

Table S1 The significant function enrichment of KEGG pathway based on DEGs between patients with AF and SR

Category		Subcategory	ID	Description	Gene ratio	BgRatio	P value	Padjust	q value	Gene ID	Count
hsa05140	Human Diseases	Infectious disease: parasitic	hsa05140	Leishmaniasis	9/158	77/8842	8.45E-06	0.001235	0.001057	FCGR3B/NCF2/HLA-DPB1/FCGR2C/HLA-DRA/CYBA/CYBB/TNF/IL1B	9
hsa05150	Human Diseases	Infectious disease: bacterial	hsa05150	Staphylococcus aureus infection	10/158	100/8842	1.09E-05	0.001235	0.001057	FCGR3B/C1QC/HLA-DPB1/FCGR2C/HLA-DRA/CFD/C1QA/C1QB/FPR3/KRT18	10
hsa05310	Human Diseases	Immune disease	hsa05310	Asthma	6/158	31/8842	1.51E-05	0.001235	0.001057	FCER1A/HLA-DPB1/HLA-DRA/MS4A2/FCER1G/TNF	6
hsa05323	Human Diseases	Immune disease	hsa05323	Rheumatoid arthritis	9/158	94/8842	4.30E-05	0.002645	0.002264	HLA-DPB1/HLA-DRA/CCL5/CXCL12/IL18/TNF/IL1B/CXCL6/CXCL1	9
hsa04061	Environmental Information Processing	Signaling molecules and interaction	hsa04061	Viral protein interaction with cytokine and cytokine receptor	9/158	100/8842	7.02E-05	0.003455	0.002957	CXCR2/PPBP/CCL5/CXCL12/CCR2/IL18/TNF/CXCL6/CXCL1	9
hsa04380	Organismal Systems	Development and regeneration	hsa04380	Osteoclast differentiation	10/158	142/8842	0.00022	0.009005	0.007707	FCGR3B/NCF2/TYROBP/FCGR2C/CYBA/FHL2/PIK3CA/BLNK/TNF/IL1B	10
hsa05133	Human Diseases	Infectious disease: bacterial	hsa05133	Pertussis	7/158	78/8842	0.000465	0.01633	0.013975	C1QC/LY96/C1QA/C1QB/TNF/IL1B/CXCL6	7
hsa04216	Cellular Processes	Cell growth and death	hsa04216	Ferroptosis	5/158	42/8842	0.000853	0.026229	0.022447	CYBB/SLC7A11/ALOX15/TFRC/SLC39A8	5
hsa04664	Organismal Systems	Immune system	hsa04664	Fc epsilon RI signaling pathway	6/158	69/8842	0.001403	0.038338	0.03281	ALOX5AP/FCER1A/MS4A2/PIK3CA/FCER1G/TNF	6
hsa05417	Human Diseases	Cardiovascular disease	hsa05417	Lipid and atherosclerosis	11/158	216/8842	0.001664	0.040351	0.034532	NCF2/CYBA/CYBB/LY96/CCL5/PIK3CA/IL18/TNF/IL1B/SOD2/CXCL1	11
hsa05144	Human Diseases	Infectious disease: parasitic	hsa05144	Malaria	5/158	50/8842	0.001894	0.040351	0.034532	COMP/ACKR1/IL18/TNF/IL1B	5
hsa04145	Cellular Processes	Transport and catabolism	hsa04145	Phagosome	9/158	157/8842	0.001968	0.040351	0.034532	FCGR3B/NCF2/COMP/HLA-DPB1/FCGR2C/HLA-DRA/CYBA/CYBB/TFRC	9
hsa05142	Human Diseases	Infectious disease: parasitic	hsa05142	Chagas disease	7/158	103/8842	0.002404	0.043973	0.037632	C1QC/C1QA/CCL5/PIK3CA/C1QB/TNF/IL1B	7
hsa04060	Environmental Information Processing	Signaling molecules and interaction	hsa04060	Cytokine-cytokine receptor interaction	13/158	298/8842	0.002584	0.043973	0.037632	CXCR2/TNFRSF17/PPBP/CCL5/CSF2RB/CXCL12/CCR2/IL18/TNF/IL1B/CXCL6/BMPR1B/CXCL1	13
hsa04064	Environmental Information Processing	Signal transduction	hsa04064	NF-kappa B signaling pathway	7/158	105/8842	0.002681	0.043973	0.037632	BCL2A1/LY96/CXCL12/BLNK/TNF/IL1B/CXCL1	7
hsa05134	Human Diseases	Infectious disease: bacterial	hsa05134	Legionellosis	5/158	56/8842	0.003135	0.045036	0.038542	NAIP/IL18/TNF/IL1B/CXCL1	5
hsa05322	Human Diseases	Immune disease	hsa05322	Systemic lupus erythematosus	8/158	139/8842	0.003395	0.045036	0.038542	FCGR3B/C1QC/HLA-DPB1/HLA-DRA/C1QA/C1QB/TNF/GRIN2A	8
hsa05171	Human Diseases	Infectious disease: viral	hsa05171	Coronavirus disease - COVID-19	11/158	238/8842	0.003543	0.045036	0.038542	C1QC/CYBB/CFD/C1QA/PIK3CA/RPL23/TLR8/RPL3L/C1QB/TNF/IL1B	11
hsa05164	Human Diseases	Infectious disease: viral	hsa05164	Influenza A	9/158	172/8842	0.003644	0.045036	0.038542	HLA-DPB1/HLA-DRA/CCL5/PIK3CA/TPSAB1/RSAD2/IL18/TNF/IL1B	9
hsa05418	Human Diseases	Cardiovascular disease	hsa05418	Fluid shear stress and atherosclerosis	8/158	141/8842	0.003705	0.045036	0.038542	NCF2/KLF2/CYBA/PIK3CA/GSTM5/TNF/IL1B/BMPR1B	8
hsa05020	Human Diseases	Neurodegenerative disease	hsa05020	Prion disease	12/158	278/8842	0.00409	0.045036	0.038542	NCF2/C1QC/CYBA/CYBB/C1QA/CCL5/PIK3CA/C1QB/KIF5C/TNF/IL1B/GRIN2A	12
hsa05143	Human Diseases	Infectious disease: parasitic	hsa05143	African trypanosomiasis	4/158	37/8842	0.004097	0.045036	0.038542	IL18/TNF/IL1B/HPR	4
hsa04936	Human Diseases	Endocrine and metabolic disease	hsa04936	Alcoholic liver disease	8/158	144/8842	0.004211	0.045036	0.038542	C1QC/LY96/C1QA/C1QB/TNF/IL1B/CXCL1/ADIPOQ	8

AF, atrial fibrillation; KEGG, Kyoto Encyclopedia of Genes and Genomes; SR, sinus rhythm.

Table S2 The significant function enrichment of gene ontology analysis based on DEGs between patients with AF and SR

Ontology	ID	Description	Gene ratio	BgRatio	P value	Padjust	q value	Gene ID	Count
BP	GO:0036230	granulocyte activation	11/295	49/18870	1.95E-10	6.81E-07	5.63E-07	CXCR2/TYROBP/FCER1A/DNASE1L3/CCL5/FCER1G/CCR2/IL18/PLA2G2A/TNF/CXCL6	11
BP	GO:0042119	neutrophil activation	9/295	42/18870	1.40E-08	2.45E-05	2.03E-05	CXCR2/TYROBP/DNASE1L3/CCL5/FCER1G/IL18/PLA2G2A/TNF/CXCL6	9
BP	GO:0006959	humoral immune response	19/295	258/18870	2.62E-08	3.06E-05	2.53E-05	S100A12/IGHM/S100A9/C1QC/PPBP/FCN1/CFD/C1QA/RGCC/RNASE6/BLNK/C1QB/CCR2/TNF/IL1B/SUSD4/CXCL6/SLPI/CXCL1	19
BP	GO:0002443	leukocyte mediated immunity	25/295	466/18870	9.24E-08	7.62E-05	6.30E-05	IGHM/CLC/TYROBP/IGHD/GAPT/C1QC/IGKC/FCER1A/HLA-DRA/DNASE1L3/C1QA/CSF2RB/ADGRE2/CRTAM/FCER1G/TLR8/C1QB/RSAD2/CCR2/IL18/TFRC/TNF/IL1B/SUSD4/CXCL6	25
BP	GO:0030593	neutrophil chemotaxis	12/295	107/18870	1.13E-07	7.62E-05	6.30E-05	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/CCL5/FCER1G/IL1B/CXCL6/CXADR/CXCL1	12
BP	GO:0071621	granulocyte chemotaxis	13/295	130/18870	1.31E-07	7.62E-05	6.30E-05	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/CCL5/ADGRE2/FCER1G/IL1B/CXCL6/CXADR/CXCL1	13
BP	GO:0097529	myeloid leukocyte migration	17/295	242/18870	2.83E-07	0.000141	0.000117	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/CCL5/ADGRE2/PLA2G7/CXCL12/FCER1G/CCR2/CD200/IL1B/CXCL6/CXADR/CXCL1	17
BP	GO:0002444	lymphocyte mediated immunity	21/295	368/18870	3.74E-07	0.000164	0.000135	IGHM/CLC/IGHD/GAPT/C1QC/IGKC/FCER1A/HLA-DRA/C1QA/CSF2RB/CRTAM/FCER1G/TLR8/C1QB/RSAD2/CCR2/IL18/TFRC/TNF/IL1B/SUSD4	21
BP	GO:1990266	neutrophil migration	12/295	129/18870	8.75E-07	0.000323	0.000268	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/CCL5/FCER1G/IL1B/CXCL6/CXADR/CXCL1	12
BP	GO:0006956	complement activation	9/295	67/18870	9.54E-07	0.000323	0.000268	IGHM/C1QC/FCN1/CFD/C1QA/RGCC/C1QB/IL1B/SUSD4	9
BP	GO:0097530	granulocyte migration	13/295	156/18870	1.08E-06	0.000323	0.000268	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/CCL5/ADGRE2/FCER1G/IL1B/CXCL6/CXADR/CXCL1	13
BP	GO:0050900	leukocyte migration	21/295	396/18870	1.23E-06	0.000323	0.000268	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/SELL/CCL5/ADGRE2/PLA2G7/CXCL12/LYVE1/CRTAM/FCER1G/CCR2/CD200/TNF/IL1B/CXCL6/CXADR/CXCL1	21
BP	GO:0030595	leukocyte chemotaxis	16/295	240/18870	1.27E-06	0.000323	0.000268	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/CCL5/ADGRE2/PLA2G7/CXCL12/FCER1G/CCR2/IL1B/CXCL6/CXADR/CXCL1	16
BP	GO:0002274	myeloid leukocyte activation	16/295	241/18870	1.34E-06	0.000323	0.000268	S100A12/CXCR2/TYROBP/FCER1A/DNASE1L3/C1QA/CCL5/ADGRE2/FCER1G/CCR2/IL18/CD200/PLA2G2A/TNF/CXCL6/ITGB8	16
BP	GO:0060537	muscle tissue development	22/295	433/18870	1.39E-06	0.000323	0.000268	NRAP/RCAN1/FHL2/PRMT1/MYL3/TCF21/POPCD3/RPL3L/ERBB4/DKK1/TNN/HEG1/XK/CDON/HCN4/WT1/NEB/TNNI1/CXADR/RBP4/LRP2/DNER	22
BP	GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	20/295	380/18870	2.49E-06	0.000543	0.000449	IGHM/CLC/IGHD/GAPT/C1QC/IGKC/FCER1A/HLA-DRA/C1QA/CSF2RB/FCER1G/TLR8/C1QB/RSAD2/CCR2/IL18/TFRC/TNF/IL1B/SUSD4	20
BP	GO:0016064	immunoglobulin mediated immune response	14/295	205/18870	4.47E-06	0.000881	0.000729	IGHM/IGHD/GAPT/C1QC/IGKC/FCER1A/C1QA/CSF2RB/FCER1G/TLR8/C1QB/TFRC/TNF/SUSD4	14
BP	GO:0042742	defense response to bacterium	18/295	330/18870	4.87E-06	0.000881	0.000729	S100A12/S100A8/IGHM/S100A9/MPEG1/PPBP/CYBA/RNASE6/FCER1G/RNASE1/NAIP/IL18/PLA2G2A/TNF/IL1B/CXCL6/SLPI/HP	18
BP	GO:0006935	chemotaxis	22/295	468/18870	4.89E-06	0.000881	0.000729	S100A12/S100A8/CXCR2/S100A9/S100A4/PROK2/PPBP/CMTM2/PIIB/CCL5/ADGRE2/PLA2G7/CXCL12/FCER1G/CYSLTR1/CCR2/FPR3/IL1B/CXCL6/CXADR/CXCL1/FLRT3	22
BP	GO:0042330	taxis	22/295	470/18870	5.23E-06	0.000881	0.000729	S100A12/S100A8/CXCR2/S100A9/S100A4/PROK2/PPBP/CMTM2/PIIB/CCL5/ADGRE2/PLA2G7/CXCL12/FCER1G/CYSLTR1/CCR2/FPR3/IL1B/CXCL6/CXADR/CXCL1/FLRT3	22
BP	GO:0019724	B cell mediated immunity	14/295	208/18870	5.29E-06	0.000881	0.000729	IGHM/IGHD/GAPT/C1QC/IGKC/FCER1A/C1QA/CSF2RB/FCER1G/TLR8/C1QB/TFRC/TNF/SUSD4	14
BP	GO:0007159	leukocyte cell-cell adhesion	20/295	419/18870	1.06E-05	0.001692	0.0014	S100A8/S100A9/HLA-DPB1/HLA-DRA/SELL/CCL5/PDE5A/PIK3CA/CXCL12/CRTAM/CCR2/IL18/TFRC/PLA2G2A/TNF/IL1B/SHB/SLC39A8/EFNB3/GPAM	20
BP	GO:0014706	striated muscle tissue development	15/295	264/18870	1.88E-05	0.002859	0.002365	NRAP/FHL2/PRMT1/MYL3/RPL3L/ERBB4/DKK1/HEG1/HCN4/WT1/NEB/TNNI1/CXADR/RBP4/LRP2	15
BP	GO:0070663	regulation of leukocyte proliferation	15/295	267/18870	2.15E-05	0.003128	0.002587	MNDA/CLC/TYROBP/HLA-DPB1/CCL5/CSF2RB/PDE5A/CRTAM/LST1/CCR2/IL18/TFRC/PLA2G2A/IL1B/GPAM	15
BP	GO:0050670	regulation of lymphocyte proliferation	14/295	238/18870	2.43E-05	0.003403	0.002815	MNDA/CLC/TYROBP/HLA-DPB1/CCL5/PDE5A/CRTAM/LST1/CCR2/IL18/TFRC/PLA2G2A/IL1B/GPAM	14
BP	GO:0050729	positive regulation of inflammatory response	11/295	152/18870	2.78E-05	0.003653	0.003022	S100A12/S100A8/S100A9/ALOX5AP/PLA2G7/NAIP/CCR2/IL18/PLA2G2A/TNF/IL1B	11
BP	GO:0046651	lymphocyte proliferation	16/295	307/18870	2.87E-05	0.003653	0.003022	MNDA/CLC/TYROBP/GAPT/HLA-DPB1/CCL5/PDE5A/CRTAM/LST1/CCR2/IL18/TFRC/PLA2G2A/IL1B/SHB/GPAM	16
BP	GO:0032944	regulation of mononuclear cell proliferation	14/295	242/18870	2.92E-05	0.003653	0.003022	MNDA/CLC/TYROBP/HLA-DPB1/CCL5/PDE5A/CRTAM/LST1/CCR2/IL18/TFRC/PLA2G2A/IL1B/GPAM	14
BP	GO:0048738	cardiac muscle tissue development	14/295	247/18870	3.66E-05	0.00437	0.003615	NRAP/FHL2/PRMT1/MYL3/ERBB4/DKK1/HEG1/HCN4/WT1/NEB/TNNI1/CXADR/RBP4/LRP2	14
BP	GO:0032943	mononuclear cell proliferation	16/295	314/18870	3.77E-05	0.00437	0.003615	MNDA/CLC/TYROBP/GAPT/HLA-DPB1/CCL5/PDE5A/CRTAM/LST1/CCR2/IL18/TFRC/PLA2G2A/IL1B/SHB/GPAM	16
BP	GO:0070661	leukocyte proliferation	17/295	350/18870	3.95E-05	0.00437	0.003615	MNDA/CLC/TYROBP/GAPT/HLA-DPB1/CCL5/CSF2RB/PDE5A/CRTAM/LST1/CCR2/IL18/TFRC/PLA2G2A/IL1B/SHB/GPAM	17
BP	GO:0002703	regulation of leukocyte mediated immunity	14/295	249/18870	4.00E-05	0.00437	0.003615	CLC/TYROBP/HLA-DRA/DNASE1L3/ADGRE2/CRTAM/RSAD2/CCR2/IL18/TFRC/TNF/IL1B/SUSD4/CXCL6	14
BP	GO:0001819	positive regulation of cytokine production	21/295	499/18870	4.16E-05	0.00441	0.003648	TYROBP/IGHD/HLA-DPB1/FCN1/CYBA/HTR2B/CYBB/LY96/RGCC/CRTAM/FCER1G/TLR8/NAIP/RSAD2/CCR2/IL18/CD200/HEG1/TNF/IL1B/ADIPOQ	21
BP	GO:0050727	regulation of inflammatory response	19/295	425/18870	4.34E-05	0.004464	0.003693	S100A12/S100A8/S100A9/ALOX5AP/DNASE1L3/CCL5/CMA1/PLA2G7/NAIP/CCR2/IL18/CD200/ALOX15/PLA2G2A/TNF/IL1B/IER3/SLC39A8/ADIPOQ	19
BP	GO:0098883	synapse pruning	4/295	14/18870	5.18E-05	0.005174	0.00428	C1QC/C1QA/C1QB/DKK1	4
BP	GO:0150146	cell junction disassembly	5/295	27/18870	5.49E-05	0.005339	0.004417	C1QC/C1QA/SNAI2/C1QB/DKK1	5
BP	GO:0060326	cell chemotaxis	16/295	325/18870	5.68E-05	0.005373	0.004444	S100A12/S100A8/CXCR2/S100A9/PPBP/PIIB/CCL5/ADGRE2/PLA2G7/CXCL12/FCER1G/CCR2/IL1B/CXCL6/CXADR/CXCL1	16
BP	GO:0031349	positive regulation of defense response	20/295	480/18870	7.27E-05	0.006695	0.005539	S100A12/S100A8/MNDA/S100A9/TYROBP/ALOX5AP/FCN1/CYBA/LY96/CCL5/PLA2G7/CRTAM/TLR8/NAIP/RSAD2/CCR2/IL18/PLA2G2A/TNF/IL1B	20
BP	GO:0070098	chemokine-mediated signaling pathway	8/295	91/18870	8.97E-05	0.008044	0.006654	CXCR2/PPBP/ACKR1/CCL5/CXCL12/CCR2/CXCL6/CXCL1	8
BP	GO:0022407	regulation of cell-cell adhesion	20/295	493/18870	0.000105	0.009143	0.007564	HLA-DPB1/HLA-DRA/EPCAM/CCL5/PDE5A/PIK3CA/RGCC/CXCL12/CRTAM/CCR2/IL18/ANK3/TFRC/PLA2G2A/TNF/IL1B/SHB/EFNB3/GPAM/ADIPOQ	20
BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	16/295	346/18870	0.000118	0.010079	0.008338	IGHM/MNDA/TYROBP/IGHD/IGKC/FCER1A/HLA-DPB1/FCN1/CYBA/FYB1/LY96/PIK3CA/FCER1G/BLNK/FPR3/SHB	16
BP	GO:0002764	immune response-regulating signaling pathway	20/295	500/18870	0.000126	0.010523	0.008705	IGHM/MNDA/TYROBP/IGHD/IGKC/FCER1A/HLA-DPB1/FCN1/CYBA/FYB1/LY96/PIK3CA/FCER1G/TLR8/BLNK/NAIP/RSAD2/FPR3/TNF/SHB	20
BP	GO:0042129	regulation of T cell proliferation	11/295	182/18870	0.000142	0.011431	0.009456	CLC/HLA-DPB1/CCL5/PDE5A/CRTAM/CCR2/IL18/TFRC/PLA2G2A/IL1B/GPAM	11
BP	GO:0002697	regulation of immune effector process	17/295	389/18870	0.000144	0.011431	0.009456	CLC/TYROBP/FCN1/HLA-DRA/DNASE1L3/ADGRE2/CRTAM/RSAD2/CCR2/IL18/TFRC/TNF/IL1B/SHB/SUSD4/CXCL6/RBP4	17
BP	GO:0006968	cellular defense response	6/295	52/18870	0.000154	0.011778	0.009743	CXCR2/MNDA/NCF2/TYROBP/LY96/CCR2	6
BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	15/295	318/18870	0.000155	0.011778	0.009743	IGHM/MNDA/TYROBP/IGHD/IGKC/HLA-DPB1/FCN1/CYBA/FYB1/LY96/PIK3CA/FCER1G/BLNK/FPR3/SHB	15
BP	GO:1990868	response to chemokine	8/295	99/18870	0.000162	0.011823	0.00978	CXCR2/PPBP/ACKR1/CCL5/CXCL12/CCR2/CXCL6/CXCL1	8
BP	GO:1990869	cellular response to chemokine	8/295	99/18870	0.000162	0.011823	0.00978	CXCR2/PPBP/ACKR1/CCL5/CXCL12/CCR2/CXCL6/CXCL1	8
BP	GO:0002757	immune response-activating signaling pathway	19/295	473/18870	0.000176	0.012592	0.010417	IGHM/MNDA/TYROBP/IGHD/IGKC/HLA-DPB1/FCN1/CYBA/FYB1/LY96/PIK3CA/FCER1G/TLR8/BLNK/NAIP/RSAD2/FPR3/TNF/SHB	19
BP	GO:0002544	chronic inflammatory response	4/295	19/18870	0.000188	0.013185	0.010907	S100A8/S100A9/CCL5/TNF	4
BP	GO:0032729	positive regulation of type II interferon production	7/295	77/18870	0.000201	0.013763	0.011385	HLA-DPB1/CRTAM/TLR8/CCR2/IL18/TNF/IL1B	7
BP	GO:0002455	humoral immune response mediated by circulating immunoglobulin	6/295	55/18870	0.000211	0.014218	0.011762	IGHM/C1QC/C1QA/C1QB/TNF/SUSD4	6
BP	GO:0019233	sensory perception of pain	7/295	78/18870	0.000218	0.014358	0.011877	PROK2/NPY1R/CXCL12/GPR171/CCR2/TNF/GRIN2A	7
BP	GO:0002526	acute inflammatory response	8/295	107/18870	0.000277	0.01797	0.014866	CXCR2/ALOX5AP/FCER1A/DNASE1L3/TFRC/TNF/IL1B/HP	8
BP	GO:0090026	positive regulation of monocyte chemotaxis	4/295	21/18870	0.000284	0.018058	0.014939	CCL5/PLA2G7/CXCL12/CCR2	4
BP	GO:0002369	T cell cytokine production	5/295	38/18870	0.000297	0.018218	0.015071	CLC/RSAD2/CCR2/IL18/IL1B	5
BP	GO:0002724	regulation of T cell cytokine production	5/295	38/18870	0.000297	0.018218	0.015071	CLC/RSAD2/CCR2/IL18/IL1B	5
BP	GO:0001776	leukocyte homeostasis	8/295	109/18870	0.000315	0.018984	0.015704	CXCR2/TFNRSF17/GAPT/TSC22D3/CCR2/SLC7A11/CXCL6/GPAM	8
BP	GO:0002699	positive regulation of immune effector process	13/295	270/18870	0.000347	0.020577	0.017022	TYROBP/FCN1/HLA-DRA/ADGRE2/CRTAM/RSAD2/CCR2/IL18/TFRC/TNF/IL1B/SHB/RBP4	13
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	16/295	382/18870	0.00036	0.021011	0.017381	HLA-DPB1/HLA-DRA/CCL5/IGKC/HLA-DPB1/FCN1/CYBA/FYB1/LY96/PIK3CA/CXCL12/CRTAM/CCR2/IL18/TFRC/PLA2G2A/TNF/IL1B/SHB/EFNB3/GPAM	16
BP	GO:0042554	superoxide anion generation	5/295	41/18870	0.000427	0.024463	0.020237	NCF2/TYROBP/CYBA/CYBB/SOD2	5
BP	GO:0006958	complement activation, classical pathway	5/295	42/18870	0.000478	0.026975	0.022315	IGHM/C1QC/C1QA/C1QB/SUSD4	5
BP	GO:0014002	astrocyte development	5/295	43/18870	0.000534	0.02966	0.024536	S100A8/S100A9/C1QA/TNF/IL1B	5
BP	GO:0042098	T cell proliferation	11/295	213/18870	0.000549	0.029989	0.024808	CLC/HLA-DPB1/CCL5/PDE5A/CRTAM/CCR2/IL18/TFRC/PLA2G2A/IL1B/GPAM	11
BP	GO:0060343	trabecula formation	4/295	26/18870	0.000667	0.035892	0.029691	FHL2/FBN2/SFRP1/RBP4	4
BP	GO:0050804	modulation of chemical synaptic transmission	18/295	489/18870	0.00073	0.038362	0.031735	TYROBP/YWHAH/RAB8A/CCR2/SLC7A11/ARHGAP44/DKK1/MCTP2/TNF/CNTN4/CBLN2/IL1B/BCHE/GRIN2A/EFNB3/SYT4/NMU/ADIPOQ	18
BP	GO:0048545	response to steroid hormone	14/295	330/18870	0.000735	0.038362	0.031735	LBH/CYBB/YWHAH/PIK3CA/TCF21/GABRB1/MGARP/SFRP1/TNF/PAPPA/BCHE/AREG/CLDN1/ADIPOQ	14
BP	GO:0099177	regulation of trans-synaptic signaling	18/295	490/18870	0.000747	0.038419	0.031782	TYROBP/YWHAH/RAB8A/CCR2/SLC7A11/ARHGAP44/DKK1/MCTP2/TNF/CNTN4/CBLN2/IL1B/BCHE/GRIN2A/EFNB3/SYT4/NMU/ADIPOQ	18
BP	GO:0002706	regulation of lymphocyte mediated immunity	10/295	188/18870	0.000775	0.039289	0.032501	CLC/HLA-DRA/CRTAM/RSAD2/CCR2/IL18/TFRC/TNF/IL1B/SUSD4	10
BP	GO:0009636	response to toxic substance	12/295	258/18870	0.000789	0.039405	0.032597	S100A9/ALOX5AP/SELENOT/CCL5/ALDH1A1/SLC7A11/GABRB1/TNF/SOD2/SLC39A8/CLDN1/HP	12
BP	GO:0061383	trabecula morphogenesis	5/295	47/18870	0.000809	0.039859	0.032973	FHL2/FBN2/HEG1/SFRP1/RBP4	5
BP	GO:0002275	myeloid cell activation involved in immune response	7/295	98/18870	0.000874	0.042468	0.035131	TYROBP/FCER1A/DNASE1L3/ADGRE2/FCER1G/CCR2/TNF	7
BP	GO:0014015	positive regulation of gliogenesis	6/295	72/18870	0.000913	0.043134	0.035682	CYSLTR1/PTPRZ1/MYRF/TNF/IL1B/LRP2	6
BP	GO:0097327	cellular response to toxic substance	8/295	128/18870	0.000918	0.043134	0.035682	S100A9/ALOX5AP/SELENOT/ALDH1A1/TNF/SOD2/SLC39A8/HP	8
BP	GO:1903706	regulation of hemopoiesis	16/295	417/18870	0.000925	0.043134	0.035682	TYROBP/EV2B/C1QC/TCIM/HLA-DRA/PRMT1/CRTAM/SNAI2/GPR171/CCR2/TMEM176A/IL18/SFRP1/TNF/SHB/ADIPOQ	16
BP	GO:0035589	G protein-coupled purinergic nucleotide receptor signaling pathway	3/295	13/18870	0.000963	0.043607	0.036074	GPR34/PTRY13/GPR171	3
BP	GO:0070486	leukocyte aggregation	3/295	13/18870	0.000963	0.043607	0.036074	S100A8/S100A9/IL1B	3
BP	GO:0042692	muscle cell differentiation	16/295	419/18870	0.000972	0.043607	0.036074	NRAP/COMP/RCAN1/FHL2/CDK9/POPCD3/RPL3L/DKK1/	

Table S3 The significantly enriched Hallmark gene sets based on GSEA of AF samples and SR samples

ID	Description	Set size	Enrichment score	NES	P value	Padjust	q value	Rank	Leading edge	Core enrichment
HALLMARK_OXIDATIVE_PHOSPHORYLATION	HALLMARK_OXIDATIVE_PHOSPHORYLATION	199	0.548756	2.428418	1.00E-10	2.50E-09	1.32E-09	5284	tags=54%, list=25%, signal=41 %	TOMM22/NQO2/IDH3A/PDK4/ATP6V1C1/DLD/ACAT1/MRPL35/NDUFB7/HSPA9/ATP5MC2/GLUD1/GPX4/OGDH/MRPL34/NDUFS7/MRPS12/SLC25A6/ECHS1/FDX1/IDH2/UQCRC1/NDUFS3/BAX/ABCB7/FXN/MGST3/COX11/NDUFS8/COX17/ETFB/SLC25A5/NDUFV1/MPC1/NDUFV2/ETFA/MTRF1/HCCS/TIMM50/COX8A/SLC25A20/GPI/COX5B/NDUFA5/PDHX/HADHA/PHB2/UQCRH/CYC1/ALAS1/NDUFB6/SLC25A12/DLAT/OXA1L/SDHC/ATP5PO/PDP1/SUPV3L1/ATP5MC1/NDUFB5/IDH3G/ECH1/MRPL15/COX7A2/ECI1/PMPCA/DECR1/SLC25A4/NDUFS1/NNT/UQCRCQ/ETFDH/UQCRC2/NDUFA3/ATP6V1G1/COX7B/NDUFA9/NDUFC2/UQCRC11/ATP5PD/SLC25A11/IMMT/ATP6V1F/POLR2F/COX6A1/SUCLA2/NDUFB2/MDH1/TIMM8B/NDUFB4/VDAC3/ATP5F1E/ATP6V0B/ATP5F1C/ACADM/NDUFB3/NDUFA7/COX6B1/LDHB/NDUFA4/ALDH6A1/RHOT2/NDUFB1/ISCA1/NDUFB8/ATP5MC3/NDUFA8/MTX2
HALLMARK_ALLOGRAFT_REJECTION	HALLMARK_ALLOGRAFT_REJECTION	200	0.530551	2.347447	1.00E-10	2.50E-09	1.32E-09	4258	tags=46%, list=20%, signal=37 %	HLA-DRA/FYB1/IGSF6/CCL5/GZMA/CRTAM/RPL3L/CCR2/CD28/SOCS1/ITGB2/ITK/LYN/CD74/FCGR2B/CD86/TGFB1/ABH1/CD2/GPR65/CCL19/NCF4/HLA-DMB/CXCL9/HLA-DMA/IRF8/CD3D/TRAT1/TLR1/PTPRC/IL18RAP/SPI1/ST8SIA4/LY86/CTSS/IFNGR1/GCNT1/CCL13/LCP2/RPS9/CD1D/CXCL13/NLRP3/KLRD1/CFP/LY75/PSMB10/IFNGR2/ABCE1/CD47/PRF1/GZMB/NOS2/CSK/CCL11/ELANE/PTPN6/HLA-E/ITGAL/CD96/ETS1/CD247/HCLS1/EREG/LTB/FGR/AKT1/CD79A/CD3G/CCL4/TLR2/EIF3A/IL2RG/MMP9/UBE2D1/CCR1/RPS19/EIF3D/TAP2/CD3E/CCL7/NME1/MAP4K1/PF4/GALNT1/B2M/IL2RB/PRKCB/LCK/CXCR3/EIF5A/CD40LG
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	197	0.491107	2.165264	8.16E-10	1.36E-08	7.16E-09	4104	tags=40%, list=20%, signal=33 %	IFIT2/CCL5/CSF2RB/GZMA/CXCL11/RSAD2/SOCS1/IFI44L/CD74/CD69/ISG15/PLSCR1/IFI30/MX2/CD86/EIF4E3/FPR1/OAS2/P2RY14/CXCL9/XCL1/PTGS2/HLA-DMA/LAP3/IRF8/CASP1/ST8SIA4/CASP8/EPST1/SLAMF7/LCP2/MTHFD2/NFKBIA/CDKN1A/PSMB10/RNF213/IRF2/MARCHF1/VAMP8/BPGM/ISG20/IRF9/PSME1/VCAM1/TXNIP/PTPN6/IFI44/MT2A/OASL/BST2/RAPGEF6/GBP4/IFIT1/CD38/PSMB8/CMKLR1/UBE2L6/HLA-B/MYD88/MX1/PNPT1/RTP4/FGI2/CXCL10/NMI/SAMD9L/IFITM3/IL18BP/OAS3/PARP12/IL15RA/CCL7/TOR1B/SAMHD1/B2M/PSMB9/IL2RB/SOCS3/CASP4
HALLMARK_COMPLEMENT	HALLMARK_COMPLEMENT	198	0.452356	1.996998	7.32E-08	9.14E-07	4.81E-07	2956	tags=32%, list=14%, signal=28 %	S100A12/S100A9/C1QC/FCN1/G1QA/CCL5/PIK3CA/PLA2G7/GZMA/FCER1G/DOCK10/SERPINA1/LYN/PLSCR1/GNB2/KYNU/ITGAM/PPP4C/ANG/LAP3/PLEK/GZMK/CTSC/CASP1/LIPA/PFN1/LGMN/CTSS/FDX1/CALM1/LCP2/CR1/OLR1/USP15/CTSO/CSRP1/IRF2/CD36/DUSP6/LGALS3/AKAP10/GZMB/CP/CD46/ANXA5/SERPINE1/PRKCD/CASP10/CTSV/GNG2/APOBEC3G/PIK3CG/COL4A2/USP8/CTSB/DUSP5/GNAI2/PREP/PRCP/PDP1/NOTCH4/ITIH1/CEBPB/PIK3R5
HALLMARK_INTERFERON_ALPHA_RESPONSE	HALLMARK_INTERFERON_ALPHA_RESPONSE	97	0.526948	2.106783	7.79E-07	7.79E-06	4.10E-06	3606	tags=40%, list=17%, signal=33 %	IFIT2/SELL/CXCL11/RSAD2/LPAR6/IFI44L/CD74/ISG15/PLSCR1/IFI30/LAMP3/ELF1/LAP3/CASP1/CASP8/MOV10/EPST1/IRF2/CD47/ISG20/IRF9/PSME1/TXNIP/IFI44/OASL/BST2/GBP4/MVB12A/PSMB8/UBE2L6/SAMD9/MX1/PNPT1/RTP4/CXCL10/NMI/SAMD9L/IFITM3/PARP12
HALLMARK_PI3K_AKT_MTOR_SIGNALING	HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	0.463564	1.877045	6.56E-05	0.0004690	0.00247	4769	tags=42%, list=23%, signal=32 %	CXCR4/SLA/ARF1/PIK3R3/PFN1/PRKAG1/ATF1/CAB39L/ACTR2/GSK3B/PPP1CA/CDKN1A/RALB/RIT1/UBE2D3/EIF4E/HRAS/AKT1S1/DAPP1/CSNK2B/GNA14/MAP2K6/MKNK2/HSP90B1/AKT1/CDK4/MYD88/TBK1/PIN1/IL2RG/PLA2G12A/ACTR3/AP2M1/CFL1/PDK1/DUSP3/CDK2/MAPK9/PRKCB/LCK/ARPC3/RAC1/RAF1/EC5IT
HALLMARK_MYC_TARGETS_V1	HALLMARK_MYC_TARGETS_V1	197	0.390608	1.722169	5.99E-05	0.0004690	0.00247	4663	tags=36%, list=22%, signal=28 %	MYC/AP3S1/ILF2/PSMB3/LSM2/HSPE1/DUT/PABPC4/PHB1/POLD2/UBE2L3/HNRNPU/SRSF1/C1QBP/XPOT/ABCE1/PTGES3/EIF4E/SNRPD3/RPS5/RRM1/RANBP1/TXNL4A/PRDX4/GSPT1/PSMA7/NCBP1/SNRPD2/TFDP1/PHB2/CYC1/LSM7/PSMC4/SYNCRIP/UBA2/SNRPB/CDK4/SRSF3/RSL1D1/KPNB1/MRPL23/TCP1/SRSF7/CCT7/USP1/ACP1/SNRPD1/EIF3D/YWHAQ/PSMC6/RNPS1/NHP2/CCNA2/RACK1/ERH/MCM4/NME1/CDK2/TRA2B/POLE3/TUFM/NCBP2/SNRPB/PSMB2/EPRS1/HNRNPD/VDAC3/HDAC2/CNBP/IMPDH2/RPS6
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	200	0.378508	1.674727	0.00011	0.0006860	0.00361	3526	tags=36%, list=17%, signal=30 %	COMP/PPIB/CRLF1/FBN2/CXCL12/SNAI2/IGFBP3/FBLN5/IGFBP2/TGFB1/SFRP4/FAP/GEM/RHOB/TNC/COL1A2/FBLN1/COL6A3/CCN2/CTHRC1/SERPINH1/LOXL1/LGALS1/WIPF1/FOXC2/ID2/CD44/PFN2/MYLK/FUCA1/EDIL3/COL6A2/MGP/SDC1/TPM4/NT5E/MYL9/VIM/VCAM1/CADM1/CDH11/DAB2/VEGFC/SERPINE1/SGCD/GJA1/GLIPR1/COL16A1/MMP1/COL4A2/THBS2/PCOLCE/EFEMP2/IL32/COL5A1/DCN/MSX1/SLC6A8/BASP1/OXTR/NNMT/MFAP5/PDGFRB/CALU/SCG2/ACTA2/MMP2/TNFRSF11B/ITGB3/DPYSL3/COL8A2/SLIT3
HALLMARK_ESTROGEN_RESPONSE_EARLY	HALLMARK_ESTROGEN_RESPONSE_EARLY	200	-0.364399	-1.648477	0.0001360	0.0007540	0.00397	3194	tags=28%, list=15%, signal=24 %	SVIL/XBP1/SLC7A2/GFRA1/ENDOD1/FRK/ALDH3B1/ADCY1/FCMR/ESRP2/B4GALT1/KRT8/NCOR2/PGR/TUBB2B/BHLHE40/RASGRP1/MINDY1/ANXA9/SLC24A3/TMEM164/NAV2/FLNB/TPD52L1/AR/REEP1/SCARB1/TGM2/TOB1/ABHD2/THSD4/SLC22A5/PMAIP1/ABAT/PEX11A/TPBG/KLF10/SLC26A2/EEIG1/SEMA3B/STC2/CELSR2/CALB2/SLC1A1/BCL2/MAPT/NHERF1/FASN/LRIG1/CLK10/AQP3/TFAP2C/PAPSS2/KRT18/CA12/AREG/KRT19
HALLMARK_KRAS_SIGNALING_UP	HALLMARK_KRAS_SIGNALING_UP	199	0.373934	1.654775	0.0001530	0.0007660	0.00403	1810	tags=26%, list=9%, signal=24 %	PPBP/CD37/LY96/CLEC4A/FCER1G/TLR8/IGFBP3/NRP1/LCP1/CSF2RA/CXCR4/ANO1/ITGB2/EPB41L3/IL7R/IL33/ARG1/GYPC/MAFB/PTGS2/LAPTM5/IRF8/DOCK2/C3AR1/APOD/NR1H4/CTSS/ACE/MPZL2/MAP3K1/ID2/CAB39L/PDCD1LG2/SPON1/GNG11/RELN/FUCA1/ADGRL4/MALL/DUSP6/PRELID3B/BPGM/PRDM1/G0S2/SNAP25/TRIB2/ADAMDEC1/AKAP12/IKZF1/ITGBL1/LAT2
HALLMARK_MTORC1_SIGNALING	HALLMARK_MTORC1_SIGNALING	199	0.368295	1.629824	0.0002660	0.0012090	0.00636	3643	tags=31%, list=17%, signal=26 %	P4HA1/DDIT4/SLC6A6/RPN1/CXCR4/SLA/ITGB2/CORO1A/SYTL2/IFI30/CYB5B/HSPA9/RPA1/PIK3R3/CTSC/CD9/VLDLR/SSR1/PDAP1/LGMN/HSPE1/SERPINH1/EEF1E1/GOT1/CFP/ACTR2/GSK3B/MTHFD2/CDKN1A/TP11/MTHFD2L/RIT1/UBE2D3/GPI/UCHL5/PITPNB/DAPP1/ERO1A/PSMC4/TUBG1/TCEA1/GBE1/NFIL3/G6PD/HSP90B1/ATP5MC1/BTG2/ADD3/RRM2/TBK1/NUPR1/FGI2/LTA4H/PSMC6/CACYBP/ACTR3/SEC11A/SLC1A5/IMMT/MCM4/USO1
HALLMARK_IL2_STAT5_SIGNALING	HALLMARK_IL2_STAT5_SIGNALING	199	0.358919	1.588329	0.0005340	0.0022270	0.001172	4304	tags=34%, list=21%, signal=27 %	P4HA1/SELL/CD48/NRP1/MYC/IL1R2/SOCS1/PLSCR1/SWAP70/CD86/GPR65/RHOB/GPX4/IRF8/DENND5A/HYCC2/GUCY1B1/TNFRSF4/RRAGD/FLT3LG/IFNGR1/CD44/GLIPR2/IGF2R/TLR7/P2RX4/CST7/PENK/KLF6/ANXA4/PHTF2/SOCS2/NT5E/RNH1/GBP4/TTCC39B/S100A1/DHRS3/MXD1/NFIL3/SYNGR2/PTGER2/ITIH5/LTB/ST3GAL4/RHOH/ITGAE/FGI2/CXCL10/SH3BGR2/COL6A1/BATF/DCPS/IFITM3/SLC1A5/IL1RL1/UCK2/MYO1E/SCN9A/NDRG1/IL3RA/ENO3/IL2RB/AHCY/AMACR/CYFIP1/SPP1/LRRC8C
HALLMARK_ESTROGEN_RESPONSE_LATE	HALLMARK_ESTROGEN_RESPONSE_LATE	200	-0.325082	-1.470609	0.0027720	0.0106610	0.005611	2177	tags=21%, list=10%, signal=19 %	PTGER3/JAK1/KIF20A/NCOR2/PGR/GAL/TFPI2/ANXA9/SLC24A3/FLNB/TPD52L1/SCARB1/TSPAN13/TRIM29/TOB1/ABHD2/SLC22A5/MAPK13/CACNA2D2/LAMC2/TPBG/SLC26A2/TOP2A/PRKAR2B/EEIG1/SEMA3B/AGR2/CELSR2/BCL2/MAPT/NHERF1/BTG3/GFGR3/CLK10/TFAP2C/PAPSS2/PCP4/CA12/AREG/KRT19/CLK11/NMU
HALLMARK_HYPOXIA	HALLMARK_HYPOXIA	200	0.335798	1.485754	0.003293	0.01176	0.00619	2525	tags=24%, list=12%, signal=21 %	DPYSL4/S100A4/P4HA1/PPP1R3C/IGFBP3/DDIT4/SLC6A6/CXCR4/PLAC8/MIF/CITED2/HMOX1/VLDLR/RRAGD/CCN2/CCNG2/CCN5/SRPX/MAP3K1/PGAM2/STBD1/CDKN1A/NAGK/CAVIN1/PRDX5/MYH9/TP11/KLF6/CP/ISG20/AKAP12/TMEM45A/SERPINE1/MT2A/HEXA/GPI/ERRF11/ETS1/KDELRL3/GPC3/ERO1A/FOS/MT1E/BNIP3L/COL5A1/GBE1/NFIL3/TGFB3
HALLMARK_IL6_JAK_STAT3_SIGNALING	HALLMARK_IL6_JAK_STAT3_SIGNALING	87	0.417758	1.622222	0.004426	0.01433	0.007542	3900	tags=45%, list=19%, signal=37 %	CSF2RB/CXCL11/CSF2RA/IL1R2/SOCS1/TGFB1/STAM2/CXCL9/HMOX1/CD9/IFNGR1/CXCL13/CSF3R/CD44/ITGA4/IFNGR2/CD36/CD14/IRF9/HAX1/CNTFR/IL1R1/REG1A/CD38/LTB/TLR2/MYD88/PIK3R5/IL2RG/CXCL10/CCR1/ITGB3/IL15RA/CCL7/IL10RB/EBI3/IL3RA/IL6ST/PF4
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	113	0.381778	1.556406	0.004586	0.01433	0.007542	4375	tags=35%, list=21%, signal=28 %	DDIT4/HSPA9/CKS1B/BANF1/SSR1/NFYB/SKIC3/PDIA5/MTHFD2/TUBB2A/XPOT/ATP6V0D1/EIF4E/DNAJA4/SPCS3/EDC4/DCTN1/GOSR2/KDELRL3/IFIT1/ERO1A/EIF4EBP1/IMP3/EXOSC2/TARS1/HSP90B1/LSM1/CEBPB/NFYA/H2AX/IGFBP1/POP4/NHP2/SEC11A/EIF4A2/LSM4/EXOSC4/RPS14/SLC30A5/SERP1
HALLMARK_INFLAMMATORY_RESPONSE	HALLMARK_INFLAMMATORY_RESPONSE	200	0.322295	1.426009	0.0068930	0.020272	0.01067	3769	tags=32%, list=18%, signal=26 %	PROK2/CYBB/SELL/CCL5/CD48/CXCL11/MYC/C5AR1/LYN/RGS1/CD69/IL7R/FPR1/ABH1/LAMP3/CXCL9/CLEC5A/TLR1/IL18RAP/C3AR1/CALCRL/LCP2/NLRP3/CSF3R/OLR1/P2RX4/NFKBIA/CDKN1A/IFNGR2/EDN1/KLF6/CD14/PTGER4/SERPINE1/SLC31A2/IL1R1/BST2/SCARF1/CXCR6/MSR1/PTAFR/FFAR2/GPC3/P2RY2/MXD1/EREG/PTGER2/CMKLR1/BTG2/ATP2C1/TLR2/PIK3R5/RTP4/CXCL10/NMI/ITGB3/GNA15/NMUR1/IL15RA/CCL7/AQP9/EMP3/EBI3/SLAMF1
HALLMARK_MYOGENESIS	HALLMARK_MYOGENESIS	198	0.327225	1.44459	0.0083550	0.0232090	0.012215	3019	tags=26%, list=14%, signal=23 %	CNN3/COL15A1/CFD/MYL3/PPP1R3C/IGFBP3/TGFB1/FXYD1/MEF2C/CSRP3/MYOZ1/FABP3/PFKM/TNNT3/AEBP1/APOD/COL6A3/PGAM2/MYOM2/PTP4A3/MYLK/LSP1/IGF1/CDKN1A/COL6A2/TNNC2/CD36/GSN/MYH9/RYR1/RIT1/PICK1/SGCA/GABARAPL2/HDAC5/DES/SGCD/SORBS1/TNNC1/HSPB2/PKIA/COL4A2/CRAT/TCAP/PDE4DIP/SYNGR2/SLC6A8/RB1/CKMT2/VIPR1/CRYAB/CKM
HALLMARK_UV_RESPONSE_UP	HALLMARK_UV_RESPONSE_UP	158	0.327287	1.394567	0.0102990	0.0271020	0.014264	4020	tags=32%, list=19%, signal=26 %	RRAD/EPCAM/RPN1/PSMC3/ATP6V1C1/LYN/IGFBP2/CYB5B/EPHX1/RHOB/BSG/SHOX2/EIF2S3/HMOX1/PDAP1/ARRB2/NFKBIA/HNRNPU/PPP1R2/PDLIM3/STK25/PRKCD/CTSV/CYP1A1/FMO1/ALAS1/BID/TMBIM6/CCK/FOS/PLCL1/TARS1/MSX1/BTG2/SLC6A8/MRPL23/KLHDC3/H2AX/PRKACA/SLC25A4/EIF5/CREG1/SULT1A1/ATP6V1F/JUNB/CDC34/CHKA/CDK2/IL6ST/POLE3/RAB27A
HALLMARK_GLYCOLYSIS	HALLMARK_GLYCOLYSIS	200	0.310881	1.375507	0.0123370	0.0308430	0.016233	2660	tags=20%, list=13%, signal=18 %	DPYSL4/P4HA1/IGFBP3/DDIT4/CXCR4/DLD/MIF/CITED2/TXN/ANG/FUT8/PGAM1/VLDLR/RRAGD/ARPP19/GOT1/PGAM2/CD44/ALG1/PKP2/TP11/SDC1/ISG20/STMN1/NT5E/HAX1/LCT/SPAG4/CENPA/KDELRL3/SDHC/GPC3/SOD1/ERO1A/PSMC4/PGLS/COL5A1/GUSB/G6PD/NDUFV3/DCN
HALLMARK_FATTY_ACID_METABOLISM	HALLMARK_FATTY_ACID_METABOLISM	155	0.331549	1.404983	0.0142430	0.0339120	0.017848	3348	tags=30%, list=16%, signal=26 %	YWHAH/ALDH1A1/DLD/SMS/MIF/PTPRG/EPHX1/HSD17B11/ECHS1/HPGD/LGALS1/CD1D/BCKDHB/CA4/CD36/G0S2/LTC4S/NTHL1/PSME1/MCEE/HCCS/ADH1C/PTS/GSTZ1/IL411/CYP1A1/BPHL/FMO1/PCBD1/OSTC/UROS/VNN1/MLYCD/SDHC/CBR3/CRAT/UBE2L6/IDH3G/MGLL/ECH1/ECI1/ECI2/DECR1/ETFDH/GPD1/NCAPH2/TDO2
HALLMARK_TGF_BETA_SIGNALING	HALLMARK_TGF_BETA_SIGNALING	54	0.41226	1.476588	0.0160290	0.035169	0.01851	2239	tags=24%, list=11%, signal=22 %	ID1/CDK9/TGFB1/ID3/ID2/PPP1CA/FKBP1A/IFNGR2/PPM1A/UBE2D3/CTNNB1/SERPINE1/APC
HALLMARK_UV_RESPONSE_DN	HALLMARK_UV_RESPONSE_DN	142	0.345226	1.440756	0.0161780	0.035169	0.01851	3179	tags=30%, list=15%, signal=26 %	ID1/FHL2/SNAI2/NRP1/MYC/FBLN5/CITED2/ATRN/PIK3R3/NEK7/COL1A2/VLDLR/GCNT1/DBP/INPP4B/BCKDHB/PDLIM5/ANXA4/AKT3/SYNJ2/MTA1/SPOP/DAB2/PRKCE/TGFB2/SERPINE1/MRPS31/GJA1/ADGRL2/ATP2B4/MT1E/CACNA1A/ADD3/ATP2C1/MGLL/DUSP1/KIT/NR1D2/PLPP3/RASA2/PDGFRB/MMP16/CAV1
HALLMARK_ADIPOGENESIS	HALLMARK_ADIPOGENESIS	198	0.313687	1.384821	0.01707	0.0355630	0.018717	3592	tags=31%, list=17%, signal=26 %	COL15A1/IDH3A/CAT/DLD/NDUFB7/SLC66A3/GPX4/OMD/RTN3/DGRAM2/TANK/ECHS1/CCNG2/IFNGR1/APOE/UQCRC1/NDUFS3/MYLK/MGST3/CHCHD10/CD36/PDCD4/CAVIN1/ETFB/DNAJC15/LTC4S/PTCD3/COX8A/SORBS1/NDUFA5/CYC1/CDKN2C/ORM1/DLAT/SDHC/SOD1/G3BP2/ATP5PO/LPCAT3/CRAT/GBE1/ITIH5/BCL2L13/GHITM/IDH3G/MGLL/ECH1/MRPL15/ATP1B3/SAMM50/RREB1/DECR1/UQCRCQ/COX7B/UQCRC11/UCP2/COQ9/SLC1A5/SCP2/IMMT/SULT1A1
HALLMARK_XENOBIOTIC_METABOLISM	HALLMARK_XENOBIOTIC_METABOLISM	197	0.306103	1.349593	0.0198460	0.039692	0.02089	3737	tags=29%, list=18%, signal=24 %	PDK4/SLC6A6/CAT/FMO3/KYNU/ARG1/SAR1B/EPHX1/IRF8/HMOX1/BLVRB/FBLN1/TAT/ARPP19/PGD/APOE/ID2/SSR3/MAN1A1/IGF1/PSMB10/PDLIM5/CD36/PTGES3/SLC35D1/ADH1C/PTS/DHRS1/SERPINE1/MT2A/PTGES/IL1R1/AKR1C2/CYP1A1/BPHL/FMO1/VNN1/ALAS1/ETS2/TMBIM6/REG1A/SLC22A1/ITIH1/GART/ECH1/ACOX2/GSTM4/ACP1/ETFDH/IGFBP1/TDO2/PTGR1/NINJ1/SLC1A5/FBP1/CYP2C18/AQP9

AF, atrial fibrillation; GSEA, gene set enrichment analysis; NES, normalized enrichment score; SR, sinus rhythm.

Table S4 Identification of significantly enriched chemical and genetic perturbations and canonical pathways through GSEA of DEGs in neutrophils between AF and SR via single-cell transcriptomic analysis

ID	Description	Set size	Enrichment score	NES	P value	P.adjust	q value	Rank	Leading edge	Core enrichment
REACTOME_CRISTAE_FORMATION	REACTOME_CRISTAE_FORMATION	16	-0.809555	-2.502822	2.07E-07	0.000184	0.000168	199	tags=88%, list=16%, signal=74%	HSPA9/MICOS10/ATP5PF/ATP5F1C/ATP5PB/ATP5F1D/ATP5PO/ATP5F1A/ATP5MC2/ATP5MG/ATP5ME/ATP5F1E/ATP5F1B/ATP5MF
REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COUPLING	14	-0.829776	-2.469899	1.32E-07	0.000184	0.000168	168	tags=86%, list=14%, signal=75%	ATP5PF/ATP5F1C/ATP5PB/ATP5F1D/ATP5PO/ATP5F1A/ATP5MC2/ATP5MG/ATP5ME/ATP5F1E/ATP5F1B/ATP5MF
REACTOME_MITOCHONDRIAL_BIOGENESIS	REACTOME_MITOCHONDRIAL_BIOGENESIS	18	-0.743429	-2.369531	1.74E-06	0.001031	0.000943	199	tags=78%, list=16%, signal=66%	HSPA9/MICOS10/ATP5PF/ATP5F1C/ATP5PB/ATP5F1D/ATP5PO/ATP5F1A/ATP5MC2/ATP5MG/ATP5ME/ATP5F1E/ATP5F1B/ATP5MF
REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE	REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE	33	-0.611223	-2.305634	7.37E-06	0.003283	0.003001	201	tags=58%, list=16%, signal=50%	RP2/HSPA9/MICOS10/DYNLRB1/ATP5PF/CCT5/ATP5F1C/ATP5PB/ATP5F1D/DYNC1H1/ATP5PO/ATP5F1A/ATP5MC2/ATP5MG/ATP5ME/ATP5F1E/ATP5F1B/SEPTIN2/ATP5MF
MENSE_HYPOXIA_UP	MENSE_HYPOXIA_UP	18	0.719057	2.33041	1.05E-05	0.003741	0.003421	255	tags=78%, list=21%, signal=63%	SLC2A3/CEBPB/VEGFA/GNA13/INSIG1/ATF3/RBPJ/PFKFB3/NDRG1/CEBPD/ADM/PLIN2/NAMPT/TIPARP
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_INFLUENZA_A_DEL_NS1_INFECTION_UP	BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_INFLUENZA_A_DEL_NS1_INFECTION_UP	100	0.413908	1.970206	1.65E-05	0.004905	0.004484	297	tags=48%, list=24%, signal=40%	THAP9-AS1/C3AR1/APOBEC3A/LY6E/CEBPB/IFITM3/IFI6/KLF10/DUSP1/GNA13/IFRD1/HBEGF/TRIB1/DUSP2/TNFAIP8/METRNL/TAGAP/SOCS3/THEMIS2/OLR1/IFI16/LAP3/NFKBIA/PLSCR1/TLR2/RASGEF1B/SP100/PARP14/ID2/TNFSF10/TRIM22/TNFSF13B/ADM/STAT1/SCO2/CXCL16/CCNL1/NFKBD/ICAM1/RNF213/SERPINB9/TIPARP/LMO2/CXCL3/PLAUR/RIPK2/CARD16/MX2
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	13	0.752681	2.234426	4.57E-05	0.010311	0.009428	199	tags=77%, list=16%, signal=65%	HLA-DQA1/HLA-DRB5/HLA-DPA1/HLA-DPB1/HLA-DQB1/HLA-DMA/HLA-DRA/SSB/FCGR2A/CD86
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	27	0.608535	2.212958	4.63E-05	0.010311	0.009428	305	tags=67%, list=25%, signal=51%	C3AR1/UPP1/IFI6/CD163/SOCS3/KLF6/OLR1/IFI16/DUSP6/BTG1/TLR2/NDRG1/STAT1/CPD/ARL4A/ANXA2/ACSL1/FNDC3B
KIM_GLIS2_TARGETS_UP	KIM_GLIS2_TARGETS_UP	23	0.644833	2.243947	6.22E-05	0.010749	0.009828	235	tags=65%, list=19%, signal=54%	HLA-DQA1/IFITM3/HLA-DRB5/ISG15/SOCS3/HLA-DQB1/CASP4/HLA-DMA/HLA-DRA/TLR2/PYCARD/LILRB3/FCGR2A/TNFSF13B/ICAM1
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	11	0.780508	2.209238	6.64E-05	0.010749	0.009828	202	tags=82%, list=16%, signal=69%	HLA-DQA1/HLA-DRB5/HLA-DPA1/HLA-DPB1/HLA-DQB1/HLA-DMA/HLA-DRA/CD86/TNFSF13B
BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_CALU3_CELLS_UP	BLANCO_MELO_COVID19_SARS_COV_2_INFECTION_CALU3_CELLS_UP	54	0.495451	2.104512	6.57E-05	0.010749	0.009828	297	tags=56%, list=24%, signal=44%	MT2A/KLF10/DUSP1/HBEGF/ISG15/ATF3/TAGAP/THEMIS2/KLF6/IFI16/PMAIP1/ISG20/NFKBIA/RASGEF1B/SP100/PARP14/MAP3K8/NLRP3/G0S2/TNFSF10/TRIM22/TNFSF13B/STAT1/ICAM1/RNF213/SERPINB9/TIPARP/LMO2/CXCL3/MX2
DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP	DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP	52	0.497279	2.105553	7.39E-05	0.010972	0.010032	208	tags=42%, list=17%, signal=37%	SLC2A3/CEBPB/IFITM3/IFI6/GABARAPL1/DUSP1/GNA13/IFRD1/ISG15/ATF3/RSRC2/KLF6/IFI16/PMAIP1/ISG20/NFKBIA/PLSCR1/SP100/NR4A2/TRIM22/ADM/STAT1
ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	45	0.511224	2.108764	8.02E-05	0.010985	0.010044	212	tags=49%, list=17%, signal=42%	MT2A/SLA/UPP1/ISG15/TIMP1/ATF3/PFKFB3/GK/SOCS3/IFI16/CASP4/NFKBIA/TLR2/MAP3K8/CEBPD/LILRB3/FCGR2A/RAB20/CD14/ADM/STAT1/LITAF
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	34	0.557162	2.131986	0.000107	0.013597	0.012432	263	tags=56%, list=21%, signal=45%	HLA-DQA1/SLC11A1/HLA-DRB5/PTPN1/FKBP5/ISG15/PLAC8/IFI16/HLA-DQB1/HLA-DMA/HLA-DRA/NFKBIA/GIMAP4/CD14/STAT1/LITAF/ICAM1/NAMPT/EIF1AX
ABBUD_LIF_SIGNALING_1_UP	ABBUD_LIF_SIGNALING_1_UP	10	0.798546	2.183486	0.000136	0.015402	0.014083	112	tags=80%, list=9%, signal=73%	CEBPB/UPP1/KLF10/PTPN1/TNFRSF1A/STAT3/SOCS3/GPCPD1
BROWNE_HCMV_INFECTION_16HR_UP	BROWNE_HCMV_INFECTION_16HR_UP	20	0.652194	2.17346	0.000204	0.015402	0.014083	152	tags=50%, list=12%, signal=45%	TFRC/PPP1R2/IFI6/VEGFA/GNA13/FKBP5/REL/GK/HLA-DPB1/PLSCR1
HARRIS_HYPOXIA	HARRIS_HYPOXIA	18	0.66249	2.147079	0.000216	0.015402	0.014083	217	tags=56%, list=17%, signal=47%	ALDOA/TFRC/SLC2A3/SAT1/VEGFA/LDHA/CDKN1B/FOS/ADM/APEX1
MANNE_COVID19_NONICU_VS_HEALTHY_DONOR_PLATELETS_UP	MANNE_COVID19_NONICU_VS_HEALTHY_DONOR_PLATELETS_UP	12	0.730339	2.127904	0.000202	0.015402	0.014083	158	tags=67%, list=13%, signal=59%	LY6E/IFITM3/IFI6/ISG15/HMGA1/SLC25A37/PFDN2/PARP14
GROSS_HYPOXIA_VIA_ELK3_DN	GROSS_HYPOXIA_VIA_ELK3_DN	44	0.518413	2.121228	0.000169	0.015402	0.014083	224	tags=48%, list=18%, signal=41%	CEBPB/SAT1/UPP1/THBD/VEGFA/IFRD1/HSPA5/HBEGF/RBPJ/DUSP2/PFKFB3/SLC20A1/KLF6/IFI16/SKIL/NFKBIA/NDRG1/FOS/ADM/JMJD1C/IL13RA1
CHEN_HOXA5_TARGETS_9HR_UP	CHEN_HOXA5_TARGETS_9HR_UP	49	0.497094	2.0809	0.000139	0.015402	0.014083	326	tags=57%, list=26%, signal=44%	THAP9-AS1/CEBPB/SAT1/GABARAPL1/VEGFA/KLF10/ZNF331/IFRD1/ATF3/RSRC2/GADD45B/KLF6/IFI16/PMAIP1/DUSP6/NFKBIA/TAF1D/FOS/CCNL1/JMJD1C/AKIRIN1/TIPARP/ARID4B/PPIG/RIPK2/RLF/PPP1R12A/FOSL2
WP_OXIDATIVE_PHOSPHORYLATION	WP_OXIDATIVE_PHOSPHORYLATION	27	-0.583561	-2.079483	0.000206	0.015402	0.014083	198	tags=52%, list=16%, signal=45%	NDUFA3/NDUFB9/NDUFB1/ATP5PF/ATP5PB/ATP5F1D/ATP5PO/ATP5F1A/ATP5MC2/ATP5MG/ATP5ME/ATP5F1E/ATP5F1B/ATP5MF
NAGASHIMA_NRG1_SIGNALING_UP	NAGASHIMA_NRG1_SIGNALING_UP	61	0.463376	2.02119	0.000198	0.015402	0.014083	255	tags=48%, list=21%, signal=40%	CEBPB/VEGFA/KLF10/DUSP1/ZNF331/IFRD1/HBEGF/REL/ATF3/GADD45B/TRIB1/DUSP2/PFKFB3/AREG/PHLDA2/KLF6/PMAIP1/ISG20/MAP3K8/FOS/NR4A1/NR4A2/IER3/ADM/CCNL1/IER5/ZFAND5/AKIRIN1/TIPARP
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP	HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP	59	0.45438	1.973086	0.000183	0.015402	0.014083	256	tags=49%, list=21%, signal=41%	TFRC/HLA-DQA1/MT2A/SAT1/IFI6/DUSP1/DSE/TIMP1/HLA-DPA1/TUBA1A/DUSP2/STAT3/ACSL3/PFKFB3/AREG/MAFB/PHLDA2/HLA-DPB1/BTG1/FOS/NR4A1/ID2/NR4A2/IER3/STAT1/IL13RA1/RPS20/SPTLC2/POLR2L
STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN	STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN	96	-0.398946	-1.921295	0.000207	0.015402	0.014083	185	tags=29%, list=15%, signal=27%	MICOS10/OGFRL1/TRA2B/DYNLRB1/ATP5PF/ROMO1/TMEM256/CCT5/ATP5F1C/COMT/ATP5PO/SEC22B/IDH3G/HSPE1/PET100/RTRAF/ATP5MG/RAB5IF/ELOB/ATP5ME/RPL36A/ATP5F1E/TRIR/UGP2/SELENOH/ATP5MF/NME2/ELOC
LIU_OVARIAN_CANCER_TUMORS_AND_XENOGRAFTS_XDGS_DN	LIU_OVARIAN_CANCER_TUMORS_AND_XENOGRAFTS_XDGS_DN	202	0.311946	1.690752	0.000216	0.015402	0.014083	292	tags=36%, list=23%, signal=33%	DOCK10/C3AR1/GPR183/SLC2A3/HLA-DQA1/MT2A/SAT1/SLA/UPP1/SLC11A1/THBD/DUSP1/HLA-DRB5/RGCC/FKBP5/HBEGF/TIMP1/EPB41L3/HLA-DPA1/GADD45B/CD163/DUSP2/TNFAIP8/VAMP5/TAGAP/SOCS3/KLF6/OLR1/IFI16/HLA-DPB1/HLA-DQB1/HLA-DMA/HLA-DRA/APBB1IP/FPR1/TLR2/RNASE6/NLRP3/G0S2/SERPINB1/GIMAP4/LGALS1/PYCARD/CEBPD/FOS/OSM/NR4A1/LILRB3/FCGR2A/TNFSF10/LY96/CD86/TRIM22/TNFSF13B/CD14/ADM/CLEC2B/WIPF1/HCST/CD52/ICAM1/SERPINB9/C1orf162/TIPARP/LMO2/MS4A6A/IGSF6/CXCL3/SH3BGR/LRAB31/PLAUR/CLEC7A/CARD16
MITSIADES_RESPONSE_TO_APLIDIN_UP	MITSIADES_RESPONSE_TO_APLIDIN_UP	95	0.387756	1.823756	0.000274	0.018752	0.017145	155	tags=28%, list=12%, signal=27%	THAP9-AS1/C3AR1/SLC2A3/CEBPB/PPR12/IFITM3/GABARAPL1/DUSP1/IFRD1/HBEGF/TIMP1/RSRC2/GADD45B/TRIB1/DUSP2/ARF6/PFKFB3/AREG/THEMIS2/KLF6/PFDN2/DUSP6/ISG20/SKIL/NFKBIA/PLSCR1/TAF1D
HUMMERICH_SKIN_CANCER_PROGRESSION_UP	HUMMERICH_SKIN_CANCER_PROGRESSION_UP	23	0.6138	2.135956	0.000306	0.02017	0.018442	174	tags=48%, list=14%, signal=42%	MT2A/IFITM3/HSPA5/TNFRSF1A/GADD45B/STAT3/IFI16/HLA-DQB1/SERPINB1/PYCARD/FOS
WP_NETWORK_MAP_OF_SARS_COV_2_SIGNALING_PATHWAY	WP_NETWORK_MAP_OF_SARS_COV_2_SIGNALING_PATHWAY	36	0.530955	2.065364	0.000339	0.02154	0.019694	215	tags=50%, list=17%, signal=43%	DDIT4/CEBPB/IFITM3/IFI6/DUSP1/HLA-DRB5/CD163/PTPN6/HLA-DRA/RHEB/NLRP3/FOS/FYN/TNFSF10/ACTG1/CD14/STAT1/CXCL16
QI_HYPOXIA	QI_HYPOXIA	15	0.685081	2.099177	0.000364	0.022282	0.020373	224	tags=67%, list=18%, signal=55%	ALDOA/MT2A/DDIT4/VEGFA/DUSP1/INSIG1/NDRG1/IER3/ADM/IL13RA1
CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	28	0.557468	2.040102	0.000375	0.022282	0.020373	255	tags=57%, list=21%, signal=46%	MT2A/DDIT4/CEBPB/RGCC/FKBP5/ATF3/GADD45B/CD163/AREG/NFKBIA/CEBPD/BTG2/IER5/PLIN2/ZFAND5/TIPARP
ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	57	0.453712	1.939145	0.000428	0.024604	0.022496	219	tags=44%, list=18%, signal=38%	TFRC/DUSP1/FKBP5/HBEGF/PLAC8/ATF3/VMP1/TRIB1/PFKFB3/METRNL/SLC20A1/SOCS3/GPCPD1/OLR1/MAP3K8/ZFP36L1/NDRG1/CEBPD/FOS/NR4A1/NR4A2/IER3/ADM/CCNL1/CHMP1B
ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN	ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN	23	0.601574	2.093411	0.000487	0.025758	0.023551	270	tags=65%, list=22%, signal=52%	MT2A/DDIT4/CEBPB/HSPA5/INSIG1/ATF3/KLF6/ID2/TAX1BP1/FCGR2A/IER3/IER5/AAK1/RTN4/LMO2
WP_ONCOSTATIN_M_SIGNALING_PATHWAY	WP_ONCOSTATIN_M_SIGNALING_PATHWAY	16	0.660912	2.076113	0.000517	0.025758	0.023551	208	tags=56%, list=17%, signal=47%	CEBPB/VEGFA/CDKN1B/STAT3/SOCS3/NFKBIA/FOS/OSM/STAT1
PILON_KLF1_TARGETS_UP	PILON_KLF1_TARGETS_UP	19	-0.635751	-2.051604	0.000521	0.025758	0.023551	243	tags=63%, list=20%, signal=52%	TMEM30A/HLA-A/USP8/PICALM/HSPA9/OGFRL1/HIPK2/CPEB4/IRS2/CYLD/SEPTIN2/ELOC
SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	42	0.499839	2.03148	0.000473	0.025758	0.023551	233	tags=45%, list=19%, signal=38%	C3AR1/SLC2A3/CEBPB/SLA/THBD/VEGFA/HBEGF/DSE/INSIG1/TNFRSF1A/PFKFB3/FPR1/TLR2/FCGR2A/IER3/CD14/ADM/PLIN2/IFNGR2
FEVR_CTNNB1_TARGETS_UP	FEVR_CTNNB1_TARGETS_UP	81	0.405414	1.873261	0.0005	0.025758	0.023551	228	tags=42%, list=18%, signal=37%	LY6E/MIDN/HLA-DQA1/MT2A/CEBPB/UPP1/GABARAPL1/DUSP1/GNA13/EPB41L3/ATF3/GADD45B/CD163/STAT3/GK/VAMP5/SLC20A1/SOCS3/CASP4/HLA-DMA/DUSP6/G0S2/SERPINB1/LGALS1/FOS/RAB20/BTG2/TNFSF13B/ADM/STAT1/LITAF/CXCL16/IL13RA1/IER5
HECKER_IFNB1_TARGETS	HECKER_IFNB1_TARGETS	14	0.698071	2.118744	0.000608	0.02929	0.026781	211	tags=79%, list=17%, signal=66%	C3AR1/APOBEC3A/LY6E/IFI6/ISG15/CD163/LAP3/PLSCR1/G0S2/STAT1/SCO2
MANNE_COVID19_COMBINED_COHORT_VS_HEALTHY_DONOR_PLATELETS_UP	MANNE_COVID19_COMBINED_COHORT_VS_HEALTHY_DONOR_PLATELETS_UP	12	0.704291	2.052012	0.00063	0.02951	0.026982	133	tags=58%, list=11%, signal=53%	LY6E/IFITM3/IFI6/ISG15/HMGA1/SLC25A37/PFDN2
ROSS_ACUTE_MYELOID_LEUKEMIA_CBF	ROSS_ACUTE_MYELOID_LEUKEMIA_CBF	12	0.701795	2.044739	0.000674	0.030764	0.028128	232	tags=75%, list=19%, signal=62%	HLA-DPA1/DUSP2/VAMP5/HLA-DPB1/PMAIP1/DUSP6/ISG20/WIPF1/CD52
ELVIDGE_HYPOXIA_UP	ELVIDGE_HYPOXIA_UP	33	0.525385	2.001516	0.000773	0.033587	0.03071	313	tags=64%, list=25%, signal=49%	DDIT4/SAT1/VEGFA/DUSP1/PLAC8/ATF3/GADD45B/RBPJ/PFKFB3/TNFAIP8/KLF6/ISG20/NDRG1/FOS/FYN/ADM/PLIN2/TIPARP/PLAUR/RLF/BHLHE40
HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP	HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP	48	0.465475	1.955593	0.000759	0.033587	0.03071	214	tags=42%, list=17%, signal=36%	SLC2A3/SAT1/UPP1/VEGFA/DUSP1/IFRD1/TIMP1/STAT3/ACSL3/TNFAIP8/SOCS3/OLR1/CASP4/PMAIP1/ISG20/PLSCR1/SERPINB1/FYN/LY96/CLEC2B
XIE_ST_HSC_S1PR3_OE_UP	XIE_ST_HSC_S1PR3_OE_UP	16	0.651627	2.046946	0.000832	0.035082	0.032076	236	tags=69%, list=19%, signal=56%	LY6E/IFITM3/IFI6/HBEGF/ISG15/ISG20/PLSCR1/ID2/STAT1/CD52/RNF213
DAZARD_RESPONSE_TO_UV_SCC_DN	DAZARD_RESPONSE_TO_UV_SCC_DN	17	0.638116	2.036443	0.000881	0.035082	0.032076	99	tags=41%, list=8%, signal=38%	MT2A/DDIT4/THBD/ARL4C/TNFRSF1A/RBPJ/TNFAIP8
ELVIDGE_HYPOXIA_BY_DMOG_UP	ELVIDGE_HYPOXIA_BY_DMOG_UP	23	0.584552	2.034175	0.00086	0.035082	0.032076	207	tags=57%, list=17%, signal=48%	DDIT4/SAT1/VEGFA/PLAC8/ATF3/PFKFB3/TNFAIP8/KLF6/ISG20/NDRG1/FOS/FYN/ADM
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	17	0.6368	2.032245	0.000926	0.035082	0.032076	199	tags=59%, list=16%, signal=50%	HLA-DQA1/HLA-DRB5/HLA-DPA1/PTPN6/HLA-DPB1/HLA-DQB1/HLA-DRA/MAP3K8/FYN/CD86
NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	30	0.534214	1.987401	0.00091	0.035082	0.032076	208	tags=50%, list=17%, signal=43%	C3AR1/MT2A/SAT1/SLC11A1/IFRD1/ATF3/GK/SLC20A1/IFI16/CASP4/APBB1IP/NFKBIA/CEBPD/IER3/STAT1
WINTER_HYPOXIA_METAGENE	WINTER_HYPOXIA_METAGENE	50	0.458681	1.924679	0.000901	0.035082	0.032076	235	tags=50%, list=19%, signal=42%	ALDOA/TFRC/SLC2A3/DDIT4/SAT1/VEGFA/LDHA/HSPA5/INSIG1/PNN/CDKN1B/RBPJ/PFKFB3/SLC20A1/HLA-DQB1/BTG1/NDRG1/LGALS1/FOS/NR4A1/ID2/ADM/EIF4A3/PLIN2/ICAM1
KEGG_LEISHMANIA_INFECTION	KEGG_LEISHMANIA_INFECTION	22	0.575391	1.984174	0.000989	0.035963	0.032882	233	tags=64%, list=19%, signal=53%	HLA-DQA1/HLA-DRB5/HLA-DPA1/PTPN6/HLA-DPB1/HLA-DQB1/HLA-DMA/HLA-DRA/NFKBIA/TLR2/FOS/FCGR2A/STAT1/IFNGR2
WALLACE_PROSTATE_CANCER_RACE_UP	WALLACE_PROSTATE_CANCER_RACE_UP	64	0.423353	1.853762	0.000969	0.035963	0.032882	242	tags=42%, list=19%, signal=36%	DOCK10/GPR183/HLA-DQA1/SLA/IFITM3/IFI6/THBD/ARL4C/ISG15/PLAC8/DUSP2/THEMIS2/IFI16/HLA-DPB1/HLA-DQB1/HLA-DRA/ISG20/RNASE6/CEBPD/FYN/NR4A2/LY96/CD86/STAT1/WIPF1/CD52/SERPINB9
REACTOME_INTERFERON_GAMMA_SIGNALING	REACTOME_INTERFERON_GAMMA_SIGNALING	26	0.557063	1.99983	0.00103	0.036675	0.033533	235	tags=58%, list=19%, signal=48%	HLA-DQA1/MT2A/HLA-DRB5/PTPN1/HLA-DPA1/SOCS3/PTPN6/HLA-DPB1/HLA-DQB1/HLA-DRA/SP100/TRIM22/STAT1/IFNGR2/ICAM1
BASSO_CD40_SIGNALING_UP	BASSO_CD40_SIGNALING_UP	30	0.526744	1.959611	0.001122	0.039172	0.035816	235	tags=57%, list=19%, signal=47%	GPR183/HLA-DQA1/DDIT4/GADD45B/DUSP2/TNFAIP8/HLA-DPB1/HLA-DQB1/HLA-DMA/NFKBIA/MAP3K8/ZFP36L1/LGALS1/IER3/STAT1/LITAF/ICAM1
DELACROIX_RAR_TARGETS_UP	DELACROIX_RAR_TARGETS_UP	11	0.713758	2.0203	0.00137	0.046917	0.042897	142	tags=55%, list=11%, signal=49%	CEBPB/SAT1/DUSP1/HMGA1/DUSP6/SKIL
BOQUEST_STEM_CELL_DN	BOQUEST_STEM_CELL_DN	30	0.518224	1.927912	0.001422	0.047785	0.043691	169	tags=47%, list=14%, signal=41%	HLA-DQA1/UPP1/THBD/HBEGF/HLA-DPA1/AREG/HLA-DPB1/HLA-DQB1/HLA-DMA/DUSP6/HLA-DRA/ISG20/G0S2/GIMAP4

AF, atrial fibrillation; GSEA, gene set enrichment analysis; NES, normalized enrichment score; SR, sinus rhythm.

Table S5 Identification of significantly enriched hallmark gene sets through GSEA of DEGs in neutrophils between AF and SR via single-cell transcriptomic analysis

ID	Description	Set size	Enrichment score	NES	P value	P.adjust	q value	Rank	Leading edge	Core enrichment
HALLMARK_TNFA_SIGNALING_VIA_NFKB	HALLMARK_TNFA_SIGNALING_VIA_NFKB	84	0.475638	2.220009	9.84E-07	3.84E-05	2.80E-05	290	tags=52%, list=23%, signal=43%	GPR183/SLC2A3/CEBPB/SAT1/VEGFA/KLF10/DUSP1/HBEGF/REL/ATF3/GADD45B/TRIB1/DUSP2/PFKFB3/AREG/TNFAIP8/PHLDA2/SOCS3/KLF6/OLR1/BTG1/NFKBIA/TLR2/MAP3K8/G0S2/CEBPD/FOS/NR4A1/ID2/NR4A2/BTG2/IER3/NINJ1/LITAF/CCNL1/IER5/IFNGR2/ICAM1/NAMPT/TIPARP/CXCL3/PLAUR/RIPK2/ATP2B1
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	48	0.527321	2.226431	1.62E-05	0.000316	0.00023	297	tags=62%, list=24%, signal=49%	LY6E/HLA-DQA1/MT2A/IFITM3/UPP1/PTPN1/ISG15/STAT3/VAMP5/SOCS3/PTPN6/CASP4/HLA-DMA/BTG1/ISG20/LAP3/FPR1/NFKBIA/PLSCR1/PARP14/TNFSF10/CD86/STAT1/ICAM1/RNF213/NAMPT/ARL4A/VAMP8/RIPK2/MX2
HALLMARK_HYPOXIA	HALLMARK_HYPOXIA	44	0.47761	1.987776	0.00065	0.008445	0.006154	207	tags=45%, list=17%, signal=39%	ALDOA/SLC2A3/MT2A/DDIT4/VEGFA/DUSP1/LDHA/HSPA5/PLAC8/ATF3/CDKN1B/RBPJ/PFKFB3/KLF6/BTG1/ISG20/NDRG1/FOS/IER3/ADM

AF, atrial fibrillation; DEGs, differentially expressed genes; GSEA, gene set enrichment analysis; NES, normalized enrichment score; SR, sinus rhythm.

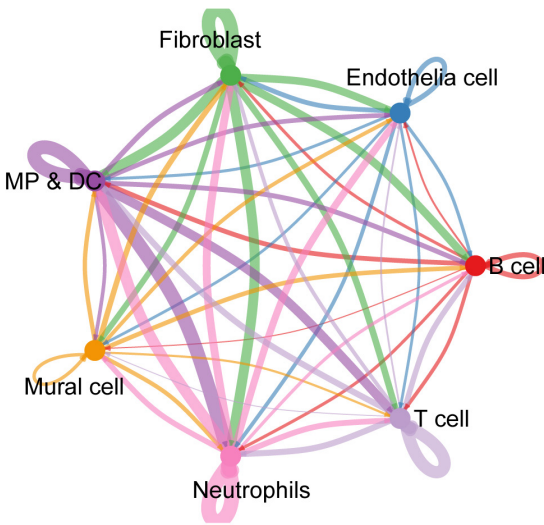


Figure S1 CellChat analysis of the communications between neutrophils and other immune cells. DC, dendritic cell; MP, macrophage.