# SUPPLEMENTAL FIGURES- PROTEOMICS

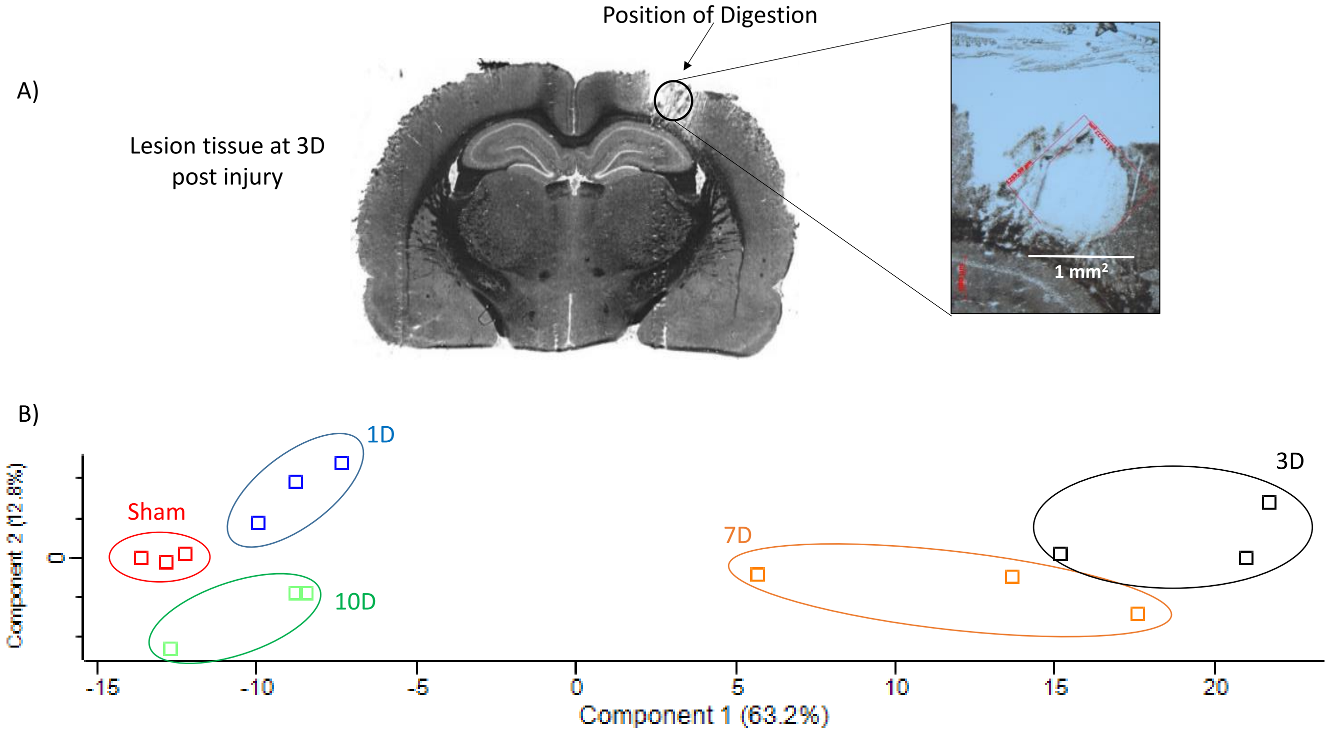

**Figure S1:** A) Optical image of lesion segment at 3 days post injury along with a zoom image of the area of tryptic digestion and peptide extraction. B) Principal component analysis showing the first two components (1 and 2) of the spatially-resolved microproteomics analysis for all three replicates of each of the following: sham, 1D, 3D, 7D, and 10D post injury.

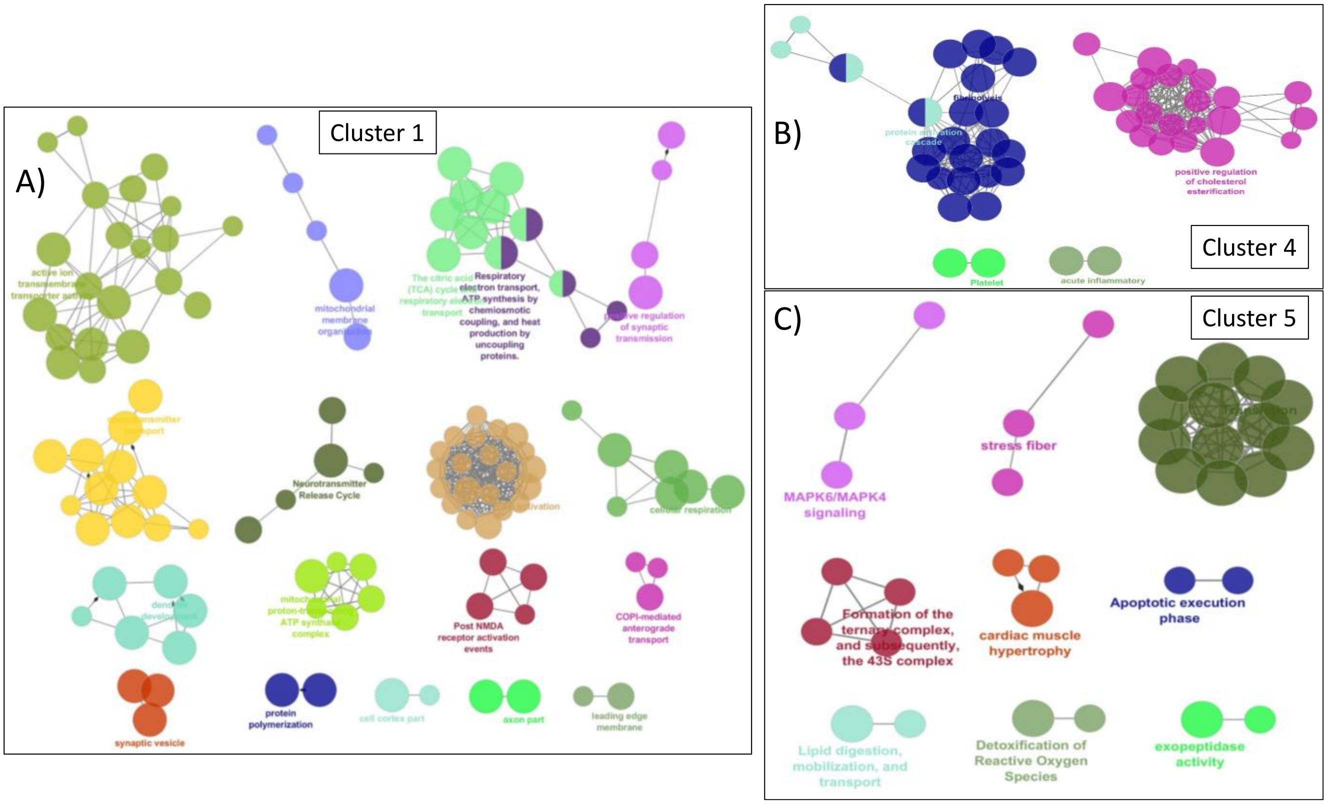

**Figure S2:** A) ClueGo terms involved in proteins over-expressed in cluster 1. B) ClueGo terms involved in proteins over-expressed in cluster 4. C) ClueGo terms involved in proteins over-expressed in cluster 5.

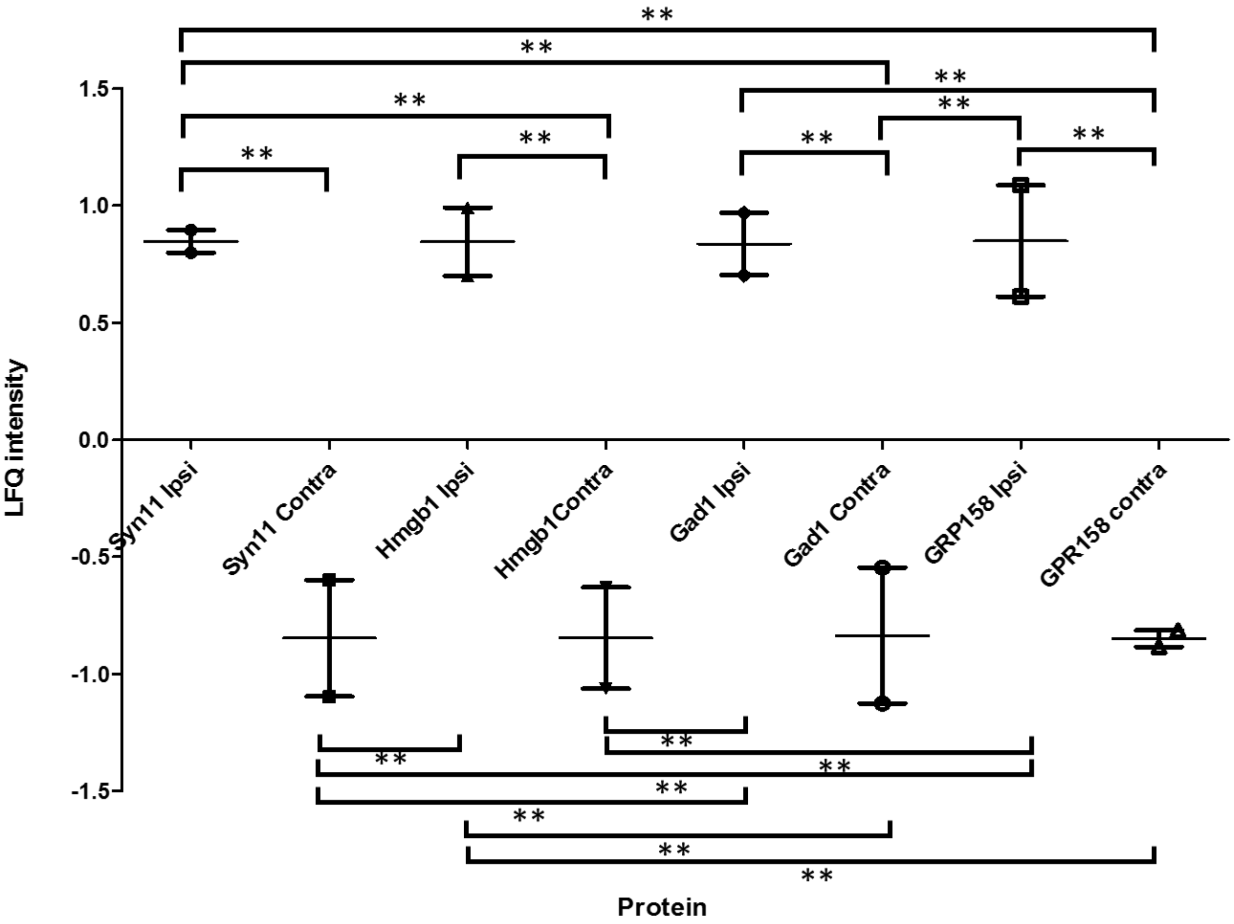

**Figure S3.** From LFQ data, quantitative expression level of 4 different proteins upregulated in SN ipsilateral (Syn11, HMGB1, Gad1, and GPR158), is represented when compared to the contralateral substantia nigra, along with the significant values with a threshold of < 0.05 (**).

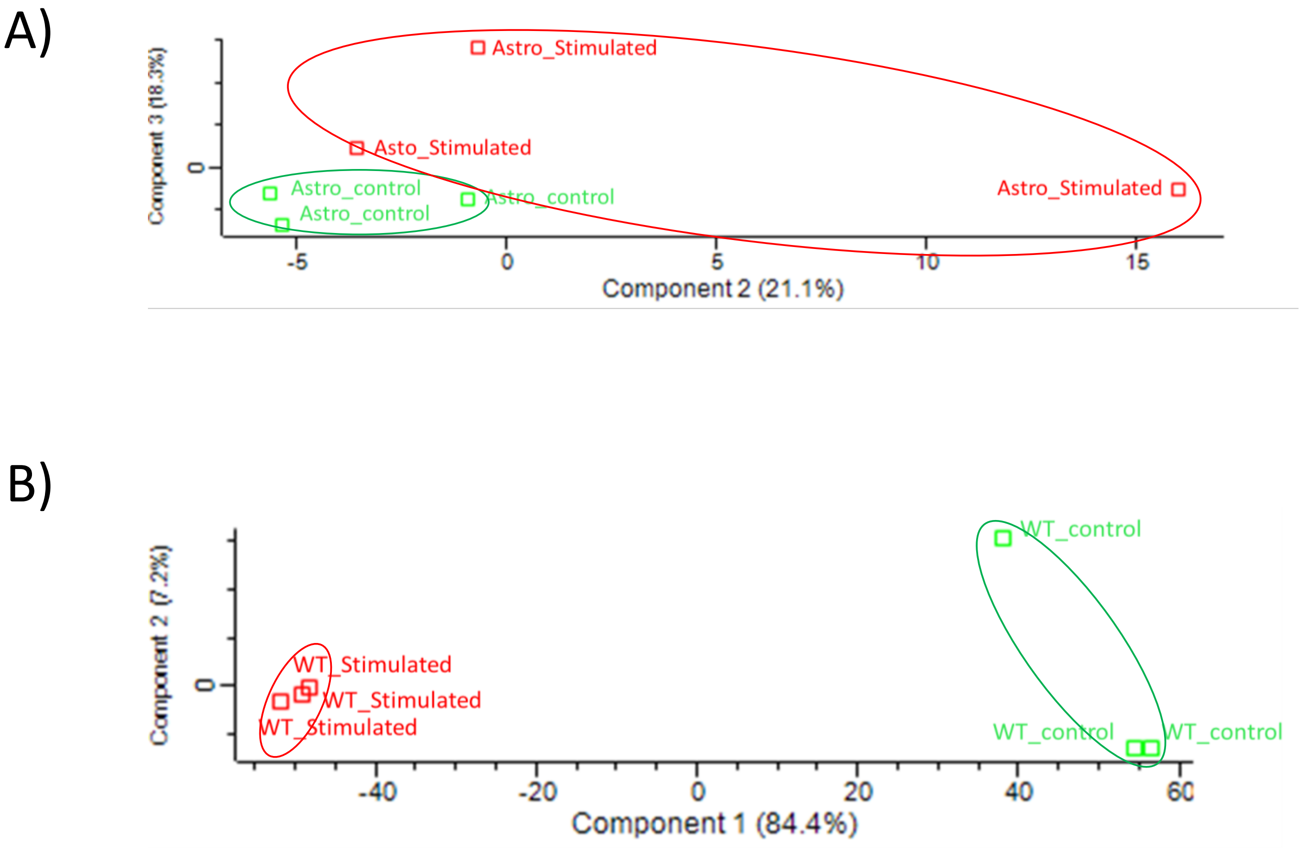

**Figure S4:** Principle Component analysis of identified proteins between the palmitoylcarnitine stimulated condition or not in A) astrocytes and B) Macrophages.

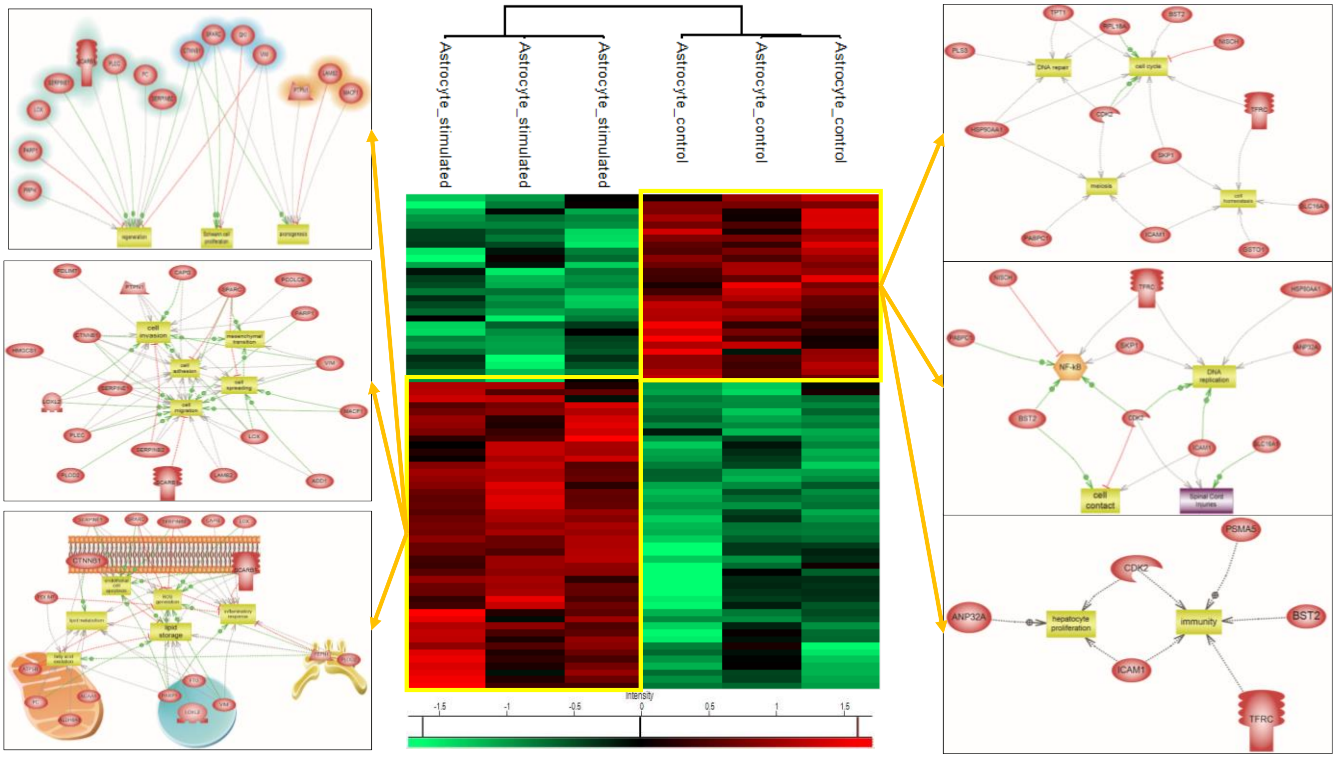

**Figure S5:** Heat map based on the hierarchical clustering analysis of the LFQ value corresponding to the detected proteins extracted from macrophages stimulated with palmitoylcarnitine or not. Distinct clusters are highlighted. The system biology analysis for network identification for each of the highlighted clusters issued from heat map of proteins is also shown.