https://doi.org/10.17305/bb.2023.8997

Biomolecules and Biomedicine

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

Journal Impact Factor® (2021): 3.76

CiteScore® (2021): 5.2

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SUPPLEMENTAL DATA

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

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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 statistics
LA: left atrium; LV: left ventricle; RV: right ventricle

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	CH	HF
LA	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
	collagen-containing extracellular matrix	haptoglobin-hemoglobin complex
	micturition	distal axon; myelin sheath; terminal bouton
	transmembrane receptor protein STK signaling pathway	presynapse; neurofilament; axon terminus
	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
LV	muscle contraction	fat cell differentiation
	extracellular matrix organization	**extracellular matrix organization**
	extracellular structure organization	**extracellular structure organization**

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	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

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

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;

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	CH	HF
LA	**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
	Drug metabolism - cytochrome P450	Hippo signaling pathway
	Ras signaling pathway	
	Metabolism of xenobiotics by cytochrome P450	
	Butanoate metabolism	
	Fatty acid degradation	
	Tryptophan metabolism	
	Glutamatergic synapse	
	cAMP signaling pathway	
LV	**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**
	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
	p53 signaling pathway	Dilated cardiomyopathy
		Glycosphingolipid biosynthesis - ganglio series
	Circadian entrainment	**Circadian entrainment**
	Oxytocin signaling pathway	**Oxytocin signaling pathway**
	African trypanosomiasis	Vascular Smooth Muscle Contraction
	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;

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	CH		HF
LA	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
	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
LV	**Extracellular matrix organization**		**Assembly of collagen fibrils and other multimeric structures**
	Assembly of collagen fibrils and other multimeric structures		**Extracellular matrix organization**
	Collagen formation		**Collagen formation**
	Integrin cell surface interactions		**Collagen biosynthesis and modifying enzymes**
	Degradation of the extracellular matrix		**Integrin cell surface interactions**

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	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
RV	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
	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	Collagen formation
	Phase 0 - rapid depolarisation	Collagen biosynthesis and modifying enzymes
	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

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	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;

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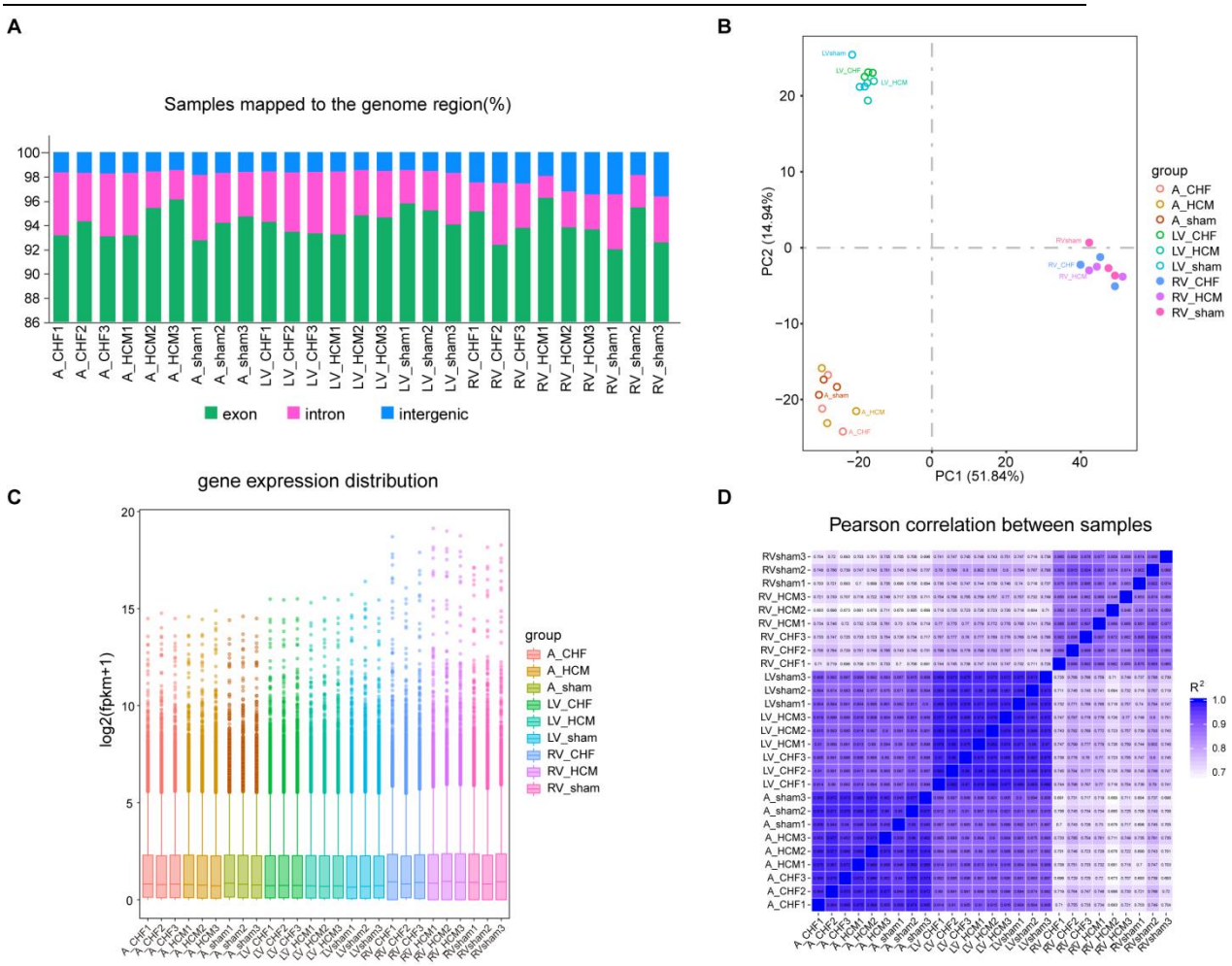

Figure S1 Quality control and quantitative analysis of sequencing data from all samples. (A) Reads of all samples were aligned to the reference genome. (B) PCA using FPKM of samples. The samples were clustered according to the sampling location. (C) Boxplots of gene expression distribution. The X-axis is the name of the samples; Y-axis is $\log_2$ (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;

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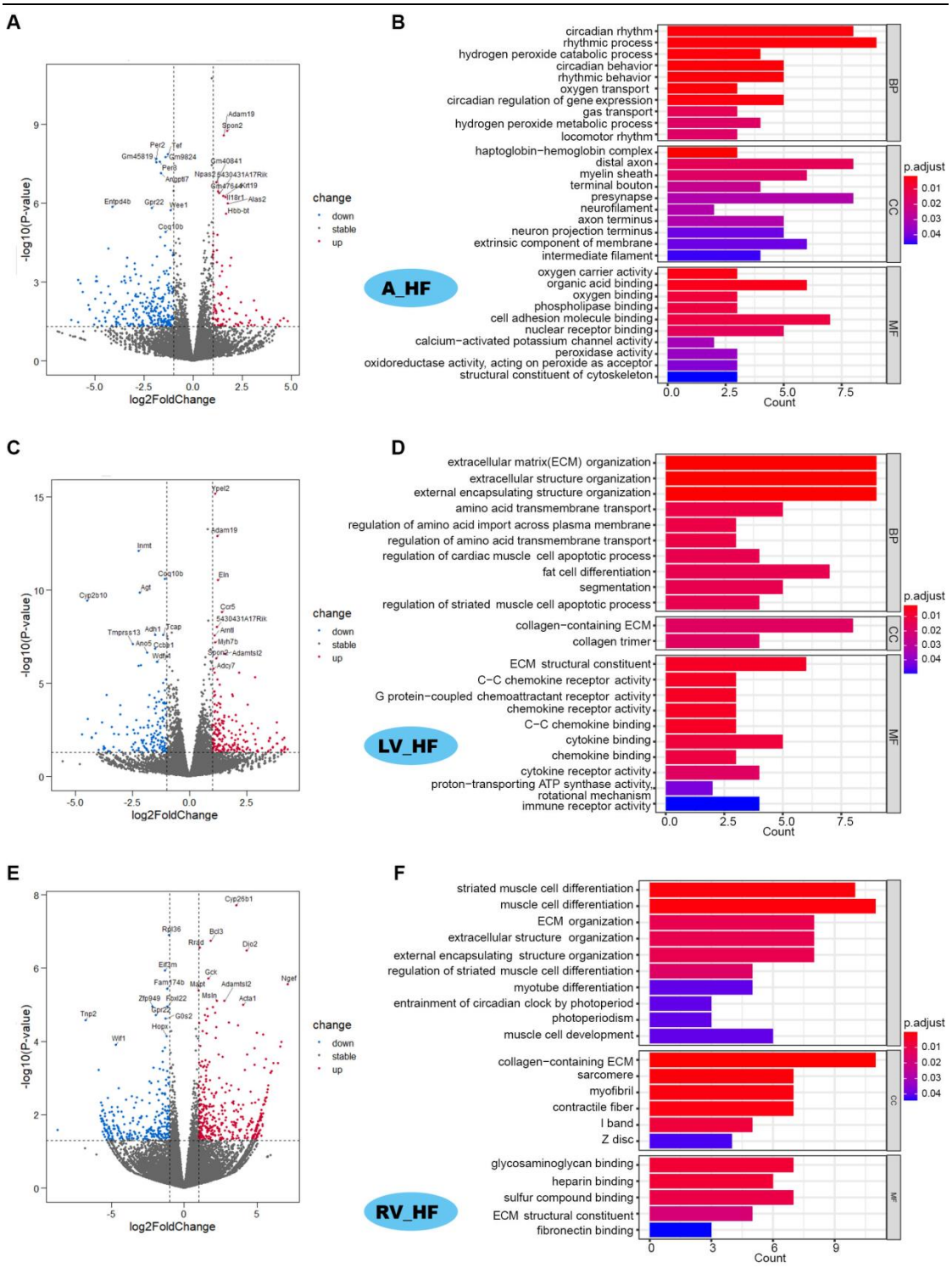

Figure S2 Analysis of differentially expressed genes (DEGs) in the same position under the HF-sham. Volcano plots of DEGs for in LA (A), LV (C), and RV (E), blue dots represent down-regulated DEGs; red dots represent up-regulated DEGs. The most significant 10 DEGs gene names are shown. The top 10 GO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

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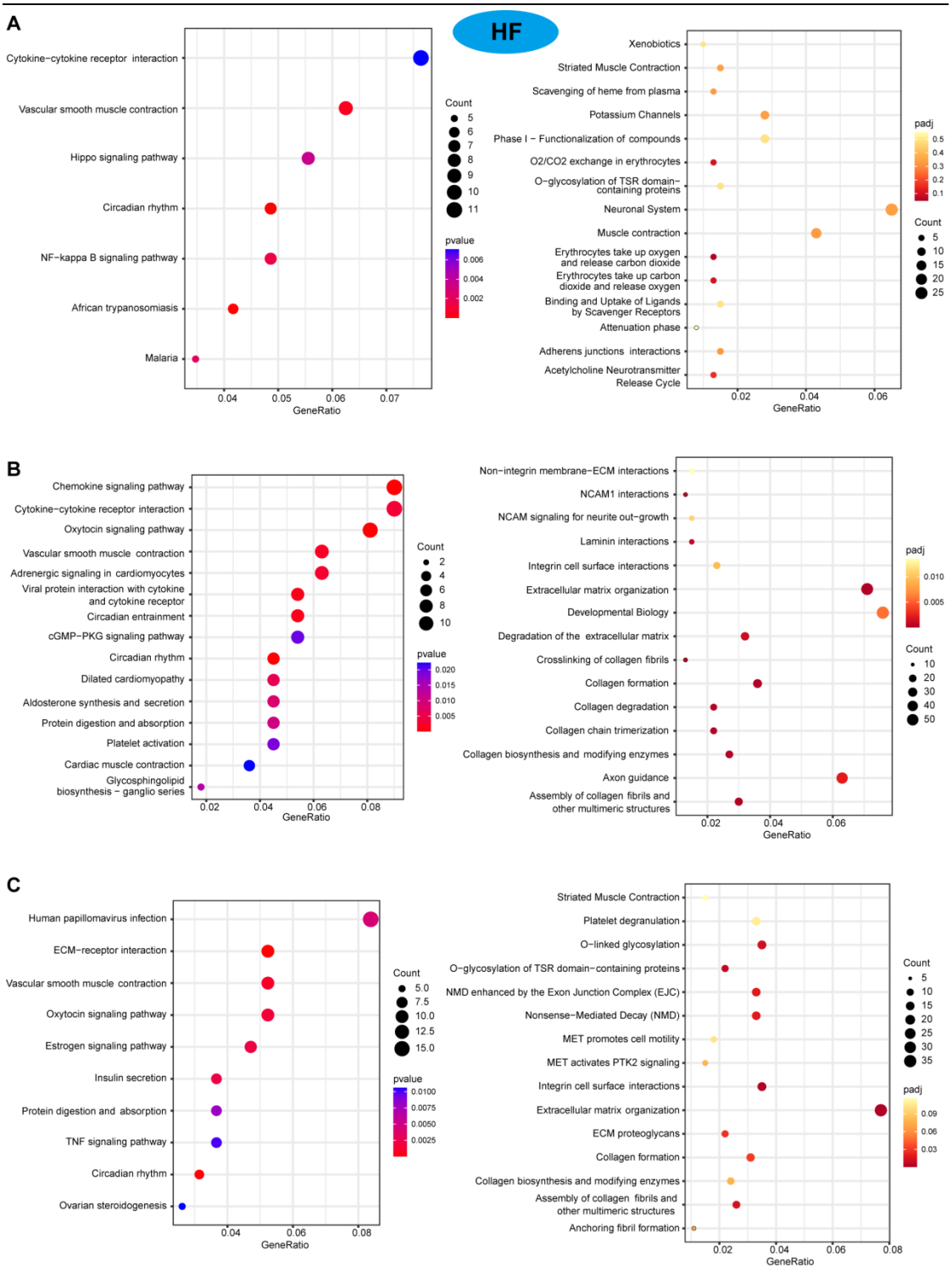

Figure S3 Statistics of pathway enrichment of DEG from the LA, LV, and RV of HF condition in mice. The KEGG enrichment pathway is on the left, and the Reactome enrichment pathway is on the right in the picture. (A) Enrichment pathway of the DEGs in the LA; (B) Enrichment pathway of the DEGs in LV; (C)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

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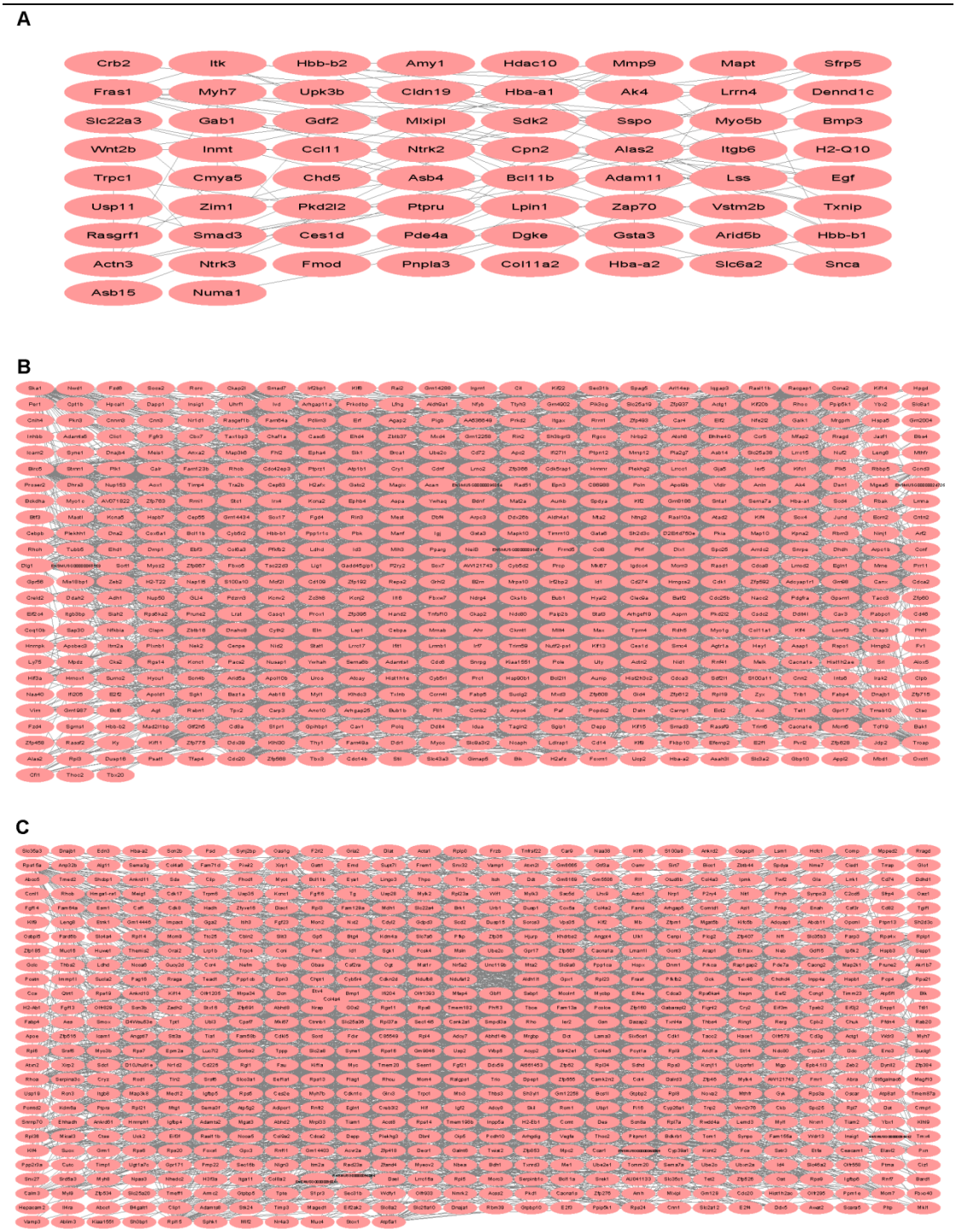

Figure S4 Constructing PPI network shared in CH and HF in LA, LV, and RV, respectively. (A) The PPI network of DEGs is shared in CH and HF in LA. (B) in LV. (C) in RV performed by the MCODE plugin in Cytoscape software

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.

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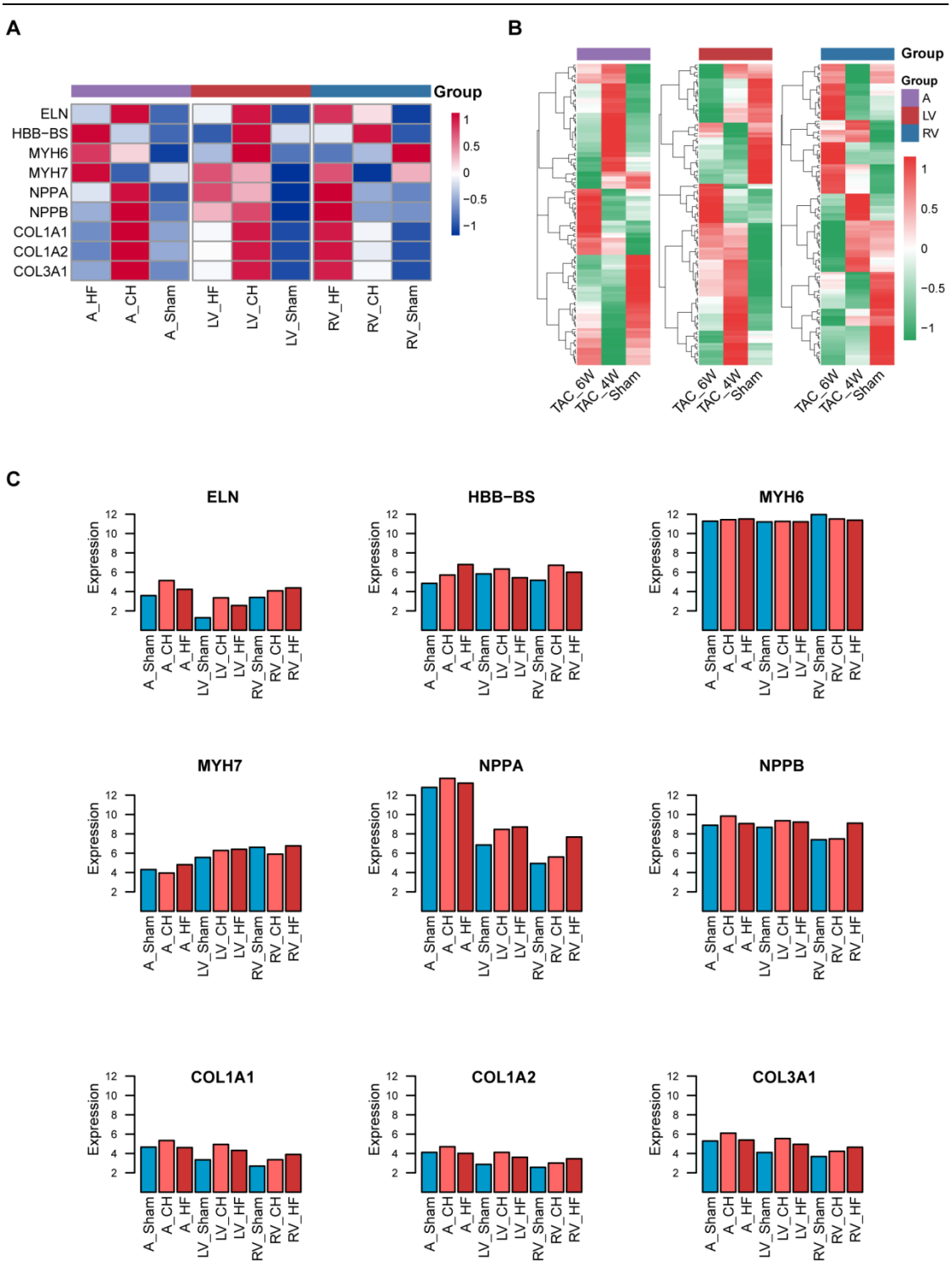

Figure S5 Expression of genes associated with cardiac hypertrophy and heart failure. (A) The heatmap of nine DEGs encoding cardiac myosin and natriuretic peptide hormones, fibrosis, and identified biomarkers in our study. (B) Heat maps of 123 genes may be known to be associated with hypertrophy and heart 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