

AVENIO Tumor Tissue Surveillance Kit

Longitudinal Tumor Burden Monitoring and MRD Detection



The AVENIO Tumor Tissue Surveillance Kit is an NGS assay that is designed to enable researchers to establish a baseline for tumor burden monitoring in lung and colorectal cancer, as well as to assess for minimal residual disease (MRD). This assay contains **471 frequently mutated regions** associated with the presence of disease across **197 genes, including those in the U.S. National Comprehensive Cancer Network (NCCN) Guidelines.¹**



Benefits

- Confidently report **all four mutation classes**: SNVs, indels, fusions, and CNVs.
- Delivers exceptional analytical performance supported by enzymatic error suppression and molecular barcodes.
- Uses an **intelligent algorithm** that applies population-scale data from multiple cancer databases to design a panel with **broad research subject coverage**.²
- Enables researchers to detect aberrations derived from a variety of solid tumor indications using a single,
 streamlined workflow[†]
- Establishes **baseline tumor profiles** to enhance subsequent tumor burden monitoring using ctDNA.

Research focus

Primary: Lung, Colorectal

Secondary: Breast, Gastric, Prostate, Glioma, Melanoma, Ovarian, Thyroid, and Pancreatic

Applications

- Tumor profiling
- Detection of resistance biomarkers
- Establishment of a baseline for tumor burden monitoring
- Detection of minimal residual disease (MRD)

Performance metrics²

	Mutation Class	SNVs		In	Indels Fusions		sions	CNVs	
	Mutant Allele Frequency/ Copy Number	5%		5%		5%		5 copies	
		Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV	Sensitivity	PPV
	Sensitivity and PPV	>99%	>99%	>99%	>99%	>99%	>99%	>99%	>99%

Samples: 2 x 10 µm FFPE tissue curls/sections DNA input: 20 ng of amplifiable DNA, total DNA amount for each sample determined by input QC

Source: Data on file.

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 loci of interest. 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.

Specifications

Panel size	198 kb
Sample size	2 x 10 µm FFPET curls/sections
DNA input*	20 ng of amplifiable DNA

Reactions per kit	24
Turnaround time	5 days from extraction to results

Assay targets

Seq Target	SNV	Indel*	Fusion"	CNV"
Selected Regions				
Selected Regions				
Selected Regions				
All Coding Regions				
All Coding Regions				
Selected Regions				
All Coding Regions				
All Coding Regions		•		•
Selected Regions		•		
	Selected Regions Selected Regions Selected Regions All Coding Regions All Coding Regions Selected Regions All Coding Regions All Coding Regions All Coding Regions	Selected Regions Selected Regions Selected Regions All Coding Regions All Coding Regions Selected Regions All Coding Regions All Coding Regions All Coding Regions All Coding Regions	Selected Regions Selected Regions Selected Regions All Coding Regions All Coding Regions Selected Regions All Coding Regions All Coding Regions All Coding Regions All Coding Regions All Coding Regions All Coding Regions	Selected Regions Selected Regions Selected Regions - All Coding Regions All Coding Regions Selected Regions All Coding Regions All Coding Regions All Coding Regions All Coding Regions - All Coding Regions - Selected Regions - All Coding Regions - All Coding Regions

Gene	Seq Target	SNV	Indel*	Fusion"	CNV"
KRAS	All Coding Regions				
MET	All Coding Regions				
NRAS	Selected Regions	•			
PDGFRA	Selected Regions				
RET	Selected Regions				
ROS1	Selected Regions				
TP53	All Coding Regions				
UGT1A1***	Selected Regions				

All coding regions are based on the longest transcript from Ensembl build 82

Frequently mutated select regions of these genes included to monitor tumor burden (n=180)

ABCC5	CDH9	DMD	GBP7	HTR2C	LRRC7	NRXN1	RNASE3	TMEM200A
ABCG2	CDKN2A	DNTTIP1	GJA8	IFI16	LRRTM1	NXPH4	ROBO2	TNFRSF21
ACTN2	CHRM2	DOCK3	GPR139	IL7R	LRRTM4	NYAP2	SEMA5B	TNN
ADAMTS12	CNTN5	DSC3	GRIA2	INSL3	LTBP4	OPRD1	SLC18A3	TNR
ADAMTS16	CNTNAP2	DSCAM	GRIK3	ITGA10	MAP2	P2RY10	SLC39A12	TRHDE
ARFGEF1	CPXCR1	EGFLAM	GRIN2B	ITSN1	MAP7D3	PAX6	SLC6A5	TRIM58
ASTN1	CPZ	EPHA5	GRIN3B	KCNA5	MKRN3	PCDH15	SLC8A1	TRPS1
ASTN2	CRMP1	EPHA6	GRM1	KCNB2	MMP16	PDYN	SLITRK1	UGT3A2
AVPR1A	CSMD1	EYS	GRM5	KCNC2	MTX1	PDZRN3	SLITRK4	USH2A
BCHE	CSMD3	FAM135B	GRM8	KCNJ3	MYH7	PGK2	SLITRK5	USP29
BPIFB4	CTNNB1	FAM151A	GSX1	KCTD8	MYT1L	PHACTR1	SLPI	VPS13B
BRINP2	CTNND2	FAM71B	HACD1	KEAP1	NAV3	PIK3CA	SMAD4	WBSCR17
BRINP3	CYBB	FAT1	HCN1	KIAA1211	NEUROD4	PIK3CG	SOX9	WIPF1
C6	DCAF12L1	FBN2	HCRTR2	KIF17	NFE2L2	PKHD1L1	SPTA1	WSCD2
C6orf118	DCAF12L2	FBXL7	HEBP1	KIF19	NLGN4X	POLE	ST6GALNAC3	ZC3H12A
CA10	DCAF4L2	FBXW7	HECW1	KLHL31	NLRP3	POM121L12	STK11	ZFPM2
CACNA1E	DCLK1	FCRL5	HS3ST4	KPRP	NMUR1	PREX1	SV2A	ZIC1
CDH12	DCSTAMP	FOXG1	HS3ST5	LPPR4	NOL4	RALYL	T	ZIC4
CDH18	DDI1	FRYL	HTR1A	LRFN5	NPAP1	RFX5	THSD7A	ZNF521
CDH8	DLGAP2	GBA3	HTR1E	LRP1B	NR0B1	RIN3	TIAM1	ZSCAN1

AVENIO family of NGS oncology assays

AVENIO Tumor Tissue Surveillance Kit is a part of the AVENIO family of NGS oncology assays which includes three tumor tissue assays and three corresponding ctDNA assays. By using the wider family of AVENIO assays, labs can obtain detailed molecular findings across all four mutation classes from both tissue and plasma samples.

Published by:

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Indianapolis, IN 46256

For more information about the AVENIO Tumor Tissue Analysis Kits,

*Required hardware: Illumina NextSeq 500/550 sequencers and Roche Oncology Analysis Server. NextSeq 500/550 instruments and associated sequencing reagents are manufactured and sold by Illumina and are not supplied by Roche.

please contact your Roche Sequencing representative.

qo.roche.com/assays

^{*}Total DNA amount for each sample determined by input QC

^{*} Indels are limited to variants in a pre-specified list of positions, referred to as "Loci of Interest", except for EGFR exon 19 long deletions, EGFR exon 20 long insertions, and MET long insertions, which are not restricted to a pre-defined set of Indels.

^{**} Detection of Fusions and CNVs are limited to variants in a pre-specified list of positions, referred to as "Loci of Interest" in the AVENIO analysis software.

^{***} UGT1A1*28 allele sequenced but not currently called by the AVENIO analysis software.

^{1.} National Comprehensive Cancer Network. http://www.nccn.org. October 15, 2016.

^{2.} Newman AM, Bratman SV, To J, et al. An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage. Nature Medicine. 2014;20(5):548-554. doi:10.1038/nm.3519

^{3.} Data on file.