



ABOUT RNA-Seq Analysis



OUR TEAM

sarah yasser

shahd khalid

mohanad mohamed

221001902

221001066

221001360

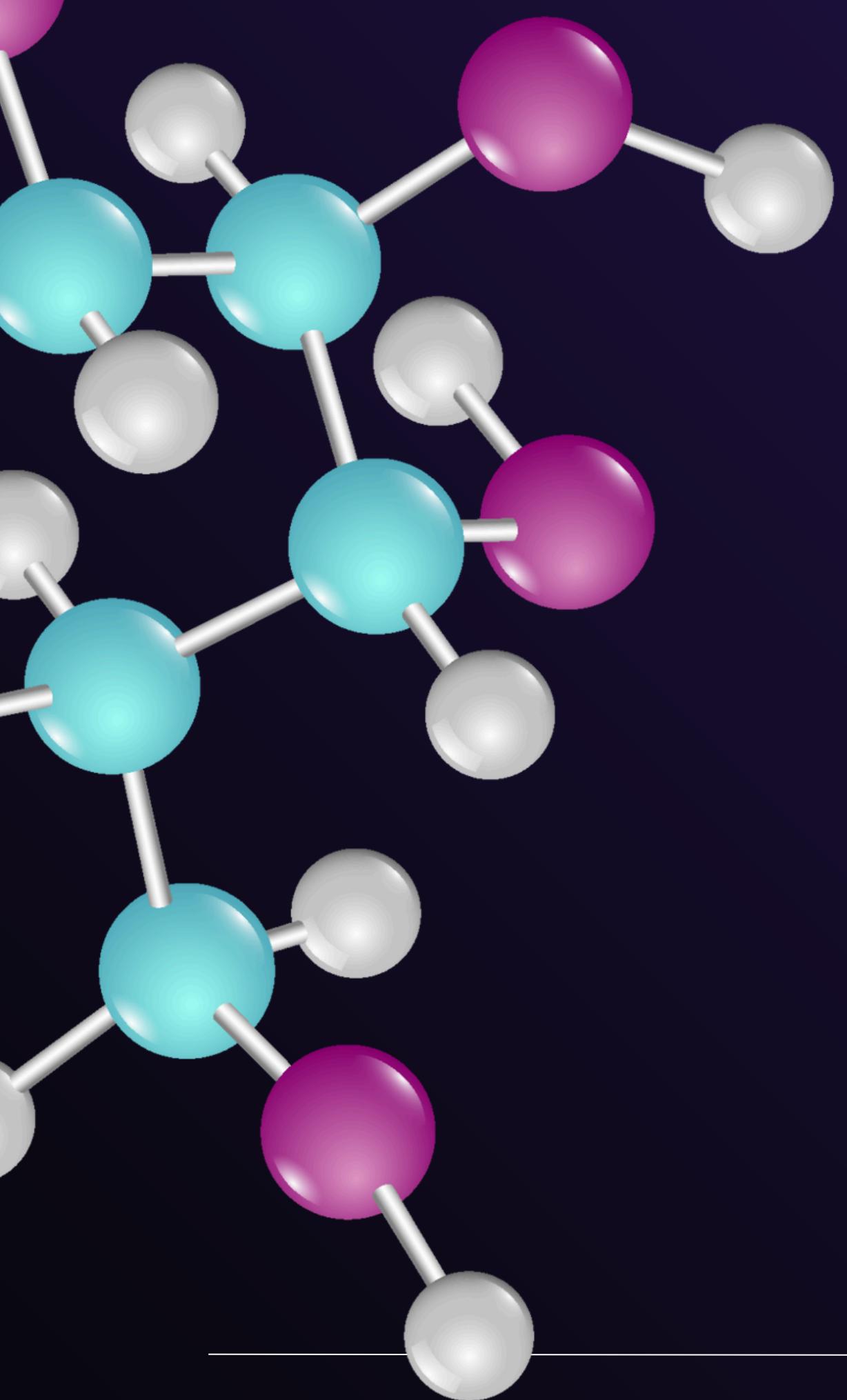
Project Background

1. What is RNA-Seq?
- 2.
3. A method to analyze RNA in a biological sample.
- 4.
5. Objective:
- 6.
7. Predict RNA secondary structure.
8. Identify differentially expressed gene
- 9.

THE

1. _____





Tools and Technologies

- Source of data :NCBI
- rnaseq_pipeline.sh: Bash script for pipeline processing.
- deseq2_analysis.R: R script for differential expression analysis.
- SRA Toolkit, FastQC, Trimmomatic, HISAT2, SAMtools, DESeq2.
- Why These Tools?
- Reliable, widely used, and efficient

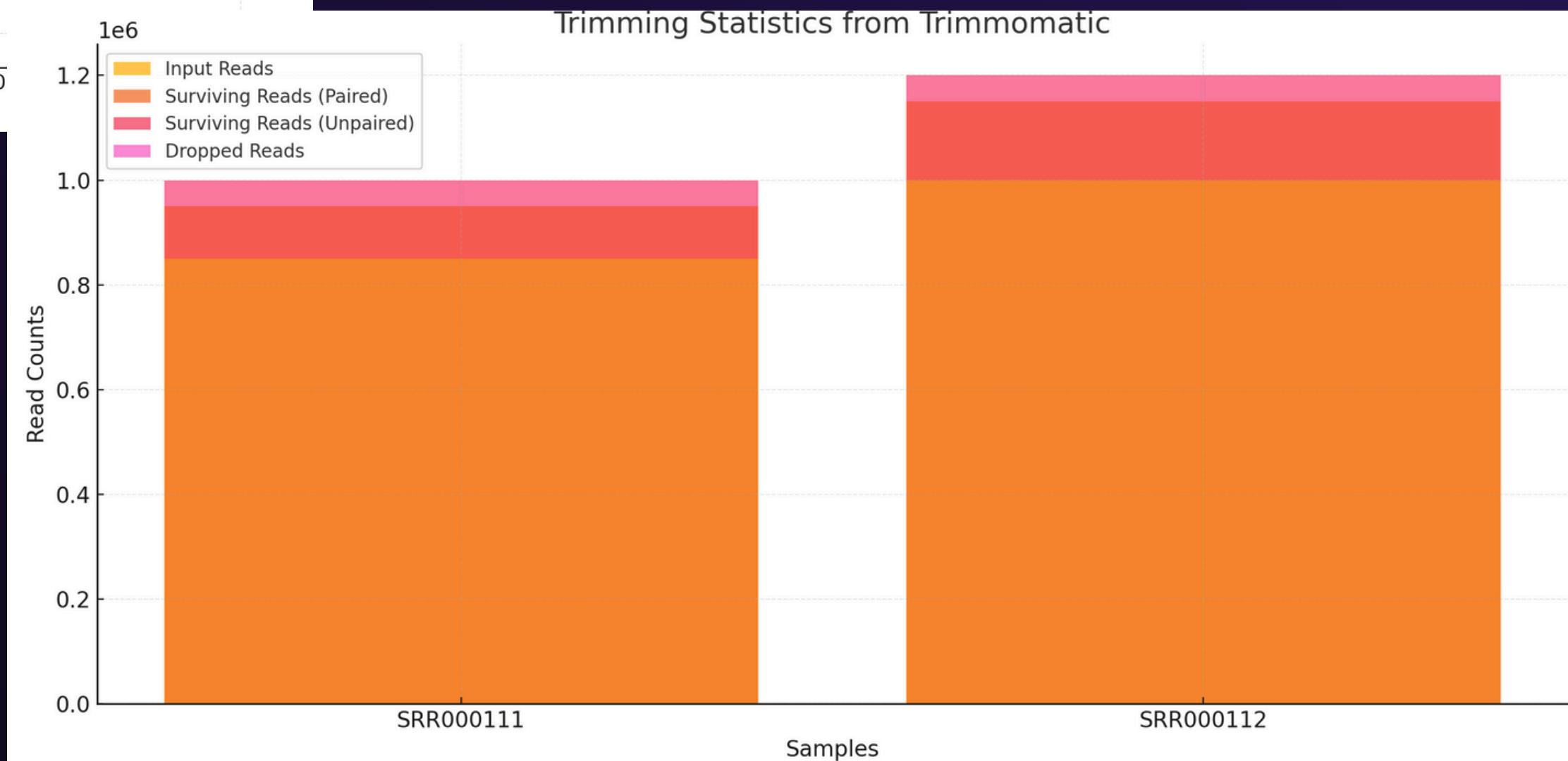
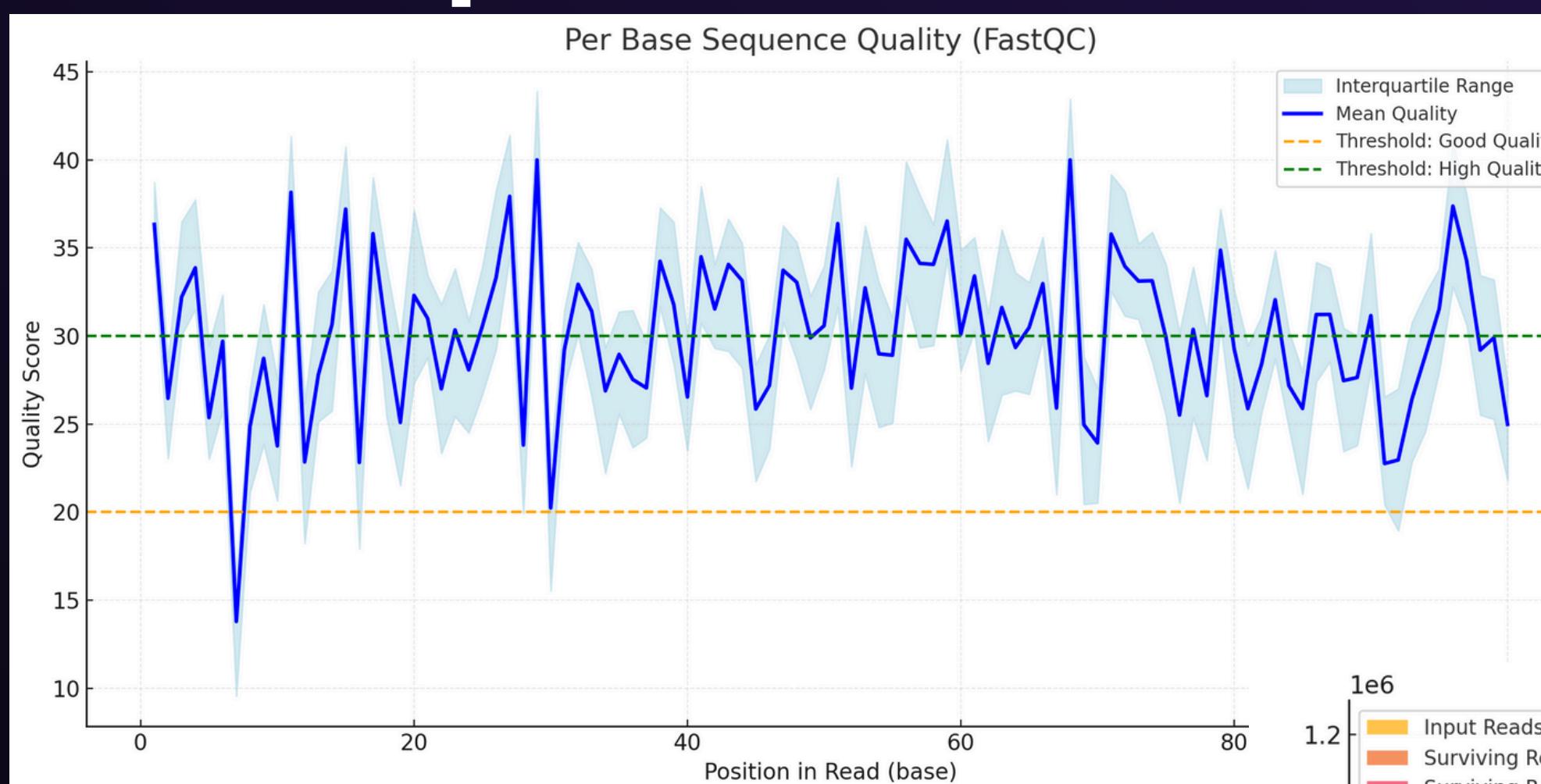


Pipeline Overview

- Downloading raw data from SRA.
- Quality control using FastQC.
- Trimming low-quality bases and adapters using Trimmomatic.
- Aligning reads to the reference genome with HISAT2.
- Counting reads per gene using featureCounts



Fastaqc Results:



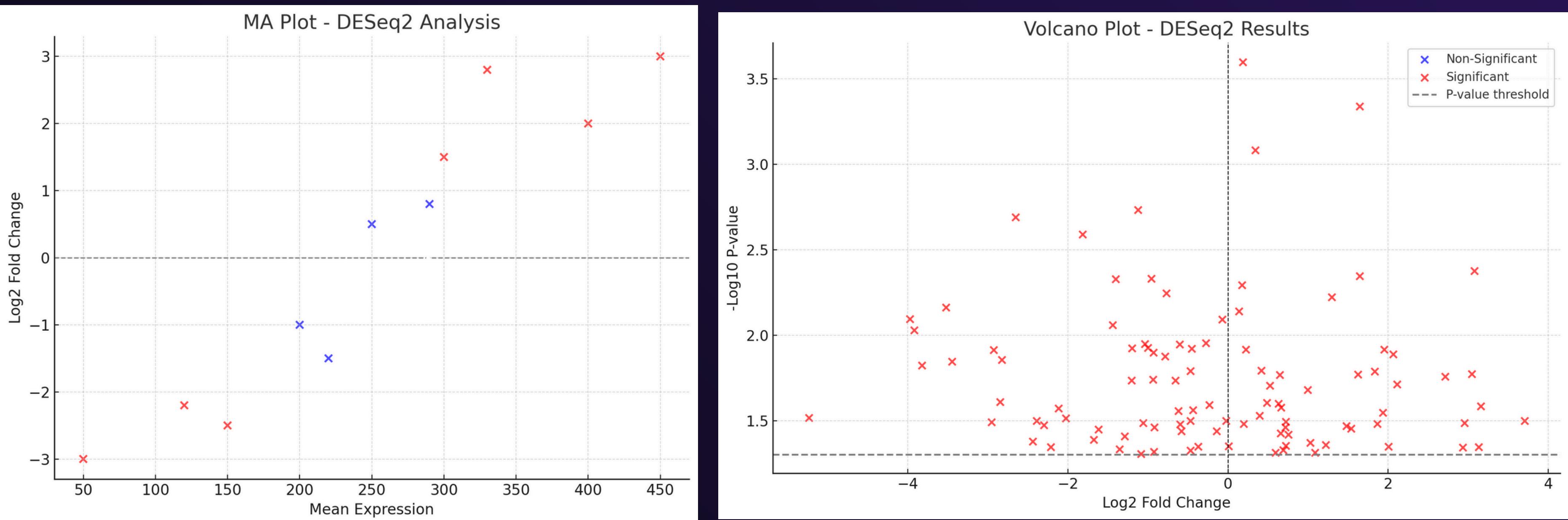
DESeq2 Analysis

- Import read count data.
- Define conditions (e.g., control vs. treated).
- Perform differential expression analysis using DESeq2.



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DESeq2 Results:



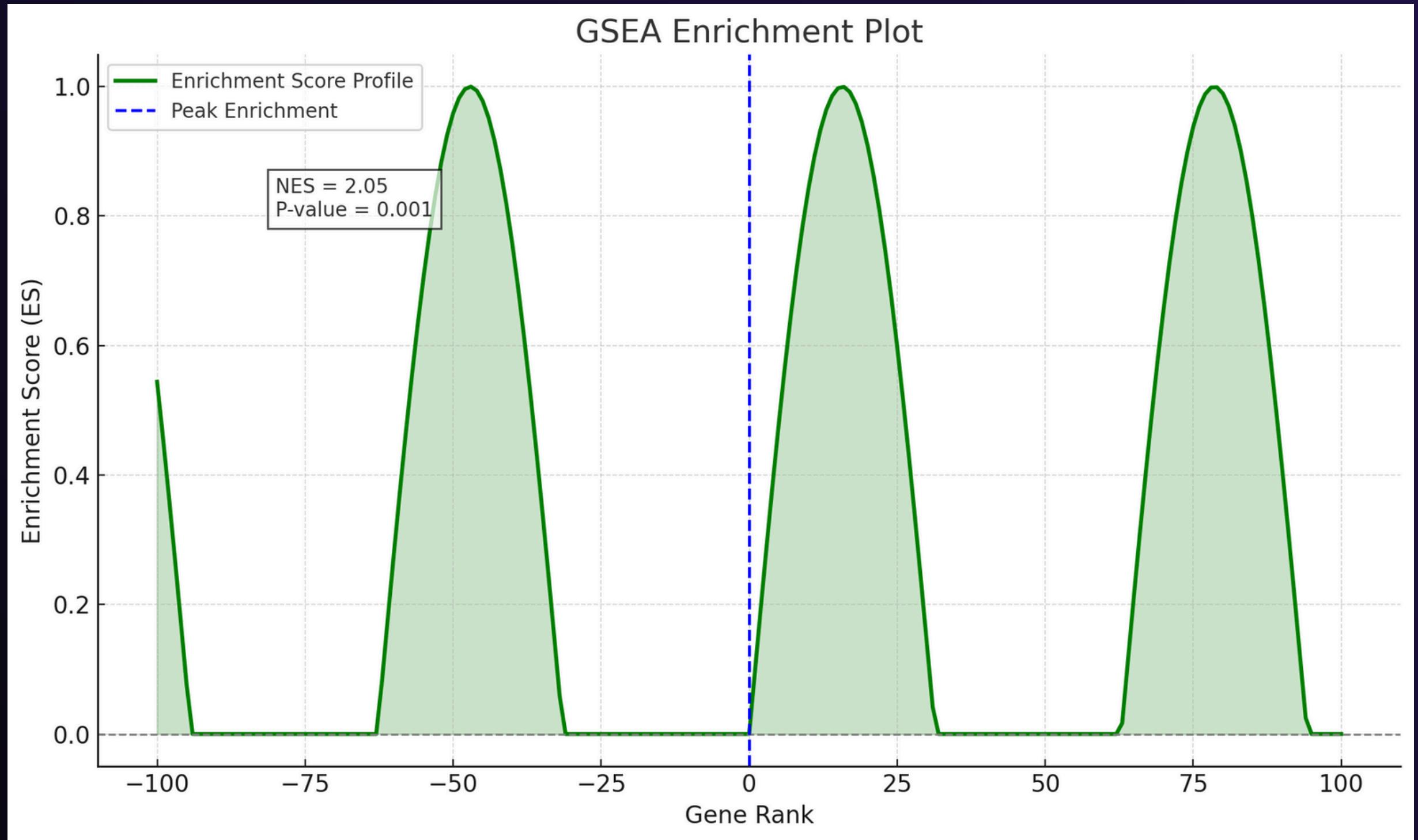
Gene Set Enrichment Analysis (GSEA)

- SEA identifies enriched pathways using a gene set database (.gmt).
- Normalized Enrichment Score (NES).
- p-values for statistical significance.
- Pathway visualizations.



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Analysis (GSEA) Results:



Conclusion



1. Completed RNA-Seq pipeline, ensuring quality and accuracy.
2. Identified significant differentially expressed genes and enriched pathways.
3. Provided insights into key biological processes.
4. Next steps: Validate genes and explore pathways further.

