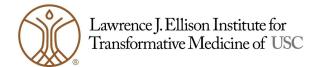
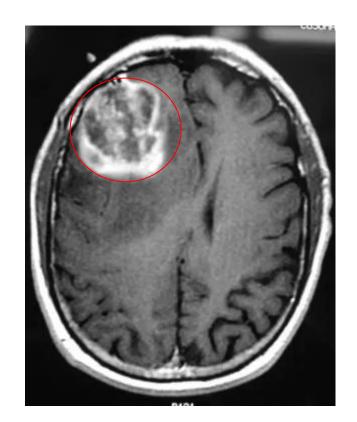
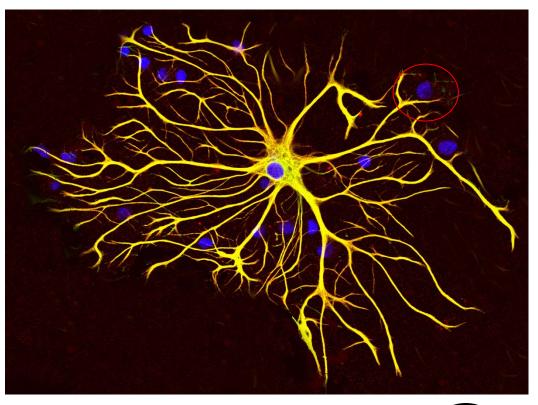
Clinical and Multi-Omic Prognostic Factors of Glioblastomas

Hirad Hosseini, Amir Arya, Talha Rafique QBIO 490: Multi-Omic Data Analysis Fall 2022













Comparing 5-year survival rate of GBM to other cancers worldwide

Overall 5-year survival rate for patients with GBM: Less than 3%

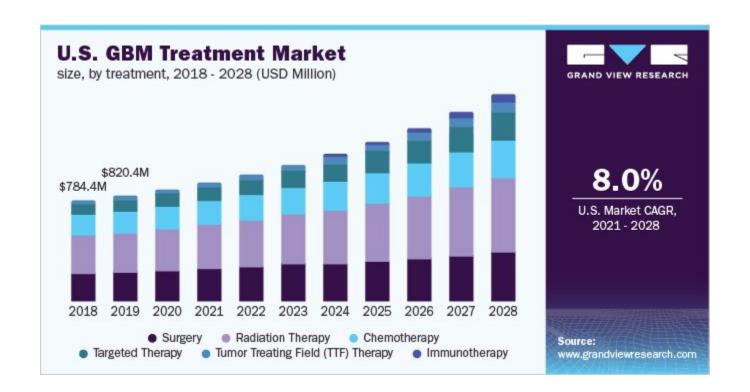
Overall 5-year survival rate for breast cancer patients: Up to 89%

GBM = Glioblastoma

Source: Roche











Methods

Statistical analyses → RStudio IDE (R), Jupyter Notebook (Python)

Datasets → TCGA (Accession: TCGA-GBM), CPTAC (Accession: Gbm)

590 TCGA & 115 CPTAC patients post-processing

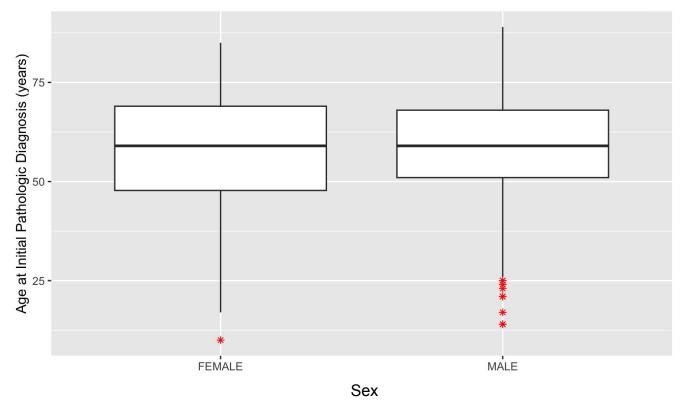








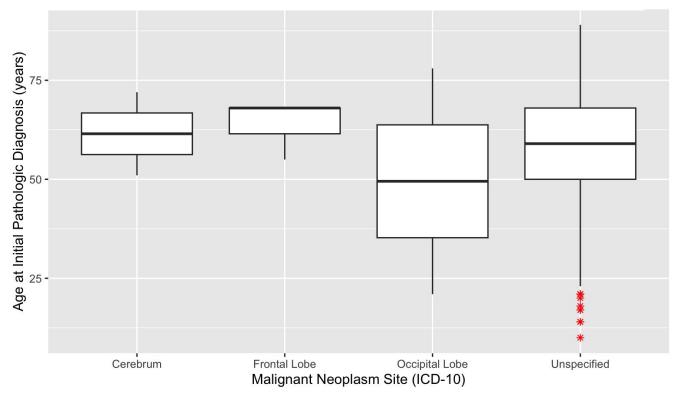
No Significant Variation in Age at Diagnosis Based Upon Patient Sex







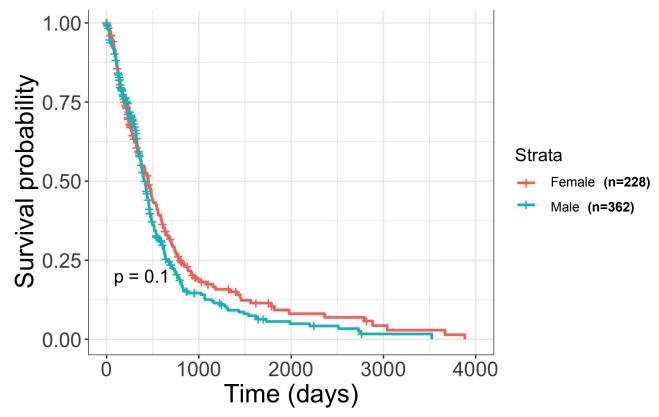
No Significant Variation in Age at Diagnosis Based Upon GBM Site

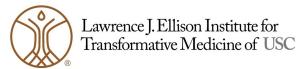






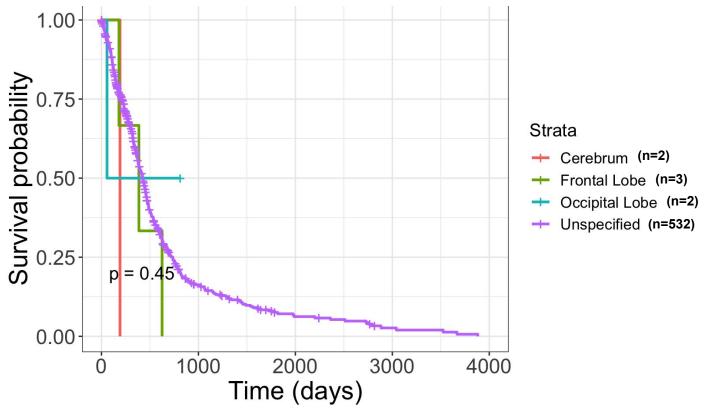
Patient Sex Is Not a Significant Discriminating Factor for GBM Prognosis







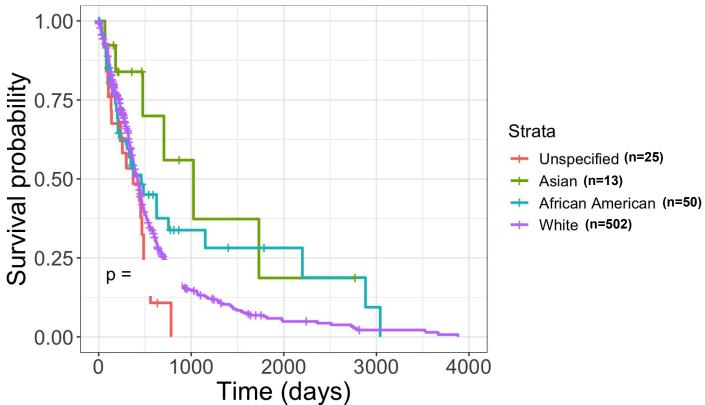
Tumor Site Is Not a Significant Discriminating Factor for GBM Prognosis





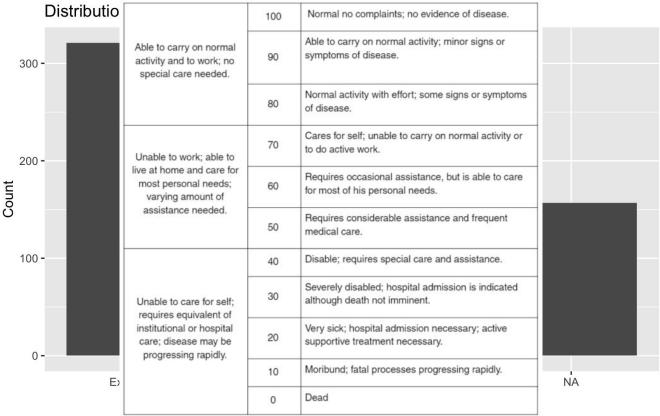


Potential Racial Differences in GBM Prognosis



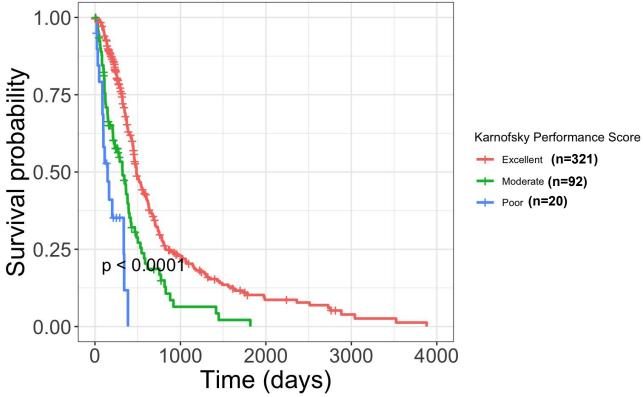


KARNOFSKY PERFORMANCE STATUS SCALE DEFINITIONS RATING (%) CRITERIA



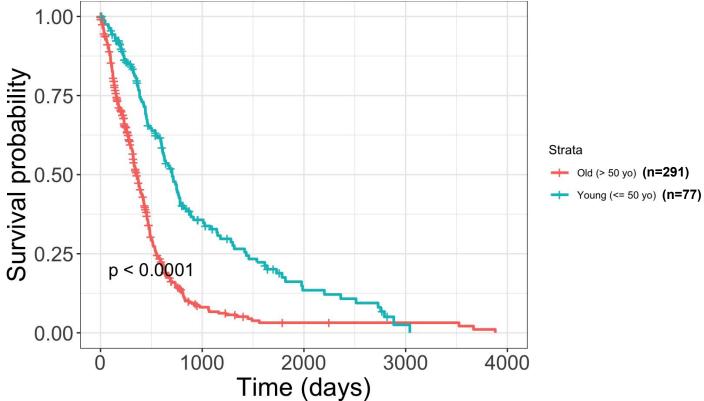


Lower Karnofsky Scores Are Associated with Poor GBM Prognosis



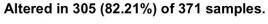


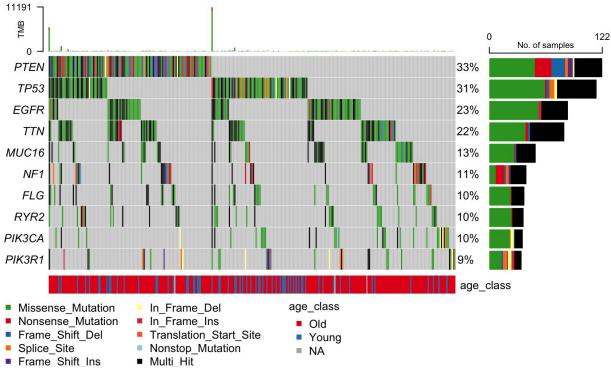
Older Patients (> 50 Years Old) Exhibit Poor GBM Prognosis



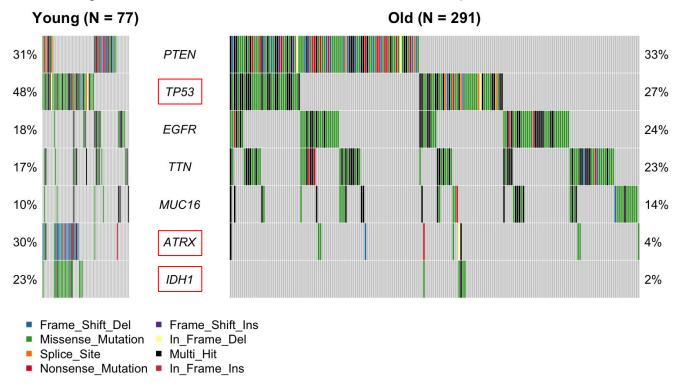


Overall GBM Patient Cohort Demonstrates Commonly Mutated Cancer Genes





Age-Stratified GBM Patient Cohorts Demonstrate Unique Mutation Profiles



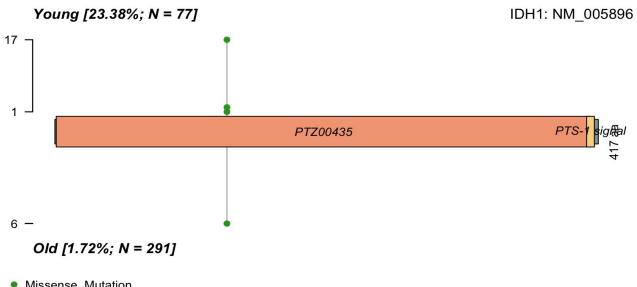


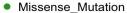
ATRX: Chromatin remodeling/DNA methylation

Young [29.87%; N = 77] ATRX: NM_000489 5 ADDZ ATRX DEMB&_N HELICC 2495 5 Old [3.78%; N = 291]Nonsense_MutationFrame_Shift_Ins Frame Shift Del In Frame Del Missense_Mutation



IDH1: Isocitrate dehydrogenase





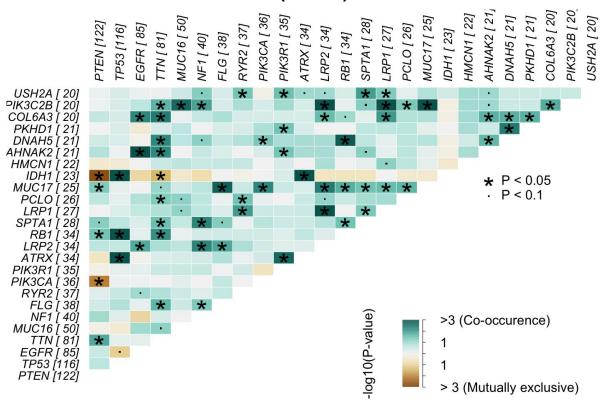


TP53: general tumor suppressor gene

Young [48.05%; N = 77]TP53: NM 000546 1 396 aa P53 P53 tetramer 8 Old [27.15%; N = 291]Splice_Site In Frame Del • Frame Shift Del Frame Shift Ins Missense_MutationNonsense_Mutation

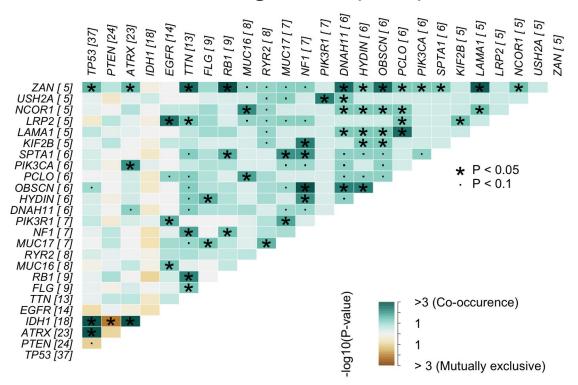


Overall Genomic Mutation Profile Shows Various Co-Occurrences and Mutual Exclusivities (n=368)



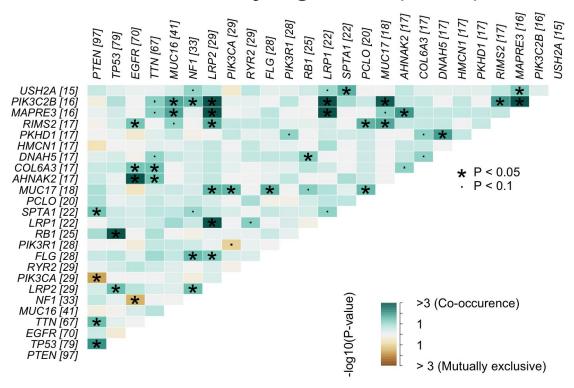


Young Genomic Mutation Profile Demonstrates Unique Mutual Exclusivity Signature (n=77)





Old Genomic Mutation Profile Demonstrates Unique Mutual Exclusivity Signature (n=291)

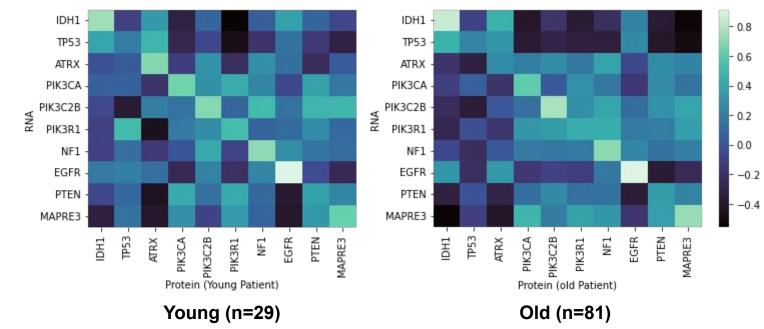




Overall IDH1 - 0.8 TP53 - 0.6 ATRX PIK3CA - 0.4 PIK3C2B - 0.2 PIK3R1 - 0.0 NF1 EGFR -- -0.2 PTEN MAPRE3 PIK3C2B -TP53 ATRX PIK3CA EGFR PTEN **MAPRE3** NF1 댎



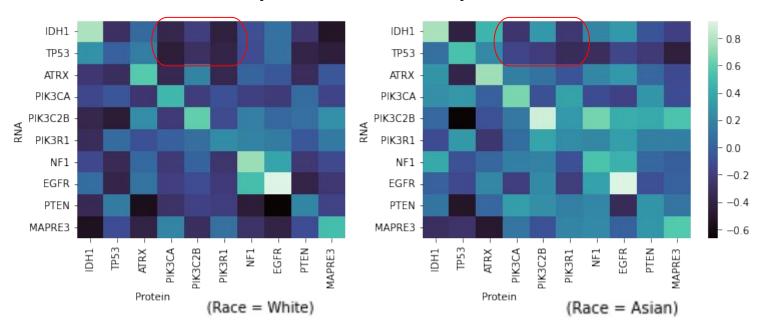
Age-Stratified Heatmaps Don't Demonstrate Significant Differences in Transcriptome/Proteome Expression





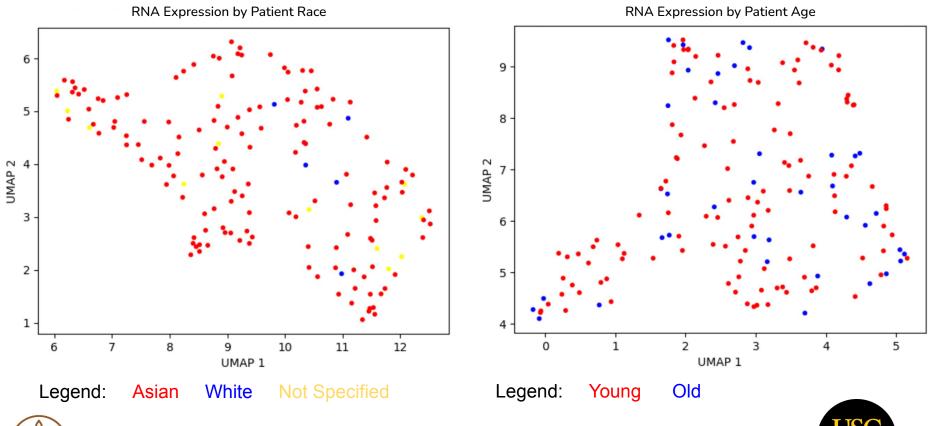


Race-Stratified Heatmaps Demonstrate Minor Differences in Transcriptome/Proteome Expression



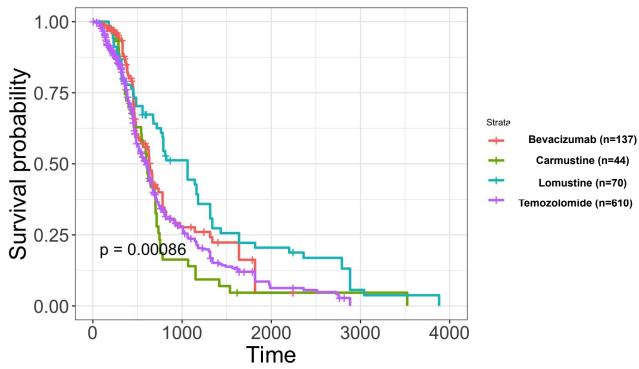


UMAP Plots of Race and Age Do Not Demonstrate Clear Clustering



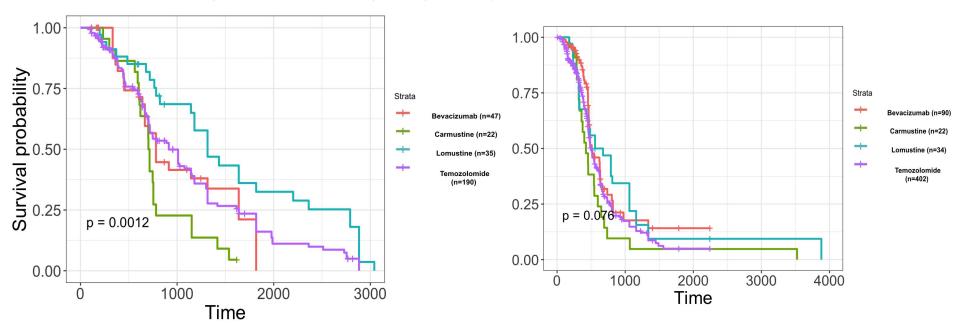
Conclusion

Patient age is a statistically significant prognostic factor for GBM.



Conclusion

Patient age can inform us regarding efficacy of different treatments for each patient.



Young (n=294)

Lawrence J. Ellison Institute for Transformative Medicine of USC

Old (n=548)



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Q&A Segment

