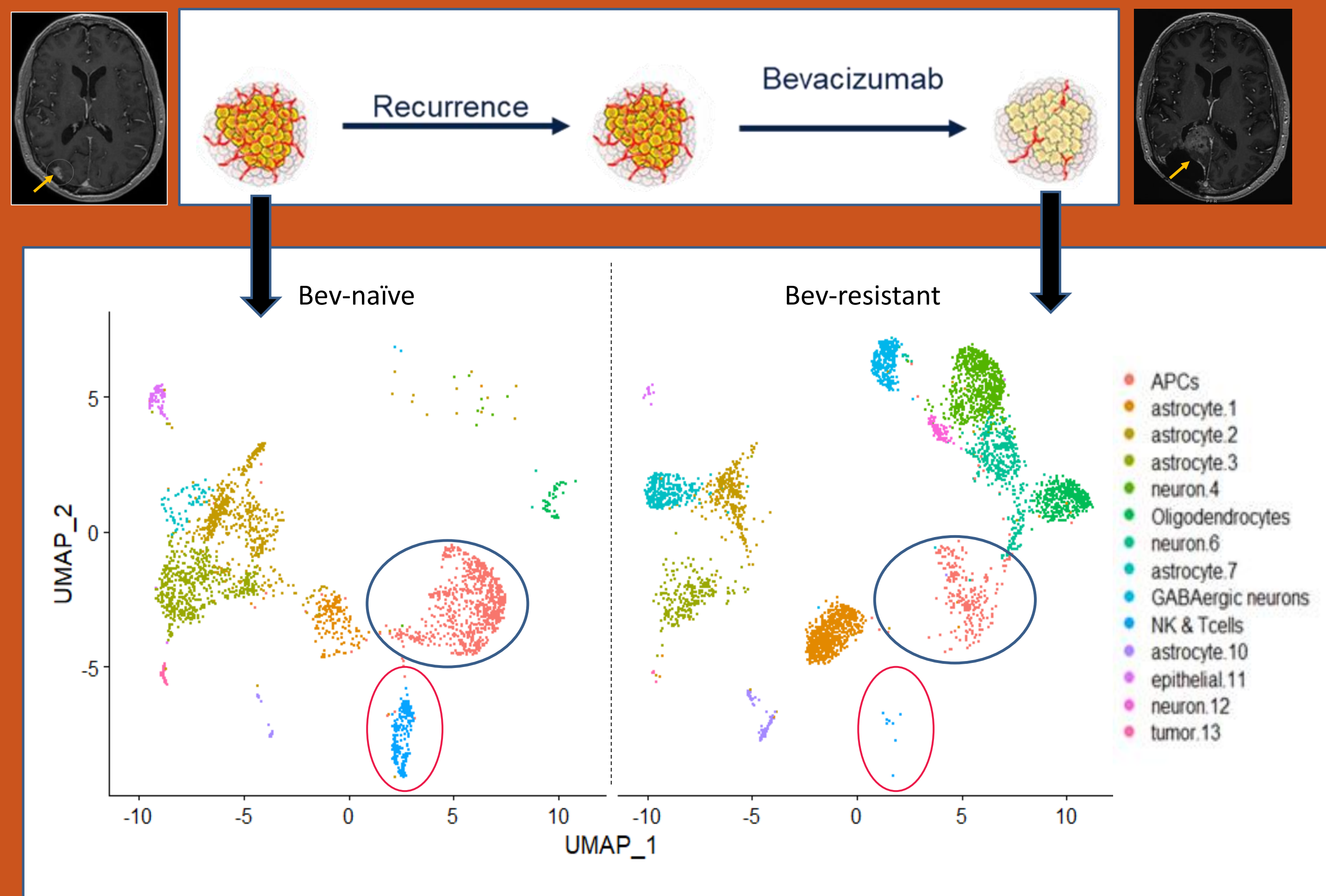


Case Report: single-nucleus RNA sequencing reveals relative immune depletion in recurrent GBM treated with antiangiogenic immunotherapy



Immune Depletion in Bevacizumab-treated Glioblastoma

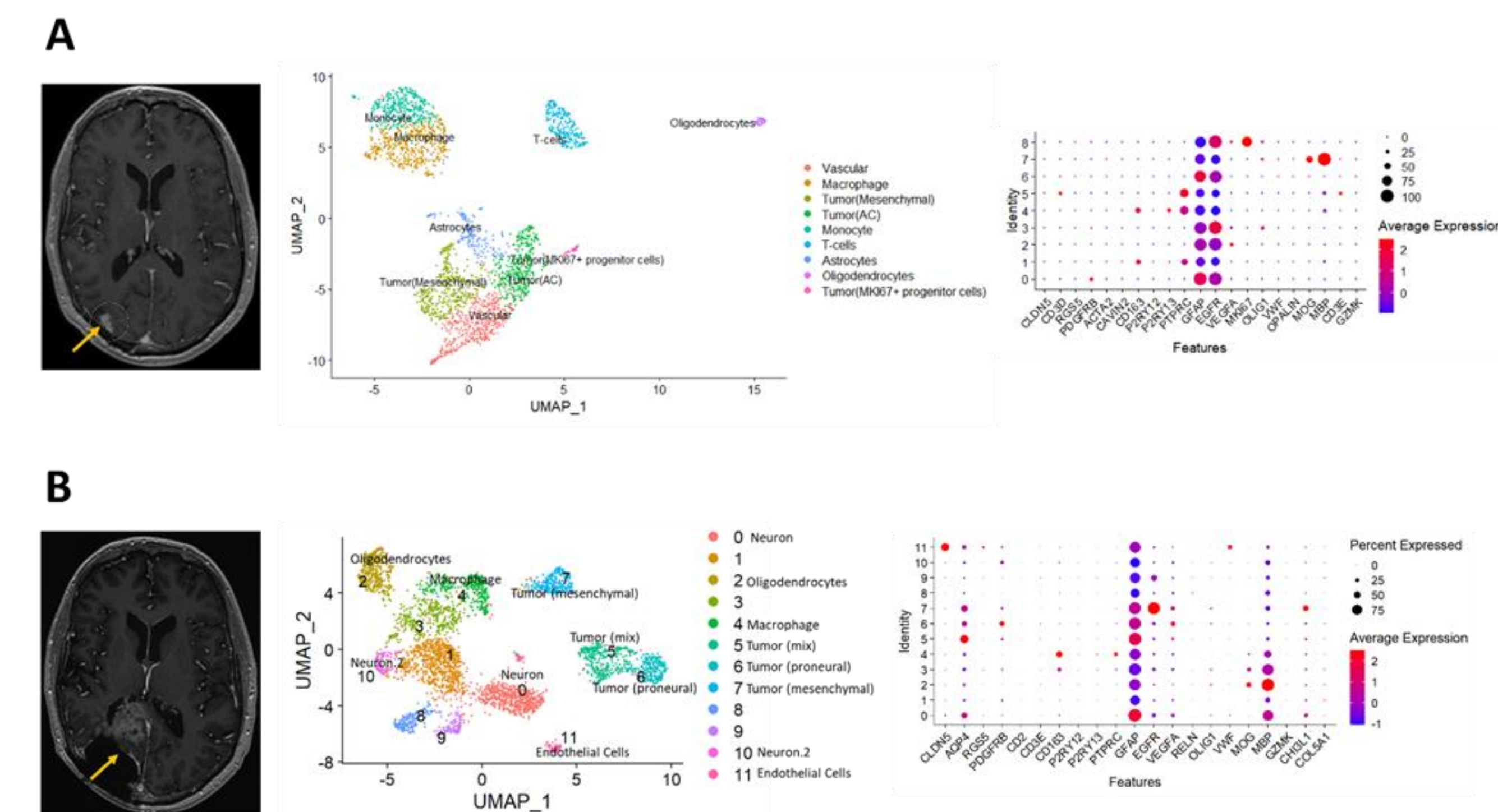
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Introduction

While the antiangiogenic agent bevacizumab is FDA-approved for the treatment of recurrent glioblastoma (GBM), efficacy is transient. We used single-nucleus sequencing to compare bevacizumab-naïve glioblastoma cells to glioblastoma cells that progressed during bevacizumab treatment.

Methods

Two human glioblastoma samples from a single patient harvested in our were prepared for single-nucleus RNA capture and sequencing. One of these samples was a primary GBM tumor and the second a recurrent bevacizumab-treated GBM tumor. Single-nucleus (sn) RNA libraries were generated and sequenced. Raw sequence data was processed and loaded into Seurat package for Uniform Manifold Approximation and Projection (UMAP) visualization and were analyzed on RStudio.

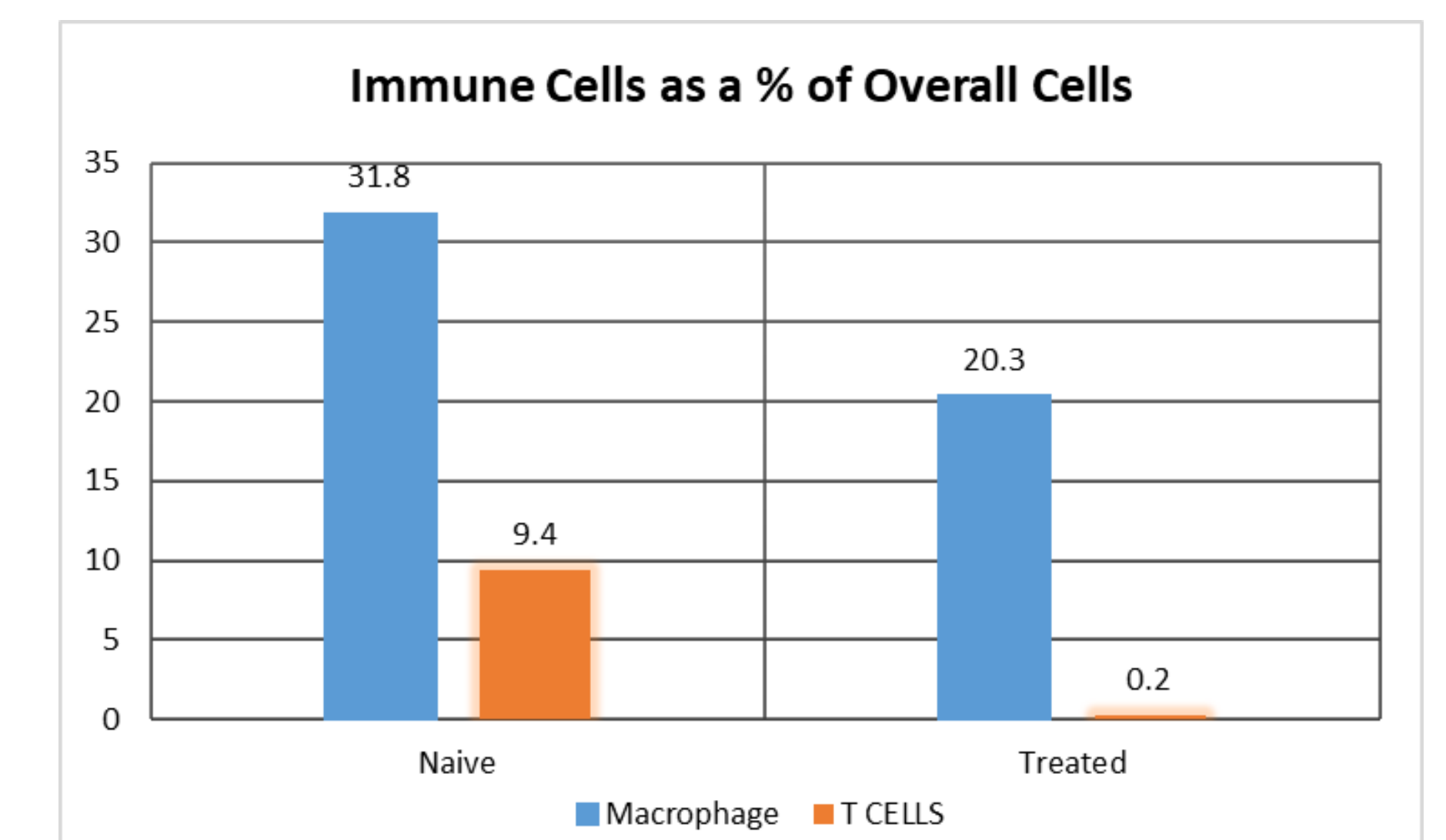
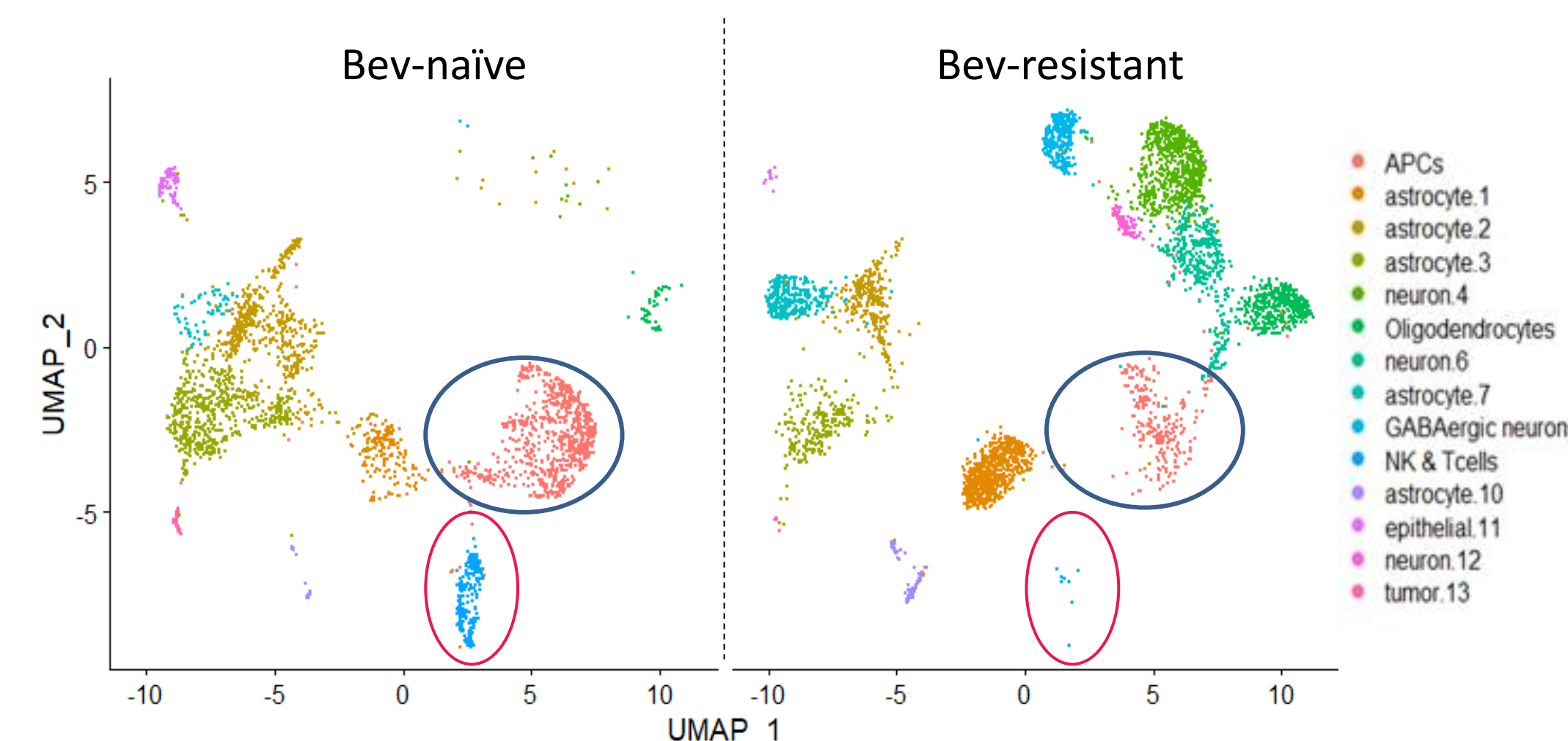


Discussion

Comparison of gene expression at the single-nucleus level between naïve and bevacizumab-treated GBM revealed a scarcity of T-cell and monocytic cell populations in the treated tumor. This points to a potential alteration of immune populations as a result of bevacizumab treatment.

Results

The bevacizumab-naïve (BN) sample composed of 2481 nuclei and bevacizumab-treated (BT) sample composed of 3760 nuclei. Merged gene expression data used to visually compare cell expression between both tumors.



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