

We can now align the viral reads to a known reference sequence.

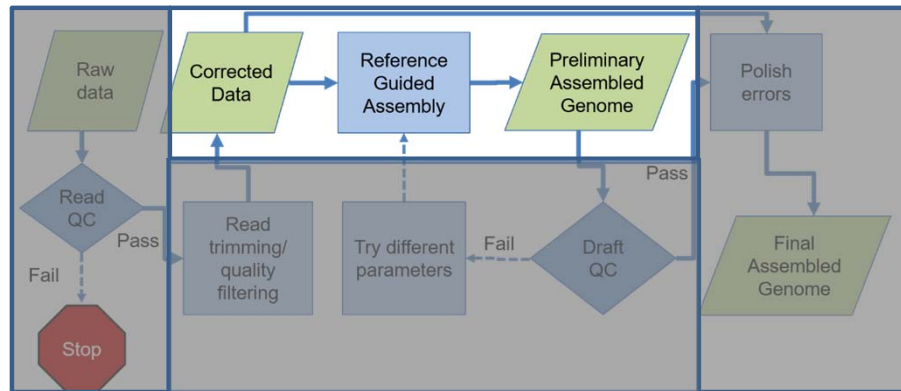
Sequence of the reference strain (already known).



Quality Viral Reads,
from the previous step.

- **Use the “bwa” program to map the viral reads to the known reference assembly.**

Reference Guided Assembly



- Start with quality reads and a reference genome.
- The reference genome is the known sequence from the same species.
- Reads are mapped to the reference genome, creating a preliminary draft of the sample genome.

