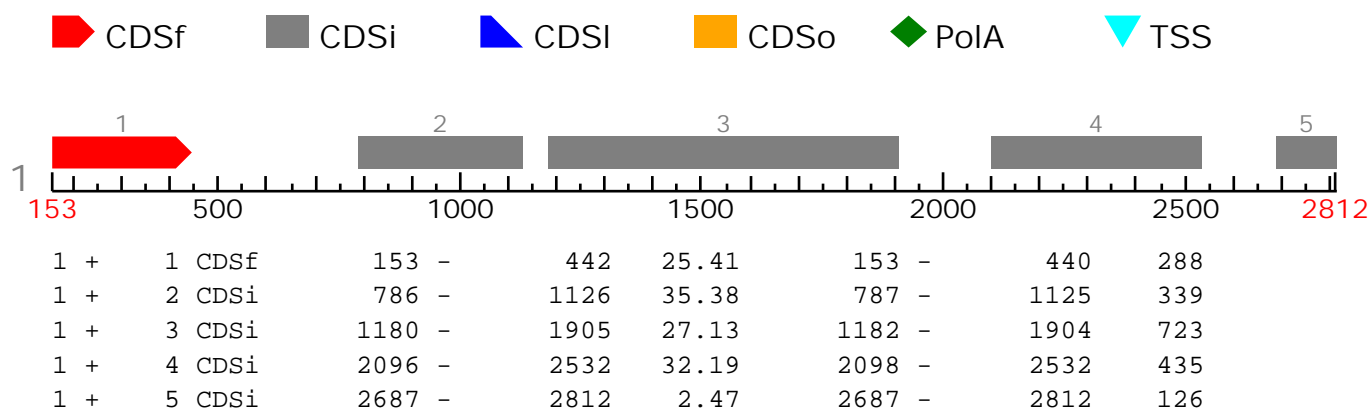


FGENESH 2.6 Prediction of potential genes in *Trichinella_spiralis* genomic DNA
 Seq name: gb|JAECWH010001149.1| Dtropicalis01
 Length of sequence: 2856
 Number of predicted genes 1: in +chain 1, in -chain 0.
 Number of predicted exons 5: in +chain 5, in -chain 0.
 Positions of predicted genes and exons: Variant 1 from 1, Score:103.489978



Predicted protein(s):

```
>FGENESH:[mRNA] 1 5 exon (s) 153 - 2812 1920 bp, chain +
ATGAAATATTGCAAATTTTGCTGCAAAGCTGTGACTGGAGTGAAATTAATTCACGTGCCG
AAGTGTGCTATTAAGAGAAAATTGTGGGAGCAGAGCCTTGGGTGCAGCCTTGGTGAAAAC
TCCCAAATTTGTGATACCCACTTTAATGATTTCGCAGTGAAGGCTGCACCTGCAAAAGGT
CAGACATTTAAAGGAGGCGACTTAACGCAGATGCATTACCTAGTAAAGTGATAGAGCCT
GAACCAGAAAAGATAAAAGAAGGCTATAACAGTGGGAGTACACAAACAGAATGGTTATCA
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GACGAGATGAAGGTCGCTGCTGCCTTTCGAGTATGACAGCTCTCCTGATATTGTTTACGAG
CCAAGCGACTATGTACAACCTGGCTATTGTTTCGTGGTCTAAAAAATCGTGGAAGCAGCCA
GTTTTTTTTCGATTTTAATACCCGAATGGACCCGGATACTCTTAACAATATATTAAGGAAA
CTGCATAGTAAAGGATATTTAGTAGTTGCAATTGTCTCCGATTTAGGTACCGGAAACCAA
AAGCTATGGACAGAGCTCGGTATATCAGAATCAAAAACCTGGTTTAGCCATCCTGCAGAT
GACCAGTTAAAGATTTTCGTTTTTTCGGATACGCCACATTTAATTAAGTTAGTCCGTAAC
CACTATGTGGATTCCGAATTAACAATAAATGGAAAAAATTAACAAAAAACAATTCAG
GAGGCACTTCATCTTTGCAACAAGTCCGATCTGTCTATCCTCTTTAAATTAATGAAAAT
CACATTAATGTTTCGATCGCTCGCAAAACAGAAGGTTAAATTGGCTACCCAGCTGTTTTCG
AATACCACCGCTAGCTCGATCAGACGCTGCTATTCATTGGGGTATGACATTGAAAATGCC
ACCGAAACTGCGGACTTCTTCAAATTGATGAATGATTGGTTTCGACATTTTAAATTCTAAA
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AGGCTCCCATTTTCAAAAAGGTATCATTGTGAATAATGCTTCGCTTGATGGCTTGATATAA
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GTGGAGCATTTTTTTGGCAGCATGCGATCGAGAGGTGGACAATTCGACCATCCCACTCCA
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TATGTCATTAAAAAATTGAGAATCAGTGACAAAGTAAAAGAAAATTTGACATTTACATAC
GTCGACGAGGTGTCTTACGGCGGACTTATTAAGCCGTCCGAAAAATTTCAAGAGAAGCTA
```

AAAGAGCTAGAATGTATTTTTTGCATTATACAAATAATAATAATTTTGAAATTACAAAT
AATGTAAAGGAAAAATTAATATTAGCAGGGCAAAACGTCGATGTTGATAACAATTAATT
TCAAACCCACGGACATGCTAAGGGTTAATCAACAATCATATCGCTGTCTCACTCAGACT
CAATACGACACTCAGAATACTATTCTTTCACTCGCACTTATTGCAAGCATACGTTAAGT
>FGENESH: 1 5 exon (s) 153 - 2812 640 aa, chain +
MKYCKFCCKAVTGVKLIHVPKCAIKRKLWEQSLGCSLGENSQICDTHFNDSQWKAAPAKG
QTFKRRLNADALPSKVIEPEPEKIKEGYTSGSTQTEWLSDVDIKRGCLDVVDKLCVLAF
DEMKVAAAFEYDSSPDIVYEPSDYVQLAIVRGLKKS WKQPVFFDFNTRMDPDTLNNILRK
LHSGYLVVAIVSDLGTGNQKLWTELGISSEKTFWFSHPADDQLKIFVFS DTPHLIKLVRN
HYVDSELTINGKKLT KKTIQEALHLCNKSDLSILFKINENHINVRSLAKQKVKLATQLFS
NTTASSIRRCYSLGYDIENATETADFFKLMNDWFDIFNSKLSTSN CIEWSQPYGKQLDIQ
NDILNRMSVIMRKGILDKPKRLPFQKGIIVNNASLDGLYKYLQENFSMQYILTSRLNQDI
VEHFFGSMRSRGGQFDHPTPLQFKYRLRKYIKARNT EMLRNSGNIEEENSESWLNLD FSS
KEKENKTKDDEPVDEMSRYIYVDVTEMDELTVDAMEYIAGYVIKKLRISDKVKENLTFTY
VDEVSYGGLIKPSEKFQEKLKELECI FLHYTNNNNF EITNNVKEKLILAGQNVDVDKQLI
SNPTDMLRVNQSYRCLTQTQYDTQNTIPFTRTYCKHTLS