

Figure S1. Volcano plots of DEGs. Volcano plot of (A) LADEGs, (B) RADEGs, and (C) DADEGs. All the three types of DEGs were selected using a threshold of $|\text{fold change}| > 1.5$ and $P < 0.05$. LA, left atria; RA, right atria; DEGs, differentially expressed genes; LADEGs, differentially expressed genes in LA; RADEGs, differentially expressed genes in RA; DADEGs, differentially expressed genes in the LA/RA ratio; UP, upregulated; DOWN, downregulated; NOT, not changed.

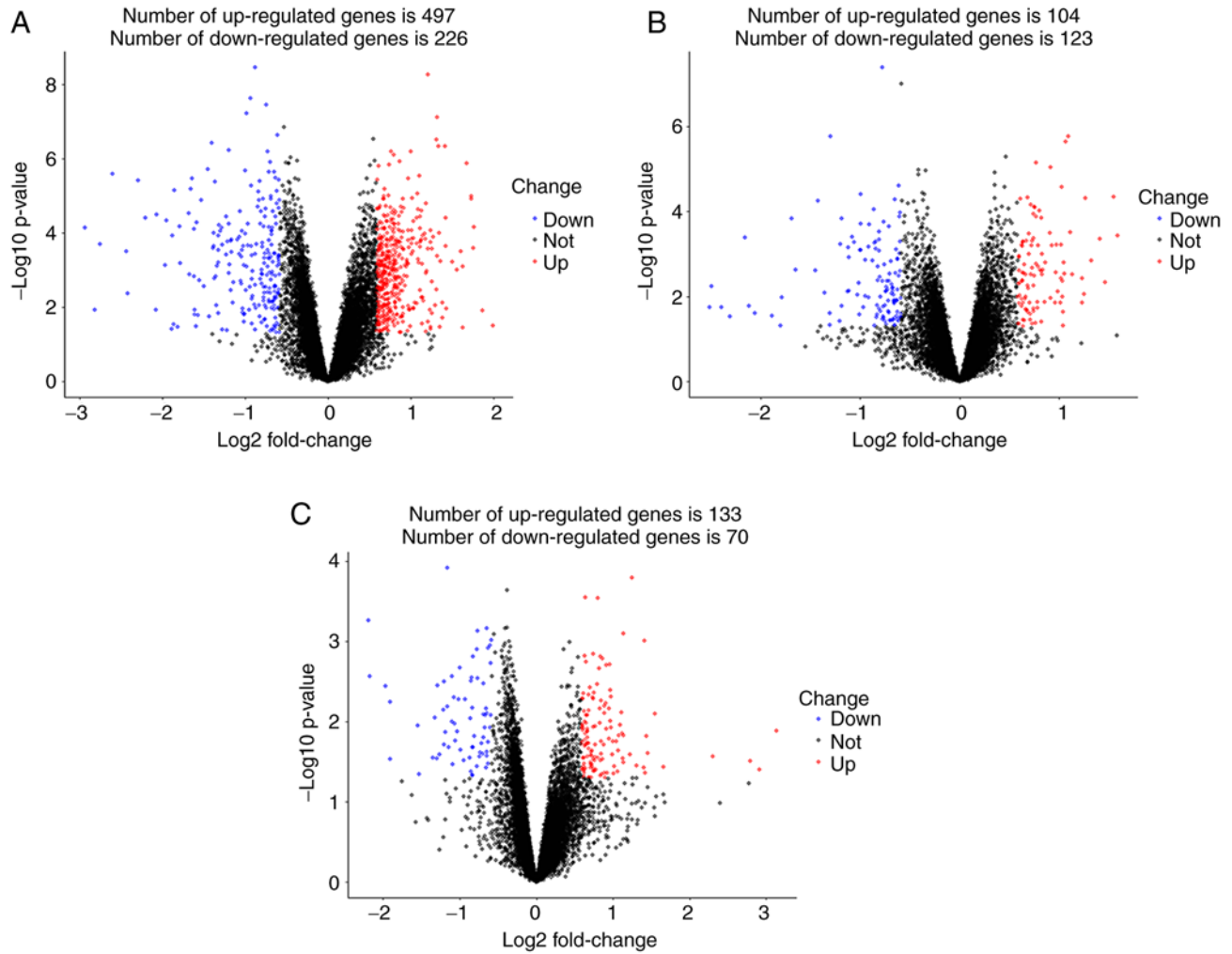


Table SI. Characteristics of the patients.

Age	Sex	Status
53	Female	AF
47	Female	AF
46	Male	AF
46	Female	AF
32	Female	AF
71	Male	AF
43	Male	AF
60	Male	SR
77	Female	SR
33	Male	SR
74	Female	SR
62	Female	SR
76	Female	SR

AF, atrial fibrillation; SR, sinus rhythm.

Table SII. KEGG enrichment analysis of DEGs.

DEG category	Direction	ID	Description	P-value	Count
LA	DOWN	hsa04530	Tight junction	0.003151	7
LA	DOWN	hsa04514	Cell adhesion molecules	0.005858	6
LA	DOWN	hsa04151	PI3K-Akt signaling pathway	0.007337	10
LA	DOWN	hsa04976	Bile secretion	0.009008	4
LA	DOWN	hsa04390	Hippo signaling pathway	0.009764	6
LA	DOWN	hsa04216	Ferroptosis	0.009928	3
LA	DOWN	hsa04610	Complement and coagulation cascades	0.010507	4
LA	DOWN	hsa04360	Axon guidance	0.017957	6
LA	DOWN	hsa00910	Nitrogen metabolism	0.018521	2
LA	DOWN	hsa04972	Pancreatic secretion	0.021204	4
LA	UP	hsa05140	Leishmaniasis	5.50E-08	13
LA	UP	hsa04672	Intestinal immune network for IgA production	4.81E-07	10
LA	UP	hsa05150	Staphylococcus aureus infection	7.68E-07	10
LA	UP	hsa05310	Asthma	8.38E-06	7
LA	UP	hsa05323	Rheumatoid arthritis	1.98E-05	11
LA	UP	hsa05332	Graft-versus-host disease	3.10E-05	7
LA	UP	hsa04145	Phagosome	3.48E-05	14
LA	UP	hsa05322	Systemic lupus erythematosus	3.48E-05	12
LA	UP	hsa05330	Allograft rejection	6.01E-05	7
LA	UP	hsa04940	Type I diabetes mellitus	0.00013	7
RA	DOWN	hsa03320	PPAR signaling pathway	0.000211	5
RA	DOWN	hsa05133	Pertussis	0.002078	4
RA	DOWN	hsa05143	African trypanosomiasis	0.002369	3
RA	DOWN	hsa04512	ECM-receptor interaction	0.003408	4
RA	DOWN	hsa05150	Staphylococcus aureus infection	0.004961	3
RA	DOWN	hsa05134	Legionellosis	0.007101	3
RA	DOWN	hsa05140	Leishmaniasis	0.013389	3
RA	DOWN	hsa04151	PI3K-Akt signaling pathway	0.014296	7
RA	DOWN	hsa04145	Phagosome	0.016851	4
RA	DOWN	hsa04610	Complement and coagulation cascades	0.01709	3
RA	UP	hsa04270	Vascular smooth muscle contraction	0.00338	4
RA	UP	hsa04921	Oxytocin signaling pathway	0.008093	4
RA	UP	hsa04022	cGMP-PKG signaling pathway	0.008911	4
RA	UP	hsa05418	Fluid shear stress and atherosclerosis	0.031832	3
RA	UP	hsa04910	Insulin signaling pathway	0.034534	3
RA	UP	hsa04371	Apelin signaling pathway	0.035228	3
RA	UP	hsa04072	Phospholipase D signaling pathway	0.043338	3
RA	UP	hsa04924	Renin secretion	0.04372	2
LA/RA ratio	DOWN	hsa04530	Tight junction	0.000142	5
LA/RA ratio	DOWN	hsa05130	Pathogenic Escherichia coli infection	0.009161	2
LA/RA ratio	DOWN	hsa04514	Cell adhesion molecules (CAMs)	0.009603	3
LA/RA ratio	DOWN	hsa04360	Axon guidance	0.018391	3
LA/RA ratio	DOWN	hsa05211	Renal cell carcinoma	0.01902	2
LA/RA ratio	DOWN	hsa04610	Complement and coagulation cascades	0.02257	2
LA/RA ratio	DOWN	hsa04015	Rap1 signaling pathway	0.025411	3
LA/RA ratio	DOWN	hsa01521	EGFR tyrosine kinase inhibitor resistance	0.026374	2
LA/RA ratio	DOWN	hsa04670	Leukocyte transendothelial migration	0.046344	2
LA/RA ratio	UP	hsa05140	Leishmaniasis	5.94E-05	6
LA/RA ratio	UP	hsa05150	Staphylococcus aureus infection	0.000109	5
LA/RA ratio	UP	hsa04640	Hematopoietic cell lineage	0.000337	6
LA/RA ratio	UP	hsa05322	Systemic lupus erythematosus	0.000545	6
LA/RA ratio	UP	hsa04610	Complement and coagulation cascades	0.000913	5
LA/RA ratio	UP	hsa04672	Intestinal immune network for IgA production	0.001102	4
LA/RA ratio	UP	hsa05310	Asthma	0.002476	3
LA/RA ratio	UP	hsa05330	Allograft rejection	0.005515	3
LA/RA ratio	UP	hsa04928	Parathyroid hormone synthesis, secretion and action	0.005555	5
LA/RA ratio	UP	hsa05143	African trypanosomiasis	0.006002	3

KEGG, kyoto encyclopedia of genes and genomes; DEGs, differentially expressed genes; LA, left atria; RA, right atria; DOWN, downregulated; UP, upregulated; hsa, Homo sapiens.

Table SIII. GO enrichment analysis of DEGs.

DEG category	Direction	Category	ID	Description	P-value	Count
LA	UP	BP	GO:0060333	Interferon-gamma-mediated signaling pathway	9.13E-05	10
LA	UP	BP	GO:0008015	Blood circulation	0.000118	28
LA	UP	BP	GO:0003013	Circulatory system process	0.000159	28
LA	UP	BP	GO:0098542	Defense response to another organism	0.000305	25
LA	UP	BP	GO:0009266	Response to temperature stimulus	0.000347	15
LA	UP	BP	GO:0071677	Positive regulation of mononuclear cell migration	0.000351	5
LA	DOWN	BP	GO:0015701	Bicarbonate transport	1.29E-05	6
LA	DOWN	BP	GO:0043588	Skin development	8.69E-05	14
LA	DOWN	BP	GO:0015711	Organic anion transport	0.000122	16
LA	DOWN	BP	GO:0098742	Cell-cell adhesion via plasma-membrane adhesion molecules	0.000151	11
LA	DOWN	BP	GO:0050805	Negative regulation of synaptic transmission	0.000193	6
LA	DOWN	BP	GO:0070268	Cornification	0.000276	7
LA	UP	MF	GO:0003823	Antigen binding	1.31E-05	9
LA	UP	MF	GO:0042605	Peptide antigen binding	0.000341	5
LA	UP	MF	GO:0019956	Chemokine binding	0.001302	5
LA	UP	MF	GO:0019888	Protein phosphatase regulator activity	0.00139	8
LA	UP	MF	GO:0016493	C-C chemokine receptor activity	0.002284	4
LA	UP	MF	GO:0019865	Immunoglobulin binding	0.002284	4
LA	DOWN	MF	GO:0017171	Serine hydrolase activity	0.000117	10
LA	DOWN	MF	GO:0004866	Endopeptidase inhibitor activity	0.000167	9
LA	DOWN	MF	GO:0061135	Endopeptidase regulator activity	0.000223	9
LA	DOWN	MF	GO:0030414	Peptidase inhibitor activity	0.000234	9
LA	DOWN	MF	GO:0001618	Virus receptor activity	0.000271	6
LA	DOWN	MF	GO:0104005	Hijacked molecular function	0.000271	6
LA	UP	CC	GO:0042613	MHC class II protein complex	8.44E-06	5
LA	UP	CC	GO:0042611	MHC protein complex	0.000175	5
LA	UP	CC	GO:0005798	Golgi-associated vesicle	0.000176	14
LA	UP	CC	GO:0071556	Integral component of luminal side of endoplasmic reticulum membrane	0.000691	5
LA	UP	CC	GO:0098553	Luminal side of endoplasmic reticulum membrane	0.000691	5
LA	UP	CC	GO:0012507	ER to Golgi transport vesicle membrane	0.000851	7
LA	DOWN	CC	GO:0016324	Apical plasma membrane	3.88E-06	15
LA	DOWN	CC	GO:0045177	Apical part of cell	4.04E-05	15
LA	DOWN	CC	GO:0031528	Microvillus membrane	8.81E-05	4
LA	DOWN	CC	GO:0031012	Extracellular matrix	8.94E-05	17
LA	DOWN	CC	GO:0043235	Receptor complex	9.18E-05	15
LA	DOWN	CC	GO:0031253	Cell projection membrane	0.000178	13
RA	UP	BP	GO:0008015	Blood circulation	2.54E-06	13
RA	UP	BP	GO:0003013	Circulatory system process	3.09E-06	13
RA	UP	BP	GO:0007263	Nitric oxide mediated signal transduction	0.000387	3
RA	UP	BP	GO:0043666	Regulation of phosphoprotein phosphatase activity	0.000478	5
RA	UP	BP	GO:0044057	Regulation of system process	0.000813	10
RA	UP	BP	GO:0035304	Regulation of protein dephosphorylation	0.001033	5
RA	DOWN	BP	GO:0019432	Triglyceride biosynthetic process	0.000101	4
RA	DOWN	BP	GO:0046460	Neutral lipid biosynthetic process	0.000114	4
RA	DOWN	BP	GO:0046463	Acylglycerol biosynthetic process	0.000114	4
RA	DOWN	BP	GO:0001654	Eye development	0.000186	10
RA	DOWN	BP	GO:0150063	Visual system development	0.00019	10
RA	DOWN	BP	GO:0048880	Sensory system development	0.000215	10
RA	UP	MF	GO:0019888	Protein phosphatase regulator activity	0.001146	4
RA	UP	MF	GO:0050786	RAGE receptor binding	0.001615	2
RA	UP	MF	GO:0019208	Phosphatase regulator activity	0.002157	4
RA	UP	MF	GO:0005523	Tropomyosin binding	0.003215	2
RA	UP	MF	GO:0008528	G-protein coupled peptide receptor activity	0.00766	4
RA	UP	MF	GO:0001653	Peptide receptor activity	0.008752	4
RA	DOWN	MF	GO:0017134	Fibroblast growth factor binding	0.000384	3
RA	DOWN	MF	GO:0050840	Extracellular matrix binding	0.000477	4
RA	DOWN	MF	GO:0017171	Serine hydrolase activity	0.001468	6

Table SIII. Continued.

DEG category	Direction	Category	ID	Description	P-value	Count
RA	DOWN	MF	GO:0019199	Transmembrane receptor protein kinase activity	0.002235	4
RA	DOWN	MF	GO:0016303	1-phosphatidylinositol-3-kinase activity	0.003193	3
RA	DOWN	MF	GO:0004252	Serine-type endopeptidase activity	0.004199	5
RA	UP	CC	GO:0034774	Secretory granule lumen	0.002047	7
RA	UP	CC	GO:0060205	Cytoplasmic vesicle lumen	0.002819	7
RA	UP	CC	GO:0031983	Vesicle lumen	0.002871	7
RA	UP	CC	GO:0030016	Myofibril	0.007729	5
RA	UP	CC	GO:0005788	Endoplasmic reticulum lumen	0.0082	6
RA	UP	CC	GO:0043292	Contractile fiber	0.009623	5
RA	DOWN	CC	GO:0043235	Receptor complex	8.17E-05	11
RA	DOWN	CC	GO:0005938	Cell cortex	0.004119	7
RA	DOWN	CC	GO:0072562	Blood microparticle	0.005477	4
RA	DOWN	CC	GO:1904724	Tertiary granule lumen	0.00606	3
RA	DOWN	CC	GO:0031012	Extracellular matrix	0.006214	9
RA	DOWN	CC	GO:0045177	Apical part of cell	0.013035	7
LA/RA ratio	UP	BP	GO:0032649	Regulation of interferon-gamma production	8.03E-05	6
LA/RA ratio	UP	BP	GO:1904018	Positive regulation of vasculature development	9.86E-05	8
LA/RA ratio	UP	BP	GO:0050878	Regulation of body fluid levels	0.000117	13
LA/RA ratio	UP	BP	GO:0032609	Interferon-gamma production	0.000149	6
LA/RA ratio	UP	BP	GO:0048732	Gland development	0.000151	12
LA/RA ratio	UP	BP	GO:0009612	Response to mechanical stimulus	0.000219	8
LA/RA ratio	DOWN	BP	GO:0044089	Positive regulation of cellular component biogenesis	0.000179	9
LA/RA ratio	DOWN	BP	GO:0098742	Cell-cell adhesion via plasma-membrane adhesion molecules	0.000303	6
LA/RA ratio	DOWN	BP	GO:0043588	Skin development	0.000371	7
LA/RA ratio	DOWN	BP	GO:0070268	Cornification	0.000709	4
LA/RA ratio	DOWN	BP	GO:0003158	Endothelium development	0.001101	4
LA/RA ratio	DOWN	BP	GO:0046879	Hormone secretion	0.001235	6
LA/RA ratio	UP	MF	GO:0042277	Peptide binding	0.000166	9
LA/RA ratio	UP	MF	GO:0033218	Amide binding	0.000166	10
LA/RA ratio	UP	MF	GO:0019199	Transmembrane receptor protein kinase activity	0.000461	5
LA/RA ratio	UP	MF	GO:0008528	G-protein coupled peptide receptor activity	0.00056	6
LA/RA ratio	UP	MF	GO:0001653	Peptide receptor activity	0.000687	6
LA/RA ratio	UP	MF	GO:0034236	Protein kinase A catalytic subunit binding	0.004728	2
LA/RA ratio	DOWN	MF	GO:0004869	Cysteine-type endopeptidase inhibitor activity	0.001498	3
LA/RA ratio	DOWN	MF	GO:0004714	Transmembrane receptor protein tyrosine kinase activity	0.002334	3
LA/RA ratio	DOWN	MF	GO:0004857	Enzyme inhibitor activity	0.002619	6
LA/RA ratio	DOWN	MF	GO:0004866	Endopeptidase inhibitor activity	0.003777	4
LA/RA ratio	DOWN	MF	GO:0072509	Divalent inorganic cation transmembrane transporter activity	0.00414	2
LA/RA ratio	DOWN	MF	GO:0061135	Endopeptidase regulator activity	0.004335	4
LA/RA ratio	UP	CC	GO:0098552	Side of membrane	5.89E-09	19
LA/RA ratio	UP	CC	GO:0009897	External side of plasma membrane	3.82E-07	13
LA/RA ratio	UP	CC	GO:0042613	MHC class II protein complex	0.003657	2
LA/RA ratio	UP	CC	GO:0030669	Clathrin-coated endocytic vesicle membrane	0.004231	3
LA/RA ratio	UP	CC	GO:0009898	Cytoplasmic side of plasma membrane	0.006708	5
LA/RA ratio	UP	CC	GO:0031092	Platelet alpha granule membrane	0.00683	2
LA/RA ratio	DOWN	CC	GO:0044295	Axonal growth cone	0.000163	3
LA/RA ratio	DOWN	CC	GO:0005911	Cell-cell junction	0.000266	8
LA/RA ratio	DOWN	CC	GO:0031256	Leading edge membrane	0.000513	5
LA/RA ratio	DOWN	CC	GO:0001533	Cornified envelope	0.000842	3
LA/RA ratio	DOWN	CC	GO:0005923	Bicellular tight junction	0.001027	4
LA/RA ratio	DOWN	CC	GO:0016328	Lateral plasma membrane	0.00108	3

GO, gene ontology; DEGs, differently expressed genes; LA, left atria; RA, right atria; DOWN, down-regulated; UP, up-regulated; BP, biological process; MF, molecular function; CC, cellular component.

Table SIV. Validation of hub genes in the external datasets.

Gene	Datasets							
	GSE115574						GSE2240	
	AF (14) vs. SR (15) in LA		AF (14) vs. SR (16) in RA		AF vs. SR in LA to RA		AF (10) vs. SR (20) in RA	
	log2FC	P-value	log2FC	P-value	log2FC	P-value	log2FC	P-value
ACAT1	0.09	0.63	0.27	0.06	-0.18	0.44	0.06	0.53
CRADD	0.11	0.58	0.42	0.01	-0.32	0.18	0.05	0.43
GIN1	0.04	0.87	0.16	0.38	-0.13	0.65	-0.03	0.77
FTX	-0.1	0.46	-0.24	0.05	0.13	0.46	-0.61	0.01
TCEAL2	-0.53	0.22	-0.35	0.31	-0.18	0.73	-0.82	0.02
MCM3AP	0.09	0.35	-0.05	0.61	0.15	0.31	0	1

AF, atrial fibrillation; SR, sinus rhythm; LA, left atria; RA, right atria; FC, fold change; CAT1, acetyl-CoA Acetyltransferase 1; CRADD, death domain-containing protein CRADD; GIN1, gypsy retrotransposon integrase 1; FTX, FTX transcript, XIST regulator; TCEAL2, transcription elongation factor A like 2; MCM3AP, minichromosome maintenance complex component 3 associated protein.