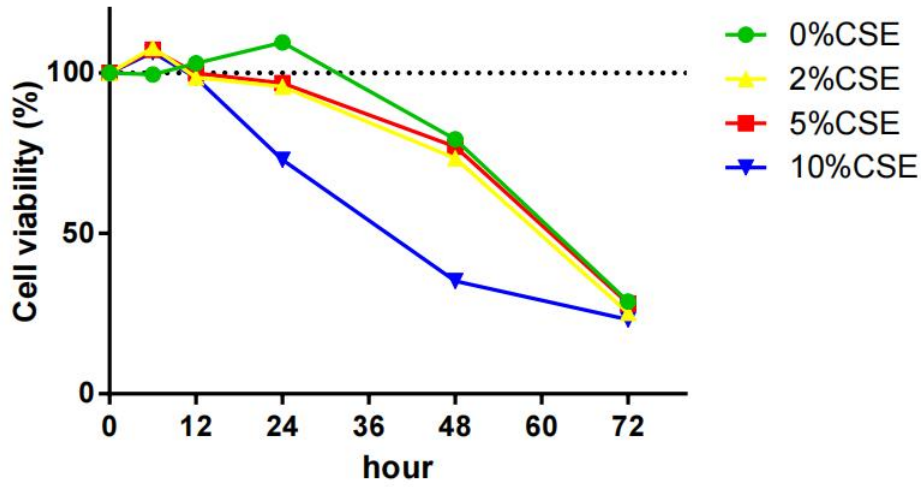
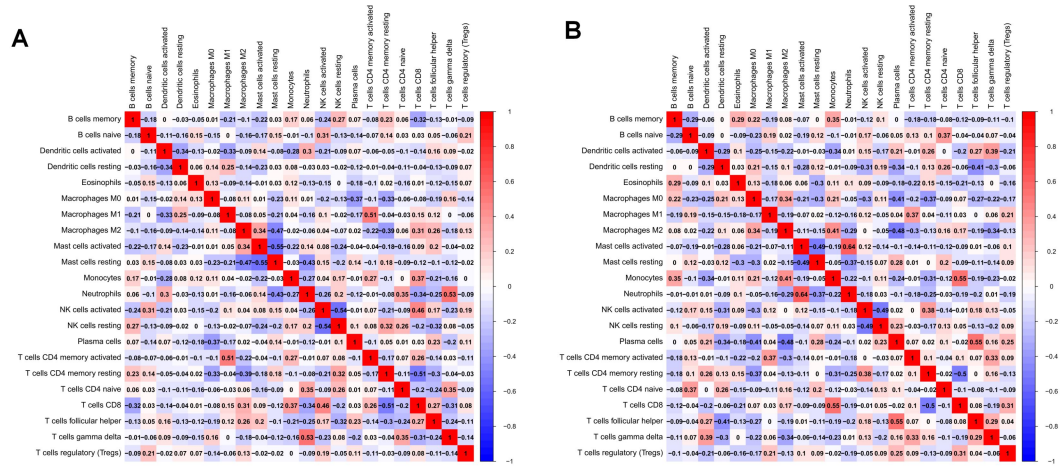


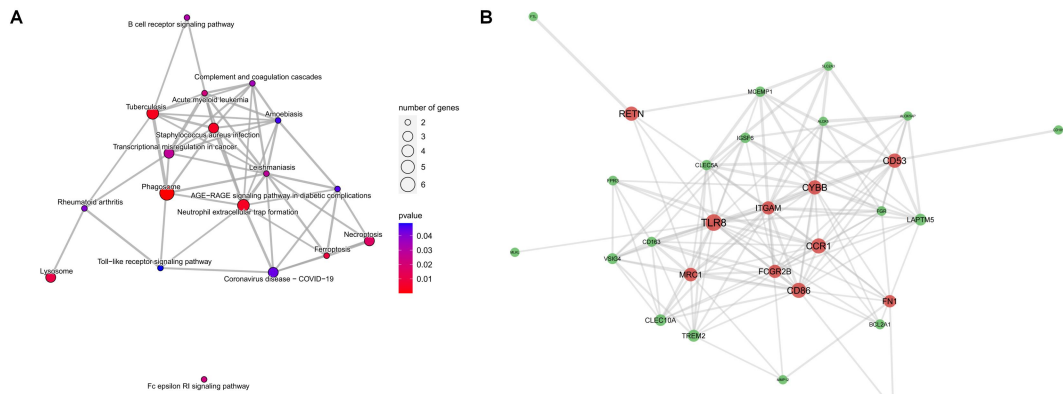
CCK-8



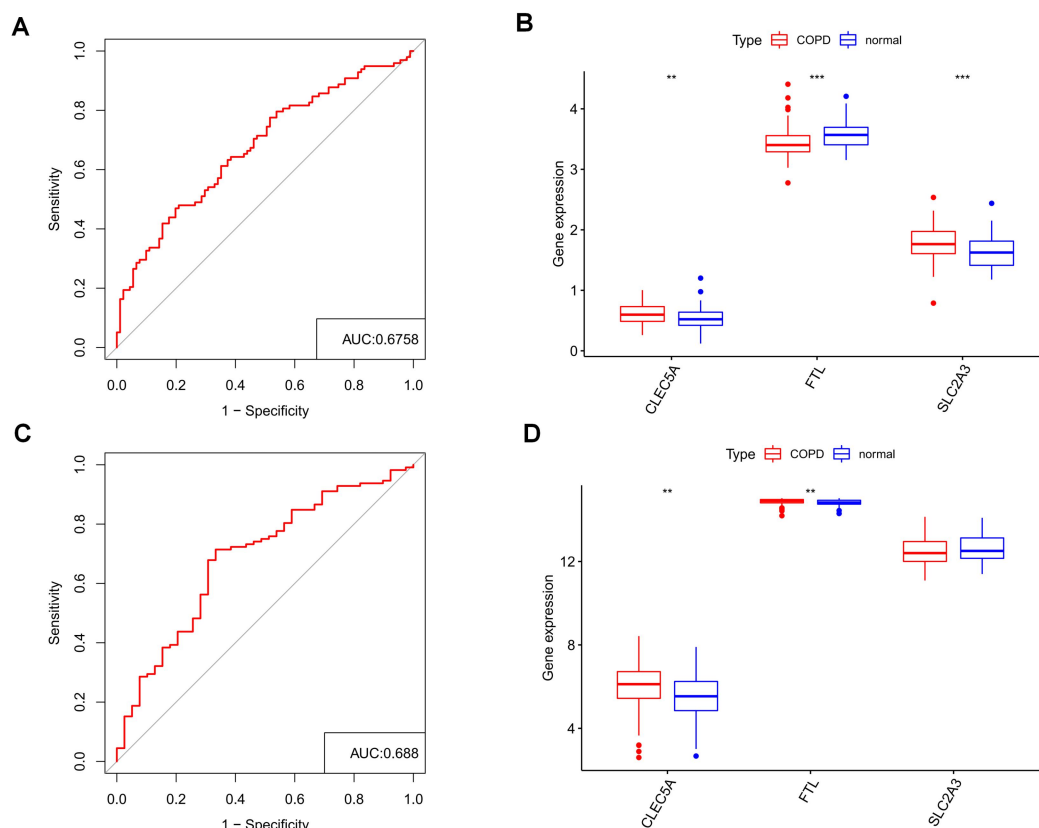
Supplementary Figure 1: Determination of Cell Viability



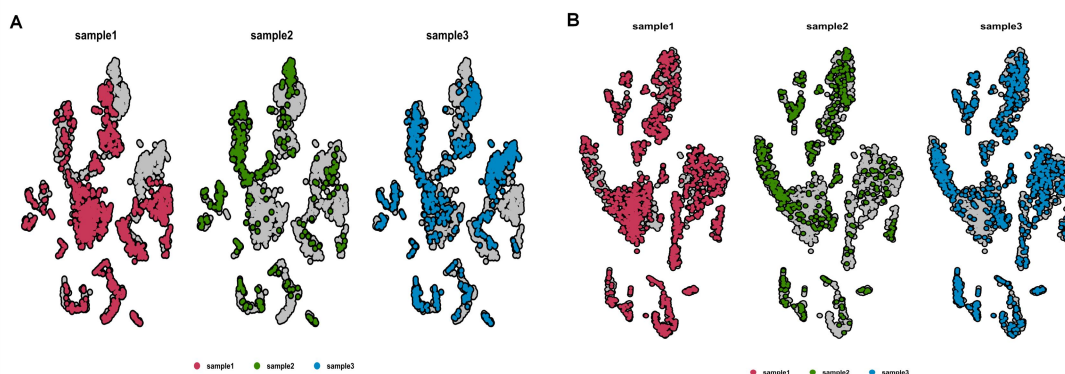
Supplementary Figure 2. Correlation between immune cells in GSE20257(A) and GSE10006(B).



Supplementary Figure 3. Kyoto encyclopedia of genes and genomes and Protein-Protein Interaction Networks. (A) Network diagram of KEGG enrichment analyses. (B) PPI network. Red represents hub genes.



Supplementary Figure 4. Identification of 3 gene signatures in lung tissue. auc for predicted outcomes in GSE57148 (A) and GSE76925 (B). expression of CLEC5A, FTL and SLC2A3 in COPD patients and healthy controls in GSE57148 (C) and GSE76925 (D). ns, not significant; * $P < 0.05$, ** $P < 0.01$, *** $p < 0.001$.



Supplementary Figure 5. tSNE plots before (A) and after (B) correction of the "harmony" R package batch.

Supplementary Table 1. GO enrichment analysis of 41 candidate genes.

ONTO LOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adju st	qvalu e	geneID	Coun t
BP	GO:0001819	positive regulation of cytokine production	8/37	475/18800	3.17E-06	0.0015 24512	0.0009 85909	CLEC5A/CYBB/MMP12/CD86/TREM2/TLR8/LAPTM5/FGR	8
BP	GO:0050866	negative regulation of cell activation	6/37	216/18800	3.71E-06	0.0015 24512	0.0009 85909	CD86/TREM2/LAPTM5/FGR/VSIG4/FCGR2B	6
BP	GO:0002697	regulation of immune effector process	7/37	353/18800	4.92E-06	0.0015 24512	0.0009 85909	CD86/TREM2/ITGAM/LAPTM5/FGR/VSIG4/FCGR2B	7
BP	GO:0045088	regulation of innate immune response	6/37	231/18800	5.45E-06	0.0015 24512	0.0009 85909	MMP12/TREM2/TLR8/FGR/VSIG4/FCGR2B	6
BP	GO:0002274	myeloid leukocyte activation	6/37	232/18800	5.59E-06	0.0015 24512	0.0009 85909	TREM2/ITGAM/FN1/FGR/VSIG4/FCGR2B	6
BP	GO:0031348	negative regulation of defense response	6/37	268/18800	1.27E-05	0.0023 83418	0.0015 41368	ALOX5/MMP12/TREM2/FGR/VSIG4/FCGR2B	6
BP	GO:0051250	negative regulation of lymphocyte activation	5/37	161/18800	1.51E-05	0.0023 83418	0.0015 41368	CD86/LAPTM5/FGR/VSIG4/FCGR2B	5
BP	GO:0002683	negative regulation of immune system process	7/37	425/18800	1.64E-05	0.0023 83418	0.0015 41368	MMP12/CD86/TREM2/LAPTM5/FGR/VSIG4/FCGR2B	7
BP	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	4/37	79/18800	1.72E-05	0.0023 83418	0.0015 41368	TREM2/FN1/FGR/PIK3AP1	4
BP	GO:0032102	negative regulation of response to external stimulus	7/37	429/18800	1.75E-05	0.0023 83418	0.0015 41368	ALOX5/MMP12/TREM2/NRP1/FGR/VSIG4/FCGR2B	7
BP	GO:0048015	phosphatidylinositol-mediated signaling	5/37	177/18800	2.39E-05	0.0027 88243	0.0018 0317	CA8/TREM2/FN1/FGR/PIK3AP1	5
BP	GO:0050777	negative regulation of immune response	5/37	179/18800	2.52E-05	0.0027 88243	0.0018 0317	MMP12/TREM2/FGR/VSIG4/FCGR2B	5
BP	GO:0048017	inositol lipid-mediated signaling	5/37	181/18800	2.66E-05	0.0027 88243	0.0018 0317	CA8/TREM2/FN1/FGR/PIK3AP1	5
BP	GO:0002862	negative regulation of inflammatory response to antigenic stimulus	3/37	31/18800	3.04E-05	0.0029 58606	0.0019 13344	TREM2/FGR/FCGR2B	3
BP	GO:0002695	negative regulation of leukocyte	5/37	193/18800	3.61E-05	0.0031 40918	0.0020 31247	CD86/LAPTM5/FGR/VSIG4/FCGR2B	5

		activation										
		immune									TREM2/TLR8/LAPTM	
BP	GO:0002	response-regulating signaling pathway	7/37	482/18800	3.68E-05	0.0031	0.0020	40918	31247		5/FPR3/FGR/PIK3AP1/FCGR2B	7
BP	GO:0042	macrophage activation	4/37	106/18800	5.46E-05	0.0041	0.0026	54008	86417		TREM2/ITGAM/VSIG4/FCGR2B	4
BP	GO:0007	integrin-mediated signaling pathway	4/37	107/18800	5.67E-05	0.0041	0.0026	54008	86417		ITGAM/FN1/NRP1/FGFR	4
BP	GO:0002	regulation of response to biotic stimulus	6/37	351/18800	5.79E-05	0.0041	0.0026	54008	86417		MMP12/TREM2/TLR8/FGFR/VSIG4/FCGR2B	6
BP	GO:0045	positive regulation of axon extension	3/37	39/18800	6.11E-05	0.0041	0.0026	58771	89497		TRPV2/FN1/NRP1	3
BP	GO:0014	regulation of phosphatidylinositol 3-kinase signaling	4/37	111/18800	6.54E-05	0.0041	0.0026	58771	89497		TREM2/FN1/FGR/PIK3AP1	4
BP	GO:0001	negative regulation of cytokine production	6/37	363/18800	6.97E-05	0.0041	0.0026	58771	89497		TREM2/TLR8/LAPTM/FGFR/VSIG4/FCGR2B	6
BP	GO:0002	acute inflammatory response	4/37	113/18800	7.01E-05	0.0041	0.0026	58771	89497		ALOX5AP/FN1/CD163/FCGR2B	4
BP	GO:0002	regulation of inflammatory response to antigenic stimulus	3/37	45/18800	9.41E-05	0.0051	0.0033	28686	16746		TREM2/FGR/FCGR2B	3
BP	GO:0002	regulation of humoral immune response	3/37	45/18800	9.41E-05	0.0051	0.0033	28686	16746		TREM2/VSIG4/FCGR2B	3
BP	GO:0002	activation of immune response	6/37	386/18800	9.78E-05	0.0051	0.0033	28686	16746		TREM2/LAPTM5/FPR3/FGR/VSIG4/FCGR2B	6
BP	GO:0050	negative regulation of T cell activation	4/37	125/18800	0.0001037	0.0052	0.0033	89	43266	90845	CD86/LAPTM5/VSIG4/FCGR2B	4
BP	GO:0050	regulation of inflammatory response	6/37	394/18800	0.0001094	0.0053	0.0034	01	29387	4654	ALOX5/ALOX5AP/TREM2/FGR/PIK3AP1/FCGR2B	6
BP	GO:0002	positive regulation of immune effector process	5/37	248/18800	0.0001184	0.0055	0.0035	57	22743	71584	CD86/TREM2/ITGAM/LAPTM5/FGR	5
BP	GO:0043	regulation of leukocyte degranulation	3/37	49/18800	0.0001214	0.0055	0.0035	68	22743	71584	ITGAM/FGR/FCGR2B	3
BP	GO:0048	autophagic cell death	2/37	10/18800	0.0001679	0.0071	0.0046	23	69216	36366	TREM2/LAPTM5	2

BP	GO:1904	response to amyloid-beta	3/37	55/18800	0.0001715	0.0071	0.0046	MMP12/TREM2/FCGR2B	3
BP	GO:0014	phosphatidylinositol 3-kinase signaling	4/37	144/18800	0.0001791	0.0071	0.0046	TREM2/FN1/FGR/PIK3AP1	4
BP	GO:1903	negative regulation of leukocyte cell-cell adhesion	4/37	144/18800	0.0001791	0.0071	0.0046	CD86/LAPTM5/VSIG4/FCGR2B	4
BP	GO:0046	viral entry into host cell	4/37	146/18800	0.0001888	0.0071	0.0046	MRC1/CLEC5A/CD86/NRP1	4
BP	GO:0001	positive regulation of cytokine-mediated signaling pathway	3/37	57/18800	0.0001908	0.0071	0.0046	MMP12/TREM2/LAPTM5	3
BP	GO:0032	positive regulation of response to external stimulus	6/37	442/18800	0.0002045	0.0071	0.0046	ALOX5AP/MMP12/TREM2/TLR8/NRP1/CCR1	6
BP	GO:0019	lipoygenase pathway	2/37	11/18800	0.0002049	0.0071	0.0046	ALOX5/ALOX5AP	2
BP	GO:0098	synapse pruning	2/37	11/18800	0.0002049	0.0071	0.0046	TREM2/ITGAM	2
BP	GO:0002	regulation of myeloid leukocyte mediated immunity	3/37	59/18800	0.0002114	0.0072	0.0046	ITGAM/FGR/FCGR2B	3
BP	GO:0044	entry into host	4/37	153/18800	0.0002259	0.0073	0.0047	MRC1/CLEC5A/CD86/NRP1	4
BP	GO:0002	leukocyte activation involved in immune response	5/37	285/18800	0.0002264	0.0073	0.0047	CD86/TREM2/ITGAM/FGR/FCGR2B	5
BP	GO:0044	biological process involved in symbiotic interaction	5/37	286/18800	0.0002301	0.0073	0.0047	MRC1/CLEC5A/CD86/FN1/NRP1	5
BP	GO:0002	cell activation involved in immune response	5/37	289/18800	0.0002415	0.0074	0.0048	CD86/TREM2/ITGAM/FGR/FCGR2B	5
BP	GO:0043	regulation of macrophage activation	3/37	62/18800	0.0002449	0.0074	0.0048	TREM2/VSIG4/FCGR2B	3
BP	GO:0032	interleukin-2 production	3/37	63/18800	0.0002568	0.0074	0.0048	CD86/LAPTM5/VSIG4	3
BP	GO:0032	regulation of interleukin-2 production	3/37	63/18800	0.0002568	0.0074	0.0048	CD86/LAPTM5/VSIG4	3
BP	GO:0060	positive regulation of response to cytokine stimulus	3/37	64/18800	0.0002691	0.0076	0.0049	MMP12/TREM2/LAPTM5	3

BP	GO:1901	positive regulation of NIK/NF-kappaB signaling	3/37	67/18800	0.0003082	0.0084	0.0054	CD86/TREM2/LAPTM	3
	224				3	48572	63731	5	
BP	GO:0007	negative regulation of cell adhesion	5/37	305/18800	0.0003096	0.0084	0.0054	MMP12/CD86/LAPTM	5
	162				98	48572	63731	5/VSIG4/FCGR2B	
BP	GO:0070	protein homotrimerization	2/37	15/18800	0.0003893	0.0101	0.0065	ALOX5AP/MLKL	2
	207				98	27459	49476		
BP	GO:1902	regulation of neutrophil activation	2/37	15/18800	0.0003893	0.0101	0.0065	ITGAM/FCGR2B	2
	563				98	27459	49476		
BP	GO:0052	movement in host environment	4/37	177/18800	0.0003935	0.0101	0.0065	MRC1/CLEC5A/CD86/ NRP1	4
	126				16	27459	49476		
BP	GO:0002	inflammatory response to antigenic stimulus	3/37	75/18800	0.0004297	0.0105	0.0067	TREM2/FGR/FCGR2B	3
	437				92	08667	96004		
BP	GO:0050	negative regulation of inflammatory response	4/37	182/18800	0.0004372	0.0105	0.0067	ALOX5/TREM2/FGR/ FCGR2B	4
	728				41	08667	96004		
BP	GO:0002	negative regulation of humoral immune response	2/37	16/18800	0.0004444	0.0105	0.0067	VSIG4/FCGR2B	2
	921				74	08667	96004		
BP	GO:0023	CD40 signaling pathway	2/37	16/18800	0.0004444	0.0105	0.0067	CD86/TREM2	2
	035				74	08667	96004		
BP	GO:0043	leukocyte degranulation	3/37	76/18800	0.0004468	0.0105	0.0067	ITGAM/FGR/FCGR2B	3
	299				49	08667	96004		
BP	GO:0050	positive regulation of axonogenesis	3/37	77/18800	0.0004643	0.0107	0.0069	TRPV2/FN1/NRP1	3
	772				36	3483	42265		
BP	GO:0034	toll-like receptor 2 signaling pathway	2/37	17/18800	0.0005031	0.0112	0.0072	TREM2/PIK3AP1	2
	134				13	49947	75394		
BP	GO:0070	protein trimerization	2/37	17/18800	0.0005031	0.0112	0.0072	ALOX5AP/MLKL	2
	206				13	49947	75394		
BP	GO:0051	biological process involved in interaction with host	4/37	191/18800	0.0005245	0.0115	0.0074	MRC1/CLEC5A/CD86/ NRP1	4
	701				36	3979	62837		
BP	GO:1903	regulation of leukocyte cell-cell adhesion	5/37	344/18800	0.0005367	0.0116	0.0075	ALOX5/CD86/LAPTM	5
	037				81	21726	15825	5/VSIG4/FCGR2B	
BP	GO:0002	humoral immune response mediated by circulating immunoglobulin	2/37	18/18800	0.0005653	0.0120	0.0077	TREM2/FCGR2B	2
	923				01	47984	91489		
BP	GO:0050	negative regulation of lymphocyte proliferation	3/37	84/18800	0.0005991	0.0125	0.0081	CD86/VSIG4/FCGR2B	3
	672				39	72693	3082		

BP	GO:0022	negative regulation of cell-cell adhesion	4/37	199/18800	0.0006119 86	0.0126 26552	0.0081 65651	CD86/LAPTM5/VSIG4 /FCGR2B	4
BP	GO:0032	negative regulation of mononuclear cell proliferation	3/37	85/18800	0.0006202 19	0.0126 26552	0.0081 65651	CD86/VSIG4/FCGR2B	3
BP	GO:0043	negative regulation of macrophage activation	2/37	19/18800	0.0006310 25	0.0126 5761	0.0081 85737	VSIG4/FCGR2B	2
BP	GO:0031	cell-substrate adhesion	5/37	364/18800	0.0006932 19	0.0134 53071	0.0087 00165	PARVB/MMP12/ITGA M/FN1/NRP1	5
BP	GO:0002	regulation of antigen processing and presentation	2/37	20/18800	0.0007002 7	0.0134 53071	0.0087 00165	TREM2/FCGR2B	2
BP	GO:0097	dendritic spine maintenance	2/37	20/18800	0.0007002 7	0.0134 53071	0.0087 00165	TREM2/FCGR2B	2
BP	GO:0070	negative regulation of leukocyte proliferation	3/37	91/18800	0.0007566 94	0.0138 73742	0.0089 72214	CD86/VSIG4/FCGR2B	3
BP	GO:0019	leukotriene biosynthetic process	2/37	21/18800	0.0007730 24	0.0138 73742	0.0089 72214	ALOX5/ALOX5AP	2
BP	GO:0030	regulation of complement activation	2/37	21/18800	0.0007730 24	0.0138 73742	0.0089 72214	TREM2/VSIG4	2
BP	GO:0032	positive regulation of interferon-alpha production	2/37	21/18800	0.0007730 24	0.0138 73742	0.0089 72214	MMP12/TLR8	2
BP	GO:0150	cell junction disassembly	2/37	21/18800	0.0007730 24	0.0138 73742	0.0089 72214	TREM2/ITGAM	2
BP	GO:0002	myeloid cell activation involved in immune response	3/37	93/18800	0.0008060 92	0.0140 96277	0.0091 16129	TREM2/ITGAM/FGR	3
BP	GO:0030	regulation of axon extension	3/37	93/18800	0.0008060 92	0.0140 96277	0.0091 16129	TRPV2/FN1/NRP1	3
BP	GO:0007	leukocyte cell-cell adhesion	5/37	381/18800	0.0008512 09	0.0146 9683	0.0095 04509	ALOX5/CD86/LAPTM 5/VSIG4/FCGR2B	5
BP	GO:0002	production of molecular mediator involved in inflammatory response	3/37	97/18800	0.0009109 44	0.0155 31593	0.0100 44355	ALOX5/ALOX5AP/TR EM2	3
BP	GO:0050	regulation of phagocytosis	3/37	99/18800	0.0009664 61	0.0162 74732	0.0105 24946	TREM2/FGR/FCGR2B	3
BP	GO:0002	positive regulation of humoral immune	2/37	24/18800	0.0010122 04	0.0164 36268	0.0106 29413	TREM2/FCGR2B	2

		response								
BP	GO:0045	positive regulation of osteoclast differentiation	2/37	24/18800	0.0010122	0.0164	0.0106		TREM2/CCR1	2
	672				04	36268	29413			
BP	GO:0060	positive regulation of syncytium formation by plasma membrane fusion	2/37	24/18800	0.0010122	0.0164	0.0106		TREM2/CD53	2
	143				04	36268	29413			
BP	GO:0071	cellular response to molecule of bacterial origin	4/37	229/18800	0.0010331	0.0165	0.0107		MRC1/CD86/TREM2/F	4
	219				4	78855	21624		CGR2B	
BP	GO:0006	substrate-dependent cell migration	2/37	25/18800	0.0010988	0.0172	0.0111		FN1/NRP1	2
	929				6	28101	41494			
BP	GO:0043	positive regulation of leukocyte degranulation	2/37	25/18800	0.0010988	0.0172	0.0111		ITGAM/FGR	2
	302				6	28101	41494			
BP	GO:0002	myeloid leukocyte mediated immunity	3/37	104/18800	0.0011145	0.0172	0.0111		ITGAM/FGR/FCGR2B	3
	444				23	75101	7189			
BP	GO:0007	cell-matrix adhesion	4/37	235/18800	0.0011369	0.0174	0.0112		MMP12/ITGAM/FN1/	4
	160				31	24426	68459		NRP1	
BP	GO:0002	regulation of leukocyte mediated immunity	4/37	236/18800	0.0011549	0.0175	0.0113		TREM2/ITGAM/FGR/	4
	703				15	03385	19522		FCGR2B	
BP	GO:0002	immune response-regulating cell surface receptor signaling pathway	2/37	26/18800	0.0011889	0.0176	0.0113		FGR/FCGR2B	2
	433				58	27591	99847			
BP	GO:0038	involved in phagocytosis	2/37	26/18800	0.0011889	0.0176	0.0113		FGR/FCGR2B	2
	096				58	27591	99847			
BP	GO:0061	regulation of extent of cell growth	3/37	108/18800	0.0012427	0.0182	0.0117		TRPV2/FN1/NRP1	3
	387				55	21973	84236			
BP	GO:0034	substrate adhesion-dependent cell spreading	3/37	109/18800	0.0012762	0.0182	0.0117		PARVB/FN1/NRP1	3
	446				03	21973	84236			
BP	GO:0032	interferon-alpha production	2/37	27/18800	0.0012824	0.0182	0.0117		MMP12/TLR8	2
	607				85	21973	84236			
BP	GO:0032	regulation of interferon-alpha production	2/37	27/18800	0.0012824	0.0182	0.0117		MMP12/TLR8	2
	647				85	21973	84236			
BP	GO:1901	regulation of	3/37	110/18800	0.0013102	0.0184	0.0119		CD86/TREM2/LAPTM	3

	222	NIK/NF-kappaB signaling			14	24035	14911	5		
		negative regulation of interleukin-2 production								
BP	GO:0032703		2/37	28/18800	0.0013794	0.0191	0.0124		LAPTM5/VSIG4	2
					28	99389	16336			
BP	GO:0071216	cellular response to biotic stimulus	4/37	256/18800	0.0015580	0.0213	0.0138		MRC1/CD86/TREM2/F	4
					33	85237	29934		CGR2B	
BP	GO:0038094	Fc-gamma receptor signaling pathway	2/37	30/18800	0.0015835	0.0213	0.0138		FGR/FCGR2B	2
		regulation of syncytium formation by plasma membrane fusion								
BP	GO:0060142		2/37	30/18800	0.0015835	0.0213	0.0138		TREM2/CD53	2
					11	85237	29934			
BP	GO:0030282	bone mineralization	3/37	121/18800	0.0017225	0.0228	0.0147		ALOX5/FGR/CCR1	3
					2	10844	51881			
BP	GO:0048675	axon extension	3/37	121/18800	0.0017225	0.0228	0.0147		TRPV2/FN1/NRP1	3
					2	10844	51881			
BP	GO:0002224	toll-like receptor signaling pathway	3/37	123/18800	0.0018052	0.0236	0.0153		TREM2/TLR8/PIK3AP	3
					15	76087	11437	1		
BP	GO:0022407	regulation of cell-cell adhesion	5/37	456/18800	0.0018873	0.0239	0.0154		ALOX5/CD86/LAPTM	5
					59	62981	96973		5/VSIG4/FCGR2B	
BP	GO:0002443	leukocyte mediated immunity	5/37	457/18800	0.0019055	0.0239	0.0154		TREM2/TLR8/ITGAM/	5
					28	62981	96973		FGR/FCGR2B	
BP	GO:0002431	Fc receptor mediated stimulatory signaling pathway	2/37	33/18800	0.0019149	0.0239	0.0154		FGR/FCGR2B	2
					3	62981	96973			
BP	GO:0036336	dendritic cell migration	2/37	33/18800	0.0019149	0.0239	0.0154		ALOX5/CCR1	2
		negative regulation of antigen receptor-mediated signaling pathway								
BP	GO:0050858		2/37	33/18800	0.0019149	0.0239	0.0154		LAPTM5/FCGR2B	2
					3	62981	96973			
BP	GO:1903532	positive regulation of secretion by cell	4/37	274/18800	0.0019969	0.0245	0.0158		TREM2/ITGAM/RETN	4
					05	2903	6304		/FGR	
BP	GO:0006911	phagocytosis, engulfment	3/37	128/18800	0.0020227	0.0245	0.0158		TREM2/ITGAM/FCGR	3
		antigen processing and presentation of peptide antigen via MHC class II								
BP	GO:0002495		2/37	34/18800	0.0020320	0.0245	0.0158		TREM2/FCGR2B	2
					97	2903	6304			
BP	GO:0006691	leukotriene metabolic process	2/37	34/18800	0.0020320	0.0245	0.0158		ALOX5/ALOX5AP	2
					97	2903	6304			
BP	GO:0050869	negative regulation of B cell activation	2/37	35/18800	0.0021525	0.0257	0.0166		LAPTM5/FCGR2B	2
					89	55541	5623			

BP	GO:1902 105	regulation of leukocyte differentiation	4/37	283/18800	0.0022456 37	0.0266 35203	0.0172 25112	CD86/TREM2/FCGR2 B/CCR1	4
BP	GO:0002 504	antigen processing and presentation of peptide or polysaccharide	2/37	36/18800	0.0022763 94	0.0267 67252	0.0173 10509	TREM2/FCGR2B	2
BP	GO:0045 730	antigen via MHC class II respiratory burst	2/37	37/18800	0.0024034 98	0.0280 06994	0.0181 12256	CYBB/TREM2	2
BP	GO:0031 349	positive regulation of defense response	4/37	289/18800	0.0024228 92	0.0280 06994	0.0181 12256	ALOX5AP/MMP12/TR EM2/TLR8	4
BP	GO:0099 024	plasma membrane invagination	3/37	137/18800	0.0024539 8	0.0281 27968	0.0181 9049	TREM2/ITGAM/FCGR 2B	3
BP	GO:0043 410	positive regulation of MAPK cascade	5/37	491/18800	0.0026033 49	0.0289 36924	0.0187 13646	TREM2/LAPTM5/NRP 1/FCGR2B/CCR1	5
BP	GO:1901 652	response to peptide	5/37	491/18800	0.0026033 49	0.0289 36924	0.0187 13646	CYBB/MMP12/TREM 2/RETN/FCGR2B	5
BP	GO:0050 921	positive regulation of chemotaxis	3/37	140/18800	0.0026094 15	0.0289 36924	0.0187 13646	TREM2/NRP1/CCR1	3
BP	GO:1903 305	regulation of regulated secretory pathway	3/37	140/18800	0.0026094 15	0.0289 36924	0.0187 13646	ITGAM/FGR/FCGR2B	3
BP	GO:0038 061	NIK/NF-kappaB signaling	3/37	141/18800	0.0026625 49	0.0291 08364	0.0188 24517	CD86/TREM2/LAPTM 5	3
BP	GO:0097 242	amyloid-beta clearance	2/37	39/18800	0.0026675 55	0.0291 08364	0.0188 24517	TREM2/ITGAM	2
BP	GO:0002 429	immune response-activating cell surface receptor signaling pathway	4/37	300/18800	0.0027725 68	0.0295 45178	0.0191 07006	LAPTM5/FPR3/FGR/F CGR2B	4
BP	GO:0002 757	immune response-activating signal transduction	4/37	300/18800	0.0027725 68	0.0295 45178	0.0191 07006	LAPTM5/FPR3/FGR/F CGR2B	4
BP	GO:0051 047	positive regulation of secretion	4/37	300/18800	0.0027725 68	0.0295 45178	0.0191 07006	TREM2/ITGAM/RETN /FGR	4
BP	GO:0010 324	membrane invagination	3/37	144/18800	0.0028259 63	0.0298 80725	0.0193 24007	TREM2/ITGAM/FCGR 2B	3
BP	GO:0022 604	regulation of cell morphogenesis	4/37	305/18800	0.0029424 21	0.0306 60417	0.0198 28237	PARVB/FN1/NRP1/FG R	4
BP	GO:0042 119	neutrophil activation	2/37	41/18800	0.0029446 59	0.0306 60417	0.0198 28237	ITGAM/FCGR2B	2
BP	GO:0034	toll-like receptor 4	2/37	42/18800	0.0030880	0.0319	0.0206	TREM2/PIK3AP1	2

	142	signaling pathway			71	10071	36394		
BP	GO:0006	phagocytosis	4/37	310/18800	0.0031192	0.0319	0.0206	TREM2/ITGAM/FCGR2B	4
	909				93	90339	88304		
BP	GO:0070	regulation of ERK1 and ERK2 cascade	4/37	311/18800	0.0031555	0.0321	0.0207	TREM2/FN1/NRP1/CC	4
	372				22	20386	72406	R1	
BP	GO:1901	regulation of neuron death	4/37	313/18800	0.0032288	0.0322	0.0208	TREM2/ITGAM/NRP1	4
	214				44	05411	27392	/FCGR2B	
BP	GO:0008	regulation of cell shape	3/37	151/18800	0.0032310	0.0322	0.0208	PARVB/FN1/FGR	3
	360				04	05411	27392		
BP	GO:0042	superoxide anion generation	2/37	43/18800	0.0032347	0.0322	0.0208	CYBB/ITGAM	2
	554				08	05411	27392		
BP	GO:0006	humoral immune response	4/37	317/18800	0.0033789	0.0331	0.0214	ALOX5/TREM2/VSIG	4
	959				76	5772	43254	4/FCGR2B	
BP	GO:0019	viral life cycle	4/37	317/18800	0.0033789	0.0331	0.0214	MRC1/CLEC5A/CD86/	4
	058				76	5772	43254	NRP1	
BP	GO:0050	regulation of axonogenesis	3/37	154/18800	0.0034149	0.0332	0.0215	TRPV2/FN1/NRP1	3
	770				44	71314	16717		
BP	GO:1904	cellular response to amyloid-beta	2/37	45/18800	0.0035376	0.0342	0.0221	TREM2/FCGR2B	2
	646				01	21903	31467		
BP	GO:1902	positive regulation of leukocyte differentiation	3/37	157/18800	0.0036051	0.0343	0.0222	CD86/TREM2/CCR1	3
	107				97	88028	38901		
BP	GO:1903	positive regulation of hemopoiesis	3/37	157/18800	0.0036051	0.0343	0.0222	CD86/TREM2/CCR1	3
	708				97	88028	38901		
BP	GO:0002	response-regulating cell surface receptor signaling pathway	4/37	328/18800	0.0038163	0.0355	0.0229	LAPTM5/FPR3/FGR/F	4
	768				36	12293	65968	CGR2B	
BP	GO:0001	microglial cell activation	2/37	47/18800	0.0038532	0.0355	0.0229	TREM2/ITGAM	2
	774				4	12293	65968		
BP	GO:0002	regulation of acute inflammatory response	2/37	47/18800	0.0038532	0.0355	0.0229	ALOX5AP/FCGR2B	2
	673				4	12293	65968		
BP	GO:0036	granulocyte activation	2/37	47/18800	0.0038532	0.0355	0.0229	ITGAM/FCGR2B	2
	230				4	12293	65968		
BP	GO:0097	dendritic cell differentiation	2/37	47/18800	0.0038532	0.0355	0.0229	TREM2/FCGR2B	2
	028				4	12293	65968		
BP	GO:0070	leukocyte proliferation	4/37	330/18800	0.0038997	0.0357	0.0230	CD86/TREM2/VSIG4/	4
	661				98	00165	87466	FCGR2B	
BP	GO:0030	positive regulation of cell growth	3/37	163/18800	0.0040049	0.0358	0.0231	TRPV2/FN1/NRP1	3
	307				08	01056	52713		
BP	GO:0099	postsynapse organization	3/37	163/18800	0.0040049	0.0358	0.0231	TREM2/NRP1/FCGR2	3
	173				08	01056	52713	B	
BP	GO:0006	acute-phase response	2/37	48/18800	0.0040158	0.0358	0.0231	FN1/CD163	2

BP	GO:0006 887	exocytosis	4/37	357/18800	0.0051509 33	0.0413 28665	0.0267 27443	ITGAM/FGR/FCGR2B /CCR1	4
BP	GO:0008 361	regulation of cell size	3/37	179/18800	0.0051994 69	0.0414 74131	0.0268 21517	TRPV2/FN1/NRP1	3
BP	GO:0002 763	positive regulation of myeloid leukocyte differentiation	2/37	55/18800	0.0052412 64	0.0415 64444	0.0268 79923	TREM2/CCR1	2
BP	GO:0050 767	regulation of neurogenesis	4/37	361/18800	0.0053567 12	0.0422 34426	0.0273 13204	TRPV2/TREM2/FN1/N RP1	4
BP	GO:0046 456	icosanoid biosynthetic process	2/37	57/18800	0.0056191 47	0.0440 48949	0.0284 86664	ALOX5/ALOX5AP	2
BP	GO:0032 481	positive regulation of type I interferon production	2/37	58/18800	0.0058126 54	0.0451 74571	0.0292 14609	MMP12/TLR8	2
BP	GO:0071 706	tumor necrosis factor superfamily cytokine production	3/37	187/18800	0.0058690 32	0.0451 74571	0.0292 14609	CYBB/CD86/TREM2	3
BP	GO:1903 555	necrosis factor superfamily cytokine production	3/37	187/18800	0.0058690 32	0.0451 74571	0.0292 14609	CYBB/CD86/TREM2	3
BP	GO:1903 706	regulation of hemopoiesis	4/37	371/18800	0.0058952 15	0.0451 74571	0.0292 14609	CD86/TREM2/FCGR2 B/CCR1	4
BP	GO:0000 768	syncytium formation by plasma membrane fusion	2/37	59/18800	0.0060091 88	0.0452 84706	0.0292 85834	TREM2/CD53	2
BP	GO:0001 755	neural crest cell migration	2/37	59/18800	0.0060091 88	0.0452 84706	0.0292 85834	FN1/NRP1	2
BP	GO:0140 253	cell-cell fusion	2/37	59/18800	0.0060091 88	0.0452 84706	0.0292 85834	TREM2/CD53	2
BP	GO:1903 409	reactive oxygen species biosynthetic process	2/37	61/18800	0.0064112 88	0.0480 49434	0.0310 73797	CYBB/ALOX5	2
BP	GO:0002 712	regulation of B cell mediated immunity	2/37	62/18800	0.0066168 31	0.0489 98856	0.0316 87792	TREM2/FCGR2B	2
BP	GO:0002 889	regulation of immunoglobulin mediated immune response	2/37	62/18800	0.0066168 31	0.0489 98856	0.0316 87792	TREM2/FCGR2B	2
BP	GO:0006 949	syncytium formation	2/37	63/18800	0.0068253 54	0.0489 98856	0.0316 87792	TREM2/CD53	2
BP	GO:0032 613	interleukin-10 production	2/37	63/18800	0.0068253 54	0.0489 98856	0.0316 87792	TREM2/FCGR2B	2
BP	GO:0032	interleukin-12	2/37	63/18800	0.0068253	0.0489	0.0316	TLR8/LAPTM5	2

	615	production			54	98856	87792			
BP	GO:0032	regulation of interleukin-10	2/37	63/18800	0.0068253	0.0489	0.0316	TREM2/FCGR2B		2
	653	production			54	98856	87792			
BP	GO:0032	regulation of interleukin-12	2/37	63/18800	0.0068253	0.0489	0.0316	TLR8/LAPTM5		2
	655	production			54	98856	87792			
BP	GO:0048	antigen processing and presentation of peptide antigen	2/37	63/18800	0.0068253	0.0489	0.0316	TREM2/FCGR2B		2
	002				54	98856	87792			
BP	GO:0045	regulation of osteoclast differentiation	2/37	64/18800	0.0070368	0.0502	0.0324	TREM2/CCR1		2
	670				44	52644	98623			
BP	GO:0009	response to virus	4/37	392/18800	0.0071417	0.0507	0.0328	MLKL/MMP12/TLR8/ FGR		4
	615				25	36008	11217			
BP	GO:0043	cellular component maintenance	2/37	65/18800	0.0072512	0.0512	0.0331	TREM2/FCGR2B		2
	954				89	47455	41972			
BP	GO:0017	regulation of exocytosis	3/37	204/18800	0.0074575	0.0522	0.0337	ITGAM/FGR/FCGR2B		3
	157				42	42451	85441			
BP	GO:0050	regulation of antigen receptor-mediated signaling pathway	2/37	66/18800	0.0074686	0.0522	0.0337	LAPTM5/FCGR2B		2
	854				79	42451	85441			
BP	GO:0043	regulation of neuron apoptotic process	3/37	207/18800	0.0077617	0.0540	0.0349	TREM2/ITGAM/NRP1		3
	523				49	15438	3204			
BP	GO:0042	negative regulation of T cell proliferation	2/37	68/18800	0.0079122	0.0547	0.0354	CD86/VSIG4		2
	130				42	8324	28581			
BP	GO:0050	positive regulation of phagocytosis	2/37	71/18800	0.0085993	0.0592	0.0383	TREM2/FCGR2B		2
	766				73	40123	10868			
BP	GO:0016	immunoglobulin mediated immune response	3/37	216/18800	0.0087181	0.0597	0.0386	TREM2/TLR8/FCGR2 B		3
	064				86	56812	45013			
BP	GO:0010	regulation of cell-substrate adhesion	3/37	217/18800	0.0088285	0.0597	0.0386	MMP12/FN1/NRP1		3
	810				45	77779	58573			
BP	GO:0006	superoxide metabolic process	2/37	72/18800	0.0088341	0.0597	0.0386	CYBB/ITGAM		2
	801				79	77779	58573			
BP	GO:0016	viral process	4/37	418/18800	0.0089132	0.0597	0.0386	MRC1/CLEC5A/CD86/ NRP1		4
	032				54	77779	58573			
BP	GO:0050	synapse organization	4/37	419/18800	0.0089866	0.0597	0.0386	TREM2/ITGAM/NRP1 /FCGR2B		4
	808				31	77779	58573			
BP	GO:0019	B cell mediated immunity	3/37	219/18800	0.0090517	0.0597	0.0386	TREM2/TLR8/FCGR2 B		3
	724				33	77779	58573			
BP	GO:0001	ossification	4/37	420/18800	0.0090604	0.0597	0.0386	CLEC5A/ALOX5/FGR /CCR1		4
	503				04	77779	58573			

BP	GO:0045	negative regulation of innate immune response	2/37	73/18800	0.0090718 48	0.0597 77779	0.0386 58573	MMP12/VSIG4	2
BP	GO:0150	neuroinflammatory response	2/37	73/18800	0.0090718 48	0.0597 77779	0.0386 58573	TREM2/ITGAM	2
BP	GO:0002	positive regulation of leukocyte activation	4/37	421/18800	0.0091345 75	0.0598 10844	0.0386 79956	CD86/TREM2/ITGAM/ FGR	4
BP	GO:0070	positive regulation of ERK1 and ERK2 cascade	3/37	220/18800	0.0091645 65	0.0598 10844	0.0386 79956	TREM2/NRP1/CCR1	3
BP	GO:0002	regulation of immunoglobulin production	2/37	74/18800	0.0093123 67	0.0604 8604	0.0391 16609	CD86/FCGR2B	2
BP	GO:0050	positive regulation of neurogenesis cytokine production	3/37	222/18800	0.0093927 1	0.0607 18749	0.0392 67103	TRPV2/FN1/NRP1	3
BP	GO:0002	involved in inflammatory response regulation of cytokine production	2/37	75/18800	0.0095557 25	0.0611 92531	0.0395 73499	ALOX5/TREM2	2
BP	GO:1900	involved in inflammatory response	2/37	75/18800	0.0095557 25	0.0611 92531	0.0395 73499	ALOX5/TREM2	2
BP	GO:0050	regulation of chemotaxis	3/37	225/18800	0.0097411 5	0.0620 88453	0.0401 52897	TREM2/NRP1/CCR1	3
BP	GO:0048	developmental cell growth	3/37	227/18800	0.0099776 07	0.0632 99798	0.0409 36279	TRPV2/FN1/NRP1	3
BP	GO:0050	positive regulation of cell activation	4/37	436/18800	0.0102953 92	0.0649 85249	0.0420 26268	CD86/TREM2/ITGAM/ FGR	4
BP	GO:0050	regulation of lymphocyte proliferation	3/37	230/18800	0.0103385 62	0.0649 85249	0.0420 26268	CD86/VSIG4/FCGR2B	3
BP	GO:0072	reactive oxygen species metabolic process	3/37	231/18800	0.0104605 57	0.0654 50458	0.0423 27121	CYBB/ALOX5/ITGA M	3
BP	GO:0051	regulation of nervous system development	4/37	440/18800	0.0106204 35	0.0661 47367	0.0427 77815	TRPV2/TREM2/FN1/N RP1	4
BP	GO:0032	regulation of mononuclear cell proliferation	3/37	233/18800	0.0107070 68	0.0662 52395	0.0428 45738	CD86/VSIG4/FCGR2B	3
BP	GO:0097	dendritic spine organization	2/37	80/18800	0.0108147 02	0.0662 52395	0.0428 45738	TREM2/FCGR2B	2
BP	GO:0045	regulated exocytosis	3/37	234/18800	0.0108315	0.0662	0.0428	ITGAM/FGR/FCGR2B	3

	055				87	52395	45738			
		developmental								
BP	GO:0060	growth involved in	3/37	234/18800	0.0108315	0.0662	0.0428			
	560	morphogenesis				87	52395	45738	TRPV2/FN1/NRP1	3
BP	GO:0030	regulation of bone mineralization	2/37	81/18800	0.0110748	0.0674	0.0435		ALOX5/CCR1	2
BP	GO:0045	positive regulation of cell adhesion	4/37	446/18800	0.0111204	0.0674	0.0435		ALOX5/CD86/FN1/NR	4
	785	regulation of response to endoplasmic reticulum stress				33	14537	97301	P1	
BP	GO:1905	response to endoplasmic reticulum stress	2/37	82/18800	0.0113377	0.0681	0.0440		ALOX5/FCGR2B	2
	897					67	28528	59042		
BP	GO:0098	import into cell	3/37	238/18800	0.0113381	0.0681	0.0440		TRPV2/TREM2/SLC2	3
	657					06	28528	59042	A3	
BP	GO:0014	neural crest cell development	2/37	83/18800	0.0116034	0.0691	0.0446		FN1/NRP1	2
	032					27	13863	96263		
BP	GO:0045	positive regulation of exocytosis	2/37	83/18800	0.0116034	0.0691	0.0446		ITGAM/FGR	2
	921					27	13863	96263		
BP	GO:0051	neuron apoptotic process	3/37	241/18800	0.0117268	0.0695	0.0449		TREM2/ITGAM/NRP1	3
	402					91	45563	75445		
BP	GO:0001	regulation of leukocyte mediated cytotoxicity	2/37	85/18800	0.0121429	0.0717	0.0463		ITGAM/FCGR2B	2
	910					47	01214	69515		
BP	GO:0022	cellular component disassembly	4/37	460/18800	0.0123459	0.0725	0.0469		MMP12/TREM2/ITGA	4
	411					93	43092	13962	M/DNASE2B	
BP	GO:0006	receptor-mediated endocytosis	3/37	246/18800	0.0123918	0.0725	0.0469		MRC1/ITGAM/FCGR2	3
	898					92	43092	13962	B	
BP	GO:0001	negative regulation of cytokine-mediated signaling pathway	2/37	87/18800	0.0126933	0.0736	0.0476		MMP12/TREM2	2
	960					26	75306	46169		
BP	GO:1901	positive regulation of neuron death	2/37	87/18800	0.0126933	0.0736	0.0476		ITGAM/FCGR2B	2
	216					26	75306	46169		
BP	GO:0014	mesenchymal cell development	2/37	88/18800	0.0129725	0.0746	0.0482		FN1/NRP1	2
	031					59	60638	83388		
BP	GO:0048	stem cell development	2/37	88/18800	0.0129725	0.0746	0.0482		FN1/NRP1	2
	864					59	60638	83388		
BP	GO:0070	chemokine-mediated signaling pathway	2/37	89/18800	0.0132544	0.0756	0.0489		TREM2/CCR1	2
	098					74	44781	19839		
BP	GO:0106	neuron projection organization	2/37	89/18800	0.0132544	0.0756	0.0489		TREM2/FCGR2B	2
	027					74	44781	19839		
BP	GO:0070	regulation of leukocyte proliferation	3/37	254/18800	0.0135004	0.0767	0.0496		CD86/VSIG4/FCGR2B	3
	663					11	27338	19933		
CC	GO:0070	tertiary granule	6/38	73/19594	5.45E-09	5.88E-	4.64E-		MCEMP1/CLEC5A/C	6

	821	membrane				07	07	YBB/ITGAM/SLC2A3/ CD53	
CC	GO:0035	specific granule	6/38	91/19594	2.08E-08	7.79E-	6.15E-	MCEMP1/CLEC5A/C	
	579	membrane				07	07	YBB/ITGAM/SLC2A3/ CD53	6
CC	GO:0042	specific granule	7/38	160/19594	2.17E-08	7.79E-	6.15E-	MCEMP1/CLEC5A/C	
	581					07	07	YBB/ITGAM/RETN/S LC2A3/CD53	7
CC	GO:0070	tertiary granule	6/38	164/19594	6.94E-07	1.87E-	1.48E-	MCEMP1/CLEC5A/C	
	820					05	05	YBB/ITGAM/SLC2A3/ CD53	6
CC	GO:0009	external side of plasma membrane	7/38	455/19594	2.35E-05	0.0005	0.0003	CD86/TLR8/ITGAM/C	
	897					02552	96751	LEC10A/CD163/FCGR 2B/CCR1	7
CC	GO:0030	secretory granule membrane	6/38	312/19594	2.79E-05	0.0005	0.0003	MCEMP1/CLEC5A/C	
	667					02552	96751	YBB/ITGAM/SLC2A3/ CD53	6
CC	GO:0034	secretory granule lumen	4/38	322/19594	0.0034021	0.0431	0.0340	ALOX5/FN1/RETN/FG	
	774				61	35046	53984	R	4
CC	GO:0060	cytoplasmic vesicle lumen	4/38	325/19594	0.0035167	0.0431	0.0340	ALOX5/FN1/RETN/FG	
	205				48	35046	53984	R	4
CC	GO:0031	vesicle lumen	4/38	327/19594	0.0035945	0.0431	0.0340	ALOX5/FN1/RETN/FG	
	983				87	35046	53984	R	4
MF	GO:0001	opsonin binding	2/38	16/18410	0.0004888	0.0209	0.0143	ITGAM/VSIG4	
	846				29	3728	45069		2
MF	GO:0001	virus receptor activity	3/38	76/18410	0.0005140	0.0209	0.0143	MRC1/CLEC5A/CD86	
	618				37	3728	45069		3
MF	GO:0140	exogenous protein binding	3/38	77/18410	0.0005341	0.0209	0.0143	MRC1/CLEC5A/CD86	
	272				17	3728	45069		3
MF	GO:0038	cargo receptor activity	3/38	79/18410	0.0005757	0.0209	0.0143	MRC1/ITGAM/CD163	
	024				69	3728	45069		3
MF	GO:0001	amyloid-beta binding	3/38	81/18410	0.0006194	0.0209	0.0143	TREM2/ITGAM/FCGR	
	540				46	3728	45069	2B	3
MF	GO:0001	complement binding	2/38	20/18410	0.0007699	0.0216	0.0148	ITGAM/VSIG4	
	848				58	87143	58834		2
MF	GO:0016	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	2/38	24/18410	0.0011126	0.0255	0.0174	ALOX5/ALOX5AP	
	702				57	1557	81861		2
MF	GO:0016	oxidoreductase activity, acting on	2/38	25/18410	0.0012078	0.0255	0.0174	ALOX5/ALOX5AP	
	701				38	1557	81861		2

		single donors with							
		incorporation of							
		molecular oxygen							
MF	GO:0003	NAD+ nucleosidase	2/38	28/18410	0.0015159	0.0284	0.0195	TLR8/PIK3AP1	2
	953	activity			48	66138	03427		
MF	GO:0030	carbohydrate binding	4/38	270/18410	0.0022564	0.0381	0.0261	MRC1/CLEC5A/CLEC	4
	246				36	33775	27158	10A/SLC2A3	
MF	GO:0140	immune receptor	3/38	148/18410	0.0034950	0.0536	0.0367	FPR3/FCGR2B/CCR1	3
	375	activity			95	97374	90478		
MF	GO:0015	coreceptor activity	2/38	47/18410	0.0042296	0.0576	0.0394	CD86/NRP1	2
	026				03	33976	8762		
MF	GO:0005	fatty acid binding	2/38	49/18410	0.0045893	0.0576	0.0394	FABP6/ALOX5AP	2
	504				84	33976	8762		
		hydrolase activity,							
		hydrolyzing							
MF	GO:0016	N-glycosyl	2/38	50/18410	0.0047744	0.0576	0.0394	TLR8/PIK3AP1	2
	799	compounds			12	33976	8762		

Supplementary Table 2.KEGG enrichment analysis of 41 candidate genes.

ID	Description	GeneRatio	BgRat io	pvalue	p.adjust	qvalue	geneID	Count
hsa04	Phagosome	6月28日	152/8	9.95E-0	0.00086	0.00072	MRC1/CYBB/ITGAM/TUB	6
145			190	6	5869	2867	B6/ATP6V0D2/FCGR2B	
hsa05	Tuberculosis	4月28日	180/8	0.00305	0.08992	0.07507	MRC1/ITGAM/ATP6V0D2/	4
152			190	8108	4986	3491	FCGR2B	
hsa04	Neutrophil extracellular	4月28日	190/8	0.00371	0.08992	0.07507	CYBB/TLR8/ITGAM/FPR3	4
613	trap formation		190	499	4986	3491		
hsa05	Staphylococcus aureus	3月28日	96/81	0.00413	0.08992	0.07507	ITGAM/FPR3/FCGR2B	3
150	infection		90	4482	4986	3491		
hsa04	Ferroptosis	2月28日	41/81	0.00851	0.14482	0.12091	FTL/CYBB	2
216			90	232	9432	0234		
hsa04	Lysosome	3月28日	132/8	0.00998	0.14482	0.12091	LAPTM5/DNASE2B/ATP6	3
142			190	8237	9432	0234	V0D2	
hsa04	Necroptosis	3月28日	159/8	0.01648	0.20485	0.17101	FTL/CYBB/MLKL	3
217			190	2274	1126	9089		
hsa05	Acute myeloid leukemia	2月28日	67/81	0.02173	0.21599	0.18032	ITGAM/BCL2A1	2
221			90	2762	6693	3918		
hsa04	Fc epsilon RI signaling	2月28日	68/81	0.02234	0.21599	0.18032	ALOX5/ALOX5AP	2
664	pathway		90	4485	6693	3918		
hsa05	Transcriptional	3月28日	193/8	0.02738	0.22276	0.18597	CD86/ITGAM/BCL2A1	3
202	misregulation in cancer		190	3717	1174	1216		
hsa05	Leishmaniasis	2月28日	77/81	0.02816	0.22276	0.18597	CYBB/ITGAM	2
140			90	5206	1174	1216		
hsa04	B cell receptor signaling	2月28日	82/81	0.03163	0.22935	0.19147	PIK3AP1/FCGR2B	2

662	pathway		90	5174	5013	6055		
hsa04	Complement and	2月28日	86/81	0.03452	0.23106	0.19290	ITGAM/VSIG4	2
610	coagulation cascades		90	7258	7034	5328		
hsa05	Rheumatoid arthritis	2月28日	93/81	0.03982	0.23554	0.19664	CD86/ATP6V0D2	2
323			90	6821	6779	5224		
hsa05	Coronavirus disease -	3月28日	232/8	0.04366	0.23554	0.19664	CYBB/TLR8/NRP1	3
171	COVID-19		190	7813	6779	5224		
hsa04	AGE-RAGE signaling		100/8	0.04541	0.23554	0.19664		
933	pathway in diabetic	2月28日	190	6004	6779	5224	CYBB/FN1	2
	complications							
hsa05	Amoebiasis	2月28日	102/8	0.04706	0.23554	0.19664	ITGAM/FN1	2
146			190	3907	6779	5224		
hsa04	Toll-like receptor		104/8	0.04873	0.23554	0.19664		
620	signaling pathway	2月28日	190	3816	6779	5224	CD86/TLR8	2

Supplementary Table 3. Protein Interaction Networks of 41 Candidate Genes.

from	to	weight
SLC2A3	CD53	902
BCL2A1	LAPTM5	428
IGSF6	LAPTM5	526
CD53	LAPTM5	910
CLEC10A	CCR1	424
BCL2A1	CCR1	431
CD53	CCR1	551
LAPTM5	CCR1	402
RETN	TLR8	490
CLEC10A	TLR8	744
BCL2A1	TLR8	451
IGSF6	TLR8	555
CCR1	TLR8	590
MLKL	TLR8	449
SLC2A3	MCEMP1	912
RETN	MCEMP1	628
CD53	MCEMP1	918
LAPTM5	MCEMP1	471
TLR8	MCEMP1	438
CLEC10A	CD86	587
NRP1	CD86	489
BCL2A1	CD86	464
CD53	CD86	571
LAPTM5	CD86	403
CCR1	CD86	702
TLR8	CD86	786

CLEC10A	FPR3	445
CCR1	FPR3	932
TLR8	FPR3	532
NRP1	FN1	533
CCR1	FN1	415
TLR8	FN1	483
CD86	FN1	429
CLEC10A	FCGR2B	430
IGSF6	FCGR2B	435
CD53	FCGR2B	505
LAPTM5	FCGR2B	524
CCR1	FCGR2B	496
TLR8	FCGR2B	615
CD86	FCGR2B	829
CLEC10A	CD163	535
IGSF6	CD163	552
CCR1	CD163	456
TLR8	CD163	594
CD86	CD163	740
FPR3	CD163	547
FCGR2B	CD163	674
CD53	CD101	731
TLR8	TREM2	462
CD86	TREM2	449
FCGR2B	TREM2	424
CD163	TREM2	419
IGSF6	FGR	571
CD53	FGR	527
LAPTM5	FGR	575
CCR1	FGR	441
TLR8	FGR	638
CD86	FGR	400
FN1	FGR	531
FCGR2B	FGR	436
TLR8	ALOX5	450
CD86	ALOX5	406
FGR	ALOX5	615
CLEC10A	VSIG4	437
IGSF6	VSIG4	499
TLR8	VSIG4	448
CD86	VSIG4	470
FPR3	VSIG4	555
CD163	VSIG4	870
TREM2	VSIG4	586

RETN	FTL	902
SLC2A3	CYBB	904
BCL2A1	CYBB	444
IGSF6	CYBB	415
CD53	CYBB	955
LAPTM5	CYBB	529
CCR1	CYBB	546
TLR8	CYBB	703
MCEMP1	CYBB	928
CD86	CYBB	641
FPR3	CYBB	471
FN1	CYBB	468
FCGR2B	CYBB	493
FGR	CYBB	461
ALOX5	CYBB	460
SLC2A3	ITGAM	906
RETN	ITGAM	498
CLEC10A	ITGAM	624
CD53	ITGAM	952
LAPTM5	ITGAM	536
CCR1	ITGAM	748
TLR8	ITGAM	769
MCEMP1	ITGAM	932
CD86	ITGAM	920
FN1	ITGAM	589
FCGR2B	ITGAM	895
CD163	ITGAM	759
TREM2	ITGAM	569
FGR	ITGAM	664
ALOX5	ITGAM	681
VSIG4	ITGAM	540
CYBB	ITGAM	977
SLC2A3	CLEC5A	900
CD53	CLEC5A	926
TLR8	CLEC5A	589
MCEMP1	CLEC5A	935
CD86	CLEC5A	401
TREM2	CLEC5A	647
VSIG4	CLEC5A	447
CYBB	CLEC5A	932
ITGAM	CLEC5A	947
RETN	MRC1	501
CLEC10A	MRC1	531
CCR1	MRC1	425

TLR8	MRC1	583
CD86	MRC1	814
FCGR2B	MRC1	725
CD163	MRC1	900
TREM2	MRC1	590
VSIG4	MRC1	501
CYBB	MRC1	424
ITGAM	MRC1	832
CLEC5A	MRC1	474
FN1	MMP12	570
TREM2	MMP12	410
ITGAM	MMP12	443
MRC1	MMP12	422
IGSF6	ALOX5AP	616
CD53	ALOX5AP	632
LAPTM5	ALOX5AP	728
CCR1	ALOX5AP	409
FGR	ALOX5AP	564
ALOX5	ALOX5AP	997
ITGAM	ALOX5AP	658