

Preliminary
Assembled
Genome

trimmedR
1_paired.f
astq

trimmedR
2_paired.f
astq

- Map the quality filtered reads to the preliminary assembly.
- Save output as an alignment (.sam) file. This indicates where, and how well, the reads map to the assembly.

Specify
mapping
algorithm.

Preliminary assembly

Trimmed, quality
filtered reads

```
bwa mem prelim_assembly.fasta trimmedR1_paired.fastq \
trimmedR2_paired.fastq > alignment.sam
```

Trimmed, quality filtered
reads, cont.

Save the output as a
.sam file.

alignment.
sam

Continue with
the “polish
errors” section