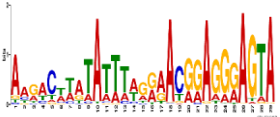
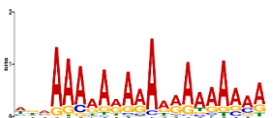
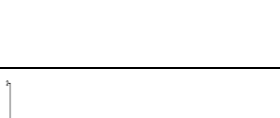
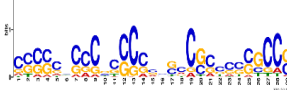
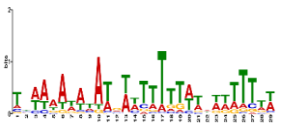
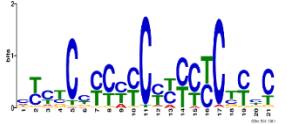
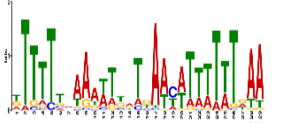
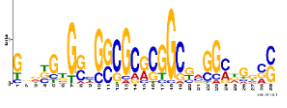
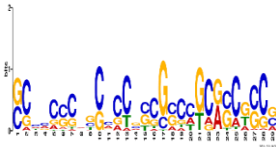
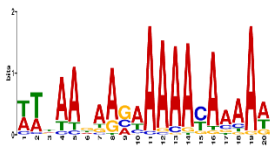
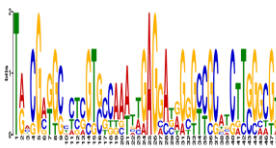
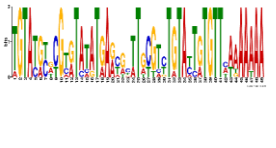
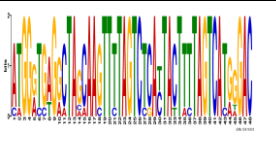


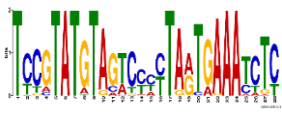
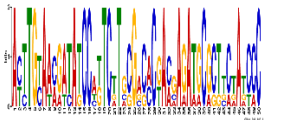
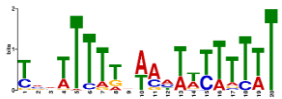
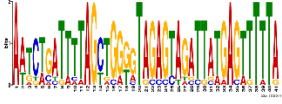
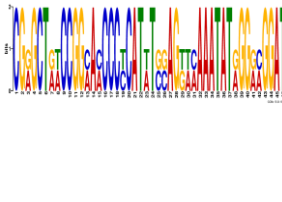
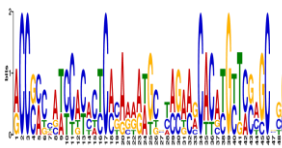
Supplementary File 1

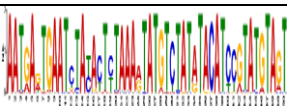
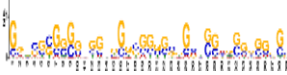
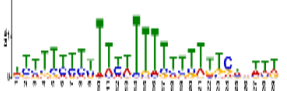
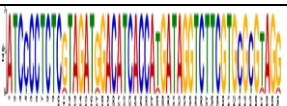
Twenty significant motifs were detected with lengths ranging from 15 to 50aa in the promoter of DEGs. The GOMO analysis for the motifs discovered by MEME identified several biological functions.

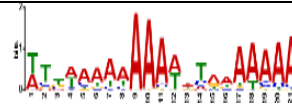
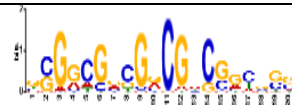
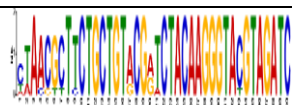
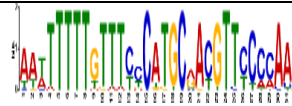
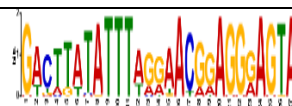
Detected motifs related to the promoters of the up-regulated genes							
	Motif Logo		Width	E-value	Number of Genes contain the motif	Best match in JASPAR and PLACE	Top 5 Significant GO term identified by GOMO
Motif 1		AAGACW WATATTT WGRAACG GAGGGAG TA	29	7.2e-077	218	MA1416.1 (RAMOSA1)	MF transcription factor activity (GO :0003700) CC nucleus (GO :0005634) BP regulation of transcription (GO :0045449) CC plasma membrane MF kinase activity (GO :0005886)
Motif 2		WDAAAAR ARAAAAR AAAAAAA	21	2.3e-072	401	MA1268.1 (AT1G69570) c2h2	MF transcription factor activity (GO :0003700) CC nucleus (GO :0005634) CC plasma membrane (GO :0005886) BP regulation of transcription, DNA-dependent (GO :0006355) BP transmembrane receptor protein tyrosine kinase signaling pathway (GO :0007169)
Motif 3		SCSYCCBC SCCSBCBC CBBCSSCS SCRBCMS CCSCBCSC CC	41	3.9e-081	568	MA1053.1 (ERF109) AP2	CC mitochondrion (GO :0005739) MF nucleotide binding (GO :0000166) CC chloroplast envelope (GO :0009941) CC CUL4 RING ubiquitin ligase complex (GO :0080008) BP translation (GO :0006412)
Motif 4		TDTWTAT WDWHAT WTTTTWD WATDTWK DTHATTT WTT	38	7.2e-048	442	MA1267.1 (AT5G66940) c2h2	MF transcription factor activity (GO :0003700) CC endomembrane system (GO :0012505) CC plasma membrane (GO :0005886) CC nucleus (GO :0005634) BP regulation of transcription, DNA-

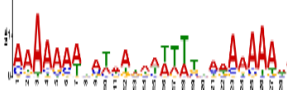
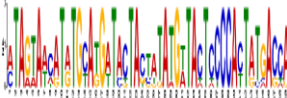
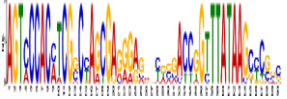
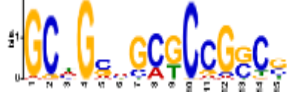
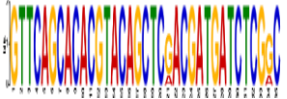
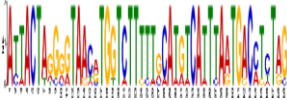
							dependent (GO :0006355)
Motif 5		CSSSCBCC CBCSCCVB SCCSCCCS SGCCS	29	7.8e-019	419	MA1264.1 (ESE1) AP2	CC mitochondrion (GO:0005739) MF monooxygenase activity (GO :0004497) MF nucleotide binding (GO :0000166) BP translation (GO :0006412) CC chloroplast envelope (GO :0009941)
Motif 6		THWAAA WAWATR WWTTTTT WWDWWT TTTW	29	3.1e-012	356	MA1274.1 (OBP3) c2h2	MF transcription factor activity (GO :0003700) CC endomembrane system (GO :0012505) MF oxygen binding (GO :0019825) BP regulation of transcription, DNA-dependent (GO :0006355) CC plasma membrane (GO :0005886)
Motif 7		MYYTCYY CYCYYY CYCYBC	21	1.6e-008	304	MA1404.1 (BPC1) AP2	MF transcription factor activity (GO :0003700) CC nucleus (GO :0005634) CC chloroplast (GO :0009507) CC plasma membrane (GO :0005886) MF protein binding (GO :0005515)
Motif 8		KTTTTTDA AAWTKRT KAAYWTT TTWTDAA	29	1.1e-003	211	MA1379.1 (SOL1) other	MF transcription factor activity (GO :0003700) BP regulation of transcription (GO :0045449)
Motif 9		GBDBGKG SHGSCGCR CGGCKVG GMDGGVS	29	8.8e-006	194	MA0980.1 (RAP2-10) AP2	CC chloroplast (GO :0009507) CC mitochondrion (GO :0005739) BP translation (GO :0006412) MF structural constituent of ribosome (GO :0003735) MF nucleotide binding (GO :0000166)

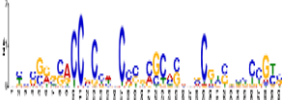
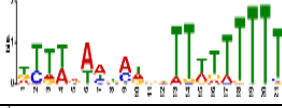
Motif 10		SCHVCSCV GCMCCSS CGSCCGC RSCKSCS	29	2.0e-005	359	MA0992.1 (ERF4) AP2	CC mitochondrion (GO :0005739) MF nucleotide binding (GO :0000166) MF structural constituent of ribosome (GO :0003735) CC chloroplast envelope (GO :0009941) CC chloroplast stroma (GO :0009570)
Motif 11		WWDAAD AAVAAAA AYAAAAW	20	3.1e-004	291	MA1267.1 (AT5G66940) c2h2	MF transcription factor activity (GO :0003700) CC plasma membrane (GO :0005886) BP regulation of transcription (GO :0045449) BP transmembrane receptor protein tyrosine kinase signaling pathway (GO :0007169) CC nucleus (GO :0007169)
Motif 12		TRMCGMK GCYYYS TSSCAAAT WGAGGAB RGSYCG CATCTTSG GCGKGA	50	1.2e+000	30	MA0946.1 (ARR11)	CC chloroplast (GO :0009507) BP mitochondrial transport (GO :0006839) CC mitochondrial inner membrane (GO :0005743) BP protein amino acid glycosylation (GO :0006486) BP translation (GO :0006412)
Motif 13		TGTATGY DCGTRTA TATGARY GYTTGCG TYTGTAY TGTGTH AAAAAAA	49	3.0e+002	93	MA1208.1 (GT2)	MF transcription factor activity (GO :0003700) CC endomembrane system (GO :0012505) BP regulation of transcription (GO :0045449)
Motif 14		ATGGRTG AGGCTAG CAAGTTTT AGTCTCA YTACTTTT AGTCATG GGAC	48	5.1e+002	28	MA1272.1 (AT2G28810) c2h2	no significant GO-term could be associated with this motif

Motif 15		TCCGTAT GTAGTCY YYTARTG AAATCTC	28	1.7e+003	73	MA1035.1 (TCP4)	CC endomembrane system (GO :0012505) MF transcription factor activity (GO :0003700)
Motif 16		AYTTGYA AMGATAT CCAKTCTT GCGACMC KAMGAGA TGCCTTC TATCCC	50	3.7e+003	11	MA0947.1 (ARR14)	no significant GO-term could be associated with this motif .
Motif 17		TVHTTTTT VWAMTW YTTTTT	20	2.0e+003	182	M1159.1 (SGR5) c2h2	MF transcription factor activity (GO :0003700)
Motif 18		AATCTGA TTTTAGCT GGKGTAG AGTAGAT TATGAGT TTTTA	41	4.2e+003	40	MA1317.1 (WRKY50)	no significant GO-term could be associated with this motif
Motif 19		CGRGCTR WCCGGM AMCCCYC ATWTSSA GKWMAA ATATRGG RMGGAT	46	7.2e+003	21	MA1056.1 (SPL11)	no significant GO-term could be associated with this motif
Motif 20		RCCSMCC AWYCAY MCYCMSA RRRWGCN YMSAMRC ACAYGYT MSMGCNS SC	50	5.0e+002	64	MA1048.1 (ERF018) AP2	CC chloroplast (GO :0009507) CC mitochondrion (GO :0005739) BP protein modification process (GO :0006464)

Detected motifs related to the promoters of the down-regulated genes							
	Motif Logo		Width	E-value	Number of Genes contain the motif	Best match in JASPAR and PLACE	Top 5 Significant GO term identified by GOMO
Motif 1		DAAAYYW HTAAAAA GACTTAT ATTTWGR AACGGAG GGAG	39	7.5e-058	244	MA1403.1 (BPC5)	MF transcription factor activity (GO :0003700) BP regulation of transcription (GO :0045449)
Motif 2		AATGART GAATCTA YACTYTA AARTATG TCTATATA CATCCGT ATGTAGT	50	3.1e-052	152	MA1190.1 (At4g01280), HTH (MYB)	MF transcription factor activity (GO :0003700) CC endomembrane system (GO :0012505) BP regulation of transcription (GO :0045449)
Motif 3		GVBSSGSGS SGNNGNG GGSGGSGS GGVBSSGM GSGVSGSG V	39	6.2e-049	603	MA1257.1 (ERF9), AP2	CC mitochondrion (GO :0005739) MF monooxygenase activity (GO :0004497) BP translation (GO :0006412) MF structural constituent of ribosome (GO :0003735) CC ribosome (GO :0005840)
Motif 4		TTTTTYTT TTYTTTTT TTTTTTTC WDWTT	29	1.8e-046	490	MA1267.1 (AT5G66940), c2h2	MF transcription factor activity (GO :0003700) CC nucleus (GO :0005634) CC plasma membrane (GO :0005886) BP regulation of transcription, DNA-dependent (GO :0006355) BP transmembrane receptor protein tyrosine kinase signaling pathway (GO :0007169)
Motif 5		ATCCCCTC TCGTAGA TGGACAT CACCATG ATAGGTC TTCGTGC	50	1.1e-026	21	MA1202.1 (AGL55), MAdS	no significant GO-term could be associated with this motif

		GCGTAGG					
Motif 6		WTTWAAA AAAAWAT AAAAAAA	21	1.5e-017	233	MA1268.1 (AT1G69570), c2h2	MF transcription factor activity (GO :0003700)
Motif 7		GGRRGRG RGRGGRG G	15	2.3e-012	227	MA1416.1 (RAMOSA1), c2h2	MF transcription factor activity (GO :0003700) CC nucleus (GO :0005634) CC chloroplast (GO :0009507) MF protein binding (GO :0005515) MF microtubule motor activity (GO :0003777)
Motif 8		GSGGCGR CGRCGAC SGYGSS	20	1.9e-010	175	MA1257.1 (ERF9), AP2	CC mitochondrion (GO :0005739) BP nitrogen compound metabolic process (GO :0006807) MF nucleotide binding (GO :0000166) BP translation (GO :0006412) CC chloroplast stroma (GO :0009570)
Motif 9		CTAACGC TTCTGCTG TACGRTCT ACAAGGG TACGTAG ATC	40	3.2e-010	25	MA1038.1 (MYB3),	no significant GO-term could be associated with this motif
Motif 10		AAWTTTT TGTTYCC ATGCRAC GTTYCCC AAC	32	3.0e-009	31	MA1365.1 (AT5G47660),	MF transcription factor activity (GO :0003700)
Motif 11		GACTTAT ATTTAGG AACGGAG GGAGTA	27	4.4e-009	259	MA0955.1 (POPTR_0002s00440g)	MF transcription factor activity (GO :0003700) BP regulation of transcription (GO :0045449)

Motif 12		AAAAAAW NATAADA WTTTDA AAAAAAW A	29	1.0e-009	399	MA1267.1 (AT5G66940), c2h2	MF transcription factor activity (GO :0003700) BP regulation of transcription (GO :0045449) CC plasma membrane (GO :0005886) CC nucleus (GO :0005634) MF protein heterodimerization activity (GO :0046982)
Motif 13		MTAGTAW CATRTGC ATGATAC TACTATAT GWTACTC CCCACTA TGACCA	49	7.1e-006	25	MA0987.1 (PHYPADRAFT_140773)	CC endomembrane system (GO :0012505) MF transcription factor activity (GO :0003700)
Motif 14		AGTCCCA CMTCGSC YAGCGAG GGAGDNY DVGACCG GTTTATA AGCYCSSC	50	1.2e-009	25	MA1266.1 (RAP21), AP2	no significant GO-term could be associated with this motif
Motif 15		GCHGSMG CKCCGSCS	15	1.9e-005	104	MA0980.1 (RAP2-10), AP2	CC chloroplast (GO :0009507) CC mitochondrion (GO :0005739) BP translation (GO :0006412) MF structural constituent of ribosome (GO :0003735) CC ribosome (GO :0005840)
Motif 16		GTTCAGC ACACGTA CAGCTCG ACGATGA TCTCGGC	35	1.6e-003	28	MA0978.1 (DREB1E),	no significant GO-term could be associated with this motif
Motif 17		ATTACTA GGGGTAA CRTGGTCT TTTTGCAT GTCATTTA ATGACMT CTAGT	50	2.4e-002	22	MA0990.1 (EDT1),	no significant GO-term could be associated with this motif

Motif 18		NYBCSRSS ACCVCCH NCCSKCG CMSVNVC GBSBBBCC GYS	40	1.6e-007	358	MA1242.1 (AT3G57600), AP2	CC mitochondrion (GO :0005739) CC chloroplast stroma (GO :0009570) CC chloroplast envelope (GO :0009941) MF nucleotide binding (GO :0000166) CC chloroplast thylakoid membrane (GO :0009535)
Motif 19		KTTWVWH KMDDKTT WTTTTTT	21	9.2e-002	227	MA1279.1 (COG1), c2h2	MF transcription factor activity (GO :0003700) CC plasma membrane (GO :0005886)
Motif 20		TTTWGCA TGTCATTT AATAACT TCTWVTA	29	1.2e+001	38	MA1209.1 (ATHB20),	MF transcription factor activity (GO :0003700) CC endomembrane system (GO :0012505) BP regulation of transcription, DNA-dependent (GO :0006355)