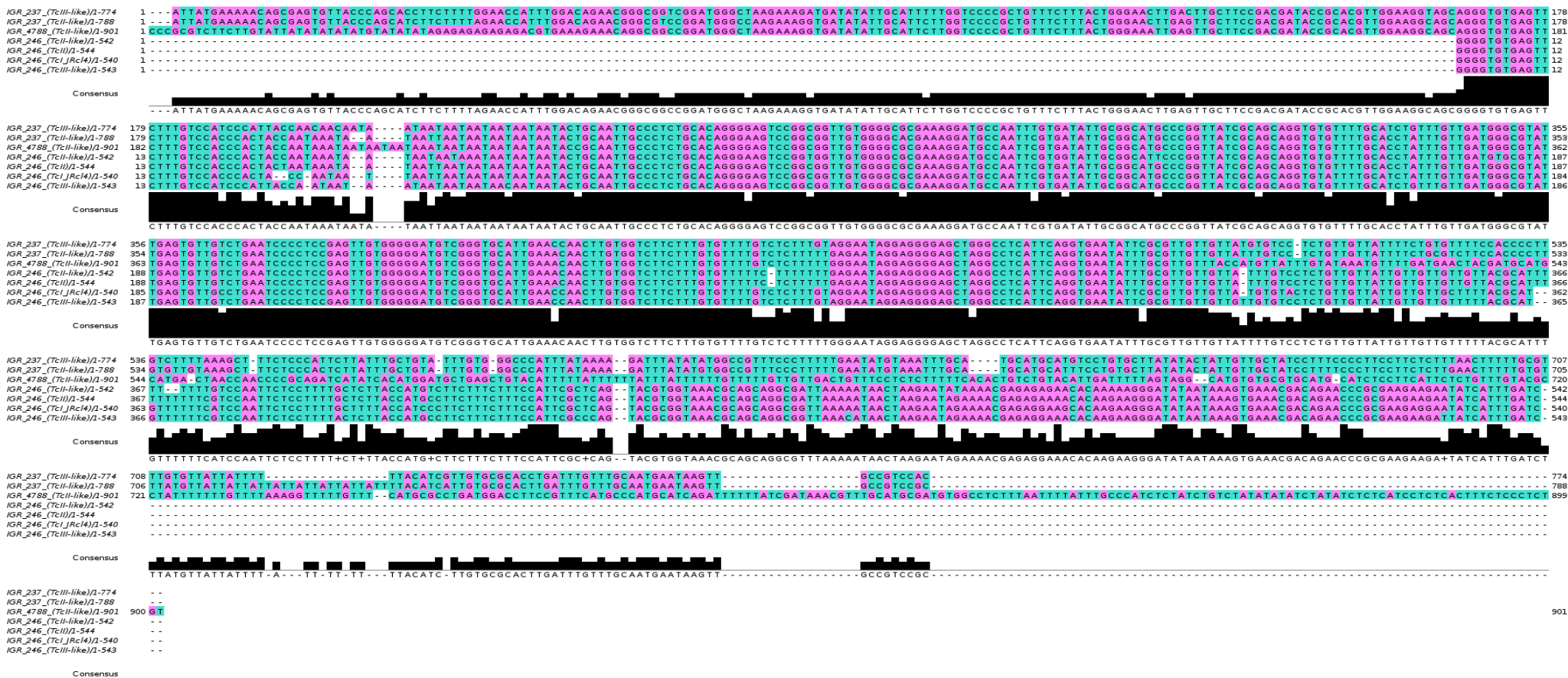
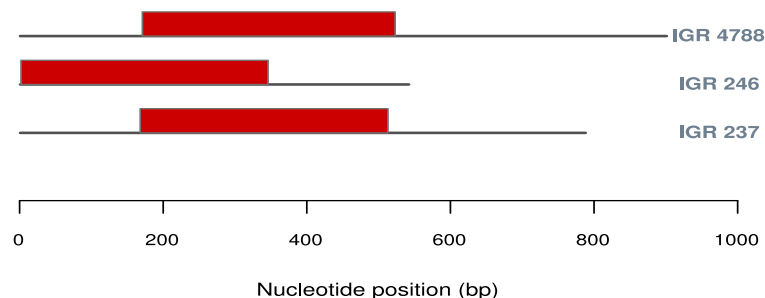


## Motif #1

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
1	237	TcCLB.508277.20	protein kinase, putative	TcCLB.509941.120	protein kinase, putative	TcCLB.508277.30	hypothetical protein, conserved	TcCLB.509941.140	hypothetical protein, conserved
	246	TcCLB.508277.140	phosphomevalonate kinase protein, putative	TcCLB.507913.20	phosphomevalonate kinase protein, putative	TcCLB.508277.150	proliferative cell nuclear antigen (PCNA), putative	TcCLB.507913.30	proliferative cell nuclear antigen (PCNA), putative
	4788	TcCLB.508277.220	hypothetical protein	TcCLB.509945.30	hypothetical protein	TcCLB.508277.230	nucleolar RNA binding protein, putative	No ortholog	-



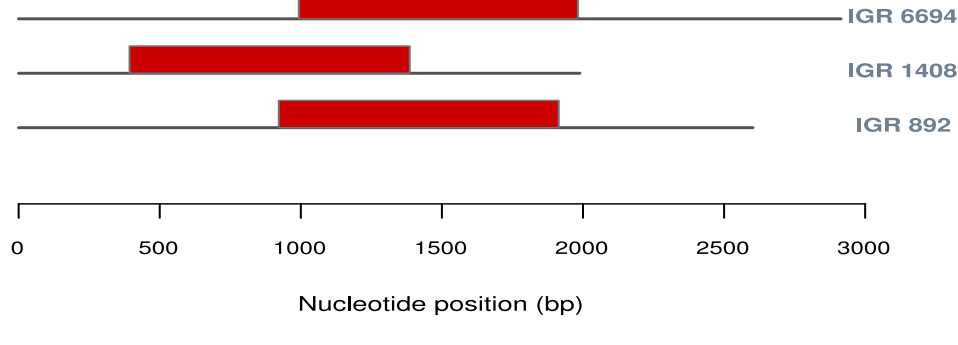






### Motif #3

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
3	892	TCCLB.509233.50	hypothetical protein, conserved	TCCLB.509437.70	hypothetical protein, conserved	TCCLB.509233.60	hypothetical protein, conserved	TCCLB.509437.60	hypothetical protein, conserved
	1408	TCCLB.510257.80	peptidase M20/M25/M40, putative	TCCLB.509213.120	peptidase M20/M25/M40, putative	TCCLB.510257.90	autophagocytosis associated protein, putative	TCCLB.509213.130	autophagocytosis associated protein, putative
	6694	TCCLB.510761.44	cyclophilin-like protein, putative	No_ortholog	-	TCCLB.510761.60	casein kinase II, putative	No_ortholog	-



1 ATAAAGCGGAGCAAGATCCAGCTCAAGACTGAAAAAAGAAAGTAGAGACAAAATACACATAAATATATCCACAGTATTAAAAACAAACAAAAAAGAA 100  
1 ATAAAGCGAGAGCAAGATCCAGCTCAAGACTGAAAAAAGAAAGTAGAGACAAAATACACATAAATATATCCACAGTATTAAAAACAAACAAAAAAGAA 100

Consensus

HGR\_892\_(TcIII-like)/1-2601 46 TGGAAATGGAAACG - - - - - GGGTGAAG - - - - - GGAATTCGTTGTGTTCCACAGCTGTGGCTCATTTGGCAGCT - - - - - TT - - - - - ATTGGTGCCTTT 118  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 101 TGCATGAAAAGAAAGAGAGGGGTAAAAAATAAGGGGTGAGGATCCAGAGCTCGGACGCATTTTCGACACAAAGTTTCCTGTGTGTTGATTAAAA 200  
HGR\_6694\_(TcII)/1-2893 101 TGCATGAAAAGAAAGAGAGGGGTAAA - - - - - AAAAATAAGGGGTGAGGATCCAGAGCTCGGACGCATTTTCGACACAAAGTTTCCTGTGTGTTGATTAAAA 198

Consensus

TGCATGAAAAGAAAGAGAGGGGTAAA - - - - - AAAAATAAGGGGTGAGGATCCAGAGCTCGGACGCATTTTCGACACAAAGTTTCCTGTGTGTTGATTAAAA

HGR\_892\_(TcIII-like)/1-2601 119 GCAAGCTCTCTCCCTGTAA - - - - - TGTGGGTGTGGTGTATGGATGGTGGATGGCAGGGGGGGGGAGGGGAATATTGCTGAGCGCATTTGTTTGTAT 210  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 201 GAAAAACAATCACTACAGACGCGGCATACACGTTTTTTTTTAAAAGCGAAGGCGGTGTGGTGCAGTAATGAACCTGACATAGCAGCGCATTTTCGTTATA 300  
HGR\_6694\_(TcII)/1-2893 199 GAAAAACAATCACTACAGACGCGGCATACACGTTTTTTTTTAAAAGCGAAGGCGGTGTGGTGCAGTAATGAACCTGACATAGCAGCGCATTTTCGTTATA 298

Consensus

GAAAAACAATCACTACAGACGCGGCATACACGTTTTTTTTTAAAAGCGAAGGCGGTGTGGTGCAGTAATGAACCTGACATAGCAGCGCATTTTCGTTATA

HGR\_892\_(TcIII-like)/1-2601 211 - - - - - GTCTCTTGCAATGGTGTATTTCAT - - - - - GCGATG - - - - - CGAAGAAGTTCACACGCCACGCA 268  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 201 TTTTGTCTTCTTTGGATTGCCAGCCTCTTCTCCAACTGCGATGCTTTATTTTGGACGTAAAAATATTCGGTTTGCAGATCTCTTTAAAAATTAAAGCA 400  
HGR\_6694\_(TcII)/1-2893 201 TTTTGTCTTCTTTGGATTGCCAGCCTCTTCTCCAACTGCGATGCTTTATTTTGGACGTAAAAATATTCGGTTTGCAGATCTCTTTAAAAATTAAAGCA 398

Consensus

TTTGTCTTCTTTGGATTGCCAGCCTCTTCTCCAACTGCGATGCTTTATTTTGGACGTAAAAATATTCGGTTTGCAGATCTCTTTAAAAATTAAAGCA

HGR\_892\_(TcIII-like)/1-2601 269 ACATACATATACACACAGGAAAAAAGAAAGTAGAAGTAATGGAGGGAATGCCCTTTTGTGTAATATTTCAATGTTTTTTTTTTTGT 368  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 401 AGGTCCAA - - - - - CACCGAA - - - - - CAAGAAAAAAGAAAG - - - - - GCTTCAT - - - - - GTGTGTGTACCTGGA 457  
HGR\_6694\_(TcII)/1-2893 399 AGGTCCAA - - - - - CACCGAA - - - - - CAAGAAAA - - - - - GCTTCAT - - - - - GTGTGTGTACCTGGA 454

Consensus

AGGTCCAA - - - - - CACCGAA - - - - - CAAGAAAAAAGAAAG - - - - - GCTTCAT - - - - - GTGTGTGTACCTGGA

HGR\_892\_(TcIII-like)/1-2601 369 ATTGTGTGTTGCTTTTCTGTTATATGAAGCAAGTTTTTATTTTATTACTATATTTTTTTTTTTTTTTTGGTGTAAAAAAGAAAAACAT 468  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 458 AAAGAGGAAA - - - - - AAGGAAACAG - - - - - CGATAGTCAACGAAAAAAGAAAGGAT 515  
HGR\_6694\_(TcII)/1-2893 458 AAAGAGGAAA - - - - - AAGGAAACAG - - - - - CGATAGTCAACGAAAA - - - - - AAAAAAAGGAT 500

Consensus

AAAGAGGAAA - - - - - AAGGAAACAG - - - - - CGATAGTCAACGAAAAAAGAAAGGAT

HGR\_892\_(TcIII-like)/1-2601 469 GTGGAGGGAATGT-GCACCCTGTGAGGCTTAATACG - - - - - TGAATGGGTGTTTTATTCATCTGCCCTGTTTTGTACAA - - - - - TAACCTGAATT 557  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 511 GTGGAGGGAATGT-GCACCCTGTGAGGCTTAATACG - - - - - TGAATGGGTGTTTTATTCATCTGCCCTGTTTTGTACAA - - - - - TAACCTGAATT 609  
HGR\_6694\_(TcII)/1-2893 504 GTGGAGGGAATGT-GCACCCTGTGAGGCTTAATACG - - - - - TGAATGGGTGTTTTATTCATCTGCCCTGTTTTGTACAA - - - - - TAACCTGAATT 601

Consensus

GTGGAGGGAATGT-GCACCCTGTGAGGCTTAATACG - - - - - TGAATGGGTGTTTTATTCATCTGCCCTGTTTTGTACAA - - - - - TAACCTGAATT

HGR\_892\_(TcIII-like)/1-2601 558 TTTTGTCTCAATGATGCCAGTTGGAGGGTGGCAGGCTAGTCTCTCTTAAGGTCCACCCCACTCCCAATCCAGTGTAAAG - - - - - ACTGACCTCCAC 653  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 612 TTTTGTCTCAATGATGCCAGTTGGAGGGTGGCAGGCTAGTCTCTCTTAAGGTCCACCCCACTCCCAATCCAGTGTGTAAAG - - - - - ACTGACCTCCAC 653  
HGR\_6694\_(TcII)/1-2893 610 TTTTGTCTCAATGATGCCAGTTGGAGGGTGGCAGGCTAGTCTCTCTTAAGGTCCACCCCACTCCCAATCCAGTGTGTAAAG - - - - - ACTGACCTCCAC 653

Consensus

TTTTTGTCTCAATGATGCCAGTTGGAGGGTGGCAGGCTAGTCTCTCTTAAGGTCCACCCCACTCCCAATCCAGTGTGTAAAG - - - - - ACTGACCTCCAC

HGR\_892\_(TcIII-like)/1-2601 747 GGGATTGGTTTATGAGAGAAATGGTTTACTGGCTGTACGTTGGTGGAGGTGAATCGAACCCGAAGTGAATTGGAG - - - - - ATGT 826  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 706 GGGATTGGTTTATGAGAGAAATGGTTTACTGGCTGTACGTTGGTGGAGGTGAATCGAACCCGAAGTGAATTGGAG - - - - - ATGT 826  
HGR\_6694\_(TcII)/1-2893 706 GGGATTGGTTTATGAGAGAAATGGTTTACTGGCTGTACGTTGGTGGAGGTGAATCGAACCCGAAGTGAATTGGAG - - - - - ATGT 826

Consensus

GGATTGGTTTATGAGAGAAATGGTTTACTGGCTGTACGTTGGTGGAGGTGAATCGAACCCGAAGTGAATTGGAG - - - - - ATGT

HGR\_892\_(TcIII-like)/1-2601 827 TGGCGAATTGAGTTGGAGTAATTTGTCTCTCGTGTTCTTTTTTTTTTCTTTCTT - - - - - CATCCATCAAGGATGGCCGCTTCTCTC - - - - - TCTACACATC 922  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 894 GGGCTCTGATGAACGGGATGACCTTGTCTGTGGATGGTGGAGATGATAGGATGAGGACGATGACGCGGTGTGCGAAAGCGCGCGGGCATGCGAC 993  
HGR\_6694\_(TcII)/1-2893 885 GGGCTCTGATGAACGGGATGACCTTGTCTGTGGATGGTGGAGATGATAGGATGAGGACGATGACGCGGTGTGCGAAAGCGCGCGGGATGACGCG 984

Consensus

GGCTCTGATGAACGGGATGACCTTGTCTGTGGATGGTGGAGATGATAGGATGAGGACGATGACGCGGTGTGCGAAAGCGCGCGGGCATGCGAC

HGR\_892\_(TcIII-like)/1-2601 1023 AATTCTCAGCGGACAAATGCCAGGCCATCGGGGATCAACAGCATCTTTGCGCTCTCTCTCAATGACAGCTTGTGGCTGAGGAAAGAGGGATCGG - 1121  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 1094 AATTCTCAGCGGACAAATGCCAGGCCATCGGGGAGCCACAGCATCTTTGCGCTCTCTCTCAATGACAGCTTGTGGCTGAGGAAAGAGGGATCGG - 1190  
HGR\_6694\_(TcII)/1-2893 1083 AATTCTCAGCGGACAAATGCCAGGCCATCGGGGAGCCACAGCATCTTTGCGCTCTCTCT - - - - - AATGCG - - - - - AGCTGGCGCTGAGGAAAGAGGGATCGG - 1178

Consensus

AATTCTCAGCGGACAAATGCCAGGCCATCGGGGAGCCACAGCATCTTTGCGCTCTCTCTCAATGACAGCTTGTGGCTGAGGAAAGAGGGATCGG -

HGR\_892\_(TcIII-like)/1-2601 1192 - - - - - TGTGATCCTCGCGGAAGGCTCTCCGCGAGAAGTGCAGGACTTTTGGGAAAAAGGAGAGCGACCGTTGACGAGGAAAGAGGCTTGGAGAAAGCGAGCG 1218  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 1191 - - - - - TGTGATCCTCGCGGAAGGCTCTCCGCGAGAAGTGCAGGACTTTTGGGAAAAAGGAGAGCGACCGTTGACGAGGAAAGAGGCTTGGAGAAAGCGAGCG 1218  
HGR\_6694\_(TcII)/1-2893 1179 - - - - - TGTGATCCTCGCGGAAGGCTCTCCGCGAGAAGTGCAGGACTTTTGGGAAAAAGGAGAGCGACCGTTGACGAGGAAAGAGGCTTGGAGAAAGCGAGCG 1218

Consensus

- - - - - TGTGATCCTCGCGGAAGGCTCTCCGCGAGAAGTGCAGGACTTTTGGGAAAAAGGAGAGCGACCGTTGACGAGGAAAGAGGCTTGGAGAAAGCGAGCG

HGR\_892\_(TcIII-like)/1-2601 1219 TGGCGAGTTCAACCCCAACCGCGTGGTGTCACTCCCTGGCGTCCAAGCGTGGCTTGTCCCGTGGGAACTCTAGCATCTCTGTTTTGCGACGGC 1318  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(TcII-like)/1-2913 1282 TGGCGAGTTCAACCCCAACCGCGGAGGTGGCACTCCCTGGGTCCAAGCGTGGCTTGTCCCGTGGGAACTCTAGCATCTCTGTTTTGCGACGGC 1375  
HGR\_6694\_(TcII)/1-2893 1276 TGGCGAGTTCAACCCCAACCGCGGAGGTGGCACTCCCTGGGTCCAAGCGTGGCTTGTCCCGTGGGAACTCTAGCATCTCTGTTTTGCGACGGC 1375

Consensus

TGGCGAGTTCAACCCCAACCGCGGAGGTGGCACTCCCTGGGTCCAAGCGTGGCTTGTCCCGTGGGAACTCTAGCATCTCTGTTTTGCGACGGC

HGR\_892\_(TcIII-like)/1-2601 1319 GGGGGGAGATGTTGTTGGCGGTGAGCT-CCCGAATGCAATGCGTCTCCCTCCACTGCCCCAGGCTCGGCCAACGACGTTGCCAGCCGGGAATTTGTCGGGG 1418  
HGR\_1408\_(TcII)/1-1988  
HGR\_6694\_(Tc



#### Motif #4

[illegible]



















# Motif #9

Motif #	IGR ID	CDS A		CDS B	
		TcII-like	TcIII-like	TcII-like	TcIII-like
		Product Description	Product Description	Product Description	Product Description
3	1208	TCCLB.503715.10	splicing factor TSR1, putative	TCCLB.508569.10	hypothetical protein, conserved
	1211	TCCLB.505869.70	hypothetical protein, conserved	TCCLB.508569.80	phosphoacetylglucosamine mutase
<div><div><div></div><div></div></div><div><div></div><div></div></div></div> <div><div>IGR 1211</div><div>IGR 120E</div></div> <div><div>0</div><div>2000</div><div>4000</div><div>6000</div><div>8000</div></div> <div>Nucleotide position (bp)</div>					
<div><div><div>IGR 1208 (TcII-like)/J-7616</div><div>IGR 1211 (TcII-like)/J-1265</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 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(TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 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(TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 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(TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J-1318</div><div>IGR 1211 (TcII-like)/J</div></div></div>					

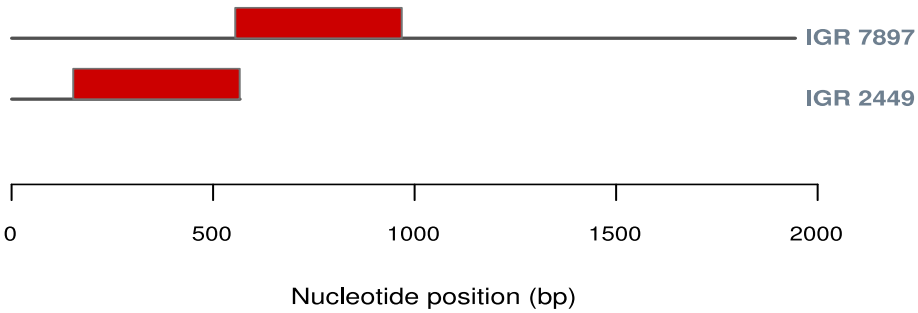






Motif #11

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
11	2449	TcCLB.505965.50	phosphonopyruvate decarboxylase, putative	TcCLB.510903.50	phosphonopyruvate decarboxylase, putative	TcCLB.505965.60	hypothetical protein, conserved	TcCLB.510903.40	hypothetical protein, conserved
	7897	No_ortholog		TcCLB.510901.250	hypothetical protein, conserved	No_ortholog		TcCLB.510901.230	hypothetical protein, conserved



IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1 TTTTATGGCTGCGATTCTGTACGGAAACCCACACAATACTATAACTAAAAGATAACGTGGAGGATAAGTAACCTCGACGGTACTTTTTTAGTCTTATTTA100

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

101 TTTATTTATTTATTTTCTTTTCTGTCGCAATTTTTTTTTTTTTTTTCTTACCCCTTCTCTCTCCCCCTCAATTCTTGTTGGTTTTGCCTTTTCGCTAAT200

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

201 GGGAAATGTTAACATAGTCCACCGTTGTATTTATAATCTCTTTTCTTTTCTTTTACTTTTCTTTACTTTAGAGTCTTTGAGAAGAGTAGTGGGGCTCTACA300

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

301 TGTGCCAATATTTTTTTTTTTTCTTTTCTTTTGTGCTTAATGCCATGGATAATGCGAGGTCTTCTTGGGTGTTTGCTAGGCAGTGATTTTTATTTTATT400

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

401 TCTCTGGAACCTCGAGGGGAAGGAAGTGAAATTGGGACGATGTAGGCGATGATTTTTCAGCCTGTGGGGTTTTTAA-TGGCCATGCAATGATCGTGCGTGCT103

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

104 CTCTTACCGTTTCTAAAA-----ACT-ATATCTGCCTGGAAGAGATTTCAGTTTTTGGAGGGAATTTGCGATCATATGTGGGGGAAGGGAGGCTAA193

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

194 GGAGGAGGTTGGCGTGGTTTTCTCATCCCCCACCATT---ATTTTTTCTTTCTTTTTACATGTTGGTGCCTGCGAGGACATCGAGTGCAATTTCTTTTTGT290

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

291 TTTCTGTCCTTGCACTCGCCGACTTTCTTAAGACTAATACCGCTGCAGCAACTTGCCACACGGAGGGAATTCTGGCGGTTGCGGTGGCCCTTTTGAAGAC390

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

391 TGCCGCCTCAGCGTGGTGCGCCAGGGTCAATCGCCCCGTATTGTGGGGGAGGCCAGGGGCCAGCCATGCTTTCCCTCACGGGCTTGTTGGTGCAGGGCTG490

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

491 ACGGCATGTATTTTGTGAATATCTTTGTTTGTGGGTGCGTGCCTGTTGGATAAAATTGTTTCTGAATTGTGTGCGGG-----566

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1093 GTTTTGTTCTGGATGGTACCAATTATTTATAGTCTTGATGTATGCCTGTGTGTGTGTGTGTGCTGGTGTGTAAATACCTTTTAATTTATTTTTTAA1192

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1193 TATTTGTTTTGCTGCGTTTTCTCCCATTCACAATTGTTGCCGTGTGACGTGGTTTTTTTCCCTTTCCCTGTTGGTGTTAACCTTTGAAAGTTGAAAAAGCA1292

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1293 AGCCATCAAAATGCAGATTGTGACGGGCCAGCACTTCAGCGGTGGCGTTCAACGGAGTGAGGCGCTGGAGGATTCCGCCACGGCACTGAAGCATTCATGCG1392

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1393 AGATGGGCCGTTTTTTTGCCTACTACACGCATCCACACCGTCTGCCGCTTAGTCAGAGCGCGGAGGAGCCGATGTGTGAGAAGCTGCCACGCGATGAGGCG1492

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1493 GATGCTTGCGCCAGGGGACTTTACTTTCTCTCCCACACCAGACGTACTGTGGCCGGACAACGGTTGACAAAGTGCTCTACAAGCAATTGCCTGAGCCTTGAT1592

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1693 GAGAAATAATTAGAGCAGCAGCAACAGTGATGGCGGTTGTATTTGTTTTACTTTGTCTTACTCTCCTTTTTTCTCCTTCTTCTAACATTGCCCTTCTTC1792

Consensus

IGR\_2449\_(TcII)/1-566  
IGR\_2449\_(TcII-like)/1-565  
IGR\_2449\_(TcIII-like)/1-566  
IGR\_7897\_(TcIII-like)/1-1944

1893 GGAGGGGAGAGGCAGAGGAAGTGTCTCTCTCTCTGTGTGGTCTCTTTACGC1944

Consensus



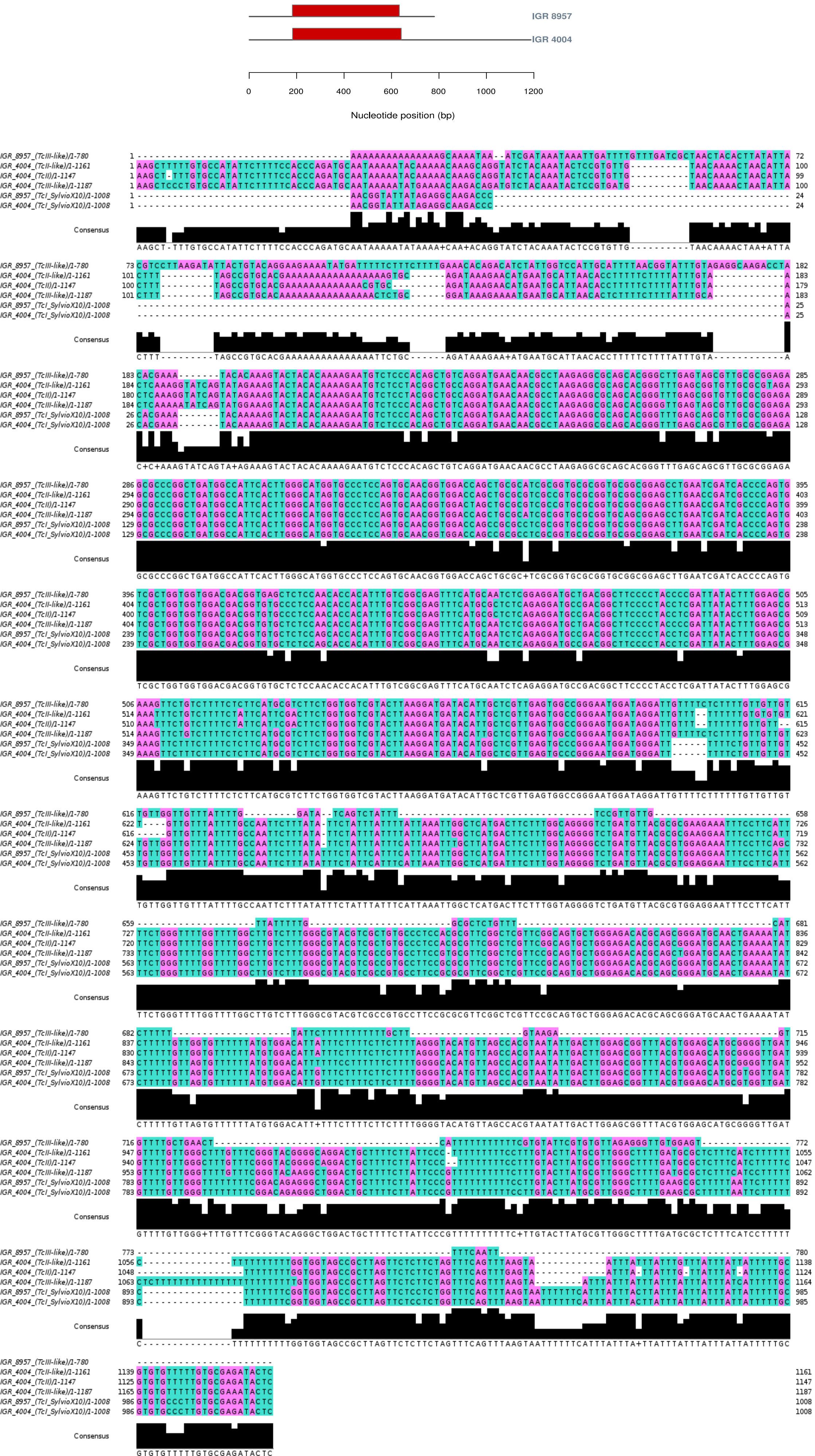
## Motif #12

[illegible]



Motif #13

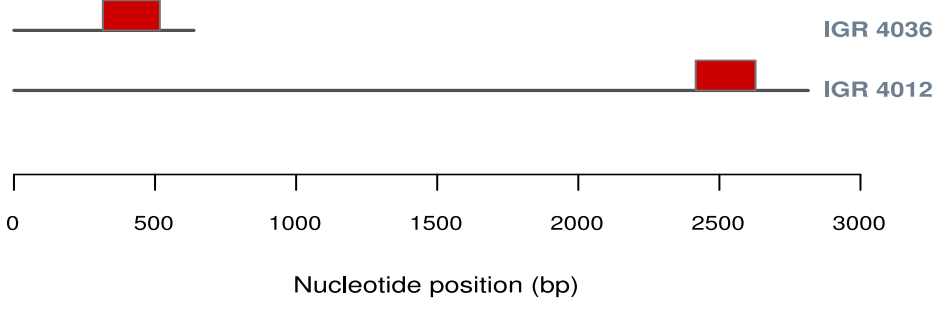
Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
13	4004	TCLB.511445.140	hypothetical protein	TCLB.503703.60	hypothetical protein	TCLB.511445.160	copper-transporting ATPase-like protein, putative	TCLB.503703.50	copper-transporting ATPase-like protein, putative
	8957	TCLB.511445.160	copper-transporting ATPase-like protein, putative	TCLB.503703.50	copper-transporting ATPase-like protein, putative	TCLB.503893.30	hypothetical protein, conserved	TCLB.503703.40	hypothetical protein, conserved





### Motif #14

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
14	4012	TCCLB.503893.100	hypothetical protein, conserved	TCCLB.508057.40	hypothetical protein, conserved	TCCLB.503893.120	calcium uniporter protein, mitochondrial, putative	TCCLB.508057.50	calcium uniporter protein, mitochondrial, putative
	4036	TCCLB.509831.20	vesicular-fusion ATPase-like protein, putative	TCCLB.506629.60	vesicular-fusion ATPase-like protein, putative	TCCLB.509831.30	hypothetical protein, conserved	TCCLB.506629.50	hypothetical protein, conserved



IGR\_4012\_(Tcl-like)/2-2814  
1 AGGAAAGGATCTTACGAAACCAAAAAAAGGAGGGGTAAAAGGTAAAGCATAGAGAAGAAACCGTCATGACTTTTCTTTTGT194  
IGR\_4012\_(Tcl)/1-2532  
1 AGGAAAGGATCTTACGAAACCAAAAAACCAAGGAGGGGTAAAAGGTAAAGCATAGAGAAGAAACCGTCATGACTTTTCTTTTGT192  
IGR\_4036\_(Tcl-like)/1-637  
IGR\_4036\_(Tcl-like)/1-646  
IGR\_4036\_(Tcl|Rc14)/1-642  
IGR\_4036\_(Tcl\_SylvioX10)/2-640

AGGAAAGGATCTACGAAACCAAAAAAAAAAAAAAAGGGAGGGGTAAAGGTAAGCATAGAGAAGAAACCGTCATGACTTTT-----TTTTTTTT

IGR\_4012 (TcII-like)/I-1017 101 A TTTTTCACGTCGGCAGCATGCTGGGAAGTTGTGATGGGAAGGAAGATGACGACCCCTGCTGTGACACTGTATTATCGCGGCCCACTCGTAATGCAATGA203

IGR\_4012 (TcII-like)/I-2014 95 A TTTTTCACGGCGTCATGCTGATGCTGGGAAGTTGTGATGGGAAGGAAGATGACGACCCCTGCTGTGACACTGTATTATCGCGGCCCACTCGTAATGCAATGA197

IGR\_4012 (TcII)/I-2532 93 A TTTTTCACGCGCCGTCATGCTGGGAAGTTGTGATGGGAAGGAAGATGACGACCCCTGCTGTGACACTGTATTATCGCGGCCCACTCGTAATGCAATGA195

IGR\_4036 (TcII-like)/I-637 -----

IGR\_4036 (TcII-like)/I-646 -----

IGR\_4036 (TcI 1Rc14)/I-642 -----

Consensus

ATTTTACGCGCCTGCATGCTGGGGAAGTTGTGATGGGACGGAAGATGACGCCCTTGCTGTGACATCTGATTCATGCCGCCCACTCGTAACTGCAATGA

IGR\_4012 (TcIII-like) (1-1017

IGR\_4012 (TcIII-like) (1-2814

IGR\_4012 (TcIII-2-2532

204 AAGTACGGGTACTTTT - - - - - TTTTITTTTGTGTGTGTCACAGGGATGGGTGAAGACCGTGATGGGGGGAGTGTGAGAAGCAAGAAGATATT 298

198 AAGTACGGGTATGTTGTTTGTGTTTITTTTGTGTGTCACAGGGATGGGTGAAGACCGTGATGAGGGAGAGCGGCGAAGCAAGAAGATATT 300

196 AAGTACGGGTATGTTTGTGTTG - - - - - TTTTITTTTGTGTGTGTCACAGGGATGGGTGAAGACCGTGATGAGGGAGAGCGGCGAAGCAAGAAGATATT 295

*IGR\_4036\_[TcI]\_Rc1A)*/1-642  
*IGR\_4036\_[TcI]\_Rc1A)*/1-646  
*IGR\_4036\_[TcI]\_Rc1A)*/1-642  
*IGR\_4036\_[TcI]\_SylvioX10)*/1-640

Consensus

AAGTACGGGTATGTTGTTGTTG - - TTTT TTTTGTGTGTGTGTGCCACAGGGATTGGGTGAAGACC GTGGATGAGGGAGAGCGCGCAGAGAAGCAAGAGATATT

IGR\_4012\_(TcIII-like)/J-2014  
IGR\_4012\_(TcIII-like)/J-2014  
IGR\_4012\_(TcII)/J-2332  
IGR\_4036\_(TcIII-like)/J-637  
IGR\_4036\_(TcIII-like)/J-646  
IGR\_4036\_(TcI/Rc4)/J-642  
IGR\_4036\_(TcI\_SylvioX10)/J-640

CACACATATATATATATATATATA-----TATATATGTCATTGTGTTGGGAGCTTGTGAAACTACTGTTTGTGAGAGGGCGTGCCTAAC  
 IGR\_4012 (TcIII-like)/I-1017 385 TAAITTAATTAATGTAATTAAGAAGAAAGAAAAAGAAATATTATTAACGAITCCTTCGCATCTTATGAATCTTTGGAAGACGCAATGGGAAGGAGCCAA487  
 IGR\_4012 (TcIII-like)/I-2814 404 TAAITTAATTAATGTAATTAAGAAGAAAGAAAAAGAAATATTATTAACGAITCCTTCGCATCTTATGAATCTTTGGAAGACGCAATGGGAAGGAGCCAA496  
 IGR\_4012 (TcII)/I-2532 376 TAAITTAATTAATGTAATTAAGAAGAAAGAAAAAGAAATATTATTAACGAITCCTTCGCATCTTATGAATCTTTGGAAGACGCAATGGGAAGGAGCCAA478  
 IGR\_4036 (TcIII-like)/I-637 .....  
 IGR\_4036 (TcIII-like)/I-646 .....  
 IGR\_4036 (TcI IRcI4)/I-642 .....

Consensus

TAATTTAATTAATGATGATTATAAGAAAGAAAGAAACGAAGATATTTTATACGATCTCTTCGCATCTTATGAATCTTTGGAAGACCGCAATGGGAGGAGCCA

IGR\_4012\_(TcIII-like)1-1017

IGR\_4012\_(TcIII-like)2-2814

IGR\_4012\_(TcIII)-2532

IGR\_4036\_(TcII-like)1-637  
IGR\_4036\_(TcIII-like)1-646  
IGR\_4036\_(TcI\_Rc14)1-642  
IGR\_4036\_(TcI\_SylvioX10)1-640

Consensus

ATGAACCGATAACGTCAAGACGAAGCATTTTTTTTTTTTTTTTTTTT-TTTTTTTT-----TGGAGGGGGTTTGTTGTTGTTGTTTATTTTCGCCGTCCTCCACTCG

IGR\_4012\_(TcIII-like)/I-101/ 591 **G**CACATTTTTTTCGATTAC-CCCCCACCTTGGAGGCGGTGTCITGGGCTGGAGGAA|CCCCAAATTTTCTACCTTCGTAGTAAATAATAIATAATATG|GTAGAA|G692  
 IGR\_4012\_(TcIII-like)/I-2814 605 GCATTTTTTTCGTATTAC-CCCCCACCTTGGAGAGCGGTGTCITGGGCTGGAGGAA|CCCCAAATTTTACCAATTCGTAAATAATAAAACATCTCCAAATCCGAAAT706  
 IGR\_4012\_(TcII)/I-2532 568 **G**CATTTTTTTCGATTACCCGCCCCACCTTGGAGAGCGGTGTCITGGGCTGGAGGAA|CCCCAAATTTTACCAATTCGTAAATAATAAAACATCTCCAAATCCGAAAT670  
 IGR\_4036\_(TcI)/I-637 .....  
 IGR\_4036\_(TcI-like)/I-646 .....  
 IGR\_4036\_(TcI)Rc14/I-642 .....  
 IGR\_4036\_(TcI)SylvioX10/I-640 .....

[illegible][illegible]

IGR\_4036\_(TcII-like)/J2-637  
IGR\_4036\_(TcIII-like)/J2-646  
IGR\_4036\_(TcI\_Rc14)/J2-642  
IGR\_4036\_(TcI\_SylvioX10)/J2-640

Consensus

CACCGCCTCTCTTTACCCCTCTTTTATCAGCCTGTTTAAATTATAAGTTCTGTATTTGCGAGCAGCCCAAGGCAATATTTTTTTTTTTCTTTATGTT

[illegible]

T A T T A T T G G A A G G T G G G T G A A A T T T T T T C - A A - A G G - T T C G T T T G T C T G - - - C G T G G C G T T C T C C G T C A T T C T T C T C G T G C G T G G G G G C G G A

IGR\_4012 (TcIII-like)1-1017 943 T G T G A T A T G T T T T T T A T G G T A A G G T A G A G T C T C A G A A T G T T T T C T C T T G T A G A A C A G A C G C T A C G G A T G A A - - - 1017

IGR\_4012 (TcIII-like)2-2814 1000 T G A C - - - G G T G T T T T C A T G C A C T G G T G G T A C C A G G A A A T C T C A C A G A A G - A A A C C A A C A G C G G G G G A G A G G T G G C G C A A G A T G C C C A A A A A G G G C 1058

IGR\_4012 (TcIII)-2532 977 T G A C - - - G G T G T T T T C A T G C A C T G G T G G T A C C A G G A A A T C C T C A C A G A A G - A A A C C A A C A G C G G G G G A G A G G T G G C G C A A G A T G C C C A A A A A G G G G C 1075

IGR\_4032 (TcIII-like)1-637

IGR\_4036 (TcIII-like)1-646

IGR\_4036 (TcI18A4)1-640

[illegible]

IGR\_4036\_(TcII-like)/I-637 .....  
 IGR\_4036\_(TcIII-like)/I-646 .....  
 IGR\_4036\_(TcI/RcI4)/I-642 .....  
 IGR\_4036\_(TcI\_SylvioX10)/I-640 .....

Consensus

ATCGGACGACGTCCATGTTCACACAACCGGGGTGGGGGAACTCGTTTTCACAGTTGGTCAAGCACGTGAAGGTGATGGTGCTGGTGGAAACAAAAGTGGATAAA

IGR\_4012\_(TcIII-like)/J-1017  
IGR\_4012\_(TcIII-like)/J-2814  
IGR\_4012\_(TcII)/J-2532  
IGR\_4036\_(TcIII-like)/J-637  
IGR\_4036\_(TcIII-like)/J-646  
IGR\_4036\_(TcI)Rc14/J-642  
IGR\_4036\_(TcI)\_SylvioX10/J-640

AGAGAGGAACCAAAATAAAAGATAAAATGCCGTGAACCAAGAGGTGAGGGGGGTGAAAAATAAGAGGGGAATATTGGCCTT-TTTT-CTG-CCGCTCA

IGR\_4012 (TcIII-like)/J1-1017  
IGR\_4012 (TcII-like)/J2-2814  
IGR\_4012 (TcII)/J2-2532  
IGR\_4036 (TcII-like)/J2-637  
IGR\_4036 (TcII-like)/J1-646

1305 TTTATTTTTCCTTACTGTTTTTTCGGTGTCTTGGAGTGGCAGTTTTTCCCGCTCTCAATATCCCTCCTGTCTATTGTACTGTAGTAGTGATGTTTTT  
1282 TTTATTTTTCCTTACTGTTTTTTCGGTGTCTTGGAGTGGCAGTTTTTCCCGCTCTCAATATCCCTCCTGTCTATTGTACTGTAGTAGTGATGTTTTT 1384

IGR\_4036\_(TcI\_SylvioX10)/I-640

Consensus

TTTATTTTTCTTTACTGTTTTTTCCGTGCTTTGGATGGCAGTTTTTCCCCCTCTCAATATCCCTCCTGTCATTGTTACTGTGAGTAGTGAATGTTTTT

IGR\_4012\_(TcIII-like)/I-1017

IGR\_4012\_(TcIII-like)/I-2814

1408 TTT - GTTTTTTTTTTTTTTCTCAAGAGGGTTTGGCCCCAGCAATCTACAGCTGGTCTGAGCGCTGGTCTGATGCCCTGAGCCCTGCGCCAAAAAGCAATGACCCCGT 1509

IGR\_4036\_(TcII-like)/J-637 .....  
IGR\_4036\_(TcIII-like)/J-646 .....  
IGR\_4036\_(TcI\_JRcl4)/J-642 .....  
IGR\_4036\_(TcI\_SylvioX10)/J-640 .....

Consensus

T - T - GTTTTTTTTTTTCTCAAGAGGGTTTGCCCCAGCAATTACACAGCTGGTTCGAGCGCTGGTCGATGCCGTACGCCCTGCGCCAAAAAACAATGACCCCGT

IGR\_4012\_(TcIII-like)/I-1017  
IGR\_4012\_(TcIII-like)/I-2814  
IGR\_4012\_(TcII)/I-2532  
IGR\_4036\_(TcIII-like)/I-637  
IGR\_4036\_(TcIII-like)/I-646  
IGR\_4036\_(TcI/Rc14)/I-642  
IGR\_4036\_(TcI\_SylvioX10)/I-640

IGR\_4012 (TcIII-like)/J-1017  
IGR\_4012 (TcIII-like)/J-2814  
IGR\_4012 (TcIII)/J-2532  
IGR\_4036 (TcIII-like)/J-637  
IGR\_4036 (TcIII-like)/J-646

IGR\_4036\_(Tcl\_SylvioX10)/2-640

Consensus

IGR\_4012\_(TcIII-like)/1-1017

IGR\_4012\_(TcII-like)/2-2814

1716 GCGCTGGCAATAGACTGTGATACGGGCATTGCCAACTTCGCGATTATTCATCGCCGCTGTCTCCGGGTACAGGTGCTTTTGC.CCTGCAGGAATGCCGCTGGCAT1817

IGR\_4036\_(TcII-like)/I-637  
IGR\_4036\_(TcIII-like)/I-646  
IGR\_4036\_(TcI\_JRc4)/I-642  
IGR\_4036\_(TcI\_SylvioX10)/I-640

Consensus

G-CTGGCAATAGACTGTGATACGCGCAATTGCCAACTTCGCAATTATTG-TCGCGCTGTCTCCGGGTCAAGGTGCTTTGC-CCTGCAAGGAATGCCGCTGGCAT

IGR\_4012\_(TcIII-like)/J-1017  
 IGR\_4012\_(TcII-like)/J-2614  
 IGR\_4012\_(TcII)/J-2532  
 IGR\_4036\_(TcII-like)/J-637  
 IGR\_4036\_(TcII-like)/J-646  
 IGR\_4036\_(TcI\_JRc4)/J-642  
 IGR\_4036\_(TcI\_SylvioX10)/J-640

[illegible]

IGR\_4036\_(TcI\_SylvioX10)/2-640

Consensus

CTTCCCGAAGAATTGCACCCGTTGCTCTCGGTGATAGGCTCTGGCACTACGGT-ATGTAGTC-AC-ATGAAGACACCGGTTTTTT-...-TCTGGTTGTTGT-

IGR\_4012\_(TcIII-like)/1-1017

IGR\_4012\_(TcIII-like)/2-2814

2024 GTTTTTTTTTTTTTTTTTTTTTTTTATGCCGGTGTGTTTTCAATTAATCCCGATTACACTTTCAATCCGATGGGTAGAGAGAGAGAAAAA...GGGGAAAAAC 2118

IGR\_4036\_(TcII-like)/J-637 1 ..... GATGTTAGTCAAAGGGATGTGAGGAGGGGAAAAAGGGAGAGAAGGAACAAAAA51  
IGR\_4036\_(TcIII-like)/J-646 1 ..... GATGTTAATCAAAGGGATGTGAGGAGGGGAAAAAGGGAGAGAAGGAACAAAAA51  
IGR\_4036\_(TcI)Rc4/J-642 1 ..... GATGCGTTAATCAAAGGGATGTGAGGAGGGGAAAAAGGGAGAGAAGGAACAAAAA51  
IGR\_4036\_(TcI)SylvioX10/J-640 1 ..... GATGCGTTAATCAAAGGGATGTGAGGAGGGGAAAAAGGGAGAGAAGGAACAAAAA51

Consensus

-----TTTTTT-TTTTTATGCGGCTGTGTTTTCAATTATCCGAGTATAGATGTGTAATCAAAGGGATGTGAGGAGGGGAAAAAGGGAGAGAAGGAACAAAAA

[illegible]

Consensus

GGGTGTGGGAAACGAATAATACGAGAGGGAGGAGGTCCACTGGC+TTGTA+CGGTAGCTGTGCCATG+CATAAATT-----GATGACCTCCGGAAG

IGR\_4012 (TcIII-like)/1-1017

IGR\_4012 (TcIII-like)/2-2614

IGR\_4012 (TcIII)/2-2532

IGR\_4036 (TcIII-like)/1-637

IGR\_4036 (TcIII-like)/2-646

2217 G T A T A T T T A T T T A T A T T A T T A T T A T A T C C T G A T A A A C G C A T G C A C T C C T T T A T G A A A C T T T T C C T G T C T T A T G A A T T T G G G A A G G C C A G A C C T T A A 2319

144 G G A A T G C C T T A T A C C A T T A G A - - - A C - C A A A A A G C T C C A A G G C T T G C C T G A A G C A G A A G C A A T T G A C A A A A A A G A A A A T G T G T T G G A 238

144 G A G A G A T C C T T C T A A C C A T T A G A - - - A C - C A A A A A G C T C C A A G G C T T G A T T G A G A C A G A A G C A A A A G G A A A T G T G T T G G A 238

IGR\_4036 (Tc<sub>II</sub>SylvioX10)/I-640

144 GGAGATGCCTTCTATACCCATTGAG-----GC--CAAGAAGCGTCCAAAGGCTTGGATTGAAGACAGAAGACGAATTGACAAAAAAGAGGAATGTGTTGGA238

Consensus

GGAGATGCCTTCTATACCCATTGAG-----+C--CAAGAAGCGTCCAAAGGCTTGGATTGAAGACAGAAGACGAATTGACAAAAAAGAGGAATGTGTTGGA

IGR\_4012 (TcIII-like)/I-1017

IGR\_4012 (TcIII-like)/I-2814

2320 G-----GACATCGAGGAAACGATAGAGGCGAGATAATTTTTTATTTTTATTTTCAACCTCTCACCCACACCTCTTTTTTCATCCCCACAGGGGGG2412

IGR\_4036\_[TcII-like)]/I-637 239 G C A A A A T A C G A G T G A T T A T G G A A A A A A G G T T T A A C C A T T T T T A C T T T T T A T C  
IGR\_4036\_[TcIII-like)]/I-646 239 G C A A A A T A C G A G T G A T T T G G G A A G A G A A A A G G T T T A A C C A T T T T T A C T T T T T A T C  
IGR\_4036\_[TcI]Rc(I4)]/I-642 239 G C A A A A T A C G A G T G A T T A T G G G A A G A G A A A A G G T T T A A C C A T T T T T A C T T T T T A T C  
IGR\_4036\_[TcI\_SylvioX10)]/I-640 239 G C A A A A T A C G A G T G A T T A T G G G A A G A G A A A A G G T T T A A C C A T T T T T A C T T T T T A T C

Consensus  
G C A A A A T A C G A G T G A T T A T G G G A A G A G A A A A G G T T T A A C C A T T T T T A C T T T T T A T C - - - - - T T C C C A C C C A C C C A C C A C T T T G + G A

[illegible]

Consensus

GGTCTCTGTGGCTGGAGGATCCCAAAGTTTGCTACCTCGTA+GTAATATATATATATATATATGTTGATAGAT+GTACACTTACCTGGT+TTAAACTTCGAG

IGR\_4012 (TcIII-like)/I-2017

IGR\_4012 (TcIII-like)/I-2014

IGR\_4012 (TcIII-like)/I-2532

IGR\_4036 (TcIII-like)/I-637

IGR\_4036 (TcIII-like)/I-646

2516 GATATGGTGAATCCCACTCTTTATTCCTATCTCTTTCTATTCCTATCGGGTTTGTTTTCTCTCTATTATTTGATAAACTCGAGGATTTGGCGAGGGCCAG 2618

2234 GATATGGTGAATCCCACTCTTTATTCCTATTAACCTCTTCTCTATTCCTATCGGGTTTGTTTTCTCTCTATTATTTGATAAACTCGAGGATTCGGCGAGGGCCAG 2396

405 GATATGGTGAATCCCACTCTTTATTCCTATCTCTTTCTATTCCTATCGGGTTTGTTTTCTCTCTATTATTTGATAAACTCGAGGATTTGGCGAGGGCCAG 507

412 GATATGGTGAATCCCACTCTTTATTCCTATTCCTCTTCTCTATTCCTATCGGGTTTGTTTTCTCTCTATTTGATAAACTCGAGGATTCGGCGAGGGCCAG 511

IGR\_4036\_(TcI\_SylvioX10)/I-640

418 GACATGGTGAAATCCCACTCGTATTCGGTTATCCCTCCCTATTCCTATCGGGTTTGTTTCTCCTATTATTGATGAACTCAGGACTTGGCCAGCGGCCAG520

Consensus

GATATGGTGAAATCCCACTCTTATCCATTTATC+CTTTCTCTATTCCTATCGGGTTTGTTTCTCCTATTATTGAT+AACTCAGGATTGGCCAGCGGCCAG

IGR\_4012\_(TcIII-like)/I-1017

IGR\_4012\_(TcIII-like)/I-2614

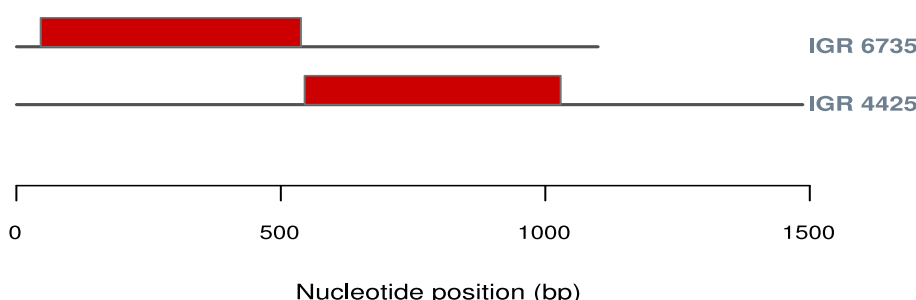
2619 AAGATATTACAGTGTGTATGGAGGGGGGAATTCGCTCTCTTCTCTCTCTCTCGAATAGATTATATTTATATGCGACTTTGGCCCTTTAAATAAGTTT...TT2719

[illegible][illegible]



## Motif #15

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
15	4425	TcCLB.507683.34	hypothetical protein, conserved	TcCLB.511291.50	hypothetical protein, conserved	TcCLB.507683.40	protein kinase, putative	TcCLB.511291.40	protein kinase, putative
	6735	TcCLB.506211.114	C-terminal motor kinesin, putative	TcCLB.510901.50	C-terminal motor kinesin, putative	TcCLB.506211.120	hypothetical protein, conserved	TcCLB.511289.110	hypothetical protein, conserved



IGR\_6735\_(TcII-like)/1-1099  
IGR\_6735\_(TcII)/1-1097  
IGR\_4425\_(TcII-like)/1-1486  
IGR\_4425\_(TcII-like)/1-1426

1 CGCGGCACATTCTTTCTTTTTTTTTTTTTTTTTTTTTCTTTTAAAGGAAAGATGCTCTGATGCTGAATGCATTATATCCCGATAATCGTCTTATTTTCCC 100  
1 CGCGGCACATTCTTTCTTTTTTTTTTTTTTTTTTTTTCTTTTAAAGGAAAGCTGCTCTGATGCTGAATGCATTATATCCCGATAATCGTCTTATTTTCTT 89

[illegible]

IGR\_6735\_(TcII-like)/I-1099 1 ..... GGT - 3  
IGR\_6735\_(TcII)/I-1097 1 ..... GGT - 3  
IGR\_4425\_(TcII-like)/I-1486 101 TGC AAAAAAAAAAGAGGGGGGAAAAAAAAAGAGAA TTTTGAGAAGGAAT AAATATATTTCTATTTTATTTCTTGAGAAGCTTAGGGATATGCGTC AGTGAGAAGGGGAT 200  
IGR\_4425\_(TcII-like)/I-1426 90 TGC AAAAAAAAAA AAGGGGGAAGAAAGAGAAATTTTGAGAAGGAAT AAATATATTTCTATTTTATTTCTTGAGAAGCTTAGGGACATGCGTC AGTGAGAAGGAAT 188

Consensus

IGCAAAAAAAAAA-A-GGGGAAAAAAAAAGAGAAATTT-GAGAAAGGAATAAAATATATTTCTATTTATCTTIGAGAAGCTTAGGGA-ATGCGTCGGGIGAGAAGG-ATA

IGR\_6735\_(TcII-like)/I-1099 4 .....CTAACGAGAAGAAAAACA ..... 20  
 IGR\_6735\_(TcII)/I-1097 4 .....CTAACGAGAAGAAAAACA ..... 20  
 IGR\_4425\_(TcII-like)/I-1486 201 ATGTGGAGCCCCACCCCTACCACTGCCCCCTCTCTCCCTTAAAGGGGGGAGAACAGTGGTCCAAAAGTATTTCAAACAATCGCTTATGTTTATTTT 300  
 IGR\_4425\_(TcII-like)/I-1426 189 ATGTGGAGCCCCACCCCTACCAACCCGCCCCCTCTCTCCCTTAAAGGGGGGAGAACAGTGGTTCAAAAGTATTTCAAACAATCGC-----TTATTTT 282

Consensus

ATG TGG AGC CCCC ACC CCA TACC ACC - GCC CCA TCT C TCC C + T A ACG + G + + G A + A A C A G T G G T - C A A A A C T G A T T T T C A A A C A A T C G C - - - - - T A T A T T T

IGR\_6735\_(TcII-like)/1-1099  
IGR\_6735\_(TcII)/1-1097  
IGR\_4425\_(TcII-like)/1-1486 301 GTGGATGGAGGGGAAATAGGAGGAAATTGTTGCTGTCCTGCGCTTCCCTTTCACCTCTATTTTATTATTATTATTATTATTATTATTTTGGTTT 400  
IGR\_4425\_(TcII-like)/1-1426 283 GTGGATGGAGGAGAATAGGAGGAAATTGTTGCTGTCCTGCGCTTCCCTTTCACCTCTATTTTATTATTATTATTATTATTATTATTTTGGTTT 367

Consensus   
GIGGAIGGAGG-GAATAGGAGG-AAATGIGCGICGICGCGTICGCTTACACTTAAITTTAATTT-ITATTTAA.....TIGGTTT

IGR\_6735\_(TcII-like)/1-1099 21 - - - - - TATTTGTACGAGTGTATGTGTGCAT - - - - - 45  
IGR\_6735\_(TcII)/1-1097 21 - - - - - TATTTGTACGAGTGTGTGTGTGCAT - - - - - 45  
IGR\_4425\_(TcII-like)/1-1486 401 GTTGTTTGTTTTTTTTTTTTGTGTGTGTGTTTCGTACTTACTCTCTCCGTTTTTTTACTCTCTCTATGTGGGAAATGATGTTTCAGAAATTCCTTAAT 500  
IGR\_4425\_(TcII-like)/1-1426 368 GTTG - - - - - GTTTTTGTGTGTTGTTGTTGCTACTTACTCTCTCCACTCTTTAATCTCATATGTGGGAAATGATGTTTCAGAAATTCCTTAAT 458

Consensus

GTTG-----TTTTTGT+GA+TGTTTGT+TGCATACTTACTCTCTCC--T-TTTA-TCITC-TATGTGGGAATGATGTTCAGAAATCTTAA

IGR_6735_(TcII-like)/1-1099	46	-----	TTGTTGTCGATGCTCT	GGAAGAAATGTGCGGCCAGATGGGACTCGGAAATGAT	100	
IGR_6735_(TcII)/1-1097	46	-----	TTGTTGTCGATGCTCT	GGAAGAAATGTGCGGCCAGATGGGACTCGGAAATGAT	100	
IGR_4425_(TcII-like)/1-1486	501	TAGAGACATTGACCTCGATTGCCCTTTTA	-TTTTCTTCTTTTTTA	TATTGTCGATGCTCT	GGAAGAAATGTGCGGCCAGATGGGACTCGGAAATGAT	599
IGR_4425_(TcII-like)/1-1426	459	TAGAGACATTGATTTCGATTACCCCTTTTA	TTTTTCTTCTTTTTTA	TATTGTCGATGCTCT	GGAAGAAATGTGCGGCCAGATGGGACTCGGAAATGAT	558

Consensus

TAGAGACATTGA-TTCGATT-CC-TTTTA-TTTT-TTCTTTTTTATT+TTGTCGATGCTTCTGGAAAGAAATGTGCGGCCAGATGGGACTCGGGAAATGAT

IGR_6735_(TcII-like)/1-1099	101	AG	TGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAACTGATTTGGGCTTTCTAACTGTGCACG	-TTGGAAGACAGCGAGTGGCGTTCCTTC	199
IGR_6735_(TcII)/1-1097	101	AG	TGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAACTGATTTGGGCTTTCTAACTGTGCACG	-TTGGAAGACAGCGAGTGGCGTTCCTTC	199
IGR_4425_(TcII-like)/1-1486	600	AG	TGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAACTGATTTGGGCTTTCTAACTGTGCACG	-TTGGAAGACAGCGAGTGGCGTTCCTTC	698
IGR_4425_(TcII-like)/1-1426	559	AG	TGCTGTTTGTTTAACTTCCCTTTCCTTTTATATATCTGTCAACTGATTTGGGCTTTCTAACTGTGCACG	-TTGGAAGGACAGCGAGTGGCGTTCCTTC	658

Consensus

AGTGTCTGTTTGTAACTTCCCTTTCCTTTTATATATCTGTCAACTGATTTGGGCTTTCTAACTGTGCACG-TTGGAAAGACAAGCAGTGGCGTTCTTTC

IGR\_6735\_(TcII-like)/1-1099 200 A T G T G - - T G T G T G T C T G T G T T T G T G T T T T T G T G T A T T T C C A C C C C T G C T G C C T C C A C G C G G A G A G G C A T C C G G C G G C T G C G G G G C T T T A T A A A T 297  
IGR\_6735\_(TcII)/1-1097 200 A T G T G - - T G T G T G T C T G T G T T T G T G T T T T T G T G T A T T T C C A C C C C T G C T G C C T C C A C G C G G A G A G G C A T C C G G C G G C T G C G G G G C T T T A T A A A T 297  
IGR\_4425\_(TcII-like)/1-1486 699 A T G T G - - - - - - - - - T G T G T C T G T G T T T T T G T G T A T T T C C A C C C C T G C T G C C T C C A C G C G G A G A G G C A T C C G G C G G C T G C G G G G C T T T A T A A A T 788  
IGR\_4425\_(TcII-like)/1-1426 659 T T G T G T G T G T G T C T G T G T C T G T G T T T T T G T A T T T C C A C C C C T G C T G C C T C C A C G C G G A G A G G C A T C C G G C G G C T G C G G G G C T T T A T A A A T 758

Consensus

ATGTG--TGTTGTCTGTGTGT+TGTGTGTTTTTGTGTAATTCACCCCCCTGCTGCCCCCACCAGCGGAGAGGCATCCGGCGGGCTGCGGGGCTTTATAAAT

IGR_6735_(TcII-like)/1-1099	298	G	A	C	T	G	C	C	A	C	T	G	T	G	A	G	C	T	C	A	G	C	G	A	A	C	C	C	G	T	T	C	T	A	T	G	A	C	C	A	C	A	T	G	T	T	T	C	T	G	A	A	T	T	T	G	T	A	C	T	G	A	T	G	T	A	T	G	A	G	T	G	T	T	G	T	G	A	A	T	C	T	T	C	T	C	T	C		397
IGR_6735_(TcII)/1-1097	298	G	A	C	T	G	C	C	A	C	T	G	T	G	A	G	C	T	C	A	G	C	G	A	A	C	C	C	G	T	T	C	T	A	T	G	A	C	C	A	C	A	T	G	T	T	T	C	T	G	A	A	T	T	T	G	T	A	C	T	G	A	T	G	A	T	G	A	G	T	G	T	T	G	T	G	A	A	T	C	T	T	C	T	C		397			
IGR_4425_(TcII-like)/1-1486	789	G	A	C	T	G	C	C	A	C	T	G	T	G	A	G	C	T	C	A	G	C	G	A	A	C	C	C	G	T	T	C	T	A	T	G	A	C	C	A	C	A	T	G	T	T	T	C	T	G	A	A	T	T	T	G	T	A	C	T	G	A	T	G	A	T	G	A	G	T	G	T	T	G	T	G	A	A	T	C	T	T	C	T	C		888			
IGR_4425_(TcII-like)/1-1426	759	G	A	C	T	G	C	C	A	C	T	T	T	G	G	G	C	T	C	A	G	C	G	A	A	C	C	C	G	T	T	C	T	A	T	G	A	C	C	A	C	A	T	G	T	T	T	C	T	G	A	A	T	T	T	G	T	A	C	T	G	A	T	G	A	T	G	A	T	G	A	G	T	G	T	T	G	T	G	A	A	T	C	T	T	C		858		

Consensus

GACTGCCACCTCGTGAAGCTCACAGCGA+CCCGGTTCTTATGACCACATGTTTTCTGAATCCATTTGTGTACTGATGTATGAGTGTTTGGTGAATCTTCTC

IGR\_6735\_(TcII-like)/I-1099 398 TGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCTCACATTGCGTCAATTGCCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACGCGCA 497  
IGR\_6735\_(TcII)/I-1097 398 TGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCTCACATTGCGTCAATTGCCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACGCGCA 497  
IGR\_4425\_(TcII-like)/I-1486 889 TGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCTCACATTGCGTCAATTGCCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACGCGCA 988  
IGR\_4425\_(TcII-like)/I-1426 859 TGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCTCACATTGCGTCAATTGCCCTCCGTGGGCATAAAGAAAAGTGCCCTCATCCACGCGCA 958

Consensus

TGGATTGTGGGAAGATGCTGGGCGCAGTGAGCAAAAATGCCATCTCACATTGCGTCATTGCCCTCCGTGGGCATAAAGAAAAGGGCCTCATCCACGCGCA

IGR\_6735\_(TcII-like)/I-1099 498 GG TTT GCT GTT GCT CTT ACG CGT CCG GGA TGG CGG CCA GA - - - - GAACAT GGAGG - - - GAAC TGG CGAG TAA AGG ACG TGT GAAG - - - - - GAC AG 581  
IGR\_6735\_(TcII)/I-1097 498 GG TTT GCT TTT GCT CTT GCG CGT CCG GGG TGG CGG CCA GA - - - - GAACAT GGAGG - - - GAAC TGG CGAG TAA AGG ACG TGT GAAG - - - - - GAC AG 581  
IGR\_4425\_(TcII-like)/I-1486 989 GG TTT GCT TTT GCT CTT GCG CGT CCG GGG TGG CGG CCA GGA AAG ACG AAT ATG AAA AGG AT GAG CTT TAA AG TTA AGG CTC ATG CGG AG CC ATT AT AAA AA 1088  
IGR\_4425\_(TcII-like)/I-1426 959 GG TTT GCT GTT GCT CTT GCG CGT CCG GGG TGG CGG CCA GGA AAG ACG AAT ATG AAA AGG AT GAG CTT TAA AG TTA AGG CTC ATG CGG AG CC ATT AT AAA AA 105

Consensus

GGTTTGCT+TTGCTCTTGC GCGTCCGGGGTGGGCGGCCAGAGAAGACGAA+ATG+A+GGATGA+CT+G++++TAAAG++C+TG+G+AGCC-TTAT+A+AG

IGR_6735_(TcII-like)/1-1099	582	TGGAAATTAATTTG	TTTTGCCTTG	TTTATTGTCCTTTTCT	ACTTTATTTGGAGCTTATACCTATTGGAGATG	CCTTTTTCGATTATGCATTCAATATC	681	
IGR_6735_(TcII)/1-1097	582	TGGAAATTAATTTG	TTTTGCCTTG	TTTATTGTCCTTTTCT	ACTTTATTTGGAGCTTATACCTATTGGAGATG	CCTTTTTCGATTATGCATTCAATATC	681	
IGR_4425_(TcII-like)/1-1486	1089	TGAAGGAAGGAAGA	TTTGGCTTTT	TTTTCTTTTCTTTT	-----	-----	ATGTAAATG	1147
IGR_4425_(TcIII-like)/1-1426	1059	TGAAGGAAGGAAGA	TTTGGCTTT	-----	TTTTT	-----	ATGTAAATG	1147

Consensus

IGR_6735_(TcII-like)/1-1099	682	TTGGGTGCCGCTGTACATTTTCACAGTATAAATTTCTAGGGGAGAATA	TGCTTTT	-	-	ACGGTATTTTGACTTTCTGTATCTCTCATATTCATCTCTTACT	779
IGR_6735_(TcII)/1-1097	682	TTGGGTGCCGCTGTACATTTTCACAGTATAAATTTCTAGGGGAGAATA	TGCTTTT	-	-	ACGGTATTTTGACTTTCTGTATCTCTCATATTCATCTCTTACT	779
IGR_4425_(TcII-like)/1-1486	1148	TGCGCCACAACTACTGTTTCTTATCATCAG	-----	-----	-----	TTCTTTTGAATGGTTTGGTGTGTTGTGTTCTGCAACGCTGCTTTTATT	1228
IGR_4425_(TcII-like)/1-1426	1107	TGCGCCACAACTACTGTTTCTTATCATCAG	-----	-----	-----	TTCTTTTGAATGGTTTGGTGTGTTGTGTTCTGCAACGCTGCTTTTATT	1187

Consensus

[illegible]

Consensus

IGR\_6735\_(TcII-like)/1-1099 853 TTTTCTCTAAATTTTCATTGG - - - - AGAAAGAAAGTCGCACAGGCGTGACAAAAGTAGCATTTTATTGCTGAC - - - - GCTCACCGTTAGTGGGAAA 942  
 IGR\_6735\_(TcII)/1-1097 851 TTTTCTCTAAATTTTCATTGG - - - - AGAAAGAAAGTCGCACAGGCGTGACAAAAGTAGCATTTTATTGCTGAC - - - - GTTACCGTTAGTGGGAAA 940  
 IGR\_4425\_(TcII-like)/1-1486 1317 TTTTCTCTCAGTCGGCCTGTGGCTTCCGGTGAATTGGCGAGCAGCG-TGCTCGCTTTGCAATCGGAACGGTGGGCAATTAGCACAGTGTGCGTGTGGAG 1415

Consensus

IGR\_6735\_(TcII-like)/1-1099 943 AG TCG - - - - GAAAAGCC ACCAGGAAAAAGAAAGAAAAGAAAGAAAAAAAAG TGGTGTCATCGATTGTATTGGCGACATCATCTCTCTTTGAGTGCT 1037  
 IGR\_6735\_(TcII)/1-1097 941 AG TCG - - - - GAAAAGCC ACCAGGAAAAAGAAAGAAAAGAAAGAAAAAAAAG TGGTGTCATCGATTGTATTGGCGACATCATCTCTCTTTGAGTGTT 1035  
 IGR\_4425\_(TcII-like)/1-1486 1416 CGTGACGCACGCACACAGACACACGGGTC AAGGGAGCAGGGGGGACGAGCCAA - - - - TATTGGGTGT - 1476

[illegible]

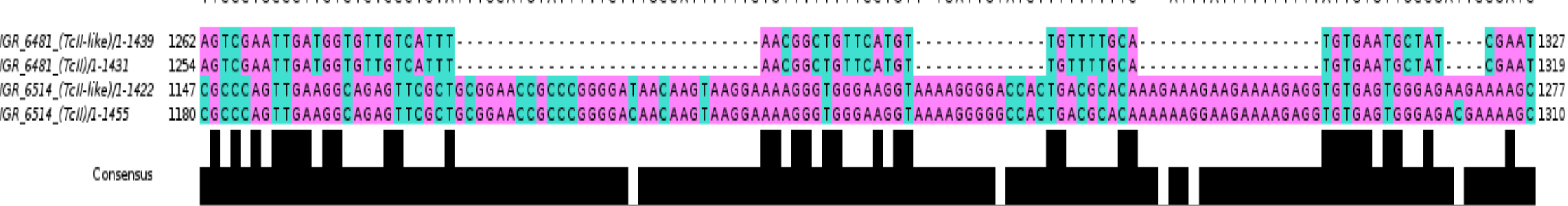
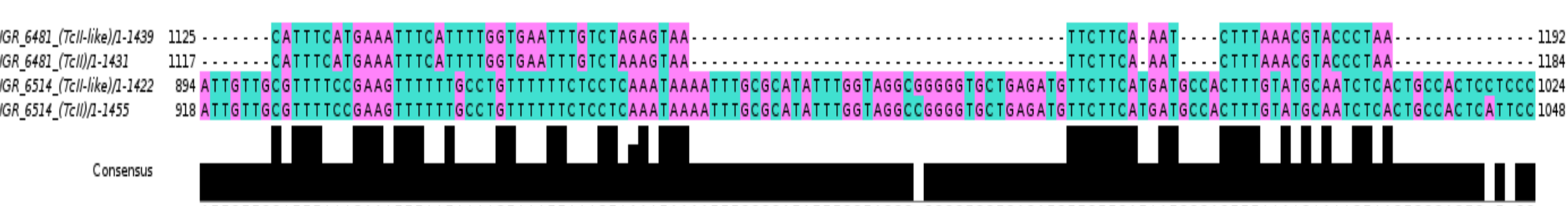
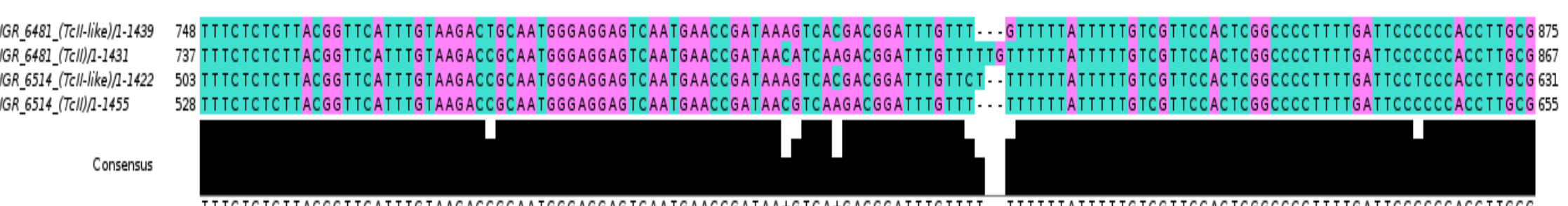
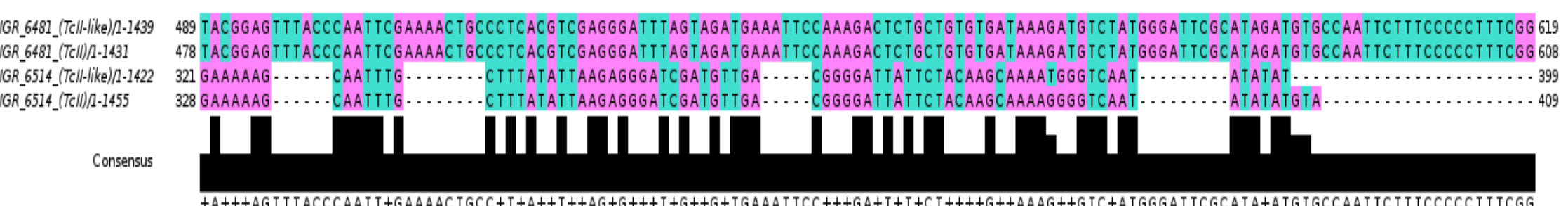
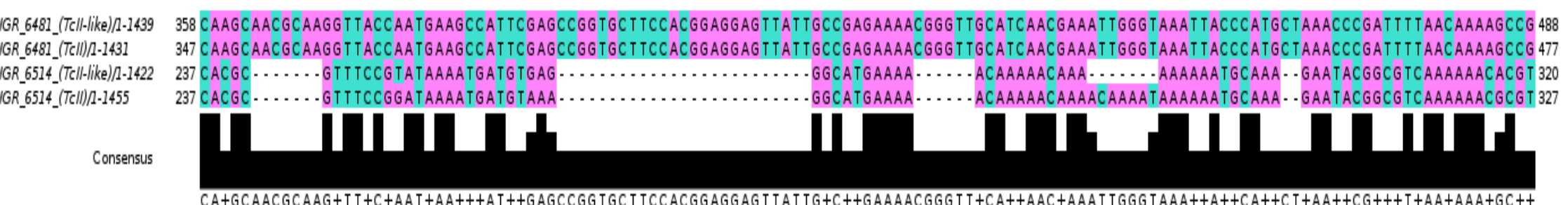
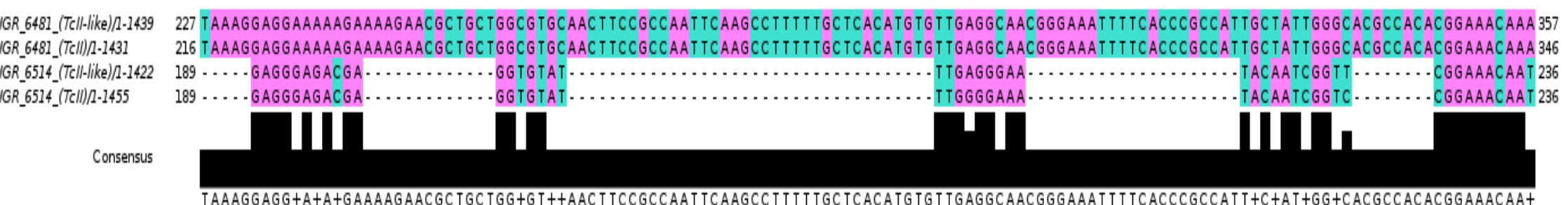
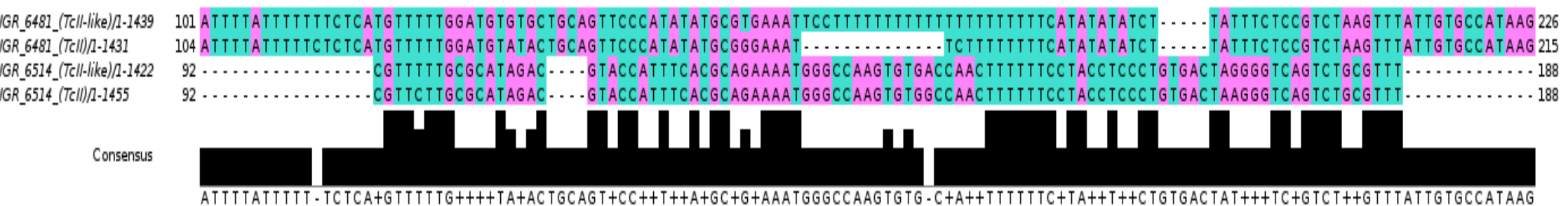
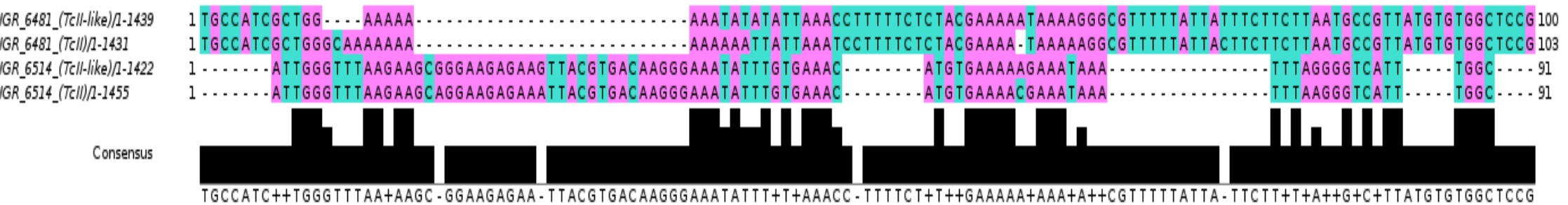
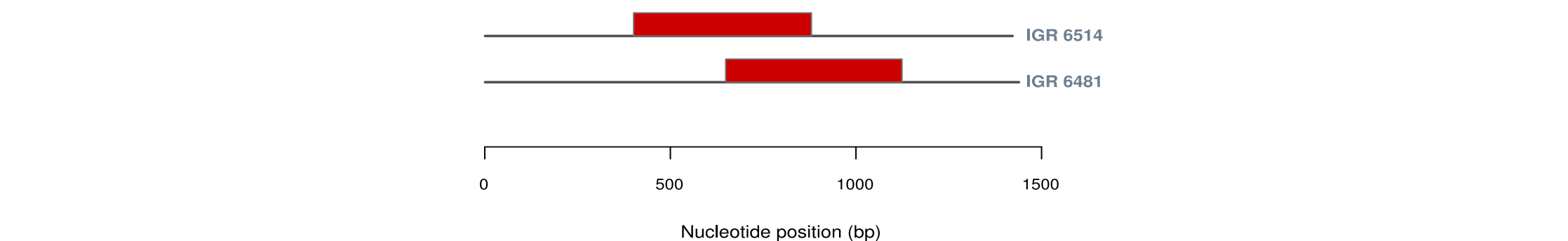
		1038	ATCGCACGCAT	ACTGCAT	ATTTTT	AGGTTT	GGAATG	CATTCA	TAGCAT	CATTTTTT	CGAAC	1099
IGR_6735_(TcII-like)/1-1099		1038	ATCGCACGCAT	ACTGCAT	ATTTTT	AGGTTT	GGAATG	CATTCA	TAGCAT	CATTTTTT	CGAAC	1099
IGR_6735_(TcII)/1-1097		1036	ATCGCACGCAT	ACTGCAT	ATTTTT	AGGTTT	GGAATG	CATTCA	TAGCAT	CATTTTTT	CGAAC	1097
IGR_4425_(TcII-like)/1-1486		1477	- - -	CGCG -	- - -	- - -	- - -	- - -	GAGCA -	- - -	- - -	1486

Consensus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Consensus	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100



## Motif #16

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
16	6481	TcCLB.506925.70	epsin, putative	No_ortholog	-	TcCLB.506925.80	hypothetical protein, conserved	No_ortholog	-
	6514	TcCLB.506925.480	ribokinase, putative	No_ortholog	-	TcCLB.506925.490	hypothetical protein, conserved	No_ortholog	-



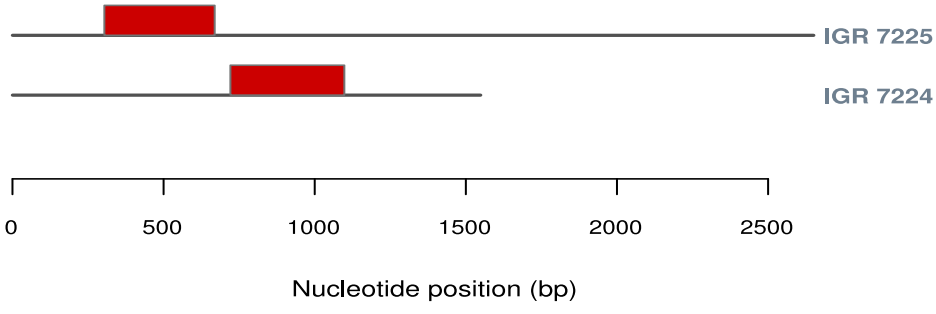






Motif #18

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
18	7224	No_ortholog	-	TCCLB.511807.160	hypothetical protein, conserved	No_ortholog	-	TCCLB.511807.180	hypothetical protein, conserved
	7225	No_ortholog	-	TCCLB.511807.180	hypothetical protein, conserved	No_ortholog	-	TCCLB.511807.190	hypothetical protein, conserved

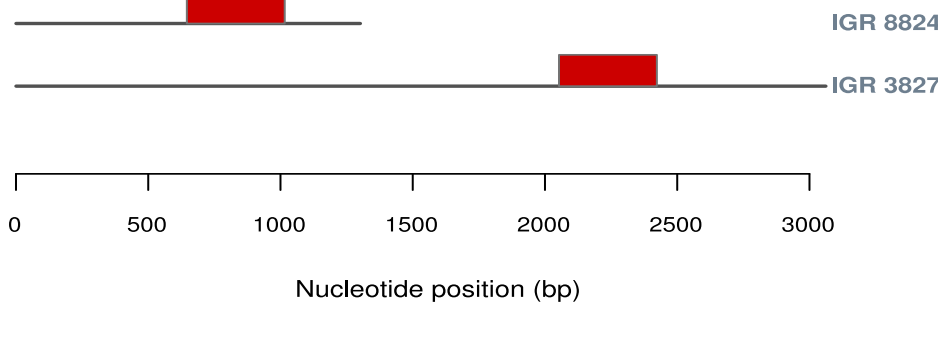


IGR_7225_(TcIII-like)/I-2650	1	-----AAGAAAGAAA-----	10
IGR_7224_(TcIII-like)/I-1548	1	1GACCTCTCTGTGTTTTTATTTTCCCTTTCTTTTCGGCTTTACATGCGGACTTCATGTATTATATGCATATGCAACGACATTGTGTTGTATTTTTGTTACGG	100
Consensus		-----A-G-A-GA-A-----	
IGR_7225_(TcIII-like)/I-2650	11	-----ATAAAGGAATTACT-----GATGGCGAC	34
IGR_7224_(TcIII-like)/I-1548	101	CTGCATTACTGTGTTTTTTTTTTTTTCTGTTTCATTGACTTGTGTTTTAGTGCAGTGGGACGCTCTCGCATAGAAGCTTTCACCAAGAGGGCGGGGAT	200
Consensus		-----ATA-AAG--T-AC-----G--GG-GA-----	
IGR_7225_(TcIII-like)/I-2650	35	ATTT-----TGATTAAA-----AAATGAGAAAACTGTCTTCGGTCTGTA	76
IGR_7224_(TcIII-like)/I-1548	201	GCTTTATATATATATATATATAGAGAACTTGTGCTCTCAAAGTGTATGGAGGAGAAAACTGGGCAGTACTTGTGCTTCCTTTTTTTTTTTTTTTTTTTGA	300
Consensus		--TT-----TG-T-AAA-----A-GAGAAAC--G-C--T-GTG-----GA	
IGR_7225_(TcIII-like)/I-2650	77	GAAGGATTGAGGGGTGGAA-----CATGCGCAAAACAGAAATACTTTTCAA--AAAAATAAACAAACAAACAGCAACAAAAACAATATCTC	165
IGR_7224_(TcIII-like)/I-1548	301	CACGCATTACAGGCATATGAATTTTCTGTTATGCACGCATAGAGCTGCGCCGATCCAGCCAGCGATGGATGAAAGGAGGAAATAAATAATATGATAATTGA	400
Consensus		-A-G-ATT-AGG--T--GAA-----ATGC-C-A-A-AG--C--TC-A--A--AT--A-A-A-A-A--A-AA-A--ATA--T-	
IGR_7225_(TcIII-like)/I-2650	166	TAAAAAATTAAAGTGATGCT-----ATGTGAATGGAACAGGGTCCGGGTGAAACAGGT-----GAGGGCG	224
IGR_7224_(TcIII-like)/I-1548	401	TAAATATATTTCTGTGTGCTGTTTCACTTACCTTTTCTGTTGGGAGAAAGGAGCGAGGGAGGGTGGGAGGGGGTGCCTTTTTTTTAAAGCTGCAGGGGAGTG	500
Consensus		TAAA-A-ATT--TG-TGC-----G--A-GGA-C--GG--GG-G-GAA--GGT--G--G-G	
IGR_7225_(TcIII-like)/I-2650	225	CTATTAGGACGATATATACACTTGTGCG-----GTGAACAGTTTTTTGTCTTTTTT-----TTATATCC	284
IGR_7224_(TcIII-like)/I-1548	501	GGGTAGGTCTGTGTTTTTTTTTTTTTACGCTCTCTGGTGTGTTGGAGGTTCTTCCGTCTCTGCTGGGGATGTGCGTCTCGGGGATTAAACGCGCCATTCCG	600
Consensus		---TAGG-C--T-T-T---TT-TT--G-----GTG-A--T-TT--GTCCT-T-T-----AT--GC	
IGR_7225_(TcIII-like)/I-2650	285	TG-----AATTAAAAAAGGACAA-----	303
IGR_7224_(TcIII-like)/I-1548	601	CGACTGAGAGAGACGGAAGAAAAGGCGGAAACAAAGACGGGGGTTTTAGCACAAACAAAAGGTGGTCAACGAAAAAAAATAAAAAAAAAGAAGAAG	700
Consensus		-G-----AAT-AAAAAA--A-AA-----	
IGR_7225_(TcIII-like)/I-2650	304	-----AAAAAGTTGTGCCGACAGAAAATGTGAGTTGCTTGCAAGATGCACCACGGGGGGGCTTGTGCGTGAGAGGATGTGTGACA	383
IGR_7224_(TcIII-like)/I-1548	701	AGGGAAAAGAAGAAATGGAGAAAAGTTGTGCTGACAGAAAGTGTGAGTTGCTTGCAAGATGCACCACGGGGGGGCTTGTGCGTGAGAGGATGTGTGACA	800
Consensus		-----AAAAAGTTGTGC-GACAGAAA-TGTGAGTTGCTTGCAAGATGCACCACGGGGGGGCTTGTGCGTGAGAGGATGTGTGACA	
IGR_7225_(TcIII-like)/I-2650	384	TCACGCCACGGGGTTCCCTGTGCCCTCACTGGCGCGCACAGGGTGGGCCCTGTTCTCCACAGGGCCTGCTTGGGCATACACCGCGTCCAAAGGGGGAG	483
IGR_7224_(TcIII-like)/I-1548	801	TCACGCCACGGGGTTCCCTGTGCCCTCACTGGCGCGCACAGGGTGGGCCCTGTTCTCCACAGGGCCTGCTTGGGCATACACCGCGTCCAAAGGGGAAG	900
Consensus		TCACGCCACGGGGTTCCCTGTGCCCTCACTGGC-CGCACAAGGGTGGGCCCTGTTCTCCACAGGGCCTGCTTGGGCATACACCGCGTCCAAAGGGG-AG	
IGR_7225_(TcIII-like)/I-2650	484	GGAGACATGTTGTCATGTTTTATCTTCCCGCATTTCCTCTTTTTTCTTTTGTGTTGTT-----TTTGGACTCACGCACGACGGCCAATGCCATGGGC	576
IGR_7224_(TcIII-like)/I-1548	901	GGAGGCATGTTGTCATGTTTTATCTTCCCGCATTTCCTCTTTTTTCTTTTGTGTTGTTTATTGTTTGGACTCACGCACGACGGCCAATGCCATGGGC	998
Consensus		GGAG-CATGTTGTCATGTTTTATTCTTCCCGCATTTCCT--TTTTTTTT-TTTTGTTGT-----TTTGGACTCACGCACGACGGCCAATGCCATGGGC	
IGR_7225_(TcIII-like)/I-2650	577	CGCATGAGCGGGAAGGGGCGCGTGAACCTCTAGAGAGAGAGAGGTGTGTGTGTGT-----TCCGGGTCTGGCACACAGTTTCGTCCTTTTTTCTTTTTT	669
IGR_7224_(TcIII-like)/I-1548	999	CGCATGAGCGGGAAGGGGCGCGTGAACCTCTACAGAGAGAGAGGTGTGTGTGTGTGTGTGGACGGGTCTGGCACACAGTTTCGTCCTTTTTTTTTTCTCT	1098
Consensus		CGCATGAGCGGGAAGGGGCGCGTGAACCTCTA-AGAGAGAGAGGTGTGTGTGTGT-----CGGGTCTGGCACACAGTTTCGTCCTTTTTTT-TTT--T	
IGR_7225_(TcIII-like)/I-2650	670	GTTGAATGTTGAGTGGTTTTTTTTTTTTTGGGCGAAATTTTATTTCTTCTCTTTTTATTTATTTTTTTTTTGTGAGAAACGCATGCATGAATTT	769
IGR_7224_(TcIII-like)/I-1548	1099	-----TTTTTTTTTTTTT-----AAATT-----	1116
Consensus		-----TTTTTTTTTTTTT-----AAATT-----	
IGR_7225_(TcIII-like)/I-2650	770	ATAAGCTTTTTTTTTTCTTTTTGTGTGTGTGCCATTATTGTTGGTGTATGTGCGTTGATTTTCTTTGGCTTTGTGTGTGTGTGGGGGGGGGGGG	869
IGR_7224_(TcIII-like)/I-1548			
Consensus			
IGR_7225_(TcIII-like)/I-2650	870	GGGGCGATGGAGCGGAGGTGAAAGGACGTGGAGGGCGGTACATGTATGTATGCATGCAATGTTGACTGTTTGTACGATGTAAACGGTGGGAAGACACATGA	969
IGR_7224_(TcIII-like)/I-1548	1117	-----CCGTACGT-----	1124
Consensus		-----CCGTAC-T-----	
IGR_7225_(TcIII-like)/I-2650	970	GGAGGGATGAGACGAGGGGAGTTGGGTTTTGTGGCGAGTGAGGAGTGAAACGGTCAAAAAAAAAAAAAAAAAAATAATAATGCGTCATCGACACAACA	1069
IGR_7224_(TcIII-like)/I-1548	1125	--AGGGTTTCAG-----TAGGGTTTG--GGTGACGTA-----CGACATCGA-----	1160
Consensus		--AGGG-T-AG-----T-GG-TTTG--GG-GA-TGA-----CG-CATCGA-----	
IGR_7225_(TcIII-like)/I-2650	1070	ATAAACACAATCTGATGTTGTGTGGTTTGGATTGCCITCCAATGAGATACCGTCTTCTTTCTTAGTGGGACTTATATGGGGTGAAGGCTTGTGTTGTTT	1169
IGR_7224_(TcIII-like)/I-1548	1161	-----TTGTG-----CCAAAGA-----ACGAAGATTTTTTTTTT	1190
Consensus		-----TTGTG-----CCAA-GA-----GAAG--TT-TTT-TTT	
IGR_7225_(TcIII-like)/I-2650	1170	TGTTTATTTATTTTATTTTTATTGTGTTTTTTTTTCTGCGTGTATTGAAAGAGAAAAACAAACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1269
IGR_7224_(TcIII-like)/I-1548	1191	T-----TTTTCTTGTGCTT-----AGTG-----GAAAGAGTAAC-----GACAGACAAAAGGAG-----	1236
Consensus		T-----TTTTT-TTGTG-TT-----GTG--GAAAGAG-AAAC-----GA-AGA-AAAAGG-----	
IGR_7225_(TcIII-like)/I-2650	1270	GATTTCTCTTATATGTTTGCTCACGTGATTGCCGGGATATATAAATATAAATATATCTGCATGCATGCACATGAATAAACAGTCGGAGAGAGAGAGGA--	1367
IGR_7224_(TcIII-like)/I-1548	1237	-----TGCTAACG-----CCAAGGCGACACGACG	1261
Consensus		-----TGCT-ACG-----C-AG-G-GA-A-GA-----	
IGR_7225_(TcIII-like)/I-2650	1368	GGGTAAATTGGTATAAATTTTTTTTTTTTTTTTTTTTTTGGGGAGGGTTTAAATGGCCGGTGTGTTTGATTTTTTACTTGCTTTTTTCTTTAAGT	1467
IGR_7224_(TcIII-like)/I-1548	1262	GGGCAAGACCAAAA-----AGGAAGGTTG-----	1286
Consensus		GGG-AA--A-AA-----GGA-GGTT-----	
IGR_7225_(TcIII-like)/I-2650	1468	TTTCTGCGTGTAACGCTGCAAAAATGGGAGGGAGCGGGACACGCAGCGTGATGCGCGCATTCGGTTTGGCGGCTGGTAACGTTGCGCGGCAAAAAA	1567
IGR_7224_(TcIII-like)/I-1548	1287	-----AGGAAGGGTGA AAAAGAGCG-----	1307
Consensus		-----AGG-AGG-G-GA-A-AGCG-----	
IGR_7225_(TcIII-like)/I-2650	1568	AACAACAACAACAACAATACTGGGAGAAGGCCGCTACAGTCAGGGTGAAGGGAGAAAGGGGAAAAAGTAAAGAGAAATTCATATTTTTATATA	1667
IGR_7224_(TcIII-like)/I-1548	1308	-----AAGAACAACA-----GAAAGAAAAAGGAAAAAACAACA-----	1341
Consensus		-----AA-AACAACA-----GAA-G-A-AAG-GGAAAAA--AA-A-----	
IGR_7225_(TcIII-like)/I-2650	1668	TTCAAGGACGAGATACGGATGAGACAGAGGTACATGTCTACGTGCATGCAACGATTCGACATGAATACGCAAAATAAGGAAAAATAAATAACTCAATTTAA	1767
IGR_7224_(TcIII-like)/I-1548	1342	-----AACAAACAACAACGACAGA-----TCAATT-----	1369
Consensus		-----AA-A--CAAA-AAA-GA-AA-A-----TCAATT-----	
IGR_7225_(TcIII-like)/I-2650	1768	TGTTATATAGAATACAATACAGGTTTATATGAAGTAAAGTTGTGAACATTTTATTTCTTTTCAACATATTTTATTTACTTTCTTTTGTGTGCGGAGTTG	1867
IGR_7224_(TcIII-like)/I-1548	1370	-----TTTTGT-----	1375
Consensus		-----TTTTGT-----	
IGR_7225_(TcIII-like)/I-2650	1868	GCTGAGGGAGGAAAGGAGGGGAAGGGAGGGGAGGGGGCCAGAAATATGAAGAGAAATGAATGGAACCAAGAGTGGGATTCCCTATGAAAAAGAGAAGAAG	1967
IGR_7224_(TcIII-like)/I-1548			
Consensus			
IGR_7225_(TcIII-like)/I-2650	1968	GAAAAAAGTATTTGGGTGACTTGGTTAACAGAGCAACGGGAATTTTCTTTTTTTTTTGTGGGGGGGGCTGCGTGATGTATGTGTGTGTGTGTGTGTGTGT	2067
IGR_7224_(TcIII-like)/I-1548	1376	-----ACGGAAGTTTTTCTTTTTT-----TATCCGTG-----	1404
Consensus		-----ACGG-A-TTTT-T-TTTTTTT-----T-T--GTG-----	
IGR_7225_(TcIII-like)/I-2650	2068	TGCGTTGAGAGCGGTACTATTTTGTGATTGCAACCAAGGCAAAAAATAGTTCCGCAAAATGAAGAAGCAAAATTGACCGGAGTGGCGAGCCAAATGTGTGTTA	2167
IGR_7224_(TcIII-like)/I-1548	1405	CGAGCTCAGCCAG-----AGGAATCAGCAAGAA-----AGGGGG-----AAACGTG-----	1449
Consensus		-G-G-T-AG-GC-G-----G-AA-CA-GCAA-AA-----G-G-GG-----AAA-GTG-----	
IGR_7225_(TcIII-like)/I-2650	2168	TAAACCTGTATATAAATCTACGGGATTCCTTTCTTTTTTTTTTTTTTCTTCTTTTCTGGTGGCGTTTATGTTGCAAAAGGAATGGTTACTGCATGTA	2267
IGR_7224_(TcIII-like)/I-1548			
Consensus			
IGR_7225_(TcIII-like)/I-2650	2268	TATATTTGTGTGTGTCTGTGTGCATGTGCGCCATCTTGTCTTGATGCTCCTTTGGTTCTCTCTCTTTTTTTCTTTTCTCTCGGCCCTTGTCATTTCTA	2367
IGR_7224_(TcIII-like)/I-1548	1450	-----GGACGCTGGACACACATCGCCT-----	1473
Consensus		-----G--GC-TG--C-C-A--T-G-CT-----	
IGR_7225_(TcIII-like)/I-2650	2368	AGATAATTACCATCTGGCATCCGTGTACAGTACATTGACCGGCAGAGAAGAAGGTATCTGTTTATTAATTTTTTATAGACAGGAGGCCCATATAGAGAG	2467
IGR_7224_(TcIII-like)/I-1548	1474	-----TCACCA-----AAG-----	1482
Consensus		-----T-ACCA-----AAG-----	
IGR_7225_(TcIII-like)/I-2650	2468	TAACTTCTTGAGGAGTGAGCGAGTGGGTTGGGCAAAATAGAAGGAGGACTGAGGGAGTGGAGTACATTTTTTGGCCATTTTTTTCAAGTTAAATTTT	2567
IGR_7224_(TcIII-like)/I-1548	1483	T-----AGGAGGGAATAACAAG--GTTGGAAGAAACAGCA-----ACCAACGGA-----CAACAAAC-----	1534
Consensus		T-----AGGAG-GA--A--A-G--GT-GG-A-AA-AG-A--AC--A-GGA-----CAA--AA-----	
IGR_7225_(TcIII-like)/I-2650	2568	TTTTTAGGGGTGTGTGTGGGGAGCATTGCCTGCAATTTTTGCTCGGGGGAAAGGTGGTGGGGTGGGAGAAGAAAGAAAGAA	2650
IGR_7224_(TcIII-like)/I-1548	1535	-----AACAAACAAAAAAG-----	1548
Consensus		-----A--A--AA-AA-A-----	



### Motif #19

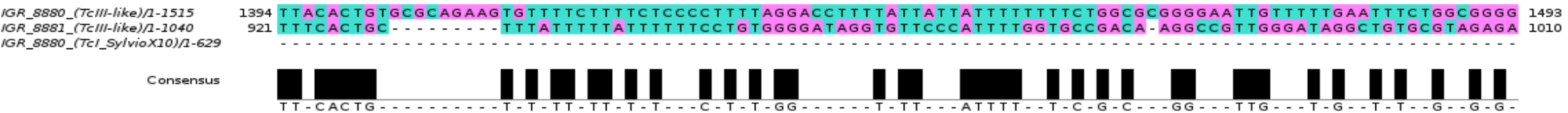
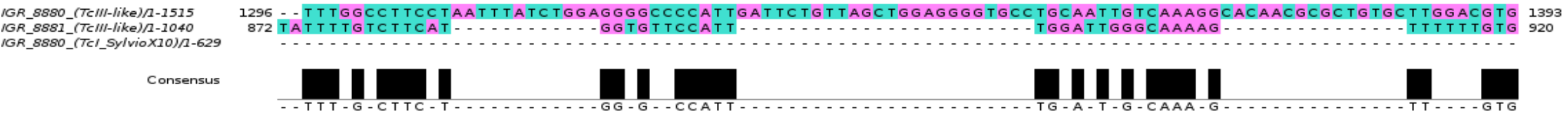
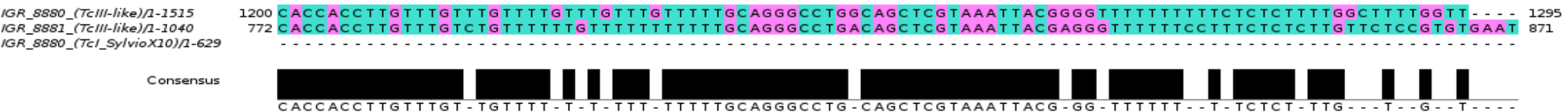
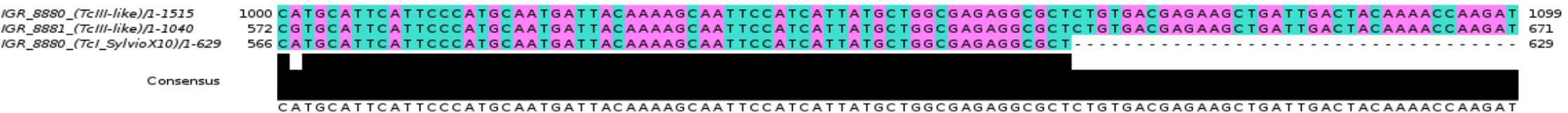
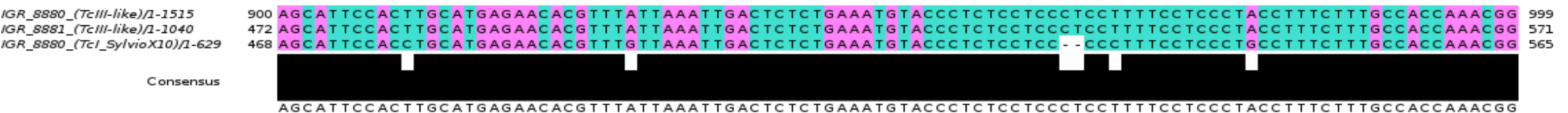
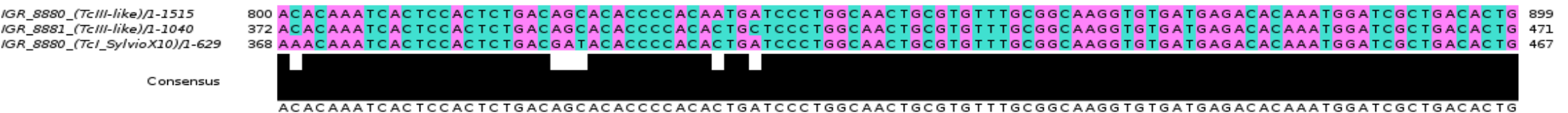
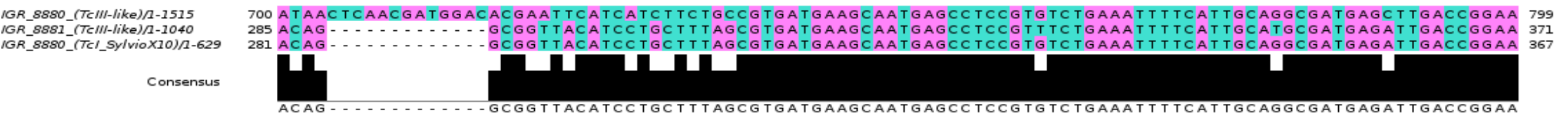
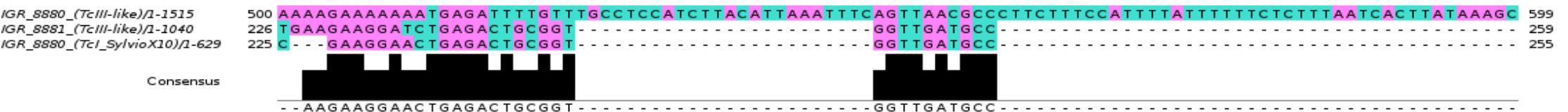
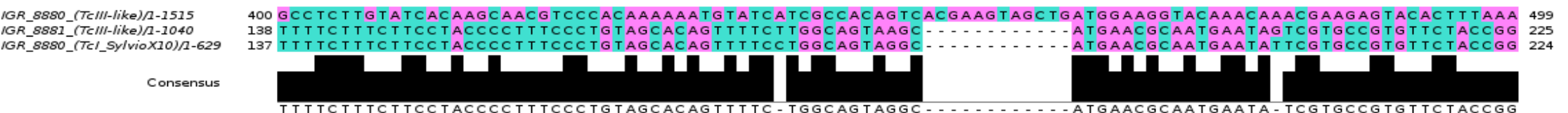
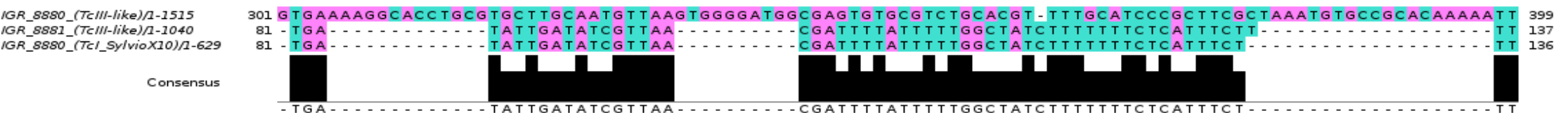
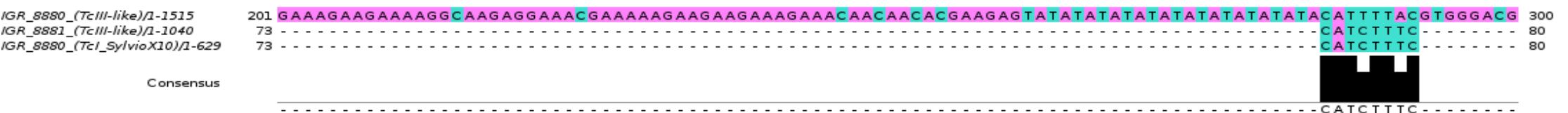
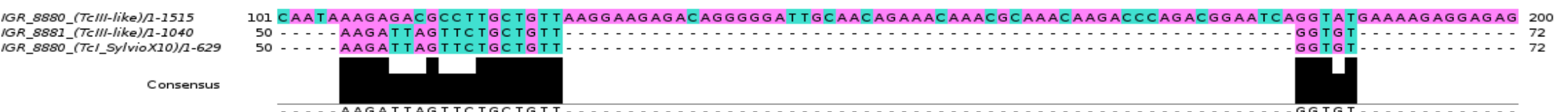
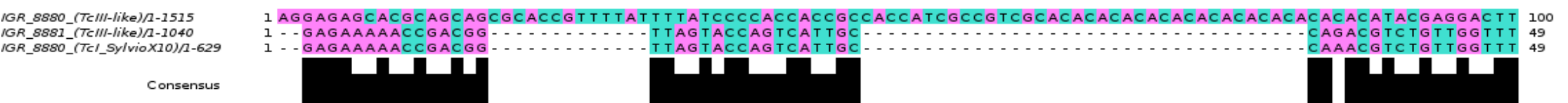
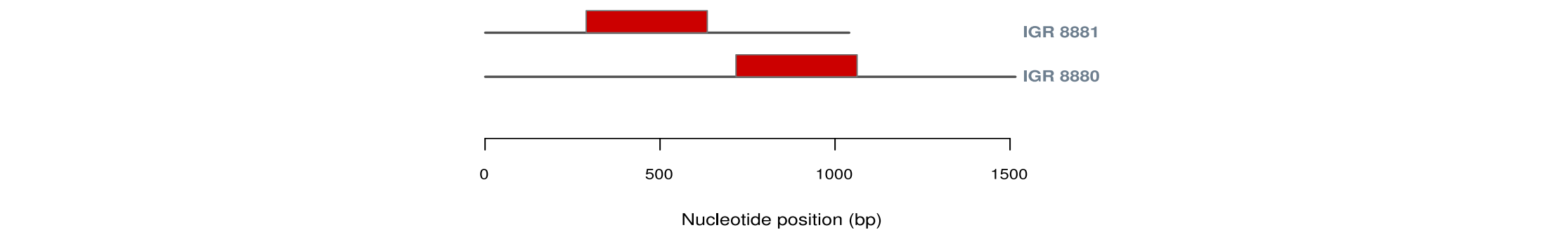
Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
19	3827	TCLB.507677.150	CYC2-like cyclin, putative,G1 cyclin Cyc64, putative	TCLB.504021.10	CYC2-like cyclin, putative,G1 cyclin Cyc64, putative	TCLB.507677.140	hypothetical protein, conserved	TCLB.504021.20	hypothetical protein, conserved
	8824	No_ortholog		TCLB.509647.150	calcium-transporting ATPase, putative	No_ortholog		TCLB.509647.140	hypothetical protein, conserved

[illegible]



## Motif #20

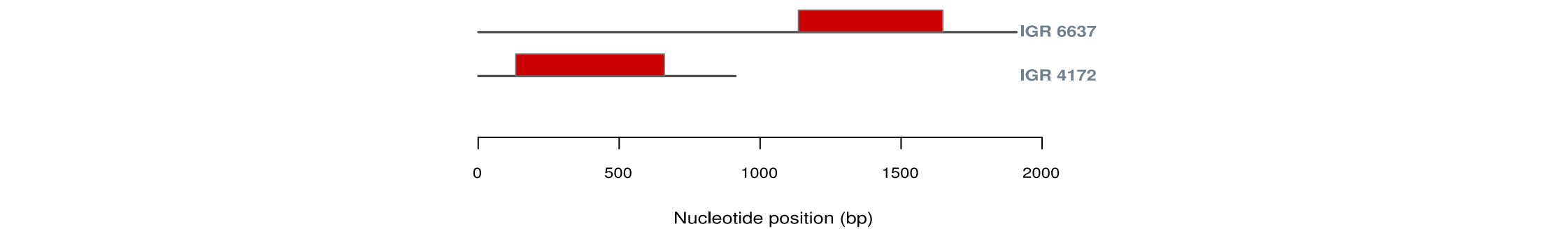
Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
20	8880	No_ortholog	-	TcCLB.510187.270	COP-coated vesicle membrane protein erv25 precursor, putative	No_ortholog	-	TcCLB.510187.260	hypothetical protein, conserved
	8881	No_ortholog	-	TcCLB.510187.260	hypothetical protein, conserved	No_ortholog	-	TcCLB.510187.250	hypothetical protein, conserved





Motif #21

Motif #	IGR ID	CDS A				CDS B			
		TcII-like		TcIII-like		TcII-like		TcIII-like	
		CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description	CDS ID	Product Description
21	4172	TcCLB.506147.180	DNA polymerase epsilon catalytic subunit, putative	TcCLB.510733.60	DNA polymerase epsilon catalytic subunit, putative	TcCLB.506147.170	hypothetical protein, conserved	TcCLB.510735.9	hypothetical protein, conserved
	6637	TcCLB.509551.110	hypothetical protein, conserved	TcCLB.507007.34	hypothetical protein, conserved	TcCLB.509551.100	hypothetical protein, conserved	TcCLB.507007.40	hypothetical protein, conserved



IGR\_4172\_(TcII-like)/1-912 1-----GGCTAGC-----TGGCGATGGA-----AACAG 22  
IGR\_4172\_(TcII)/1-864 1-----GGCTAGC-----TGGCGATGGA-----AACAG 22  
IGR\_6637\_(TcII-like)/1-1909 1GCGGATTGTTTGGGCAGCGCTCTCCATGCGGACACACCGAGCGCGGAGATAGAAAGTGG+GATGGAAAAAGGGTCATGTTGATGGTGGGGAGTTTAAACAG 100  
IGR\_6637\_(TcII)/1-1884 1GCGGATTGTTTGGGCAGCGCTCTCCATGCGGACACACCGAGCGCGGAGATAGAAAGTGGAGATGGAAAAAGGGTCATGTTGATGGTGGGGAGTTTAAACAA 100

Consensus  
GCGGATTGTTTGG++AGCGCTCTCCATGCGGACACACCGAGCGCGGAGATAGAAAGTGG+GATGGAAAAAGGGTCATGTTGATGGTGGGGAGTTTAAACAG

IGR\_4172\_(TcII-like)/1-912 23ATACTCGCAAAGCAAAAAGA--AAAGAGAGAGAGCGAAGGAGG-----64  
IGR\_4172\_(TcII)/1-864 23ATACTCGCAAAGCAAAAAGA--AAAGAGAGAGAGCGAAGGAGG-----64  
IGR\_6637\_(TcII-like)/1-1909 101ACACACACACACAAAAAAGGGTAAATGATGAGAGTGGAAAGAGGGAATTATGGATCTCGTTACTGGATGAATGCGGATTGGAATGCGTCAGAGCAAATG 200  
IGR\_6637\_(TcII)/1-1884 101ACACACACACA--CAAAAAGGGTAAATGATGAGAGTGGAAAGAGGGAATTATGGATCTCGTTACTGGATGAATGCGGATTGGAATGCGTCAGAGCAAATG 198

Consensus  
A+AC+C+CA+AAGCAAAAAG+GTAAA++++GAGAG+G+A+GAGGGAATTATGGATCTCGTTACTGGATGAATGCGGATTGGAATGCGTCAGAGCAAATG

IGR\_4172\_(TcII-like)/1-912 65-----GGGAAAC-----GCGGTGT-----79  
IGR\_4172\_(TcII)/1-864 65-----GGGAAAC-----GCGGTGT-----79  
IGR\_6637\_(TcII-like)/1-1909 201ACGTTTTTCCCTGATTTCGGGAGGACATTCCCAACCACTCTCCACCAGAAGCAGCGGTGATTGTAACGGTAGCTGATGTTGACGTCATGTTGGATTG 300  
IGR\_6637\_(TcII)/1-1884 199ACGTTTTTCCCTGATTTCGGGAGGACATTCCCAACCACTCTCCACCAGAAGCAGCGGTGATTGTAACGGTAGCTGATGTTGACGTCATGTTGGATTG 298

Consensus  
ACGTTTTTCCCTGATTTCGGGA++ACATTCCCA-CACCATCTCCACCAGAAGCAGCGGTGATTGTAACGGTAGCTGATGTTGACGTCATGTTGGATTG

IGR\_4172\_(TcII-like)/1-912 80-----TTTTTT-----95  
IGR\_4172\_(TcII)/1-864 80-----TTTTTT-----87  
IGR\_6637\_(TcII-like)/1-1909 301CTACTTTTTTTCCTTCCAAATTTTGTTTTACCCCTCCCCACGGCCGGAGTAGTGAAGTATGGACCACGAAAGGTTTATGCGTGTTTTTTTTTTTTT 400  
IGR\_6637\_(TcII)/1-1884 299CTAC-TTTTTTCCTTCAAATTTTGTTTTACCCCTCCCCACGGCCGGAGTAGTGAAGTATGGACCACGAAAGGTTTATGCG-----TTGTGTTTTT 391

Consensus  
CTAC-TTTTTTCCTTC-AAATTTTGTTTTTACCCCTCCCCACGGCCGGAGTAGTGAAGTATGGACCACGAAAGGTTTATGCG-----TTTTTTTTTT

IGR\_4172\_(TcII-like)/1-912 96TTACTAA-----AATTACT-----109  
IGR\_4172\_(TcII)/1-864 88TTACTAA-----AATTACT-----101  
IGR\_6637\_(TcII-like)/1-1909 401TTAGCAGTCCGATGGCGAGAGATAAAAAACGCTCTAGCGATTACTTGACAAACATGGCATGTTTTTTTTTCTATTTTTTTTTTTTTTTGTTTTTTTGC 500  
IGR\_6637\_(TcII)/1-1884 392TTAGCAGTCCGATGGCGAGAGATAAAAAACGCTCTAGCGATTACTTGACAAACATGCATTATTGTTTTTTTTTCTATTTTTTTTTTTGTTTTTTTGC 491

Consensus  
TTA++A+TCCGATGGCGAGAGATAAAAAACGCTCTAGC+ATTACTTGACAAACATG---T-TT-TTTTTT-T--TT-TTTTTTTTTTGTTTTTTT--

IGR\_4172\_(TcII-like)/1-912 501CATTCTTTTTTTTTTGGTTTTGTTTTGTTTTGCACTTTTTAAGGAGATAGGCTGCTTACAATGTTGGCTTTGGTAAAACGGCAATGCGGCTCGGAGAAT 600  
IGR\_4172\_(TcII)/1-864 492TACATTTCTTTTTTTGGTTTTGTTTTGTTTTGCACTTTTTAAGGAAATAGGCTGCTTACAATGTTGGCTTTGGTAAAACGGCAATGCGGCTCGGAGAAT 591  
IGR\_6637\_(TcII-like)/1-1909 501CATTCTTTTTTTTTTGGTTTTGTTTTGTTTTGCACTTTTTAAGGAGATAGGCTGCTTACAATGTTGGCTTTGGTAAAACGGCAATGCGGCTCGGAGAAT 600  
IGR\_6637\_(TcII)/1-1884 492TACATTTCTTTTTTTGGTTTTGTTTTGTTTTGCACTTTTTAAGGAAATAGGCTGCTTACAATGTTGGCTTTGGTAAAACGGCAATGCGGCTCGGAGAAT 591

Consensus  
-A---T-TTTTTTTTGGTTTTGTTTTGTTTTGCACTTTTTAAGGA-ATAGGCTGCTTACAATGTTGGCTTTGGTAAAACGGCAATGCGGCTCGGAGAAT

IGR\_4172\_(TcII-like)/1-912 110-----CAAAGAGGCCGGT-----123  
IGR\_4172\_(TcII)/1-864 102-----CAAAGAGGCCGGT-----115  
IGR\_6637\_(TcII-like)/1-1909 601AGCCATGCTTTCTACGGGGCCTACCATAGCGGGTGGCGAAACAAAGCTGGCGGATATTGTTTGCATGCCGATCCTTTTTGTCGCCGCTAGGGTCTTCTCT 700  
IGR\_6637\_(TcII)/1-1884 592AGCCATGCTTTCTACGGGGCCTACCATAGCGGGTGGCGAAACAAAGCTGGCGGATATTGTTTGCATGCCGATCCTTTTTGTCGCCGCTAGGGTCTTCTCT 691

Consensus  
AGCCATGCTTTCTACGGGGCCTACCATAGCGGGTGGC+AAA+A+GC+GG+GGATATTGTTTGCATGCCGATCCTTTTTGTCGCCGCTAGGGTCTTCTCT

IGR\_4172\_(TcII-like)/1-912 701CGCAAGTTGAACTGACATCTTCCGTAGATTTGTCTCATTTTACGCTTGCTGTGTTGCGGCATTTTATATACATACGGATGGAGTTTTTGTGCGCTGCC 800  
IGR\_4172\_(TcII)/1-864 692CGCAAGTTGAACTGACATCTTCCGTAGATTTGTCTCATTTTACGCTTGCTGTGTTGCGGCATTTTATATACATATGGATGGAGTTTTTGTGCGCTGCC 791  
IGR\_6637\_(TcII-like)/1-1909 701CGCAAGTTGAACTGACATCTTCCGTAGATTTGTCTCATTTTACGCTTGCTGTGTTGCGGCATTTTATATACATACGGATGGAGTTTTTGTGCGCTGCC 800  
IGR\_6637\_(TcII)/1-1884 692CGCAAGTTGAACTGACATCTTCCGTAGATTTGTCTCATTTTACGCTTGCTGTGTTGCGGCATTTTATATACATATGGATGGAGTTTTTGTGCGCTGCC 791

Consensus  
CGCAAGTTGAACTGACATCTTCCGTAGATTTGTCTCATTTTACGCTTGCTGTGTTGCGGCATTTTATATACATA-GGATGGAGTTTTTGTGCGCTGCC

IGR\_4172\_(TcII-like)/1-912 124-----TCTTAAGTT-----132  
IGR\_4172\_(TcII)/1-864 116-----TCTTAAGTT-----124  
IGR\_6637\_(TcII-like)/1-1909 801CGTAAGCCGTTATCATTTGGAATAAATTGAGTACTTTTTCTTGCCATACCTGCAGTGGAGACC GTTG-TTTTTTATTTCAAGTTATTTGGCAGGGATTGCGG 900  
IGR\_6637\_(TcII)/1-1884 792CGTAAGCCGTTATCATTTGGAATAAATTGAGTACTTTTTCTTGCCATACCTGCAGTGGAGACC GTTG-TTTTTTATTTCAAGTTATTTGGCAGGGATTGCGG 890

Consensus  
CGTAAGCCGTTATCATTTGGAATAAATTGAGTACTTTTTCTTGCCATACCTGCAGTGGAGACC GTTG-TTTTTTAT+T+AAGTTATTTGGCAGGGATTGCGG

IGR\_4172\_(TcII-like)/1-912 901TGTAATTCCTTTACGCATTGACGTCTTGAGAAGTGGACACCGGCGTTATTTGAGAATTTACCGCAAGCATCTTTTTCTGTGGTTTGAGCTCCTCGTCTAC 1000  
IGR\_4172\_(TcII)/1-864 891TGTAATTCCTTTACGCATTGACGTCTTGAGAAGCGGACACCGGCGTTATTTGAGAATTTACCGCAAAACATCTTTTTCTGTGGTTTGAGCTCCTCGTCTAC 990  
IGR\_6637\_(TcII-like)/1-1909 901TGTAATTCCTTTACGCATTGACGTCTTGAGAAGTGGACACCGGCGTTATTTGAGAATTTACCGCAAGCATCTTTTTCTGTGGTTTGAGCTCCTCGTCTAC 1000  
IGR\_6637\_(TcII)/1-1884 891TGTAATTCCTTTACGCATTGACGTCTTGAGAAGCGGACACCGGCGTTATTTGAGAATTTACCGCAAAACATCTTTTTCTGTGGTTTGAGCTCCTCGTCTAC 990

Consensus  
TGTAATTCCTTTACGCATTGACGTCTTGAGAAG-GGACACCGGCGTTATTTGAGAATTTACCGCAA-CATCTTTTTCTGTGGTTTGAGCTCCTCGTCTAC

IGR\_4172\_(TcII-like)/1-912 1001TTTGGATACAGGCCAGAGCTGAGGAACAAAATGGACGCAAAAGTAAAGGGAACCTGAGGCTTATTTGGATACAACGAAACACCACTCCCAAAAAATTG 1100  
IGR\_4172\_(TcII)/1-864 991TTTGGATACAGGCCAGAGCTGAGGAACAAAATGGACGCAAAAGTAAAGGGAACCTGAGGCTTATTTGGATACAACGAAACACCACTCCCAAAAAATTG 1090  
IGR\_6637\_(TcII-like)/1-1909 1001TTTGGATACAGGCCAGAGCTGAGGAACAAAATGGACGCAAAAGTAAAGGGAACCTGAGGCTTATTTGGATACAACGAAACACCACTCCCAAAAAATTG 1100  
IGR\_6637\_(TcII)/1-1884 991TTTGGATACAGGCCAGAGCTGAGGAACAAAATGGACGCAAAAGTAAAGGGAACCTGAGGCTTATTTGGATACAACGAAACACCACTCCCAAAAAATTG 1090

Consensus  
TTTGGATACAGGCCAGAGCTGAGGAACAAAATGGACGCAAAAGTAAAGGGAACCTGAGGCTTATTTGGATACAACGAAACACCACTCCCAAAAAATTG

IGR\_4172\_(TcII-like)/1-912 133-----TCTTCTCTTTTTTAGGAGCTGTGTGAAGAGAAGGATCGCGGGAGAGCTGGCAAACCTTAAT 194  
IGR\_4172\_(TcII)/1-864 125-----TCTTCTCTTTTTTAGGAGCTGTGTGAAGAGAAGGATCGCGGGAGAGCTGGCAAACCTTAAT 186  
IGR\_6637\_(TcII-like)/1-1909 1101TGTTATGGAAAAGTGAGTGATTATTATTATTATTA-----TTTTCTCTTTTTTAAAGGAGCTGTGTGAAGAGAAGGATCGCGGGAGAGCTGGCAAACCTTAAT 1197  
IGR\_6637\_(TcII)/1-1884 1091TGTTATGGAAAAGTGAGTGATTATTATTATTATTA-----TTTTCTCTTTTTTAAAGGAGCTGTGTGAAGAGAAGGATCGCGGGAGAGCTGGCAAACCTTAAT 1190

Consensus  
TGTTATGGAAAAGTGAGTGATTATTATTATTATTA---T+TTT+TCTTTTTT+AGGAGCTGTGTGAAGAGAAGGATCGCGGGAGAGCTGGC+AACCTTAAT

IGR\_4172\_(TcII-like)/1-912 195TAATGCATATATGTATCCGGGTAAAACGAATGCAATCCTTTATGACACTTTCCTACCGTATGAAATTTGGGAAGGTCACGACTTTTAGGAGGAGCGGGGA 294  
IGR\_4172\_(TcII)/1-864 187TAATGCATATATGTATCCGGGTAAAACGAATGCAATCCTTTATGACACTTTCCTACCGTATGAAATTTGGGAAGGTCACGACTTTTAGGAGGAGCGGGGA 286  
IGR\_6637\_(TcII-like)/1-1909 1198TAATGCATATATGTATCCGGGTAAAACGAATGCAATCCTTTATGACACTTTCCTACCGTATGAAATTTGGGAAGGTCACGACTTTTAGGAGGAGCGGGGA 1297  
IGR\_6637\_(TcII)/1-1884 1191TAATGCATATATGTATCCGGGTAAAACGAATGCAATCCTTTATGACACTTTCCTACCGTATGAAATTTGGGAAGGTCACGACTTTTAGGAGGAGCGGGGA 1290

Consensus  
TAATGCATATATGTATCCGGGTAAAACGAATGCAATCCTTTATGACACTTTCCTACCGTATGAAATTTGGGAAGGTCACGACTTTTAGGAGGAGCGGGGA

IGR\_4172\_(TcII-like)/1-912 295ACCGATAGCGGCCGGTTAATTATTTATTTTTATTTTTGCCATCCCACCGCACTCTTTTGGTTCTTACCCTGGCGGGGGTCTTGTGGCTGGAGGAGCC 394  
IGR\_4172\_(TcII)/1-864 287ACCGATAGCGGCCGGTTAATTATTTATTTTTATTTTTGCCATCCCACCGCACCTCTTTGGTTCTTACCCTGGCGGGGGTCTTGTGGCTGGAGGAGCC 386  
IGR\_6637\_(TcII-like)/1-1909 1298ACCGATAGCGGCCGGTTAATTATTTATTTTTATTTTTGCCATCCCACCGCCCCCTTTGGTTCTTACCCTGGCGGGGGTCTTGTGGCTGGAGGAGCC 1397  
IGR\_6637\_(TcII)/1-1884 1291ACCGATAGCGGCCGGTTAATTATTTATTTTTATTTTTGCCATCCCACCGCCCCCTTTGGTTCTTACCCTGGCGGGGGTCTTGTGGCTGGAGGAGCC 1390

Consensus  
ACCGATAGCGGCCGGTTAATTATTTATTTTTATTTTTGCCATCCCACCGC+CCCTTTTGGTTCTTACCCTGCGGGCGGGTCTTGTGGCTGGAGGAGCCC

IGR\_4172\_(TcII-like)/1-912 395AAAGTATGCCACTTCGTAAGTGATATAAAATAATATACAATAAATATATATGATATCCCATCCGAATAGGGTGAACGGGTCACAATTGTGGCTAACGGATG 494  
IGR\_4172\_(TcII)/1-864 387AAAGTATGCCACTTCGTAAGTGATATAAAATAATATACAATAAATATATATGATATCCCATCCGAATAGGGTGAACGGGTCACAATTGTGGCTAACGGATG 486  
IGR\_6637\_(TcII-like)/1-1909 1398AAAGTATGCCACTTCGTAAGTAATATAAAATAAATATACAATAAATATATATGTA--CCATCCGAATAGGGTGAACGGGTCACAATTGTGGCTAACGGATG 1495  
IGR\_6637\_(TcII)/1-1884 1391AAAGTATGCCACTTCGTAAGTAATATAAAATAAATATACAATAAATATATATATA--CCATCCGAATAGGGTGAACGGGTCACAATTGTGGCTAACGGATG 1488

Consensus  
AAAGTATGCCACTTCGTAAGT+ATATAAAATAAATATACAATAAATATATATGATATCCCATCCGAATAGGGTGAACGGGTCACAATTGTGGCTAACGGATG

IGR\_4172\_(TcII-like)/1-912 495ATATATATATATGATATATATATATATAAATGTGTGCTTACTTGCTGTTAACTTTGAGGATATGGTAAATCTATTCTTATTCATTGCTCTTTTCT 594  
IGR\_4172\_(TcII)/1-864 487-----ATATATATATATATATATATGTTGCTTACTTGCTGTTAACTTTGAGGATATGGTAAATCTATTCTTATTCATTGCTCTTTTCT 571  
IGR\_6637\_(TcII-like)/1-1909 1496-----ATATATATATATATATATGTTGCTTACTTGCTGTTAACTTTGAGGATATGGTAAATCCATTCTTATTCATTGCTCTTTTCT 1582  
IGR\_6637\_(TcII)/1-1884 1489-----ATATATGAATATATATATGTTGCTTACTTGCTGTTAACTTTGAGGATATGGTGAATCCATTCTTATTCATTGCTCTTTTCT 1575

Consensus  
-----ATATATATATATATATATGTTGCTTACTTGCTGTTAACTTTGAGGATATGGT+AATC+ATTCTTATTCATTT+CCTCTTTTCT

IGR\_4172\_(TcII-like)/1-912 595CTATTTCATCTTGTGTTGTTTCTATTATTGATAAACTCATGATTCGGCCAGCAGCCCAGAAGATTATCCGTTTTCTCTCTCTCTCTCCCTTGTGTGTT 694  
IGR\_4172\_(TcII)/1-864 572CTATTTCATCTTGTGTTGTTTCTATTATTGATAAACTCATGATTTGGCCAGCAGCCCAGGAGATTATCCGTTTTCTCTCTCTCTCTCCCTTGTGTGTT 671  
IGR\_6637\_(TcII-like)/1-1909 1583TTATTTCATCTTGTGTTGTTTCTATTATTGATAAACTCATGATTTGGCCAGCAGCCCAGGAGATTATTCCTTTTTTTTTTTTTTTTTTTTTTTT 1682  
IGR\_6637\_(TcII)/1-1884 1576-----TTCCATCTTGTTGTTT-CTATTATTGATAAACTCATGATTTGGCCAGCAGCCCAGGAGATT-----TATTTCCTTTTTTTTTTTTTTTG 1657

Consensus  
CTATTTCATCTTGTGTTGTTTCTATTATTGATAAACTCATGATTTGGCCAGCAGCCCAGGAGATTATCCGTTTTCTCTCT+TCTCT++TTT+TT+TT

IGR\_4172\_(TcII-like)/1-912 695TG-----TGTGTTG-TGTTCTGCTGCCGAGTCCATTAAACGGACCATTGAAAAGGCAGTCGATAACAAATTTGGAGAAATG 768  
IGR\_4172\_(TcII)/1-864 672TG-----TGTGTTG-TGTTCTGCTGCCGAGTCCATTAAACGGACCATTGAAAAGGCAGTCGATAACAAATTTGGAGAAATG 745  
IGR\_6637\_(TcII-like)/1-1909 1683TGATATTCCGTGTTTCAGGAATTGGCGATTTTTTG-TGCTCTTCGCATA-TTTAACGACTGCGCAT-----GTCTCTGCATGCATTATTGCGTTATATG 1775  
IGR\_6637\_(TcII)/1-1884 1658TGATATTCCGTGTTTCAGGGATTAGCGATTTTTTTGTGTCCTTCTGCATA-TTTAACGACTGCGCAT-----GTCTCTGCATGCATTATTGCGTTATATG 1751

Consensus  
TGATATTCCGTGTTTCAGG-ATT-GCGAT+T+T-TGTC+TCTGTC++AGT++A++++AC+G++CATGAAAAG+CCTGTC++++A++A+TT++G++A+ATG

IGR\_4172\_(TcII-like)/1-912 769AGACGAAATAAATTTCCGTGTGGATTCTATTTTTTGTGGAGCGCTTTTTTTTTTTTTTTGTTCTTTTTTAATTTAACTTTATTTTAACTTTTAT 868  
IGR\_4172\_(TcII)/1-864 746AGACGAAATAAATTTCCGTGTGGATTCTATTTTTTGTGGAGCGCTTTTTTT-----TGTTCTTTTTTAACTTTTAACTTTTAT 818  
IGR\_6637\_(TcII-like)/1-1909 1776-----GAATTAATTT-GTGTG-----TTTCATGGCAAGAGACCG-----AGAGAAATATTTCACTCTGACCTCACTT 1835  
IGR\_6637\_(TcII)/1-1884 1752-----GAATTAATTT-GTGTG-----TTTCATGGCAAGAGACCG-----AGAGAAATATTTCACTCTGACCTCACTT 1811

Consensus  
AGACGAA+TAATTTGCCGTGTGGATTT++A++++++GA+CG--TTTTTT-----AGAGAAATATTTCA+T+TGAC+TCACCTT

IGR\_4172\_(TcII-like)/1-912 869CTCTTT--TTTTTTTTTTTTTTTTTTTTATAAGT--GAACG-----AAACAC-----912  
IGR\_4172\_(TcII)/1-864 819TTATTTTGGCTTTTATCT-CTTTTTTTTATAAGT--GAACG-----AAACAC-----864  
IGR\_6637\_(TcII-like)/1-1909 1835TTTTTT--CTTCCGTTCTGTTTTTTGTAACGTGTCGAGAAATGTAAGGAGGTCGGTGTAGCGGTAAATACGTTGG-----1909  
IGR\_6637\_(TcII)/1-1884 1812TTTTTT--CTTCCGTTCTGTTTTTTGTAACGTGTCGAGAAATGTAAGGAGGTCGGTGTAGCGGTAAATACGTTGG-----1884

Consensus  
TTTTTT--CTTT++GTTCTGCTTTTTTTT+A+++++GTCGAGAA+GTAAAGGAGGTCGGTGTAGCGGTAA+ACGTTGG