

Real-World Molecular Profiling in Stage IV NSCLC: Preliminary Results from A Population-Based Study from Southwestern Ontario



Jonathan J Moroniti¹, Saritha Surapaneni^{2,3}, Sarah Ma^{1,2}, Ana Carolina da Cruz⁴, Mehdi Qiabi^{1,2,3}, Mark Vincent^{1,2,3}, Michael Sanatani^{1,2,3}, Jawaid Younus^{1,2,3}, Daniel Breadner^{1,2,3}, Phillip Blanchette^{1,2,3}, Hamid Mithoowani^{1,2,3}, Diane Logan^{1,2,3}, Jacques Raphael^{1,2,3}, Robin Sachdeva⁵, M. Sara Kuruvilla^{1,2,3}

¹Schulich School of Medicine and Dentistry, Western University, London, ON, Canada, ²London Health Sciences Centre Research Institute, ON, Canada, ³Department of Oncology, Verspeeten Family Cancer Centre, London Health Sciences Centre, London, ON, Canada, ⁴Department of Statistical and Actuarial Sciences, Western University, London, ON, Canada, ⁵Precision Medicine Group, LLC, London, Ontario, Canada

INTRODUCTION

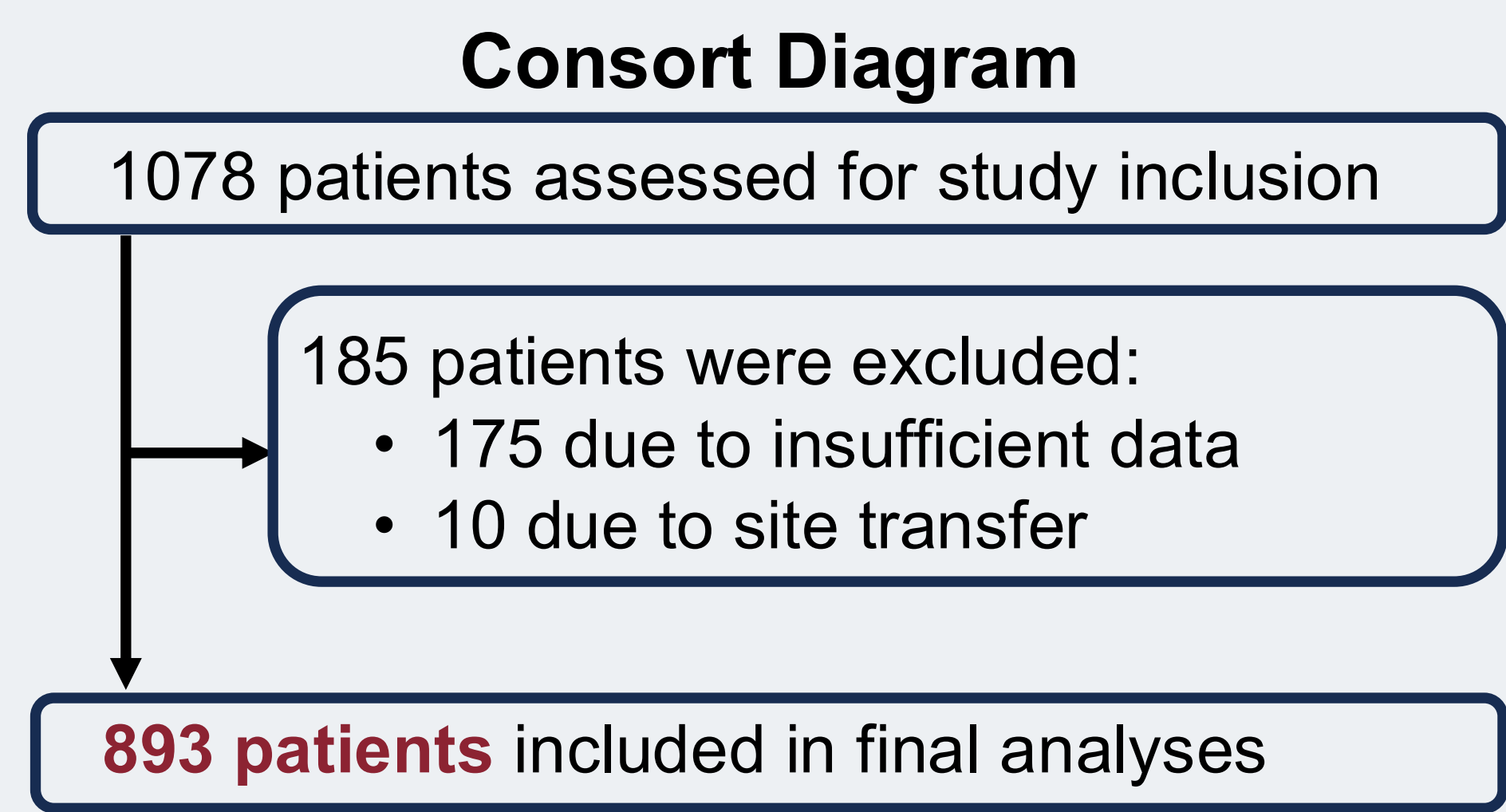
- Stage IV non-small cell lung cancer (NSCLC) carries a poor 5-year survival of <10%^{1,2}
- Molecular profiling** has become central to the management of advanced non-small cell lung cancer (NSCLC), enabling biomarker-driven treatment selection³⁻⁵
- However, **real-world data describing the molecular landscape of stage IV NSCLC** remain limited⁶⁻⁷
- Southwestern Ontario** represents a demographically diverse population with a broad spectrum of care settings⁶⁻⁷

Objectives

- To characterize the molecular landscape of advanced NSCLC, **including patterns of genomic alterations and co-mutations**, and evaluate their associations with clinical characteristics and/or outcomes.

METHODS

Retrospective, observational study of adult patients diagnosed with Stage IV NSCLC at London Health Sciences Centre (LHSC) from January 1st, 2017, to December 31st, 2021.



Data Collection: Demographic, clinical, and molecular variables; treatment data including first-line regimens; survival data.

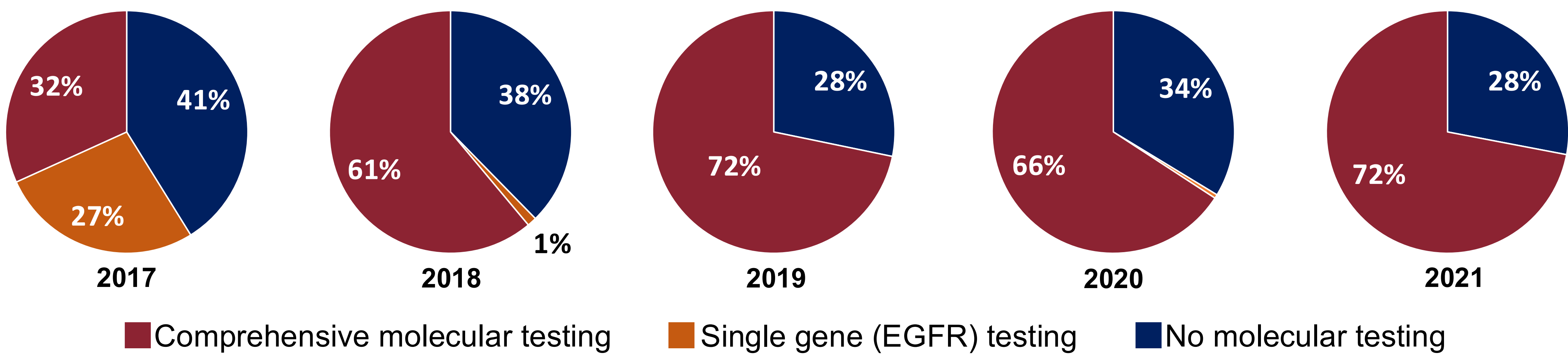
Outcomes: Real-world use of molecular profiling; distribution of mutations

Statistical Analyses: Descriptive statistics summarized cohort characteristics

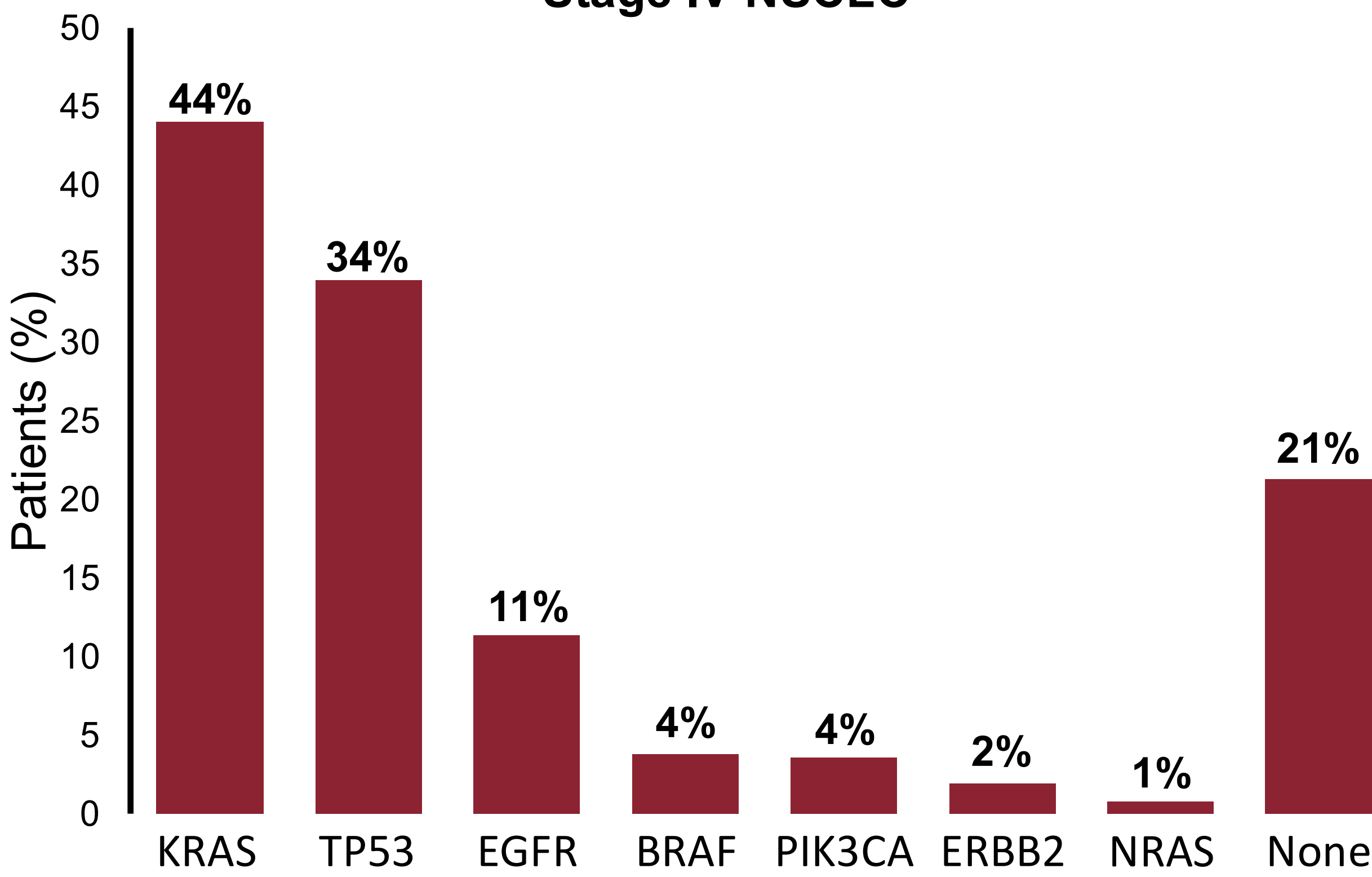
RESULTS

Demographic Characteristics		Clinical Features		Histology and Biomarkers	
Age (years)		Date of Diagnosis		Histology	
Median (IQR)	70 (63, 76)	2017	192 (21.5%)	Non-squamous	683 (76.5%)
Sex		2018	239 (26.8%)	Squamous	126 (14.1%)
Female	455 (51%)	2019	216 (24.2%)	Not Specified	84 (9.4%)
Male	433 (48%)	2020	196 (21.9%)	PD-L1 Status	
Unknown	5 (1%)	2021	50 (5.6%)	Negative, <1%	174 (19.5%)
Smoking History		ECOG Performance Status		Weak, 1-49%	200 (22.4%)
Never	86 (9.6%)	0	73 (8.2%)	Strong, ≥50%	226 (25.3%)
Former	579 (64.8%)	1	320 (35.8%)	Unknown	293 (32.8%)
Current	179 (20.0%)	2+	280 (31.4%)		
Unknown	49 (5.5%)	Unknown	220 (24.6%)		

Uptake of Comprehensive Molecular Testing in Our Cohort



Distribution of Molecular Alterations in Stage IV NSCLC^{a,b}



^a Comprehensive molecular testing predominantly utilized a DNA based panel during the period of interest, n = 527.
^b ALK was assessed by immunohistochemistry and is therefore not captured here.

Co-Mutations	Number of Patients (%) ^a
KRAS-TP53	59 (11.2%)
KRAS-EGFR	20 (3.8%)

^aIn patients who underwent comprehensive molecular testing, n = 527; panel included KRAS, TP53, EGFR, BRAF, PIK3CA, ERBB2, NRAS.

KRAS Mutation	Number of Patients (%) ^c
Gly12Cys	105 (45.26)
Gly12Val	50 (21.55)
Gly12Asp	25 (10.78)
Gln61His	10 (4.31)
Gly12Ala	9 (3.88)
Gly13Asp	6 (2.59)
Other	27 (11.64)

^cIn patients who were identified to have KRAS mutations, n = 232.

DISCUSSION

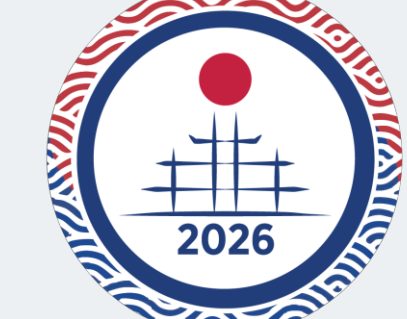
Actionable Take Away Message:

- NGS became the predominant molecular testing strategy at our centre, **increasing from 32% in 2017 to ~70% by 2019-2021**, with near-complete replacement of single-gene testing.
- A persistent testing gap remains despite widespread NGS adoption. Nevertheless, the histological diagnoses of **untested patients shifted from predominantly non-squamous in 2017–2018 to predominantly squamous in later years, reflecting broader NGS uptake among non-squamous NSCLC over time.**
- KRAS** represents the dominant molecular alteration in our real-world stage IV NSCLC population (~44%), with KRAS G12C accounting for nearly half (45.3%) of KRAS-mutated cases
- Mutations in TP53 were the second most common (~34%); **~11% had KRAS-TP53 co-mutations, which have been associated with a more unfavorable prognosis⁸.**

Future Direction for Research:

- Identify barriers** to molecular testing among the persistent untested population.
- Characterize the clinical relevance of specific co-mutation patterns, **particularly KRAS/TP53**, in patients with advanced non-squamous NSCLC and evaluate their associations with **clinicopathologic characteristics as well as responsiveness to treatments such as immunotherapy.**

REFERENCES



IASLC 2026 World Conference on Lung Cancer
SEPTEMBER 12 - 15, 2026
SEOUL, REPUBLIC OF KOREA

Artificial Intelligence (AI) Use Disclaimer
The authors declare that no AI was used in the creation of this poster.

Acknowledgements
We gratefully acknowledge the patients and families whose care made this work possible, and the clinicians, data abstractors, and administrative staff who supported data collection. We also thank colleagues in the thoracic oncology program for their feedback on study design and interpretation.

