

INTRODUCTION

Non-small cell lung cancer (NSCLC) remains a leading cause of cancer mortality, with survival influenced by disease stage, performance status, tumour histology, and molecular characteristics.¹ Advances in molecular testing and targeted therapy have improved outcomes for patients with actionable genomic alterations (AGA).² However, real-world evidence from developing countries remains limited, where delayed presentation and unequal access to molecular profiling and targeted treatments may affect survival.³ Identifying stage-specific clinical and molecular factors associated with prognosis is therefore essential. This study evaluated factors associated with overall survival among patients with Stage I–IV NSCLC in a real-world, resource-limited setting.

METHODS

This retrospective study examined data of patients diagnosed with NSCLC between January 2017 and December 2023 at a tertiary referral centre. Demographic, clinicopathological, and molecular-testing data were extracted from medical records. Patients were stratified into Stage I/II, Stage III, and Stage IV groups. Descriptive and multivariable analyses were performed to evaluate factors associated with overall survival. Statistical analyses were performed using JAMOVl.

RESULTS

- Among 577 patients, 62 had Stage I/II, 73 had Stage III, and 442 had Stage IV disease. The mean age at diagnosis was 63.2 years; patients with Stage I/II disease were significantly older than those with Stage IV disease (66.2 vs 62.5 years; $p=0.011$).
- Overall, EGFR mutation is the most common AGA detected, present in 52.8% patients. Most patients were tested by single gene testing (81.6%).
- Median overall survival decreased with advancing stage: 28 months for Stage I/II, 18 months for Stage III, and 8 months for Stage IV disease. Twelve-month mortality was significantly highest among patients with Stage IV disease ($p<0.001$).
- Poor ECOG performance status and negative molecular-testing results were associated with poorer survival ($p=0.008$). Conversely, EGFR-sensitising mutations were associated with longer survival, particularly among patients with Stage IV disease ($p=0.001$).

DISCUSSION AND CONCLUSION

DISCUSSION: Survival declined markedly with advancing disease stage. Median overall survival was 28 months for Stage I/II, 18 months for Stage III, and 8 months for Stage IV disease, while 12-month mortality reached 63% among patients with Stage IV disease. In the multivariable analysis, Stage IV disease and an ECOG performance status of 3–4 were independent predictors of death within 12 months, highlighting the adverse effects of late presentation and poor functional status.⁴

Patients with negative molecular-testing results had a higher risk of early death than those with EGFR mutations. The longer survival observed in EGFR-mutated disease likely reflects the clinical benefit and availability of targeted therapies. These findings support earlier diagnosis, timely molecular characterization, and equitable access to targeted treatments in resource-constrained settings. Broader genomic profiling may also identify AGAs among patients whose initial limited-panel testing yields negative results.

However, this study is limited by its retrospective nature, single-centre study design, limited NGS testings, missing data, and changes in treatment availability and access during the study period.

CONCLUSION: Disease stage, performance status, and molecular-testing results were important determinants of survival in this real-world NSCLC cohort. Patients with Stage IV disease, poor ECOG performance status, or undetected AGA were at greatest risk of early mortality. Strategies promoting earlier diagnosis, molecular profiling, and improved access to targeted therapies are needed to improve NSCLC outcomes in developing countries.

REFERENCES & ACKNOWLEDGEMENTS

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References:
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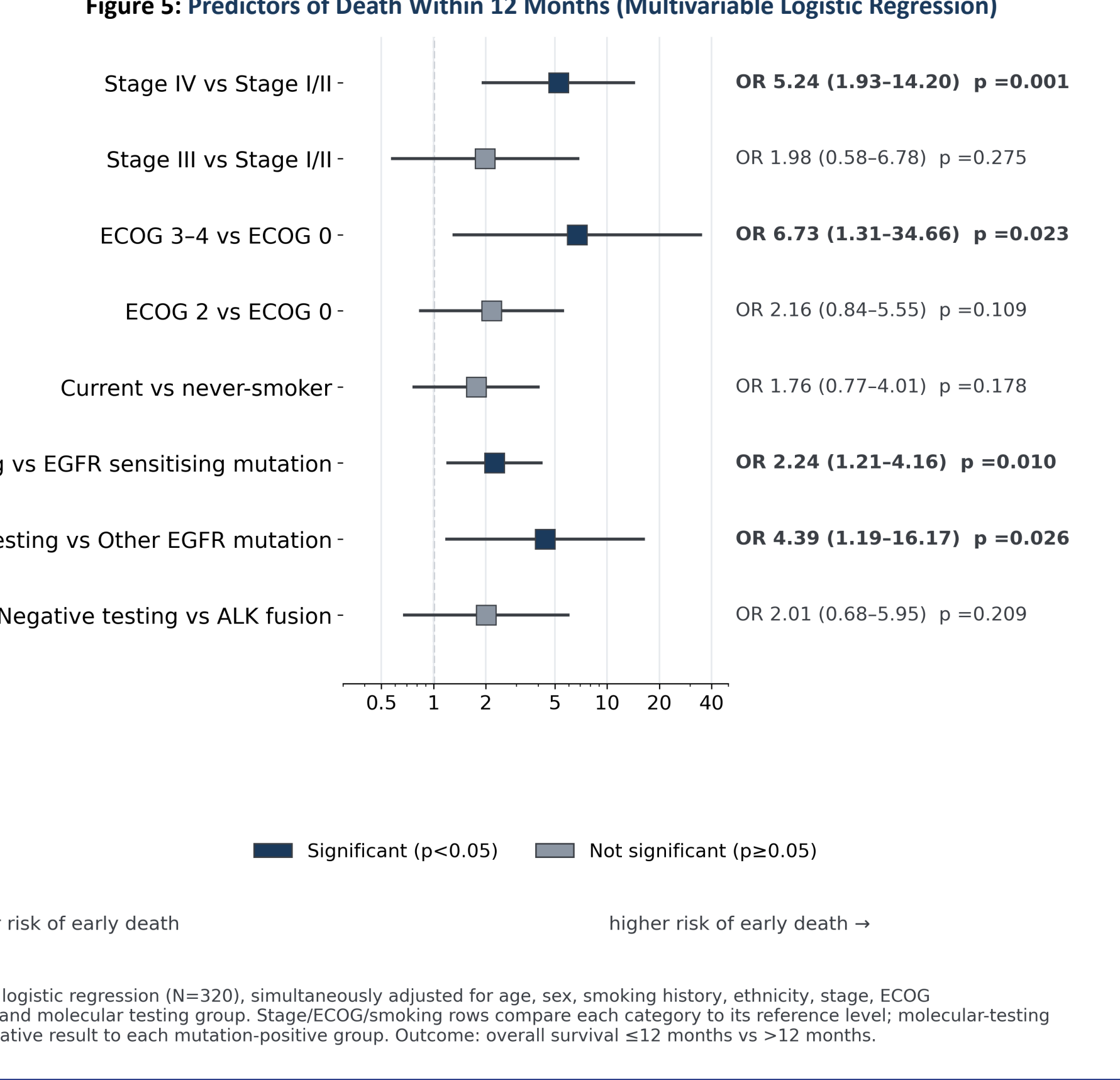
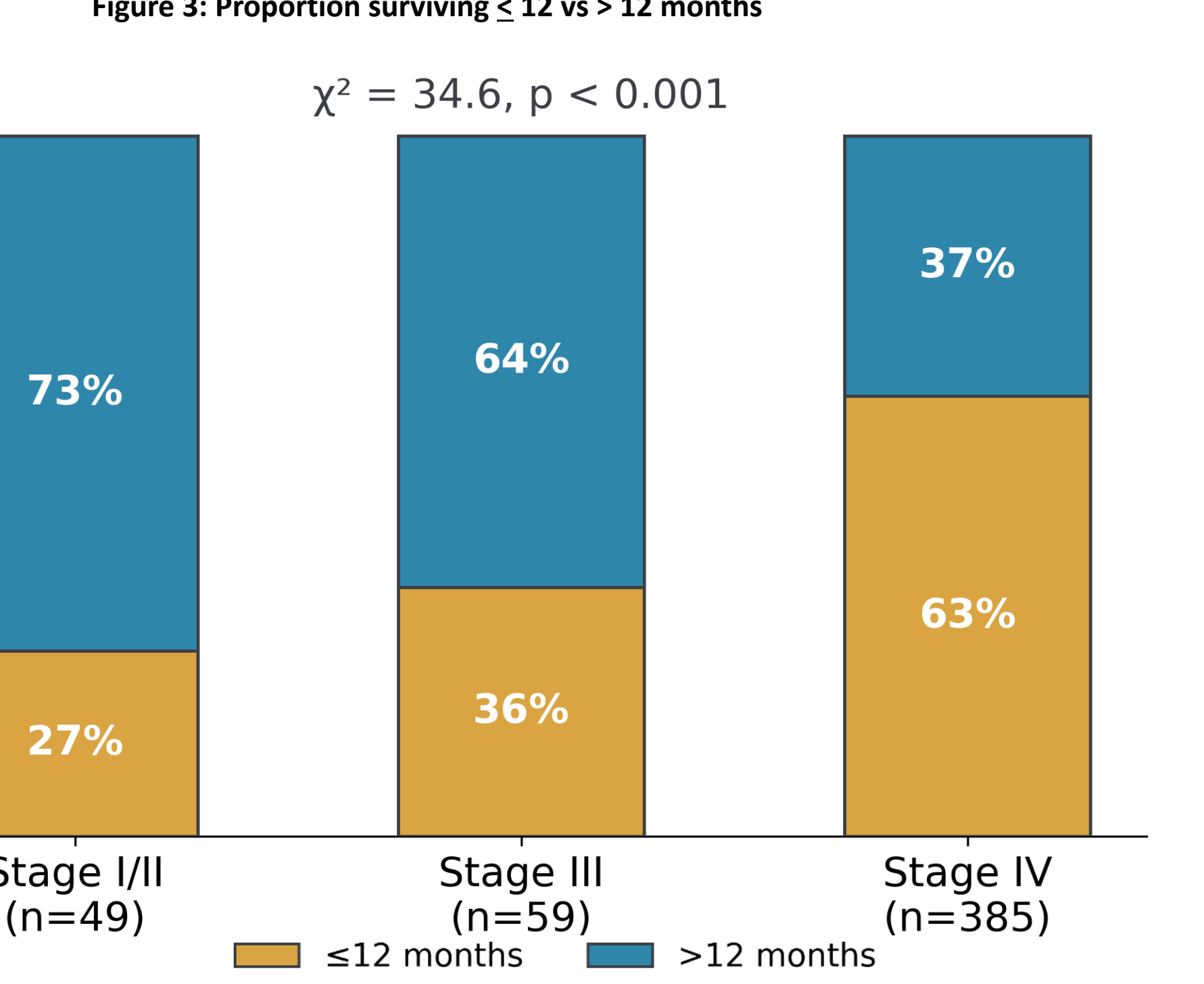
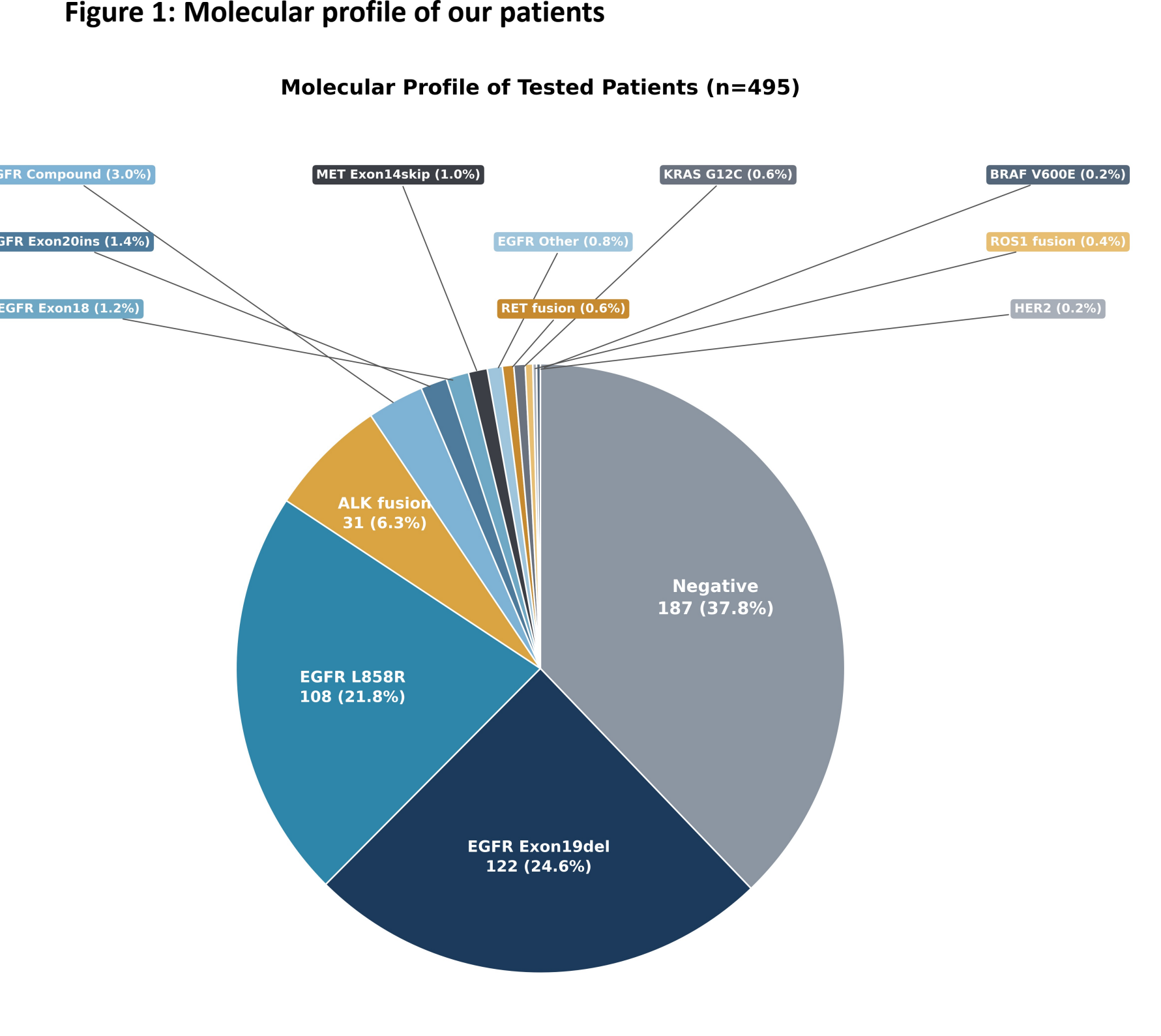
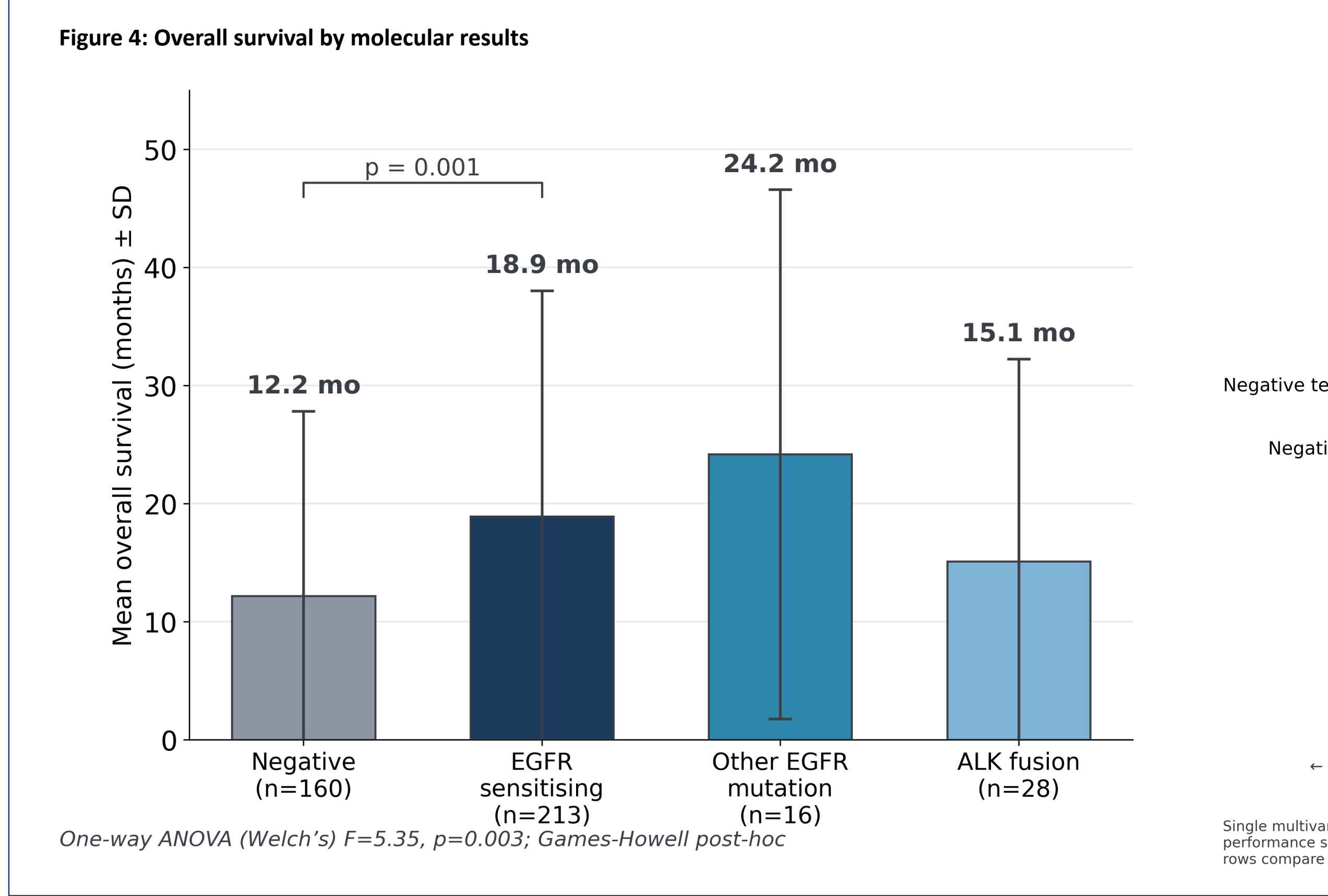
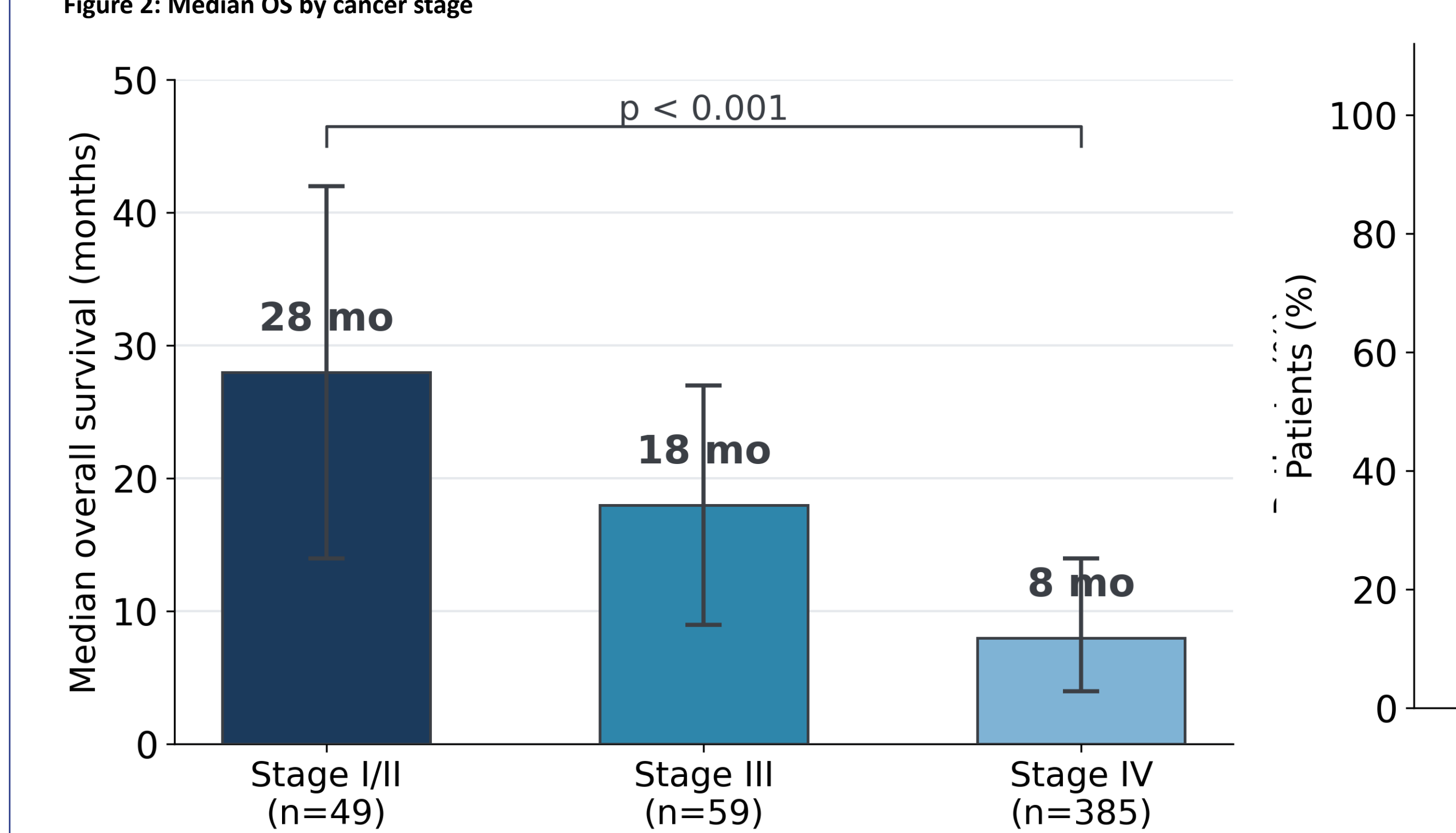
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RESULTS

Table 1: Baseline characteristics of the patients					
Variable	Overall (n=577)	Stage I/II (n=62)	Stage III (n=73)	Stage IV (n=442)	p
Median age, years [IQR]	64.0 [57.0, 71.0]	66.50 [60.25, 73.00]	65.00 [58.00, 75.00]	64.00 [55.25, 70.00]	0.014
Sex, n (%)					
Male	311 (53.9)	30 (48.4)	44 (60.3)	237 (53.6)	0.374
Female	266 (46.1)	32 (51.6)	29 (39.7)	205 (46.4)	—
Smoking status, n (%)					
Never	286 (49.6)	33 (53.2)	31 (42.5)	222 (50.2)	0.248
Ex-smoker	91 (15.8)	11 (17.7)	13 (17.8)	67 (15.2)	—
Current	176 (30.5)	16 (25.8)	29 (39.7)	131 (29.6)	—
Missing	24 (4.2)	2 (3.2)	0 (0.0)	22 (5.0)	—
Ethnicity, n (%)					
Malay	107 (18.5)	9 (14.5)	14 (19.2)	84 (19.0)	0.417
Chinese	230 (39.9)	32 (51.6)	33 (45.2)	165 (37.3)	—
Iban	135 (23.4)	9 (14.5)	14 (19.2)	112 (25.3)	—
Bidayuh	63 (10.9)	9 (14.5)	7 (9.6)	47 (10.6)	—
Indian / Other	42 (7.3)	3 (4.8)	5 (6.8)	34 (7.7)	—
ECOG performance status, n (%)					
0	60 (10.4)	17 (27.4)	12 (16.4)	31 (7.0)	<0.001
1	239 (41.4)	27 (43.5)	33 (45.2)	179 (40.5)	—
2	96 (16.6)	3 (4.8)	7 (9.6)	86 (19.5)	—
3–4	50 (8.7)	1 (1.6)	3 (4.1)	46 (10.4)	—
Missing	132 (22.9)	14 (22.6)	18 (24.7)	100 (22.6)	—
Histology, n (%)					
Adenocarcinoma	473 (82.0)	51 (82.3)	44 (60.3)	378 (85.5)	<0.001
Squamous cell	69 (12.0)	5 (8.1)	19 (26.0)	45 (10.2)	—
Adenosquamous / other	35 (6.1)	6 (9.7)	10 (13.7)	19 (4.3)	—

Age: Kruskal–Wallis test. Categorical variables: χ^2 test.



Single multivariable logistic regression (N=320), simultaneously adjusted for age, sex, smoking history, ethnicity, stage, ECOG performance status and molecular testing group. Stage/ECOG/smoking rows compare each category to its reference level; molecular-testing rows compare a negative result to each mutation-positive group. Outcome: overall survival ≤12 months vs >12 months.