related to mesenchymal transition in GBM such as NF-kB and CEBPB were accessible from normal to tumor-associated microglia. On the other hand, tissue-associated macrophages exhibited enhanced calcium-regulated NEAT TF accessibility. Tumor-associated IWP and IWR myeloid cells also showed a gain of DGE of apoptosis and a reduction of proliferation-related genes.

Conclusions Our studies demonstrate that in addition to the previous dogma of myeloid mediated immune suppression that contributes to tumor immune escape, epigenomic reprogramming in the brain TIME leads to unexpected activation of transcriptional pathways that can trigger transdifferentiation and cell death of myeloid cells further promoting tumor progression. In summary, we provide an unparalleled epigenomic landscape of glioma-associated myeloid cells that may have translational implications.

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Trial Registration NA

Ethics Approval The brain tumor/tissue samples were collected as per MD Anderson internal review board (IRB)-approved protocol numbers LAB03-0687 and, LAB04-0001. One non-tumor brain tissue sample was collected from a patient undergoing neurosurgery for epilepsy as per Baylor College of Medicine IRB-approved protocol number H-13798. All experiments were compliant with the review board of MD Anderson Cancer Center, USA.

Consent Written informed consent was obtained from the patient for publication of this abstract and any accompanying images. A copy of the written consent is available for review by the Editor of this journal

Conclusions Taken together, we have established a rapid, efficient and convenient method to achieve in situ genome editing of liver resident macrophages in vivo. By targeting essential genes that instruct macrophage polarization, this method could be used as immunotherapy for liver diseases, including cancers.

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Immune cell types

835 STRUCTURAL DIFFERENCE CAUSED BY MUTATED RESIDUES IS CORRELATED WITH IMMUNOGENICITY OF NEOANTIGENS AND SPECIFICITY OF REACTIVE T CELLS

Tomoyo Shinkawa*, Serina Tokita, Takayuki Kanaseki, Toshihiko Torigoe. Sapporo Medical University, Sapporo, Japan

Background Host T-cell response is limited to only a small fraction of nonsynonymous mutations; however, the molecular properties of those immunogenic neoantigens remain elusive.

Methods Here, we interrogated the HLA class I ligandome of a microsatellite instability (MSI)-type cancer cell line using a proteogenomic approach, and found an immunogenic 9-mer neoantigen, AKF9. The AKF9 was a non-anchor type neoantigen that harbored a single amino-acid substitution (Asn > Lys) at position 8, which did not affect the HLA-binding affinity.

Results In order to assess a determinant of the immunogenicity, we prepared a panel of AKF9 variants with substitutions at position 8, and found that CD8+ T-cell responses were biased toward residues with structural difference from the wild-type. Interestingly, a substitution with moderate structural change (Asp) also induced reactive T cells; however, in contrast to the others, induced T cells frequently cross-reacted to the wild type HLA ligand. To validate these findings, we used in silico prediction of accessible surface areas and scored the difference between neoantigens and wild types (AASA). Evaluation of reported clinical datasets demonstrated that patient T-

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