

Name	:	Centre Details	:
Age	:	Sex:	Accession.ID
Collection Date	:	07/Apr/2026 02:22PM	Referred By
Received Date	:	07/Apr/2026 02:22PM	Report Date
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DEPARTMENT OF MOLECULAR DIAGNOSTICS-II

OncqSol CGP 270+

Next Generation Sequencing

Clinical Indication: Metastatic Carcinoma-Lung

Specimen: 10 Unstained Slides from FFPE Block: H-4771/25 (2)

Tumor Content & Cellularity: 50%; Adequate

Site: Right supraclavicular lymph node biopsy

Test Result Summary

POSITIVE

Clinically relevant **MET exon 14 skipping Variant** detected

Fusion Gene	Breakpoint	Total Reads	Variant Classification
MET(13) - MET(15)	chr7:116411708 -chr7:116414935	1424	Tier I: A FDA Approved Drugs: capmatinib &tepotinib

*Genetic test results are reported based on the recommendations of AMP-ASCO-CAP guidelines. #Correlation of the genetic findings with the clinical condition of the patient is required to arrive at an accurate diagnosis, prognosis or therapeutic decisions

Multi-gene Biomarker Results:

Biomarker	Status/Score
Microsatellite Instability (MSI)	Stable
Microsatellite Instability Score	13.21

***MSI Score Interpretation: 1-18 (Stable), 18-19 (No call), >19 (Unstable)

Additional Biomarker Detected

This section provides information about variant that do not have any therapeutic value. However, these variant may or may not have a likely oncogenic effect.

Gene	CDS details	Amino acid change/ Exon No.	Overall depth/ Mutant Allele Percentage	Locus	Transcript	Variant Effect
TP53	c.844C>G	p.Arg282Gly/Exon 8	1999x/30.77	chr17:7577094	NM_000546.6	missense

Variant Classification as per AMP-ASCO-CAP Guidelines

Variant	A change in a gene. This could be disease causing (pathogenic) or not disease causing (benign).
Level A	biomarkers that predict response or resistance to US FDA-approved therapies for a specific type of tumor or



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Tier I: Variants of Strong Clinical Significance	have been included in professional guidelines as therapeutic, diagnostic, and/or prognostic biomarkers for specific types of tumors; Level B , biomarkers that predict response or resistance to a therapy based on well- powered studies with consensus from experts in the field or have diagnostic and/or prognostic significance of certain diseases based on well-powered studies with expert consensus.
Tier II: Variants of Potential Clinical Significance	Level C , biomarkers that predict response or resistance to therapies approved by FDA or professional societies for a different tumor type (i.e., off-label use of a drug), serve as inclusion criteria for clinical trials, or have diagnostic and/or prognostic significance based on the results of multiple small studies. Level D , biomarkers that show plausible therapeutic significance based on preclinical studies or may assist disease diagnosis and/or prognosis themselves or along with other biomarkers based on small studies or multiple case reports with no consensus.
Tier III: Variants of unknown clinical significance	Not observed at a significant allele frequency in the general or specific subpopulation or pan cancer or tumor specific variant databases. No convincing published evidence of Cancer Association

Test Attributes, Methodology:

- This is a **Next Generation Sequencing based test** which identifies genetic alterations in a comprehensive panel of >270 genes which can impact response to approved therapy for a particular cancer type. Some of the alterations detected may have bearing on prognosis and/or therapeutic options and may provide relevant information that allows doctor to consider various lines of targeted treatment for the patient.
- Sample preparation and Library preparation:** DNA isolated from FFPE or any other fresh tumor tissue source was used to perform targeted gene capture using a custom capture kit. In process quality controls were determined for prepared library. The libraries were sequenced to mean >500X coverage on Thermofisher S5plus sequencing platform. This is a targeted, next-generation sequencing (NGS) assay that provides a comprehensive genomic profiling solution appropriate for formalin-fixed paraffin-embedded (FFPE) tissues. The assay allows concurrent analysis of DNA and RNA to simultaneously detect multiple biomarkers associated with targeted and immune checkpoint research, including comprehensive targets that are relevant in cancer, in a single workflow.
- Bioinformatics Analysis and Reporting:** The sequences obtained are aligned to human reference genome (GRCh37/hg19) and variant analysis is performed using set of Bioinformatics Pipeline. Variant calling, annotation and classification of the variants were done using ion reporter 5.2.0 software. Clinically relevant mutations are annotated using published variants in literature and a set of databases – ClinVar, COSMIC and dbSNP. Common variants are filtered based on allele frequency in 1000 Genome Phase 3, ExAC, EVS, dbSNP147, etc. Non-synonymous variants effect is calculated using multiple algorithms such as PolyPhen-2, SIFT, MutationTaster2, Mutation Assessor and LRT. Silent variations that do not result in any change in amino acid in the coding region are not reported. It enables the identification of SNV, Indels, Gene level copy number variants, MSI status, and gene fusions.

Comprehensive Genomic Panel gene list:

DNA Gene List				
A	AKT2	GATA2	GATA3	FLT3
AR	ARAF	AKT3	ALK	GNA11
ATR	ATRX	ARID1A	ARID5B	APC
BCOR	BCORL1	AXL	BAP1	ATM
BRCA2	BRIP1	BLM	BRAF	BARD1
CCND1	CCND3	BTK	CBL	BRCA1
CCND2	CDK4	CCNE1	CDH1	CCND1
CDKN2B	CHEK1	CDK6	CDKN1B	CDK12
CSF1R	CSMD3	CHEK2	CIC	CDKN2A
DICER1	DPYD	CTCF	CTNNB1	CREBBP



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EP300	EPCAM	ERBB2	EGFR	DDR2
ERCC2	ESR1	EZH1	ERBB3	EIF1AX
FANCC	FANCD2	FANCE	EZH2	ERBB4
FANCI	FANCL	FARSB	FANCF	FANCA
FGFR2	FBXW7	FGF19	FAT1	FANCG
FUBP1	FGFR3	FGFR4	FGF3	FGFR1
FOXL2	U2AF1	KMT2D	KNSTRN	MDM4
GNAQ	IDH1	MAP2K1	MAP2K2	MLH3
GNAS	JAK3	MAX	MDM2	MSH6
HRAS	KMT2C	MET	MLH1	MYCL
JAK2	MAGOH	MSH2	MSH3	NF2
KIT	MEN1	MUTYH	MYC	PALB2
MAPK1	MRE11	NBN	NF1	PIK3CA
MED12	MYD88	NOTCH2	NOTCH3	PMS1
MPL	NOTCH1	NTRK2	NTRK3	PPP2R1A
MTOR	NTRK1	PDGFRB	PICALM	PTPN11
MYCN	PDGFRA	PIK3R1	PIK3R2	RAD51C
NFE2L2	PIK3CD	POLE	RAD51B	RB1
NRAS	POLD1	PTEN	RAF1	RICTOR
PBRM1	PTCH1	RAD51	RHOA	SDHA
PIK3CB	RAD50	RAD54L	ROS1	SF3B1
PMS2	RAD52	RHEB	SETD2	SMARCB1
PPP2R2A	RET	RNF43	SMARCA4	STK11
RAC1	RNF213	SDHD	STAT3	TET2
RAD51D	SDHC	SMAD4	TERT	TP53
RBM10	SLX4	SRC	TSC2	TSHR
RIT1	SPOP	SYN2	XRCC2	UGT1A1*
SDHB	SUZ12	TSC1	HNFI1A	VHL
SLC5A5	TP53	XPO1	JAK1	WT1
SMO	VHL	HIST1H3C	KEAP1	XRCC2
SUFU	IDH2	IGF1R	KRAS	XRCC3
TOP1	KDM6A	KDR	MAP2K4	ZRSR2
TSC1	PIM1	PIM1	PARP2	STAG2
TSC2	MCL1	PAX5	PARP3	STAT1
BCL6	BCR	PARP1	SPEN	ETV6

RNA Gene list				
AKT1	ERBB4	MET	NTRK3	RET
AKT2	ERG	MTAP	NUTM1	ROS1
AKT3	ESR1	MYB	PIK3CA	RSP02
ALK	ETV1	MYBL1	PIK3CB	RSP03
AR	ETV4	NOTCH1	PPARG	STAT6
BRAF	ETV5	NOTCH2	PRKACA	TERT
BRCA1	FGFR1	NOTCH3	PRKACB	TFE3
CDKN2A	FGFR2	NRG1	RAF1	TFEB
EGFR	FGFR3	NTRK1	RARA	YAP1
ERBB2	MAP3K8	NTRK2	RELA	

Disclaimer:

DNA studies do not constitute a definitive test for the selected condition(s) in all individuals. It should be realized that there are possible



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sources of error. Errors can result from trace contamination, rare technical errors, rare genetic variants that interfere with analysis, recent scientific developments, and alternative classification systems. This test should be one of the many aspects used by the healthcare provider to help with a diagnosis and treatment plan. The contents of this test should be carefully assessed by the treating physician and further interpreted along with clinical, histopathological findings, contraindications and guidelines before deciding the course of therapy. Most recent block is recommended for testing as the mutation profile may change in response to treatment and hence differ at different sampling points. Certain genes may not be covered completely, and few mutations could be missed. A negative result cannot rule out the possibility that the tested tumor sample carries mutations not previously associated with cancer and hence not included in the panel. The accuracy and completeness may vary due to variable information available in different databases. The classification of variants of unknown significance can change over time. Synonymous mutations were not considered while preparing this report. The mutations have not been confirmed using Sanger sequencing and/or alternate technologies. To rule out germ line mutations i.e. variant with variant allele frequency at nearly 50% or 100%, whole blood sample is recommended to process along with tissue sample. No other variant that warrants to be pathogenic was detected. Variations with high minor allele frequencies which are benign/likely benign will be given upon request. Due to poor quality of FFPE DNA, indeterminate result due to low gene coverage or low variant depth cannot be ruled out. The sensitivity of the assays depends on the quality of the block, and tumor content

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Note: The performance of this Test has been evaluated at Oncquest Laboratories Ltd.

*** End Of Report ***

Disclaimer: All Results released pertain to the specimen submitted to the lab
 1. Test results are dependent on the quality of the sample received by the lab
 2. Tests are performed as per schedule given in the test listing and in any unforeseen circumstances, report delivery may be delayed
 3. Test results may show interlaboratory variations
 4. All dispute and claims are subjected to local jurisdiction only. Clinical correlation advised.
 5. Test results are not valid for medico legal purposes
 6. For all queries, feedbacks, suggestions, and complaints, please contact customer care support +0124 665 0000



Sample Cancer Type: Lung Cancer

Relevant Lung Cancer Findings

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	MET exon 14 skipping		

Relevant Biomarkers

Genomic Alteration	Relevant Therapies (In this cancer type)	Relevant Therapies (In other cancer type)	Clinical Trials
MET exon 14 skipping	capmatinib ¹ tepotinib ¹ crizotinib	None*	26

* Public data sources included in relevant therapies: NCCN, ESMO, FDA¹

 Alerts informed by public data sources:  Contraindicated,  Resistance,  Breakthrough,  Fast Track

MET exon 14 skipping  crizotinib¹

Public data sources included in alerts: NCCN, ESMO, FDA¹

Biomarker Descriptions

MET exon 14 skipping

MET proto-oncogene, receptor tyrosine kinase

Background: The MET gene encodes the MET proto-oncogene, encodes a receptor tyrosine kinase for the hepatocyte growth factor (HGF) protein, which is expressed by mesenchymal cells¹. MET is expressed as multiple isoforms with transcript variant 1 (NM_001127500.3) encoding a 1408 amino acid protein and transcript variant 2 (NM_000245.4) encoding a 1390 amino acid protein, both of which possess an intact protein kinase domain¹. Ubiquitin-dependent proteolysis is responsible for regulating the steady-state level of the MET protein via recognition of the tyrosine phosphorylation site Y1003(NM_000245.4), sometimes referred to as Y1021 (NM_001127500.3), in the MET Cbl-binding domain within the juxtamembrane region^{2,3,4}. Growth factor signaling leads to MET dimerization and subsequent initiation of downstream effectors, including those involved in the RAS/RAF/MEK/ERK and PI3K/AKT signaling pathways, which regulate cell migration, proliferation, and survival^{5,6}.

Alterations and prevalence: Somatic mutations in MET are observed in 10% of uterine corpus endometrial carcinoma, 9% of skin cutaneous melanoma, 8% of kidney renal papillary cell carcinoma (PRCC), 4% of lung adenocarcinoma, colorectal adenocarcinoma, bladder urothelial carcinoma, and uterine carcinosarcoma, and 2% of diffuse large B-cell lymphoma, esophageal adenocarcinoma, glioblastoma multiforme, lung squamous cell carcinoma, stomach adenocarcinoma, and sarcoma^{7,8}. Recurrent somatic mutations fall into two classes, mutations in the MET kinase domain, which are uncommon, and splice-site mutations affecting exon 14⁹. Recurrent kinase domain mutations are observed in PRCC and include M1250T, H1094Y, and V1070E (NM_000245.4)^{7,8,9}. Mutation of the

Disclaimer: The data presented here are from a curated knowledge base of publicly available information, but may not be exhaustive. The data version is 2026.03(005). The content of this report has not been evaluated or approved by the FDA, EMA or other regulatory agencies.

Biomarker Descriptions (continued)

Y1003 phosphorylation site is reported in approximately 2% of MET altered lung cancer¹⁰. In contrast, splice-site mutations flanking exon 14 are observed in 3-4% of all non-small cell lung cancer (NSCLC)¹¹. These mutations include canonical splice site mutations affecting exon 14 and deletions that extend into the splicing motifs within intron 13^{10,12}. Such mutations disrupt splicing leading to the formation of an alternative transcript that joins exon 13 directly to exon 15 and skips exon 14 entirely. The MET exon 14 skipping transcript lacks the juxtamembrane domain that contains the recognition motif for ubiquitin-dependent proteolysis and thus leads to a marked increase in the steady-state level of the MET protein¹³. MET exon 14 skipping mutations act as oncogenic drivers in lung cancer mutually exclusive to activating mutations in EGFR and KRAS and other oncogenic fusions such as ALK and ROS1^{12,14,15}. MET amplification is observed in 3% of esophageal adenocarcinoma, ovarian serous cystadenocarcinoma, stomach adenocarcinoma, and glioblastoma multiforme, and 2% of lung adenocarcinoma, liver hepatocellular carcinoma, bladder urothelial carcinoma, diffuse large B-cell lymphoma, kidney renal papillary cell carcinoma, skin cutaneous melanoma, sarcoma, and kidney chromophobe^{7,8}. Recurrent MET fusions, although infrequent, are observed in adult and pediatric glioblastoma, papillary renal cell carcinoma, lung cancer, liver cancer, thyroid cancer, and melanoma^{16,17,18}. MET alterations are believed to be enriched in late-stage cancers where they drive tumor progression and metastasis^{19,20,21}. Alterations in MET are rare in pediatric cancers^{7,8}. Somatic mutations are observed in less than 1% of embryonal tumors (3 in 332 cases), bone cancer (2 in 327 cases), glioma (1 in 297 cases), leukemia (1 in 354 cases), peripheral nervous system cancers (2 in 1158 cases), and Wilms tumor (1 in 710 cases)^{7,8}. Amplification of MET is observed in less than 1% of Wilms tumor (1 in 136 cases) and B-lymphoblastic leukemia/lymphoma (3 in 731 cases)^{7,8}.

Potential relevance: In 2020, the FDA granted accelerated approval to capmatinib²² for NSCLC harboring MET exon 14 skipping positive as detected by an FDA-approved test. The kinase inhibitor, tepotinib²³, is also approved (2021) for MET exon 14 skipping mutations in NSCLC. MET exon 14 skipping mutations confer sensitivity to approved kinase inhibitors including crizotinib (2011), which is recommended for MET amplifications and exon 14 skipping mutations^{12,14,15,24}. The FDA also granted breakthrough therapy designation (2018) to crizotinib for metastatic non-small cell lung cancer (NSCLC) with MET exon 14 alterations with disease progression on or after platinum-based chemotherapy²⁵. MET amplification has been observed to mediate resistance to EGFR tyrosine kinase inhibitors (TKIs)^{26,27,28,29,30}. The FDA has granted fast track designation (2021) to the MET/CSF1R/SRC small molecule inhibitor, elzovantinib (TPX-0022)³¹, for MET amplified advanced or metastatic gastric cancer and gastroesophageal junction adenocarcinoma (GEJ) after prior chemotherapy. Tepotinib has also been recommended for treatment of NSCLC with high-level MET amplification²⁴. The FDA has granted fast track designation (2025) to the ATP-competitive c-Met inhibitor, savolitinib³², in combination with osimertinib for the treatment of patients with EGFR-mutated NSCLC with MET overexpression or amplification whose disease progressed on treatment with osimertinib. As a MET amplification is a diagnostic marker of infant-type hemispheric glioma^{33,34}.

Clinical Trials Summary

MET exon 14 skipping		
NCT ID	Title	Phase
No NCT ID	An Exploratory Multi-cohort Clinical Study of Glumetinib in the Treatment of Advanced Non-small Cell Lung Cancer Brain Metastases with MET Alterations (BRAIN-MET01)	IV
No NCT ID	Phase IIIb clinical study of Baricitinib in patients with locally advanced/metastatic non-small cell lung cancer with MET exon 14 mutation	III
NCT05989542	An Open, Multi-center, Single-arm Phase IIIb Confirmatory Clinical Study to Evaluate the Efficacy, Safety and Tolerability of Vebreltinib in Patients With Locally Advanced or Metastatic Non-small Cell Lung Cancer With MET Exon 14 Mutation	III
No NCT ID	A multicenter, single-arm, open label phase III confirmatory clinical study evaluating the efficacy and safety of oral glutecitinib in patients with advanced non-small cell lung cancer with MET exon 14 skipping mutation	III
NCT06074588	A Randomized, Open-label, Phase III Study of MK-2870 vs Chemotherapy (Docetaxel or Pemetrexed) in Previously Treated Advanced or Metastatic Nonsquamous Non-small Cell Lung Cancer (NSCLC) With EGFR Mutations or Other Genomic Alterations	III

Clinical Trials Summary (continued)

MET exon 14 skipping (continued)

NCT ID	Title	Phase
No NCT ID	A Phase II, Open label, Single arm study to assess the Efficacy of Cabozantinib in Patients with Advanced/Metastatic Non-Small Cell Lung cancer harboring MET exon14 alterations, who developed acquired resistance to Tepotinib or Capmatinib (CAPTURE Trial)	II
NCT04322890	Treatment Strategies and Survival Outcome for Non-small Cell Lung Cancer With Oncogenic Mutation.	II
No NCT ID	A Single-Arm, Multicenter Phase II Clinical Study to Evaluate the Efficacy of Ensartinib in Patients With Advanced or Metastatic Non-Small Cell Lung Cancer Harboring MET 14 Exon Skipping Mutation	II
NCT06868836	A Phase II Study of JS207 (PD-1/VEGF Bispecific Antibody) in Combination With Pemetrexed and Platinum in Advanced Non-small Cell Lung Cancer With Actionable Genomic Alterations and TKI Therapy Failure	II
NCT06563999	Neoadjuvant Umbrella Trial Directed by Next Generation Sequencing for Patients With Unresectable Stage III NSCLC Harboring Rare Mutations (Without EGFR Sensitizing Mutations)	II
NCT03574402	An Open-label, Multi-center, Phase II Umbrella Study to Assess Efficacy of Targeted Therapy or Immunotherapy Directed by Next Generation Sequencing (NGS) in Chinese Patients With Advanced NSCLC (TRUMP)	II
NCT04647838	A Phase II Study of Tepotinib in Patients With Solid Cancers Harboring c-MET Amplification or Exon 14 Mutation Who Progressed After Standard Treatment for Advanced/Metastatic Disease	II
NCT05800340	Neoadjuvant Toripalimab Combined With Chemotherapy in Rare Mutations Stage IIB-IIIB NSCLC	II
NCT05541822	A Phase II Multicenter, Open-Label, Parallel Cohort Expansion Study to Evaluate the Efficacy, Safety, Tolerability and Pharmacokinetic Profile of ABN401 in Patients With Advanced Solid Tumors Harboring c-Mesenchymal-epithelial Transition Factor (c-MET) Dysregulation	II
NCT03175224	Phase I/II Multicenter Study of the Safety, Pharmacokinetics, and Preliminary Efficacy of APL-101 in Subjects With Non-Small Cell Lung Cancer With c-Met EXON 14 Skip Mutations and c-Met Dysregulation Advanced Solid Tumors.	I/II
NCT04868877	Phase 1/2 Dose Escalation and Expansion Study Evaluating MCLA-129, a Human Anti-EGFR and Anti-c-MET Bispecific Antibody, in Patients with Advanced NSCLC and Other Solid Tumors	I/II
NCT04930432	A Phase I/II Study of MCLA-129, a Human Anti-EGFR and Anti-c-Met Bispecific Antibody, in Patients With Advanced NSCLC and Other Solid Tumors, Evaluating Safety, Pharmacokinetic Characteristics and Antitumor Activity	I/II
NCT06669117	A First-In-Human (FIH) Phase I/II Open-label, Multicentre, Dose Escalation and Expansion Trial of VERT-002 in Patients With Locally Advanced or Metastatic Solid Tumors Including Non-small Cell Lung Cancer (NSCLC) Harboring Mesenchymal-Epithelial Transition (MET) Alterations	I/II
NCT06328439	A Phase I Study to Evaluate the Safety, Tolerability, Pharmacokinetics, and Preliminary Efficacy of ANS014004 Monotherapy in Subjects With Locally Advanced or Metastatic Solid Tumors	I
NCT02929290	Safety, Efficacy and Pharmacokinetic of BPI-9016M in Patients With c-Met- Dysregulated Advanced NSCLC: A Phase Ib Study,Open-label,Dose-expansion Study	I
NCT06081907	A Prospective, Multi-cohort Study on Efficacy and Safety of IBI363 for Advanced Solid Tumors	I
NCT06592417	To Evaluate the Phase I Clinical Study of JSKN016 in Chinese Patients With Advanced Malignant Solid Tumors	I

Clinical Trials Summary (continued)

MET exon 14 skipping (continued)

NCT ID	Title	Phase
No NCT ID	Phase I Clinical Trial of the Safety, Tolerability, Pharmacokinetics and Preliminary Efficacy of ST-1898 Tablets in Patients with Advanced Solid Tumors	I
No NCT ID	A Phase I clinical study to evaluate the safety, tolerability, pharmacokinetic characteristics and preliminary efficacy of SYS6023 in the treatment of patients with advanced solid tumors	I
NCT07110883	A Phase I Clinical Study Evaluating the Safety, Tolerability, Pharmacokinetic Profiles, and Preliminary Efficacy of SYS6023 in Patients With Advanced Solid Tumors	I
NCT06386705	A Multicenter, Open-label, Phase Ia/Ib Study to Evaluate the Safety, Tolerability, Pharmacokinetics, Pharmacodynamics, and Preliminary Efficacy of TSN084 Tablets in Patients With Advanced Malignant Tumors.	I

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