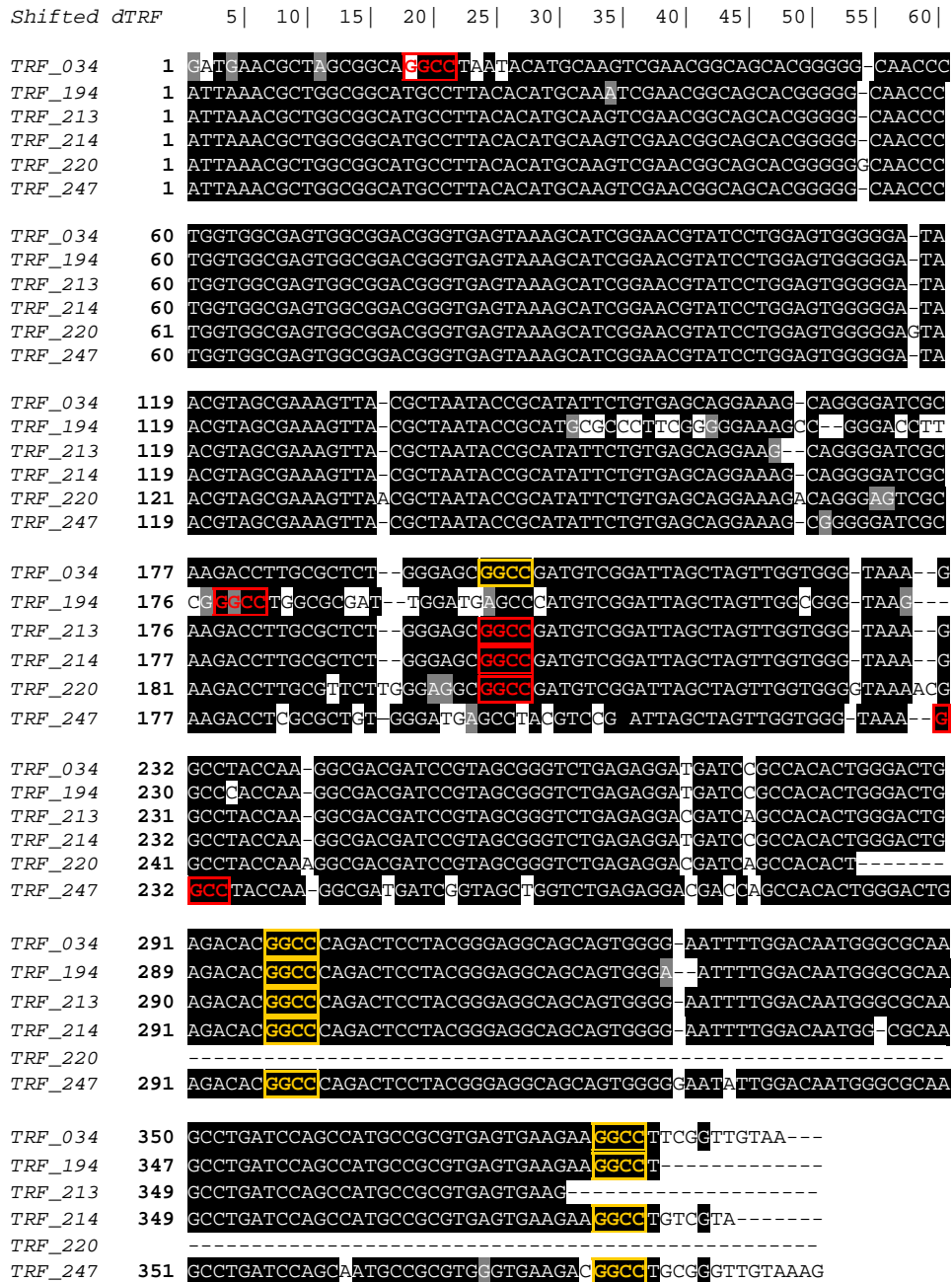


**Additional file 7****Figure AF7.1 – Alignment of sequences affiliating with *Rhodocyclus tenuis* (accession number AB200295), and exhibiting different T-RFs.**

Sequence similarities are given in black. The first HaeIII-related ‘GG<sup>^</sup>CC’ restriction sites are given in red. Further restriction sites are given in yellow. The horizontal scale bar provides the number of characters per line, including alignment gaps. The bold numbers indicate the actual position in the sequence, excluding alignment gaps. The shifted dT-RF size is obtained by adding the forward primer length (20 bp) and subtracting the shift between dT-RFLP and eT-RFLP profiles (-5 bp) to the position of the first restriction site.

Weissbrodt D.G. and Shani N., et al., **Additional files**, PyroTRF-ID.

Shifted dTRF      5| 10| 15| 20| 25| 30| 35| 40| 45| 50| 55| 60|

TRF\_161      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA  
 TRF\_163      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA  
 TRF\_164      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA  
 TRF\_165      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA  
 TRF\_166      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA  
 TRF\_168      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA  
 TRF\_171      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA  
 TRF\_174      1 GATC-AACGCTAGCGG-CGTGCCTTATG-CATGC-AAGTC-GAACGGTCTTAAG----CA

TRF\_161      52 ATT--AAGA--TAGTGGCGAACGG-TGAGTAACGCGTAAGTAACCTACCTACCTAAGTGGGG  
 TRF\_163      52 ATT--AAGA--TAGTGGCGAACGGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGG  
 TRF\_164      52 ATT--AAGA--TAGTGGCGAACGGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGG  
 TRF\_165      52 ATT--AAGA--TAGTGGCGAACGGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGG  
 TRF\_166      52 ATT--AAGA--TAGTGGCGAACGGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGG  
 TRF\_168      52 ATT--AAGA--TAGTGGCGAACGGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGG  
 TRF\_171      56 GTT--GTA--TCTTAGTGGCGAACGGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGG  
 TRF\_174      58 ATT--AAGA--TAGTGGCGAACGGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGG

TRF\_161      107 -A--TAGCTTCGGG--AAAC--T--GAGGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT  
 TRF\_163      108 GA--TAGCTTCGGG--AAAC--T--GAAGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT  
 TRF\_164      108 GA--TAGCTTCGGG--AAACGT--GAAGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT  
 TRF\_165      108 GAGTAGCTTCGGG--AAACGT--GAAGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT  
 TRF\_166      108 GAGTAGCTTCGGG--AAACGT--GAAGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT  
 TRF\_168      108 GAGTAGCTTCGGG--AAACGTAGAAGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT  
 TRF\_171      114 GAGTAGCTTCGGG--AAACGT--GAAGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT  
 TRF\_174      118 GATAGCTTCGGG--AAAC--T--GAAGGTAATA--CCGC--ATGTGGTG--GGCC--G--ACATATGTT

TRF\_161      159 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG  
 TRF\_163      161 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG  
 TRF\_164      162 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG  
 TRF\_165      163 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG  
 TRF\_166      164 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG  
 TRF\_168      167 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG  
 TRF\_171      169 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG  
 TRF\_174      172 GGTTCACTAAAGCCGTAAGGCGCTT--GGTGAGGGGC--TTGCGTCCGATTAGCTAG--TTG

TRF\_161      216 GTGGGGTAA--TGGCC--TACCAAGGCTT--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC  
 TRF\_163      217 GTGGGGTAA--TGGCC--TACCAAGGCTT--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC  
 TRF\_164      218 GTGGGGTAA--C--GGCC--TACCAAGGCGA--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC  
 TRF\_165      222 GTGGGGTAA--GTG--ACTACCAAGGCTT--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC  
 TRF\_166      222 GTGGGGTAA--GTG--ACTACCAAGGCTT--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC  
 TRF\_168      225 GTGGGGTAA--TGGCC--TACCAAGGCTT--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC  
 TRF\_171      225 GTGGGGTAA--TGGCC--TACCAAGGCTT--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC  
 TRF\_174      231 GTGGGGTAA--TGGCC--TACCAAGGCTT--CGATCGGTAGCTGGTCTGAGAGGATGATCAGCC

TRF\_161      274 AC--ACTGGGAC--TGAGAC--ACGGTCCAGACTCCTACGGGAGGCA--GCAGTGGGGAA--TAT  
 TRF\_163      275 AC--ACTGGGAC--TGAGAC--ACGGTCCAGACTCCTACGGGAGGCA--GCAGTGGGGAA--TAT  
 TRF\_164      276 ACCACGGTACCGGTCTTAG--ACGACCGGAAACCCGACCCCTACCTTACCGGTAACCGGGA  
 TRF\_165      281 AC--ACTGGGAC--TGAGAC--ACGGTCCAGACTCCTACGGGAGGCA--GCAGTGGGGAAATAT  
 TRF\_166      280 AC--ACTGGGAC--TGAGAC--ACGGTCCAGACTCCTACGGGAGGCA--GCAGTGGGGAAATAT  
 TRF\_168      284 AC--ACTGGGAC--TGAGAC--ACGGTCCAGACTCCTACGGGAGGCA--GCAGTGGGGAA--  
 TRF\_171      284 AC--ACTGGGAC--TGAGAC--ACGGTCCAGACTCCTACGGGAGGCA--GCAGTGGGGAA--  
 TRF\_174      289 ACTACTGGGAC--TGAGAC--AC-----

TRF\_161      330 TGGTCAATGGACGCAAGTCTGAACCCAGCATGCGCGTGCAGGAA-----  
 TRF\_163      330 TGGTCAATGGGCGCAAGCTCTGAACCCAGCAATGCGCGTGCAGTATGAA--GGCC--TTAGGGTT  
 TRF\_164      335 CGGACGAC--TACGTAAGGCTAAAGGTAATTTAGGTTACGGAAACTAAGGTAGGGGACG  
 TRF\_165      337 TGGTCAATGGG-----  
 TRF\_166      338 TGGTCAATGGGCGCAAGCTCTGAACCCAGCAACCGCGCGTGCAGGATGAAGC-----  
 TRF\_168      -----  
 TRF\_171      -----  
 TRF\_174      -----

TRF\_161      -----  
 TRF\_163      390 GTAAAGCTCTTTCCGACCGCAGCATGATGACGGTAGCGTGAGAAGAAGCCCCGGCTAACT  
 TRF\_164      395 GAACCTACC-----  
 TRF\_165      -----  
 TRF\_166      -----

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TRF_168 -----  
TRF_171 -----  
TRF_174 -----  
  
TRF_161 -----  
TRF_163 450 TCGTGCCAGCAGCCGCGGTAAT  
TRF_164 -----  
TRF_165 -----  
TRF_166 -----  
TRF_168 -----  
TRF_171 -----  
TRF_174 -----
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**Figure AF7.2 – Alignment of sequences affiliating with *Dehalococcoides* sp. (accession number EF059529), and exhibiting different dT-RFs.**

Sequence similarities are given in black. The first HaeIII-related ‘GG<sup>^</sup>CC’ restriction sites are given in red. Further restriction sites are given in yellow. The horizontal scale bare provides the number of characters per line, including alignment gaps. The bold numbers indicate the actual position in the sequence, excluding alignment gaps. The shifted dT-RF size is obtained by adding the forward primer length (20 bp) and subtracting the shift between dT-RFLP and eT-RFLP profiles (-5 bp) to the position of the first restriction site.