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# Identification of core genes and outcomes related to the effect of Crizotinib on gastric cancer using bioinformatics analysis

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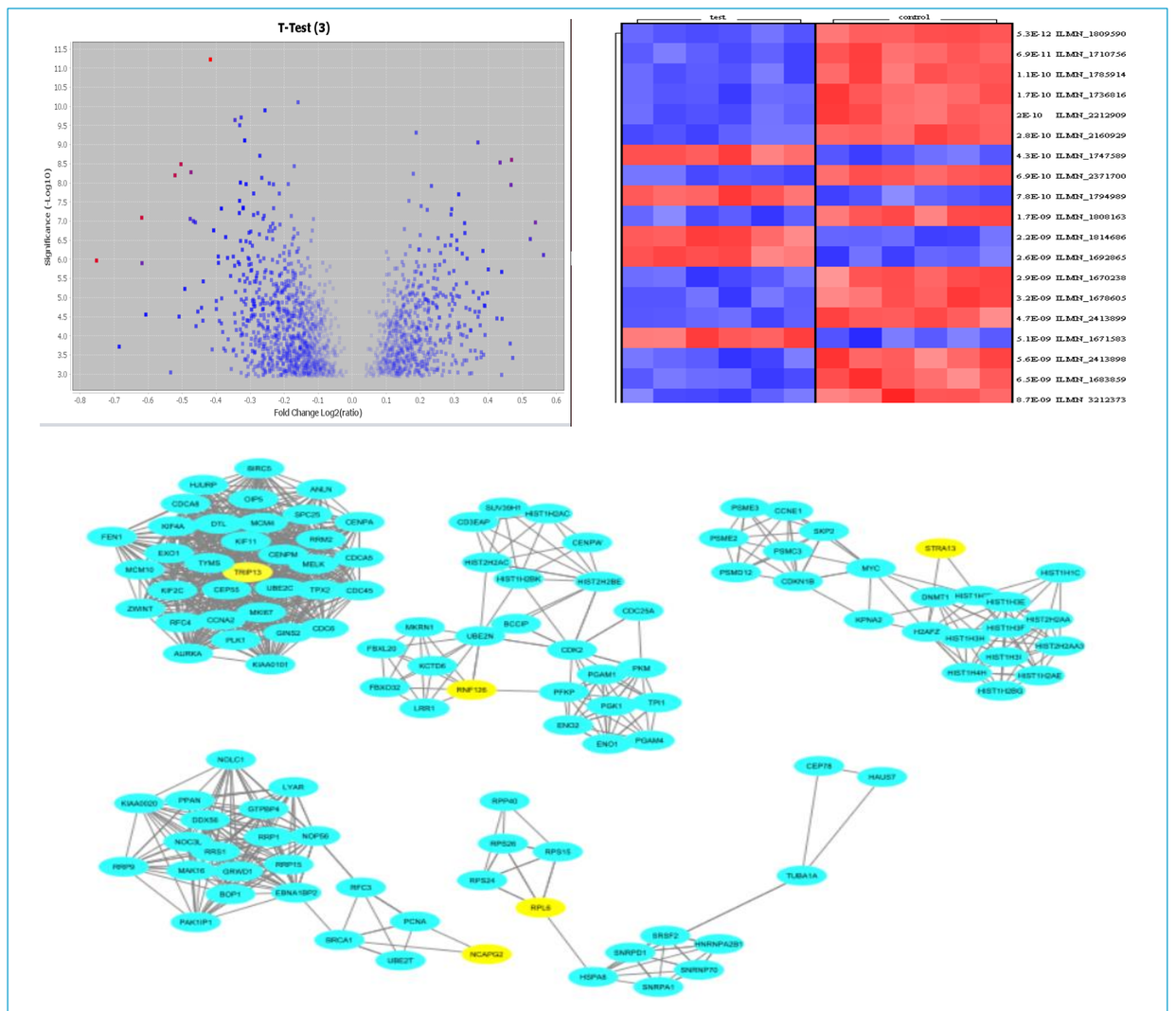
## Abstract

Gastric cancer (GC) is a common malignant neoplasm of gastrointestinal tract. Currently, gastric cancer therapies mainly include surgery, adjuvant and palliative chemotherapy, biologic therapy, targeted therapy, and radiation therapy. However, most gastric cancer patients have missed the chance of surgery at the time of diagnosis. Traditional radiotherapy and chemotherapy are less effective and molecular targeted drugs for gastric cancer are also limited. Therefore there is a great need for screening new targets and developing and approving targeted drugs. Recent studies have shown that preoperative chemotherapy with FLOT regimens (5-FU, leucovorin, oxaliplatin, and docetaxel without radiotherapy) are the standard treatment in the West. Two-drug chemotherapy is the best primary treatment for the metastatic disease. It is better than S-1 monotherapy (4), but studies on the safest drug with the least side effects and longer patient survival are still ongoing.

## Results




FIGURES: Clusters network & Protein-protein interaction of significant genes that determined the sub- network of seed genes connected to first connected nodes

## Methods

The list of proteins that make up the disease network was then mapped to the HIPPIE,Bisogenet & STRING database

the network was introduced into CYTOSCAPE and the MCODE program was implemented to obtain meaningful subnetworks

The common genes between the drug and the disease were then identified and Enrich's significant datasets

common functional pathways between and within the motif were identified and predicted and plotted with the cytoscape.

## Discussion, Conclusion and Suggestions

The majority of the top genes and biological processes which scored in the two types of analysis, were all verified in other published experimental studies about GC. Those studies were used to verify the PPI network and based on this ground we recommended the other genes available in the models for further investigation of their probable role in the effect of Critozinib on gastric cancer.

Pathway enrichment analysis was performed to find pathways that are statistically involved in Gastric cancer and crizotinib. The identification of significant pathways, such as cell cycle, Oocyte meiosis, progesterone-mediate Oocyte maturation and viral carcinogenesis between gastric cancer and crizotinib.

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---|---|---|---|---|---|---|---|---|
| ☐ | KEGG_PATHWAY | Cell cycle | RT | | 8 | 38.1 | 1.6E-9 | 8.4E-8 |
| ☐ | KEGG_PATHWAY | Progesterone-mediated oocyte maturation | RT | | 4 | 19.0 | 6.4E-4 | 1.7E-2 |
| ☐ | KEGG_PATHWAY | Hepatitis B | RT | | 4 | 19.0 | 2.8E-3 | 4.9E-2 |
| ☐ | KEGG_PATHWAY | Oocyte meiosis | RT | | 3 | 14.3 | 2.1E-2 | 2.6E-1 |
| ☐ | KEGG_PATHWAY | Epstein-Barr virus infection | RT | | 3 | 14.3 | 2.5E-2 | 2.6E-1 |
| ☐ | KEGG_PATHWAY | PI3K-Akt signaling pathway | RT | | 4 | 19.0 | 3.0E-2 | 2.6E-1 |
| ☐ | KEGG_PATHWAY | DNA replication | RT | | 2 | 9.5 | 7.1E-2 | 5.3E-1 |

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