# Bioinformatics Somatic Mutation Analysis Report

## Introduction

This report summarizes the bioinformatics pipeline for identifying somatic mutations in tumor samples compared to normal tissue. The analysis involves alignment, variant calling, custom analysis, and annotation steps.

## Workflow Summary

1. Alignment: Tumor and normal samples were aligned to the human genome (hg38) using BWA.

2. Variant Calling: Somatic mutations were identified using Mutect2 and filtered.

3. Custom Analysis: Median background mutation level was calculated from normal tissue.

4. Annotation: Somatic mutations were annotated using snpEff.

## Results Summary

Total Somatic Variants Identified: 589

Median Background Mutation Level (AF): 0.5

Reads per Million Required: 1,000,000