Pancreatic Sample
Michael Schmidt

Diagnosis
Acinar cell carcinoma

Accession No.
9628

xT

Date of Birth
1992-05-25

Sex
Male

Physician
Dr. Jerome House

Institution
Schmidt, Gutierrez and Lynch

Tumor specimen:
source Pancreatic
CollectedDate 2023-07-03
ReceivedDate 2023-07-03
TumorPercentage 60%

Normal specimen:
source Blood
CollectedDate 2023-07-10
ReceivedDate 2023-07-15

GENOMIC VARIANTS

Somatic - Potentially Actionable		variant allele fraction
MSH2	c.1906G>C p.A636P Nonsense-LOF	3.22%
PTEN	c.389G>C p.R130Q Spliceregionvariant-GOF	12.8%
U2AF1	c.3113A>G p.S34X Spliceregionvariant-GOF	29.63%
HRAS	c.35G>A p.G12D Nonsense-GOF	18.37%

Somatic - Biologically Relevant

NCSTN	c.3113A>G p.G12X Spliceregionvariant-GOF	4.75%

Germline - Pathogenic

No Germline - Pathogenic variants were found in the limited set of genes on which we report.

Pertinent Negatives

DICER1 STAG2

IMMUNOTHERAPY MARKERS

Tumor Mutational Burden

3 m/Mb 90%

Microsatellite Instability Status

Stable | Equivocal | High

FDA-APPROVED THERAPIES, Current Diagnosis

KRAS G12C Inhibitors	**Sotorasib**	NCCN, Consensus, Non-Small Cell Lung Cancer MSK OncoKB, Level 1 KRASp.G12C G12C-GOF

FDA-APPROVED THERAPIES, Other Indications

KRAS G12C Inhibitors	**Sotorasib**	NCCN, Consensus, Non-Small Cell Lung Cancer MSK OncoKB, Level 1 KRASp.G12C G12C-GOF

ADDITIONAL INDICATORS

Unfavorable Prognosis	NCCN, Consensus, Non-Small Cell Lung Cancer KRASp.G12C Gain-of-function

CLINICAL TRIALS

A Study of VS-6766 v. VS-6766 + Defactinib in Recurrent G12V, Other KRAS and BRAF Non-Small Cell Lung Cancer	**Phase 2** City, state - x mi **KRAS mutation**
A Phase 1/2 Study of MRTX849 in Patients With Cancer Having a KRAS G12C Mutation KRYSTAL-1	**Phase 1/2** City, state - x mi **KRAS mutation** **STK11 mutation**
First-in-human Study of DRP-104 (Sirpiglenastat) as Single Agent and in Combination With Atezolizumab in Patients With Advanced Solid Tumors. (NCT04471415)	**Phase 1/2** City, state - x mi **NFE2L2 mutation** **STK11 mutation**

VARIANTS OF UNKNOWN SIGNIFICANCE

Somatic	Mutation effect	Variant allele fraction
HRAS	c.35_36delinsAT p.G12X Nonsense-LOF NM_001011645	15.88%
PHF6	c.3113A>G p.R225X Missensevariant(exon2)-GOF NM_001011645	18.85%
PDGFRB	c.3113A>G p.T681I Nonsense-GOF NM_001011645	4.67%
PDGFRB	c.3113A>G p.T681I Spliceregionvariant-LOF NM_001011645	6.65%
FBXW7	c.1394G>A p.R465H Spliceregionvariant-LOF NM_001011645	2.73%
KIT	c.2458G>T p.G648D Frameshift-LOF NM_001011645	5.95%
SDHD	c.34G>A p.G12S Nonsense-GOF NM_001011645	2.19%
BLM	c.2207_2212delinsTAGATTC p.Y736fs*4 Spliceregionvariant-GOF NM_001011645	6.96%
KIT	c.1676T>A p.L813P Spliceregionvariant-LOF NM_001011645	2.61%
CTNNB1	c.94G>A p.G34E Nonsense-LOF NM_001011645	4.01%
ARHGAP45	c.416G>A p.R139H Nonsense-GOF NM_001011645	6.73%
HDAC2	c.3113A>G p.E455fs*7 Frameshift-LOF NM_001011645	3.19%

LOW COVERAGE REGIONS

NF1 FBXW7 ARID2

SOMATIC VARIANT DETAILS - POTENTIALLY ACTIONABLE

MSH2 c.1906G>C p.A636P Nonsense-LOF VAF: 3.22%

FAT1 encodes a transmembrane protein involved in tumor suppressor signaling. FAT1 protein can regulate transcriptional activity by sequestering beta-catenin, thereby preventing it from entering the nucleus. Loss of function mutations and copy number loss of FAT1 are associated with cancer progression.

PTEN c.389G>C p.R130Q Spliceregionvariant-GOF VAF: 12.8%

PTEN encodes a phosphatase that acts as a tumor suppressor by negatively regulating the PI3K-AKT-mTOR pathway. Loss of function mutations, copy number loss, and underexpression of PTEN are associated with cancer progression.

U2AF1 c.3113A>G p.S34X Spliceregionvariant-GOF VAF: 29.63%

TP53 encodes a protein that is a transcription factor that regulates the expression of genes involved in cell cycle arrest, apoptosis, and DNA repair. TP53 is a tumor suppressor gene that is mutated in many cancers. Mutations in TP53 are associated with cancer progression.

HRAS c.35G>A p.G12D Nonsense-GOF VAF: 18.37%

RBM10 encodes a protein that contains a RNA-binding motif and interacts with RNA homopolymers, and is thought to function in regulating alternative splicing. Loss of function mutations and copy number loss of RBM10 are associated with cancer progression.

SOMATIC VARIANT DETAILS - BIOLOGICALLY RELEVANT

NCSTN c.3113A>G p.G12X Spliceregionvariant-GOF VAF: 4.75%

ARID2 encodes a protein that is a subunit of the SWI/SNF chromatin remodeling complex SWI/SNF-B or PBAF. This complex functions in ligand-dependent transcriptional activation. Loss of function mutations and copy number loss of ARID2 are associated with cancer progression.

CLINICAL HISTORY

Diagnosed on

2023-07-02