Taipei Veterans General Hospital

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Sample Information

Patient Name: 劉國台
Gender: Male
ID No.: K120115468
History No.: 38145787
Age: 67

Ordering Doctor: DOC1242E 劉峻宇
Ordering REQ.: 0CRVRHA
Signing in Date: 2023/10/13

Path No.: M112-00265
MP No.: F23074
Assay: Oncomine Focus Assay
Sample Type: FFPE
Block No.: S112-84501A
Percentage of tumor cells: 20%

Reporting Doctor: DOC5466K 葉奕成 (Phone: 8#5466)

Note:

Sample Cancer Type: Non-Small Cell Lung Cancer

Report Highlights

0 Relevant Biomarkers
0 Therapies Available
0 Clinical Trials

Relevant Non-Small Cell Lung Cancer Variants

Gene	Finding	Gene	Finding
ALK	None detected	NTRK1	None detected
BRAF	None detected	NTRK2	None detected
EGFR	None detected	NTRK3	None detected
ERBB2	None detected	RET	None detected
KRAS	None detected	ROS1	None detected
MET	None detected		

Relevant Biomarkers

No relevant biomarkers found in this sample.

Prevalent cancer biomarkers without relevant evidence based on included data sources
MYC amplification

Variant Details

DNA Sequence Variants

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
JAK1	p.(P733=)	c.2199A>G	.	chr1:65310489	51.65%	NM_002227.4	synonymous	2000
ALK	p.(D1529E)	c.4587C>G	.	chr2:29416366	50.75%	NM_004304.5	missense	1998
ALK	p.(G1125=)	c.3375C>A	.	chr2:29445458	50.10%	NM_004304.5	synonymous	1998
PDGFRA	p.(G313=)	c.939T>G	.	chr4:55133726	52.91%	NM_006206.6	synonymous	1996
PDGFRA	p.(V824=)	c.2472C>T	.	chr4:55152040	54.48%	NM_006206.6	synonymous	1997
FGFR4	p.(P136L)	c.407C>T	.	chr5:176517797	99.65%	NM_213647.3	missense	2000

Copy Number Variations

Gene	Locus	Copy Number
MYC	chr8:128748885	30.6

Biomarker Descriptions

MYC (MYC proto-oncogene, bHLH transcription factor)

Background: The MYC gene encodes the MYC proto-oncogene (c-MYC), a basic helix-loop-helix transcription factor that regulates the expression of numerous genes that control cell cycle progression, apoptosis, metabolic pathways, and cellular transformation[1,2,3,4]. MYC is part of the MYC oncogene family that includes related transcription factors MYCN and MYCL that regulate transcription in 10-15% of promoter regions[5]. MYC functions as a heterodimer in complex with the transcription factor MAX[2,6].

Alterations and prevalence: Recurrent somatic alterations are observed in both solid and hematological cancers. Recurrent somatic mutations in MYC, including codon T58, are infrequent and hypothesized to increase the stability of the MYC protein[7,8]. MYC gene amplification is particularly common in diverse solid tumors. MYC amplification is observed in 30% of serous ovarian cancer, 20% of uterine serous carcinoma, 15% of esophageal and breast cancers, and is common (1-10%) in numerous other cancer types[9,10,11]. MYC is the target of the t(8;14)(q24;32) chromosomal translocation in Burkitt's lymphoma that places MYC coding sequences adjacent to immunoglobulin region regulatory sequences, which results in increased MYC expression[12,13].

Potential relevance: B-cell lymphoma with MYC translocations that co-occur with BCL2 or BCL6 are referred to as double hit lymphoma, while co-occurrence with BCL2 and BCL6 rearrangements is referred to as triple-hit lymphoma[14,15]. MYC translocations are also indicative of high risk for multiple myeloma and is associated with poor risk in acute lymphoblastic leukemia[16,17]. Currently, no therapies are approved for MYC aberrations. Due to the high frequency of somatic MYC alterations in cancer, many approaches are being investigated in clinical trials including strategies to disrupt complex formation with MAX, including inhibition of MYC expression and synthetic lethality associated with MYC overexpression[1,18,19,20].

Clinical Trials in Taiwan region:

References

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