

Supplementary Table S1: Extracted ion intensities (XIC) from dual mass spectrometry of insoluble brain fraction from individual cases in 5 control and 6 FAD with PSEN1 mutations (left) and proteomic spectral counts of pooled insoluble fractions from control and sAD cases in our previously published dataset (right) [3]. The average fold change of protein enrichment in FAD and sAD as compared to control within each group is shown. Protein spectral counts are shown for the control/sAD comparison instead of XIC values because the original proteomic sequencing run was not optimized for obtaining XIC values.

	Control					PSEN1(FAD)						Control vs FAD	Control vs FAD
	B-1313	B-1471	B-1517	B-2027	B-2066	E10-110	W-238	W-24	W-301	W-304	W-328	p-values*	Fold change in FAD
APP	19.69	68.73	26.81	16.34	12.98	943.14	652	862.1	426.72	609.31	483.63	0.00008	22.9
Tau	206.04	195.09	175.6	134.7	230.24	4347.5	3924	3976	3496.6	976.62	3865.07	0.00025	18.2
ApoE	90.31	52.07	128.1	36.5	25.35	417.74	500	263.1	376.57	391.65	521.21	0.00003	6.2
Clusterin	112.54	182.89	126.7	191.9	200.28	237.61	205.2	371.6	197.04	407.99	222.67	0.03437	1.7
Collagen a1-(XXV)	11.16	6.19	7.97	8.24	3.93	399.83	233.1	24.28	211.62	14.69	186.39	0.02749	23.8
U1-70k	2.07	2.43	1.48	1.6	1.49	15.51	9.64	29.33	14.45	50.06	19.13	0.01129	12.7
U1-A	11.79	8.13	6.73	8.54	7.56	9.16	8.74	38.31	12.4	56.98	10.07	0.16080	2.6
Sm B	17.04	24.03	14.03	26.26	23.97	28.22	15.36	66.3	16.16	136.67	41.01	0.19218	2.4
Sm D1	2.99	13.73	4.35	3.58	4.53	3.85	4.4	25.67	4.31	29.77	13.64	0.19406	2.3
Sm D2, isoform 1	4.69	5.6	4.38	5.16	4.96	12.17	11.19	15.5	9.68	20.66	13.75	0.00074	2.8
Sm D2, isoform 2	2.89	3.95	2.82	4.28	3.6	6.58	11.56	10.23	7.59	13.18	8.87	0.00045	2.8
Sm D3	15.87	24.08	27.99	19.03	16.05	19.58	16.25	62.94	16.45	45.37	32.72	0.21857	1.6
Luc7-like	5.87	10.32	9.98	2.45	4.26	5.24	11.35	13.6	8.51	20.48	11.03	0.09221	1.8
DDX46/Prp5	2.67	3.7	2.19	1.1	2.05	2.57	5.18	13.76	3.33	7.65	4.78	0.07044	2.7

	Control		sAD		Control vs sporadic AD
	Control Pool A	Control Pool B	AD Pool A	AD Pool B	Fold change in sAD**
APP	9	31	169	196	9.1
Tau	10	11	824	989	86.3
ApoE	1	1	49	92	70.5
Clusterin	87	78	72	75	0.9
Collagen a1-(XXV)	1	0	23	24	47.0
U1-70k	2	2	31	39	17.5
U1-A	0	1	12	22	34.0
Sm B	6	6	15	15	2.5
Sm D1	7	2	11	11	2.4
Sm D2, isoform 1	10	11	20	14	1.6
Sm D2, isoform 2	***	***	***	***	***
Sm D3	6	3	5	6	1.2
Luc7-like	0	1	5	14	19.0
DDX46/Prp5	0	0	9	12	10.5

B: Baltimore Longitudinal Study of Aging; E: Emory; W: University of Washington; FAD: familial Alzheimer's disease; sAD: sporadic late-onset Alzheimer's disease. *p-values calculated using Student's ttest. **Unable to perform statistical analysis for significance comparing control and sAD due to nature of dataset with pooled cases. ***Unique peptides to SmD2, isoform 2 were not sequenced.