Supporting information

Figure S1 The sequences of wheat *DREB* genes. (a), (b) and (c) represent the nucleotide sequence and amino acid sequence of *DREB2*, *DREB6* and *Wdreb2*, respectively. The box and underline denote nuclear localization signal and AP2/EREBP domain, respectively.

Figure S2 Alignments of wheat DREBs. (a) and (b) represent the alignments of AP2/EREBP domain and amino acid sequence of *DREB2*, *DREB6* and *Wdreb2*. The similar and consistent amino acids are indicated in blue or dark blue, respectively. β-sheet and α-helix are indicated with long arrow and dotted line, the conserved residues at 14 th and 19 th are marked with short arrow.

Figure S3 Multiple alignment of wheat DREBs and its homologous sequences. (a), (b) and (c) are the alignment on some homologous sequences of wheat DREB2, DREB6 and Wdreb2, respectively. The underline denotes the AP2/EREBP domain.

Figure S4 Promoter regions of wheat *DREB* genes. (a), (b) and (c) represent the promoter sequences and some *cis*-acting elements of *DREB2*, *DREB6* and *Wdreb2*, respectively.

Figure S5 Prediction of CpG islands in the promoter regions of wheat *DREB* genes. (a), (b) and (c) represent the location of putative CpG islands in the promoter regions of *DREB2*, *DREB6* and *Wdreb2*, respectively. The CpG island regions between two arrows below each diagram were examined using BSP, respectively.

Figure S6 Bisulfite sequencing analysis on the promoter regions of wheat *DREB* genes using CyMATE. (a), (b) and (c) indicate methylation sites in the promoter regions of *DREB2*, *DREB6* and W*dreb2* in wheat leaves. Circles, squares and triangles represent CG, CHG or CHH, filled and hollow circles denote methylated and unmethylated cytosine. Each row represents the sequencing result of one positive clone. The length of CpG island sequence is visualized above each diagram and the potential methylation sites are displayed below.

Table S1 Homologous amino acid sequences of wheat DREBs by BLASP

The homologous sequences of wheat DREB2, DREB6 and Wdreb2 were retrieved with BlastP algorithm, which are mainly from some species in Gramineae. The homologous sequences having higher identity with wheat DREBs were selected from some Genera in Gramineae, and were further analyzed.

Table S2 The *cis*-acting elements in the promoter of *DREB2*

Table S3 The *cis*-acting elements in the promoter of *DREB6*

Table S4 The *cis*-acting elements in the promoter of *Wdreb2*

Table S5 Correlation between promoter methylation and expression of *DREB* genes. Pearson's r represents the relationship between expression levels of *DREB2*, *DREB6*, *Wdreb2* in wheat leaves and methylation rates at CG, CHG or CHH sites in their promoter regions under the treatment of 15% PEG_{6000} solution. According to the expression level and methylation rate when wheat seedlings incubated in PEG_{6000} solution for 12 h, Pearson's r analysis of *DREBs* were performed.

Table S6 Primers used in this study

(a)

```
1      CTACTCCCTGCACGGTCCTCCCATTACCACGAGCGAGCGCGTGTCATCTCATACGGGCACGCGGGGCTACGTGGT
76     GCTCTCTGCGCGCACATGGCGGCGAGCGAGCAGAGCTCCGAGTCCTCGTCGACGTCCTGCACTTCCTCCTACTCC
1                      M  A  A  S  E  Q  S  S  E  S  S  S  T  S  C  T  S  S  Y  S
151    ACGTCCTCGTGCTCCCCCAGGGCCGACGACAAGAAGCGGAACGGCGGCGGCAAGCGGAAGCGCGCAGCGGCGGCC
21      T  S  S  C  S  P  R  A  D  D  K  K  R  N  G  G  G  K  R  K  R  A  A  A  A
226    GACGAGGAGCCGGCCCCGGCGGCGGCGGCGGCGTCGTATCGCGGCGTGCGGATGCGGGCGTGGGGCAAGTGGGTG
46      D  E  E  P  A  P  A  A  A  A  S  Y  R  G  V  R  M  R  A  W  G  K  W  V
301    TCGGAGATCAGGGAGCCGCGCAAGAAGTCCCGCATCTGGCTCGGCACCTTCCCGTGCCCGGAGATGGCCGCGCGC
71      S  E  I  R  E  P  R  K  K  S  R  I  W  L  G  T  F  P  C  P  E  M  A  A  R
376    GCCCACGACGCCGCCGCGCTCAGCATCAAGGGCGCCCGCGCCGTGCTTAACTTCCCGGACCTCGCGCCCGCGCTC
96      A  H  D  A  A  A  L  S  I  K  G  A  R  A  V  L  N  F  P  D  L  A  P  A  L
451    CCTCGCCCGGCCTCCCTCGCCCCGTGCGACGTCCAGGCCGCCGCCGCGCGCGCCGCCCTCATGCACGACCACGAC
121     P  R  P  A  S  L  A  P  C  D  V  Q  A  A  A  A  R  A  A  L  M  H  D  H  D
526    CACCAGTGCTGCTCCGCCTCAACCTCCCCCGCCGCCGCGCCGGACTCCGCGCGCGGCAATGCCCCGGCGCCATGC
146     H  Q  C  C  S  A  S  T  S  P  A  A  A  P  D  S  A  R  G  N  A  P  A  P  C
601    GACCAGCCGGCCGCGCGAGACGAGCCGGAGCATGAGCCGCCGTTCCAGCCGAGCCAGGGAAATGAGCAGCAGCTC
171     D  Q  P  A  A  R  D  E  P  E  H  E  P  P  F  Q  P  S  Q  G  N  E  Q  Q  L
676    ACGGCTGCACAGGTGGAGATGGTGTTCGACGAGCTGGCGCCGCTGTGGGTGGAGAACGTGGTGGATTTCGCGCCG
196     T  A  A  Q  V  E  M  V  F  D  E  L  A  P  L  W  V  E  N  V  V  D  F  A  P
751    TCCGATCACTGCTGGACGGCGTACGATTGTCTCGACCCAATCGGCTTCCAGCCTCTCCTGTGGGAGTATTAGGCT
221     S  D  H  C  W  T  A  Y  D  C  L  D  P  I  G  F  Q  P  L  L  W  E  Y
```

(b)

```
1      TCGTCCCTCTTCTCGCTCCATGGAGACCGGGGGTAGCAAGCGGGAAGGAGACTGCCCCGGGCAGGAAAGgtgagc
1                             M  E  T  G  G  S  K  R  E  G  D  C  P  G  Q  E  R
76     gccggaaccactccctccatctctacttgtatcccgccgcgtttcgctcgaatctacgggcattgctgaggcggc
151    ggcggcgcgccgtcgccgcgacatggaatttgcgcgtgtttccgcggttggtcggtgctgtgaaacatgcccatc
226    taaagcagttatccgctactcgtttcctgttaccgcggcgcgtgtcggactagtcgtaggtcggcggtggtcgcc
301    ctaggtcgatggctgtcctccagttcggttcgccgggtttccgccggctgtagaattatggtttcctccgtcttc
376    tcggttggggattggagttcggcgagattcagagcggtgcgtggcgaactgtcggtgttgggtcgggtgaggcgg
451    cgccgtcctctgaatcggatgcagaagtccccatgtccatggcggcggtcggggattgcccatgccatggcggta
526    cgattgctggtgcacagcatcataaactatatcttcgggagctcgattgcggttggtacccaacccaagtgataa
601    taatctccttgactttttccaccaaggaaacaaggatagccctgcttcgttttgttttagatttatacgacttt
676    ttttttctgtgagaaagattcatatgactctgactgcttatgtttttggtttcaacgtgttttcaccttgtgata
751    tggattgccttgatgaacagGAAGAAGAAAGTGCGCAGGAGAAGCACTGGTCCTGATTCGGTTGCTGAAACCATC
1                          K  K  K  V  R  R  R  S  T  G  P  D  S  V  A  E  T  I
826    AAGAAGTGGAAGGAGGAAAACCAGAAGCTCCAGCAAGAGAATGGATCCCGGAAAGCACCGGCCAAGGGTTCCAAG
36      K  K  W  K  E  E  N  Q  K  L  Q  Q  E  N  G  S  R  K  A  P  A  K  G  S  K
901    AAAGGGTGCATGGCAGGGAAAGGAGGTCCAGAGAATTCAAACTGCGCTTACCGCGGTGTGAGGCAGAGGACGTGG
61      K  G  C  M  A  G  K  G  G  P  E  N  S  N  C  A  Y  R  G  V  R  Q  R  T  W
976    GGGAAATGGGTTGCTGAGATCCGTGAGCCCAACCGTGGCAATCGGCTGTGGCTTGGTTCATTCCCTACCGCAGTC
86      G  K  W  V  A  E  I  R  E  P  N  R  G  N  R  L  W  L  G  S  F  P  T  A  V
1051   GAAGCTGCACGTGCATATGATGATGCGGCAAGGGCAATGTATGGCGCCAAAGCACGTGTCAACTTCTCAGAGCAG
111     E  A  A  R  A  Y  D  D  A  A  R  A  M  Y  G  A  K  A  R  V  N  F  S  E  Q
1126   TCCCCGGATGCCAACTCTGGTTGCACGCTGGCACCTCCATTGCCGATGTCTAATGGGGCAACCGCTGCGTCACAT
136     S  P  D  A  N  S  G  C  T  L  A  P  P  L  P  M  S  N  G  A  T  A  A  S  H
1201   CCTTCTGATGGGAAGGATGAATCGGAGTCTCCTCCTTCTCTTATCTCAAATGCGCCGACAGCTGCGCTGCATCGG
161     P  S  D  G  K  D  E  S  E  S  P  P  S  L  I  S  N  A  P  T  A  A  L  H  R
1276   TCTGATGCTAAGGATGAGTCTGAGTCTGCAGGGACCGTGGCACGTAAGGTGAAAAAAGAAGTGAGCAATGATTTG
186     S  D  A  K  D  E  S  E  S  A  G  T  V  A  R  K  V  K  K  E  V  S  N  D  L
1351   AGAAGTACCCATGAGGAGCACAAGACCCTGGAAGTATCCCAACCAAAAGGGAAGGCTTTACATAAAGCAGCGAAC
211     R  S  T  H  E  E  H  K  T  L  E  V  S  Q  P  K  G  K  A  L  H  K  A  A  N
1426   GTAAGTTATGATTACTTCAACGTCGAGGAAGTTCTTGACATGATAATTGTGGAATTGAGTGCTGATGTAAAAATG
235     V  S  Y  D  Y  F  N  V  E  E  V  L  D  M  I  I  V  E  L  S  A  D  V  K  M
1501   GAAGCACATGAAGAGTACCAAGATGGTGATGATGGGTTTAGTCTTTTCTCATATTAGGGTTTTAGCTATGAGGGT
261     E  A  H  E  E  Y  Q  D  G  D  D  G  F  S  L  F  S  Y
```

(c)

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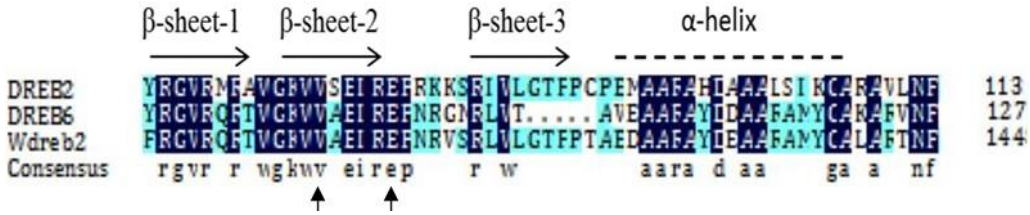
1       AAGAAAACAGGCGACAAGATTGCGAACGCTAGATATCTGGACCCGATCCGGATCGGGTCGGCCATGACGGTAGAT
1                                                                       M  T  V  D
76      CGGAAGCACGCCGAGGCGGCGGCGGCGGCGCCCTTCGAGATCCCGGCGCTCCAGCCTGGAAGGAAAAAGCGACCT
5        R  K  H   A  E   A  A   A  A  A  P   F  E  I   P  A  L   Q  P   G  R   K  K   R  P
151     CGGAGATCACGTGATGGGCCTAATTCAGTCTCTGAAACGATCAGGCGATGGAAAGAAGTGAACCAACAACTGGAG
30       R  R  S   R  D   G  P   N  S  V  S   E  T  I   R  R  W   K  E   V  N   Q  Q   L  E
226     CATGATCCACAGGGTGCAAAGAGGGCGAGGAAGCCACCTGCAAAGGGTTCGAAGAAGGGCTGTATGCTGGGGAAA
55       H  D  P   Q  G   A  K   R  A  R  K   P  P  A   K  G  S   K  K   G  C   M  L   G  K
301     GGAGGACCTGAGAATACACAATGTGGATTCCGTGGTGTAAGGCAACGTACTTGGGGGAAGTGGGTTGCTGAAATT
80       G  G  P   E  N   T  Q   C  G  F  R   G  V  R   Q  R  T   W  G   K  W   V  A   E  I
376     CGGGAGCCAAATCGGGTGAGCAGGCTCTGGCTGGGAACGTTCCCCACTGCTGAGGATGCTGCCCGTGCTTATGAC
105      R  E  P   N  R   V  S   R  L  W  L   G  T  F   P  T  A   E  D   A  A   R  A   Y  D
451     GAGGCAGCCAGAGCAATGTATGGCGCACTGGCTCGTACCAACTTCCCTGTGCATCCTGCACAAGCTCCTGCTGTG
130      E  A  A   R  A   M  Y   G  A  L  A   R  T  N   F  P  V   H  P   A  Q   A  P   A  V
526     GCTGTACCAGCGGCAATCGAAGGTGTTGTACGTGGTGCTTCAGCATCATGCGAGTCTACTACAACGTCCACCAAC
155      A  V  P   A  A   I  E   G  V  V  R   G  A  S   A  S  C   E  S   T  T   T  S   T  N
601     CACTCAGATGTTGCTTCTTCCTTGCCGAGACAAGCTCAAGCTCCTGAGATTTACTCCCAGCCAGATGCGCTTGAG
180      H  S  D   V  A   S  S   L  P  R  Q   A  Q  A   P  E  I   Y  S   Q  P   D  A   L  E
676     TCCACAGAATCAGTTGTGCTGGAGTCTGTCGAGCATTACAGCCATCAAGACACTGTTCCTGACGCTGGCTCAAGC
205      S  T  E   S  V   V  L   E  S  V  E   H  Y  S   H  Q  D   T  V   P  D   A  G   S  S
751     ATTTCAAGGAGCACATCCGAAGAGGATGTGTTCGAGCCATTGGAGCCTATTTCCAGTTTGCCGGATGGAGAAGCA
230      I  S  R   S  T   S  E   E  D  V  F   E  P  L   E  P  I   S  S   L  P   D  G   E  A
826     GACGGTTTTGATATAGAAGAATTATTGAGATTGATGGAAGCCGACCCAATTGAAGTCGAGCTGGTCACTGGGGGC
255      D  G  F   D  I   E  E   L  L  R  L   M  E  A   D  P  I   E  V   E  L   V  T   G  G
901     TCCTGGAATGGTGGAGCCAACACTGGCGTGGAGATGGGCCAGCAGGAACCTCTCTACCTGGATGGCTTGGACCAA
280      S  W  N   G  G   A  N   T  G  V  E   M  G  Q   Q  E  P   L  Y   L  D   G  L   D  Q
976     GGCATGCTGGAGGGCATGCTGCAGTCTGATTATCCTTACCCAATGTGGATATCAGAGGATCGGGCCATGCACAAC
305      G  M  L   E  G   M  L   Q  S  D  Y   P  Y  P   M  W  I   S  E   D  R   A  M   H  N
1051    TCTGCCTTCCATGATGCTGAGATGAGCGAGTTCTTCGAAGGGTTGTGATCCCCTACCGGCG
330      S  A  F   H  D   A  E   M  S  E  F   F  E  G   L
```

Figure S1 The sequences of wheat *DREB* genes. (a), (b) and (c) represent the nucleotide sequence and amino acid sequence of *DREB2*, *DREB6* and *Wdreb2*, respectively. The box and underline denote nuclear localization signal and AP2/EREBP domain, respectively.

(a)



(b)

Figure S2 Alignments of wheat DREBs. (a) and (b) represent the alignments of AP2/EREBP domain and amino acid sequence of *DREB2*, *DREB6* and *Wdreb2*. The similar and consistent amino acids are indicated in blue or dark blue, respectively. β-sheet and α-helix are indicated with long arrow and dotted line, the conserved residues at 14 th and 19 th are marked with short arrow.

(a)

```
DREB2                                  MAASEQSSESSS...TSCTSSYSTSSCSPR............ADDKKRNGGGKRKRAAAADEEPAPAAAA.ASYRGVRM   63
Aegilops tauschii ERF                  MAASEQSSESSS...TSCTSSYSTSSCSPR............ADDKKQNGGNKRKRAAAADEEPAPAAASSASYRGVRM   64
Brachypodium distachyon ERF            MAASEQSSDSNSSTTTTTSSSCSASSCSPRSTADADADAAIGIQNKPQTQHGDNKRKRARVEASASASAN...YRGVRM   76
Dichanthelium oligosanthes DREB3       ..MSDLSSDTSS..TSSYSSSPSTSSSSP...............KSGRGGGKSKRPRAHDGGDGAGVPA...YRGVRM   56
Oryza sativa TINY                      MAASEQSSESSS...TASTS.....SCG................KKQQVAGKRKREDVGGGGEQAAAVA...YRGVRM   51
Setaria italica ERF                    MAASEQSSESSS...TASTS.....SCG................KKQQVAGKRKREDVGGGGEQAAAVA...YRGVRM   51
Sorghum bicolor TINY                   MAMSELSSDTSS...TSSYSSDPSTSTSPR.........AAAPCSAAAAVSG.KKRPRSN.GGGESGSAP..AYRGVRM   63
Zea mays TINY                          MAMSEPSSDTSC...TSSCSSGPSTSTSPR.........AAPSAAAAAASGGGKKRPRSDDGGSSSSSAP..AYRGVRM   65
Domain

DREB2                                  RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDAAALSIKGARAVLNFPDLAPALPRPASLAPCDVQAAAARAALMH  142
Aegilops tauschii ERF                  RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDAAALSIKGARAVLNFPDLAPALPRPASLAPCDVQAAAARAALMH  143
Brachypodium distachyon ERF            RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDAAALCVKGARAVLNFPDLAHALPRPASLAPRDVQAAAARAALMH  155
Dichanthelium oligosanthes DREB3       RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDVAALSIKGARAVLNFPDLAPALPRPASLAPRDVQAAAARAALMQ  135
Oryza sativa TINY                      RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDVAALSIKGARAVLNFPDLAPALPRPASLAPRDVQAAAALAAVMH  130
Setaria italica ERF                    RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDVAALSIKGARAVLNFPDLAPALPRPASLAPRDVQAAAALAAVMH  130
Sorghum bicolor TINY                   RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDVAALSIKGARAVLNFPDLARHLPRPASLAPRDVQAAAARAALMH  142
Zea mays TINY                          RAWGKWVSEIREPRKKSRIWLGTFPCPEMAARAHDAAALSVKGARAVLNFPGLARHLPRPASLAPRDVQAAAARAALMH  144
Domain

DREB2                                  DHDHQC....CSASTS.P......AAAPDSARGNAPAPC.......DQPAARDEPEHEPPFQPSQGNEQQLTAAQVEMV  203
Aegilops tauschii ERF                  DHDHQC....CSASTS.P......AAAPASPRGNTPAPC.......GQPAARDEPEHQPPFQPSQGNEQQLTAAQVEMV  204
Brachypodium distachyon ERF            PERAEE....GAIDDD.........DAPLAGGGEPSPSP.......SPETKENEPSRGS....EETAEAEAEAQ..ELV  208
Dichanthelium oligosanthes DREB3       QQQQKQQSSGGTASSSSPDTPAAVAAAAAAAADDAQRPA.......DAPAHHHHEREPEPSRDQEREPAQVEVA..ELV  205
Oryza sativa TINY                      HHKHPS....SSTSTSSP......PAAPPPDEHHPRHEP.......QQPESSREDDQQQ..QPAAAAAAQMAVA..ELV  188
Setaria italica ERF                    HHKHPS....SSTSTSSP......PAAPPPDEHHPRHEP.......QQPESSREDDQQQ..QPAAAAAAQMAVA..ELV  188
Sorghum bicolor TINY                   MHSDG..AGSGSGSGGSSS.....PSSSSSSSTRDAADT.......DGAAAHDEPEPEPE.PQRQHERQPVEMA.AELV  205
Zea mays TINY                          HSSAGCCCCGGGGGGGSTA.....TATSSSSSSSAAADVGGCGQRRDGAAAHDEPEPE.........RQPLEVA.AELV  208

DREB2                                  FDELAPLWVENVVDFA..PSDH..CWT.AYDCL..DPIGF...QPLLWEY.                             243
Aegilops tauschii ERF                  FDELAPLWVEDVVDFA..PSDH..CWT.AYDCL..DPIGF...QPLLWEY.                             244
Brachypodium distachyon ERF            FDELAPLWVEDVVDFA..PSDH..CWTAAYDALGLDPVGF...QPLLWEY.                             251
Dichanthelium oligosanthes DREB3       FDELAPLWVEDVVEFE..PSDH..SWT.PYDGF..DAVGF...QPLLWEY.                             245
Oryza sativa TINY                      FDELAPLWVEDVVEFG..TSDH..CWT.AYDAL..DPIGF...QPLLWEY.                             228
Setaria italica ERF                    FDELAPLWVEDVVEFG..TSDH..CWT.AYDAL..DPIGF...QPLLWEY.                             228
Sorghum bicolor TINY                   FDELAPLWVEDVVEFGGPPSDH..TWT.PCDGLD.AAVGFLHPLPLLWDY.                             251
Zea mays TINY                          FDELAPLWVEDVVELG.PSADHPWPWT.PCDGLD.IAAGF.HPLPLLWDDY                             255
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(b)

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DREB6                          METGGSKREGDCPGQER.KKKVRRRSTGPDSVAETIKKWKEENQKLLQENGSRKAPAKGSKKGCMAGKGGPENSNCAYR  78
Aegilops biuncialis DREB2      METGGSKREGDCPGQER.KKKVRRRSTGPDSVAETIKKWKEENQKLQQENGSRKAPAKGSKKGCMAGKGGPENSNCAYR  78
Agropyron mongolocum AP2EREBP  METGGSKREGDCPGQER.KKKVRRRSTGPDSVAETIKKWKEQNQKLQQENGFRKAPAKGSKKGCMAGKGGPENSNCAYR  78
Dasypyrum villosum DREB        ................KKKVRRRSTGPDSVAETIKKWKEQNQKLQQENGSRKAPAKGSKKGCMAGKGGPENSNCAYR  61
Leymus multicaulis DREB2       .............MSR.KKKVRRRSTGPDSVAETIKKWKEQNQKLQQENRSRKAPAKGSKKGCMAGKGGPENSNCAYR  64
Thinopyrum bessarabicum DREB   METGGSKREGDCPGQERRKKKVRRRSTGPDSVAETIKKWKEENQKLQQENGSRKAPAKGSKKGCMAGKGGPENSNCAYR  79
Thinopyrum elongatum AP2EREBP  METGGSKREGDCPGQER.KKKVRRRSTGPDSVAETIKKWKEENQKLQQENGSRKAPAKGSKKGCMAGKGGPENSNCAYR  78
Triticum aestivum DREBW73      METGGSKREGDCPGQER.KKKVRRRSTGPDSVAETIKKWKEENQKLQQENGSRKAPAKGSKKGCMAGKGGPENSNCAYR  78
Domain                                                                                                  ——

DREB6                          GVRQRTWGKWVAEIREPNRGNRLWT.....AVEAARAYDDAARAMYGAKARVNFSEQSPDASSGCTLAPPLLMSNGATA 152
Aegilops biuncialis DREB2      GVRQRTWGKWVAEIREPNRGNRLWLGSFPTAVEAARAYDDAARAMYGAKARVNFSEQSPDANSGCTLAPPLPMSNGATA 157
Agropyron mongolocum AP2EREBP  GVRQRTWGKWVAEIREPNRGNRLWLGSFPTAVEAARAYDDAARAMYGAKARVNFSEQSPDANSGCTLASPLLMSNGATS 157
Dasypyrum villosum DREB        GVRQRTWGKWVAEIREPNRGNRLWLGSFPTAVEAARAYDDAARAMYGAKARVNFSEQSPDANSGCTLAPPVLMSNGATA 140
Leymus multicaulis DREB2       GVRQRTWGKWVAEIREPNRGNRLWLGSFPTAVEAARAYDDAARAMYGAKARVNFSEQSPDANSGCT......SNGATA 136
Thinopyrum bessarabicum DREB   GVRHRTWGKWVAEIREPNRGNRLWLGSFPTAVEAARAYDDAARAMYGAKAR........ANSGCTLAPPLPMSNGATA 149
Thinopyrum elongatum AP2EREBP  GVRQRTWGKWVAEIREPNRGNRLWLGSFPTAVEAARAYDDAARAMYGAKARV......PDASSGCTLAPPLLLSNGATA 151
Triticum aestivum DREBW73      GVRQRTWGKWVAEIREPNRGNRLWLGSFPTAVEAARAYDDAA......KARVNFSEQSPDANSGCTLAPPLLTSNGATA 151
Domain                         ————————————————————————————————————————————————————————————————————————————

DREB6                          ASHPSDGKDESE.......................SAGTVAHKVKKEVSNDLRSTHEEHKTLEVSQPKGKALHKEANV 207
Aegilops biuncialis DREB2      ASHPSDGKDESESPPSLISDAPTAPLHRSDAKGESESAGTVARKVKKEVSNDLRSTHEEHKTLEVSQPKGKALHKEANV 236
Agropyron mongolocum AP2EREBP  ASHPSDGKDESESPPSLISNAPTA........AQSESAGTVAHKVKTEVSNDLRSTHEEHKTLEVSQPKGKALHKEANV 228
Dasypyrum villosum DREB        ASHPSDGKDESESPPSLISNAPTAALHRSDAKDESESAGTMAHKVKTEVSNDLRSSHEEHKTLEVSQPKGKALHREANV 219
Leymus multicaulis DREB2       ASHPSDGKDESESPPPLISNAPTAALHQSDAKDESESAGTVAHKVKTEVSNDLRSTHEEHKTLEVSQPKGKALHKEANV 215
Thinopyrum bessarabicum DREB   VSHPSDGKDESGSPPSLISNAPTAALHRSDAKDESESAGTVAHKVKKEVSNDLRSTHEEHKTPEVSQPKGKALHKEANV 228
Thinopyrum elongatum AP2EREBP  ASHPSDGKDESESPPSLISNAPAAALHRSDAKDESESAGTMAHKVKKEVSNDLRSTHEEHKTLEVSQPKGKALHKEANV 230
Triticum aestivum DREBW73      ASHPSDGKDESESPPSLISNGPTAALRRSDAKDESESAGTVARKVKKEVSNDLRSTHEEHKTLEVSQPKGKALHKEANV 230

DREB6                          SYDYFNVEEVLDMIVELSADVKMEAHEEYQDGDDGFSLFSY 249
Aegilops biuncialis DREB2      SYDYFNVEEVLDMIVELSADVKTEAHEEYQDGDDGFSLFSY 278
Agropyron mongolocum AP2EREBP  SYDYFNVEEVLDMIVELSADVKMEAHEEYQDGDDGFSLFSY 270
Dasypyrum villosum DREB        SYDYFNVEEVLDMIVELSADVKMEAHEEYQDGDDGFSLFSY 261
Leymus multicaulis DREB2       SYDYFNVEEVLDMIVELSADVKMEAHEEYQDGDDGFSLFSY 257
Thinopyrum bessarabicum DREB   SYNYFNVEEVLDMIMELSADVKMEAHEEYQDGDDGFSLFSY 270
Thinopyrum elongatum AP2EREBP  SYDHFNVEEVLDMIVELSADVKMEAHEEYQDGDDGFSLFSY 272
Triticum aestivum DREBW73      SYDYFNVEEVLDMIVELSADVKMEAHEEYQDGDDGFSLFSY 272
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(c)

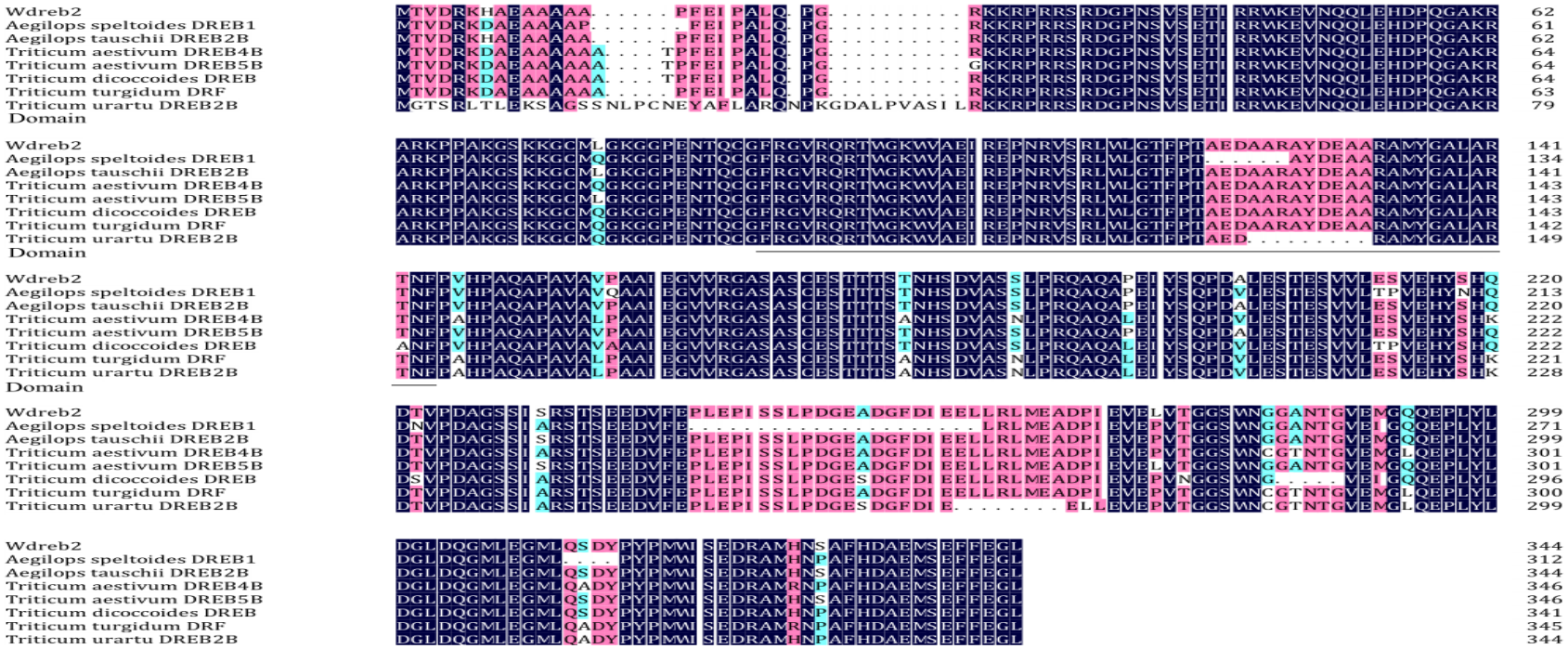

Figure S3 Multiple alignment of wheat DREBs and its homologous sequences. (a), (b) and (c) are the alignment on some homologous sequences of wheat DREB2, DREB6 and Wdreb2, respectively. The underline denotes the AP2/EREBP domain.

(a)

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GGTCGGCAGC ACTACTATGC TCGCCTCATT GCCCTGCAAA AGCCTGAACC GCCACCCACC GATGTGATAT CGCTTCCCCG

GCCATCCCTC TAATCCTCCT TCCCCCAACC CAAACAATAA ACCCTCTTAT TCCCTCCCGT TTTCAACGCC GTGCTCGTGG
                                         CAAT-box
CTGCATTGAA ATCAATTGAT GCATCATTGT TTTTAGGTGT ATGAGCTTTA ACCCAATTTT TTTACTATTT ATTATTAGGG
AT-rich element CAAT-box          TATA-box              GT1-motif
TCTGAGCAAT AACTATCTCT AAGTTCACCA CTAACCATCC TAACATGAGA CTTATACAAG TACAAAAGAC ACGACAAGAT
      CAAT-box
CTTGATCAGA TGGTTATCAA TATCAAATGC AAAACATTTT TGGAGCCGGC CCTTTGCTGA AGATTGTTGG AACTTTGTTT

ATCCCTGAAG AAACATAAAT CTGTTGCTCT TGAGGCCAGA TCCAAAGGAA AAGTCAAGGG TGCCTTTCTT TATGGAAATT
                      GARE-motif
ATTGTACTTG CTTCCTGGGC CATCTGGATT TCCAAAAGCA ATAAGATATT CATATGAGGC GTGCAGTTTA ATGAGATGGA
                                          CAAT-box
AATAAATTTG CCCCCAAGAG CTCACCCTGC TGAAATTTAG GATTAAGAGG AGACATGAAG TTGTTTTTGT CTTCAGGTCC

GACTCCTTTT GTAAACTTTA ATCTGTAATC TTTCTTTCCT TCCTTTTTTT TTCTTCCTTA TTAGGCTTAT CTGTAGTCAT
      P-box
TTGTTGATAT TGTTTAAATT CTTTCATTAA GAGTGAATTC TATTATTTTT ACCTCTTAGT GTCACGTTTG AGACATCAAC
                                              TATA-box          G-box            MBS
TGCTATATTT AACTTCCCGC AAAAAAAAGA ACTGCTATAT TTAACAGGTT TTCACATATT TACCCAATTT AAGCAAACTG
                                                                     CAAT-box
GTGCGACAAA TTATCCTATT TTTTTCTCTT TAAATGTTGA TTGTACATGC CATTTTGGCT GTTTTTTTTA CTTTTTATTT
                                                                   TATA-box  TATA-box
GCTCTTGATT TGTCAAGGGA TGGGTCCTAC CTGCCAGTTG GGGAGCAAGA AATATGAGTG AAAAATTGGA GTACGGCTGT

AGTTTGAACC CGAAATCTCC CCCCCGCAGAC AGGTAAGACT CATCCCCCCGC CGGACCGAGA GCAAACCAGA CAAAACCAAA
           LTR       GC-motif        TCA-motif     GC-motif                ARE       ARE
CAGTAAAACA AACCAGCCAA TATGGCATGC ACAGTCAACA CTGATTCAGA AAATAAATAA ATAAATGGGG ATAATTTGTG
           ARE
GCACAATTTT GCTTACATTG GGTAAAAGTA CATGGAAAAA CTACCAAATG GGACAATTCT TGTCACAAAC GTGAAACGTG
  CAAT-box                                                CAAT-box          ABRE      ABRE
GGGTACAAAT AGAATTAACC CTGATGTAAT TCCATTTGTA CATTTTCCTC TGACAATTAT TGAAAAAGTA GAGTTACAGT
               GT1-motif                                  CAAT-box
AGGGTTTTAC CCTACTATTT TTCTCAAAAA AAAAGAATTC ACTCTTTAAT TAATTTATAA AAATTGTAGT GGGGTATTAT
     TATA-box
CCTACCGTTG CCCTTCAAAA GAAAAATGTC GAGTGAGAAA TAATTATTTC TAATTCGACC GTGCTATAGA CGTTTTTATT
    CCAAT-box                                                                  TATA-box
TCTAAGACAA CATATACTGC GTTCTGAAAT GTCAGGGAGT CCAAGTGAAT CGTTGGGAGG AATTGAATGT CTAGGTGTAG

CAGGGCATGG AGTCAGGAGA GGGAGGCATG CAGCCCCGCC CGGTCCTGTC CGACCCTGCG AGAGACCATG CGACCCTAAT

TATTGATGAT CATGGCGGAG TCAGCTGTCG TTCATGGGTT CCTATCCCAC GCCACGTTGC CTCCACTCTC CTCTACATAT
                          TGA-element  GATA-motif TATC-box  G-box
ACAGCACCAC CTCCCTCTTC CTCCTCGCTC TACCCCTCTC CTTGCTCGCA GTAACTCGAG TCCTACTCCC TGCACGGTCC

TCCCATTACC ACGAGCGAGC GCGTGTCATC TCATACGGGC ACGCGGGGCT ACGTGGTGCT CTCTGCGCGC ACATG
 Sp1                   Skn-1-motif                       ABRE
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(b)

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TTCCCCACTA GAAGCATAAC TTATGCATCT GCACTATGAG TGGACGGGGA AATAGATGCT TAGTGGTGGC AGTGTTTTGA
                                              A-box
ACCTCTTTAG CGGAATATGT TGTTGTCATC GTTTTGCTTC TGTCGTTGCT TCAGTTACAA ATGGTTCTCT TTGAAGGCCA
                                            TGA-element
GACATATCCA TCTGACACAA ACCGTGTGAT GATATAACGA AGTTCCAATT CACGATGTGA AGTGCTCATG TGATGTATTT
                                                CAAT-box
CTATATTAGG TGATCCCACA TGAGCATCGA GAAAACTCAA GATCTTAAAA TGCCAAAAAA CGGTCATATC TTTTATGTCC
TATA-box                                                          MBSI        TATA-box
TCGCAAGGAG ATGCCTAATT TCATCATGAA CCCACTCTGG CCATGGCACC AATACTAATC ATGCCAAGAT AGATCGTCCG
                                                      CAAT-box
AACACTATAC CTACGTACAC TTACATCTAC CATGAGACCT CAAACAAGAG CCTCACGTGT CATGCACCAC TGGATATCAG
            G-box                                       ABRE
ACGAAAGCCT TAGTGCATAT CTCTTGACAA CAAGACAACT GATGCCGATG TTGTGTCCAT TCCCAATGTC ACCTTTTTCC
                                        MBS                         CAAT-box
GCCCCGTCTC CTCACGACGA GAAGAGGATA CAGGTCTGTT TGGATGACGC TGACAACGCC CCCGCAAAAA ATGGATGTGC
SP1                                   GARE-motif   CGTCA-motif        GC-motif
CAATAATTTC AAGGAGGAAT TCAGATCCTT GGTTTCGCCA ACACGTAGTG TGTAGAAATT GAACCGACGA TCGAAAAGTT
CAAT-box                         ACE          ABRE
GGTGGAGGTT CAAACGTTCG CCCATGCTCC CGGTCCATGC TGAAAAAATG GTGTGGAGAG ACCTGATTTT CACAAGCCCA
                                   AuxRR-core
CTTTGACCAT GGTACCAGCC ATGCCAAGAT AGATCGTCCG AACACTATAC CCATGCAGTC GAGCTACATG CACTTGTCTG
  W-box
GTTCGATTGT TCAGTGGCTC TTTCTAAGAG GCGGGGAATG TAAATAGAAA ACATCCCACG AGGAAGGAAT CAAGTGGGAC

CGAGAGATCA TTGCTCATTC GGTGGTTGCC CTCCCCCCCT AATAAGTAAT CCCTCTGCAA AGTAATATAA GAGCGTTTAG

ATCACTATAA AAGGGAGTAC CTATCAAGAA TTGGGCCAGT TAGTATTTTC ATAGAAAAAA AATACCCTTT CCAGGTTTAA
                    Box-E                 MBS
TGATCAAACA TCATCTAGAT AATGACAACG TACCGAGTAG GCCCTACATC TATCGGGGAG CTCACATCCT CACAAGAGCG
                      Skn-1 motif          ABRE
AGGCACATAC TCTCGTGTCT ATATCACGAG ATCTCGAACA AGAGCCATGT GTGACGTCTA CCGTGGGGTC TCAAACGGCA
                                                      TGACG-motif
ACCCCGCGTG TCTATCTGTT GACATCAAGA CAACTGCCAG CGATGCTCTT GTCCATTTTC AACGTCACCT TTTCCCGCCC
                                 MBS                                CGTCA-motif
GCCTTCCCTC GGCGGGAAGA AAGATACGTG TCTATTTGGA GCGGCGCCCA CGCCAACCCC ACAAACTCGG GCGCGCCAAT
                            ABRE
AATTTGACGA AGGAATTTAC ATCATCGGTT TCACCGACAC ACGTGGCGTA AAAGCTGAAC CAACTACTGA AAAGTCGGCG
                                            ABRE
GAGGTCCACG TGCACCGATG CCGAAAATTG ATAGGGCAGC TCCAGACAGC ATTCCAAACA AACCCTACAT AGTGGCAACA
                       LTR
TCACACGAAA AATGTTGAGA TCAGCCTCTC CCGCTCCCTC TTTTCATCAA AAGGAAAACG GCGGAAACGA AATTTGAAAT
                                                                                ERE
CGGCGCCCGA CGGTGATACT CCTATATCGC AGCGAATCCA GGGGGGATCG AGTCGGCGTG TCCGTCCGTT TGGAAGGCTG
      CRT/DRE                                  SP1                  A-box
CCTGCAAGCA GGTTACGACT TGCCTTTACT GG
```

(c)

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ATCCGTTCAC ATGGACAGCG GGCGAGCCTT AGGTTTGCTC GAAGCATTAT GCCAGCGTTT TCATCCGTTT TAATTCAAAC
                              MRE
AGACACACTA GAATCAAAAT GCATCGACAC GTTGGAGTTA CCCTTACAAT GGAGAAGAGA AGACCACGCC GGCCACCACT
                          ABRE                CAAT-box
GATCCATGCA ACCAAAGGCG TCTCACGCCG TCTCAAGAAT AAAAAATGCC TCACGATCCA CCGTGTCATC CCGACTGCCC
                                                                   O2-site
ACGTGTCGTC TCCTATATCG ACTCAGCCCC CAGCCACTGG CCACATGTAG ACGTACACGT GGAACCCACC CAACAGCAGC
ABRE          TATA-box              CAT-box                      ABRE
ACGTCCAATC CACCCCGAAA GAAAAGCACC GGTAGCACTC GAAAGCGTAA AGGAGAAGCC GAGTTTCCTT CGGCACCAAG
     CAAT-box      LTR
TCTCGGGAAG TTTCCCCGCA CCACGGCACA GCTGACGTCA CGCGTCCGCA GCCTCACCCC CACGCACCAG GCCCACGCGG
                                 TGACG-motif
ACCGCGTCGC TTACATCCGG GCCCCACGCG CCAACGCCCC GCACGCGAGT GACCTAGATA ATTCCGTGAG TCCGGAGCAC

GGAGCACCCC GATCCGGGCT ATAAATAGGCG CCCCGGCGTG AGCCCCTGGG GTTTCCGACT TTCTTTCTCT CTTCCTCCAA
                      TATA-box
CTCTCTATCC AAGTCGACGC AGCGAAGAAA CAGGCGACAA GATTGCGAAC GCTAGATATC TGGACCCGAT CCGGATCGGG
                                             CAAT-box
TCGGCCATC
```
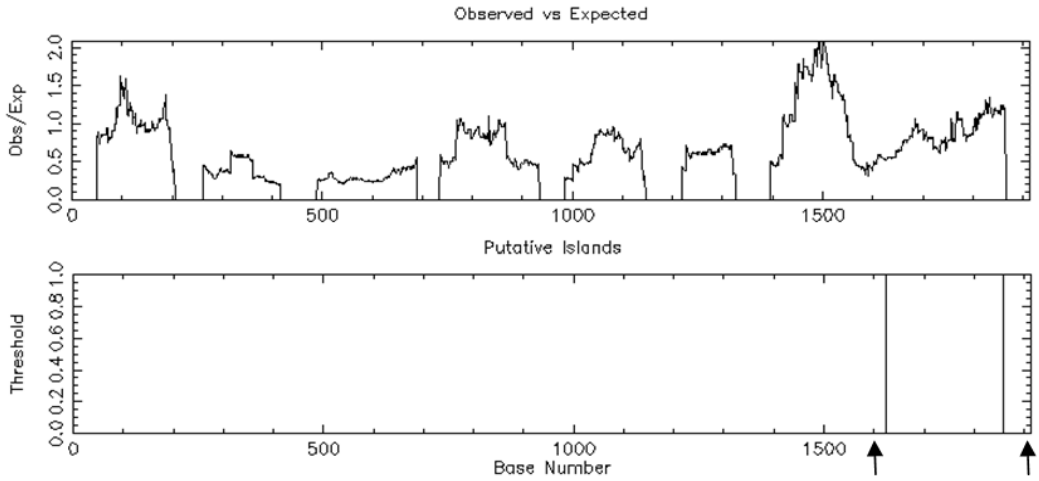
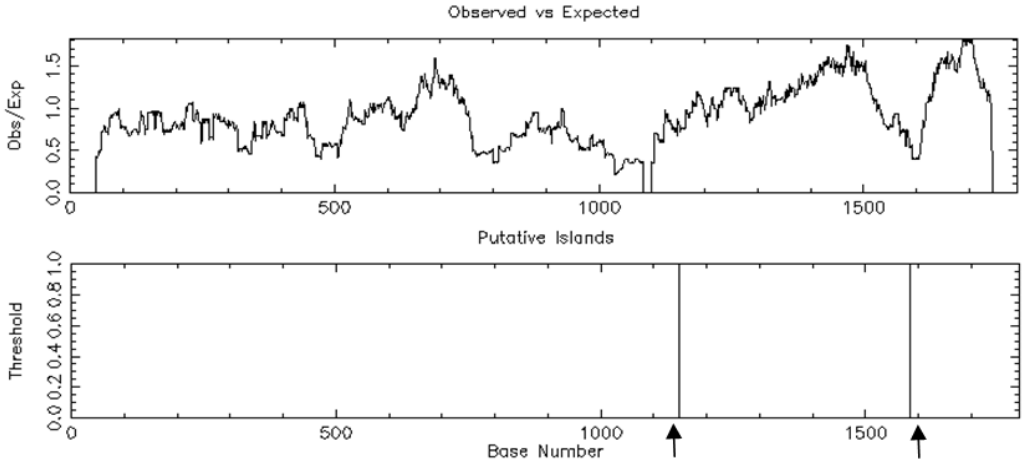

Figure S4 Promoter regions of wheat *DREB* genes. (a), (b) and (c) represent the promoter sequences and some *cis*-acting elements of *DREB2*, *DREB6* and *Wdreb2*, respectively.

(a)



(b)



(c)

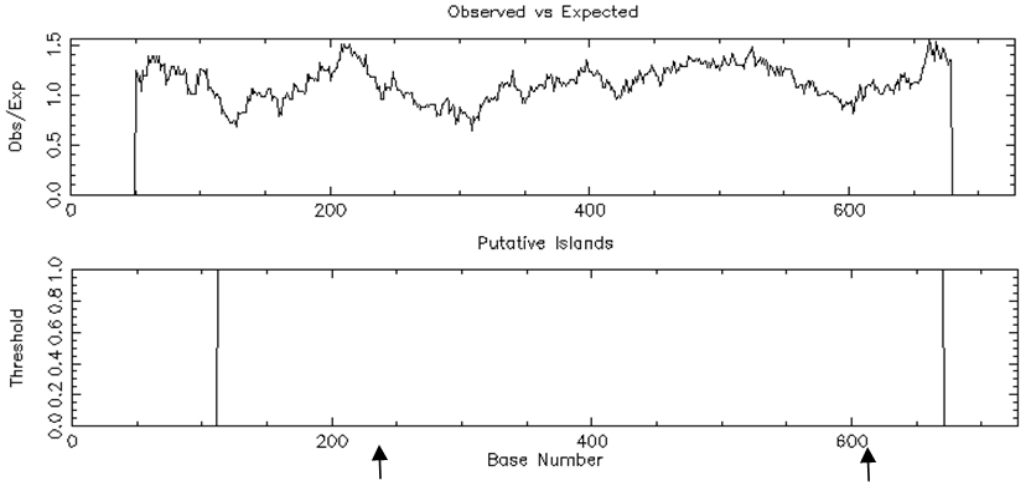
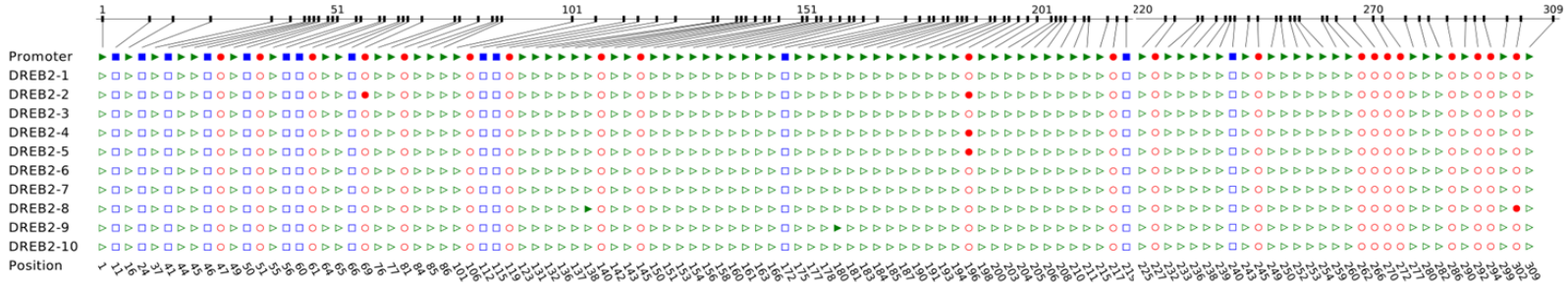
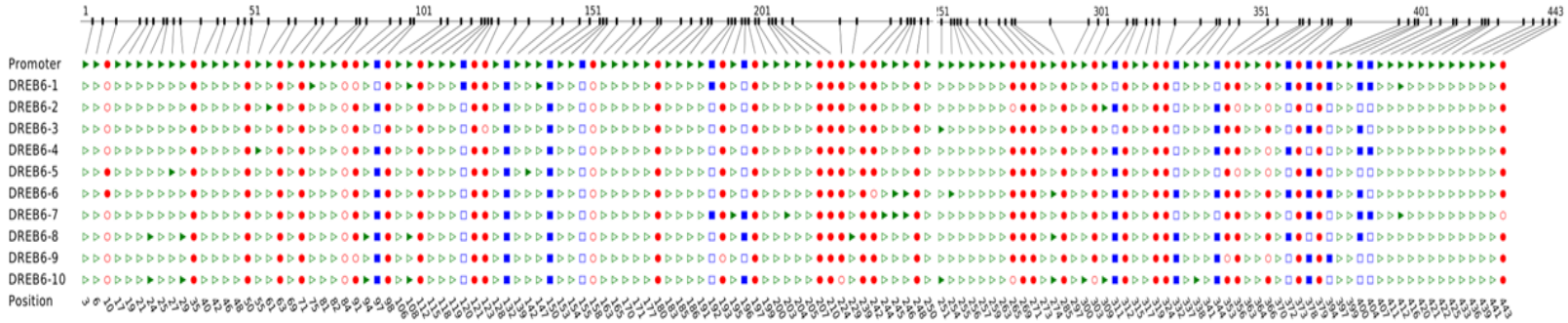


Figure S5 Prediction of CpG islands in the promoter regions of wheat *DREB* genes. (a), (b) and (c) represent the location of putative CpG islands in the promoter regions of *DREB2*, *DREB6* and *Wdreb2*, respectively. The CpG island regions between two arrows below each diagram were examined using BSP, respectively.

(a)



(b)



(c)

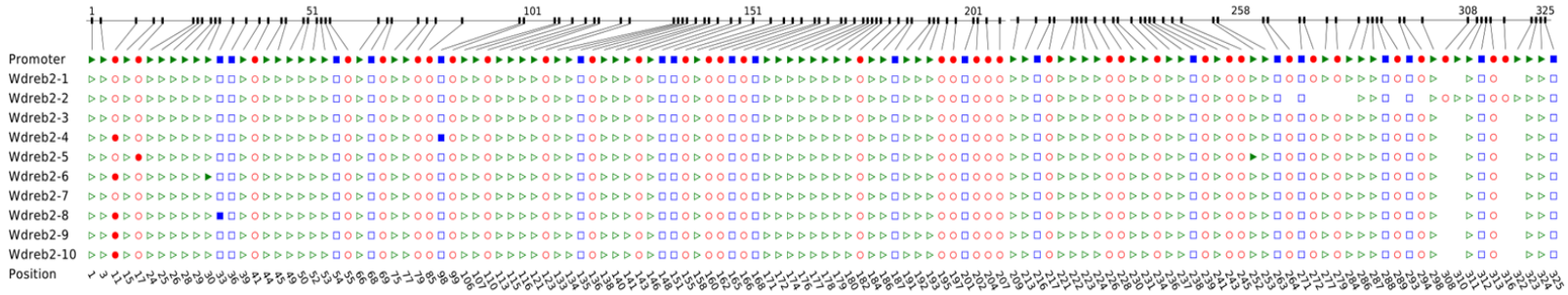


Figure S6 Bisulfite sequencing analysis on the promoter regions of wheat *DREB* genes using CyMATE. (a), (b) and (c) indicate methylation sites in the promoter regions of *DREB2*, *DREB6* and W*dreb2* in wheat leaves. Circles, squares and triangles represent CG, CHG or CHH, filled and hollow circles denote methylated and unmethylated cytosine. Each row represents the sequencing result of one positive clone. The length of CpG island sequence is visualized above each diagram and the potential methylation sites are displayed below.

Table S1 Homologous amino acid sequences of wheat DREBs by BLASP

	Protein	Accession Number	Identity
DREB2	*Aegilops tauschii* ERF	XP-020183719.1	95%
	Setaria italica ERF	XP-004968548.2	66%
	Oryza sativa TINY	XP-015644400.1	64%
	Brachypodium distachyon ERF	XP-010233006.1	64%
	Dichanthelium oligosanthes DREB3	OEL19602.1	61%
	Sorghum bicolor TINY	XP-002454993.1	61%
	Zea mays TINY	XP-020398183.1	59%
DREB6	*Thinopyrum elongatum* AP2/EREBP	AEI98920.1	98%
	Triticum aestivum DREBW73	AAY44604.1	98%
	Agropyron mongolocum AP2/EREBP	AJD80690.1	94%
	Aegilops biuncialis DREB2	CBX87024.1	97%
	Leymus multicaulis DREB2	AFO12475.1	97%
	Thinopyrum bessarabicum DREB	AIY22662.1	96%
	Dasypyrum villosum DREB	AIY22669.1	97%
Wdreb2	*Aegilops tauschii* DREB2B	XP-020156298.1	99%
	Triticum aestivum DREB5B	AAX13287.1	99%
	Aegilops speltoides DREB1	AC035588.1	96%
	Triticum turgidum DRF	AFO10996.1	95%
	Triticum aestivum DREB4B	AAX13283.1	94%
	Triticum dicoccoides DREB	ADM93284.1	93%
	Triticum urartu DREB2B	EMS45041.1	93%

The homologous sequences of wheat DREB2, DREB6 and Wdreb2 were retrieved with BlastP algorithm, which are mainly from some species in Gramineae. The homologous sequences having higher identity with wheat DREBs were selected from some Genera in Gramineae, and were further analyzed.

Table S2 The *cis*-acting elements in the promoter of *DREB2*

Element	Sequence	Function	Number
TATA-box	TATAWAW	Core promoter element around -30 of transcription start	13
CAAT-box	CAAT	Common cis-acting element in promoter and enhancer regions	34
ABRE	CGTACGTGCA	*Cis*-acting element involved in the abscisic acid responsiveness	5
ACE	AAAACGTTTA	*Cis*-acting element involved in light responsiveness	1
ARE	TGGTTT	*Cis*-acting regulatory element essential for the anaerobic induction	3
MBS	CAACTG	MYB binding site involved in drought-inducibility	2
LTR	CCGAAA	*Cis*-acting element involved in low-temperature responsiveness	1
G-box	(T/C)ACGT(C/G/T)	*Cis*-acting regulatory element involved in light responsiveness	6
C-repeat/DRE	TGGCCGAC	Regulatory element involved in cold- and dehydration-responsiveness	1
EIER	TTCGACC	Elicitor responsive element	1
TGACG-motif	TGACG	*Cis*-acting regulatory element involved in the MeJA-responsiveness	1
Skn-1-motif	GTCAT	*Cis*-acting regulatory element required for endosperm expression	1
SP1	CC(G/A)CCC	Light responsive element	4
GARE-motif	TCTGTTG	Gibberellin responsive element	1
TCA-element	TCAGAAGAGG	*Cis*-acting element involved in salicylic acid responsiveness	2
TGA-element	AACGAC	Auxin responsive element	1
OCT	CGCGGATC	*Cis*-acting regulatory element related to meristem specific activation	1
TATC-box	TATCCCA	*Cis*-acting element involved in gibberellins responsiveness	1
Circadian	CAANNNNATC	*Cis*-acting regulatory element involved in circadian control	1
MNF	GTGCCC(A/T)	Light responsive element	1
HD-Zip	CAAT(A/T)ATTG	Element involved in differentiation of the palisade mesophyll cells	1
GT1-motif	GGTTAAT	Light responsive element	2
GC-motif	CCCCCG	Enhancer-like element involved in anoxic specific inducibility	2
TATC-box	TATCCCA	*Cis*-acting element involved in gibberellins responsiveness	1
P-box	CCTTTTG	Gibberellins responsive element	1

Table S3 The *cis*-acting elements in the promoter of *DREB6*

Element	Sequence	Function	Number
TATA-box	TATAWAW	Core promoter element around -30 of transcription start	10
CAAT-box	CAAT	Common *cis*-acting element in promoter and enhancer regions	19
ABRE	CGTACGTGCA	*Cis*-acting element involved in the abscisic acid responsiveness	10
ACE	AAAACGTTTA	*Cis*-acting element involved in light responsiveness	2
ARE	TGGTTT1	*Cis*-acting regulatory element essential for the anaerobic induction	1
MBS	CAACTG	MYB binding site involved in drought-inducibility	5
LTR	CCGAAA	*Cis*-acting element involved in low-temperature responsiveness	1
AuxRR-core	GGTCCAT	*Cis*-acting regulatory element involved in auxin responsiveness	1
TGA-element	AACGAC	Auxin responsive element	1
TGACG-motif	TGACG	*Cis*-acting regulatory element involved in the MeJA-responsiveness	4
CGTCA-motif	CGTCA	*Cis*-acting regulatory element involved in the MeJA-responsiveness	3
CAT-box	GCCACT	*Cis*-acting regulatory element related to meristem expression	2
G-box	(C/T)ACG(T/A)G	*Cis*-acting regulatory element involved in light responsiveness	11
MBSI	aaAaaC(G/C)GTTA	MYB binding site involved in flavonoid biosynthetic genes regulation	1
A-box	CCGTCC	*Cis*-acting regulatory element	2
GARE-motif	AAACAGA	Gibberellin responsive element	2
P-box	CCTTTTG	Gibberellin responsive element	1
Circadian	CAANNNNATC	*Cis*-acting regulatory element involved in circadian control	1
DRE/CRT	RCCGAC	Drought, high salt and cold-responsive element	1
ERE	ATTTCAAA	Ethylene-responsive element	1
SP1	GGGCGG	Light responsive element	6
Box I	TTTCAAA	Light responsive element	1
GC-motif	CCCCCG	Enhancer-like element involved in anoxic specific inducibility	1
W-box	TTGACC	Fungal elicitor responsive element	1

Table S4 The *cis*-acting elements in the promoter of *Wdreb2*

Element	Sequence	Function	Number
5UTRpy-rich stretch	TTTCTTCTCT	*Cis*-acting element conferring high transcription levels	1
TATA-box	TATAWAW	Core promoter element around -30 of transcription start	5
CAAT-box	CAAT	Common *cis*-acting element in promoter and enhancer regions	4
CAT-box	GCCACT	*Cis*-acting regulatory element related to meristem expression	1
ABRE	CGTACGTGCA	*Cis*-acting element involved in the abscisic acid responsiveness	8
ACE	AAAACGTTTA	*Cis*-acting element involved in light responsiveness	1
O2-site	GATGACATGG	*Cis*-acting regulatory element involved in zein metabolism	1
C-repeat/DRE	TGGCCGAC	Regulatory element involved in cold and dehydration responsiveness	1
C-box	CTGACGTCAG	*Cis*-acting regulatory element involved in light responsiveness	1
CE3	GACGCGTGTC	*Cis*-acting element involved in ABA and VP1 responsiveness	1
G-box	CACGT(G/C/T)	*Cis*-acting regulatory element involved in light responsiveness	7
MRE	AACCTAA	MYB binding site involved in light responsiveness	1
LTR	CCGAAA	*Cis*-acting element involved in low-temperature responsiveness	1
TGACG-motif	TGACG	*Cis*-acting regulatory element involved in the MeJA-responsiveness	2
GARE-motif	TCTGTTG	Gibberellin responsive element	1
SP1	CCGCCC	Light responsive element	2
as1	TGACGTCA	*Cis*-acting regulatory element involved in the root specificexpression	1
CGTCA-motif	CGTCA	*Cis*-acting regulatory element involved in the MeJA-responsiveness	2

Table S5 Correlation between promoter methylation and expression of *DREB* genes

Gene / Methylation type	Pearson's r		
	DREB2	*DREB6*	*Wdreb2*
CG	-0.952	-0.981	-0.986
CHG	-0.327	-0.950	-0.973
CHH	-0.509	0.656	-0.878

Pearson's r represents the relationship between expression levels of *DREB2*, *DREB6*, *Wdreb2* in wheat leaves and methylation rates at CG, CHG or CHH sites in their promoter regions under the treatment of 15% PEG_{6000} solution. According to the expression level and methylation rate when wheat seedlings incubated in PEG_{6000} solution for 12 h, Pearson's r analysis of *DREBs* were performed.

Table S6 Primers used in this study

Experiment	Primer	Sequence（5’ to 3’）
Gene cloning	*DREB2*-F	CTACTCCCTGCACGGTCCT
	DREB2-R	GCCAAGCCTAATACTCCCAC
	DREB6-F	CGTCCCTCTTCTCGCTCCA
	DREB6-R	CTAATATGAGAAAAGACTAAACCC
	Wdreb2-F	AAGAAAACAGGCGACAAGAT
	Wdreb2-R	ACGAAGCACAAAAAACTAGC
qRT-PCR	*β-Actin*-F	CCAAGGCGGAGTACGATGAGTCT
	β-Actin-R	TTCATACAGCAGGCAAGCACCAT
	DREB2-F	GCGTACAACACCTTGATTTCC
	DREB2-R	AAACTCAACTCACATCTAAGC
	DREB6-F	CGGCTGTGGCTTGGTTCATTC
	DREB6-R	CAGTTGCCCCATTAGACATC
	Wdreb2-F	AGATGTTGCTTCTTCCTTGCC
	Wdreb2-R	GATGTGCTCCTTGAAATGCTTG
Promoter cloning	*DREB2*-F	CCCAAGCTTGGTCGGCAGCACTACTATG
	DREB2-R	CATGCCATGGCATGTGCGCGCAGAGAGC
	DREB6-F	CCCAAGCTTTTCCCCACTAGAAGCATAAC
	DREB6-R	AACTGCAGCCAGTAAAGGCAAGTCGTAA
	Wdreb2-F	CCCAAGCTTATCCGTTCACATGGACAGC
	Wdreb2-R	AACTGCAGGATGGCCGACCCGATCCGGAT
BSP	*DREB2*-F	GTTTAGGTGTAGTAGGGTATGGAG
	DREB2-R	AAAAACACCACRTAACCC
	DREB6-1-F	TTTATATTTATYGGGGAGTTTATA
	DREB6-1-R	AAAACCRATAATATAAATTCCTTC
	DREB6-2-F	TGTTAGYGATGTTTTTGTTTAT
	DREB6-2-R	CAACATTTTTCRTATAATATTACCAC
	Wdreb2-F	GTTATATGTAGAYGTATAYGTGGA
	Wdreb2-R	AAAACCCCAAAAACTCAC