Posterior fossa type A (PFA) ependymoma is a lethal brain cancer mostly diagnosed in infants and young children. This tumor type lacks recurrent genetic mutations. However, PFA ependymoma is defined by a characteristic DNA methylation profile and global loss of the histone mark H3K27me3. It has therefore been suggested that PFA ependymoma is an example of an epigenetically-driven malignancy. In this study, we investigated whether the epigenomic characteristics of PFA ependymoma result in disease-specific 3D genome architecture. We uncovered new 3D genome structures in PFA ependymoma that we call TULIPs. TULIPs are present in all PFA ependymomas, occur at recurrent genome coordinates and are important for tumor cell fitness. Therefore, although PFA ependymoma lacks recurrent genetic mutations, it is characterized by recurrent 3D genome structures that could present translational opportunities.