Lung Cancer

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3.1 Genome Analysis Toolkit

Genome analysis toolkit (GATK) is a software package for variant discovery among sequencing data (Van der Auwera et al., 2013; DePristo et al., 2011).

3.2 Alignment

3.2.1 Burrows-Wheeler Aligner

Burrows-Wheeler Aligner (BWA) is a software package for aligning short-read sequences unto a large reference genome (Li & Durbin, 2009). BWA-MEM is one of the contained algorithms in BWA software package, is a novel algorithm for mapping sequence reads on a large reference genome (Li, 2013).

3.2.2 Bowtie2

Bowtie 2 is an efficient and fast software package for aligning sequencing reads against long reference sequences (Langmead & Salzberg, 2012).

3.2.3 STAR

STAR is a swift universal RNA-seq alignment tool (Dobin et al., 2013).

3.2.4 Samtools

Samtools is a suite software packages for discovering in high-throughput sequencing data (Li et al., 2009).

3.3 Quality Check

3.3.1 FastQC

FastQC is a software package which aims to provide a productive method to do quality control check on raw sequence data (Andrews et al., 2012).

3.3.2 Sequenza

Sequenza is a software package to investigate genomic sequencing data, such as cellularity and ploidy estimation, from paired normal-tumor samples (Favero et al., 2015).

4 Results

4.1 FastQC

5 Discussion

6 References

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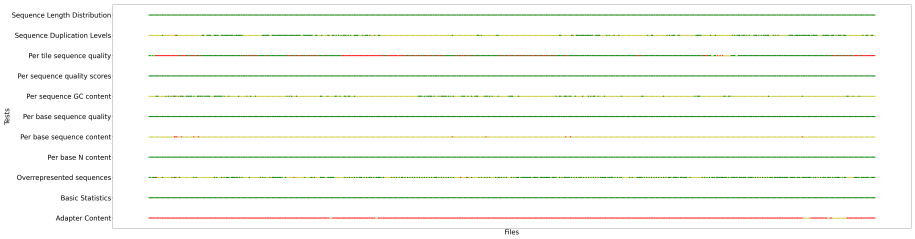

Figure 1: FastQC with WES data

Figure 2: FastQC with WTS data