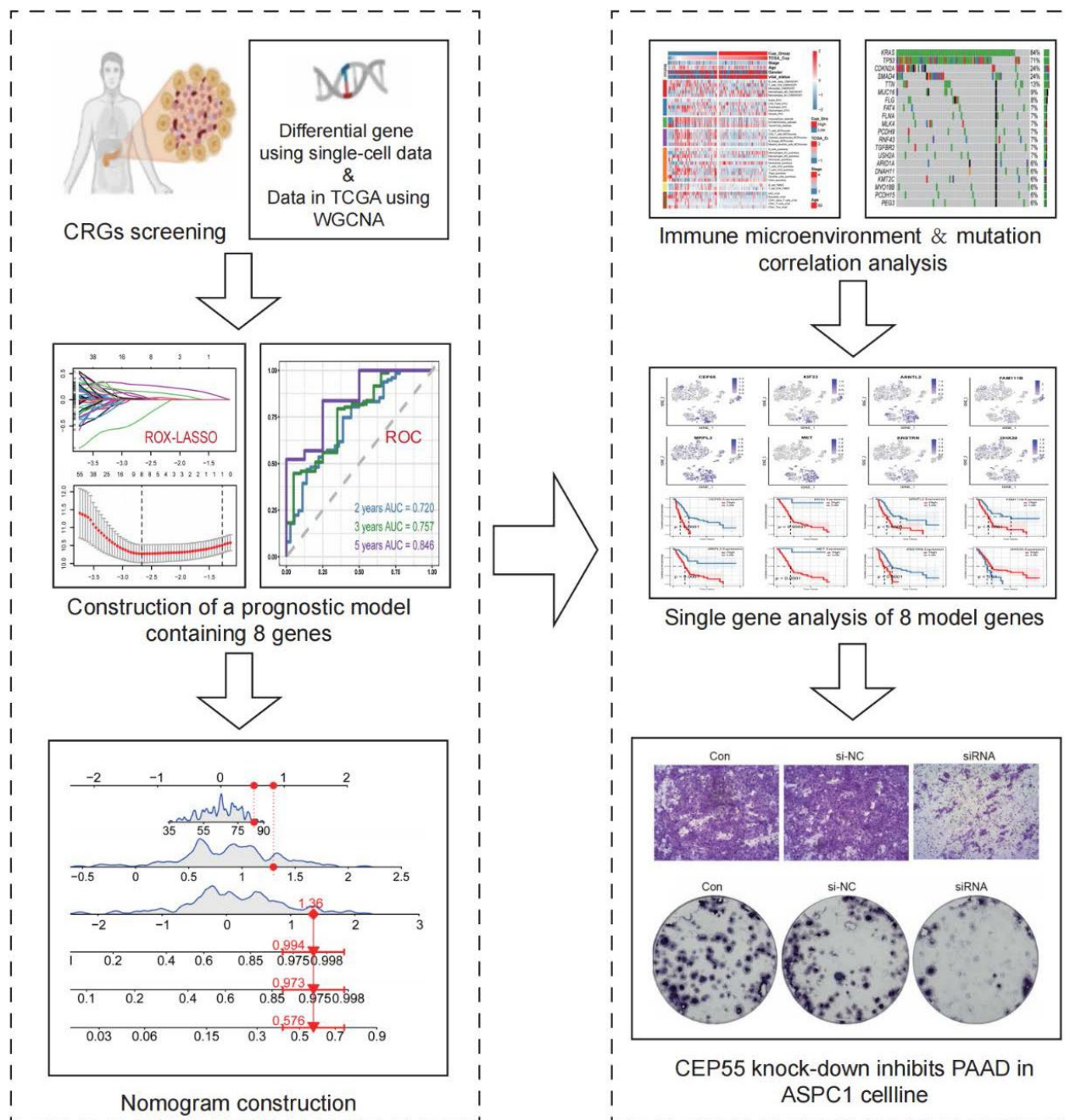


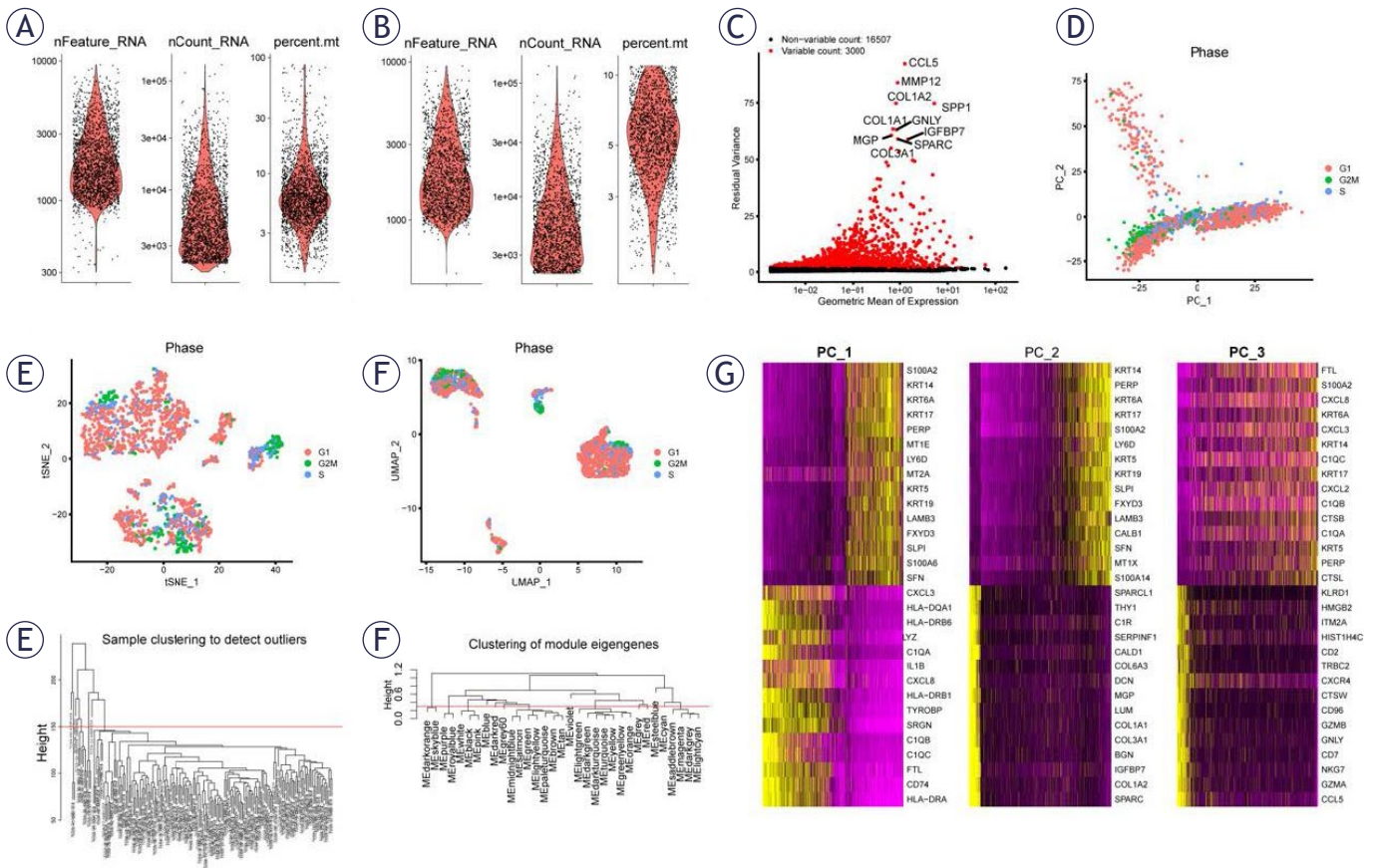
Cuproptosis-related gene *CEP55* as a biomarker of pancreatic adenocarcinoma via multi-omics techniques and experimental validation

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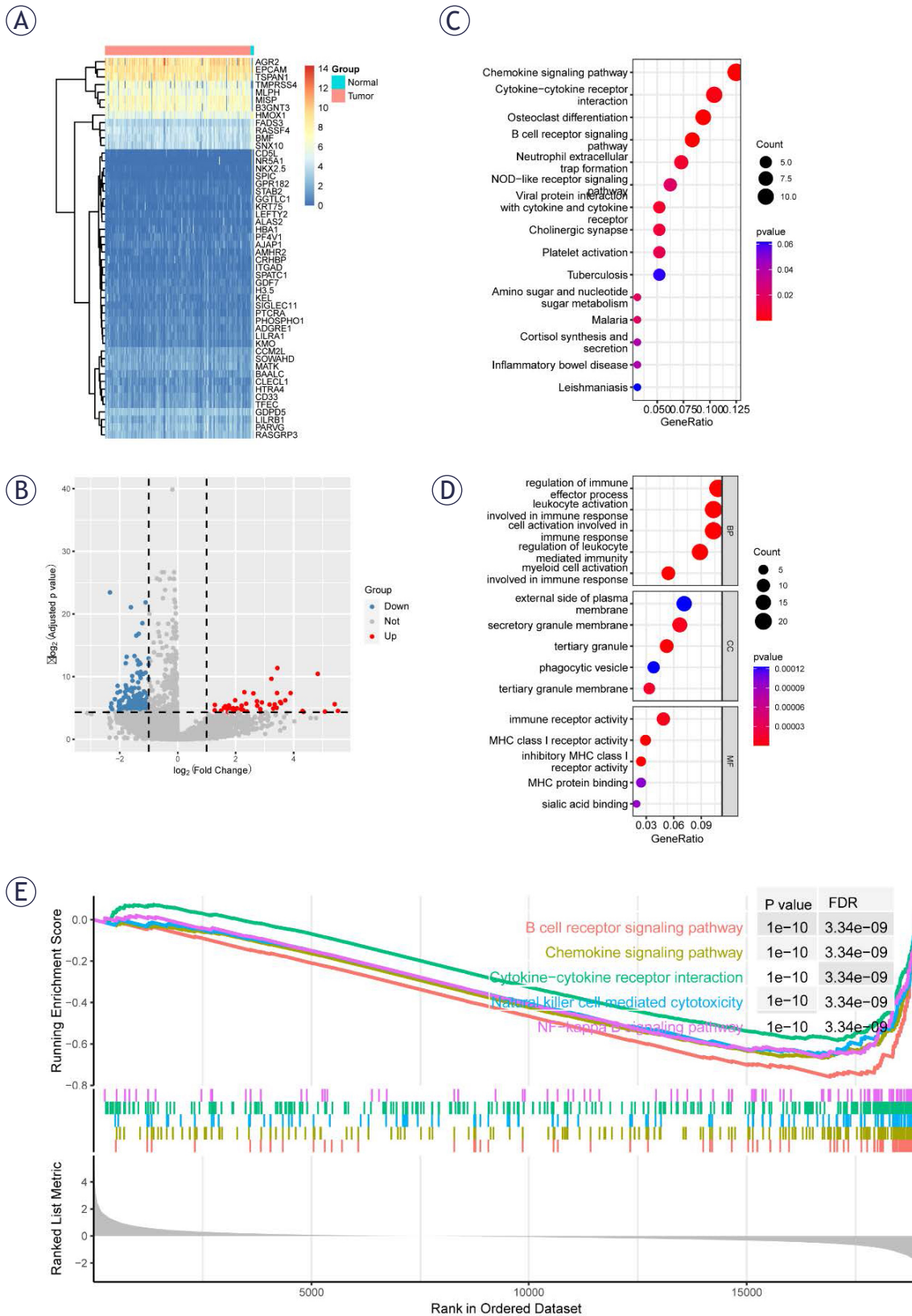
doi: 10.2478/raon-2025-0042



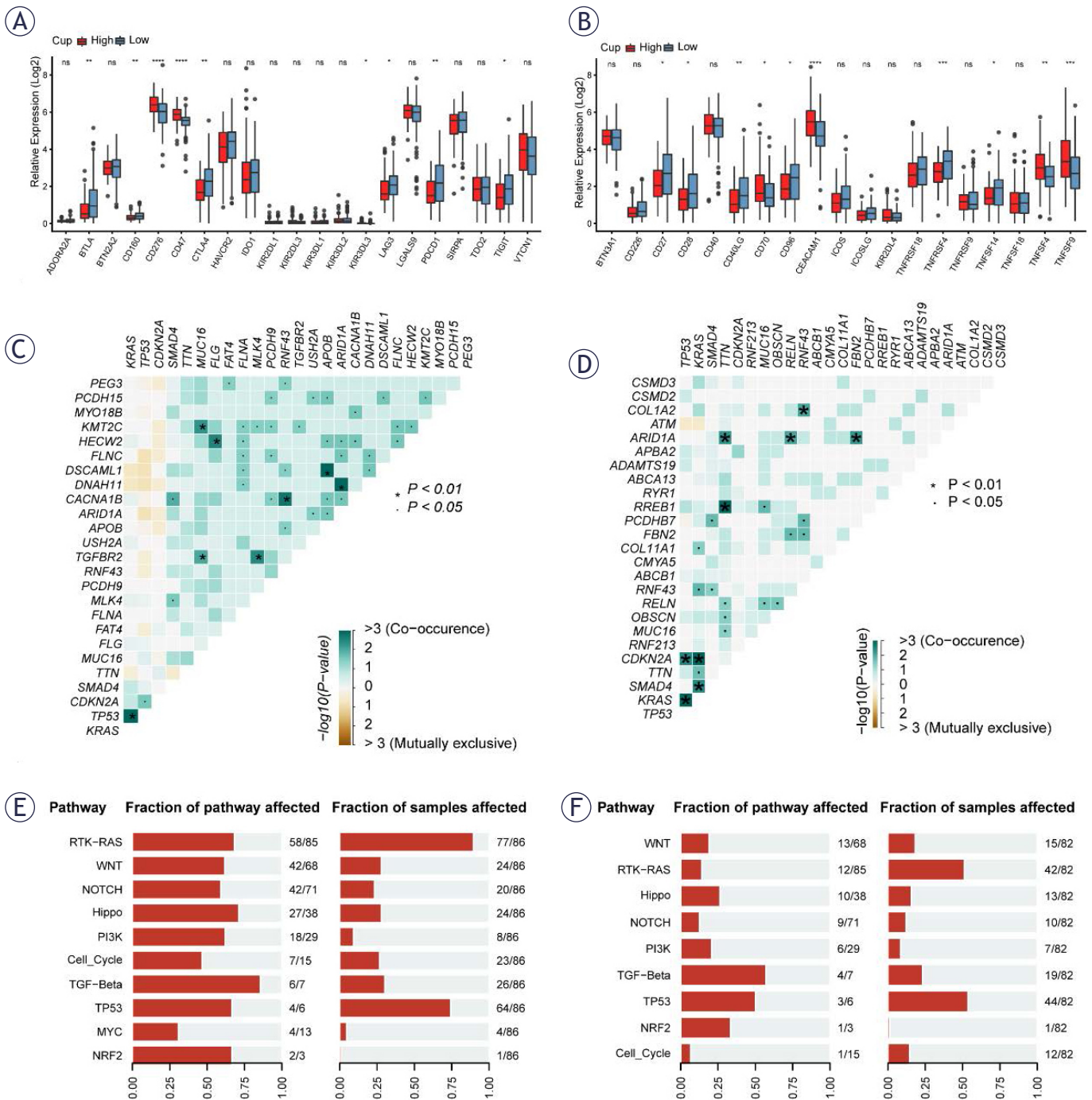
SUPPLEMENTARY FIGURE 1. Flow chart.



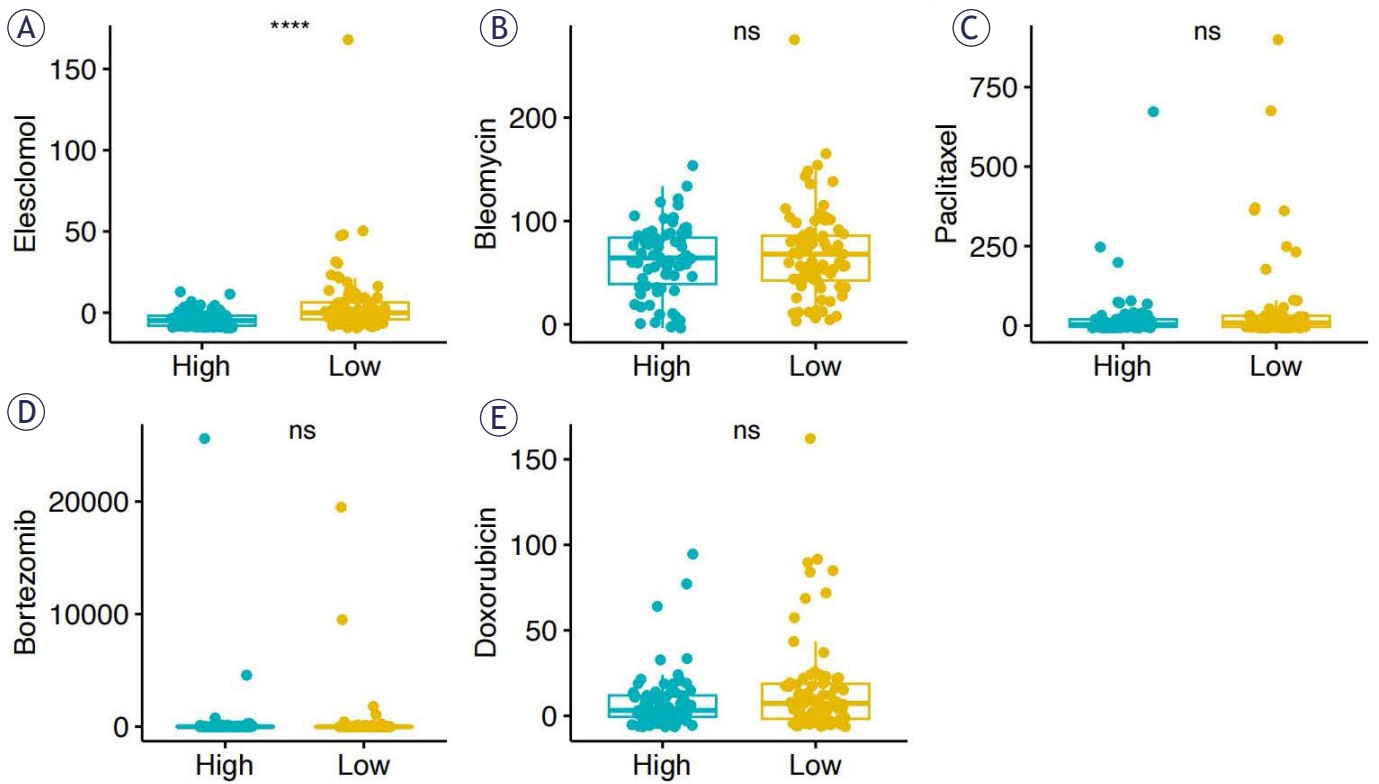
SUPPLEMENTARY FIGURE 2. Single-cell analysis quality control process. (A-F) The quality control process of the single-cell analysis.



SUPPLEMENTARY FIGURE 3. Differential expression analysis and enrichment analysis. **(A, B)** Differential expression analysis. **(C-E)** Enrichment analysis. The identification of key pathways, such as chemokine signaling, cytokine-cytokine receptor interaction, and B cell receptor signaling, underscores the pivotal role of immune-related processes in PAAD



SUPPLEMENTARY FIGURE 5. The results of immune infiltration analysis and tumor mutation analysis. **(A, B)** Differential expression of immune checkpoint-related genes. **(C, D)** Analysis of the correlation of mutated genes. **(E, F)** Analysis results of pathways related to mutated genes. The results indicate mutations in key pathways, encompassing RTK-RAS, WNT, TGF-Beta, and TP53.



SUPPLEMENTARY FIGURE 6. Drug sensitivity between high and low cuproptosis-related genes groups. (A-E) IC50 of five copper metabolism-related drugs in two CRGs group.