Relative expression of the MRPS18 family genes in glioblastomas

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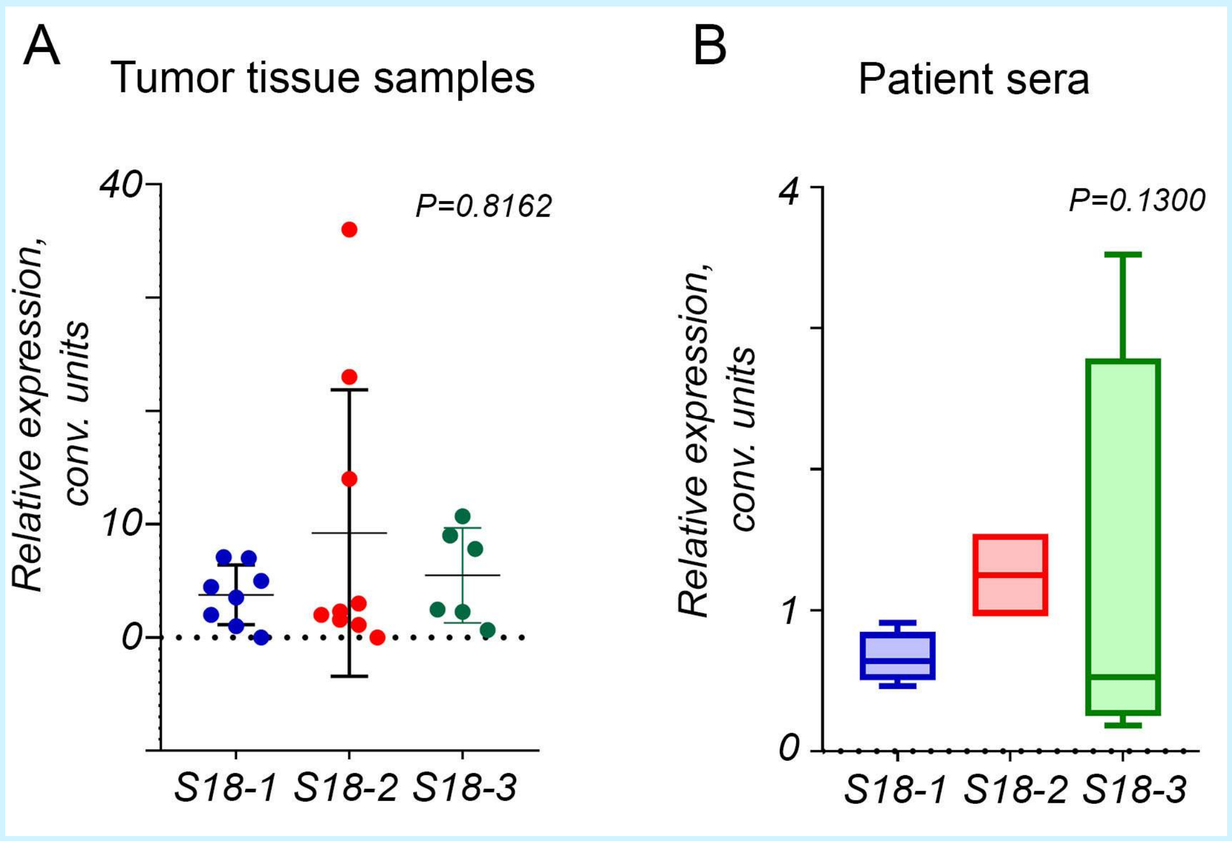
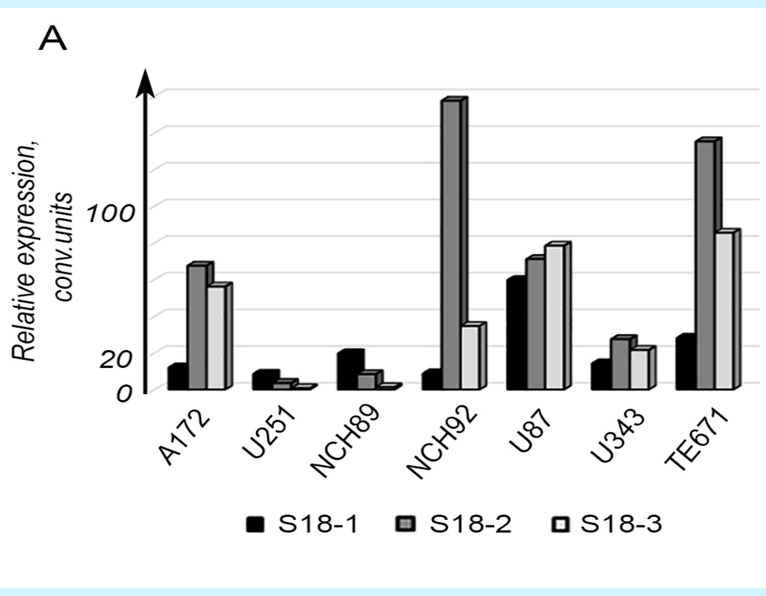
Background: The three mitochondrial ribosomal proteins S18 (MRPS18-1-3) form a family. The proteins show low homology to each other and might play different roles in cancerogenesis (Mushtaq M., et al., Oncotarget, 2016). Taking into consideration the crucial role of MRPS18-2 in tumor development, it is important, to study an expression pattern of other two family members in various cancer types.

Aim: to compare relative expression levels of the S18 family genes in glioblastoma patients, in both, tumor tissue samples and in blood sera, and in established glioma cell lines as well.

Materials and methods: the tissue and blood serum of nine patients with glioblastoma of the brain; 2 cell lines, obtained from glioblastoma, 2 cell lines, produced from astrocytoma, 2 primary cultures of glioblastoma, and the rhabdomyosarcoma cell line. RNA isolation from the tissue and serum, a quantitative PCR (qPCR) analysis, a bioinformatic analysis of the publicly available data bases on expression. All experiments on human samples were performed, according to the Declaration of Helsinki.

The MRPS18 family genes demonstrated various expression patterns in glioblastomas and in glioma cell lines.





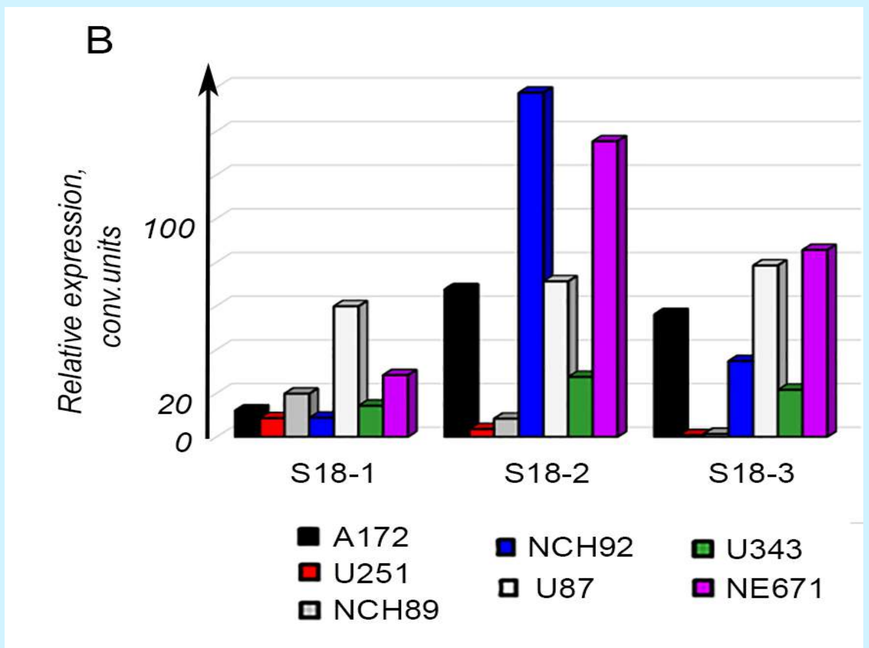
The relative expression of the *MRPS18-2* gene at mRNA and protein levels was the highest, compared to other two family members.

In glioblastoma patient sera the highest expression levels was detected for the *MRPS18-3* gene.

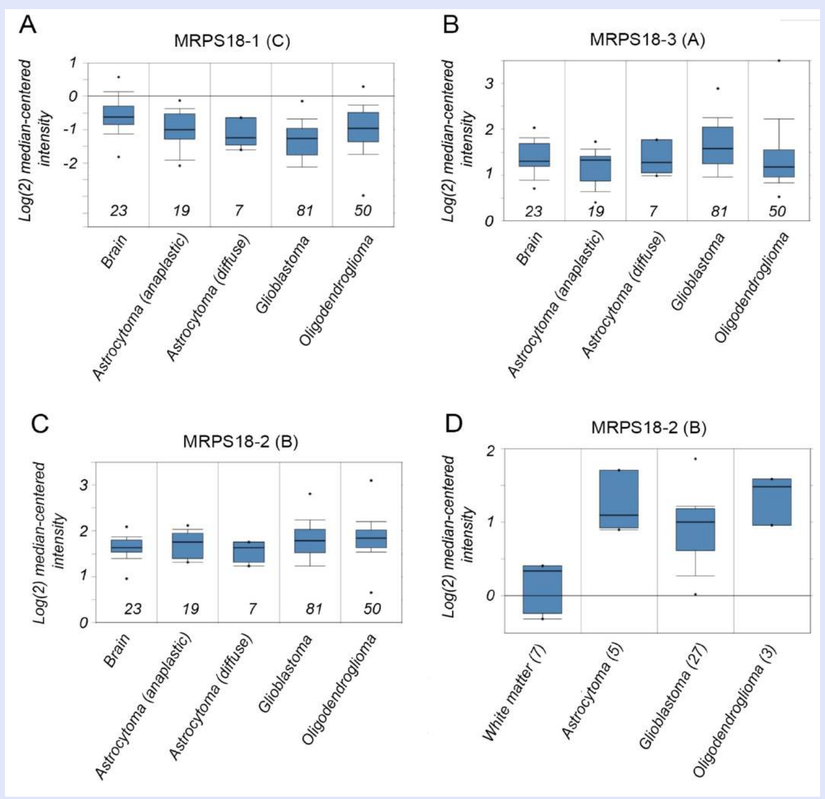
The relative expression of all MRPS18 family genes in patient sera was one magnitude lower, than in tissue.

The cell lines: A172, U87, produced from glioblastoma; U251, produced from astrocytoma and U343, sub-clone of U251, selected in vitro; NCH89 and NCH92, low passage glioblastoma culture; TE671, rhabdomyosarcoma.

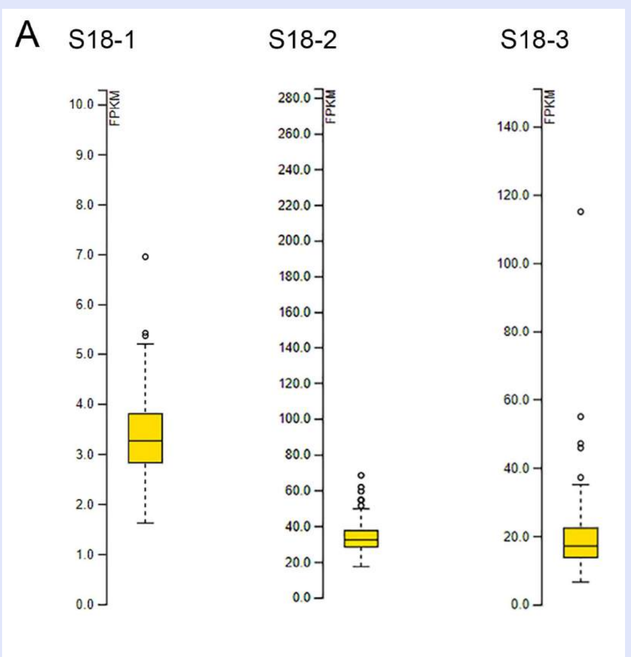
All cells were from a Cell bank at R.E. Kavetsky IEPOR.

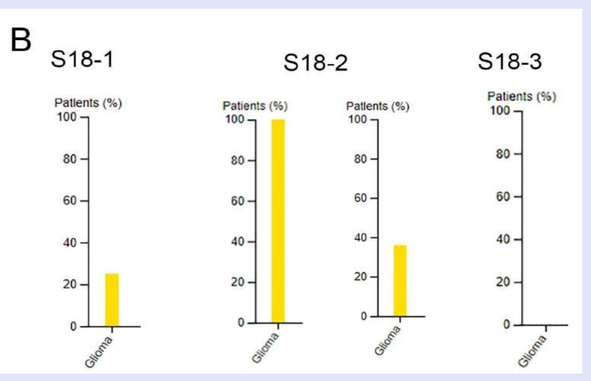


The bioinformatic analysis of the data deposited to Oncomine and Protein Atlas portals, corroborated our experimental results.



A bioinformatic analysis on expression of S18 family genes was performed, using the data deposited to a portal Oncomine. The highest expression was found for *S18-2* and *S18-3* genes, while *S18-1* was almost undetectable.





The bioinformatic analysis of expression of S18 family genes at mRNA and protein levels on a platform Protein Atlas revealed that S18-2 and S18-3 are highly expressed in gliomas, according to the data of RNA sequencing.

Conclusions: The relative expression level of the *MRPS18-2* gene is high in glioblastoma tumor tissues and glioma-derived cell lines, compared to other two members of the MRPS18 family. A larger cohort of glioblastoma patients should be studied, to confirm these preliminary data.

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