UEG Parts B-C Worksheet

Name:

Instructions: One copy of this worksheet will be randomly selected from your group at the end **Week 5's** lab, where you will complete Parts D and E. Make sure to answer questions completely and clearly, fully indicating your reasoning/thoughts (often writing in complete sentences is helpful). I expect the responses to **have no typos and minimal grammatical error**. You are allowed and encouraged to discuss questions with your labmates.

B1. How many genes are there in contig1, and what are the names of these genes?
B2. Which gene has the largest span (i.e., the largest distance between the start and end of the gene)?
B3. What is the relationship between the bases displayed when the arrow is pointed to the left versus when it is pointed to the right?
B4. Explain the difference between exons and introns. How many exons does tra-RA contain? How many introns does tra-RA contain?
DE Militale condition for the control of the contro

B5. Which reading frame contains the amino acid sequence for the second CDS (coding sequence of coding exon) of tra-RA? Explain your reasoning.

а	a. First CDS:		
b	b. Middle CDS:		
c	c. Last CDS:		
C1. Describe TWO ways in which the histograms are similar and ONE way in which they differ (other than color). This is a descriptive exercise to compare your two datasets.			
• Similarities:			
• Differences: C2. Do females or males make more <i>transformer</i> mRNA, or do they express it at about the same level?			
C3. Share the following information you've gathered:			
а			
b			
С			
d			
е	Last three nucleotides of tra-RA exon 2:		
f			
g	First two nucleotides of tra-RA intron 2:		
h			
i	Coordinate of the first nucleotide of tra-RA exon 3:		
	•		

B6. For the following components of a protein-coding gene, explain if you must have, can have,

or will never have a start or stop codon.

C4. Using the information you've gathered above, make a graphical picture of the tra-RA (female specific) isoform with 3 exons and 2 introns. Represent exons as rectangular boxes and introns as lines connecting the boxes. Number each exon and intron (start from the left with "exon 1"). Add the coordinates for the first and last nucleotide of the exons that you have found so far (you may feel that you're missing some positions - don't worry, we'll pick them up in the next section). Add the sequences of the splice donor and splice acceptor sites at the appropriate locations.

- **C5.** Where does transcription *start* in your diagram? On your diagram above, mark the putative Transcription Start Site (TSS) in your diagram with a bent arrow pointing in the direction of transcription. The region right before the TSS is the promoter region.
- **C6.** Do you notice any patterns about the splice acceptors and splice donors? Look at the nucleotides at the start and ends of introns. Is there a pattern? Why might this be useful?