

# MusVar: Output (v1.0.1)

## Introduction

The output consists of the raw output files from the TEMPO pipeline along with some simple post-processing of the mutation tables to filter for non-silent events.

## Directory Structure

```
{outdir}
├── post
│   ├── reports
│   │   ├── {projectNum}_mutationReport_v1.xlsx
│   │   └── output.html
│   ├── pipeline_info
│   │   ├── version.txt
│   │   └── output.html
│   └── plots
│       └── facets
└── tempo
    └── {projectNum}
        ├── bams
        ├── cohort_level
        ├── runlog
        └── somatic
```

## Tempo Output

The core output is from the [Tempo](#) research pipeline from MSKCC CMO Computational Science group. The raw output from Tempo is in the `tempo` subfolder, and a detailed description of these files can be found here: [//outputs.html](https://tempo.mskcc.org/outputs.html). *N.B.*, to save space, the `bam` and `snp-pileup` files are not delivered by default. If you require them, please contact us.

## Post folder

The post folder contains a number of useful files that give an overall summary of the pipeline and results.

# Reports

In the reports folder, there is a mutation summary report in excel format which has the following three sheets:

1. *Sample Data*: Provides summary information on samples including TMB and sample purity.
2. *Gene Stats*: Lists genes mutated in more than two samples, with mutation count, frequency, and affected samples.
3. *Mutations*: Displays a table of all non-silent mutations detected.

## Pipeline Info

Information on the pipeline including: `version.txt` file contains details about the software version used for analysis along with other run information and an HTML version of this document (`output.html`).

## Plots Folder

The plots folder contains copy number profile plots generated by FACET for each sample, providing convenient access to visual representations of copy number alterations.