Henry Ford Health System
CENTER FOR PRECISION DIAGNOSTICS

Henry Ford Comprehensive Solid Tumor Fusion 50 Gene Panel

Gene fusions play a key role in carcinogenesis. Many of the driver gene rearrangements / mutations are in genes that express kinases, as indicated in the tables below. Fusions in these genes often unlink the kinase domains of the proteins from regulatory subunits, resulting in constitutive activation of the kinase function. This test is used for diagnostic, prognostic, and predictive purposes.

Testing Method

Anchored Multiplex PCR (AMP™), a target enrichment chemistry used to create target enrichment libraries for next generation sequencing (NGS). AMP leverages the power of unidirectional gene specific primers (GSPs), sample indexes and barcodes for multiplex targeted NGS using low input sample types such as formalin fixed, paraffin embedded (FFPE) sections.

Highlights of the Henry Ford Comprehensive Solid Tumor Fusion 50 Gene Panel

- Permits the **simultaneous detection** of both known recurrent fusions as well as previously unidentified fusions at key breakpoints in target genes.
- **Targeted sequencing assay** that simultaneously detects and identifies fusions and other mutations (such as exon skipping) associated with genes linked to various carcinomas
- The dilution series of the known positive control shows **0.3% technical sensitivity**

Fusions Detected and Genes Targeted

Gene	Transcript	Exons	Direction	Type
AKT3	NM_005465	1, 2, 3	5'	Fusion
ALK	NM_004304	19, (intron 19), 20, 21, 22	5'	Fusion
ARHGAP26	NM_015071	2, 10, 11, 12	5'	Fusion
AXL	NM_021913	19, 20	3'	Fusion
BRAF	NM_004333	7, 8	3'	Fusion
BRAF	NM_004333	7, 8, 9, 10, 11, 12	5'	Fusion
BRAF	NM_004333	15	5'	Fusion
BRAF	NM_004333	V600E	n/a	Mutation
BRD3	NM_007371	9, 10, 11, 12	3'	Fusion
BRD4	NM_014299	10, 11	3'	Fusion
EGFR	NM_005228	7, 9, 16, 20	5'	Fusion
EGFR	NM_005228	8, (2-7 exon skipping event)	n/a	Mutation
EGFR	NM_005228	24, 25	3'	Fusion
ERG	NM_004449	2, 3, 4, 5, 6, 7, 8, 9, 10, 11	5'	Fusion
ESR1	NM_001122742	3, 4, 5, 6	3'	Fusion
ETV1	NM_004956	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13	5'	Fusion
ETV4	NM_001986	2, 4, 5, 6, 7, 8, 9, 10	5'	Fusion
ETV5	NM_004454	2, 3, 7, 8, 9	5'	Fusion
ETV6	NM_001987	1, 2, 3, 4, 5, 6	3'	Fusion
ETV6	NM_001987	2, 3, 5, 6, 7	5'	Fusion
EWSR1	NM_005243	4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14	3'	Fusion
FGFR1	NM_015850	2, 8, 9, 10, 17	5'	Fusion
FGFR2	NM_000141	2, 8, 9, 10	5'	Fusion
FGFR2	NM_000141	17	3'	Fusion
FGFR3	NM_000142	17, intron 17	3'	Fusion
FGFR3	NM_000142	8, 9, 10	5'	Fusion
FGR	NM_005248	2	5'	Fusion
INSR	NM_000208	20, 21, 22	3'	Fusion
INSR	NM_000208	12, 13, 14, 15, 16, 17, 18, 19	5'	Fusion
MAML2	NM_032427	2, 3	5'	Fusion
MAST1	NM_014975	7, 8, 9, 18, 19, 20, 21	5'	Fusion
MAST2	NM_015112	2, 3, 5, 6	5'	Fusion
MET	NM_000245	13	3'	Fusion
MET	NM_000245	13, 15 (exon 14 skipping event)	n/a	Mutation
MSMB	NM_002443	2, 3, 4	3'	Fusion
MUSK	NM_005592	7, 8, 9, 11, 12, 13, 14	5'	Fusion

Gene	Transcript	Exons	Direction	Type
MYB	NM_001130173	7, 8, 9, 11, 12, 13, 14, 15, 16	3'	Fusion
NOTCH1	NM_017617	2, 4, 29, 30, 31	3'	Fusion
NOTCH1	NM_017617	26, 27, 28, 29 (internal exon 3-27 deletion)	5'	Fusion
NOTCH2	NM_024408	5, 6, 7	3'	Fusion
NOTCH2	NM_024408	26, 27, 28	5'	Fusion
NRG1	NM_004495	1, 2, 3, 6	5'	Fusion
NTRK1	NM_002529	8, 10, 11, 12, 13	5'	Fusion
NTRK2	NM_006180	11, 12, 13, 14, 15, 16, 17	5'	Fusion
NTRK3	NM_002530	13, 14, 15, 16	5'	Fusion
NTRK3	NM_001007156	15	5'	Fusion
NUMBL	NM_004756	3	5'	Fusion
NUTM1	NM_175741	3	5'	Fusion
PDGFRA	NM_006206	7 (exon 8 deletion)	n/a	Mutation
PDGFRA	NM_006206	10, 11, 12, 13, 14	5'	Fusion
PDGFRA	NM_006206	T674I, D842V	n/a	Mutation
PDGFRB	NM_002609	8, 9, 10, 11, 12, 13, 14	5'	Fusion
PIK3CA	NM_006218	2	5'	Fusion
PKN1	NM_002741	10, 11, 12, 13	5'	Fusion
PPARG	NM_015869	1, 2, 3	5'	Fusion
PRKCA	NM_002737	4, 5, 6	5'	Fusion
PRKCB	NM_002738	3	5'	Fusion
RAF1	NM_002880	4, 5, 6, 7, 9	3'	Fusion
RAF1	NM_002880	4, 5, 6, 7, 9, 10, 11, 12	5'	Fusion
RELA	NM_021975	3, 4	5'	Fusion
RET	NM_020630	8, 9, 10, 11, 12, 13	5'	Fusion
ROS1	NM_002944	31, 32, 33, 34, 35, 36, 37	5'	Fusion
RSPO2	NM_178565	1, 2	5'	Fusion
RSPO3	NM_032784	2	5'	Fusion
TERT	NM_198253	2	5'	Fusion
TFE3	NM_006521	2, 3, 4, 5, 6	3'	Fusion
TFE3	NM_006521	2, 3, 4, 5, 6, 7, 8	5'	Fusion
TFEB	NM_007162	1, 2	5'	Fusion
THADA	NM_022065	28	3'	Fusion
TMPRSS2	NM_005656	1, 2, 3, 4, 5, 6	3'	Fusion
TMPRSS2	NM_001135099	1	3'	Fusion

Ordering Information

Get started: Print a Solid Tumor test requisition form online at www.HenryFord.com/HFCPD

Specimen 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 micro-dissected to enrich for neoplastic cells.

- Formalin-fixed, paraffin-embedded tissue, preferably no older than 2 years
- 5-6 tissue sections at 5-6 micron thickness (please include H&E slide and a copy of pathology report)
- Cytology slides (cell block with 500+ tumor cells, submit block or 5-6 tissue sections at 5-10 micron thickness depending on cellularity)

TAT: 5-10 business days

Mail test material to:
Henry Ford Center for Precision Diagnostics
Pathology and Laboratory Medicine
Clinic Building, K6, Core Lab, E-655
2799 W. Grand Blvd., Detroit, MI 48202

CPT Codes: 81455

Contact us: Client Services, Account and Billing Set-up, and connect with a Molecular Pathologist at (313) 916-4DNA (4362)

For more information on Comprehensive Molecular Services please visit our website www.HenryFord.com/HFCPD