Table 1. Lesson Timeline

Activity	Description	Time	Notes
Module 1. Introduction to the Genome Browser: What is a Gene?			
Warm up	Discuss the question: What is a gene? (Perhaps discuss with a partner, then as a class, or start with whole class discussion.) Emphasize the function of a gene; consider how the structure of the gene is related to its function.	10 minutes	
Investigation	1. Watch Genome Browser video at https://youtu.be/suMC7wmP7tA. 2. Work through Module 1, stopping on page 4 to watch the Evidence Tracks video at https://youtu.be/BwwP7cOqr0Y.	50 minutes-1 hour 40 minutes	Module 1 is provided as Supporting File S1
Conclusion	Conclude with discussion of the following points: • Genes may run in either direction on a chromosome; • Genes are represented on the genome browser as blocks connected by lines; • Eukaryotic genes are made up of protein-coding exons (the blocks) connected by introns; • Proteins usually begin with a Methionine (M) and end at a stop codon (*)	15 minutes	
Module 2. Transcription Part I			
Warm up	1. Discuss the questions: What is transcription? What cellular proteins are required for transcription? How does it work mechanistically? What is/are the products of transcription? (students discuss in pairs, then as a class) 2. Describe regulatory signals: Transcription Start Site (TSS), and AATAAA sequence (site of transcript cleavage for termination).	10 minutes	
Investigation	Work through Module 2, stopping at page 4 to watch the RNA-Seq and TopHat video at https://youtu.be/qepVXEsfLMM and at page 10 to learn about the Short Match functionality of the Genome Browser at https://youtu.be/eoeWufgcdvg	50 minutes - 1.5 hours	Module 2 is provided as Supporting File S2
Conclusion	Conclude by challenging students to think about these questions: 1. How important is it for RNA polymerase II to recognize the promoter sequence? 2. Do you think it is possible for a gene to have more than one transcriptional start site? 3. How would RNA polymerase II know which one to choose? 4. When would it make a difference in the protein product, and when not?	15 minutes	
Module 3. Transcription Part II			
Warm up	1. Discuss the questions: What happens to the initial (pre-mRNA) transcript made by RNA pol II? Does it leave the nucleus 'as is'? Or do changes have to occur? (Hint: introns vs. exons) 2. Mini-presentation illustrating that during pre-mRNA processing, three events occur: - 5′ capping, - 3′ polyadenylation, - splicing out of introns	10 minutes	
Investigation	Work through Module 3.	50 minutes - 1.5 hours	Module 3 is provided as Supporting File S3
Conclusion	Conclude with a discussion of mRNA processing, emphasizing the three steps: • 5′ capping, • 3′ polyadenylation, • removal of introns through splicing (via spliceosome)	15 minutes	

Activity	Description	Time	Notes
Module 4. Splicing			
Warm up	1. Review mRNA processing. 2. Introduce splicing and the spliceosome.	10 minutes	
Investigation	1. Work through Module 4, Investigation 1. Watch RNA-Seq and TopHat video at https://youtu.be/qepVXEsfLMM. When students work on page 6 of the Module, they should also watch the Genes and Isoforms video at https://youtu.be/8jtTp_6vN4M. 2. Work through Investigations 2 and 3.	50 minutes-1.5 hours	Module 4 is provided as Supporting File S4
Conclusion	1. Discuss the length of the pre-mRNA vs. the length of the spliced mRNA 2. Identify isoforms of *tra* with different transcription start sites or alternative splicing patterns.	15 minutes	
Module 5. Translations			
Warm up	1. Review the process of translation: Overview of the ribosome, tRNAs, and associated proteins involved in translation (Initiation Factors, Elongation Factors and Release Factors). 2. Review genetic code table.	10 minutes	
Investigation	1. Work through Module 5 2. When working through page 8 of the Module, watch the Splicing and Phase video at https://youtu.be/JsvUfHy3eHE.	50 minutes-1.5 hours	Module 5 is provided as Supporting File S5
Conclusion	Discuss the following points: • mRNAs are translated into amino acids using triplet codons • Identification of ORFs • The ORF must be maintained across splice sites to generate a working mRNA • The assembled ORF begins with a start codon and ends with a stop codon.	15 minutes	
Module 6. Alternative Splicing			
Warm up	Introduce students to tra-RB, the second isoform of *tra*.	10 minutes	
Investigation	1. Work through Module 6 2. When working through page 2 of the Module, students may wish to rewatch the RNA-Seq and TopHat video at https://youtu.be/qepVXEsfLMM. 3. When working through page 4 of the Module, students may wish to rewatch the Splicing and Phase video at https://youtu.be/JsvUfHy3eHE. 4. When working through page 6 of the Module, students may wish to rewatch the Genes and Isoforms video at https://youtu.be/8jtTp_6vN4M.	50 minutes-1.5 hours	Module 6 is provided as Supporting File S6
Conclusion	1. Discuss gene models. 2. Discuss the following points: How does the polypeptide translated from the tra-RB isoform differ from the polypeptide translated from the tra-RA isoform? What are the consequences of these differences on protein function? 3. Discuss how the bigger mRNA leads to creation of a smaller polypeptide! 4. Consider how alternative splicing could allow many different proteins to be encoded by the same gene. 5. Based on the gene structure of the two isoforms of tra shown in the "FlyBase Genes" track, provide a hypothesis that could explain this difference in RNA-Seq read coverage between the adult males sample and adult females sample.	15 minutes	