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Tai21      ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
Tai30      ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
Tai15b     ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
Tai15a     ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
GE22850    ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
GE19852    ATGCAAGAGGTGACCTCATTCAAG-TGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 59
Tai6       ATGCAAGAGGTGACCTCATTCAAG-TGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 59
Tai18      ATGCAAGAGGTGACCTCATTCAAG-TGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 59
Tai59      ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
Tai37      ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
Tai26      ATGCAAGAGGTGACCTCATTCAAG-TGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 59
Tai27      ATGCAAGAGGTGACCTCATTCAAGCTGGTTCTTCTCGGAGACGGAGGAACTGGGAAAGCC 60
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Tai21      ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 120
Tai30      ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 120
Tai15b     ACATTTATCAAGCGACACCTGACTGGCGAGTTCGATAGGCGATAACATTGCGATCCTGGGT 120
Tai15a     ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 120
GE22850    ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 120
GE19852    ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 119
Tai6       ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 119
Tai18      ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 119
Tai59      ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 120
Tai37      ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 120
Tai26      ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 119
Tai27      ACATTTATCAAGCGACACCTGACCGGCGAGTTCGAGAGGCGATAACATTGCGACCCTGGGT 120
*****

Tai21      GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180
Tai30      GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180
Tai15b     GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180
Tai15a     GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180
GE22850    GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180
GE19852    GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 179

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Tai6 GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 179
 Tai18 GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 179
 Tai59 GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180
 Tai37 GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180
 Tai26 GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 179
 Tai27 GTGGAGGTCCATCCAATACTCTTCCACACCAACCGAGGAGTGTACCGCTTCTATGTGTGG 180

Tai21 GACTGCGGTCAGGAGAAGTTCGGTGGCTACAAGATGGGTATTATGTCCAAGGTCAA 240
 Tai30 GACTGCGGTCAGGAGAAGTTCGGTGGCTACAAGATGGGTATTATGTCCAAGGTCAA 240
 Tai15b GACTGCGGTCAGGAGAAGTTCGGTAGCCTACAAGATGGGTATTATGTCCAAGGTCAA 240
 Tai15a GACTGCGGTCAGGAGAAGTTCGGTGGCTACAAGATGGGTATTATGTCCAAGGTCAA 240
 GE22850 GACTGCGGTCAGGAGAAGTTCGGTGGCTACAAGATGGGTATTATGTCCA----- 234
 GE19852 GACAC-----AAGATGGGTATTATGTCCAAGGTCAA 210
 Tai6 GACAC-----AAGATGGGTATTATGTCCAAGGTCAA 210
 Tai18 GACAC-----AAGATGGGTATTATGTCCAAGGTCAA 210
 Tai59 GACTGCGGTCAGGAGAAGTTCGGTGGCTACAAGATGGGTATTATGTCCAAGGTCAA 240
 Tai37 GACTGCGGTCAGGAGAAGTTCGGTGGCTACAAGATGGGTATTATGTCCAAGGTCAA 240
 Tai26 GACTGCGGTCAGGAGAAGTTCGGTGGCTACAAGATGGGTATTATGTCCAAGGTCAA 239
 Tai27 GACTGCGGTCAGGAGAAGTTCGGT-----AGACGGGTATTATGTCCAAGGTCAA 232

Tai21 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 300
 Tai30 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 300
 Tai15b TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 300
 Tai15a TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 300
 GE22850 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 294
 GE19852 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 270
 Tai6 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 270
 Tai18 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 270
 Tai59 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 300
 Tai37 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 300
 Tai26 TGTGCCATAAAATTGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 299
 Tai27 TGTGCCATAATAATGTTTCGACGTGAGCTCGAGAATTACCTACAAGAATGTGGCACGTTGG 292

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Tai21	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	360
Tai30	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	360
Tai15b	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	360
Tai15a	CACCGCGACTTGGTGAGTGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	360
GE22850	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	354
GE19852	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	330
Tai6	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	330
Tai18	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	330
Tai59	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	360
Tai37	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	360
Tai26	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	359
Tai27	CACCGCGACTTGGTGAGGGTATGCGGCAATATTCCGATTGTTTTGTGTGGAAACAAGGTG	352

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Tai21	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	420
Tai30	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	420
Tai15b	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAGGAAAAACCTC	420
Tai15a	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	420
GE22850	GATATCAAGCAACGGAAGGTTAGGCCCTAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	414
GE19852	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	390
Tai6	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	390
Tai18	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	390
Tai59	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	420
Tai37	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	420
Tai26	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	419
Tai27	GATATCAAGCAACGGAAGGTTAGGCCCAGGCGCTTTGACTTTCATCGTAAGAAAAACCTC	412

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Tai21	CACTACATTGAAATGTCCGCCAAGTCAAACCTATA----ACATTGAGAGTCCCTTCGTCTA	476
Tai30	CACTACATTGAAATGTCCGCCAAGTCAAACCTATA----ACATTGAGAGTCCCTTCGTCTA	476
Tai15b	CACTACATTGAAATGTCCGCCAAGTCAAACCTATA----ACATTGAGAGTCCCTTCGTCTA	476
Tai15a	CACTACATTGAAATGTCCGCCAAGTCAAACCTATA----ACATTGAGAGTCCCTTCGTCTA	476

GE22850 CACTACATTG-----TCCGCCAAGTCAAACATAA----ATATTGAGAGTCCCTTCGTCTA 465
 GE19852 CACTACATTGAAATGTCCGCCAAGTCAAACATAA----ACATTGAGAGTCCCTTCGTCTA 446
 Tai6 CACTACATTGAAATGTCCGCCAAGTCAAACATAA----ACATTGAGAGTCCCTTCGTCTA 446
 Tai18 CACTACATTGAAATGTCCGCCAAGTCAAACATAA----ACATTGAGAGTCCCTTCGTCTA 446
 Tai59 CACTGCATTGAAATGTCCGCCAAGTCAAACATAA**CTTGA**CATTGATAGTCCCTTCGTCTA 480
 Tai37 CACTGCATTGAAATGTCCGCCAAGTCAAACATAA**CTTGA**CATTGATAGTCCCTTCGTCTA 480
 Tai26 CACTACATTGAAATGTCCGCCAAGTCAAACATAA----ACATTGAGAGTCCCTTCGTCTA 475
 Tai27 CACTACATTGAAATGTCCGCCAAGTCAAACATAA----ACATTGAGAGTCCCTTCGTCTA 468

Tai21 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 536
 Tai30 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 536
 Tai15b TCTGTTGCGGAAGTTGATTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 536
 Tai15a TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTTAAGAACCCCGCTCTAAA 536
 GE22850 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 525
 GE19852 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGGACCCCGCTCTAAA 506
 Tai6 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGGACCCCGCTCTAAA 506
 Tai18 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGGACCCCGCTCTAAA 506
 Tai59 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 540
 Tai37 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 540
 Tai26 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 535
 Tai27 TCTGTTGCGGAAGTTGGTTGATGATCCCAACTTGCAATTGGTCAAGAACCCCGCTCTAAA 528

Tai21 ACCCCCAGAAGTGGTTTTTACCGACGACG**CG**-----AATGGA 571
 Tai30 ACCCCCAGAAGTGGTTTTTACCGACGACG**CG**-----AATGGA 571
 Tai15b ACCCCCAGAAGTGGTTTTTACCGACGACG**CG**-----AATGGA 571
 Tai15a ACCCCCAGAAGTGTCTTTTACCGACGAGATGCGCCGTCAAGTGAACGCGGGTTAATGGA 596
 GE22850 ACCCCCAGATGTGGTTTTTACCGACGAGATGCGCCGTCAAGTGAACGCGGGTTAATGGA 585
 GE19852 ACCCCCAGAAGTGGTTTTTACCGACGAGATGCGCCGTCAAGTGAACGCGGGTTAATGGA 566
 Tai6 ACCCCCAGAAGTGGTTTTTACCGACGAGATGCGCCGTCAAGTGAACGCGGGTTAATGGA 566
 Tai18 ACCCCCAGAAGTGGTTTTTACCGACGAGATGCGCCGTCAAGTGAACGCGGGTTAATGGA 566
 Tai59 ACCCCCAGAAGTGGTTTTTACCGACGAGATGCGCCGTCAAGTGAACGCGGGTTAATGGA 600
 Tai37 ACCCCCAGAAGTGGTTTTTACCGACGAGATGCGCCGTCAAGTGAACGCGGGTTAATGGA 600

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Tai26      ACTCCCAGAAGTTGTTTTTACCGACGAGATGCGCCGTCAAGTGGAACGCGGGTTAATGGA 595
Tai27      ACCCCCAGAAGTGGTTTTTACCGACGAGATGCGCCGTCAAGTGGAACGCGGGTTAATGGA 588
          ** ***** ** ** ********** *****

Tai21      GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 620
Tai30      GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 620
Tai15b     GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 620
Tai15a     GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 645
GE22850    GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 634
GE19852    GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 615
Tai6       GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 615
Tai18      GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 615
Tai59      GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 649
Tai37      GGCCAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 649
Tai26      GGCAAGCTTCTATCCTCTGCCCACTTATAACGATGATGATGATCTGTAA 644
Tai27      G-----ATGTTAATGATGATGATCTGTAA 612
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FIGURE S3.—Alignment of *ran-like* disabled sequences from several strains of *D. yakuba*. See Materials and Methods and Results for more details.

Blue highlights deletions or insertions that change the frame (i.e. deletions that are not multiple of 3 base pairs). Deletions with insertion are marked in orange and they all change frame. The first premature stop codon in frame is shown in red.