AVENIO Tumor Tissue **CGP Kit**
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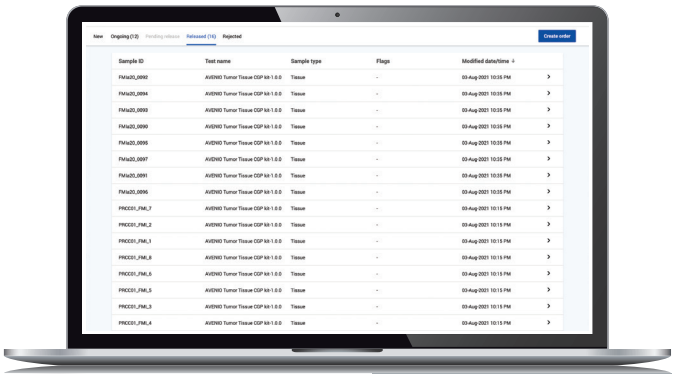
FoundationONE® Analysis Platform + AVENIO Connect Software

Secondary analysis and workflow manager software



Evidence-driven variant calling knowledgebase

- Built on insights from FMI's experience in profiling over 500,000+ samples.
- Continuously evolving based on evidence compiled by a multidisciplinary team of cancer biologists from scientific publications, conferences, and online databases (COSMIC, dbSNP, gnomAD, 1000 Genomes).

Broad genomic coverage

- Identifies all four types of genetic variants including Single Nucleotide Variants (SNV), InDels, Copy Number Alterations (CNA), and Rearrangements.
- Calculates genomic signatures such as TMB, MSI, and LOH.
- Variant calls in all captured regions, not limited to pre-defined set of hotspots.

Cloud-based computing for efficient analysis

- Converts uploaded BCL files to FASTQ, demultiplexes reads, and downsamples.*
- Enables regular updates to minimize downtime and manual intervention.

Confidence in high-quality results

- QC metrics, including median coverage and potential contamination, used to assess data quality.

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

* BCL files are the raw data files generated by the Illumina sequencers. FASTQ format is a text- based format for storing both a biological sequence and its corresponding quality scores.

TMB, tumor mutational burden. MSI, Microsatelite instability. LOH, loss of heterozygosity. QC, quality control.

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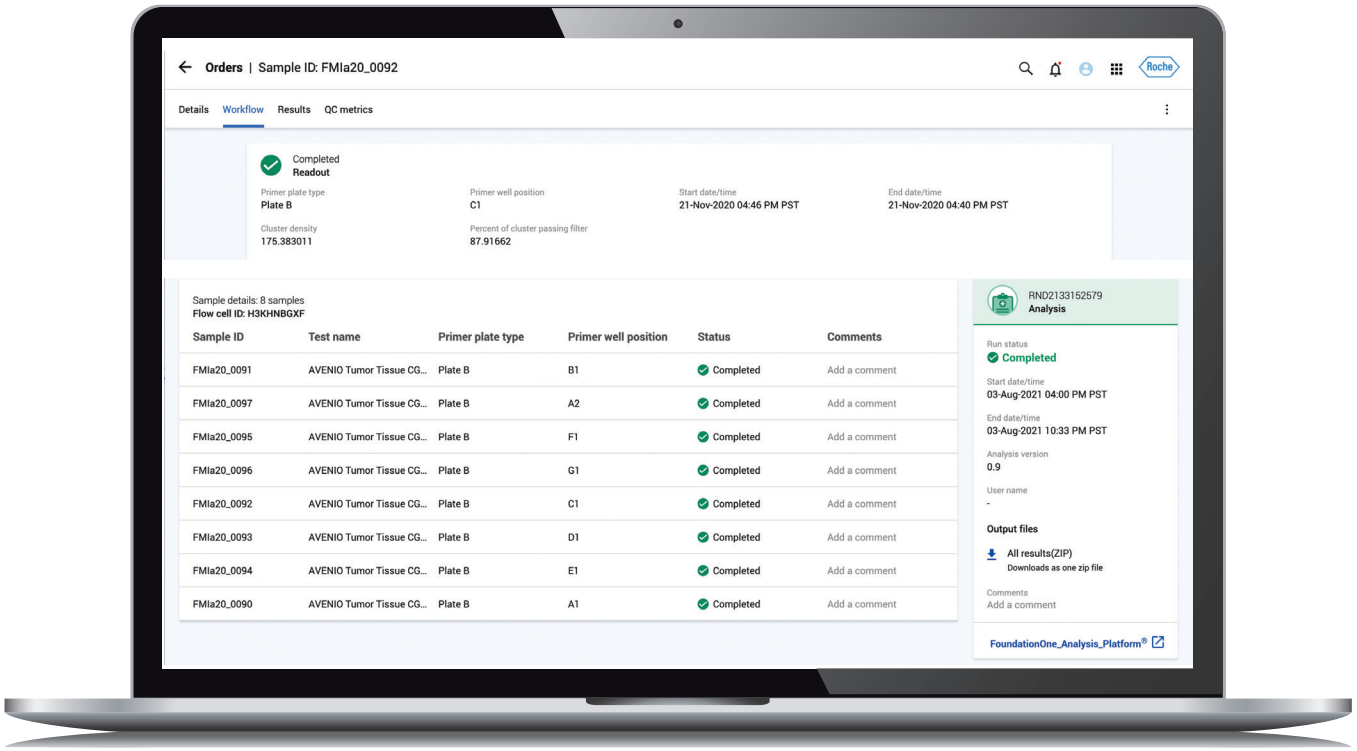
Gain access to clear information and results

Web application for download of analysis output files

- VCF (SNVs and InDels)
- JSON (CNAs, rearrangements, TMB, MSI, and LOH)
- CSV (QC metrics & variants combined)
- BAM (alignment file)



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SNV, single nucleotide variant. InDel, Insertion and deletion. CNA, copy number alteration. TMB, tumor mutational burden. MSI, Microsatellite instability. LOH, Loss of heterozygosity. QC, Quality control.

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For more information on FoundationONE® Analysis Platform and AVENIO Connect Software please reach out to your local Roche Sequencing representative.

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