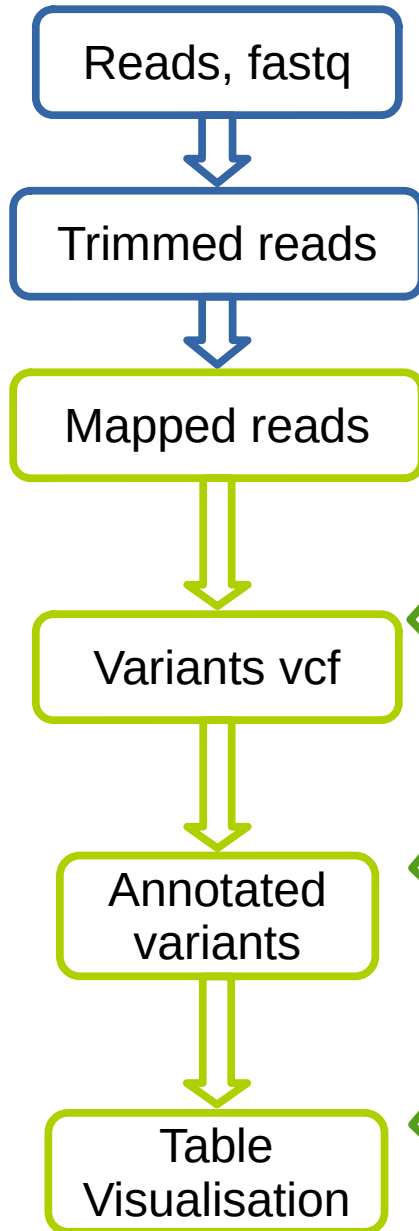


RNA-seq data of 29 tumour-only breast cancer cell lines



Filter steps:

- Mapping quality <20
- Cluster of ≥ 3 variants within 35bp
- Depth <5x
- RNA edit sites
- Low complexity regions (LCRs)
- Common SNPs
 - 1000 genomes
 - GnomAD
 - dbSNP
- Frequency >20% samples