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Histone modifications

Defining the cell of origin for diffuse midline gliomas

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K27M mutation of histone H3 has been identified as a driver event in diffuse midline glioma. Two studies used comprehensive multi-model single-cell genomic, epigenomic and chromatin structure analysis to characterize the cell of origin and find a distinct etiology of H3K27M between pontine and thalamic tumors, and show that pontine gliomas harbor more immature oligodendrocyte-precursor-like cells.

Previous studies on spatiotemporal specificity of genetic alterations have suggested that aberrant development plays a role in high-grade glioma pathogenesis[7]. Through analysis of single-cell transcriptomes, chromatin