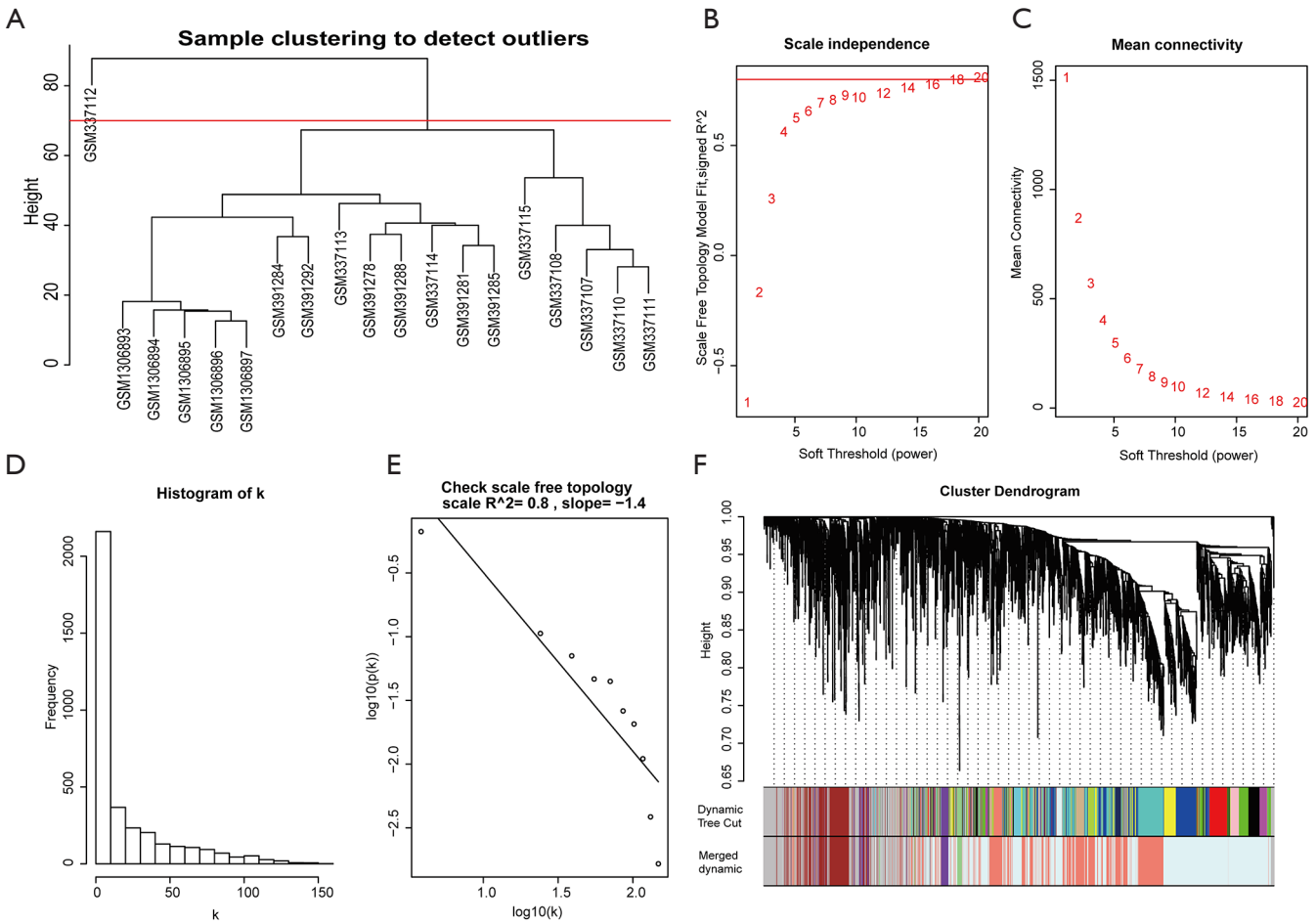

Figure S1 Construction of weighted gene co-expression network of unruptured IA samples. (A) Sample clustering detected 1 outliers (GSM337112). (B,C) The cut-off was set to be 0.8 and β=18 was chosen to be the soft-threshold power. (D,E) The histogram and the linear fitting plot showed that the co-expression network we constructed met the requirement of scale-free topology. (F) 5 modules were detected after merging modules generated by dynamic tree cut. IA, intracranial aneurysm.

Table S1 KEGG pathways for gene modules of ruptured IA and unruptured IA

Ruptured IA	KEGG pathways	Count	PValue	Unruptured IA	KEGG pathways	Count	PValue
	Blue				Brown		
	hsa04142:Lysosome	40	1.75E-19		hsa04151:PI3K-Akt signaling pathway	15	0.015286
	hsa05152:Tuberculosis	37	2.92E-11		hsa04514:Cell adhesion molecules (CAMs)	13	4.64E-05
	hsa04145:Phagosome	31	2.14E-09		hsa04510:Focal adhesion	12	0.004471
	hsa04380:Osteoclast differentiation	30	3.22E-10		hsa04723:Retrograde endocannabinoid signaling	11	5.33E-05
	hsa04062:Chemokine signaling pathway	29	3.61E-06		hsa04724:Glutamatergic synapse	11	1.49E-04
	hsa04015:Rap1 signaling pathway	25	0.001318		hsa04014:Ras signaling pathway	11	0.022573
	hsa04060:Cytokine-cytokine receptor interaction	25	0.008707		hsa04728:Dopaminergic synapse	10	0.001599
	hsa05164:Influenza A	24	2.10E-04		hsa04713:Circadian entrainment	9	9.09E-04
	hsa05323:Rheumatoid arthritis	23	4.24E-09		hsa04727:GABAergic synapse	8	0.002165
	hsa05150:Staphylococcus aureus infection	22	7.99E-13		hsa05032:Morphine addiction	8	0.003192
	hsa05140:Leishmaniasis	22	3.29E-10		hsa05033:Nicotine addiction	7	1.81E-04
	hsa04650:Natural killer cell mediated cytotoxicity	22	7.45E-06		hsa04911:Insulin secretion	7	0.009415
	hsa04514:Cell adhesion molecules (CAMs)	22	7.89E-05		hsa04726:Serotonergic synapse	7	0.031154
	hsa04620:Toll-like receptor signaling pathway	21	2.87E-06		hsa04670:Leukocyte transendothelial migration	7	0.036154
	hsa05145:Toxoplasmosis	20	1.93E-05		hsa04730:Long-term depression	6	0.00885
	hsa04670:Leukocyte transendothelial migration	20	3.68E-05		hsa04976:Bile secretion	6	0.015641
	hsa04611:Platelet activation	20	2.01E-04		hsa04012:ErbB signaling pathway	6	0.038014
	hsa01130:Biosynthesis of antibiotics	20	0.044292		hsa04512:ECM-receptor interaction	6	0.038014
	hsa04662:B cell receptor signaling pathway	18	3.18E-07		hsa05020:Prion diseases	5	0.00564
	hsa05142:Chagas disease (American trypanosomiasis)	18	1.08E-04		hsa05014:Amyotrophic lateral sclerosis (ALS)	5	0.021554
	hsa04666:Fc gamma R-mediated phagocytosis	17	2.52E-05		hsa05214:Glioma	5	0.049708
	hsa05162:Measles	17	0.004935		hsa00340:Histidine metabolism	4	0.010932
	hsa05133:Pertussis	16	2.46E-05		hsa00260:Glycine, serine and threonine metabolism	4	0.049933
	hsa04660:T cell receptor signaling pathway	16	7.03E-04		Lightcyan		
	hsa04664:Fc epsilon RI signaling pathway	15	3.26E-05		hsa05200:Pathways in cancer	61	2.13E-06
	hsa04640:Hematopoietic cell lineage	15	5.11E-04		hsa04151:PI3K-Akt signaling pathway	44	0.004626
	hsa01200:Carbon metabolism	15	0.006405		hsa05205:Proteoglycans in cancer	38	2.60E-06
	hsa05134:Legionellosis	14	1.05E-05		hsa04810:Regulation of actin cytoskeleton	37	2.10E-05
	hsa03320:PPAR signaling pathway	14	1.19E-04		hsa04510:Focal adhesion	34	1.80E-04
	hsa05132:Salmonella infection	14	0.001044		hsa04022:cGMP-PKG signaling pathway	33	1.67E-06
	hsa04066:HIF-1 signaling pathway	14	0.003973		hsa04390:Hippo signaling pathway	30	1.52E-05
	hsa05169:Epstein-Barr virus infection	14	0.027185		hsa04015:Rap1 signaling pathway	30	0.004558
	hsa05416:Viral myocarditis	13	9.48E-05		hsa01130:Biosynthesis of antibiotics	29	0.00963
	hsa04064:NF-kappa B signaling pathway	13	0.004781		hsa04550:Signaling pathways regulating pluripotency of stem cells	27	7.58E-05
	hsa05321:Inflammatory bowel disease (IBD)	12	0.001149		hsa04024:cAMP signaling pathway	27	0.013237
	hsa05146:Amoebiasis	12	0.047315		hsa04270:Vascular smooth muscle contraction	25	2.68E-05
	hsa04672:Intestinal immune network for IgA production	11	3.31E-04		hsa04261:Adrenergic signaling in cardiomyocytes	25	3.99E-04
	hsa00520:Amino sugar and nucleotide sugar metabolism	10	0.001702		hsa00230:Purine metabolism	24	0.020098
	hsa04621:NOD-like receptor signaling pathway	10	0.005067		hsa04310:Wnt signaling pathway	23	0.002229
	hsa00010:Glycolysis / Gluconeogenesis	10	0.016177		hsa05010:Alzheimer's disease	22	0.039192
	hsa04610:Complement and coagulation cascades	10	0.019342		hsa04611:Platelet activation	21	0.005249
	hsa01230:Biosynthesis of amino acids	10	0.024898		hsa04921:Oxytocin signaling pathway	21	0.023828
	hsa04612:Antigen processing and presentation	10	0.033951		hsa04932:Non-alcoholic fatty liver disease (NAFLD)	20	0.045518
	hsa05144:Malaria	9	0.007326		hsa04152:AMPK signaling pathway	19	0.013022
	hsa05332:Graft-versus-host disease	8	0.002652		hsa04713:Circadian entrainment	18	0.001976
	hsa05330:Allograft rejection	8	0.005214		hsa05146:Amoebiasis	18	0.006372
	hsa04940:Type I diabetes mellitus	8	0.010606		hsa05222:Small cell lung cancer	17	0.001538
	hsa00480:Glutathione metabolism	8	0.028953		hsa04114:Oocyte meiosis	17	0.021193
	hsa05320:Autoimmune thyroid disease	8	0.031826		hsa01200:Carbon metabolism	17	0.024691
	hsa05310:Asthma	7	0.007206		hsa04350:TGF-beta signaling pathway	16	0.003636
	hsa05340:Primary immunodeficiency	7	0.013381		hsa05414:Dilated cardiomyopathy	16	0.003636
	hsa00052:Galactose metabolism	6	0.029335		hsa04512:ECM-receptor interaction	16	0.005121
	hsa00511:Other glycan degradation	5	0.018893		hsa04066:HIF-1 signaling pathway	16	0.012695
	hsa00531:Glycosaminoglycan degradation	5	0.022844		hsa04916:Melanogenesis	16	0.01807
	hsa04614:Renin-angiotensin system	5	0.043381		hsa04070:Phosphatidylinositol signaling system	15	0.032
	hsa00603:Glycosphingolipid biosynthesis - globo series	4	0.045674		hsa04915:Estrogen signaling pathway	15	0.034539
	hsa00290:Valine, leucine and isoleucine biosynthesis	3	0.019254		hsa04924:Renin secretion	14	0.002047
	Cyan				hsa05410:Hypertrophic cardiomyopathy (HCM)	14	0.011718
	hsa05200:Pathways in cancer	17	3.05E-04		hsa04970:Salivary secretion	14	0.025141
	hsa05166:HTLV-I infection	11	0.005568		hsa04666:Fc gamma R-mediated phagocytosis	13	0.044988
	hsa04151:PI3K-Akt signaling pathway	11	0.039259		hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	12	0.021728
	hsa05205:Proteoglycans in cancer	9	0.011744		hsa04971:Gastric acid secretion	12	0.038381
	hsa04510:Focal adhesion	9	0.013855		hsa05217:Basal cell carcinoma	11	0.012622
	hsa04668:TNF signaling pathway	8	0.001247		hsa04962:Vasopressin-regulated water reabsorption	10	0.009238
	hsa04310:Wnt signaling pathway	8	0.005254		hsa00280:Valine, leucine and isoleucine degradation	10	0.014206
	hsa05202:Transcriptional misregulation in cancer	8	0.014295		hsa04923:Regulation of lipolysis in adipocytes	10	0.040653
	hsa04978:Mineral absorption	7	5.10E-05		hsa00270:Cysteine and methionine metabolism	8	0.035282
	hsa04550:Signaling pathways regulating pluripotency of stem cells	7	0.020677		hsa00640:Propanoate metabolism	7	0.025374
	hsa05222:Small cell lung cancer	6	0.009778		hsa04710:Circadian rhythm	7	0.040145
	hsa04974:Protein digestion and absorption	6	0.011264		Lightgreen		
	hsa04916:Melanogenesis	6	0.01874		hsa04978:Mineral absorption	7	2.55E-08
	hsa05217:Basal cell carcinoma	5	0.009332		hsa00010:Glycolysis / Gluconeogenesis	5	1.86E-04
	hsa04640:Hematopoietic cell lineage	5	0.044799		hsa01130:Biosynthesis of antibiotics	5	0.012817
	hsa05323:Rheumatoid arthritis	5	0.046396		hsa01230:Biosynthesis of amino acids	4	0.003645
	Green				hsa01200:Carbon metabolism	4	0.012692
	hsa04141:Protein processing in endoplasmic reticulum	17	3.89E-07		hsa04068:FoxO signaling pathway	4	0.019992
	hsa04151:PI3K-Akt signaling pathway	15	0.012926		Purple		
	hsa04510:Focal adhesion	14	3.54E-04		hsa04510:Focal adhesion	14	1.43E-09
	hsa04512:ECM-receptor interaction	11	1.19E-05		hsa04512:ECM-receptor interaction	10	8.92E-09
	hsa05205:Proteoglycans in cancer	10	0.024122		hsa04151:PI3K-Akt signaling pathway	10	7.29E-04
	hsa01130:Biosynthesis of antibiotics	10	0.03342		hsa04670:Leukocyte transendothelial migration	7	1.67E-04
	hsa03050:Proteasome	9	2.84E-06		hsa04810:Regulation of actin cytoskeleton	7	0.003903
	hsa05222:Small cell lung cancer	8	0.001924		hsa05222:Small cell lung cancer	6	3.50E-04
	hsa04145:Phagosome	8	0.037561		hsa05146:Amoebiasis	6	9.65E-04
	hsa04974:Protein digestion and absorption	7	0.010067		hsa04514:Cell adhesion molecules (CAMs)	6	0.003508
	hsa05146:Amoebiasis	7	0.023388		hsa05205:Proteoglycans in cancer	6	0.014498
	hsa05169:Epstein-Barr virus infection	7	0.042388		hsa05100:Bacterial invasion of epithelial cells	5	0.002373
	hsa00510:N-Glycan biosynthesis	6	0.003409		hsa05410:Hypertrophic cardiomyopathy (HCM)	5	0.002373
	hsa05130:Pathogenic Escherichia coli infection	6	0.004062		hsa05414:Dilated cardiomyopathy	5	0.003109
	hsa05131:Shigellosis	5	0.044513		hsa05322:Systemic lupus erythematosus	5	0.015874
	Greenyellow				hsa05150:Staphylococcus aureus infection	4	0.006908
	hsa00330:Arginine and proline metabolism	4	0.00468		hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	4	0.012492
	hsa04971:Gastric acid secretion	4	0.013313		hsa04530:Tight junction	4	0.024986
	hsa00340:Histidine metabolism	3	0.009675		hsa04974:Protein digestion and absorption	4	0.025738
	hsa05020:Prion diseases	3	0.02231		Salmon		
	hsa04978:Mineral absorption	3	0.036037		hsa04510:Focal adhesion	14	1.43E-09
	Lightcyan				hsa04512:ECM-receptor interaction	10	8.92E-09
	no significant results				hsa04151:PI3K-Akt signaling pathway	10	7.29E-04
	Midnightblue				hsa04670:Leukocyte transendothelial migration	7	1.67E-04
	hsa05200:Pathways in cancer	6	0.02592		hsa04810:Regulation of actin cytoskeleton	7	0.003903
	hsa05146:Amoebiasis	5	0.001072		hsa05222:Small cell lung cancer	6	3.50E-04
	hsa04020:Calcium signaling pathway	5	0.007159		hsa05146:Amoebiasis	6	9.65E-04
	hsa00562:Inositol phosphate metabolism	4	0.003503		hsa04514:Cell adhesion molecules (CAMs)	6	0.003508
	hsa04512:ECM-receptor interaction	4	0.0062		hsa05205:Proteoglycans in cancer	6	0.014498
	hsa04611:Platelet activation	4	0.018456		hsa05100:Bacterial invasion of epithelial cells	5	0.002373
	hsa04310:Wnt signaling pathway	4	0.021598		hsa05410:Hypertrophic cardiomyopathy (HCM)	5	0.002373
	hsa04261:Adrenergic signaling in cardiomyocytes	4	0.021598		hsa05414:Dilated cardiomyopathy	5	0.003109
	Purple				hsa05322:Systemic lupus erythematosus	5	0.015874
	hsa05200:Pathways in cancer	52	1.53E-04		hsa05150:Staphylococcus aureus infection	4	0.006908
	hsa04151:PI3K-Akt signaling pathway	42	0.003677		hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	4	0.012492
	hsa04810:Regulation of actin cytoskeleton	39	5.84E-07		hsa04530:Tight junction	4	0.024986
	hsa04510:Focal adhesion	36	7.26E-06		hsa04974:Protein digestion and absorption	4	0.025738
	hsa04022:cGMP-PKG signaling pathway	34	1.06E-07				
	hsa05205:Proteoglycans in cancer	30	7.40E-04				
	hsa05166:HTLV-I infection	30	0.022645				
	hsa04270:Vascular smooth muscle contraction	27	6.94E-07				
	hsa01130:Biosynthesis of antibiotics	25	0.039129				
	hsa04390:Hippo signaling pathway	24	0.00131				
	hsa04921:Oxytocin signaling pathway	21	0.011863				
	hsa04114:Oocyte meiosis	20	8.23E-04				
	hsa04550:Signaling pathways regulating pluripotency of stem cells	20	0.011685				
	hsa04611:Platelet activation	19	0.011418				
	hsa04070:Phosphatidylinositol signaling system	18	0.001308				
	hsa04915:Estrogen signaling pathway	18	0.001469				
	hsa04152:AMPK signaling pathway	18	0.013961				
	hsa04670:Leukocyte transendothelial migration	17	0.015824				
	hsa05414:Dilated cardiomyopathy	16	0.001837				
	hsa01200:Carbon metabolism	16	0.028066				
	hsa05410:Hypertrophic cardiomyopathy (HCM)	15	0.002453				
	hsa05215:Prostate cancer	15	0.007525				
	hsa05146:Amoebiasis	15	0.0344				
	hsa04668:TNF signaling pathway	15	0.03688				
	hsa04931:Insulin resistance	15	0.039485				
	hsa04725:Cholinergic synapse	15	0.048084				
	hsa04350:TGF-beta signaling pathway	14	0.012308				
	hsa04530:Tight junction	14	0.016271				
	hsa04540:Gap junction	14	0.017786				
	hsa04916:Melanogenesis	14	0.045246				
	hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	13	0.004975				
	hsa05100:Bacterial invasion of epithelial cells	13	0.016553				
	hsa04925:Aldosterone synthesis and secretion	13	0.021828				
	hsa05222:Small cell lung cancer	13	0.030675				
	hsa04924:Renin secretion	12	0.009609				
	hsa04115:p53 signaling pathway	12	0.013453				
	hsa00562:Inositol phosphate metabolism	12	0.020263				
	hsa04730:Long-term depression	11	0.01631				
	hsa04520:Adherens junction	11	0.046735				
	hsa00020:Citrate cycle (TCA cycle)	9	0.001602				
	hsa05213:Endometrial cancer	9	0.045888				
	hsa04710:Circadian rhythm	7	0.029759				
	Salmon						
	hsa04060:Cytokine-cytokine receptor interaction	8	0.001183				
	hsa04062:Chemokine signaling pathway	5	0.03741				

KEGG, Kyoto encyclopedia of genes and genomes; IA, intracranial aneurysm.

Table S2 Hub genes of each gene module

Module	Gene ID	Gene symbol	Official full name
Ruptured IA			
Blue	9056	SLC7A7	Solute carrier family 7 member 7
Cyan	9945	GFPT2	Glutamine-fructose-6-phosphate transaminase 2
Green	378	ARF4	ADP ribosylation factor 4
Green yellow	4118	MAL	Mal, T cell differentiation protein
Lightcyan	257240	KLHL34	Kelch like family member 34
Midnightblue	5332	PLCB4	Phospholipase C beta 4
Purple	5592	PRKG1	Protein kinase cGMP-dependent 1
Salmon	8875	VNN2	Vanin 2
Unruptured IA			
Brown	590	BCHE	Butyrylcholinesterase
Lightcyan	4012	LNPEP	Leucyl and cystinyl aminopeptidase
Lightgreen	4495	MT1G	Metallothionein 1G
Purple	91663	MYADM	Myeloid associated differentiation marker
Salmon	963	CD53	CD53 molecule

IA, intracranial aneurysm.

Table S3 Validation of key genes using dataset GSE122897

Gene symbol	t	P value	P value summary
CXCR4	2.029	0.0492	*
AQP9	2.374	0.0225	*
SLA	2.712	0.0098	**
MPP1	4.044	0.0002	***
PDZRN3	2.639	0.0118	*
ANGPT1	3.017	0.0044	**
FPR1	2.430	0.0197	*
ANPEP	3.111	0.0034	**
SRGN	2.417	0.0203	*
C15orf48	3.314	0.0020	**
NCF2	2.732	0.0093	**
C1orf162	3.024	0.0043	**
TCIRG1	3.018	0.0044	**
FGR	2.259	0.0294	*

*, P<0.05; **, P<0.01; ***, P<0.001.

Table S4 ROC analysis of key genes

Gene symbol	AUC	SE	P value
CXCR4	0.703	0.082	0.024
AQP9	0.717	0.082	0.016
SLA	0.726	0.080	0.012
MPP1	0.821	0.069	0.000
PDZRN3	0.692	0.085	0.034
ANGPT1	0.766	0.077	0.003
FPR1	0.696	0.081	0.030
ANPEP	0.737	0.078	0.009
SRGN	0.714	0.082	0.017
C15orf48	0.764	0.076	0.003
NCF2	0.728	0.078	0.011
C1orf162	0.757	0.081	0.004
TCIRG1	0.766	0.077	0.003
FGR	0.712	0.080	0.019

ROC, receiver operating characteristic; AUC, area under curve; SE, standard error.