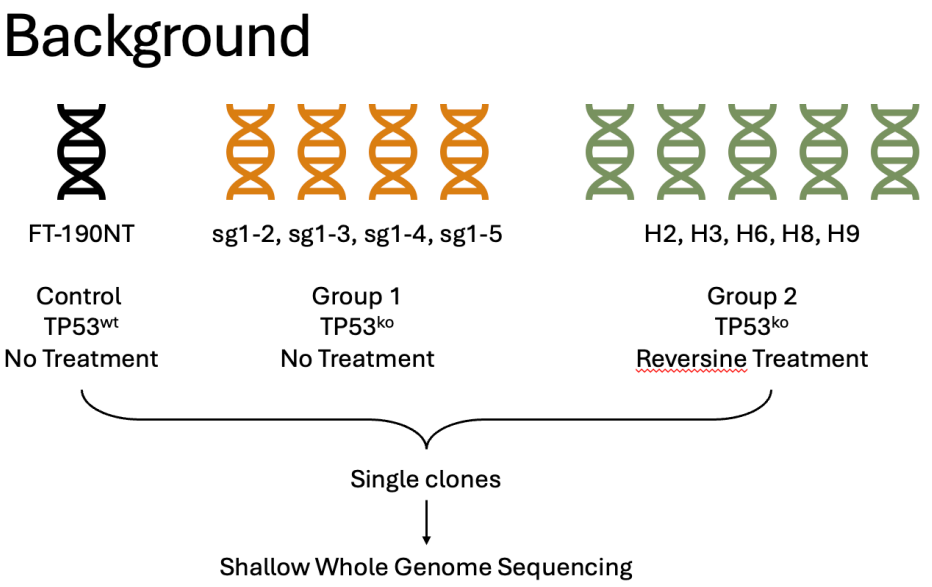
01.Overview

Data stored in Agothos

Introduction

Use Shallow Whole Genome to see evolution of aneuploidy in HGSOC cancers

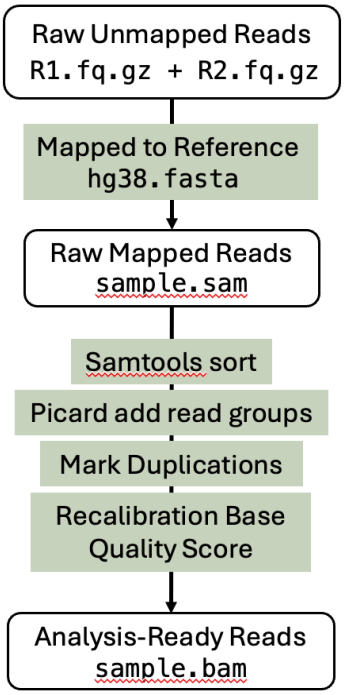


- [x] Download data and upload to HPC to alignment
- [x] Run QDNAseq on the data

Update 1:

Data aligned –– Quality of bam checked by samtools stats, average percentage of properly paired reads: 98.75%

GATK Data-Preprocessing Pipeline



Quality of bam checked by samtools stats, average percentage of properly paired reads: 98.75%

https://gatk.broadinstitute.org/hc/en-us/articles/360035535912-Data-pre-processing-for-variant-discovery

QDNAseq not very smooth, issues:

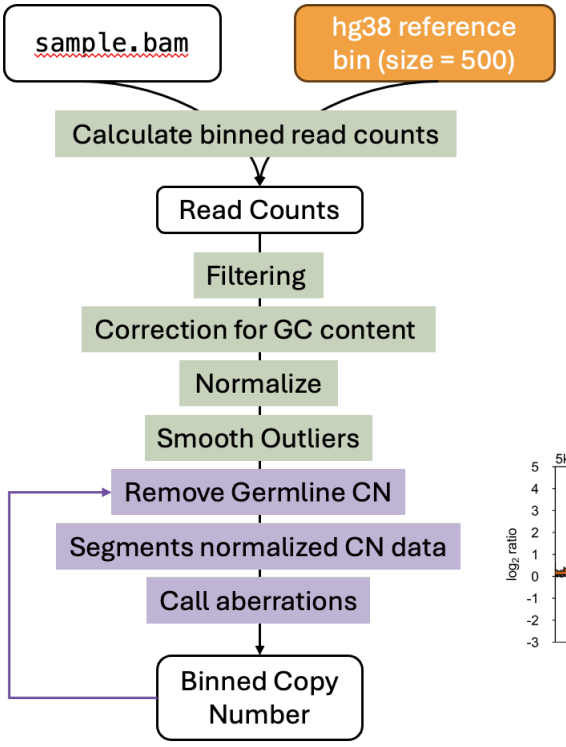
1. Too many segments in the data
2. The normal sample have aneuploidy -– how can it be??

- [x] Improve segmentation

Update 2:

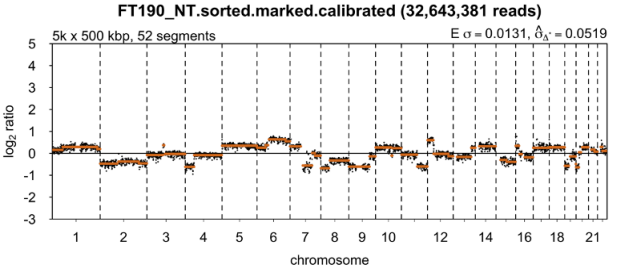
Segment at 500 bin results in smooth arm-level aneuploidies.

- [x] Remove backgrounds?



Analyzing Chromosomal Aberrations Using QDNA-seq

https://bioconductor.org/packages/devel/bioc/vignettes/QDNAseq/inst/doc/QDNAseq.pdf



Extract the copy number matrix from the control QDNA-seq object and use it as background noise to normalise all other treatment objects.