

Bioinformatics Analysis Report

Comprehensive Analysis Report for Somatic Mutation Detection and Background Mutation Estimation

Workflow Summary:

1. Alignment of tumor and normal samples using BWA.
2. Somatic mutation identification using Mutect2 and VarScan2.
3. Custom analysis using Samtools and bcftools for mutation detection.
4. Annotation of somatic variants using snpEff.
5. Calculation of median background mutation level from the normal sample.

Results Summary:

- Total Somatic Variants Identified: 589
- Median Background Mutation Level (AF): 0.5
- Reads per Million Required to Confidently Call a Mutation: 1,000,000

Tools and Software Used:

- BWA for alignment
- Samtools and bcftools for mutation detection
- Mutect2 for variant calling
- snpEff for variant annotation
- Python (pandas) for custom analysis