



Integrative analyses of leprosy susceptibility genes indicate a common autoimmune profile

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ARTICLE INFO

Article history:

Received 1 August 2015

Received in revised form 14 December 2015

Accepted 5 January 2016

Keywords:

Leprosy
Susceptibility gene
Enrichment
Autoimmune
Network

ABSTRACT

Background: Leprosy is an ancient chronic infection in the skin and peripheral nerves caused by *Mycobacterium leprae*. The development of leprosy depends on genetic background and the immune status of the host. However, there is no systematic view focusing on the biological pathways, interaction networks and overall expression pattern of leprosy-related immune and genetic factors.

Objectives: To identify the hub genes in the center of leprosy genetic network and to provide an insight into immune and genetic factors contributing to leprosy.

Methods: We retrieved all reported leprosy-related genes and performed integrative analyses covering gene expression profiling, pathway analysis, protein–protein interaction network, and evolutionary analyses.

Results: A list of 123 differentially expressed leprosy related genes, which were enriched in activation and regulation of immune response, was obtained in our analyses. Cross-disorder analysis showed that the list of leprosy susceptibility genes was largely shared by typical autoimmune diseases such as lupus erythematosus and arthritis, suggesting that similar pathways might be affected in leprosy and autoimmune diseases. Protein–protein interaction (PPI) and positive selection analyses revealed a co-evolution network of leprosy risk genes.

Conclusions: Our analyses showed that leprosy associated genes constituted a co-evolution network and might undergo positive selection driven by *M. leprae*. We suggested that leprosy may be a kind of autoimmune disease and the development of leprosy is a matter of defect or over-activation of body immunity.

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1. Introduction

Leprosy is an ancient chronic infectious disease caused by *Mycobacterium leprae* and causes a variety of disabilities [1]. Epidemiological survey have found that less than 10% of people in contact with *M. leprae* would develop the disease and the current prevalence rate was estimated as 0.31–0.32 per 10,000 population [2–4]. In the long evolutionary process of interaction with the host,

M. leprae lost about 50% coding genes in its genome, making it a stringent host-dependent intracellular parasite [5,6]. Development of leprosy is determined by the host immune status and genetic background, and there are little differences among different *M. leprae* strains [2,7]. Genomes or genetic susceptibility factors and immune response of those susceptible individuals may be shaped by selection pressure driven by this ancient pathogen [8].

Leprosy can be classified into multibacillary (MB) and paucibacillary (PB) leprosy based on the clinical manifestations and the number of skin lesions according to the World Health Organization (WHO) guidelines [9,10]. Leprosy can also be classified into five subtypes, including two polar forms of leprosy (lepromatous leprosy [LL, belongs to MB] and tuberculoid leprosy [TT, belongs to PB]) and three immunologically unstable borderline forms (borderline tuberculoid leprosy [BT], mid-borderline leprosy

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[BB], borderline lepromatous leprosy [BL]) [10]. The immune responses of patients with leprosy include type I and type II reactions [11–14]. Type I leprosy reaction is mainly characterized by up-regulation of Th1 type T cells expressing IL-2 and IFN- γ , whereas type II reaction is mainly up-regulated by Th2 type T cells and increases proinflammatory cytokines such as TNF- α , IL-6, and IL-1 β . The TT is characterized by a strong Th1 cellular immunity with type I reaction, whereas the LL is caused by the defect of cellular immunity with complicated type II reactions or erythema nodosum leprosum reactions [11–14]. However, it is unclear whether there is leprosy-specific immune profile that would distinguish it from other infectious or immune diseases.

Genetic linkage analysis [15], association analyses [16–21] and genome-wide association study (GWAS) [22,23] have reported numerous leprosy susceptibility genes, most of which are involved in the immune system. Pattern recognition receptors (PRRs) play a key role in pathogen recognition and signal transduction [24]. Genetic polymorphisms of these genes, including Toll-like receptors outside the cell membrane and intracellular NOD-like receptors, have been widely reported to be associated with leprosy [18,25]. Genetic polymorphisms of cytokines, such as TNF- α [26], IFN- γ [19], interleukin (ILs) [27], and human leukocyte antigen (HLA) [28,29] that were involved in type I and type II reactions have been identified to be related to leprosy susceptibility. Although the associations of several top genes such as *IL10*, *TNF*, *NOD2*, *PARK2*, Toll-like receptors (e.g., *TLR1* and *TLR4*), and HLA alleles (e.g., *HLA-DRB1*) with leprosy have been well replicated, a number of leprosy associated genes were analyzed in different populations with insufficient replications (cf. <https://phgkb.cdc.gov/HuGENavigator/startPagePhenoPedia.do>). There were successful attempts using animal experiments with *M. leprae* strains to study the pathobiology of leprosy [30], yet functional investigation of

potential leprosy causal genes is still a challenge. What's more, reported genetic association studies had paid limited attention to the gene expression pattern of leprosy susceptibility genes.

Hitherto, there is no report for integrative analyses of leprosy. In this study, we collected all reported leprosy-related genes and performed integrative analyses, to fully characterize host immune response and genetic background that influence the development and susceptibility to leprosy.

2. Materials and methods

2.1. Research strategy

We took the following strategies in our integrative analyses (Fig. 1): First, we retrieved all leprosy-associated genes from published sources as a preliminary gene set. Second, the preliminary gene set was checked and filtered with gene expression profiling. Third, Gene Ontology (GO) enrichment analysis [31] for terms of Biological Process (BP), Cellular Component (CC), Molecular Function (MF) was conducted for the filtered gene set. Fourth, cross-disorder analysis was performed for the gene set to identify shared genetic factors between typical infectious and immune diseases. Fifth, protein–protein interaction and co-expression network analysis [32] was performed for the genes in the gene set [33–35]. Finally, the leprosy susceptibility genes were analyzed for positive selection among populations by using an integrated method CMS (Composite of Multiple Signals) [36].

2.2. Gene set compilation and assignment

Four public data sources were employed to compile the complete gene list of all reported leprosy associated genes: (1)

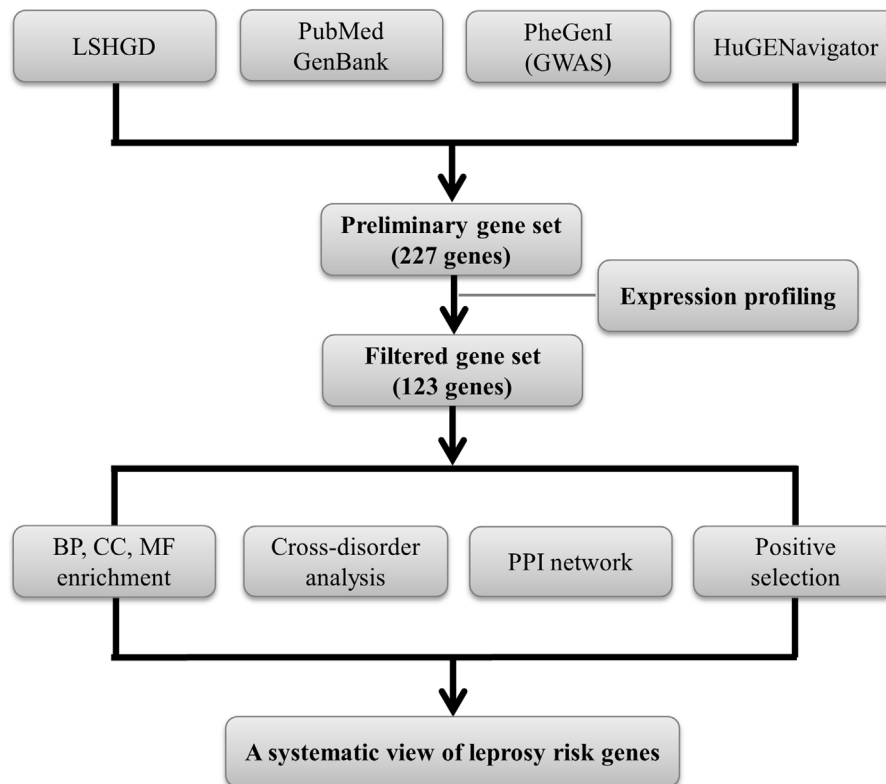


Fig. 1. Study design of the integrative analyses.

We retrieved all leprosy-related genes from published sources. The preliminary gene set were checked and filtered by referring to gene expression profiling. The filtered gene set was used for Gene Ontology (GO) enrichment analysis for Biological Process (BP), Cellular Component (CC), and Molecular Function (MF), cross-disorder analysis [31], protein–protein interaction and co-expression network analysis [35], and positive selection analysis.

Table 1
Expression changes of 123 leprosy associated genes.

Gene	PB		MB		R1		R2	
	adj.P.Val	logFC	adj.P.Val	logFC	adj.P.Val	logFC	adj.P.Val	logFC
CCL3	2.8E-12	5.38	1.1E-16	6.41	1.5E-14	6.59	1.2E-09	6.30
PSMB9	5.3E-15	2.61	1.3E-15	2.49	6.7E-16	2.88	5.3E-09	2.73
PRKCQ	7.8E-14	3.61	1.7E-15	3.38	2.2E-14	3.93	2.4E-08	2.90
BATF	1.2E-14	3.37	2.1E-15	3.53	6.7E-19	4.06	1.2E-09	3.36
HLA-DPB1	1.7E-12	2.05	5.6E-14	2.45	6.9E-17	2.74	6.6E-09	2.02
PTPN22	4.2E-13	3.47	5.8E-14	3.70	3.7E-15	4.23	1.2E-08	3.26
IL10RA	2.7E-11	2.49	1.6E-13	2.69	4.4E-17	3.12	1.2E-09	2.83
TAP1	2.3E-13	1.89	1.9E-13	1.65	2.4E-12	2.19	6.1E-06	1.76
HLA-DMB	1.2E-12	2.60	2.1E-13	2.97	4.1E-17	3.24	4.7E-10	2.65
HLA-DPA1	2.2E-11	2.33	3.4E-13	2.61	7.8E-16	3.52	6.2E-09	2.31
AIF1	2.9E-13	2.48	4.6E-13	3.29	1.6E-16	3.41	8.9E-12	3.80
CCL5	4.0E-10	3.28	8.1E-13	3.56	8.0E-13	3.79	8.0E-07	2.84
HLA-G	5.6E-14	1.85	1.1E-12	2.06	3.2E-15	2.28	3.7E-08	1.86
HLA-DOA	1.3E-11	3.04	1.2E-12	3.67	9.7E-16	4.05	4.4E-07	2.60
HLA-F	2.8E-12	2.06	1.6E-12	1.95	1.4E-14	2.21	3.7E-08	1.95
HLA-DQA1	5.8E-11	2.21	1.6E-12	2.35	1.4E-13	2.67	3.9E-07	2.10
HLA-B	8.4E-07	1.91	2.4E-12	2.33	1.1E-12	2.48	6.2E-07	1.88
LTB	9.8E-13	4.52	2.9E-12	2.91	7.0E-15	4.67	1.5E-07	3.25
HLA-DMA	4.4E-12	2.52	3.2E-12	3.07	2.3E-17	3.29	2.0E-09	2.61
PSMB8	1.1E-13	1.57	1.1E-11	1.49	2.1E-14	1.79	8.6E-09	1.85
NCR3	2.1E-12	3.34	1.3E-11	2.83	7.8E-13	3.42	5.5E-03	1.23
FCN1	2.7E-12	2.13	1.5E-11	2.22	6.6E-13	2.77	6.8E-10	3.10
HLA-DQB1	2.4E-08	2.05	2.1E-11	2.22	3.0E-12	2.61	6.8E-07	2.00
HLA-DOB	1.2E-11	2.40	2.2E-11	1.99	8.7E-14	2.55	3.9E-05	1.43
HLA-DRB1	1.2E-10	2.07	2.4E-11	2.23	4.6E-15	2.62	1.3E-08	2.10
NLRP3	1.8E-11	2.53	4.9E-11	2.62	7.2E-14	3.17	1.3E-09	3.45
TAP2	2.4E-11	2.36	9.6E-11	1.86	3.9E-14	2.67	2.9E-06	2.10
GPSM3	3.6E-11	2.29	1.4E-10	2.36	9.3E-18	2.90	5.7E-09	2.49
CCDC88B	7.5E-09	2.19	1.8E-10	2.01	1.4E-14	2.73	4.9E-06	1.67
HLA-DRA	1.0E-10	2.58	2.4E-10	2.65	2.7E-12	3.06	5.6E-09	2.67
HLA-A	1.5E-10	1.81	3.5E-10	2.06	3.3E-14	2.49	4.3E-06	1.92
BATF3	4.0E-09	1.95	6.3E-10	1.74	3.1E-13	2.51	6.7E-06	2.42
ICAM1	7.7E-10	2.34	6.9E-10	2.63	1.3E-14	3.35	4.2E-10	3.84
CFB	1.2E-08	2.15	1.3E-09	1.92	2.2E-12	2.81	1.4E-10	3.82
LST1	1.1E-06	1.33	3.3E-09	1.47	1.4E-11	1.79	5.3E-08	1.57
TLR2	2.2E-08	1.53	1.2E-08	2.09	2.2E-14	2.53	4.3E-11	3.23
HLA-C	1.6E-09	1.85	3.6E-08	1.62	2.1E-10	1.99	2.1E-07	1.89
C3	7.7E-09	2.12	8.8E-08	1.70	1.6E-10	2.51	2.8E-05	1.68
MICB	7.3E-08	1.17	1.0E-07	1.25	8.8E-13	1.10	1.7E-06	0.94
ALS2CL	3.9E-06	-1.39	1.3E-07	-1.53	4.5E-11	-1.72	2.2E-07	-1.88
TLR4	5.4E-06	1.00	1.6E-07	2.19	1.1E-11	2.07	5.3E-09	2.61
TNF	5.1E-08	2.52	3.4E-07	2.21	5.5E-14	3.51	3.3E-07	2.62
IFNGR1	1.3E-07	0.78	9.9E-07	1.09	4.4E-10	1.04	1.9E-05	1.00
C6orf26	1.6E-04	-1.59	1.4E-06	-1.43	1.6E-10	-2.00	5.4E-10	-2.71
RAB32	3.5E-07	0.91	1.6E-06	1.45	1.3E-10	1.45	1.6E-08	1.67
PPT2	1.6E-05	-0.95	1.6E-06	-1.07	2.9E-09	-1.26	5.3E-06	-1.14
FAM89A	1.4E-04	-0.88	2.0E-06	-1.01	4.1E-09	-1.35	1.3E-02	-0.55
CSNK2B	1.3E-03	-0.38	2.5E-06	-0.49	6.2E-07	-0.57	1.0E-05	-0.63
VDR	7.7E-07	-0.73	2.6E-06	-1.10	3.3E-07	-0.85	6.9E-03	-0.43
TNFRSF25	8.0E-04	-0.44	4.1E-06	-1.30	1.8E-07	-0.99	5.5E-08	-1.65
GNG2	3.2E-05	0.85	5.1E-06	1.03	6.0E-07	1.17	1.0E-03	0.75
IL6R	2.5E-05	1.15	7.3E-06	1.18	1.9E-09	1.58	1.2E-05	1.33
IL6	9.3E-05	1.84	8.5E-06	1.69	1.8E-07	2.52	3.6E-08	6.50
NOD1	1.7E-05	0.63	9.8E-06	0.68	5.5E-11	0.99	1.9E-08	1.60
LY6G5C	4.7E-06	1.20	1.0E-05	1.20	8.2E-06	1.33	1.9E-03	0.89
LTA4H	1.3E-05	0.89	1.1E-05	1.64	1.9E-09	1.79	4.1E-03	1.10
TGFB1	1.1E-07	1.19	1.2E-05	1.30	9.7E-12	1.78	5.2E-08	1.68
ERBB2	1.1E-05	-1.16	1.2E-05	-1.53	3.8E-11	-2.09	9.6E-08	-2.09
TLR1	2.0E-05	1.83	1.3E-05	2.19	3.5E-14	2.91	8.9E-12	3.59
EGFL8	1.2E-05	-0.83	1.9E-05	-1.08	1.1E-09	-1.22	8.4E-09	-1.61
HSPA1B	2.1E-02	-0.96	2.6E-05	-1.37	1.2E-07	-2.00	1.0E-05	-1.56
DDAH2	7.9E-06	-0.87	3.7E-05	-0.59	6.2E-05	-0.88	3.0E-05	-0.99
LY6G6D	2.5E-03	-1.59	4.0E-05	-1.79	1.1E-06	-2.24	6.2E-05	-2.30
C4B	6.7E-03	0.98	4.7E-05	1.53	8.0E-09	1.57	3.8E-09	2.24
FKBP1	2.6E-04	-0.88	5.9E-05	-0.91	9.4E-04	-1.00	2.7E-02	-0.61
RGNEF	2.3E-05	-1.06	8.7E-05	-1.19	7.0E-09	-1.81	1.8E-07	-2.12
HCP5	1.7E-03	0.80	1.2E-04	0.75	5.5E-10	1.18	8.7E-04	0.62
NEBL	1.5E-05	-1.43	1.2E-04	-1.50	1.2E-10	-2.42	3.2E-06	-2.18
IL4R	4.9E-06	0.85	1.7E-04	0.65	2.1E-10	1.23	9.5E-07	1.42
PRRT1	1.4E-04	-0.67	2.0E-04	-0.61	1.7E-05	-0.79	3.4E-05	-0.97
DEFB1	5.0E-05	-1.42	2.1E-04	-1.69	4.9E-11	-2.48	1.7E-03	-1.60
MEN1	2.9E-03	-0.50	2.1E-04	-0.59	7.6E-04	-0.50	9.4E-05	-0.62
IL13RA1	2.2E-04	0.44	2.2E-04	0.56	1.5E-09	0.86	8.4E-09	1.60
C2	5.6E-03	0.86	2.3E-04	1.08	2.1E-10	1.35	4.9E-06	1.19

Table 1 (Continued)

Gene	PB		MB		R1		R2	
	adj.P.Val	logFC	adj.P.Val	logFC	adj.P.Val	logFC	adj.P.Val	logFC
STK19	1.0E-03	-1.15	2.9E-04	-1.14	3.6E-04	-1.22	5.9E-03	-1.14
MAPT	3.1E-05	-1.07	2.9E-04	-1.37	2.9E-06	-1.68	1.6E-07	-3.04
BCHE	6.6E-05	-1.13	3.3E-04	-1.83	8.7E-08	-2.19	1.4E-05	-2.38
TOLLIP	4.9E-05	-0.56	4.0E-04	-0.45	2.1E-06	-0.60	8.5E-04	-0.57
GNL1	2.3E-03	-0.68	5.5E-04	-0.81	7.2E-06	-0.89	8.5E-06	-1.47
RDBP	2.7E-02	-0.17	5.6E-04	-0.26	4.0E-06	-0.33	1.2E-01	-0.15
RIPK2	4.6E-04	0.51	6.0E-04	0.64	1.9E-07	0.98	1.0E-03	0.76
APOM	1.1E-04	-0.65	7.5E-04	-0.62	2.8E-07	-0.94	3.5E-03	-0.69
PSORS1C1	6.3E-03	-1.45	1.0E-03	-1.60	4.4E-05	-1.51	2.3E-03	-1.54
TGFBR1	6.1E-03	0.44	1.5E-03	0.77	1.8E-07	1.02	3.1E-07	1.33
ATP6V1G2	5.0E-03	0.76	1.7E-03	0.82	3.6E-05	0.79	7.9E-01	0.08
PACRG	2.3E-04	-0.69	2.2E-03	-0.66	2.3E-06	-0.89	2.7E-05	-0.95
IL18RAP	5.7E-05	1.90	2.3E-03	1.12	1.3E-08	2.44	5.8E-06	2.17
MICA	2.4E-01	0.17	3.2E-03	0.34	2.3E-03	0.40	4.6E-02	0.44
GTF2H4	2.3E-03	-0.53	3.6E-03	-0.52	7.1E-02	-0.35	2.8E-01	-0.20
IL10RB	3.2E-02	0.21	3.7E-03	0.51	7.1E-08	0.64	1.8E-06	0.83
NINJ1	1.2E-02	0.38	4.4E-03	0.56	7.8E-07	0.92	3.5E-03	0.91
NLRP1	4.3E-01	-0.16	4.5E-03	-0.39	6.6E-01	0.09	3.1E-05	-0.79
TGFBR2	2.3E-03	1.07	4.5E-03	0.76	3.9E-06	1.28	2.9E-04	0.86
NFKBIL1	5.9E-03	-0.46	6.4E-03	-0.38	2.4E-04	-0.45	2.3E-02	-0.30
HSPA1A	4.3E-01	-0.27	7.9E-03	-0.46	7.3E-05	-0.73	1.4E-02	-0.53
GSTM1	1.0E-02	-0.61	8.0E-03	-0.70	6.3E-04	-0.91	8.9E-04	-1.06
CD209	3.7E-02	0.70	8.6E-03	1.03	5.9E-08	1.55	3.0E-06	1.69
CCHCR1	9.0E-03	-0.37	1.3E-02	-0.40	4.2E-06	-0.59	8.1E-06	-0.71
MAP4K2	1.7E-04	0.73	1.3E-02	0.45	1.7E-05	0.75	1.1E-01	0.27
BRD2	9.2E-04	0.24	1.3E-02	0.16	1.3E-02	0.24	4.1E-01	-0.09
APOE	3.9E-01	0.19	1.7E-02	0.63	1.2E-04	0.66	7.3E-01	0.11
TIRAP	4.8E-01	0.08	2.0E-02	0.26	7.3E-03	0.26	1.8E-02	0.30
PBX2	3.2E-04	0.74	2.3E-02	0.45	7.7E-02	0.47	1.3E-01	0.40
LGALS3	1.1E-03	-0.44	2.5E-02	0.62	1.4E-01	-0.25	9.7E-05	-0.69
NOTCH4	8.3E-03	-0.57	2.6E-02	-0.35	1.1E-01	-0.32	6.1E-01	0.14
RNF5	3.8E-01	-0.07	3.3E-02	-0.18	6.8E-01	-0.04	9.6E-04	-0.35
EHMT2	2.7E-01	-0.13	4.3E-02	-0.22	3.2E-01	-0.11	3.2E-03	-0.34
AGPAT1	2.1E-02	-0.41	5.9E-02	-0.35	4.8E-03	-0.44	1.5E-02	-0.47
C7orf44	2.6E-02	0.22	6.2E-02	0.21	1.0E-02	0.27	6.2E-04	0.46
C6orf27	6.9E-02	-0.17	6.6E-02	-0.25	2.3E-04	-0.37	1.2E-02	-0.36
FLOT1	1.4E-01	0.21	7.0E-02	0.25	1.6E-02	0.34	1.1E-05	0.89
SDHD	5.6E-01	0.05	8.2E-02	0.17	2.7E-03	0.30	4.2E-02	0.28
TNXB	1.1E-02	-0.33	8.4E-02	-0.51	4.1E-01	-0.14	1.4E-05	-0.75
AGER	2.0E-03	0.49	1.1E-01	0.18	5.7E-05	0.51	2.1E-01	0.18
C6orf48	8.5E-03	0.21	1.6E-01	0.15	3.5E-02	0.24	9.5E-02	-0.30
SNCA	2.5E-02	-0.56	1.7E-01	0.39	1.2E-01	-0.40	2.9E-01	-0.22
LY6G6C	3.4E-01	-0.31	1.8E-01	-0.35	5.0E-02	-0.35	5.4E-03	-0.77
SLC11A1	2.7E-01	-0.16	2.6E-01	0.38	1.1E-01	0.31	4.8E-08	1.94
CLIC1	9.3E-01	-0.01	3.2E-01	0.10	9.0E-02	0.12	1.5E-02	0.30
TRIM10	2.5E-01	0.27	4.3E-01	-0.18	2.0E-02	0.68	3.6E-04	1.78
LSM2	3.3E-02	0.13	4.7E-01	0.06	3.5E-02	0.14	8.1E-03	0.27
NOS3	5.3E-01	-0.12	6.1E-01	0.11	8.6E-01	-0.04	2.2E-03	0.84
CFH	3.6E-01	0.21	8.2E-01	0.07	3.2E-02	0.47	3.0E-01	-0.14

Note: MB—multibacillary leprosy; PB—paucibacillary leprosy; R1—type I reaction; R2—type II reaction; adj.P.Val—FDR adjusted *P*-value; logFC—log of Fold Change compared with controls.

LSHGD (<http://info.vit.ac.in/leprosy/leprosy.htm>) [37], a database for human leprosy susceptible genes developed in 2012; (2) the Human Genome Epidemiology (HuGE) Navigator (<https://phgkb.cdc.gov/HuGENavigator/startPagePhenoPedia.do>) [38]; (3) The Phenotype–Genotype Integrator (PheGenI, <http://www.ncbi.nlm.nih.gov/gap/phegeni>), which provides the NHGRI genome-wide association study (GWAS) catalog data; (4) PubMed and/or GenBank. For those reports published before September 2012, we directly obtained the leprosy associated gene list (*N* = 47) from LSHGD [37]. We searched PubMed and/or GenBank using “leprosy”, “association”, “gene”, and “genetic variants” as keywords and we retrieved 98 genes reported in leprosy genetic association studies. For the PheGenI; GWAS data [22] with a *P*-value < 5.0×10^{-5} were retrieved and we got 107 leprosy-associated SNPs from 39 genes. From the HuGENavigator; we compiled 224 leprosy-related genes. All genes from these four sources were merged as the preliminary gene set; which contains 227 genes

after the exclusion of the overlapping genes. Hitherto; there is limited number of risk genes reported in leprosy compared with other common diseases. Therefore; we kept all reported leprosy-related genes in the gene set; ignoring the sample size and allele frequency in the original study; as the enrichment analysis requires a relatively larger gene number. We used gene expression change as the criterion to filter the gene list in following analyses (Fig. 1).

2.3. Gene expression profiling

Expression data was retrieved from the Gene Expression Omnibus (GEO, <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE74481>) [39]. In this microarray data, 16487 genes were analyzed for the leprosy skin lesions from 66 patients including 20 PB (10 TT + 10 BT), 24 MB (10 BB + 10 BL + 4 LL), 14 type I reaction (R1), and 10 type II reaction (R2) patients, and normal skin biopsies

from 9 healthy individuals. We screened mRNA expression data of the genes in the preliminary gene set ($N=227$) and retrieved the top differently expressed gene with a cut-off P -value $< 5.0 \times 10^{-6}$ (experiment-wide significance) in PB and MB patients.

2.4. Enrichment analysis

GO enrichment analysis using terms of Biological Process (BP), Cellular Component (CC), and Molecular Function (MF) [31] was performed for the leprosy susceptibility gene set. We used the Database for Annotation, Visualization and Integrated Discovery v6.7 (DAVID, <http://david.abcc.ncifcrf.gov/>) [31], which provides a comprehensive set of functional annotation tools, to perform the enrichment analysis and to infer potential biological meanings behind our list of genes.

2.5. Protein–protein interaction (PPI) and co-expression network analysis

PPI network analysis was performed by a biological network integrator: the GeneMANIA prediction server (<http://www.genemania.org/>), which contains physical protein–protein interaction, pathway analysis, and co-expression analysis [33–35]. The list of leprosy susceptibility genes was set as the input seed. Both direct and indirect interaction networks were included in our analysis.

2.6. Cross-disorder analysis

To clarify whether the leprosy associated genes involved in immune response are leprosy-specific or common for other infectious and/or immune diseases, we performed a cross-disorder analysis. The list of leprosy associated genes were screened in the disease association dataset (Genetic Association DB Disease: <http://geneticassociationdb.nih.gov/>) using DAVID [31].

2.7. Positive selection analysis

We used the positive selection data produced by an integrated method CMS [36], a tool for identifying regions that are under positive selection in the genome using whole-genome sequencing data from the 1000 Genomes project (www.1000genomes.org/) [40]. It generates a composite score based on three distinct

Table 2

Top 10 terms of the GO and KEGG pathway enrichment of 123 leprosy related genes.

Term	Count	% ^a	Fold of enrichment	P-value	FDR
Biological process					
GO:0006955 ~ immune response	52	43.0	9.5	8.1E-38	1.4E-34
GO:0006952 ~ defense response	42	34.7	8.6	6.1E-28	1.0E-24
GO:0019882 ~ antigen processing and presentation	22	18.2	33.5	1.2E-26	2.0E-23
GO:0002684 ~ positive regulation of immune system process	24	19.8	12.7	4.4E-19	7.5E-16
GO:0006954 ~ inflammatory response	26	21.5	10.1	2.7E-18	4.5E-15
GO:0048584 ~ positive regulation of response to stimulus	23	19.0	12.3	6.2E-18	1.0E-14
GO:0009611 ~ response to wounding	30	24.8	7.2	3.6E-17	6.1E-14
GO:0048002 ~ antigen processing and presentation of peptide antigen	11	9.1	49.7	6.6E-15	1.1E-11
GO:0050778 ~ positive regulation of immune response	16	13.2	14.0	3.8E-13	6.5E-10
GO:0002252 ~ immune effector process	15	12.4	14.2	2.1E-12	3.6E-09
Cellular component					
GO:0042611 ~ MHC protein complex	16	13.2	35.9	1.2E-19	1.5E-16
GO:0042613 ~ MHC class II protein complex	10	8.3	44.1	6.1E-13	7.6E-10
GO:0042825 ~ TAP complex	7	5.8	127.8	1.3E-12	1.6E-09
GO:0044459 ~ plasma membrane part	48	39.7	2.8	3.1E-12	3.9E-09
GO:0042824 ~ MHC class I peptide loading complex	7	5.8	99.4	1.5E-11	1.9E-08
GO:0005886 ~ plasma membrane	59	48.8	2.0	1.6E-09	2.0E-06
GO:0005615 ~ extracellular space	23	19.0	4.3	9.0E-09	1.1E-05
GO:0005887 ~ integral to plasma membrane	30	24.8	3.2	1.3E-08	1.6E-05
GO:0031226 ~ intrinsic to plasma membrane	30	24.8	3.2	2.1E-08	2.6E-05
GO:0044421 ~ extracellular region part	24	19.8	3.2	8.2E-07	1.0E-03
Molecular function					
GO:0032395 ~ MHC class II receptor activity	10	8.3	69.0	4.7E-15	6.3E-12
GO:0051059 ~ NF-kappaB binding	7	5.8	31.7	6.5E-08	8.8E-05
GO:0042288 ~ MHC class I protein binding	6	5.0	49.2	9.0E-08	1.2E-04
GO:0042287 ~ MHC protein binding	6	5.0	31.5	1.0E-06	1.4E-03
GO:0019955 ~ cytokine binding	9	7.4	10.8	1.6E-06	2.2E-03
GO:0050785 ~ advanced glycation end-product receptor activity	4	3.3	131.1	1.7E-06	2.2E-03
GO:0032393 ~ MHC class I receptor activity	5	4.1	38.6	6.7E-06	9.1E-03
KEGG pathways					
hsa05332:Graft-versus-host disease	16	13.2	27.8	1.2E-18	1.3E-15
hsa05330:Allograft rejection	15	12.4	28.3	1.5E-17	1.6E-14
hsa04940:Type I diabetes mellitus	15	12.4	24.2	2.0E-16	2.3E-13
hsa04612:Antigen processing and presentation	17	14.0	13.9	1.8E-14	1.9E-11
hsa05320:Autoimmune thyroid disease	14	11.6	18.6	1.4E-13	1.4E-10
hsa05416:Viral myocarditis	15	12.4	14.3	6.7E-13	7.1E-10
hsa05310:Asthma	11	9.1	25.7	3.7E-12	3.9E-09
hsa04672:Intestinal immune network for IgA production	12	9.9	16.6	5.4E-11	5.8E-08
hsa05322:Systemic lupus erythematosus	14	11.6	9.6	1.0E-09	1.1E-06
hsa04514:Cell adhesion molecules (CAMs)	15	12.4	7.7	3.8E-09	4.1E-06

Note—The top 10 terms are defined by the top 10 smallest P values in each category. The entire list is included in Supplementary Table 1.

^a The percentage is defined by the number of gene count for each terms divided by 123 leprosy associated genes.

signatures of selection: long-range haplotypes, differentiated alleles, and high frequency derived alleles. By combining several, nearly-independent signals, CMS detects signals of positive selection at a much higher resolution than the conventional tests, often at the level of single genes. We searched the CMS Viewer tool (<http://www.broadinstitute.org/mpg/cmsviewer/>) [36] to explore positive selection in three populations (European [CEU], African [YRI], and East Asian [CHB + JPT]) for regions of interest (here refer to the leprosy associated genes). A CMS score of one site greater than 3.0 ($FDR < 0.05$) was set as positive selection threshold [36].

3. Results

3.1. mRNA expression profiling and filtered leprosy susceptibility gene set

We screened the mRNA expression changes by using a skin microarray data (16487 genes) of 76 individuals (GSE74481) available in NCBI GEO [39]. At the experiment-wide significance level (P -value $< 5.0 \times 10^{-6}$), there were 2134 genes differentially expressed in PB or MB patients. When we restricted the analysis to 227 leprosy-associated genes in the preliminary gene set, 123 genes were found to be differentially expressed in patient skin lesions (Table 1) and were subjected to following analyses.

3.2. GO terms enrichment

We performed the GO enrichment analyses based on the terms of BP, CC, and MF for the 123 leprosy susceptibility genes using DAVID [31], to understand the potential biological implication

behind this list of genes. For GO term BP, we got 511 terms in total, with 82 terms having a false discovery rate (FDR) < 0.05 (Supplementary Table S1). The top 10 terms were involved in activation and regulation of immune response and inflammatory response (Table 2). For GO term CC, we got 34 terms in total (Supplementary Table S1), with 13 terms having a $FDR < 0.05$ (Table 2). The top significant terms included extracellular space, plasma membrane, and MHC protein complex. For MF terms, we got 56 terms in total, with 7 terms having a $FDR < 0.05$. The top significant terms were “MHC class II receptor activity” and “NF- κ B binding” (Supplementary Table S1).

For pathway analysis, the 123 leprosy associated genes were enriched in 21 KEGG (Kyoto Encyclopedia of Genes and Genomes: <http://www.genome.jp/kegg/>) pathways, with 11 pathways having a $FDR < 0.05$ (Table 2). The top pathways were associated to autoimmune disorders (e.g., allograft rejection, type I diabetes mellitus, and systemic lupus erythematosus) (Supplementary Table S1).

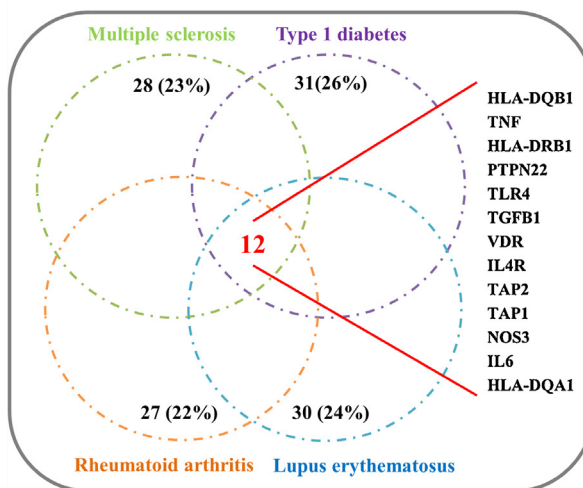
3.3. Cross-disorder feature

We performed a cross-disorder analysis to test whether the 123 leprosy associated genes were leprosy-specific or common for other infectious and/or immune diseases (Fig. 2 and Supplementary Table S2). A total of 85 diseases or disease-related phenotypes showed a significant enrichment of the leprosy related genes ($FDR < 0.05$). Typical autoimmune diseases, such as type I diabetes (enrichment $P = 1.89 \times 10^{-13}$), multiple sclerosis (enrichment $P = 7.44 \times 10^{-13}$), and systemic lupus erythematosus (enrichment $P = 3.52 \times 10^{-12}$), and well-studied infectious diseases, e.g., HIV

(a) Top hits of disease enrichment analysis for leprosy susceptibility genes

Disease	Shared gene Count (%)	Fold Enrichment	P-value	Bonferroni	FDR
Type 1 diabetes	31 (25.6)	6.0	7.96E-17	1.74E-13	1.89E-13
Multiple sclerosis	28 (23.1)	6.5	4.77E-16	6.97E-13	7.44E-13
Rheumatoid arthritis	27 (22.3)	6.9	5.98E-16	8.71E-13	9.33E-13
Systemic lupus erythematosus	23 (19.0)	8.5	2.06E-15	3.31E-12	3.52E-12
Lupus erythematosus	18 (14.9)	9.6	7.00E-13	1.10E-09	1.17E-09
Asthma	26 (21.5)	4.9	7.03E-12	1.10E-08	1.18E-08
Tuberculosis	20 (16.5)	12.8	5.10E-17	7.99E-14	8.51E-14
HIV	20 (16.5)	10.0	1.05E-14	1.65E-11	1.76E-11
Hepatitis B	17 (14.0)	15.0	1.41E-15	2.26E-12	2.41E-12
Psoriasis	19 (15.7)	10.7	1.46E-14	2.28E-11	2.43E-11

(b) Autoimmune disorders



(c) Infection

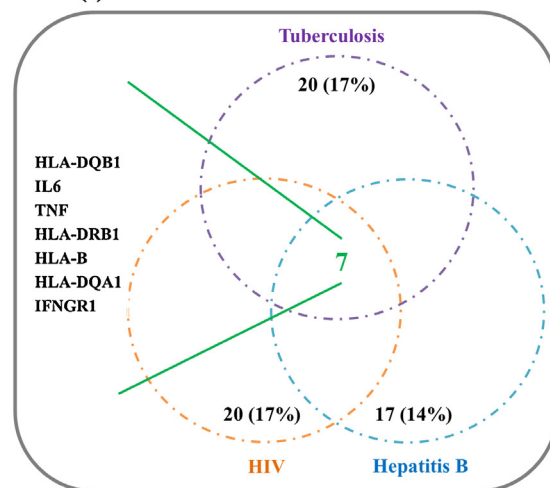


Fig. 2. Cross-disorder analysis showing that leprosy shared similar genetic risk factors with other autoimmune diseases.

The list of leprosy associated genes were screened in the disease association dataset (Genetic Association DB Disease: <http://geneticassociationdb.nih.gov/>) using DAVID [31]. Typical autoimmune diseases and well-studied infectious diseases showed the largest enrichment of leprosy associated genes (a). There are 13 genes shared by leprosy and four typical autoimmune diseases (b) and 7 genes shared by leprosy and typical infectious diseases (c).

(a) Enriched pathways of autoimmune diseases shared genes

KEGG_pathway	Count (%)	Fold Enrichment	P-value	Bonferroni	FDR
hsa05332:Graft-versus-host disease	5 (38.5)	59.3	6.0E-07	2.5E-05	5.6E-04
hsa04672:Intestinal immune network for IgA production	5 (38.5)	47.2	1.5E-06	6.4E-05	0.001
hsa04612:Antigen processing and presentation	5 (38.5)	27.8	1.3E-05	5.4E-04	0.012
hsa05310:Asthma	4 (30.8)	63.8	1.9E-05	8.2E-04	0.018
hsa05330:Allograft rejection	4 (30.8)	51.4	3.8E-05	0.002	0.035
hsa04940:Type I diabetes mellitus	4 (30.8)	44.0	6.0E-05	0.003	0.056
hsa04640:Hematopoietic cell lineage	4 (30.8)	21.5	5.1E-04	0.021	0.475
hsa05322:Systemic lupus erythematosus	4 (30.8)	18.7	7.8E-04	0.032	0.718
hsa05320:Autoimmune thyroid disease	3 (23.1)	27.2	0.004	0.163	3.835
hsa05416:Viral myocarditis	3 (23.1)	19.5	0.008	0.288	7.204

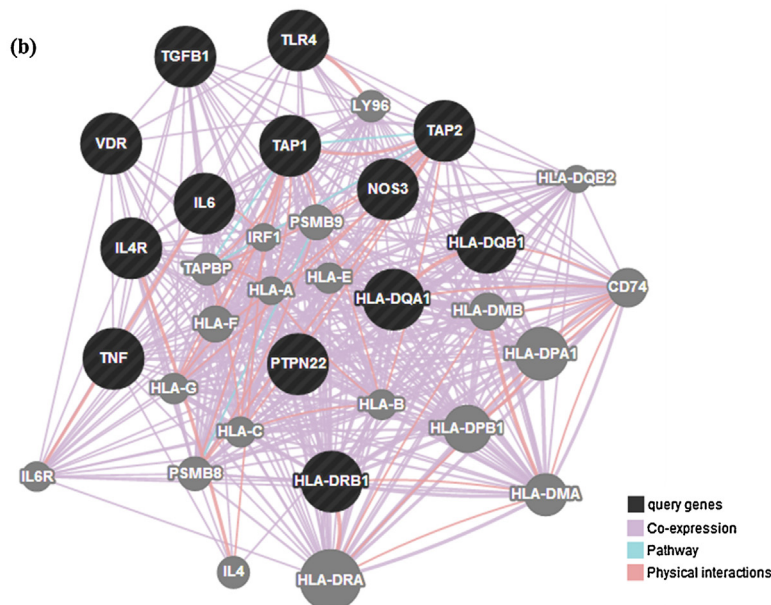


Fig. 3. Protein–protein interaction (PPI), co-expression network and enriched pathways of the 13 genes shared by leprosy and autoimmune diseases. KEGG pathway enrichment analysis (a) was performed by using DAVID [31]. PPI and co-expression network analyses (b) were performed by using the GeneMANIA prediction server (<http://www.genemania.org/>) [35].

infection (enrichment $P = 1.76 \times 10^{-11}$) and tuberculosis (enrichment $P = 5.81 \times 10^{-14}$), showed the largest enrichment of leprosy risk genes (Fig. 2 and Supplementary Table S2). In particular, 13 out of the 123 leprosy-associated genes were shared by leprosy and four other typical autoimmune diseases (multiple sclerosis, type 1 diabetes, rheumatoid arthritis, and lupus erythematosus) (Fig. 2). The leprosy shared autoimmune genes were also enriched in other typical autoimmune reactions such as graft-versus-host disease and allograft rejection, and in “antigen processing and presentation” and “IgA production” pathways (Fig. 3a). Comparatively, only 7 genes were shared by leprosy and the typical infectious diseases. This observation showed that leprosy shared similar genetic risk factors with other autoimmune diseases.

As the majority of the leprosy candidate genes in previous case-control studies were chosen among immune-associated genes, we need to surpass the argument in a circle through a bottom-up strategy. Therefore, we set all 2134 differently expressed ($P < 5.0 \times 10^{-6}$) genes in leprosy skin tissues as another gene set for enrichment analysis. Analysis of this enlarged bottom-up gene set showed a similar pattern as the above results (Table 3).

3.4. Interaction network

We performed the PPI and co-expression network analyses to detect whether the 13 autoimmune genes shared by leprosy and other autoimmune diseases would constitute a network

underlying the regulation of immune response during leprosy onset. As expected, these genes/proteins were involved in one interaction network, with HLA-DQA1, HLA-DQB1, VDR, TNF, and TGFBI being the central nodes (Fig. 3b). It should be mentioned that the important role of TNF and VDR had been also confirmed by previous microRNA studies [30,41]. This observation indicates a common and synergistic effect of these leprosy risk genes in host immune response.

3.5. Positive selection of the leprosy susceptibility genes

M. leprae lost nearly half of its coding genes during the long evolutionary process of interaction with the host [42]. Previous studies have shown that development of leprosy is determined by host genetic background [2]. It is reasonable to speculate that leprosy associated genes may be shaped and retained in populations by positive selection. To test this speculation, we investigated the positive selection effect on these leprosy-related genes. We used an integrated method CMS [36], a tool for identifying regions that are under positive selection in the genome, and took advantage of the available data from the 1000 Genomes project (www.1000genomes.org/) [40]. We observed 18 positively selected genes in Europeans, 14 positively selected genes in East Asians, and 8 positively selected genes in Africans, respectively (Supplementary Table S3). Compared with Africans, Europeans had a significantly increased number of positively selected leprosy risk

Table 3

Top 10 terms the GO and KEGG pathway enrichment of 2134 differentially expressed genes in leprosy skin lesions.

Term	Count	% ^a	Fold of enrichment	P-value	FDR
Cross-disorders					
Hepatitis B	27	1.30	4.22	5.56E-12	9.60E-09
Diabetes, type 1	67	3.24	2.30	5.94E-12	1.03E-08
Infection	86	4.15	1.92	1.78E-10	1.31E-07
Multiple sclerosis	55	2.66	2.28	9.75E-10	1.68E-06
Immune	173	8.36	1.45	1.54E-09	1.13E-06
Lupus erythematosus	31	1.50	2.93	1.50E-08	2.59E-05
Rheumatoid arthritis	49	2.37	2.21	3.19E-08	5.52E-05
Tuberculosis	27	1.30	3.07	5.02E-08	8.67E-05
Systemic lupus erythematosus	38	1.84	2.48	5.70E-08	9.85E-05
HIV	30	1.45	2.65	3.79E-07	6.55E-04
KEGG pathways					
hsa05416:Viral myocarditis	35	1.69	3.55	4.34E-12	5.38E-09
hsa05340:Primary immunodeficiency	22	1.06	4.52	2.55E-10	3.16E-07
hsa05330:Allograft rejection	22	1.06	4.40	5.32E-10	6.61E-07
hsa04612:Antigen processing and presentation	33	1.59	2.86	1.61E-08	2.00E-05
hsa04650:Natural killer cell mediated cytotoxicity	44	2.13	2.38	2.86E-08	3.55E-05
hsa04660:T cell receptor signaling pathway	38	1.84	2.53	4.97E-08	6.16E-05
hsa04062:Chemokine signaling pathway	54	2.61	2.08	1.06E-07	1.32E-04
hsa04940:Type I diabetes mellitus	21	1.01	3.60	1.39E-07	1.72E-04
hsa05332:Graft-versus-host disease	20	0.97	3.69	1.82E-07	2.25E-04
GO biological process terms					
GO:0006955 ~ immune response	205	9.90	2.60	9.35E-41	1.74E-37
GO:0001775 ~ cell activation	88	4.25	2.68	1.56E-18	2.90E-15
GO:0045321 ~ leukocyte activation	79	3.82	2.86	1.83E-18	3.41E-15
GO:0046649 ~ lymphocyte activation	70	3.38	3.08	2.22E-18	4.14E-15
GO:0042110 ~ T cell activation	52	2.51	3.61	3.74E-17	6.96E-14
GO:0002684 ~ positive regulation of immune system process	75	3.62	2.76	1.26E-16	2.11E-13
GO:0030217 ~ T cell differentiation	75	1.55	4.31	3.21E-13	5.97E-10
GO:0030098 ~ lymphocyte differentiation	75	1.98	3.48	5.58E-13	1.04E-09
GO:0050865 ~ regulation of cell activation	75	2.66	2.75	3.03E-12	5.63E-09
GO:0050863 ~ regulation of T cell activation	75	2.08	3.22	3.23E-12	6.02E-09

^a The percentage is defined by the number of gene count for each terms divided by 2134 genes differentially expressed in PB or MB patients.

genes ($P=0.027$). Among these positively selected genes, *TLR1* had been previously shown to be under selection caused by *M. leprae* or other pathogens that could be recognized by TLR1 and its co-receptors [8]. Therefore, our current analyses provided a bird view for the natural selection imprints on leprosy associated genes and added more support to the notion that the genetic basis of leprosy might be shaped by population evolutionary history.

4. Discussion

Leprosy has complex clinical features [1]. Little differences have been observed among different *M. leprae* strains across the world [6,42,43] and the diversified clinical symptoms are highly determined by host immune status and genetic background [2]. Moreover, less than 10% of people in contact with *M. leprae* would develop the disease [44,45], suggesting strong effects of host genetic background and environmental factors (e.g., nutrition). Previous studies have identified numerous leprosy risk alleles [19,20,27,46–49]. In this study, we retrieved all reported leprosy-related genes (227 genes) and performed integrated analyses, to obtain an overview of the genetic and immune basis of leprosy. After having filtered these 227 genes by referring to the mRNA expression changes in leprosy skin lesions, we got a list of 123 leprosy associated genes with evidence at both the genetic association and differential expression levels (Table 1), providing an updated preliminary gene set for further screening, fine-mapping, and functional studies. We observed no significant *M. leprae*-infection-specific signal in our results. However, we found that leprosy susceptibility genes were enriched in activation and regulation of immune response, including innate and adaptive immune response, and inflammatory response (Fig. 2). Biological

processes involving interleukins, interferons, pattern recognition receptors, and components of the complement system play essential and extensive roles in host immune responses against pathogens [11]. Intriguingly, the mRNA expression pattern of these susceptibility genes was similar between leprosy patients with different subtypes (Table 1), suggesting that these leprosy risk genes might represent a common immune and genetic profile for leprosy *per se*.

The list of leprosy susceptibility genes was largely shared by typical autoimmune diseases such as lupus erythematosus, type I diabetes, and arthritis (Figs. 2 and 3). This observation suggested that similar pathways might be affected in leprosy and autoimmune diseases. Note that *M. leprae* could be latent for many years before the clinical manifestations. In our pathway analysis, we found that the leprosy-shared autoimmune genes were enriched in other typical autoimmune reactions such as graft-versus-host disease and allograft rejection, the “antigen processing and presentation” and “IgA production” pathways (Fig. 3). On this point, we suggested that leprosy might be a kind of autoimmune disease. Interestingly, the very recent GWAS follow-up study [48] also indicated an autoimmune profile of leprosy susceptibility, adding robust support to our hypothesis.

It should be mentioned that the most shared risk genes for leprosy distilled from the cross-disorder analysis were *TNF*, *HLA-DRB1*, *HLA-DQB1*, *IL10*, *IL6*, *HLA-DQA1*, and *IFNG* (Supplementary Table S2). It is not unexpected that HLA genes have a very large effect because the HLA region is highly associated with multiple diseases as revealed by GWASs (cf. the NHGRI GWAS Catalog: <http://www.genome.gov/gwastudies/>). Genes *TNF*, *IFNG*, *IL6*, *IL10*, *NOD2*, *TLR4*, *SLC11A1*, *RIPK2*, and *BCL10* contributed the lead signal for enrichment of BP terms (Supplementary Table S1). Four genes,

TNF, *IFNG*, *IL6*, and *IL10*, which contributed most of the signals in both cross-disorder analysis and term enrichment, play an essential role in related diseases and are worthy of attention. Five genes (*NOD2*, *TLR4*, *SLC11A1*, *RIPK2*, and *BCL10*), especially *RIPK2* and *BCL10*, showed only the lead signal in BP term enrichment for leprosy but no signal in cross-disorders. *NOD2*, *RIPK2*, *TLR4*, *TLR1*, *TLR2*, and *TIRAP* were positively selected among populations (Supplementary Table S3). These leprosy associated genes might be driven by co-evolution against *M. leprae*. In addition, our analyses showed that Europeans have a significantly increased number of positively selected leprosy risk genes compared with Africans. This pattern may be caused by historical pandemics [50,51]. Interaction of evolutionary selection driven genetic background, and host immune status and environments might jointly promote the susceptibility and development of leprosy.

Why there is a common autoimmune profile of leprosy and other infectious diseases? Does this mean a universal therapy to target all these related diseases? Or can we speculate an immune nature of leprosy and related diseases, rather than disorder-specific pathology? Apparently, more assays shall be carried out to answer these questions. Nonetheless, it seems that susceptibility to leprosy or development of the disease is only a matter of defect or over-activation of host immunity. Genetic studies aiming at identifying leprosy-specific risk factors may be questionable.

In summary, the current study revealed the hub genes that were located in the center of leprosy genetic network through a comprehensive integration analysis, providing an insight into immune and genetic factors contributing to leprosy. The results also offered thoughts for further fine-mapping and functional investigation. Nevertheless, there are limitations of the current study because of the paucity of information on leprosy. Moreover, conclusions revealed by our integrative analyses were heavily dependent on limited number of reported susceptibility genes, which might show population specific association pattern. The causality of these genes in leprosy remains undefined. The overall profile revealed by this study needs further validation in the future.

Acknowledgement

This work was supported by the National Natural Science Foundation of China (31271346).

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.jdermsci.2016.01.001>.

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Table S1. Biological Process (BP), Cellular Component (CC), and Molecular Function (MF) enrichment analysis for 123 leprosy associated genes

Category	Term	Count	Fold of enrichment	P-value	Bonferroni	FDR	Genes
BP	GO:0006955~immune response	52	9.528050928	8.11E-38	1.43E-34	1.37E-34	MICB, MICA, TOLLIP, SNCA, TLR1, TLR2, TIRAP, TLR4, HLA-DMB, HLA-DMA, TGFB1, IL4R, CFH, LTB, GNL1, ICAM1, IL18RAP, C4B, HLA-A, HLA-C, HLA-B, IL6R, NLRP3, HLA-DQA1, HLA-G, HLA-F, NCR3, HLA-DPA1, HLA-DRA, HLA-DQB1, CCL3, LST1, TNF, HLA-DRB1, C3, GPSM3, MAP4K2, CCL5, SLC11A1, IL10RB, TAP2, TAP1, FCN1, C2, HLA-DPB1, HLA-DOA, HLA-DOB, DEFB1, IL6, CFB,
BP	GO:0006952~defense response	42	8.63423752	6.10E-28	1.07E-24	1.03E-24	LY6G6D, C6ORF26, CCL3, MICA, TNF, AIF1, TOLLIP, C3, TLR1, SNCA, TIRAP, TLR2, TLR4, CCL5, TGFB1, SLC11A1, NOD1, IL10RB, TAP2, TAP1, CFH, HCP5, C2, DDAH2, DEFB1, APOM, IL6, IL18RAP, C4B, CFB, CSNK2B, HLA-C, CLIC1, HLA-B, IL6R, NLRP3, AGER, NLRP1, HLA-G, NCR3, RIPK2, LTA4H, HLA-DRA
BP	GO:0019882~antigen processing and presentation	22	33.51154149	1.20E-26	2.11E-23	2.04E-23	HLA-DQB1, ICAM1, MICB, MICA, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, PSMB8, HLA-G, HLA-F, PSMB9, SLC11A1, TAP2, CD209, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-
BP	GO:0002684~positive regulation of immune system process	24	12.74923427	4.41E-19	7.75E-16	7.47E-16	ICAM1, IL6, MICB, MICA, CFB, C4B, C3, TGFB2, TLR2, PTPN22, TLR4, IL6R, HLA-DMA, TGFB1, NCR3, SLC11A1, PRKCQ, TAP2, IL4R, CFH, RIPK2, C2, IL13RA1, HLA-DRA
BP	GO:0006954~inflammatory response	26	10.11439252	2.67E-18	4.70E-15	4.53E-15	CCL3, TNF, AIF1, C3, TOLLIP, TLR1, TIRAP, TLR2, TLR4, CCL5, TGFB1, SLC11A1, NOD1, IL10RB, CFH, C2, IL6, IL18RAP, CFB, C4B, IL6R, NLRP3, AGER, NCR3, RIPK2, LTA4H
BP	GO:0048584~positive regulation of response to stimulus	23	12.32155869	6.16E-18	1.08E-14	1.04E-14	IL6, MICB, MICA, TNF, CFB, C4B, C3, TLR2, PTPN22, TLR4, IL6R, CCL5, HLA-DMA, AGER, TGFB1, NCR3, SLC11A1, NOD1, TAP2, CFH, RIPK2, C2, HLA-DRA
BP	GO:0009611~response to wounding	30	7.156409804	3.59E-17	6.31E-14	6.08E-14	CCL3, TNF, AIF1, C3, TOLLIP, ERBB2, TLR1, TIRAP, TLR2, NINJ1, TLR4, CCL5, TGFB1, SLC11A1, NOD1, IL10RB, CFH, C2, IL6, IL18RAP, C4B, CFB, TGFB2, IL6R, NLRP3, AGER, NCR3, PRKCQ, SLC11A1, MICA, TAP2, CD209, HLA-A, HLA-C, HLA-B, HLA-DOA, HLA-DMA, HLA-G, HLA-DRA, HLA-F
BP	GO:0048002~antigen processing and presentation of peptide	11	49.66889186	6.63E-15	1.17E-11	1.13E-11	SLC11A1, MICA, TAP2, CD209, HLA-A, HLA-C, HLA-B, HLA-DOA, HLA-DMA, HLA-G, HLA-DRA, HLA-F
BP	GO:0050778~positive regulation of immune response	16	13.95088624	3.83E-13	6.73E-10	6.48E-10	MICB, MICA, CFB, C3, C4B, TLR2, PTPN22, TLR4, HLA-DMA, NCR3, SLC11A1, TAP2, CFH, RIPK2, C2, HLA-DRA
BP	GO:0002252~immune effector process	15	14.15260148	2.14E-12	3.77E-09	3.63E-09	ICAM1, IL6, MICA, C3, C4B, CFB, IL6R, NLRP3, HLA-DMA, SLC11A1, FCN1, CFH, C2, GNL1, HLA-DRA

BP	GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via	10	38.31209289	2.60E-12	4.57E-09	4.40E-09	HLA-DQB1, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DOA, HLA-DOB, HLA-DMA, HLA-DQA1, HLA-DRA
BP	GO:0010033~response to organic substance	27	4.734545737	3.47E-11	6.09E-08	5.87E-08	LY6G6D, C6ORF26, TNF, ERBB2, SNCA, TLR2, HSPA1A, TLR4, HSPA1B, CCL5, TGFB1, SLC11A1, BCHE, APOE, TAP2, NOS3, GNG2, DDAH2, APOM, IL6, CFB, TGFB1, TGFB2, CSNK2B, CLIC1, IL6R, IL18RAP, C3, C4B, CFB, SNCA, TLR1, TIRAP, TLR2, TLR4, TGFB1, SLC11A1, CFH, C2, DEFB1
BP	GO:0045087~innate immune response	14	12.8262224	5.18E-11	9.11E-08	8.78E-08	IL18RAP, C3, C4B, CFB, SNCA, TLR1, TIRAP, TLR2, TLR4, TGFB1, SLC11A1, CFH, C2, DEFB1
BP	GO:0001775~cell activation	18	7.929401804	7.97E-11	1.40E-07	1.35E-07	ICAM1, IL6, MICB, MICA, TNF, TOLLIP, SNCA, TGFB2, TLR1, TLR2, PTPN22, TLR4, HLA-DMA, NFKBIL1, TGFB1, SLC11A1, RIPK2, LTB
BP	GO:0050865~regulation of cell activation	15	10.83684913	8.19E-11	1.44E-07	1.39E-07	IL6, LST1, ERBB2, SNCA, TGFB2, TLR4, HLA-DMA, TGFB1, PRKCQ, APOE, IL4R, RIPK2, NOS3, IL13RA1, HLA-DOA
BP	GO:0051240~positive regulation of multicellular organismal process	16	8.290485675	6.82E-10	1.20E-06	1.16E-06	IL6, TNF, SNCA, TLR2, TLR4, IL6R, NLRP3, CCL5, TGFB1, NFKBIL1, SLC11A1, NOD1, RIPK2, NOS3, LTB, AGPAT1
BP	GO:0001817~regulation of cytokine production	14	9.779108793	1.54E-09	2.71E-06	2.61E-06	IL6, TNF, TLR1, TLR2, TLR4, IL6R, NLRP3, TGFB1, PRKCQ, SLC11A1, NOD1, RIPK2, LTB, AGPAT1
BP	GO:0001819~positive regulation of cytokine production	11	15.45254413	1.92E-09	3.38E-06	3.26E-06	SLC11A1, IL6, NOD1, TNF, TLR2, RIPK2, TLR4, IL6R, NLRP3, TGFB1, AGPAT1
BP	GO:0048660~regulation of smooth muscle cell proliferation	9	24.73628606	2.22E-09	3.90E-06	3.75E-06	IL6, TNF, NOTCH4, TGFB2, NOS3, IL6R, AGER, FKBPL, AGPAT1
BP	GO:0002253~activation of immune response	11	14.79498906	2.96E-09	5.21E-06	5.02E-06	MICB, MICA, C3, CFB, C4B, CFH, TLR2, PTPN22, RIPK2, TLR4, C2
BP	GO:0048661~positive regulation of smooth muscle cell proliferation	8	32.62707266	3.34E-09	5.88E-06	5.66E-06	IL6, TNF, NOTCH4, TGFB2, IL6R, AGER, FKBPL, AGPAT1
BP	GO:0009617~response to bacterium	14	9.171081304	3.38E-09	5.93E-06	5.72E-06	SLC11A1, IL6, MICA, NOD1, TNF, TAP2, SNCA, TLR2, RIPK2, NOS3, TLR4, IL6R, CCL5, DEFB1
BP	GO:0032755~positive regulation of interleukin-6 production	7	46.57943925	5.01E-09	8.81E-06	8.49E-06	IL6, NOD1, TNF, TLR2, RIPK2, TLR4, IL6R
BP	GO:0032675~regulation of interleukin-6 production	8	28.09553479	1.03E-08	1.81E-05	1.74E-05	IL6, NOD1, TNF, TLR1, TLR2, RIPK2, TLR4, IL6R
BP	GO:0007584~response to nutrient	12	10.83684913	1.18E-08	2.08E-05	2.00E-05	LY6G6D, VDR, C6ORF26, MICB, BCHE, CFB, TGFB2, CSNK2B, CLIC1, DDAH2, APOM, TGFB1
BP	GO:0002237~response to molecule of bacterial	10	14.70115192	2.20E-08	3.87E-05	3.72E-05	SLC11A1, IL6, TAP2, SNCA, TLR2, RIPK2, NOS3, TLR4, IL6R, CCL5

BP	GO:0002443~leukocyte mediated immunity	10	14.70115192	2.20E-08	3.87E-05	3.72E-05	ICAM1, SLC11A1, IL6, C3, C4B, IL6R, C2, GNL1, HLA-DMA, HLA-DRA
BP	GO:0044093~positive regulation of molecular function	21	4.530764569	2.33E-08	4.09E-05	3.94E-05	ICAM1, IL6, TNF, TGFBR1, ERBB2, TGFBR2, TLR2, TLR4, NLRP3, NLRP1, TGFB1, PSMB8, PSMB9, MEN1, SLC11A1, PRKCQ, VDR, NOD1, APOE, RIPK2, NOS3
BP	GO:0051092~positive regulation of NF-kappaB transcription factor activity	8	24.66925006	2.68E-08	4.71E-05	4.54E-05	ICAM1, PRKCQ, IL6, TNF, TLR2, RIPK2, TLR4, TGFB1
BP	GO:0045321~leukocyte activation	14	7.314126825	5.07E-08	8.92E-05	8.59E-05	ICAM1, MICB, MICA, TOLLIP, TLR1, TGFBR2, SNCA, TLR2, PTPN22, TLR4, HLA-DMA, TGFB1, SLC11A1, RIPK2
BP	GO:0002694~regulation of leukocyte activation	12	9.139511316	6.93E-08	1.22E-04	1.17E-04	PRKCQ, IL6, LST1, ERBB2, IL4R, SNCA, TGFBR2, RIPK2, HLA-DOA, IL13RA1, HLA-DMA, TGFB1
BP	GO:0051090~regulation of transcription factor activity	10	12.27474821	1.07E-07	1.89E-04	1.82E-04	MEN1, ICAM1, PRKCQ, IL6, TNF, TLR2, RIPK2, TLR4, NLRP3, TGFB1
BP	GO:0002250~adaptive immune response	9	14.77752154	1.46E-07	2.57E-04	2.48E-04	ICAM1, SLC11A1, C3, C4B, TLR4, C2, GNL1, HLA-DMA, HLA-DRA
BP	GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	9	14.77752154	1.46E-07	2.57E-04	2.48E-04	ICAM1, SLC11A1, C3, C4B, TLR4, C2, GNL1, HLA-DMA, HLA-DRA
BP	GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	6	44.62231996	1.54E-07	2.71E-04	2.61E-04	MICA, TAP2, HLA-A, HLA-C, HLA-B, HLA-G, HLA-F
BP	GO:0042742~defense response to bacterium	10	11.28838451	2.22E-07	3.90E-04	3.76E-04	SLC11A1, IL6, MICA, NOD1, TNF, TLR2, RIPK2, TLR4, IL6R, DEFB1
BP	GO:0051249~regulation of lymphocyte activation	11	9.396817378	2.35E-07	4.13E-04	3.98E-04	PRKCQ, IL6, LST1, ERBB2, IL4R, TGFBR2, RIPK2, HLA-DOA, IL13RA1, HLA-DMA, TGFB1
BP	GO:0031667~response to nutrient levels	12	7.701314104	3.93E-07	6.91E-04	6.66E-04	LY6G6D, VDR, C6ORF26, MICB, BCHE, CFB, TGFBR2, CSNK2B, CLIC1, DDAH2, APOM, TGFB1
BP	GO:0051091~positive regulation of transcription factor activity	8	16.85732087	4.08E-07	7.17E-04	6.90E-04	ICAM1, PRKCQ, IL6, TNF, TLR2, RIPK2, TLR4, TGFB1
BP	GO:0051101~regulation of DNA binding	10	10.44875261	4.31E-07	7.57E-04	7.29E-04	MEN1, ICAM1, PRKCQ, IL6, TNF, TLR2, RIPK2, TLR4, NLRP3, TGFB1
BP	GO:0042127~regulation of cell proliferation	22	3.534254058	6.34E-07	0.00111362	0.001073305	IL6, TNF, LST1, AIF1, ERBB2, TGFBR1, TGFBR2, IL6R, AGER, NFKBIL1, TGFB1, MEN1, PRKCQ, VDR, APOE, NOTCH4, RIPK2, NOS3, IL13RA1, LTB, FKBPL, AGPAT1

BP	GO:0010740~positive regulation of protein kinase cascade	11	8.327718395	7.21E-07	0.001267303	0.001221518	<i>IL6, NOD1, TNF, ERBB2, TGFB1, RIPK2, TLR4, IL6R, LTB, NFKBIL1, TGFB1</i>
BP	GO:0051222~positive regulation of protein transport	8	15.09610824	8.78E-07	0.001541945	0.001486439	<i>PRKCQ, IL6, TNF, TGFB1, NLRP3, LTB, NFKBIL1, TGFB1</i>
BP	GO:0042981~regulation of apoptosis	22	3.459524806	8.97E-07	0.001576137	0.001519427	<i>IL6, TNF, TNFRSF25, ERBB2, TGFB1, SNCA, TLR2, HSPA1A, TLR4, IL6R, HSPA1B, NLRP3, NLRP1, NFKBIL1, TGFB1, MEN1, VDR, NOD1, APOE, RIPK2, NOS3, DDAH2, LTB</i>
BP	GO:0043067~regulation of programmed cell death	22	3.425440818	1.05E-06	0.001849699	0.001783388	<i>IL6, TNF, TNFRSF25, ERBB2, TGFB1, SNCA, TLR2, HSPA1A, TLR4, IL6R, HSPA1B, NLRP3, NLRP1, NFKBIL1, TGFB1, MEN1, VDR, NOD1, APOE, RIPK2, NOS3, DDAH2, LTB</i>
BP	GO:0010941~regulation of cell death	22	3.412831833	1.12E-06	0.001963028	0.001892761	<i>IL6, TNF, TNFRSF25, ERBB2, TGFB1, SNCA, TLR2, HSPA1A, TLR4, IL6R, HSPA1B, NLRP3, NLRP1, NFKBIL1, TGFB1, MEN1, VDR, NOD1, APOE, RIPK2, NOS3, DDAH2, LTB</i>
BP	GO:0009991~response to extracellular stimulus	12	6.89617672	1.18E-06	0.002066595	0.001992722	<i>LY6G6D, VDR, C6ORF26, MICB, BCHE, CFB, TGFB2, CSNK2B, CLIC1, DDAH2, APOM, TGFB1</i>
BP	GO:0002449~lymphocyte mediated immunity	8	14.44913218	1.19E-06	0.002084452	0.002009958	<i>ICAM1, SLC11A1, C3, C4B, C2, GNL1, HLA-DMA, HLA-DRA</i>
BP	GO:0043388~positive regulation of DNA binding	8	14.44913218	1.19E-06	0.002084452	0.002009958	<i>ICAM1, PRKCQ, IL6, TNF, TLR2, RIPK2, TLR4, TGFB1</i>
BP	GO:0002697~regulation of immune effector process	9	11.26603128	1.20E-06	0.002114499	0.002038963	<i>ICAM1, MICB, IL6, TNF, C3, TAP2, IL13RA1, TGFB1, NCR3</i>
BP	GO:0006986~response to unfolded protein	8	14.24562327	1.31E-06	0.002297417	0.002215547	<i>LY6G6D, C6ORF26, CFB, CSNK2B, HSPA1A, CLIC1, HSPA1B, DDAH2, APOM</i>
BP	GO:0051050~positive regulation of transport	12	6.803403043	1.34E-06	0.002360217	0.00227618	<i>PRKCQ, SLC11A1, IL6, TNF, C3, APOE, TGFB1, SNCA, NLRP3, LTB, NFKBIL1, TGFB1</i>
BP	GO:0002274~myeloid leukocyte activation	7	19.2393336	1.46E-06	0.002559217	0.002468339	<i>SLC11A1, SNCA, TGFB2, TLR1, TLR2, TLR4, TGFB1</i>
BP	GO:0051130~positive regulation of cellular component organization	11	7.68358548	1.51E-06	0.002643406	0.002549644	<i>MEN1, PRKCQ, SLC11A1, TNF, C3, MAPT, TGFB1, SNCA, LTB, NFKBIL1, TGFB1</i>
BP	GO:0031349~positive regulation of defense response	8	13.85533222	1.58E-06	0.002778213	0.002679849	<i>IL6, MICA, C3, TLR2, RIPK2, TLR4, CCL5, NCR3</i>
BP	GO:0010647~positive regulation of cell communication	14	5.379996023	1.71E-06	0.003003154	0.002897149	<i>IL6, TNF, ERBB2, TGFB1, SNCA, TLR4, IL6R, TGFB1, NFKBIL1, MEN1, NOD1, RIPK2, LTB, AGPAT1</i>
BP	GO:0051789~response to protein stimulus	9	10.6342912	1.87E-06	0.003278962	0.003163655	<i>LY6G6D, C6ORF26, CFB, CSNK2B, HSPA1A, CLIC1, HSPA1B, DDAH2, APOM, TGFB1</i>

BP	GO:0043410~positive regulation of MAPKKK cascade	7	18.4376947	1.89E-06	0.00330935	0.003193023	<i>IL6, NOD1, TNF, ERBB2, RIPK2, TLR4, IL6R</i>
BP	GO:0007568~aging	9	10.34426508	2.30E-06	0.004040982	0.003900354	<i>PRKCQ, TGFB1, NOTCH4, NOS3, CCL5, AGER, TGFB1, FKBPL,</i>
BP	GO:0050867~positive regulation of cell	9	10.2510735	2.47E-06	0.004326225	0.004176262	<i>PRKCQ, IL6, IL4R, TGFB2, RIPK2, TLR4, IL13RA1, HLA-DMA, TGFB1</i>
BP	GO:0051099~positive regulation of binding	8	12.9671699	2.49E-06	0.004359201	0.004208164	<i>ICAM1, PRKCQ, IL6, TNF, TLR2, RIPK2, TLR4, TGFB1</i>
BP	GO:0051098~regulation of binding	10	8.263392584	3.09E-06	0.00541107	0.005226321	<i>MEN1, ICAM1, PRKCQ, IL6, TNF, TLR2, RIPK2, TLR4, NLRP3, TGFB1</i>
BP	GO:0009967~positive regulation of signal transduction	13	5.571487407	3.27E-06	0.005735223	0.0055403	<i>MEN1, IL6, NOD1, TNF, ERBB2, TGFB1, RIPK2, TLR4, IL6R, LTB, NFKBIL1, TGFB1, AGPAT1</i>
BP	GO:0050863~regulation of T cell activation	9	9.725377426	3.66E-06	0.006421336	0.006205212	<i>PRKCQ, IL6, ERBB2, IL4R, TGFB2, RIPK2, HLA-DOA, HLA-DMA, TGFB1</i>
BP	GO:0010627~regulation of protein kinase cascade	12	6.093007544	3.92E-06	0.006871855	0.006642058	<i>MEN1, IL6, NOD1, TNF, ERBB2, TGFB1, RIPK2, TLR4, IL6R, LTB, NFKBIL1, TGFB1</i>
BP	GO:0032101~regulation of response to external	10	7.951566449	4.24E-06	0.007418711	0.007172581	<i>IL6, C3, APOE, TGFB2, NOS3, TLR4, IL6R, CCL5, AGER, TGFB1</i>
BP	GO:0042116~macrophage activation	5	42.14330218	4.55E-06	0.007964479	0.007702337	<i>SLC11A1, SNCA, TLR1, TLR2, TLR4</i>
BP	GO:0043065~positive regulation of apoptosis	15	4.410345577	6.38E-06	0.011155638	0.01080566	<i>TNF, TNFRSF25, TGFB1, TLR2, TLR4, NLRP3, NLRP1, TGFB1, NFKBIL1, MEN1, VDR, NOD1, APOE, RIPK2, LTB</i>
BP	GO:0043068~positive regulation of programmed cell death	15	4.37978891	6.91E-06	0.012072276	0.011698902	<i>TNF, TNFRSF25, TGFB1, TLR2, TLR4, NLRP3, NLRP1, TGFB1, NFKBIL1, MEN1, VDR, NOD1, APOE, RIPK2, LTB</i>
BP	GO:0010942~positive regulation of cell death	15	4.35965195	7.28E-06	0.012719687	0.012330284	<i>TNF, TNFRSF25, TGFB1, TLR2, TLR4, NLRP3, NLRP1, TGFB1, NFKBIL1, MEN1, VDR, NOD1, APOE, RIPK2, LTB</i>
BP	GO:0032103~positive regulation of response to external stimulus	7	13.82827103	1.04E-05	0.018133615	0.017626273	<i>IL6, C3, TLR4, IL6R, CCL5, AGER, TGFB1</i>
BP	GO:0051251~positive regulation of lymphocyte activation	8	10.42720879	1.07E-05	0.018633039	0.018116273	<i>PRKCQ, IL6, IL4R, TGFB2, RIPK2, IL13RA1, HLA-DMA, TGFB1</i>
BP	GO:0002526~acute inflammatory response	8	10.3208087	1.14E-05	0.01992521	0.019385209	<i>IL6, C3, CFB, C4B, CFH, TLR4, IL6R, C2</i>
BP	GO:0032722~positive regulation of chemokine production	4	72.24566088	1.60E-05	0.027731673	0.027086724	<i>IL6, TNF, RIPK2, IL6R</i>

BP	GO:0002696~positive regulation of leukocyte activation	8	9.541879739	1.92E-05	0.033123119	0.032441526	<i>PRKCQ, IL6, IL4R, TGFB2, RIPK2, IL13RA1, HLA-DMA, TGFB1</i>
BP	GO:0048545~response to steroid hormone stimulus	10	6.584890966	1.94E-05	0.033604132	0.032920706	<i>IL6, TNF, BCHE, ERBB2, TGFB1, TGFB2, NOS3, IL6R, CCL5, TGFB1</i>
BP	GO:0008284~positive regulation of cell	14	4.275407468	2.06E-05	0.035507123	0.034818762	<i>IL6, TNF, ERBB2, TGFB1, TGFB2, IL6R, AGER, TGFB1, PRKCQ, NOTCH4, RIPK2, IL13RA1, FKBPL, AGPAT1</i>
BP	GO:0042306~regulation of protein import into nucleus	6	17.2404418	2.29E-05	0.039424229	0.038737413	<i>PRKCQ, TNF, TGFB1, NLRP3, NFKBIL1, TGFB1</i>
BP	GO:0043408~regulation of MAPKKK cascade	8	9.279259196	2.30E-05	0.039596585	0.038910199	<i>MEN1, IL6, NOD1, TNF, ERBB2, RIPK2, TLR4, IL6R</i>
BP	GO:0008285~negative regulation of cell	13	4.552877521	2.51E-05	0.043122509	0.042451702	<i>IL6, LST1, TNF, AIF1, ERBB2, TGFB2, TGFB1, NFKBIL1, MEN1, VDR, APOE, NOS3, LTB</i>
BP	GO:0051953~negative regulation of amine	4	63.21495327	2.54E-05	0.043754945	0.0430883	<i>TNF, SNCA, LTB, NFKBIL1</i>
BP	GO:0043271~negative regulation of ion transport	5	27.48476229	2.81E-05	0.048227746	0.047602468	<i>TNF, NOS3, LTB, NFKBIL1, TGFB1</i>
BP	GO:0007242~intracellular signaling cascade	25	2.51651884	3.03E-05	0.051807611	0.051230604	<i>TNF, TOLLIP, ERBB2, TLR1, TLR2, MAP4K2, TIRAP, TLR4, MEN1, VDR, NOD1, APOE, GNG2, DDAH2, LTB, FKBPL, AGPAT1, TGFB1, RGFNEF, AGER, NFKBIL1, PRKCQ, RAB32, CD209, NOTCH4</i>
BP	GO:0009628~response to abiotic stimulus	13	4.466273872	3.03E-05	0.051835736	0.051259162	<i>MEN1, PRKCQ, MICB, MICA, TNF, TGFB1, TGFB2, NOS3, IL6R, LTB, NFKBIL1, TGFB1, FKBPL</i>
BP	GO:0032496~response to lipopolysaccharide	7	11.49362787	3.03E-05	0.051905206	0.051329705	<i>SLC11A1, SNCA, RIPK2, NOS3, TLR4, IL6R, CCL5</i>
BP	GO:0051223~regulation of protein transport	8	8.872274143	3.07E-05	0.052601422	0.052036956	<i>PRKCQ, IL6, TNF, TGFB1, NLRP3, LTB, NFKBIL1, TGFB1</i>
BP	GO:0007243~protein kinase cascade	13	4.442131851	3.19E-05	0.054581237	0.054050969	<i>TNF, TGFB1, ERBB2, TLR1, TLR2, TIRAP, MAP4K2, TLR4, AGER, MEN1, NOTCH4, FKBPL, AGPAT1</i>
BP	GO:0006959~humoral immune response	7	11.20264995	3.51E-05	0.059838084	0.059418956	<i>IL6, TNF, C3, CFB, C4B, CFH, C2</i>
BP	GO:0048534~hemopoietic or lymphoid organ	11	5.348957584	3.65E-05	0.062106006	0.061744011	<i>MEN1, TNF, TGFB1, NOTCH4, TGFB2, TIRAP, PTPN22, TRIM10, LTB, HLA-DMA, TGFB1</i>
BP	GO:0006917~induction of apoptosis	12	4.741121495	4.11E-05	0.069683134	0.0695526	<i>VDR, NOD1, TNF, TNFRSF25, APOE, TGFB1, TLR2, NLRP3, LTB, NLRP1, NFKBIL1, TGFB1</i>
BP	GO:0012502~induction of programmed cell death	12	4.726351646	4.23E-05	0.071615276	0.071553842	<i>VDR, NOD1, TNF, TNFRSF25, APOE, TGFB1, TLR2, NLRP3, LTB, NLRP1, NFKBIL1, TGFB1</i>
BP	GO:0070201~regulation of establishment of protein localization	8	8.359002085	4.51E-05	0.076226347	0.076346539	<i>PRKCQ, IL6, TNF, TGFB1, NLRP3, LTB, NFKBIL1, TGFB1</i>

BP	GO:0050670~regulation of lymphocyte proliferation	7	10.6627632	4.65E-05	0.078446969	0.078663088	<i>PRKCQ, IL6, LST1, ERBB2, RIPK2, IL13RA1, TGFB1</i>
BP	GO:0032944~regulation of mononuclear cell	7	10.53582555	4.97E-05	0.083712314	0.084178056	<i>PRKCQ, IL6, LST1, ERBB2, RIPK2, IL13RA1, TGFB1</i>
BP	GO:0070663~regulation of leukocyte proliferation	7	10.53582555	4.97E-05	0.083712314	0.084178056	<i>PRKCQ, IL6, LST1, ERBB2, RIPK2, IL13RA1, TGFB1</i>
BP	GO:0002757~immune response-activating signal transduction	6	14.58806614	5.21E-05	0.087523402	0.088189438	<i>MICB, MICA, TLR2, PTPN22, RIPK2, TLR4</i>
BP	GO:0043085~positive regulation of catalytic	15	3.647016535	5.29E-05	0.08881856	0.089556442	<i>TNF, ERBB2, TGFB1, TGFB2, NLRP3, NLRP1, PSMB8, TGFB1, PSMB9, MEN1, SLC11A1, VDR, NOD1, APOE, NOS3</i>
BP	GO:0050829~defense response to Gram-negative bacterium	4	50.57196262	5.39E-05	0.090431478	0.091261526	<i>SLC11A1, IL6, TLR4, IL6R</i>
BP	GO:0033157~regulation of intracellular protein	6	14.31281961	5.72E-05	0.095622281	0.096769343	<i>PRKCQ, TNF, TGFB1, NLRP3, NFKBIL1, TGFB1</i>
BP	GO:0042110~T cell	8	8.027295653	5.84E-05	0.097592596	0.09886819	<i>ICAM1, SLC11A1, MICB, MICA, PTPN22, RIPK2, HLA-DMA, TGFB1</i>
BP	GO:0002520~immune system development	11	5.038873087	6.04E-05	0.100671884	0.102157461	<i>MEN1, TNF, TGFB1, NOTCH4, TGFB2, TIRAP, PTPN22, TRIM10, LTB, HLA-DMA, TGFB1</i>
BP	GO:0051094~positive regulation of developmental process	11	5.002622201	6.41E-05	0.106597175	0.10851831	<i>MEN1, IL6, TNF, MAPT, IL4R, TGFB2, NOS3, IL6R, CCL5, HLA-DMA, TGFB1</i>
BP	GO:0002478~antigen processing and presentation of exogenous	4	45.97451147	7.37E-05	0.121542615	0.124749835	<i>TAP2, HLA-DOA, HLA-DMA, HLA-DRA</i>
BP	GO:0002764~immune response-regulating signal transduction	6	13.54606142	7.47E-05	0.123062103	0.126415368	<i>MICB, MICA, TLR2, PTPN22, RIPK2, TLR4</i>
BP	GO:0032270~positive regulation of cellular protein metabolic process	10	5.426176246	8.81E-05	0.143435241	0.149026978	<i>MEN1, IL6, TNF, APOE, TGFB1, TLR4, IL6R, PSMB8, TGFB1, PSMB9</i>
BP	GO:0046822~regulation of nucleocytoplasmic	6	13.07895585	8.85E-05	0.144085139	0.14975702	<i>PRKCQ, TNF, TGFB1, NLRP3, NFKBIL1, TGFB1</i>
BP	GO:0032680~regulation of tumor necrosis factor production	5	20.39192041	9.52E-05	0.154122711	0.161102641	<i>NOD1, TLR1, TLR2, RIPK2, TLR4</i>
BP	GO:0032880~regulation of protein localization	8	7.329269944	1.04E-04	0.16682818	0.175656572	<i>PRKCQ, IL6, TNF, TGFB1, NLRP3, LTB, NFKBIL1, TGFB1</i>

BP	GO:0031401~positive regulation of protein modification process	9	6.084861812	1.09E-04	0.174488154	0.184537546	<i>MEN1, IL6, TNF, TGFBR1, TLR4, IL6R, PSMB8, TGFB1, PSMB9</i>
BP	GO:0050866~negative regulation of cell	6	12.43572851	1.13E-04	0.179860099	0.190814601	<i>LST1, APOE, ERBB2, IL4R, NOS3, TGFB1</i>
BP	GO:0051247~positive regulation of protein metabolic process	10	5.202876812	1.21E-04	0.19203055	0.205187588	<i>MEN1, IL6, TNF, APOE, TGFBR1, TLR4, IL6R, PSMB8, TGFB1, PSMB9</i>
BP	GO:0009725~response to hormone stimulus	12	4.133947898	1.40E-04	0.217947548	0.236523075	<i>PRKCQ, IL6, TNF, BCHE, ERBB2, TGFBR1, TGFB2, NOS3, GNG2, IL6R, CCL5, TGFB1</i>
BP	GO:0019884~antigen processing and presentation of exogenous	4	36.12283044	1.60E-04	0.244997683	0.270345092	<i>TAP2, HLA-DOA, HLA-DMA, HLA-DRA</i>
BP	GO:0032642~regulation of chemokine production	4	33.71464174	1.99E-04	0.294818887	0.33590428	<i>IL6, TNF, RIPK2, IL6R</i>
BP	GO:0032760~positive regulation of tumor necrosis factor production	4	33.71464174	1.99E-04	0.294818887	0.33590428	<i>NOD1, TLR2, RIPK2, TLR4</i>
BP	GO:0006957~complement activation, alternative pathway	4	33.71464174	1.99E-04	0.294818887	0.33590428	<i>C3, CFB, CFH, C2</i>
BP	GO:0032386~regulation of intracellular transport	6	10.68421745	2.32E-04	0.334951154	0.392140647	<i>PRKCQ, TNF, TGFBR1, NLRP3, NFKBIL1, TGFB1</i>
BP	GO:0002429~immune response-activating cell surface receptor signaling pathway	5	16.20896238	2.37E-04	0.340988279	0.400890011	<i>MICB, MICA, TLR2, PTPN22, RIPK2</i>
BP	GO:0042035~regulation of cytokine biosynthetic process	6	10.2510735	2.82E-04	0.390666704	0.476055899	<i>PRKCQ, IL6, TNF, TLR1, TLR4, LTB</i>
BP	GO:0050714~positive regulation of protein secretion	5	15.41828129	2.89E-04	0.397892813	0.487492232	<i>PRKCQ, IL6, TNF, NLRP3, TGFB1</i>
BP	GO:0046330~positive regulation of JNK cascade	4	29.7482133	2.94E-04	0.403176673	0.49594105	<i>NOD1, TNF, RIPK2, TLR4</i>
BP	GO:0051241~negative regulation of multicellular organismal process	8	6.167312514	3.02E-04	0.411776964	0.509852503	<i>SLC11A1, IL6, TNF, BCHE, APOE, TGFBR2, NOS3, IL6R</i>
BP	GO:0006956~complement activation	5	15.05117935	3.17E-04	0.427287511	0.535458734	<i>C3, CFB, C4B, CFH, C2</i>

BP	GO:0002768~immune response-regulating cell surface receptor signaling pathway	5	15.05117935	3.17E-04	0.427287511	0.535458734	<i>MICB, MICA, TLR2, PTPN22, RIPK2</i>
BP	GO:0050870~positive regulation of T cell	6	9.981308411	3.19E-04	0.429461594	0.53910268	<i>PRKCQ, IL6, IL4R, TGFB2, RIPK2, HLA-DMA</i>
BP	GO:0009719~response to endogenous stimulus	12	3.746071305	3.28E-04	0.437854207	0.553299605	<i>PRKCQ, IL6, TNF, BCHE, ERBB2, TGFB1, TGFB2, NOS3, GNG2, IL6R, CCL5, TGFB1</i>
BP	GO:0002541~activation of plasma proteins involved in acute inflammatory	5	14.70115192	3.47E-04	0.457120083	0.586700218	<i>C3, CFB, C4B, CFH, C2</i>
BP	GO:0070723~response to cholesterol	3	94.82242991	3.61E-04	0.47012066	0.609908983	<i>TGFB1, TGFB2, TGFB1</i>
BP	GO:0002037~negative regulation of L-glutamate transport	3	94.82242991	3.61E-04	0.47012066	0.609908983	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0043281~regulation of caspase activity	6	9.602271383	3.82E-04	0.489319615	0.645235627	<i>MEN1, NOD1, TNF, SNCA, NLRP3, NLRP1</i>
BP	GO:0034097~response to cytokine stimulus	6	9.602271383	3.82E-04	0.489319615	0.645235627	<i>SLC11A1, SNCA, RIPK2, NOS3, IL6R, CCL5</i>
BP	GO:0002218~activation of innate immune response	4	26.61682243	4.14E-04	0.516738224	0.698036901	<i>MICA, TLR2, RIPK2, TLR4</i>
BP	GO:0002758~innate immune response-activating signal	4	26.61682243	4.14E-04	0.516738224	0.698036901	<i>MICA, TLR2, RIPK2, TLR4</i>
BP	GO:0045597~positive regulation of cell differentiation	9	4.968860956	4.33E-04	0.53305459	0.730885014	<i>MEN1, IL6, MAPT, IL4R, TGFB2, IL6R, CCL5, HLA-DMA, TGFB1</i>
BP	GO:0045089~positive regulation of innate immune response	5	13.74238115	4.51E-04	0.547683264	0.761316729	<i>MICA, TLR2, RIPK2, TLR4, NCR3</i>
BP	GO:0052548~regulation of endopeptidase activity	6	9.250968771	4.54E-04	0.550065525	0.766364615	<i>MEN1, NOD1, TNF, SNCA, NLRP3, NLRP1</i>
BP	GO:0010638~positive regulation of organelle organization	6	9.139511316	4.80E-04	0.570280308	0.810295803	<i>MEN1, PRKCQ, TNF, MAPT, LTB, NFKBIL1</i>
BP	GO:0050830~defense response to Gram-positive bacterium	4	25.28598131	4.84E-04	0.572881904	0.816097741	<i>IL6, NOD1, RIPK2, IL6R</i>

BP	GO:0031399~regulation of protein modification	10	4.285759544	5.10E-04	0.591999101	0.859837237	<i>MEN1, IL6, TNF, TGFB1, SNCA, TLR4, IL6R, PSMB8, TGFB1, PSMB9</i>
BP	GO:0030097~hemopoiesis	9	4.821479487	5.29E-04	0.605382995	0.891684372	<i>MEN1, TNF, NOTCH4, TGFB2, TIRAP, PTPN22, TRIM10, HLA-DMA,</i>
BP	GO:0042108~positive regulation of cytokine biosynthetic process	5	13.16978193	5.32E-04	0.607320402	0.896382879	<i>PRKCQ, TNF, TLR1, TLR4, LTB</i>
BP	GO:0070304~positive regulation of stress-activated protein kinase signaling pathway	4	24.08188696	5.61E-04	0.627261585	0.94612309	<i>NOD1, TNF, RIPK2, TLR4</i>
BP	GO:0052547~regulation of peptidase activity	6	8.820691154	5.66E-04	0.630106925	0.953434399	<i>MEN1, NOD1, TNF, SNCA, NLRP3, NLRP1</i>
BP	GO:0002036~regulation of L-glutamate transport	3	75.85794393	5.99E-04	0.651185739	1.009398814	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0001934~positive regulation of protein amino acid	6	8.523364486	6.62E-04	0.687649851	1.114628125	<i>IL6, TNF, TGFB1, TLR4, IL6R, TGFB1</i>
BP	GO:0051051~negative regulation of transport	7	6.555624784	6.66E-04	0.690126598	1.122210924	<i>TNF, SNCA, NOS3, NLRP3, LTB, NFKBIL1, TGFB1</i>
BP	GO:0045580~regulation of T cell differentiation	5	12.39508888	6.71E-04	0.692473464	1.129451668	<i>ERBB2, IL4R, TGFB2, HLA-DOA, HLA-DMA</i>
BP	GO:0016064~immunoglobulin mediated immune	5	11.70647283	8.33E-04	0.769108988	1.402044227	<i>C3, C4B, C2, HLA-DMA, HLA-DRA</i>
BP	GO:0045088~regulation of innate immune response	5	11.70647283	8.33E-04	0.769108988	1.402044227	<i>MICA, TLR2, RIPK2, TLR4, NCR3</i>
BP	GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	5	11.49362787	8.93E-04	0.792241766	1.502260263	<i>SLC11A1, C3, TAP2, IL4R, TGFB1</i>
BP	GO:0044070~regulation of anion transport	3	63.21495327	8.94E-04	0.792364615	1.502821459	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0070372~regulation of ERK1 and ERK2 cascade	3	63.21495327	8.94E-04	0.792364615	1.502821459	<i>NOD1, RIPK2, TLR4</i>
BP	GO:0051956~negative regulation of amino acid transport	3	63.21495327	8.94E-04	0.792364615	1.502821459	<i>TNF, LTB, NFKBIL1</i>

BP	GO:0070374~positive regulation of ERK1 and ERK2 cascade	3	63.21495327	8.94E-04	0.792364615	1.502821459	<i>NOD1, RIPK2, TLR4</i>
BP	GO:0032768~regulation of monooxygenase activity	4	20.22878505	9.49E-04	0.811478564	1.594405337	<i>VDR, TNF, APOE, SNCA</i>
BP	GO:0002819~regulation of adaptive immune response	5	11.28838451	9.56E-04	0.814036157	1.607352405	<i>SLC11A1, C3, TAP2, IL4R, TGFB1</i>
BP	GO:0019724~B cell mediated immunity	5	11.28838451	9.56E-04	0.814036157	1.607352405	<i>C3, C4B, C2, HLA-DMA, HLA-DRA</i>
BP	GO:0046649~lymphocyte activation	8	5.082609308	9.57E-04	0.814262951	1.608508981	<i>ICAM1, SLC11A1, MICB, MICA, PTPN22, RIPK2, HLA-DMA, TGFB1</i>
BP	GO:0042327~positive regulation of phosphorylation	6	7.82040659	9.78E-04	0.820916338	1.643076587	<i>IL6, TNF, TGFB1, TLR4, IL6R, TGFB1</i>
BP	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	6	7.82040659	9.78E-04	0.820916338	1.643076587	<i>NOD1, TNF, RIPK2, TLR4, LTB, NFKBIL1</i>
BP	GO:0010604~positive regulation of macromolecule metabolic	17	2.50794447	9.98E-04	0.82714739	1.676623321	<i>IL6, TNF, TGFB1, SNCA, TLR1, TLR4, IL6R, PSMB8, TGFB1, PSMB9, MEN1, SLC11A1, PRKCQ, APOE, NOTCH4, PBX2, LTB</i>
BP	GO:0050900~leukocyte migration	5	11.09034268	0.0010225	0.834439693	1.717439112	<i>ICAM1, IL6, TNF, IL6R, CCL5</i>
BP	GO:0002637~regulation of immunoglobulin	4	19.45075485	0.0010663	0.846736278	1.790475725	<i>IL6, TNF, IL13RA1, TGFB1</i>
BP	GO:0050708~regulation of protein secretion	5	10.89912987	0.0010917	0.853418305	1.832637578	<i>PRKCQ, IL6, TNF, NLRP3, TGFB1</i>
BP	GO:0010562~positive regulation of phosphorus metabolic process	6	7.585794393	0.0011214	0.860896486	1.882141734	<i>IL6, TNF, TGFB1, TLR4, IL6R, TGFB1</i>
BP	GO:0045937~positive regulation of phosphate metabolic process	6	7.585794393	0.0011214	0.860896486	1.882141734	<i>IL6, TNF, TGFB1, TLR4, IL6R, TGFB1</i>
BP	GO:0043280~positive regulation of caspase	5	10.71439886	0.0011641	0.870956123	1.953063618	<i>MEN1, NOD1, TNF, NLRP3, NLRP1</i>
BP	GO:0010952~positive regulation of peptidase activity	5	10.71439886	0.0011641	0.870956123	1.953063618	<i>MEN1, NOD1, TNF, NLRP3, NLRP1</i>
BP	GO:0006916~anti-	8	4.909899283	0.0011703	0.87237749	1.963523558	<i>TNF, APOE, TGFB1, SNCA, RIPK2, NOS3, HSPA1A, HSPA1B,</i>

BP	GO:0032268~regulation of cellular protein metabolic process	12	3.200757128	0.0012052	0.879967877	2.021411696	<i>MEN1, IL6, TNF, APOE, TGFB1, SNCA, TLR4, IL6R, APOM, PSMB8, TGFB1, PSMB9</i>
BP	GO:0001774~microglial cell activation	3	54.18424566	0.0012449	0.888071031	2.087355997	<i>SNCA, TLR2, TLR4</i>
BP	GO:0002456~T cell mediated immunity	3	54.18424566	0.0012449	0.888071031	2.087355997	<i>ICAM1, SLC11A1, GNL1</i>
BP	GO:0042129~regulation of T cell proliferation	5	10.19596021	0.0014014	0.915023477	2.346842192	<i>PRKCQ, IL6, ERBB2, RIPK2, TGFB1</i>
BP	GO:0050921~positive regulation of chemotaxis	4	17.4386078	0.0014733	0.925122806	2.465787387	<i>IL6, IL6R, AGER, TGFB1</i>
BP	GO:0045619~regulation of lymphocyte differentiation	5	10.03411957	0.0014875	0.926974065	2.489305027	<i>ERBB2, IL4R, TGFB2, HLA-DOA, HLA-DMA</i>
BP	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	6	7.08952747	0.0015166	0.93062274	2.537436832	<i>NOD1, TNF, RIPK2, TLR4, LTB, NFKBIL1</i>
BP	GO:0042493~response to drug	8	4.682589131	0.0015378	0.933165153	2.572481118	<i>BCHE, ERBB2, SNCA, TGFB2, TLR2, NOS3, CCL5, TGFB1</i>
BP	GO:0033043~regulation of organelle organization	8	4.661010379	0.001579	0.937840972	2.640524434	<i>MEN1, PRKCQ, TNF, MAPT, SNCA, LTB, NFKBIL1, NEBL</i>
BP	GO:0050729~positive regulation of inflammatory response	4	16.85732087	0.0016277	0.942948999	2.7209107	<i>IL6, C3, TLR4, CCL5</i>
BP	GO:0042990~regulation of transcription factor import into nucleus	4	16.85732087	0.0016277	0.942948999	2.7209107	<i>PRKCQ, TNF, NLRP3, NFKBIL1</i>
BP	GO:0032388~positive regulation of intracellular transport	4	16.85732087	0.0016277	0.942948999	2.7209107	<i>PRKCQ, TNF, TGFB1, TGFB1</i>
BP	GO:0051047~positive regulation of secretion	6	6.959444397	0.0016463	0.944784513	2.751549666	<i>PRKCQ, IL6, TNF, SNCA, NLRP3, TGFB1</i>
BP	GO:0009615~response to virus	6	6.959444397	0.0016463	0.944784513	2.751549666	<i>IL6, MICA, TNF, CCL5, NLRP3, IFNGR1</i>
BP	GO:0002495~antigen processing and presentation of peptide antigen via MHC class II	3	47.41121495	0.0016514	0.945279825	2.759990457	<i>HLA-DOA, HLA-DMA, HLA-DRA</i>
BP	GO:0010543~regulation of platelet activation	3	47.41121495	0.0016514	0.945279825	2.759990457	<i>APOE, NOS3, TLR4</i>

BP	GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC	3	47.41121495	0.0016514	0.945279825	2.759990457	<i>HLA-DOA, HLA-DMA, HLA-DRA</i>
BP	GO:0046328~regulation of JNK cascade	5	9.725377426	0.0016706	0.947100519	2.79168158	<i>MEN1, NOD1, TNF, RIPK2, TLR4</i>
BP	GO:0050920~regulation of chemotaxis	4	16.31353633	0.0017919	0.95727445	2.991482433	<i>IL6, IL6R, AGER, TGFB1</i>
BP	GO:0043066~negative regulation of apoptosis	10	3.571466286	0.0018354	0.96042319	3.062991786	<i>IL6, TNF, APOE, ERBB2, TGFB1, SNCA, RIPK2, NOS3, HSPA1A, HSPA1B, DDAH2</i>
BP	GO:0043069~negative regulation of programmed cell death	10	3.521724416	0.0020192	0.971368822	3.364823669	<i>IL6, TNF, APOE, ERBB2, TGFB1, SNCA, RIPK2, NOS3, HSPA1A, HSPA1B, DDAH2</i>
BP	GO:0060548~negative regulation of cell death	10	3.511941848	0.0020576	0.973244814	3.427885187	<i>IL6, TNF, APOE, ERBB2, TGFB1, SNCA, RIPK2, NOS3, HSPA1A, HSPA1B, DDAH2</i>
BP	GO:0070302~regulation of stress-activated protein kinase signaling pathway	5	9.161587431	0.0020828	0.974404674	3.469103585	<i>MEN1, NOD1, TNF, RIPK2, TLR4</i>
BP	GO:0046325~negative regulation of glucose	3	42.14330218	0.0021124	0.97570414	3.517540176	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0032874~positive regulation of stress-activated MAPK cascade	3	42.14330218	0.0021124	0.97570414	3.517540176	<i>NOD1, RIPK2, TLR4</i>
BP	GO:0052200~response to host defenses	3	42.14330218	0.0021124	0.97570414	3.517540176	<i>TLR2, TLR4, TGFB1</i>
BP	GO:0052173~response to defenses of other organism during symbiotic	3	42.14330218	0.0021124	0.97570414	3.517540176	<i>TLR2, TLR4, TGFB1</i>
BP	GO:0075136~response to	3	42.14330218	0.0021124	0.97570414	3.517540176	<i>TLR2, TLR4, TGFB1</i>
BP	GO:0051952~regulation of amine transport	4	15.32483716	0.0021504	0.977280629	3.579870534	<i>TNF, SNCA, LTB, NFKBIL1</i>
BP	GO:0048520~positive regulation of behavior	4	14.87410665	0.0023452	0.983880319	3.898081304	<i>IL6, IL6R, AGER, TGFB1</i>
BP	GO:0050806~positive regulation of synaptic transmission	4	14.87410665	0.0023452	0.983880319	3.898081304	<i>TNF, SNCA, LTB, NFKBIL1</i>
BP	GO:0001932~regulation of protein amino acid phosphorylation	7	5.115660958	0.0023829	0.984915948	3.959532014	<i>MEN1, IL6, TNF, TGFB1, TLR4, IL6R, TGFB1</i>

BP	GO:0032872~regulation of stress-activated MAPK cascade	3	37.92897196	0.002627	0.990189314	4.356666224	<i>NOD1, RIPK2, TLR4</i>
BP	GO:0010829~negative regulation of glucose transport	3	37.92897196	0.002627	0.990189314	4.356666224	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0032891~negative regulation of organic acid transport	3	37.92897196	0.002627	0.990189314	4.356666224	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0051955~regulation of amino acid transport	3	37.92897196	0.002627	0.990189314	4.356666224	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0031328~positive regulation of cellular biosynthetic process	14	2.583968893	0.0026553	0.990667736	4.402715152	<i>ICAM1, IL6, TNF, TGFBR1, TLR1, TLR4, TGFB1, MEN1, PRKCQ, SLC11A1, APOE, NOTCH4, PBX2, LTB</i>
BP	GO:0002366~leukocyte activation during immune response	4	14.04776739	0.0027667	0.992331458	4.583355625	<i>ICAM1, SLC11A1, TLR2, TLR4</i>
BP	GO:0002263~cell activation during immune	4	14.04776739	0.0027667	0.992331458	4.583355625	<i>ICAM1, SLC11A1, TLR2, TLR4</i>
BP	GO:0050727~regulation of inflammatory response	5	8.317757009	0.0029645	0.994589291	4.903356478	<i>IL6, C3, APOE, TLR4, CCL5</i>
BP	GO:0051971~positive regulation of transmission of nerve impulse	4	13.668098	0.0029938	0.994861784	4.950680055	<i>TNF, SNCA, LTB, NFKBIL1</i>
BP	GO:0009891~positive regulation of biosynthetic process	14	2.546789484	0.0030089	0.994996136	4.974935666	<i>ICAM1, IL6, TNF, TGFBR1, TLR1, TLR4, TGFB1, MEN1, PRKCQ, SLC11A1, APOE, NOTCH4, PBX2, LTB</i>
BP	GO:0032965~regulation of collagen biosynthetic process	3	34.4808836	0.0031944	0.996392235	5.273893771	<i>IL6, IL6R, TGFB1</i>
BP	GO:0051384~response to glucocorticoid stimulus	5	8.104481189	0.0032569	0.996769185	5.374534676	<i>IL6, TNF, BCHE, IL6R, CCL5</i>
BP	GO:0060341~regulation of cellular localization	8	4.078384082	0.0033435	0.997226944	5.513694541	<i>PRKCQ, IL6, TNF, TGFBR1, SNCA, NLRP3, NFKBIL1, TGFB1</i>
BP	GO:0007259~JAK-STAT cascade	4	12.9671699	0.0034817	0.997826571	5.735188409	<i>NOTCH4, AGER, FKBPL, AGPAT1</i>
BP	GO:0031646~positive regulation of neurological system process	4	12.9671699	0.0034817	0.997826571	5.735188409	<i>TNF, SNCA, LTB, NFKBIL1</i>

BP	GO:0042325~regulation of phosphorylation	11	2.984396936	0.0035514	0.998078274	5.846883619	<i>MEN1, SLC11A1, IL6, TNF, APOE, ERBB2, TGFBR1, TGFBR2, TLR4, IL6R, TGFB1</i>
BP	GO:0051341~regulation of oxidoreductase activity	4	12.64299065	0.0037427	0.998628777	6.152499556	<i>VDR, TNF, APOE, SNCA</i>
BP	GO:0010712~regulation of collagen metabolic process	3	31.60747664	0.0038137	0.998790166	6.265630305	<i>IL6, IL6R, TGFB1</i>
BP	GO:0060389~pathway-restricted SMAD protein phosphorylation	3	31.60747664	0.0038137	0.998790166	6.265630305	<i>TGFBR1, TGFBR2, TGFB1</i>
BP	GO:0002675~positive regulation of acute inflammatory response	3	31.60747664	0.0038137	0.998790166	6.265630305	<i>IL6, C3, CCL5</i>
BP	GO:0042060~wound	7	4.633556784	0.0038877	0.998938401	6.38357238	<i>PRKCQ, SLC11A1, IL6, ERBB2, TGFBR2, NINJ1, TGFB1</i>
BP	GO:0040012~regulation of locomotion	7	4.609423676	0.0039881	0.99911077	6.543208832	<i>ICAM1, IL6, APOE, SNCA, IL6R, AGER, TGFB1</i>
BP	GO:0002700~regulation of production of molecular mediator of immune	4	12.33462503	0.0040154	0.999152589	6.586563231	<i>IL6, TNF, IL13RA1, TGFB1</i>
BP	GO:0002683~negative regulation of immune system process	5	7.61625943	0.0040727	0.999234047	6.677459411	<i>MICB, LST1, ERBB2, IL4R, TGFB1</i>
BP	GO:0050804~regulation of synaptic transmission	6	5.577789995	0.0042964	0.999483939	7.031775034	<i>TNF, BCHE, APOE, SNCA, LTB, NFKBIL1</i>
BP	GO:0031960~response to corticosteroid stimulus	5	7.437053326	0.0044344	0.999595553	7.24976461	<i>IL6, TNF, BCHE, IL6R, CCL5</i>
BP	GO:0051605~protein maturation by peptide bond cleavage	5	7.350575962	0.0046231	0.999710187	7.547054458	<i>C3, CFB, C4B, CFH, C2</i>
BP	GO:0019220~regulation of phosphate metabolic	11	2.867482416	0.004702	0.999747896	7.671112098	<i>MEN1, SLC11A1, IL6, TNF, APOE, ERBB2, TGFBR1, TGFBR2, TLR4, IL6R, TGFB1</i>
BP	GO:0051174~regulation of phosphorus metabolic process	11	2.867482416	0.004702	0.999747896	7.671112098	<i>MEN1, SLC11A1, IL6, TNF, APOE, ERBB2, TGFBR1, TGFBR2, TLR4, IL6R, TGFB1</i>
BP	GO:0002699~positive regulation of immune effector process	4	11.49362787	0.0049049	0.999823818	7.989244003	<i>C3, TAP2, IL13RA1, NCR3</i>
BP	GO:0045069~regulation of viral genome replication	3	27.09212283	0.0052048	0.999896297	8.457779353	<i>CCL3, TNF, CCL5</i>
BP	GO:0002224~toll-like receptor signaling pathway	3	27.09212283	0.0052048	0.999896297	8.457779353	<i>TLR2, RIPK2, TLR4</i>

BP	GO:0050795~regulation of behavior	4	10.99390492	0.0055587	0.999944521	9.007701121	<i>IL6, IL6R, AGER, TGFB1</i>
BP	GO:0001816~cytokine production	4	10.99390492	0.0055587	0.999944521	9.007701121	<i>SLC11A1, NOD1, TLR4, NLRP3</i>
BP	GO:0051969~regulation of transmission of nerve	6	5.160404349	0.0059588	0.999972654	9.625654225	<i>TNF, BCHE, APOE, SNCA, LTB, NFKBIL1</i>
BP	GO:0016477~cell	8	3.664634972	0.0059729	0.999973325	9.64729185	<i>ICAM1, IL6, TNF, TGFB1, NOS3, IL6R, CCL5, TGFB1</i>
BP	GO:0002687~positive regulation of leukocyte migration	3	25.28598131	0.005975	0.999973426	9.650578397	<i>ICAM1, IL6, IL6R</i>
BP	GO:0030099~myeloid cell differentiation	5	6.797306803	0.0060974	0.999978598	9.83875715	<i>TNF, TGFB2, TIRAP, TRIM10, TGFB1</i>
BP	GO:0050764~regulation of phagocytosis	3	23.70560748	0.0067938	0.999993759	10.90269343	<i>SLC11A1, C3, TGFB1</i>
BP	GO:0031644~regulation of neurological system	6	4.958035551	0.007035	0.999995928	11.2683771	<i>TNF, BCHE, APOE, SNCA, LTB, NFKBIL1</i>
BP	GO:0040017~positive regulation of locomotion	5	6.450505436	0.007323	0.999997555	11.70320433	<i>ICAM1, IL6, IL6R, AGER, TGFB1</i>
BP	GO:0051272~positive regulation of cell motion	5	6.450505436	0.007323	0.999997555	11.70320433	<i>ICAM1, IL6, TGFB1, IL6R, TGFB1</i>
BP	GO:0043269~regulation of ion transport	5	6.385348815	0.0075862	0.999998466	12.09882521	<i>TNF, NOS3, LTB, NFKBIL1, TGFB1</i>
BP	GO:0044246~regulation of multicellular organismal metabolic process	3	22.31115998	0.0076605	0.999998655	12.21020517	<i>IL6, IL6R, TGFB1</i>
BP	GO:0032890~regulation of organic acid transport	3	22.31115998	0.0076605	0.999998655	12.21020517	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0002221~pattern recognition receptor signaling pathway	3	22.31115998	0.0076605	0.999998655	12.21020517	<i>TLR2, RIPK2, TLR4</i>
BP	GO:0033993~response to	3	21.07165109	0.0085743	0.999999734	13.56917795	<i>TGFB1, TGFB2, TGFB1</i>
BP	GO:0042345~regulation of NF-kappaB import into nucleus	3	21.07165109	0.0085743	0.999999734	13.56917795	<i>PRKCQ, TNF, NLRP3</i>
BP	GO:0009595~detection of biotic stimulus	3	21.07165109	0.0085743	0.999999734	13.56917795	<i>NOD1, TLR4, NLRP3</i>
BP	GO:0002706~regulation of lymphocyte mediated immunity	4	9.365178262	0.0086823	0.99999978	13.72849742	<i>C3, TAP2, TGFB1, NCR3</i>

BP	GO:0015833~peptide transport	4	9.365178262	0.0086823	0.99999978	13.72849742	<i>IL6, TAP2, CD209, TAP1</i>
BP	GO:0051250~negative regulation of lymphocyte activation	4	9.365178262	0.0086823	0.99999978	13.72849742	<i>LST1, ERBB2, IL4R, TGFB1</i>
BP	GO:0006919~activation of caspase activity	4	9.365178262	0.0086823	0.99999978	13.72849742	<i>NOD1, TNF, NLRP3, NLRP1</i>
BP	GO:0080135~regulation of cellular response to stress	5	6.137374104	0.0087013	0.999999787	13.75639202	<i>MEN1, NOD1, TNF, RIPK2, TLR4</i>
BP	GO:0050671~positive regulation of lymphocyte proliferation	4	9.194902294	0.0091317	0.999999901	14.38834911	<i>PRKCQ, IL6, RIPK2, IL13RA1</i>
BP	GO:0070665~positive regulation of leukocyte proliferation	4	9.03070761	0.0095945	0.999999956	15.0629008	<i>PRKCQ, IL6, RIPK2, IL13RA1</i>
BP	GO:0032946~positive regulation of mononuclear cell proliferation	4	9.03070761	0.0095945	0.999999956	15.0629008	<i>PRKCQ, IL6, RIPK2, IL13RA1</i>
BP	GO:0009408~response to	4	9.03070761	0.0095945	0.999999956	15.0629008	<i>PRKCQ, MICB, MICA, NOS3</i>
BP	GO:0009612~response to mechanical stimulus	4	9.03070761	0.0095945	0.999999956	15.0629008	<i>TNF, TGFB2, LTB, NFKBIL1</i>
BP	GO:0002695~negative regulation of leukocyte activation	4	8.872274143	0.0100707	0.999999981	15.75186396	<i>LST1, ERBB2, IL4R, TGFB1</i>
BP	GO:0048870~cell motility	8	3.294590398	0.0104259	0.99999999	16.26241348	<i>ICAM1, IL6, TNF, TGFB1, NOS3, IL6R, CCL5, TGFB1</i>
BP	GO:0051674~localization of cell	8	3.294590398	0.0104259	0.99999999	16.26241348	<i>ICAM1, IL6, TNF, TGFB1, NOS3, IL6R, CCL5, TGFB1</i>
BP	GO:0002685~regulation of leukocyte migration	3	18.96448598	0.0105401	0.999999992	16.42577045	<i>ICAM1, IL6, IL6R</i>
BP	GO:0051607~defense response to virus	3	18.96448598	0.0105401	0.999999992	16.42577045	<i>IL6, MICA, NLRP3</i>
BP	GO:0044057~regulation of system process	8	3.273266189	0.0107788	0.999999995	16.76665076	<i>PRKCQ, TNF, BCHE, APOE, SNCA, NOS3, LTB, NFKBIL1</i>
BP	GO:0007565~female pregnancy	5	5.746813934	0.0109006	0.999999996	16.94005007	<i>MEN1, VDR, TGFB1, TGFB2, TGFB1</i>
BP	GO:0016485~protein processing	5	5.644192256	0.0115891	0.999999999	17.91362742	<i>C3, CFB, C4B, CFH, C2</i>
BP	GO:0019216~regulation of lipid metabolic process	5	5.644192256	0.0115891	0.999999999	17.91362742	<i>TNF, APOE, SNCA, APOM, TGFB1</i>

BP	GO:0050792~regulation of viral reproduction	3	18.06141522	0.0115905	0.999999999	17.91556717	<i>CCL3, TNF, CCL5</i>
BP	GO:0002673~regulation of acute inflammatory	3	18.06141522	0.0115905	0.999999999	17.91556717	<i>IL6, C3, CCL5</i>
BP	GO:0002703~regulation of leukocyte mediated	4	8.290485675	0.0121117	1	18.64550102	<i>C3, TAP2, TGFB1, NCR3</i>
BP	GO:0030100~regulation of endocytosis	4	8.290485675	0.0121117	1	18.64550102	<i>SLC11A1, C3, SNCA, TGFB1</i>
BP	GO:0006928~cell motion	10	2.661682243	0.0122019	1	18.77126456	<i>ICAM1, CCL3, IL6, TNF, ERBB2, TGFB1, NOS3, IL6R, CCL5, TGFB1</i>
BP	GO:0010564~regulation of cell cycle process	5	5.54517134	0.0123049	1	18.91456902	<i>PRKCQ, TNF, LTB, NFKBIL1, TGFB1</i>
BP	GO:0043525~positive regulation of neuron apoptosis	3	17.2404418	0.0126849	1	19.44120501	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0045670~regulation of osteoclast differentiation	3	17.2404418	0.0126849	1	19.44120501	<i>TNF, TLR4, CCL5</i>
BP	GO:0007249~I-kappaB kinase/NF-kappaB cascade	4	8.027295653	0.0132147	1	20.17014079	<i>TLR1, TIRAP, TLR2, TLR4</i>
BP	GO:0010557~positive regulation of macromolecule	12	2.319814799	0.0133687	1	20.38091314	<i>MEN1, PRKCQ, SLC11A1, IL6, TNF, TGFB1, NOTCH4, TLR1, TLR4, PBX2, LTB, TGFB1</i>
BP	GO:0032269~negative regulation of cellular protein metabolic process	6	4.214330218	0.0135814	1	20.67105999	<i>MEN1, SNCA, APOM, PSMB8, TGFB1, PSMB9</i>
BP	GO:0045471~response to ethanol	4	7.901869159	0.013787	1	20.95060697	<i>APOE, NOS3, TLR4, IL6R</i>
BP	GO:0031400~negative regulation of protein modification process	5	5.312180947	0.0142168	1	21.53193477	<i>MEN1, SNCA, PSMB8, TGFB1, PSMB9</i>
BP	GO:0033273~response to vitamin	4	7.662418578	0.0149736	1	22.54582112	<i>VDR, MICB, BCHE, TGFB1</i>
BP	GO:0009620~response to fungus	3	15.80373832	0.0150029	1	22.58482927	<i>TLR2, TLR4, TGFB1</i>
BP	GO:0014070~response to organic cyclic substance	5	5.224376303	0.0150314	1	22.62276577	<i>PRKCQ, TGFB1, TGFB2, NOS3, TGFB1</i>
BP	GO:0051604~protein maturation	5	5.181553547	0.0154495	1	23.17714181	<i>C3, CFB, C4B, CFH, C2</i>
BP	GO:0002384~hepatic immune response	2	126.4299065	0.0156104	1	23.38940411	<i>IL6, IL6R</i>

BP	GO:0045602~negative regulation of endothelial cell differentiation	2	126.4299065	0.0156104	1	23.38940411	<i>TGFB1, NOTCH4</i>
BP	GO:0051248~negative regulation of protein metabolic process	6	4.056574541	0.0157837	1	23.61756769	<i>MEN1, SNCA, APOM, PSMB8, TGFB1, PSMB9</i>
BP	GO:0045669~positive regulation of osteoblast differentiation	3	15.17158879	0.016225	1	24.19539264	<i>MEN1, IL6, IL6R</i>
BP	GO:0051785~positive regulation of nuclear	3	15.17158879	0.016225	1	24.19539264	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0001910~regulation of leukocyte mediated cytotoxicity	3	15.17158879	0.016225	1	24.19539264	<i>ICAM1, TAP2, NCR3</i>
BP	GO:0045840~positive regulation of mitosis	3	15.17158879	0.016225	1	24.19539264	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0031099~regeneration	4	7.329269944	0.0168586	1	25.01798839	<i>PRKCQ, TGFB1, NINJ1, TGFB1</i>
BP	GO:0046635~positive regulation of alpha-beta T cell activation	3	14.58806614	0.0174882	1	25.82697063	<i>IL4R, TGFB2, RIPK2</i>
BP	GO:0051353~positive regulation of oxidoreductase activity	3	14.58806614	0.0174882	1	25.82697063	<i>VDR, TNF, APOE</i>
BP	GO:0051270~regulation of cell motion	6	3.930463416	0.0178519	1	26.2905246	<i>ICAM1, IL6, APOE, TGFB1, IL6R, TGFB1</i>
BP	GO:0045859~regulation of protein kinase activity	8	2.931707978	0.018718	1	27.38363226	<i>MEN1, SLC11A1, TNF, APOE, ERBB2, TGFB1, TGFB2, TGFB1</i>
BP	GO:0006875~cellular metal ion homeostasis	6	3.870303261	0.0189502	1	27.67407149	<i>VDR, SLC11A1, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0002521~leukocyte differentiation	5	4.825568952	0.0195447	1	28.41260134	<i>TNF, TGFB2, PTPN22, HLA-DMA, TGFB1</i>
BP	GO:0045833~negative regulation of lipid metabolic process	3	13.54606142	0.0201352	1	29.1392497	<i>TNF, APOE, APOM</i>
BP	GO:0007159~leukocyte adhesion	3	13.54606142	0.0201352	1	29.1392497	<i>ICAM1, TNF, CD209</i>
BP	GO:0031341~regulation of cell killing	3	13.54606142	0.0201352	1	29.1392497	<i>ICAM1, TAP2, NCR3</i>
BP	GO:0051046~regulation of secretion	6	3.755343759	0.0212788	1	30.52679874	<i>PRKCQ, IL6, TNF, SNCA, NLRP3, TGFB1</i>

BP	GO:0045807~positive regulation of endocytosis	3	13.07895585	0.0215176	1	30.8132411	<i>SLC11A1, C3, SNCA</i>
BP	GO:0006958~complement activation, classical	3	13.07895585	0.0215176	1	30.8132411	<i>C3, C4B, C2</i>
BP	GO:0043549~regulation of kinase activity	8	2.833163172	0.0220985	1	31.50556296	<i>MEN1, SLC11A1, TNF, APOE, ERBB2, TGFBR1, TGFBR2, TGFB1</i>
BP	GO:0055065~metal ion homeostasis	6	3.700387509	0.0225102	1	31.99224708	<i>VDR, SLC11A1, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3	12.64299065	0.0229383	1	32.49484075	<i>SLC11A1, C3, TAP2</i>
BP	GO:0030278~regulation of ossification	4	6.483584951	0.0232778	1	32.89097149	<i>MEN1, IL6, IL6R, TGFB1</i>
BP	GO:0033083~regulation of immature T cell	2	84.28660436	0.0233248	1	32.94567126	<i>ERBB2, RIPK2</i>
BP	GO:0032966~negative regulation of collagen biosynthetic process	2	84.28660436	0.0233248	1	32.94567126	<i>IL6, IL6R</i>
BP	GO:0070102~interleukin-6-mediated signaling	2	84.28660436	0.0233248	1	32.94567126	<i>IL6, IL6R</i>
BP	GO:0046629~gamma-delta T cell activation	2	84.28660436	0.0233248	1	32.94567126	<i>MICB, MICA</i>
BP	GO:0002455~humoral immune response mediated by circulating	3	12.23515225	0.0243966	1	34.18097235	<i>C3, C4B, C2</i>
BP	GO:0043112~receptor metabolic process	3	12.23515225	0.0243966	1	34.18097235	<i>TNF, SNCA, TGFB1</i>
BP	GO:0002821~positive regulation of adaptive immune response	3	12.23515225	0.0243966	1	34.18097235	<i>SLC11A1, C3, TAP2</i>
BP	GO:0008219~cell death	12	2.110095798	0.0250946	1	34.97387596	<i>MICB, IL6, MICA, NOD1, TNF, TNFRSF25, RIPK2, NLRP3, LTB, NLRP1, NFKBIL1, TGFB1</i>
BP	GO:0070664~negative regulation of leukocyte proliferation	3	11.85280374	0.025892	1	35.86867997	<i>LST1, ERBB2, TGFB1</i>

BP	GO:0045582~positive regulation of T cell differentiation	3	11.85280374	0.025892	1	35.86867997	<i>IL4R, TGFBR2, HLA-DMA</i>
BP	GO:0050672~negative regulation of lymphocyte proliferation	3	11.85280374	0.025892	1	35.86867997	<i>LST1, ERBB2, TGFB1</i>
BP	GO:0032945~negative regulation of mononuclear cell proliferation	3	11.85280374	0.025892	1	35.86867997	<i>LST1, ERBB2, TGFB1</i>
BP	GO:0060021~palate development	3	11.85280374	0.025892	1	35.86867997	<i>MEN1, TGFB1, TGFBR2</i>
BP	GO:0016265~death	12	2.095523313	0.0262359	1	36.25097965	<i>MICB, IL6, MICA, NOD1, TNF, TNFRSF25, RIPK2, NLRP3, LTB, NLRP1, NFKBIL1, TGFB1</i>
BP	GO:0051338~regulation of transferase activity	8	2.718922721	0.0268942	1	36.97687895	<i>MEN1, SLC11A1, TNF, APOE, ERBB2, TGFB1, TGFBR2, TGFB1</i>
BP	GO:0009266~response to temperature stimulus	4	6.093007544	0.027341	1	37.46512976	<i>PRKCQ, MICB, MICA, NOS3</i>
BP	GO:0045596~negative regulation of cell differentiation	6	3.511941848	0.0274185	1	37.54951204	<i>MEN1, IL4R, TGFB1, NOTCH4, TLR4, TGFB1</i>
BP	GO:0050871~positive regulation of B cell	3	11.49362787	0.0274237	1	37.55513187	<i>IL6, IL13RA1, TGFB1</i>
BP	GO:0046324~regulation of glucose import	3	11.49362787	0.0274237	1	37.55513187	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0006873~cellular ion homeostasis	8	2.704383028	0.0275834	1	37.72848407	<i>VDR, SLC11A1, CCL3, APOE, ERBB2, SNCA, CCL5, TGFB1</i>
BP	GO:0002705~positive regulation of leukocyte mediated immunity	3	11.15557999	0.0289911	1	39.23762357	<i>C3, TAP2, NCR3</i>
BP	GO:0000060~protein import into nucleus,	3	11.15557999	0.0289911	1	39.23762357	<i>SLC11A1, TNF, TGFB1</i>
BP	GO:0002708~positive regulation of lymphocyte mediated immunity	3	11.15557999	0.0289911	1	39.23762357	<i>C3, TAP2, NCR3</i>
BP	GO:0010827~regulation of glucose transport	3	11.15557999	0.0289911	1	39.23762357	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0002573~myeloid leukocyte differentiation	3	11.15557999	0.0289911	1	39.23762357	<i>TNF, TGFBR2, TGFB1</i>

BP	GO:0007166~cell surface receptor linked signal transduction	23	1.566749919	0.0291419	1	39.3972533	<i>CCL3, MICB, MICA, IL18RAP, TNFRSF25, C3, ERBB2, TGFB1, TGFB2, TIRAP, CSNK2B, TLR2, PTPN22, CCL5, AGER, TGFB1, APOE, NOTCH4, RIPK2, NOS3, GNG2, IL13RA1, DEFB1</i>
BP	GO:0010324~membrane invagination	6	3.44808836	0.0293599	1	39.62726533	<i>SLC11A1, APOE, CD209, SNCA, FCN1, TGFB2</i>
BP	GO:0006897~endocytosis	6	3.44808836	0.0293599	1	39.62726533	<i>SLC11A1, APOE, CD209, SNCA, FCN1, TGFB2</i>
BP	GO:0055082~cellular chemical homeostasis	8	2.661682243	0.0297231	1	40.00867584	<i>VDR, SLC11A1, CCL3, APOE, ERBB2, SNCA, CCL5, TGFB1</i>
BP	GO:0045621~positive regulation of lymphocyte differentiation	3	10.83684913	0.0305936	1	40.91358023	<i>IL4R, TGFB2, HLA-DMA</i>
BP	GO:0045860~positive regulation of protein kinase activity	6	3.401701521	0.0308718	1	41.200086	<i>SLC11A1, TNF, ERBB2, TGFB1, TGFB2, TGFB1</i>
BP	GO:0002220~innate immune response activating cell surface receptor signaling pathway	2	63.21495327	0.0309793	1	41.31048735	<i>MICA, TLR2</i>
BP	GO:0044252~negative regulation of multicellular organismal metabolic	2	63.21495327	0.0309793	1	41.31048735	<i>IL6, IL6R</i>
BP	GO:0002548~monocyte chemotaxis	2	63.21495327	0.0309793	1	41.31048735	<i>IL6, IL6R</i>
BP	GO:0010713~negative regulation of collagen metabolic process	2	63.21495327	0.0309793	1	41.31048735	<i>IL6, IL6R</i>
BP	GO:0045601~regulation of endothelial cell	2	63.21495327	0.0309793	1	41.31048735	<i>TGFB1, NOTCH4</i>
BP	GO:0070391~response to lipoteichoic acid	2	63.21495327	0.0309793	1	41.31048735	<i>TLR2, RIPK2</i>
BP	GO:0010544~negative regulation of platelet activation	2	63.21495327	0.0309793	1	41.31048735	<i>APOE, NOS3</i>
BP	GO:0007346~regulation of mitotic cell cycle	5	4.158878505	0.03152	1	41.86251143	<i>PRKCQ, TNF, LTB, NFKBIL1, TGFB1</i>
BP	GO:0046634~regulation of alpha-beta T cell activation	3	10.53582555	0.0322304	1	42.58055845	<i>IL4R, TGFB2, RIPK2</i>
BP	GO:0030193~regulation of blood coagulation	3	10.53582555	0.0322304	1	42.58055845	<i>APOE, NOS3, TLR4</i>

BP	GO:0001776~leukocyte homeostasis	3	10.53582555	0.0322304	1	42.58055845	<i>MEN1, IL6, TGFB1</i>
BP	GO:0031344~regulation of cell projection	4	5.682242991	0.0326839	1	43.03443422	<i>PRKCQ, APOE, MAPT, TGFB1</i>
BP	GO:0030335~positive regulation of cell migration	4	5.682242991	0.0326839	1	43.03443422	<i>ICAM1, IL6, IL6R, TGFB1</i>
BP	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	6	3.341759644	0.0329628	1	43.31194138	<i>VDR, SLC11A1, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0042592~homeostatic process	12	2.020184925	0.0330618	1	43.41016472	<i>MEN1, VDR, SLC11A1, CCL3, IL6, APOE, ERBB2, SNCA, TRIM10, CCL5, APOM, TGFB1</i>
BP	GO:0043523~regulation of neuron apoptosis	4	5.619106957	0.0336236	1	43.96436125	<i>TNF, SNCA, LTB, NFKBIL1</i>
BP	GO:0030595~leukocyte chemotaxis	3	10.2510735	0.0339011	1	44.23624735	<i>IL6, IL6R, CCL5</i>
BP	GO:0019722~calcium-mediated signaling	3	10.2510735	0.0339011	1	44.23624735	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0033674~positive regulation of kinase	6	3.283893676	0.0351405	1	45.43535463	<i>SLC11A1, TNF, ERBB2, TGFB1, TGFB2, TGFB1</i>
BP	GO:0001818~negative regulation of cytokine production	3	9.981308411	0.0356049	1	45.87846911	<i>SLC11A1, TNF, IL6R</i>
BP	GO:0006935~chemotaxis	5	3.950934579	0.0370039	1	47.19271667	<i>CCL3, IL6, IL6R, CCL5, DEFB1</i>
BP	GO:0042330~taxis	5	3.950934579	0.0370039	1	47.19271667	<i>CCL3, IL6, IL6R, CCL5, DEFB1</i>
BP	GO:0042102~positive regulation of T cell proliferation	3	9.725377426	0.0373413	1	47.50517893	<i>PRKCQ, IL6, RIPK2</i>
BP	GO:0060326~cell	3	9.725377426	0.0373413	1	47.50517893	<i>IL6, IL6R, CCL5</i>
BP	GO:0002282~microglial cell activation during immune response	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0052556~positive regulation by symbiont of host immune response	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0052305~positive regulation by organism of innate immunity in other organism during symbiotic interaction	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>

BP	GO:0042535~positive regulation of tumor necrosis factor	2	50.57196262	0.0385744	1	48.6323271	<i>TLR1, TLR4</i>
BP	GO:0052306~modulation by organism of innate immunity in other organism during symbiotic	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0002251~organ or tissue specific immune	2	50.57196262	0.0385744	1	48.6323271	<i>IL6, IL6R</i>
BP	GO:0052552~modulation by organism of immune response of other organism during symbiotic	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0052166~positive regulation by symbiont of host innate immunity	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0052167~modulation by symbiont of host innate immunity	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0034380~high-density lipoprotein particle	2	50.57196262	0.0385744	1	48.6323271	<i>APOE, APOM</i>
BP	GO:0052555~positive regulation by organism of immune response of other organism during symbiotic interaction	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0052553~modulation by symbiont of host immune response	2	50.57196262	0.0385744	1	48.6323271	<i>TLR2, TLR4</i>
BP	GO:0051224~negative regulation of protein transport	3	9.482242991	0.0391097	1	49.11446454	<i>TNF, NLRP3, NFKBIL1</i>
BP	GO:0060627~regulation of vesicle-mediated transport	4	5.267912773	0.0395544	1	49.51184287	<i>SLC11A1, C3, SNCA, TGFB1</i>
BP	GO:0055066~di-, tri-valent inorganic cation	6	3.173972549	0.0397588	1	49.69349392	<i>VDR, SLC11A1, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0006979~response to oxidative stress	5	3.854570321	0.0399398	1	49.85377171	<i>MICB, APOE, SNCA, TLR4, CCL5</i>

BP	GO:0051347~positive regulation of transferase activity	6	3.160747664	0.040361	1	50.22504498	<i>SLC11A1, TNF, ERBB2, TGFBR1, TGFB2, TGFB1</i>
BP	GO:0002761~regulation of myeloid leukocyte differentiation	3	9.250968771	0.0409094	1	50.70454509	<i>TNF, TLR4, CCL5</i>
BP	GO:0050818~regulation of coagulation	3	9.250968771	0.0409094	1	50.70454509	<i>APOE, NOS3, TLR4</i>
BP	GO:0050801~ion	8	2.472956607	0.041652	1	51.34694885	<i>VDR, SLC11A1, CCL3, APOE, ERBB2, SNCA, CCL5, TGFB1</i>
BP	GO:0050868~negative regulation of T cell	3	9.03070761	0.0427399	1	52.27376974	<i>ERBB2, IL4R, TGFB1</i>
BP	GO:0048585~negative regulation of response to stimulus	4	5.057196262	0.043784	1	53.14768169	<i>MEN1, MICB, APOE, TGFB1</i>
BP	GO:0048872~homeostasis of number of cells	4	5.057196262	0.043784	1	53.14768169	<i>MEN1, IL6, TRIM10, TGFB1</i>
BP	GO:0030334~regulation of cell migration	5	3.740529779	0.0437919	1	53.15424364	<i>ICAM1, IL6, APOE, IL6R, TGFB1</i>
BP	GO:0045667~regulation of osteoblast differentiation	3	8.820691154	0.0446005	1	53.82061575	<i>MEN1, IL6, IL6R</i>
BP	GO:0060391~positive regulation of SMAD protein nuclear	2	42.14330218	0.0461106	1	55.0411718	<i>TGFBR1, TGFB1</i>
BP	GO:0019062~virion attachment to host cell surface receptor	2	42.14330218	0.0461106	1	55.0411718	<i>ICAM1, CD209</i>
BP	GO:0009405~pathogenesis	2	42.14330218	0.0461106	1	55.0411718	<i>HLA-DRB1, HLA-DPB1</i>
BP	GO:0034384~high-density lipoprotein particle	2	42.14330218	0.0461106	1	55.0411718	<i>APOE, APOM</i>
BP	GO:0052564~response to immune response of other organism during symbiotic interaction	2	42.14330218	0.0461106	1	55.0411718	<i>TLR2, TLR4</i>
BP	GO:0052255~modulation by organism of defense response of other organism during symbiotic	2	42.14330218	0.0461106	1	55.0411718	<i>TLR2, TLR4</i>
BP	GO:0052572~response to host immune response	2	42.14330218	0.0461106	1	55.0411718	<i>TLR2, TLR4</i>

BP	GO:0060390~regulation of SMAD protein nuclear translocation	2	42.14330218	0.0461106	1	55.0411718	<i>TGFB1, TGFB1</i>
BP	GO:0045071~negative regulation of viral genome replication	2	42.14330218	0.0461106	1	55.0411718	<i>TNF, CCL5</i>
BP	GO:0052031~modulation by symbiont of host defense response	2	42.14330218	0.0461106	1	55.0411718	<i>TLR2, TLR4</i>
BP	GO:0002544~chronic inflammatory response	2	42.14330218	0.0461106	1	55.0411718	<i>TNF, CCL5</i>
BP	GO:0052509~positive regulation by symbiont of host defense response	2	42.14330218	0.0461106	1	55.0411718	<i>TLR2, TLR4</i>
BP	GO:0052510~positive regulation by organism of defense response of other organism during symbiotic interaction	2	42.14330218	0.0461106	1	55.0411718	<i>TLR2, TLR4</i>
BP	GO:0032943~mononuclear cell proliferation	3	8.620220901	0.0464908	1	55.34368616	<i>SLC11A1, RIPK2, TGFB1</i>
BP	GO:0070661~leukocyte proliferation	3	8.620220901	0.0464908	1	55.34368616	<i>SLC11A1, RIPK2, TGFB1</i>
BP	GO:0044092~negative regulation of molecular function	7	2.64972858	0.0473959	1	56.05611177	<i>MEN1, APOE, SNCA, NOS3, NLRP3, PSMB8, PSMB9</i>
BP	GO:0048878~chemical homeostasis	9	2.222400701	0.0477132	1	56.30335883	<i>VDR, SLC11A1, CCL3, APOE, ERBB2, SNCA, CCL5, APOM, TGFB1</i>
BP	GO:0009749~response to glucose stimulus	3	8.428660436	0.0484101	1	56.84170727	<i>PRKCQ, TGFB2, TGFB1</i>
BP	GO:0051336~regulation of hydrolase activity	7	2.626140492	0.0491157	1	57.38045479	<i>MEN1, NOD1, TNF, SNCA, NOS3, NLRP3, NLRP1</i>
BP	GO:0043627~response to estrogen stimulus	4	4.816377392	0.0493755	1	57.57723323	<i>TGFB1, TGFB2, NOS3, TGFB1</i>
BP	GO:0030003~cellular cation homeostasis	6	2.986533225	0.049377	1	57.57833589	<i>VDR, SLC11A1, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0045834~positive regulation of lipid metabolic process	3	8.245428688	0.0503579	1	58.31352563	<i>TNF, APOE, TGFB1</i>

BP	GO:0040008~regulation of growth	7	2.595335325	0.0514684	1	59.13138216	<i>MEN1, PRKCQ, APOE, MAPT, TGFB1, TGFB2, TGFB1</i>
BP	GO:0051345~positive regulation of hydrolase activity	5	3.531561635	0.0521031	1	59.59203104	<i>MEN1, NOD1, TNF, NLRP3, NLRP1</i>
BP	GO:0031346~positive regulation of cell projection organization	3	8.069994035	0.0523336	1	59.7581049	<i>PRKCQ, MAPT, TGFB1</i>
BP	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	3	8.069994035	0.0523336	1	59.7581049	<i>IL6, TLR4, IL6R</i>
BP	GO:0048638~regulation of developmental growth	3	8.069994035	0.0523336	1	59.7581049	<i>APOE, MAPT, TGFB2</i>
BP	GO:0034284~response to monosaccharide stimulus	3	8.069994035	0.0523336	1	59.7581049	<i>PRKCQ, TGFB2, TGFB1</i>
BP	GO:0009746~response to hexose stimulus	3	8.069994035	0.0523336	1	59.7581049	<i>PRKCQ, TGFB2, TGFB1</i>
BP	GO:0048525~negative regulation of viral reproduction	2	36.12283044	0.0535882	1	60.65081168	<i>TNF, CCL5</i>
BP	GO:0060558~regulation of calcidiol 1-monooxygenase activity	2	36.12283044	0.0535882	1	60.65081168	<i>VDR, TNF</i>
BP	GO:0045084~positive regulation of interleukin-12 biosynthetic process	2	36.12283044	0.0535882	1	60.65081168	<i>TLR4, LTB</i>
BP	GO:0033160~positive regulation of protein import into nucleus,	2	36.12283044	0.0535882	1	60.65081168	<i>TGFB1, TGFB1</i>
BP	GO:0051491~positive regulation of filopodium assembly	2	36.12283044	0.0535882	1	60.65081168	<i>PRKCQ, TGFB1</i>
BP	GO:0002825~regulation of T-helper 1 type immune response	2	36.12283044	0.0535882	1	60.65081168	<i>SLC11A1, IL4R</i>
BP	GO:0051489~regulation of filopodium assembly	2	36.12283044	0.0535882	1	60.65081168	<i>PRKCQ, TGFB1</i>
BP	GO:0032494~response to peptidoglycan	2	36.12283044	0.0535882	1	60.65081168	<i>IL6, RIPK2</i>

BP	GO:0006874~cellular calcium ion homeostasis	5	3.454369031	0.0556533	1	62.07978026	<i>VDR, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0048705~skeletal system morphogenesis	4	4.515353805	0.0577595	1	63.48684995	<i>MEN1, TGFB1, TGFB2, TGFB1</i>
BP	GO:0055074~calcium ion homeostasis	5	3.362497514	0.0602709	1	65.10033564	<i>VDR, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0050864~regulation of B cell activation	3	7.437053326	0.0605049	1	65.24720417	<i>IL6, IL13RA1, TGFB1</i>
BP	GO:0030857~negative regulation of epithelial cell differentiation	2	31.60747664	0.0610077	1	65.56086176	<i>TGFB1, NOTCH4</i>
BP	GO:0045075~regulation of interleukin-12 biosynthetic process	2	31.60747664	0.0610077	1	65.56086176	<i>TLR4, LTB</i>
BP	GO:0002281~macrophage activation during immune response	2	31.60747664	0.0610077	1	65.56086176	<i>TLR2, TLR4</i>
BP	GO:0006527~arginine catabolic process	2	31.60747664	0.0610077	1	65.56086176	<i>NOS3, DDAH2</i>
BP	GO:0007626~locomotory behavior	6	2.768538099	0.064169	1	67.47252114	<i>CCL3, IL6, SNCA, IL6R, CCL5, DEFB1</i>
BP	GO:0006898~receptor-mediated endocytosis	3	7.156409804	0.0647441	1	67.8093706	<i>APOE, SNCA, TGFB2</i>
BP	GO:0051173~positive regulation of nitrogen compound metabolic	10	1.963197307	0.0655614	1	68.28242521	<i>MEN1, ICAM1, SLC11A1, IL6, TNF, APOE, TGFB1, NOTCH4, PBX2, TGFB1</i>
BP	GO:0001558~regulation of cell growth	5	3.258502746	0.0660736	1	68.57558207	<i>PRKCQ, APOE, MAPT, TGFB1, TGFB1</i>
BP	GO:0043086~negative regulation of catalytic	6	2.738553932	0.066582	1	68.86399757	<i>MEN1, APOE, SNCA, NOS3, PSMB8, PSMB9</i>
BP	GO:0030826~regulation of cGMP biosynthetic process	2	28.09553479	0.0683697	1	69.85852682	<i>APOE, NOS3</i>
BP	GO:0033158~regulation of protein import into nucleus, translocation	2	28.09553479	0.0683697	1	69.85852682	<i>TGFB1, TGFB1</i>
BP	GO:0042346~positive regulation of NF-kappaB import into nucleus	2	28.09553479	0.0683697	1	69.85852682	<i>PRKCQ, TNF</i>

BP	GO:0043537~negative regulation of blood vessel endothelial cell migration	2	28.09553479	0.0683697	1	69.85852682	<i>APOE, TGFB1</i>
BP	GO:0044003~modification by symbiont of host morphology or physiology	2	28.09553479	0.0683697	1	69.85852682	<i>TLR2, TLR4</i>
BP	GO:0034405~response to fluid shear stress	2	28.09553479	0.0683697	1	69.85852682	<i>NOS3, TGFB1</i>
BP	GO:0002446~neutrophil mediated immunity	2	28.09553479	0.0683697	1	69.85852682	<i>IL6, IL6R</i>
BP	GO:0051044~positive regulation of membrane protein ectodomain proteolysis	2	28.09553479	0.0683697	1	69.85852682	<i>TNF, APOE</i>
BP	GO:0043011~myeloid dendritic cell	2	28.09553479	0.0683697	1	69.85852682	<i>TGFB2, TGFB1</i>
BP	GO:0051023~regulation of immunoglobulin secretion	2	28.09553479	0.0683697	1	69.85852682	<i>IL6, TNF</i>
BP	GO:0001773~myeloid dendritic cell activation	2	28.09553479	0.0683697	1	69.85852682	<i>TGFB2, TGFB1</i>
BP	GO:0048771~tissue remodeling	3	6.773030708	0.0712835	1	71.41578527	<i>ERBB2, NOS3, TGFB1</i>
BP	GO:0007088~regulation of mitosis	3	6.773030708	0.0712835	1	71.41578527	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0051783~regulation of nuclear division	3	6.773030708	0.0712835	1	71.41578527	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0019725~cellular homeostasis	8	2.170470499	0.073286	1	72.44175893	<i>VDR, SLC11A1, CCL3, APOE, ERBB2, SNCA, CCL5, TGFB1</i>
BP	GO:0048704~embryonic skeletal system morphogenesis	3	6.654205607	0.0735094	1	72.55405421	<i>MEN1, TGFB1, TGFB2</i>
BP	GO:0045787~positive regulation of cell cycle	3	6.654205607	0.0735094	1	72.55405421	<i>TNF, LTB, NFKBIL1</i>
BP	GO:0055080~cation homeostasis	6	2.652375662	0.074123	1	72.86023763	<i>VDR, SLC11A1, CCL3, APOE, CCL5, TGFB1</i>
BP	GO:0034341~response to interferon-gamma	2	25.28598131	0.0756744	1	73.62014675	<i>SLC11A1, SNCA</i>
BP	GO:0002690~positive regulation of leukocyte chemotaxis	2	25.28598131	0.0756744	1	73.62014675	<i>IL6, IL6R</i>

BP	GO:0048535~lymph node development	2	25.28598131	0.0756744	1	73.62014675	<i>LTB, TGFB1</i>
BP	GO:0030823~regulation of cGMP metabolic process	2	25.28598131	0.0756744	1	73.62014675	<i>APOE, NOS3</i>
BP	GO:0042534~regulation of tumor necrosis factor biosynthetic process	2	25.28598131	0.0756744	1	73.62014675	<i>TLR1, TLR4</i>
BP	GO:0045073~regulation of chemokine biosynthetic process	2	25.28598131	0.0756744	1	73.62014675	<i>IL6, TNF</i>
BP	GO:0033138~positive regulation of peptidyl-serine phosphorylation	2	25.28598131	0.0756744	1	73.62014675	<i>IL6, TGFB1</i>
BP	GO:0009743~response to carbohydrate stimulus	3	6.321495327	0.0803188	1	75.77711375	<i>PRKCQ, TGFB2, TGFB1</i>
BP	GO:0007179~transforming growth factor beta receptor signaling pathway	3	6.321495327	0.0803188	1	75.77711375	<i>TGFB1, TGFB2, TGFB1</i>
BP	GO:0016192~vesicle-mediated transport	9	1.97546729	0.0823798	1	76.68014343	<i>SLC11A1, CCL3, APOE, CD209, SNCA, FCN1, TGFB2, MAP4K2, CCL5</i>
BP	GO:0006968~cellular defense response	3	6.217864256	0.0826309	1	76.78795929	<i>TAP2, CCL5, HLA-G</i>
BP	GO:0044409~entry into	2	22.98725573	0.0829224	1	76.91254957	<i>ICAM1, CD209</i>
BP	GO:0031663~lipopolysaccharide-mediated signaling pathway	2	22.98725573	0.0829224	1	76.91254957	<i>RIPK2, NOS3</i>
BP	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	2	22.98725573	0.0829224	1	76.91254957	<i>IL6, IL6R</i>
BP	GO:0051897~positive regulation of protein kinase B signaling cascade	2	22.98725573	0.0829224	1	76.91254957	<i>TGFB1, TGFB1</i>
BP	GO:0002688~regulation of leukocyte chemotaxis	2	22.98725573	0.0829224	1	76.91254957	<i>IL6, IL6R</i>
BP	GO:0052192~movement in environment of other organism during symbiotic interaction	2	22.98725573	0.0829224	1	76.91254957	<i>ICAM1, CD209</i>

BP	GO:0032729~positive regulation of interferon-gamma production	2	22.98725573	0.0829224	1	76.91254957	<i>SLC11A1, RIPK2</i>
BP	GO:0046718~entry of virus into host cell	2	22.98725573	0.0829224	1	76.91254957	<i>ICAM1, CD209</i>
BP	GO:0052126~movement in host environment	2	22.98725573	0.0829224	1	76.91254957	<i>ICAM1, CD209</i>
BP	GO:0030260~entry into host cell	2	22.98725573	0.0829224	1	76.91254957	<i>ICAM1, CD209</i>
BP	GO:0051828~entry into other organism during symbiotic interaction	2	22.98725573	0.0829224	1	76.91254957	<i>ICAM1, CD209</i>
BP	GO:0051806~entry into cell of other organism during symbiotic	2	22.98725573	0.0829224	1	76.91254957	<i>ICAM1, CD209</i>
BP	GO:0022604~regulation of cell morphogenesis	4	3.860455162	0.0836061	1	77.20229429	<i>LST1, APOE, MAPT, TGFB1</i>
BP	GO:0048514~blood vessel morphogenesis	5	2.995969349	0.0840305	1	77.38041687	<i>APOE, TGFB1, NOTCH4, TGFB2, NOS3</i>
BP	GO:0022415~viral reproductive process	3	6.117576123	0.0849634	1	77.76740152	<i>ICAM1, CD209, TGFB1</i>
BP	GO:0045765~regulation of angiogenesis	3	6.02047174	0.0873158	1	78.71573001	<i>IL6, ERBB2, NOS3</i>
BP	GO:0030879~mammary gland development	3	6.02047174	0.0873158	1	78.71573001	<i>ERBB2, NOTCH4, TGFB1</i>
BP	GO:0001666~response to hypoxia	4	3.774027061	0.0880746	1	79.01343317	<i>PRKCQ, TGFB1, NOS3, TGFB1</i>
BP	GO:0048732~gland development	4	3.746071305	0.0895863	1	79.59484276	<i>ERBB2, TGFB1, NOTCH4, TGFB1</i>
BP	GO:0051235~maintenance of location	3	5.926401869	0.0896877	1	79.63328153	<i>TNF, APOE, NFKB1L1</i>
BP	GO:0065005~protein-lipid complex assembly	2	21.07165109	0.0901141	1	79.79423598	<i>APOE, APOM</i>
BP	GO:0050766~positive regulation of phagocytosis	2	21.07165109	0.0901141	1	79.79423598	<i>SLC11A1, C3</i>
BP	GO:0034375~high-density lipoprotein particle remodeling	2	21.07165109	0.0901141	1	79.79423598	<i>APOE, APOM</i>
BP	GO:0008354~germ cell migration	2	21.07165109	0.0901141	1	79.79423598	<i>TGFB1, TGFB1</i>

BP	GO:0006809~nitric oxide biosynthetic process	2	21.07165109	0.0901141	1	79.79423598	<i>NOS3, DDAH2</i>
BP	GO:0034377~plasma lipoprotein particle	2	21.07165109	0.0901141	1	79.79423598	<i>APOE, APOM</i>
BP	GO:0051926~negative regulation of calcium ion transport	2	21.07165109	0.0901141	1	79.79423598	<i>NOS3, TGFB1</i>
BP	GO:0030217~T cell differentiation	3	5.835226456	0.0920786	1	80.52043626	<i>PTPN22, HLA-DMA, TGFB1</i>
BP	GO:0030155~regulation of cell adhesion	4	3.691384133	0.0926424	1	80.72425923	<i>ICAM1, TNF, ERBB2, TGFB1</i>
BP	GO:0016310~phosphorylation	11	1.738411215	0.0962807	1	81.99214393	<i>PRKCQ, TNF, TOLLIP, ERBB2, TGFB1, SNCA, TGFB2, MAP4K2, RIPK2, STK19, TGFB1</i>
BP	GO:0006525~arginine metabolic process	2	19.45075485	0.0972499	1	82.31641653	<i>NOS3, DDAH2</i>
BP	GO:0042993~positive regulation of transcription factor import into nucleus	2	19.45075485	0.0972499	1	82.31641653	<i>PRKCQ, TNF</i>
BP	GO:0002286~T cell activation during immune	2	19.45075485	0.0972499	1	82.31641653	<i>ICAM1, SLC11A1</i>
BP	GO:0031056~regulation of histone modification	2	19.45075485	0.0972499	1	82.31641653	<i>MEN1, SNCA</i>
BP	GO:0046209~nitric oxide metabolic process	2	19.45075485	0.0972499	1	82.31641653	<i>NOS3, DDAH2</i>
BP	GO:0051043~regulation of membrane protein ectodomain proteolysis	2	19.45075485	0.0972499	1	82.31641653	<i>TNF, APOE</i>
BP	GO:0032770~positive regulation of monooxygenase activity	2	19.45075485	0.0972499	1	82.31641653	<i>TNF, APOE</i>
BP	GO:0045730~respiratory	2	19.45075485	0.0972499	1	82.31641653	<i>PRKCQ, SLC11A1</i>
BP	GO:0070482~response to oxygen levels	4	3.586664015	0.0988828	1	82.8503218	<i>PRKCQ, TGFB1, NOS3, TGFB1</i>
BP	GO:0043405~regulation of MAP kinase activity	4	3.586664015	0.0988828	1	82.8503218	<i>TNF, APOE, ERBB2, TGFB1</i>
BP	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	3	5.577789995	0.0993613	1	83.00389425	<i>IL6, TLR4, IL6R</i>
BP	GO:0006915~apoptosis	9	1.890148104	0.0998845	1	83.17032561	<i>IL6, NOD1, TNF, TNFRSF25, RIPK2, NLRP3, LTB, NLRP1, NFKB1</i>

CC	GO:0042611~MHC protein complex	16	35.87929825	1.19E-19	2.38E-17	1.50E-16	HLA-DQB1, MICB, MICA, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-G, HLA-DQA1, HLA-F, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA
CC	GO:0042613~MHC class II protein complex	10	44.07586207	6.10E-13	1.21E-10	7.64E-10	HLA-DQB1, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DOA, HLA-DOB, HLA-DMA, HLA-DQA1, HLA-DRA
CC	GO:0042825~TAP	7	127.82	1.29E-12	2.56E-10	1.61E-09	TAP2, TAP1, HLA-DMB, HLA-DOB, HLA-DMA, PSMB8, HLA-DRA
CC	GO:0044459~plasma membrane part	48	2.78500227	3.12E-12	6.21E-10	3.91E-09	MICB, MICA, TOLLIP, AIF1, TLR1, TLR2, TLR4, HLA-DMB, HLA-DMA, APOE, MAPT, IL4R, GNG2, NOS3, IL13RA1, APOM, IFNGR1, AGPAT1, ICAM1, FLOT1, HLA-A, HLA-C, IL6R, HLA-B, HLA-DQA1, HLA-G, HLA-F, NCR3, PRKCQ, HLA-DPA1, HLA-DRA, HLA-DQB1, TNF, HLA-DRB1, TNFRSF25, ERBB2, SLC11A1, IL10RB, TAP2, TAP1, HLA-DPB1, HLA-DOA, HLA-DOB, FKBPL, IL6, TGFB1, TGFB2, TAP2, TAP1, HLA-DMB, HLA-DOB, HLA-DMA, PSMB8, HLA-DRA
CC	GO:0042824~MHC class I peptide loading complex	7	99.41555556	1.53E-11	3.04E-09	1.91E-08	TAP2, TAP1, HLA-DMB, HLA-DOB, HLA-DMA, PSMB8, HLA-DRA
CC	GO:0005886~plasma membrane	59	1.996658724	1.62E-09	3.22E-07	2.03E-06	MICB, MICA, AIF1, TOLLIP, SNCA, TLR1, TLR2, TIRAP, TLR4, HLA-DMB, HLA-DMA, APOE, IL4R, MAPT, GNG2, NOS3, IL13RA1, APOM, IFNGR1, AGPAT1, ICAM1, FLOT1, HLA-A, HLA-C, IL6R, HLA-B, CLIC1, HLA-DQA1, HLA-G, HLA-F, NCR3, PRKCQ, HLA-DPA1, HLA-DRA, HLA-DQB1, LY6G6D, TNF, HLA-DRB1, TNFRSF25, ERBB2, LY6G6C, MAP4K2, SLC11A1, IL10RB, TAP2, IL10RA, TAP1, HLA-DPB1, HLA-DOA, HLA-DOB, FKBPL, IL6, LGALS3, CFB, TGFB1, ICAM1, CCL3, IL6, MICA, TNF, TNXB, C4B, C3, IL6R, CCL5, AGER, TGFB1, BCHE, APOE, NOTCH4, FCN1, CFH, C2, GNL1, APOM, LTB, MICB, MICA, TNF, HLA-DRB1, TNFRSF25, TOLLIP, TLR1, TLR2, TLR4, SLC11A1, IL10RB, IL4R, TAP2, TAP1, IL13RA1, APOM, IFNGR1, ICAM1, IL6, TGFB1, TGFB2, HLA-A, HLA-C, IL6R, HLA-B, AGER, HLA-DQA1, NCR3, NOTCH4, HLA-DPA1, HLA-DRA
CC	GO:0005615~extracellular space	23	4.291766423	9.01E-09	1.79E-06	1.13E-05	MICB, MICA, TNF, HLA-DRB1, TNFRSF25, TOLLIP, TLR1, TLR2, TLR4, SLC11A1, IL10RB, IL4R, TAP2, TAP1, IL13RA1, APOM, IFNGR1, ICAM1, IL6, TGFB1, TGFB2, HLA-A, HLA-C, IL6R, HLA-B, AGER, HLA-DQA1, NCR3, NOTCH4, HLA-DPA1, HLA-DRA
CC	GO:0005887~integral to plasma membrane	30	3.227777778	1.25E-08	2.49E-06	1.57E-05	ICAM1, IL6, CCL3, MICA, TNF, TNXB, LGALS3, C4B, C3, IL6R, CCL5, AGER, TGFB1, BCHE, APOE, NOTCH4, FCN1, CFH, C2, GNL1, APOM, LTB, FKBPL, AGPAT1
CC	GO:0031226~intrinsic to plasma membrane	30	3.156049383	2.07E-08	4.12E-06	2.59E-05	MICB, MICA, TNF, HLA-DRB1, TNFRSF25, TOLLIP, TLR1, TLR2, TLR4, SLC11A1, IL10RB, IL4R, TAP2, TAP1, IL13RA1, APOM, IFNGR1, ICAM1, IL6, TGFB1, TGFB2, HLA-A, HLA-C, IL6R, HLA-B, AGER, HLA-DQA1, NCR3, NOTCH4, HLA-DPA1, HLA-DRA
CC	GO:0044421~extracellular region part	24	3.1955	8.21E-07	1.63E-04	0.001028501	ICAM1, IL6, CCL3, MICA, TNF, TNXB, LGALS3, C4B, C3, IL6R, CCL5, AGER, TGFB1, BCHE, APOE, NOTCH4, FCN1, CFH, C2, GNL1, APOM, LTB, FKBPL, AGPAT1
CC	GO:0042612~MHC class I protein complex	6	27.39	2.15E-06	4.27E-04	0.002690375	MICB, MICA, HLA-A, HLA-C, HLA-B, HLA-G, HLA-F
CC	GO:0043235~receptor	9	9.917068966	3.11E-06	6.18E-04	0.003891745	IL6, TOLLIP, IL10RB, ERBB2, TGFB1, TGFB2, TLR4, IL6R, IL13RA1

CC	GO:0005576~extracellular region	35	2.225721393	3.76E-06	7.48E-04	0.004707349	C6ORF27, CCL3, MICA, TNF, C3, TNFRSF25, ERBB2, CCL5, TGFB1, BCHE, APOE, IL4R, FCN1, CFH, C2, DEFB1, APOM, LTB, GNL1, FKBPL, AGPAT1, ICAM1, LY6G5C, IL6, TNXB, LGALS3, C4B, CFB, CSNK2B, HLA-C, IL6R, HLA-B, AGER, CD209, NOTCH4, EGFL8
CC	GO:0009925~basal plasma membrane	5	24.58076923	4.44E-05	0.008798613	0.055601929	ERBB2, NOTCH4, AGER, FKBPL, AGPAT1
CC	GO:0045178~basal part of	5	21.30333333	7.95E-05	0.015695686	0.09951159	ERBB2, NOTCH4, AGER, FKBPL, AGPAT1
CC	GO:0009986~cell surface	11	4.040287356	3.57E-04	0.068575375	0.446078538	ICAM1, MICA, TNF, APOE, NOTCH4, TGFB2, TLR2, TLR4, IL6R, TGFB1, HLA-DRA
CC	GO:0009897~external side of plasma membrane	7	5.263176471	0.0020473	0.33490572	2.533919725	ICAM1, TNF, APOE, TGFB2, TLR2, TLR4, HLA-DRA
CC	GO:0031224~intrinsic to membrane	58	1.351606199	0.0022513	0.361422356	2.783158955	C7ORF44, MICB, MICA, TOLLIP, TLR1, TLR2, TIRAP, TLR4, HLA-DMB, HLA-DMA, IL4R, PRRT1, IL13RA1, APOM, LTB, IFNGR1, AGPAT1, ICAM1, IL18RAP, FLOT1, HLA-A, HLA-C, IL6R, HLA-B, CLIC1, HLA-DQA1, HLA-G, HLA-F, NCR3, EGFL8, HLA-DPA1, HLA-DRA, HLA-DQB1, LY6G6D, LST1, TNF, HLA-DRB1, TNFRSF25, ERBB2, LY6G6C, NINJ1, ATP6V1G2, SLC11A1, IL10RB, TAP2, IL10RA, TAP1, HLA-DPB1, HLA-DOA, HLA-DOB, IL6, TGFB1, TGFB2,
CC	GO:0016021~integral to membrane	56	1.351315839	0.0030995	0.460852255	3.813182943	C7ORF44, MICB, MICA, TOLLIP, TLR1, TLR2, TLR4, HLA-DMB, HLA-DMA, IL4R, PRRT1, IL13RA1, APOM, LTB, IFNGR1, AGPAT1, ICAM1, IL18RAP, FLOT1, HLA-A, HLA-C, IL6R, HLA-B, CLIC1, HLA-DQA1, HLA-G, HLA-F, NCR3, EGFL8, HLA-DPA1, HLA-DRA, HLA-DQB1, LY6G6D, LST1, TNF, HLA-DRB1, TNFRSF25, ERBB2, NINJ1, ATP6V1G2, SLC11A1, IL10RB, TAP2, IL10RA, TAP1, HLA-DPB1, HLA-DOA, HLA-DOB, IL6, TGFB1, TGFB2, AGER, NFKBIL1, RNF5,
CC	GO:0045121~membrane	6	5.363076923	0.0050385	0.634029003	6.130097206	TNF, ERBB2, FLOT1, TGFB2, NOS3, TLR4
CC	GO:0005773~vacuole	7	3.550555556	0.0135064	0.933202514	15.65903382	SLC11A1, PPT2, ATP6V1G2, HLA-DMB, HLA-DOB, HLA-DMA, HLA-BCHE, TAP2, TAP1, HLA-DMB, HLA-DOB, HLA-DMA, PSMB8, HLA-DRA
CC	GO:0044432~endoplasmic reticulum part	8	2.94685879	0.0180937	0.973579474	20.44124737	ERBB2, TGFB1, NOTCH4, AGER, FKBPL, AGPAT1
CC	GO:0016323~basolateral plasma membrane	6	3.777931034	0.0206823	0.984375858	23.02847553	IL6, IL6R
CC	GO:0005896~interleukin-6 receptor complex	2	85.21333333	0.0230581	0.99036438	25.33459917	TGFB1, TGFB2
CC	GO:0070022~transforming growth factor beta receptor complex	2	85.21333333	0.0230581	0.99036438	25.33459917	SLC11A1, PPT2, HLA-DMB, HLA-DOB, HLA-DMA, HLA-DRA
CC	GO:0000323~lytic vacuole	6	3.634691943	0.0239656	0.991991289	26.19856492	SLC11A1, PPT2, HLA-DMB, HLA-DOB, HLA-DMA, HLA-DRA
CC	GO:0005764~lysosome	6	3.634691943	0.0239656	0.991991289	26.19856492	LY6G6D, C6ORF26, TNFRSF25, CFB, SNCA, TGFB2, CSNK2B, CLIC1, PSMB8, PSMB9, MEN1, TAP2, MAPT, RIPK2, NOS3, DDAH2,
CC	GO:0005829~cytosol	18	1.729894737	0.0260318	0.994746971	28.1315233	

CC	GO:0005625~soluble	7	2.858594249	0.0345893	0.999092787	35.65135816	<i>MEN1, PRKCQ, CCL3, MAP4K2, NOS3, CLIC1, CCL5</i>
CC	GO:0005901~caveola	3	7.374230769	0.0613313	0.999996612	54.735956	<i>FLOT1, TGFB2, NOS3</i>
CC	GO:0005770~late	3	6.8475	0.0698423	0.999999447	59.61569155	<i>SLC11A1, APOE, HLA-DMA</i>
CC	GO:0001772~immunological synapse	2	25.564	0.0748336	0.99999981	62.24727122	<i>ICAM1, PRKCQ</i>
CC	GO:0034362~low-density lipoprotein particle	2	19.66461538	0.0961827	0.999999998	71.81824657	<i>APOE, APOM</i>
CC	GO:0005768~endosome	6	2.434666667	0.0976132	0.999999999	72.37178368	<i>SLC11A1, TNF, APOE, HLA-A, HLA-DMB, HLA-DMA</i>
KEGG	hsa05332:Graft-versus-host disease	16	27.81538462	1.176E-18	9.63935E-17	1.25584E-15	<i>HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, HLA-G, HLA-F, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa05330:Allograft rejection	15	28.25	1.529E-17	1.25399E-15	1.63373E-14	<i>HLA-DQB1, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-G, HLA-DQA1, HLA-F, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa04940:Type I diabetes mellitus	15	24.21428571	1.982E-16	1.82077E-14	2.33147E-13	<i>HLA-DQB1, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-G, HLA-DQA1, HLA-F, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa04612:Antigen processing and presentation	17	13.88674699	1.793E-14	1.47482E-12	1.9218E-11	<i>HLA-DQB1, HLA-DRB1, HLA-A, HSPA1A, HLA-C, HSPA1B, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, HLA-G, HLA-F, TAP2, TAP1, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa05320:Autoimmune thyroid disease	14	18.61176471	1.352E-13	1.10794E-11	1.4434E-10	<i>HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-G, HLA-DQA1, HLA-F, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa05416:Viral myocarditis	15	14.32394366	6.679E-13	5.47686E-11	7.1354E-10	<i>HLA-DQB1, ICAM1, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-G, HLA-DQA1, HLA-F, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa05310:Asthma	11	25.71724138	3.66E-12	3.00162E-10	3.91058E-09	<i>HLA-DQB1, TNF, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DOA, HLA-DOB, HLA-DMA, HLA-DQA1, HLA-DRA</i>
KEGG	hsa04672:Intestinal immune network for IgA	12	16.60408163	5.407E-11	4.43402E-09	5.77675E-08	<i>HLA-DQB1, IL6, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DOA, HLA-DOB, HLA-DMA, HLA-DQA1, TGFB1, HLA-DRA</i>
KEGG	hsa05322:Systemic lupus erythematosus	14	9.587878788	1.02E-09	8.36547E-08	1.08987E-06	<i>HLA-DQB1, TNF, HLA-DRB1, C3, C4B, HLA-DMB, HLA-DMA, HLA-DQA1, HLA-DPA1, HLA-DPB1, C2, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa04514:Cell adhesion molecules (CAMs)	15	7.704545455	3.828E-09	3.13931E-07	4.08997E-06	<i>HLA-DQB1, ICAM1, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-G, HLA-DQA1, HLA-F, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA</i>
KEGG	hsa04060:Cytokine-cytokine receptor	16	4.140458015	3.766E-06	0.000308732	0.004022776	<i>CCL3, IL6, TNF, IL18RAP, TNFRSF25, TGFB1, TGFB2, IL6R, CCL5, TGFB1, IL10RB, IL10RA, IL4R, IL13RA1, LTB, IFNGR1</i>
KEGG	hsa04620:Toll-like receptor signaling pathway	9	6.041584158	9.364E-05	0.007649106	0.099987447	<i>CCL3, IL6, TNF, TOLLIP, TLR1, TIRAP, TLR2, TLR4, CCL5</i>
KEGG	hsa04621:NOD-like receptor signaling pathway	7	7.65483871	0.0002496	0.020262102	0.266335286	<i>IL6, NOD1, TNF, RIPK2, CCL5, NLRP3, NLRP1</i>

KEGG	hsa04650:Natural killer cell mediated cytotoxicity	9	4.587969925	0.0006256	0.050019747	0.666302407	ICAM1, MICB, MICA, TNF, HLA-A, HLA-C, HLA-B, IFNGR1, HLA-G, NCR3
KEGG	hsa04640:Hematopoietic cell lineage	6	4.730232558	0.0079451	0.480091951	8.168806148	IL6, TNF, HLA-DRB1, IL4R, IL6R, HLA-DRA
KEGG	hsa04610:Complement and coagulation cascades	5	4.913043478	0.0175287	0.765453391	17.21494367	C3, CFB, C4B, CFH, C2
KEGG	hsa04630:Jak-STAT signaling pathway	7	3.061935484	0.024537	0.869597838	23.31027386	IL6, IL10RB, IL10RA, IL4R, IL6R, IL13RA1, IFNGR1
KEGG	hsa04144:Endocytosis	7	2.579347826	0.0502763	0.985446165	42.3673873	TGFBR1, TGFBR2, HLA-A, HLA-C, HSPA1A, HLA-B, HSPA1B, HLA-G,
KEGG	hsa05212:Pancreatic	4	3.766666667	0.0866186	0.999406424	62.01249306	ERBB2, TGFBR1, TGFBR2, TGFB1
KEGG	hsa05020:Prion diseases	3	5.811428571	0.0913998	0.999614015	64.0838166	IL6, HSPA1A, HSPA1B, CCL5
MF	GO:0004896~cytokine receptor activity	6	14.30633609	5.71E-05	0.01814849	0.077001553	IL10RB, IL10RA, IL4R, IL6R, IL13RA1, IFNGR1
MF	GO:0019838~growth factor binding	7	8.742760943	1.40E-04	0.043865292	0.188482355	IL10RB, IL10RA, ERBB2, IL4R, TGFBR1, TGFBR2, IL6R
MF	GO:0046982~protein heterodimerization activity	8	5.043900544	9.88E-04	0.271997344	1.326280346	APOE, TAP2, ERBB2, TGFBR1, NOTCH4, TAP1, TGFBR2, TGFB1
MF	GO:0042834~peptidoglycan binding	3	43.71380471	0.0019615	0.467542963	2.615934487	NOD1, TLR2, NLRP3
MF	GO:0046983~protein dimerization activity	12	2.903499944	0.0025382	0.557707738	3.372884206	BATF3, BATF, SLC11A1, APOE, TAP2, ERBB2, TGFBR1, NOTCH4, TAP1, TGFBR2, IL6R, TGFB1
MF	GO:0042802~identical protein binding	13	2.663809975	0.0031074	0.631764508	4.114743467	SLC11A1, NOD1, TNF, APOE, TAP2, ERBB2, MAPT, SNCA, TAP1, CSNK2B, IL6R, TGFB1, ALS2CL
MF	GO:0005539~glycosaminoglycan binding	6	5.62034632	0.0041332	0.735394118	5.438289443	NOD1, TNXB, APOE, TGFBR2, TLR2, NLRP3
MF	GO:0042277~peptide	7	4.522117729	0.0043386	0.752348828	5.7012902	TAP2, CD209, HLA-DMB, HLA-DOB, HLA-DMA, PSMB8, HLA-DRA
MF	GO:0030246~carbohydrate binding	9	3.334103749	0.0052755	0.816938005	6.892239146	NOD1, TNXB, LGALS3, APOE, CD209, FCN1, TGFBR2, TLR2, NLRP3
MF	GO:0030247~polysaccharide binding	6	5.109405746	0.0061711	0.862900262	8.017558361	NOD1, TNXB, APOE, TGFBR2, TLR2, NLRP3
MF	GO:0001871~pattern	6	5.109405746	0.0061711	0.862900262	8.017558361	NOD1, TNXB, APOE, TGFBR2, TLR2, NLRP3
MF	GO:0005160~transforming growth factor beta receptor binding	3	23.1426025	0.0071244	0.899251583	9.201733949	TGFBR1, TGFBR2, TGFB1
MF	GO:0005164~tumor necrosis factor receptor	3	18.73448773	0.0107876	0.969242993	13.62163422	TNF, LTB, NFKBIL1
MF	GO:0004920~interleukin-10 receptor activity	2	131.1414141	0.0150403	0.992285085	18.50254987	IL10RB, IL10RA
MF	GO:0046703~natural killer cell lectin-like receptor	2	131.1414141	0.0150403	0.992285085	18.50254987	MICB, MICA

MF	GO:0019969~interleukin-10 binding	2	131.1414141	0.0150403	0.992285085	18.50254987	<i>IL10RB, IL10RA</i>
MF	GO:0004674~protein serine/threonine kinase activity	9	2.744820296	0.0159374	0.994241627	19.49900416	<i>PRKCQ, BRD2, TGFB1, TGFB2, MAP4K2, GTF2H4, CSNK2B, RIPK2, STK19</i>
MF	GO:0019899~enzyme	10	2.507484018	0.01716	0.996136424	20.83885698	<i>BCHE, ERBB2, MAPT, TGFB1, TGFB2, TLR4, IL6R, LSM2, NLRP1,</i>
MF	GO:0043028~caspase regulator activity	3	13.56635319	0.0200577	0.998502514	23.93242026	<i>NOD1, SNCA, NLRP1</i>
MF	GO:0032813~tumor necrosis factor receptor superfamily binding	3	12.69110459	0.0227501	0.999380824	26.70606317	<i>TNF, LTB, NFKB1</i>
MF	GO:0008034~lipoprotein binding	3	11.24069264	0.0285503	0.999908395	32.36620308	<i>APOE, MAPT, TLR2</i>
MF	GO:0046978~TAP1	2	65.57070707	0.0298566	0.999940525	33.58375791	<i>TAP2, TAP1</i>
MF	GO:0046979~TAP2	2	65.57070707	0.0298566	0.999940525	33.58375791	<i>TAP2, TAP1</i>
MF	GO:0046977~TAP binding	2	65.57070707	0.0298566	0.999940525	33.58375791	<i>TAP2, TAP1</i>
MF	GO:0001875~lipopolysaccharide receptor activity	2	52.45656566	0.0371818	0.999994779	40.04377465	<i>TLR2, TLR4</i>
MF	GO:0048156~tau protein binding	2	52.45656566	0.0371818	0.999994779	40.04377465	<i>APOE, SNCA</i>
MF	GO:0004672~protein kinase activity	10	2.164049738	0.0392269	0.999997362	41.74044987	<i>PRKCQ, BRD2, ERBB2, TGFB1, TGFB2, MAP4K2, GTF2H4, CSNK2B, RIPK2, STK19</i>
MF	GO:0008134~transcription factor binding	9	2.300726564	0.0399098	0.9999979	42.29702576	<i>BATF3, LY6G6D, VDR, C6ORF26, CFB, CSNK2B, CLIC1, DDAH2, APOM</i>
MF	GO:0005114~type II transforming growth factor beta receptor binding	2	43.71380471	0.0444523	0.999999542	45.87588224	<i>TGFB1, TGFB1</i>
MF	GO:0042056~chemoattractant activity	2	43.71380471	0.0444523	0.999999542	45.87588224	<i>CCL3, CCL5</i>
MF	GO:0030554~adenyl nucleotide binding	19	1.580017038	0.0469396	0.999999802	47.74736067	<i>ERBB2, TGFB1, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, NOD1, TAP2, TAP1, RIPK2, NOS3, STK19, HLA-DOB, HLA-DRA</i>
MF	GO:0046332~SMAD	3	8.552700922	0.0470913	0.999999811	47.85953199	<i>MEN1, TGFB1, TGFB2</i>
MF	GO:0005524~ATP binding	18	1.598202745	0.04973	0.999999923	49.77537745	<i>ERBB2, TGFB1, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, NOD1, TAP2, TAP1, RIPK2, STK19, HLA-DOB, HLA-DRA</i>
MF	GO:0050700~CARD domain binding	2	37.46897547	0.0516684	0.99999996	51.14107139	<i>NOD1, RIPK2</i>
MF	GO:0005138~interleukin-6 receptor binding	2	37.46897547	0.0516684	0.99999996	51.14107139	<i>IL6, IL6R</i>

MF	GO:0001883~purine nucleoside binding	19	1.556331586	0.0530885	0.999999975	52.11967901	ERBB2, TGFB1, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, NOD1, TAP2, TAP1, RIPK2, NOS3, STK19, HLA-DOB, HLA-DRA
MF	GO:0032559~adenyl ribonucleotide binding	18	1.576850671	0.0552225	0.999999988	53.55608858	ERBB2, TGFB1, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, NOD1, TAP2, TAP1, RIPK2, STK19, HLA-DOB, HLA-DRA
MF	GO:0001882~nucleoside binding	19	1.545711457	0.0560921	0.999999991	54.12992145	ERBB2, TGFB1, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, NOD1, TAP2, TAP1, RIPK2, NOS3, STK19, HLA-DOB, HLA-DRA
MF	GO:0005125~cytokine	5	3.362600363	0.0600498	0.999999998	56.65956685	CCL3, IL6, TNF, CCL5, LTB
MF	GO:0015399~primary active transmembrane transporter activity	4	4.299718496	0.0647852	1	59.51637702	TAP2, SNCA, TAP1, ATP6V1G2
MF	GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity	4	4.299718496	0.0647852	1	59.51637702	TAP2, SNCA, TAP1, ATP6V1G2
MF	GO:0003823~antigen	3	7.0254329	0.0667823	1	60.66808194	TAP2, CD209, FCN1
MF	GO:0015197~peptide transporter activity	2	26.22828283	0.0729947	1	64.05962246	TAP2, TAP1
MF	GO:0050431~transforming growth factor beta binding	2	26.22828283	0.0729947	1	64.05962246	TGFB1, TGFB2
MF	GO:0017076~purine nucleotide binding	21	1.435854899	0.079737	1	67.43272154	TGFB1, ERBB2, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, RAB32, NOD1, TAP2, TAP1, RIPK2, NOS3, STK19, GNL1, HLA-DOB, HLA-DRA
MF	GO:0001530~lipopolysaccharide binding	2	21.85690236	0.0869478	1	70.71414554	TLR2, TLR4
MF	GO:0032553~ribonucleotide binding	20	1.42855571	0.092076	1	72.85849863	TGFB1, ERBB2, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, RAB32, NOD1, TAP2, TAP1, RIPK2, STK19, GNL1, HLA-DOB, HLA-DRA
MF	GO:0032555~purine ribonucleotide binding	20	1.42855571	0.092076	1	72.85849863	TGFB1, ERBB2, TGFB2, MAP4K2, HSPA1A, HSPA1B, HLA-DMB, NLRP3, HLA-DMA, NLRP1, PSMB8, PRKCQ, RAB32, NOD1, TAP2, TAP1, RIPK2, STK19, GNL1, HLA-DOB, HLA-DRA
MF	GO:0001540~beta-amyloid binding	2	20.17560218	0.0938462	1	73.56432701	BCHE, APOE
MF	GO:0032395~MHC class II receptor activity	10	69.02179692	4.71E-15	1.50E-12	6.29E-12	HLA-DQB1, HLA-DRB1, HLA-C, HLA-DPA1, HLA-DPB1, HLA-B, HLA-DOA, HLA-DOB, HLA-DMA, HLA-DQA1, HLA-DRA
MF	GO:0051059~NF-kappaB binding	7	31.6548241	6.54E-08	2.10E-05	8.83E-05	LY6G6D, C6ORF26, CFB, CSNK2B, CLIC1, DDAH2, APOM

MF	GO:0042288~MHC class I protein binding	6	49.1780303	9.04E-08	2.90E-05	1.22E-04	<i>TAP2, HLA-DMB, HLA-DOB, HLA-DMA, PSMB8, HLA-DRA</i>
MF	GO:0042287~MHC protein binding	6	31.47393939	1.04E-06	3.34E-04	0.001407037	<i>TAP2, HLA-DMB, HLA-DOB, HLA-DMA, PSMB8, HLA-DRA</i>
MF	GO:0019955~cytokine	9	10.82819016	1.60E-06	5.14E-04	0.002164079	<i>TNFRSF25, IL10RB, IL10RA, IL4R, TGFBR1, TGFBR2, IL6R, IL13RA1,</i>
MF	GO:0050785~advanced glycation end-product receptor activity	4	131.1414141	1.66E-06	5.32E-04	0.002240111	<i>NOTCH4, AGER, FKBPL, AGPAT1</i>
MF	GO:0032393~MHC class I receptor activity	5	38.57100416	6.74E-06	0.002160408	0.009095796	<i>MICA, HLA-A, HLA-C, HLA-B, HLA-G, HLA-F</i>

Note - Gene Ontology (GO) enrichment analysis for Biological Process (BP), Cellular Component (CC), and Molecular Function (MF) was performed by using DAVID.

Table S2. Diseases enrichment analysis for 123 leprosy associated genes

Term	Count	Fold of enrichment	P-value	Bonferroni	FDR	Genes
diabetes, type 1	31	5.9864796	7.96E-17	1.74E-13	1.89E-13	HLA-DQB1, MICA, TNF, LST1, HLA-DRB1, AIF1, TNFRSF25, TLR2, PTPN22, TLR4, HSPA1A, HSPA1B, TGFB1, VDR, SLC11A1, APOE, IL4R, TAP2, TAP1, CFH, NOS3, HLA-DPB1, ICAM1, IL6, HLA-A, HLA-C, HLA-B, NFKBIL1, PSMB8, HLA-DQA1, PSMB9, HLA-DPA1, HLA-DRA
multiple sclerosis	28	6.5419753	4.77E-16	6.97E-13	7.44E-13	HLA-DQB1, CCL3, TNF, HLA-DRB1, PTPN22, TLR4, HSPA1A, HSPA1B, CCL5, HLA-DMA, TGFB1, VDR, SLC11A1, APOE, IL4R, TAP2, TAP1, NOS3, HLA-DPB1, IFNGR1, ICAM1, IL6, HLA-A, HLA-C, HLA-B, PSMB8, HLA-G, HLA-DQA1, NOTCH4, HLA-DRA
rheumatoid arthritis	27	6.8587248	5.98E-16	8.71E-13	9.33E-13	HLA-DQB1, MICB, MICA, TNF, HLA-DRB1, TLR2, PTPN22, TLR4, HLA-DMB, CCL5, HLA-DMA, TGFB1, GSTM1, VDR, SLC11A1, TAP2, IL4R, TAP1, NOS3, LTB, IFNGR1, IL6, HLA-G, HLA-DQA1, NFKBIL1, PSMB9, NOTCH4
asthma	26	4.9452261	7.03E-12	1.10E-08	1.18E-08	HLA-DQB1, TNF, HLA-DRB1, C3, TLR2, AIF1, TG2, HSPA1A, TLR4, HSPA1B, CCL5, TGFB1, GSTM1, VDR, NOD1, IL4R, TAP1, NOS3, HLA-DPB1, IL13RA1, DEFB1, LTB, IFNGR1, HLA-A, HLA-C, HLA-B, HLA-DQA1, NFKBIL1, LTA4H
systemic lupus erythematosus	23	8.4519417	2.06E-15	3.31E-12	3.52E-12	HLA-DQB1, IL6, MICA, TNF, HLA-DRB1, CFB, C4B, C3, TLR2, PTPN22, TLR4, HLA-DMB, HLA-DMA, HLA-DQA1, TGFB1, GSTM1, VDR, TAP2, IL4R, TAP1, C2, IFNGR1, HLA-DRA
tuberculosis	20	12.830508	5.10E-17	7.99E-14	8.51E-14	HLA-DQB1, IL6, TNF, HLA-DRB1, C3, TIRAP, TLR2, PTPN22, HLA-C, TLR4, HLA-B, NFKBIL1, HLA-DQA1, TGFB1, SLC11A1, VDR, TAP2, CD209, TAP1, HLA-DPB1, IFNGR1
HIV	20	9.9605263	1.05E-14	1.65E-11	1.76E-11	HLA-DQB1, IL6, CCL5, TNF, HLA-DRB1, TLR2, HLA-A, HLA-C, TLR4, HLA-B, CCL5, HLA-DMA, HLA-DQA1, HLA-G, TAP2, IL4R, IL10RA, CD209, NOS3, DEFB1, IFNGR1
psoriasis	19	10.733582	1.46E-14	2.28E-11	2.43E-11	HLA-DQB1, MICB, MICA, TNF, HLA-DRB1, HLA-A, PTPN22, HLA-C, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1, PSMB8, PSMB9, GSTM1, CCHCR1, VDR, TAP2, TAP1, PSORS1C1
lupus erythematosus	18	9.5957746	7.00E-13	1.10E-09	1.17E-09	HLA-DQB1, MICB, IL6, MICA, TNF, HLA-DRB1, C4B, HLA-A, PTPN22, HLA-C, HLA-B, HLA-DMB, CCL5, HLA-DMA, HLA-DQA1, TAP2, TAP1, HLA-DPB1, IL6, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B, CCL5, HLA-DQA1, PSMB8, TGFB1, PSMB9, VDR, TAP2, IL4R, TAP1, HLA-DPB1, IFNGR1
hepatitis B	17	14.963953	1.41E-15	2.26E-12	2.41E-12	ICAM1, IL6, TNF, HLA-DRB1, SNCA, HLA-A, HSPA1A, HSPA1B, PSMB9, SLC11A1, VDR, BCHE, APOE, TAP2, MAPT, NOTCH4, NOS3, APOM
celiac disease	16	10.093333	9.48E-12	1.49E-08	1.58E-08	HLA-DQB1, ICAM1, MICB, IL6, MICA, TNF, HLA-DRB1, HLA-A, PTPN22, HLA-C, HLA-B, CCL5, HLA-DQA1, TGFB1, CD209, HLA-DPB1, HLA-DRA

schizophrenia	16	2.1027778	0.0063781	0.999956349	10.137745	HLA-DQB1, ICAM1, MICB, IL6, TNF, TNFA, HLA-DRB1, TGFB2, HLA-A, HSPA1A, HSPA1B, HLA-DQA1, GSTM1, APOE, TAP2, IL10RA, NOTCH4
diabetes, type 2	16	2.0955017	0.0065861	0.999968571	10.451493	HLA-DQB1, ICAM1, IL6, TNF, HLA-DRB1, CFB, IL6R, CCL5, AGER, HLA-DQA1, TGFB1, VDR, BCHE, APOE, NOS3, APOM
sarcoidosis	15	12.903409	1.28E-12	2.01E-09	2.14E-09	HLA-DQB1, IL6, CCL3, HLA-DRB1, TLR2, HLA-A, HLA-C, TLR4, HLA-B, CCL5, HLA-G, TGFB1, SLC11A1, NOD1, HLA-DPB1, HLA-DRA
arthritis	15	10.322727	3.87E-11	6.07E-08	6.46E-08	HLA-DQB1, ICAM1, IL6, MICA, TNF, HLA-DRB1, HLA-C, TLR4, HLA-B, HLA-DQA1, NFKBIL1, SLC11A1, VDR, TAP2, IL4R, TAP1
Crohn's disease	15	9.4625	1.39E-10	2.18E-07	2.32E-07	HLA-DQB1, ICAM1, TNF, HLA-DRB1, TLR2, TLR4, HSPA1A, HLA-C, HSPA1B, HLA-B, GSTM1, VDR, SLC11A1, IL4R, PSORS1C1, HLA-DRA
preeclampsia	15	7.8854167	1.87E-09	2.94E-06	3.13E-06	HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-A, HSPA1A, HSPA1B, HLA-DQA1, HLA-G, TGFB1, GSTM1, APOE, TAP2, IL4R, TAP1, NOS3
periodontitis	15	7.1867089	6.75E-09	1.06E-05	1.13E-05	HLA-DQB1, ICAM1, IL6, TNF, HLA-DRB1, TLR2, HLA-A, HLA-C, TLR4, IL6R, HLA-B, CCL5, TGFB1, VDR, DEFB1, IFNGR1
atherosclerosis, coronary	15	3.6629032	3.24E-05	0.049531102	0.0540739	HLA-DQB1, ICAM1, IL18RAP, TNF, HLA-DRB1, TLR2, TLR4, CCL5, VDR, NOD1, BCHE, APOE, CFH, NOS3, IFNGR1
breast cancer	15	1.9851399	0.0143032	1	21.390034	HLA-DQB1, GSTM1, VDR, IL6, TNF, HLA-DRB1, APOE, TGFB1, ERBB2, TGFB2, NOS3, HLA-DPB1, EHMT2, TGFB1, HLA-DQA1
ankylosing spondylitis	14	17.663333	7.91E-14	1.24E-10	1.32E-10	HLA-DQB1, IL6, MICA, TNF, HLA-DRB1, HSPA1A, HLA-C, TLR4, HSPA1B, HLA-B, PSMB8, HLA-DQA1, TGFB1, PSMB9, TAP2, TAP1
hepatitis C	14	7.4633803	1.64E-08	2.58E-05	2.75E-05	HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B, CCL5, TGFB1, SLC11A1, APOE, TAP2, IL10RA, IL4R, IFNGR1
juvenile arthritis	13	16.967241	1.54E-12	2.41E-09	2.57E-09	HLA-DQB1, IL6, TNF, HLA-DRB1, PSMB8, HLA-DQA1, TGFB1, PSMB9, SLC11A1, TAP2, IL4R, TAP1, HLA-DPB1
nasopharyngeal cancer	13	13.298649	4.65E-11	7.30E-08	7.77E-08	HLA-DQB1, MICA, TNF, HLA-DRB1, HLA-A, TLR4, HSPA1A, HLA-C, HSPA1B, HLA-B, HLA-DQA1, GSTM1, TAP1, HLA-DPA1, HLA-DPB1
inflammatory bowel disease	13	10.696739	8.10E-10	1.27E-06	1.35E-06	HLA-DQB1, ICAM1, TNF, HLA-DRB1, C3, TLR4, TGFB1, SLC11A1, NOD1, APOE, IL4R, HLA-DPA1, IFNGR1
graft-versus-host disease	13	10.696739	8.10E-10	1.27E-06	1.35E-06	HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-A, HLA-C, TLR4, HLA-B, HLA-DQA1, TGFB1, VDR, IL10RB, IL4R, HLA-DPB1
pregnancy loss, recurrent	13	8.6324561	1.17E-08	1.84E-05	1.96E-05	HLA-DQB1, IL6, TNF, MICA, HLA-DRB1, HLA-A, HLA-C, HLA-B, TGFB1, HLA-DQA1, HLA-G, VDR, APOE, NOS3
prostate cancer	13	2.8944118	0.0012534	0.860244814	2.0734607	ICAM1, IL6, TNF, ERBB2, TGFB1, TLR1, HLA-A, TIRAP, TLR4, TGFB1, GSTM1, VDR, NOS3
lymphoma	12	10.093333	9.33E-09	1.46E-05	1.56E-05	HLA-DQB1, TNF, HLA-DRB1, TLR1, HLA-A, TLR2, TLR4, HLA-C, HLA-B, HLA-DQA1, GSTM1, IL10RA, HLA-DPB1
cervical cancer	12	8.9058824	3.86E-08	6.05E-05	6.45E-05	GSTM1, HLA-DQB1, SLC11A1, MICA, TNF, HLA-DRB1, ERBB2, TAP1, HLA-A, HLA-C, HLA-DPB1, HLA-B, HLA-DQA1

H. pylori infection	11	13.878333	1.62E-09	2.54E-06	2.70E-06	HLA-DQB1, IL6, TNF, HLA-DRB1, IL10RA, IL4R, HLA-A, HLA-C, TLR4, HLA-B, IFNGR1, HLA-DQA1
sclerosis, systemic	11	11.252703	1.62E-08	2.54E-05	2.70E-05	HLA-DQB1, IL6, TNF, HLA-DRB1, AIF1, TAP2, TAP1, PTPN22, NOS3, HLA-DPB1, CCL5
hepatitis C, chronic	11	10.40875	3.69E-08	5.79E-05	6.17E-05	HLA-DQB1, IL6, TNF, HLA-DRB1, TAP2, TAP1, HLA-A, HLA-C, HLA-B, CCL5, HLA-DQA1, TGFB1
endometriosis	11	7.7101852	7.76E-07	0.001216676	0.0012962	GSTM1, HLA-DQB1, ICAM1, IL6, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-DPB1, HLA-B, CCL5, HLA-DQA1
stroke, ischemic	11	7.4348214	1.11E-06	0.001735034	0.0018489	HLA-DQB1, ICAM1, IL6, TNF, HLA-DRB1, APOE, NOS3, HLA-C, HSPA1A, TLR4, HLA-B, HSPA1B, HLA-DRA
stomach cancer	11	4.3369792	1.50E-04	0.210324018	0.2511035	GSTM1, HLA-DQB1, IL6, TNF, HLA-DRB1, ERBB2, IL4R, TGFB1, TLR4, HLA-DQA1, TGFB1
myocardial infarct	11	3.4127049	0.0010599	0.810593958	1.7559772	ICAM1, VDR, IL6, APOE, IL4R, CFH, NOS3, ATP6V1G2, LTA4H, TLR4,
colorectal cancer	11	2.071393	0.0340607	1	43.949986	GSTM1, ICAM1, VDR, IL6, TNF, APOE, TGFB1, TGFB2, TLR2, NOS3,
Behcet's disease	10	10.513889	1.88E-07	2.95E-04	3.14E-04	MICB, MICA, TAP2, TAP1, HLA-A, TLR2, NOS3, HLA-C, HLA-B, NLRP3,
atopy	10	8.8023256	9.71E-07	0.001523075	0.0016229	HLA-DQB1, SLC11A1, IL6, TNF, HLA-DRB1, IL4R, TAP1, HLA-C, TLR4, HLA-DPB1, HLA-B
ulcerative colitis	10	8.6022727	1.20E-06	0.001874341	0.0019975	HLA-DQB1, MICB, MICA, TNF, HLA-DRB1, TLR2, HLA-C, TLR4, HLA-B, NFKBIL1, HLA-DRA
Parkinson's disease	10	2.8246269	0.0073288	0.99999028	11.563405	GSTM1, IL6, TNF, APOE, MAPT, PACRG, SNCA, CFH, NOS3, HSPA1A, HLA-DRB1, TAP2, TAP1, HLA-C, HLA-DPA1, HLA-DPB1, HLA-B, HLA-DMB, HLA-DMA, HLA-DQA1
measles	9	37.85	1.32E-12	2.08E-09	2.21E-09	HLA-DQB1, IL6, TNF, TAP2, IL4R, TAP1, CCL5, HLA-DQA1, TGFB1
allergic rhinitis	9	18.925	5.32E-09	8.35E-06	8.89E-06	HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-A, PTPN22, NOS3, HLA-C, HLA-B,
cirrhosis, biliary primary	9	17.0325	1.47E-08	2.30E-05	2.45E-05	ICAM1, IL6, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-B, HLA-DQA1, TGFB1
bone marrow transplantation	9	14.81087	5.37E-08	8.42E-05	8.96E-05	HLA-DQB1, IL6, HLA-DRB1, TAP2, HLA-A, PTPN22, HLA-C, HLA-B, HLA-DQA1, TGFB1
Sjogren's syndrome	9	14.81087	5.37E-08	8.42E-05	8.96E-05	HLA-DQB1, TNF, HLA-DRB1, HLA-A, TLR2, HLA-C, TLR4, HLA-DPB1,
malaria, plasmodium falciparum	9	13.626	1.13E-07	1.78E-04	1.90E-04	IL6, MICA, TNF, IL4R, NOS3, HSPA1A, TLR4, HSPA1B, CCL5, TGFB1
kidney transplant	9	11.355	5.52E-07	8.66E-04	9.23E-04	HLA-DQB1, ICAM1, IL6, TNF, HLA-DRB1, TAP2, TAP1, PTPN22, HLA-
Graves' disease	9	9.7328571	2.00E-06	0.003131191	0.0033391	HLA-DQB1, MICB, MICA, HLA-DRB1, ATP6V1G2, HLA-DPA1, HLA-DPB1, HLA-DQA1, NFKBIL1
cardiomyopathy	9	8.7346154	4.80E-06	0.007505289	0.008021	ICAM1, NOD1, TNF, HLA-DRB1, PTPN22, NOS3, TLR4, HLA-G, NFKBIL1
Crohn's disease ulcerative colitis	9	7.57	1.48E-05	0.022984013	0.0247545	GSTM1, IL6, TNF, APOE, NOS3, HSPA1A, HSPA1B, CCL5, DEFB1, TGFB1
chronic obstructive pulmonary disease/COPD	9	6.3083333	5.91E-05	0.088630994	0.0987668	GSTM1, HLA-DQB1, VDR, IL6, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DQA1, TGFB1
melanoma	9	5.9763158	8.82E-05	0.12920133	0.1471922	

longevity	9	4.7978873	4.22E-04	0.484647143	0.7033335	GSTM1, IL6, TNF, C3, APOE, C4B, HSPA1A, TLR4, HSPA1B, TGFB1
leukemia	9	4.0553571	0.0013157	0.873268393	2.1754014	GSTM1, HLA-DQB1, VDR, HLA-DRB1, HLA-A, HLA-C, HLA-DPB1, HLA-B, HLA-DQA1, TGFB1
ovarian cancer	9	4.0553571	0.0013157	0.873268393	2.1754014	GSTM1, HLA-DQB1, IL6, HLA-DRB1, ERBB2, TGFBR1, HLA-A, NOS3,
bone density	9	3.2442857	0.0054063	0.999797643	8.6581451	GSTM1, ICAM1, VDR, IL6, TNF, APOE, TGFBR2, NOS3, TGFB1
hypertension	9	1.8820442	0.0966773	1	81.705392	GSTM1, VDR, IL6, TNF, HLA-DRB1, APOE, NOS3, NLRP3, TGFB1
rheumatic heart disease	8	27.527273	1.91E-09	3.00E-06	3.19E-06	HLA-DQB1, HLA-DRB1, HLA-A, TLR2, HLA-C, TLR4, HLA-B, HLA-DQA1,
leprosy	8	23.292308	9.53E-09	1.50E-05	1.59E-05	SLC11A1, MICB, MICA, TNF, HLA-DRB1, PACRG, TLR2, IFNGR1
Q fever	8	17.811765	9.93E-08	1.56E-04	1.66E-04	ICAM1, VDR, SLC11A1, IL6, TNF, HLA-DRB1, HLA-C, HLA-B, TGFB1
cholangitis, sclerosing	8	15.14	3.72E-07	5.83E-04	6.21E-04	HLA-DQB1, ICAM1, NOD1, TNF, HLA-DRB1, HLA-C, TLR4, HLA-B, HLA-
myasthenia gravis	8	13.763636	7.84E-07	0.001228908	0.0013093	HLA-DQB1, TNF, HLA-DRB1, HLA-A, PTPN22, HLA-C, HLA-B, HLA-DQA1, HLA-DRA
psoriatic arthritis	8	10.093333	7.91E-06	0.012326978	0.0132057	CCHCR1, MICA, TNF, HLA-DRB1, PSORS1C1, HLA-A, PTPN22, HLA-C,
retinopathy, diabetic	8	9.1757576	1.56E-05	0.024140113	0.0260148	HLA-DQB1, ICAM1, TNF, HLA-DRB1, APOE, NOS3, HLA-DPB1, HLA-
kidney transplant complications	8	8.9058824	1.92E-05	0.029681611	0.0320765	HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-A, NOS3, HLA-C, HLA-B, TGFB1
dermatitis and eczema	8	8.1837838	3.45E-05	0.05269918	0.0576268	NOD1, TNF, TOLLIP, IL4R, CCL5, NLRP3, DEFB1, NLRP1
preterm delivery	8	7.9684211	4.14E-05	0.062916203	0.0691655	GSTM1, IL6, TNF, TLR2, NOS3, TLR4, IL6R, TGFB1
coronary artery disease	8	4.2647887	0.0021833	0.967593842	3.5855597	IL6, TNF, BCHE, APOE, TAP1, NOS3, CCL5, TGFB1
infection, post allograft	7	29.438889	2.06E-08	3.23E-05	3.44E-05	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-DPB1, HLA-B,
berylliosis	7	29.438889	2.06E-08	3.23E-05	3.44E-05	HLA-DQB1, TNF, HLA-DRB1, HLA-DPA1, HLA-DPB1, HLA-DQA1, TGFB1
dermatitis, atopic	7	26.495	5.04E-08	7.91E-05	8.42E-05	TAP2, IL4R, TAP1, HLA-A, HLA-C, HLA-B, PSMB8, PSMB9
alopecia areata	7	18.925	6.63E-07	0.001039529	0.0011074	HLA-DQB1, HLA-DRB1, NOTCH4, HLA-A, PTPN22, HLA-C, HLA-B, HLA-
pemphigus	7	18.925	6.63E-07	0.001039529	0.0011074	HLA-DQB1, IL6, HLA-DRB1, TAP2, IL4R, HLA-A, HLA-C, HLA-B
arthritis, juvenile	7	16.559375	1.70E-06	0.002656474	0.0028322	HLA-DQB1, VDR, TNF, HLA-DRB1, HLA-A, PSMB8, HLA-DQA1
periodontal disease	7	16.559375	1.70E-06	0.002656474	0.0028322	IL6, TNF, IL4R, TLR2, NOS3, TLR4, DEFB1
arthritis, rheumatoid	7	15.585294	2.57E-06	0.004017852	0.0042865	HLA-DQB1, ICAM1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA1,
kidney cancer	7	9.1362069	7.67E-05	0.113350693	0.1280121	GSTM1, HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-DQA1, TGFB1
Lupus	7	8.8316667	9.39E-05	0.13694982	0.1566943	VDR, IL6, TNF, HLA-DRB1, TAP2, HLA-C, HLA-B, IFNGR1
nephropathy in other diseases	7	8.2796875	1.37E-04	0.193949321	0.2293034	HLA-DQB1, HLA-DRB1, APOE, NOS3, HLA-DPB1, CCL5, HLA-DQA1
cystic fibrosis	7	7.7926471	1.96E-04	0.264311308	0.326286	GSTM1, IL6, TNF, TAP2, TAP1, TLR4, DEFB1
Crohn's disease; ulcerative colitis	7	6.9723684	3.69E-04	0.439992714	0.6154393	ICAM1, SLC11A1, MICB, MICA, TNF, PTPN22, TLR4
macular degeneration	7	6.1616279	7.35E-04	0.684696195	1.2214199	HLA-DQB1, HLA-DRB1, CFB, APOE, CFH, TLR4, C2
head and neck cancer	7	4.9990566	0.0022504	0.970835068	3.6936795	GSTM1, HLA-DQB1, TNF, HLA-DRB1, SDHD, HLA-A, HLA-C, HLA-B
restenosis	7	4.0761538	0.0063169	0.999951924	10.045301	ICAM1, IL6, TNF, APOE, IL4R, NOS3, HSPA1A, HSPA1B
HIV; cytomegalovirus retinitis	6	37.85	6.27E-08	9.83E-05	1.05E-04	HLA-DQB1, MICA, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DQA1
Plasmodium falciparum infection	6	37.85	6.27E-08	9.83E-05	1.05E-04	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-DPB1, HLA-B, HLA-DQA1
cytokine resposne	6	37.85	6.27E-08	9.83E-05	1.05E-04	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-B, HLA-DQA1
IgA, IgD, IgG, IgM	6	37.85	6.27E-08	9.83E-05	1.05E-04	HLA-DQB1, TNF, HLA-A, HLA-C, HLA-B, HLA-DQA1, HLA-DRA

vitiligo	6	25.233333	1.24E-06	0.001938782	0.0020663	HLA-DQB1, HLA-DRB1, HLA-A, PTPN22, HLA-C, HLA-B, HLA-DQA1
hematopoietic stem cell transplantation	6	25.233333	1.24E-06	0.001938782	0.0020663	HLA-DQB1, TNF, HLA-DRB1, IL4R, HLA-A, HLA-C, HLA-B
spondyloarthropathies	6	22.71	2.42E-06	0.003795035	0.0040483	MICA, HLA-C, HSPA1A, HLA-B, HSPA1B, PSMB8, HLA-DRA, PSMB9
biliary atresia	6	20.645455	4.35E-06	0.006805572	0.0072707	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-DPB1, HLA-B, HLA-DQA1
carbamazepine hypersensitivity	6	17.469231	1.16E-05	0.018090997	0.0194367	TNF, HLA-A, HLA-C, HSPA1A, HLA-B, HSPA1B, HLA-DQA1, HLA-DRA
oral submucous fibrosis	6	17.469231	1.16E-05	0.018090997	0.0194367	HLA-DQB1, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B, TGFB1
antiphospholipid syndrome	6	17.469231	1.16E-05	0.018090997	0.0194367	HLA-DQB1, TNF, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA1
osteoporosis, postmenopausal	6	17.469231	1.16E-05	0.018090997	0.0194367	HLA-DQB1, VDR, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DQA1
HIV infection	6	16.221429	1.77E-05	0.02743803	0.0296182	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B, CCL5, HLA-DRA
cirrhosis	6	16.221429	1.77E-05	0.02743803	0.0296182	HLA-DQB1, TNF, HLA-DRB1, C3, IL10RA, TGFB1
uveitis	6	16.221429	1.77E-05	0.02743803	0.0296182	HLA-DQB1, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B, CCL5
respiratory syncytial virus	6	13.358824	5.15E-05	0.077673129	0.086053	ICAM1, IL6, TNF, IL4R, TLR4, TGFB1
diabetes, type 2; diabetes, type 1	6	11.952632	9.29E-05	0.135695406	0.1551503	HLA-DQB1, MICA, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DQA1
liver transplant	6	10.814286	1.56E-04	0.217259565	0.2604722	HLA-DQB1, IL6, TNF, HLA-DRB1, CCL5, TGFB1
Diabetic Nephropathy	6	8.4111111	5.48E-04	0.576671173	0.9110795	GSTM1, TNF, APOE, NOS3, AGER, TGFB1
thyroid cancer	6	7.3258065	0.0010623	0.811300551	1.7598868	GSTM1, HLA-DQB1, LGALS3, HLA-DRB1, SDHD, HLA-DQA1
malaria	6	7.3258065	0.0010623	0.811300551	1.7598868	HLA-DQB1, ICAM1, TNF, HLA-DRB1, TLR2, TLR4
atherosclerosis	6	6.3083333	0.0021284	0.964668239	3.4967892	GSTM1, IL6, TNF, APOE, NOS3, TLR4
osteoarthritis	6	4.2849057	0.0114724	0.999999986	17.53218	HLA-DQB1, VDR, TNF, HLA-DRB1, IL4R, HLA-DQA1
pancreatitis, autoimmune; pancreatitis, chronic calcifying	5	37.85	2.11E-06	0.003299406	0.0035187	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-DPB1, HLA-B
multiple sclerosis; optic neuritis	5	37.85	2.11E-06	0.003299406	0.0035187	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DQA1
scleroderma; jaundice	5	37.85	2.11E-06	0.003299406	0.0035187	HLA-DQB1, HLA-DRB1, HLA-A, HLA-DPB1, HLA-DQA1
multiple sclerosis; IgA	5	37.85	2.11E-06	0.003299406	0.0035187	TAP2, TAP1, HLA-DMB, HLA-DMA, PSMB9
graft-versus-host disease; psoriasis; celiac disease Genomewide Association Study of an AIDS-Nonprogression Cohort Emphasizes the Role Played by HLA Genes (ANRS Genomewide Association Study 2007)	5	37.85	2.11E-06	0.003299406	0.0035187	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-DPB1, HLA-B
diabetes, latent autoimmune arthritis, psoriatic	5	31.541667	6.19E-06	0.009670931	0.0103466	HLA-DQB1, MICA, HLA-DRB1, HLA-C, HLA-B, HLA-DQA1
maternal microchimerism	5	31.541667	6.19E-06	0.009670931	0.0103466	MICB, MICA, TNF, HLA-DRB1, HLA-C, HLA-B
typhoid fever	5	27.035714	1.42E-05	0.021980845	0.0236621	GSTM1, HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
pneumonia, atypical; Rheiter's syndrome; urogenital disorders	5	27.035714	1.42E-05	0.021980845	0.0236621	HLA-DQB1, TNF, HLA-DRB1, HLA-A, HLA-C, HLA-B
						TNF, HLA-DRB1, TAP2, TAP1, HSPA1A, HSPA1B

celiac disease; Wegener's granulomatosis; cervical cancer	5	21.027778	4.90E-05	0.07399685	0.0818211	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B, HLA-DQA1
Wegener's granulomatosis	5	17.204545	1.23E-04	0.175903554	0.2057804	HLA-DQB1, TNF, PTPN22, CCL5, TGFB1
Guillain-Barre syndrome	5	15.770833	1.81E-04	0.247591104	0.3024335	HLA-DQB1, HLA-DRB1, APOE, TLR4, HLA-DQA1
Addison's disease	5	15.770833	1.81E-04	0.247591104	0.3024335	HLA-DQB1, VDR, MICA, HLA-DRB1, HLA-DQA1
hepatocellular carcinoma	5	14.557692	2.57E-04	0.331560435	0.427968	GSTM1, HLA-DQB1, HLA-DRB1, HLA-DPB1, HLA-DQA1
chronic fatigue syndrome	5	12.616667	4.71E-04	0.522424534	0.7837889	HLA-DQB1, IL6, TNF, HLA-DRB1, HLA-DQA1
meningioma	5	12.616667	4.71E-04	0.522424534	0.7837889	HLA-DQB1, HLA-DRB1, TGFB2, HLA-A, TGFB1
giant cell arteritis	5	12.616667	4.71E-04	0.522424534	0.7837889	ICAM1, TNF, HLA-DRB1, NOS3, CCL5
Graves disease	5	11.828125	6.16E-04	0.619406609	1.0232906	HLA-DQB1, HLA-DRB1, HLA-C, HLA-B, HLA-DQA1, PSMB9
chronic obstructive pulmonary disease	5	11.132353	7.89E-04	0.710176627	1.3100044	GSTM1, TNF, TLR4, DEFB1, TGFB1
pancreatitis, chronic	5	9.0119048	0.0018326	0.943755051	3.0178822	GSTM1, ICAM1, IL6, TNF, TGFB1
bone mineral density	5	9.0119048	0.0018326	0.943755051	3.0178822	VDR, IL6, TNF, APOE, TGFB1
lung function	5	8.2282609	0.002606	0.983330985	4.2656047	GSTM1, TNF, IL10RA, IL4R, IL13RA1
abdominal aortic aneurysm	5	7.2788462	0.0041462	0.998524635	6.705467	HLA-DQB1, HLA-DRB1, NOS3, HLA-DQA1, TGFB1
sepsis	5	6.3083333	0.0070232	0.999984244	11.107452	IL6, TNF, HSPA1A, TLR4, HSPA1B, DEFB1
coronary heart disease	5	3.5707547	0.047871	1	55.934642	IL6, TNF, APOE, NOS3, AGER
diabetes, type 2; alveolitis, extrinsic allergic	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
myositis, sporadic inclusion-body	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
nasal polyps	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, CCL5, HLA-DQA1
psoriasis; celiac disease	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
Pigeon breeders disease	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
interferon response	4	37.85	6.71E-05	0.099985448	0.1121013	TAP2, TAP1, PSMB8, PSMB9
arthrofibrosis	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
stem cell transplantation outcome	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
pancreatitis, autoimmune	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, TNF, HLA-DRB1, NFKBIL1
leukemia lymphoma	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
hepatitis C sicca syndrome	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
hepatosplenic schistosomiasis japonica	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-DPA1, HLA-DQA1
neuropathy, small fiber	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
alveolitis, extrinsic allergic	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
alveolar echinococcosis	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
pulmonary hypertension; thrombosis, deep vein; pulmonary thromboembolism	4	37.85	6.71E-05	0.099985448	0.1121013	HLA-DRB1, HLA-A, HLA-C, HLA-DPB1, HLA-B

Lyme disease	4	30.28	1.65E-04	0.227726116	0.2747672	HLA-DQB1, HLA-DRB1, TLR1, TLR2
diabetes, type 1; measles	4	30.28	1.65E-04	0.227726116	0.2747672	HLA-DQB1, TNF, HLA-DRB1, TAP1
nut allergy	4	30.28	1.65E-04	0.227726116	0.2747672	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
sporadic inclusion body myositis	4	30.28	1.65E-04	0.227726116	0.2747672	HLA-DQB1, HLA-DRB1, APOE, HLA-A
cirrhosis, primary biliary	4	25.233333	3.23E-04	0.397792656	0.5385303	HLA-DQB1, HLA-DRB1, HLA-DPB1, HLA-DQA1
vaccine response	4	25.233333	3.23E-04	0.397792656	0.5385303	HLA-DQB1, HLA-DRB1, IL4R, HLA-DPB1
diabetes, type 1 diabetic nephropathy	4	25.233333	3.23E-04	0.397792656	0.5385303	ICAM1, TGFBR1, TGFBR2, TGFB1
pityriasis rosea	4	25.233333	3.23E-04	0.397792656	0.5385303	HLA-DQB1, HLA-DRB1, HLA-A, HLA-C, HLA-B
leishmaniasis	4	25.233333	3.23E-04	0.397792656	0.5385303	HLA-DQB1, HLA-DPA1, HLA-DPB1, HLA-DQA1
renal allograft outcome	4	25.233333	3.23E-04	0.397792656	0.5385303	IL6, TNF, IL4R, TGFB1
Chlamydia	4	25.233333	3.23E-04	0.397792656	0.5385303	HLA-DQB1, HLA-DRB1, TLR2, TLR4
acute coronary syndrome						
atherosclerosis, coronary cholesterol, LDL smoking	4	25.233333	3.23E-04	0.397792656	0.5385303	HLA-DRB1, C4B, HLA-A, HLA-C, HLA-B
allergies; common cold	4	21.628571	5.55E-04	0.581445191	0.9230444	ICAM1, IL6, TNF, IL4R
leukemia, chronic lymphocytic	4	21.628571	5.55E-04	0.581445191	0.9230444	HLA-DQB1, HLA-DRB1, HLA-C, HLA-DPB1, HLA-B
atherothrombosis	4	21.628571	5.55E-04	0.581445191	0.9230444	HLA-DQB1, HLA-DRB1, TLR4, HLA-DQA1
antibody formation Crohn's disease ulcerative colitis	4	21.628571	5.55E-04	0.581445191	0.9230444	NOD1, TLR1, TLR2, TLR4
rheumatic fever	4	21.628571	5.55E-04	0.581445191	0.9230444	HLA-DQB1, HLA-DRB1, TLR2, HLA-DQA1
scleroderma	4	21.628571	5.55E-04	0.581445191	0.9230444	HLA-DQB1, TNF, HLA-DRB1, HLA-DPB1
allergy	4	21.628571	5.55E-04	0.581445191	0.9230444	HLA-DQB1, HLA-DRB1, IL4R, HLA-DQA1
autoimmune thyroid disease; thyroid disease, autoimmune	4	18.925	8.71E-04	0.745277935	1.4455668	HLA-DQB1, HLA-DRB1, HLA-A, HLA-DQA1
bacterial infection	4	16.822222	0.0012824	0.866457162	2.1208589	IL6, TNF, TLR2, TLR4
silicosis	4	15.14	0.0017977	0.940576095	2.9610926	HLA-DQB1, TNF, HLA-DRB1, HLA-DPB1
renal disease, end stage	4	15.14	0.0017977	0.940576095	2.9610926	HLA-DQB1, HLA-DRB1, NOS3, HLA-DQA1
Chagas Disease	4	15.14	0.0017977	0.940576095	2.9610926	HLA-DQB1, SLC11A1, HLA-DRB1, HLA-DQA1
graft rejection, liver	4	15.14	0.0017977	0.940576095	2.9610926	IL6, TNF, HLA-DRB1, TGFB1
hypothyroidism	4	15.14	0.0017977	0.940576095	2.9610926	TNF, HLA-A, HLA-C, HSPA1A, HLA-B, HSPA1B
renal transplantation, rejection	4	13.763636	0.0024255	0.977858301	3.9757705	IL6, TNF, IL4R, TGFB1
brucellosis	4	13.763636	0.0024255	0.977858301	3.9757705	IL6, TNF, TLR4, TGFB1
heart transplant complications	4	12.616667	0.0031736	0.993176126	5.1716697	IL6, TNF, CCL5, TGFB1
liver disease	4	12.616667	0.0031736	0.993176126	5.1716697	HLA-DQB1, HLA-DRB1, TAP2, PSMB8
arthritis; asthma; diabetes, type 1; pemphigus; IL-1RI	4	12.616667	0.0031736	0.993176126	5.1716697	IL6, TNF, IL4R, TGFB1

lupus erythematosus; rheumatoid arthritis	4	12.616667	0.0031736	0.993176126	5.1716697	HLA-DRB1, TLR2, PTPN22, TLR4
sarcoidosis tuberculosis	4	11.646154	0.0040487	0.998279774	6.5528144	HLA-DQB1, HLA-DRB1, TLR2, HLA-DQA1
atopic dermatitis	4	10.814286	0.0050568	0.999648838	8.1204832	NOD1, IL4R, CCL5, TGFB1
psoriasis psoriatic arthritis	4	10.814286	0.0050568	0.999648838	8.1204832	MICA, TNF, HLA-A, HLA-C, HLA-B
measles vaccine immunity	4	10.814286	0.0050568	0.999648838	8.1204832	IL10RB, IL10RA, IL4R, IFNGR1
narcolepsy	4	10.814286	0.0050568	0.999648838	8.1204832	HLA-DQB1, TNF, HLA-DRB1, HLA-DQA1
C-reactive protein	4	9.4625	0.0074928	0.999992499	11.807089	IL6, TNF, TLR2, TLR4
subarachnoid hemorrhage	4	9.4625	0.0074928	0.999992499	11.807089	IL6, TNF, APOE, NOS3
testicular cancer	4	8.9058824	0.0089293	0.999999227	13.915459	HLA-DQB1, TNF, HLA-DRB1, TGFB1
hepatitis B, chronic	4	8.4111111	0.0105162	0.999999937	16.189504	HLA-DQB1, HLA-DRB1, CCL5, HLA-DQA1
acute coronary syndrome	4	8.4111111	0.0105162	0.999999937	16.189504	NOS3, TLR4, PSMB8, PSMB9
vascular disease	4	7.2095238	0.0162056	1	23.886523	IL6, IL10RA, IL4R, NOS3
dementia	4	7.2095238	0.0162056	1	23.886523	BCHE, APOE, MAPT, SNCA
pancreatitis	4	6.8818182	0.0184177	1	26.695635	GSTM1, TNF, HSPA1A, HSPA1B, TGFB1
pulmonary fibrosis	4	6.3083333	0.0233214	1	32.579156	HLA-DQB1, IL6, HLA-DRB1, HLA-C, HLA-B
glaucoma, primary open-angle	4	5.4071429	0.0350479	1	44.899329	GSTM1, APOE, TAP2, TAP1
multiple myeloma	4	5.2206897	0.0383756	1	47.989179	GSTM1, IL6, TNF, IL4R
nephropathy, IgA	4	4.4529412	0.0573153	1	62.694509	IL6, TNF, NOS3, TGFB1
alcohol abuse	4	3.6047619	0.0950046	1	81.131158	GSTM1, TNF, APOE, SNCA
cardiovascular	4	3.6047619	0.0950046	1	81.131158	IL6, APOE, NOS3, TGFB1
leptospirosis	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, TNF, HLA-DRB1
myositis	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
H. pylori infection; Helicobacter pylori infection	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
beryllium disease	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DPB1
cutaneous neonatal lupus	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, TNF, HLA-DRB1
hepatitis type 1, autoimmune	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
recurrent respiratory	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, TAP1
diabetes, type 1; blood group incompatibility	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
Vogt-Koyanagi-Harada syndrome	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
Graves' disease; Hashimoto's thyroiditis; autoimmune polyglandular syndrome	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
diabetes, type 1; autoimmune diabetes; diabetes, autoimmune	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1

anti-islet autoantibodies diabetes, type 1	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DPB1
psychological distress	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
asthma; urticaria	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DPB1
autoimmune polyglandular syndrome	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
dermatomyositis myopathy, idiopathic inflammatory polymyositis	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, TNF, HLA-C, HLA-B
polymyositis and hypersomnolence	3	37.85	0.0019826	0.955570485	3.2610778	MICA, TNF, HLA-DRB1
measles antibody level	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
pulmonary tuberculosis	3	37.85	0.0019826	0.955570485	3.2610778	VDR, HLA-DRB1, IFNGR1
immunology study	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DPB1
posttreatment Th2 immune response to S. mansoni Ags	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
graft acceptance, liver	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DPB1
inflammatory myopathies	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
celiac disease diabetes, type 1	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
insulin response, first phase; insulinitis	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
pemphigoid, bullous	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
lung cancer; Lambert-Eaton myasthenic syndrome	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-C, HLA-B, HLA-DQA1
physiologic constitutions, Traditional Chinese Med. Defined	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DPB1
human papilloma virus/HPV	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-C, HLA-B
hepatitis, fulminant non-A, nonB	3	37.85	0.0019826	0.955570485	3.2610778	HLA-A, HLA-C, HLA-B, HLA-DRA
warts	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
multiple sclerosis; diabetes, type	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
pneumoconiosis	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, TGFB1
cytokine response to measles vaccine	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DPB1
bee venom allergy	3	37.85	0.0019826	0.955570485	3.2610778	HLA-DQB1, HLA-DRB1, HLA-DQA1
diabetes, type 1 thyroid autoimmunity	3	28.3875	0.0038981	0.997819362	6.3165479	HLA-DQB1, HLA-DRB1, PTPN22
Fuchs heterochromic cyclitis	3	28.3875	0.0038981	0.997819362	6.3165479	HLA-DQB1, TNF, HLA-DRB1
allograft dysfunction, renal	3	28.3875	0.0038981	0.997819362	6.3165479	IL6, TNF, TGFB1
nasal polyposis	3	28.3875	0.0038981	0.997819362	6.3165479	HLA-DQB1, TNF, HLA-DQA1

HIV; sclerosis, systemic	3	28.3875	0.0038981	0.997819362	6.3165479	HLA-DQB1, HLA-DRB1, HLA-DQA1
Rheumatoid arthritis, susceptibility to	3	25.029545	0.0056195	0.618503079	6.6504323	HLA-DRB1, PTPN22, NFKBIL1
Common variants at CD40 and other loci confer risk of rheumatoid arthritis	3	25.029545	0.0056195	0.618503079	6.6504323	PRKCQ, HLA-DRB1, PTPN22
kidney graft survival	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
jaundice	3	22.71	0.0063871	0.999956966	10.151356	HLA-DQB1, HLA-DRB1, HLA-DQA1
Rubella vaccine, cytokine response to	3	22.71	0.0063871	0.999956966	10.151356	HLA-DRB1, HLA-A, HLA-C, HLA-B
hepatitis C infection	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
appendicitis	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TLR4
parvovirus	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
multiple sclerosis; diabetes, gestational; insulin; diabetes, type 1; rhinitis	3	22.71	0.0063871	0.999956966	10.151356	HLA-DQB1, HLA-DRB1, HLA-DQA1
cell-surface B7 expression; cytokine production	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
inflammatory markers	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, NOS3
osteoporosis, postmenopausal; estradiol	3	22.71	0.0063871	0.999956966	10.151356	VDR, IL6, TGFB1
parvovirus B19 infection	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
bronchiolitis obliterans syndrome	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
allergies	3	22.71	0.0063871	0.999956966	10.151356	HLA-DQB1, HLA-DRB1, HLA-DPB1
allograft outcome	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
Alzheimer's disease; dementia	3	22.71	0.0063871	0.999956966	10.151356	TNF, NOS3, HSPA1A, HSPA1B
graft-vs-host disease	3	22.71	0.0063871	0.999956966	10.151356	IL6, TNF, TGFB1
polyangiitis	3	18.925	0.0094191	0.999999644	14.623426	HLA-DQB1, HLA-DRB1, HLA-C, HLA-B
bronchiectasis	3	18.925	0.0094191	0.999999644	14.623426	TAP2, TAP1, TLR2
bacterial vaginosis	3	18.925	0.0094191	0.999999644	14.623426	IL6, TNF, TLR4
idiopathic pulmonary fibrosis	3	18.925	0.0094191	0.999999644	14.623426	IL6, TNF, TGFB1
mediterranean visceral	3	18.925	0.0094191	0.999999644	14.623426	HLA-DQB1, TNF, HLA-DRB1
urinary tract infection	3	18.925	0.0094191	0.999999644	14.623426	TNF, TLR1, HSPA1A, HSPA1B
keloid disease	3	18.925	0.0094191	0.999999644	14.623426	TGFBR1, TGFBR2, TGFB1
lymphoproliferative disorders, post-transplant	3	18.925	0.0094191	0.999999644	14.623426	IL6, TNF, TGFB1
lung transplant complications	3	16.221429	0.0129647	0.999999999	19.587593	IL6, TNF, TGFB1
G6PD deficiency	3	16.221429	0.0129647	0.999999999	19.587593	IL6, TNF, TGFB1

colorectal cancer; Tourette syndrome; bone density; pregnancy loss, recurrent; cleft lip without cleft palate; juvenile polyposis; cleft palate	3	16.221429	0.0129647	0.999999999	19.587593	TGFBR1, TGFBR2, TGFB1
liver transplantation, immunosuppression after	3	16.221429	0.0129647	0.999999999	19.587593	IL6, TNF, TGFB1
Kaposi's sarcoma	3	16.221429	0.0129647	0.999999999	19.587593	HLA-DQB1, HLA-DRB1, HLA-C, HLA-B
allograft rejection, heart	3	14.19375	0.0169959	1	24.901493	IL6, TNF, TGFB1
Idiopathic Dilated	3	14.19375	0.0169959	1	24.901493	TNF, NOS3, TGFB1
asthma; candidiasis; high-altitude illness	3	14.19375	0.0169959	1	24.901493	TNF, HSPA1A, TLR4, HSPA1B
HIV, tuberculosis, cleft lip with cleft palate; cleft lip without cleft palate	3	12.616667	0.0214855	1	30.430419	IL6, TNF, IL4R
sickle cell anemia	3	12.616667	0.0214855	1	30.430419	HLA-DQB1, HLA-DRB1, NOS3
Alzheimer`s Disease	3	12.616667	0.0214855	1	30.430419	IL6, BCHE, APOE
human longevity	3	11.355	0.0264074	1	36.051054	GSTM1, IL6, TNF
Alzheimer's disease; Parkinson's disease	3	11.355	0.0264074	1	36.051054	ICAM1, APOE, CCL5
disc disease, intervertebral	3	11.355	0.0264074	1	36.051054	IL6, TNF, IL4R
aging	3	11.355	0.0264074	1	36.051054	IL6, TNF, TGFB1
graft-versus-host disease; longevity; spondyloarthropathies; aphthous stomatitis	3	9.4625	0.0374494	1	47.145891	IL6, TNF, TGFB1
rhinitis	3	9.4625	0.0374494	1	47.145891	HLA-DRB1, TAP2, TAP1
diabetes mellitus	3	9.4625	0.0374494	1	47.145891	TNF, HLA-DRB1, HLA-DPB1
azoospermia	3	9.4625	0.0374494	1	47.145891	HLA-DQB1, BRD2, HLA-DRB1
bone mass	3	8.7346154	0.0435222	1	52.448989	VDR, IL6, TNF
bullous pemphigoid	3	8.7346154	0.0435222	1	52.448989	IL6, TNF, IL4R
heart transplant	3	8.7346154	0.0435222	1	52.448989	IL6, TNF, TGFB1
arthritis; osteoarthritis	3	8.7346154	0.0435222	1	52.448989	GSTM1, IL6, TNF
systemic sclerosis	3	8.1107143	0.0499331	1	57.502128	HLA-DRB1, NOS3, TGFB1
hematology indices	3	8.1107143	0.0499331	1	57.502128	ICAM1, NOS3, TLR4
Total IgE	3	8.1107143	0.0499331	1	57.502128	HLA-DRB1, IL13RA1, TGFB1
atherosclerosis, carotid	3	7.57	0.0566608	1	62.259432	IL6, PTPN22, NOS3
cerebral infarct, atherothrombotic	3	7.57	0.0566608	1	62.259432	IL6, APOE, CCL5
kawasaki disease	3	6.3083333	0.0785442	1	74.501145	IL6, TNF, NOS3
heart failure	3	5.9763158	0.0863427	1	77.876369	IL6, TNF, TGFB1

graft versus host disease	3	5.9763158	0.0863427	1	77.876369	IL6, TNF, TGFB1
kidney failure, chronic	3	5.9763158	0.0863427	1	77.876369	IL6, TNF, NOS3
Genome-wide association study targeting HIV1 viral setpoint.	2	66.745455	0.0292073	0.993710322	30.37107	HCP5, HLA-C, HLA-B
Abacavir hypersensitivity, susceptibility to	2	66.745455	0.0292073	0.993710322	30.37107	HLA-A, HLA-C, HLA-B
Macular degeneration, age-related, reduced risk of	2	66.745455	0.0292073	0.993710322	30.37107	CFB, C2
TRAF1-C5 as a risk locus for rheumatoid arthritis--a genomewide study	2	66.745455	0.0292073	0.993710322	30.37107	HLA-DRB1, PTPN22
Celiac disease, susceptibility to	2	44.49697	0.0434954	0.999501702	41.9032	HLA-DQB1, HLA-DQA1
Malaria, cerebral, susceptibility	2	44.49697	0.0434954	0.999501702	41.9032	ICAM1, TNF
Colorectal cancer, susceptibility	2	44.49697	0.0434954	0.999501702	41.9032	TLR2, TLR4
hepatitis B vaccination, humoral immune response	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
celiac disease gluten intolerance	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DQA1
respiratory papillomatosis, juvenile-onset; recurrent	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DQA1
IL6 preterm delivery	2	37.85	0.0515074	1	58.663348	IL6, IL6R
latex-fruit syndrome	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRA
human papillomavirus infection	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
hypertension, pulmonary arterial	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
juvenile arthritis; measles	2	37.85	0.0515074	1	58.663348	HLA-DPA1, HLA-DPB1
diabetes, type 1; celiac disease	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DQA1
medicamentosa like dermatitis, trichloroethylene-induced	2	37.85	0.0515074	1	58.663348	HLA-DMB, HLA-DMA
peanut allergy	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
body mass; lipoproteins; blood pressure; CrossLaps, urinary; osteocalcin	2	37.85	0.0515074	1	58.663348	VDR, ERBB2
hepatitis C; hepatitis B	2	37.85	0.0515074	1	58.663348	HLA-A, HLA-C, HLA-B
autoimmune-associated congenital heart block.	2	37.85	0.0515074	1	58.663348	TNF, TGFB1
Alzheimer's disease; Lewy body disease	2	37.85	0.0515074	1	58.663348	APOE, NOS3
condyloma acuminata	2	37.85	0.0515074	1	58.663348	HLA-DMB, HLA-DMA
nasopharyngeal carcinoma	2	37.85	0.0515074	1	58.663348	HLA-A, HSPA1A, HSPA1B

pollen allergy	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
myopathy, idiopathic	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
sensorineural hearing loss	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
pregnancy loss, recurrent; rhinitis	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
Meniere's disease	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
birth weight gestational infections	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DQA1
lupus erythematosus; nasopharyngeal cancer	2	37.85	0.0515074	1	58.663348	MICB, MICA
hypothyroidism, goitrous juvenile autoimmune	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
hepatitis type 2, autoimmune	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
neuropathy, Alzheimer's disease related	2	37.85	0.0515074	1	58.663348	BCHE, APOE
Vogt-Koyanagi-Harada's disease	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
diabetes, type 1; Addison's	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
IgE response	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
gastric adenocarcinoma	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
HLA-DR2 specificity	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
HIV; Toxoplasmic encephalitis	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
atherosclerosis, coronary carotid artery damage	2	37.85	0.0515074	1	58.663348	TNF, HSPA1A, HSPA1B
inflammatory urogenital disease	2	37.85	0.0515074	1	58.663348	TAP2, TAP1
lupus erythematosus; antiphospholipid syndrome	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
urticaria	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
dermatitis and eczema, trichoroethylene-induced	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DQA1
glomerulonephritis, Hepatitis B virus-associated	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
H. pylori infection; thrombocytopenic purpura, idiopathic	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
pelvic inflammatory disease	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DQA1
leprosy type	2	37.85	0.0515074	1	58.663348	VDR, SLC11A1
asthma lung function	2	37.85	0.0515074	1	58.663348	MICB, MICA
malaria; hypoglycemia; hyperparasitemia	2	37.85	0.0515074	1	58.663348	TAP1, PSMB9
rheumatoid arthritis, extra-	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1

posterior cortical atrophy	2	37.85	0.0515074	1	58.663348	APOE, MAPT
Alzheimers disease; juvenile	2	37.85	0.0515074	1	58.663348	PSMB8, PSMB9
vulval lichen sclerosus	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
thyroiditis, chronic lymphocytic	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
lung disease, mycobacteria	2	37.85	0.0515074	1	58.663348	TLR2, IFNGR1
retinopathy, diabetic; diabetes, type 1	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
hepatitis C viral load	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
liver cancer; lymphoma	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
C-reactive protein intima-media thickness	2	37.85	0.0515074	1	58.663348	TLR2, TLR4
paracoccidioidomycosis	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
nonfamilial idiopathic dilated cardiomyopathy	2	37.85	0.0515074	1	58.663348	HLA-DRB1, NEBL
bacteremia malaria, plasmodium falciparum pneumonia	2	37.85	0.0515074	1	58.663348	TLR2, TLR4
tuberculosis Brain aging	2	37.85	0.0515074	1	58.663348	IL6, APOE
coronary artery ectasia	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
asthma; allergic rhinitis; atopic dermatitis	2	37.85	0.0515074	1	58.663348	TLR2, TLR4
celiac disease; colitis	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
multiple sclerosis narcolepsy	2	37.85	0.0515074	1	58.663348	HLA-DQB1, HLA-DRB1
frontotemporal lobar	2	25.233333	0.0762697	1	73.42908	APOE, MAPT
early onset ischemic heart	2	25.233333	0.0762697	1	73.42908	APOE, TGFB1
filiariasis	2	25.233333	0.0762697	1	73.42908	TLR2, TLR4
chronic lung disease	2	25.233333	0.0762697	1	73.42908	TNF, TGFB1
birth weight diabetes, type 1 head circumference at birth	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DQA1
primary sclerosing cholangitis	2	25.233333	0.0762697	1	73.42908	TNF, HLA-C, HLA-B
infertility, tubal factor	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DQA1
Juvenile Myoclonic Epilepsy	2	25.233333	0.0762697	1	73.42908	BRD2, HLA-DRB1
lipid metabolism disorders; hyperlipidemia	2	25.233333	0.0762697	1	73.42908	TNF, APOE
diabetes, type 1; Graves' disease; Hashimoto's thyroiditis	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DRB1
silicosis tuberculosis	2	25.233333	0.0762697	1	73.42908	SLC11A1, TNF
Primary Biliary Cirrhosis	2	25.233333	0.0762697	1	73.42908	VDR, HLA-DPB1

asthma Chlamydomphila pneumoniae infection	2	25.233333	0.0762697	1	73.42908	TNF, CCL5
Crohn's disease; ulcerative colitis; pancolitis	2	25.233333	0.0762697	1	73.42908	TLR1, TLR2
prometastatic vitreoretinopathy rhegmatogenous retinal detachment	2	25.233333	0.0762697	1	73.42908	IL6, TGFB1
Goodpasture's disease	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DRB1
thyroiditis, Hashimoto's	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DRB1
autoimmune response	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DQA1
cirrhosis, biliary primary; diabetes, gestational	2	25.233333	0.0762697	1	73.42908	HLA-A, HLA-C, HLA-B
thyroid autoimmunity	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DQA1
echinococcosis	2	25.233333	0.0762697	1	73.42908	TAP2, TAP1
arthritis, rheumatoid Sjogren's syndrome	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, TNF
birth weight body mass	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DRB1
asthma, aspirin-intolerant	2	25.233333	0.0762697	1	73.42908	TNF, HLA-DPB1
frontotemporal dementia	2	25.233333	0.0762697	1	73.42908	APOE, MAPT
psoriasis; psoriatic arthritis	2	25.233333	0.0762697	1	73.42908	CCHCR1, HLA-C, HLA-B
pemphigus vulgaris	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DRB1
Brugada syndrome	2	25.233333	0.0762697	1	73.42908	HLA-DQB1, HLA-DRB1
aspergillosis	2	25.233333	0.0762697	1	73.42908	TLR1, TLR4
creatinine kidney function lead toxicity	2	25.233333	0.0762697	1	73.42908	VDR, NOS3
duodenal ulcer gastritis	2	25.233333	0.0762697	1	73.42908	NOD1, TLR4
dental implants	2	25.233333	0.0762697	1	73.42908	IL6, TGFB1
LOC1 Related to Metabolic-Syndrome Pathways Including LEPR, HNF1A, IL6R, and GCKR Associate with Plasma C-Reactive Protein: The Women's Genome Health Study	2	22.248485	0.0851324	0.999999753	66.262722	APOE, IL6R
Multiple sclerosis, susceptibility	2	22.248485	0.0851324	0.999999753	66.262722	HLA-DQB1, HLA-DRB1

Table S3. Positively selected leprosy susceptibility genes among populations

Population	YRI	CEU	CHB+JPT
Number of positively selected genes	8	18	14
<i>TLR1</i>	NO	YES	NO
<i>NOD2</i>	NO	YES	NO
<i>TLR2</i>	YES	NO	NO
<i>TLR4</i>	NO	NO	YES
<i>VDR</i>	YES	NO	NO
<i>MBL2</i>	YES	NO	NO
<i>RIPK2</i>	NO	YES	YES
<i>LACC1</i>	NO	YES	NO
<i>PARK2</i>	NO	YES	YES
<i>CCDC122</i>	NO	YES	NO
<i>COL3A1</i>	NO	NO	YES
<i>TIRAP</i>	NO	NO	YES
<i>HLA-DRB1</i>	NO	YES	NO
<i>PACRG</i>	NO	YES	NO
<i>HLA-DQB1</i>	NO	YES	NO
<i>HLA-DQA1</i>	NO	YES	NO
<i>CCL5</i>	NO	YES	NO
<i>LAMA2</i>	NO	NO	YES
<i>TNFSF8</i>	YES	NO	NO
<i>KIR2DL1</i>	NO	NO	YES
<i>CUBN</i>	YES	YES	YES
<i>NEBL</i>	NO	YES	NO
<i>MASP2</i>	YES	NO	YES
<i>IRGM</i>	YES	YES	NO
<i>NLRP1</i>	NO	YES	YES
<i>IL23R</i>	NO	NO	YES
<i>IL18RAP</i>	NO	NO	YES
<i>IL18R1</i>	NO	NO	YES
<i>IL6</i>	NO	YES	YES
<i>CFH</i>	NO	YES	NO
<i>DEC1</i>	YES	YES	NO

Note - Data of the 1000 genome project were used for the positive selection test

YRI - Yoruba in Ibadan, Nigeria [YRI]; CEU - Utah residents (CEPH) with Northern and Western European ancestry [CEU]; CHB+JPT - Han Chinese in Beijing [CHB] + Japanese in Tokyo [JPT]



Erratum

Erratum to “Integrative analyses of leprosy susceptibility genes indicate a common autoimmune profile” [J. Dermatol. Sci. 82 (2016) 18–27.



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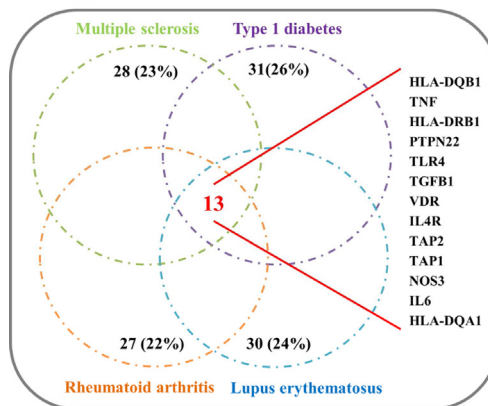
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The publisher regrets that there was an error in Fig. 2 of this paper. The correct figure can be found below:

(a) Top hits of disease enrichment analysis for leprosy susceptibility genes

Disease	Shared gene Count (%)	Fold Enrichment	P-value	Bonferroni	FDR
Type 1 diabetes	31 (25.6)	6.0	7.96E-17	1.74E-13	1.89E-13
Multiple sclerosis	28 (23.1)	6.5	4.77E-16	6.97E-13	7.44E-13
Rheumatoid arthritis	27 (22.3)	6.9	5.98E-16	8.71E-13	9.33E-13
Systemic lupus erythematosus	23 (19.0)	8.5	2.06E-15	3.31E-12	3.52E-12
Lupus erythematosus	18 (14.9)	9.6	7.00E-13	1.10E-09	1.17E-09
Asthma	26 (21.5)	4.9	7.03E-12	1.10E-08	1.18E-08
Tuberculosis	20 (16.5)	12.8	5.10E-17	7.99E-14	8.51E-14
HIV	20 (16.5)	10.0	1.05E-14	1.65E-11	1.76E-11
Hepatitis B	17 (14.0)	15.0	1.41E-15	2.26E-12	2.41E-12
Psoriasis	19 (15.7)	10.7	1.46E-14	2.28E-11	2.43E-11

(b) Autoimmune disorders



(c) Infection

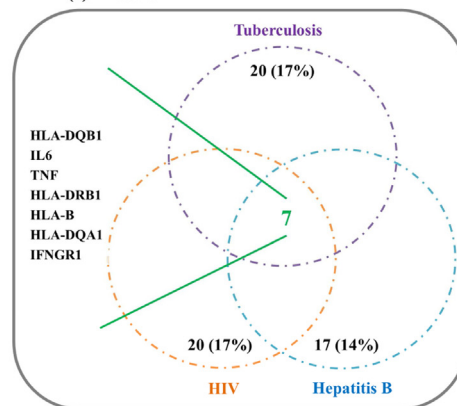


Fig. 2. Cross-disorder analysis showing that leprosy shared similar genetic risk factors with other autoimmune diseases.

The publisher would like to apologise for any inconvenience caused.

DOI of original article: <http://dx.doi.org/10.1016/j.jdermsci.2016.01.001>

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<http://dx.doi.org/10.1016/j.jdermsci.2016.03.008>

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