A Novel Algorithm to Determine the Functionality of Brain Stem Glioma Associated Single Nucleotide Polymorphisms

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Genetic mutations, often characterized by single-nucleotide polymorphisms (SNP), have been shown to act as the main cause of varying gene expression, leading to the onset of many cancers. In order to correlate a specific SNP to a multitude of cancers, an algorithm was created to identify different cross sectional genes. Once the algorithm was run, several SNP's were found using the following main criteria: upstream/downstream gene distances, chromosome number and risk allele frequency. The SNPid, rs2763100, was selected for further investigation, based upon its previously identified role in normal lung development. However, a novel association to Glioma was sought out due its effects as a catalytic subunit of the enzyme Telomerase. Furthermore, an SNP analysis was utilized to conclude that the designated SNP was positioned on the TERT gene on the 5th chromosome. A DNA microarray was executed in order to understand gene expression levels. From this, a heat map was constructed concluding that the onset of the cancer was linked to an overexpression of the TERT gene, rather than a suppression of the surrounding genes. A DNA methylation chart was also created to confirm the previously noted results using methylation rates of the TERT gene. Additionally, a network visualization analysis was constructed to determine the location of other genes. Overexpression of the TERT gene supported the role of the TERT gene in development of both Glioma and Lung cancer. The correlated SNP was shown to block the beta pathway leading to both Glioma and Lung cancer.

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