

Identification of survival pathways through integrated analysis of the transcriptome of Medulloblastoma

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Brain tumors are the leading cause of cancer related death in children and medulloblastoma is the most common malignant brain tumor of children. Transcriptome analysis has revealed four major molecular subtypes, WNT, SHH, Group C and D. Through integrated analysis on multiple studies, we were able to identify the core genes for each molecular subtype. By using a seed-and-grow greedy search algorithm, we reconstructed the signaling pathways underlying each molecular subtype. More importantly, we were able to associate key pathway structures to the patient survival information. In particular, identified a set of pathway modules differentially activated by Myc between WNT and Group C subtypes. These differences are significantly associated with patient survival outcomes, where WNT subtype has the best survival and GroupC subtype has the poorest survival. Overall, our integrated analysis provides a detailed pathway landscape of Medulloblastoma in each molecular subtype.

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