## Proteomic analysis of cerebrospinal fluid from children with central nervous system tumors identifies candidate proteins relating to tumor metastatic spread

## SUPPLEMENTARY MATERIALS

Supplementary Data 1: List of proteins and peptides identified by mass spectrometry after the SEQUEST searcher for each sample
See Supplementary Data 1
Supplementary Data 2: Spectral count of the 558 identified proteins
See Supplementary Data 2
Supplementary Data 3: List of the 558 NCBI annotated proteins identified in both case and control groups after
label free spectral counting (scaffold analysis) of the LC-MS/MS results
See Supplementary Data 3

Supplementary Data 4: Protein identifiers in column A were downloaded from CSF proteome database www.biosino. org/bodyfluid. This database provides International Protein Index (IPI) identifiers corresponding to 1286 unique proteins. As our proteins were identified by NCBI GI accession numbers, we used David gene ID conversion tool (https://david.ncifcrf.gov) to convert the NCBI GI accession numbers to IPI identifiers in order to compare our and Biosino lists (column B). We were able to confidently (status: identical) convert 504 of the 558 NCBI GI accession numbers to 1926 IPI identifiers. In column C the total list of IPI identifiers (3212, both databases); in column D 2878 unique identifiers. Thus 334 identifiers overlapped between the two lists, 1592 identifiers were unique (column E) for our study and 948 unique in Biosino database

See Supplementary Data 4

Supplementary Data 5: After the conversion from IPI identifiers to UniProt accession numbers we compared through PANTHER system Uniprot annotations included in Biosino database (column A) with those identified by us (Column B): 793 and 487 annotations, respectively (total annotations in column C, unique in column D). 212 uniprot accession number overlapped; 275 out of 487 annotations (56%) did not overlap Biosino database

See Supplementary Data 5

S	up	ple	ementary	<b>Table</b>	1:	Cellular	com	ponents	according	to:	the	PA	١N	THER	databas	e

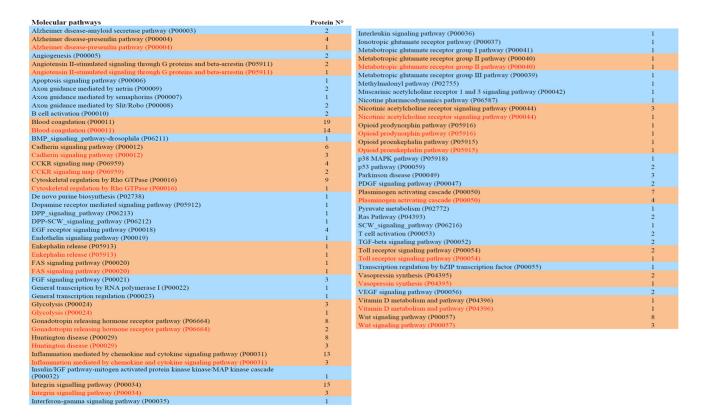
See Supplementary File 1

**Supplementary Table 2: Protein classes according to the PANTHER database** 

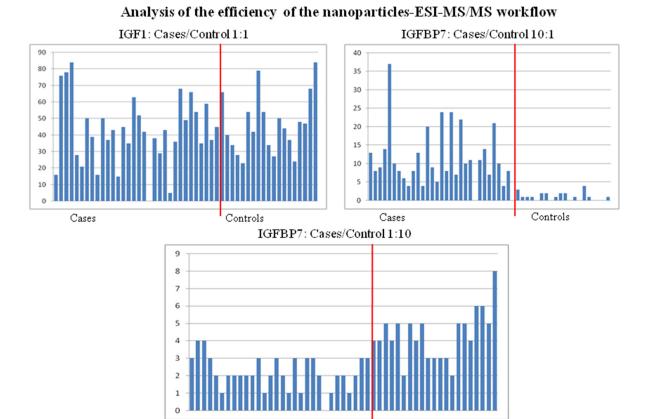
See Supplementary File 1

Supplementary Table 3: Molecular pathways according to the PANTHER database

See Supplementary File 1



Supplementary Figure 1: Overview of the distribution of molecular functions in control (red) and cases (black) and shared (highlighted in orange) according to the PANTHER database.



Supplementary Figure 2: Two chemokines IGFBP7 and IGF-1 were spiked in the CSF samples before nanoparticles incubation as control standards in order to evaluate the performance of nanoparticles harvesting. These chemokines were spiked in cases versus controls in a ratio of 10:1, 1:1, respectively. After Scaffold analysis, they were found to be differentially abundant with a ratio similar to the expected one, (actual ratio of 11.1 and 0.92) in brain tumor samples versus controls.

Controls

Cases