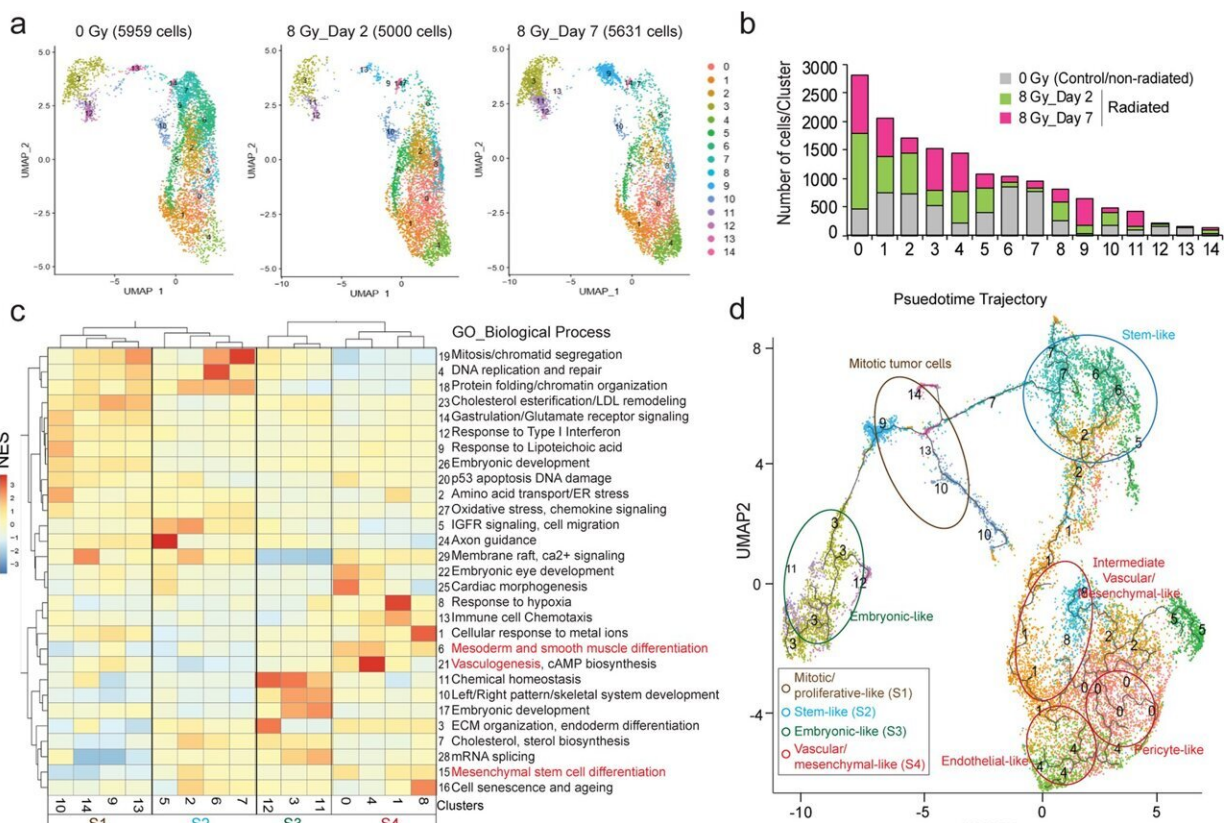


Researchers identify a gene as a potential target in treatment-resistant brain cancer glioblastoma multiforme

October 19 2022



Single-cell sequencing reveals the diverse functional states of glioma cells post-radiation. **a** UMAP plot of cell clusters from control (0 Gy) and 2- and 7-days radiated (8 Gy) fractions. **b** Histogram shows the number of cells per cluster in each group. **c** Heatmap shows Louvain clustering of co-expressed gene network modules and EnrichR GO_terms associated with each cluster. Each subgroup is highlighted by a black box. **d** Pseudotime trajectory analysis, subgroups are

highlighted in colored circles and their functional cell states indicated in the inset. **e** Heatmap of average expression of markers of proliferation, glioma stem cells (GSC), Neural crest-mesenchymal stem cells (NC-MS), pericytes, mesodermal and endothelial cells. **f** Heatmap of normalized enrichment scores (NES) of gene sets in glioma cells 2- and 7-days post-radiation. $N = 3$ biological replicates and only gene sets with p

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