



Figure S1 Weighted co-expression network construction for non-dilated PVAT. (A) No outliers were detected by sample clustering. (B,C) The soft-threshold β was chosen to be 10. (D,E) The network we constructed met the requirements of scale-free topology. (F) After dynamic tree cut and merging, 5 gene modules were detected.

Table S1 GO-BP terms for up-regulated DEGs and down-regulated DEGs

	GO Terms	Count	P value
Up-regulated	GO:0006954--inflammatory response	19	1.98E-12
	GO:0030593--neutrophil chemotaxis	9	2.64E-09
	GO:0032496--response to lipopolysaccharide	10	2.82E-07
	GO:0006935--chemotaxis	9	3.44E-07
	GO:0032870--cellular response to hormone stimulus	6	4.55E-06
	GO:0051591--response to cAMP	6	5.08E-06
	GO:0006955--immune response	12	1.87E-05
	GO:0044344--cellular response to fibroblast growth factor stimulus	5	2.07E-05
	GO:0002523--leukocyte migration involved in inflammatory response	4	2.54E-05
	GO:0060326--cell chemotaxis	6	2.82E-05
	GO:0042493--response to drug	10	4.32E-05
	GO:0045597--positive regulation of cell differentiation	5	4.85E-05
	GO:0070374--positive regulation of ERK1 and ERK2 cascade	8	4.93E-05
	GO:0050729--positive regulation of inflammatory response	6	4.95E-05
	GO:0050830--defense response to Gram-positive bacterium	6	1.03E-04
	GO:0031668--cellular response to extracellular stimulus	4	1.22E-04
	GO:0035914--skeletal muscle cell differentiation	5	1.48E-04
	GO:0007229--integrin-mediated signaling pathway	6	2.11E-04
	GO:0045944--positive regulation of transcription from RNA polymerase II promoter	16	2.69E-04
	GO:0009612--response to mechanical stimulus	5	3.05E-04
	GO:0008285--negative regulation of cell proliferation	10	3.19E-04
	GO:0048661--positive regulation of smooth muscle cell proliferation	5	3.25E-04
	GO:0051090--regulation of sequence-specific DNA binding transcription factor activity	4	3.35E-04
	GO:0071356--cellular response to tumor necrosis factor	6	3.44E-04
	GO:0001666--response to hypoxia	7	3.64E-04
	GO:0006366--transcription from RNA polymerase II promoter	11	4.96E-04
	GO:0045893--positive regulation of transcription, DNA-templated	11	5.11E-04
	GO:0007165--signal transduction	17	5.26E-04
	GO:0070098--chemokine-mediated signaling pathway	5	6.19E-04
	GO:0071347--cellular response to interleukin-1	5	6.19E-04
	GO:0031663--lipopolysaccharide-mediated signaling pathway	4	7.04E-04
	GO:0043524--negative regulation of neuron apoptotic process	6	7.92E-04
	GO:0043066--negative regulation of apoptotic process	10	8.65E-04
	GO:0043407--negative regulation of MAP kinase activity	4	9.97E-04
	GO:0045080--positive regulation of chemokine biosynthetic process	3	0.001299
	GO:0002548--monocyte chemotaxis	4	0.001565
	GO:0045429--positive regulation of nitric oxide biosynthetic process	4	0.001676
	GO:0007568--aging	6	0.002131
	GO:0031100--organ regeneration	4	0.002168
	GO:0001649--osteoblast differentiation	5	0.002556
	GO:0007267--cell-cell signaling	7	0.002722
	GO:0071277--cellular response to calcium ion	4	0.00274
	GO:0042542--response to hydrogen peroxide	4	0.00274
	GO:0000187--activation of MAPK activity	5	0.002833
	GO:0034097--response to cytokine	4	0.002897
	GO:0010628--positive regulation of gene expression	7	0.003172
	GO:0050829--defense response to Gram-negative bacterium	4	0.003398
	GO:0030335--positive regulation of cell migration	6	0.00341
	GO:0071222--cellular response to lipopolysaccharide	5	0.003448
	GO:0042127--regulation of cell proliferation	6	0.00349
	GO:0045766--positive regulation of angiogenesis	5	0.003671
	GO:0007155--cell adhesion	9	0.003677
	GO:0071346--cellular response to interferon-gamma	4	0.00376
	GO:0006915--apoptotic process	10	0.003865
	GO:0051412--response to corticosterone	3	0.004291
	GO:0034142--toll-like receptor 4 signaling pathway	3	0.004291
	GO:0045669--positive regulation of osteoblast differentiation	4	0.004346
	GO:0030198--extracellular matrix organization	6	0.004459
	GO:0050900--leukocyte migration	5	0.004531
	GO:0009611--response to wounding	4	0.004985
	GO:0019221--cytokine-mediated signaling pathway	5	0.005824
	GO:0006952--defense response	4	0.005919
	GO:0043065--positive regulation of apoptotic process	7	0.006109
	GO:0051092--positive regulation of NF-kappaB transcription factor activity	5	0.006141
	GO:0090023--positive regulation of neutrophil chemotaxis	3	0.006387
	GO:0035690--cellular response to drug	4	0.006424
	GO:0071300--cellular response to retinoic acid	4	0.006685
	GO:0008360--regulation of cell shape	5	0.007342
	GO:0045444--fat cell differentiation	4	0.007507
	GO:0051602--response to electrical stimulus	3	0.007577
	GO:0001525--angiogenesis	6	0.007627
	GO:0007186--G-protein coupled receptor signaling pathway	12	0.009962
	GO:0048247--lymphocyte chemotaxis	3	0.010231
	GO:0070488--neutrophil aggregation	2	0.010928
	GO:0048662--negative regulation of smooth muscle cell proliferation	3	0.01095
	GO:0030307--positive regulation of cell growth	4	0.011015
	GO:0043547--positive regulation of GTPase activity	9	0.012273
GO:0043200--response to amino acid	3	0.012453	
GO:0045765--regulation of angiogenesis	3	0.012453	
GO:0046677--response to antibiotic	3	0.013236	
GO:0032355--response to estradiol	4	0.013665	
GO:0008284--positive regulation of cell proliferation	8	0.014033	
GO:0071364--cellular response to epidermal growth factor stimulus	3	0.01404	
GO:0032602--chemokine production	2	0.016347	
GO:0071409--cellular response to cycloheximide	2	0.016347	
GO:1990646--cellular response to prolactin	2	0.016347	
GO:0000122--negative regulation of transcription from RNA polymerase II promoter	10	0.017045	
GO:0034605--cellular response to heat	3	0.017462	
GO:0007596--blood coagulation	5	0.018475	
GO:0006953--acute-phase response	3	0.019292	
GO:0032570--response to progesterone	3	0.019292	
GO:0045471--response to ethanol	4	0.019967	
GO:0043280--positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	3	0.020235	
GO:0007346--regulation of mitotic cell cycle	3	0.020235	
GO:0010574--regulation of vascular endothelial growth factor production	2	0.021738	
GO:0032119--sequestering of zinc ion	2	0.021738	
GO:0002793--positive regulation of peptide secretion	2	0.021738	
GO:0035556--intracellular signal transduction	7	0.023322	
GO:0006879--cellular iron ion homeostasis	3	0.024199	
GO:0043434--response to peptide hormone	3	0.024199	
GO:0032755--positive regulation of interleukin-6 production	3	0.025235	
GO:0032729--positive regulation of interferon-gamma production	3	0.02629	
GO:0003151--outflow tract morphogenesis	3	0.02629	
GO:0014910--regulation of smooth muscle cell migration	2	0.027099	
GO:0032760--positive regulation of tumor necrosis factor production	3	0.027362	
GO:0009408--response to heat	3	0.028451	
GO:0006909--phagocytosis	3	0.028451	
GO:0032494--response to peptidoglycan	2	0.032431	
GO:0048146--positive regulation of fibroblast proliferation	3	0.035342	
GO:0060548--negative regulation of cell death	3	0.036547	
GO:0007204--positive regulation of cytosolic calcium ion concentration	4	0.037324	
GO:0010629--negative regulation of gene expression	4	0.039448	
GO:0070373--negative regulation of ERK1 and ERK2 cascade	3	0.040257	
GO:0071407--cellular response to organic cyclic compound	3	0.041524	
GO:0050679--positive regulation of epithelial cell proliferation	3	0.042806	
GO:0043433--negative regulation of sequence-specific DNA binding transcription factor activity	3	0.042806	
GO:2001020--regulation of response to DNA damage stimulus	2	0.043008	
GO:0071223--cellular response to lipoteichoic acid	2	0.048254	
GO:0060452--positive regulation of cardiac muscle contraction	2	0.048254	
GO:0051384--response to glucocorticoid	3	0.049433	
Down-regulated	GO:0006936--muscle contraction	12	6.58E-13
	GO:0030049--muscle filament sliding	5	1.84E-05
	GO:0007015--actin filament organization	5	2.30E-04
	GO:0008016--regulation of heart contraction	4	2.87E-04
	GO:0060048--cardiac muscle contraction	4	8.68E-04
	GO:0055119--relaxation of cardiac muscle	3	0.0011
	GO:0010881--regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	3	0.002798
	GO:0007010--cytoskeleton organization	5	0.004568
	GO:0007517--muscle organ development	4	0.006099
	GO:0007420--brain development	5	0.008146
	GO:1901877--negative regulation of calcium ion binding	2	0.00832
	GO:1901894--regulation of calcium-transporting ATPase activity	2	0.00832
	GO:1901077--regulation of relaxation of muscle	2	0.012455
	GO:1901020--negative regulation of calcium ion transmembrane transporter activity	2	0.012455
	GO:0070527--platelet aggregation	3	0.012649
	GO:1903779--regulation of cardiac conduction	3	0.022824
	GO:0045822--negative regulation of heart contraction	2	0.028823
	GO:0051694--pointed-end actin filament capping	2	0.028823
	GO:0035865--cellular response to potassium ion	2	0.032873
	GO:0071313--cellular response to caffeine	2	0.032873
	GO:0090281--negative regulation of calcium ion import	2	0.032873
	GO:1904706--negative regulation of vascular smooth muscle cell proliferation	2	0.032873
	GO:0043086--negative regulation of catalytic activity	3	0.039106
	GO:0007155--cell adhesion	6	0.042448
	GO:0006600--creatine metabolic process	2	0.044924
	GO:0006813--potassium ion transport	3	0.045943
	GO:0030007--cellular potassium ion homeostasis	2	0.048908
	GO:0086004--regulation of cardiac muscle cell contraction	2	0.048908
	GO:0008154--actin polymerization or depolymerization	2	0.048908

Table S2 KEGG pathways for up-regulated DEGs and down-regulated DEGs

	KEGG pathways	Count	P value	
Up-regulated	hsa05132:Salmonella infection	9	7.21E-07	
	hsa04380:Osteoclast differentiation	10	2.48E-06	
	hsa04668:TNF signaling pathway	9	5.02E-06	
	hsa05134:Legionellosis	6	1.23E-04	
	hsa05323:Rheumatoid arthritis	7	1.40E-04	
	hsa05161:Hepatitis B	8	3.30E-04	
	hsa04620:Toll-like receptor signaling pathway	7	3.87E-04	
	hsa05140:Leishmaniasis	6	4.49E-04	
	hsa05166:HTLV-I infection	10	4.57E-04	
	hsa05133:Pertussis	6	5.78E-04	
	hsa05152:Tuberculosis	8	0.001088	
	hsa05150:Staphylococcus aureus infection	5	0.001434	
	hsa05142:Chagas disease (American trypanosomiasis)	6	0.002516	
	hsa05031:Amphetamine addiction	5	0.003011	
	hsa04060:Cytokine-cytokine receptor interaction	8	0.006451	
	hsa04062:Chemokine signaling pathway	7	0.006823	
	hsa05030:Cocaine addiction	4	0.009997	
	hsa05144:Malaria	4	0.009997	
	hsa04915:Estrogen signaling pathway	5	0.012573	
	hsa04621:NOD-like receptor signaling pathway	4	0.014377	
	hsa05146:Amoebiasis	5	0.015826	
	hsa05202:Transcriptional misregulation in cancer	6	0.01798	
	hsa05164:Influenza A	6	0.021085	
	hsa05168:Herpes simplex infection	6	0.025569	
	hsa04010:MAPK signaling pathway	7	0.027535	
	hsa04151:PI3K-Akt signaling pathway	8	0.037242	
	hsa05020:Prion diseases	3	0.038381	
	hsa04064:NF-kappa B signaling pathway	4	0.04507	
	hsa04640:Hematopoietic cell lineage	4	0.04507	
	hsa04012:ErbB signaling pathway	4	0.04507	
	Down-regulated	hsa05414:Dilated cardiomyopathy	7	1.60E-06
		hsa05410:Hypertrophic cardiomyopathy (HCM)	6	2.22E-05
		hsa04022:cGMP-PKG signaling pathway	7	6.11E-05
hsa04510:Focal adhesion		7	2.64E-04	
hsa04260:Cardiac muscle contraction		5	3.28E-04	
hsa04270:Vascular smooth muscle contraction		5	0.001754	
hsa04261:Adrenergic signaling in cardiomyocytes		5	0.003204	
hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)		4	0.003267	
hsa04512:ECM-receptor interaction	4	0.006802		

Table S5 Hub genes for modules of dilated PVTA and non-dilated PVAT

Modules	Gene symbol	Official full name
Dilated PVAT		
Black	PROK2	Prokineticin 2
Blue	PPARG	Peroxisome proliferator activated receptor gamma
Brown	NUBPL	Nucleotide binding protein like
Red	ITGB1	Integrin subunit beta 1
Turquoise	MAP4K1	Mitogen-activated protein kinase kinase kinase kinase 1
Yellow	DACT3	Dishevelled binding antagonist of beta catenin 3
Non-dilated PVAT		
Blue	MTARC1	Mitochondrial amidoxime reducing component 1
Brown	RPL23AP87	Ribosomal protein L23a pseudogene 87
Green	CASQ2	Calsequestrin 2
Turquoise	SP140	SP140 nuclear body protein
Yellow	PLA2G2D	Phospholipase A2 group IID