

# Lung Cancer

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# 1 Introduction

# 2 Materials

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## 3.1 General Usage

### 3.1.1 Genome Analysis Toolkit

Genome analysis toolkit (GATK) is a software package for variant discovery among sequencing data (Van der Auwera et al., 2013; DePristo et al., 2011).

### 3.1.2 Samtools

Samtools is a suite software packages for discovering in high-throughput sequencing data (Li et al., 2009).

## 3.2 Alignment

### 3.2.1 Burrows-Wheeler Aligner

Burrows-Wheeler Aligner (BWA) is a software package for aligning short-read sequences unto a large reference genome (Li & Durbin, 2009). BWA-MEM is one of the contained algorithms in BWA software package, is a novel algorithm for mapping sequence reads on a large reference genome (Li, 2013).

### 3.2.2 STAR

STAR is a swift universal RNA-seq alignment tool (Dobin et al., 2013).

## 3.3 Quality Check

### 3.3.1 FastQC

FastQC is a software package which aims to provide a productive method to do quality control check on raw sequence data (Andrews et al., 2012).

### 3.3.2 Sequenza

Sequenza is a software package to investigate genomic sequencing data, such as cellularity and ploidy estimation, from paired normal-tumor samples (Favero et al., 2015).

## 3.4 SNV Detection Workflow

# 4 Results

## 4.1 FastQC

# 5 Discussion

# 6 References

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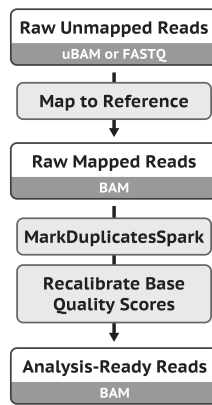


Figure 1: Data pre-processing for variant discovery (Van der Auwera et al., 2013; DePristo et al., 2011)

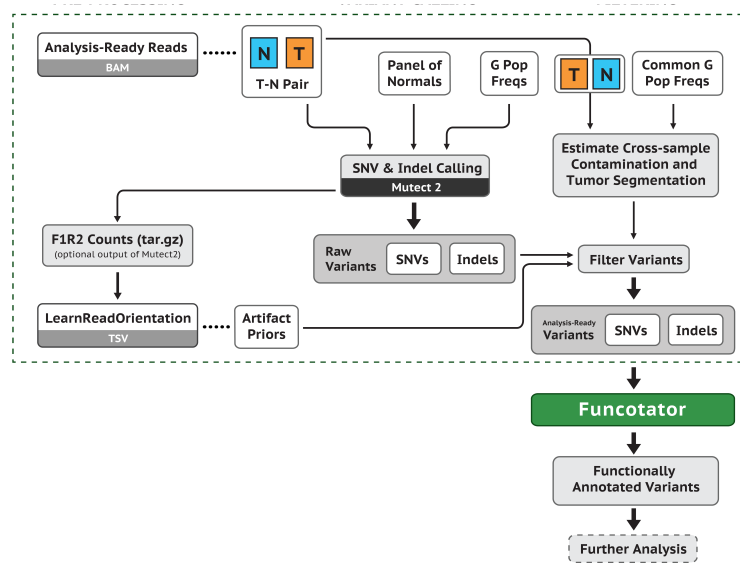


Figure 2: Somatic short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

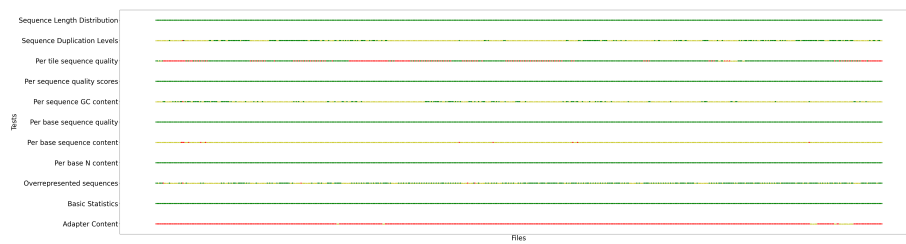


Figure 3: FastQC with WES data

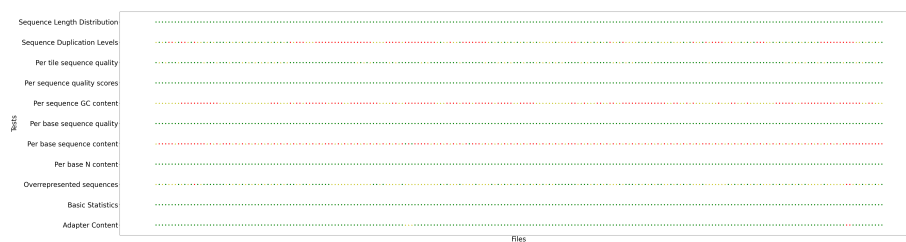


Figure 4: FastQC with WTS data

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