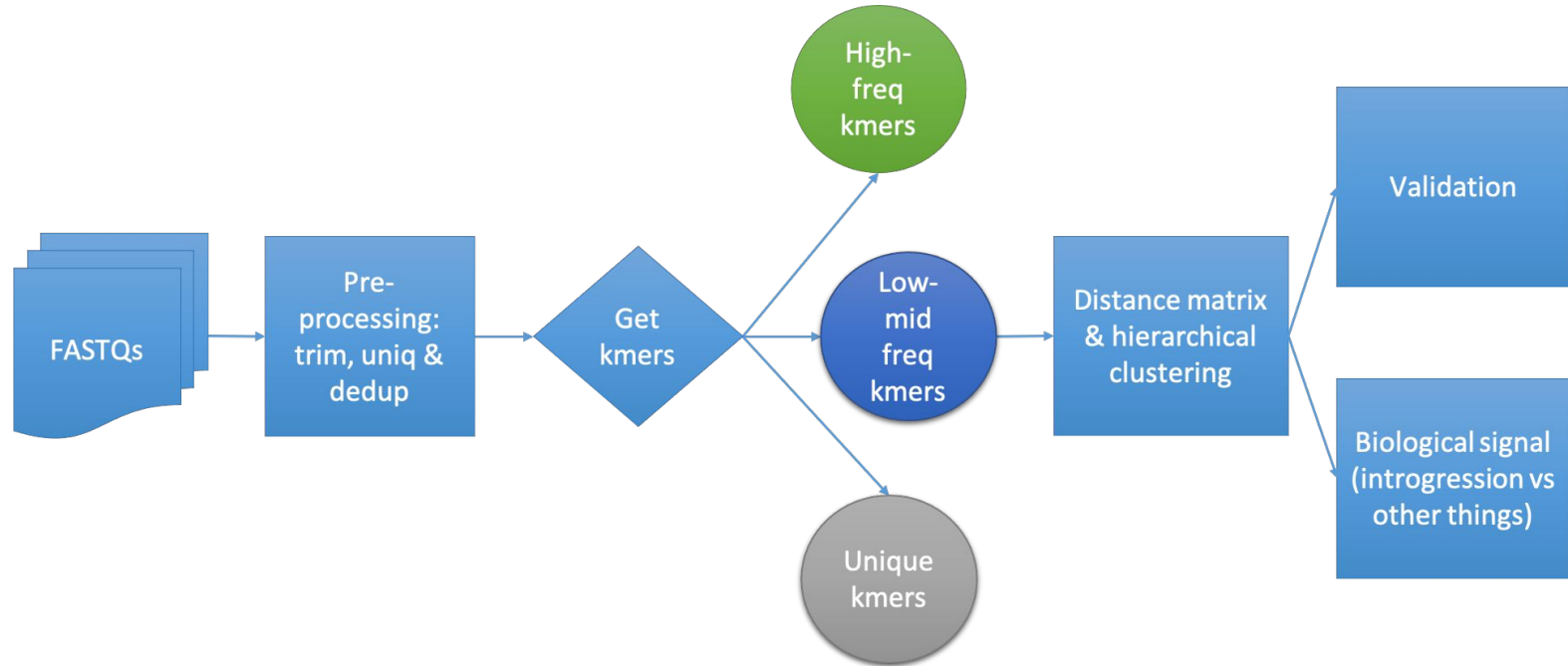


# Group 3- pipeline

12 Oct

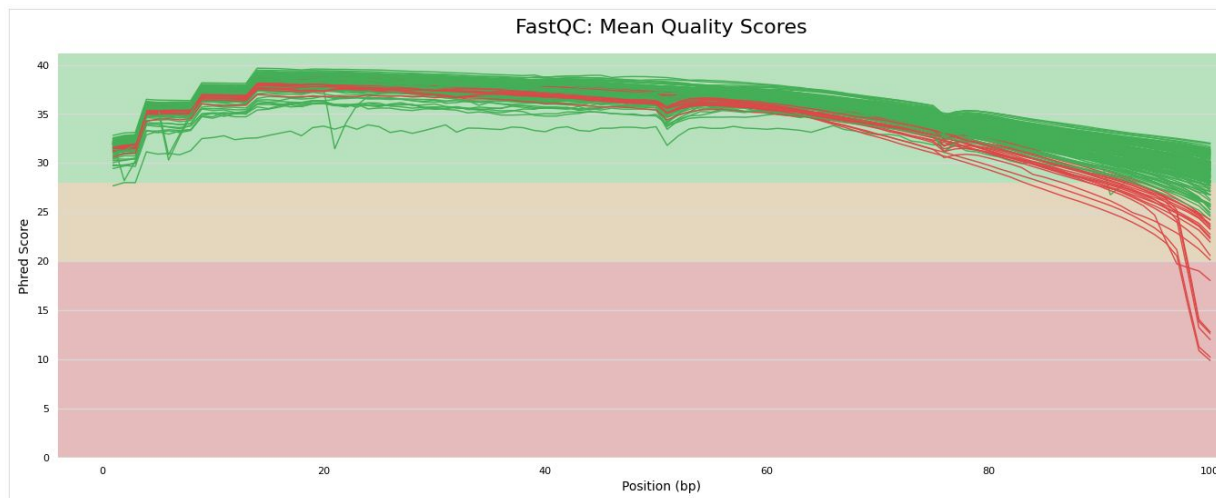


*In a single reseq sample:*

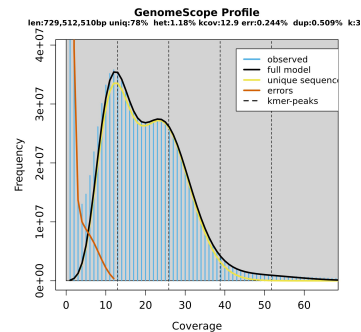
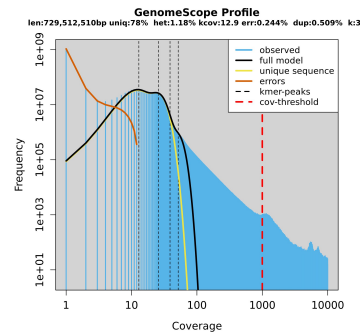
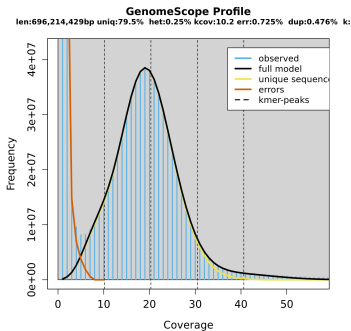
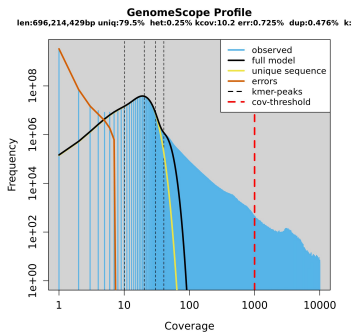


# Progress

- Downloaded short reads 84 tomato lines `sra_fastq_importer`
- Quality control of reads `fastqc`
- Trimming `flexbar_fastq_read_trimmer` (5base,q>20N)

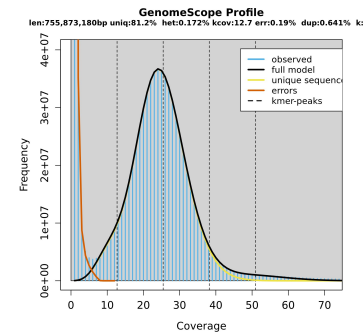
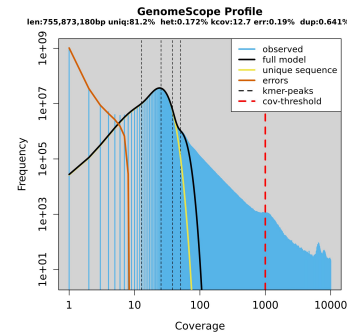
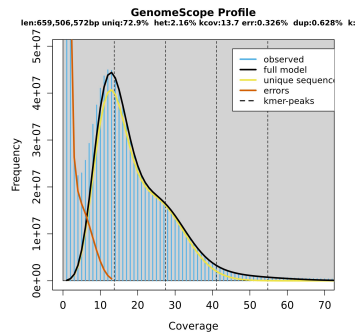
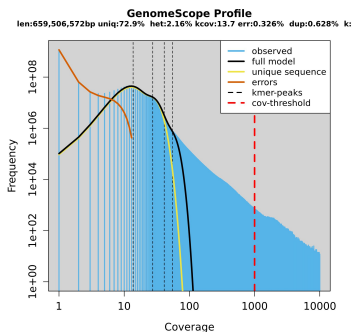


# ● Jellyfish `jellyfish_and_genomescope`



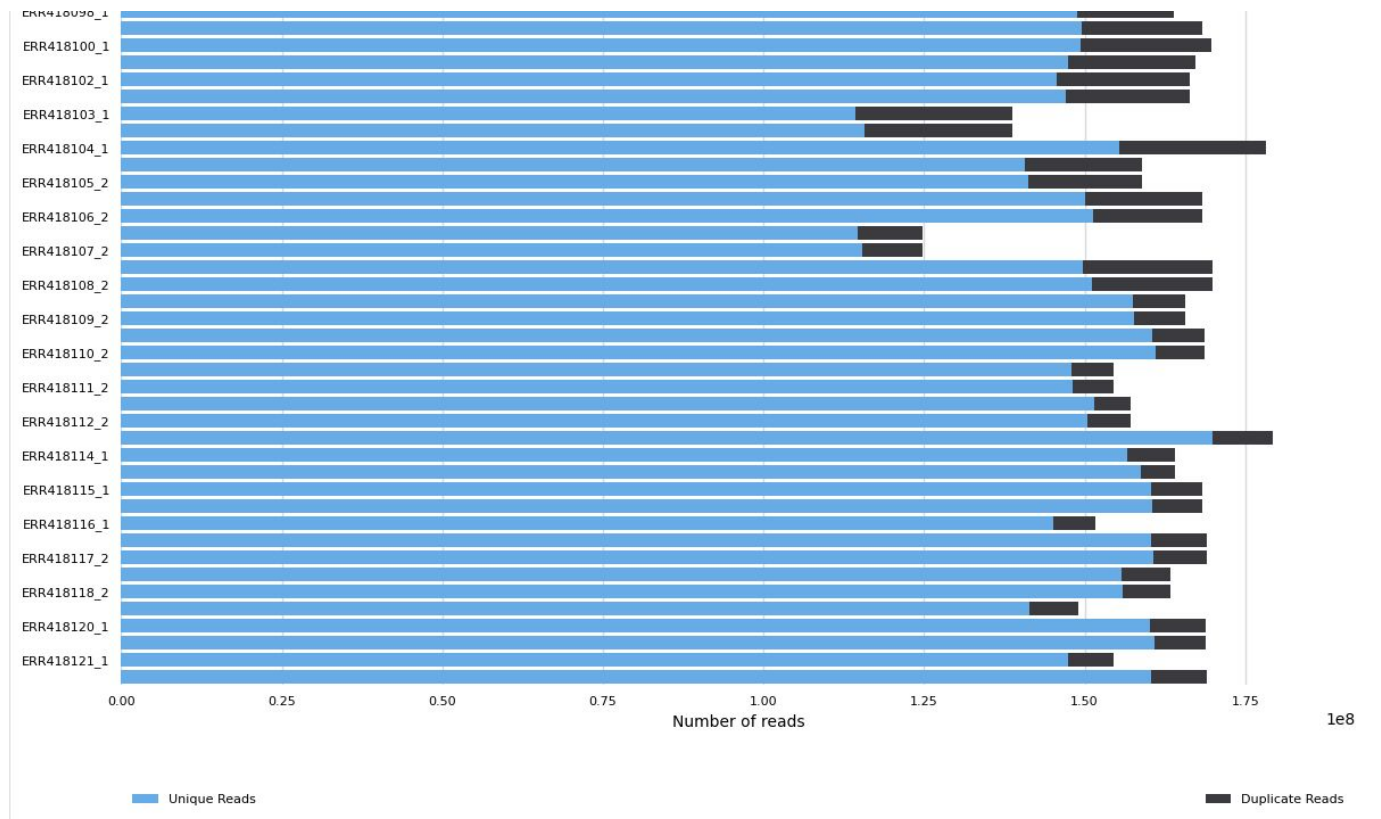
ERR418040 (*S. lycopersicum-elit*)

ERR418100 (*S. habrochaites-wild*)



ERR418108 (*S. huaylasense-wild*)

ERR418099 (*S. habrochaites-wild*)



Subsampling all samples `SwissArmyKnife-> seqtk`