

Supplementary Material

1. Section S1: The alignment of *TaCHI* promoters

```
1
TaCHI-A1 AAAAGAATTGCCAGTTAAGCACAAGATAATTCCAAAAGGTTGTGATTTTACTCGTAGTACAAACAATTGGAGCTTTTCCACACCCACAAAGGTGATTTC
TaCHI-D1 GGAGCTTTTCCACACCCATAAAGGTGGTTTC
TaCHI-B1 CGGACCCAAACGGACAAAAAGCGAAC
101
TaCHI-A1 TTTAAT-----ATCGGTCTGCAGTGCAGGTGCAGTTTATGTT-TTATATCTTTTTTGAACATGCAGTTTATGTTGGTGATATGTTGAGTTCC
TaCHI-D1 TTTAATCTGTTGAGATCGGTCTGCAGTGCAGGTGTTTGT-TT-----TGTTTTTGAACATGCAGTTTATGTTGGTGATATGTTGAGTTCC
TaCHI-B1 AAAAT-----CACCGTCTTGGTGGGTGGGACCGTTGGAGTTGCTCTAATCTTATTATTCATGCC---TGAGGTAGGCGAACATTA----CT
201
TaCHI-A1 TTTCTTTGCGACACGGCAGACCTGTCATCGGCCAACAC-ACACGAGCGTCTCGTCTGGGCTCTCGCTGAGTT-----GAATGGTA-
TaCHI-D1 TTTGCTTTACGACACGGCAGACCTGTCATCGGCCAGCA-ACACGAGTGTCTGGTCTGGACTCGTGCCTGAGTTT-----TTTGGAGGACTCTGTC
TaCHI-B1 CTTGCTTACCCGTAGGTTGTTCTTTGAGATCGGTGTGCTTTGGTGACATGT-TGAGCGTGTGTCTGGTGT-----GGGCTCGTGC
301
TaCHI-A1 -----GCTCGCTTGACCTCGCCGCAAAACCTGGCGCGGGCCAGTCCGT-----CCTCTCAAGTGCCTCTCCTAACTACCACTAAC
TaCHI-D1 GTGAGTTGAATGTTAGCTTGACCTCGCCGCAAAACCTGGCGCGGGACACGTCTCTCTCT-----GCCCTCAAGTGCCTCTCCTAACTACCACTAAC
TaCHI-B1 GTGAGTTGAATGTTAGCTTGACCTCGCCGCAAAACCTGGCGCGGGCCAGTCCGTCTCTCTCTTTGCCCTCAAGTGCCTCTCCTAACTACCACTAAC
401
TaCHI-A1 ACGCCCCCAGACGCGCCACAAACTACATCTTTGCCACAAGGCACAA-AGTTACCCCTCCGTCTACG-----CGTAGGCCAAAGAACTAGAC
TaCHI-D1 ACGCCCCCAGATGCGCCACAAACTACATCTCTGCCACAAGGCACAA-AGTTACCCCTCCGTCTACGCTAGTCTAGGCCGCTAGGCCAGAGAACAGAC
TaCHI-B1 ACGCCCCCATATGCGCACACAAACTACATCTTTGCCACAAGGCACAAAGTTACCCCTCCGTCTACGCTAGTCTAGGCCGCTAGGCCAGAGAACAGAC
501
TaCHI-A1 CAGATTACGCGCGTGGCATAATCGCAATTACGGGACAGAGTCCACGGGCGTTTATATAGCCGCTGGGGTGTATATAGGAGAGG---GCACCACCAACCCCA
TaCHI-D1 CAGATTACGCGCGTGGCATAATCGCAATTACGGGACAGAGTCCACGGGCGTTTATATAGCCGTTGCGGTGTATATAGGAGGAGGACACCAACCAACCCCA
TaCHI-B1 CAGATTACGCGCGTGGCATAATCGCAATTACGGGACAGAGTCCACGGGCGTTTATATAGCCGTTGCGGTGTATATAGGAGGAGGACACCAACCAACCCCA
601
TaCHI-A1 GCTGACCATCCCGTGCGCCACGCTTCAAAGATCGCACCTACCCCTGCGCGGCGGCTGCCCCATCACATCAATACAAGCGTTGCTGCTACGTGCC
TaCHI-D1 GCTACCCATCCCGTGCGCCACGCTTCAAAGATCGCACCTACCCCTGCGCGG-----CCTGCCCCATCACATCAATACAAGTGTGCTGCTACGTGCC
TaCHI-B1 GCTACCCATCCCGTGCGCCACGCTTCAAAGATCGCACCTACCCCTGCGCGG-----CCTGCCCCGTCCTATCAATACAAGTGTGCTGCTACGTGCC
701
TaCHI-A1 GTC-----GTCTCCGAGACCCCTCCGCGCA-CCA-CCG-----AGACC
TaCHI-D1 GTC-----GTCTCCGAGACCCCTCCGTCGA-CCA-CC
TaCHI-B1 GTCGTCGTCTCCGAGACCCCTCCATCCATCCATCCGGGATATACC
```

2. Section S2: The alignment of *TaF3H* promoters

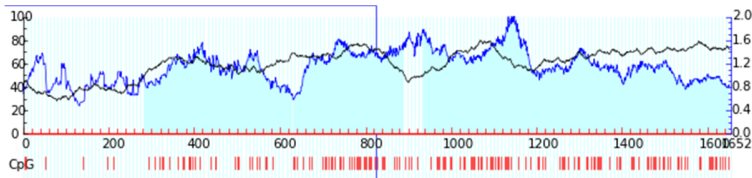
```
1
TaF3H-B1 TCTACAAGCCATGGAAATATGACGTGTCATGATGTATAGGTTTATAGATATTGGCGAACCAATCTGTGGTTGGATGTTAAAGGGACTCTGATATCCCA
TaF3H-B2 ATTTGCAACCGAGCGAGC--TTAGATGGTTAGATATTTCTTG-----TGGTGAACATA
101
TaF3H-B1 GTCCACTAAGGTTCAAA--TCTGGTGCTTGAGTTTATTC--TGGATTATTTAGGA-TTTTCGACGATGTGCATTCAGTAGGAGAAGACGTTCCCGTCCGA
TaF3H-B2 GCCCATCATGTTTCATAGTCTTAAGGCTTATTTGGTTTGGAGGAATTTATAGGACTTTTATACGATAGGATTTCTTATAGGAATTT--TTCTTAAAGC
201
TaF3H-B1 CAACGAGTTGCCACGATGACTTCGTAAATTTCAAGATAATATCCGATTCGGTCTTTCGGAGGTGCTCATAGGGGTAGGGTGTGCGTGTGTCGCTTTAT
TaF3H-B2 CTATTAAATTCATAGGAATGAATT--TTATTCTTACATAGAAAT-TGGTTCTATCCTTCA-----CACTTTAAAGTAAATATAA---TATGAATCTAG
301
TaF3H-B1 AGGGATGAGTGATGCACTATATGAGCGCTTGATCTGGAAGTGTGTTAAAAAAGTTCTAGATCTTGGTTGGTGTATAGCGGGTGTCCAGTGGTGT
TaF3H-B2 ACTCACTGGAATAAATCATAT-TATG-----TGAACTCATAGGATTTGAGAGACTTGTG--ATCTCATTTCCATA---CAAGTTTCTATT---T
401
TaF3H-B1 GTGTGCTTGATGTGTGTGTGTGCGTATATGGATCGATCGATACGGTGGATGGATGCAATGGGTGCGGCCGGTGTAGTTCGCGACCTAACACGAGTGC
TaF3H-B2 CTATGATAATGGTATAT-----CGTAT--GAACCAAAAGAACG--CTAATTTGACACTCGTGCATG--CATTTTCTGAATTTATTTCA-----
501
TaF3H-B1 CCGAGGGCGACTTCCTTGGTTAGTTGCGTGCACACGCGGACTTGCAGGTGCGGTCTGCCCCATCTTCCAAAGTATATACAAATGCCCTCTTCCCG
TaF3H-B2 -----GACTTTCT--GGTGTGTTTCAATCA-GTGGAGACAT-----CT--CCCTAATTTAAAGATGTTGTG--CCGGTTCAGTATTTC--
601
TaF3H-B1 GCCGTATATATCCCGGTGCGTACAACGTCAGAAAAACCAACCCAAACGGCCGAGCCTTTCATCAAGGAACAAACCATCATACGAGACAGACGCGCGCC
TaF3H-B2 -----AAAGGTACTCAGCGTTTATAGGC---ATCTCCCTAATTTAAATATATGTACCCCTCTTTC---ATCTAATCATACGAGACAGAGCTA--CA
701
TaF3H-B1 GCGACACAAGCGGACGATCCCGGAGTGCAGATCG
TaF3H-B2 GATCGATAACTGGTAGATAGCG
```

3. Section S3:CpG island prediction in promoters of *TaCHI* and *TaF3H* genes made with MethPrimer 2.0

Sequence Name: **Triticum aestivum chalcone flavanone isomerase (Chi-A1)**

Sequence Length: 1652 bp

Promoter Sequence: 1-754 bp



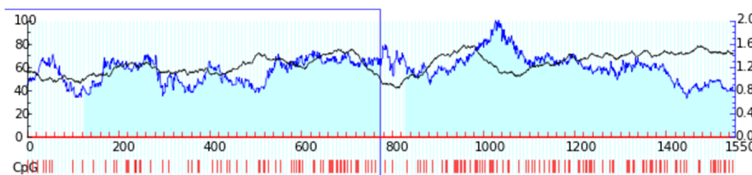
CpG Island Prediction

No.	Island size	Island start	Island end	GC% percent	O/E ratio
Island 1	346	284	629	50.0	0.6
Island 2	258	632	889	50.0	0.6

Sequence Name: **Triticum aestivum chalcone flavanone isomerase (Chi-B1)**

Sequence Length: 1550 bp

Promoter Sequence: 1-636 bp



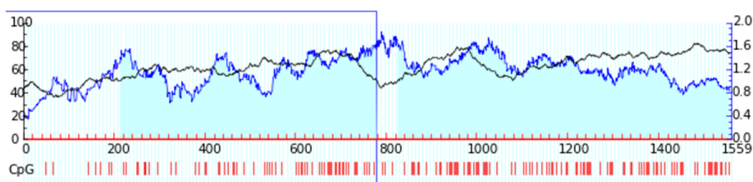
CpG Island Prediction

No.	Island size	Island start	Island end	GC% percent	O/E ratio
Island 1	645	128	772	50.0	0.6
Island 2	719	831	1549	50.0	0.6

Sequence Name: **Triticum aestivum chalcone flavanone isomerase (Chi-D1)**

Sequence Length: 1559 bp

Promoter Sequence: 1-645 bp



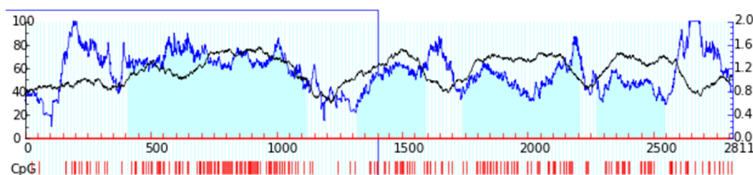
CpG Island Prediction

No.	Island size	Island start	Island end	GC% percent	O/E ratio
Island 1	564	215	778	50.0	0.6
Island 2	733	826	1558	50.0	0.6

Sequence Name: **Triticum aestivum flavanone 3-hydroxylase (F3H-B1)**

Sequence Length: 2811 bp

Promoter Sequence: 1-731 bp



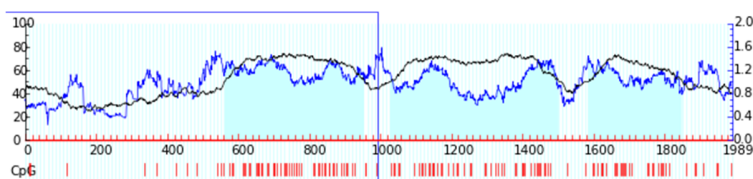
CpG Island Prediction

No.	Island size	Island start	Island end	GC% percent	O/E ratio
Island 1	711	409	1119	50.0	0.6
Island 2	271	1324	1594	50.0	0.6
Island 3	462	1746	2207	50.0	0.6
Island 4	273	2273	2545	50.0	0.6

Sequence Name: **Triticum aestivum flavanone 3-hydroxylase (F3H-B2)**

Sequence Length: 1989 bp

Promoter Sequence: 1-577 bp



CpG Island Prediction

No.	Island size	Island start	Island end	GC% percent	O/E ratio
Island 1	393	562	954	50.0	0.6
Island 2	474	1029	1502	50.0	0.6
Island 3	264	1586	1849	50.0	0.6

Roots *TaChi-A1*

1102030405060708090100110120130

Chi-R1-r-1

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-2

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-3

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-4

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-8

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-7

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-6

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-5

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-9

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1-r-10

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Chi-R1

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

Consensus

AAAGGATTTGTTAGTTAGTATAGCATATTTAAAGGTTGCTGATTTATTTGATGATAAATATTGGAGTTTTATATTTATAGGCGATTTTTTATATTTGGTTGAGTATGGGTGAG

131140150160170180190200210220230240250261

Chi-R1-r-1

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-2

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-3

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-4

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-8

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-7

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-6

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-5

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-9

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1-r-10

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Chi-R1

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

Consensus

TTTAGTTTATATTTTTTGAAATATGTAGTTTATTTTGGTGATATGTTGAGTTTTTTTGTAGATGGTAGATTTGATTTGGTTATAGTATGAGGTGTTTGTGGGTTTGTGTGTA

261270280290300310320330340350360370380390

Chi-R1-r-1

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-2

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-3

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-4

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-8

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-7

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-6

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-5

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-9

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1-r-10

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Chi-R1

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

Consensus

GTTGARATGAGTTGTTGTGATTTGTTGTAAATTTGGTGTGGTATGTTGTTGTTTAAATGTTGTTTTTATATATATTAATATGTTTATAGATGCTTTAAATATATTTTGTATATA

391400410420430440450460470480490500510520

Chi-R1-r-1

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-2

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-3

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-4

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-8

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-7

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-6

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-5

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-9

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1-r-10

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Chi-R1

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

Consensus

GGTARAGTTTATTTTTGTTATGCTGAGGTAAAGAAATAGATAGATTATGGTTGGTATATATGATTATGGGAGAGTTATGGGTTTATATAGTTGTGGGGTGTATATAGAGAGGGGT

521530540550560570580590600610620630640651

Chi-R1-r-1

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-2

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-3

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-4

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-8

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-7

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-6

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-5

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-9

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1-r-10

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Chi-R1

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

Consensus

ATATATATTTAGTTGATTTATTTGTGTGTATGTTTAAATAGATGATTTATTTGTTGGGTGGTGTGTTTTATATATTAATATAGTGTTTGTGTATGTGTGTGTTTTGGGAGTTTT

651660670680690700710720730

Chi-R1-r-1

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-2

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-3

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-4

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-8

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-7

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-6

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-5

TGTGTATATTTAGATATGGTGTGTGTTTGTAGTTTGAAGTTGATGGTGTGTTTTT-TGTGTTGTTGTTGTTGGTGG

Chi-R1-r-9

CCGCGCATCATGGAGCATGTCGCGGCTGTGGTGTGAGGTCGATGGTGTGTTTTTTCGTCGTTGTTGTTGTTGGTGG

Chi-R1-r-10

CCGCGCATCATGGAGCATGTCGCGGCTGTGGTGTGAGGTCGATGGTGTGTTTTTTCGTCGTTGTTGTTGTTGGTGG

Chi-R1

CCGCGCATCATGGAGCATGTCGCGGCTGTGGTGTGAGGTCGATGGTGTGTTTTTTCGTCGTTGTTGTTGTTGGTGG

Consensus

CCGCGCATCATGGAGCATGTCGCGGCTGTGGTGTGAGGTCGATGGTGTGTTTTTTCGTCGTTGTTGTTGTTGGTGG

Coleoptiles *TaChi-B1*

[illegible]

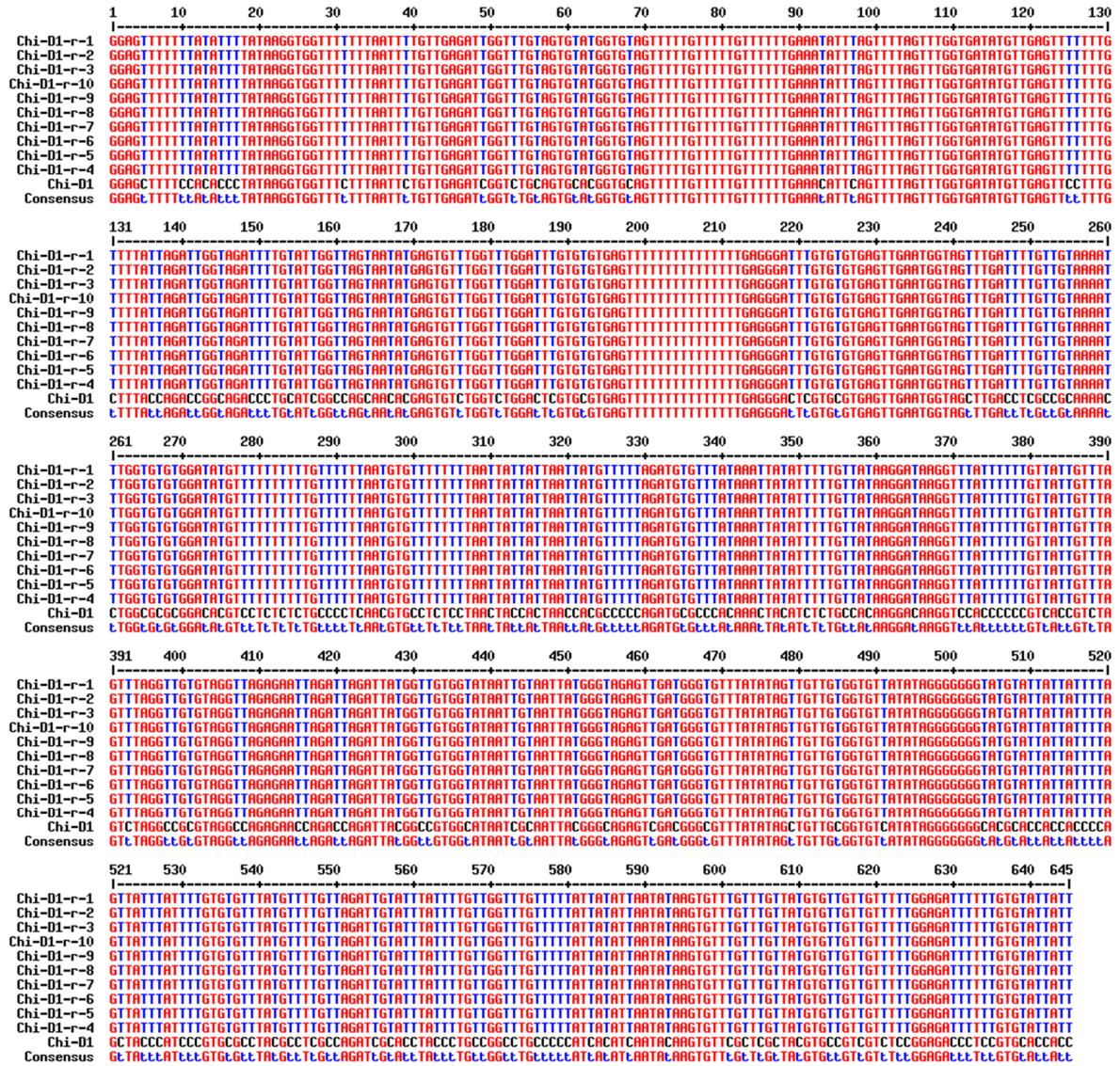
Roots *TaChi-B1*

Figure 1. Consensus sequence of the 100 bp DNA fragments. The figure displays a grid of DNA sequences for 100 bp fragments, organized into 10 rows (Chi-B1-r-1 to Chi-B1-r-10) and 10 columns (1 to 100). Each row represents a different fragment, and each column represents a specific position within the 100 bp fragment. The sequences are shown in a color-coded format, with each nucleotide (A, T, C, G) represented by a unique color. The consensus sequence for each fragment is indicated by a horizontal line at the bottom of each column, showing the most frequent nucleotide at that position. The consensus sequence for the entire 100 bp fragment is shown at the bottom of the grid.

Coleoptiles *TaChi-D1*

Figure 1. Schematic representation of the genomic organization of the *hTERT* gene. The gene is located on chromosome 5p15.3 and consists of 11 exons and 10 introns. The exons are numbered 1 to 11, and the introns are numbered 1 to 10. The gene structure is shown as a series of boxes representing exons and lines representing introns. The scale bar at the top indicates the position of the gene on the chromosome, with markers at 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, and 130. The scale bar at the bottom indicates the position of the gene on the chromosome, with markers at 261, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, and 390. The gene structure is shown as a series of boxes representing exons and lines representing introns. The scale bar at the top indicates the position of the gene on the chromosome, with markers at 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, and 130. The scale bar at the bottom indicates the position of the gene on the chromosome, with markers at 261, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, and 390.

Roots *TaChi-D1*



Coleoptiles *TaF3H-B1*

[illegible]

Roots *TaF3H-B1*

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
F3H-B1-r-1	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-2	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-3	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-8	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-4	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-5	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-6	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-7	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-9	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1-r-10	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
F3H-B1	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
Consensus	TTTATAGGATATGGAARATATGATGCTATGATGATATGAGTTTACGATATTTGGGTGAATTAATTTGGTGTGGATGGTTAARGGGATTTTGATATCCCTAGTCCCTARGGTTCAARATCTGGGTTTGAG													
	131	140	150	160	170	180	190	200	210	220	230	240	250	261
F3H-B1-r-1	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-2	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-3	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-8	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-4	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-5	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-6	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-7	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-9	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1-r-10	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
F3H-B1	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
Consensus	TTTATCTCGGATATTTCCAGGATTTTCAGCATGATGTTATTAGTAGGAGAGAGCGTTTCGTCGATARCAGAGTTGTCATGATGATTCGTAARATTCARGATATATGTCGATTCCGGTCTTCGGAGG													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
F3H-B1-r-1	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-2	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-3	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-8	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-4	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-5	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-6	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-7	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-9	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1-r-10	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
F3H-B1	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
Consensus	TGCTCATAGGGGATAGGGGTGCGGTGTCGCTTTATAGGAGTGAAGTATGACGATATATGAGGCCCTTGATCTGGATGCTGTGTAAARAAAGGTTTAGATTTGGTGGGTATATGTTGGGTTTAG													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
F3H-B1-r-1	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-2	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-3	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-8	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-4	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-5	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-6	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-7	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-9	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1-r-10	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
F3H-B1	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
Consensus	TGGTGTGTGTGTTGATGTGTGTGTTGTGTGTATATGATGATGATGATGGTGGATGGATGATGGGGTGGGTTGGTATGTGCGTATTAATATGAGTGTGTGAGGGGATTTTTGGGTAG													
	521	530	540	550	560	570	580	590	600	610	620	630	640	651
F3H-B1-r-1	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGCTC													
F3H-B1-r-2	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-3	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-8	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-4	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-5	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-6	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-7	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-9	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1-r-10	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
F3H-B1	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
Consensus	TGTGTGCGCATGTGTGACTGTAGGGTCGCGTTGCCCTTATCTTTCARATGATGATATATATGCTCTCTTTTGGTCGATATATCTGTGTGCGATACACGTTAGAAAATATAAATTAACGGTC													
	651	660	670	680	690	700	710	720	730	740	750	760	766	
F3H-B1-r-1	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCGA													
F3H-B1-r-2	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCGA													
F3H-B1-r-3	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCGA													
F3H-B1-r-8	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCGA													
F3H-B1-r-4	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCTGA													
F3H-B1-r-5	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCTGA													
F3H-B1-r-6	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCTGA													
F3H-B1-r-7	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCTGA													
F3H-B1-r-9	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCGA													
F3H-B1-r-10	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCGA													
F3H-B1	GAGTGTGTTTATAGGGAATAAATATATATGAGATAGATGTTGGTGTGATATAGTGGATGATTTTGGAGTGGATGATGTGGTGTGTTGGTGAATACAGAGAGCTTCTCCCGA													
Consensus	GAGGCTTTTATCAGAGGAACACACCTATACAGAGACAGCGCCCGCCAGACAGCGGACGATCCCGGAGTCGATATCCGGTCGCTGAGCAGCAGAGAGCTTCTCCCGA													
	GAGGCTTTTATCAGAGGAACACCTATACAGAGACAGCGCCCGCCAGACAGCGGACGATCCCGGAGTCGATATCCGGTCGCTGAGCAGCAGAGAGCTTCTCCCGA													
	GAGGCTTTTATCAGAGGAACACCTATACAGAGACAGCGCCCGCCAGACAGCGGACGATCCCGGAGTCGATATCCGGTCGCTGAGCAGCAGAGAGCTTCTCCCGA													

Coleoptiles *TaF3H-B2*

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
F3h-B2-c-1	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-2	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-3	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-4	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-5	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-6	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-7	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-8	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-9	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2-c-10	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
F3h-B2	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
Consensus	ATT	TGT	AAT	GAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG	TAG
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
F3h-B2-c-1	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-2	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-3	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-4	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-5	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-6	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-7	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-8	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-9	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2-c-10	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
F3h-B2	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
Consensus	AGG	AAT	TTT	TTA	AAAG	TTT	TTA	TAAT	TAT	AGG	AAT	GAAT	TTT	TAT
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
F3h-B2-c-1	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-2	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-3	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-4	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-5	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-6	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-7	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-8	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-9	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2-c-10	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
F3h-B2	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
Consensus	TGT	GAAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT	TTT	TAG	GAT
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
F3h-B2-c-1	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-2	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-3	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-4	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-5	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-6	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-7	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-8	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-9	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2-c-10	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
F3h-B2	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
Consensus	ATT	TAG	AT	TTT	TGG	TAT	TTT	TAG	TAT	TTT	TGG	TAT	TTT	TAG
	521	530	540	550	560	570	577							
F3h-B2-c-1	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-2	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-3	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-4	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-5	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-6	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-7	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-8	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-9	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2-c-10	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
F3h-B2	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT
Consensus	TTT	TTT	TAT	TAT	AT	TAT	GAT	AT	AT	TAT	GAT	AT	AT	TAT

Roots *TaF3H-B2*

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
F3h-B2-r-1	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-2	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-3	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-4	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-10	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-9	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-8	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-7	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-6	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-5	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
Consensus	ATT	TG	TAA	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
F3h-B2-r-1	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-2	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-3	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-4	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-10	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-9	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-8	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-7	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-6	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2-r-5	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
F3h-B2	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
Consensus	AGG	AA	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT	TT
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
F3h-B2-r-1	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-2	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-3	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-4	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-10	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-9	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-8	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-7	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-6	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-5	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
Consensus	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
F3h-B2-r-1	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-2	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-3	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-4	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-10	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-9	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-8	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-7	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-6	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2-r-5	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
F3h-B2	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
Consensus	ATT	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG	TG
	521	530	540	550	560	570	577							
F3h-B2-r-1	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-2	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-3	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-4	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-10	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-9	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-8	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-7	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-6	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2-r-5	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
F3h-B2	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
Consensus	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT

5. Section S5: Results of the signal scan search request in promoters of *TaCHI* and *TaF3H* genes made with New PLACE and PlantPAN 3.0

The diagrams show the arrangement of elements in the promoter, the tables contain a description of the elements. Elements in the tables are highlighted in colors: light-dependent activation (yellow), TF-dependent elements (red), tissue- specific elements (green), stress-specific elements (blue). Sequences that correspond to methylation labels are highlighted in bold.

(+) = Current Strand
(-) = Opposite Strand

>TaChi-A1

AAAAGAATTGCCAGTTAAGCACAAGATAATTCCAAAAGGTTGTGATTTTACTCGTAGTACAAACAATTGGAGCTTTTCCA
CACCTTACAAGGTGATTTCTTTAATATCGGTCTGCAGTGCACGGTGCAGTTTATGTTTATATTCTTTTTTGAACATGCA
GTTTTAGTTTGGTGATATGTTGAGTTCCTTTTCTTTGCCAGACCGGCAGACCTGCATCGGCCAACAGCAGAGCGTCTCG
TCTGGGCTCCTGCGTGAGTTGAATGGTAGCTCGCTTGACCTCGCCGCAAAACCTGGCGCGCGGCCACGTCCGTCTCTCAA
CGTGCTCTCCTAACTACCACTAACCACGCCCCCAGACGCGCCCAAACTACATCTTTGCCACAAGGCACAAGTTCACCC
CCCGTCTACCGGTAGGCCAAAGAAGTACAGGATTACGGCCGTGGCATAATCGCAATTACGGCGAGAGTCCACGGGCGTT
TATATAGCCGCTGGGGTGTCTATATAGGAGAGAGGCCACCACCCAGCTGACCATCCCGTGCAGCCACGCTCAACAGATC
GCACCTACCCCTGCCGGGCCGCTGCCCCATCACATCAATACAAGCGTTCTGCTCGCTACGTGCCGCTCGTCTCCGGAGACC
CTCCGCGCACACCAGAGACCATGGCCGTGTCCGAGCTCGAGGTCGACGGCGTCTCTTCCCGCCGCTCGCCGCCGCGCGG

AAAAGAATTGCCAGTTAAGCACAAGATAATTCCAAAAGGTTGTGATTTTACTCGTAGTACAAACAATTGGAGCTTTTCCAACCTTACAAGGTGATTTCC 100
TTTTCTTAACGGTCAATTCTGTCTCTATTAAGGTTTCCAACTATAAATGAGCATCATGTTTGTAACTCGAAAAGGTGGGATGTTCCACTAAAG
TTTTAATATCGTCTGCAGTGCACGGTGCAGTTTATGTTTATATTCTTTTTGAAAATGCACTGAGTTTATGTTTGGTGATATGTTGAGTTCTTTCTTTTGC 200
AAATTTATAGCCAGACGTCACTGTCACGTCCTCAAAATCAAAATATAAGAAAACTTTGTACGTCAAAATCAACCACTATACAACCTCAAGGAAAGGAAACG
CAGACCGGCAGACCTGCATCGGCCAACAGCAGAGCGTCTCGTCTGGGCTCTGCGTGAGTTGAATGGTAGCTCGCTTGACCTCGCCGCAAAACCTGGC 300
GTCTGGCGCTCTGGGACGTAGCCGTTGTCTGCTCGCAGAGCAGACCCGAGGACGCACTCAACTTACATCGAGCGAAGTGGAGCGGCTTTGGACCGC
GCGCGGCACGTCCGTCTCTCAACGTGCTCTCTTAACCTACCACTAACTACGCGCCAGAGCGCGCCACAACTACATCTTTGCCACAAGGCACAAGTT 400
CGCGCGGTGCAAGGAGGAGTTGCACGGAGAGGATTGATGGTGATTGTTGCGGGGTCTGCGCGGTGTTTGTATGTAAGAACGGTGTTCGGTGTTCAA
CACCCCGCTCTACGCGTAGGCCAAAGAAGTACAGCAGATTACGGCGTGGCAATATCGCAATTACGGGAGAGTCCACGGGCGTTTATATAGCGCTGG 500
GTGGGGGCGAGATGCGCATCCGGTTCTTGAATCTGCTCTAATGCCGGCACCGTATTAGCGTTAATGCCGCTCTCAGGTGCCCGCAATATATCGCGCACC
GGTGTCTATATAGGAGAGGGCACCACCACTCAGCTGACCATCCGTGCGCCACGCTCAACAGATCGCACCTACCTGCGGGCGGCTGCCCCATC 600
CCACAGTATATCTCTCCCGTGTGGTGGGGTCACTGGTAGGGCAGCGGGTGGCGAGTTGTCTAGCTGGATGGACGGCCCGGCGGACGGGGGTAG
ACATCAATACAAGCGTTCTGCTCGCTACGTGCGCTCTCCGGAGACCTCCGCGACACCAGAGACCATGGCCGTGTCGAGCTCGAGGTCGACGGCGT 700
TGTAGTTATGTTTCGCAAGCGAGCGATGACGGCAGCAGAGGCTCTGGGAGGCGCTGGTGGCTCTGGTACCGGCACAGGCTCGAGCTCCAGCTGCGCA
CGTCTTCCCGCGCTCGCCGCCGCGCGG 800
GCAGAAAGGCGCGAGCGGGCGGGCGGC

TF_motif_seq_0246:	TF_motif_seq_0256:	TF_motif_seq_0257:
TF_motif_seq_0266:	TF_motif_seq_0312:	TF_motif_seq_0316:
TF_motif_seq_0327:	TF_motif_seq_0356:	TF_motif_seq_0422:
TF_motif_seq_0430:	TF_motif_seq_0446:	TF_motif_seq_0508:
TF_motif_seq_0002:	TF_motif_seq_0025:	TF_motif_seq_0037:
TF_motif_seq_0039:	TF_motif_seq_0068:	TF_motif_seq_0070:
TF_motif_seq_0238:	TF_motif_seq_0259:	TF_motif_seq_0274:
TF_motif_seq_0294:	TF_motif_seq_0297:	TF_motif_seq_0309:
TF_motif_seq_0310:	TF_motif_seq_0321:	TF_motif_seq_0333:
TF_motif_seq_0334:	TF_motif_seq_0343:	TF_motif_seq_0350:
TF_motif_seq_0353:	TF_motif_seq_0358:	TF_motif_seq_0360:
TF_motif_seq_0372:	TF_motif_seq_0406:	TF_motif_seq_0425:
TF_motif_seq_0427:	TF_motif_seq_0429:	TF_motif_seq_0436:
TF_motif_seq_0440:	TF_motif_seq_0454:	TF_motif_seq_0458:
TF_motif_seq_0488:	TF_motif_seq_0503:	

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
DOFCOREZM	2 (+) AAAG		S000265
EECCRAH1	5 (+) GANTTNC		S000494
CAATBOX1	7 (-) CAAT		S000028
MYB2AT	13 (-) TAACTG		S000177

MYB2CONSENSUSAT	13 (-)	YAACKG	S000409
MYBCORE	13 (+)	CNGTTR	S000176
GATABOX	26 (+)	GATA	S000039
GT1CONSENSUS	26 (+)	GRWAAW	S000198
IBOXCORE	26 (+)	GATAA	S000199
PYRIMIDINEBOXOSRAMY1A	35 (-)	CCTTTT	S000259
DOFCOREZM	36 (+)	AAAG	S000265
GTGANTG10	43 (+)	GTGA	S000378
ARR1AT	44 (+)	NGATT	S000454
CACTFTPPCA1	50 (+)	YACT	S000449
CACTFTPPCA1	57 (-)	YACT	S000449
CURECORECR	58 (-)	GTAC	S000493
CURECORECR	58 (+)	GTAC	S000493
EBOXBNNA	65 (-)	CANNTG	S000144
MYCCONSUSAT	65 (-)	CANNTG	S000407
CAATBOX1	65 (+)	CAAT	S000028
EBOXBNNA	65 (+)	CANNTG	S000144
MYCCONSUSAT	65 (+)	CANNTG	S000407
CAATBOX1	67 (-)	CAAT	S000028
CCAATBOX1	67 (-)	CCAAT	S000030
DOFCOREZM	74 (-)	AAAG	S000265
GT1CONSENSUS	75 (-)	GRWAAW	S000198
GTGANTG10	93 (+)	GTGA	S000378
ARR1AT	94 (+)	NGATT	S000454
POLLEN1LELAT52	97 (-)	AGAAA	S000245
DOFCOREZM	100 (-)	AAAG	S000265
TAAAGSTKST1	100 (-)	TAAAG	S000387
ROOTMOTIFTAPOX1	104 (-)	ATATT	S000098
GATABOX	106 (-)	GATA	S000039
CACTFTPPCA1	117 (-)	YACT	S000449
ROOTMOTIFTAPOX1	141 (+)	ATATT	S000098
-10PEHVPSBD	142 (+)	TATTCT	S000392
DOFCOREZM	146 (-)	AAAG	S000265
RYREPEATBNNA	157 (+)	CATGCA	S000264
MYBPLANT	169 (-)	MACCWAMC	S000167
GTGANTG10	174 (+)	GTGA	S000378
GATABOX	176 (+)	GATA	S000039
RAV1AAT	180 (-)	CAACA	S000314
EECCRCAH1	184 (+)	GANTTNC	S000494
DOFCOREZM	190 (-)	AAAG	S000265
DOFCOREZM	195 (-)	AAAG	S000265
INTRONLOWER	214 (-)	TGCAGG	S000086
MYBCORE	225 (-)	CNGTTR	S000176
RAV1AAT	225 (+)	CAACA	S000314
RHERPATEXPA7	230 (+)	KCACGW	S000512
SURECOREATSULTR11	238 (-)	GAGAC	S000499
SITEIIATCYTC	246 (+)	TGGGCY	S000474
GTGANTG10	257 (+)	GTGA	S000378
CAREOSREP1	259 (-)	CAACTC	S000421
S1FBOXSORPS1L21	266 (+)	ATGGTA	S000223
ELRECOREPCR1	278 (+)	TTGACC	S000142
WBOXATNPR1	278 (+)	TTGAC	S000390
QELEMENTZM13	279 (-)	AGGTCA	S000254
WRKY71OS	279 (+)	TGAC	S000447
WBOXNTERF3	279 (+)	TGACY	S000457
CGCGBOXAT	299 (-)	VCGCGB	S000501
CGCGBOXAT	299 (+)	VCGCGB	S000501
CGCGBOXAT	301 (-)	VCGCGB	S000501

CGCGBBOXAT	301 (+)	VCGCGB	S000501
ABREOSRAB21	305 (-)	ACGTSSSC	S000012
BOXIIPCCHS	306 (-)	ACGTGGC	S000229
ACGTABREMOTIFA2OSEM	306 (-)	ACGTGKC	S000394
SORLIP1AT	306 (+)	GCCAC	S000482
ABRELATERD1	308 (-)	ACGTG	S000414
ACGTATERD1	309 (-)	ACGT	S000415
ACGTATERD1	309 (+)	ACGT	S000415
PALBOXAPC	313 (+)	CCGTCC	S000137
BP5OSWX	322 (+)	CAACGTG	S000436
T/GBOXATPIN2	323 (+)	AACGTG	S000458
ABRERATCAL	323 (+)	MACGYGB	S000507
ACGTATERD1	324 (-)	ACGT	S000415
RHERPATEXPA7	324 (-)	KCACGW	S000512
ABRELATERD1	324 (+)	ACGTG	S000414
ACGTATERD1	324 (+)	ACGT	S000415
CACTFTPPCA1	343 (+)	YACT	S000449
SV40COREENHAN	345 (-)	GTGGWWHG	S000123
MYBATRD22	345 (+)	CTAACCA	S000175
MYB1AT	346 (+)	WAACCA	S000408
CGCGBBOXAT	361 (-)	VCGCGB	S000501
CGCGBBOXAT	361 (+)	VCGCGB	S000501
NODCON1GM	378 (-)	AAAGAT	S000461
OSE1ROOTNODULE	378 (-)	AAAGAT	S000467
DOFCOREZM	380 (-)	AAAG	S000265
SORLIP1AT	384 (+)	GCCAC	S000482
GTGANTG10	400 (-)	GTGA	S000378
CGCGBBOXAT	413 (-)	VCGCGB	S000501
CGCGBBOXAT	413 (+)	VCGCGB	S000501
DOFCOREZM	424 (+)	AAAG	S000265
PRECONSCRHSP70A	437 (-)	SCGAYNRNNNNNNNNNNNNNNNNHND	S000506
ARR1AT	437 (+)	NGATT	S000454
SORLIP1AT	448 (-)	GCCAC	S000482
ARR1AT	455 (-)	NGATT	S000454
CAATBOX1	460 (+)	CAAT	S000028
TATAPVTRNALEU	485 (+)	TTTATATA	S000340
TATABOX4	486 (-)	TATATAA	S000111
BIHD1OS	503 (+)	TGTCA	S000498
WRKY71OS	504 (-)	TGAC	S000447
EBOXBNNAPA	531 (-)	CANNTG	S000144
MYCCONSENSUSAT	531 (-)	CANNTG	S000407
EBOXBNNAPA	531 (+)	CANNTG	S000144
MYCCONSENSUSAT	531 (+)	CANNTG	S000407
WBOXNTCHN48	534 (+)	CTGACY	S000508
WRKY71OS	535 (+)	TGAC	S000447
WBOXNTERF3	535 (+)	TGACY	S000457
BOXLCOREDPCAL	537 (+)	ACCWWCC	S000492
MYBCORE	559 (-)	CNGTTR	S000176
RAV1AAT	559 (+)	CAACA	S000314
MYBPLANT	569 (+)	MACCWAMC	S000167
BOXLCOREDPCAL	570 (+)	ACCWWCC	S000492
MYBPZM	571 (+)	CCWACC	S000179
SORLIP2AT	582 (+)	GGGCC	S000483
GTGANTG10	599 (-)	GTGA	S000378
CAATBOX1	605 (+)	CAAT	S000028
ACGTATERD1	626 (-)	ACGT	S000415
RHERPATEXPA7	626 (-)	KCACGW	S000512
ABRELATERD1	626 (+)	ACGTG	S000414
ACGTATERD1	626 (+)	ACGT	S000415

HEXAMERATH4	631 (+)	CCGTCG	S000146
CGACGOSAMY3	632 (-)	CGACG	S000205
SURECOREATSULTR11	636 (-)	GAGAC	S000499
SURECOREATSULTR11	643 (+)	GAGAC	S000499
CGCGBOXAT	651 (-)	VCGCGB	S000501
CGCGBOXAT	651 (+)	VCGCGB	S000501
DRE1COREZMRAB17	660 (+)	ACCGAGA	S000401
SURECOREATSULTR11	663 (+)	GAGAC	S000499
CRTDREHVCBF2	690 (-)	GTCGAC	S000411
CBFHV	690 (-)	RYCGAC	S000497
CRTDREHVCBF2	690 (+)	GTCGAC	S000411
CBFHV	690 (+)	RYCGAC	S000497
HEXAMERATH4	692 (-)	CCGTCCG	S000146
CGACGOSAMY3	692 (+)	CGACG	S000205
CGACGOSAMY3	698 (-)	CGACG	S000205
//			

>TaChi-B1

CGGACCCAAACGGACAAAAAGCGAACAAAATCACCGTCCGTTTGGGTCGGCACCGTTGGAGTTGCTCTAATCCTTATTAAT
TCATGCCTGAGGTAGGCGGAACATTACTCTTGCCCTACCCCGTAGGGTGGTTTCTTTTGGATCGGTGTGCTTTGGTGACAT
GTTGAGCCGTTGTGTCTGGTGTGGGCTCGTGCGTGAGTTGAATGGTAGCTTGACGTCGCCGCAAAACCTGGCGCGCGGCCA
CGTCCGTCCTCTCTTTGCCCTCAACGTGCCTCTCCCAACTACCCTAACACGCCCCCATATGCGCACACAACTACATC
TTTGCCACAAGGCACAAGGTCCACCTCCGTTACCGTCTAGTCTAGGCCGCGTAGGCCAGAGAACCAGACCAGATTACAGC
CGTGGCACAATCGCAATTACGGGCAGAGTGTACGGGCGTTTATATAGCTGTTGCGGTGTCTATAGGGGGGGGCACGCACCA
CCACCCAGCTACCCATCCCGTGCGCCACGCCCTCGCCAGATCGCACCTACCTGCGGCCCTGCCCGCGTCCCATCAATAC
AAGTGTTTGTCTCGCTACGTGCCGTCCGTCTCTCCGAGACCTCCATCCATCCATCCGGCGATATACC

CGGACCCAAACGGACAAAAAGCGAACAAAATCACCGTCCGTTTGGGTCGGCACCGTTGGAGTTGCTCTAATCCTTATTAATT
CATGCCTGAGGTAGGCGGAACATTACTCTTGCCCTACCCCGTAGGGTGGTTTCTTTTGGATCGGTGTGCTTTGGTGACAT
GTTGAGCCGTTGTGTCTGGTGTGGGCTCGTGCGTGAGTTGAATGGTAGCTTGACGTCGCCGCAAAACCTGGCGCGCGGCCA
CGTCCGTCCTCTCTTTGCCCTCAACGTGCCTCTCCCAACTACCCTAACACGCCCCCATATGCGCACACAACTACATC
TTTGCCACAAGGCACAAGGTCCACCTCCGTTACCGTCTAGTCTAGGCCGCGTAGGCCAGAGAACCAGACCAGATTACAGC
CGTGGCACAATCGCAATTACGGGCAGAGTGTACGGGCGTTTATATAGCTGTTGCGGTGTCTATAGGGGGGGGCACGCACCA
CCACCCAGCTACCCATCCCGTGCGCCACGCCCTCGCCAGATCGCACCTACCTGCGGCCCTGCCCGCGTCCCATCAATAC
AAGTGTTTGTCTCGCTACGTGCCGTCCGTCTCTCCGAGACCTCCATCCATCCATCCGGCGATATACC

CGGACCCAAACGGACAAAAAGCGAACAAAATCACCGTCCGTTTGGGTCGGCACCGTTGGAGTTGCTCTAATCCTTATTAATT
CATGCCTGAGGTAGGCGGAACATTACTCTTGCCCTACCCCGTAGGGTGGTTTCTTTTGGATCGGTGTGCTTTGGTGACAT
GTTGAGCCGTTGTGTCTGGTGTGGGCTCGTGCGTGAGTTGAATGGTAGCTTGACGTCGCCGCAAAACCTGGCGCGCGGCCA
CGTCCGTCCTCTCTTTGCCCTCAACGTGCCTCTCCCAACTACCCTAACACGCCCCCATATGCGCACACAACTACATC
TTTGCCACAAGGCACAAGGTCCACCTCCGTTACCGTCTAGTCTAGGCCGCGTAGGCCAGAGAACCAGACCAGATTACAGC
CGTGGCACAATCGCAATTACGGGCAGAGTGTACGGGCGTTTATATAGCTGTTGCGGTGTCTATAGGGGGGGGCACGCACCA
CCACCCAGCTACCCATCCCGTGCGCCACGCCCTCGCCAGATCGCACCTACCTGCGGCCCTGCCCGCGTCCCATCAATAC
AAGTGTTTGTCTCGCTACGTGCCGTCCGTCTCTCCGAGACCTCCATCCATCCATCCGGCGATATACC

AACATTACTCTTGCCCTACCCGTTAGGGTGGTTTCTTTTGGATCGGTGTGCTTTGGTGACATGTTGAGCCGTTGTCTGGTGTGGGCT
CGTGCCTGAGT
TTGTAATGAGAACGGATGGCGCATCCACCAAGAACTCTAGCCACACGAAACCTGTACAACTCGGCAACACAGACACACCCGAGCAGGCATCA

TGAATGGTAGCTTGAAGTCGCGCAAAACCTGGCGCGCGCCACGTCCGTCCTCTCTTGCCCTCAACGTGCTCTCCCAACTACCACTAACACGCCCC
ACTTACCATCGAATCGAGCGCGCTTTGGACCGCGCGCGGTGCAAGCAGGAGAGAAACGGGAGTTGACGAGAGAGGGTTGATGGTGATTGGTGGCGG

CCATATGCGCACACAACTACATCTTTGCCACAAGGCACAAGGTCCACCTCCGTTACCGTCTAGTCTAGGCCGCGTAGGCCAGAGAACCAGACCAGATT
GGTATACCGGTGTGTTTGTAGTGAAGACGGTGTTCCGTGTTCCAGGTGGGAGGCAATGGCAGATCAGATCCCGCGCATCCGGTCTCTTGGTCTGGTCTAA

ACAGCGTGGCACAATCGCAATTACGGGCAGAGTGTACGGGCGTTTATATAGCTGTTGCGGTGTCTATAGGGGGGGGCACGCACCAACCACCCAGCTAC
TTGTCGGCACCGTGTTAGCGTTAATGCCGCTCTCACATGCCGCAATATATCGACAACGCCACAGTATATCCCGCCGTGCGTGGTGGGGTTCGATGG

CATCCCGTGGCGCCACGCTCGCCAGATCGCACCTACCTGCGGCCCTGCCCGCTCCCATCAATACAAGTGTTTGTCTGCTACGTGCCGTCCGTCGTCT
GTAGGCAACCGCGGTGCGGAGCGGTCTAGCTGGATGGGACGGCGGACGGGGCAGGGTAGTTATGTTCAACAACGAGCGATGCACGGCAGGCAGAGA

CCGAGACCTCCATCCATCCATCCGCGATATACC
GGCCCTCGGGAGGTAGGTAGTAGCGCGTATATGG

TF_motif_seq_0246:		TF_motif_seq_0256:		TF_motif_seq_0257:	
TF_motif_seq_0266:		TF_motif_seq_0292:		TF_motif_seq_0312:	
TF_motif_seq_0316:		TF_motif_seq_0327:		TF_motif_seq_0347:	
TF_motif_seq_0422:		TF_motif_seq_0431:		TF_motif_seq_0446:	
TF_motif_seq_0508:		TF_motif_seq_0002:		TF_motif_seq_0025:	
TF_motif_seq_0031:		TF_motif_seq_0037:		TF_motif_seq_0039:	
TF_motif_seq_0068:		TF_motif_seq_0121:		TF_motif_seq_0132:	
TF_motif_seq_0238:		TF_motif_seq_0259:		TF_motif_seq_0274:	
TF_motif_seq_0283:		TF_motif_seq_0297:		TF_motif_seq_0310:	
TF_motif_seq_0324:		TF_motif_seq_0334:		TF_motif_seq_0344:	
TF_motif_seq_0353:		TF_motif_seq_0358:		TF_motif_seq_0360:	
TF_motif_seq_0372:		TF_motif_seq_0380:		TF_motif_seq_0406:	
TF_motif_seq_0425:		TF_motif_seq_0427:		TF_motif_seq_0429:	
TF_motif_seq_0440:		TF_motif_seq_0454:		TF_motif_seq_0458:	
TF_motif_seq_0488:		TF_motif_seq_0503:			

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
MYBCOREATCYCB1	9 (+) AACGG		S000502
DOFCOREZM	18 (+) AAAG		S000265
ARR1AT	29 (-) NGATT		S000454

GTGANTG10	31 (-) GTGA	S000378
PALBOXAPC	34 (+) CCGTCC	S000137
MYBCOREATCYCB1	38 (-) AACGG	S000502
LTRECOREATCOR15	46 (-) CCGAC	S000153
DRECRTCOREAT	46 (-) RCCGAC	S000418
CBFHV	46 (-) RYCGAC	S000497
MYB2CONSENSUSAT	53 (-) YAACKG	S000409
MYBCOREATCYCB1	53 (-) AACGG	S000502
MYBCORE	53 (+) CNGTTR	S000176
CAREOSREP1	59 (-) CAACTC	S000421
EECCRCAH1	59 (+) GANTTNC	S000494
ARR1AT	69 (-) NGATT	S000454
TATABOX3	75 (+) TATTAAT	S000110
MYBPZM	92 (-) CCWACC	S000179
CACTFTPPCA1	106 (+) YACT	S000449
NODCON2GM	108 (+) CTCTT	S000462
OSE2ROOTNODULE	108 (+) CTCTT	S000468
MYBPZM	114 (+) CCWACC	S000179
MYB1AT	128 (-) WAACCA	S000408
POLLEN1LELAT52	131 (-) AGAAA	S000245
DOFCOREZM	134 (-) AAAG	S000265
DOFCOREZM	151 (-) AAAG	S000265
GTGANTG10	156 (+) GTGA	S000378
BIHD1OS	157 (-) TGTCA	S000498
WRKY71OS	157 (+) TGAC	S000447
RAV1AAT	162 (-) CAACA	S000314
MYB2CONSENSUSAT	169 (-) YAACKG	S000409
MYBCOREATCYCB1	169 (-) AACGG	S000502
MYBCORE	169 (+) CNGTTR	S000176
DPBFCOREDCDC3	178 (-) ACACNNG	S000292
SITEIIATCYTC	184 (+) TGGGCY	S000474
RHERPATExPA7	189 (-) KCACGW	S000512
GTGANTG10	195 (+) GTGA	S000378
CAREOSREP1	197 (-) CAACTC	S000421
S1FBOXSORPS1L21	204 (+) ATGGTA	S000223
WBOXATNPR1	212 (+) TTGAC	S000390
HEXMOTIFTAH3H4	213 (-) ACGTCA	S000053
ASF1MOTIFCAMV	213 (+) TGACG	S000024
TGACGTVMAMY	213 (+) TGACGT	S000377
WRKY71OS	213 (+) TGAC	S000447
ACGTCBOX	214 (-) GACGTC	S000131
ACGTCBOX	214 (+) GACGTC	S000131
ACGTATERD1	215 (-) ACGT	S000415
ABREOSRAB21	215 (+) ACGTSSSC	S000012
ACGTATERD1	215 (+) ACGT	S000415
CGACGOSAMY3	216 (-) CGACG	S000205
CGCGBOXAT	233 (-) VCGCGB	S000501
CGCGBOXAT	233 (+) VCGCGB	S000501
CGCGBOXAT	235 (-) VCGCGB	S000501
CGCGBOXAT	235 (+) VCGCGB	S000501
ABREOSRAB21	239 (-) ACGTSSSC	S000012
BOXIIPCCHS	240 (-) ACGTGCC	S000229
ACGTABREMOTIFA2OSEM	240 (-) ACGTGKC	S000394
SORLIP1AT	240 (+) GCCAC	S000482
ABRELATERD1	242 (-) ACGTG	S000414
ACGTATERD1	243 (-) ACGT	S000415
ACGTATERD1	243 (+) ACGT	S000415
PALBOXAPC	247 (+) CCGTCC	S000137
NODCON2GM	254 (+) CTCTT	S000462

OSE2ROOTNODULE	254 (+)	CTCTT	S000468
DOFCOREZM	256 (-)	AAAG	S000265
E2FCONSENSUS	257 (+)	WTTSSCSS	S000476
BP5OSWX	266 (+)	CAACGTG	S000436
T/GBOXATPIN2	267 (+)	AACGTG	S000458
ABRERATCAL	267 (+)	MACGYGB	S000507
ACGTATERD1	268 (-)	ACGT	S000415
RHERPATEXPA7	268 (-)	KCACGW	S000512
ABRELATERD1	268 (+)	ACGTG	S000414
ACGTATERD1	268 (+)	ACGT	S000415
UPRMOTIFIIAT	279 (+)	CCNNNNNNNNNNNNNCCACG	S000426
CACTFTPPCA1	287 (+)	YACT	S000449
SV40CORENHAN	289 (-)	GTGGWWHG	S000123
MYBATRD22	289 (+)	CTAACCA	S000175
MYB1AT	290 (+)	WAACCA	S000408
EBOXBNNAPA	302 (-)	CANNTG	S000144
CATATGGMSAUR	302 (-)	CATATG	S000370
MYCCONSENSUSAT	302 (-)	CANNTG	S000407
EBOXBNNAPA	302 (+)	CANNTG	S000144
CATATGGMSAUR	302 (+)	CATATG	S000370
MYCCONSENSUSAT	302 (+)	CANNTG	S000407
NODCON1GM	322 (-)	AAAGAT	S000461
OSE1ROOTNODULE	322 (-)	AAAGAT	S000467
DOFCOREZM	324 (-)	AAAG	S000265
SORLIP1AT	328 (+)	GCCAC	S000482
MYB2CONSENSUSAT	352 (-)	YAACKG	S000409
MYBCOREATCYCB1	352 (-)	AACGG	S000502
MYBCORE	352 (+)	CNGTTR	S000176
CGCGBOXAT	372 (-)	VCGCGB	S000501
CGCGBOXAT	372 (+)	VCGCGB	S000501
PRECONSCRHSP70A	396 (-)	SCGAYNRNNNNNNNNNNNNNNHND	S000506
ARR1AT	396 (+)	NGATT	S000454
SORLIP1AT	407 (-)	GCCAC	S000482
CAATBOX1	413 (+)	CAAT	S000028
ARR1AT	414 (-)	NGATT	S000454
CAATBOX1	419 (+)	CAAT	S000028
CACTFTPPCA1	432 (-)	YACT	S000449
CURECORECR	435 (-)	GTAC	S000493
CURECORECR	435 (+)	GTAC	S000493
TATAPVTRNALEU	444 (+)	TTTATATA	S000340
TATABOX4	445 (-)	TATATAA	S000111
MYBCORE	453 (+)	CNGTTR	S000176
RAV1AAT	454 (-)	CAACA	S000314
BIHD1OS	462 (+)	TGTCA	S000498
WRKY71OS	463 (-)	TGAC	S000447
UPRMOTIFIIAT	499 (+)	CCNNNNNNNNNNNNNCCACG	S000426
MYBPLANT	531 (+)	MACCWAMC	S000167
BOXLCOREDCPAL	532 (+)	ACCWWCC	S000492
MYBPZM	533 (+)	CCWACC	S000179
GCCORE	541 (+)	GCCGCC	S000430
PALBOXAPC	553 (+)	CCGTCC	S000137
CAATBOX1	562 (+)	CAAT	S000028
EBOXBNNAPA	567 (-)	CANNTG	S000144
DPBFCOREDCDC3	567 (-)	ACACNNG	S000292
MYCCONSENSUSAT	567 (-)	CANNTG	S000407
EBOXBNNAPA	567 (+)	CANNTG	S000144
MYCCONSENSUSAT	567 (+)	CANNTG	S000407
CACTFTPPCA1	569 (-)	YACT	S000449

MYBCORE	39 (+)	CNGTTR	S000176
RAV1AAT	40 (-)	CAACA	S000314
CACTFTPPCA1	57 (-)	YACT	S000449
SEF4MOTIFGM7S	70 (+)	RTTTTTTR	S000103
ANAERO1CONSENSUS	73 (-)	AAACAAA	S000477
SEF4MOTIFGM7S	76 (+)	RTTTTTTR	S000103
ANAERO1CONSENSUS	79 (-)	AAACAAA	S000477
INRNTPSADB	95 (+)	YTCANTYY	S000395
MYBPLANT	105 (-)	MACCWAMC	S000167
GTGANTG10	110 (+)	GTGA	S000378
GATABOX	112 (+)	GATA	S000039
RAV1AAT	116 (-)	CAACA	S000314
EECCRCAH1	120 (+)	GANTTNC	S000494
DOFCOREZM	126 (-)	AAAG	S000265
DOFCOREZM	131 (-)	AAAG	S000265
TAAAGSTKST1	131 (-)	TAAAG	S000387
GT1CONSENSUS	132 (-)	GRWAAW	S000198
INTRONLOWER	150 (-)	TGCAGG	S000086
RAV1AAT	164 (+)	CAACA	S000314
DPBFCOREDCDC3	166 (+)	ACACNNG	S000292
DPBFCOREDCDC3	169 (-)	ACACNNG	S000292
CACTFTPPCA1	171 (-)	YACT	S000449
RHERPATEXPA7	187 (-)	KCACGW	S000512
GTGANTG10	193 (+)	GTGA	S000378
MARTBOX	198 (+)	TTWTWTTWTT	S000067
MARTBOX	199 (+)	TTWTWTTWTT	S000067
MARTBOX	200 (+)	TTWTWTTWTT	S000067
MARTBOX	201 (+)	TTWTWTTWTT	S000067
MARTBOX	202 (+)	TTWTWTTWTT	S000067
MARTBOX	203 (+)	TTWTWTTWTT	S000067
RHERPATEXPA7	220 (-)	KCACGW	S000512
GTGANTG10	226 (+)	GTGA	S000378
CAREOSREP1	228 (-)	CAACTC	S000421
S1FBOXSORPS1L21	235 (+)	ATGGTA	S000223
ELRECOREPCR1	243 (+)	TTGACC	S000142
WBOXATNPR1	243 (+)	TTGAC	S000390
QELEMENTZMZM13	244 (-)	AGGTCA	S000254
WRKY71OS	244 (+)	TGAC	S000447
WBOXNTERF3	244 (+)	TGACY	S000457
CGCGBOXAT	264 (-)	VCGCGB	S000501
CGCGBOXAT	264 (+)	VCGCGB	S000501
CGCGBOXAT	266 (-)	VCGCGB	S000501
CGCGBOXAT	266 (+)	VCGCGB	S000501
ACGTABREMOTIFA2OSEM	271 (-)	ACGTGKC	S000394
GADOWNAT	271 (-)	ACGTGTC	S000438
ABRELATERD1	273 (-)	ACGTG	S000414
ACGTATERD1	274 (-)	ACGT	S000415
ACGTATERD1	274 (+)	ACGT	S000415
BP5OSWX	293 (+)	CAACGTG	S000436
T/GBOXATPIN2	294 (+)	AACGTG	S000458
ABRERATCAL	294 (+)	MACGYGB	S000507
ACGTATERD1	295 (-)	ACGT	S000415
RHERPATEXPA7	295 (-)	KCACGW	S000512
ABRELATERD1	295 (+)	ACGTG	S000414
ACGTATERD1	295 (+)	ACGT	S000415
CACTFTPPCA1	314 (+)	YACT	S000449
SV40COREENHAN	316 (-)	GTGGWWHG	S000123
MYBATRD22	316 (+)	CTAACCA	S000175

MYB1AT	317 (+)	WAACCA	S000408
EBOXBNNAPA	329 (-)	CANNTG	S000144
MYCCONSENSUSAT	329 (-)	CANNTG	S000407
EBOXBNNAPA	329 (+)	CANNTG	S000144
MYCCONSENSUSAT	329 (+)	CANNTG	S000407
SORLIP1AT	355 (+)	GCCAC	S000482
ASF1MOTIFCAMV	379 (-)	TGACG	S000024
WRKY71OS	380 (-)	TGAC	S000447
GTGANTG10	381 (-)	GTGA	S000378
CGCGBOXAT	398 (-)	VCGCGB	S000501
CGCGBOXAT	398 (+)	VCGCGB	S000501
PRECONSCRHSP70A	422 (-)	SCGAYNRNNNNNNNNNNNNNNNNH	S000506
ARR1AT	422 (+)	NGATT	S000454
SORLIP1AT	433 (-)	GCCAC	S000482
ARR1AT	440 (-)	NGATT	S000454
CAATBOX1	445 (+)	CAAT	S000028
CRTDREHVCBF2	459 (-)	GTCGAC	S000411
CBFHV	459 (-)	RYCGAC	S000497
CRTDREHVCBF2	459 (+)	GTCGAC	S000411
CBFHV	459 (+)	RYCGAC	S000497
HEXAMERATH4	461 (-)	CCGTCG	S000146
CGACGOSAMY3	461 (+)	CGACG	S000205
TATAPVTRNALEU	470 (+)	TTTATATA	S000340
TATABOX4	471 (-)	TATATAA	S000111
MYBCORE	479 (+)	CNGTTR	S000176
RAV1AAT	480 (-)	CAACA	S000314
BIHD1OS	488 (+)	TGTCA	S000498
WRKY71OS	489 (-)	TGAC	S000447
MYBPLANT	557 (+)	MACCWAMC	S000167
BOXLCOREDPCAL	558 (+)	ACCWWCC	S000492
MYBPZM	559 (+)	CCWACC	S000179
GTGANTG10	582 (-)	GTGA	S000378
CAATBOX1	588 (+)	CAAT	S000028
EBOXBNNAPA	593 (-)	CANNTG	S000144
DPBFCOREDCDC3	593 (-)	ACACNNG	S000292
MYCCONSENSUSAT	593 (-)	CANNTG	S000407
EBOXBNNAPA	593 (+)	CANNTG	S000144
MYCCONSENSUSAT	593 (+)	CANNTG	S000407
CACTFTPPCA1	595 (-)	YACT	S000449
CANBNNAPA	596 (-)	CNAACAC	S000148
ACGTATERD1	609 (-)	ACGT	S000415
RHERPATExPA7	609 (-)	KCACGW	S000512
ABRELATERD1	609 (+)	ACGTG	S000414
ACGTATERD1	609 (+)	ACGT	S000415
HEXAMERATH4	614 (+)	CCGTCG	S000146
CGACGOSAMY3	615 (-)	CGACG	S000205
SURECOREATSULTR11	619 (-)	GAGAC	S000499
SURECOREATSULTR11	626 (+)	GAGAC	S000499
//			

>TaF3H-B1

TCTACAAGCCATGGAAATATGACGTGTCATGATGTATAGGTTTTAGATATTGGGCGAACCAATCTGTGGTTGGATGGTTAA
AGGGACTCTGATATCCCCAGTCCACTAAGGTTCAAATCTGGTGCTTGAGTTTATTCCTGGATTATTTTCAGGATTTTCGACG
ATGTGCATTTCAGTAGGAGAAGACGTTCCCGTCGACAACGAGTTGCCACGATGACTTCGTAAATTTCAAGATAATATGCCG
ATTCGGTCTTTTCGGAGGTGCTCATAGGGGTAGGGTGTGCGTGTGTGCGTTTATAGGGATGAGTGTATGCACGTATATATGA
GCGCTTGATCTGGACTGTGTTAAAAAAAGTTCTAGATCTTGGTTGGTGTATAGCGGGTGTCCAGTGGTGTGTGTGCTTG
TGATGTGTGTGTTGTGCGTATATGGATCGATCGATACGGCTGGATGGATGCATGGGTGCGGCCCCGGTTAGTTGCGCACCTA
ACACGAGTGCCCCGAGGGCGACTTTCCTTGTTAGTTGCGTGCGCACGCGCGACTTGCAGGTGCGGTCTGCCCTCATCTTCC

AACGTTAGTATACACAATGCCCTCTTCCCGGCCGTATATATCCGCGTGCGTACAACGTCCAGAAAACCACAACCCAAACGGC
CGAGCCTTTTCATCAAGGAACAAACCATCATACGAGACAGACGCCGCGCGACACAAGCGGACGATCCCCGGAGTGCGGAT
CGATGGCGCCCGGTGAGCAACGAGACGTTCTCTCCCGA

TCTACAAGCCATGGAATATGACGTGCTATGATGTATAGTTTTAGATATTGGGCGAACCAATCTGTGGTTGGATGTTAAAGGGACTCTGATATCCCA 100
AGATGTTTCGGTACCTTTATCTGCACAGTACTACATATCCAAAATCTATAACCCGCTTGGTTAGACACCAACCCTACCAATTTCCCTGAGACTATAGGGT

GTCCACTAAGGTTCAAACTGTGGTCTTATCTCTGGATTAATTTCAAGGATTTTTCGACGATGTGCAATTCAGTAGGAGAAGACGTTCCCGTCGACAAAC 200
CAGGTGATTTCCAAGTTTAGACCACGAACCTAAATAAGGACCTAATAAAGTCCATAAAGCTGCTACACGTAAGTCATCTCTCTGCAAGGGCAGCTGTTG

GAGTTGCGCCACGATGACTTCGTAATTTCAAGATAATATGCCGATTCTGCTCTTTCGAGGTTGCTCATAGGGGTAGGGTGTGCGTGTGTGCGTTTATAGGG 300
CTCAACGGGTGCTACTGAAGCATTTAAAGTTCTATTATACGGCTAAGCCAGAAAGCCTCCACGAGTATCCCATCCACACGCAACACGCAATATCCG





























ATGAGTGTATGCACGTATATATGAGCGCTTGTATCTGGAAGTGTATAAAAAAGTTCTAGATCTTGGTTGGTGTATAGCGGGTGTCCAGTGGTGTGTGT 400
TACTCACATACGTGCATATATATACTCGCAACATAGACCTGACACAAATTTTTTTTCAAGATCTAGAACCACACATATCGCCACAGGTCAACACACACA

GCTTGTGATGTGTGTGTGTGCGTATATGGATCGATCGATACGGCTGGATGGATGCATGGGTGCGGCCCGGTTAGTTGCGCACCTAACACAGTGCCTCGA 500
CGAACACTACACACACAACACGCATATACCTAGCTAGCTATGCGGACCTACCTACGTACCCACGCCGGGCAATCAACGCGTGGATTGTGCTACGGGCT

GGGCGACTTCCTTGGTTAGTTGCGTGCACGCGCGACTTGCAGGTGCGCTCTGCCCCCTCATCTTCAACGTAGTATACACAATGCCCTCTTCCCGCGCG 600
CCGCTGAAGGAACTAATCAACGCACGCTGCGCGCTGAACGTCCAGCGCAGACGGGAGTAGAAGGTTGCATCATATGTGTTACGGGAGAAAGGCGCGC

TATATATCCCGGTGCGTCAACGTCAGAAAAACCAACCAACCGCGGAGCTTTTCATCAAGGAACAAACCATCATACGAGACAGACCGCGCGCGCA 700
ATATATAGGCGCAGCATGTTGCAGGTCTTTTGGTGTGGTTTGGCGGCTCGGAAAGTAGTTCCTTGTGTTGGTAGTATGCTCTGTCTGCGGCCGCGCGT

CAACGCGGACGATCCCCGGAGTGCGGATCGATGGCGCGGTGAGCAACGAGACGTTCTCTCCGA 800
GTGTTGCGCTGCTAGGGGCTCACGCTAGCTACCGCGGCACTCGTTGCTCTGCAAGGAGGGCT

TF_motif_seq_0011:		TF_motif_seq_0025:		TF_motif_seq_0031:	
TF_motif_seq_0068:		TF_motif_seq_0103:		TF_motif_seq_0121:	
TF_motif_seq_0231:		TF_motif_seq_0238:		TF_motif_seq_0259:	
TF_motif_seq_0274:		TF_motif_seq_0283:		TF_motif_seq_0297:	
TF_motif_seq_0310:		TF_motif_seq_0321:		TF_motif_seq_0333:	
TF_motif_seq_0334:		TF_motif_seq_0344:		TF_motif_seq_0350:	
TF_motif_seq_0353:		TF_motif_seq_0358:		TF_motif_seq_0363:	
TF_motif_seq_0372:		TF_motif_seq_0378:		TF_motif_seq_0380:	
TF_motif_seq_0387:		TF_motif_seq_0389:		TF_motif_seq_0390:	
TF_motif_seq_0425:		TF_motif_seq_0427:		TF_motif_seq_0429:	
TF_motif_seq_0440:		TF_motif_seq_0458:			

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
GT1CONSENSUS	13 (+) GRWAAW		S000198
ROOTMOTIFTAPOX1	16 (-) ATATT		S000098
HEXMOTIFTAH3H4	20 (-) ACGTCA		S000053
ASF1MOTIFCAMV	20 (+) TGACG		S000024
TGACGTVMAMY	20 (+) TGACGT		S000377
WRKY71OS	20 (+) TGAC		S000447
ACGTATERD1	22 (-) ACGT		S000415
ACGTABREMOTIFA2OSEM	22 (+) ACGTGKC		S000394
ABRELATERD1	22 (+) ACGTG		S000414
ACGTATERD1	22 (+) ACGT		S000415
GADOWNAT	22 (+) ACGTGTC		S000438
BIHD1OS	25 (+) TGTCA		S000498
WRKY71OS	26 (-) TGAC		S000447
GATABOX	46 (+) GATA		S000039
ROOTMOTIFTAPOX1	47 (+) ATATT		S000098
CAATBOX1	49 (-) CAAT		S000028
CCAATBOX1	49 (-) CCAAT		S000030
REALPHALGLHCB21	57 (+) AACCAA		S000362
CCAATBOX1	59 (+) CCAAT		S000030
CAATBOX1	60 (+) CAAT		S000028
ARR1AT	61 (-) NGATT		S000454
SV40COREENHAN	66 (+) GTGGWWHG		S000123
BOXLCOREDCPAL	73 (-) ACCWWCC		S000492
MYB1AT	76 (-) WAACCA		S000408
GT1CORE	77 (+) GGTAA		S000125
TAAAGSTKST1	80 (+) TAAAG		S000387































DOFCOREZM	81 (+) AAAG	S000265
GATABOX	92 (+) GATA	S000039
GATABOX	94 (-) GATA	S000039
MYBST1	94 (-) GGATA	S000180
CACTFTPPCA1	105 (+) YACT	S000449
ARR1AT	117 (-) NGATT	S000454
POLASIG1	132 (-) AATAAA	S000080
POLASIG3	144 (-) AATAAT	S000088
TATABOX5	145 (+) TTATTT	S000203
ARR1AT	153 (+) NGATT	S000454
EECCRCAH1	154 (+) GANTTNC	S000494
GT1CONSENSUS	155 (-) GRWAAW	S000198
CGACGOSAMY3	160 (+) CGACG	S000205
CACTFTPPCA1	175 (-) YACT	S000449
ACGTATERD1	186 (-) ACGT	S000415
ACGTATERD1	186 (+) ACGT	S000415
HEXAMERATH4	192 (+) CCGTCC	S000146
CGACGOSAMY3	193 (-) CGACG	S000205
CRTDREHVCBF2	194 (-) GTCGAC	S000411
CBFHV	194 (-) RYCGAC	S000497
CRTDREHVCBF2	194 (+) GTCGAC	S000411
CBFHV	194 (+) RYCGAC	S000497
CAREOSREP1	203 (-) CAACTC	S000421
EECCRCAH1	203 (+) GANTTNC	S000494
WBOXHVIS01	217 (+) TGACT	S000442
WRKY71OS	217 (+) TGAC	S000447
WBOXNTERF3	217 (+) TGACY	S000457
GATABOX	235 (+) GATA	S000039
GT1CONSENSUS	235 (+) GRWAAW	S000198
IBOXCORE	235 (+) GATAA	S000199
ROOTMOTIFTAPOX1	238 (-) ATATT	S000098
ARR1AT	245 (+) NGATT	S000454
DOFCOREZM	254 (-) AAAG	S000265
LTRE1HVBLT49	255 (-) CCGAAA	S000250
MYBPZM	274 (-) CCWACC	S000179
AMMORRESIIUDCRNIA1	274 (+) GGWAGGGT	S000374
DPBFCOREDCDC3	286 (-) ACACNNG	S000292
PREATPROD	305 (-) ACTCAT	S000450
CACTFTPPCA1	308 (-) YACT	S000449
RHERPATEXPA7	315 (+) KCACGW	S000512
ABRELATERD1	316 (-) ACGTG	S000414
ACGTATERD1	317 (-) ACGT	S000415
ACGTATERD1	317 (+) ACGT	S000415
GATABOX	336 (-) GATA	S000039
DOFCOREZM	357 (+) AAAG	S000265
REALPHALGLHCB21	370 (-) AACCAA	S000362
MYBPLANT	372 (-) MACCWAMC	S000167
MYBPZM	372 (-) CCWACC	S000179
BOXLCOREDCPAL	372 (-) ACCWWCC	S000492
BS1EGCCR	383 (+) AGCGGG	S000352
DPBFCOREDCDC3	385 (-) ACACNNG	S000292
CACTFTPPCA1	394 (-) YACT	S000449
GTGANTG10	410 (+) GTGA	S000378
RAV1AAT	420 (-) CAACA	S000314
GATABOX	444 (+) GATA	S000039
RYREPEATLEGUMINBOX	459 (-) CATGCAY	S000100
RYREPEATGMY2	459 (-) CATGCAT	S000105
RYREPEATBNNA	460 (-) CATGCA	S000264
SORLIP2AT	471 (-) GGGCC	S000483

MYBCORE	475 (+) CNGTTR	S000176
MYB1LEPR	477 (+) GTTAGTT	S000443
MYBPLANT	487 (+) MACCWAMC	S000167
CANBNNAFA	490 (+) CNAACAC	S000148
CACTFTPPCA1	499 (-) YACT	S000449
EECCRCAH1	512 (+) GANTTNC	S000494
REALPHALGLHCB21	519 (-) AACCAA	S000362
MYBATRD22	520 (-) CTAACCA	S000175
MYB1AT	520 (-) WAACCA	S000408
MYB1LEPR	522 (+) GTTAGTT	S000443
ABRERATCAL	536 (+) MACGYGB	S000507
CGCGBOXAT	537 (-) VCGCGB	S000501
CGCGBOXAT	537 (+) VCGCGB	S000501
EECCRCAH1	543 (+) GANTTNC	S000494
INTRONLOWER	547 (+) TGCAGG	S000086
ACGTATERD1	577 (-) ACGT	S000415
ACGTATERD1	577 (+) ACGT	S000415
CACTFTPPCA1	581 (-) YACT	S000449
CAATBOX1	589 (+) CAAT	S000028
NODCON2GM	596 (+) CTCCTT	S000462
OSE2ROOTNODULE	596 (+) CTCCTT	S000468
GATABOX	613 (-) GATA	S000039
MYBST1	613 (-) GGATA	S000180
REBETALGLHCB21	613 (-) CGGATA	S000363
CGCGBOXAT	616 (-) VCGCGB	S000501
ABRERATCAL	616 (-) MACGYGB	S000507
CGCGBOXAT	616 (+) VCGCGB	S000501
CURECORECR	624 (-) GTAC	S000493
CURECORECR	624 (+) GTAC	S000493
ACGTATERD1	629 (-) ACGT	S000415
ACGTATERD1	629 (+) ACGT	S000415
SEF3MOTIFGM	646 (+) AACCCA	S000115
MYBCOREATCYCB1	652 (+) AACGG	S000502
DOFCOREZM	663 (-) AAAG	S000265
AACACOREOSGLUB1	675 (+) AACAAAC	S000353
MYB1AT	678 (+) WAACCA	S000408
SORLIP4AT	681 (-) GTATGATGG	S000485
ARFAT	690 (-) TGTCTC	S000270
SEBFCONSSTPR10A	690 (-) YTGTCWC	S000391
SURECOREATSULTR11	690 (+) GAGAC	S000499
PRECONSCRHSP70A	706 (+) SCGAYNRNNNNNNNNNNNNNNHHD	S000506
CACTFTPPCA1	731 (-) YACT	S000449
//		

>TaF3h-B2

ATTTGCAACCGAGCGAGCTTAGATGGTTAGATATTTCTTGTGGTGGAAGTAGCCCATCATGGTTTCATAGTCCTAAGGCCTT
 ATTTGGTTTGGAGGAATTTTCATAGGACTTTTATACGATAGGATTCTTATAGGAAATTTTCTTAAAGCCTATTAATTCATA
 GGAATGAATTTTTATTCTACATAGAATTGGTTCCTATCCTTCACACTTTAAAGTAAATATGAATCTAGACTCACT
 GGAAAAAATCATATTATGTGAAACTCATAGGATTTGAGAGACTTGTCTATCTCATTTCCTACAAGTTTCTATTTCTATGA
 TAATGGTATATCGTATGAACCAAAGAAGCCTAATTTGACACTCGTGCATGCATTTTCTGAATTTATTTTCAGACTTTCTG
 GTGATGTTTCATTTCAGTGCGAGACATCTCCCTAATTTAAAGATGTTGTGCCGTTTCAGTATTTCAAAGGTACTCAGGCGTTC
 ATAGGCATCTCCCTAATTTAAATATATGTACCCTCCTTTCCATCTATAATCATACGAGACAGACGTACAGATCGATAACTG
 GTAGATAGCG

ATTTGCAACCGAGCGAGCTTAGATGGTTAGATATTTCTTGTTGGTGAAGCTAGCCCATCATGGTTCATAGTCCTAAGGCCTTATTTGGTTGGAGGAATTT
 TAAACGTGGCTCGCTCGAATCTACCAATCTATAAAGAACCACCTTGTATCGGGTAGTACCAAGTATCAGGATTCGGGAATAAACCAACCTCCTTAAA
 CATAGGACTTTTATACGATAGGATCTTATAGGAAATTTTCTTAAAGCCTATTAATTCATAGGAATGAATTTTATTCCTACATAGAATTGGTTCCTAT
 GTATCCTGAAATATGCTATCTTAAGAAATATCTTTAAAAAGAATTCGATAAATTAAATATCTTACCTTAAATAAAGGATGTATCTTAAACCAAGGATA
 CCTTCACACTTTAAAGTAAATAAATATGAATCTAGACTCACTGGAAAAAATCATATTAATGTGAAACTCATAGGATTTGAGAGACTTGTCTCTCATTT
 GGAAGTGTGAAATTTCTATTTTATTTATCTTAGATCTGAGTGACCTTTTCTTAGTATAATACACTTTGAGTATCTCTAAACCTCTGAACAGTAGAGTAAA
 CCTACAAGTTTCTATTTCTATGATAATGGTATATCGTATGAACCAAAAGAAGCCTAATTTGACACTCGTGCATGCATTTTCTGAATTTATTTAGACT
 GGATGTTCAAAAGATAAGATACTATTACCATATAGCATACTGGTTTCTTCGGATTAACACTGTGAGCACGTACGTAAAAAGACTTAAATAAAGTCTGA
 TTCTGGTGATGTTCAATTCAGTGCGAGACATCTCCCTAATTTAAAGATGTTGTGCGGGTTCAGTATTTCAAAGGTACTCAGGCCTCATAGGCATCTCCCT
 AAGACCATAACAAGTAAAGTACAGCTCTGTAGAGGGATTAAATTTCTACAACACGGCCAAGTCATAAAGTTTCCATGAGTCCGCAACTATCCCTAGAGGGA
 AATTTAAATAATGTATGACCTCCTTTCCATCTATAATCATACGAGACAGAGCTACAGATCGATAACTGGTAGATAGCG
 TTAATTTATATACATGGAGGAAAGGTAGATATTAGTATGCTCTGTCTGCATGTCTAGCTATTGACCATCTATCGC

TF_motif_seq_0246:  TF_motif_seq_0256:  TF_motif_seq_0257: 
 TF_motif_seq_0266:  TF_motif_seq_0282:  TF_motif_seq_0316: 
 TF_motif_seq_0327:  TF_motif_seq_0335:  TF_motif_seq_0347: 
 TF_motif_seq_0386:  TF_motif_seq_0422:  TF_motif_seq_0508: 
 TF_motif_seq_0002:  TF_motif_seq_0031:  TF_motif_seq_0192: 
 TF_motif_seq_0238:  TF_motif_seq_0259:  TF_motif_seq_0274: 
 TF_motif_seq_0082:  TF_motif_seq_0321:  TF_motif_seq_0334: 
 TF_motif_seq_0350:  TF_motif_seq_0372:  TF_motif_seq_0380: 
 TF_motif_seq_0387:  TF_motif_seq_0389:  TF_motif_seq_0390: 
 TF_motif_seq_0391:  TF_motif_seq_0392:  TF_motif_seq_0397: 

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
MYBCORE	6 (-) CNGTTR		S000176
MYBATRD22	24 (-) CTAACCA		S000175
MYB1AT	24 (-) WAACCA		S000408
GATABOX	30 (+) GATA		S000039
ROOTMOTIFTAPOX1	31 (+) ATATT		S000098
POLLEN1LELAT52	34 (-) AGAAA		S000245
SITEIIATCYTC	51 (-) TGGGCY		S000474
CARGATCONSENSUS	79 (-) CCWWWWWGG		S000404
CARGATCONSENSUS	79 (+) CCWWWWWGG		S000404
TATABOX5	81 (+) TTATTT		S000203
REALPHALGLHCB21	85 (-) AACCAA		S000362
MYB1AT	86 (-) WAACCA		S000408
EECCRAH1	96 (+) GANTTNC		S000494
DOFCOREZM	109 (-) AAAG		S000265
GATABOX	118 (+) GATA		S000039
ARR1AT	122 (+) NGATT		S000454
GT1CONSENSUS	133 (+) GRWAAW		S000198
TAAAGSTKST1	146 (+) TAAAG		S000387
DOFCOREZM	147 (+) AAAG		S000265
TATABOX3	153 (+) TATTAAT		S000110
INRNTPSADB	165 (-) YTCANTYY		S000395
SEF4MOTIFGM7S	172 (+) RTTTTTTR		S000103
POLASIG1	175 (-) AATAAA		S000080
BOXIINTPATPB	186 (+) ATAGAA		S000296
CAATBOX1	191 (-) CAAT		S000028
CCAATBOX1	191 (-) CCAAT		S000030
REALPHALGLHCB21	192 (-) AACCAA		S000362
GATABOX	200 (-) GATA		S000039
MYBST1	200 (-) GGATA		S000180
GTGANTG10	206 (-) GTGA		S000378
CACTFTPPCA1	209 (+) YACT		S000449
NTBBF1ARROLB	215 (-) ACTTTA		S000273
TAAAGSTKST1	215 (+) TAAAG		S000387
DOFCOREZM	216 (+) AAAG		S000265
CACTFTPPCA1	218 (-) YACT		S000449

TATABOX5	222 (-)	TTATTT	S000203
SEF1MOTIF	223 (-)	ATATTAWW	S000006
POLASIG1	223 (+)	AATAAA	S000080
ROOTMOTIFTAPOX1	227 (-)	ATATT	S000098
ARR1AT	233 (-)	NGATT	S000454
GTGANTG10	242 (-)	GTGA	S000378
CACTFTPPCA1	243 (+)	YACT	S000449
PYRIMIDINEBOXHVEPB1	247 (-)	TTTTTTCC	S000298
GT1CONSENSUS	247 (+)	GRWAAW	S000198
GT1CONSENSUS	248 (+)	GRWAAW	S000198
GT1GMSCAM4	248 (+)	GAAAAA	S000453
ARR1AT	254 (-)	NGATT	S000454
ROOTMOTIFTAPOX1	258 (+)	ATATT	S000098
GTGANTG10	265 (+)	GTGA	S000378
EECCRCAH1	267 (-)	GANTTNC	S000494
PREATPROD	270 (+)	ACTCAT	S000450
ARR1AT	277 (+)	NGATT	S000454
SURECOREATSULTR11	286 (+)	GAGAC	S000499
BIHD1OS	292 (+)	TGTCA	S000498
WRKY71OS	293 (-)	TGAC	S000447
INRNTPSADB	298 (+)	YTCANTYY	S000395
GT1CONSENSUS	301 (-)	GRWAAW	S000198
SURE1STPAT21	313 (-)	AATAGAAAA	S000186
POLLEN1LELAT52	314 (-)	AGAAA	S000245
BOXIINTPATPB	315 (-)	ATAGAA	S000296
POLLEN1LELAT52	320 (-)	AGAAA	S000245
BOXIINTPATPB	321 (-)	ATAGAA	S000296
GATABOX	327 (+)	GATA	S000039
GT1CONSENSUS	327 (+)	GRWAAW	S000198
IBOXCORE	327 (+)	GATAA	S000199
S1FBOXSORPS1L21	331 (+)	ATGGTA	S000223
GATABOX	337 (-)	GATA	S000039
REALPHALGLHCB21	346 (+)	AACCAA	S000362
DOFCOREZM	351 (+)	AAAG	S000265
WBOXATNPR1	365 (+)	TTGAC	S000390
BIHD1OS	366 (-)	TGTCA	S000498
WRKY71OS	366 (+)	TGAC	S000447
DPBFCORECDC3	368 (+)	ACACNNG	S000292
CACTFTPPCA1	369 (+)	YACT	S000449
RHERPATEXPA7	372 (-)	KCACGW	S000512
RYREPEATLEGUMINBOX	374 (-)	CATGCAY	S000100
RYREPEATBNNAPA	375 (-)	CATGCA	S000264
RYREPEATLEGUMINBOX	377 (+)	CATGCAY	S000100
RYREPEATGMGY2	377 (+)	CATGCAT	S000105
RYREPEATBNNAPA	377 (+)	CATGCA	S000264
GT1CONSENSUS	383 (-)	GRWAAW	S000198
GT1GMSCAM4	383 (-)	GAAAAA	S000453
POLLEN1LELAT52	385 (-)	AGAAA	S000245
POLASIG1	393 (-)	AATAAA	S000080
TATABOX5	394 (+)	TTATTT	S000203
EECCRCAH1	402 (+)	GANTTNC	S000494
DOFCOREZM	404 (-)	AAAG	S000265
POLLEN1LELAT52	405 (-)	AGAAA	S000245
GTGANTG10	411 (+)	GTGA	S000378
ARFAT	430 (-)	TGTCTC	S000270
SURECOREATSULTR11	430 (+)	GAGAC	S000499
TAAAGSTKST1	447 (+)	TAAAG	S000387
DOFCOREZM	448 (+)	AAAG	S000265

NODCON1GM	448 (+) AAAGAT	S000461
OSE1ROOTNODULE	448 (+) AAAGAT	S000467
RAV1AAT	453 (-) CAACA	S000314
CACTFTPPCA1	467 (-) YACT	S000449
ERELEE4	470 (+) AWTTCAAA	S000037
DOFCOREZM	475 (+) AAAG	S000265
CURECORECR	479 (-) GTAC	S000493
CURECORECR	479 (+) GTAC	S000493
CACTFTPPCA1	480 (+) YACT	S000449
SEF1MOTIF	510 (-) ATATTTAWW	S000006
TATABOXOSPAL	511 (-) TATTTAA	S000400
ROOTMOTIFTAPOX1	514 (-) ATATT	S000098
CURECORECR	521 (-) GTAC	S000493
CURECORECR	521 (+) GTAC	S000493
DOFCOREZM	529 (-) AAAG	S000265
ARR1AT	541 (-) NGATT	S000454
ARFAT	549 (-) TGTCTC	S000270
SEBFCONSSTPR10A	549 (-) YTGTCWC	S000391
SURECOREATSULTR11	549 (+) GAGAC	S000499
ACGTATERD1	556 (-) ACGT	S000415
ACGTATERD1	556 (+) ACGT	S000415
CURECORECR	558 (-) GTAC	S000493
CURECORECR	558 (+) GTAC	S000493
MYBCORE	570 (-) CNGTTR	S000176
MYB2AT	570 (+) TAACTG	S000177
MYB2CONSENSUSAT	570 (+) YAACKG	S000409
GATABOX	579 (+) GATA	S000039
//		