CHE 4320 Day 4 of class/DNA Sequence Project Day 3 Name:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

1. Find your gene in FlyBase. Scroll down to the section called “Transcript data”. Click to expand it if necessary. How many different annotated transcripts have been reported from your gene? You may want to copy and paste the information in the table
2. Go to the Gene Model and Products section and match the information in the table with the graphical representation of the transcripts of your gene. Discuss how the mRNAs from your gene are similar and how are they different. Also: what are the gray and orange colors in the transcript section representing?
3. Scroll down to the External Data right above Gene Ontology. There is a cross- reference to the Eukaryotic Promoter Database. How many experimentally validated promoters does your gene have?
   1. Each person in your group can pick one promoter, follow the link, then find Position in the genome. Record that number
   2. Map the position in genome back to your gene in FlyBase. Which transcript(s) start from that promoter?
4. Toward the top of the FlyBase gene entry, in the Genomic Location section, under Genomic Maps, click on GBrowse. How is GBrowse similar to the Gene Model and Products section you explored for Q2? How are they different from each other? It might help to have both open on two different computers and to work on this as a group.
5. Look at the RNA-Seq data in GBrowse (scroll down toward the bottom). What can you quickly tell about the expression of your gene based on this information? We will try to look at this data more carefully next class.
6. What questions do you have about what we’ve covered? What would you like to know more about?