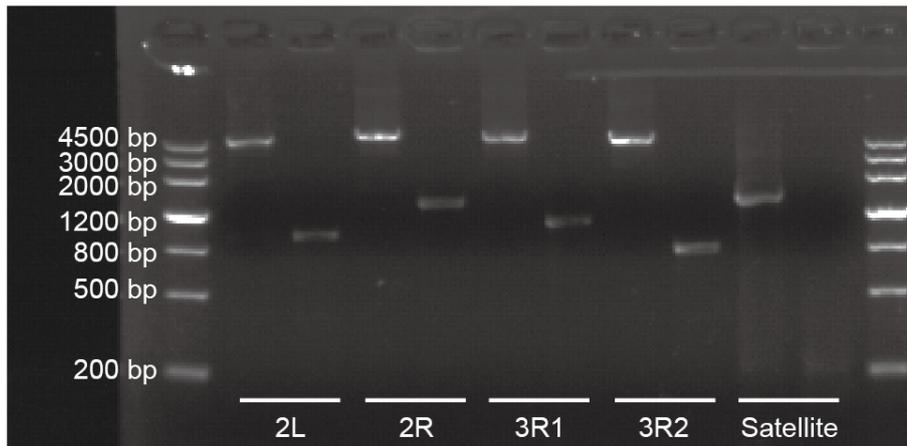


PCR and Sanger sequencing results of five loci of *CG17604_r*.

The information about locations and primers can be found in Supplemental Table 6. For the first four locations, we performed the PCR experiment in one randomly-chosen line containing this retrocopy and the reference iso-1 as the negative control, using the primers targeting both flanking regions of the retroposed locus. For the retrocopy inserted in a satellite, the primers target the satellite and internal retrocopy, which is why there is no band in iso-1.



Sequence alignment

The 'p_LTR' sequence is artificially constructed on the basis of the parental gene and LTR retrotransposon sequences encoded in the iso-1 genome. The eight nucleotide changes shared by retrocopies present in different insertion sites were marked as 1-8. The alignment is color-coded as:

5' and 3' LTR repeat zone

Coding region of LTR retrotransposon *BLASTOPIA*

Microsimilarity shared by LTR retrotransposon and retrocopy

Retrocopy

```
>CG17604_p_LTR          TGTAACATG-AGTAAGGCTGAAGGCTGGCAACAACCCGGTTGGCAGCGCTGTT-GAGCAG
>CG17604_r_satellite   -----
>CG17604_r_2L          TGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCGGTTGGCAGCGCTGTT-GAGCAG
>CG17604_r_2R          TGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCGGTTGGCAGCGCTGTT-GAGCAG
>CG17604_r_3R1         TGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCGGTTGGCAGCGCTGTT-GAGCAG
>CG17604_r_3R2         TGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCGGTTGGCAGCGCTGTTTGGAGCAG
*****
>CG17604_p_LTR          CAACATGATTGTCGAAATCCAAGTTATCGACAATCAGTCATCGAAGGA-CGATCGCA-G
>CG17604_r_satellite   -----
>CG17604_r_2L          CAACATGATTGTCGAAATCGAAGTTATCGACAATCAGTCATCGAAGGAACGATCGCAAG
>CG17604_r_2R          CAACATGATTGTCGAAATCGAAGTTATCGACAATCAGTCATCGAAGGAACGATCGCAAG
>CG17604_r_3R1         CAACATGATTGTCGAAATCGAAGTTATCGACAATCAGTCATCGAAGGAACGATCGCAAG
>CG17604_r_3R2         CAACATGATTGTCGAAATCGAAGTTATCGACAATCAGTCATCGAAGGAACGATCGCAAG
*****
>CG17604_p_LTR          G-CAGCAGTAGAGGCGAGTGGAAGTCAGCGTTGCAGTCAGTCGAGTTCTCAGCAGCAGTC
>CG17604_r_satellite   -----
>CG17604_r_2L          G-CAGCAGTGG-----AGTCGAGTTCTCAGCAGCAGTC
>CG17604_r_2R          G-CAGCAGTGGAGTCGAGTGGAAGTCAGCGTTGCAGTCAGTCGAGTTCTCAGCAGCAGTC
>CG17604_r_3R1         G-CAGCAGTGGAGTCAAGTGGAAGTCAGCGTTGCAGTCAGTCGAGTTCTCAGCAGCAGTC
>CG17604_r_3R2         GGCAGCAGTGGAGTCGAGTGGAAGTCAGCGTTGCAGTCAGTCGAGTTCTCAGCAGCAGTC
* ***** *
>CG17604_p_LTR          -GTTTCGGTCCACAACTAAG--AAATACTTT-ATATAATTACC-GCATTTAGAATTAAC
>CG17604_r_satellite   -----
>CG17604_r_2L          CGTTCGGT-CA-----
>CG17604_r_2R          -GTTTCGGT-CACAACTAAG--AAATACTTT-ATATAATTACC-GCATTTAGAATTAAC
>CG17604_r_3R1         -GTTTCGGT-CACAAA-CTAA--AAATACTTT-ATATAATTACC-GCATTAAAATTAAC
>CG17604_r_3R2         GTTTCGGT-CACAACTAAGAAATACTTTTATATAATTACCCGCATTTAGAATTA--
*****
>CG17604_p_LTR          TAATAATTAATTAATAATAACAATAATAACAATCTTACATGGGGGCTCGTCCAG
>CG17604_r_satellite   -----
```

>CG17604_r_2L -----
>CG17604_r_2R TAATAATTAATAATAATAAAACAATAATAATAACAATCTTACATGGGGGCTCGTCCAG
>CG17604_r_3R1 TAATAATTAATAATAATAAAACAATAATAATAACAATCTTACATGGGGGCTCGTCCAG
>CG17604_r_3R2 -----

>CG17604_p_LTR **TCCTAAATCGGTTATATGAAGGTGCAGTTGTTAAAGAAAAAGACATTGTTGTGTGCGT**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R TCCTAAATCGGTTATATGAAGGTGCAGTTGTTAAAGAAAAAGACATTGTTGTGTGCGT
>CG17604_r_3R1 TCCTAAATCGGTTATATGAAGGTGCAGTTGTTAAAGAAAAAGACATTGTTGTGTGCGT
>CG17604_r_3R2 -----

>CG17604_p_LTR **GGGTATAGTCTTTAAAAACGTGTGAAAGTTGTGGCTATATCTATTGCATTTAAAGTTGGAA**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R GGGTATAGTCTTTAAAA- GTTGTAAAGTTGTGGCTATATCTATTGCATTTAAAGTTGGAA
>CG17604_r_3R1 GGGTATAGTCTTTAAAA- GTTGTAAAGTTGTGGCTATATCTATTGCATTTAAAGTTGGAA
>CG17604_r_3R2 -----

>CG17604_p_LTR **AAATCAGTTGTACAGATTTTGTGTTGAACACAAGTCGGTAAAAAGTCGGGAAAGCTGCTAGA**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R AAATCAGTTGTACAGATTTTGTGTTGAACACAAGTCGGTAAAAAGTCGGGAAAGCTGCTAGA
>CG17604_r_3R1 AAATCAGTTGTACAGATTTTGTGTTGAACACAAGTCGGTAAAAAGTCGGGAAAGCTGCTAGA
>CG17604_r_3R2 -----

>CG17604_p_LTR **GAGAACTGATAAAGTTGAAATTGTCGCTGTGCGTGGATTTAGTCTTTAAAGTTGTAAGTT**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R GAGAACTGATAAAGTTGAAATTGTCGCTGTGCGTGGATTTAGTCTTTAAAGTTGTAAGTT
>CG17604_r_3R1 GAGAACTGATAAAGTTGAAATTGTCGCTGTGCGTGGATTTAGTCTTTAAAGTTGTAAGTT
>CG17604_r_3R2 -----

>CG17604_p_LTR **ATGGCTACGTCTACTGCATTGAAAGTTGAAAAATCGATTGAACTCATACTCAAGT**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R ATGGCTACGTCTACTGCATTGAAAGTTGAAAAATCGATTGAACTCATACTCAAGT
>CG17604_r_3R1 ATGGCTACGTCTACTGCATTGAAAGTTGAAAAATCGATTGAACTCATACTCAAGT
>CG17604_r_3R2 -----

>CG17604_p_LTR **CGTTTTGCTGTTGTGGAATTTAAAACAATTAATGCAAAGGTGGTCAAATTCGTTTCTA**
 >CG17604_r_satellite -----
 >CG17604_r_2L -----
 >CG17604_r_2R **CGTTTTGCTGTTGTGGAATTTAAAACAATTAATGCAAAGGTGGTCAAATTCGTTTCTA**
 >CG17604_r_3R1 **CGTTTTGCTGTTGTGGAATTTAAAACAATTAATGCAAAGGTGGTGA-----**
 >CG17604_r_3R2 -----

>CG17604_p_LTR **ACGAAAATCAAATTTGTCCTTTAACCGGTGGCGCCGTCTGCAAATCGACTACCGTCGC**
 >CG17604_r_satellite -----
 >CG17604_r_2L -----
 >CG17604_r_2R **ACGAAAATCAAATTTGTCCTTTAACCGGTGGCGCCGTCTGCAAATCGACTACCGTCGC**
 >CG17604_r_3R1 -----
 >CG17604_r_3R2 -----

>CG17604_p_LTR **GCCGTTAGAACATTGTCGTTGTTGCTGGTGTAGTGCCTTGTGCGGAATGTTACACG**
 >CG17604_r_satellite -----
 >CG17604_r_2L -----
 >CG17604_r_2R **GCCGTTAGAACATTGTCGTTGTTGCTGGTGTAGTGCCTTGTGCGGAATGTTACACG**
 >CG17604_r_3R1 -----
 >CG17604_r_3R2 -----

>CG17604_p_LTR **TACACCACCTACAAATAAAAACTTAACACCGACCAAATACAAGCAATTCTAGAGAACGA**
 >CG17604_r_satellite -----
 >CG17604_r_2L -----
 >CG17604_r_2R **TACACCACCTACAAATAAAAACTTAACACCGACCAAATACAAGCAATTCTAGAGAACGA**
 >CG17604_r_3R1 -----
 >CG17604_r_3R2 -----

>CG17604_p_LTR **AA- GCGAGGACGAAAGCAGAAAAGAAAAATGAACGAAGAAGATCAAAGTTGGCGCCTG**
 >CG17604_r_satellite -----
 >CG17604_r_2L -----
 >CG17604_r_2R **AAAGCGAGGACGAAAGCAGAAAAGAAAAATGAACGAAGAAGATCAAAGTTG-----**
 >CG17604_r_3R1 -----
 >CG17604_r_3R2 -----

** *****

>CG17604_p_LTR **TAGGAGAAGCAGAGGCAAAGAAGCAGAATAAAGACGCTAGTGCTAAAGTCGAAGAGAAAT**
 >CG17604_r_satellite -----

>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR **TTGAACAAATGATGAATACTCTAACCCAGAGCATGTTGGCAAATCTAAACAAGAGGGGC**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR **AAGTAATTATCGCTGCAGAAAAATTTGAAAAAGTTGTAAGTGAAGTGTGATGGCAAATCAA**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR **TTCCTATTAATAAAAAATGGTTTGAAATTTTTGAGAAAAATGCCGAGGCATATGAACTTTTCGG**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR **AGAAACAAAAATATGTTCAAGCCAGAAGTAAGATGATTGGATCAGCAGAACTTTTCTTAG**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR **AATCTGAATGTGTCAGTGGATACACTGAACTCAAAGAGTTACTAATTGAAGAATTTTCAG**
>CG17604_r_satellite -----
>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR GCAGCTATAATAGCGCCGTATTTCACAAAAAGTTGCAAGACAGGAAGAAGAAGAGGGAGG
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>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR AACTCTACACGACTATTTGTTACAAATGAAGAAAATAGCAGCCTTAGGTGAAGTTGAAA
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>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR CAGTTGCTTTGATAACTCATATCGTAAACGGCCTCGACATTAAGGAGTATAAGGGTG
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>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

>CG17604_p_LTR CTATGCTCCGTTGTAAAACCTTAAGGAATTAAGCAAGAATTCGAAATCTACGAGAGTC
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>CG17604_r_2L -----
>CG17604_r_2R -----
>CG17604_r_3R1 -----
>CG17604_r_3R2 -----

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>CG17604_r_satellite -----
>CG17604_r_2L ----- AACCAAAACCAAAGCAAATTACACAAGGTGTAA
>CG17604_r_2R -----
>CG17604_r_3R1 -----
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>CG17604_r_satellite -----

>CG17604_r_2L AAGCAGATCACTGCTTCAACTGTGGTTTCGAGGGAACACAAACGAAAGGATTGTACTTTC
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>CG17604_r_3R2 -----

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>CG17604_r_2L CTACCAAATGTTTCAGCTGTAATCAAGAGGGCCATATCTCAAGCAAGTGCCAGAAAAAG
>CG17604_r_2R CTACCAAATGTTTCAGCTGTAATCAAGAGGGCCATATCTCAAGCAAGTGCCAGAAAAAG
>CG17604_r_3R1 ----- TTTCAGCTGTAATCAAGAGGGCCATATCTCAAGCAAGTGCCAGAAAAAG
>CG17604_r_3R2 ---- CAAATGTTTCAGCTGTAATCAAGAGGGCCATATCTCAAGCAAGTGCCAGAAAAAG

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>CG17604_r_satellite -----
>CG17604_r_2L TAAACAGCATGCGCATTACGTTGATAGTGCACGAACAAAGCCAGTAATCATAAATGGGA
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>CG17604_r_3R1 TAAACAGCATGCGCATTACGTTGATAGTGCACGAACAAAGCCAGTAATCATAAATGGGA
>CG17604_r_3R2 TAAACAGCATGCGCATTACGTTGATAGTGCACGAACAAAGCCAGTAATCATAAATGGGA

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>CG17604_r_satellite -----
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>CG17604_r_2R TTATCATCAACTGTCTGGTGGACACAGGATCAGATGTGACCATAATTAAGAAGCTATAT
>CG17604_r_3R1 TTATCATCAACTGTCTGGTGGACACAGGATCAGATGTGACCATAATTAAGAAGCTATAT
>CG17604_r_3R2 TTATCATCAACTGTCTGGTGGACACAGGATCAGATGTGACCATAATTAAGAAGCTATAT

>CG17604_p_LTR TCAAGAAGATGAAAGATGTTGATTTAAACCGCACTGCAACAGTATTGCGAGGTTTGGGAA
>CG17604_r_satellite -----
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>CG17604_r_2R TCAAGAAGATGAAAGATGTTGATTTAAACCGCACTGCAACAGTATTGCGAGGTTTGGGAA
>CG17604_r_3R1 TCAAGAAGATGAAAGATGTTGATTTAAACCGCACTGCAACAGTATTGCGAGGTTTGGGAA
>CG17604_r_3R2 TCAAGAAGATGAAAGATGTTGATTTAAACCGCACTGCAACAGTATTGCGAGGTTTGGGAA

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>CG17604_r_satellite -----
>CG17604_r_2L ATGCCTCAACACAGCCGATTGGATGCTTCAGAGCATTAAATCAAGACCGACCAGGTGGAAG
>CG17604_r_2R ATGCCTCAACACAGCCGATTGGATGCTTCAGAGCATTAAATCAAGACCGACCAGGTGGAAG
>CG17604_r_3R1 ATGCCTCAACACAGCCGATTGGATGCTTCAGAGCATTAAATCAAGACCGACCAGGTGGAAG
>CG17604_r_3R2 ATGCCTCAACACAGCCGATTGGATGCTTCAGAGCATTAAATCAAGACCGACCAGGTGGAAG

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>CG17604_r_satellite -----

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>CG17604_r_2R CAAGCCACAACGTTTTAGTCGTCCACGATTCTAAATTCAGTTGCGATGGAATAGTGGGAC

>CG17604_r_3R1 CAAGCCACAACGTTTTAGTCGTCCACGATTCTAAATTCAGTTGCGATGGAATAGTGGGAC

>CG17604_r_3R2 CAAGCCACAACGTTTTAGTCGTCCACGATTCTAAATTCAGTTGCGATGGAATAGTGGGAC

>CG17604_p_LTR ACGATTTTATCAGCAAGTTTCGTCTTATCTGTAGTGCAGAAGGCTATACTTTTCTTGACC

>CG17604_r_satellite -----

>CG17604_r_2L ACGATTTTATCAGCAAGTTTCGTCTTATCTGTAGTGCAGAAGGCTATACTTTTCTTGACC

>CG17604_r_2R ACGATTTTATCAGCAAGTTTCGTCTTATCTGTAGTGCAGAAGGCTATACTTTTCTTGACC

>CG17604_r_3R1 ACGATTTTATCAGCAAGTTTCGTCTTATCTGTAGTGCAGAAGGCTATACTTTTCTTGACC

>CG17604_r_3R2 ACGATTTTATCAGCAAGTTTCGTCTTATCTGTAGTGCAGAAGGCTATACTTTTCTTGACC

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>CG17604_r_satellite ----- AGCAGCGACTTAAATGCAA

>CG17604_r_2L TGGAAGCAGATAAAAAACAAGCGGCAAACATTTTACAATTAAGCAGCGACTTAAATGCAA

>CG17604_r_2R TGGAAGCAGATAAAAAACAAGCGGCAAACATTTTACAATTAAGCAGCGACTTAAATGCAA

>CG17604_r_3R1 TGGAAGCAGATAAAAAACAAGCGGCAAACATTTTACAATTAAGCAGCGACTTAAATGCAA

>CG17604_r_3R2 TGGAAGCAGATAAAAAACAAGCGGCAAACATTTTACAATTAAGCAGCGACTTAAATGCAA

>CG17604_p_LTR AGATGCTTGACTGCGCCAGCTTGAAGATCGCATTGAGCAGCTGCCAATAGAGGCCAACA

>CG17604_r_satellite AGATGCTTGACTGCGCCAGCTTGAAGATCGCATTGAGCAGCTGCCAATAGAGGCCAACA

>CG17604_r_2L AGATGCTTGACTGCGCCAGCTTGAAGATCGCATTGAGCAGCTGCCAATAGAGGCCAACA

>CG17604_r_2R AGATGCTTGACTGCGCCAGCTTGAAGATCGCATTGAGCAGCTGCCAATAGAGGCCAACA

>CG17604_r_3R1 AGATGCTTGACTGCGCCAGCTTGAAGATCGCATTGAGCAGCTGCCAATAGAGGCCAACA

>CG17604_r_3R2 AGATGCTTGACTGCGCCAGCTTGAAGATCGCATTGAGCAGCTGCCAATAGAGGCCAACA

>CG17604_p_LTR AAGCTTTGTGCGAACTGCAACGTGATTTAGAAGCCAGTGAATTGCAGTTCGTGGATCAGC

>CG17604_r_satellite AAGCTTTGTGCGAACTGCAACGTGATTTAGAAGCCAGTGAATTGCAGTTCGTGGATCAGC

>CG17604_r_2L AAGCTTTGTGCGAACTGCAACGTGATTTAGAAGCCAGTGAATTGCAGTTCGTGGATCAGC

>CG17604_r_2R AAGCTTTGTGCGAACTGCAACGTGATTTAGAAGCCAGTGAATTGCAGTTCGTGGATCAGC

>CG17604_r_3R1 AAGCTTTGTGCGAACTGCAACGTGATTTAGAAGCCAGTGAATTGCAGTTCGTGGATCAGC

>CG17604_r_3R2 AAGCTTTGTGCGAACTGCAACGTGATTTAGAAGCCAGTGAATTGCAGTTCGTGGATCAGC

>CG17604_p_LTR AACGATTGACTGATCAGGCAACGAGGGAAGCTCGAAGTTGTTTCGCAATGAGATAAATACGT

>CG17604_r_satellite AACGATTGACTGATCAGGCAACGAGGGAAGCTCGAAGTTGTTTCGCAATGAGATAAATACGT

>CG17604_r_2L AACGATTGACTGATCAGGCAACGAGGGAACCGAACTTGTTTCGCAATGAGATAAATACGT
>CG17604_r_2R AACGATTGACTGATCAGGCAACGAGGGAACCGAACTTGTTTCGCAATGAGATAAATTCGT
>CG17604_r_3R1 AACGATTGACTGATCAGGCAACGAGGGAACCGAACTTGTTTCGCAATGAGATAAATACGT
>CG17604_r_3R2 AACGATTGACTGATCAGGCAACGAGGGAACCGAACTTGTTTCGCAATGAGATAAATACGT

***** **

>CG17604_p_LTR **TTAAGACTCTTATTGAGGAAAAGGAAAAGAAGACATGTTCCCTAAGTGATGAACTAACTC**
>CG17604_r_satellite TTAAGACTCTTATTGAGGAAAAGGAAAAGAAGACATGTTCCCTAAGTGATGAACTAACTC
>CG17604_r_2L TTAAGACTCTTATTGAGGAAAAGGAAAAGAAGACATGTTCCCTAAGTGATGAACTAACTC
>CG17604_r_2R TTAAGACTCTTATTGAGGAAAAGGAAAAGAAGACATGTTCCCTAAGTGATGAACTAACTC
>CG17604_r_3R1 TTAAGACTCTTATTGAGGAAAAGGAAAAGAAGACATGTTCCCTAAGTGATGAACTAACTC
>CG17604_r_3R2 TTAAGACTCTTATTGAGGAAAAGGAAAAGAAGACATGTTCCCTAAGTGATGAACTAACTC

>CG17604_p_LTR **AAATGACGGAGAGATTGAGCGAGCTCGCTGATATCAACGAAAAGTTATATCAATGAGTTGA**
>CG17604_r_satellite AAATGACGGAGAGATTGAGCGAGCTCGCTGATATCAACGAAAAGTTATATCAATGAGTTGA
>CG17604_r_2L AAATGACGGAGAGATTGAGCGAGCTCGCTGATATCAACGAAAAGTTATATCAATGAGTTGA
>CG17604_r_2R AAATGACGGAGAGATTGAGCGAGCTCGCTGATATCAACGAAAAGTTATATCAATGAGTTGA
>CG17604_r_3R1 AAATGACGGAGAGATTGAGCGAGCTCGCTGATATCAACGAAAAGTTATATCAATGAGTTGA
>CG17604_r_3R2 AAATGACGGAGAGATTGAGCGAGCTCGCTGATATCAACGAAAAGTTATATCAATGAGTTGA

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>CG17604_r_2L CTGAAACAAAATTGAAGCACTCCCAGGAAATAAAAGATCAAGCAGATGCCTACGAGATTG
>CG17604_r_2R CTGAAACAAAATTGAAGCACTCCCAGGAAATAAAAGATCAAGCAGATGCCTACGAGATTG
>CG17604_r_3R1 CTGAAACAAAATTGAAGCACTCCCAGGAAATAAAAGATCAAGCAGATGCCTACGAGATTG
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>CG17604_r_2L TTGTTCAAGAGTTAAAAGAGAGCTTGAACAAGGCTTCAGTTGATTTTACTCAGCTAAAAA
>CG17604_r_2R TTGTTCAAGAGTTAAAAGAGAGCTTGAACAAGGCTTCAGTTGATTTTACTCAGCTAAAAA
>CG17604_r_3R1 TTGTTCAAGAGTTAAAAGAGAGCTTGAACAAGGCTTCAGTTGATTTTACTCAGCTAAAAA
>CG17604_r_3R2 TTGTTCAAGAGTTAAAAGAGAGCTTGAACAAGGCTTCAGTTGATTTTACTCAGCTAAAAA

>CG17604_p_LTR **GCAACAGTGAGAAGCTACACAAAGAAACCTTCTGCAGGTCTCCGAACTGCAGGAAAAAC**
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>CG17604_r_2L GCAACAGTGAGAAGCTACACAAAGAAACCTTCTGCAGGTCTCCGAACTGCAGGAAAAAC
>CG17604_r_2R GCAACAGTGAGAAGCTACACAAAGAAACCTTCTGCAGGTCTCCGAACTGCAGGAAAAAC
>CG17604_r_3R1 GCAACAGTGAGAAGCTACACAAAGAAACCTTCTGCAGGTCTCCGAACTGCAGGAAAAAC
>CG17604_r_3R2 GCAACAGTGAGAAGCTACACAAAGAAACCTTCTGCAGGTCTCCGAACTGCAGGAAAAAC

>CG17604_p_LTR **TTATAGAAATGGTGTCCCATCGCAGCAATCAGGAAGAGCTAATAAAGCGTCTTGGAATG**
 >CG17604_r_satellite TTATAGAAATGGTGTCCCATCGCAGCAATCAGGAAGAGCTAATAAAGCGTCTTGGAATG
 >CG17604_r_2L TTATAGAAATGGTGTCCCATCGCAGCAATCAGGAAGAGCTAATAAAGCGTCTTGGAATG
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 >CG17604_r_3R1 TTATAGAAATGGTGTCCCATCGCAGCAATCAGGAAGAGCTAATAAAGCGTCTTGGAATG
 >CG17604_r_3R2 TTATAGAAATGGTGTCCCATCGCAGCAATCAGGAAGAGCTAATAAAGCGTCTTGGAATG

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 >CG17604_r_2L AAATTCAAGAAAAA ACTCATAATTTTGAAGAAGAACTCAAAAAGGCAACAGGAGCAGCTTG
 >CG17604_r_2R AAATTCAAGAAAAA ACTCATAATTTTGAAGAAGAACTCAAAAAGGCAACAGGAGCAGCTTG
 >CG17604_r_3R1 AAATTCAAGAAAAA ACTCATAATTTTGAAGAAGAACTCAAAAAGGCAACAGGAGCAGCTTG
 >CG17604_r_3R2 AAATTCAAGAAAAA ACTCATAATTTTGAAGAAGAACTCAAAAAGGCAACAGGAGCAGCTTG

>CG17604_p_LTR **CTAATCAAATGCAGATGAAGGCCACTGAAGTTGAGAGCGAAAATAAGCGAAACGCTGTTG**
 >CG17604_r_satellite CTAATCAAATGCAGACGAAGGCCACTGAAGTTGAGAGCGAAAATAAGCGAAACGCTGTTG
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 >CG17604_r_2R CTAATCAAATGCAGACGAAGGCCACTGAAGTTGAGAGCGAAAATAAGCGAAACGCTGTTG
 >CG17604_r_3R1 CTAATCAAATGCAGACGAAGGCCACTGAAGTTGAGAGCGAAAATAAGCGAAACGCTGTTG
 >CG17604_r_3R2 CTAATCAAATGCAGACGAAGGCCACTGAAGTTGAGAGCGAAAATAAGCGAAACGCTGTTG

*****1*****

>CG17604_p_LTR **AAATACAAAAAGTTAAATTTAGCGAGGAATTACAGTCTCAGAAAGATAACCTAATGAAA**
 >CG17604_r_satellite AAATAC- AAAAAGTTAAATTTAGCGAGGAATTACAGTCTCAGAAAGATAACCTAATGAAA
 >CG17604_r_2L AAATAC- AAAAAGTTAAATTTAGCGAGGAATTACAGTCTCAGAAAGATAACCTAATGAAA
 >CG17604_r_2R AAATAC- AAAAAGTTAAATTTAGCGAGGAATTACAGTCTCAGAAAGATAACCTAATGAAA
 >CG17604_r_3R1 AAATAC- AAAAAGTTAAATTTAGCGAGGAATTACAGTCTCAGAAAGATAACCTAATGAAA
 >CG17604_r_3R2 AAATAC- AAAAAGTTAAATTTAGCGAGGAATTACAGTCTCAGAAAGATAACCTAATGAAA

*****2*****

>CG17604_p_LTR **AAGGTATCCGAATTGGAGCTTGAAATTTAAAAGAAAAGAAACCGAATTGATTGAACCTTGAG**
 >CG17604_r_satellite AAGGTATCCGAATTGGAGCTTGAAATTTAAAAGAAAAGAAACCGAATTGATTGAACCTTGAG
 >CG17604_r_2L AAGGTATCCGAATTGGAGCTTGAAATTTAAAAGAAAAGAAACCGAATTGATTGAACCTTGAG
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 >CG17604_r_3R1 AAGGTATCCGAATTGGAGCTTGAAATTTAAAAGAAAAGAAACCGAATTGATTGAACCTTGAG
 >CG17604_r_3R2 AAGGTATCCGAATTGGAGCTTGAAATTTAAAAGAAAAGAAACCGAATTGATTGAACCTTGAG

*****3*****

>CG17604_p_LTR **CGTGAAGAACAATGAAATGGCTGTGCTACAATTTAAAATGAATCGAATTAACGCTG**

>CG17604_r_satellite CGCGAAAAGAACAATGAAATGGCTGTGCTACAATTTAAAATGAATCGAATTAATTGCCTG
>CG17604_r_2L CGCGAAAAGAACAATGAAATGGCTGTGCTACAATTTAAAATGAATCGAATTAATTGCCTG
>CG17604_r_2R CGCGAAAAGAACAATGAAATGGCTGTGCTACAATTTAAAATGAATCGAATTAATTGCCTG
>CG17604_r_3R1 CGCGAAAAGAACAATGAAATGGCTGTGCTACAATTTAAAATGAATCGAATTAATTGCCTG
>CG17604_r_3R2 CGCGAAAAGAACAATGAAATGGCTGTGCTACAATTTAAAATGAATCGAATTAATTGCCTG
4***5*****

>CG17604_p_LTR ATCGACCAACCAGTGACCACAATTAACAGCTAAAAGATTCCAAAGGGCCAACCAGAACT
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>CG17604_r_2L ATCGACCAACCAGTGACCACAATTAACAGCTAAAAGATTCCAAAGGGCCAACCAGAACT
>CG17604_r_2R ATCGACCAACCAGTGACCACAATTAACAGCTAAAAGATTCCAAAGGGCCAACCAGAACT
>CG17604_r_3R1 ATCGACCAACCAGTGACCACAATTAACAGCTAAAAGATTCCAAAGGGCCAACCAGAACT
>CG17604_r_3R2 ATCAACCAACCAGTGACCACAATTAACAGCTAAAAGATTCCAAAGGGCCAACCAGAACT
*** *****

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>CG17604_r_2L GAGAGCATTCTACTAAGGTGCA- GCCGAAAATGCAGACCTATTGTCATCCGGGTCGGAT
>CG17604_r_2R GAGAGCATTCTACTAAGGTGCA- GCCGAAAATGCAGACCTATTGTCATCCGGGTCGGAT
>CG17604_r_3R1 GAGAGCATTCTACTAAGGTGCA- GCCGAAAATGCAGACCTATTGTCATCCGGGTCGGAT
>CG17604_r_3R2 GAGAGCATTCTACTAAGGTGCA- GCCGAAAATGCAGACCTATTGTCATCCGGGTCGGAT
*****67*****8*****

>CG17604_p_LTR GATGATGATCAGGAGGGCCGAATGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCG
>CG17604_r_satellite GATGATGATCAGGAGGGCCGAATGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCG
>CG17604_r_2L GATGATGATCAGGAGGGCCGAATGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCG
>CG17604_r_2R GATGATGATCAGGAGGGCCGAATGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCG
>CG17604_r_3R1 GATGATGATCAGGAGGGCCGAATGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCG
>CG17604_r_3R2 GATGATGATCAGGAGGGCCGAATGTAACATGGAGTAAGGCTGAAGGCTGGCAACAACCCG

>CG17604_p_LTR GTTGGCAGCGCTGTTGAGCAGCAACATGATTGTCGGAATCGAAGTTATCGACAATCAGT
>CG17604_r_satellite GTTGGCAGCGCTGTTGAGCAGCAACATGATTGTCGGAATCGAAGTTATCGACAATCAGT
>CG17604_r_2L GTTGGCAGCGCTGTTGAGCAGCAACATGATTGTCGGAATCGAAGTTATCGACAATCAGT
>CG17604_r_2R GTTGGCAGCGCTGTTGAGCAGCAACATGATTGTCGGAATCGAAGTTATCGACAATCAGT
>CG17604_r_3R1 GTTGGCAGCGCTGTTGAGCAGCAACATGATTGTCGGAATCGAAGTTATCGACAATCAGT
>CG17604_r_3R2 GTTGGCAGCGCTGTTGAGCAGCAACATGATTGTCGGAATCGAAGTTATCGACAATCAGT

>CG17604_p_LTR CATCGAAGGAACGATCGCAAGGCAGCAGTGGAGTCGAGTGAAGTCAGCGTTGCAGTCAG
>CG17604_r_satellite CATCGAAGGAACGATCGCAAGGCAGCAGTGGAGTCGAGTGAAGTCAGCGTTGCAGTCAG
>CG17604_r_2L CATCGAAGGAACGATCGCAAGGCAGCAGTGG-----AG
>CG17604_r_2R CATCGAAGGAACGATCGCAAGGCAGCAGTGG-----AG
>CG17604_r_3R1 CATCGAAGGAACGATCGCAAGGCAGCAGTGGAGTCGAGTGAAGTCAGCGTTGCAGTCAG

>CG17604_r_3R2 CATCGAAGGAACGATCGCAAGGCAGCAGTGGAGTCGAGTGGAAAGTCAGCGTTGCAGTCAG
***** **

>CG17604_p_LTR TCGAGTTCTCAGCAGCAGTCGTTCCGGTCACAAACTAAGAATACTTTATATAATTACCGCA
>CG17604_r_satellite TCGAGTTCTCAGCAGCAGTCGTTCCGGTCACAAACTAAGAATACTTTATATAATTACCGCA
>CG17604_r_2L TCGAGTTCTCAGCAGCAGTCGTTCCGGTCACAAACTAAGAATACTTTATATAATTACCGCA
>CG17604_r_2R TCGAGTGGAAAGTCAGCG-----
>CG17604_r_3R1 TCGAGTTCTCAGCAGCAGTCGTTCCGGTCACAAACTAAGAATACTTTATATAATTACCGCA
>CG17604_r_3R2 TCGAGTTCTCAGCAGCAGTCGTTCCGGTCACAAACTAAGAATACTTTATATAATTACCGCA
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>CG17604_p_LTR TTTAGAATTAAACTAATAATTAATTAATAATAAACAATAATAATAAACAATCTTACA
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>CG17604_r_2L TTTAGAATTAAACTAATAATTAATTAATAATAAACAATAATAATAAACAATCTTAC-
>CG17604_r_2R -----
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