



Figure S1 Data preprocessing. (A) Pre-normalization for GSE55235 and GSE55457. (B) Post-normalization for GSE55235 and GSE55457. (C-D) Principal component analysis (PCA) for GSE55235 and GSE55457. (E) Pre-normalization for GSE28829 and GSE41571. (F) Post-normalization for GSE28829 and GSE41571. (G-H) PCA for GSE28829 and GSE41571. HC, healthy controls; RA, rheumatoid arthritis; EAP, early atherosclerotic plaque; AAP, advanced atherosclerotic plaque.

Table S1 Gene Ontology and Kyoto Encyclopedia of Genes and Genomes pathway enrichment analyses of common differentially expressed genes.

ONTOLOGY	ID	Description	GeneRatio	BgRatio	P value	p.adjust	qvalue	geneID	Count
BP	GO:0050900	leukocyte migration	17/60	499/18670	1.85598E-13	3.23684E-10	2.02205E-10	CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/CD300A/IGLV1-44/SLAMF8	17
BP	GO:0051249	regulation of lymphocyte activation	16/60	485/18670	1.75971E-12	1.52661E-09	9.53674E-10	CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	16
BP	GO:0042119	neutrophil activation	16/60	498/18670	2.62606E-12	1.52661E-09	9.53674E-10	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	16
BP	GO:0006909	phagocytosis	14/60	369/18670	8.27003E-12	3.60573E-09	2.25249E-09	CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/IGLL5	14
BP	GO:0050864	regulation of B cell activation	11/60	184/18670	1.42121E-11	4.9572E-09	3.09675E-09	FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	11
BP	GO:0043312	neutrophil degranulation	15/60	485/18670	2.43026E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002283	neutrophil activation involved in immune response	15/60	488/18670	2.65098E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002446	neutrophil mediated immunity	15/60	499/18670	3.62817E-11	7.9094E-09	4.94099E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0030595	leukocyte chemotaxis	11/60	224/18670	1.18654E-10	2.29925E-08	1.43634E-08	NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8	11
BP	GO:0002697	regulation of immune effector process	14/60	458/18670	1.45234E-10	2.45605E-08	1.53429E-08	CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/SLAMF8	14
CC	GO:0009897	external side of plasma membrane	11/63	393/19717	4.17226E-08	6.67562E-06	3.90875E-06	CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5	11
CC	GO:0070820	tertiary granule	7/63	164/19717	9.06323E-07	7.25059E-05	4.24541E-05	CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A	7
CC	GO:0101002	ficolin-1-rich granule	7/63	185/19717	2.02926E-06	0.000108227	6.33699E-05	ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A	7
CC	GO:0030667	secretory granule membrane	8/63	298/19717	4.66784E-06	0.000186714	0.000109326	CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A	8
CC	GO:0030666	endocytic vesicle membrane	6/63	167/19717	1.5378E-05	0.000450681	0.000263885	CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A	6
CC	GO:0042613	MHC class II protein complex	3/63	16/19717	1.69005E-05	0.000450681	0.000263885	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042611	MHC protein complex	3/63	25/19717	6.80025E-05	0.001552276	0.000908899	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042571	immunoglobulin complex, circulating	4/63	72/19717	8.27284E-05	0.001552276	0.000908899	IGHM/IGKC/IGLC1/IGLL5	4
CC	GO:0070821	tertiary granule membrane	4/63	73/19717	8.73155E-05	0.001552276	0.000908899	CYBA/ITGB2/VAMP8/CD300A	4
CC	GO:0030670	phagocytic vesicle membrane	4/63	76/19717	0.000102188	0.001635005	0.000957338	CYBA/RAC2/VAMP8/CORO1A	4
MF	GO:0003823	antigen binding	7/59	160/17697	9.95363E-07	0.000230924	0.000183356	CD48/HLA-DRA/IGHM/IGKC/IGLC1/IGLV1-44/IGLL5	7
MF	GO:0023026	MHC class II protein complex binding	3/59	16/17697	1.91121E-05	0.002217009	0.001760329	HLA-DMA/HLA-DMB/HLA-DRA	3
MF	GO:0023023	MHC protein complex binding	3/59	25/17697	7.68384E-05	0.00594217	0.004718148	HLA-DMA/HLA-DMB/HLA-DRA	3
MF	GO:0034987	immunoglobulin receptor binding	4/59	76/17697	0.000119512	0.006931719	0.00550386	IGHM/IGKC/IGLC1/IGLL5	4
MF	GO:0048020	CCR chemokine receptor binding	3/59	43/17697	0.000395083	0.018331851	0.014555689	CCL13/CCL18/CCL19	3
MF	GO:0008009	chemokine activity	3/59	49/17697	0.000581514	0.019537216	0.015512762	CCL13/CCL18/CCL19	3
MF	GO:0019864	IgG binding	2/59	11/17697	0.000589485	0.019537216	0.015512762	FCGR1B/FCGR2B	2
MF	GO:0005178	integrin binding	4/59	132/17697	0.000979876	0.02841641	0.022562939	ITGB2/LCP1/SPP1/ITGBL1	4
MF	GO:0042379	chemokine receptor binding	3/59	66/17697	0.00138748	0.033384871	0.026507951	CCL13/CCL18/CCL19	3
MF	GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	2/59	17/17697	0.001439003	0.033384871	0.026507951	CYBA/KMO	2
KEGG	hsa04145	Phagosome	9/42	152/8076	6.13591E-08	7.42445E-06	5.29626E-06	CD14/CTSS/CYBA/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A	9
KEGG	hsa05416	Viral myocarditis	6/42	60/8076	5.55121E-07	3.35848E-05	2.39578E-05	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/RAC2	6
KEGG	hsa05152	Tuberculosis	8/42	180/8076	3.21921E-06	0.000129841	9.26229E-05	CD14/CTSS/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A	8
KEGG	hsa04672	Intestinal immune network for IgA production	5/42	49/8076	4.7939E-06	0.000145016	0.000103447	CD86/HLA-DMA/HLA-DMB/HLA-DRA/CXCR4	5
KEGG	hsa04640	Hematopoietic cell lineage	6/42	99/8076	1.06974E-05	0.000258877	0.000184671	CD14/CD37/CSF1R/HLA-DMA/HLA-DMB/HLA-DRA	6
KEGG	hsa05330	Allograft rejection	4/42	38/8076	4.10371E-05	0.000771375	0.000550263	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa05140	Leishmaniasis	5/42	77/8076	4.4625E-05	0.000771375	0.000550263	CYBA/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05332	Graft-versus-host disease	4/42	42/8076	6.12967E-05	0.000905209	0.000645734	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04940	Type I diabetes mellitus	4/42	43/8076	6.73296E-05	0.000905209	0.000645734	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04514	Cell adhesion molecules	6/42	149/8076	0.000108131	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/PTPRC	6
KEGG	hsa05323	Rheumatoid arthritis	5/42	93/8076	0.000110414	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05150	Staphylococcus aureus infection	5/42	96/8076	0.000128378	0.001294476	0.000923419	FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05320	Autoimmune thyroid disease	4/42	53/8076	0.000153857	0.001345905	0.000960106	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04061	Viral protein interaction with cytokine and cytokine receptor	5/42	100/8076	0.000155725	0.001345905	0.000960106	CSF1R/CCL13/CCL18/CCL19/CXCR4	5
KEGG	hsa04670	Leukocyte transendothelial migration	5/42	114/8076	0.00028782	0.002321749	0.001656228	CYBA/ITGB2/MMP9/RAC2/CXCR4	5
KEGG	hsa04062	Chemokine signaling pathway	6/42	192/8076	0.000429397	0.003247314	0.002316483	DOCK2/RAC2/CCL13/CCL18/CCL19/CXCR4	6
KEGG	hsa05310	Asthma	3/42	31/8076	0.000531305	0.003781638	0.002697645	HLA-DMA/HLA-DMB/HLA-DRA	3
KEGG	hsa04612	Antigen processing and presentation	4/42	78/8076	0.000682249	0.00458623	0.003271604	CTSS/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04064	NF-kappa B signaling pathway	4/42	104/8076	0.001994807	0.012068582	0.008609167	BCL2A1/CD14/CCL13/CCL19	4
KEGG	hsa04620	Toll-like receptor signaling pathway	4/42	104/8076	0.001994807	0.012068582	0.008609167	CD14/CD86/SPP1/TLR8	4
KEGG	hsa05145	Toxoplasmosis	4/42	112/8076	0.002614852	0.015066527	0.010747762	ALOX5/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa05202	Transcriptional misregulation in cancer	5/42	192/8076	0.003002662	0.016514642	0.01178078	BCL2A1/CD14/CD86/CSF1R/MMP9	5
KEGG	hsa04060	Cytokine-cytokine receptor interaction	6/42	295/8076	0.00390778	0.02055832	0.014665353	CSF1R/CSF2RB/CCL13/CCL18/CCL19/CXCR4	6
KEGG	hsa05321	Inflammatory bowel disease	3/42	65/8076	0.004567287	0.023026738	0.016426207	HLA-DMA/HLA-DMB/HLA-DRA	3
KEGG	hsa05221	Acute myeloid leukemia	3/42	67/8076	0.004973176	0.023513674	0.016773565	BCL2A1/CD14/CSF1R	3
KEGG	hsa04210	Apoptosis	4/42	136/8076	0.005246853	0.023513674	0.016773565	BCL2A1/CTSC/CSF2RB/CTSS	4
KEGG	hsa05322	Systemic lupus erythematosus	4/42	136/8076	0.005246853	0.023513674	0.016773565	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04662	B cell receptor signaling pathway	3/42	82/8076	0.008711718	0.037647067	0.026855672	CD72/FCGR2B/RAC2	3
KEGG	hsa04658	Th1 and Th2 cell differentiation	3/42	92/8076	0.011918685	0.049729685	0.035474852	HLA-DMA/HLA-DMB/HLA-DRA	3
ONTOLOGY	ID	Description	GeneRatio	BgRatio	P value	p.adjust	qvalue	geneID	Count
BP	GO:0050900	leukocyte migration	17/60	499/18670	1.85598E-13	3.23684E-10	2.02205E-10	CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/CD300A/IGLV1-44/SLAMF8	17
BP	GO:0051249	regulation of lymphocyte activation	16/60	485/18670	1.75971E-12	1.52661E-09	9.53674E-10	CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	16
BP	GO:0042119	neutrophil activation	16/60	498/18670	2.62606E-12	1.52661E-09	9.53674E-10	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	16
BP	GO:0006909	phagocytosis	14/60	369/18670	8.27003E-12	3.60573E-09	2.25249E-09	CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/IGLL5	14
BP	GO:0050864	regulation of B cell activation	11/60	184/18670	1.42121E-11	4.9572E-09	3.09675E-09	FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	11
BP	GO:0043312	neutrophil degranulation	15/60	485/18670	2.43026E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002283	neutrophil activation involved in immune response	15/60	488/18670	2.65098E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002446	neutrophil mediated immunity	15/60	499/18670	3.62817E-11	7.9094E-09	4.94099E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0030595	leukocyte chemotaxis	11/60	224/18670	1.18654E-10	2.29925E-08	1.43634E-08	NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8	11
BP	GO:0002697	regulation of immune effector process	14/60	458/18670	1.45234E-10	2.45605E-08	1.53429E-08	CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/SLAMF8	14
CC	GO:0009897	external side of plasma membrane	11/63	393/19717	4.17226E-08	6.67562E-06	3.90875E-06	CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5	11
CC	GO:0070820	tertiary granule	7/63	164/19717	9.06323E-07	7.25059E-05	4.24541E-05	CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A	7
CC	GO:0101002	ficolin-1-rich granule	7/63	185/19717	2.02926E-06	0.000108227	6.33699E-05	ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A	7
CC	GO:0030667	secretory granule membrane	8/63	298/19717	4.66784E-06	0.000186714	0.000109326	CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A	8
CC	GO:0030666	endocytic vesicle membrane	6/63	167/19717	1.5378E-05	0.000450681	0.000263885	CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A	6
CC	GO:0042613	MHC class II protein complex	3/63	16/19717	1.69005E-05	0.000450681	0.000263885	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042611	MHC protein complex	3/63	25/19717	6.80025E-05	0.001552276	0.000908899	HLA-DMA/HLA-DMB/HLA-DRA	

Table S1 (continued)

ONTOLOGY	ID	Description	GeneRatio	BgRatio	P value	p.adjust	qvalue	geneID	Count
KEGG	hsa05321	Inflammatory bowel disease	3/42	65/8076	0.004567287	0.023026738	0.016426207	HLA-DMA/HLA-DMB/HLA-DRA	3
KEGG	hsa05221	Acute myeloid leukemia	3/42	67/8076	0.004973176	0.023513674	0.016773565	BCL2A1/CD14/CSF1R	3
KEGG	hsa04210	Apoptosis	4/42	136/8076	0.005246853	0.023513674	0.016773565	BCL2A1/CTSC/CSF2RB/CTSS	4
KEGG	hsa05322	Systemic lupus erythematosus	4/42	136/8076	0.005246853	0.023513674	0.016773565	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04662	B cell receptor signaling pathway	3/42	82/8076	0.008711718	0.037647067	0.026855672	CD72/FCGR2B/RAC2	3
KEGG	hsa04658	Th1 and Th2 cell differentiation	3/42	92/8076	0.011918685	0.049729685	0.035474852	HLA-DMA/HLA-DMB/HLA-DRA	3
ONTOLOGY	ID	Description	GeneRatio	BgRatio	P value	p.adjust	qvalue	geneID	Count
BP	GO:0050900	leukocyte migration	17/60	499/18670	1.85598E-13	3.23684E-10	2.02205E-10	CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/CD300A/IGLV1-44/SLAMF8	17
BP	GO:0051249	regulation of lymphocyte activation	16/60	485/18670	1.75971E-12	1.52661E-09	9.53674E-10	CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	16
BP	GO:0042119	neutrophil activation	16/60	498/18670	2.62606E-12	1.52661E-09	9.53674E-10	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	16
BP	GO:0006909	phagocytosis	14/60	369/18670	8.27003E-12	3.60573E-09	2.25249E-09	CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/IGLL5	14
BP	GO:0050864	regulation of B cell activation	11/60	184/18670	1.42121E-11	4.9572E-09	3.09675E-09	FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	11
BP	GO:0043312	neutrophil degranulation	15/60	485/18670	2.43026E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002283	neutrophil activation involved in immune response	15/60	488/18670	2.65098E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002446	neutrophil mediated immunity	15/60	499/18670	3.62817E-11	7.9094E-09	4.94099E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0030595	leukocyte chemotaxis	11/60	224/18670	1.18654E-10	2.29925E-08	1.43634E-08	NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8	11
BP	GO:0002697	regulation of immune effector process	14/60	458/18670	1.45234E-10	2.45605E-08	1.53429E-08	CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/SLAMF8	14
CC	GO:0009897	external side of plasma membrane	11/63	393/19717	4.17226E-08	6.67562E-06	3.90875E-06	CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5	11
CC	GO:0070820	tertiary granule	7/63	164/19717	9.06323E-07	7.25059E-05	4.24541E-05	CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A	7
CC	GO:0101002	ficolin-1-rich granule	7/63	185/19717	2.02926E-06	0.000108227	6.33699E-05	ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A	7
CC	GO:0030667	secretory granule membrane	8/63	298/19717	4.66784E-06	0.000186714	0.000109326	CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A	8
CC	GO:0030666	endocytic vesicle membrane	6/63	167/19717	1.5378E-05	0.000450681	0.000263885	CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A	6
CC	GO:0042613	MHC class II protein complex	3/63	16/19717	1.69005E-05	0.000450681	0.000263885	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042611	MHC protein complex	3/63	25/19717	6.80025E-05	0.001552276	0.000908899	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042571	immunoglobulin complex, circulating	4/63	72/19717	8.27284E-05	0.001552276	0.000908899	IGHM/IGKC/IGLC1/IGLL5	4
CC	GO:0070821	tertiary granule membrane	4/63	73/19717	8.73155E-05	0.001552276	0.000908899	CYBA/ITGB2/VAMP8/CD300A	4
CC	GO:0030670	phagocytic vesicle membrane	4/63	76/19717	0.000102188	0.001635005	0.000957338	CYBA/RAC2/VAMP8/CORO1A	4
MF	GO:0003823	antigen binding	7/59	160/17697	9.95363E-07	0.000230924	0.000183356	CD48/HLA-DRA/IGHM/IGKC/IGLC1/IGLV1-44/IGLL5	7
MF	GO:0023026	MHC class II protein complex binding	3/59	16/17697	1.91121E-05	0.002217009	0.001760329	HLA-DMA/HLA-DMB/HLA-DRA	3
MF	GO:0023023	MHC protein complex binding	3/59	25/17697	7.68384E-05	0.00594217	0.004718148	HLA-DMA/HLA-DMB/HLA-DRA	3
MF	GO:0034987	immunoglobulin receptor binding	4/59	76/17697	0.000119512	0.006931719	0.00550386	IGHM/IGKC/IGLC1/IGLL5	4
MF	GO:0048020	CCR chemokine receptor binding	3/59	43/17697	0.000395083	0.018331851	0.014555689	CCL13/CCL18/CCL19	3
MF	GO:0008009	chemokine activity	3/59	49/17697	0.000581514	0.019537216	0.015512762	CCL13/CCL18/CCL19	3
MF	GO:0019864	IgG binding	2/59	11/17697	0.000589485	0.019537216	0.015512762	FCGR1B/FCGR2B	2
MF	GO:0005178	integrin binding	4/59	132/17697	0.000979876	0.02841641	0.022562939	ITGB2/LCP1/SPP1/ITGBL1	4
MF	GO:0042379	chemokine receptor binding	3/59	66/17697	0.00138748	0.033384871	0.026507951	CCL13/CCL18/CCL19	3
MF	GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	2/59	17/17697	0.001439003	0.033384871	0.026507951	CYBA/KMO	2
KEGG	hsa04145	Phagosome	9/42	152/8076	6.13591E-08	7.42445E-06	5.29626E-06	CD14/CTSS/CYBA/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A	9
KEGG	hsa05416	Viral myocarditis	6/42	60/8076	5.55121E-07	3.35848E-05	2.39578E-05	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/RAC2	6
KEGG	hsa05152	Tuberculosis	8/42	180/8076	3.21921E-06	0.000129841	9.26229E-05	CD14/CTSS/FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/CORO1A	8
KEGG	hsa04672	Intestinal immune network for IgA production	5/42	49/8076	4.7939E-06	0.000145016	0.000103447	CD86/HLA-DMA/HLA-DMB/HLA-DRA/CXCR4	5
KEGG	hsa04640	Hematopoietic cell lineage	6/42	99/8076	1.06974E-05	0.000258877	0.000184671	CD14/CD37/CSF1R/HLA-DMA/HLA-DMB/HLA-DRA	6
KEGG	hsa05330	Allograft rejection	4/42	38/8076	4.10371E-05	0.000771375	0.000550263	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa05140	Leishmaniasis	5/42	77/8076	4.4625E-05	0.000771375	0.000550263	CYBA/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05332	Graft-versus-host disease	4/42	42/8076	6.12967E-05	0.000905209	0.000645734	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04940	Type I diabetes mellitus	4/42	43/8076	6.73296E-05	0.000905209	0.000645734	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04514	Cell adhesion molecules	6/42	149/8076	0.000108131	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2/PTPRC	6
KEGG	hsa05323	Rheumatoid arthritis	5/42	93/8076	0.000110414	0.001214553	0.000866406	CD86/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05150	Staphylococcus aureus infection	5/42	96/8076	0.000128378	0.001294476	0.000923419	FCGR2B/HLA-DMA/HLA-DMB/HLA-DRA/ITGB2	5
KEGG	hsa05320	Autoimmune thyroid disease	4/42	53/8076	0.000153857	0.001345905	0.000960106	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04061	Viral protein interaction with cytokine and cytokine receptor	5/42	100/8076	0.000155725	0.001345905	0.000960106	CSF1R/CCL13/CCL18/CCL19/CXCR4	5
KEGG	hsa04670	Leukocyte transendothelial migration	5/42	114/8076	0.00028782	0.002321749	0.001656228	CYBA/ITGB2/MMP9/RAC2/CXCR4	5
KEGG	hsa04062	Chemokine signaling pathway	6/42	192/8076	0.000429397	0.003247314	0.002316483	DOCK2/RAC2/CCL13/CCL18/CCL19/CXCR4	6
KEGG	hsa05310	Asthma	3/42	31/8076	0.000531305	0.003781638	0.002697645	HLA-DMA/HLA-DMB/HLA-DRA	3
KEGG	hsa04612	Antigen processing and presentation	4/42	78/8076	0.000682249	0.00458623	0.003271604	CTSS/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04064	NF-kappa B signaling pathway	4/42	104/8076	0.001994807	0.012068582	0.008609167	BCL2A1/CD14/CCL13/CCL19	4
KEGG	hsa04620	Toll-like receptor signaling pathway	4/42	104/8076	0.001994807	0.012068582	0.008609167	CD14/CD86/SPP1/TLR8	4
KEGG	hsa05145	Toxoplasmosis	4/42	112/8076	0.002614852	0.015066527	0.010747762	ALOX5/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa05202	Transcriptional misregulation in cancer	5/42	192/8076	0.003002662	0.016514642	0.01178078	BCL2A1/CD14/CD86/CSF1R/MMP9	5
KEGG	hsa04060	Cytokine-cytokine receptor interaction	6/42	295/8076	0.00390778	0.02055832	0.014665353	CSF1R/CSF2RB/CCL13/CCL18/CCL19/CXCR4	6
KEGG	hsa05321	Inflammatory bowel disease	3/42	65/8076	0.004567287	0.023026738	0.016426207	HLA-DMA/HLA-DMB/HLA-DRA	3
KEGG	hsa05221	Acute myeloid leukemia	3/42	67/8076	0.004973176	0.023513674	0.016773565	BCL2A1/CD14/CSF1R	3
KEGG	hsa04210	Apoptosis	4/42	136/8076	0.005246853	0.023513674	0.016773565	BCL2A1/CTSC/CSF2RB/CTSS	4
KEGG	hsa05322	Systemic lupus erythematosus	4/42	136/8076	0.005246853	0.023513674	0.016773565	CD86/HLA-DMA/HLA-DMB/HLA-DRA	4
KEGG	hsa04662	B cell receptor signaling pathway	3/42	82/8076	0.008711718	0.037647067	0.026855672	CD72/FCGR2B/RAC2	3
KEGG	hsa04658	Th1 and Th2 cell differentiation	3/42	92/8076	0.011918685	0.049729685	0.035474852	HLA-DMA/HLA-DMB/HLA-DRA	3
ONTOLOGY	ID	Description	GeneRatio	BgRatio	P value	p.adjust	qvalue	geneID	Count
BP	GO:0050900	leukocyte migration	17/60	499/18670	1.85598E-13	3.23684E-10	2.02205E-10	CD48/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/CD300A/IGLV1-44/SLAMF8	17
BP	GO:0051249	regulation of lymphocyte activation	16/60	485/18670	1.75971E-12	1.52661E-09	9.53674E-10	CD86/FCGR2B/NCKAP1L/HLA-DMB/IGHM/IGKC/IGLC1/PTPRC/RAC2/CCL19/CORO1A/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	16
BP	GO:0042119	neutrophil activation	16/60	498/18670	2.62606E-12	1.52661E-09	9.53674E-10	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/FCGR2B/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	16
BP	GO:0006909	phagocytosis	14/60	369/18670	8.27003E-12	3.60573E-09	2.25249E-09	CD14/CYBA/DOCK2/FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CORO1A/CD300A/IGLV1-44/IGLL5	14
BP	GO:0050864	regulation of B cell activation	11/60	184/18670	1.42121E-11	4.9572E-09	3.09675E-09	FCGR2B/NCKAP1L/IGHM/IGKC/IGLC1/PTPRC/CD300A/MZB1/SLAMF8/SAMSN1/IGLL5	11
BP	GO:0043312	neutrophil degranulation	15/60	485/18670	2.43026E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002283	neutrophil activation involved in immune response	15/60	488/18670	2.65098E-11	6.60473E-09	4.12596E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0002446	neutrophil mediated immunity	15/60	499/18670	3.62817E-11	7.9094E-09	4.94099E-09	ALOX5/CD14/CTSC/CTSS/CYBA/DOCK2/NCKAP1L/ITGB2/MMP9/SERPINA1/PTPRC/S100A9/SLC2A5/VAMP8/CD300A	15
BP	GO:0030595	leukocyte chemotaxis	11/60	224/18670	1.18654E-10	2.29925E-08	1.43634E-08	NCKAP1L/ITGB2/RAC2/S100A9/CCL13/CCL18/CCL19/CXCR4/PLA2G7/CORO1A/SLAMF8	11
BP	GO:0002697	regulation of immune effector process	14/60	458/18670	1.45234E-10	2.45605E-08	1.53429E-08	CD86/FCGR2B/HLA-DMB/IGKC/IGLC1/ITGB2/PTPRC/RAC2/CCL19/VAMP8/CD300A/IGLV1-44/MZB1/SLAMF8	14
CC	GO:0009897	external side of plasma membrane	11/63	393/19717	4.17226E-08	6.67562E-06	3.90875E-06	CD14/CD86/FCGR2B/IGHM/IGKC/IGLC1/ITGB2/PTPRC/CXCR4/TLR8/IGLL5	11
CC	GO:0070820	tertiary granule	7/63	164/19717	9.06323E-07	7.25059E-05	4.24541E-05	CTSS/CYBA/NCKAP1L/ITGB2/MMP9/VAMP8/CD300A	7
CC	GO:0101002	ficolin-1-rich granule	7/63	185/19717	2.02926E-06	0.000108227	6.33699E-05	ALOX5/CTSS/NCKAP1L/ITGB2/MMP9/SERPINA1/CD300A	7
CC	GO:0030667	secretory granule membrane	8/63	298/19717	4.66784E-06	0.000186714	0.000109326	CD14/CYBA/NCKAP1L/ITGB2/PTPRC/SLC2A5/VAMP8/CD300A	8
CC	GO:0030666	endocytic vesicle membrane	6/63	167/19717	1.5378E-05	0.000450681	0.000263885	CYBA/FCGR1B/HLA-DRA/RAC2/VAMP8/CORO1A	6
CC	GO:0042613	MHC class II protein complex	3/63	16/19717	1.69005E-05	0.000450681	0.000263885	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042611	MHC protein complex	3/63	25/19717	6.80025E-05	0.001552276	0.000908899	HLA-DMA/HLA-DMB/HLA-DRA	3
CC	GO:0042571	immunoglobulin complex, circulating	4/63	72/19717	8.27284E-05</				

Table S2 Detail information of two key functional modules.

Cluster	Score	Nodes	Edges	Node IDs
Module 1	6.571	15	46	DOCK2, TLR8, CD52, HLA-DRA, CSF1R, CD300A, EVI2B, MMP9, CD86, LCP1, NCKAP1L, CD14, CTSS, RAC2, S100A9
Module 2	5.429	8	19	CD48, FCGR2B, CYTIP, CSF2RB, ITGB2, PTPRC, CCL19, CORO1A

Table S3 Gene Ontology and Kyoto Encyclopedia of Genes and Genomes pathway enrichment analyses of hub genes.

ONTOLOGY	ID	Description	P value	p.adjust	geneID	Count
BP	GO:0070661	leukocyte proliferation	2.48847E-09	2.22718E-06	CD86/CSF1R/DOCK2/NCKAP1L/PTPRC/RAC2/CD300A	7
BP	GO:0007159	leukocyte cell-cell adhesion	5.83685E-09	2.61199E-06	CD86/NCKAP1L/ITGB2/PTPRC/RAC2/S100A9/CD300A	7
BP	GO:0042110	T cell activation	5.27508E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/LCP1/PTPRC/RAC2/CD300A	7
BP	GO:0046651	lymphocyte proliferation	6.41178E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/PTPRC/RAC2/CD300A	6
BP	GO:0032943	mononuclear cell proliferation	6.69642E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/PTPRC/RAC2/CD300A	6
BP	GO:0043312	neutrophil degranulation	7.14053E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
BP	GO:0002283	neutrophil activation involved in immune response	7.44788E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
BP	GO:0046631	alpha-beta T cell activation	8.39338E-08	7.60517E-06	CD86/DOCK2/NCKAP1L/PTPRC/CD300A	5
BP	GO:0042119	neutrophil activation	8.55476E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
BP	GO:0002446	neutrophil mediated immunity	8.67274E-08	7.60517E-06	DOCK2/NCKAP1L/ITGB2/MMP9/PTPRC/S100A9/CD300A	7
CC	GO:0070820	tertiary granule	7.76795E-06	0.000419077	NCKAP1L/ITGB2/MMP9/CD300A	4
CC	GO:0101002	ficolin-1-rich granule	1.25022E-05	0.000419077	NCKAP1L/ITGB2/MMP9/CD300A	4
CC	GO:0101003	ficolin-1-rich granule membrane	1.53321E-05	0.000419077	NCKAP1L/ITGB2/CD300A	3
CC	GO:0030667	secretory granule membrane	8.06369E-05	0.001653057	NCKAP1L/ITGB2/PTPRC/CD300A	4
CC	GO:0009897	external side of plasma membrane	0.00023395	0.002871573	CD86/ITGB2/PTPRC/TLR8	4
CC	GO:0005925	focal adhesion	0.000262428	0.002871573	ITGB2/LCP1/PTPRC/RAC2	4
CC	GO:0005924	cell-substrate adherens junction	0.000269922	0.002871573	ITGB2/LCP1/PTPRC/RAC2	4
CC	GO:0030055	cell-substrate junction	0.000280154	0.002871573	ITGB2/LCP1/PTPRC/RAC2	4
CC	GO:0070821	tertiary granule membrane	0.00156887	0.014294145	ITGB2/CD300A	2
CC	GO:0005884	actin filament	0.003579709	0.029353613	LCP1/RAC2	2
MF	GO:0048365	Rac GTPase binding	0.001322735	0.074331524	DOCK2/NCKAP1L	2
MF	GO:0005178	integrin binding	0.004738111	0.074331524	ITGB2/LCP1	2
MF	GO:0032395	MHC class II receptor activity	0.00788484	0.074331524	HLA-DRA	1
MF	GO:0017048	Rho GTPase binding	0.008364282	0.074331524	DOCK2/NCKAP1L	2
MF	GO:0019887	protein kinase regulator activity	0.008639343	0.074331524	NCKAP1L/RAC2	2
MF	GO:0008429	phosphatidylethanolamine binding	0.008670141	0.074331524	CD300A	1
MF	GO:0050786	RAGE receptor binding	0.008670141	0.074331524	S100A9	1
MF	GO:0035325	Toll-like receptor binding	0.009454864	0.074331524	S100A9	1
MF	GO:0036041	long-chain fatty acid binding	0.011022581	0.074331524	S100A9	1
MF	GO:0019207	kinase regulator activity	0.011295508	0.074331524	NCKAP1L/RAC2	2
KEGG	hsa05416	Viral myocarditis	1.30353E-06	0.000102979	CD86/HLA-DRA/ITGB2/RAC2	4
KEGG	hsa04514	Cell adhesion molecules	4.90976E-05	0.001939354	CD86/HLA-DRA/ITGB2/PTPRC	4
KEGG	hsa05323	Rheumatoid arthritis	0.000301683	0.00794431	CD86/HLA-DRA/ITGB2	3
KEGG	hsa04670	Leukocyte transendothelial migration	0.00054926	0.010847895	ITGB2/MMP9/RAC2	3
KEGG	hsa05330	Allograft rejection	0.001381269	0.019940988	CD86/HLA-DRA	2
KEGG	hsa05332	Graft-versus-host disease	0.001686132	0.019940988	CD86/HLA-DRA	2
KEGG	hsa04940	Type I diabetes mellitus	0.001766923	0.019940988	CD86/HLA-DRA	2
KEGG	hsa04672	Intestinal immune network for IgA production	0.002289738	0.021126162	CD86/HLA-DRA	2
KEGG	hsa05202	Transcriptional misregulation in cancer	0.002484004	0.021126162	CD86/CSF1R/MMP9	3
KEGG	hsa05320	Autoimmune thyroid disease	0.002674198	0.021126162	CD86/HLA-DRA	2
KEGG	hsa04015	Rap1 signaling pathway	0.003205535	0.023021569	CSF1R/ITGB2/RAC2	3
KEGG	hsa04810	Regulation of actin cytoskeleton	0.003563773	0.023461508	NCKAP1L/ITGB2/RAC2	3
KEGG	hsa05140	Leishmaniasis	0.005566922	0.033829758	HLA-DRA/ITGB2	2
KEGG	hsa04657	IL-17 signaling pathway	0.00820029	0.042117858	MMP9/S100A9	2
KEGG	hsa05150	Staphylococcus aureus infection	0.008540762	0.042117858	HLA-DRA/ITGB2	2
KEGG	hsa04666	Fc gamma R-mediated phagocytosis	0.008713375	0.042117858	PTPRC/RAC2	2
KEGG	hsa04640	Hematopoietic cell lineage	0.009063336	0.042117858	CSF1R/HLA-DRA	2
KEGG	hsa04620	Toll-like receptor signaling pathway	0.009965657	0.043738161	CD86/TLR8	2