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DRAGEN TruSight Oncology 500 ctDNA Analysis Software v1.2 on ICA

User Guide

For Research Use Only. Not for use in diagnostic procedures.

Table of Contents

Getting Started

You can execute DRAGEN™ TruSight™ Oncology 500 (TSO 500) ctDNA Analysis Software v1.2 on Illumina® Connected Analytics (ICA) v2.

Use the following instructions to configure an analysis run in the ICA interface using graphical mode or command-line interface (CLI). For more information about using ICA, refer to the Illumina Connected Analytics support site page. For more information about running a TSO 500 analysis on ICA, refer to the TruSight Oncology 500 ctDNA support site page.

Prerequisites

To use ICA to perform interactive data analysis, complete the following prerequisites:

1. Purchase ICA and enable ICA Flow.
2. Upload sequencing data files to an ICA project.
3. Make sure a TSO 500 bundle is available when setting up a project.

Analysis Modes and Configuration

In ICA v2, there are two modes available to launch analysis:

- Graphical user interface
- Command-line interface (CLI)

When starting a new analysis for DRAGEN TSO 500 ctDNA Analysis Software v1.2, select a TSO 500 project, TSO 500 pipeline, and the appropriate storage size.

For DRAGEN TSO 500 ctDNA Analysis Software v1.2 on ICA v2, a small storage size is typically not sufficient. Using the medium or large storage option is recommended.

Graphical Mode

In graphical mode, the following pipeline run settings must be configured to initiate a DRAGEN TSO 500 ctDNA Analysis Software v1.2 run successfully.

Name	Type	Required	Description
`sample_sheet`	File	Yes	The path to the `samplesheet.csv` file.
`run_folder`	Folder	Yes	The path to the run folder containing BCL files.

`fastq_folder`	Folder	No	The path to the FASTQ folder containing FASTQ files. If starting from BCL files, this folder is optional.
`resource_folder`	Folder	Yes	The path to the resource folder.
`sample_ids`	String	No	A comma-delimited list of sample IDs to process. Use this field to restrict analysis to a subset of sample IDs.
`first_tile_only`	Bool	No	A flag to specify using only the first flow cell tile.
`start_from_fastq`	Bool	No	A flag to specify starting from FASTQ files. This flag must be set to true if `fastq_folder` is provided. The flag must be set to false if starting from BCL files.

ICA CLI

The same configuration fields as described in *Graphical Mode* on page 1 must be modified for each ICA CLI run.

Analysis Methods

The DRAGEN TSO 500 ctDNA Analysis Software v1.2 uses the following tools to analyze sequencing data.

- Sample Sheet Validation
- Resource Verification
- Run QC
- FASTQ Generation
- FASTQ Validation
- Align Collapse Fusion Caller
- Stitched Realigned
- Copy Number Variant (CNV) Caller
- Microsatellite Instability (MSI) Scoring
- DNA Fusion Filtering
- Small Variant Calling
- Small Variant Filtering
- Phased Variant Calling
- Annotation
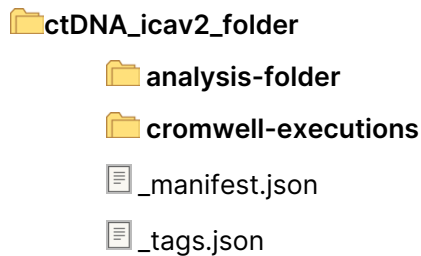- Tumor Mutational Burden (TMB) Scoring

- Max Somatic VAF
- Variant Matching
- Merged Annotation
- Contamination
- DNA QC Metrics
- Sample Analysis Results
- Combined Variant Output
- Metrics Output
- Clean Up

For more information on analysis methods, refer to *DRAGEN TruSight Oncology 500 ctDNA Analysis Software v1.2 User Guide (Document # 200017080)*.
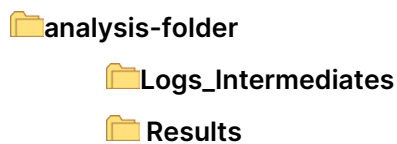
Output Folders

This section describes each output folder generated during analysis and where to find metric and analytic files when the pipeline is executed on ICA.

High-Level Folder Structure

📁 **ctDNA_icav2_folder**

    📁 **analysis-folder**

    📁 **cromwell-executions**

    📄 _manifest.json

    📄 _tags.json

Analysis Folder

The analysis folder contains the following two subfolders:

📁 **analysis-folder**

    📁 **Logs_Intermediates**

    📁 **Results**

Results—Contains the aggregated `MetricsOutput.tsv` file and the combined `dsdm.json` file at the root level. Additionally, the `Results` folder contains a subfolder for each sample.

📁 **analysis-folder/Results**
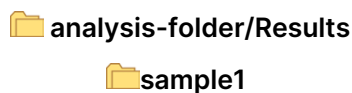
    📁 **sample1**

📁 **sample2**

📁 **...**

📄 dsdm.json

📄 MetricsOutput.tsv

Each sample subfolder contains files required for generating result metrics and the files relevant for analysis.

📁 **analysis-folder/Results/sample1**

📄 CombinedVariantOutput.tsv

📄 CopyNumberVariants.vcf

📄 Fusions.csv

📄 MergedSmallVariantsAnnotated.json.gz

📄 MergedSmallVariants.genome.vcf

📄 MergedSmallVariants.vcf

📄 TMB_Trace.tsv

Logs_Intermediates—Contains folders for each task in the DRAGEN TSO 500 ctDNA Analysis Software v1.2 on ICA pipeline. The folders contain a copy of all the relevant files required to create the metric output files and report files. Each folder for a pipeline task contains combined log files at the root level and subfolders for each sample. The sample-specific files include log files, console output, error output, and any intermediate results.

📁 **analysis-folder/Logs_Intermediates**

📁 **AlignCollapseFusionCaller**

📁 **Annotation**

📁 **Cleanup**

📁 **CnvCaller**

📁 **CombinedVariantOutput**

📁 **Contamination**

📁 **DnaFusionFiltering**

📁 **DnaQCMetrics**

📁 **FastqGeneration**

📁 **FastqValidation**

📁 **MaxSomaticVaf**

📁 **MergedAnnotation**

📁 **MetricsOutput**

📁 **Msi**

📁 **PhasedVariants**

📁 **ResourceVerification**

📁 **RunQc**

📁 **SampleAnalysisResults**

📁 **SamplesheetValidation**

📁 **SmallVariantFilter**

📁 **StitchedRealigned**

📁 **Tmb**

📁 **VariantCaller**

📁 **VariantMatching**

If an analysis run is unsuccessful, the analysis folder reflects the state of the system at the time of analysis failure. For example, if the analysis run was unsuccessful, the `Results` folder might not have been created and intermediate folders called `Analysis_Node_1` to `Analysis_Node_6` might be present.

Cromwell Executions

Cromwell log files are generated from the execution of the DRAGEN TSO 500 ctDNA Analysis Software v1.2 on ICA pipeline.

The files are grouped by the subworkflow and the pipeline task that is being executed.

Revision History

Document	Date	Description of Change
Document # 200015532 v00	August 2022	Initial Release

Document # 200015532 v00

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