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Master's Degree Project Report

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# 1 Abstract

Provide a concise summary of the project (150–300 words):

- Background
  - Objective
  - Methods
  - Key results
  - Conclusion
- 

## 2 1. Introduction

### 2.1 1.1 Background

Introduce the scientific or technical context of your project.

### 2.2 1.2 Problem Statement

Clearly define the research problem.

### 2.3 1.3 Objectives

- Primary objective
  - Secondary objectives
- 

## 3 2. Materials and Methods

### 3.1 2.1 Dataset Description

Describe:

- Data source
- Number of samples
- File format (FASTQ, BAM, etc.)

- Sequencing platform
- Read length

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### 3.2 2.2 Tool Parameters

Input Parameter	Value
Raw read data from current history	
Contaminant list	
Adapter list	
Submodule and limit specifying file	
Disable grouping of bases for reads > 50 bp	FALSE
Lower limit on sequence length shown in report	N/A
Length of k-mer analyzed	7

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### 3.3 2.3 Data Preprocessing

Describe all preprocessing steps:

- Quality filtering
  - Adapter trimming
  - Removal of low-quality reads
  - Deduplication (if applicable)
- 

### 3.4 2.4 Statistical / Computational Analysis

Describe:

- Quality metrics evaluated
  - K-mer analysis
  - Statistical methods
  - Software tools used
-

## **4 3. Results**

### **4.1 3.1 Quality Control Metrics**

Interpretation:

Explain what the results show.

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### **4.2 3.2 GC Content Analysis**

Interpretation:

Discuss GC distribution and potential bias.

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### **4.3 3.3 Adapter Contamination**

Interpretation:

Explain findings.

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### **4.4 3.4 K-mer Analysis**

Interpretation:

Discuss overrepresented sequences.

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## **5 4. Discussion**

Interpret your findings:

- Major quality issues
  - Comparison with expectations
  - Technical or biological implications
  - Impact on downstream analysis
- 

## **6 5. Limitations**

Discuss:

- Data limitations
  - Parameter sensitivity
  - Computational constraints
- 

## 7 6. Conclusion

Summarize:

- Overall data quality
  - Suitability for downstream analysis
  - Final recommendations
- 

## 8 7. Reproducibility

```
## R version 4.5.0 (2025-04-11)
## Platform: x86_64-pc-linux-gnu
## Running under: Debian GNU/Linux 13 (trixie)
##
## Matrix products: default
## BLAS/LAPACK: /usr/lib/x86_64-linux-gnu/libmkl_rt.so; LAPACK version 3.8.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C          LC_TIME=C
##  [4] LC_COLLATE=C          LC_MONETARY=C        LC_MESSAGES=C
##  [7] LC_PAPER=C            LC_NAME=C             LC_ADDRESS=C
## [10] LC_TELEPHONE=C        LC_MEASUREMENT=C      LC_IDENTIFICATION=C
##
## time zone: Europe/Amsterdam
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] dplyr_1.1.4  ggplot2_4.0.0 knitr_1.50
##
## loaded via a namespace (and not attached):
```

##	[1]	vctrs_0.6.5	cli_3.6.5	rlang_1.1.6	xfun_0.53
##	[5]	generics_0.1.4	S7_0.2.0	glue_1.8.0	htmltools_0.5.8.1
##	[9]	scales_1.4.0	rmarkdown_2.30	grid_4.5.0	evaluate_1.0.5
##	[13]	tibble_3.3.0	fastmap_1.2.0	yaml_2.3.10	lifecycle_1.0.4
##	[17]	compiler_4.5.0	RColorBrewer_1.1-3	pkgconfig_2.0.3	rstudioapi_0.17.1
##	[21]	farver_2.1.2	digest_0.6.37	R6_2.6.1	tidyselect_1.2.1
##	[25]	dichromat_2.0-0.1	pillar_1.11.1	magrittr_2.0.4	withr_3.0.2
##	[29]	tools_4.5.0	gtable_0.3.6		

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## 9 8. References

Add references here (BibTeX recommended if submitting PDF).

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