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**SURVEYING THE MOLECULAR LANDSCAPE OF
PEDIATRIC BRAIN TUMORS VIA SPATIALLY
RESOLVED TRANSCRIPTOMICS**

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Due to their intrinsic heterogeneity and plasticity, pediatric brain tumors present highly complex clinical challenges. To provide insight into the molecular scene of these tumors, we generated spatial transcriptomics data from 19 distinct patients, 7 of which suffered a relapse of the disease. In this cohort, spanning 59 tissue sections across 8 diagnoses and 4 tumor grades, we recovered diagnosis-specific gene expression patterns that could be linked to processes characteristic of developmental stages. We also identified between 2 to 4 spatial archetypal niches per section, which could then be related to 11 main biological themes, and to distinct celltype-like transcriptomic signatures. For example, we noted strong spatial correlations between developmental archetypes and oligodendrocyte lineage signal in pilocytic astrocytoma. Lastly, we utilised spatially inferred copy-number variants for the profiling of relapse-associated tentative tumor clones. These clones were then related via spatial geographical analysis to regions with strong blood vessel signatures. Overall, these results provide vital details into the progression and maintenance of pediatric brain tumors, offering novel edges to be exploited in personalized medicine.