Name:

Date:

RNA Sequencing: Advanced Activity

1. In this example, what happens when the read length is doubled? Does knowing the identity of additional bases in your read help to tell whether Spliceform 1 or 2 is correct?

2. In this example, Spliceform 1 has two exons and Spliceform 2 has three exons. Describe the situation in the example where the original read’s paired-end mate still aligns to both spliceforms. In otherwords, which exon does the mate (in orange) align to in Spliceform 1? Which exon does it align to in Spliceform 2??

3. The paired-end sequence information did not help to tell if Spliceform 1 or Spliceform 2 is correct. What additional information was needed that tells us that Spliceform 1 is the correct alignment?