

## INTRODUCTION

Lung cancer remains the leading cause of cancer-related death worldwide. Young adults with non-small cell lung cancer (NSCLC) represent a distinct subgroup, often with limited tobacco exposure and a high frequency of actionable genomic alterations. However, access to broad genomic testing remains uneven, particularly in settings with limited resources. This study aimed to describe the demographic characteristics, genomic profile, and clinical outcomes of young adults with NSCLC followed in Brazilian clinical practice.

## METHODS

This multicenter retrospective study included patients aged 18–50 years with NSCLC who were followed at Oncologia D’Or centers in Brazil between January 2020 and December 2025. Clinical, pathological, and genomic data were collected from medical records. Actionable genomic alterations were defined as alterations associated with targeted therapies available in current clinical practice. Descriptive statistics were used for the initial data analysis, based on the characteristics of the variables. This preliminary analysis included patients from states of Bahia and São Paulo and is part of a broader multicenter study with ongoing data collection across Brazil.

## DISCUSSION AND CONCLUSION

The high frequency of actionable genomic alterations in this cohort (80.4%) is consistent with large sequencing studies showing that young adults with NSCLC are more likely than older patients to harbor targetable alterations [1–3] A Peruvian study also reported actionable alterations in 84.4% of young patients, suggesting a similar genomic profile among young Latin American populations [4]. The low frequency of tobacco exposure in our cohort (17.7%) further supports the distinct profile of NSCLC in young adults and never-smokers, in whom EGFR mutations and ALK rearrangements are more common.[5]

These findings support broad genomic testing in this population, including in settings where access remains limited, so that eligible patients can receive targeted therapies without unnecessary delays.

## REFERENCES & ACKNOWLEDGEMENTS

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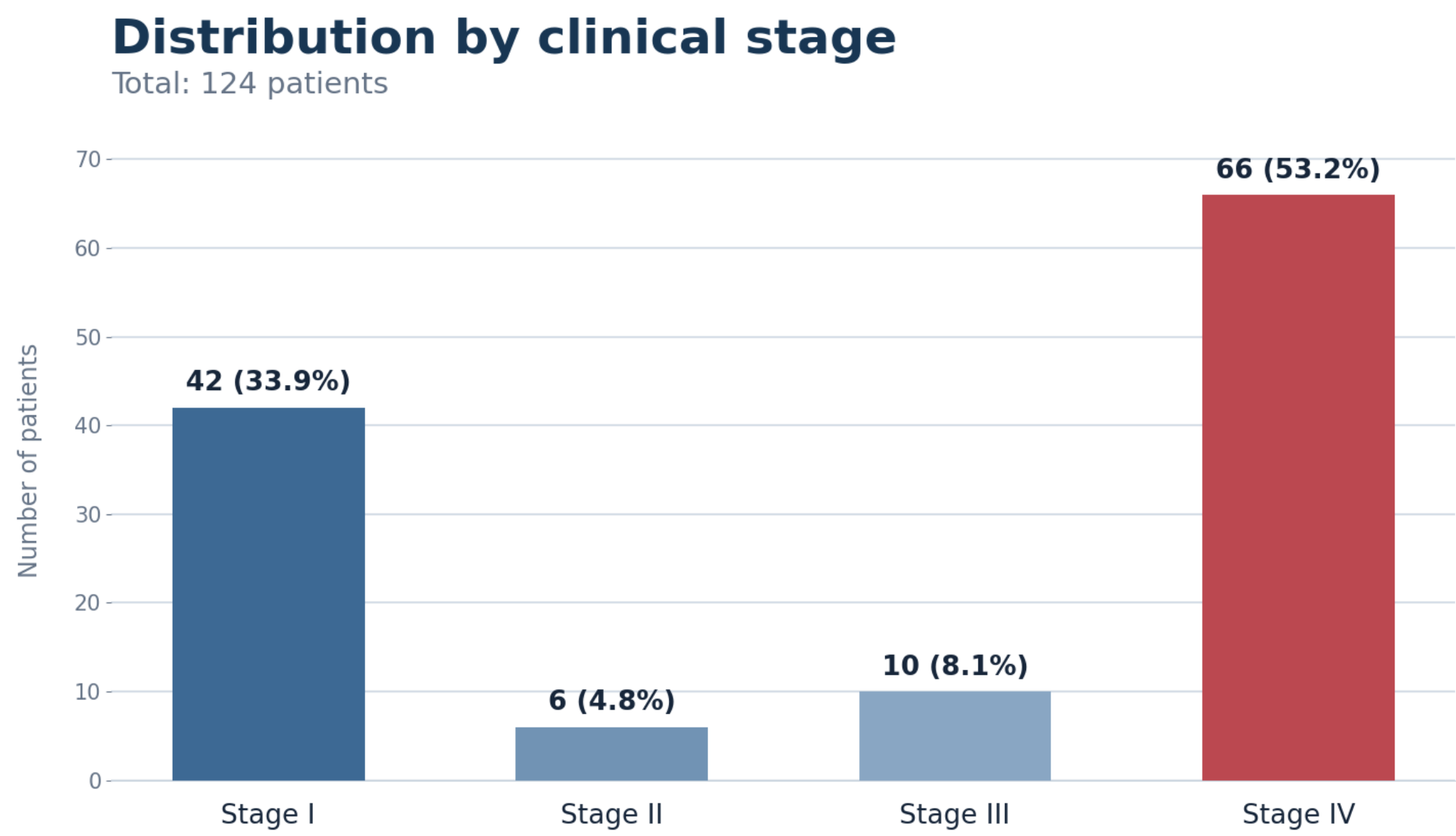
### Artificial Intelligence (AI) Use Disclaimer

ChatGPT (OpenAI) was used to assist with the creation of graphs, grammatical editing, and translation into English. All AI-assisted outputs were reviewed and validated by the authors, who retained full responsibility for the accuracy and integrity of the content.

## RESULTS

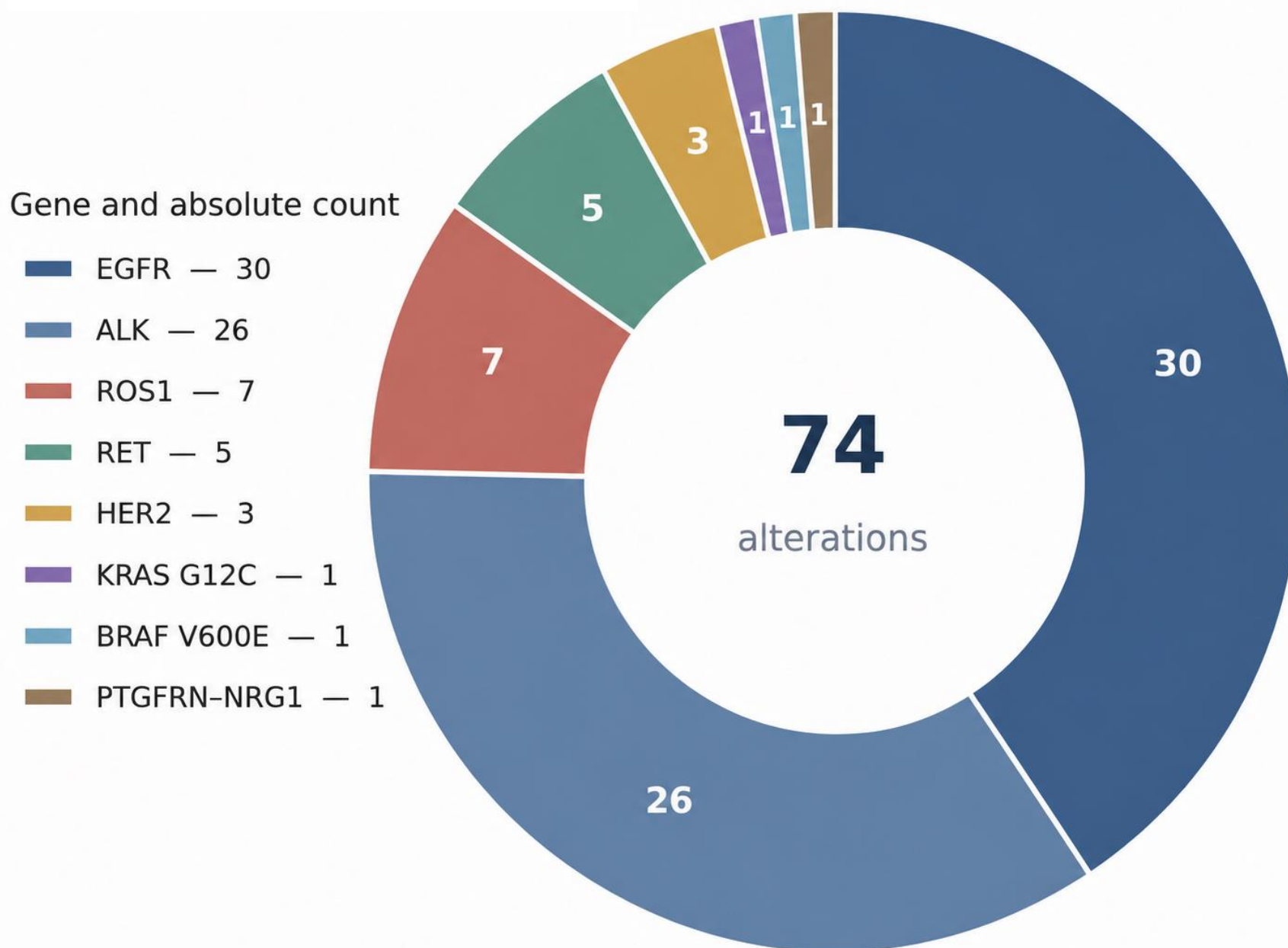
The medical records of 319 patients were reviewed, of whom 124 were included in the study after excluding patients with incomplete medical records, carcinoid tumors, small-cell lung cancer (SCLC), or other predefined exclusion criteria. Of the included patients, 31 (25.0%) were from Bahia and 92 (75.0%) from São Paulo. The median age was 43 years, and 86 patients (69.4%) were diagnosed between 41 and 50 years of age. Most patients were women (n=71; 57.3%), and adenocarcinoma was the predominant histology (n=119; 96.0%). Only 22 patients (17.7%) had a history of smoking.

At diagnosis, 66 patients (53.2%) had stage IV disease. Brain metastases were identified in 33 patients (26.6%) and were present at diagnosis in 18 (14.5%).



### Driver mutations

Absolute number of positive results



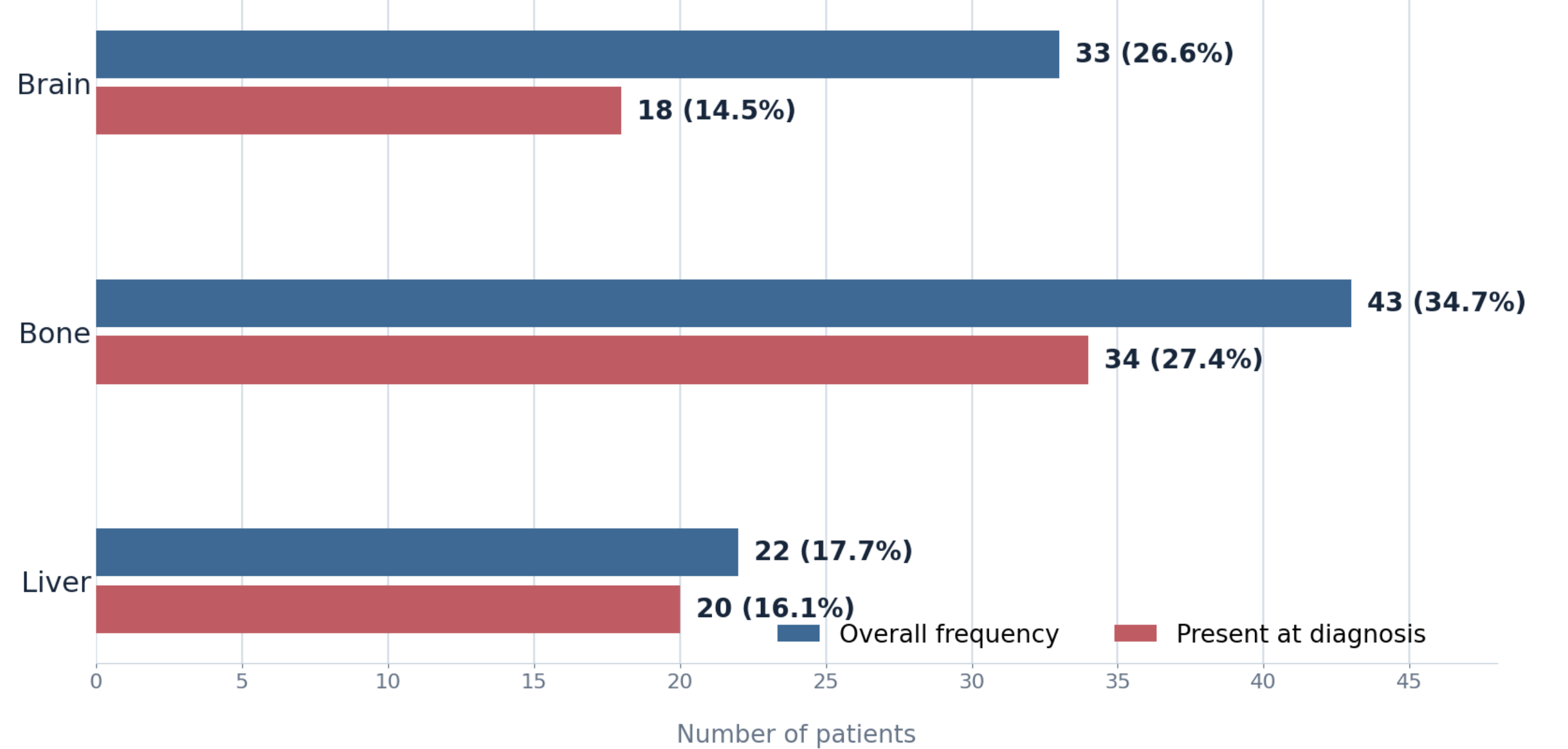
### Patient characteristics

Clinical and demographic profile

| Characteristic                  | Category                       | Value       |
|---------------------------------|--------------------------------|-------------|
| Gender, n (%)                   | Male                           | 53 (42.7%)  |
|                                 | Female                         | 71 (57.3%)  |
| Median age (range)              |                                | 43 (27–50)  |
| Histology, n (%)                | Adenocarcinoma                 | 119 (96.0%) |
|                                 | Squamous cell carcinoma        | 3 (2.4%)    |
|                                 | Adenosquamous carcinoma        | 1 (0.8%)    |
|                                 | NSCLC, not otherwise specified | 1 (0.8%)    |
| Smoking history, n (%)          | No                             | 102 (82.3%) |
|                                 | Yes                            | 22 (17.7%)  |
| Family history of cancer, n (%) | Any type of cancer             | 79 (63.7%)  |
|                                 | Lung cancer                    | 20 (16.1%)  |
|                                 | Missing information            | 18 (14.5%)  |

### Metastatic sites

Overall frequency and presence at diagnosis



Molecular data were available for 92 patients. Testing was performed using next-generation sequencing (NGS) in 72 patients and immunohistochemistry and/or polymerase chain reaction in 18. For the remaining two patients, the testing method was not documented. Among the 92 patients with molecular data, 74 (80.4%) had an actionable genomic alteration. All 32 patients without molecular data had stage I disease. The most frequent driver alterations were EGFR mutations (30/92; 32.6%), ALK rearrangements (26/90; 28.9%), ROS1 fusions (7/74; 9.5%), RET fusions (5/74; 6.8%), HER2 alterations (3/72; 4.2%), and KRAS G12C mutations (1/74; 1.4%). Other KRAS mutations were found in five patients (5/74; 6.8%). Among the co-alterations, TP53 mutations were the most common (21/72; 29.2%), followed by CDKN2A/B alterations (12/72; 16.7%) and MTAP loss (5/72; 6.9%).