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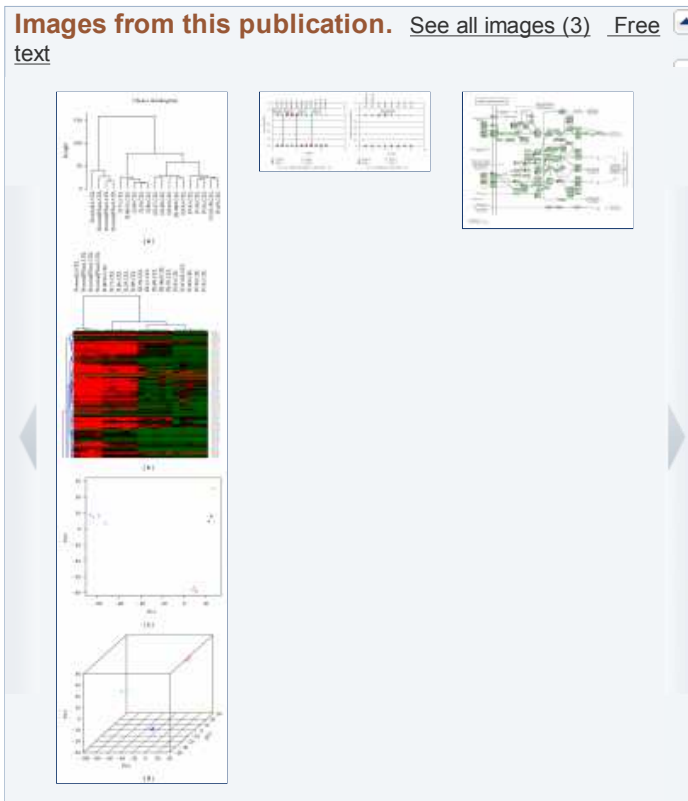
Gene expression profiling in human high-grade astrocytomas.

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Abstract

Diffuse astrocytoma of (WHO grade II) has a tendency to progress spontaneously to anaplastic astrocytoma (WHO grade III) and/or glioblastoma (WHO grade IV). However, the molecular basis of astrocytoma progression is still poorly understood. In current study, an essential initial step toward this goal is the establishment of the taxonomy of tumors on the basis of their gene expression profiles. We have used gene expression profiling, unsupervised (hierarchical cluster (HCL) and principal component analysis (PCA)) and supervised (prediction analysis for microarrays (PAM)) learning methods, to demonstrate the presence of three distinct gene expression signatures of astrocytomas (ACMs), which correspond to diffuse or low-grade astrocytoma (WHO grade II), Anaplastic astrocytoma (WHO grade III) and Glioblastoma multiforme (WHO grade IV). We also demonstrate a 171 gene-based classifier that characterize the distinction between these pathologic/molecular subsets of astrocytomas. These results further define molecular subtypes of astrocytomas and may potentially be used to define potential targets and further refine stratification approaches for therapy. In addition, this study demonstrates that combining gene expression analysis with detailed annotated pathway and gene ontology (GO) category resources was applied to highly enriched normal and tumor population; it can yield an understanding of the critical biological mechanism of astrocytomas.

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