

## Expression Analysis Exercises

### A. RNA-Seq alignment exercise

1. What difficulties did you have with the alignment?
2. What would you expect to find in a human genome that we mostly don't see here?
3. Were there mistakes in these data? What were they? How would you determine if they are features or mistakes?
4. What did you do with "reads" that matched two places?

### B. How would you design an algorithm to map exon-exon splitting reads?

### C. What properties of the transcripts in a cell will determine the probability of finding a read from it in our RNA-seq library?