
MODULE TSS2

Q1. Using RNA-Seq data, which represents the level of mRNA expression, can you identify the TSS for Antp-RM in *D. eugracilis*?

Q2. Using the BLAT Alignment of *D. melanogaster* Transcripts, RNA-Seq and TopHat evidence, what is the approximate coordinate of the first nucleotide Antp-RM exon 1? For a refresher on RNA-Seq and TopHat, watch the [video](#).

Q3. The first nucleotide of exon 1 in *D. melanogaster* Antp-RM aligns with the *D. eugracilis* scaffold. Based on the *blastn* alignment, what is the coordinate of the first nucleotide of exon 1 of Antp-RM in *D. eugracilis*?

Q4. Does the *D. eugracilis* sequence in the first alignment ("Range 1: 38407 to 39378") match the *D. melanogaster* exon 1 sequence exactly?

Q5. Starting with the "A" nucleotide at the 5' end of exon 1, how many nucleotides can be aligned between *D. melanogaster* and *D. eugracilis*?

Q6. Under "Comparative Genomics", click on the blue "Drosophila Conservation (28 Species)" link. Scroll down to the section marked "Display Conventions and Configuration" under "Gap Annotation". What do the double lines mean in the *D. sukikii* sequence?

Q7. The Inr motif is sometimes found at the beginning of exon 1 of genes in *Drosophila*. At which two nucleotide positions are there degenerate bases in the Inr motif consensus sequence?

Q8. Is there an Inr motif in this region? If so, what are the coordinates for the motif? Remember that motifs on the minus strand will have coordinates preceded by a minus sign (-), and motifs on the plus strand will have coordinates preceded by a plus sign (+).

Q9. Analyze the BRE^d motif instances on the Short Match track (you may need to zoom in). Is there a BRE^d motif at -23 relative to the start of transcription (+1)? Note that the core promoter motif should be in the same orientation as the direction of transcription. Based on the information about the characteristics of core promoter motifs above, is there a canonical BRE^d motif for the core promoter of Antp-RM?

Q10. Perform Short Match searches for the rest of the core promoter motifs in Table 2. Are any of these motifs located in the correct positions relative to the TSS of Antp-RM?

Motif	Coordinates (plus strand only)	Correct position?
BRE ^u		
TATA Box		
BRE ^d		
Inr		
MTE		
DPE		
Ohler motif1		
DRE		
Ohler motif5		
Ohler motif6		
Ohler motif7		
Ohler motif8		