Name:

Date:

RNA Sequencing: Activity 3

1. In the Activity 3 presentation, what happened when you increased the read length? Did knowing the identity of more of the base pairs in the read help you decide whether Alignment 1, 2 or 3 was the correct alignment?

2. Did adding paired-end sequencing information allow the researcher to tell whether Alignment 1 or Alignment 2 was correct? Describe the situation in the example where the paired-end sequencing information can match both Alignment 1 and Alignment 2.

3. In the example, could you tell if Alignment 1 or Alignment 2 is correct when you have the following information? Explain why.

a) Additional Fragment Length Information: The RNA fragments that you sequenced were 100-200 base pairs long (bp).

b) Fragment length based on possible alignments of paired-end reads: Alignment 1 = 150 bp, Alignment 2 = 500 bp

Challenge Question

You are analyzing RNA from an organism with a small genome that has very few repeated sequences. There is almost no chance of seeing multimappers. Which modifications (increasing read length, using paired-end data, using fragment length information) would you choose, if any?