

Abstract: Incorporating RNA-Sequencing data from adult gliomas, pediatric gliomas and contrasting it with gene expression data for GTEx-defined normal brain regions, can increase our understanding of all brain diseases. We apply uniform manifold approximation and projection (UMAP), a non-linear dimension reduction tool, to bulk gene expression data and build a BRAIN-UMAP and further overlay copy number and mutation calls on the same to understand the landscape of brain diseases.

Fig 1: Constructing the BRAIN-UMAP

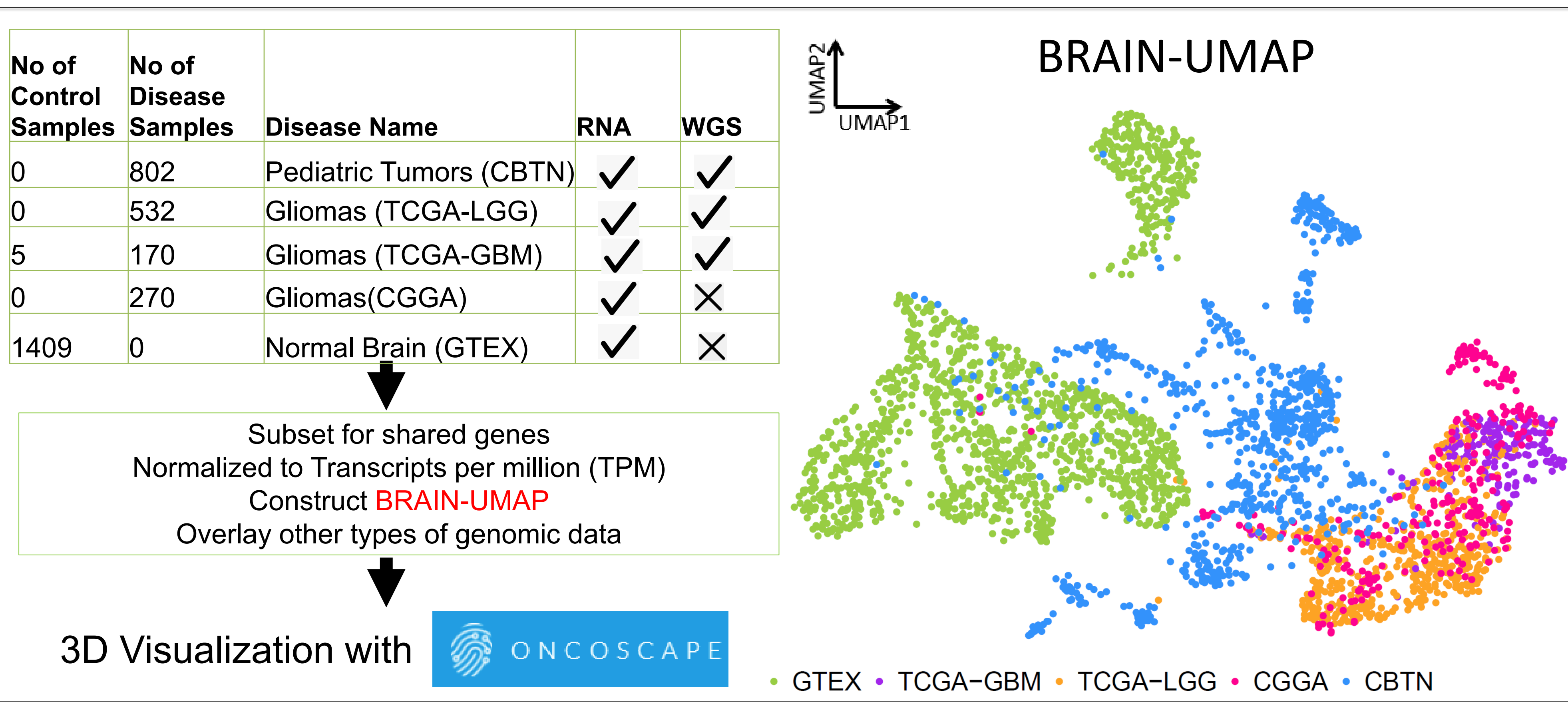


Fig 2: Regions of Healthy Brain

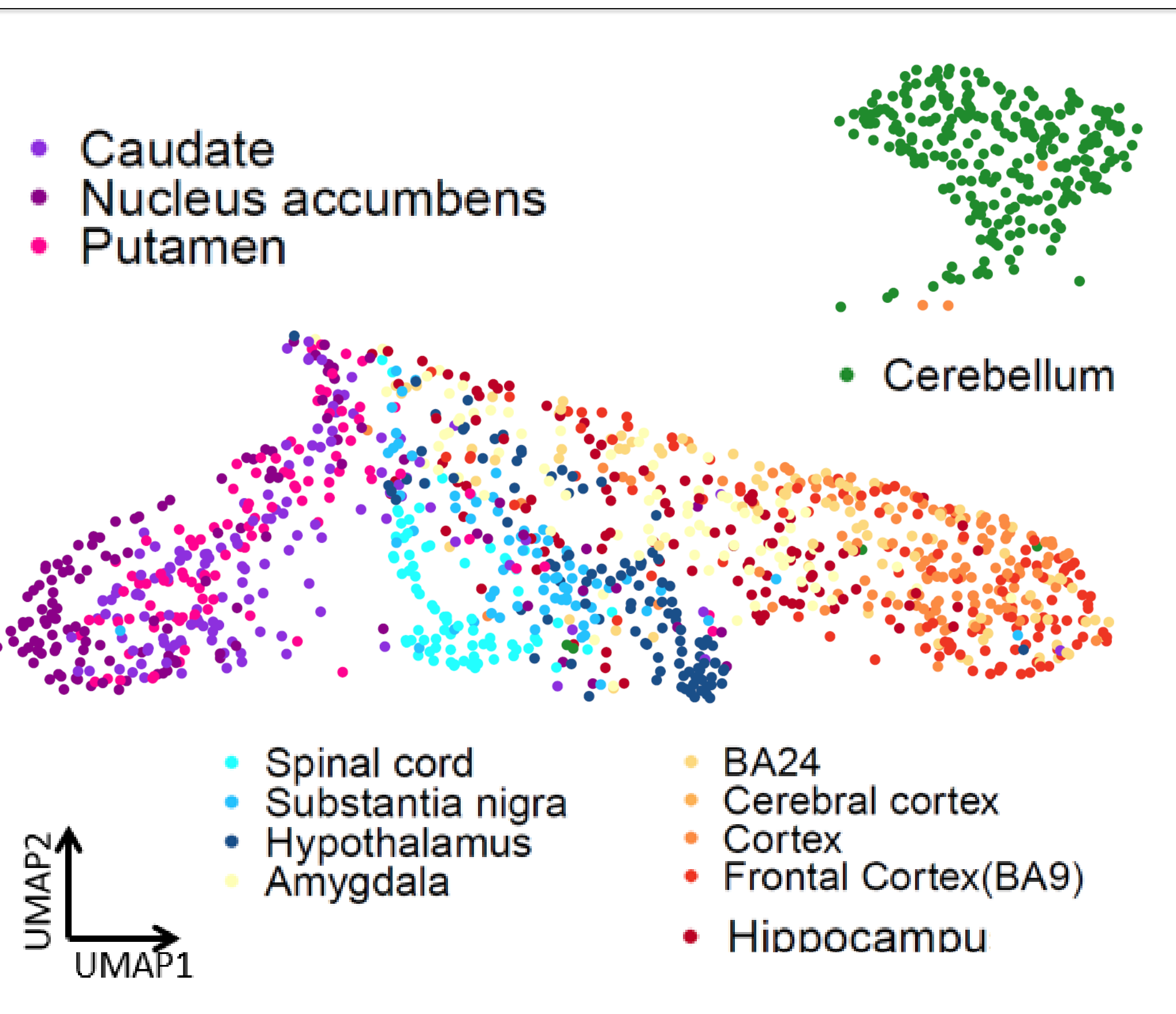


Fig 3: TCGA Glioma landscape

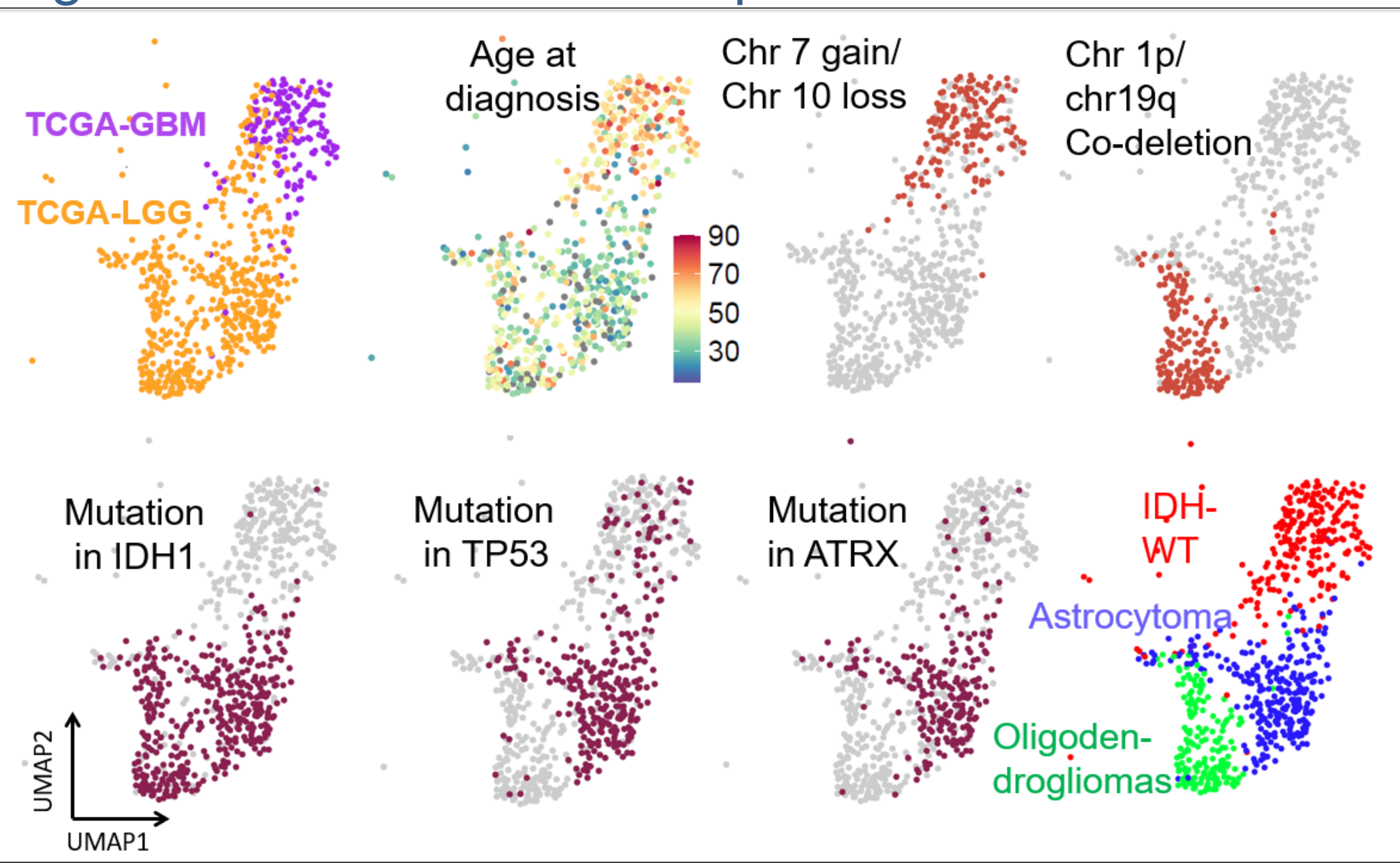


Fig 4: Glioma landscape is consistent across TCGA and CGGA

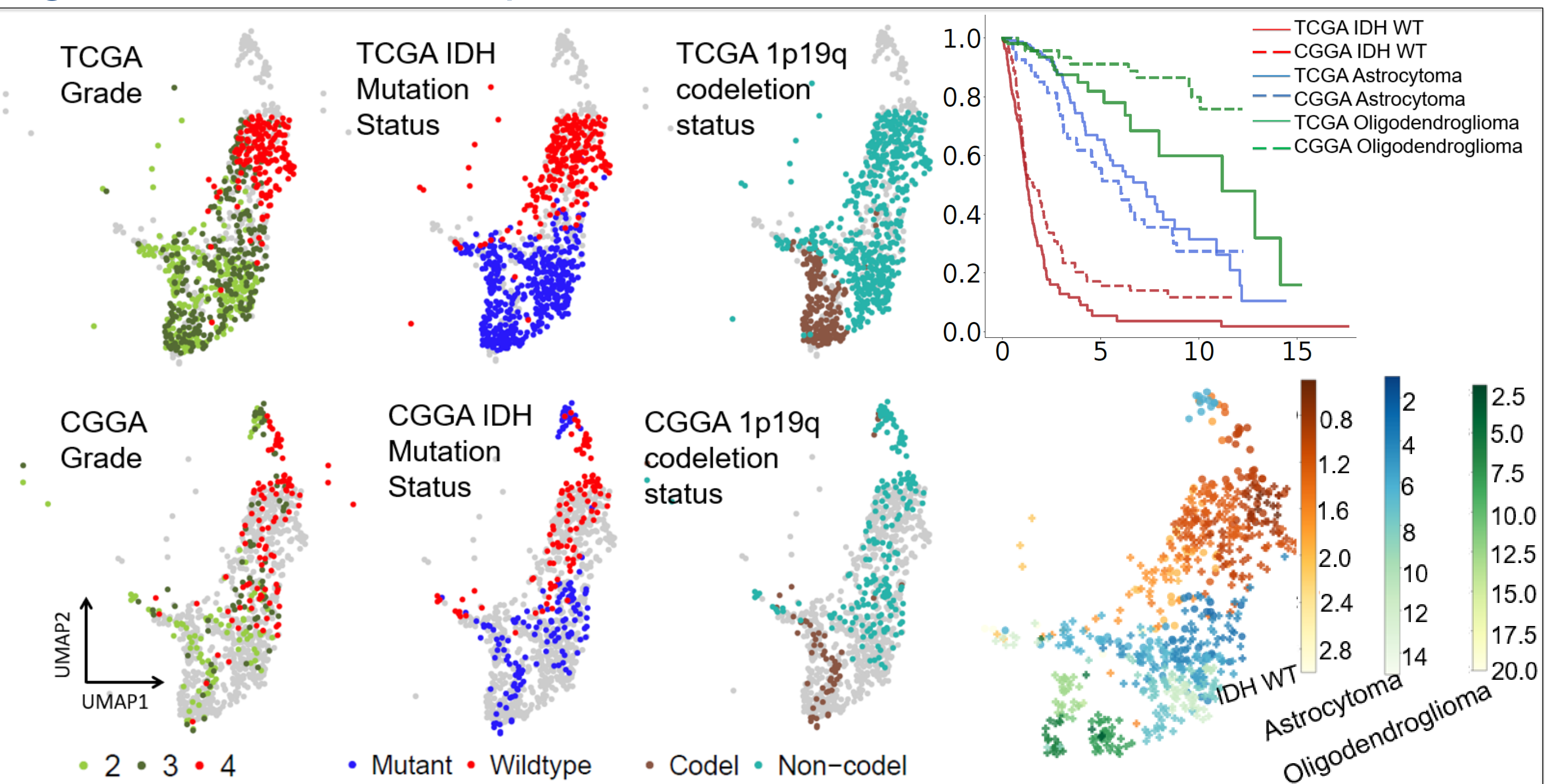


Fig 5: Contrasting Adult & Pediatric Gliomas

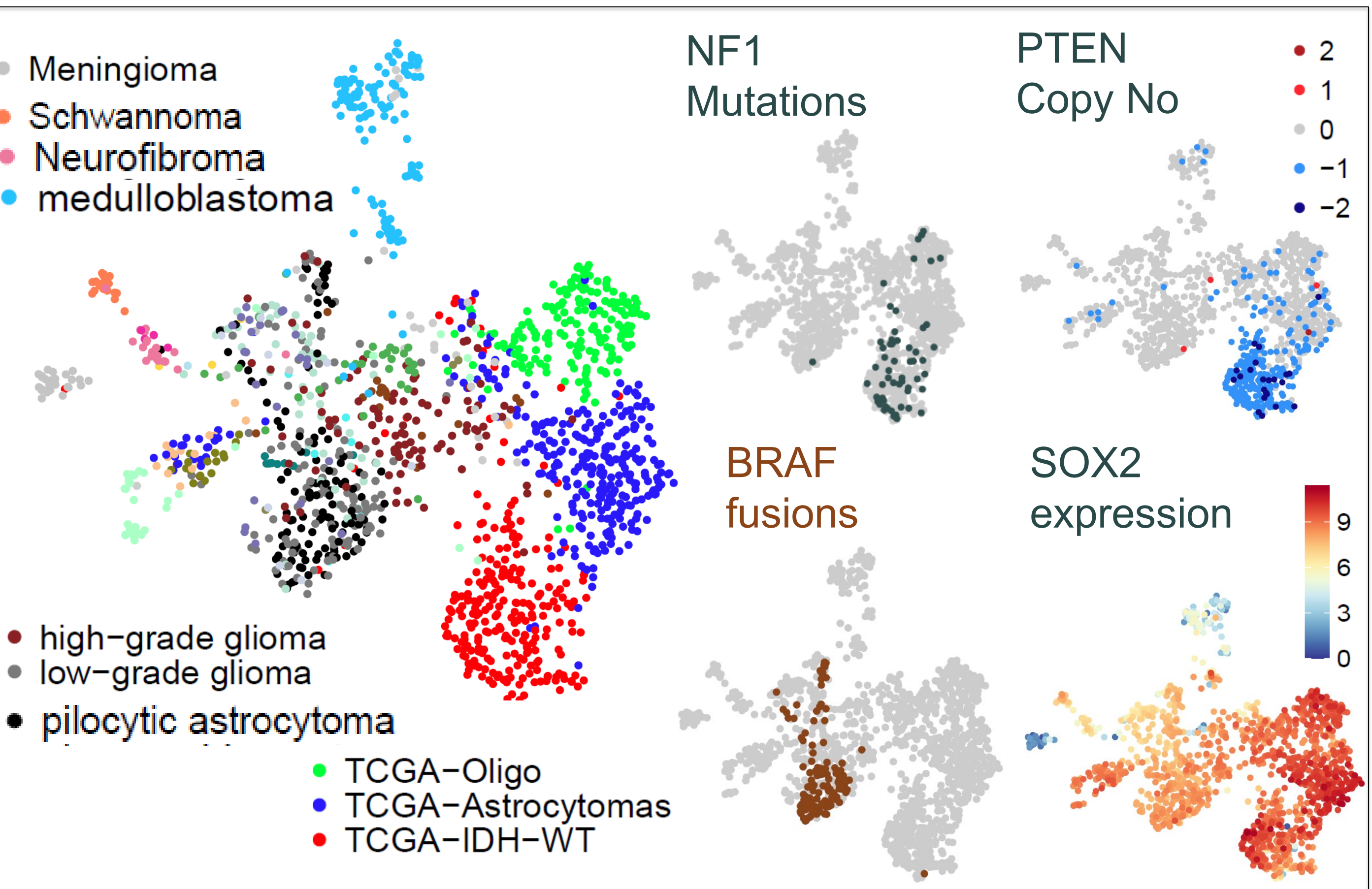
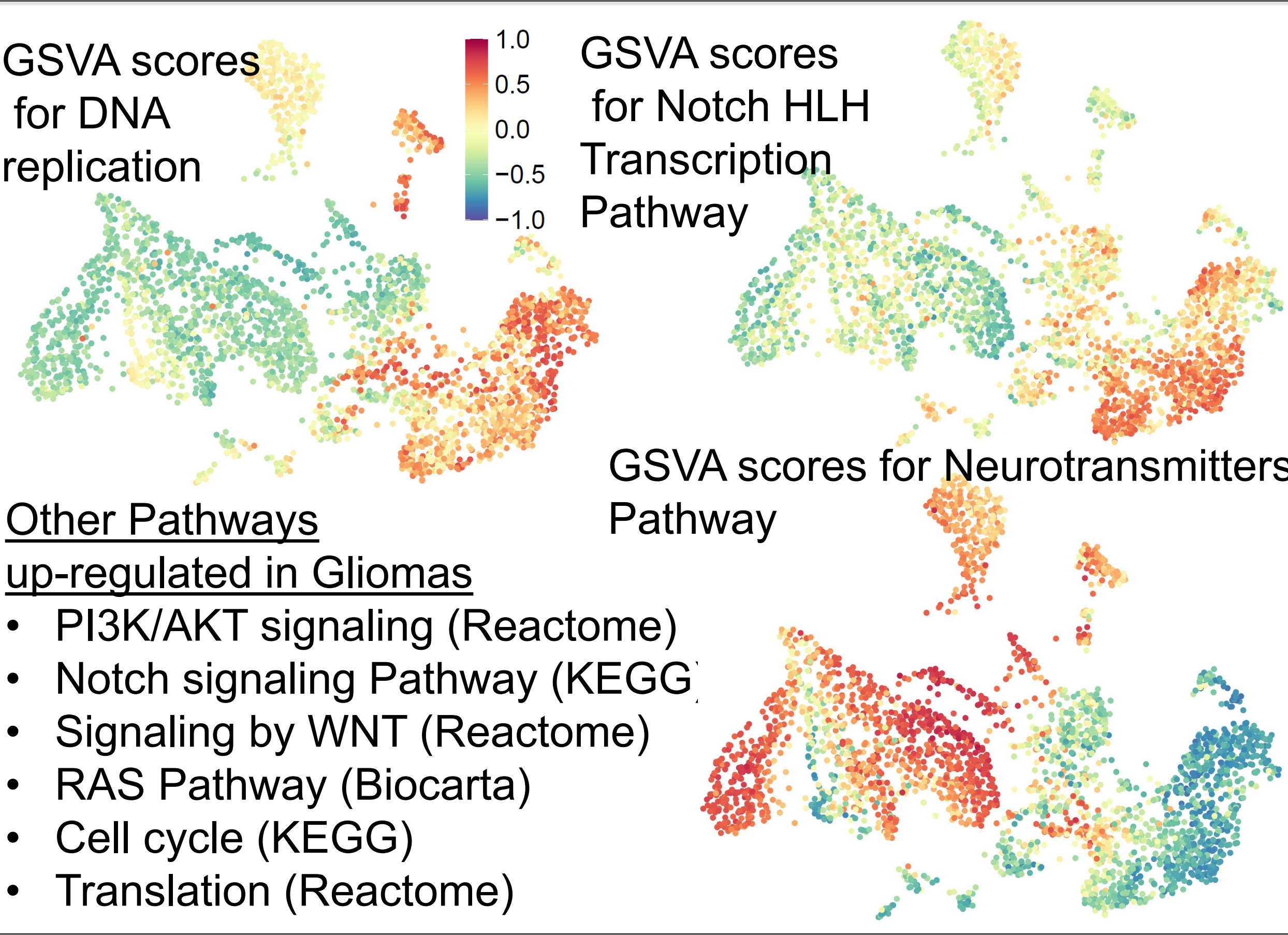


Fig 6: Different Pathways regulated in Gliomas



*CGGA and TCGA greyed out in top and bottom panel respectively

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