

Solid Tumor Mutation Panel, Sequencing

Last Literature Review: August 2022 Last Update: September 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.

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

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
AKT1	NM_001014431.1	3, 4, 6
ALK	NM_004304.4	16-29
APC	NM_000038.5	16 ^a
ATM	NM_000051.3	8, 9, 12, 17, 26, 34-36, 39, 50, 54-56, 59, 61, 63
BRAF	NM_004333.4	11, ^b 14, 15
CDH1	NM_004360.4	3, 8, 9

CDKN/2A NML.001904.3 3 ODR2 NML.001904.3 3 CORR NML.005228.4 18-21 EGGR NML.005228.4 18-21 ERBB2 NML.00448.3 8,17-22 ERBB4 NML.005235.2 3,4.6-9.15,23 EZH2 NML.004486.4 16.18 ⁶ FBXW7 NML.03110.2 4,7 FGFR1 NML.023110.2 4,7 FGFR2 NML.00141.4 7,9.12 FGFR3 NML.00142.4 7,9.14.16.18 CMA11 NML.002024.4 5° GNA3 NML.002024.4 5° GNA4 NML.002024.4 5° GNA5 NML.005343.3 2-4 IDH1 NML.005343.3 2-4 IDH2 NML.002024.3 4 KDR NML.002383.2 6,7.11.19.21.26.27.30 AVT NML.002833.2 2,9.10.11.13.14.15.17.18 KRAS NML.002752.3 2,9.10.11.13.14.15.16.19 MACT NML.002752.3 2,7.8.10.11.13.14.15.16.19	Gene	Accession No.	Targeted Exons
DDP2 NML001014796-1 18 EGFR NML005228-4 18-21 ERBB2 NML00448-3 8,17-22 ERBB4 NML005235-2 3,4,69,15,23 EZH2 NML00456-4 16,189 FEXW7 NML033632-3 5,8-11 FGFR1 NML033110.2 4,7 FGFR2 NML000141.4 7,9,12 FGFR3 NML000142.4 7,9,14,16,18 GMAJ11 NML002067.4 5 GMAQ NML002072.4 9 ^b GMAS NML002072.4 9 ^b GMAS NML005343.3 2-4 IDH1 NML005896.3 4 IDH2 NML002168.3 4 KDR NML002253.2 6,7,11,19,21,26,27,30 KIT NML002252.2 2,9,10,11,13,14,15,17,18 KRAS NML002953.3 2,3,4 MAP2K1 NML004985.4 2,3,4 MAP2K1 NML0017617.4 26,27,34 ³ MFT NML004988.3 27:58 NOTCH1	CDKN2A	NM_000077.4	2 ^b
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PTEN NM_000314.6 1,b 2,b 3, 4-9b RB1 NM_000321.2 4, 6, 10, 11, 14, 17, 18, 20, 21, 22 RET NM_020975.4 6, 7, 8, 10-13, 15, 16 ROS1 NM_002944.2 7, 31-36, 38, 40, 41 SMAD4 NM_005359.5 3-12	PDGFRA	NM_006206.4	12, 14, 15, 18
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RET NM_020975.4 6, 7, 8, 10-13, 15, 16 ROS1 NM_002944.2 7, 31-36, 38, 40, 41 SMAD4 NM_005359.5 3-12	PTEN	NM_000314.6	1, ^b 2, ^b 3, 4-9 ^b
ROS1 NM_002944.2 7, 31-36, 38, 40, 41 SMAD4 NM_005359.5 3-12	RB1	NM_000321.2	4, 6, 10, 11, 14, 17, 18, 20, 21, 22
SMAD4 NM_005359.5 3-12	RET	NM_020975.4	6, 7, 8, 10-13, 15, 16
	ROS1	NM_002944.2	7, 31-36, 38, 40, 41
SMO NM_005631.4 3, 5, 6, 9-11	SMAD4	NM_005359.5	3-12
	SMO	NM_005631.4	3, 5, 6, 9-11

Gene	Accession No.	Targeted Exons
STK11	NM_000455.4	1, 4, 5, 6, 8
TERT Promoter	NM_198253.2.1	Selected promoter region variants ^e
TP53 ^f	NM_000546.5	2-11
VHL	NM_000551.3	1-3

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

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.

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

 $^{{}^{\}rm b}{\rm Exon\ known\ to\ contain\ known\ pseudogenes,\ homologous\ genomic\ regions,\ and/or\ low-mappability\ regions.}$

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

^dc.7168-c.7657

 $^{^{}e} Only\ c.-124 C>T,\ c.-146 C>T,\ c.-57\ A>C,\ c.-125_124 delins\ TT,\ and\ c.-139_-138 delins\ TT\ hotspot\ promoter\ variants\ reported.$

For detection of sequence variants in the TP53 gene alone, see Somatic TP53 Mutations in Formalin-Fixed, Paraffin-Embedded (FFPE) Tissue 3017688

^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

- 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

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Related Information

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

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