

REP sequences in flanking regions upstream IS1106 transposases in *Neisseria meningitidis* Z2491

1	130
2'-727827	CCGTCATTCCCGCGCAGCGGGAATCTAGTCT-GTTCGGTTTCAGTTATTTCCGATAAATGCCTGTTGCTTTTCATTTCCTAGATTCCACATTTTCGTGGGAATGACGGGATTTTAGGTTTCTGATTTTGGT
3'-1063489	CCGTCATTCCCGCGCAGCGGGAATCTAGTCT-GTTCGGTTTCAGTTATTTCCGATAAATGCCTGTTGCTTTTCATTTCCTAGATTCCACATTTTCGTGGGAATGACGA-ATTTTAGGTTTCTGATTTTGGT
4-1179979	CCGTCATTCCCGCGCAAGCGGGAATCTAGGTTCGTTCGGTTTCAGTTATTTCCGATAGATTCTGCGCGGTTGGGGTCTGGATTCCCGCTGCGCGGGAATGACGA-ATTTTAGGTTTCTGATTTTGGT
Consensus	CCGTCATTCCCGCGCAgCGGGAATCTAGtct.GTtCGGTTTCaGTTATTTtCGATAaATgCCTGttGctTtttcattTCtaGATTCCcCaCtttCGcGGGAATGACGa.ATTTtAGGTTtCTGaTTTtGGT
131	260
2'-727827	TTTCTGTCTTGTGGAATGACGGGATGTAG-GTTCGTAGGAATGA-----CGTGGTGCAGGTTTCCGTGCGGATGGATTCGTCATT-----
3'-1063489	TTTCTGTCTTGTGGAATGACGGGATATAG-GTTCGTAGGAATGA-----CGTGGTGCAGGTTTCCGTGCGGATGGATTCGTCATT-----CCC GCGCAGGCGGGAATCCAGACCTTAAGGCAGCG
4-1179979	TTTCTGTCTTGTGAAAATAACAGGATGAGATCTTTGCAAAATTCCTTTCCTCCCGACAGCCGAAACCAACACAGGTTTTCGTCTATTTTCGCCCAATACCTCTAATTTTACCAAATACCCCC
Consensus	TTTCTGTccTTGTGggAATgACgGGATgtag.gTtCgtAggAaTga.....CgtggtGCaGgtttCCgtgCggAtGgaTTCGTcatT.....ccc.....c.....a.....acg..aa...c..c.
261	390
2'-727827	-----
3'-1063489	GCAATATTCAAAGATTATCTGAAAGTCTGAGATTCTAGATTCCACATTTTCGTGGGAATGACGTTCA-----GTTGCTACGGTTACTGTAGGTTTCGGTTATGTGGAATTTCCGGGAAC
4-1179979	TTAACCCCTCCCGGATACCCGATAATCAGGCAATCC--GGTCTCCTTTTAGGCGGCAGCGGGCGCACATTAGCTTGTGCGGCTTTCAACAGGTTCAAAACATCGCCTTCAGATGGCTTGCACACTCAC
Consensus	..aa...tc...g..ta.c.ga.a.tc.g..at.c..g.t..cc..tt..g.gg.a..g...g..c.....tt.c.ac.g.t.c...ca..t..c..t.a..t.g...t.....ac
391	520
2'-727827	-----CCCGCGCAGGCGGGAATCTG-----GAATTTCATGCTCAAGAATTATCGGAAAAACCAAAAC-----CCTTCGGTCATCATTC-----
3'-1063489	TTAT-----GAATCGTCATTCCCGCGCAGGCGGGAATCTG-----GAATTTCATGCTCAAGAATTATCGGAAAAACCAAAAC-----CCTTCGGTCATCATTC-----
4-1179979	TTTAATCAGTCCGAAATAGGCTGCCCCGCGCATAGCGGAATTTACGGTGTCAGCGTACCGAAGCTCTGTTTCGACCATATAGTGGATTAAATTTAAACCAGTACGGCGTTGCCTCGCCTTGCCGTACTATT
Consensus	tt.....gaa.....t.CCCGCGCaggcgGGAATcTg.....GAAttTCaTgCctCaAgAatTtaTcGgaaAAaccAAAc.....CcTTCgTCatCaTtCC.....
521	650
2'-727827	-----CGCAAAAGCGGGAATCTAGAAATGAAAAGCAACAGGAATTTATCGGAAATGACCGAAA--CTGAACGGACTGGATTCCCGCTTTTGCGG-GAATGACGGCGACAGGGTT-GCTGTTAT
3'-1063489	-----CGCAAAAGCGGGAATCTAGAAATGAAAAGCAACAGGAATTTATCGGAAATGACCGAAA--CTGAACGGACTGGATTCCCGCTTTTGCGG-GAATGACGGCGACAGGGTT-GCTGTTAT
4-1179979	TGTAATGTCGTCGCTTCGTCGCCTTGTCTGATTTAAATTTAATCCACTATAACGGGTCTTCGACAAATACCGGTTGCGTTTGGTTCGCTTCCGACAGCGGACGGTTGCGGCAGGCTTTGCGCATAA
Consensus	CGcaaaaGcgGgaaTcTagaaATgaAAAGcaAcaggAaTtTATCGGaaaTgaccgAAA...CtGaacyGacTGGaTtCcctcTtttgCgG.GaAtGacyGCGaCAGGgTT.GCtgtTAT
651	780
2'-727827	AGTGGATGAACAAAACCGGTACGGCGTTGTCTCGCCTTAGCTCGAAGAGAACGATTCTCTAAGGTGCTGAAGCACCAAGTGAATCGGTTC-CGTACTATCTGTACTGTCTGCGGCTTCGTCTGCTTTGTC
3'-1063489	AGTGGATGAACAAAACCGGTACGGCGTTGTCTCGCCTTAGTTCTGAAGAGAACGATTCTCTAAGGTGCTGAAGCACCAAGTGAATCGGTTC-CGTACTATCTGTACTGTCTGCGGCTTCGTCTGCTTTGTC
4-1179979	TGCCGTCCAACTGATGTTCTTCAGATGTTGCGGTTTTCGCACTGTCGTAGCCTTTGTGCGCATAGACGGTCTGACCTTTGGGAGTCCCTTCCAACAACGGCGGCGAGGTGTTTGCACTCATGGGC
Consensus	aGtgGatgAACAAAaaccGgTacygCgttgtctCgCctTagttCGaAgaGaacyAttCTcTaaGtgGtcTgaAgcacCaagtgaatCGGttc.CgTactAtCtgtactGtCtGcgGcTTcgtGctcTtGtC
781	910
2'-727827	CT-----GATTTTGTGTTAATTCATATATCGACATCGCCAAACGAACTTCGTTCATCGCCGTTTC-GTCTTTGTCTAAAACCAAAACCGAA----ACCAACAACCCCAAAGGTATCGCCCATACTAT
3'-1063489	CT-----GATTTTGTGTTAATTCATATATCGACATCGCCAAACGAACTTCGTTCATCGCCGTTTC-GTCTTTGTCTAAAACCAAAACCGAA----ACCAACAACCCCAAAGGTATCGCCCATACTAT
4-1179979	ATTGGCGGGGTAATGTGAGTTTTCGATATAGCCTTCGCACTCGGTACGGGTATGTTGTTTGAACGAGTTGTAGAGATCCAACGGGCATCTTTGTCTTTACTCGGTGTGGTTTGCCCGCTGATTT
Consensus	cT.....GattTtTGttaATTCaCtATATcGaCaTcGcCAaacGaAacttcgTcaTcgccGtttc.GtcTTTGTctAaAaCCAAaaccgAa....acCaacAacCcaaaaGGTaTcGCCcaTacTaT

911	Left End	orf	1040
2'-727827	CGAATACCTTAAATAAACACAAGGTC-----GAGACCTTTGCATAATCCCCATAATCCCTTAAATTCCACCAAGCCATTTAGGGGATTTTCATGAGCACCTTCTTCC		
3'-1063489	CGAATACCTTAAATAAACACAAGGTC-----GAGACCTTTGCATAATCCCCATAATCCCTTAAATTCCACCAAGCCATTTAGGGGATTTTCATGAGCACCTTCTTCC		
4-1179979	GTCCCTTCTCGTCAACTTCTATGGCTGGCGCTGTTTGTGCTGCCGGCGGTCTGAGACCTTTGCATAATCCCCATAATCCCTTAAATTCCACCAAGCCATTTAGGGGATTTTCATGAGCACCTTCTTCC		
Consensus	cgaaTaCcTtaaaAAacaCaAgGtC.....GAGACCTTTGCATAATCCCCATAATCCCTAAaTTCCACCAAGcCATTTAGGGGATTTtcCATGAGCACCTTCTTCC		
1041	orf		1170
2'-727827	GGCAAACCGCACAAGCCATGATTGCCAAACACATCGACCGTTTCCCCTATTGAAGTTGGACCAGGTGATTGATTGGCAACCGATCGAACAATACCTGAACCGTCAAAAACCCGTTACCTTAAGAGACCA		
3'-1063489	GGCAAACCGCACAAGCCATGATTGCCAAACACATCGACCGCTTCCCCTATTGAAGTTGGACCAGGTGATTGATTGGCAACCAATCGAACAATACCTGAACCGTCAAAAACCCGTTACCTTCGAGACCA		
4-1179979	GGCAAACCGCACAAGCCATGATTGCCAAACACATCGACCGTTTCCCCTATTGAAGTTGGACCAGGTGATTGATTGGCAACCGATCGAACAATACCTGAACCGTCAAAAACCCGTTACCTTAAGAGACCA		
Consensus	GGCAAACCGCACAAGCCATGATTGCCAAACACATCGACCGtTTCCCgCTATTGAAGTTGGACCAGGTGATTGATTGGCAgCCgATCGAACAATACCTGAACCGTCAAAAaAAaCCGTTACCTTaGAGACCA		
1171	orf		1300
2'-727827	CCGCGGCCGTCCCGCTACCCCTCTGCTGTCCATGTTCAAAGCCGTCCTGCTCGGACAATGGCACAGCCTCTCCGATCCCGAAGTCAACACAGCCTCATCACCCGCATCGATTCAACCTGTTTGGCGT		
3'-1063489	CCGCGGCCGTCCCGCTACCCGCTGCTGTCCATGTTCAAAGCCGTCCTGCTCGGACAATGGCACAGCCTCTCCGATCCCGAAGTCAACACAGCCTCATCACCCGCATCGATTCAACCTGTTTGGCGT		
4-1179979	CCGCGGCCGTCCCGCTACCCCTCTGCTGTCCATGTTCAAAGCCGTCCTGCTCGGACAATGGCACAGCCTCTCCGATCCCGAAGTCAACACAGCCTCATCACCCGCATCGATTCAACCTGTTTGGCGT		
Consensus	CCGCGGCCGTCCCGCTACCCtCTGCTGTCCATGTTCAAAGCCGTCCTGCTCGGACAATGGCACAGCCTCTCCGATCCCGAAGTCAACACAGCCTCATCACCCGCATCGAtTTCAACCTGTTTGGCGT		
1301	orf		1430
2'-727827	TTTGACGAAGTGTATCATCCCCGATTACAGTACCTTATGCCGCTACCGCAACTGGCTGGCGCAAGACGACACCCCTGTCCGAATTACTCAAAGTATTAACTGCCAACTGACCGAAAAAGGCCATAAAATAG		
3'-1063489	TTTGACGAAGTGTATCATCCCCGATTACAGCACCTTATGCCGCTACCGCAACTGGCTGGCGCAAGACGACACCCCTGTCCGAATTACTCAAAGTATTAACTGCCAACTGACCGAAAAAGGCCATAAAATAG		
4-1179979	TTTGACGAAGTGTATCATCCCCGATTACAGTACCTTATGCCGCTACCGCAACTGGCTGGCGCAAGACGACACCCCTGTCCGAATTACTCAAAGTATTAACTGCCAACTGACCGAAAAAGGCCATAAAATAG		
Consensus	TTcGACGAAGTGTATCATCCCCGATTACAGtACCTTATGCCGCTACCGCAACTGGCTGGCGCAAGACGACACCCCTGTCCGAATTACTCAAAGTATTAACTGCCAACTGACCGAAAAAGGCCATAAAATAG		
1431	orf		1560
2'-727827	AGAAAGCATCCGCCGCCGTCGTTGATGCCACCATTATCCAGACCGCCGGCAGCAAAACAGCGTCAGGCCATAGAAGTTGACGAAGAAGGACAAATCAGCGGTCAAACCACACCGAGTAAGGACAGCGATGC		
3'-1063489	AGAAAGCATCCGCCGCCGTCGTTGATGCCACCATTATCCAGACCGCCGGCAGCAAAACAGCGTCAGGCCATAGAAGTTGACGAAGAAGGACAAATCAGCGGTCAAACCACACCGAGTAAGGACAGCGATGC		
4-1179979	AGAAAGCATCCGCCGCCGTCGTTGATGCCACCATTATCCAGACCGCCGGCAGCAAAACAGCGTCAGGCCATAGAAGTTGACGAAGAAGGACAAATCAGCGGTCAAACCACACCGAGTAAGGACAGCGATGC		
Consensus	AGAAAGCATCCGCCGCCGTCGTTGATGCCACCATTATCCAGACCGCCGGCAGCAAAACAGCGTCAGGCCATAGAAGTTGACGAAGAAGGACAAATCAGCGGTCAAACCACACCGAGTAAGGACAGCGATGC		
1561	orf		1690
2'-727827	CCGTTGGATCAAGAAAAACGGCCTCTACAAACTCGGTTACAAACAACATACCCGTACCGATGTGGAAGGCTATATCGAGAAACTGTACATCACTCCCACCAATGCCCATGAGTGCAACACCTGTGCGCG		
3'-1063489	CCGTTGGATTAAGAAAAACGGCCTCTACAAACTCGGTTACAAACAACATACCCGTACCGATGTGGAAGGCTATATCGAGAAACTGTACATCACTCCCACCAATGCCCATGAGTGCAACACCTGTGCGCG		
4-1179979	CCGTTGGATTAAGAAAAACGGCCTCTACAAACTCGGTTACAAACAACATACCGTACCGATGTGGAAGGCTATATCGAGAAACTGCACATTACTCCCGCCAATGCCCATGAGTGCAACACCTGTGCGCG		
Consensus	CCGTTGGATaAAGAAAAACGGCCTCTACAAACTCGGTTACAAACAACATACcGTACCGATGcGGAAGGCTATATCGAGAAACTGtACATcACTCCCACCAATGCCCATGAGTGCAcACACCTGTGCGCG		
1691	orf		1820
2'-727827	TTGTTGGAAGGACTGCCAAAGGTACGACCGTCTATGCCGACAAAGGCTATGACAGTGCAGGAAAACCGGCAACATCTGGAAGAACATCAGTTGcAGGACGGCATTATGCGCAAGCCTGCCGCAACCGTC		
3'-1063489	TTGTTGGAAGGACTGCCAAAGGTACGACCGTCTATGCCGACAAAGGCTATGACAGTGCAGGAAAACCGGCAACATCTGGAAGAACATCAGTTGcAGGACGGCATTATGCGCAAGCCTGCCGCAACCGCC		
4-1179979	TTGTTGGAAGGTTACCCGAAGGTACGACCGTCTATGCCGACAAAGGCTACGACAGTGCAGGAAAACCGGCAACATCTGGAAGAACATCAGTTGTTGGACGGCATTATGCGCAAGCCTGCCGCAACCGCC		
Consensus	TTGTTGGAAGGAcTgCCCaAAGGTACGACCGTCTATGCCGACAAAGGCTAtGACAGTGCAGGAAAACCGGCAACATCTGGAAGAACATCAGTTGcaGGACGGCATTATGCGCAAGCCTGCCGCAACCGCc		
1821	orf		1950

2'-727827 CGCTGTCGGAAACGCAACCAAAACGCGACCGGTATTTGTGCGAAGACCCGTGGCGATGTGTTGAACCTGTTGAAAGCCGCCA-----ACAGGCTAAGTGCGCCG-----CT
3'-1063489 CGCTGTCGGGAAGTGCAAAACCAAACGCAACCGATATTTGTGCGAAGACCCGTATGTGGTTGAACAGAGCTTCGGTACGCTGCACCGTAAATTCGGCTACGCTCGGGCAGCCTATTTCGGACTGATTAAAGT
4-1179979 CGCTGTCGGGAAGTGCAAAACCAAACGCAACCGATATTTGTGCGAAGACCCGTATGTGGTTGAACAGAGCTTCGGTACGCTGCACCGTAAATTCGGCTACGCTCGGGCAGCCTATTTCGGACTGATTAAAGT
Consensus CGCTGTCGGGAAGTGCAAAACCAAACGCAACCGATATTTGTGCGAAGACCCGTatGtggTtgaacAgagctTcGgtAcgCtgCAccgtaaatccgctacgctcgggCAGcCTAttTcgGacTgattaaagT

1951 orf 2032
2'-727827 GCCGCCCAAAAGCGACCGGATGCCTGATTATCGGGTATCTAGGGAG-----GATTAA
3'-1063489 GAGTGCGCAAAGCCACCTGAAAGCGATGTGTTTGAACCTGTTGAAAGCGGCCAACAGGTTAAGTGCGCCCGCTGCCGCCTAA
4-1179979 GAGTGCGCAAAGCCACCTGAAAGCGATGTGTTTGAACCTGTTGAAAGCGGCCAACAGGTTAAGTGCGCCCGCTGCCGCCTAA
Consensus GagtGcGcAAAGcCacCtGaAaGcGatgTgtTtGaaccTgTtGaaAGcggccaacaGgTTAAgtgcgcccgctgccgcctaa

REP sequences in flanking regions downstream IS1106 transposases in *Neisseria meningitidis* Z2491

1 Righth End 130
1'-209578 AAAGGCGGGCCCGGATGCCTGATTATCGGGTATCCGGGCAGGATTAAGGGGGGATTTGGGTAGAATTAGGAGGTATTTGG-GGCGAAAAACAGCCGAAAAACCTGTGTTGGGGTTTCGGTTGTTGGG-GGGAA
6-1673919 AAAGCGAGCCCGGATGCCTGATTATCGGGTATCCGGGGAGGATTAAGGGGGTATTTGGGTAGAATTAGGAGGTATTTGG-GGCGAAAAACAGCCGAAAAACCTGTGTTGGGGTTTCGGCTGTCCGGAGGGAA
5'-1550999 AAAGGCGGGCCCGGATGCCTGATTATCGGGTATCCGGG---GATTAAGGGGGTATTTGGGTAGAATTAGGAGGTATTTGGTAGCGAAAAACAGCTGAAAAACCTGTGTTGGGGTTTCGGCTGTCCGGAGGGAA
Consensus AAAGGCGGGCCCGGATGCCTGATTATCGGGTATCCGGG.agGATTAAGGGGGTATTTGGGTAGAATTAGGagGTatTTGG.gGCGAAAAACAGCcGAAAAACCTGTGTTtGGGTTTCGGcGTcGGGaGGGAA

131 Righth End 260
1'-209578 AGGAATTTTGCAAAGGTCTCCGTCCGGCATCTGCAGCCGTTATTCCCGCGCAGGCGGGAACTCTAGTCTGTTCCGGTTTCAGTTATTTCCGATAAATGCCTGTGTCTTTTCATTTCTAGATTCCCACTTTTCG
6-1673919 GGGAATTTTGCAAAGGTCTCA-----TCCTGTTATTTTCACAAAAACAGAAAAAC-----CAAAAAACAGCAACCTGAAAATTCGT-----CATTCCCGCGCAGG
5'-1550999 AGGAATGTTTGCAAAGGTCTC-----TCCTGTTATTTTCACAAAAACAGAAAAAC-----CAAAAAACAGCAACCTGAAAATTCGT-----CATTCCCGCGCAGG
Consensus aGGAATtTTGCAAAGGTCTC.....c.gttatt..c.c..a..c.g.aa.c.....c.a.aa..gc....tg.tttTCgT.....cATTCCCgC....g

261 390
1'-209578 TGGGAATGACGGTTTCACTGCTACGGTTACTGTCAGGTTTCGGTTATGTTGGAATTTTCGGGAACCTTATGAAATCGTCATTCCCGCGCAGGCGGGAATCTAGAACATTCATGCTAAGGCAATTTATCGGGA
6-1673919 CGGGAATC-----CAGTGCGTTGAGTTTCAG-----CTATTTAGAATAAATTTTGAAACTCTAATCG--CGTCATTCCCGCGCAAGTTGGAATCCAGTTTCTTGAGTTTCAGTCATCCCGATAAA
5'-1550999 -----CAGTGCGTTGAGTTTCAG-----CTATTTAGAATAAATTTTGAAACTCTAATCG--CGTCATTCCCGCGCAACCGGGAATCTAGAACTCTCGACTTTTCAGATAATCTTTGAAT
Consensus .gggaat.....cagt...t....gtt.c.g.....c..tt..g....aattt.g..acaCTtaT...CGTCATTCCCGCGaA.GcgGGAATCtAGa.tcTcga..tT.aggcaattc.t.gaaa

391 520
1'-209578 ATGACTGAACTCAAAAAATGGATTCCCACTTTTCGTGGGAATGACGGGATTTTAGGTTCTGATTTTGGTTTTCCTGTTTGTAGGAATGATGAAATTTTGAGTTTATAGGAATTTACCGGAAA-----AA
6-1673919 TTGCCTTAGCATTTGAATGTCTAGATTCCCGCCTTCCCGGGAATGACGGCGGAGC-GGTTTCTGTTTTT---TCCGGTAAATACCCACAAGCTAAAATCCCGTTATTTTCACAAAAACAGAAAAACAAA
5'-1550999 ATTGCTGTTGTCTAAGGTCTAGATTCCCGCGTTTCGCGGGAATGACGG-----TTCAGTTGCTACGGTTATGTCAGGTTTGGTTATGTTGGAAATTTTCGGGAAC-----
Consensus aTg.CTga...Tc.AA.gtCTaGATTCCCGc.TtCGCGGGAATGACGG.....ggtttctg.tttt...TtC.GTt..Tac.g..Atg.T.AaaTtttG.tttTtt.g.AattaC.GgAAAC...aa

521 650
1'-209578 ACAGAAACCGTTCTGTTCGTCAATCCCGCGCAGGCGGGAATCTAGACATTCAATGCTAAGGCAATTTATCGGGAATGACTGAAACTCAAAAAATGGATTCCCACTTTTCGTGGGAATGACGGGATGTAGGT

6-1673919 ACAGCAACCTGAAATTCGTCATTCCCGCGCAGGCGGGAATCCAGTGTGTTGA-GTTTCAGCTATTTAGAATAAATTT-TGAAACTCTAATCGCGTCATTCCACGAAAGTGGGAATCCAGTTTCTTGAGT
5'-1550999 -----TTATGAAT-----TGAGACCTTTGCAAAATAGTCTGTAAACGAATTTGACGCATAAAAATGCGCCAAAAAATTTTCAATTGCCATAAACCTTCTCTAA-----
Consensus acag.aacc.....TcgTcAtTcccgcgcGgCGggaaTccAga.att..atGtTaa.GcaATTTa.cg.aaAt.a.TGaaaCtcaAAA..ct..ATTcCCac.aacgTgggaAt...g.....t..gt

651 780
1'-209578 TCGTGGGAATGACGGGATGTAGGTTCCGTACGGATGGATTCGTCATTCCCGCGCAGGCGGGAATCTAGACCTTGGGATAACAGCAATATTCAAAGATTATCTGAAAGTTTGAGATTCTGGATTCCCACT
6-1673919 TTCAGTCATTTCCGATAAATTGCCTTAGCATTGAATG---TCTAGATTCCCGCTGCGCGGGAATGACGGCGGAGCGGTTTCTGTTTTTCCGGTAAATACCCACAG-----CTAAATCCTGT
5'-1550999 -----TATTGAGCAAAAGTAGGAAAATCAGAAA-----AGTTTGCATT
Consensus t...g..a.t..cg..a..t.g..tt.....g.atg...tc...attccgc...gcgggaat...g.c...g.g.tttcaGcaatat.cag.aAatAtc.gaAG..ctagatTcccatT

781 910
1'-209578 TTCGTGGGAATGACGGGATGAGTTTCAAAATTTATTTCTAAATAGCTGAAGCTCAACGCACCTGGATTCCCGCTGCGCGGGAATGACGAATTTTAGGTTTCTGATT--TTGTTTTTCTGTTTGTGTTGGG
6-1673919 ATTTTCACAAACAGAAACCAAAACAGCAACCTG---AAATTCGTCATTCCCGCGCAGGCGGGAATCTGGTTTCGTTTCGGTTTCGCTGTTTTTAAGTTTCGGGTAACTTCCACTTCGTCATTCCCGCG
5'-1550999 TTGAAAATGAGATTGAGCATAAATTTTAGTAACCTATGTTATTGCAAGGCTCTC-----TTTTCGTCATTCCCGCC
Consensus tT..t.a.aA.aacgggaata.AatttcAg.Aacct.t.taAaT.c.t.a.tCtC.....gg....c.g..t....gg..t..c...tttta.gtttc.g.t...tt..ttTTCgtcaTTcccGcg

911 1040
1'-209578 AATGATGAAAT-----TTGAGTTTtagGAATTTATCGGAAAAACAGAAACCGCTCTGCCTGTCATTCCCG-CGCAGGCGGGAATCTAGACCTTGAACAAACAGTAATATTCAAAGATTATCTGAAAG
6-1673919 CAACTGGGAATCCAGTGCCTTtagTTTCAGCTATTTA-GAATAAATTTTGAAATCTAATCGCGTCATTCCCA-CGAAAGTGGGAATCCAGTTTGTAGTTTCAGTCATTCCGATAAATTGCCTTAGC
5'-1550999 ACTTTT-----CGTCATTCCCTCGAAAGCGGGAATCTAGAAATCTCGGACTTTCAGATAATCTTTGAATATTGCTGTTG
Consensus aatgttg.aat.....ttgagttt.ag..attta.....aaa....gaaac.....t..CGTCATTCCC..CGaAaGcGGGAATcTAgA.ttt.Gaacttcagtaatatcc.a.aAttttcct.a.g

1041 1170
1'-209578 TCCGGGATTCCTGGATTCCCACTTCGCGGGAATGACGAATTTTAGGTTCTCTGATTTGGTTTTCTGTTTGTGGGAATGATGAAATTTGAGTTTtagGAATTTATCGGAAAAACAGAAACCGCTCCG
6-1673919 ATTGAATGTCTAGATTCTCGCTGCGCGGGAATGACGAATCCATCCATACGGAAACCTGCATCCGTCATTCC-----CACGAACCTGTATC
5'-1550999 TTCTAAGGTCTAGATTTCGCGCTTCGCGGGAATGACGGTTCAGTTGCTACGGTTATTGTCA-----GGTTTCGGTTATG
Consensus ttcgaa.gTCTaGATTccCgC.TtCGCGGGAATGACGaaTc..t.g.TaCgGatattggcat.c.gt..tt.....cag.aaCcg.Tatg

1171 1300
1'-209578 CCGTCATTCCCGCGCAGGCGGGAATCCAGACCTTAGAACACAGTAATATTCAAAGATTATCTGAAAGTCCGGGATTCCTGGATTCCCACTTTCTGGGAATGACGGGATGAGGTTCCGTGCGGATGGA
6-1673919 CCGTCATTCCACGAAAGTGGGAATCCAGCTTTTtagTTTCAGTCATTTCGATAAATGCTTtagCATTTAGATGCTAGATTCCCGCTGCGCGGGAATGACGGGATTTGAAATTGCGGC-----AT
5'-1550999 TTGGAATTCGGGAACTTATGAATTGAGACCTTTGCAAAA-----ATAGTCTGTTACGAATTTGACGCATAAAAATGCGCCAAAAAATTTCAATTGC-----
Consensus ccGtcATTcCcgcaA.gtggGAATccAGaccTTtGaa.aacagt.at.t.c.a..a.t...c..aaagtctg..a.tctagaTTccCgC.T.cg.ggGaatgAcgggATT..aaTTgCg.....

1301 1430
1'-209578 TTCGTCATTCCCGCGCAGGCGGGAATCTAGACCTTAGAACAAACAGCAATATCAAGATTATCTGAAAGTCCGGGATTCCTGGATTCCCACTTTCTGGGAATGACGGGATTTAGGTTCTGTGTTTGGT
6-1673919 TTATCGGGAGCAACAGAAAGCGCTCTGCCGTCATTCCCACGAAGTGGGAATCCAGCTTTTtagT-----TTCAGTCATTTCCGATAAATTGCC----TTAGCATTTGAATGCTCTAGA
5'-1550999 -----CTAAACCTTCTAATATTGAGCAAAAGTAGGAAAAATCAGAAAAGTTTGC-----ATTTGAAAATGAGA-----TTGAGCATAAAATTTAGT
Consensus tt.....c..C..AagCcg..cT...gtc.ttc.aCaa.AG.aa.AaTCaaa.atTTt.tG.....ttc...c.tTT.tGa.AATgag.....Ttagg.tT.aattTTaGt

1431 1560
1'-209578 TTTCTGTTTGTAGGAATGATGAAATTTGAGTTTtagGAATTTATCGGAAAAACAGAAACCGCTCTGCGTCATTCCCGCGCAGGCGGGAATCTAGACATTCAATTCTAAGGCAATTTATCGGGAAAT

6-1673919 **TTCCCGCCTGCGCGGGAATGACGG**GATTT-GAGATTGCGGCATTATCAGGAGCAACAGAAGCCGCTCTG**CCGTCATTCCCACGAAAGTGGGAATCCAGTT**TTT**TGAGTTTCAGTCATTCCCGATAAATT**
 5'-1550999 AACCTATGTTATTGCAAGGTCTCGAATT-----GTCATTCCCACGCAGGCGGGAATCTAGTCTGTTCGGTTTCAGTTATTTCCGATAAATT
 Consensus ttcCtgt.Tt.gtgggAATGacg.gAtTT.gag.tt..gg.atttatc.g.a..aacagaa.ccgctctgccGTCATTCCCaCGcAgGcGGGAATCtAGtcttTt.agTtTcAGtcAtTtccgataaAtT

1561 1606
 1'-209578 GACTGAACTCAAAAA**CTGGATTCCCTACTTTCGTGGGAATGACGG**
 6-1673919 GCCTTAGCAT**TGAATGCTGGATTCCCGCCTGCGCGGGAATGACGG**
 5'-1550999 CCTGCTGCTTTT**ATTCTAGATTCCCACTTTCGTGGGAATGACGA**
 Consensus gcct.agc.Tt.aAt.tCTgGATTCCCaCtTtCGtGGGAATGACGg

>7'-1683921
 ACAAAAACAGTACGGCGTTGCCTCGCCTTAGCTCAAAGAGAACGATTCTCTAAGGTGCTGAAGCACCAAGTGAATCGGTTCCGTACTATTGTACTGTCTGCGGCTTTGCCGCCTTGTCTGATTTTTGTTAATCCACTATATG
 AATCGTCATTCCCGCGCAGGCGGGAATCCAGACATTCAATGCTAAGGCAATTTATCGGGAATGACTGAAACTCAAAAA**GCTGGATTCCCACTTTCGTGGGAATGACGG**GATTAGAGTTTCAAATTTATTCTAAATAGCTGAAAC
 TCAACGC**ACTGGATTCCCGCCTGCGCGGGAATGACGA**ATTTTCAGGTTGCTGTTTTTGGTTTTCTATTTTTGTGAAAATAACGGGATTTTCAGCTTGTGGGTATTTACCAGAAAAACAGAAACCGCTCCG**CCGTCATTCCC**
GGCGGAATCTAGACATTCAATGCTAAGGCAATTTATCGGAAATGACTGAAACTCAAAAA**ACTGGATTCCCACTTTCGTGGGAATGACAC**GATTAGAGTTTCAAATTTATTCTAAATAGCTGAAACTCAAAAA**CTGGATTCCC**
GCCTGCGCGGGAATGACGAAGTGGAAGTTACCCGAAATTTAAACAAGCGAAACCGAACGA**GCCGGATTCCCGCTTTCGTGGGAATGACGA**ATTTTCAGGTTGCTGTTTTTGGTTTTCTGTTTTGTGAAAATAACGGGATTTAG
 CTTGTGGGTATTTACCGGAAAAACAGAAACCGCTCCG**CCGTCATTCCC**
 GTGGAAGTTACCCGAAACTTAAACAAGCGAAACCGAACGA**ACTAGATTCCCACTTTCGTGGGAATGACGG**CAGAGCGGCTTCTGTTGCTCCCGATAAATGCCGCAATCTCAAATCCCGTCATTCCCGCGCAGGCGGGAATCTAG
 GTCTGTCAGTGCGGAAACTTATCAGGTAAACGGTTTCTTGAGATTTTGCGTCCTGGATTCCCACT

The copy 7 is not aligned with the copies 1, 6 and 5 because is a remnant without the end of the IS.
 REP sequences are in green background