

Supplementary statistical analysis

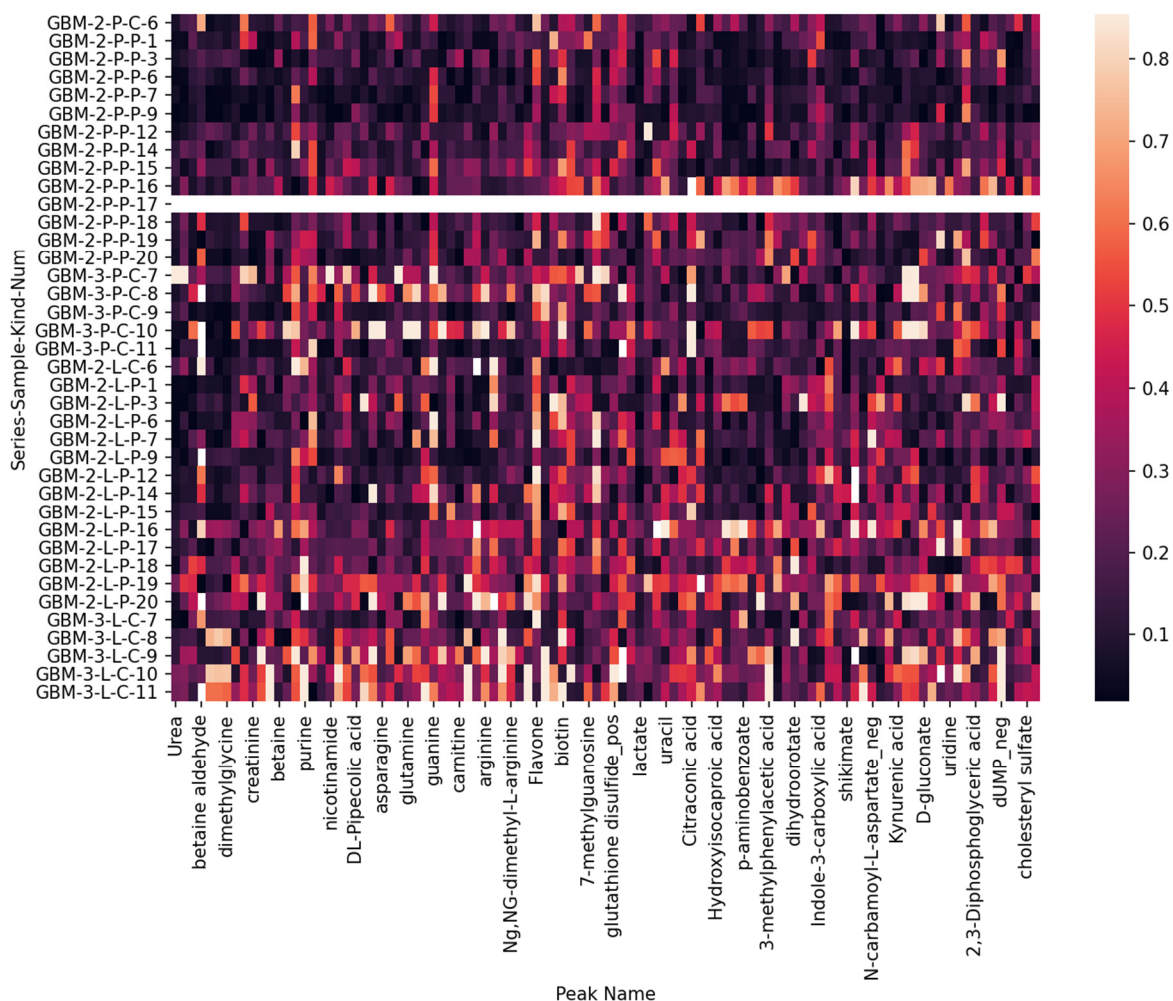


Figure S1. Relative variation of metabolite levels over three experimental replicas. The notations of the rows (vertical axis) correspond to the individuals (patients and control), those of the columns (horizontal axis) to the metabolites, respectively. Individual code is composed of internal identifier (GBM-X), plasma or CSF (P or L), patient or control (P or C) and positional number.

To illustrate variation of metabolites levels over the three measurements replicas the corresponding score was calculated. Standard deviation of a metabolite level divided to its mean was depicted on Figure S1. The score for the 17th patient's plasma sample is absent as only one replica was done in its case. Mean values were calculated without missing values.

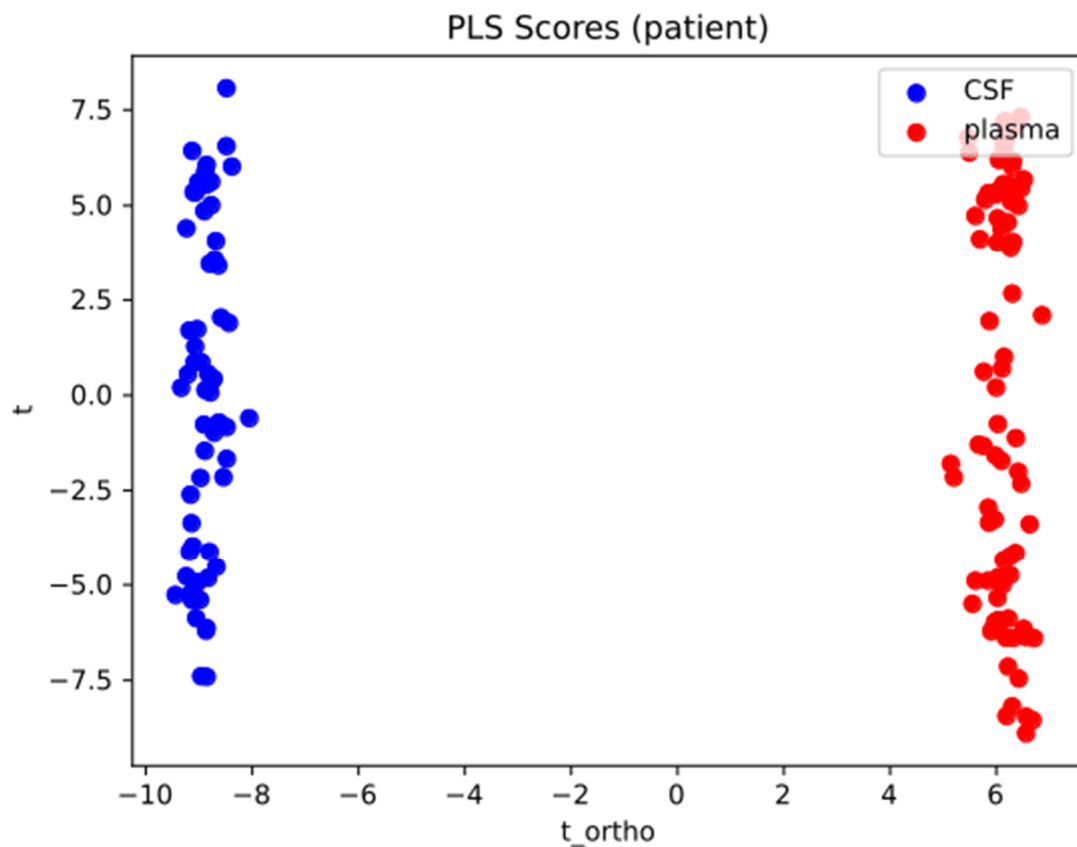


Figure S2. OPLS-DA separation of plasma samples from CSF ones.

OPLS-DA was conducted to better separate between groups of samples studied (see Fig. S2 and S3). When cross-validating this separation between patients and control ones via stratified 10-fold validation 129 metabolites were found significant ($p < 0.05$). Similar analysis for separation between plasma and CSF samples 138 metabolites were found to be significant ($p < 0.05$) discriminants.

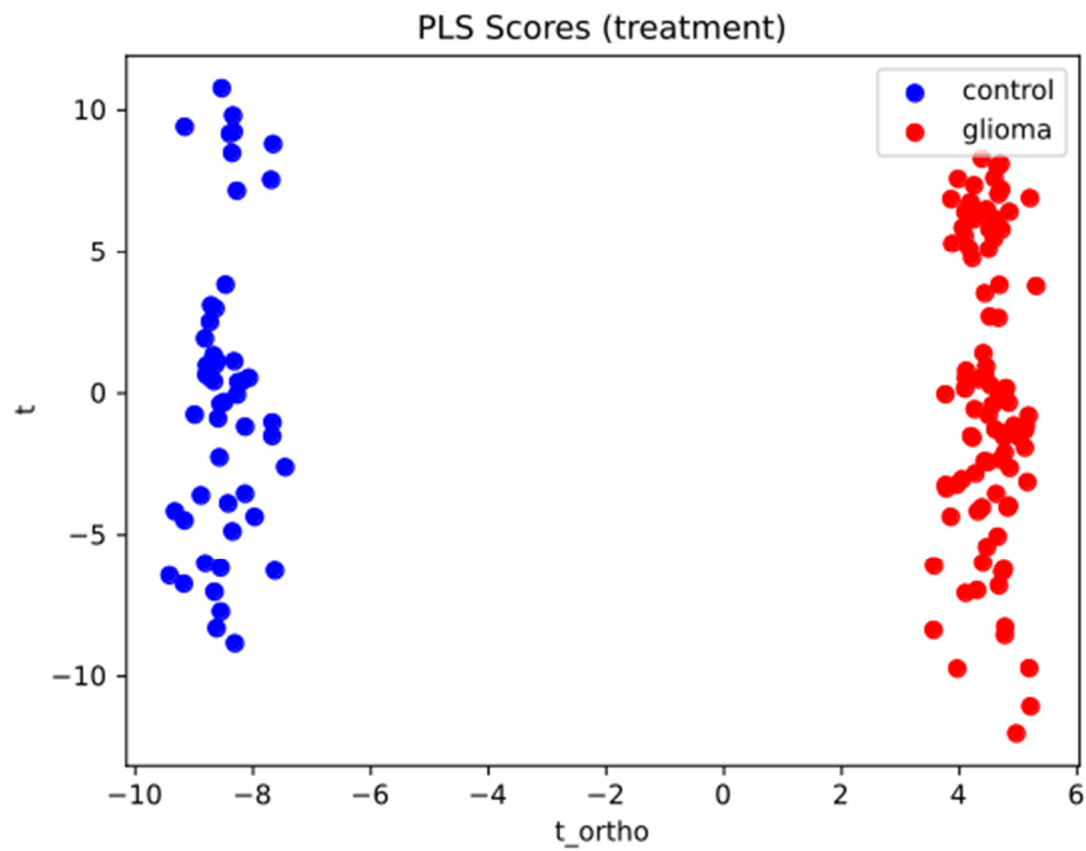


Figure S3. OPLS-DA separation of glioma patients from control ones.

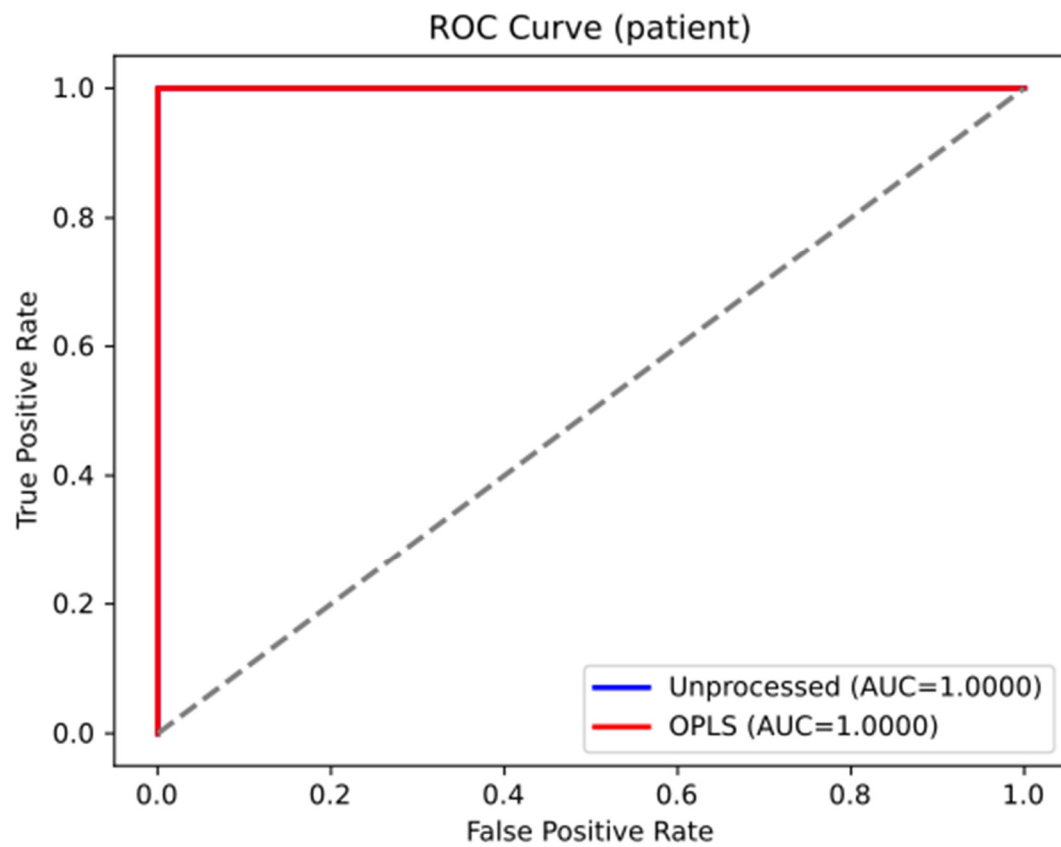


Figure S4. ROC curves for PLS-DA (blue) and OPLS-DA (red) cross-validation of separation between plasma and CSF samples.

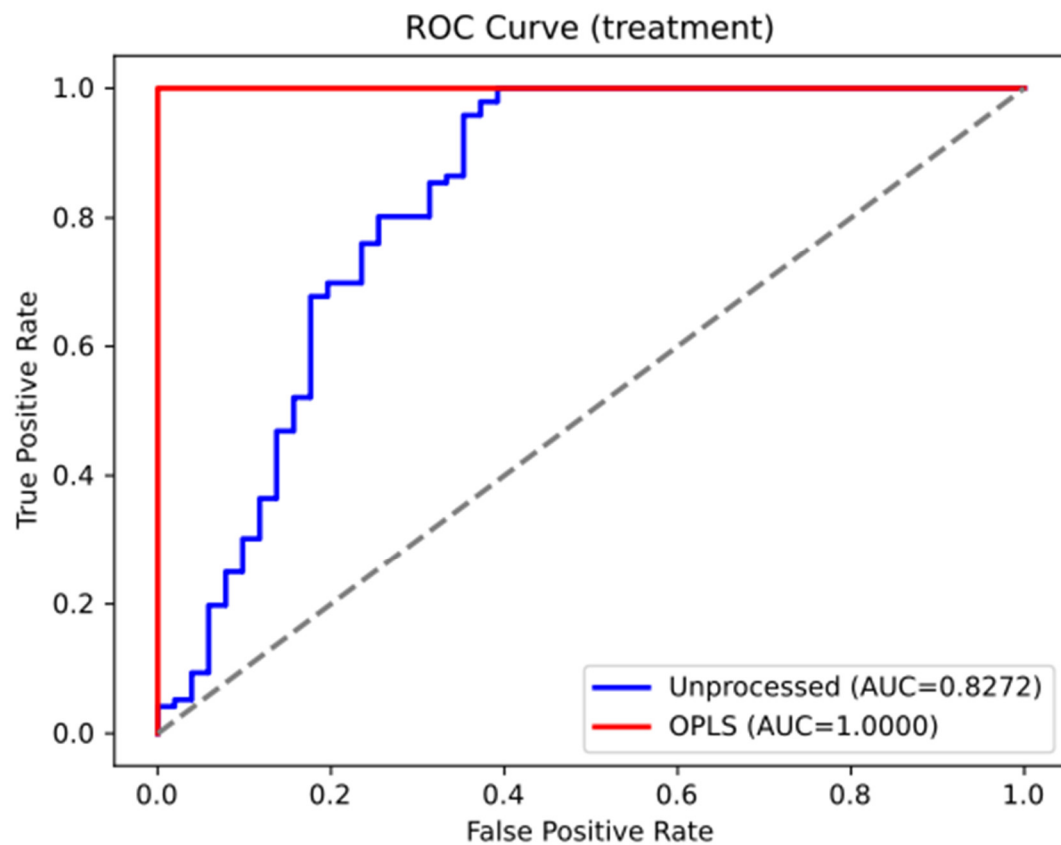


Figure S5. ROC curves for PLS-DA (blue) and OPLS-DA (red) cross-validation of separation between glioma patients and control.

Corresponding ROC curves were shown on Figures S4 and S5.

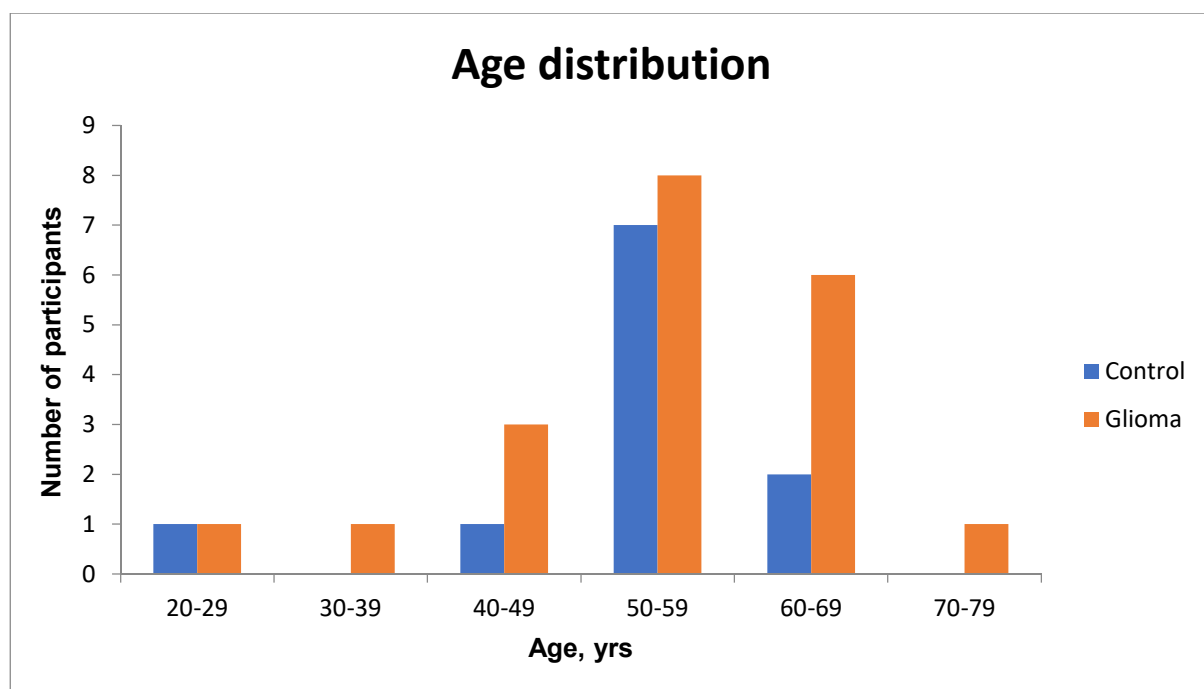


Figure S6. Participants' age distribution.