

Lung Precancer Analysis

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Overview

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2 Materials

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Introduction

Lung Cancer

- Squamous cell carcinoma
- Adenocarcinoma

Precancer

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 + Transcriptome
- 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
 - ② Normal - AAH - AIS - MIA - ADC
- Total 112 samples

Materials

Sample Count

Sample Count in WES

Sample Count in Transcriptome

Methods

Methods

Workflows

Data pre-processing for variant discovery

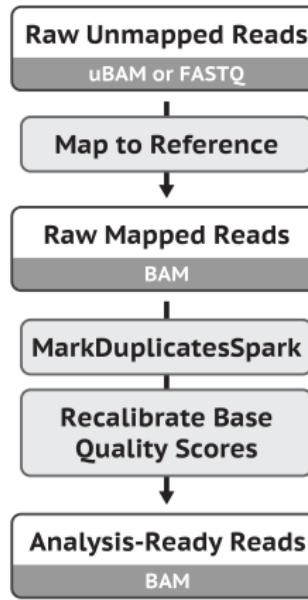


Figure: Data pre-processing for variant discovery (Van der Auwera et al., 2013; DePristo et al., 2011)

Somatic short variant discovery

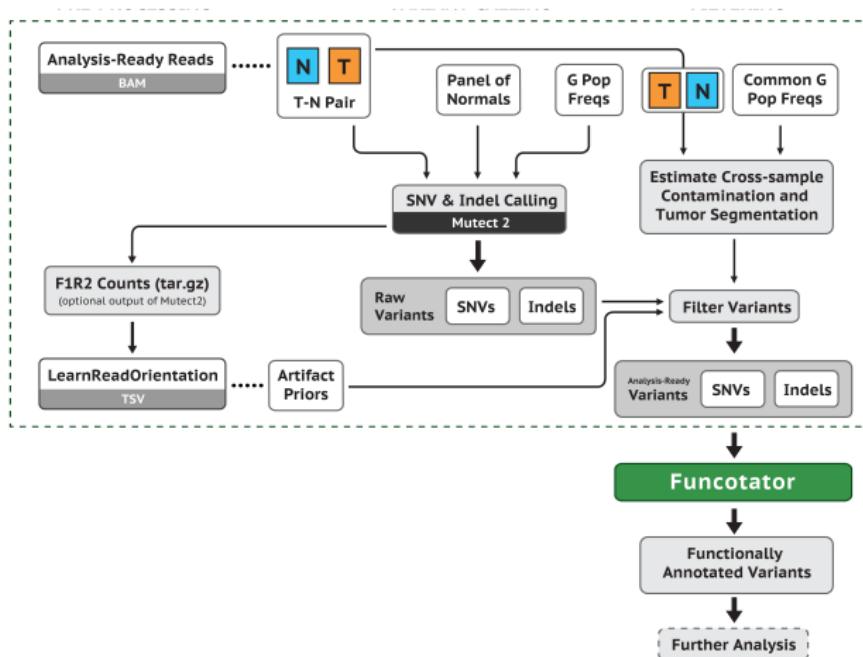


Figure: Somatic short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

Germline short variant discovery

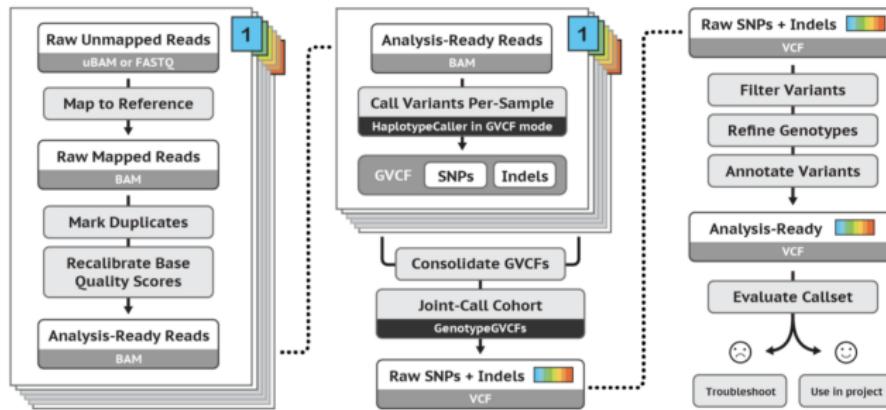


Figure: Germline short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

RNA-seq short variant discovery

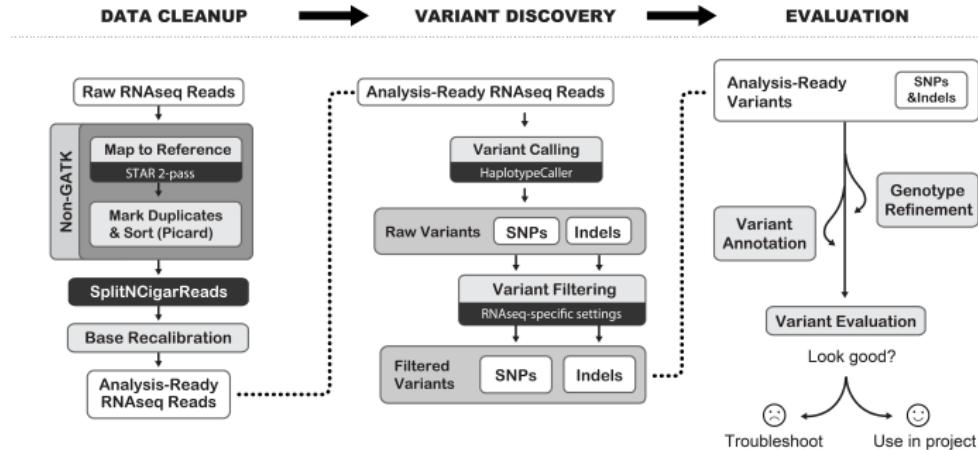


Figure: RNA-seq short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

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?

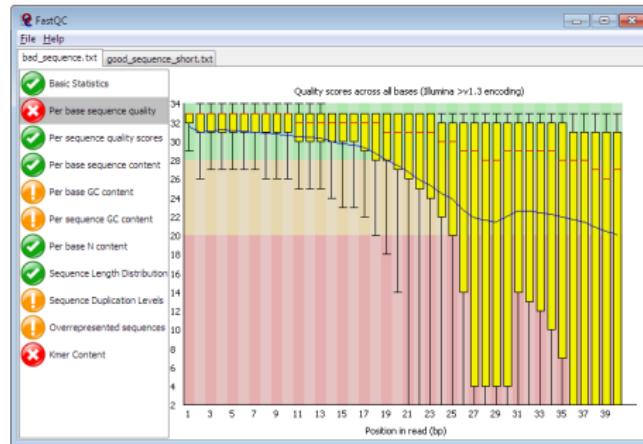


Figure: Example of FastQC Result (Andrews et al., 2012)

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

FastQC on WES

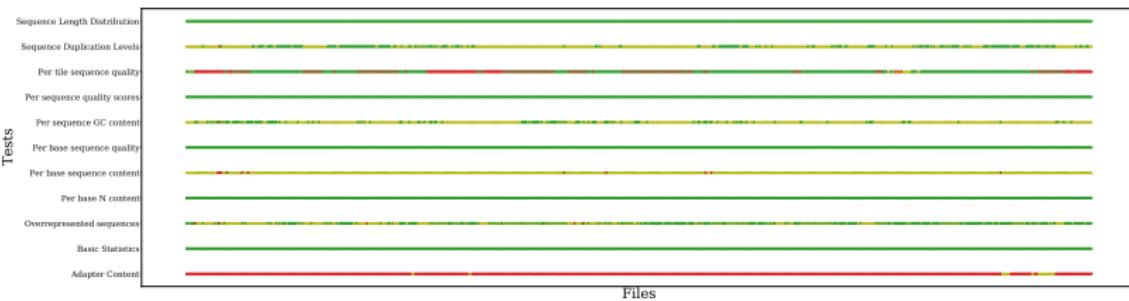


Figure: FastQC with WES data

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

FastQC on WTS

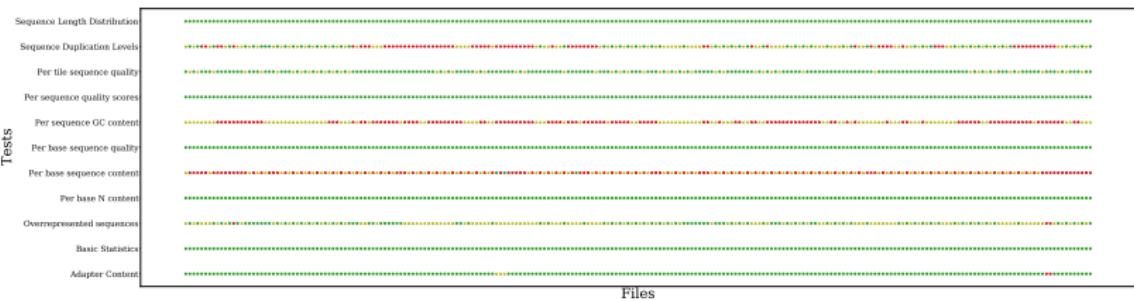


Figure: FastQC with WTS data

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

Results

Quality Checks with Sequenza

Sequenza?

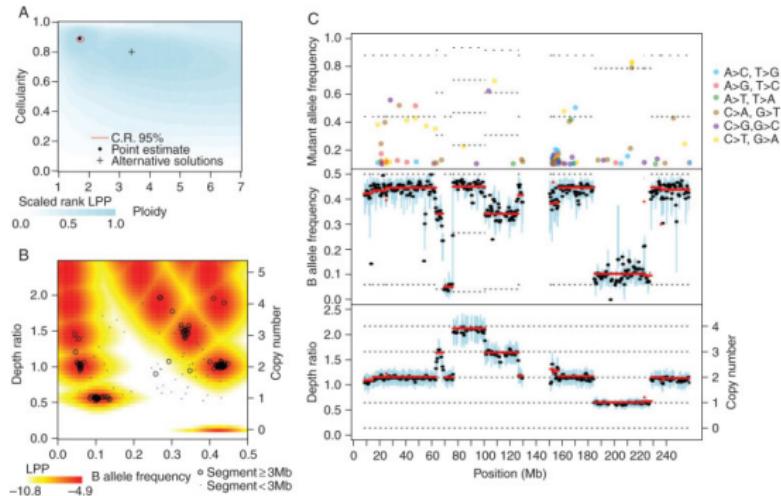


Figure: Representative Output of the Sequenza (Favero et al., 2015)

Cellularity & Ploidy on WES

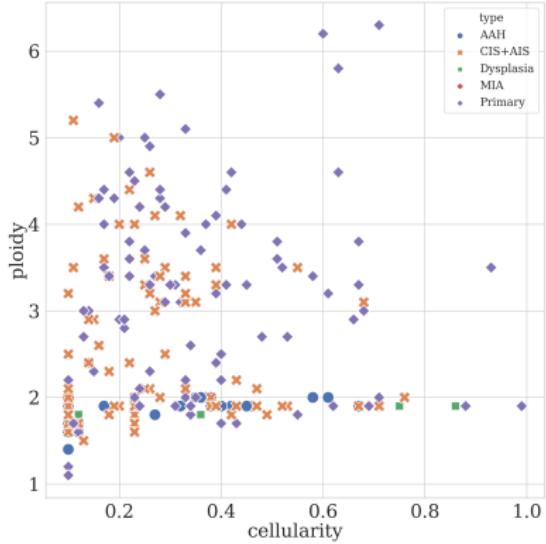


Figure: Cellularity and Ploidy from Sequenza

CNV of SQC

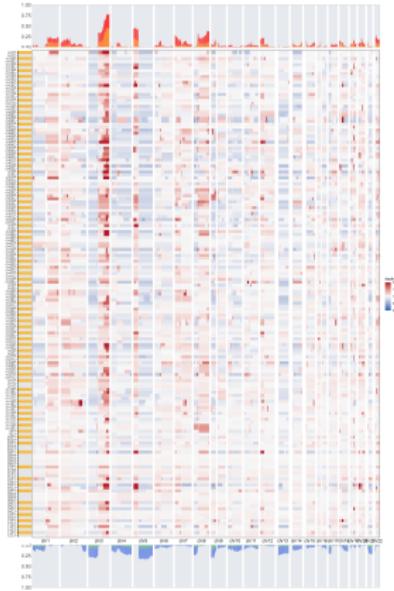


Figure: CNV Plot with SQC Patients

CNV of ADC

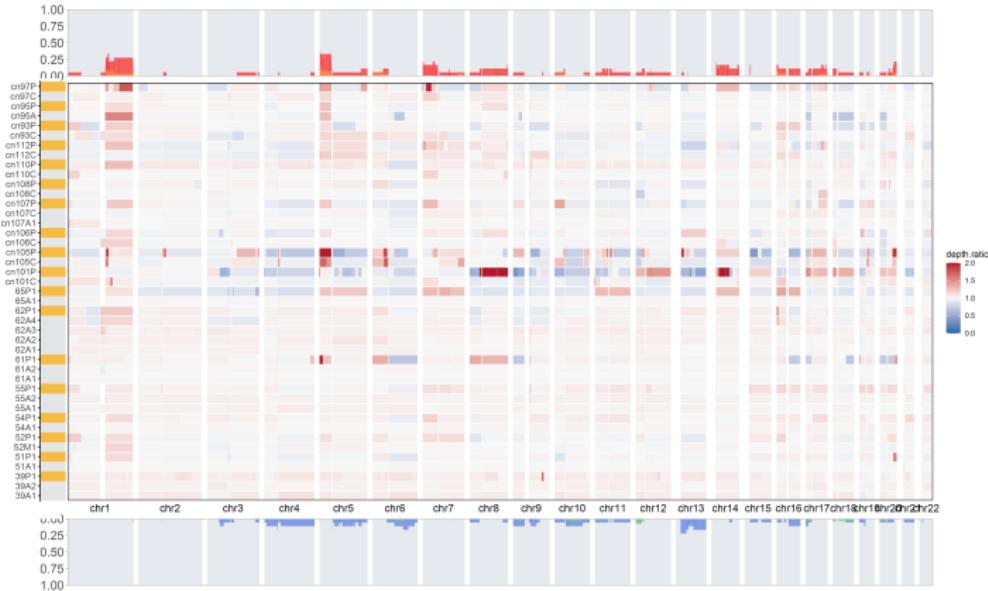


Figure: CNV Plot with ADC Patients

Results

Mutect2

Mutect2?

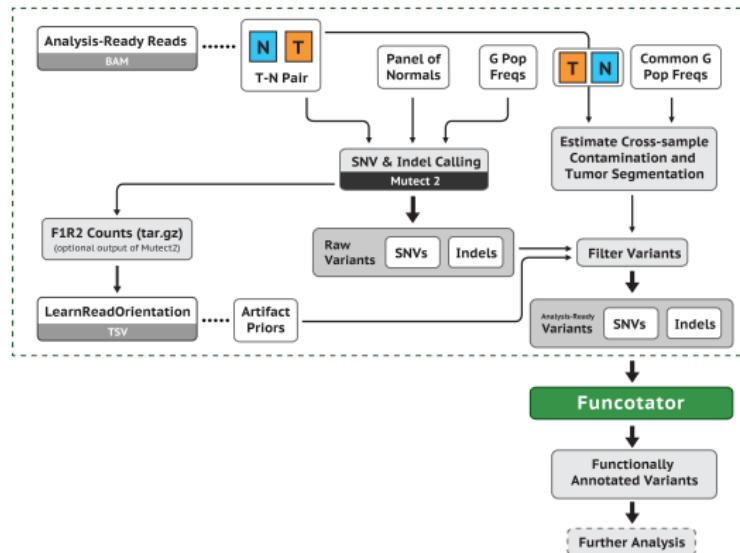


Figure: Somatic short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

Witer?

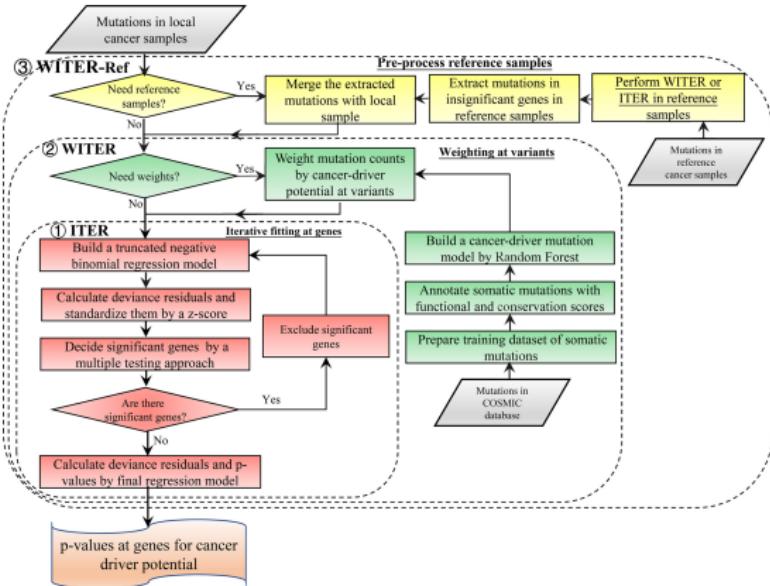


Figure: Witer diagram for detecting cancer-drive genes (Jiang et al., 2019)

Somatic Variant in SQC

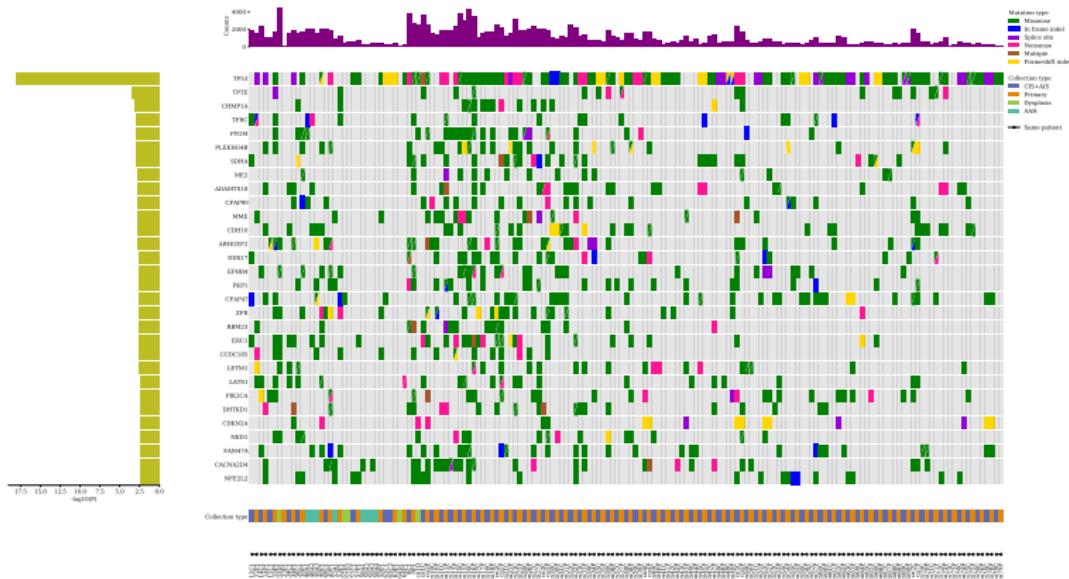


Figure: Comut Plot with SQC Patients

Somatic Variant in ADC

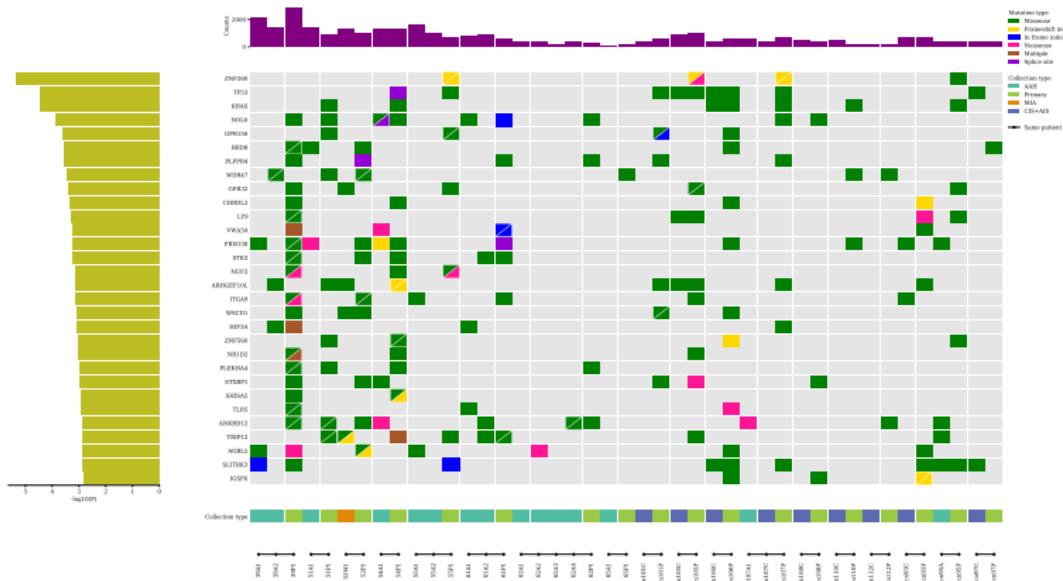


Figure: Comut Plot with ADC Patients

Discussion

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