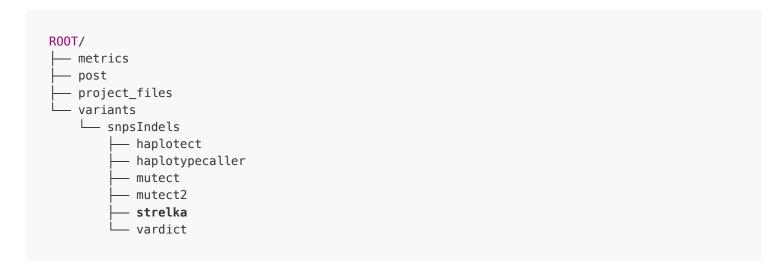
# **BIC@MSKCC M-IMPACT Pipeline: Output**

## Introduction

# **Directory Structure**



#### **Post**

These are the primary mutation call lists. They have the filtered annotated output.

### **Matrics**

The raw output of a number of metrics computed with the PICARD toolkit. The are summarized in the file: Proj\_15402\_QC\_Report.pdf and for the individual metrics there are .txt files which are the raw output from PICARD.

# Project\_files

The files used for running the pipeline. They contain the mapping data, pairing and grouping data.

## **Variants**

The folders here have the raw output of the various callers run in the pipeline. For the filtered results only the following callers are used: mutect, haplotype. But depending on the run there may be additional raw output included.