

# Lung Precancer Analysis

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# Overview

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# Introduction

# Lung Cancer

- Squamous cell carcinoma
- Adenocarcinoma

# Precancer

## Introduction

## Study Objectives

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- Find different mutations
  - between WES
  - between WTS
  - from cancer
  - from precancer
- Pathway examine from the mutations
  - of WES
  - of RNA-seq
- Ultra-deep sequencing to find an *infinitesimal* quantity of Non-Circulating Tumor DNA
  - from blood
  - from urine
  - from bronchus
- Diagnostic performance

# Materials

# Lung Cancer Data

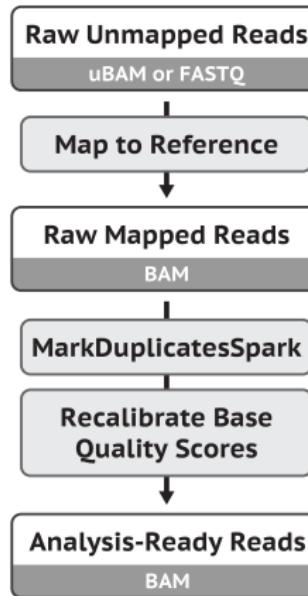
- WES (n=289) + Transcriptome (n=166)
- Normal + {Primary, CIS + AIS, AAH, Dysplasia, MIA}
  - Carcinoma in situ
  - Adenocarcinoma in situ
  - Atypical adenomatous hyperplasia
  - Dysplasia
  - Minimally invasive adenocarcinoma
- Squamous cell carcinoma (SQC) & Adenocarcinoma (ADC)
  - ① Normal - Dysplasia - CIS - SQC (n=80)
  - ② Normal - AAH - AIS - MIA - ADC (n=28)

# Methods

## Methods

## Workflows

# Data pre-processing for variant discovery



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

# Somatic short variant discovery

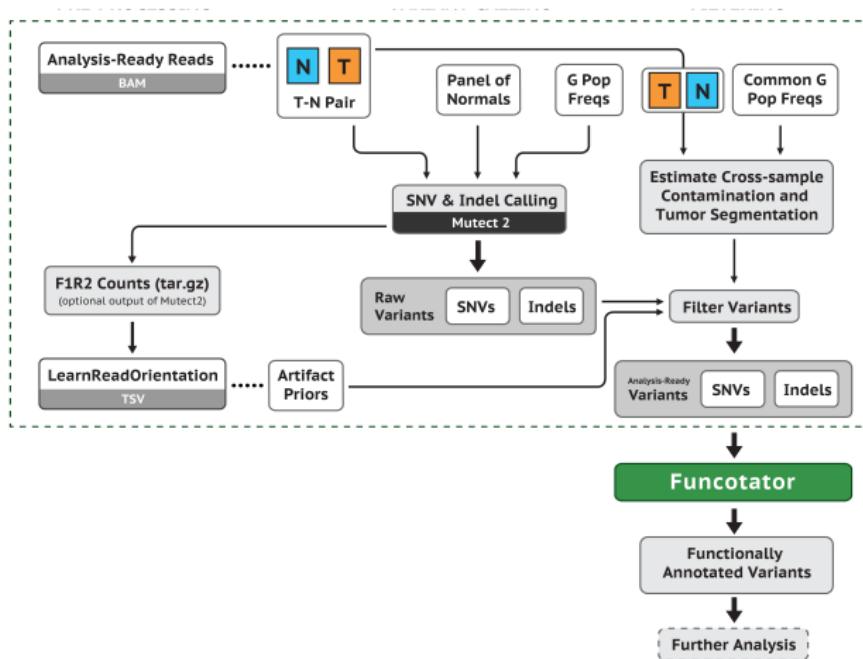
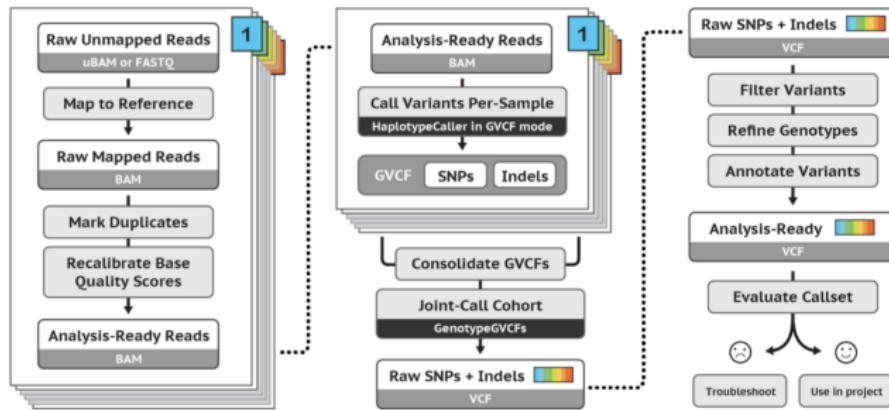


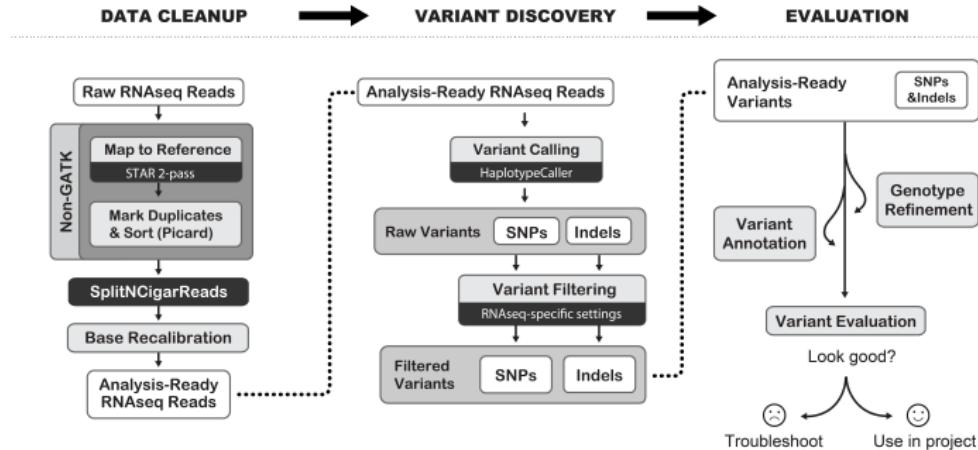
Figure: Somatic short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

# Germline short variant discovery



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

# RNA-seq short variant discovery



**Figure:** RNA-seq short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

## Methods

## Miscellaneous

# Used Bioinformatics Tools

- FastQC (Andrews et al., 2012)
- Sequenza (Favero et al., 2015)
- BWA (Li & Durbin, 2009; Li, 2013)
- STAR (Dobin et al., 2013)
- Bowtie2 (Langmead & Salzberg, 2012)
- Samtools (Li et al., 2009)
- GATK (Van der Auwera et al., 2013; DePristo et al., 2011)
- Picard (*Picard toolkit*, 2019)
- VCF2MAF (Kandoth et al., 2018)
- VEP (McLaren et al., 2016)
- Witer (Jiang et al., 2019)

# Python Packages

- Pandas (pandas development team, 2020; Wes McKinney, 2010)
- Sequenza-utils (Favero et al., 2015)
- Matplotlib (Hunter, 2007)
- Seaborn (Waskom & the seaborn development team, 2020)
- CoMut (Crowdis, He, Reardon, & Van Allen, 2020)

# Results

# Results

## Quality Checks with FastQC

# FastQC?

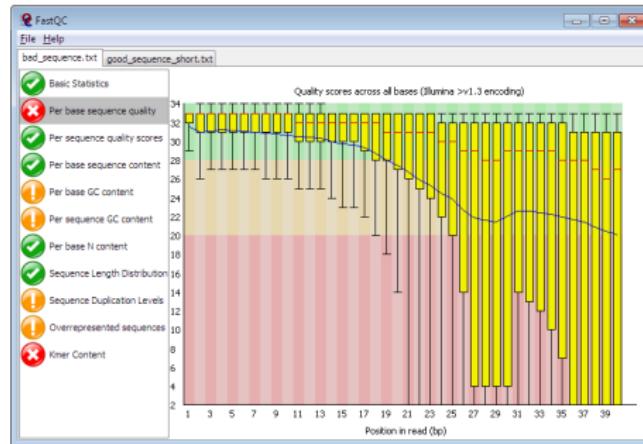


Figure: Example of FastQC Result (Andrews et al., 2012)

- A quality check tool for sequence data
- Give an overview that which test may be problems

# FastQC on WES

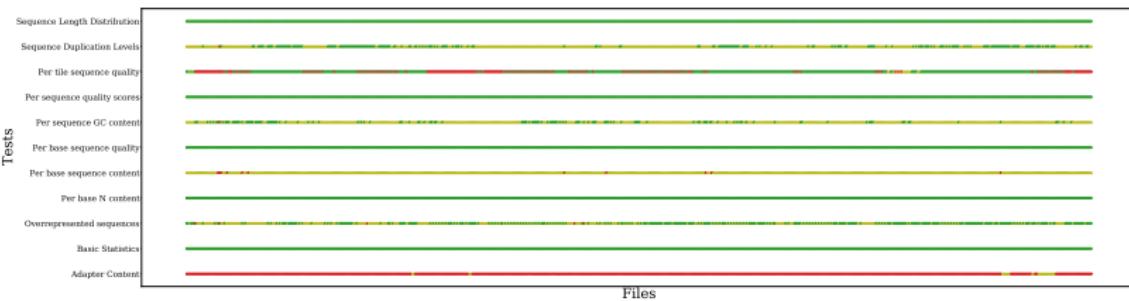
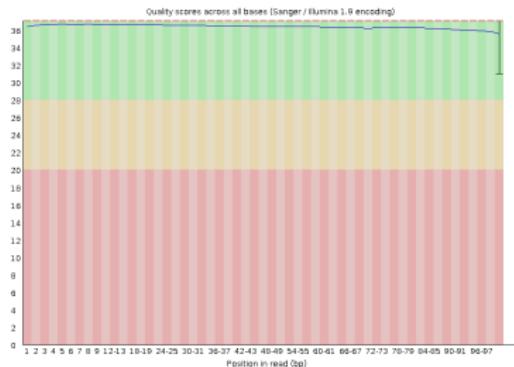


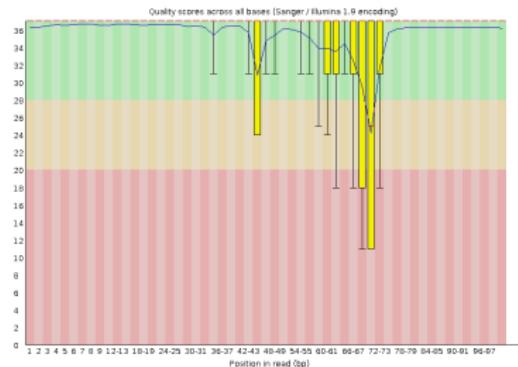
Figure: FastQC with WES data

∴ Only 33P1 has more than 3 failures: 6 FAILs.  
∴ 33P1 is excluded at further analysis.

# Failure on 33P1 I



(a) 33N



(b) 33P1

Figure: Per Base Sequence Quality Results

# Failure on 33P1 II

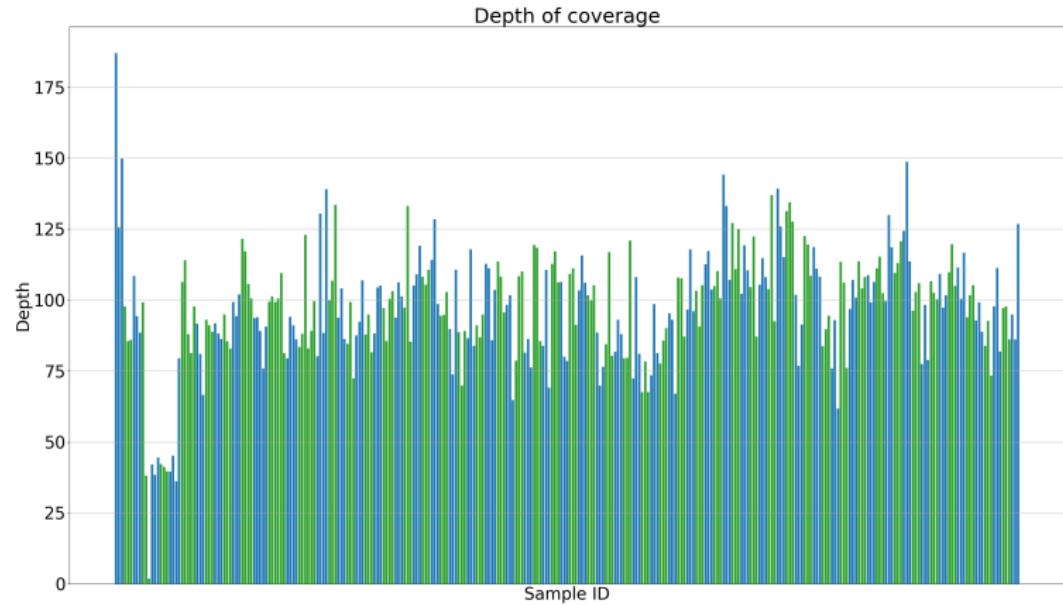


Figure: Coverage Depth Plot

# FastQC on WTS

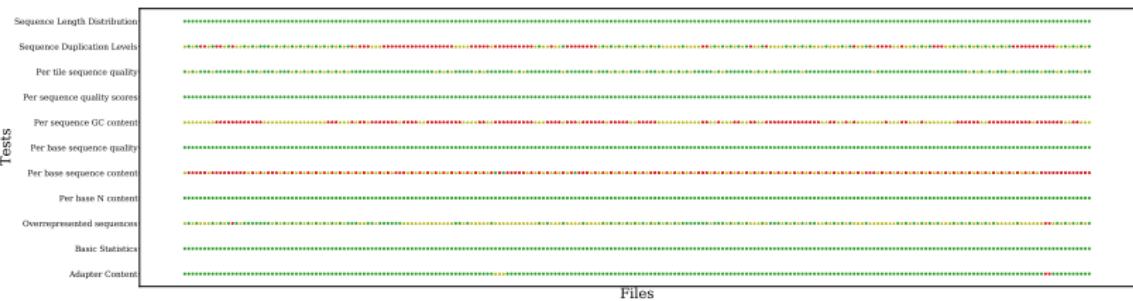


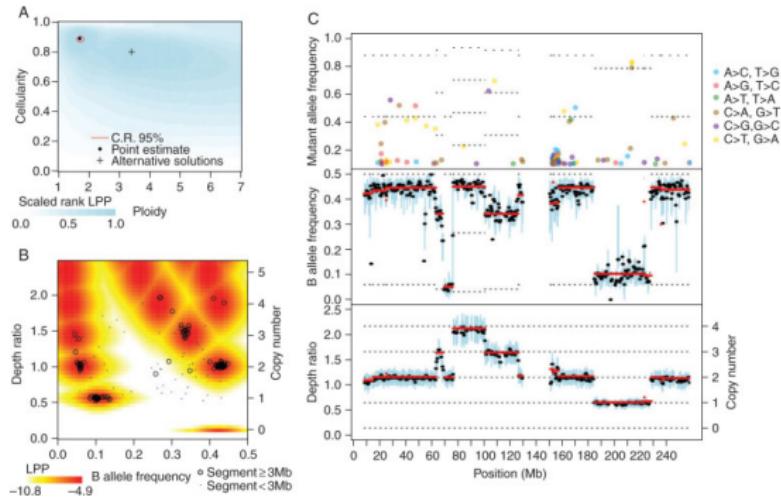
Figure: FastQC with WTS data

∴ No sample has more than 5 failures.  
∴ All sample are good to analysis.

# Results

## Quality Checks with Sequenza

# Sequenza?



**Figure:** Representative Output of the Sequenza (Favero et al., 2015)

# Cellularity & Ploidy on WES

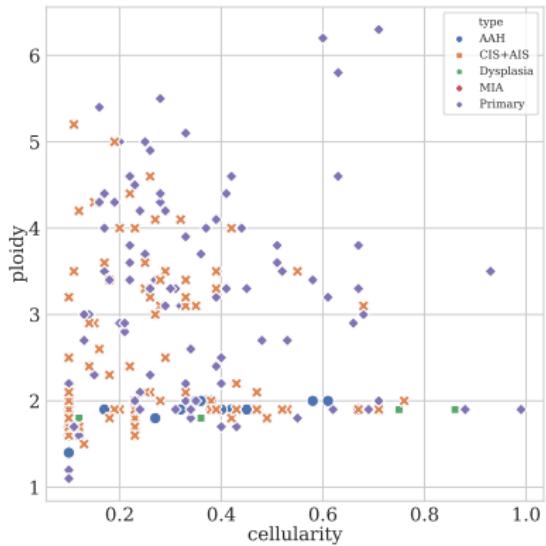


Figure: Cellularity and Ploidy from Sequenza

# Genome View on Patient #57

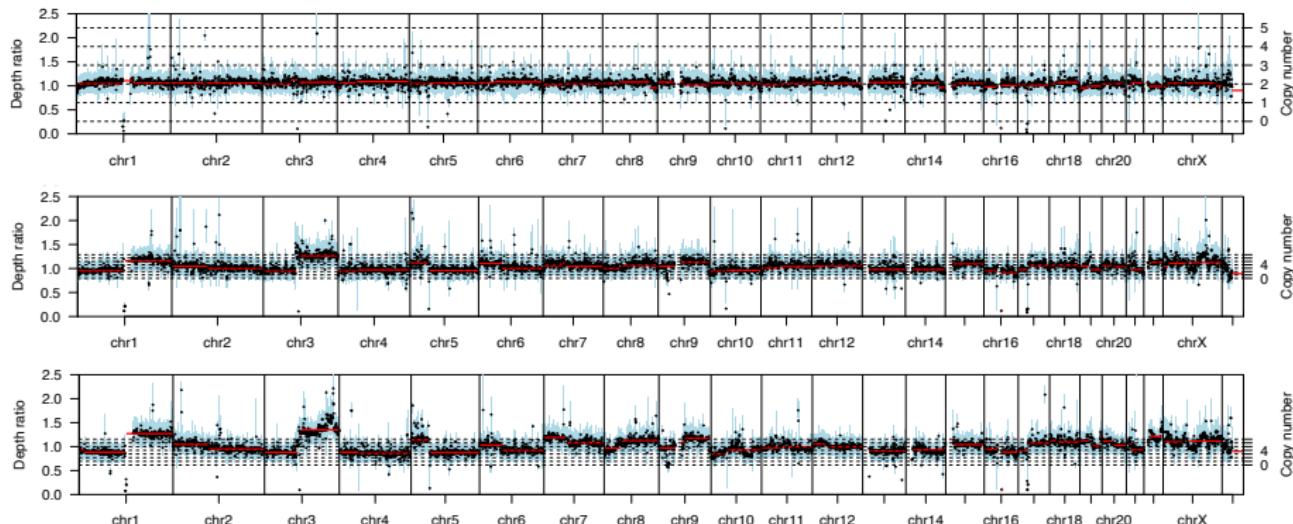
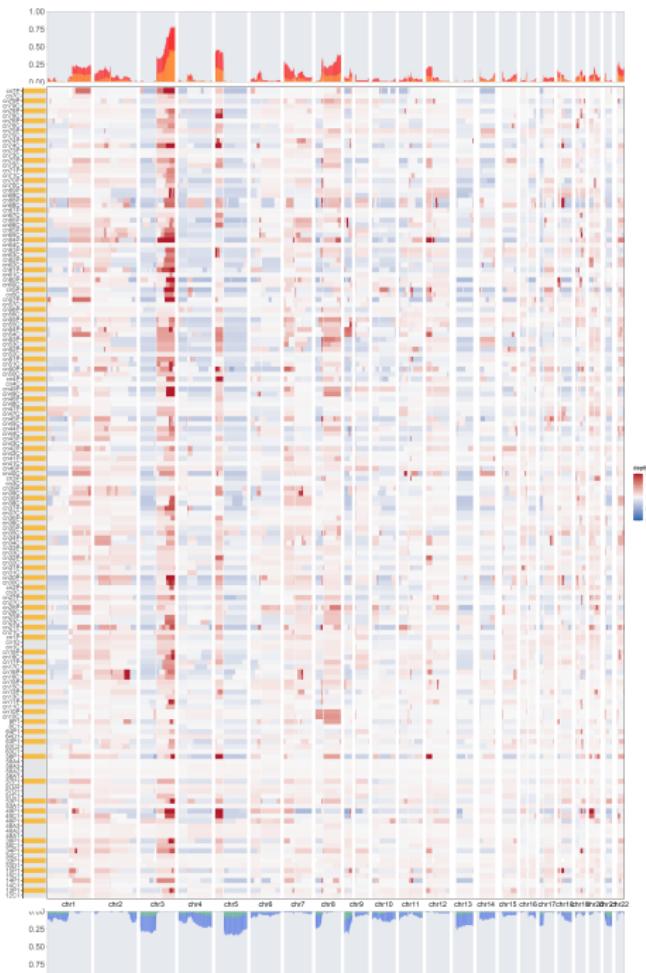


Figure: Dysplasia-CIS-Primary tumor



# CNV of ADC

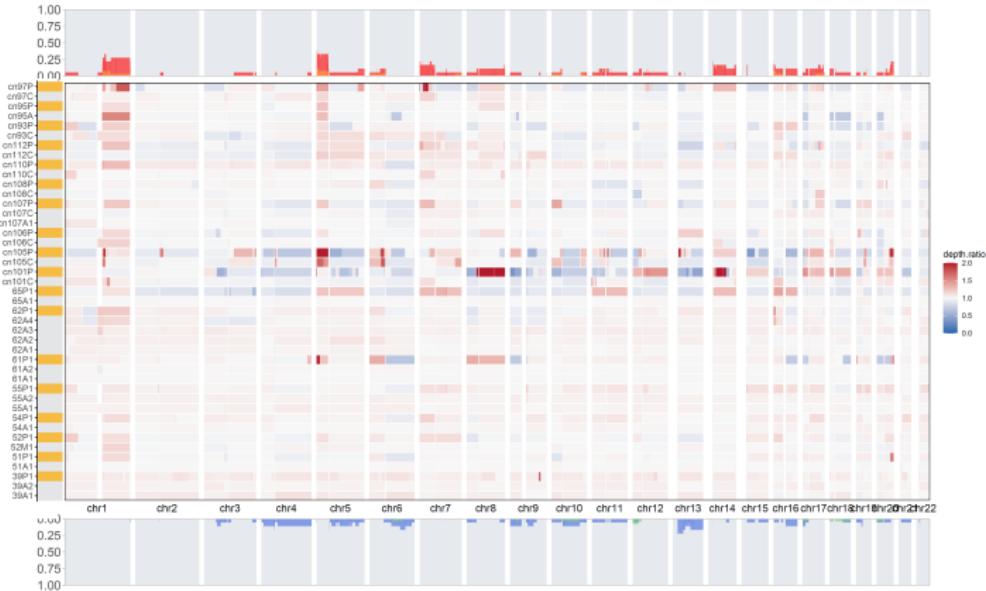
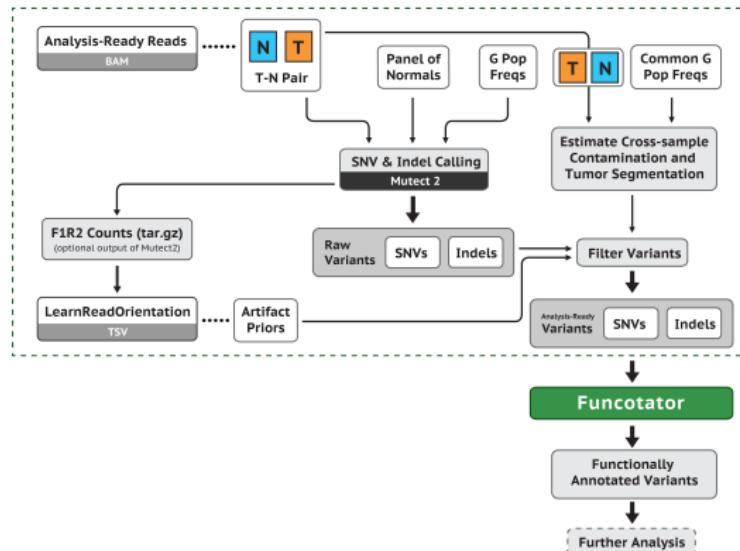


Figure: CNV Plot with ADC Patients

# Results

## Mutect2

# Mutect2?



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

# Witer?

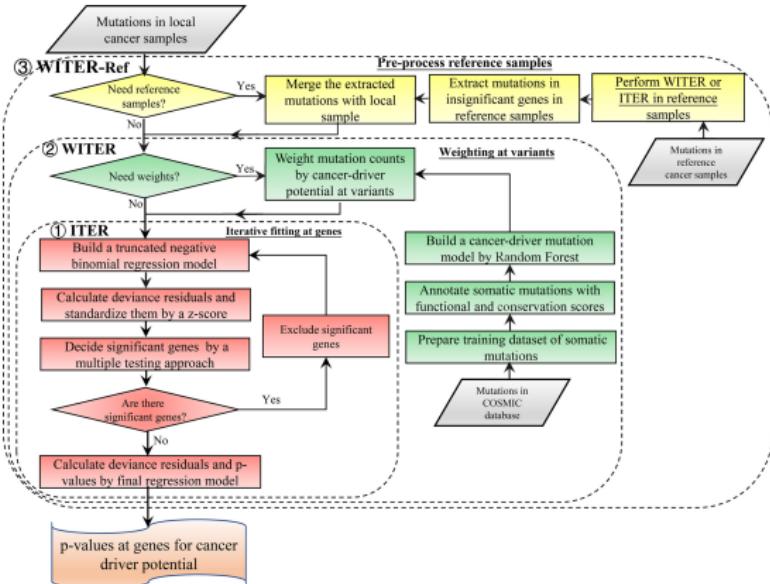


Figure: Witer diagram for detecting cancer-drive genes (Jiang et al., 2019)

# Somatic Variant in SQC

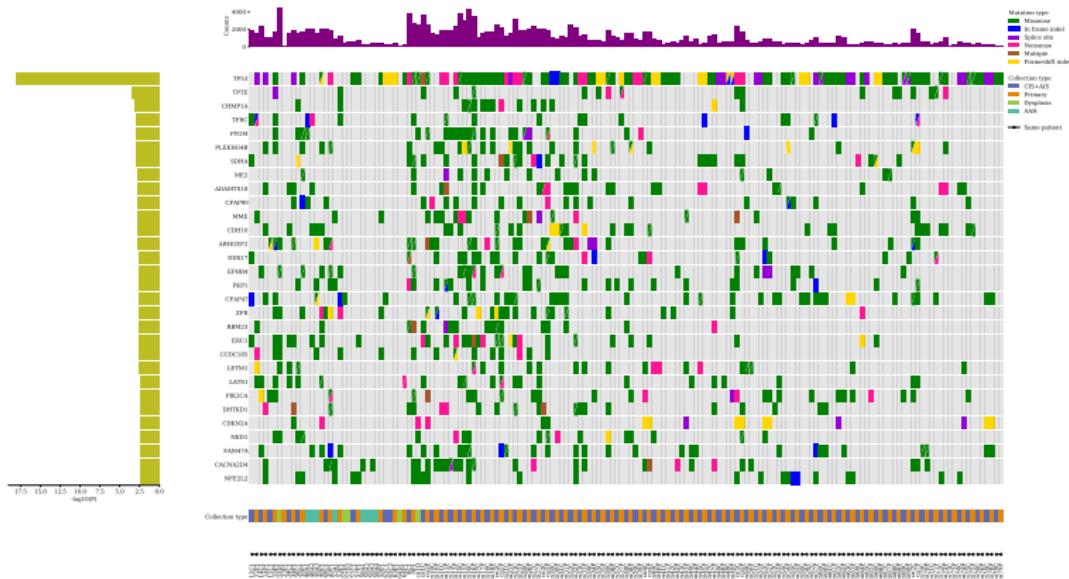
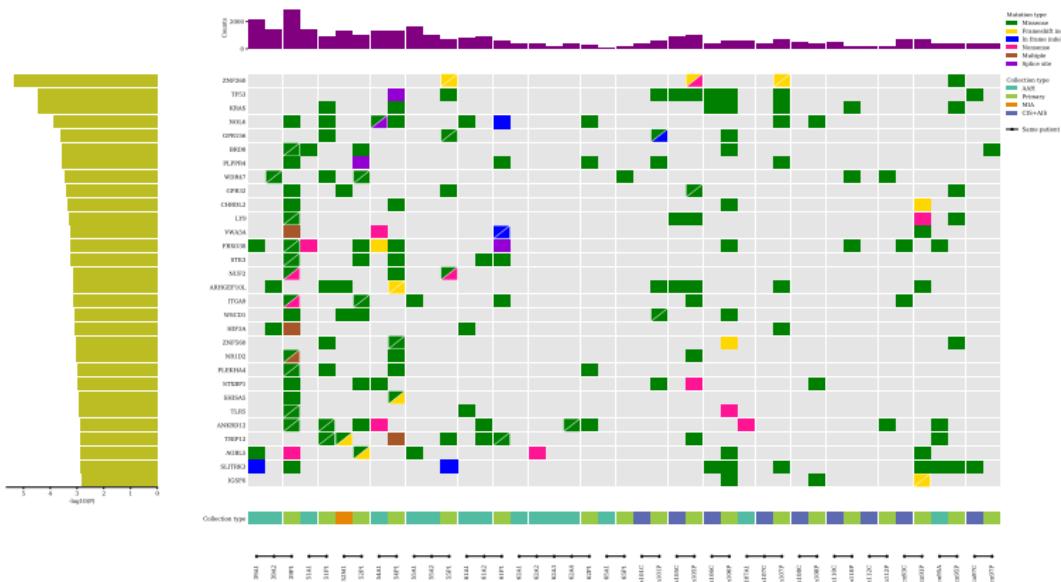


Figure: CoMut Plot with SQC Patients

## Somatic Variant in ADC



## Figure: CoMut Plot with ADC Patients

## Discussion

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