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PDCD5-Related Prognostic Genes in Lung Adenocarcinoma: An Integrated Analysis of Bulk and Single-Cell RNA Sequencing

T. Zhang¹; J. Zhang¹; G. Qiao²

¹Shenzhen Hospital, Southern Medical University, Shenzhen, China

²Zhujiang Hospital, The Second School of Clinical Medicine, Southern Medical University, Guangzhou, China

PDCD5 marked an adverse LUAD phenotype

Integrated multi-omics workflow

Bulk RNA-seq | TCGA-LUAD

Survival, pathways, immune infiltration and immunotherapy sensitivity

Single-cell RNA-seq | GSE149655

Cell annotation, communication networks and epithelial pseudotime

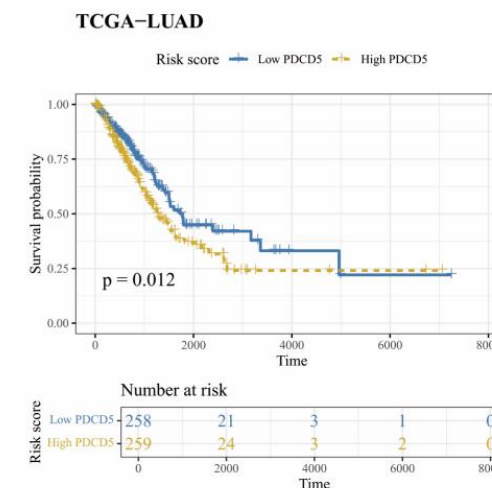
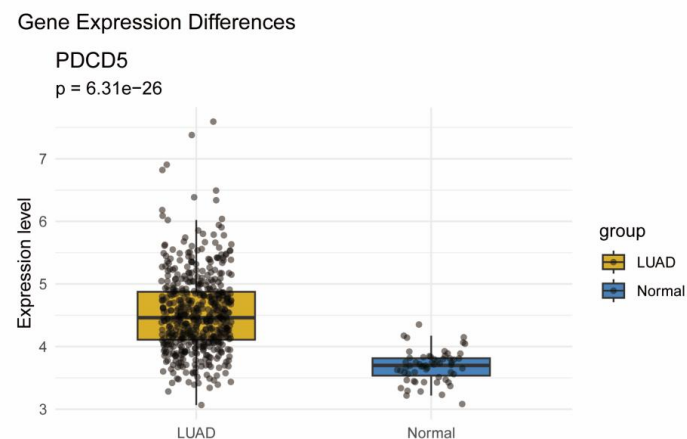
Candidate genes

LUAD DEGs $\cap$ PDCD5-related DEGs $\cap$ epithelial differentiation genes

Clinical model

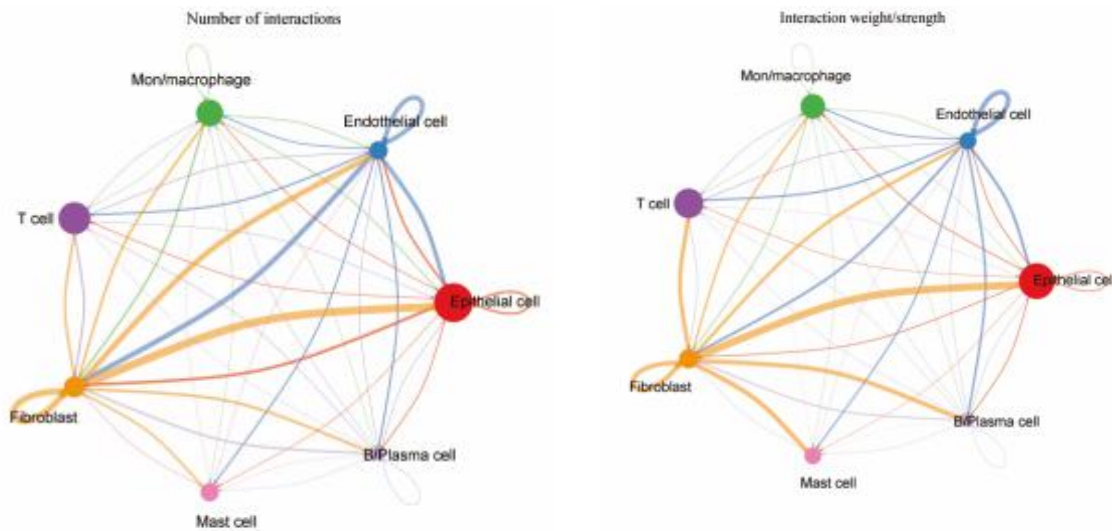
Regression $\rightarrow$ two-gene risk score $\rightarrow$ nomogram $\rightarrow$ molecular validation

PDCD5 was elevated in LUAD and associated with worse survival

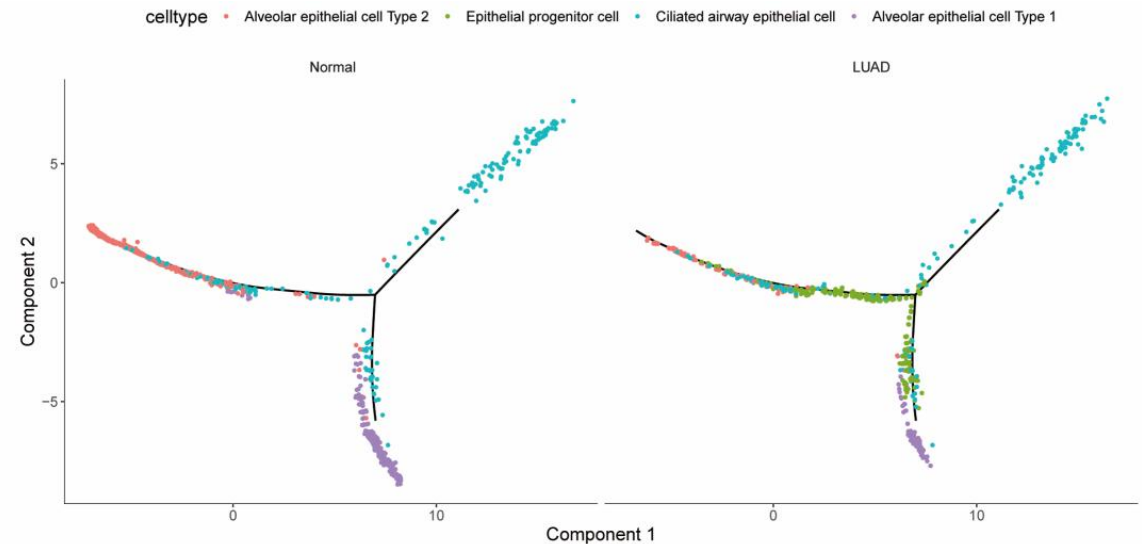


Single-cell analysis linked PDCD5 to epithelial-state remodeling

LUAD strengthened epithelial–fibroblast communication



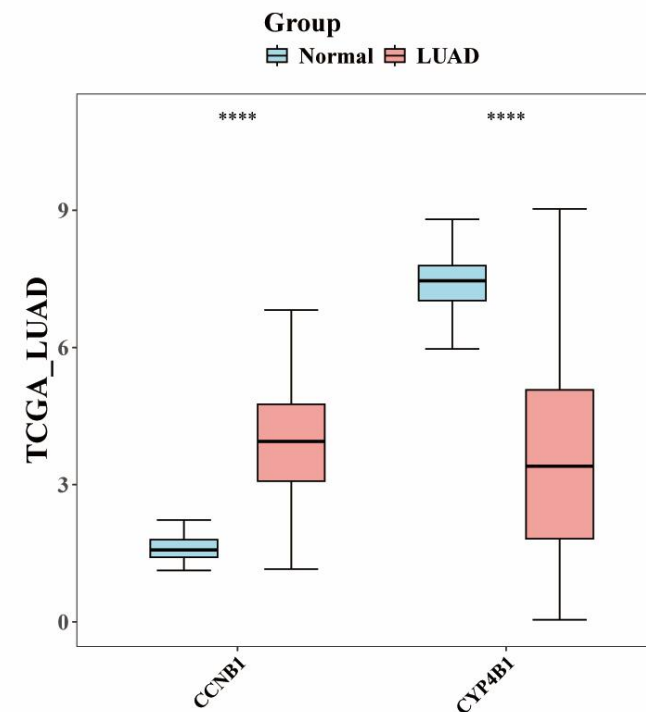
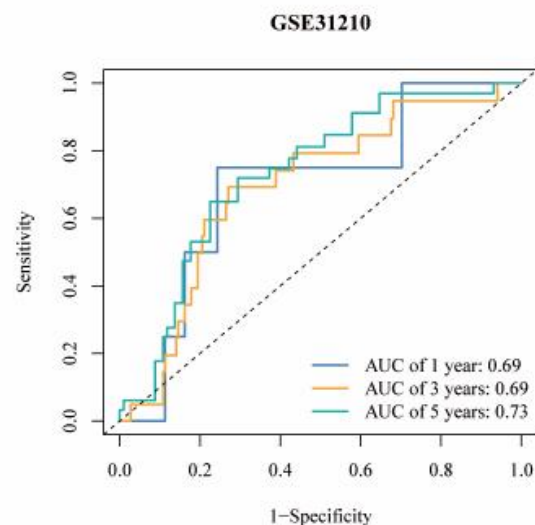
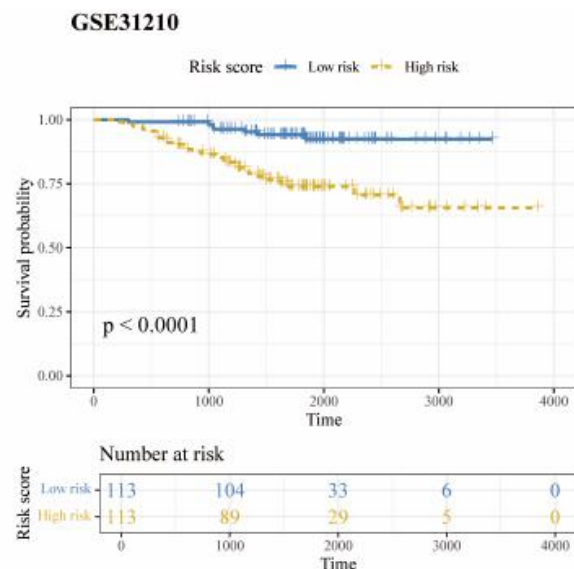
Pseudotime resolved divergent epithelial differentiation states



Two genes stratified prognosis; prospective validation is next

GSE31210: survival $P < 0.0001$; time-dependent AUC 0.69–0.73

TCGA: CCNB1 $\uparrow$ / CYP4B1 $\downarrow$; RT-qPCR: PDCD5 $\uparrow$ / CYP4B1 $\downarrow$



Disclosure

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