

Potential Neuroprotective Mechanisms of Methamphetamine Treatment in Traumatic Brain Injury Defined by Large-Scale IonStar-Based Quantitative Proteomics

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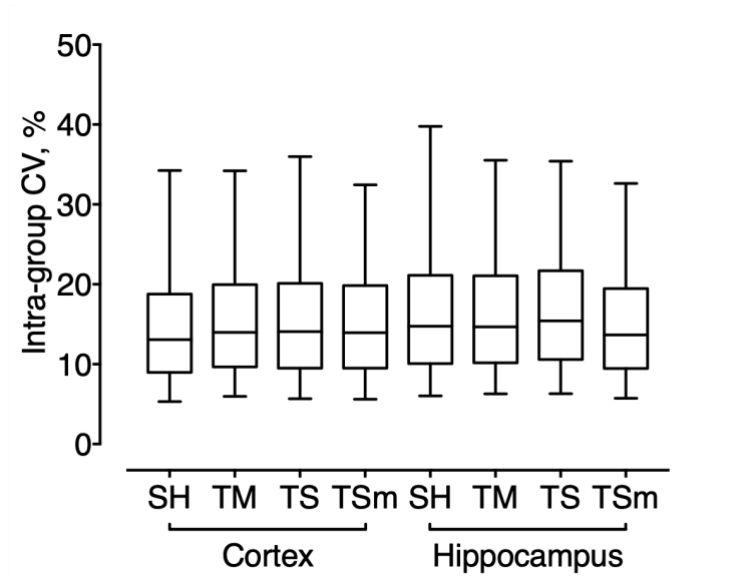
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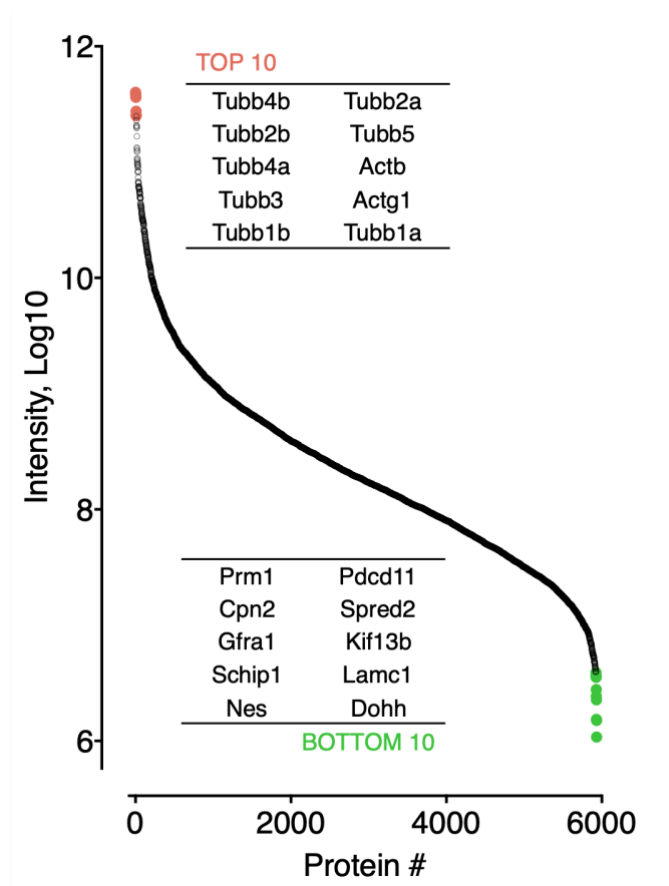
Supplementary Materials

Supplementary Figure S1 – S5.

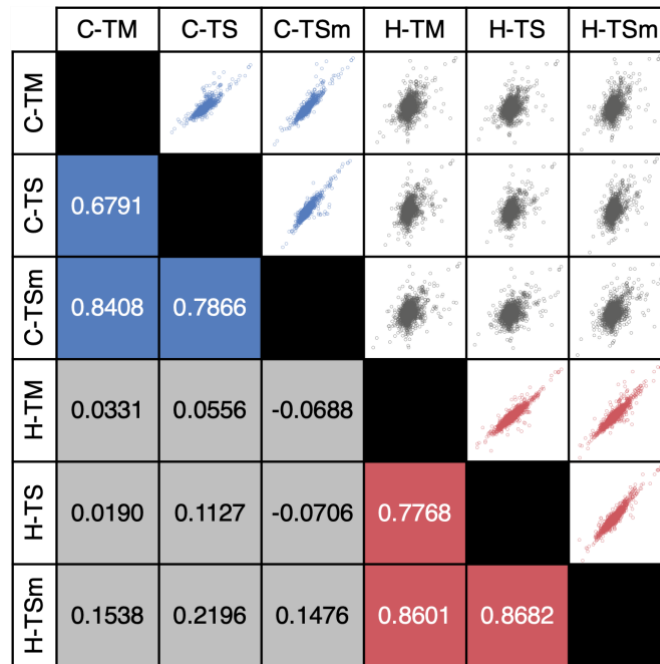
Supplementary Table S1 – S4.



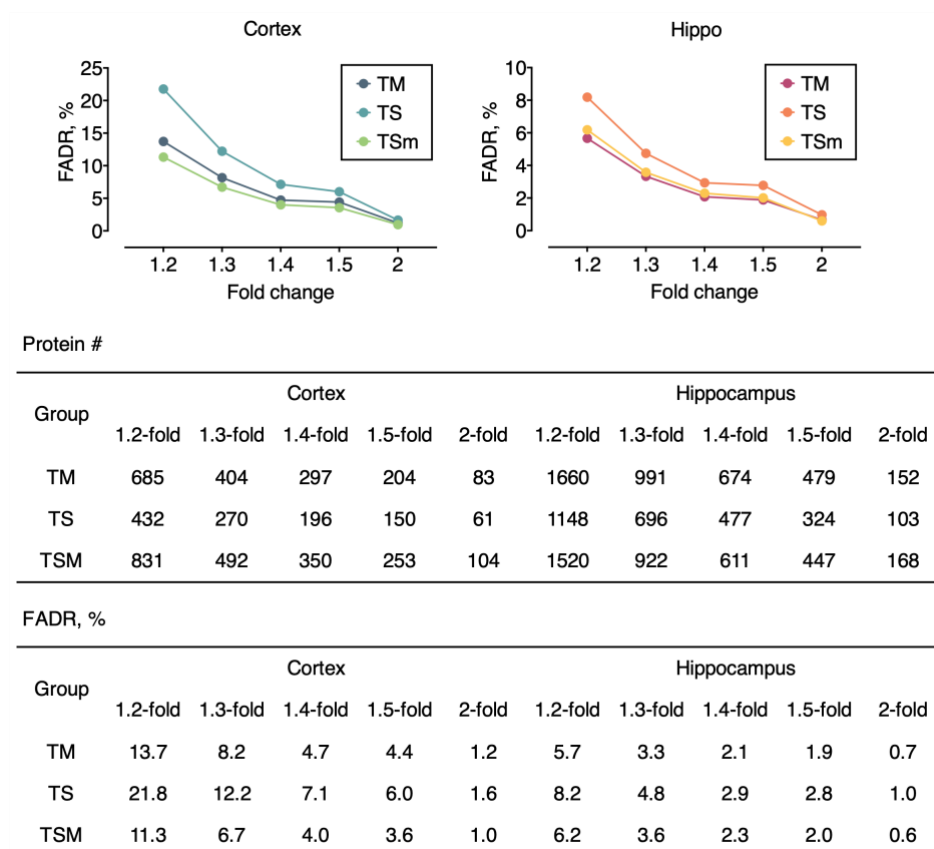
Supplementary Figure S1. Intra-group coefficient of variation (CV) of biological replicates from cortex and hippocampus.



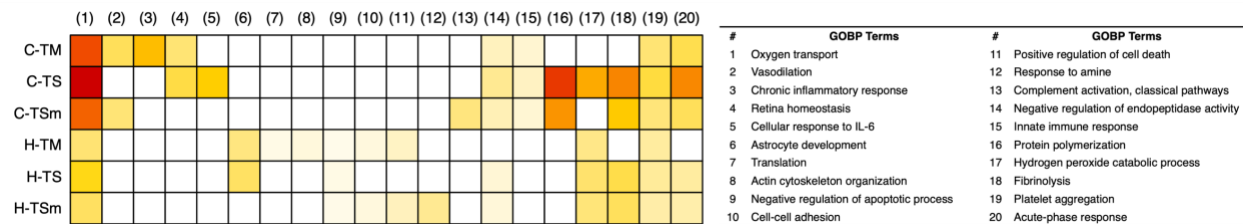
Supplementary Figure S2. Abundance rank of proteins quantified in the study. Proteins with the highest (TOP10) and lowest (BOTTOM10) abundances are highlighted.



Supplementary Figure S3. R-squared values from Pearson correlation of protein ratios (compared to the SH group).



Supplementary Figure S4. Optimization of protein fold change (FC) thresholds for determining altered proteins (APs) using an Experimental Null (EN) method. 1.4-fold protein FC was selected based on the consideration to control False Altered-protein Discovery Rate (FADR) low and obtain a reasonable number of APs.



Supplementary Figure S5. Gene Ontology Biological Processes (GOBP) enriched from APs using DAVID.

Supplementary Table S1. Quantification results of rat cortical tissues.

Supplementary Table S2. Quantification results of rat hippocampal tissues.

Supplementary Table S3. Altered proteins (APs) of rat cortical tissues and classification results.

Supplementary Table S4. Altered proteins (APs) of rat hippocampal tissues and classification results.

****All Supplementary Tables are provided as separate Excel files.**