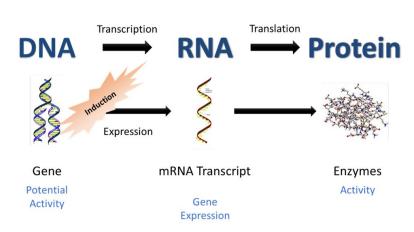
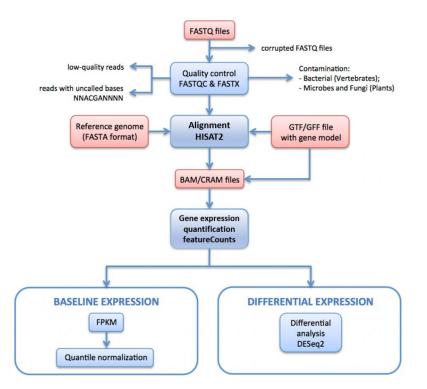
# Bora Öden Past Works and Abroad Experience

Mersin University - Faculty of Medicine

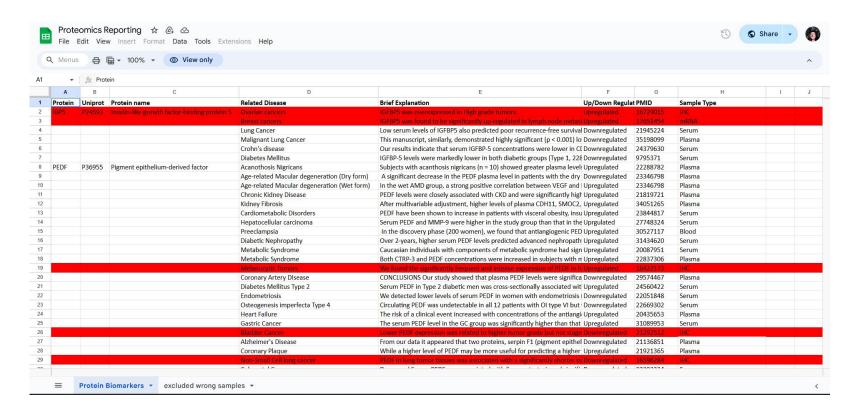
Summer 2022: SciLifeLab - Mardinoğlu Group / Stockholm



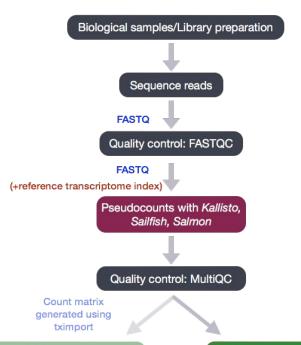




#### **July 2022 - Proteomics Literature Review and Analysis**



## August 2022: RStudio, DeSeq2, Kallisto Analysis



#### **About**

**kallisto** is a program for quantifying abundances of transcripts from bulk and single-cell RNA-Seq data, or more generally of target sequences using high-throughput sequencing reads. It is based on the novel idea of *pseudoalignment* for rapidly determining the compatibility of reads with targets, without the need for alignment. On benchmarks with standard RNA-Seq data, **kallisto** can quantify 30 million human reads in less than 3 minutes on a Mac desktop computer using only the read sequences and a transcriptome index that itself takes less than 10 minutes to build. Pseudoalignment of reads preserves the key information needed for quantification, and **kallisto** is therefore not only fast, but also as accurate as existing quantification tools. In fact, because the pseudoalignment procedure is robust to errors in the reads, in many benchmarks **kallisto** significantly outperforms existing tools. **kallisto** is described in detail in:



DGE with R: DESeq2, EdgeR, limma:voom DGE or isoform-level DE with R: Sleuth

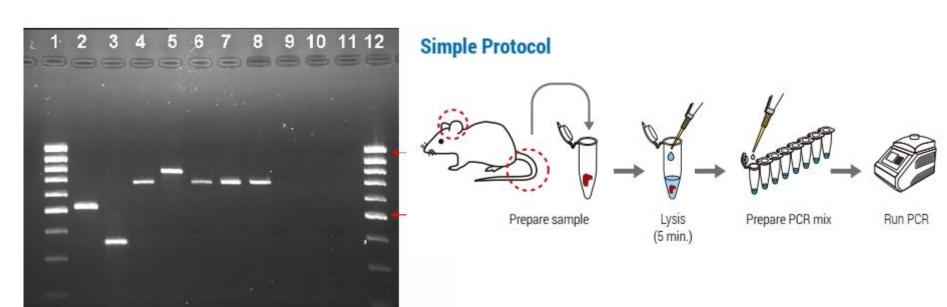
### **Spring 2023 / Erasmus at University of Pisa Faculty of Medicine**



#### Summer 2023: Universitätsklinikum Ulm



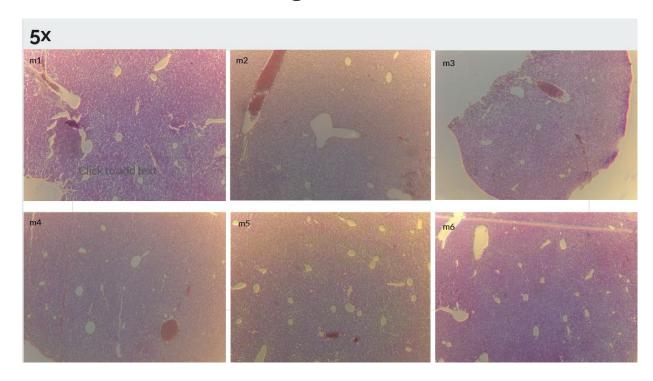
## Regenotyping with PCR



# **Cell culture of mice macrophages**



# **Mice Livers Histological Examination and Presentation**



link to my presentation

the end.

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thank you for your attention.