

1	REP fragments	DR	Left End	orf A	130
IS8-1	TGA AAAAC TTC CGCACG CAGTTGAG GTTA TCGTTCC T CACGCTC CAG TGGACTGCCCCAAGAAGTTGGACACCAATCCGACCTAATGGGGGTGTTCAA ATGGCCAAGTATTCAGAGCAATTC AAAGCT				
IS8-2	CACGATAG TT ACGCTT TA GC TC CAGACAC CTG- TCGTTC CC TACGCT CTG TGGACTGCCCCAAGAAGTTGGACACCAATCCGACCTAATGGGGGTGTTCAA ATGGCCAAGTATTCAGAGCAATTC AAAGCT				
IS8-3	TCTTCGCGAACAGTTTCGCTCCCACAGGG CCATGTGTGCCCGT AAA TGGACTGCCCCAAGAAGTTGGACACCAATCCGACCTAATGGGGGTGTTCAA ATGGCCAAGTATTCAGAGCAATTC AAAGCT				
IS8-4	CGCTCAG CT CATACG CA CTCTG AAAGAG- CCC G AAA AGCT TGG TTT TGG ACTGCCCCAAGAAGTTGGACACCAATCCGACCTAATGGGGGTGTTCAA ATGGCCAAGTATTCAGAGCAATTC AAAGCT				
IS8-5	CGGTCCT CT TCG CGAC-TC AGAG CGTCG AGAG CTGC ATT CCC AC CGG TGGACTGCCCCAAGAAGTTGGACACCAATCCGACCTAATGGGGGTGTTCAA ATGGCCAAGTATTCAGAGCAATTC AAAGCT				
Consensus	cgC g aaacc T aC g ac ac aaC t c g aa ag gggc CgT g caT c aC g ctc ag TGG ACTGCCCCAAGAAGTTGGACACCAATCCGACCTAATGGGGGTGTTCAA ATGGCCAAGTATTCAGAGCAATTC AAAGCT				
131 orf A 260					
IS8-1	CACCGTC GTCAAAGCCTATCTTGCAGGCAACATAGGCTTT CG AAAGGTG TCC AGCCAGTTCTCGATCGATTCCAGCCTGCTTCGACGCTGGGTCGCCAATTACAAGAGCCATGGGCACACAGGCCATCGT				
IS8-2	CACCGTC GTCAAAGCCTATCTTGCAGGCAACATAGGCTTT CG AAAGGTG TCC AGCCAGTTCTCGATCGATTCCAGCCTGCTTCGACGCTGGGTCGCCAATTACAAGAGCCATGGGCACACAGGCCATCGT				
IS8-3	CACCGTC GTCAAAGCCTATCTTGCAGGCAACATAGGCTTT CG AAAGGTG TCC AGCCAGTTCTCGATCGATTCCAGCCTGCTTCGACGCTGGGTCGCCAATTACAAGAGCCATGGGCACACAGGCCATCGT				
IS8-4	CACCGTC GTCAAAGCCTATCTTGCAGGCAACATAGGCTTT CG AAAGGTG TCC AGCCAGTTCTCGATCGATTCCAGCCTGCTTCGACGCTGGGTCGCCAATTACAAGAGCCATGGGCACACAGGCCATCGT				
IS8-5	CACCGTC GTCAAAGCCTATCTTGCAGGCAACATAGGCTTT CG AAAGGTG TCC AGCCAGTTCTCGATCGATTCCAGCCTGCTTCGACGCTGGGTCGCCAATTACAAGAGCCATGGGCACACAGGCCATCGT				
Consensus	CACCGTC GTCAAAGCCTATCTTGCAGGCAACATAGGCTTT CG AAAGGTG TCC AGCCAGTTCTCGATCGATTCCAGCCTGCTTCGACGCTGGGTCGCCAATTACAAGAGCCATGGGCACACAGGCCATCGT				
261 orf A 390					
IS8-1	AAGCCTGG TCTTCGGTACAGCGAAGCCTTCAAACGCTCAGTGCTGGAGCACAAGCGCGAGCACGGGCTGTCCCTTCGCCAGACCGCAGCGCATTTTGGTATTGGTGATCCTGGCCAAATAGTCATTTGGG				
IS8-2	AAGCCTGG TCTTCGGTACAGCGAAGCCTTCAAACGCTCAGTGCTGGAGCACAAGCGCGAGCACGGGCTGTCCCTTCGCCAGACCGCAGCGCATTTTGGTATTGGTGATCCTGGCCAAATAGTCATTTGGG				
IS8-3	AAGCCTGG TCTTCGGTACAGCGAAGCCTTCAAACGCTCAGTGCTGGAGCACAAGCGCGAGCACGGGCTGTCCCTTCGCCAGACCGCAGCGCATTTTGGTATTGGTGATCCTGGCCAAATAGTCATTTGGG				
IS8-4	AAGCCTGG TCTTCGGTACAGCGAAGCCTTCAAACGCTCAGTGCTGGAGCACAAGCGCGAGCACGGGCTGTCCCTTCGCCAGACCGCAGCGCATTTTGGTATTGGTGATCCTGGCCAAATAGTCATTTGGG				
IS8-5	AAGCCTGG TCTTCGGTACAGCGAAGCCTTCAAACGCTCAGTGCTGGAGCACAAGCGCGAGCACGGGCTGTCCCTTCGCCAGACCGCAGCGCATTTTGGTATTGGTGATCCTGGCCAAATAGTCATTTGGG				
Consensus	AAGCCTGG TCTTCGGTACAGCGAAGCCTTCAAACGCTCAGTGCTGGAGCACAAGCGCGAGCACGGGCTGTCCCTTCGCCAGACCGCAGCGCATTTTGGTATTGGTGATCCTGGCCAAATAGTCATTTGGG				
391 orf A 520					
IS8-1	AACAGCAG CATTACAGTAACGATCTAGCCCCCTACGTTCCCAAGAGAAGAAAGTCTGTTGCCATGCCCAAGAAGCCTTATCCACCGCACCAGTAATCGACGACGATACGCAGAAGACGCGTGACCAGTT				
IS8-2	AACAGCAG CATTACAGTAACGATCTAGCCCCCTACGTTCCCAAGAGAAGAAAGTCTGTTGCCATGCCCAAGAAGCCTTATCCACCGCACCAGTAATCGACGACGATACGCAGAAGACGCGTGACCAGTT				
IS8-3	AACAGCAG CATTACAGTAACGATCTAGCCCCCTACGTTCCCAAGAGAAGAAAGTCTGTTGCCATGCCCAAGAAGCCTTATCCACCGCACCAGTAATCGACGACGATACGCAGAAGACGCGTGACCAGTT				
IS8-4	AACAGCAG CATTACAGTAACGATCTAGCCCCCTACGTTCCCAAGAGAAGAAAGTCTGTTGCCATGCCCAAGAAGCCTTATCCACCGCACCAGTAATCGACGACGATACGCAGAAGACGCGTGACCAGTT				
IS8-5	AACAGCAG CATTACAGTAACGATCTAGCCCCCTACGTTCCCAAGAGAAGAAAGTCTGTTGCCATGCCCAAGAAGCCTTATCCACCGCACCAGTAATCGACGACGATACGCAGAAGACGCGTGACCAGTT				
Consensus	AACAGCAG CATTACAGTAACGATCTAGCCCCCTACGTTCCCAAGAGAAGAAAGTCTGTTGCCATGCCCAAGAAGCCTTATCCACCGCACCAGTAATCGACGACGATACGCAGAAGACGCGTGACCAGTT				
521 orf A Intergenic region 650					
IS8-1	AATGGCCG AGCTCGAATACCTGCGCATGGAGAACGCTTACCTAAAAAAGTTGGAAGAGTTGAAGGAGCAGCAACGACGGCAAAGAAAAAGCCCTGATCGTCAAACAAC TGAGGAGCCGCTTCTCGCTCT				
IS8-2	AATGGCCG AGCTCGAATACCTGCGCATGGAGAACGCTTACCTAAAAAAGTTGGAAGAGTTGAAGGAGCAGCAACGACGGCAAAGAAAAAGCCCTGATCGTCAAACAAC TGAGGAGCCGCTTCTCGCTCT				
IS8-3	AATGGCCG AGCTCGAATACCTGCGCATGGAGAACGCTTACCTAAAAAAGTTGGAAGAGTTGAAGGAGCAGCAACGACGGCAAAGAAAAAGCCCTGATCGTCAAACAAC TGAGGAGCCGCTTCTCGCTCT				
IS8-4	AATGGC AGAGCTCGAATACCTGCGCATGGAGAACGCTTACCTAAAAAAGTTGGAAGAGTTGAAGGAGCAGCAACGACGGCAAAGAAAAAGCCCTGATCGTCAAACAAC TGAGGAGCCGCTTCTCGCTCT				
IS8-5	AATGGCCG AGCTCGAATACCTGCGCATGGAGAACGCTTACCTAAAAAAGTTGGAAGAGTTGAAGGAGCAGCAACGACGGCAAAGAAAAAGCCCTGATCGTCAAACAAC TGAGGAGCCGCTTCTCGCTCT				
Consensus	AATGGCCG AGCTCGAATACCTGCGCATGGAGAACGCTTACCTAAAAAAGTTGGAAGAGTTGAAGGAGCAGCAACGACGGCAAAGAAAAAGCCCTGATCGTCAAACAAC TGAGGAGCCGCTTCTCGCTCT				
651 Intergenic region orf B 780					
IS8-1	GCGCCCTT CTGACGCTGGCGGGCT TGG CGCGCAGTACGTTCTACTATCAGGTT CC AGGTG CAATCC AGACCGGATCCAGATGCTGCTCTAAAGCAGGAGGTAGAGCGGATTTATCAGGAGAGAGGGTCT				

IS8-2 GCGCCCTTCTGACGCTGGCGGGCTTGGCGCGCAGTACGTTCTACTATCAGGTTTCAGGTGCAATCCAGACCCGATCCAGATGCTGCTCTAAAGCAGGAGGTAGAGCGGATTTATCACGAGGAGAGAGGTC
IS8-3 GCGCCCTTCTGACGCTGGCGGGCTTGGCGCGCAGTACGTTCTACTATCAGGTTTCAGGTGCAATCCAGACCCGATCCAGATGCTGCTCTAAAGCAGGAGGTAGAGCGGATTTATCACGAGGAGAGAGGTC
IS8-4 GCGCCCTTCTGACGCTGGCGGGCTTGGCGCGCAGTACGTTCTACTATCAGGTTTCAGGTGCAATCCAGACCCGATCCAGATGCTGCTCTAAAGCAGGAGGTAGAGCGGATTTATCACGAGGAGAGAGGTC
IS8-5 GCGCCCTTCTGACGCTGGCGGGCTTGGCGCGCAGTACGTTCTACTATCAGGTTTCAGGTGCAATCCAGACCCGATCCAGATGCTGCTCTAAAGCAGGAGGTAGAGCGGATTTATCACGAGGAGAGAGGTC
Consensus GCGCCCTTCTGACGCTGGCGGGCTTGGCGCGCAGTACGTTCTACTATCAGGTTTCAGGTGCAATCCAGACCCGATCCAGATGCTGCTCTAAAGCAGGAGGTAGAGCGGATTTATCACGAGGAGAGAGGTC

781 orf B 910

IS8-1 TTATGGGGCTCGGCGCATCACAGCGGTTATCCGCAACTCAGGCACGCTGGTCAACAAGAAGGTTGTGGAGAGATTGATGGCTGAACTGGGTCTGCGCTCCGTTGTTTCGACCAAAAAAATACCGTTCCTAT
IS8-2 TTATGGGGCTCGGCGCATCACAGCGGTTATCCGCAACTCAGGCACGCTGGTCAACAAGAAGGTTGTGGAGAGATTGATGGCTGAACTGGGTCTGCGCTCCGTTGTTTCGACCAAAAAAATACCGTTCCTAT
IS8-3 TTATGGGGCTCGGCGCATCACAGCGGTTATCCGCAACTCAGGCACGCTGGTCAACAAGAAGGTTGTGGAGAGATTGATGGCTGAACTGGGTCTGCGCTCCGTTGTTTCGACCAAAAAAATACCGTTCCTAT
IS8-4 TTATGGGGCTCGGCGCATCACAGCGGTTATCCGCAACTCAGGCACGCTGGTCAACAAGAAGGTTGTGGAGAGATTGATGGCTGAACTGGGTCTGCGCTCCGTTGTTTCGACCAAAAAAATACCGTTCCTAT
IS8-5 TTATGGGGCTCGGCGCATCACAGCGGTTATCCGCAACTCAGGCACGCTGGTCAACAAGAAGGTTGTGGAGAGATTGATGGCTGAACTGGGTCTGCGCTCCGTTGTTTCGACCAAAAAAATACCGTTCCTAT
Consensus TTATGGGGCTCGGCGCATCACAGCGGTTATCCGCAACTCAGGCACGCTGGTCAACAAGAAGGTTGTGGAGAGATTGATGGCTGAACTGGGTCTGCGCTCCGTTGTTTCGACCAAAAAAATACCGTTCCTAT

911 orf B 1040

IS8-1 AAGGGCACCGTCGGAAAAATTCACCGAATTTGCTGGAGCGCAATTCACGGCGCAACGCCGAACCAGAAATGGGTGACCGATGTGACCGAGTTTAAAGTGGCCAATCGAAAGCTGTATCTCTCGCCTG
IS8-2 AAGGGCACCGTCGGAAAAATTCACCGAATTTGCTGGAGCGCAATTCACGGCGCAACGCCGAACCAGAAATGGGTGACCGATGTGACCGAGTTTAAAGTGGCCAATCGAAAGCTGTATCTCTCGCCTG
IS8-3 AAGGGCACCGTCGGAAAAATTCACCGAATTTGCTGGAGCGCAATTCACGGCGCAACGCCGAACCAGAAATGGGTGACCGATGTGACCGAGTTTAAAGTGGCCAATCGAAAGCTGTATCTCTCGCCTG
IS8-4 AAGGGCACCGTCGGAAAAATTCACCGAATTTGCTGGAGCGCAATTCACGGCGCAACGCCGAACCAGAAATGGGTGACCGATGTGACCGAGTTTAAAGTGGCCAATCGAAAGCTGTATCTCTCGCCTG
IS8-5 AAGGGCACCGTCGGAAAAATTCACCGAATTTGCTGGAGCGCAATTCACGGCGCAACGCCGAACCAGAAATGGGTGACCGATGTGACCGAGTTTAAAGTGGCCAATCGAAAGCTGTATCTCTCGCCTG
Consensus AAGGGCACCGTCGGAAAAATTCACCGAATTTGCTGGAGCGCAATTCACGGCGCAACGCCGAACCAGAAATGGGTGACCGATGTGACCGAGTTTAAAGTGGCCAATCGAAAGCTGTATCTCTCGCCTG

1041 orf B 1170

IS8-1 TGATGGACCTGTACAACGGTGAGATCGTGGCGTACGAATTTGCTACCAGGCCGTGCTTTGAGCTGGTCACCAGTATGCTGGACAAGGCGTTGCAGCAGTTGCAAGACGAGCCGAAGCTTGTGATGCACTC
IS8-2 TGATGGACCTGTACAACGGTGAGATCGTGGCGTACGAATTTGCTACCAGGCCGTGCTTTGAGCTGGTCACCAGTATGCTGGACAAGGCGTTGCAGCAGTTGCAAGACGAGCCGAAGCTTGTGATGCACTC
IS8-3 TGATGGACCTGTACAACGGTGAGATCGTGGCGTACGAATTTGCTACCAGGCCGTGCTTTGAGCTGGTCACCAGTATGCTGGACAAGGCGTTGCAGCAGTTGCAAGACGAGCCGAAGCTTGTGATGCACTC
IS8-4 TGATGGACCTGTACAACGGTGAGATCGTGGCGTACGAATTTGCTACCAGGCCGTGCTTTGAGCTGGTCACCAGTATGCTGGACAAGGCGTTGCAGCAGTTGCAAGACGAGCCGAAGCTTGTGATGCACTC
IS8-5 TGATGGACCTGTACAACGGTGAGATCGTGGCGTACGAATTTGCTACCAGGCCGTGCTTTGAGCTGGTCACCAGTATGCTGGACAAGGCGTTGCAGCAGTTGCAAGACGAGCCGAAGCTTGTGATGCACTC
Consensus TGATGGACCTGTACAACGGTGAGATCGTGGCGTACGAATTTGCTACCAGGCCGTGCTTTGAGCTGGTCACCAGTATGCTGGACAAGGCGTTGCAGCAGTTGCAAGACGAGCCGAAGCTTGTGATGCACTC

1171 orf B 1300

IS8-1 GGATCAAGGCTGGCAGTATCAACACGCGCAGTACCGTCAGAAACTGGCGGCAAAGGGTGTGAAGCAAAGCATGTCTCGTAAGGGAATTCGCTGGACAACGCTGCGATGGAAAGCTTTTTTGGTACGCTT
IS8-2 GGATCAAGGCTGGCAGTATCAACACGCGCAGTACCGTCAGAAACTGGCGGCAAAGGGTGTGAAGCAAAGCATGTCTCGTAAGGGAATTCGCTGGACAACGCTGCGATGGAAAGCTTTTTTGGTACGCTT
IS8-3 GGATCAAGGCTGGCAGTATCAACACGCGCAGTACCGTCAGAAACTGGCGGCAAAGGGTGTGAAGCAAAGCATGTCTCGTAAGGGAATTCGCTGGACAACGCTGCGATGGAAAGCTTTTTTGGTACGCTT
IS8-4 GGATCAAGGCTGGCAGTATCAACACGCGCAGTACCGTCAGAAACTGGCGGTAAGGGTGTGAAGCAAAGCATGTCTCGTAAGGGAATTCGCTGGACAACGCTGCGATGGAAAGCTTTTTTGGTACGCTT
IS8-5 GGATCAAGGCTGGCAGTATCAACACGCGCAGTACCGTCAGAAACTGGCGGCAAAGGGTGTGAAGCAAAGCATGTCTCGTAAGGGAATTCGCTGGACAACGCTGCGATGGAAAGCTTTTTTGGTACGCTT
Consensus GGATCAAGGCTGGCAGTATCAACACGCGCAGTACCGTCAGAAACTGGCGGCAAAGGGTGTGAAGCAAAGCATGTCTCGTAAGGGAATTCGCTGGACAACGCTGCGATGGAAAGCTTTTTTGGTACGCTT

1301 orf B 1430

IS8-1 AAGTCCGAGTTTTTCTACTTGAAACGATTTGAAAGCATAGAAGAGCTGACGGCAGGTCTGGAGGAGTACATCCGCTACTACAACCATGACCGCATTAAGCTGAAGCTAGGCGGCCTGAGCCCCGTAAAAT
IS8-2 AAGTCCGAGTTTTTCTACTTGAAACGATTTGAAAGCATAGAAGAGCTGACGGCAGGTCTGGAGGAGTACATCCGCTACTACAACCATGACCGCATTAAGCTGAAGCTAGGCGGCCTGAGCCCCGTAAAAT
IS8-3 AAGTCCGAGTTTTTCTACTTGAAACGATTTGAAAGCATAGAAGAGCTGACGGCAGGTCTGGAGGAGTACATCCGCTACTACAACCATGACCGCATTAAGCTGAAGCTAGGCGGCCTGAGCCCCGTAAAAT
IS8-4 AAGTCCGAGTTTTTCTACTTGAAACGATTTGAAAGCATAGAAGAGCTGACGGCAGGTCTGGAGGAGTACATCCGCTACTACAACCATGACCGCATTAAGCTGAAGCTAGGCGGCCTGAGCCCCGTAAAAT
IS8-5 AAGTCCGAGTTTTTCTACTTGAAACGATTTGAAAGCATAGAAGAGCTGACGGCAGGTCTGGAGGAGTACATCCGCTACTACAACCATGACCGCATTAAGCTGAAGCTAGGCGGCCTGAGCCCCGTAAAAT

Consensus AAGTCCGAGTTTTTCTACTTGAAACGATTTGAAAGCATAGAAGAGCTGACGGCAGGTCTGGAGGAGTACATCCGCTACTACAACCATGACCGCATTAAAGCTGAAGCTAGGCGGCCTGAGCCCCGTAAAAAT

1431 orf B Right End DR REP fragments 1555

IS8-1 ACAGGACTCAGGCGGCAAGCTAAAACTGTCCAACCTCCGGGGGGCAGTCCA CAGCGTAGGAATGCCGTGGGTGACGCTCTGCGTCA CAAATCTGCGCTGCGCCGCATACTCAAGACCGGACGC
IS8-2 ACAGGACTCAGGCGGCAAGCTAAAACTGTCCAACCTCCGGGGGGCAGTCCA CTGCGTGGGAATGCCTTGCGTGACGCTCCGCGTCA CAGGTTTGGCAGCGTCGCCGATAGTGCAAGGCGAT
IS8-3 ACAGGACTCAGGCGGCAAGCTAAAACTGTCCAACCTCCGGGGGGCAGTCCA AAAATGTGGGAGTGACCGGGGCGCGATCCGCATTG CTCACGAAGAGGCCGTGCAGCCGCTGATGTATCAG
IS8-4 ACAGGACTCAGGCGGCAAGCTAAAACTGTCCAACCTCCGGGGGGCAGTCCA TTTTGTGGGAGTGGACTTGTCCGCGAT--GGTTGCGAAGCGGCCCTAAACCAGACGACTTGGTTGCGCCT
IS8-5 ACAGGACTCAGGCGGCAAGCTAAAACTGTCCAACCTCCGGGGGGCAGTCCA CCGGGGGCGTA-GGGAACCATAGCCCTGACTATCGTGCTGAAATTCTGTGTGGATATGCTGATCTCAACTAT
Consensus ACAGGACTCAGGCGGCAAGCTAAAACTGTCCAACCTCCGGGGGGCAGTCCA cagcGTGGGAaTGccctgGgtggCGcTccGcgTcgCaaagcagcgCtgcGcCGcaacacctGatcgacct.