What am i about to say?

Intro

Sample collection and DNA extraction

Sequencing

Preprocessing:

qsub ./my\_fastX\_trimmer.py 🡺 WERKT NIET OP GZ FILES 🡺 eerst unzippen dan file kopieren 🡺zulke dingen nakijken later op de job

Q33 or Phred score = error van 10^-4

Germ line variant calling

First we unzip the files because the BWA algorithm does not work with zipped files 🡺 for file in `ls |grep gz`; do gunzip $file; done

GATK:

Provides VDA(variant discovery analysis) in HTS data 🡺 provides workflow to do so

Reads are not all the same size

Picard is crazy to use

Read group adding = little identifier

BWA: is a software package for mapping low-divergent sequences against a large reference genome, such as the human genome. It consists of three algorithms: BWA-backtrack, BWA-SW and BWA-MEM. The first algorithm is designed for Illumina sequence reads up to 100bp, while the rest two for longer sequences ranged from 70bp to 1Mbp. BWA-MEM and BWA-SW share similar features such as long-read support and split alignment, but BWA-MEM, which is the latest, is generally recommended for high-quality queries as it is faster and more accurate. BWA-MEM also has better performance than BWA-backtrack for 70-100bp Illumina reads.

Depending on the questions we use the right algorithm

Using bwa mem does everything in 1 time

ID=sample, SM=sample name, LB= sample name, PL= Illumina , PU= sample name

Base quality recalibratos = tells you if there are systematic errors => detect systematic errors

**Samtools flaggstat : To run SAMTOOLS with Paco zijn script heb ik eerst een directory nodig waar alle files die ik met bwa\_mem heb gerund in zitten**

1= mkdir No\_MAPQ 2= make the SAMQ directory

Replace all the bwa\_mem files to No\_MAPQ directory and run samtools on this map

**Use the BIT09 script 🡺 get the overall score??**

./bit09-filtering-samtools.sh /nlustre/users/junior/OmegaFastq/No\_MAPQ/ 20 /nlustre/users/junior/OmegaFastq/SAMQ/

**For every sample we run qaulimap and run multiqc again**

=> reference genome:

qualimap bamqc -bam [infile] -gff /nlustre/users/fourie/H.sapiens/intervals/trusight\_cancer\_manifest\_a.bed -outdir [outdir]

(/nlustre/users/fourie/H.sapiens/gatk\_resources\_bundle/2.8/hg19/uscs.hg19.fasta) 🡺 does not ask for a reference genome because it is normally already inbedded in the bam files

Qaulimap gene annotation files:

/nlustre/users/fourie/BIFHons/Mapping/ucsc\_hg19\_refseq.gtf

File that came with the kit

Picard:

Retrieves duplicated and adds a label to the reads to say that they are independent reads…

HaplotypeCaller:

The HaplotypeCaller can call SNPs and indels simultaneously via local de-novo assembly of haplotypes in an active region. In other words, whenever the program encounters a region showing signs of variation, it discards the existing mapping information and completely reassembles the reads in that region. This allows the HaplotypeCaller to be more accurate when calling regions that are traditionally difficult to call, for example when they contain different types of variants close to each other. It also makes the HaplotypeCaller much better at calling indels than position-based callers like UnifiedGenotyper.

In the so-called GVCF mode used for scalable variant calling in DNA sequence data, HaplotypeCaller runs per-sample to generate an intermediate genomic gVCF (gVCF), which can then be used for joint genotyping of multiple samples in a very efficient way, which enables rapid incremental processing of samples as they roll off the sequencer, as well as scaling to very large cohort sizes (e.g. the 92K exomes of ExAC).

In addition, HaplotypeCaller is able to handle non-diploid organisms as well as pooled experiment data. Note however that the algorithms used to calculate variant likelihoods is not well suited to extreme allele frequencies (relative to ploidy) so its use is not recommended for somatic (cancer) variant discovery. For that purpose, use MuTect2 instead.