

## Dissection of Differentially-Expressed Genes in Resveratrol-Induced Breast Cancer Cells by Bioinformatics Analysis

Masoumeh Farahani <sup>1,\*</sup>, Hakimeh Zali <sup>2</sup>, Mostafa Rezaei Tavirani <sup>1</sup>

<sup>1</sup> Proteomics Research Center, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran

<sup>2</sup> School of Advanced Technologies in Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

\*Corresponding Author: Masoumeh Farahani, Proteomics Research Center, School of Allied Medical Sciences, Shahid Beheshti University of Medical Sciences, Tehran, Iran. E-mail: mfarahani@sbmu.ac.ir

DOI: 10.21859/mci-sup-64

### Keywords:

Resveratrol  
Breast Cancer  
Differentially-expressed Genes

### Abstract

**Introduction:** Resveratrol is a polyphenol compound found in a wide variety of plants like grapes, berries and peanuts and is known to have several antitumor characteristics. It is emerging as a promising anticancer agent because of its chemopreventive and pro-apoptotic attributes. Herein, via bioinformatics approaches, we investigated the biological processes, pathways and underlying mechanisms of the resveratrol-induced breast cancer cells.

**Materials and Methods:** Initially, GSE25412 datasets were extracted from the Gene Expression Omnibus (GEO) database (<https://www.ncbi.nlm.nih.gov/geo/>). Significant differentially expressed genes (DEGs) were filtered with GEO2R. Afterwards, through gene ontology (GO) analysis, significant terms were enriched and identified, and also, we performed KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway analysis for differentially expressed genes through GeneTrail2 bioinformatics resource (<http://genetrail2.bioinf.uni-sb.de/>). Furthermore, the transcription factors which target the DEGs, were enriched. Statistical significance based on p-values was calculated by false discovery rate (FDR) estimation (FDR adjustment (Benjamini)) and significance level: 0.05.

**Results:** In this study, several enriched GO terms were identified via biological process analyses, which among them “cell cycle phase & mitotic cell cycle phase” (GO: 0022403, adj.P-Value: 5.13e-20) was disclosed as top category containing 221 genes. Significant terms for Cellular Component were mined, for instance “chromosome centromeric region” (adj.P-Value: 2.76e-13, 124 genes) was designated as a top term. The KEGG pathway analysis indicated “Cell cycle” term as the top pathway including 97 genes, and adj. p-value: 1.49e-8. Also, transcription factor enrichment analysis revealed E2F1 transcription factor (adj.P-Value: 9.34e-6) that targets 51 genes in the DEGs and plays a crucial role in the control of cell cycle and action of tumor suppressor proteins.

**Conclusions:** The results indicate that resveratrol treatment can be involved in expression of key regulatory enzymes and proteins is required for cell growth and death, and DNA replication.