

## Djerba: Generating Clinical Genome Interpretation Reports for Cancer

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## Introduction: What is <u>Dierba</u>?

- A system to merge **genomic information** for a **cancer** patient into a **clinically actionable** report.
- Diverse set of inputs, with more under active development
- Named for a Mediterranean island, pronounced "jerba".

#### How is it made?





- Main codebase in **Python**
- Data analysis and plotting in R
- HTML templating in **Mako**
- Archiving reports in <u>CouchDB</u>

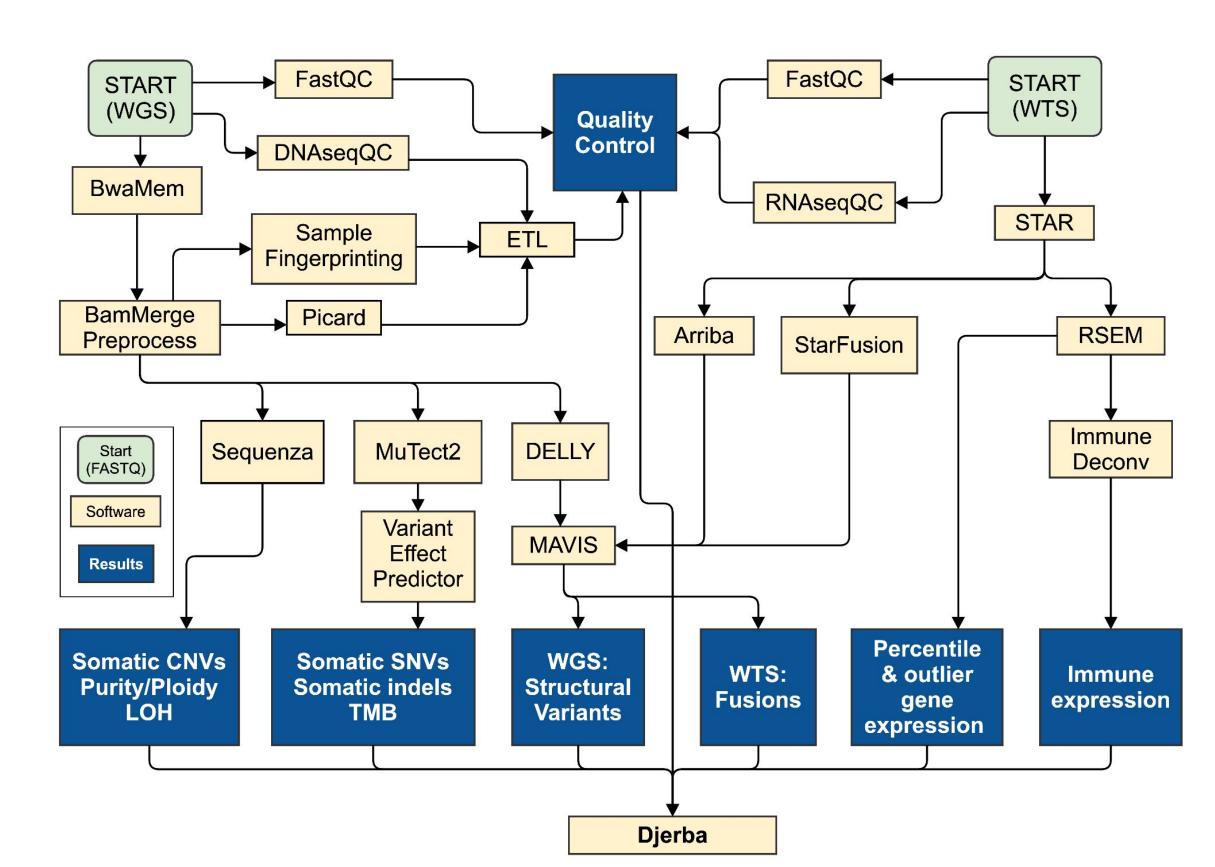




## Sequencing & Workflows







BCL files from

with sequencing.

Clinical reporting begins

tumour/normal Whole Genome Sequencing (WGS) and Whole Transcriptome Sequencing (WTS) are converted to FASTQ and input to the OICR clinical pipelines.

The pipelines are fully automated, implemented in WDL (Workflow **Description Language**) and run by the **Shesmu** and **Vidarr** systems developed at OICR.

Figure 1: Flowchart of WGS and WTS workflows and outputs at OICR.

# Machine Readable



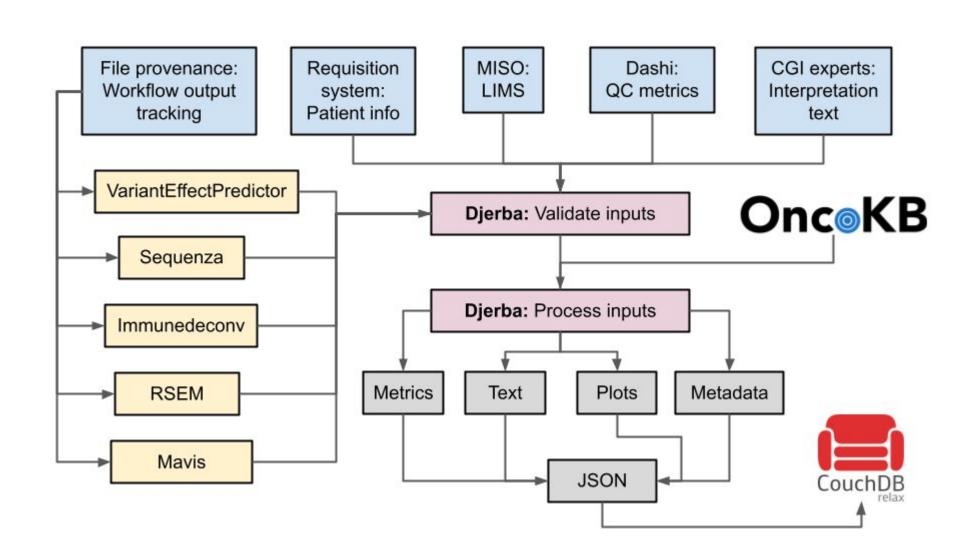


Figure 2: Workflow of the Djerba system to produce JSON from a range of inputs.

Djerba takes input from workflows, other OICR systems, and customized interpretation text; applies annotation from **OncoKB**; generates metrics and plots; and outputs a self-contained **JSON** document.

The JSON is uploaded to a CouchDB database, and used to make the human-readable clinical report.

The JSON data structure

document using Mako, a

populates an HTML

flexible and powerful

templating system for

converted to PDF to

produce the final clinical

Python. HTML is

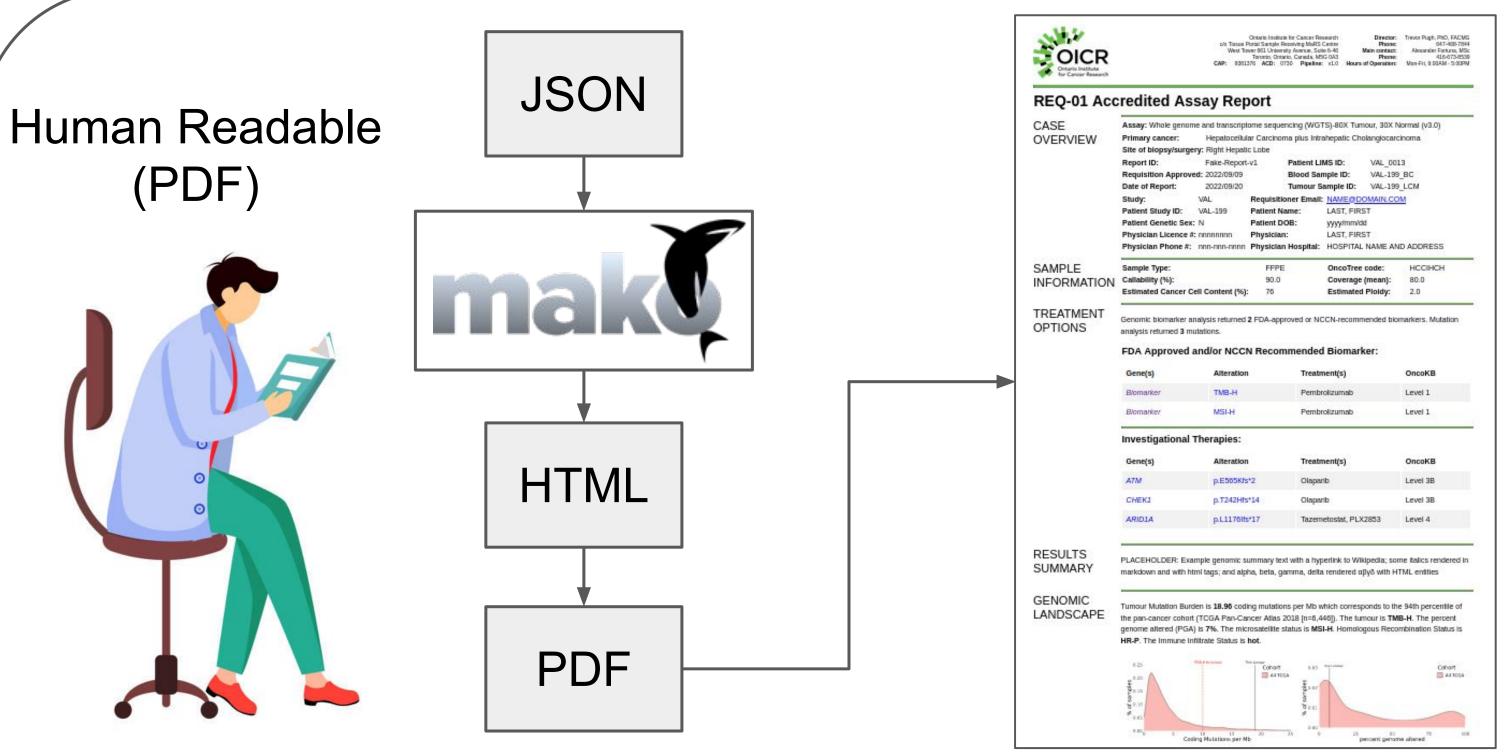
report document.

Djerba operations

nputs

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Djerba



inputs to build clinically

Figure 3: Workflow of the Djerba system to produce PDF from JSON.

## Summary

**Djerba** brings together a rich and diverse set of actionable reports.