Differential Impacts of EGFR L858R and Exon19 Deletion Mutations on Downstream Pathways in LUAD Patients

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Abstract:

Lung adenocarcinoma (LUAD) is the most common subtype of lung cancer, with EGFR mutations playing a pivotal role in its pathogenesis. Among these, L858R and Exon19 deletions are the most frequent. While these mutations show distinct therapeutic responses and prognostic outcomes, their downstream biological impacts remain inadequately understood. Understanding these molecular differences can provide critical insights to guide mutation-specific therapeutic strategies.

This study aims to identify the differential downstream pathways associated with EGFR L858R and Exon19 deletion mutations, offering insights into tailored treatment strategies for LUAD patients.

Transcriptome data from LUAD patients with EGFR L858R and Exon19 deletion mutations were obtained via the NIH GDC Portal. Differential gene expression analysis and Gene Ontology (GO) Biological Process (BP) Gene Set Enrichment Analysis (GSEA) were conducted. The results were visualized using Cytoscape's Enrichment Map to identify key pathways.

L858R mutations were predominantly associated with metabolic pathways, whereas Exon19 deletions were linked to immune evasion mechanisms. These findings highlight distinct molecular characteristics between the two mutations.

This study reveals significant downstream pathway differences between EGFR L858R and Exon19 deletion mutations in LUAD patients, providing crucial guidance for mutation-specific precision therapies and advancing personalized medicine in lung cancer treatment.