

Biomolecules and Biomedicine

ISSN: 2831-0896 (Print) | ISSN: 2831-090X (Online)

Journal Impact Factor® (2021): 3.76

CiteScore® (2021): 5.2 www.biomolbiomed.com | blog.biomolbiomed.com

SUPPLEMENTAL DATA

Deciphering transcriptional dynamics of cardiac hypertrophy and failure in a chamber-specific manner

Sample ID	Tissues	raw_reads number	clean_reads number	clean_bases	error_rate	Q30	GC (%)
A_CHF1	atrium	51086866	50601886	7.59G	0.03	92.87	48.83
A_CHF2	atrium	46548484	46108434	6.92G	0.03	93.04	48.57
A_CHF3	atrium	47358694	46925514	7.04G	0.03	93.12	48.89
A_HCM1	atrium	46677678	46296298	6.94G	0.03	93.14	48.91
A_HCM2	atrium	46908252	46563004	6.98G	0.03	92.55	49.07
A_HCM3	atrium	49608912	49187858	7.38G	0.03	93.37	48.24
A_sham1	atrium	45706142	45025986	6.75G	0.03	93.34	48.79
A_sham2	atrium	45489412	44822164	6.72G	0.03	93.37	48.73
A_sham3	atrium	47544878	47048378	7.06G	0.03	93.14	48.91
LV_CHF1	left ventricle	46716808	46195920	6.93G	0.03	92.58	47.18
LV_CHF2	left ventricle	46182796	45628840	6.84G	0.03	93.28	47.3
LV_CHF3	left ventricle	46450658	45837024	6.88G	0.03	92.95	47.16
LV_HCM1	left ventricle	46476284	45909980	6.89G	0.03	92.8	47.62
LV_HCM2	left ventricle	47613930	47157086	7.07G	0.03	93.09	47.41
LV_HCM3	left ventricle	45201762	44682114	6.7G	0.03	93.18	47.34
LV_sham1	left ventricle	46297952	45844554	6.88G	0.03	92.76	47.03
LV_sham2	left ventricle	47473316	46840548	7.03G	0.03	92.98	44.41
LV_sham3	left ventricle	46983382	46527468	6.98G	0.03	93.03	47.2
RV_CHF1	right ventricle	47248666	46444388	6.97G	0.03	92.16	40.51
RV_CHF2	right ventricle	45278016	43648060	6.55G	0.03	92.42	44.66
RV_CHF3	right ventricle	47637072	46997014	7.05G	0.03	92.37	41.72
RV_HCM1	right ventricle	47051652	46289232	6.94G	0.03	92.61	40.18
RV_HCM2	right ventricle	47109924	46395186	6.96G	0.03	92.23	40.17
RV_HCM3	right ventricle	46032126	45054048	6.76G	0.03	91.71	40.51
RV_sham1	right ventricle	51678400	50798664	7.62G	0.03	91.48	41.95
RV_sham2	right ventricle	47078410	46588702	6.99G	0.03	92.62	41.51
RV_sham3	right ventricle	46801706	45751680	6.86G	0.03	91.79	40.73

Table S1 Sample information and sequencing statisticsLA: left atrium; LV: left ventricle; RV: right ventricle

	СН	HF				
	muscle contraction	circadian rhythm; rhythmic process				
	extracellular matrix organization	hydrogen peroxide metabolic/catabolic process				
	extracellular structure organization	circadian behavior; rhythmic behavior; locomotor rhythm				
	external encapsulating structure organization	circadian regulation of gene expression				
	muscle system process	oxygen transport; gas transport haptoglobin-bemoglobin complex				
	collagen-containing extracellular matrix	HF circadian rhythm; rhythmic process hydrogen peroxide metabolic/catabolic process circadian behavior; rhythmic behavior; locomotor rhythm circadian regulation of gene expression oxygen transport; gas transport haptoglobin-hemoglobin complex distal axon; myelin sheath; terminal bouton presynapse; neurofilament; axon terminus neuron projection terminus extrinsic component of membrane intermediate filament oxygen carrier activity; oxygen binding organic acid binding; phospholipase binding calcium-activated potassium channel activity peroxidase activity; oxidoreductase activity structural constituent of cytoskeleton fat cell differentiation				
	micturition	HIFcircadian rhythm; rhythmic processhydrogen peroxide metabolic/catabolic processcircadian behavior; rhythmic behavior; locomotor rhythmcircadian regulation of gene expressionoxygen transport; gas transporthaptoglobin-hemoglobin complexdistal axon; myelin sheath; terminal boutonpresynapse; neurofilament; axon terminusneuron projection terminusextrinsic component of membraneintermediate filamentoxygen carrier activity; oxygen bindingorganic acid binding; phospholipase bindingcell adhesion molecule binding; nuclear receptor bindingcalcium-activated potassium channel activityperoxidase activity; oxidoreductase activitystructural constituent of cytoskeletonfat cell differentiationextracellular matrix organizationextracellular structure organization				
	transmembrane receptor protein STK signaling pathway	presynapse; neurofilament; axon terminus				
LA	excretion	neuron projection terminus				
	regulation of smooth muscle contraction	extrinsic component of membrane				
	phasic smooth muscle contraction	intermediate filament				
	neuronal cell body membrane	oxygen carrier activity; oxygen binding				
	cell body membrane	organic acid binding; phospholipase binding				
	dendrite membrane	cell adhesion molecule binding; nuclear receptor binding				
	dendritic spine membrane	calcium-activated potassium channel activity				
		peroxidase activity; oxidoreductase activity				
		structural constituent of cytoskeleton				
	muscle contraction	fat cell differentiation				
LV	extracellular matrix organization	extracellular matrix organization				
	extracellular structure organization	extracellular structure organization				

	external encapsulating structure organization	external encapsulating structure organization
	muscle system process	extracellular matrix structural constituent
	collagen-containing extracellular matrix	collagen-containing extracellular matrix
	regulation of cardiac muscle cell membrane repolarization	amino acid transmembrane transport
	cardiac muscle cell membrane repolarization	regulation of amino acid import across plasma membrane
	regulation of membrane repolarization	regulation of amino acid transmembrane transport
	membrane repolarization	regulation of cardiac muscle cell apoptotic process
	regulation of heart rate	segmentation; collagen trimer
	chromosome, centromeric region	regulation of striated muscle cell apoptotic process
	condensed chromosome	C-C chemokine receptor activity; C-C chemokine binding
	voltage-gated sodium channel complex	G protein-coupled chemoattractant receptor activity
	myosin filament	chemokine receptor activity; cytokine receptor activity
	chromosomal region	cytokine binding; chemokine binding
	sodium channel complex	proton-transporting ATP synthase activity, rotational mechanism
		immune receptor activity
	negative regulation of transmembrane receptor protein STK signaling pathway	striated muscle cell differentiation
	extracellular matrix organization	extracellular matrix organization
	extracellular structure organization	extracellular structure organization
RV	external encapsulating structure organization	external encapsulating structure organization
	regulation of transmembrane receptor protein STK signaling pathway	collagen-containing extracellular matrix
	respiratory electron transport chain	extracellular matrix structural constituent
	L-glutamate transmembrane transporter activity	muscle cell differentiation; muscle cell development

tetrapyrrole binding	heparin binding sulfur compound binding: fibronectin binding
acidic amino acid transmembrane transporter activity	I band; Z disc
NAD(P)H oxidoreductase activity	sarcomere; myofibril; contractile fiber
retinoic acid binding	entrainment of circadian clock by photoperiod
C4-dicarboxylate transmembrane transporter activity	myotube differentiation
retinoic acid 4-hydroxylase activity	regulation of striated muscle cell differentiation

Table S2 Top 10 BP, CC, and MF GO terms in CH and HF, respectively

Note: GO terms with a red background denote Gene Ontology (GO) terms enriched in both the LA and LV, GO terms with a blue background represent GO terms shared between the LA and RV, and yellow in LV and RV. Without any background color, unique GO terms are enriched in each chamber; for example, no shared GO terms between the atrium and left ventricle.

Entries in bold denote GO terms enriched in CH and HF in the LA, LV, and RV, respectively.

CH- cardiac hypertrophy, HF- heart failure, LA- left atrium, LV- left ventricule, RV- right ventricule, BP- biological process, CC- cellular component, MF- molecular function;

	СН	HF					
	Cytokine-cytokine receptor interaction	Cytokine-cytokine receptor interaction					
	Vascular smooth muscle contraction	Vascular Smooth Muscle Contraction					
	Salivary secretion	Circadian Rhythm					
	Calcium signaling pathway	African trypanosomiasis					
	Pyruvate metabolism	NF-kappa B signaling pathway					
	Neuroactive ligand-receptor interaction	Malaria					
та	Drug metabolism - cytochrome P450	Hippo signaling pathway					
LA	Ras signaling pathway						
	Metabolism of xenobiotics by cytochrome P450						
	Butanoate metabolism						
	Fatty acid degradation						
	Tryptophan metabolism						
	Glutamatergic synapse						
	cAMP signaling pathway						
	Cytokine-cytokine receptor interaction	Cytokine-cytokine receptor interaction					
	Chemokine signaling pathway	Chemokine signaling pathway					
	Adrenergic signaling in cardiomyocytes	Adrenergic signaling in cardiomyocytes					
	Aldosterone synthesis and secretion	Aldosterone synthesis and secretion					
	Protein digestion and absorption	Platelet activation					
LV	Platelet activation	Cardiac muscle contraction					
	Cardiac muscle contraction	Protein digestion and absorption					
	Cell cycle	Vascular Smooth Muscle Contraction					
	Progesterone-mediated oocyte maturation	Circadian rhythm					
	Oocyte meiosis	Oxytocin signaling pathway					
	ECM-receptor interaction	Viral protein interaction with cytokine and cytokine receptor					

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Diabetic cardiomyopathy		Circadian entrainment							
	Homologous recombination	cGMP-PKG signaling pathway							
Diabetic cardiomyopathyCircadian entrainmentHomologous recombinationcGMP-PKG signaling pathwayp53 signaling pathwayDilated cardiomyopathy Glycosphingolipid biosynthesis - ganglio seFCircadian entrainmentCircadian entrainmentOxytocin signaling pathwayOxytocin signaling pathwayAfrican trypanosomiasisVascular Smooth Muscle ContractionAdrenergic signaling in cardiomyocytesCircadian RhythmMucin type O-glycan biosynthesiscGMP-PKG signaling pathwayPrimary immunodeficiencyViral protein interaction with cytokine and of ECM-receptor interactionRVMAPK signaling pathwayEstrogen signaling pathwayIntestinal immune network for IgA productionInsulin secretionCholesterol metabolismTNF signaling pathwayVitamin digestion and absorptionOvarian steroidogenesisMalariaCalcium signaling pathway	Dilated cardiomyopathy								
		Glycosphingolipid biosynthesis - ganglio series							
	Circadian entrainment	Circadian entrainment							
	Oxytocin signaling pathway	Oxytocin signaling pathway							
	African trypanosomiasis	Vascular Smooth Muscle Contraction							
RV M Ci Ai Ai Ni M Pr T In Oi Cl Vi M	Adrenergic signaling in cardiomyocytes	Circadian Rhythm							
	Natural killer cell mediated cytotoxicity	Protein digestion and absorption							
	Mucin type O-glycan biosynthesis	cGMP-PKG signaling pathway							
	Primary immunodeficiency	Viral protein interaction with cytokine and cytokine receptor							
RV	MAPK signaling pathway	ECM-receptor interaction							
	T cell receptor signaling pathway	Estrogen signaling pathway							
	Intestinal immune network for IgA production	Insulin secretion							
	One carbon pool by folate	Human papillomavirus infection							
	Cholesterol metabolism	TNF signaling pathway							
	Vitamin digestion and absorption	Ovarian steroidogenesis							
	Malaria	Calcium signaling pathway							
		Drug metabolism - other enzymes							

Table S3 The top 15 KEGG pathways in CH and HF

Note: KEGG pathway terms with a red background denote the KEGG pathway enriched in both the LA and LV, KEGG pathways with a blue background represent the KEGG pathway shared between the LA and RV, and yellow in LV and RV. Without any background color, unique KEGG pathways are enriched in each chamber. KEGG pathways in bold denote the KEGG pathway enriched in CH and HF in the LA, LV, and RV, respectively.

CH- cardiac hypertrophy, HF- heart failure, LA- left atrium, LV- left ventricule, RV- right ventricule, BP- biological process, CC- cellular component, MF- molecular function, KEGG- Kyoto Encyclopedia of Genes and Genomes;

	СН		HF
	Degradation of the extracellular matrix		Erythrocytes take up oxygen and release carbon dioxide
	Extracellular matrix organization		Erythrocytes take up carbon dioxide and release oxygen
	Assembly of collagen fibrils and other multimeric structures		O2/CO2 exchange in erythrocytes
	Collagen formation		Acetylcholine Neurotransmitter Release Cycle
	Collagen biosynthesis and modifying enzymes		Scavenging of heme from plasma
	Crosslinking of collagen fibrils		Adherens junctions interactions
	Integrin cell surface interactions		Neuronal System
LA	Non-integrin membrane-ECM interactions		Potassium Channels
	Collagen degradation		Phase I - Functionalization of compounds
	Collagen chain trimerization		Binding and Uptake of Ligands by Scavenger Receptors
	Muscle contraction		Muscle contraction
	Striated Muscle Contraction		Striated Muscle Contraction
	ECM proteoglycans		O-glycosylation of TSR domain-containing proteins
	NCAM1 interactions		Xenobiotics
	NCAM signaling for neurite out-growth		Attenuation phase
	Extracellular matrix organization		Assembly of collagen fibrils and other multimeric structures
	Assembly of collagen fibrils and other multimeric structures		Extracellular matrix organization
LV	Collagen formation		Collagen formation
	Integrin cell surface interactions		Collagen biosynthesis and modifying enzymes
	Degradation of the extracellular matrix		Integrin cell surface interactions

	Collagen biosynthesis and modifying enzymes	Crosslinking of collagen fibrils							
	Collagen degradation	Collagen degradation							
	Collagen chain trimerization	Collagen chain trimerization							
	Crosslinking of collagen fibrils	Non-integrin membrane-ECM interactions							
	Non-integrin membrane-ECM interactions	Degradation of the extracellular matrix							
	Laminin interactions	Laminin interactions							
	Elastic fibre formation	Axon guidance							
	Signaling by Rho GTPases	Developmental Biology							
	Kinesins	NCAM signaling for neurite out-growth							
	Anchoring fibril formation	NCAM1 interactions							
	Respiratory electron transport	Extracellular matrix organization							
	Complex I biogenesis	Integrin cell surface interactions							
	The citric acid (TCA) cycle and respiratory electron transport	Assembly of collagen fibrils and other multimeric structures							
H S H A H C T H C T H C T H C C H C T H C C T H C C T H C C T H C C T H C C T H C C T H C C T H C C T H C C T H C C T T T T	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	Collagen formation							
DV	Phase 0 - rapid depolarisation	Collagen biosynthesis and modifying enzymes							
RV	Cardiac conduction	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)							
	Erythrocytes take up carbon dioxide and release oxygen	Nonsense-Mediated Decay (NMD)							
	O2/CO2 exchange in erythrocytes	O-linked glycosylation							
	Sema4D in semaphorin signaling	ECM proteoglycans							
	Signaling by Retinoic Acid	Anchoring fibril formation							

GPVI-mediated activation cascade	MET activates PTK2 signaling
Collagen degradation	MET promotes cell motility
Collagen chain trimerization	Platelet degranulation
Muscle contraction	O-glycosylation of TSR domain-containing proteins
Striated Muscle Contraction	Striated Muscle Contraction

Table S4 The top 15 Reactome pathways in CH and HF

Note: Reactome pathway terms with a red background denote the Reactome pathway enriched in both the LA and LV, Reactome pathways with a blue background represent the Reactome pathway shared between the LA and RV, and yellow in LV and RV. Without any background color, unique Reactome pathways are enriched in each chamber.

Reactome pathways in bold denote the Reactome pathway enriched in CH and HF in the LA, LV, and RV, respectively.

CH- cardiac hypertrophy, HF- heart failure, LA- left atrium, LV- left ventricule, RV- right ventricule, BP- biological process, CC- cellular component, MF- molecular function;



Figure S1 Quality control and quantitative analysis of sequencing data from all samples. (A) Reads of all samples were aligned to the reference genome. (B) PCA using FPKM of samples. The samples were clustered according to the sampling location. (C) Boxplots of gene expression distribution. The X-axis is the name of the samples; Y-axis is log₂ (FPKM+1). (D) Correlation of gene expression levels among samples based on Pearson correlation between samples. Atrium (left), LV- left ventricule, RV- right ventricule, PCA-principal component analysis, FPKM- Fragments Per Kilobase of transcript sequence per Millions base pairs;



Figure S2 Analysis of differentially expressed genes (DEGs) in the same position under the HF-sham. Volcano plots of DEGs for in LA (A), LV (C), and RV (E), blue dots represent down-regulated DEGs; red dots represent up-regulated DEGs. The most significant 10 DEGs gene names are shown. The top 10 GO terms in BP, CC, and MF for DEGs in LA, LV, and RV are shown in the right part of the picture (B, D, F)

CH- cardiac hypertrophy, HF- heart failure, A- atrium (left), LV- left ventricule, RVright ventricule, BP- biological process, CC- cellular component, MF- molecular function:



Figure S3 Statistics of pathway enrichment of DEG from the LA, LV, and RV of HF condition in mice. The KEGG enrichment pathway is on the left, and the Reactome enrichment pathway is on the right in the picture. (A) Enrichment pathway of the DEGs in the LA; (B) Enrichment pathway of the DEGs in LV; (C) Enrichment pathway of the DEGs in RV. The size of the point represents the number of DEGs

CH- cardiac hypertrophy, HF- heart failure, A- atrium (left), LV- left ventricule, RV- right ventricule, BP- biological process, CC- cellular component, MF- molecular function; KEGG- Kyoto Encyclopedia of Genes and Genomes

Α

Crb2	ltk		Hbb-b2		Amy1		Hdac10		Mmp9		Mapt		Sfrp5
Fras1	Myh7		Upk3b	X	Cldn19	X	Hba-a1	X	Ak4	X	Lrrn4	H	Dennd1c
SIc22a3	Gab1	X	Gdf2		Mixipi		Sdk2		Sspo	Ì	Myo5b	H	Bmp3
Wnt2b	Inmt	X	Ccl11		Ntrk2	X	Cpn2	E	Alas2		ltgb6		H2-Q10
Trpc1	Cmya5		Chd5		Asb4		Bcl11b		Adam11		Lss	R	Egf
Usp11	Zim1		Pkd2l2	X	Ptpru	Ż	Lpin1		Zap70		Vstm2b		Txnip
Rasgrf1	Smad3	X	Ces1d		Pde4a		Dgke	×	Gsta3		Arid5b		Hbb-b1
Actn3	Ntrk3		Fmod		Pnpla3		Col11a2		Hba-a2		SIc6a2		Snca
Asb15	Numa1												

В													
Skat Nedt Fedd Soen2 Rere Chap	21 Smad7 Irf2bp1	KIB Rai2	Gm14298	ligmt Cil	K/22 Sec31	b Spag5	Arit4ap	Equaps	Rasif1b	Racgap1	Cena2	K#14	Hpgd
Pert Catto 2 Hosait 2 Dappi insigi 2 Uhrt	fi ivd Artigap11	Privedbp Ling	AldhGal	Nfyb Ttyn3	Gm4002 Pik3o	9 SI026a19	Zip037	Actg1	K#206	Rhoe	Ppip5k1	Ybx2	Sidea1
Inhab Allavitad Clot Fgirld Clot? Taxib	Data Chafla Casof	End4 Zbib37	Mide	Gm12258 Rin2	Shibgrid Rgo	Nrbp2	Alaho	Ehhe40	Curs	Map2	Rragd	Jasti	Dbat
loam2 Syne1 Dnajb4 Meis1 Anxa2 Map3	HO FhQ Ephad	Sik1 Broat	Uba2o	Cd72 Apri2	IN2711 Plpn1	2 Mmp12	Pla207	Ap014	8425138	Lire15	NUR	Lange	MINT
Bro5 Strint S Pikt Call Samt Famil28 Rho	e Cdo42ep3 Ptprz1	Atp1b1 Cry1	Cdm	L/mo2 Z#p366	Cdk5rap1 Hmm	r Plekhg2	Lince1	Gja5	lető	Kifo1	PIK5	Rbbp5	Cond3
Proser2 Dhra3 Nup153 Aox1 Timp4 Tra2	tb Cep83 HQafx	Gato2 Magix	Acan Dila	105 6000000000 H054 Rad51	Epn3 CB096	18 Poin	Apolijb	Vidir	Anin	Ak4	Dan1	Mgea5 De	Serus G 000 0002 472 6
Dekeha Myo1e A\071822 Zfp763 Rwi1 Stel	1 Init Kona2	Epho4 Aspa	Ywnag	Denf Mat2a	Ausb Spdy	HID NO	Grm0100	Gitat	Sema7a	Hba-at	Ecd4	Rbak	Lima
RF3 Matti Kona5 Hapb7 Gep55 Gm14	434 Sox17 Fg64	Rina Mest	DbM	Arpo3 Dex20b	Althial Mai	Ning2	Rasi10a	A162	KIM	Sox4	Jund	Ecrn2	Cntn2
Cabpb Plekhni Dna2 Cox8a1 Bol11b Cyb5	ir2 Hbb-b1 Ppp1r1c	Pbk Marf	1gi	Gata3 Mapk10	Timm10 Gata	5 Sh2d3o	D2844750+	Pkia	Map10	Kpna2	Rbm3	Ninj1	Art2
Rhoh Tubbő Ehdi Dmpi Eb/3 Coló	a3 Pfkb2 Ldhd	Id3 Mih3	Pparg	NelD ENSAUS CODODDIN	4 Frendt Coll	Pur	Dist	Spc26	And d2	Snipe	Dhdh	Alpeta	Conf
0-46 Matthet Zak2 H0.722 Nas16 800a	10 Met21 Cet109	Zinte2 Ren2	GHND I	ECm Mrast0	HTEP MRD	CATA	Himara2	Calu	27+4922	Adapantet	Greek	Cany	Crical
Creid2 Ddah2 Adht Nup50 GLI4 Pdzr	n3 Konv2 Zo3n8	Kenj2 III8	Fbxw7	Ndrg4 Cks1b	Bub1 Hyal	Clacka	Butto	C de25b	Nacc2	Pdgfra	Gpsrm1	Tacc3	Z1p80
Ef2o4 Rgb3bp Slah2 Rps0ka2 Prune2 Lraf	t Casq1 Prox1	Ztp305 Hand2	Tritatio	Ckap2 Ndd80	Pak20 Brat	Artigefil	Aspm	Pk.6212	Cade2	DdHI	Cava	Pabpot	C 340
Gog10b Sap20 NRbia Glaps Zbtb18 Dnah	cyth2 Elin	Lap1 Cabya	Mmab	Ahr Gamtt	MIM Max	Tpm4	Rdh5	Myo1g	Celt1a1	KE4	Londa	Diap3	Phil
Hnmpk Apobeci Ibm2a Plunbl 1 Nek2 Cenp	Nic2 Statl	Lrro17 Htt	Limbi	Inf7 Trim59	Nut2-ps1 KF12	Gestd	Smo4	Agtria	Heyt	Asap1	Rapot	Hengb2	Fy1
Ly76 Mpdz Cks2 Rgs14 Konct Pacs	2 Nusap1 Ywhah	Sema0b Adamtal	Card	Shipg Haat651	Pole Uty	Adtr2	Nidt	Rnf41	Malk	Caonata	HistitiZae	Bri	Aloz5
HIDa Hmoxt Sums2 Hyout Son4b Arlas	5a Apol10b Uros	Alloay Histihile	Gyatiri	Pro1 HapDOb1	Bol211 Auri	Hist2h0c2	Cdoad	50211	6100a11	Gnn2	Ints0	Irak2	Сірь
Naa40 If205 E22 Apole1 Spt1 Bazt	Ta Asb10 Myll	Hindea Txinb	Gern4l	Fabp5 Sudig2	Mxd3 Z(960	Gid4	Zfp812	Rpi19	Zyx	Trb1	Fabp4	Dnajb1	26715
Vim Gmf987 : BoB Agt 2 Ribnt Tpd	2 Ckp3 Ano10	Artigap25 Bub1b	PII	Conb2 Arpo4	Par Popdi	2 Data	Carnp1	Eet2	Axi	Tet1	Gpr17	Trablo	Ctsc
Zfo450 Rassf2 Ky Kit11 Z5/75 D5/3	a sipin spinopi	Famil@a Ddr1	Myos	BicBa3r2 Noaph	Ldirap1 Cd1-	KING	Fkbp10	Eferno2	E211	Pvrg	Z10828	Jdp2	Troap
Alas2 Rpl3 Dusp18 Psatt Ttap4 Cdr2	20 Z 1588 Tbx3	Cdc14b SH	Sic43a3	Gimap6 Bik	H2afz Form	Uep2	Hba-a2	AsaNI	Sle3#2	Gbp10	App12	Mbd1	Oxet1
С													
Sio35a3 Dnajb1 Edn3 Hba-a2 Son2b Pad Si	yrj2bp Oastg F2rl2	Griaz Diat	Acta1 Rpip	0 Frzb Tritist	2 Carl Nas	38 KIB	6100w8	Arkid2 C	Isgepit L	Hol Hol	c1 Comp	Mpped2	Rragd
Aboo5 Tmed2 Shdop1 Ankid11 Sda Cip F	Thodt Myot Builth	Eyat Lingo3	Thpo Tre	Buh Dat	Gm8169 Cm5	506 R11	Osudite	Cul4a0	Ipmà T		Last	Cd74	Dahdt
Conti Rhob Mergel-rel Meigt Cok17 Trpm6 U	Jap35 Konct Fig#18	Tg Usp28	Nyk2 Rpl21	la WH Myk	Sacod Lib	9 Atto:	Nrp1	P2ry4	Net P	hyh Syng	o 3 C2od	Stp4	Oazt
Fgl14 Fambla Eam1 Cell Call Hadh 21	tyve16 Diect RpD	Fam128a Mdh1	BicZarl Bis 1	Urb1 Durp	Confis Cold	a2 Fanti	Artigapo	Comtd1	Azil P	nàp En	en Cartor	C 482	Tan
Killi Lengi Eriki Gini 4446 impaci i Ggaz i Odolf Pardto Siotal Roll Mend Tuch C	hih3 Fgf23 Mon2	N x2 Cdyl2	Gdpd3 Sod3 Silo7a6 P to	2 Dusp15 Soros	3 Vps35 Kit	2 Mb	Ztpm1 Certoi	Mgattb Pice2	H01050 Adi	oyapt Abd	11 Opon 567 Paro7	Prpn13 Rostx	Rolo1
Zp165 Must6 Huve1 Themis2 Ora2 Lp1b 1	Trpol Con Pert	Id1 SgA1	Posk4 Msk	Ube2o Opr1	Z\$0007 Cace	ata Lmanti	Gent3	Arapt	Elflax 1	140 00	15 T IDEN 2	Hapb3	Bepp1
Gele Those Lidho Neead Guoy2d Cor4 H	Netm Svip Gbas	Cat2ra Ogt	Matr Nr6a	2 Une119b Mtad	Stolug Ppp	еа Нарх	Onm1	Price R	ap1gap2 Pr	1e7a Cao	1g2 Map2k	Prune2	AArtb7
Postn inmp11 Sucia2 Pag10 Rraga Teast P	pp1db Epn3 Chps1	Cyb6r4 Cakras	Noubli Noute	A2 Aldri	e Opict Rat	E) Frast	PK82	Oca	Taxel0 Ch	chdi Inpp	4a Hapbi	P cp4	Rpa21
Cos Gett Rps/9 Ankd/0 Kit/4 2 OH/205 M H2-461 Fg/13 OH/209 Ser36 Zadh2 Ser36 Z	trpa34 Don Co Ce601 Abhd0 Nrep	x4a4 Rg+11	Rps0 Tmam	102 Ph#3 Teor	Fam 13a P co	ce Zb160	Cdca3 Gatarapi2	Figri2	Cry2 E	el2 Cor fàm Tee	g1 7 Timm2 62 8 EX012	Engel	Tel
Fabp4 Aes Smox D4vysd3e Tpt Ubl3 C	Cpst7 Mki07 Camb1	SIc25a36 Rpl37a	Sect 48 Cank 2	tal SmpdDa Rho	ler2 Os	n Dazap2	ToriHa	Those	Ringt R	erg Cp	2 Chuk	PAD14	Rab20
Apoe Zb516 loam1 Angp#7 Stt2a Tiat Fa	am59b Cdkl5 Sord	Fdr (95549	Rp14 Adoy	7 Abhd14b Mrgb	Da Lan	a7 Slutbost	CdM	Taco2	Hace1 / OF	1679 Cd	No Actual	AMR453	Myh7
Rpi6 Sref5 Myo20 Rps7 Epm2a Luc72 S	lorbs2 Tppp Skc2a8	Syne1 Rps18	Gm 9046 Usp:	2 Weps Aop	2 BdH2e1 CoH	a5 Poytia	Rpla	Atdia	St14 N	scill) Cyp	2s1 Dob	Enol	Suckyl
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Usp19 Ron8 ligb9 Map3x8 Hed12 ligbp5 F	Rps5 Ces2e Myh7b	Counte Gina	Trpol Mtx3	3 Thosa Shay	1 Gm12258 Bos	11 Gtpbp2	Rpil8	Nova2	MIDIT	ByA RDI	3 a 0 90 a r	ArpBat	Tmen87a
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Figure S4 Constructing PPI network shared in CH and HF in LA, LV, and RV, respectively. (A) The PPI network of DEGs is shared in CH and HF in LA. (B) in LV. (C) in RV performed by the MCODE plugin in Cytoscape software PPI- protein-protein interaction, CH- cardiac hypertrophy, HF- heart failure, DEGs- differentially expressed genes, LA- left atrium, LV- left ventricule, RV-right ventricule, MCODE- molecular complex detection.



Figure S5 Expression of genes associated with cardiac hypertrophy and heart failure. (A) The heatmap of nine DEGs encoding cardiac myosin and natriuretic peptide hormones, fibrosis, and identified biomarkers in our study. (B) Heat maps of 123 genes may be known to be associated with hypertrophy and heart failure based on our gene expression dataset. (C) The expression of single DEG in LA, LV, and RV in different states

DEGs- differentially expressed genes, LA- left atrium, LV- left ventricule, RV-right ventricule