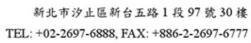


金萬林實驗室





廣泛型癌症循環核酸檢測報告書

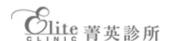
送檢資料1

CIM X III	
送檢單位:****/**	送檢醫師:***醫師
性 別:□男 ■女	聯絡電話:**_*****
檢體編號:******	電子郵件:****@**.***
檢測流水號:NGS******	(用以寄送檢測報告電子檔)
	採檢日期(YYYY/MM/DD): ****/**
檢體種類: ■ 血液	
根據該樣品「檢測申請書/檢測同意	書」所述,
「運送條件及樣本質量請參閱送檢	須知,若不符合允收標準或檢測標準是否仍要進行檢測?
□ 是。仍要進行檢測。(本實驗)	室保留最終解釋權。)
■ 否。予以退件。」	

岭豐 只 盾 2,3,4

从胜时只		
收檢品質	:	檢體 符合 允收標準。
		檢體量 未達 允收標準。
		檢體運送條件 <u>未達</u> 允收標準。
檢測品質	:	檢體 符合 檢測標準。
		檢體 DNA 去氧核醣核酸濃度未達檢測標準。
		檢體次世代定序平均深度 <u>未達</u> 檢測標準。
冷糠昭片	:	





金萬林實驗室





TEL: +02-2697-6888, FAX: +886-2-2697-6777

Gene Testing Report^{5,6}

檢測項目:廣泛型癌症循環核酸檢測	報告編號: NGS*****R				
收件時間(YYYY/MM/DD): ****/**	檢測區間(YYYY/MM/DD): ****/**-***/**				
報告時間(YYYY/MM/DD): ****/**	檢測週期: 10 工作天				
检测技術哲昌 (Testing method)					

檢測技術背景 (Testing method)

廣泛型癌症循環核酸檢測係利用標的擴增方式(target amplification),分析多個癌症相關基因變異狀 態。此檢測於單一工作流程下,使用次世代定序方法檢測 46 個基因之變異,包含單點變異(Single Nucleotide Variant, SNV)與片段插入或缺失(insertion or deletion, indel)。

檢測侷限 (Testing limitations)

- 1. 單點變異與片段插入或缺失的變異位點頻率(allele frequency)偵測極限為 0.5%。
- 2. 當送檢樣本未符合允收標準,可能導致檢測不確定性(Uncertainty)。

檢測基因 (Testing genes)

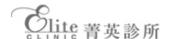
SNV and indel:

AKT1, ALK, APC, AR, ARAF, BRAF, CHEK2, CTNNB1, DDR2, EGFR, ERBB2, ERBB3, ESR1, FBXW7, FGFR1, FGFR2, FGFR3, FGFR4, FLT3, GNA11, GNAQ, GNAS, HRAS, IDH1, IDH2, KIT, KRAS, MAP2K1, MAP2K2, MET, MTOR, NRAS, NTRK1, NTRK3, PDGFRA, PIK3CA, PTEN, RAF1, RET, ROS1, SF3B1, SMAD4, SMO, TP53

核酸品質3

DNA 去氧核醣核酸濃度: <u>12.7</u>	ng/μl	■ DNA 去氧核糖核酸濃度 符合 檢測標準 ■ DNA 去氧核糖核酸濃度 未達 檢測標準
註:檢測標準:DNA 去氧核醣核酸濃度 ≥1 ng/μl		
定序品質 4		
次世代定序平均深度: 83,815		■ 定序平均深度 <u>符合</u> 檢測標準
	倍	

註:檢測標準:次世代定序平均深度 ≥ 20,000 倍



金萬林實驗室





TEL: +02-2697-6888, FAX: +886-2-2697-6777

重要單點變異與片段插入或缺失 7,8,9,10,11

基因名稱	變異類型	核酸變異	胺基酸變異	位點深度	變異位點 頻率	變異位點闡述
Gene	Alteration	Mutation	Amino acid change	Depth	Allele frequency	Variant interpretation
KRAS	SNV	c.35G>A	p.(G12D)	82,637	2.40%	Pathogenic

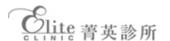
未檢出變異位點 10

SNV and indel:

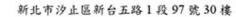
AKT1, ALK, APC, AR, ARAF, BRAF, CHEK2, CTNNB1, DDR2, EGFR, ERBB2, ERBB3, ERG, ESR1, FBXW7, FGFR1, FGFR2, FGFR3, FGFR4, FLT3, GNA11, GNAQ, GNAS, HRAS, IDH1, IDH2, KIT, MAP2K1, MAP2K2, MET, MTOR, MYC, NRAS, NTRK1, NTRK3, PIK3CA, PTEN, RAF1, RET, ROS1, SF3B1, SMAD4, SMO, TP53



檢測人員	報告簽署
62.00.0	600 (00-
	300



金萬林實驗室





TEL: +02-2697-6888, FAX: +886-2-2697-6777

Sample Cancer Type: Lung Cancer

Variant Details

D 1 1 4	_					
ΙΙΝΙΔ	~ or	HOT	100	Wa	ria	nte.
DNA	, occ	ucı		V C	1161	III S

Gene	Amino Acid Change	Coding	Locus	Allele Frequency	Transcript	Variant Effect	Oncomine Variant Class
KRAS	p.(G12C)	c.34G>T	chr12:25398285	21.52%	NM_033360.4	missense	Hotspot
PDGFRA	p.(P567=)	c.1701A>G	chr4:55141055	100.00%	NM_006206.6	synonymous	
TP53	p.(H193L)	c.578A>T	chr17:7578271	23.99%	NM_000546.6	missense	





Disclaimer: The data presented here is from a curated knowledgebase of publicly available information, but may not be exhaustive. The data version is 2024.03(005). The content of this report has not been evaluated or approved by FDA, EMA or other regulatory agencies.



金萬林實驗室

新北市汐止區新台五路1段97號30樓



TEL: +02-2697-6888, FAX: +886-2-2697-6777

Biomarker Descriptions

KRAS G12C

KRAS proto-oncogene, GTPase

Background: The KRAS proto-oncogene encodes a GTPase that functions in signal transduction and is a member of the RAS superfamily which also includes NRAS and HRAS. RAS proteins mediate the transmission of growth signals from the cell surface to the nucleus via the PI3K/AKT/MTOR and RAS/RAF/MEK/ERK pathways, which regulate cell division, differentiation, and survival^{1,2,3}.

Alterations and prevalence: Recurrent mutations in RAS oncogenes cause constitutive activation and are found in 20-30% of cancers. KRAS mutations are observed in up to 10-20% of uterine cancer, 30-35% of lung adenocarcinoma and colorectal cancer, and about 60% of pancreatic cancer⁴. The majority of KRAS mutations consist of point mutations occurring at G12, G13, and Q61^{4,5,6}. Mutations at A59, K117, and A146 have also been observed but are less frequent^{7,8}.

Potential relevance: The FDA has approved the small molecule inhibitors, sotorasib⁹ (2021) and adagrasib¹⁰ (2022), for the treatment of adult patients with KRAS G12C-mutated locally advanced or metastatic non-small cell lung cancer (NSCLC). Sotorasib and adagrasib are also useful in certain circumstances for KRAS G12C-mutated pancreatic adenocarcinoma¹¹. The FDA has also granted breakthrough therapy designation (2022) to the KRAS G12C inhibitor, GDC-6036¹², for KRAS G12C-mutated non-small cell lung cancer. The SHP2 inhibitor, BBP-398¹³ was granted fast track designation (2022) in combination with sotorasib for previously treated patients with KRAS G12C-mutated metastatic NSCLC. The RAF/MEK clamp, avutometinib¹⁴ was also granted fast track designation (2024) in combination with sotorasib for KRAS G12C-mutated metastatic NSCLC who have received at least one prior systemic therapy and have not been previously treated with a KRAS G12C inhibitor. The PLK1 inhibitor, onvansertib¹⁵, was granted fast track designation (2020) in combination with bevacizumab and FOLFIRI for second-line treatment of patients with KRAS-mutated metastatic colorectal cancer (mCRC). The EGFR antagonists, cetuximab¹⁶ and panitumumab¹⁷, are contraindicated for treatment of colorectal cancer patients with KRAS mutations in exon 2 (codons 12 and 13), exon 3 (codons 59 and 61), and exon 4 (codons 117 and 146)⁸. Additionally, KRAS mutations are associated with poor prognosis in NSCLC¹⁸.



Disclaimer: The data presented here is from a curated knowledgebase of publicly available information, but may not be exhaustive. The data version is 2024.03(005).