```
                   10        20        30        40        50        60        70        80        90       100
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001 -------------------------------------------------------------------------------------TATGCCAAGTTCTTA
TsuRTP002 ----------------------------------------------------------------------------------------------------
TsuRTP003 ----------------------------------------------------------------------------------------------------
TsuRTP004 ----------------------------------------------------------------------------------------------------
TsuRTP005 ----------------------------------------------------------------------------------------------------
TsuRTP011 ----------------------------------------------------------------------------------------------------
TsuRTP012 ----------------------------------------------------------------------------------------------------
TsuRTP013 ----------------------------------------------------------------------------------------------------
TsuRTP014 ----------------------------------------------------------------------------------------------------
TsuRTP015 ----------------------------------------------------------------------------------TTTGTGACAATTGTAGTA
TsuRTP016 ----------------------------------------------------------------------------------------------------
TsuRTP017 -----------------------------------CAGCCTAGTACTTCACCTTGGGGAGCTCCAGT-ATGTTGTGAGGAAGAAAGACGGAACCTTGAGG
TsuRTP018 -----------------------------------------------------------------------ACTGAAGACCTGATGCGACGTTTTGTTTG
TsuRTP019 ----------------------------CAACCCAAGCAGGTAGTGGGGCTCGGGGGAGGCCCTGTGGATAGGCTAAGCGGGAATCCATCGCCTGAGAGC
TsuRTP020 -------------------------------------------TTCTTGCACACTTTGGCCTTATAATCTGAAAATACACAAAAGTGGCCTTAAACACTG
TsuRTP021 --GATTTACATGCTTAAAGAAGATTCTCGCATTCAACGTTTCCAATTTCTCGTTCATCTATAGATTTTTCGTATGTTCTACTTGCTATAAATTTTTATAA
TsuRTP022 ----------------------------------------------------------------------------------------------------

                  110       120       130       140       150       160       170       180       190       200
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001 AAGGAGCTTTGCACCACTAGGAAGAGGATGTCGACCAAGGAGGTGGTAAAAGGTAGGTGAAAAATGTCTCCGCCATCTTGCAACGCAAACTACCCCCCAA
TsuRTP002 ---------------------TTGTCAGGTCTACTGTTAGAATGGTTTGATGTCGAGGCTCTTCGATCCATCATGATGACATGTATTATTGTCCAACAAT
TsuRTP003 ----------------------------------------------------------------------------------------------------
TsuRTP004 ----------------------------------------------------------------------------------------------------
TsuRTP005 ----------------------------------------------------------------------------------------------------
TsuRTP011 --------------------------------------------------AGGCATTTTAGGCGTGAGGTGTAGGCGAAATCACGCCACAGAGGACATAT
TsuRTP012 ----------------------------------------------------------ACCTTCTCGTTGACTTTTTATAAAATTTGTCGCCACCTTAGC
TsuRTP013 --------------------AAACCATCATCACCAATCTGCCGCAAGCAAAGGA-AAGGAGATTAGATTCACTCAATTGTGGGCTCTTCATTCTGAGTTT
TsuRTP014 --------------------ATTCTTGAGCTTAAACCATTGCCGGATCATTTGAAGTATGTCTATTTGGGAGAGAATGAGACGTTGCCCGTCATAGTTTC
TsuRTP015 ATGATGTAAGTAGGGATCGTTCTAACCGGGGATTAACTAGGGGTGCTAAACACTTGACTCAAATAAATAAAACTAATCTTTTAAAAACACTTAACTCACT
TsuRTP016 ---------ATAGACGTAAGGTTAGCCATTTGGAGTTGTAACTCAGAAATAGAACTTACCTCATTTACATGATATGGCCGTGGGGTGTCTCTCTGCCCAA
TsuRTP017 CTATGTATTGATTATCGACAATTGAATCGGGTGACGATTAAAAACCGTTATCCGTTGCCGCGTATTGATGATTTGTTTGATCAGCTTCGAGGTGCTTGTG
TsuRTP018 AGTATTTACACACTCAAGGGGGAGTATCAGATCAGGAATGTGATTGTGTAAATCCTAGTGTATCTAGGAGTATCTTGTATATTCCTATTAGGAGTTGATT
TsuRTP019 CTAATGGCTGTGTGATGTGTGGCTGACCTCGGGGTGACCCGACTTGAATTCTTCTGTTTTCCTTTGTCAGAATCTGGAAAAAGAACGGGATGCATACAGG
TsuRTP020 AAATAGATAAGTAAACACAACATAAATGCACGAGAACAAGCTAATTAAGTCGCATGAATATGCTCCTATCAGTTAGTTTCCTCCTTTAGTGGATCAACCT
TsuRTP021 AATTATTTGAATAAAAGTATAAGAAAAATACAATGATAAGAAATTTGGAAACCACAATGAATGAAGCTTCCTACTTTCAAAGATCCGGATCAAGTGATGG
TsuRTP022 -----------GGAATAGCTGGCTCCATGCTCAAGAGTAACGGATAGTGGTCTGAGCCACGCACTATGCAATGAGATTGCCAACTTCCATTAACTAGGCC

                  210       220       230       240       250       260       270       280       290       300
          ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001 ATGCAAAGATCCGGGTAGTTTTACCATTCCTTGTGTCATAGGTAACACGCGTTTTAAATCTGCCATGCTAGACCTAGGTGTTGGAAGTATGCCCACAAAG
TsuRTP002 ATGATTGTGGAAGATGAGTATGATTATGATGTCGTCGATGAATACGAGCCAAATCTAATGAACAATTCAAGAACACGTTGTTGGAAGTATGCCCACAAAG
TsuRTP003 ------------------------------------------CGTACTACAATTGCATAATTTATAGGGTTTAATATGTGTTGGAAGTATGCCCACAAAG
TsuRTP004 --------------GAAGAATTATTTTGCAGAGCTGAATCAGGTTGGTTGATGCACCAACATCTTGCGATCACCTTGCTGTTGGAAGTATGCCCACAAAG
TsuRTP005 -----ACAAGTAACTACAAACAAGCATAAACCAAAGAGTATATCAAACGTCCATCCATGTTTGTAACTTTCTTTAACCTGTTGGAAGTATGCCCACAAAG
TsuRTP011 CTTCCAAATCCGAGTCACAACTTTGATTCTGTAGGTTGCTTAACTAGTATTGCAATGACTTTAAAACCAAGTCACTTTTGTTGGAAGTATGCCCACAAAG
TsuRTP012 TTATTTTGACGCCTTGATTCCAAATCCGCACTTCGTTTCCCCAAATTTAATTGTCTTAGTGAAGTTTTACTAATGGGTTGTTGGAAGTATGCCTACAAAG
TsuRTP013 GTTGAACTAATTTTTGGGTGTATTTCTATTCTTATATTTCAATGTCTAATTCATGTAATCTTTGTTTTTGCTCTGAGTTGTTGGAAGTATGCCCACAAAG
TsuRTP014 CTCATCCCTCACGTCAATGGAGGAGGAGAAATTGGATTCGGGGTGTTGAAAGAGCACAAAAACGGCCATAGGATGGACTGTTGGAAGTATGCCCACAAAG
TsuRTP015 TAACGAAAACTCAAAATAAGTCCACAAGACTCCAAATACTTAAAAACACAAAATAAGATAGATTAAGACTAAACAAAATGTTGGAAGTATGCCCACAAAG
TsuRTP016 CACCTTCATATTGTTGTGGATTGAGTGCTCGATTAGCAATGAGAGTTTTGGCATCCCTAGGTGTCTTGTCCACTAGAGTGTTGGAAGTATGCCCACAAAG
TsuRTP017 TATTCTCCAAGATTGACTTGAGGTCGGGTTACCATCAGCTGAAGATTAGTAGGGATGATGTTCCTAAGACGGCGTTCATGTTGGAAGTATGCCCATAAAG
TsuRTP018 ACCTATTAAGAGATGTAATCCTAAAAGGGTATGGATTCTTCCTATCATACTACTATAAATAAAGGCATAAGGGGGTGATGTTGGAAGTATGCCTACAAAG
TsuRTP019 GAATTAAGCCCTTGAATTAAACCACAAGAATTGCAACACAACAGGATTTAAAGCTCAAGAACGCAAGATAGTGATATATGTTGGAAGTATGCCCACAAAG
TsuRTP020 TCGTGTCAGCTTCTCACATGCTGCACATCCAGACAATTGACAAGTGTAGCAATCTGCAAGTTATTTTCCCCATGGTCCTGTTGGAAGTATGGCCACAAAG
TsuRTP021 AGATTGCAATGTAGCACCACCACAATGATCCACAAGGCTCAACGCGATGGCTAAATGAGCAACTTTGCCATCATGGAGTGTTGGAAGTATGCCCACAAAG
TsuRTP022 CCAATTGAGACGTTTATGCACCAGGGTATTATTCCTAGTGCCCCGTGAAGTTTGGGCCGCTAAAACCTAAGTCAATCATGTTGGAAGTATGCCCACAAAG
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                   310       320       330       340       350       360       370       380       390       400
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP002   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTA---------TGAAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP003   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP004   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP005   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGCATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP011   CCACTCATTT-GATGTAATAGCTTTTTTGGAATACTTAATGTATTAAACTTTTATATGTTTAATGAAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP012   CCACTCATTT-GATGTAATAGCTTTTTTGGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP013   CCACTCATTTTGATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP014   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGCATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP015   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP016   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAATTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP017   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTTTATTG
TsuRTP018   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGCATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATTACTATTT-ATTG
TsuRTP019   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP020   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP021   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
TsuRTP022   CCACTCATTT-GATGTAATAGCTTTTT-GGAATACTTAATGTATTAAACTTTTATATGTTTAATGGAGGGCAAAGCTTATTGTTAATCACTATTT-ATTG
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                   410       420       430       440       450       460       470       480       490       500
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP002   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCCCTTATGTT
TsuRTP003   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAATGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP004   TATCTTGTGTTTAAGCAATAAGGGA-TCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP005   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP011   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP012   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCGAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP013   TATCTTGTGTTTAAGAAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP014   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP015   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAAAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP016   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTTTCGAGACCTTTCTCTTATGTT
TsuRTP017   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP018   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP019   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP020   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP021   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGATCTAAGTAAGTTAGATTTT-CGAGACCTTTCTCTTATGTT
TsuRTP022   TATCTTGTGTTTAAGCAATAAGGGAATCCAAGGAATGTATTTGATCTAAGAGATAAGTGTGTAGACATCGAAATTTCGGTGAAACAAATGTTCACCAATG
            *************** ********* *********************** ****** ** *

                   510       520       530       540       550       560       570       580       590       600
            ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001   TCATTACTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP002   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP003   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP004   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP005   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP011   TCATTCCTAAAAAGTTCCTAGCCATAGGATTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP012   TCATTCCTAAAATGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP013   TCATTCCTAAAAAGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCTGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP014   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATTGATATGACAA
TsuRTP015   TCATTCCTAAAAAGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCACTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP016   TCATTCCTAAAACATTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCTCTAAGGTTAGTATGTGTTATGTCGACTCAAGTATGGATATGACAA
TsuRTP017   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTCG------------------
TsuRTP018   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTTAGTATGTGTTATGTC-------------------
TsuRTP019   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGCATTGACAATCCGCTAAGGTT----------------------------------
TsuRTP020   TCATTCCTAAAACGTTCCTAGCCACAGGGTTGCCAATTGGGCATTGACAATCCGCT----------------------------------------
TsuRTP021   TCATTCCTAAAACGTTCCTAGCCATAGGGTTGCCAATTGGGC-------------------------------------------------------
TsuRTP022   CATTAAAGTTTTGACGTGTCAAGGCATACATGGCATACGCCACGTGTTGTACAAATTG-TACACATGGCGTGTGACTCAACAAAATAGGAAGAAATACC
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                 610       620       630       640       650       660       670       680       690       700
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001  GTCTCAAGTCATTTAGTGTT-GGAC-ACTAAGACAAACACATAGGT------------------------------------------------------
TsuRTP002  GTCTCAAGTCATTTAGTGTT-GGAC-ACTAAGACAAACACATAGGT------------------------------------------------------
TsuRTP003  GTCTCAAGTCATTTAGTGTT-GGAC-ACTAAGACAAACACATAGGTGCTCGAAAAAAGTAATCGAGTACACTGAACTAGGATCAAAAGAGAGTTCAAACA
TsuRTP004  GTCTCAAGTCATTTAGTGTTTGGAC-ACTAAGACAAACACATAGGTGCTCGAAAGA-GTAATCGAGTACACTGAACTATGATCAAAAGAGAGTTCAAACA
TsuRTP005  GTCTCAAGTCATTTAGTGTTGGTACGACTAAGACAAACACATAGATGCTCGAAAGA-GTAATCGAGTACACTGAACTATGATCAAAAGAGAGTTCAAACA
TsuRTP011  GTCTCAAGTCATTTAGTGTT-GGAC-ACTAAGACAAACACATAGGTGCTCGAAAGA-GTAATCGAGTACACTGAACTATGATCAAAAGAGAG--------
TsuRTP012  GTCTCAAGTCATTTAGTGTT-GGAC-ACTAAGACAAACACATAGGTGCTCGAAAGA-GTAATCGAGTACACTGAACTATGATCAAAAGAGAGTT------
TsuRTP013  GTCTCAAGTCATTTAGTGTT-GGAC-ACTAAGACAAACACATAGGTGCTCGAAAGA-GTAATC-------------------------------------
TsuRTP014  GTCTCAAGTCATTTAGTGTT-GGAC-ACTAAGACAAACACATAGG-------------------------------------------------------
TsuRTP015  GTCTCAAGTCATTT--------------------------------------------------------------------------------------
TsuRTP016  GTCTCAAGTCATT---------------------------------------------------------------------------------------
TsuRTP017  ----------------------------------------------------------------------------------------------------
TsuRTP018  ----------------------------------------------------------------------------------------------------
TsuRTP019  ----------------------------------------------------------------------------------------------------
TsuRTP020  ----------------------------------------------------------------------------------------------------
TsuRTP021  ----------------------------------------------------------------------------------------------------
TsuRTP022  CTTGAAGGATTAAACAAGTTTTTACTTCTTCATTTTTGGG------------------------------------------------------------

                 710       720       730       740       750       760       770
           ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
TsuRTP001  -------------------------------------------------------------------------
TsuRTP002  -------------------------------------------------------------------------
TsuRTP003  TACATGTCATGTAAGAACTCGATGGTTACAATATGCAAAGTAGTCCTTTGACCTGAGGCATCATAGATGTCTA
TsuRTP004  TACATGTCATGTAAGAACTCGATGGTTACAATATGG-------------------------------------
TsuRTP005  TACATGTCATGTAAGAACT------------------------------------------------------
TsuRTP011  -------------------------------------------------------------------------
TsuRTP012  -------------------------------------------------------------------------
TsuRTP013  -------------------------------------------------------------------------
TsuRTP014  -------------------------------------------------------------------------
TsuRTP015  -------------------------------------------------------------------------
TsuRTP016  -------------------------------------------------------------------------
TsuRTP017  -------------------------------------------------------------------------
TsuRTP018  -------------------------------------------------------------------------
TsuRTP019  -------------------------------------------------------------------------
TsuRTP020  -------------------------------------------------------------------------
TsuRTP021  -------------------------------------------------------------------------
TsuRTP022  -------------------------------------------------------------------------
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Supplemental Fig. 1.

Nucleotide sequences of 17 RBIP markers of 5′-LTR insertions. Forward primers are indicated by underlined, and reverse primers are indicated by italics.