

INTRODUCTION

- Approximately 30% of non-small cell lung cancer (NSCLC) cases are diagnosed at **early stages** and primarily managed by **surgical resection** and **adjuvant therapy**.
- Disease **recurrence** remains common within the first two years (35% of patients).
- Liquid biopsy-based surveillance via **cell-free DNA (cfDNA)** is a promising tool for recurrence detection.

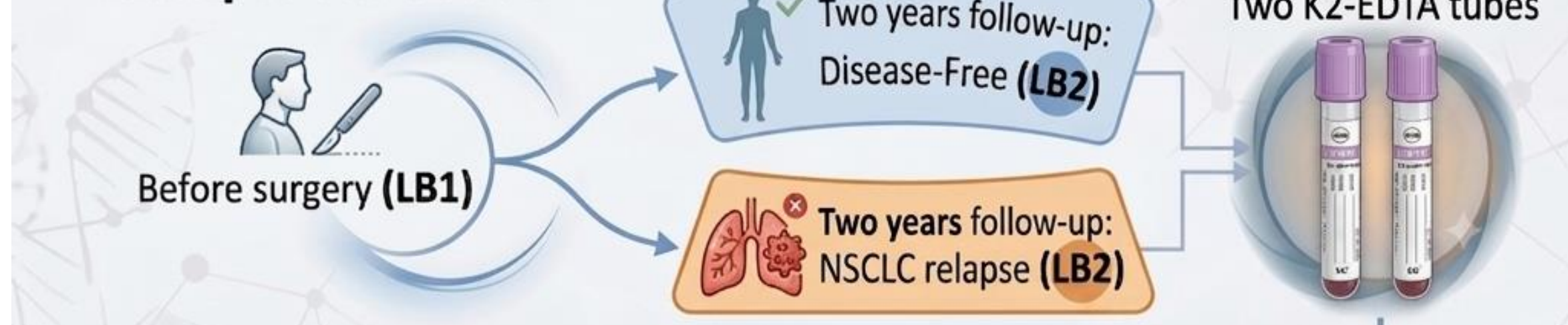
Objective: To evaluate the **prognostic value of cfDNA** as a marker for **clinical progression** in patients with resected early-stage NSCLC who received adjuvant therapy.

METHODS

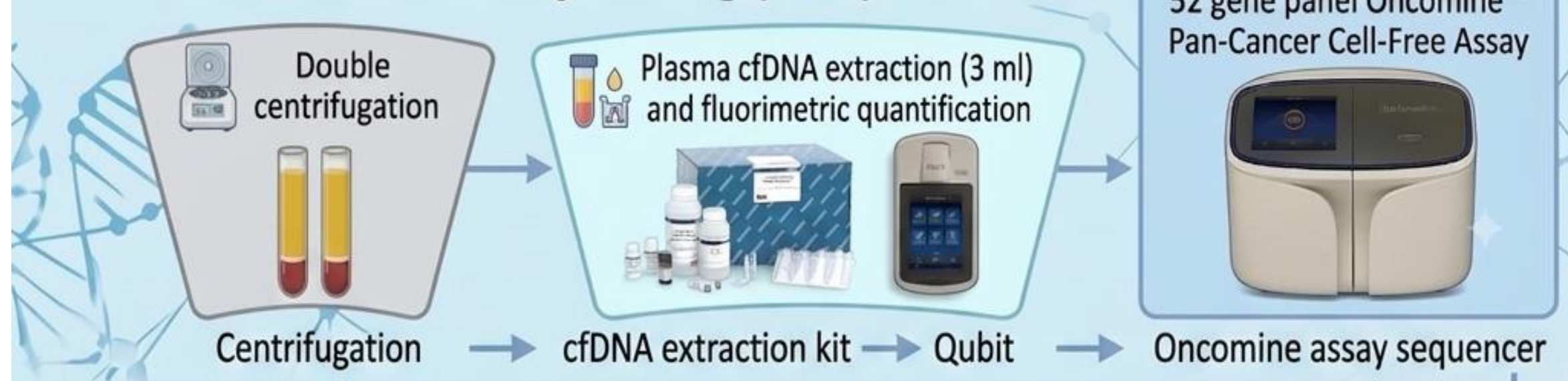
Design:

This is a prospective cohort study of patients with resectable NSCLC at the Cruces University Hospital in the Basque Country, Spain.

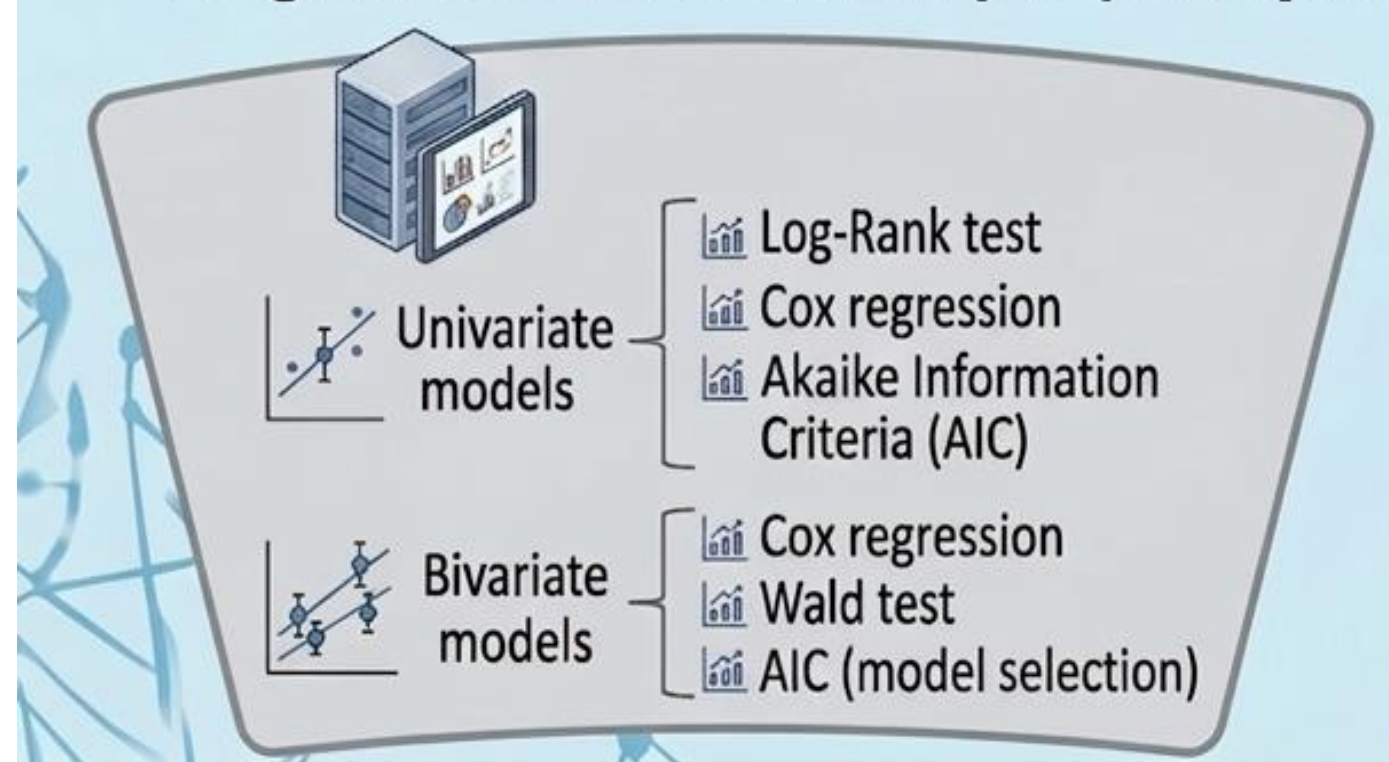
Sample collection



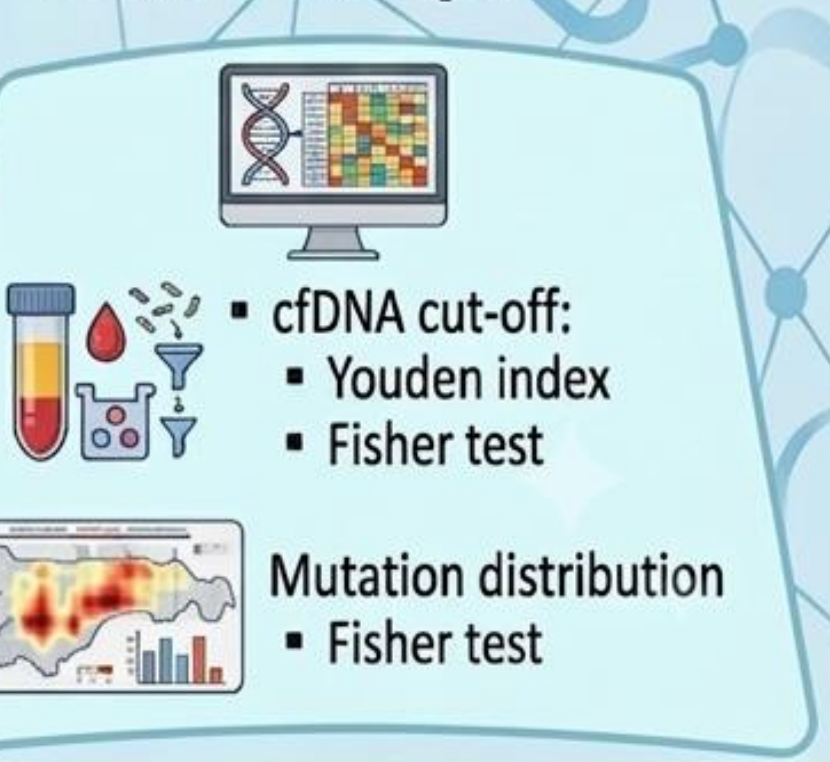
Next Generation Sequencing (NGS) workflow



Progression-Free Survival (PFS) analysis



Genetic analysis



DISCUSSION AND CONCLUSION

- Longitudinal monitoring of cfDNA concentration and mutational status provides powerful prognostic indicators of NSCLC recurrence.**
- cfDNA concentration offers a rapid, quantifiable metric to identify high-risk patients who may benefit from intensified surveillance or early therapeutic intervention.**
- Large-scale prospective trials are warranted to validate these personalized surveillance biomarkers and bridge the gap between surgical resection and radiological progression.**

REFERENCES & ACKNOWLEDGEMENTS

ctDNA-LUNG-DETECT Study



Plasma vs. Tissue DNA Mutations in NSCLC



DISCLOSURES

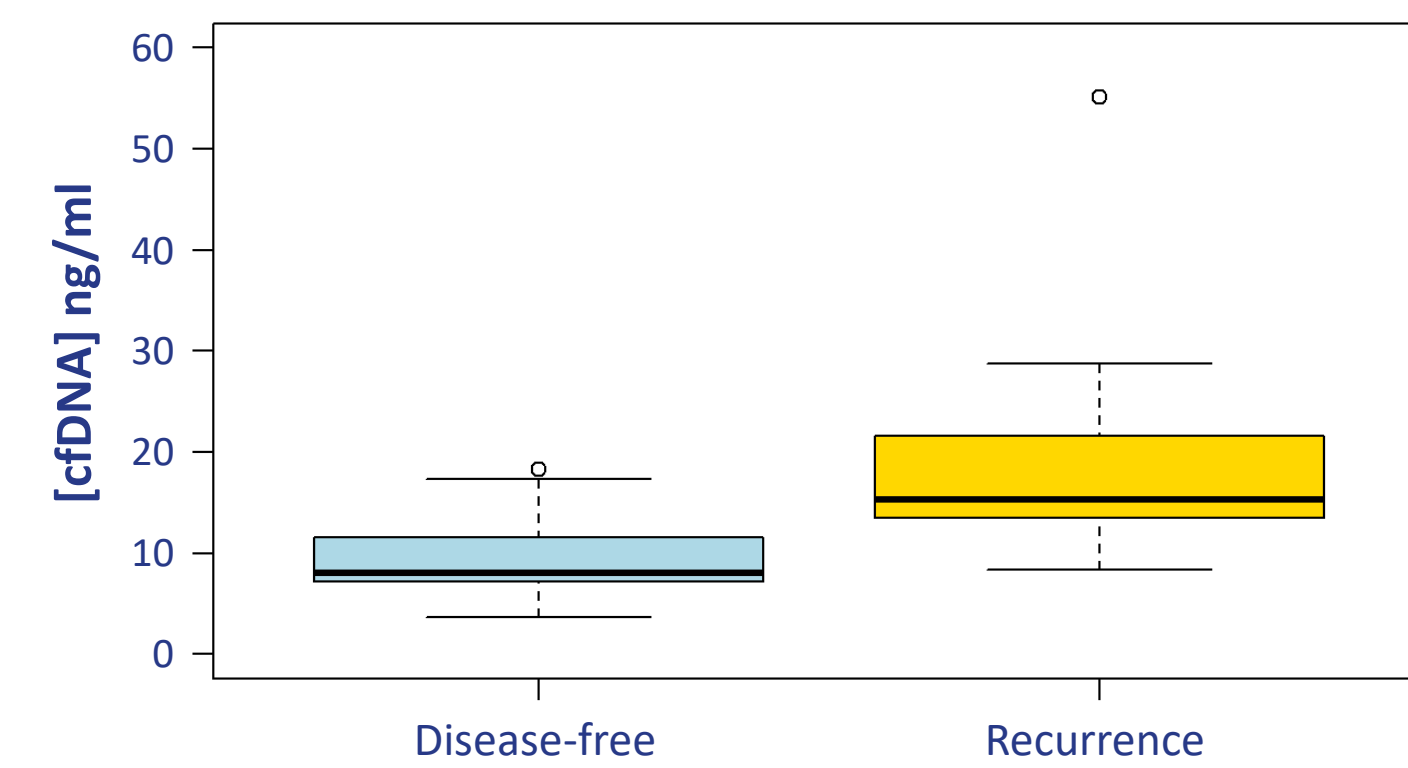
- Funding:** This work was funded by “BIOEF-EITB Telemaratoia” (Code: BIO19/CP/003).
- AI disclosures:** Google Gemini was used for methodology diagram generation and text editing.

RESULTS

Clinical Data

Cohort characteristics	2-Year Clinical Outcomes
31 patients. - Mean age 63.2 ± 6.6 years. - Sex distribution (M:F): 2.44 ratio.	- Follow-up period: 2 years. - Recurrence rate: 29%; Median Progression Free Survival (PFS) not achieved. - Median time to progression: 8.4 months (6.6 - 16.1).

cfDNA concentration in Follow-Up



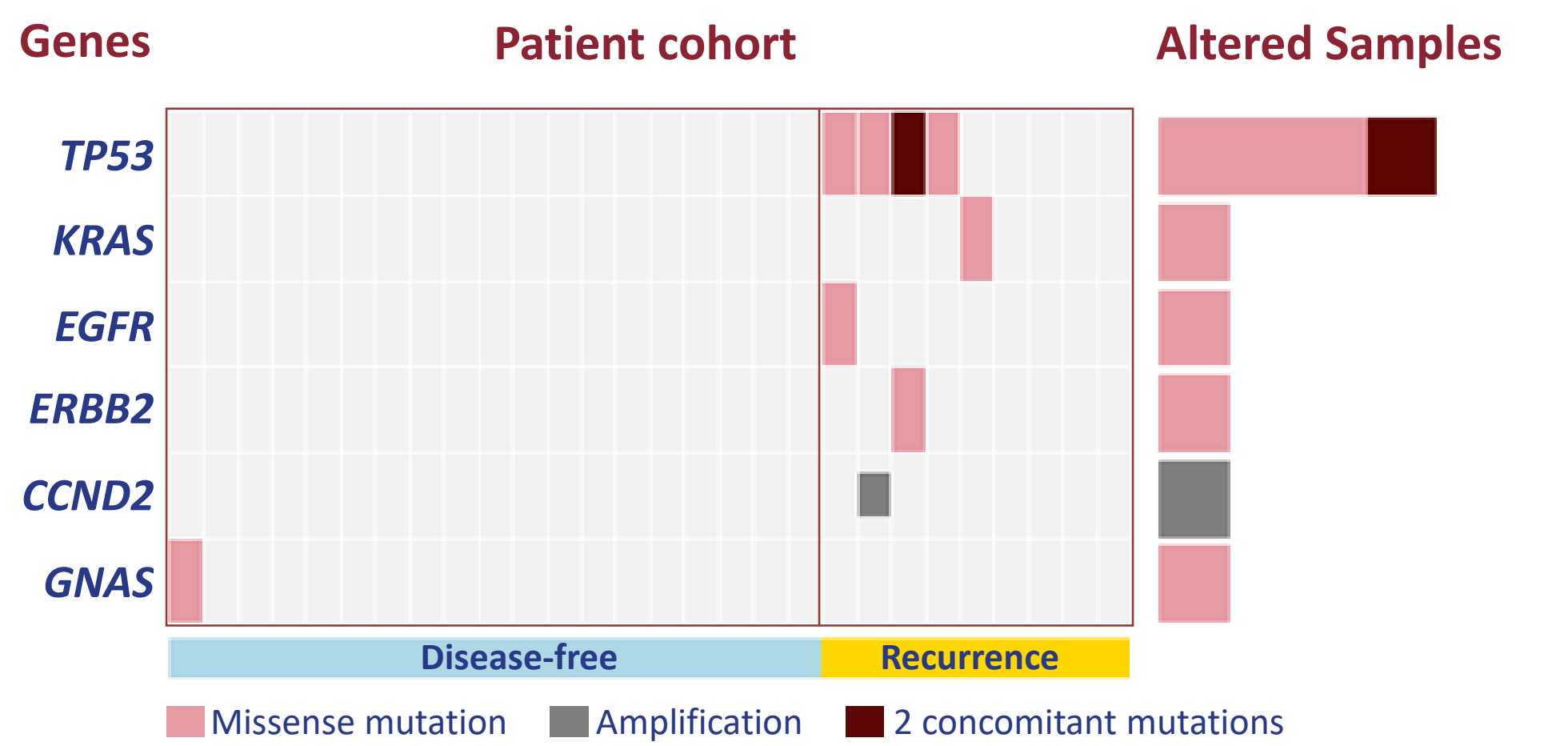
cfDNA cut-off

- Accuracy: 0.86
- Sensitivity: 0.78
- Specificity: 0.89
- p = 0.001

Molecular Profile

Elevated cfDNA levels correlate with disease recurrence in follow-up (LB2) samples. Patients with recurrence showed significantly higher cfDNA concentrations (p = 0.0008). Median (IQR): Disease-free 8.08 ng/ml (7.16–11.58); Recurrence 15.30 ng/ml (13.53–21.56).

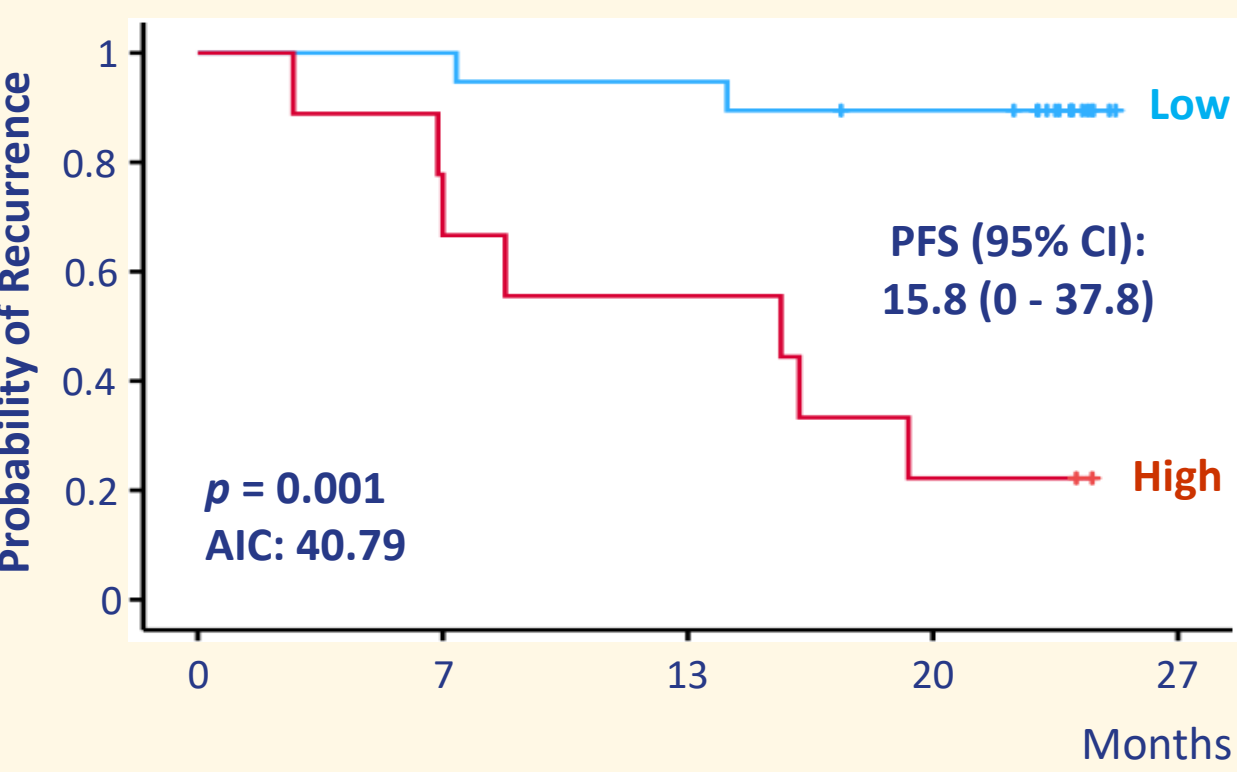
Genetic Alterations by Disease Status



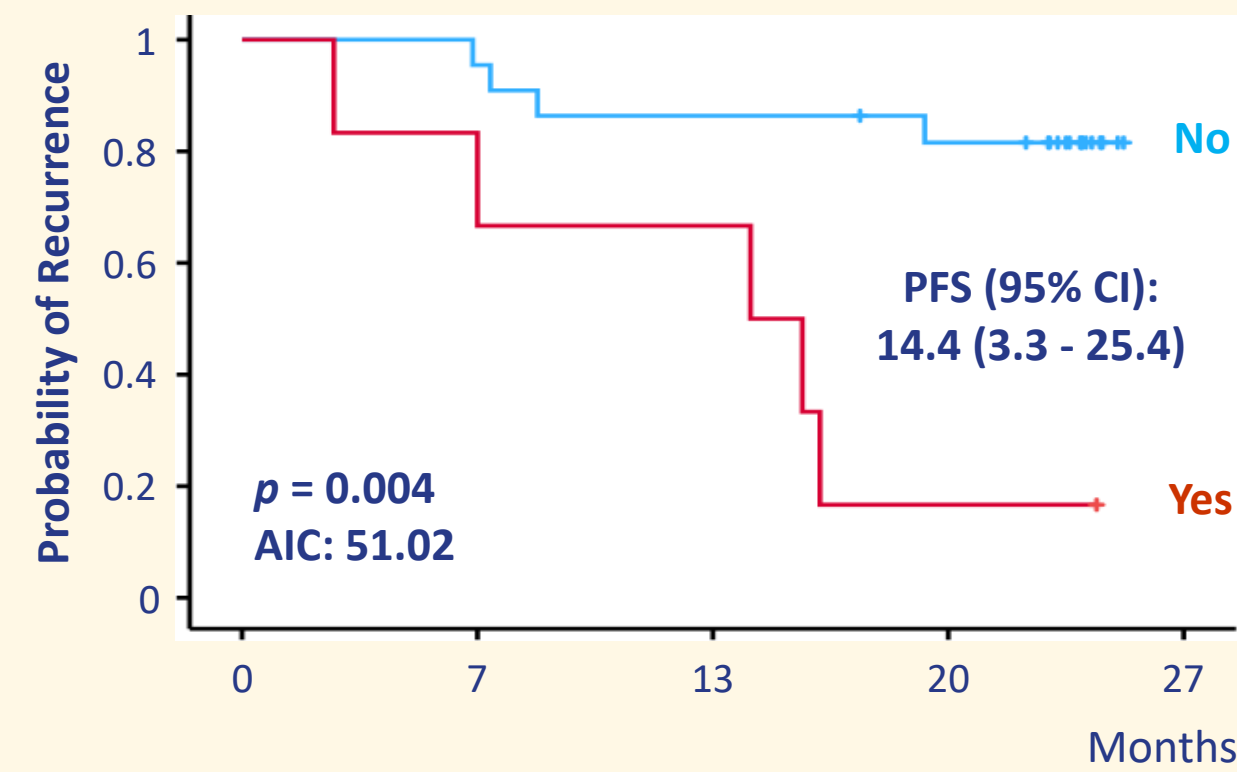
Distribution of genetic alterations by disease status. In the LB2 cohort, 10 genetic alterations were identified across 6 patients. Variant prevalence was significantly higher in **recurrent cases** compared to disease-free patients (56% vs. 5.3%, p = 0.011), with TP53 representing the most frequent alteration (50%).

Univariate Predictors of Progression-Free Survival (PFS)

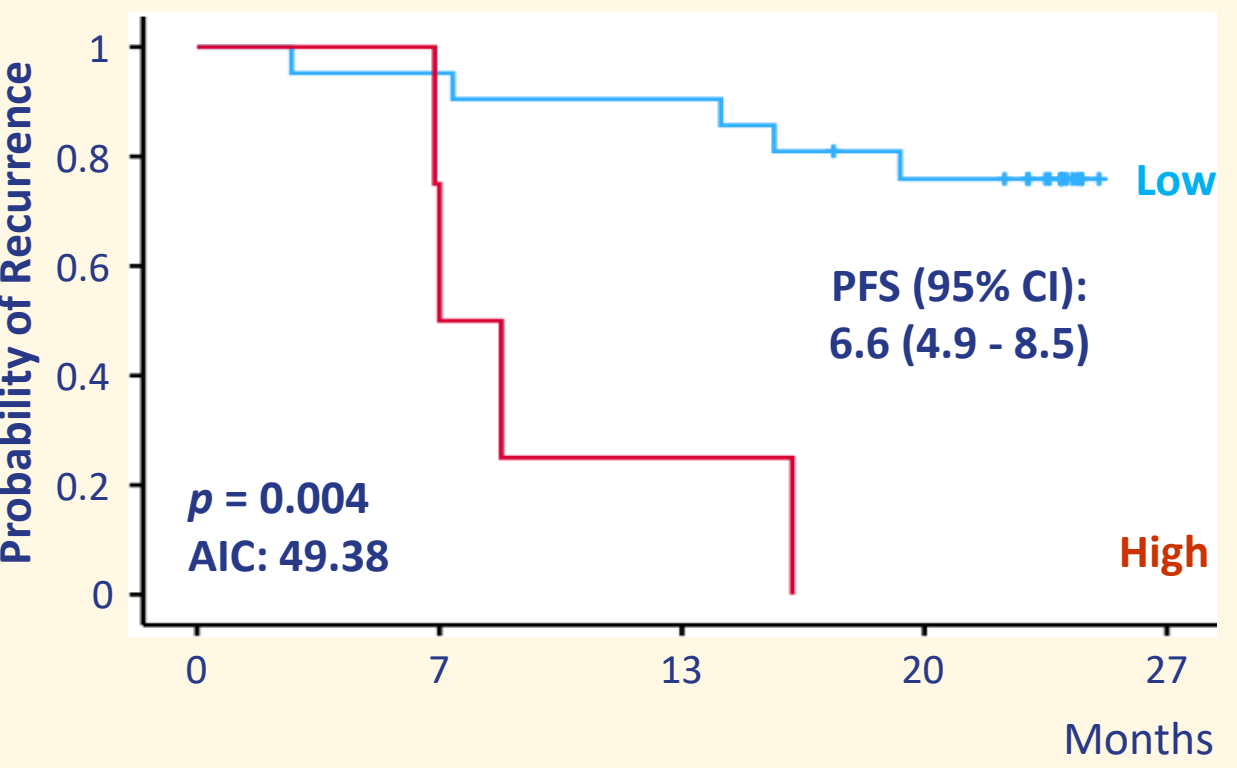
A cfDNA concentration (LB2)



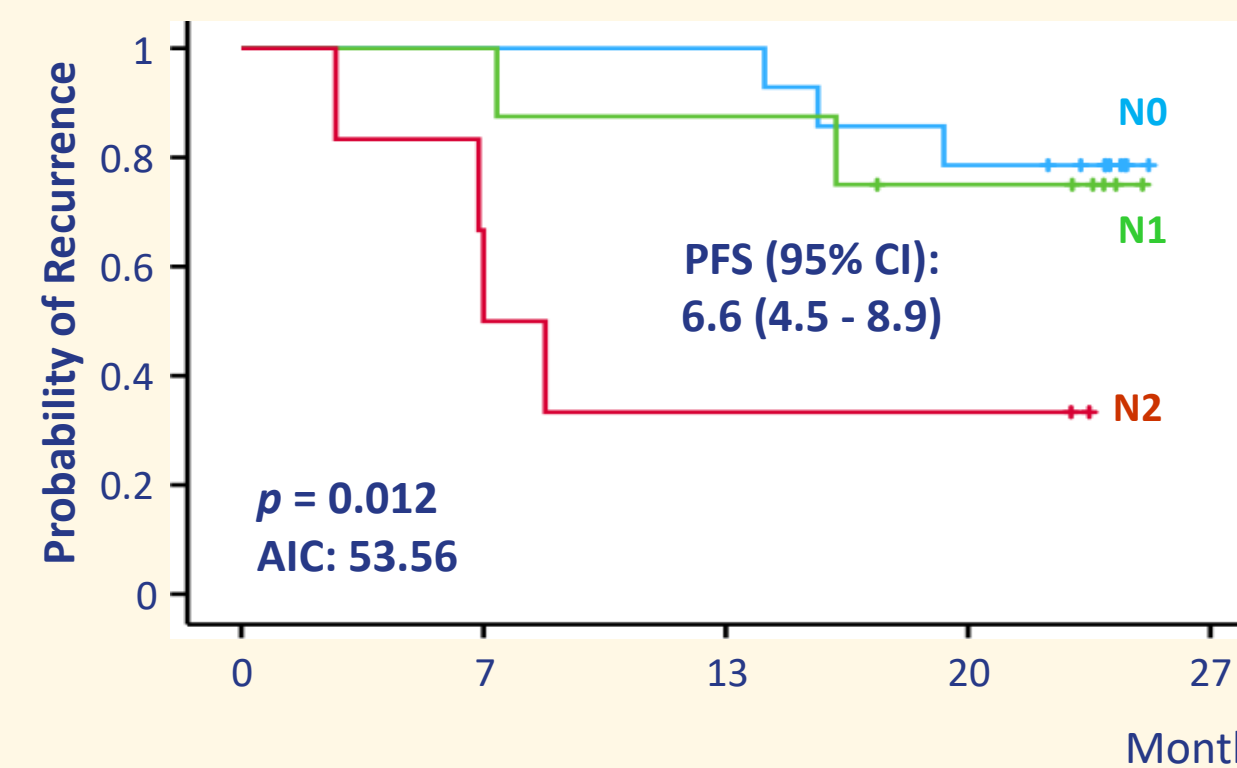
B Presence of mutations (LB2)



C CYFRA 21-1 levels (LB2)



D Lymph Node Status (LB1)



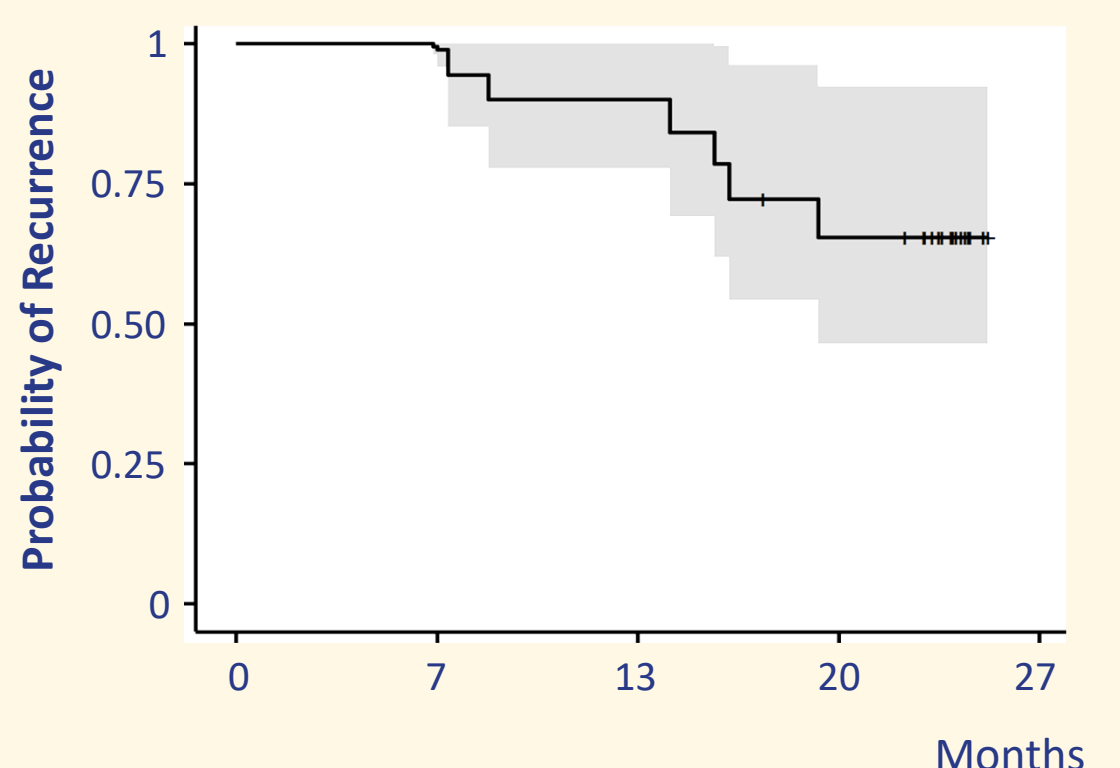
Factors associated with Progression-Free Survival (PFS): All variables significantly predicted recurrence (p < 0.05). LB2 cfDNA concentration showed the best model fit (lowest AIC: 40.79, p = 0.001). All variables except Lymph Node Status (D) were measured at LB2. LB1 variables were not significant (p > 0.05). AIC: Akaike Information Criterion; CI: Confidence Interval.

Predicting Recurrence: Optimal Multivariate Model

	Model	HR 95% CI	p-value	AIC
1	cfDNA	1.082 - 1.493	0.004	38.92
	N Status	0.993 - 7.574	0.052	
2	CYFRA 21-1	1.019 - 3.152	0.043	50.95
	N Status	0.497 - 4.179	0.501	
3	cfDNA	1.061 - 1.351	0.003	38.28
	CYFRA 21-1	0.892 - 3.053	0.111	
4	cfDNA	1.038 - 1.435	0.016	39.44
	CYFRA 21-1	0.562 - 3.196	0.509	
	N Status	0.491 - 6.865	0.367	

Survival Analysis

Best model: cfDNA concentration & Lymph Node Status



Cox regression of the optimal model (cfDNA + lymph node status). Grey shaded area represents the 95% confidence interval (CI) for recurrence probability. Combining both variables improves model stability compared to univariate analyses. HR: Hazard Ratio; AIC: Akaike Information Criterion.