```
                   10        20        30        40        50        60        70        80        90       100
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP006  -------------------------------------------------------------------------AAATCCTCAAAG-----------AAGA
TsuRTP007  ------------------------------------------------------------------------------------G-----------AAAA
TsuRTP008  --------------------------------------------------------------------------AATCCTCAAAG-----------AAGA
TsuRTP009  ATCCATTTCATCTTCACACAATATCTTTGGTGTGGAGACTTAGAGACACCAAACTTTTGGTGTTTTGGAGATCAAATCCTCAAAG-----------AAGA
TsuRTP010  --------CATCTTCACACAACATCTTTGGTGTGGAGACTTAGAGACACCAAACTTTTGGTGTTTTGGAGAACAAATCCTCAAAATCCTCAAAAGAAGAA
                                                                                                           *  *

                  110       120       130       140       150       160       170       180       190       200
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP006  AA-GGAGCACTAAAAGGGAGGAAATCACAAGGAAGATTCAAGGAGCAAGGAGGTGACTTGAAGGCCCTCCACTTGGGTGAATCCCTTGT-GCAATCAAGG
TsuRTP007  AG-GAGACACTAAAAGGGAGGAAATCACAAGGAAGATTCAAGGAGCAAGGAGGTGACTTGAAGGCCCTC-ACTTGGGTGAATCCCTTGTAGCAATCAAGG
TsuRTP008  AAAGGAGCACTAAAAGGGAGGAAATCACAAGGAAGATTCAAGGAGCAAGGAGGTGACTTGAAGGCCCTCCACTTGGGTGAATCCCTTGT-GCAATCAAGG
TsuRTP009  AAAGGAGCACTAAAAGGGAGGAAATCACAAGGAAGATTCAAGGAGCAAGGAGGTGACTTGAAGGCCCTCCACTTGGGTGAATCCCTTGT-GTAATCAAGG
TsuRTP010  AAAGGAGCACTAAAAGGGAGAAAATCACAAGGAAGATCCAAGGAGCAAGGAGGTGACTTGAAGGCCCTCCACTTGGGTGAATCCCTTGT-GCAATCAAGG
           *  *   ************* **************** ******************************* ******************* * ********

                  210       220       230       240       250       260       270       280       290       300
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP006  ATGAGCTTCAAGGGTAAAGAATCTCTAAATTCTTATTCTCTTTAATTTTGTTAAAGAGTCTTATGGTTCACCATATACTAGGCTTTGAAAGTCATGGGTT
TsuRTP007  ATGAGCTTCAAGGGTAAAGAATCTCTAAATTCTTATTCTCTTTAATTTTGTTAAAGAGTCTTATGGTTCACCATATACTAGGCTTTGAAAGTCATGGGTT
TsuRTP008  ATGAGCTTCAAGGGTAAAGAATCTCTAAATTCTTATTCTCTTTAATTTTGTTAAAGAGTCTTATGGTTCACCATATACTAGGCTTTGAAAGTCATGGGTT
TsuRTP009  ATGAGCTTCAAGGGTAAAGAATCTCTAAATTCTTATTCTCTTTAATTTTGTTAAAGAGTCTTATGGTTCACCATATACTAGGCTTTGAAAGTCATGGGTT
TsuRTP010  ATGAGCTTCAAGGGTAAAGAATCTCTAAATTCTTATTCTCTTTAATTTTGTTAAAGAGTCTTATGGTTCACCATATACTAGGCTTTGAAAGTCATGGGTT
           ****************************************************************************************************

                  310       320       330       340       350       360       370       380       390       400
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP006  TTATGAATTGTTTTT--AATGCATGCCTACTTTAAAGAGTTATTAGTTTGCATATGTATTCAAATGTTCTTACATGTTCTTAGCTAGGACAAAAATTTTT
TsuRTP007  TTATGAATTGTTTTTTGAATGCATGCCTACTTTAAAGAGTTATTAGTTTGCATATGTATTCAAATGTTCTTACATGTTCTTAGCTAGGACAAAA-TTTTT
TsuRTP008  TTATGAATTGTTTTT-GAATGCATGCCTACTTTAAAGAGTTATTAGTTTGCATATGTATTCAAATGTTCTTACATGTTCTTAGCTAGGACAAAA-TTTTT
TsuRTP009  TTATGAATTGTTTT--GAATGCATGCCTACTTTAAAGAGTTATTAGTTTGCATATGTATTCAAATGTTCTTACATGTTCTTAGCTAGGACAAAA-TTTTT
TsuRTP010  TTATGAATTGTTTTT-GAATGCATGCCTACTTTAAAGTGTTATTAGTTTGCATATGTATTCAAATGTTCTTACATGTTCTTAGCTAGGACAAAA-TTTTT
           **************   ******************** ******************************************************** *****

                  410       420       430       440       450       460       470       480       490       500
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP006  CCTTCAATAGGACTGCAACACTCCCTCTTGAGTGTGTAAAATACTCAAACAAATTACCTATCAGGTCTTCAGCGATGAAGTTCAATTGATGGAGTCATCG
TsuRTP007  CCTTCAAATATAACATACTACGTATAGTATGAAAATACTTACCATATCTAGTTCAAAGCTCCAAATTTCAAAGCTCCGTTTAAGAACCAAATAAAAGTTA
TsuRTP008  CCTTCACGTTCACTATAAGAACCCATGATGGACTTAAGGAATTTGGGCTTAGGGCCCAGCCTAAAAGGCCTAGGGCCTGAGGTGAAAGGAAACGGCTCGA
TsuRTP009  CCTTCAGAAGAGACCATCAGAAGTTCTTTGCACCTCCAATCCCAAGAAGTAATGGAGGGGCCCCAAAATCCTTAACAGGAAAAGCTTAACGGAGTTTGTG
TsuRTP010  CCTTCACACAGCACAAGTCCTTCTTCTTCCTTCCTTGCTACGGCACTCTTTATATTTTTCTCTCTGAAATTCTCTCTAAAGCTCTCTAATTTTGTGCGGC
           ******

                  510       520       530       540       550       560       570       580       590       600
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP006  GCACAATGAGCGAATGCGAGTCTCAGATAAAACGAAAGAATGTATAAAAAGGTAAAAACTCACAAAAACCTTGCTATGGTAAAAACCCAAGGTGGGATAA
TsuRTP007  GGAATGTGATGAATAGAAATATATCAATTAGAAGCCCAGTTGTGA-------------------------------------------------------
TsuRTP008  AGGCCTTAAGCCTTTAAAGGCTTGGGTTTTAAGGCGCACGGGCCTAAGGCTCCAAAGGGGGACATGGCCCAAAGGCCTCAGGGTTTTAAACAATTAAATA
TsuRTP009  AATAAAACGTTGACAGACAGTGGCATTAGGTCCGGTGACAAGAATGTCATCGACATAGACCAAAAACAAGAACAGGAAA---------------------
TsuRTP010  ATAAT-----------------------------------------------------------------------------------------------

                  610       620       630       640       650       660       670       680       690       700
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP006  AAAACTCGTAGACT------------------------------------------------------------------------------------
TsuRTP007  --------------------------------------------------------------------------------------------------
TsuRTP008  AAAATTAAAAGGGTTGGGTTGGGGTTTAGGCACGGCCCAAAAGGGCCTGGGTTCGAATGGGCTTAGGCCCGAAGGTCTGGTTCCCTGATCTCGCCAGA
TsuRTP009  --------------------------------------------------------------------------------------------------
TsuRTP010  --------------------------------------------------------------------------------------------------
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Supplemental Fig. 2.

Nucleotide sequences of five RBIP markers of 3′-LTR insertions. Forward primers are indicated by italics, and reverse primers are indicated by underlined.