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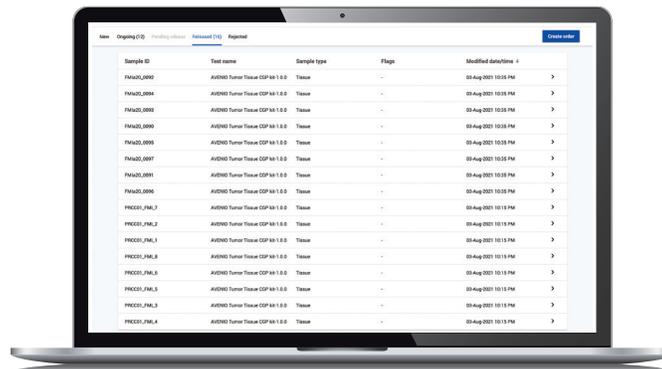

FoundationOne® Analysis Platform + AVENIO Connect Software
Secondary analysis and data management software

Thoroughly validated variant calling knowledgebase

- Built on insights from Foundation Medicine's experience in profiling over 1.3 million+ samples.[1]
- Continuously evolving based on evidence compiled from databases such as COSMIC, dbSNP, gnomAD, 1000 Genomes.[2]

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.
- Allows for seamless hardware integration.

Broad genomic coverage

- Identifies all four types of genomic variants including Single Nucleotide Variants, Insertions and Deletions, Copy Number Alterations, and Rearrangements.[3,4]
- Calculates genomic signatures such as TMB, MSI, gLOH, and newly added HRD signature (HRDsig).[3-5]
- Variant calls in all captured regions, not limited to pre-defined set of hotspots.

Confidence in high-quality results

- 14+ QC metrics, including median coverage and potential contamination, used to assess data quality.[4]
- Enables users to filter and annotate genomic data for criticality, relevance and biological significance.[3]

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TMB, tumor mutational burden. MSI, Microsatelite instability. gLOH, genomic loss of heterozygosity. HRD, homologous recombination deficiency. QC, quality control.
* 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.

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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, REs, TMB, MSI, gLOH and HRDsig)
- CSV (QC metrics & variants combined)
- BAM (alignment file)

1. Foundation Medicine Biopharma services. Available at: https://www.foundationmedicine.com/info/biopharma-overview (Accessed July 2024).
2. Foundation Medicine® About Us. Available at: https://www.foundationmedicine.com/info/detail/our-story (Accessed July 2024).
3. Data on file.
4. AVENIO Tumor Tissue CGP Kit V2 Instructions for Use June 2024.
5. Chen KT et al. A Novel HRD Signature Is Predictive of FOLFIRINOX Benefit in Metastatic Pancreatic Cancer. Oncologist. 2023 Aug 3;28(8):691-698. doi: 10.1093/oncolo/oyad178.

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SNV=Single Nucleotide Variant, InDel=Insertion and Deletion, CNA=Copy Number Alteration, TMB=Tumor Mutational Burden, MSI=Microsatellite Instability, gLOH=genomic Loss of Heterozygosity, HRDsig=Homologous Recombination Deficiency Signature, QC=Quality Control

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

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