

Computational Analyses to Identify Genes Disproportionately Affected by NFKBIA Deletions and Implicated in Breast Cancer and Glioblastoma Tumorigenesis

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NFKBIA deletions are extremely prevalent in cases of both Breast Cancer and Glioblastoma, and this study aims at identifying genes disproportionately affected by these deletions. First, gene-expression data relating to Glioblastoma Multiforme and Breast Cancer was downloaded from the Genomic Data Commons Data Portal. Using the programming language R and the BioMart database, the genes present in this dataset were found. Also using R, two correlation analyses were performed to determine which genes were significant in relation to NFKBIA. From these important genes, median absolute deviation statistics were used to identify those genes that were differentially expressed. A differential gene analysis was then performed on these genes using the EdgeR package in R to further condense the list of those genes that were truly significant in relation to NFKBIA. Last, using the clusterProfiler package in R and the PANTHER application, a gene ontology enrichment analysis was performed to identify the biological processes, cellular components, and molecular functions of these genes. The results of these analyses showed that the loss of NFKBIA in these diseases does in fact have an effect on transcription. Specifically, this study found that the loss of NFKBIA increased the severity of GBM and the likelihood of breast cancers to metastasize to the brain, which suggests that targeting developmental processes may offer new therapies to treat these two diseases. The analyses also determined that patients with breast cancers that had metastasized to the brain exhibited loss of the sense of smell. Although loss of smell has been detected in brain tumors, it has yet to be associated with breast cancers, and this phenotype may serve as a method of early detection of the disease.

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