

P. papatasi tra-2 partial gene model

Scaffold1530_Length=36934

Figure S17. Manually-curated *P. papatasi* tra-2 partial gene model. Exonic sequences are indicated by black cases; black upper cases indicate coding sequences. Intronic sequences are indicated by grey lower cases. Start and stop codons are highlighted in green and red, respectively. Underlined cases indicate putative alternatively spliced exon, predicted on the basis of sequence conservation with the corresponding exon of *P. perniciosus* tra-2 gene. It is interesting to observe the sequence of the putative alternative N-terminus (MTSDQK) which is identical between the two *Phlebotomus* species. Exon start/end positions in the scaffold/s are indicated. Intron boundaries were predicted using transcripts vs genome alignments and confirmed by *de novo* prediction with Berkeley BDGP Splice Site Prediction Tool with default parameters (http://www.fruitfly.org/seq_tools/splice.html); prediction scores are indicated in red. Interestingly, the BDGP Splice Site Prediction Tool fails to predict the 5' alternative donor splicing site downstream the putative alternatively spliced exon of *P. papatasi* tra-2, indicating that this splicing site is suboptimal and it could need an activation by unknown factors.

P. bergeroti tra-2 partial gene model

Contig_173972_Length=4440

2942
|
2966
| 0.99 ctaatac**GT**aaatcc
DNA: tgcatctctagagccaaaaagccaatttctccatttcacactttcataatagttttcccactaaaatagctacattgt**GTAAGTACTCGTCCTACTATAG****GTAAAGTCACCAAAAAGTCATAAATTGCTTTCCATGAATAAAATCCCACACCCGGCTTGCGTCGCATGGCAGAAAAGTCATCAAAGACTGCGATGCATTGTC**
-3fr
·'S··T··R··T··Y··W··S··S··Q··K··S··I··C··L··S··M··N··K··I··P··K··Q··P··A··C··R··V··V··A··M··A··K··K··C··I··K··D··C··D··A··F··C··P··Q··G··S··L··

2341

0.77 aagtgc

Gtaagtgc

C
 DNA: CCAGCGAGGAACGACATACATCTCTCGAGCAGGTTCACTCCGGAGAGAATGGAGACTACAGAAAGTCCCGAAATCGCTCTCGTAGTCGAGGAGCCTACAGATCTCGTCAGGTTACAGGATCTCGTGTGAGAACGTTACAGAAGCAAGTCACCGCCGCCACGATAGGAAACGCTCTACCCAGGGCCCAATTCTCCCGTCGCAGACAGTACAGTCGAGtaagtgc
 -3fr: P-S-E-R-H-Y-I-S-R-A-G-S-S-R-E-N-G-D-Y-R-K-S-R-K-S-S-S-R-S-R-S-R-S-R-C-E-K-R-Y-R-S-K-S-P-P-R-H-D-R-K-R-S-Y-S-R-S-P-N-S-S-R-R-R-H-V-A-S-R-

1884

|

0.66 gggaaattgtaatcatttcAGacggggttacggggctt
ACGGGGTGTTCACGGGGCTTTGTGTTGTCACT

DNA: cctaggccggaaagttaatctcatatgttagatctgtctgatttggtagataatatccggaaaatttagaatgataccacactcatagcttcaagagttcaattgggtttcattaaaggcattccggacatttcactcaatcaattccacagatgttagatttaatttggaaattgtaatcatttcagACGGGGTGTTCACGGGGCTTTGTGTTGTCACT
-3fr: T-G-C-S-B-G-F-C-F-V-Y-

DNA: ccaatattctctaaatcaaataaaaaatacgccctctaagattttaattcgaaaaaaaacgttgtaaaccaggatagactttatgtggctactgtttatcacacttgacatt

Figure S18. Manually-curated *P. bergeroti* tra-2 partial gene model. Exonic sequences are indicated by black cases; black upper cases indicate coding sequences. Intronic sequences are indicated by grey lower cases. Start and stop codons are highlighted in green and red, respectively. Underlined cases indicate putative alternatively spliced exon, predicted on the basis of sequence conservation with the corresponding exon of *P. perniciosus* tra-2 gene. It is interesting to observe the sequence of the putative alternative N-terminus (MTSDQK) which is identical between the two *Phlebotomus* species. Exon start/end positions in the scaffold/s are indicated. Intron boundaries were predicted using transcripts vs genome alignments and confirmed by *de novo* prediction with Berkeley BDGP Splice Site Prediction Tool with default parameters (http://www.fruitfly.org/seq_tools/splice.html); prediction scores are indicated in red. Interestingly, the BDGP Splice Site Prediction Tool fails to predict the 5' alternative donor splicing site downstream the putative alternatively spliced exon of *P. bergeroti* tra-2, indicating that this splicing site is suboptimal and it could need an activation by unknown factors.

P. duboscqi tra-2 partial gene model

Contig_637001_Length=1709

Figure S19. Manually-curated *P. duboscqi* tra-2 partial gene model. Exonic sequences are indicated by black cases; black upper cases indicate coding sequences. Intronic sequences are indicated by grey lower cases. Start and stop codons are highlighted in green and red, respectively. Underlined cases indicate putative alternatively spliced exon, predicted on the basis of sequence conservation with the corresponding exon of *P. perniciosus* tra-2 gene. It is interesting to observe the sequence of the putative alternative N-terminus (MTSDQK) which is identical between the two *Phlebotomus* species. Exon start/end positions in the scaffold/s are indicated. Intron boundaries were predicted using transcripts vs genome alignments and confirmed by *de novo* prediction with Berkeley BDGP Splice Site Prediction Tool with default parameters (http://www.fruitfly.org/seq_tools/splice.html); prediction scores are indicated in red. Interestingly, the BDGP Splice Site Prediction Tool predicts the 5' alternative donor splicing site downstream the putative alternatively spliced exon of *P. duboscqi* tra-2 as very weak, indicating that this splicing site is suboptimal and it could need an activation by unknown factors.