

Flanking regions upstream ISPa11 orfs

	1		90
ISPa11-1	CGGATCCTGGCCGGGCGGCGGCAGCAGGAGGATGTCGATGATCGGCTTGGCGTCGAGCCCGGGCA	CCGCGGTGCTGCCGACATGCTCGAT	
ISPa11-2	CAAGGGCGGGCGGCGGATAGTCGGCGCCTGGCCGCTGGAGGATGTTCCGCTGAGCCGCTCGCAGCGCATCGAGCTGC	AACGGCAACTG	
ISPa11-4	AGGTGAAGTACGTGACCTGTCTCGACCTCGCGGCTGGGCGCGGTGTTACCGAGGGCTGGGA	CCGCCAGGTACGGTTCGTGCCGAG	
ISPa11-3	GCCGCCCTCAAGGGCTGATCCCGGGCGTACCCCGCCGAGGCGGCGATTAACCGCGTGGCGTTATTG	CCCTACACGGGGAGGGG	
ISPa11-5	CGGCGACAGCTGGTTCGTAGCAAGGCA	CCCCGGTGCTCTGGGAGGTGTCGACGGCGGCTTCGTCAAGCACTACTACGGCGTG	
ISPa11-6	AGACGCCGGTGGAAT--ACCGCAACCCGCGCCACCCCTCGGCCAGCACACCGACGAGT	CCTCGAGACGCTCCTCGGCCTGGAC	
Consensus	g..g..cgg..gg.....c..c.....g..ccc..gg.....g..t...cg..c..gg..cc..c...g..c...ac...gc...g..g		
	91		180
ISPa11-1	GCCCAGCCGGGCAGCGCCAGCGCCGTCGTCGGATGGCCTCGGCTTC	-GGCGCGAAGTGTGTGTTGTT-----GGCCAGGCGGGGTC	
ISPa11-2	GCCGCCCGCGGACACGATCCGGGCGCGGTGGATGGCATCA---TC	-GGCGCCAATACGCGCA-----AGGCGATCCGCGCC	
ISPa11-4	G---AGGGCAAGAAGATCAAGACCGAGATCAATGGCGTGTGGATCTACCCGCGCGCGCGGA	-----CGCGCCGTGGCGC	
ISPa11-3	ACAAGCGGTAGGGCGAATAACGCGCCAGGCGTTATCCGCCGAAACG	CGCTGCCGAGGTGGCGG-----ATAACCGCGTAGCGGTT	
ISPa11-5	GCTTGAGACACCG-AAGAGACGGCGAGCCGTTACGCAAGGCGTG	CGCTGCGGCGCTGCCAACCCCTCGACACGCCCCCGTAGGGCGAAT	
ISPa11-6	GCG-GCCGCGCTG-GAAAGGCTGCGCGACGGCAAGGTGATCTGAGCC	CCCGCGCCCGCCECA-----GCGACGCATCGCGGAC	
Consensus	gc.....gc.....ga...a..gCg..g..gg..t.gc.....c..ccgcc.....gc..a.....c.c....g..gg..c		
	181		270
ISPa11-1	GGCAGGCAGCACCTCGATGCGTCTGTCGTCGCGGCTGCTCCAGCGTTGG	CCGTGGAAGC---GGGGCGGTTGGGTGAGGACATGGCGGA	
ISPa11-2	TGCCAGCAGGAGTTCGGCTGCGCGCGGACGGGCTATCCGACCCCGCGCTGCT	CGACCG---CCTGCGGACGCCATAGGGCCGCCGGCGG	
ISPa11-4	TGGCGGCGGCCGACCGCTGATTCCGGTGGTGGCGTAGGGCGATTTC	CCCTCACCCCAA---CCCTCTCCCGCAGGCGGGAGAGGATGCC	
ISPa11-3	ATTCGCCC-----TACACGGGGAGAGGACAAAGCGGTAGGGCGAAT	AACGCCCAGGCGGTTATCCGCGGAAACGCCTGCCGAGGTGGCGGA	
ISPa11-5	AAACCGCTCGCGGTATCCGCGGTGAAACCCGCTCGTAACGCGGAT	AGCGCTGCGCGCTATTCCGCTTACCGGCAAGC-----CG	
ISPa11-6	AAACGCCACCCGTACCCCGCGCAACACCGCGACGTAG-GGCGCAT	AACCGCAAACGCGGTTATCCGCGGCCAGCCGAGCATCG--GCGGA	
Consensus	..ccg..c..gc..g..tc..cg..g.....cggcg..t..ggCg..t..c..cc..cg..cg....ccg..Cg..c..g....g..g....g..gg..		
	271	REP frg	Left End
ISPa11-1	CTCGGGGAT-----ATGCGGGAGATTGGCGGCGATGGAGAGCTGGG	GTAGGGCAATGAAATGGACTCCTCCCTCCTACGGCGTCAAGCG	
ISPa11-2	AGCTTACGACCCACGTCCGCGCGACCGCTCGCGGCACACCGGTTG	GTAGGGCAATGAAATGGACTCCTCCCTCCTACGGCGTCAAGCG	
ISPa11-4	GTGCAGCGTAGAGGGATGCAGCGG--CGCGCGGATGCCTGGCTTCG	GTAGGGCAATGAAATGGACTCCTCCCTCCTACGGCGTCAAGCG	
ISPa11-3	TAAACCGCTGCGCGTTATTCCGCTGCGCGGG--AGGGAGCAAGCG	GTAGGGCAATGAAATGGACTCCTCCCTCCTACGGCGTCAAGCG	
ISPa11-5	TTACGCCCGGCG-----ACGCTGCCAACCCCTCGACATGTCCCC	GTAGGGCAATGAAATGGACTCCTCCCTCCTACGGCGTCAAGCG	
ISPa11-6	TACGCGCCTGCGGTTATTCCGCTACCGTACCCCGCGCAGCACCA	GTAGGGCAATGAAATGGACTCCTCCCTCCTACGGCGTCAAGCG	
Consensus	...c..cg.....gc..c..c.....a..c.....GTAGGGCAATGAAATGGACTCCTCCCTCCTACGGCGTCAAGCG		
	361	Left End	orf
ISPa11-1	CCAGACTAATGGTGCAGCCACAAGTCCCGGAGGGGGAGTCAGC	ATGAACCTTAGTCGCATTGGTCTGGATCTGGCAAAACAAGTATTCCA	
ISPa11-2	CCAGACTAATGGTGCAGCCACAAGTCCCGGAGGGGGAGTCAGC	ATGAACCTTAGTCGCATTGGTCTGGATCTGGCAAAACAAGTATTCCA	
ISPa11-4	CCAGACTAATGGTGCAGCCACAAGTCCCGGAGGGGGAGTCAGC	ATGAACCTTAGTCGCATTGGTCTGGATCTGGCAAAACAAGTATTCCA	
ISPa11-3	CCAGACTAATGGTGCAGCCACAAGTCCCGGAGGGGGAGTCAGC	ATGAACCTTAGTCGCATTGGTCTGGATCTGGCAAAACAAGTATTCCA	

ISPa11-5 CCAGACTAATGGTGCAGCCACAAGTCCCGGAGGGGGAGTCAGCATGAACCTTAGTCGCATTGGTCTGGATCTGGCAAAACAAGTATTCCA
ISPa11-6 CCAGACTAATGGTGCAGCCACAAGTCCCGGAGGGGGAGTCAGCATGAACCTTAGTCGCATTGGTCTGGATCTGGCAAAACAAGTATTCCA
Consensus CCAGACTAATGGTGCAGCCACAAGTCCCGGAGGGGGAGTCAGCATGAACCTTAGTCGCATTGGTCTGGATCTGGCAAAACAAGTATTCCA

451 orf 540

ISPa11-1 GGTGCACGGCGTTGATCGTCACGAGCATGTGGTATGTCGTCGCCAACTCAAGCGGGCACAGGTGCGGGATTCTTTTCGCCAACTGCCGCC
ISPa11-2 GGTGCACGGCGTTGATCGTCACGAGCATGTGGTATGTCGTCGCCAACTCAAGCGGGCACAGGTGCGGGATTCTTTTCGCCAACTGCCGCC
ISPa11-4 GGTGCACGGCGTTGATCGTCACGAGCATGTGGTATGTCGTCGCCAACTCAAGCGGGCACAGGTGCGGGATTCTTTTCGCCAACTGCCGCC
ISPa11-3 GGTGCACGGCGTTGATCGTCACGAGCATGTGGTATGTCGTCGCCAACTCAAGCGGGCACAGGTGCGGGATTCTTTTCGCCAACTGCCGCC
ISPa11-5 GGTGCACGGCGTTGATCGTCACGAGCATGTGGTATGTCGTCGCCAACTCAAGCGGGCACAGGTGCGGGATTCTTTTCGCCAACTGCCGCC
ISPa11-6 GGTGCACGGCGTTGATCGTCACGAGCATGTGGTATGTCGTCGCCAACTCAAGCGGGCACAGGTGCGGGATTCTTTTCGCCAACTGCCGCC
Consensus GGTGCACGGCGTTGATCGTCACGAGCATGTGGTATGTCGTCGCCAACTCAAGCGGGCACAGGTGCGGGATTCTTTTCGCCAACTGCCGCC

541 orf 630

ISPa11-1 GTGCCTGGTGGCGATGGAGGCCTGCGGCAGTGCGCACTACTGGGCGCGGAGTTGCGGGAGCTGGGCCACACGGTACGCCTGATCGCACC
ISPa11-2 GTGCCTGGTGGCGATGGAGGCCTGCGGCAGTGCGCACTACTGGGCGCGGAGTTGCGGGAGCTGGGCCACACGGTACGCCTGATCGCACC
ISPa11-4 GTGCCTGGTGGCGATGGAGGCCTGCGGCAGTGCGCACTACTGGGCGCGGAGTTGCGGGAGCTGGGCCACACGGTACGCCTGATCGCACC
ISPa11-3 GTGCCTGGTGGCGATGGAGGCCTGCGGCAGTGCGCACTACTGGGCGCGGAGTTGCGGGAGCTGGGCCACACGGTACGCCTGATCGCACC
ISPa11-5 GTGCCTGGTGGCGATGGAGGCCTGCGGCAGTGCGCACTACTGGGCGCGGAGTTGCGGGAGCTGGGCCACACGGTACGCCTGATCGCACC
ISPa11-6 GTGCCTGGTGGCGATGGAGGCCTGCGGCAGTGCGCACTACTGGGCGCGGAGTTGCGGGAGCTGGGCCACACGGTACGCCTGATCGCACC
Consensus GTGCCTGGTGGCGATGGAGGCCTGCGGCAGTGCGCACTACTGGGCGCGGAGTTGCGGGAGCTGGGCCACACGGTACGCCTGATCGCACC

631 orf 666..... .

ISPa11-1 GCAGTTCGTAAAACCTACGTCAAGGGTGACAAGCA..... .
ISPa11-2 GCAGTTCGTAAAACCTACGTCAAGGGTGACAAGCA..... .
ISPa11-4 GCAGTTCGTAAAACCTACGTCAAGGGTGACAAGCA..... .
ISPa11-3 GCAGTTCGTAAAACCTACGTCAAGGGTGACAAGCA..... .
ISPa11-5 GCAGTTCGTAAAACCTACGTCAAGGGTGACAAGCA..... .
ISPa11-6 GCAGTTCGTAAAACCTACGTCAAGGGTGACAAGCA..... .
Consensus GCAGTTCGTAAAACCTACGTCAAGGGTGACAAGCA..... .

Flanking regions downstream ISPa11 orfs

	1	orf	Right End	90
ISPa11-1	CCTGGCCAACAAGAAATGCCCGGATCCTTTGGGCTTTACTCAGCCGGGAGACATGCTACCGGCCCGGTTGAGCGTTTCCTGCCACACCGTAG			
ISPa11-2	CCTGGCCAACAAGAAATGCCCGGATCCTTTGGGCTTTACTCAGCCGGGAGACATGCTACCGGCCCGGTTGAGCGTTTCCTGCCACACCGTAG			
ISPa11-3	CCTGGCCAACAAGAAATGCCCGGATCCTTTGGGCTTTACTCAGCCGGGAGACATGCTACCGGCCCGGTTGAGCGTTTCCTGCCACACCGTAG			
ISPa11-5	CCTGGCCAACAAGAAATGCCCGGATCCTTTGGGCTTTACTCAGCCGGGAGACATGCTACCGGCCCGGTTGAGCGTTTCCTGCCACACCGTAG			
ISPa11-4	CCTGGCCAACAAGAAATGCCCGGATCCTTTGGGCTTTACTCAGCCGGGAGACATGCTACCGGCCCGGTTGAGCGTTTCCTGCCACACCGTAG			
ISPa11-6	CCTGGCCAACAAGAAATGCCCGGATCCTTTGGGCTTTACTCAGCCGGGAGACATGCTACCGGCCCGGTTGAGCGTTTCCTGCCACACCGTAG			
Consensus	CCTGGCCAACAAGAAATGCCCGGATCCTTTGGGCTTTACTCAGCCGGGAGACATGCTACCGGCCCGGTTGAGCGTTTCCTGCCACACCGTAG			
	91	Right End		180
ISPa11-1	TTGAAACATCCACCACGATTGCTCAGTGAATGACAATGATGACGAACCGGTCGAACCGGCCTGCATGAAACCTGGTTTATACGTGGGCTC			
ISPa11-2	TTGAAACATCCACCACGATTGCTCAGTGAATGACAATGATGACGAACCGGTCGAACCGGCCTGCATGAAACCTGGTTTATACGTGGGCTC			
ISPa11-3	TTGAAACATCCACCACGATTGCTCAGTGAATGACAATGATGACGAACCGGTCGAACCGGCCTGCATGAAACCTGGTTTATACGTGGGCTC			
ISPa11-5	TTGAAACATCCACCACGATTGCTCAGTGAATGACAATGATGACGAACCGGTCGAACCGGCCTGCATGAAACCTGGTTTATACGTGGGCTC			
ISPa11-4	TTGAAACATCCACCACGATTGCTCAGTGAATGACAATGATGACGAACCGGTCGAACCGGCCTGCATGAAACCTGGTTTATACGTGGGCTC			
ISPa11-6	TTGAAACATCCACCACGATTGCTCAGTGAATGACAATGATGACGAACCGGTCGAACCGGCCTGCATGAAACCTGGTTTATACGTGGGCTC			
Consensus	TTGAAACATCCACCACGATTGCTCAGTGAATGACAATGATGACGAACCGGTCGAACCGGCCTGCATGAAACCTGGTTTATACGTGGGCTC			
	181	Right End		270
ISPa11-1	CCTGCTGCAGTGAAGCAAAGCCGTTAGGGCGATCAGGTATGCAGGCGCGCATTTTCATCAGGGCTCGGGAGTTGCAACACCACTCCATGAA			
ISPa11-2	CCTGCTGCAGTGAAGCAAAGCCGTTAGGGCGATCAGGTATGCAGGCGCGCATTTTCATCAGGGCTCGGGAGTTGCAACACCACTCCATGAA			
ISPa11-3	CCTGCTGCAGTGAAGCAAAGCCGTTAGGGCGATCAGGTATGCAGGCGCGCATTTTCATCAGGGCTCGGGAGTTGCAACACCACTCCATGAA			
ISPa11-5	CCTGCTGCAGTGAAGCAAAGCCGTTAGGGCGATCAGGTATGCAGGCGCGCATTTTCATCAGGGCTCGGGAGTTGCAACACCACTCCATGAA			
ISPa11-4	CCTGCTGCAGTGAAGCAAAGCCGTTAGGGCGATCAGGTATGCAGGCGCGCATTTTCATCAGGGCTCGGGAGTTGCAACACCACTCCATGAA			
ISPa11-6	CCTGCTGCAGTGAAGCAAAGCCGTTAGGGCGATCAGGTATGCAGGCGCGCATTTTCATCAGGGCTCGGGAGTTGCAACACCACTCCATGAA			
Consensus	CCTGCTGCAGTGAAGCAAAGCCGTTAGGGCGATCAGGTATGCAGGCGCGCATTTTCATCAGGGCTCGGGAGTTGCAACACCACTCCATGAA			
	271	Right End	REP fragment	360
ISPa11-1	GCCGGATATACGGATGCAGTCGTACACAGGTTTGAATCAAGACAAACACTGGCAAACCGGGAGGAGTCCATATACGAATAACGCCAGCG			
ISPa11-2	GCCGGATATACGGATGCAGTCGTACACAGGTTTGAATCAAGACAAACACTGGCAAACCGGGAGGAGTCCATATACGGATAACGCCATGG			
ISPa11-3	GCCGGATATACGGATGCAGTCGTACACAGGTTTGAATCAAGACAAACACTGGCAAACCGGGAGGAGTCCATATACGAATAACGCCCCAG			
ISPa11-5	GCCGGATATACGGATGCAGTCGTACACAGGTTTGAATCAAGACAAACACTGGCAAACCGGGAGGAGTCCATATACGAATAACCGCTC-G			
ISPa11-4	GCCGGATATACGGATGCAGTCGTACACAGGTTTGAATCAAGACAAACACTGGCAAACCGGGAGGAGTCCATATACGAATAACCGCGAAG			
ISPa11-6	GCCGGATATACGGATGCAGTCGTACACAGGTTTGAATCAAGACAAACACTGGCAAACCGGGAGGAGTCCATATACGCATAAACCGCAACG			
Consensus	GCCGGATATACGGATGCAGTCGTACACAGGTTTGAATCAAGACAAACACTGGCAAACCGGGAGGAGTCCATATACGaATAAC...C...g			

REP fragment

450

ISPa11-1 GCGTTATCCGCCTTCC-GCGAGCGGGGTGCGGGTAAACCCGGGAGTCTCAGAAGTCCAGTGCTGCACCCCTGGATGCTGCGGATCGAA
 ISPa11-2 GCGTTATCCGCGCGCTG-CGGCGTCCAGGACCTAGTCAATCCGCGCAGAACCAGGATAGCGTCCGCCACCTGGGTGGCCGCTCGCGCTG
 ISPa11-3 GCGTTATCCGCGCGAAACGCTGCGAGGTGGCGGATAACCGGTAGCGGTTAT--TCGCCCTACACGGGGAGGGAGCAAGCGGTAGGGCG
 ISPa11-5 CCGTTATCCGCGCGTGAAACCCGGCGTAACGGCGCATAGCGCTGCGGCGCTAT--TCGCCCTACCTCGGCAAGCCGTTCGCCCGGAGGCG
 ISPa11-4 CCGTTATCCGCGCGTTGCCTCGGTTCTCTTGGAGCGTGCTCTTCAGCGCTGGCGTTCCACCGCCGGACGGGCGAGCAGAAGGCGCAACG
 ISPa11-6 CCGTTATCCGCGCGGCCAGCCGAGCATCGGCGGATAACGCCCTGGCGTCAT----TCGCCCTACCGACCCGTGTAGAAGGCGGTCGATG
 Consensus g.GTTATCCGCcg.....cc.g.c.....g...a.a.Cc.c...g...ct.....tc.ccct.C.....c..g.....g.cg...g..g

451

540

ISPa11-1 CCCATCCAGGCGCATGCGCTCGGCGAATGCCCTCCGCGCCGCTCTCCCTGGAGAAACGCGCTCCGCGCGAGGCCAGTCGTCCGGTTG
 ISPa11-2 CGGAAATGGCCGACGCCCTCCAGCA--CCAGCCGCTGGTAACGCCCGCTGAAGTAGTGCTCGCGTCCGCGGGAGCCGTCTGGGTGGTG
 ISPa11-3 AATAACGCCCCAGGCGTTATCCGCGCAACGCCTGCCGAGGTGGCG--GATAAACCGCGTAGCGGTTATTGCGCCTACACGGGGAGGGAGC
 ISPa11-5 CTGCCAGCCCTCGACATGTCCCGTAGGGCGAATAACCGTCCGCG--GTTATCCGCCGTG--AAACCCGGCGTAACGGCGGATAGCGC
 ISPa11-4 AGGCCCCAGCGTTTCGCGCATGACCCAGGCCGTGAGCGGGCTG-----GAAGTCCAGCGTGAGCCCGGCAACCCGGCGCAGGTCATCTAC
 ISPa11-6 CCGGCGCCTCGATGGAAGCGCACTCAGGCCGCCAGGCGGCCGCCGCGGATCGCCTCGAGGCGCTTGAGCATGGCCCGCAACAGCACCGC
 Consensus c.g..c....c.....ctcc.c..a.gccgcc.....g..g.c...g....cc...g.g..c.....cg.....c....g....g..c

541

630

ISPa11-1 CAGCCGTACCATCCAGCCCTCGCCGTAGCAAT---CCCGGTTGATCAGCGCCGGGCGCTTGACCACCGCCGGGTTGCTCGCCAGCAGGG
 ISPa11-2 CAGGCATCCGCGCCGCGGTGCAAGCACCAGGGT---CGGCAGCGCCAGCGCGGTGCCGGGAGCAAGCGCTGTTCCGCGCCCCGTAGCG
 ISPa11-3 AAGCGGTAGGGCGAATAACGCCCCAGGCGTATCCGCGGTAGCCTCTGCCGAGCTGGCGGTTATTCGTCTACGCCGGGCTTTCCTCCA
 ISPa11-5 CTGGCGCGCTATTGCGCCTACCGGCAAGCCGTTACGCCCGGCGACGCTGCCCAACCCTCGACATGTCCCGTAGGGCGAA-TAACCGCTC
 ISPa11-4 CAGCCGCGCCATCGCCTGGCCCGGCTCGGCTTT-CAGCAGAGCCGCCGCGGCTGCGCGGTTTCGGCGCTGCCGCGCCAGAGCAGGAGTTCG
 ISPa11-6 GCAGCCGGCGGCCAGGTCGTCCGGGCTGGCGTT-CTCGATCTCGTTGTGGCTGATGCCGTTCTCGCAGGGCACGAAGATCATCCCCGCCG
 Consensus cagccg..c...c.....C.g....g...T..c.cc.....gc.c.Gcc..g..c.....c.....c.....g.....c.ccg

631

654

ISPa11-1 TCCCGGCCAACGGGCTGCGG
 ISPa11-2 CGGCTTCCCCGCGACGAAGCCC
 ISPa11-3 GCGGCTGCTCGCGCAGCAG
 ISPa11-5 GCGGTATCCGCGGTGAAACCCGG
 ISPa11-4 CGCGCTTTCGCGCAGGCGCT
 ISPa11-6 GACCGAGTTCGGCGAGGAAG
 Consensust...cgcg..g.ag.....