Doctoral Thesis

<Lung Precancer Analysis>

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<2021>

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Abstract

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I Introduction

1.1 Lung Cancer

Lung cancer is the most common form of cancer as 12.3 % of all cancers (Minna, Roth, & Gazdar, 2002).

1.2 Non-small cell lung cancer

Lung adenocarcinoma (LUAD)

Lung squamous cell carcinoma (LUSC)

1.3 Lung Precancer

1.4 Study Objectives

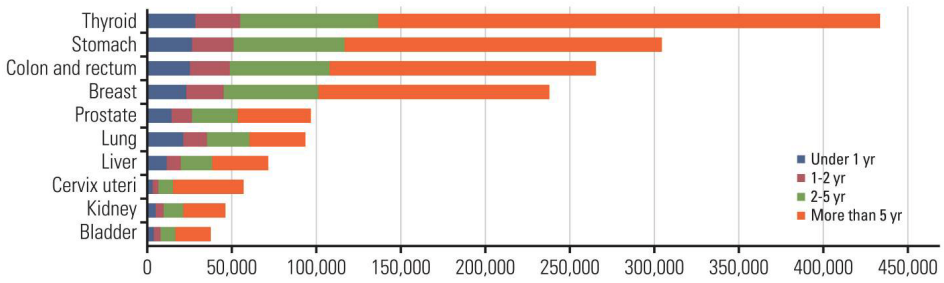


Figure 1: Common cancer survival rates (Hong et al., 2021)

II Materials

2.1 List of IPNs

Carcinoma *in situ*

Carcinoma *in situ* (CIS)

Adenocarcinoma *in situ*

Adenocarcinoma *in situ* (AIS)

Atypical Adenomatous Hyperplasia

Atypical adenomatous hyperplasia (AAH)

Dysplasia

Minimally Invasive Adenocarcinoma

Minimally invasive adenocarcinoma (MIA)

2.2 Data Composition

III Methods

3.1 Workflows

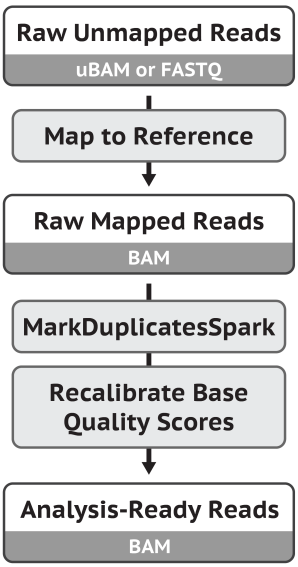


Figure 2: Workflow for data pre-processing for variant discovery (Van der Auwera et al., 2013; DePristo et al., 2011)

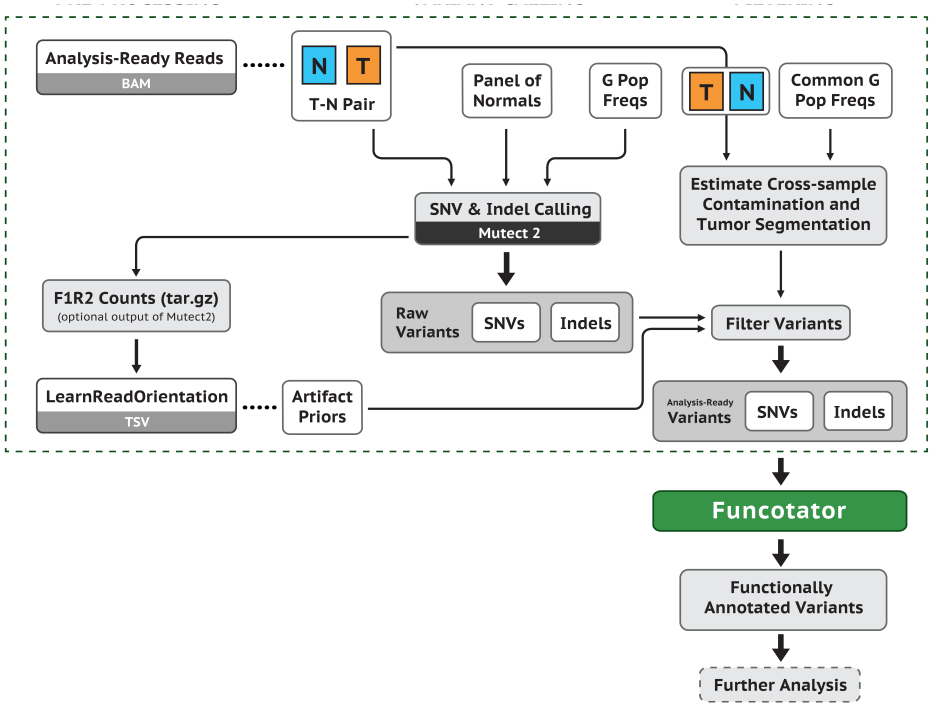


Figure 3: Somatic short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

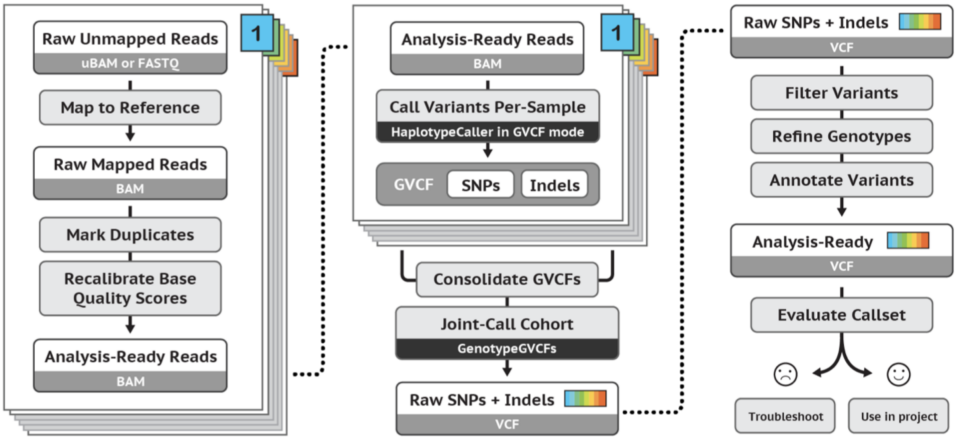


Figure 4: Germline short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

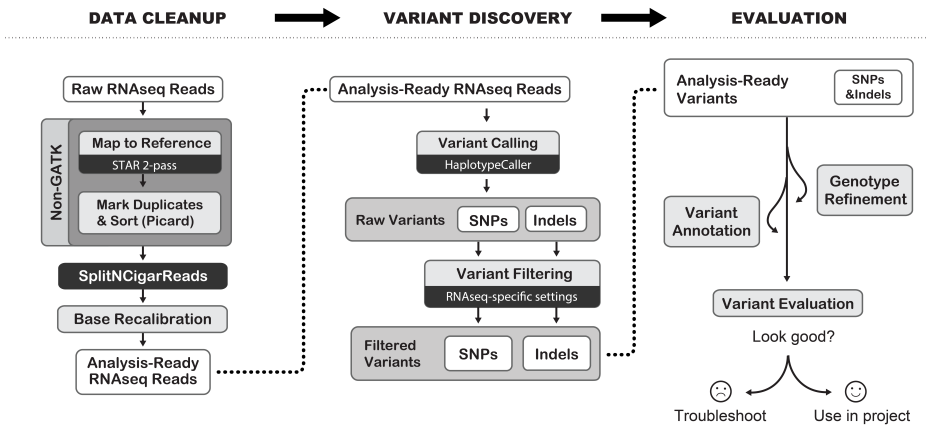


Figure 5: RNA-seq short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

IV Results

4.1 Quality Checks

Quality Checks with FastQC

Quality Checks with Picard

Findings in Quality Checks

4.2 Copy Number Variation Analyses

Purity and Ploidy

Copy Number Variation Plot

Findings in Copy Number Variation Analyses

4.3 Somatic Short Variation Analyses

Somatic Short Variation Analyses with Mutect2

Somatic Short Variant with Clinical Data

Findings in Somatic Short Variation Analyses

4.4 Variant Allele Frequency Analyses

Findings in Variant Allele Frequency Analyses

4.5 Gene Fusion Analyses

Findings in Gene Fusion Analyses

4.6 Differences in Gene Expression levels

4.7 Bulk Cell Deconvolution Analyses

Single-cell Reference Data

GSE131907 as Reference

GSE162498 as Reference

GSE179994 as Reference

Findings in Bulk Cell Deconvolution Analyses

4.8 Mutational Signature Analyses

Single Base Substitutions

Double Base Substitutions

Insertions and Deletions

Findings in Mutational Signature Analyses

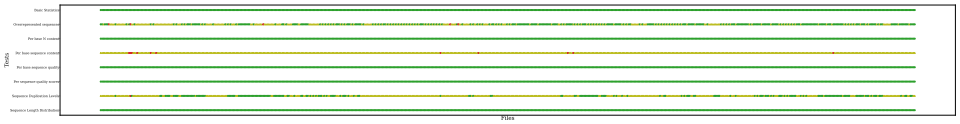


Figure 6: FastQC results with WES data

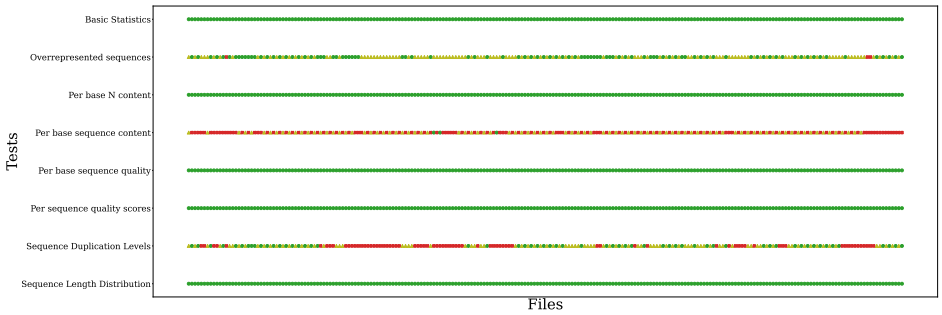
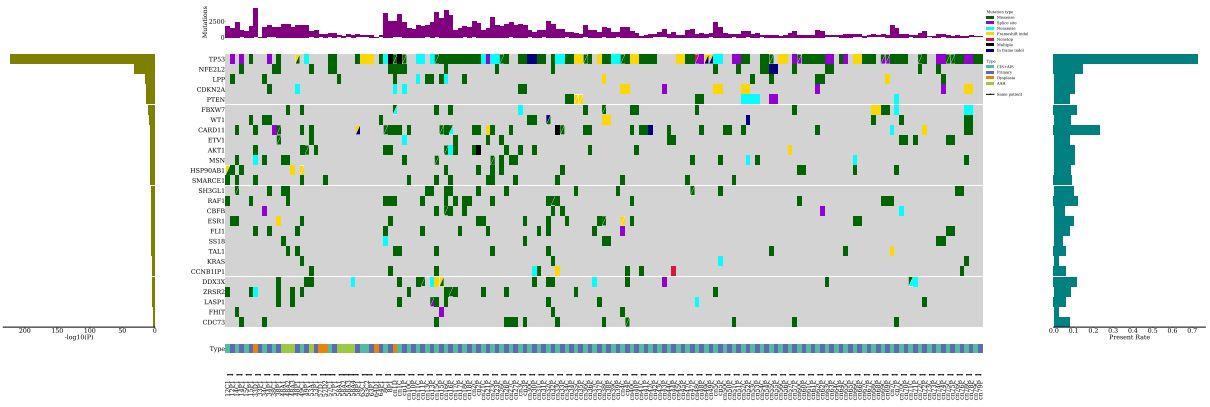
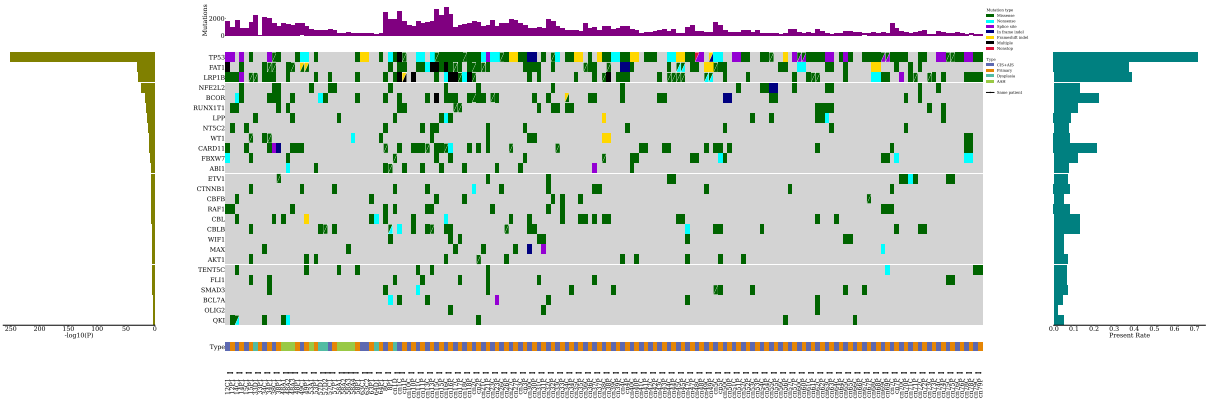


Figure 7: FastQC results with WTS data

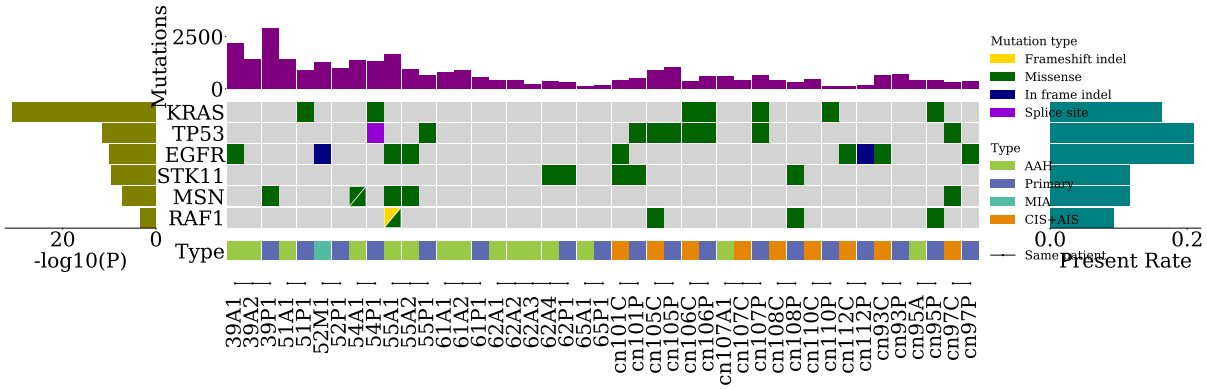


(a) BWA

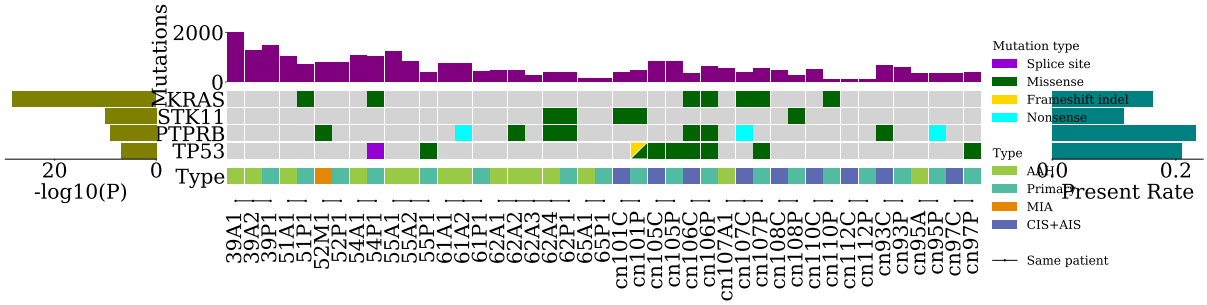


(b) Bowtie2

Figure 8: Comut Plot by LUSC



(a) BWA



(b) Bowtie2

Figure 9: Comut Plot by LUAD

V Discussion

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Acknowledgements

Thank you very much.