Colorectal Sample
Micheal Baker

Diagnosis
Lymphoma

Accession No.
9716

xT

Date of Birth
1964-04-29

Sex
Female

Physician
Dr. Joshua Villa

Institution
Contreras PLC

Tumor specimen:
source Colorectal
CollectedDate 2023-11-28
ReceivedDate 2023-12-02
TumorPercentage 92%

Normal specimen:
source Blood
CollectedDate 2023-12-02
ReceivedDate 2023-12-02

GENOMIC VARIANTS

Somatic - Potentially Actionable — **variant allele fraction**

AKT1	c.49G>A p.E17K Stopgain-LOF	39.66%

Somatic - Biologically Relevant

IKZF1	c.3113A>G p.E17K Nonsense-LOF	26.49%
PIK3CA	c.1635G>T p.H1047X Frameshift-LOF	3.5%

Germline - Pathogenic

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

Pertinent Negatives

HDAC2 | PIK3CA | PDGFRA

IMMUNOTHERAPY MARKERS

Tumor Mutational Burden

25 m/Mb 37%

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
CHEK2	c.1283C>T p.S428F Spliceregionvariant-LOF NM_001011645	21.2%
PRKCA	c.1387G>C p.D463H Spliceregionvariant-GOF NM_001011645	19.37%
RNF43	c.954G>T p.P154L Frameshift-LOF NM_001011645	1.85%
CSF3R	c.3113A>G p.G751A Spliceregionvariant-LOF NM_001011645	5.63%
MUTYH	c.1014G>C p.Q338H Frameshift-GOF NM_001011645	6.94%
RNF43	c.420C>G p.E318D Nonsense-GOF NM_001011645	1.17%
ERCC2	c.3113A>G p.F332V Spliceregionvariant-GOF NM_001011645	4.21%
BRCA1	c.68_69delAG p.E23Vfs*17 Spliceregionvariant-GOF NM_001011645	3.49%
B2M	c.2T>G p.M1R Spliceregionvariant-GOF NM_001011645	9.45%
PRKCA	c.1387G>C p.D463H Spliceregionvariant-GOF NM_001011645	8.16%

LOW COVERAGE REGIONS

BLM

SOMATIC VARIANT DETAILS - POTENTIALLY ACTIONABLE

AKT1 c.49G>A p.E17K Stopgain-LOF VAF: 39.66%

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.

SOMATIC VARIANT DETAILS - BIOLOGICALLY RELEVANT

IKZF1 c.3113A>G p.E17K Nonsense-LOF VAF: 26.49%

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.

PIK3CA c.1635G>T p.H1047X Frameshift-LOF VAF: 3.5%

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.

CLINICAL HISTORY

Diagnosed on

2023-11-27