

Supplementary legends

Table S2: USSC secretome. All proteins identified in 7 independent USSC secretomes are listed (1520 proteins). Classically secreted proteins (385 proteins) predicted by SignalP are indicated by “Y” (row J). Proteins secreted by alternative pathways predicted by SecretomeP (276 proteins) are listed by NN-score (row K) which was interpreted as a high probability of secretion with a value of > 0.6 . Proteins predicted by UniProt annotation to be localized extracellular (row L) or at the cell surface (row M) are indicated by “1” including 487 and 8 unique proteins, respectively. All other proteins (364) were predicted to be intracellular proteins / contaminants. Rows N-AD include proteins assigned to cellular components and rows AE-AV proteins assigned to biological process annotated by UniProt database. Additionally, score, coverage, number of proteins, unique peptides, peptides, number of amino acids and molecular weight for each protein are listed (row C-I).

Table S3: Proteins categorized in GO term biological processes. Overview of all GO terms found to be enriched by DAVID database with $FDR < 0.05$. In each spreadsheet, proteins assigned to one gene ontology term are listed. Classically secreted proteins are indicated by “Y”. NN-scores for each non-classically secreted protein are listed. Extracellular annotated proteins are indicated by “1”. Spreadsheet order from lowest to highest FDR per category as indicated in overview table.

Table S4: Protein abundances. Proteins were quantified and ranked into three classes based on their abundance. Abundance classes are indicated in orange, blue and green. Neurite growth promoting factors are indicated in red. The standard deviation (SD) and coefficient of variation (CV) of protein mean concentrations depicted in fmol/ml and the common logarithm are listed. Protein concentrations quantified only in one or two runs are indicated by NA. Taking into account that MS1 peak intensity methods suffer from large quantification errors of small proteins likely resulting from protein-to-protein variation as well as limited number of peptides for accurate quantification, absolute quantification could include quantification errors (70).