

Conserved sequence motif #1

IGR 23711-540 (*TcIII-like*)/1-348

IGR_237/1-538_(TcII-like)/1-346

JGR_4788/1-550_(TcII-like)/1-353

IGR_246/1-542_(TcII-like)/1-345

IGR_246/1-544_(TcII)/1-345

IGR_246/1-540_(Tcl_JRcl4)/1-343

IGR_246/1-543_(TcIII-like)/1-346

Consensus

IGR_23711-540_(TcIII-like)/1-348

IGR_237/1-538_(TcII-like)/1-346

JGR_4788/1-550_(TcII-like)/1-353

IGR_246/1-542_(TcII-like)/1-345

IGR_246/1-544_(TcII)/1-345

IGR_246/1-540_(Tcl_JRcl4)/1-343

IGR_246/1-543_(TcIII-like)/1-346

Consensus

IGR_237/1-540_(TcIII-like)/1-348

IGR_237/1-538_(TcII-like)/1-346

IGR_4788/1-550_(TcII-like)/1-353

IGR_246/1-542_(TcII-like)/1-345

IGR_246/1-544_(TcII)/1-345

IGR_246/1-540_(Tcl_JRcl4)/1-343

IGR_246/1-543_(TcIII-like)/1-346

Consensus

IGR_23711-540_(TcIII-like)/1-348

IGR_237/1-538_(TcII-like)/1-346

IGR_4788/1-550_(TcII-like)/1-353

IGR_246/1-542_(TcII-like)/1-345

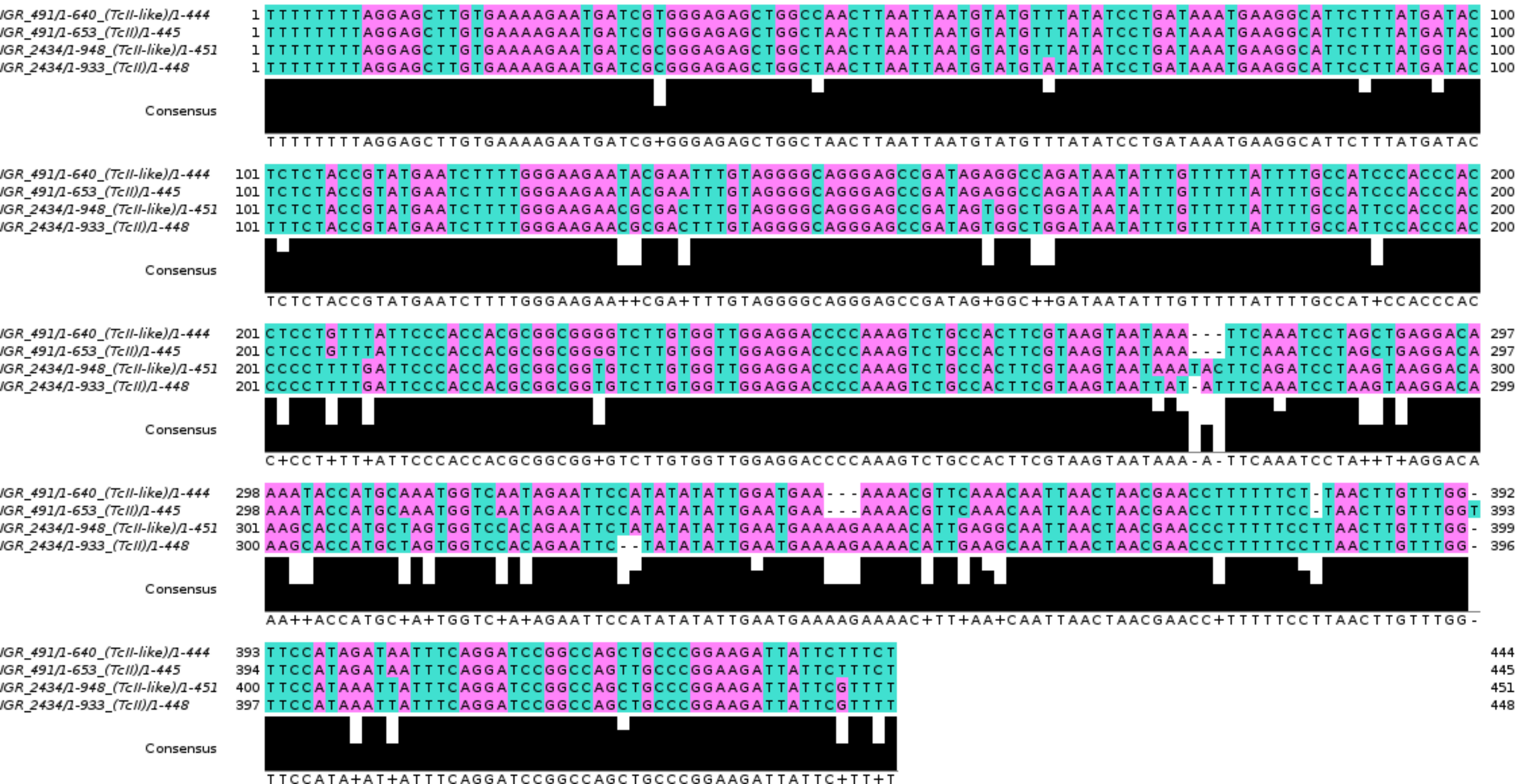
IGR_246/1-544_(TcII)/1-345

IGR_246/1-540_(Tcl_JRcl4)/1-343

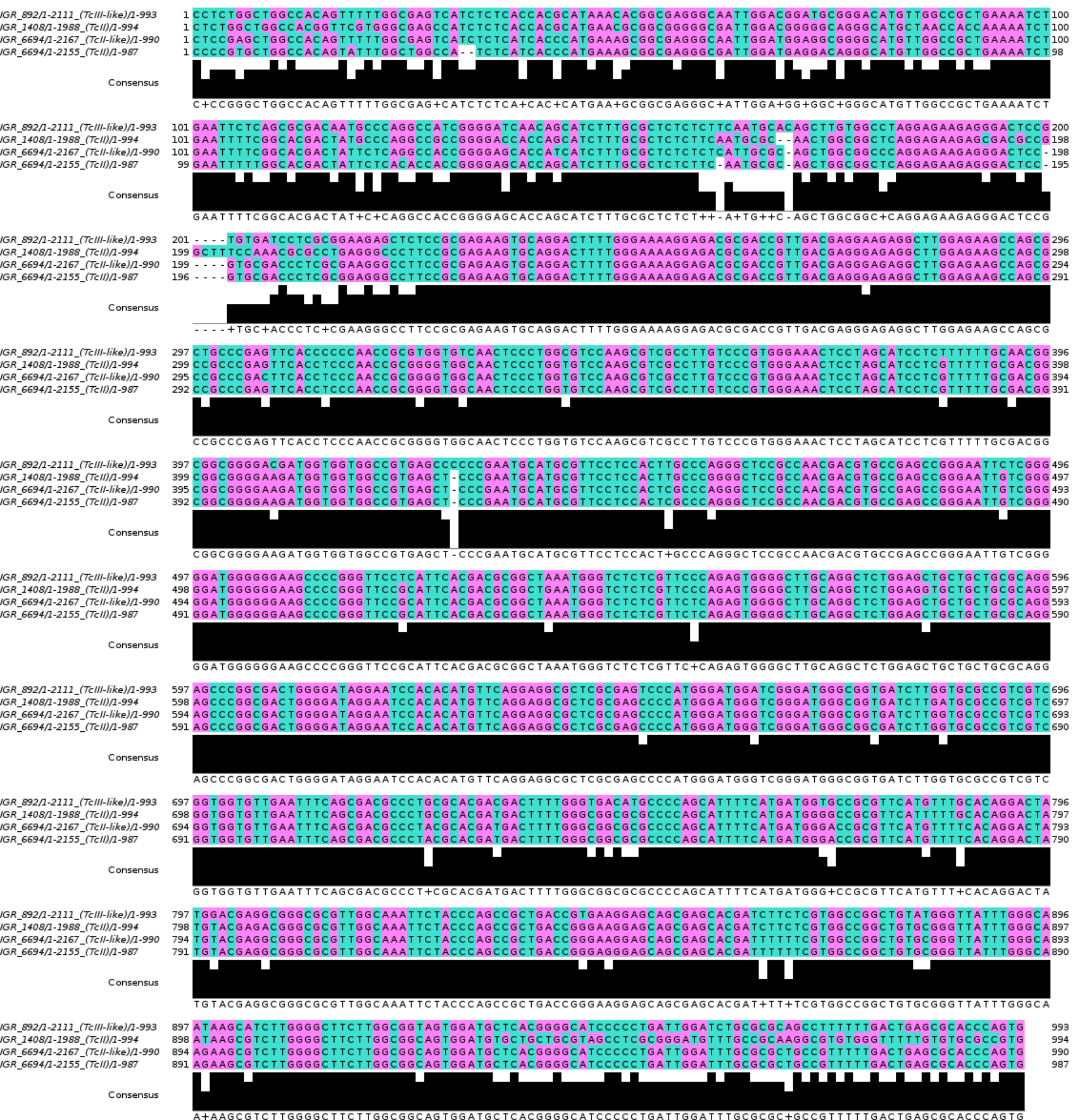
IGR_246/1-543_(TcIII-like)/1-346

Consensus

Conserved sequence motif #2



Conserved sequence motif #3



Conserved sequence motif #4

JGR_1869/1-1196 (TcIII-like)/1-434 1 ACGTGCATCTATACAGGACC AAAT AAAAGGG CAGGGGTATTTCATCGATCC AACCTGTTTGTTTACAATTTGATGATTGGATTGGTTACC AAAGAC ACCGC 100
JGR_1869/1-1190 (TcI_SylvioX10)/1-430 1 ATTTGCATCTATACAGGACC AAAT AAAAGGG CAGGGTTCCTTCATCGATCC AACCTGTTTGTTTACAATTTGATGATTGAATTGGTTACC AAAGAC ACCGC 100
JGR_1861/1-1131 (TcIII-like)/1-434 1 ATGTGCATCTATACAGGAAC AAAT AAAAGGG CAGGGGTATTTCATCGATCC AACCTGTTTGTTTACAATTTGATGATTGGATTGGTTACC AAAGAC ACCGC 100
JGR_1861/1-1147 (TcI_SylvioX10)/1-430 1 ATGTGCATCTATACAGGACC AAAT AAAAGGG CAGGGGTCTTTCATCGTTC AACCTGTTTGTTTACAATTTGATGATTGAATTGGTTACC AAAGAC ACCGC 100
JGR_1861/1-1145 (TcII-like)/1-437 1 ATGTGCATCTATACAGGACC AAAT AAAAGGG CAGGGGCCCTTCATCGATCC ATCCTGTTTGTTTACAATTTGATGACTGAATTGGTTACC AAAGAC ACCGC 100
JGR_1861/1-1165 (TcII)/1-437 1 ATGTGCATCTATACAGGACC AAAT AAAAGGG CAGGGGCCCTTCATCGATCC ATCCTGTTTGTTTACAATTTGATGACTGAATTGGTTACC AAAGAC ACCGC 100

Consensus

ATGTGCATCTATACAGGACC AAAT AAAAGGG CAGGGGTCTTTCATCGATCC AACCTGTTTGTTTACAATTTGATGATTGAATTGGTTACC AAAGAC ACCGC

JGR_1869/1-1196 (TcIII-like)/1-434 101 GTTGGAGGATGGCGAGGAGTAGTTGTCTCGTCCATCTCGCTCAGCCCCGACGACGACTACTCTCCACGCAGAGGAAAGTCCGACGGTTGTGGGACCCCG 200
JGR_1869/1-1190 (TcI_SylvioX10)/1-430 101 GTTGGAGGATAGCGAGGAGTAGTTGTCTCGTCCATCTCACTCAG - CCCCCGACGACGACTACTCTCCACGCAGAGGAAAGTCCGACGGTTGTGGGACCCCG 199
JGR_1861/1-1131 (TcIII-like)/1-434 101 GTTGGAGGATGGCGAGGAGTAGTTGTCTCGTCCATCTCGCTCAGCCCCGACGACGACTACTCTCCACGCAGAGGAAAGTCCGACGGTTGTGGGACCCCG 200
JGR_1861/1-1147 (TcI_SylvioX10)/1-430 101 GTTGGAGGATAGCGAGGAGTAGTTGTCTCGTCCATCTCACTCAG - CCCCCGACGACGACTACTCTCCACGCAGAGGAAAGTCCGACGGTTGTGGGACCCCG 199
JGR_1861/1-1145 (TcII-like)/1-437 101 GTTGCAGGATAGCGAGGAGTAGTTGTCTCGTCCATCTCACTCAGCCCCGACGACGACTACTCTCCACGCAGAGGAAAGTCCGACGGTTGTGGGACCCCG 200
JGR_1861/1-1165 (TcII)/1-437 101 GTTGCAGGATAGCGAGGAGTAGTTGTCTCGTCCATCTCACTCAGCCCCGACGACGACTACTCTCCACGCAGAGGAAAGTCCGACGGTTGTGGGACCCCG 200

Consensus

GTTGGAGGATAGCGAGGAGTAGTTGTCTCGTCCATCTCACTCAGCCCCGACGACGACTACTCTCCACGCAGAGGAAAGTCCGACGGTTGTGGGACCCCG

JGR_1869/1-1196 (TcIII-like)/1-434 201 GGAAAAACCTGCTGCTTTGCGGGGTTACGGCGAGCCCGGCTATCATGGATTGCTTTGTGACCCAAACTGCCCCACCGTTGATGTATGCATGTGGACTCAAC 300
JGR_1869/1-1190 (TcI_SylvioX10)/1-430 200 GGAAAAACCCGCTGCTTTGCGGGGTTACGGCGAGCCCGGCCATCATGGATTGCTTTGTGACCCAAACTGCCCCACCGTTGATGTATGCATGTGGACTCAAC 299
JGR_1861/1-1131 (TcIII-like)/1-434 201 GGAAAAACCTGCTGCTTTGCGGGGTTACGGCGAGCCCGGCTATCATGGATTGCTTTGTGACCCAAACTGCCCCACCGTTGATGTATGCATGTGGACTCAAC 300
JGR_1861/1-1147 (TcI_SylvioX10)/1-430 200 GGAAAAACCCGCTGCTTTGCGGGGTTACGGCGAGCCCGGCCATCATGGATTGCTTTGTGACCCAAACTGCCCCACCGTTGATGTATGCATGTGGACTCAAC 299
JGR_1861/1-1145 (TcII-like)/1-437 201 GGAAAAACCTGCCACTTTGCGGGGTTACGGCGAGCCCGGCTATCATGGATTGCTTTGTGACCCAAACTGCCCCACCGTTGATGTATGCATGTGGACTCAAC 300
JGR_1861/1-1165 (TcII)/1-437 201 GGAAAAACCTGCCACTTTGCGGGGTTACGGCGAGCCCGGCTATCATGGATTTCTTTGTGACCCAAACTGCCCCACCGTTGATGTATGCATGTGGACTCAAC 300

Consensus

GGAAAAACCTGCTGCTTTGCGGGGTTACGGCGAGCCCGGCTATCATGGATTGCTTTGTGACCCAAACTGCCCCACCGTTGATGTATGCATGTGGACTCAAC

JGR_1869/1-1196 (TcIII-like)/1-434 301 CCCTTCTGAAGTGGGAAATGTTGAGCCCATCAAAATGAATTTTGATCTTCTT - - - TTGTTGTTGTTGTTGTTGTTGTTCCGTGTCTTTTTGTAGGAATAGGA 396
JGR_1869/1-1190 (TcI_SylvioX10)/1-430 300 CCCTTCTGAAGTGGGAAATGTTGAGCCCATCAAAATAAACCGTGATCTTCTT - - - - - TTGTTGTTGTTGTTGTTGTTGTTCCGTGTCTTTTTGTAGGAATAGGA 392
JGR_1861/1-1131 (TcIII-like)/1-434 301 CCCTTCTGAAGTGGGAAATGTTGAGCCCATCAAAATGAATTGTGATCTTCTT - - - TTGTTGTTGTTGTTGTTGTTGTTCCGTGTCTTTTTGTAGGAATAGGA 396
JGR_1861/1-1147 (TcI_SylvioX10)/1-430 300 CCCTTCTGAAGTGGGAAATGTTGAGCCCATGAAAATAAACCGTGATCTTCTT - - - - - TTGTTGTTGTTGTTGTTGTTGTTCCGTGTCTTTTTGTAGGAATAGGA 392
JGR_1861/1-1145 (TcII-like)/1-437 301 CCCTTCTGAAGTGGGAAATGTTGAGCCCATCAAAATAAACTGTGATTTTCTTTTTTTTGTGTTGTTGTTGTTGTTGTTGTTCCGTGTCTCTTTGTAGGAATAGGA 400
JGR_1861/1-1165 (TcII)/1-437 301 CCCTTCTGAAGTGGGAAATGTTGAGCCCATCAAAATAAACTGTGATTTTCTTTTTTGTGTTGTTGTTGTTGTTTGTGTTCCGTGTCTCTTTGTAGGAATAGGA 400

Consensus

CCCTTCTGAAGTGGGAAATGTTGAGCCCATCAAAATAAACTGTGATCTTCTTTTTT - TTGTTGTTGTTGTTGTTGTTGTTCCGTGTCTTTTTGTAGGAATAGGA

JGR_1869/1-1196 (TcIII-like)/1-434 397 GGAAAAATTTCTCAGTCAGACGCATATTGTGATTTATTG 434
JGR_1869/1-1190 (TcI_SylvioX10)/1-430 393 GGAAAAATTTCTCAACCAGACGCATATTGTGTTTTCTTG 430
JGR_1861/1-1131 (TcIII-like)/1-434 397 GGAAAAATTTCTCAGTCAGACGCATATTGTGTTTTCTTG 434
JGR_1861/1-1147 (TcI_SylvioX10)/1-430 393 GGAAAAATTTCTCAACCAGACGCATATTGTGTTTTCTTG 430
JGR_1861/1-1145 (TcII-like)/1-437 401 GG - AAATGTCTCAGCCAGACGCATATTGTGTTTTCTTG 437
JGR_1861/1-1165 (TcII)/1-437 401 GG - AAATGTCTCAGCCAGATGCATATTGTGTTTTCTTG 437

Consensus

GGAAAAATTTCTCAGCCAGACGCATATTGTGTTTTCTTG

Conserved sequence motif #5

[illegible]

Consensus

ATCCACAACCAACCACCTTCTCTGTTGCCCTCCACGCTGAGGGGGAGTGTGCAACGGCTGCGGGGCCCTTAAA+AAAAAAAAAGACTCCACCTTGTGAGTTTAT

| | | | | | | | | | |
|---|-----|----------------------|------------|--------------|---------------------|--------------------|------------------|------------------|-----|
| <i>JGR_2865/1-830 (TcIII-like)/1-302</i> | 96 | AAGGAGCCCGGCTGCCATAA | CTTTCATGCA | TTTCATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | AGTGTGTGGG - GG | TGTTGGGCCAAACTG | 196 |
| <i>JGR_2865/1-812 (TcI_JRcl4)/1-308</i> | 101 | AAGGAGCCCGGCTGCCATAA | CTTTCATGCA | TTTCATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTATTGTGTGGGGGT | TGTTGGGCCAAACTG | 202 |
| <i>JGR_2865/1-817 (TcI_SylvioX10)/1-305</i> | 98 | AAGGAGCCCGGCTGCCATAA | CTTTCATGCA | TTTCATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTATTGTGTGGGGGT | TGTTGGGCCAAACTG | 199 |
| <i>JGR_2848/1-810 (TcII-like)/1-311</i> | 98 | AAGGAACCCGACTGCCATAA | CTTTCATGCA | TTTATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTAGTGTGTGGG - G | TGTTGGGCCAAACTG | 198 |
| <i>JGR_2848/1-803 (TcIII-like)/1-305</i> | 99 | AAGGAGCCCGGCTGCCATAA | CTTTTATGCA | TTTCATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTAGTGTGTGGG - G | TGTTGGGTCAAAC TG | 199 |
| <i>JGR_2848/1-790 (TcI_JRcl4)/1-307</i> | 100 | AAGGGGCCCGGCTGCCATAA | CTTTCATGCA | TTTCATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTATTGTGTGGGGGT | TGTTGGGCCAAACTG | 201 |
| <i>JGR_2848/1-788 (TcI_SylvioX10)/1-307</i> | 101 | AAGGAGCCCGGCTGCCATAA | CTTTCATGCA | TTTCATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTATTGTGTGGG - G | TGTTGGGCCAAACTG | 201 |
| <i>JGR_2854/1-1199 (TcIII-like)/1-304</i> | 98 | AAGGAGCCCGGCTGCCATAA | CTTTTATGCA | TTTCATTTGTTT | ACGGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTAGTGTGTGGG - G | TGTTGGGTCAAAC TG | 198 |
| <i>JGR_2854/1-1296 (TcII-like)/1-310</i> | 97 | AAGGAGCCCGACTGCCATAA | CTTTCATGCA | TTTCATTTGTTT | ACGGGTGCGTGAGTGT | TGGATGAATTTACTTCTT | GTAGTGTGTGGG - G | TGTTGGGCCAAACTG | 197 |
| <i>JGR_2854/1-462 (TcII)/1-227</i> | 15 | AAGGAGCCCGACTGCCATAA | CTTTCATGCA | TTCTATTGTTT | CA - CGGTGTGTGAGTGT | TGGATGAATTTACTTCTT | GTAGTGTGTGGG - T | GGTTGGGCCAAACTA | 114 |

Consensus

AAGGAGCCCCGGCTGCCATAACTTTTCATGCATTCAATTTGTTTACGGGGTGTGTGAGTGTGGGATGAATTTACTTCGTAGTGTGTGGGGGTGTTGGGCCAAACTG

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|---|-----|--|--|---|-----|
| <i>UGR_2865/1-830 (TcIII-like)/1-302</i> | 197 | CCACTCCCCGTTGTGTCTCACACACACACAAACCTCTCTCCCTTTCTCGGTGTG | --- | TCTTTTTTCTTTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 291 |
| <i>UGR_2865/1-812 (TcI_JrCl4)/1-308</i> | 203 | CCACTCCCCGTTGTGTCTCACACACGACACAAACCTCTCTCCCTTTCTCGGTGTG | --- | TCTTTTTTCTATTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 297 |
| <i>UGR_2865/1-817 (TcI_SylvioX10)/1-305</i> | 200 | CCACTCCCCGTTGTGTCTGCACACGACACAAACCTCTCTCCCTTTCTCGGTGTG | --- | TCTTTTTTCTGTTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 294 |
| <i>UGR_2848/1-810 (TcII-like)/1-311</i> | 199 | CCACTCCCCGTTGTGTCTCACACACACACACACACAAACCTCTCTCCCTTTCTCG | GCGTGTCTTTTTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 300 | |
| <i>UGR_2848/1-803 (TcIII-like)/1-305</i> | 200 | CCACTCCCCCTTTGTGTCTCACACACACACAAACCTCTCTCCCTTTCTCG | --- | TGTGTCTTTTTTCTTTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 294 |
| <i>UGR_2848/1-790 (TcI_JrCl4)/1-307</i> | 202 | CCACTCCCCGTTGTGTCTCACACACGACACAAACCTCTCTCCCTTTCTCG | --- | TGTGTCTTTTTTCTATTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 296 |
| <i>UGR_2848/1-788 (TcI_SylvioX10)/1-307</i> | 202 | CCACTCCCCGTTGTGTCTGCACACGACACAAACCTCTCTCCCTTTCTCG | --- | TGTGTCTTTTTTCTATTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 296 |
| <i>UGR_2854/1-1199 (TcIII-like)/1-304</i> | 199 | CCACTCCCCGTTGTGTCTCACACACACACAAACCTCTCTCCCTTTCTCGGTGTG | --- | TCTTTTTTCTTTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 293 |
| <i>UGR_2854/1-1296 (TcII-like)/1-310</i> | 198 | CCACTCCCCGTTGAGTCTCACACACACACACACACGACACAAACCTCTCTCCCTTTCTCG | GCGTGTCTTTTTTTGTAGGAATAGGGGACAGGGTCTTGGAAAGG | 299 | |
| <i>UGR_2854/1-462 (TcII)/1-227</i> | 115 | GCCACTCCCCGTTTCGAGTGTACACACACACACACACAAACCTCTCTCCCTTTCTCG | GCGTGTCTTTTTTTGTAGGAATAGGGGACAGGGTCTTGGACAGG | 216 | |

Consensus

CCACTCCCCGTTGTGTACACACACACAACCTCTCTCCCTTTCTCCGTGTGTTT++++TCTTTTTTCTTTTTGTAGGAATAGGGGGACAGGGTCTTGGACAGG

| | | | |
|--------------------------------------|-----|--------------|-----|
| JGR_2865/1-830_(TcIII-like)/1-302 | 292 | AGCGTATTCCTT | 302 |
| JGR_2865/1-812_(TcI_JRcl4)/1-308 | 298 | GGCGTGTAATA | 308 |
| JGR_2865/1-817_(TcI_SylvioX10)/1-305 | 295 | GGCGTGTAATA | 305 |
| JGR_2848/1-810_(TcII-like)/1-311 | 301 | GGCGTATACTT | 311 |
| JGR_2848/1-803_(TcIII-like)/1-305 | 295 | AGCGTATTCCTT | 305 |
| JGR_2848/1-790_(TcI_JRcl4)/1-307 | 297 | GGCGTATACTT | 307 |
| JGR_2848/1-788_(TcI_SylvioX10)/1-307 | 297 | GGCGTATACTT | 307 |
| JGR_2854/1-1199_(TcIII-like)/1-304 | 294 | AGCGTATACTT | 304 |
| JGR_2854/1-1296_(TcII-like)/1-310 | 300 | GGCGTGTAATA | 310 |
| JGR_2854/1-462_(TcII)/1-227 | 217 | GGCGTGTAATA | 227 |

Consensus

GGCGTACTT

Conserved sequence motif #6

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| <i>JGR_176/1-734_(TcII-like)/1-295</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | G | G | C | A | G | C | G | A | G | T | G | C | C | G | T | T | T | C | T | T | T | A | T | T | T | G | T | T | G | C | C | T | C | T | 100 | |
| <i>JGR_176/1-726_(TcI/Rc14)/1-292</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | G | G | C | A | G | C | G | G | T | T | C | T | T | T | A | T | T | T | C | G | T | T | G | C | C | C | C | - | 99 | | | | | | | |
| <i>JGR_176/1-728_(TcIII-like)/1-293</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | G | G | C | A | G | C | G | A | G | T | G | C | C | G | T | T | G | C | T | T | T | A | C | T | T | C | G | T | T | G | C | C | C | C | - | 99 |
| <i>JGR_149/1-777_(TcI/Rc14)/1-291</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | G | G | C | A | G | C | G | A | G | T | G | C | C | G | T | T | C | T | T | T | A | T | T | T | C | G | T | T | G | C | C | C | C | 99 | | |
| <i>JGR_149/1-806_(TcII-like)/1-297</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | T | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | G | G | C | A | G | C | G | A | G | T | G | C | C | G | T | T | C | T | T | T | A | T | T | T | C | G | T | T | G | C | C | T | C | T | 100 |
| <i>JGR_149/1-771_(TcIII-like)/1-293</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | G | G | C | A | G | G | G | A | G | T | G | C | C | G | T | T | C | T | T | T | A | C | T | T | C | G | T | T | G | C | C | - | - | 97 | | |
| <i>JGR_175/1-842_(TcII-like)/1-295</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | T | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | A | G | C | A | G | C | G | A | G | T | G | C | C | G | T | T | C | T | T | T | A | T | T | T | C | G | T | T | G | C | C | T | C | T | 100 |
| <i>JGR_175/1-830_(TcIII-like)/1-293</i> | 1 | T | T | G | T | T | T | A | G | C | C | G | C | C | T | G | C | T | T | C | T | T | T | A | T | T | A | T | T | G | A | C | T | T | T | A | T | T | T | C | C | A | T | C | G | A | T | A | C | C | A | G | C | C | G | G | G | G | A | G | G | C | A | G | C | G | A | G | T | G | C | C | G | T | T | C | T | T | T | A | C | T | T | C | G | T | T | G | C | C | C | C | 100 | | |

Consensus

TTGTTTATAGCCGCCCTTGCTTCCTTTTATTATTGACTTTTATTTCCCATCGATACACGCCGGGGAGGCAGCGAGTGCCGTTCCTTTATTTCGTTGCCCT

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|--|-----|-----------------------------|----------------------|------------|--------|---------|----------|-----|--------|----------|------|----------|-----|
| <i>UGR_176/1-734_(TcII-like)/1-295</i> | 101 | CCCTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGGT | - - | TTTTTTC | AAAGACTG | CCG | CACCGT | GACTTTG | CAAC | GAGAGATC | 198 |
| <i>UGR_176/1-726_(TcI/Rc14)/1-292</i> | 100 | - -CTGCCGCCGTTCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | -TC- | TTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGGGATC | 195 |
| <i>UGR_176/1-728_(TcIII-like)/1-293</i> | 100 | - -CTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | TTT- | TTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGCTC | 196 |
| <i>UGR_149/1-777_(TcI/Rc14)/1-291</i> | 100 | - - -TGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | TC - - | TTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGATC | 194 |
| <i>UGR_149/1-806_(TcII-like)/1-297</i> | 101 | CCCTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | TTTT | TTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGATC | 200 |
| <i>UGR_149/1-771_(TcIII-like)/1-293</i> | 98 | CCCTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGG | TTTT - | TTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGATC | 196 |
| <i>UGR_175/1-842_(TcII-like)/1-295</i> | 101 | CCCTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGAGGAGGCTGGC | GGTTGCGGG | T - T | TTTTTTC | AAGGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGATC | 198 |
| <i>UGR_175/1-830_(TcIII-like)/1-293</i> | 101 | - - -TGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | TTT - | TTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGATC | 196 |
| <i>UGR_156/1-593_(TcII-like)/1-295</i> | 101 | CCCTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGAGGAGGCTGGC | GGTTGCGGG | T - T | TTTTTTC | AAAGACTG | CC | GACCG | TGACTTTG | CAAC | GAGAGATC | 198 |
| <i>UGR_156/1-577_(TcIII-like)/1-293</i> | 100 | - -CTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | TTT - | CTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGCTC | 196 |
| <i>UGR_189/1-839_(TcII-like)/1-295</i> | 101 | CCCTGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | T - T | TTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGATC | 198 |
| <i>UGR_189/1-752_(TcIII-like)/1-293</i> | 101 | - - -TGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | TTT - | CTTTTTC | AAAGACTG | CC | ACCCG | TGACTTTG | CAAC | GAGAGATC | 196 |
| <i>UGR_189/1-666_(TcI_SylvioX10)/1-292</i> | 101 | - - -TGCTGCCGTCCCTCCCTCACCA | CGTGGGAGGGGGAGGCTGGC | GGTTGCGGG | T - C | TTTTTTC | AAAGATTG | CC | ACCCG | TGACTTTG | CAAC | GAGGGATC | 195 |

Consensus

CCCTGCTGCGCTCC TCCCTCACCACGTGGGAGGGGGAGGC TGGCGGTTCGCGGGTTT - TTTTTCCTCAAAGACTGCCACCCCGTGACTTTTGCAACGAGAGATC

| | | | | | | | | | |
|--|-----|--------------------|------------|------------|-----------------------------|-------------------|--------------|-------|-----|
| <i>JGR_176/1-734_(TcII-like)/1-295</i> | 199 | CCGGCTGCTGGTGGCGTG | TGCCCTTTTG | CATGCGTGCG | TTTTAATGGTAGTGTATGCATGCGCGG | TGAATCCTCTCTGAGG | TGTGTGTTTTGT | AGGGG | 295 |
| <i>JGR_176/1-726_(TcI/Rc14)/1-292</i> | 196 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGTTTTGT | AGGGG | 292 |
| <i>JGR_176/1-728_(TcIII-like)/1-293</i> | 197 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGTTTTGT | ATGGG | 293 |
| <i>JGR_149/1-777_(TcI/Rc14)/1-291</i> | 195 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCCGAGG | TGTGTGTTTTGT | AGGGG | 291 |
| <i>JGR_149/1-806_(TcII-like)/1-297</i> | 201 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAATGGTAGTGTATGCATGCGCGG | TGAATCCTCTCTGAGG | TGTGTGTTTTGT | AGGGG | 297 |
| <i>JGR_149/1-771_(TcIII-like)/1-293</i> | 197 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGTTTTGT | AGGGG | 293 |
| <i>JGR_175/1-842_(TcII-like)/1-295</i> | 199 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAATGGTAGTGTATGCATGCGCGG | TGAATCCTCTCTGAGG | TGTGTGTTTTGT | AGGGG | 295 |
| <i>JGR_175/1-830_(TcIII-like)/1-293</i> | 197 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGTTTTGT | ATGGG | 293 |
| <i>JGR_156/1-593_(TcII-like)/1-295</i> | 199 | CCGGCTGCTGGTGGCGTG | TGCCCTTTTG | CATGCGTGCG | TTTTAATGGTAGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGCTTTGT | AGGGG | 295 |
| <i>JGR_156/1-577_(TcIII-like)/1-293</i> | 197 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGTTTTGT | ATGGG | 293 |
| <i>JGR_189/1-839_(TcII-like)/1-295</i> | 199 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAATGGTAGTGTATGCATGCGCGG | TGAATCCTCTCTGAGG | TGTGTGTTTTGT | AGGGG | 295 |
| <i>JGR_189/1-752_(TcIII-like)/1-293</i> | 197 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGTTTTGT | ATGGG | 293 |
| <i>JGR_189/1-666_(TcI_SylvioX10)/1-292</i> | 196 | CCGGCTGCTGGTGGCGTA | TGCCCTTTTG | CATGCGTGCG | TTTTAGTGGTGGTGTATGCATGCGCGG | TGAATCCCCCTCTGAGG | TGTGTGTTTTGT | AGGGG | 292 |

Consensus

CCGGCTGCTGGTGGCGTATGCCTTTTCATGCGTGCGTTTTAGTGGTGGTGTATGCATGCGCGGTGAATCCCCCTCTGAGGTGTGTGTTTTTGTAGGGG

Conserved sequence motif #7

| | | | |
|--|-----|---|-----|
| <i>JGR_973/1-1858 (TcIII-like)/1-543</i> | 1 | T T T T T T T T T T A T A T T C A T T T T C T T A T T G G T G C A A T T T T T T G G A G G G A - - A G A G T G T G C G G C A T T T A T G A A T G G A G G G G G A G G G A A G G A G G A G T C A A C G A T G | 100 |
| <i>JGR_982/1-3518 (TcII-like)/1-544</i> | 1 | T T T T T T T T T T - - A A T C C A T T T T C T T A T T G G T G C A A T T T T T T G T A G A G A A G A G A G T G T G C G G C A T T T A T G A G T G G A G G G G G A G G G G A G G A G G A G T C A A C G A T G | 100 |
| <i>JGR_982/1-3486 (TcIII-like)/1-539</i> | 1 | T T T T T T T T T T A T A T T C A T T T T C T T A T T G G T G G A A T T T T T T G G A G A G A - - A G A G T G T G C G G C A T T T A T G A A T G G A G G G G G A G G G A A G G A G G A G T C A A C G A T G | 100 |
| Consensus | | T T T T T T T T T T A T A T T C A T T T T C T T A T T G G T G C A A T T T T T T G G A G A G A - - A G A G T G T G C G G C A T T T A T G A A T G G A G G G G G A G G G A A G G A G G A G T C A A C G A T G | |
| <i>JGR_973/1-1858 (TcIII-like)/1-543</i> | 101 | G A T G G T G C C T C T T T T T T T G A A C G T T C C C G C C C A C C C G A G T T T C G G T T G C C C G A T T T T T C T C T T A A A G A C A C C G C C T T G G A G G G C A G C G A G T G C A G T T T T C T T T | 202 |
| <i>JGR_982/1-3518 (TcII-like)/1-544</i> | 101 | G A T G G T G C C T C T T T T T T T G A A C C T T C C C G C C C A C T T G A G T T T C G G T T G C C T G A T T T T C C T C T T A A A G A C A C C G C C T T G G A G G G C A G C G A G T G C A G T T T T C T T T | 202 |
| <i>JGR_982/1-3486 (TcIII-like)/1-539</i> | 101 | G A T G G T G C C T C T T T T T T T G A G C C T T C C C G C C C A C T C G A G T T T C G G T T G C C C G A T T T T T C T C T T A A A G A C A C C G C C T T G G A G G G C A G C G A G T G C A G T T T T C T T T | 202 |
| Consensus | | G A T G G T G C C T C T T T T T T T G A A C C T T C C C G C C C A C T C G A G T T T C G G T T G C C C G A T T T T T C T C T T A A A G A C A C C G C C T T G G A G G G C A G C G A G T G C A G T T T T C T T T | |
| <i>JGR_973/1-1858 (TcIII-like)/1-543</i> | 203 | T T A T T T T C T C A T T C C A C C C G C C C A C T C C C T - - - C A C C A C C A C C A C C A C T A C T A C T G T G A C T C T C C G C A T G G G G G G A G T T T T G T T G G C T G C G A G G C T C C C C C T | 301 |
| <i>JGR_982/1-3518 (TcII-like)/1-544</i> | 203 | T T A T T T T T C A T T C C A C C C G C C C A C T C C C T C A C C A C C A C C A C C A C T A C T A C T G T G A C T C T C C G C A T G G A G G G G A G T T T T G T T G G C T G C A A G G C T C C C C C - | 303 |
| <i>JGR_982/1-3486 (TcIII-like)/1-539</i> | 203 | T T A T T T T T C A T T C C A C C C G C C C A C T C C C T - - - C A C C A C C A C C A C C A C T A C T A C T G T G A C T C T C C G C A T G G A G G G G A G T T T T G T T G G C T G C G A G G C T C C C C C - | 300 |
| Consensus | | T T A T T T T T C A T T C C A C C C G C C C A C T C C C T - - - C A C C A C C A C C A C C A C T A C T A C T G T G A C T C T C C G C A T G G A G G G G A G T T T T G T T G G C T G C G A G G C T C C C C C - | |
| <i>JGR_973/1-1858 (TcIII-like)/1-543</i> | 302 | T T T T T T T T T T T T T T A G G G A C C G C C G C T T C G T G G G G T C C G C A G C G C G C C C G G T T T T C A T A G G A C G A G C C T C A A T G G A C C G A T T G G T T T A C T G A T G T A T G G G C G | 403 |
| <i>JGR_982/1-3518 (TcII-like)/1-544</i> | 304 | T T T T T T T T T T T T T T A G G G A C C G C C G C T T C G T G G G G T C C A C A G C G C G C C C G G T T G T C A T A G G A C G A G C C T C A A T G G A C C G A T T G G T T T A C T G A T G T A T G G G C G | 405 |
| <i>JGR_982/1-3486 (TcIII-like)/1-539</i> | 301 | - - - C T T T T T T T T T T T T A G G G A C C G C C G C T T C G T G G G G T C C G C A G C G C G C C C G G T T T T C A T A G G A C G A G C C T C A A T G G A C C G A T T G G T T T A C T G A T G T A T G G G C G | 399 |
| Consensus | | T T T T T T T T T T T T T T A G G G A C C G C C G C T T C G T G G G G T C C G C A G C G C G C C C G G T T T T C A T A G G A C G A G C C T C A A T G G A C C G A T T G G T T T A C T G A T G T A T G G G C G | |
| <i>JGR_973/1-1858 (TcIII-like)/1-543</i> | 404 | T G G G G T G A A T T T T T T C A C T A C G A G T G C G G G G G C T G C C A G G C G C A C T G A A C C C A G C C G T C A T C T C C C C A C C G T T G C C C C T T C T C T G T C T G T G G G A A T A G G G G | 505 |
| <i>JGR_982/1-3518 (TcII-like)/1-544</i> | 406 | T G G G G T G A A T T T T T T C A C T A C G A G T G C G G G G G C T G C C A G G C G C A C T G A A C C C A G C T G T C A T C T C C C C A C C G T T G - C C C C T T C T C T G T C T G T A G G A A T A G G G G | 506 |
| <i>JGR_982/1-3486 (TcIII-like)/1-539</i> | 400 | T G G G G A G A A T T T T T T C A C T A C G A G T G C G G G G G C T G C C A G G C G C A C T G A A C C C A G C C G T C A T C T C C C C A C C G T T G C C C C T T C T C T G T C T G T A G G A A T A G G G G | 501 |
| Consensus | | T G G G G T G A A T T T T T T C A C T A C G A G T G C G G G G G C T G C C A G G C G C A C T G A A C C C A G C C G T C A T C T C C C C A C C G T T G C C C C T T C T C T G T C T G T A G G A A T A G G G G | |
| <i>JGR_973/1-1858 (TcIII-like)/1-543</i> | 506 | G G A C C A G G C C G C A T C C C G G C G C A C A T T A C T T T C T T T T C | 543 |
| <i>JGR_982/1-3518 (TcII-like)/1-544</i> | 507 | G G A C C A G G C C G C A T C C C G G C G C A C A T T A C T T T C T T T T C | 544 |
| <i>JGR_982/1-3486 (TcIII-like)/1-539</i> | 502 | G G A C C A G G C C G C G T C C C G G C G C A C A T T A C T T T C T T T T C | 539 |
| Consensus | | G G A C C A G G C C G C A T C C C G G C G C A C A T T A C T T T C T T T T C | |

Conserved sequence motif #8

UGR_933/1-783_(TcII-like)/1-370 1 TTTTTCCTTCTTTT TTTT TACGTGTGGATTGGGTTGTTTCTTAAGATGCCGCGAGGGGAAGGCAGGAAGTGGAGGTCTTTTTTCCTTTTGTTCCACTCTCT 100
UGR_949/1-745_(TcIII-like)/1-373 1 TTCCTTTTTTTTTCTTTT CCGCGTGGATTGGGTTGTTTCTTAAGATGCCGCGAGGGGAAGGCAGGAAGTGGAGGTCTTTTTTCCTTTTGTTCCACTCTCT 100
UGR_949/1-725_(TcII-like)/1-370 1 TTTT TTTT TCTTCTTTT TACGTGTGGATTGGGTTGTTTCTTAAGATGCCGCGAGGGGAAGGCAGGAAGTGGAGGTCTTTTTTCCTTTTGTTCCACTCTCT 100
UGR_949/1-710_(TcII)/1-366 1 TTTT - - - TTTCTTCTTTT TACGTGTGGATTGGGTTGTTTCTTAAGATGCCGCGAGGGGAAGGCAGGAAGTGGAGGTCTTT - TTTCTTTTGTTCCACTCTCT 96

Consensus

TTTTTTTTTTT+TTCTTTTACGTGTGGATTGGGTTGTTTCTTAAGATGCCGCGAGGGGAAGGCAGGAAGTGGAGGTCTTTTTTCCTTTTGTTCCACTCTCT

UGR_933/1-783_(TcII-like)/1-370 101 TTCTACTGCTGCTCTCTCCACGAGGGGAGGTTGGGAGGTGGCGGGGCGCTCTTGATGAATGCCACGTTGTCCTTTTTCACAAAGAGGCCCGGTGATCATTGCGG 200
UGR_949/1-745_(TcIII-like)/1-373 101 TTCTACTGCTGCTCTCTCCACGAGGGGAGGTTGGGAGGTGGCGGGGCGCTCTTGATGAATGCCACGTTGTCCTTTTTCACAAAGAGGCCCGGTGATCATTGCGG 200
UGR_949/1-725_(TcII-like)/1-370 101 TTCTACTGCTGATCTCTCCACGAGGGGAGGTTGGGAGGTGGCGGGGCGCTCTTTATGAATGCCACGTTGTCCTTTTTCACAAAGAGGCCCGGTGATCATTGCGG 200
UGR_949/1-710_(TcII)/1-366 97 TTCTACTGCTGATCTCTCCACGAGGGGAGGTTGGGAGGTGGCGGGGCGCTCTTGATGAATGCCACGTTGTCCTTTTTCACAAAGAGGCCCGGTGATCATTGCGG 196

Consensus

TTCTACTGCTG+TCTCCACGAGGGGAGGTTGGGAGGTGGCGGGGCGCTCTTGATGAATGCCACGTTGTCCTTTTTCACAAAGAGGCCCGGTGATCATTGCGG

UGR_933/1-783_(TcII-like)/1-370 201 TTTTTATTTATGAACACATCCTTCTACGTTTGTGCGATGCGTGTTTGAATGGGTCTCAGTCGGAGTGTGGGGGATGTTGGGCGCATGGAACCAAACGGTCA 300
UGR_949/1-745_(TcIII-like)/1-373 201 TTTTTATTTATGAACACATCCTTCTACGTTTGTGCGATGCGTGTTTGAATGGGTCTCAGTCGGAGTGTGGGGGATGTTGGGCGCATGGAACCAAACGGTCA 300
UGR_949/1-725_(TcII-like)/1-370 201 TTTTTATTTATGAACACATCCTTCTACGTTTGTGCGATGCGTGTTTGAATGGGTCTCAGTCGGAGTGTGGGGGATGTTGGGCGCATGGAACCAAACGGTCA 300
UGR_949/1-710_(TcII)/1-366 197 TTTTTATTGATGAACACATCCTTCTACGTTTGTGCGATGCGTGTTTGAATGGGTCTCAGTCGGAGTGTGGGGGATGTTGGGCGCATGGAACCAAACGGTCA 296

Consensus

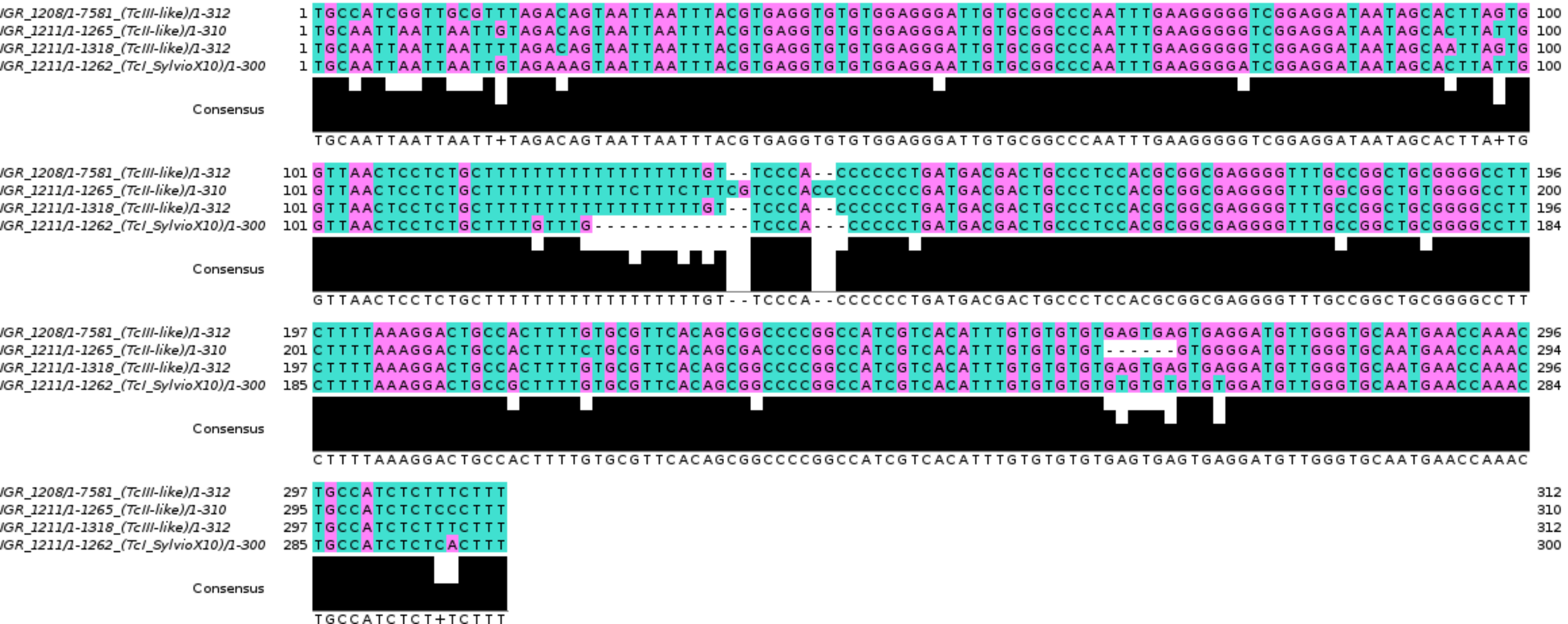
TTTTTATTTATGAACACATCCTTCTACGTTTGTGCGATGCGTGTTTGAATGGGTCTCAGTCGGAGTGTGGGGGATGTTGGGCGCATGGAACCAAACGGTCA

UGR_933/1-783_(TcII-like)/1-370 301 TCTCC - - - GCCCGTTGTGTCTGCTCCGCTCCGTCTTTGTGGGCACGCGGGCCTCAGCTAAGCGCACATGTCTACA 370
UGR_949/1-745_(TcIII-like)/1-373 301 TCTCCTCCGCCCGTTGTGTTCTGCTCCGCTCCGTCTTTGTGGGCACGCGGGACCTCAGCTAAGCGCACATTTTATTTA 373
UGR_949/1-725_(TcII-like)/1-370 301 TCTCC - - - GCCCGTTGTGTCTGCTCCGCTCCGTCTTTGTGGGCACGCGGGCCTCAGCTAAGCGCACATTTTTTTA 370
UGR_949/1-710_(TcII)/1-366 297 TCTCC - - - GCCCGTTGTGTCTGCTCCGCTCCGTCTTTGTGGGCACGCGGGCCTCAGCTAAGCGCACTATTTTTTT 366

Consensus

TCTCC - - - GCCCGTTGTGTCTGCTCCGCTCCGTCTTTGTGGGCACGCGGGCCTCAGCTAAGCGCACATTTTTTTA

Conserved sequence motif #9



Conserved sequence motif #10

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| <i>JGR_1292/1-1237 (TcIII-like)/1-460</i> | 1 | T | T | T | T | T | T | G | A | G | C | T | T | G | C | G | G | G | A | G | G | A | A | T | A | T | G | T | G | A | C | C | A | G | A | T | G | G | G | G | C | C | G | A | A | C | C | G | A | T | G | A | T | A | A | C | G | C | G | T | C | T | C | G | G | A | T | G | C | A | T | T | C | C | T | T | G | G | C | T | T | T | T | A | T | T | G | A | A | G | C | C | T | G | A | T | G | T | 100 | |
| <i>JGR_1292/1-1227 (TcII-like)/1-448</i> | 1 | T | T | T | T | T | T | G | A | G | C | T | T | G | C | G | G | G | A | G | A | A | T | T | T | G | T | G | A | C | C | A | G | A | T | G | G | G | G | C | C | G | A | A | C | C | G | A | T | G | A | T | A | A | C | G | C | G | T | C | T | C | G | G | A | T | G | C | A | T | T | C | C | T | T | G | G | C | T | T | T | T | A | C | T | G | A | A | A | T | C | C | T | G | A | T | G | T | 100 | |
| <i>JGR_1292/1-1216 (TcII)/1-448</i> | 1 | T | T | T | T | T | T | G | A | G | C | T | T | G | C | G | G | G | A | G | A | A | T | G | T | G | T | G | A | C | C | A | G | A | T | G | G | G | G | C | C | G | A | A | C | C | G | A | T | G | A | T | A | A | C | G | C | G | T | C | T | C | G | G | A | T | G | C | A | T | T | C | C | T | T | G | G | C | T | T | T | T | A | T | T | G | A | A | A | T | C | C | T | G | A | T | G | T | 100 | |
| <i>JGR_1305/1-1326 (TcI/RcI4)/1-455</i> | 1 | T | T | A | C | T | T | C | G | A | G | C | A | - | - | - | - | C | G | A | G | G | A | A | T | G | T | G | T | G | A | C | C | A | G | A | T | G | G | G | G | C | C | G | A | A | T | C | G | A | T | G | A | T | A | A | C | G | C | G | T | C | T | C | G | A | A | T | G | C | A | T | T | C | C | T | T | G | G | C | T | T | T | T | A | T | T | G | A | A | G | C | C | T | A | A | T | G | T | 96 |
| <i>JGR_1305/1-1317 (TcII-like)/1-448</i> | 1 | T | T | A | C | T | T | C | G | A | G | C | T | T | G | C | G | G | G | A | G | A | A | T | T | T | G | T | G | A | C | C | A | G | A | T | G | G | G | G | C | C | G | A | A | C | C | G | A | T | G | A | T | A | A | C | G | C | G | T | C | T | C | G | G | A | T | G | C | A | T | T | C | C | T | T | G | G | C | T | T | T | T | A | T | T | G | A | A | A | T | C | C | T | G | A | T | G | T | 100 |
| <i>JGR_1305/1-1302 (TcII)/1-448</i> | 1 | T | T | A | C | T | T | C | G | A | G | C | T | T | G | C | G | G | G | A | G | A | A | T | G | T | G | T | G | A | C | C | A | G | A | T | G | G | G | G | C | C | G | A | A | C | C | G | A | T | G | A | T | A | A | C | G | C | G | T | C | T | C | G | G | A | T | G | C | A | T | T | C | C | T | T | G | G | C | T | T | T | T | A | T | T | G | A | A | A | T | C | C | T | G | A | T | G | T | 100 |

Consensus

TT++TT+GAGCTTGCGGGAGGAATGTGTGACCAGATGGGGCCGAACCGATGATAACGCGTCTCGGATGCATTCTTGGCTTTTTTATTGAAATCCTGATGT

| | | | |
|---|-----|---|-----|
| <i>JGR_1292/1-1237 (TcIII-like)/1-460</i> | 101 | TTGTTGTTAACGGTATCGCGTTGGAGGGTGGCAAGTGCAGCTTTTGTTTCACTCTGTTGTCCCAGTCACTCTCTCGGTGACTCTTTCACGCGGAGATGAGTTC | 200 |
| <i>JGR_1292/1-1227 (TcII-like)/1-448</i> | 101 | TTGTTGTTAACGGTATCGCGTTGGAGGGTGGCGAGTGCAGCTTTTGTTCCACTCTGTTGTTCAGCCACTCTCTCGGTGGCTCTTTCACGCGGAGAGGAGTTC | 200 |
| <i>JGR_1292/1-1216 (TcII)/1-448</i> | 101 | TTGTTGTTAACGGTATCGCGTTGGAGGGTGGCGAGTGCAGCTTTTGTTCCACTCTGTTGTTCAGCCACTCTCTCGGTGACTCTTTCACGCGGAGAGGAGTTC | 200 |
| <i>JGR_1305/1-1326 (TcI/RcI4)/1-455</i> | 97 | TTGTTGTTAACGGTATCGCGTTGGAGGGTGGCAAGTGCAGCTTTTGCTCCA TCTGTTTTCCTAGCCACTCTCTCGGTGACTCTTTCACGCGGAGATGAGTTC | 196 |
| <i>JGR_1305/1-1317 (TcII-like)/1-448</i> | 101 | TTGTTGTTAACGGTATCGCGTTGGAGGGTGGCGAGTGCAGCTTTTGTTCCACTCTGTTGTCCCAGCCACTCTCTCGGTGACTCTTTCACGCGGAGAGGAGTTC | 200 |
| <i>JGR_1305/1-1302 (TcII)/1-448</i> | 101 | TTGTTGTTAACGGTATCGCGTTGGAGGGTGGCGAGTGCAGCTTTTGTTCCACTCTGTTGTTCAGCCACTCTCTCGGTGGCTCTTTCACGCGGAGAGGAGTTC | 200 |

Consensus

T T G T T G T T A A C G G T A T C G C G T T G G A G G G T G G C G A G T G C A G C T T T T G T T C C A T C T G T T G T + C C A G C C A C C T C C T C C G T G A C T C T T C A C G C G G A G A G G A G T C

| | | | |
|---|-----|---|-----|
| <i>JGR_1292/f1-1237_(TcIII-like)/f1-460</i> | 201 | C G G C A G C T G C G G G G G C A C T T G T A A T G A C T G C C A C T T C G T G A G C T C A C A A C G A G C C T G G C T G T C A T G G A T G A A C T T G G G A A C C G T T T G G T T T A C T G G T G T G | 300 |
| <i>JGR_1292/f1-1227_(TcII-like)/f1-448</i> | 201 | C G G C A G C T G C G G A G G C A C T T G T A A T G A C T G C C G C T T C G T G A G C T C A C A A C G A G C C T G G C T G T C A T G G A T G A A C T T G G G A C C C G T T T G G T T T A C T G G T G T T | 300 |
| <i>JGR_1292/f1-1216_(TcII)/f1-448</i> | 201 | C G G C A G C T G C G G G G G C A C T T G T A A T G A C T G C C G C T T C G T G A G C T C A C A A C G A G C C T G G C T G T C A T G G A T G A A C T T G G G A A C C G T T T G G T T T A C T G G T G T G | 300 |
| <i>JGR_1305/f1-1326_(TcI/Rc14)/f1-455</i> | 197 | C G G C A G C T G C G G G G G C A T C T G T A A T G A C T G C C A C T T C G T G A G C T C A C A A C G A G C C T G G C T G T C A T G G A T G A A C T T G G G A A C C G T T T G G T T T A C T A G T G T G | 296 |
| <i>JGR_1305/f1-1317_(TcII-like)/f1-448</i> | 201 | C G G C A G C T G C G G G G G C A C T T G T A A T G A C T G C C A C T T C G T G A G C T C A C A A C G A G C C T G G C T G T C A T G G A T G A A C T T G G G A C C C G T T T G G T T T A C T G G T G T G | 300 |
| <i>JGR_1305/f1-1302_(TcII)/f1-448</i> | 201 | C G G C A G C T G C G G G G G C A C T T G T A A T G A C T G C C A C T T C G T G A G C T C A C A A C G A G C C T G G C T G T C A T G G A T G A A C T T G G G A A C C G T T T G G T T T A C T G G T G T G | 300 |

Consensus

CGGCAGCTGCGGGGGCACATTGTAAATGACTGCCACTTCGTGAGCTCACAAACGAGCCTGGCTGTTCATGGATGAACCTTGGGAACCGTTTGGTTTACTGGTGTG

| | | | |
|---|-----|---|-----|
| <i>JGR_1292/f1-1237_(TcIII-like)/f1-460</i> | 301 | C G T G T A T G T G T T T G T G T G C G T T G G G T G A A T T T T C T T T G A A T T A T G G G G G A T G T T G G G T A C A G T G A A C C A A G C T G T T G C C T C C C A C T G T G C T T T G C C C T T T | 400 |
| <i>JGR_1292/f1-1227_(TcII-like)/f1-448</i> | 301 | T G - - - - - - - - - - T G T G T G C T G G G T G A A T T T C C T T T G A A T T A T G G G G G A T G T T G G G T A C A G T G A A C C A A G C T G T G C C T C C C A C T G T G T T T T G C C C T T T | 388 |
| <i>JGR_1292/f1-1216_(TcII)/f1-448</i> | 301 | C G - - - - - - - - - - T G G G T G T T G G G T G A A T T T C C T T T G A A T T A T G G G G G A T G T T G G G T A C A G T G A A C C A A G C T G T G C C T C C C A C T G T G C T T T G C C C T T T | 388 |
| <i>JGR_1305/f1-1326_(TclJRcI4)/f1-455</i> | 297 | A G T G T G T G T G T T T G T G T G T T G G G T G A A T T T C C T T T G A A T T A T G G G G G A T G T T G G G T A C A G T G A A C C A A G C T G T T G C C T C C C A C T G T G C T T T G C C C T T T | 396 |
| <i>JGR_1305/f1-1317_(TcII-like)/f1-448</i> | 301 | C G T - - - - - - - - - - G G G T G T T G G G T G A A T T T C C T T T G A A T T A T G G G G G A T G T T G G G T A C A G T G A A C C A A G C T G T G C C T C C C A C T G T G T T T T G C C C T T T | 388 |
| <i>JGR_1305/f1-1302_(TcII)/f1-448</i> | 301 | C G T - - - - - - - - - - G T G T G T T G G G C G A A T T T C C T T T G A A T T A T G G G G G A T G T T G G G T A C A G T G A A C C A A G C T G T G C C T C C C A C T G T G T T T T G C C C T T T | 388 |

Consensus

CGTGT-TGTGTTTGTGTGTGTTGGGTGAATTTCCTTTGAATTATGGGGGATGTTGGGTACAGTGAACCAAGCTGTGGCTCCCACTGTGT+TTTGGCCCTTT

| | | | |
|---|-----|---|-----|
| <i>JGR_1292/1-1237_(TcIII-like)/1-460</i> | 401 | C T T C T T T C T G G G G G G C A T G T G A C G A G G C C T C A C C C A G G C A C A A T A T T T G A C T T T G T T T A T T | 460 |
| <i>JGR_1292/1-1227_(TcII-like)/1-448</i> | 389 | C T T T T T T C T G G G G G G C A T G T G A C G A G G C C T C A C C C A G G C G C A T A T T T G A C T T T G T T T A T T | 448 |
| <i>JGR_1292/1-1216_(TcII)/1-448</i> | 389 | C T T T T T T C T G G G G G G C A T G T G A C G A G G C C T C A C C C A G G C G C A T A T T T G A C T T T G T T T A T T | 448 |
| <i>JGR_1305/1-1326_(TcI/RcI4)/1-455</i> | 397 | C T T C T T T C T G - G G G G C A T G T G A C G A G G C C T C A C C C A G G C G C A T A T T T G A C T T T G T T A T T | 455 |
| <i>JGR_1305/1-1317_(TcII-like)/1-448</i> | 389 | C T T T T T T C T G G G G G G C A T G T G A C G A G G C C T C A C C C A G G C G C A T A T T T G A C T T T G T T T A T T | 448 |
| <i>JGR_1305/1-1302_(TcII)/1-448</i> | 389 | C T T T T T T C T G G G G G G C A T G T G A C G A G G C C T C A C C C G G G C G C A T A T T T G A C T T T G T T T A T T | 448 |

Consensus

CTTTTTTC TGGGGGGGCATGTGACGAGGCC TCACCCAGGCGCATATTTGACTTTGTTTATT

Conserved sequence motif #11

JGR_2449/1-566_(TcII)/1-413 1 GGAGGGAATTTGCGATCATATGTGGGGGAAGGGAGGCTAAGGAGGAGGTTGGCGTGGTTTTTCTCATCCCCACCATT- - -ATTTTTTCTTTCTTTTACATG 99
JGR_2449/1-565_(TcII-like)/1-412 1 GGAGGGAATTTGCGATCATATGTGGGGGAAGGGAGGCTAAGGAGGAGGTTGGCGTGGTTTTTCTCATCCCCACCATT- - -ATTTTT- TTTTCTTTTACATG 98
JGR_2449/1-566_(TcIII-like)/1-414 1 GGAGGGAATGTGCGATCATATGG- -GGGAAGGGAGGCTAAGGAGGAGGTTGGCGTGGTTTTTCTCATCCCCCACCATTATTATTATTTTTTCTTTTACATG 100
JGR_7897/1-572_(TcIII-like)/1-414 1 GGAGGGAATGTGCG- -ATCATATGGGGGAAGGGAGGCTAAGGAGGAGGTTGGCGTGGTTTTTCTCATCCCCCACCATTATTATTATTTTTTCTTTTACATG 100

Consensus

GGAGGGAAT+TGCGATCATATGTGGGGGAAGGGAGGCTAAGGAGGAGGTTGGCGTGGTTTTTCTCATCCCC++C++TTAT++TT+TTTTTCTTTTACATG

JGR_2449/1-566_(TcII)/1-413 100 TTGGTGCCTGCAAGGACATCGAGTGCATTTCTTTTGTTCCTTGCCTCGCCGACTTTCTTAAGACTAATACCGCTGCAGCAACTTGCCACGCGGA 201
JGR_2449/1-565_(TcII-like)/1-412 99 TTGGTGCCTGCAAGGACATCGAGTGCATTTCTTTTGTTCCTTGCCTCGCCGACTTTCTTAAGACTAATACCGCTGCAGCAACTTGCCACGCGGA 200
JGR_2449/1-566_(TcIII-like)/1-414 101 TTGGTGCCTGCAAGGACATCGAGTGCATTTCTTTGTGTTTCCTGTCCTTGCCTCGCCGACTTTCTTAAGACTAATACCGCTGCAGCAACTTGCCACGCGGA 202
JGR_7897/1-572_(TcIII-like)/1-414 101 TTGGTGCCTGCAAGGACATCGAGTGCATTTCTTTGTGTTTCCTGTCCTTGCCTCGCCGACTTTCTTAAGACTAATACCGCTGCAGCAAAATTGCCACGCGGA 202

Consensus

TTGGTGCCTGCAAGGACATCGAGTGCATTTCTTT+TGTTTCCTGTCCTTGCCTCGCC+ACTTTCTTAAGACTAATACCGCTGCAGCAACTTGCCACGCGGA

JGR_2449/1-566_(TcII)/1-413 202 GGGAATTCTGGCGGTGCGGTGGCCCTTTTGAAGACTGCCGCTCAGCGTGGTGCGCCAGGGTCAATCGCCCCGTATTGTCGGGGGAGGCCAGGGGCCAGCC 303
JGR_2449/1-565_(TcII-like)/1-412 201 GGGAATTCTGGCGGTGCGGTGGCCCTTTTGAAGACTGCCGCTCAGCGTGGTGCGCCAGGGTCAATCGCCCCGTATTGTCGGGGGAGGCCAGGAGCCAGCC 302
JGR_2449/1-566_(TcIII-like)/1-414 203 GGGAATTCTGGCGGTGCGGTGGCCCTTTTGAAGACTGCCGCTCAGCGTGGTGCGCCAGGGTCAATCGCCCCCTATTGTCGGGGGAGGCCAGGAGCCAGCC 304
JGR_7897/1-572_(TcIII-like)/1-414 203 GGGAATTCTGGCGGTGCGGTGGCCCTTTTGAAGACTGCCGCTCAGCGTGGTGCGCCAGGGTCAATCGCCCCCTATTGTCGGGGGAGGCCAGGAGCCAGCC 304

Consensus

GGGAATTCTGGCGGTGCGGTGGCCCTTTTGAAGACTGCCGCTCAGCGTGGTGCGCCAGGGTCAATCGCCCC+TATTGTC+GGGGAGGCCAGGAGCCAGCC

JGR_2449/1-566_(TcII)/1-413 304 ATGTTTCCCTCACGGGCTTGTTGGTGCAGGGCTGACGGCATGTATTTTGTGAATATCTTTGTTTGTGGGTGCGTGCGTGTGGATAAATTGTTTCTGAATTG 405
JGR_2449/1-565_(TcII-like)/1-412 303 ATGTTTCCCTCACGGGCTTGTTGGTGCAGGGCTGACGGCATGTATTTTGTGAATATCTTTGTTTGTGGGTGCGTGCGTGTGGATAAATTGTTTCTGAATTG 404
JGR_2449/1-566_(TcIII-like)/1-414 305 ATGTTTCCCTCACGGGCTTGTTGGTGCAGGGCTGACGGCATGTATTTTGTGAATATCTTTGTTTGTGGGTGCGTGCGTGTGGATAAATTGTTTCTGAATTG 406
JGR_7897/1-572_(TcIII-like)/1-414 305 ATGTTTCCCTCACGGGCTTGTTGGTGCAGGGCTGACGGCATGTATTTTGTGAATATCTTTTGTGGGTGCGTGCGTGTGGATAAATTGTTTCTGAATTG 406

Consensus

ATGTTTCCCTCACGGGC+TGTTGGTGCAGGGCTGACGGCATGTATTTTGTGAATATCTTTGTTTGTGGGTGCGTGCGTGTGGATAAATTGTTTCTGAATTG

JGR_2449/1-566_(TcII)/1-413 406 TGTGTGGG 413
JGR_2449/1-565_(TcII-like)/1-412 405 TGTGCGGG 412
JGR_2449/1-566_(TcIII-like)/1-414 407 TTTGCGGG 414
JGR_7897/1-572_(TcIII-like)/1-414 407 TTTGCGGG 414

Consensus

T+TGCGGG

Conserved sequence motif #12

JGR_3859/1-3342_(TcII-like)/1-294 1 GCACTGCCCTTTGAAGGCTTGCTGGCCAGTTCGGCAATGGGTCGTTCAGTTCAGAAACAAGCTCACTTTTAAAGTACAACGCGTCTACGTTCCTGGGC AAG 100
JGR_3860/1-526_(TcIII-like)/1-294 1 GCACTGCCCTTTGAAGGCTTGCTGGCCAGTTCGGCAATGGGTCGTTCAGTTCAGAAACAAGCTCACTTTTAAAGTACAACGCGTCTACGTTCCTGGGC GAG 100
JGR_3860/1-527_(TcII-like)/1-292 1 GCACTGCCCTTTGAAGGCTTGCTGGCCAGTTCGGCAATGGGTCGTTCAGTTCAGAAACAAGCTCACTTTTAAAGTACAACGCGTCTACGTTCCTGGGC AAG 100
JGR_3860/1-521_(TcII)/1-287 1 GCACTGCCCTTTGAAGGCTTGCTGGCCAGTTCGGCAATGGGTCGTTCAGTTCAGAAACAAGCTCACTTTTAAAGTACAACGCGTCTACGTTCCTGGGC AAG 100

Consensus

GCAC TGCCCTTTGAAGGCTTGCTGGCCAGTTCGGCAATGGGTCGTTCAGTTCAGAAACAAGCTCACTTTTAAAGTACAACGCGTCTACGTTCCTGGGC AAG

JGR_3859/1-3342_(TcII-like)/1-294 101 GGGATGTCTCTTCTCTGCTTACCCATTGTAGGGGACAGGAAAAGAACTGACTGCCTCTTATTAAAAGAAAAAAGGAAAAAAGGAAAAAAGGAAGGATC 200
JGR_3860/1-526_(TcIII-like)/1-294 101 GGGATGTCTCTTCTCTGTTTACCCCTTGTGGGGGACAGGAAAAGAACTGACTGCCTCTTATTAAAAAAGGAAAAAAGGGAAGGGTC 200
JGR_3860/1-527_(TcII-like)/1-292 101 GGGATGTCTCTTCTCTG - CTACCCCTTGTAGGGGACAGGAAAAGAACTGACTGCCTCTTATTAAAAGAAAAAAGGAAAAAAGGGAAGGATC 198
JGR_3860/1-521_(TcII)/1-287 101 GGGATGTCTCTTCTCTG - CTACCCCTTGTAGGGGACAGGAAAAGAACTGACTGCCTCTTATTAAAAGAAAAAAGGAAAA - - - - AAAAAAGGGAAGGATC 193

Consensus

GGGATGTCTCTTCTCTG - +TACCCCTTGTAGGGGACAGGAAAAGAACTGACTGCCTCTTATTAAAAGAAAAAAGGAAAAAAGGGAAGGATC

JGR_3859/1-3342_(TcII-like)/1-294 201 GGGGAATGAAGGGGAAATAAGTAAAAATAATTAAATCAAAAACCTCTCATATTCTCGATCCTTGCGCAGCGCGTGGGAGGGTAAATAGCAAATAAAA 294
JGR_3860/1-526_(TcIII-like)/1-294 201 GGGGAATGAAGGGGAAATAAGTAAAAATAATTAAATCAACAGCCCTCATATTCTCGATCCTTGCGCAGCGCGTGGGAGGGTAAATAGCAAATAAAA 294
JGR_3860/1-527_(TcII-like)/1-292 199 GGGGAATGAAGGGGAAATAAGTAAAAATAATTAAATCAAAAACCTCTCATATTCTCGATCCTTGCGCAGCGCGTGGGAGGGTAAATAGCAAATAAAA 292
JGR_3860/1-521_(TcII)/1-287 194 GGGGAATGAAGGGGAAATAAGTAAAAATAATTAAATCAAAAACCTCTCATATTCTCGATCCTTGCGCAGCGCGTGGGAGGGTAAATAGCAAATAAAA 287

Consensus

GGGGAATGAAGGGGAAATAAGTAAAAATAATTAAATCAAAAACCTCTCATATTCTCGATCCTTGCGCAGCGCGTGGGAGGGTAAATAGCAAATAAAA

Conserved sequence motif #13

JGR_8957/1-780_(TcIII-like)/1-452 1 ACACGAAA - - - - - TACACAAAGTACTACACAAAAGAATGTCTCCCACAGCTGTCAGGATGAACAACGCCTAAGAGGCGCAGCACGGGCTTGAGTAGCG 93
JGR_4004/1-1065_(TcII-like)/1-453 1 ACTCAAAGGTATCAGTATAGAAAGTACTACACAAAAGAATGTCTCCTACGGCTGCCAGGATGAACAACGCCTAAGAGGCGCAGCACGGGTTTGAGCGGTG 100
JGR_4004/1-1055_(TcII)/1-450 1 ACTCAAAGGTATCAGTATAGAAAGTACTACACAAAAGAATGTCTCCTACGGCTGCCAGGATGAACAACGCCTAAGAGGCGCAGCACGGGTTTGAGCGGTG 100
JGR_4004/1-1087_(TcIII-like)/1-459 1 ACTCAAAAATATCAGTATGGAAAGTACTACACAAAAGAATGTCTCCCACAGCTGTCAGGATGAACAACGCCTAAGAGGCGCAGCACGGGGTTTGAGTAGCG 100
JGR_8957/1-936_(TcI_SylvioX10)/1-446 1 ACACGAAA - - - - - TACAAAAGTACTACACAAAAGAATGTCTCCCACAGCTGTCAGGATGAACAACGCCTAAGAGGCGCAGCACGGGTTTGAGCAGCG 93
JGR_4004/1-936_(TcI_SylvioX10)/1-446 1 ACACGAAA - - - - - TACAAAAGTACTACACAAAAGAATGTCTCCCACAGCTGTCAGGATGAACAACGCCTAAGAGGCGCAGCACGGGTTTGAGCAGCG 93

Consensus

AC+C+AAAGTATCAGTA+AGAAAGTACTACACAAAAGAATGTCTCCCACAGCTGTCAGGATGAACAACGCCTAAGAGGCGCAGCACGGGTTTGAGCAGCG

JGR_8957/1-780_(TcIII-like)/1-452 94 TTGCGCGGAGAGCGCCCGGCTGATGGCCATTCACTTGGGCATGGTGCCCTCCAGTGCAACGGTGGACCAGCTGCGCATCGCGGTGCGCGGTGCGGCGGAG 193
JGR_4004/1-1065_(TcII-like)/1-453 101 TTGCGCGTAGAGCGCCCGGCTGATGGCCATTCACTTGGGCATAGTGCCCTCCAGTGCAACGGTGGACCAGCTGCGCGTCGCCGTGCGCGGTGCGGCGGAG 200
JGR_4004/1-1055_(TcII)/1-450 101 TTGCGCGGAGAGCGCCCGGCTGATGGCCATTCACTTGGGCATGGTGCCCTCCAGTGCAACGGTGGACTAGCTGCGCGTCGCCGTGCGCGGTGCGGCGGAG 200
JGR_4004/1-1087_(TcIII-like)/1-459 101 TTGCGCGGAGAGCGCCCGGCTGATGGCCATTCACTTGGGCATGGTGCCCTCCAGTGCAACGGTGGACCAGCTGCGCATCGCGGTGCGCGGTGCGAGCGGAG 200
JGR_8957/1-936_(TcI_SylvioX10)/1-446 94 TTGCGCGGAGAGCGCCCGGCTGATGGCCATTCACTTGGGCATGGTGCCCTCCAGTGCAACGGTGGACCAGCCGCGCCTCGCGGTGCGCGGTGCGGCGGAG 193
JGR_4004/1-936_(TcI_SylvioX10)/1-446 94 TTGCGCGGAGAGCGCCCGGCTGATGGCCATTCACTTGGGCATGGTGCCCTCCAGTGCAACGGTGGACCAGCCGCGCCTCGCGGTGCGCGGTGCGGCGGAG 193

Consensus

TTGCGCGGAGAGCGCCCGGCTGATGGCCATTCACTTGGGCATGGTGCCCTCCAGTGCAACGGTGGACCAGCTGCGC+TCGCGGTGCGCGGTGCGGCGGAG

JGR_8957/1-780_(TcIII-like)/1-452 194 CCTGAATCGATCACCCAGTGTCGCTGGTGGTGGACGACGGTGAGCTCTCCAACACCACATTTGTTCGGCGAGTTTCATGCAATCTCGGAGGATGCTGACG 293
JGR_4004/1-1065_(TcII-like)/1-453 201 CTTGAACCGATCGCCCCAGTGTCGCTGGTGGTGGACGACGGTGTCCTCCAACACCACATTTGTTCGGCGAGTTTCATGCGCTCTCAGAGGATGCCGACG 300
JGR_4004/1-1055_(TcII)/1-450 201 CTTGAACCGATCGCCCCAGTGTCGCTGGTGGTGGACGACGGTGTCCTCCAACACCACATTTGTTCGGCGAGTTTCATGCGCTCTCAGAGGATGCCGACG 300
JGR_4004/1-1087_(TcIII-like)/1-459 201 CCTGAATCGATCACCCAGTGTCGCTGGTGGTGGACGACGGTGTCCTCCAACACCACATTTGTTCGGCGAGTTTCATGCAATCTCGGAGGATGCTGACG 300
JGR_8957/1-936_(TcI_SylvioX10)/1-446 194 CTTGAATCGATCACCCAGTGTCGCTGGTGGTGGACGACGGTGTCCTCCAAGCACCACATTTGTTCGGCGAGTTTCATGCAATCTCAGAGGATGCCGACG 293
JGR_4004/1-936_(TcI_SylvioX10)/1-446 194 CTTGAATCGATCACCCAGTGTCGCTGGTGGTGGACGACGGTGTCCTCCAAGCACCACATTTGTTCGGCGAGTTTCATGCAATCTCAGAGGATGCCGACG 293

Consensus

CTTGAATCGATCACCCAGTGTCGCTGGTGGTGGACGACGGTGTCCTCCAACACCACATTTGTTCGGCGAGTTTCATGCAATCTCAGAGGATGCCGACG

JGR_8957/1-780_(TcIII-like)/1-452 294 GCTTCCCCTACCTCGATTATACTTTGGAGCGAAAGTTCTGTCTTTTCTCTTCATGCGTCTTCTGGTGGTTCGTACTTAAGGATGATACATTGCTCGTTGAG 393
JGR_4004/1-1065_(TcII-like)/1-453 301 GCTTCCCCTACCTCGATTATACTTTGGAGCGAAATTTCTGTCTTTTCTATTCAATTCGACTTCTGGTGGTTCGTACTTAAGGATGATACATTGCTCGTTGAG 400
JGR_4004/1-1055_(TcII)/1-450 301 GCTTCCCCTACCTCGATTATACTTTGGAGCGAAATTTCTGTCTTTTCTATTCAATTCGACTTCTGGTGGTTCGTACTTAAGGATGATACATTGCTCGTTGAG 400
JGR_4004/1-1087_(TcIII-like)/1-459 301 GCTTCCCCTACCTCGATTATACTTTGGAGCGAAAGTTCTGTCTTTTCTCTTCATGCGTCTTCTGGTGGTTCGTACTTAAGGATGATACATTGCTCGTTGAG 400
JGR_8957/1-936_(TcI_SylvioX10)/1-446 294 GCTTCCCCTACCTCGATTATACTTTGGAGCGAAAGTTCTTTCTTTTCTCTTCATGCGTCTTCTGGTGGTTCGTACTTAAGGATGATACATGGCTCGTTGAG 393
JGR_4004/1-936_(TcI_SylvioX10)/1-446 294 GCTTCCCCTACCTCGATTATACTTTGGAGCGAAAGTTCTTTCTTTTCTCTTCATGCGTCTTCTGGTGGTTCGTACTTAAGGATGATACATGGCTCGTTGAG 393

Consensus

GCTTCCCCTACCTCGATTATACTTTGGAGCGAAAGTTCTGTCTTTTCTCTTCATGCGTCTTCTGGTGGTTCGTACTTAAGGATGATACATTGCTCGTTGAG

JGR_8957/1-780_(TcIII-like)/1-452 394 TGGCCGGGAATGGATAGGATTGTTTTCTCTTTTGTTGTTGTTGTTGGTTGTTTATTTTG 452
JGR_4004/1-1065_(TcII-like)/1-453 401 TGGCCGGGAATGGATAGGATTGTTT - - TTTTGTGTGTT - - - GTTGTTTATTTTG 453
JGR_4004/1-1055_(TcII)/1-450 401 TGGCCGGGAGTGGATAGGATTGTTT - - TTTTGTGTGTT - - - - GTTGTTTATTTTG 450
JGR_4004/1-1087_(TcIII-like)/1-459 401 TGGCCGGGAATGGATAGGATTGTTTTCTCTTTTGTTGTTGTTGTTGGTTGTTTATTTTG 459
JGR_8957/1-936_(TcI_SylvioX10)/1-446 394 TGCCCGGGGAATGGATGGGATT - - - - - TTTTCTGTGTGTTGTTGTTGGTTGTTTATTTTG 446
JGR_4004/1-936_(TcI_SylvioX10)/1-446 394 TGCCCGGGGAATGGATGGGATT - - - - - TTTTCTGTGTGTTGTTGTTGGTTGTTTATTTTG 446

Consensus

TGGCCGGGAATGGATAGGATTGTTTTCTTTTTGTTGTTGTTGTTGGTTGTTTATTTTG

Conserved sequence motif #14

| | | | | | | | |
|---|---|-----------|-----------------|-----------------|----------|---|-----|
| <i>JGR_4012/1-694 (TcII-like)/1-213</i> | 1 | TCTTG | TGGCTGGAGGACCTC | AAAGTTTGCTACCTC | GTAAGTAA | TATATATATATATATATGTATGTATTTAGATGTACACTTACTTGGTTTTAAACTTCGAG | 100 |
| <i>JGR_4012/1-443 (TcII)/1-192</i> | 1 | - - - - - | - - - - - CTC | AAAGTTTGCTACCTC | GTAAGTAA | - - - TATATATATATATATATATGTAGATGTACACTTACTTGGTTTTAAACTTCGAG | 79 |
| <i>JGR_4036/1-637 (TcII-like)/1-203</i> | 1 | TCTTG | TGGCTGGAGGACCCC | AAAGTTTGCTACCTC | GTAAGTAA | TATATATA - - - - - TATATGTAG - - ATGTACACTTACCTGGTTTTAAACTTCGAG | 90 |
| <i>JGR_4036/1-646 (TcIII-like)/1-202</i> | 1 | TCTTG | TGGCTGGAGGATCCC | AAAGTTTCTACCTC | GTAGGTAA | TATATATA - - - - - TATGTGTAGATGTGTACACTTACCTGGTGTAAACCTCGAG | 92 |
| <i>JGR_4036/1-642 (TcI/RcI4)/1-209</i> | 1 | TCTTG | TGACTGGAGGATCCC | AAAGTTTGCTACCTC | GTAGGTAA | TATATATATATA - - - - - TATGTGTGTAGATGTATACACTTACCTGGTGTAAACTTTGAG | 96 |
| <i>JGR_4036/1-640 (TcI_SylvioX10)/1-207</i> | 1 | TCTTG | TGACTGGAGGATCCC | AAAGTTTGCTACCTC | GTAGGTAA | TATATATATA - - - - - TATGTGTGTAGATGTATACACTTACCTGGTGTAAACTTTGAG | 94 |

Consensus

TC TTG TGG C TGG AGG AT C C C A A A G T T T G C T A C C T C G T A + G T A A T A T A T A T A T A T A T A T A T G T G T A G A T + T G T A C A C T T A C C T G G T + T T A A A C T T C G A G

| | | | | | | | |
|---|-----|-------------|-------------------|-------------------------|--------------------------------|---------------------------|-----|
| <i>UGR_4012/1-694_(TcII-like)/1-213</i> | 101 | GATATGGTGAA | TCCCCACTCTTATTCCA | TTCATCTCTTTCCCTATTCCATA | TCGGGTTTGTTTTCTCCTATTATTGAT | TAAACTCAGGATTTGGCCAGCGGCC | 200 |
| <i>UGR_4012/1-443_(TcII)/1-192</i> | 80 | GATATGGTGAA | TCCCCACTCTTATTCCA | TTTAACTCTTTCCCTATTCCATA | TCGGGTTTGTTTTCTCCTATTATTGAT | TAAACTCAGGATTCGGCCAGCGGCC | 179 |
| <i>UGR_4036/1-637_(TcII-like)/1-203</i> | 91 | GATATGGTGAA | TCCCCACTCTTATTCCA | TTTATCTCTTTCCCTATTCCATA | TCGGGTTTGTTTTCTCCTATTATTGAT | TGAACTCAGGATTTGGCCAGCGGCC | 190 |
| <i>UGR_4036/1-646_(TcIII-like)/1-202</i> | 93 | GATATGGTGAA | TCCCCACTCTTTTCCA | TTTATCCCTTTCCCTATTCCATA | TCGGGTTTGTTTTCTCCTAT - - - TGA | TAAACTCAGGATTCGGCCAGCGGCC | 189 |
| <i>UGR_4036/1-642_(TcI/RcI4)/1-209</i> | 97 | GACATGGTGAA | TCCCCACTCGTATTCCG | TTTATCCCTTTCCCTATTCCATA | TCGGGTTTGTTTTCTCCTATTATTGAT | TGAACTCAGGACTTGGCCAGCGGCC | 196 |
| <i>UGR_4036/1-640_(TcI_SylvioX10)/1-207</i> | 95 | GACATGGTGAA | TCCCCACTCGTATTCCG | TTTATCCCTTTCCCTATTCCATA | TCGGGTTTGTTTTCTCCTATTATTGAT | TGAACTCAGGACTTGGCCAGCGGCC | 194 |

Consensus

GATATGGTGAATCCCCACTCTTATTCCATTTATC+CTTTCCTATTCCATATCGGGTTTGTTTTCTCCTATTATTGAT+AACTCAGGGATTTGGCCAGCGGGC

| | | | |
|--------------------------------------|-----|----------------|-----|
| IGR_4012/1-694_(TcII-like)/1-213 | 201 | CAGAAAGATTATTC | 213 |
| IGR_4012/1-443_(TcII)/1-192 | 180 | CAGAAAGATTATTC | 192 |
| IGR_4036/1-637_(TcII-like)/1-203 | 191 | CAGAAAGATTATTC | 203 |
| IGR_4036/1-646_(TcIII-like)/1-202 | 190 | CAGAGGATTATTC | 202 |
| IGR_4036/1-642_(TcI_JRcI4)/1-209 | 197 | CAGAGGATTATTC | 209 |
| IGR_4036/1-640_(TcI_SylvioX10)/1-207 | 195 | CAGAGGATTATTC | 207 |

Consensus

CAGA+GATTATTC

Conserved sequence motif #15

JGR_6735/1-1085_(TcII-like)/1-493 1 TTGTTGTCGATGCTTCTGGAAAGAATGTGCGGCCAGATGGGACTCGGGAAATGATAGTGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAA 100
JGR_6735/1-1083_(TcII)/1-493 1 TTGTTGTCGATGCTTCTGGAAAGAATGTGCGGCCAGATGGGACTCGGGAAATGATAGTGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAA 100
JGR_4425/1-1300_(TcII-like)/1-485 1 TTATTGTCGATGCTTCTGGAAAGAATGTGCGGCCAGTTGGGACTCGGGAAATGATAGTGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAA 100
JGR_4425/1-1252_(TcIII-like)/1-496 1 TTATTGTCGATGCTTCTGGAAAGAATGTGCGGCCAGATGGGACTCGGGAAATGATAGTGCTGTTTGTTTAACTCCCTTTCCTTTTATATATCTGTCAA 100

Consensus

TT+TTGTCGATGCTTCTGGAAAGAATGTGCGGCCAGATGGGACTCGGGAAATGATAGTGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAA

JGR_6735/1-1085_(TcII-like)/1-493 101 CTGATTTTGGGCTTTCTAACTGTGCACG - TTGGAAGACAGCGAGTGGCGTTCTTTTCATGTG - - TGTGTGTCTGTGTGTTTGTGTGTTTTGTGTATTTCCA 197
JGR_6735/1-1083_(TcII)/1-493 101 CTGATTTTGGGCTTTCTAACTGTGCACG - TTGGAAGACAGCGAGTGGCGTTCTTTTCATGTG - - TGTGTGTCTGTGTGTTTGTGTGTTTTGTGTATTTCCA 197
JGR_4425/1-1300_(TcII-like)/1-485 101 CTGATTTTGGGCTTTCTAACTGTGCACG - TTGGAAGACAGCGAGTGGCGTTCTTTTCATGTG - - - - - TGTGTGTCTGTGTGTTTGTGTATTTCCA 189
JGR_4425/1-1252_(TcIII-like)/1-496 101 CTGATTTTGGGCTTTCTAACTGTGCACGTTTGGGAAGGCGAGTGGCGTTCTTTCTTGTGTGTGTGTGTCTGTGTGTTTTGTGTATTTCCA 200

Consensus

CTGATTTGGGCTTTCTAACTGTGCACG - TTGGAAGACAGCGAGTGGCGTTCTTTTCATGTG - - TGTGTGTCTGTGTGT+TGTGTGTTTTGTGTATTTCCA

JGR_6735/1-1085_(TcII-like)/1-493 198 CCCCCTGCTGCGCCTCCACGCGGAGAGGCATCCGGCGGCTGCGGGGCTTTATAAATGACTGCCACCTCGTGAGCTCACAGCGA+CCCGGTTCTTATGACCA 297
JGR_6735/1-1083_(TcII)/1-493 198 CCCCCTGCTGCGCCTCCACGCGGAGAGGCATCCGGCGGCTGCGGGGCTTTATAAATGACTGCCACCTCGTGAGCTCACAGCGAGCCCGGTTCTTATGACCA 297
JGR_4425/1-1300_(TcII-like)/1-485 190 CCCCCTGCTGCGCCTCCACGCGGAGAGGCATCCGGCGGCTGCGGGGCTTTATAAATGACTGCCACCTCGTGAGCTCACAGCGA+CCCGGTTCTTATGACCA 289
JGR_4425/1-1252_(TcIII-like)/1-496 201 CCCCCTGCTGCGCCTCCACGCGGAGAGGCATCCGGCGGCTGCGGGGCTTTTTAAAGGACTGCCACTTCTTGGGCTCACAGCGAGCCCGGTTCTCATGACCA 300

Consensus

CCCCCTGCTGCGCCTCCACGCGGAGAGGCATCCGGCGGCTGCGGGGCTTTATAAATGACTGCCACCTCGTGAGCTCACAGCGA+CCCGGTTCTTATGACCA

JGR_6735/1-1085_(TcII-like)/1-493 298 CATGTTTTCTGAATCCATTTGTGTACTGATGTATGAGTGTTTGGTGAATCTTCTCTGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCT 397
JGR_6735/1-1083_(TcII)/1-493 298 CATGTTTTCTGAATCCATTTGTGTACTGATGTATGAGTGTTTGGTGAATCTTCTCTGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCT 397
JGR_4425/1-1300_(TcII-like)/1-485 290 CATGTTTTCTGAATCCATTTGTGTACTGATGTATGAGTGTTTGGTGAATCTTCTCTGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCT 389
JGR_4425/1-1252_(TcIII-like)/1-496 301 CATGTTTTCTGAATCCATTTGTTACTGATGTATGAGTGTTTGGTGAATCTTCTCTGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCT 400

Consensus

CATGTTTTCTGAATCCATTTGTGTACTGATGTATGAGTGTTTGGTGAATCTTCTCTGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCT

JGR_6735/1-1085_(TcII-like)/1-493 398 CACATTGCGTCATTGCGCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACGCGCAGGTTTGCTGTTGCTCTTACGCGTCCGGGGTGGGCAGCCAGA 493
JGR_6735/1-1083_(TcII)/1-493 398 CACATTGCGTCATTGCGCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACGCGCAGGTTTGCTTTTGTCTTTGCGCGTCCGGGGTGGGCAGCCAGA 493
JGR_4425/1-1300_(TcII-like)/1-485 390 CACATTGCGTCATTGCGCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACACGCGAGGTTTGCTTTTGTCTTTGCGCGTCCGGGGTGGGCAGCCAGA 485
JGR_4425/1-1252_(TcIII-like)/1-496 401 CACATTGCGTCATTGCGCCTCCGTGGGCATAAAGAAAAGTGCCTCATCCACGCGCAGGTTTGCTGTTGCTCTTGCAGCGTCCGGGGTGGGCAGCCAGA 496

Consensus

CACATTGCGTCATTGCGCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACGCGCAGGTTTGCT+TTTGCTCTTGCAGCGTCCGGGGTGGGCAGCCAGA

Conserved sequence motif #16

JGR_6481/1-1432_(TcII-like)/1-476 1 TTGA - - - CATTTCGATTTTGTGAAAAGAATGATTGCGAGAGGGCTGGCCACCCAAATTTAATATGACATCCTGATAAGACGAAAATATTTATTTACAATT 97
 JGR_6481/1-1424_(TcII)/1-479 1 TTGA - - - CATTTCGATTTTGTGAAAAGAATGATTGCGAGAGGGCTAGCCACCCAAATTTAATATGACATCCTGATAAGACGAAAATATTTATTTACAATT 97
 JGR_6514/1-1422_(TcII-like)/1-480 1 TTGATTGTGTTGGGAGCTTGTGAAAAGAATGATTGCGAGAGGGCTGGCCACCCGAATTTAATATGACATCCTGATAAGACGAAAACATTTATTTACAATT 100
 JGR_6514/1-1455_(TcII)/1-479 1 TTGATTGTGTTAGGAGCTTGTGAAAAGAATGATTGCGAGAGGGCTGGCCACCCAAATTTAATATGACATCCTGATAAGACGAAAATATTTATTTACAATT 100

Consensus

TTGATTG++TTT+GA++TTGTGAAAAGAATGATTGCGAGAGGGCTGGCCACCCAAATTTAATATGACATCCTGATAAGACGAAAATATTTATTTACAATT

JGR_6481/1-1432_(TcII-like)/1-476 98 ATTTTCTCTCTTACGGTTCATTTGTAAAGACTGCAATGGGAGGAGTCAATGAACCGATAAAGTCACGACGGAATTTGTTT - - - GTTTTTATTTTTGTCGTTT 194
 JGR_6481/1-1424_(TcII)/1-479 98 ATTTTCTCTCTTACGGTTCATTTGTAAAGACCGCAATGGGAGGAGTCAATGAACCGATAACATCAAGACGGAATTTGTTTTTGTTTTTTATTTTTGTCGTTT 197
 JGR_6514/1-1422_(TcII-like)/1-480 101 ATTTTCTCTCTTACGGTTCATTTGTAAAGACCGCAATGGGAGGAGTCAATGAACCGATAAAGTCACGACGGAATTTGTTCT - - - TTTTTTAATTTTTGTCGTTT 198
 JGR_6514/1-1455_(TcII)/1-479 101 ATTTTCTCTCTTACGGTTCATTTGTAAAGACCGCAATGGGAGGAGTCAATGAACCGATAACGTCAGACGGAATTTGTTT - - - TTTTTTAATTTTTGTCGTTT 197

Consensus

ATTTTCTCTCTTACGGTTCATTTGTAAAGACCGCAATGGGAGGAGTCAATGAACCGATAA+GTCA+GACGGATTTGTTTT - - - TTTTTATTTTTGTCGTTT

JGR_6481/1-1432_(TcII-like)/1-476 195 CACTCGGCCCTTTTGAATTCCTCCACCTTGCGGCGGTGTCTTGTTGGCAGGAGGACCTCAAATTCTACCAATTTTTTAACATAATAAACATCCCCAATCC 294
 JGR_6481/1-1424_(TcII)/1-479 198 CACTCGGCCCTTTTGAATTCCTCCACCTTGCGGCGGTGTCTTGTTGGCAGGAGGACCTCAAATTCTACCAATTTTTTAACATAATAAACATCCCCAATCC 297
 JGR_6514/1-1422_(TcII-like)/1-480 199 CACTCGGCCCTTTTGAATTCCTCCACCTTGCGGCGGTGTCTTGTTGGCAGGAGGACCTTAAATTCCACCAATTTTTTAACATAATAAACATCCCCAATCC 298
 JGR_6514/1-1455_(TcII)/1-479 198 CACTCGGCCCTTTTGAATTCCTCCACCTTGCGGCGGTGTCTTGTTGGCTGGAGGACCTCAAATTCTACCAATTTTTTAACATAATAAACATCCCCAATCC 297

Consensus

CACTCGGCCCTTTTGAATTCCTCCACCTTGCGGCGGTGTCTTGTTGGCAGGAGGACCTCAAATTCTACCAATTTTTTAACATAATAAACATCCCCAATCC

JGR_6481/1-1432_(TcII-like)/1-476 295 GAATAGAGCGCAACATGTACGAGAGCGGCAATTTGAATAAATCTATCTATCTATATATACTTGAAGCAAACATGGAGGATATGGCGAGGCCACCGCC 394
 JGR_6481/1-1424_(TcII)/1-479 298 GAATAGAGCGCAACATGTACGAGAGCGGCAATTTGAATAAATCTATCTATCTATATATACTTGAAGCAAACATGGAGGATATGGCGAGGCCACCGCC 397
 JGR_6514/1-1422_(TcII-like)/1-480 299 GAATAGAGCGCAACATGTACGAGAGCGGCAATTTGAATAAATCTATCTATCTATATATACTTGAAGCAAACATGGAGGATATGGCGAGGCCACCGCC 398
 JGR_6514/1-1455_(TcII)/1-479 298 GAATAGAGCGCAACATGTACGAGAGCGGCAATTTGAATAAATCTATCTATCTATATATACTTGAAGCAAACATGGAGGATATGGCGAGGCCACCGCC 397

Consensus

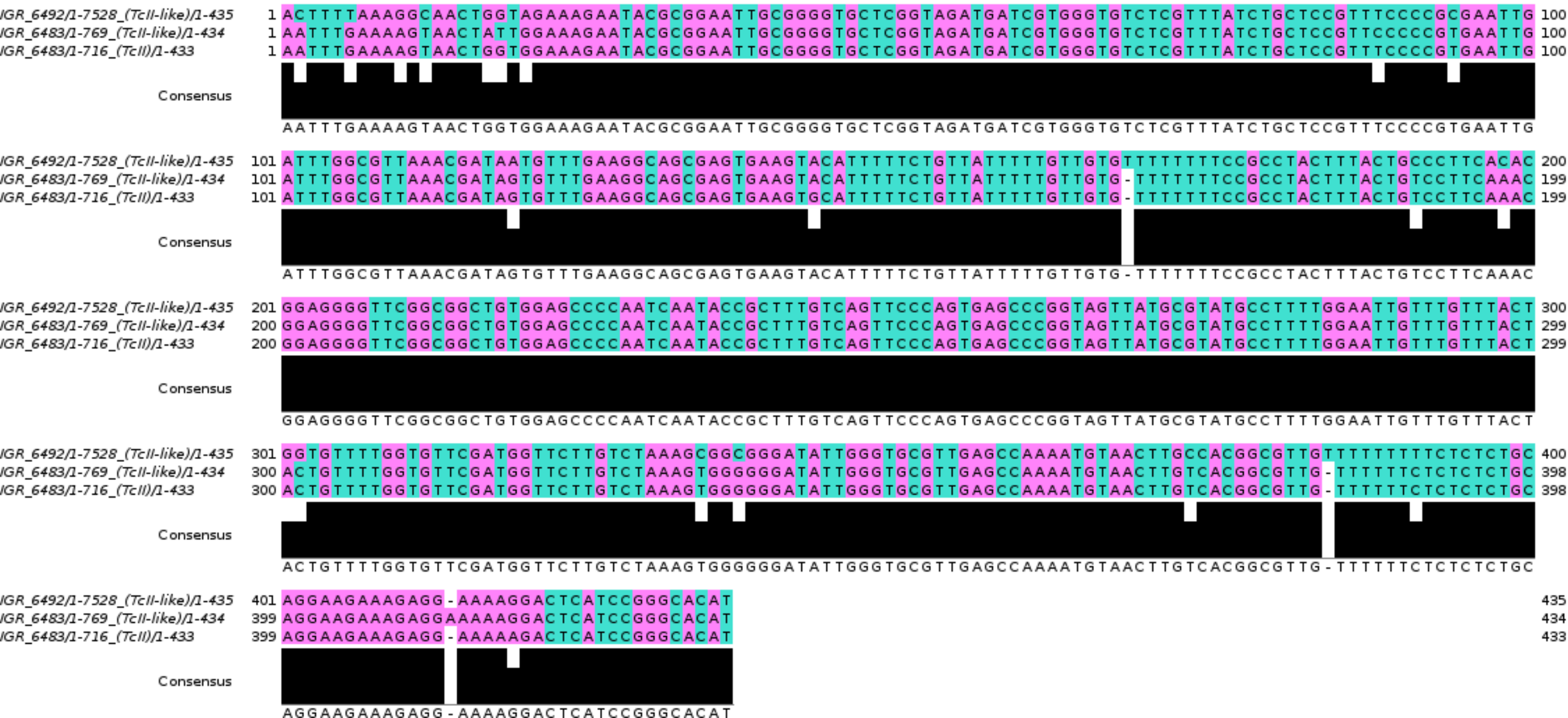
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JGR_6481/1-1432_(TcII-like)/1-476 395 TCTCCTTTACCTTTTCTTTCTTGTCTTATTTTTATTTCTTTAGAGAGGTTTCGGGATCTGGCTAGCAGCAGAGGTGAGTATTT 476
 JGR_6481/1-1424_(TcII)/1-479 398 TCTCCTTTACCTTTTCTTTCTTGTCTTATTTTTATTTCTTTAGAGAGGTTTCGGGATCTGGCTAGCAGCAGAGGTGAGTATTT 479
 JGR_6514/1-1422_(TcII-like)/1-480 399 TCTCCTTTACCTTTTCTTTCTTGTCTTATTTTTATTTCTTTAGAGAGGTTTCAGGATCTGGCTAGCAGCCAGGC GGATGTTT 480
 JGR_6514/1-1455_(TcII)/1-479 398 TCTCCTTTACCTTTTCTTTCTTGTCTTATTTTTATTTCTTTAGAGAGGTTTCGGGATCTGGCTAGCAGCCAGGC GGATGTTT 479

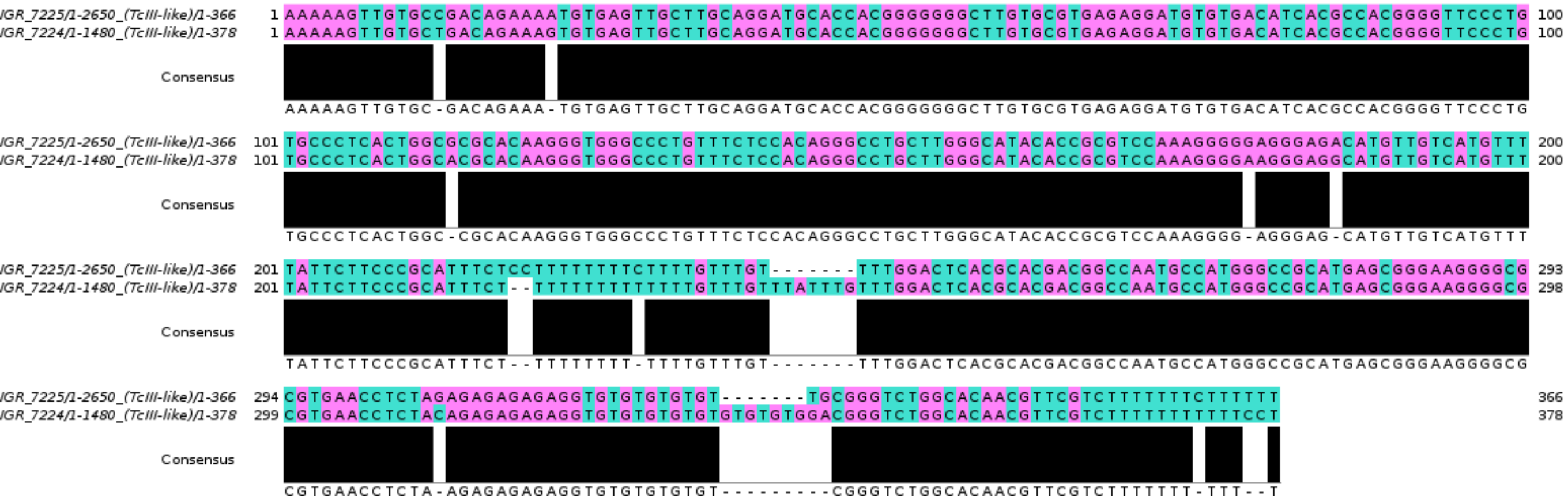
Consensus

TCTCCTTTACCTTTTCTTTCTTGTCTTATTTTTATTTCTTTAGAGAGGTTTCGGGATCTGGCTAGCAGC++AGG+G++T+TTT

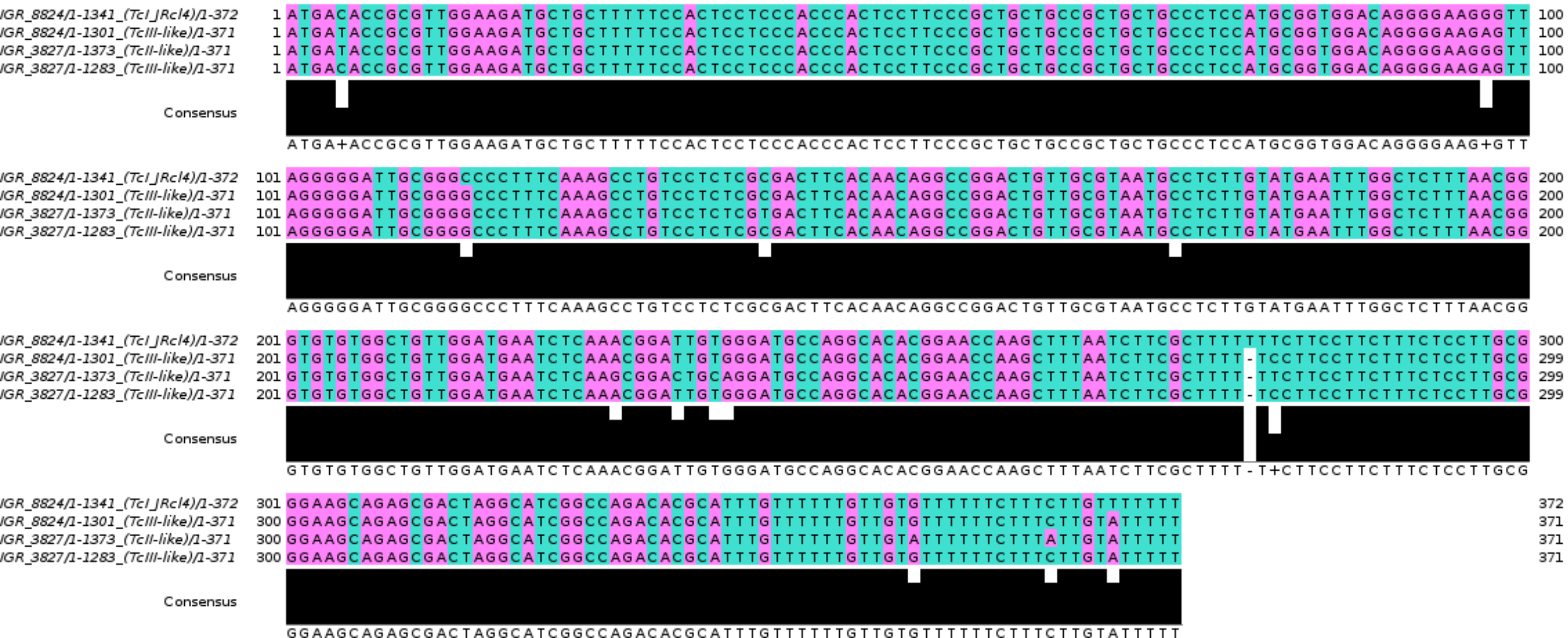
Conserved sequence motif #17



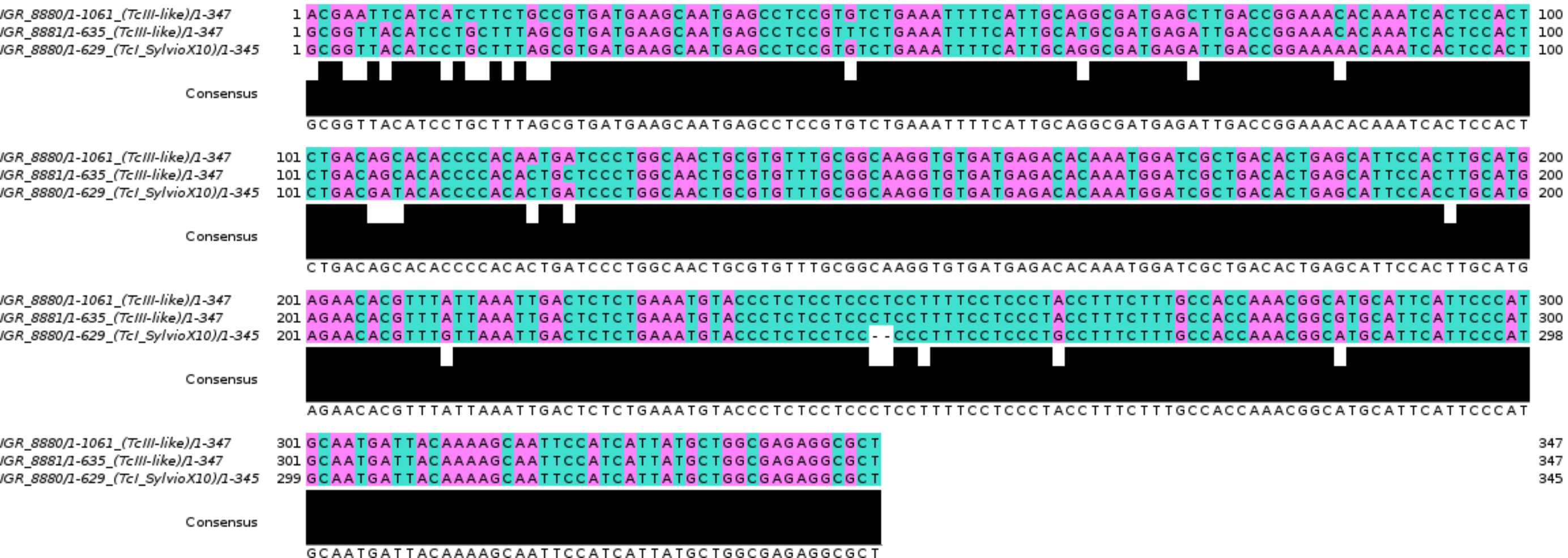
Conserved sequence motif #18



Conserved sequence motif #19



Conserved sequence motif #20



Conserved sequence motif #21

