

S1 Table. Description of the raw data and scores for narrowing down the selection of candidate proteins

Protein name	Gene name	"-Log(P-value) in 1st set"	Difference (Log2Foldchange) in 1st SET	"-Log(P-value) in 2nd set"	Difference (Log2Foldchange) in 2nd set	ROC (AUC value)	SCORE		SCORE 3: AUC	SCORE 4: Multiple regression modeling 1	SCORE 5: Multiple regression modeling 2	Sum of five scores	Rank
							1: 1st fold-change Score	2: 2nd fold-change Score					
Alpha-2-macroglobulin	<i>A2M</i>	2.85381613	4.50576	10.11450924	5.511215164	0.986	5	6	10	10	10	40	1
Cofilin-1	<i>CFL1</i>	3.299330024	3.70566	2.651602382	1.628830782	0.803	4	2	4	10	10	29	2
Apolipoprotein A-I	<i>APOA1</i>	2.446607348	3.56486	6.081590897	4.30588865	0.898	4	4	6	10		24	3
Inter-alpha-trypsin inhibitor heavy chain H2	<i>ITIH2</i>	5.726811153	4.43631	4.392752992	2.983399958	0.898	4	3	6	-	10	23	4
Afamin	<i>AFM</i>	3.269501158	2.15676	6.702358989	2.007927237	0.949	2	2	8	-	10	22	5
Fibrinogen beta chain	<i>FGB</i>	6.8033265	6.65579	6.005915497	4.744389442	0.933	7	5	8	-	-	19	6
Cell division cycle 5-like protein	<i>CDC5L</i>	2.363678632	1.90223	5.285292126	1.321161714	0.887	2	1	6	10	-	19	7
CD5 antigen-like	<i>CD5L</i>	4.739899978	4.57045	2.198924371	1.961528501	0.752	5	2	2	10	-	19	8
Fibrinogen gamma chain	<i>FGG</i>	3.540535136	5.23772	6.217428389	5.041801739	0.947	5	5	8	-	-	18	9
Complement C3	<i>C3</i>	3.394467628	4.41276	6.966474391	4.339245433	0.937	4	4	8	-	-	17	10
Complement factor H	<i>CFH</i>	4.97094105	4.53503	5.505663063	3.60581189	0.928	5	4	8	-	-	16	11
Protein S isoform 1	<i>PROS1</i>	2.696179958	2.5525	5.034412876	2.863956838	0.919	3	3	8	-	-	13	12
Apolipoprotein C-III	<i>APOC3</i>	2.572817484	3.59382	4.339920935	3.591881942	0.894	4	4	6	-	-	13	13
Apolipoprotein M	<i>APOM</i>	1.825323949	1.94726	5.617349202	2.163536325	0.914	2	2	8	-	-	12	14
Heparin cofactor 2	<i>SERPIND1</i>	2.211264022	1.38109	5.408781564	2.473802496	0.944	1	2	8	-	-	12	15
Rho GDP	<i>ARHGDI</i>	5.534562122	4.58498	3.838979607	2.578171797	0.831	5	3	4	-	-	11	16

dissociation inhibitor (GDI) beta, isoform CRA_a													
Complement component C9	<i>C9</i>	2.591737981	3.06952	3.682511307	1.914698593	0.87	3	2	6	-	-	11	17
Proenkephalin-A	<i>PENK</i>	2.116403288	2.5838	4.015143833	2.282791747	0.863	3	2	6	-	-	11	18
Plasminogen	<i>PLG</i>	1.970644635	1.02685	5.211532536	1.474719475	0.91	1	1	8	-	-	11	19
Antithrombin-III	<i>SERPINC1</i>	2.439119399	1.50534	5.012623878	2.459498133	0.875	2	2	6	-	-	10	20
Heat shock protein HSP 90-beta	<i>HSP90AB1</i>	2.558430537	2.66912	2.787216262	2.473571038	0.782	3	2	2	-	-	7	21
Serum amyloid P-component;Pentaxin	<i>APCS</i>	2.559768064	3.78168	1.904305582	1.788756785	0.743	4	2	0	-	-	6	22
Myosin light polypeptide 6	<i>MYL6</i>	4.941881583	3.94346	1.987436676	1.533932082	0.743	4	2	0	-	-	5	23
Protein IGLV3-19	<i>IGLV3-19</i>	2.319897563	2.42852	2.894478155	2.074889668	-	2	2	0	-	-	-	-
Ig gamma-4 chain C region	<i>IGHG4</i>	2.191019057	2.66229	2.733874052	1.530675178	-	3	2	0	-	-	-	-
IGL@ protein	<i>IGL@</i>	3.106141739	4.01097	7.10992347	2.389454719	-	4	2	0	-	-	-	-
IGL@ protein	<i>IGL@</i>	3.106141739	4.01097	6.082814679	1.520416717	-	4	2	0	-	-	-	-

References

1. Han D, Jin J, Woo J, Min H, Kim Y. Proteomic analysis of mouse astrocytes and their secretome by a combination of FASP and StageTip based, high pH, reversed-phase fractionatio. *Proteomics*. 2014;14:1604-9.
2. Woo J, Han D, Park J, Kim SJ, Kim Y. In-depth characterization of the secretome of mouse CNS cell lines by LC-MS/MS without prefractionation. *Proteomics*. 2015;15:3617–22.