Analysis report of RNA-Seq data from Sus scrofa, (pig)

1   introduction

The rnaseq-pipeline of nf-core project was used for initial processing of the provided data. In addition to the reads a reference genome and annotation file are required to successfully run the pipeline. The pipeline performs three basic processing steps:

1. quality check (FastQC/MultiyQC)

2. adapter trimming (Cutadapt)

3. alignment (STAR)

In addition the pipeline performs a number of anylses

- biotype counts (featureCounts)

- alignment quality check (QualiMap)

- duplication rates (DupRadar)

- sample similarity (edgeR)

- complexity estimation (Preseq)

- pression quantification (Salmon)

The results of the Salmon gene expression qunatification then are further analyzed using the DESeq2 R-package, providing a matrix of differntially expressed genes. The resulting DESeq-matrix is analyzed using KeyPathwayMiner (KPM)

in order to extract the pathways. The protein-protein-interaction network necessary for this is downloaded from the STRING database via cytoscape. finally

a GO-Term enrichment was done with g:Profiler, based on the results KPM provided, to identify over- or under-represented genes in the extracted pathway.

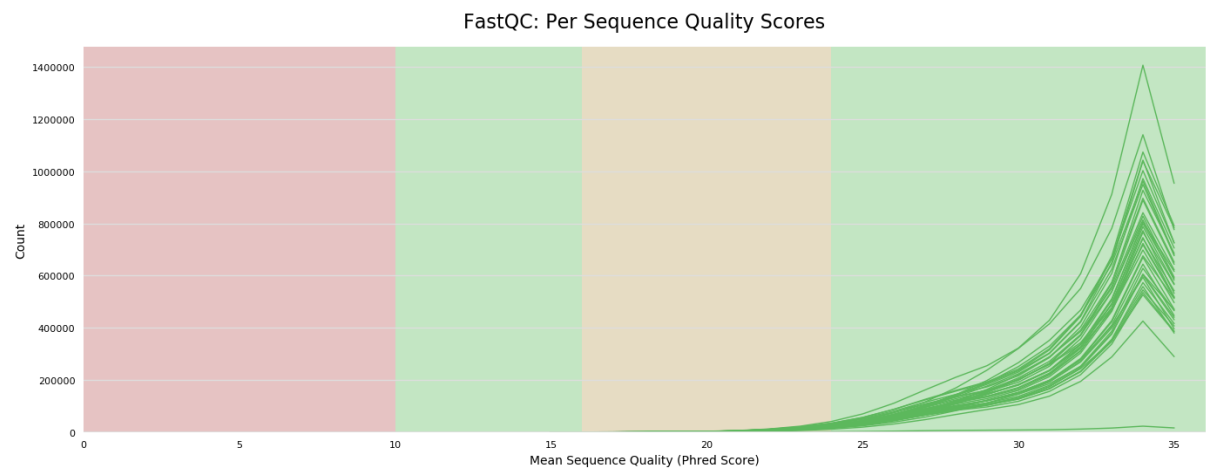# Results

Quality Control

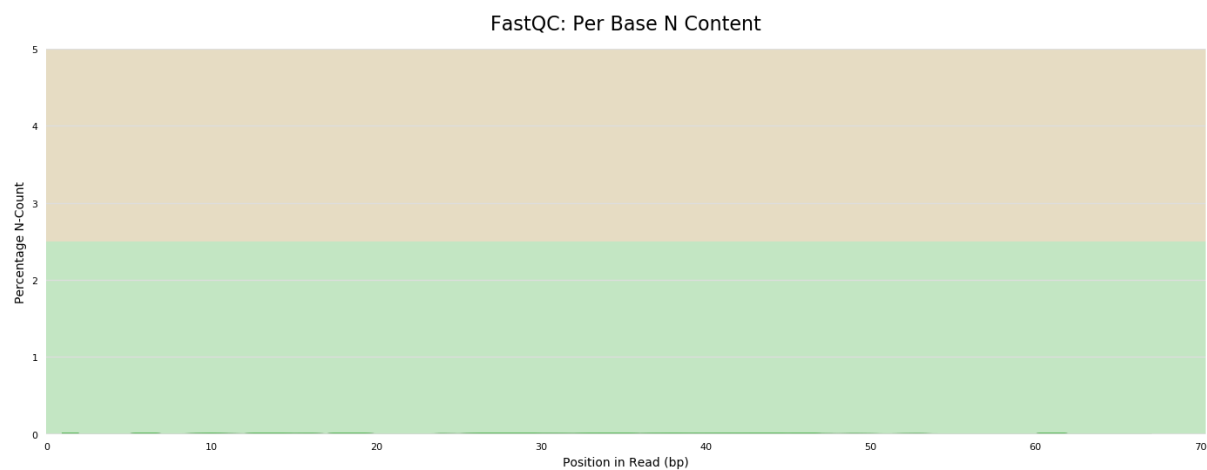
Figure 1: Sus scrofa, (pig)

Figure 2: Sus scrofa, (pig)

FastQC: Per Base N Content

Figure 3: Sus scrofa, (pig)

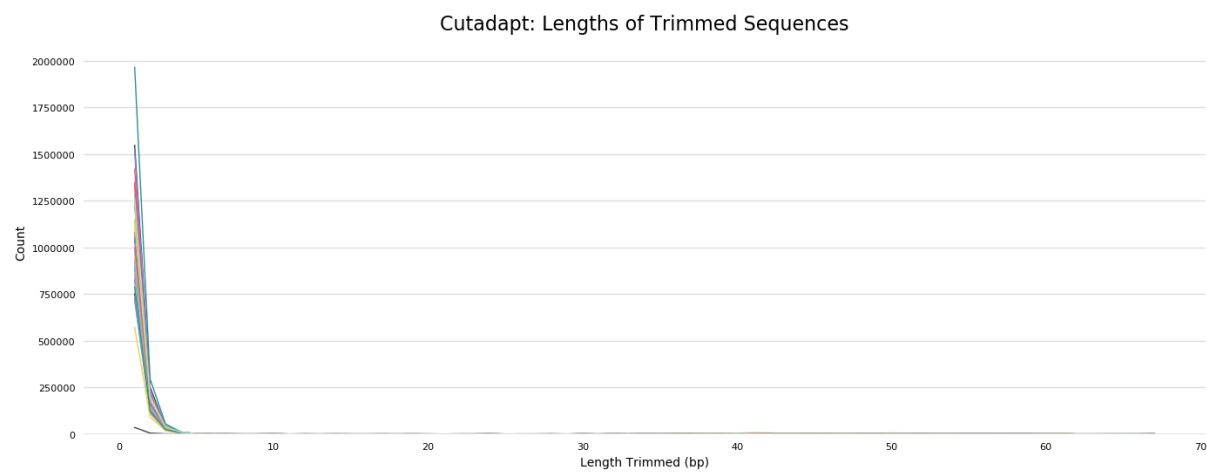# Trimming

Cutadapt: Lengths of Trimmed Sequences

Figure 4: Sus scrofa, (pig)

Alignment

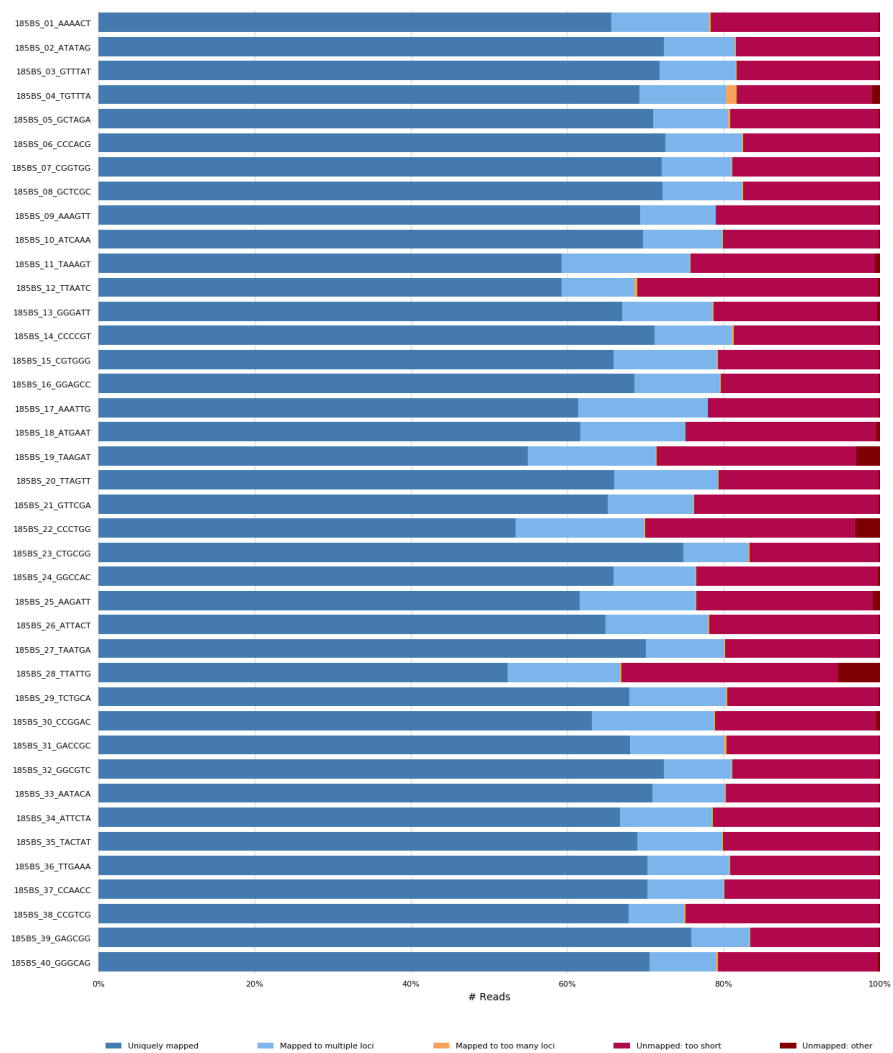

Figure 5: Sus scrofa, (pig)

BiotypeCounts
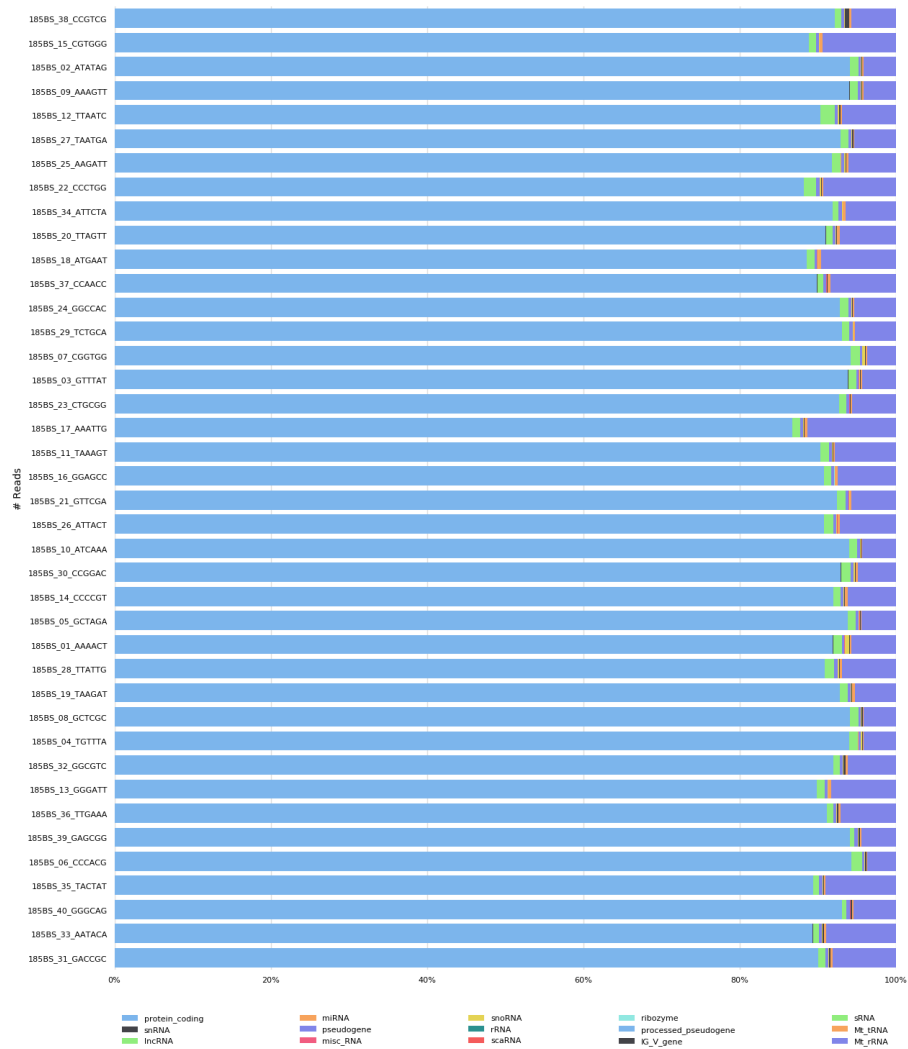

Figure 6: Sus scrofa, (pig)

Alignment Quality Check

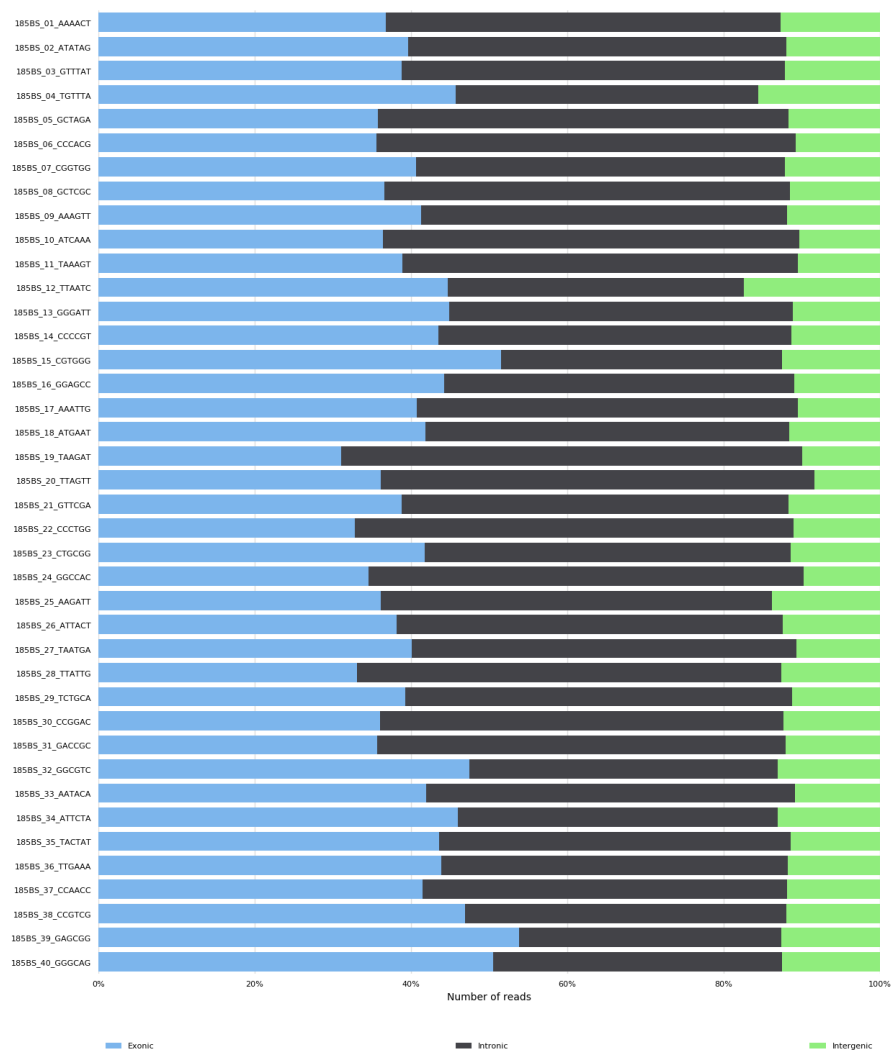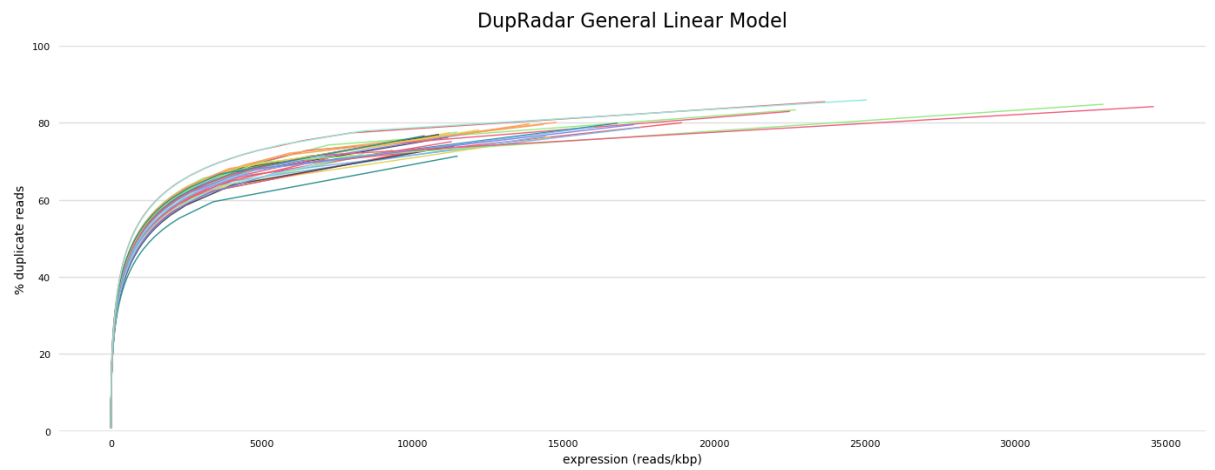Figure 7: Sus scrofa, (pig)

Duplication Rates

Figure 8: Sus scrofa, (pig)
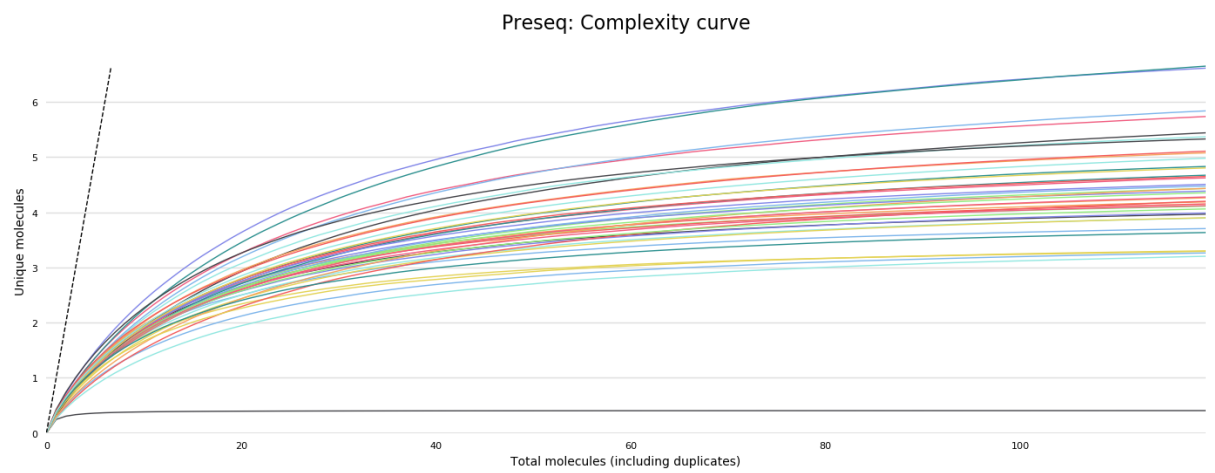
Sample Similarity

Complexity Estimation

Figure 9: Sus scrofa, (pig)

Gene Expression Quantification

More detailed and interactive results from the rnaseq-pipeline can be viewed with the multiqc_report.html in the MultiQC folder in the output directory.
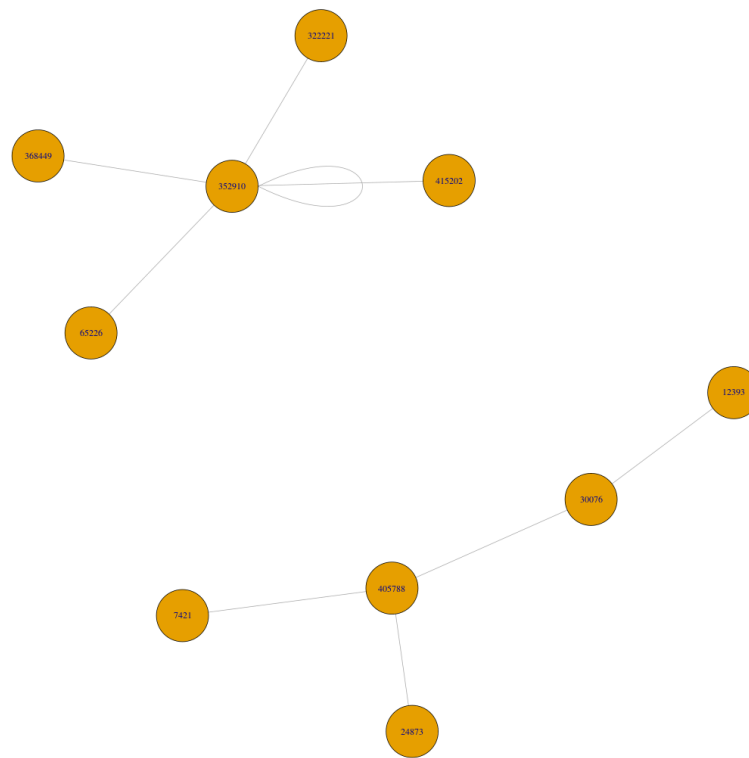
Differentially Expressed Genes

KeyPathwayMiner

Figure 10: Sus scrofa, (pig)

Additional plots and graphs from the MultiQC run can be found in the output directory of the RNA-Seq run in the MultiQC/multiqc_report.html html-file