1. Less than 2k
2. Before: 7.050350 M (94.004667%) After: 6.490441 M (95.318169%)
3. Duplication rate: 4.784%
4. There is a decline in both after base position 100
5. A few seconds and a bit longer
6. Read 1 aligned better if I am reading the output correctly
7. Reads that don’t map could represent changes in the nucleotides of the transcript, like if there was a frameshift mutation or a translocation event the reads may not align quite right. There are quite a few reasons though these are just the ones I can think of.
8. The head of the sam file: @HD VN:1.5 SO:unsorted GO:query@SQ SN:Chromosome\_10A LN:23813772@SQ SN:Chromosome\_10B LN:20101091@SQ SN:Chromosome\_1A LN:40621098

I would say it is a perfect match

I was having gzip header errors with Jbrowse so I am just going to look at the screenshotted image.

A screenshot of a computer

Description automatically generated

1. In the viewer 597bp.
2. I think there are two variants. I think one variant has differences before 11,912,100 and another after 11,913,300. The other I think has differences before 11,912,100 and a different mismatch in the same spot as the other variant 11,913,300. There is a lot of matching though in general in the reads.