

Lung Precancer Study

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Overview

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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

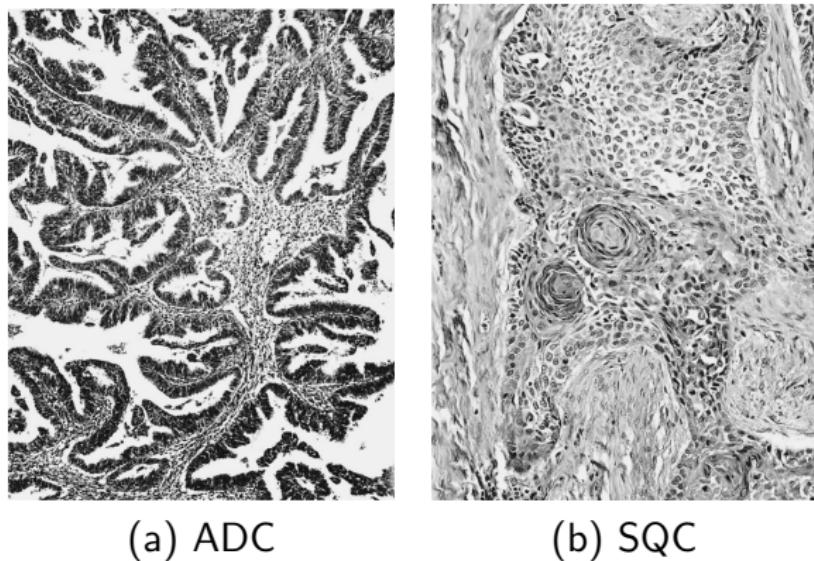
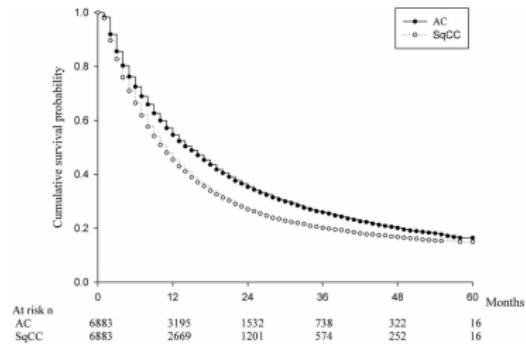
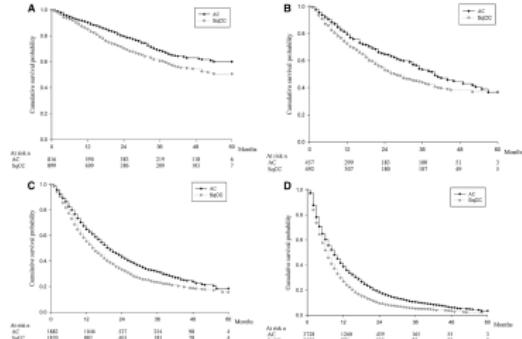


Figure: ADC and SQC histology in Lung cancer (Travis, 2002)

ADC vs. SQC II



(a) All patients



(b) By cancer stages

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

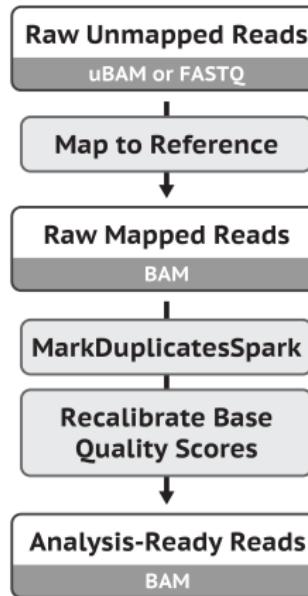


Figure: Data pre-processing for variant discovery (Van der Auwera et al., 2013; DePristo et al., 2011)

Somatic short variant discovery

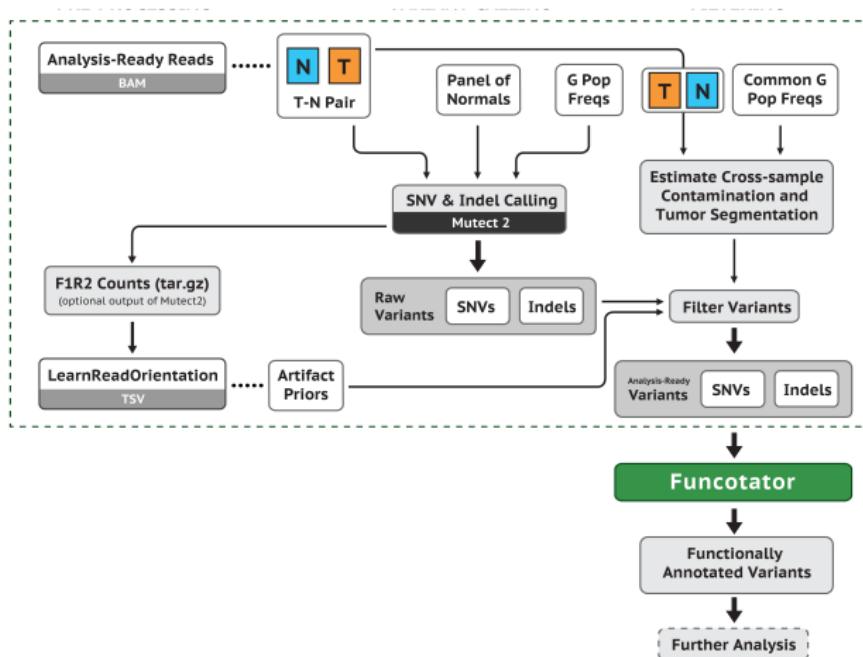


Figure: Somatic short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

Germline short variant discovery

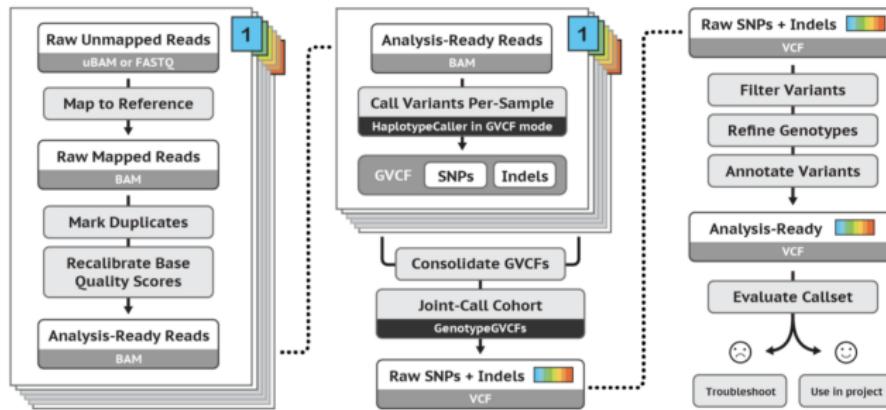


Figure: Germline short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

RNA-seq short variant discovery

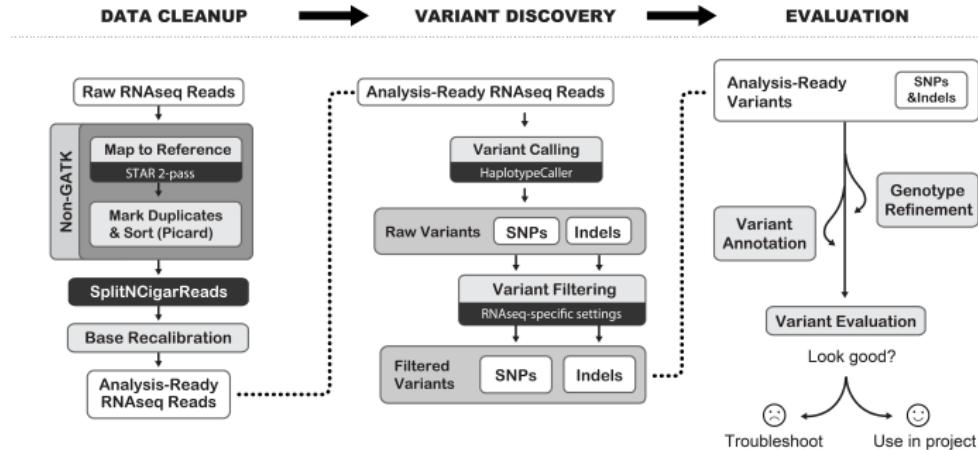


Figure: RNA-seq short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

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?

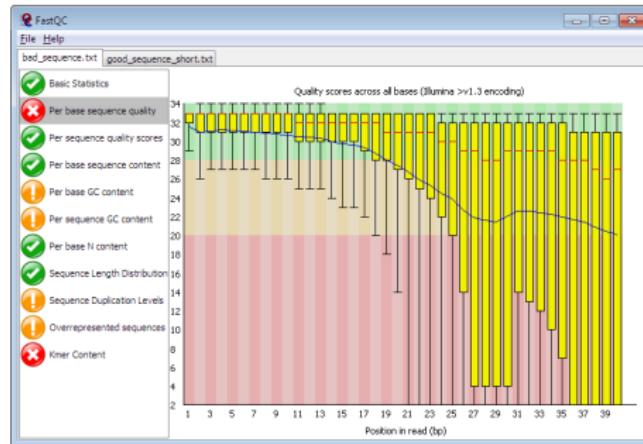


Figure: Example of FastQC Result (Andrews et al., 2012)

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

FastQC on WES

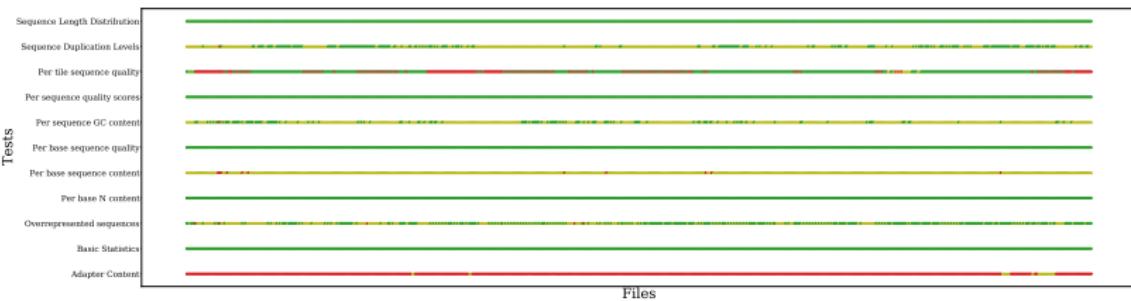
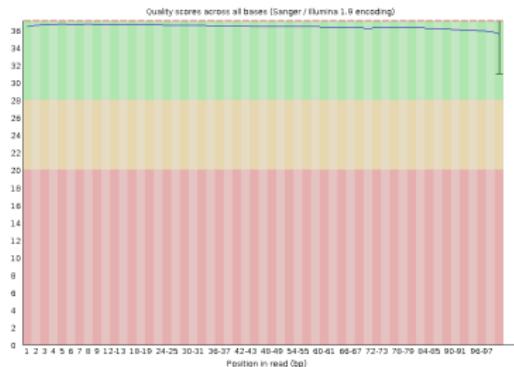


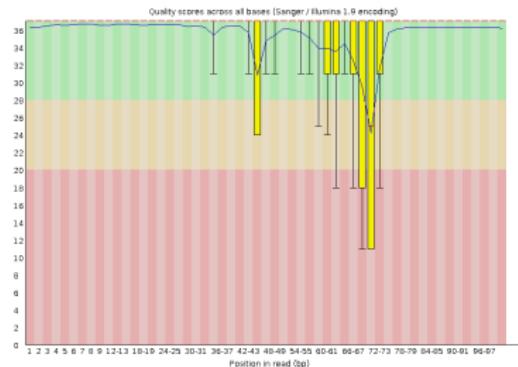
Figure: FastQC with WES data

∴ 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

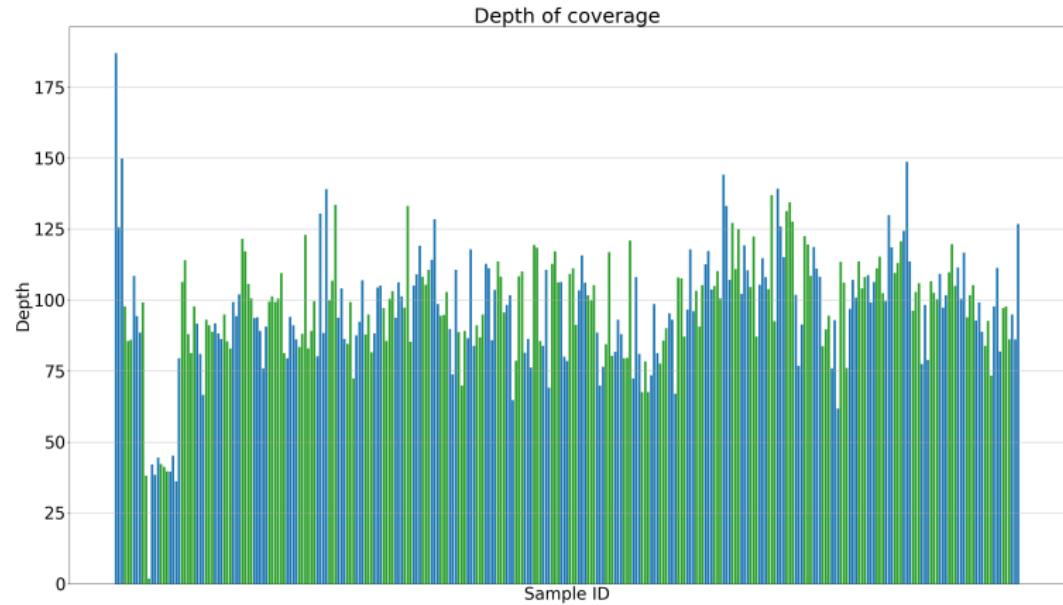


Figure: Coverage Depth Plot

FastQC on WTS

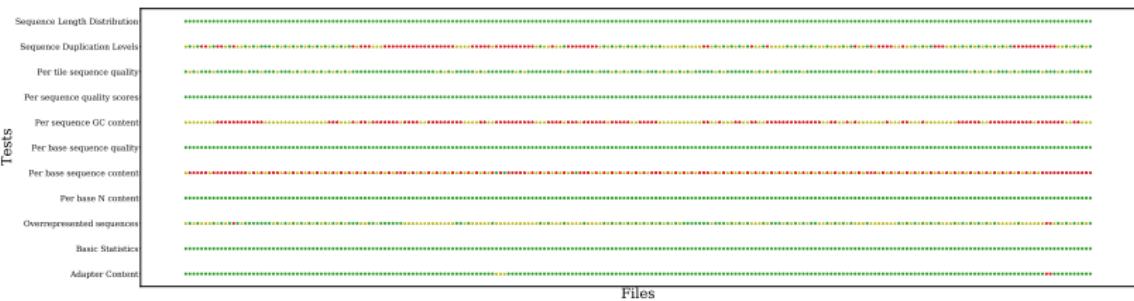


Figure: FastQC with WTS data

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

Results

Quality Checks with Sequenza

Sequenza?

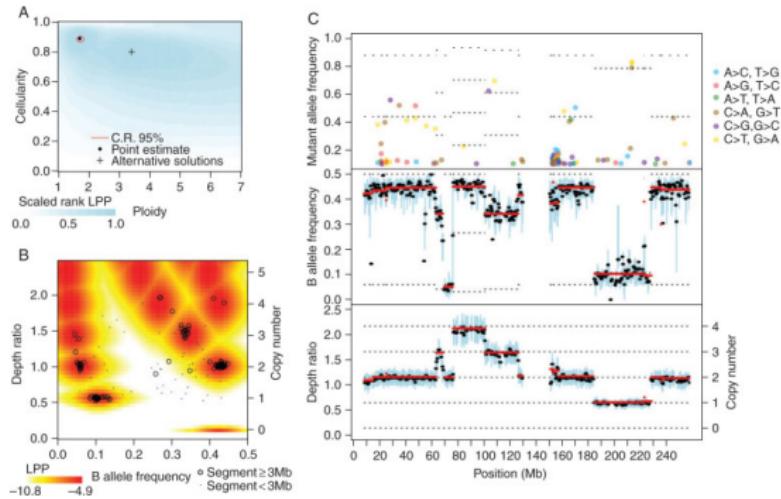
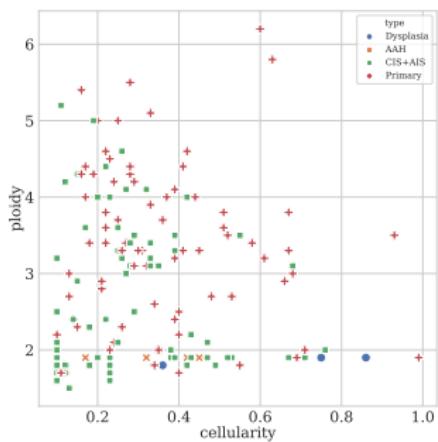
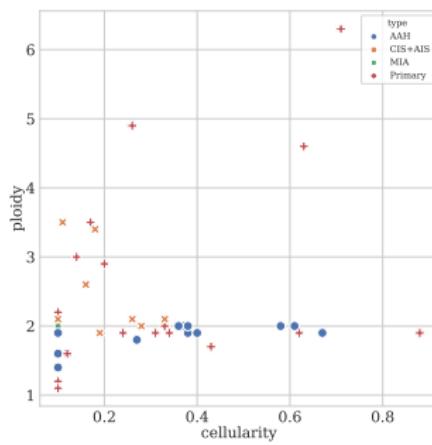


Figure: Representative Output of the Sequenza (Favero et al., 2015)

Cellularity & Ploidy on WES



(a) SQC Samples



(b) ADC Samples

Figure: Cellularity and Ploidy from Sequenza

Genome View on Patient #57

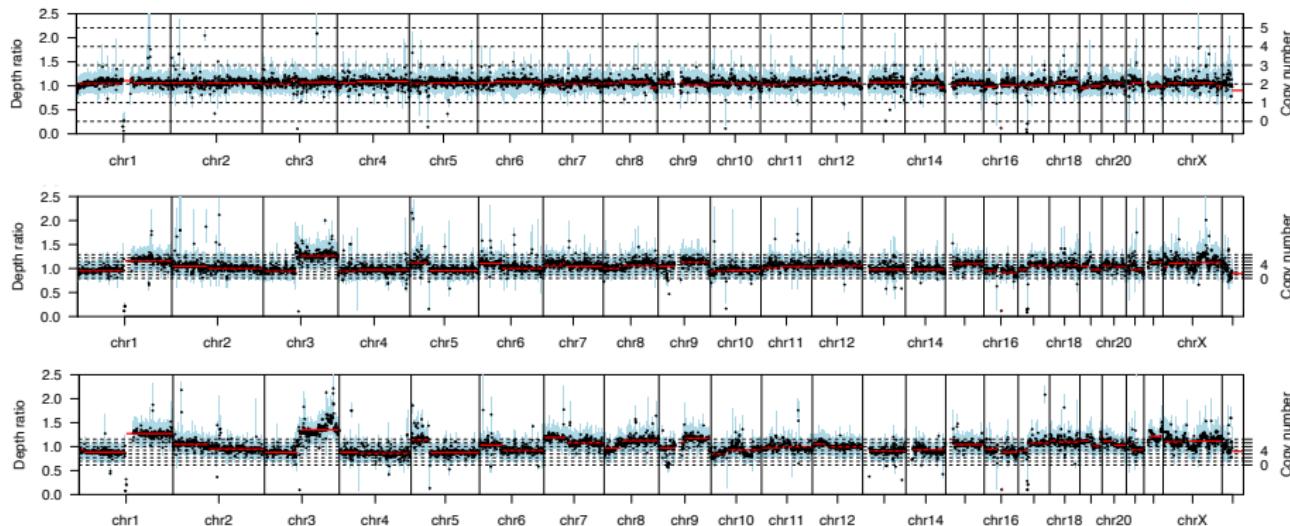


Figure: Dysplasia-CIS-Primary tumor

CNV of SQC

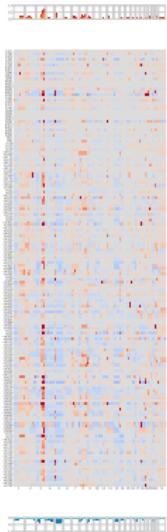


Figure: CNV Plot with SQC Patients

CNV of ADC

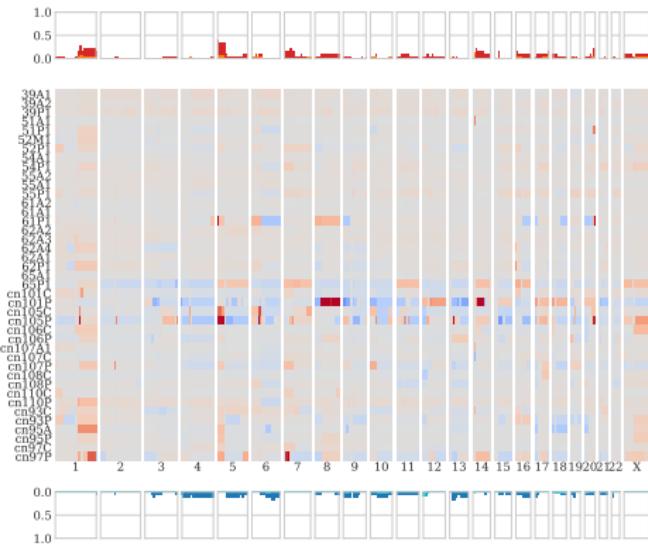


Figure: CNV Plot with ADC Patients

Results

Find SNVs with Mutect2

Mutect2?

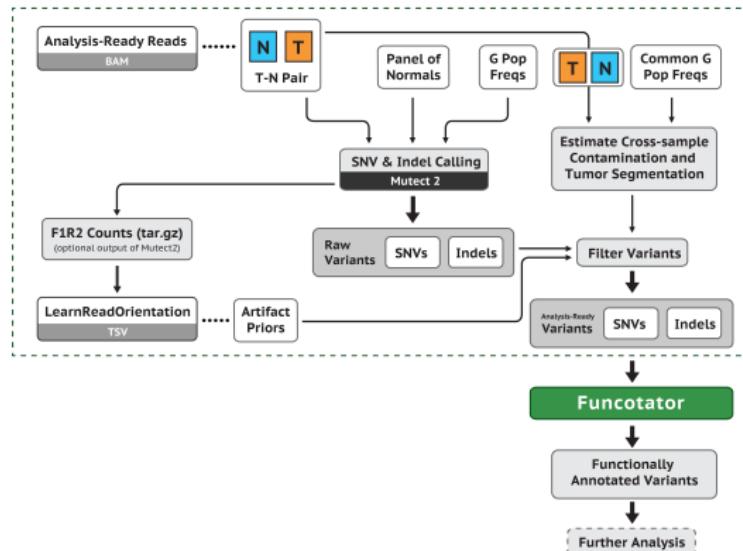


Figure: Somatic short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

Witer?

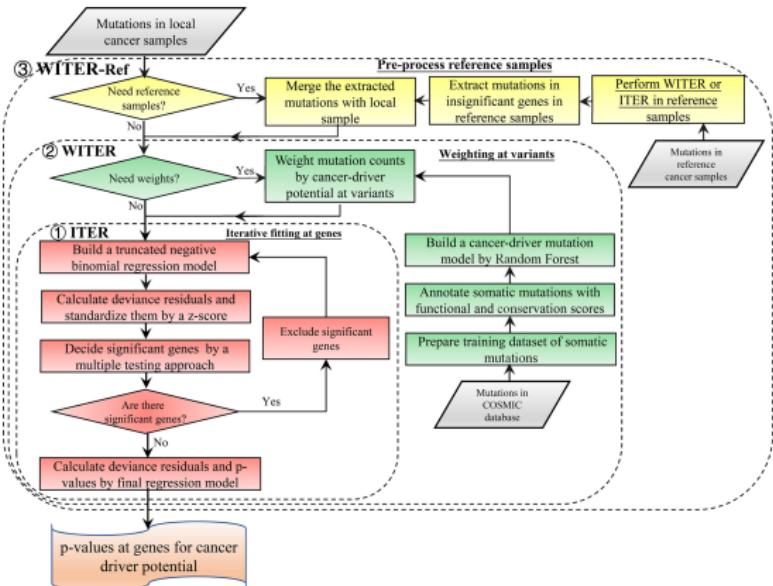


Figure: Witer diagram for detecting cancer-drive genes (Jiang et al., 2019)

Somatic Variant in SQC

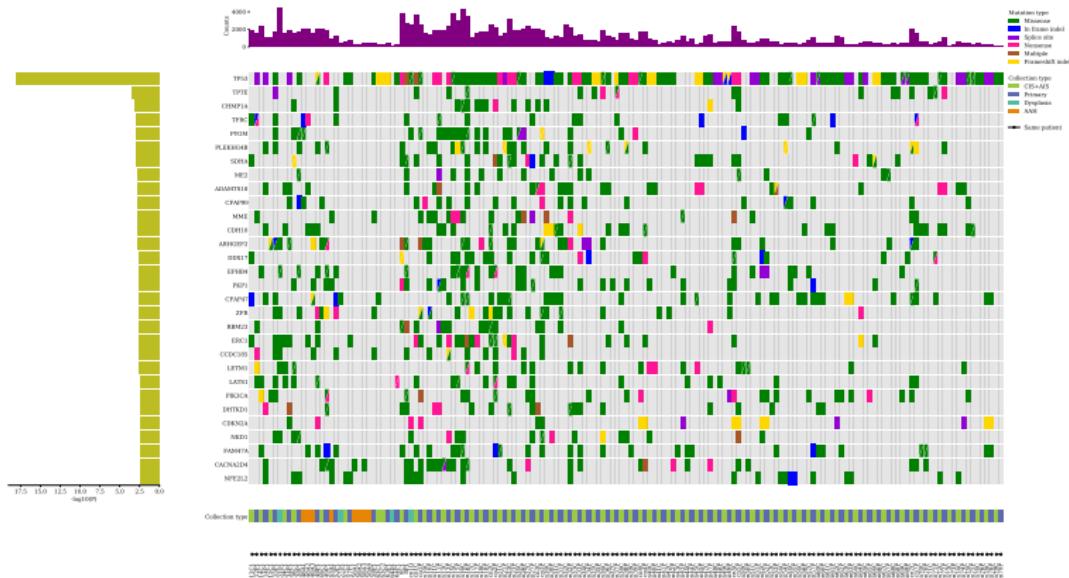


Figure: CoMut Plot with SQC Patients

Somatic Variant in ADC

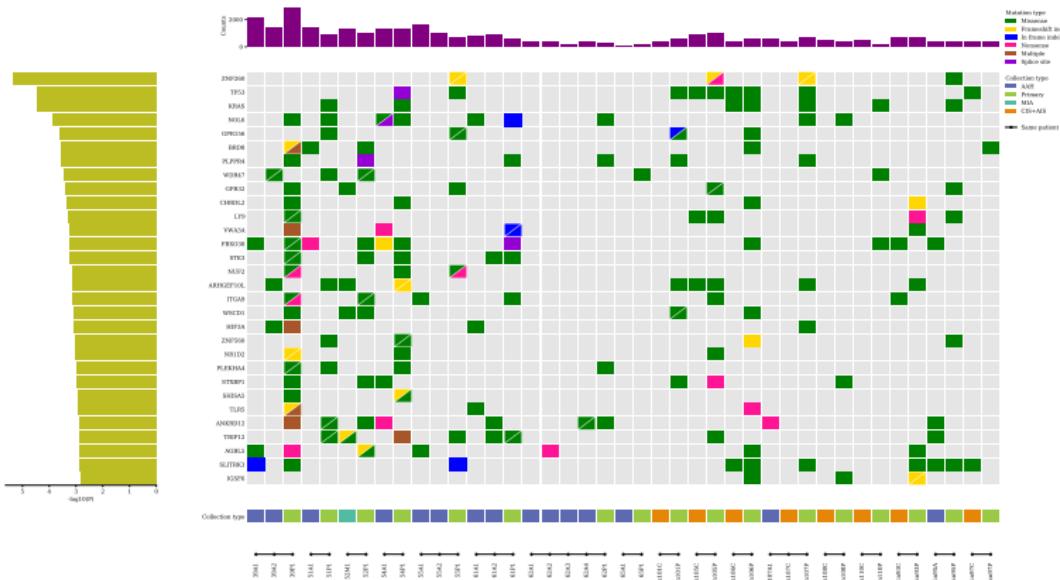


Figure: CoMut Plot with ADC Patients

Results

Gene Expression Levels from RSEM

RSEM?

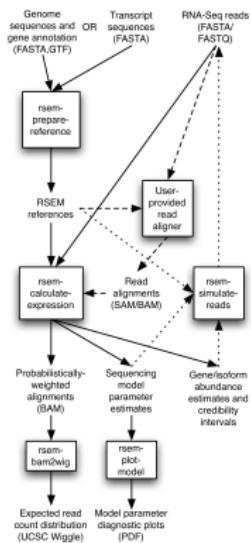
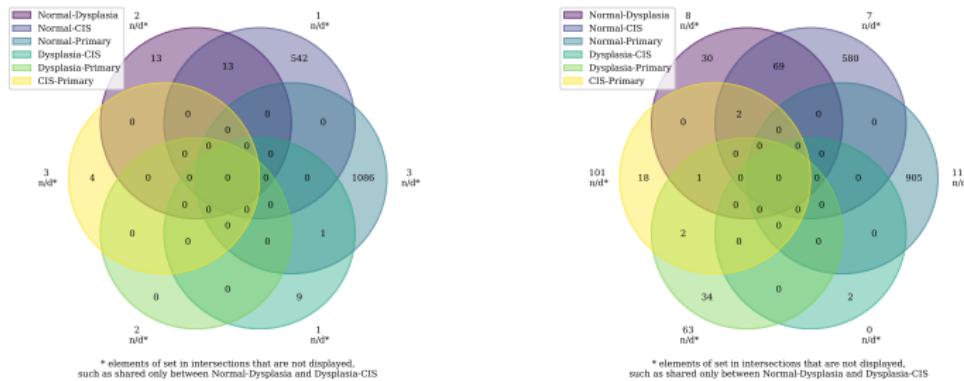


Figure: The RSEM workflow (B. Li & Dewey, 2011)

DEG Pseudo-Venn Diagram with Bowtie2 in SQC

Normal → Dysplasia → CIS → Primary (SQC)



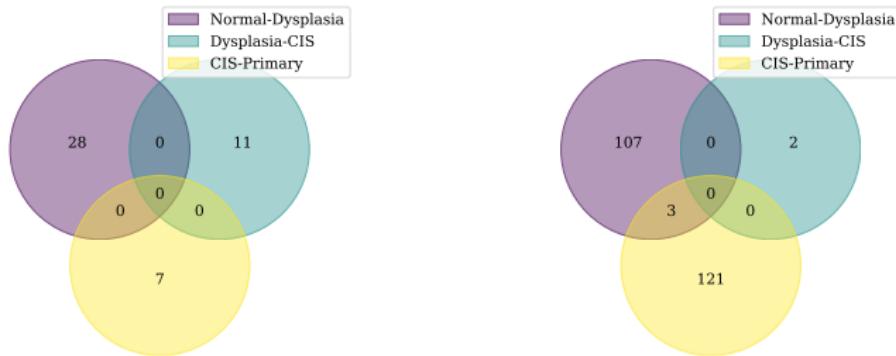
(a) Up-regulated

(b) Down-regulated

Figure: DEG Pseudo-Venn Diagram with Bowtie2 in SQC

DEG Venn Diagram with Bowtie2 in SQC

Normal → Dysplasia → CIS → Primary (SQC)



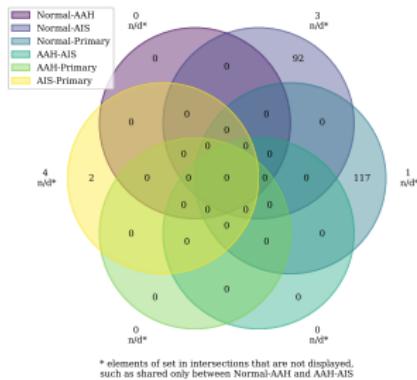
(a) Up-regulated

(b) Down-regulated

Figure: DEG Venn Diagram with Bowtie2 in SQC

DEG Pseudo-Venn Diagram with Bowtie2 in ADC

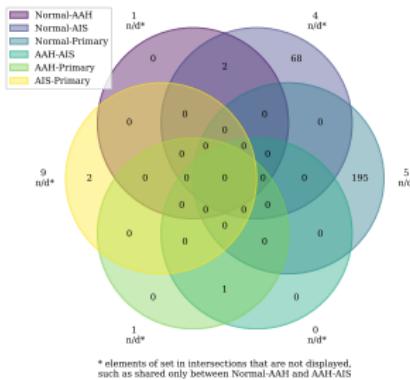
Normal → AAH → AIS → MIA → Primary (ADC)



(a) Up-regulated

(b) Down-regulated

Figure: DEG Pseudo-Venn Diagram with Bowtie2 in ADC



DEG Venn Diagram with Bowtie2 in ADC

Normal → AAH → AIS → MIA → Primary (ADC)

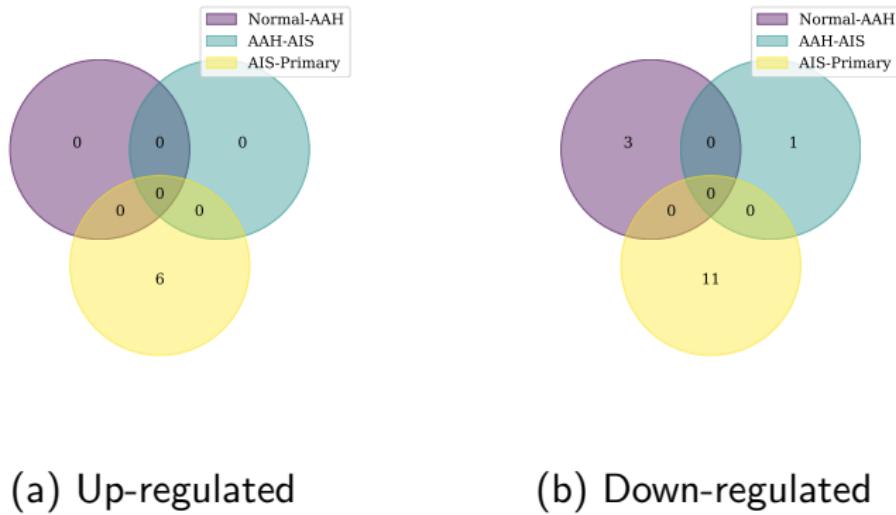


Figure: DEG Venn Diagram with Bowtie2 in ADC

Results

Tumor Evolution with MesKit

MesKit?

Results

Estimated Cell Types with CIBERSORTx

CIBERSORTx?

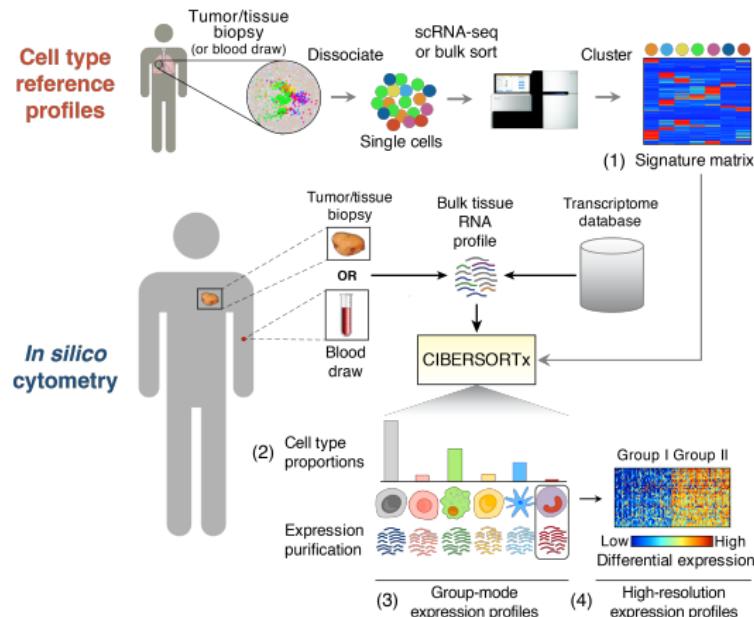


Figure: CIBERSORTx workflow (Steen et al., 2020)

CIBERSORTx with SQC

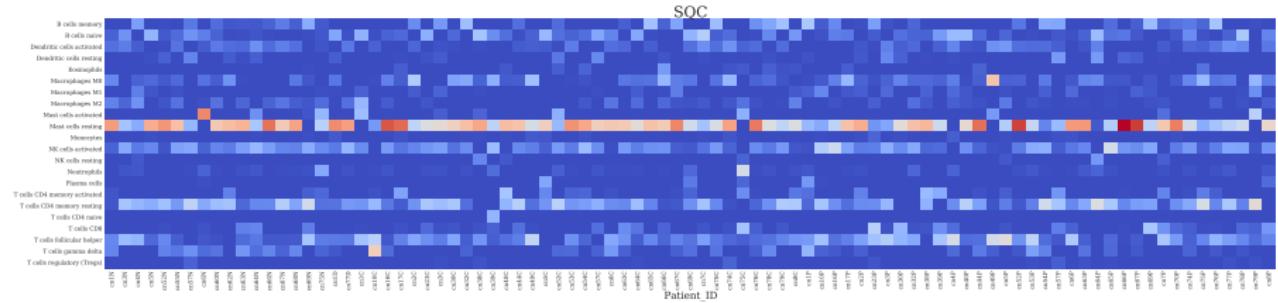


Figure: Estimated Cell Types with SQC Samples

CIBERSORTx with ADC

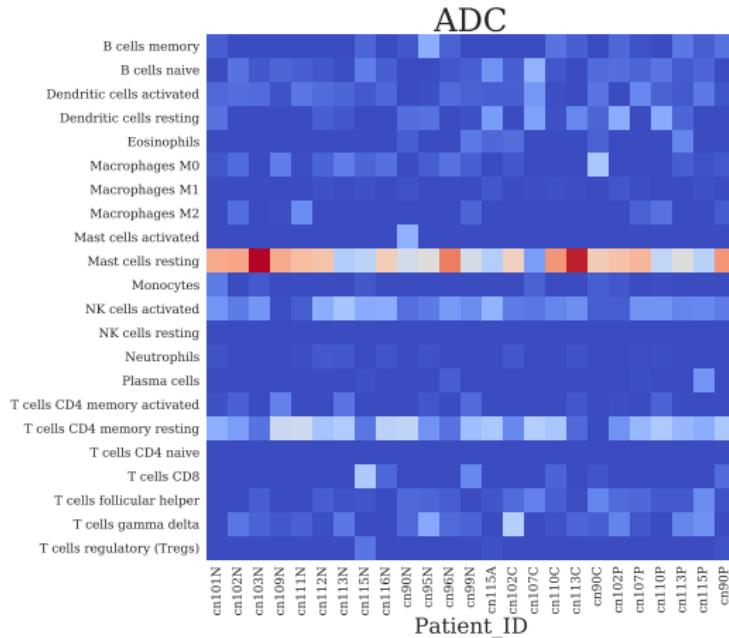


Figure: Estimated Cell Types with ADC Samples

Discussion

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