

ATF1 Regulating Signaling Pathways between Nasopharyngeal Carcinoma Cells and Immortalized Epithelial Cells

Fangfang Wang^{1,2}, Hua Chen³, Jing Wang^{1,2}, Huiyuan Cao^{1,2}, Ning Wang^{1,2},
Jie Ding^{1,2} and Guo-Liang Huang^{1,2,*}

¹*Guangdong Provincial Key Laboratory of Medical Molecular Diagnostics,
The First Dongguan Affiliated Hospital, Guangdong Medical University, Dongguan, China*
²*China-America Cancer Research Institute, Key Laboratory for Epigenetics of Dongguan City,
Guangdong Medical University, Dongguan, China*
³*The second tumor department, Maoming People's Hospital,
Maoming, Guangdong, 525 000, China*

KEYWORDS Apoptosis. ATF1. Cancer. Metabolism. Proliferation

ABSTRACT This study aims to provide a comprehensive pathway regulated by ATF1 and screen for differences between cancer and normal cells. Genome-wide mRNA expression microarrays were performed using RNA isolated from ATF1 over-expressing CNE1 and NP69 cells. The ATF1 regulating expression pattern and signaling was investigated by GO annotation, KEGG pathway and PPI network. A total of 1651 genes were found to be expressed differentially between CNE1-ATF1 and CNE1-control cells, 4304 genes were shown to be expressed differentially between NP69-ATF1 and NP69-control cells. In the GO annotation, KEGG analysis and PPI networks, pathways associated with cancer, apoptosis and cell proliferation exhibited the most significant correlation with ATF1 modulation in both cells. Different pathways were suggested as immune response in CNE1 cells and metabolism in NP69 cells. Taken together, the data of this study provide a comprehensive signaling pathway regulated by ATF1 and figure out the differences between cancer and normal cells.