Breast Sample
Rachel Anderson

Diagnosis
Invasive lobular carcinoma

Accession No.
4816

xT

Date of Birth
1951-07-18

Sex
Male

Physician
Dr. Jessica Morgan

Institution
Williams Ltd

Tumor specimen:
source Breast
CollectedDate 2023-12-28
ReceivedDate 2023-12-30
TumorPercentage 50%

Normal specimen:
source Blood
CollectedDate 2023-12-31
ReceivedDate 2023-12-31

GENOMIC VARIANTS

Somatic - Potentially Actionable		variant allele fraction
IDH1	c.394_395delinsGT p.R132S Spliceregionvariant-GOF	35.31%
BTK	c.3113A>G p.C481X Spliceregionvariant-LOF	2.98%
PDGFRA	c.1154_1155delinsTA p.D842V Nonsense-LOF	1.26%

Somatic - Biologically Relevant		
CTNNB1	c.122_123delinsTT p.S37C Frameshift-LOF	12.4%
BRAF	c.1798G>A p.S45P Stopgain-LOF	7.19%
TP53	c.638G>T p.R248W Spliceregionvariant-GOF	13.7%

Germline - Pathogenic

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

Pertinent Negatives

MPL EGFR JAK2

IMMUNOTHERAPY MARKERS

Tumor Mutational Burden

16 m/Mb 65%

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**
NF1	c.6926del p.N1465S Spliceregionvariant-LOF NM_001011645	12.41%
BRCA1	c.68_69delAG p.Q1756Pfs Frameshift-GOF NM_001011645	9.58%
NCSTN	c.3113A>G p.A572G Spliceregionvariant-GOF NM_001011645	10.81%
FGFR3	c.746C>G p.G380R Nonsense-GOF NM_001011645	7.54%
SMO	c.3113A>G p.A374E Missensevariant(exon2)-GOF NM_001011645	6.67%
PTPN11	c.1508G>C p.G503A Stopgain-LOF NM_001011645	7.27%
CSF3R	c.3113A>G p.G751A Frameshift-LOF NM_001011645	2.92%
Germline	**Mutation effect**	**Condition**
PAX5	c.547G>A p.A322T Spliceregionvariant-LOF NM_001011645	important

LOW COVERAGE REGIONS

FGFR4 HBB

SOMATIC VARIANT DETAILS - POTENTIALLY ACTIONABLE

IDH1 c.394_395delinsGT p.R132S Spliceregionvariant-GOF VAF: 35.31%

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.

BTK c.3113A>G p.C481X Spliceregionvariant-LOF VAF: 2.98%

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PDGFRA c.1154_1155delinsTA p.D842V Nonsense-LOF VAF: 1.26%

BCL11B encodes a C2H2-type zinc finger protein that functions as a transcriptional repressor and plays a role in T-cell development and survival. Loss of function mutations, copy number loss, and fusions resulting in the underexpression of BCL11B are associated with cancer progression.

SOMATIC VARIANT DETAILS - BIOLOGICALLY RELEVANT

CTNNB1 c.122_123delinsTT p.S37C Frameshift-LOF VAF: 12.4%

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.

BRAF c.1798G>A p.S45P Stopgain-LOF VAF: 7.19%

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.

TP53 c.638G>T p.R248W Spliceregionvariant-GOF VAF: 13.7%

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.

CLINICAL HISTORY

Diagnosed on

2023-12-20