Lung Cancer

Jaewoong Lee

Ulsan National Institute of Science and Technology

jwlee230@unist.ac.kr

2021-01-22

Overview

1. Introduction
2. Materials
3. Methods
4. Results
5. Proceedings

Introduction

Objectives

- Find different mutation between WES & WTS in Lung cancer & pre-cancer.

Materials

Lung Cancer Data

- WES + WTS
- Normal + {Primary, CIS AIS, AAH, Dysplasia, MIA}
- Total 112 samples

Methods

Data pre-processing for variant discovery

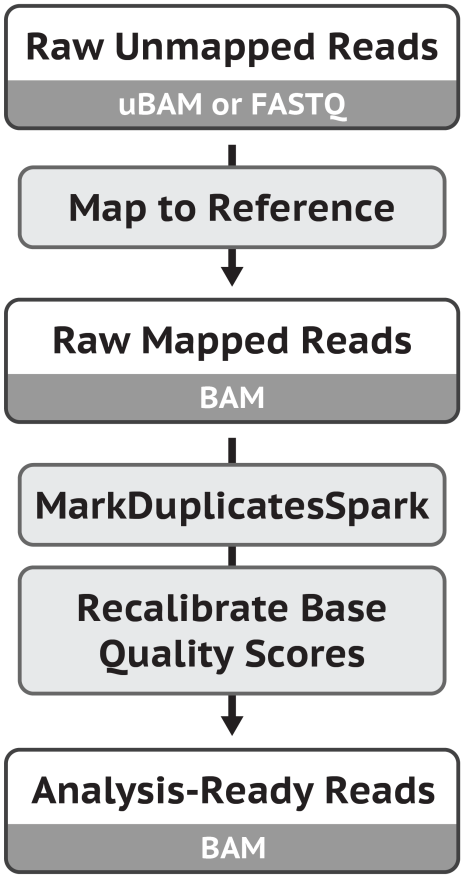

Figure: Data pre-processing for variant discovery (Van der Auwera et al., 2013; DePristo et al., 2011)

Somatic short variant discovery

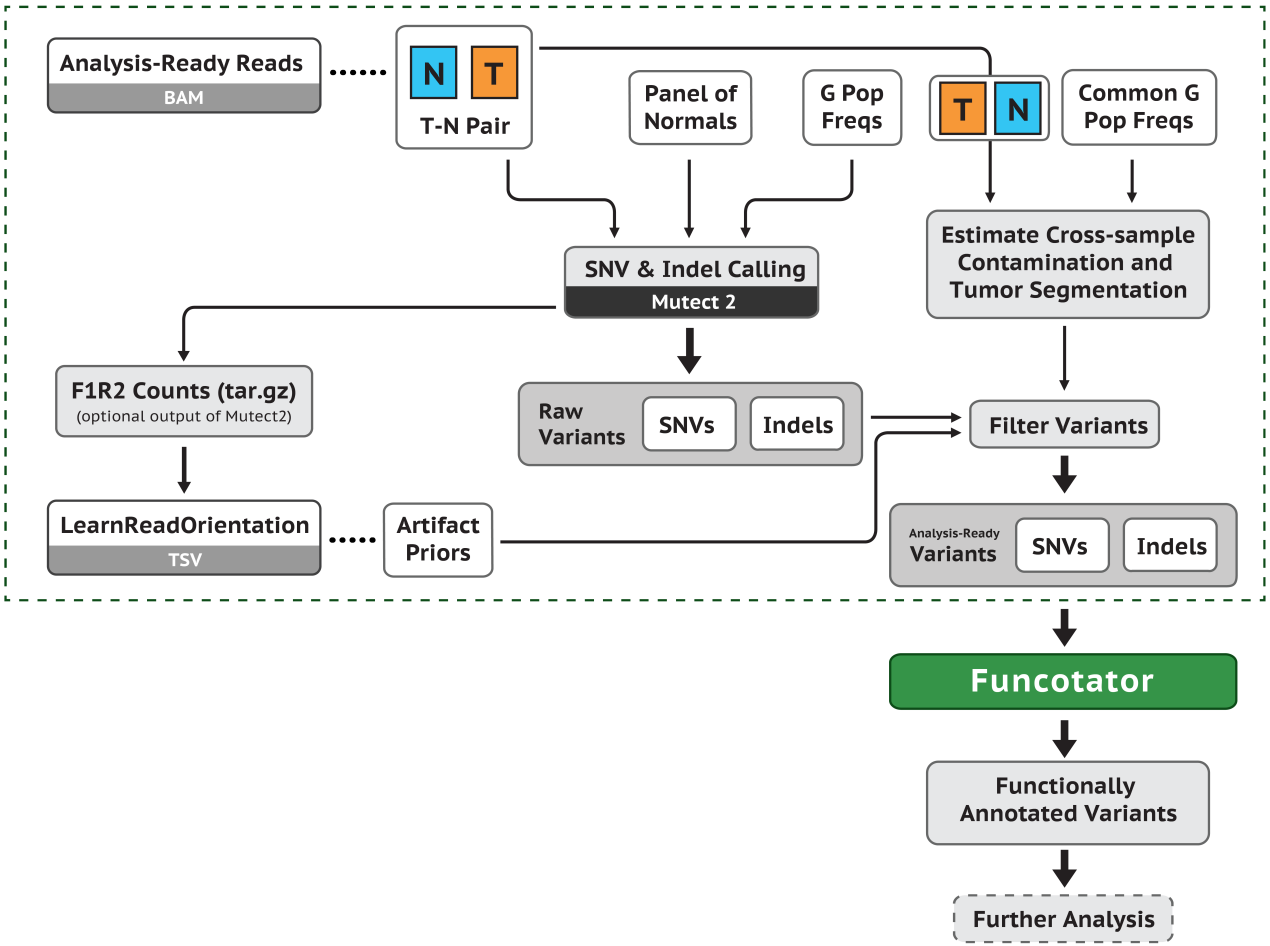

Figure: Somatic short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

RNA-seq short variant discovery

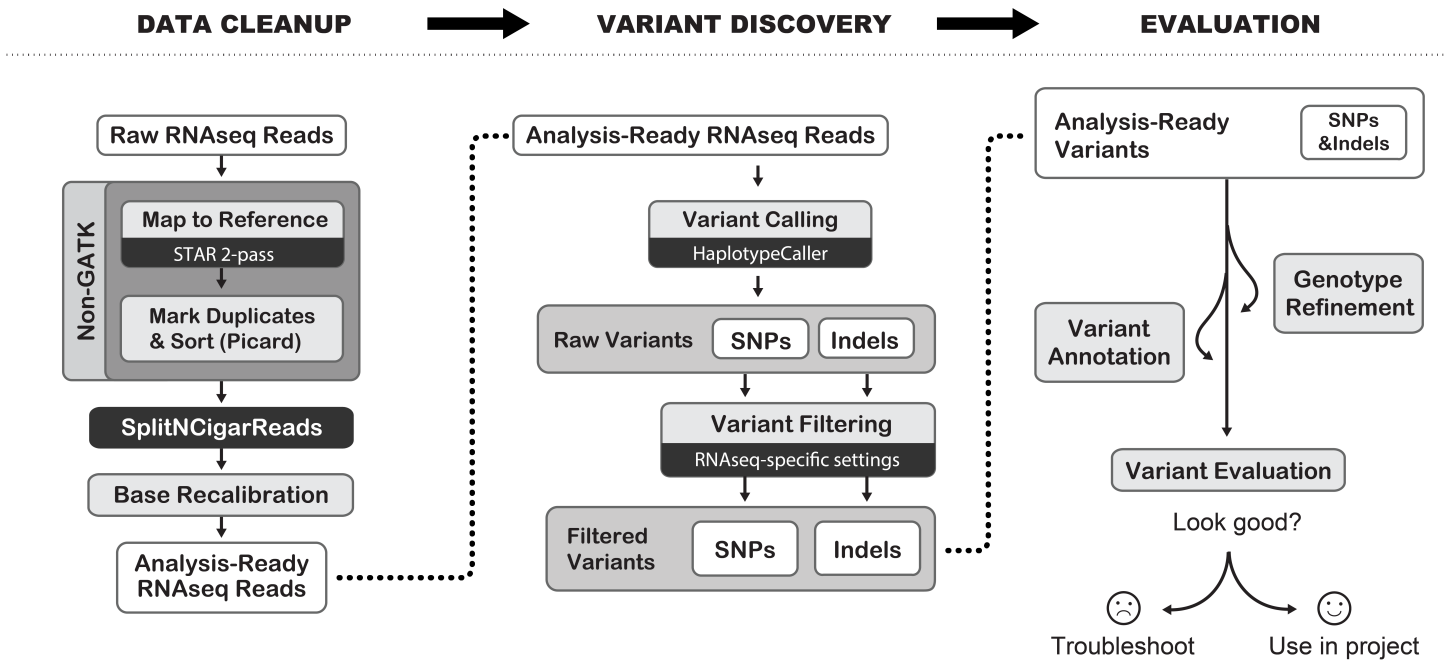

Figure: RNA-seq short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

Results

FastQC

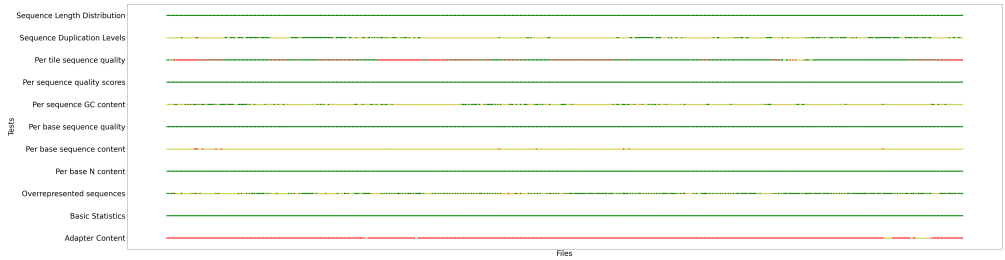

Figure: FastQC with WES data

Figure: FastQC with WTS data

$\therefore$ All PASS at *per base sequence quality*!

Proceedings

To-do Lists I

- Alignment WES with BWA
- Alignment WES with Bowtie2

References I

DePristo, M. A., Banks, E., Poplin, R., Garimella, K. V., Maguire, J. R., Hartl, C., ... others (2011). A framework for variation discovery and genotyping using next-generation dna sequencing data. *Nature genetics*, *43*(5), 491.

Van der Auwera, G. A., Carneiro, M. O., Hartl, C., Poplin, R., Del Angel, G., Levy-Moonshine, A., ... others (2013). From fastq data to high-confidence variant calls: the genome analysis toolkit best practices pipeline. *Current protocols in bioinformatics*, *43*(1), 11–10.