frontiers | Frontiers in Molecular Biosciences

TYPE Original Research
PUBLISHED 21 August 2024
DOI 10.3389/fmolb.2024.1425422

OPEN ACCESS

EDITED BY
Shengxi Chen,
Arizona State University, United States

REVIEWED BY
Sowmya Ramesh,
Johns Hopkins University, United States
Parmanand Malvi,
University of Alabama at Birmingham, United States

*CORRESPONDENCE
Muzafar A. Macha,
muzafar.macha@iust.ac.in,
muzafar.aiiims@gmail.com
Ajaz A. Bhat,
abhat@sidra.org

RECEIVED 29 April 2024
ACCEPTED 30 July 2024
PUBLISHED 21 August 2024

CITATION
Khurshid S, Usmani S, Ali R, Hamid S, Masoodi T, Sadida HQ, Ahmed I, Khan MS, Abeer I, Albalawi IA, Bedaiwi RI, Mir R, Al-Shabeeb Akil AS, Bhat AA and Macha MA (2024) Integrating network analysis with differential expression to uncover therapeutic and prognostic biomarkers in esophageal squamous cell carcinoma.
Front. Mol. Biosci. 11:1425422.
doi: 10.3389/fmolb.2024.1425422

Integrating network analysis with differential expression to uncover therapeutic and prognostic biomarkers in esophageal squamous cell carcinoma

Sana Khurshid[1], Shahabuddin Usmani[2], Raiyan Ali[3], Saira Hamid[1], Tariq Masoodi[4], Hana Q. Sadida[2], Ikhlak Ahmed[2], Mohd Shahnawaz Khan[5], Inara Abeer[6], Ibrahim Altedlawi Albalawi[7], Ruqaiah I. Bedaiwi[8], Rashid Mir[8], Ammira S. Al-Shabeeb Akil[2], Ajaz A. Bhat[2]* and Muzafar A. Macha[1]*

[1]Watson-Crick Centre for Molecular Medicine, Islamic University of Science and Technology, Awantipora, India, [2]Department of Human Genetics-Precision Medicine in Diabetes, Obesity and Cancer Program, Sidra Medicine, Doha, Qatar, [3]Council of Scientific and Industrial Research-Institute of Genomics and Integrative Biology, Delhi, India, [4]Human Immunology Department, Research Branch, Sidra Medicine, Doha, Qatar, [5]Department of Biochemistry, College of Sciences, King Saud University, Riyadh, Saudi Arabia, [6]Department of Pathology, Sker-I-Kashmir Institute of Medical Sciences, Srinagar, India, [7]Department of Surgical Oncology, Faculty of Medicine, University of Tabuk, Tabuk, Saudi Arabia, [8]Faculty of Applied Medical Sciences, Medical Laboratory Technology, University of Tabuk, Tabuk, Saudi Arabia

Introduction: Esophageal squamous cell carcinoma (ESCC) accounts for over 90% of all esophageal tumors. However, the molecular mechanism underlying ESCC development and prognosis remains unclear, and there are still no effective molecular biomarkers for diagnosing or predicting the clinical outcome of patients with ESCC. Here, we used bioinformatics analysis to identify potential biomarkers and therapeutic targets for ESCC.

Methodology: Differentially expressed genes (DEGs) between ESCC and normal esophageal tissue samples were obtained by comprehensively analyzing publicly available RNA-seq datasets from the TCGA and GTEX. Gene Ontology (GO) annotation and Reactome pathway analysis identified the biological roles of the DEGs. Moreover, the Cytoscape 3.10.1 platform and subsidiary tools such as CytoHubba were used to visualize the DEGs' protein-protein interaction (PPI) network and identify hub genes, Furthermore our results are validated by using Single-cell RNA analysis. Results: Identification of 2524 genes exhibiting altered expression enriched in pathways including keratinization, epidermal cell differentiation, G alpha(s) signaling events, and biological process of cell proliferation and division, extracellular matrix (ECM) disassembly, and muscle function. Moreover, upregulation of hallmarks E2F targets, G2M checkpoints, and TNF signaling. CytoHubba revealed 20 hub genes that had a valuable influence on the progression of ESCC in these patients. Among these, the high expression levels of four genes, CDK1 MAD2L1, PLK1, and TOP2A, were