Lab 6 UEG Parts D-E Worksheet
Name:

Instructions: One copy of your worksheets will be randomly selected from your group at the end of the lab. 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.

D1. Give the coordinates for the entire start codon for tra-RA (start codon coordinates should be three consecutive numbers, for example: nucleotides 212-214).

D2. Which reading frame should we follow along for CDS-1 to see the predicted amino acid sequence of tra-RA?

D3. Zoom out to see the entire exon containing CDS-1. Are there any stop codons in the reading frame you chose for question D2? Explain whether you would expect to see stop codons.

D4. How many bases are left in the codon before the 3' splice site of intron 2 (i.e., is the start of CDS-2 in phase 0, phase 1, or phase 2)?

D6. Give the coordinates for the bases in the stop codon for tra-RA.

D7. Look at the map of tra-RA you drew in C4. Indicate the coordinate for the end of the translated region on your drawing in question C4. In the space below, provide a map of the processed mRNA after intron removal and indicate the regions that are translated into a protein. (Color coding may be helpful.)

E1. Given that exons are shown by the black boxes, and introns are shown by thin lines with arrowheads in the FlyBase Genes track, what does this tell us about the first intron of *tra-RB* compared to that of *tra-RA*?

E2. Share the following information you've gathered:

a	Coordinate of the first nucleotide of tra-RB exon 1:	
b	Coordinate of the last nucleotide of tra-RB exon 1:	
c	Phasing at the end of tra-RB exon 1:	
d	The first two nucleotides of tra-RB intron 1:	
e	Last two nucleotides of tra-RB intron 1:	
f	Coordinate of the first nucleotide of tra-RB exon 2:	
g	Phasing at the start of tra-RB exon 2:	
h	Reading frame for tra-RB exon 2:	
i	Coordinates of the stop codon in exon 2:	

E3. Draw a gene model for tra-RB, similar to the one you drew in C4 (you do not need to also draw the processed mRNA, but you do need all positions and the splice donor/acceptor sequences marked).

E4. Calculate the number of amino acids for the tra-RA protein, and the number of amino acids for the tra-RB protein. Show your work. Note that your total number of bases across all translated regions (excluding your stop codons) divided by three should give you this value.
HINT 1: Your total bases should be divisible by three.
HINT 2: Consider a codon in positions 200-202 (positions 200, 201, 202). Note that if I subtract, I get 202-200=2, which is only two bases. Thus I needed to add one while subtracting to account for three bases. Adjust your math accordingly.

E5. Is it likely that the protein translated from tra-RB could play the same functional role played by the protein translated from tra-RA? Explain your reasoning on whether you do or do not find it likely.