#### Generate consensus sequence:

* + Make a copy of the final VCF file (final\_variants.vcf) with a new name (final\_variants.phageD.vcf).
  + Compress the copied VCF file using bgzip.
  + Create an index file for the compressed VCF file using bcftools index.
  + Use bcftools consensus to generate a consensus sequence from the reference genome and the compressed VCF file.
  + Specify the output file as final.consensus.fasta in the sample's mapping directory.