

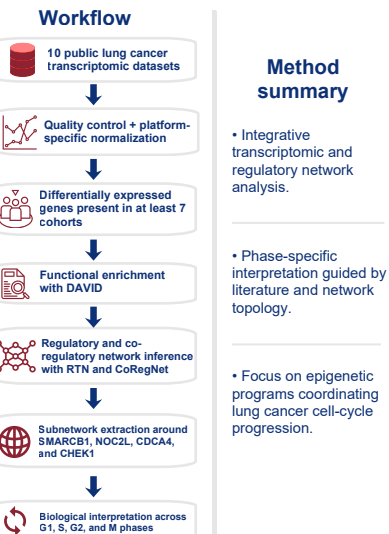
1 BACKGROUND / INTRODUCTION

- Lung cancer progression is sustained by uncontrolled proliferation, genomic instability, and altered checkpoint regulation.
- Beyond genetic mutations, epigenetic mechanisms shape chromatin accessibility, transcriptional control, and damage-response pathways across the cell cycle.
- DNA methylation, histone acetylation, phosphorylation, ubiquitination, chromatin remodeling, hydroxylation, and microRNA regulation interact with cell-cycle machinery in a phase-dependent manner.
- However, an integrated framework linking epigenetic regulatory networks to G₁, S, G₂, and M phases in lung cancer remains incompletely characterized.

2 OBJECTIVE

- To define the epigenetic regulatory landscape of lung cancer across cell-cycle phases.
- To identify core transcriptional and regulatory axes centered on SMARCB1, NOC2L, CDCA4, and CHEK1.
- To generate a biologically coherent, phase-oriented systems framework with translational relevance.

3 METHODS



4 RESULTS

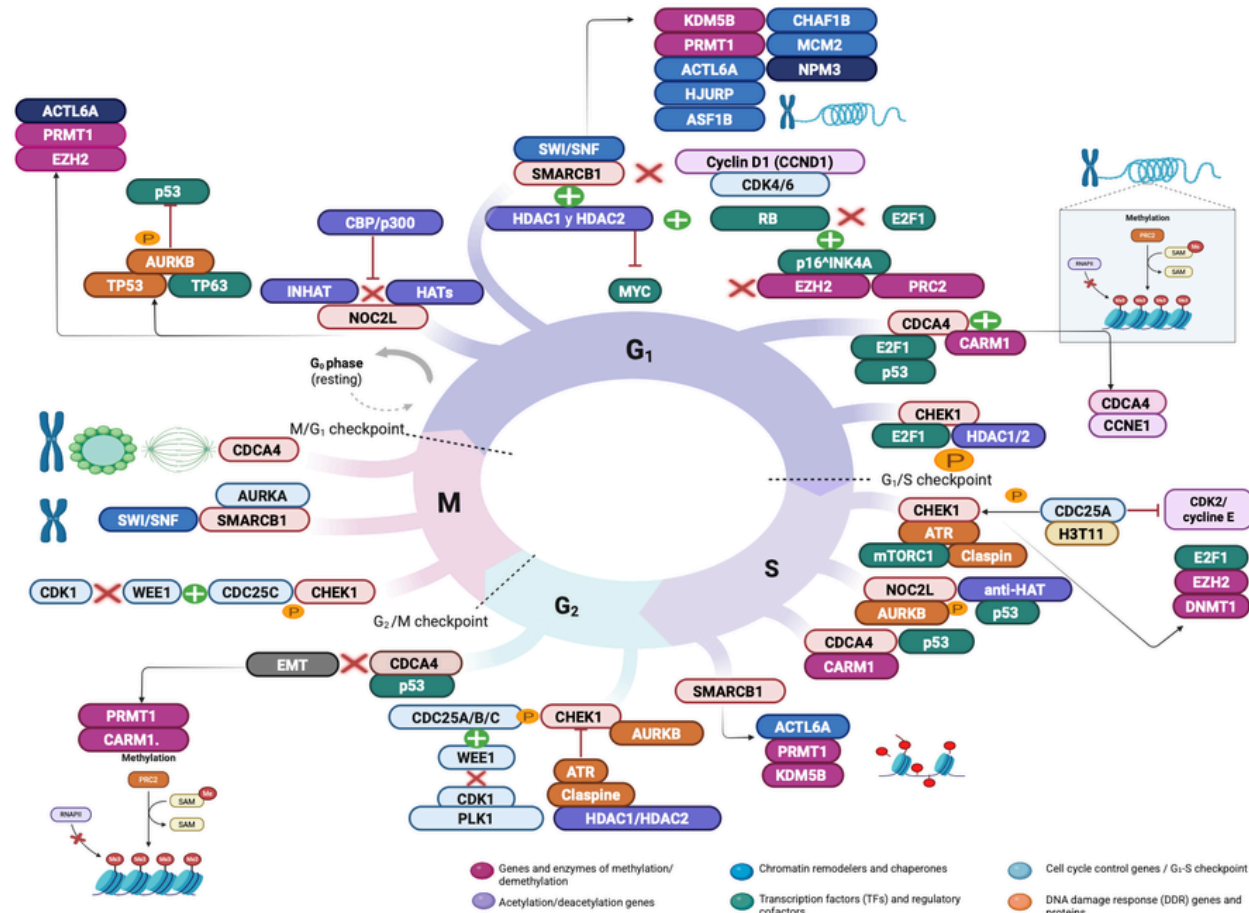
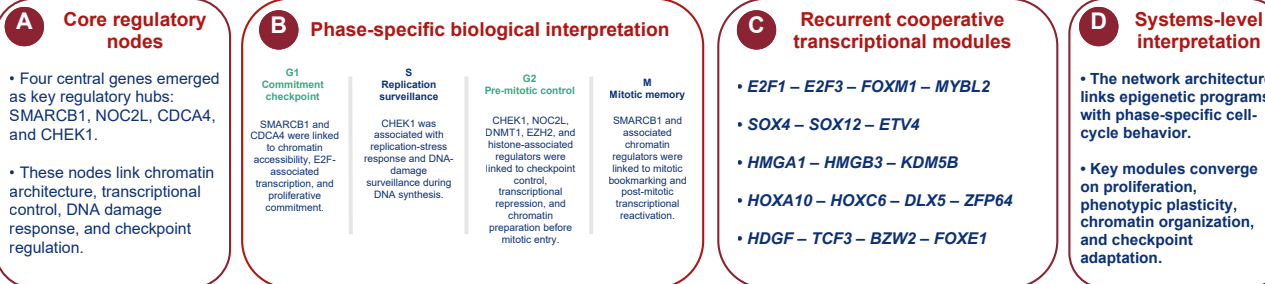


Figure 1. Phase-oriented epigenetic regulatory model of lung cancer centered on SMARCB1, NOC2L, CDCA4, and CHEK1.



5 DISCUSSION / CONCLUSION

- Lung cancer cell-cycle progression appears to be sustained not by a single molecular defect, but by a multilayered epigenetic and post-translational landscape in which multiple regulatory mechanisms converge.
- A phase-by-phase reading of these networks provides a biologically coherent framework for interpreting tumor behavior.
- This systems-level model may help prioritize candidate biomarkers and therapeutic vulnerabilities relevant to precision oncology.

6 CLINICAL / TRANSLATIONAL RELEVANCE

Actionable Take-Home Message

- Phase-oriented network interpretation may improve biomarker prioritization.
- CHEK1-linked checkpoint dependency and associated epigenetic regulators may represent therapeutic vulnerabilities.
- Integrating transcriptomics with network biology can support precision-oncology hypothesis generation.

7 FUTURE DIRECTIONS

- Validate the proposed phase-specific network in independent lung cancer cohorts.
- Integrate survival, treatment-response, and clinicopathological variables.
- Evaluate whether these regulatory modules are tumor-cell-intrinsic or shaped by the microenvironment.
- Experimentally test key checkpoint-related and epigenetic regulatory axes.

8 ACKNOWLEDGEMENTS / FUNDING / DISCLOSURES

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9 AI USE DISCLOSURE

OpenAI was used only for language editing, grammar correction, and improvement of text clarity. Gemini (Google) was used to assist with literature searches and data organization. All scientific content, interpretation, and final approval were controlled by the authors.