HENRY FORD HEALTH
CENTER FOR PRECISION DIAGNOSTICS

PAN Solid Tumor Gene Fusion Panel

Gene fusions play a key role in carcinogenesis. Many of the driver gene rearrangements / mutations are in genes that express kinases. Fusions in these genes often unlink the kinase domains of the proteins from regulatory subunits, resulting in constitutive activation of the kinase function.

Testing Method and Background

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. This test is used for diagnostic, prognostic, and predictive purposes.

Highlights of the Henry Ford PAN Solid Tumor Gene Fusion Panel

Targeted Regions

ACVR2A, AKT1, AKT2, AKT3, ALK, AR, ARHGAP26, ARHGAP6, AXL, BCOR, BRAF, BRD3, BRD4, CAMTA1, CCNB3, CCND1, CIC, CRTC1, CSF1, CSF1R, DNAJB1, EGF, EGFR, EPC1, ERBB2, ERBB4, ERG, ESR1, ESRRA, ETV1, ETV4, ETV5, ETV6, EWSR1, FGF1, FGFR1, FGFR2, FGFR3, FGR, FOS, FOSB, FOXO1, FOXO4, FOXR2, FUS, GLI1, GRB7, HMGA2, IGF1R, INSR, JAK2, JAK3, JAZF1, KIT, MAML2, MAP2K1, MAST1, MAST2, MBTD1, MDM2, MEAF6, MET, MGEA5, MKL2, MN1, MSMB, MUSK, MYB, MYBL1, MYC, NCOA1, NCOA2, NCOA3, NFATC2, NFE2L2, NFIB, NOTCH1, NOTCH2, NR4A3, NRG1, NTRK1, NTRK2, NTRK3, NUMBL, NUTM1, PAX3, PAX8, PDGFB, PDGFD, PDGFRA, PDGFRB, PHF1, PHKB, PIK3CA, PKN1, PLAG1, PPARG, PRDM10, PRKACA, PRKACB, PRKCA, PRKCB, PRKCD, PRKD1, PRKD2, PRKD3, RAD51B, RAF1, RELA, RET, ROS1, RSPO2, RSPO3, SS18, SS18L1, STAT6, TAF15, TCF12, TERT, TFE3, TFEB, TFG, THADA, TMPRSS2, USP6, VGLL2, WWTR1, YAP1, YWHAE
* ***Specific exon coverage listed on next page***

Ordering Information

Get started (non-HFHS): Print a Molecular Solid Tumor Testing requisition form online at www.HenryFord.com/HFCPD

Get started (HFHS): Order through Epic using test "PAN Solid Tumor Gene Fusion Panel" (test code coming soon)

Specimen requirements:

A surgical pathologist should confirm the presence of adequate tumor in materials submitted for analysis. 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, 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)
- Extracted RNA - from a CLIA-certified Laboratory

Cause for Rejection: Fresh unfixed tissue, paraffin materials that do not contain tumor cells, improperly labeled specimens, archival paraffin material subjected to acid decalcification.

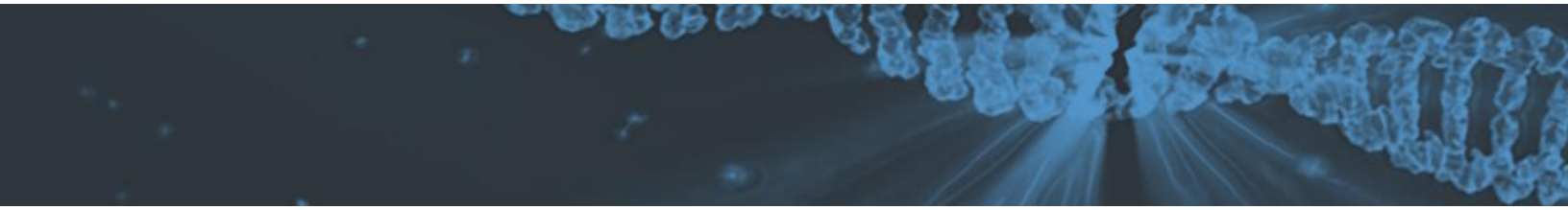
TAT: 5-10 business days (after Prior Authorization obtained)

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: 81445, G0452

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, visit our website www.HenryFord.com/HFCPD

Revision: 1; 04-22-2025



PAN Solid Tumor Gene Fusion Panel

Gene	Accession	Exon (5')	Exon (3')
ACVR2A	NM_001616	1, 2, 3	
AKT1	NM_005163	2, 3, 4, 5, mid-exon5	
AKT2	NM_001626	2*, 5	11
AKT3	NM_005465	2, 3, 4, 9	6, 7, 8
ALK	NM_004304	2, 4, 6, 8, 10, 12, 14, 16, 17, 18, 19, intron19, 20, mid-exon20, 21, 22, 23, 26	1, 2
AR	NM_001011645		1
AR	NM_000044		1, 2, 3, 4, 5, 6, 7, 8*
ARHGAP26	NM_015071	2, 10, 11, 12	
ARHGAP6	NM_006125	2	
AXL	NM_021913	11	18, 19, mid-exon20, 20
BCOR	NM_017745	8	
BCOR	NM_001123385	mid-exon2, 3, 4, mid-exon4, 5, 6, 7, 8, 9, 11, 15	2, 4, mid-exon4, 6, 7, mid-exon7, 10, 12, 14, 15
BRAF	NM_004333	2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 15, 16	1, 2, 3, 7, 8, 10, 13, 14, 18
BRD3	NM_007371		9, 10, 11, 12
BRD4	NM_058243	2*	10, 11, 12, 13, 14
CAMTA1	NM_015215	8, 9, mid-exon9, 10	3
CCNB3	NM_033031	2*, 3, 4, 5, 6, mid-exon 6, 7	
CCND1	NM_053056	1*, 2, 3, 4, 5	1, 2, 3, 4, mid-exon5*, 5*
CIC	NM_015125	12	14, 15, 16, 17, 18, mid-exon19, 19, mid-exon20, 20*
CRTC1	NM_015321		1, 2, 3, 4
CSF1	NM_000757	2, 3, 4, 5, 6	5, 6, 7, 8*, mid-exon9*
CSF1	NM_172212		9*
CSF1R	NM_005211	11, 12, 13	
DNAJB1	NM_006145		1, 2
EGF	NM_001963	16, 17, 18, 19	
EGFR	NM_005228	7, 8, 9, 14, 15, 16, 17, 18, 19, 20	1, 24, 25, mid-exon25, 26
EPC1	NM_025209		9, 10, 11
ERBB2	NM_004448	4, 5, 13, 15, 17	15, 23, 24, 25, mid-exon26, 26
ERBB4	NM_005235	2, 3, 4, 14, 15, 16, 17, 18, 23	
ERG	NM_004449	2*, 3*, 4, 5, 6, 7, 8, 9, 10, 11	
ESR1	NM_000125	5, 6, 7, 8	1, 2, 3, 4, 5, 6, 7
ESRRA	NM_004451		2, 3
ETV1	NM_004956	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13	
ETV4	NM_001986	2, 3, 4, 5, 6, 7, 8, 9, 10	
ETV5	NM_004454	2*, 3, 7, 8, 9	
ETV6	NM_001987	2, 3, 4, 5, 6, 7	1, 2, 3, 4, 5, 6
EWSR1	NM_005243	8	4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14
FGF1	NM_00800	mid-exon 2, 2	
FGFR1	NM_015850	2*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 17	12, 17
FGFR2	NM_000141	2*, 3, 5, 6, 7, 8, 9, 10	16, 17, 18
FGFR3	NM_000142	3, 5, 8, 9, 10, 11, 12, 13, 14	16, 17, intron17, mid-exon18
FGR	NM_005248	2*, 3	
FOS	NM_005252		mid-exon4
FOSB	NM_006732	1*, mid-exon1*, 1, 2	
FOXO1	NM_002015	1*, 2, 3*	1*, 2*, 3*
FOXO4	NM_005938	2, mid-exon2, 3	
FOXR2	-	cryptic upstream exon2,3 (chrX:55562068, chrX:55634636)	
FUS	NM_004960		3, 4, 5, mid-exon6, 6, 7, 8, 9, 10,11, 13, 14
GLI1	NM_005269	4, 5, 6, 7	4, 5, mid-exon5, 6, 7
GRB7	NM_005310	10, 11, 12	
HMGA2	NM_003483		1, 2, 3, 4, mid-exon5*, 5*
IGF1R	NM_000875	13, 14, 15	
INSR	NM_000208	2, 12, 13, 14, 15, 16, 17, 18, 19	20, 21, 22
JAK2	NM_004972	6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20	9, 10, 11, 12, 22
JAK3	NM_000215	10, 11, 12, 17, 18, 19	23
JAZF1	NM_175061		2, 3, 4
KIT	NM_000222	8	1
MAML2	NM_032427	2, 3	2
MAP2K1	NM_002755	2	
MAST1	NM_014975	7, 8, 9, 18, 19, 20, 21	
MAST2	NM_015112	2, 3, 5, 6	15, 16, 17
MBTD1	NM_017643	3*	15, 16, 17
MDM2	NM_002392	5, 9	2, 4, 6, 8, 10
MEAF6	NM_001270875		4, 5
MET	NM_000245	2, 4, 5, 6, 13, 14, 15, 16, 17, 21	2, 13
MGEA5	NM_012215	4, 5, 6, 7, 8, 9, 12, 13, 14, 15	
MKL2	NM_014048	11, 12, 13	
MN1	NM_002430		1, 2

*Indicates exons that are entirely untranslated region (UTR), or for which the UTR is targeted.

Gene	Accession	Exon (5')	Exon (3')
MSMB	NM_002443		2, 3, 4
MUSK	NM_005592	7, 9, 10, 12, 13, 14, 15	
MYB	NM_001130173		7, 8, 9, 11, 12, 13, 14, 15, 16
MYBL1	NM_001080416		8, 9, mid-exon10, 10, 11, 12, 13, 14, 15
MYC	NM_002467	1*, mid-exon1*, 2, 3	1, 2
NCOA1	NM_147223	11, 12, 13, 14, 15	
NCOA2	NM_006540	11, 12, 13, 14, intron14, 15, 16, 22	14
NCOA3	NM_006534	2*, 13, 14, 15, 16	20
NFATC2	NM_012340	2, 3, 9, 10	
NFE2L2	NM_006164	1, 2, 3, 4, 5	
NFIB	NM_001369458	10, 11	
NFIB	NM_005596	9*, mid-exon 9	2
NOTCH1	NM_017617	5, 24, 25, 26, 27, 28, 29	2, 4, 24, 29, 30, 31
NOTCH2	NM_024408	24, 25, 26, 27, 28, 29	5, 6, 7
NR4A3	NM_173200	2*, 3*, 4, 5, 7, 9	8
NRG1	NM_001159996	1*, 3, 4, 5	
NRG1	NM_004495	1, 2, 3, 4, 5, 6	
NRG1	NM_013958	1*	
NRG1	NM_013959	1*, 3	
NRG1	NM_013962	1*	1
NTRK1	NM_001007792	1, 2	
NTRK1	NM_002529	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14	
NTRK2	NM_006180	4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18	11, 14
NTRK3	NM_001007156	15	
NTRK3	NM_002530	3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16	13, 14, 15, 17
NUMBL	NM_004756	2, 3	
NUTM1	NM_175741	2*, 3, mid-exon3, 4, 5, mid-exon6, 6	
PAX3	NM_181459	2, 4, 8	3, 5, 6, 7, 8
PAX8	NM_003466	3	1*, 2, 6, 7, 8, 9, 10
PDGFB	NM_002608	2, 3	
PDGFD	NM_025208	5, 6, 7	
PDGFRA	NM_006206	10, 11, 12, mid-exon12, 13, 14, 15	7
PDGFRB	NM_002609	8, 9, 10, 11, 12, mid-exon12, 13, 14	
PHF1	NM_024165	1*, 2	10, 11, 12
PHKB	NM_000293		4
PIK3CA	NM_006218	2, 15	
PKN1	NM_002741	10, 11, 12, 13	
PLAG1	NM_002655	1, 2, 3, 4	
PPARG	NM_015869	1, 2, 3	
PRDM10	NM_020228	13, 14	
PRKACA	NM_002730	2	
PRKACB	NM_182948	2, 3, 4	
PRKCA	NM_002737	4, 5, 6, 9, 15	
PRKCB	NM_002738	1, 3, 7, 8, 9	
PRKCD	NM_006254	9, 10, 11, 12, 15	18
PRKD1	NM_002742	2, 10, 11, 12, 13	
PRKD2	NM_016457	10, 11, 12, 13	
PRKD3	NM_005813	10, 11, 12, 13	
RAD51B	NM_133509	8	3, 4, 5, 6, 7, 8, 9
RAF1	NM_002880	2*, 4, 5, 6, 7, 8, 9, 10, 11, 12	4, 5, 6, 7, 8, 9
RELA	NM_021975	1, 2, 3, 4, 11	
RET	NM_020630	2, 4, 6, 8, 9, 10, 11, mid-exon11,12, 13, 14	
ROS1	NM_002944	2, 4, 7, 31, 32, 33, 34, 35, 36, 37	
RSPO2	NM_178565	1, 2*, 3*	
RSPO3	NM_032784	2	
SS18	NM_001007559	2, 3, 4, 5, 6, 10, 11	4, 5, 6, 8, 9, 10
SS18L1	NM_198935		1, 2, 3, 8, 9, 10
STAT6	NM_001178078	1*, 2*, 3, 4, 5, 6, 7, 15, 16, 17, 18, 19, 20	
TAF15	NM_139215	6, 7	5, 6, 7, 9
TCF12	NM_207036		4, 5, 6
TERT	NM_198253	2, 3, 5, 7, 10, 11, 12	3, 9, 15
TFE3	NM_006521	2, 3, 4, 5, 6, 7, 8	2, 3, 4, 5, 6
TFEB	NM_007162	1*, 2*, 3, mid-exon3, 4, mid-exon4, mid-exon 5, 6	9, mid-exon 10
TFG	NM_006070	6	3, 4, 5, 6, 7, mid-exon8
THADA	NM_022065		24, 25, 26, 27, 28, 29, 30, 31, 36, 37
TMPRSS 2	NM_001135099		1
TMPRSS 2	NM_005656		1*, 2, 3, 4, 5, 6
USP6	NM_004505	1*, mid-exon1*, 2*, 3	
VGLL2	NM_182645		1, 2, 3, intron3, 4
WWTR1	NM_015472	3, 4	3, 4
YAP1	NM_001130145	1, mid-exon1, 2, 3, 4, 8, 9	1, 2, 3, 4, 5, 6, 7
YWHAE	NM_006761		5