Supplementary file 2
Acaryochloris marina MBIC11017 uid58167 TnpPred annotation in genbank format (.gbk)

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LOCUS       NC_009925                  0 bp    DNA     linear   UNK
ACCESSION   unknown
COMMENT     This looks like a good IS fragment prediction
FEATURES             Location/Qualifiers
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                     SLS"
                     /note="IS5_IS1031  e-value= 1.3e-110 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
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                     length is 314aa with 37 gaps, 1 stops, absolute frame=
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                     length is 314aa with 37 gaps, 1 stops, absolute frame=
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                     ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                     /note="IS630  e-value= 1.1e-13 fragment hit coverage=
                     38.83%, between model( 376 aa) positions 188; 333 length
                     is 129aa with 20 gaps, 0 stops, absolute frame= Plus1"
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                     QYKRCSFLIIANYPFSEWDIIFR-DSMMMVVAVDRLVHHALIIEIKAESY"
                     /note="IS21_ORF2   e-value= 4.1e-16 fragment hit coverage=
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                     is 92aa with 2 gaps, 1 stops, absolute frame= Plus1"
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                     TLYYRRqiSSETIQTILQSHAEGSSLRGLSRITGVAFNTCVSVIR"
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                     36.40%, between model( 239 aa) positions 1; 87 length is
                     88aa with 1 gaps, 0 stops, absolute frame= Plus1"
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                     CMDIENRF"
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                     33.77%, between model( 154 aa) positions 1; 52 length is
                     47aa with 5 gaps, 0 stops, absolute frame= Plus1"
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                     CM"
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                     coverage= 30.07%, between model( 153 aa) positions 1; 46
                     length is 41aa with 5 gaps, 0 stops, absolute frame=
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     CDS             689875..690138
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                     /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
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                     88aa with 2 gaps, 0 stops, absolute frame= Plus1"
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                     frame= Plus1"
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                     ARGQPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKT
                     KV-KRKRTtnsehsfprYGNRVLNLSIDHPEQVWVADITYIRLQ--QEFVYLAVVmDV
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                     SLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS407_ORF2    e-value= 6.3e-13 complete sequence
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                     344 length is 349aa with 10 gaps, 4 stops, absolute
                     frame= Plus1"
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                     /evidence=predicted
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                     QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALER----ATPEIHHSDQGVQ
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                     HIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 4.3e-49 complete sequence
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                     frame= Plus1"
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                     QLTLRALNKALERAT-PEIHHSDQGVQYAAA----AYMQLLQQHQVQISMAEVGQAWQ
                     NGYAERLMRTIKEEEVDLSD---YRNFTEAYEHIEQFLEDvYMHKRIHSSLGYLTPCE
                     YEQQWRQQNNHYCMNKEDS"
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                     length is 295aa with 58 gaps, 0 stops, absolute frame=
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                     QYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEH
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                     frame= Plus1"
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                     coverage= 25.29%, between model( 344 aa) positions 60;
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     CDS             850450..851301
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                     FVYLAVVMDVFTRAIRGWH------LSRHIDQQLTLRALNK---ALERATPEIHH-SD
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                     frame= Plus1"
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                     AIRGWHLSRHIDQQLTLRALNKALERAT---PEIHHS-----DQGVQYAAAAYMQLLQ
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                     HKRIHSSLGYLTPCEYEQQWRQQ"
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                     /note="IS3_IS51_ORF1     e-value= 6.3e-51 complete sequence
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                     /note="IS3_IS3_ORF1      e-value= 9.5e-54 complete sequence
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                     frame= Plus1"
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                     LTPCEYEQQWRQQNN"
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                     frame= Plus1"
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                     288 length is 272aa with 19 gaps, 0 stops, absolute
                     frame= Plus1"
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                     -CVNHKRVARLMRQ"
                     /note="IS3_IS2_ORF2      e-value= 9.1e-09 fragment hit
                     coverage= 18.87%, between model( 302 aa) positions 48;
                     104 length is 53aa with 5 gaps, 0 stops, absolute frame=
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                     SSLGYLTPCEYEQQWRQQNNH"
                     /note="IS3_IS51_ORF2     e-value= 1.9e-38 fragment hit
                     coverage= 74.76%, between model( 317 aa) positions 73;
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                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
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                     RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                     ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                     /note="IS630 e-value= 1.1e-13 fragment hit coverage=
                     38.83%, between model( 376 aa) positions 188; 333 length
                     is 129aa with 20 gaps, 0 stops, absolute frame= Plus1"
     CDS             1334545..1335405
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IQVELRGSIHXplNLKMVRHPYDTDLTLDQWELLRPLLPKAK--
                     -----SGGRPRRVNLLAVVNAIFYLLRSGCPWRLIPHDFPAWQTVYTYFRQWEADGTW
                     ERLNRALREKLRIQAGRHRHPSAACVDSQSVKTAGAAQE--KGFDGGKKVKGRKRTIL
                     VDTMGLLIGATVHSARRSDHQ-GMILLGLWFSAFWQSIQLIWTDQTFGGQAFTAWFQK
                     TFGWTMEVVKRPEEQQGFEVLPRRWVVERTFAWFGHYRRLSKDYEYLPTTSEMMLYAA
                     MVNLMLKRLAXIFSNTLLEAV"
                     /note="IS5_IS1031  e-value= 2.7e-109 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 287aa with 10 gaps, 2 stops, absolute frame=
                     Plus1"
     CDS             1334545..1335384
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IQVELRGSIHXPLNLKMVRHPYDTDLTLDQWELLRPLLPKAKSG
                     -------------------------GRPRRVNLLAVVNAIFYLLRSGCPWRL--IPHD
                     FPAWQTVYTYFRQWEADGTWERLNRALREKLRIQAG---RHRHPSAACVDSQSVKTAG
                     A---------------------------------------------------------
                     ----------------------------------------AQEKGFDGGKKVKGRKRT
                     ILVDTMGLLIGA---------------TVHSARRSDHQGMILLGLWFSAFWQSIQLIW
                     TDQTFGGQAFTAWFQKTFGWTMEVVKRPEEQQGFEVLPRRWVVERTFAWFGHYRRLSK
                     DYEYLPTTSEMMLYAAMVNLMLKRLAXIFS"
                     /note="IS5_IS5     e-value= 6.1e-15 complete sequence hit
                     coverage= 100%, between model( 422 aa) positions 1; 422
                     length is 280aa with 142 gaps, 2 stops, absolute frame=
                     Plus1"
     CDS             1334599..1335378
                     /colour="255 0 0"
```

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                /evidence=predicted
                /translation="RHPYDTDLTLDQWELLRPLLPKAK-------SGGRPRRVNLLAV
                VNAIFYLLRSGCPWRLIPHDFPAWQTVYTYFRQWEADGTWERLNRALREKLRIQAGRH
                RHPSAACVDSQSVKTAGAAQE--KGFDGGKKVKGRKRTILVDTMGLLIGATVHSARRS
                DHQ-GMILLGLWFSAFWQSIQLIWTDQTFGGQAFTAWFQKTFGWTMEVVKRPEEQQGF
                EVLPRRWVVERTFAWFGHYRRLSKDYEYLPTTSEMMLYAAMVNLMLKRLAXI"
                /note="IS5_IS1031  e-value= 3.5e-110 fragment hit
                coverage= 91.53%, between model( 295 aa) positions 17;
                286 length is 260aa with 10 gaps, 1 stops, absolute
                frame= Plus1"
CDS             1334629..1334862
                /colour="255 0 0"
                /evidence=predicted
                /translation="DQWELLRPLLP--KAKSGGRPRRVNLLAVVNAIFYLLRSGCPWR
                LIPHDFPAWQTVYTYFRQWEADGTWERLNRALREKL"
                /note="IS5_IS427   e-value= 7.9e-16 fragment hit coverage=
                27.03%, between model( 296 aa) positions 129; 208 length
                is 78aa with 2 gaps, 0 stops, absolute frame= Plus1"
CDS             1334704..1334931
                /colour="255 0 0"
                /evidence=predicted
                /translation="AVVNAIFYLLRSGCPWRL--IPHDFPAWQTVYTYFRQWEADGTW
                ERLNRALREKLRIQAG---RHRHPSAACVDSQSVKTA"
                /note="IS5_IS5     e-value= 7.9e-09 fragment hit coverage=
                19.19%, between model( 422 aa) positions 79; 159 length
                is 76aa with 5 gaps, 0 stops, absolute frame= Plus1"
CDS             1334932..1335384
                /colour="255 0 0"
                /evidence=predicted
                /translation="GAAQEKGFDGGKKVKGRKRTILVDTMGLLIGA------------
                ---TVHSARRSDHQGMILLGLWFSAFWQSIQLIWTDQTFGGQAFTAWFQKTFGWTMEV
                VKRPEEQQGFEVLPRRWVVERTFAWFGHYRRLSKDYEYLPTTSEMMLYAAMVNLMLKR
                LAXIFS"
                /note="IS5_IS5     e-value= 1.2e-15 fragment hit coverage=
                39.34%, between model( 422 aa) positions 257; 422 length
                is 151aa with 15 gaps, 1 stops, absolute frame= Plus1"
CDS             1474789..1475553
                /colour="255 0 0"
                /evidence=predicted
                /translation="-----TGVYKQTFkrMLHAWHTHHLGRSN--AGRPPKLCRPDQL
                LVALQYWREYRTYFHIAGDWEVSESTVCRIVHQVETALMNSGLFRLPGQKSLLQGFER
                PDVVVMDVTETPIERPQKRQKAYYSGKKRDIPSNARLSLTAT--LXRLSV--------
                XALAQAVGMIFrssrfqvSISIQIPRVCKIADIKGLQPT--TPTAM----FLSRSHNT
                VNXLPCSESITVlxvknEWAlntlNRSLKIFRILSERYRNRRRRYTLRCNLIAALYNH
                EL"
                /note="IS5_ISL2    e-value= 2.2e-49 complete sequence hit
                coverage= 100%, between model( 260 aa) positions 1; 260
                length is 255aa with 23 gaps, 3 stops, absolute frame=
                Plus1"
CDS             1474852..1475160
                /colour="255 0 0"
                /evidence=predicted
                /translation="RSNAGRPPKLCRPDQLLVALQYWREYRTYFHIAGDWEVSESTVC
                RIVHQVETALMNSGLFRLPGQKSLLQGFERPDVVVMDVTETPIERPQKRQKAYYSGKK
                R"
                /note="IS5_ISL2    e-value= 1.5e-44 fragment hit coverage=
                39.62%, between model( 260 aa) positions 27; 129 length
                is 103aa with 0 gaps, 0 stops, absolute frame= Plus1"
CDS             1475446..1475553
                /colour="255 0 0"
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                     /evidence=predicted
                     /translation="NRSLKIFRILSERYRNRRRRYTLRCNLIAALYNHEL"
                     /note="IS5_ISL2    e-value= 1.1e-16 fragment hit coverage=
                     13.85%, between model( 260 aa) positions 225; 260 length
                     is 36aa with 0 gaps, 0 stops, absolute frame= Plus1"
     CDS             1499707..1499970
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                     DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVR"
                     /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
                     36.40%, between model( 239 aa) positions 1; 87 length is
                     88aa with 2 gaps, 0 stops, absolute frame= Plus1"
     CDS             1585042..1585257
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="REIHEAIGVSIRTIERVRMRFVEEG---LEAAINQRsGAGRKRK
                     IQGEQEAHLIALRCSEPPVG----HARWTLRLLAD"
                     /note="IS630 e-value= 9.9e-08 fragment hit coverage=
                     20.74%, between model( 376 aa) positions 44; 121 length
                     is 72aa with 7 gaps, 0 stops, absolute frame= Plus1"
     CDS             1602370..1602585
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="REIHEAIGVSIRTIERVRMRFVEEG---LEAAINQRsGAGRKRK
                     IQGEQEAHLIALRCSEPPVG----HARWTLRLLAD"
                     /note="IS630 e-value= 9.9e-08 fragment hit coverage=
                     20.74%, between model( 376 aa) positions 44; 121 length
                     is 72aa with 7 gaps, 0 stops, absolute frame= Plus1"
     CDS             2373475..2374293
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-IEYPQFLQLLEQAELKHNERKaeiexhksRVNAK-GGGRKPLL
                     SVAEEVCLCLFYLRHYPTFEVLGLQFGVSKSEANDTVHYWLSMLRVLL-----PASLL
                     EQVDSNPsdyAIVqewltqfqlIVDTFEQARERPIdnDEQRSYFSGKKQQHTFKSQIV
                     TLPGGKDIVDAIAGkKGPTSDISVFREHQSQFAPGQGFDGDKAYVGAQNVQ----TPH
                     KKPRGKELTPKQKAQNKKfSSTRRIFVEHTIRLVRIFRVAQERFRLRHDTYEQVILTV
                     CGLVRLRL"
                     /note="IS5_ISL2    e-value= 1.6e-11 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 273aa with 11 gaps, 0 stops, absolute frame=
                     Plus1"
     CDS             2373877..2374236
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QRSYFSGKKQQHTFKSQIVTLPGGKDIVDAIAGkKGPTSDISVF
                     REHQSQFAPGQGFDGDKAYVGAQNVQ----TPHKKPRGKELTPKQKAQNKKfSSTRRI
                     FVEHTIRLVRIFRVAQERFRLR"
                     /note="IS5_ISL2    e-value= 8.7e-11 fragment hit coverage=
                     46.92%, between model( 260 aa) positions 120; 241 length
                     is 120aa with 4 gaps, 0 stops, absolute frame= Plus1"
     CDS             2559835..2560116
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SMECPYCQSEK-ILKRGFDSlqdgTLVQRYQCKDCNRRFN-ERT
                     GTPMARLRtasSVVSYAIKARTEGMGVRSAGRTFGKSHTTIMRWEKRLADQA"
                     /note="IS1_ORF1    e-value= 3.2e-11 fragment hit coverage=
                     37.24%, between model( 239 aa) positions 5; 93 length is
                     94aa with 2 gaps, 0 stops, absolute frame= Plus1"
     CDS             2630473..2630631
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                /colour="255 0 0"
                /evidence=predicted
                /translation="HHPHPRVQRRMEVLYLKSQGLPHAQICQLCQISRPTLAKTLRLY
                QQGGIEGLK"
                /note="IS481 e-value= 1.1e-08 fragment hit coverage=
                15.10%, between model( 351 aa) positions 1; 53 length is
                53aa with 0 gaps, 0 stops, absolute frame= Plus1"
CDS             2982304..2983041
                /colour="255 0 0"
                /evidence=predicted
                /translation="-----TGVYKQTF-KRMLHAWHTYHlSHSNAERPPKLCRPDQLL
                VALQYWREYRTYFHIAGDWDVSESTVCRIVQQVESALMNSGLFRLPGKKHLIQGFERP
                DVVVMDVTETPIERPQKGQKAYYSGKKRDIPSNARLSLTVALXRLSALT---------
                -LAKVVGMIFrssrfqvSTSIQIprVCKIADiKGLQPI-----TPIAM----FLSRSH
                NTVNXLPSSESTTVLXVRNEWALNTLIAAXRFSEFCRSAIVIVVVATRCGVTX"
                /note="IS5_ISL2    e-value= 2.8e-20 complete sequence hit
                coverage= 100%, between model( 260 aa) positions 1; 260
                length is 246aa with 25 gaps, 5 stops, absolute frame=
                Plus1"
CDS             2982364..2982675
                /colour="255 0 0"
                /evidence=predicted
                /translation="SHSNAERPPKLCRPDQLLVALQYWREYRTYFHIAGDWDVSESTV
                CRIVQQVESALMNSGLFRLPGKKHLIQGFERPDVVVMDVTETPIERPQKGQKAYYSGK
                KR"
                /note="IS5_ISL2    e-value= 1.3e-41 fragment hit coverage=
                40%, between model( 260 aa) positions 26; 129 length is
                104aa with 0 gaps, 0 stops, absolute frame= Plus1"
CDS             3974686..3975072
                /colour="255 0 0"
                /evidence=predicted
                /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                /note="IS630 e-value= 1.1e-13 fragment hit coverage=
                38.83%, between model( 376 aa) positions 188; 333 length
                is 129aa with 20 gaps, 0 stops, absolute frame= Plus1"
CDS             3975325..3976020
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                51.23%, between model( 486 aa) positions 1; 249 length is
                232aa with 27 gaps, 0 stops, absolute frame= Plus1"
CDS             3975325..3976452
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
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                /note="IS4   e-value= 9.9e-07 complete sequence hit
                coverage= 100%, between model( 486 aa) positions 1; 486
                length is 376aa with 117 gaps, 0 stops, absolute frame=
                Plus1"
CDS             4217206..4217592
                /colour="255 0 0"
                /evidence=predicted
                /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                /note="IS630  e-value= 1.1e-13 fragment hit coverage=
                38.83%, between model( 376 aa) positions 188; 333 length
                is 129aa with 20 gaps, 0 stops, absolute frame= Plus1"
CDS             4225801..4226796
                /colour="255 0 0"
                /evidence=predicted
                /translation="CIAVAILRRTXTREVFHSFCSVMPKIYSYdlRCKVIDAIeLDGM
                RPSEASELFHIRRNTINQWQHLKAETG-----DLHPKP-VHCPDHSHKIK--------
                DWDKFRAFAYKHRHKTQAQMAQLWDGE----ISERTISRALQNIGFT-RKKTYGYR--
                ERD--EHKR----AAFIKRLSTVDP-DDIVYADESGMDHRDEYDY-AYGPKGE-----
                ------RVYA-LKSG-TRKGRVNMIAALRAKQL--MAPFTIEGACNRTVFEvwlERCL
                IPMLKPGQKLVI--DNATFHKAGRIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWI
                K--SRIRHQLDHFGSLREAMEHVLHLTSXIEWRLLXNKLCNNLKRIIL"
                /note="IS630  e-value= 1.2e-10 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 332aa with 50 gaps, 3 stops, absolute frame=
                Plus1"
CDS             4226083..4226673
                /colour="255 0 0"
                /evidence=predicted
                /translation="AFAYKHRHKTQAQMAQLWDGEISERTISRALQNIGFT-RKKTYG
                YR--ERD--EHKR----AAFIKRLSTVDP-DDIVYADESGMDHRDEYDY-AYGPKGE-
                ----------RVYA-LKSG-TRKGRVNMIAALRAKQL--MAPFTIEGACNRTVFEvwl
                ERCLIPMLKPGQKLVI--DNATFHKAGRIQELVEKAG--CEVWYLPPYSPDLNKIERS
                WSWIKSRIR"
                /note="IS630  e-value= 1.2e-14 fragment hit coverage=
                59.57%, between model( 376 aa) positions 110; 333 length
                is 197aa with 30 gaps, 0 stops, absolute frame= Plus1"
CDS             4227730..4228050
                /colour="255 0 0"
                /evidence=predicted
                /translation="FPDAQQVHVVLDNLNTHtpaalyKTFKPDEALRILS-RIQFHYT
                PKHGSWLNMVEFEFSALSRQCLNRRIP-DIEKLRHEVTAWEQRRNWDKAMVNWLFTVD
                DARTKLS"
                /note="IS630  e-value= 3.3e-07 fragment hit coverage=
                27.39%, between model( 376 aa) positions 274; 376 length
                is 107aa with 2 gaps, 0 stops, absolute frame= Plus1"
CDS             5176546..5176935
                /colour="255 0 0"
                /evidence=predicted
                /translation="FFMDESGFSLVPCIPY-GWQPIG-------------TYL-EIPT
                RSSKRLNVLGFLSRRQGL--HAYTSEQTITSEVVShCIDTFFADV--ELPTVIVVDQA
                PIHTSQsiyEMKAEWAERG--ITLFELPSYSPHLNLIERLWQFMKYQWI"
                /note="IS630  e-value= 6.5e-11 fragment hit coverage=
                39.10%, between model( 376 aa) positions 187; 333 length
                is 130aa with 21 gaps, 0 stops, absolute frame= Plus1"
CDS             5240533..5240919
                /colour="255 0 0"
                /evidence=predicted
                /translation="YADESGMEHRDEYDY-AYGPKGE-----------RAYA-LKSG-
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                RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFEIWLercLIPMLKPGQKLVI--DN
                ATFHKGGQIQELVEAAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                /note="IS630 e-value= 4e-14 fragment hit coverage=
                38.83%, between model( 376 aa) positions 188; 333 length
                is 129aa with 20 gaps, 0 stops, absolute frame= Plus1"
CDS             5297623..5297775
                /colour="255 0 0"
                /evidence=predicted
                /translation="QLCLILDNNPTHKG-KMRSQLAIHLEqmgltqsiQVEFLYLPSY
                SPKLNLVE"
                /note="IS630 e-value= 4.3e-06 fragment hit coverage=
                11.70%, between model( 376 aa) positions 279; 322 length
                is 51aa with 1 gaps, 0 stops, absolute frame= Plus1"
CDS             5359111..5359329
                /colour="255 0 0"
                /evidence=predicted
                /translation="RIRFVYIPKHTSWLNQIECWFSILVRRLIRRGNFTSKDDLQQRI
                LEFIEYFNHtMAKPFQWQFKGFQPRLXLM"
                /note="IS630 e-value= 4e-10 fragment hit coverage=
                19.15%, between model( 376 aa) positions 305; 376 length
                is 73aa with 0 gaps, 1 stops, absolute frame= Plus1"
CDS             5359159..5359269
                /colour="255 0 0"
                /evidence=predicted
                /translation="IECWFSILVRRLIR--RGNFTSKDDLQQRILEFIEYFNH"
                /note="IS3_IS150_ORF2   e-value= 2e-08 fragment hit
                coverage= 10.03%, between model( 389 aa) positions 329;
                367 length is 37aa with 2 gaps, 0 stops, absolute frame=
                Plus1"
CDS             5666503..5666847
                /colour="255 0 0"
                /evidence=predicted
                /translation="CGNANIMXYLY--------------RNIEKGEYMVELGgfrRYF
                YELARHKESVIEEGHLMPDHVHKLLSIPPKYSVSNVVGYVKGKVPFISPESXA-----
                --------------IVGMRQAI------SFGLEDILC-QQSAKMRKXSVDISG"
                /note="IS605 e-value= 9.1e-06 complete sequence hit
                coverage= 100%, between model( 152 aa) positions 1; 152
                length is 115aa with 40 gaps, 3 stops, absolute frame=
                Plus1"
CDS             5666590..5666721
                /colour="255 0 0"
                /evidence=predicted
                /translation="FYELARHKESVIEEGHLMPDHVHKLLSIPPKYSVSNVVGYVKGK
                "
                /note="IS200 e-value= 1.3e-14 fragment hit coverage=
                28.57%, between model( 154 aa) positions 41; 84 length is
                44aa with 0 gaps, 0 stops, absolute frame= Plus1"
CDS             5666590..5666721
                /colour="255 0 0"
                /evidence=predicted
                /translation="FYELARHKESVIEEGHLMPDHVHKLLSIPPKYSVSNVVGYVKGK
                "
                /note="IS200_IS605 e-value= 1.4e-14 fragment hit
                coverage= 28.76%, between model( 153 aa) positions 41; 84
                length is 44aa with 0 gaps, 0 stops, absolute frame=
                Plus1"
CDS             5666629..5666721
                /colour="255 0 0"
                /evidence=predicted
                /translation="EGHLMPDHVHKLLSIPPKYSVSNVVGYVKGK"
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                     /note="IS605  e-value= 2.2e-10 fragment hit coverage=
                     20.39%, between model( 152 aa) positions 54; 84 length is
                     31aa with 0 gaps, 0 stops, absolute frame= Plus1"
     CDS             5747743..5747880
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                     RWHRR"
                     /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Plus1"
     CDS             5903662..5904156
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LEKAGIESKKKTYGYR--ERD--ETQR---QEFIERLKTKHA--
                     HQIVYVDEAGIDNRADYPY-GYGPIG-----------QRFYD-LKSG-KRTERVSFIA
                     ALKEGQL--FSPMTFEGSCNWLLFEAWLQQSLIPQLQPgdIIVI-DNASFHHGLSIEE
                     IVAEAG--CEIWYLPSYSPDLNKIERWWFVLKN"
                     /note="IS630  e-value= 4e-13 fragment hit coverage=
                     50.80%, between model( 376 aa) positions 140; 330 length
                     is 165aa with 28 gaps, 0 stops, absolute frame= Plus1"
     CDS             6055453..6056127
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGRQFL--ST
                     YSKRGYSDWTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQVGVLLPDAYDPDD-
                     -----IP---QVGELDELETFVGKKRNKVWIW-TVVDHFHPG--ILGWVVGDHSAETF
                     RPLWqaIVCWQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLARLHR
                     KTLCYSKSVDMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 5.8e-42 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 225aa with 19 gaps, 1 stops, absolute frame=
                     Plus1"
     CDS             6055453..6056127
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGRQFL--ST
                     YSKRGYSDWTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQVGVLLPDAYDPDD-
                     -----IP---QVGELDELETFVGKKRNKVWIW-TVVDHFHPG--ILGWVVGDHSAETF
                     RPLWqaIVCWQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLARLHR
                     KTLCYSKSVDMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 3.3e-41 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 225aa with 19 gaps, 1 stops, absolute frame=
                     Plus1"
     CDS             6055453..6056133
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGR----QFL
                     STYSKRGysdwTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQV--GVLLPDAYD
                     PDDIPQVGELDELETFVGKKRNKVWIWTVVDHFHPGILGWVVGDHSAETFRPLWQAIV
                     CWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGENTRLRHYLARLHRKTL
                     CYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 3.9e-29 complete sequence hit
                     coverage= 100%, between model( 237 aa) positions 1; 237
                     length is 227aa with 14 gaps, 1 stops, absolute frame=
                     Plus1"
     CDS             6055732..6056133
                     /colour="255 0 0"
                     /evidence=predicted
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                     /translation="DPDDIPQVGELDELETFVGKKRNKVWIWTVVDHFHPGILGWVVG
                     DHSAETFRPLWQAIVCWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGEN
                     TRLRHYLARLHRKTLCYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 8.3e-32 fragment hit coverage=
                     59.07%, between model( 237 aa) positions 98; 237 length
                     is 134aa with 6 gaps, 0 stops, absolute frame= Plus1"
     CDS             6108877..6109140
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                     DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVR"
                     /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
                     36.40%, between model( 239 aa) positions 1; 87 length is
                     88aa with 2 gaps, 0 stops, absolute frame= Plus1"
     CDS             6307891..6308655
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SPYQHLSLYLKKLRLSHMLTHWESIESQA-MQENWSYAEFLLAL
                     CETKAQRREQARLKRALTEARLPNA-KSFTNFDFSHCPQLNPAPLMQLAAdPGWLERA
                     ENCLILGPSGVGKTHLATGVSKKMLEFGKRVKFFAANALVQHLQQAKLQLQLH-PMLK
                     KLDRYDLLVLDDLGYCKKSEAETSVLFELIAHRYERKSLLITANQPFSQWDDIFT-DS
                     MMAVAAIDRLIHHGLIIKIQADSYRRKSATQRTAQTQSPPQ"
                     /note="IS21_ORF2   e-value= 7.2e-80 complete sequence hit
                     coverage= 100%, between model( 258 aa) positions 1; 258
                     length is 255aa with 4 gaps, 0 stops, absolute frame=
                     Plus1"
     CDS             6307891..6308655
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SPYQHLSLYLKKLRLSHMLTHWESIESQA-MQENWSYAEFLLAL
                     CETKAQRREQARLKRALTEARLPNA-KSFTNFDFSHCPQLNPAPLMQLAAdPGWLERA
                     ENCLILGPSGVGKTHLATGVSKKMLEFGKRVKFFAANALVQHLQQAKLQLQLH-PMLK
                     KLDRYDLLVLDDLGYCKKSEAETSVLFELIAHRYERKSLLITANQPFSQWDDIFT-DS
                     MMAVAAIDRLIHHGLIIKIQADSYRRKSATQRTAQTQSPPQ"
                     /note="IS21_ORF2   e-value= 1.9e-80 complete sequence hit
                     coverage= 100%, between model( 258 aa) positions 1; 258
                     length is 255aa with 4 gaps, 0 stops, absolute frame=
                     Plus1"
     CDS             6335869..6336906
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630 e-value= 4.9e-24 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Plus1"
     CDS             6335869..6336906
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
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                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630 e-value= 6.7e-25 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Plus1"
     CDS             6335929..6336087
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                     QQGGIEGLK"
                     /note="IS481 e-value= 3.7e-09 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Plus1"
     CDS             6483169..6483501
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QRVKDRAAMIRLSHQGMYVEKIAALFQCNVRTARQTFHRWQQKG
                     ---LGGLWDAPHPGAQRRWHPED-IEYLETCLRQEERTY-------NSQQLSRKLAKE
                     RNVHLSADRIRQILKKRGXS"
                     /note="IS630 e-value= 6e-07 fragment hit coverage=
                     32.45%, between model( 376 aa) positions 25; 146 length
                     is 111aa with 11 gaps, 1 stops, absolute frame= Plus1"
     CDS             59159..60220
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IVKRXKN------EQCIVSHpYPALXPPQPLAQG---ISSA---
                     --RQXHFXESEQRRQRXSENCSVRASSRPIDAAIRDRKKSLNVLTP--NQKRQMVRQL
                     QQDYSIRQICQVLNYPRSQVYYHARGQP-----DESELKAAIAGVAGAYP-TYGYRRI
                     TAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-RKRTTNSEHSfpRYGNRVLNLS
                     --IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNK
                     ALERAT---PEIHHS-----DQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAER
                     LMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYMHKRIHSSLGYLTPCEYEQQWRQ
                     Q"
                     /note="IS3_IS150_ORF2    e-value= 1.7e-22 complete sequence
                     hit coverage= 100%, between model( 389 aa) positions 1;
                     389 length is 354aa with 39 gaps, 5 stops, absolute
                     frame= Plus2"
     CDS             59198..60244
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HPYPALXPPQ--PLAQGI--SSARQXHFXESEQRRQRXSENCSV
                     RASSRPIDAAiRDRKKslnVLTPNQKRQMVRQLQQDY--SIRQICQVLNYPRSQVYYH
                     ARGQPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKT
                     KV-KRKRTtnsehsfprYGNRVLNLSIDHPEQVWVADITYIRLQ--QEFVYLAVVmDV
                     FTRAIRGWHLSRHIDQQLTLRALNKALE-RATPEIHHSDQGVQYAAAAYMQLLQQHQV
                     QISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDvYMHKRIHS
                     SLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS407_ORF2    e-value= 6.3e-13 complete sequence
                     hit coverage= 100%, between model( 344 aa) positions 1;
                     344 length is 349aa with 10 gaps, 4 stops, absolute
                     frame= Plus2"
     CDS             59333..60217
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PIDAAIRDRKKSLnVLTPNQKRQMVRQLQQDYSIRQICQVLNYP
                     RSQVYYHARGQPDESELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMR
                     QIGIMAKTKVK----RKRTTNSEHSF-PRYGNRvlNLSIDHPEQVWVADITYIRL--Q
                     QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALER----ATPEIHHSDQGVQ
                     YAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFT--EAYE
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                     HIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 4.3e-49 complete sequence
                     hit coverage= 100%, between model( 306 aa) positions 1;
                     306 length is 295aa with 14 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59369..60253
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LNVLTPNQKRQMVRQLQQD-YSIRQICQVLNYPRSQVVYYHARGQ
                     PD--------------------ESELKAAIAGVAGAYPTYGYRRITAQLQRQGYC---
                     VNHKRVARLMRQIGIMAKTKVKRKR-TTNSEHSFPRYGnRVLNLSIDHPEQVWVADIT
                     YI-------------RLQQ--------EFVYLAVVMDVFTRAIRGWHLSRH----IDQ
                     QLTLRALNKALERAT-PEIHHSDQGVQYAAA----AYMQLLQQHQVQISMAEVGQAWQ
                     NGYAERLMRTIKEEEVDLSD---YRNFTEAYEHIEQFLEDvYMHKRIHSSLGYLTPCE
                     YEQQWRQQNNHYCMNKEDS"
                     /note="IS481 e-value= 2.9e-08 complete sequence hit
                     coverage= 100%, between model( 351 aa) positions 1; 351
                     length is 295aa with 58 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             59369..60253
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LNVLTPNQK-RQMVRQLQqdYSIRQICQVLNYP---RSQVVYYHA
                     RgQPDESELKA--AIAGV-------AGA---YPTYGYRRITAQLQRQGYCVNHKRVAR
                     LMRQIGIMAKTKVKRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEF
                     VYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALERATPE--------IHHSDQGV
                     QYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEH
                     IEQFLEDV--YMHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNKEDS"
                     /note="IS3_IS51_ORF2     e-value= 1.6e-26 complete sequence
                     hit coverage= 100%, between model( 317 aa) positions 1;
                     317 length is 295aa with 27 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59375..59629
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VLTPNQKRQMVRQLQQDY--SIRQICQVLNYPRSQVVYYHARGQP
                     DESELKAAIAGVAGAYPTYGYRRITAQLQRQGYCVNHKRVARL"
                     /note="IS3_IS407_ORF2    e-value= 1.2e-17 fragment hit
                     coverage= 25.29%, between model( 344 aa) positions 60;
                     146 length is 85aa with 2 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             59378..60229
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LTPNQKRQMVRQL-QQDYSIRQICQVLNYPRSQVVYYHARG----
                     -------QPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGY-----CVNHKRVARLM
                     RQIGIM--AKTKVKRK-RttnsehsfpRYGNRVLnlsIDHPEQVWVAD-ITYIRLQQE
                     FVYLAVVMDVFTRAIRGWH------LSRHIDQQLTLRALNK---ALERATPEIHH-SD
                     QGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEA
                     YEHIEQFLEDvYMHKRIHSSLGYLTPCEYEQQWRQQNNH"
                     /note="IS3_IS2_ORF2      e-value= 2.2e-08 complete sequence
                     hit coverage= 100%, between model( 302 aa) positions 1;
                     302 length is 284aa with 31 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59393..60220
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KRQMVRQLQQDYSIRQICQVLNYPRSQVVYYHARGQP-----DES
                     ELKAAIAGVAGAYP-TYGYRRITAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-
                     RKRTTNSEHSfpRYGNRVLNLS--IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTR
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                     AIRGWHLSRHIDQQLTLRALNKALERAT---PEIHHS-----DQGVQYAAAAYMQLLQ
                     QHQVQISMAEVGQAWQNGYAERLMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYM
                     HKRIHSSLGYLTPCEYEQQWRQQ"
                     /note="IS3_IS150_ORF2    e-value= 2.2e-47 fragment hit
                     coverage= 76.09%, between model( 389 aa) positions 94;
                     389 length is 276aa with 23 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59396..60244
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RQMVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                     QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                     KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                     IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                     HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                     MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 8.1e-53 complete sequence
                     hit coverage= 100%, between model( 307 aa) positions 1;
                     307 length is 283aa with 25 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59396..60244
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RQMVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                     QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                     KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                     IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                     HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                     MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 6.3e-51 complete sequence
                     hit coverage= 100%, between model( 307 aa) positions 1;
                     307 length is 283aa with 25 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59399..60214
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QMVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                     ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                     VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 9.5e-54 complete sequence
                     hit coverage= 100%, between model( 286 aa) positions 1;
                     286 length is 272aa with 15 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59399..60214
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QMVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                     ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                     VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 2.5e-54 complete sequence
                     hit coverage= 100%, between model( 286 aa) positions 1;
                     286 length is 272aa with 15 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             59402..60217
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                /colour="255 0 0"
                /evidence=predicted
                /translation="MVRQLQQDYSIRQICQVLNYPRSQVYYHARGQPDESELKAAIAG
                V-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVK----RKRTTNSE
                HSF-PRYGNRvlNLSIDHPEQVWVADITYIRL--QQEFVYLAVVMDVFTRAIRGWHLS
                RHIDQQLTLRALNKALER----ATPEIHHSDQGVQYAAAAYMQLLQQHQVQISMAEVG
                QAWQNGYAERLMRTIKEEEVDLSDYRNFT--EAYEHIEQFLEDVYMHKRIHSSLGYLT
                PCEYEQQWRQ"
                /note="IS3_IS150_ORF1    e-value= 6.3e-50 fragment hit
                coverage= 92.81%, between model( 306 aa) positions 23;
                306 length is 272aa with 14 gaps, 0 stops, absolute
                frame= Plus2"
CDS             59411..60226
                /colour="255 0 0"
                /evidence=predicted
                /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                LTPCEYEQQWRQQNN"
                /note="IS3_IS3_ORF2      e-value= 1.2e-64 complete sequence
                hit coverage= 100%, between model( 288 aa) positions 1;
                288 length is 272aa with 19 gaps, 0 stops, absolute
                frame= Plus2"
CDS             59411..60226
                /colour="255 0 0"
                /evidence=predicted
                /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                LTPCEYEQQWRQQNN"
                /note="IS3_IS3_ORF2      e-value= 3.3e-65 complete sequence
                hit coverage= 100%, between model( 288 aa) positions 1;
                288 length is 272aa with 19 gaps, 0 stops, absolute
                frame= Plus2"
CDS             59480..59638
                /colour="255 0 0"
                /evidence=predicted
                /translation="YHARgQPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGY----
                -CVNHKRVARLMRQ"
                /note="IS3_IS2_ORF2      e-value= 9.1e-09 fragment hit
                coverage= 18.87%, between model( 302 aa) positions 48;
                104 length is 53aa with 5 gaps, 0 stops, absolute frame=
                Plus2"
CDS             59546..60229
                /colour="255 0 0"
                /evidence=predicted
                /translation="YPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                TTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                HLSRHIDQQLTLRALNKALERATPE--------IHHSDQGVQYAAAAYMQLLQQHQVQ
                ISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEHIEQFLEDV--YMHKRIH
                SSLGYLTPCEYEQQWRQQNNH"
                /note="IS3_IS51_ORF2     e-value= 1.9e-38 fragment hit
                coverage= 74.76%, between model( 317 aa) positions 73;
                309 length is 228aa with 11 gaps, 0 stops, absolute
                frame= Plus2"
CDS             86624..87475
```

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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                     ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVH
                     INEHLRMQERVSEDRHPSPSAAICDAQSVKVGNPRCH-SIGFDGGKMVKGRKRHVLVD
                     TLGLVLMVMVTAANISDQR-GAKILFWKARRQGaslSRLVRIWADAGYQGQALMKWVM
                     DRFQYVLEVVKRSDNLAGFQVVSKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALAYV
                     AMIRLMVRRLAQEHXNFSNSLS"
                     /note="IS5_IS1031  e-value= 1.9e-108 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 284aa with 14 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             86666..87475
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                     IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRMQERVSEDRHPSP
                     SAAICDAQSVKVGNPRCH-SIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
                     -GAKILFWKARRQGaslSRLVRIWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGF
                     QVVSKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALAYVAMIRLMVRRLAQEHXNFSN
                     SLS"
                     /note="IS5_IS1031  e-value= 1.3e-110 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             86675..86914
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRM"
                     /note="IS5_IS427   e-value= 3.3e-18 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             104411..105622
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
                     A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVTNSVMEEVKDWRSRP
                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 1.4e-166 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             104411..105622
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
                     A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVTNSVMEEVKDWRSRP
                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 3.7e-167 complete sequence hit
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                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             159026..160063
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630 e-value= 6.7e-25 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             159026..160063
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630 e-value= 4.9e-24 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             159086..159244
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                     QQGGIEGLK"
                     /note="IS481 e-value= 3.7e-09 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Plus2"
     CDS             249134..249991
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="CRISDRNLRAM-----STAYDSDLTAEQWELLEPLIPAAK----
                     ---PGGRPRTTDMLSVVNAIFYLVVTGCQWRQLPHDFHCWSTVYSYFRKWRDDGTWRQ
                     INEHLRMQVRVSEDRHPSPSAAICDAQSVKVGNPRCQ-SIGFDGGKLIKGRKRHVLVD
                     TLGLILMVVVTAANISDQR-GAKILFWKARRQGAslgRLVRIWADAGYQGEALMQWVM
                     DRFRYILEVIKRSDNLAGFKVVPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                     AMIRLMVRRLAQEyxTFQTASKMW"
                     /note="IS5_IS1031  e-value= 6.8e-110 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 286aa with 14 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             249164..249424
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MSTAYDSDLTAEQWELLEPLIPAAKP-GGRPRT-TDMLSVVNAI
                     FYLVVTGCQWRQLPHDFHCWSTVYSYFRKWRDDGTWRQINEHLRM"
                     /note="IS5_IS427   e-value= 1e-22 fragment hit coverage=
                     30.07%, between model( 296 aa) positions 118; 206 length
                     is 87aa with 2 gaps, 0 stops, absolute frame= Plus2"
```

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     CDS             249176..249991
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTAEQWELLEPLIPAAK-------PGGRPRTTDMLSVVNA
                     IFYLVVTGCQWRQLPHDFHCWSTVYSYFRKWRDDGTWRQINEHLRMQVRVSEDRHPSP
                     SAAICDAQSVKVGNPRCQ-SIGFDGGKLIKGRKRHVLVDTLGLILMVVVTAANISDQR
                     -GAKILFWKARRQGAslgRLVRIWADAGYQGEALMQWVMDRFRYILEVIKRSDNLAGF
                     KVVPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEyxTFQT
                     ASKMW"
                     /note="IS5_IS1031  e-value= 1.4e-111 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 272aa with 9 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             440219..441070
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                     ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQ
                     INEHLRMQVRVSEDRHPSPSAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVD
                     TLGLVLMVMVTAANISDQR-GAKILFWKARRQGaslSRLVRIWADAGYQGQALMKWVM
                     DRSQYVLEVIKRSDNLAGFQVVSKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                     AMIRLMVRRLAQEHXNFSNSLS"
                     /note="IS5_IS1031  e-value= 2.3e-109 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 284aa with 14 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             440261..441070
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                     IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSEDRHPSP
                     SAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
                     -GAKILFWKARRQGaslSRLVRIWADAGYQGQALMKWVMDRSQYVLEVIKRSDNLAGF
                     QVVSKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHXNFSN
                     SLS"
                     /note="IS5_IS1031  e-value= 1.5e-111 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             440270..440509
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRM"
                     /note="IS5_IS427   e-value= 2e-19 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             720377..721051
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGRQFL--ST
                     YSKRGYSDWTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQVGVLLPDAYDPDD-
                     -----IP---QVGELDELETFVGKKRNKVWIW-TVVDHFHPG--ILGWVVGNHSAETF
                     RPLWqaIVCWQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLARLHR
                     KTLCYSKSVDMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 4e-41 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 225aa with 19 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             720377..721051
```

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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGRQFL--ST
                     YSKRGYSDWTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQVGVLLPDAYDPDD-
                     -----IP---QVGELDELETFVGKKRNKVWIW-TVVDHFHPG--ILGWVVGNHSAETF
                     RPLWqaIVCWQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLARLHR
                     KTLCYSKSVDMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 2.4e-40 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 225aa with 19 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             720377..721057
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGR----QFL
                     STYSKRGysdwTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQV--GVLLPDAYD
                     PDDIPQVGELDELETFVGKKRNKVWIWTVVDHFHPGILGWVVGNHSAETFRPLWQAIV
                     CWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGENTRLRHYLARLHRKTL
                     CYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 1.5e-28 complete sequence hit
                     coverage= 100%, between model( 237 aa) positions 1; 237
                     length is 227aa with 14 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             720656..721057
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DPDDIPQVGELDELETFVGKKRNKVWIWTVVDHFHPGILGWVVG
                     NHSAETFRPLWQAIVCWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGEN
                     TRLRHYLARLHRKTLCYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 3e-31 fragment hit coverage=
                     59.07%, between model( 237 aa) positions 98; 237 length
                     is 134aa with 6 gaps, 0 stops, absolute frame= Plus2"
     CDS             748838..749635
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IRVSCVVAQGDGSTALQAIHQAFGLEGxlfGCKLHPPLYCKKEN
                     DLVIKRGHSRICIWIXVRTAVVVLT-QKQWXTHSDYTLSAVTSKRLFEK-------XV
                     KLSRYXsVNTQTLDRTXRAMPTAYDSDLTTLQWELLEPLIPAAKP-GGRPRT-TDMLS
                     VLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSE--
                     ---------------------------DRHPSPSAAICDAQSVkvgnpRCHLIGFDGG
                     KMVKGRKRHVLVDTLGLVLMVMVTAANIS"
                     /note="IS5_IS427   e-value= 2.8e-07 complete sequence hit
                     coverage= 100%, between model( 296 aa) positions 1; 296
                     length is 266aa with 39 gaps, 5 stops, absolute frame=
                     Plus2"
     CDS             749108..749977
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="EKXVKLSRYXSVNTQTLDRTXramptaYDSDLTTLQWELLEPLI
                     PAAKPG-----GRPRTTDML--------------------SVLNAIFYLVVTGCQWRQ
                     --LPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSED---RHPSPSAAICDAQ
                     SVK------------------------------VGNpRcHLIGFD--------GGKM-
                     --------------------------------------------VKGRKRHVLVD-TL
                     GLVLMVMVTAANISDQRGAK----------------------ILFWKAQRQGASLSRL
                     VR----IWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWL
                     LWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHX"
                     /note="IS5_IS5     e-value= 1.8e-09 complete sequence hit
                     coverage= 100%, between model( 422 aa) positions 1; 422
                     length is 290aa with 140 gaps, 4 stops, absolute frame=
                     Plus2"
```

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     CDS             749147..749998
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                     ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQ
                     INEHLRMQVRVSEDRHPSPSAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVD
                     TLGLVLMVMVTAANISDQR-GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVM
                     DRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                     AMIRLMVRRLAQEHXNFSNSLX"
                     /note="IS5_IS1031  e-value= 1.8e-111 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 284aa with 14 gaps, 3 stops, absolute frame=
                     Plus2"
     CDS             749189..749998
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                     IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSEDRHPSP
                     SAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
                     -GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGF
                     QVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHXNFSN
                     SLX"
                     /note="IS5_IS1031  e-value= 1.2e-113 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             749198..749437
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRM"
                     /note="IS5_IS427   e-value= 2e-19 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             791804..792046
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Plus2"
     CDS             940328..941023
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Plus2"
     CDS             940328..941455
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
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                AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                /note="IS4   e-value= 9.9e-07 complete sequence hit
                coverage= 100%, between model( 486 aa) positions 1; 486
                length is 376aa with 117 gaps, 0 stops, absolute frame=
                Plus2"
CDS             942041..942427
                /colour="255 0 0"
                /evidence=predicted
                /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                /note="IS630 e-value= 1.1e-13 fragment hit coverage=
                38.83%, between model( 376 aa) positions 188; 333 length
                is 129aa with 20 gaps, 0 stops, absolute frame= Plus2"
CDS             1009808..1010014
                /colour="255 0 0"
                /evidence=predicted
                /translation="IKANILKGQLIQADETPIKMVK---RE--TGYVWVFTTTD----
                ---------AVLYFFKSTRKAFFLKELLKDFTGVLISDFYAGY"
                /note="IS66_ORF2   e-value= 1e-08 fragment hit coverage=
                16.26%, between model( 535 aa) positions 243; 329 length
                is 69aa with 18 gaps, 0 stops, absolute frame= Plus2"
CDS             1009844..1010014
                /colour="255 0 0"
                /evidence=predicted
                /translation="ADETPIKMV-----KRETGYVWVFTTTD---------AVLYFFK
                STRKAFFLKELLKDFTGVLISDFYAGY"
                /note="IS66_ORF3   e-value= 3.6e-07 fragment hit coverage=
                12.72%, between model( 558 aa) positions 287; 357 length
                is 57aa with 14 gaps, 0 stops, absolute frame= Plus2"
CDS             1313054..1314091
                /colour="255 0 0"
                /evidence=predicted
                /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
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                -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                /note="IS630 e-value= 6.7e-25 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Plus2"
CDS             1313054..1314091
                /colour="255 0 0"
                /evidence=predicted
                /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
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                -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                /note="IS630 e-value= 4.9e-24 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
```

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                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Plus2"
CDS             1313114..1313272
                /colour="255 0 0"
                /evidence=predicted
                /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                QQGGIEGLK"
                /note="IS481 e-value= 3.7e-09 fragment hit coverage=
                15.10%, between model( 351 aa) positions 1; 53 length is
                53aa with 0 gaps, 0 stops, absolute frame= Plus2"
CDS             1525481..1525684
                /colour="255 0 0"
                /evidence=predicted
                /translation="QRYQCKDCNRRFN-ERTGTPMARLRtasSVVSYAIKARTEGMGV
                RAAGRTFGKSHTTIMRWEKRLADQA"
                /note="IS1_ORF1    e-value= 2.6e-10 fragment hit coverage=
                27.62%, between model( 239 aa) positions 28; 93 length is
                68aa with 1 gaps, 0 stops, absolute frame= Plus2"
CDS             1529090..1529305
                /colour="255 0 0"
                /evidence=predicted
                /translation="REIHEAIGVSIRTIERVRMRFVEEG---LEAAINQRsGAGRKRK
                IQGEQEAHLIALRCSEPPVG----HARWTLRLLAD"
                /note="IS630 e-value= 9.9e-08 fragment hit coverage=
                20.74%, between model( 376 aa) positions 44; 121 length
                is 72aa with 7 gaps, 0 stops, absolute frame= Plus2"
CDS             1580969..1581355
                /colour="255 0 0"
                /evidence=predicted
                /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFEIWLercLIPMLKPGQKLVI--DN
                ATFHKGGRIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                /note="IS630 e-value= 6.9e-14 fragment hit coverage=
                38.83%, between model( 376 aa) positions 188; 333 length
                is 129aa with 20 gaps, 0 stops, absolute frame= Plus2"
CDS             1587323..1587460
                /colour="255 0 0"
                /evidence=predicted
                /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                RWHRR"
                /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                20.68%, between model( 237 aa) positions 164; 212 length
                is 46aa with 3 gaps, 0 stops, absolute frame= Plus2"
CDS             1631051..1631893
                /colour="255 0 0"
                /evidence=predicted
                /translation="LDRTLRAMPTA--------YDSDLTTLQWELLEPLIPAAK----
                ---PGGRPRTTDMRSVLNAILYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVH
                INEHLRMQERVSEDRHPSPRAAICDAQSVKVGNPRCH-SIGFDGGKQIKGRKRHVLVD
                TLGLVLMVIVTAANISDQR-GAKILFWKARRQGaslSRLVRIWADAGYQGQAFMKWVM
                DRFQYVLEVIKRSDNLAGFQVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                AMIRLMVRRLTEEAXNFSNSLL"
                /note="IS5_IS1031  e-value= 2.8e-110 complete sequence hit
                coverage= 100%, between model( 295 aa) positions 1; 295
                length is 281aa with 17 gaps, 1 stops, absolute frame=
                Plus2"
CDS             1631084..1631893
                /colour="255 0 0"
                /evidence=predicted
                /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMRSVLNA
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                     ILYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRMQERVSEDRHPSP
                     RAAICDAQSVKVGNPRCH-SIGFDGGKQIKGRKRHVLVDTLGLVLMVIVTAANISDQR
                     -GAKILFWKARRQGaslSRLVRIWADAGYQGQAFMKWVMDRFQYVLEVIKRSDNLAGF
                     QVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYYVAMIRLMVRRLTEEAXNFSN
                     SLL"
                     /note="IS5_IS1031  e-value= 1.4e-112 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             1631093..1631332
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMRSVLNAILYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRM"
                     /note="IS5_IS427   e-value= 1.2e-18 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             2086388..2086531
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VIVIDNASFHHGQRIEEIVAEAG--CEIWYLPSYSPDLNKIERW
                     WFVLKN"
                     /note="IS630 e-value= 1.7e-14 fragment hit coverage=
                     13.30%, between model( 376 aa) positions 281; 330 length
                     is 48aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             2216453..2216695
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Plus2"
     CDS             2274167..2274631
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LSIYYPKHASPKLR---TFSA--RLXLLHISnagXRSSIKKSIV
                     ENHLGNYAVtrlTILKGMVSKDHDHTLIEYPPSKSISDIAKRLKGFTSRRLQQEYREL
                     ERRYWDKYLWALGYGAWSTGNISEQMVEEYLEHHRLVSNNDINTFMLEXIKTLVLRRI
                     "
                     /note="IS200 e-value= 1.5e-09 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 155aa with 5 gaps, 3 stops, absolute frame=
                     Plus2"
     CDS             2274167..2274628
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LSIYYPKHASPKLR---TFSARLXLLHISNAGXRSSIKKSIVEn
                     hLGNYAvtRLTILKGMVSKDHDHTLIEYPPSKSISDIAKRLKGFTSRRLQQEYRELER
                     RYWDKYLWALGYGAWSTGNISEQMVEEYLEHHRLVSNNDINTFMLEXIKTLVLRR"
                     /note="IS200_IS605 e-value= 3.6e-09 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 154aa with 3 gaps, 3 stops, absolute frame=
                     Plus2"
     CDS             2274320..2274559
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TILKGMVSKDHDHTLIEYPPSKSISDIAKRLKGFTSRRLQQEYR
                     ELERRYWDKYLWALGYGAWSTGNISEQMVEEYLEHH"
                     /note="IS200 e-value= 3.2e-19 fragment hit coverage=
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                     51.95%, between model( 154 aa) positions 51; 130 length
                     is 80aa with 0 gaps, 0 stops, absolute frame= Plus2"
     CDS             2274320..2274559
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TILKGMVSKDHDHTLIEYPPSKSISDIAKRLKGFTSRRLQQEYR
                     ELERRYWDKYLWALGYGAWSTGNISEQMVEEYLEHH"
                     /note="IS200_IS605 e-value= 7.4e-15 fragment hit
                     coverage= 52.29%, between model( 153 aa) positions 51;
                     130 length is 80aa with 0 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             2409029..2410090
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IVKRXKN------EQCIVSHpYPALXPPQPLAQG---ISSA---
                     --RQXHFXESEQRRQRXSENCSVRASSRPIDAAIRDRKKSLNVLTP--NQKRQMVRQL
                     QQDYSIRQICQVLNYPRSQVYYHARGQP-----DESELKAAIAGVAGAYP-TYGYRRI
                     TAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-RKRTTNSEHSfpRYGNRVLNLS
                     --IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNK
                     ALERAT---PEIHHS-----DQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAER
                     LMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYMHKRIHSSLGYLTPCEYEQQWRQ
                     Q"
                     /note="IS3_IS150_ORF2    e-value= 1.7e-22 complete sequence
                     hit coverage= 100%, between model( 389 aa) positions 1;
                     389 length is 354aa with 39 gaps, 5 stops, absolute
                     frame= Plus2"
     CDS             2409203..2410087
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PIDAAIRDRKKSLnVLTPNQKRQMVRQLQQDYSIRQICQVLNYP
                     RSQVYYHARGQPDESELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMR
                     QIGIMAKTKVK----RKRTTNSEHSF-PRYGNRvlNLSIDHPEQVWVADITYIRL--Q
                     QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALER----ATPEIHHSDQGVQ
                     YAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFT--EAYE
                     HIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 4.3e-49 complete sequence
                     hit coverage= 100%, between model( 306 aa) positions 1;
                     306 length is 295aa with 14 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409239..2410123
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LNVLTPNQK-RQMVRQLQqdYSIRQICQVLNYP---RSQVYYHA
                     RgQPDESELKA--AIAGV-------AGA---YPTYGYRRITAQLQRQGYCVNHKRVAR
                     LMRQIGIMAKTKVKRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEF
                     VYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALERATPE--------IHHSDQGV
                     QYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEH
                     IEQFLEDV--YMHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNKEDS"
                     /note="IS3_IS51_ORF2     e-value= 1.6e-26 complete sequence
                     hit coverage= 100%, between model( 317 aa) positions 1;
                     317 length is 295aa with 27 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409245..2409499
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VLTPNQKRQMVRQLQQDY--SIRQICQVLNYPRSQVYYHARGQP
                     DESELKAAIAGVAGAYPTYGYRRITAQLQRQGYCVNHKRVARL"
                     /note="IS3_IS407_ORF2    e-value= 1.2e-17 fragment hit
                     coverage= 25.29%, between model( 344 aa) positions 60;
                     146 length is 85aa with 2 gaps, 0 stops, absolute frame=
```

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                     Plus2"
     CDS             2409263..2410090
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KRQMVRQLQQDYSIRQICQVLNYPRSQVYYHARGQP-----DES
                     ELKAAIAGVAGAYP-TYGYRRITAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-
                     RKRTTNSEHSfpRYGNRVLNLS--IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTR
                     AIRGWHLSRHIDQQLTLRALNKALERAT---PEIHHS-----DQGVQYAAAAYMQLLQ
                     QHQVQISMAEVGQAWQNGYAERLMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYM
                     HKRIHSSLGYLTPCEYEQQWRQQ"
                     /note="IS3_IS150_ORF2    e-value= 2.2e-47 fragment hit
                     coverage= 76.09%, between model( 389 aa) positions 94;
                     389 length is 276aa with 23 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409266..2410114
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RQMVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                     QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                     KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                     IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                     HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                     MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 8.1e-53 complete sequence
                     hit coverage= 100%, between model( 307 aa) positions 1;
                     307 length is 283aa with 25 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409266..2410114
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RQMVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                     QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                     KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                     IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                     HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                     MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 6.3e-51 complete sequence
                     hit coverage= 100%, between model( 307 aa) positions 1;
                     307 length is 283aa with 25 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409269..2410084
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QMVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                     ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                     VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 9.5e-54 complete sequence
                     hit coverage= 100%, between model( 286 aa) positions 1;
                     286 length is 272aa with 15 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409269..2410084
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QMVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                     ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
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                     VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 2.5e-54 complete sequence
                     hit coverage= 100%, between model( 286 aa) positions 1;
                     286 length is 272aa with 15 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409272..2410087
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MVRQLQQDYSIRQICQVLNYPRSQVYYHARGQPDESELKAAIAG
                     V-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVK----RKRTTNSE
                     HSF-PRYGNRvlNLSIDHPEQVWVADITYIRL--QQEFVYLAVVMDVFTRAIRGWHLS
                     RHIDQQLTLRALNKALER----ATPEIHHSDQGVQYAAAAYMQLLQQHQVQISMAEVG
                     QAWQNGYAERLMRTIKEEEVDLSDYRNFT--EAYEHIEQFLEDVYMHKRIHSSLGYLT
                     PCEYEQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 6.3e-50 fragment hit
                     coverage= 92.81%, between model( 306 aa) positions 23;
                     306 length is 272aa with 14 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409281..2410096
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                     KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                     EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWRQQNN"
                     /note="IS3_IS3_ORF2      e-value= 1.2e-64 complete sequence
                     hit coverage= 100%, between model( 288 aa) positions 1;
                     288 length is 272aa with 19 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409281..2410096
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                     KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                     EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWRQQNN"
                     /note="IS3_IS3_ORF2      e-value= 3.3e-65 complete sequence
                     hit coverage= 100%, between model( 288 aa) positions 1;
                     288 length is 272aa with 19 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2409350..2409508
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YHARgQPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGY----
                     -CVNHKRVARLMRQ"
                     /note="IS3_IS2_ORF2      e-value= 9.1e-09 fragment hit
                     coverage= 18.87%, between model( 302 aa) positions 48;
                     104 length is 53aa with 5 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             2409416..2410099
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERATPE--------IHHSDQGVQYAAAAYMQLLQQHQVQ
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                     ISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEHIEQFLEDV--YMHKRIH
                     SSLGYLTPCEYEQQWRQQNNH"
                     /note="IS3_IS51_ORF2     e-value= 1.9e-38 fragment hit
                     coverage= 74.76%, between model( 317 aa) positions 73;
                     309 length is 228aa with 11 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2500838..2501899
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IVKRXKN------EQCIVSHpYPALXPPQPLAQG---ISSA---
                     --RQXHFXESEQRRQRXSENCSVRASSRPIDAAIRDRKKSLNVLTP--NQKRQMVRQL
                     QQDYSIRQICQVLNYPRSQVYYHARGQP-----DESELKAAIAGVAGAYP-TYGYRRI
                     TAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-RKRTTNSEHSfpRYGNRVLNLS
                     --IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNK
                     ALERAT---PEIHHS-----DQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAER
                     LMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYMHKRIHSSLGYLTPCEYEQQWRQ
                     Q"
                     /note="IS3_IS150_ORF2    e-value= 1.7e-22 complete sequence
                     hit coverage= 100%, between model( 389 aa) positions 1;
                     389 length is 354aa with 39 gaps, 5 stops, absolute
                     frame= Plus2"
     CDS             2501012..2501896
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PIDAAIRDRKKSLnVLTPNQKRQMVRQLQQDYSIRQICQVLNYP
                     RSQVYYHARGQPDESELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMR
                     QIGIMAKTKVK----RKRTTNSEHSF-PRYGNRvlNLSIDHPEQVWVADITYIRL--Q
                     QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALER----ATPEIHHSDQGVQ
                     YAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFT--EAYE
                     HIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 4.3e-49 complete sequence
                     hit coverage= 100%, between model( 306 aa) positions 1;
                     306 length is 295aa with 14 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2501048..2501932
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LNVLTPNQK-RQMVRQLQqdYSIRQICQVLNYP---RSQVYYHA
                     RgQPDESELKA--AIAGV-------AGA---YPTYGYRRITAQLQRQGYCVNHKRVAR
                     LMRQIGIMAKTKVKRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEF
                     VYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALERATPE--------IHHSDQGV
                     QYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEH
                     IEQFLEDV--YMHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNKEDS"
                     /note="IS3_IS51_ORF2     e-value= 1.6e-26 complete sequence
                     hit coverage= 100%, between model( 317 aa) positions 1;
                     317 length is 295aa with 27 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2501054..2501308
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VLTPNQKRQMVRQLQQDY--SIRQICQVLNYPRSQVYYHARGQP
                     DESELKAAIAGVAGAYPTYGYRRITAQLQRQGYCVNHKRVARL"
                     /note="IS3_IS407_ORF2    e-value= 1.2e-17 fragment hit
                     coverage= 25.29%, between model( 344 aa) positions 60;
                     146 length is 85aa with 2 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             2501072..2501899
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KRQMVRQLQQDYSIRQICQVLNYPRSQVYYHARGQP-----DES
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                ELKAAIAGVAGAYP-TYGYRRITAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-
                RKRTTNSEHSfpRYGNRVLNLS--IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTR
                AIRGWHLSRHIDQQLTLRALNKALERAT---PEIHHS-----DQGVQYAAAAYMQLLQ
                QHQVQISMAEVGQAWQNGYAERLMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYM
                HKRIHSSLGYLTPCEYEQQWRQQ"
                /note="IS3_IS150_ORF2    e-value= 2.2e-47 fragment hit
                coverage= 76.09%, between model( 389 aa) positions 94;
                389 length is 276aa with 23 gaps, 0 stops, absolute
                frame= Plus2"
CDS             2501075..2501923
                /colour="255 0 0"
                /evidence=predicted
                /translation="RQMVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                /note="IS3_IS51_ORF1     e-value= 8.1e-53 complete sequence
                hit coverage= 100%, between model( 307 aa) positions 1;
                307 length is 283aa with 25 gaps, 0 stops, absolute
                frame= Plus2"
CDS             2501075..2501923
                /colour="255 0 0"
                /evidence=predicted
                /translation="RQMVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                /note="IS3_IS51_ORF1     e-value= 6.3e-51 complete sequence
                hit coverage= 100%, between model( 307 aa) positions 1;
                307 length is 283aa with 25 gaps, 0 stops, absolute
                frame= Plus2"
CDS             2501078..2501893
                /colour="255 0 0"
                /evidence=predicted
                /translation="QMVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                LTPCEYEQQWR"
                /note="IS3_IS3_ORF1      e-value= 9.5e-54 complete sequence
                hit coverage= 100%, between model( 286 aa) positions 1;
                286 length is 272aa with 15 gaps, 0 stops, absolute
                frame= Plus2"
CDS             2501078..2501893
                /colour="255 0 0"
                /evidence=predicted
                /translation="QMVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                LTPCEYEQQWR"
                /note="IS3_IS3_ORF1      e-value= 2.5e-54 complete sequence
                hit coverage= 100%, between model( 286 aa) positions 1;
                286 length is 272aa with 15 gaps, 0 stops, absolute
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                     frame= Plus2"
     CDS             2501081..2501896
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MVRQLQQDYSIRQICQVLNYPRSQVYYHARGQPDESELKAAIAG
                     V-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVK----RKRTTNSE
                     HSF-PRYGNRvlNLSIDHPEQVWVADITYIRL--QQEFVYLAVVMDVFTRAIRGWHLS
                     RHIDQQLTLRALNKALER----ATPEIHHSDQGVQYAAAAYMQLLQQHQVQISMAEVG
                     QAWQNGYAERLMRTIKEEEVDLSDYRNFT--EAYEHIEQFLEDVYMHKRIHSSLGYLT
                     PCEYEQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 6.3e-50 fragment hit
                     coverage= 92.81%, between model( 306 aa) positions 23;
                     306 length is 272aa with 14 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2501090..2501905
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                     KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                     EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWRQQNN"
                     /note="IS3_IS3_ORF2      e-value= 1.2e-64 complete sequence
                     hit coverage= 100%, between model( 288 aa) positions 1;
                     288 length is 272aa with 19 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2501090..2501905
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                     KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                     EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWRQQNN"
                     /note="IS3_IS3_ORF2      e-value= 3.3e-65 complete sequence
                     hit coverage= 100%, between model( 288 aa) positions 1;
                     288 length is 272aa with 19 gaps, 0 stops, absolute
                     frame= Plus2"
     CDS             2501159..2501317
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YHARgQPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGY----
                     -CVNHKRVARLMRQ"
                     /note="IS3_IS2_ORF2      e-value= 9.1e-09 fragment hit
                     coverage= 18.87%, between model( 302 aa) positions 48;
                     104 length is 53aa with 5 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             2501225..2501908
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERATPE--------IHHSDQGVQYAAAAYMQLLQQHQVQ
                     ISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEHIEQFLEDV--YMHKRIH
                     SSLGYLTPCEYEQQWRQQNNH"
                     /note="IS3_IS51_ORF2     e-value= 1.9e-38 fragment hit
                     coverage= 74.76%, between model( 317 aa) positions 73;
                     309 length is 228aa with 11 gaps, 0 stops, absolute
```

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                frame= Plus2"
CDS             2629103..2629798
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                51.23%, between model( 486 aa) positions 1; 249 length is
                232aa with 27 gaps, 0 stops, absolute frame= Plus2"
CDS             2629103..2630230
                /colour="255 0 0"
                /evidence=predicted
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                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                /note="IS4   e-value= 9.9e-07 complete sequence hit
                coverage= 100%, between model( 486 aa) positions 1; 486
                length is 376aa with 117 gaps, 0 stops, absolute frame=
                Plus2"
CDS             2631026..2631439
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                I--PISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKECL
                YSKYYSDFHSFKGAIQQCIDQCNTEHKAKLTSLLSLKFQSFQK"
                /note="IS630 e-value= 1.1e-17 fragment hit coverage=
                38.56%, between model( 376 aa) positions 232; 376 length
                is 138aa with 7 gaps, 0 stops, absolute frame= Plus2"
CDS             2714843..2715040
                /colour="255 0 0"
                /evidence=predicted
                /translation="GKHKQILLVLDGAGWHTC---KNRVVPPG--IHLKILPPYSPEL
                QPAERLWRLADEPLAN-QCFETLDDLED"
                /note="IS630 e-value= 1.4e-09 fragment hit coverage=
                19.15%, between model( 376 aa) positions 275; 346 length
                is 66aa with 6 gaps, 0 stops, absolute frame= Plus2"
CDS             2845484..2846386
                /colour="255 0 0"
                /evidence=predicted
                /translation="QRFIQGLSPETIHLLSRIHRHSYHHQVRQRAHCILLSFEGFNVT
                ELMSIFAVTRKTVYTWLDDWDNHC---LVGLYDQPGRGRKPKLNDVQ-KEQIRAWAKM
                TP---------HNLNAVLAKIKEAWNIAVSKTTLKRILKSCSMSWRRLRRVVAGQPDP
                VEYETK-----RHQLEVLKRQEEKGELdlrYLDESGFCLVPYVPY-AWQEKG------
                --------ETLGLPSQRSSRFNVLGLMNRHNDL-TSYVFDKSITSAVVVACIDDFSRT
                C--DQHTVVVMDQASVHKNAEIEEKIEDWKAkNVEIFWLPTYSPHLNLIEIFWRFMKY
                EWI"
                /note="IS630 e-value= 1.1e-24 fragment hit coverage=
                88.56%, between model( 376 aa) positions 1; 333 length is
                301aa with 36 gaps, 0 stops, absolute frame= Plus2"
CDS             2845484..2846518
                /colour="255 0 0"
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                     /evidence=predicted
                     /translation="QRFIQGLSPETIHLLSRIHRHSYHHQVRQRAHCILLSFEGFNVT
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                     TP---------HNLNAVLAKIKEAWNIAVSKTTLKRILKSCSMSWRRLRRVVAGQPDP
                     VEYETK-----RHQLEVLKRQEEKGELdlrYLDESGFCLVPYVPY-AWQEKG------
                     --------ETLGLPSQRSSRFNVLGLMNRHNDL-TSYVFDKSITSAVVVACIDDFSRT
                     C--DQHTVVVMDQASVHKNAEIEEKIEDWKAkNVEIFWLPTYSPHLNLIEIFWRFMKY
                     EWIEFAAYKCLGSLSLYIDKILKGFgKDYVIDFGXVLINFXLTTQLL"
                     /note="IS630 e-value= 5.3e-21 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 345aa with 36 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             3258380..3259537
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SSNSFRAKTPSIXKVG-ILNSNHQIT---------FHVSSTQVF
                     ACCPVCNQITHRVHSRYERTLRDLPCVDFCLTILLQVCKFFCRNeaCKRCIFTErlpk
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                     -PAPTPKILGVDDFAFQRG--HHYGTILVDLEHH----RTIALLPDRDAKTLVAWLEE
                     HP------GVEILSRDRSKTYKSAISEGAPNAIQVADRFHLLKNLQEVLEKVF-----
                     -------------------HSNYPALKSVDAALLKS-EVPEPHAPESNEKSKVP-PDE
                     QgPRSRAH-----RLNNYQQTHALKQQGYXVTDIAHHLGIAKRTAYQ-YLSHPFFPEH
                     QPYTRKVPTVIEP-YKDY---------LYQEWMAGRQNSYCTK------YRdALIGHK
                     SIKCVKTNDLD"
                     /note="ISL3  e-value= 4e-07 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
                     length is 386aa with 75 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             3258827..3259108
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TPKILGVDDFAFQRG--HHYGTILVDLEHH----RTIALLPDRD
                     AKTLVAWLEEHP------GVEILSRDRSKTYKSAISEGAPNAIQVADRFHLLKNLQEV
                     LEKV"
                     /note="ISL3  e-value= 1.4e-18 fragment hit coverage=
                     23.50%, between model( 451 aa) positions 157; 262 length
                     is 94aa with 12 gaps, 0 stops, absolute frame= Plus2"
     CDS             3307874..3309085
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
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                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 1.4e-166 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             3307874..3309085
                     /colour="255 0 0"
                     /evidence=predicted
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                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
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                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
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                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 3.7e-167 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             3753371..3754582
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
                     A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVTNSVMEEVKDWRSRP
                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
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                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 1.4e-166 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             3753371..3754582
                     /colour="255 0 0"
                     /evidence=predicted
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                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
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                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 3.7e-167 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
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     CDS             3911570..3912511
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 1.1e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             3911570..3912511
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
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                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 2.2e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             4126139..4127350
                     /colour="255 0 0"
                     /evidence=predicted
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                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
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                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
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                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 1.4e-166 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             4126139..4127350
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
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                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 3.7e-167 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Plus2"
     CDS             4199279..4199470
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ATPIELSQQQHHCLLQIVRQTINPYRLVRRASIILSAASGKSNT
                     QISRQWQLDRNQVRYWRQRW"
                     /note="IS630 e-value= 8.9e-08 fragment hit coverage=
                     17.02%, between model( 376 aa) positions 1; 64 length is
                     64aa with 0 gaps, 0 stops, absolute frame= Plus2"
     CDS             4226972..4227316
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KYIVTLTPEERSELIQLTRRRTLSARKMKRAQILMLADEGHKDD
                     TITQMLNAGISTVHRTRQKFVEGG---VEfALNERPRPGGQKKLDSKAEALLIATACS
                     DPPTG----CCRWTMQLLAE"
                     /note="IS630 e-value= 1.2e-15 fragment hit coverage=
                     32.18%, between model( 376 aa) positions 1; 121 length is
                     115aa with 7 gaps, 0 stops, absolute frame= Plus2"
     CDS             4926788..4927030
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Plus2"
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CDS             5053775..5054902
                /colour="255 0 0"
                /evidence=predicted
                /translation="PFASIIEHFSDLDDPRAAHRIEYSLEDIIFITLCAVLCGADNWV
                EVANYGCSKAQWLKQWIALPNG------IPSHDTFEWVFARLKPQQLQQCFLNWTQAI
                YHLSAGA-LIAIDGKTLRGAIATGEQRSLIHMVSAWASHNRLVLGQRTVEEKSNEITA
                IPELLKILELEG-ALVSIDAMGCQTAIAETIIEGQG-DYVLALKGNQGDLYNDVVQLF
                dhaCQTQFQGIEHDSYQTVEKGHGRIEHRTYWTMGQTDYLLGAE-RWAQLKSIGCVES
                CRRQPGHPG---TLQRRYYLLSIESDAQR---FADAVRSHWGIENQLHWILDVGFRED
                KLRACQGYSAQNLSVIRHIAANLLQQESTAKCGVKAKRLKAGWDDDYLVKILSAAAKG
                "
                /note="ISAs1 e-value= 1.9e-150 complete sequence hit
                coverage= 100%, between model( 389 aa) positions 1; 389
                length is 376aa with 16 gaps, 0 stops, absolute frame=
                Plus2"
CDS             5053775..5054902
                /colour="255 0 0"
                /evidence=predicted
                /translation="PFASIIEHFSDLDDPRAAHRIEYSLEDIIFITLCAVLCGADNWV
                EVANYGCSKAQWLKQWIALPNG------IPSHDTFEWVFARLKPQQLQQCFLNWTQAI
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                IPELLKILELEG-ALVSIDAMGCQTAIAETIIEGQG-DYVLALKGNQGDLYNDVVQLF
                dhaCQTQFQGIEHDSYQTVEKGHGRIEHRTYWTMGQTDYLLGAE-RWAQLKSIGCVES
                CRRQPGHPG---TLQRRYYLLSIESDAQR---FADAVRSHWGIENQLHWILDVGFRED
                KLRACQGYSAQNLSVIRHIAANLLQQESTAKCGVKAKRLKAGWDDDYLVKILSAAAKG
                "
                /note="ISAs1 e-value= 1.5e-144 complete sequence hit
                coverage= 100%, between model( 389 aa) positions 1; 389
                length is 376aa with 16 gaps, 0 stops, absolute frame=
                Plus2"
CDS             5055743..5055940
                /colour="255 0 0"
                /evidence=predicted
                /translation="ASPIELSQQQHHCLTQIVRQTTNPYRLVRRASIILSAASGESNT
                QISRQWQLDRNQVRYWRQRWLD"
                /note="IS630 e-value= 4e-07 fragment hit coverage=
                17.55%, between model( 376 aa) positions 1; 66 length is
                66aa with 0 gaps, 0 stops, absolute frame= Plus2"
CDS             5176034..5176441
                /colour="255 0 0"
                /evidence=predicted
                /translation="MLLVRPISTESLRLLHRIYHSSRHHQVRQRAHCLILFAQGWPPY
                TLASLFSVSPKTVYNWLKAWNNRG---FAGLYNHPGRGRKPMFNPDQQQQIYEWT-QA
                SPIQ---------LNQVLAQIEQQWSVRVSKATVKRVLKQMDMSWHR"
                /note="IS630 e-value= 8.7e-15 fragment hit coverage=
                39.63%, between model( 376 aa) positions 1; 149 length is
                136aa with 13 gaps, 0 stops, absolute frame= Plus2"
CDS             5176094..5176432
                /colour="255 0 0"
                /evidence=predicted
                /translation="SSRHHQVRQRAHCLILFAQGWPPYTLASLFSVSPKTVYNWLKAW
                NNRGFAGLYNH---PGRGRKPMfNPDQQQQIYEWTQASPIQLNQVLAQIEQQWSVR--
                -VSKATVKRVLKQMDMS"
                /note="IS481 e-value= 3.5e-09 fragment hit coverage=
                33.62%, between model( 351 aa) positions 1; 118 length is
                113aa with 6 gaps, 0 stops, absolute frame= Plus2"
CDS             5341466..5341705
                /colour="255 0 0"
                /evidence=predicted
                /translation="RNQQHYIRQRLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKY
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                     LDGGLQGLVQPI--RHQKPSRLSPEEQQQLKEMVLTQR"
                     /note="IS481 e-value= 1.2e-07 fragment hit coverage=
                     23.36%, between model( 351 aa) positions 1; 82 length is
                     80aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             5341493..5341900
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKYLDGG---LQ
                     GLVQPIRHQKPSRLSPEEQQQLKEMVLTQRPTDYGIDRNMWTGAILAVVIEQRFEVQL
                     KDSRIYELLSELGLSYQRAHRDYA--NADLNAQKEWVAA"
                     /note="IS630 e-value= 1.9e-29 fragment hit coverage=
                     37.50%, between model( 376 aa) positions 30; 170 length
                     is 136aa with 5 gaps, 0 stops, absolute frame= Plus2"
     CDS             5545037..5545732
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMInDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
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                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEGDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGAAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 2.3e-13 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Plus2"
     CDS             5545037..5546200
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMInDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkSLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEGDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGAAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDSCP-----------------VANQHFaQHPWWDNQNGWKNLLNNV
                     RLIIQPLISWNLLKSWLE--VFPIRALKKGFEQLTSKMEAFCC"
                     /note="IS4   e-value= 1.2e-06 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 388aa with 105 gaps, 0 stops, absolute frame=
                     Plus2"
     CDS             5653406..5653864
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTHRKLSHSVWECKYHVVFVPKYRKGRIYGQIRXNSGDIFH-EL
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                     HKFWSRGYFVSTVG-RDEAMIRRYIRHQGQEEQKLEQLNLFraXPKSPLRGSNS"
                     /note="IS200 e-value= 6.3e-51 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 153aa with 3 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             5653406..5653864
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTHRKLSHSVWECKYHVVFVPKYRKGRIYGQIRXNSGDIFH-EL
                     ARHKKNVIEEGHLMPDHVHMLLSIPLKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEAMIRRYIRHQGQEEQKLEQLNLFraXPKSPLRGSNS"
                     /note="IS200 e-value= 5.1e-50 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 153aa with 3 gaps, 2 stops, absolute frame=
                     Plus2"
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     CDS             5653406..5653861
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTHRKLSHSVWECKYHVVFVPKYRKGRIYGQ-IRXNSGDIFHEL
                     ARHKKNVIEEGHLMPDHVHMLLSIPLKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEAMIRRYIRHQGQEEQKLEQLNLFraXPKSPLRGSN"
                     /note="IS200_IS605 e-value= 2.2e-50 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 152aa with 3 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             5653406..5653861
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTHRKLSHSVWECKYHVVFVPKYRKGRIYGQ-IRXNSGDIFHEL
                     ARHKKNVIEEGHLMPDHVHMLLSIPLKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEAMIRRYIRHQGQEEQKLEQLNLFraXPKSPLRGSN"
                     /note="IS200_IS605 e-value= 5.6e-51 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 152aa with 3 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             5653406..5653861
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTHRKLSHSVWECKYHVVFVPKYRKGRIYGQIRXNSGDIFHEL
                     ARHKKNVIEEGHLMPDHVHMLLSIPLKYSVSNVVGYVKGKSAIYIARELGNSRN-ATG
                     HKFWSRGYFVSTVGRDEAMIRRYIRHQGQEEQKLEQLNLfrAXPKSPLRGSN"
                     /note="IS605 e-value= 6.9e-45 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 152aa with 2 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             5653406..5653861
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTHRKLSHSVWECKYHVVFVPKYRKGRIYGQIRXNSGDIFHEL
                     ARHKKNVIEEGHLMPDHVHMLLSIPLKYSVSNVVGYVKGKSAIYIARELGNSRN-ATG
                     HKFWSRGYFVSTVGRDEAMIRRYIRHQGQEEQKLEQLNLfrAXPKSPLRGSN"
                     /note="IS605 e-value= 8.2e-45 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 152aa with 2 gaps, 2 stops, absolute frame=
                     Plus2"
     CDS             5747213..5747476
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                     DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVR"
                     /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
                     36.40%, between model( 239 aa) positions 1; 87 length is
                     88aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             5896091..5896333
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Plus2"
     CDS             5908769..5909158
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FFMDESGFSLVPCIPY-GWQPIG-------------TYL-EIPT
```

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                     RSSKRLNVLGFLSRRQGL--HAYTSEQTITSEVVShCIDTFFADV--ELPTVIVVDQA
                     PIHTSQsiyEMKAEWAERG--ITLFELPSYSPHLNLIERLWQFMKYQWI"
                     /note="IS630 e-value= 6.5e-11 fragment hit coverage=
                     39.10%, between model( 376 aa) positions 187; 333 length
                     is 130aa with 21 gaps, 0 stops, absolute frame= Plus2"
     CDS             5942117..5942839
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="----MAHLSPESFXCRATSEVVPSRST---------ISGPSILa
                     risdLFPHCWRLGSLXIN---GLPYSPPGRDRS-----DELRTLP----PTRQETSNT
                     RIXAAXCCRDGCDXDTDXTSpKRTKSVLFRKKKRHTLKCQIIADRNTLEVICLSFGPG
                     RRHDFQIFKGSGIHIHPNTESLQDSGYQGIAAYHANSYVPFKKPQHGELTSLQREYNC
                     ALSQERMGIEHINRSLKISRILSERYRNRRCRYALRCNLIAALYNHEL"
                     /note="IS5_ISL2    e-value= 1e-38 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 241aa with 25 gaps, 6 stops, absolute frame=
                     Plus2"
     CDS             5942438..5942839
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KKKRHTLKCQIIADRNTLEVICLSFGPGRRHDFQIFKGSGIHIH
                     PNTESLQDSGYQGIAAYHANSYVPFKKPQHGELTSLQREYNCALSQERMGIEHINRSL
                     KISRILSERYRNRRCRYALRCNLIAALYNHEL"
                     /note="IS5_ISL2    e-value= 2.1e-57 fragment hit coverage=
                     51.54%, between model( 260 aa) positions 127; 260 length
                     is 134aa with 0 gaps, 0 stops, absolute frame= Plus2"
     CDS             6104879..6105265
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                     RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFEIWLercLIPMLKPGQKLVI--DN
                     ATFHKGGRIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                     /note="IS630 e-value= 6.9e-14 fragment hit coverage=
                     38.83%, between model( 376 aa) positions 188; 333 length
                     is 129aa with 20 gaps, 0 stops, absolute frame= Plus2"
     CDS             6243806..6244048
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Plus2"
     CDS             6501464..6501685
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YASDLTAEQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                     ILYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTW"
                     /note="IS5_IS1031  e-value= 3.3e-39 fragment hit coverage=
                     27.46%, between model( 295 aa) positions 20; 100 length
                     is 74aa with 7 gaps, 0 stops, absolute frame= Plus2"
     CDS             6501473..6501685
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTAEQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAILYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTW"
                     /note="IS5_IS427   e-value= 7.3e-19 fragment hit coverage=
                     24.66%, between model( 296 aa) positions 125; 197 length
                     is 71aa with 2 gaps, 0 stops, absolute frame= Plus2"
     CDS             316002..316943
```

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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 1.1e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             316002..316943
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 2.2e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             469320..469814
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LEKTGIESKKKTYGYR--ERD--ETQR---QAFIERLQTKHP--
                     HQIVYVDEAGIDNRADYPY-GYCPVG-----------QRFYD-LKSG-KRTERVSFIA
                     ALKEGQL--FSPMTFEGSCNRLLFEAWLQQSLI-SQLQLgdVIVIDNASFHHGQRIEE
                     IVAEAG--CEIWYLPSYSPDLNKIERWWFVLKN"
                     /note="IS630  e-value= 3e-16 fragment hit coverage=
                     50.80%, between model( 376 aa) positions 140; 330 length
                     is 165aa with 28 gaps, 0 stops, absolute frame= Plus3"
     CDS             471168..471305
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYSRQLPNE---TIHHVSKALTQRLERTNGILRQQAG
                     RWHRR"
                     /note="IS1_ORF2    e-value= 3.3e-13 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Plus3"
     CDS             516039..516734
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Plus3"
     CDS             516039..517166
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
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                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             666744..667439
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Plus3"
     CDS             666744..667871
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             690405..690542
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                     RWHRR"
                     /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Plus3"
     CDS             972294..973070
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PYXXXEKAXISLVLEASKNAXISLLSXGwVQAPTTIRIAGLARL
                     IAWA--VCFANPASSXEL--PLYSGSFSLSI---------SKYRTGCLERLFEKXVKL
                     SRYXsVNTQTLDRTXRAMPTAYDSDLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVL
                     NAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSE----
                     -------------------------DRHPSPSAAICDAQSVkvgnpRCHLIGFDGGKM
                     VKGRKRHVLVDTLGLVLMVMVTAANIS"
                     /note="IS5_IS427   e-value= 8.6e-07 complete sequence hit
                     coverage= 100%, between model( 296 aa) positions 1; 296
                     length is 259aa with 44 gaps, 10 stops, absolute frame=
                     Plus3"
```

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     CDS             972543..973412
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="EKXVKLSRYXSVNTQTLDRTXramptaYDSDLTTLQWELLEPLI
                     PAAKPG-----GRPRTTDML--------------------SVLNAIFYLVVTGCQWRQ
                     --LPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSED---RHPSPSAAICDAQ
                     SVK------------------------------VGNpRcHLIGFD--------GGKM-
                     --------------------------------------------VKGRKRHVLVD-TL
                     GLVLMVMVTAANISDQRGAK----------------------ILFWKAQRQGASLSRL
                     VR----IWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWL
                     LWSRRLNKDYEVLTRTAEALVYYVAMIRLMVRRLAQEHX"
                     /note="IS5_IS5     e-value= 1.8e-09 complete sequence hit
                     coverage= 100%, between model( 422 aa) positions 1; 422
                     length is 290aa with 140 gaps, 4 stops, absolute frame=
                     Plus3"
     CDS             972582..973433
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                     ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQ
                     INEHLRMQVRVSEDRHPSPSAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVD
                     TLGLVLMVMVTAANISDQR-GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVM
                     DRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                     AMIRLMVRRLAQEHXNFSNSLX"
                     /note="IS5_IS1031  e-value= 1.8e-111 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 284aa with 14 gaps, 3 stops, absolute frame=
                     Plus3"
     CDS             972624..973433
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                     IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSEDRHPSP
                     SAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
                     -GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGF
                     QVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYYVAMIRLMVRRLAQEHXNFSN
                     SLX"
                     /note="IS5_IS1031  e-value= 1.2e-113 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 2 stops, absolute frame=
                     Plus3"
     CDS             972633..972872
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRM"
                     /note="IS5_IS427   e-value= 2e-19 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Plus3"
     CDS             1016775..1017812
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSRHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630 e-value= 3.1e-22 complete sequence hit
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                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             1016775..1017812
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSRHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630  e-value= 3.5e-21 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             1016835..1016993
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                     QQGGIEGLK"
                     /note="IS481  e-value= 3.7e-09 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Plus3"
     CDS             1099857..1100243
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                     RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                     ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                     /note="IS630  e-value= 1.1e-13 fragment hit coverage=
                     38.83%, between model( 376 aa) positions 188; 333 length
                     is 129aa with 20 gaps, 0 stops, absolute frame= Plus3"
     CDS             1100496..1101191
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Plus3"
     CDS             1100496..1101623
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
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                     Plus3"
     CDS             1211556..1212239
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LHLXYFRRQYQCGGQHIHKNGHRR-GKQNHICVACGR----QFL
                     STYSKRGysdwTKRLCLRMYVNGMGLQGIERVIGVAHTTVIRWVQQV--GVLLPDAYD
                     PDDIPQVGELDELETFVGQKRNKVWIWTVVDHFHPGILGWVVGDHSAETFRPLWQAIV
                     CWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGENTRLRHYLARLHRKTL
                     CYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 4.1e-24 complete sequence hit
                     coverage= 100%, between model( 237 aa) positions 1; 237
                     length is 228aa with 13 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             1211586..1212233
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QCGGQH-IHKNGHRR-GKQNHICVACGRQFL--STYSKRGYSDW
                     TKRLCLRMYVNGMGLQGIERVIGVAHTTVIRWVQQVGVLLPDAYDPDD------IP--
                     -QVGELDELETFVGQKRNKVWIW-TVVDHFHPG--ILGWVVGDHSAETFRPLWqaIVC
                     WQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLARLHRKTLCYSKSV
                     DMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 5.5e-39 fragment hit coverage=
                     96.23%, between model( 239 aa) positions 10; 239 length
                     is 216aa with 19 gaps, 0 stops, absolute frame= Plus3"
     CDS             1211586..1212233
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="---------QCGGQH-IHKNGHRR-GKQNHICVACGRQFL--ST
                     YSKRGYSDWTKRLCLRMYVNGMGLQGIERVIGVAHTTVIRWVQQVGVLLPDAYDPDD-
                     -----IP---QVGELDELETFVGQKRNKVWIW-TVVDHFHPG--ILGWVVGDHSAETF
                     RPLWqaIVCWQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLARLHR
                     KTLCYSKSVDMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 5.6e-36 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 216aa with 28 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             1211838..1212239
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DPDDIPQVGELDELETFVGQKRNKVWIWTVVDHFHPGILGWVVG
                     DHSAETFRPLWQAIVCWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGEN
                     TRLRHYLARLHRKTLCYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 1.9e-31 fragment hit coverage=
                     59.07%, between model( 237 aa) positions 98; 237 length
                     is 134aa with 6 gaps, 0 stops, absolute frame= Plus3"
     CDS             1474827..1475525
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RMAYPSsrSLKCRASSKVVSPXSTIGGSS---------ILAGIS
                     DLFPYCWRLGSLXINCLPYCppGRNRSDELRTLSLTWSEISATR---------VXATG
                     CRCDGCDXNAHXTSPEKTKSVLF----REKKRHTLKCQIIADRNTLEIICLSFGPGRR
                     HDFQIFKVSGIHIHPNTESLQDSGYQGIAAYHANSYVPFKKSQHSELTSLQREYNRAL
                     SQERMGIEHIK---------SQPEDFQNSVGALPXSSSSLHAAVXL"
                     /note="IS5_ISL2    e-value= 5e-10 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 233aa with 31 gaps, 7 stops, absolute frame=
                     Plus3"
     CDS             1475154..1475444
                     /colour="255 0 0"
                     /evidence=predicted
```

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                /translation="KKRHTLKCQIIADRNTLEIICLSFGPGRRHDFQIFKVSGIHIHP
                NTESLQDSGYQGIAAYHANSYVPFKKSQHSELTSLQREYNRALSQERMGIEHI"
                /note="IS5_ISL2    e-value= 4.6e-35 fragment hit coverage=
                37.31%, between model( 260 aa) positions 128; 224 length
                is 97aa with 0 gaps, 0 stops, absolute frame= Plus3"
CDS             1500237..1500374
                /colour="255 0 0"
                /evidence=predicted
                /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                RWHRR"
                /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                20.68%, between model( 237 aa) positions 164; 212 length
                is 46aa with 3 gaps, 0 stops, absolute frame= Plus3"
CDS             1586793..1587056
                /colour="255 0 0"
                /evidence=predicted
                /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVR"
                /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
                36.40%, between model( 239 aa) positions 1; 87 length is
                88aa with 2 gaps, 0 stops, absolute frame= Plus3"
CDS             2912997..2913938
                /colour="255 0 0"
                /evidence=predicted
                /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                LN-RMIQIAKPETVWVE"
                /note="IS5_IS903   e-value= 1.1e-96 complete sequence hit
                coverage= 100%, between model( 347 aa) positions 1; 347
                length is 314aa with 37 gaps, 1 stops, absolute frame=
                Plus3"
CDS             2912997..2913938
                /colour="255 0 0"
                /evidence=predicted
                /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                LN-RMIQIAKPETVWVE"
                /note="IS5_IS903   e-value= 2.2e-96 complete sequence hit
                coverage= 100%, between model( 347 aa) positions 1; 347
                length is 314aa with 37 gaps, 1 stops, absolute frame=
                Plus3"
CDS             2982312..2983067
                /colour="255 0 0"
                /evidence=predicted
                /translation="LQANLQTHAPRMAHLSPKSLXCRATSKVVPPRSTIsgpSILARI
                SDLFPHCWRLGRFXIN-----GLPYSPAGR---ECSDELRTLP----PTRQETSNTRI
                XATXCCRDGCDXDTDXTsSKRTKSVLFRKKKRHTLKCQIIANRSTLEIICLNFGKGRR
                HDFQIFKVSGIHIHPNTESLQDSGYQGITAYHSNSYVPFKKPQHGELTSLQREYNRAL
                SQERMGIEHINRSLKIFRILSERYRNRRRRYALRCNLIAALYNHEL"
                /note="IS5_ISL2    e-value= 4.5e-45 complete sequence hit
                coverage= 100%, between model( 260 aa) positions 1; 260
                length is 252aa with 12 gaps, 6 stops, absolute frame=
```

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               Plus3"
CDS            2982666..2983067
               /colour="255 0 0"
               /evidence=predicted
               /translation="KKKRHTLKCQIIANRSTLEIICLNFGKGRRHDFQIFKVSGIHIH
               PNTESLQDSGYQGITAYHSNSYVPFKKPQHGELTSLQREYNRALSQERMGIEHINRSL
               KIFRILSERYRNRRRRYALRCNLIAALYNHEL"
               /note="IS5_ISL2    e-value= 5.1e-63 fragment hit coverage=
               51.54%, between model( 260 aa) positions 127; 260 length
               is 134aa with 0 gaps, 0 stops, absolute frame= Plus3"
CDS            3307083..3307769
               /colour="255 0 0"
               /evidence=predicted
               /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
               NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
               A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVTNSVMEEVKDWRSRP
               LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
               FWLSVLTDLKNRGTQDILM"
               /note="IS256 e-value= 1.9e-79 fragment hit coverage=
               56.59%, between model( 410 aa) positions 1; 232 length is
               229aa with 8 gaps, 0 stops, absolute frame= Plus3"
CDS            3307083..3309647
               /colour="255 0 0"
               /evidence=predicted
               /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
               NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
               A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVTNSVMEEVKDWRSRP
               LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
               FWLSVLTDLKNRGTQDilmglfrvlckrsriqthqetvrclerkklpiesmncxmnss
               ertlnrkifwanqdclndsanaxwneplqvnxlitcsnpptisqvmrilmapeivamv
               trkrpsslnkerwtyrflvtvaaslslswclkasdasqgsmrksspymlgaxppvife
               pnwwscmgpislklxlvtspiaswkrsktgvqgrwmrcirlsilmrcmxtsksmvksa
               selsmslwqxlwratrncwdygxeplnereqnsgfrcsqtlkieelrisxllavmdsk
               vflkrlsrstlrprcrfvlsilfviafamcrgrkvepxlqtsspftkrplwkslrlrw
               mhlpingtrrilalaksgydigimlprcfntqwpsvrlstppmplsrstahxerxlrp
               krfslmkslstnxcfxrxgifrsdgpdqfxigrrrcpillfcsqhdstieytaaytki
               xtlSLIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPWKESRAVAADLKPI
               YQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQYPMAIRKVIYTTN
               AIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPILNWKAALSHFAIL
               FPTRFNYXIH"
               /note="IS256 e-value= 4.1e-83 complete sequence hit
               coverage= 100%, between model( 410 aa) positions 1; 410
               length is 855aa with 11 gaps, 1 stops, absolute frame=
               Plus3"
CDS            3309117..3309647
               /colour="255 0 0"
               /evidence=predicted
               /translation="LIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPWKES
               RAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQYPM
               AIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPILNW
               KAALSHFAILFPTRFNYXIH"
               /note="IS256 e-value= 5.1e-77 fragment hit coverage=
               43.90%, between model( 410 aa) positions 231; 410 length
               is 177aa with 3 gaps, 1 stops, absolute frame= Plus3"
CDS            3315393..3316334
               /colour="255 0 0"
               /evidence=predicted
               /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
               TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
               RRKGQLSISLPVIPKQGAIHVVIDSTGIKVYG------------EGEWKTRQHGVS-K
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                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 9.4e-98 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             3315393..3316334
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGIKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 1.7e-97 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             3758064..3758450
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                     RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                     ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                     /note="IS630 e-value= 1.1e-13 fragment hit coverage=
                     38.83%, between model( 376 aa) positions 188; 333 length
                     is 129aa with 20 gaps, 0 stops, absolute frame= Plus3"
     CDS             4200300..4200518
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRFVYIPKHTSXLNQIECWFSILVRRLIRRGNFTSTDDLQQRI
                     LDFIEYFNHtMAKPFQWQFKGFTPHGXLM"
                     /note="IS630 e-value= 5.4e-08 fragment hit coverage=
                     19.15%, between model( 376 aa) positions 305; 376 length
                     is 73aa with 0 gaps, 2 stops, absolute frame= Plus3"
     CDS             4200348..4200458
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IECWFSILVRRLIR--RGNFTSTDDLQQRILDFIEYFNH"
                     /note="IS3_IS150_ORF2    e-value= 4.8e-09 fragment hit
                     coverage= 10.03%, between model( 389 aa) positions 329;
                     367 length is 37aa with 2 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             4250727..4251422
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Plus3"
     CDS             4250727..4251854
                     /colour="255 0 0"
```

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                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             4281402..4281956
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HLSKTTQVNPKNQGLNINKVACSSQSW---------NDCLLMPV
                     SLKFFPLSLXFLLISEYMNSGL------ISLMPKHMKHLR----------LFFTVYPE
                     XspACVKQHDTKQRPHEPRQA------VLLLSLRXQIKITLX----------------
                     ------------------------------RLLYVPLKKPQQGELTPLEXEYNRALSQ
                     ERMGIEHINRSLKIFRILSERYRSRSRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 3.9e-10 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 185aa with 77 gaps, 5 stops, absolute frame=
                     Plus3"
     CDS             4281750..4281956
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YVPLKKPQQGELTPLEXEYNRALSQERMGIEHINRSLKIFRILS
                     ERYRSRSRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 3.1e-31 fragment hit coverage=
                     26.54%, between model( 260 aa) positions 192; 260 length
                     is 69aa with 0 gaps, 1 stops, absolute frame= Plus3"
     CDS             5056764..5056982
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRFVYIPKHTSWLNQIECWFSILVRRLIRRGNFTSKDDLQQRI
                     LEFIEYFNHtMAKPFQWQFKGFQPRLXLM"
                     /note="IS630  e-value= 4e-10 fragment hit coverage=
                     19.15%, between model( 376 aa) positions 305; 376 length
                     is 73aa with 0 gaps, 1 stops, absolute frame= Plus3"
     CDS             5056812..5056922
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IECWFSILVRRLIR--RGNFTSKDDLQQRILEFIEYFNH"
                     /note="IS3_IS150_ORF2    e-value= 2e-08 fragment hit
                     coverage= 10.03%, between model( 389 aa) positions 329;
                     367 length is 37aa with 2 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             5147340..5148377
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
```

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                /note="IS630 e-value= 6.7e-25 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Plus3"
CDS             5147340..5148377
                /colour="255 0 0"
                /evidence=predicted
                /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                /note="IS630 e-value= 4.9e-24 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Plus3"
CDS             5147400..5147558
                /colour="255 0 0"
                /evidence=predicted
                /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                QQGGIEGLK"
                /note="IS481 e-value= 3.7e-09 fragment hit coverage=
                15.10%, between model( 351 aa) positions 1; 53 length is
                53aa with 0 gaps, 0 stops, absolute frame= Plus3"
CDS             5209563..5210690
                /colour="255 0 0"
                /evidence=predicted
                /translation="PFASIIEHFSDLDDPRAAHRIEYSLEDIIIITLCAVLCGADNWV
                EVANYGRSKAQWLKQWIALPNG------VPSHDTFEWVFARLKPQQLQQCFLNWTQAI
                YQLSAGE-LIAIDGKTLRGAIAPGEQCSLIHMVSAWASHNRLVLGQRTVDEKSNEITA
                IPELLKVLELEG-ALVSIDAMGCQTAIAETIIEGQG-DYVLALKGNQGDLYNDVVQLF
                dhaCQTQFQGIEHDSYQTVEKGHGRIEHRTYWTMGQTDYLLGAE-RWAQLKSIGCVES
                CRRQPGHPG---TLQRRYYLLSIESDAQR---FADAVRSHWGIENQLHWILDVGFRED
                KLRACQGCSAQNLSVIRHIAANLLQQESTAKCGVKAKRLKAGWDDNYLVKILSVAAKG
                "
                /note="ISAs1 e-value= 2.4e-150 complete sequence hit
                coverage= 100%, between model( 389 aa) positions 1; 389
                length is 376aa with 16 gaps, 0 stops, absolute frame=
                Plus3"
CDS             5209563..5210690
                /colour="255 0 0"
                /evidence=predicted
                /translation="PFASIIEHFSDLDDPRAAHRIEYSLEDIIIITLCAVLCGADNWV
                EVANYGRSKAQWLKQWIALPNG------VPSHDTFEWVFARLKPQQLQQCFLNWTQAI
                YQLSAGE-LIAIDGKTLRGAIAPGEQCSLIHMVSAWASHNRLVLGQRTVDEKSNEITA
                IPELLKVLELEG-ALVSIDAMGCQTAIAETIIEGQG-DYVLALKGNQGDLYNDVVQLF
                dhaCQTQFQGIEHDSYQTVEKGHGRIEHRTYWTMGQTDYLLGAE-RWAQLKSIGCVES
                CRRQPGHPG---TLQRRYYLLSIESDAQR---FADAVRSHWGIENQLHWILDVGFRED
                KLRACQGCSAQNLSVIRHIAANLLQQESTAKCGVKAKRLKAGWDDNYLVKILSVAAKG
                "
                /note="ISAs1 e-value= 1.8e-144 complete sequence hit
                coverage= 100%, between model( 389 aa) positions 1; 389
                length is 376aa with 16 gaps, 0 stops, absolute frame=
                Plus3"
CDS             5296908..5297147
                /colour="255 0 0"
                /evidence=predicted
                /translation="RNQQHYIRQRLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKY
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                     LDGGLQGLVQPI--RHQKPSRLSPEEQQQLKEMVLTQR"
                     /note="IS481 e-value= 1.2e-07 fragment hit coverage=
                     23.36%, between model( 351 aa) positions 1; 82 length is
                     80aa with 2 gaps, 0 stops, absolute frame= Plus3"
     CDS             5296935..5297342
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKYLDGG---LQ
                     GLVQPIRHQKPSRLSPEEQQQLKEMVLTQRPTDYGIDRNMWTGAILAVVIEQRFEVQL
                     KDSRIYELLSELGLSYQRAHRDYA--NADLNAQKEWVAA"
                     /note="IS630 e-value= 1.9e-29 fragment hit coverage=
                     37.50%, between model( 376 aa) positions 30; 170 length
                     is 136aa with 5 gaps, 0 stops, absolute frame= Plus3"
     CDS             5342181..5342333
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLCLILDNNPTHKG-KMRSQLAIHLEqmgltqsiQVEFLYLPSY
                     SPKLNLVE"
                     /note="IS630 e-value= 4.3e-06 fragment hit coverage=
                     11.70%, between model( 376 aa) positions 279; 322 length
                     is 51aa with 1 gaps, 0 stops, absolute frame= Plus3"
     CDS             5352645..5353340
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Plus3"
     CDS             5352645..5353772
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             5358090..5358287
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ASPIELSQQQHHCLTQIVRQTTNPYRLVRRASIILSAASGESNT
                     QISRQWQLDRNQVRYWRQRWLD"
                     /note="IS630 e-value= 4e-07 fragment hit coverage=
                     17.55%, between model( 376 aa) positions 1; 66 length is
                     66aa with 0 gaps, 0 stops, absolute frame= Plus3"
     CDS             5653053..5653250
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GKHKQILLVLDGAGWHTC---KNRVVPPG--IHLKILPPYSPEL
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                     QPAERLWRLADEPLAN-QCFETLDDLED"
                     /note="IS630 e-value= 1.4e-09 fragment hit coverage=
                     19.15%, between model( 376 aa) positions 275; 346 length
                     is 66aa with 6 gaps, 0 stops, absolute frame= Plus3"
     CDS             5666475..5666576
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKHRKGRIYGRIRR"
                     /note="IS200 e-value= 1.1e-12 fragment hit coverage=
                     22.08%, between model( 154 aa) positions 1; 34 length is
                     34aa with 0 gaps, 0 stops, absolute frame= Plus3"
     CDS             5666475..5666933
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKHRKGRIYGRIRRIXAIFLXAGT
                     SXRECHRrrsFNARSCSX-----VVEYSAEILRVQCGGLRKRKSAIYIARELGNSRNA
                     -TGHKFWSRGYFVSTVG-KDEEMICXYIRpgiRSKKSKSXSNXTCFGRSPSPLXGVPI
                     "
                     /note="IS200 e-value= 3.1e-10 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 153aa with 7 gaps, 8 stops, absolute frame=
                     Plus3"
     CDS             5666475..5666576
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKHRKGRIYGR-IRR"
                     /note="IS200_IS605 e-value= 1.5e-13 fragment hit
                     coverage= 22.88%, between model( 153 aa) positions 1; 35
                     length is 34aa with 1 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             5666475..5666906
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKHRKGRIYGR--IRRIXAIFLXA
                     GTsxRECHRrrsFNARSCSX-----VVEYSAEILRVQCGGLRKRKSAIYIARELGNSR
                     NA-TGHKFWSRGYFVSTVG-KDEEMICXYIR-----PGIRSKKSKSXSNXTCFGRS"
                     /note="IS200_IS605 e-value= 5.4e-10 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 144aa with 14 gaps, 6 stops, absolute frame=
                     Plus3"
     CDS             5666475..5666576
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTYRKLSHSVWECKYHVVFVPKHRKGRIYGRIRR"
                     /note="IS605 e-value= 1.1e-11 fragment hit coverage=
                     23.03%, between model( 152 aa) positions 1; 35 length is
                     34aa with 1 gaps, 0 stops, absolute frame= Plus3"
     CDS             5666475..5666906
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTYRKLSHSVWECKYHVVFVPKHRKGRIYGRIRRIXAIFLXAG
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                     ATGHKFWSRGYFVSTVGKDEEMICXYIRPGIRSKK-----SKSXSNXTCFGRS"
                     /note="IS605 e-value= 1.7e-10 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 144aa with 11 gaps, 7 stops, absolute frame=
                     Plus3"
     CDS             5666769..5666846
                     /colour="255 0 0"
                     /evidence=predicted
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                     /translation="GHKFWSRGYFVSTVG-KDEEMICXYIR"
                     /note="IS200 e-value= 3.8e-10 fragment hit coverage=
                     17.53%, between model( 154 aa) positions 102; 128 length
                     is 26aa with 1 gaps, 1 stops, absolute frame= Plus3"
     CDS             5666769..5666846
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GHKFWSRGYFVSTVG-KDEEMICXYIR"
                     /note="IS200_IS605 e-value= 1.3e-09 fragment hit
                     coverage= 17.65%, between model( 153 aa) positions 102;
                     128 length is 26aa with 1 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             5666769..5666846
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GHKFWSRGYFVSTVGKDEEMICXYIR"
                     /note="IS605 e-value= 5.7e-09 fragment hit coverage=
                     17.11%, between model( 152 aa) positions 102; 127 length
                     is 26aa with 0 gaps, 1 stops, absolute frame= Plus3"
     CDS             5908257..5908664
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MLLVRPISTESLRLLHRIYHSSRHHQVRQRAHCLILFAQGWPPY
                     TLASLFSVSPKTVYNWLKAWNNRG---FAGLYNHPGRGRKPMFNPDQQQQIYEWT-QA
                     SPIQ---------LNQVLAQIEQQWSVRVSKATVKRVLKQMDMSWHR"
                     /note="IS630 e-value= 8.7e-15 fragment hit coverage=
                     39.63%, between model( 376 aa) positions 1; 149 length is
                     136aa with 13 gaps, 0 stops, absolute frame= Plus3"
     CDS             5908317..5908655
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SSRHHQVRQRAHCLILFAQGWPPYTLASLFSVSPKTVYNWLKAW
                     NNRGFAGLYNH---PGRGRKPMfNPDQQQQIYEWTQASPIQLNQVLAQIEQQWSVR--
                     -VSKATVKRVLKQMDMS"
                     /note="IS481 e-value= 3.5e-09 fragment hit coverage=
                     33.62%, between model( 351 aa) positions 1; 118 length is
                     113aa with 6 gaps, 0 stops, absolute frame= Plus3"
     CDS             5916063..5917301
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IRIPLNLPDI--RVLELSKTERGDWL------IKIESTLQGTTC
                     HQCGREITDL-HCHDQ-PFRIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWH
                     EPRSPNTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADL
                     KVMGMDEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-I
                     DLRQTIERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRR
                     ELS------------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLER
                     LFA--YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTT
                     INNWMDEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQT
                     FAVTXTL"
                     /note="ISL3  e-value= 1.8e-43 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
                     length is 413aa with 44 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             5916222..5917301
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWHEPRSP
                     NTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADLKVMGM
                     DEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-IDLRQT
                     IERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRRELS--
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                ----------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLERLFA--
                YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTTINNWM
                DEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQTFAVTX
                TL"
                /note="ISL3  e-value= 1e-49 fragment hit coverage= 86.03%,
                between model( 451 aa) positions 64; 451 length is 360aa
                with 34 gaps, 1 stops, absolute frame= Plus3"
CDS             5942076..5942741
                /colour="255 0 0"
                /evidence=predicted
                /translation="-----TGVYKQTF-KRMLHAWHTYHlSHSNAGRPPKLCRPDQLL
                VALQYWREYRTYFHIAGDWEVSESTVCRIVHQVETALMNSGLFRLPGKKHLIQGFERP
                DVVVMDVTETPIERPQKGQKAYYSGKKRDIPSNARLLLTAT--LXRLSV--------X
                ALAQAVGMIFR-------------YSRVQVSIS--IQIPRVCKIADIKGLQPTTPTAM
                FLS--------RSHNMVNXLPCSESITVHXVRNEWALNTLIAA"
                /note="IS5_ISL2    e-value= 1.8e-23 complete sequence hit
                coverage= 100%, between model( 260 aa) positions 1; 260
                length is 222aa with 39 gaps, 4 stops, absolute frame=
                Plus3"
CDS             5942136..5942447
                /colour="255 0 0"
                /evidence=predicted
                /translation="SHSNAGRPPKLCRPDQLLVALQYWREYRTYFHIAGDWEVSESTV
                CRIVHQVETALMNSGLFRLPGKKHLIQGFERPDVVVMDVTETPIERPQKGQKAYYSGK
                KR"
                /note="IS5_ISL2    e-value= 5e-44 fragment hit coverage=
                40%, between model( 260 aa) positions 26; 129 length is
                104aa with 0 gaps, 0 stops, absolute frame= Plus3"
CDS             5992275..5993312
                /colour="255 0 0"
                /evidence=predicted
                /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                /note="IS630 e-value= 6.7e-25 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Plus3"
CDS             5992275..5993312
                /colour="255 0 0"
                /evidence=predicted
                /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                /note="IS630 e-value= 4.9e-24 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Plus3"
CDS             5992335..5992493
                /colour="255 0 0"
                /evidence=predicted
                /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
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                     QQGGIEGLK"
                     /note="IS481 e-value= 3.7e-09 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Plus3"
     CDS             6109407..6109544
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                     RWHRR"
                     /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Plus3"
     CDS             6263616..6264854
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IRIPLNLPDI--RVLELSKTERGDWL------IKIESTLQGTTC
                     HQCGREITDL-HCHDQ-PFRIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWH
                     EPRSPNTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADL
                     KVMGMDEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-I
                     DLRQTIERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRR
                     ELS------------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLER
                     LFA--YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTT
                     INNWMDEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQT
                     FAVTXTL"
                     /note="ISL3  e-value= 1.8e-43 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
                     length is 413aa with 44 gaps, 1 stops, absolute frame=
                     Plus3"
     CDS             6263775..6264854
                     /colour="255 0 0"
                     /evidence=predicted
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                     NTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADLKVMGM
                     DEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-IDLRQT
                     IERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRRELS--
                     ----------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLERLFA--
                     YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTTINNWM
                     DEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQTFAVTX
                     TL"
                     /note="ISL3  e-value= 1e-49 fragment hit coverage= 86.03%,
                     between model( 451 aa) positions 64; 451 length is 360aa
                     with 34 gaps, 1 stops, absolute frame= Plus3"
     CDS             6300402..6300794
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VDTHGQSEVGFAFCYLLNFQLMPRFKGINKQKLYLPMsGQKKKY
                     VYLKAIVKRPMRWDLVREQYEPMIQFTTAMKQGTAEPEAILSRFTRNNIKHPTYLALA
                     ELGRAIKTIFLCQYLHDEALRQEINEGLN"
                     /note="Tn3   e-value= 7.4e-17 fragment hit coverage=
                     12.95%, between model( 1004 aa) positions 764; 893 length
                     is 131aa with 0 gaps, 0 stops, absolute frame= Plus3"
     CDS             6306396..6307874
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DSYHTRVYMNGRDLGLKQAEAAYIAEISTRTGQRIEAGTHQPNR
                     -GRLQD-------QRTVPDPLADVWE---DELEPMLRRDPRLKPMTLYEYLQD-KYPG
                     QYPQVlrtlQRRVRTWKALHGPS-----PEVMFELRHEPGVQGFSDFTELKGITITIA
                     GQPFEHLIYHYRLGYSGWRYAQIIQGgESFVALSEGLQNAFAACGGVPQQHRTDSLSA
                     AYRNMGGRRS-KNLTRLYDELCDHYRLEPTRNNKG--IAHENGSIESPHGHLKNRIKQ
                     AIYLRGSAD-----FTSVAEYQALIDAQVAKLNQQCQTK------YEQEKDHLQPLPK
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                     YRTPDYEVLTA----KVSKRSTIDVRCILYTVPSRLIGRQLELHLYHDRIVGYLERHP
                     VVELPRKRVSGkGKRRDRCINYRHVIGSMRLKPRAFIYCTWQSDLLPNPEYRQIWEQL
                     KAQFDLEQAAKIIVEALYIAAVQDKEQAVAVYLQQQLQASSLTLNRLKKQFEPPQMKQ
                     VPDLSIeQHS----LELYDKLLPS"
                     /note="IS21_ORF1   e-value= 1.3e-21 complete sequence hit
                     coverage= 100%, between model( 525 aa) positions 1; 525
                     length is 493aa with 39 gaps, 0 stops, absolute frame=
                     Plus3"
     CDS             6306666..6307496
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QYPQVLRTLQRRVRTWKALHGPS-----PEVMFELRHEPGVQGF
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                     GGVPQQHRTDSLSAAYRNMGGRRS-KNLTRLYDELCDHYRLEPTRNNKG--IAHENGS
                     IESPHGHLKNRIKQAIYLRGSAD-----FTSVAEYQALIDAQVAKLNQQCQTK-----
                     -YEQEKDHLQPLPKYRTPDYEVLTA----KVSKRSTIDVRCILYTVPSRLIGRQLELH
                     LYHDRIVGY-----LERHPVVELPRKRVS"
                     /note="IS21_ORF1   e-value= 1e-29 fragment hit coverage=
                     57.90%, between model( 525 aa) positions 99; 402 length
                     is 277aa with 28 gaps, 0 stops, absolute frame= Plus3"
     CDS             complement(6395489..6394549)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 1.1e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Minus1"
     CDS             complement(6395489..6394549)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 2.2e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Minus1"
     CDS             complement(6348974..6348694)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SISFRaMQCIHCQSEN-VVKNGTKT-LKtaqvvQYFLCKDCGRR
                     FN-ERSGTPMARLRtpvETISMAINARTEGLGIRAAGRVLGKSPTSILLWEKR"
                     /note="IS1_ORF1    e-value= 9.8e-10 fragment hit coverage=
                     36.82%, between model( 239 aa) positions 1; 88 length is
                     94aa with 3 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(6343880..6343381)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QVTLIEAAVETTQQRFGWRVYVTNAPLEELSFEEAVLTVRDAWI
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                     QESGFSRLKGNPLGASPLFVQRDDHAKGLMHLLSLGLRILTLIEFVVQRRLKQ-----
                     --------------HKEkLFGLFPGNPKRATTRPTTERILRAFKDISLTILGVKDeey
                     ghVSPLTSLQQRILELLGLAPDIYSS"
                     /note="IS4   e-value= 3e-08 fragment hit coverage= 37.04%,
                     between model( 486 aa) positions 307; 486 length is 167aa
                     with 19 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(6314132..6313894)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TLAKLDHFELFILDEIGYDIKTDDETSIQSELIVHRYERRSFKI
                     TANHPFSTRXCIFC-DSSMTVAAIDRFVYHAFIIEIK"
                     /note="IS21_ORF2   e-value= 1.3e-09 fragment hit coverage=
                     31.40%, between model( 258 aa) positions 157; 237 length
                     is 80aa with 1 gaps, 1 stops, absolute frame= Minus1"
     CDS             complement(6234089..6232612)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DSYHTRVYMNGRDLGLKQAEAAYIAEISTRTGQRIEAGTHQPNR
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                     QYPQVlrtlQRRVRTWKALHGPS-----PEVMFELRHEPGVQGFSDFTELKGITITIA
                     GKPFEHLIYHYRLGYSGWRYAQIIQGgESFVALSEGLQNAFAACGGVPTQHRTDSLSA
                     AYRNMGGRRS-KNLTRLYDELCDHYRLEPTRNNKG--VAHENGSIESPHGHLKNRIKQ
                     AIYLRGSAD-----FTSVGEYQALIDAQVA---KLNQQC---QAKYEQEKEHLQPLPK
                     YRTPDYEVLTA----KVSKRSTIDVRCILYTVPSRLIGRQLELHLYHDRIVGYLERHP
                     VVELPRKRVSGkGKRRDRCINYRHVIGSMRLKPRAFIYCTWQSDLLPNPEYRQIWEQL
                     KAQFDLEQAAKIIVEALYIAAVQDKEQAVAVYLQQQLRSSSLTLNRLKKQFEPPQMKQ
                     VPDLSIeQHS----LELYDKLLPS"
                     /note="IS21_ORF1   e-value= 3.3e-24 complete sequence hit
                     coverage= 100%, between model( 525 aa) positions 1; 525
                     length is 493aa with 39 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(6233819..6232990)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QYPQVLRTLQRRVRTWKALHGPS-----PEVMFELRHEPGVQGF
                     SDFTELKGITITIAGKPFEHLIYHYRLGYSGWRYAQIIQGgESFVALSEGLQNAFAAC
                     GGVPTQHRTDSLSAAYRNMGGRRS-KNLTRLYDELCDHYRLEPTRNNKG--VAHENGS
                     IESPHGHLKNRIKQAIYLRGSAD-----FTSVGEYQALIDAQVA---KLNQQC---QA
                     KYEQEKEHLQPLPKYRTPDYEVLTA----KVSKRSTIDVRCILYTVPSRLIGRQLELH
                     LYHDRIVGY-----LERHPVVELPRKRVS"
                     /note="IS21_ORF1   e-value= 4.2e-32 fragment hit coverage=
                     57.90%, between model( 525 aa) positions 99; 402 length
                     is 277aa with 28 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(6059630..6059137)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LEKTGIESKKKTYGYR--ERD--ETQR---QAFIERLQTKHP--
                     HQIVYVDEAGIDNRADYPY-GYCPVG------------QRFYD-LKSG-KRTERVSFIA
                     ALKEGQL--FSPMTFEGSCNRLLFEAWLQQSLI-SQLQLgdVIVIDNASFHHGQRIEE
                     IVAEAG--CEIWYLPSYSPDLNKIERWWFVLKN"
                     /note="IS630 e-value= 3e-16 fragment hit coverage=
                     50.80%, between model( 376 aa) positions 140; 330 length
                     is 165aa with 28 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(6014810..6014614)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ASPIELSQQQHHCLTQIVRQTTNPYRLVRRASIILSAASGESNT
                     QISRQWQLDRNQVRYWRQRWLD"
                     /note="IS630 e-value= 4e-07 fragment hit coverage=
                     17.55%, between model( 376 aa) positions 1; 66 length is
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                     66aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5728283..5728174)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VMKVMI-CPHCQSDR-LSKNGKRR-NQQCYVCKDCRKQFV"
                     /note="IS1_ORF1    e-value= 4.1e-06 fragment hit coverage=
                     16.74%, between model( 239 aa) positions 1; 40 length is
                     37aa with 3 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5719823..5719186)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MASKTTNVkPVVVSLWKLLSKSELIHPLKAXSISYCLKRYLWQV
                     L-----PGS------VMFLKAGYKSTXTVsMKQCLVLXTYHQKKGR------------
                     ---LTLQCDEMWSFVNDKSNKQWIWLALDVITREIVGVYVGARSKQGARQLWNSLPGI
                     YRQCAVaYTDFWDAYGCVFPKQ-RHQAVGKETGQTCYIERFNCTMRQRVSRLVRKTLS
                     FSKKLENHIGAIWMFVHHYNAS"
                     /note="IS1_ORF2    e-value= 4.6e-13 complete sequence hit
                     coverage= 100%, between model( 237 aa) positions 1; 237
                     length is 213aa with 27 gaps, 3 stops, absolute frame=
                     Minus1"
     CDS             complement(5719571..5719195)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DEMWSFVNDKSNKQWIWLALDVITREIVGVYVGA----RSKQGA
                     RQLwNSLPGIYRQCAVAYTDFWDAYgCVFPKQRHQAVGKEtgQTCYIERFNCTMRQRV
                     SRLVRKTLSFSKKLENHIGAIWMF---VHHY"
                     /note="IS1_ORF1    e-value= 4.6e-14 fragment hit coverage=
                     53.97%, between model( 239 aa) positions 111; 239 length
                     is 126aa with 7 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5719571..5719186)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DEMWSFVNDKSNKQWIWLALDVITREIVGVYVGARSKQGARQLW
                     NSLPGIYRQCAVaYTDFWDAYGCVFPKQ-RHQAVGKETGQTCYIERFNCTMRQRVSRL
                     VRKTLSFSKKLENHIGAIWMFVHHYNAS"
                     /note="IS1_ORF2    e-value= 6.2e-32 fragment hit coverage=
                     54.43%, between model( 237 aa) positions 109; 237 length
                     is 129aa with 1 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5718014..5717818)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ASPIELSQQQHHCLTQIVRQTTNPYRLVRRASIILSAASGESNT
                     QISRQWQLDRNQVRYWRQRWLD"
                     /note="IS630 e-value= 4e-07 fragment hit coverage=
                     17.55%, between model( 376 aa) positions 1; 66 length is
                     66aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5509199..5509063)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                     RWHRR"
                     /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5354885..5354170)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YLSPES-LXCRASSKVVSMXSTVGSPS---------ILARISDL
                     FPHCWRLGSLXINCLPYCppGRDRSDELRTLSLTRSEISATR---------VRATGCR
                     CDGCDXNAHXTSPDKTKSVLF----RKKKRHTFKCQIIANRNTLEIICLNVGPGRRHD
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                     FQISKVSGIHIHPDTESLQDSGYQGIAAYHANSYVPLKKPQHGELTSLQREYNRALSQ
                     ERMGIEHINRSLKIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 8.9e-38 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 239aa with 23 gaps, 5 stops, absolute frame=
                     Minus1"
     CDS             complement(5354570..5354170)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KKKRHTFKCQIIANRNTLEIICLNVGPGRRHDFQISKVSGIHIH
                     PDTESLQDSGYQGIAAYHANSYVPLKKPQHGELTSLQREYNRALSQERMGIEHINRSL
                     KIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 4.7e-61 fragment hit coverage=
                     51.54%, between model( 260 aa) positions 127; 260 length
                     is 134aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5242232..5241538)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5242232..5241106)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT--------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(5175581..5174845)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-----TGVYKRTFkrMLHAWHTYHLSRSN--AGRPPKLCQCDQL
                     LVTLQYWREYRTYFHIAGDWEVSESTVCRIVHQVETALMNSGLFRLPGQKSLLQGFER
                     PDVVVMDVTETPIERPQTRQKAYYSGKKRDIPSNARLSLTATLXrlsaltLVQVVG--
                     -------MIFRSSRVQVSISIQIPRVCKIADIKGLQ-----PIMP-TAMFLSRSHNTV
                     NXLPCSESITVLXVRNEWALNTLIAAXRFSEFCRSAIAIVVVATRCGVTX"
                     /note="IS5_ISL2    e-value= 3.2e-21 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 246aa with 22 gaps, 5 stops, absolute frame=
                     Minus1"
     CDS             complement(5175521..5175211)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SRSNAGRPPKLCQCDQLLVTLQYWREYRTYFHIAGDWEVSESTV
                     CRIVHQVETALMNSGLFRLPGQKSLLQGFERPDVVVMDVTETPIERPQTRQKAYYSGK
                     KR"
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                     /note="IS5_ISL2    e-value= 7.6e-44 fragment hit coverage=
                     40%, between model( 260 aa) positions 26; 129 length is
                     104aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(5069105..5069026)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TFSCLNRYRRLGKDYELYPETSEAMIY"
                     /note="IS5_IS1031  e-value= 5.8e-07 fragment hit coverage=
                     9.15%, between model( 295 aa) positions 246; 272 length
                     is 27aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4933280..4932616)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKYLHLGMMsDIKHKSLPAIARICGLANEQGLLHFLTESPWRPS
                     aLEQaRLNLILQVLSGRPLTLIID------------------ETEDRKKGKQTDYVQR
                     QYLGNLGKVDNGIvAVTAYGVVEHMTLPLMFRVYKPKsRLQSGD---------VYHSK
                     PEIAVSMIDELLAHGCQFDLVLADSLYGESGSTFVSHLQALQLPYVVAIRSNHGLWLP
                     KEQRVRCNRWRAFEHVFSDGS---------------CETRYIREVI"
                     /note="IS4   e-value= 4.5e-12 fragment hit coverage=
                     53.29%, between model( 486 aa) positions 1; 259 length is
                     222aa with 42 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4933280..4932184)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKYLHLGMMsDIKHKSLPAIARICGLANEQGLLHFLTESPWRPS
                     aLEQaRLNLILQVLSGRPLTLIID------------------ETEDRKKGKQTDYVQR
                     QYLGNLGKVDNGIvAVTAYGVVEHMTLPLMFRVYKPKsRLQSGD---------VYHSK
                     PEIAVSMIDELLAHGCQFDLVLADSLYGESGSTFVSHLQALQLPYVVAIRSNHGLWLP
                     KEQRVRCNRWRAFEHVFSDGS----------------------------CETRYIREV
                     IYGQR----LAQQfWDITTDPQNLPKASTW------------------------YVMS
                     EIE---GVKYHQIGNFYGLRNWVEYGLKQSKN-ELGWADFRVTDYDQIERWWQVVMSA
                     YLMVSLHSDRFEL----------------------------------PTGLSMKQQVP
                     PVIETFSQ-----HRYWQTGKGWKHLLNNLRLVIIQSLILFD"
                     /note="IS4   e-value= 1.2e-06 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 366aa with 126 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(4908698..4908313)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                     RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                     ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                     /note="IS630 e-value= 1.1e-13 fragment hit coverage=
                     38.83%, between model( 376 aa) positions 188; 333 length
                     is 129aa with 20 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4716020..4715806)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="REIHEAIGVSIRTIERVRMRFVEEG---LEAAINQRsGAGRKRK
                     IQGEQEAHLIALRCSEPPVG----HARWTLRLLAD"
                     /note="IS630 e-value= 9.9e-08 fragment hit coverage=
                     20.74%, between model( 376 aa) positions 44; 121 length
                     is 72aa with 7 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4612568..4612411)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLPHAQICQLCQISRPTLAKTLRLY
                     QQGGIEGLK"
                     /note="IS481 e-value= 1.1e-08 fragment hit coverage=
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                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4319990..4319854)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                     RWHRR"
                     /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4252406..4251982)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GRQRFNVLGALNAVTKEvTSITNHTYINSHSMCLLLAKLALLDP
                     VI--PISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKEC
                     LYSKYYSDFHSFKGAIQQCIDQCNTEHKAKLTSLLSLKFQSFQK"
                     /note="IS630 e-value= 6.2e-18 fragment hit coverage=
                     38.56%, between model( 376 aa) positions 232; 376 length
                     is 142aa with 4 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4222007..4221850)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLPHAQICQLCQISRPTLAKTLRLY
                     QQGGIEGLK"
                     /note="IS481 e-value= 1.1e-08 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4221497..4221091)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MLLVRPISTESLRLLHRIYHSSRHHQVRQRAHCLILFAQGWPPY
                     TLASLFSVSPKTVYNWLKAWNNRG---FAGLYNHPGRGRKPMFNPDQQQQIYEWT-QA
                     SPIQ---------LNQVLAQIEQQWSVRVSKATVKRVLKQMDMSWHR"
                     /note="IS630 e-value= 8.7e-15 fragment hit coverage=
                     39.63%, between model( 376 aa) positions 1; 149 length is
                     136aa with 13 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4221437..4221100)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SSRHHQVRQRAHCLILFAQGWPPYTLASLFSVSPKTVYNWLKAW
                     NNRGFAGLYNH---PGRGRKPMfNPDQQQQIYEWTQASPIQLNQVLAQIEQQWSVR--
                     -VSKATVKRVLKQMDMS"
                     /note="IS481 e-value= 3.5e-09 fragment hit coverage=
                     33.62%, between model( 351 aa) positions 1; 118 length is
                     113aa with 6 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4218878..4218454)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GRQRFNVLGALNAVTKEvTSITNHTYINSHSMCLLLAKLALLDP
                     VI--PISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKEC
                     LYSKYYSDFHSFKGAIQQCIDQCNTEHKAKLTSLLSLKFQSFQK"
                     /note="IS630 e-value= 6.2e-18 fragment hit coverage=
                     38.56%, between model( 376 aa) positions 232; 376 length
                     is 142aa with 4 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(4135019..4134772)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MQCPLCGHPT-THXHGKTSKGSQRYRCLHCXRTFSEtfDTLYYH
                     RQISPQTLQTILQSHAEGSSLRGLARITGVAYNTCVSVVR"
                     /note="IS1_ORF1    e-value= 2.5e-12 fragment hit coverage=
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                     34.31%, between model( 239 aa) positions 6; 87 length is
                     83aa with 1 gaps, 2 stops, absolute frame= Minus1"
     CDS             complement(4135019..4134334)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-----MQCPLCGHPT-THXHGKTSKGSQRYRCLHCXRTFSEtfD
                     TLYYHRQISPQTLQTILQSHAEGSSLRGLARITGVAYNTCVSVVRSA--SHKAQMIHN
                     Q-------EGQAVSTDVinaDALWSFVKKSKsTVNRKNXASAIAGXRX-------VLP
                     KTVAXCS--VVVLANIPTSSLKHXLRILKAKPPVtIGKRMVETVTHANYPMRXSItxV
                     RPXRNAXSgpmeyyGNRPGAGIDDKTNLV-KSGNRV"
                     /note="IS1_ORF1    e-value= 1.6e-06 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 229aa with 25 gaps, 10 stops, absolute frame=
                     Minus1"
     CDS             complement(4134977..4134790)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GKTSKGSQRYRCLHCXRTFSETFdtLYYHRQisPQTLQTILQSH
                     AEGSSLRGLARITGVAYNT"
                     /note="IS1_ORF2    e-value= 4.3e-06 fragment hit coverage=
                     24.89%, between model( 237 aa) positions 21; 79 length is
                     63aa with 0 gaps, 1 stops, absolute frame= Minus1"
     CDS             complement(3406541..3406153)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FFMDESGFSLVPCIPY-GWQPIG-------------TYL-EIPT
                     RSSKRLNVLGFLSRRQGL--HAYTSEQTITSEVVShCIDTFFADV--ELPTVIVVDQA
                     PIHTSQsiyEMKAEWAERG--ITLFELPSYSPHLNLIERLWQFMKYQWI"
                     /note="IS630 e-value= 6.5e-11 fragment hit coverage=
                     39.10%, between model( 376 aa) positions 187; 333 length
                     is 130aa with 21 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(2707001..2705968)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QRFIQGLSPETIHLLSRIHRHSYHHQVRQRAHCILLSFEGFNVT
                     ELMSIFAVTRKTVYTWLDDWDNHC---LVGLYDQPGRGRKPKLNDVQ-KEQIRAWAKM
                     TP---------HNLNAVLAKIKEAWNIAVSKTTLKRILKSCSMSWRRLRRVVAGQPDP
                     VEYETK-----RHQLEVLKRQEEKGELdlrYLDESGFCLVPYVPY-AWQEKG------
                     --------ETLGLPSQRSSRFNVLGLMNRHNDL-TSYVFDKSITSAVVVACIDDFSRT
                     C--DQHTVVVMDQASVHKNAEIEEKIEDWKAkNVEIFWLPTYSPHLNLIEIFWRFMKY
                     EWIEFAAYKCLGSLSLYIDKILKGFgKDYVIDFGXVLTKAVFISDIY"
                     /note="IS630 e-value= 1.1e-19 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 345aa with 36 gaps, 1 stops, absolute frame=
                     Minus1"
     CDS             complement(2707001..2706100)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QRFIQGLSPETIHLLSRIHRHSYHHQVRQRAHCILLSFEGFNVT
                     ELMSIFAVTRKTVYTWLDDWDNHC---LVGLYDQPGRGRKPKLNDVQ-KEQIRAWAKM
                     TP---------HNLNAVLAKIKEAWNIAVSKTTLKRILKSCSMSWRRLRRVVAGQPDP
                     VEYETK-----RHQLEVLKRQEEKGELdlrYLDESGFCLVPYVPY-AWQEKG------
                     --------ETLGLPSQRSSRFNVLGLMNRHNDL-TSYVFDKSITSAVVVACIDDFSRT
                     C--DQHTVVVMDQASVHKNAEIEEKIEDWKAkNVEIFWLPTYSPHLNLIEIFWRFMKY
                     EWI"
                     /note="IS630 e-value= 1.1e-24 fragment hit coverage=
                     88.56%, between model( 376 aa) positions 1; 333 length is
                     301aa with 36 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(2587106..2586868)
                     /colour="255 0 0"
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                     /evidence=predicted
                     /translation="RNQQHYIRQRLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKY
                     LDGGLQGLVQPI--RHQKPSRLSPEEQQQLKEMVLTQR"
                     /note="IS481 e-value= 1.2e-07 fragment hit coverage=
                     23.36%, between model( 351 aa) positions 1; 82 length is
                     80aa with 2 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(2587079..2586673)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKYLDGG---LQ
                     GLVQPIRHQKPSRLSPEEQQQLKEMVLTQRPTDYGIDRNMWTGAILAVVIEQRFEVQL
                     KDSRIYELLSELGLSYQRAHRDYA--NADLNAQKEWVAA"
                     /note="IS630 e-value= 1.9e-29 fragment hit coverage=
                     37.50%, between model( 376 aa) positions 30; 170 length
                     is 136aa with 5 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(2498918..2498134)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="CLAAXPNATLSHFQQSMKCLYCVIM--EHNSTHCLPLMGGRHQI
                     KALSQSNRRLKMGLIGFTRSWISPNELNLHRWHQEVEXAASSKRLFEK-----XVKLS
                     RYXsVNTQTLDRTXRAMPTAYDSDLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLN
                     AIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRMQERVSE-----
                     ------------------------DRHPSPSAAICDAQSVKVGNPRCHSIGFDGgkmv
                     KGRKRHVLVDTLGLVL-MVMVTAAN"
                     /note="IS5_IS427   e-value= 7.3e-07 complete sequence hit
                     coverage= 100%, between model( 296 aa) positions 1; 296
                     length is 262aa with 39 gaps, 5 stops, absolute frame=
                     Minus1"
     CDS             complement(2498615..2497765)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                     ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVH
                     INEHLRMQERVSEDRHPSPSAAICDAQSVKVGNPRCH-SIGFDGGKMVKGRKRHVLVD
                     TLGLVLMVMVTAANISDQR-GAKILFWKARRQGaslSRLVRIWADAGYQGQALMKWVM
                     DRSQYVLEVIKRSDNLAGFQVVSKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                     AMIRLMVRRLAQEHXNFSNSLX"
                     /note="IS5_IS1031  e-value= 3.2e-108 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 284aa with 14 gaps, 3 stops, absolute frame=
                     Minus1"
     CDS             complement(2498573..2497765)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                     IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRMQERVSEDRHPSP
                     SAAICDAQSVKVGNPRCH-SIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
                     -GAKILFWKARRQGaslSRLVRIWADAGYQGQALMKWVMDRSQYVLEVIKRSDNLAGF
                     QVVSKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHXNFSN
                     SLX"
                     /note="IS5_IS1031  e-value= 2.1e-110 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 2 stops, absolute frame=
                     Minus1"
     CDS             complement(2498564..2498326)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRM"
                     /note="IS5_IS427   e-value= 3.3e-18 fragment hit coverage=
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                27.70%, between model( 296 aa) positions 125; 206 length
                is 80aa with 2 gaps, 0 stops, absolute frame= Minus1"
CDS             complement(2405255..2405098)
                /colour="255 0 0"
                /evidence=predicted
                /translation="HHPHPRVQRRMEVLYLKSQGLPHAQICQLCQISRPTLAKTLRLY
                QQGGIEGLK"
                /note="IS481  e-value= 1.1e-08 fragment hit coverage=
                15.10%, between model( 351 aa) positions 1; 53 length is
                53aa with 0 gaps, 0 stops, absolute frame= Minus1"
CDS             complement(2383214..2382808)
                /colour="255 0 0"
                /evidence=predicted
                /translation="MLLVRPISTESLRLLHRIYHSSRHHQVRQRAHCLILFAQGWPPY
                TLASLFSVSPKTVYNWLKAWNNRG---FAGLYNHPGRGRKPMFNPDQQQQIYEWT-QA
                SPIQ---------LNQVLAQIEQQWSVRVSKATVKRVLKQMDMSWHR"
                /note="IS630  e-value= 8.7e-15 fragment hit coverage=
                39.63%, between model( 376 aa) positions 1; 149 length is
                136aa with 13 gaps, 0 stops, absolute frame= Minus1"
CDS             complement(2383154..2382817)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SSRHHQVRQRAHCLILFAQGWPPYTLASLFSVSPKTVYNWLKAW
                NNRGFAGLYNH---PGRGRKPMfNPDQQQQIYEWTQASPIQLNQVLAQIEQQWSVR--
                -VSKATVKRVLKQMDMS"
                /note="IS481  e-value= 3.5e-09 fragment hit coverage=
                33.62%, between model( 351 aa) positions 1; 118 length is
                113aa with 6 gaps, 0 stops, absolute frame= Minus1"
CDS             complement(2285066..2284843)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SQMSTLTCPNCRSQN-VVKNGRIHNGKQNHKCKTCGRQFV--EA
                PQQKRIDSSTKGLIDKLLLEKIPLAGIARVCDVS"
                /note="IS1_ORF1    e-value= 3.6e-14 fragment hit coverage=
                32.64%, between model( 239 aa) positions 1; 78 length is
                75aa with 3 gaps, 0 stops, absolute frame= Minus1"
CDS             complement(1924193..1923499)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                51.23%, between model( 486 aa) positions 1; 249 length is
                232aa with 27 gaps, 0 stops, absolute frame= Minus1"
CDS             complement(1924193..1923067)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                /note="IS4   e-value= 9.9e-07 complete sequence hit
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                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(1895579..1895383)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ASPIELSQQQHHCLTQIVRQTTNPYRLVRRASIILSAASGESNT
                     QISRQWQLDRNQVRYWRQRWLD"
                     /note="IS630 e-value= 4e-07 fragment hit coverage=
                     17.55%, between model( 376 aa) positions 1; 66 length is
                     66aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(1336244..1335394)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TQTLDRTXRAM-----PTAYDSDLTAEQWELLEPLIPAAK----
                     ---PGGRPRTTDMRSVLNAILYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVH
                     INEHLRMQERVSEDRHPSPRAAICDAQSVKVGNPRCH-SIGFDGGKQIKGRKRHVLVD
                     TLGLVLMVIVTAANISDQR-GAKILFWKARRQGaslSRLVRIWADAGYQGQAFMKWVM
                     DRFQYVLEVIKRSDNLAGFQVVPKRWIVERTFGWLLWSRRLNKDYELLTRTAEALAYV
                     AMIRLMVRRLAQEYXNFSNSLX"
                     /note="IS5_IS1031  e-value= 3e-112 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 284aa with 14 gaps, 3 stops, absolute frame=
                     Minus1"
     CDS             complement(1336202..1335394)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTAEQWELLEPLIPAAK-------PGGRPRTTDMRSVLNA
                     ILYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRMQERVSEDRHPSP
                     RAAICDAQSVKVGNPRCH-SIGFDGGKQIKGRKRHVLVDTLGLVLMVIVTAANISDQR
                     -GAKILFWKARRQGaslSRLVRIWADAGYQGQAFMKWVMDRFQYVLEVIKRSDNLAGF
                     QVVPKRWIVERTFGWLLWSRRLNKDYELLTRTAEALAYVAMIRLMVRRLAQEYXNFSN
                     SLX"
                     /note="IS5_IS1031  e-value= 2.4e-114 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 2 stops, absolute frame=
                     Minus1"
     CDS             complement(1336193..1335955)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTAEQWELLEPLIPAAKP-GGRPRT-TDMRSVLNAILYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRM"
                     /note="IS5_IS427   e-value= 1.2e-20 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(1225547..1225171)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="EHRKSEDFALCMQYLVDGLFPQADKLHVVLDNLNTHspaalyKT
                     FNPDEALRILK-RIQFHYTPKHGSWLNMIEFEFSALSRQCLNRRIP-DIEQLRYEVTA
                     WEKRRNHDKATVNWLFTVDDARTKLS"
                     /note="IS630 e-value= 2.3e-07 fragment hit coverage=
                     32.45%, between model( 376 aa) positions 255; 376 length
                     is 126aa with 2 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(1184315..1183279)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
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                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSRHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630 e-value= 3.5e-21 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(1184315..1183279)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSRHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630 e-value= 3.1e-22 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(1184255..1184098)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                     QQGGIEGLK"
                     /note="IS481 e-value= 3.7e-09 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(1119713..1118947)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="--IYPSFITLGRXKNRLLDLLHnxvcdMVLSHSNAGRPPKLCRP
                     DQLLVALQDWREYRTYFHIAGDWGVSESTVCRIVQQVEtaHELRTLP----PTRQETS
                     NTRIXAAXCCRDGCDXDTDXTSpKRTKSVLCRKKKRHTLKCQIIADRNTLEIICLSFG
                     KGRRHDFQVFKVSGVHIHPDTESLLDSGYQG------NSYVPLKKPQQGELTSLEREY
                     NHALSQERIGIEHINRSLKMFRILSERYCNRRRRYSLRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 6.5e-76 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 256aa with 12 gaps, 5 stops, absolute frame=
                     Minus1"
     CDS             complement(1119629..1118947)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SHSNAGRPPKLCRPDQLLVALQDWREYRTYFHIAGDWGVSESTV
                     CRIVQQVEtaHELRTLP----PTRQETSNTRIXAAXCCRDGCDXDTDXTSpKRTKSVL
                     CRKKKRHTLKCQIIADRNTLEIICLSFGKGRRHDFQVFKVSGVHIHPDTESLLDSGYQ
                     G------NSYVPLKKPQQGELTSLEREYNHALSQERIGIEHINRSLKMFRILSERYCN
                     RRRRYSLRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 1.1e-77 fragment hit coverage=
                     90.38%, between model( 260 aa) positions 26; 260 length
                     is 228aa with 10 gaps, 4 stops, absolute frame= Minus1"
     CDS             complement(826598..826267)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QRVKDRAAMIRLSHQGMYVEKIAALFQCNVRTVRQTLHRWQQKG
                     ---LGGLWDAPHPGAQRRWNPED-IEYLETCLRQEERTY-------NSQQLSQKLAKE
                     RNVHLSADRIRQILKKRGXS"
                     /note="IS630 e-value= 8.8e-10 fragment hit coverage=
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                     32.45%, between model( 376 aa) positions 25; 146 length
                     is 111aa with 11 gaps, 1 stops, absolute frame= Minus1"
     CDS             complement(741935..741721)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="REIHEAIGVSIRTIERVRMRFVEEG---LEAAINQRsGAGRKRK
                     IQEEQEAHLIALRCSEPPVG----HARWTLRLLAD"
                     /note="IS630  e-value= 2.5e-08 fragment hit coverage=
                     20.74%, between model( 376 aa) positions 44; 121 length
                     is 72aa with 7 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(669422..669199)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SQMSTLTCPNCRSQN-VVKNGRIHNGKQNHKCKTCGRQFV--EA
                     PQQKRIDSSTKGLIDKLLLEKIPLAGIARVCDVS"
                     /note="IS1_ORF1    e-value= 3.6e-14 fragment hit coverage=
                     32.64%, between model( 239 aa) positions 1; 78 length is
                     75aa with 3 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(517589..517393)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GKHKQILLVLDGAGWHTC---KNRVVPPG--IHLKILPPYSPEL
                     QPAERLWRLADEPLAN-QCFETLDDLED"
                     /note="IS630  e-value= 1.4e-09 fragment hit coverage=
                     19.15%, between model( 376 aa) positions 275; 346 length
                     is 66aa with 6 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(481079..480364)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YLSPES-LXCRASSKVVSMXSTVGSPS---------ILARISDL
                     FPHCWRLGSLXINRLPYCppGRDRSDELRTLSLTRSEISATR---------VRATGCR
                     CDGCDXNAHXTSPDKTKSVLF----RKKKRHTFKYQIIANRNTLEIICLNVGPGRRHD
                     FQIFKVSGIHIHPDTESLQDSGYQGIAAYHTNSYVPLKKPQHGELTSLQREYNRALSQ
                     ERMGIEHINRSLKIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 1e-38 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 239aa with 23 gaps, 5 stops, absolute frame=
                     Minus1"
     CDS             complement(480764..480364)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KKKRHTFKYQIIANRNTLEIICLNVGPGRRHDFQIFKVSGIHIH
                     PDTESLQDSGYQGIAAYHTNSYVPLKKPQHGELTSLQREYNRALSQERMGIEHINRSL
                     KIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 2.5e-62 fragment hit coverage=
                     51.54%, between model( 260 aa) positions 127; 260 length
                     is 134aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(476648..475171)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DSYHTRVYMNGRDLGLKQAEAAYIAEISTRTGQRIEAGTHQPNR
                     -GRLQD-------QRTVPDPLADVWE---DELEPMLRRDPRLKPMTLYEYLQD-KYPG
                     QYPQVlrtlQRRVRTWKALHGPS-----PEVMFELRHEPGVQGFSGFTELKGITITIA
                     GQPFEHLIYHYRLGYSGWRYAQIIQGgESFVALSEGLQNAFAACGGVPQQHRTDSLSA
                     AYRNMGGRRS-KNLTRLYDELCDHYRLEPTRNNKG--IAHENGSIESPHGHLKNRIKQ
                     AIYLRGSAD-----FTSVAEYQALIDAQVAKLNQQCQTK------YEQEKDHLQPLPK
                     YRTPDYEVLTA----KVSKRSTIDVRCILYTVPSRLIGRQLELHLYHDRIVGYLERHP
                     VVELPRKRVSGkGKRRDRCINYRHVIGSMRLKPRAFIYCTWQSDLLPNPEYRQIWEQL
                     KAQFDLEQAAKIIVEALYIAAVQDKEQAVAVYLQQQLQASSLTLNRLKKQFEPPQMKQ
                     VPDLSIeQHS----LELYDKLLPS"
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                /note="IS21_ORF1   e-value= 5e-20 complete sequence hit
                coverage= 100%, between model( 525 aa) positions 1; 525
                length is 493aa with 39 gaps, 0 stops, absolute frame=
                Minus1"
CDS             complement(476378..475549)
                /colour="255 0 0"
                /evidence=predicted
                /translation="QYPQVLRTLQRRVRTWKALHGPS-----PEVMFELRHEPGVQGF
                SGFTELKGITITIAGQPFEHLIYHYRLGYSGWRYAQIIQGgESFVALSEGLQNAFAAC
                GGVPQQHRTDSLSAAYRNMGGRRS-KNLTRLYDELCDHYRLEPTRNNKG--IAHENGS
                IESPHGHLKNRIKQAIYLRGSAD-----FTSVAEYQALIDAQVAKLNQQCQTK-----
                -YEQEKDHLQPLPKYRTPDYEVLTA----KVSKRSTIDVRCILYTVPSRLIGRQLELH
                LYHDRIVGY-----LERHPVVELPRKRVS"
                /note="IS21_ORF1   e-value= 3.2e-28 fragment hit coverage=
                57.90%, between model( 525 aa) positions 99; 402 length
                is 277aa with 28 gaps, 0 stops, absolute frame= Minus1"
CDS             complement(408932..408064)
                /colour="255 0 0"
                /evidence=predicted
                /translation="EKXVKLSRYXSVNTQTLDRTXramptaYDSDLTTLQWELLEPLI
                PAAKPG-----GRPRTTDML--------------------SVLNAIFYLVVTGCQWRQ
                --LPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSED---RHPSPSAAICDAQ
                SVK------------------------------VGNpRcHLIGFD--------GGKM-
                --------------------------------------------VKGRKRHVLVD-TL
                GLVLMVMVTAANISDQRGAK----------------------ILFWKAQRQGASLSRL
                VR----IWADAGYQGQALMKWVMDRFQYVLEVIKRSDNLAGFQVVPKRWIVERTFGWL
                LWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHX"
                /note="IS5_IS5     e-value= 1.3e-09 complete sequence hit
                coverage= 100%, between model( 422 aa) positions 1; 422
                length is 290aa with 140 gaps, 4 stops, absolute frame=
                Minus1"
CDS             complement(408893..408043)
                /colour="255 0 0"
                /evidence=predicted
                /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQ
                INEHLRMQVRVSEDRHPSPSAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVD
                TLGLVLMVMVTAANISDQR-GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVM
                DRFQYVLEVIKRSDNLAGFQVVPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                AMIRLMVRRLAQEHXNFSNSLL"
                /note="IS5_IS1031  e-value= 4.2e-111 complete sequence hit
                coverage= 100%, between model( 295 aa) positions 1; 295
                length is 284aa with 14 gaps, 2 stops, absolute frame=
                Minus1"
CDS             complement(408851..408043)
                /colour="255 0 0"
                /evidence=predicted
                /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSEDRHPSP
                SAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
                -GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVMDRFQYVLEVIKRSDNLAGF
                QVVPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHXNFSN
                SLL"
                /note="IS5_IS1031  e-value= 2.8e-113 fragment hit
                coverage= 93.56%, between model( 295 aa) positions 20;
                295 length is 270aa with 9 gaps, 1 stops, absolute frame=
                Minus1"
CDS             complement(408842..408604)
                /colour="255 0 0"
                /evidence=predicted
```

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                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRM"
                     /note="IS5_IS427   e-value= 2e-19 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(129620..128584)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630  e-value= 4.9e-24 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(129620..128584)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                     QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                     -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                     ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                     DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                     CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                     /note="IS630  e-value= 6.7e-25 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 33 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(129560..129403)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                     QQGGIEGLK"
                     /note="IS481  e-value= 3.7e-09 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(105725..105655)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HVHMLISIPPKYSVLNVMGYIKGK"
                     /note="IS200  e-value= 5.3e-11 fragment hit coverage=
                     15.58%, between model( 154 aa) positions 61; 84 length is
                     24aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(105725..105655)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HVHMLISIPPKYSVLNVMGYIKGK"
                     /note="IS200_IS605 e-value= 2.1e-10 fragment hit
                     coverage= 15.69%, between model( 153 aa) positions 61; 84
                     length is 24aa with 0 gaps, 0 stops, absolute frame=
                     Minus1"
     CDS             complement(105725..105655)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HVHMLISIPPKYSVLNVMGYIKGK"
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                     /note="IS605 e-value= 2.8e-08 fragment hit coverage=
                     15.79%, between model( 152 aa) positions 61; 84 length is
                     24aa with 0 gaps, 0 stops, absolute frame= Minus1"
     CDS             complement(100253..99016)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IRIPLNLPDI--RVLELSKTERGDWL------IKIESTLQGTTC
                     HQCGREITDL-HCHDQ-PFRIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWH
                     EPRSPNTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADL
                     KVMGMDEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-I
                     DLRQTIERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRR
                     ELS------------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLER
                     LFA--YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTT
                     INNWMDEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQT
                     FAVTXTL"
                     /note="ISL3  e-value= 1.8e-43 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
                     length is 413aa with 44 gaps, 1 stops, absolute frame=
                     Minus1"
     CDS             complement(100094..99016)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWHEPRSP
                     NTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADLKVMGM
                     DEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-IDLRQT
                     IERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRRELS--
                     ----------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLERLFA--
                     YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTTINNWM
                     DEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQTFAVTX
                     TL"
                     /note="ISL3  e-value= 1e-49 fragment hit coverage= 86.03%,
                     between model( 451 aa) positions 64; 451 length is 360aa
                     with 34 gaps, 1 stops, absolute frame= Minus1"
     CDS             complement(6333589..6332766)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="XRIKXKNYILINSNXXKINIKLNYKLKIRRXAF------IGNEV
                     PIXLKXLNYXQLDKLKXRLMQWLKKKLVKQRFKPTQLVXSIVEVVtlrtfpklsaITX
                     RLFEKXVKLSRYXsVNTQTLDRTXRAMPTAYDSDLTTLQWELLEPLIPAAKP-GGRPR
                     T-TDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQ
                     VRVSE-----------------------------DRHPSPSAAICDAQSVkvgnpRCH
                     LIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANIS"
                     /note="IS5_IS427   e-value= 2.1e-06 complete sequence hit
                     coverage= 100%, between model( 296 aa) positions 1; 296
                     length is 275aa with 37 gaps, 14 stops, absolute frame=
                     Minus2"
     CDS             complement(6333292..6332424)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="EKXVKLSRYXSVNTQTLDRTXramptaYDSDLTTLQWELLEPLI
                     PAAKPG-----GRPRTTDML--------------------SVLNAIFYLVVTGCQWRQ
                     --LPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSED---RHPSPSAAICDAQ
                     SVK------------------------------VGNpRcHLIGFD--------GGKM-
                     --------------------------------------------VKGRKRHVLVD-TL
                     GLVLMVMVTAANISDQRGAK----------------------ILFWKAQRQGASLSRL
                     VR----IWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWL
                     LWSRRLNKDYEVLTRTAEALVYYVAMIRLMVRRLAQEHX"
                     /note="IS5_IS5     e-value= 1.8e-09 complete sequence hit
                     coverage= 100%, between model( 422 aa) positions 1; 422
                     length is 290aa with 140 gaps, 4 stops, absolute frame=
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           Minus2"
CDS        complement(6333253..6332403)
           /colour="255 0 0"
           /evidence=predicted
           /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
           ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQ
           INEHLRMQVRVSEDRHPSPSAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVD
           TLGLVLMVMVTAANISDQR-GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVM
           DRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
           AMIRLMVRRLAQEHXNFSNSLL"
           /note="IS5_IS1031  e-value= 3.6e-111 complete sequence hit
           coverage= 100%, between model( 295 aa) positions 1; 295
           length is 284aa with 14 gaps, 2 stops, absolute frame=
           Minus2"
CDS        complement(6333211..6332403)
           /colour="255 0 0"
           /evidence=predicted
           /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
           IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSEDRHPSP
           SAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
           -GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGF
           QVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHXNFSN
           SLL"
           /note="IS5_IS1031  e-value= 2.4e-113 fragment hit
           coverage= 93.56%, between model( 295 aa) positions 20;
           295 length is 270aa with 9 gaps, 1 stops, absolute frame=
           Minus2"
CDS        complement(6333202..6332964)
           /colour="255 0 0"
           /evidence=predicted
           /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
           CQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRM"
           /note="IS5_IS427   e-value= 2e-19 fragment hit coverage=
           27.70%, between model( 296 aa) positions 125; 206 length
           is 80aa with 2 gaps, 0 stops, absolute frame= Minus2"
CDS        complement(6280795..6279558)
           /colour="255 0 0"
           /evidence=predicted
           /translation="IRIPLNLPDI--RVLELSKTERGDWL------IKIESTLQGTTC
           HQCGREITDL-HCHDQ-PFRIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWH
           EPRSPNTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADL
           KVMGMDEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-I
           DLRQTIERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRR
           ELS------------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLER
           LFA--YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTT
           INNWMDEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQT
           FAVTXTL"
           /note="ISL3  e-value= 1.8e-43 complete sequence hit
           coverage= 100%, between model( 451 aa) positions 1; 451
           length is 413aa with 44 gaps, 1 stops, absolute frame=
           Minus2"
CDS        complement(6280636..6279558)
           /colour="255 0 0"
           /evidence=predicted
           /translation="RIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWHEPRSP
           NTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADLKVMGM
           DEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-IDLRQT
           IERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRRELS--
           ----------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLERLFA--
           YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTTINNWM
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                     DEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQTFAVTX
                     TL"
                     /note="ISL3  e-value= 1e-49 fragment hit coverage= 86.03%,
                     between model( 451 aa) positions 64; 451 length is 360aa
                     with 34 gaps, 1 stops, absolute frame= Minus2"
     CDS             complement(6250273..6249804)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="EAVYILDGLLKN--TSEIQPDTIHGDTQSQSCTVFALAFLLGIT
                     LMPRIRGWQNLAFYRPsRGTRYK--HLDSLFTEVTDWDLIETHLPDMLRVALSIKDGK
                     VQASTLLRKLGTNSRKNKLFQAFHELGGVLRTIFLLQYINDPQMQETIHAETNKCEAF
                     N"
                     /note="Tn3   e-value= 2.6e-14 fragment hit coverage=
                     15.94%, between model( 1004 aa) positions 740; 899 length
                     is 157aa with 4 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(6238489..6238101)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FFMDESGFSLVPCIPY-GWQPIG-------------TYL-EIPT
                     RSSKRLNVLGFLSRRQGL--HAYTSEQTITSEVVShCIDTFFADV--ELPTVIVVDQA
                     PIHTSQsiyEMKAEWAERG--ITLFELPSYSPHLNLIERLWQFMKYQWI"
                     /note="IS630  e-value= 6.5e-11 fragment hit coverage=
                     39.10%, between model( 376 aa) positions 187; 333 length
                     is 130aa with 21 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(6232594..6231831)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SPYQHLSLYLKKLRLSHMLTHWESIESQA-MQENWSYAEFLLAL
                     CETEAQRREQARLKRALTEARLPNA-KSFTNFDFSHCPQLNPAPLMQLAAdPGWLERA
                     ENCLILGPSGVGKTHLATGVSKKMLEFGKRVKFFAANALVQHLQQAKLQLQLH-PMLK
                     KLDRYDLLVLDDLGYCKKSEAETSVLFELIAHRYERKSLLITANQPFSQWDDIFT-DS
                     MMAVAAIDRLIHHGLIIKIQADSYRRKSATQRTAQTQSPPQ"
                     /note="IS21_ORF2   e-value= 1.3e-82 complete sequence hit
                     coverage= 100%, between model( 258 aa) positions 1; 258
                     length is 255aa with 4 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(6232594..6231831)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SPYQHLSLYLKKLRLSHMLTHWESIESQA-MQENWSYAEFLLAL
                     CETEAQRREQARLKRALTEARLPNA-KSFTNFDFSHCPQLNPAPLMQLAAdPGWLERA
                     ENCLILGPSGVGKTHLATGVSKKMLEFGKRVKFFAANALVQHLQQAKLQLQLH-PMLK
                     KLDRYDLLVLDDLGYCKKSEAETSVLFELIAHRYERKSLLITANQPFSQWDDIFT-DS
                     MMAVAAIDRLIHHGLIIKIQADSYRRKSATQRTAQTQSPPQ"
                     /note="IS21_ORF2   e-value= 3.4e-83 complete sequence hit
                     coverage= 100%, between model( 258 aa) positions 1; 258
                     length is 255aa with 4 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(6209392..6208452)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 1.1e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
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                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(6209392..6208452)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 2.2e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(6167842..6167601)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(6120718..6119784)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="CWVGIDVSKQNLDIHIRPSGH-----IFQHPNDKDGISALVASL
                     ESVS-----IERIVLEATGGMELPAAVALSQA---GMAVAVVNPRQARDFA-KATGQI
                     AKTDTIDAAILAHFA--EAIRPETRPLASEESQLLGELVTRRHQIVDMITAEKNRLAA
                     MHGPM--KEHIEQHIE------------------------------------------
                     ----------------------------WLKTQLNELDEQLQRTIRQTPVWCEQAKLL
                     KS---------VPGVGDVLSSVLLVDLP-ELGKLDSR-KIACLVGLAPLNRDSG-KFR
                     -GKRMIWGGRGRVRTALYMPTLVAIRYNPVLKAFYERLVGQGK---PKKVALTACMRK
                     LLIILNAMVKNNQQWNPEMARGAX"
                     /note="IS110 e-value= 6.8e-68 complete sequence hit
                     coverage= 100%, between model( 416 aa) positions 1; 416
                     length is 312aa with 104 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(6120718..6119784)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="CWVGIDVSKQNLDIHIRPSGH-----IFQHPNDKDGISALVASL
                     ESVS-----IERIVLEATGGMELPAAVALSQA---GMAVAVVNPRQARDFA-KATGQI
                     AKTDTIDAAILAHFA--EAIRPETRPLASEESQLLGELVTRRHQIVDMITAEKNRLAA
                     MHGPM--KEHIEQHIE------------------------------------------
                     ----------------------------WLKTQLNELDEQLQRTIRQTPVWCEQAKLL
                     KS---------VPGVGDVLSSVLLVDLP-ELGKLDSR-KIACLVGLAPLNRDSG-KFR
                     -GKRMIWGGRGRVRTALYMPTLVAIRYNPVLKAFYERLVGQGK---PKKVALTACMRK
                     LLIILNAMVKNNQQWNPEMARGAX"
                     /note="IS110 e-value= 2.2e-68 complete sequence hit
                     coverage= 100%, between model( 416 aa) positions 1; 416
                     length is 312aa with 104 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(6013789..6013572)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRFVYIPKHTSWLNQIECWFSILVRRLIRRGNFTSKDDLQQRI
                     LEFIEYFNHtMAKPFQWQFKGFQPRLXLM"
                     /note="IS630 e-value= 4e-10 fragment hit coverage=
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                     19.15%, between model( 376 aa) positions 305; 376 length
                     is 73aa with 0 gaps, 1 stops, absolute frame= Minus2"
     CDS             complement(6013741..6013632)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IECWFSILVRRLIR--RGNFTSKDDLQQRILEFIEYFNH"
                     /note="IS3_IS150_ORF2    e-value= 2e-08 fragment hit
                     coverage= 10.03%, between model( 389 aa) positions 329;
                     367 length is 37aa with 2 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(5927854..5927166)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TDLFKWRHYQFEIILLNVRWYCRYTLSYRNLEEMMG-RGFKVDH
                     ITIHRWVFKYSSELDKR-CRHLKP-THASSRVDETYVKIHXQWRYLYRAVDSE-SYTL
                     DFLLTAKRDTKAAKRFLTKALNTXDSWVXISSIQCGRHPAYPPAVEQLQADERIPEKE
                     KVRQVKYLNNRVEQDRIGIKKLVNPGMGFGSCNSARRTLKGFESMNMICKVQIKNVGK
                     DDVIG-QIYFINQIFGL"
                     /note="IS6   e-value= 1.5e-77 complete sequence hit
                     coverage= 100%, between model( 235 aa) positions 1; 235
                     length is 230aa with 5 gaps, 3 stops, absolute frame=
                     Minus2"
     CDS             complement(5927854..5927166)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TDLFKWRHYQFEIILLNVRWYCRYTLSYRNLEEMMG-RGFKVDH
                     ITIHRWVFKYSSELDKR-CRHLKP-THASSRVDETYVKIHXQWRYLYRAVDSE-SYTL
                     DFLLTAKRDTKAAKRFLTKALNTXDSWVXISSIQCGRHPAYPPAVEQLQADERIPEKE
                     KVRQVKYLNNRVEQDRIGIKKLVNPGMGFGSCNSARRTLKGFESMNMICKVQIKNVGK
                     DDVIG-QIYFINQIFGL"
                     /note="IS6   e-value= 6.2e-80 complete sequence hit
                     coverage= 100%, between model( 235 aa) positions 1; 235
                     length is 230aa with 5 gaps, 3 stops, absolute frame=
                     Minus2"
     CDS             complement(5746405..5745369)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="CMIKIDFTAEEIQHLNYERYHHPHPRVQRRMEVLYLKSQGLPHA
                     QICQLCQISRPTLAKTLRLYQQGG---IEGLKTLEYKGQSSSLNAHS-DSVRAYFEQH
                     PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRSRKVGYVPGKSSLP
                     -EKIEEQEQFRQTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-LWCLRRI-----
                     ---------FIPSPS-GRQRFNVLGALNAVTKEvTSITNHTYINSHSMCLLLAKLALL
                     DPVI--PISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRK
                     ECLYSKYYSDFHSFKGAIQQCIDQCNTEHKAKLTSLLSLKFQSFQK"
                     /note="IS630 e-value= 4e-22 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 346aa with 34 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(5746345..5746188)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HHPHPRVQRRMEVLYLKSQGLPHAQICQLCQISRPTLAKTLRLY
                     QQGGIEGLK"
                     /note="IS481 e-value= 1.1e-08 fragment hit coverage=
                     15.10%, between model( 351 aa) positions 1; 53 length is
                     53aa with 0 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(5746339..5745369)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PHPRVQRRMEVLYLKSQGLPHAQICQLCQISRPTLAKTLRLYQQ
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                     GG---IEGLKTLEYKGQSSSLNAHS-DSVRAYFEQHPP---------RTSAEAQAVIE
                     QLTGIKRSPTQIKAFLKRIGCRSRKVGYVPGKSSLP-EKIEEQEQFRQTRLEPLleeA
                     QRQERLVFFVDAAHFVHRAYLGF-LWCLRRI--------------FIPSPS-GRQRFN
                     VLGALNAVTKEvTSITNHTYINSHSMCLLLAKLALLDPVI--PISVILDNARYQKCQL
                     VTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKECLYSKYYSDFHSFKGAIQQCI
                     DQCNTEHKAKLTSLLSLKFQSFQK"
                     /note="IS630  e-value= 9.5e-24 fragment hit coverage=
                     94.15%, between model( 376 aa) positions 23; 376 length
                     is 324aa with 34 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(5716993..5716776)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRFVYIPKHTSWLNQIECWFSILVRRLIRRGNFTSKDDLQQRI
                     LEFIEYFNHtMAKPFQWQFKGFQPRLXLM"
                     /note="IS630  e-value= 4e-10 fragment hit coverage=
                     19.15%, between model( 376 aa) positions 305; 376 length
                     is 73aa with 0 gaps, 1 stops, absolute frame= Minus2"
     CDS             complement(5716945..5716836)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IECWFSILVRRLIR--RGNFTSKDDLQQRILEFIEYFNH"
                     /note="IS3_IS150_ORF2    e-value= 2e-08 fragment hit
                     coverage= 10.03%, between model( 389 aa) positions 329;
                     367 length is 37aa with 2 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(5652220..5652039)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="AVAESFFGTLKTELIYSTTFANRA--MAKTAIAEWIEVFYNRQR
                     LHSTIGHCAPVQFEENYWR"
                     /note="IS3_IS150_ORF1    e-value= 1.1e-07 fragment hit
                     coverage= 20.59%, between model( 306 aa) positions 244;
                     306 length is 61aa with 2 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(5652220..5652060)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="AVAESFFGTLKTELIY--STTFANRAMAKTAIAEWIEvFYNRQR
                     LHSTIGHCAPVQ"
                     /note="IS3_IS150_ORF2    e-value= 3.7e-12 fragment hit
                     coverage= 14.14%, between model( 389 aa) positions 327;
                     381 length is 54aa with 2 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(5652220..5652042)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="AVAESFFGTLK--TELIYSTTFANRAMAKTAIAEWIEVFYNRQR
                     LHSTIGHCAPVQFEENYW"
                     /note="IS3_IS3_ORF1      e-value= 3.3e-23 fragment hit
                     coverage= 21.68%, between model( 286 aa) positions 225;
                     286 length is 60aa with 2 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(5652220..5652030)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="AVAESFFGTLKTELIYSTTFANRAMAKTAIAEWIEVFYNRQRLH
                     STIGHCAPVQFEENYWRTRH"
                     /note="IS3_IS3_ORF2      e-value= 1.9e-21 fragment hit
                     coverage= 22.22%, between model( 288 aa) positions 225;
                     288 length is 64aa with 0 gaps, 0 stops, absolute frame=
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                    Minus2"
     CDS            complement(5652220..5652012)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="AVAESFFGTLKTELIYS----TTFANRAMAKTAIAEWIEVFYNR
                    QRLHSTIGHCAPVQFEENYWRTRHQTLVAX"
                    /note="IS3_IS51_ORF1     e-value= 1.5e-22 fragment hit
                    coverage= 24.10%, between model( 307 aa) positions 234;
                    307 length is 70aa with 4 gaps, 1 stops, absolute frame=
                    Minus2"
     CDS            complement(5652220..5652030)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="AVAESFFGTLKTELIYSTTFANRAMAKTAIAEWIEVFYNRQRLH
                    STIGHCAPVQFEENYW-RTRH"
                    /note="IS3_IS51_ORF2     e-value= 2.3e-14 fragment hit
                    coverage= 20.50%, between model( 317 aa) positions 245;
                    309 length is 64aa with 1 gaps, 0 stops, absolute frame=
                    Minus2"
     CDS            complement(5522092..5521956)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="WQTDGWEGYSRQLADE---VIHHVSKALTQRLERTNGILRQQTG
                    RWHRR"
                    /note="IS1_ORF2    e-value= 1.6e-12 fragment hit coverage=
                    20.68%, between model( 237 aa) positions 164; 212 length
                    is 46aa with 3 gaps, 0 stops, absolute frame= Minus2"
     CDS            complement(5510998..5509761)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="IRIPLNLPDI--RVLELSKTERGDWL------IKIESTLQGTTC
                    HQCGREITDL-HCHDQ-PFRIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWH
                    EPRSPNTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADL
                    KVMGMDEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-I
                    DLRQTIERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRR
                    ELS------------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLER
                    LFA--YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTT
                    INNWMDEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQT
                    LVVHQRS"
                    /note="ISL3  e-value= 4.5e-44 complete sequence hit
                    coverage= 100%, between model( 451 aa) positions 1; 451
                    length is 413aa with 44 gaps, 0 stops, absolute frame=
                    Minus2"
     CDS            complement(5510839..5509761)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="RIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWHEPRSP
                    NTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADLKVMGM
                    DEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-IDLRQT
                    IERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRRELS--
                    ----------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLERLFA--
                    YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTTINNWM
                    DEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQTLVVHQ
                    RS"
                    /note="ISL3  e-value= 2.6e-50 fragment hit coverage=
                    86.03%, between model( 451 aa) positions 64; 451 length
                    is 360aa with 34 gaps, 0 stops, absolute frame= Minus2"
     CDS            complement(5509729..5509467)
                    /colour="255 0 0"
                    /evidence=predicted
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                     /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                     DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVR"
                     /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
                     36.40%, between model( 239 aa) positions 1; 87 length is
                     88aa with 2 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(5475031..5474574)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFH-EL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSNS"
                     /note="IS200 e-value= 9.6e-56 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 153aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(5475031..5474574)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFH-EL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSNS"
                     /note="IS200 e-value= 5.7e-55 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 153aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(5475031..5474577)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGR-IRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSN"
                     /note="IS200_IS605 e-value= 8.6e-58 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 152aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(5475031..5474577)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGR-IRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSN"
                     /note="IS200_IS605 e-value= 2.2e-58 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 152aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(5475031..5474577)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRN-ATG
                     HKFWSRGYFVSTVGRDEEVIRRYIRHQEQEEQKLEQLNLfrAXPKSPLRGSN"
                     /note="IS605 e-value= 1e-51 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 152aa with 2 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(5475031..5474577)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRN-ATG
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                     HKFWSRGYFVSTVGRDEEVIRRYIRHQEQEEQKLEQLNLfrAXPKSPLRGSN"
                     /note="IS605 e-value= 5.5e-52 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 152aa with 2 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(5354932..5354196)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-----TGVYKRTFkpMLHAWHTYHLSRSN--AGRPPKLCRCDQL
                     LVALQYWREYRTYFHIAGDWEVSESTVCRIVHQVETALMNSGLFRLPGQKSLLQGFER
                     PDVVVMDVTETPIERPQTRQKAYYSGKKRDIPSNARLSLTATLXRLSALT--------
                     --LVQVVGMIFrsprfqvSISIQIPRVCKIADIKGLQ-----PIMP-TAMFLSRSHNT
                     VNXLPCSESITVLXVRNEWALNTLIAAXRFSEFCRSAIAIVVVATRCGVTX"
                     /note="IS5_ISL2    e-value= 9.6e-21 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 246aa with 23 gaps, 5 stops, absolute frame=
                     Minus2"
     CDS             complement(5354872..5354562)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SRSNAGRPPKLCRCDQLLVALQYWREYRTYFHIAGDWEVSESTV
                     CRIVHQVETALMNSGLFRLPGQKSLLQGFERPDVVVMDVTETPIERPQTRQKAYYSGK
                     KR"
                     /note="IS5_ISL2    e-value= 9.3e-44 fragment hit coverage=
                     40%, between model( 260 aa) positions 26; 129 length is
                     104aa with 0 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(5338738..5338023)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YLSPES-LQCRASSKVVSMXSTVGSPS---------ILARISDL
                     FPHCWRLGSLXINCLPYCppGRDRSDELRTLSLTRSEISATR---------VRATGCR
                     CDGCDXNAHXTSPDKTKSVLF----RKKKRHTFKCQIIANRNTLEIICLNVGPGRRHD
                     FQIFKGSGIHIHPDTESLQDSGYQGIAAYHANSYVPLKKPQHGELTSLQREYNRALSQ
                     ERMGIEHINRSLKIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 6.9e-39 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 239aa with 23 gaps, 4 stops, absolute frame=
                     Minus2"
     CDS             complement(5338423..5338023)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KKKRHTFKCQIIANRNTLEIICLNVGPGRRHDFQIFKGSGIHIH
                     PDTESLQDSGYQGIAAYHANSYVPLKKPQHGELTSLQREYNRALSQERMGIEHINRSL
                     KIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 6.5e-62 fragment hit coverage=
                     51.54%, between model( 260 aa) positions 127; 260 length
                     is 134aa with 0 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(4930255..4929975)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SMECPYCQSEK-ILKRGFDSlqdgTLVQRYQCKDCNRRFN-ERT
                     GTPMARLRtasSVVSYAIKARTEGMGVRSAGRTFGKSHTTIMRWEKRLADQA"
                     /note="IS1_ORF1    e-value= 3.2e-11 fragment hit coverage=
                     37.24%, between model( 239 aa) positions 5; 93 length is
                     94aa with 2 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(4612015..4611591)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GRQRFNVLGALNAVTKEvTSITNHTYINSHSMCLLLAKLALLDP
                     VI--PISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKEC
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                LYSKYYSDFHSFKGAIQQCIDQCNTEHKAKLTSLLSLKFQSFQK"
                /note="IS630 e-value= 6.2e-18 fragment hit coverage=
                38.56%, between model( 376 aa) positions 232; 376 length
                is 142aa with 4 gaps, 0 stops, absolute frame= Minus2"
CDS             complement(4461124..4460748)
                /colour="255 0 0"
                /evidence=predicted
                /translation="EHRKSEDFALCMQYLVDGLFPQADKLHVVLDNLNTHspaalyKT
                FNPDEALRILK-RIQFHYTPKHGSWLNMIEFEFSALSRQCLNRRIP-DIEQLRYEVTA
                WEKRRNHDKATVNWLFTVDDARTKLS"
                /note="IS630 e-value= 2.3e-07 fragment hit coverage=
                32.45%, between model( 376 aa) positions 255; 376 length
                is 126aa with 2 gaps, 0 stops, absolute frame= Minus2"
CDS             complement(4320520..4320258)
                /colour="255 0 0"
                /evidence=predicted
                /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVR"
                /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
                36.40%, between model( 239 aa) positions 1; 87 length is
                88aa with 2 gaps, 0 stops, absolute frame= Minus2"
CDS             complement(4297825..4296789)
                /colour="255 0 0"
                /evidence=predicted
                /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                /note="IS630 e-value= 6.7e-25 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Minus2"
CDS             complement(4297825..4296789)
                /colour="255 0 0"
                /evidence=predicted
                /translation="PMIKIDFTAEEIQQLNYERYHHPHPRVQRRMEVLYLKSQGLSHT
                QICQLCQISRPTLAKTLRQYQQGG---IEGLKTLEYKGQPSLLNAHS-DSVRAYFEQH
                PP---------RTSAEAQAVIEQLTGIKRSPTQIKAFLKRIGCRYRKVGYVPGKSSLP
                -EKIEEQEQFRHTRLEPLleeAQRQERLVFFVDAAHFVHRAYLGF-VWCITRI-----
                ---------FIPSPS-GRQRFNVLGALDAITKDLVSVTNHTYINSHSMCLLLAKLALL
                DPV-IPISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKE
                CLYSKYYADFPAFKGAIQQCIDQCNGEHKAKLTTLLSLKFQSFKK"
                /note="IS630 e-value= 4.9e-24 complete sequence hit
                coverage= 100%, between model( 376 aa) positions 1; 376
                length is 346aa with 33 gaps, 0 stops, absolute frame=
                Minus2"
CDS             complement(4297765..4297608)
                /colour="255 0 0"
                /evidence=predicted
                /translation="HHPHPRVQRRMEVLYLKSQGLSHTQICQLCQISRPTLAKTLRQY
                QQGGIEGLK"
                /note="IS481 e-value= 3.7e-09 fragment hit coverage=
                15.10%, between model( 351 aa) positions 1; 53 length is
                53aa with 0 gaps, 0 stops, absolute frame= Minus2"
CDS             complement(4135960..4135503)
                /colour="255 0 0"
                /evidence=predicted
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                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFH-EL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSNS"
                     /note="IS200 e-value= 9.6e-56 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 153aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(4135960..4135503)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFH-EL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSNS"
                     /note="IS200 e-value= 5.7e-55 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 153aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(4135960..4135506)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGR-IRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSN"
                     /note="IS200_IS605 e-value= 8.6e-58 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 152aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(4135960..4135506)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MTYRKLSHSVWECKYHVVFVPKYRKRRIYGR-IRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRNA-TG
                     HKFWSRGYFVSTVG-RDEEVIRRYIRHQEQEEQKLEQLNLFraXPKSPLRGSN"
                     /note="IS200_IS605 e-value= 2.2e-58 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 152aa with 3 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(4135960..4135506)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRN-ATG
                     HKFWSRGYFVSTVGRDEEVIRRYIRHQEQEEQKLEQLNLfrAXPKSPLRGSN"
                     /note="IS605 e-value= 1e-51 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 152aa with 2 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(4135960..4135506)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-MTYRKLSHSVWECKYHVVFVPKYRKRRIYGRIRQNLGDIFHEL
                     ARHKESAIEEGHLMLDHVHMLLSIPPKYSVSNVVGYVKGKSAIYIARELGNSRN-ATG
                     HKFWSRGYFVSTVGRDEEVIRRYIRHQEQEEQKLEQLNLfrAXPKSPLRGSN"
                     /note="IS605 e-value= 5.5e-52 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 152aa with 2 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(3914230..3913173)
                     /colour="255 0 0"
                     /evidence=predicted
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                    /translation="ACSRCRHTFT-DXSSQSEDIEGSQKPHGCMGSESSCTT------
                    ---WRISGASSQH---TDGDSSALE---RMGXVKSPSRGLAVSDPgDLAGKVRVRQ-L
                    QQDYSIRQICQVLNYPRSQVYYHARGQP-----DESELKAAIAGVAGAYP-TYGYRRI
                    TAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-RKRTTNSEHSfpRYGNRVLNLS
                    --IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNK
                    ALERAT---PEIHHS-----DQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAER
                    LMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYMHKRIHSSLGYLTPCEYEQQWRQ
                    Q"
                    /note="IS3_IS150_ORF2    e-value= 5e-28 complete sequence
                    hit coverage= 100%, between model( 389 aa) positions 1;
                    389 length is 353aa with 40 gaps, 2 stops, absolute
                    frame= Minus2"
     CDS            complement(3914146..3913149)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="MGSESSCTTWRISGASSQHTDGDS--SALERMGXVK-----SPS
                    RGLAVSDPGDLAGKVRVRQLQQ-----------DYSIRQICQVLNYPRSQVYYHARGQ
                    PDESELKAAIAGVAGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV-K
                    RKRTtnsehsfprYGNRVLNLSIDHPEQVWVADITYIRLQ--QEFVYLAVVmDVFTRA
                    IRGWHLSRHIDQQLTLRALNKALE-RATPEIHHSDQGVQYAAAAYMQLLQQHQVQISM
                    AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDvYMHKRIHSSLGY
                    LTPCEYEQQWRQQNNHYCMNK"
                    /note="IS3_IS407_ORF2    e-value= 1.2e-11 complete sequence
                    hit coverage= 100%, between model( 344 aa) positions 1;
                    344 length is 333aa with 22 gaps, 1 stops, absolute
                    frame= Minus2"
     CDS            complement(3914050..3913176)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="VKSPSRGLAVSDPgdLAGKVR----VRQLQQDYSIRQICQVLNY
                    PRSQVYYHARGQPDESELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLM
                    RQIGIMAKTKVK----RKRTTNSEHSF-PRYGNRvlNLSIDHPEQVWVADITYIRL--
                    QQEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALER----ATPEIHHSDQGV
                    QYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFT--EAY
                    EHIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ"
                    /note="IS3_IS150_ORF1    e-value= 2.2e-46 complete sequence
                    hit coverage= 100%, between model( 306 aa) positions 1;
                    306 length is 292aa with 18 gaps, 0 stops, absolute
                    frame= Minus2"
     CDS            complement(3914026..3913140)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="AVSDPGDLAGKVRVRQLQQDYSIRQICQVLNYPRSQVYYHARGQ
                    PD--------------------ESELKAAIAGVAGAYPTYGYRRITAQLQRQGYC---
                    VNHKRVARLMRQIGIMAKTKVKRKR-TTNSEHSFPRYGnRVLNLSIDHPEQVWVADIT
                    YI-------------RLQQ--------EFVYLAVVMDVFTRAIRGWHLSRH----IDQ
                    QLTLRALNKALERAT-PEIHHSDQGVQYAAA----AYMQLLQQHQVQISMAEVGQAWQ
                    NGYAERLMRTIKEEEVDLSD---YRNFTEAYEHIEQFLEDvYMHKRIHSSLGYLTPCE
                    YEQQWRQQNNHYCMNKEDS"
                    /note="IS481 e-value= 2.7e-07 complete sequence hit
                    coverage= 100%, between model( 351 aa) positions 1; 351
                    length is 296aa with 57 gaps, 0 stops, absolute frame=
                    Minus2"
     CDS            complement(3914008..3913140)
                    /colour="255 0 0"
                    /evidence=predicted
                    /translation="----DLAGKVRVRQLQQDYSIRQICQVLNYP---RSQVYYHARg
                    QPDESELKA--AIAGV-------AGA---YPTYGYRRITAQLQRQGYCVNHKRVARLM
                    RQIGIMAKTKVKRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVY
                    LAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALERATPE--------IHHSDQGVQY
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                     AAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEHIE
                     QFLEDV--YMHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNKEDS"
                     /note="IS3_IS51_ORF2     e-value= 3.7e-25 complete sequence
                     hit coverage= 100%, between model( 317 aa) positions 1;
                     317 length is 290aa with 30 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3914005..3913164)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-LAGKV--RVRQL-QQDYSIRQICQVLNYPRSQVYYHARG----
                     -------QPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGY-----CVNHKRVARLM
                     RQIGIM--AKTKVKRK-RttnsehsfpRYGNRVLnlsIDHPEQVWVAD-ITYIRLQQE
                     FVYLAVVMDVFTRAIRGWH------LSRHIDQQLTLRALNK---ALERATPEIHH-SD
                     QGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEA
                     YEHIEQFLEDvYMHKRIHSSLGYLTPCEYEQQWRQQNNH"
                     /note="IS3_IS2_ORF2      e-value= 3.7e-08 complete sequence
                     hit coverage= 100%, between model( 302 aa) positions 1;
                     302 length is 281aa with 34 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3913996..3913149)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KVRVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                     QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                     KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                     IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                     HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                     MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 3e-51 complete sequence
hit

                     coverage= 100%, between model( 307 aa) positions 1; 307
                     length is 283aa with 25 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(3913996..3913149)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KVRVRQLQQDYSIRQICQVLNYPRSQVYYHA-----------RG
                     QPDEsELKAAIAGV-AGAYPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKV
                     KRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRA
                     IRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQYAAAAYMQLLQQ
                     HQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVY
                     MHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 3.9e-53 complete sequence
                     hit coverage= 100%, between model( 307 aa) positions 1;
                     307 length is 283aa with 25 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3913993..3913179)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VRVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                     ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                     VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 7.6e-54 complete sequence
                     hit coverage= 100%, between model( 286 aa) positions 1;
                     286 length is 272aa with 15 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3913993..3913179)
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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VRVRQLQQDYSIRQICQVLNYPRSQVYYHARG--QPD-----ES
                     ELKAAI-AGVAGAYPTYGYRRITAQLQ-RQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                     VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 2e-54 complete sequence
hit
                     coverage= 100%, between model( 286 aa) positions 1; 286
                     length is 272aa with 15 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(3913981..3913167)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                     KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                     EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWRQQNN"
                     /note="IS3_IS3_ORF2      e-value= 3.3e-65 complete sequence
                     hit coverage= 100%, between model( 288 aa) positions 1;
                     288 length is 272aa with 19 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3913981..3913167)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLQQDYSIRQICQVLNYPRSQVYYHARGQPDE---------SEL
                     KAAIAGVAGaypTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                     EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWRQQNN"
                     /note="IS3_IS3_ORF2      e-value= 1.2e-64 complete sequence
                     hit coverage= 100%, between model( 288 aa) positions 1;
                     288 length is 272aa with 19 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3913978..3913173)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LQQDYSIRQICQVLNYPRSQVYYHARGQP-----DESELKAAIA
                     GVAGAYP-TYGYRRITAQLQ---RQGYCVNHKRVARLMRQIGIMAKTKVK-RKRTTNS
                     EHSfpRYGNRVLNLS--IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALERAT---PEIHHS-----DQGVQYAAAAYMQLLQQHQVQIS
                     MAEVGQAWQNGYAERLMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYMHKRIHSS
                     LGYLTPCEYEQQWRQQ"
                     /note="IS3_IS150_ORF2    e-value= 2.2e-46 fragment hit
                     coverage= 74.29%, between model( 389 aa) positions 101;
                     389 length is 269aa with 23 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3913963..3913176)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SIRQICQVLNYPRSQVYYHARGQPDESELKAAIAGV-AGAYPTY
                     GYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVK----RKRTTNSEHSF-PRYGN
                     RvlNLSIDHPEQVWVADITYIRL--QQEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTL
                     RALNKALER----ATPEIHHSDQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAE
                     RLMRTIKEEEVDLSDYRNFT--EAYEHIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWR
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                     Q"
                     /note="IS3_IS150_ORF1    e-value= 1.4e-49 fragment hit
                     coverage= 89.87%, between model( 306 aa) positions 32;
                     306 length is 263aa with 14 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3913963..3913764)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SIRQICQVLNYPRSQVYYHARGQPDESELKAAIAGVAGAYPTYG
                     YRRITAQLQRQGYCVNHKRVARL"
                     /note="IS3_IS407_ORF2    e-value= 2e-15 fragment hit
                     coverage= 19.48%, between model( 344 aa) positions 80;
                     146 length is 67aa with 0 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(3913912..3913755)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YHARgQPDESELKAAIAGVAGAYPTYGYRRITAQLQRQGY----
                     -CVNHKRVARLMRQ"
                     /note="IS3_IS2_ORF2      e-value= 9.1e-09 fragment hit
                     coverage= 18.87%, between model( 302 aa) positions 48;
                     104 length is 53aa with 5 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(3913846..3913164)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YPTYGYRRITAQLQRQGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERATPE--------IHHSDQGVQYAAAAYMQLLQQHQVQ
                     ISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEHIEQFLEDV--YMHKRIH
                     SSLGYLTPCEYEQQWRQQNNH"
                     /note="IS3_IS51_ORF2     e-value= 1.9e-38 fragment hit
                     coverage= 74.76%, between model( 317 aa) positions 73;
                     309 length is 228aa with 11 gaps, 0 stops, absolute
                     frame= Minus2"
     CDS             complement(3759763..3758637)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(3759763..3759069)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
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                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(3688744..3687618)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(3688744..3688050)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(3511168..3510495)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGRQFL--ST
                     YSKRGYSDWTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQVGvllPNAYDPDDI
                     PQ------------VGELDELETFVGKKRNKVWIW-TVVDHFHPG--ILGWVVGDHSA
                     ETFRPLWqaIVCWQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLAR
                     LHRKTLCYSKSVDMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 3.5e-42 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 225aa with 22 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(3511168..3510495)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGRQFL--ST
                     YSKRGYSDWTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQVGvllPNAYDPDDI
                     PQ------------VGELDELETFVGKKRNKVWIW-TVVDHFHPG--ILGWVVGDHSA
                     ETFRPLWqaIVCWQCFFWVSDGNPVYpgFIPEgDQIVSKTYMTRVEGENTRLRHYLAR
                     LHRKTLCYSKSVDMLKHSIRLL---IHYL"
                     /note="IS1_ORF1    e-value= 1.9e-41 complete sequence hit
                     coverage= 100%, between model( 239 aa) positions 1; 239
                     length is 225aa with 22 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(3511168..3510489)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SXGICMKCPECGGQH-IHKNGHRR-GKQNHICVTCGR----QFL
                     STYSKRGysdwTKRLCLRMYVNGMGLKGIERVIGVAHTTVIHWVQQV--GVLLPNAYD
                     PDDIPQVGELDELETFVGKKRNKVWIWTVVDHFHPGILGWVVGDHSAETFRPLWQAIV
                     CWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGENTRLRHYLARLHRKTL
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                     CYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 3.2e-29 complete sequence hit
                     coverage= 100%, between model( 237 aa) positions 1; 237
                     length is 227aa with 14 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(3510889..3510489)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DPDDIPQVGELDELETFVGKKRNKVWIWTVVDHFHPGILGWVVG
                     DHSAETFRPLWQAIVCWQ-CFFWVSDGNPVYPGFIPEG----DQIVSKTYMTRVEGEN
                     TRLRHYLARLHRKTLCYSKSVDMLKHSIRLLI-HYLKF"
                     /note="IS1_ORF2    e-value= 8.3e-32 fragment hit coverage=
                     59.07%, between model( 237 aa) positions 98; 237 length
                     is 134aa with 6 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(3407053..3406647)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MLLVRPISTESLRLLHRIYHSSRHHQVRQRAHCLILFAQGWPPY
                     TLASLFSVSPKTVYNWLKAWNNRG---FAGLYNHPGRGRKPMFNPDQQQQIYEWT-QA
                     SPIQ---------LNQVLAQIEQQWSVRVSKATVKRVLKQMDMSWHR"
                     /note="IS630 e-value= 8.7e-15 fragment hit coverage=
                     39.63%, between model( 376 aa) positions 1; 149 length is
                     136aa with 13 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(3406993..3406656)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SSRHHQVRQRAHCLILFAQGWPPYTLASLFSVSPKTVYNWLKAW
                     NNRGFAGLYNH---PGRGRKPMfNPDQQQQIYEWTQASPIQLNQVLAQIEQQWSVR--
                     -VSKATVKRVLKQMDMS"
                     /note="IS481 e-value= 3.5e-09 fragment hit coverage=
                     33.62%, between model( 351 aa) positions 1; 118 length is
                     113aa with 6 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2632693..2631567)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(2632693..2631999)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2586391..2586240)
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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QLCLILDNNPTHKG-KMRSQLAIHLEqmgltqsiQVEFLYLPSY
                     SPKLNLVE"
                     /note="IS630 e-value= 4.3e-06 fragment hit coverage=
                     11.70%, between model( 376 aa) positions 279; 322 length
                     is 51aa with 1 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2459947..2458710)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IRIPLNLPDI--RVLELSKTERGDWL------IKIESTLQGTTC
                     HQCGREITDL-HCHDQ-PFRIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWH
                     EPRSPNTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADL
                     KVMGMDEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-I
                     DLRQTIERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRR
                     ELS------------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLER
                     LFA--YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTT
                     INNWMDEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQT
                     FAVTXTL"
                     /note="ISL3  e-value= 1.8e-43 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
                     length is 413aa with 44 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(2459788..2458710)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWHEPRSP
                     NTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADLKVMGM
                     DEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-IDLRQT
                     IERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRRELS--
                     ----------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLERLFA--
                     YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVLKSDiKEFDCFLTTINNWM
                     DEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQTFAVTX
                     TL"
                     /note="ISL3  e-value= 1e-49 fragment hit coverage= 86.03%,
                     between model( 451 aa) positions 64; 451 length is 360aa
                     with 34 gaps, 1 stops, absolute frame= Minus2"
     CDS             complement(2413129..2412849)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMSHLIDTLKQVPDFRSARGRTHPLWLLLLLMVMGMLAGYQGYC
                     PLETFTSDYQQPLCELLGLENF-----QVPSHCTFRRVMKGLDFQSLSHQFEAWM"
                     /note="ISAs1 e-value= 1.2e-14 fragment hit coverage=
                     25.45%, between model( 389 aa) positions 1; 99 length is
                     94aa with 5 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2413129..2412096)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMSHLIDTLKQVPDFRSARGRTHPLWLLLLLMVMGMLAGYQGYC
                     PLETFTSDYQQPLCELLGLENF-----QVPSHCTFRRVMKGLDFQSLSHQFEAWMlsk
                     aqthspDNYAASMDGK-RIC---QGLTDENGKQRFVG---LVSIFAVEAGITLKLEAL
                     TQEDNsEIKVVQALLETLQLDG-LLITMDALHAQKNTSAS-CGFGX------------
                     XLSYRRXAQSGPSLRPPPDLL-XVSXTHGxayplHTEXRTRGTSVYPGLXACRHSPTR
                     -VGSHSLGALCPAMGYSSRQG----VSQH-----GLLHQFS-----------CHLTPS
                     LAISGPRALGHXKS-----------VALAEGCGLWXRXLSTRGXTSTAQLVSAXNHCD
                     XYSASKRLSIPQ"
                     /note="ISAs1 e-value= 7e-07 complete sequence hit
                     coverage= 100%, between model( 389 aa) positions 1; 389
                     length is 345aa with 59 gaps, 13 stops, absolute frame=
                     Minus2"
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     CDS             complement(2404702..2404278)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GRQRFNVLGALNAVTKEvTSITNHTYINSHSMCLLLAKLALLDP
                     VI--PISVILDNARYQKCQLVTDFAEIVD--IELVYLPSYSPHLNLIERLWRFVRKEC
                     LYSKYYSDFHSFKGAIQQCIDQCNTEHKAKLTSLLSLKFQSFQK"
                     /note="IS630  e-value= 6.2e-18 fragment hit coverage=
                     38.56%, between model( 376 aa) positions 232; 376 length
                     is 142aa with 4 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2284996..2284359)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MASKTTNVkPVVVSLWKLLSKSELIHPLKAXSISYCLKRYLWQV
                     L-----PGS------VMFLKAGYKSTXTVsMKQCLVLXTYHQKKGR------------
                     ---LTLQCDEMWSFVNDKSNKQWIWLALDVITREIVGVYVGARSKQGARQLWNSLPGI
                     YRQCAVaYTDFWDAYGCVFPKQ-RHQAVGKETGQTCYIERFNCTMRQRVSRLVRKTLS
                     FSKKLENHIGAIWMFVHHYNAS"
                     /note="IS1_ORF2    e-value= 4.6e-13 complete sequence hit
                     coverage= 100%, between model( 237 aa) positions 1; 237
                     length is 213aa with 27 gaps, 3 stops, absolute frame=
                     Minus2"
     CDS             complement(2284744..2284368)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DEMWSFVNDKSNKQWIWLALDVITREIVGVYVGA----RSKQGA
                     RQLwNSLPGIYRQCAVAYTDFWDAYgCVFPKQRHQAVGKEtgQTCYIERFNCTMRQRV
                     SRLVRKTLSFSKKLENHIGAIWMF---VHHY"
                     /note="IS1_ORF1    e-value= 4.6e-14 fragment hit coverage=
                     53.97%, between model( 239 aa) positions 111; 239 length
                     is 126aa with 7 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2284744..2284359)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DEMWSFVNDKSNKQWIWLALDVITREIVGVYVGARSKQGARQLW
                     NSLPGIYRQCAVaYTDFWDAYGCVFPKQ-RHQAVGKETGQTCYIERFNCTMRQRVSRL
                     VRKTLSFSKKLENHIGAIWMFVHHYNAS"
                     /note="IS1_ORF2    e-value= 6.2e-32 fragment hit coverage=
                     54.43%, between model( 237 aa) positions 109; 237 length
                     is 129aa with 1 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2088655..2088024)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                     ---PGGRPRTTDMRSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVH
                     INEHLRMQERVSEDRHPSPSAAICDAQSVKVG--NPR---------------------
                     --------------CHTNS----LIEXPLXSKHPR---------YKNIPLEKPPPSGR
                     GYXYAQIKRSP-------VPQ-----------------XNQSFCLXKAFLGPAIIALP
                     DXVLdyETAVQSATHSQAIEP"
                     /note="IS5_IS1031  e-value= 3.4e-16 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 211aa with 86 gaps, 7 stops, absolute frame=
                     Minus2"
     CDS             complement(2088613..2088297)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMRSVLNA
                     IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRMQERVSEDRHPSP
                     SAAICDAQSVK"
                     /note="IS5_IS1031  e-value= 7.2e-51 fragment hit coverage=
                     38.31%, between model( 295 aa) positions 20; 132 length
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                     is 106aa with 7 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2088604..2088366)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMRSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWVHINEHLRM"
                     /note="IS5_IS427   e-value= 9.2e-19 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(2087236..2086668)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SQISIRKGLGM-----RDKY-------------------Q----
                     -------QRATP-------IIQVTH-----------------IWNWY-----------
                     ---------------------------------HSI----GFDGGKMVKGRKRHVLVD
                     TLGLVLMVMVTAANISDQR-GAKMLFWKARRQGaslSRLVRIWADAGYQGQAFMKWVM
                     DRFQYVLEVIKRSDNLAGFQVVPKRWIVERTFGWLLWSRRLNKDYEVLTRTTEALAYV
                     AMIRLMVRRLAQEYXNFSNSLX"
                     /note="IS5_IS1031  e-value= 2.9e-19 complete sequence hit
                     coverage= 100%, between model( 295 aa) positions 1; 295
                     length is 190aa with 108 gaps, 2 stops, absolute frame=
                     Minus2"
     CDS             complement(2087131..2086668)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR-GAKMLF
                     WKARRQGaslSRLVRIWADAGYQGQAFMKWVMDRFQYVLEVIKRSDNLAGFQVVPKRW
                     IVERTFGWLLWSRRLNKDYEVLTRTTEALAYVAMIRLMVRRLAQEYXNFSNSLX"
                     /note="IS5_IS1031  e-value= 2.2e-60 fragment hit coverage=
                     51.86%, between model( 295 aa) positions 143; 295 length
                     is 155aa with 1 gaps, 2 stops, absolute frame= Minus2"
     CDS             complement(1894558..1894341)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RIRFVYIPKHTSWLNQIECWFSILVRRLIRRGNFTSKDDLQQRI
                     LEFIEYFNHtMAKPFQWQFKGFQPRLXLM"
                     /note="IS630  e-value= 4e-10 fragment hit coverage=
                     19.15%, between model( 376 aa) positions 305; 376 length
                     is 73aa with 0 gaps, 1 stops, absolute frame= Minus2"
     CDS             complement(1894510..1894401)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IECWFSILVRRLIR--RGNFTSKDDLQQRILEFIEYFNH"
                     /note="IS3_IS150_ORF2    e-value= 2e-08 fragment hit
                     coverage= 10.03%, between model( 389 aa) positions 329;
                     367 length is 37aa with 2 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(1226248..1225905)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KYIVTLTPEERSELIQLTRRRTLSARKMKRAQILMLADEGHKDD
                     TITQMLNAGISTVHRTRQKFVEGG---VEfALNERPRPGGQKKLDSKAEALLIATACS
                     DPPTG----CCRWTMQLLAE"
                     /note="IS630  e-value= 1.2e-15 fragment hit coverage=
                     32.18%, between model( 376 aa) positions 1; 121 length is
                     115aa with 7 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(1119469..1119321)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LMNSGLFRLPGKKHLIQGFERPDVVVMDVTETPIERPQKGQKAY
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                     YAGKKR"
                     /note="IS5_ISL2    e-value= 1.8e-17 fragment hit coverage=
                     19.23%, between model( 260 aa) positions 80; 129 length
                     is 50aa with 0 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(669352..668715)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MASKTTNVkPVVVSLWKLLSKSELIHPLKAXSISYCLKRYLWQV
                     L-----PGS------VMFLKAGYKSTXTVsMKQCLVLXTYHQKKGR------------
                     ---LTLQCDEMWSFVNDKSNKQWIWLALDVITREIVGVYVGARSKQGARQLWNSLPGI
                     YRQCAVaYTDFWDAYGCVFPKQ-RHQAVGKETGQTCYIERFNCTMRQRVSRLVRKTLS
                     FSKKLENHIGAIWMFVHHYNAS"
                     /note="IS1_ORF2    e-value= 4.6e-13 complete sequence hit
                     coverage= 100%, between model( 237 aa) positions 1; 237
                     length is 213aa with 27 gaps, 3 stops, absolute frame=
                     Minus2"
     CDS             complement(669100..668724)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DEMWSFVNDKSNKQWIWLALDVITREIVGVYVGA----RSKQGA
                     RQLwNSLPGIYRQCAVAYTDFWDAYgCVFPKQRHQAVGKEtgQTCYIERFNCTMRQRV
                     SRLVRKTLSFSKKLENHIGAIWMF---VHHY"
                     /note="IS1_ORF1    e-value= 4.6e-14 fragment hit coverage=
                     53.97%, between model( 239 aa) positions 111; 239 length
                     is 126aa with 7 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(669100..668715)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DEMWSFVNDKSNKQWIWLALDVITREIVGVYVGARSKQGARQLW
                     NSLPGIYRQCAVaYTDFWDAYGCVFPKQ-RHQAVGKETGQTCYIERFNCTMRQRVSRL
                     VRKTLSFSKKLENHIGAIWMFVHHYNAS"
                     /note="IS1_ORF2    e-value= 6.2e-32 fragment hit coverage=
                     54.43%, between model( 237 aa) positions 109; 237 length
                     is 129aa with 1 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(557656..557520)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYSRQLANE---VIHHVSKALTQRLERTNGILRQQTS
                     RWHRR"
                     /note="IS1_ORF2    e-value= 1.2e-12 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(522460..522219)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(481126..480390)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-----TGVYKRTFkpMLHAWHTYHLSRSN--AGRPPKLCRCDQL
                     LVALQYWREYRTYFHIAGDWEVSESTVCRIVHQVETALMNSGLFRLPGQKSLLQGFER
                     PDVVVMDVTETPIERPQTRQKAYYSGKKRDIPSNTRLSLTATLXRLSALT--------
                     --LVQVVGMIFrssrfqvSISIQIPRVCKIADIKGLQPII--PTAM----FLSRSHNT
                     VNXLPCSESITVLXVRNEWALNTLIAAXRFSEFCRSAIAIVVVATRCGVTX"
                     /note="IS5_ISL2    e-value= 1.9e-21 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
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                length is 246aa with 23 gaps, 5 stops, absolute frame=
                Minus2"
CDS             complement(481066..480756)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SRSNAGRPPKLCRCDQLLVALQYWREYRTYFHIAGDWEVSESTV
                CRIVHQVETALMNSGLFRLPGQKSLLQGFERPDVVVMDVTETPIERPQTRQKAYYSGK
                KR"
                /note="IS5_ISL2    e-value= 9.3e-44 fragment hit coverage=
                40%, between model( 260 aa) positions 26; 129 length is
                104aa with 0 gaps, 0 stops, absolute frame= Minus2"
CDS             complement(475153..474390)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SPYQHLSLYLKKLRLSHMLTHWESIESQA-MQENWSYAEFLLAL
                CETKAQRREQARLKRALTEARLPNA-KSFTNFDFSHCPQLNPAPLMQLAAdPGWLERA
                ENCLILGPSGVGKTHLATGVSKKMLEFGKRVKFFAANALVQHLQQAKLQLQLH-PMLK
                KLDRYDLLVLDDLGYCKKSEAETSVLFELIAHRYERKSLLITANQPFSQWDDIFT-DS
                MMAVAAIDRLIHHGLIIKIQADSYRRKSATQRTAQTQSPPQ"
                /note="IS21_ORF2   e-value= 7.2e-80 complete sequence hit
                coverage= 100%, between model( 258 aa) positions 1; 258
                length is 255aa with 4 gaps, 0 stops, absolute frame=
                Minus2"
CDS             complement(475153..474390)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SPYQHLSLYLKKLRLSHMLTHWESIESQA-MQENWSYAEFLLAL
                CETKAQRREQARLKRALTEARLPNA-KSFTNFDFSHCPQLNPAPLMQLAAdPGWLERA
                ENCLILGPSGVGKTHLATGVSKKMLEFGKRVKFFAANALVQHLQQAKLQLQLH-PMLK
                KLDRYDLLVLDDLGYCKKSEAETSVLFELIAHRYERKSLLITANQPFSQWDDIFT-DS
                MMAVAAIDRLIHHGLIIKIQADSYRRKSATQRTAQTQSPPQ"
                /note="IS21_ORF2   e-value= 1.9e-80 complete sequence hit
                coverage= 100%, between model( 258 aa) positions 1; 258
                length is 255aa with 4 gaps, 0 stops, absolute frame=
                Minus2"
CDS             complement(466177..466083)
                /colour="255 0 0"
                /evidence=predicted
                /translation="AERG--ITLVELPSYSPHLNLIERLWQFMKYQWI"
                /note="IS630 e-value= 1.7e-09 fragment hit coverage=
                9.04%, between model( 376 aa) positions 300; 333 length
                is 32aa with 2 gaps, 0 stops, absolute frame= Minus2"
CDS             complement(339451..339123)
                /colour="255 0 0"
                /evidence=predicted
                /translation="MVENRRGNHTVTRLTVHIVWVTKYRYQVLKGEVQKRCRELLIQI
                CDAEDIRILKGVVSKDHVHMLIEYPPSKSISDIVKCLKGRTSRRLQQEYREXEKRYWG
                KHLWAIGY"
                /note="IS605 e-value= 3e-25 fragment hit coverage=
                72.37%, between model( 152 aa) positions 1; 110 length is
                110aa with 0 gaps, 1 stops, absolute frame= Minus2"
CDS             complement(339451..338973)
                /colour="255 0 0"
                /evidence=predicted
                /translation="MVENRRGNHTVTRLTVHIVWVTKYRYQVLKGEVQKRCRELLIQI
                CDAEDIRILKGVVSKDHVHMLIEYPPSKSISDIVKCLKGRTSRRLQQEYREXEKRYWG
                KHLWAIGYGAWSTGnISEQMVEEYLEHHrlvsnnDLDTFMLEXIrTLVLRGTGLSVDK
                "
                /note="IS605 e-value= 2.6e-17 complete sequence hit
                coverage= 100%, between model( 152 aa) positions 1; 152
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                     length is 160aa with 0 gaps, 2 stops, absolute frame=
                     Minus2"
     CDS             complement(339448..339063)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VENRRGNHTVTRLTVHIVWVTKYRYQVLKGEVQKRCRELLI-QI
                     CDAEDIRILKGVVSKDHVHMLIEYPPSKSISDIVKCLKGRTSRRLQQEYREXEKRYWG
                     KHLWAIGYGAWSTGNISEQMVEEYLEHH"
                     /note="IS200 e-value= 1.2e-47 fragment hit coverage=
                     84.42%, between model( 154 aa) positions 1; 130 length is
                     129aa with 1 gaps, 1 stops, absolute frame= Minus2"
     CDS             complement(339448..339015)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VENRRGNHTVTRLTVHIVWVTKYRYQVLKGEVQKRCRELLI-QI
                     CDAEDIRILKGVVSKDHVHMLIEYPPSKSISDIVKCLKGRTSRRLQQEYREXEKRYWG
                     KHLWAIGYGAWSTGNISEQMVEEYLEHHRLVSNNDL--------DTFMLEXI"
                     /note="IS200 e-value= 1.5e-46 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 145aa with 9 gaps, 2 stops, absolute frame=
                     Minus2"
     CDS             complement(339448..339063)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VENRRGNHTVTRLTVHIVWVTKYRYQVLKGE-VQKRCRELLIQI
                     CDAEDIRILKGVVSKDHVHMLIEYPPSKSISDIVKCLKGRTSRRLQQEYREXEKRYWG
                     KHLWAIGYGAWSTGNISEQMVEEYLEHH"
                     /note="IS200_IS605 e-value= 1.3e-45 fragment hit
                     coverage= 84.97%, between model( 153 aa) positions 1; 130
                     length is 129aa with 1 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(339448..338994)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VENRRGNHTVTRLTVHIVWVTKYRYQVLKGE-VQKRCRELLIQI
                     CDAEDIRILKGVVSKDHVHMLIEYPPSKSISDIVKCLKGRTSRRLQQEYREXEKRYWG
                     KHLWAIGYGAWSTGNISEQMVEEYLEHHRLVSNNDLDTFMLEXIRTLVLRG"
                     /note="IS200_IS605 e-value= 4.2e-45 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 152aa with 1 gaps, 2 stops, absolute frame=
                     Minus2"
     CDS             complement(323713..323475)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RNQQHYIRQRLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKY
                     LDGGLQGLVQSI--RHQKPSRLSPEEQQQLKEMVLTQR"
                     /note="IS481 e-value= 6.3e-08 fragment hit coverage=
                     23.36%, between model( 351 aa) positions 1; 82 length is
                     80aa with 2 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(323686..323280)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RLTAIKLLNEGHSRTQVSEQVGCSYDTLTRWMDKYLDGG---LQ
                     GLVQSIRHQKPSRLSPEEQQQLKEMVLTQRPTDYGIDRNMWTGAILAVVIEQRFEVQL
                     KDSRIYELLSELGLSYQRAHRDYA--NADLNAQKEWVAA"
                     /note="IS630 e-value= 9.2e-30 fragment hit coverage=
                     37.50%, between model( 376 aa) positions 30; 170 length
                     is 136aa with 5 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(322042..321891)
                     /colour="255 0 0"
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                     /evidence=predicted
                     /translation="QLCLILDNNPTHKG-KMRSQLAIHLEqmgltqsiQVEFLYLPSY
                     SPKLNLVE"
                     /note="IS630 e-value= 4.3e-06 fragment hit coverage=
                     11.70%, between model( 376 aa) positions 279; 322 length
                     is 51aa with 1 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(259486..259350)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="WQTDGWEGYARQLPDE---VVHEVSKALTQRLERTNGIVRQQTG
                     RWHRR"
                     /note="IS1_ORF2    e-value= 1.8e-11 fragment hit coverage=
                     20.68%, between model( 237 aa) positions 164; 212 length
                     is 46aa with 3 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(127654..127374)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="PMSHLIDTLKQVPDFRSARGRTHPLWLLLLLMVMGMLAGYQGYC
                     PLETFTSDYQQPLCELLGLENF-----QVPSHCTFRRVMKGLDFQSLSHQFEAWM"
                     /note="ISAs1 e-value= 1.2e-14 fragment hit coverage=
                     25.45%, between model( 389 aa) positions 1; 99 length is
                     94aa with 5 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(105898..105813)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ITYHKLFHTEWECKYRVVFIPKYCQKCIY"
                     /note="IS200 e-value= 2.1e-06 fragment hit coverage=
                     18.83%, between model( 154 aa) positions 1; 29 length is
                     29aa with 0 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(105898..105807)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ITYHKLFHTEWECKYRVVFIPKYCQKCIYSN"
                     /note="IS200_IS605 e-value= 4.7e-06 fragment hit
                     coverage= 20.26%, between model( 153 aa) positions 1; 31
                     length is 31aa with 0 gaps, 0 stops, absolute frame=
                     Minus2"
     CDS             complement(105892..105807)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="---YHKLFHTEWECKYRVVFIPKYCQKCIYSN"
                     /note="IS605 e-value= 9.3e-06 fragment hit coverage=
                     21.05%, between model( 152 aa) positions 1; 32 length is
                     29aa with 3 gaps, 0 stops, absolute frame= Minus2"
     CDS             complement(62245..61035)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
                     A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVTNSVMEEVKDWRSRP
                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 1.4e-166 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Minus2"
     CDS             complement(62245..61035)
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                /colour="255 0 0"
                /evidence=predicted
                /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
                A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVTNSVMEEVKDWRSRP
                LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQCIVHLIRNSLRHVPW
                KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                LNWKAALSHFAILFPTRFNYXIH"
                /note="IS256 e-value= 3.7e-167 complete sequence hit
                coverage= 100%, between model( 410 aa) positions 1; 410
                length is 404aa with 11 gaps, 1 stops, absolute frame=
                Minus2"
CDS             complement(6379401..6378635)
                /colour="255 0 0"
                /evidence=predicted
                /translation="PCLGRFILYFTKLQLPPQKKYCDLEXWIISA---IILGYNGGEF
                RXLIQPIIwLVLMPVAFRIALLSDIKNLV---------FPSILSXRLFEKXV----KL
                SRYXsVNTQTLDRTXRAMPTAYDSDLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVL
                NAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSE----
                -------------------------DRHPSPSAAICDAQSVkvgnpRCHLIGFDGGKM
                VKGRKRHVLVDTLGLVLMVMVTAANIS"
                /note="IS5_IS427   e-value= 4.4e-06 complete sequence hit
                coverage= 100%, between model( 296 aa) positions 1; 296
                length is 256aa with 47 gaps, 6 stops, absolute frame=
                Minus3"
CDS             complement(6379161..6378293)
                /colour="255 0 0"
                /evidence=predicted
                /translation="EKXVKLSRYXSVNTQTLDRTXramptaYDSDLTTLQWELLEPLI
                PAAKPG-----GRPRTTDML--------------------SVLNAIFYLVVTGCQWRQ
                --LPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSED---RHPSPSAAICDAQ
                SVK------------------------------VGNpRcHLIGFD--------GGKM-
                --------------------------------------------VKGRKRHVLVD-TL
                GLVLMVMVTAANISDQRGAK----------------------ILFWKAQRQGASLSRL
                VR----IWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWL
                LWSRRLNKDYEVLTRTAEALVYYVAMIRLMVRRLAQEHX"
                /note="IS5_IS5     e-value= 1.8e-09 complete sequence hit
                coverage= 100%, between model( 422 aa) positions 1; 422
                length is 290aa with 140 gaps, 4 stops, absolute frame=
                Minus3"
CDS             complement(6379122..6378272)
                /colour="255 0 0"
                /evidence=predicted
                /translation="TQTLDRTXRAM-----PTAYDSDLTTLQWELLEPLIPAAK----
                ---PGGRPRTTDMLSVLNAIFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQ
                INEHLRMQVRVSEDRHPSPSAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVD
                TLGLVLMVMVTAANISDQR-GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVM
                DRFQYVLEVVKRSDNLAGFQVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYV
                AMIRLMVRRLAQEHXNFSNSLL"
                /note="IS5_IS1031  e-value= 3.6e-111 complete sequence hit
                coverage= 100%, between model( 295 aa) positions 1; 295
                length is 284aa with 14 gaps, 2 stops, absolute frame=
                Minus3"
CDS             complement(6379080..6378272)
                /colour="255 0 0"
                /evidence=predicted
                /translation="YDSDLTTLQWELLEPLIPAAK-------PGGRPRTTDMLSVLNA
                IFYLVVTGCQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRMQVRVSEDRHPSP
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                     SAAICDAQSVKVGNPRCH-LIGFDGGKMVKGRKRHVLVDTLGLVLMVMVTAANISDQR
                     -GAKILFWKAQRQGaslSRLVRIWADAGYQGQALMKWVMDRFQYVLEVVKRSDNLAGF
                     QVIPKRWIVERTFGWLLWSRRLNKDYEVLTRTAEALVYVAMIRLMVRRLAQEHXNFSN
                     SLL"
                     /note="IS5_IS1031  e-value= 2.4e-113 fragment hit
                     coverage= 93.56%, between model( 295 aa) positions 20;
                     295 length is 270aa with 9 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(6379071..6378833)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DLTTLQWELLEPLIPAAKP-GGRPRT-TDMLSVLNAIFYLVVTG
                     CQWRQLPHDFPCWSTVYSYFRRWRDDGTWSQINEHLRM"
                     /note="IS5_IS427   e-value= 2e-19 fragment hit coverage=
                     27.70%, between model( 296 aa) positions 125; 206 length
                     is 80aa with 2 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6361275..6360608)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QRFIQGLSPETIHLLSRIHRHSHHHQVRQRAHCILLSFEGFNVT
                     ELMSIFAVTRKTVYTWLDAWDNHC---LVGLYDQPGRGRKPKLRDVQ-KEQIREWAKM
                     TP---------HNLNVVLAKIKEAWNIEVSKTTLKRILKSCSMSWRRLRRVVAGQPDP
                     VEYATK-----RHQLEVLKRQEEKGELdlrYLDESGFCLVPYVPY-AWQEKG-ETLGL
                     PSQRSGRFNVLGLMNRHNDLTSYVF"
                     /note="IS630 e-value= 4.6e-12 fragment hit coverage=
                     63.83%, between model( 376 aa) positions 1; 240 length is
                     223aa with 20 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6361275..6360251)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="QRFIQGLSPETIHLLSRIHRHSHHHQVRQRAHCILLSFEGFNVT
                     ELMSIFAVTRKTVYTWLDAWDNHC---LVGLYDQPGRGRKPKLRDVQ-KEQIREWAKM
                     TP---------HNLNVVLAKIKEAWNIEVSKTTLKRILKSCSMSWRRLRRVVAGQPDP
                     VEYATK-----RHQLEVLKRQEEKGELdlrYLDESGFCLVPYVPY-AWQEKG------
                     --------ETLGLPSQRSGRFNVLGLMNRHNDLtSYVFDKSITSAVVVACIDDFSQTC
                     DQHT----VVVMDQASIHKNTEIEENIEDWKAkNVEIFWLPTYSPHLNLIEIFWRFMK
                     YEWLEFDAYKCLGSLSLYIDKILKGFGR--DYVIDFGXVLSVLLFGY"
                     /note="IS630 e-value= 3.7e-16 complete sequence hit
                     coverage= 100%, between model( 376 aa) positions 1; 376
                     length is 342aa with 39 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(6360546..6360377)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DQHTVVVMDQASIHKNTEIEENIEDWKAkNVEIFWLPTYSPHLN
                     LIEIFWRFMKYEW"
                     /note="IS630 e-value= 1.9e-12 fragment hit coverage=
                     14.89%, between model( 376 aa) positions 277; 332 length
                     is 57aa with 0 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6350184..6349745)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-RNVTXEAKSYDMGLHHIVFIPKRRRRVIYGSLRIRLGVLFRDL
                     AEQRDVEILEGHLLPDHVHMCMSIPPKHAVSGVVGFMKGKSAIAIARQFMGKRRNYSG
                     ESFWAXGYYVSTVDLYEGMVRAYIRNQELEDARLEQLSLPLGX----CXR"
                     /note="IS605 e-value= 1e-36 complete sequence hit
                     coverage= 100%, between model( 152 aa) positions 1; 152
                     length is 147aa with 5 gaps, 4 stops, absolute frame=
                     Minus3"
     CDS             complement(6350172..6349730)
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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="XEAKSYDMGLH----HIVFIPKRRRRVIYGSLRIRLGVLFR-DL
                     AEQRDVEILEGHLLPDHVHMCMSIPPKHAVSGVVGFMKGKSAIAIARQFMGKRRNYSG
                     ESFWAXGYYVSTVD-LYEGMVRAYIRNQELEDARLEQLSLPLGXCXRVAPWG"
                     /note="IS200 e-value= 2.5e-35 complete sequence hit
                     coverage= 100%, between model( 154 aa) positions 1; 154
                     length is 148aa with 6 gaps, 4 stops, absolute frame=
                     Minus3"
     CDS             complement(6350172..6349733)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="XEAKSYDMGLH----HIVFIPKRRRRVIYGS-LRIRLGVLFRDL
                     AEQRDVEILEGHLLPDHVHMCMSIPPKHAVSGVVGFMKGKSAIAIARQFMGKRRNYSG
                     ESFWAXGYYVSTVD-LYEGMVRAYIRNQELEDARLEQLSLPLGXCXRVAPW"
                     /note="IS200_IS605 e-value= 8.1e-37 complete sequence hit
                     coverage= 100%, between model( 153 aa) positions 1; 153
                     length is 147aa with 6 gaps, 4 stops, absolute frame=
                     Minus3"
     CDS             complement(6350139..6349763)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HIVFIPKRRRRVIYGSLRIRLGVLFR-DLAEQRDVEILEGHLLP
                     DHVHMCMSIPPKHAVSGVVGFMKGKSAIAIARQFMGKRRNYSGESFWAXGYYVSTVD-
                     LYEGMVRAYIRNQELEDARLEQLSLP"
                     /note="IS200 e-value= 1.2e-40 fragment hit coverage=
                     83.12%, between model( 154 aa) positions 16; 143 length
                     is 126aa with 2 gaps, 1 stops, absolute frame= Minus3"
     CDS             complement(6350139..6349760)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HIVFIPKRRRRVIYGS-LRIRLGVLFRDLAEQRDVEILEGHLLP
                     DHVHMCMSIPPKHAVSGVVGFMKGKSAIAIARQFMGKRRNYSGESFWAXGYYVSTVD-
                     LYEGMVRAYIRNQELEDARLEQLSLPL"
                     /note="IS200_IS605 e-value= 7.4e-40 fragment hit
                     coverage= 84.31%, between model( 153 aa) positions 16;
                     144 length is 127aa with 2 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(6350139..6349760)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HIVFIPKRRRRVIYGSLRIRLGVLFRDLAEQRDVEILEGHLLPD
                     HVHMCMSIPPKHAVSGVVGFMKGKSAIAIARQFMGKRRNYSGESFWAXGYYVSTVDLY
                     EGMVRAYIRNQELEDARLEQLSLPL"
                     /note="IS605 e-value= 2.1e-41 fragment hit coverage=
                     83.55%, between model( 152 aa) positions 17; 143 length
                     is 127aa with 0 gaps, 1 stops, absolute frame= Minus3"
     CDS             complement(6347595..6346655)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 1.1e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
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                     Minus3"
     CDS             complement(6347595..6346655)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TKNRXPMSYQIRNWSEYNAGLKQRGSVTFWLEQS--AIVHWLET
                     TPRQKRGASLTYSDTAISTFETVKCIYGLAGRQTEGFLNSLFELMGIELPVCDHSTVS
                     RRKGQLSISLPVIPKQGAIHVVIDSTGVKVYG------------EGEWKTRQHGVS-K
                     RRTWRKLHLSVDESTGEILTGVVTTNDVQDGEVFEDLLEGIDD-----EIEQVSAD-G
                     AYDQSHCYDALMERNATAAIPPRKNA-------------KIWQHGNC--NApphpRDQ
                     NLRAIRKQGRKRWKKQAHYHRRSLAETTMFRFKTIFGGQVRSRNFDNQATELLLQCAA
                     LN-RMIQIAKPETVWVE"
                     /note="IS5_IS903   e-value= 2.2e-96 complete sequence hit
                     coverage= 100%, between model( 347 aa) positions 1; 347
                     length is 314aa with 37 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(6338160..6337466)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                     /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                     51.23%, between model( 486 aa) positions 1; 249 length is
                     232aa with 27 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6338160..6337034)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus3"
     CDS             complement(6335550..6334313)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="IRIPLNLPDI--RVLELSKTERGDWL------IKIESTLQGTTC
                     HQCGREITDL-HCHDQ-PFRIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWH
                     EPRSPNTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADL
                     KVMGMDEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-I
                     DLRQTIERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRR
                     ELS------------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLER
                     LFA--YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVlKSGIKEFDSFLTT
                     INNWMDEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQT
                     FAVTXTL"
                     /note="ISL3  e-value= 1.2e-45 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
                     length is 413aa with 44 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(6335391..6334313)
                     /colour="255 0 0"
```

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                     /evidence=predicted
                     /translation="RIRHLPLFEVPVYLEIRPKRYRCKYCDDhpTTTQHLEWHEPRSP
                     NTKAYERWLLRILIN-STVSDVARKLGVSEDIVSGIIDRWIAAQVDWSEYADLKVMGM
                     DEISLKRG--HR---DFVVLITIPTTdgVDILAVLADRKQQTVANFLQSIP-IDLRQT
                     IERVCTDMYQGFVSAVREQLPQAKIVIDRFHVTKAYRNCADTVRKREVKRLRRELS--
                     ----------KQEYD-----------SIKGAMWPFRKRPENLKES-EQQLLERLFA--
                     YSPQLKQAYNLREKLTQIFEGRYTKHGAKcAIRAWCKQVlKSGIKEFDSFLTTINNWM
                     DEMTNYFLEG-WTSGFVEGFNNRVKVLKRRCYGIFDIERLFQRISLDLNGYQTFAVTX
                     TL"
                     /note="ISL3  e-value= 8.8e-52 fragment hit coverage=
                     86.03%, between model( 451 aa) positions 64; 451 length
                     is 360aa with 34 gaps, 1 stops, absolute frame= Minus3"
     CDS             complement(6315477..6314273)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TCSFFLTSXVSAIESGLLKRLSKRLVERALAGELTHHLQQSSND
                     QS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRIA-
                     GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVINSVMEEVKDWRSRPLD
                     EV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAKFW
                     LSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPWKE
                     SRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQYP
                     MAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPILN
                     WKAALSHFAILFPTRFNYXIH"
                     /note="IS256 e-value= 6.6e-165 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 402aa with 11 gaps, 2 stops, absolute frame=
                     Minus3"
     CDS             complement(6315435..6314273)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SGLLKRLSKRLVERALAGELTHHLQQSSNDQS-GDeNSNGPRNS
                     RNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRIA-GLDEKIIALYARGM
                     TTRDIRAQLVELYG--ANISEALISDVINSVMEEVKDWRSRPLDEV--YPIVYLDALY
                     VNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAKFWLSVLTDLKNRGTQD
                     ILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPWKESRAVAADLKPIYQA
                     ATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQYPMAIRKVIYTTNAIE
                     SLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPILNWKAALSHFAILFPT
                     RFNYXIH"
                     /note="IS256 e-value= 1.1e-164 fragment hit coverage=
                     96.59%, between model( 410 aa) positions 15; 410 length
                     is 388aa with 11 gaps, 1 stops, absolute frame= Minus3"
     CDS             complement(6239001..6238595)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MLLVRPISTESLRLLHRIYHSSRHHQVRQRAHCLILFAQGWPPY
                     TLASLFSVSPKTVYNWLKAWNNRG---FAGLYNHPGRGRKPMFNPDQQQQIYEWT-QA
                     SPIQ---------LNQVLAQIEQQWSVRVSKATVKRVLKQMDMSWHR"
                     /note="IS630 e-value= 8.7e-15 fragment hit coverage=
                     39.63%, between model( 376 aa) positions 1; 149 length is
                     136aa with 13 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6238941..6238604)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SSRHHQVRQRAHCLILFAQGWPPYTLASLFSVSPKTVYNWLKAW
                     NNRGFAGLYNH---PGRGRKPMfNPDQQQQIYEWTQASPIQLNQVLAQIEQQWSVR--
                     -VSKATVKRVLKQMDMS"
                     /note="IS481 e-value= 3.5e-09 fragment hit coverage=
                     33.62%, between model( 351 aa) positions 1; 118 length is
                     113aa with 6 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6207357..6205703)
```

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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FQQFLPCQDTLHLDSWDLDSTNHQMT---------FHVSSTQAL
                     ACCPVCHQTSHRVHSRYERTLRDLPCVEFCLTILLQVCKFFCsnKTCKRRIfterlpQ
                     VAVPWARRTVRFAEHLSSIGLALGGAAAARLSYQINYGSSRNT----MLRALFKLPLP
                     -SVTTPKILGVDDFALRRG--HEYGTILVDLEKH----QPIVLLTDRKADTLADWLNE
                     HP------GVEVISRDRSKAYKSGASEGAPDALQVADRFHLLQNLEEILENVF-----
                     -------------------SSHSQ----VIKTVEYTLLKATLAEHQDTEAMSQPvvkp
                     qvdpnsrkaqnrarrlekyeqthalrkqgylikdiahhlgigkrtvytylaadtfqey
                     kthprrgwsglnpykaylleqwnkgrqnskqllaeiqqqgfkgsytmvvrythklrqs
                     lppqpprdslnelpgrgpvpeaqeliqkpltvqraawlvmrkvenlTEEDETILE-QL
                     SSQPELSKAIDLAQSLLFIVR-KRLPQHLDPWLDRAKN--SALKPFQSFAKGLLDDYE
                     AVKA-ALTLEVSNGQVEGQNNRLK--------------MVKRQMYGRAGLDLLNKRLV
                     L"
                     /note="ISL3  e-value= 9.2e-10 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
                     length is 552aa with 73 gaps, 0 stops, absolute frame=
                     Minus3"
     CDS             complement(6206910..6206654)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="TTPKILGVDDFALRRG--HEYGTILVDLEKH----QPIVLLTDR
                     KADTLADWLNEHP------GVEVISRDRSKAYKSGASEGAPDALQVADRFHLLQ"
                     /note="ISL3  e-value= 1.5e-21 fragment hit coverage=
                     21.73%, between model( 451 aa) positions 156; 253 length
                     is 86aa with 12 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6206475..6206177)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="RLEKYEQTHALRKQGYLIKDIAHHLGIGKRTVYTYLAADTFQEY
                     KTHPRR-------GWSGLNPYKAYLLEQWNKGRQNSKQ--------LLAEIQQQGFKG
                     SYTMVVRYTHKLR"
                     /note="IS21_ORF1   e-value= 2.7e-14 fragment hit coverage=
                     21.90%, between model( 525 aa) positions 1; 115 length is
                     100aa with 15 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6206010..6205742)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LEQLSSQPELSKAIDLAQSLLFIVR-KRLPQHLDPWLDRAKN--
                     SALKPFQSFAKGLLDDYEAVKA-ALTLEVSNGQVEGQNNRLKMVKRQMYG"
                     /note="ISL3  e-value= 1.6e-06 fragment hit coverage=
                     20.84%, between model( 451 aa) positions 331; 424 length
                     is 90aa with 4 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(6205539..6203885)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FQQFLPCQDTLHLDSWDLDSTNHQMT---------FHVSSTQAL
                     ACCPVCHQTSHRVHSRYERTLRDLPCVEFCLTILLQVCKFFCsnKTCKRRIfterlpQ
                     VAVPWARRTVRFAEHLSSIGLALGGAAAARLSYQINYGSSRNT----MLRALFKLPLP
                     -SVTTPKILGVDDFALRRG--HEYGTILVDLEKH----QPIVLLTDRKADTLADWLNE
                     HP------GVEVISRDRSKAYKSGASEGAPDALQVADRFHLLQNLEEILENVF-----
                     -------------------SSHSQ----VIKTVEYTLLKATLAEHQDTEAMSQPvvkp
                     qvdpnsrkaqnrarrlekyeqthalrkqgylikdiahhlgigkrtvytylaadtfqey
                     kthprrgwsglnpykaylleqwnkgrqnskqllaeiqqqgfkgsytmvvrythklrqs
                     lppqpprdslnelpgrgpvpeaqeliqkpltvqraawlvmrkvenlTEEDETILE-QL
                     SSQPELSKAIDLAQSLLFIVR-KRLPQHLDPWLDRAKN--SALKPFQSFAKGLLDDYE
                     AVKA-ALTLEVSNGQVEGQNNRLK--------------MVKRQMYGRAGLDLLNKRLV
                     L"
                     /note="ISL3  e-value= 9.2e-10 complete sequence hit
                     coverage= 100%, between model( 451 aa) positions 1; 451
```

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                length is 552aa with 73 gaps, 0 stops, absolute frame=
                Minus3"
CDS             complement(6205092..6204836)
                /colour="255 0 0"
                /evidence=predicted
                /translation="TTPKILGVDDFALRRG--HEYGTILVDLEKH----QPIVLLTDR
                KADTLADWLNEHP------GVEVISRDRSKAYKSGASEGAPDALQVADRFHLLQ"
                /note="ISL3  e-value= 1.5e-21 fragment hit coverage=
                21.73%, between model( 451 aa) positions 156; 253 length
                is 86aa with 12 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(6204657..6204359)
                /colour="255 0 0"
                /evidence=predicted
                /translation="RLEKYEQTHALRKQGYLIKDIAHHLGIGKRTVYTYLAADTFQEY
                KTHPRR-------GWSGLNPYKAYLLEQWNKGRQNSKQ--------LLAEIQQQGFKG
                SYTMVVRYTHKLR"
                /note="IS21_ORF1   e-value= 2.7e-14 fragment hit coverage=
                21.90%, between model( 525 aa) positions 1; 115 length is
                100aa with 15 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(6204192..6203924)
                /colour="255 0 0"
                /evidence=predicted
                /translation="LEQLSSQPELSKAIDLAQSLLFIVR-KRLPQHLDPWLDRAKN--
                SALKPFQSFAKGLLDDYEAVKA-ALTLEVSNGQVEGQNNRLKMVKRQMYG"
                /note="ISL3  e-value= 1.6e-06 fragment hit coverage=
                20.84%, between model( 451 aa) positions 331; 424 length
                is 90aa with 4 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(6061491..6061148)
                /colour="255 0 0"
                /evidence=predicted
                /translation="KYIVTLTPEERSELIQLTRRRTLSARKMKRAQILMLADEGHKDD
                TITQMLNAGISTVHRTRQKFVEGG---VEfALNERPRPGGQKKLDSKAEALLIATACS
                DPPTG----CCRWTMQLLAE"
                /note="IS630 e-value= 1.2e-15 fragment hit coverage=
                32.18%, between model( 376 aa) positions 1; 121 length is
                115aa with 7 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(5745174..5744480)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                51.23%, between model( 486 aa) positions 1; 249 length is
                232aa with 27 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(5745174..5744048)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                /note="IS4   e-value= 9.9e-07 complete sequence hit
```

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                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus3"
     CDS             complement(5719893..5719670)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SQMSTLTCPNCRSQN-VVKNGRIHNGKQNHKCKTCGRQFV--EA
                     PQQKRIDSSTKGLIDKLLLEKIPLAGIARVCDVS"
                     /note="IS1_ORF1    e-value= 3.6e-14 fragment hit coverage=
                     32.64%, between model( 239 aa) positions 1; 78 length is
                     75aa with 3 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(5522628..5522375)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HIEFSyplMQCPLCGHPK-IYKHGKTSKGSQRXRCPHCHQTFS-
                     DtfDTLYYRRQiSPQTIQVILQSHAEGSSFRGLPRITGVAYNT"
                     /note="IS1_ORF1    e-value= 9e-13 fragment hit coverage=
                     33.89%, between model( 239 aa) positions 1; 81 length is
                     85aa with 2 gaps, 1 stops, absolute frame= Minus3"
     CDS             complement(5391534..5391422)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KDYERXTDSTEVMIYICMIRLMVRRVAXTLRRWSLFTH"
                     /note="IS5_IS1031  e-value= 2.7e-08 fragment hit coverage=
                     12.88%, between model( 295 aa) positions 258; 295 length
                     is 38aa with 0 gaps, 2 stops, absolute frame= Minus3"
     CDS             complement(5338785..5338049)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="-----TGVYKRTFkpMLHAWHTYHLSRSN--AGRPPKLCRCDQL
                     LVALQYWREYRTYFHIAGDWEVSESTVCRIVHQVETALMNSGLFRLPGQKSLLQGFER
                     PDVVVMDVTETPIERPQTRQKAYYSGKKRDIPSNARLSLTATLXrlsaltLVQVVG--
                     -------MIFRSSRVQVSISIQIPRVCKIADIKGLQ-----PIMP-TAMFLSRSHNTV
                     NXLPCSESITVLXVRNEWALNTLIAAXRFSEFCRSAIAIVVVATRCGVTX"
                     /note="IS5_ISL2    e-value= 3.1e-21 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 246aa with 22 gaps, 5 stops, absolute frame=
                     Minus3"
     CDS             complement(5338725..5338415)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SRSNAGRPPKLCRCDQLLVALQYWREYRTYFHIAGDWEVSESTV
                     CRIVHQVETALMNSGLFRLPGQKSLLQGFERPDVVVMDVTETPIERPQTRQKAYYSGK
                     KR"
                     /note="IS5_ISL2    e-value= 9.3e-44 fragment hit coverage=
                     40%, between model( 260 aa) positions 26; 129 length is
                     104aa with 0 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(5175534..5174819)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YLSPES-LQCRASSKVVSMXSTVGNPS---------ILARISDL
                     FPHCWRLGSLXINRLPYCppGRDRSDELRTLSLTRSEISATR---------VRATGCR
                     CDGCDXNAHXTSPDKTKSVLF----RKKKRHTFKCQIIANRNTLEIICLNVGPGRRHD
                     FQIFKGSGIHIHPDTESLQDSGYQGIAAYHANSYVPLKKPQHGELTSLQREYNRALSQ
                     ERMGIEHINRSLKIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                     /note="IS5_ISL2    e-value= 1.5e-39 complete sequence hit
                     coverage= 100%, between model( 260 aa) positions 1; 260
                     length is 239aa with 23 gaps, 4 stops, absolute frame=
                     Minus3"
     CDS             complement(5175219..5174819)
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                /colour="255 0 0"
                /evidence=predicted
                /translation="KKKRHTFKCQIIANRNTLEIICLNVGPGRRHDFQIFKGSGIHIH
                PDTESLQDSGYQGIAAYHANSYVPLKKPQHGELTSLQREYNRALSQERMGIEHINRSL
                KIFRILSERYRNRRRRYALRCNLIAAIYNYEL"
                /note="IS5_ISL2   e-value= 6.5e-62 fragment hit coverage=
                51.54%, between model( 260 aa) positions 127; 260 length
                is 134aa with 0 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(5122416..5122250)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SRRRAYPNDMSDTEWDVLRPLLPPANGFR-------RPRTVNLR
                EILNAIFYVQRSGYQWEML"
                /note="IS5_IS1031  e-value= 1.2e-20 fragment hit coverage=
                21.36%, between model( 295 aa) positions 15; 77 length is
                56aa with 7 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(4461825..4461482)
                /colour="255 0 0"
                /evidence=predicted
                /translation="KYIVTLTPEERSELIQLTRRRTLSARKMKRAQILMLADEGHKDD
                TITQMLNAGISTVHRTRQKFVEGG---VEfALNERPRPGGQKKLDSKAEALLIATACS
                DPPTG----CCRWTMQLLAE"
                /note="IS630 e-value= 1.2e-15 fragment hit coverage=
                32.18%, between model( 376 aa) positions 1; 121 length is
                115aa with 7 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(4252959..4252802)
                /colour="255 0 0"
                /evidence=predicted
                /translation="HHPHPRVQRRMEVLYLKSQGLPHAQICQLCQISRPTLAKTLRLY
                QQGGIEGLK"
                /note="IS481 e-value= 1.1e-08 fragment hit coverage=
                15.10%, between model( 351 aa) positions 1; 53 length is
                53aa with 0 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(4219197..4219103)
                /colour="255 0 0"
                /evidence=predicted
                /translation="AERG--ITLFELPSYSPHLNLIERLWQFMKYQWI"
                /note="IS630 e-value= 1.8e-09 fragment hit coverage=
                9.04%, between model( 376 aa) positions 300; 333 length
                is 32aa with 2 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(4134504..4134368)
                /colour="255 0 0"
                /evidence=predicted
                /translation="WQTDGXDGYSRQLPDE---VIHHVSKALTQRLERTNGILWQQTG
                RWHRR"
                /note="IS1_ORF2   e-value= 3.9e-08 fragment hit coverage=
                20.68%, between model( 237 aa) positions 164; 212 length
                is 46aa with 3 gaps, 1 stops, absolute frame= Minus3"
CDS             complement(3873963..3873578)
                /colour="255 0 0"
                /evidence=predicted
                /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                /note="IS630 e-value= 1.1e-13 fragment hit coverage=
                38.83%, between model( 376 aa) positions 188; 333 length
                is 129aa with 20 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(3585738..3585497)
                /colour="255 0 0"
                /evidence=predicted
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                /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                19.91%, between model( 422 aa) positions 23; 106 length
                is 81aa with 3 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(3216468..3216083)
                /colour="255 0 0"
                /evidence=predicted
                /translation="YADESGMDHRDEYDY-AYGPKGE-----------RVYA-LKTG-
                RRSGRVNMIAALRAKQL--MAPFTIEGACNRTVFELwLERCLIPvlKPGQKLVI--DN
                ATFHKGGQIQELVEKAG--CEVWYLPPYSPDLNKIERSWSWIKSRIR"
                /note="IS630  e-value= 1.1e-13 fragment hit coverage=
                38.83%, between model( 376 aa) positions 188; 333 length
                is 129aa with 20 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(2709669..2709254)
                /colour="255 0 0"
                /evidence=predicted
                /translation="IERLQTKHP--HQIVYVDEAGIDNRADYPY-GYCPVG-------
                ----QRFYD-LKSG-KRTERVSFIAALKEGQL--FSPMIFEGSCNRLLFEAWLQQSLI
                -SQLQLgdVIVIDNASFHHGQRIEEIVAEAG--CEIWYLPSYSPDLNKIERWWFVLKN
                "
                /note="IS630  e-value= 7.3e-15 fragment hit coverage=
                42.02%, between model( 376 aa) positions 173; 330 length
                is 139aa with 21 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(2412987..2412026)
                /colour="255 0 0"
                /evidence=predicted
                /translation="LLRAIISSLyVSCWDWR-TSKFR------LTVPFDAXXRGLTSN
                RXATNLKLGCSRKLRLTLPIIMQHPWMangFVRGSpMKTASSVLXDWXV------YSQ
                WKQASPSSSKPS---------LRRIIAKS-KSSRLywkHYNSMACXSPWMP----YTP
                KKT----------------L----------------QQVVASVN-DYLIAVKRNQGRL
                YDHLQTYFeCLKPMAEHTHS-----IQSRGREEHRCIQVYEPVGI---ALQEWEAIRS
                VLCVQRWGTRQGKAY----HNTAYYISSAATSPHH---WQSLVREHWGIENRLHWPKD
                VVFGEDDYRLEDEQALLNWSVLRTIVINILRLNG--YQSLKTAMTKLANRVDIIFSLL
                TXNSPA"
                /note="ISAs1  e-value= 1.9e-08 complete sequence hit
                coverage= 100%, between model( 389 aa) positions 1; 389
                length is 321aa with 77 gaps, 7 stops, absolute frame=
                Minus3"
CDS             complement(2412552..2412110)
                /colour="255 0 0"
                /evidence=predicted
                /translation="DYLIAVKRNQGRLYDHLQTYFeCLKPMAEHTHS-----IQSRGR
                EEHRCIQVYEPVGI---ALQEWEAIRSVLCVQRWGTRQGKAY----HNTAYYISSAAT
                SPHH---WQSLVREHWGIENRLHWPKDVVFGEDDYRLEDEQALLNWSVLRTIVINILR
                LNG"
                /note="ISAs1  e-value= 2.4e-27 fragment hit coverage=
                41.65%, between model( 389 aa) positions 198; 359 length
                is 148aa with 15 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(2404083..2403389)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                /note="IS4    e-value= 4.7e-14 fragment hit coverage=
                51.23%, between model( 486 aa) positions 1; 249 length is
                232aa with 27 gaps, 0 stops, absolute frame= Minus3"
```

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CDS             complement(2404083..2402957)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                /note="IS4   e-value= 9.9e-07 complete sequence hit
                coverage= 100%, between model( 486 aa) positions 1; 486
                length is 376aa with 117 gaps, 0 stops, absolute frame=
                Minus3"
CDS             complement(2382702..2382314)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FFMDESGFSLVPCIPY-GWQPIG-------------TYL-EIPT
                RSSKRLNVLGFLSRRQGL--HAYTSEQTITSEVVShCIDTFFADV--ELPTVIVVDQA
                PIHTSQsiyEMKAEWAERG--ITLFELPSYSPHLNLIERLWQFMKYQWI"
                /note="IS630 e-value= 6.5e-11 fragment hit coverage=
                39.10%, between model( 376 aa) positions 187; 333 length
                is 130aa with 21 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(2279970..2279714)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SMECPCCQSQK-IHKRGFDSlqdgTLVQRYQCEDCNRRFK-ERT
                GNPMARLRTtslVVSYAIKARTKGMGVRATGRTFGTSHTTIMRW"
                /note="IS1_ORF1    e-value= 8.4e-08 fragment hit coverage=
                33.89%, between model( 239 aa) positions 5; 85 length is
                86aa with 2 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(1504611..1503287)
                /colour="255 0 0"
                /evidence=predicted
                /translation="CDSDVTLDF----YQDHPLCVQFSDLDLSSDVGILLAAQAESRI
                HICQDIADCIEEWRDPDKLTHSLPQLVAQRVYQLIGGYEDANDSDSLRHDPIFKIACE
                YLPIPESnVLASQLTISRLENQVTTDQTAAMRRQFIDRFIA-----SYPHPPSTIVLD
                IDGWDDPTHGDQEGSAFHGYYGQHMYFPVLINE----AQSGFPLVCQLRRGNSHPGKA
                VAGILRWLFWRLKRAWPGVT-------------IVLRADAGFSLPEILRVCERSGIHY
                AIGFSSNAVLKRKISNV-LEQARLQYCRTQQKARL-----FDDVYYAAATWDYPRRLV
                MKAEYLPKGANPRFVLTD-MMLSPQQLYDTFYVQRGGDSEHpIKELKRGIQADRLSCH
                RFTANQFRLLLA-------------QAAYLLMITLRXAAQ-GTELATAQVERLRCALI
                KGAARVRVSVRRVLVELATFCPFEKEIRLIAQRLCDPMP"
                /note="IS1380 e-value= 2.1e-64 complete sequence hit
                coverage= 100%, between model( 487 aa) positions 1; 487
                length is 442aa with 47 gaps, 1 stops, absolute frame=
                Minus3"
CDS             complement(1504542..1503287)
                /colour="255 0 0"
                /evidence=predicted
                /translation="LSSDVGILLAAQAESRIHICQDIADCIEEWRDPDKLTHSLPQLV
                AQRVYQLIGGYEDANDSDSLRHDPIFKIACEYLPIPESnVLASQLTISRLENQVTTDQ
                TAAMRRQFIDRFIA-----SYPHPPSTIVLDIDGWDDPTHGDQEGSAFHGYYGQHMYF
                PVLINE----AQSGFPLVCQLRRGNSHPGKAVAGILRWLFWRLKRAWPGVT-------
                ------IVLRADAGFSLPEILRVCERSGIHYAIGFSSNAVLKRKISNV-LEQARLQYC
                RTQQKARL-----FDDVYYAAATWDYPRRLVMKAEYLPKGANPRFVLTD-MMLSPQQL
                YDTFYVQRGGDSEHpIKELKRGIQADRLSCHRFTANQFRLLLA-------------QA
                AYLLMITLRXAAQ-GTELATAQVERLRCALIKGAARVRVSVRRVLVELATFCPFEKEI
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                     RLIAQRLCDPMP"
                     /note="IS1380 e-value= 1.5e-67 fragment hit coverage=
                     94.46%, between model( 487 aa) positions 28; 487 length
                     is 419aa with 43 gaps, 1 stops, absolute frame= Minus3"
     CDS             complement(691935..690725)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
                     A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVINSVMEEVKDWRSRP
                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256  e-value= 3.8e-165 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(691935..690725)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DELIGENPQPEdiLGESGLLKRLSKRLVERALAGELTHHLQQSS
                     NDQS-GDeNSNGPRNSRNGYSKKTVQSEQG-EMDLSIPRDRCG-EFEPVLVPKGQRRI
                     A-GLDEKIIALYARGMTTRDIRAQLVELYG--ANISEALISDVINSVMEEVKDWRSRP
                     LDEV--YPIVYLDALYVNIKVNGQVSKRAVYVALAVTVEGNKELLGLWIGAAerEGAK
                     FWLSVLTDLKNRGTQDILIACCDGLKGFPQAIESVYPQTQVQVCIVHLIRNSLRHVPW
                     KESRAVAADLKPIYQAATLE-ESEAALDAFAH-KWDETYPGISQIWIRHWDNVAPLFQ
                     YPMAIRKVIYTTNAIESLNRSLRKVIKTKAVFPNEESVYKLMFLAMRNISKR-WTRPI
                     LNWKAALSHFAILFPTRFNYXIH"
                     /note="IS256  e-value= 9.9e-166 complete sequence hit
                     coverage= 100%, between model( 410 aa) positions 1; 410
                     length is 404aa with 11 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(558171..557924)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MQCPLCGHPK-THKHGKTSKGSQRYRCPHCHQTFS--ETFDTLH
                     YRRQISSEtiqtILQSHAEGSSLRGLSRITGVAYNTCVSVIR"
                     /note="IS1_ORF1    e-value= 2.1e-12 fragment hit coverage=
                     34.31%, between model( 239 aa) positions 6; 87 length is
                     83aa with 3 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(483540..483299)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VKLAELIPWESFESEYADQFSQ---TMGAPAKPFRVALGTLIIK
                     EKLGISDAETVEQIRENPYLQYFLGFSEYRESAPFDASML"
                     /note="IS5_IS5     e-value= 2.6e-06 fragment hit coverage=
                     19.91%, between model( 422 aa) positions 23; 106 length
                     is 81aa with 3 gaps, 0 stops, absolute frame= Minus3"
     CDS             complement(477669..477176)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LEKTGIESKKKTYGYR--ERD--ETQR---QAFIERLQTKHP--
                     HQIVYVDEAGIDNRADYPY-GYCPVG-----------QRFYD-LKSG-KRTERVSFIA
                     ALKEGQL--FSPMTFEGSCNRLLFEAWLQQSLI-SQLQLgdVIVIDNASFHHGQRIEE
                     IVAEAG--CEIWYLPSYSPDLNKIERWWFVLKN"
                     /note="IS630  e-value= 3e-16 fragment hit coverage=
                     50.80%, between model( 376 aa) positions 140; 330 length
                     is 165aa with 28 gaps, 0 stops, absolute frame= Minus3"
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     CDS             complement(474207..474032)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GXHPIAQICQVLNYPRSQVYYHARGQP-----DESELKAAIAGV
                     AGAYP-TYGYRRITAQLQ---RQG"
                     /note="IS3_IS150_ORF2    e-value= 2.1e-06 fragment hit
                     coverage= 17.48%, between model( 389 aa) positions 103;
                     170 length is 59aa with 9 gaps, 1 stops, absolute frame=
                     Minus3"
     CDS             complement(474183..474032)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="CQVLNYPRSQVYYHARGQPDESELKAAIAGVAGAYPTYGYRRIT
                     AQLQRQG"
                     /note="IS3_IS407_ORF2    e-value= 1.2e-07 fragment hit
                     coverage= 14.83%, between model( 344 aa) positions 85;
                     135 length is 51aa with 0 gaps, 0 stops, absolute frame=
                     Minus3"
     CDS             complement(474147..474035)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YHARgQPDESELKAAIAGVAGAYPTYGYRRITAQLQRQ"
                     /note="IS3_IS2_ORF2      e-value= 9.4e-07 fragment hit
                     coverage= 12.25%, between model( 302 aa) positions 48; 84
                     length is 38aa with 0 gaps, 0 stops, absolute frame=
                     Minus3"
     CDS             complement(472965..471914)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MSPLMMKTSVFE------GLGLGTQPRTTISHEERLVLSGNlsN
                     XISVKFGTMDTTIMQGXigtrpLTTEDRMLRQTHKXTQARTHQYRIhxLKXRVFTGAK
                     -----AAIQSLAELTQMVE------------NHKG--NECDDSLTLKQSVYFI-----
                     -DCFSRLLXSKLK-----GYCVNHKRVARLMRQIGIMAKTKVK-RKRTTNSEHSfpRY
                     GNRVLNLS--IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTRAIRGWHLSRHIDQQ
                     LTLRALNKALERAT---PEIHHS-----DQGVQYAAAAYMQLLQQHQVQISMAEVGQA
                     WQNGYAERLMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYMHKRIHSSLGYLTPC
                     EYEQQWRQQ"
                     /note="IS3_IS150_ORF2    e-value= 4.3e-13 complete sequence
                     hit coverage= 100%, between model( 389 aa) positions 1;
                     389 length is 351aa with 50 gaps, 5 stops, absolute
                     frame= Minus3"
     CDS             complement(472827..471917)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MDTTIMQGXIGTRplTTEDRMLRQTHKXTQARTHQYRIHXLKXR
                     VFTGAKAAIQSLAELTQMVENhkgneCDDSLTLKQSVYFIDCFSRLLXSKlkGYCVNH
                     KRVARLMRQIGIMAKTKVK----RKRTTNSEHSF-PRYGNRvlNLSIDHPEQVWVADI
                     TYIRL--QQEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALER----ATPEI
                     HHSDQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYRN
                     FT--EAYEHIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 6.7e-29 complete sequence
                     hit coverage= 100%, between model( 306 aa) positions 1;
                     306 length is 304aa with 13 gaps, 5 stops, absolute
                     frame= Minus3"
     CDS             complement(472827..471890)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="MDTTIMQGXI------------GTRPLTTEDRMLRQTHKXT---
                     QARTHQYRIHXLKXRVFTGAKA--AIQSLAELTQMVE--------------NHKGNEC
                     DDSLTLKQSVYFI----DCF-SRLLXSKL--KGYCVNHKRVARLMRQIGIMAKTKV-K
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                     RKRTtnsehsfprYGNRVLNLSIDHPEQVWVADITYIRLQ--QEFVYLAVVmDVFTRA
                     IRGWHLSRHIDQQLTLRALNKALE-RATPEIHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDvYMHKRIHSSLGY
                     LTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS407_ORF2    e-value= 9.2e-07 complete sequence
                     hit coverage= 100%, between model( 344 aa) positions 1;
                     344 length is 313aa with 42 gaps, 5 stops, absolute
                     frame= Minus3"
     CDS             complement(472785..471890)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="LTTEDRmLRQTH------KXTQARTHQYRIHXLKXRVFTGAKAA
                     IQSLAELTQMVEN-HKGNECddsltlkqsVYFIDCFSRLLXSklKGYCVNHKRVARLM
                     RQIGIMAKTKVKRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEFVY
                     LAVVMDVFTRAIRGWHLSRHIDQQLT-LRALNKALERATPE-------IHHSDQGVQY
                     AAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDL---S-DYRNFTEAY
                     EHIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 2.6e-25 complete sequence
                     hit coverage= 100%, between model( 307 aa) positions 1;
                     307 length is 299aa with 20 gaps, 4 stops, absolute
                     frame= Minus3"
     CDS             complement(472752..471881)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="HKXTQARTH-QYRIHXLKX------RVFTGA---KAAIQSLAEL
                     TQMvENHKGNECDDSL-----TLKQS-----VYFIDCFSRLLxsKLKGYCVNHKRVAR
                     LMRQIGIMAKTKVKRKRTTNSEHSFPRYGNRVL-NLSIDHPEQVWVADITYIRLQQEF
                     VYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALERATPE--------IHHSDQGV
                     QYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIKEEEVDLSDYrnFTEAYEH
                     IEQFLEDV--YMHKRIHSSLGYLTPCEYEQQWRQQNNHYCMNKEDS"
                     /note="IS3_IS51_ORF2     e-value= 1.6e-14 complete sequence
                     hit coverage= 100%, between model( 317 aa) positions 1;
                     317 length is 291aa with 31 gaps, 3 stops, absolute
                     frame= Minus3"
     CDS             complement(472737..471908)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="ARTHQYRIHXLkXRVFT----GAKAAIQSLAELTQMVENHKGNE
                     CDDSLTLKQSVYFIDCFSRLLXSklKGYCVNHKRVARLMRQIGIMAKTKVKRKRTTNS
                     EHSFPRY---GNRVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHL
                     SRHIDQQLTLRALNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISM
                     AEVGQAWQNGYAERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWRQQNN"
                     /note="IS3_IS3_ORF2      e-value= 7.9e-44 complete sequence
                     hit coverage= 100%, between model( 288 aa) positions 1;
                     288 length is 277aa with 14 gaps, 3 stops, absolute
                     frame= Minus3"
     CDS             complement(472722..471920)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="YRIHXLKXRVFTGAKAAIQSLAELT--QMVEN--HKG--NECDD
                     SLTLKQSVYFID-----CFSRLLXSKL--KGYCVNHKRVARLMRQIGIMAKTKVKRKR
                     TTNSEHSfPRYGNRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGW
                     HLSRHIDQQLTLRALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAE
                     VGQAWQNGYAERLMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGY
                     LTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 1.8e-35 complete sequence
                     hit coverage= 100%, between model( 286 aa) positions 1;
                     286 length is 268aa with 19 gaps, 3 stops, absolute
                     frame= Minus3"
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     CDS             complement(472551..471914)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="SKLKGYCVNHKRVARLMRQIGIMAKTKVK-RKRTTNSEHSfpRY
                     GNRVLNLS--IDHPEQVWVADITYIRLQ-QEFVYLAVVMDVFTRAIRGWHLSRHIDQQ
                     LTLRALNKALERAT---PEIHHS-----DQGVQYAAAAYMQLLQQHQVQISMAEVGQA
                     WQNGYAERLMRTIKEEEVD--LSDYRNFTEAYEHIEQFLEdVYMHKRIHSSLGYLTPC
                     EYEQQWRQQ"
                     /note="IS3_IS150_ORF2    e-value= 3.3e-35 fragment hit
                     coverage= 57.58%, between model( 389 aa) positions 166;
                     389 length is 213aa with 14 gaps, 0 stops, absolute
                     frame= Minus3"
     CDS             complement(472548..471917)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="KLKGYCVNHKRVARLMRQIGIMAKTKVK----RKRTTNSEHSF-
                     PRYGNRvlNLSIDHPEQVWVADITYIRL--QQEFVYLAVVMDVFTRAIRGWHLSRHID
                     QQLTLRALNKALER----ATPEIHHSDQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQ
                     NGYAERLMRTIKEEEVDLSDYRNFT--EAYEHIEQFLEDVYMHKRIHSSLGYLTPCEY
                     EQQWRQ"
                     /note="IS3_IS150_ORF1    e-value= 2.3e-40 fragment hit
                     coverage= 72.55%, between model( 306 aa) positions 85;
                     306 length is 211aa with 13 gaps, 0 stops, absolute
                     frame= Minus3"
     CDS             complement(472548..471920)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="K-LKGYCVNHKRVARLMRQIGIMAKTKVKRKRKRTTNSEHSfPRYG
                     NRVLNLS-IDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTL
                     RALNKALERA-TPE--IHHSDQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAER
                     LMRTIK-EEEVDL-SDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWR"
                     /note="IS3_IS3_ORF1      e-value= 2.3e-45 fragment hit
                     coverage= 75.52%, between model( 286 aa) positions 71;
                     286 length is 210aa with 7 gaps, 0 stops, absolute frame=
                     Minus3"
     CDS             complement(472539..471908)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="GYCVNHKRVARLMRQIGIMAKTKVKRKRKRTTNSEHSFPRY---GN
                     RVLNLSIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRA
                     LNKALER----ATPE---IHHSDQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYA
                     ERLMRTIKEEEVDLSDYRNFTEAYEHIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ
                     QNN"
                     /note="IS3_IS3_ORF2      e-value= 7.7e-58 fragment hit
                     coverage= 76.74%, between model( 288 aa) positions 68;
                     288 length is 211aa with 10 gaps, 0 stops, absolute
                     frame= Minus3"
     CDS             complement(472530..471890)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="VNHKRVARLMRQIGIMAKTKVKRKRKRTTNSEHSFPRYGNRVL-NL
                     SIDHPEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHLSRHIDQQLT-LRALNKA
                     LERATPE-------IHHSDQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLM
                     RTIKEEEVDL---S-DYRNFTEAYEHIEQFLEDVYMHKRIHSSLGYLTPCEYEQQWRQ
                     QNNHYCMNK"
                     /note="IS3_IS51_ORF1     e-value= 9.6e-44 fragment hit
                     coverage= 73.94%, between model( 307 aa) positions 81;
                     307 length is 214aa with 13 gaps, 0 stops, absolute
                     frame= Minus3"
     CDS             complement(472518..471905)
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                /colour="255 0 0"
                /evidence=predicted
                /translation="RVARLMRQIGIMAKTKVKRKRTTNSEHSFPRYGNRVL-NLSIDH
                PEQVWVADITYIRLQQEFVYLAVVMDVFTRAIRGWHLSRHIDQQLTLRALNKALERAT
                PE--------IHHSDQGVQYAAAAYMQLLQQHQVQISMAEVGQAWQNGYAERLMRTIK
                EEEVDLSDYrnFTEAYEHIEQFLEDV--YMHKRIHSSLGYLTPCEYEQQWRQQNNH"
                /note="IS3_IS51_ORF2     e-value= 1.8e-35 fragment hit
                coverage= 67.51%, between model( 317 aa) positions 96;
                309 length is 205aa with 11 gaps, 0 stops, absolute
                frame= Minus3"
CDS             complement(470568..470162)
                /colour="255 0 0"
                /evidence=predicted
                /translation="MSLVRPISTESLRLLHRIYHSSRHHQVRQRAHCLILFAQGWPPY
                TLASLFSVSPKTVYNWLKAWNNRG---FAGLYNHPGRGRKPMFNPDQQQQIYEWT-QA
                SPIQ---------LNQVLAQIEQQWSVRVSKATVKRVLKQMDMSWHR"
                /note="IS630 e-value= 3.4e-15 fragment hit coverage=
                39.63%, between model( 376 aa) positions 1; 149 length is
                136aa with 13 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(470508..470171)
                /colour="255 0 0"
                /evidence=predicted
                /translation="SSRHHQVRQRAHCLILFAQGWPPYTLASLFSVSPKTVYNWLKAW
                NNRGFAGLYNH---PGRGRKPMfNPDQQQQIYEWTQASPIQLNQVLAQIEQQWSVR--
                -VSKATVKRVLKQMDMS"
                /note="IS481 e-value= 3.5e-09 fragment hit coverage=
                33.62%, between model( 351 aa) positions 1; 118 length is
                113aa with 6 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(260016..259754)
                /colour="255 0 0"
                /evidence=predicted
                /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVR"
                /note="IS1_ORF1    e-value= 1.7e-15 fragment hit coverage=
                36.40%, between model( 239 aa) positions 1; 87 length is
                88aa with 2 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(260016..259316)
                /colour="255 0 0"
                /evidence=predicted
                /translation="LFYFLMQCPLCGHPK-THKHGKTSKGSQRYRCPHCQQTFS-Etf
                DTLCYRRQiSPETIQTILQAHVEGSSLRGLSRITGVAYNTCVSVVRSA---SHKSQMI
                HNGEVQAVAT---DVINADELWSFVKkskstVSRRSXGXATAGXHXVLRKRVVSCSVA
                VLADIPTSXLknxLKILRAKPPVIIGK----------RMVGKGTH-----DNYPMRSS
                MKXVKPXPNAxsgpmascVSRPGVGIDDRINLA-KSGNRV"
                /note="IS1_ORF1    e-value= 2.6e-07 complete sequence hit
                coverage= 100%, between model( 239 aa) positions 1; 239
                length is 234aa with 24 gaps, 7 stops, absolute frame=
                Minus3"
CDS             complement(220944..220250)
                /colour="255 0 0"
                /evidence=predicted
                /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                AEQAVFAEPWQSFERTFSNGTTETRYrQEIIYGqrhhQKRY"
                /note="IS4   e-value= 4.7e-14 fragment hit coverage=
                51.23%, between model( 486 aa) positions 1; 249 length is
                232aa with 27 gaps, 0 stops, absolute frame= Minus3"
CDS             complement(220944..219818)
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                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="FKHLHLGMIsDIKRKSLPAIARAVGLENHQSLHHFLSESPWVAS
                     hLSDkRLDIILKILDGRRLILLID------------------ETGDCKKGKSTDYVKR
                     QYIGNVGKKENGIvAVTAYGLFQGMILPLSFEVYKPR---------ErLKEEDEYLSK
                     PQIAAGMIRQLQGMGFCFELVLADSLYGEAQTNFVNVLEELKLPYILAIRSNHAVWLP
                     AEQAVFAEPWQSFERTFSNGT-------------------------------TETRYR
                     QEIIYGQRHHQKRyWLLTTDPQTLPENSTS-----------------------YVMAA
                     APE----IKLDEIGDCYGFRTWIEYGLKQSKD-TLGWADFRMTHYEQIEKWWEIVMSA
                     FLMVSLFADVFNDS-------------------------CPVAHQHFAQHPwWDNQNG
                     WKNLLNNVR--LIIQPLIS----WNLLKRWLEVFPSRALKKGF"
                     /note="IS4   e-value= 9.9e-07 complete sequence hit
                     coverage= 100%, between model( 486 aa) positions 1; 486
                     length is 376aa with 117 gaps, 0 stops, absolute frame=
                     Minus3"
     CDS             complement(127077..126635)
                     /colour="255 0 0"
                     /evidence=predicted
                     /translation="DYLIAVKRNQGRLYDHLQTYFeCLKPMAEHTHS-----IQSRGR
                     EEHRCIQVYEPVGI---ALQEWEAIRSVLCVQRWGTRQGKAY----HNTAYYISSAAT
                     SPHH---WQSLVREHWGIENRLHWPKDVVFGEDDYRLEDEQALLNWSVLRTIVINILR
                     LNG"
                     /note="ISAs1 e-value= 2.4e-27 fragment hit coverage=
                     41.65%, between model( 389 aa) positions 198; 359 length
                     is 148aa with 15 gaps, 0 stops, absolute frame= Minus3"

//
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