

Figure S1 Clusters characterized by different immune signatures in Liu_Data. (A) Cluster 1 (LIG) and cluster 2 (HIG) divided by K-means clustering based on signatures of 29 immune-related hallmarks. (B) The infiltration levels of 22 immune cells between HIG and LIG samples. (C) Estimation of StromaScore, ImmuneScore, ESTIMATEScore, and TumorPurity. (D) Expression profiles of HLA genes. (E) Landscapes of 29 immune-related hallmarks in two groups. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. LIG, low-immune-infiltration group; HIG, high-immune-infiltration group.

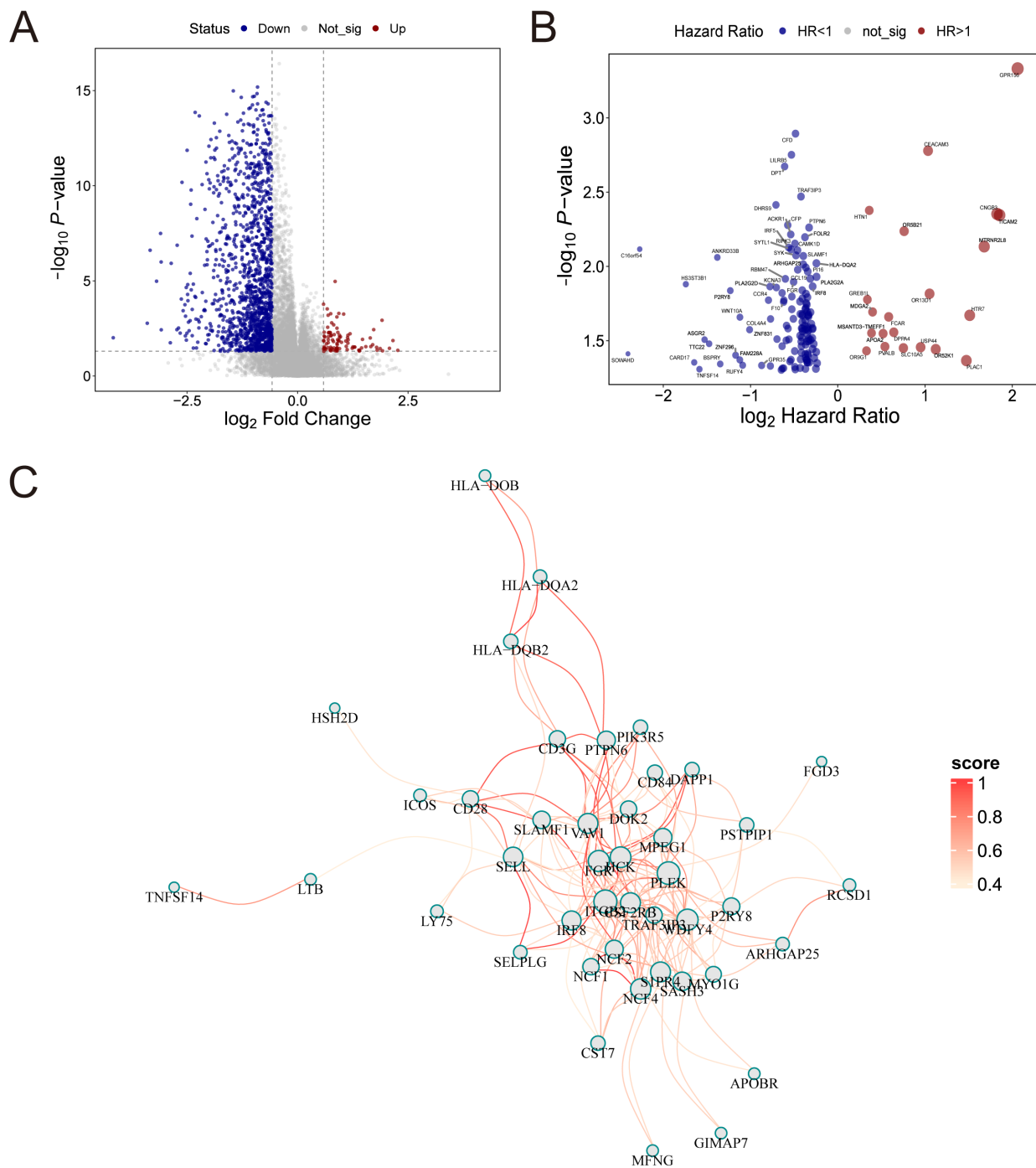


Figure S2 DEGs between the HIG and LIG clusters based on the Liu_Data cohort. (A) The volcano plots and (B) hazard ratios of DEGs. (C) Protein-protein interaction network with 59 hub DEGs. DEGs, differentially expressed genes.

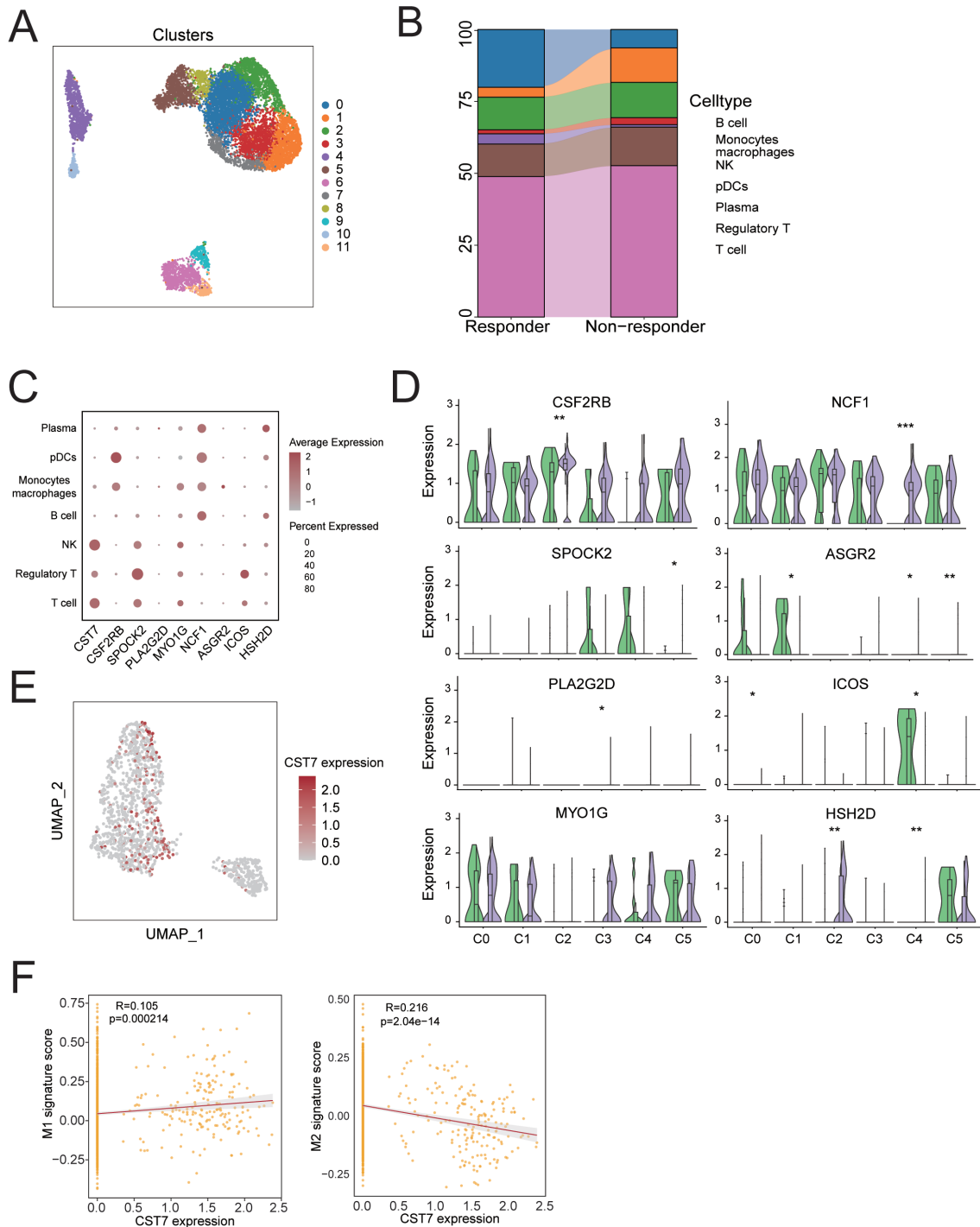


Figure S3 The correlation between immune cells and therapeutic response. (A) UMAP plot of 11 immune cell clusters. (B) Box plots presenting the different proportions of seven cell clusters between responder and non-responder groups. (C) Dot plot indicating the expression of prognostic genes in seven main cell types. (D) Violin plots suggesting the differential expression of eight prognostic genes across six monocytes/macrophages subpopulations between responders and non-responders. (E) UMAP plot visualizing CST7 expression levels in monocytes/macrophages. (F) Dot plot showing the correlation between CST7 expression and M1/M2 scores. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. UMAP, uniform manifold approximation and projection.

Table S1 The 59 prognostic DEGs between HIG and LIG clusters shared by two cohorts of TCGA-SKCM and Liu_Data

Gene names
<i>FGR</i>
<i>TRAF3IP3</i>
<i>LY75</i>
<i>CD84</i>
<i>DAPP1</i>
<i>CST7</i>
<i>MFNG</i>
<i>NCF4</i>
<i>CSF2RB</i>
<i>HCK</i>
<i>SPOCK2</i>
<i>SELPLG</i>
<i>PTPN6</i>
<i>PLEK</i>
<i>NCF2</i>
<i>SLAMF1</i>
<i>PLA2G2D</i>
<i>SASH3</i>
<i>LAX1</i>
<i>ZNF831</i>
<i>HS3ST3B1</i>
<i>TNFSF14</i>
<i>S1PR4</i>
<i>FGD3</i>
<i>WDFY4</i>
<i>ADAMDEC1</i>
<i>MYO1G</i>
<i>PSTPIP1</i>
<i>IRF8</i>
<i>PIK3R5</i>
<i>VAV1</i>
<i>FGD2</i>
<i>DOK2</i>
<i>NCF1</i>

Table S1 (continued)

Table S1 (continued)

Gene names
<i>ITGB2</i>
<i>CD3G</i>
<i>ASGR2</i>
<i>ARHGAP25</i>
<i>ICOS</i>
<i>CCDC88B</i>
<i>KCNA3</i>
<i>CD28</i>
<i>GIMAP7</i>
<i>CAMK1D</i>
<i>CCR4</i>
<i>APOBR</i>
<i>C16orf54</i>
<i>RUFY4</i>
<i>SELL</i>
<i>HSH2D</i>
<i>MPEG1</i>
<i>CCDC69</i>
<i>RCSD1</i>
<i>LTB</i>
<i>HLA-DQB2</i>
<i>HLA-DQA2</i>
<i>HLA-DOB</i>
<i>SLC10A5</i>
<i>P2RY8</i>

HIG, high-immune-infiltration group; LIG, low-immune-infiltration group.

Table S2 GO terms enriched by the 59 DEGs

Ontology	ID	Description	Gene ratio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	Gene name	Rich factor
BP	GO:0007159	Leukocyte cell-cell adhesion	12/56	366/18862	6.17009E-10	4.85996E-07	3.43954E-07	283234/940/29851/3689/54900/26279/5777/54440/6402/6404/8740/7409	12	CCDC88B/CD28/ICOS/ITGB2/LAX1/PLA2G2D/PTPN6/SASH3/SELL/SELPLG/TNFSF14/VAV1	0.214285714
BP	GO:0006909	Phagocytosis	12/56	381/18862	9.7394E-10	4.85996E-07	3.43954E-07	9938/57118/917/2268/3055/3394/3689/64005/4688/4689/6504/7409	12	ARHGAP25/CAMK1D/CD3G/FGR/HCK/IRF8/ITGB2/MYO1G/NCF2/NCF4/SLAMF1/VAV1	0.214285714
BP	GO:1903037	Regulation of leukocyte cell-cell adhesion	10/56	330/18862	4.09229E-08	1.36137E-05	9.63483E-06	283234/940/29851/3689/54900/26279/5777/54440/8740/7409	10	CCDC88B/CD28/ICOS/ITGB2/LAX1/PLA2G2D/PTPN6/SASH3/TNFSF14/VAV1	0.178571429
BP	GO:0045730	Respiratory burst	5/56	36/18862	6.75272E-08	1.6848E-05	1.19239E-05	57118/3055/653361/4688/4689	5	CAMK1D/HCK/NCF1/NCF2/NCF4	0.089285714
BP	GO:0042110	T cell activation	11/56	474/18862	1.20685E-07	2.40887E-05	1.70483E-05	283234/940/917/29851/54900/26279/5777/54440/8740/7409/57705	11	CCDC88B/CD28/CD3G/ICOS/LAX1/PLA2G2D/PTPN6/SASH3/TNFSF14/VAV1/WDFY4	0.196428571
BP	GO:0050867	Positive regulation of cell activation	10/56	412/18862	3.22022E-07	5.3563E-05	3.79082E-05	283234/940/2268/29851/3689/5341/5777/54440/8740/7409	10	CCDC88B/CD28/FGR/ICOS/ITGB2/PLEK/PTPN6/SASH3/TNFSF14/VAV1	0.178571429
BP	GO:1903039	Positive regulation of leukocyte cell-cell adhesion	8/56	234/18862	4.23401E-07	5.85191E-05	4.14158E-05	283234/940/29851/3689/5777/54440/8740/7409	8	CCDC88B/CD28/ICOS/ITGB2/PTPN6/SASH3/TNFSF14/VAV1	0.142857143
BP	GO:0050863	Regulation of T cell activation	9/56	327/18862	4.69091E-07	5.85191E-05	4.14158E-05	283234/940/29851/54900/26279/5777/54440/8740/7409	9	CCDC88B/CD28/ICOS/LAX1/PLA2G2D/PTPN6/SASH3/TNFSF14/VAV1	0.160714286
BP	GO:0022407	Regulation of cell-cell adhesion	10/56	437/18862	5.52185E-07	6.12312E-05	4.33352E-05	283234/940/29851/3689/54900/26279/5777/54440/8740/7409	10	CCDC88B/CD28/ICOS/ITGB2/LAX1/PLA2G2D/PTPN6/SASH3/TNFSF14/VAV1	0.178571429
BP	GO:0031295	T cell costimulation	5/56	57/18862	7.15318E-07	7.13887E-05	5.0524E-05	940/29851/5777/8740/7409	5	CD28/ICOS/PTPN6/TNFSF14/VAV1	0.089285714
BP	GO:0031294	Lymphocyte costimulation	5/56	59/18862	8.51435E-07	7.72484E-05	5.46711E-05	940/29851/5777/8740/7409	5	CD28/ICOS/PTPN6/TNFSF14/VAV1	0.089285714
BP	GO:0002429	Immune response-activating cell surface receptor signaling pathway	10/56	481/18862	1.31792E-06	0.000101176	7.16054E-05	940/917/2268/3055/3118/3120/54900/64005/5777/7409	10	CD28/CD3G/FGR/HCK/HLA-DQA2/HLA-DQB2/LAX1/MYO1G/PTPN6/VAV1	0.178571429
BP	GO:0002757	Immune response-activating signal transduction	10/56	481/18862	1.31792E-06	0.000101176	7.16054E-05	940/917/2268/3055/3118/3120/54900/64005/5777/7409	10	CD28/CD3G/FGR/HCK/HLA-DQA2/HLA-DQB2/LAX1/MYO1G/PTPN6/VAV1	0.178571429
BP	GO:0022409	Positive regulation of cell-cell adhesion	8/56	276/18862	1.46845E-06	0.00010468	7.40851E-05	283234/940/29851/3689/5777/54440/8740/7409	8	CCDC88B/CD28/ICOS/ITGB2/PTPN6/SASH3/TNFSF14/VAV1	0.142857143
BP	GO:0002696	Positive regulation of leukocyte activation	9/56	401/18862	2.53978E-06	0.00016898	0.000119592	283234/940/2268/29851/3689/5777/54440/8740/7409	9	CCDC88B/CD28/FGR/ICOS/ITGB2/PTPN6/SASH3/TNFSF14/VAV1	0.160714286
BP	GO:0002703	Regulation of leukocyte mediated immunity	7/56	209/18862	2.7147E-06	0.00016933	0.00011984	940/8832/2268/3689/5777/54440/7409	7	CD28/CD84/FGR/ITGB2/PTPN6/SASH3/VAV1	0.125
BP	GO:0050870	Positive regulation of T cell activation	7/56	212/18862	2.98338E-06	0.000175142	0.000123953	283234/940/29851/5777/54440/8740/7409	7	CCDC88B/CD28/ICOS/PTPN6/SASH3/TNFSF14/VAV1	0.125
BP	GO:0045785	Positive regulation of cell adhesion	9/56	425/18862	4.07938E-06	0.000226179	0.000160074	283234/940/29851/3689/5777/54440/9806/8740/7409	9	CCDC88B/CD28/ICOS/ITGB2/PTPN6/SASH3/SPOCK2/TNFSF14/VAV1	0.160714286
BP	GO:0019882	Antigen processing and presentation	7/56	234/18862	5.71744E-06	0.000300316	0.000212543	3112/3118/3120/653361/4688/4689/57705	7	HLA-DOB/HLA-DQA2/HLA-DQB2/NCF1/NCF2/NCF4/WDFY4	0.125
BP	GO:0014068	Positive regulation of phosphatidylinositol 3-kinase signaling	5/56	90/18862	6.97019E-06	0.000347812	0.000246158	940/2268/653361/23533/5777	5	CD28/FGR/NCF1/PIK3R5/PTPN6	0.089285714
BP	GO:0002478	Antigen processing and presentation of exogenous peptide antigen	6/56	177/18862	1.38033E-05	0.000655983	0.00046426	3112/3118/3120/653361/4688/4689	6	HLA-DOB/HLA-DQA2/HLA-DQB2/NCF1/NCF2/NCF4	0.107142857
BP	GO:0007229	Integrin-mediated signaling pathway	5/56	106/18862	1.55035E-05	0.000701564	0.000496518	2268/3055/3689/5341/7409	5	FGR/HCK/ITGB2/PLEK/VAV1	0.089285714
BP	GO:0002695	Negative regulation of leukocyte activation	6/56	182/18862	1.61683E-05	0.000701564	0.000496518	8832/8530/2268/54900/26279/5777	6	CD84/CST7/FGR/LAX1/PLA2G2D/PTPN6	0.107142857
BP	GO:0019884	Antigen processing and presentation of exogenous antigen	6/56	185/18862	1.77376E-05	0.00073759	0.000522016	3112/3118/3120/653361/4688/4689	6	HLA-DOB/HLA-DQA2/HLA-DQB2/NCF1/NCF2/NCF4	0.107142857
BP	GO:0048002	Antigen processing and presentation of peptide antigen	6/56	194/18862	2.31982E-05	0.000916635	0.000648731	3112/3118/3120/653361/4688/4689	6	HLA-DOB/HLA-DQA2/HLA-DQB2/NCF1/NCF2/NCF4	0.107142857
BP	GO:0042098	T cell proliferation	6/56	195/18862	2.38803E-05	0.000916635	0.000648731	283234/940/26279/5777/54440/8740	6	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3/TNFSF14	0.107142857
BP	GO:1903131	Mononuclear cell differentiation	8/56	411/18862	2.70042E-05	0.000981516	0.00069465	940/917/3394/4242/26279/5777/54440/7409	8	CD28/CD3G/IRF8/MFNG/PLA2G2D/PTPN6/SASH3/VAV1	0.142857143

Table S2 (continued)

Table S2 (continued)

Ontology	ID	Description	Gene ratio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count	Gene name	Rich factor
BP	GO:0050866	Negative regulation of cell activation	6/56	200/18862	2.75375E-05	0.000981516	0.00069465	8832/8530/2268/54900/26279/5777	6	CD84/CST7/FGR/LAX1/PLA2G2D/PTPN6	0.107142857
BP	GO:0014066	Regulation of phosphatidylinositol 3-kinase signaling	5/56	127/18862	3.70975E-05	0.001276667	0.000903537	940/2268/653361/23533/5777	5	CD28/FGR/NCF1/PIK3R5/PTPN6	0.089285714
BP	GO:0002699	Positive regulation of immune effector process	6/56	219/18862	4.57641E-05	0.00152242	0.001077464	940/8832/2268/3689/54440/7409	6	CD28/CD84/FGR/ITGB2/SASH3/VAV1	0.107142857
BP	GO:0006801	Superoxide metabolic process	4/56	70/18862	5.52241E-05	0.001727076	0.001222305	3689/653361/4688/4689	4	ITGB2/NCF1/NCF2/NCF4	0.071428571
BP	GO:0002433	Immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	5/56	139/18862	5.71077E-05	0.001727076	0.001222305	917/2268/3055/64005/7409	5	CD3G/FGR/HCK/MYO1G/VAV1	0.089285714
BP	GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	5/56	139/18862	5.71077E-05	0.001727076	0.001222305	917/2268/3055/64005/7409	5	CD3G/FGR/HCK/MYO1G/VAV1	0.089285714
BP	GO:0038094	Fc-gamma receptor signaling pathway	5/56	140/18862	5.90897E-05	0.001734457	0.00122753	917/2268/3055/64005/7409	5	CD3G/FGR/HCK/MYO1G/VAV1	0.089285714
BP	GO:0002431	Fc receptor mediated stimulatory signaling pathway	5/56	145/18862	6.98103E-05	0.001990592	0.001408804	917/2268/3055/64005/7409	5	CD3G/FGR/HCK/MYO1G/VAV1	0.089285714
BP	GO:0051251	Positive regulation of lymphocyte activation	7/56	356/18862	8.42381E-05	0.002281639	0.001614788	283234/940/29851/5777/54440/8740/7409	7	CCDC88B/CD28/ICOS/PTPN6/SASH3/TNFSF14/VAV1	0.125
BP	GO:0008360	Regulation of cell shape	5/56	151/18862	8.45898E-05	0.002281639	0.001614788	221472/89846/2268/3055/3689	5	FGD2/FGD3/FGR/HCK/ITGB2	0.089285714
BP	GO:0030098	Lymphocyte differentiation	7/56	358/18862	8.72373E-05	0.002291128	0.001621503	940/917/4242/26279/5777/54440/7409	7	CD28/CD3G/MFNG/PLA2G2D/PTPN6/SASH3/VAV1	0.125
BP	GO:0014065	Phosphatidylinositol 3-kinase signaling	5/56	154/18862	9.28279E-05	0.002375442	0.001681174	940/2268/653361/23533/5777	5	CD28/FGR/NCF1/PIK3R5/PTPN6	0.089285714
BP	GO:0042129	Regulation of T cell proliferation	5/56	168/18862	0.000139748	0.003486707	0.002467652	283234/940/26279/5777/54440	5	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3	0.089285714
BP	GO:0042554	Superoxide anion generation	3/56	35/18862	0.000151664	0.003652341	0.002584876	3689/653361/4688	3	ITGB2/NCF1/NCF2	0.053571429
BP	GO:0060333	Interferon-gamma-mediated signaling pathway	4/56	91/18862	0.000153706	0.003652341	0.002584876	3055/3118/3120/3394	4	HCK/HLA-DQA2/HLA-DQB2/IRF8	0.071428571
BP	GO:0002683	Negative regulation of immune system process	7/56	403/18862	0.00018152	0.004164775	0.002947541	8832/8530/2268/3112/54900/26279/5777	7	CD84/CST7/FGR/HLA-DOB/LAX1/PLA2G2D/PTPN6	0.125
BP	GO:0046651	Lymphocyte proliferation	6/56	282/18862	0.000183617	0.004164775	0.002947541	283234/940/26279/5777/54440/8740	6	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3/TNFSF14	0.107142857
BP	GO:0048010	Vascular endothelial growth factor receptor signaling pathway	4/56	96/18862	0.000188958	0.004190669	0.002965868	653361/4688/4689/7409	4	NCF1/NCF2/NCF4/VAV1	0.071428571
BP	GO:0032943	Mononuclear cell proliferation	6/56	285/18862	0.000194435	0.004218391	0.002985487	283234/940/26279/5777/54440/8740	6	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3/TNFSF14	0.107142857
BP	GO:0048015	Phosphatidylinositol-mediated signaling	5/56	192/18862	0.000260116	0.005523307	0.003909017	940/2268/653361/23533/5777	5	CD28/FGR/NCF1/PIK3R5/PTPN6	0.089285714
BP	GO:0043300	Regulation of leukocyte degranulation	3/56	43/18862	0.000281202	0.005710413	0.004041438	8832/2268/3689	3	CD84/FGR/ITGB2	0.053571429
BP	GO:0045454	Cell redox homeostasis	3/56	43/18862	0.000281202	0.005710413	0.004041438	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
BP	GO:0048017	Inositol lipid-mediated signaling	5/56	196/18862	0.000286093	0.005710413	0.004041438	940/2268/653361/23533/5777	5	CD28/FGR/NCF1/PIK3R5/PTPN6	0.089285714
BP	GO:0070661	Leukocyte proliferation	6/56	312/18862	0.000316224	0.006188073	0.004379493	283234/940/26279/5777/54440/8740	6	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3/TNFSF14	0.107142857
BP	GO:0050852	T cell receptor signaling pathway	5/56	204/18862	0.000343919	0.006600592	0.004671445	940/917/3118/3120/5777	5	CD28/CD3G/HLA-DQA2/HLA-DQB2/PTPN6	0.089285714
BP	GO:0050851	Antigen receptor-mediated signaling pathway	6/56	323/18862	0.000380321	0.007161524	0.005068434	940/917/3118/3120/54900/5777	6	CD28/CD3G/HLA-DQA2/HLA-DQB2/LAX1/PTPN6	0.107142857
BP	GO:0002697	Regulation of immune effector process	7/56	465/18862	0.000432057	0.007985051	0.00565127	940/8832/2268/3689/5777/54440/7409	7	CD28/CD84/FGR/ITGB2/PTPN6/SASH3/VAV1	0.125
BP	GO:0002886	Regulation of myeloid leukocyte mediated immunity	3/56	52/18862	0.000494139	0.008836742	0.006254039	8832/2268/3689	3	CD84/FGR/ITGB2	0.053571429
BP	GO:0050670	Regulation of lymphocyte proliferation	5/56	221/18862	0.000495849	0.008836742	0.006254039	283234/940/26279/5777/54440	5	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3	0.089285714
BP	GO:0032944	Regulation of mononuclear cell proliferation	5/56	223/18862	0.000516585	0.008900129	0.006298899	283234/940/26279/5777/54440	5	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3	0.089285714
BP	GO:0002705	Positive regulation of leukocyte mediated immunity	4/56	125/18862	0.000517242	0.008900129	0.006298899	940/3689/54440/7409	4	CD28/ITGB2/SASH3/VAV1	0.071428571
BP	GO:0061756	Leukocyte adhesion to vascular endothelial cell	3/56	54/18862	0.000552275	0.009341867	0.006611531	3689/6402/6404	3	ITGB2/SELL/SELPLG	0.053571429
BP	GO:0038093	Fc receptor signaling pathway	5/56	239/18862	0.00070686	0.011757437	0.008321106	917/2268/3055/64005/7409	5	CD3G/FGR/HCK/MYO1G/VAV1	0.089285714

Table S2 (continued)

Table S2 (continued)

Ontology	ID	Description	Gene ratio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count	Gene name	Rich factor
BP	GO:0070663	Regulation of leukocyte proliferation	5/56	241/18862	0.000733893	0.011918868	0.008435355	283234/940/26279/5777/54440	5	CCDC88B/CD28/PLA2G2D/PTPN6/SASH3	0.089285714
BP	GO:0032615	Interleukin-12 production	3/56	60/18862	0.000752393	0.011918868	0.008435355	3394/4050/6504	3	IRF8/LTB/SLAMF1	0.053571429
BP	GO:0032655	Regulation of interleukin-12 production	3/56	60/18862	0.000752393	0.011918868	0.008435355	3394/4050/6504	3	IRF8/LTB/SLAMF1	0.053571429
BP	GO:0030217	T cell differentiation	5/56	246/18862	0.000804865	0.012550856	0.008882633	940/917/26279/54440/7409	5	CD28/CD3G/PLA2G2D/SASH3/VAV1	0.089285714
BP	GO:0046631	Alpha-beta T cell activation	4/56	149/18862	0.000998518	0.015331092	0.010850293	940/26279/54440/57705	4	CD28/PLA2G2D/SASH3/WDFY4	0.071428571
BP	GO:0051250	Negative regulation of lymphocyte activation	4/56	153/18862	0.001101626	0.016657918	0.011789329	2268/54900/26279/5777	4	FGR/LAX1/PLA2G2D/PTPN6	0.071428571
BP	GO:0045123	Cellular extravasation	3/56	70/18862	0.001178592	0.017530045	0.01240656	3689/6402/6404	3	ITGB2/SELL/SELPLG	0.053571429
BP	GO:0002706	Regulation of lymphocyte mediated immunity	4/56	157/18862	0.001211997	0.017530045	0.01240656	940/5777/54440/7409	4	CD28/PTPN6/SASH3/VAV1	0.071428571
BP	GO:0030168	Platelet activation	4/56	157/18862	0.001211997	0.017530045	0.01240656	23533/5341/5777/7409	4	PIK3R5/PLEK/PTPN6/VAV1	0.071428571
BP	GO:0002479	Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	3/56	75/18862	0.001438711	0.020445422	0.014469864	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
BP	GO:0072593	Reactive oxygen species metabolic process	5/56	281/18862	0.001454534	0.020445422	0.014469864	3689/653361/4688/4689/7409	5	ITGB2/NCF1/NCF2/NCF4/VAV1	0.089285714
BP	GO:0042590	Antigen processing and presentation of exogenous peptide antigen via MHC class I	3/56	80/18862	0.001732297	0.024011557	0.01699373	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
BP	GO:0051897	Positive regulation of protein kinase B signaling	4/56	175/18862	0.001805805	0.024584544	0.01739925	940/29851/23533/7409	4	CD28/ICOS/PIK3R5/VAV1	0.071428571
BP	GO:0001819	Positive regulation of cytokine production	6/56	437/18862	0.001822902	0.024584544	0.01739925	283234/940/2268/3394/4050/54440	6	CCDC88B/CD28/FGR/IRF8/LTB/SASH3	0.107142857
BP	GO:0071346	Cellular response to interferon-gamma	4/56	177/18862	0.001882269	0.025046721	0.017726347	3055/3118/3120/3394	4	HCK/HLA-DQA2/HLA-DQB2/IRF8	0.071428571
BP	GO:0045061	Thymic T cell selection	2/56	22/18862	0.001925069	0.025279198	0.017890878	940/917	2	CD28/CD3G	0.035714286
BP	GO:0022604	Regulation of cell morphogenesis	5/56	305/18862	0.002082443	0.026925537	0.019056044	221472/89846/2268/3055/3689	5	FGD2/FGD3/FGR/HCK/ITGB2	0.089285714
BP	GO:0043302	Positive regulation of leukocyte degranulation	2/56	23/18862	0.002104401	0.026925537	0.019056044	2268/3689	2	FGR/ITGB2	0.035714286
BP	GO:0032753	Positive regulation of interleukin-4 production	2/56	24/18862	0.002291346	0.028946374	0.020486254	940/54440	2	CD28/SASH3	0.035714286
BP	GO:0001562	Response to protozoan	2/56	25/18862	0.002485861	0.030628259	0.021676576	283234/3394	2	CCDC88B/IRF8	0.035714286
BP	GO:0042832	Defense response to protozoan	2/56	25/18862	0.002485861	0.030628259	0.021676576	283234/3394	2	CCDC88B/IRF8	0.035714286
BP	GO:0051056	Regulation of small GTPase mediated signal transduction	5/56	319/18862	0.002529575	0.030786781	0.021788767	9938/221472/89846/286530/7409	5	ARHGAP25/FGD2/FGD3/P2RY8/VAV1	0.089285714
BP	GO:0050764	Regulation of phagocytosis	3/56	94/18862	0.002744669	0.031521217	0.02230855	57118/2268/3055	3	CAMK1D/FGR/HCK	0.053571429
BP	GO:0034341	Response to interferon-gamma	4/56	197/18862	0.002774426	0.031521217	0.02230855	3055/3118/3120/3394	4	HCK/HLA-DQA2/HLA-DQB2/IRF8	0.071428571
BP	GO:0042113	B cell activation	5/56	326/18862	0.002777629	0.031521217	0.02230855	940/54900/4242/5777/54440	5	CD28/LAX1/MFNG/PTPN6/SASH3	0.089285714
BP	GO:0002273	Plasmacytoid dendritic cell differentiation	1/56	1/18862	0.002968932	0.031521217	0.02230855	3394	1	IRF8	0.017857143
BP	GO:0010920	Negative regulation of inositol phosphate biosynthetic process	1/56	1/18862	0.002968932	0.031521217	0.02230855	5341	1	PLEK	0.017857143
BP	GO:0010924	Regulation of inositol-polyphosphate 5-phosphatase1/56 activity	1/56	1/18862	0.002968932	0.031521217	0.02230855	5341	1	PLEK	0.017857143
BP	GO:0010925	Positive regulation of inositol-polyphosphate 5-phosphatase activity	1/56	1/18862	0.002968932	0.031521217	0.02230855	5341	1	PLEK	0.017857143
BP	GO:0030845	Phospholipase C-inhibiting G protein-coupled receptor signaling pathway	1/56	1/18862	0.002968932	0.031521217	0.02230855	5341	1	PLEK	0.017857143
BP	GO:0032685	Negative regulation of granulocyte macrophage colony-stimulating factor production	1/56	1/18862	0.002968932	0.031521217	0.02230855	8832	1	CD84	0.017857143

Table S2 (continued)

Table S2 (continued)

Ontology	ID	Description	Gene ratio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count	Gene name	Rich factor
BP	GO:0060305	Regulation of cell diameter	1/56	1/18862	0.002968932	0.031521217	0.02230855	5341	1	PLEK	0.017857143
BP	GO:0071976	Cell gliding	1/56	1/18862	0.002968932	0.031521217	0.02230855	64005	1	MYO1G	0.017857143
BP	GO:0120117	T cell meandering migration	1/56	1/18862	0.002968932	0.031521217	0.02230855	64005	1	MYO1G	0.017857143
BP	GO:0002507	Tolerance induction	2/56	28/18862	0.003114369	0.032366141	0.022906529	1233/29851	2	CCR4/ICOS	0.035714286
BP	GO:0002474	Antigen processing and presentation of peptide antigen via MHC class I	3/56	99/18862	0.003178238	0.032366141	0.022906529	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
BP	GO:0019886	Antigen processing and presentation of exogenous peptide antigen via MHC class II	3/56	99/18862	0.003178238	0.032366141	0.022906529	3112/3118/3120	3	HLA-DOB/HLA-DQA2/HLA-DQB2	0.053571429
BP	GO:0042102	Positive regulation of T cell proliferation	3/56	99/18862	0.003178238	0.032366141	0.022906529	283234/940/54440	3	CCDC88B/CD28/SASH3	0.053571429
BP	GO:0043304	Regulation of mast cell degranulation	2/56	29/18862	0.003338711	0.033320335	0.023581843	8832/2268	2	CD84/FGR	0.035714286
BP	GO:0050690	Regulation of defense response to virus by virus	2/56	29/18862	0.003338711	0.033320335	0.023581843	940/3055	2	CD28/HCK	0.035714286
BP	GO:0002495	Antigen processing and presentation of peptide antigen via MHC class II	3/56	103/18862	0.003553724	0.033935795	0.024017422	3112/3118/3120	3	HLA-DOB/HLA-DQA2/HLA-DQB2	0.053571429
BP	GO:0030593	Neutrophil chemotaxis	3/56	103/18862	0.003553724	0.033935795	0.024017422	57118/3689/7409	3	CAMK1D/ITGB2/VAV1	0.053571429
BP	GO:0032743	Positive regulation of interleukin-2 production	2/56	30/18862	0.003570399	0.033935795	0.024017422	940/54440	2	CD28/SASH3	0.035714286
BP	GO:0033006	Regulation of mast cell activation involved in immune response	2/56	30/18862	0.003570399	0.033935795	0.024017422	8832/2268	2	CD84/FGR	0.035714286
BP	GO:0050901	Leukocyte tethering or rolling	2/56	30/18862	0.003570399	0.033935795	0.024017422	6402/6404	2	SELL/SELPLG	0.035714286
BP	GO:0002504	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	3/56	104/18862	0.003651646	0.034380594	0.024332221	3112/3118/3120	3	HLA-DOB/HLA-DQA2/HLA-DQB2	0.053571429
BP	GO:0002861	Regulation of inflammatory response to antigenic stimulus	2/56	32/18862	0.004055638	0.037171391	0.026307355	940/26279	2	CD28/PLA2G2D	0.035714286
BP	GO:0032673	Regulation of interleukin-4 production	2/56	32/18862	0.004055638	0.037171391	0.026307355	940/54440	2	CD28/SASH3	0.035714286
BP	GO:0002708	Positive regulation of lymphocyte mediated immunity	3/56	108/18862	0.004059801	0.037171391	0.026307355	940/54440/7409	3	CD28/SASH3/VAV1	0.053571429
BP	GO:0002449	Lymphocyte mediated immunity	5/56	360/18862	0.004239826	0.038466788	0.027224148	940/64005/5777/54440/7409	5	CD28/MYO1G/PTPN6/SASH3/VAV1	0.089285714
BP	GO:0032633	Interleukin-4 production	2/56	33/18862	0.004309101	0.038743087	0.027419694	940/54440	2	CD28/SASH3	0.035714286
BP	GO:0018108	Peptidyl-tyrosine phosphorylation	5/56	369/18862	0.00470468	0.041922057	0.02966955	2268/3055/3689/653361/5777	5	FGR/HCK/ITGB2/NCF1/PTPN6	0.089285714
BP	GO:0018212	Peptidyl-tyrosine modification	5/56	372/18862	0.00486741	0.042988275	0.030424146	2268/3055/3689/653361/5777	5	FGR/HCK/ITGB2/NCF1/PTPN6	0.089285714
BP	GO:0045066	Regulatory T cell differentiation	2/56	36/18862	0.005112343	0.044755428	0.031674815	940/26279	2	CD28/PLA2G2D	0.035714286
BP	GO:0050868	Negative regulation of T cell activation	3/56	119/18862	0.005321588	0.046182129	0.032684536	54900/26279/5777	3	LAX1/PLA2G2D/PTPN6	0.053571429
BP	GO:0032733	Positive regulation of interleukin-10 production	2/56	38/18862	0.00568312	0.046872092	0.033172845	940/54440	2	CD28/SASH3	0.035714286
BP	GO:1990266	Neutrophil migration	3/56	123/18862	0.005832518	0.046872092	0.033172845	57118/3689/7409	3	CAMK1D/ITGB2/VAV1	0.053571429
BP	GO:0002522	Leukocyte migration involved in immune response	1/56	2/18862	0.005929207	0.046872092	0.033172845	3055	1	HCK	0.017857143
BP	GO:0002587	Negative regulation of antigen processing and presentation of peptide antigen via MHC class II	1/56	2/18862	0.005929207	0.046872092	0.033172845	3112	1	HLA-DOB	0.017857143
BP	GO:0033277	Abortive mitotic cell cycle	1/56	2/18862	0.005929207	0.046872092	0.033172845	5777	1	PTPN6	0.017857143
BP	GO:0038043	Interleukin-5-mediated signaling pathway	1/56	2/18862	0.005929207	0.046872092	0.033172845	1439	1	CSF2RB	0.017857143

Table S2 (continued)

Table S2 (continued)

Ontology	ID	Description	Gene ratio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count	Gene name	Rich factor
BP	GO:0045914	Negative regulation of catecholamine metabolic process	1/56	2/18862	0.005929207	0.046872092	0.033172845	3689	1	ITGB2	0.017857143
BP	GO:0045963	Negative regulation of dopamine metabolic process	1/56	2/18862	0.005929207	0.046872092	0.033172845	3689	1	ITGB2	0.017857143
BP	GO:0050902	Leukocyte adhesive activation	1/56	2/18862	0.005929207	0.046872092	0.033172845	6404	1	SELPLG	0.017857143
BP	GO:0070560	Protein secretion by platelet	1/56	2/18862	0.005929207	0.046872092	0.033172845	5341	1	PLEK	0.017857143
BP	GO:2000349	Negative regulation of CD40 signaling pathway	1/56	2/18862	0.005929207	0.046872092	0.033172845	6504	1	SLAMF1	0.017857143
BP	GO:0071621	Granulocyte chemotaxis	3/56	124/18862	0.005964685	0.046872092	0.033172845	57118/3689/7409	3	CAMK1D/ITGB2/VAV1	0.053571429
BP	GO:0051896	Regulation of protein kinase B signaling	4/56	247/18862	0.006186141	0.048232572	0.034135698	940/29851/23533/7409	4	CD28/ICOS/PIK3R5/VAV1	0.071428571
BP	GO:0032735	Positive regulation of interleukin-12 production	2/56	40/18862	0.006281723	0.048598134	0.034394418	3394/4050	2	IRF8/LTB	0.035714286
CC	GO:0032010	Phagolysosome	3/58	6/19520	4.94757E-07	6.9266E-05	4.73925E-05	653361/4688/4689	3	NCF1/NCF2/NCF4	0.051724138
CC	GO:0043020	NADPH oxidase complex	3/58	12/19520	5.37371E-06	0.00037616	0.000257373	653361/4688/4689	3	NCF1/NCF2/NCF4	0.051724138
CC	GO:0005767	Secondary lysosome	3/58	16/19520	1.35634E-05	0.000474718	0.000324807	653361/4688/4689	3	NCF1/NCF2/NCF4	0.051724138
CC	GO:0042613	MHC class II protein complex	3/58	16/19520	1.35634E-05	0.000474718	0.000324807	3112/3118/3120	3	HLA-DOB/HLA-DQA2/HLA-DQB2	0.051724138
CC	GO:0042611	MHC protein complex	3/58	25/19520	5.46578E-05	0.001530419	0.001047129	3112/3118/3120	3	HLA-DOB/HLA-DQA2/HLA-DQB2	0.051724138
CC	GO:0030139	Endocytic vesicle	6/58	307/19520	0.000293403	0.006164261	0.004217652	3118/3120/219972/653361/4688/4689	6	HLA-DQA2/HLA-DQB2/MPEG1/NCF1/NCF2/NCF4	0.103448276
CC	GO:0042105	Alpha-beta T cell receptor complex	2/58	9/19520	0.000308213	0.006164261	0.004217652	917/5777	2	CD3G/PTPN6	0.034482759
CC	GO:0001931	Uropod	2/58	13/19520	0.000662709	0.010004902	0.006845459	9051/6404	2	PSTPIP1/SELPLG	0.034482759
CC	GO:0031254	Cell trailing edge	2/58	13/19520	0.000662709	0.010004902	0.006845459	9051/6404	2	PSTPIP1/SELPLG	0.034482759
CC	GO:0045335	Phagocytic vesicle	4/58	136/19520	0.000714636	0.010004902	0.006845459	219972/653361/4688/4689	4	MPEG1/NCF1/NCF2/NCF4	0.068965517
CC	GO:0031252	Cell leading edge	6/58	411/19520	0.00134936	0.017173668	0.011750404	221472/89846/2268/64005/5341/9051	6	FGD2/FGD3/FGR/MYO1G/PLEK/PSTPIP1	0.103448276
CC	GO:0031256	Leading edge membrane	4/58	173/19520	0.001741635	0.01956038	0.013383418	221472/2268/64005/5341	4	FGD2/FGR/MYO1G/PLEK	0.068965517
CC	GO:0001726	Ruffle	4/58	175/19520	0.001816321	0.01956038	0.013383418	221472/89846/2268/5341	4	FGD2/FGD3/FGR/PLEK	0.068965517
CC	GO:0030027	Lamellipodium	4/58	196/19520	0.002739509	0.024469624	0.016742374	221472/89846/64005/9051	4	FGD2/FGD3/MYO1G/PSTPIP1	0.068965517
CC	GO:0032587	Ruffle membrane	3/58	95/19520	0.002838977	0.024469624	0.016742374	221472/2268/5341	3	FGD2/FGR/PLEK	0.051724138
CC	GO:0001891	Phagocytic cup	2/58	27/19520	0.002903592	0.024469624	0.016742374	9938/64005	2	ARHGAP25/MYO1G	0.034482759
CC	GO:0030526	Granulocyte macrophage colony-stimulating factor receptor complex	1/58	1/19520	0.002971311	0.024469624	0.016742374	1439	1	CSF2RB	0.017241379
CC	GO:0071556	Integral component of luminal side of endoplasmic reticulum membrane	2/58	29/19520	0.003345801	0.024653272	0.016868028	3118/3120	2	HLA-DQA2/HLA-DQB2	0.034482759
CC	GO:0098553	Luminal side of endoplasmic reticulum membrane	2/58	29/19520	0.003345801	0.024653272	0.016868028	3118/3120	2	HLA-DQA2/HLA-DQB2	0.034482759
CC	GO:0044853	Plasma membrane raft	3/58	111/19520	0.004399681	0.02868915	0.019629419	3055/3689/6404	3	HCK/ITGB2/SELPLG	0.051724138
CC	GO:1990204	Oxidoreductase complex	3/58	111/19520	0.004399681	0.02868915	0.019629419	653361/4688/4689	3	NCF1/NCF2/NCF4	0.051724138
CC	GO:0005884	Actin filament	3/58	113/19520	0.00462468	0.02868915	0.019629419	3055/9051/92241	3	HCK/PSTPIP1/RCSD1	0.051724138
CC	GO:0030665	Clathrin-coated vesicle membrane	3/58	117/19520	0.005095323	0.02868915	0.019629419	917/3118/3120	3	CD3G/HLA-DQA2/HLA-DQB2	0.051724138
CC	GO:0098576	Luminal side of membrane	2/58	36/19520	0.005123063	0.02868915	0.019629419	3118/3120	2	HLA-DQA2/HLA-DQB2	0.034482759
CC	GO:0098636	Protein complex involved in cell adhesion	2/58	36/19520	0.005123063	0.02868915	0.019629419	940/3689	2	CD28/ITGB2	0.034482759
CC	GO:0034687	Integrin alpha-beta2 complex	1/58	2/19520	0.005933946	0.028924152	0.019790209	3689	1	ITGB2	0.017241379

Table S2 (continued)

Table S2 (continued)

Ontology	ID	Description	Gene ratio	BgRatio	pvalue	p.adjust	qvalue	genelD	Count	Gene name	Rich factor
CC	GO:0034688	Integrin alpham-beta2 complex	1/58	2/19520	0.005933946	0.028924152	0.019790209	3689	1	ITGB2	0.017241379
CC	GO:0034689	Integrin alphax-beta2 complex	1/58	2/19520	0.005933946	0.028924152	0.019790209	3689	1	ITGB2	0.017241379
CC	GO:0030669	Clathrin-coated endocytic vesicle membrane	2/58	39/19520	0.005991431	0.028924152	0.019790209	3118/3120	2	HLA-DQA2/HLA-DQB2	0.034482759
CC	GO:0009897	External side of plasma membrane	5/58	402/19520	0.006769849	0.03159263	0.02161601	1233/940/917/3689/4065	5	CCR4/CD28/CD3G/ITGB2/LY75	0.086206897
MF	GO:0043325	Phosphatidylinositol-3,4-bisphosphate binding	4/56	29/18337	1.75017E-06	0.000199826	0.000142094	27071/64005/653361/5341	4	DAPP1/MYO1G/NCF1/PLEK	0.071428571
MF	GO:0016176	Superoxide-generating NADPH oxidase activator activity	3/56	10/18337	3.18871E-06	0.000199826	0.000142094	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
MF	GO:0032395	MHC class II receptor activity	3/56	10/18337	3.18871E-06	0.000199826	0.000142094	3112/3118/3120	3	HLA-DOB/HLA-DQA2/HLA-DQB2	0.053571429
MF	GO:0016175	Superoxide-generating NAD(P)H oxidase activity	3/56	11/18337	4.37498E-06	0.000205624	0.000146217	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
MF	GO:0001784	Phosphotyrosine residue binding	4/56	44/18337	9.66868E-06	0.000363542	0.00025851	2268/3055/5777/7409	4	FGR/HCK/PTPN6/VAV1	0.071428571
MF	GO:0050664	Oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	3/56	16/18337	1.46883E-05	0.000460234	0.000327266	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
MF	GO:0045309	Protein phosphorylated amino acid binding	4/56	56/18337	2.54578E-05	0.000683725	0.000486187	2268/3055/5777/7409	4	FGR/HCK/PTPN6/VAV1	0.071428571
MF	GO:0140375	Immune receptor activity	5/56	136/18337	5.87727E-05	0.001381159	0.000982123	1233/1439/3112/3118/3120	5	CCR4/CSF2RB/HLA-DOB/HLA-DQA2/HLA-DQB2	0.089285714
MF	GO:0035091	Phosphatidylinositol binding	6/56	253/18337	0.000118483	0.002458124	0.001747938	27071/221472/64005/653361/4689/285180	6	DAPP1/FGD2/MYO1G/NCF1/NCF4/RUFY4	0.107142857
MF	GO:0140031	Phosphorylation-dependent protein binding	2/56	6/18337	0.000136331	0.002458124	0.001747938	5777/7409	2	PTPN6/VAV1	0.035714286
MF	GO:0051219	Phosphoprotein binding	4/56	87/18337	0.000143826	0.002458124	0.001747938	2268/3055/5777/7409	4	FGR/HCK/PTPN6/VAV1	0.071428571
MF	GO:1901981	Phosphatidylinositol phosphate binding	5/56	171/18337	0.00017297	0.002709856	0.001926941	27071/221472/64005/4689/285180	5	DAPP1/FGD2/MYO1G/NCF4/RUFY4	0.089285714
MF	GO:0042169	SH2 domain binding	3/56	38/18337	0.000210976	0.003051038	0.002169551	54900/5777/6504	3	LAX1/PTPN6/SLAMF1	0.053571429
MF	GO:0005543	Phospholipid binding	7/56	451/18337	0.000425676	0.00571622	0.004064726	27071/221472/64005/653361/4689/26279/285180	7	DAPP1/FGD2/MYO1G/NCF1/NCF4/PLA2G2D/RUFY4	0.125
MF	GO:0038024	Cargo receptor activity	3/56	75/18337	0.001559109	0.019540836	0.013895219	55911/433/3689	3	APOBR/ASGR2/ITGB2	0.053571429
MF	GO:0016651	Oxidoreductase activity, acting on NAD(P)H	3/56	102/18337	0.00374076	0.043953933	0.031255037	653361/4688/4689	3	NCF1/NCF2/NCF4	0.053571429
MF	GO:0005164	Tumor necrosis factor receptor binding	2/56	31/18337	0.004024289	0.044503905	0.031646114	4050/8740	2	LTB/TNFSF14	0.035714286

DEGs, differently expressed genes.

Table S3 KEGG pathways enriched by the 59 DEGs

Pathway name	pathwayHits	oriBaits
hsa04145 Phagosome - Homo sapiens (human) (6)	HLA-DOB HLA-DQA2 ITGB2 NCF2 NCF4 NCF1	hsa:3112 hsa:3118 hsa:3689 hsa:4688 hsa:4689 hsa:653361
hsa04062 Chemokine signaling pathway - Homo sapiens (human) (6)	CCR4 FGR PIK3R5 HCK NCF1 VAV1	hsa:1233 hsa:2268 hsa:23533 hsa:3055 hsa:653361 hsa:7409
hsa04670 Leukocyte transendothelial migration - Homo sapiens (human) (5)	ITGB2 NCF2 NCF4 NCF1 VAV1	hsa:3689 hsa:4688 hsa:4689 hsa:653361 hsa:7409
hsa04660 T cell receptor signaling pathway - Homo sapiens (human) (5)	ICOS PTPN6 VAV1 CD3G CD28	hsa:29851 hsa:5777 hsa:7409 hsa:917 hsa:940
hsa04613 Neutrophil extracellular trap formation - Homo sapiens (human) (5)	ITGB2 NCF2 NCF4 SELPLG NCF1	hsa:3689 hsa:4688 hsa:4689 hsa:6404 hsa:653361
hsa05323 Rheumatoid arthritis - Homo sapiens (human) (5)	HLA-DOB HLA-DQA2 ITGB2 LTB CD28	hsa:3112 hsa:3118 hsa:3689 hsa:4050 hsa:940
hsa04672 Intestinal immune network for IgA production - Homo sapiens (human) (4)	ICOS HLA-DOB HLA-DQA2 CD28	hsa:29851 hsa:3112 hsa:3118 hsa:940
hsa05417 Lipid and atherosclerosis - Homo sapiens (human) (4)	NCF2 NCF4 NCF1 VAV1	hsa:4688 hsa:4689 hsa:653361 hsa:7409
hsa05416 Viral myocarditis - Homo sapiens (human) (4)	HLA-DOB HLA-DQA2 ITGB2 CD28	hsa:3112 hsa:3118 hsa:3689 hsa:940
hsa05150 Staphylococcus aureus infection - Homo sapiens (human) (4)	HLA-DOB HLA-DQA2 ITGB2 SELPLG	hsa:3112 hsa:3118 hsa:3689 hsa:6404
hsa05166 Human T-cell leukemia virus 1 infection - Homo sapiens (human) (4)	HLA-DOB HLA-DQA2 ITGB2 CD3G	hsa:3112 hsa:3118 hsa:3689 hsa:917
hsa04060 Cytokine-cytokine receptor interaction - Homo sapiens (human) (4)	CCR4 CSF2RB LTB TNFSF14	hsa:1233 hsa:1439 hsa:4050 hsa:8740
hsa04650 Natural killer cell mediated cytotoxicity - Homo sapiens (human) (3)	ITGB2 PTPN6 VAV1	hsa:3689 hsa:5777 hsa:7409
hsa04666 Fc gamma R-mediated phagocytosis - Homo sapiens (human) (3)	HCK NCF1 VAV1	hsa:3055 hsa:653361 hsa:7409
hsa05322 Systemic lupus erythematosus - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD28	hsa:3112 hsa:3118 hsa:940
hsa05168 Herpes simplex virus 1 infection - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 TNFSF14	hsa:3112 hsa:3118 hsa:8740
hsa04810 Regulation of actin cytoskeleton - Homo sapiens (human) (3)	ITGB2 VAV1 FGD3	hsa:3689 hsa:7409 hsa:89846
hsa04659 Th17 cell differentiation - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD3G	hsa:3112 hsa:3118 hsa:917
hsa05169 Epstein-Barr virus infection - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD3G	hsa:3112 hsa:3118 hsa:917
hsa05332 Graft-versus-host disease - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD28	hsa:3112 hsa:3118 hsa:940
hsa04940 Type I diabetes mellitus - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD28	hsa:3112 hsa:3118 hsa:940

Table S3 (continued)

Table S3 (continued)

Pathway name	pathwayHits	oriBaits
hsa04658 Th1 and Th2 cell differentiation - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD3G	hsa:3112 hsa:3118 hsa:917
hsa04380 Osteoclast differentiation - Homo sapiens (human) (3)	NCF2 NCF4 NCF1	hsa:4688 hsa:4689 hsa:653361
hsa05020 Prion disease - Homo sapiens (human) (3)	NCF2 NCF4 NCF1	hsa:4688 hsa:4689 hsa:653361
hsa04640 Hematopoietic cell lineage - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD3G	hsa:3112 hsa:3118 hsa:917
hsa05167 Kaposi sarcoma-associated herpesvirus infection - Homo sapiens (human) (3)	CCR4 PIK3R5 HCK	hsa:1233 hsa:23533 hsa:3055
hsa05145 Toxoplasmosis - Homo sapiens (human) (3)	PIK3R5 HLA-DOB HLA-DQA2	hsa:23533 hsa:3112 hsa:3118
hsa05415 Diabetic cardiomyopathy - Homo sapiens (human) (3)	NCF2 NCF4 NCF1	hsa:4688 hsa:4689 hsa:653361
hsa05162 Measles - Homo sapiens (human) (3)	SLAMF1 CD3G CD28	hsa:6504 hsa:917 hsa:940
hsa05235 PD-L1 expression and PD-1 checkpoint pathway in cancer - Homo sapiens (human) (3)	PTPN6 CD3G CD28	hsa:5777 hsa:917 hsa:940
hsa05152 Tuberculosis - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 ITGB2	hsa:3112 hsa:3118 hsa:3689
hsa04662 B cell receptor signaling pathway - Homo sapiens (human) (3)	DAPP1 PTPN6 VAV1	hsa:27071 hsa:5777 hsa:7409
hsa05320 Autoimmune thyroid disease - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD28	hsa:3112 hsa:3118 hsa:940
hsa05330 Allograft rejection - Homo sapiens (human) (3)	HLA-DOB HLA-DQA2 CD28	hsa:3112 hsa:3118 hsa:940
hsa05133 Pertussis - Homo sapiens (human) (2)	IRF8 ITGB2	hsa:3394 hsa:3689
hsa04061 Viral protein interaction with cytokine and cytokine receptor - Homo sapiens (human) (2)	CCR4 TNFSF14	hsa:1233 hsa:8740
hsa04630 JAK-STAT signaling pathway - Homo sapiens (human) (2)	CSF2RB PTPN6	hsa:1439 hsa:5777
hsa05130 Pathogenic Escherichia coli infection - Homo sapiens (human) (2)	PTPN6 MYO1G	hsa:5777 hsa:64005
hsa04015 Rap1 signaling pathway - Homo sapiens (human) (2)	ITGB2 VAV1	hsa:3689 hsa:7409
hsa04612 Antigen processing and presentation - Homo sapiens (human) (2)	HLA-DOB HLA-DQA2	hsa:3112 hsa:3118
hsa05208 Chemical carcinogenesis - reactive oxygen species - Homo sapiens (human) (2)	NCF2 NCF1	hsa:4688 hsa:653361
hsa05418 Fluid shear stress and atherosclerosis - Homo sapiens (human) (2)	NCF2 NCF1	hsa:4688 hsa:653361
hsa04921 Oxytocin signaling pathway - Homo sapiens (human) (2)	PIK3R5 CAMK1D	hsa:23533 hsa:57118
hsa04080 Neuroactive ligand-receptor interaction - Homo sapiens (human) (2)	P2RY8 S1PR4	hsa:286530 hsa:8698

Table S3 (continued)

Table S3 (continued)

Pathway name	pathwayHits	oriBaits
hsa05321 Inflammatory bowel disease - Homo sapiens (human) (2)	HLA-DOB HLA-DQA2	hsa:31112 hsa:31118
hsa04064 NF-kappa B signaling pathway - Homo sapiens (human) (2)	LTB TNFSF14	hsa:4050 hsa:8740
hsa05310 Asthma - Homo sapiens (human) (2)	HLA-DOB HLA-DQA2	hsa:31112 hsa:31118
hsa05164 Influenza A - Homo sapiens (human) (2)	HLA-DOB HLA-DQA2	hsa:31112 hsa:31118
hsa05205 Proteoglycans in cancer - Homo sapiens (human) (2)	PTPN6 VAV1	hsa:5777 hsa:7409

DEGs, differently expressed genes.