AVENIO Oncology Analysis Software

Exceptional performance, minimal effort

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The AVENIO Oncology Analysis Software processes sequencing data from plasma and tissue samples run using the AVENIO ctDNA Analysis Kits V2 and AVENIO Tumor Tissue Analysis Kits V2.

The interface guides users confidently through the post-sequencing workflow. Intelligent bioinformatics with advanced proprietary algorithms and error suppression strategies deliver comprehensive results with proven accuracy and reproducibility.[1,2]

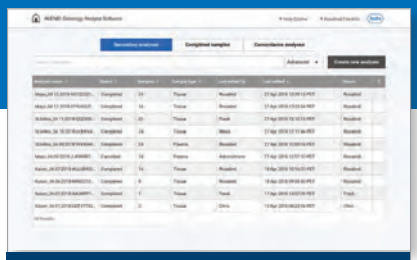
Powerful and intuitive, the AVENIO Oncology Analysis Software offers simplicity, efficiency and accuracy.

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

Log-in

Select plasma or tissue

Run settings



Analysis

Results

Reporting

Set up and run the analysis with ease

The AVENIO Oncology Analysis Software requires minimal expertise to set up and run an analysis. This allows laboratory and bioinformatics professionals to focus more of their time on the findings and insights, and less on managing information systems.

Intuitive user interface:

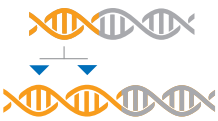
- Select plasma or tissue
- Offers two user types (Admin, Lab User)
- Provides real-time tracking of analysis status
- Enables filtering, custom annotation, and analytical concordance reporting between tissue and plasma
- Provides reports in PDF format, as well as variant results in VCF and BAM file formats.

With its ability to process approximately 800 million reads in less than a day, the AVENIO Oncology Analysis Software can be set up to run in the evening, delivering results ready for review in the morning.

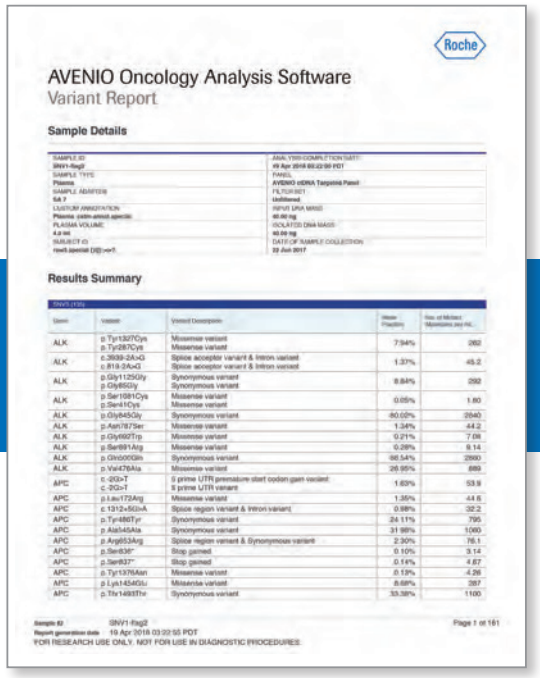
SNV
Single Nucleotide Variant

Indel
Insertion or Deletion

Fusion



CNV
Copy Number Variant



Detect all four mutation classes in a single DNA workflow

The software's bioinformatic algorithms and checkpoints have been optimized to enable accurate variant calls across all four mutation classes.[1]

Detect low frequency alleles with exceptional sensitivity and specificity

The AVENIO Oncology Analysis Software employs integrated digital error suppression (iDES) strategies in the ctDNA workflow, combining molecular barcodes with in silico error suppression techniques. This proprietary method enables detection of low frequency alleles down to 0.1% with exceptional sensitivity and specificity.[1,2] The tumor tissue workflow employs enzymatic error suppression and molecular barcodes for accurate detection of all four mutation classes from DNA only.

Performance metrics[1]

AVENIO ctDNA Analysis Kits V2

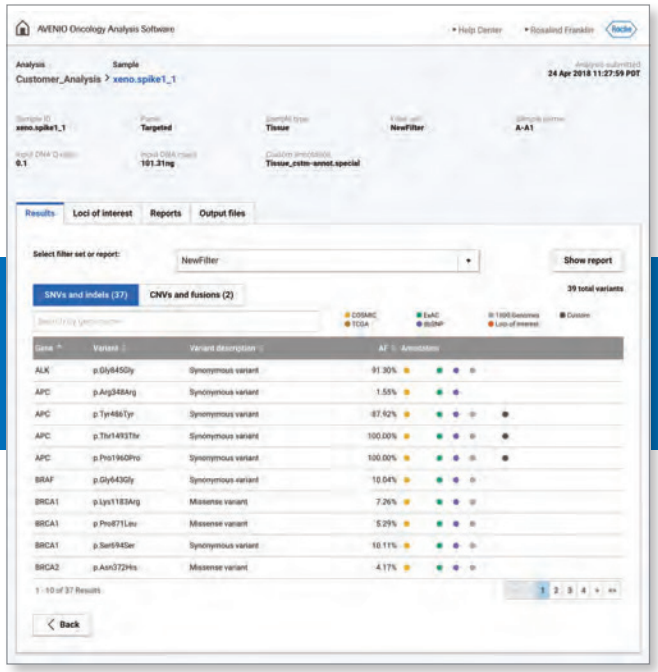
Mutant Allele Frequency/ Copy Number	SNVs		Indels		Fusions		CNVs**	
	0.5%*		1.0%*		1.0%			
AVENIO Tissue Kit V2	Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV
Targeted	>99%	>99%	>99%	>99%	>99%	>99%	SD	>99%
Expanded	>99%	>95%	>99%	>99%	>99%	>99%	SD	>99%
Surveillance	>99%	>99%	>99%	>99%	>99%	>99%	SD	>99%

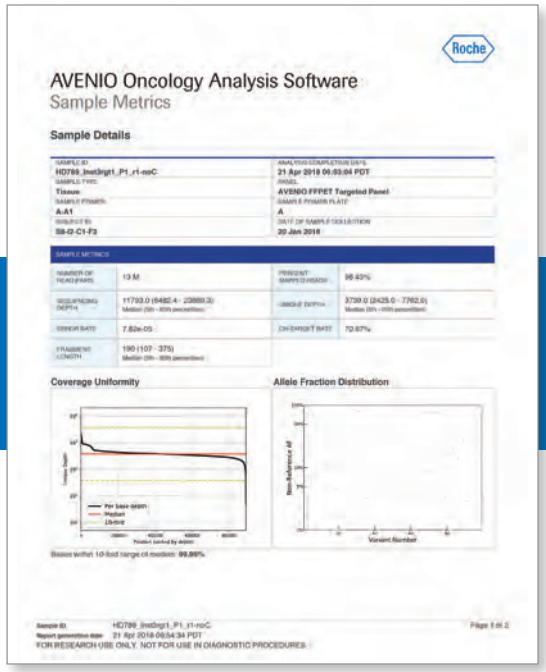
SD: Sample dependent; * Detects variants down to 0.1%; **Can detect ERBB2, EGFR and MET CNVs. Performance dependent on input sample type and input concentration(10 ng - 50 ng per reaction). Performance samples: Seraseq ctDNA Complete Mutation Mixes (SeraCare), healthy donor cfDNA. Sensitivity and Positive Predictive Value (PPV) metrics based on observed product performance. Sensitivity and PPV performance reported per variant. Sensitivity was determined using commercially available reference samples containing verified mutations at the stated allele frequencies. SNV performance data based on hotspot calls. The AVENIO ctDNA Analysis Kit V2 can achieve>99.99% per base specificity across each of the panels. Stated performance requires at least 40 million reads per sample for all AVENIO ctDNA Panels V2. Sequencing performed on an Illumina® NextSeq™ 500/550/550Dx instrument.

AVENIO Tumor Tissue Analysis Kits V2

Mutant Allele Frequency/ Copy Number	SNVs		Indels		Fusions		CNVs	
	5%*		5%		5%			
AVENIO ctDNA Kit V2	Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV
Targeted	>99%	>99%	>99%	>98%	>99%	>99%	SD	>99%
Expanded	>99%	>99%	>99%	>99%	>99%	>99%	SD	>99%
Surveillance	>99%	>99%	>99%	>99%	>99%	>99%	SD	>99%

SD: Sample dependent; Samples: FFPE tissue curls/ sections, DNA input: ≥20 ng of FFPET DNA, total DNA amount for each sample determined by input QC DNA. Sensitivity and Positive Predictive Value (PPV) metrics based on observed product performance. Sensitivity and PPV performance reported per variant. Sensitivity was determined using commercially available reference samples containing verified mutations at the stated allele frequencies. SNV performance is panel wide. Indel, Fusion and CNV performance based on whitelist variants. AVENIO Tumor Tissue Analysis Kits V2 achieve >99.99% per base specificity across each of the panels. Stated performance requires at least 20 million reads per sample for Targeted, Expanded and Surveillance Kits V2. Sequencing performed on an Illumina® NextSeq ™ 500/550/550Dx instrument.





Call mutations with confidence

Five leading oncology databases, a curated loci of interest list and a customizable annotation database are integrated into the AVENIO Oncology Analysis Software. This allows quick and easy access to trusted public resources for cross-referencing and verification of results:

- COSMIC
- TCGA
- ExAC
- dbSNP
- 1000 Genomes

These annotation databases can help users call mutations with increased confidence.

Control quality across the workflow

The AVENIO Oncology Analysis Software provides a sequencing quality report with key metrics such as sequencing depth, number of reads, on-target rate, coverage uniformity, and error rate to confirm quality at different stages in the workflow.

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1. Data on file with Roche.
2. Newman AM, Lovejoy AF, Klass DM, et al. Integrated digital error suppression for improved detection of circulating tumor DNA. Nature Biotechnology. 2016;34(5):547–555. doi:10.1038/nbt.3520.

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