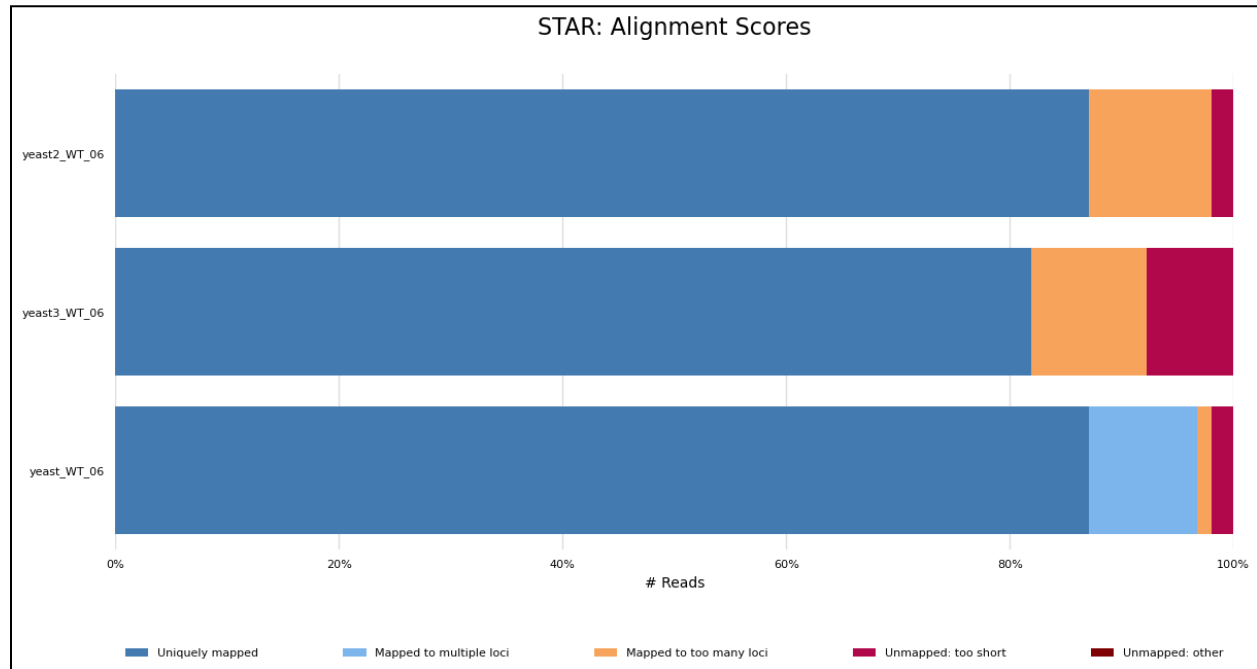
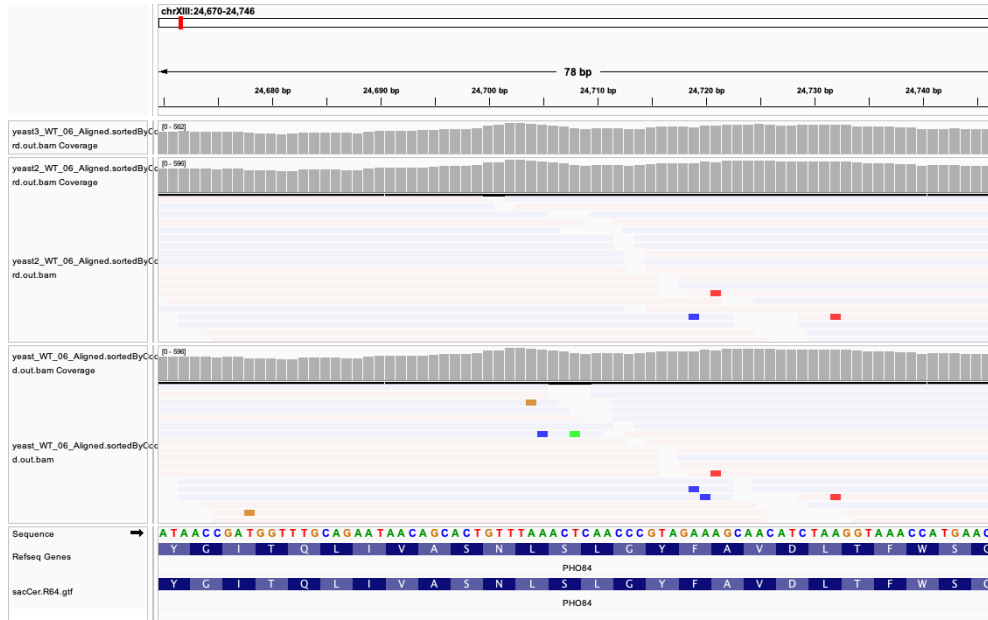


1)



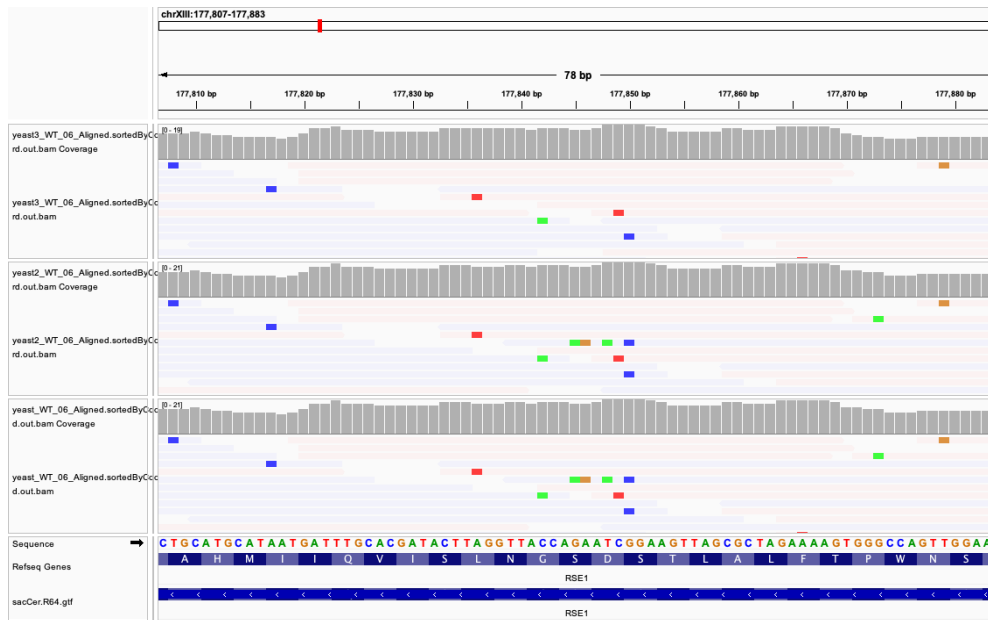
These reads align relatively well, with each run having over 80% of the reads being uniquely mapped despite the STAR options. The default setting is displayed at bottom and has the greatest proportion of uniquely mapped and mapped to multiple loci reads. In comparison, the “--outFilterMultimapNmax 1” star option, represented as the top bar, had the same high proportion of uniquely mapped reads but had more reads mapped to too many loci; this option’s focus on uniquely mapped reads may have caused this change from mappings to multiple loci to too many loci. Lastly, the “--outFilterScoreMinOverLread 0.96” option, represented in the middle bar, demonstrated the least amount of uniquely mapped readings and a relatively similar proportion of readings mapped to too many loci; this may be due to the setting only requiring the aligned read to get 96% of the maximum score, resulting in a decrease in the uniquely mapped readings and increase in unmapped readings.

**2) Comparison IGV plot with the three BAM files showing some reads that disappear when the option `--outFilterMultimapNmax 1` is used:**



These reads might have disappeared because they are not uniquely mapped to that region, which is filtered by this STAR option. Since these readings may be mapped to other loci, these reads were not considered with the new STAR option.

**3) Comparison IGV plot with the three BAM files showing some reads that disappear when the added option `--outFilterScoreMinOverLread 0.96` is used:**



These reads might have disappeared because they did not meet 96% of the maximum score, so a score above 46. This STAR option would have then caused less of these readings to be present.

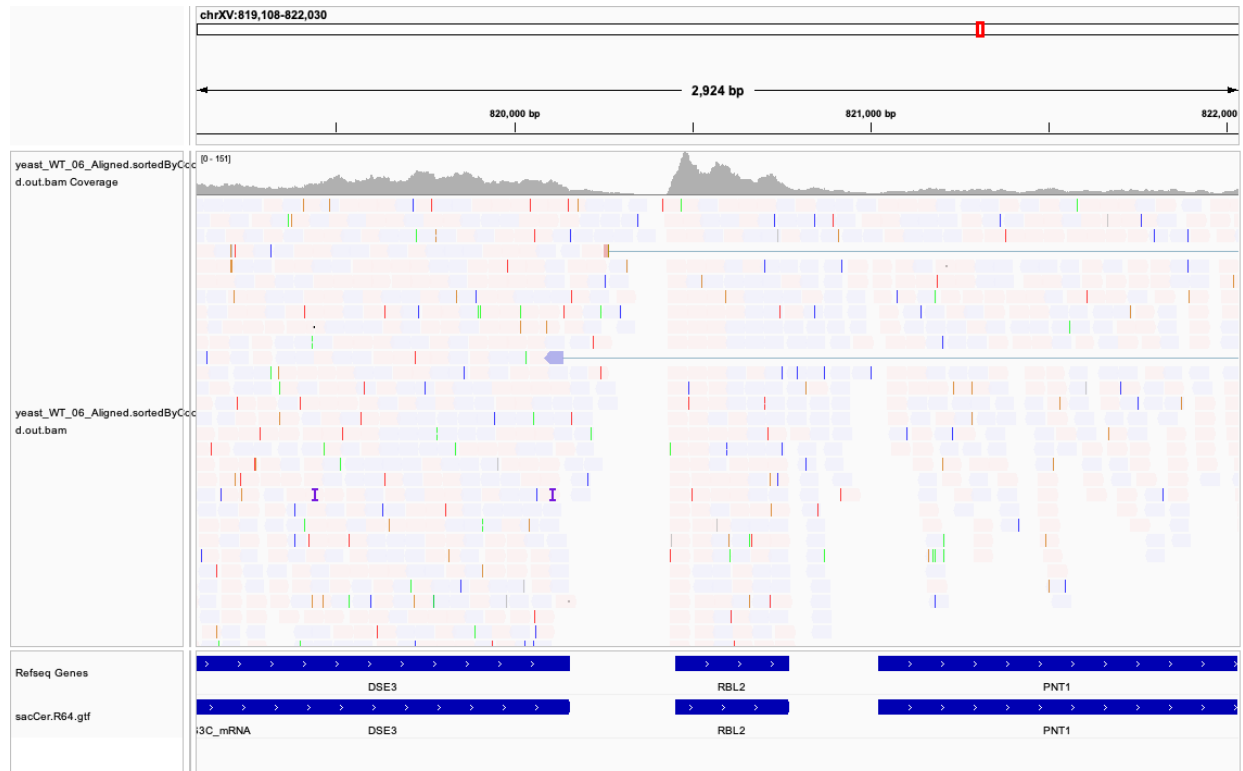
#### 4) Single BAM file IGV plot showing an insertion:



#### 5) Single BAM file IGV plot showing a deletion:



## 6) Single BAM file IGV plot showing spliced reads:



## 7) Table of possible read scores, with total number of reads for each score, for all three BAM files:

All BAM files:

```

93 53
112 32
9502 33
10287 35
10443 34
11129 37
11931 36
12363 39
14527 38
16694 41
18938 40
35519 43
42053 42
102940 45
128981 44
277276 51
629767 47
969209 46
1561431 49
9520841 48
34936300 50

```

Default Setting:

```

31 53
112 32
5371 33
5868 35
5949 34
6371 37
6840 36
7162 39
8328 38
9533 41
11076 40
19725 43
23687 42
56801 45
72398 44
93936 51
354385 47
540735 46
611354 49
3669028 48
13386396 50

```

Option 1:

```

31 53
4131 33
4419 35
4494 34
4758 37
5091 36
5201 39
6199 38
7161 41
7862 40
15794 43
18366 42
46139 45
56583 44
91670 51
275382 47
428474 46
475041 49
2925907 48
10774952 50

```

Option 2:

```

31 53
91670 51
475036 49
2925906 48
10774952 50

```

Highest score possible = 53

8) Single BAM file IGV plot showing a read with the highest score possible:

