Online Supplemental materials for:

Identification of Hub Genes Related to Alzheimer's Disease and Major Depressive Disorder

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Online Supplemental Figure S1

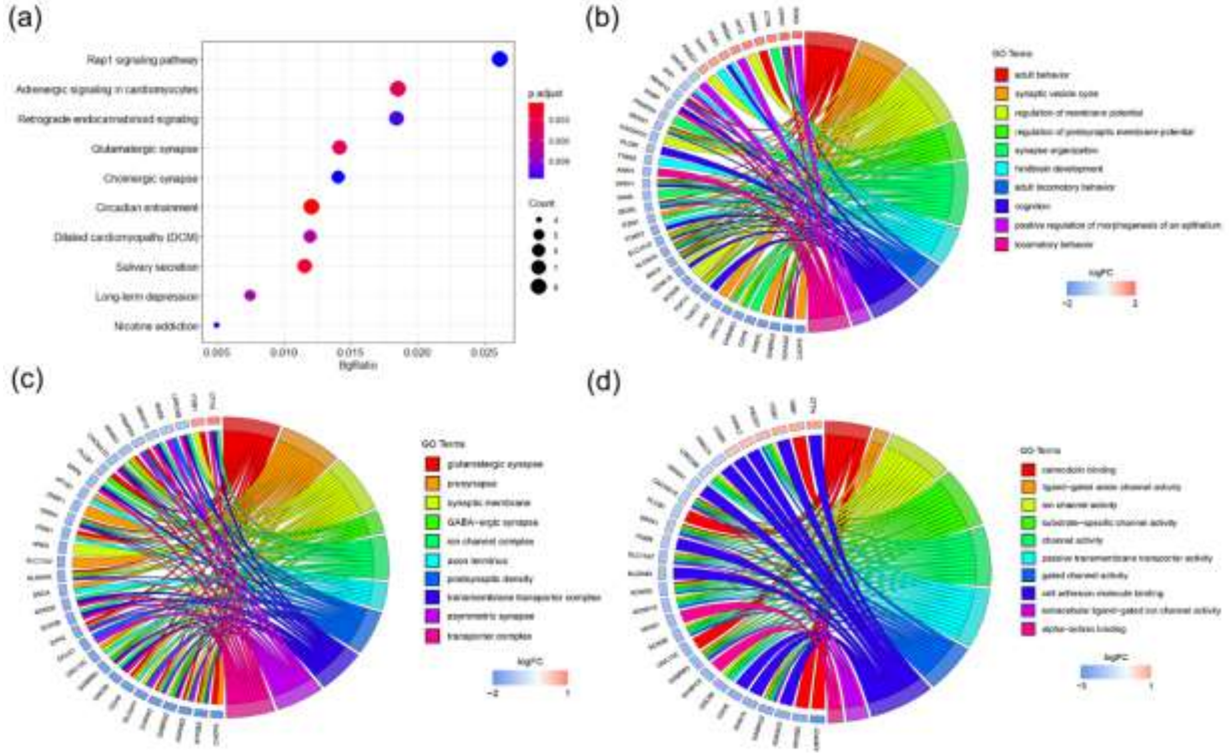

Figure S1. Functional characteristics analysis for DEGs of AD-related datasets. (a) KEGG pathway enrichment analyses. (b) The BP category of GO enrichment analyses. (c) The CC category of GO enrichment analyses. (d) The MF category of GO enrichment analyses.

Online Supplemental Figure S2

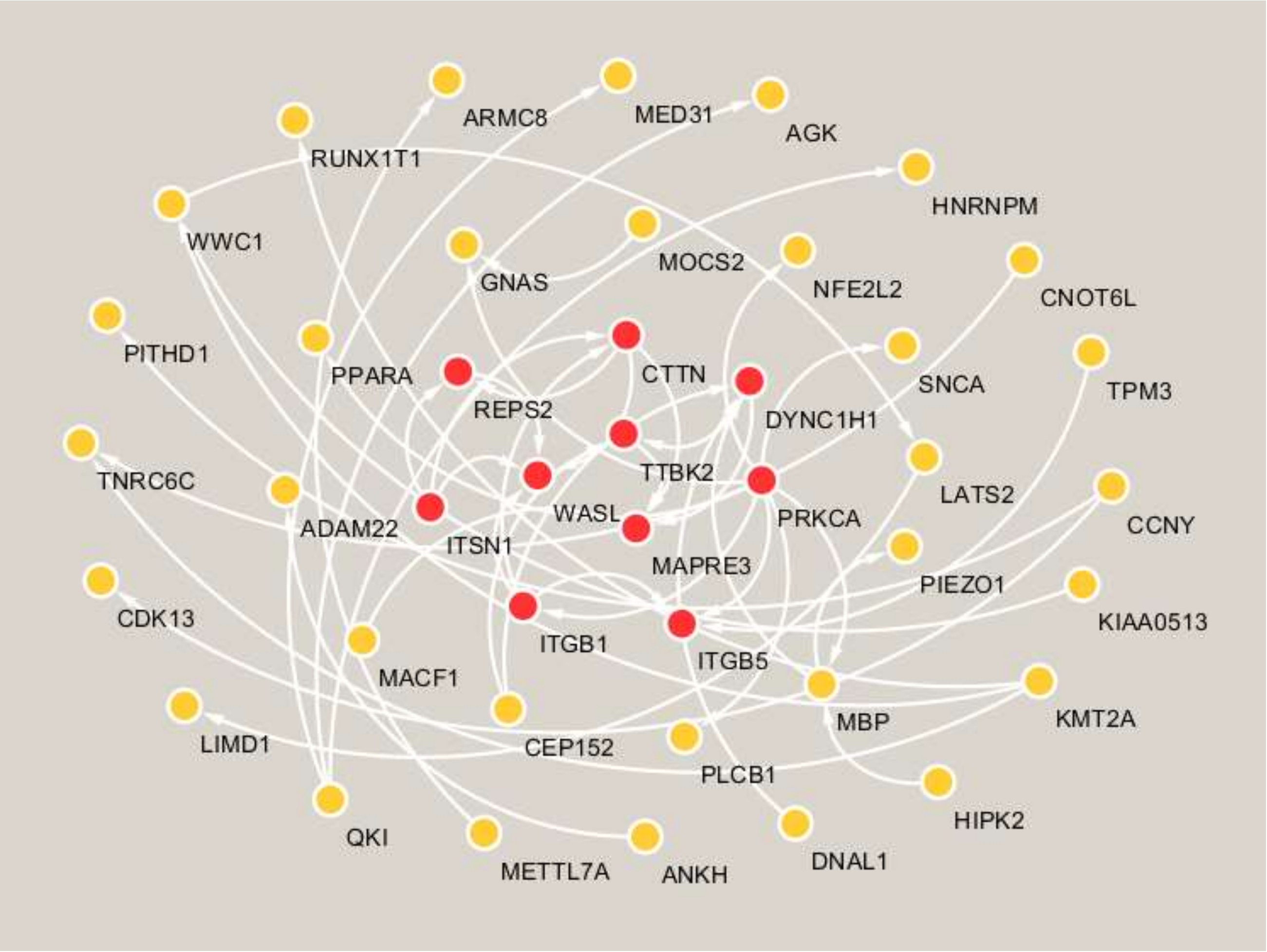

Figure S2. Establishment of the protein- protein interaction network. Nine hub genes are shown in red.

Table S1 Significant top 10 enrichments of KEGG pathways of 171 DEGs of AD-related datasets.

ID	Description	Term Candidate Gene Num	Total Candidate Gene Num	Term Gene Num	Total Gene Num	Rich Ratio*	p.value	p.adjust	q.value
hsa04713	Circadian entrainment	8	73	97	8041	0.109589	2.36E-06	0.000494	0.000358
hsa04970	Salivary secretion	7	73	91	8041	0.09589	1.67E-05	0.001748	0.001268
hsa04261	Adrenergic signaling in cardiomyocytes	8	73	149	8041	0.109589	5.59E-05	0.003765	0.002731
hsa04724	Glutamatergic synapse	7	73	114	8041	0.09589	7.21E-05	0.003765	0.002731
hsa04730	Long-term depression	5	73	60	8041	0.068493	0.000199	0.007703	0.005587
hsa05414	Dilated cardiomyopathy (DCM)	6	73	96	8041	0.082192	0.000221	0.007703	0.005587
hsa04723	Retrograde endocannabinoid signaling	7	73	148	8041	0.09589	0.000366	0.010939	0.007934
hsa05033	Nicotine addiction	4	73	40	8041	0.054795	0.000446	0.011423	0.008285
hsa04725	Cholinergic synapse	6	73	113	8041	0.082192	0.000534	0.011423	0.008285
hsa04015	Rap1 signaling pathway	8	73	210	8041	0.109589	0.000592	0.011423	0.008285

* The rich ratio is the ratio of the value of "Term Candidate Gene Num" to the value of " Total Candidate Gene Num ". It means that the higher the rich ratio’s value of the pathway, the greater the correlation between the pathway and AD.

Table S2 Significant top 10 of GO enrichment analyses of 171 DEGs of AD-related datasets.

	ID	**Description**	**Term Candidate Gene Num**	**Total Candidate Gene Num**	**Term Gene Num**	**Total Gene Num**	**Rich Ratio***	**p.value**
BP	GO:0030534	adult behavior	10	148	144	18670	0.067567568	2.24E-07
	GO:0099504	synaptic vesicle cycle	10	148	194	18670	0.067567568	3.42E-06
	GO:0042391	regulation of membrane potential	14	148	434	18670	0.094594595	9.45E-06
	GO:0060078	regulation of postsynaptic membrane potential	8	148	140	18670	0.054054054	1.59E-05
	GO:0050808	synapse organization	13	148	408	18670	0.087837838	2.27E-05
	GO:0030902	hindbrain development	8	148	152	18670	0.054054054	2.89E-05
	GO:0008344	adult locomotory behavior	6	148	77	18670	0.040540541	3.34E-05
	GO:0050890	cognition	10	148	296	18670	0.067567568	0.000128069
	GO:1905332	positive regulation of morphogenesis of an epithelium	4	148	35	18670	0.027027027	0.000163979
	GO:0007626	locomotory behavior	8	148	198	18670	0.054054054	0.000184398
CC	GO:0098978	glutamatergic synapse	13	156	349	19717	0.083333333	4.29E-06
	GO:0098793	presynapse	15	156	491	19717	0.096153846	8.58E-06
	GO:0097060	synaptic membrane	14	156	432	19717	0.08974359	8.96E-06
	GO:0098982	GABA-ergic synapse	6	156	71	19717	0.038461538	2.09E-05
	GO:0034702	ion channel complex	11	156	301	19717	0.070512821	2.86E-05
	GO:0043679	axon terminus	7	156	119	19717	0.044871795	4.53E-05
	GO:0014069	postsynaptic density	11	156	324	19717	0.070512821	5.58E-05
	GO:1902495	transmembrane transporter complex	11	156	324	19717	0.070512821	5.58E-05
	GO:0032279	asymmetric synapse	11	156	328	19717	0.070512821	6.23E-05
	GO:1990351	transporter complex	11	156	332	19717	0.070512821	6.95E-05
MF	GO:0005516	calmodulin binding	8	147	200	17697	0.054421769	0.000269809
	GO:0099095	ligand-gated anion channel activity	3	147	20	17697	0.020408163	0.000577097
	GO:0005216	ion channel activity	11	147	416	17697	0.074829932	0.000718978

GO:0022838	substrate-specific channel activity	11	147	428	17697	0.074829932	0.000906803
GO:0015267	channel activity	11	147	456	17697	0.074829932	0.001507154
GO:0022803	passive transmembrane transporter activity	11	147	457	17697	0.074829932	0.001533502
GO:0022836	gated channel activity	9	147	343	17697	0.06122449	0.002303175
GO:0050839	cell adhesion molecule binding	11	147	499	17697	0.074829932	0.003033698
GO:0005230	extracellular ligand-gated ion channel activity	4	147	75	17697	0.027210884	0.003518131
GO:0051393	alpha-actinin binding	3	147	37	17697	0.020408163	0.00354801

* The rich ratio is the ratio of the value of "Term Candidate Gene Num" to the value of " Total Candidate Gene Num ". It means that the higher the rich ratio’s value of the GO term, the greater the correlation between the GO term and AD.

Table S3 Significant top 10 enrichments of KEGG pathways of 79 DEGs shared by AD and MDD.

ID	Description	Term Candidate Gene Num	Total Candidate Gene Num	Term Gene Num	Total Gene Num	Rich Ratio*	p.value	p.adjust	q.value
hsa04730	Long-term depression	4	33	60	8041	0.121212	9.75E-05	0.014432	0.00924
hsa04392	Hippo signaling pathway - multiple species	3	33	26	8041	0.090909	0.000214	0.015359	0.00983
hsa04540	Gap junction	4	33	88	8041	0.121212	0.00043	0.015359	0.00983
hsa04970	Salivary secretion	4	33	91	8041	0.121212	0.000489	0.015359	0.00983
hsa05414	Dilated cardiomyopathy (DCM)	4	33	96	8041	0.121212	0.000599	0.015359	0.00983
hsa04713	Circadian entrainment	4	33	97	8041	0.121212	0.000623	0.015359	0.00983
hsa04961	Endocrine and other factor-regulated calcium reabsorption	3	33	53	8041	0.090909	0.001283	0.027126	0.01736
hsa04611	Platelet activation	4	33	124	8041	0.121212	0.00156	0.028854	0.01847
hsa04270	Vascular smooth muscle contraction	4	33	132	8041	0.121212	0.001963	0.032281	0.02066
hsa04924	Renin secretion	3	33	69	8041	0.090909	0.002744	0.033403	0.02138

* The rich ratio is the ratio of the value of "Term Candidate Gene Num" to the value of " Total Candidate Gene Num ". It means that the higher the rich ratio’s value of the pathway, the greater the correlation between the pathway and AD and MDD.

Table S4 Significant top 10 of GO enrichment analyses of 79 DEGs shared by AD and MDD.

	ID	Description	Term Candidate Gene Num	Total Candidate Gene Num	Term Gene Num	Total Gene Num	Rich* Ratio	pvalue
BP	GO:0033962	cytoplasmic mRNA processing body assembly	3	68	21	18670	0.044118	5.86E-05
	GO:0007626	locomotory behavior	6	68	198	18670	0.088235	8.36E-05
	GO:0008344	adult locomotory behavior	4	68	77	18670	0.058824	0.000178
	GO:0030534	adult behavior	5	68	144	18670	0.073529	0.00018
	GO:0097581	lamellipodium organization	4	68	82	18670	0.058824	0.000227
	GO:0035329	hippo signaling	3	68	38	18670	0.044118	0.000356
	GO:1904526	regulation of microtubule binding	2	68	10	18670	0.029412	0.000577
	GO:0061013	regulation of mRNA catabolic process	5	68	199	18670	0.073529	0.000791
	GO:0035330	regulation of hippo signaling	2	68	12	18670	0.029412	0.000843
	GO:1901215	negative regulation of neuron death	5	68	208	18670	0.073529	0.000965
CC	GO:0030027	lamellipodium	6	73	193	19717	0.082192	8.04E-05
	GO:0031252	cell leading edge	7	73	403	19717	0.09589	0.000723
	GO:0016607	nuclear speck	6	73	397	19717	0.082192	0.00351
	GO:0008076	voltage-gated potassium channel complex	3	73	87	19717	0.041096	0.004131
	GO:0030139	endocytic vesicle	5	73	303	19717	0.068493	0.005314
	GO:0034705	potassium channel complex	3	73	96	19717	0.041096	0.005438
	GO:0005938	cell cortex	5	73	308	19717	0.068493	0.005689
	GO:0008305	integrin complex	2	73	31	19717	0.027397	0.005865
	GO:0019867	outer membrane	4	73	203	19717	0.054795	0.006827
	GO:0051233	spindle midzone	2	73	34	19717	0.027397	0.007026
MF	GO:0005178	integrin binding	4	67	132	17697	0.059701	0.001576
	GO:0051010	microtubule plus-end binding	2	67	17	17697	0.029851	0.001851
	GO:0051959	dynein light intermediate chain binding	2	67	29	17697	0.029851	0.005367
	GO:0003779	actin binding	6	67	431	17697	0.089552	0.00575

GO:0003713	transcription coactivator activity	5	67	319	17697	0.074627	0.007157
GO:0043014	alpha-tubulin binding	2	67	37	17697	0.029851	0.008634
GO:0015631	tubulin binding	5	67	336	17697	0.074627	0.008849
GO:0019894	kinesin binding	2	67	42	17697	0.029851	0.011027
GO:0001221	transcription cofactor binding	2	67	43	17697	0.029851	0.011537
GO:0048156	tau protein binding	2	67	45	17697	0.029851	0.012588

* The rich ratio is the ratio of the value of "Term Candidate Gene Num" to the value of " Total Candidate Gene Num ". It means that the higher the rich ratio’s value of the GO term, the greater the correlation between the GO term and AD and MDD.

Table S5 The top 10 of Degree, MNC, DMNC, MCC using the CytoHubba plugin

Degree		MNC		DMNC		MCC	
Gene Symbol	score	Gene Symbol	score	Gene Symbol	score	Gene Symbol	score
PRKCA	8	WASL	4	REPS2	0.46346	CTTN	9
DYNC1H1	5	CTTN	4	ITSN1	0.46346	PRKCA	8
CTTN	5	REPS2	3	WASL	0.37893	WASL	8
MAPRE3	4	DYNC1H1	3	CTTN	0.37893	REPS2	6
ITGB1	4	TTBK2	3	DYNC1H1	0.30898	DYNC1H1	6
WASL	4	ITSN1	3	TTBK2	0.30898	ITSN1	6
ITSN1	3	MAPRE3	2	MAPRE3	0.30779	MBP	4
ITGB5	3	ITGB5	2	ITGB5	0.30779	MAPRE3	4
REPS2	3	ITGB1	2	ITGB1	0.30779	ITGB1	4
TTBK2	3	PRKCA	2	PRKCA	0.30779	TTBK2	4
KMT2A	3	CEP152	2	CEP152	0.30779		
WWC1	3						
QKI	3						

Abbreviations: MNC: Maximum Neighborhood Component; DMNC: Density of maximum neighborhood component; MCC: Maximal Clique Centrality.

Table S6 The top five target genes of TF-target regulatory network.

Target Genes	Degree*	TF
PPARA	9	RELA
ITGB1	6	FOXF2
IGF2BP2	3	HMGA2
MBP	3	SOX10
REPS2	2	NFKB1

Abbreviations: TF: transcription factor. *Degree is a algorithm to assess the importance of genes in TF-target regulatory network.

Table S7 The top five target genes of miRNA-target regulatory network.

Target Genes	Degree*	MicroRNA
QKI	45	hsa-mir-16-5p
HIPK2	39	hsa-mir-124-3p
KMT2A	33	hsa-mir-155-5p
WASL	32	hsa-mir-1-3p
IL6ST	31	hsa-mir-23b-3p

*Degree is a algorithm to assess the importance of genes in TF-target regulatory network.

Table S8 Gene symbol of 171 DEGs from AD-related datasets.

Gene symbol	Gene symbol	Gene symbol	Gene symbol	Gene symbol	Gene symbol
CCNY	SEZ6L	HIPK2	AP1S1	LIMD1	LRIG1
CDH8	GABRG2	PCDH7	DYNC1H1	COG1	DOCK6
ITSN1	SYNPO2	BCAP29	PITHD1	ABHD12	DOCK1
SNCA	HIF3A	FRMPD4	TMED5	KCNQ5	TMEM178B
ACSS3	GUCY1B3	REPS2	TNRC6C	SOX9	SLC22A23
NLGN4X	RALGAPA2	TUSC3	CECR6	DLGAP1	DKK3
AKT2	CADPS	PREPL	ST3GAL3	POU3F2	SEC16B
ANKRD36	SLC17A7	RHEB	C17orf51	FOXP2	CADM2
MED31	EMX1	SOBP	ZNRF1	ELFN2	DCLK1
RGS12	IKZF2	MOCS2	DCAF8	KIAA0513	ARL10
MBP	CYGB	WASL	GNAS	CDK13	LMBRD2
CHRM3	HNRNPM	TTBK2	FRYL	RHOJ	PPARA
KAZN	CEP152	LGALSL	ITGB1	CTTN	ST8SIA3
AMBRA1	BCAT1	ANKRD50	RUNX1T1	FABP3	UNC13C
RAPH1	NPAS3	METTL7A	PCSK2	WWC1	KIAA0754
ARMC8	PRKCA	SMARCA2	GREM2	AGK	ITGB8
MAPRE3	GRIN1	DIRAS1	LRRC8B	PIEZO1	IGF2BP2
DENND5B	EPB41L4B	RPS6KA5	UNC80	LATS2	ANKH
FGF14	SLC3A1	TPM3	RAB1A	IQCA1	GART
CSRNP3	NFE2L2	PTPN5	DNAL1	ZKSCAN8	DLL3
B3GALNT1	ZNF709	QKI	ANK2	PMP2	ATP6V1H
RREB1	ATP2B2	AHI1	CEBPZOS	MSI2	CDC42EP4
EPHA6	NUB1	KCNK10	ZNF224	IL6ST	TIMM50
WNT2B	NRXN1	ICA1L	TLL2	ZNF800	ITGB5
GIPC3	UBE2QL1	MAGI1	PXDC1	ADAM22	MEG3
KITLG	SYN2	DPP6	PLCB1	SCN2B	NDUFA10
CCDC88A	ARPP21	CACNA1C	PRKG1	CNOT6L	FMNL2
GABRB3	KMT2A	LOC101930370		PET117///KAT14	
MIR4683///FZD8	LOC100506718///FLRT2	LINC00461///MIR9-2	TUBA3D///TUBA3C	/	/
LOC101930404///SNORD116-28///SNORD115-26///SNORD115-13///SNORD115-7///SNORD116-22///SNORD116-4///PWARSN///SNORD107///SNRPN///IPW					

Table S9 Gene symbol of 79 DEGs from AD and MDD.

Gene symbol	Gene symbol	Gene symbol	Gene symbol	Gene symbol
TPM3	DCAF8	TIMM50	KIAA0513	ITGB1
SOBP	CCNY	TTBK2	ARMC8	PPARA
LGALSL	RHEB	GNAS	CEBPZOS	MOCS2
TMED5	CDK13	FRYL	PLCB1	SLC22A23
MED31	SMARCA2	DPP6	CTTN	ZNF800
DNAL1	RUNX1T1	RREB1	NPAS3	QKI
ADAM22	RGS12	TNRC6C	PRKCA	IL6ST
CDC42EP4	BCAP29	SLC3A1	ITGB5	MBP
WASL	ZNF224	KMT2A	KCNQ5	DYNC1H1
SNCA	CCDC88A	REPS2	ANKH	ABHD12
CECR6	CNOT6L	METTL7A	AGK	PIEZO1
PITHD1	NFE2L2	ZNRF1	ANKRD36	KAZN
LRIG1	GUCY1B3	CEP152	GART	HIPK2
HNRNPM	ITSN1	LIMD1	LATS2	WWC1
KIAA0754	AMBRA1	IGF2BP2	MAPRE3	NDUFA10
LOC100506718///FLRT2		PET117///KAT14	/	/
LOC101930404///SNORD116-28///SNORD115-26///SNORD115-13///SNORD115-7///SNORD116-22///SNORD116-4///PWARSN///SNORD107///SNRPN///IPW				