

SOMAscan Proteomics Identifies Novel Plasma Proteins in Amyotrophic Lateral Sclerosis Patients

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Table S1. Upregulated and Downregulated proteins between ALS patients and neurologically healthy controls using SAM Analysis of SOMAscan Results.

Increased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
SH21A	SH2D1A	1.689103	0.019616
TIMP-3	TIMP3	1.292908	0.003370
PDGF-BB	PDGFB	1.205864	0.005048
TARC	CCL17	1.081839	0.003579
PKC-D	PRKCD	1.004368	0.011062
Gro-b/g	CXCL3 CXCL2	1.003084	0.009649
NID2	NID2	0.515259	0.011365
Nidogen	NID1	0.419618	0.012383
Decreased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
Ephrin-A2	EFNA2	-0.281950	0.024822
RGMB	RGMB	-0.313691	0.018977
VCAM-1	VCAM1	-0.315918	0.007538
sTie-1	TIE1	-0.334705	0.015354
TLR4	TLR4	-0.371138	0.006458
RGM-C	HJV	-0.388838	0.008869
IGF-I sR	IGF1R	-0.415958	0.025886
BMPRI1A	BMPRI1A	-0.449027	0.015265
LYPD3	LYPD3	-0.456034	0.011876
NCAM-L1	L1CAM	-0.482127	0.003169
BCAM	BCAM	-0.485299	0.031243
sTie-2	TEK	-0.488869	0.014479
Ephrin-A3	EFNA3	-0.514959	0.002038
MASP3	MASP1	-0.536970	0.011929
Kallikrein 7	KLK7	-0.553409	0.024028
Nectin-like protein 2	CADM1	-0.559252	0.045222
RET	RET	-0.566935	0.019690
IR	INSR	-0.594081	0.024830
TLR4:MD-2 complex	TLR4 LY96	-0.597382	0.007250
IL-13 Ra1	IL13RA1	-0.597611	0.014114
CD23	FCER2	-0.602595	0.046311
HAI-1	SPINT1	-0.620640	0.008536
sE-Selectin	SELE	-0.625872	0.024278
TECK	CCL25	-0.655796	0.041103
Carbonic anhydrase I	CA1	-0.703275	0.003678
ISLR2	ISLR2	-0.738526	0.000955
IL-5 Ra	IL5RA	-0.742331	0.026171
kallikrein 8	KLK8	-0.791363	0.021481
Growth hormone receptor	GHR	-0.820837	0.004480
BST1	BST1	-0.884313	0.037880
CYTT	CST2	-0.905443	0.017786
IL-18 BP α	IL18BP	-0.906512	0.001023
TF	F3	-1.041923	0.001738
ENPP7	ENPP7	-1.261712	0.003212

Table S2. Upregulated and Downregulated proteins between ALS patients and neurologically healthy controls using limma analysis of SOMAScan Results.

Increased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
Troponin T	TNNT2	1.477579	0.000924
TIMP-3	TIMP3	1.292908	0.003370
PDGF-BB	PDGFB	1.205864	0.005048
TARC	CCL17	1.081839	0.003579
Gro-b/g	CXCL3 CXCL2	1.003084	0.009649
DKK1	DKK1	0.826350	0.004899
CSRP3	CSRP3	0.786139	0.002050
Dkk-4	DKK4	0.685932	0.008682
Decreased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
TLR4:MD-2 complex	TLR4 LY96	-0.597382	0.007250
HAI-1	SPINT1	-0.620640	0.008536
Carbonic anhydrase I	CA1	-0.703275	0.003678
ISLR2	ISLR2	-0.738526	0.000955
Growth hormone receptor	GHR	-0.820837	0.004480
IL-1a	IL1A	-0.849595	0.003406
IL-18 BP _a	IL18BP	-0.906512	0.001023
TF	F3	-1.041923	0.001738
ENPP7	ENPP7	-1.261712	0.003212

Table S3. Upregulated and Downregulated proteins between S-ALS patients and neurologically healthy controls using SAM Analysis of SOMAscan Results.

Increased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
TIMP-3	TIMP3	1.488049	0.003717
TARC	CCL17	1.451586	0.000576
Protein disulfide isomerase A3	PDIA3	1.020243	0.031587
AN32B	ANP32B	0.618600	0.002078
NID2	NID2	0.602565	0.011215
Decreased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
Ephrin-A2	EFNA2	-0.337748	0.021640
sTie-1	TIE1	-0.346598	0.031437
IL-16	IL16	-0.354345	0.054714
VCAM-1	VCAM1	-0.368661	0.007593
ULBP-2	ULBP2	-0.457169	0.010375
VEGF sR3	FLT4	-0.469542	0.004093
Ephrin-A3	EFNA3	-0.504992	0.008539
BMPRI1A	BMPRI1A	-0.514741	0.017360
BCAM	BCAM	-0.515190	0.050522
IGF-I	IGF1	-0.516672	0.013849
LYPD3	LYPD3	-0.532839	0.011828
Cathepsin S	CTSS	-0.546092	0.033920
sTie-2	TEK	-0.554973	0.017552
NCAM-L1	L1CAM	-0.571303	0.002630
IL-18 Ra	IL18R1	-0.602471	0.038568
TLR4:MD-2 complex	TLR4 LY96	-0.661724	0.010767
IL-13 Ra1	IL13RA1	-0.681839	0.016537
Kallikrein 7	KLK7	-0.696381	0.014740
granzyme A	GZMA	-0.710334	0.004400
RET	RET	-0.749046	0.007686
ISLR2	ISLR2	-0.787154	0.002363
IR	INSR	-0.791866	0.009677
IL-18 BPa	IL18BP	-0.844704	0.006945
sE-Selectin	SELE	-0.860835	0.007021
CD23	FCER2	-0.896461	0.009192
Myostatin	MSTN	-0.897505	0.056884
kallikrein 8	KLK8	-0.924181	0.021588
Lactoferrin	LTF	-0.957086	0.031620
Growth hormone receptor	GHR	-1.138476	0.000460

Table S4. Downregulated proteins between F-ALS patients and neurologically healthy controls using SAM Analysis of SOMAscan Results. No significantly up-regulated proteins were identified.

Decreased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
RNF43	RNF43	-0.403979	0.027766
TLR4	TLR4	-0.434531	0.006334
RGM-C	HFE2	-0.481616	0.006041
ISLR2	ISLR2	-0.689897	0.002233
Carbonic anhydrase I	CA1	-0.812518	0.002971
Discoidin domain receptor 2	DDR2	-1.138072	0.003942
TF	F3	-1.466182	0.000018
ENPP7	ENPP7	-1.498924	0.000856

Table S5. Upregulated and Downregulated proteins between S-ALS patients and neurologically healthy controls using limma Analysis of SOMAscan Results.

Increased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
TIMP-3	TIMP3	1.488049	0.003717
Troponin T	TNNT2	1.483767	0.003801
TARC	CCL17	1.451586	0.000576
G-CSF-R	CSF3R	1.193777	0.008583
IGFBP-2	IGFBP2	1.114518	0.003953
DKK1	DKK1	0.978497	0.004176
Dkk-4	DKK4	0.863833	0.004338
FGF-10	FGF10	0.754318	0.009419
LIMP II	SCARB2	0.628880	0.004092
AN32B	ANP32B	0.618600	0.002078
SDF-1	CXCL12	0.616372	0.003589
CD22	CD22	0.592353	0.009333
Decreased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
Nogo Receptor	RTN4R	-0.590989	0.001815
granzyme A	GZMA	-0.710334	0.004400
RET	RET	-0.749046	0.007686
ISLR2	ISLR2	-0.787154	0.002363
IR	INSR	-0.791866	0.009677
IL-18 BP α	IL18BP	-0.844704	0.006945
sE-Selectin	SELE	-0.860835	0.007021
CD23	FCER2	-0.896461	0.009192
Growth hormone receptor	GHR	-1.138476	0.000460

Table S6. Upregulated and Downregulated proteins between F-ALS patients and neurologically healthy controls using READAT Analysis of Somascan Results.

Increased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
PDE5A	PDE5A	2.515048	0.003031
M2-PK	PKM	2.282772	0.004186
AMPM2	METAP2	2.111687	0.008841
FER	FER	1.846274	0.008930
MAPK2	MAPKAPK2	1.693216	0.002242
CPNE1	CPNE1	1.667009	0.007142
DLRB1	DYNLRB1	1.655651	0.005362
Troponin T	TNNT2	1.471392	0.002702
PKC-D	PRKCD	1.426355	0.001771
EGF	EGF	1.385597	0.002806
Gro-b/g	CXCL3 CXCL2	1.213105	0.008527
C5a	C5	1.196144	0.008846
CAMK2A	CAMK2A	1.189491	0.003996
cGMP-stimulated PDE	PDE2A	1.012715	0.003776
C6	C6	0.941726	0.008187
CSRP3	CSRP3	0.845542	0.000344
Calcineurin B a	PPP3R1	0.807205	0.008612
Decreased in ALS patients			
Target Fullname	Entrez Gene Sym	logFC	p-value
calreticulin	CALR	-0.583783	0.004835
ISLR2	ISLR2	-0.689897	0.002233
TECK	CCL25	-0.808331	0.009408
Carbonic anhydrase I	CA1	-0.812518	0.002971
BMP-6	BMP6	-0.885880	0.000407
IL-18 BP _a	IL18BP	-0.968319	0.001700
Discoidin domain receptor 2	DDR2	-1.138072	0.003942
α 2-Macroglobulin	A2M	-1.438991	0.004912
TF	F3	-1.466182	0.000018
ENPP7	ENPP7	-1.498924	0.000856
Thrombin	F2	-1.509842	0.007796
C3b	C3	-1.703522	0.003412

Table S7. List of GO Annotation for TARC, TIMP-3, NID1 and NID2. Abbreviations: P-Pathway, F-Function; C- Cellular.

TARC

Qualifier	GO Term	GO Name	Reference	GO Aspect
involved_in	GO:0043547	positive regulation of GTPase activity	PMID:21873635	P
enables	GO:0008009	chemokine activity	PMID:21873635	F
involved_in	GO:0048247	lymphocyte chemotaxis	PMID:21873635	P
is_active_in	GO:0005615	extracellular space	PMID:21873635	C

involved_in	GO:0070098	chemokine-mediated signaling pathway	PMID:21873635	P
involved_in	GO:0070374	positive regulation of ERK1 and ERK2 cascade	PMID:21873635	P
involved_in	GO:0071346	cellular response to type II interferon	PMID:21873635	P
involved_in	GO:0071347	cellular response to interleukin-1	PMID:21873635	P
involved_in	GO:0071356	cellular response to tumor necrosis factor	PMID:21873635	P
involved_in	GO:0030593	neutrophil chemotaxis	PMID:21873635	P
involved_in	GO:0002548	monocyte chemotaxis	PMID:21873635	P
involved_in	GO:0006954	inflammatory response	PMID:21873635	P
involved_in	GO:0007186	G protein-coupled receptor signaling pathway	PMID:21873635	P
enables	GO:0048020	CCR chemokine receptor binding	PMID:21873635	F
enables	GO:0008009	chemokine activity	GO_REF:0000002	F
located_in	GO:0005576	extracellular region	GO_REF:0000002	C
involved_in	GO:0006955	immune response	GO_REF:0000002	P
located_in	GO:0005615	extracellular space	GO_REF:0000043	C
located_in	GO:0005576	extracellular region	GO_REF:0000043	C
enables	GO:0005125	cytokine activity	GO_REF:0000043	F
involved_in	GO:0006935	chemotaxis	GO_REF:0000043	P
involved_in	GO:0006954	inflammatory response	GO_REF:0000043	P
enables	GO:0008009	chemokine activity	PMID:9743322	F
enables	GO:0005102	signaling receptor binding	PMID:8702936	F
enables	GO:0005102	signaling receptor binding	PMID:9743322	F
involved_in	GO:0006935	chemotaxis	PMID:9743322	P
involved_in	GO:0007267	cell-cell signaling	PMID:8702936	P
located_in	GO:0005576	extracellular region	Reactome:R-HSA-443986	C
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
enables	GO:0005515	protein binding	PMID:28381538	F
involved_in	GO:0045662	negative regulation of myoblast differentiation	GO_REF:0000107	P
enables	GO:0031729	CCR4 chemokine receptor binding	GO_REF:0000107	F
located_in	GO:0005576	extracellular region	GO_REF:0000044	C
involved_in	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	PMID:12949249	P
involved_in	GO:0031640	killing of cells of another organism	PMID:12949249	P
involved_in	GO:0031640	killing of cells of another organism	PMID:12949249	P

TIMP-3

Qualifier	GO Term	GO Name	Reference	GO Aspect
enables	GO:0002020	protease binding	PMID:21873635	F
enables	GO:0008191	metalloendopeptidase inhibitor activity	PMID:21873635	F
involved_in	GO:0051045	negative regulation of membrane protein	PMID:21873635	P

ectodomain proteolysis				
is_active_in	GO:0005615	extracellular space	PMID:21873635	C
involved_in	GO:0009725	response to hormone	PMID:21873635	P
involved_in	GO:0010033	response to organic substance	PMID:21873635	P
involved_in	GO:0010951	negative regulation of endopeptidase activity	PMID:21873635	P
is_active_in	GO:0031012	extracellular matrix	PMID:21873635	C
involved_in	GO:0034097	response to cytokine	PMID:21873635	P
enables	GO:0008191	metalloendopeptidase inhibitor activity	GO_REF:0000002	F
enables	GO:0008191	metalloendopeptidase inhibitor activity	GO_REF:0000043	F
involved_in	GO:0050896	response to stimulus	GO_REF:0000043	P
enables	GO:0030414	peptidase inhibitor activity	GO_REF:0000043	F
involved_in	GO:0007601	visual perception	GO_REF:0000043	P
involved_in	GO:0010466	negative regulation of peptidase activity	GO_REF:0000043	P
located_in	GO:0005576	extracellular region	GO_REF:0000043	C
enables	GO:0004857	enzyme inhibitor activity	GO_REF:0000043	F
enables	GO:0046872	metal ion binding	GO_REF:0000043	F
located_in	GO:0005576	extracellular region	Reactome:R-HSA-481009	C
located_in	GO:0031089	platelet dense granule lumen	Reactome:R-HSA-481009	C
enables	GO:0005515	protein binding	PMID:18344519	F
involved_in	GO:0071310	cellular response to organic substance	GO_REF:0000107	P
located_in	GO:0005604	basement membrane	GO_REF:0000107	C
involved_in	GO:1904684	negative regulation of metalloendopeptidase activity	GO_REF:0000107	P
enables	GO:0008191	metalloendopeptidase inhibitor activity	PMID:18638486	F
involved_in	GO:1903984	positive regulation of TRAIL-activated apoptotic signaling pathway	PMID:19962668	P
part_of	GO:0062023	collagen-containing extracellular matrix	PMID:25037231	C
part_of	GO:0062023	collagen-containing extracellular matrix	PMID:28675934	C
part_of	GO:0062023	collagen-containing extracellular matrix	PMID:25037231	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:27559042	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:27068509	C
colocalizes_with	GO:0062023	collagen-containing extracellular matrix	PMID:20551380	C
involved_in	GO:0051045	negative regulation of membrane protein ectodomain proteolysis	PMID:18383040	P
involved_in	GO:0070373	negative regulation of ERK1 and ERK2 cascade	PMID:19962668	P
involved_in	GO:1904684	negative regulation of metalloendopeptidase activity	GO_REF:0000024	P
enables	GO:0005515	protein binding	PMID:18638486	F
located_in	GO:0005634	nucleus	PMID:21630459	C
NID1				
Qualifier	GO Term	GO Name	Reference	GO Aspect
is_active_in	GO:0005886	plasma membrane	PMID:21873635	C
enables	GO:0005509	calcium ion binding	GO_REF:0000002	F
involved_in	GO:0007160	cell-matrix adhesion	GO_REF:0000002	P
located_in	GO:0005576	extracellular region	GO_REF:0000043	C

located_in	GO:0005604	basement membrane	GO_REF:0000043	C
involved_in	GO:0007155	cell adhesion	GO_REF:0000043	P
located_in	GO:0005576	extracellular region	Reactome:R-HSA-2426450	C
located_in	GO:0005576	extracellular region	Reactome:R-HSA-3791319	C
enables	GO:0005518	collagen binding	GO_REF:0000107	F
involved_in	GO:0010811	positive regulation of cell-substrate adhesion	GO_REF:0000107	P
located_in	GO:0071944	cell periphery	GO_REF:0000107	C
located_in	GO:0031012	extracellular matrix	GO_REF:0000107	C
located_in	GO:0005604	basement membrane	GO_REF:0000107	C
involved_in	GO:0030198	extracellular matrix organization	GO_REF:0000107	P
involved_in	GO:0032836	glomerular basement membrane development	GO_REF:0000107	P
involved_in	GO:0007160	cell-matrix adhesion	GO_REF:0000107	P
enables	GO:0043237	laminin-1 binding	GO_REF:0000107	F
enables	GO:0050840	extracellular matrix binding	GO_REF:0000107	F
located_in	GO:0005604	basement membrane	PMID:22952693	C
enables	GO:0005518	collagen binding	PMID:22952693	F
enables	GO:0043236	laminin binding	PMID:22952693	F
involved_in	GO:0071711	basement membrane organization	PMID:22952693	P
enables	GO:0005201	extracellular matrix structural constituent	PMID:25037231	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:25037231	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:28675934	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:20551380	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:27559042	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:27068509	F
part_of	GO:0062023	collagen-containing extracellular matrix	PMID:25037231	C
part_of	GO:0062023	collagen-containing extracellular matrix	PMID:25037231	C
part_of	GO:0062023	collagen-containing extracellular matrix	PMID:28675934	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:27559042	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:27068509	C
colocalizes_with	GO:0062023	collagen-containing extracellular matrix	PMID:20551380	C
colocalizes_with	GO:0062023	collagen-containing extracellular matrix	PMID:22261194	C
enables	GO:0005201	extracellular matrix structural constituent	GO_REF:0000024	F
enables	GO:0043394	proteoglycan binding	PMID:22952693	F
located_in	GO:0005604	basement membrane	GO_REF:0000044	C
involved_in	GO:0110011	regulation of basement membrane organization	PMID:2119632	P
involved_in	GO:0045785	positive regulation of cell adhesion	PMID:3794389	P
involved_in	GO:0051149	positive regulation of muscle cell differentiation	PMID:26555376	P
located_in	GO:0098637	protein complex involved in cell-matrix adhesion	PMID:3109910	C
involved_in	GO:2001046	positive regulation of integrin-mediated signaling pathway	PMID:23948589	P
located_in	GO:0005604	basement membrane	PMID:1678389	C
located_in	GO:0070062	extracellular exosome	PMID:23533145	C
located_in	GO:0070062	extracellular exosome	PMID:19056867	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:23658023	C

located_in	GO:0110165	cellular anatomical entity	GO_REF:0000117	C
NID2				
Qualifier	GO Term	GO Name	Reference	GO Aspect
is_active_in	GO:0005615	extracellular space	PMID:21873635	C
is_active_in	GO:0005604	basement membrane	PMID:21873635	C
involved_in	GO:0007160	cell-matrix adhesion	PMID:21873635	P
enables	GO:0005509	calcium ion binding	GO_REF:0000002	F
involved_in	GO:0007160	cell-matrix adhesion	GO_REF:0000002	P
located_in	GO:0005576	extracellular region	GO_REF:0000043	C
located_in	GO:0005604	basement membrane	GO_REF:0000043	C
involved_in	GO:0007155	cell adhesion	GO_REF:0000043	P
enables	GO:0005518	collagen binding	PMID:9733643	F
located_in	GO:0005604	basement membrane	PMID:9733643	C
involved_in	GO:0007155	cell adhesion	PMID:9733643	P
located_in	GO:0005576	extracellular region	Reactome:R-HSA-2426450	C
located_in	GO:0031012	extracellular matrix	GO_REF:0000107	C
located_in	GO:0005604	basement membrane	GO_REF:0000107	C
involved_in	GO:0007160	cell-matrix adhesion	GO_REF:0000107	P
located_in	GO:0005604	basement membrane	PMID:22952693	C
involved_in	GO:0071711	basement membrane organization	PMID:22952693	P
enables	GO:0005201	extracellular matrix structural constituent	PMID:28675934	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:20551380	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:27559042	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:27068509	F
enables	GO:0005201	extracellular matrix structural constituent	PMID:28327460	F
part_of	GO:0062023	collagen-containing extracellular matrix	PMID:28675934	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:28327460	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:27559042	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:27068509	C
colocalizes_with	GO:0062023	collagen-containing extracellular matrix	PMID:20551380	C
enables	GO:0005201	extracellular matrix structural constituent	GO_REF:0000024	F
located_in	GO:0005604	basement membrane	GO_REF:0000044	C
located_in	GO:0005886	plasma membrane	GO_REF:0000052	C
located_in	GO:0070062	extracellular exosome	PMID:23533145	C
located_in	GO:0062023	collagen-containing extracellular matrix	PMID:23658023	C
enables	GO:0005515	protein binding	PMID:11956183	F
located_in	GO:0110165	cellular anatomical entity	GO_REF:0000117	C

Table S8. ROC curve data of ALS, S-ALS and F-ALS versus controls (H-CTR and NoH-CTR).

ALS versus controls

Protein Name	AUC	P value	Z score	Sensitivity	Specificity	Optimal cut-off point
TARC	0.68	0.0034	2.93	0.56	0.72	57.22
TIMP3	0.60	0.14194	1.47	-	-	-
NID1	0.52	0.78816	0.27	-	-	-
NID2	0.58	0.22565	1.27	-	-	-

S-ALS versus controls						
Protein Name	AUC	P value	Z score	Sensitivity	Specificity	Optimal cut-off point
TARC	0.67	0.00915	2.60	0.562	0.722	57.22
TIMP3	0.67	0.00827	2.64	0.656	0.694	49.4
NID1	0.54	0.55898	0.58	-	-	-
NID2	0.51	0.89388	0.13	-	-	-
F-ALS versus controls						
Protein Name	AUC	P value	Z score	Sensitivity	Specificity	Optimal cut-off point
TARC	0.72	0.00856	2.63	1	0.375	31.49
TIMP3	0.65	0.1389	1.48.			
NID1	0.53	0.79092	0.26.			
NID2	0.81	0.00002	4.32.	0.583	0.938	22.74

Table S9. Stepwise logistic regression analysis of ALS, S-ALS and F-ALS versus controls (H-CTR and NoH-CTR). Abbreviations: VIF-Variance Inflation Factor

ALS versus controls		
Protein Name	P value	VIF
TARC	0.00836	1.360
NID1	0.03857	1.360
S-ALS versus controls		
Protein Name	P value	VIF
TARC	0.00240	1.428
NID1	0.05980	1.428
F-ALS versus controls		
Protein Name	P value	VIF
TARC	0.07890	1.113
TIMP3	0.02540	1.087
NID2	0.02120	1.026