

INTRODUCTION

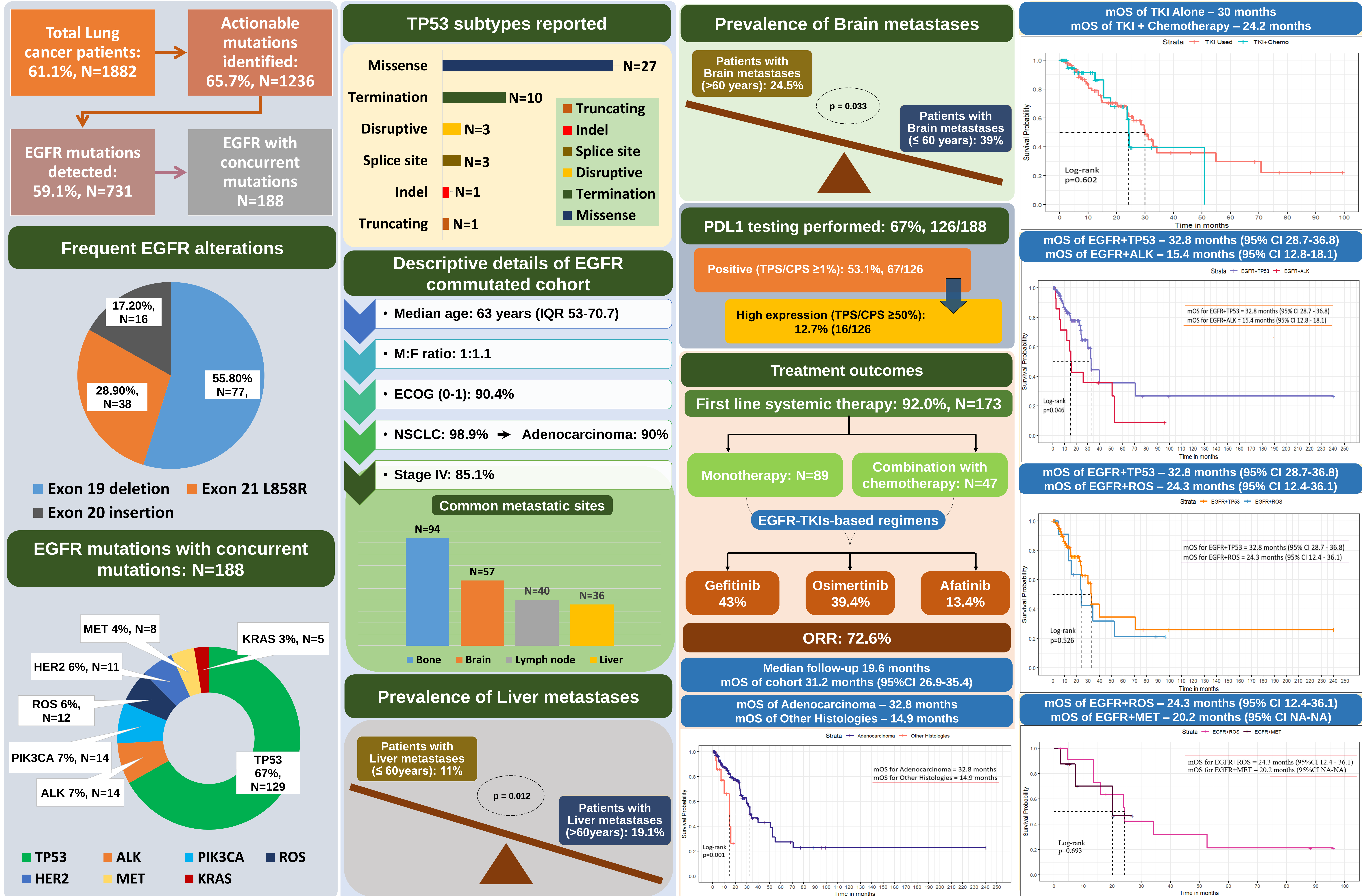
While EGFR mutations are common and actionable in NSCLC, the broader spectrum of concurrent genomic co-mutations and their clinical implications remain inadequately characterized in Indian real-world settings.

METHODS

Consecutive patients with EGFR-mutated lung cancer harboring co-mutations, treated between March 2018 and December 2025 were retrospectively evaluated.

- Co-mutation profiles, clinicopathological characteristics, treatment patterns and outcomes were retrieved from electronic medical records.
- Survival outcomes were analyzed using the Kaplan-Meier method.

RESULTS



CONCLUSION

- Concurrent co-mutations in EGFR-mutated lung cancer significantly influence clinical outcomes, highlighting the critical role of comprehensive genomic profiling in optimizing personalized therapeutic strategies in real-world settings