

We now have a preliminary assembly

Preliminary Assembly



Improve the quality of the assembly: Polishing



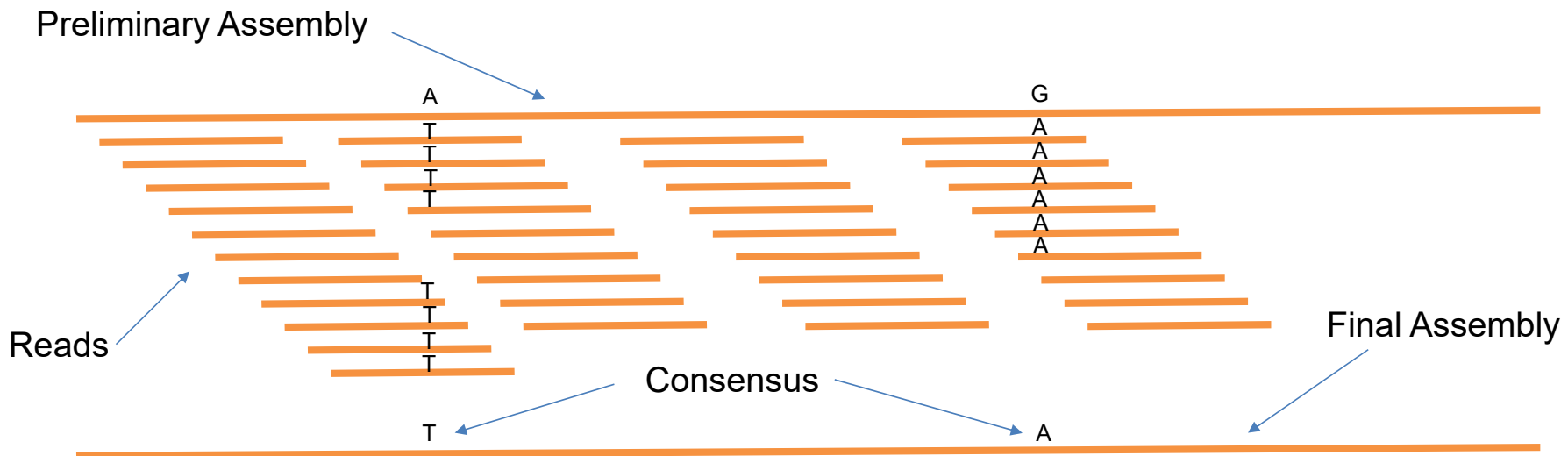
- **We can map the quality filtered reads to this preliminary assembly.**
- **This is similar to the initial read mapping to the reference genome done previously.**

Improve the quality of the assembly: Polishing



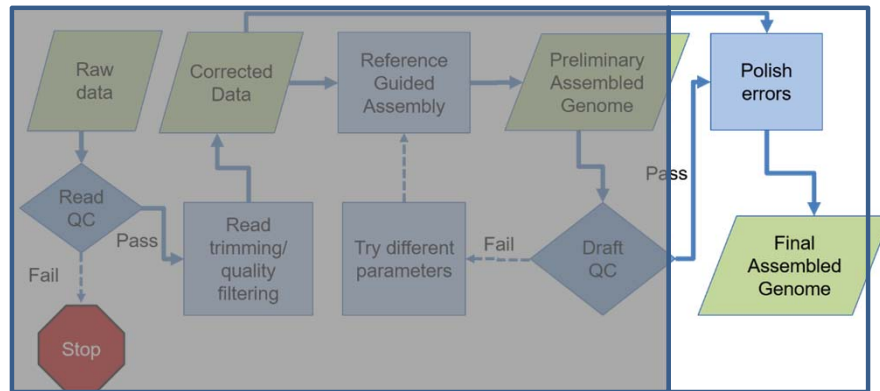
- The read sequences may disagree with the assembly sequence at certain positions. The divergent sequences are known as “variants.”
- Identifying these differences will enable us to correct small-scale errors, yielding a more accurate final assembly.

Improve the quality of the assembly: Polishing



- **A final assembly is generated with the consensus sequences, which are generally the most common sequence at the position.**

Polishing the Genome



- “Polish” out errors in the assembly by mapping the reads back to the assembly.
- Identify positions where the read sequences differ from the draft genome.
- Correct the draft sequence at those positions, producing a higher quality final assembled genome.

