

Introduction

- Lung cancer is the second most common cancer worldwide.
- Although the management of lung cancer has improved over the past decade, early detection is one of the crucial facets of outcomes of successful treatment and improved survival.
- In the landscape of the pathways underlying the pathogenesis and progression of Lung cancer are those that disrupt the regular regulation of cell cycle as its precise regulation is crucial to maintain normal cell homeostasis.
- The goal of this study is to evaluate the profiles of genes/pathways that play a pivotal role in the dysregulation of the cell cycle in lung cancer pathogenesis.

Methods and Materials

	Male	Female	Dead	Alive	Female /Dead	Female/Alive	Male/Dead	Male/Alive
SCLC	18	1	17	2	1	0	16	2
NSCLC	59	23	50	32	10	13	40	19

Table 1. Patient Population characteristics

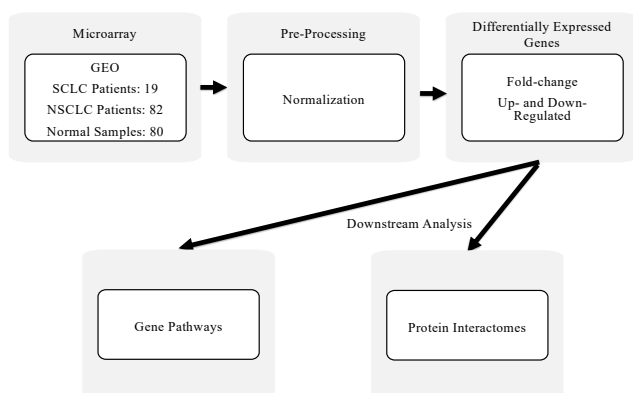


Figure 1. Analysis Pipeline

Results

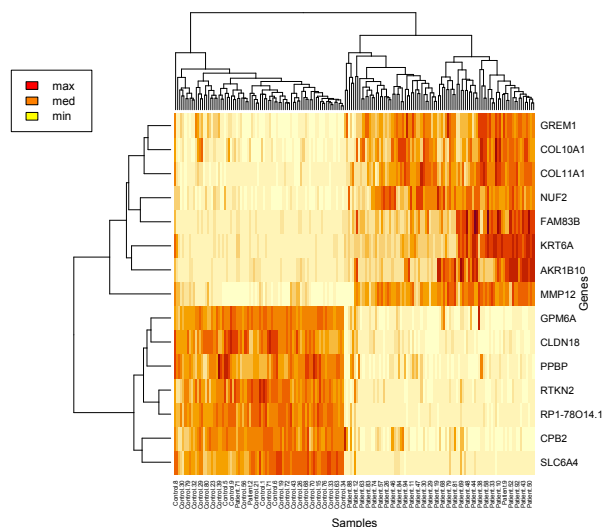
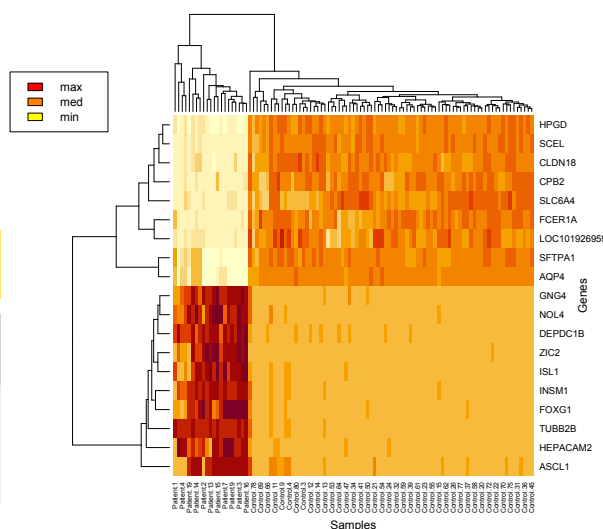


Figure 2. Up: Top DEG in SCLC. Down: Top DEG in NSCLC

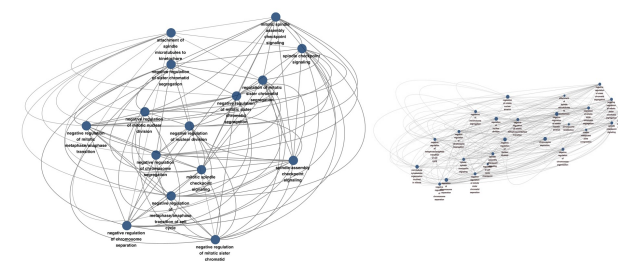


Figure 3. Left: Pathway interactome in SCLC. Right: Protein interactome in NSCLC

Conclusions and Next Steps

Known Genes involved in lung cancer: SCEL, SLC6A4, ASCL1, NOL4

Genes involved in cell cycle: HEPACAM2, TUBB2B

Genes involved in other cancer types: GNG4, CLDN18

Future Scope of the Study

- Replicate the study with improved patient sample size
- Find the metadata to conduct a survival analysis
- Understand the role of genes involved in other cancer types and if they are related to SCLC and NSCLC
- In vitro and in vivo validation of significant genes

Conclusion

- Collectively findings from our study provide novel insights into cell cycle associated genes and pathways that can aid in developing a biosignature, allowing for earlier detection of lung cancer at more treatable stages.
- Gene set enrichment analysis indicated that the top 50 up and down-regulated genes were associated with multiple cell-cycle processes including mitotic spindle assembly checkpoint, metaphase/anaphase transition, transcription regulatory, tissue morphogenesis, chromosome segregation, immune infiltration and nuclear division.
- Importantly, the genes associated with most of the dysregulated cell cycle processes are part of the kinetochore complex components (NUF2 and SPC25) and protein kinases (TTK).

Acknowledgements & Literature Cited

We acknowledge the microarray datasets provided from the following studies that were used in this analysis.

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