

Consulting physician		Patient		Sample	
Provider	General Hospital	Name	Michelle Doe	Accession Number	D19-03598_S3
Physician	Dr. E Smith	Age	54	Collection site	Bone Marrow
Pathologist	Dr. R Jones	Gender	Female	Type	Biopsy
Report Date	Sep 1, 2020	Diagnosis	Acute myeloid leukemia	Collection date	Sep 1, 2020

## Panel Analysis: Hematological Cancer

Comprehensive genomic next generation sequencing test that targets variants in key genes known to be involved in myeloid malignancies such as AML, MDS, MPN, CML, CMML, and JMML.

### Overall comment

Patient specific comment

NPM1 mutations in the presence of FLT3-ITD have been associated with an intermediate prognosis [PMID:16076867, PMID:18450602, PMID:16455956, PMID:27288520, PMID:27055875].

### Analysis results: Positive

2 Variants of strong clinical significance, Tier 1	Approved treatments	Other findings
FLT3: p.Y597_E598insDYVDFREY, Pathogenic	Midostaurin	Trials: 1 Expanded Access 2 Phase 3 2 Phase 2 1 Phase 1/Phase 2
NPM1: p.W288fs*?, Pathogenic	-	Trials: 1 Phase 2
2 Variants of potential clinical significance, Tier 2	Approved treatments	Other findings
RAD21 †: p.L183fs*7, Likely Pathogenic	-	-
WT1: p.A387fs*4, Pathogenic	-	-
3 Variants of uncertain significance, Tier 3		

† Allele Fraction (AF) >40%. AF suggests that it may be germline and pathogenic or likely pathogenic. Recommend obtaining confirmatory germline testing.


### Interactions

Clinically relevant co-occurring variants are reported in the "interactions" section starting on page 2.

### Guidelines

Potentially relevant guidelines are reported in the "guidelines" section starting on page 2.

### Approval



Electronically signed on: Sep 1, 2020 by Dr. Jones, Lab Director

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## GUIDELINES

The 2017 ELN recommendations for AML note that screening for mutations in NPM1, CEBPA, RUNX1, FLT3 (for ITD and TKD alterations as well as mutant-to-wild-type ratio), TP53, and ASXL1 may be useful for diagnosis, risk assessment, prognostication, and treatment [31]. The 2017 ELN recommendations place AML patients with wild-type NPM1 plus a high allelic ratio of FLT3-ITD (greater than or equal to 0.5) in the adverse risk category, while patients with mutated NPM1 plus a high allelic ratio of FLT3-ITD, as well as patients with wild-type NPM1 plus a low allelic ratio of FLT3-ITD (less than 0.5), are placed in the intermediate risk category.; AML patients with mutated NPM1 and a low allelic ratio of FLT3 are placed in the favorable risk category [31]. These guidelines additionally state that midostaurin plus standard chemotherapy may be considered for both induction and consolidation therapy in AML patients aged 18-60 years with an activating FLT3 mutation [31].

## INTERACTIONS

NPM1 mutations in the presence of FLT3-ITD have been associated with an intermediate prognosis [112, 110, 124, 83, 130].

## TREATMENT OPTIONS

### Therapies with potential clinical benefit (1)

#### MIDOSTAURIN

Midostaurin, a kinase inhibitor, is FDA- and EMA-approved for treating adult patients with aggressive systemic mastocytosis (ASM), systemic mastocytosis with associated hematological neoplasm (SM-AHN), or mast cell leukemia (MCL); midostaurin is FDA-approved for treating adult patients with newly diagnosed acute myeloid leukemia (AML) that is FLT3 mutation-positive, as detected by an FDA-approved test, in combination with standard cytarabine and daunorubicin induction and cytarabine consolidation (midostaurin is not indicated as a single-agent induction therapy for the treatment of patients with AML); midostaurin is EMA-approved for treating adult patients with newly diagnosed acute myeloid leukaemia (AML) who are FLT3 mutation-positive, in combination with standard daunorubicin and cytarabine induction and high-dose cytarabine consolidation chemotherapy, and for patients in complete response followed by midostaurin single agent maintenance therapy.

#### Sensitive

Gene	Classification	Variant
<b>FLT3</b>	Tier 1A Pathogenic	p.Y597_E598insDYVDFREY c.1770_1793dupCTACGTTGATTCAGAGAATATGA

## AVAILABLE CLINICAL TRIALS

### Expanded Access clinical trials (1)

#### CRENOLANIB

Compassionate Use of Crenolanib for Cancers With Platelet Derived Growth Factor Receptor Alpha (PDGFRa) Mutations, PDGFRa Amplifications or Fms-like Tyrosine Kinase 3 (FLT3) Mutations

[NCT03620318](#)

#### Qualifying variant

Gene	Classification	Variant	Contact
<b>FLT3</b>	Tier 1A Pathogenic	p.Y597_E598insDYVDFREY c. 1770_1793dupCTACGTTGATTC AGAGAATATGA	Vinay Jain, MD; info@arogpharma.com; 214-593-0500;

### Phase 3 clinical trials (2)

#### GILTERITINIB, MIDOSTAURIN

A Phase 3, Multicenter, Open-label, Randomized, Study of Gilteritinib Versus Midostaurin in Combination With Induction and Consolidation Therapy Followed by One-year Maintenance in Patients With Newly Diagnosed Acute Myeloid Leukemia (AML) or Myelodysplastic Syndromes With Excess Blasts-2 (MDS-EB2) With FLT3 Mutations Eligible for Intensive Chemotherapy (HOVON 156 AML / AMLSG 28-18)

[NCT04027309](#)

#### Qualifying variant

Gene	Classification	Variant	Contact
<b>FLT3</b>	Tier 1A Pathogenic	p.Y597_E598insDYVDFREY c. 1770_1793dupCTACGTTGATTC AGAGAATATGA	M. Raaijmakers, Prof. Dr.; hdc@erasmusmc.nl; +31 (0)10 7041560;

#### IDARUBICIN, CRENOLANIB, CYTARABINE, FLUDARABINE PHOSPHATE, MITOXANTRONE

Phase III Randomized, Double-blind, Placebo-controlled Study Investigating the Efficacy of the Addition of Crenolanib to Salvage Chemotherapy Versus Salvage Chemotherapy Alone in Subjects ≤ 75 Years of Age With Relapsed/Refractory FLT3 Mutated Acute Myeloid Leukemia

[NCT03250338](#)

#### Qualifying variant

Gene	Classification	Variant	Contact
			United States: CA, FL, IL, KS, MI, NC, NY General Contact; info@arogpharma.com; 214-593-0500;

## Phase 3 clinical trials (2)

Gene	Classification	Variant
<b>FLT3</b>	Tier 1A Pathogenic	p.Y597_E598insDYVDFREY c. 1770_1793dupCTACGTTGATTC AGAGAATATGA

## Phase 2 clinical trials (3)

### PONATINIB

Phase 2 Study of Ponatinib (Iclusig) for Prevention of Relapse After Allogeneic Stem Cell Transplantation (Allo-SCT) in FLT3-ITD AML Patients: the PONALLO Trial."

[NCT03690115](#)

#### Qualifying variant

Gene	Classification	Variant
<b>FLT3</b>	Tier 1A Pathogenic	p.Y597_E598insDYVDFREY c. 1770_1793dupCTACGTTGATTC AGAGAATATGA

#### Contact

Laure MORISSET; lморisset@ch-versailles.fr;  
 +33139239785;

### DECITABINE, MIDOSTAURIN

A Randomized Phase II Multicenter Study to Assess the Tolerability and Efficacy of the Addition of Midostaurin to 10-day Decitabine Treatment in Unfit Adult Acute Myeloid Leukemia and High Risk Myelodysplasia Patients

[NCT04097470](#)

#### Qualifying variant

Gene	Classification	Variant
<b>FLT3</b>	Tier 1A Pathogenic	p.Y597_E598insDYVDFREY c. 1770_1793dupCTACGTTGATTC AGAGAATATGA

#### Contact

Gerwin Huls, Prof.; g.huls@umcg.nl;  
 +31503612354;

### PEMBROLIZUMAB, 5-AZACYTIDINE

MRD-guided Treatment With Pembrolizumab and Azacitidine in NPM1mut AML Patients With an Imminent Hematological Relapse

[NCT03769532](#)

#### Qualifying variant

Gene	Classification	Variant
<b>NPM1</b>	Tier 1A Pathogenic	p.W288fs*? c.860_863dupTCTG

#### Contact

Uwe Platzbecker, MD; Uwe.Platzbecker@medizin.uni-leipzig.de;  
 +49 351 458 x2722;

## Phase 1/Phase 2 clinical trials (1)

### NMS-03592088

A Phase I/II Study of NMS-03592088, a FLT3, KIT and CSF1R Inhibitor, in Patients With Relapsed or Refractory AML or CMML

[NCT03922100](#)

#### Qualifying variant

Gene	Classification	Variant
<b>FLT3</b>	Tier 1A Pathogenic	p.Y597_E598insDYVDFREY c. 1770_1793dupCTACGTTGATTC AGAGAATATGA

#### Contact

Frank Gan; frank.gan@nervianoms.com;  
 +39.334.6513171;

## VARIANT DETAILS

### Variants of strong clinical significance (2)

#### FLT3 Y597\_E598insDYVDFREY

**Gene:** FLT3

**Exon:** 14

**Nucleotide:**

NM\_004119.2:

g.28608262\_2860826

3insTCATATTCTCTGA

AATCAACGTAG

c.1770\_1793dupCTAC

GTTGATTTCAGAGAATA

**Biomarker summary:** FLT3-Y597\_E598insDYVDFREY is predicted to be an activating mutation.

**Clinical relevance:** Activating FLT3 alterations have been reported to promote proliferation, inhibit apoptosis, and result in oncogenic transformation [48, 72, 140, 71, 84]. Activating alterations in FLT3 may predict sensitivity to small molecule multi-tyrosine kinase inhibitors, several of which have been approved by numerous agencies for certain indications [109, 105, 151, 78]. Midostaurin has been approved by the EMA for FLT3-positive acute myelocytic leukemia patients [118]. Additional second-generation inhibitors with greater specificity for Flt3 are also in clinical development [135, 25, 43].

## Variants of strong clinical significance (2)

TGA

**Amino Acid:** p.

Y597\_E598insDYVDFREY

**Allelic Fraction:** 31.0% (of 13551 reads)

**Classification:** Tier 1A

**Assessment:** Pathogenic

### Treatment options

1 Sensitive

6 Trials

**Disease summary:** Constitutive activation of Flt3 by internal tandem duplication (ITD) or tyrosine kinase domain (TKD) mutations has been reported to result in the activation of several signaling pathways, including those of Akt and Stat5, and has been reported to promote proliferation, survival, and transformation of myeloid cells [20, 60, 10, 96, 61, 76]. FLT3 mutations have been associated with elevated white blood cell and bone marrow blast counts in studies of acute myelocytic leukemia (AML), and have been reported most commonly in patients with normal cytogenetics [117, 42, 65, 6]. FLT3-ITD mutations in normal karyotype AML have been associated with poor prognosis in numerous scientific studies [98, 117, 134, 42, 65, 69]. However, recent studies have suggested that AML patients with a low allelic ratio of FLT3-ITD (generally defined as a mutant-to-wild-type ratio of lower than 0.5 as determined by quantitative DNA fragment length analysis) and concurrent NPM1 mutations have a favorable prognosis; patients with wild-type NPM1 and a low allelic ratio of FLT3-ITD or mutant NPM1 and a high allelic ratio of FLT3-ITD (greater than or equal to 0.5) have an intermediate prognosis; and patients with wild-type NPM1 and a high allelic ratio of FLT3-ITD have a poor prognosis [31, 49, 101, 132, 115].

**Molecular function:** The FLT3 alteration reported here results in the insertion of a single amino acid followed by the tandem duplication of seven amino acids within exon 14, corresponding to the juxtamembrane domain of the Flt3 protein (Integrative Genomics Viewer, v.2.3). FLT3-ITD alterations similar to the one reported here have been found to result in ligand-independent dimerization, constitutive Flt3 kinase activity, activation of downstream signaling pathways, and oncogenic transformation [82, 20, 61, 62, 60]. Therefore, although this alteration has not been functionally characterized, is predicted to be activating.

**Incidence:** FLT3 mutations have been reported in 23% (16351/70387) of Acute myelocytic leukemia (AML) samples analyzed in COSMIC (May 2020). FLT3 mutations have been reported in 6.7-30% of Acute myelocytic leukemia (AML) samples (cBioPortal for Cancer Genomics, May 2020). FLT3 mutations have been reported as the most common alteration in AML, with FLT3 internal tandem duplication (FLT3-ITD) and tyrosine kinase domain (FLT3-TKD) mutations cited in 12-35% and 4-10% of cases, respectively, and found to occur more frequently in AML with a normal karyotype [17, 35, 146, 80, 94, 108, 58, 85, 125, 6, 7, 61, 29].

## NPM1 W288fs\*?

**Gene:** NPM1

**Exon:** 11

**Nucleotide:**

NM\_002520.6:

g.170837543\_170837

544insTCTG

c.860\_863dupTCTG

**Amino Acid:** p.W288fs\*?

**Allelic Fraction:** 40.0% (of 3453 reads)

**Classification:** Tier 1A

**Assessment:** Pathogenic

### Treatment options

1 Trial

**Biomarker summary:** NPM1-W288fs exhibits altered function compared to wild-type.

**Clinical relevance:** NPM1 encodes nucleophosmin (Npm1), a multifunctional protein that regulates the ARF/p53 pathway and enhances Myc oncogenic activities [45, 75, 59, 77]. NPM1 mutations, particularly C-terminal truncations, have been reported frequently in myeloid malignancies, and although mutation has not been commonly found in solid tumors, overexpression of the Npm1 protein has been reported [41, 124, 40, 59, 95, 57]. There are currently no therapeutic approaches targeting alterations in NPM1 or changes in Npm1 protein expression.

**Disease summary:** NPM1 mutation in AML has been shown to result in the aberrant cytoplasmic localization of Npm1, in contrast to its normal nucleolar localization, and has been reported to play a role in the development of AML through the mislocalization and inhibition of Npm1 binding partners, including the tumor suppressor ARF [37, 38, 150, 24, 40]. NPM1 mutations in AML have been associated with M4 and M5 morphology, increased leukocyte and bone marrow blast counts, female sex, and decreased expression of CD34; NPM1 mutations have been reported more frequently in cytogenetically normal AML (CN-AML) and often occur in combination with FLT3, IDH1/2, NRAS, and DNMT3A mutations [32, 112, 124, 131, 93, 91, 107]. AML with mutant NPM1 is recognized as a subtype of AML with recurrent genetic abnormalities in the WHO classification of myeloid neoplasms and acute leukemia [3]. NPM1 mutations in the absence of FLT3-ITD have been associated with favorable outcomes in AML, especially in cytogenetically normal AML (CN-AML), while NPM1 mutations in the presence of FLT3-ITD have been associated with an intermediate prognosis [112, 110, 124, 83, 130]. Additionally, monitoring of mutant NPM1 transcript levels has been reported to be useful in the detection of minimal residual disease (MRD) and prediction of disease relapse [111, 68, 113, 53, 56].

**Molecular function:** NPM1 W288fs is expected to effectively truncate the Npm1 protein at amino acid 288 of 294 (UniProt). This truncation results in the loss of two tryptophan residues, W288 and W290, that are critical for nucleolar localization of Npm1 [88, 39]. In addition, the resulting protein would also lack a lysine residue at position 292, one of six lysines that undergo acetylation, which enhances the interaction of Npm1 with acetylated histones and is required for the enhancement of chromatin transcription [121]. Several C-terminal NPM1 W288 truncating and frameshift alterations have been reported to result in mislocalization of Npm1, as well as a gain in oncogenic function through deregulation of downstream pathways [24, 39, 40, 19, 103, 38]. The most common NPM1 W288fs alteration, type A, is the result of the insertion/duplication of a TCGT tetranucleotide, but many similar alterations resulting in W288fs have been reported [2, 5]. Therefore, although this alteration results in loss of the nucleolar localization domain, it is predicted to be associated with promotion of tumorigenesis.

**Incidence:** NPM1 mutations have been reported in 31% (6308/20330) of Acute myelocytic leukemia (AML) samples analyzed in COSMIC (May 2020). NPM1 mutations have been reported in 0.7-27% of Acute myelocytic leukemia (AML) samples (cBioPortal for Cancer Genomics, May 2020). NPM1 mutations, predominately resulting in C-terminal truncations, have been reported in 14-35% of AML samples and in 46-53% of cytogenetically normal AML (CN-AML) samples analyzed in scientific studies [100, 145, 8, 16, 124, 110, 32, 112, 131, 93]. In addition, one study analyzing the TAGE dataset has reported NPM1 mutations in 7.6% (66/869) of pediatric AML cases [138].

## Variants of potential clinical significance (2)

### RAD21 L183fs\*7

**Gene:** RAD21  
**Exon:** 6  
**Nucleotide:**  
NM\_006265.2:  
g.117869645\_117869  
646delTA  
c.548\_549delTA  
**Amino Acid:** p.L183fs\*7  
**Allelic Fraction:** 44.0% (of 6364 reads)  
**Classification:** Tier 2C  
**Assessment:** Likely Pathogenic

**Biomarker summary:** RAD21-L183fs\*7 is an inactivating mutation.

**Clinical relevance:** RAD21 encodes the Rad21 protein, a key component of the cohesin complex which maintains fidelity in chromosome segregation [64, 139, 12, 13]. At present, there are no therapies that directly address loss of Rad21 activity; however, inactivation of Rad21 and other cohesin complex components has been associated with enhanced sensitivity to PARP inhibitors in preclinical models [81, 9]. Although Rad21 has been implicated as a tumor suppressor in some contexts, it has also been described as activated or essential for cell proliferation and survival in various cancer cell line lineages [79, 4, 28, 147, 141]. Therefore, the potential relevance of any targeted therapies must be carefully considered in each situation.

**Disease summary:** RAD21 mutations have been reported in 3.3% (165/4946) of Acute myelocytic leukemia (AML) samples analyzed in COSMIC (May 2020). RAD21 mutations have been reported in 0.7-3.0% of Acute myelocytic leukemia (AML) samples (cBioPortal for Cancer Genomics, May 2020). Literature studies have reported RAD21 mutations in 2-17% of AML samples [127, 126, 30]. The role of RAD21 in AML has not been a significant subject of study reported in the scientific literature (PubMed, May 2019).

**Molecular function:** The RAD21 frameshift alteration reported here is expected to effectively truncate the 631-amino acid Rad21 protein prior to or within the C-terminal Smc1-binding domain (UniProt, Interpro) [137, 27]. The interaction between Rad21 and Smc1 is required for the formation of the cohesin complex [128, 15]. In addition, one study has reported RAD21 truncation alterations (including I621fs) in myeloid malignancies and that the alterations correlated with low RAD21 expression [127]. Therefore, this alteration is predicted to be inactivating.

**Incidence:** RAD21 mutations have been reported in 3.3% (165/4946) of Acute myelocytic leukemia (AML) samples analyzed in COSMIC (May 2020). RAD21 mutations have been reported in 0.7-3.0% of Acute myelocytic leukemia (AML) samples (cBioPortal for Cancer Genomics, May 2020). Literature studies have reported RAD21 mutations in 2-17% of AML samples [127, 126, 30].

### WT1 A387fs\*4

**Gene:** WT1  
**Exon:** 7  
**Nucleotide:**  
NM\_024426.6:  
g.32417907\_3241790  
8insCCGA  
c.1156\_1159dupTCGG  
**Amino Acid:** p.A387fs\*4  
**Allelic Fraction:** 20.0% (of 13717 reads)  
**Classification:** Tier 2C  
**Assessment:** Pathogenic

**Biomarker summary:** WT1-A387fs\*4 is an inactivating mutation.

**Clinical relevance:** WT1 encodes the Wilms tumor 1 protein (Wt1). Wt1 has been reported to have both tumor suppressive and tumorigenic properties [54, 119]. There are no approved targeted therapies for WT1 mutations or expression. Wt1 vaccines are in clinical trials for Wt1-expressing hematologic and solid tumor cancers, including renal cell carcinoma, biliary tract cancers, and non-small cell lung cancer [119, 89, 123, 122]. In the case of an inactivating alteration, as reported here, Wt1 vaccines are not expected to be relevant.

**Disease summary:** In studies of AML, both overexpression of WT1 mRNA and inactivating mutations of WT1 have been reported [102]. WT1 mRNA transcript levels have been reported to be elevated in the blood and bone marrow of leukemia patients and have been reported to serve in minimal residual disease monitoring [46, 104, 70, 97, 67]. WT1 mRNA expression has been positively associated with relapse and poor overall survival in several studies of AML [148, 46, 44, 114, 99, 144, 52, 87, 142]. WT1 mutations, predominately resulting in protein truncation, have been associated with younger patient age, cytogenetically normal (CN) AML, and the presence of FLT3 internal tandem duplication (ITD) mutations [18, 106, 52, 51, 14]. WT1 mutations have also been associated with reduced relapse-free, event-free, and overall survival in studies of AML, particularly in CN-AML patients [55, 106, 133, 52, 92, 51, 66, 33].

**Molecular function:** The WT1 frameshift alteration reported here is expected to effectively truncate the Wt1 protein before or within the zinc finger region, resulting in disruption of this region (UniProt). The zinc finger domains of Wt1 have been reported to be necessary for DNA binding and proper nuclear localization of the protein [21, 47, 36, 11]. Therefore, this alteration is expected to be inactivating.

**Incidence:** WT1 mutations have been reported in 7.8% (525/6762) of Acute myelocytic leukemia (AML) samples analyzed in COSMIC (May 2020). WT1 mutations have been reported in 3.3-6.5% of Acute myelocytic leukemia (AML) samples (cBioPortal for Cancer Genomics, May 2020). WT1 mutations, predominately resulting in protein truncation, have been reported in 4-7% of AML cases overall, with higher frequency of 7-13% observed in cytogenetically normal AML (CN-AML) and in pediatric AML cases [50, 18, 148, 34, 1, 66, 133, 52, 149, 129].

## Variants of uncertain significance (3)

Gene	Variant	Allelic fraction	Classification
BCORL1	c.1123G>C p.A375P	13.0% (of 2140 reads)	Tier 3, Uncertain Significance
BCORL1	c.3073G>A p.V1025M	44.0% (of 5452 reads)	Tier 3, Uncertain Significance
STAG2	c.1580G>T p.C527F	20.0% (of 825 reads)	Tier 3, Uncertain Significance

## REPORT INFORMATION

### Genes tested (54)

*ABL1, ASXL1, ATRX, BCOR, BCORL1, BRAF, CALR, CBL, CBLB, CBLC, CDKN2A, CEBPA, CSF3R, CUX1, DNMT3A, EZH2, FBXW7, FLT3, GATA1, GATA2, GNAS, HRAS, IDH1, IDH2, IKZF1, JAK2, JAK3, KDM6A, KIT, KRAS, MPL, MYD88, NOTCH1, NPM1, NRAS, PDGFRA, PHF6, PTEN, PTPN11, RAD21, RUNX1, SETBP1, SF3B1, SMC1A, SMC3, SRSF2, STAG2, TET2, TP53, U2AF1, WT1, ZRSR2, ETV6, KMT2A*

### Methods and limitations

EXAMPLE Statement including sample type (FFPE, etc), method of extraction, amplification reactions, panel targeted regions, sequencing technology, etc. Additionally, a description of the data analysis software(s), genome of reference and the sensitivity of the methods should be described.

**QIAGEN Clinical Insight (QCI™)** is a variant analysis, interpretation and decision support tool for research and clinical labs analyzing human genetics data and is not intended to be used for diagnostic purposes. QCI Interpret software includes the following underlying databases, data reference sets and tools; QIAGEN Clinical Insight-Interpret (6.0.20200609), Ingenuity Knowledge Base (X-release), CADD (v1.4), Allele Frequency Community (2019-09-25), EVS (ESP6500SI-V2), Refseq Gene Model (2019-10-01), JASPAR (2013-11), Ingenuity Knowledge Base Snapshot Timestamp (2020-08-19 13:28:30.0), Vista Enhancer hg18 (2012-07), Vista Enhancer hg19 (2012-07), Clinical Trials (X-release), PolyPhen-2 (v2.2.2), 1000 Genome Frequency (phase3v5b), ExAC (0.3.1), iva (May 11 16:21 iva-1.0.1458.jar), PhyloP hg18 (2009-11), PhyloP hg19 (2009-11), DbSNP (151), TargetScan (7.2), GENCODE (Release 31), CentoMD (5.3), OMIM (May 26, 2017), gnomAD (2.1.1), BSIFT (2016-02-23), TCGA (2013-09-05), Clinvar (2019-11-06), DGV (2016-05-15), COSMIC (v89), HGMD (2020.2), OncoTree (oncotree\_2019\_03\_01), SIFT4G (2016-02-23)

### Clinical significance of variants based on AMP / ASCO / CAP guidelines\*

#### Strong clinical significance

Tier 1A Biomarker predicts response or resistance to an FDA or EMA approved therapy, according to drug label or professional guidelines for this diagnosis  
Biomarker included in professional guidelines is prognostic or diagnostic for this diagnosis

Tier 1B Biomarker predicts response or resistance to a therapy for this diagnosis based on well-powered studies  
Biomarker is prognostic or diagnostic for this diagnosis based on well-powered studies

#### Potential clinical significance

Tier 2C Biomarker is associated with response or resistance to an FDA or EMA approved therapy, according to drug label or professional guidelines but only for different diagnosis  
Biomarker is an inclusion criterion for an active clinical trial  
Biomarker is prognostic or diagnostic based on multiple small studies

Tier 2D Biomarker shows plausible response or resistance based on case or preclinical studies  
Biomarker may assist in disease diagnosis or prognosis based on small studies

#### Uncertain clinical significance

Tier 3 Biomarker has uncertain clinical significance and not known to be likely benign or benign

\*Adapted from PMID:27993330 [jmd.amjpathol.org/article/S1525-1578\(16\)30223-9/pdf](http://jmd.amjpathol.org/article/S1525-1578(16)30223-9/pdf)

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