Name:

Date:

RNA Sequencing: Activity 4

1. What would be a reasonable hypothesis if you had a lot of RNA reads align with a part of the genome containing no known genes?

2. RNA-seq can identify different spliceforms. What were the example diseases that can change RNA splicing?

3. How does RNA-seq allow you to see how much of one type of spliceform is expressed compared to another type of spliceform? Hint: If you have your aligned reads for the spliceforms, what would you do next to compare the two spliceforms?