Henry Ford Health System
CENTER FOR PRECISION DIAGNOSTICS

Solid Tumor Gene Sequencing (Customizable: 1-4 Genes / 5-50 Genes)

AKT1	*ALK*	*ARID1A*	*BRAF*	*BRCA1*	*BRCA2*	*CDK4*	*CDKN2A*	*CTNNB1*	*DDR2*
DICER1	*EGFR*	*ERBB2*	*ERBB4*	*ESR1*	*FBXW7*	*FGFR1*	*FGFR2*	*FGFR3*	*FOXL2*
GNA11	*GNAQ*	*GNAS*	*H3F3A*	*H3F3B*	*HIST1H3B*	*HRAS*	*IDH1*	*IDH2*	*KIT*
KMT2A	*KMT2D*	*KRAS*	*MAP2K1*	*MAP2K2*	*MET*	*MTOR*	*MYOD1*	*NRAS*	*PDGFRA*
PIK3CA	*POLE*	*PTEN*	*PTPN11*	*RAC1*	*RAF1*	*RET*	*ROS1*	*SF3B1*	*SMAD4*
TERT	*TGFBR2*	*TP53*							

Indication

Diagnosis, prognosis and treatment of solid tumors relies on identification of molecular genetic alterations that are characteristic to specific tumor subtypes or have prognostic or therapeutic relevance with the potential to guide patient management. This Solid Tumor Gene Sequencing assay enables analytically sensitive mutation detection within multiple cancer types, including lung, colon, GIST, glioma, breast, ovarian, prostate, melanoma and sarcoma. The panel is customizable and includes 53 genes with known associations to cancer, targeting clinically relevant somatic mutations across the hotspot regions of oncogenes (e.g., *BRAF*, *KRAS*, *NRAS*, *PIK3CA*, *KIT*, *PDGFRA*, *MET*, *IDH1*, *IDH2* and many others) as well as analysis of the entire coding sequence of several tumor suppressor genes (e.g., *BRCA1*, *BRCA2*, *TP53*). In addition, this assay detects copy number aberrations in 43 target genes.

Testing method

This Solid Tumor Gene Sequencing assay utilizes next generation sequencing (NGS) technology for detection of hotspot mutations and copy number alterations in multiple cancer-related genes. For each gene included on the clinical panel (listed below), the target exons are enriched by hybrid capture method followed by NGS analysis on the Illumina MiSeq instrument. This method was optimized for use with low quantity of input DNA (50 ng) obtained from formalin-fixed, paraffin-embedded (FFPE) tissues providing high on-target coverage with coverage uniformity above 95% throughout the entire target region. Data analysis is performed using SOPHiA DDM platform, which provides sequence alignment to reference genome, variant detection and annotation, interpretation of clinically significant genomic alterations and their association to approved or investigational therapies.

Diagnostic sensitivity: This assay is designed to detect known single nucleotide variants, insertions, deletions, and copy number alterations only within defined target regions. Large insertions and deletions that include genomic sequence outside of the defined target regions may not be detected. Gene rearrangements are not detected.

Technical sensitivity: This assay may not detect certain mutations if the proportion of tumor cells in the sample studied is less than 20%. Sensitivity for detection of copy number variants is reduced in samples with tumor fraction below 50%.

Clinical Panel

Gene	Exon / Amino Acid (AA) Coverage	Annotation Transcript
AKT1	Exon 4	NM_001014432
ALK	Exons 21-25	NM_004304
ARID1A	Exons 1, 2, 5, 15, 18-20 (partial coverage)	NM_006015
BRAF	Exons 11, 15	NM_004333
BRCA1	Full	NM_007294
BRCA2	Full	NM_000059
CDK4	Exon 2	NM_000075
CDKN2A	Full	NM_000077
CTNNB1	Exon 3	NM_001904
DDR2	Exon 17	NM_006182
DICER1	Exons 24, 25	NM_177438
EGFR	Exons 18-21	NM_005228
ERBB2	Exons 8, 17, 20	NM_004448
ERBB4	Exons 10, 12	NM_005235
ESR1	Exons 2-8	NM_000125
FBXW7	Exons 7-11	NM_033632
FGFR1	Exons 12, 14	NM_023110
FGFR2	Exons 7, 12, 14	NM_000141
FGFR3	Exons 7, 9, 14, 16	NM_000142
FOXL2	Full	NM_023067
GNA11	Exons 4, 5	NM_002067
GNAQ	Exons 4, 5	NM_002072
GNAS	Exon 8	NM_000516
H3F3A	Exon 2	NM_002107
H3F3B	Exon 2	NM_005324
HIST1H3B	Full	NM_003537
HRAS	Exons 2-4	NM_005343
IDH1	Exon 4	NM_001282387
IDH2	Exon 4	NM_002168
KIT	Exons 8-11, 13, 17, 18	NM_000222
KMT2A	Exons 3, 5 (partial coverage)	NM_005933
KMT2D	Exons 10, 11, 28, 34, 39 (partial coverage)	NM_003482
KRAS	Exons 2-4	NM_004985
MAP2K1	Exons 2, 3	NM_002755
MAP2K2	Exons 2-7	NM_030662
MET	Exons 2, 14-20	NM_001127500
MTOR	Exons 46-52	NM_004958
MYOD1	Exon 1	NM_002478
NRAS	Exons 2-4	NM_002524
PDGFRA	Exons 12, 14, 18	NM_006206
PIK3CA	Exons 2, 3, 6, 8, 10, 21	NM_006218
POLE	Exons 9, 13, 14, 34	NM_006231
PTEN	Exons 5-9	NM_000314
PTPN11	Exon 3	NM_002834
RAC1	Exon 3	NM_006908
RAF1	Exons 7, 10, 12-15	NM_002880

RET	Exons 11, 13, 15, 16	NM_020975
ROS1	Exons 38, 41	NM_002944
SF3B1	Exons 15-17	NM_012433
SMAD4	Exons 8-12	NM_005359
TERT	Promoter, Exons 1, 8, 9, 13	NM_198253
TGFBR2	Exons 3, 4, 6, 7 (partial coverage)	NM_003242
TP53	Full	NM_000546

Genes Targeted for Copy Number Analysis

ALK, ARID1A, BRAF, BRCA1, BRCA2, CDK4, CDKN2A, CTNNB1, DICER1, EGFR, ERBB2, ERBB4, ESR1, FBXW7, FGFR1, FGFR2, FGFR3, FOXL2, GNAQ, HIST1H3B, HRAS, KIT, KMT2D, KRAS, MAP2K1, MAP2K2, MET, MTOR, MYOD1, NRAS, PDGFRA, PIK3CA, POLE, PTEN, PTPN11, RAF1, RET, ROS1, SF3B1, SMAD4, TERT, TGFBR2, TP53

Turnaround time

5-10 business days

Sample requirements

The presence of adequate tumor in the material submitted for analysis should be confirmed by a surgical pathologist. A section from archival paraffin material or frozen surgical biopsies should be confirmed to contain > 50% tumor by a surgical pathologist. If the submitted material for analysis contains < 50% of tumor, areas of predominant tumor will be microdissected, if possible, to enrich for neoplastic cells.

- Formalin-fixed, paraffin-embedded tissue
- 5-6 tissue sections (please include H&E slide and a copy of pathology report)
- Cytology slides

CPT codes

1-4 Genes: Enquire for CPT codes

5-50 Genes: 81445, G0452 (88363 or 88381 may apply)

Ship Specimens to:

Henry Ford Center for Precision Diagnostics
Henry Ford Hospital
Clinic Building, K6, Core Lab E-655
2799 W. Grand Blvd.
Detroit, MI 48202