Supplementary Figure 1 – [^{35}S]-amino acid uptake by cultured hippocampal neurons. The cells (7 DIV) were starved from methionine and cysteine for 30 min and were then incubated with [^{35}S]cysteine and [^{35}S]methionine for the indicated periods of time. Uptake of [^{35}S]-radiolabelled amino acids was then measured after washing the cells with Na^+-medium. The results are the average ± SEM of 3 different experiments, performed in independent preparations.

Supplementary Figure 2 – Two-dimensional gel electrophoresis of proteins from hippocampal neurons. Representative two-dimensional autoradiography images showing [^{35}S]-labelled proteins from the soluble fraction (**A**) or the S126 fraction (**B**). Proteins were focused using IPG strips pH 4.5-5.5, 5.0-6.0, 5.5-6.7, and 6.0-9.0. After running the second dimension, the gels were dried and placed in contact with a phosphor screen. Images were acquired using a STORM laser scanner (see caption of Fig. 2 and Experimental procedures section for further details). All gels shown are oriented with the anode (acidic) to the left and cathode (basic) to the right, and the second dimension was performed in 10% polyacrylamide.

Supplementary Figure 3 - Two-dimensional gel electrophoresis of proteins from control or BDNF-treated hippocampal neurons. Representative two-dimensional autoradiography images showing [^{35}S]-labelled proteins from the soluble fraction of control **(A)** and BDNF-treated (12h) hippocampal neurons **(B)**. Proteins were focused using IPG strips pH 5.5-6.7. After running the second dimension, the gels were dried and placed in contact with a phosphor screen. Images were acquired using a STORM laser scanner (see caption of Fig. 2 and Experimental procedures section for further details). The gels shown

are oriented with the anode (acidic) to the left and cathode (basic) to the right, and the second dimension was performed in 10% polyacrylamide. Gel complexity clearly shows the need of supervised software analysis for quantitative analysis, including spot volume normalization across different gel images.

Supplementary Figure 4 –Two dimensional gel mapping of proteins from hippocampal neurons. Preparative gels of the soluble fraction (**A**) and the S126 fraction (**B**) were stained with ruthenium II tris (bathophenanthroline disulfonate) followed by colloidal Coomassie and used for protein identification by mass spectrometry (Supplementary Table I) with Swiss-Prot accession numbers displayed in the identified spots (see caption of Fig. 2 and Experimental procedures section for further details).

Supplementary Figure 5 – Differences between the spot pattern in autoradiograms (radiolabelled proteins) and silver stained gels (total protein content). Radiolabelled proteins were treated as indicated in the caption of Fig. 2B (soluble fraction, pH 5.5-6.7) except that the gel was silver stained before being dried, and was then exposed to a phosphor screen. The same gel was scanned in an office scanner for silver staining (**A**), and in a laser scanner for radiolabelling (**B**). The zoomed images (C-D) show spot patterns in both images that are either conserved (red ellipses) or not (yellow ellipses).

Supplementary Figure 6 – Sars and Eef2 identification by mass spectrometry. Proteinscape screenshots with protein identification by MALDI-TOF-TOF from 2D-gel spots corresponding to Sars (A) and Eef2 (B) proteins (Supplementary Table I and

Supplementary Figure 2). Identified peptides are highlighted in red with 30.7% and 46.8% sequence coverage and Mascot scores of 113 and 265 for Sars and Eef2, respectively.

Supplementary Figure 7 – Relative expression of *Map2* and *Gapdh* genes in the neurite and soma compartments. Hippocampal neurons were cultured for 14-15 DIV and the total RNA from neurites and soma compartments was mechanically separated to get pure preparations; 250-500 ng were used in the reverse transcription reaction. *Map2* expression was used as a dendritic marker. Gene expression was normalized using *Pgk1*, *Tbp* and *Ppia* as internal control genes. The results are the average ± SEM of 5 independent transcription reactions, performed in independent preparations.