Tissue Culture-Induced Novel Epialleles of a Myb Transcription Factor Encoded by pericarp color1 in Maize

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Figure S1.—Methylation profile of individual clones in the wild type (P1-wr:DP15), leaky (p1-ww:DP3), and silent (p1-ww:DP6) alleles in the R-III region of second intron. Shown here are the methylation patterns of cytosine residues in all the clones sequenced after bisulfite treatment. Location of individual CG (ovals), CNG (squares), and CHH (triangles) sites in R-III in the reference P1-wr sequence is shown at the top. In sequenced clones, open and filled shapes represent non-methylated and methylated sites, respectively. Some discrepancies between certain sites in the reference sequence and the corresponding sites in the cloned sequences indicate sequence polymorphisms. Coordinates of individual cytosine residues are shown at the bottom. For each genotypes, the clones were divided into groups based on their methylation profile and/or sequence polymorphisms. The groups are indicated on right and percentage of these clones is shown in parentheses. Grey shaded boxes mark the three HpaII sites that are covered in R-III; two adjacent sites that were partially methylated in p1-ww:DP3 in DNA gel blot analysis are at nt positions 4671 and 4675 (on the anti-sense strand) in the middle of the region.
**TABLE S1**

Details of three regions analyzed through genomic bisulfite sequencing

<table>
<thead>
<tr>
<th>Region</th>
<th>Coordinates (Size)</th>
<th>Target strand</th>
<th>Primers used for amplification</th>
</tr>
</thead>
</table>
| R-I    | -169 to 157 (326-bp) | Sense         | Forward-Prom: 5’-AGTAAAGGGTTAATAATTGT-3’  
Reverse-Prom: 5’-AAATCACAATCTACTTTA-3’ |
| R-II   | 4093 to 3800 (294-bp) | Antisense     | Forward-SalI: 5’-AGATGGAAGGAAAGTTGAGT-3’ 
Reverse-SalI: 5’-CATAACCTACTTTACCCACATTA-3’ |
| R-III  | 4781 to 4532 (250-bp) | Antisense     | Forward-Hpa: 5’-GGGAAATTATTAGGGAGGG-3’  
Reverse-Hpa: 5’-CTCTTCATTCAAACTAACTAA-3’ |