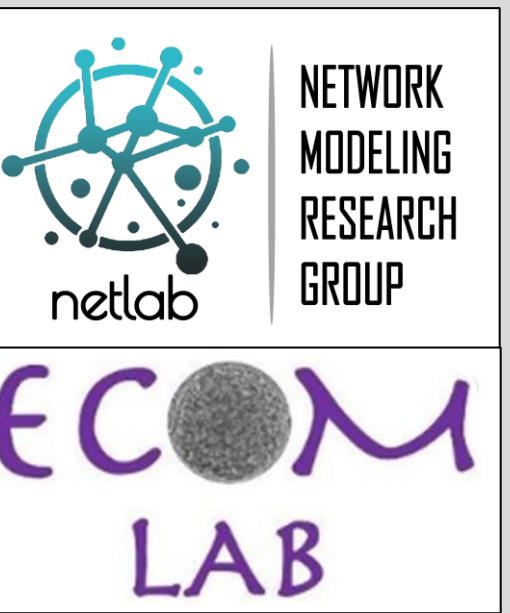


Extracellular Matrix-Driven Stratification and Network Modeling of Patients Reveal Distinct Molecular Grades with Potential Clinical Implications

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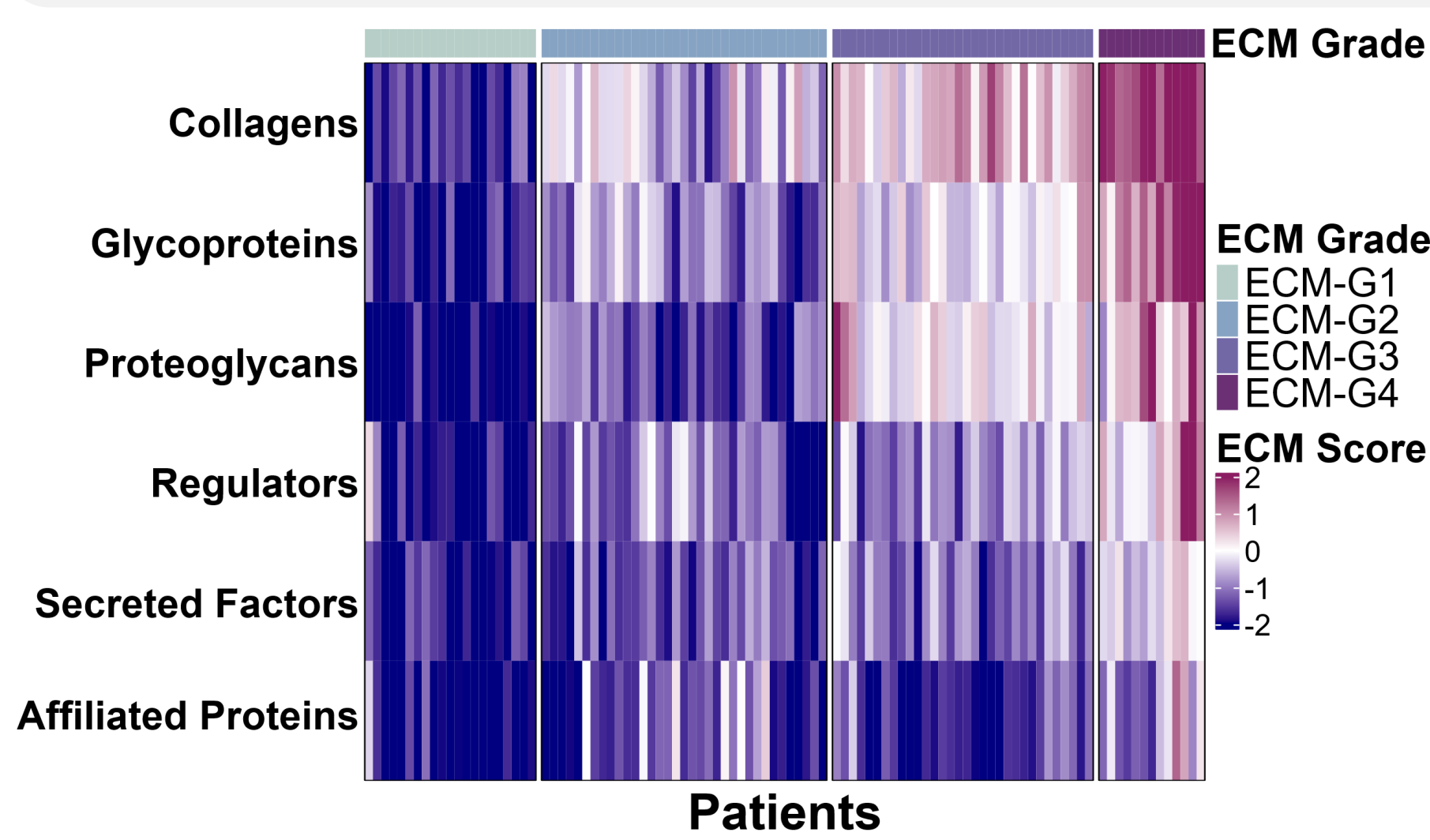


Aim

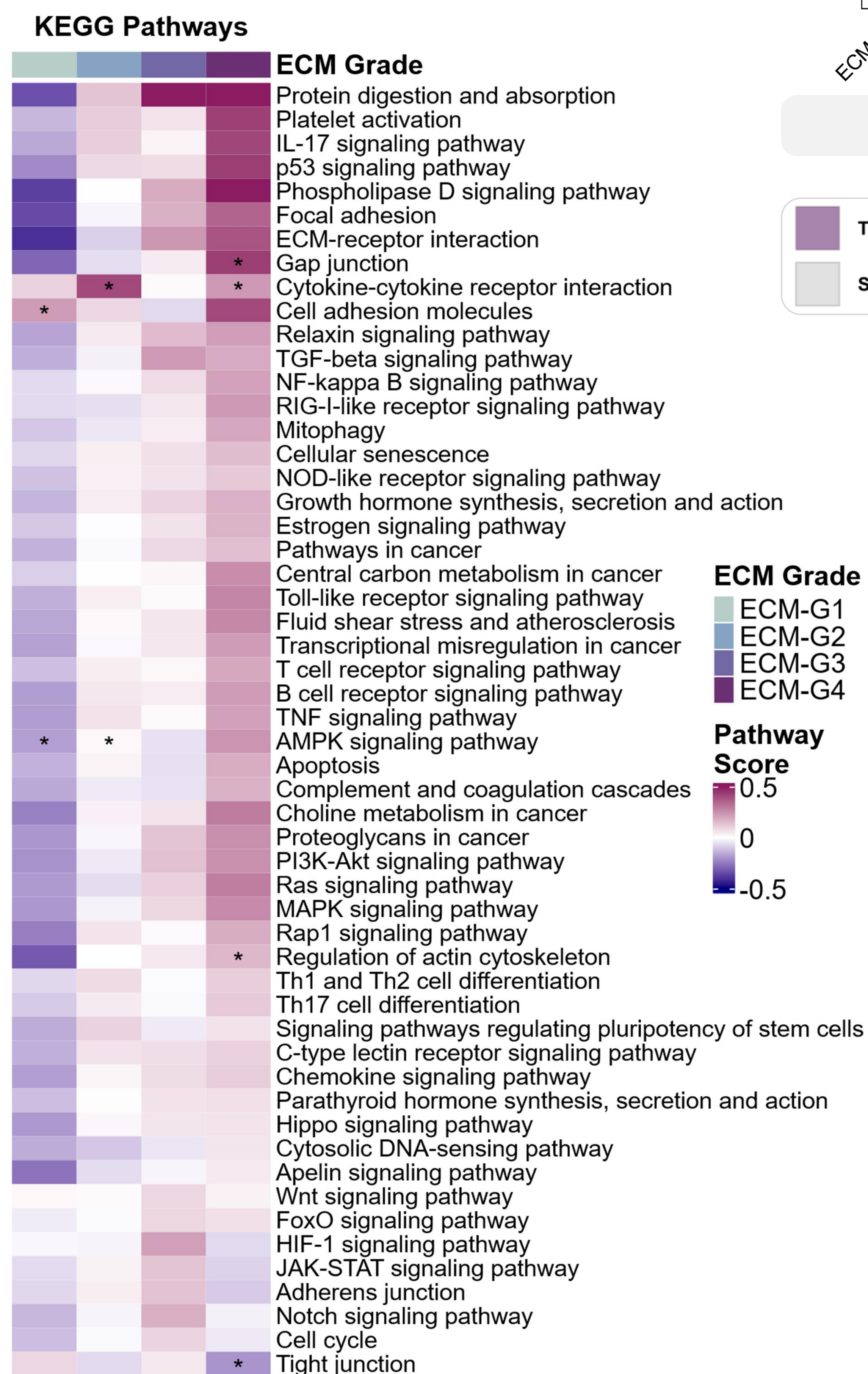
The extracellular matrix (ECM) plays a crucial role in tumor initiation, progression, and drug response. Consequently, the gene/protein expression signatures of ECM in tumors could serve as significant prognostic factors. This study aims to stratify lung adenocarcinoma (LUAD) patients using an ECM-guided multi-omic approach and further define ECM profiles of these groups through network modeling, providing deeper insights into prognosis and facilitating the selection of patient-specific therapies.

Results

Multi-omic ECM barcodes reveal four consensus clusters with significant alteration in ECM



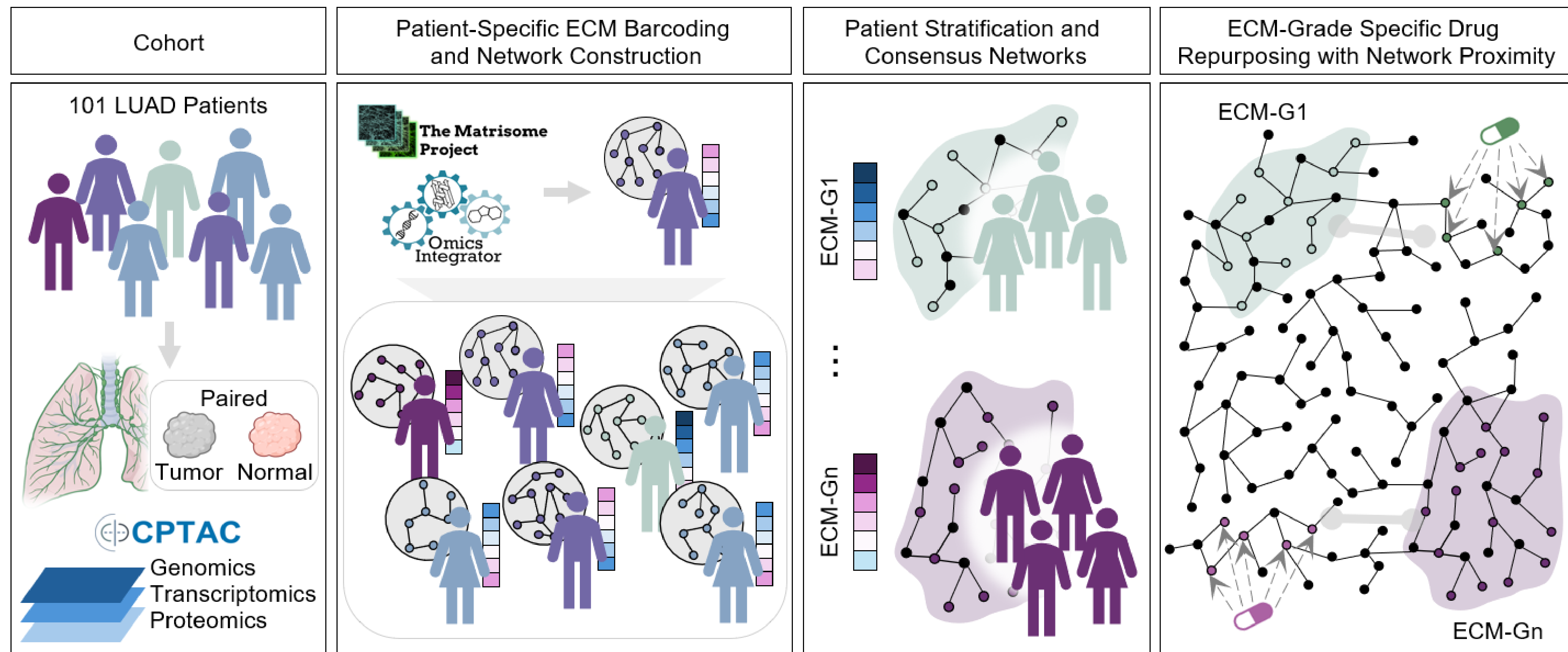
Functional enrichment on patient-specific networks reveal high impact of ECM on pathways



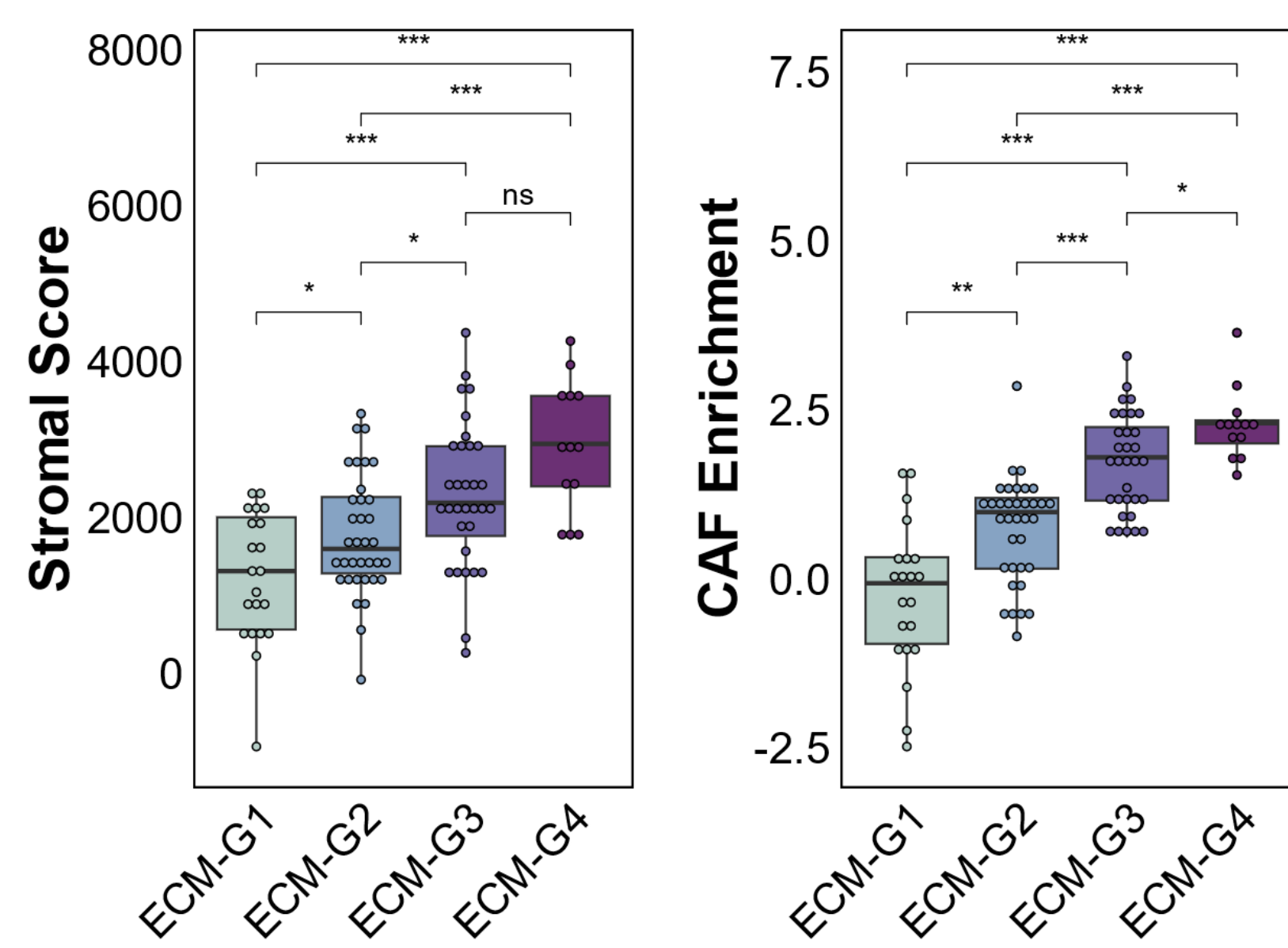
Conclusion

- Scoring and subsequent consensus clustering of patients revealed four distinct clusters and resulting clusters showed different abundances in ECM content.
- Network and enrichment analysis revealed cluster specific pathways and therapeutics.

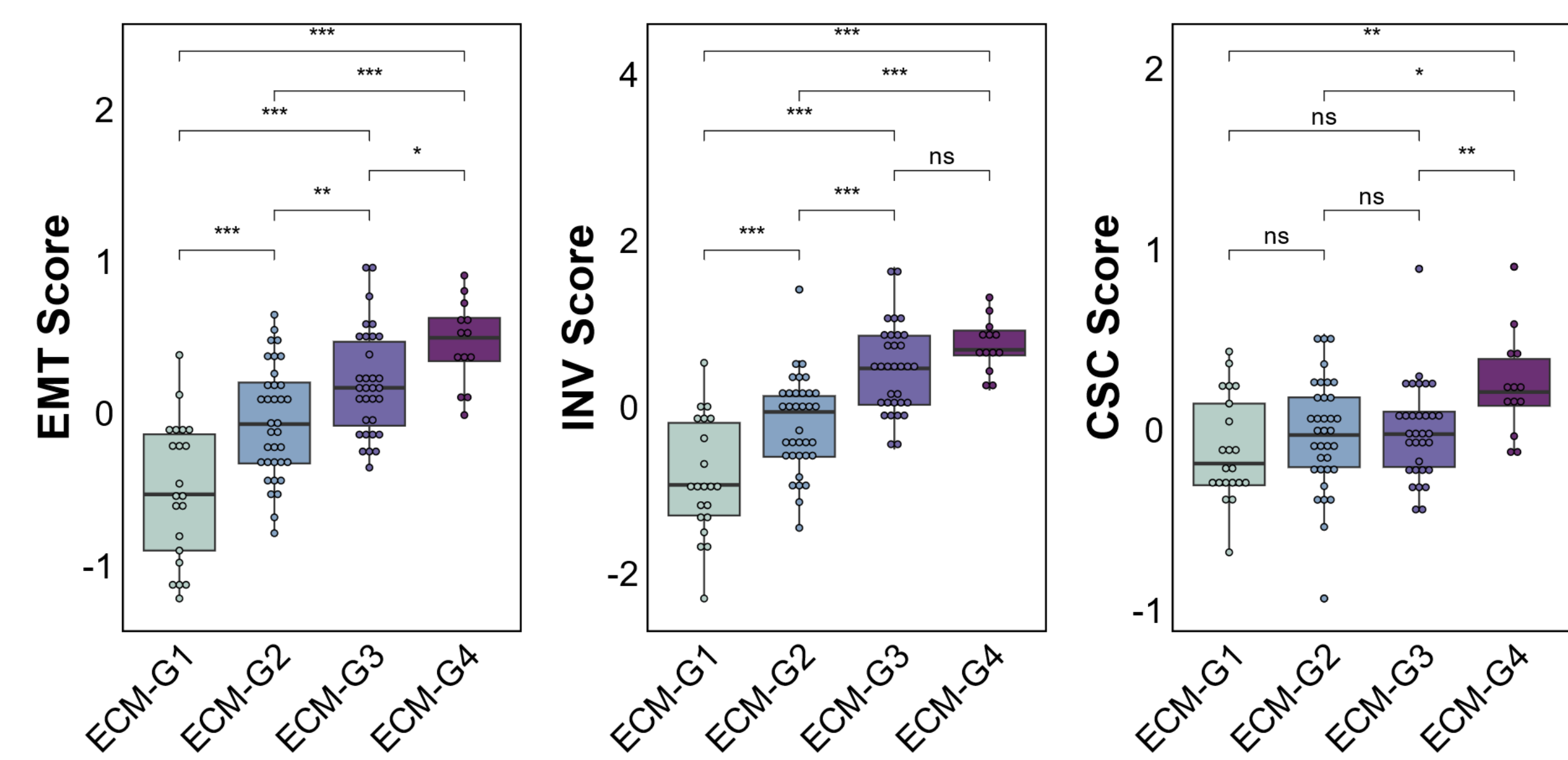
Acknowledgements: This work was funded by The Scientific and Technological Research Council of Türkiye (TUBITAK), project number: 121E245, Travel support was provided by Graduate School of Sciences and Engineering, Koç University.



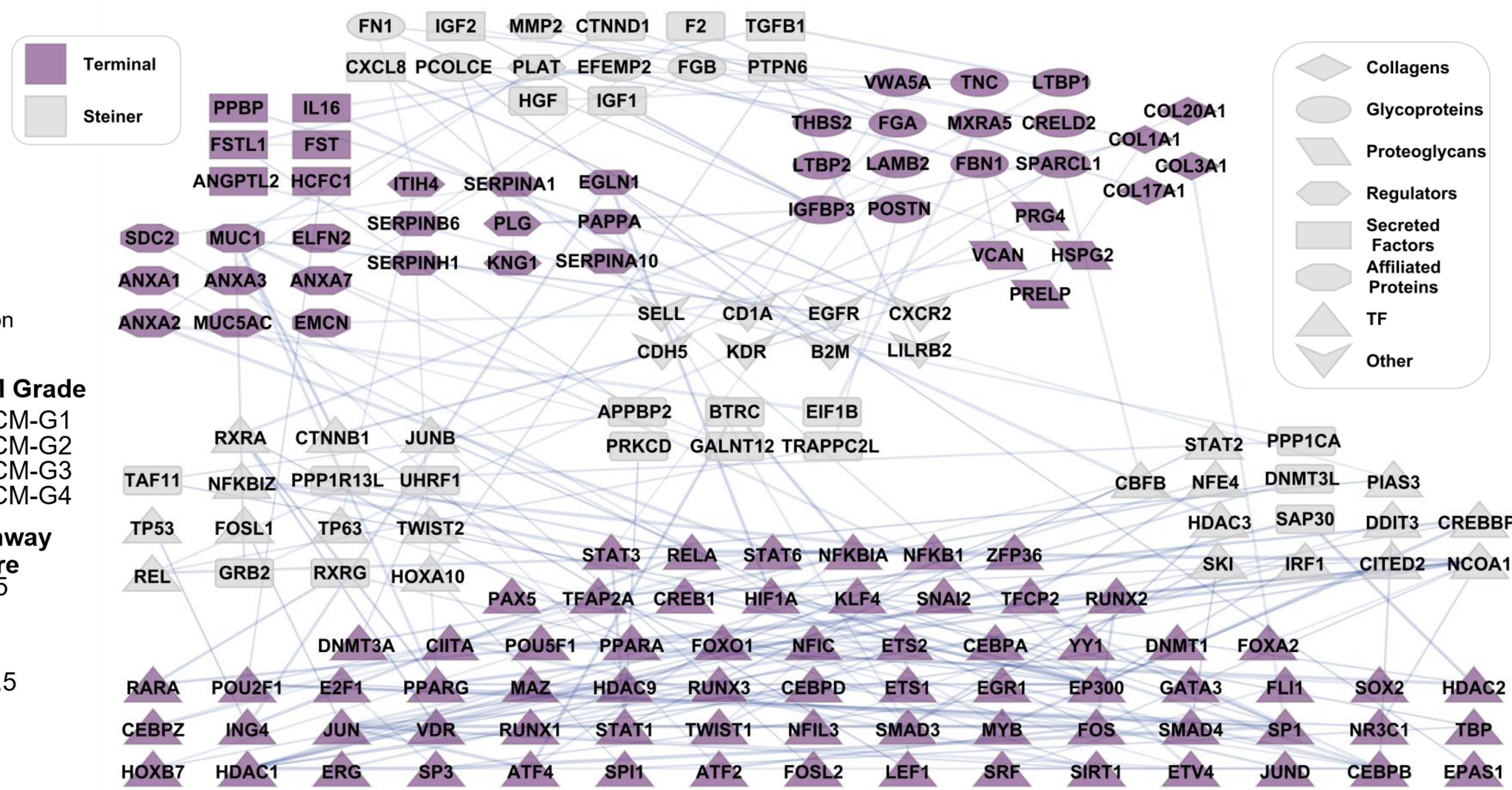
Higher ECM grades show higher stromal content and CAF enrichment



EMT, invasiveness and cancer stem cell maintenance increases with elevated ECM grade



ECM grade-specific networks represent both unique and shared characteristics among groups



Network-based drug screening followed by experimental validation reveals

ECM-dependent and independent hits

