

Supporting Information

In-Plant Persistence and Systemic Transport of *Nicotiana benthamiana* Retrozyme RNA

The following Supporting Information is available for this article:

Figure S1. Sequence similarity between LTR regions of *F. ananassa* and *N. benthamiana* retrozymes.

Figure S2. Sequences of full-length *N. benthamiana* retrozymes.

Figure S3. Sequence alignment of *N. benthamiana* Group 1 retrozymes.

Figure S4. Sequence alignment of *N. benthamiana* Group 2 retrozymes.

Figure S5. Conserved region in the LTRs of Group 1 and Group 2 retrozymes.

Figure S6. Analysis of potential ribozyme structures in *N. benthamiana* retrozymes.

Figure S7. 5'-RACE analysis of LTR-GFP transcription product.

Figure S8. Sequence analysis of Group 1 retrozyme (-) strand-specific amplification product obtained with divergent primers.

Figure S9. Sequence analysis of NbRZ1-Tag amplification products obtained for upper leaves of plants agroinfiltrated for expression of NbRZ1-Tag.

Table S1. Retrozyme-containing *N. benthamiana* genomic scaffolds.

Table S2. Contigs assembled from retrozyme-specific HTS reads.

Table S3. Retrozyme-specific small RNAs in *N. benthamiana* plants.

Table S4. Primers used in this study.

F.ananassa_Rtz-Fa-49c_LTR NbRZ1 (Niben101Scf01887)	TGTCACGTTCCGCTTTTGGGAGTGTTCATCATGGGCGACACTGGTTGTCAAGCTGCATGGA TGTCACGACCCGATTGTGCG---TGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTGGA ***** *** * * * * * * * * ** ****
F.ananassa_Rtz-Fa-49c_LTR NbRZ1 (Niben101Scf01887)	TATGCGGGGTTGCGCTCCAAGATCAAGGAGTGTAGGGGCATACGTGCAGTCCCTTTGGAG TTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGC-GATAAGGCGTTCTCCCTTAGATG * * * * * * * * * * * * * * * *
F.ananassa_Rtz-Fa-49c_LTR NbRZ1 (Niben101Scf01887)	T-----TCAGGCAGGCCGACCCGGTTGAGTTGGGGAGCTTGTGCGTGGT CTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTGGGGAGCTTGTGCGTGGT *****
F.ananassa_Rtz-Fa-49c_LTR NbRZ1 (Niben101Scf01887)	CGAGGACTTAACGCTGAAGAGGGGACTAGGCCATCCCTACACAACTGGTCGGGGTCTGG CATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGGGACAACCTGGTCGGGGGCTAG * * * * * * * * * * * *
F.ananassa_Rtz-Fa-49c_LTR NbRZ1 (Niben101Scf01887)	AGCCGATCCCTTGACGAGCCCAAGGCAGGGCGAAACCAGT-CGTTGCCTCGGTTGATAAG TGCCGCTCCCTTGATGAGCCCAAGGCAGGGCGAAACCAGTTGGCTTCCGCATGTGGTAAG *****
F.ananassa_Rtz-Fa-49c_LTR NbRZ1 (Niben101Scf01887)	GCTGG-CTCCC-TGGCATGGGA-----GCGCCGCATGGGCCAAGTGTGGTGGCCGAA GCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGC-CG ***** * * * * * * * * * *
F.ananassa_Rtz-Fa-49c_LTR NbRZ1 (Niben101Scf01887)	AGGGCTAGGCCCGTGACA GACTCTCGTCCCGTGACA * * * *

Figure S1. Sequence similarity between LTR regions of *F. ananassa* and *N. benthamiana* retrozymes. Sequence alignment of 352-nucleotide-long LTR of the *F. ananassa* retrozyme Rtz-Fa-49c (GeneBank accession number KX281162.1) with LTR of retrozyme identified in *N. benthamiana* genomic scaffold Niben101Scf01887 (<https://solgenomics.net>) referred to as NbRZ1. The ribozyme region is shown by gray shading. Asterisks indicate identical residues.

>NbrZ1 (Niben101Scf01887)

TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGCT
TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGT
AGCCGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCGATGTGGTAAGGCTGGTCTGGGGT
GGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAATTGCTGTTGTTGCGCG
TTTATGGTGGGGTCCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCTAGGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGA
CCGGATGGCCACCAAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGCGCGCATAGCAGTATTGTACGGGATCCTTGGGCAGAGTCC
TTCTCCCCCTACAGCACGAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAA**TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTG**
GATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTT
GGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGGGACAAC**TGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGG**
CAGGCGAAACCGGTTGGCTTCCGCGTGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGT
CCCGTGACA

>NbrZ2 (Niben101Scf00825)

TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGCT
TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGT
AGCCGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCGTGTGGTAAGGCTGGTCTGGGGT
GGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAATTGCTGTTGTTGCGCG
TTTATGGTGGGGTCCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCTAGGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGA
CCGGATGGCCACCAAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGCGCGCATAGCAGTATTGTACGGGATCCTTGGGCAGAGTCC
TTCTCCCCCTACAGCACGAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAA**TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTG**
GATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTT
GGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGGGACAAC**TGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGG**
CAGGCGAAACCGGTTGGCTTCCGCGTGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGT
CCCGTGACA

>NbrZ3 (Niben101Scf04922)

CCGTGACAAGTGGTATCAGAGCCGGACGTAATTGCTGTTGTTGCGCGTTTATGGTGGGGTCCCTCGGGGAGGACTGTGCGGGTGCGTTGCTAGGGGGTGGCT
CGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGACCGGATGGCCACCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACA
CGCGCGCGCGATAGCAGTATTGTACGGGATCCTTGGGCAGAGTCCTTCTCCCCCTACAGCACGAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAA**TGTCACGACC**
CGATTGTCGTGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAG
ATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGG
GACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCGTGTGGTAAGGCTGGTCTGGGGTGGTATGGGAC
GCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAATTGCTGTTGTTGCGCGTTTATGGTGG
GGTCCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCTAGGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGACCGGGATGGC
CACCAGCAAGGACCGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGCGCGCATAGCAGTATTGTACGGGATCCTTGGGCAGAGTCCTTCTCCCCCT
ACAGCACGAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAA**TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTGGATTTTCGTC**
GTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTG
TCGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGGGACAAC**TGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAA**
CCGGTTGGCTTCCGCGATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGGCCCGTGACA

>NbrZ4 (Niben101Scf19517)

TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAATGAAAAGCGTGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGACATTAGCGATAAGGCGCT
TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGT
AGCCGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCGTGTGGTAAGGCTGGTCTGGGGT
GGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAATTGCTGTTGTTGCGCG
TTTATGGTGGGGTCCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCTAGGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGA
CCGGATGGCCACCAAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGCGCGCATAGCAGTATTGTACGGGATCCTTGGGCAGAGTCC
TTCTCCCCCTACAGCACGAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAA**TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAATGAAAGAGCGGGCCATCTG**
GATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTT
GGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGGGACAAC**TGGTCGGGGGCTAGTGCCGCTCCCTAATGAGCCCAAGG**
CAGGCGAAACCGGTTGGCTTCCGCGATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCTACGGGCGCTGTGCGCTGCGCCGGACTCTCGG
CCCGTGACA

>NbrZ5 (Niben101Scf00321)

TGTCACGACCCAATTGTCGTGACCGTTAAGATCAAAGAAAGAGCGGACCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAATGGCATTAGCAATAAGGCGCT
TCTCCCTAAGATGCTTTGGTCTTGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGTGCTTGTGCTGGTTCATGGACTTGACTATGAAGCAGACCGAAGC
AATCCTAAGGGACAACCTGGTCGGGAGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCGATGTGGTAAGGCTGGTCTCGGGG
TGGTATGGGACGCCTCGGGACGCTGCACGGGCGCTGTGTGCTGCGCCGGACTCTCGGCCCGTGACAAGTGGTATCAGAGCAGGACGTAATTGCTGTTGTTGGC
CGTTATGGTGGGATCCTCAGGGGAGGATTGTGCGGGTGCGGTTGGCTTAAGTTTAAATCCCGGACGCTGAGGGCATCGTGGCAGCTGAGCACTGCCCATCC
TGCAAGGTCAACCGGGTAGCCGGTGGATAGCTACCAGCAAGCCCGGTTGCAACAGGCGTGATGCGACTGAGCCCAAAGGGATGCGCGCGCAAGAGCAGTATTGT
ACGGGATCCTTGGGCAGAGTCCTTCTCCCCAACAGCACGAGGGCGTGCTGGATTTTGGGTGGGGGAGAA**TGTCACGACCCGATTGTCGTGACTGTTAAGATCA**
AATGAAAGAGCGGACCATCTGGATTTTCGTTGTTGGGAAATAAAGGGAACGGCATTAGCAATAAGGGCGTTCTCCCTAAGATGCTTTGGTCTTGCCGAGTTAG
GCAGGCCGACCCGGTTAAGTTTGGGGCGCTTGTGCTGGTTCATGGACTTGACTATGAAGCAGACCGAAGCAATCCTAAGGGACAAC**TGGTCGGGAGCTAGTGC**
CGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCGATGTGGTAAGGCTGGTCTCAGGTTGGTATGGGACGCCTCGGGACACCGCACGGGCG
CTGTGTGCTGCGCCGGACTCTCGGCCCGTGACA

>NbrZ6 (Niben101Scf06068)

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TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAAGGCAGGTGACCCGGTTAAGTTTGGGGTGCTTGTGCTGGTTCATGGACTTGACAACGAAGGGGACCAAAGT
AGGCCTAAGGGATAAACTGGTCGGGGGCTAGTTCCGCTCCCTGATGAGCCCAAGTCAGGGCAAAACCGGTTGGCTTCCGCGTGTGGTAAGGCTTGTCTCGAG

GTAGTGGGCGGCCTCAGGACGCCGCACAGGCGCTGTGTGCTGCGCCGACTCTTAGCCCGTGACAATTGGTATCAGAGCGGGACGTACTTGTGCTGCGCGTT
ATGGTGGGGTCCTCAAGGGAGGACTGTGCGGGTGCCTTGCCTAGCGGGGGGGGGGCTCGTGCCGACGACTGCCCCATCTGCTATGGTCTGCAGGGGAAAG
ACCGGTATGGCCACCAGCAAGGCCGCTTGACAGAGGTGAGGTGCGATTGAGCAAAAGAGACGGCGCGTTAAGCAGTATTGTGCGGGTTCTGGGTGGAGTCC
TTCTTCCCAACAGCACGAGGACGTGCTGGGTTTTGGGTGGGGAGAAATGTCACGACCCGTTTGTGCTGATCGTGTAGTCCAAAGGAAAGAGCGGGCCATCTGG
AACTTTTTCGTTGGGTACGGGGACGACATTAGCAATAAGACGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCGGGCTGACCCGTTAAGTTTAGGG
TGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGGACCGAAGTAAGCCTAAAGGATCAACTGGTCGGGGGCTAGTGCCGCTCCCTAATGAGCCCAAGGCAA
GGCGAAACCGGTTGGCTTCCGCGTATGTTAAGGCTTGTCTCGAGGTAGTGGGCTGCCTCGAGACGCTGCACGGGCGCTGTGTGCTGCGCCGAACCTCTCAGCCC
GTGACA

>NbRZ7 (Niben101Scf00379)

TGTCACGACCCGATTGTCTGTGACCGATGAGATCACATGAAAGAGCGGACCCTCTGGCAATTTGTGCTTGGGAATAAGGGAACGGCATTAGCAATAAGGACGTT
CTCCCTAAGATGCTTTGGTCTTGTGAGTCAGGCAGGCCACCCGTTAAGTTTGGGGCGCTTGTGCTTGTCTTGGAAATGACTATGAAGTTGACCGAAGCA
ATCCTAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTTGACGAGCCCAAGGCAGGGCGAAACAGTTGGCATCCGCGTACAGGATTAGGCTTGTCTCGGG
GTATGGCGGGCCTTGGGACGCCGACGGGCGCCGCACGCTGTGCGGACTCTCAGCCCCTGACAAAGTGGTATCAGAGCAGGACGTACATTTGTCTGGGTCTGCG
CGCTATGGTGGGGTCTTACAGAAAGGACTGAGCGGTCGCTTTGCCTACACACACATTCCGGATGGTGAGCGCAGCACCGTGGCAGCAGTACGACGATGCC
CTATCCTGCAAGGTCTTTCCGGACGACCGGTGGATGGCCACCAAGCCATGCCCGTTGCCATCAAGTGACTGGGCACAATCACGCGGCGCTATAGCAGCATTTG
TACGGGATCCTTGGGCAGAGTCCTTCTCCCCATCAGCACGAGGACGTGCTGCGACATGGGTGGGGGAGAAATGTCACGACCCGATTGTCTGTAACGATGAGATC
ACATGAAAGAGCAGACCATCTGGCAATTCTGCTGTTGGGAATAAGGGAACGGCATTAGCAATAAGGGCGTTCTCCCTAAGATGCTTTGGTCTTGGCGAGTCAGG
CAGGCCGACCCGTTAAGTTTGGGGCGCTTGTGCTTGTCTTGGACATGACTATGAAGTTGACCGAAGCAATCCTAAGGGACAACCTGGTCGGGGGCTAGTGCC
GCTCCCTTGACGAGCCCAAGGCAGGGCGAAACAGTTGGCATCCGCGTACACGATTAGGCTTGTCTGCTGGTATGGCGGGGCGCTCGGGACGCCGACGGGCGC
CACACGCTGCGCCGACTCTCAGCCCGTGACA

>NbRZ8 (Niben101Scf00177)

TGTCACGTCCTCAGAGAAGGGGCAAAGTAAAGCGTGCGGATTGGCATCAAACCTGCCTTGGAGAGGGGAGGCGTCTCTAGCCATTAAGGCGCTCTGCCCTAGTT
GCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAAGTTTGGGGAGCATGTGCTTGTCTTGGACATGACTATGAAGGGAGCCGAAGCATAACGAGGGG
CACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACAGTCTGCGCGCACAGGCAGGACGGGCGTGTCCGGGGCGGTATGGGA
CGCCTCGGGCGCGGAGCGCCGCGGTCCGTGTCAATTGGTATCAGAGCAAACATGCTCTTCAACTTCTGTGGCGAGGTGTCAAGCTCATGAATGCACAAAGCTA
GCGGAAGGCATAAGTGCAAAGATGGGGGCGCTGAGTTACAGAGTGGGGCATGACGGTCCTTGGGGCAAACATACTACTTCTCCGCCAAAGTAAAGCGGGCTTG
AGCAATGAAATTGTTGCGAACTCTAGATGAAACCAGAAAGTGGACGCGCCGACGAAGTGTGAAGCTCTCCATGGTTTCGTGCCTAAGTCCGAGGTAGGCAGC
ACGAGGAGGTATTGCTAGCATGATGGGTGCAATGTTCCGAGTGGAAAGACGAAAGGAGTAGCAGCGAAAGTAATGCGTCGGGTCCCGCATCAGCCAGGTGGGG
TAGGGTTGTACAGTCCTCAGAGAAGGGGCAAAGTAAAGCGTGCGGATTGGCATCAAACCTGCCTTGGAGAGGGGAGGCGTCTCTAGCCATTAAGGCGCTCTGCC
CTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAAGTTTGGGGAGCATGTGCTTGTCTTGGACATGACTATGAAGGGAGCCGAAGCATAC
GAGGGGCGACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACAGTCTGCGCGCACAGGCAGGACGGGCGTGTCCGGGGCGGT
ATGGGACGCCTCGGGCGCGGAGCGCCGCGGTCCGTGTCA

>NbRZ9 (Niben101Scf03939)

GTCCGTGACA GAGTGGTATTAGAGCAAACATGCTCTTCAACTTCTCTTGGCAGGTGTACGCTCATGAATGTAAGAGCTCGAGTGAATGCTACAAGTGCAAAGA
TGGGGGCGCTGAGTGACAGAGTGGAGCATGACGGTCCTTGGGCAAACATACTACTTCTCTGCCAAAGTAAAGCGGGCTTGAAGCAATGAAATTGTTGCGAACTC
TAGATGAAACCACGAAGTGGACGCACCGACGAAGTGTGATGCCGTCTCCATGATTACGTGCCTGAGTCCCAAAGTTGGCAGCACGAGGAGGTGTGGTGCAAGC
ATGAATGAGGGTGCAAGTTCCGTGTGGAAGACGAAAGGAGTTGACGCGAAAGTAATGCGTCGGGTCCCGCATCATCGGGTGGGGGAGAGTTGTACACGGCCTC
AGAGTAGGGGACAAAGAAAAGCGTGCGGATTGGCATCAAACCTGCCTTGGGGAGGGGAGGTGCCTCTAGCCATAAAGGCGCTCTGCCCTAGTTGCGTATTGGCTT
GGCCGAGTTAGGCATGCCGACCCGATTAAAGTTTGGGGAGCATGTGCTTGTCTTGGACATGACTATGAAGGGAGCCGAAGCATAACGGGGGCGACAGCTGGTCG
GGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACAGTCTGCGCGCTAGGTGCGACGGGCGTGTCCGGGGCGGTATGGGACGCCCTCGGGCGC
GAAGCGCCGCGGTCCGTGACA TTTGGTATCAGAGCAAACATGCTCTTCAACTTCTCTTGAAGGTGTACGCTCATGAATGCACAAGCTCGGGTGAATGCTACA
AGTGCAAAGATGGGGGCGCTGAGTGACAGAGTGGAGCATGACGGTCCTTGGGCAAACATACTACTTCTCCGCCAAAGTAAAGCGGGCTTGAAGCAATGAAATTG
TTGCGAACTCTAGATGAAACCACGAAGTGGACGCACCGACGAAGTGTGATGCCGTCTCCATGATTACGTGCCTGAGTCCCAAAGTTGGCAGCACGAGGAGGTG
TGGTGCAAGCATGAATGAGGGTGCAAGTTCCGTGTGGAAGACGAAAGGAGTTGCAGCAAAATTAATGCGTCGGGTCCCGCATCATCGGGTGGGGGAGAGTTG
TCAAGGCCTCAGAGCAGGGCAAAGTAAAGCGTGCGGATTGGCATCAAACCTGCTTGGGAAGGAGAGGTGCCTCTAGCCATAAAGGCGCTCTGCCCTAGTTGC
GTATTGGCTTGGCCGAATTAGGCATGCCGACCCGATTAGTTTGGGGAGCATATGCTTGTGACTTGGACATGACTATGAAGGGAGCCGAAGCATAACGGGGGCA
GAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGGCGAAACAGTCTGCGCGCTAGGTGCGACGAGCGTGTCCGCGCGGTTATGAGAC
GCCTCGGGCGCGAAGCGCCGCGGTCCGTGACA

Figure S2. Sequences of full-length *N. benthamiana* retrozymes. Scaffolds containing the retrozymes are indicated in parentheses (<https://solgenomics.net>). LTR regions are marked with yellow color.

NbRZ1 **TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAAATGAAAGAGCGGGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATT**
NbRZ2 TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAAATGAAAGAGCGGGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATT
NbRZ3 TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAAATGAAAGAGCGGGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATT
NbRZ4 TGTCACGACCCGATTGTCGTGACCGTAAAGACCAAAATGAAAGAGCGTGCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATT
NbRZ6 TGTCACGACCCGTTTGTGTCGTGACCGTGTAGTCCAAAGGAAAGAGCGGGCCATCTGGAACTTCGCCATTGGG---CTACGGGGACGACATT
NbRZ5 TGTCACGACCCAAATTGTCGTGACCGTTAAGATCAA-AGAAAGAGCGGACCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAATGGCATT
NbRZ7 TGTCACGACCCGATTGTCGTGACCGATGAGATCACATGAAAGAGCGACCATCTGGCAATTGTCGTTGGG-AATAA-GGGAACGGCATT

NbRZ1 **AGCGAT-AAGGCGT---TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCGCTGGT**
NbRZ2 AGCGAT-AAGGCGT---TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCGCTGGT
NbRZ3 AGCGAT-AAGGCGT---TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCGCTGGT
NbRZ4 AGCGAT-AAGGCGT---TCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTGCGCTGGT
NbRZ6 AGCAATAA-GGCGTTGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGTCGACCCGGTTAAGCTTGGGGTGTCTGTCGCTGGT
NbRZ5 AGCAATAAGGCGT---TCTCCCTAAGATGCTTTGGTCTTGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGTGTCTGTCGCTGGT
NbRZ7 AGCAATAAGGACGT---TCTCCCTAAGATGCTTTGGTCTTGCTGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGGCGCTTGTGCTGCTTGT

NbRZ1 **CATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAG-GGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGG**
NbRZ2 CATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAG-GGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGG
NbRZ3 CATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAG-GGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGG
NbRZ4 CATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAG-GGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGG
NbRZ6 CATGGACTTGACAACGAAGGGGACCAAGTAGGCTTAAGGATAAACTGGTCGGGGGCTAGTCCGCTCCCTGATGAGCCCAAGGCAGG
NbRZ5 CATGGACTTGACTATGAGACGACCGAAGCAATCCTAAG-GGACAACCTGGTCGGGGGCTAGTGCAGCCGCTCCCTGATGAGCCCAAGGCAGG
NbRZ7 CTTGGAATGACTATGAAGTTGACCGAAGCAATCCTAAG-GGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGG
* ****

NbRZ1 **GCGAAACCGGTGGCTTCCGCGATGT--GGTAAGGCTGGTCT-GGGGTGGTATGGGACGCCTCA-GACGCCGCACGGGCGCTGTGCGCTGC**
NbRZ2 GCGAAACCGGTGGCTTCCGCGTGT--GGTAAGGCTGGTCT-GGGGTGGTATGGGACGCCTCA-GACGCCGCACGGGCGCTGTGCGCTGC
NbRZ3 GCGAAACCGGTGGCTTCCGCGTGT--GGTAAGGCTGGTCT-GGGGTGGTATGGGACGCCTCA-GACGCCGCACGGGCGCTGTGCGCTGC
NbRZ4 GCGAAACCGGTGGCTTCCGCGTGT--GGTAAGGCTGGTCT-GGGGTGGTATGGGACGCCTCA-GACGCCGCACGGGCGCTGTGCGCTGC
NbRZ6 GCGAAACCGGTGGCTTCCGCGTGT--GGTAAGGCTGGTCT-GGGGTGGTATGGGACGCCTCA-GACGCCGCACGGGCGCTGTGCGCTGC
NbRZ5 GCGAAACCGGTGGCTTCCGCGTGT--GGTAAGGCTGGTCT-GGGGTGGTATGGGACGCCTCA-GACGCCGCACGGGCGCTGTGCGCTGC
NbRZ7 GCGAAACCGGTGGCTTCCGCGTGT--GGTAAGGCTGGTCT-GGGGTGGTATGGGACGCCTCA-GACGCCGCACGGGCGCTGTGCGCTGC
** *****

NbRZ1 **GCCGGACTCTCGTCCCGTGACA**AGTGGTATCAGAGCCGGACGTAC--TTGCTGTTGTTGCGCGTTTATGGTGGGG-TCCTCGGGGG-AGG
NbRZ2 GCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAC--TTGCTGTTGTTGCGCGTTTATGGTGGGG-TCCTCGGGGG-AGG
NbRZ3 GCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAC--TTGCTGTTGTTGCGCGTTTATGGTGGGG-TCCTCGGGGG-AGG
NbRZ4 GCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAC--TTGCTGTTGTTGCGCGTTTATGGTGGGG-TCCTCGGGGG-AGG
NbRZ6 GCCGGACTCTTAGCCCGTGACAATTGGTATCAGAGCCGGACGTAC--TTGCTG--CTGCGCGT-TATGGTGGGG-TCCTCAAGGG-AGG
NbRZ5 GCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTAC--TTGCTGTTGTTGCGCGT-TATGGTGGGA-TCCTCAGGGG-AGG
NbRZ7 GCCGGACTCTCAGCCCGTGACAAGTGGTATCAGAGCCGGACGTACATTGCTGGGTCTGCGCGC-TATGGTGGGGTCTCTACAGAAAGG

NbRZ1 ACTGTGCG**GGTGCGCGT**-----**TGCCTAGGGG**-----**GTTGGCTCGCACT**GAAGACGGCCCCATCTGCAATGGT
NbRZ2 ACTGTGCGGGTGCGCGT-----TGCTAGGGG-----GTGGCTCGCACTGAAGACGGCCCCATCTGCAATGGT
NbRZ3 ACTGTGCGGGTGCGCGT-----TGCTAGGGG-----GTGGCTCGCACTGAAGACGGCCCCATCTGCAATGGT
NbRZ4 ACTGTGCGGGTGCGCGT-----TGCTAGGGG-----GTGGCTCGCACTGAAGACGGCCCCATCTGCAATGGT
NbRZ6 ACTGTGCGGGTGCGTTG-CCTA-----GGCGGGGGG-----GGGCTCGTGCCGACGACTGCCCATCTGCTATGGT
NbRZ5 ATTGTGCGGGTGCGTTGGCCCTAAGTTTA-ATCCCGGACGGTGAGGGC---ATCGTGGCAGCACTGAAGACTGCCCATCTGCAA-GGT
NbRZ7 ACTGAGCGGGTGCGTTTGCCTACACACACTTCCGGATGGTGAGCGACGACCGTGGCAGCACTGACGACTGCCCTTCCCTGCAA-GGT
* ** *****

NbRZ1 CTGCAGGGGCAAGACCGG--GATGGCCA-CCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGG-CCAAAACACGCGGCGCGCATAG
NbRZ2 CTGCAGGGGCAAGACCGG--GATGGCCA-CCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGG-CCAAAACACGCGGCGCGCATAG
NbRZ3 CTGCAGGGGCAAGACCGG--GATGGCCA-CCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGG-CCAAAACACGCGGCGCGCATAG
NbRZ4 CTGCAGGGGCAAGACCGG--GATGGCCA-CCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGG-CCAAAACACGCGGCGCGCATAG
NbRZ6 CTGCAGGGGAAAGACCGG--TATGGCCA-CCAGCAAGGCGGGTTGCACGAGGTGAGGTGCGATTGAG-CAAAGAGACGCGGCGCGTTAAG
NbRZ5 CAACCGGT---GACCGGTGGATAGCTA-CCAGCAAGGCGGGTTGCACAAGGCGTATGCGACTGAGCCAAAGGATCGCGGCGCAAG
NbRZ7 CTTTCCCGAC--GACCGGTGGATGGCCACCAAGCCTGCCCCTTGC-----CATCAAGTGACTGGG-CACAATCAGCGGCGCGTATAG
* ** *****

NbRZ1 CAGTATTGTACGGGATCCTTGGGCAGAGTCCTTCTCCCCCTACAGCAGAGGGCGTGTGCGTTTTTCGGTGGGGGAGAA**TGTCACGACCC**
NbRZ2 CAGTATTGTACGGGATCCTTGGGCAGAGTCCTTCTCCCCCTACAGCAGAGGGCGTGTGCGTTTTTCGGTGGGGGAGAAATGTCACGACCC
NbRZ3 CAGTATTGTACGGGATCCTTGGGCAGAGTCCTTCTCCCCCTACAGCAGAGGGCGTGTGCGTTTTTCGGTGGGGGAGAAATGTCACGACCC
NbRZ4 CAGTATTGTACGGGATCCTTGGGCAGAGTCCTTCTCCCCCTACAGCAGAGGGCGTGTGCGTTTTTCGGTGGGGGAGAAATGTCACGACCC
NbRZ6 CAGTATTGTGCGGGTCTCT-GGGTGAGTCTTCTT-CCCAACAGCAGGAGGACGTGCTGGTTTTGGTGGGGGAGAAATGTCACGACCC
NbRZ5 CAGTATTGTACGGGATCCTTGGGCAGAGTCCTTCTC-CCCAACAGCAGAGGGCGTGTGGAATTTGGTGGGGGAGAAATGTCACGACCC
NbRZ7 CAGCATTGTACGGGATCCTTGGGCAGAGTCCTTCTC-CCCATCAGCAGGAGGACGTGCTGCGACATGGGTGGGGGAGAAATGTCACGACCC
*** *****

NbRZ8 **TGTCACGTCCTCAGAGAAGGGGCAAAGTAAAGCGTGCGGATTGGCATCAAAC**TGCCTTGGAGAGGGGAGGCGTCTCTAGCCATTAAGGCG
NbRZ9 TGTCACGGCCTCAGAGTAGGGACAAAGAAAAGCGTGCGGATTGGCATCAAACTGCCTTGGGAGGGGAGGTGCCTCTAGCCATAAAGGCG

NbRZ8 **CTCTGCGCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGAGCATGTCGCTTGTCTTGGACATGACTA**
NbRZ9 CTCTGCGCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGAGCATGTCGCTTGTCTTGGACATGACTA

NbRZ8 **TGAAGGGAGCCGAAGCATACGAGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACCACTGTC**
NbRZ9 TGAAGGGAGCCGAAGCATACGAGGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACCACTGTC

NbRZ8 **GCGCACAGGCAGGACGGGCGTGTCCGGGGCGG-TATGGGACGCCTCGGGCGCGGAGCGCCGCGGTCCGTGTCA**TTTGGTATCAGAGCAA
NbRZ9 GCGCT-AGGTTCGACGGGCGTGTCCGGGGCGGTATGGGACGCCTCGGGCGCGAAGCGCCGCGGTCCGTACATTTGGTATCAGAGCAA

NbRZ8 CATGCTCTTCAACTTCTGTGGCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCG-GAAGGC-ATAAGTGCAAAGATGGGGGCGCTGAG
NbRZ9 CATGCTCTTCAACTTCTGTGCAAGGTGTCA-GCTCATGAATGCACAA-GCTCGGGTGAATGCTACAGTGCAAAGATGGGGGCGCTGAG

NbRZ8 TTACAGAGTGGGGCATGACGGTCCTTGGGGCAAACATACTACTTCTCCGCCAAAGTAAAGCGGGCTTGAGCAAATGAAATTGTTGCGAAC
NbRZ9 TGACAGAGTGGAGCATGACGGTCCTTGG-GCAAACATACTACTTCTCCGCCAAAGTAAAGCGGGCTTGAGC-AATGAAATTGTTGCGAAC
* *****

NbRZ8 TCTAGATGAAACCACGAAGTGGACGCGCCGACGAAGTGTGAAGC--TCTCCATGGTTTCGTGCCTAAGTCCGAG-GTAGGCAGCACGAGG
NbRZ9 TCTAGATGAAACCACGAAGTGGACGCGCCGACGAAGTGTGATGCGCTTCCATGATTACGTGCCTGAGTCCCAAAGTTGGCAGCACGAGG

NbRZ8 AGGTA---GCTAGCATGA---TGGGTGCAATGTTCCGAGTGAAGACGAAAGGAGTAGCAGCGAAAGTAATGCGTCGGGTCGCCGCATC
NbRZ9 AGGTGTGGTGCAAGCATGAATGAGGGTGCAA-GTTCGTGTGGAAGACGAAAGGAGTTGCAGCAAAATTAATGCGTCGGGTCGCCGCATC

NbRZ8 AGCCAGGTGGGGTAGGGT**TGTCACGTCCTCAGAGAAGGGGCAAAGTAAAGCGTGCGGATTGGCATCAAAC**TGCCTTGGAGAGGGGAGGCG
NbRZ9 ATCG-GGTGGGGGAGAGTTGTCAAGGCCTCAGAGCAGGGACAAAGTAAAGCGTGCGGATTGGCATCAAACTGCTTGGGAAGGAGAGGTG
* *****

NbRZ8 **TCTCTAGCCATTAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGAGCATGTCGC**
NbRZ9 CCTCTAGCCATAAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAATTAGGCATGCCGACCCGATTTAGTTTGGGAGCATATCGC

NbRZ8 **TTGTCTTGGACATGACTATGAAGGGAGCCGAAGCATACGAGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGC**
NbRZ9 TTGACTTGGACATGACTATGAAGGGAGCCGAAGCATACGAGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGC

NbRZ8 **A-GGGCGAAACCACTGTCGCGCACAGGCAGGACGGGCGTGTCCGGGGCGG-TATGGGACGCCTCGGGCGCGGAGCGCCGCGGTCCGTGTCA**
NbRZ9 AGGGGCGAAACCACTGTCGCGCT-AGGTTCGACGAGCGTGTCCGCGCGGTATGAGACGCCTCGGGCGCGAAGCGCCGCGGTCCGTGACA
* *****

Figure S4. Sequence alignment of *N. benthamiana* Group 2 retrozymes. In the NbRZ8 sequence, LTR regions are marked with yellow color and ribozyme sequences are shown in bold. Asterisks indicate invariant residues.

```

NbRZ1  CGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
NbRZ2  CGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
NbRZ3  CGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
NbRZ4  CGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
NbRZ5  TGGTCTTGGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGTGCCTTGTCGCTGGTCATGGACTTGACTATGAAGCAGACCGAAGCAAT
NbRZ6  CGATCTGGCCGAGTCAGGCAGGTCGACCCGGTTAAGCTTGGGGTGCCTTGTCGCTGGTCATGGACTTGACAACGAAGGGGACCAAAGTAGG
NbRZ7  TGGTCTTGCTGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGCGCTTGTCGCTTGCTTTGGAAATGACTATGAAGTTGACCGAAGCAAT
NbRZ8  TGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGAGCATGTCGCTTGCTTTGGACATGACTATGAAGGGAGCCGAAGCATA
NbRZ9  TGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGAGCATGTCGCTTGCTTTGGACATGACTATGAAGGGAGCCGAAGCATA
      *   *  **  *****  *  *****  *****  *****  **  *****  **  *****  *****  *  **  *

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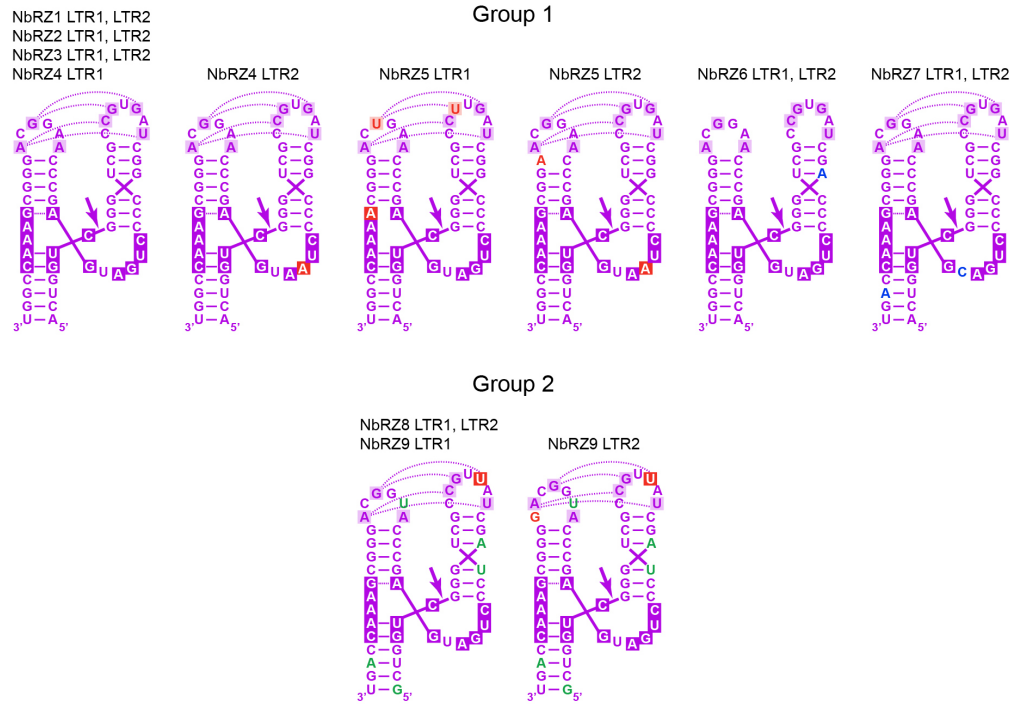
```

NbRZ1  CGAAAG-GGACAACTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCC
NbRZ2  CGAAAG-GGACAACTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCC
NbRZ3  CGAAAG-GGACAACTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCC
NbRZ4  CGAAAG-GGACAACTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCC
NbRZ5  CCTAAG-GGACAACTGGTCGGGAGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCC
NbRZ6  CCTAAGGGATAACTGGTCGGGGGCTAGTTCCGCTCCCCTGATGAGCCCAAGTCAGGGCAAACCGGTTGGCTTCC
NbRZ7  CCTAAG-GGACAACTGGTCGGGGGCTAGTGCCGCTCCCCTGACGAGCCCAAGGCAGGGCGAAACCGGTTGGCATCC
NbRZ8  CGAGGG-GCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACCGTCTGCGCGC
NbRZ9  CGGGGG-GCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACCGTCTGCGCGC
      *       *  *   *  *****  *****  *  *****  *****  *  *****  *****  **  **  *

```

Figure S5. Conserved region in the LTRs of Group 1 and Group 2 retrozymes. Sequence alignment of region conserved in LTRs of Group 1 and Group 2 retrozymes is presented. Ribozyme sequences are shown in bold. Asterisks indicate invariant residues.

A



B

Group	Retrozyme	Mismatches between two LTRs
Group 1	NbRZ1	1
	NbRZ2	0
	NbRZ3	2
	NbRZ4	7
	NbRZ5	9
	NbRZ6	32
	NbRZ7	11
Group 2	NbRZ8	0
	NbRZ9	15

Figure S6. Analysis of potential ribozyme structures in *N. benthamiana* retrozymes. **(A)** Predicted structure of ribozymes in two LTR regions of NbRZ1-NbRZ9. For Group 1 retrozymes, substitutions potentially affecting the ribozyme structure/function are shown in red color, those having no effect - in blue color. In NbRZ4 and NbRZ5, the ribozyme sequences did not match in two LTRs, with mutations being located at essential residues, and NbRZ5 ribozyme contained as many as five substitutions in two LTRs. Therefore, potential transcripts of NbRZ4 and NbRZ5 might be incapable of self-cleavage at both LTRs. For Group 2 retrozymes, substitutions affecting non-essential residues and preserving base pairing of the retrozyme fold are shown in green, a substitution of residue involved in non-canonical interactions of two retrozyme loops is shown in red. **(B)** Numbers of mismatches between two LTRs of *N. benthamiana* retrozymes.

```

GTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGTACGCGGGGGGGGCTAGTGCCGCTCCCCTGATGAGCCCA
AGGCAGGGCGAAACCGGTTGGCTTCCGCATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGC
TGTGCGCTGCGCCGACTCTCGTCCCGTGACACCATGGTGAGTAAAGGAGAAGAAGCTTTTCACTGGAGTTGTCCCAATTCTTG
TTAAATTAGATGGTGATGTTAATGGGCACAAATTTTCTGTCACTGGAGAGGGTGAAGGTGATGCTACATACGGAAAGCTTACC
CTTAAATTTATTTGCACTACTGGAAAACTACCTGTTCCCTTGGCCAACACTTGTCACTACTTTCTCTTATGGTGTTCAATGCTT
TTCCCGTTATCCGGATCATATGAAACGGCATGACTTTTTCAAGAGTGCCATGCCCCGAAGGTATGTACAGGAACGCACTATAT
CTTTCAAAGATGACGGGAACTACAAGACACGTGCTGAAGTCAAGTTTGAAGGTGATACCCCTTGTTAATCGTATCGAGTTAAAA
GGTATTGATTTTAAAGAAGATGGAAACATTCTCGGACACAACTGGAGTACAACCTATAA

```

Figure S7. 5'-RACE analysis of LTR-GFP transcription product. Sequence of 5'-RACE product obtained on RNA from *N. benthamiana* leaves infiltrated with agrobacteria carrying the LTR-GFP construct. Gray color indicates a sequence derived from 5'-RACE adaptor and amplification primers, yellow color - the LTR sequence, green color - the GFP sequence. *NcoI* site used for cloning is shown in bold.

NbRZ1	GACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTACTTGCTGTTG
NbRZ2	GACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTACTTGCTGTTG
NbRZ3	GACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTACTTGCTGTTG
NbRZ4	GACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTACTTGCTGTTG
1x1-423	GACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTACTTGCTGTTG
2RC-425	GACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTACTTGCTGTTG
4RC-425	GACGCCGCACGGGCGCTGTGCGCTGCGCCGGACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGGACGTACTTGCTGTTG
1x2-423	GACGCCGCACGGGCGCTGTGCTCTGCGCCGGACTCTCGTCCCGTGACAAGTAGTATCAGAGCCGGACGTACTTGCTGTTG
1x3RC-423	GACGCCGCACGGGCGCTGTGCTCTGCGCCGGACTCTCGTCCCGTGACAAGTAGTATCAGAGCCGGACGTACTTGCTGTTG
1x4RC-423	GACGCCGCACGGGCGCTGTGCTCTGCGCCGGACTCTCGTCCCGTGACAAGTAGTATCAGAGCCGGACGTACTTGCTGTTG
5-425	GACGCCGCACGGGCGCTGTGCTCTGCGCCGGACTCTCGTCCCGTGACAAGTAGTATCAGAGCCGGACGTACTTGCTGTTG
1RC-425	GACGCCGCACGGGCGCTGTGCTCTGCGCCGGACTCTCGTCCCGTGACAAGTAGTATCAGAGCCGGACGTACTTGCTGTTG

NbRZ1	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
NbRZ2	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
NbRZ3	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
NbRZ4	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGTGCGCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
1x1-423	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
2RC-425	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
4RC-425	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
1x2-423	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
1x3RC-423	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
1x4RC-423	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
5-425	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC
1RC-425	TTGCGCGTTTATGGTGGGGTCCTCGGGGAGGACTGTGCGGGT--GCGTTGCCTAGGGGGTGGCTCGCACTGAAGACGGC

NbRZ1	CCCATCCTGCAATGGTCTGCAGGGGCAAG
NbRZ2	CCCATCCTGCAATGGTCTGCAGGGGCAAG
NbRZ3	CCCATCCTGCAATGGTCTGCAGGGGCAAG
NbRZ4	CCCATCCTGCAATGGTCTGCAGGGGCAAG
1x1-423	CCCATCCTGCAATGGTCTGCAGGGGCAAG
2RC-425	CCCATCCTGCAATGGTCTGCAGGGGCAAG
4RC-425	CCCATCCTGCAATGGTCTGCAGGGGCAAG
1x2-423	CCCATCCTGCAATGGTCTGCAGGGGCAAG
1x3RC-423	CCCATCCTGCAATGGTCTGCAGGGGCAAG
1x4RC-423	CCCATCCTGCAATGGTCTGCAGGGGCAAG
5-425	CCCATCCTGCAATGGTCTGCAGGGGCAAG
1RC-425	CCCATCCTGCAATGGTCTGCAGGGGCAAG

Figure S8. Sequence analysis of Group 1 retrozyme (-) strand-specific amplification product obtained with divergent primers. Sequences of eight independent clones were aligned with the corresponding region of NbRZ1-NbRZ4. Mismatches are shown by gray shading.

A

NbRZ1-Tag
1RC_426
2RC_426
1RC_430
3RC_430

```

GATTACAAGGATGACGATGACAAGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGACCG
GATTACAAGGATGACGATGACAAGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGACCG
GATTACAAGGATGACGATGACAAGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGACCG
GATTACAAGGATGACGATGACAAGGGGTGGCTCGCACTGAAGACGGCCCCATCCTGCAATGGTCTGCAGGGGCAAGACCG
*****

```

NbRZ1-Tag
1RC_426
2RC_426
1RC_430
3RC_430

```

GGATGGCCACCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGGCGCGCATAGCAGTATTGTAC
GGATGGCCACCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGGCGCGCATAGCAGTATTGTAC
GGATGGCCACCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGGCGCGCATAGCAGTATTGTAC
GGATGGCCACCAGCAAGGACGGTTGCACGAGGTGAGGTGCGACTGGGCCAAAACACGCGGCGCGCATAGCAGTATTGTAC
*****

```

NbRZ1-Tag
1RC_426
2RC_426
1RC_430
3RC_430

```

GGGATCCTTGGGCA
GGGATCCTTGGGCA
GGGATCCTTGGGCA
GGGATCCTTGGGCA
GGGATCCTTGGGCA
*****

```

B

NbRZ1-Tag
2RC_438
3RC_438
4RC_438

```

GAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAATGTACGACCCGATTGTCTGTGACCGTAAAGACCAATGAAAGAGCGGGC
GAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAATGTACGACCCGATTGTCTGTGACCGTAAAGACCAATGAAAGAGCGGGC
GAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAATGTACGACCCGATTGTCTGTGACCGTAAAGACCAATGAAAGAGCGGGC
GAGGGCGTGCTGCGTTTTTCGGTGGGGGAGAATGTACGACCCGATTGTCTGTGACCGTAAAGACCAATGAAAGAGCGGGC
*****

```

NbRZ1-Tag
2RC_438
3RC_438
4RC_438

```

CATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCC
CATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCC
CATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCC
CATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCC
*****

```

NbRZ1-Tag
2RC_438
3RC_438
4RC_438

```

GAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCTGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
GAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCTGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
GAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCTGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
GAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGAGCTTGTCTGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGC
*****

```

NbRZ1-Tag
2RC_438
3RC_438
4RC_438

```

CGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCATG
CGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCATG
CGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCATG
CGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCCTGATGAGCCCAAGGCAGGGCGAAACCGGTTGGCTTCCGCATG
*****

```

NbRZ1-Tag
2RC_438
3RC_438
4RC_438

```

TGTTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCGGACTCTCGTCCCCT
TGTTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCGGACTCTCGTCCCCT
TGTTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCGGACTCTCGTCCCCT
TGTTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGCACGGGCGCTGTGCGCTGCGCGGACTCTCGTCCCCT
*****

```

NbRZ1-Tag
2RC_438
3RC_438
4RC_438

```

GACAAGTGGTATCAGAGCCGGACGTAAGTGTGTTGTCGCGTTTATGGTGGGGTCTCGGGGAGGACTGTGCGGGTG
GACAAGTGGTATCAGAGCCGGACGTAAGTGTGTTGTCGCGTTTATGGTGGGGTCTCGGGGAGGACTGTGCGGGTG
GACAAGTGGTATCAGAGCCGGACGTAAGTGTGTTGTCGCGTTTATGGTGGGGTCTCGGGGAGGACTGTGCGGGTG
GACAAGTGGTATCAGAGCCGGACGTAAGTGTGTTGTCGCGTTTATGGTGGGGTCTCGGGGAGGACTGTGCGGGTG
*****

```

NbRZ1-Tag
2RC_438
3RC_438
4RC_438

```

CGCGTTGCCTAGGGATTACAAGGATGACGATGACAAGGGGTGGCT
CGCGTTGCCTAGGGATTACAAGGATGACGATGACAAGGGGTGGCT
CGCGTTGCCTAGGGATTACAAGGATGACGATGACAAGGGGTGGCT
CGCGTTGCCTAGGGATTACAAGGATGACGATGACAAGGGGTGGCT
*****

```

Figure S9. Sequence analysis of NbRZ1-Tag amplification products obtained for upper leaves of plants agroinfiltrated for expression of NbRZ1-Tag. **(A)** Clones of the (-) strand-specific PCR product obtained with primers specific for the NbRZ1-Tag CR (Figure 4B). **(B)** Clones of the (+) strand-specific PCR product obtained with divergent primers, one of which was complementary to the tag sequence (Figure 4E). Mismatches to the NbRZ1-Tag sequence are shown by gray shading.

Table S1. Retrozyme-containing *N. benthamiana* genomic scaffolds. Genomic scaffolds that contain sequences exhibiting significant (e-value < 1e-10) similarity to the LTR of *N. benthamiana* retrozyme found in the scaffold Niben101Scf01887.

BLASTN 2.6.0+			
Database: Niben.genome.v1.0.1.scaffolds.nrcontigs.fasta			
56,094 sequences; 2,969,810,994 total letters			
Sequences producing significant alignments	Coverage (%)	Score (Bits)	E Value
Niben101Scf01887	cov=13.0	689	0.0
Niben101Scf04922	cov=14.0	684	0.0
Niben101Scf00825	cov=13.9	684	0.0
Niben101Scf01870	cov=12.7	678	0.0
Niben101Scf19517	cov=14.4	673	0.0
Niben101Scf09914	cov=12.0	553	3e-155
Niben101Scf00321	cov=13.5	531	1e-148
Niben101Scf08455	cov=13.9	507	2e-141
Niben101Scf05269	cov=13.7	505	8e-141
Niben101Scf01476	cov=13.6	505	8e-141
Niben101Scf00305	cov=13.1	503	3e-140
Niben101Scf01313	cov=13.2	494	2e-137
Niben101Scf04505	cov=14.1	490	2e-136
Niben101Scf22660	cov=13.9	484	1e-134
Niben101Scf04528	cov=13.6	484	1e-134
Niben101Scf00961	cov=14.5	479	5e-133
Niben101Scf17535	cov=6.6	473	2e-131
Niben101Scf20037	cov=13.6	457	2e-126
Niben101Scf02207	cov=14.9	457	2e-126
Niben101Scf01485	cov=12.9	451	1e-124
Niben101Scf16010	cov=13.5	446	5e-123
Niben101Scf06068	cov=13.6	438	8e-121
Niben101Scf03766	cov=14.1	438	8e-121
Niben101Scf29314	cov=5.7	435	1e-119
Niben101Scf12469	cov=13.9	433	4e-119
Niben101Scf00530	cov=14.5	433	4e-119
Niben101Scf11350	cov=17.5	429	5e-118
Niben101Scf08394	cov=14.1	429	5e-118
Niben101Scf07841	cov=14.1	425	7e-117
Niben101Scf00110	cov=13.2	418	1e-114
Niben101Scf00751	cov=13.9	416	4e-114
Niben101Ctg13204	cov=15.0	412	5e-113
Niben101Scf18195	cov=15.8	412	5e-113
Niben101Scf08936	cov=13.4	412	5e-113
Niben101Scf12763	cov=12.0	409	7e-112
Niben101Scf00409	cov=12.8	409	7e-112
Niben101Scf02601	cov=13.2	405	9e-111
Niben101Scf31750	cov=13.2	403	3e-110
Niben101Scf21557	cov=13.1	403	3e-110
Niben101Scf11260	cov=12.5	401	1e-109
Niben101Scf00177	cov=13.9	401	1e-109
Niben101Scf06096	cov=13.5	399	4e-109
Niben101Scf05191	cov=13.4	394	2e-107
Niben101Scf13530	cov=14.0	392	7e-107
Niben101Scf03092	cov=13.2	388	9e-106
Niben101Ctg05563	cov=4.0	385	1e-104
Niben101Scf08627	cov=13.8	385	1e-104
Niben101Scf03457	cov=14.1	385	1e-104
Niben101Scf00291	cov=12.0	385	1e-104
Niben101Scf00542	cov=13.8	383	4e-104
Niben101Scf07034	cov=13.4	379	5e-103
Niben101Scf00379	cov=13.6	379	5e-103
Niben101Scf07364	cov=13.2	377	2e-102
Niben101Scf38783	cov=3.4	370	3e-100
Niben101Scf00420	cov=14.0	370	3e-100
Niben101Scf09236	cov=13.1	368	1e-99
Niben101Scf02182	cov=13.8	359	7e-97
Niben101Scf00690	cov=13.4	350	4e-94

Niben101Scf15824	cov=14.8	346	5e-93
Niben101Scf03128	cov=13.2	346	5e-93
Niben101Scf03432	cov=14.6	331	1e-88
Niben101Scf13344	cov=14.1	329	5e-88
Niben101Scf09015	cov=12.8	327	2e-87
Niben101Scf10940	cov=14.3	316	4e-84
Niben101Scf11496	cov=13.5	311	2e-82
Niben101Scf07849	cov=14.7	303	3e-80
Niben101Scf39306	cov=3.0	302	1e-79
Niben101Scf06158	cov=13.6	296	5e-78
Niben101Scf07320	cov=15.5	294	2e-77
Niben101Scf03243	cov=14.7	289	9e-76
Niben101Scf01596	cov=13.7	289	9e-76
Niben101Scf03253	cov=14.5	281	1e-73
Niben101Scf00381	cov=13.6	270	3e-70
Niben101Scf09960	cov=15.0	267	4e-69
Niben101Scf02136	cov=14.0	261	2e-67
Niben101Scf17891	cov=12.9	257	3e-66
Niben101Scf04976	cov=15.3	257	3e-66
Niben101Scf01599	cov=13.6	257	3e-66
Niben101Scf01538	cov=13.7	252	1e-64
Niben101Scf08374	cov=13.8	213	6e-53
Niben101Scf01506	cov=14.8	207	3e-51
Niben101Ctg08192	cov=10.0	204	3e-50
Niben101Scf39521	cov=17.8	204	3e-50
Niben101Scf13540	cov=13.8	204	3e-50
Niben101Scf34433	cov=5.6	189	9e-46
Niben101Scf07466	cov=13.8	187	3e-45
Niben101Scf07288	cov=13.8	182	2e-43
Niben101Scf02606	cov=14.9	180	6e-43
Niben101Scf09087	cov=14.7	176	7e-42
Niben101Scf25048	cov=8.9	174	3e-41
Niben101Ctg01052	cov=5.0	172	9e-41
Niben101Scf11453	cov=13.3	172	9e-41
Niben101Scf01388	cov=14.3	172	9e-41
Niben101Scf12045	cov=13.4	167	4e-39
Niben101Scf07207	cov=13.1	167	4e-39
Niben101Scf05435	cov=13.1	167	4e-39
Niben101Ctg09397	cov=9.0	165	2e-38
Niben101Scf00090	cov=13.3	165	2e-38
Niben101Scf05417	cov=13.4	163	6e-38
Niben101Scf11399	cov=14.5	161	2e-37
Niben101Scf07896	cov=13.5	161	2e-37
Niben101Scf05621	cov=13.7	161	2e-37
Niben101Scf15391	cov=13.9	159	7e-37
Niben101Scf06611	cov=12.4	159	7e-37
Niben101Scf05997	cov=15.7	159	7e-37
Niben101Scf01502	cov=14.7	159	7e-37
Niben101Scf01063	cov=15.0	159	7e-37
Niben101Scf21165	cov=13.9	158	3e-36
Niben101Scf02461	cov=13.1	158	3e-36
Niben101Scf01319	cov=14.7	158	3e-36
Niben101Scf12790	cov=14.9	156	9e-36
Niben101Scf11106	cov=14.4	156	9e-36
Niben101Scf03939	cov=14.3	156	9e-36
Niben101Scf00246	cov=13.4	156	9e-36
Niben101Scf24096	cov=13.1	154	3e-35
Niben101Scf05884	cov=15.0	154	3e-35
Niben101Scf05809	cov=13.7	154	3e-35
Niben101Scf05348	cov=13.4	154	3e-35
Niben101Scf02852	cov=13.7	154	3e-35
Niben101Scf00998	cov=13.8	154	3e-35
Niben101Scf00460	cov=13.6	154	3e-35
Niben101Scf33522	cov=13.7	152	1e-34
Niben101Scf07035	cov=13.3	152	1e-34
Niben101Scf02844	cov=13.3	152	1e-34
Niben101Scf00823	cov=13.6	150	4e-34

Niben101Scf19986	cov=9.6	148	2e-33
Niben101Scf10322	cov=14.3	148	2e-33
Niben101Scf09648	cov=12.3	148	2e-33
Niben101Scf06465	cov=14.1	148	2e-33
Niben101Scf05549	cov=13.2	148	2e-33
Niben101Scf04286	cov=14.0	148	2e-33
Niben101Scf02870	cov=12.3	148	2e-33
Niben101Scf01241	cov=13.7	148	2e-33
Niben101Scf01994	cov=13.7	145	2e-32
Niben101Scf01154	cov=13.1	145	2e-32
Niben101Scf07712	cov=13.1	143	7e-32
Niben101Scf03326	cov=14.0	143	7e-32
Niben101Scf00797	cov=13.4	143	7e-32
Niben101Scf00492	cov=14.2	143	7e-32
Niben101Scf04451	cov=11.7	141	3e-31
Niben101Scf02085	cov=13.9	141	3e-31
Niben101Scf01658	cov=13.9	139	1e-30
Niben101Scf08564	cov=13.7	137	3e-30
Niben101Scf03340	cov=12.8	137	3e-30
Niben101Ctg12727	cov=16.0	134	4e-29
Niben101Scf01947	cov=14.2	132	2e-28
Niben101Scf01534	cov=13.8	132	2e-28
Niben101Ctg15019	cov=16.0	128	2e-27
Niben101Scf11139	cov=12.7	128	2e-27
Niben101Scf02621	cov=14.1	122	1e-25
Niben101Ctg11055	cov=18.0	121	3e-25
Niben101Scf10336	cov=13.4	115	2e-23
Niben101Scf36875	cov=6.1	113	6e-23
Niben101Scf06898	cov=13.0	108	3e-21
Niben101Scf04477	cov=14.8	108	3e-21
Niben101Scf01013	cov=12.9	108	3e-21
Niben101Scf07129	cov=12.0	102	1e-19
Niben101Scf04448	cov=11.8	102	1e-19
Niben101Scf05226	cov=14.2	100	5e-19
Niben101Scf02174	cov=14.2	100	5e-19
Niben101Scf00620	cov=13.9	100	5e-19
Niben101Scf02285	cov=14.0	99.0	2e-18
Niben101Ctg14852	cov=19.0	97.1	6e-18
Niben101Scf29015	cov=13.6	97.1	6e-18
Niben101Scf03898	cov=14.7	97.1	6e-18
Niben101Scf02195	cov=13.1	95.3	2e-17
Niben101Scf00470	cov=14.0	95.3	2e-17
Niben101Scf39198	cov=12.0	93.5	8e-17
Niben101Scf03652	cov=13.4	93.5	8e-17
Niben101Scf07030	cov=13.1	91.6	3e-16
Niben101Scf06698	cov=14.4	91.6	3e-16
Niben101Scf08368	cov=13.5	89.8	1e-15
Niben101Scf04875	cov=13.0	89.8	1e-15
Niben101Scf04556	cov=13.3	89.8	1e-15
Niben101Ctg02061	cov=10.0	87.9	4e-15
Niben101Scf08018	cov=14.8	87.9	4e-15
Niben101Scf16024	cov=13.8	86.1	1e-14
Niben101Scf02738	cov=15.1	86.1	1e-14
Niben101Scf02111	cov=13.3	84.2	5e-14
Niben101Scf14881	cov=13.0	80.5	6e-13
Niben101Scf03700	cov=13.3	80.5	6e-13
Niben101Scf03450	cov=14.6	80.5	6e-13
Niben101Scf03367	cov=15.6	80.5	6e-13
Niben101Scf04049	cov=14.1	78.7	2e-12
Niben101Scf03396	cov=14.2	78.7	2e-12
Niben101Scf03279	cov=12.2	78.7	2e-12
Niben101Scf14323	cov=13.7	76.8	8e-12
Niben101Scf11770	cov=14.0	76.8	8e-12
Niben101Scf05132	cov=13.5	76.8	8e-12
Niben101Scf03607	cov=14.9	76.8	8e-12
Niben101Ctg13528	cov=12.0	73.1	1e-10

Table S2. Contigs assembled from retrozyme-specific HTS reads. Contigs were obtained by constrained assembly of retrozyme-specific reads generated by high-throughput sequencing of *N. benthamiana* leaf RNA.

Name	Number of reads	Sequence
>contig 1	36	GCGGGCCATCTGGATTTTCGTCGTTGGGTACGGGAACGGCATTAGCGATAAGGCGTTGTCTTCCTT AGATGCTTTGGTCTTGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGCGCTTGTGCGCTTGTG
>contig 2	2	GGCCATCTGGATTTTCGTCGTTGGGATAAAAGGGAACGGCATTAGTGATAAGGCGTTCTCCCTTAG ATGCTTCGATCTGGCCGAGTCAAGCAGGCCGACCCGATTAAGTTTGGGGAGC
>contig 3	59	TTAGCGATAAGGCGTTCTCGCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAG TTTGGGGAGCTTGTGCGTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGGGACAAAC TGGTCGGGGGCTAGTGGCGCTCCCTGATGACCCCAAGGCAGGGCGAAACCGTTGGCTTCCGCGTG TGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACCCGCGACGGGCGCTGTGCGCTGCGCCGG ACTCTCGTCCCGTGACAAGTGGTATCAGAGCCGACGTACTTGTGTTGTGCGCGTTTATGGTGGG GTCCTCGGGGGAGGACTGTGCGGGTGCGCGTTGCCTAGGGGGTG
>contig 4	4	GGGGCGCTTGTGCGTGGTGGTGGACTTGACAATGAAGGGCACCAGAAATAGGCCTAAGGGATCAACTG GTTGGGGCTAGTGCCGCTCCCTGATGAGCCCATGGCAGCG
>contig 5	16	ACCGAAGCAATCCTAAGGGACAACCTGGTTGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGG GCGAAACAGGTTGGCTTCCGCATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCTCAGACGCGG CACGG
>contig 6	2	CCGAAAGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGG TTGGCTTCCGCATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCTCA
>contig 7	8	GTTGGGGGCTAGTGCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGTTGGCTTCCGCATGTG GTAAGGCTGGTCTAGGGTGGTATGGGACGCTCAGA
>contig 8	4	GTCTAGGGTGGTATGGGACGCTCAGACGCGCACGGGCGCTGTGCGCTGCGCCGACTCTCAGCCT GTGACAAGTGGTATCAGAGCGGGACGTACTTGCTGCTGTT
>contig 9	38	CCGGACTCTCAGCCTGTGACAAGTGGTATCAGAGCGGGACGTACTTGCTGCTGTTGTGCGTTATGGT GGGATTTCTCAGGGGAGGACTGTGCGGGTGCGTTGCCTGGGGGGGCTCGCGCCGACGACTGCCCCATC CTGCAATGGTCTGCAGGGGCAAGACCGGGATGGCTACCAGCAAGGCCGGTTGCACGAGG
>contig 10	14	CGTGCTGCGTTTGGGTGGGGGAGAATGTACGACCCGATGTGCTGACCGTTAAAGATCAAATGAA AGAGCGGGCCATCTGGCAATTCGTCGTTGGGTACGGGAACGGCATTAGCGATA
>contig 11	2	GTGGGGGAGAATGTACGACCCGATTTTCGTGACCGTTAAGGTCAAATGAAAGAGCGGGCCATCTGG AAATTCGTCGTTGGGATACGGGAACGGCATTAGCG
>contig 12	27	GTTTGGGGTGTGTCGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGGCCAAAGGGATCA ACTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGTTGGCTTCCGCG TGTGGAAGG
>contig 13	5	GGGCGCTTGTGCGCAGGTCATAGACTTGACAATGAAGGGGACCGAAGTAGGCAAAAGGGATCAACTGG TCGGGGGCTAGTGCTGCTCCCTGATGAGCCCA
>contig 14	27	GGGGGTGCTTGTGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGGCCAAAGGGATCAACT GGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCGTTGGCTTCCGCGTGT GGAAAGG
>contig 15	2	GTTCACTCAATGTGATGTGTACGACCCGATTGTCGTGACCGTTAAAGATCAAATGAAAGAGCGG GCCATCTGGATTTTCGTCGTTGGGTACGGGAACGGCATTAA
>contig 16	2	GGGCGCTTGTGCGTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGGCAAAAGGGATCAACTGG TCGGGGGCTAGTGCCGCTCCCTGATGAGCCCA
>contig 17	2	GACCGGGATGGCTACCAGCAAGGCCGGTTGCACGAGGTGAGGTGCGCTTGGGCAAAACACGCGGCGC GTATAGCAGTATTGTACGTGATCCTTGGCAGAGTCCTTCTCCCAACAGCACGA
>contig 18	2	GTGGGGGAGAATGTACGACCCGATTGTCGTGACCGTTAAAGATCAAATGAAAGAGCGGGCCATCTGG ATTTTCGTCGTTGGGATAAAAGGGAACGGCATTAG
>contig 19	5	GGGGGGAGAATGTACGACCCGATTGTCGTGACCGTTAAAGATCAAATGAAAGAGCGGGCCATCTGG CAATTCGTCGTTGGGTACGGGAACGGCATTAGCGATA
>contig 20	33	GGGGGTGCTTGTGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGGCCAAAGGGATCAACT GGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGAGCGAAACCGTTGGCTTCCGCGTGT GGTAA
>contig 21	4	AGGGGACCGAAGTAGGCCTAAGGGATCAACTGGTCGGGGGCTAGTGCCGCTCCCTGATGAGCCAC GGCAGGGCGAAACTGGTTGGCTTCCGCGTGTGGTAAGGCTTGCTCG
>contig 22	2	GGCCAAAACACGCGCGCGCATAGTAGTATTGTACGGGATCCTTGGGTAGAGTCCTTCTCCCCAACA GCACGAGGGCGTGCTGCGTTTGGGTGGGGAGA
>contig 23	3	GCGCTGTGTGCTGCGCCGACTCTCAGCCCGTGACAAGTGGTATCAGAGCGGGACATACTTGCTGCT GTTGCGATGATTGGTCTTATAGAGAGAGGACTG
>contig 24	2	GGCGGTATAGCAGTATTGTACGTGATCCTTGGGCAGAGTCCTTCTCCCCAACAGCACGAGGACGTG CTGCGTTTGGGTGGGGGAGAATGTACGACCCGATTGTCGTGACCGATAA
>contig 25	13	GGCGGTATAGCAGTATTGTACGTGATCCTTGGGCAGAGTCCTTCTCCCCAACAGCACGAGGACGTG CTGCGTTTGGGTGGGGGAGAATGTACGACCCGATTGTCGTGACCGTTAAAGATCAAATGAAAG

>contig 26	11	CGGGCAGAGTCTTCTCCCCAACAGCACGAGGACGTGCTGCGTTTTGGGTGGGGGAGAATGTCACGA CCCGATTGTCGTGACCGTTAAAGATCAAATGAAAG
>contig 27	11	AGGGCAGAGTCTTCTCCCCAACAGCACGAGGACGTGCTGCGTTTTGGGTGGGGGAGAATGTCACGA CCCGATTGTCGTGACCGTTAAAGATCAAATGAAAG
>contig 28	26	GCGGGCCATCTGGCAATTCGTGCTTGGGTACGGGAACGGCATTAGCGATAAGGCGTTGTTCTTCCTT AGATGCTTTGGTCTTGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGCGCTTGTCGCTTGTCTC
>contig 29	7	GCGGGCCATCTGGCAATTCGTGCTTGGGTACGGGAACGGCATTAGCGATAAGGCGTTGTTCTTCCTT AGATGCTTTGGTCTTGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGC
>contig 30	3	GCCGCACGGGCGCTGTGTGCTGCGCCGACTCTCAGCCCGTAACATTACGCTGTTGAATACAATAGG ATAAGAAGCACAATAATTAACAATATTACTCTGTCTTCTTGA
>contig 31	4	CCCTGTAGTCCAAAGGAAAGAGCGGGCCATCTGGAACATTGCCGTTGGGTTATGGGGACGACATTAG CATTAAAGCGTTGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTT
>contig 32	19	GTCCGAAGGAAAGAGCGGGCCATCTGGAACATTGTGCTTGGGTTATGGGGACGATATTAGCATTAAAG GCGTTGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGTAGGCCGACCCGGTTAAGTTTGGGGT GCTTGTCGCTGGTC
>contig 33	11	CGGGCCATATGGAACCTTCGTGCGTTGGGTTATAGGGTCGACATTAGCATTAAAGCGTTGTTCTCCCT TAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGTGCTTGTCGCTGGTC
>contig 34	2	GGGCCATCTGGAACCTTCGTGCTTGGGTTATGGGGACGATAATAGCATTAGGGCGTTGTTCTCCCTTA GATGCTTCGATCTGGCCGAGTCAGGCTGGACGACCCGGTT
>contig 35	8	GTCATATGGAACCTTCGTGCGTTGGGTTATAGGGTCGACATTAGCATTAAAGCGTTGTTCTCCCTTAG ATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGTGCTTGTCGCTGGTC
>contig 36	2	GCTCCCTGATGAGCCCAAGGCAGAGCGAAACCGGTTGGCTTCCGCGTGTGGTAAGGCTTGTCCTCGA GGTAGTGGGCGGCCCTCGGGACGCCGACGGGCGCTGT
>contig 37	21	CCGGACTCTCAGCCTGTGACAAAGTGGTATCAGAGCGGGACGTACTTGCTGCTGTTGTGCGTTATGGT GGGATTCTCAGGGGAGGACTGTGCGGGTGCGTTGCCTGGGGGGCTCGCGCCGACGACTGCCCATC CTGCAATGGTCTGCAAGGGCAAGACCGGGATGGCTACCAGCAAGACCGGTTG
>contig 38	2	GTCGGCTATTTTCGTGAGTTGGTGTGTTGGTTGCCGCGGGGCTGTTTTAGAGTGACATAAAACGAGC CCGTGACAAATGGTATCAGAGCGGGCCAGGTTTCATGACTAGGTGAGATGGAC
>contig 39	2	CCCGTGAAAAGTGGTATCAGAGAGGGACGTACTTGCTGCTGCGCGTTATGGTGGGGTCCTCGAGGGG AGGACTGTGCGGGTGCGTTTGTCTAGGCGGGGGC
>contig 40	2	GCTGCTGCGCGATATGGTGGGGTCCTCGGGGGAGGACTGTGCGGGTGCGTTGCCTAGGCGGGGGGCT CGCGCCGACGACTGCCCCATCTGTGAAGTCTGCAAGG
>contig 41	4	GCGGGTGCGTTGCCTAGGCGGGGGGCTCGCGCCGACGACTGCCCATCCTGCTAAGGTCTGCAAGGG CAAGACCGGATGGCCACCAGCAAGGCCGGTTG
>contig 42	5	TGGTGCGTTGCCTGGGGGGGCTCGCGCCGACGACTGCCCATCCTGCAATGGTCTGCAGGGGCAAGA CCGGGATGGCTACCAGCAAGGCCGGTTGCACGAGG
>contig 43	2	GCCGGGATGGCCACCAGCAAGGCCGGTTGCACAAAGTGAGGTGCGACTGAGCGAAGATACGCGGCGC GTTAAGCAGTATTGTGCGGGTCTCTGGGCGGAG
>contig 44	3	GCGACTGAGCGAAGAGACGCGGTGCGTTAAGCAGTATTATGCGGGACCTGGGCGGAGTCCTTCTCC CCAACAGCACGAGGACGTGCTGGGTTTTAGTGGGGGAGAATGTCACGA
>contig 45	2	GGCGCTTTAGCAGTATTGTGCGGGATCCTGGGCGGAGTCCTTCTCCCAACAGCACGAGGACGTGCT GGGTTTTGGGTGGGGGAGAATGTACAGGCCTGT
>contig 46	5	GTATTGTGCGGGTTCCTGGGCGGAGTCCTTCTCCCAACAGCACGAGGACGTGCTGGGTTTTGGGTG GGGGAGAATGTCACGACCCGTTTGTGCGTACCCTGTAGATCAAAAGAAAGAGCGGGC
>contig 47	5	GGTGCGGGTTCCTGGGCGGAGTCCTTCTCCCAACAGCACGAGGACGTGCTGGGTTTTGGGTGGGGG AGAATGTCACGACCCGTTTGTGCTGACCGTGTAGATCAAAAGAAAGAGCGGGC
>contig 48	3	GGACGTGCTGGGTTTTGGGTGGGGGAGAATGTCACGACCCGTTTGTGCTGACCATATAGTCCAAAGG AAAGAGCGGGCCATCTGGAACCTTCGTGCTTGGGTGATGGGACGACATTAG
>contig 49	4	GCTGGGTTTTGGGTGGGGGAGAATGTCACGACCCGTTTGTGCTGACCGTGTAGTCCGAAGGAAAGAG CGGGCCATCTGGAACATTGTGCTTGGGTTATGGGACGATATTAGCATT
>contig 50	3	GTTTTGGGTGGGGGAGAATGTCACGACCCGTTTGTGCTGACCGTGTAGTCCAAAGGAAAGAGCGGGC TATCTGGAACCTTCGTGCTGACTCATGGGACGACATTAGCAT
>contig 51	4	ACCCGTTAAGTTTTGGGTGCTTGTGCTGGTTCATGGACTTAACAATGAAGGGGACCGAAGTAGGCC TAAGGGATCAACTGGTGGGGGCTAGTGCCGCT
>contig 52	3	GGGGTGCTTGTGCTGGTTCATGACTTGACAATGATGGGGACCGAAGTAGGCCTAAGGGATCAACTG GTCGGGGGCTAGTGCCGCTCCCTGATGAACCCA
>contig 53	2	GGTTGGCTTCCGCATGTGGTAAGGCTGGTCTAGGGTGGTATGGGACGCCCTAGACGCCGACGGGCG CTGTGCGCTGCGCCGACTCTCAGCCTGTGACAA
>contig 54	34	GTTGGCTTCCGCATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGACGGGCGC TGTGCGCTGCGCCGACTCTCAGCCTGTGACAGATGTGATGGATGACATTATTAGGACAATTTCCCT TC
>contig 55	25	GGTTCCGCATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGACGGGCGCTGT GCGCTGCGCCGACTCTCAGCCTGTGACAGATGTGATGGATGACATTATTAGGACAATTTCCCTTC
>contig 56	24	GTCCGCATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCTCAGACGCCGACGGGCGCTGTGCG CTGCGCCGACTCTCAGCCTGTGACAGATGTGATGGATGACATTATTAGGACAATTTCCCTTC
>contig 57	2	GGGGTGGTATGGGACGCCTCAGACGCCGACGGGCGCTGTGCGCTGCGCCGACTCTCGGCCCGTGA CATTATAATGAGACAAGTACAATAGCCTTAAAGAC
>contig 58	9	CCGTGCTTGGGTACGGGAACGGCATTAGCGATAAGGCGTTGTTCTTCTTCTTAGATGCTTTGGTCTTGC CGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGCGCTTGTGCTTGTG

>contig 59	4	AGGCGTTGTTCTTCCTTAGATGCTTTGGTCTTGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGG GAGCTTGTCGCTTGCTTGACATGACTATGAAGTGGACCGAAGCAATCCTAAGG
>contig 60	20	AGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGCGCTTGTCGCTTGCTTGACATGACTATGAAGTT GACCGAAGCAATCCTAAGGGACAACCTGGTTGGGGGCTAGTGCAGCTCCCTGATGAGCCCAAGGCAG GGC
>contig 61	24	AGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGCGCTTGTCGCTTGCTTGACATGACTATGAAGTT GACCGAAGCAATCCTAAGGGACAACCTGGTTGGGGGCTAGTGCAGCTCCCTGATGAGCCCAAGGCA
>contig 62	2	CCGGTTAAGTTTGGGGAGCTTGTCGCTTGCTTGACATGACTATGAAGTGGACCGAAGCAATCCTA AGGGACAACCTGGTCGGGGGCTAGTGCCGCTCCC
>contig 63	2	GGGGCGCTTGTCGCTTGCTTGACATGACTATGAAGTTGACCGAAGCAATCCTAAGGAACAACCTGG TTGGGGGCTAGTGCCGCTCCCTGATGAGCCCA
>contig 64	2	GGGGCGCTTGTCGCTTGCTTGACATGACTATGAAGTTGACCGAAGCAATCCTAAGGGACAACCTGG TCGGGGGCTAGTGTCGCTCCCTGACGAGCCCA
>contig 65	56	GCAGCGAAAGTAATGCGTCGGGTCGCCGCATCATCGGGTGGGGGAGAGTTGTACGGCCCTCAAAGTA GGGACAAAGCGTGCGTGCGGATTGGCATCAAACCTGCCTTGGGGAGGGGAGGCGCCTCTAGCCATAAA GGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGA G
>contig 66	12	GCGGAAACTTTTGAAGGGAGTATGGAGTGAAAAGTTCGAAATGAAGACTGAAGTGTACGGCCCTCAG AGTAGGGACAAAGCGTGCGTGCCGATTGGCATCAAACCTGCCTTGGGGAGGGGAGGCGCCTCTAGCCA TAAAGGCGCTCTGCCCGAGT
>contig 67	2	CGGGTGGGGGAGAGTTGTACGGCCTCAAAGTAGGGACAAAGCGTGCGTGCGGATTGGCATCAAAC TGCCTTGGGGAGGGGAGGCGCCTCTAGCCATAATGGCGCT
>contig 68	37	CGGGGAGAGTTGTACGGCCTCAAAGTAGGGACAAAGCGTGCGTGCGGATTGGCATCAAACCTGCCT TGGGGAGGGGAGGCGCCTCTAGCCATAAAGGCGCTCTGCCTAGTTGCGTATTGGCTTGGCCGAGTT AGGCATGCCGACCCGATTAAGTTTGGGGAG
>contig 69	17	GTCACGGCCTCAGAGTAGGGACAAAGCGTCGTCGCCGATTGGCATCAAACCTGCCTTGGGGAGGGGAG GCGCCTCTAGCCATAAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGAC CCGATTAAGTTTGGGGAG
>contig 70	16	CCACGGCCTCAGAGTAGGGACAAAGCGTGCGTGCCGATTGGCATCAAACCTGCCTTGGGGAGGGGAGG CGCCTCTAGCCATAAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACC CGATTAAGTTTGGGGAG
>contig 71	11	GGACGGCGTTGTATTGGCGTCGAAGCGTGCGTGCTGACTGGCATCAAACCTGCCTTGGGGAGGGGAGG CGTATCTAGCAATAAGACGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCAT
>contig 72	10	CGGCCTCAGAGTAGTGACTATGACGGCGCTGTATTTGGCGTCGAAGCGTGCGTGCTGACTGGCAATC AAACTGCCTTGGGGAGGGGAGGCGCTCTAGCCATAAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTG GC
>contig 73	6	GTGCTTGCGGATTGGCATCAAACCTGCCTTGGGGAGGGGAGGCGCCTCTAGCCATAAAGGCGCTCTGC CCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGAG
>contig 74	8	CTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGAGCAT GTCGCTTGCTTTGAACATGACTATGAAGGGAGCCGAAGCATAACGGGGGGCACAGCTGG
>contig 75	26	CTCAGAGAAGGGGCAAGTAAGCGTGCGGATTGGCATCAAACCTGCCTTGGAGAGGGGAGGCGCTCTC TAGCCATTAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTA AGTTTGGGGAGCATGTCGCTTGCTTGACATGACTATGAAGGGAGCCGAAGCATAACGGGGGGGCAC AGCTGG
>contig 76	2	GTATTGGCTTGGCCGAGTTAAGCATGCCGACCCGATTAAGTTTGGGAGCATGTCGCTTGCTTTGGA CAGGACTATGAAGGGAGCTGAAGCATACGGGGG
>contig 77	2	ATTGGCTTGCCGAGTTAGGCATGCCGACTGATTAAGTTTGGGGAGCATGTCGCTTGCTTTGGACA TGACTATGAAGGGAGCTGAAGCATACGGGGGGC
>contig 78	4	GTTTGGGGAGCATGTCGCTTGCTTTGAACATGACTATGAAGGGAGCCGAAGCATAACGGGGGGGCACA GCTGGTCGGGAGCTATTACCGCTTCCCTGATGAGCCC
>contig 79	2	CGCTTGCTTTGGACATGACTATGAAGGGAGCCGAAGCATAACGGGGGGCTCAGCTGGTCGGGAGCTAT TGCCGCTTCCCTGATGAGCCCATGGCAGGGCGA
>contig 80	7	TGAAGGGAGCCGAAGCATAACGGGGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCC CATGGCAGGGCGAAACAGTCTGCGCGCTAGGTTCGGACGGGCGTGTCCGGGGGCGGT
>contig 81	10	GGGAGCTGAAGCATAACGGGGGGGCACAGTTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGG CAGGGCGAACCAGTCTGTACGCTATTTCGGACGGGCGAGTCCGGGTGGTATGGGACGCCCTCGGGCGC CGCGGG
>contig 82	6	GGAGCTGAAGCATAACGGGGGGCACAACTGGTCGGGAGCTATTGCCGCTTCCGTAATGAGCCCATGGCA GGGCGAAACAGTCTGTACGCTATTTCGGACGGGCGAGTTCCGGGTGGTATGGGACGCCTCG
>contig 83	15	AGCCGAAGCATAACGGGGGGGCACAGCTGGTCGGGAGCTATTACCGCTTCCCTGATGAGCCCATGGCA GGGCGAAACAGTCTGCGCGCTAGGTTCGGACGGGCGTGTCCGGGGCGTTTATGGGACGCCCTCGGGCG CGAAGCGCCGCGTCCGTACAGAAAGGATCAGGAAATATAAGCACTCAAAGTTCAAATGGATTATA AAGAATT
>contig 84	5	AGCTGAAGAATAACGGGGGGGCACAGTTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAG GGCGAACCAGTCTGTACGCTATTTCGGACGGGCGAGTCCGGGTGGTATGGGACGCCCTCGGGCGCCGC GGG
>contig 85	6	GGCCGAAGCATAACGGGGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCA GGGCGAAACAGTCTGCGCGCTAGGTTCGGACGGGCGTGTCCGGGGCGGT
>contig 86	2	GCATACGGGGGCACAGCTGGTTGGGAGCTATTGCCGCTTCCCTGATGAGCCCATGGCAGGGCGAAAC

		CTGTCTGTACGCTATTTGGACGGGCGAGTCTGGGGTGGTAT
>contig 87	13	CGGGGGGGGCACAGTGGTTCGGGAGCTATTACCGCTTCCCTGATGAGCCCATGGCAGGGCGAAACCA GTCTGCGCGTAGGTTCGGACGGGCGTGTCCGGGGCGTTTATGGGACGCCTCGGGCGCGAAGCGCCGC GGTCCGTACAGAAGGATCAGGAAATATAAGCACTCAAAAGTTCAAATGGATTATAAAGAATT
>contig 88	10	ACCCAGTCTGCGCGTAGGTTCGGACGGGCGTGTCCGGGGCGTTTATGGGACGCCTCGGGCGCGAAGC GCCGCGGTCCGTACAGAAGGATCAGGAAATATAAGCACTCAAAAGTTCAAATGGATTATAAAGAAT T
>contig 89	25	CCAGTCTGCGCGTAGGTTCGGACGGGCGTGTCCGGGGCGGTTATGGGACGCCTCGGGCGCGAAGCGC CGCGGTCCGTACATATGGTATCAGAGCAAACATGCTCTTCAACTTCTCTTGCAGGTGTCTAGCTCA TG
>contig 90	22	CGTCGGACGGGCGTGTCCGGGGCGGTTATGGGACGCCTCGGGCGCGAAGCGCGCGGTCCGTACAT ATGGTATCAGAGCAAACATGCTCTTCAACTTCTCTTGCAGGTGTCTAGCTCATG
>contig 91	2	GTCAGCTCATGAATGCACAAGCTCGGGTGAATGCTACAAGTGCAAAGATGGGGCGCTGAGTGACAG AGTGGAGCATGACGGTCTTGGGCAAACATACTACTTCTCCGCCAAAGTAAAGC
>contig 92	2	CTTGGGTGAATGCTACAAGTGCAAAGATGGGGGCGCTGAGTGACAGAGTGGAGCATGACGGTCTTTG GGCAAACATACTACTTCTCCGCCAAAGTAAAGC
>contig 93	5	GGATGCTATAAGTGCACAAGATGGGGATGCTGAGTGACAGAGTGGAGCATGACGATTTTGGGCAAAGA GACTACTTCTCCGCCAAAGTAAAGCGGCTTGAGCAATGAAATTGTTGTGAAGTCTAAATGAAACCAC GAAGTGGACACACCGACGAAGTGCG
>contig 94	43	TGGGGGCGCTGAGTGACAGAGTGGAGCATGACGGTCTTTGGGCAAACATACTACTTCTCCGCCAAAG TAAAGCGGGCTTGAGCAATGAAATTATTGTGAAGTCTAGATGAAACCACGAAGTGGACGCACCGACG AAGTG
>contig 95	32	TGGGGCGCTGAGTGACAGAGTGGAGCATGACGGTCTTTGGGCAAACATACTACTTCTCCGCCAAAGT AAAGCGGGCTTGAGCAATGAAATTATTGTGAAGTCTAGATGAAACCACGAAGTGGACGCACCGACGA AGTG
>contig 96	22	CTGGGCGCTGAGTGACAGAGTGGAGCATGACGGTCTTTGGGCAAACATACTACTTCTCCGCCAAAGT AAAGCGGGCTTGAGCAATGAAATTATTGTGAAGTCTAGATGAAACCACGAAGTGGACGCACCGACGA AGTG
>contig 97	11	GCTCCTTGGGCAAACATACTACTTCTCCGCCAAAGTAAAGCGGGCTTGAGCAATGAAATTATTGTGA ACTCTAGATGAAACCACGAAGTGGACGCACCGACGAAGTG
>contig 98	17	AGCGGGCTTGAGCAATGAAATTATTGTGAAGTCTAGATGAAACCACGAAGTGGACGCACCGACGAAG TGTGATGCCGTCTCCATGATTACGTGCCTGAGTCCCAAAGTTGG
>contig 99	3	GCACCGACGAAGTGTGATGCCGTCTCCATGATTACGTGCCTGAGTCCCAAAGTTGGCAGCACGAAGA GGTGTGGTGCAAGCATGAATGAGGGTGCAAGTTCCGTGTGGAACACGAAAGGAGTT
>contig 100	13	GGCAGCACGAAGAGGTGTGGTGCAAGCATGAATGAGGGTGCAAGTTCCGTGTGGAACACGAAAGGAG TTGCAGCGAAAGTAATGCGTCGGGTCGCCGCATCATCGGGTGGGGGAGAGTTGTACGGCCTCAAAG T
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>contig 103	7	GTTAGCATGAATTAGGGTGCAAGATCCGTGCGGAAACGAAAGGAGTTGCAGCGAAAGTAATGCGTCG GGTCGCCGCATCATCGGGTGGGGGAGAGTTGTACGGCCTCAGAGTAGTGACTATGGACGGCGTTGT ATTGGCGTCGAAGCGTGCCTGCTGACTGGCATCAAAC
>contig 104	7	GCATGAATTAGGGTGCAAGTTCCGTGTGGAACACGAAAGGAGTTGCAGCGAAAGTAAATGCGTCGGGTC GCCGCATCATCGGGTGGGGGAGAGTTGTACGGCCTCAGAGTAGTGACTATGGACGGCGTTGTATTG GCGTCGAAGCGTGCCTGCTGACTGGCATCAAAC
>contig 105	2	CATGAATTAGGGTGGAAGTTCCGTGTGGAACACGAAAGGGGTGCAGCGAAAGTAATGCGTCGGGTGCG CCGCATCATCGGGTGGGGAAGAGTTGTACGGCCTCAGAGAAGT
>contig 106	18	CTCAGAGAAGGGGCAAAGTAAAGCGTTCGGATTGGCATCAAACGCTTGGAGAGGGGAGGCGTCTC TAGCCATTAAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCACCCGATTA AGTTTGGGGAGCATGTCGCTGTGCTTGGACATGACTATGAAGGGAGCCGAAGCATACGGGGGGC
>contig 107	3	GGGGAGGGGAGGCGTCTCTAGCCATAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAG GCATGCCTACCCGATTAAGTTTGGGGAGCATGTC
>contig 108	5	GCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGAGCTTGTGCTTGTCTTGGACATGAC TATGAAGGGAGCTGAAGCATACGGGGGCACAGCTGGT
>contig 109	2	GGGGAGCAAGTCGCTTGTCTTGGACATGACTATGAAGGGAGCTGAAGCATACGGGGGCACAACTGGT CGGGAGCTATGCGGCTTCCGTAATGAGCCCATG
>contig 110	2	GGCAGGACGGGCGTGTCCGGGGCGGTATGGGACGCCTCGGGCGCGGAGAGCCGCGGTCCGTGTCATT TGGTATCAGAGCAAACATGCTCTTCAACTTCTGTGGCGAG
>contig 111	3	GGCGTGTCCGGGGCGGTATGGGACGCTCGGGCGCGAAGCGCGCGGTCCGTGTCACTTGGCTCAAG CTTATTTTAAATCAATTATCAAGAAGTAGAAAGACACAGCGTAAT
>contig 112	2	GTCCAGGGAGGTATGGGACCTCGGGCGCGGAGCGCCGCGGTCCGTGTCATTATGCTAGGGAATGTT TCAAAGCTGGACTTGAGCACAGTGGTGAAAGTATG
>contig 113	2	ACCGGGCGGTATGGGACGCTCGGGCGCGAAGCGCCGCGGTCCGTGTCACTTGGCTCAAGCTTATT TTAATCAATTATCAAGAAGTAGAAAGACACAGCGTAAT
>contig 114	2	GGCGATTGTGACTAAGGCGCACGGAAGATAGCTAGGGAGTTATCCGGTCCGTGACAGTTGGTATC AGAGCAAACATGCTCTTCAACTTCTGTGGCGAGGTGCC
>contig 115	3	CCGTGTCATTGGTACCAGAGCAAACATGCTCTTCAACTTCTGTGGCGAGGTGTCAAGCTCATGAAT

		GCACAAAGCTAGCGGAAGGCGTAAGTGCAAAGA
>contig 116	3	TGGCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCGTAAGTGCAAAGATGGGGGCGCT GAGTTACAGAGTGGGGCATGACGGTCTTTGGGGC
>contig 117	4	GTGCAAAGATGGGGGCGCTGAGTTACAGAGTGGGGCATGACGGTCTTTGGGAAAACTACTACTTC TCCGCCAAAGTAAAGCGGGCTTGAGCAAATGAAATTGTTGCGAACTCTAGATGAAACCACGAAGTGG
>contig 118	50	TTGCACTTCAACTTCTGTGGCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGT GCAAAGATGGGGGCGCTGAGTTACAGAGTGGGGCATGACGGTCTTTGGGGCAAACATACTACTTCTC CGCCAAAGTAAAGTGGGCTTGAGCAAATGAAATTGTTGCGAACTCTAAAAGAAACCACGAAG
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>contig 120	51	GGCTTGAGCAAATGAAATTGTTGCGAACTCTAGATGAAACCACGAAGTGGACGCGCCGACGAAGTGT GAAGCTCTCCATGGTTTCGTGCCTAAGTCCGAGGTAGGCAGCACGAGGAGGTATTGCTAGCATGATG GGTGAATGTTCCGAGTGGAGACGAAAGGAGTAGCAGCGAAAGTAATGCGTCGGGTGCGCCGATCA GCCAGGTGGGGGAGGTTGTACGTCCTCAGAGAAGGGGC
>contig 121	2	GGCTTGAGCAAATGAAATTGTTGCGAACTCTAAAAGAAACCACGAAGTGGACGCGCCGACGAAGTGT GAAGCTCTCCATCGTTTCGTGCCTAAGTCCGAG
>contig 122	2	GTCCGAGGTAGGCAGCACGAGGAGGTATCGCTTGATGATGGGTGCAATGTTCCGAGTGGAGACGA AAGGAGTAGCAGCGAAAGTAATGCGTCGGGTCTG
>contig 123	52	TTGTTGCGAACTCTAGATGAAACCACGAAGTGGACGCGCCGACGAAGTGTGAAGCTCTCCATGGTTT CGTGCCTAAGTCCGAGGTAGGCAGCACGAGGAGGTATTGCTAGCATGATGGGTGCAATGTTCCGAGT GGAAGACGAAAGGAGTAGCAGCGAAAGTAATGCGTCGGGTGCGCCGATCAGCCAGGTGGGGGAGGGT TGTCACGTCCTCAGAGAAGAGGCAAAGTAAAGCGTGCGGATTGGCATCAAACGCCAGATCGGA
>contig 124	10	GGTGGGGAGGGTTGTACGTCCTCAGAGAGAGGCAAAGTAAAGCGTGCGGATTGGCATCAAACGTG CCTTGGAGAGGGGAGGCGTCTCTAGCCATTAAGGCGCT
>contig 125	11	CGGGGAGGGTTGTACGTCCTCAGAGAAGAGGCAAAGTAAAGCGTGCGGATTGGCATCAAACGCC TTGGAGAGGGGAGGCGTCTCTAGCCATTAAGGCGCT
>contig 126	3	GGGGAGGGTTGTACGTCCTCAGAGAAGGGGCAAAGTAAAGCGTGCGGATTGGCATCAAACGCCCTT AGAGAGGGGAGGCGTCTCTAGCCATTAAGGCGC
>contig 127	4	GGGGAGCTTGTGCGTTGTCTTGACATGACTATGAAGGGAGCTGAAGCATACGGGGGCACAGCTGGT TGGGAGCTATTGCGGCTTCCCTGATGAGCCCATG
>contig 128	3	AGACCAAATGAAAGAGCGGGCCATCTGGATTTTCGTCGTTGGGAAATAAAGGGAACGGCATTAGCGA TAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGC
>contig 129	12	CTGTTTGTGCTGATCGTGTAGATCAAAAGAATGAACGGGCCATCTGTAACCTTCGTCGTTGGGATACG GGAACGGCATTAGCGATAAGGCTGTGGAAGAGGATTGCTATTAATATTGTAGGGAG
>contig 130	12	TTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAG TTTGGGGAGCTTGTGCTGGTCATGGACTTGACAATGAAGGGGACCGAAGTAGCCGAAAGGGACAAC TGGCCGGG
>contig 131	3	CTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTGACTGTATTTATGTTTCC TATGTTTTTCATAATTATTTACGTTATTTCTGCGGG
>contig 132	2	GGCCGAGTCAGGCAGGCCGACCCGATTAAAGTTTGGGGTGCTTGTGCTGGTCATGGACTTGACAATG AAGGGGACTGAAGTAGACCTAAGGGATCAACTA
>contig 133	2	AAGGGGACCGAAGTAGCCGAAAGGACAACTGGTCGGTGGCATCGGAATCGAGGCGTCAGACGTGCA ATCGACGCGGAAACCAAGCAAGAAAGGTCC
>contig 134	2	AGGCAGGGCGAAACCGGTTGCGCTTCGCGATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCCA GACGCCGACGAGCGCTGTGCGCTGCGCCGGACC
>contig 135	42	ATGTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCCTCAGACGCCGACGAGCGCTGTGCGCTGCGC CGGACTCTCAGCCCGTGACAAGTGGTATCAGAGCGGGACGTAATTGCTGTTGTTGCGCGTTATGGTG GGGTCTCGGGGGAGG
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>contig 137	2	CCGTGACAAGTGGTATCAGAGCGGGACGTAATTGCTGTTGTTGCGCGTTATGGTGGGGTCTCGGGG GAGGACTGTGCGGGTGCGTTGCCTAGGCGGGAG
>contig 138	4	CGCGTTATGGTGGGGTCTCGGGGGAGGACTGTGCGGGTGCGTTGCC TAGCGGGGAGGGCTCGCACT GAAGACGGCCCCATCTTGCAATGGTCTGCAGGGGCAAGACCGGGAT
>contig 139	5	GTTTATGGTGGGGTCTCGGGGGAGGACTGTGCGGGTGCGCGTTGCC TAGGGGGTGGCTCGCACTGA AGACGGCCCCATCTGCAATGGTCTGCAGGGGCG
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>contig 142	9	CCCATCTTGCAATGGTCTGCAGGGGCAAGACCGGGATGGCCACCAGCAAGGCCGGTTGCACGAGGTG TGGTGCAGCTGGGCAAAAACACGCGGCGCGATAGCAGTATTGTACGTGATCCTTGGGCC
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>contig 144	2	TTGCAAGAGTGTGTGCTGCGACTGGGCAAAAACACGCGGCGCGATAGCAGTATTGTACGTGATCCTT GGGCAGAGTCTTCTCCCTACAGCACGAGGGCG
>contig 145	40	GCAGAGTCTTCTCCCTACAGCAGAGGGCGTGCTGCGTTTTGGGTGGGGGAGAATGTACGACCC GATTGTGCTGACCGTGAAGATCAAAAGAAATAGCGGACCATCTGGATTTTCGTCGTTGGGAAATAAG

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>contig 147	8	ATTAAGGCGTTGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGATTAAAGTT TGGGGTGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGG
>contig 148	3	CTGACTGTATGCTAGGCAGGGCAACAGGACGACCCGAGTTCAGGGGCAACGTGTCACGACCCGATTG TCGTGACCGTAAAGACCAAATGAAAGAGCGGGC
>contig 149	6	TTAGCGATAAGGCGTTCTCCCTTAGATGCTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAG TTTGGGGAGCTTGTGCTGGTTCATGGACTTGACAATGAAGGGG
>contig 150	2	GCGTTGTTCTCCCTTAGATGCTTCGATCTAGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGGT GGTTGTCGCTGGTTCATGGACTTGACAATGAAGGGGAC
>contig 151	27	GTGGTAAGGCTGGTCTGGGGTGGTATGGGACGCCCTCAGACGCCGACGAGCGCTGTGCGCTGCGCCG GACTCTCAGCCCGTGACAAGTGGTATCAGAGCGGGACGTAATTGCTGTTGTTGCGCGTTATGGTGGG GTCCCCGG
>contig 152	6	CCGATGACTGCCCATCCTGCTAAGGTCTGGGGTAAGACCTGGATGGCCATCAGCGAGGCCCGGTTG CACGAGGTGAGGTGCGACTGAGCGAAGAAATACGGCGC
>contig 153	4	TCCTTCTCCCCCTACAGCACGAGGGCGTGCTGCGTTTTTGGTGGGGGAGAATGTCACGACCCGATTG TCGTGACCGTAAAGACCAAATGAAAGAGCGGGC
>contig 154	4	GTTGTTCTCCCTTAGATACTTCGATCTGGCCGAGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGTGC TTGTGCTGCTGATGACTTGACAATGAAGGGGAC
>contig 155	2	AGTCAGGCAGGCCGACCCGGTTAAGTTTGGGGTGGTGTGCTGCTGGTTCATGGACTTGACAATGAAGGA GACCGAAGTAGGCCAAAGGGATCAACTGGTCGGGG
>contig 156	10	CTTCCGATCTGGTCTGGGGTGGTATGGGACGCCCTCAGACGCCGACGAGCGCTGTGCGCTGCGCCGG ACTCTCAGCCCGTGACAAGTGGTATCAGAGCGGGACGTAATTGCTGTTGTTGCGCGTTATGGTGGGG TCCTCGGGGGAGG
>contig 157	2	CGAGATCATGGGCGAGTGGCAAGGCATGATCGAGATCATGGGCGAGTGACAAGTGGTATCAGAGCCG GACGTACTTGCTGTTGTTGCGCGTTTATGGTGGGGTCCTCGGGGGAG
>contig 158	2	TCTGCAGGGGCAAGACCGGGATGGCCACCAACAAGGCCGTTGACAGAGGTGAGGTGCGACTGAGCAA AGTGACGCGCGCTGCTTTAGCAGTATTGTACGGGATCCTTGGG
>contig 159	2	GAAACGTTTTTTATAGAGCTTGTGTGTCACGACCCGATTGTCGTGACCGTGAAGATCAAAAGAAATAGC GGACCATCTGGATTTTCGTGCTTGGGAAATAAGG
>contig 160	3	CCTCGGGAGGCCGACGGGCGCTGTGTGCTGCGCCGACTCTTAGCCCGTGACAGTGGTATCAGAGC GGTACGTACTTGCTGCTGTTGCGCGTTATGGTG
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>contig 163	2	AGTCCTTCTCCCCAACAGCACGAGGACGTGCTAGATTTTGGGTGGGGGAGAATGTCACGACCCGTTT GTCGTGACCGTGAGATCAAAAGAAAGAGCGGGCCAATTGGAACCTCGTTCGATG
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>contig 165	20	ATATTTGTACATATTTAGTAGATTTCTAAACACATGTACAGGTTTGAGCCGAATGTCACGACCCGTT TGTCGTGACCGTGTAGATCAAAAGAAAGAGCGGGCC
>contig 166	5	ATATTTGTACATATTTAGTAGATTTCTAAACACATGTACAGGTTTGAGCCGAATGTCACGACCCGTT TGTCGTGACCGTGTAGATCAAAAGAAAGAGCGGGAC
>contig 167	2	CAATGATTCTGTGTAATAATTACAGAAACATTACTTTAAACTACGAGCCGTTTGTACAGACCCGTTT GTCGTGACCGTGTAGATCAAAAGAAAGAGCGGGCC
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>contig 169	3	TAAGGCTTGTCTCGAGGTAGTGGGCGGCCCTCGGGACGCCGACGGGCGCTGTGTGCTGCGCCGACT CTAAGCCCGTGACAAGTGGTATCAGAGCGGGAC
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>contig 173	5	GAGTCCTTCTCCCAAACAGCACGAGGACGTGCTGGGTTTTGGGTGGGGGAGAATGTCACGACCCGTT TGTCGTGACCGTGTAGATCAAAAGAAAGAGCGGGC
>contig 174	2	CCCAACAGCACGAGGACGTCTGGGTTTTGGGTGGGGGAGAATGTCACGACAAACGGGTGCGGGGCT AGTGCCGCTCCCCTGATACTCAAGGCAGGGC
>contig 175	2	GGGTTTTGGGTGGGGGAGAATGTCACGACCCGTTTGTGCTGACCGTGTAGATCAAAAGAAAGAGCGG GCCATCTGGAACCTTCGTGCTGGGTTATTGGGGAG
>contig 176	4	GGTTTTGGGTGGGGGAGAATGTCACGACCCGTTTGTGCTGACCGTGTAGTCCAAAGGAAAGAGCGGT CCATCTGGAACCTTCGTGCTGGGTTATGGGGACGACATTAGCATTAAGG
>contig 177	8	CATGTACAGGTTTGAAGCCGAATGTCACGACCCGTTTGTGCTGACCGTGTAGATCAAAAGAAAGAGCG GGCCATCTGGAACCTTCGTGCTGGGTTATTAGGGAG
>contig 178	2	GATCAACTGGTCGGGGCTAGTGCCGCTCCCTGATGAGCCCAAGGCAGGGCGAAACCCGTTGGCTTC

		CGCGTGTGGTAAGGCTTGTCTTGAGGTAGTGGGC
>contig 179	5	CTCAGACGCCGCACGAGCGCTGTGCGCTGCGCCGACTCTCAGCCCGTGACAAGTGGTATCAGAGCG GGACGTAATTGCTGTTGTTGCGCGTTATGGTGGGGTCCCTCGGGGGTGG
>contig 180	2	GGGGTCCCTCGGGGAGGACTGTGCGGGTGCAGCTTGCCTAGGGGGTGGCTCGCACTGAAGACGGCCC CATCCTGCAATGGTCTGCAGGGGCAAGACCGGGATGGC
>contig 181	18	GGCGTTGTTCTTCTTAGATGCTTTGGTCTTGCCGAGTTAGGCAGGCCGACCCGGTTAAGTTTGGGG AGCTTGTGCTTGTCTTGGACATGACTATGAAGGGAGCCGAAGCATACGAGGGGACACAGCTGGTCGG GG
>contig 182	34	ATTAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTT GTGGAGCATGTCGCTTGTCTTGGACATGACTATGAAGGGAGCCGAAGCATACGAGGGGCTCAGCTGG T
>contig 183	2	GCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGAGCA TGTCGCTTGTCTTGGACATGACTATGAGGGGAG
>contig 184	2	GACATGACTATGAAGGGAGCCGAAGCATACGGGGGGCACAGCTGGTCTTGCCTAGAATCGTACTAAG GGAATGCTGGATAGCAACACAGAAATTCAGAG
>contig 185	3	AAAGCGTGCGGATTGGCATCAAACCTGCCCTGGAGAGGGGAGGCGTCTTTAGCCATTAAGGCGCTCTG CCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGTGGAGC
>contig 186	16	AGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGG AGCATGTGCTTGTCTTGGACATGACTATGAAGGGAGCCGAAGCATACGAGGGGACACAGCTGGTCGG G
>contig 187	3	ATTAAGGCGCTCTGCCCTAGTTGCGTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTT GTGGAGCATGTCGCTTGTCTTGGACATGACTATGGAGGG
>contig 188	2	AGGGAGCCGAAGCATACGAGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCCTGATGAGCCCATG GCAGGGCGAAACAGTCTGCGCGCACAGGCAGGTCCGG
>contig 189	4	GACACTATATAGAAGTGGTATTGGATTGATTGACATATGCCGCTTCCCTGATGAGCCCATGGCAG GGCGAAACCAGTCTGCGCGCACAGGCAGGACGGGCGG
>contig 190	3	CACTATATAGAAGTGGTATTGGATTGATTGACATATGCCGCTTCCCTGATGAGCCCATGGCAGGG CGAAACCAGTCTGCGCGCACAGGCAGGACGGGCGTGTCCGGG
>contig 191	2	CAGGACGGGCGTGTCCGGGGCGGTATGGGACGCCCTCGGGCGCGGAGCGCCGCGGTCCGTGTCATTTG GTATCAGAGCAAACATGCTCTTCAACTTCTGTGGCGAG
>contig 192	4	GGACGGGCGTGTCCGGGGCGGTATGGGACGCCCTCGGGCGCTGAGCGCCGCGGTCCGTGTCATTTGGT ATCAGAGCAAACATGCTCTTCAACTTCTGTGGCGAGGTGTCAAGCTCATGAATGCACC
>contig 193	3	GATCTCGGGCGTGTCCGGGGCGGTATGGGACGCCCTCGGGCGCTGAGCGCCGCGGTCCGTGTCATTTG GTATCAGAGCAAACATGCTCTTCAACTTCTGTGGCGAGGTGTCAAGCTCATGAATGCACC
>contig 194	11	GCTGAGCGCGCGGTCCGTGTCATTTGGTATCAGAGCAAACATGCTCTTCAACTTCTGTGGCGAGGT GTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGTGCAAAGATGGGGGC
>contig 195	2	CAGGCGCCGCTAGGCGCGTGCGCCACGGTCCGTTCCAGGTCCGTTTCATATGGTATCAGAGCAA CATGCTCTTCTACTTCTGTTGCAAGGTGTGGGC
>contig 196	33	TTGCACTTCAACTTCTGTGGCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGT GCAAAGATGGGGGCGCTGAGTTACAGAGTGGGGCATGACGGTCCCTGGGGCAC
>contig 197	32	CGTCTGTGGCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGTGCAAAGATGGG GGCGTGAGTTACAGAGTGGGGCATGACGGTCCCTGGGGCAC
>contig 198	5	TGGCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGTGCAAAGATGGGGGCGCT GAGTTACAGAGTGGAGCATGACGGTCCCTGGGGC
>contig 199	2	GGCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGTGCAAAGATGGGGGCGCTG AGTTACAGAGTGGAGCATGACGGTCCCTCGGGG
>contig 200	14	GGCTAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGTGCAAAGATGGGGGCGCTG AGTTACAGAGTGGGGCATGACGGTCCCTGGGGCAAACATACTACTTCTCCGCCAAAGTAAAGTGGGC TTGAGC
>contig 201	14	ATCTCGAGGTGTCAAGCTCATGAATGCACAAAGCTAGCGGAAGGCACAAGTGCAAAGATGGGGGCGC TGAGTTACAGAGTGGGGCATGACGGTCCCTGGGGCAAACATACTACTTCTCCGCCAAAGTAAAGTGGG GCTTGAGC
>contig 202	3	GCGGAAGGCACAAGTGCAAAGATGGGGGCGCTGAGTTACAGAGTGGAGCATGACGGTCCCTGGGGCA AACATACTACTTCTCCGCCAAAGTAAAGTGGGC
>contig 203	2	GCTTGAGCAAATGAACTGTGCGAATCTAGAAGAAACCACGAAGTGGACGCGCCGACGAAGTGTG AAGCTCTCCATGGTTTCGTGCCCTAAGTCCGAGG
>contig 204	2	ACAGCTGGTCTCTCCATGGTTTCGTGCCCTAAGTCCGAGGTAGGCAGCACGAGGAGGTATTGCTAGC ATGATGGGTGCAATGTTCCGAGTGAAGACGAG
>contig 205	5	CCAGGGTTGGCAGCACGAGGAAGTATGGCTGTGTAGCATGATACTGGGTGCAAGTTCCGTGCGGAGAC GAAAGGAGTTGCAGCGAAAGTAATGCGTCGGGTCGCCGTATCATCTAGTGGGGGAG
>contig 206	27	TCTCGAGGAGTATTGCTAGCATGATGGGTGCAATGTTCCGAGTGAAGACGAAAGGAGTAGCAGCG AAAGTAATGCGTCGGGTCGCCGCATCAGCCAGGTGGGGGAGGGTTGTACGTCCTCAGAGAAGGGGC
>contig 207	7	CAATGTTCCGAGTGAAGACGAAAGGAGTAGCAGCGAAAGTAATGCGTCGGGTCGCCGCATCAGCCA GGTGGGGTAGGGTTGTACGTCCTCAGAGAAGGGGC
>contig 208	10	AATGTTCCGAGTGAAGACGAAAGGAGTAGCAGCGAAAGTAATGCGTCGGGTCGCCGCATCAGCCAG GTGGGGGAGTGTGTCACGTCTCAGAGAAGGGGCAAAGTAAAGCGTGC
>contig 209	4	CGTCGGGTCGCCGCATCAGCCAGGTGGGGGAGGGTTGTACGTCCTCAGAGAAGGGGCAAAGTAAAG CGTGCAGATTGGCATCAAACGCTTGGAGAGGGGC
>contig 210	4	GTCGGGTGCGCCGCATCAGCCAGGTGGGGGAGTGTGTACGTCCTCAGAGAAGGGGCAAAGTAAAGC

		GTGCGGATTGGCATCAAAC TGCCTTGGAGAGGGGAGGC
>contig 211	6	ATCTATTGGCTTGGCCGAGTTAGGCATGCCGACCCGATTAAGTTTGGGGAGCATGTCGCTTGTCTTG GACATGACTATGAAGGGAGCCGAAGCATAACGAGGGGC
>contig 212	4	GGAGCCGAAGCATAACGAGGGGCACAGCTGGTCGGGAGCTATTGCCGCTTCCTGATGAGCCCATGGC GGGGCGAAACCAGTCTGCGCGCACAGGCAGGACGGGCG

Table S3. Retrozyme-specific small RNAs in *N. benthamiana* plants. Small RNAs sequence reads, which exactly match the retrozyme sequences, were identified in publicly available libraries of HTS reads obtained for small RNA fractions isolated from different organs of *N. benthamiana* plants.

Dataset	Tissue	Run	Number of matches	Total for dataset
Experiment 1				
SRX1081187	Root	SRR2087151	92	214
		SRR2087152	122	
SRX1081185	Leaf	SRR2087149	132	215
		SRR2087150	83	
SRX1081184	Seedling	SRR2087147	74	306
		SRR2087148	232	
SRX1081183	Flower	SRR2087143	369	450
		SRR2087144	81	
SRX1081188	Stem	SRR2087153	47	267
		SRR2087154	220	
Experiment 2				
SRX2502227	Leaf	SRR5186275	114	114
SRX2502225	Root	SRR5186273	59	59
SRX2502223	Stem	SRR5186271	105	105

Table S4. Primers used in this study.

NbRZ1 cloning		
NbRZ-P-Xho	CGCTCGAGATGTTAACCTTTGTTATAAAAGGAGC	
NbRZ-3-M	GCTCTAGAGCAGTGGGAGGAGCCAGGTGT	
LTR-GFP cloning		
RZ-LTR-P	CGCGAATTCTGTCACGACCCGATTGTCGTG	
RZ-LTR-M	CCGCCATGGTGTGTCACGGGACGAGAGTCCG	
35S-NbRZ1-Tag cloning		
NbRz-FLAG1-P	GATTACAAGGATGACGATGACAAGGGGTGGCTCGCACTGAAGA	
NbRz-FLAG1-M	CTTGTGTCATCGTCATCCTTGTAATCCCTAGGCAACGCGCACCCG	
Bisulfite sequencing		
RZ-BisS-P1	ATAAGATGTTAAYTTTGTATATAAAGGAG	
RZ-BisS-M1	CCCACCATAAACRCRCAACAACA	
prPDSb-P320	GTGGGAGATGTGTGYAAAGTGGT	
prPDSb-M	CTRTTACCCACAAAAARATACCCCT	
Detection of Group 1 retrozyme RNA in <i>N. benthamiana</i> plants		
RZ-PP4-F	TGCCCCAAGGATCCCGTACAA	Expected product size: 117 bp
RZ-PP4-R	AATGGTCTGCAGGGGCAAG	
Detection of Group 2 retrozyme RNA in <i>N. benthamiana</i> plants		
RZ8-PP5-F	TCAACTTCTGTGGCGAGGTG	Expected product size: 217 bp
RZ8-PP5-R	AGAGCTTCACACTTCGTCGG	
RZ9-PP1-F	GAAGTGTGATGCCGTCTCCA	Expected product size: 111 bp
RZ9-PP1-R	CCTTTCGTCTTCCACACGGA	
Detection of NbRZ1-Tag		
NbRZ-int-M	TCTGCCCCAAGGATCCCGTACAA	Expected product size: 176 bp
FLAG-det-P	GATTACAAGGATGACGATGACAAG	
Detection of circular (+) strand of NbRZ1-Tag in upper leaves		
RZ (-) circ-det-D1	GAGGGCGTGCTGCGTTTTTC	Expected product size: 525 bp
FLAG-det-M2	AGCCACCCCTTGTCATCGTC	
Detection of NbRZ circular (+) strand		
RZcirc-det-C1	AGTCCTTCTCCCCCTACAGC	Expected product size: 665 bp
RZ-PP4-R	AATGGTCTGCAGGGGCAAG	
Detection of NbRZ circular (-) strand		
RZcirc-det-A1	CTTGCCCCTGCAGACCATT	Expected product size: 588 bp
RZcirc-det-A2	TTGTACGGGATCCTTGGGCA	
Detection of GFP mRNA		
GFP-C3-PP1-F	TCAGTGGAGAGGGTGAAGGT	Expected product size: 240 bp
GFP-C3-PP1-R	GCGTCTTGTA GTTCCCCTCA	
Detection of F-box protein gene and mRNA		
F-Box-F	GGCACTCACAAACGTCTATTTTC	Expected product size: 127 bp
F-Box-R	ACCTGGGAGGCATCCTGCTTAT	
Retrozyme 5'-RACE		
RZ-RACE-OUT	ACGCGCAACAACAGCAAGTAC	
RZ-RACE-IN	TCCGGCTCTGATACCACTTGT	
LTR-GFP 5'-RACE		
GFP-C3-DetR (outer)	ATGTGTAATCCCAGCAGCAGT	
GFP-C3-ovlX-M (inner)	ATAGTTGTACTCCAGTTTGTGTCCG	