**Transposon-induced inversions activate gene expression in Maize pericarp**

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**Supplemental Information**



**Figure S1:** Southern Blot gel images using A) *Hpa*I and B) *Eco*RV restriction enzymes with fragment-15 (within the *p1* enhancer) as a probe. Lane 1, DNA ladder, black arrow points to 10 kb fragment on each gel; Lane 2, J (*p1-ww*); Lane 3, *P1-rr4B2*; Lane 4, *p1-wwB54*; Lane 5, 140; Lane 6, E1; Lane 7, TZ3-4; Lane 8, SP1-18; Lane 9, S25; and Lane 10, TZ2-7.

**Figure S2: RT-PCR sequence aligned to *p1* and *p2* exons 1, 2 and 3. The middle sequence is RT-PCR product from E1 (one of the inversions), the upper sequence is from *p1* and the lower sequence is from *p2*. At three sites, SNPs in the RT-PCR product match *p2* (lower) but not *p1* (upper). Two additional SNPs in the RT-PCR product likely represent amplification or sequencing artefacts.**

Exon 1

381 GCGGA**-A**GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAG

 ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||

3 GCGGA**TG**GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAG

 ||||| **|**|||||||||||||||||||||||||||||||||||||||||||||||||||||

279 GCGGA**-G**GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAG

GTCGCTGCCCAAGAATGCAG 459

||||||||||||||||||||

GTCGCTGCCCAAGAATGCAG 82

||||||||||||||||||||

GTCGCTGCCCAAGAATGCAG 357

Exon 2

580 GCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTACCT**T**CGGG

 ||||||||||||||||||||||||||||||||||||||||||||||||| ||||

83 GCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTACCT**C**CGGG

 |||||||||||||||||||||||||||||||||||||||||||||||||**|**||||

475 GCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTACCT**C**CGGG

CGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAGCTCCACG

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

CGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAGCTCCACG

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CGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAGCTCCACG

CCACCCTCGG**C**AACAG 709

|||||||||| |||||

CCACCCTCGG**G**AACAG 212

||||||||||**|**|||||

CCACCCTCGG**G**AACAG 610

Exon 3

5309 GTGGTCCCTGATCGCCAGCCACCTCCCC**-**GGCCGAAC 5344

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213 GTGGTCCCTGATCGCCAGCCACCTCCCC**C**GGCCGAAC 249

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4425 GTGGTCCCTGATCGCCAGCCACCTCCCC**-**GGCCGAAC 4460

**Table S1: Primers used for screening for inversions**

|  |  |  |
| --- | --- | --- |
| Set 1  | GAACAGTGATGGGAATGTTG | CTGCTAGCTGCTAGCTGTTAGGCTC |
| Set 2  | GAGTCGCGAGCAGTGGAG | CTGCTAGCTGCTAGCTGTTAGGCTC |
| *fAc-p1* junction | GACCGTGACCTGTCCGCTC | TGCCATCTTCCACTCCTCGGCTTTAG |
| Nested | GGCATAGTGAGACCCATTCCTCCTTC | CCTCTCCATGAGCAATGTGTCTTAT |

**Table S2: Primers for sequencing inversion endpoints**

Primers for *Ac* side

|  |
| --- |
| *Ac* primer: GCTCTACCGTTTCCGTTTCCGTTTACCG |
| 140, E1, TZ3-4, SP1-18 | TTATACTTGCGACGCTGTGG |
| S25​ | TCTTTTGGCCATACGTCTCC |
| TZ2-7​ | CTTGGAGGACGAGGGATGGCAATGGG |

Primers for *fAc* side

|  |
| --- |
| *fAc* primer: CTGCTAGCTGCTAGCTGTTAGGCTC |
| 140, E1, TZ3-4, SP1-18 | GCAGCCTTTTCTTGCAGTCA |
| S25​ | CCCTCGTCCTCCAAGATTCTCCCCCTG |
| TZ2-7​ | GATTGGCTGAACCGTGACGT |

**Table S3: Primers used for RT-PCR**

|  |  |  |
| --- | --- | --- |
| *p2*  | GCGGAGGAGGACCAGTTAC | CTGAGGTGCGAGTTCCAGTAG |
| Beta-tubulin  | CTACCTCACGGCATCTGCTATGT | GTCACACACACTCGACTTCACG |

**Table S4: Inversion alleles, Target Site Duplications, and relevant distances (in basepairs)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **Target Site Duplication** | **Distance from TSS** | **E-P distance** | **Size of Inverted fragment** |
| 140 | CCGGTGGC | 3505 | 8235 | 81800 |
| E1​ | CAGCCAGG​ | 3387 | 8117 | 81682 |
| TZ3-4​ | TGTGTAGT | 3376 | 8106 | 81671 |
| SP1-18 | GTCGGGGC​ | 3203 | 7933 | 81498 |
| S25​ | CTCGTCGA​ | 3070 | 7800 | 81365 |
| TZ2-7​ | ATCTCTTC | 2692 | 7422 | 80987 |