#### RNAseq Workshop

Monash Genomics and Bioinformatics Platform (MGBP)  $\,$ 

Compiled: May 06, 2024

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# Getting started

Instructors:

#### 1.1 Summary

Important links:

## Introduction

## Experimental design

- 3.1 Sequencing methods
- 3.2 Cost optimisation approaches
- 3.3 Sequencing
- 3.4 Batches and replicates (technical/biological)

## Library Preparation

- 4.1 Read length/type, paired/single
- 4.2 Enrichment/depletion
- 4.3 cDNA synthesis

## Pipeline Overview

- 5.1 Sequencing
- 5.2 (fastq)QC
- 5.3 multiQC interpretation
- 5.4 Mapping
- 5.5 Proper references and annotated genome references
- 5.6 multiQC interpretation
- 5.7 Counting
- 5.8 Feature counts
- **5.9** UMIs
- 5.10 Show them where they my run it

## Differential Expression

#### 6.1 Normalisation

#### 6.2 analysis ie DEG

( should we go into more details on design matrices, contrast matrices, fitting linear models etc.?) ## QC of results ### MDA/PCA plots and running additional adjustments such as RUVseq or adding covariates in DGE

## Post Analysis

- 7.1 Discuss additional plots and variations
- 7.2 Discuss Network analysis
- 7.3 Discuss Multivariate integration
- 7.4 Discuss Single Cell