Sequencing Metrics

The following data is taken from the *SequencingMetrics.txt* file located on ARC in the following location: */nobackup/medlste/data/RNAseq/PvR_consolidated/SequencingMetrics.txt*. From the original set of sequencing metrics (183 samples across 92 patients) I removed the following samples:

- Those which are absent from the metadata file (10 samples across 5 patients). Agreed in previous meeting that these should not be included in analysis.
- Those which we previously agreed to filter out based on metadata values (55 samples across 28 patients).
- This left us with 118 samples across 59 patients. This is the data I have used in the below sequencing metrics analysis.
- The differential expression analysis includes the s341 samples (both primary and recurrent). This is not present in the sequencing metrics file.
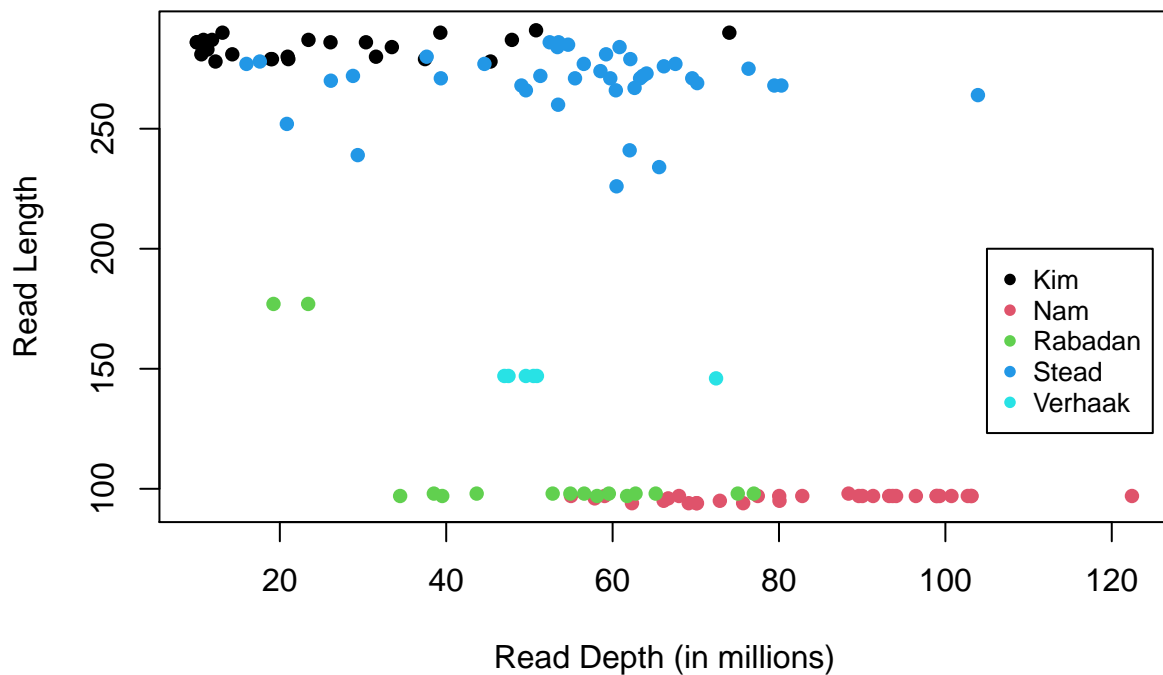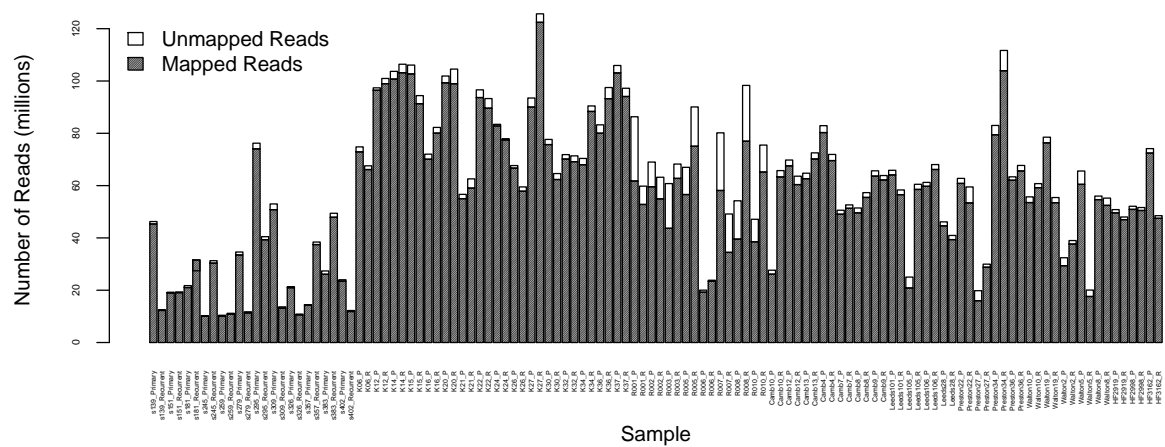

Figure 1: Read depth and length by sample source

Figure 2: Number of mapped and unmapped reads. Total number of samples = 118 (59 patients). Samples grouped by source in the following order: Kim, Nam, Rabadan, Stead, Verhaak.
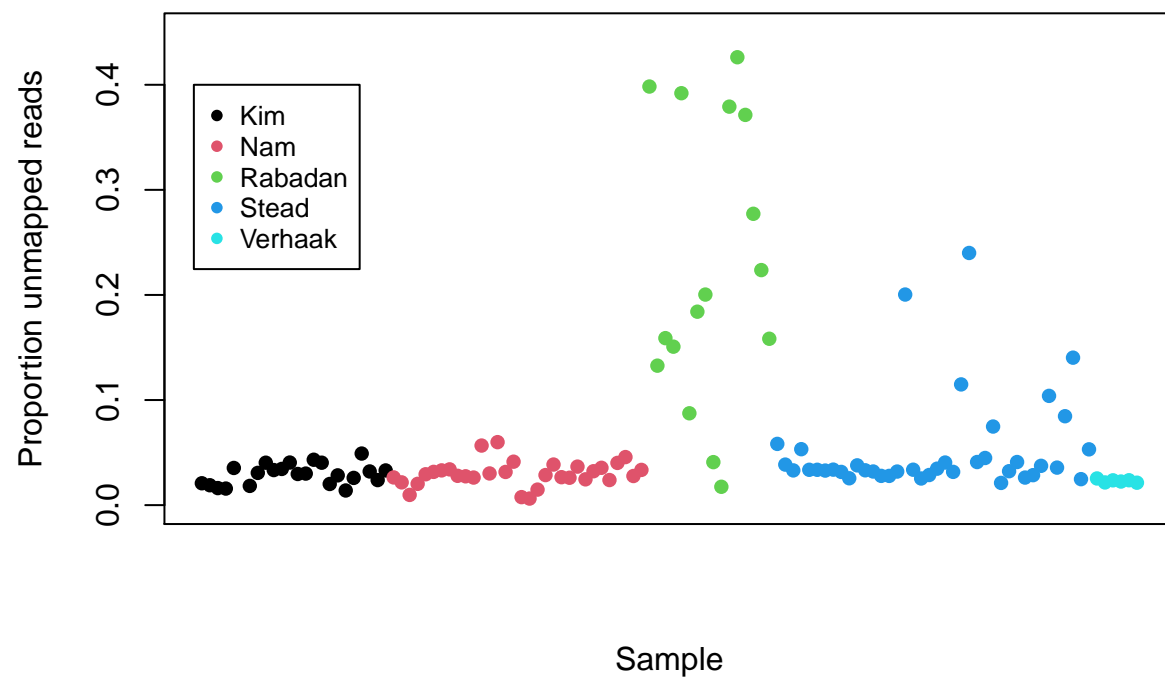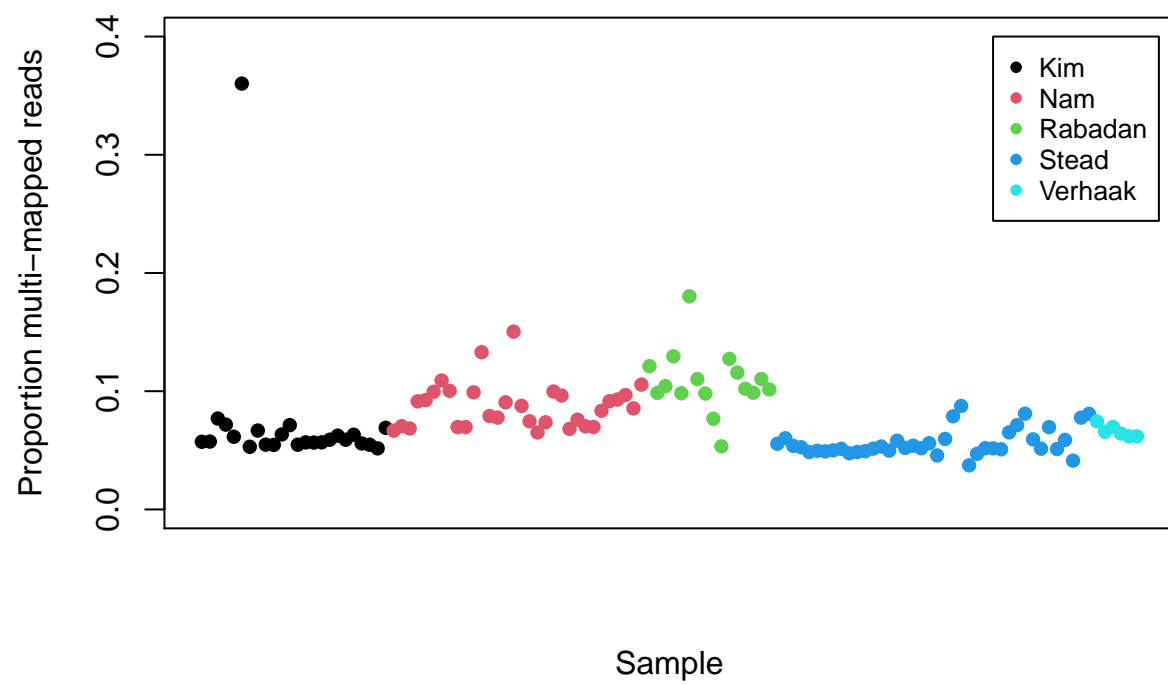

Figure 3: Proportion unmapped reads

Figure 4: Proportion multi-mapped reads