MODULE 4: SPLICING

ANSWER SHEET

Questions:

Q1. List two ways in which the histograms are similar.

a. ____

b. ____

Q2. List one way that the histograms differ (other than color).

a. ____

Q3. Recall that our other evidence (see Module 3) indicates that tra-RA extends from 9,851 to 10,846. How many gaps do you see in the histograms in this interval?

Q4. How many exons do you see?

Q5. Do females or males make more *transformer* mRNA or do they express it at about the same level?

Q6. Using the information you've gathered so far, make a diagram of the *tra-RA* (female specific) isoform with 3 exons and 2 introns. Represent exons as rectangular boxes, and introns as lines that connect the boxes. Number each exon and intron (start from left with 'exon 1').

Q7. Where is the promoter in relation to the exons and introns? Mark the putative Transcription Start Site with a bent arrow, pointing in the direction of transcription.

Q8. What is the coordinate of the last nucleotide in the female tra-RA exon 1?

Q9. What are the first two nucleotides of the female tra-RA intron 1?

Q10. What are the last two nucleotides of the female tra-RA intron 1?

Q11. What is the coordinate of the first nucleotide in the female tra-RA exon 2?

Summary Question 1. What are the last three nucleotides of the female tra-RA exon 2?

Summary Question 2. What is the coordinate of the last nucleotide in the female tra-RA exon 2?

Summary Question 3. What are the first two nucleotides of the female tra-RA intron 2?

Summary Question 4. What are the last two nucleotides of the female tra-RA intron 2?

Summary Question 5. What is the coordinate of the first nucleotide in the female tra-RA exon 3?

Summary Question 6. Using the information you've gathered so far, make a graphical picture of the tra-RA (female specific) isoform with 3 exons and 2 introns. Number each exon and intron. Add the coordinates for first and last nucleotide of the exons that you have found so far. Add the sequences of the splice donor and splice acceptor sites at the appropriate locations.

Summary Question 7. Where do you think the promoter is located in relation to your gene model? What <u>evidence</u> do you have to support your idea, using the evidence tracks we have displayed (Base Position, RNA-Seq Coverage, Exon Junctions)?

Bonus Question 1. Support your hypothesis by gathering additional data. Recall our explorations in Modules 2 and 3. You might want to open the tracks “D. mel. cDNAs,” and “TSS Annotations,” both in **full.** What type of evidence is shown by each of these tracks (refer to Module 2)? Finally, to see tra-RA as currently annotated in FlyBase, open the “tra Isoform” track on **full,** or to see both isoforms open the “FlyBase Genes” track in **pack.** Do these results support your model? Do any ambiguities remain?

MODULE 4 HOMEWORK: SPLICING ANSWER SHEET

DETERMINING SPLICE SITES FOR THE *SPD*-2 GENE

Summary Question 1. How many exons does *spd-2* have? _____

Summary Question 2. How many introns does *spd-2* have? _____

Summary Question 3. What are the last three nucleotides of exon 1? ____

Summary Question 4. What is the coordinate of the last nucleotide in exon 1? ______
What are the first two nucleotides of intron 1? ______

Summary Question 5. What are the last two nucleotides of intron 1? _____

Summary Question 6. What is the coordinate of the first nucleotide in exon 2? ______

Summary Question 7. What are the last three nucleotides of exon 2? _____

Summary Question 8. What is the coordinate of the last nucleotide in exon 2? _______

Summary Question 9. What are the first two nucleotides of intron 2? ______

Summary Question 10. What are the last two nucleotides of intron 2? _____

Summary Question 11. What is the coordinate of the first nucleotide in exon 3? _____

Summary Question 12. Using the information you've gathered so far, make a graphical picture of the *spd-2* gene with 3 exons and 2 introns. Number each exon and intron. Add the coordinates for first and last nucleotide of the exons that you have found so far. Add the sequences of the splice donor and splice acceptor sites at the appropriate locations. Finally, add a bent arrow for the transcription start site.