

# Lung Precancer Study

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# Overview

1 Introduction

2 Materials

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# Introduction

# Introduction

## Lung Cancer

# Lung Cancer?

- The most common form of cancer (12.3 % of all cancers) (Minna, Roth, & Gazdar, 2002)
- The most important factor: **Tobacco**

# Type of Lung Cancer

Types of lung cancer:

- Adenocarcinoma (ADC) (40 %) ★
- Squamous cell carcinoma (SQC) (25 %) ★
- Small cell carcinoma (20 %)
- Large cell carcinoma (10 %)
- Adenosquamous carcinoma
- Carcinoid
- Bronchioalveolar (Bronchial gland carcinoma)

(Vincent et al., 1977; Collins, Haines, Perkel, & Enck, 2007)

# ADC vs. SQC I

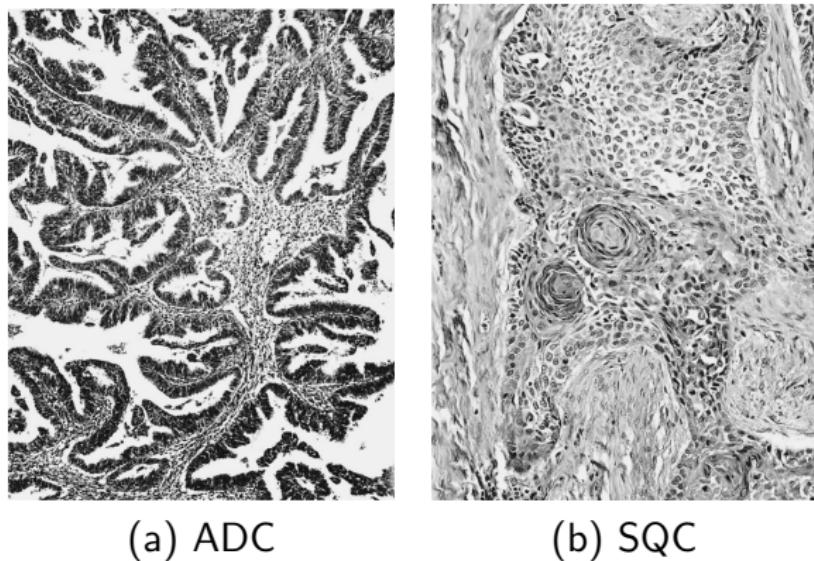


Figure: ADC and SQC histology in Lung cancer (Travis, 2002)

# ADC vs. SQC II

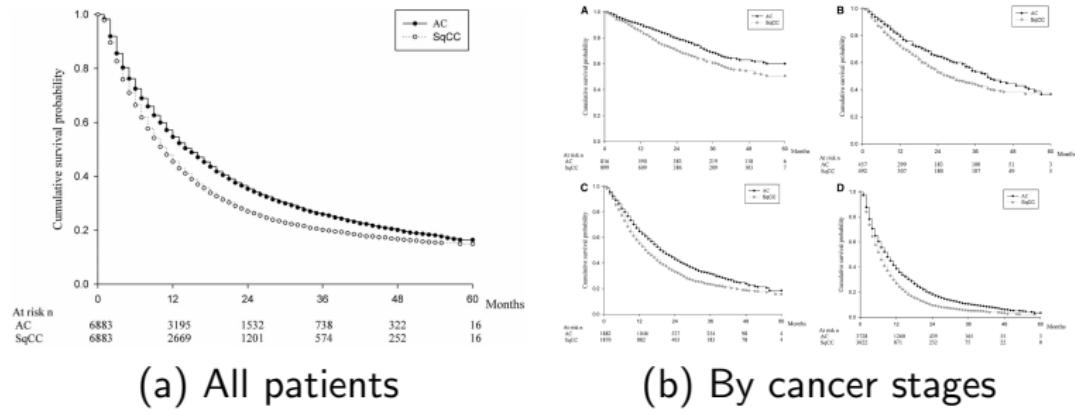


Figure: Kaplan-Meier survival curves for ADC & SQC (Wang et al., 2020)

∴ In every plots,  $p < 0.001$

∴ SQC is more dangerous than ADC.

## Introduction

## Study Objectives

# Study Objectives

- 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

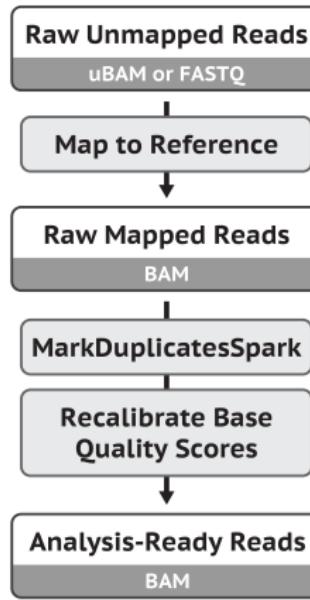
- WES (n=289) + Transcriptome (n=166)
- Normal + {Primary, CIS + AIS, AAH, Dysplasia, MIA}
  - Carcinoma in situ
  - Adenocarcinoma in situ
  - Atypical adenomatous hyperplasia
  - Dysplasia
  - Minimally invasive adenocarcinoma
- Squamous cell carcinoma (SQC) & Adenocarcinoma (ADC)
  - ① Normal - Dysplasia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

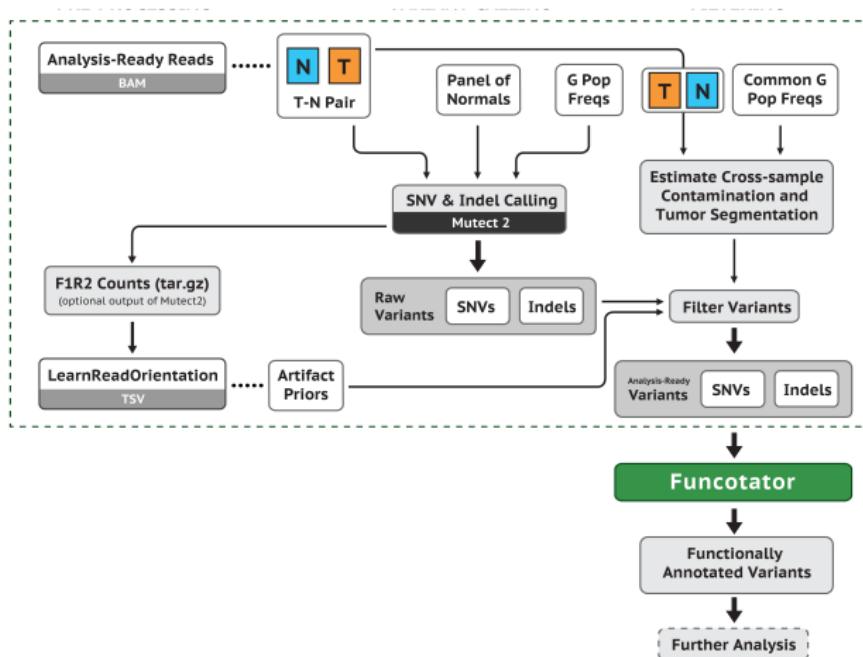
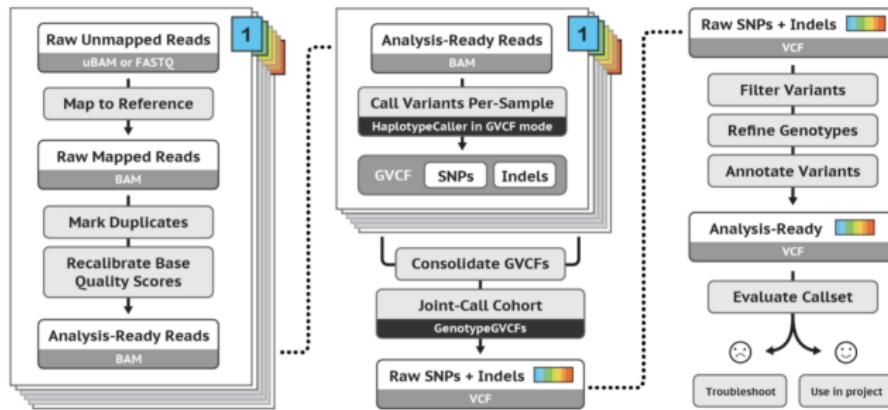


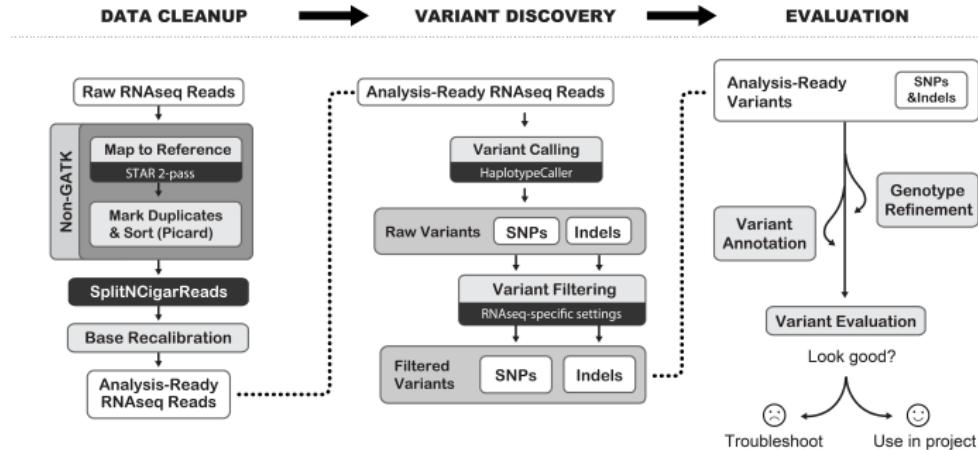
Figure: Somatic short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

# 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)
- BWA (H. Li & Durbin, 2009; H. Li, 2013)
- STAR (Dobin et al., 2013)
- Bowtie2 (Langmead & Salzberg, 2012)
- Samtools (H. Li et al., 2009)
- GATK (Van der Auwera et al., 2013; DePristo et al., 2011)
- Picard (*Picard toolkit*, 2019)
- VCF2MAF (Kandoth et al., 2018)
- BCFtools (Danecek et al., 2021)
- VEP (McLaren et al., 2016)
- RSEM (B. Li & Dewey, 2011)
- CIBERSORTx (Steen, Liu, Alizadeh, & Newman, 2020)

# R Packages

- Sequenza (Favero et al., 2015)
- Copynumber (Nilsen, Liestol, & Lingjaerde, 2013; Nilsen et al., 2012)
- DESeq2 (Love, Huber, & Anders, 2014)

# 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)
- PyClone (Roth et al., 2014)
- Statannot

# Results

# Results

## Quality Checks with FastQC

# FastQC?

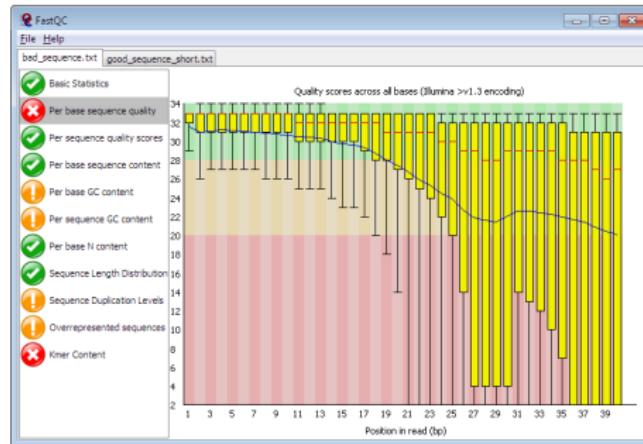


Figure: Example of FastQC Result (Andrews et al., 2012)

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

# FastQC on WES

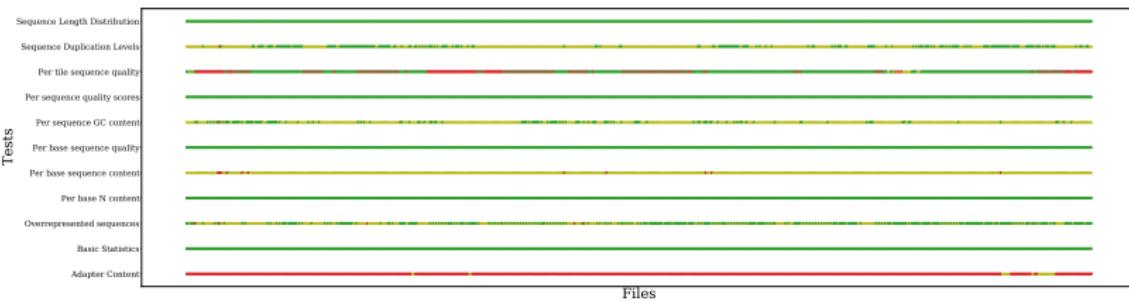
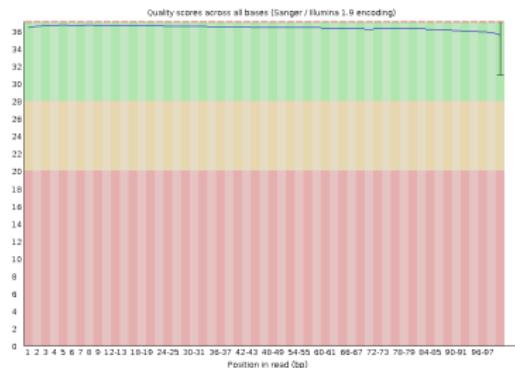


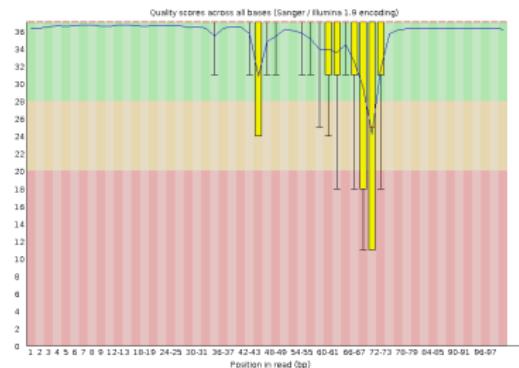
Figure: FastQC with WES data

∴ 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

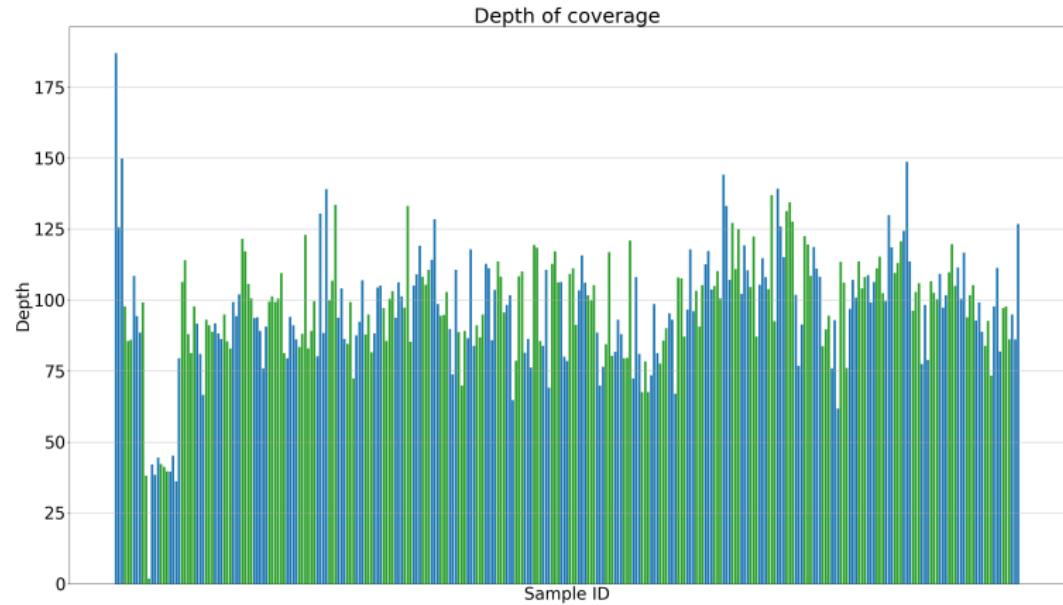


Figure: Coverage Depth Plot

# FastQC on WTS

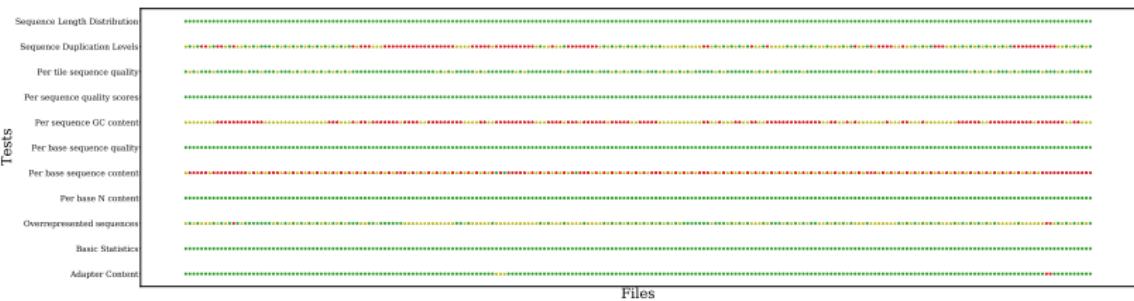


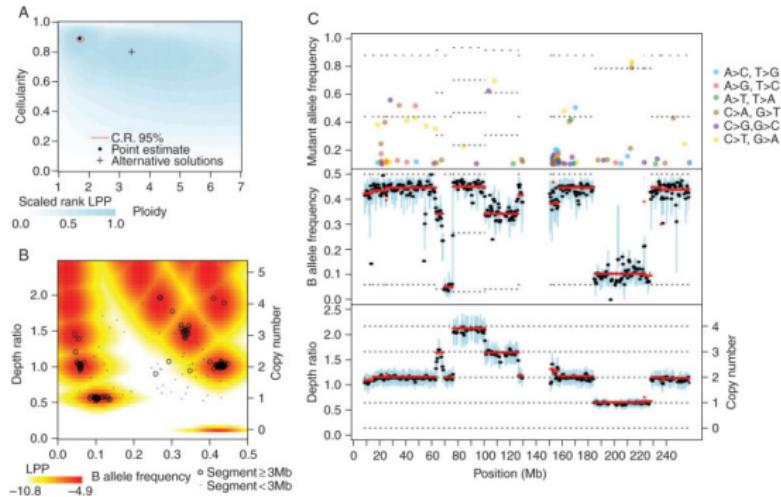
Figure: FastQC with WTS data

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

# Results

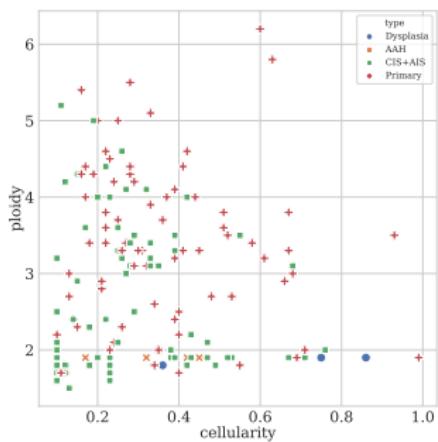
## Quality Checks with Sequenza

# Sequenza?

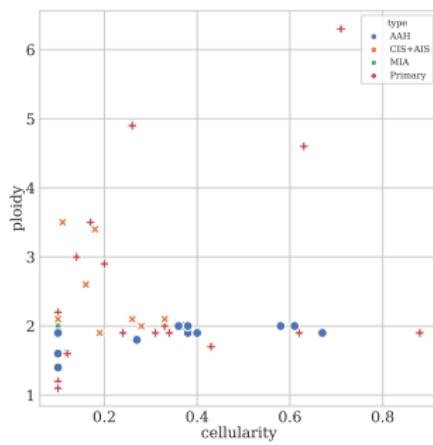


**Figure:** Representative Output of the Sequenza (Favero et al., 2015)

# Cellularity & Ploidy on WES



(a) SQC Samples



(b) ADC Samples

Figure: Cellularity and Ploidy from Sequenza

# Genome View on Patient #57

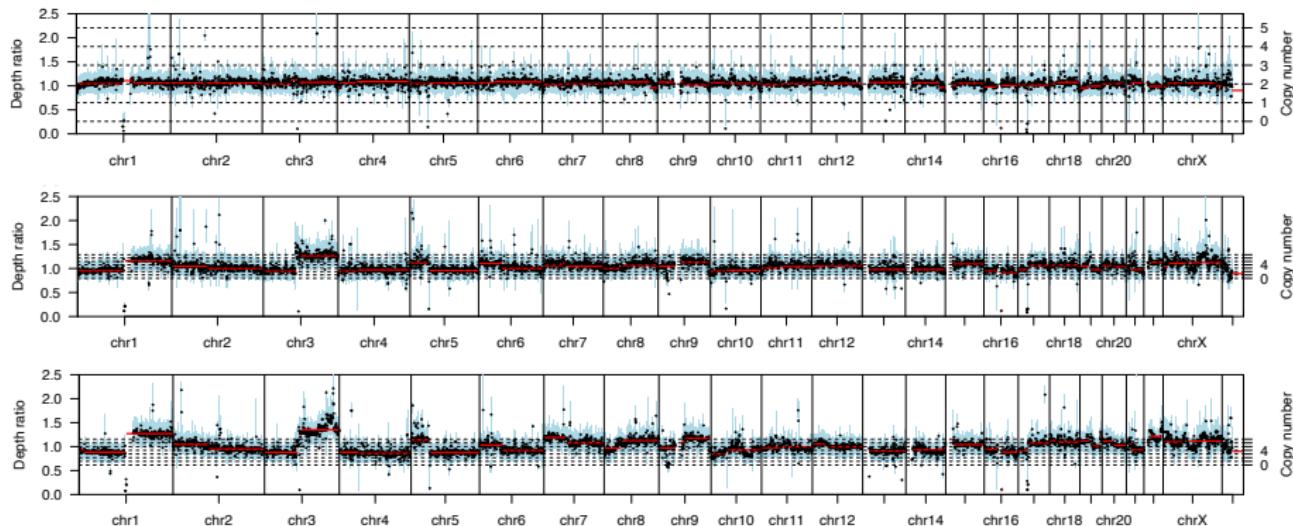
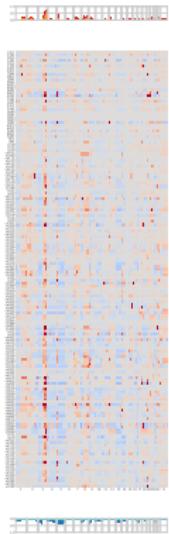


Figure: Dysplasia-CIS-Primary tumor

CNV of SQC



## Figure: CNV Plot with SQC Patients

# CNV of ADC

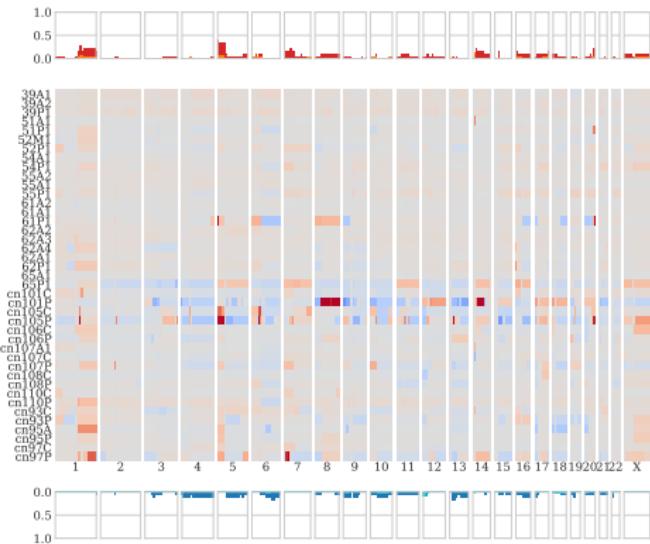
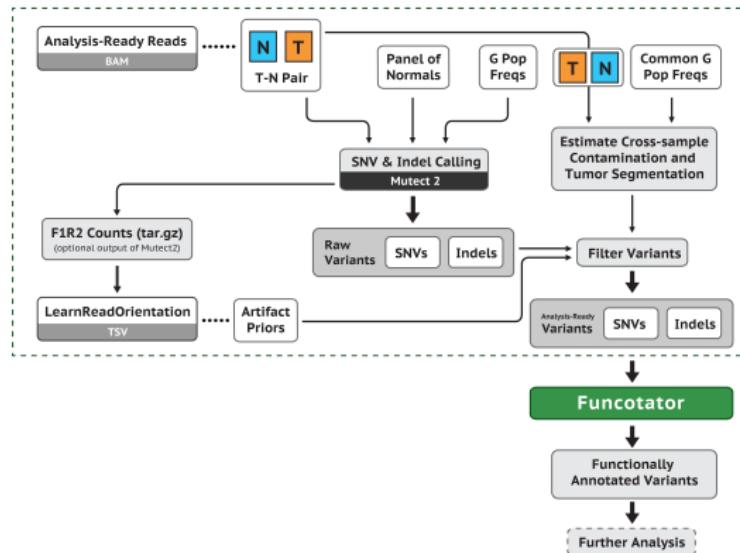


Figure: CNV Plot with ADC Patients

# Results

Find SNVs with Mutect2

# Mutect2?



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

# Witer?

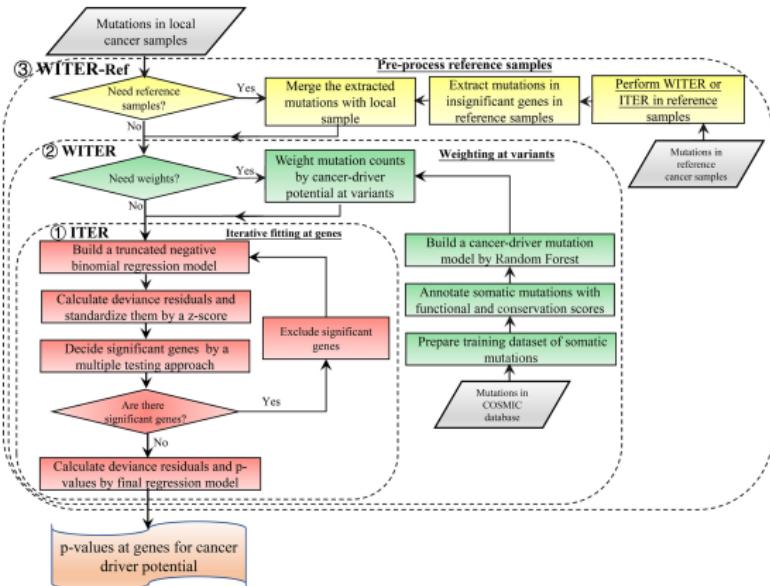


Figure: Witer diagram for detecting cancer-drive genes (Jiang et al., 2019)

# Somatic Variant in SQC

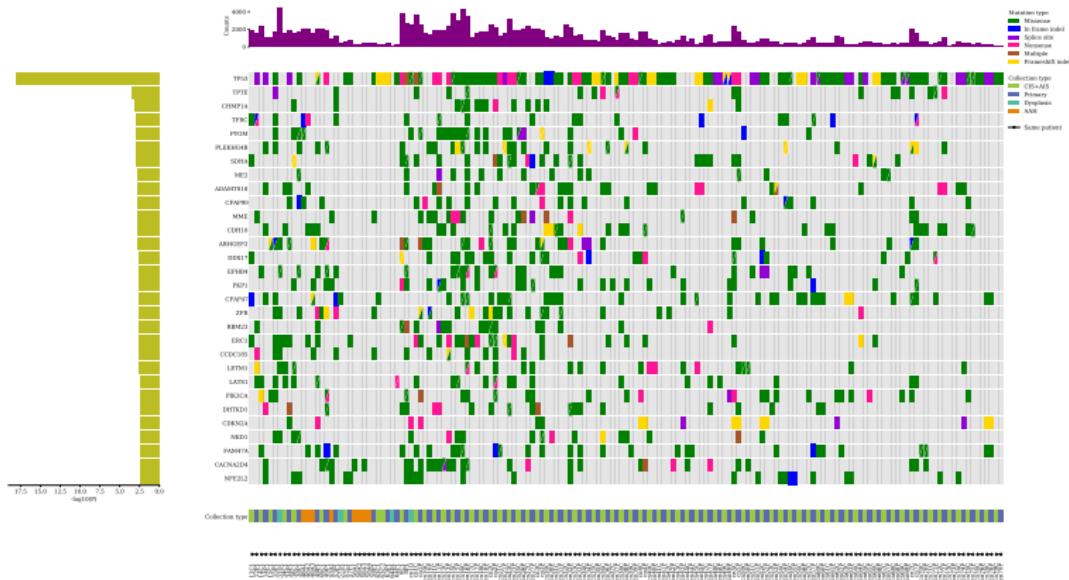
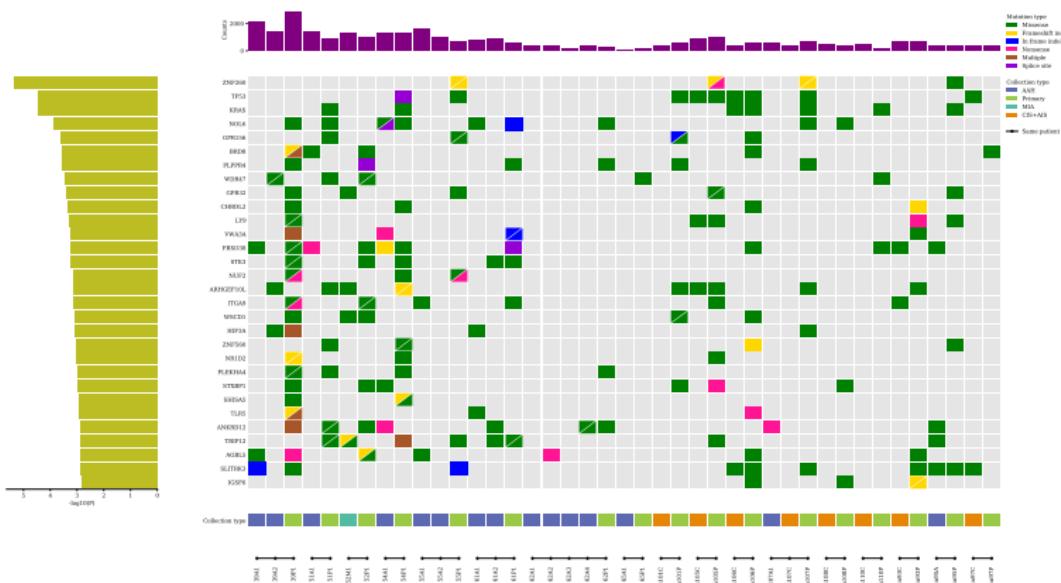


Figure: CoMut Plot with SQC Patients

## Somatic Variant in ADC



## Figure: CoMut Plot with ADC Patients

# Results

## Gene Expression Levels from RSEM

# RSEM?

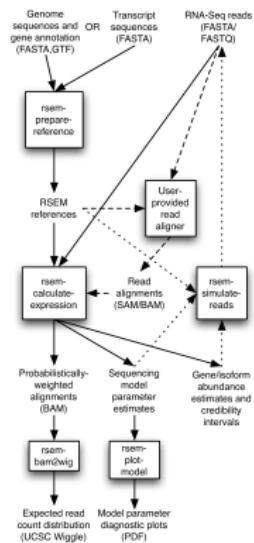


Figure: The RSEM workflow (B. Li & Dewey, 2011)

# Volcano Plot in SQC

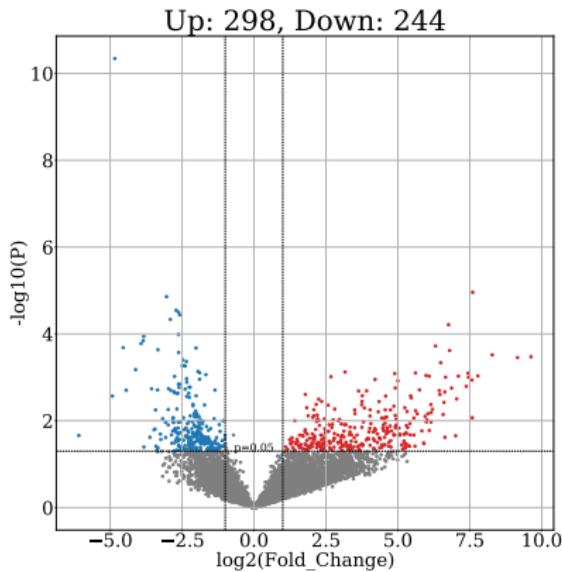


Figure: Volcano Plot in SQC

# Volcano Plot in ADC

# Results

## Tumor Evolution with MesKit

# MesKit?

# Results

## Estimated Cell Types with CIBERSORTx

# CIBERSORTx?

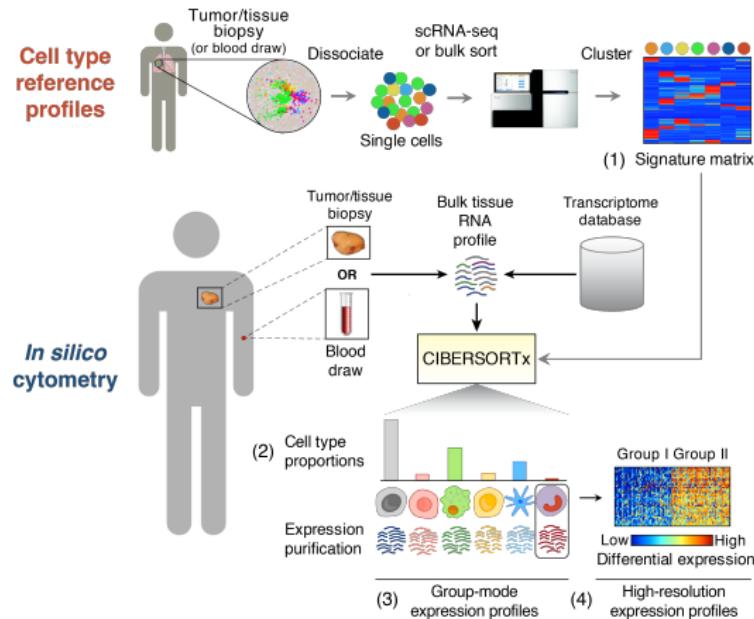
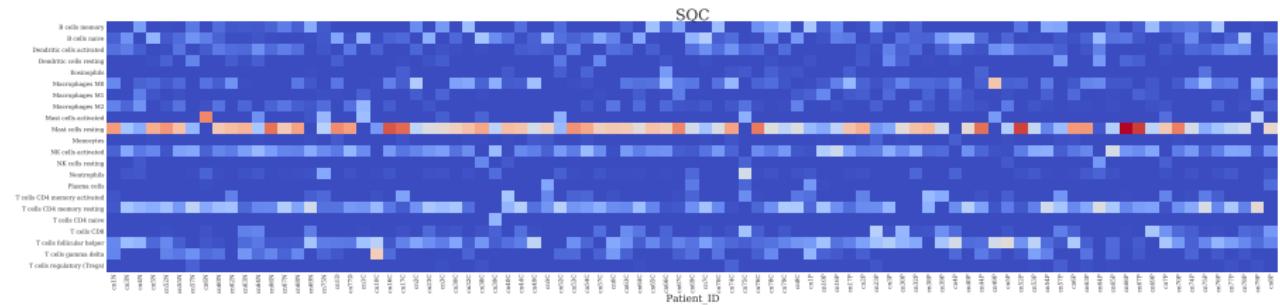


Figure: CIBERSORTx workflow (Steen et al., 2020)

CIBERSORTx with SQC



## Figure: Estimated Cell Types with SQC Samples

# CIBERSORTx with ADC

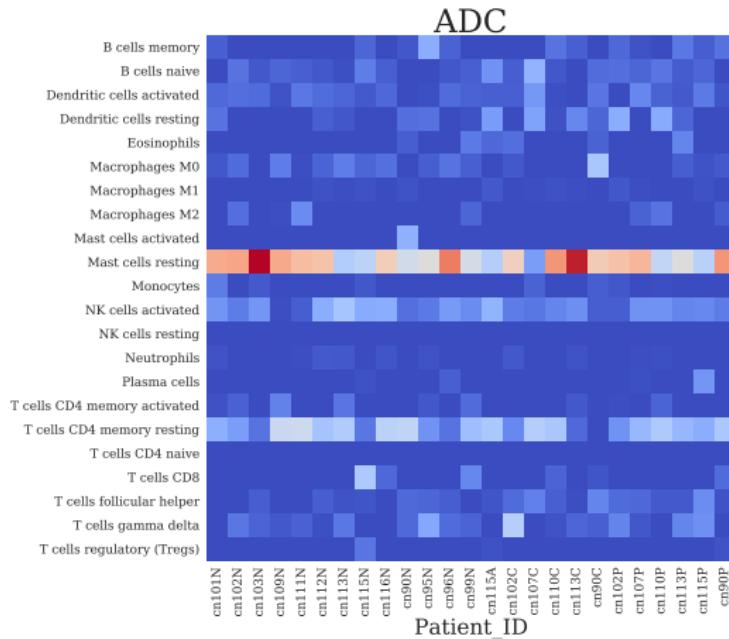


Figure: Estimated Cell Types with ADC Samples

## Discussion

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