COMPARATIVE ANALYSIS OF AGING AND SENESCENCE-RELATED MOLECULAR SIGNATURES IN YOUNG AND ELDERLY GLIOBLASTOMA PATIENTS

Gravina, T.; [1,2] Favero, F.; [1,2] Centonze, S.; [1,2] Orso, F.; [1] Pelicci, G.; [1,3] and Corà, D. [1,2]

(1) Department of Translational Medicine, University of Piemonte Orientale, 28100 Novara, Italy.
(2) Center for Translational Research on Allergic and Autoimmune Diseases (CAAD), University of PiemonteOrientale, 28100 Novara, Italy.
(3) Department of Experimental Oncology, European Institute of Oncology (IEO), IRCCS, Milan 20139, Italy.

SUMMARY

Glioblastoma (GBM) is a highly malignant and fatal type of adult diffuse glioma that originates from neuroglial progenitor cells, and it has a remarkable ability to infiltrate normal brain parenchyma. Despite being a rare tumor, it is the most common Central Nervous System (CNS) malignancy. The median age at diagnosis is 65 years, indicating that GBM predominantly affects older adults, although rare cases also occur in younger individuals. In this study, we present a bioinformatics analysis aimed at identifying differences between younger and older GBM patient groups by analyzing RNA-Seq data and metadata from the TCGA cohort, as reported by Wang et al. (2021).

METHODS
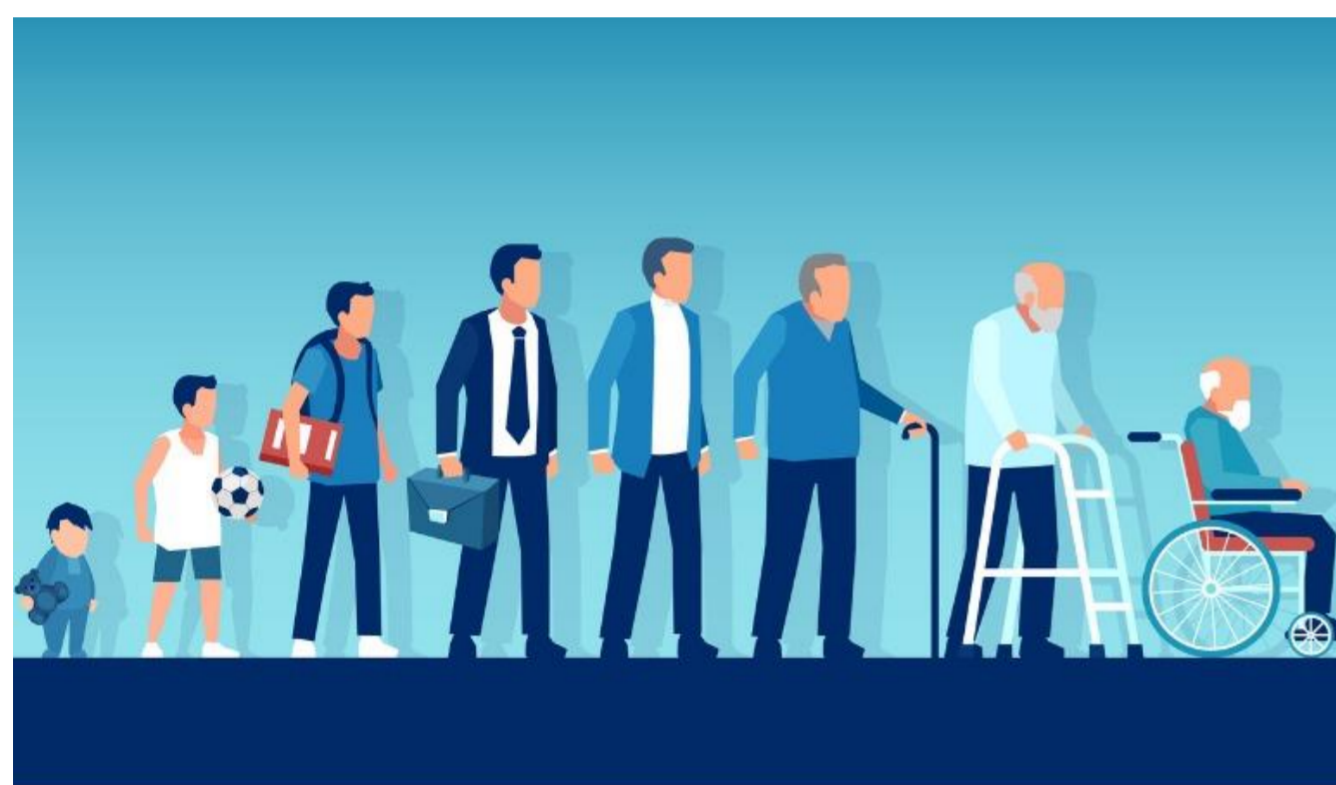
**Wang et al. (2021)
RNA- Seq**

**10 young patients
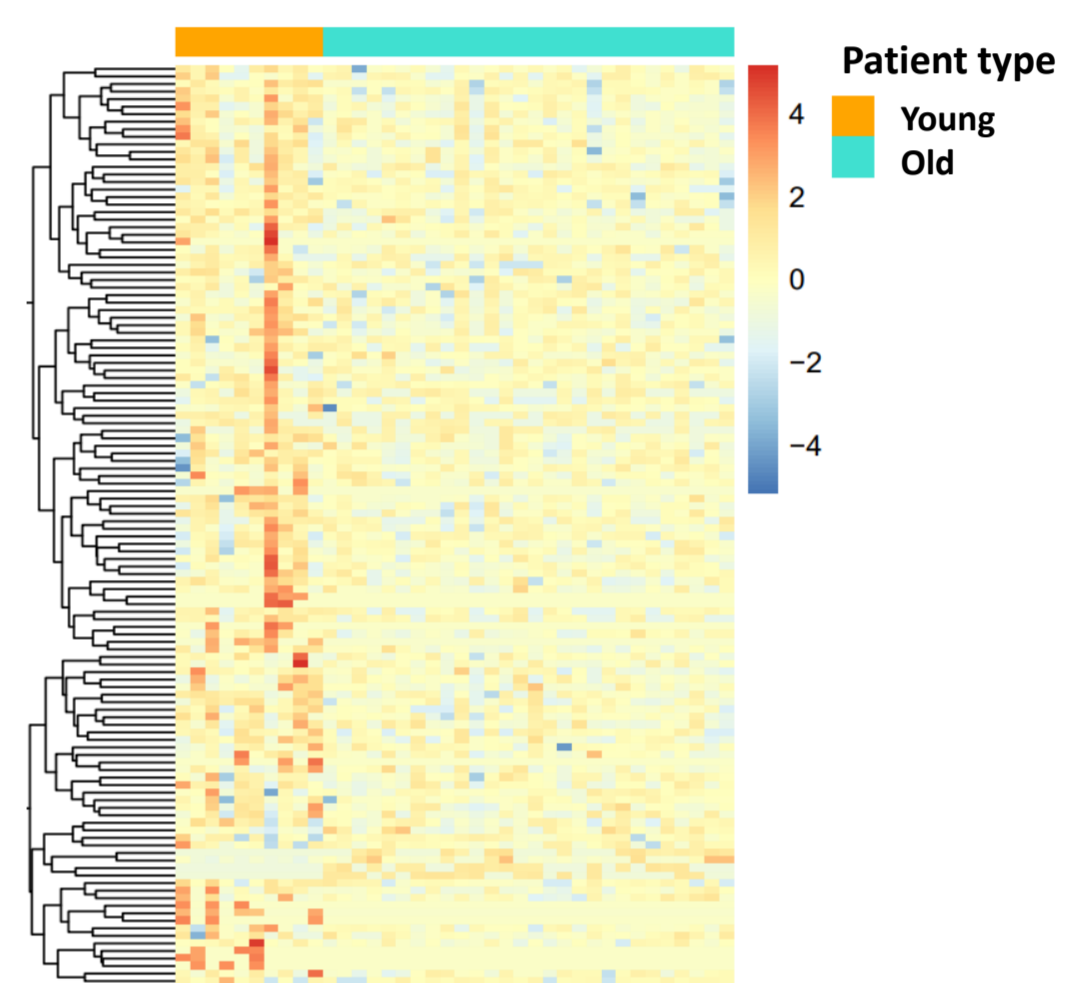(<40 years)**

**28 old patients
(>65 years)**

**DEGs analysis (Young vs Old):
edgeR with
|log2FC| > 1.5 and FDR < 0.05**

121 upregulated genes

5 downregulated genes

RNA-Seq data matrix from Wang et al. 2021

**Gene Set Enrichment Analysis (GSEA)
considering aging (https://agingsignature.webhosting.rug.nl) and
senescence (SAUL_SEN - GSEA M45803) signatures.
(Young vs Old; NES >1; FDR < 0.05)**
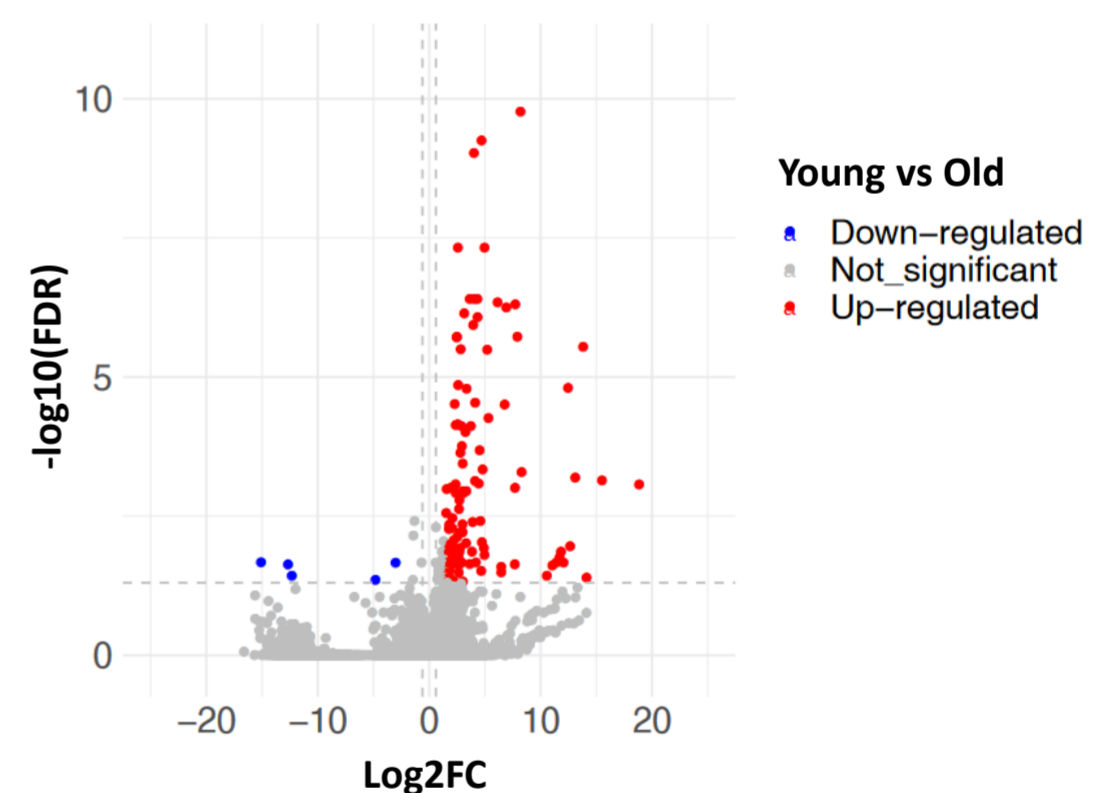
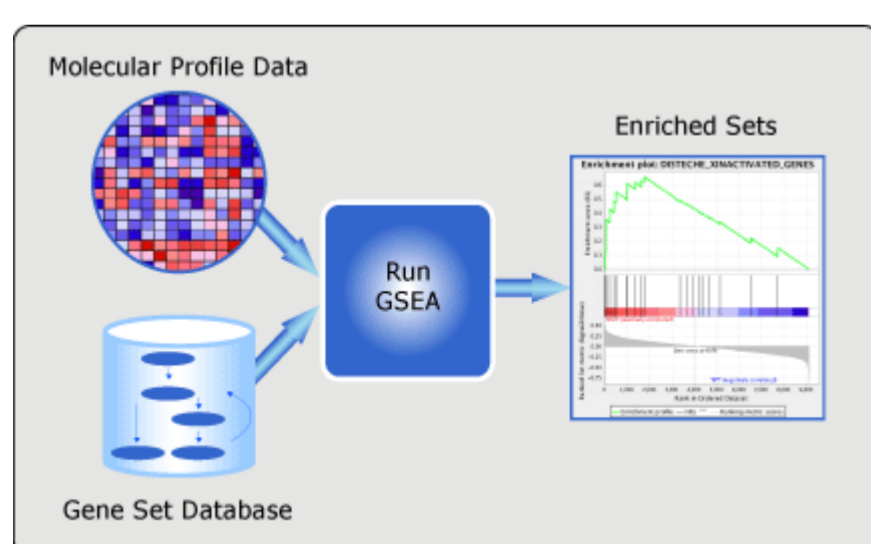## RESULTS

Differentially expressed genes (DEGs)

Heatmap showing the unsupervised hierarchical clustering of 126 DEGs (Young vs Old)

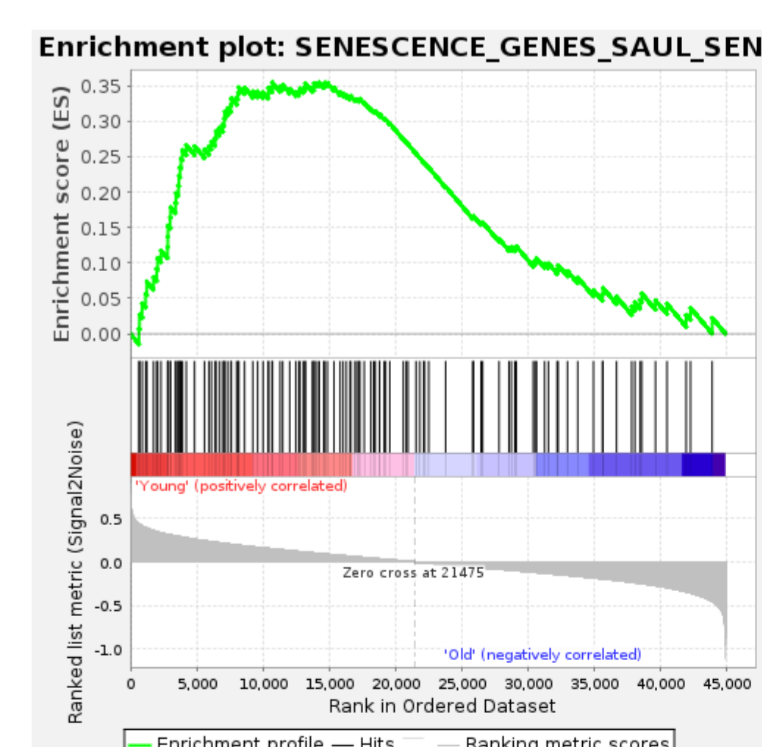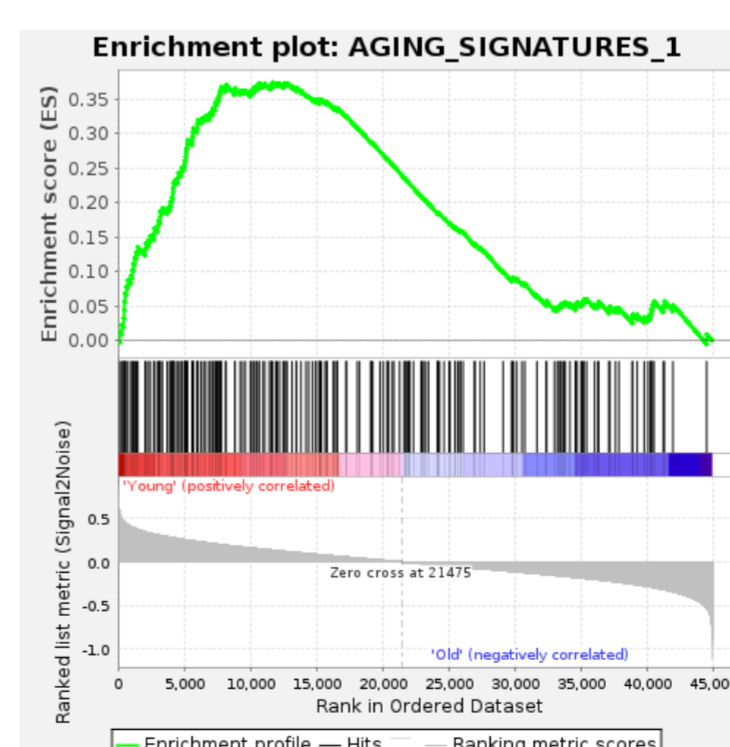**Volcano plot with 121 upregulated genes and 5 downregulated genes**

GSEA results

REFERENCE:
Wang, L. B., Karpova, A., Gritsenko, M. A., Kyle, J. E., Cao, S., Li, Y., Rykunov, D., Colaprico, A., Rothstein, J. H., Hong, R., Stathias, V., Cornwell, M., Petralia, F., Wu, Y., Reva, B., Krug, K., Pugliese, P., Kawaler, E., Olsen, L. K., Liang, W. W., ... Clinical Proteomic Tumor Analysis Consortium (2021). Proteogenomic andmetabolomic characterization of human glioblastoma. Cancer cell, 39(4), 509–528.e20

UPO AGING PROJECT
UNIVERSITÀ DEL PIEMONTE ORIENTALE