

Solid Tumor Profile Plus

Patient Name:		Ordering Physician:	
Date of Birth:		Accession #:	
Gender (M/F):		Specimen Type:	TISSUE
Client:		Specimen ID:	
Case #:			
Body Site:			

Collected Date:			Tumor Type:	pancreatic adenocarcinoma
Received Date:				
Reported Date:				

Detected Genomic Alterations				
Level 1 (FDA-Approved)	Level 2 (Standard of Care)	Level 3 (Clinical Evidence)	Level 4 (Biological Evidence)	Other
KRAS (G12D)	-Homologous recombination deficiency (HRD): Positive-High -No evidence of microsatellite instability -Tumor Mutation Burden Low: 1 Mut/Mb	TP53 (2 mutations), SF3B1	MSH6, CTC1, DPP4	Autosomal chromosomal structural analysis shows 1q+, 3p-, -4, 5q-, 6p+ (proximal, CCND3 and VEGFA amplification), 9p- (CDKN2A/B deletion), 12q+, 13q+, 15q-, 17q+ (proximal), 19p+ and others

Results Summary

- **-Mutations in KRAS (G12D), TP53 (2 mutations), MSH6, CTC1, SF3B1, and DPP4 genes**
- Homologous recombination deficiency (HRD): Positive-High**
- No evidence of microsatellite instability**
- Tumor Mutation Burden Low: 1 Mut/Mb**
- No evidence of BRCA1/2 or PALB2 mutations**
- No evidence of fusion mRNA involving ALK, RET, ROS1, or NTRK**
- EBV, HPV, TTV, and HTLV viral mRNA: Not detected**
- HLA Genotyping:**
 - HLA-A: A*31:01-A*32:01**
 - HLA-B: B*08:01-B*53:01**
 - HLA-C: C*04:01-C*07:912**
- Autosomal chromosomal structural analysis shows 1q+, 3p-, -4, 5q-, 6p+ (proximal, CCND3 and VEGFA amplification), 9p- (CDKN2A/B deletion), 12q+, 13q+, 15q-, 17q+ (proximal), 19p+ and others**
- Increased CA15-3, CEA, MET, ERBB2, VEGFA, TROP2 mRNA**

-The FDA has approved NALIRIFOX (combination of liposomal irinotecan, 5-fluorouracil, and oxaliplatin) for the treatment of metastatic pancreatic cancer.

-KRAS mutation suggests possible response to pan-RAS inhibitors (daraxonrasib etc).

-Positive homologous recombination deficiency (HRD) suggests response to platinum-based chemotherapy and PARP inhibitors.

-VEGFA gene amplification suggests possible response to anti-VEGF or anti-VEGFR therapy.

-TP53 mutations suggest possible response to eprenetapopt (APR-246), Aurora kinase A and Wee1 inhibitors.

-See additional report information at the end of the report

Tumor Heterogeneity

There is a dominant abnormal clone with KRAS mutation. The TP53 (2 mutations), MSH6, CTC1, SF3B1, and DPP4 mutations are detected in subclones.

Expression

Increased CA15-3, CEA, MET, ERBB2, VEGFA, TROP2 mRNA

Diagnostic Implications

KRAS, TP53 (2 mutations), MSH6, CTC1, SF3B1, DPP4

The findings are consistent with pancreatic cancer

FDA-Approved Therapeutics

KRAS (G12D)

Daraxonrasib

FDA-Approved Therapeutics in Other Tumor Types

HRD Positive

Niraparib + platinum-based chemotherapy

Relevant Alteration Associated with Resistance

KRAS mutations suggest resistance to targeted anti-EGFR therapy

TP53 mutation is associated with resistance to therapy.

Levels 2, 3 & 4 (Standard of Care and Clinical/Biological Evidence)

KRAS

pan-RAS inhibitors

TP53

Aurora kinase A inhibitors, Wee1 inhibitors, Chk1 inhibitors, kevetrin, APR-246, nutlins, gene therapy

SF3B1	Spliceosome modifiers
HRD Positive	PARP Inhibitors & Platinum based chemotherapy

Relevant Genes with NO Alteration

-No evidence of mutation in NRAS, EGFR, BRAF, or BRCA 1/2 -No specific mutation in DPYD gene, associated with enzymatic deficiency	No evidence of fusion mRNA involving ALK, RET, ROS1, or NTRK	-No evidence of METex14 skipping or EGFRvIII -No evidence of ERBB2 (HER2) amplification
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Test Description:

This is a comprehensive molecular profile which uses next generation sequencing (NGS) to identify molecular abnormalities, including single nucleotide variants (SNVs), insertions/deletions (indels), copy number variants (CNVs), fusions, tumor mutational burden (TMB), microsatellite instability (MSI), homologous recombination deficiency (HRD), B- and T-cell clonality, and viruses (HPV, EBV, HTLV1, and TTV), in DNA of 434 genes and RNA in greater than 1600 genes implicated in solid tumors. Whenever possible, clinical relevance and implications of detected abnormalities are described below.

Biological relevance of detected Alterations

- **KRAS.** This gene, a Kirsten ras oncogene homolog from the mammalian ras gene family, encodes a protein that is a member of the small GTPase superfamily. A single amino acid substitution is responsible for an activating mutation. The transforming protein that results is implicated in various malignancies, including lung adenocarcinoma, mucinous adenoma, ductal carcinoma of the pancreas and colorectal carcinoma. Alternative splicing leads to variants encoding two isoforms that differ in the C-terminal region. [provided by RefSeq, Jul 2008]
- **TP53.** This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons from identical transcript variants (PMIDs: 12032546, 20937277). [provided by RefSeq, Dec 2016]
- **MSH6.** This gene encodes a member of the DNA mismatch repair MutS family. In E. coli, the MutS protein helps in the recognition of mismatched nucleotides prior to their repair. A highly conserved region of approximately 150 aa, called the Walker-A adenine nucleotide binding motif, exists in MutS homologs. The encoded protein heterodimerizes with MSH2 to form a mismatch recognition complex that functions as a bidirectional molecular switch that exchanges ADP and ATP as DNA mismatches are bound and dissociated. Mutations in this gene may be associated with hereditary nonpolyposis colon cancer, colorectal cancer, and endometrial cancer. Transcripts variants encoding different isoforms have been described. [provided by RefSeq, Jul 2013]
- **CTC1.** This gene encodes a component of the CST complex. This complex plays an essential role in protecting telomeres from degradation. This protein also forms a heterodimer with the CST complex subunit STN1 to form the enzyme alpha accessory factor. This enzyme regulates DNA replication. Mutations in this gene are the cause of cerebroretinal microangiopathy with calcifications and cysts. Alternate splicing results in both coding and non-coding variants. [provided by RefSeq, Mar 2012]
- **SF3B1.** This gene encodes subunit 1 of the splicing factor 3b protein complex. Splicing factor 3b, together with splicing factor 3a and a 12S RNA unit, forms the U2 small nuclear ribonucleoproteins complex (U2 snRNP). The splicing factor 3b/3a complex binds pre-mRNA upstream of the intron's branch site in a sequence independent manner and may anchor the U2 snRNP to the pre-mRNA. Splicing factor 3b is also a component of the minor U12-type spliceosome. The carboxy-terminal two-thirds of subunit 1 have 22 non-identical, tandem HEAT repeats that form rod-like, helical structures. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2008]
- **DPP4.** The DPP4 gene encodes dipeptidyl peptidase 4, which is identical to adenosine deaminase complexing protein-2, and to the T-cell activation antigen CD26. It is an intrinsic type II transmembrane glycoprotein and a serine exopeptidase that cleaves X-proline dipeptides from the N-terminus of polypeptides. Dipeptidyl peptidase 4 is highly involved in glucose and insulin metabolism, as well as in immune regulation. This protein was shown to be a functional receptor for Middle East respiratory syndrome coronavirus (MERS-CoV), and protein modeling suggests that it may play a similar role with SARS-CoV-2, the virus responsible for COVID-19. [provided by RefSeq, Apr 2020]

Drug Information

Daraxonrasib

Daraxonrasib (RMC-6236) is an orally administered, non-covalent RAS(ON) inhibitor designed to target the active, GTP-bound state of RAS proteins, including multiple oncogenic RAS variants. By inhibiting aberrant RAS signaling, daraxonrasib is intended to suppress a key driver of tumor growth and survival in RAS-mutated cancers. The drug has demonstrated clinically meaningful antitumor activity in patients with advanced solid tumors, particularly pancreatic adenocarcinoma, and is being investigated across a broader range of RAS-mutated malignancies, including non-small cell lung cancer and colorectal cancer.

Olaparib (Lynparza)

Olaparib (Lynparza) is an antineoplastic agent, Poly(ADP-ribose) Polymerase 1;2;3 inhibitor. (PARP 1;2;3 inhibitor).

Lynparza is a poly (ADP-ribose) polymerase (PARP) inhibitor indicated for the treatment of adult patients with deleterious or suspected deleterious germline BRCA-mutated advanced ovarian cancer who have been treated with three or more prior lines of chemotherapy. Select patients for therapy based on an FDA-approved companion diagnostic for Lynparza.

Talazoparib

Talazoparib is a poly(ADP-ribose) Polymerase 1, 2 (PARP 1;2 inhibitor).

Talazoparib was approved by the FDA for use in germline BRCA mutated, HER2 negative, locally advanced or metastatic breast cancer on October 16, 2018 under the trade name Talzenna. Talazoparib prevents PARP-mediated repair of DNA damage in cancer cells, allowing accumulation of damage and PARP-DNA complexes. Repair related errors by error prone secondary repair pathways may also contribute to the cytotoxicity of Talazoparib. Talazoparib is indicated for the treatment of deleterious or suspected deleterious germline BRCA mutated, HER2 negative locally advanced or metastatic breast cancer in adults.

Niraparib (Zejula)

Niraparib (ZEJULA) is an inhibitor of poly (ADP-ribose) polymerase (PARP) with potential antineoplastic activity. PARP Inhibitor MK4827 inhibits PARP activity, enhancing the accumulation of DNA strand breaks and promoting genomic instability and apoptosis. The PARP family of proteins detect and repair single strand DNA breaks by the base-excision repair (BER) pathway. The specific PARP family member target for PARP inhibitor MK4827 is unknown. (NCI Thesaurus)

ZEJULA is a poly(ADP-ribose) polymerase (PARP) inhibitor indicated for the maintenance treatment of adult patients with recurrent epithelial ovarian, fallopian tube, or primary peritoneal cancer who are in a complete or partial response to platinum-based chemotherapy.

Rucaparib (Rubraca)

Rucaparib is a potent mammalian poly(ADP-ribose) polymerase 1, 2 and 3 inhibitor with anticancer properties (PARP 1;2;3 inhibitor).

Rucaparib is an inhibitor of PARP-1, PARP-2, and PARP-3. Via an inhibitory effect on the PARP enzymatic activity, rucaparib decreases the formation of PARP-DNA complexes resulting in DNA damage, apoptosis, and cell death. It is proposed that PARP inhibition specifically targets tumor cells with preexisting HRD, such as those cells possessing mutations in the BRCA1 or BRCA2 genes.

Irinotecan

Irinotecan is a topoisomerase inhibitor used for chemotherapy. It is a water-soluble analogue of camptothecin, which is extracted from Camptotheca acuminata tree. The bis-piperidine side chain in the structure of irinotecan bestows enhanced water solubility. As an anticancer drug, irinotecan was first commercially available in Japan in 1994 to treat various cancers such as lung, cervical and ovarian cancer. Approved by the FDA in 1996, irinotecan is used to treat colorectal cancer and pancreatic adenocarcinoma. Irinotecan liposome was approved by the FDA in February 2024.

Tegafur

Tegafur (INN, BAN, USAN) is a prodrug of Fluorouracil (5-FU), an antineoplastic agent used as the treatment of various cancers such as advanced gastric and colorectal cancers. It is a pyrimidine analogue used in combination therapies as an active chemotherapeutic agent in conjunction with Gimeracil and Oteracil, or along with Fluorouracil as Tegafur-uracil. Tegafur is usually given in combination with other drugs that enhance the bioavailability of the 5-FU by blocking the enzyme responsible for its degradation, or serves to limit the toxicity of 5-FU by ensuring high concentrations of 5-FU at a lower dose of tegafur. When converted and bioactivated to 5-FU, the drug mediates an anticancer activity by inhibiting thymidylate synthase (TS) during the pyrimidine pathway involved in DNA synthesis.

Oxaliplatin

Oxaliplatin is a platinum-based chemotherapy drug in the same family as cisplatin and carboplatin. Like most platinum-based compounds,

oxaliplatin's mechanism of action is primarily through DNA damage through DNA crosslinking. However, due to the structure of oxaliplatin, its adducts make the binding of mismatch repair protein to DNA harder compared to cisplatin or carboplatin's adducts, resulting in greater cytotoxic effects. Oxaliplatin, in combination with infusional fluorouracil and leucovorin, is indicated for the treatment of advanced colorectal cancer and adjuvant treatment of stage III colon cancer in patients who have undergone complete resection of the primary tumor.

Cobimetinib

Cobimetinib is a reversible inhibitor of mitogen-activated protein kinase 1 (MAPK)/extracellular signal regulated kinase 1 (MEK1) and MEK2. MEK inhibitor Cobimetinib specifically binds to and inhibits the catalytic activity of MEK1, resulting in inhibition of extracellular signal-related kinase 2 (ERK2) phosphorylation and activation and decreased tumor cell proliferation. Cobimetinib targets kinase activity in the RAS/RAF/MEK/ERK pathway.

APR-246

APR-246 is a first-in-class agent targeting mutant p53. In vitro and in vivo preclinical models have demonstrated that APR-246 has excellent efficacy in OC (both adenocarcinoma and squamous cell carcinoma) and potently synergises with chemotherapies used in the treatment of OC, restoring sensitivity to chemotherapy-resistant tumours. An initial phase I clinical trial has shown APR-246 to be safe in humans and early results from a currently running phase Ib/II trial of APR-246 with carboplatin and liposomal doxorubicin in ovarian cancer have been promising. Together, these data provide a strong rationale for investigating the efficacy of APR-246 in OC.

APR-246 has been used in trials studying the treatment of Prostatic Neoplasms, Hematologic Neoplasms, and Platinum Sensitive Recurrent High-grade Serous Ovarian Cancer With Mutated p53.

APR-246 is an analogue of PRIMA-1, which modifies the core domain of mutant p53, resulting in restoration of wild-type p53 conformation and reactivation of normal p53 function, leading to increased cell cycle arrest and tumor cell death (PMID: 20498645).

Luspatercept-aamt

Luspatercept-aamt (REBLOZYL) is approved for adult patients with very low- to intermediate-risk myelodysplastic syndromes with ring sideroblasts (MDS-RS) or with myelodysplastic/myeloproliferative neoplasm with ring sideroblasts and thrombocytosis (MDS/MPN-RS-T).

H3B-8800

H3B-8800 is a spliceosome inhibitor. H3B-8800 preferentially targets cells with spliceosome complexes containing mutant splicing factor 3B1 (SF3B1) protein, modulating intron splicing leading to increased death in cancer cells while having little effect on the viability cells with wild-type SF3B1. Both normal and aberrant mature mRNA are suppressed in mutant and wild-type cells, the selectivity of the lethal effect is thought to be due to the presence of mutant SF3B1 and its implications rather than a change in mechanism or potency of effect on the mutant protein over the wild-type. H3B-8800 was granted orphan drug status by the FDA in August 2017 and is in clinical trials for the treatment of acute myelogenous leukemia and chronic myelomonocytic leukemia.

Imetelstat

Imetelstat directly and competitively inhibits human telomerase. It is used to treat anemia in patients with myelodysplastic syndromes (MDS). It is indicated for the treatment of adult patients with low- to intermediate-risk MDS with transfusion-dependent anemia requiring four or more red blood cell units over eight weeks who have not responded to, are no longer responsive to, or are ineligible for erythropoiesis-stimulating agents.

Potential Clinical Trials

Trial URL	Status	Title	Disease	Drug	Sites
https://clinicaltrials.gov/study/NCT07020221	Recruiting	A Phase 1/2, Open-label Study of VS-7375, a KRAS G12D (ON/OFF) Inhibitor, as Monotherapy and in Combination, in Patients With Advanced KRAS G12D-Mutated Solid Tumors	Pancreatic Cancer	VS-7375, Cetuximab, Carboplatin + Pemetrexed + Pembrolizumab, Gemcitabine, Gemcitabine + Nab-paclitaxel	Cedars-Sinai Medical Center, Los Angeles, California 90048

https://clinicaltrials.gov/study/NCT07409272	Recruiting	A Phase 3, Double-blind, Placebo-controlled, Randomized Study to Assess the Efficacy and Safety of ASP3082 in Combination With mFOLFIRINOX or NALIRIFOX as First-line Treatment in Participants With KRAS G12D Mutated Metastatic Pancreatic Adenocarcinoma	Pancreatic Cancer	Setidegrasib, Oxaliplatin, Leucovorin, Irinotecan, fluorouracil, liposomal irinotecan, Placebo	University of Arizona Cancer Center - North Campus, Tucson, Arizona 85719
https://clinicaltrials.gov/study/NCT06586515	Recruiting	A Phase 1a/1b Trial of LY3962673 in Participants With KRAS G12D-Mutant Solid Tumors	Pancreatic Cancer	LY3962673, Cetuximab, Gemcitabine, nab-paclitaxel, Oxaliplatin, leucovorin, Irinotecan, 5-fluorouracil	City of Hope, Duarte, California 91010

Detailed Results

Single Nucleotide Variant (SNV) and Insertions-Deletions (INDELS)								
Gene name	Hgvsnp	Hgvsc	Amino acids	Codons	Consequence	Allele frequency	Read depth	Predicted effect on protein
KRAS	NP_203524.1:p.Gly12Asp	NM_033360.2:c.35G>A	G/D	gGt/gAt	missense_variant	70.77	65	deleterious
TP53	NP_000537.3:p.Ser392PhefsTer79	NM_000546.5:c.1174dup	S/FX	tca/tTca	frameshift_variant	31.43	105	0
TP53	NP_000537.3:p.Ser392LeufsTer79	NM_000546.5:c.1173dup	-/X	-/C	frameshift_variant	25.71	105	0
MSH6	NP_000170.1:p.Trp365Arg	NM_000179.2:c.1093T>C	W/R	Tgg/Cgg	missense_variant	24.35	115	deleterious
CTC1	NP_079375.3:p.Arg542Gln	NM_025099.5:c.1625G>A	R/Q	cGg/cAg	missense_variant	23.53	68	tolerated
SF3B1	NP_036565.2:p.Lys666Thr	NM_012433.3:c.1997A>C	K/T	aAg/aCg	missense_variant	23.36	107	deleterious
DPP4 (RNA)	NP_001926.2:p.Gln505Ter	NM_001935.3:c.1513C>T	Q/*	Cag/Tag	stop_gained	27.74	137	0

Methodology and Test Background

This is a next generation sequencing (NGS) test that involves separate analysis of DNA and RNA panels for abnormalities that are reported to be altered in various types of solid tumors. The DNA panel is composed of 434 genes and the RNA panel is composed of >1600 genes. The DNA and RNA components of this assay were developed, validated, and set up as separate workflows, with independent extraction, library preparation, sequencing, and analysis pipelines. The NGS assay also detects several viruses that are important in oncology, including EBV, HPV, HTLV1, and TTV. TTV (torque teno virus) was first discovered in a patient with non-A-E hepatitis and is now regarded as a part of the human virome. In general, TTV does not cause pathology in immunocompetent individuals. TTV is considered as a marker of immune competence in patients with immunological impairment and inflammatory disorders. High TTV load is associated with increased risk of infection. In patients with organ transplant, low TTV load is associated with an increased risk of rejection.

Nucleic acid is isolated from paraffin-embedded tissue. For optimal results neoplastic cells should be greater than 30% of the analyzed cells. H&E-sections are reviewed by a pathologist and tumor-enrichment is performed by macrodissection when possible. Testing is performed using massive parallel sequencing of the coding DNA of the listed genes. This includes sequencing of all the exons as well as approximately 50 nucleotides at the 5' and 3' ends of each coding exon to detect splice site abnormalities. The TERT promoter region, including the hotspots at -124 and -146 bp, is also covered. Our DNA sequencing method has a sensitivity of 3% for detecting hotspot mutations and 5% for detecting single nucleotide variants (SNVs) and small (<60 bp) insertions/ deletions (indels). MSI status is inferred by interrogating all available genomic microsatellites covered. Borderline MSI results by NGS are confirmed by fragment analysis. Tumor mutational burden (TMB) is measured by counting all nonsynonymous variants and filter settings as follows: (A) Pass all filters; (B) inside genes; (C) had a mutant allele frequency >5%; (D) not found in the dbSNP (to exclude germline variations). The median for TMB is 10 mutations/Mb based on lung carcinoma analysis. The cut off for other types of tumors is not well-established at this time. Significant gene amplification and deletion (copy number variants) are also reported. Targeted RNA NGS is performed by hybrid capture and duplicates are excluded for levels measurements. The Universal Human Reference (UHR) RNA is used as control. All detected fusion transcripts are reported. While the major focus of the RNA analysis is the detection of fusion mRNA, mutations in the expressed RNA of the analyzed genes, HLA class I genotyping, and Epstein-Barr virus (EBV), human papillomavirus (HPV), human T-lymphotropic virus type-1 (HTLV1), and torque teno virus (TTV) viral RNA are also analyzed and reported. B- and T-cell clonality will be reported, if clonal or clinically relevant. The sensitivity of this assay in detecting fusion mRNA is between 5% and 10%. This test specifically covers translocations that lead to the expression of fusion RNA. Translocations that lead to deregulation of expression can be addressed by this test if compared to the expression proper normal control. Since the clinical relevance of the RNA expression level of most of the genes is not characterized at this time, only a few specific genes will be commented on when abnormalities are detected. CD274 (PD-L1) mRNA levels are reported when they are significantly elevated. This assay is not designed to detect minimal residual disease and should be used for diagnosis. Performance of the assays may vary dependent on the quantity and quality of nucleic acid, sample preparation and sample age. Decalcified specimens have not been validated. Decalcification with strong acids is not recommended and may lead to poor nucleic acid quality and suboptimal results. The testing is not validated to detect germline abnormalities. Potential germline mutations detected incidentally should be confirmed by tests specifically designed for detecting germline abnormalities.

Based on our validation study, the following exonic regions of the genes listed below are not covered appropriately <100X coverage and sequencing by NGS may not be reliable in these regions. The poor coverage is primarily due to the inherent difficulty in obtaining adequate sequencing coverage in regions with high GC content. No well-characterized hotspots are present in these regions. ASXL1 NM_001164603 20:30946620-30946635, ATM NM_000051 11:108186550-108186638, BAP1 NM_004656 3:52443858-52443894, BCR NM_004327 22:23652510-23652620, BRD4 NM_058243 19:15353808-15354193, 5355041-15355411, CCNE1 NM_001238 19:30303463-30303485, CD274 NM_001267706 9:5456109-5456165, CD79A NM_001783 19:42384736-42384805, CSF3R NM_000760 1:36937667-36937740, DDX11 NM_001257144 12:31240872-31240917, ERBB3 NM_001982 12:56492284-56492359, FANCI NM_001113378 15:89835919-89836052, FLT3 NM_004119 13:28674605-28674652, FLT4 NM_002020 5:180035281-180035284, GEN1 NM_001130009 2:17954486-17954525, H3-3A NM_002107 1:226259140-226259180, IRS2 NM_003749 13:110437126-110437363, 110437805-110437899, 110438359-110438400, JAK1 NM_002227 1:65309747-65309771, MAGI2 NM_012301 7:77648719-77649044, MITF NM_000248 3:70005606-70005681, MYCL NM_001033081 1:40367518-40367565, NF1 NM_000267 17:29664837-29664898, NOTCH2 NM_001200001 1:120572528-120572610, PBRM1 NM_018313 3:52677264-52677322, PIK3R2 NM_005027 19:18272089-18272305, PMS2 NM_000535 7:6013024-6013173, RANBP2 NM_006267 2:109363166-109363254, 109367779-109367838, 109367984-109368069, 109369453-109369497, 109378578-109378651, RHEB NM_005614 7:151216546-151216597, SUFU NM_001178133 10:104263911-104264039, TNFRSF14 NM_003820 1:2494304-2494335. Data was annotated against GRCh37 (hg19) reference human genome using Nirvana v3.17.0. This human reference is based on the GRCh37.p6 version of the human genome assembly.

The table below may contain a partial list of the tested DNA genes. For a complete list, please go to:
<https://genomictestingcooperative.com/genomic-tests/solid-tumor-profile-plus/> (click the DNA tab)

The table below contains a partial list of the tested RNA genes (Fusions/Expression). For a complete list, please go to:
<https://genomictestingcooperative.com/genomic-tests/solid-tumor-profile-plus/> (click the RNA tab)

Tested genes

Genes Tested for Abnormalities in Coding Sequence																
ABCB7	ATRX	BTK	CDKN2B	DKC1	FANCA	FLI1	GREM1	INPP4B	LIG4	MSH2	NSD2 (WHSC1)	POLE	RAF1	SDHD	STAG2	TP53
ABL1	AURKA	CALR	CDKN2C	DNM2	FANCB	FLT1	GRIN2A	IRF2	LMO1	MSH6	NTRK1	POT1	RANBP2	SEC23B	STAT3	TRAF3
ABL2	AURKB	CARD11	CEBPA	DNMT3A	FANCC	FLT3	GRM3	IRF4	LPIN2	MTOR	NTRK2	PPM1D	RARA	SETBP1	STAT4	TSC1
ABRAXAS1	AURKC	CBFB	CHD2	DOT1L	FANCD2	FLT4	GSK3B	IRS2	LRP1B	MUTYH	NTRK3	PPP2R1A	RB1	SETD2	STAT6	TSC2
ACD	AXIN1	CBL	CHD4	EED	FANCE	FOXL2	GSKIP	JAGN1	LYN	MVK	NUP93	PRDM1	RBBP6	SF3B1	STK11	TSHR
ACVR1B	AXIN2	CBLB	CHEK1	EGFR	FANCF	FOXP1	H3-3A (H3F3A)	JAK1	LYST	MYC	PAK3	PREX2	RBM10	SLIT2	SUFU	U2AF1
ADA	AXL	CBLC	CHEK2	EGLN1	FANCG	FRS2	H3C2	JAK2	LZTR1	MYCL	PALB2	PRKAR1A	RBM8A	SLX4	SUZ12	U2AF2
ADGRA2	B2M	CCN6 (WISP3)	CIC	ELANE	FANCI	FUBP1	HAX1	JAK3	MAGI2	MYCN	PAX5	PRKCI	REEP5	SMAD2	SYK	VEGFA
AK2	BAP1	CCND1	CREBBP	EMSY	FANCL	G6PC3	HGF	JUN	MAP2K1	MYD88	PBRM1	PRKDC	RET	SMAD3	TAF1	VHL
AKT1	BARD1	CCND2	CRKL	EP300	FANCM	GABRA6	HNF1A	KAT6A	MAP2K2	NBN	PDCD1LG2	PRKN (PARK2)	RHEB	SMAD4	TAL1	WAS
AKT2	BCL2	CCND3	CRLF2	EPAS1	FAS	GALNT12	HOXA11	KDM5A	MAP2K4	NF1	PDGFRA	PRSS1	RHOA	SMAD9	TBX3	WT1
AKT3	BCL2L1	CCNE1	CSF1R	EPCAM	FAT1	GATA1	HOXB13	KDM5C	MAP3K1	NF2	PDGFRB	PRSS8	RICTOR	SMARCA4	TCF3	XPO1
ALK	BCL2L2	CD274	CSF3R	EPHA3	FBXW7	GATA2	HRAS	KDM6A	MAP3K14	NFE2L2	PDK1	PSTPIP1	RIT1	SMARCB1	TCIRG1	XRCC2
AMER1	BCL6	CD79A	CTC1	EPHA5	FGF10	GATA3	HSD3B1	KDR	MAPK1	NFKBIA	PHF6	PTCH1	RNF168	SMC1A	TENT5C (FAM46C)	XRCC3
ANKRD26	BCOR	CD79B	CTCF	EPHA7	FGF14	GATA4	HSP90AA1	KEAP1	MCL1	NHP2	PIK3C2B	PTEN	RNF43	SMC3	TERC	ZBTB2
APC	BCORL1	CDAN1	CTNNA1	EPHB1	FGF19	GATA6	ID3	KEL	MDM2	NKX2-1	PIK3CA	PTPN11	ROS1	SMO	TERF1	ZNF217
AR	BCR	CDC73	CTNNA1	ERBB2	FGF23	GEN1	IDH1	KIF23	MDM4	NLRP3	PIK3CB	QKI	RPTOR	SNCAIP	TERF2	ZNF703
ARAF	BIRC3	CDH1	CUL3	ERBB3	FGF3	GFI1	IDH2	KIT	MED12	NME1	PIK3CG	RAB27A	RTEL1	SOC1	TERF2IP	ZRSR2
ARFRP1	BLM	CDIN1 (C15orf41)	CUX1	ERBB4	FGF4	GFI1B	IGF1R	KLF1	MEF2B	NOP10	PIK3R1	RAC1	RUNX1	SOX10	TERT	-
ARID1A	BMPR1A	CDK12	CXCR4	ERCC4	FGF6	GID4	IGF2	KLHL6	MEFV	NOTCH1	PIK3R2	RAD21	RUNX1T1	SOX2	TET2	-
ARID1B	BRAF	CDK4	CYLD	ERG	FGFR1	GLI1	IKBKE	KLLN	MEN1	NOTCH2	PIM1	RAD50	SAMD9L	SOX9	TGFBR2	-
ARID2	BRCA1	CDK6	DAXX	ERRF1	FGFR2	GLI2	IKZF1	KMT2A	MET	NOTCH3	PLCG1	RAD51	SBDS	SPEN	TNFAIP3	-
ASXL1	BRCA2	CDK8	DDR2	ESR1	FGFR3	GNA11	IKZF3	KMT2B	MITF	NPM1	PLCG2	RAD51B	SBF2	SPOP	TNFRSF14	-
ATG2B	BRD4	CDKN1A	DDX11	ETV6	FGFR4	GNA13	IL2RG	KMT2C	MLH1	NR0B1	PMS1	RAD51C	SDHA	SPTA1	TNFRSF1A	-
ATM	BRIP1	CDKN1B	DDX41	EXO1	FH	GNAQ	IL7R	KMT2D	MPL	NRAS	PMS2	RAD51D	SDHB	SRC	TOP1	-
ATR	BTG1	CDKN2A	DICER1	EZH2	FLCN	GNAS	INHBA	KRAS	MRE11	NSD1	POLD1	RAD54L	SDHC	SRSF2	TOP2A	-

RNA Fusions/Expression

Fusion/Expression													
ABL1	BCL6	CD274 (PD-L1)	EGFR	ESR1	FLI1	IKZF3	MAP3K1	NRG1	NUP98	PML	RET	SS18	THADA
AKT3	BRAF	CIC	ERG	FGFR1	FOXO1	JAK2	MECOM	NTRK1	PAX8	PPARG	RHOA	STAT6	TMPSR2
ALK	CAMTA1	CREB1	ETS1	FGFR2	FUS	KIAA1549	MYB	NTRK2	PDGFRA	PRKACA	ROS1	TAL1	YAP1
AR	CBFB	CREBBP	ETV1	FGFR3	GLI1	KMT2A	MYC	NTRK3	PDGFRB	RAF1	RUNX1	TCF3	YWHA
BCL2	CCND1	ERBB2	ETV6	FIP1L1	HMG2	MAML2	NOTCH1	NUP214	PICALM	RARA	RUNX1T1	TFG	ZFTA

Reference

1. Daraxonasib in Advanced RAS-Mutated Pancreatic Cancer. Sun X, Chen B, Wang S. N Engl J Med. 2026 Jul 23;395(4):414. doi: 10.1056/NEJMc2607459. PMID: 42485639.
2. PARPs and PARP inhibitors: molecular mechanisms and clinical applications. Wang F, Guo Z, Carr MJ, Shi W. Mol Biomed. 2025 Dec 29;6(1):152. doi: 10.1186/s43556-025-00385-1. PMID: 41460301.
3. Advances in pancreatic cancer early diagnosis, prevention, and treatment: The past, the present, and the future. Mannucci A, Goel A. CA Cancer J Clin. 2026 Jan-Feb;76(1):e70035. doi: 10.3322/caac.70035. Epub 2025 Sep 19. PMID: 40971231.

Electronic Signature

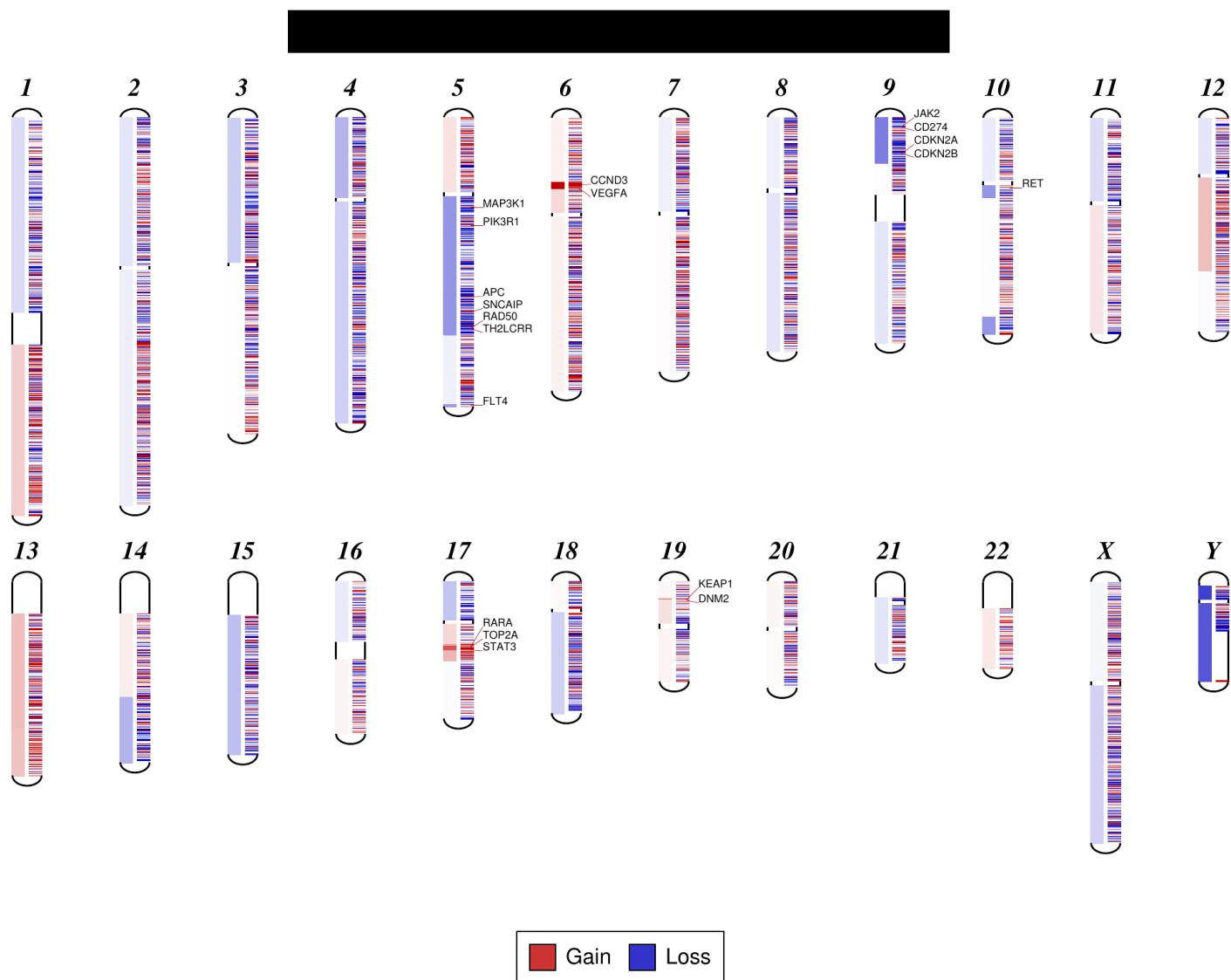
Ahmad Charifa, M.D.

TX Genomic Testing Cooperative, LCA serves as the coordinating laboratory for this assay and is responsible for overall test performance and reporting. The test (sample processing, sequencing and data generation) was performed at TX Genomic Testing Cooperative, LCA, 8800 Technology Forest Place Suite 140 The Woodlands, TX 77381. Medical Director Maher Albitar, M.D. Analysis of the data was performed by Genomic Testing Cooperative, LCA, 25371 Commercentre Drive, Lake Forest, CA 92630. Medical Director: Maher Albitar, M.D. (CLIA #: 05D2111917 CAP #: 9441574). The signing pathologist / Medical Director is responsible for the accuracy and interpretation of results and the release of this report.

The test was developed and its performance characteristics have been determined by TX Genomic Testing Cooperative, LCA. This test has not been approved by the FDA. The FDA has determined such clearance or approval is not necessary. This laboratory is CLIA certified to perform high complexity clinical testing.

Additional Report Information

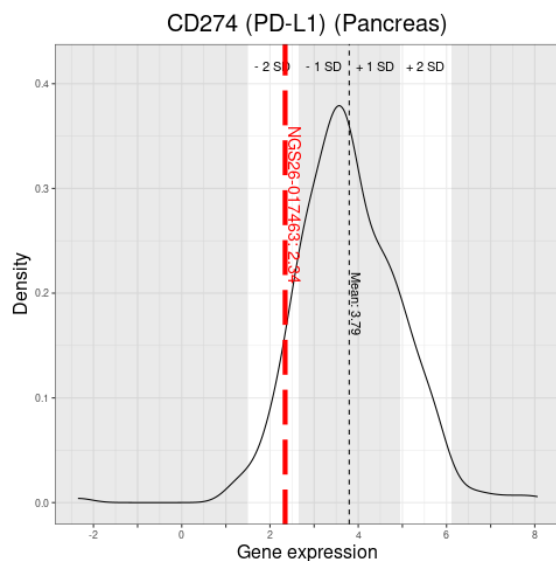
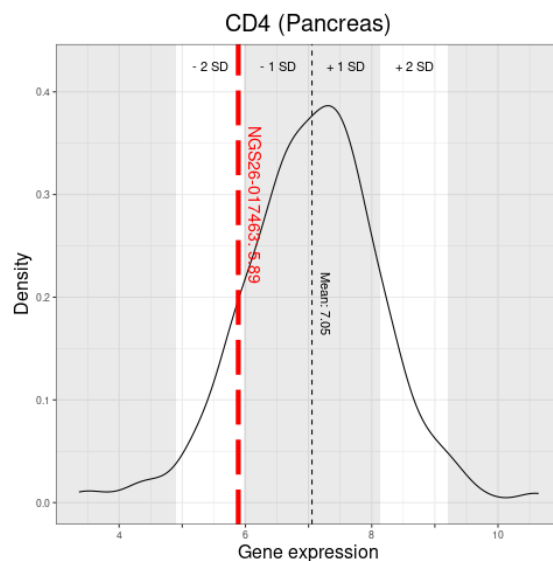
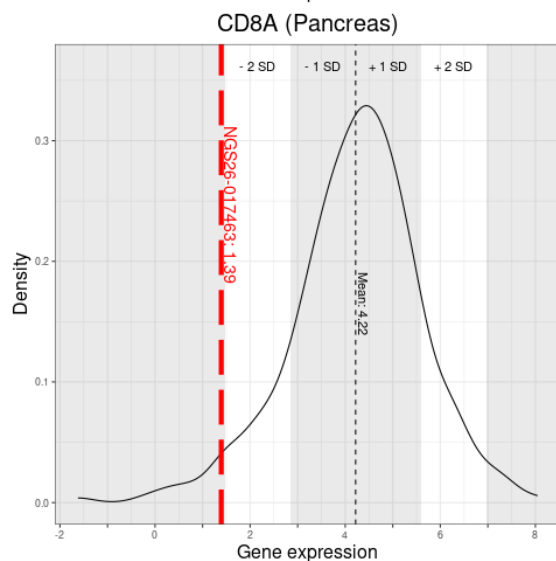
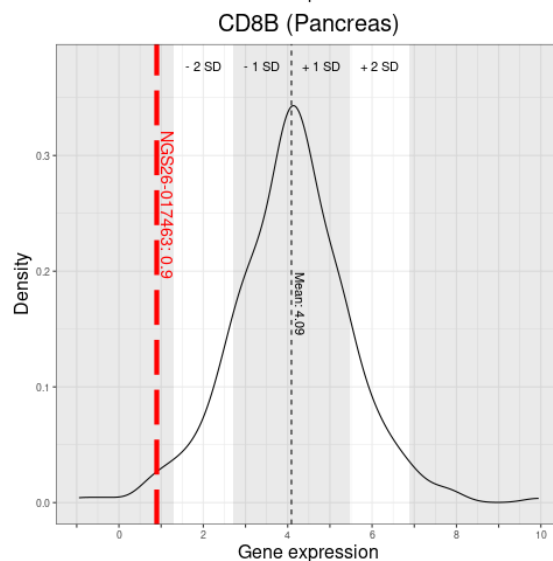
Chromosomal Abnormality Graph



Additional Report Information

RNA Expression Plots

These plots represent the distribution of the expression in log2 transformed TPM (transcript per million) for each gene across GTC's history for the specified disease. The mean for each distribution is denoted by the black dotted line, while the alternating shaded areas depict the standard deviation. The expression for the current patient is marked by the red dotted line.



Additional Report Information

RNA Expression Plots

