

Table S1. List of primer sets for MITE insertion polymorphism (MIP) PCR analysis.

| MITE name | Primer name | Primer sequence (5'→3') | Inserted size (bp) | Excised size (bp) |
|------------------|-----------------------------|----------------------------|--------------------|-------------------|
| <i>PTE-2</i> | <i>PTE-2</i> F ^Z | TATACATGACGAGTATACGAGGG | 835 | 562 |
| | <i>PTE-2</i> R | CCACAAGTGATCGTTGTCTAG | | |
| <i>PTE-2_c1</i> | <i>PTE-2_c1</i> F | CATGTAGATTTACCCCAACG | 631 | 394 |
| | <i>PTE-2_c1</i> R | CGCCTAGTCTCAACTTCAAA | | |
| <i>PTE-2_c2</i> | <i>PTE-2_c2</i> F | CACGATGATGGCGAGATTATT | 749 | 513 |
| | <i>PTE-2_c2</i> R | TGTTGAACTATGACCGAGTGG | | |
| <i>PTE-2_c3</i> | <i>PTE-2_c3</i> F | TTGGTATGCATGAATGGCAC | 679 | 449 |
| | <i>PTE-2_c3</i> R | GGTACCTGCTTGGTGTACATT | | |
| <i>PTE-2_c4</i> | <i>PTE-2_c4</i> F | ATTGTACCAGAAAAGATGTATATT | 618 | 356 |
| | <i>PTE-2_c4</i> R | GTCAAGTTCATTTACATACTC | | |
| <i>PTE-2_c5</i> | <i>PTE-2_c5</i> F | GCCACACGAGCCTGATGC | 727 | 477 |
| | <i>PTE-2_c5</i> R | GCGGTGATGTTTAATCCAGCG | | |
| <i>PTE-2_c6</i> | <i>PTE-2_c6</i> F | GCCCAACAACAACAATAATAAT | 730 | 500 |
| | <i>PTE-2_c6</i> R | CCGAATCCAGATCCAGGT | | |
| <i>PTE-2_c7</i> | <i>PTE-2_c7</i> F | AGACCCTAAGTGTAATCAA | 595 | 358 |
| | <i>PTE-2_c7</i> R | AAAGATAAAGATGTAGAGTTGTT | | |
| <i>PTE-2_c8</i> | <i>PTE-2_c8</i> F | TGCATGAATGATTATGTCGAT | 749 | 511 |
| | <i>PTE-2_c8</i> R | GGAATGTGAGTAGTATGAAG | | |
| <i>PTE-2_c9</i> | <i>PTE-2_c9</i> F | CATCTCTATTTCTCTATTTCCAA | 353 | 112 |
| | <i>PTE-2_c9</i> R | TGGAAATAGAGGTGGAATA | | |
| <i>PTE-2_c10</i> | <i>PTE-2_c10</i> F | TCTCTATGAATCCCAACTTA | 909 | 679 |
| | <i>PTE-2_c10</i> R | CTTTCAGTAGGGTAGCAT | | |
| <i>PTE-2_c11</i> | <i>PTE-2_c11</i> F | CTAATCGCCACATAAACTAACC | 528 | 283 |
| | <i>PTE-2_c11</i> R | TAACACGAGAGTAGTCAATAGG | | |
| <i>PTE-2_c12</i> | <i>PTE-2_c12</i> F | GAAACCAGAGAAACACCATAC | 775 | 548 |
| | <i>PTE-2_c12</i> R | TGTGAAATGTTCTGGTTACTCTT | | |
| <i>PTE-2_c13</i> | <i>PTE-2_c13</i> F | TTC AAT AGT AGT TCA CCG | 478 | 238 |
| | <i>PTE-2_c13</i> R | TTC ATC TTG TAA TCT GTA AT | | |
| <i>PTE-2_c14</i> | <i>PTE-2_c14</i> F | CTCCTACTTCATCTCTTCAAG | 840 | 569 |
| | <i>PTE-2_c14</i> R | CTAACTTCTGTTACAGTCAATG | | |

^ZF, forward primer; R, reverse primer

Table S2. Distribution of MITE family in 'CT001' genome.

| | 1kup ^z | Intron | Exon | 1kdn ^y | Intergenic | Total |
|-----|-------------------|--------|------|-------------------|------------|---------|
| DTH | 28,546 | 9,159 | 808 | 18,945 | 67,419 | 124,877 |
| DTA | 1,269 | 564 | 44 | 735 | 2,847 | 5,459 |
| DTC | 6 | 6 | 0 | 17 | 96 | 125 |
| DTM | 1,798 | 426 | 7 | 765 | 2,041 | 5,037 |
| DTT | 35,682 | 13,859 | 114 | 22,786 | 72,562 | 145,003 |

^z: 1kup, 1k bp upstream from gene locus. ^y:1kdn, 1k bp downstream from gene locus.