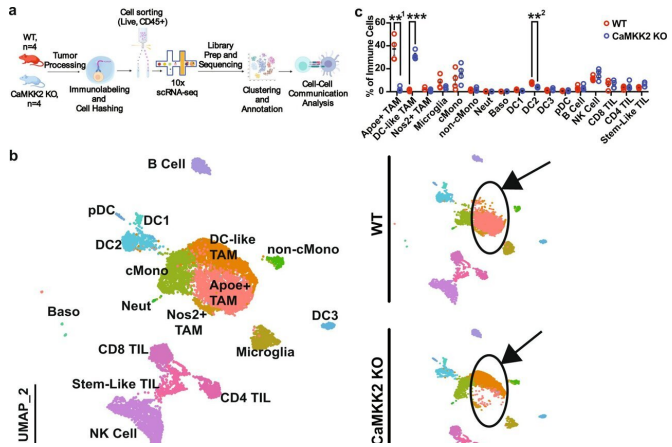
Mechanism identified for drug resistance in glioblastoma brain tumors

3 November 2022, by Sarah Avery



Pro-tumor immune programming in the glioma microenvironment is CaMKK2 dependent. a Schematic depicting scRNA-seq experimental design. n = 4 WT and CaMKK2 KO mice had 50k CT2a orthotopically implanted. On D14 tumors were harvested and underwent tumor processing. Samples were labeled with a Live-Dead viability Dye, CD45, and TotalSeqB anti-mouse Hashtag antibodies. CD45+ Live cells were sorted, and then pooled in equal parts by genotype. Graphic was created with BioRender.com. b 14k CD45+ Live Immune cells were sorted from WT and CaMKK2 KO tumor-bearing hemispheres on D14 p.i. HTO and Gene Expression libraries were prepared using the 10X platform. UMAP plots of the cell types identified using unsupervised clustering methods are shown for the aggregate dataset and stratified by genotype. c Abundance of immune cell types identified by scRNA-seq. n = 4 per genotype, two-way RM ANOVA p

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