

Solid Tumor Mutation Panel, Sequencing

Last Literature Review: August 2022 Last Update: December 2025

Individuals diagnosed with a solid tumor cancer may benefit from testing for genetic mutations and variants that can affect treatment options and prognosis. Solid tumor cancers that may benefit from this testing include melanoma,¹ gastrointestinal stromal tumors (GISTs),² hepatocellular carcinomas,³ primary brain tumors,⁴ colorectal,⁵ bladder,⁶ and thyroid cancer,⁷ among others. Testing can be useful at initial diagnosis or in the presence of refractory disease.

Disease Overview

Diagnosis

- Genetic targets contained in the panel, including extended *RAS* targets,⁵ are relevant across the spectrum of solid tumors.
- Identification of one or more variants may aid in diagnostic subclassification.

Prognosis and Treatment

- Certain gene variants may have prognostic significance.
- Certain gene variants may confer sensitivity or resistance to available targeted therapies.

Genetics

Genes

AKT1, ALK, APC, ATM, BRAF, CDH1, CDKN2A, CTNNB1, DDR2, EGFR, ERBB2, ERBB4, EZH2, FBXW7, FGFR1, FGFR2, FGFR3, GNA11, GNAQ, GNAS, HRAS, IDH1, IDH2, KDR, KIT, KRAS, MAP2K1, MET, MTOR, NOTCH1, NRAS, NTRK1, PDGFRA, PIK3CA, PTEN, RB1, RET, ROS1, SMAD4, SMO, STK11, TERT promoter, TP53, VHL

Variants Detected

- This test is intended to detect somatic mutations, but germline alterations may also be detected.
- The assay does not distinguish between somatic and germline findings.
- Consultation with a genetic counselor is advised if there is any clinical suspicion for a germline alteration.

Solid Panel Targeted Regions

Gene	Accession No.	Targeted Exons
<i>AKT1</i>	NM_001014431.1	3, 4, 6
<i>ALK</i>	NM_004304.4	16-29
<i>APC</i>	NM_000038.5	16 ^a
<i>ATM</i>	NM_000051.3	8, 9, 12, 17, 26, 34-36, 39, 50, 54-56, 59, 61, 63
<i>BRAF</i>	NM_004333.4	11, ^b 14, 15
<i>CDH1</i>	NM_004360.4	3, 8, 9
<i>CDKN2A</i>	NM_000077.4	2 ^b

Featured ARUP Testing

[Solid Tumor Mutation Panel, Sequencing 3004294](#)

Method: Massively Parallel Sequencing

- Use to assess for targeted variants that are useful for prognosis and/or treatment of individuals with solid tumor cancers, including melanoma, GIST, colorectal, bladder, and hepatocellular carcinomas, at initial diagnosis or in the presence of refractory disease
- If the clinical indication is lung cancer, additional molecular genetic testing may be considered for detection of gene rearrangements and/or c-MET exon 14-skipping alterations.
- For evaluation of microsatellite instability, additional molecular testing should be considered.
- For detection of sequence variants in the *TP53* gene alone, see [Somatic *TP53* Mutations in Formalin-Fixed, Paraffin-Embedded \(FFPE\) Tissue 3017688](#)

Gene	Accession No.	Targeted Exons
<i>CTNNB1</i>	NM_001904.3	3
<i>DDR2</i>	NM_001014796.1	18
<i>EGFR</i>	NM_005228.4	18-21
<i>ERBB2</i>	NM_004448.3	8, 17-22
<i>ERBB4</i>	NM_005235.2	3, 4, 6-9, 15, 23
<i>EZH2</i>	NM_004456.4	16, 18 ^b
<i>FBXW7</i>	NM_033632.3	5, 8-11
<i>FGFR1</i>	NM_023110.2	4, 7
<i>FGFR2</i>	NM_000141.4	7, 9, 12
<i>FGFR3</i>	NM_000142.4	7, 9, 14, 16, 18
<i>GNA11</i>	NM_002067.4	5
<i>GNAQ</i>	NM_002072.4	5 ^b
<i>GNAS</i>	NM_000516.5	8, 9
<i>HRAS</i>	NM_005343.3	2-4
<i>IDH1</i>	NM_005896.3	4
<i>IDH2</i>	NM_002168.3	4
<i>KDR</i>	NM_002253.2	6, 7, 11, 19, 21, 26, 27, 30
<i>KIT</i>	NM_000222.2	2, 9, 10, 11, 13, 14, 15, 17, 18
<i>KRAS</i>	NM_004985.4	2, 3, 4
<i>MAP2K1</i>	NM_002755.3	2, ^b 3, 6, 7, ^b 11 ^b
<i>MET</i>	NM_001127500.2	2, ^c 11, 13, 14, 15, 16, 19, intron 14
<i>MTOR</i>	NM_004958.3	27-58
<i>NOTCH1</i>	NM_017617.4	26, 27, 34 ^d
<i>NRAS</i>	NM_002524.4	2-5
<i>NTRK1</i>	NM_002529.3	5-15, 17
<i>PDGFRA</i>	NM_006206.4	12, 14, 15, 18
<i>PIK3CA</i>	NM_006218.2	2, 5, 7, 8, 10, ^b 14, ^b 19, 21
<i>PTEN</i>	NM_000314.6	1, ^b 2, ^b 3, 4-9 ^b
<i>RB1</i>	NM_000321.2	4, 6, 10, 11, 14, 17, 18, 20, 21, 22
<i>RET</i>	NM_020975.4	6, 7, 8, 10-13, 15, 16
<i>ROS1</i>	NM_002944.2	7, 31-36, 38, 40, 41
<i>SMAD4</i>	NM_005359.5	3-12
<i>SMO</i>	NM_005631.4	3, 5, 6, 9-11
<i>STK11</i>	NM_000455.4	1, 4, 5, 6, 8
<i>TERT</i> Promoter	NM_198253.2.1	Selected promoter region variants ^e

Gene	Accession No.	Targeted Exons
TP53 ^f	NM_000546.5	2-11
VHL	NM_000551.3	1-3

^ac.2390-c.2879, c.3128-c.3497, c.3730-4932

^bExon known to contain known pseudogenes, homologous genomic regions, and/or low-mappability regions.

^cc.374-c.743, c.815-c.1200+10

^dc.7168-c.7657

^eOnly c.-124C>T, c.-146C>T, c.-57 A>C, c.-125_124delinsTT, and c.-139_-138delinsTT hotspot promoter variants reported.

^fFor detection of sequence variants in the TP53 gene alone, see [Somatic TP53 Mutations in Formalin-Fixed, Paraffin-Embedded \(FFPE\) Tissue 3017688](#)

Test Interpretation

Analytic Sensitivity

Variant Class	No. of Variants Tested	PPA (%)	PPA (%), 95% Tolerance at 95% Reliability
SNVs	177	99	97.4-99.9
MNVs	42	93	82.2-98.0
Small insertions and duplications ^a	42	100	95.6-100.0
Medium insertions and duplications ^b	10	100	82.9-100.0
Large insertions ^c	1	100	22.9-100.0
Small deletions ^a	80	100	97.6-100.0
Medium deletions ^b	14	100	71.2-99.2
Large deletions ^d	22	64	42.9-81.1

^a≤21 bp.

^b22-60 bp.

^c≥61 bp and ≤64 bp.

^d≥61 bp and ≤13547 bp.

bp, base pairs; MNV, multinucleotide variant; PPA, positive percent agreement; SNV, single nucleotide variant

Results

Results	Variants Detected	Interpretation
Positive	Variants in ≥1 of the 44 genes were detected	Clinical relevance (diagnosis, prognosis, or therapy) will be correlated, if known
Negative	No pathogenic variants were detected	n/a
n/a, not available		

Limitations

- Does not detect copy number alterations, translocations, microsatellite instability (MSI), gene rearrangements, and tumor mutational burden
- Variants in areas outside the targeted genomic regions or below the limit of detection (LOD) of 5% variant allele frequency for SNVs or small- to medium-sized MNVs (<60 bp) will not be detected.
- 10 ng input DNA from extracted tissue sample is minimally required, but 50 ng input DNA is recommended for optimal results.

- Large variants (>60 bp) may not be detected.
- Variants in known pseudogenes, homologous genomic regions, and/or low-mappability regions may not be detected (see the [Solid Panel Targeted Regions table](#)).
- Not intended to detect minimal residual disease
- Does not distinguish between somatic and germline variants

References

1. Seth R, Messersmith H, Kaur V, et al. [Systemic therapy for melanoma: ASCO guideline](#). *J Clin Oncol*. 2020;38(33):3947-3970.
2. von Mehren M, Joensuu H. [Gastrointestinal stromal tumors](#). *J Clin Oncol*. 2018;36(2):136-143.
3. Cancer Genome Atlas Research Network. [Comprehensive and integrative genomic characterization of hepatocellular carcinoma](#). *Cell*. 2017;169(7):1327-1341.e23.
4. Kristensen BW, Priesterbach-Ackley LP, Petersen JK, et al. [Molecular pathology of tumors of the central nervous system](#). *Ann Oncol*. 2019;30(8):1265-1278.
5. Sepulveda AR, Hamilton SR, Allegra CJ, et al. [Molecular biomarkers for the evaluation of colorectal cancer: guideline from the American Society for Clinical Pathology, College of American Pathologists, Association for Molecular Pathology, and the American Society of Clinical Oncology](#). *J Clin Oncol*. 2017;35(13):1453-1486.
6. Loriot Y, Necchi A, Park SH, et al. [Erdafitinib in locally advanced or metastatic urothelial carcinoma](#). *N Engl J Med*. 2019;381(4):338-348.
7. Nikiforov YE. [Role of molecular markers in thyroid nodule management: then and now](#) [published correction appears in *Endocr Pract*. 2017;23(11):1362]. *Endocr Pract*. 2017;23(8):979-988.

Related Information

[Colorectal \(Colon\) Cancer](#)
[Gastrointestinal Stromal Tumors \(GISTs\)](#)
[Lynch Syndrome - Hereditary Nonpolyposis Colorectal Cancer \(HNPCC\)](#)
[Non-Small Cell Lung Cancer Molecular Markers](#)
[Melanoma](#)

ARUP Laboratories is a nonprofit enterprise of the University of Utah and its Department of Pathology. 500 Chipeta Way, Salt Lake City, UT 84108
 (800) 522-2787 | (801) 583-2787 | [aruplab.com](#) | [arupconsult.com](#)