

Prelim_alignment.sam

- Sort the alignment file (.sam) by location in the reference genome, and save as a bam.
- This makes the data easier to process by downstream programs.

Sort the .sam by
reference location.

Save the output in
.bam format

The input file

```
samtools sort -O BAM Prelim_alignment.sam > Prelim_alignment.bam
```

Save the output in a .bam file.

Prelim_alignment.bam



Continue Reference
Based Assembly