

Supplementary Table 2: Pathway analyses for AD- and tau-related proteins. For each pathway, enrichment in different groups of proteins are indicated (i.e., AD, all studies; AD, clinical; AD, biomarker; t-tau), as well as the overlap between the input and pathway proteins.

Pathway		AD, total			AD, clinical			AD, biomarker			t-tau		
Pathway name	Total genes	overlap	Genes in overlap	FDR (p value)	overlap	Genes in overlap	FDR (p value)	overlap	Genes in overlap	FDR (p value)	overlap	Genes in overlap	FDR (p value)
Platelet activation, signaling and aggregation	262	8	[APOH COL1A2 HRG AHSG YWHAZ FGB IGF2 A2M]	0.00078***	4	[ALB HRG AHSG A2M]	0.013*	4	[APOH FGB IGF2 CLU]	0.013*	4	[HGF VEGFA SERPINE1 SOD1]	0.016*
Platelet degranulation	128	6	[APOH HRG AHSG FGB IGF2 A2M]	0.00078***	4	[ALB HRG AHSG A2M]	0.002**	4	[APOH FGB IGF2 CLU]	0.0016**	4	[HGF VEGFA SERPINE1 SOD1]	0.0033**
Response to elevated platelet cytosolic Ca2+	133	6	[APOH HRG AHSG FGB IGF2 A2M]	0.00078***	4	[ALB HRG AHSG A2M]	0.002**	4	[APOH FGB IGF2 CLU]	0.0016**	4	[HGF VEGFA SERPINE1 SOD1]	0.0033**
Plasma lipoprotein assembly	19	3	[APOC2 APOA2 A2M]	0.0028**	2	[APOE A2M]	0.0076	-	-	-	1	[APOE]	0.042
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	124	5	[IGFBP5 AHSG IGF2 C3 APOA2]	0.0045**	5	[CHGB APOE ALB AHSG C3]	0.00011***	4	[VGF SCG2 IGF2 C3]	0.0016**	2	[APOE SPP1]	0.042
Retinoid metabolism and transport	44	3	[RBP1 APOC2 APOA2]	0.015*	1	[APOE]	0.076	1	[TTR]	0.075	1	[APOE]	0.094
Post-translational protein phosphorylation	107	4	[IGFBP5 AHSG C3 APOA2]	0.015*	5	[CHGB APOE ALB AHSG C3]	0.00011***	3	[VGF SCG2 C3]	0.013*	2	[APOE SPP1]	0.042
Metabolism of fat-soluble vitamins	48	3	[RBP1 APOC2 APOA2]	0.015*	1	[APOE]	0.083	1	[TTR]	0.075	1	[APOE]	0.1
Extracellular matrix organization	301	6	[NCAM1 LTBP2 COL1A2 NRXN1 FGB A2M]	0.015*	1	[A2M]	0.42	3	[NRXN1 TTR FGB]	0.064	2	[SERPINE1 SPP1]	0.15
Plasma lipoprotein assembly, remodeling, and clearance	72	3	[APOC2 APOA2 A2M]	0.038*	3	[APOE ALB A2M]	0.0045**	-	-	-	1	[APOE]	0.15
Binding and Uptake of Ligands by Scavenger Receptors	129	2	[HP COL1A2]	0.15	3	[HP APOE ALB]	0.014*	-	-	-	2	[APOE FTH1]	0.042

Transport of small molecules	731	5	[APOC2 ATP6AP1 AZGP1 APOA2 A2M]	0.15	5	[APOD APOE ALB AZGP1 A2M]	0.048*	-	-	-	2	[APOE FTH1]	0.49
Neutrophil de-granulation	480	5	[HP CHI3L1 NFASC AHSG C3]	0.15	4	[HP CHI3L1 AHSG C3]	0.048*	4	[CHI3L1 NFASC TTR C3]	0.064	3	[CHI3L1 MIF FTH1]	0.091
Constitutive Signaling by Aberrant PI3K in Cancer	86	-	-	-	-	-	-	-	-	-	4	[HGF KITLG HBEGF TGFA]	0.0033**
PI3K/AKT Signaling in Cancer	113	-	-	-	-	-	-	-	-	-	4	[HGF KITLG HBEGF TGFA]	0.0033**
Diseases of signal transduction	403	2	[RBP1 FGB]	0.46	-	-	-	2	[TTR FGB]	0.14	4	[HGF KITLG HBEGF TGFA]	0.035*
Transcriptional regulation by the AP-2 (TFAP2) family of transcription factors	37	-	-	-	1	[APOE]	0.066	-	-	-	3	[VEGFA APOE TGFA]	0.0033**
Generic Transcription Pathway	1233	1	[YWHAZ]	0.99	1	[APOE]	0.9	-	-	-	7	[VEGFA APOE SERPINE1 TGFA SPP1 TN- FRSF10C FAS]	0.042*
RNA Polymerase II Transcription	1355	1	[YWHAZ]	1	1	[APOE]	0.93	-	-	-	7	[VEGFA APOE SERPINE1 TGFA SPP1 TN- FRSF10C FAS]	0.042*
Gene expression (Transcription)	1497	1	[YWHAZ]	1	1	[APOE]	0.94	-	-	-	7	[VEGFA APOE SERPINE1 TGFA SPP1 TN- FRSF10C FAS]	0.042*
Hemostasis	722	8	[APOH COL1A2 HRG AHSG YWHAZ FGB IGF2 A2M]	0.075	4	[ALB HRG AHSG A2M]	0.066	4	[APOH FGB IGF2 CLU]	0.073	7	[HGF VEGFA MIF ANGPT2 F3 SERPINE1 SOD1]	0.0073**
Signaling by Interleukins	639	5	[NCAM1 IGHG1 COL1A2 YW- HAZ FGB]	0.15	-	-	-	1	[FGB]	0.65	7	[HGF VEGFA MIF KITLG HBEGF TGFA SOD1]	0.0048**
Cytokine Signaling in Immune system	953	5	[NCAM1 IGHG1 COL1A2 YW- HAZ FGB]	0.3	-	-	-	1	[FGB]	0.8	8	[HGF VEGFA MIF CD40 KITLG HBEGF TGFA SOD1]	0.0073**
FLT3 Signaling	277	2	[NCAM1 FGB]	0.29	-	-	-	1	[FGB]	0.36	4	[HGF KITLG HBEGF TGFA]	0.016*

Other inter-leukin signaling	300	2	[NCAM1 FGB]	0.32	-	-	-	1	[FGB]	0.39	4	[HGF KITLG HBEGF TGFA]	0.021*
Immune System	2370	11	[HP TREM2 CHI3L1 NCAM1 NFASC IGHG1 COL1A2 AHSG YWHAZ FGB C3]	0.3	5	[HP CHGA CMGA CHI3L1 AHSG C3]	0.43	6	[CHI3L1 NFASC TTR FGB C3 CLU]	0.17	11	[HGF VEGFA CHGA CMGA CHI3L1 MIF CD40 KITLG HBEGF TGFA FTH1 SOD1]	0.033*
Signaling by Receptor Tyrosine Kinases	487	3	[COL1A2 ATP6AP1 IGF2]	0.29	1	[APOE]	0.59	1	[IGF2]	0.55	8	[HGF VEGFA APOE KITLG HBEGF TGFA SPP1]	0.0013**
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	115	-	-	-	-	-	-	-	-	-	4	[HGF KITLG HBEGF TGFA]	0.0033**
Negative regulation of the PI3K/AKT network	122	-	-	-	-	-	-	-	-	-	4	[HGF KITLG HBEGF TGFA]	0.0033**
MAPK1/MAPK3 signaling	266	2	[NCAM1 FGB]	0.27	-	-	-	1	[FGB]	0.35	4	[HGF KITLG HBEGF TGFA]	0.016*
PIP3 activates AKT signaling	275	-	-	-	-	-	-	-	-	-	4	[HGF KITLG HBEGF TGFA]	0.016*
MAPK family signaling cascades	305	2	[NCAM1 FGB]	0.33	-	-	-	1	[FGB]	0.39	4	[HGF KITLG HBEGF TGFA]	0.022*
Intracellular signaling by second messengers	314	-	-	-	-	-	-	-	-	-	4	[HGF KITLG HBEGF TGFA]	0.023*
Signal Transduction	2768	12	[NCAM1 COL1A2 RBP1 APOC2 ATP6AP1 YWHAZ FGB IGF2 C3 APOA2 A2M TAC1]	0.37	4	[APOE AGT C3 A2M]	0.77	5	[TTR FGB IGF2 C3 TAC1]	0.47	11	[HGF VEGFA APOE KITLG SERPINE1 HBEGF TGFA SPP1 PPY FAS]	0.042*
RAF/MAP kinase cascade	259	2	[NCAM1 FGB]	0.26	-	-	-	1	[FGB]	0.34	4	[HGF KITLG HBEGF TGFA]	0.016*
Vesicle-mediated transport	761	3	[HP COL1A2 YWHAZ]	0.57	3	[HP APOE ALB]	0.15	-	-	-	5	[SORT1 APOE HBEGF TGFA FTH1]	0.042*

*, FDR p value < 0.05; **, FDR p value < 0.01; ***, FDR p value < 0.001; -, no overlap between input and pathway proteins. Pathways are only considered to be significantly enriched if the overlap between input and pathway genes is at least 3.