

## Supplementary Data

Clinical Data						
Cohort	Gender	Age	Education	MMSE	APOE	
AD Treated	F	69	8	21	3,4	
AD Treated	F	77	10	25	2,4	
AD Treated	F	61	10	26	4,4	
AD Treated	F	71	15	29	3,4	
AD Treated	F	81	14	22	3,3	
AD Treated	F	79	14	26	3,4	
AD Treated	F	78	12	28	3,3	
AD Treated	F	79	12	29	3,3	
AD Treated	F	84	9	22	3,4	
AD Treated	F	81	11	23	3,4	
AD Treated	F	85	12	26	3,3	
AD Treated	F	83	11	29	3,4	
AD Treated	F	89	11	22	2,3	
AD Treated	F	67	15	24	4,4	
AD Treated	M	90	7	22	3,3	
AD Treated	M	84	12	22	3,4	
AD Treated	M	80	8	25	3,3	
AD Treated	F	84	15	22	2,3	
AD Treated	F	86	12	25	3,3	
AD Treated	F	83	10	25	3,3	
AD Treated	F	80	8	27	nm	
AD Treated	M	84	13	25	3,4	
AD Treated	M	86	7	26	3,3	
AD Treated	M	83	15	30	3,3	
AD Untreated	F	66	12	26	3,4	
AD Untreated	F	72	11	27	3,4	
AD Untreated	F	62	17	27	3,3	
AD Untreated	F	75	13	21	nm	
AD Untreated	F	76	4	24	3,4	

AD Untreated	F	77	9	26	3,3
AD Untreated	F	85	11	23	3,3
AD Untreated	F	84	16	24	3,3
AD Untreated	F	80	14	24	3,3
AD Untreated	F	79	10	25	3,3
AD Untreated	F	78	16	29	3,3
AD Untreated	M	76	12	23	2,3
AD Untreated	M	72	25	23	3,3
AD Untreated	M	73	14	25	3,3
AD Untreated	M	78	35	29	2,3
AD Untreated	M	84	7	22	3,4
AD Untreated	M	84	15	22	3,4
AD Untreated	M	79	7	25	3,3
AD Untreated	M	80	15	28	nm
Healthy	F	66	11	30	nm
Healthy	F	64	18	30	nm
Healthy	F	64	12	30	nm
Healthy	F	63	18	30	nm
Healthy	F	63	17	30	nm
Healthy	F	68	18	30	nm
Healthy	F	68	12	30	nm
Healthy	F	68	16	30	nm
Healthy	F	67	15	30	nm
Healthy	F	66	12	30	nm
Healthy	F	71	15	28	nm
Healthy	F	72	13	30	nm
Healthy	F	69	15	30	nm
Healthy	F	68	15	30	nm
Healthy	F	72	8	nm	nm
Healthy	F	76	20	23	nm
Healthy	F	73	22	29	nm
Healthy	F	72	13	29	nm
Healthy	F	76	10	30	nm
Healthy	F	73	14	30	nm
Healthy	M	72	11	29	nm
Healthy	M	71	9	29	nm

Healthy	M	67	12	30	nm
Healthy	M	66	18	30	nm
Healthy	F	76	3	28	nm
Healthy	F	78	7	29	nm
Healthy	F	78	17	29	nm
Healthy	F	79	16	29	nm
Healthy	F	76	20	30	nm
Healthy	M	80	16	30	nm
Healthy	M	80	16	30	nm
Healthy	M	81	16	30	nm
Healthy	M	81	10	30	nm

**Supplementary Table 1:** Clinical data for the 19 Alzheimer Untreated (AD Untreated), 25 Alzheimer Treated (AD Treated) and 33 Normal (Healthy) samples. The abbreviation ‘nm’ stands for ‘not measured’.

Protein Identification Summary					
Gene Name	Protein Accession	Hits	Coverage	Mean Mass Diff (ppm)	Mean RT Diff (min)
TYR	IPI00218270.1	4	0.182	5.1	3.2
BDNF	IPI00012058.1	3	0.176	14.4	5.8
CHRNA1	IPI00298986.1	3	0.107	10.2	4.3
CRB1	IPI00607891.1	3	0.091	7.2	1
UNC5C	IPI00293757.3	3	0.071	11.7	2.6
GRIN2A	IPI00029768.1	5	0.068	7.1	3.8
COL4A4	IPI00334166.3	3	0.067	8.9	3.3
PARD3	IPI00163608.1	5	0.066	6.9	2.8
ADAM23	IPI00021903.1	3	0.063	7.5	2.5
COL1A2	IPI00164755.4	5	0.061	13	1.7
PCDH18	IPI00030618.2	3	0.056	10.1	2

**Supplementary Table 2:** Summary of the protein identification results by mass and retention time fingerprinting. Coverage is the number of peptides assigned divided by the maximum number of tryptic peptides theoretically identifiable by mass and retention time fingerprinting for the protein. Mean mass and

retention time differences are calculated over all assigned peptides to the protein.

Peptide Identification									
Gene Name	Fraction	MZ	RT	CH	Sequence	Sequence Mass	Sequence RT	Mass Diff (ppm)	RT Diff (min)
TYR	6	452.7174	1.8	2	SPCGQLSGR	903.4234	1.7	4.6	-0.1
TYR	3	438.5263	5.3	3	FGFWGPNCTER	1312.566	9.9	8.2	4.6
TYR	1	641.3190	14.5	3	DIDFAHEAPAFLPWHR	1920.9273	16.2	-3.2	1.6
TYR	3	634.6553	12.9	3	NTLEEMGFLHVGWAGLK	1900.9508	19.6	4.5	6.7
BDNF	6	666.6599	17.1	3	MTILFLTMVISYFGCMK	1996.9901	22.0	17.0	4.8
BDNF	4	643.2933	15.9	2	NYLDAANMSMR	1284.5591	9.2	-9.3	-6.7
BDNF	2	637.3112	11.0	3	GELSVCDSEWVTAADK	1908.8777	17.0	-16.9	6.0
CHRNA1	4	500.7326	2.8	2	GTDEYFIR	999.4663	7.3	16.8	4.5
CHRNA1	3	514.9473	13.8	3	KPPSDFLFPKPNR	1541.8357	10.4	11.2	-3.4
CHRNA1	2	727.3522	8.0	2	QLQEEDHDALK	1452.6848	3.1	-2.7	-5.0
CRB1	6	452.7174	1.8	2	NSLCQPSR	903.4233	1.8	4.5	0.0
CRB1	3	466.7550	3.3	2	GSVCNIALR	931.491	6.0	-3.5	2.7
CRB1	6	623.8468	11.8	2	GDVIYIGGLPDK	1245.6609	12.0	-13.6	0.3
UNC5C	3	466.7550	3.3	2	EVSIEISR	931.4975	3.9	3.4	0.6
UNC5C	4	732.1094	20.5	4	NQAAQQQWEDVV VVGEENFTTPCYIK	2924.3653	16.5	-14.1	-4.0
UNC5C	6	692.3395	11.6	2	VYCLDDTQDALK	1382.6391	8.4	-17.6	-3.2
GRIN2A	3	795.3441	9.4	2	NNYPYMHQYMTK	1588.6803	7.5	4.8	-1.9
GRIN2A	3	530.5737	9.4	3	NNYPYMHQYMTK	1588.6803	7.5	-10.8	-1.9
GRIN2A	3	886.9331	16.1	4	QIDLALLQFVGDGEM EELETLWLTGICHNEK	3543.7272	22.3	7.4	6.2
GRIN2A	2	528.9387	7.0	3	GIYSCIHGVIIEEK	1583.7768	9.5	-9.9	2.5
GRIN2A	2	410.7166	2.2	2	AADFIQR	819.424	3.8	7.8	1.5
GRIN2A	2	660.3030	1.8	3	YLPEEMAHSDISETSNR	1977.8739	8.6	-5.8	6.9
COL4A4	4	942.8499	19.8	3	LPSQGPPGPPGPQGP IGPLGAPGPIGLSGEK	2825.5085	13.2	-6.3	-6.6

COL4A4	4	436.2366	4.0	2	GHPGPPGPR	870.4463	1.7	-12.9	-2.3
COL4A4	3	501.6202	13.8	3	GAPGPPGLPGSVDLLR	1501.8257	12.6	-7.5	-1.2
PARD3	3	612.8166	8.3	2	GTEGLGFSITSR	1223.6148	8.5	-2.2	0.2
PARD3	7	692.8344	10.9	2	QFSDASQLDFVK	1383.6672	11.2	10.1	0.4
PARD3	3	421.5350	7.9	3	NGYLGGHGFNAR	1261.5953	5.6	10.9	-2.2
PARD3	6	784.8528	8.1	2	QPPSEGPSNYDSYK	1567.6792	1.9	-6.8	-6.1
PARD3	6	523.5746	8.0	3	QPPSEGPSNYDSYK	1567.6792	1.9	-13.5	-6.1
PARD3	3	640.8311	7.3	2	QDVPPSPSQVAR	1279.6522	2.1	4.5	-5.2
ADAM23	2	607.2909	3.0	2	SSHAHTNNFAK	1212.5635	1.7	-2.1	-1.3
ADAM23	6	623.8468	11.8	2	QHADAVHLISR	1245.6579	7.2	-16.1	-4.6
ADAM23	3	421.5350	7.9	3	SSLSYFGGVCSSR	1261.5761	9.4	-4.3	1.6
COL1A2	7	484.7414	5.5	2	MLSFVDTR	967.4798	9.6	13.1	4.1
COL1A2	7	420.7316	2.3	2	GVVGPQGAR	839.4615	1.8	16.7	-0.5
COL1A2	2	455.7340	3.3	2	GHNGLDGLK	909.4671	2.9	16.2	-0.5
COL1A2	6	487.9299	9.4	3	GLHGEFGLPGPAGPR	1460.7528	9.8	-9.2	0.5
COL1A2	3	610.3253	6.1	2	TGHPGTVGPAGIR	1218.6472	3.4	10.0	-2.8
PCDH18	3	419.2069	3.6	2	IYEEQR	836.4029	1.6	5.7	-2.0
PCDH18	3	466.7550	3.3	2	LHGHHGFK	931.4778	2.0	-17.7	-1.3
PCDH18	1	1037.1622	16.9	3	SCDIHTNVSMDSVP YTEWELSVIIQDK	3108.4423	19.6	-6.7	2.7

**Supplementary Table 3:** Peptide identification results supporting Supplementary Table 2. Fraction is the strong cation exchange fraction that the peptide was detected in. MZ, RT, CH are the observed peptide m/z, RPLC retention time and charge. Sequence mass and Sequence RT are the theoretical mass and RPLC retention times. Mass Diff and RT Diff are the differences between the observed and theoretical mass and RPLC retention time.