**File S1.** Genomic sequences of *p1-ww-id1* and *p1-ww-id4* at inverted duplication junctions. Fragments were obtained from genomic PCR and sequenced using indicated primer *P1-*15588F. The 2 bp "footprints" remaining after the excision of *Ac* and *fAc* termini are shown in red font. Sequences of the progenitor *p1-vv-9D9A* allele are shown for comparison.

> *p1-ww-id1*\_*P1*-15588F

NNNNNNNNNANNNATCCNCGTGCATGCATGCCACTGTAGCGCCGTAATATAATGATAGATATGCGCTATTGCTCCTACAACTACAAGTCTACAACCCACATGGTGTTGCGAGAGCTAGCGGTGCCACACAGTCATGGAAACATGGTTTGTGAAAGCAGCTTAACTAATTACTAGCTTAACTAATTACTAACTAATTACTAGCCTGCACTAATAAGGCTTAAAACAAGTGATCCTCGCAGGTATGTTTGTCTCAATTGTTGTACATGTCATCATTATAAATTCTCAATTAATCAAATGTCAATTATTGTAGGTACGATGCAATTTGTCCTAAAGCCGAGGAGTGGAAAGATGGCAA

> *p1-ww-id4*\_*P1*-15588F

NNNNNNNNNNNNNNNTCCNCGTGCATGCATGCCACTGTAGCGCCGTAATATAATGATAGATATGCGCTATTGCTCCTACAACTACAAGTCTACAACCCACATGGTGTTGCGAGAGCTAGCGGTGCCACACAGTCATGGAAACATGGTTTGTGAAAGCAGCTTAACTAATTACTAGCTTAACTAATTACTAACTAATTACTAGCCTGCACTAATAAGGCTTAAAACAAGTGATCCTCGCAGGTATGTTTGTCTCAATTGTTGTACATGTCATCATTATAAATTCTCAATTAATCAAATGTCAATTATTGTAGGTACGATGCAATTTGTCCTAAAGCCGAGGAGTGGAAGATGGCAA

>*p1-vv-9D9A*

AGAAATCATCTAACAAAACTGGCGAGCTATCAAACAGGACACGGGAGAGAATAGATGATTAAACAATAATCCCTCGTGCAATGCATGCCACTGTAGCGCCGTAATATAATGATAGATATGCGCTATTGCTCCTACAACTACAA**CA**CTACAACCCACATGGTGTTGCGAGAGCTAGCGGTGCCACACAGTCATGGAAACATGGTTTGTGAAAGCAGCTTAACTAATTACTAGCTTAACTAATTACTAACTAATTACTAGCCTGCACTAATAAGGCTTAAAACAAGTGATCCTCGCAGGTATGTTTGTCTCAATTGTTGTACATGTCATCATTATAAATTCTCAATTAATCAAA

id1 CGCTATTGCTCCTACAACTACAAGTCTACAACCCACATGGTGTTGCGAGAGCTAGCGGTG 123

id4 CGCTATTGCTCCTACAACTACAAGTCTACAACCCACATGGTGTTGCGAGAGCTAGCGGTG 124

9D9A CGCTATTGCTCCTACAACTACAA**CA**CTACAACCCACATGGTGTTGCGAGAGCTAGCGGTG 180

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**File S2.** Genomic sequences showing junctions of Composite Insertion termini and flanking DNA in *p1-ww-id1* and *p1-ww-id4*. Fragments were obtained from genomic PCR and sequenced using indicated primers Ac264r, Ac4436f, and Ac120r. Underlined regions indicate *Ac* or *fAc;* motifs in yellow highlight indicate 8 bp Target Site Duplications flanking each Composite Insertion. Note that the 8 bp Target Site Duplications for each allele are shown as reverse complements due to the opposite orientation of sequencing reactions.

> *p1-ww-id1\_*Ac\_Ac264r\_912121.seq

NNNNNNNNNNGNTTCGTTCGTTTTCGTTTTTTACCTCGGGTTCGAAATCGATCGGGATAAAACTAACAAAATCGGTTATACGATAACGGTCGGTACGGGATTTTCCCATCCTACTTTCATCCCTGAGCGAGGCGGCGGCTACGAATTGTGGCTGCTGTTAGTTGTTGCTCAACTCACGATGATGCAAAGCTAGCTAGCTAGCATCGATCGATCGGCATCATGCAATTTGATGACGATCCTAGCTAGCTCTAGCTACATGTATATGCATATCCTAGGCAGCTAGCTTCCCACACCNGGCTGATCGGN

> *p1-ww-id1\_*fAc\_Ac4436f\_912122.seq

NNNNNNNNNNNNNNTTTTCGTNNNNNNNNCAAGTTAAATATGAAAATGAAAACGGTAGAGGTATTTTACCGACCGTTACCGACCGTTTTCATCCCTAGCCTCGCTCGCTCATGGGTTCTATCACATCGCGCGCCCACAGATGCTCCACAGCTTTACTTGCGCATATCGTTTTCTTCTCCGCGTTGCCGTACAAGCCTGGGCAATCGTGGTGGCACGTGCACGTTCATGCTAATATGGAAACAGATAGGCTAGCTGCTAGGTAGGAAACCATCCCAGCTAACCAGAGCCGCCAAGAGAGATACTCCCTCCGTTNNNNN

> *p1-ww-id4*\_Ac120r\_793173.seq

NNNNNNNNNNNNNNCGNNCGNNNNNACTAACANAATCGGTTATACGATAACGGTCGGTACGGGATTTTCCCATCCTACTTTCATCCCTGGCCCGGATGCTGATGTAGCGACGATGCCCTGTACGGAACGATGATGGTGACGGCACGCATCGGATTCCATTCCGTTCCAGCGGGAGGGGCGAGGGGAGGGAGGAG

> *p1-ww-id4*\_ac4436f\_792285.seq

NNNNNNNNNNNNNNTNTTCGTNNNNNNNNNAAGTTAAATATGAAAATGAAAACGGTAGAGGTATTTTANNNNNNNNNANNGACCGTTTTCATCCCTAATCCGGGCGCTGATGGGGGTGTCTCCCTAGTAGTTTTAAAATGCCAATGTAATCAGCGTCTTTTTAGATGCGAAAGCCAGCCAGCTCCCATCCAGTTGAAGCGATGACGACGGGCGCAAGAGAAAGAAAAGCATGTATGCGTGCCAAATTAAAGCAAGGAGATGGAATTTTGCCAGCCCAACGAAAAGGCCATTGTGCGATTCAGCGGCTCATTAAATTATTGGCTCTCTGTTCTGTTCACATCTGAACGAACCACCAGCGTGGCGTACGACCGTGATTCTTCTTGTCAAGACAGT

**File S3.** Sequences of *p1-ww-id1* root chimeric transcript.

**A**. Composite Insertion transcript in *p1-ww-id1* includes Intron 1 of host gene Zm00001d028930. Sequences were obtained from 5' region of *p1-ww-id1* root transcript using primer 70849f located in Exon 1 of host gene Zm00001d028930. id1-c: cDNA; id1-g: genomic DNA.

Exon of Zm00001d028930

Intron of Zm00001d028930

Ac TIR

*Ac* Intron

id1-c\_70849f\_880508.seq NNNNNNNNNNNNNNNGGCCGGCGNNCTGCGGCGCGGGCCTTGGACGGTGG 50

id1-g\_70849f\_881603.seq ---NNNNNNNNNNNNNNNCGGCGANCTGCGGCGCGGGCCTTGGACGGTGG 47

\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq ACGAGGACCTCCAGCTGGTCAACTACGTCGACGCGCACGGCGAGGGCCGC 100

id1-g\_70849f\_881603.seq ACGAGGACCTCCAGCTGGTCAACTACGTCGACGCGCACGGCGAGGGCCGC 97

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq TGGAACTCGCTCGCCCGATCAGCAGGKGTGGGAAGCTAGCTGCCTAGGAT 150

id1-g\_70849f\_881603.seq TGGAACTCGCTCGCCCGATCAGCAGGTGTGGGAAGCTAGCTGCCTAGGAT 147

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq ATGCATATACATGTAGCTAGAGCTAGCTAGGATCGTCATCAAWTTGCATG 200

id1-g\_70849f\_881603.seq ATGCATATACATGTAGCTAGAGCTAGCTAGGATCGTCATCAAATTGCATG 197

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq ATGCCGATCGATCGATGCTAGCTAGCTAGCATTTGCATCATCGTGAGTTG 250

id1-g\_70849f\_881603.seq ATGCCGATCGATCGATGCTAGCTAGCTAGC-TTTGCATCATCGTGAGTTG 246

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq AGCAACAACTAACAGCAGCCACAATTCGTAGCCGCCGCCTCGCTCAGGGA 300

id1-g\_70849f\_881603.seq AGCAACAACTAACAGCAGCCACAATTCGTAGCCGCC**GCCTCGCT**CAGGGA 296

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq TGAAAGTAGGATGGGAAAATCCCGTACCGACCGTTATCGTATAACCGATT 350

id1-g\_70849f\_881603.seq TGAAAGTAGGATGGGAAAATCCCGTACCGACCGTTATCGTATAACCGATT 346

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq TTGTTAGTTTTATCCCGATCGATTTCGAACCCGAGGTAAAAAACGAAAAC 400

id1-g\_70849f\_881603.seq TTGTTAGTTTTATCCCGATCGATTTCGAACCCGAGGTAAAAAACGAAAAC 396

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq GGAACGGAAACGGGATATACWARRCGGTAAACGGAAACGGAAACGGTAGA 450

id1-g\_70849f\_881603.seq GGAACGGAAACGGGATATACAAAACGGTAAACGGAAACGGAAACGGTAGA 446

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq GCTAGTTTCCCGACCGTTTCACCGGGATCCCGTTTTTAATCGGGATGATC 500

id1-g\_70849f\_881603.seq GCTAGTTTCCCGACCGTTTCACCGGGATCCCGTTTTTAATCGGGATGATC 496

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq CCGTTTCGTTACCGTATTTTCTAATTCGGGATGACTGCAATATGGCCAGC 550

id1-g\_70849f\_881603.seq CCGTTTCGTTACCGTATTTTCTAATTCGGGATGACTGCAATATGGCCAGC 546

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq NNCCAACTCCCATCCATAACCACTGAGGCCCAGCCCATGTAAGAAATACC 600

id1-g\_70849f\_881603.seq TCC-AACTCCCATCCATAACCACTGAGGCCCAGCCCATGTAAGAAATACC 595

\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

id1-c\_70849f\_880508.seq TAGCGAACGCTGCTCTGCCTCTCTCCCAGGCGGCCAGGCACCACANGAGT 650

id1-g\_70849f\_881603.seq TAGCGAACGCTGCTCTGCCTCTCTCCCAGGCGGCCAGGCACCACACGAGT 645

**B.** Composite Insertion transcript in *p1-ww-id1* includes Intron 1 of *Ac*. Sequences were obtained from 3' region of *p1-ww-id1* root transcript using primer Ac1568r. Upper sequence is from cDNA of chimeric transcript; lower sequence is from *Ac.*

rc\_id-c\_Ac1568r\_881604.seq GCTMAGCCAKAAGATTGGCCAAGCAGATGTCTRCTCTCAMGATTCGCCTT 700

Ac GCTCAGCCATAAGATTGGCCAAGTTGATGTCTAC-CACAAGAG-CGCCTT 120

\*\*\* \*\*\*\*\*.\*\*\*\*\*\*\*\*\*\*\*\*\* :\*\*\*\*\*\*\* \* \*:\*\* \*\* \*\*\*\*\*\*

rc\_id-c\_Ac1568r\_881604.seq NTACNGCGCAARANCAANTTTCCGTATKATGRCGCATATSGNTAAGRGTA 750

Ac CTACT-CGCAAAACAAA--TTCCGTATTCT-CTGCATATGCTCAAG-GTA 165

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rc\_id-c\_Ac1568r\_881604.seq TATATTAGMAAMAGCAGTMAGCANNNAGCATTAGGCAYTAGCTARTTGTG 800

Ac TATATTAGAAAAA-CAG-TAGCAAT-AGCATTAG-CATTA-CTAATTG-G 209

\*\*\*\*\*\*\*\* \*\* \* \*\*\* \*\*\*\* . \*\*\*\*\*\*\*\* \*\* \*\* \*\*\* \*\*\* \*

rc\_id-c\_Ac1568r\_881604.seq TTGTNGNATTGGGMANNCATCTATATTGMAATGTMGAATWATAYNWWAWA 850

Ac TTGTAG-ATTGGGAAG-CATC-ATATTG-ACTGTAGAATAATACGAAAAA 255

\*\*\*\* \* \*\*\*\*\*\* \*. \*\*\*\* \*\*\*\*\*\* \*.\*\*\* \*\*\*\* \*\*\* . \* \*

rc\_id-c\_Ac1568r\_881604.seq TCYRTWTRYWACAGGGTTGAAAAGAAAAGCTGAAGCCTCTTCTAGTCGGA 900

Ac TCTGTTTATAACAGGGTTGAAAAGAAAAGCTGAAGCCTCTTCTAGTCGGA 305

\*\* \* \* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

rc\_id-c\_Ac1568r\_881604.seq TTCAGAATGTACGTGCACGTGCGCGTGGGCATGGATGTGGCCGCACATCA 950

Ac TTCAGAATGTACGTGCACGTGCGCGTGGGCATGGATGTGGCCGCACATCA 355

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

rc\_id-c\_Ac1568r\_881604.seq CCATCATCATCAACAGCTGAGGCCGAGAGGCATTTTATTCAGAGTGTAAG 1000

Ac CCATCATCATCAACAGCTGAGGCCGAGAGGCATTTTATTCAGAGTGTAAG 405

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

rc\_id-c\_Ac1568r\_881604.seq CAGTAGTAATGCAAATGGTACAGCTACAGATCCGAGTCAAGATGATATGG 1050

Ac CAGTAGTAATGCAAATGGTACAGCTACAGATCCGAGTCAAGATGATATGG 455

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

rc\_id-c\_Ac1568r\_881604.seq CTATTGTTCATGAACCACAACCACAACCACAACCACAACCAGAACCACAA 1100

Ac CTATTGTTCATGAACCACAACCACAACCACAACCACAACCAGAACCACAA 505

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

rc\_id-c\_Ac1568r\_881604.seq CCACAGCCACAACCTGAACCCGAAGAAGAAGCACCACAGAAGAGGGCAAA 1150

Ac CCACAGCCACAACCTGAACCCGAAGAAGAAGCACCACAGAAGAGGGCAAA 555

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