Supplemental Table 1. Topology property of Co-expression networks generated by CCA, GLASSO, Random and KEGG in UCEC

Method	Assortativity		Centralization	
	Mean	Standard Deviation	Mean	Standard Deviation
CCA	-0.2030	0.1024	0.7534	0.0116
GLASSO	-0.0346	0.1020	0.5871	0.0544
Random	-0.0595	0.0109	0.5921	0.0031
KEGG	-0.4355		0.7257	

Supplemental Table 2. Topology property of Co-expression networks generated by CCA and GLASSO with position-level and gene-level data in Glutamatergic synapse pathway

Methods	Tissues	Assortativity	Centralization
CCA	Bipolar	-0.66823575	0.78206554
	Schizophrenia	-0.61958925	0.85395689
	Normal	-0.57458829	0.83041518
GLASSO	Bipolar	0.01021008	0.76448247
	Schizophrenia	0.05301971	0.75174821
	Normal	-0.08047029	0.74837798
Random		-0.02759387	0.7233384

Supplemental Table 3 P-value for testing differential expression of specific alleles

Table S3. P-value for testing differential expression of specific alleles

					P-values					
					Schizophrenia		Bipolar			
Gene	Chr	hg18_pos	hg19_pos	dbsnp	Major	Minor	Major	Minor	Function	Associated Disease
PSEN1	chr14	72674749		-	0.1333	0.0388	0.0414	0.0406		
PSEN1	chr14	72675292		-	0.0268	0.0230	0.1376	0.0903		
PSEN1	chr14	72675376		-	0.0344	0.4528	0.0594	0.0354		
PSEN1	chr14	72675654		-	0.4435	0.0406	0.2586	0.0473		
PSEN1	chr14	72687408		-	0.1549	0.0788	0.1192	0.1242		
PSEN1	chr14	72719852		-	0.0275	0.0361	0.0983	0.0258		
PSEN1	chr14	72720113		-	0.6507	0.0113	0.0915	0.0517		
PSEN1	chr14	72741870		-	0.2620	0.0835	0.0454	0.0296		
PSEN1	chr14	72756063	73686310	rs362384	0.2090	0.3571	0.8719	0.0990	*nonsyn[1]	Alzheimer's Disease
PPP3R1	chr2	68235048		-	0.0490	0.4060	0.0659	0.1166		
PPP3R1	chr2	68235099		-	0.1343	0.0461	0.0318	0.0189		
PPP3R1	chr2	68259869		-	0.6914	0.9007	0.0166	0.0021		
PPP3R1	chr2	68260165		-	0.9268	0.3556	0.0063	0.5822		
PPP3R1	chr2	68260297		-	0.2712	0.9511	NA	0.0066		
PPP3R1	chr2	68260787		-	0.7151	0.7362	0.3583	0.0027		
PPP3R1	chr2	68261162		-	0.8777	0.9597	0.0206	0.0075		
PPP3R1	chr2	68261430	68407926	rs875	0.5513	0.9643	0.0148	0.0968		
PPP3R1	*chr2*	*6.8E+07*	*68409037*	*[6]rs1868402*	-----	-----	-----	-----		*Alzheimer's disease*
PPP3R1	chr2	68269271	68415767	rs11692815	0.7297	0.8015	0.0283	0.0377	*nonsyn:stop-gain[1]	
PPP3R1	chr2	68283567		-	0.1833	0.1012	0.4540	0.0444		
PPP3R1	chr2	68283577		-	0.1272	0.2011	0.7265	0.0201		
PPP3R1	chr2	68289733		-	0.1055	0.0232	0.0365	0.1019		
AXIN1	chr16	276661	336660	rs11647490	0.7000	0.0196	0.0097	0.8629	*nonsyn[1]	
AXIN1	chr16	276692		-	0.3487	0.1757	0.3269	0.0835		
AXIN1	chr16	276917	336916	rs1048786	0.6683	0.3171	0.0606	0.0790	*nonsyn[1,2]	
AXIN1	chr16	277128		-	0.2707	0.5653	0.0995	0.0157		
AXIN1	chr16	291164		-	0.0644	0.0420	0.0289	0.0467		
AXIN1	chr16	295611		-	0.0434	0.5367	0.1015	0.3354		
AXIN1	chr16	313300		-	0.0086	0.0269	0.1116	0.2810		
TBL1XR1	chr3	1.78E+08	176738798	rs6983	0.5372	0.4510	0.0901	0.2691		
TBL1XR1	chr3	1.78E+08	176739388	rs3188954	0.9245	0.5504	0.0243	0.9914		
TBL1XR1	chr3	1.78E+08	176739404	rs3188952	0.9056	0.1264	0.0202	0.8172	nonsyn[1]	
TBL1XR1	chr3	1.78E+08	176739663	rs1130272	0.5568	0.2734	0.0334	0.1158	nonsyn[1]	
TBL1XR1	chr3	1.78E+08	176739694	rs73881945	0.2695	0.9989	0.4204	0.0071		
TBL1XR1	chr3	1.78E+08		-	0.2156	0.0496	0.0134	0.0166		
TBL1XR1	*chr3*	*1.8E+08*	*176828751*	*[6]rs1564764*	----	----	----	----		*schizophrenia(P<0.02247)[5]*
TBL1XR1	chr3	1.78E+08		-	0.0431	0.3572	0.2620	0.2971		

TBL1XR1	chr3	1.78E+08	176889360	rs12485447	0.3131	0.0080	0.1863	0.2507		
CCND3	chr6	42010985	41903007	rs9529	0.1552	0.8015	0.1076	0.1765	*nonsyn[1];exonic splicing enhancer[3]	Alzheimer's disease
CCND3	chr6	42011718		-	0.4127	0.2174	0.0156	0.0150		
RAC1	chr7	6403328		-	0.0305	0.1779	0.0389	0.0121		
RAC1	chr7	6408668	6442143	rs2303366	0.3358	0.7679	0.2053	0.1766	nonsyn[1]	
RAC1	chr7	6408681	6442156	rs2303367	0.3146	0.6075	0.1618	0.1252	nonsyn[1]	
RAC1	chr7	6408706		-	0.1068	0.3115	0.0388	0.3115		
RAC1	chr7	6408896	6442371	rs9374	0.3847	0.4918	0.4126	0.0160	nonsyn[1]	
RAC1	chr7	6408958	6442433	rs12977	0.3579	0.4513	0.0141	0.2538		
RAC1	chr7	6409188		-	0.3832	0.3253	0.0135	0.3273		
RAC1	chr7	6410046		-	0.3308	0.3606	0.3269	0.0340		
SFRP4	chr7	37955114	37988589	rs2044831	0.8671	0.9812	0.1750	0.0202		
SFRP4	chr7	37956747	37990222	rs3734953	0.3640	0.8574	0.1181	0.0290		
SFRP4	chr7	37956998	37990473	rs2598094	0.7252	0.3785	0.0049	0.4994		
SFRP4	chr7	37957000	37990475	rs59667102	0.1111	0.2906	0.2054	0.0083		
SFRP4	chr7	37957022	37990497	rs58224136	0.1006	0.4330	0.2671	0.0093		
SFRP4	chr7	37957442	37990917	rs2722278	0.3167	0.6016	0.8567	0.0152		
SFRP4	chr7	37957654	37991129	rs2722279	0.8286	0.7257	0.0472	0.9330	nonsyn[1]	
SFRP4	chr7	37957711	37991186	rs1047785	0.4503	0.1068	0.3217	0.0147		
SFRP4	chr7	37957779	37991254	rs1047800	0.0874	0.1132	0.4371	0.0187	nonsyn[1]	
SFRP4	chr7	37957780	37991255	rs1047812	0.0860	0.1254	0.4395	0.0150	nonsyn[1]	
CAMK2B	chr7	44223586		-	0.1365	0.4924	0.0441	0.0238		
CAMK2B	chr7	44224249		-	0.4108	0.6855	0.2991	0.0113		
CAMK2B	chr7	44224265		-	0.6401	0.6637	0.0103	0.0038		
CAMK2B	chr7	44224663		-	0.3355	0.7756	0.3269	0.0080		
CAMK2B	chr7	44225252		-	0.3391	0.3372	0.1613	0.0181		
CAMK2B	chr7	44225407		-	0.2311	0.4715	0.0368	0.0634		
CAMK2B	chr7	44225468		-	0.1443	0.2258	0.0422	0.0926		
CAMK2B	chr7	44225489	44258964	rs13229610	0.8457	0.0086	0.0122	0.3049		
CAMK2B	chr7	44225585		-	0.2529	0.1747	0.3508	0.0226		
CAMK2B	chr7	44226231	44259706	rs1065359	0.1064	0.9904	0.7414	0.0147	[4]CpG: 25	
CAMK2B	chr7	44226396	44259871	rs1127065	0.9711	0.1800	0.0292	0.5598	[4]CpG: 25	weight gain
CAMK2B	chr7	44249393	44282868	rs11542228	0.3403	0.4425	0.1167	0.0383		bipolar ($P < 0.009138$)[5]
CAMK2B	chr7	44249402	44282877	rs11542227	0.8915	0.9966	0.0241	0.0697	exonic splicing enhancer[3]	

1: H-Inv database v 7.0; * the reference protein is found

incomplete

2: NCBI

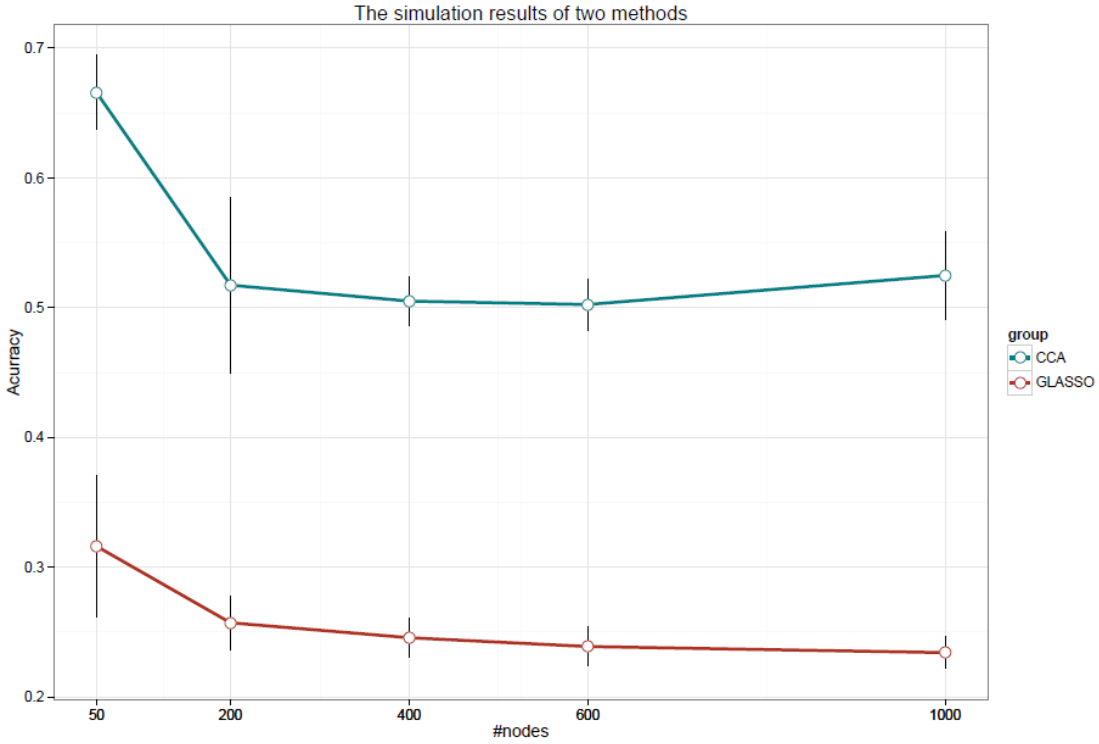
3: GeneCard

4: SNP nexus database

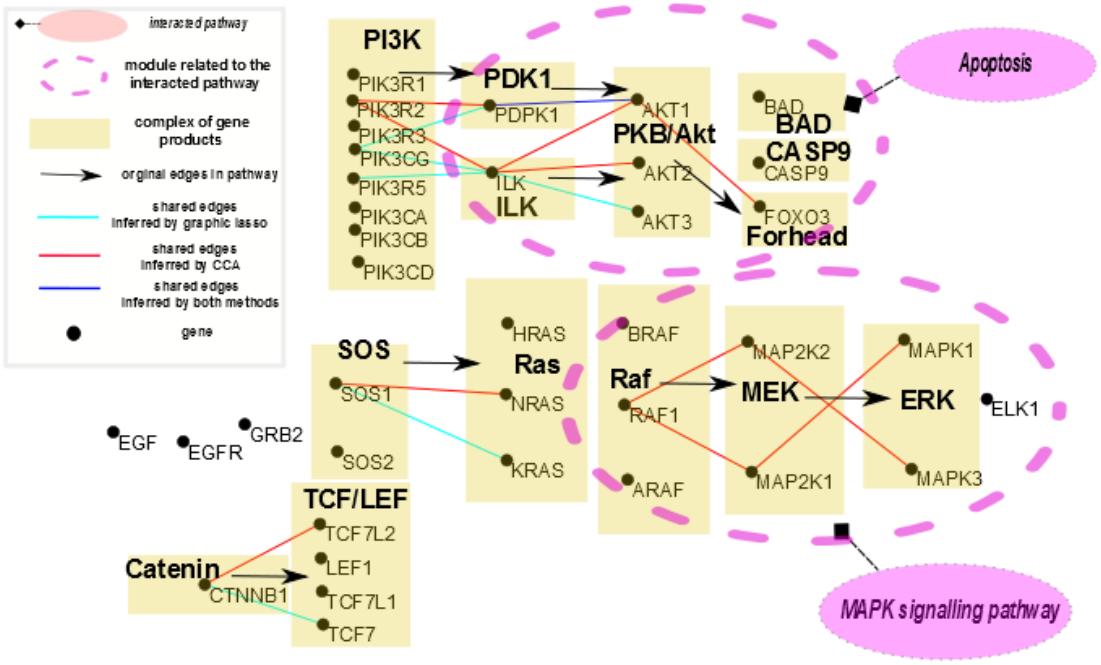
5:association tested in our study

6: *(italic) imputed SNP which was not represented in the ASE*

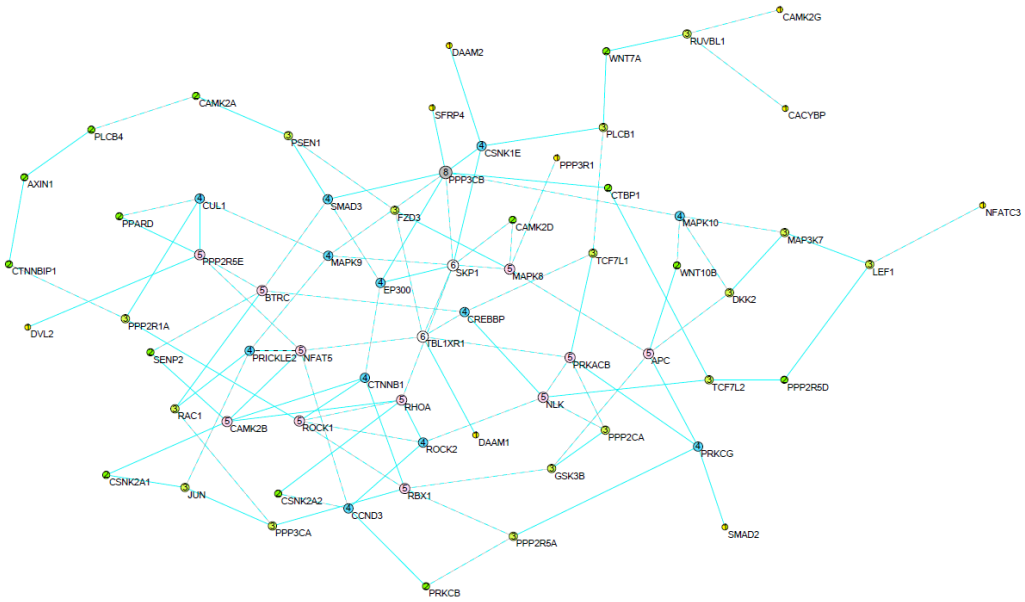
Supplemental Figure 1 The simulation results of comparison of our CCA method and GLASSO. The x-axis represented the size of network (number of nodes) and the y-axis denoted the accuracy of the method (Proportion of edges are retained in the reconstructed co-expression network by 1000 resampling) .



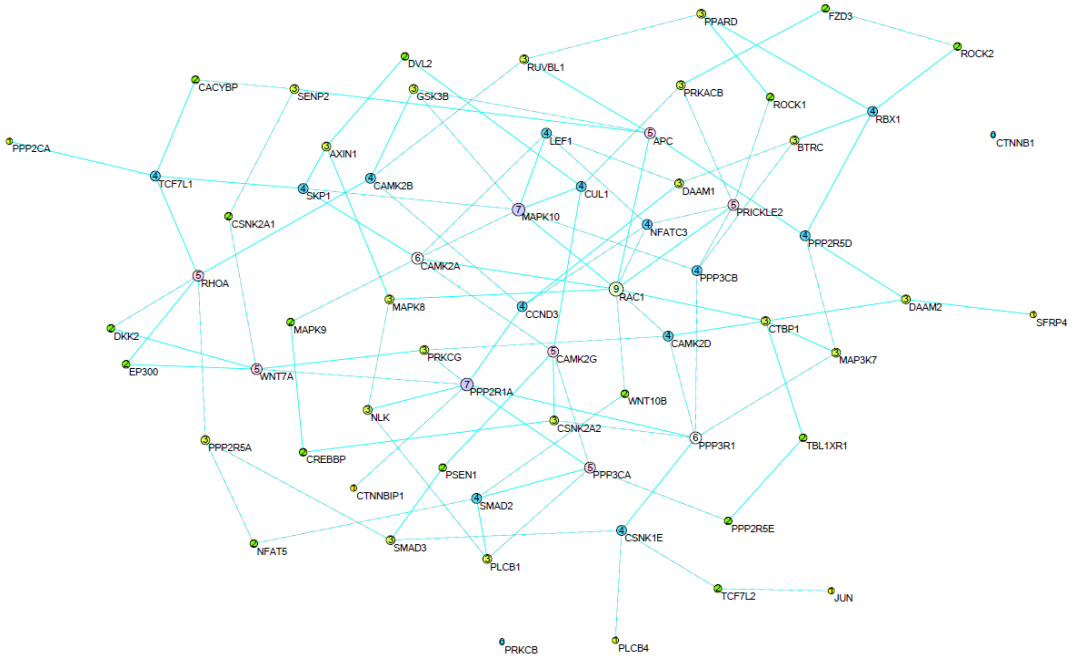
Supplementary Figure 2. The shared network structure by Endometrioid Carcinoma Pathway in KEGG and reconstructed co-expression networks using the CCA and GALSSO methods using Uterine Corpus Endometrioid Carcinoma samples in TCGA dataset.



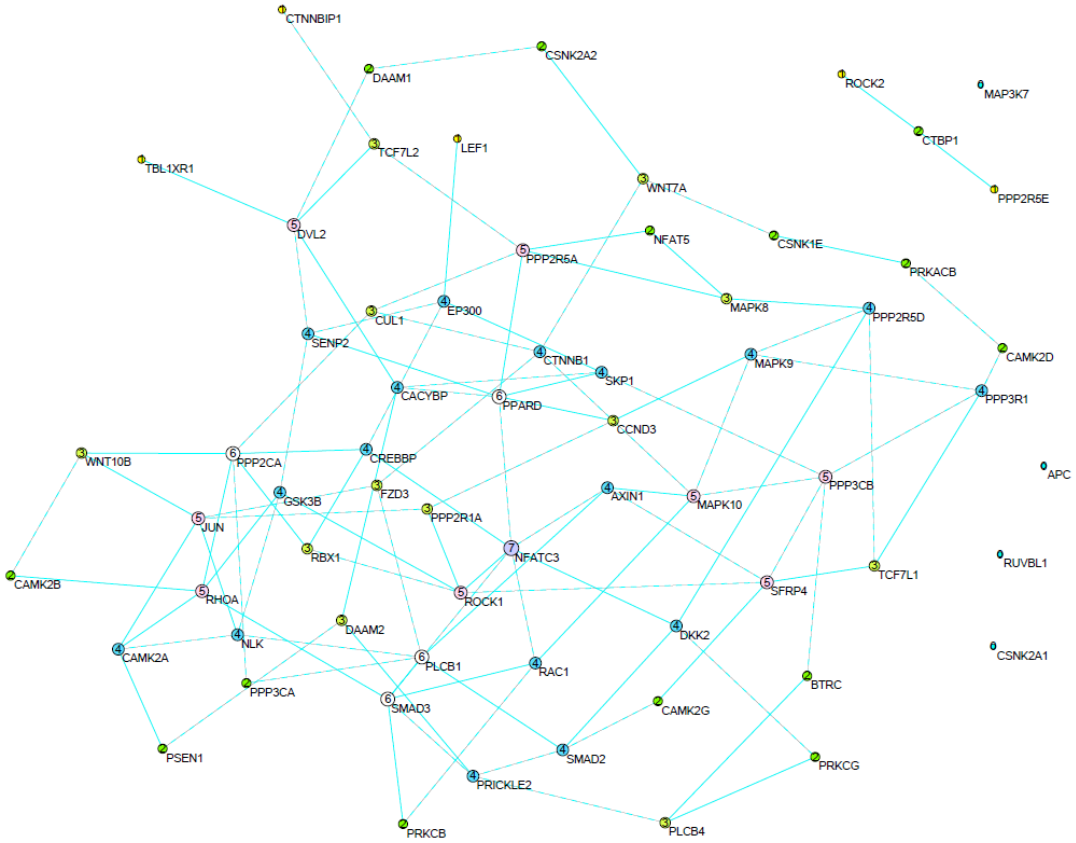
Supplemental Figure 3. The co-expression network reconstructed by GLASSO method using overall gene expression data of schizophrenia tissue samples.



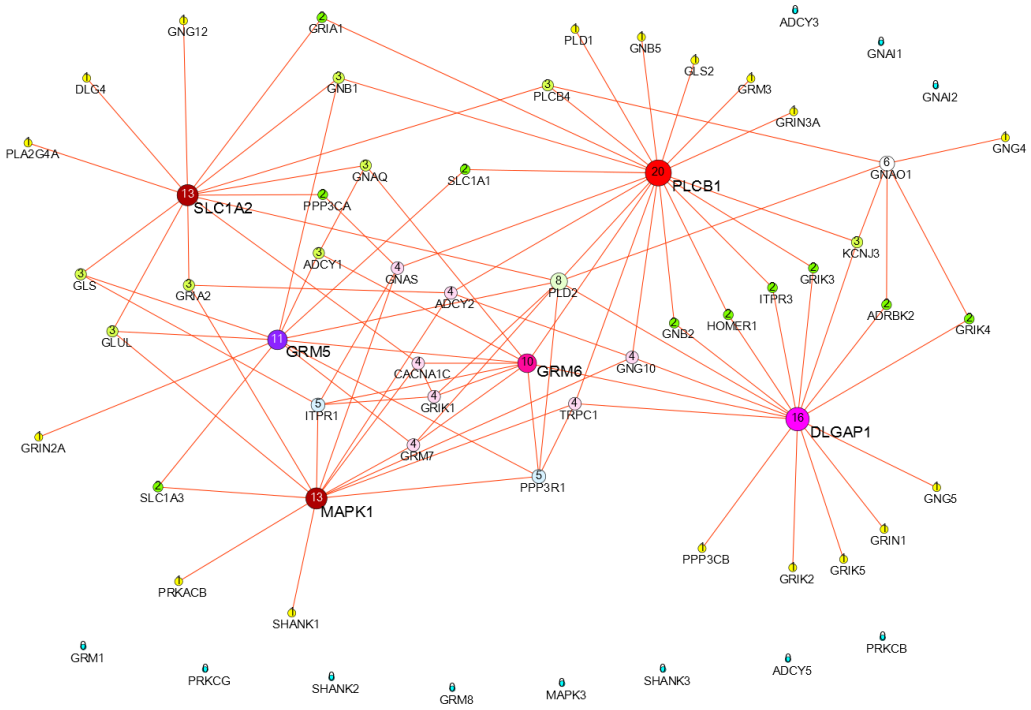
Supplemental Figure 4. The co-expression network reconstructed by GLASSO method using overall gene expression data of bipolar tissue samples.



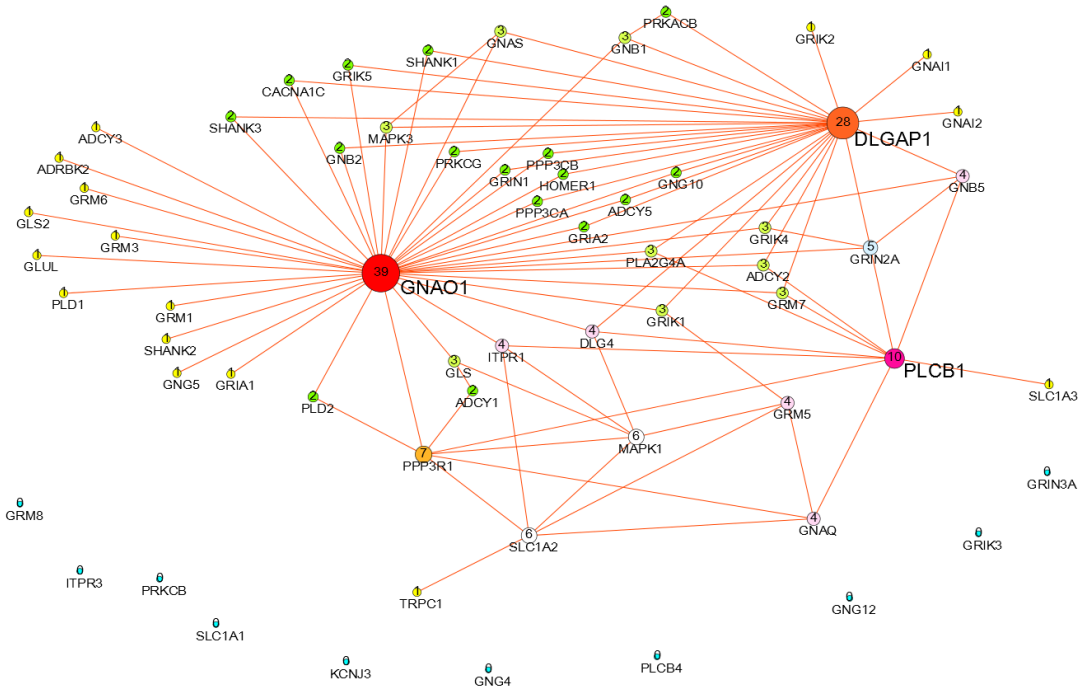
Supplemental Figure 5. The co-expression network reconstructed by GLASSO method using overall gene expression data of normal tissue samples.



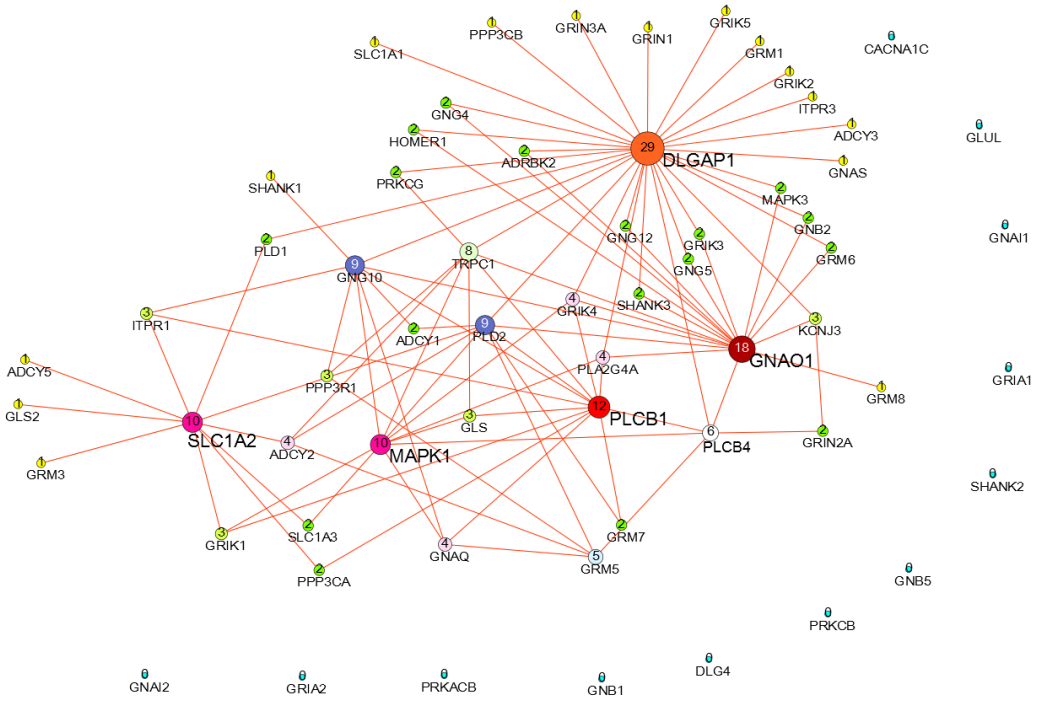
Supplementary Figure 6. The co-expression network reconstructed by CCA method using position-level RNA-seq data in Glutamatergic synapse pathway of bipolar tissue samples. Nodes are sized, numbered and colored by their degree value.



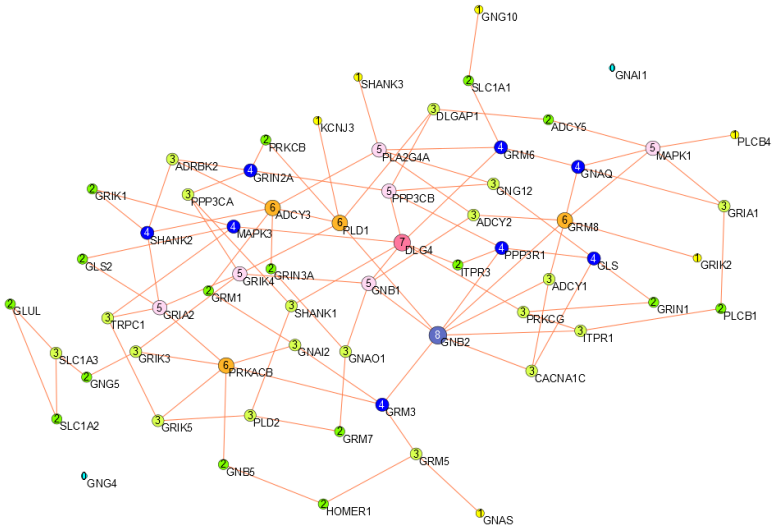
Supplementary Figure 7. The co-expression network reconstructed by CCA method using position-level RNA-seq data in Glutamatergic synapse pathway of schizophrenia tissue samples. Nodes are sized, numbered and colored by their degree value.



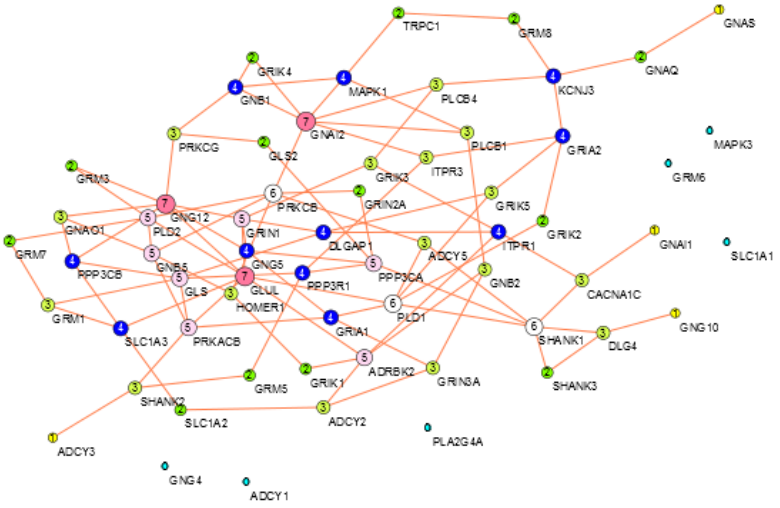
Supplementary Figure 8 . The co-expression network reconstructed by CCA method using position-level RNA-seq data in Glutamatergic synapse pathway of normal tissue samples. Nodes are sized, numbered and colored by their degree value.



Supplementary Figure 9. The co-expression network reconstructed by GLASSO method using position-level RNA-seq data in Glutamatergic synapse pathway of bipolar tissue samples. Nodes are sized, numbered and colored by their degree value.



Supplementary Figure 10. The co-expression network reconstructed by GLASSO method using position-level RNA-seq data in Glutamatergic synapse pathway of schizophrenia tissue samples. Nodes are sized, numbered and colored by their degree value.



Supplementary Figure 11 . The co-expression network reconstructed by GLASSO method using position-level RNA-seq data in Glutamatergic synapse pathway of normal tissue samples. Nodes are sized, numbered and colored by their degree value.