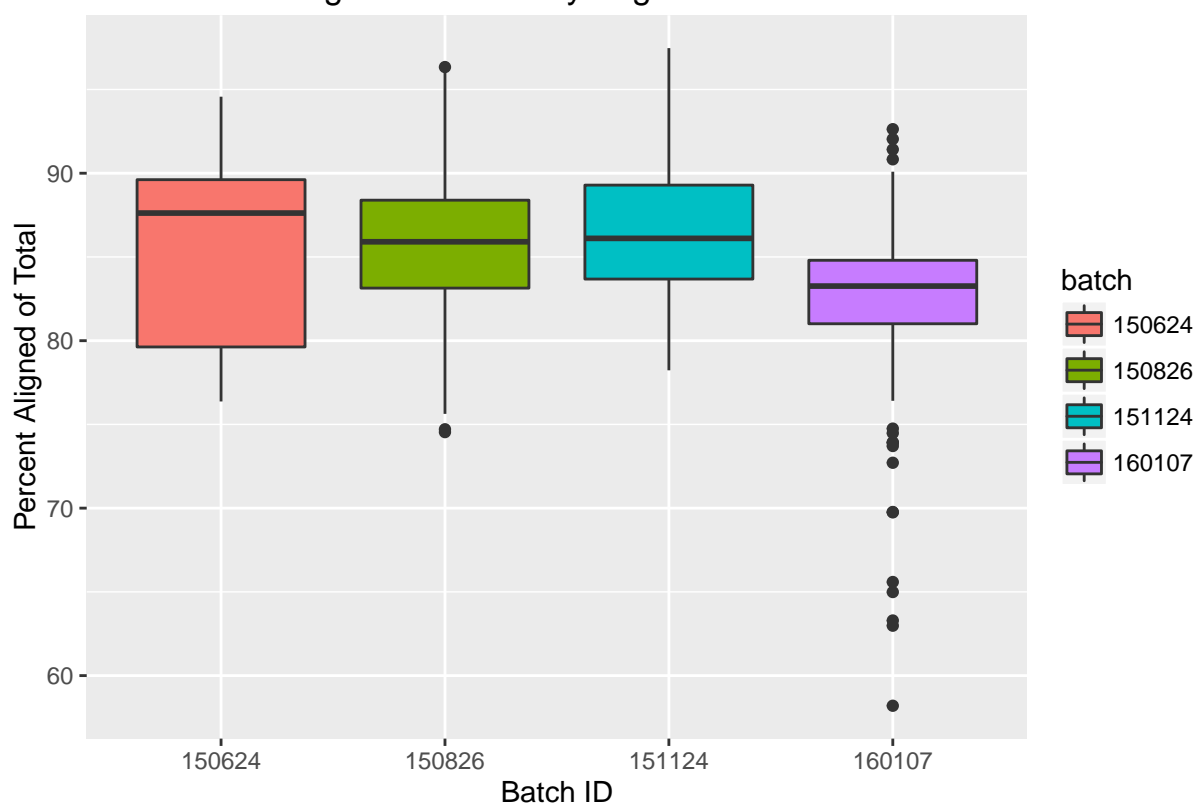# MiXCR_batch_compare

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Objective

We're having issues with out MiXCR output. Different runs of the 160107 batch were compared in the MiXCR_QC_analysis.Rmd, but this will compare the different batches, all run using the same parameters.

Results

We've generally had pretty good alignment (based on observations from the 160107 batch), with most failed alignments due to bad J reads. Let's see how this looks for all of the batches:

Fig. 1 Successfully Aligned Reads

Alignment percentages are relatively consistent. Turns out the 160107 batch was the worst of them. Let's look at the reasons for failure:

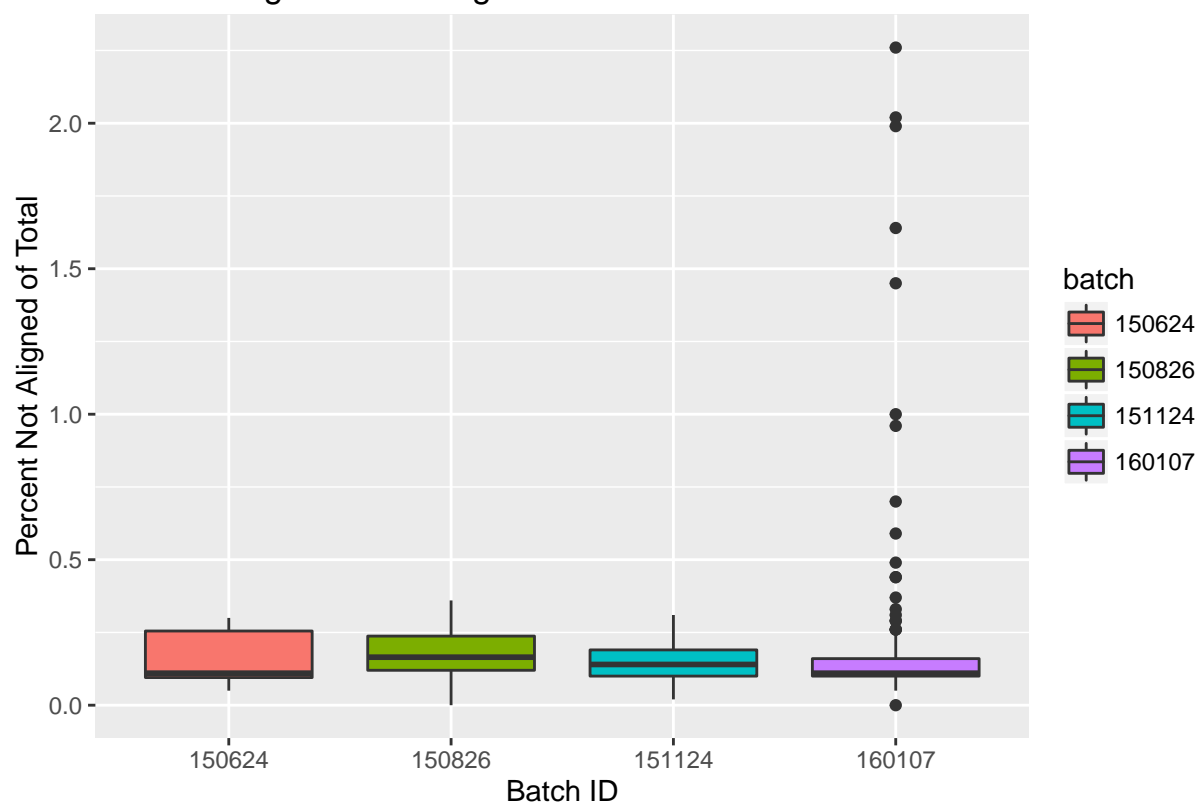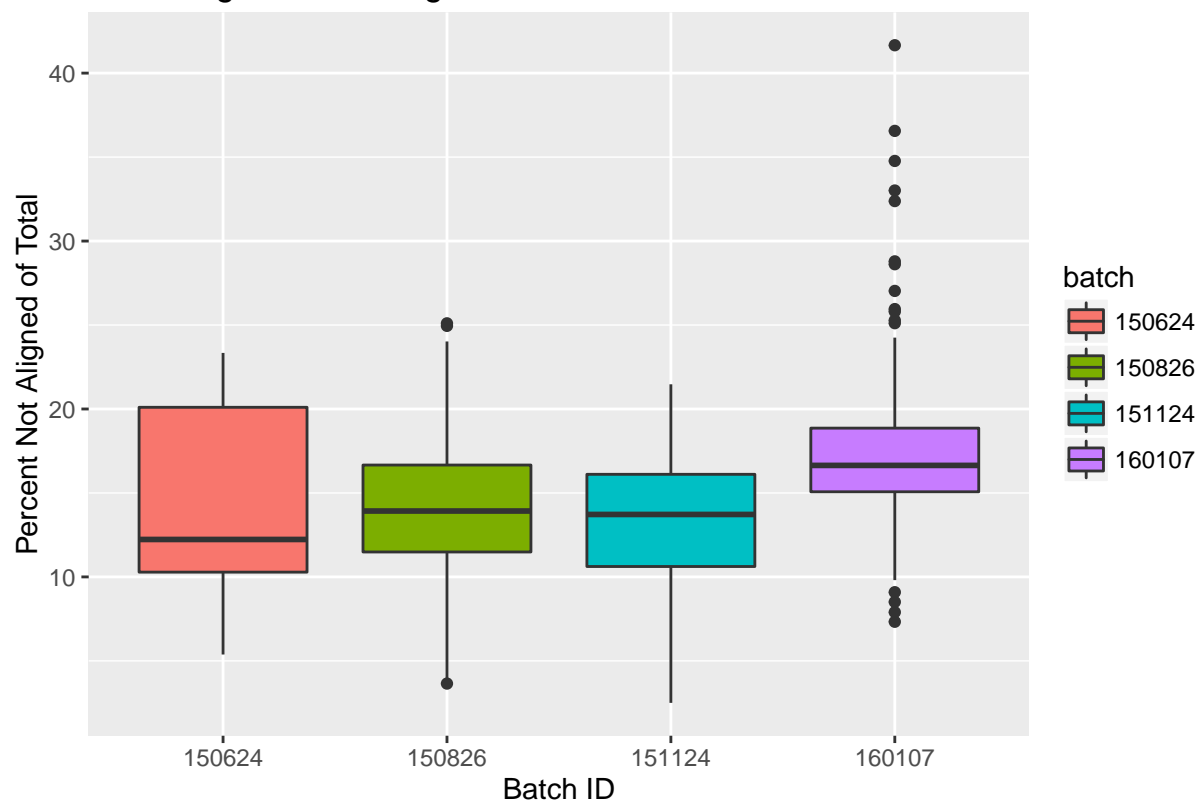## Fig. 2 Failed Alignments Due to Low Score

Fig. 3 Failed Alignments Due to Absence of J Hit

Everything looks pretty standard between the different batches. Let's look at the assembly statistics:
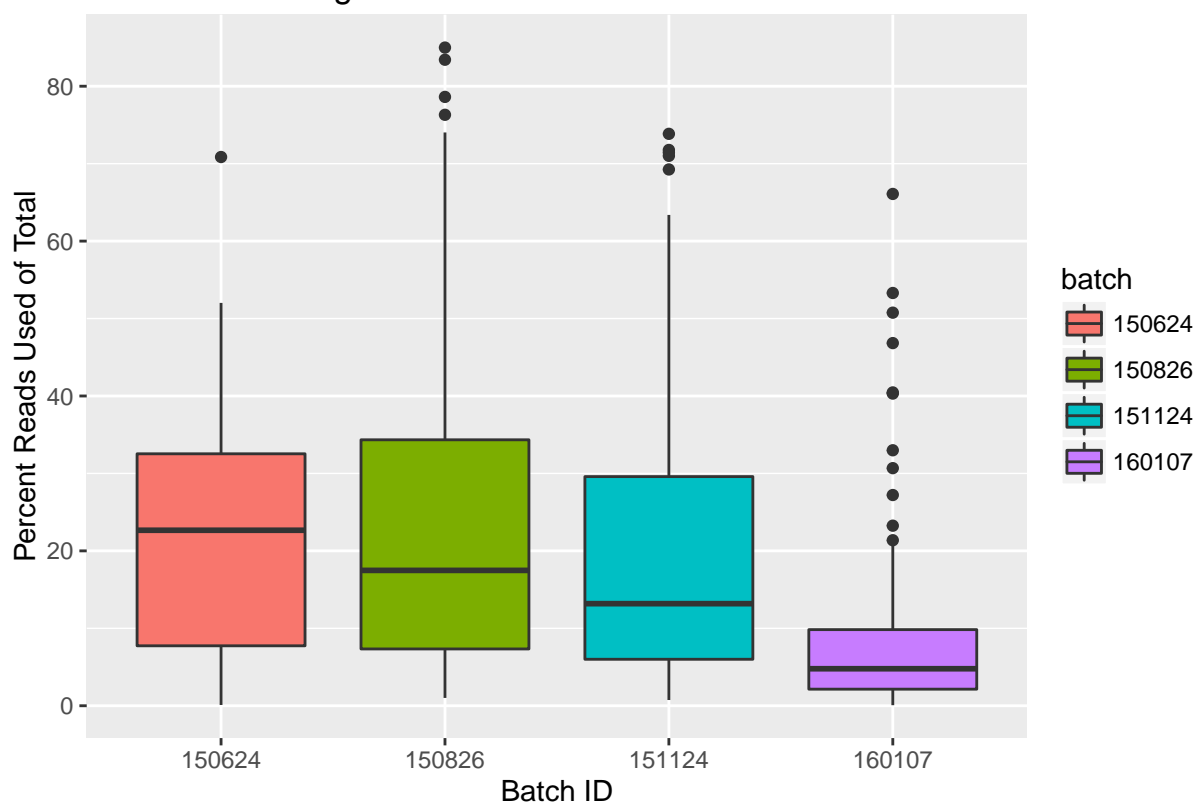
Fig. 4 Percent Assembled Reads
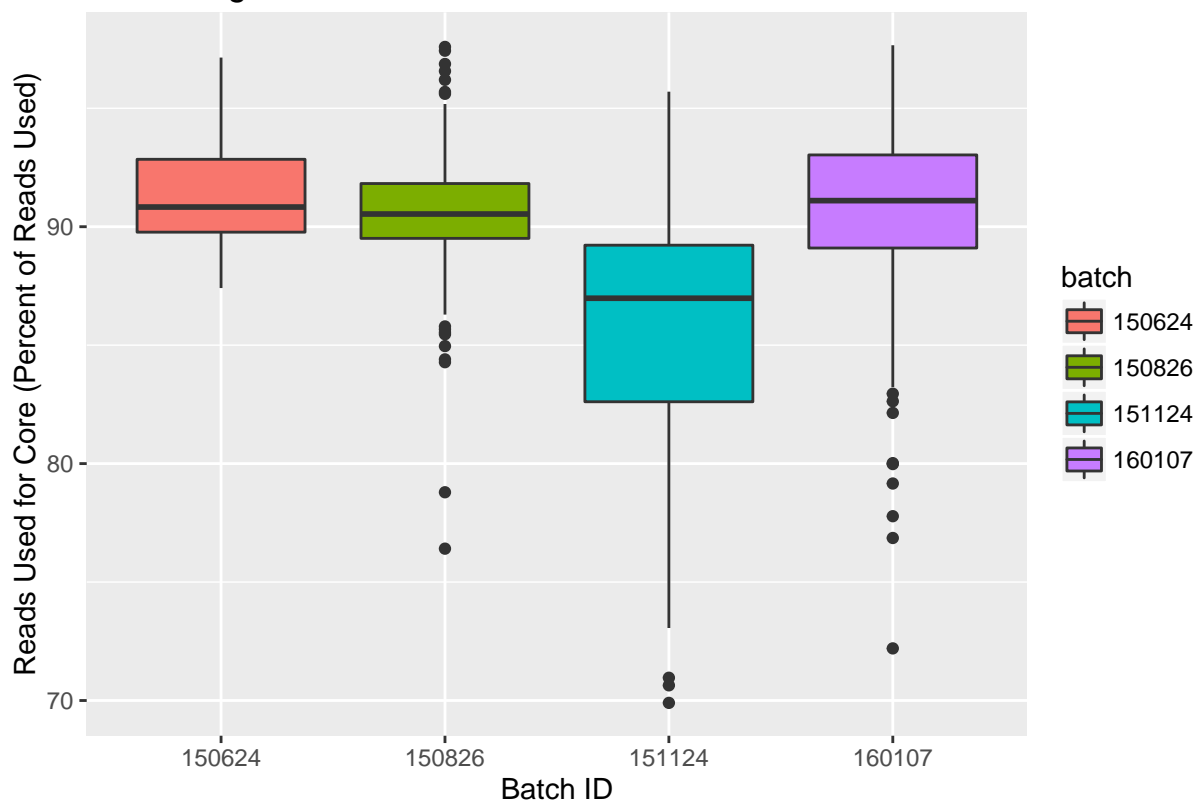

Fig. 5 Assembled Reads Used as Core Clones

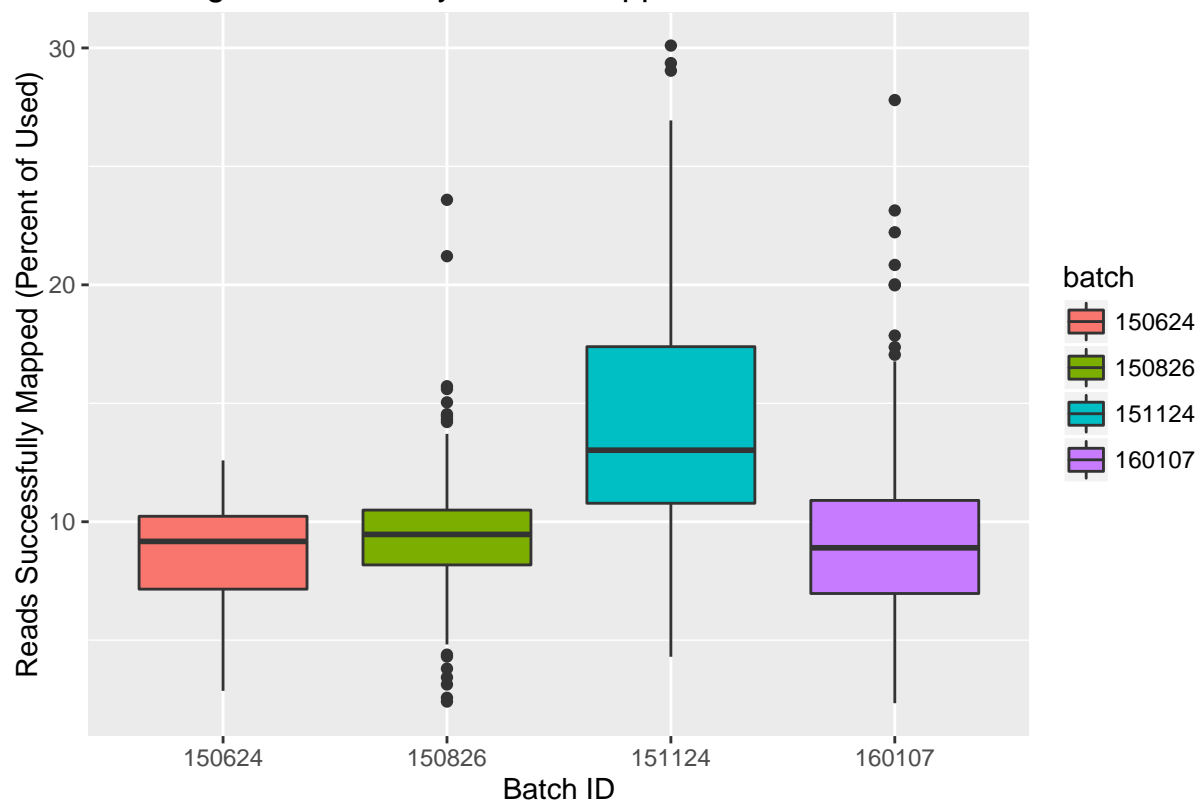Fig. 6 Low Quality Reads Mapped to Core Clones

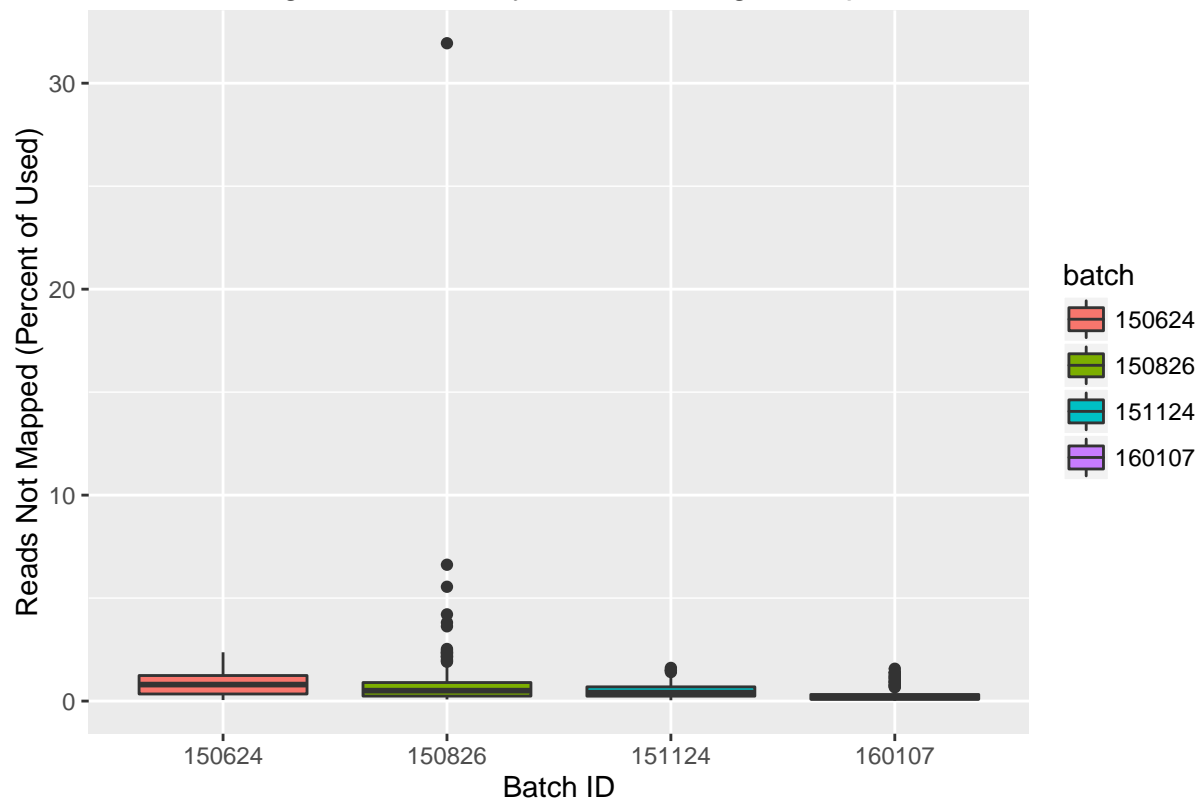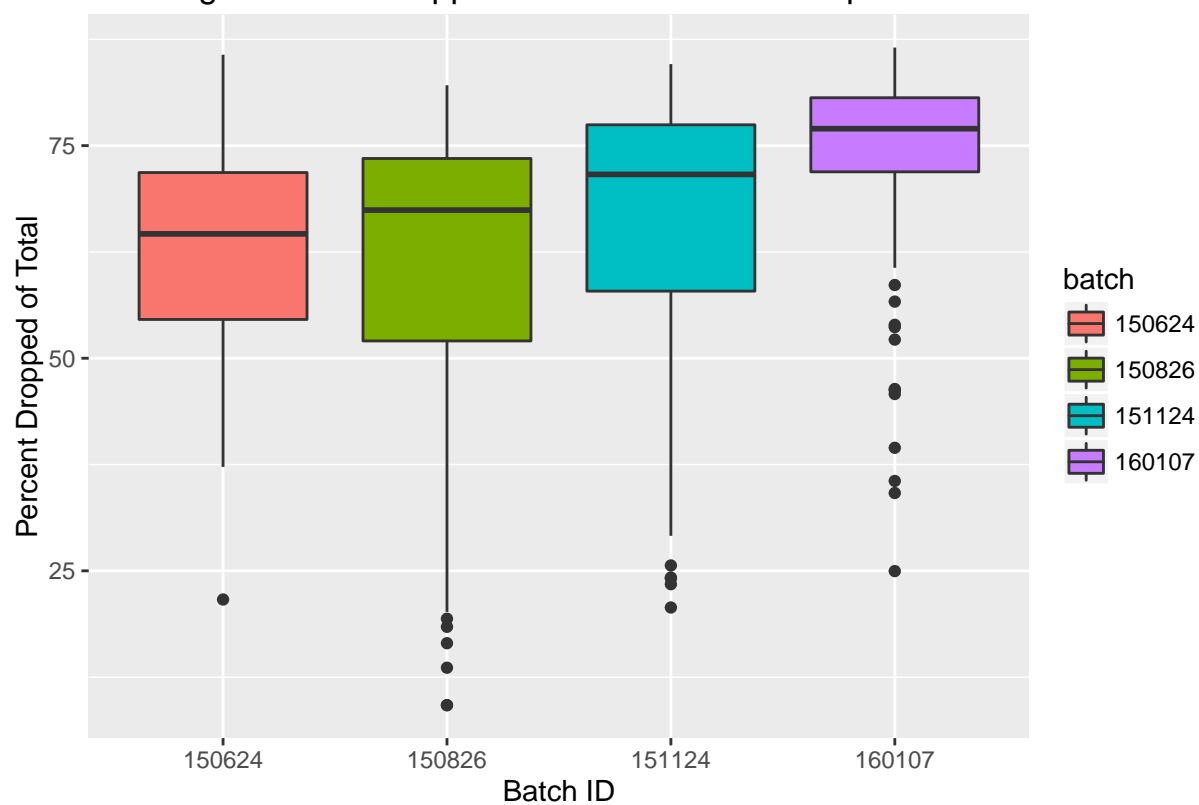Fig. 7 Low Quality Reads Failing to Map

Fig. 8 Reads Dropped Due to No Clonal Sequence

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Fig. 9 Clonotypes eliminated by PCR Error Correction