

Title: Exploring gene regulatory interaction networks and predicting therapeutic molecules for hypopharyngeal cancer and EGFR-mutated lung adenocarcinoma

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Abstract: Hypopharyngeal cancer is a disease that is associated with EGFR-mutated lung adenocarcinoma. Here we utilized a bioinformatics approach to identify genetic commonalities between these two diseases. To this end, we examined microarray datasets from GEO (Gene Expression Omnibus) to identify differentially expressed genes, common genes, and hub genes between the selected two diseases. Our analyses identified potential therapeutic molecules for the selected diseases based on 10 hub genes with the highest interactions according to the degree topology method and the maximum clique centrality (MCC). These therapeutic molecules may have the potential for simultaneous treatment of these diseases.

Keywords: EGFR-mutated lung adenocarcinoma; Gene Expression Omnibus; Degree topology, Therapeutic molecule; Hub gene; Hypopharyngeal cancer.

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