LINUX WORKSHOP

03 Visualising Result

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28/02/2025

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Visualising the variant calling result

To view the variant calling result, we need to import our data into a genome browser.

A genome browser is a graphical interface for displaying information for genomic data.

IGV (Integrated Genomics Viewer) is a powerful, interactive visualisation tool for browsing and analysing large genomic datasets, such as BAM, VCF, BED, and BigWig files. It allows researchers to explore sequencing alignments, variants, gene annotations, and other genomic data efficiently.

Visualising the variant calling result

IGV requires BAM files have an associated index. We can use `index` command from SAMtools.

```
samtools index [aligned.sorted.bam]
```

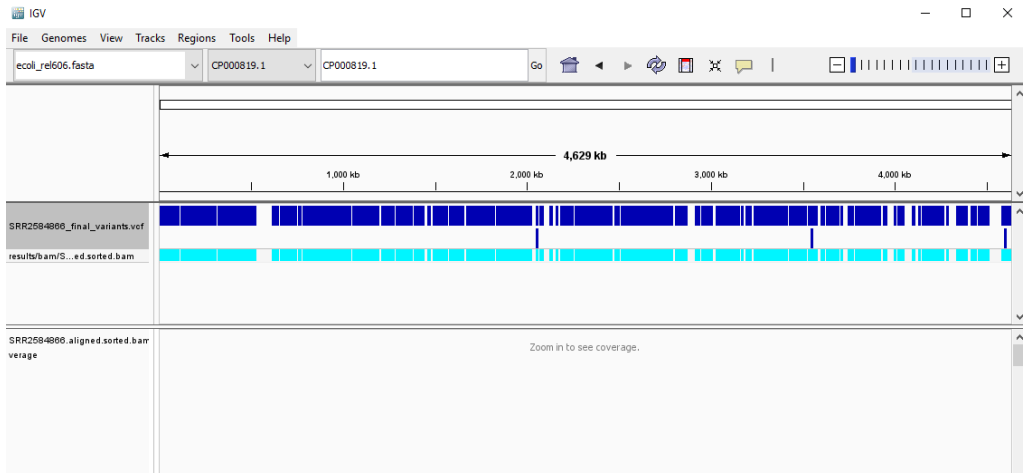
```
-rw-r--r-- 1 jiajia jiajia 206M Feb 24 14:34 SRR2584863.aligned.sorted.bam
-rw-r--r-- 1 jiajia jiajia  15K Feb 24 17:14 SRR2584863.aligned.sorted.bam.bai
```

This generates a `.bai` file, and it is the index file of the sorted bam file.

Visualising the variant calling result

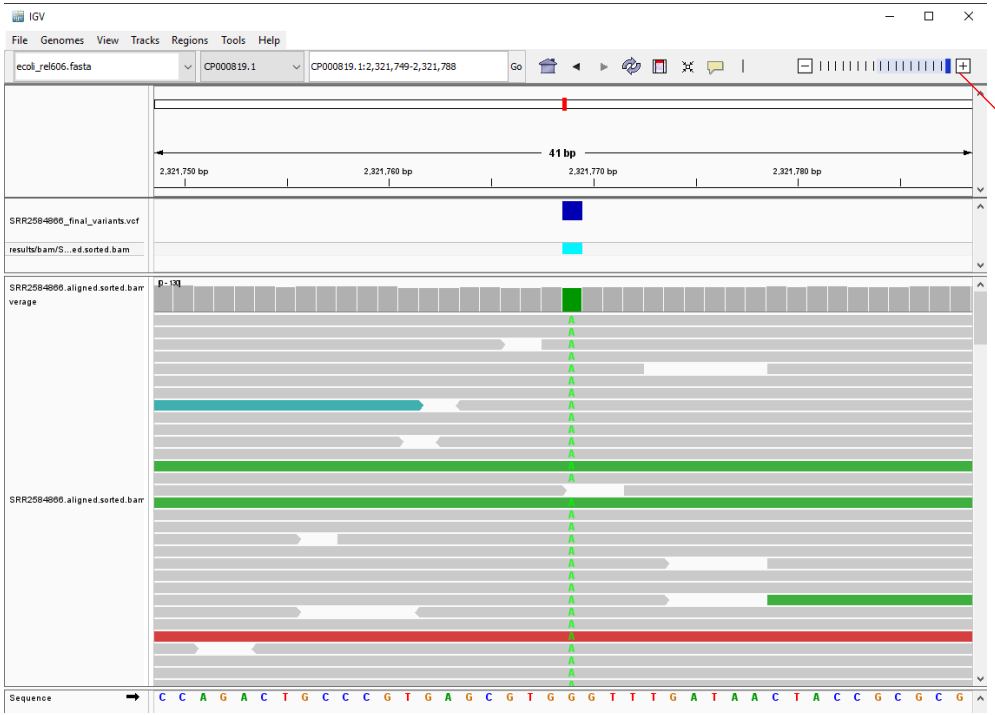
Next, we can open IGV and load files into it.

- Click Genome, and select load genome from file, select the reference genome file
- Click File, and select load from file, select the sorted BAM file
- Click File, and select load from file, select the Final VCF file



Visualising the variant calling result

Zoom in and you can see the details.



Zoom in

Visualising the variant calling result

IGV allows you to import multiple alignment together and compare them.

Read more about IGV: https://igv.org/doc/desktop/

THANK YOU

Contact Us

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