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Summary

COMPARATIVE WHOLE TRANSCRIPTOME ANALYSIS OF PAIRED GASTRIC CANCER AND ADJACENT NON-NEOPLASTIC MUCOSA REVEALS MOLECULAR SIGNATURES OF GASTRIC CARCINOGENESIS

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Whole-transcriptome RNA sequencing of 48 paired gastric cancer and adjacent non-neoplastic mucosa samples identified distinct molecular signatures with profound dysregulation of genes involved in epithelial remodeling, invasion, and loss of normal gastric function.

KEY POINTS

- Principal component analysis demonstrated clear separation between gastric cancer and non-neoplastic mucosa, indicating distinct gene expression profiles.
- The most upregulated genes in gastric cancer tissue were KRT16, CHI3L1, CLDN1, INHBA, and CEMIP, mainly associated with epithelial remodeling, invasion, and tumor progression.
- The most downregulated genes were ATP4A, ATP4B, PGA3, PGA4, and LIPF, reflecting loss of normal gastric secretory and metabolic functions.
- Subgroup analysis comparing T1-2 versus T3-4 invasion identified 11 altered genes, with KRT4, S100A7, A2ML1, and KRT23 showing the most significant overexpression in deeper invasion.
- Genes linked to epithelial differentiation and cytoskeletal organization were enriched in tumors with deeper invasion, suggesting their role in disease progression.
- The findings indicate profound molecular reprogramming during gastric carcinogenesis and may identify potential molecular biomarkers and therapeutic targets.

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