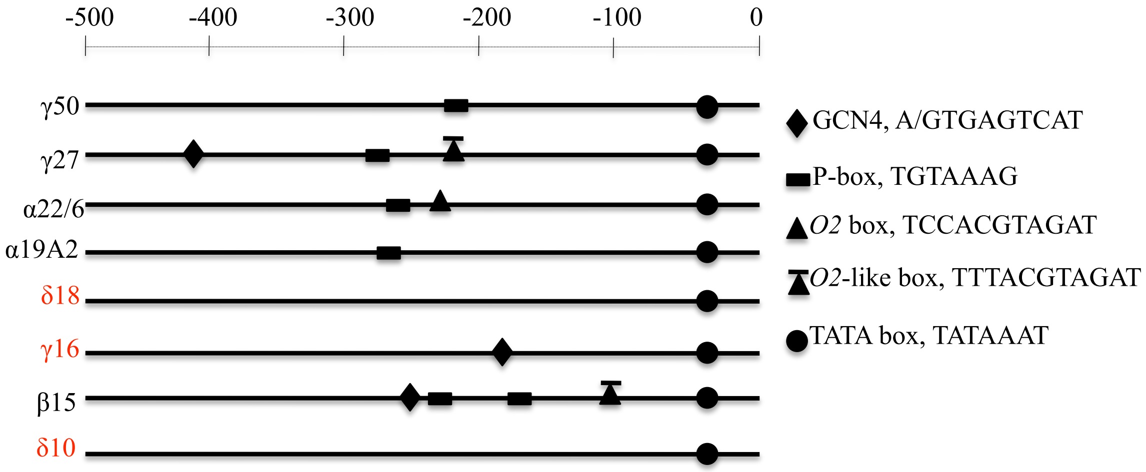
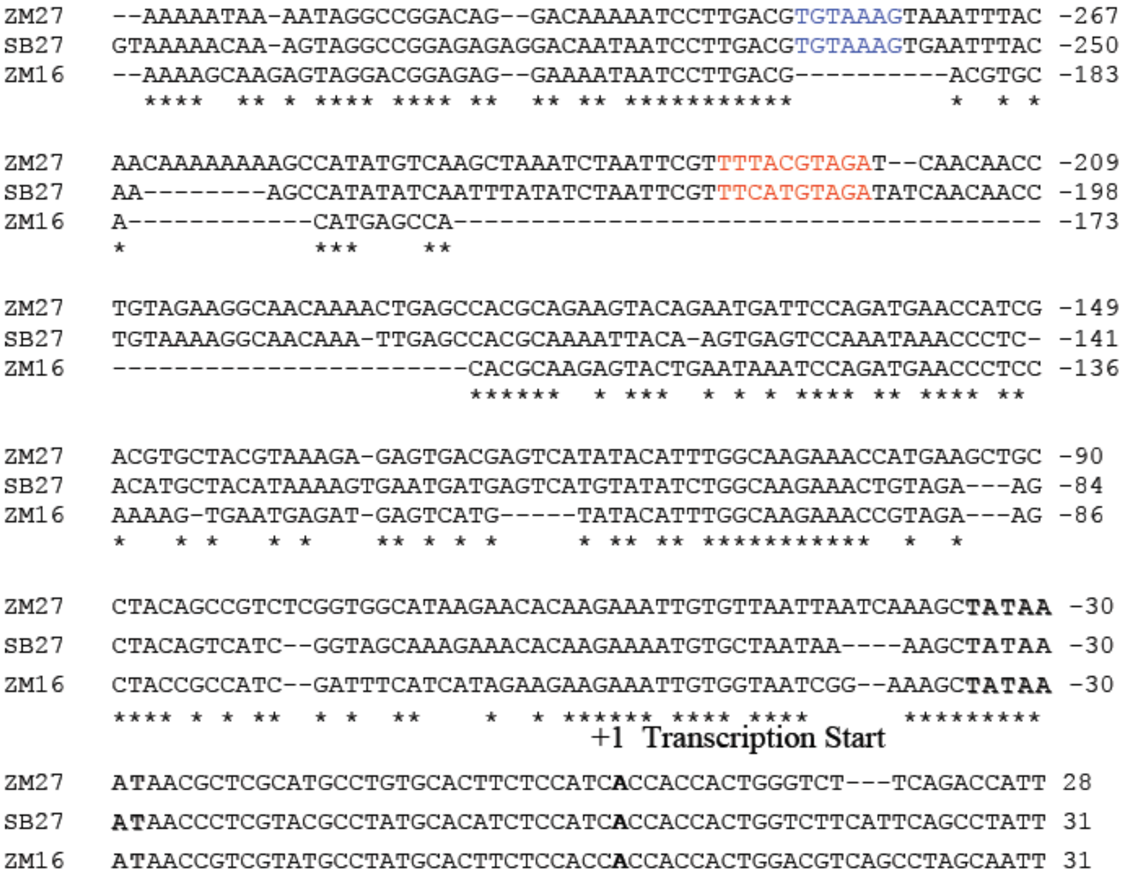


Figure S1 Cis-elements in zein-gene promoters.



```
ZM27   --AAAAATAA-AATAGGCCGGACAG--GACAAAAATCCTTGACGTGTAAAGTAAATTTAC -267
SB27   GTAAAAACAA-AGTAGGCCGGAGAGAGGACAATAATCCTTGACGTGTAAAGTGAATTTAC -250
ZM16   --AAAAGCAAGAGTAGGACGGAGAG--GAAAATAATCCTTGACG----------ACGTGC -183
         ****  ** * **** **** **  ** ** ***********          *  * *

ZM27   AACAAAAAAAAGCCATATGTCAAGCTAAATCTAATTCGTTTTACGTAGAT--CAACAACC -209
SB27   AA--------AGCCATATATCAATTTATATCTAATTCGTTTCATGTAGATATCAACAACC -198
ZM16   A------------CATGAGCCA-------------------------------------- -173
       *            ***    **

ZM27   TGTAGAAGGCAACAAAACTGAGCCACGCAGAAGTACAGAATGATTCCAGATGAACCATCG -149
SB27   TGTAAAAGGCAACAAA-TTGAGCCACGCAAAATTACA-AGTGAGTCCAAATAAACCCTC- -141
ZM16   -----------------------CACGCAAGAGTACTGAATAAATCCAGATGAACCCTCC -136
                              ******  * ***  * * * **** ** **** **

ZM27   ACGTGCTACGTAAAGA-GAGTGACGAGTCATATACATTTGGCAAGAAACCATGAAGCTGC -90
SB27   ACATGCTACATAAAAGTGAATGATGAGTCATGTATATCTGGCAAGAAACTGTAGA---AG -84
ZM16   AAAAG-TGAATGAGAT-GAGTCATG-----TATACATTTGGCAAGAAACCGTAGA---AG -86
       *   * *   * *    ** * * *     * ** ** ***********  *  *

ZM27   CTACAGCCGTCTCGGTGGCATAAGAACACAAGAAATTGTGTTAATTAATCAAAGCTATAA -30
SB27   CTACAGTCATC--GGTAGCAAAGAAACACAAGAAAATGTGCTAATAA----AAGCTATAA -30
ZM16   CTACCGCCATC--GATTTCATCATAGAAGAAGAAATTGTGGTAATCGG--AAAGCTATAA -30
       **** * * **  * *  **    *    ****** **** ****      *********
                                       +1 Transcription Start
ZM27   ATAACGCTCGCATGCCTGTGCACTTCTCCATCACCACCACTGGGTCT---TCAGACCATT 28
SB27   ATAACCCTCGTACGCCTATGCACATCTCCATCACCACCACTGGTCTTCATTCAGCCTATT 31
ZM16   ATAACCGTCGTATGCCTATGCACTTCTCCACCACCACCACTGGACGTCAGCCTAGCAATT 31
```

Figure S2 Alignment of the 27- and 16-kDa γ-zein and 27-kDa γ-kafirin promoters.

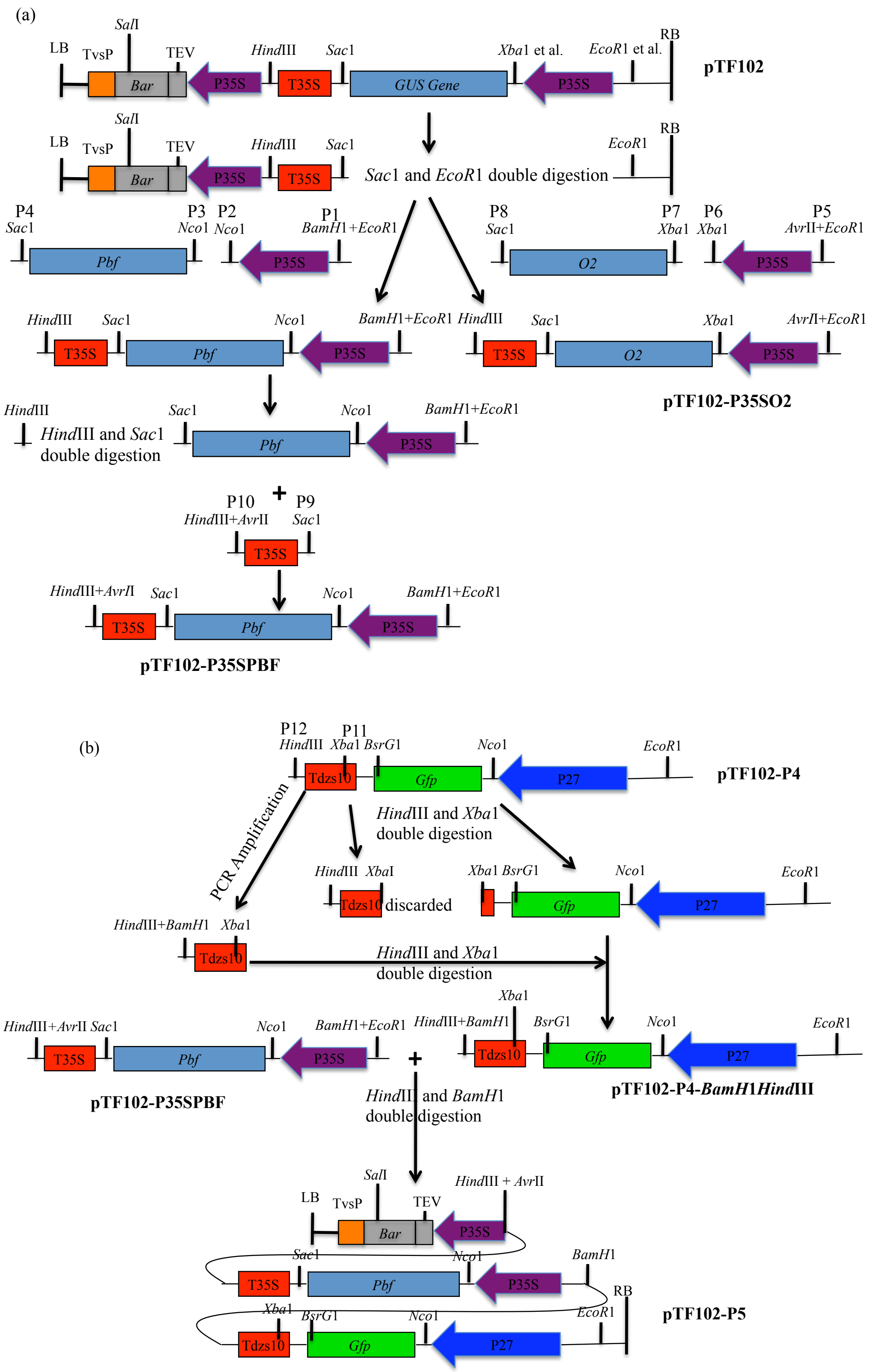
```
1     2                       3           4  5                 6
C  A  C  G  G  T  G  A  G  T  C  A  T  G  C  C  G  A  G  A  T  C  A  T
   7     8        9                       10          11          12
A  C  T  C  A  T  C  T  G  A  T  A  T  A  C  A  T  G  C  T  T  A  C  A
   13    14    15             16             17          18       19
G  C  T  C  A  C  A  A  G  A  C  A  T  T  A  C  A  A  A  C  A  A  C  T
20                   21             22                   23
C  A  T  A  T  T  G  C  A  T  T  A  C  A  A  A  G  A  T  C  G  T  T  T
24                                                    25 26          27
C  A  T  G  A  A  A  A  A  T  A  A  A  A  T  A  G  G  C  C  G  G  A  C
            28                   29 30             31
A  G  G  A  C  A  A  A  A  A  T  C  C  T  T  G  A  C  G  T  G  T  A  A
                              32       33                            34
A  G  T  A  A  A  T  T  T  A  C  A  A  C  A  A  A  A  A  A  A  A  G  C
35                   36          37                38                39
C  A  T  A  T  G  T  C  A  A  G  C  T  A  A  A  T  C  T  A  A  T  T  C
                  40                   41       42       43 44
G  T  T  T  T  A  C  G  T  A  G  A  T  C  A  A  C  A  A  C  C  T  G  T
                  45       46             47             48 49    50
A  G  A  A  G  G  C  A  A  C  A  A  A  A  C  T  G  A  G  C  C  A  C  G
51                      52                            53 54
C  A  G  A  A  G  T  A  C  A  G  A  A  T  G  A  T  T  C  C  A  G  A  T
         55 56       57       58          59       60
G  A  A  C  C  A  T  C  G  A  C  G  T  G  C  T  A  C  G  T  A  A  A  G
                     61             62                63
A  G  A  G  T  G  A  C  G  A  G  T  C  A  T  A  T  A  C  A  T  T  T  G
   64                   65 66                   67       68 69       70
G  C  A  A  G  A  A  A  C  C  A  T  G  A  A  G  C  T  G  C  C  T  A  C
      71 72       73    74                75                      76
A  G  C  C  G  T  C  T  C  G  G  T  G  G  C  A  T  A  A  G  A  A  C  A
77                                                             78
C  A  A  G  A  A  A  T  T  G  T  G  T  T  A  A  T  T  A  A  T  C  A  A
      79                            80    81    82    83          84 85
A  G  C  T  A  T  A  A  A  T  A  A  C  G  C  T  C  G  C  A  T  G  C  C
            86    87       88    89 90
T  G  T  G  C  A  C  T  T  C  T  C  C  A  (Transcription Start Site)
```

Figure S3 Cytosines in the 27-kDa γ-zein promoter. The 421-bp fragment immediately upstream of the transcription start site contains 90 cytosines, covering the P-box, O2-like box and TATA box. P-box, "ACGT" core motif and TATA box are shaded. The cytosine positions indicated in Figs. 4a and S6d are numbered in the sequence.

```
                                    1   2   3   4
Zp22/6          TGTGTAAAGGTGAAGAGATCTTGCATGTCATTC
azs22.11        TGTGTAAAGGTGAAGAGATGATGCATGTCAT-C
azs22.12        TGTGTAAAGGTGAAGAGATGATGCATGTCAT-C
azs22.13        TGTGCAAAGGTGAAGAGATCATGCATGTCATTC
azs22.4         TGTGTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.1         TGTGTAAAGGTGAAGCGATCATGCATGTCATTC
azs22.3         TGTGTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.5         TGTGTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.19        TGTGTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.7         TGTGTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.8         TGTGTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.2         TGTGTAAAGGTGAAGCGATCATGCATGTCATTC
azs22.20        TGTGTAAAGGTGAAGAGATCATGCATTTCATTC
azs22.6         TGTTTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.9         TGTGTAAAGGTGAAGAGATCATGCATGTCATTC
azs22.16        TGTGTAAAGGTGAAGAGATCATGCATGTCATTC

                5 6                7              8 9   10
Zp22/6          CACGTAGAT-AAAAAGAATGCATATATAAAAATGGCACATTTTCTTGTAGGTAGTGGAAA
azs22.11        CAAGTATATGAAAAT-AATTCCTATA-GAAAATGACACTTTTTCTTATAGGTAGTGGAAA
azs22.12        CAAGTATATGAAAAG-AATTCCTATA-GAAAATGACAATTTTTCTTGTAGGTAATGGAAA
azs22.13        CTCATGTATGGAAAG-AATTCCAATA-GAAAATGACGAATTTTCCTGTAGGTAGTGAAAA
azs22.4         CACGTAGATGAAAA--AATTCCTATATAAAAATGACACCTTTTCTTGTAGGTAGTGGAAA
azs22.1         CACGTAGATGAAAAAAAATTCCTATATAAAAATGACAATTTTTCTTGTAGGTAGTGGAAA
azs22.3         CACGTAGATGAAAAG-AATTCCTATATAAAA-TGACACCTTTTCTTGTAGGTAGTGGAAA
azs22.5         CACGTAGATGAAAAG-AATTCCTATATAAAA-TGACACCTTTTCTTGTAGGTAGTGGAAA
azs22.19        CACGTAGATGAAAAG-AATTCCTATATAAAA-TGACACCTTTTCTTGTAGGTAGTGGAAA
azs22.7         CACGTAGATGAAAAG-AATTCCTATATAAAA-TGACACCTTTTCTTGTAGGTAGTGGAAA
azs22.8         CACGTAGATGAAAAG-AATTCCTATATAAAA-TGACACCTTTTCTTGTAGGTAGTGGAAA
azs22.2         CACATAGATTAAAAA-AAATCCTATATAAAAATGACAATTTTTCTTGTAGGTAGTGGAAA
azs22.20        CACGTAGATAAAAAG-AGTTCCTATATAAGAATGGCACATTTTCTTGTAGGTAGTGGAAA
azs22.6         CACGTAGATGAAAAG-AATTCCTATATAAAA-TGACACATTTTCTTGTAGGTAGTGGAAA
azs22.9         CACGTAGATAAAAAG-AATGCCTATATAAAAATGGCACATTTTCTTGTAGGTAGTGGAAA
azs22.16        CACATAAATGAAAAG-AATTCCTATATAAAAATGACATGTTTTGTTGTAGGTAGTGGAAA

                    11 1213 14   1516         1718           19     20
Zp22/6          GTATCTTTCCAGCTAAGACC----ATATAATCCGATAAAGGTGATAACTAAATGTCGAAA
azs22.11        CTATCTTTCTA--------------TATAATCCGATGAAACCGATAACTAAATGTCGAAA
azs22.12        CTAGCTTTCCAGCAAAGACCA----TATAATCTGATGAAACTGATAACCAAATGTCGAAA
azs22.13        CTATCTTTATAGCAAAGTCCA----TATAATCATATGAAACTGATGACTAAATGTCAAAA
azs22.4         GTACCTTTCCAGCAAAGATCATATATATAATCCGATAAAGCTGAAAACTAAATGTCGAAA
azs22.1         CTATCTTTCTAGCAAAGACCATATATATAATCCGATAAAGCCGATAACTAAATGTCGAAA
azs22.3         GTATCTTTCCAGCAAAGACCATATA----ATCCGATAAAGTTGATAACTAAATGTCAAAA
azs22.5         GTATCTTTCCAGCAAAGACCATATA----ATCCAATAAAGTTGATAACTAAATGTCGAAA
azs22.19        GTATCTTTCCAGCAAAGACCATATA----ATCCGATAAAGTTGATAACTAAATGTCAAAA
azs22.7         GTATCTTTCCAGCAAAGACCATATA----ATCCGATAAAGTTGATAACTAAATGTCGAAA
azs22.8         GTATCTTTCCAGCAAATACCATATA----ATCCGATAAAGCGGATAACTAAATGTCGAAA
azs22.2         GTATCTTTCCAGCAAAGACTATATATATAATCCGATAAAGCCGATAACTAAATGTCAAAA
azs22.20        GTATCTTTCCAGCAAATACCATATA----ATCCGATAAAGATGATAACTAAATGTCGAAA
azs22.6         GTATCTTTCCAGCAAAGACTATA------ATCCGATAAAGTTGATAACTAAATGTCGAAA
azs22.9         GTATCTTTCCAGCAAAGACCATATA----ATCCGATAAAGCTGATAACTAAATGTCGAAA
azs22.16        TTATCTTTCCAGCAAAGACCATATA----ATCCGATAAAGCTGATAACTAAATGTCAAAA

                 21       2223  24 25  2627  28                     29
Zp22/6          TCGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGG--AAAAAAAAGACAAAAT
azs22.11        TTGAGTAGGTGCCATATCATCGATAGCTTATCTATTGTTTGGC--AAAAA--GACAAAAT
azs22.12        TTGAGTAGGTGCCATATCATTGATAGCTTATCTATTGTTTGGC--AAAAA--GATAAAAT
azs22.13        TTGAGTAGGTGCCATATCATCTATAGCTTATCCATTGTTGGGA--AAAAA--TACAAAAT
azs22.4         TCGAGTAGATGCCATATCATCTATACCTTATCTCTTGTTTGGA--AAAAA--GACAAAAC
azs22.1         TCGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGG---AAAAA--GACAAAAT
azs22.3         TAGAGTAGATGCCATATCATATATACCTTATCTGTTGTTTGGA--AAAAAAAGACTAAAT
azs22.5         TAGAGTAGATGCCATATCATTTATACCTTATCTGTTGTTTGGA--AAAAAA-GACTAAAT
```

```
azs22.19       TAGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGGA--AAAA---GACTAAAT
azs22.7        TAGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGGA--AAAA---GACTAAAT
azs22.8        TCGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGGA--AAAAA--GACAAAAT
azs22.2        TCGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGGA--AAAAA--GACAAAAT
azs22.20       TCGAGTAGATGCCATATCATCTATATCTTATCTGTTGTTTGGA--AAAAAA-GACAAAAT
azs22.6        AAGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGGA--AAAAAA-GACTAACT
azs22.9        TCGAGTAGATGCCATATCATCTATACCTTATCTGTTGTTTGGAAAAAAAAAAGACAAAAT
azs22.16       TCGAGTAAGTGCCATATCATCTATATCTTATCTGTTGTTTGGA—-AAAA---GACAAAAT

              3031                    32333435        36373839  40
Zp22/6         CCAAAAAA-TTTATAT----GAGATCTCACCTATATAAATAGCGCCCAAATCAGTAGTTA
azs22.11       CCAAATATATATATAT----GAGATCTCACATGTATGAATATCTCCCAAATCAGTAGTTA
azs22.12       CCAAATATATATATATATATGAGATCTCACCTATATAAATATCTCCCAAATCAGTAGTTA
azs22.13       CCAAAAA-ATATATAT----GAGACCTCACCTGTATATATAACCCCCAAATCAGTAGTTA
azs22.4        CAAAAAA--TATTTAT----GAGGTCTCACTTGTATAAATAGCTCCCAAATCAGTAGTTA
azs22.1        CCAAAAA-ATATATAT----GAGATCTCACTTGTATGAATAGCTCCCAAATCAGTAATTA
azs22.3        CCCAAAA-ATATATAT----GAGATCTCACTTGTATAAATAGCTCCCAAATTAGTAGTTA
azs22.5        CC--AAA-ATATATAT----GACATCTCACTTGTATAAATAGCTCCCAAATCAGCAGTTA
azs22.19       CCAAAAA-ATATATAT----GAGATCTCACTTGTATAAATAGCTCCCAAATCAGTAGTTA
azs22.7        CCAAAAATATATATAT----AAGATCTCACTTGTATAAATAGCTCCCAAATTAGTAGTTA
azs22.8        CCAAAAA-ATATATTT----GAGACCTCACCTGTATAAATAGCTCCCAAATCAGTAGTTA
azs22.2        CCAAAAAAATATATAT----GAGATCTCACTTGTATAAATAGCTCCCAAATCAGTAGTTA
azs22.20       CCAACAA-AAATATTC----GAGACCTCACCTATATAAATAGCTCCCATATCAGTAGTTA
azs22.6        ACAAAAA-ATATATAT----GAGATCTCACTTGTATAAATAGCTCCCAAATCAGTAGTTA
azs22.9        CCAAAAAAAAATATAA----GAGATCTCACCTATATAAATAGCTCTGAAATCAGTAGTTA
azs22.16       CCAAAAAAAAATATAT----GAGATCTCACATGTATAAATAGCTCCCAAATCAGTAGTTA

                4142
Zp22/6         ATCCA
azs22.11       ATTCA
azs22.12       ATCCA
azs22.13       ATTCA
azs22.4        ATCCA
azs22.1        ATCCG
azs22.3        A-CCA
azs22.5        A-CCA
azs22.19       A-CCA
azs22.7        A-CCA
azs22.8        ATCCA
azs22.2        ATCCA
azs22.20       ATCCA
azs22.6        A-CCA
azs22.9        ATCCA
azs22.16       ATACA
```

Figure S4 The alignment of the 22-kDa α-zein promoters from B73 and the copy Zp22/6 from BSSS53. The cytosine positions indicated in Figs. 4b, 7c and 9 are marked in the corresponding places; P-box and "ACGT" core motif are shaded.


(a)
LB
TvsP
SalI
Bar
TEV
P35S
HindIII
T35S
Sac1
GUS Gene
Xba1 et al.
EcoR1 et al.
RB
pTF102
Sac1 and EcoR1 double digestion
EcoR1
P4
Sac1
Pbf
P3
Nco1
P2
Nco1
P1
BamH1+EcoR1
P8
Sac1
O2
P7
Xba1
P6
Xba1
P5
AvrII+EcoR1
BamH1+EcoR1
HindIII
pTF102-P35SO2
HindIII and Sac1 double digestion
P10
HindIII+AvrII
+
P9
Sac1
T35S
pTF102-P35SPBF
(b)
P12
HindIII
P11
Xba1
BsrG1
Tdzs10
Gfp
Nco1
P27
EcoR1
pTF102-P4
PCR Amplification
HindIII and Xba1 double digestion
HindIII Xba1
discarded
HindIII+BamH1
Xba1
HindIII+AvrII Sac1
pTF102-P4-BamH1HindIII
HindIII and BamH1 double digestion
HindIII + AvrII
BamH1
pTF102-P5

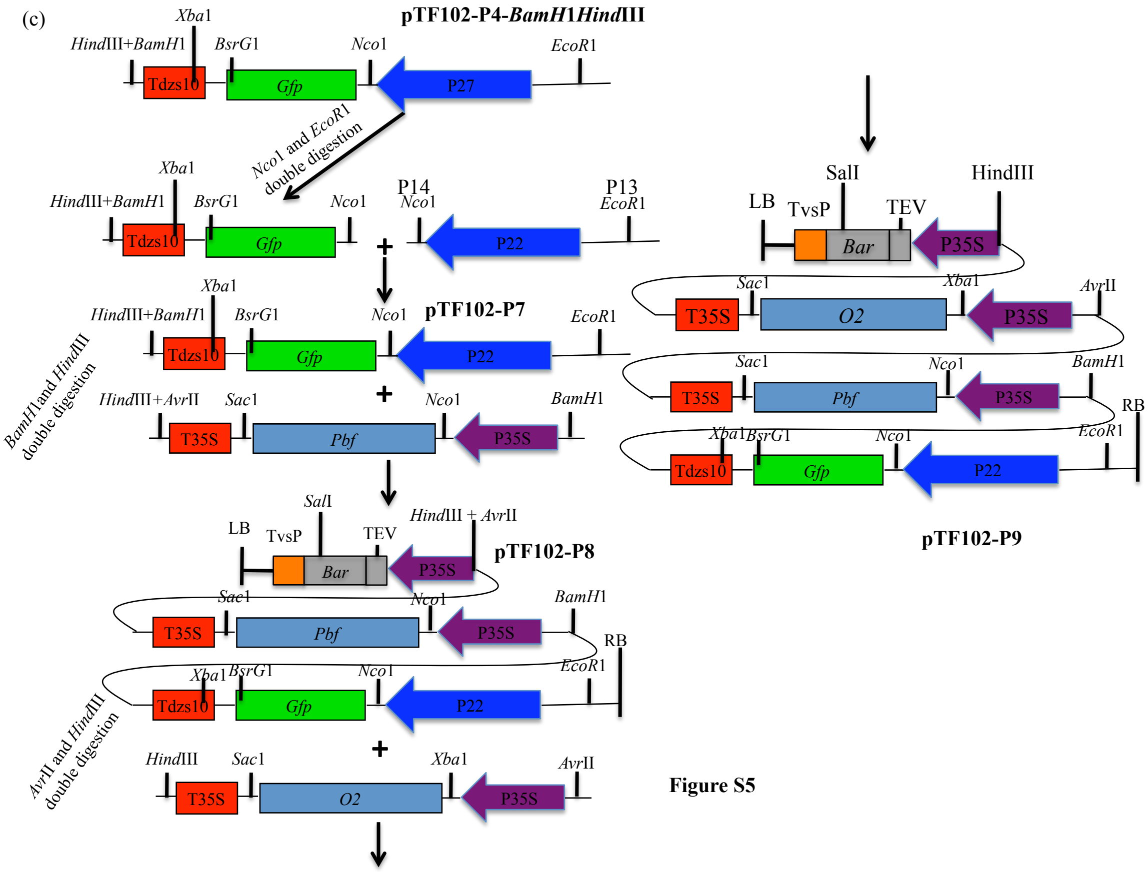


Figure S5

Figure S5 Strategies of plasmid construction. (a) P35SPBF and P35SO2 cassettes. (b) pTF102-P5. (c) pTF102-P9. Primers P1-P14 used for plasmid construction are indicated in the corresponding step.

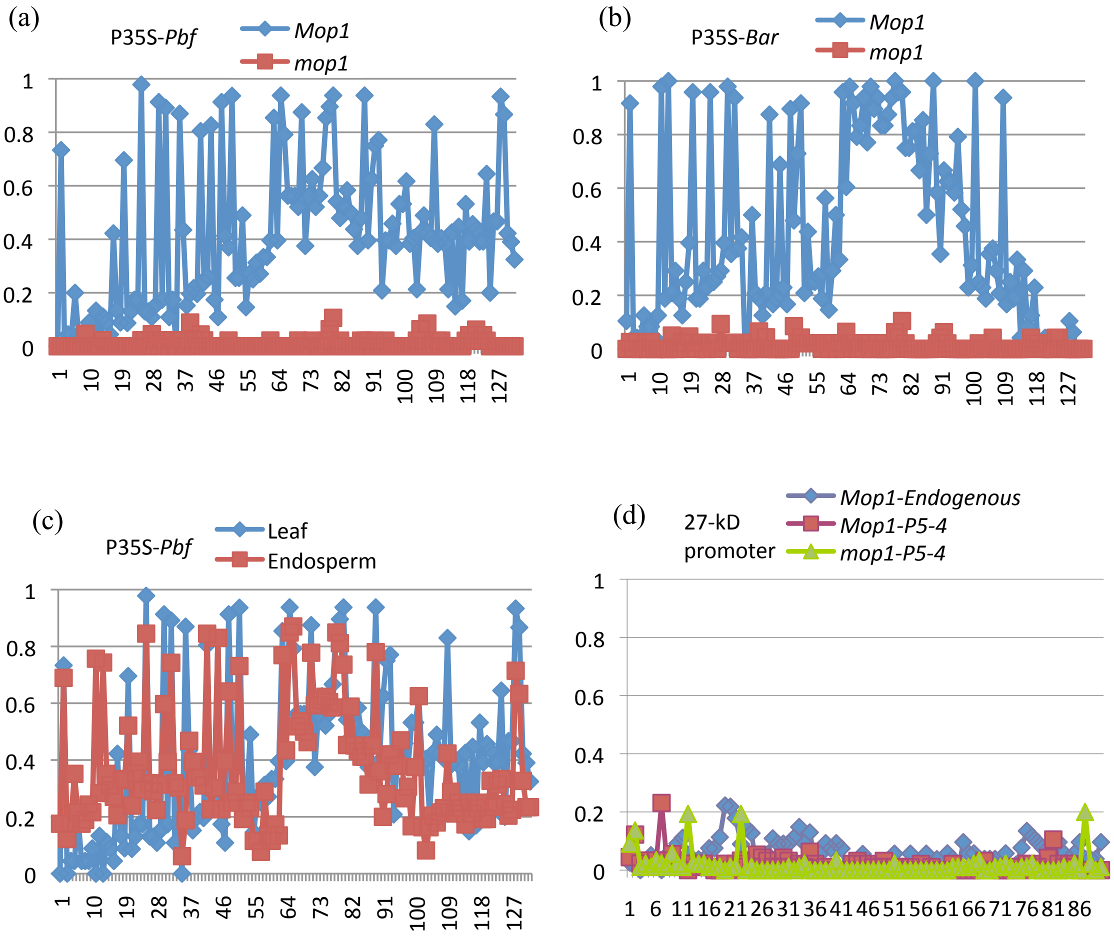


Figure S6 DNA methylation of 35S and transgenic 27-kDa γ-zein promoters in *Mop1-P5-4* and *mop1-P5-4*. (a) The 35S promoter driving the *Pbf* gene in *Mop1-P5-4 and mop1-P5-4*. (b) The 35S promoter driving the selective marker *Bar* gene in *Mop1-P5-4 and mop1-P5-4*. (c) The 35S promoter driving the *Pbf* gene in *Mop1-P5-4* leaf and endosperm. (d) The transgenic 27-kDa γ-zein promoter driving the *Gfp* gene.

```
G   A   G   C   A   A   T   G   T   A   T   T   G   G   T   T   G   T   G   A   G   T   T   T
                1           2       3       4       5
T   T   G   A   C   G   G   C   G   C   T   C   A   C   A   G   T   G   A   T   A   G   A   T
                            6                           7   8           9   10  11  12
T   T   G   T   T   A   T   C   T   A   T   A   T   G   C   C   A   G   C   C   C   C   A   G
13                      14          15  16                      17                          18
C   A   T   A   T   T   C   A   T   C   C   T   T   G   T   G   C   T   G   T   G   G   G   C
        19                              20  21          22
G   T   C   T   A   G   A   G   G   A   C   C   G   A   C   A   A   T   A   T   A   T   A   T
                                        23                      24
A   T   T   T   T   T   A   A   A   A   C   A   A   A   T   T   C   G   T   G   A   A   G   A
    25          26      27                                  28              29              30
A   C   A   T   C   A   C   A   A   G   T   T   A   T   G   C   A   T   G   C   A   A   A   C
        31      32                  33                                  34  35
T   G   C   T   C   A   A   G   T   C   A   T   G   T   G   G   A   T   C   C   A   A   G   G
36          37  38              39          40              41      42          43
C   A   T   C   C   T   A   A   C   A   A   C   T   A   G   C   A   C   A   G   C   A   T   T
    44          45
A   C   A   A   C   A   A   A   A   T   A   T   T   G   G   T   G   T   A   T   A   T   G   T
    46  47          48
G   C   C   T   A   C   A   A   T   G   A   A   G   T   G   A   A   A   G   G   T   G   A   T
                49
G   A   G   T   C   A   T   G   G   T   G   A   T   G   T   G   T   A   A   A   G   A   G   G
50                  51                                      52          52      54              55
C   A   T   T   A   C   A   A   A   G   T   T   A   G   C   T   T   C   A   C   A   A   G   C
                                    56                      57          58  59  60
G   T   A   T   G   A   A   T   T   C   A   T   T   G   A   C   A   A   C   C   C   T   T   G
    61                                                          62
A   C   A   T   G   T   A   A   A   G   T   T   G   A   T   T   C   A   T   A   T   G   T   A
                                63                                  64              65
T   A   A   G   A   A   A   G   C   T   T   A   A   T   G   A   T   C   T   A   T   C   T   G
                    66  67                  68  69                      70
T   A   A   A   T   C   C   A   A   A   T   C   C   A   T   G   T   A   C   T   A   T   G   T
        71  72      73          74              75          76      77          78
T   T   C   C   A   C   G   T   C   A   T   G   C   A   A   C   G   C   A   A   C   A   T   T
79  80                  81  82                                  83                          84
C   C   A   A   A   A   C   C   A   T   G   G   G   T   T   G   C   A   A   G   A   T   G   C
        85                          86              87  88                          89
T   G   C   A   G   A   A   T   G   C   A   A   G   C   C   A   T   G   G   A   T   C   A   T
90                                      91              92      93  94  95      96
C   T   A   T   A   A   A   T   G   G   C   T   A   G   C   T   C   C   C   A   C   A   T   A
                97                  98      99              100         101         102 103
T   G   A   A   C   T   A   G   T   C   T   C   T   A   T   C   A   T   C   A   T   C   C   A
        104 105                 106         107                 108         109
A   T   C   C   A   G   A   T   C   A   G   C   A   A   A   G   C   G   G   C   A   G   T   G
110
C   G   T   A   G   A   G   A   G   G   A   T   C   G   T   C   G   A   A   C   A   G   A   A

C   A   G   C   A   T   G
```

Figure S7 Cytosines in β-zein promoter. The 559-bp fragment upstream of the start codon contains 110 cytosines, covering the P-box, O2 box and TATA box. P-box, “ACGT” core motif and TATA box are shaded. The cytosine positions indicated in Fig. 11b are numbered in the sequence.

Table S1 List of primers

Primer	Sequence	Note
pbfBamH1	5’-AATTGGATCCACTAACCTTATTGTCCCTTG-3’	*Pbf* RNAi construct
pbfBspE1	5’-TATATCCGGAATGGACATGATCTCCGGCAG-3’	
pbfBblII	5’-AATAAGATCTATGGACATGATCTCCGGCAG-3’	
pbfSac1	5’-AATTGAGCTCACTAACCTTATTGTCCCTTG-3’	
Umc1066F	5’-ATGGAGCACGTCATCTCAATGG-3’	*O2* polymorphic markers
Umc1066R	5’-AGCAGCAGCAACGTCTATGACACT-3’	
P1	5’- TATATGAATTCAAGGATCCGCATGCCGGTCAACATGGTG -3’	P35S forward, *EcoR*1 and *BamH*1 introduced
P2	5’- AAATCCATGGTAGATCCCCCGTTCGTAAATG -3’	P35S reverse, *Nco*1 introduced
P3	5’- ATTACCATGGACATGATCTCCGGCAG -3’	*Pbf* CDS forward, *Nco*1 introduced
P4	5’- AATTGAGCTCACTAACCTTATTGTCCCTTG -3’	*Pbf* CDS reverse, *Sac*1 introduced
P5	5’- TATATGAATTCAACCTAGGGCATGCCGGTCAACATGGTG -3’	P35S forward, *EcoR*1 and *Avr*II introduced
P6	5’- AAATTCTAGAGGTAGATCCCCCGTTCGTAAATG -3’	P35S reverse, *Xba*1 introduced
P7	5’- ATTATCTAGACCATGGAGCACGTCATCTCAATG -3’	*O2* CDS forward, *Xba*1 introduced
P8	5’- TAATGAGCTCCTTATTCAGCGACGCCTG -3’	*O2* CDS reverse, *Sac*1 introduced
P9	5’-TATAGAGCTCGGCGCAAAAATCACCAGTC-3’	T35S forward, *Sac*1 introduced
P10	5’- ATTAAGCTTAATTCCTAGGTGCAGGTCACTGGATTTTGG -3’	T35S reverse, *Hind*III and *Avr*II introduced
P11	5’- AAAGCTGTACAAGTAAATAGAAATATTTGTGTTGTATCG -3’	Terminator of 10-kDa δ-zein gene, forward
P12	5’- ATCAAGCTTACTAGTGGATCCTACCAGCTGAGAATTAGGAG -3’	Terminator of 10-kDa δ-zein gene, reverse, *Hind*III and *BamH*1 introduced
P13	5’- ATTTGAATTCGTCCACGCGCAAATAGACC -3’	22-kDa zein promoter forward, *EcoR*1 introduced
P14	5’- TAATCCATGGTTGTTTGGTCGTTGCTAGTG -3’	22-kDa zein promoter

		reverse, *Nco*1 introduced
γ50F	5’-ATGAAGCTGGTGCTTGTGGTTC-3’	For γ50 RT-PCR
γ50R	5’-TAATGTCATTGCTGCTGCATGG-3’	
γ27F	5’-ATGAGGGTGTTGCTCGTTGC-3’	For γ27 RT-PCR
γ27R	5’-ACTCAACTAGCTAGCTAGCC-3’	
α22F1	5’-ACACCATATGTTCATTATTCCACAATGCTCA-3’	For α22 RT-PCR
α22R1	5’-TTAAGGATCCTATATAATCTAAAAGATGGCA-3’	
α19AF	CTCTTAa/gATTAGTAGCTAATAt/cATC	For α19A RT-PCR
α19AR	CTGGGAAGCCACAAACATCA	
α19BDF	ATTAGTCGGTAATCCATCAACC	For α19B and D RT-PCR
α19BDR	CTAGAAGATGGCACCACCAATG	
δ18F	5’-CGCCATGGCAGCCAAGATG-3’	For δ18 RT-PCR
δ18R	5’-ATGCCGACTTCATTATTGGG-3’	
γ16F	5’-TCGACACCATGAAGGTGCTG-3’	For γ16 RT-PCR
γ16R	5’-TGGTGATGGGTGACACTACG-3’	
β15F	5’-AGGATCGTCGAACAGAACAGC-3’	For β15 RT-PCR
β15R	5’-AGATGGATAGAGGAGATTTCCC-3’	
δ10F	5’-ATACTCTAGGAAGCAAGGAC-3’	For δ10 RT-PCR
δ10R	5’-TAAGAACATGGGTGGAATCG-3’	
δ18-10F	5’-CGCCATGGCAGCCAAGATG-3’	Common primer pair for δ18 and δ10 RT-PCR
δ18-10R	5’-TATCTAGAATGCAGCACCAAC-3’	
PbfF	5’-ATGGACATGATCTCCGGCAG-3’	For *Pbf* RT-PCR
PbfR	5’-ACTAACCTTATTGTCCCTTG-3’	
O2F	5’-ATGGAGCACGTCATCTCAATG-3’	For *O2* RT-PCR
O2R	5’-CCTTATTCAGCGACGCCTG-3’	
GFPF1	5’-ATGGTGAGCAAGGGCGAGG-3’	For *Gfp* RT-PCR
GFPR1	5’-TTACTTGTACAGCTCGTCC-3’	
P22F1	5’-ACATGTGTAAAGGTGAAGAG-3’	
GFPR2	5’- GTGAGCAAGGGCGAGGAGCT-3’	
P22bisulF	5’-ATATGTGTAAAGGTGAAGAG-3’	
α22bisulR	5’-CTAATATCTTAATAACCATT -3’	
GFPbisulR	5’-AACTCCTCACCCTTACTCAC-3’	
P27bisulF	5’-GAAATATGGTGAGTTATGTTGAG-3’	
γ27bisulR	5’-AAAACAACAAACAACACCCTC-3’	
P35SbisulF	5’-ATGTTGGTTAATATGGTGGAG-3’	
BarbisulR	5’-ACCACCAACATATCCACCTC-3’	
PbfbisulR	5’-CTTTAAATCCCTAACTTCCTCC-3’	

β15bisulF	5′- GAGTAATGTATTGGTTGTGAG -3′
β15bisulR	5′- CTATTCAACAATCCTCTCTAC -3′

Restriction enzyme cutting sites are colored in red.