

alignment.
sam

- Use Samtools to sort and convert alignment.sam to a sorted .bam file. This file is smaller and will be processed more quickly in future programs

Name of tool to run

Alignment file

Run the Samtools
sort tool.

Save the output as a
sorted bam file.

```
samtools view -bS alignment.sam | samtools sort - > alignment_sorted.bam
```

Read in a .sam file, and
output a .bam file
(compressed sam file).

"|" indicates to use the output of the previous
command as the input to the following command.

"-" means use the output (.bam) file from the
previous command as an argument here.

Alignment_
sorted.bam

Continue with
the "polish
errors" section