Backed by the trusted expertise and proven technology of Roche and Foundation Medicine, Inc®.

The AVENIO Tumor Tissue CGP Kit V2 is part of Roche's broad CGP portfolio that offers flexible solutions and comprehensive support services to meet your research needs.

Proven Technology

Trusted Expertise

Comprehensive Portfolio

AVENIO Tumor TIssue CGP Kit V2 is for Research Use Only. Not for use in diagnostic procedures.

References:

1. Frampton GM et al. Nat Biotechnol. 2013;31:1023–1031.
2. FoundationOne®CDx Technical Label, 2023. Available at: https://info.foundationmedicine.com/hubfs/FMI%20Labels/FoundationOne_CDx_Label_Technical_Info.pdf (Accessed July 2024).
3. FoundationOne®Liquid Technical Specifications, 2023. Available at: https://assets.ctfassets.net/w98cd481qyp0/wVEm7VtICYR0sT5C1VbU7/fd055e0476183a6acd4eae6b583e3a00/F1LCDx_Technical_Specs_072021.pdf (Accessed July 2024).
4. FoundationOne®Heme Technical Specifications, 2021. Available at: https://assets.ctfassets.net/w98cd481qyp0/42r1cTE8VR4137CaHrsaen/baf91080cb3d78a52ada10c6358fa130/FoundationOne_Heme_Technical_Specifications.pdf (Accessed July 2024).
5. He J et al. Blood. 2016;127:3004–3014.
6. Clark TA et al. J Mol Diagn. 2018;20:686–702.
7. Chalmers ZR et al. Genome Med. 2017;9:34.
8. Schrock AB et al. Clin Cancer Res. 2016;22:3281–3285.
9. Ross JS et al. Gynecol Oncol. 2013;130:554–559.
10. Hall MJ et al. J Clin Oncol. 2016;34:1523–1523.
11. Data on file at Roche.
12. Mosele F et al. Ann Oncol. 2024;35(7):588-606. DOI:https://doi.org/10.1016/j.annonc.2024.04.005.
13. AVENIO Tumor Tissue CGP Kit V2 Instructions for Use June 2024.
14. AVENIO Connect v2.2 Instructions for Use June 2024.
15. navify® Mutation Profiler v2.6 Instructions for Use June 2024.
16. Choi, J., et al. (2023). 204P Performance assessment of a comprehensive genomic profiling (CGP) NGS kit across multiple study laboratories. Annals of Oncology, 34. https://doi.org/10.1016/j.annonc.2023.09.2927
17. Foundation Medicine Biopharma services. Available at: https://www.foundationmedicine.com/info/biopharma-overview (Accessed July 2024).
18. 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

MC-US-15628 August 2024

For more information on AVENIO Tumor Tissue CGP Kit V2 visit go.roche.com/aveniocgpkit or contact your local Roche Sequencing representative

AVENIO Tumor Tissue CGP Kit V2
Powered by **FOUNDATION MEDICINE**

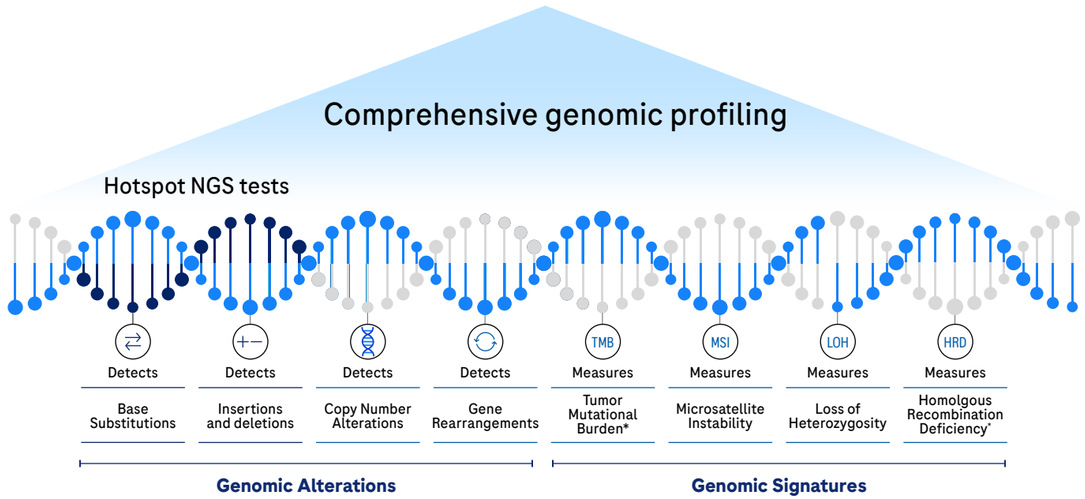
AVENIO Tumor Tissue CGP Kit V2

Powered by **FOUNDATION MEDICINE**

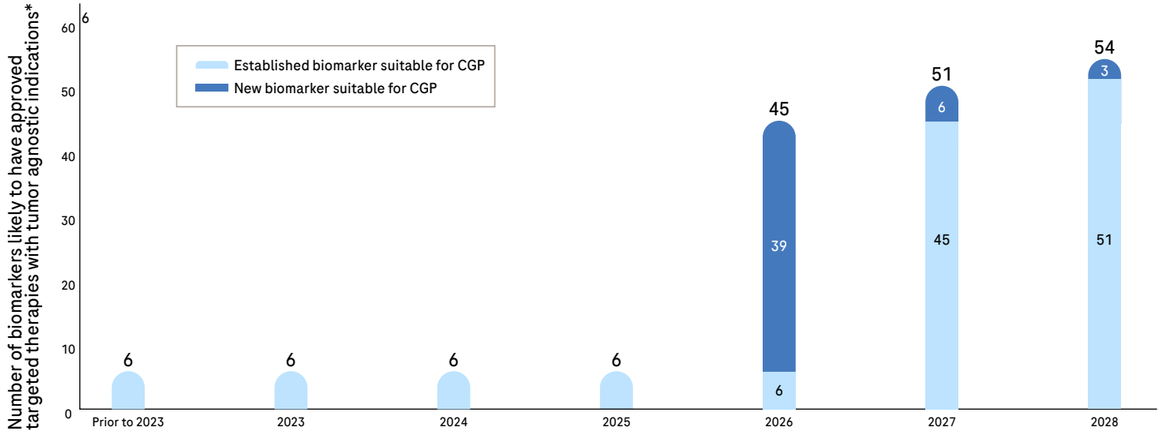
For Research Use Only. Not for use in diagnostic procedures.

The power of precision medicine

CGP offers the greatest insights from a single assay leveraging NGS to broadly analyze regions of the tumor genome that other assays miss.[1-10]



The majority of cancer research is now focused on targeted therapies and, as a result, CGP is becoming the tool of choice.[11]



Analysis includes Phase 1, Phase 2 and Phase 3 trials initiated before October 2023.

*Multiple secondary sources used to cross validate information, including Trialtrove, clinicaltrials.gov, EudraCT, ChiCTR; FDA approval timeline estimation based on Ph3 PCD + 8 months review; analysis based on current Phase 1, Phase 2 and Phase 3 trials with inclusion criteria requiring patient selection based on alterations to specific biomarkers; assumption made that all ongoing trials will lead to approval.

ESMO Precision Medicine Working Group recommends to carry out NGS in clinical research center in order to accelerate clinical research.[12]

For Research Use Only. Not for use in diagnostic procedures.
ESMO, European Society for Medical Oncology.

The enhanced AVENIO Tumor Tissue CGP Kit V2

Leveraging the FoundationOne® Analysis Platform for bioinformatics and the AVENIO workflows, the kit is part of Roche's broad portfolio that offers flexible CGP solutions and support services to meet your research needs. With the AVENIO Tumor Tissue CGP Kit V2, you can get deeper genomic insights about solid tumors right in your lab – and advance discoveries in cancer research.

Leverage the power of Roche and Foundation Medicine®

Experts in personalized medicine and comprehensive genomic profiling: 800+ peer reviewed publications, 1.3 million+ clinical samples reported.[11,17]

Unlock high-quality meaningful Genomic Insights

Analyzes 335 relevant genes, four classes of genomic alterations, and complex genomic signatures including TMB, MSI, gLOH and the newly added HRDsig.[11,13,18]

Utilize fast and convenient NGS workflows

One workflow from DNA extraction to data analysis. Fast 2-day library prep and short 1-hour ligation with a total 5-day turnaround time from DNA extraction to result generation.[11,13]

For Research Use Only. Not for use in diagnostic procedures.
TMB - Tumor Mutational Burden, MSI - Microsatellite Instability, gLOH - genomic Loss of Heterozygosity, HRDsig - Homologous Recombination Deficiency, ESMO - European Society for Medical Oncology.
*Compatible with tertiary analysis solutions such as navify® Mutation Profiler to provide meaningful genomic insights. AVENIO Tumor Tissue CGP Portfolio and navify® Mutation Profiler are For Research Use Only. Not for use in diagnostic procedures. Tertiary analysis with navify® Mutation Profiler is not part of the AVENIO Tumor Tissue CGP kit V2 and may be purchased as an add on.

Key features and benefits

AVENIO Tumor Tissue CGP Kit V2 enables users to be at the forefront of scientific advancements. It brings to you comprehensive panel content and robust performance, while incorporating efficient NGS workflows, up-to-date thoroughly validated bioinformatics algorithms, and successful incorporation of a new complex biomarker, pan-tumor HRD signature (HRDsig). The kit not only helps unlock meaningful genomic insights from your samples but it also enables you to filter and annotate them for criticality, relevance and biological significance.[11,13]

AVENIO Tumor Tissue CGP Kit V2 Features	User benefits
Comprehensive panel aligned with the FoundationOne® CDx panel design	Unlock high-quality meaningful genomic Insights from proven as well as emerging biomarkers.[11,13]
Up-to-date, thoroughly validated bioinformatics pipeline via FoundationOne® Analysis Platform	Simplify complex secondary analysis by leveraging an industry leading bioinformatics algorithm to filter and annotate genomic data for criticality, relevance and biological significance.[11,13]
Pan-cancer HRD signature based on Foundation Medicine's database, which contains comprehensive, de-identified genomic data from >600,000 samples.	Leverage a pan-cancer HRD signature score developed by Foundation Medicine (using 100+ copy number features) in the same workflow with no additional purchase required.[11,13,18]
Reduced sequencing costs due to increased multiplexing	Maximize your flowcell usage by sequencing up to 12 samples per flowcell and obtain high quality sequencing data.[11,13]
Short 2-day library preparation with a 5 day turnaround time	Utilize optimized workflows to meet your laboratory's schedule needs.[11,13]
Fast and efficient DNA extraction	Incorporate safe DNA extraction xylene-free workflow.[11,13]
Optimized compatibility with navify® Mutation Profiler for tertiary analysis	Use the same vendor for your entire CGP workflow from wet lab to secondary analysis as well as tertiary analysis.[15]
Easy data management through AVENIO Connect Software	Leverage streamlined data management for a smooth user experience.[14]

For Research Use Only. Not for use in diagnostic procedures.
FFPET, Formalin-Fixed Paraffin-Embedded Tissue; SNV, single-nucleotide variants; Indel, insertions and deletions; CNA, copy number alterations; TMB tumor mutational burden; MSI, microsatellite instability; LOH, loss of heterozygosity

Leveraging proven technology: a powerful combination

For laboratories that perform research on solid tumors.

AVENIO Tumor Tissue Workflow

An integrated end-to-end NGS workflow solution with high performance[11,13] for in-house research. The AVENIO Tumor Tissue CGP Kit V2 workflow enables a fast 2 day library prep, short 1-hour ligation as well as robust DNA extraction quality and yield of challenging FFPE tissues.[11,13]

Sample Type

- FFPE tissue curls or slides
- Extracted FFPET DNA

AVENIO Tumor Tissue CGP Panel V2

Expertly curated 335-gene panel that is aligned with the FoundationOne® CDx panel design.[11,13]

- Detects four classes of genomic alterations: SNVs, InDels, REs, and CNAs
- Detects genomic signatures TMB, MSI, gLOH, and HRDsig

FoundationOne® Analysis Platform

Expertly curated, cloud-based secondary analysis software makes it easy for you to analyze samples to identify relevant variants across multiple solid tumor types. This thoroughly validated variant calling knowledge base, is built on Foundation Medicine's proprietary algorithms based on insights from 1.3 million + high quality genomic profiles.[11,13,17]

- Broad genomic coverage
- Confidence in high-quality results
- Filtered variant calls and QC metrics
- Secure Cloud-based computing for efficient data analysis

For Research Use Only. Not for use in diagnostic procedures.
*Data on file at Roche.
FFPET, Formalin-Fixed Paraffin-Embedded Tissue; SNV, single-nucleotide variants; Indels, insertions and deletions; CNA, copy number alterations; TMB - Tumor Mutational Burden, MSI - Microsatellite Instability, gLOH - genomic Loss of Heterozygosity, HRDsig- Homologous Recombination Deficiency.

An integrated solution for an end-to-end hybrid-capture workflow

The efficient, high quality workflow of the AVENIO Tumor Tissue CGP Kit V2 includes all sample preparation reagents, input QC, robust bioinformatics and secondary analysis, all from one trusted source. It has been optimized to manage hands-on time, offer workflow flexibility depending on sample complexity allowing you to obtain reliable genomic insights from solid tumors within 5 days.[11,13]

5 day workflow from DNA isolation to result generation[13]

Day 1	Day 2	Day 3	Day 4	Day 5
DNA Isolation	Library Prep	Target Enrichment	Sequencing	Data Analysis

AVENIO Tumor Cleanup and Capture Beads V2

AVENIO Tumor DNA Isolation & QC Kit
- Extraction enzymes & buffers
- DNA elution buffer
- QC PCR reaction mix
- QC PCR primer mixes
- QC PCR DNA standard

AVENIO Tumor Library Prep Kit V2
- DNA polishing enzyme
- Fragmentation buffer & enzyme
- DNA preparation buffers & enzymes
- Ligation buffer & DNA ligase
- PCR Reaction Mix
- Universal adapters

AVENIO Tumor Sample Primers – Plate A or Plate B
- Plate A includes 24 primer pairs, **OR**
- Plate B includes 24 different primer pairs

AVENIO Tumor Enrichment Kit V2
- Universal enhancing oligos
- Hybridization supplement & buffers

AVENIO Tumor Tissue CGP Panel Kit V2
- Probes

AVENIO Post -Hybridization Kit V2
- Wash buffers
- PCR reaction mix
- PCR primer mix
- Bead wash buffer

AVENIO Connect Software

Compatible with: Illumina NextSeq 500/550/550Dx (RUO mode) System

Secondary Analysis

AVENIO Connect Software
- User interface, case and results management
- RLX – Connect (Axeda agent)

VMWare
- VM vSphere Standard*

FoundationOne® Analysis Platform
- Secondary analysis pipeline
- Viewed as a workflow / application in the Connect Software

Tertiary Analysis

Optimized compatibility with navify® Mutation Profiler for tertiary analysis**

For Research Use Only. Not for use in diagnostic procedures.
QC, Quality control.
NextSeq, instruments and associated sequencing reagents are manufactured and sold by Illumina® and are not provided by Roche. *Virtual Machine Gateway is not provided by Roche.
**navify® Mutation Profiler is for Research Use Only, not for use in diagnostic procedures. Tertiary analysis with navify® Mutation Profiler is not part of the AVENIO Tumor Tissue CGP kit V2 and may be purchased as an add on.

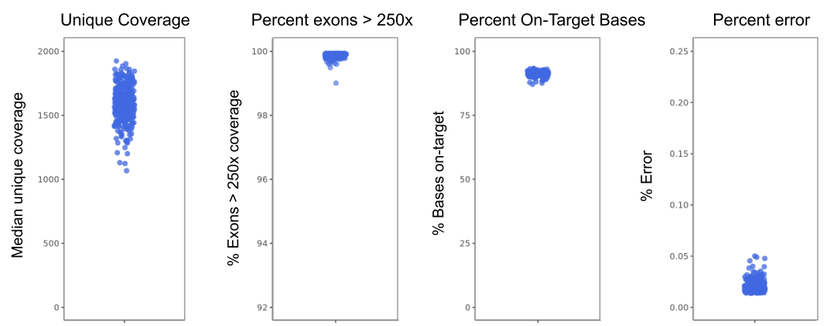
Robust analytical variant detection performance across genomic alterations and signatures

Sequencing libraries were prepared from 316 FFPE tissue-derived DNA samples on the Illumina NextSeq 550 high-throughput sequencing flowcell using the AVENIO Tumor Tissue CGP Kit V2. The percentage of expected variants detected by AVENIO Tumor Tissue CGP Kit V2 showed a high degree of alignment with the reference method for each alteration classification including short variants, rearrangements, copy number alterations as well as in genomic signatures such as MSI, TMB, gLOH and HRDsig as shown in the table below.[11,13]

Classification	Detected Variants/Signatures
Short Variants	99.7%
Rearrangements	89.9%
CNA	99.8%
MSI high	100%
TMB high	100%
gLOH high	100%
HRDsig positive	91.7%

Results are from 60 million reads per sample on Illumina NextSeq 550 (~12 samples per flowcell) to determine performance by comparing to the reference method. For this analysis, high or positive signatures were defined as follows: MSI-High ≥ 0.0124, TMB-High ≥ 10.0 mutations/Mb, gLOH-Positive ≥ 0.16, and HRDsig-Positive ≥ 0.7. Samples with scores in the marginal ranges, MSI (0.0041-0.0124; "equivocal" status), TMB (8.0-12.0 mutations/Mb), and gLOH (0.14-0.18), were excluded.The AVENIO Tumor Tissue CGP Kit V2 is a Research Use Only assay and should not be used for diagnostic procedures. Users must determine the complex signature cut-offs based on their research needs.

High performance as demonstrated by key sequencing metrics

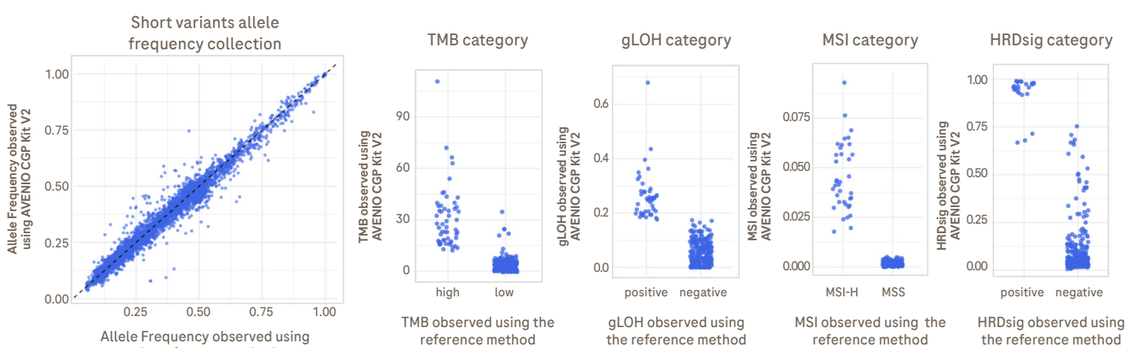


The graphs show sequencing QC metrics obtained through the FoundationOne® Analysis Platform. Results are from 60 million reads per sample (316 FFPE tissue- derived DNA samples) on Illumina NextSeq 550 (~12 samples per flowcell)[11].

For Research Use only. Not for use in diagnostic procedures.
MSI- Microsatellite Instability, TMB- Tumor Mutational Burden, gLOH- genomic Loss of Heterozygosity, HRDsig- Homologous Recombination Deficiency signature

Strong agreement in allele frequencies and signature scores to the reference method

Sequencing libraries were prepared from 316 FFPE tissue-derived DNA samples on the Illumina NextSeq 550 high-throughput sequencing flowcell using the AVENIO Tumor Tissue CGP Kit V2. Results were compared with the analytical performance of the reference method and are shown below.[11]



Results are from 60 million reads per sample on Illumina NextSeq 550 (~12 samples per flowcell) to determine performance by comparing to the reference method. For this analysis, high or positive signatures were defined as follows: MSI-High ≥ 0.0124, TMB-High ≥ 10.0 mutations/Mb, gLOH-Positive ≥ 0.16, and HRDsig-Positive ≥ 0.7. Samples with scores in the marginal ranges, MSI (0.0041-0.0124; "equivocal" status), TMB (8.0-12.0 mutations/Mb), and gLOH (0.14-0.18), were excluded. The AVENIO Tumor Tissue CGP Kit V2 is a Research Use Only assay and should not be used for diagnostic procedures. Users must determine the complex signature cut-offs based on their research needs.

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

Reliable overall kit performance across disease ontologies for all four mutation classes

Libraries were prepared from 316 FFPE tissue-derived DNA samples by the AVENIO Tumor Tissue CGP Kit V2. The expected and observed number of samples from a subset of key disease ontologies and gene mutations are shown below. The range of the allele fraction, copy number, or breakpoint reads of those samples, as measured by the AVENIO Tumor Tissue CGP Kit V2 analysis, are shown below.[11]

Disease Ontology	Genes	Mutations	No. Samples expected*	No. Samples observed	Measured Allele Fraction, Copy Number or Breakpoint Reads
non-small cell lung carcinoma	EGFR	T790M	6	6	8.4% - 51.8%
non-small cell lung carcinoma	EGFR	L858R	11	11	8.6% - 34.0%
non-small cell lung carcinoma	EGFR	Exon 19 deletion	9	9	15.0% - 61.7%
non-small cell lung carcinoma	EGFR	G719A	1	1	29.8%
non-small cell lung carcinoma	MET	Exon 14 splice mutation	2	2	21.9% - 83.3%
non-small cell lung carcinoma	BRAF	V600E	7	7	7.6% - 17.6%
colon adenocarcinoma (crc)	BRAF	V600E	9	9	8.1% - 51.5%
melanoma	BRAF	V600E/V600K	11	11	8.7% - 65.7%
colon adenocarcinoma (crc)	KRAS	Codon 12 mutation	9	9	13.0% - 47.4%
colon adenocarcinoma (crc)	KRAS	Codon 13 mutation	4	4	35.1% - 60.5%
colon adenocarcinoma (crc)	KRAS	Codon 61 mutation	3	3	29.8% - 34.2%
colon adenocarcinoma (crc)	NRAS	Codon 61 mutation	2	2	16.5% - 43.9%
breast cancer	PIK3CA	C420R/E542K/E545D/ Q546K/H1047R/H1047L	14	14	1.3% - 61.9%
breast cancer	ERBB2	ERBB2 amplification	8	8	5 - 147 copies
non-small cell lung carcinoma	ALK-ELM4	EML4-ALK fusion	5	5	3.2% - 7.6% / 18 - 41 reads

For Research Use Only. Not for use in diagnostic procedures.
FFPE, Formalin-fixed paraffin-embedded.
* Variant detection expected based on the reference method