

Supplementary Materials

Genome-wide Network-assisted Association and Enrichment Study of Amyloid Imaging Phenotype in Alzheimer's Disease

Jin Li^a, Feng Chen^a, Qiushi Zhang^b, Xianglian Meng^a, Xiaohui Yao^c, Shannon L. Risacher^d, Jingwen Yan^d, Andrew J. Saykin^d, Hong Liang^a, Li Shen^c, and for the Alzheimer's Disease Neuroimaging Initiative

^aCollege of Automation, Harbin Engineering University, Harbin, China; ^bCollege of Information Engineering, Northeast Dianli University, Jilin, China; ^cDepartment of Biostatistics, Epidemiology and Informatics, University of Pennsylvania Perelman School of Medicine, Philadelphia, USA; ^dDepartment of Radiology and Imaging Sciences, Indiana University School of Medicine, Indianapolis, USA.

Table S1: 156 genes appeared in 24 modules identified by DMS. P-values smaller than 0.001 were in bold. Top 10% of each topological centrality were separately bolded in coloured text. **Betweenness**: betweenness centrality, denotes the number of short communication paths that a node participates in; **Closeness**: closeness centrality, corresponds to the average distance (the length of the shortest paths) between a given node and the rest of the network; **PageRank**: PageRank centrality, takes into account the quantity and quality of connections to a given node; **Degree**: degree centrality, counts the number of interactions with a given node; **P-G₁**: P-value of the gene from GWA analysis of G₁ dataset; **P-G₂**: P-value of the gene from GWA analysis of G₂ dataset; **DegreeP**: degree of the gene in PPIN; **PCT**: percentage, number of genes with degree larger than the gene divided by the number of all genes; **#M**: number of identified modules containing the gene.

Gene	Betweenness	Closeness	PageRank	Degree	P-G ₁	P-G ₂	DegreeP	PCT(%)	#M
<i>APOE</i>	0.001	0.355	0.004	0.019	6.86E-16	1.28E-06	55	7.35	24
<i>TOMM40</i>	0.017	0.375	0.006	0.032	5.39E-14	2.49E-06	41	10.54	21
<i>APP</i>	0.277	0.495	0.040	0.224	5.27E-03	3.73E-02	1649	0.01	20
<i>PARK2</i>	0.192	0.489	0.031	0.179	3.66E-03	1.21E-03	314	0.33	13
<i>ACTG1</i>	0.018	0.375	0.009	0.058	1.12E-02	1.90E-01	111	2.48	9
<i>ATP5O</i>	0.002	0.364	0.006	0.032	2.86E-03	4.25E-03	25	18.32	8
<i>AARS</i>	0.003	0.336	0.005	0.026	6.93E-02	3.31E-02	40	10.84	5
<i>ACTN1</i>	0.002	0.342	0.005	0.026	1.19E-02	1.20E-01	95	3.23	5
<i>ATP5C1</i>	0.003	0.373	0.005	0.026	5.34E-03	2.80E-01	44	9.77	5
<i>CDK14</i>	0.004	0.335	0.003	0.013	1.35E-03	4.63E-03	18	24.82	5
<i>FBXO18</i>	0.000	0.335	0.003	0.013	3.62E-04	9.14E-02	11	36.21	5
<i>HSP90AA1</i>	0.232	0.474	0.037	0.192	2.92E-01	9.35E-02	630	0.06	5
<i>AHSA2</i>	0.000	0.322	0.002	0.006	1.60E-02	2.28E-02	1	83.60	4
<i>ALK</i>	0.000	0.322	0.002	0.006	1.30E-02	9.71E-05	52	7.92	4
<i>ABCA3</i>	0.000	0.292	0.002	0.006	2.74E-02	1.07E-01	2	73.34	3
<i>ABL1</i>	0.028	0.411	0.011	0.058	1.24E-01	8.14E-02	287	0.42	3
<i>ABLIM2</i>	0.002	0.303	0.003	0.013	1.80E-02	5.08E-03	4	59.37	3
<i>ACTA2</i>	0.008	0.347	0.005	0.026	5.59E-02	2.43E-03	55	7.35	3
<i>ADCY9</i>	0.000	0.292	0.002	0.006	3.32E-03	2.67E-03	1	83.60	3
<i>DDAH1</i>	0.001	0.333	0.003	0.013	4.54E-04	4.40E-03	4	59.37	3
<i>IKBKE</i>	0.016	0.366	0.012	0.071	2.68E-02	4.44E-03	299	0.38	3
<i>NRF1</i>	0.125	0.412	0.030	0.154	9.09E-02	2.51E-02	2053	0.00	3
<i>PVRL2</i>	0.002	0.265	0.005	0.019	2.46E-06	1.92E-04	11	36.21	3
<i>ABCA1</i>	0.000	0.273	0.003	0.019	9.07E-04	1.23E-02	46	9.23	2
<i>ABCC4</i>	0.002	0.304	0.005	0.026	2.30E-02	6.14E-03	7	46.48	2

<i>ABCF1</i>	0.003	0.374	0.006	0.032	2.37E-02	2.81E-01	44	9.77	2
<i>ABHD10</i>	0.000	0.351	0.003	0.013	2.50E-03	5.15E-02	3	65.54	2
<i>ACSL1</i>	0.008	0.339	0.003	0.013	7.10E-02	3.11E-02	5	54.41	2
<i>AHR</i>	0.000	0.322	0.002	0.006	3.97E-02	5.82E-02	34	13.02	2
<i>ANKS1B</i>	0.000	0.332	0.002	0.006	5.63E-04	2.07E-02	11	36.21	2
<i>ARHGAP15</i>	0.002	0.271	0.004	0.013	5.73E-03	2.16E-03	7	46.48	2
<i>CBX1</i>	0.017	0.360	0.007	0.032	5.69E-03	3.84E-02	38	11.55	2
<i>CUL1</i>	0.029	0.406	0.013	0.071	2.65E-03	2.83E-01	515	0.12	2
<i>DAGLB</i>	0.000	0.292	0.002	0.006	1.86E-03	3.20E-02	2	73.34	2
<i>PRKAB1</i>	0.011	0.363	0.008	0.045	7.69E-02	8.10E-01	141	1.60	2
<i>RNF2</i>	0.046	0.404	0.018	0.103	6.30E-02	5.39E-04	579	0.08	2
<i>SMURF1</i>	0.048	0.364	0.013	0.064	1.17E-03	2.81E-03	252	0.50	2
<i>ABR</i>	0.015	0.350	0.004	0.019	2.67E-02	1.51E-04	6	50.28	1
<i>ACACA</i>	0.003	0.347	0.006	0.038	1.69E-01	6.44E-02	57	7.02	1
<i>ACAP2</i>	0.000	0.267	0.002	0.006	4.60E-02	5.40E-03	1	83.60	1
<i>ACLY</i>	0.004	0.360	0.007	0.038	7.33E-02	1.42E-01	34	13.02	1
<i>ACTR1A</i>	0.003	0.333	0.004	0.026	1.79E-02	4.88E-01	25	18.32	1
<i>ADORA2B</i>	0.000	0.248	0.002	0.006	4.70E-02	1.18E-02	7	46.48	1
<i>AGGF1</i>	0.000	0.232	0.002	0.006	8.80E-03	3.34E-01	7	46.48	1
<i>AIDA</i>	0.000	0.338	0.003	0.013	8.08E-03	1.00E-01	4	59.37	1
<i>ALDH1A2</i>	0.000	0.277	0.002	0.006	7.61E-02	3.39E-02	2	73.34	1
<i>ALDOA</i>	0.002	0.346	0.004	0.019	2.26E-02	2.04E-01	46	9.23	1
<i>AMPH</i>	0.000	0.280	0.003	0.013	1.67E-03	1.69E-02	17	26.02	1
<i>AMY2B</i>	0.001	0.333	0.003	0.013	8.46E-02	7.81E-02	2	73.34	1
<i>ANK3</i>	0.001	0.299	0.003	0.013	2.55E-03	1.80E-02	15	28.78	1
<i>ANXA13</i>	0.000	0.265	0.002	0.006	3.66E-03	1.69E-01	3	65.54	1
<i>ANXA2</i>	0.009	0.380	0.009	0.051	5.91E-02	8.95E-03	75	4.69	1
<i>APC</i>	0.007	0.354	0.006	0.032	8.23E-02	3.23E-02	126	2.01	1
<i>APLF</i>	0.011	0.362	0.004	0.026	1.72E-01	1.32E-01	11	36.21	1
<i>ARHGAP1</i>	0.001	0.259	0.004	0.013	1.30E-01	1.63E-01	21	21.61	1
<i>ARRB1</i>	0.025	0.418	0.011	0.064	3.44E-02	3.44E-02	217	0.70	1
<i>ATF7</i>	0.000	0.256	0.002	0.006	4.27E-03	6.97E-02	20	22.54	1
<i>ATG12</i>	0.001	0.336	0.003	0.013	2.10E-01	7.36E-02	51	8.13	1
<i>ATP2B2</i>	0.001	0.257	0.003	0.013	1.16E-02	2.10E-02	9	40.79	1
<i>ATP6VIC1</i>	0.000	0.300	0.003	0.013	1.03E-01	2.06E-02	40	10.84	1
<i>BAG3</i>	0.002	0.334	0.005	0.026	1.53E-01	1.38E-01	335	0.27	1
<i>BIRC2</i>	0.010	0.340	0.008	0.045	4.89E-03	3.05E-01	81	4.14	1
<i>BTBD2</i>	0.000	0.224	0.002	0.013	1.41E-03	5.41E-03	30	15.16	1
<i>BZW2</i>	0.000	0.323	0.003	0.013	1.12E-03	6.84E-02	18	24.82	1
<i>CALCOCO2</i>	0.009	0.353	0.007	0.038	1.24E-01	4.68E-04	69	5.28	1
<i>CASP10</i>	0.000	0.282	0.002	0.006	1.77E-03	1.70E-02	39	11.15	1
<i>CASP3</i>	0.036	0.391	0.010	0.051	1.92E-01	2.47E-01	151	1.43	1
<i>CBL</i>	0.026	0.360	0.013	0.083	5.20E-03	2.30E-01	215	0.74	1

<i>CBLC</i>	0.001	0.284	0.004	0.019	1.95E-02	6.31E-02	34	13.02	1
<i>CD93</i>	0.005	0.259	0.007	0.026	2.45E-01	2.15E-02	18	24.82	1
<i>CDC40</i>	0.002	0.297	0.004	0.019	3.02E-02	1.79E-01	20	22.54	1
<i>CDC6</i>	0.001	0.257	0.004	0.013	3.30E-01	1.79E-01	38	11.55	1
<i>CDH2</i>	0.014	0.296	0.006	0.026	7.72E-03	9.03E-02	60	6.53	1
<i>CDH4</i>	0.000	0.229	0.002	0.006	7.91E-04	3.98E-03	2	73.34	1
<i>CFTR</i>	0.035	0.379	0.012	0.064	1.98E-01	5.46E-01	174	1.09	1
<i>CHD1L</i>	0.009	0.284	0.005	0.019	7.93E-02	1.19E-01	20	22.54	1
<i>CHMP1B</i>	0.002	0.306	0.003	0.013	3.96E-01	7.95E-02	16	27.31	1
<i>CISD1</i>	0.009	0.363	0.008	0.038	5.36E-01	4.35E-02	8	43.39	1
<i>CNTN2</i>	0.000	0.279	0.003	0.013	1.96E-02	3.70E-02	30	15.16	1
<i>COL4A1</i>	0.007	0.336	0.005	0.019	3.71E-03	1.43E-03	27	17.03	1
<i>COL4A2</i>	0.007	0.336	0.005	0.019	7.75E-03	3.90E-02	22	20.75	1
<i>CUX1</i>	0.000	0.232	0.002	0.006	7.83E-03	1.30E-04	24	19.09	1
<i>DBN1</i>	0.008	0.305	0.007	0.032	1.01E-02	3.43E-01	55	7.35	1
<i>DMRTA1</i>	0.005	0.331	0.004	0.019	2.84E-01	1.75E-01	4	59.37	1
<i>DOK5</i>	0.000	0.264	0.002	0.006	1.20E-02	8.30E-04	8	43.39	1
<i>DOK6</i>	0.000	0.264	0.002	0.006	3.39E-02	3.79E-04	3	65.54	1
<i>DPP4</i>	0.015	0.288	0.008	0.038	4.69E-01	1.72E-01	13	31.99	1
<i>ECT2</i>	0.030	0.302	0.012	0.058	3.64E-03	3.47E-01	125	2.04	1
<i>EEF2K</i>	0.009	0.339	0.007	0.038	2.96E-03	5.59E-02	129	1.94	1
<i>ELAVL1</i>	0.100	0.420	0.025	0.141	5.16E-03	3.69E-01	1344	0.02	1
<i>EPHA2</i>	0.004	0.391	0.006	0.032	4.39E-02	3.75E-03	34	13.02	1
<i>ESRRB</i>	0.000	0.333	0.003	0.013	1.95E-03	1.20E-01	6	50.28	1
<i>ESRRG</i>	0.000	0.361	0.003	0.013	1.57E-03	6.28E-03	24	19.09	1
<i>FMNL1</i>	0.005	0.369	0.006	0.032	2.58E-01	5.39E-01	54	7.57	1
<i>FOS</i>	0.015	0.343	0.006	0.026	1.20E-01	3.88E-01	130	1.90	1
<i>GABRR1</i>	0.000	0.258	0.002	0.006	9.92E-02	4.07E-02	13	31.99	1
<i>GPD2</i>	0.000	0.330	0.003	0.013	2.61E-01	1.84E-02	3	65.54	1
<i>GRIA1</i>	0.000	0.265	0.002	0.013	1.37E-03	4.11E-04	26	17.67	1
<i>GSK3B</i>	0.022	0.407	0.012	0.071	1.74E-01	4.00E-02	276	0.44	1
<i>HSDL2</i>	0.003	0.356	0.005	0.026	4.06E-01	3.39E-02	6	50.28	1
<i>HTRA2</i>	0.030	0.382	0.010	0.051	8.85E-01	9.32E-02	40	10.84	1
<i>IL7R</i>	0.004	0.350	0.007	0.038	2.57E-02	1.74E-03	84	3.85	1
<i>ILF3</i>	0.009	0.373	0.008	0.045	2.12E-02	4.72E-01	230	0.64	1
<i>INO80C</i>	0.001	0.333	0.003	0.013	1.97E-04	6.00E-02	16	27.31	1
<i>ITPR1</i>	0.001	0.263	0.004	0.013	1.31E-03	1.65E-02	37	11.94	1
<i>KLHL6</i>	0.000	0.322	0.002	0.006	2.04E-01	5.05E-03	2	73.34	1
<i>MAPK3</i>	0.004	0.318	0.006	0.032	3.66E-02	1.51E-01	159	1.27	1
<i>MAPK6</i>	0.026	0.342	0.010	0.051	1.30E-01	1.63E-01	139	1.63	1
<i>MGMT</i>	0.001	0.332	0.004	0.019	9.17E-03	4.47E-03	59	6.67	1
<i>MYLK4</i>	0.000	0.322	0.002	0.006	1.86E-01	2.54E-03	3	65.54	1
<i>MYO1D</i>	0.010	0.322	0.004	0.019	1.62E-03	1.20E-03	21	21.61	1

<i>NCOA3</i>	0.008	0.350	0.008	0.045	4.04E-03	3.24E-02	98	3.08	1
<i>NDFIP1</i>	0.005	0.318	0.006	0.032	1.26E-01	2.04E-01	7	46.48	1
<i>NEDD4</i>	0.037	0.360	0.014	0.071	6.13E-03	2.74E-02	232	0.64	1
<i>NEDD4L</i>	0.002	0.331	0.005	0.026	7.39E-03	1.50E-02	132	1.82	1
<i>NR4A2</i>	0.000	0.306	0.003	0.013	2.79E-01	1.95E-01	25	18.32	1
<i>ORC5</i>	0.004	0.282	0.006	0.026	8.03E-02	6.47E-02	27	17.03	1
<i>OXCT1</i>	0.000	0.276	0.004	0.019	2.07E-01	5.68E-03	34	13.02	1
<i>PAG1</i>	0.000	0.300	0.003	0.013	2.85E-02	1.78E-04	18	24.82	1
<i>PARD3</i>	0.002	0.290	0.003	0.019	1.59E-02	1.87E-03	59	6.67	1
<i>PDZK1</i>	0.030	0.354	0.008	0.038	1.10E-01	1.01E-01	28	16.40	1
<i>PLEKHF2</i>	0.008	0.357	0.005	0.026	4.60E-02	3.10E-02	29	15.84	1
<i>PSKH1</i>	0.027	0.332	0.007	0.026	2.83E-01	9.29E-02	5	54.41	1
<i>PSMA1</i>	0.005	0.385	0.008	0.045	2.35E-03	4.69E-02	99	3.01	1
<i>PSME2</i>	0.020	0.389	0.010	0.058	9.25E-01	1.76E-02	35	12.75	1
<i>PTEN</i>	0.026	0.360	0.009	0.051	7.76E-02	5.96E-01	81	4.14	1
<i>PTPRF</i>	0.000	0.264	0.002	0.013	3.55E-03	4.62E-02	25	18.32	1
<i>PTPRO</i>	0.024	0.360	0.008	0.058	4.61E-02	4.54E-04	26	17.67	1
<i>RDH13</i>	0.000	0.250	0.002	0.006	5.27E-02	6.03E-03	3	65.54	1
<i>RET</i>	0.048	0.357	0.012	0.058	1.29E-01	2.45E-03	37	11.94	1
<i>RNF141</i>	0.001	0.276	0.003	0.019	2.54E-01	2.75E-04	3	65.54	1
<i>SCYL1</i>	0.000	0.226	0.004	0.013	2.21E-01	5.66E-01	5	54.41	1
<i>SEPT11</i>	0.019	0.347	0.009	0.045	1.85E-01	1.45E-01	29	15.84	1
<i>SEPT9</i>	0.021	0.366	0.007	0.038	5.78E-02	1.13E-02	39	11.15	1
<i>SH3GL2</i>	0.017	0.354	0.007	0.038	3.24E-02	4.76E-05	54	7.57	1
<i>SH3GL3</i>	0.003	0.294	0.006	0.032	3.86E-03	7.01E-02	39	11.15	1
<i>SLC11A2</i>	0.004	0.345	0.005	0.026	1.21E-01	4.05E-02	6	50.28	1
<i>SLC22A4</i>	0.000	0.271	0.003	0.013	3.64E-01	1.09E-01	4	59.37	1
<i>SLC9A3R2</i>	0.043	0.329	0.014	0.064	6.97E-02	8.72E-02	52	7.92	1
<i>SLCO3A1</i>	0.000	0.248	0.002	0.006	6.78E-04	3.79E-03	3	65.54	1
<i>SNTA1</i>	0.010	0.301	0.009	0.045	1.41E-01	5.11E-04	71	5.08	1
<i>SREBF2</i>	0.003	0.322	0.005	0.026	3.46E-04	8.66E-04	55	7.35	1
<i>STARD13</i>	0.023	0.354	0.007	0.032	3.15E-03	1.08E-02	14	30.43	1
<i>STAT5B</i>	0.006	0.358	0.006	0.032	3.60E-02	7.25E-02	63	6.12	1
<i>STYK1</i>	0.000	0.331	0.003	0.013	3.69E-01	5.40E-03	3	65.54	1
<i>SUCLA2</i>	0.006	0.307	0.004	0.019	1.51E-01	4.79E-02	15	28.78	1
<i>SUCLG1</i>	0.009	0.300	0.009	0.051	8.25E-01	6.59E-02	11	36.21	1
<i>SUCLG2</i>	0.001	0.279	0.004	0.019	2.74E-02	3.19E-02	18	24.82	1
<i>TAX1BP1</i>	0.036	0.347	0.011	0.051	1.17E-01	9.31E-02	23	20.00	1
<i>TGM3</i>	0.014	0.341	0.007	0.038	1.31E-01	1.17E-02	8	43.39	1
<i>TPM4</i>	0.016	0.352	0.006	0.032	1.24E-01	1.28E-02	38	11.55	1
<i>TRIM24</i>	0.003	0.308	0.004	0.019	8.27E-02	2.48E-03	37	11.94	1
<i>U2AF1</i>	0.006	0.348	0.006	0.032	2.63E-04	1.11E-01	83	3.95	1
<i>USP53</i>	0.001	0.261	0.003	0.013	3.87E-02	2.11E-01	21	21.61	1

<i>WFOX</i>	0.002	0.316	0.005	0.026	1.61E-04	1.56E-03	198	0.89	1
<i>ZNF787</i>	0.005	0.349	0.006	0.032	2.02E-01	5.22E-02	5	54.41	1