

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

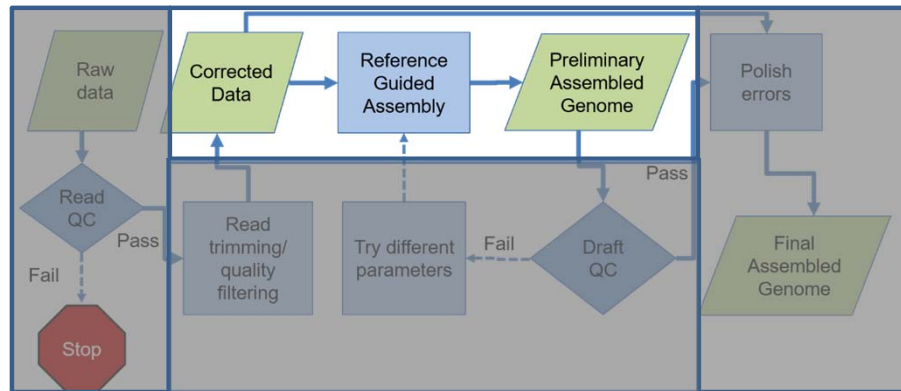
Sequence of the reference strain (already known).



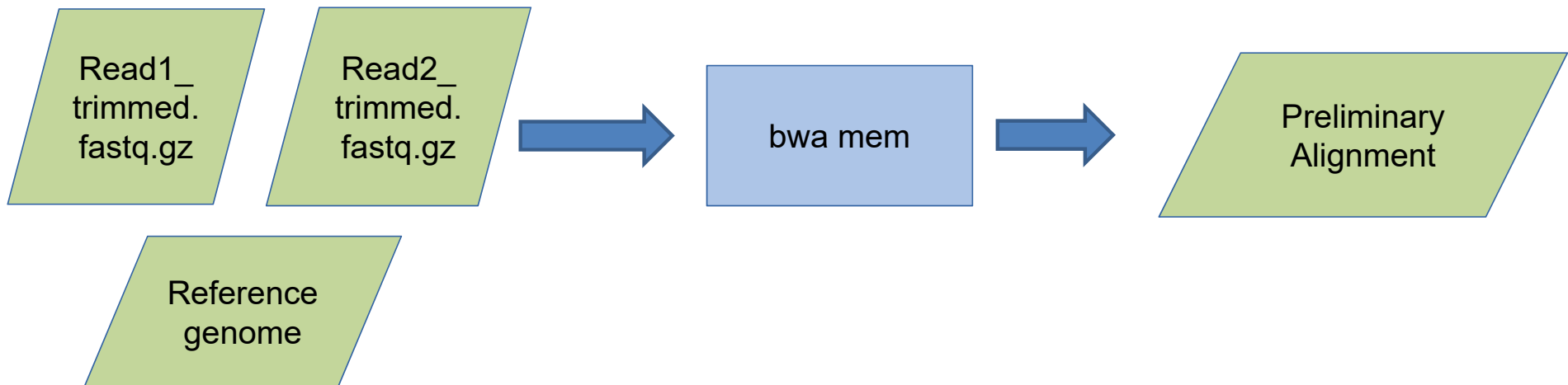
Quality Viral Reads,  
from the previous step.

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

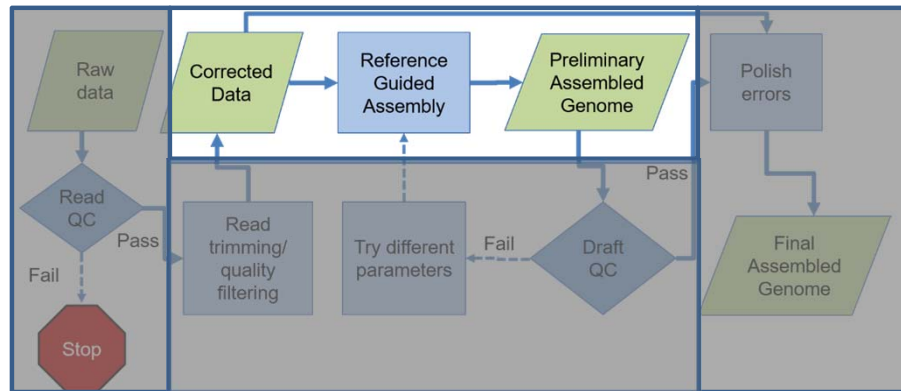
## Reference Guided Assembly, pt. 1



- 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 alignment



## Reference Guided Assembly, pt. 2



- Starting with the preliminary alignment, run the **velveth** and **velvetg** programs.
- These programs compare the aligned reads to the reference genome and output a **preliminary assembled genome**.
- This preliminary assembly is now our best guess of the genome sequence of the virus isolated from our sample.

