

Lung Precancer Study

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Overview

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2 Materials

3 Methods

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Introduction

Introduction

Lung Cancer

Lung Cancer? I

The most common cancer

The most common form of cancer:

12.3 % of all cancers (Minna, Roth, & Gazdar, 2002)

The most important factor

Tobacco

Cancer Survival Rate in Korea



Figure: Common cancer survival rates (Hong et al., 2021)

Survival rate (More than 5 yr)

- Thyroid: 68.4 %
- Lung: 35.4 %

Type of Lung Cancer

Types of lung cancer:

- ① Adenocarcinoma (ADC) (40 %) ★
- ② Squamous cell carcinoma (SQC) (25 %) ★
- ③ Small cell carcinoma (20 %)
- ④ Large cell carcinoma (10 %)
- ⑤ Adenosquamous carcinoma (< 5 %)
- ⑥ Carcinoid (< 5 %)
- ⑦ Bronchioalveolar (Bronchial gland carcinoma)

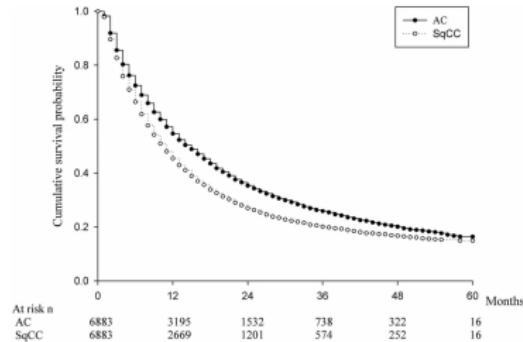
(Vincent et al., 1977; Collins, Haines, Perkel, & Enck, 2007)

ADC vs. SQC I

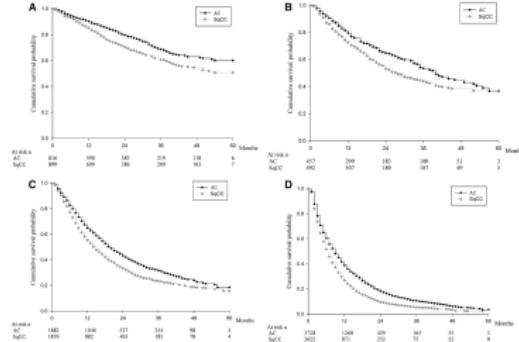


Figure: ADC and SQC histology in Lung cancer (Travis, 2002)

ADC vs. SQC II



(a) All patients



(b) By cancer stages

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

Findings

SQC is more dangerous than ADC. $\therefore p < 0.001$

Introduction

Study Objectives

Study Objectives

Find different mutations

- between WES vs. WTS
- from cancer vs. precancer

Pathway examine

- with the mutation of WES & RNA-seq
- with immune-depleted animal models

Ultra-deep sequencing

to find an *infinitesimal* quantity of Non-Circulating Tumor DNA

- from blood
- from urine
- from bronchus

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)

Results

Results

Quality Checks

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

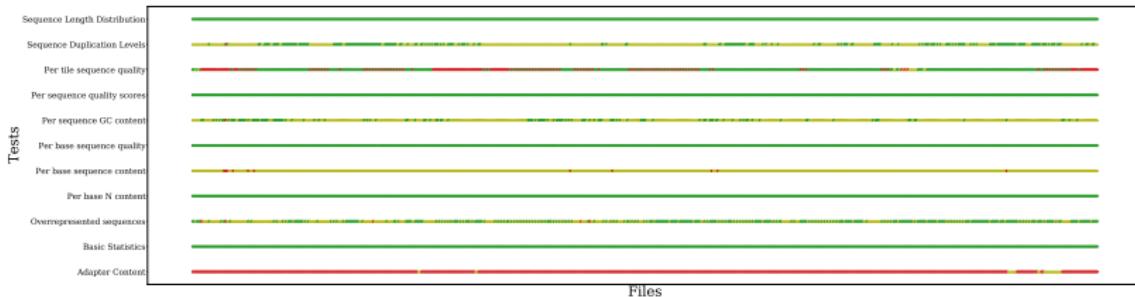


Figure: FastQC with WES data

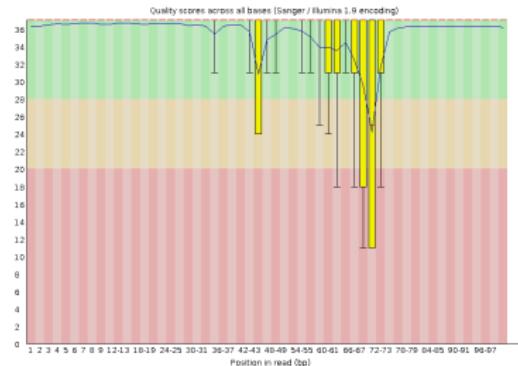
Failure on 33P1 sample

33P1 is excluded at further analysis.

Failure on 33P1 I



(a) 33N



(b) 33P1

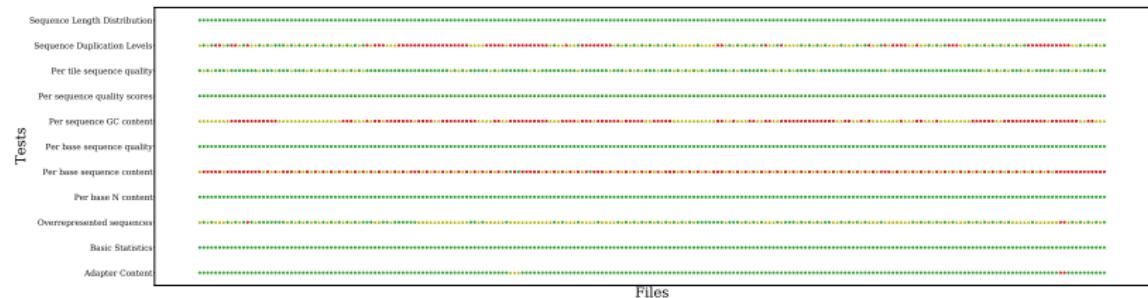
Figure: Per Base Sequence Quality Results

Failure on 33P1 II



Figure: Coverage Depth Plot

FastQC on WTS



All sample are good to analysis

⋮

∴ No sample has more than 5 failures.

Results

Copy Number Variations

Sequenza?

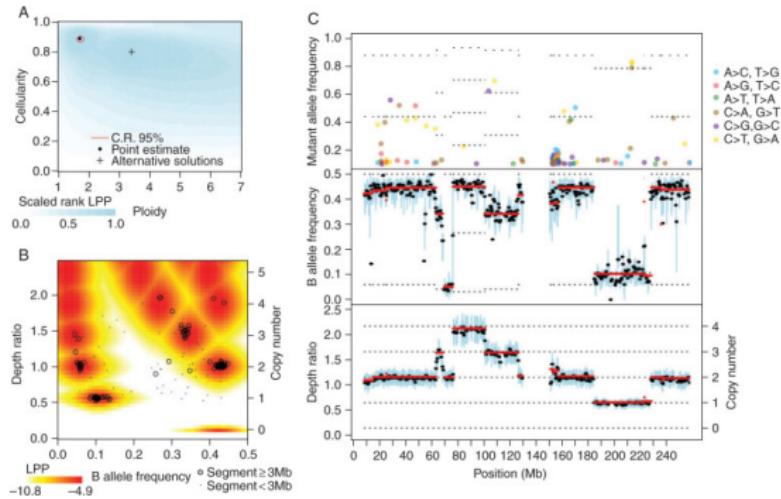
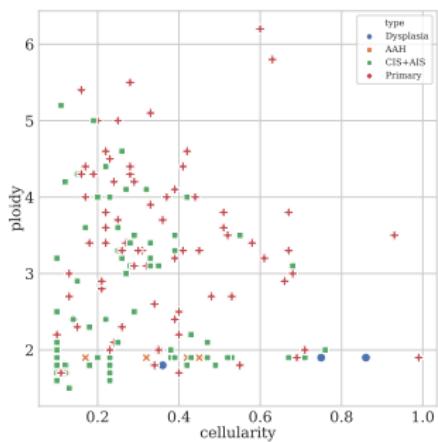
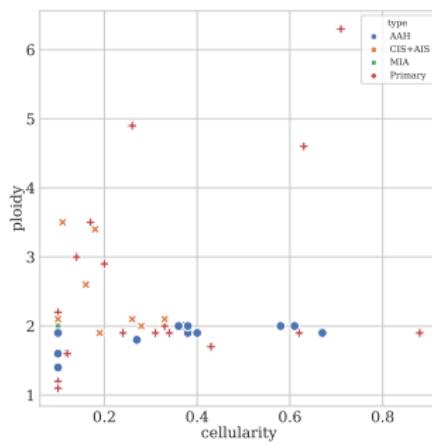


Figure: Representative Output of the Sequenza (Favero et al., 2015)

Cellularity & Ploidy on WES



(a) SQC Samples



(b) ADC Samples

Figure: Cellularity and Ploidy from Sequenza

Genome View on Patient #57

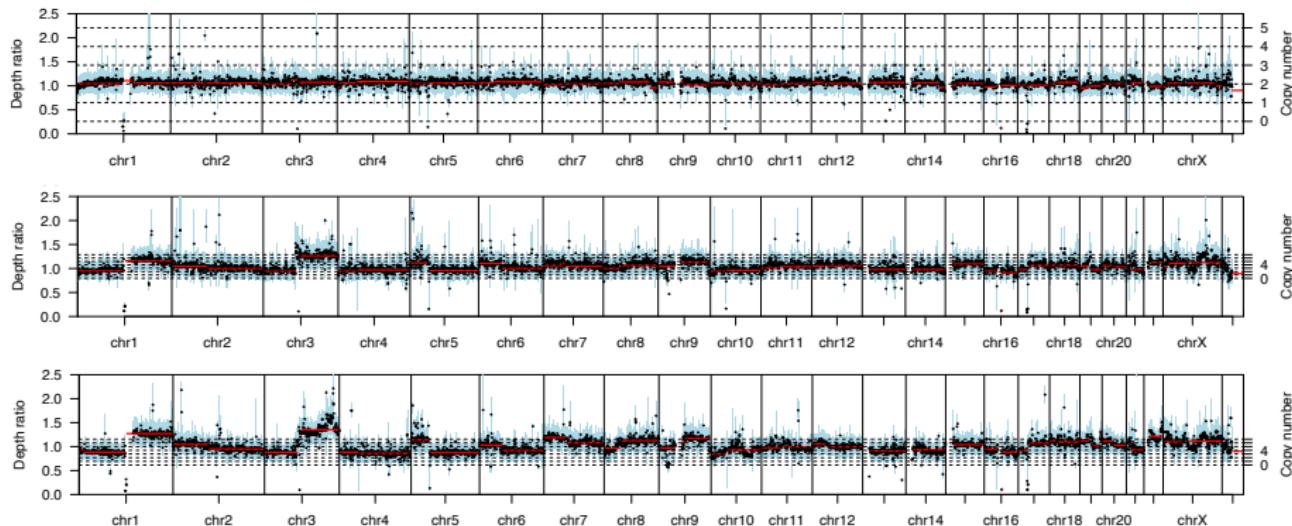


Figure: Dysplasia-CIS-Primary Tumor on Patient #57

CNVs of SQC

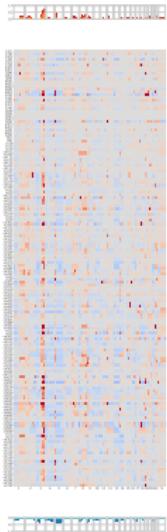
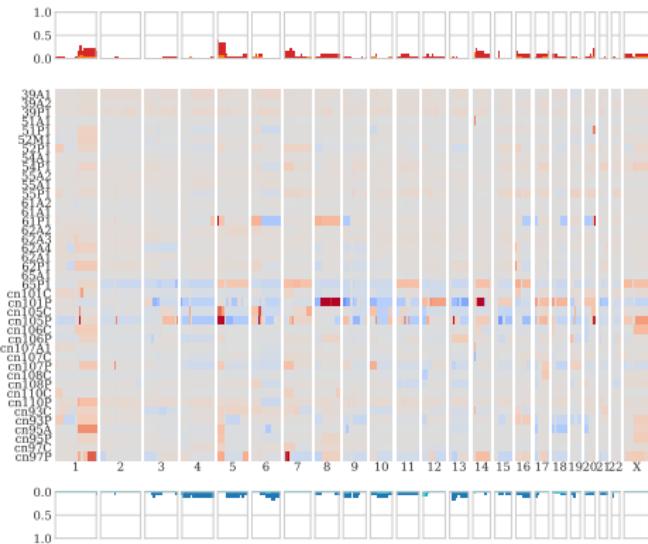


Figure: CNV Plot with SQC Patients

CNVs of ADC



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SQC vs. ADC

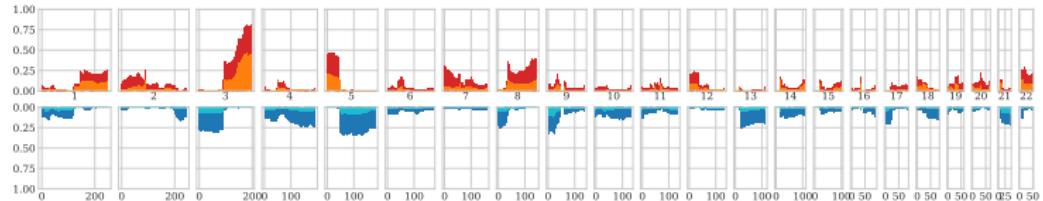


Figure: Simple CNV Plot with SQC Patients

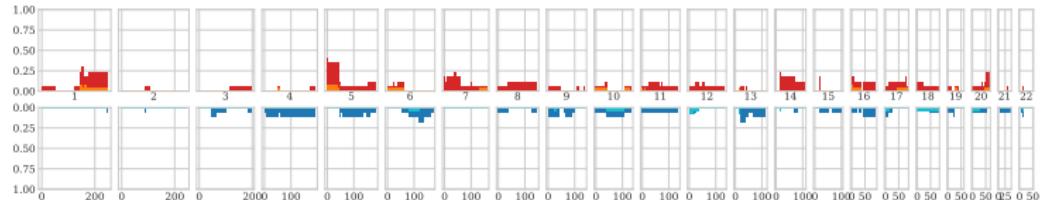


Figure: Simple CNV Plot with ADC Patients

Findings in Sequenza

Sequenza Findings

- SQC have more CNVs than ADC.
- SQC have aggressive CNVs on chromosome #3 and #5.
- ADC have aggressive CNVs on chromosome #5.

Results

SNVs Analysis

Mutect2?

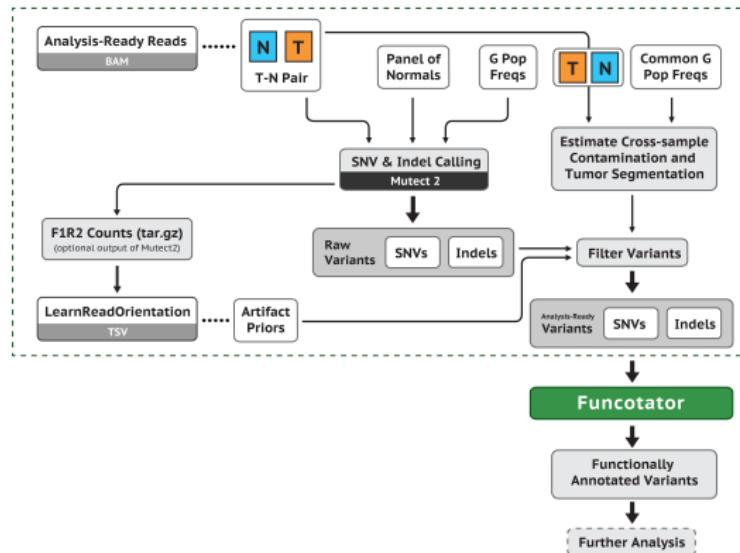


Figure: Somatic short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

MutEnricher?



Analysis summary:

Inputs:

- Somatic mutations
- Features of interest:
 - Coding genes
 - Non-coding regions
- Genomic covariates (optional)

Analyses:

- Background calculations:
 - global, local, or covariate clustered
- Mutation enrichments:
 - coding/non-coding modules

Outputs:

- Gene or non-coding region enrichments:
 - Overall genes/regions
 - Hotspots
 - Combined

Figure: Schematic representation of MunEnricher's analysis procedures (Soltis et al., 2020)

Somatic Variant in SQC

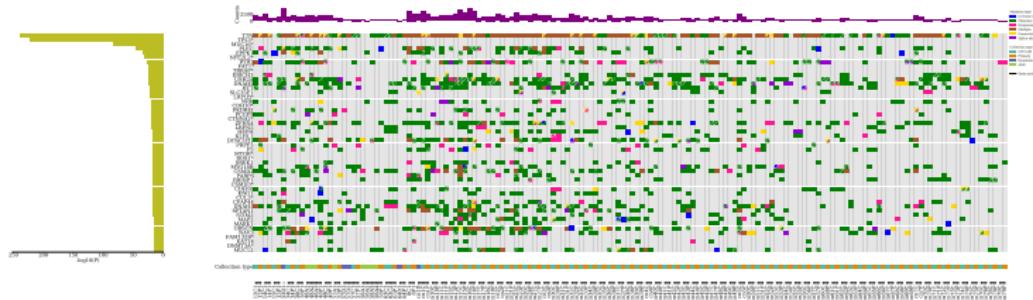


Figure: CoMut Plot with SQC Patients

Somatic Variant in ADC

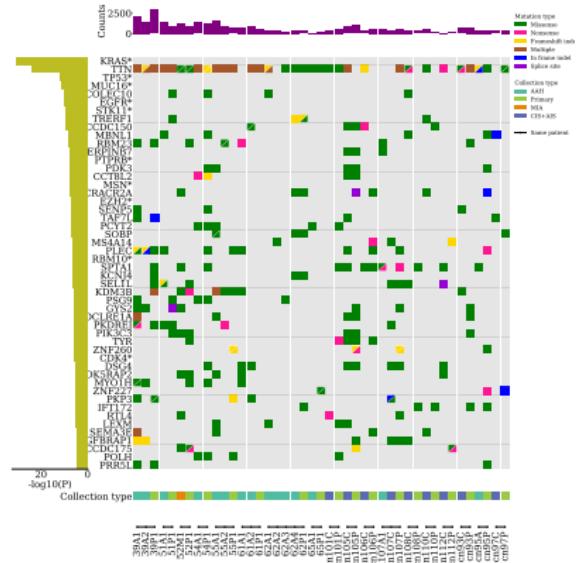


Figure: CoMut Plot with ADC Patients

Findings in SNVs Analysis

TTN

TTN is the most mutated gene both in SQC and ADC.

Results

VAF Analysis

VAF?

- Variant allele frequency
- VAF = Alternative allele read count/Total read count
- To find tumor evolution

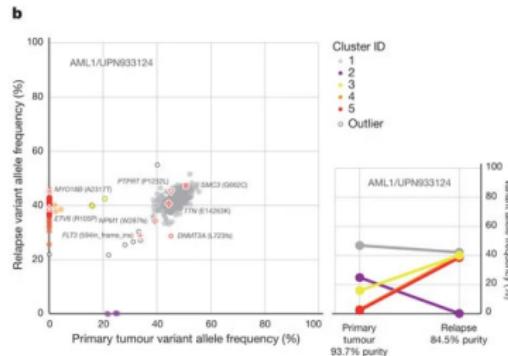


Figure: VAF distribution of validated mutations (Ding et al., 2012)

VAF Plots I

PyClone?

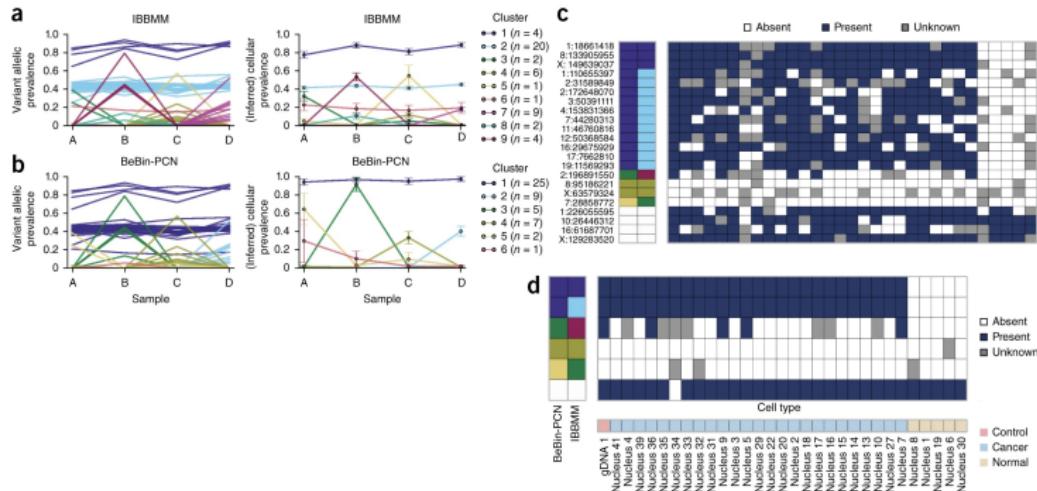


Figure: Analysis of multiple samples by PyClone (Roth et al., 2014)

PyClone Plots I

Findings in VAF Analysis

Results

Differences in Gene Expression Levels

RSEM?

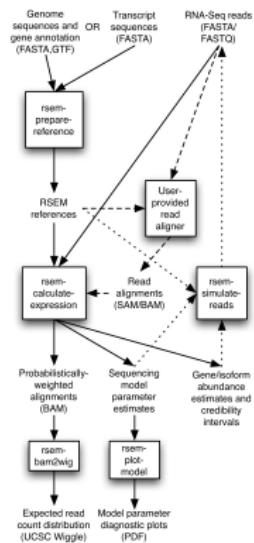


Figure: RSEM workflow (Li & Dewey, 2011)

DESeq2

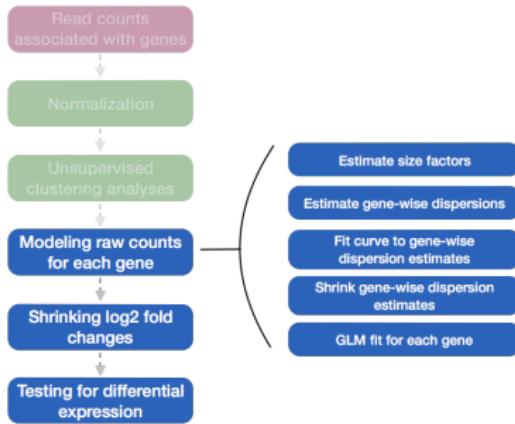


Figure: DESeq2 workflow (Love, Huber, & Anders, 2014)

DEG Selection Strategy

DEG: differentially expressed genes

Fold Change

$$\log_2(\text{Fold Change}) > 1 \vee \log_2(\text{Fold Change}) < -1$$

P-value

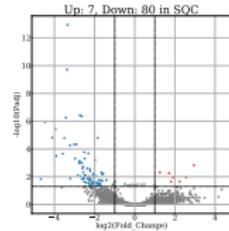
$$P\text{-value} < 0.05$$

Adjusted P-value

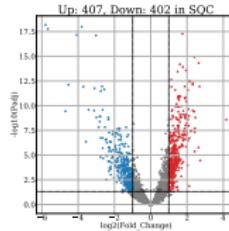
$$P_{adj} < 0.05$$

DEG Volcano Plots in SQC

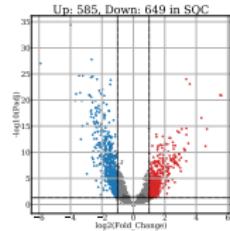
Normal → Dysplasia → CIS → Primary (SQC)



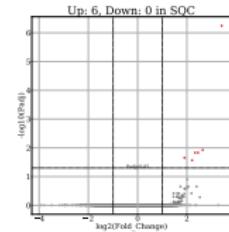
(a) Normal-Dysplasia



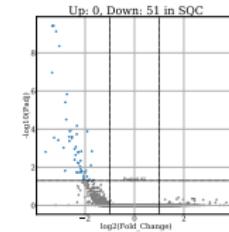
(b) Normal-CIS



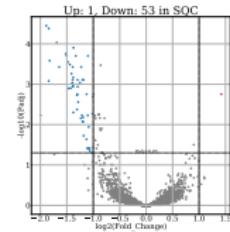
(c) Normal-Primary



(d) Dysplasia-CIS



(e) Dysplasia-Primary

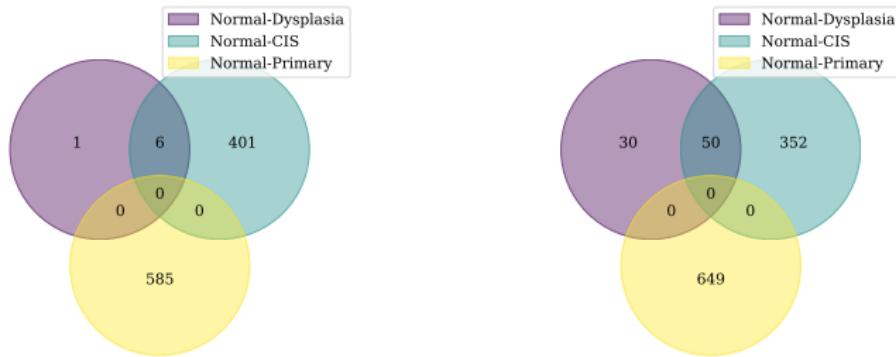


(f) CIS-Primary

Figure: DEG Volcano Plots in SQC

DEG Venn Diagram with Bowtie2 in SQC

Normal → Dysplasia → CIS → Primary (SQC)



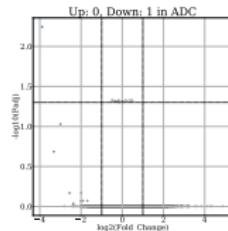
(a) Up-regulated

(b) Down-regulated

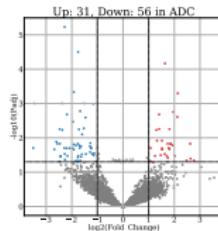
Figure: DEG Venn Diagram in SQC

DEG Volcano Plots with Bowtie2 in ADC

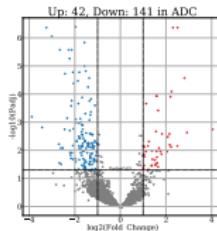
Normal → AAH → AIS → MIA → Primary (ADC)



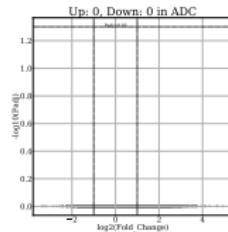
(a) Normal-AAH



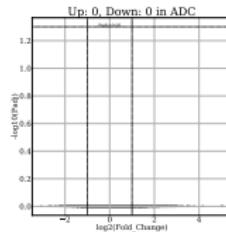
(b) Normal-AIS



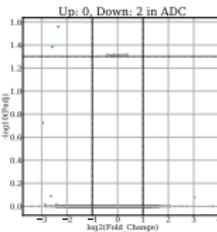
(c) Normal-Primary



(d) AAH-AIS



(e) AAH-Primary



(f) AIS-Primary

Figure: DEG Volcano Plots in ADC

DEG Venn Diagram with Bowtie2 in ADC

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



(a) Up-regulated

(b) Down-regulated

Figure: DEG Venn Diagram in ADC

Findings in DEG Analysis

Results

Bulk Cell Deconvolution

Single-cell data as Reference

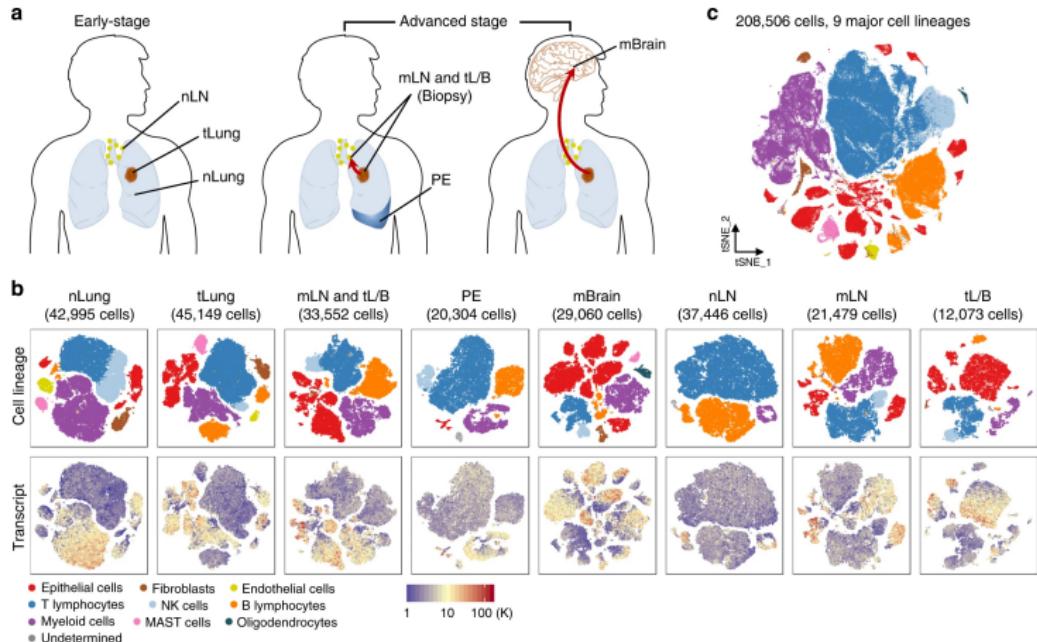


Figure: Comprehensive dissection and clustering of 208,506 single cells from LUAD patients (Kim et al., 2020)

CIBERSORTx

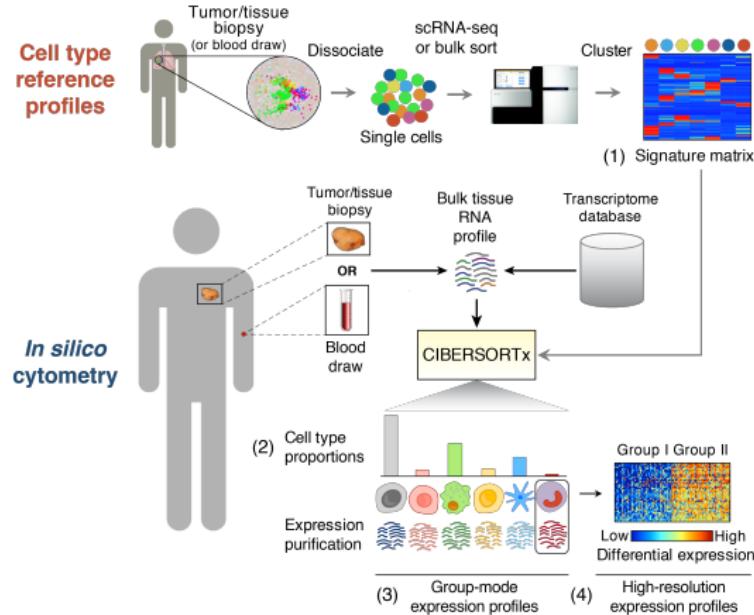


Figure: Workflow for CIBERSORTx (Steen et al., 2020; Newman et al., 2019)

Cluster Plot with Bowtie2 in ADC

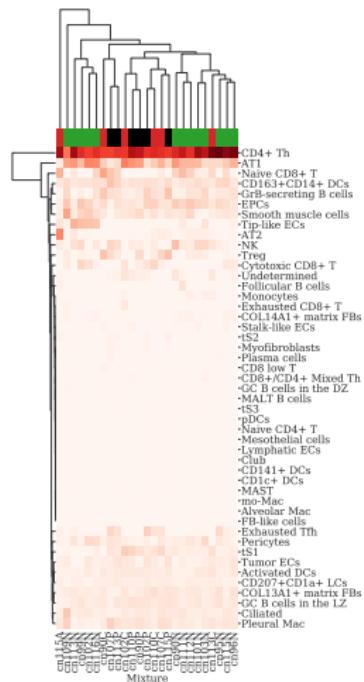


Figure: Cluster Plot in ADC

Cluster Plot with Bowtie2 in SQC

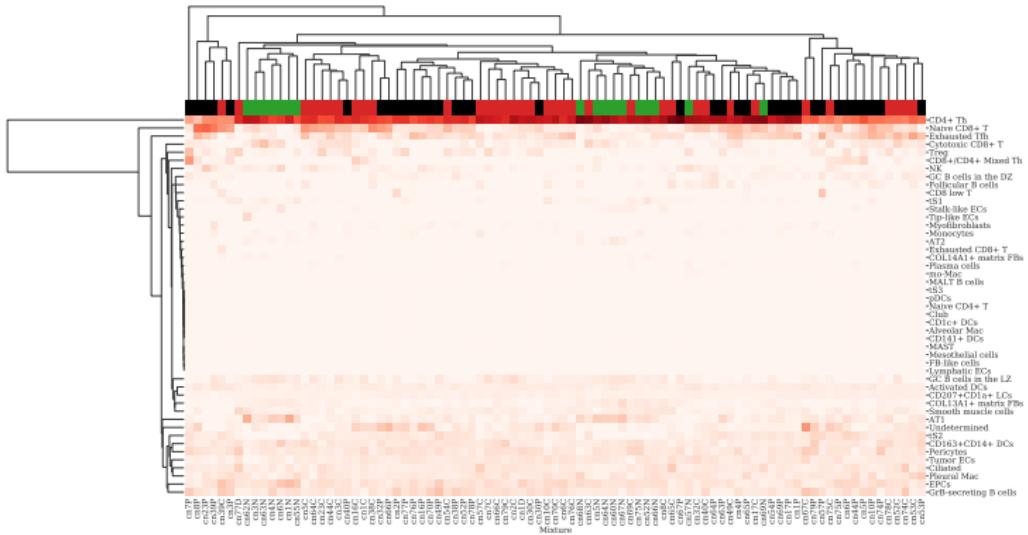


Figure: Cluster Plot in SQC

Benchmarking of Cell Deconvolution Tools

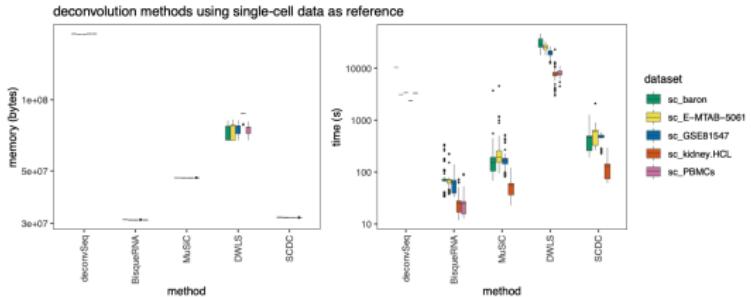


Figure: Memory and time requirements for the cell deconvolution methods (Cobos et al., 2020)

Top 3 Methods

- ① BisqueRNA (Jew et al., 2020)
- ② MuSiC (X. Wang, Park, Susztak, Zhang, & Li, 2019)
- ③ SCDC (Dong et al., 2021)

BisqueRNA?

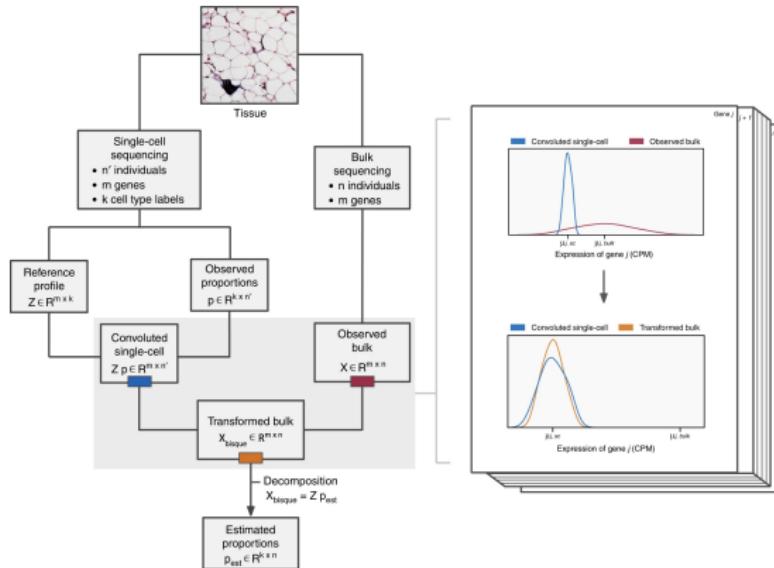


Figure: Graphical overview of the Bisque decomposition methods (Jew et al., 2020)

MuSiC?

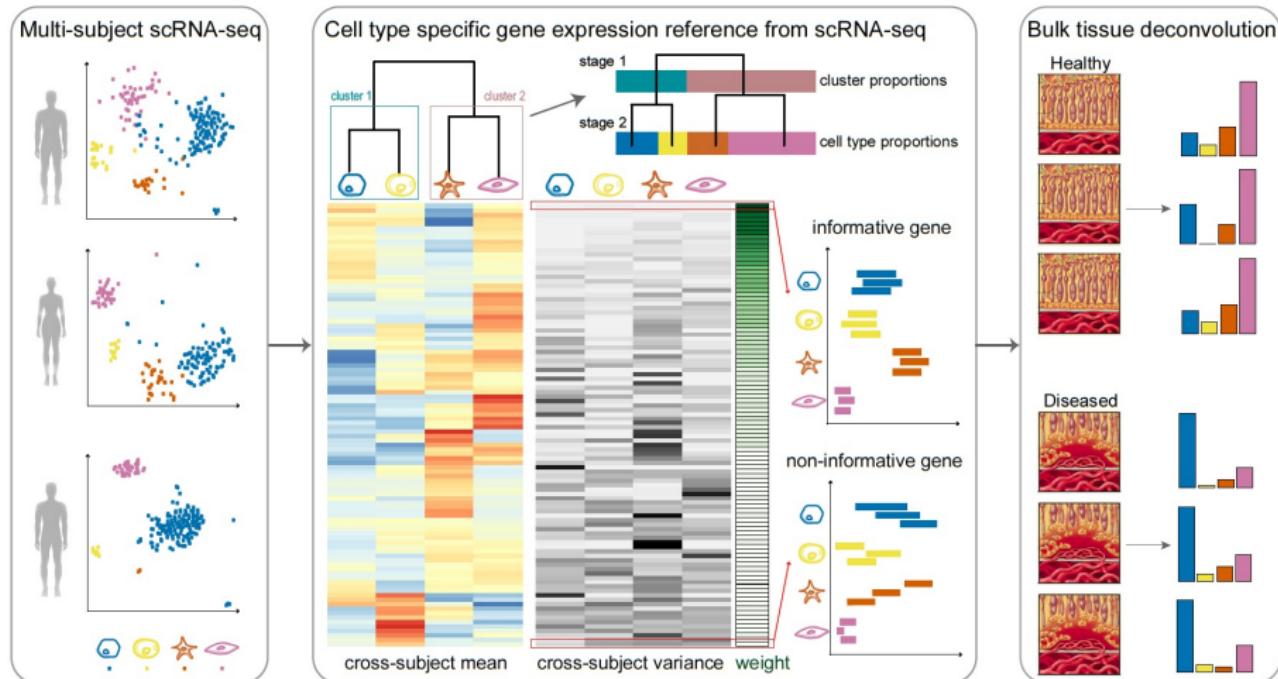
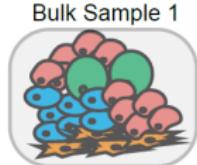


Figure: Overview of MuSiC framework (X. Wang et al., 2019)

SCDC?

Bulk RNA-seq



Bulk Sample 2

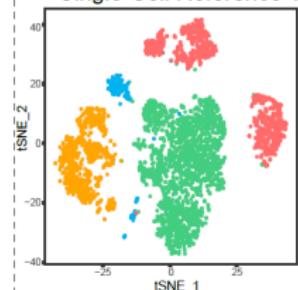


Bulk Sample 3

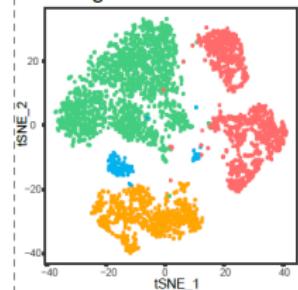


scRNA-seq

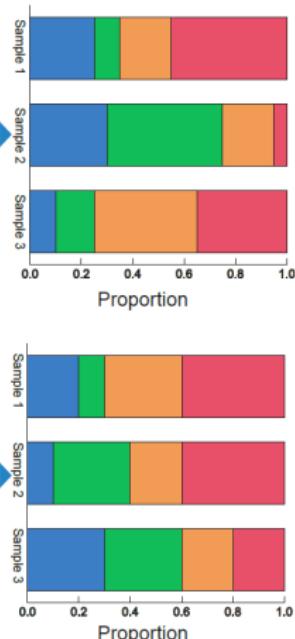
Single-Cell Reference 1



Single-Cell Reference 2



Deconvolution



ENSEMBLE

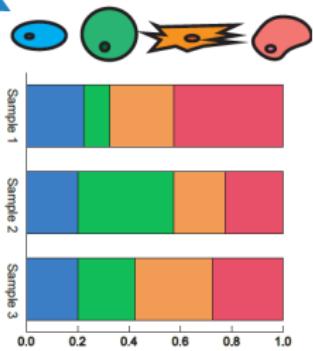


Figure: Overview of deconvolution by SCDC (Dong et al., 2021)

Findings in Bulk Cell Deconvolution

Results

Tumor Evolution Trajectories Analysis

Revolver?

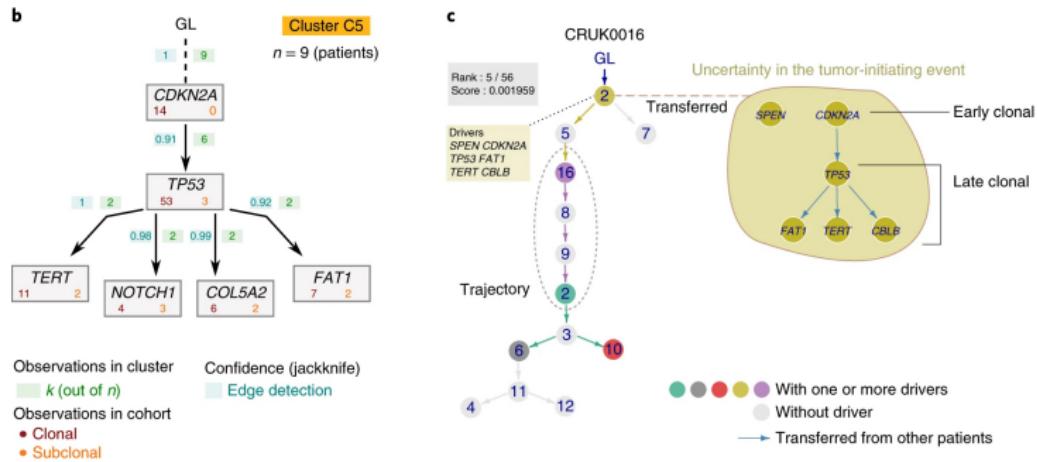


Figure: Repeated Evolutionary Trajectories (Caravagna et al., 2018)

Findings in Tumor Evolution Trajectories Analysis

Results

Discovery of Gene Fusion

Arriba?

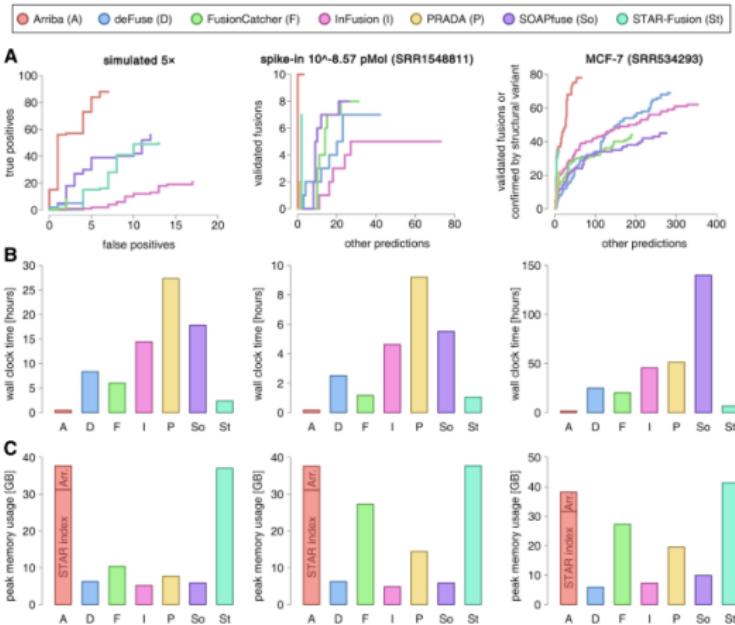


Figure: Benchmark of Arriba versus alternative methods (Uhrig et al., 2021)

FusionCatcher?

FusionCatcher – a tool for finding somatic fusion genes in paired-end RNA-sequencing data

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³Institute for Molecular Medicine Finland, P.O. Box 20,
FI-00014 Helsinki, Finland

November 19, 2014

Figure: FusionCatcher (Nicorici et al., 2014)

STAR-fusion?

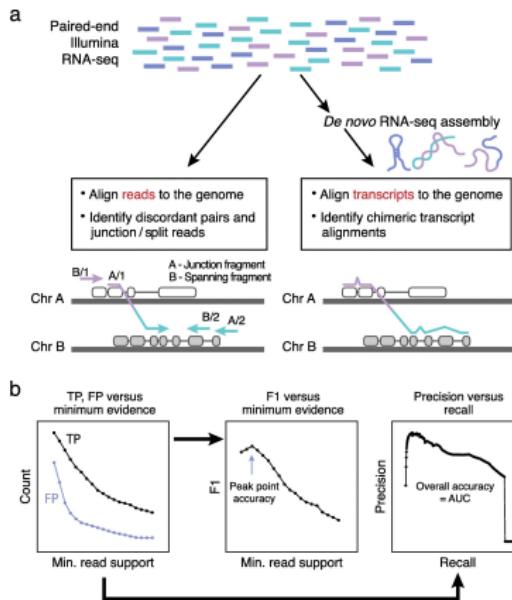


Figure: Methods for fusion transcript prediction and accuracy evaluation (Haas et al., 2019)

Findings in Gene Fusion Discovery

Discussion

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