

# AVENIO Oncology Analysis Software

*Exceptional performance, minimal effort*





## AVENIO Oncology Analysis Software

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

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.<sup>1,2</sup>

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

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



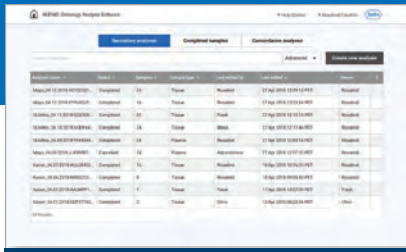
Log-in



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.







### AVENIO Oncology Analysis Software Variant Report

**Sample Details**

SAMPLE ID	AAA-1589-COMPLIATION-001
Run#-Flag#	09 Apr 2018 09:22:00 PDT
Sample Type	Panel
Platform	AVENIO ctDNA Tumor Panel
Sample ID: ADM1018	75.00001
SA F	48.00 ng
Library Amplification	Input DNA 1000
Platform: ddPCR-amplification	48.00 ng
PLASMA VOLUME	100.00 µL DNA 1000
Kit lot	48.00 ng
Run#-Flag#	DATE OF SAMPLE COLLECTION
run#-label-DE-001	22 Jun 2017

**Results Summary**

Gene	Variant	Variant Description	Allele Frequency	Pos. of Variant (Reference chr:pos)
ALK	p.Tyr1327Cys	Missense variant	7.94%	292
ALK	p.Tyr287Cys	Missense variant		
ALK	c.3039-2A>G	Splice acceptor variant & Intron variant	1.37%	45.2
ALK	c.818-28A>G	Splice acceptor variant & Intron variant		
ALK	p.Gly1125Gly	Synonymous variant	8.84%	292
ALK	p.Cys952Cys	Synonymous variant		
ALK	p.Ser1081Cys	Missense variant	0.05%	1.80
ALK	p.Ser341Cys	Missense variant		
ALK	p.Gly945Gly	Synonymous variant	90.05%	2940
ALK	p.Asp787Ser	Missense variant	1.34%	44.2
ALK	p.Gly962Tyr	Missense variant	0.21%	7.08
ALK	p.Ser981Arg	Missense variant	0.28%	8.14
ALK	p.Gln200Gln	Synonymous variant	98.54%	2960
ALK	p.Val728Asn	Missense variant	28.85%	492
APC	c.355>T	5 prime UTR premature start codon gain variant	1.65%	93.8
APC	c.355>T	5 prime UTR variant	1.35%	41.6
APC	p.Ile172Arg	Missense variant		
APC	c.1312-5G>A	Splice region variant & Intron variant	0.88%	32.2
APC	p.Tyr480Tyr	Synonymous variant	26.11%	795
APC	p.Asp454Asn	Synonymous variant	21.86%	1190
APC	p.Arg653Arg	Splice region variant & Synonymous variant	2.30%	76.1
APC	p.Ser633P	Stop gained	0.10%	3.14
APC	p.Ser837P	Stop gained	0.14%	4.67
APC	p.Tyr1376Asn	Missense variant	0.13%	4.26
APC	p.Lys1454Glu	Missense variant	8.65%	287
APC	p.The1488Thr	Synonymous variant	30.35%	1190

Sample ID: SNV1-Flag2  
Report generation date: 19 Apr 2018 03:22:05 PDT  
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## 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.<sup>1</sup>

### Performance metrics<sup>1</sup>

#### AVENIO ctDNA Analysis Kits

Mutant Allele Frequency/ Copy Number	SNVs		Indels		Fusions		CNVs	
	0.5%*		1.0%*		1.0%		At LOD**	
AVENIO Tissue Kit	Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV
<b>Targeted</b>	>99%	>99%	>99%	>99%	>99%	>99%	>99%	>99%
<b>Expanded</b>	>99%	>98%	>99%	>99%	>99%	>99%	>96%	>99%
<b>Surveillance</b>	>99%	>99%	>99%	>99%	>99%	>99%	>99%	>99%

\*Detects variants down to 0.1%. \*\*Samples tested at limit of detection (LOD): MET 2.3 copies in ctDNA; EGFR 3.2 copies in ctDNA; ERBB2 4.5 copies in ctDNA. Performance samples - cell line mixes, ctDNA 10 ng-50 ng input. Sensitivity and Positive Predictive Value (PPV) metrics based on typical product performance. Sensitivity and PPV performance reported per variant. SNV performance data based on hotspot calls; CNV performance based on ERBB2, EGFR and MET genes. Results above were tested at the stated mutant allele frequencies. The AVENIO ctDNA Analysis Kits also achieve >99.99% per base specificity across each of the panels. Stated performance requires at least 40 million reads per sample for Targeted Kit and 60 million reads per sample for Expanded and Surveillance Kits. Sequencing performed on an Illumina NextSeq 500 instrument.

#### AVENIO Tumor Tissue Analysis Kits

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

Samples: 2x10 µm FFPE tissue curls/sections DNA input: 20 ng of amplifiable DNA, total DNA amount for each sample determined by input QC. Sensitivity and Positive Predictive Value (PPV) metrics based on typical product performance. Sensitivity and PPV performance reported per variant. SNV performance is panel wide. Indel, Fusion and CNV performance based on whitelist variants. CNV performance data currently based on ERBB2 and EGFR genes. Results above were tested at the stated mutant allele frequencies. AVENIO Tumor Tissue Analysis Kits also achieve >99.999% per base specificity across each of the panels. Stated performance requires at least 20 million reads per sample for Targeted, Expanded and Surveillance Kits. Sequencing performed on an Illumina NextSeq 500 instrument.



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1. Data on file
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.

Published by:

**Roche Sequencing Solutions, Inc.**

4300 Hacienda Drive  
Pleasanton, CA 94588

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