1. Mosaic variants calling, target sequence variant calling, RNA variants calling

An html report:

1. Mulitqc for raw fastq
2. Multiqc for bam file
3. VariantQC for vcf file

For annotated vcf files with clinvar, gnomad dataset, we expect these analysis or plots,

1. <https://www.bioconductor.org/packages/release/bioc/vignettes/maftools/inst/doc/maftools.html#6_Reading_and_summarizing_maf_files>
2. <https://cancer.sanger.ac.uk/signatures/sbs/>

VCFprofile shiny

A comprehensive Shiny application for VCF analysis, mutation profiling, and statistical modeling that integrates multiple bioinformatics tools and databases.

## Features

### 🧬 Core Analysis

- \*\*VCF Processing\*\*: Support for VCF, VCF.GZ, and BCF files

- \*\*MAF Conversion\*\*: Automatic conversion from VCF to MAF format

- \*\*Multi-Sample Analysis\*\*: Handle single or multiple samples

- \*\*Genome Build Support\*\*: hg19 and hg38 compatibility

### 📊 Comprehensive Visualizations

- \*\*Mutation Summary\*\*: Overview plots and statistics

- \*\*Oncoplot\*\*: Gene mutation landscape visualization

- \*\*Rainfall Plot\*\*: Mutation distribution analysis

- \*\*TiTv Ratio\*\*: Transition/Transversion analysis

- \*\*Lollipop Plot\*\*: Protein domain mutation visualization

- \*\*Variant Classification\*\*: Distribution of mutation types

### 🔬 Advanced Analysis

- \*\*Signature Analysis\*\*: COSMIC mutational signatures

- \*\*Clinical Correlation\*\*: Survival and clinical data analysis

- \*\*Statistical Modeling\*\*: Stepwise regression with multiple models

### 📋 Reporting & Export

- \*\*Interactive Reports\*\*: HTML, PDF, Word formats

- \*\*Publication-Ready Plots\*\*: High-quality figure generation

- \*\*Data Export\*\*: MAF, VCF, CSV formats

- \*\*Comprehensive Documentation\*\*: Detailed analysis reports

**More general visualization R shiny: ggshiny**

Basic model: <https://dreamrs.github.io/esquisse/>

Advanced model: