**Comprehensive Analysis of Prognostic Value and Immune Infiltration of Src Family Kinases in Hepatocellular Carcinoma**

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**Supplementary Materials and Methods**

*Cell culture*

The normal liver cell line L02 was cultured in DMEM medium (Sigma-Aldrich) supplemented with 10% fetal bovine serum (Gibco, USA) at 37°C in a humidified incubator with 5% CO2.

*STRING*

STRING (https://string-db.org/) is an online database which offers known and predicted protein-protein interactions, including physical interactions and functional associations[1]. The protein-protein interaction networks of SFKs were constructed through STRING.

*GeneMANIA*

GeneMANIA (http://genemania.org/) is a user-friendly website providing information about gene function, analyzing gene lists and prioritizing genes for functional assays[2]. We employed GeneMANIA to explore the genetic interactions of SFKs, concerning the shared protein domains, physical interactions, co-expression, genetic interactions and pathway.

*XIANTAO* *platform*

XIANTAO platform (www.xiantao.love), an academic online analysis tools, provides researchers with a comprehensive set of functional annotation tools to understand the biological meaning of a large number of gene lists. We used XIANTAO platform for gene ontology (GO) terms analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways enrichment analysis of SFKs and 20 correlative genes from GeneMANIA database. GO terms encompasses three aspects: biological processes, cellular components and molecular functions. *p* value < 0.05 was considered to be significantly enriched.

**References**

[1] Szklarczyk D, Gable AL, Nastou KC, Lyon D, Kirsch R, Pyysalo S, *et al*. The STRING database in 2021: Customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. [Nucleic Acids Research](https://sci.justscience.cn/details.html?sci=1&id=228" \t "https://sci.justscience.cn/_blank). 2021;49(D1):D605-12.

[2]  Warde-Farley D, Donaldson SL, Comes O, Zuberi K, Badrawi R, Chao P, *et al*. The GeneMANIA prediction server: Biological network integration for gene prioritization and predicting gene function. [Nucleic Acids Research](https://sci.justscience.cn/details.html?sci=1&id=228" \t "https://sci.justscience.cn/_blank). 2010;38(Web Server issue):W214-20.