPO at <i>NotI</i> and <i>AscI</i> sites
CW2_1251R2	GTCGCGCGCCC <u>ATTAATACGATAT</u> TCAACTTTACCTTGTGG	
RTWR-10F	CCGTTGAACTTGAGAATGTTTGTAG	qRT-PCR of <i>CaWRKY10</i>
RTWR-10R	TCAATGCCAAACCGAAAAATAA	
RTWR-15F	CTCAGGTAGTAGTAGTGGTAATAGTATGGAATC	qRT-PCR of <i>CaWRKY14</i>
RTWR-15R	ACCTAAGAAAATGAATGAAACCAACA	
RTWR-16F	GGATCACCACATTACCTCACCAA	qRT-PCR of <i>CaWRKY15</i>
RTWR-16R	GTGCTGTAACATTATTAGGAGTTTCTTCTT	
RTWR-17F	AAGGATTCATGGACGAGAACAATAG	qRT-PCR of <i>CaWRKY16</i>
RTWR-17R	CTTGCCGTATTTTTTCCAGGTAA	
RTW3_1219F	TCCTTCCCAACACCAACCA	qRT-PCR of <i>CaWRKY24</i>
RTW3_1219R	GCACTCCCTTTTCCAGATG	
RTW5_2016F	TCGATGTCACCGAATTCAAGTG	qRT-PCR of <i>CaWRKY45</i>
RTW5_2016R	ACGAAGTAGTTGGTGTGTTTGCAA	
RTWR-47F	TACTGTTGTTTCTGATACTGTGTATTTCATCT	qRT-PCR of <i>CaWRKY46</i>
RTWR-47R	AGAAGAAAACACCCCAAATCAAT	
RTWR-51F	ATCGGACGAAGATCCCAATATG	qRT-PCR of <i>CaWRKY50</i>
RTWR-51R	ACGTGGCTCAGTGACATTGTTT	
RTWR-69F	CCTCCTCTATTATCAACTCTTCAATTTCA	qRT-PCR of <i>CaWRKY67</i>
RTWR-69R	GAAAACCTCAGGAAAAGGGTGGAA	
RTWR-71F	TGTCATTTTTTGTCTCAGATTTCAG	qRT-PCR of <i>CaWRKY69</i>
RTWR-71R	ATGGGATCAAGGAAGAGCAAATAAT	
RTWs1981_10F	ACCAATCCATTTGGAGAGCAA	qRT-PCR of <i>CaWRKY76</i>
RTWs1981_10R	CAACTGAATTTGGGCCTGAAA	
CaBTubRTF1	ATTCTGGTTAGGAGGCTGATGTG	qRT-PCR internal controls
CaBTubRTR1	TTAACCTCCGTTGCCCAAAT	
BSW16F1	TAAACTACTTATAAACTACAATGAGG	Bisulfite treated genomic DNA amplification around <i>CaWRKY16c</i> and <i>d</i> polyadenylation sites
BSW16R3	TTATCACAAGTAACTTCTCAATATC	
BSW16F3	ACAAGTAGCTCCAATAAATGG	
BSW16R5	TTCCATGATATTGCTTCTTTT	
pJETSeqF	CTTTAACACTTGTGCCTGAACACC	
pJETSeqF	AAGAACATCGATTTTCCATGGCAG	pJET1.2 vector specific sequencing primers

#: Underlined are the restriction enzyme site used for cloning.

Supplementary Table S2.

Group	Name	<i>C. arietinum</i>					<i>M. truncatula</i> orthologue gene ID
		CDC Frontier				ICC4958	
		Gene symbol	Contig(s) ID	Position on assembled pseudomolecule (in bp)	WRK domain(s) arrangement	CDS v2.0 ID	
I	CaWRKY18	LOC101505077	ANPC01003463	Ca2 (26835720..26832340)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_03742	Medtr5g074400
	CaWRKY20	LOC101501973	ANPC01003832	Ca2 (35373435..35377344)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HDH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_03252	Medtr5g094430
	CaWRKY21	LOC101508620	ANPC01003852	Ca2 (36092259..36090310)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HDH	Ca_03185	Medtr5g097480
	CaWRKY22	LOC101497258	ANPC01004159	Ca3 (4829553..4823609)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_05925	Medtr7g011820
	CaWRKY23	LOC101511519	ANPC01005046	Ca3 (20509024..20506092)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_05278	Medtr7g071120
	CaWRKY27	LOC101508522	ANPC01005168	Ca3 (23970068..23965853)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_06587	Medtr7g080000
	CaWRKY28	LOC101509586	ANPC01005437	Ca3 (32731074..32727857)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_07489	Medtr7g100510
	CaWRKY40	LOC101511665	ANPC01008396	Ca5 (9957299..9961738)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_12070	Medtr3g009470
	CaWRKY41	LOC101492326	ANPC01009224	Ca5 (26429936..26426762)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_12328	Medtr3g031220
	CaWRKY58	LOC101501211	ANPC01011867	Ca6 (45703332..45709711)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HDH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_12363	Medtr3g056100
	CaWRKY59	LOC101509113	ANPC01012037	Ca6 (49375743..49371400)	<b>WRKYGEK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_17886	Medtr4g013260
	CaWRKY62	LOC101514950	ANPC01012560	Ca7 (1371731..1376034)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HSN WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HDH	Ca_21836	Medtr4g130900
	CaWRKY72	LOC101496076	ANPC01019521		WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_17008	Medtr4g082580
IIa	CaWRKY5	LOC101496569	ANPC01000248	Ca1 (8829177..8828216)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_00111	Medtr3g106060
	<b>CaWRKY37</b>	LOC101508555	ANPC01007644	Ca4 (44269246..44266752)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_09705	Medtr1g013790
	<b>CaWRKY38</b>	LOC101508870	ANPC01007644	Ca4 (44274763..44273230)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH		Medtr1g013760
	CaWRKY43	LOC101512217	ANPC01009493	Ca5 (35254619..35256826)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_08384	Medtr2g105060
	CaWRKY60	LOC101512877	ANPC01012222	Ca6 (53175064..53173004)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_17473	Medtr4g007060
IIb	CaWRKY2	LOC101508161	ANPC01000149	Ca1 (5668701..5666074)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_02237	Medtr2g023930
	CaWRKY6	LOC101511587	ANPC01000429- ANPC01000430	Ca1 (14226683..14222869)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HTH	Ca_00718	Medtr4g049760
	CaWRKY9	LOC101498660	ANPC01000887	Ca1 (25444263..25447960)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_22170	Medtr2g045360
	CaWRKY11	LOC101490340	ANPC01002258	Ca2 (1135312..1132484)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH		Medtr7g009730
	CaWRKY31	LOC101489172	ANPC01005599	Ca3 (37187205..37183728)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_07178	Medtr7g110720
	CaWRKY56	LOC101507104	ANPC01010383	Ca6 (14345303..14342927)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_20512, Ca_22459	Medtr4g094412
	CaWRKY57	LOC101489116	ANPC01011138- ANPC01011140	Ca6 (32325484..32328959)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_17219	Medtr3g053330
	CaWRKY61	LOC101494311	ANPC01012547	Ca7 (887309..889467)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_22014	Medtr2g088000
	CaWRKY65	LOC101489784	ANPC01012798	Ca7 (8727845..8723652)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_21332	Medtr4g107970
	CaWRKY70	LOC101497022	ANPC01014728	Ca7 (47582247..47578004)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HDH	Ca_27185,	
	CaWRKY71	LOC101500503	ANPC01018194- ANPC01018197		WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNNH	Ca_04153, Ca_12372, Ca_29741	
IIc	CaWRKY4	LOC101514062	ANPC01000231	Ca1 (8493623..8491711)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	Ca_01920	Medtr2g033820
	CaWRKY13	LOC101498460	ANPC01002823	Ca2 (13706074..13702702)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HCH	Ca_04277	Medtr5g043880
	CaWRKY19	LOC101507353	ANPC01003785	Ca2 (34273821..34272334)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_02986	Medtr5g091390
	CaWRKY26	LOC101497701	ANPC01005152	Ca3 (23643670..23645242)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_06542	Medtr7g079010
	CaWRKY30	LOC101495104	ANPC01005589- ANPC01005590	Ca3 (36929997..36931789)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	Ca_07149	Medtr7g109800
	CaWRKY34	LOC101499569	ANPC01005906	Ca4 (7122220..7120661)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	Ca_09818	Medtr1g086790
	CaWRKY39	LOC101491983	ANPC01007652	Ca4 (44630285..44629285)	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	Ca_09592	Medtr1g015140
	CaWRKY44	LOC101505353	ANPC01009506	Ca5 (35749122..35753114)	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	Ca_15100	Medtr3g104750
	<b>CaWRKY47</b>	LOC101494696	ANPC01009859	Ca5 (46806611..46804683)	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_14119	Medtr3g095040
	<b>CaWRKY48</b>	LOC101495893	ANPC01009860	Ca5 (46829521..46830892)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HVH	Ca_14122	Medtr3g095080
	<b>CaWRKY52</b>	LOC101510823	ANPC01010131	Ca6 (7544185..7546591)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HVH	Ca_15897	Medtr8g092140
	<b>CaWRKY53</b>	LOC101494195	ANPC01010134	Ca6 (7637417..7640590)	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH		Medtr8g092010
	CaWRKY55	LOC101497541	ANPC01010376	Ca6 (14071041..14069837)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH	Ca_16651	Medtr4g094588
	CaWRKY64	LOC101498880	ANPC01012638	Ca7 (4311721..4310157)	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	Ca_19491	Medtr4g122530
	CaWRKY74	LOC101499040	ANPC01022265		WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH		Medtr7g028415
CaWRKY75	LOC101510788	ANPC01024381		WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNNH		Medtr8g007270	
IIId	CaWRKY8	LOC101493996	ANPC01000688	Ca1 (22025284..22026593)	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HRH	Ca_01816	

	CaWRKY32	LOC101511638	ANPC01005748	Ca4 (1494382..1492655)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_09008	Medtr1g070455
	CaWRKY36	LOC101509842	ANPC01007527	Ca4 (41167903..41170367)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HRH	Ca_00632	
	CaWRKY42	LOC101494382	ANPC01009453	Ca5 (34049848..34051242)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HRH	Ca_15037, Ca_15054	Medtr1g009613
	CaWRKY63	LOC101513839	ANPC01012597	Ca7 (2711950..2713117)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HQH	Ca_21554	Medtr4g127040
	CaWRKY66	LOC101493135	ANPC01012907	Ca7 (12021223..12022668)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_20866	Medtr4g094908
IIe	CaWRKY1	LOC101513300	ANPC01000094	Ca1 (3454903..3455966)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_02448	Medtr2g016770
	CaWRKY3	LOC101513524	ANPC01000222	Ca1 (7992746..7989998)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_01941	Medtr2g032030
	CaWRKY7	LOC101504205	ANPC01000478	Ca1 (15603676..15606983)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_00818	Medtr2g083870
	CaWRKY25	LOC101495745	ANPC01005151	Ca3 (23622087..23623450)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_06540	Medtr7g079040
	CaWRKY29	LOC101501992	ANPC01005588	Ca3 (36856516..36858796)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH		Medtr7g109600
	CaWRKY35	LOC101509183	ANPC01006079	Ca4 (11997480..11996221)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HTH	Ca_10152	Medtr1g099600
	CaWRKY49		ANPC01010039	Ca6 (4224846..4224511)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH		
	CaWRKY51	LOC105852239	ANPC01010064	Ca6 (5132602..5130825)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH		Medtr8g098945
	CaWRKY54	LOC101493438	ANPC01010209	Ca6 (9757404..9756155)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_16169	Medtr8g087000
	CaWRKY68	LOC101502507	ANPC01014006	Ca7 (35518134..35519911)	WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HS	Ca_20513	Medtr8g028565
	CaWRKY77	LOC101497190	ANPC01030209		WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH	Ca_24547	Medtr6g053200
	CaWRKY78	LOC101497854	ANPC01030216		WRKYGQK <sub>X13</sub> C <sub>X5</sub> C <sub>X23</sub> HNH		
	III	CaWRKY10	LOC101513740	ANPC01002171- ANPC01002172	Ca1 (47414430..47417721)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HSC	
CaWRKY14		LOC101502928	ANPC 01003341	Ca2 (24127266..24131008)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HIC	Ca_04232	Medtr5g067680
CaWRKY15		LOC101503258	ANPC 01003341	Ca2 (24147118..24143257)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC	Ca_04233	Medtr5g067700
CaWRKY16		LOC101500706	ANPC01003452- ANPC01003454	Ca2 (26650557..26680381)	<b>WKYGGK</b> <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HSC	Ca_03769	Medtr5g073620
CaWRKY24		LOC101500302	ANPC01005087	Ca3 (21367560..21365982)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC	Ca_06350	Medtr7g073430
CaWRKY45		LOC101499178	ANPC01009808	Ca5 (45068512..45066916)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC	Ca_13990	Medtr3g090860
CaWRKY46		LOC101505688	ANPC01009852- ANPC01009853	Ca5 (46423126..46424440)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC	Ca_14079, Ca_14133	Medtr3g093830
CaWRKY50		LOC101502574	ANPC01010055	Ca6 (4814316..4815651)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC	Ca_15578	Medtr8g099350
CaWRKY67		LOC105852555	ANPC01013741	Ca7 (28447994..28448999)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC	Ca_24319	Medtr8g005750
CaWRKY69		LOC101495507	ANPC01014142	Ca7 (38097610..38099228)	WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC		Medtr8g032510
CaWRKY76	LOC101503062	ANPC01028551		WRKYGQK <sub>X13</sub> C <sub>X7</sub> C <sub>X23</sub> HTC		Medtr8g027860	
Un cla ssif ied	CaWRKY12	LOC105851601	ANPC01002814	Ca2 (13332258..13330273)	<b>WKMHRKR</b> <sub>X13</sub> C <sub>X4</sub> C <sub>X22</sub> HNH <b>WTCHRRN</b> <sub>X14</sub> C <sub>X4</sub> C <sub>X16</sub> HNH		
	CaWRKY17	LOC101503578	ANPC01003463	Ca2 (26774182..26775186)	<b>WKYEEK</b> <sub>X13</sub> C <sub>X4</sub> C <sub>X22</sub> HNH		Medtr5g074200
	CaWRKY33	LOC105851868	ANPC01005830	Ca4 (4359943..4362471)	<b>WRKYGGK</b> <sub>X13</sub> C <sub>X4</sub> C <sub>X23</sub> HKH	Ca_08883	
	CaWRKY73	LOC101508010	ANPC01020275		WRKYGQK <sub>X13</sub> C <sub>X4</sub> C <sub>X23</sub> HLH		Medtr7g062220

Supplementary Table S3.

Group	Locus ID	WRKY domain	CDS coordinates (5' - 3')
I	Medtr3g009470	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	2054208 - 2057851
	Medtr3g056100	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HDH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	22291605 - 22298107
	Medtr3g031220	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	26968422 - 26964312
	Medtr4g013260	<b>WRKYGEK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	3667700 - 3670530
	Medtr4g082580	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HIH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	32111660 - 32108853
	Medtr4g130900	WRKYGQKx <sub>14</sub> Cx <sub>4</sub> Cx <sub>22</sub> HSH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HDH	54565659 - 54560408
	Medtr5g042920	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	18878155 - 18874798
	Medtr5g074400	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	31617116 - 31613612
	Medtr5g094430	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HDH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	41271053 - 41272891
	<b>Medtr5g097490</b>	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HDH	42705948 - 42704461
	<b>Medtr5g097500</b>	<b>WKKYGEK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH <b>WRKYGRK</b> x <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HDH	42713751 - 42712659
	Medtr7g011820	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	3264144 - 3257614
	Medtr7g071120	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	26333946 - 26331107
	<b>Medtr7g080000</b>	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	30399211 - 30393675
	<b>Medtr7g080020</b>	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	30411525 - 30407269
	Medtr7g100510	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>22</sub> HNH WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	40473051 - 40469910
	IIa	<b>Medtr1g013760</b>	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH
<b>Medtr1g013790</b>		WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HSH	3246467 - 3245207
Medtr2g105060		WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	45306940 - 45308082
Medtr3g106060		WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	48926629 - 48922953
Medtr4g007060		WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	926897 - 929137
IIb	Medtr2g023930	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	8498832 - 8496395
	Medtr2g045360	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	19921618 - 19925108
	Medtr2g088000	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HIH	37051419 - 37054669
	Medtr3g053330	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	21191387 - 21194666
	<b>Medtr4g049760</b>	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	17518197 - 17514648
	<b>Medtr4g049790</b>	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	17533361 - 17529826
	Medtr4g094412	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	37937888 - 37940165
	Medtr4g107970	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	44750500 - 44754582
	Medtr4g132430	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HSH	55366844 - 55364880
	Medtr7g009730	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	2212173 - 2215893
	Medtr7g110720	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	45376750 - 45373712
IIc	Medtr1g015140	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HTH	3734930 - 3734215
	Medtr1g086790	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HTH	38851136 - 38849620
	Medtr2g033820	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HTH	12870205 - 12868447
	<b>Medtr3g095040</b>	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	43387610 - 43385924
	<b>Medtr3g095080</b>	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HAH	43414727 - 43416822
	Medtr3g104750	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HTH	48289654 - 48288798
	Medtr4g094588	<b>WRKYGKK</b> x <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	38300900 - 38302481
	Medtr4g122530	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HIH	50536924 - 50538739
	Medtr5g043880	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HCH	19269496 - 19276572
	Medtr5g091390	WRKYGQKx <sub>13</sub> Cx <sub>5</sub> Cx <sub>23</sub> HNH	39836116 - 39833998
	Medtr7g028415	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	9606603 - 9608139
	Medtr7g028710	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	9834174 - 9835710
	Medtr7g079010	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	30019308-30022373
	Medtr7g109800	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HTH	44973560 - 44975020
	Medtr8g007270	WRKYGQKx <sub>13</sub> Cx <sub>4</sub> Cx <sub>23</sub> HNH	1414020-1418564



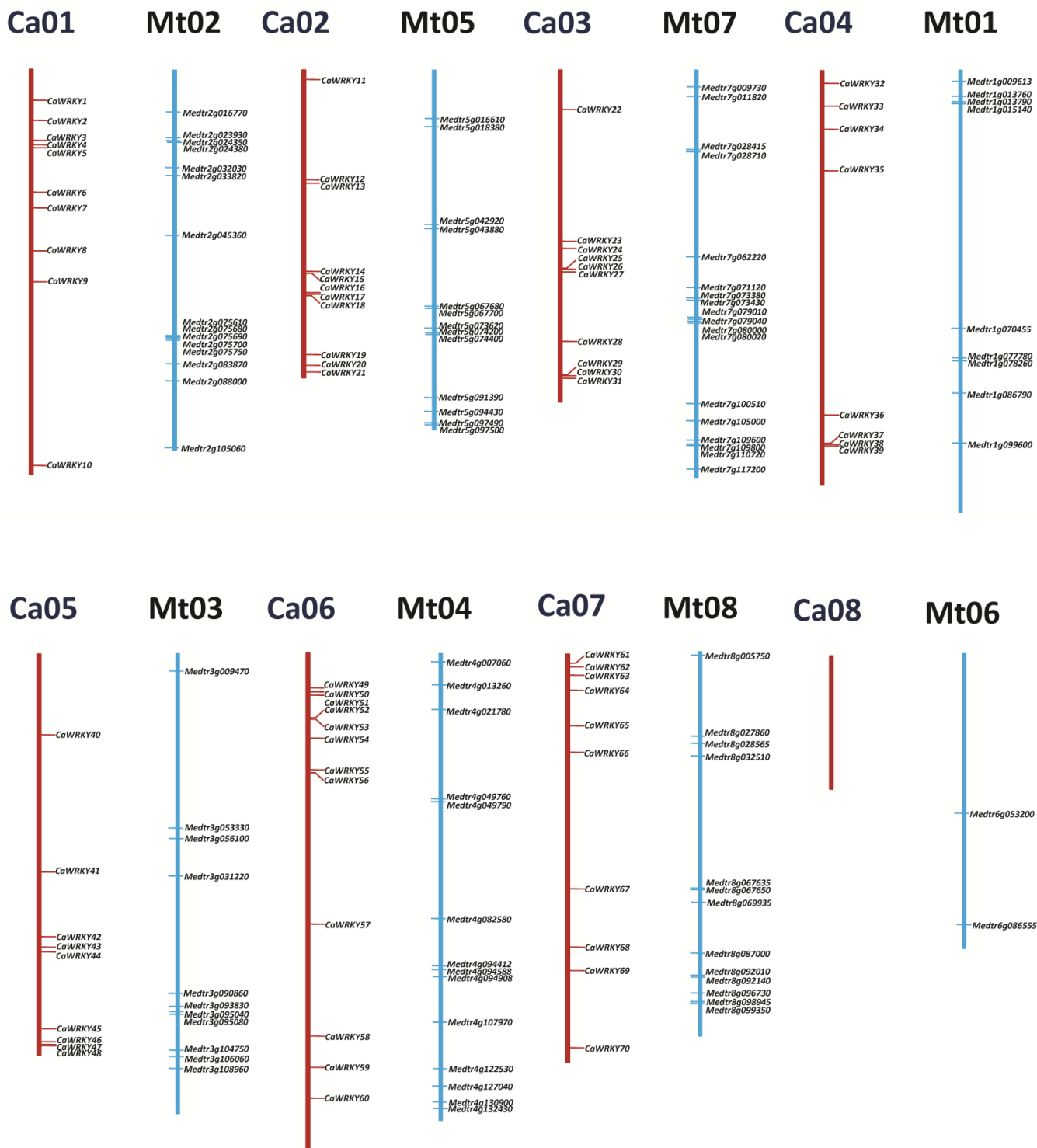
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	<a href="#">Medtr8g092140</a>	WRKYGQKX <sub>13Cx4Cx23</sub> HVH	38496852 - 38495018
	Medtr8g096730	<b>WRKYGEK</b> <sub>x13Cx4Cx23</sub> HIH	40590920 - 40591732
IId	Medtr1g009613	WRKYGQKX <sub>13Cx5Cx23</sub> HRH	1360381 - 1362350
	Medtr1g070455	WRKYGQKX <sub>13Cx5Cx23</sub> HNH	31254130 - 31252313
	Medtr3g108960	<b>WRKYGSK</b> <sub>x13Cx5Cx23</sub> HRH	50356649 - 50355064
	Medtr4g094908	WRKYGQKX <sub>13Cx5Cx23</sub> HNH	39256749 - 39255312
	Medtr4g127040	WRKYGQKX <sub>13Cx5Cx23</sub> HRH	52696299 - 52695143
	Medtr5g016610	WRKYGQKX <sub>13Cx5Cx23</sub> HNH	5978776 - 5980395
	Medtr0117s0040	<b>WRKYGSK</b> <sub>x13Cx5Cx23</sub> HHH	
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	<a href="#">Medtr2g024380</a>	WRKYGQKX <sub>13Cx5Cx23</sub> HNH	8785909 - 8787640
	Medtr2g032030	WRKYGQKX <sub>13Cx5Cx23</sub> HNH	12167936 - 12165295
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	Medtr6g053200	<b>WTKYGQK</b> <sub>x13Cx5Cx23</sub> HNH	19092662 - 19095283
	Medtr7g079040	WRKYGQKX <sub>13Cx5Cx23</sub> HNH	29998273 - 29999656
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	<a href="#">Medtr2g075680</a>	WRKYGQKX <sub>13Cx7Cx23</sub> HTC	31648412 - 31650544
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	<a href="#">Medtr2g075750</a>	WRKYGQKX <sub>13Cx7Cx23</sub> HSC	31677679 - 31678918
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	<a href="#">Medtr5g067700</a>	WRKYGQKX <sub>13Cx7Cx23</sub> HTC	28615004 - 28610470
	Medtr5g073620	<b>WTKYGMK</b> <sub>x13Cx7Cx23</sub> HTC	31317285 - 31324912
	<a href="#">Medtr7g073380</a>	WRKYGQKX <sub>13Cx7Cx23</sub> HTC	27431552 - 27430007
	<a href="#">Medtr7g073430</a>	WRKYGQKX <sub>13Cx7Cx23</sub> HTC	27449495 - 27447284
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	Medtr8g027860	WRKYGQKX <sub>13Cx7Cx23</sub> HTC	10193751 - 10196359
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	Medtr8g099350	WRKYGQKX <sub>13Cx7Cx23</sub> HTC	41854576 - 41853261
	Medtr0002s1250	<b>WRQYGQK</b> <sub>x13Cx7Cx23</sub> HTC	
	Unclassified	Medtr1g077780	<b>WRKYGEQ</b> <sub>x13Cx4Cx23</sub> HNH
Medtr1g078260		<b>WRKYGCK</b> <sub>x13Cx4Cx23</sub> HTH	35032177 - 35035171
Medtr4g021780		<b>WKYGEK</b> <sub>x12Cx4Cx22</sub> HNH	7234714 - 7234198
Medtr5g018380#		<b>WLKYDRK</b> <sub>x13Cx4Cx23</sub> HTH	6849071 - 6850162
Medtr5g074200		<b>WKYEEK</b> <sub>x13Cx4Cx22</sub> HNH	31495781 - 31496764
Medtr6g086555		<b>WHYGRK</b> <sub>x14Cx4Cx23</sub> HNH	32569398-32572647
Medtr7g062220		<b>WRQYGQK</b> <sub>x13Cx4Cx23</sub> HLH	22586277-22583775
partial WRKYs	<i>Medtr1g077760, Medtr2g075730, Medtr4g047580, Medtr4g052030, Medtr5g029850, Medtr5g044695, Medtr5g093540, Medtr6g038890, Medtr6g046600, Medtr0130s0060,</i>		

Three genomic regions encoding for WRKY-domain containing proteins were re-structured with respect to the intron-exon boundaries of annotation in Mtv4.0. The coding regions are highlighted with yellow while red colored sequences between them are introns. The deduced protein sequences are also mentioned below genomic sequence. The blue colored amino acids in

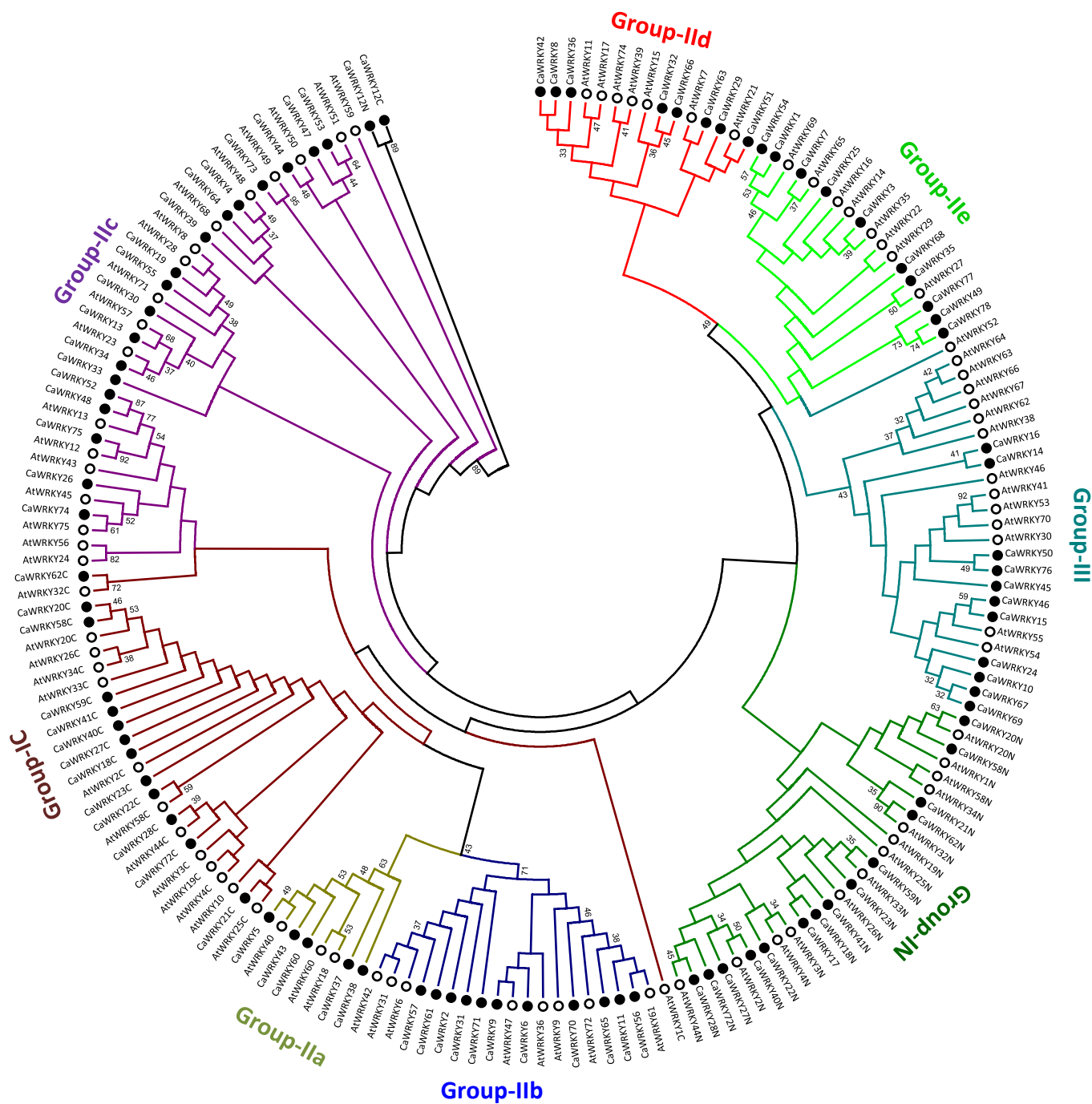




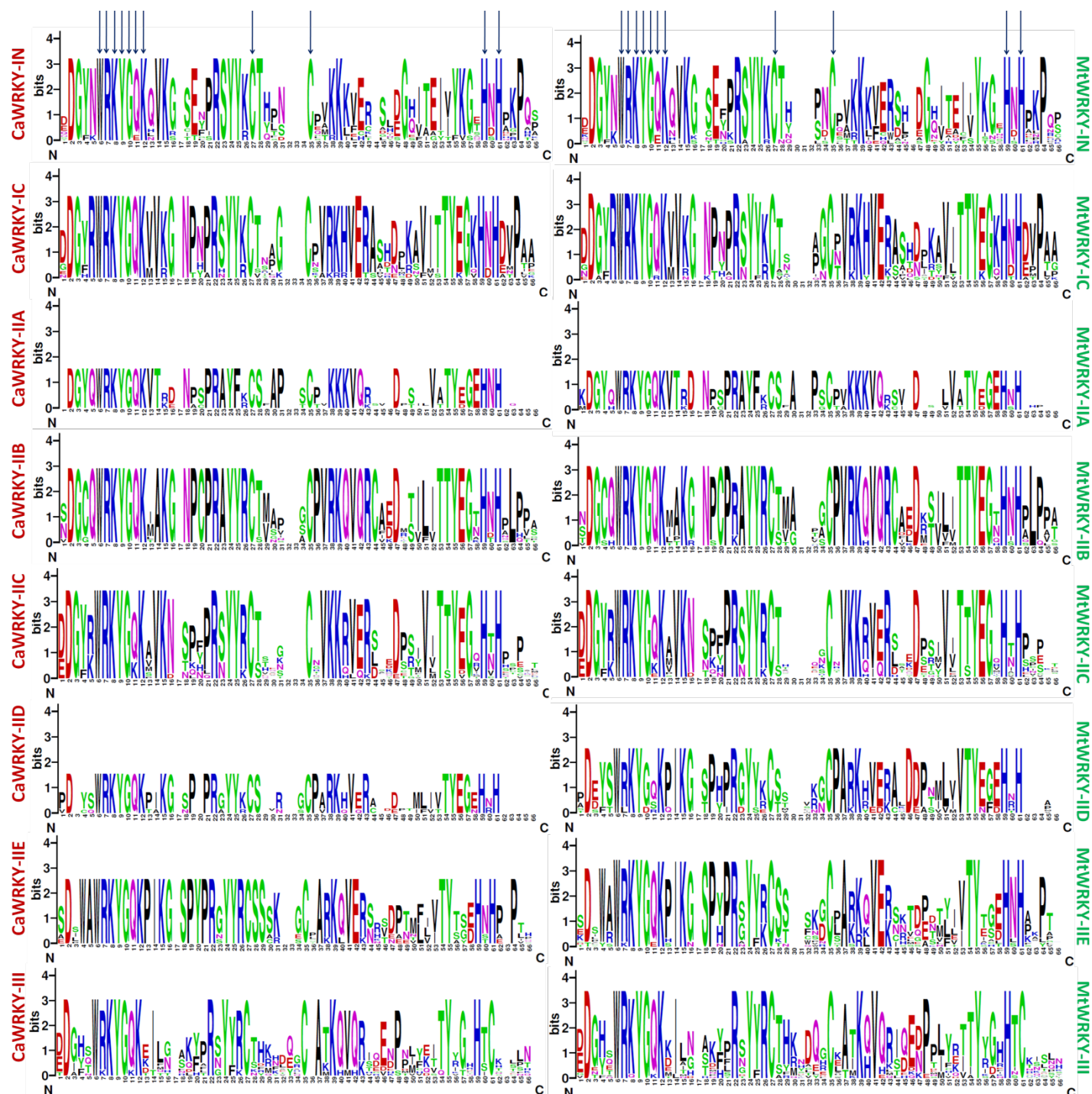
# Supplementary Fig. S1.



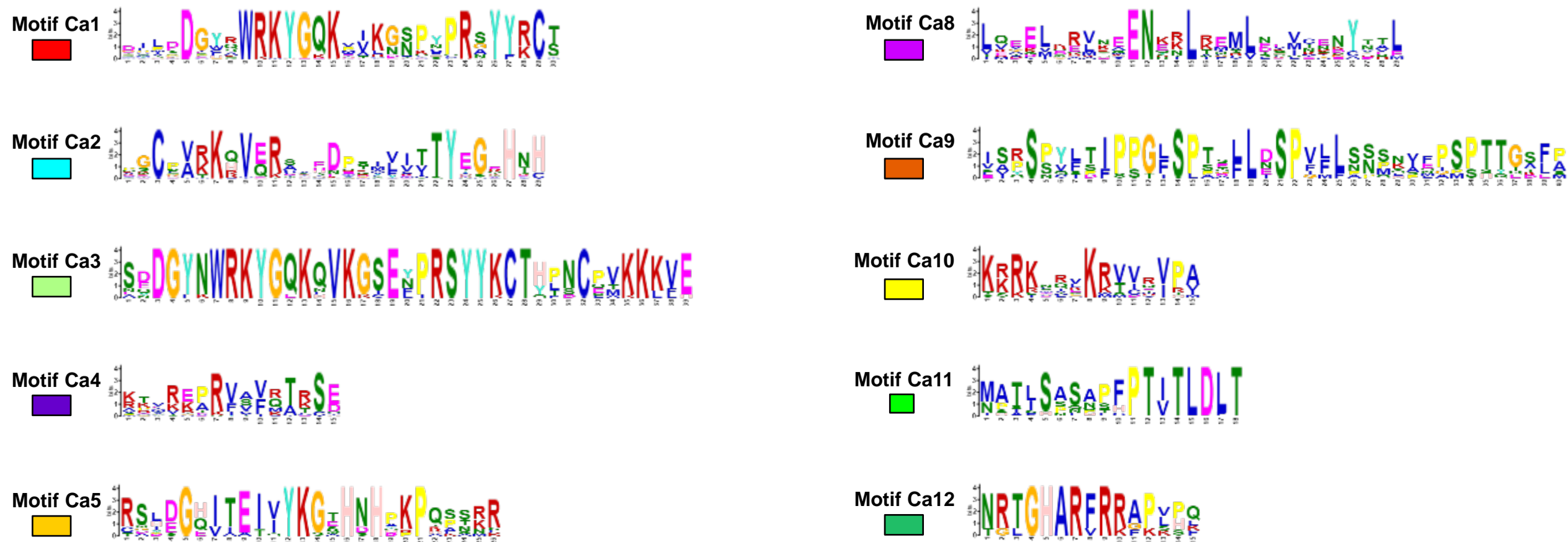
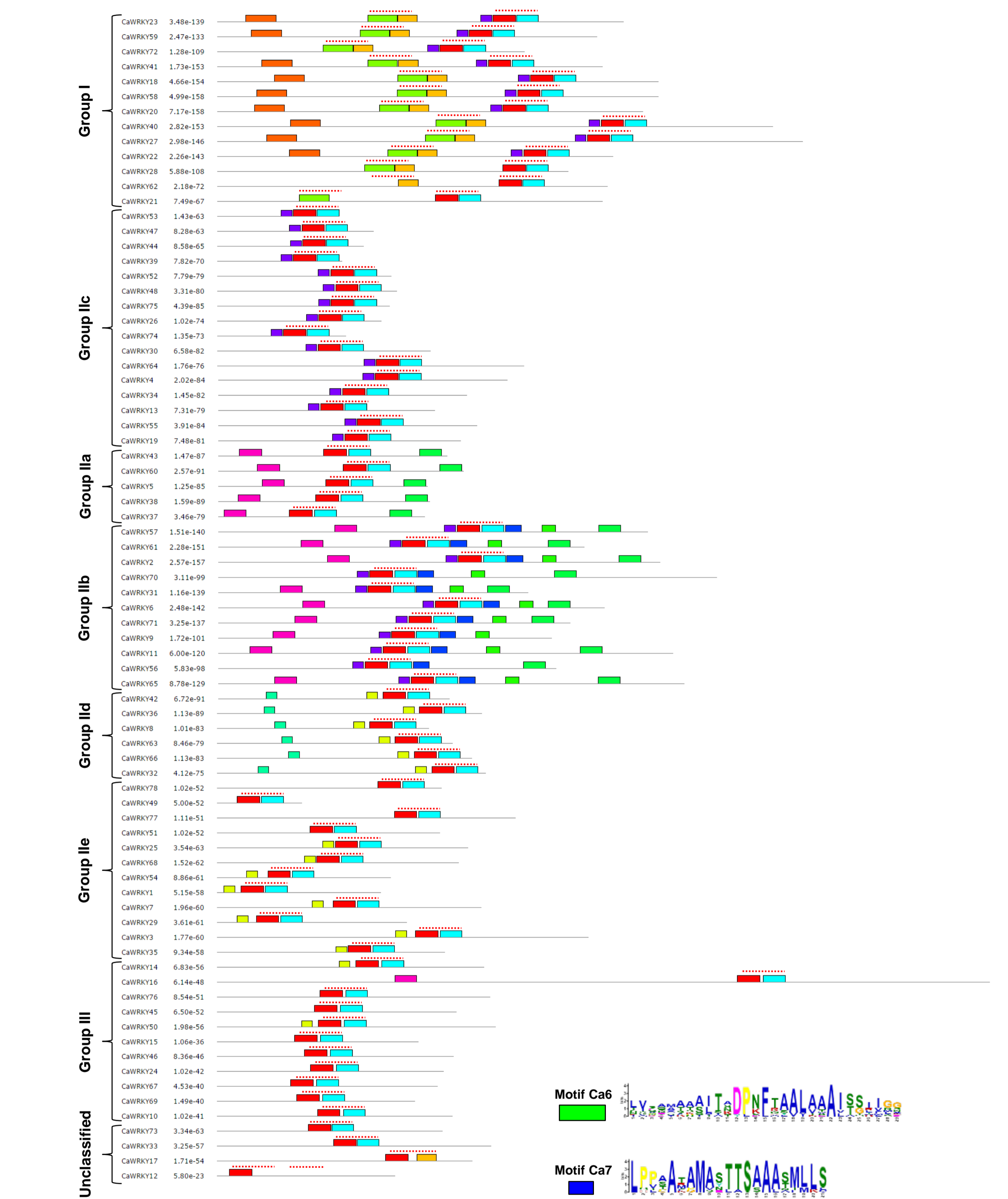
Supplementary Fig. S2.



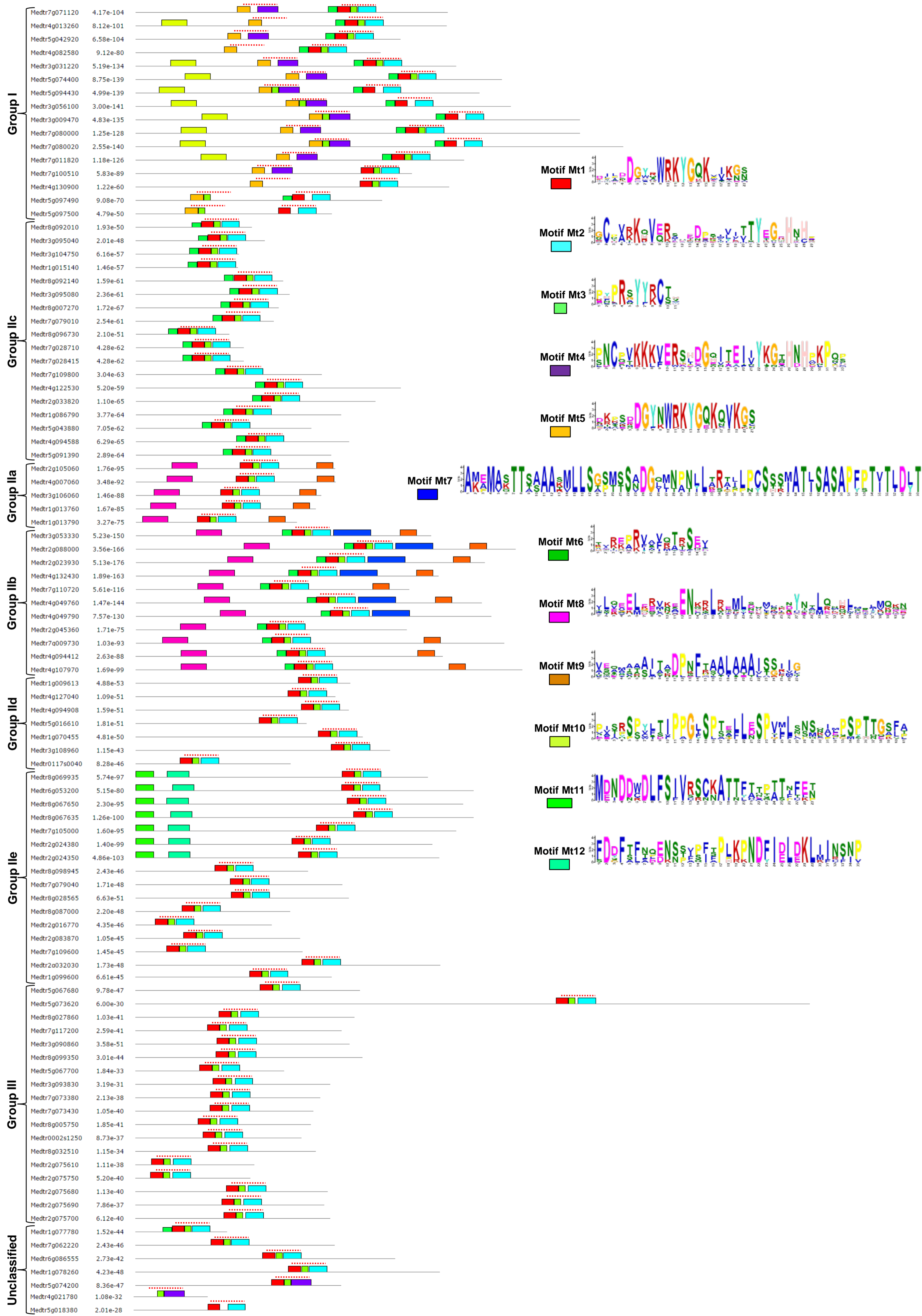
# Supplementary Fig. S3.



Supplementary Fig. S4.



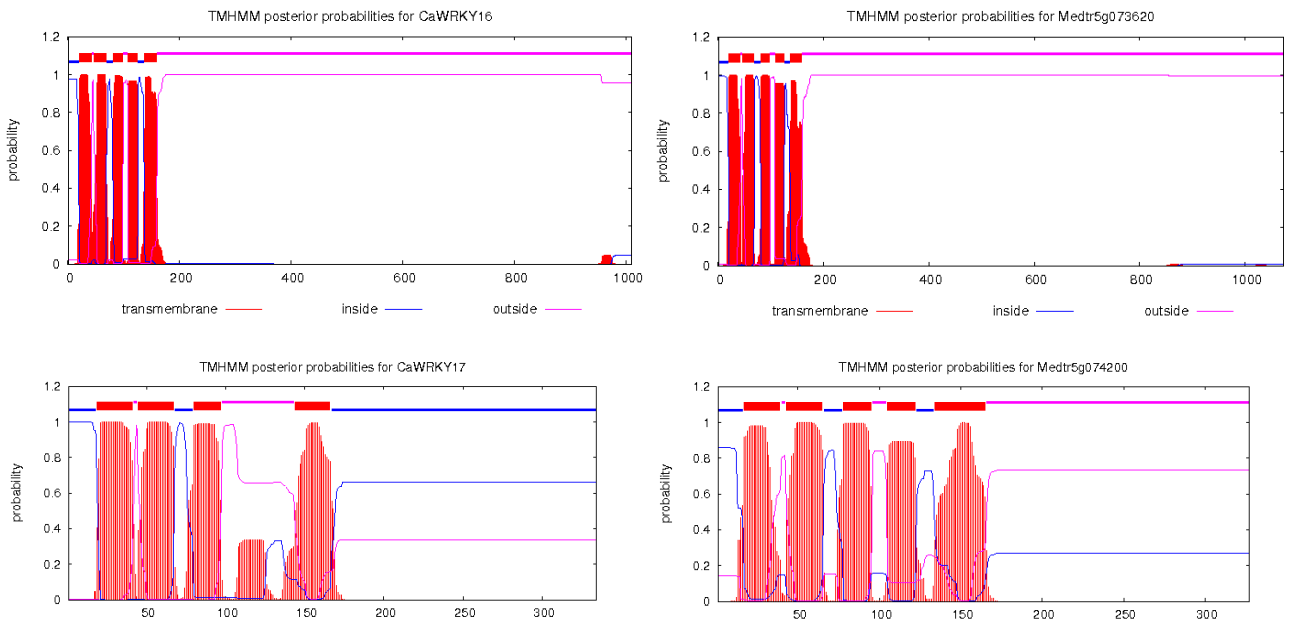
Supplementary Fig. S5.



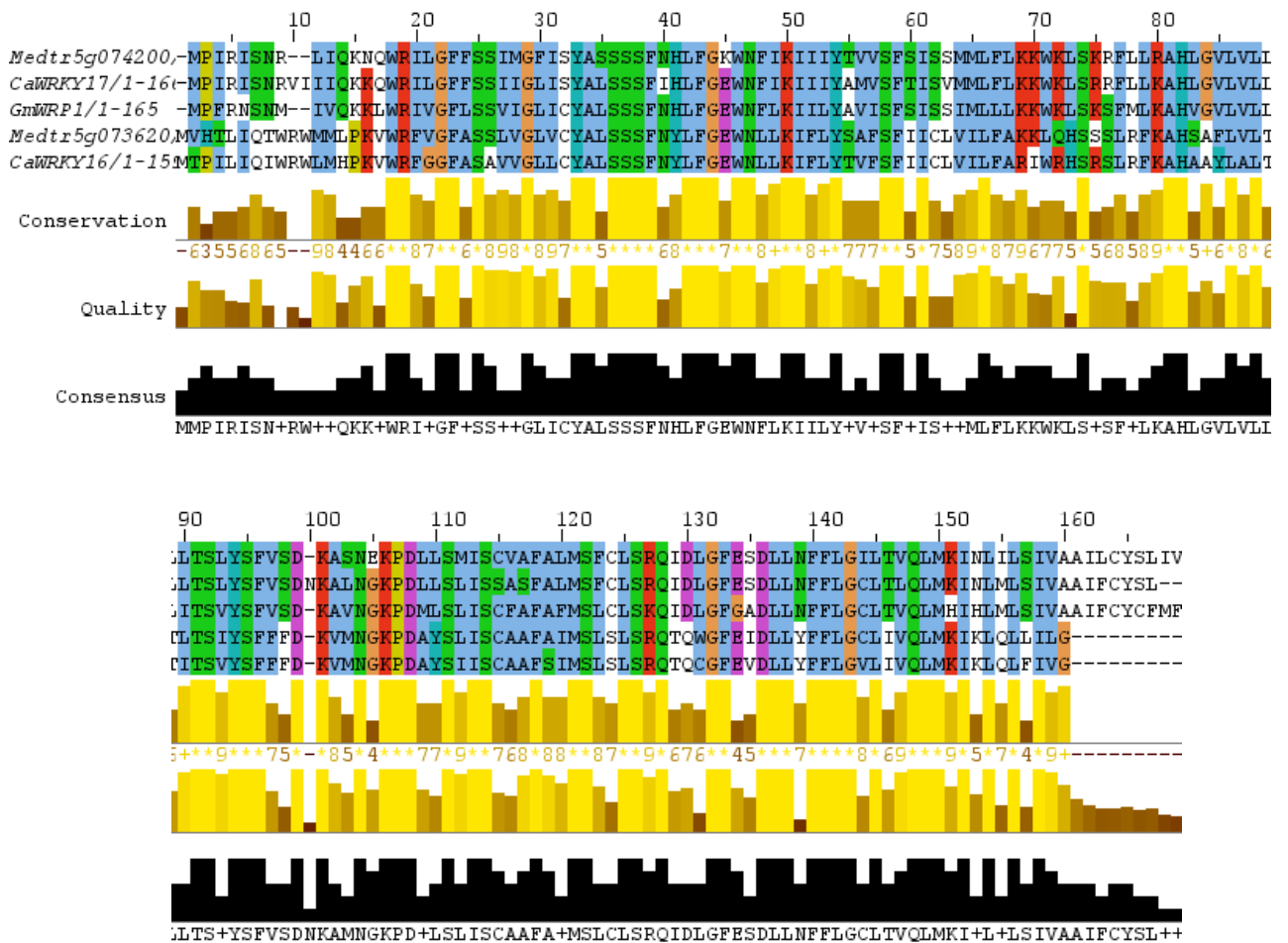


# Supplementary Fig. S6.

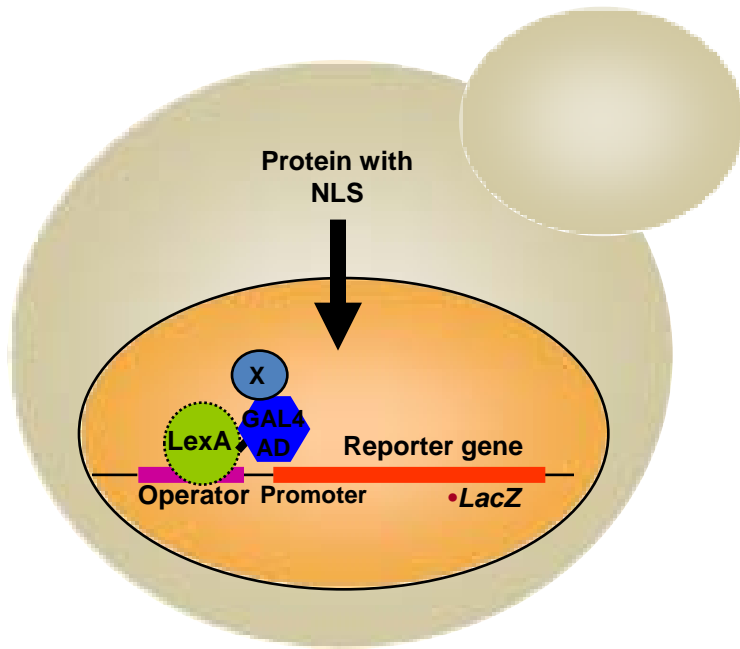
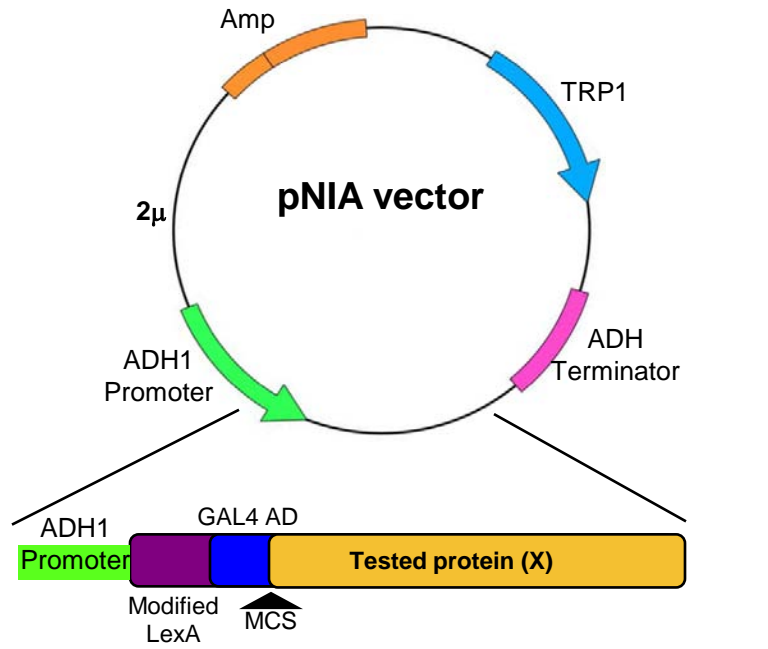
**A**



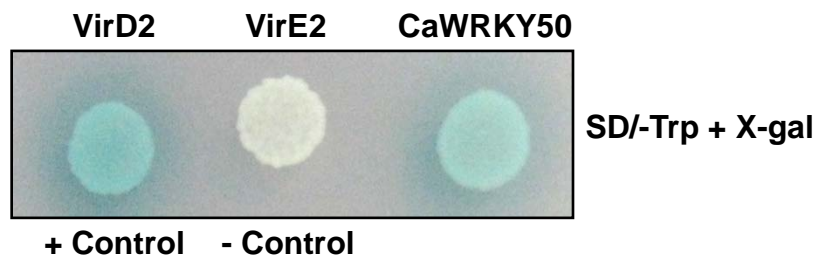
**B**



# Supplementary Fig. S7.

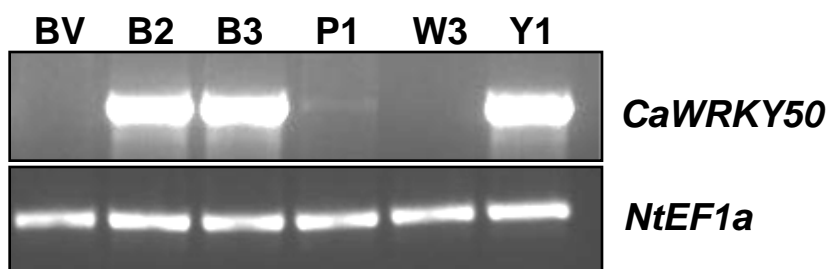


*S. cerevisiae* strain L40

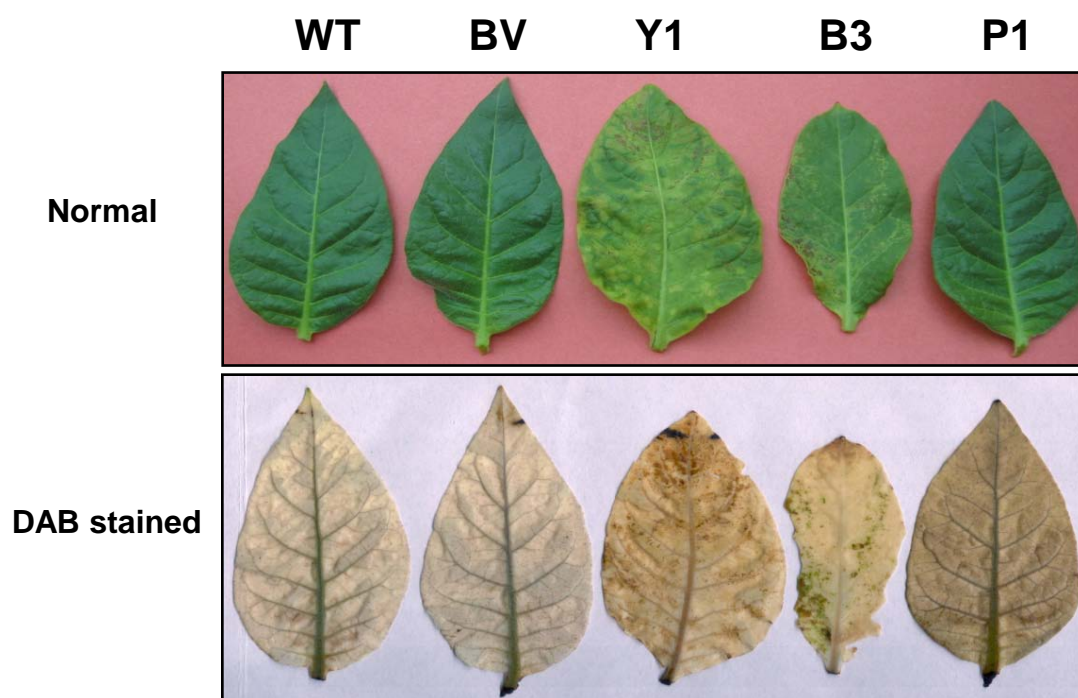


# Supplementary Fig. S8.

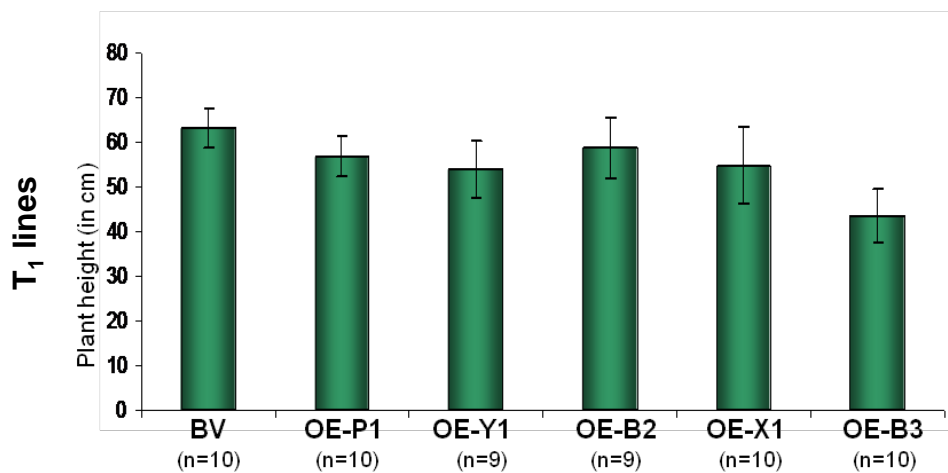
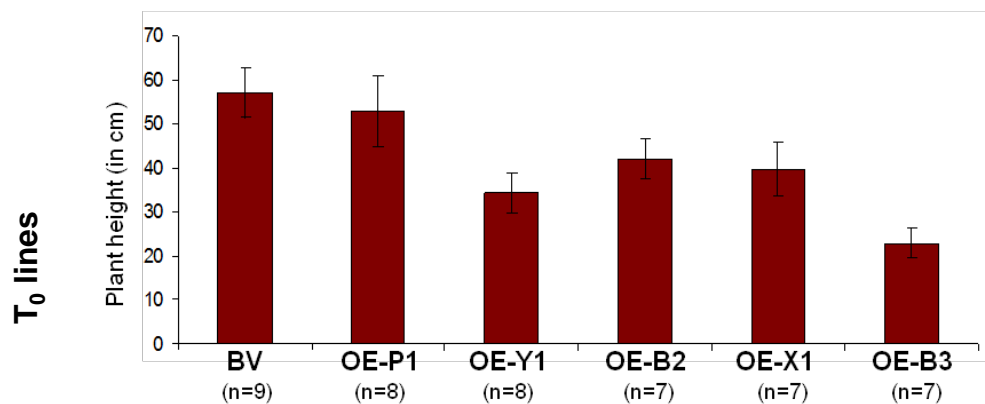
**A**



**B**



## Supplementary Fig. S9.



# Supplementary Fig. S10.

