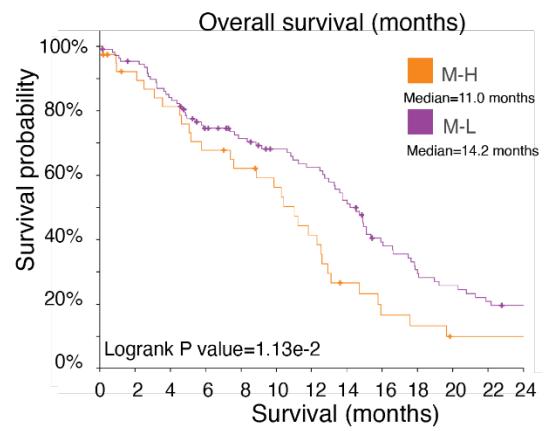
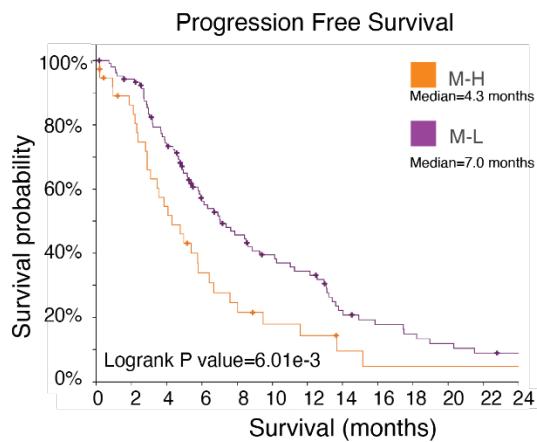
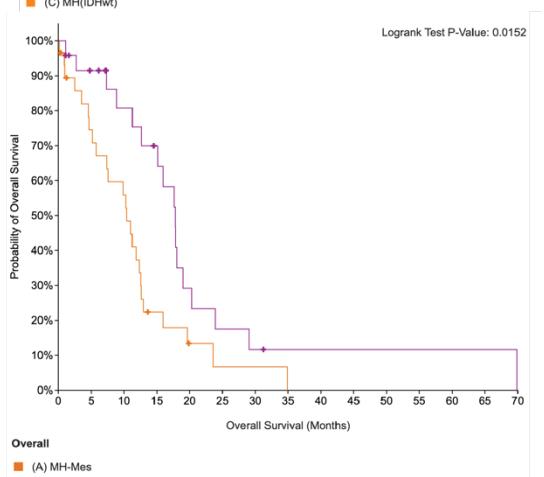
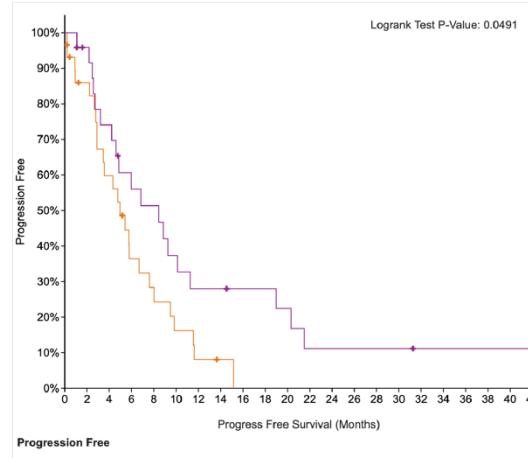
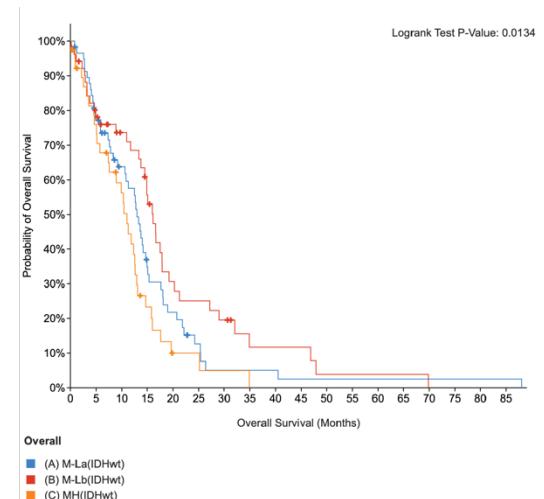
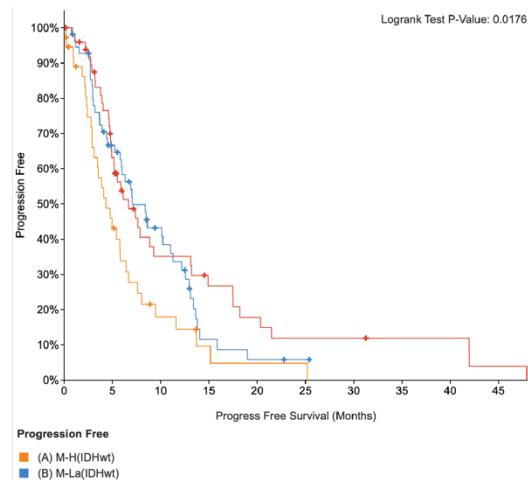
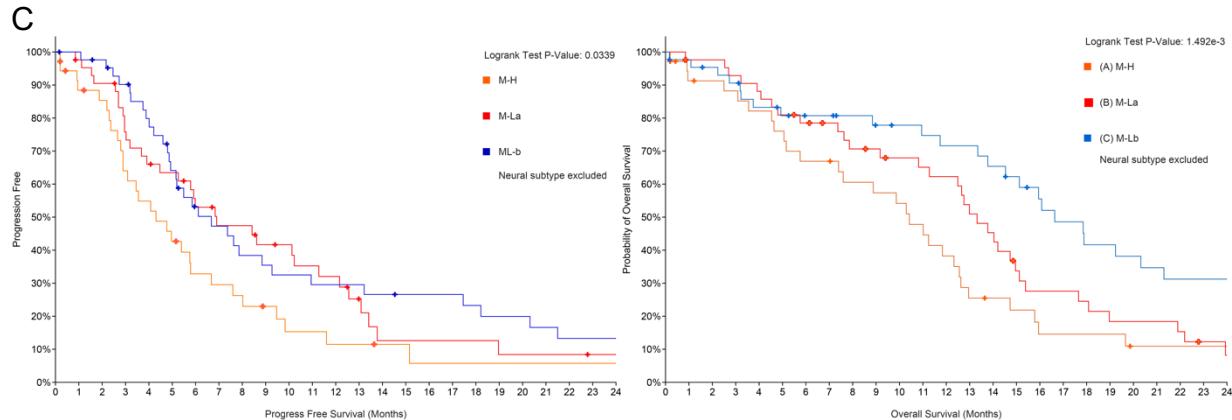


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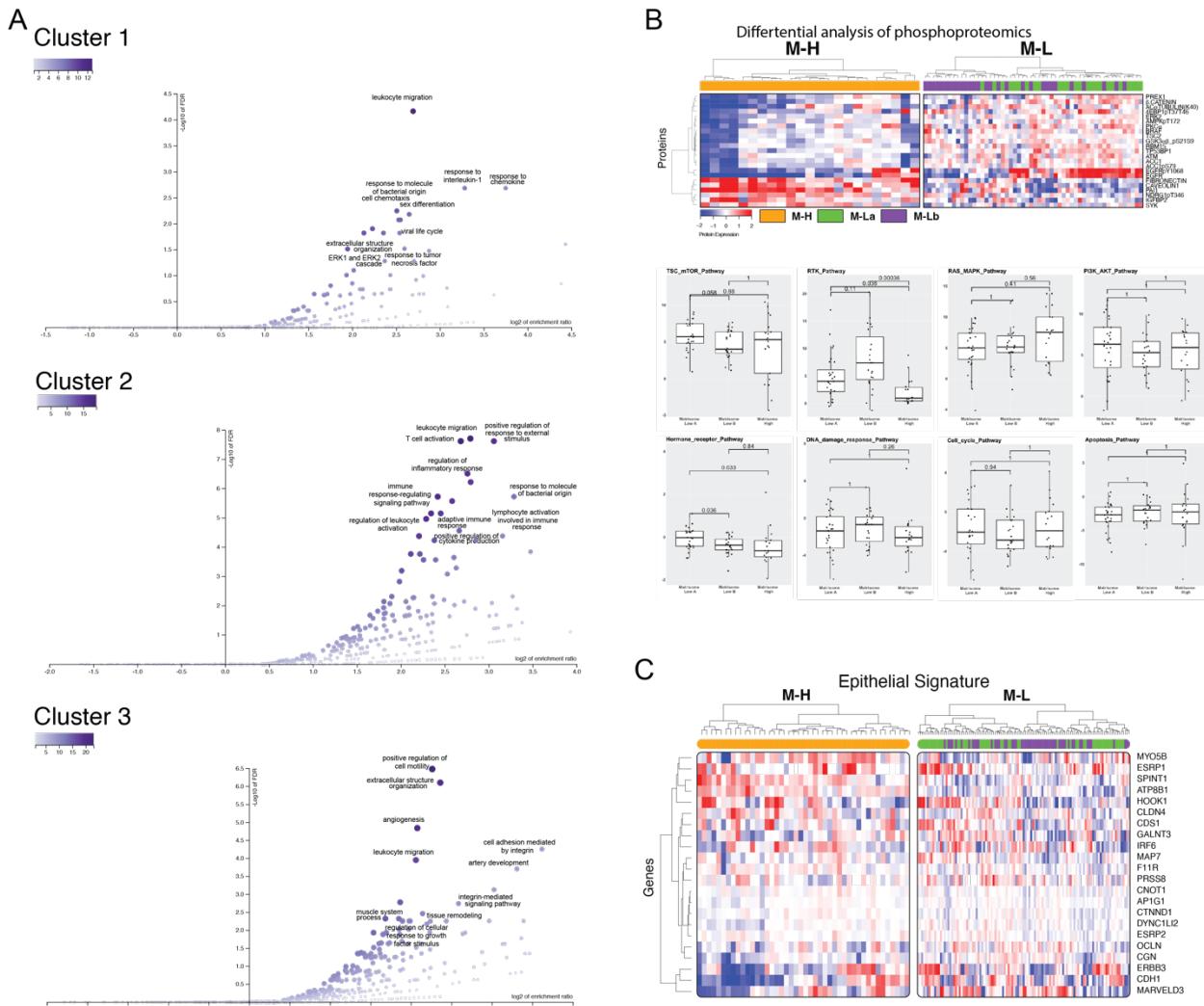


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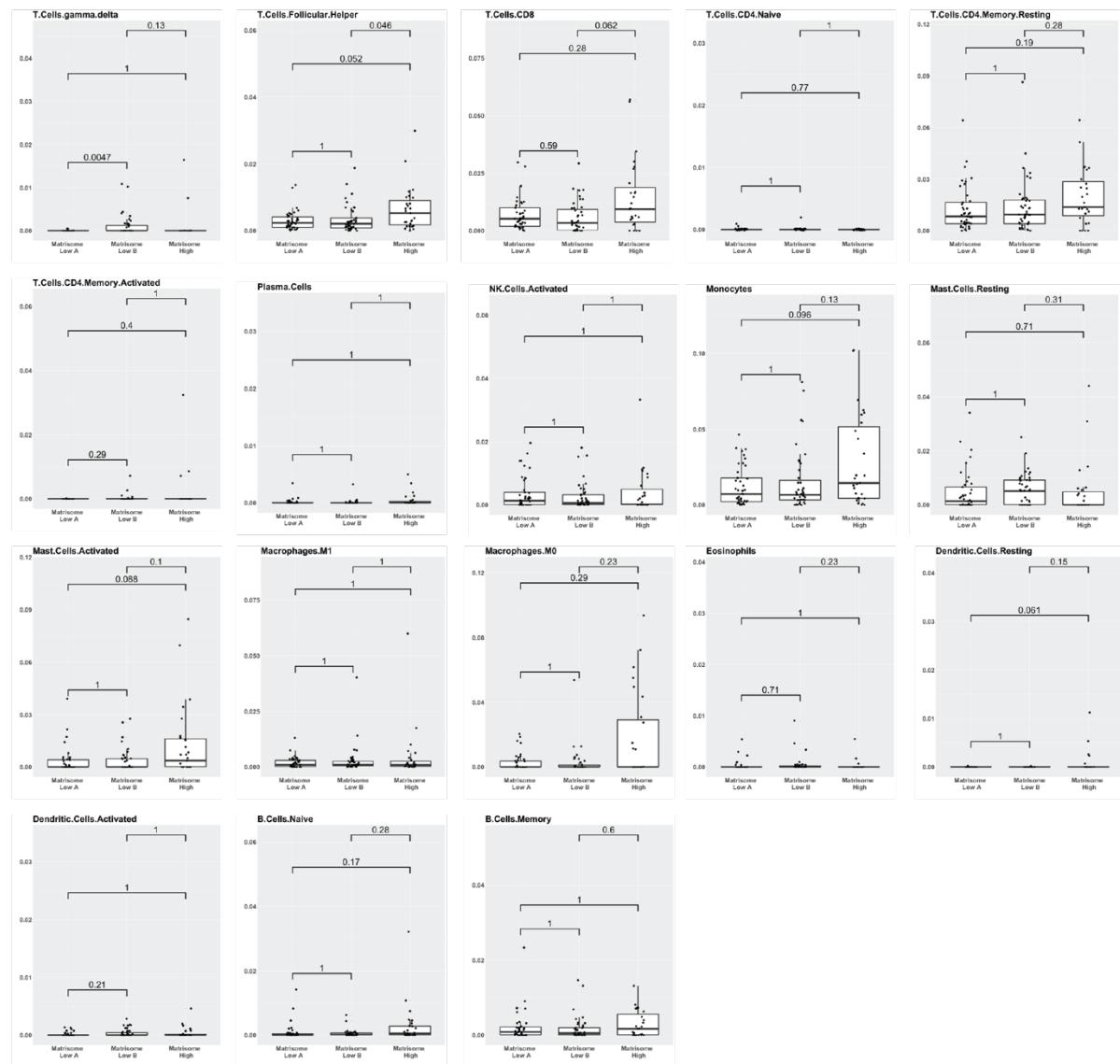


Supplementary Figure 1. The landscape of ECM composition and patient survival in glioblastoma. **A.** Kaplan-Meier analysis comparing overall and progression-free survival of the M-H subgroup with the M-La and M-Lb subgroups merged as M-L. **B.** The complete and untruncated survival curves for analyses in figure 1C and D. All underlying data and statistics are identical. **C.** Kaplan-Meier analysis comparing progression free and overall survival of the M-H subgroup with the M-La and M-Lb subgroups after exclusion of samples annotated with the neural canonical subtype.

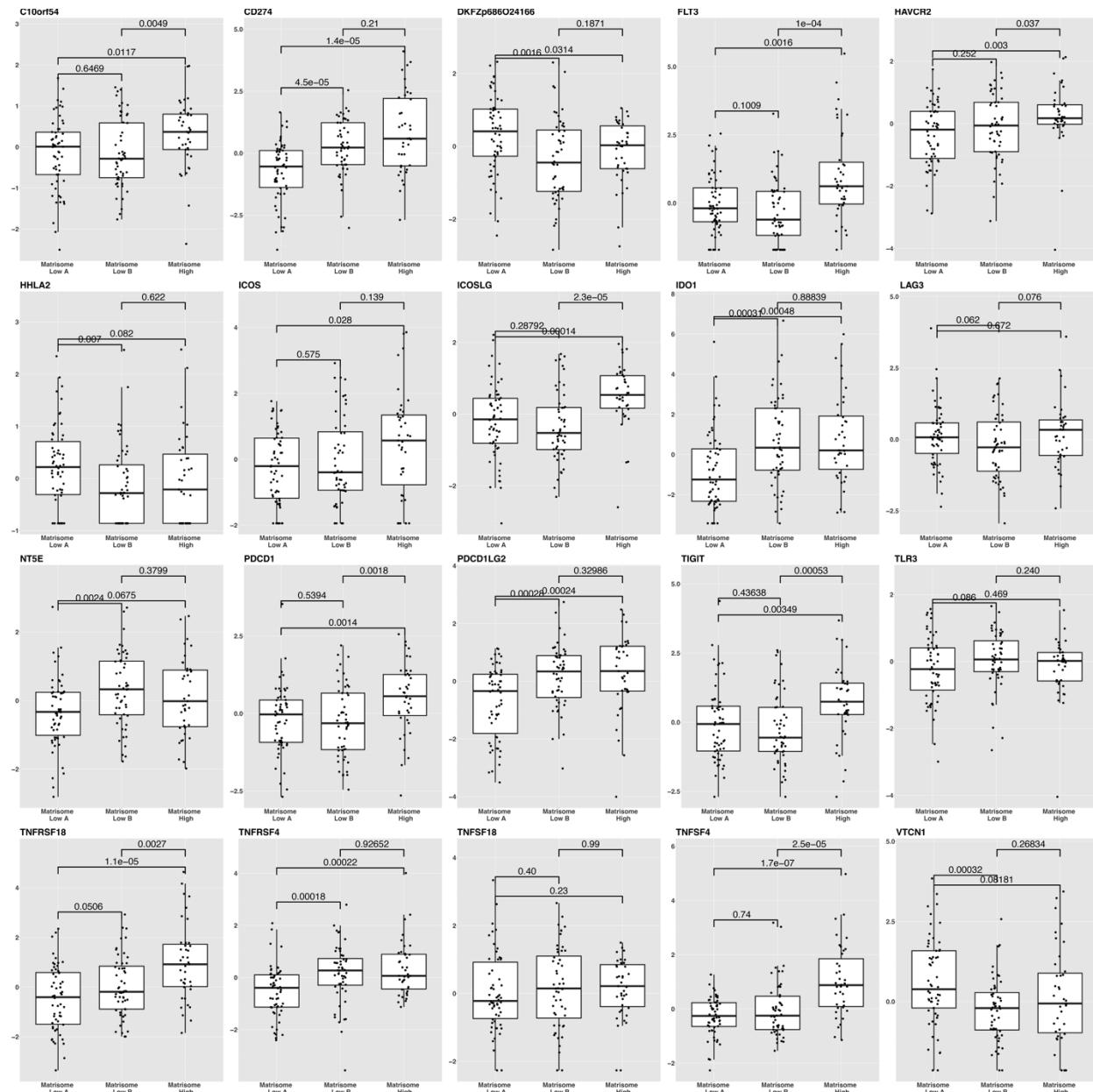


Supplementary Figure 2. The differential multi-omic landscape of matrisome-enrichment in GBM. **A.** Gene set enrichment analysis of each of the clusters in Figure 2B. **B.** The heatmap of phosphoproteomic entities with significant enrichment in M-H vs. M-L groups (top). The phosphroteomics-based pathway score differences between M-H, M-La and M-Lb groups. **C.** The transcriptomic analysis of epithelial signature (see main text figure 2 for the mesenchymal signature).

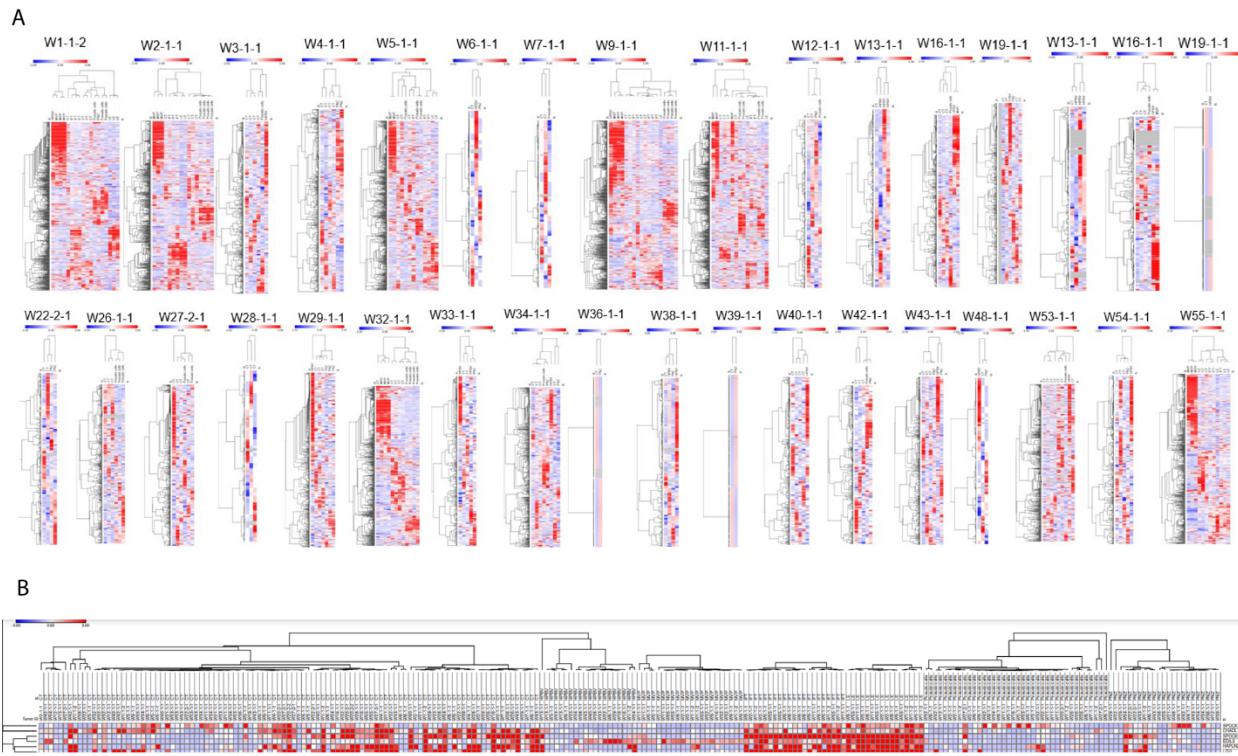
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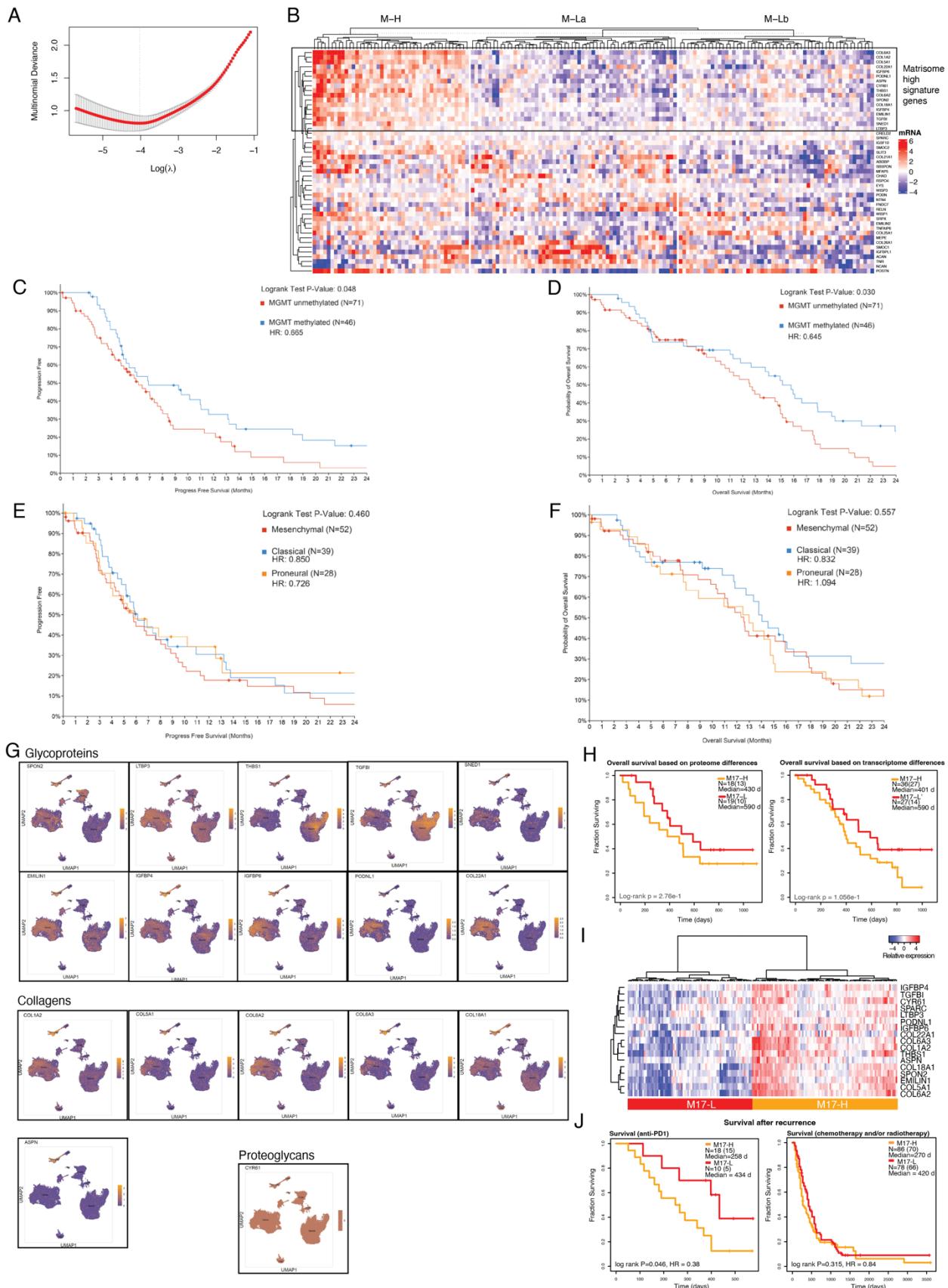
B



Supplementary Figure 3. The GBM tumor-immune interactions across matrisome subtypes. A. CIBERSORT-based analysis of immune cell type enrichment in M-H vs M-La and M-Lb groups. For statistically significant enrichments of cell types and overall immune infiltration, see figure 3A. B. The analysis of immune checkpoint expression in M-H vs M-La and M-Lb groups. For statistically significant enrichment of receptor-ligand pairs, see figure 3B.



Supplementary figure 4. The spatial compartmentalization and heterogeneity of matrisome expression. **A.** Hierarchical clustering analyses performed on multiple regional samples (Total=245 samples) of individual patients ($n=34$) show intratumoral heterogeneity based on anatomical regions. Each heatmap represents an individual patient. **B.** Supervised hierarchical clustering analysis of Oligo cell-type specific CMP genes.



Supplementary figure 5. Predictive matrisome signature and response to immunotherapy.

A. LASSO analysis to identify most discriminate matrisome genes. Multinomial deviance as a function of $\log(\lambda)$ from cross validation. The red dots and error bars represent means and standard deviations. The vertical dotted line indicates the optimal $\log(\lambda)$ where the multinomial deviance is minimal. **B.** Heatmap showing the selected 47 genes with 157 samples from M-H, M-La, and M-Lb subtypes. The black frame emphasizes the 17-gene matrisome signature genes that are elevated in the M-H subtype. **C.** Progression Free Survival of patients stratified based on MGMT promoter methylation status. Unmethylated group serves as the control for Hazard Ratio (HR) calculation. The TCGA cohort that was used in matrisome analysis is categorized based on the MGMT methylation (48 methylated samples from 46 patients, 73 methylated samples from 71 patients, 36 unclassified samples). The survival curves are truncated at 24 months while statistics is based on entire follow up period. **D.** Overall Survival of patients based on MGMT promoter methylation status. **E.** Progression Free Survival of patients stratified based on canonical (mesenchymal, proneural, classical) GBM subtypes. Mesenchymal group serves as the control for Hazard Ratio (HR) calculation. The TCGA cohort that was used in matrisome analysis is categorized based on the canonical subtypes. The survival curves are truncated at 24 months while statistics is based on entire follow up period. **F.** Overall survival of patients stratified based on canonical GBM subtypes. **G.** The single cell transcriptomic distribution of the genes across cell types in the matrisome signature as demonstrated through UMAP analysis. **H.** The overall survival of patients (Source: CPTAC, Wang et al, 2021) stratified as M-H' vs. M-L' based on the 17-gene matrisome protein (left) and mRNA (right) expression signature. **I.** The matrisome gene expression analysis of patients with recurrent/resectable GBM tumors not treated with anti-PD1 therapy (source: GLASS consortium repository, N=165). **J.** “The recurrence to death” survival period for patients treated with anti-PD1 therapy (left) and chemo/radiation therapy (GLASS consortium) (right).