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Summary

REVISITING THE ARACHIDONIC ACID PATHWAY IN GASTRIC CANCER: A TRANCRIPTOMICS APPROACH TOWARDS THE DISCOVERY OF NOVEL BIOMARKERS

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Transcriptomic analysis of 414 gastric cancer samples reveals dysregulation in over half of the arachidonic acid pathway genes, identifying potential biomarkers for prognosis and therapeutic targeting.

KEY POINTS

- A total of 53 genes in the arachidonic acid pathway were differentially expressed in gastric cancer tumors compared to normal adjacent tissue, with 29 down-regulated and 24 up-regulated, primarily involved in prostaglandin regulation and synthesis.
- Top down-regulated genes include CYP4B1, AKR1C2, HPGD and AKR1C, which encode proteins involved in arachidonic acid metabolism and prostaglandin regulation and degradation, while PTGS1 encoding COX-1 was also down-regulated.
- Top up-regulated genes include SOX9, GPX2, PON1, and FAAH2, with four genes (CYP11A1, SOX9, PON1 and FAAH2) correlating with worse overall survival in univariate analysis.
- The findings extend beyond inflammatory biomarkers and highlight the pivotal role of the arachidonic acid pathway in gastric cancer development and progression with potential for targetable therapeutic actions.

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