Lung Cancer

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Overview

Introduction

Materials

Lung Cancer Data

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

Methods

Somatic short variant discovery

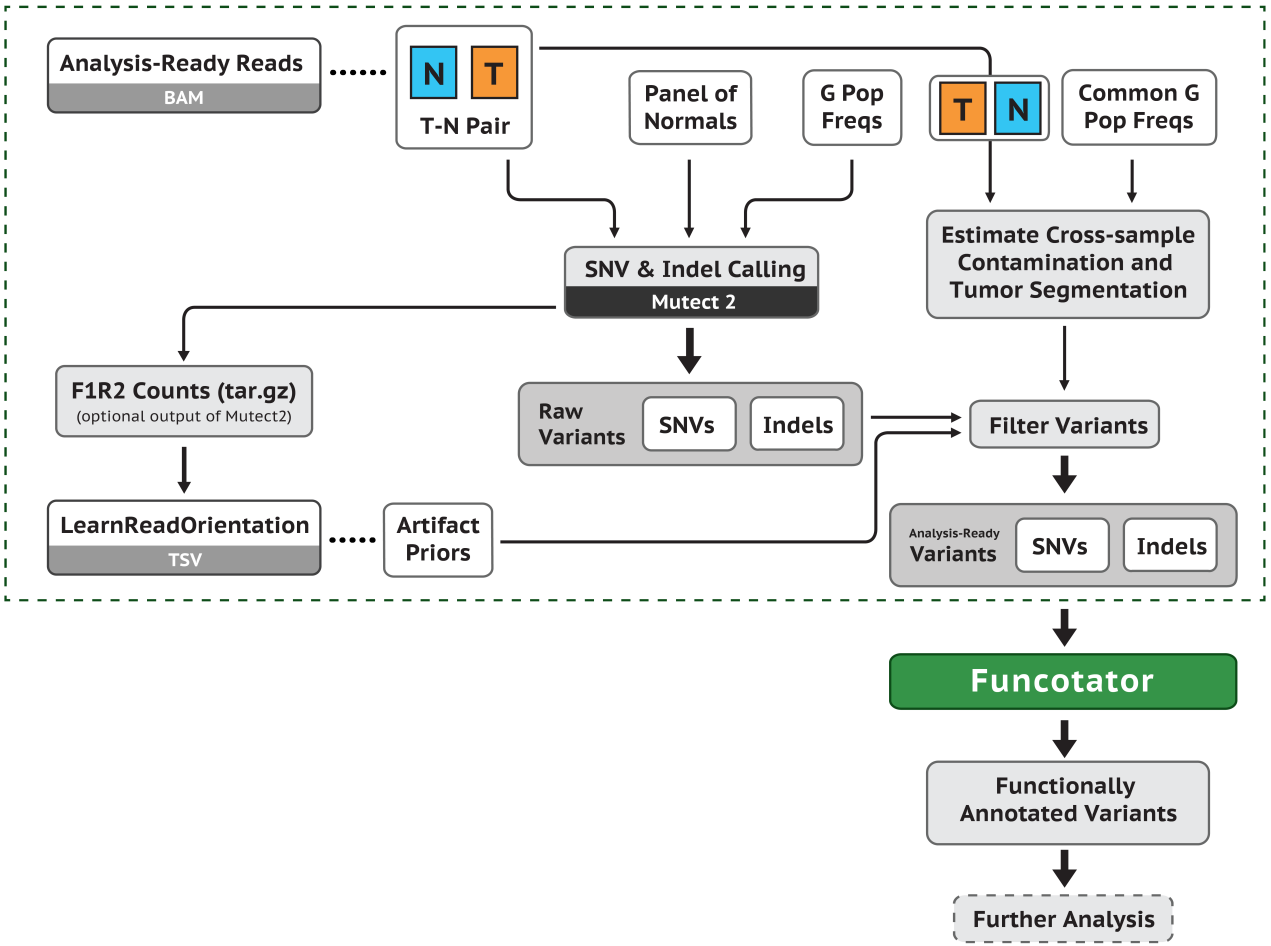

Figure: Somatic short variant (SNVs + Indels) discovery workflow (Van der Auwera et al., 2013)

Somatic CNV discovery

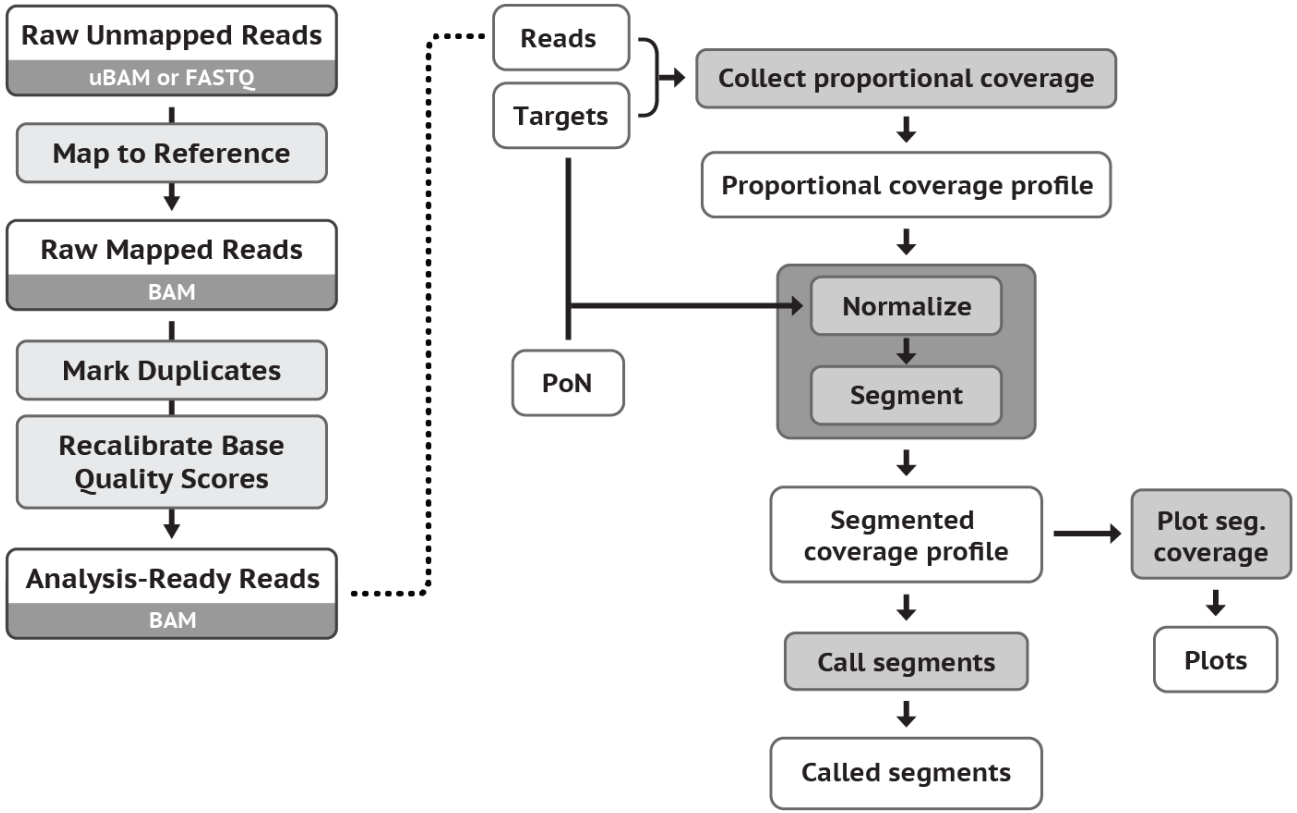

Figure: Somatic CNV (copy number variant) discovery workflow (Van der Auwera et al., 2013)

Results

FastQC

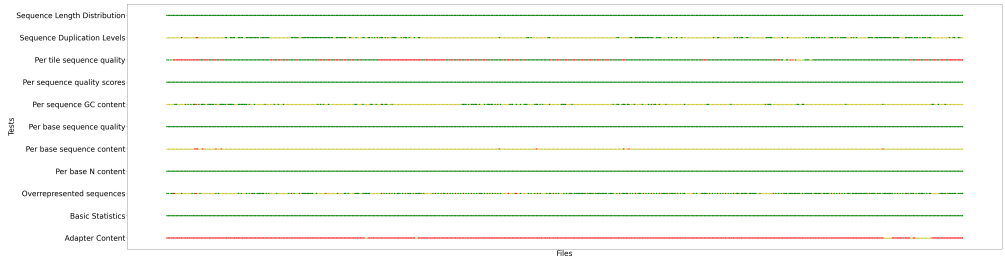

Figure: FastQC with WES data

Figure: FastQC with WTS data

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

Proceedings

References I

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.