

# Age-Specific Survival and Molecular Signatures of Glioblastoma Multiforme: Analysis of Clinical and Large-Scale Transcriptomic Data from The Cancer Genome Atlas (TCGA)

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## INTRODUCTION

- Glioblastoma multiforme (GBM) is the most common malignant brain tumor and carries a poor prognosis
- Despite aggressive multimodality treatment, the median survival is approximately 18-20 months, depending on molecular subgroups
- While it's known that older adults with GBM have a worse prognosis compared to younger patients, the precise molecular mechanism(s) and key mediator(s) of this aging-related phenomenon remain largely unknown

## OBJECTIVE

The present study was conducted to evaluate age-specific survival and molecular signatures of GBM in a large national cancer registry

## MATERIALS AND METHODS

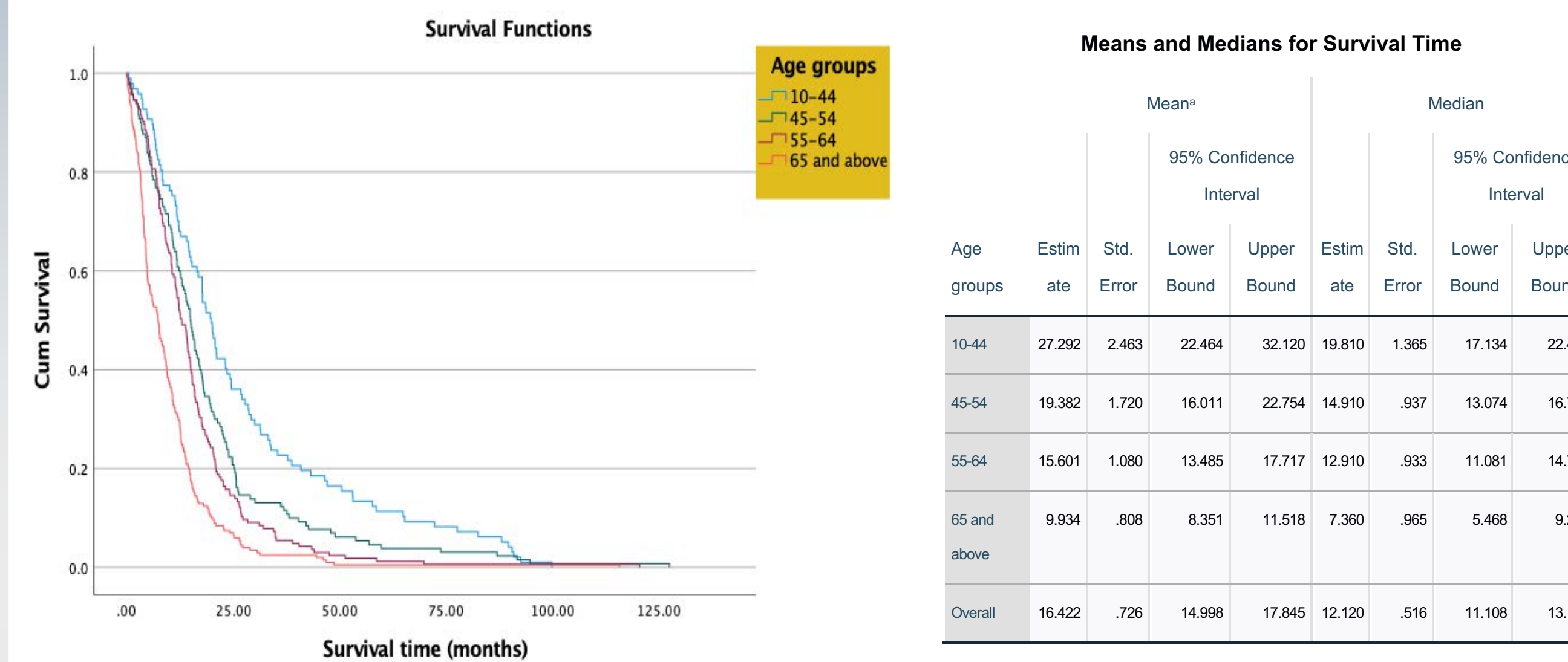
- We extracted data of 593 primary GBM patients from The Cancer Genome Atlas (TCGA) ([www.cancergenome.nih.gov](http://www.cancergenome.nih.gov))
- The data included age at diagnosis, treatment (surgical versus non-surgical), outcome (deceased versus living), survival time, Karnofsky performance score (KPS), and gene expression profile based on RNA-Sequencing (RNA-Seq) data

- For analysis, the study data was distributed into four age groups (10-44 years, 45-54 years, 55-64 years, and  $\geq 65$  years of age)

- Age-related survival and molecular signatures were identified via Kaplan-Meier survival analysis and mutational profiling

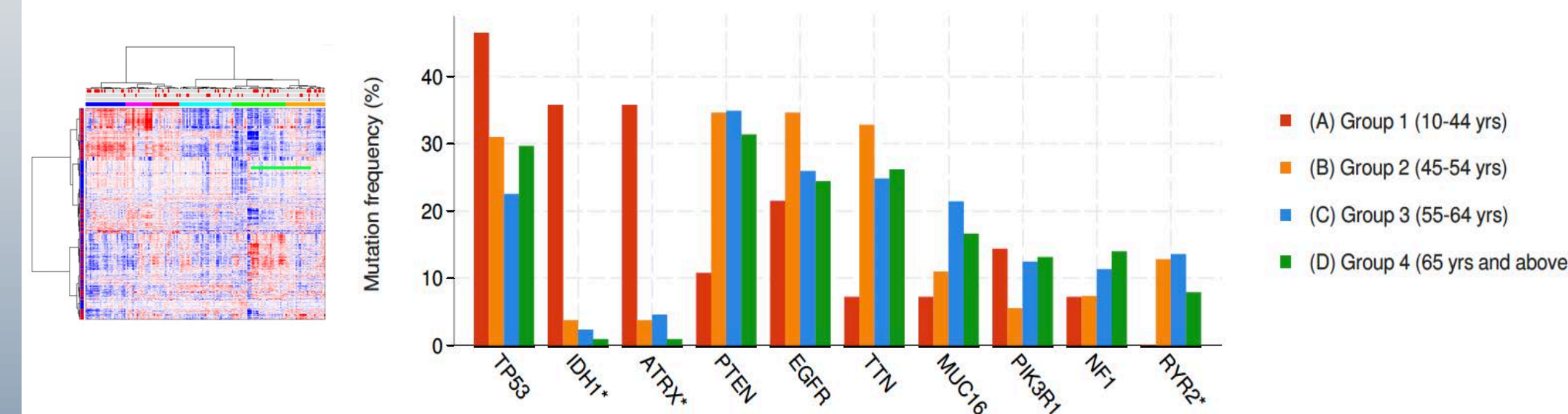
## RESULTS

### 1. Age-specific survival in GBM patients



Kaplan-Meier analysis revealed a significantly decreased survival with advancing age (log rank test,  $p < 0.0001$ ; Breslow test,  $p < 0.000$ )

### 3. RNA-Seq demonstrates differences between the four cohorts in the mutational profile of ten most mutated genes in GBM biopsies



## SUMMARY & CONCLUSIONS

- Age-specific survival analysis and RNA-Seq profiling identifies a sub-set of genes more commonly mutated in older GBM patients with shorter survival time
- Further characterization of the molecular signatures associated with aging in GBM patients will help identify mechanisms that contribute to GBM severity in this age group and may also lead to identification of potential therapeutic targets

### 2. Clinical and molecular profile of study data

