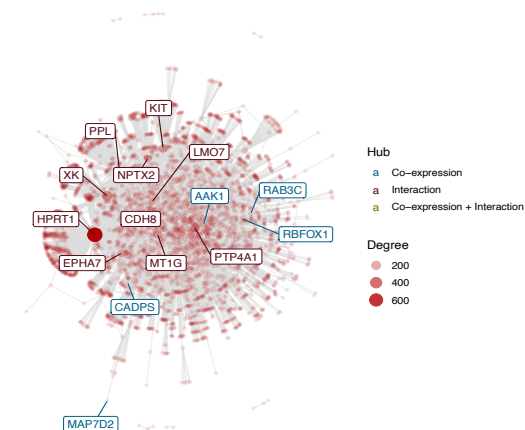


Supplementary Material

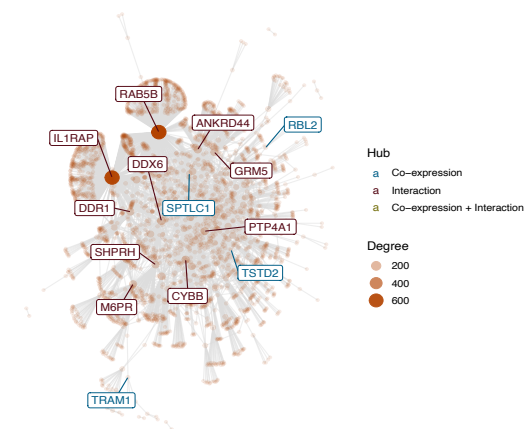
1 SUPPLEMENTARY FIGURES

The co-expression network analysis found three gene modules in Alzheimer's disease namely M1 to M3, which show 538 519, and 118 genes, respectively. Five modules M1 to M5 were found in control samples, with 384, 208, 173, 92, and 43 genes, respectively. Modules were shown in Figures S1 and Figure 2 S2.

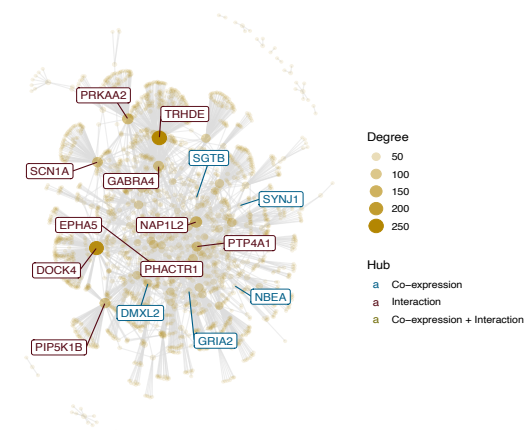
M1



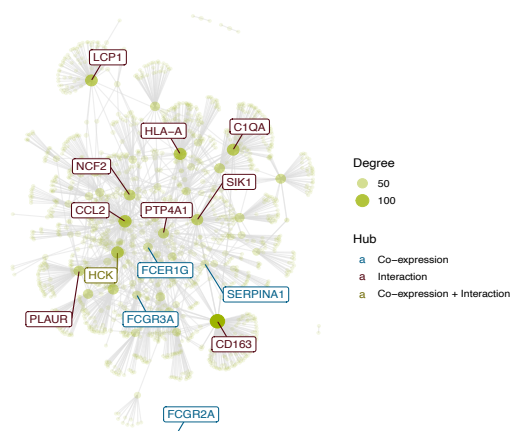
M2



M3



M4



M5

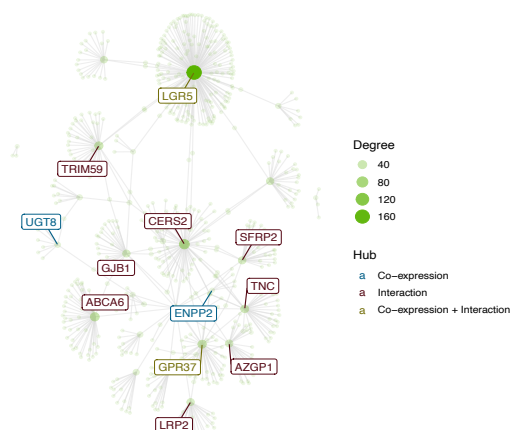


Figure S1. Gene-gene interaction networks for each co-expressed gene module identified by CEMiTool in fusiform gyrus of control samples.



Figure S2. Gene-gene interaction networks for each co-expressed gene module identified by CEMiTool in fusiform gyrus of Alzheimer's Disease.

2 SUPPLEMENTARY TABLES

Table S1: Differentially co-expressed links identified by diffcoexp ($\text{FDR} \leq 0.05$).

Gene A	Gene B	Corr. in Controls	Corr. in Cases	Corr. difference	FDR
CYP2C8	HECW1	0,295	0,810	0,516	1,65E-05
FAM153B	CAMKK1	0,334	0,852	0,517	2,20E-06
FAM153B	SYT7	0,376	0,895	0,518	9,69E-08
FAM153B	NGEF	0,321	0,849	0,529	1,99E-06
FAM153B	CHGB	0,242	0,807	0,565	5,46E-06
CKMT1B	SLC7A4	0,240	0,817	0,576	2,54E-06
FAM153B	SYP	0,270	0,834	0,563	1,99E-06
FAM153B	CRYM	0,351	0,869	0,518	1,17E-06
CYP2C8	STMN2	0,289	0,813	0,524	1,25E-05
FAM153B	STMN2	0,344	0,850	0,506	2,75E-06
FAM153B	NCALD	0,317	0,839	0,522	3,18E-06
FAM153B	NEFM	0,260	0,824	0,563	2,54E-06
CKMT1B	NEFM	0,309	0,816	0,507	1,65E-05
FAM153B	ATP1A3	0,266	0,812	0,546	7,11E-06
FAM153B	RAB3A	0,298	0,834	0,535	3,18E-06
FAM153B	PTPN5	0,366	0,879	0,512	8,35E-07
FAM153B	GDA	0,365	0,869	0,504	1,67E-06
FAM153B	RASL11B	0,322	0,854	0,532	1,73E-06
FAM153B	MCHR1	0,223	0,811	0,588	2,54E-06
FAM153B	SULT4A1	0,329	0,856	0,527	1,73E-06
CYP2C8	SNAP25	0,307	0,815	0,507	1,71E-05
FAM153B	GAD2	0,301	0,807	0,506	2,37E-05
STAT4	CYP2C8	0,277	0,819	0,542	6,02E-06
STXBP5L	CYP2C8	0,231	0,805	0,573	5,02E-06
INA	CYP2C8	0,307	0,823	0,517	9,57E-06
LRTM2	CYP2C8	0,300	0,806	0,505	2,44E-05
CREG2	CYP2C8	0,301	0,804	0,503	2,82E-05
MAP7D2	CYP2C8	0,296	0,814	0,519	1,35E-05

Table S1 continued from previous page

Gene A	Gene B	Corr. in Controls	Corr. in Cases	Corr. difference	FDR
SV2B	CYP2C8	0,302	0,805	0,503	2,64E-05
VSTM5	CYP2C8	0,251	0,816	0,565	3,40E-06
FAM153B	CLSTN3	0,322	0,846	0,523	2,42E-06
FAM153B	CDH18	0,315	0,845	0,530	2,27E-06
FAM153B	PAK1	0,324	0,854	0,530	1,73E-06
CKMT1B	CHRNA2	0,343	0,853	0,510	2,36E-06
FAM153B	LRRTM1	0,305	0,838	0,533	2,60E-06
FAM153B	NELL1	0,314	0,827	0,513	8,51E-06
FAM153B	SVOP	0,248	0,824	0,575	2,20E-06
CKMT1B	SVOP	0,321	0,853	0,532	1,73E-06
FAM153B	TMEM130	0,307	0,850	0,543	1,73E-06
FAM153B	ENTPD3	0,317	0,846	0,529	2,27E-06
FAM153B	KCNJ4	0,298	0,822	0,524	8,11E-06
FAM153B	GAP43	0,259	0,832	0,573	1,73E-06
CKMT1B	NRIP3	0,305	0,813	0,509	1,77E-05
BEX5	FAM153B	0,263	0,825	0,561	2,54E-06
AGBL4	FAM153B	0,279	0,803	0,524	1,80E-05
C2orf80	FAM153B	0,330	0,869	0,539	8,35E-07
L1CAM	FAM153B	0,330	0,830	0,500	1,02E-05