Advancing precision oncology: Bioinformatics-driven hub genes identification in gastric cancer

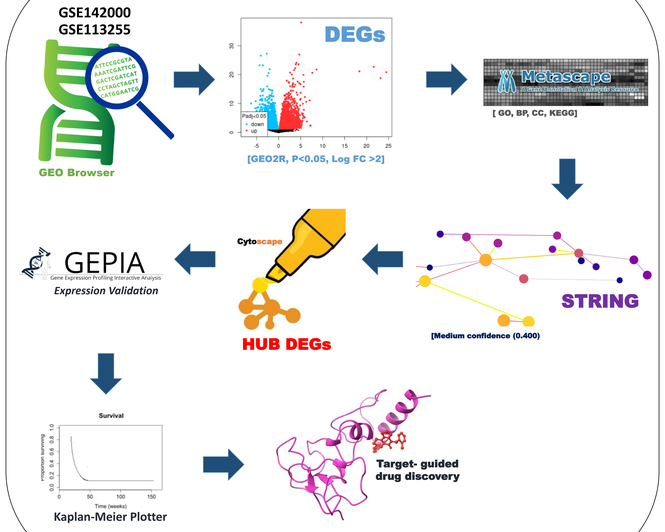
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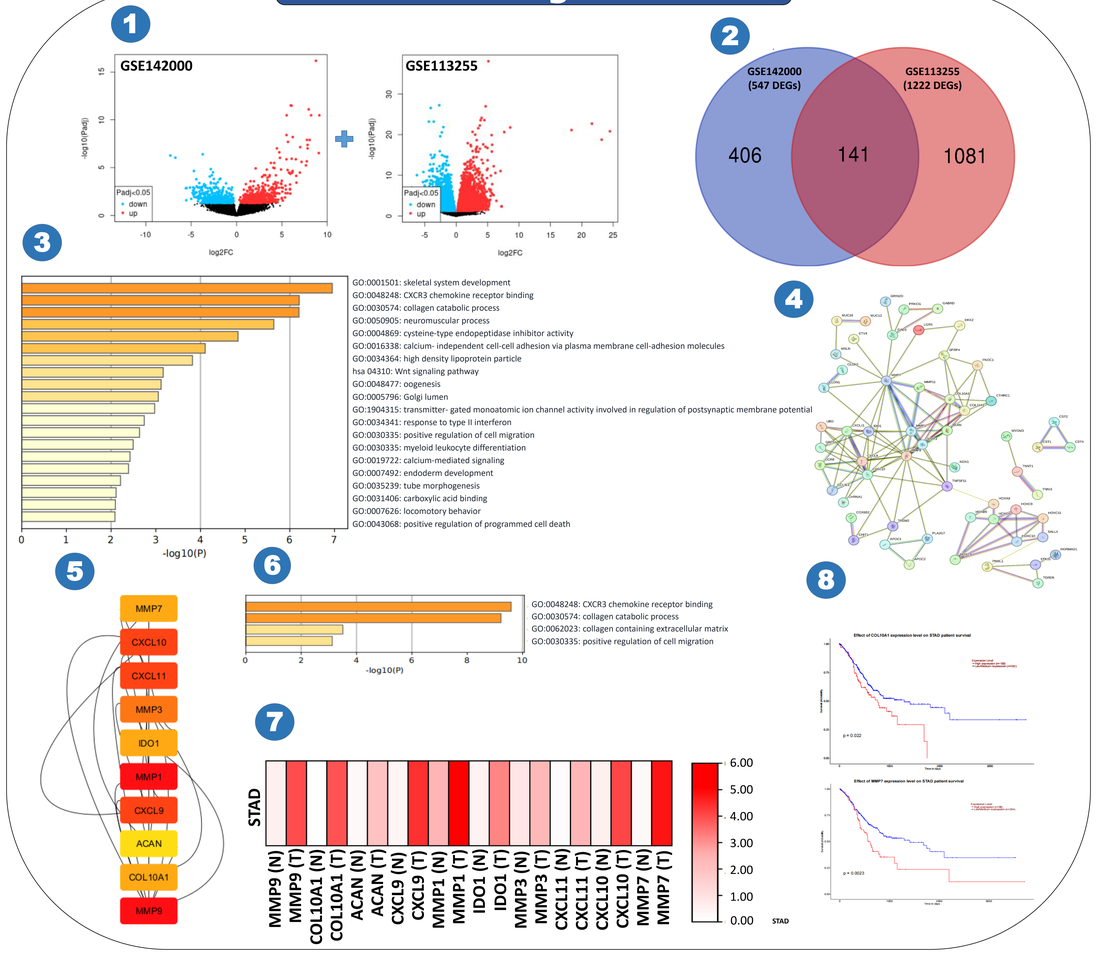
Introduction

Gastric cancer (GC) is a prevalent gastrointestinal malignancy, ranking 6th globally in incidence and 5th in mortality. The absence of tumor-specific markers poses challenges such as delayed diagnosis and worse prognosis outcomes. Therefore, our objective is to identify significant pathways and genes associated with the initiation, formation, and poor prognosis of GC using bioinformatics methods. This inquiry will further facilitate target-guided drug discovery, ultimately advancing treatment options and improving patient outcomes.

Methodology



Preliminary Results



Discussion

- CXC chemokines and their receptors drive GC inflammation, progression, and metastasis by influencing angiogenesis, invasion, and immune cell infiltration **(Ullah et al., 2023).** CXCL9, CXCL10, and CXCL11 bind to CXCR3, impacting tumor growth and metastasis **(Pan et al., 2023).** The CXCL10/CXCR3 axis activates PI3K/AKT, promoting GC cell migration and invasion **(Zhou et al., 2016).**
- Prior research indicates that most GC related DEGs were enriched in collagen catabolic processes **(Hossain et al., 2023; Wu et al., 2023; Cao et al., 2018).**
- The circulating expression level of COL10A1 significantly rises in gastric adenocarcinoma patients, correlating with poor survival **(Necula et al., 2020; Shen et al., 2020).** Additionally, COL10A1 holds promise as an immune indicator in GC as well **(Shen et al., 2022).**
- MMP7 expression is closely linked to gastric adenocarcinoma metastasis. Overexpression of EGFR and MMP7 in gastric adenocarcinoma correlates with unfavorable patient outcomes **(Ding et al., 2023).** MMP7 expression serves as a predictor of prognosis in gastric cancer patients **(Wattanawongdon et al., 2022).**

Future directions

In our upcoming research endeavors, we are dedicated to conduct target-guided drug screening utilizing the identified biomarkers. This approach entails leveraging our understanding of specific molecular targets linked to gastric cancer to identify potential therapeutic agents capable of modulating these targets effectively. Through systematic screening of a compound library against these targets, we aim to uncover avenues for combination treatments or personalized therapeutic strategies.

Looking ahead, our long-term vision involves validating these markers and identified candidate drugs in tumor cell lines (in-vitro) to ascertain their efficacy. This validation step will further solidify the potential of these biomarkers and drugs in advancing precision oncology and improving GC patient outcomes.