Name:

Date:

RNA Sequencing: Activity 2

1. When the read length was increased from 30 base pairs to 60 bp, you could tell that the Alignment 1 was wrong. How did sequencing more nucleotides (bp) allow you to tell which alignment was correct?

2. Explain how having paired-end sequence data helped tell which alignment was correct.

3. From your paired-end data, you know that your read can only align with Alignment position 2. The student helping you in your lab calculates that your paired reads at Alignment 2 must have come from a fragment that was 250 bp long. You know that all of the fragments in the sample used for your experiment were 200-300 bp long. What does this knowledge about the distance between your paired ends tell you?