Supplementary

Table S1 Enrichment analysis of DEGs between DCM and ICM groups

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04060	Cytokine-cytokine receptor interaction	22/86	295/8223	1.58E-13	1.38E-11	1.02E-11	CXCL10/CCL3/CCL8/TNFSF14/IL1RN/IL1B/CSF3/IL10/CCR5/CCR1/CCL13/OSM/CCL4/CCL2/CXCL2/IL7R/IL2RG/TNFRSF4/LIF/CCR7/CCR2/CCL21	22
hsa04061	Viral protein interaction with cytokine and cytokine receptor	15/86	100/8223	6.87E-14	1.2E-11	8.89E-12	CXCL10/CCL3/CCL8/TNFSF14/IL10/CCR5/CCR1/CCL13/CCL4/CCL2/CXCL2/IL2RG/CCR7/CCR2/CCL21	15
hsa04062	Chemokine signaling pathway	14/86	192/8223	9.27E-09	5.41E-07	4E-07	CXCL10/CCL3/CCL8/CCR5/CCR1/CCL13/JAK3/CCL4/CCL2/CXCL2/CCR7/CCR2/ITK/CCL21	14
hsa04668	TNF signaling pathway	11/86	114/8223	2.28E-08	9.99E-07	7.39E-07	SOCS3/CXCL10/IL1B/VCAM1/MMP9/JUNB/CCL2/CXCL2/PTGS2/BCL3/LIF	11
hsa04064	NF-kappa B signaling pathway	10/86	104/8223	1.08E-07	3.77E-06	2.79E-06	TNFSF14/IL1B/VCAM1/GADD45B/CCL13/CCL4/CXCL2/PTGS2/LCK/CCL21	10
hsa04640	Hematopoietic cell lineage	9/86	99/8223	7.87E-07	1.97E-05	1.46E-05	IL1B/CSF3/HLA-DQA1/IL7R/HLA-DQB1/CD8A/CD5/CD8B/HLA-DRB5	9
hsa04630	JAK-STAT signaling pathway	9/86	166/8223	5.44E-05	0.000807	0.000597	SOCS3/CSF3/IL10/JAK3/OSM/IL7R/IL2RG/MYC/LIF	9
hsa05166	Human T-cell leukemia virus 1 infection	9/86	222/8223	0.00049	0.004287	0.003172	FOSL1/HLA-DQA1/JAK3/ZFP36/HLA-DQB1/IL2RG/MYC/LCK/HLA-DRB5	9
hsa05163	Human cytomegalovirus infection	9/86	225/8223	0.00054	0.004502	0.003331	CCL3/IL1B/CCR5/CCR1/CCL4/CCL2/PTGER2/PTGS2/MYC	9
hsa04151	PI3K-Akt signaling pathway	9/86	354/8223	0.011351	0.049663	0.036743	EREG/CSF3/JAK3/OSM/IL7R/NR4A1/THBS1/IL2RG/MYC	9
hsa04657	IL-17 signaling pathway	8/86	94/8223	5.52E-06	0.000107	7.93E-05	CXCL10/FOSL1/IL1B/CSF3/MMP9/CCL2/CXCL2/PTGS2	8
hsa05144	Malaria	7/86	50/8223	7.42E-07	1.97E-05	1.46E-05	IL1B/CSF3/VCAM1/IL10/ACKR1/CCL2/THBS1	7
hsa05323	Rheumatoid arthritis	7/86	93/8223	4.9E-05	0.000807	0.000597	CCL3/IL1B/HLA-DQA1/CCL2/CXCL2/HLA-DQB1/HLA-DRB5	7
hsa05142	Chagas disease	7/86	102/8223	8.85E-05	0.001191	0.000881	CCL3/IL1B/SERPINE1/IL10/BDKRB2/CCL2/GNA15	7
hsa04659	Th17 cell differentiation	7/86	108/8223	0.000127	0.001588	0.001175	IL1B/HLA-DQA1/JAK3/HLA-DQB1/IL2RG/LCK/HLA-DRB5	7
hsa04145	Phagosome	7/86	152/8223	0.001018	0.007124	0.005271	HLA-DQA1/FCAR/HLA-DQB1/MSR1/THBS1/MPO/HLA-DRB5	7
hsa04514	Cell adhesion molecules	7/86	157/8223	0.00123	0.008276	0.006123	VCAM1/HLA-DQA1/HLA-DQB1/CD8A/CD8B/HLA-DRB5/SLITRK4	7
hsa05164	Influenza A	7/86	171/8223	0.002011	0.012133	0.008977	SOCS3/CXCL10/IL1B/HLA-DQA1/CCL2/HLA-DQB1/HLA-DRB5	7
hsa05169	Epstein-Barr virus infection	7/86	202/8223	0.005076	0.026127	0.01933	CXCL10/HLA-DQA1/GADD45B/JAK3/HLA-DQB1/MYC/HLA-DRB5	7
hsa05340	Primary immunodeficiency	6/86	38/8223	2.32E-06	5.07E-05	3.75E-05	JAK3/IL7R/CD8A/IL2RG/CD8B/LCK	6
hsa05321	Inflammatory bowel disease	6/86	65/8223	5.53E-05	0.000807	0.000597	IL1B/HLA-DQA1/IL10/HLA-DQB1/IL2RG/HLA-DRB5	6
hsa05140	Leishmaniasis	6/86	77/8223	0.000144	0.001676	0.00124	IL1B/HLA-DQA1/IL10/PTGS2/HLA-DQB1/HLA-DRB5	6
hsa04612	Antigen processing and presentation	6/86	78/8223	0.000154	0.001688	0.001249	HLA-DQA1/HLA-DQB1/IFI30/CD8A/CD8B/HLA-DRB5	6
hsa04658	Th1 and Th2 cell differentiation	6/86	92/8223	0.000381	0.003708	0.002743	HLA-DQA1/JAK3/HLA-DQB1/IL2RG/LCK/HLA-DRB5	6
hsa05150	Staphylococcus aureus infection	6/86	96/8223	0.00048	0.004287	0.003172	HLA-DQA1/IL10/FCAR/C5AR1/HLA-DQB1/HLA-DRB5	6
hsa05135	Yersinia infection	6/86	137/8223	0.003026	0.017082	0.012638	IL1B/IL10/CCL2/CD8A/CD8B/LCK	6
hsa05152	Tuberculosis	6/86	180/8223	0.011211	0.049663	0.036743	IL1B/HLA-DQA1/IL10/HLA-DQB1/ITGAX/HLA-DRB5	6
hsa05167	Kaposi sarcoma-associated herpesvirus infection	6/86	194/8223	0.015759	0.06566	0.048579	CCR5/CCR1/ZFP36/CXCL2/PTGS2/MYC	6
hsa05417	Lipid and atherosclerosis	6/86	215/8223	0.024768	0.090301	0.066809	CCL3/IL1B/VCAM1/MMP9/CCL2/CXCL2	6
hsa04610	Complement and coagulation cascades	5/86	86/8223	0.001995	0.012133	0.008977	SERPINE1/BDKRB2/C5AR1/PLAUR/ITGAX	5
hsa04625	C-type lectin receptor signaling pathway	5/86	104/8223	0.004551	0.024132	0.017854	IL1B/EGR3/IL10/PTGS2/BCL3	5
hsa04660	T cell receptor signaling pathway	5/86	104/8223	0.004551	0.024132	0.017854	IL10/CD8A/CD8B/LCK/ITK	5
hsa05145	Toxoplasmosis	5/86	112/8223	0.006221	0.031107	0.023014	HLA-DQA1/IL10/CCR5/HLA-DQB1/HLA-DRB5	5
hsa04380	Osteoclast differentiation	5/86	128/8223	0.010779	0.04964	0.036726	SOCS3/FOSL1/IL1B/JUNB/LCK	5
hsa05322	Systemic lupus erythematosus	5/86	136/8223	0.013747	0.058677	0.043412	HLA-DQA1/IL10/GRIN2A/HLA-DQB1/HLA-DRB5	5
hsa05310	Asthma	4/86	31/8223	0.000283	0.002912	0.002155	HLA-DQA1/IL10/HLA-DQB1/HLA-DRB5	4
hsa05330	Allograft rejection	4/86	38/8223	0.000628	0.004993	0.003694	HLA-DQA1/IL10/HLA-DQB1/HLA-DRB5	4
hsa05332	Graft-versus-host disease	4/86	42/8223	0.000922	0.007016	0.005191	IL1B/HLA-DQA1/HLA-DQB1/HLA-DRB5	4
hsa04940	Type I diabetes mellitus	4/86	43/8223	0.001009	0.007124	0.005271	IL1B/HLA-DQA1/HLA-DQB1/HLA-DRB5	4
hsa04672	Intestinal immune network for IgA production	4/86	49/8223	0.001651	0.010702	0.007918	HLA-DQA1/IL10/HLA-DQB1/HLA-DRB5	4
hsa05320	Autoimmune thyroid disease	4/86	53/8223	0.002211	0.012897	0.009542	HLA-DQA1/IL10/HLA-DQB1/HLA-DRB5	4
hsa04933	AGE-RAGE signaling pathway in diabetic complications	4/86	100/8223	0.02046	0.083266	0.061604	IL1B/SERPINE1/VCAM1/CCL2	4
hsa05146	Amoebiasis	4/86	102/8223	0.021829	0.086822	0.064235	IL1B/IL10/CXCL2/GNA15	4
hsa04620	Toll-like receptor signaling pathway	4/86	104/8223	0.023254	0.090301	0.066809	CXCL10/CCL3/IL1B/CCL4	4
hsa04670	Leukocyte transendothelial migration	4/86	114/8223	0.03122	0.1115	0.082494	VCAM1/MMP9/RHOH/ITK	4
hsa04650	Natural killer cell mediated cytotoxicity	4/86	131/8223	0.048053	0.161716	0.119646	SH2D1A/CD48/HCST/LCK	4
hsa05143	African trypanosomiasis	3/86	37/8223	0.006641	0.032282	0.023884	IL1B/VCAM1/IL10	3
hsa05219	Bladder cancer	3/86	41/8223	0.008842	0.041821	0.030941	MMP9/THBS1/MYC	3
hsa04978	Mineral absorption	3/86	60/8223	0.02464	0.090301	0.066809	MT1A/MT1M/MT2A	3
hsa05416	Viral myocarditis	3/86	60/8223	0.02464	0.090301	0.066809	HLA-DQA1/HLA-DQB1/HLA-DRB5	3
hsa04115	p53 signaling pathway	3/86	73/8223	0.040684	0.142393	0.105349	SERPINE1/GADD45B/THBS1	3
hsa04623	Cytosolic DNA-sensing pathway	3/86	75/8223	0.043524	0.149348	0.110495	CXCL10/IL1B/CCL4	3

ICM, ischemic cardiomyopathy; NFD, non-failing donors; DEGs, differentially expressed genes.

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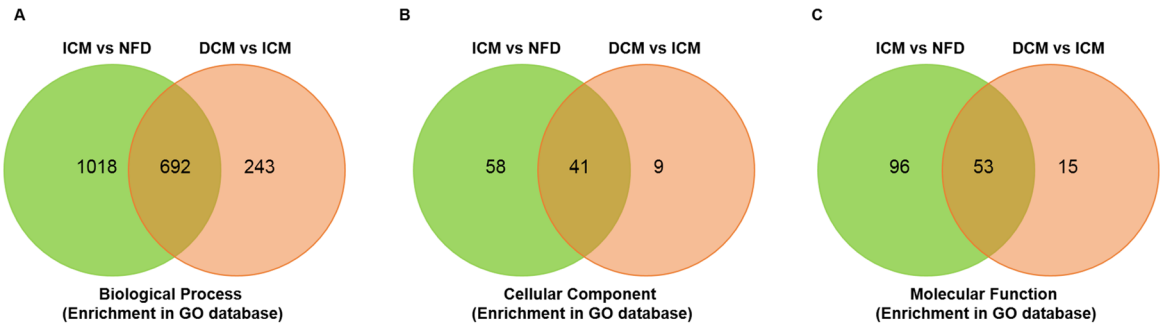

Figure S1 Intersection of enrichment analysis results in biological process (A), cellular component (B) and molecular function (C) of GO database between different comparisons in GSE116250. ICM, ischemic cardiomyopathy; NFD, non-failing donors; DCM, dilated cardiomyopathy; GO, Gene Ontology.

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Table S2 PPI network link scores of 17 T cell-related genes

#node1	node2	node1_string_id	node2_string_id	neighborhood_on_chromosome	gene_fusion	phylogenetic_cooccurrence	homology	coexpression	experimentally_determined_interaction	database_annotated	automated_textmining	combined_score
CD8A	LCK	9606.ENSP00000386559	9606.ENSP00000477713	0	0	0	0	0.471	0.903	0.9	0.998	0.999
IL7R	JAK3	9606.ENSP00000306157	9606.ENSP00000432511	0	0	0	0	0.128	0.295	0.8	0.919	0.988
CD5	CD8A	9606.ENSP00000342681	9606.ENSP00000386559	0	0	0	0	0.342	0	0	0.946	0.963
CD5	LCK	9606.ENSP00000342681	9606.ENSP00000477713	0	0	0	0	0.455	0.51	0	0.854	0.957
CD8A	LAG3	9606.ENSP00000386559	9606.ENSP00000203629	0	0	0	0	0.441	0.064	0	0.907	0.947
CD8A	IL7R	9606.ENSP00000386559	9606.ENSP00000306157	0	0	0	0	0.214	0	0	0.935	0.946
CD8A	IL1B	9606.ENSP00000386559	9606.ENSP00000263341	0	0	0	0	0.06	0	0	0.92	0.922
ITK	LCK	9606.ENSP00000398655	9606.ENSP00000477713	0	0	0.101	0.851	0.559	0	0.5	0.631	0.917
CCL21	CD8A	9606.ENSP00000259607	9606.ENSP00000386559	0	0	0	0	0.108	0	0	0.852	0.862
JAK3	LCK	9606.ENSP00000432511	9606.ENSP00000477713	0	0	0	0.673	0.159	0.045	0.4	0.73	0.852
IL1B	VCAM1	9606.ENSP00000263341	9606.ENSP00000294728	0	0	0	0	0.089	0	0	0.821	0.83
IL7R	LCK	9606.ENSP00000306157	9606.ENSP00000477713	0	0	0	0	0.177	0	0	0.778	0.809
IL7R	ITK	9606.ENSP00000306157	9606.ENSP00000398655	0	0	0	0	0.514	0	0	0.601	0.798
CD8A	TNFRSF4	9606.ENSP00000386559	9606.ENSP00000368538	0	0	0	0	0.08	0	0	0.789	0.797
LAG3	TNFRSF4	9606.ENSP00000203629	9606.ENSP00000368538	0	0	0	0	0.124	0	0	0.778	0.797
CD8A	VCAM1	9606.ENSP00000386559	9606.ENSP00000294728	0	0	0	0	0.101	0	0	0.776	0.79
CD8A	ITK	9606.ENSP00000386559	9606.ENSP00000398655	0	0	0	0	0.487	0.045	0	0.581	0.776
IL1B	IL7R	9606.ENSP00000263341	9606.ENSP00000306157	0	0	0	0	0.195	0	0	0.712	0.758
CD83	IL1B	9606.ENSP00000368450	9606.ENSP00000263341	0	0	0	0	0.223	0	0	0.663	0.727
CD83	CD8A	9606.ENSP00000368450	9606.ENSP00000386559	0	0	0	0	0.06	0	0	0.72	0.726
CD5	IL7R	9606.ENSP00000342681	9606.ENSP00000306157	0	0	0	0	0.208	0	0	0.667	0.725
BCL3	IL1B	9606.ENSP00000164227	9606.ENSP00000263341	0	0	0	0	0.213	0	0	0.657	0.719
IL1B	TNFRSF4	9606.ENSP00000263341	9606.ENSP00000368538	0	0	0	0	0.128	0	0	0.657	0.688
CD5	ITK	9606.ENSP00000342681	9606.ENSP00000398655	0	0	0	0	0.498	0	0	0.4	0.686
IL7R	LAG3	9606.ENSP00000306157	9606.ENSP00000203629	0	0	0	0	0.064	0	0	0.667	0.675
CCL21	VCAM1	9606.ENSP00000259607	9606.ENSP00000294728	0	0	0	0	0.159	0.096	0	0.58	0.653
CD8A	JAK3	9606.ENSP00000386559	9606.ENSP00000432511	0	0	0	0	0.133	0.045	0	0.581	0.623
IL7R	VCAM1	9606.ENSP00000306157	9606.ENSP00000294728	0	0	0	0	0.105	0	0	0.585	0.612
CCL21	LAG3	9606.ENSP00000259607	9606.ENSP00000203629	0	0	0.234	0	0.069	0.099	0	0.459	0.606
CD5	LAG3	9606.ENSP00000342681	9606.ENSP00000203629	0	0	0	0	0.177	0.263	0	0.396	0.602
IL7R	TNFRSF4	9606.ENSP00000306157	9606.ENSP00000368538	0	0	0	0	0.078	0	0	0.583	0.599
CCL21	IL1B	9606.ENSP00000259607	9606.ENSP00000263341	0	0	0	0	0.086	0	0	0.573	0.593
CCL21	GPR183	9606.ENSP00000259607	9606.ENSP00000365596	0	0	0	0	0.135	0	0	0.543	0.588
BCL3	NFKBID	9606.ENSP00000164227	9606.ENSP00000380109	0	0	0.12	0.69	0.085	0	0	0.512	0.572
LAG3	LCK	9606.ENSP00000203629	9606.ENSP00000477713	0	0	0	0	0.188	0.081	0	0.449	0.553
CCL21	CD83	9606.ENSP00000259607	9606.ENSP00000368450	0	0	0	0	0.106	0	0	0.508	0.541
IL1B	JAK3	9606.ENSP00000263341	9606.ENSP00000432511	0	0	0	0	0.111	0	0	0.488	0.526
GPR183	IL7R	9606.ENSP00000365596	9606.ENSP00000306157	0	0	0	0	0.276	0	0	0.359	0.516
CD5	VCAM1	9606.ENSP00000342681	9606.ENSP00000294728	0	0	0	0	0.092	0.095	0	0.431	0.491
IL1B	LAG3	9606.ENSP00000263341	9606.ENSP00000203629	0	0	0	0	0.067	0	0	0.474	0.488
IL1B	LCK	9606.ENSP00000263341	9606.ENSP00000477713	0	0	0	0	0.109	0	0	0.435	0.475
CD83	GPR183	9606.ENSP00000368450	9606.ENSP00000365596	0	0	0	0	0.329	0	0	0.247	0.474
CCL21	IL7R	9606.ENSP00000259607	9606.ENSP00000306157	0	0	0	0	0.115	0	0	0.419	0.464
CD8A	GPR183	9606.ENSP00000386559	9606.ENSP00000365596	0	0	0	0	0.198	0	0	0.356	0.461
BCL3	LCK	9606.ENSP00000164227	9606.ENSP00000477713	0	0	0	0	0	0.331	0	0.2	0.442
CD83	IL7R	9606.ENSP00000368450	9606.ENSP00000306157	0	0	0	0	0.097	0	0	0.399	0.434
CD5	IL1B	9606.ENSP00000342681	9606.ENSP00000263341	0	0	0	0	0.062	0	0	0.418	0.43
CD5	CD83	9606.ENSP00000342681	9606.ENSP00000368450	0	0	0	0	0.11	0	0	0.38	0.425
LCK	TNFRSF4	9606.ENSP00000477713	9606.ENSP00000368538	0	0	0	0	0.062	0.052	0	0.396	0.416
CD83	VCAM1	9606.ENSP00000368450	9606.ENSP00000294728	0	0	0	0	0.123	0	0	0.362	0.416
LCK	VCAM1	9606.ENSP00000477713	9606.ENSP00000294728	0	0	0	0	0.107	0.102	0	0.329	0.416
CD5	TNFRSF4	9606.ENSP00000342681	9606.ENSP00000368538	0	0	0	0	0.151	0	0	0.323	0.401

PPI, protein-protein interaction.

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