



CANCER INSTITUTE (WIA)

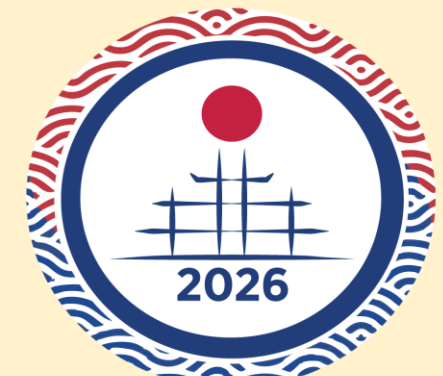
Genomic Landscape of NSCLC With Spectrum of Actionability Evaluated in 433 Indian Patients- Real-World Evidence of Precision Oncology in Practice

**Vasanthkumar Muthukumar¹, Deepika Dash¹, Sreenidhi Suresh¹, Mehanathan Kuppuloganathan¹, Neeraja Rajaraman¹, David Raj A¹, Vedhamurthy Giri¹,
Pragadeesh Thamaraiselvan², Venkatraman Radhakrishnan², Vijayalakshmi Ramshankar^{1,*}**

¹Department of Cancer Biology & Molecular Diagnostics, Cancer Institute (W.I.A), Chennai 600020, Tamil Nadu, India

²Department of Medical Oncology, Cancer Institute (W.I.A), Chennai 600036, Tamil Nadu, India

**Corresponding Author: Dr. Vijayalakshmi Ramshankar, Professor & Head, Dept. of CBMD, Cancer Institute (W.I.A); Email: r.vijayalakshmi@cancerinstitutewia.org*



IASLC 2026 World
Conference on Lung Cancer

SEPTEMBER 12 - 15, 2026
SEOUL, REPUBLIC OF KOREA

INTRODUCTION & METHODOLOGY

BACKGROUND

Non-small cell lung cancer (NSCLC) is a molecularly heterogeneous disease in which identification of actionable genomic alterations is increasingly central to treatment selection and precision oncology.

Comprehensive next-generation sequencing (NGS) enables simultaneous detection of multiple classes of genomic alterations (SNVs, indels, CNVs, and gene fusions), overcoming limitations of sequential single-gene testing and conserving tissue, especially in small biopsies.

In India, adoption of NGS is rapidly increasing, particularly in tertiary cancer centers, as it overcomes limitations of sequential single-gene testing and optimizes tissue utilization.

However, large real-world datasets describing the genomic landscape and therapeutic actionability of NSCLC in Indian patients remain limited.

Population-specific genomic data are essential, as the prevalence and co-occurrence of actionable driver alterations may differ across ethnic and geographic populations.

WHY THIS STUDY IS IMPORTANT

India has a large burden of NSCLC, with a high proportion of non-smokers and younger patients.

Distinct molecular profiles may exist in Indian patients compared with Western populations.

Real-world genomic data are critical to guide biomarker-driven therapy and optimize outcomes.

NGS allows broad genomic profiling in a single test, improving diagnostic yield and clinical decision-making.

Evidence from routine practice in resource-constrained settings supports scalable precision oncology.

STUDY CONTEXT

Conducted in a real-world tertiary cancer center setting in India.

Includes patients tested using both tissue and plasma-based specimens.

Reflects the diversity of Indian NSCLC population seen in routine practice.

STUDY OBJECTIVE

To characterize the genomic landscape, spectrum of actionable alterations, co-mutation patterns, and therapeutic actionability of NSCLC in a large real-world Indian cohort using targeted next-generation sequencing, and to demonstrate the utility of NGS in routine clinical practice.

This study provides real-world evidence of the genomic architecture of NSCLC in Indian patients and reinforces the feasibility, clinical utility, and impact of comprehensive NGS in enabling precision oncology at scale.

RESULTS & DISCUSSION

NSCLC NGS Cohort (N = 433)

TOTAL PATIENTS
433 (100%)

GENDER DISTRIBUTION

Male
251 (58.00%)

Female
182 (42.00%)

SMOKING STATUS

Non-Smoker
302 (69.75%)

Smoker
131 (30.25%)

GENDER DISTRIBUTION IN NON-SMOKERS (N = 302)

Male
149 (49.34%)

Female
153 (50.66%)

HISTOLOGY

Adenocarcinoma	327 (75.64%)
Squamous Cell Carcinoma	43 (9.93%)
Carcinoma NOS	59 (13.63%)
Adenosquamous Carcinoma	4 (0.80%)

Total (N = 433) (100.00%)

SPECIMEN TYPE

FFPE Tissue
395 (91.24%)

Plasma ctDNA
38 (8.76%)

Total (N = 433) (100.00%)

TESTING WORKFLOWS

ILLUMINA ONCOTARGET WORKFLOW (OPA = NO)
126-Gene Hybrid-Capture DNA Panel → DNA Fusion Panel (16 Genes) → ICARE Platform
295 (68.13%)
Turnaround Time ~ 16 Days

ONCOMINE PRECISION ASSAY (OPA = YES)
51-Gene Targeted Panel (DNA + RNA) → Oncomine Reporter → Clinical Report
138 (31.87%)
Turnaround Time ~ 48 Hours

KEY HIGHLIGHTS

Large Real-world NSCLC Cohort
N = 433

Adenocarcinoma Predominant
75.64%

Majority Tested on FFPE Tissue
91.24%

High Proportion of Non-Smokers
69.75%

Balanced Gender Distribution
MF = 1.38:1

OVERALL ACTIONABILITY (Patient-level)

N = 433

8.1% POTENTIALLY TARGETABLE (FDA/NCCN-SUPPORTED)
242 / 433 (55.9%)
Patients with at least one actionable biomarker with approved targeted therapy

36.0% GENOMIC ALTERATION PRESENT BUT NO MATCHED FDA/NCCN TARGETED THERAPY IDENTIFIED
156 / 433 (36.0%)

55.9%

NO REPORTABLE GENOMIC ALTERATION
35 / 433 (8.1%)

Actionability was assigned at the patient level based on biomarker-therapy associations supported by FDA-approved indications and NCCN NSCLC recommendations. Actual treatment eligibility depends on stage, prior therapy, performance status, confirmatory testing and clinical context.

BREAKDOWN OF POTENTIALLY TARGETABLE BIOMARKERS (N = 242 Patients)*			
BIOMARKER / ALTERATION	PATIENTS (N)	% OF 433	EXAMPLE FDA-APPROVED THERAPIES
EGFR (sensitizing / actionable alterations)	176	40.6%	Osimertinib, Afatinib, Erlotinib, Gefitinib, Dacomitinib, Mobocertinib, Amivantamab
ALK fusion (EML4-ALK)	30	6.9%	Alectinib, Brigatinib, Lorlatinib, Ceritinib, Crizotinib
ROS1 fusions	9	2.1%	Entrectinib, Crizotinib, Repotrectinib
KRAS G12C	8	1.8%	Sotorasib, Adagrasib
ERBB2 (HER2) activating mutations	8	1.8%	Trastuzumab deruxtecan
RET fusions (KIF5B-RET)	5	1.2%	Selpercatinib, Pralsetinib
BRAF V600E	4	0.9%	Dabrafenib + Trametinib
MET exon 14 skipping	3	0.7%	Tepotinib, Capmatinib
NRG1 fusion	1	0.2%	Zenocutuzumab

Some patients have more than one actionable alteration. Counts above are not mutually exclusive.

Unique actionable patients
242 (55.9%)

NON-TARGETABLE GENOMIC ALTERATIONS

N = 156 (36.0%)

Patients with genomic alterations without an established matched FDA/NCCN-approved targeted therapy.

Includes alterations such as:

- TP53 • CDKN2A • STK11 • KEAP1
- Other KRAS (non-G12C) • Variants of
- Uncertain Significance (VUS) • Others

NO REPORTABLE GENOMIC ALTERATION

N = 35 (8.1%)

Patients in whom no reportable genomic alteration was identified by comprehensive NGS.

Includes:

- No reportable SNVs/indels
- No reportable copy number alterations
- No gene fusions detected

TAKE-HOME MESSAGE

NGS identified potentially targetable genomic alterations in **55.9% (242/433)** of Indian NSCLC patients, while 36.0% had non-targetable genomic alterations and only 8.1% had no reportable alteration—demonstrating the substantial clinical value of comprehensive genomic profiling for precision oncology.

HIGH ACTIONABILITY
55.9% patients have a potentially actionable biomarker.

DRIVERS IDENTIFIED
Across EGFR, ALK, ROS1, KRAS G12C, RET, BRAF, HER2, MET exon 14 & NRG1.

REAL-WORLD IMPACT
Comprehensive NGS is feasible and delivers clinically meaningful results in routine practice.

PRECISION ONCOLOGY
Data supports biomarker-driven treatment decisions and improved patient management.

* Patient-level counts. Patients may harbor more than one actionable alteration. Abbreviations: NGS – Next Generation Sequencing; FDA – U.S. Food and Drug Administration; NCCN – National Comprehensive Cancer Network; NSCLC – Non-Small Cell Lung Cancer.

Total Cohort: 433 Indian NSCLC Patients

Disclosure statement: AI-assisted tools were used to support the visual design and formatting of this infographic. The scientific content and messaging were developed, reviewed, and approved by the authors.

NSCLC NGS COHORT

N = 433
Lung Cancer Patients

FFPE Tissue
n = 395 (91.2%)

Plasma ctDNA
n = 38 (8.8%)

Targeted NGS was performed in 433 lung cancer patients using FFPE tissue (n=395) and plasma ctDNA (n=38).

A ILLUMINA HYBRID-CAPTURE NGS

n = 295 (68.1%)

Hybrid-capture Libraries with UMIs → Sequencing on Illumina NextSeq 2000 → 126-Gene Panel Simultaneous detection of SNVs, indels, CNVs and gene fusions → Bioinformatics Pipeline (ICARE Platform)

BIOINFORMATICS & ANALYSIS

Alignment
GRCv38

Annotation
ClinVar, ACMG, gnomAD

Variant Classification
According to AMP/ASCO/CAP Guidelines

TURNAROUND TIME (TAT)
≤ 16 DAYS

B ONCOMINE PRECISION ASSAY (OPA) – ACROSS 50 GENES

n = 138 (31.9%)

Oncomine Precision Assay (OPA) → Genexus™ Integrated Sequencer → Automated Sequencer & Analyser → Clinical Report (Oncomine Reporter)

NUCLEIC ACID TO REPORT MODEL

Fully Automated Workflow
End-to-end automation from sequencing to analysis

Clinical Reporting
Generated using Oncomine Reporter

Evidence & Guidelines
Based on FDA/ASCO/ESMO/AMP/ClinVar

TURNAROUND TIME (TAT)
≤ 48 HOURS

WHAT WE DETECT

SNVs
Single Nucleotide Variants

Indels
Insertions/Deletions

CNVs
Copy Number Variations

Gene Fusions
Rearrangements detectable at DNA/RNA level

OncoPrint of NSCLC Genomics Profile

Age_Range: 20-29, 30-39, 40-49, 50-59
Smoking_Status: Non_Smoker, Smoker
Gender: F, M
Histology: Adenocarcinoma, Adenosquamous Carcinoma, Squamous Cell Carcinoma, Carcinoma