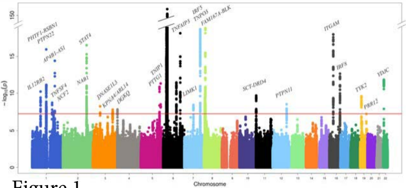
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DGKQ
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PTTG1
TNFAIP3
IRF5
TNPO3
FAM167A-BLK
LIMK1
SCT-DRD4
PTPN11
ITGAM
IRF8
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Chromosome

Figure 1

Supplementary Material Table of Contents

Online supplementary methods

Study population

This study was conducted using 12,132 affected subjects and 23,260 controls of European descent population and all of them have been included in previously published GWAS as summarized in Table S1.[1-6] Briefly, a total of 3,255 SLE cases and 9,562 ancestry matched controls were included from six countries across Europe and North America (Spain, Germany, Netherlands, Italy, UK, and USA). All of the included patients were diagnosed based on the standard American College of Rheumatology (ACR) classification criteria.[7] Previously described GWAS data from 2,363 SSc cases and 5,181 ancestry matched controls were included in the study (four case-control collections from Spain, Germany, Netherlands and USA). All the patients met the ACR Preliminary criteria for the classification of SSc or had at least 3 of the 5 CREST features.[8] A total of 4,804 RA cases and 3,793 ancestry matched controls were included from Sweden, UK and USA, obtained from the Epidemiological Investigation of RA (EIRA) project (http://www.eirasweden.se), the Wellcome Trust Case Control Consortium (WTCCC) data repositories, (http://www.wtccc.org.uk/), and the North American Rheumatoid Arthritis Consortium (NARAC), respectively. All the patients met the ACR criteria for the diagnosis of RA [9] or were diagnosed by board-certified rheumatologists. IIM GWAS data was obtained in collaboration with the MYOGEN consortium, comprising 1,710 cases and 4,724 ancestry matched controls from Europe and North America (Spain, Sweden/Netherlands, Czech Republic/Hungarian, USA and UK). The inclusion criteria were defined by proximal weakness, myopathy on electromyography, muscle biopsy consistent with idiopathic inflammatory myopathy or elevated serum muscle enzymes, and the presence of Gottron’s papules/sign or heliotrope rash, with exclusion of other causes of muscle disease per Bohan and Peter criteria. [10]

Quality control and principal component analysis

Quality control (QC) of the data was conducted for each case-control collection separately using PLINK v.1.07.[11] For the principal component analysis (PCA), ~100,000 quality-filtered independent SNPs were used on each dataset separately, using GCTA64 and R-base software under GNU Public license v.2. For that, the first ten PCs were calculated for each individual and those samples found >6 standard deviations from the cluster centroids of each set were considered outliers and were removed from the analyses.

Statistical analyses

Disease-specific association testing: Association testing for allele dosages was performed using EPACTS software,[12] adjusting by the first two or five PCs as appropriate. Additionally, prior to the meta-analysis, each individual study was adjusted by their specific inflation factor. This was performed by multiplying each standard error by the square root of the calculated inflation factor.

Cross-phenotype meta-analysis: meta-analysis was conducted with METASOFT.[13] Fixed-effects or random-effects model was applied depending on study heterogeneity (Cochran's Q test *p*-value). The lead and most significant SNP outside the extended Major Histocompatibility Complex region (xMHC [Chr6:25-34Mb]), was selected to perform sequential conditional association analyses to confirm statistical independence of associations. These analyses were carried out with the software GCTA-COJO,[14, 15] using the summary statistics from the SSc, SLE, RA and IIM meta-analysis, with the GCTA "--cojo-cond" option within a 10Mb window. A secondary signal was considered if within this window there were additional SNPs with a conditioned *p*-value passing a Bonferroni correction. Results from conditional analyses were visualized using R and depicted in Figure S2.

To annotate the association signals we utilized SNPnexus.[16] If a SNP mapped in a coding/non-coding gene region (introns, exons, UTRs), we reported the candidate gene identified by SNPnexus. If the SNP was upstream, downstream, or intergenic, the most "likely" gene was manually curated in a 500kb window and assigned based on the observed LD block and if there was evidences of previous association signals with autoimmune diseases or other immune-related phenotypes.

Model search to identify the diseases contributing to the lead signal: we conducted an exhaustive disease-subtype model search with the R statistical software package ASSET,[15] utilizing each case-control collection separately. This subset-based meta-analysis explores all possible subsets of diseases for the presence of true association signals, while adjusting for the required multiple testing.

Novelty of the variants: the observed associations were used to query the NHGRI-EBI GWAS catalog and the Phenopedia and Genopedia from HuGE Navigator.[17] The phenopedia database was queried by disease (search terms: "systemic sclerosis", "systemic lupus erythematosus", "rheumatoid arthritis", and "myositis") and the genopedia by gene name based on the annotations from SNPnexus and previously described gene prioritization. Variants were classified as "new" if they had never been associated before with a single disease at a genome-wide significance level.

Functional enrichment analysis: to characterize the functional, cellular and regulatory contribution of the associated SNPs, we conducted a non-parametric enrichment analysis with GARFIELD.[18] This software combines the summary statistics with functional annotations from the ENCODE project [19] and Roadmap Epigenomics [20] by calculating a fold enrichment, and assessing their significance via permutation testing while accounting for LD, MAF and local gene density. Functional annotation included genic elements (GENCODE), DNase hypersensitivity sites, transcription factor binding sites, histone modifications and chromatin states. Results from the functional enrichment analysis are shown in Table S3.

To determine whether any of the lead variants was an expression quantitative trait locus (eQTL) the online tools HaploReg v.4.1[21] and the Genotype-Tissue Expression project (GTEx)[22] were queried (Table 3 and Table S4). Additionally, the Capture HiC plotter [23] tool was used to displays physical interactions between restriction fragments containing the variants and the promoter of genes. This catalog of promoter-interacting regions aims to explain how the transcriptomic control of the genome works. The query was performed using the two promoter-capture datasets contained in the tool and their different cell types.[24, 25] Only the interactions between associated variants and reported genes affected by eQTLs were carried forward in the analyses (Table S6). If there was no overlap with the genes modulated by the eQTLs, the resulting interacting genes were flagged as putative candidates for the diseases. The five new shared risk-SNPs were queried as well and several putative candidates were found (Figure S4).

Drug Target Enrichment Analysis: in order to assess if associated genes were enriched in drug targets, the target genes of eQTLs that overlapped with promoter capture HiC data were used to model a protein-protein interaction (PPI) network using String v10.[26] When possible, the interaction confidence score was set in 0.9, which is the highest score calculated as a combined probability from different evidences of interactions corrected for the probability of observing an interaction by random chance (Table S6). These protein products from the risk genes and those in direct PPI with them were then used to query the OpenTargets Platform [27] for drug targets (Table S7). Additionally, the same platform was searched for drugs indicated or in different phases of drug development for the treatment of SSc, SLE, IIM and RA (Tables S8-S11). Then, Fisher's exact test was used to calculate if the results of the meta-analysis were significantly enriched in pharmacologically active drug targets. To such purpose, we used gene-products related and unrelated to the analyzed disease, drug targets indicated for the disease and coding genes of the genome that are potentially druggable (Tables S12). The Drugbank database (https://www.drugbank.ca/) and ClinicalTrials.gov (https://clinicaltrials.gov/) were searched for drugs that are currently in development for the treatment of RA and for information on publicly and privately supported clinical studies on SSc, SLE and IIM.

Supplementary figures

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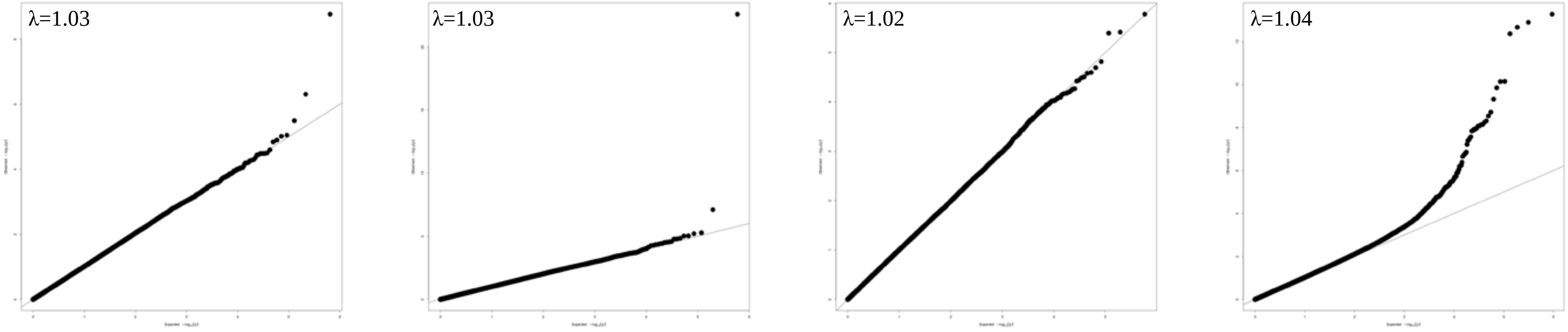

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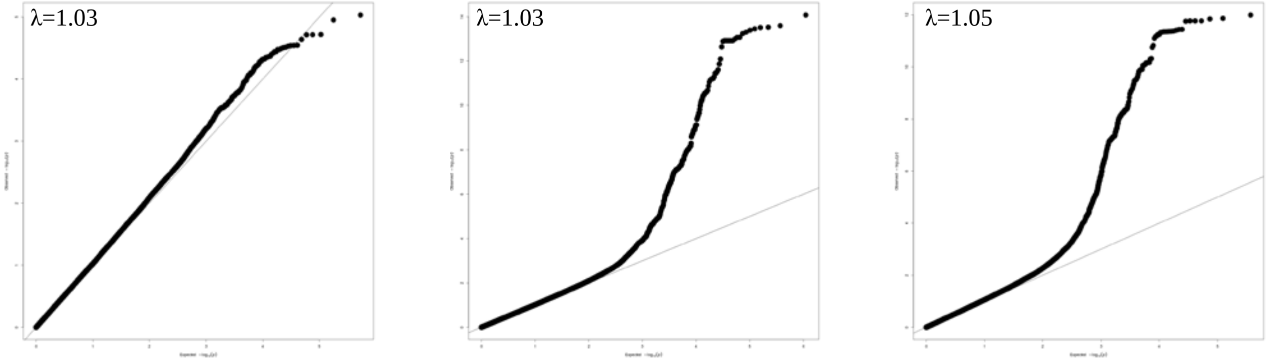

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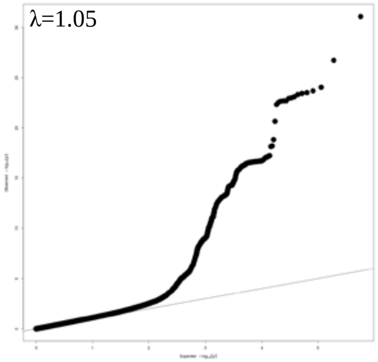

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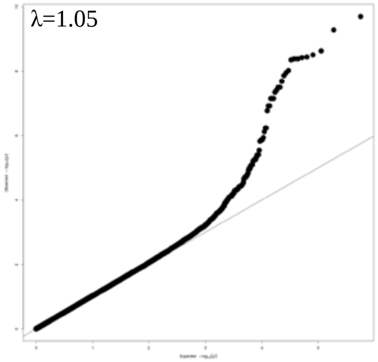

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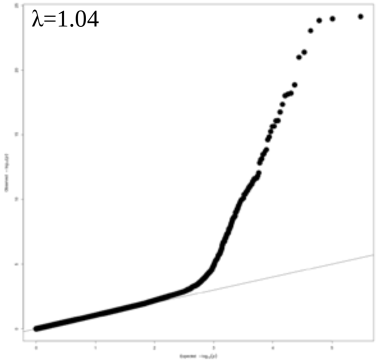

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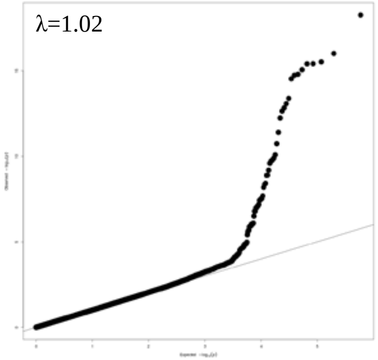

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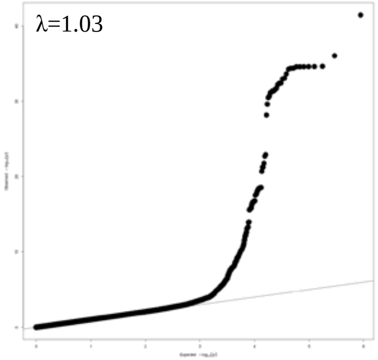

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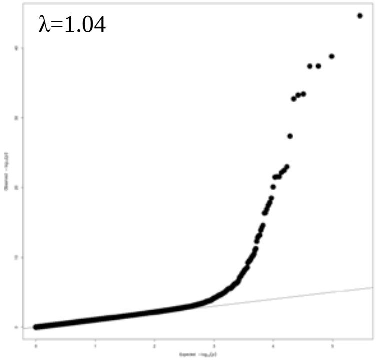

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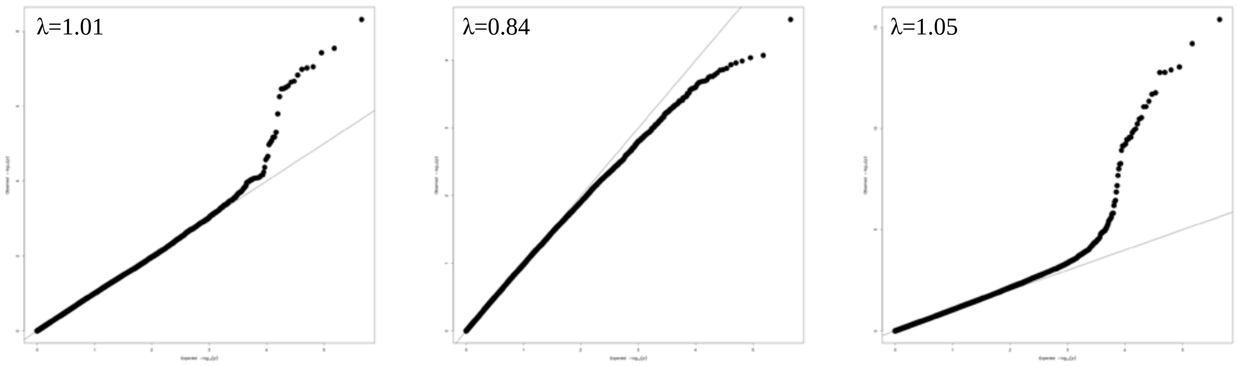

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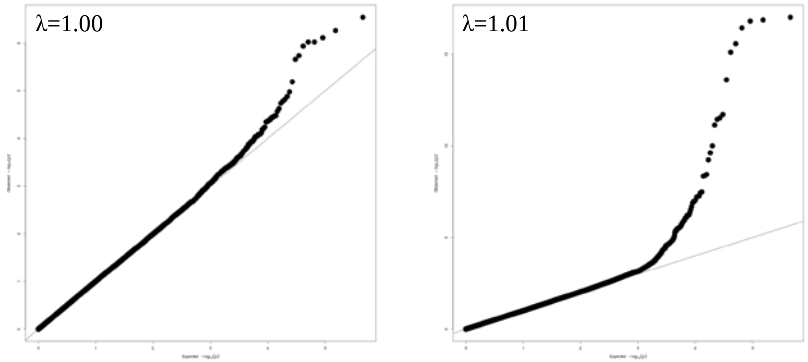
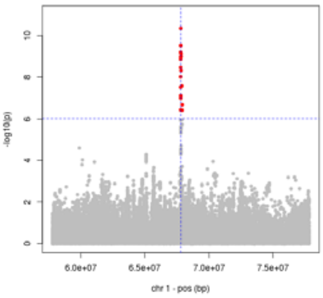


Sweden United Kingdom

Figure S1. Distribution of the observed and expected association *p*-values in each individual study that contributed to the meta-analysis. Quantile-Quantile (QQ) plots from: A) Systemic sclerosis case-control collections. B) Systemic Lupus Erythematosus. C) Rheumatoid Arthritis and D) Idiopathic Inflammatory Myopathies.

A) Non-Conditioned Analysis on variant rs6659932



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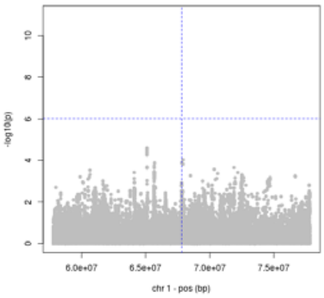

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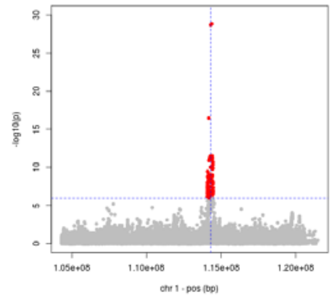

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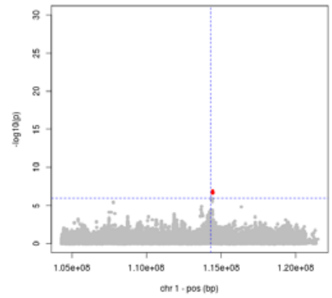

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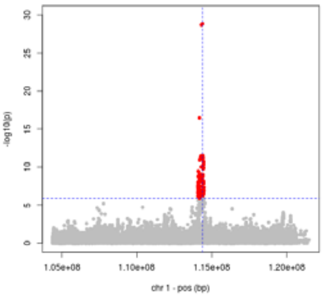

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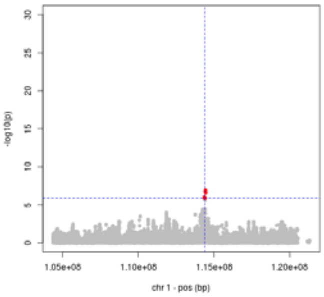

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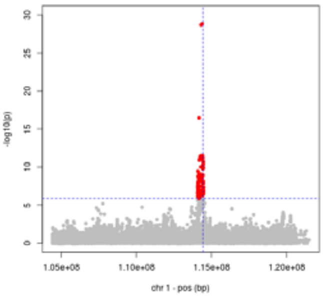

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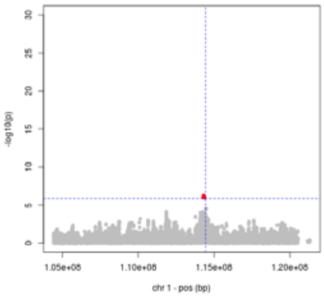

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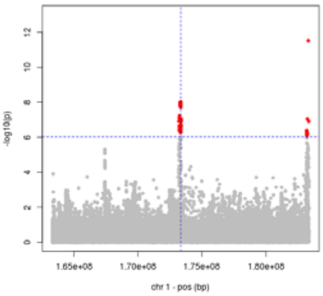

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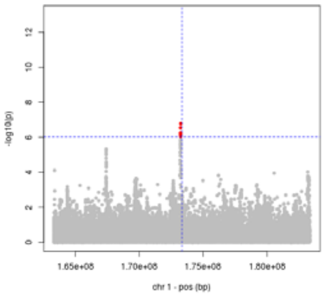

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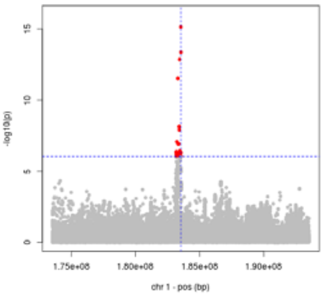

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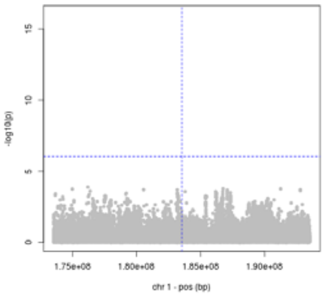

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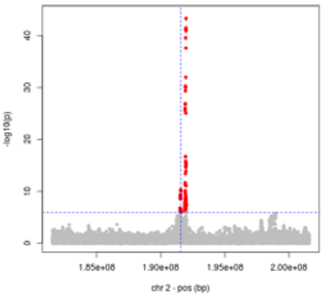

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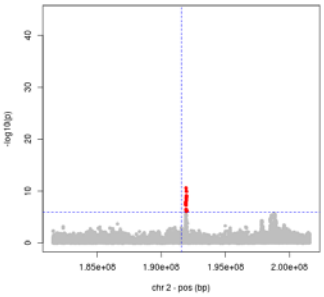

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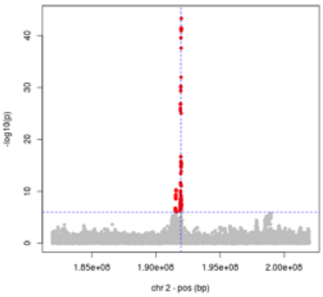

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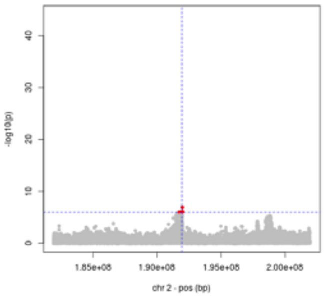

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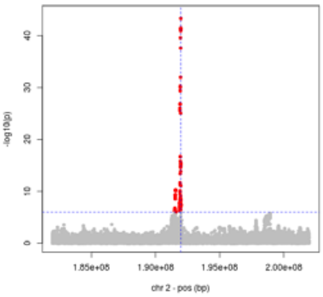

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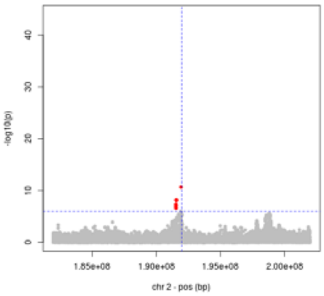

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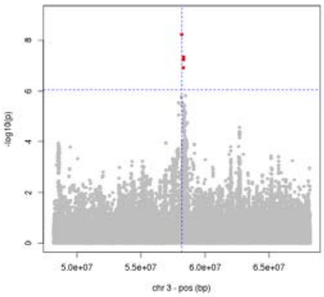

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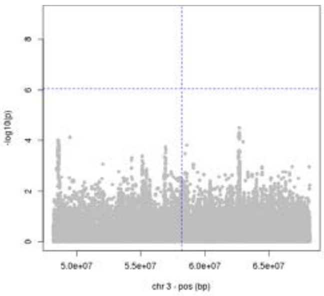

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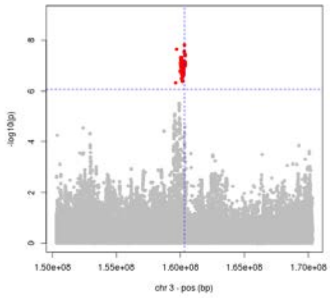

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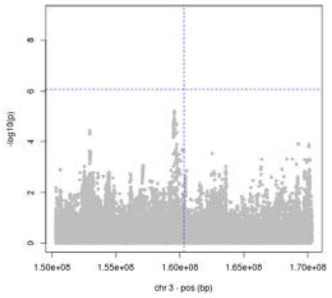

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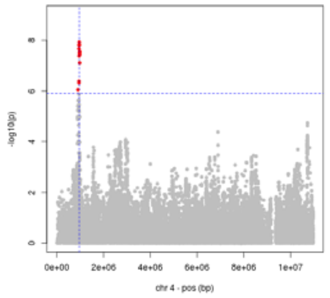

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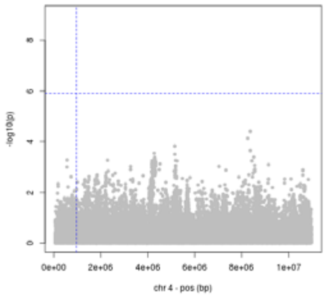

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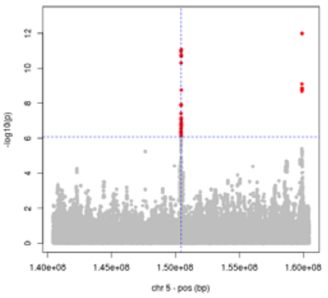

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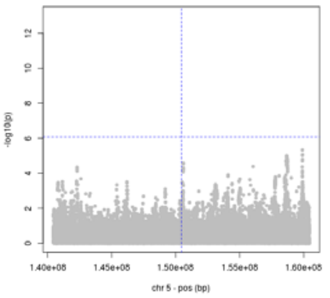

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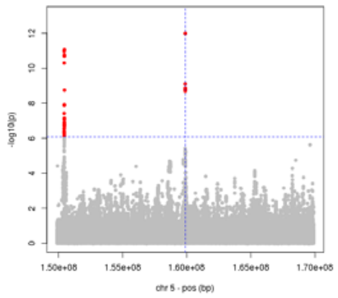

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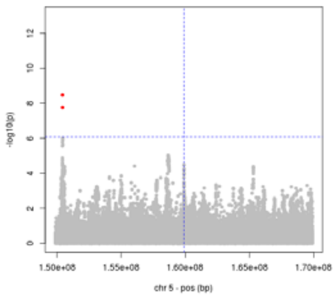

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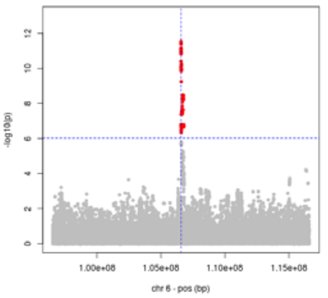

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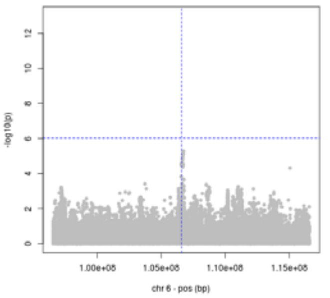

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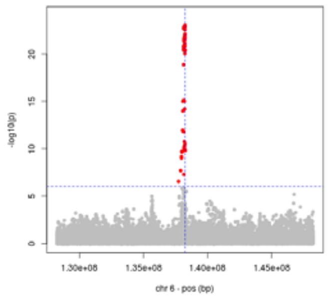

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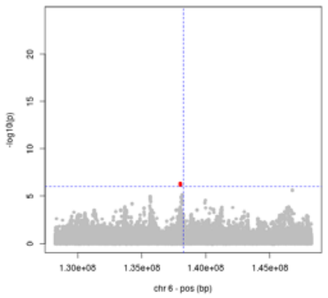

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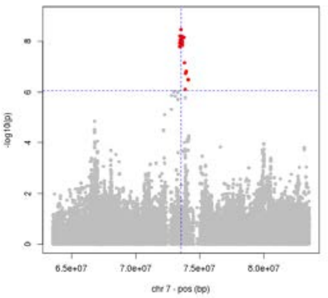

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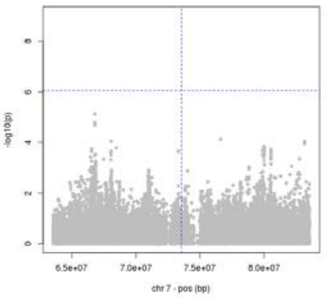

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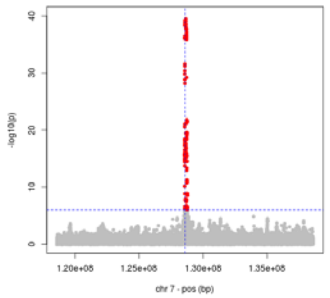

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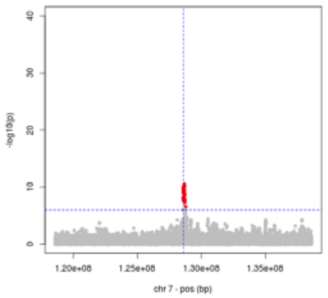

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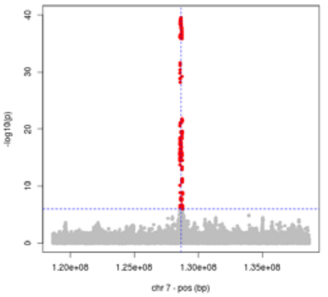

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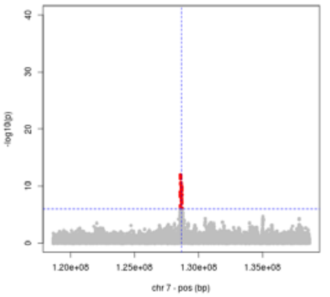

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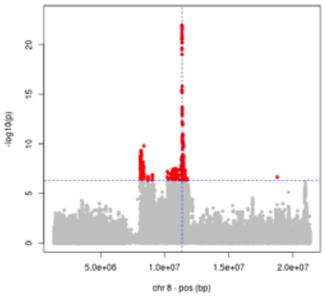
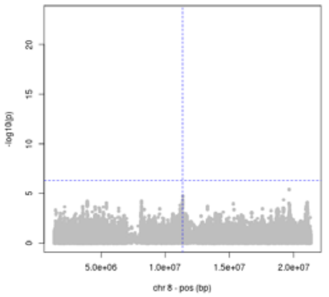
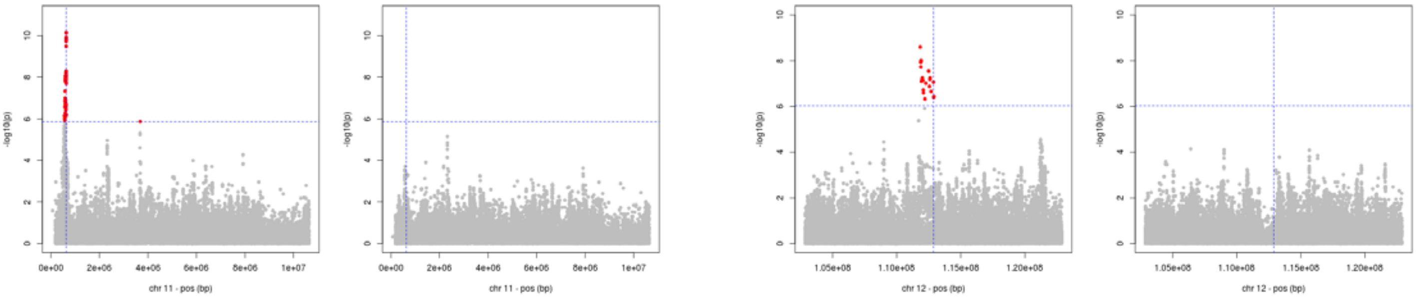


Conditioned Analysis on variant rs2736337



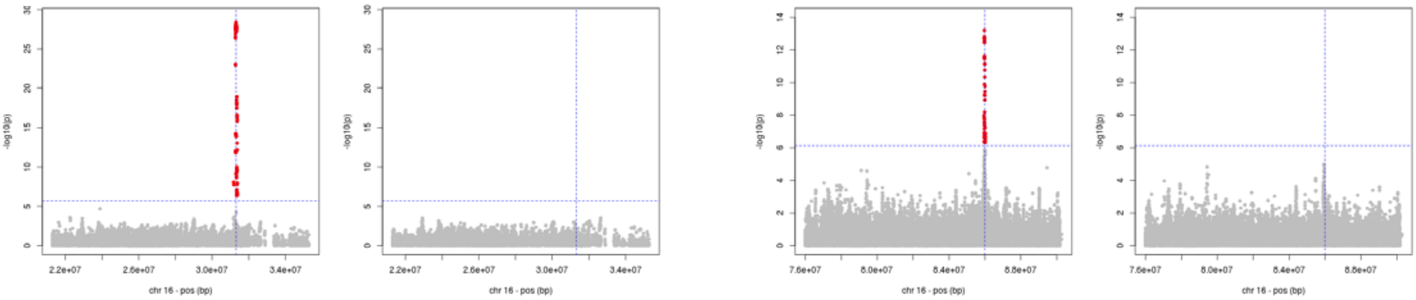


U) Non-Conditioned Analysis on variant rs7929541

Conditioned Analysis on variant rs7929541

V) Non-Conditioned Analysis on variant rs11066301

Conditioned Analysis on variant rs11066301

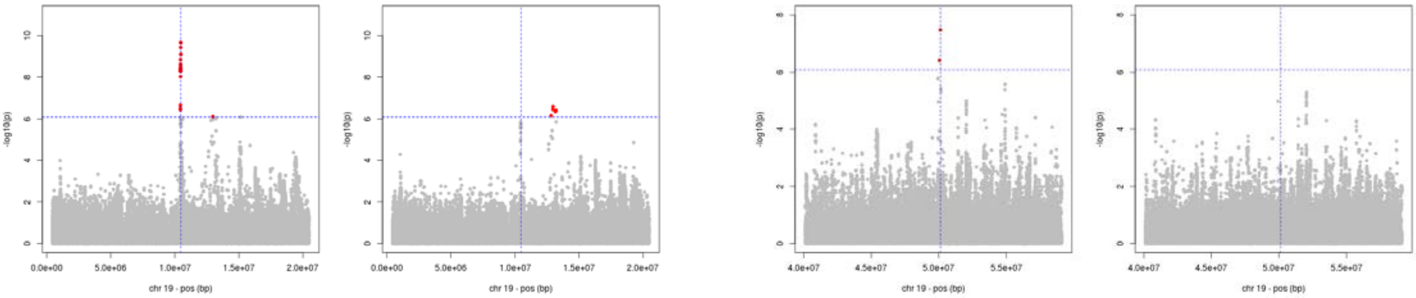


W) Non-Conditioned Analysis on variant rs12102791

Conditioned Analysis on variant rs12102791

X) Non-Conditioned Analysis on variant rs35929052

Conditioned Analysis on variant rs35929052

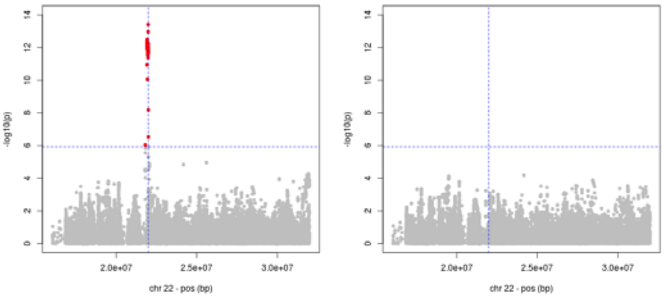


Y) Non-Conditioned Analysis on variant rs76246107

Conditioned Analysis on variant rs76246107

Z) Non-Conditioned Analysis on variant rs11085725

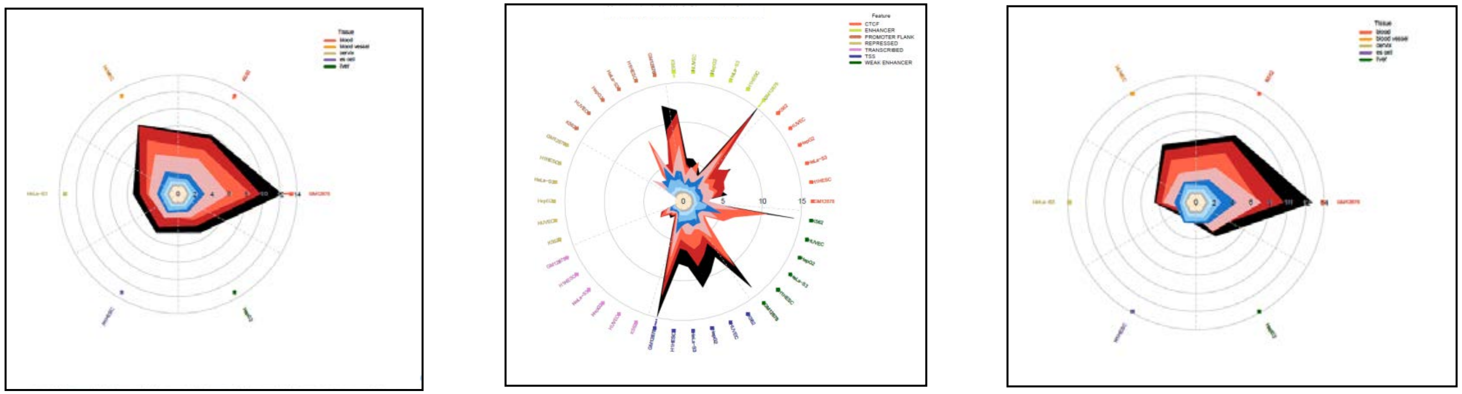
Conditioned Analysis on variant rs11085725



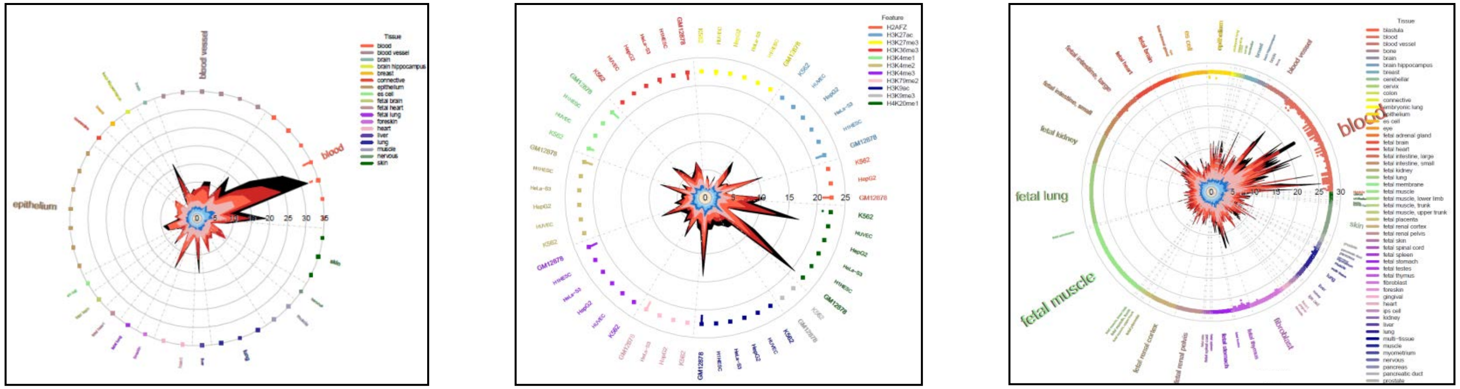
AA) Non-Conditioned Analysis on variant rs5754467

Conditioned Analysis on variant rs5754467

Figure S2. Non-Conditioned and conditioned analysis on the top associated variants from the meta-analysis. In panels where significant variants remained after conditioning, there are several independent variants in the region. In panels E, P, and Y the remaining independent variants were not significant in the meta-analysis.



TFBS Chromatin states FAIRE



Footprints Histone modifications Peaks

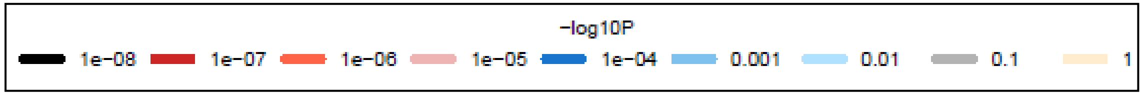
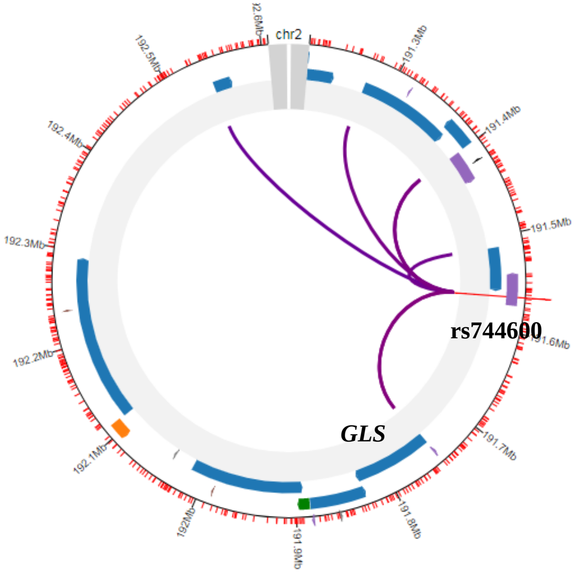
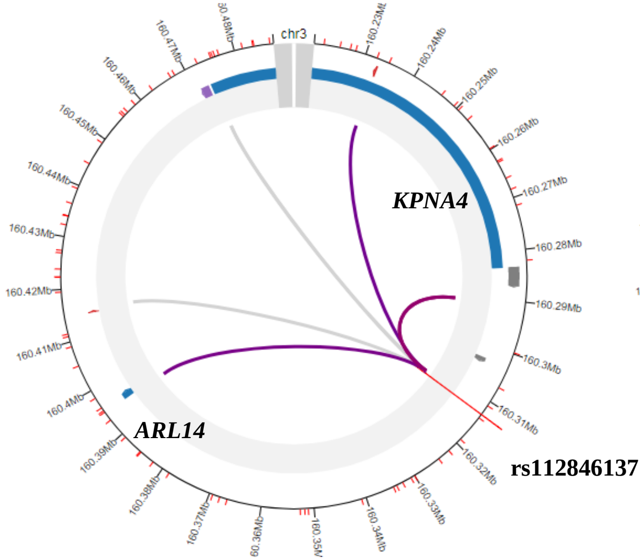


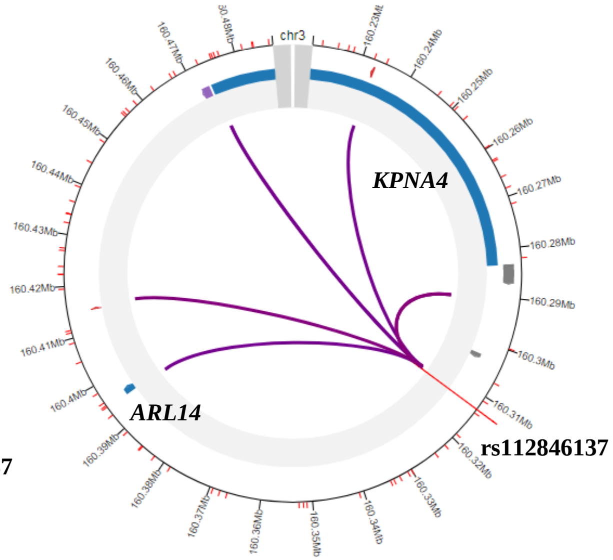
Figure S3. Wheel plots from the functional enrichment analysis with GARFIELD at different thresholds of *p*-values from the meta-analysis. Functional categories from the ENCODE project and Roadmap Epigenomics.



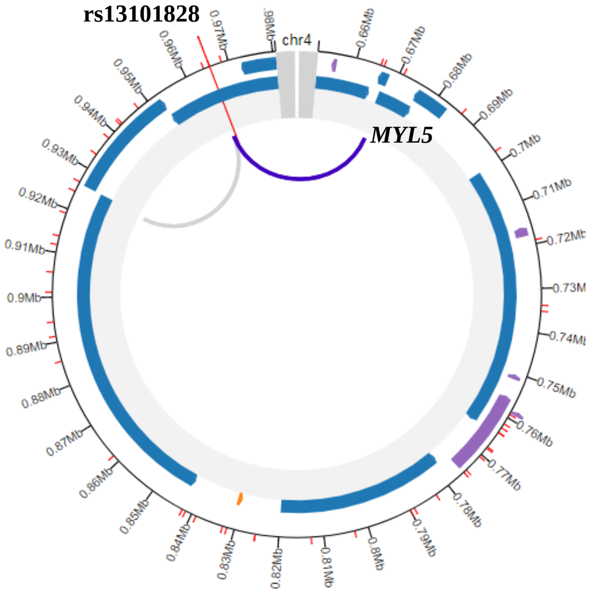
B-lymphocyte cell line



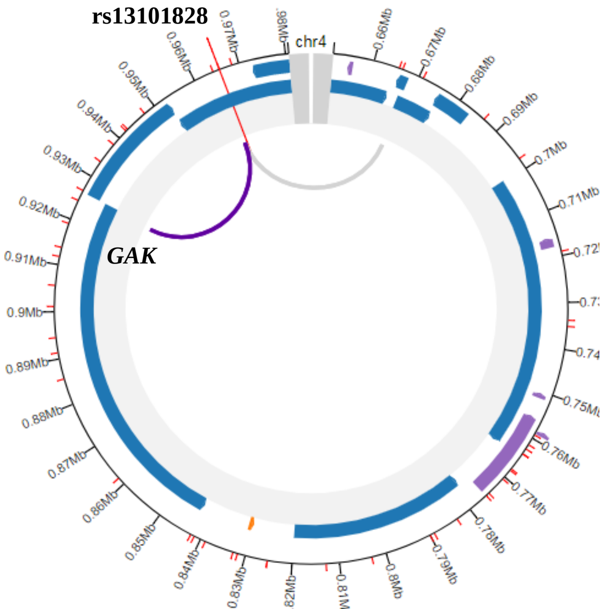
Dendritic cells



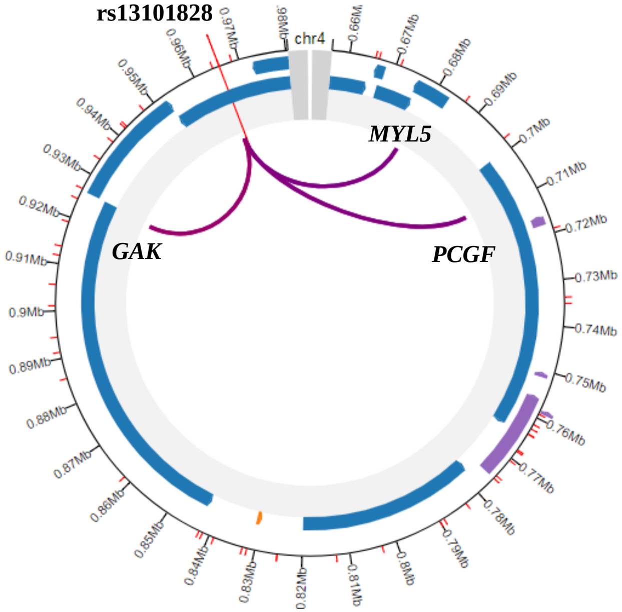
B-lymphocyte cell line



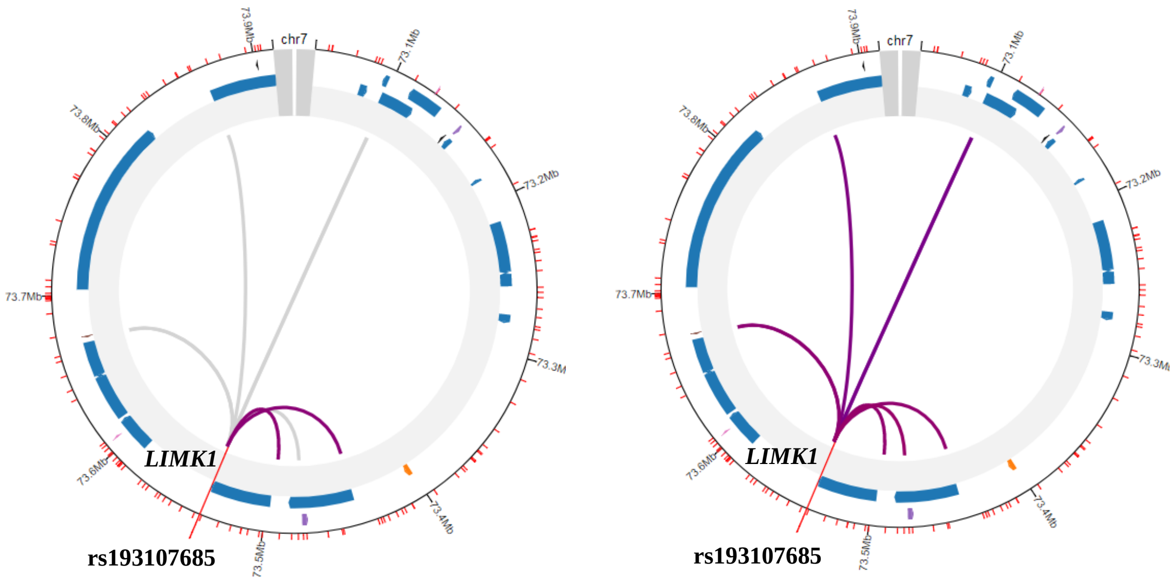
Fetal thymus



CD8+ Cells

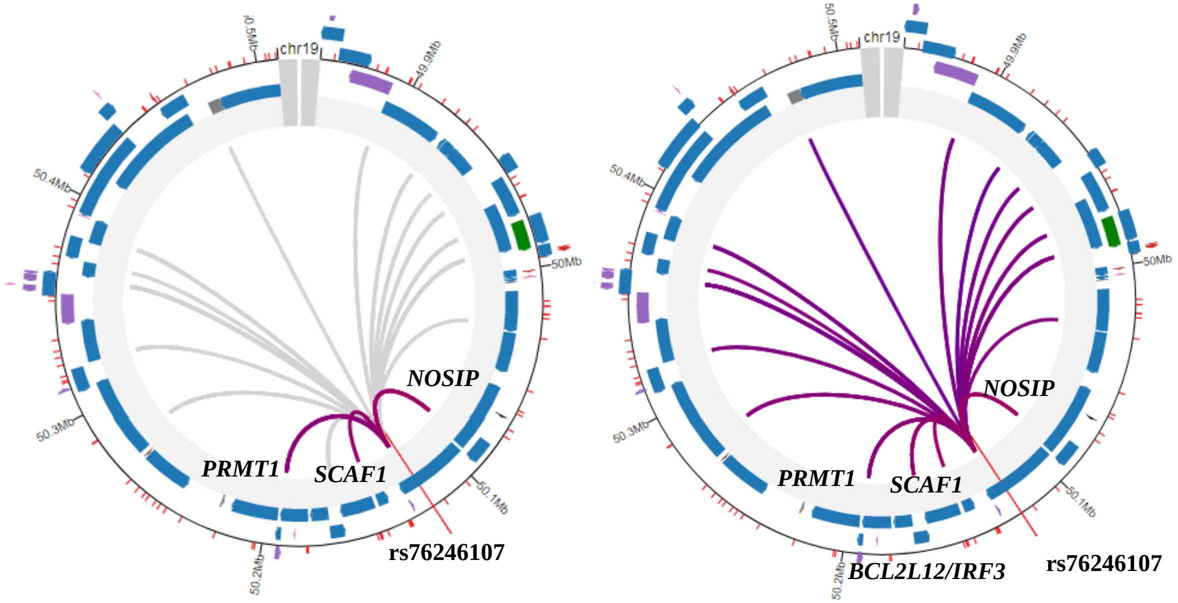


B-lymphocyte cell line



Dendritic cells

B-lymphocyte cell line



Dendritic cells

B-lymphocyte cell line

Figure S4. Circular view of the interactions from the new shared risk SNPs with genes nearby obtained from Promoter Capture HiC data in relevant immune cell types. Interactions are displayed as connecting lines depending on the confidence of the interaction. Grey lines are below threshold in the tissue. Only genes with maximum interaction score are reported.

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Table S1. Summary of the study design, utilized samples, and analyzed variants in the study.

	N (Ca/Co) postQC	Genotyping platform	Genotyped SNPs after QC	Imputed SNPs	Utilized PC	Genomic inflation factor (λ)	PMID
RA							
Sweden	1893/744	Illumina 550K, Illumina 317K	293,631	7,618,025	2	1.02	20453842
United States	875/1201		446,637	7,589,337	5	1.03	
United Kingdom	1827/1427		144,396	7,271,599	5	1.04	
SLE							
Spain	458/499	Illumina HumanOmni1Quad BeadChip, Illumina HumanOmniExpressExome 8v1.2, HumanHap300v1.1, Illumina Human Hap550	727,382	7,370,411	2	1.03	26502338, 28973304, 18204446, 20190752
Germany	199/1136		707,974	7,624,878	2	1.03	
The Netherlands	270/1675		709,969	7,494,197	2	1.05	
United Kingdom	985/1463		284,361	7,293,654	5	1.05	
Italy	335/957		719,328	7,289,469	2	1.05	
United States	907/3045		152,530	7,339,194	5	1.04	
SSc							
Spain	362/362	Illumina Human CNV370K Beadchip, Illumina 550K	317,348	7,533,253	2	1.03	20383147
Germany	255/658		290,928	7,500,879	2	1.03	
The Netherlands	182/631		286,266	7,528,731	2	1.02	
United States	1482/2759		461,068	7,617,902	5	1.04	
IIM							
Czech Republic/Hungarian	316/242	Illumina HumanHap550 BeadChip, Illumina HumanCNV370-Duo v1 BeadChip, Illumina Human610-Quad v1 BeadChip, Illumina Human660W-Quad v1 BeadChip	226,643	7,369,026	2	1.01	26291516
Spain	47/253		226,034	7,518,585	2	0.84	
United States	746/1152		220,533	7,551,455	5	1.05	
Swedish/Dutch	120/326		228,315	7,560,114	2	1.00	
United Kingdom	445/1177		227,556	7,470,059	2	1.01	

N (Ca/Co): Number of cases and controls

QC: Quality Control

Utilized PC: Utilized principal components in the logistic regressions.

RA: Rheumatoid Arthritis; SLE: Systemic Lupus Erythematosus; SSc: Systemic Sclerosis; IIM: idiopathic inflammatory myopathies

PMID: Pubmed identification number

Table S2. Number of variants and significance threshold utilized for the conditional analysis

Chr	Position[a]	SNP	Region-based *p*- value	Nº SNPs*	Bonferroni Threshold[Φ]
1	67802371	rs6659932	$4.43x10^{-11}$	52,013	$9.60x10^{-07}$
1	114303808	rs6679677	$2.10x10^{-29}$	44,915	$1.11x10^{-06}$
1	114377568	rs2476601	$1.53x10^{-29}$	37,238	$1.34x10^{-06}$
1	114433946	rs1217393	$6.51x10^{-09}$	35,757	$1.40x10^{-06}$
1	173337747	rs2422345	$9.46x10^{-09}$	54,579	$9.20x10^{-07}$
1	183532580	rs17849502	$7.33x10^{-16}$	53,361	$9.37x10^{-07}$
2	191564757	rs744600	$4.06x10^{-11}$	42,606	$1.18x10^{-06}$
2	191933283	rs13389408	$2.18x10^{-17}$	46,700	$1.07x10^{-06}$
2	191973034	rs10174238	$5.12x10^{-44}$	46,637	$1.07x10^{-06}$
3	58183636	rs35677470	$5.93x10^{-09}$	53,800	$9.29x10^{-07}$
3	160312921	rs112846137	$1.55x10^{-08}$	57,551	$8.67x10^{-07}$
4	965720	rs13101828	$1.17x10^{-08}$	40,172	$1.25x10^{-06}$
5	150438477	rs4958880	$1.04x10^{-11}$	57,108	$8.75x10^{-07}$
5	159887336	rs2431098	$1.03x10^{-12}$	58,791	$8.50x10^{-07}$
6	106569270	rs802791	$2.95x10^{-12}$	53,859	$9.28x10^{-07}$
6	138243739	rs58721818	$9.77x10^{-24}$	52,402	$9.50x10^{-07}$
7	73537902	rs193107685	$3.44x10^{-09}$	54,437	$9.18x10^{-07}$
7	128589633	rs10954214	$4.26x10^{-17}$	52,823	$9.46x10^{-07}$
7	128647942	rs13238352	$3.21x10^{-40}$	52,877	$9.45x10^{-07}$
8	11341880	rs2736337	$1.13x10^{-22}$	96,465	$5.18x10^{-07}$
11	633689	rs7929541	$7.20x10^{-11}$	36,519	$1.37x10^{-06}$
12	112871372	rs11066301	$4.75x10^{-08}$	54,795	$9.12x10^{-07}$
16	31303946	rs12102791	$4.58x10^{-29}$	23,380	$2.14x10^{-06}$
16	85994484	rs35929052	$1.17x10^{-09}$	66,226	$7.54x10^{-07}$
19	10462513	rs11085725	$2.07x10^{-10}$	61,353	$8.14x10^{-07}$
19	50121274	rs76246107	$3.36x10^{-08}$	58,435	$8.55x10^{-07}$
22	21985094	rs5754467	$3.95x10^{-14}$	42,121	$1.19x10^{-06}$

[a] Position according to build GRCh37/hg19.

Chr: Chromosome; SNP: Single Nucleotide Polymorphism.

*In a 10Mb window.

[Φ] The variants with a *p*- value lower than the Bonferroni threshold are considered independent signals.

Table S3. Functional Enrichment Analysis results for variants with p-value≤1x10^{-5} in the meta-analysis.

Category[a]	**Tissue**	**Cell type**	**Type**	**PThresh**[b]	**NAnnotThesh**[c]	**Nannot**[d]	**Nthresh**[e]	**N (LD-pruned variants)**[f]	**FE**	**EmpPval**
Chromatin_States	blood	GM12878	ENHANCER	1.00x10^{-8}	13	10944	33	416420	14.99	<1x10^{-5}
Chromatin_States	blood	GM12878	TSS	1.00x10^{-8}	12	10182	33	416420	14.87	<1x10^{-5}
Chromatin_States	blood	GM12878	ENHANCER	1.00x10^{-7}	16	10944	44	416420	13.84	<1x10^{-5}
Chromatin_States	blood	GM12878	ENHANCER	1.00x10^{-6}	22	10944	77	416420	10.87	<1x10^{-5}
Chromatin_States	blood	GM12878	ENHANCER	1.00x10^{-5}	38	10944	185	416420	7.82	<1x10^{-5}
Chromatin_States	blood	GM12878	TSS	1.00x10^{-6}	18	10182	77	416420	9.56	<1x10^{-5}
Chromatin_States	blood	GM12878	TSS	1.00x10^{-5}	32	10182	185	416420	7.07	<1x10^{-5}
Footprints	blood	GM12865	footprints	1.00x10^{-7}	12	5767	44	416420	19.69	<1x10^{-5}
Footprints	blood	GM12865	footprints	1.00x10^{-6}	15	5767	77	416420	14.07	1x10^{-5}
Footprints	blood	GM12865	footprints	1.00x10^{-5}	27	5767	185	416420	10.54	<1x10^{-5}
Footprints	blood	GM06990	footprints	1.00x10^{-8}	8	3153	33	416420	32.02	<1x10^{-5}
Footprints	blood	GM12865	footprints	1.00x10^{-8}	12	5767	33	416420	26.26	<1x10^{-5}
Genic	NA	NA	Exon	1.00x10^{-8}	12	8968	33	416420	16.89	<1x10^{-5}
Genic	NA	NA	Exon	1.00x10^{-7}	13	8968	44	416420	13.72	1x10^{-5}
Genic	NA	NA	Exon	1.00x10^{-6}	19	8968	77	416420	11.46	<1x10^{-5}
Genic	NA	NA	Exon	1.00x10^{-5}	32	8968	185	416420	8.03	<1x10^{-5}
Histone_Modifications	blood	GM12878	H2AFZ	1.00x10^{-8}	22	25824	33	416420	10.75	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K27ac	1.00x10^{-8}	22	25674	33	416420	10.81	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me1	1.00x10^{-8}	25	39871	33	416420	7.91	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me2	1.00x10^{-8}	23	34807	33	416420	8.34	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me3	1.00x10^{-8}	17	25365	33	416420	8.46	1x10^{-5}
Histone_Modifications	blood	GM12878	H3K79me2	1.00x10^{-8}	16	25683	33	416420	7.86	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K9ac	1.00x10^{-8}	21	18903	33	416420	14.02	<1x10^{-5}
Histone_Modifications	blood	GM12878	H2AFZ	1.00x10^{-7}	27	25824	44	416420	9.90	<1x10^{-5}
Histone_Modifications	blood	GM12878	H2AFZ	1.00x10^{-6}	35	25824	77	416420	7.33	<1x10^{-5}

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p* -value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Histone_Modifications	blood	GM12878	H2AFZ	1.00x10^{-5}	55	25824	185	416420	4.79	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K27ac	1.00x10^{-7}	26	25674	44	416420	9.58	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K27ac	1.00x10^{-6}	40	25674	77	416420	8.43	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K27ac	1.00x10^{-5}	66	25674	185	416420	5.79	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K36me3	1.00x10^{-6}	27	35497	77	416420	4.11	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K36me3	1.00x10^{-5}	49	35497	185	416420	3.11	<1x10^{-5}
Histone_Modifications	cervix	HeLa-S3	H3K36me3	1.00x10^{-5}	40	26849	185	416420	3.35	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me1	1.00x10^{-7}	30	39871	44	416420	7.12	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me1	1.00x10^{-6}	45	39871	77	416420	6.10	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me1	1.00x10^{-5}	77	39871	185	416420	4.35	<1x10^{-5}
Histone_Modifications	blood	K562	H3K4me1	1.00x10^{-6}	38	60235	77	416420	3.41	1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me2	1.00x10^{-7}	27	34807	44	416420	7.34	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me2	1.00x10^{-6}	40	34807	77	416420	6.21	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me2	1.00x10^{-5}	70	34807	185	416420	4.53	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me3	1.00x10^{-7}	20	25365	44	416420	7.46	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me3	1.00x10^{-6}	27	25365	77	416420	5.76	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K4me3	1.00x10^{-5}	52	25365	185	416420	4.61	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K79me2	1.00x10^{-7}	18	25683	44	416420	6.63	1x10^{-5}
Histone_Modifications	blood	GM12878	H3K79me2	1.00x10^{-6}	28	25683	77	416420	5.90	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K79me2	1.00x10^{-5}	46	25683	185	416420	4.03	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K9ac	1.00x10^{-7}	22	18903	44	416420	11.01	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K9ac	1.00x10^{-6}	30	18903	77	416420	8.58	<1x10^{-5}
Histone_Modifications	blood	GM12878	H3K9ac	1.00x10^{-5}	51	18903	185	416420	6.07	<1x10^{-5}
Hotspots	**blood**	**Adult_CD4+**	**hotspots**	**1.00x10^{-6}**	**43**	**52433**	**77**	**416420**	**4.44**	**<1x10^{-5}**
Hotspots	**blood**	**Adult_CD4+**	**hotspots**	**1.00x10^{-5}**	**77**	**52433**	**185**	**416420**	**3.31**	**1x10^{-5}**
Hotspots	**blood**	**CD20+**	**hotspots**	**1.00x10^{-6}**	**35**	**32590**	**77**	**416420**	**5.81**	**<1x10^{-5}**

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p*-value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Hotspots	**blood**	**CD20+**	**hotspots**	**1.00x10^{-5}**	**66**	**32590**	**185**	**416420**	**4.56**	**<1x10^{-5}**
Hotspots	**blood**	**GM06990**	**hotspots**	**1.00x10^{-7}**	**25**	**24839**	**44**	**416420**	**9.53**	**<1x10^{-5}**
Hotspots	**blood**	**GM06990**	**hotspots**	**1.00x10^{-6}**	**34**	**24839**	**77**	**416420**	**7.40**	**<1x10^{-5}**
Hotspots	**blood**	**GM06990**	**hotspots**	**1.00x10^{-5}**	**57**	**24839**	**185**	**416420**	**5.17**	**<1x10^{-5}**
Hotspots	**blood**	**GM12864**	**hotspots**	**1.00x10^{-7}**	**26**	**30322**	**44**	**416420**	**8.12**	**<1x10^{-5}**
Hotspots	**blood**	**GM12864**	**hotspots**	**1.00x10^{-6}**	**37**	**30322**	**77**	**416420**	**6.60**	**<1x10^{-5}**
Hotspots	**blood**	**GM12864**	**hotspots**	**1.00x10^{-5}**	**69**	**30322**	**185**	**416420**	**5.12**	**<1x10^{-5}**
Hotspots	**blood**	**GM12865**	**hotspots**	**1.00x10^{-7}**	**25**	**31195**	**44**	**416420**	**7.58**	**<1x10^{-5}**
Hotspots	**blood**	**GM12865**	**hotspots**	**1.00x10^{-6}**	**37**	**31195**	**77**	**416420**	**6.41**	**<1x10^{-5}**
Hotspots	**blood**	**GM12865**	**hotspots**	**1.00x10^{-5}**	**69**	**31195**	**185**	**416420**	**4.98**	**<1x10^{-5}**
Hotspots	**blood**	**GM12878**	**hotspots**	**1.00x10^{-7}**	**30**	**48944**	**44**	**416420**	**5.80**	**<1x10^{-5}**
Hotspots	**blood**	**GM12878**	**hotspots**	**1.00x10^{-6}**	**46**	**48944**	**77**	**416420**	**5.08**	**<1x10^{-5}**
Hotspots	**blood**	**GM12878**	**hotspots**	**1.00x10^{-5}**	**83**	**48944**	**185**	**416420**	**3.82**	**<1x10^{-5}**
Hotspots	cervix	HeLa-S3	hotspots	1.00x10^{-6}	45	56917	77	416420	4.28	<1x10^{-5}
Hotspots	cervix	HeLa-S3	hotspots	1.00x10^{-5}	87	56917	185	416420	3.44	<1x10^{-5}
Hotspots	breast	HMEC	hotspots	1.00x10^{-7}	31	55975	44	416420	5.24	<1x10^{-5}
Hotspots	breast	HMEC	hotspots	1.00x10^{-6}	48	55975	77	416420	4.64	<1x10^{-5}
Hotspots	breast	HMEC	hotspots	1.00x10^{-5}	89	55975	185	416420	3.58	<1x10^{-5}
Hotspots	muscle	HSMM	hotspots	1.00x10^{-5}	89	63035	185	416420	3.18	1x10^{-5}
Hotspots	**blood**	**Th1**	**hotspots**	**1.00x10^{-7}**	**28**	**45601**	**44**	**416420**	**5.81**	**1x10^{-5}**
Hotspots	**blood**	**Th1**	**hotspots**	**1.00x10^{-6}**	**42**	**45601**	**77**	**416420**	**4.98**	**<1x10^{-5}**
Hotspots	**blood**	**Th1**	**hotspots**	**1.00x10^{-5}**	**80**	**45601**	**185**	**416420**	**3.95**	**<1x10^{-5}**
Hotspots	**blood**	**Th2**	**hotspots**	**1.00x10^{-5}**	**56**	**25278**	**185**	**416420**	**4.99**	**<1x10^{-5}**
Hotspots	**blood**	**Jurkat**	**hotspots**	**1.00x10^{-5}**	**63**	**33879**	**185**	**416420**	**4.19**	**<1x10^{-5}**
Hotspots	**blood**	**K562**	**hotspots**	**1.00x10^{-6}**	**45**	**55105**	**77**	**416420**	**4.42**	**<1x10^{-5}**
Hotspots	breast	MCF-7	hotspots	1.00x10^{-6}	44	53837	77	416420	4.42	1x10^{-5}
Hotspots	breast	MCF-7	hotspots	1.00x10^{-5}	83	53837	185	416420	3.47	<1x10^{-5}

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p* -value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Hotspots	**blood**	**NB4**	**hotspots**	**1.00x10^{-5}**	**60**	**31772**	**185**	**416420**	**4.25**	**<1x10^{-5}**
Hotspots	skin	NHEK	hotspots	1.00x10^{-7}	31	54667	44	416420	5.37	<1x10^{-5}
Hotspots	skin	NHEK	hotspots	1.00x10^{-6}	48	54667	77	416420	4.75	<1x10^{-5}
Hotspots	skin	NHEK	hotspots	1.00x10^{-5}	88	54667	185	416420	3.62	<1x10^{-5}
Hotspots	**blood**	**GM12891**	**hotspots**	**1.00x10^{-5}**	**73**	**47554**	**185**	**416420**	**3.46**	**1x10^{-5}**
Hotspots	**blood**	**GM12892**	**hotspots**	**1.00x10^{-6}**	**39**	**50412**	**77**	**416420**	**4.18**	**<1x10^{-5}**
Hotspots	**blood**	**GM12892**	**hotspots**	**1.00x10^{-5}**	**73**	**50412**	**185**	**416420**	**3.26**	**<1x10^{-5}**
Hotspots	**blood**	**GM19238**	**hotspots**	**1.00x10^{-5}**	**75**	**46301**	**185**	**416420**	**3.65**	**<1x10^{-5}**
Hotspots	**blood**	**GM19240**	**hotspots**	**1.00x10^{-6}**	**41**	**50715**	**77**	**416420**	**4.37**	**<1x10^{-5}**
Hotspots	**blood**	**GM19240**	**hotspots**	**1.00x10^{-5}**	**81**	**50715**	**185**	**416420**	**3.60**	**<1x10^{-5}**
Hotspots	pancreatic_duct	HPDE6-E6E7	hotspots	1.00x10^{-5}	64	34673	185	416420	4.15	1x10^{-5}
Hotspots	myometrium	Myometr	hotspots	1.00x10^{-5}	68	42053	185	416420	3.64	1x10^{-5}
Hotspots	epithelium	pHTE	hotspots	1.00x10^{-5}	80	55715	185	416420	3.23	1x10^{-5}
Hotspots	liver	Stellate	hotspots	1.00x10^{-6}	39	43543	77	416420	4.84	<1x10^{-5}
Hotspots	liver	Stellate	hotspots	1.00x10^{-5}	74	43543	185	416420	3.83	<1x10^{-5}
Hotspots	urothelium	Urothelia	hotspots	1.00x10^{-5}	75	46177	185	416420	3.66	<1x10^{-5}
Hotspots	embryonic_lung	WI-38	hotspots	1.00x10^{-6}	39	40420	77	416420	5.22	<1x10^{-5}
Hotspots	embryonic_lung	WI-38	hotspots	1.00x10^{-5}	68	40420	185	416420	3.79	<1x10^{-5}
Hotspots	**blood**	**CD20+**	**hotspots**	**1.00x10^{-8}**	**19**	**32590**	**33**	**416420**	**7.36**	**<1x10^{-5}**
Hotspots	**blood**	**GM06990**	**hotspots**	**1.00x10^{-8}**	**23**	**24839**	**33**	**416420**	**11.68**	**<1x10^{-5}**
Hotspots	**blood**	**CD14_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**32**	**25266**	**77**	**416420**	**6.85**	**<1x10^{-5}**
Hotspots	**blood**	**CD14_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**53**	**25266**	**185**	**416420**	**4.72**	**1x10^{-5}**
Hotspots	**blood**	**CD14_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**28**	**23731**	**77**	**416420**	**6.38**	**<1x10^{-5}**
Hotspots	**blood**	**CD14_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**55**	**23731**	**185**	**416420**	**5.22**	**<1x10^{-5}**
Hotspots	**blood**	**GM12864**	**hotspots**	**1.00x10^{-8}**	**22**	**30322**	**33**	**416420**	**9.16**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-7}**	**25**	**29263**	**44**	**416420**	**8.09**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**38**	**29263**	**77**	**416420**	**7.02**	**<1x10^{-5}**

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p* -value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**69**	**29263**	**185**	**416420**	**5.31**	**<1x10^{-5}**
Hotspots	**blood**	**GM12865**	**hotspots**	**1.00x10^{-8}**	**22**	**31195**	**33**	**416420**	**8.90**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-7}**	**22**	**26827**	**44**	**416420**	**7.76**	**1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**34**	**26827**	**77**	**416420**	**6.85**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**63**	**26827**	**185**	**416420**	**5.29**	**<1x10^{-5}**
Hotspots	**blood**	**GM12878**	**hotspots**	**1.00x10^{-8}**	**25**	**48944**	**33**	**416420**	**6.45**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**37**	**29563**	**77**	**416420**	**6.77**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**70**	**29563**	**185**	**416420**	**5.33**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**48**	**21743**	**185**	**416420**	**4.97**	**<1x10^{-5}**
Hotspots	skin	NHEK	hotspots	1.00x10^{-8}	25	54667	33	416420	5.77	<1x10^{-5}
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**30**	**23266**	**77**	**416420**	**6.97**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**54**	**23266**	**185**	**416420**	**5.22**	**<1x10^{-5}**
Hotspots	**blood**	**CD14_Primary_Cells**	**hotspots**	**1.00x10^{-8}**	**18**	**25266**	**33**	**416420**	**8.99**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-7}**	**20**	**23015**	**44**	**416420**	**8.22**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**32**	**23015**	**77**	**416420**	**7.52**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**53**	**23015**	**185**	**416420**	**5.18**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**35**	**32550**	**77**	**416420**	**5.82**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**65**	**32550**	**185**	**416420**	**4.49**	**<1x10^{-5}**
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**34**	**31827**	**77**	**416420**	**5.78**	**<1x10^{-5}**
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**63**	**31827**	**185**	**416420**	**4.46**	**<1x10^{-5}**
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**55**	**25240**	**185**	**416420**	**4.90**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-8}**	**20**	**29263**	**33**	**416420**	**8.62**	**<1x10^{-5}**
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**35**	**32330**	**77**	**416420**	**5.85**	**<1x10^{-5}**
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**67**	**32330**	**185**	**416420**	**4.66**	**<1x10^{-5}**
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-8}**	**20**	**26827**	**33**	**416420**	**9.41**	**<1x10^{-5}**
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**28**	**24478**	**77**	**416420**	**6.19**	**<1x10^{-5}**
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**58**	**24478**	**185**	**416420**	**5.33**	**<1x10^{-5}**

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p* -value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Hotspots	**blood**	**CD19_Primary_Cells**	**hotspots**	**1.00x10^{-8}**	**20**	**29563**	**33**	**416420**	**8.54**	**1x10^{-5}**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00x10^{-7}**	**19**	**19993**	**44**	**416420**	**8.99**	**1x10^{-5}**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**28**	**19993**	**77**	**416420**	**7.57**	**<1x10^{-5}**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**50**	**19993**	**185**	**416420**	**5.63**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-8}**	**19**	**23266**	**33**	**416420**	**10.31**	**<1x10^{-5}**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00x10^{-7}**	**24**	**29207**	**44**	**416420**	**7.78**	**<1x10^{-5}**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**35**	**29207**	**77**	**416420**	**6.48**	**<1x10^{-5}**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**64**	**29207**	**185**	**416420**	**4.93**	**<1x10^{-5}**
Hotspots	**blood**	**CD3_Primary_Cells**	**hotspots**	**1.00x10^{-8}**	**19**	**23015**	**33**	**416420**	**10.42**	**<1x10^{-5}**
Hotspots	**blood**	**CD8_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**63**	**34836**	**185**	**416420**	**4.07**	**1x10^{-5}**
Hotspots	**blood**	**CD8_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**35**	**29057**	**77**	**416420**	**6.51**	**<1x10^{-5}**
Hotspots	**blood**	**CD8_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**61**	**29057**	**185**	**416420**	**4.73**	**<1x10^{-5}**
Hotspots	**blood**	**CD8_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**44**	**20073**	**185**	**416420**	**4.93**	**<1x10^{-5}**
Hotspots	fetal_intestine,_large	Fetal_Intestine_Large	hotspots	1.00x10^{-5}	50	23662	185	416420	4.76	1x10^{-5}
Hotspots	fetal_intestine,_small	Fetal_Intestine_Small	hotspots	1.00x10^{-5}	57	29749	185	416420	4.31	1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-5}	63	36246	185	416420	3.91	1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-5}	61	32612	185	416420	4.21	<1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-5}	70	39616	185	416420	3.98	<1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-5}	60	30296	185	416420	4.46	1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-6}	42	54453	77	416420	4.17	1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-5}	83	54453	185	416420	3.43	<1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-5}	57	30261	185	416420	4.24	1x10^{-5}
Hotspots	fetal_thymus	Fetal_Thymus	hotspots	1.00x10^{-5}	62	31293	185	416420	4.46	<1x10^{-5}
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00x10^{-8}**	**20**	**32330**	**33**	**416420**	**7.81**	**1x10^{-5}**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00x10^{-6}**	**33**	**29265**	**77**	**416420**	**6.10**	**<1x10^{-5}**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**61**	**29265**	**185**	**416420**	**4.69**	**<1x10^{-5}**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00x10^{-5}**	**62**	**29841**	**185**	**416420**	**4.68**	**<1x10^{-5}**

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p*-value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**56**	**27683**	**185**	**416420**	**4.55**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**60**	**30862**	**185**	**416420**	**4.38**	**1×10^{-5}**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**56**	**27484**	**185**	**416420**	**4.59**	**1×10^{-5}**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**57**	**29125**	**185**	**416420**	**4.41**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**64**	**33460**	**185**	**416420**	**4.31**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**56**	**28055**	**185**	**416420**	**4.49**	**1×10^{-5}**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-6}**	**37**	**33693**	**77**	**416420**	**5.94**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**68**	**33693**	**185**	**416420**	**4.54**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD4_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**66**	**32526**	**185**	**416420**	**4.57**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD4_Primary_Cells**	**hotspots**	**1.00×10^{-6}**	**34**	**28888**	**77**	**416420**	**6.37**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD4_Primary_Cells**	**hotspots**	**1.00×10^{-5}**	**67**	**28888**	**185**	**416420**	**5.22**	**$<1\times10^{-5}$**
Hotspots	fibroblast	Penis_Foreskin_Fibroblast_Primary_Cells	hotspots	1.00×10^{-5}	64	34505	185	416420	4.18	$<1\times10^{-5}$
Hotspots	**blood**	**CD4_Primary_Cells**	**hotspots**	**1.00×10^{-8}**	**19**	**24478**	**33**	**416420**	**9.79**	**$<1\times10^{-5}$**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00×10^{-8}**	**18**	**19993**	**33**	**416420**	**11.36**	**$<1\times10^{-5}$**
Hotspots	**blood**	**CD56_Primary_Cells**	**hotspots**	**1.00×10^{-8}**	**20**	**29207**	**33**	**416420**	**8.64**	**$<1\times10^{-5}$**
Hotspots	**blood**	**CD8_Primary_Cells**	**hotspots**	**1.00×10^{-8}**	**21**	**34836**	**33**	**416420**	**7.61**	**$<1\times10^{-5}$**
Hotspots	**blood**	**Mobilized_CD34_Primary_Cells**	**hotspots**	**1.00×10^{-8}**	**20**	**29265**	**33**	**416420**	**8.62**	**$<1\times10^{-5}$**
Peaks	blood	Adult_CD4+	peaks	1.00×10^{-6}	25	14172	77	416420	9.54	$<1\times10^{-5}$
Peaks	blood	CD34+	peaks	1.00×10^{-5}	37	11477	185	416420	7.26	$<1\times10^{-5}$
Peaks	blood	GM06990	peaks	1.00×10^{-7}	14	6433	44	416420	20.60	$<1\times10^{-5}$
Peaks	blood	GM06990	peaks	1.00×10^{-6}	18	6433	77	416420	15.13	$<1\times10^{-5}$
Peaks	blood	GM06990	peaks	1.00×10^{-5}	25	6433	185	416420	8.75	1×10^{-5}
Peaks	blood	GM12864	peaks	1.00×10^{-7}	16	9447	44	416420	16.03	$<1\times10^{-5}$
Peaks	blood	GM12864	peaks	1.00×10^{-6}	22	9447	77	416420	12.59	$<1\times10^{-5}$
Peaks	blood	GM12864	peaks	1.00×10^{-5}	33	9447	185	416420	7.86	$<1\times10^{-5}$
Peaks	blood	GM12865	peaks	1.00×10^{-7}	15	9994	44	416420	14.20	$<1\times10^{-5}$
Peaks	blood	GM12865	peaks	1.00×10^{-6}	21	9994	77	416420	11.36	$<1\times10^{-5}$

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p*-value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Peaks	blood	GM12865	peaks	$1.00x10^{-5}$	37	9994	185	416420	8.33	$<1x10^{-5}$
Peaks	blood	GM12878	peaks	$1.00x10^{-7}$	16	11758	44	416420	12.88	$1x10^{-5}$
Peaks	blood	GM12878	peaks	$1.00x10^{-6}$	25	11758	77	416420	11.50	$<1x10^{-5}$
Peaks	blood	GM12878	peaks	$1.00x10^{-5}$	39	11758	185	416420	7.47	$<1x10^{-5}$
Peaks	muscle	HSMM	peaks	$1.00x10^{-5}$	46	19514	185	416420	5.31	$1x10^{-5}$
Peaks	blood	Th1	peaks	$1.00x10^{-6}$	28	20674	77	416420	7.32	$<1x10^{-5}$
Peaks	blood	Th1	peaks	$1.00x10^{-5}$	51	20674	185	416420	5.55	$<1x10^{-5}$
Peaks	blood	Th2	peaks	$1.00x10^{-7}$	13	6321	44	416420	19.46	$<1x10^{-5}$
Peaks	blood	Th2	peaks	$1.00x10^{-6}$	17	6321	77	416420	14.54	$<1x10^{-5}$
Peaks	blood	Th2	peaks	$1.00x10^{-5}$	30	6321	185	416420	10.68	$<1x10^{-5}$
Peaks	blood	NB4	peaks	$1.00x10^{-5}$	32	10199	185	416420	7.06	$<1x10^{-5}$
Peaks	blood	GM18507	peaks	$1.00x10^{-5}$	28	8266	185	416420	7.62	$<1x10^{-5}$
Peaks	blood	GM19240	peaks	$1.00x10^{-5}$	35	12816	185	416420	6.15	$<1x10^{-5}$
Peaks	blood	CD19_Primary_Cells	peaks	$1.00x10^{-6}$	18	7245	77	416420	13.44	$<1x10^{-5}$
Peaks	blood	CD19_Primary_Cells	peaks	$1.00x10^{-5}$	27	7245	185	416420	8.39	$1x10^{-5}$
Peaks	blood	CD19_Primary_Cells	peaks	$1.00x10^{-7}$	12	6714	44	416420	16.92	$<1x10^{-5}$
Peaks	blood	CD19_Primary_Cells	peaks	$1.00x10^{-6}$	15	6714	77	416420	12.08	$1x10^{-5}$
Peaks	blood	CD19_Primary_Cells	peaks	$1.00x10^{-5}$	26	6714	185	416420	8.72	$<1x10^{-5}$
Peaks	blood	CD3_Primary_Cells	peaks	$1.00x10^{-5}$	23	5453	185	416420	9.49	$<1x10^{-5}$
Peaks	blood	CD3_Primary_Cells	peaks	$1.00x10^{-5}$	24	6742	185	416420	8.01	$<1x10^{-5}$
Peaks	blood	CD4_Primary_Cells	peaks	$1.00x10^{-5}$	29	8035	185	416420	8.12	$<1x10^{-5}$
Peaks	blood	CD4_Primary_Cells	peaks	$1.00x10^{-6}$	17	6777	77	416420	13.57	$<1x10^{-5}$
Peaks	blood	CD4_Primary_Cells	peaks	$1.00x10^{-5}$	33	6777	185	416420	10.96	$<1x10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	$1.00x10^{-7}$	14	7274	44	416420	18.22	$<1x10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	$1.00x10^{-6}$	19	7274	77	416420	14.13	$<1x10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	$1.00x10^{-5}$	31	7274	185	416420	9.59	$<1x10^{-5}$

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p* -value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Peaks	blood	GM06990	peaks	1.00×10^{-8}	13	6433	33	416420	25.50	$<1 \times 10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	1.00×10^{-7}	12	6194	44	416420	18.34	$<1 \times 10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	1.00×10^{-6}	16	6194	77	416420	13.97	$<1 \times 10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	1.00×10^{-5}	29	6194	185	416420	10.54	$<1 \times 10^{-5}$
Peaks	blood	CD8_Primary_Cells	peaks	1.00×10^{-5}	28	6932	185	416420	9.09	$<1 \times 10^{-5}$
Peaks	blood	CD8_Primary_Cells	peaks	1.00×10^{-6}	15	6315	77	416420	12.85	1×10^{-5}
Peaks	blood	CD8_Primary_Cells	peaks	1.00×10^{-5}	27	6315	185	416420	9.62	$<1 \times 10^{-5}$
Peaks	fetal_thymus	Fetal_Thymus	peaks	1.00×10^{-5}	32	10298	185	416420	6.99	$<1 \times 10^{-5}$
Peaks	fetal_thymus	Fetal_Thymus	peaks	1.00×10^{-5}	29	8423	185	416420	7.75	$<1 \times 10^{-5}$
Peaks	fetal_thymus	Fetal_Thymus	peaks	1.00×10^{-5}	36	12321	185	416420	6.58	$<1 \times 10^{-5}$
Peaks	fetal_thymus	Fetal_Thymus	peaks	1.00×10^{-5}	38	13853	185	416420	6.17	$<1 \times 10^{-5}$
Peaks	fetal_thymus	Fetal_Thymus	peaks	1.00×10^{-5}	29	8908	185	416420	7.33	$<1 \times 10^{-5}$
Peaks	blood	Mobilized_CD34_Primary_Cells	peaks	1.00×10^{-5}	35	11515	185	416420	6.84	$<1 \times 10^{-5}$
Peaks	blood	GM12864	peaks	1.00×10^{-8}	15	9447	33	416420	20.04	$<1 \times 10^{-5}$
Peaks	blood	Mobilized_CD34_Primary_Cells	peaks	1.00×10^{-5}	34	10057	185	416420	7.61	$<1 \times 10^{-5}$
Peaks	blood	Mobilized_CD4_Primary_Cells	peaks	1.00×10^{-5}	30	7522	185	416420	8.98	$<1 \times 10^{-5}$
Peaks	blood	Mobilized_CD4_Primary_Cells	peaks	1.00×10^{-5}	29	6695	185	416420	9.75	$<1 \times 10^{-5}$
Peaks	blood	Mobilized_CD56_Primary_Cells	peaks	1.00×10^{-6}	17	8145	77	416420	11.29	1×10^{-5}
Peaks	blood	Mobilized_CD56_Primary_Cells	peaks	1.00×10^{-5}	34	8145	185	416420	9.40	$<1 \times 10^{-5}$
Peaks	blood	Mobilized_CD8_Primary_Cells	peaks	1.00×10^{-5}	29	7508	185	416420	8.69	$<1 \times 10^{-5}$
Peaks	fibroblast	Penis_Foreskin_Fibroblast_Primary_Cells	peaks	1.00×10^{-5}	43	16952	185	416420	5.71	$<1 \times 10^{-5}$
Peaks	blood	GM12865	peaks	1.00×10^{-8}	14	9994	33	416420	17.68	$<1 \times 10^{-5}$
Peaks	blood	GM12878	peaks	1.00×10^{-8}	15	11758	33	416420	16.10	$<1 \times 10^{-5}$
Peaks	blood	Th2	peaks	1.00×10^{-8}	12	6321	33	416420	23.96	$<1 \times 10^{-5}$
Peaks	blood	CD19_Primary_Cells	peaks	1.00×10^{-8}	11	7245	33	416420	19.16	$<1 \times 10^{-5}$
Peaks	blood	CD19_Primary_Cells	peaks	1.00×10^{-8}	12	6714	33	416420	22.55	$<1 \times 10^{-5}$

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p* -value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S3. Continues

Category[a]	Tissue	Cell type	Type	PThresh[b]	NAnnotThesh[c]	Nannot[d]	Nthresh[e]	N (LD-pruned variants)[f]	FE	EmpPval
Peaks	blood	CD4_Primary_Cells	peaks	$1.00x10^{-8}$	11	8035	33	416420	17.28	$1x10^{-5}$
Peaks	blood	CD4_Primary_Cells	peaks	$1.00x10^{-8}$	12	6777	33	416420	22.34	$<1x10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	$1.00x10^{-8}$	13	7274	33	416420	22.55	$<1x10^{-5}$
Peaks	blood	CD56_Primary_Cells	peaks	$1.00x10^{-8}$	11	6194	33	416420	22.41	$<1x10^{-5}$
Peaks	blood	Mobilized_CD34_Primary_Cells	peaks	$1.00x10^{-8}$	12	10057	33	416420	15.06	$1x10^{-5}$
TFBS	blood	GM12878	tfbs	$1.00x10^{-8}$	19	19650	33	416420	12.20	$<1x10^{-5}$
TFBS	blood	GM12878	tfbs	$1.00x10^{-7}$	20	19650	44	416420	9.63	$1x10^{-5}$
TFBS	blood	GM12878	tfbs	$1.00x10^{-6}$	31	19650	77	416420	8.53	$<1x10^{-5}$
TFBS	blood	GM12878	tfbs	$1.00x10^{-5}$	51	19650	185	416420	5.84	$<1x10^{-5}$

[a] Functional categories from the Encode and Roadmap Epigenomics.

[b] Meta-analysis threshold.

[c] Number of LD-pruned annotated variants passing the meta-analysis threshold.

[d] Number of LD-pruned annotated variants in the reference dataset UK10K project.

[e] Number of LD-pruned variants passing the meta-analysis threshold.

[f] Number of LD-pruned variants in the reference dataset UK10K project.

LD: Linkage disequilibrium; FE: fold enrichment; EmpPval: empirical *p* -value. In boldface the enriched Hotspots in the repertoire of immune cell lines present in blood.

Table S4. Cis-eQTL *in-silico* analysis of the associated variants in the meta-analysis.

Chr	Position[a]	SNP	Allele	Tissue*	Gene*	max *p*- value*	min *p*- value*
1	67802371	rs6659932	C	nervous_system,blood	*SERBP1,IL12RB2*	$3.26x10^{-06}$	$3.72x10^{-11}$
1	114303808	rs6679677	A	blood	*PTPN22*	$4.84x10^{-10}$	$4.84x10^{-11}$
1	114377568	rs2476601	G	blood	*PTPN22*	$3.35x10^{-10}$	$3.36x10^{-10}$
1	114433946	rs1217393	A	blood_vessels,brain,gi_tract,muscle,testis,thyroid,blood	*AP4B1,AP4B1-AS1,HIPK1,PHTF1,PTPN22,RSBN1*	$5.10x10^{-04}$	$1.76x10^{-12}$
2	191564757	rs744600	T	gi_tract,heart,muscle,testis,cell_lines	*HIBCH,NAB1,TMEM194B*	$1.48x10^{-05}$	$1.30x10^{-34}$
2	191933283	rs13389408	C	muscle,blood	*GLS*	$2.97x10^{-07}$	$3.42x10^{-09}$
3	58183636	rs35677470	A	muscle,nervous_system	*PXK,RP11-802O23.3,RP11-359I18.5*	$1.13x10^{-05}$	$2.27x10^{-08}$
3	160312921	rs112846137	T	blood_vessels	*SMC4*	$1.19x10^{-06}$	$1.19x10^{-06}$
4	965720	rs13101828	G	gi_tract,heart,lung,muscle,nervous_system,pancreas,	*DGKQ,IDUA,SLC26A1,FGFRL1*	$6.49x10^{-06}$	$2.01x10^{-67}$
5	150438477	rs4958880	A	blood	*TNIP1*	$1.09x10^{-03}$	$1.09x10^{-03}$
7	128589633	rs10954214	T	blood_vessels,gi_tract,nervous_system,thyroid,blood,cell_lines	*IRF5*	$1.71x10^{-05}$	$7.54x10^{-31}$
7	129007888	rs13238352	T	cell_lines	*IRF5*	$6.22x10^{-06}$	$2.88x10^{-13}$
8	11484371	rs2736337	C	Testis,thyroid,blood	RP11-148O21,RP11-148O21.6,AF131215.9,AF131215.2	$4.14x10^{-06}$	$3.06x10^{-51}$
11	633689	rs7929541	C	adipose_tissue,blood_vessels,brain,breast,cell_lines,gi_tract, Heart,lung,muscle, Pancreas,skin,testis,thyroid,blood	*HRAS,TMEM80,EPS8L2,DRD4,PHRF1, EFCAB4A, RNH1*	$9.20x10^{-06}$	$2.24x10^{-13}$
12	112871372	rs11066301	G	skin	*ALDH2*	$3.44x10^{-10}$	$3.44x10^{-10}$
19	10462513	rs11085725	T	skin,blood,cell_lines	*TYK2 ,PDE4A*	$1.04x10^{-05}$	$2.16x10^{-06}$
19	50121274	rs76246107	A	lung,testis	*ALDH16A1,PIH1D1*	$6.45x10^{-06}$	$3.37x10^{-07}$
22	21985094	rs5754467	G	adipose_tissue,blood_vessels,brain,cell_lines,gi_tract,heart, Lung,nervous_system,pancreas,skin,blood	*CCDC116,KB-1440D3.14,UBE2L3*	$7.86x10^{-06}$	$8.42x10^{-17}$

[a] According to NCBI build GRCh37/hg19.

*Data sources: Lappalainen *Nature* 2013; Westra *Nature Genet* 2013, Ramasamy *Nature Neurosci* 2014, GTeX *Science* 2015

Table S5. Promoter CaptureHiC data for the twenty six independent variants associated at a genome-wide significance level in the meta-analysis

SNP	Interacting gene[a]	Cell type[b]	Clasification[c]	References
rs6659932	*IL12RB2*	GM12878	eQTL	Mifsud et al. Nat Genet. 2015; 47:598-606
rs6679677	*PTPN22* *HIPK1* *RSBN1* *PHTF1*	CD34/GM12878	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606
rs2476601	*HIPK1*	Macrophages Monocytes Naive and total B Naive and total CD4 Naive and total CD8 Neutrophils	eQTL	Javierre et al. Cell. 2016; 167:1369-1384.e19
		CD34		Mifsud et al.Nat Genet. 2015; 47:598-606
	AP4B1	CD34		
	PTPN22 *AP4B1* *RSBN1* *PHTF1* *HIPK1*	GM12878		Mifsud et al.Nat Genet. 2015; 47:598-606
rs1217393	*AP4B1* *HIPK1* *PTPN22* *RSBN1*	CD34/GM12878	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606
rs2422345	*SLC9C2*	GM12878	PUTATIVE CANDIDATES	Mifsud et al.Nat Genet. 2015; 47:598-606
rs17849502	*ARPC5/RGL1*	Neutrophils	PUTATIVE CANDIDATES	Javierre et al. Cell. 2016; 167:1369-1384.e19
	DHX9 *SMG7* *NMNAT2* *LAMC2* *DHX9* *TSEN15* *RGL1/APOBEC4* *ARPC5/RGL1*	GM12878		Mifsud et al.Nat Genet. 2015; 47:598-606
rs744600	***GLS***	**GM12878**	**eQTL**	**Mifsud et al.Nat Genet. 2015; 47:598-606**
rs13389408	*STAT4*	Naive and Total CD4 Naive and Total CD8	PUTATIVE CANDIDATES	Javierre et al. Cell. 2016; 167:1369-1384.e19

[a] Gene whose promoter interacts physically with the associated variant and overlap with eQTL signals.

[b] Cell type where this interaction has been observed according to Capture HiC plotter (*Schofield, Bioinformatics 2016*).

[c] Clasification according to its overlap with eQTL signals or proposal of the genes as new putative candidate locus related with the diseases.

In boldface the new associated SNPs interacting with potential new relevant candidates.

Table S5. Continues

SNP	Interacting gene[a]	Cell type[b]	Clasification[c]	References
rs10174238	*NABP1*	TOTAL CD8, CD4	PUTATIVE CANDIDATES	Javierre et al. Cell. 2016; 167:1369-1384.e19
	STAT4	CD34/GM12878		Mifsud et al.Nat Genet. 2015; 47:598-606
	MYO1B			
	NABP1	GM12878	PUTATIVE CANDIDATES	Mifsud et al.Nat Genet. 2015; 47:598-606
	SDPR			
	MFSD6			
rs35677470	*PXK*	GM12878	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606
rs112846137	***ARL14/KPNA4***	**CD34/GM12878**	**PUTATIVE CANDIDATES**	**Mifsud et al.Nat Genet. 2015; 47:598-606**
rs13101828	***MYL5***	**Fetal thymus**	**PUTATIVE CANDIDATES**	**Javierre et al. Cell. 2016; 167:1369-1384.e19**
	GAK	**CD8**		
	MYL5/MFSD7	**GM12878**		**Mifsud et al.Nat Genet. 2015; 47:598-606**
	PCGF3			
	GAK			
rs4958880	*TNIP1*	Endothelial precursors	eQTL	Javierre et al. Cell. 2016; 167:1369-1384.e19
		Macrophages		
		Monocytes		
		Neutrophils		
		GM12878		Mifsud et al.Nat Genet. 2015; 47:598-606
rs2431098	*MIR146A*	CD34/GM12878	PUTATIVE CANDIDATES	Mifsud et al.Nat Genet. 2015; 47:598-606
	ATP10B	GM12878		
rs802791	*PRDM1*	CD34	PUTATIVE CANDIDATES	Mifsud et al.Nat Genet. 2015; 47:598-606
rs58721818	*TNFAIP3*	CD34	PUTATIVE CANDIDATES	Mifsud et al.Nat Genet. 2015; 47:598-606
rs193107685	***LIMK1***	**CD34/GM12878**	**PUTATIVE CANDIDATES**	**Mifsud et al.Nat Genet. 2015; 47:598-606**
rs10954214	*TNPO3*	CD34/GM12878	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606
rs13238352	*TNPO3*	GM12878	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606
	TNPO3	CD34		
	IRF5			
rs2736337	*FAM167A*	CD34/GM12878	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606
	BLK			
	BLK	Endothelial precursors		Javierre et al. Cell. 2016; 167:1369-1384.e19
		Fetal thymus		
	FAM167A	Fetal thymus		
		Macrophages		
	BLK	Naive B		
		Naive CD4		

[a] Gene whose promoter interacts physically with the associated variant and overlap with eQTL signals.

[b] Cell type where this interaction has been observed according to Capture HiC plotter (*Schofield, Bioinformatics 2016*).

[c] Clasification according to its overlap with eQTL signals or proposal of the genes as new putative candidate locus related with the diseases.

In boldface the new associated SNPs interacting with potential new relevant candidates.

Table S5. Continues

SNP	**Interacting gene**[a]	**Cell type**[b]	**Clasification**[c]	**References**
rs2736337	*BLK*	Naive CD8 Total B cells Total CD4 Total CD8	eQTL	Javierre et al. Cell. 2016; 167:1369-1384.e19
rs7929541	*TMEM80*	Monocytes Naive CD4 Naive CD8 Total B cells Total CD4 Total CD8	eQTL	Javierre et al. Cell. 2016; 167:1369-1384.e19
rs11066301	*PTPN11*	CD34/GM12878	PUTATIVE CANDIDATES	Mifsud et al.Nat Genet. 2015; 47:598-606
rs35929052	*IRF8*	CD34/GM12878 Total B cells	PUTATIVE CANDIDATES	Mifsud et al.Nat Genet. 2015; 47:598-606 Javierre et al. Cell. 2016; 167:1369-1384.e19
rs11085725	*TYK2*	CD34/GM12878	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606
rs76246107	***NOSIP*** ***SCAF1*** ***PRMT1*** ***BCL2L12/IRF3***	**CD34/GM12878** **GM12878**	**eQTL/PUTATIVE CANDIDATES**	**Mifsud et al.Nat Genet. 2015; 47:598-606**
rs5754467	*UBE2L3*	CD34/GM12878 Total CD4 activated Total CD8 Megakaryocytes Macrophages	eQTL	Mifsud et al.Nat Genet. 2015; 47:598-606 Javierre et al. Cell. 2016; 167:1369-1384.e19

[a] Gene whose promoter interacts physically with the associated variant and overlap with eQTL signals.

[b] Cell type where this interaction has been observed according to Capture HiC plotter (*Schofield, Bioinformatics 2016*).

[c] Clasification according to its overlap with eQTL signals or proposal of the genes as new putative candidate locus related with the diseases.

In boldface the new associated SNPs interacting with potential new relevant candidates.

Table S6. Cis-eQTL gene-products and related proteins according to STRING with their confident score of interaction.

IL12RB2			IL12RB2			IL12RB2			IL12RB2		
node1	**node2**	**score**	**node1**	**node2**	**score**	**node1**	**node2**	**score**	**node1**	**node2**	**score**
IL1B	IL1R1	0.998	IL6ST	STAT3	0.980	IL12RB2	IL4	0.963	STAT4	IL12A	0.947
JAK2	STAT5A	0.998	IL12RB1	STAT4	0.979	STAT3	IFNG	0.963	IL12RB2	IFNG	0.947
JAK2	STAT3	0.996	IL12RB1	IL12B	0.979	STAT1	LCK	0.963	IL12RB1	IFNG	0.947
JAK2	STAT1	0.995	STAT5A	IL4	0.978	STAT1	IL12B	0.961	IL12B	CCL3	0.946
STAT5A	TYK2	0.995	IL12A	IL12RB2	0.978	FOS	IL1B	0.960	FOS	TYK2	0.944
STAT1	TYK2	0.994	IL12RB1	IL12A	0.978	STAT1	STAT3	0.960	GADD45G	GADD45B	0.943
JAK2	STAT6	0.993	IL12B	IFNG	0.978	STAT6	IL12B	0.959	NFKB2	IL1B	0.943
STAT6	IL4	0.993	JAK2	STAT4	0.978	STAT1	IL6ST	0.959	TYK2	IFNG	0.943
CCR5	CCL4	0.991	IL12RB2	IL12B	0.975	STAT3	IL12B	0.957	JAK2	IL1B	0.943
JAK2	SOCS1	0.990	JAK2	IL4	0.975	IL12RB1	STAT1	0.957	IL12A	IL4	0.943
CCR5	CCL3	0.989	SOCS1	STAT6	0.975	CCR5	IL12B	0.957	IL12A	IFNG	0.942
NFKB2	RELB	0.989	FOS	IL4	0.975	STAT1	IL23A	0.956	STAT5A	IL23A	0.941
STAT6	TYK2	0.988	JAK2	FOS	0.975	STAT4	IL23A	0.956	TYK2	IL23A	0.941
IL12RB1	IL23A	0.987	SOCS1	IL4	0.974	JAK2	IL6ST	0.955	IL12RB1	JAK2	0.940
TYK2	STAT3	0.986	SOCS1	IFNG	0.972	STAT5A	FOS	0.954	STAT5A	IL12B	0.940
STAT1	SOCS1	0.986	STAT4	IL12RB2	0.972	FASLG	IL12B	0.954	IL12RB1	STAT5A	0.940
SOCS1	TYK2	0.985	SOCS1	STAT3	0.971	LCK	SOCS1	0.953	STAT4	STAT3	0.940
STAT1	IFNG	0.984	IL12RB2	TBX21	0.970	JAK2	IL12RB2	0.952	CCL4	CCL3	0.940
IFNG	TBX21	0.984	TYK2	IL4	0.970	IL6ST	TYK2	0.951	IL12B	TBX21	0.939
IL1B	IL23A	0.984	IL12RB1	TBX21	0.969	JAK2	CCR5	0.951	STAT1	IL12RB2	0.939
IL12RB1	IL12RB2	0.984	STAT5A	SOCS1	0.969	IL12RB1	STAT6	0.951	STAT1	IL12A	0.939
LCK	STAT3	0.984	STAT4	TYK2	0.969	JAK2	IFNG	0.950	NOS2	TYK2	0.939
STAT3	IL23A	0.982	IL12A	EBI3	0.968	TYK2	IL12RB2	0.950	IL12RB1	IL1R1	0.938
IL12A	IL12B	0.982	STAT5A	STAT3	0.968	IL12RB2	EBI3	0.950	STAT3	IL12RB2	0.938
IFNG	IL23A	0.982	STAT5A	LCK	0.968	STAT5A	IFNG	0.949	IL6ST	EBI3	0.938
IL12RB1	IL4	0.981	STAT1	STAT5A	0.967	IL12RB1	STAT3	0.948	FASLG	FOS	0.938
IL4	IL12B	0.981	IL4	IFNG	0.967	IL12RB1	TYK2	0.948	JAK2	IL23A	0.937
STAT1	TBX21	0.981	STAT4	IFNG	0.964	FOS	IFNG	0.947	IL12A	IL1B	0.937
IL12B	IL23A	0.980	STAT4	IL12B	0.963	IL1B	IL12B	0.947	IL12A	STAT3	0.936
IL12A	TBX21	0.936	JAK2	IL12A	0.925	TYK2	GZMB	0.917	FASLG	IL12RB2	0.908

IL12RB2		
node1	**node2**	**score**
CCL4	IL12B	0.936
STAT1	EBI3	0.935
IL12RB1	CCR5	0.935
NOS2	IL23A	0.934
TYK2	IL12B	0.934
IL6ST	IL12A	0.934
IL12RB1	GZMB	0.933
JAK2	NFKB2	0.933
JAK2	FASLG	0.931
FASLG	STAT5A	0.931
STAT3	EBI3	0.931
NFKB2	TYK2	0.931
JAK2	IL12B	0.930
NOS2	IL12B	0.930
STAT5A	IL6ST	0.930
IL12RB1	SOCS1	0.930
JAK2	NOS2	0.930
JAK2	TBX21	0.929
JAK2	GZMB	0.929
TYK2	TBX21	0.929
EOMES	IFNG	0.928
IFNG	EBI3	0.928
IL6ST	IFNG	0.928
STAT6	IL12RB2	0.928
IL12RB1	EOMES	0.927
IL12RB1	IL1B	0.927
IL12A	STAT6	0.927
IL12B	GZMB	0.927
IL1B	IFNG	0.927
IL12A	CCL3	0.926
IL12RB1	SPHK2	0.900
IL12A	TYK2	0.925
IL6ST	IL12RB2	0.924
IL12RB1	FASLG	0.924
STAT4	EBI3	0.924
TYK2	IL1B	0.924
TYK2	IL1R1	0.924
IL1B	CCL3	0.924
NFKB2	IL12B	0.923
JAK2	IL1R1	0.923
SOCS1	IL12B	0.922
IL1B	IL12RB2	0.922
IL12A	CCL4	0.922
FOS	IL12B	0.922
IL12RB2	GZMB	0.922
IL12RB1	CCL3	0.921
JAK2	CCL3	0.921
STAT4	IL6ST	0.921
IL12RB1	LCK	0.920
EOMES	IL12RB2	0.920
IL12RB2	IL23A	0.920
IL1R1	IL12B	0.920
JAK2	GZMA	0.920
SOCS1	IL12A	0.919
STAT5A	EBI3	0.919
STAT5A	IL12A	0.919
JAK2	RELB	0.919
IL12B	RELB	0.919
STAT5A	IL12RB2	0.918
IL12RB1	NOS2	0.918
IL12A	IL1R1	0.917
TYK2	GADD45G	0.900
CCR5	IL12RB2	0.917
JAK2	EBI3	0.917
IL12A	CCR5	0.917
IL12RB1	CCL4	0.916
IL12RB1	FOS	0.916
JAK2	CCL4	0.916
NOS2	IL12A	0.916
FOS	IL12RB2	0.916
JAK2	GADD45B	0.915
IL12A	GZMB	0.915
IL12RB2	IL1R1	0.914
CCR5	TYK2	0.914
TYK2	EBI3	0.914
IL12RB1	GZMA	0.913
FASLG	TYK2	0.913
SOCS1	IL12RB2	0.913
JAK2	LCK	0.913
TYK2	GADD45B	0.912
IL12B	GADD45B	0.911
IL12A	GADD45B	0.911
TYK2	RELB	0.910
JAK2	TYK2	0.910
IL12RB1	GADD45B	0.910
FASLG	IL12A	0.910
GZMA	IL12B	0.910
JAK2	SPHK2	0.910
GZMA	TYK2	0.909
NFKB2	IL12A	0.909
LCK	TYK2	0.909
TYK2	CCL4	0.908
IL12RB2	RELB	0.900
TYK2	CCL3	0.908
TYK2	SPHK2	0.907
JAK2	EOMES	0.907
IL12RB1	RELB	0.907
IL12RB2	CCL3	0.907
GZMA	IL12RB2	0.907
FOS	IL12A	0.906
LCK	IL12B	0.906
IL4	TBX21	0.905
EOMES	TYK2	0.905
IL12A	RELB	0.905
NOS2	IL12RB2	0.905
IL12RB2	GADD45G	0.904
IL12RB2	GADD45B	0.903
LCK	IL12RB2	0.903
IL12RB2	CCL4	0.902
JAK2	GADD45G	0.902
STAT4	SPHK2	0.902
IL12RB1	GADD45G	0.902
LCK	IL12A	0.901
IL12A	SPHK2	0.900
IL12RB2	SPHK2	0.900
IL12RB1	NFKB2	0.900
IL12A	EOMES	0.900
NFKB2	IL12RB2	0.900
EOMES	IL12B	0.900
IL12A	GZMA	0.900
IL12A	GADD45G	0.900
SPHK2	IL12B	0.900
GADD45G	IL12B	0.900

PTPN22		
node1	node2	score
CD3E	CD3D	0.998
HLA-DRB5	HLA-DRB1	0.996
PTPN22	CSK	0.995
HLA-DRA	HLA-DRB5	0.995
HLA-DRA	HLA-DRB1	0.993
HLA-DPB1	HLA-DPA1	0.992
HLA-DPB1	HLA-DQA2	0.991
CD3G	CD3E	0.991
HLA-DRA	CD4	0.987
PTPN22	LCK	0.984
CD3G	CD3D	0.983
HLA-DRB1	CD4	0.982
LCK	CD4	0.980
HLA-DRB5	CD4	0.980
PTPN22	ZAP70	0.978
LCK	CD3D	0.977
HLA-DRB1	PTPN22	0.973
LCK	ZAP70	0.973
CD3E	LCK	0.972
CD3E	ZAP70	0.971
HLA-DQA2	HLA-DRB1	0.971
CD3D	ZAP70	0.970
HLA-DRB5	HLA-DQA2	0.970
ZAP70	CSK	0.967
CD3G	LCK	0.960
CD3G	ZAP70	0.949
HLA-DQA2	CD4	0.948
ZAP70	CD4	0.947
LCK	CSK	0.945
HLA-DPB1	HLA-DRA	0.945
HLA-DPA1	HLA-DRB1	0.944

PTPN22		
node1	node2	score
HLA-DPA1	HLA-DRB5	0.944
CD3E	CSK	0.938
HLA-DPA1	CD4	0.936
CD3E	PTPN22	0.935
HLA-DPB1	HLA-DRB1	0.933
HLA-DPB1	HLA-DRB5	0.933
CD3E	CD4	0.931
HLA-DQA2	PTPN22	0.931
HLA-DPB1	PTPN22	0.930
HLA-DRB1	LCK	0.920
HLA-DRA	PTPN22	0.920
HLA-DQA2	ZAP70	0.919
CD3G	CD4	0.919
HLA-DRA	CD3D	0.918
HLA-DPB1	CD3D	0.917
CSK	CD4	0.916
CD3D	CD4	0.916
HLA-DRB5	PTPN22	0.914
HLA-DPA1	CD3D	0.913
HLA-DRB1	CD3D	0.913
CD3G	HLA-DPB1	0.913
HLA-DRB1	ZAP70	0.911
HLA-DPB1	CD4	0.911
CD3G	HLA-DRA	0.910
HLA-DRA	LCK	0.910
CD3G	HLA-DRB1	0.910
PTPN22	CD4	0.910
HLA-DPA1	PTPN22	0.910
HLA-DRB5	CD3D	0.909
CD3G	HLA-DRB5	0.908
CD3G	HLA-DPA1	0.908

PTPN22		
node1	node2	score
HLA-DPA1	HLA-DRA	0.907
HLA-DPB1	CD3E	0.906
HLA-DPB1	LCK	0.906
CD3G	HLA-DQA2	0.905
HLA-DRA	CD3E	0.905
HLA-DPB1	ZAP70	0.905
HLA-DRB1	CSK	0.905
CD3E	HLA-DRB1	0.905
HLA-DQA2	CD3D	0.905
CD3G	PTPN22	0.905
CD3G	CSK	0.904
HLA-DRB5	CD3E	0.904
HLA-DRA	HLA-DQA2	0.904
HLA-DPA1	HLA-DQA2	0.903
HLA-DRA	ZAP70	0.903
HLA-DQA2	LCK	0.902
PTPN22	CD3D	0.902
HLA-DRB5	ZAP70	0.901
HLA-DPB1	CSK	0.901
CD3D	CSK	0.901
HLA-DPA1	LCK	0.901
HLA-DQA2	CD3E	0.901
HLA-DRB5	LCK	0.901
HLA-DPA1	CD3E	0.901
HLA-DPA1	ZAP70	0.900
HLA-DRA	CSK	0.900
HLA-DPA1	CSK	0.900
HLA-DQA2	CSK	0.900
HLA-DRB5	CSK	0.900

AP4B1		
node1	node2	score
AP1B1	AP1M2	0.999
AP4E1	AP4S1	0.999
AP1M1	AP1S1	0.999
AP1B1	AP1S1	0.999
AP2A2	AP2S1	0.999
AP2A1	AP2S1	0.999
AP4E1	AP4B1	0.999
AP4M1	AP4S1	0.998
AP4M1	AP4E1	0.998
AP1M1	AP1S2	0.998
DNAJC6	HSPA8	0.998
AP4B1	AP4S1	0.998
AP3S1	AP3B1	0.998
AP1B1	AP1S2	0.997
AP1M1	AP1B1	0.997
AP4M1	AP4B1	0.997
GAK	HSPA8	0.996
AP1M1	AP1G1	0.996
AP1G1	AP1S1	0.995
CLINT1	PICALM	0.995
AP1G1	AP1B1	0.995
AP1G1	AP1S2	0.994
DTNBP1	BLOC1S6	0.992
BLOC1S1	DTNBP1	0.992
NAPA	VAMP7	0.992
AP1G1	AP1M2	0.992
BLOC1S1	BLOC1S6	0.990
AP1G1	AP4B1	0.989
VAMP2	NAPA	0.989
SNX2	SNX5	0.987
PICALM	HIP1R	0.987

AP4B1

node1	node2	score
AP1G1	ARF1	0.987
ARF1	AP4E1	0.986
ARF1	AP4B1	0.986
GAK	HIP1R	0.985
AP4E1	AP3B1	0.985
PICALM	GAK	0.985
AP1S3	ARF1	0.984
AP1B1	ARF1	0.984
AP2A1	AP3S1	0.984
RAB5C	ARF1	0.983
AP2A1	NECAP1	0.983
AP2A2	GAK	0.983
AP1G1	AP3B1	0.982
VAMP8	NAPA	0.982
AP2A2	AP1B1	0.981
VAMP8	VAMP7	0.980
AP2A1	AP1B1	0.980
AP1S1	AP1M2	0.980
SNX9	DNM2	0.980
VAMP2	VAMP7	0.979
AP1B1	AP4E1	0.978
PICALM	PIK3C2A	0.977
PICALM	AP2A1	0.975
CLINT1	HIP1R	0.975
AP1S2	AP1M2	0.975
AP1G1	AP3S1	0.975
TGOLN2	IGF2R	0.975
AP1M1	AP3S1	0.973
AP4B1	AP1M2	0.973
ITSN1	DNM2	0.973
AP1M1	AP4B1	0.973
SNX9	SH3GL2	0.972
AP1M1	AP3B1	0.971
AP1S3	AP1B1	0.971
AP1B1	GAK	0.971
OCRL	AP2A1	0.970
AP1S3	AP1G1	0.970
AP1S2	AP4E1	0.969
AP4M1	AP2A1	0.969
ITSN1	ITSN2	0.969
AP2A1	AP1S1	0.968
AP1S3	AP4E1	0.968
AP1S1	AP4E1	0.968
AP1G1	IGF2R	0.968
AP1M1	AP4E1	0.966
AP4E1	AP1M2	0.966
AP1S3	AP1M2	0.965
AP3B1	AP1M2	0.965
AP2A1	AP4B1	0.965
ARF1	AP3B1	0.965
AP2A1	GAK	0.965
CLINT1	GAK	0.965
DNM2	GAK	0.964
PICALM	DNM2	0.964
DNM2	ITSN2	0.964
CLINT1	AP1G1	0.963
PICALM	VAMP2	0.963
GAK	AP1M2	0.963
GAK	PIK3C2A	0.962
AP1M1	AP2S1	0.961
TGOLN2	TFRC	0.961
TGOLN2	ARF1	0.961
AP1S1	AP3B1	0.960
AP1M1	GAK	0.960
GAK	AP4B1	0.959
AP1M1	AP1S3	0.959
SNX9	SNX2	0.959
AP3S1	AP1M2	0.958
AP1S2	AP3B1	0.958
CLINT1	AP1B1	0.957
ITSN2	AP4B1	0.956
DNM2	HIP1R	0.956
AP1M1	TGOLN2	0.956
IGF2R	AP4E1	0.956
GAK	AP2S1	0.955
AP1S3	AP4B1	0.955
AP1S3	AP3B1	0.955
AP1S2	AP4B1	0.955
AP1S1	AP4B1	0.955
AP3S1	AP4B1	0.955
AP1B1	AP3S1	0.955
AP1M1	ARF1	0.954
AP3S1	AP4E1	0.954
SNX9	SNX5	0.954
AP2A2	PICALM	0.952
ARRB1	AP3B1	0.951
ITSN1	AP1B1	0.951
SH3GL2	DNM2	0.951
AP1B1	ITSN2	0.951
AP2A2	AP1S1	0.951
ITSN1	AP4B1	0.951
BLOC1S1	SNX2	0.950
VAMP2	HSPA8	0.949
AP2A2	AP4M1	0.949
AP2A2	AP2A1	0.948
AP2A1	HIP1R	0.948
AP2A1	ITSN2	0.947
AP2A1	DNM2	0.947
ITSN1	AP2A1	0.947
TFRC	IGF2R	0.947
AP2A2	ITSN1	0.947
AP2A2	ITSN2	0.947
CLINT1	AP4E1	0.946
ARF1	AP1M2	0.944
PICALM	ITSN2	0.944
TFRC	ARF1	0.943
SNX2	IGF2R	0.943
AP1G1	AP4M1	0.943
PICALM	ITSN1	0.942
TFRC	VAMP2	0.942
TFRC	DNM2	0.942
DTNBP1	AP3B1	0.941
CLINT1	RAB5C	0.941
TXNDC5	HSPA8	0.941
PICALM	SH3GL2	0.941
AP1S1	ARF1	0.941
AP2A2	AP4B1	0.941
AP3B1	BLOC1S6	0.940
SH3GL2	AP2A1	0.940
AP2A2	OCRL	0.940
BLOC1S1	VAMP2	0.940
DNM2	HSPA8	0.940
CLINT1	AP4B1	0.939
SNX2	RAB5C	0.939

	AP4B1	
node1	**node2**	**score**
VAMP2	VAMP8	0.939
ARRB1	AP1B1	0.939
AP2A2	DNAJC6	0.938
PICALM	VAMP7	0.938
SNX2	VAMP7	0.938
DNM2	ARF1	0.938
ARRB1	AP2A1	0.938
TGOLN2	AP1M2	0.937
GAK	AP3B1	0.937
DNAJC6	DNM2	0.937
RAB5C	NAPA	0.937
TFRC	VAMP7	0.937
VAMP2	ARF1	0.936
SNX9	OCRL	0.936
RAB5C	VAMP7	0.936
AP1B1	AP2S1	0.935
TGOLN2	SNX2	0.935
CLINT1	NECAP1	0.935
OCRL	AP2S1	0.935
TGOLN2	VAMP2	0.935
VAMP2	BLOC1S6	0.934
TGOLN2	DNM2	0.934
AP1S1	AP1S2	0.934
YIPF6	TBC1D8B	0.934
SNX2	DNM2	0.933
PICALM	AP4B1	0.933
AP1G1	NECAP1	0.933
DNM2	VAMP2	0.933
TGOLN2	VAMP7	0.932
VAMP8	HIP1R	0.932
CLINT1	DNAJC6	0.932
OCRL	HIP1R	0.932
IGF2R	ARF1	0.932
AP1G1	OCRL	0.931
TFRC	HSPA8	0.931
OCRL	AP4E1	0.931
VAMP2	HIP1R	0.931
YIPF6	OCRL	0.931
DNM2	RAB5C	0.931
TGOLN2	CPD	0.931
AP4B1	AP3B1	0.930
ITSN1	HIP1R	0.930
NECAP1	GAK	0.930
AP1M1	AP1M2	0.930
AP1M1	PICALM	0.929
ITSN2	HIP1R	0.929
PICALM	AP1B1	0.929
AP2S1	AP4B1	0.929
AP1S2	GAK	0.928
TFRC	VAMP8	0.928
AP3S1	GAK	0.928
AP1B1	AP3B1	0.928
AP1S3	GAK	0.928
AP1S1	GAK	0.928
DNM2	AP4B1	0.927
OCRL	ARF1	0.927
DNAJC6	HIP1R	0.927
TXNDC5	GAK	0.926
PICALM	AP1M2	0.926
ARRB1	AP4B1	0.926
HIP1R	AP1M2	0.926
SH3GL2	OCRL	0.926
ARF1	VAMP7	0.926
ARF1	VAMP8	0.926
TGOLN2	VAMP8	0.926
IGF2R	CPD	0.925
RAB5C	HIP1R	0.925
DTNBP1	VAMP2	0.925
CLINT1	AP3B1	0.925
OCRL	PIK3C2A	0.925
AP1B1	DNM2	0.925
CLINT1	VAMP7	0.924
SNX5	IGF2R	0.924
DNAJC6	AP2A1	0.924
VAMP7	AP3B1	0.924
ARF1	PIK3C2A	0.924
PICALM	IGF2R	0.924
SNX2	VAMP8	0.924
TFRC	RAB5C	0.924
AP1G1	DNM2	0.923
SNX2	TFRC	0.923
CLINT1	PIK3C2A	0.923
TBC1D8B	AP3B1	0.923
DNAJC6	TXNDC5	0.923
ARRB1	DNM2	0.922
SH3GL2	VAMP2	0.922
IGF2R	DNM2	0.922
PICALM	AP3B1	0.922
SNX2	PIK3C2A	0.922
SNX2	HIP1R	0.921
ITSN1	PIK3C2A	0.921
ITSN2	PIK3C2A	0.921
DNAJC6	TFRC	0.921
DNAJC6	SNX9	0.921
AP1M1	HIP1R	0.921
SNX2	AP3B1	0.920
ITSN2	GAK	0.920
DNM2	VAMP8	0.920
ITSN1	GAK	0.920
OCRL	AP3B1	0.920
AP2A2	DNM2	0.920
AP1G1	AP4E1	0.919
CLINT1	OCRL	0.919
OCRL	AP1B1	0.919
ARRB1	TFRC	0.919
PICALM	NECAP1	0.919
DNM2	VAMP7	0.919
CLINT1	TFRC	0.919
CLINT1	AP1M1	0.919
OCRL	AP4B1	0.919
PICALM	VAMP8	0.919
ITSN1	TFRC	0.919
NECAP1	ARF1	0.919
OCRL	TFRC	0.919
DNM2	AP3B1	0.919
DNM2	AP1M2	0.918
DNM2	AP4E1	0.918
IGF2R	AP3B1	0.918
SNX2	ARF1	0.918
TBC1D8B	BLOC1S6	0.918
ARF1	HIP1R	0.918
CLINT1	SNX2	0.918
SH3GL2	TFRC	0.918
DNAJC6	SH3GL2	0.918

AP4B1		
node1	**node2**	**score**
AP1M1	DNM2	0.918
RAB5C	VAMP8	0.917
OCRL	ITSN2	0.917
GAK	ARF1	0.917
SNX9	PIK3C2A	0.917
AP2A2	SH3GL2	0.917
CLINT1	AP1M2	0.917
ITSN1	OCRL	0.917
TFRC	HIP1R	0.917
OCRL	TBC1D8B	0.917
AP1M2	HSPA8	0.917
DNM2	PIK3C2A	0.917
SNX9	ITSN1	0.916
DNAJC6	PICALM	0.916
AP1M1	TBC1D8B	0.916
SNX9	HIP1R	0.916
TGOLN2	NECAP1	0.916
NECAP1	AP1M2	0.916
TBC1D8B	GAK	0.916
TBC1D8B	ARF1	0.916
DNAJC6	ITSN1	0.916
IGF2R	VAMP7	0.916
DNAJC6	NECAP1	0.916
TGOLN2	AP3B1	0.916
AP2A1	HSPA8	0.915
TGOLN2	SNX5	0.915
IGF2R	RAB5C	0.915
SH3GL2	NECAP1	0.915
AP4M1	AP1B1	0.915
DTNBP1	AP3S1	0.915
AP1G1	HIP1R	0.915

AP4B1		
node1	**node2**	**score**
DNAJC6	IGF2R	0.915
CLINT1	SNX9	0.915
YIPF6	ARF1	0.915
ARRB1	DNAJC6	0.915
AP1M1	DNAJC6	0.915
SNX2	VAMP2	0.914
SNX2	AP3S1	0.914
AP3S1	ARF1	0.914
AP1B1	AP4B1	0.914
AP2A2	NECAP1	0.914
AP1S2	VAMP7	0.914
TBC1D8B	RAB5C	0.914
IGF2R	GAK	0.914
TFRC	GAK	0.914
AP1M1	HSPA8	0.914
AP1S1	AP2S1	0.914
CLINT1	HSPA8	0.914
IGF2R	VAMP8	0.914
DNAJC6	AP1M2	0.914
SNX9	GAK	0.914
CLINT1	PUM1	0.914
PICALM	OCRL	0.914
BLOC1S1	VAMP7	0.914
OCRL	IGF2R	0.914
AP3S1	VAMP7	0.913
PUM1	AP1G1	0.913
SNX9	TFRC	0.913
VAMP7	AP4B1	0.913
SNX9	IGF2R	0.913
DNAJC6	AP3B1	0.913
AP4E1	HIP1R	0.913

AP4B1		
node1	**node2**	**score**
ITSN1	VAMP2	0.913
DTNBP1	VAMP7	0.913
GAK	AP4E1	0.913
TGOLN2	AP1G1	0.913
PICALM	AP2S1	0.913
TXNDC5	ARF1	0.913
AP1G1	PICALM	0.913
AP2A2	HIP1R	0.913
RAB5C	VAMP2	0.913
ITSN1	SH3GL2	0.913
SNX5	TFRC	0.913
AP2A2	AP3S1	0.913
VAMP8	AP3B1	0.913
DNAJC6	ITSN2	0.913
PUM1	PIK3C2A	0.913
YIPF6	RAB5C	0.913
AP2A1	VAMP2	0.913
IGF2R	BLOC1S6	0.913
PUM1	TBC1D8B	0.912
AP1G1	TBC1D8B	0.912
TFRC	CPD	0.912
IGF2R	ITSN2	0.912
PICALM	AP4E1	0.912
TGOLN2	HSPA8	0.912
IGF2R	VAMP2	0.912
CLINT1	AP1S2	0.912
SNX9	AP1M2	0.912
AP1M1	IGF2R	0.912
NECAP1	VAMP7	0.912
TGOLN2	ITSN2	0.912
AP1S3	HIP1R	0.912

AP4B1		
node1	**node2**	**score**
BLOC1S1	RAB5C	0.912
AP1G1	SNX2	0.912
AP1S2	ARF1	0.912
TGOLN2	AP1S1	0.912
AP2A1	AP1S2	0.912
AP1M1	SNX9	0.912
SNX2	GAK	0.912
AP2A2	AP1S2	0.912
CLINT1	VAMP8	0.911
TGOLN2	DNAJC6	0.911
IGF2R	HSPA8	0.911
PICALM	CPD	0.911
SH3GL2	ARF1	0.911
SNX5	HIP1R	0.911
SNX9	ITSN2	0.911
TFRC	AP1M2	0.911
YIPF6	AP1S2	0.911
AP1G1	AP2S1	0.911
TPD52L1	PIK3C2A	0.911
HIP1R	HSPA8	0.911
SNX5	ARF1	0.911
TGOLN2	AP2S1	0.911
TBC1D8B	VAMP2	0.910
DNAJC6	AP4B1	0.910
PUM1	HSPA8	0.910
SNX9	NECAP1	0.910
VAMP2	AP1M2	0.910
ITSN2	VAMP2	0.910
ITSN1	VAMP8	0.910
AP1G1	GAK	0.910
TBC1D8B	NECAP1	0.910

AP4B1		
node1	**node2**	**score**
TGOLN2	PICALM	0.910
PUM1	AP3B1	0.910
SH3GL2	HSPA8	0.910
AP1G1	BLOC1S6	0.910
PICALM	BLOC1S6	0.910
SNX5	VAMP8	0.910
SNX2	AP4E1	0.910
CLINT1	AP3S1	0.910
TBC1D8B	VAMP8	0.910
AP1B1	TBC1D8B	0.910
AP1B1	RAB5C	0.910
VAMP7	AP4E1	0.910
ITSN2	VAMP8	0.910
IGF2R	NECAP1	0.910
ITSN1	NECAP1	0.910
AP1G1	VAMP7	0.910
DNAJC6	GAK	0.910
YIPF6	VAMP7	0.910
VAMP7	HIP1R	0.910
IGF2R	AP4B1	0.909
SH3GL2	GAK	0.909
AP2A1	VAMP8	0.909
RAB5C	AP2S1	0.909
VAMP2	AP3B1	0.909
PUM1	TGOLN2	0.909
AP1B1	VAMP7	0.909
VAMP8	AP4B1	0.909
TFRC	PIK3C2A	0.909
SNX2	TBC1D8B	0.909
AP1G1	CPD	0.909
SNX9	ARF1	0.909

AP4B1		
node1	**node2**	**score**
VAMP7	BLOC1S6	0.909
ARRB1	TGOLN2	0.909
PUM1	GAK	0.909
CLINT1	VAMP2	0.909
AP1M1	RAB5C	0.909
AP1B1	VAMP2	0.909
AP1B1	VAMP8	0.909
DTNBP1	VAMP8	0.909
VAMP2	AP4B1	0.909
VAMP7	HSPA8	0.909
RAB5C	AP1M2	0.909
SNX2	AP1M2	0.909
BLOC1S1	AP3B1	0.909
DNAJC6	SNX2	0.909
TXNDC5	DNM2	0.909
RAB5C	PIK3C2A	0.909
AP1M1	SNX2	0.909
AP1G1	PIK3C2A	0.909
PIK3C2A	AP4E1	0.909
CLINT1	TGOLN2	0.908
PIK3C2A	CPD	0.908
TBC1D8B	AP4E1	0.908
AP2S1	VAMP7	0.908
NAPA	AP1M2	0.908
AP1M1	NECAP1	0.908
SNX2	BLOC1S6	0.908
YIPF6	VAMP2	0.908
OCRL	RAB5C	0.908
SNX2	AP4B1	0.908
AP2A2	ARRB1	0.908
TGOLN2	BLOC1S6	0.908

AP4B1		
node1	**node2**	**score**
YIPF6	VAMP8	0.908
YIPF6	SNX2	0.908
AP1M1	NAPA	0.908
AP1S3	VAMP7	0.908
TGOLN2	OCRL	0.908
YIPF6	AP3B1	0.908
VAMP7	CPD	0.908
AP2A2	VAMP8	0.908
OCRL	DNM2	0.908
TPD52L1	VAMP2	0.908
DNAJC6	AP2S1	0.908
ITSN2	VAMP7	0.908
OCRL	VAMP2	0.908
TFRC	NECAP1	0.908
DNAJC6	VAMP2	0.908
RAB5C	AP1S1	0.908
AP1S1	VAMP7	0.908
NAPA	HSPA8	0.908
AP2A2	VAMP2	0.908
SNX2	AP1S2	0.907
TGOLN2	AP4B1	0.907
VAMP8	AP1M2	0.907
OCRL	GAK	0.907
SNX9	HSPA8	0.907
PUM1	SNX2	0.907
PUM1	CPD	0.907
PICALM	TFRC	0.907
CLINT1	IGF2R	0.907
TXNDC5	VAMP2	0.907
TGOLN2	AP4E1	0.907
HSPA8	CPD	0.907

AP4B1		
node1	**node2**	**score**
RAB5C	AP4B1	0.907
TBC1D8B	VAMP7	0.907
TBC1D8B	DNM2	0.907
ARRB1	ARF1	0.907
AP1M1	VAMP2	0.907
TXNDC5	DTNBP1	0.907
AP4B1	HIP1R	0.907
AP1M1	VAMP8	0.907
AP1S2	VAMP2	0.907
AP1B1	HSPA8	0.907
TXNDC5	VAMP8	0.907
TFRC	DTNBP1	0.907
PICALM	HSPA8	0.907
SNX2	AP1S1	0.907
SNX5	VAMP7	0.907
AP3B1	CPD	0.907
AP1B1	HIP1R	0.907
AP1M1	TFRC	0.907
TXNDC5	VAMP7	0.907
PIK3C2A	AP3B1	0.907
AP3B1	HIP1R	0.907
GAK	NAPA	0.907
AP3S1	BLOC1S6	0.906
AP2A2	PIK3C2A	0.906
SH3GL2	AP4B1	0.906
AP1M1	OCRL	0.906
TXNDC5	AP4E1	0.906
TFRC	TBC1D8B	0.906
TGOLN2	GAK	0.906
YIPF6	PIK3C2A	0.906
AP1G1	TXNDC5	0.906

	AP4B1	
node1	**node2**	**score**
PUM1	AP4B1	0.906
PUM1	DNAJC6	0.906
PICALM	SNX2	0.906
ITSN1	RAB5C	0.906
AP4E1	BLOC1S6	0.906
TBC1D8B	IGF2R	0.906
AP4B1	HSPA8	0.906
DNAJC6	TBC1D8B	0.906
AP1G1	RAB5C	0.906
TGOLN2	RAB5C	0.906
PUM1	IGF2R	0.906
RAB5C	AP3S1	0.906
DNM2	AP2S1	0.906
NECAP1	AP3B1	0.906
DNAJC6	AP4E1	0.906
NECAP1	HIP1R	0.906
AP4B1	BLOC1S6	0.906
ITSN2	RAB5C	0.906
PUM1	AP4E1	0.906
RAB5C	AP3B1	0.906
AP3S1	HIP1R	0.906
AP1M1	SNX5	0.906
GAK	CPD	0.906
SNX9	AP4B1	0.906
SNX5	AP1M2	0.906
TXNDC5	PIK3C2A	0.906
AP2A1	PIK3C2A	0.906
IGF2R	HIP1R	0.906
TBC1D8B	AP4B1	0.906
GAK	VAMP2	0.906
GAK	VAMP8	0.906

	AP4B1	
node1	**node2**	**score**
OCRL	AP1M2	0.906
SNX2	NAPA	0.906
SH3GL2	ITSN2	0.906
TXNDC5	RAB5C	0.906
ITSN1	AP2S1	0.906
PIK3C2A	HIP1R	0.905
AP2A1	RAB5C	0.905
PUM1	VAMP7	0.905
SNX9	VAMP2	0.905
OCRL	NAPA	0.905
TGOLN2	PIK3C2A	0.905
AP2A2	RAB5C	0.905
OCRL	VAMP8	0.905
TBC1D8B	PIK3C2A	0.905
AP1S1	VAMP2	0.905
TGOLN2	SNX9	0.905
OCRL	NECAP1	0.905
YIPF6	AP1B1	0.905
ITSN2	NECAP1	0.905
CPD	BLOC1S6	0.905
YIPF6	AP1M2	0.905
AP3S1	VAMP8	0.905
VAMP8	AP2S1	0.905
PIK3C2A	VAMP8	0.905
AP1M1	VAMP7	0.905
AP1B1	NECAP1	0.905
RAB5C	HSPA8	0.905
PUM1	PICALM	0.905
SNX5	DNM2	0.905
AP1S3	VAMP8	0.905
YIPF6	PUM1	0.905

	AP4B1	
node1	**node2**	**score**
NECAP1	VAMP2	0.905
PIK3C2A	VAMP7	0.905
RAB5C	GAK	0.905
OCRL	VAMP7	0.905
ARRB1	TBC1D8B	0.905
AP1S2	VAMP8	0.905
RAB5C	AP4E1	0.905
SNX2	OCRL	0.905
VAMP2	PIK3C2A	0.905
NAPA	CPD	0.905
VAMP7	AP1M2	0.905
PIK3C2A	HSPA8	0.905
YIPF6	AP1M1	0.905
VAMP8	HSPA8	0.905
PICALM	AP1S2	0.905
AP1S3	VAMP2	0.905
AP4E1	CPD	0.905
YIPF6	PICALM	0.905
AP1S1	VAMP8	0.905
AP3S1	VAMP2	0.905
PICALM	TBC1D8B	0.905
DNAJC6	AP1B1	0.905
YIPF6	AP4B1	0.905
VAMP2	AP2S1	0.905
ARRB1	HSPA8	0.904
TFRC	AP4B1	0.904
AP2A2	VAMP7	0.904
IGF2R	AP1M2	0.904
AP1M1	PIK3C2A	0.904
PIK3C2A	AP1M2	0.904
DTNBP1	GAK	0.904

	AP4B1	
node1	**node2**	**score**
DNAJC6	VAMP8	0.904
PUM1	AP1S2	0.904
IGF2R	AP1S2	0.904
SNX5	BLOC1S6	0.904
AP2A1	AP3B1	0.904
SNX9	AP4E1	0.904
PICALM	ARF1	0.904
SH3GL2	AP1B1	0.904
TBC1D8B	CPD	0.904
VAMP2	CPD	0.904
VAMP8	CPD	0.904
TXNDC5	AP1M2	0.904
PICALM	RAB5C	0.904
NECAP1	AP4B1	0.904
YIPF6	AP1G1	0.904
NAPA	AP4B1	0.904
SNX9	AP1B1	0.904
ITSN2	AP2S1	0.904
SNX2	AP1B1	0.904
DNM2	AP1S2	0.904
PUM1	NECAP1	0.904
SNX2	HSPA8	0.904
TFRC	ITSN2	0.904
PICALM	AP3S1	0.904
AP3S1	NAPA	0.904
DNAJC6	PIK3C2A	0.904
RAB5C	AP1S2	0.904
SH3GL2	AP2S1	0.904
AP2A1	VAMP7	0.904
SNX5	TBC1D8B	0.904
AP2A2	HSPA8	0.904

	AP4B1	
node1	**node2**	**score**
AP1S1	HSPA8	0.904
DNAJC6	OCRL	0.904
DNAJC6	AP3S1	0.904
ARRB1	HIP1R	0.904
AP1S2	HSPA8	0.904
AP1B1	NAPA	0.904
AP1M2	CPD	0.904
TPD52L1	HSPA8	0.904
TGOLN2	SH3GL2	0.904
TBC1D8B	HSPA8	0.904
SNX2	CPD	0.903
AP1S3	OCRL	0.903
AP1M1	TXNDC5	0.903
PUM1	AP1M1	0.903
AP1S3	HSPA8	0.903
YIPF6	CPD	0.903
TXNDC5	AP3S1	0.903
PUM1	TFRC	0.903
SH3GL2	VAMP8	0.903
OCRL	AP3S1	0.903
AP1S1	HIP1R	0.903
TXNDC5	SNX5	0.903
SNX9	RAB5C	0.903
SH3GL2	HIP1R	0.903
CLINT1	SNX5	0.903
PICALM	DTNBP1	0.903
SH3GL2	VAMP7	0.903
YIPF6	AP4E1	0.903
IGF2R	AP2S1	0.903
OCRL	AP1S2	0.903
OCRL	AP1S1	0.903

	AP4B1	
node1	**node2**	**score**
ITSN1	HSPA8	0.903
YIPF6	AP1S1	0.903
TFRC	AP1S1	0.903
AP1S3	NAPA	0.903
AP1S2	HIP1R	0.903
NAPA	AP3B1	0.903
AP1S3	RAB5C	0.903
YIPF6	AP1S3	0.903
YIPF6	BLOC1S6	0.903
AP3S1	AP2S1	0.903
PIK3C2A	AP2S1	0.903
BLOC1S1	NECAP1	0.903
TFRC	NAPA	0.903
TBC1D8B	NAPA	0.903
TPD52L1	IGF2R	0.903
CLINT1	TBC1D8B	0.903
AP1S1	AP3S1	0.903
IGF2R	PIK3C2A	0.903
TGOLN2	HIP1R	0.903
AP1S2	BLOC1S6	0.903
DNAJC6	RAB5C	0.903
TGOLN2	TBC1D8B	0.903
ARRB1	CPD	0.903
TGOLN2	AP1S2	0.903
TBC1D8B	HIP1R	0.903
AP1S1	NAPA	0.903
PIK3C2A	BLOC1S6	0.903
YIPF6	TGOLN2	0.903
AP2A1	IGF2R	0.903
SNX5	HSPA8	0.903
GAK	VAMP7	0.903

	AP4B1	
node1	**node2**	**score**
TPD52L1	TFRC	0.903
AP1S2	NAPA	0.903
TXNDC5	OCRL	0.903
DNM2	AP1S1	0.902
TPD52L1	SNX2	0.902
ARRB1	SNX2	0.902
SNX5	AP1B1	0.902
AP1S3	SNX2	0.902
SNX9	AP3B1	0.902
TBC1D8B	AP1M2	0.902
PICALM	SNX9	0.902
YIPF6	IGF2R	0.902
AP1G1	VAMP2	0.902
SH3GL2	SNX2	0.902
AP3B1	HSPA8	0.902
PUM1	AP1B1	0.902
PIK3C2A	AP4B1	0.902
SNX5	VAMP2	0.902
CLINT1	AP1S1	0.902
SH3GL2	AP1M2	0.902
SNX5	AP4E1	0.902
SNX9	VAMP8	0.902
OCRL	HSPA8	0.902
TPD52L1	TGOLN2	0.902
SNX5	PIK3C2A	0.902
NAPA	HIP1R	0.902
SNX5	CPD	0.902
ARRB1	OCRL	0.902
PUM1	HIP1R	0.902
PIK3C2A	NAPA	0.902
TFRC	AP1B1	0.902

	AP4B1	
node1	**node2**	**score**
ARRB1	RAB5C	0.902
AP2A2	SNX9	0.902
DNM2	CPD	0.902
AP2S1	HIP1R	0.902
CLINT1	AP1S3	0.902
AP1S3	PICALM	0.902
AP1G1	SNX9	0.902
AP1S3	DNM2	0.902
YIPF6	AP3S1	0.902
AP1M1	SH3GL2	0.902
AP1S2	AP3S1	0.902
PUM1	AP1M2	0.902
DNM2	AP3S1	0.902
TXNDC5	HIP1R	0.902
AP1G1	VAMP8	0.902
SNX5	AP4B1	0.902
TXNDC5	TFRC	0.902
AP1B1	PIK3C2A	0.902
PICALM	AP1S1	0.902
DNAJC6	DTNBP1	0.902
TXNDC5	SNX2	0.902
ARRB1	SH3GL2	0.902
PICALM	NAPA	0.902
SNX9	TXNDC5	0.902
IGF2R	AP1S1	0.902
SNX5	RAB5C	0.902
DNAJC6	NAPA	0.902
VAMP2	AP4E1	0.902
TFRC	AP3B1	0.902
NECAP1	HSPA8	0.902
ITSN1	VAMP7	0.902

AP4B1		
node1	**node2**	**score**
ARRB1	ITSN1	0.902
VAMP8	AP4E1	0.902
SNX5	OCRL	0.902
CLINT1	ARRB1	0.902
SNX5	AP1S2	0.901
AP1G1	SH3GL2	0.901
DNAJC6	AP1S1	0.901
RAB5C	CPD	0.901
AP1B1	DTNBP1	0.901
ARRB1	ITSN2	0.901
PUM1	VAMP8	0.901
SNX2	NECAP1	0.901
ARRB1	GAK	0.901
ARRB1	PIK3C2A	0.901
TPD52L1	AP1S2	0.901
NECAP1	VAMP8	0.901
YIPF6	NAPA	0.901
DTNBP1	HIP1R	0.901
TXNDC5	NAPA	0.901
TPD52L1	ARF1	0.901
ARRB1	AP1M2	0.901
NAPA	AP4E1	0.901
TBC1D8B	AP1S2	0.901
TPD52L1	VAMP7	0.901
AP4B1	CPD	0.901
AP1B1	CPD	0.901
NECAP1	AP1S1	0.901
NECAP1	AP2S1	0.901
ARRB1	PICALM	0.901
TXNDC5	IGF2R	0.901
PUM1	RAB5C	0.901
YIPF6	GAK	0.901
TXNDC5	AP1B1	0.901
ARRB1	IGF2R	0.901
TXNDC5	TBC1D8B	0.901
TPD52L1	VAMP8	0.901
BLOC1S1	AP1S1	0.901
ARRB1	VAMP8	0.901
DNAJC6	CPD	0.901
AP1G1	HSPA8	0.901
SH3GL2	CPD	0.901
AP3S1	HSPA8	0.901
AP1S3	SNX5	0.901
TPD52L1	DNM2	0.901
PUM1	AP1S1	0.901
AP1G1	NAPA	0.901
SNX5	AP1S1	0.901
ARRB1	SNX9	0.901
RAB5C	NECAP1	0.901
DNAJC6	AP1S2	0.901
TFRC	AP2A1	0.901
AP1S3	AP3S1	0.901
AP1G1	SNX5	0.901
NECAP1	AP3S1	0.901
YIPF6	NECAP1	0.901
AP1S3	NECAP1	0.901
SNX9	VAMP7	0.901
AP1S3	TXNDC5	0.901
TGOLN2	DTNBP1	0.901
TXNDC5	AP4B1	0.901
YIPF6	HSPA8	0.901
RAB5C	DTNBP1	0.901
BLOC1S1	AP3S1	0.901
TXNDC5	AP3B1	0.901
SH3GL2	AP1S2	0.901
ARRB1	AP1G1	0.901
BLOC1S1	AP1S2	0.901
TPD52L1	CPD	0.901
TXNDC5	AP1S2	0.901
PUM1	OCRL	0.901
DNAJC6	VAMP7	0.901
SH3GL2	AP3B1	0.901
SNX5	AP3S1	0.901
SH3GL2	RAB5C	0.901
PUM1	VAMP2	0.901
BLOC1S1	VAMP8	0.901
PUM1	AP1S3	0.901
ARRB1	VAMP2	0.901
SNX5	AP3B1	0.901
AP1B1	BLOC1S6	0.901
BLOC1S1	AP1S3	0.901
SH3GL2	AP4E1	0.901
SH3GL2	AP1S1	0.901
AP1S3	DNAJC6	0.901
TXNDC5	AP1S1	0.901
VAMP8	BLOC1S6	0.901
TPD52L1	NECAP1	0.901
AP2A2	TFRC	0.901
DNM2	NECAP1	0.901
AP1M1	CPD	0.901
OCRL	DTNBP1	0.901
AP2S1	HSPA8	0.901
NECAP1	AP1S2	0.901
TPD52L1	NAPA	0.901
ARRB1	AP1M1	0.901
ARRB1	PUM1	0.901
DNAJC6	AP1G1	0.901
AP1S3	AP1S1	0.900
TPD52L1	GAK	0.900
TPD52L1	AP1B1	0.900
TPD52L1	PICALM	0.900
SNX9	AP3S1	0.900
PUM1	AP3S1	0.900
AP1S1	CPD	0.900
BLOC1S1	GAK	0.900
AP2A2	TGOLN2	0.900
AP1G1	TFRC	0.900
ARRB1	NAPA	0.900
BLOC1S1	AP4B1	0.900
PUM1	SNX9	0.900
DTNBP1	CPD	0.900
TPD52L1	AP4E1	0.900
DTNBP1	AP4B1	0.900
TPD52L1	PUM1	0.900
DTNBP1	PIK3C2A	0.900
AP1G1	DTNBP1	0.900
BLOC1S1	HSPA8	0.900
ARRB1	SNX5	0.900
SH3GL2	PIK3C2A	0.900
TPD52L1	SNX9	0.900
TPD52L1	ARRB1	0.900
BLOC1S1	IGF2R	0.900
SNX9	TBC1D8B	0.900
NECAP1	DTNBP1	0.900

	AP4B1	
node1	**node2**	**score**
AP1S3	IGF2R	0.900
TPD52L1	AP1M2	0.900
NECAP1	AP4E1	0.900
ARF1	CPD	0.900
IGF2R	NAPA	0.900
SNX5	NAPA	0.900
RAB5C	BLOC1S6	0.900
AP3S1	CPD	0.900
AP1S3	CPD	0.900
IGF2R	DTNBP1	0.900
AP1B1	IGF2R	0.900
BLOC1S1	TFRC	0.900
TFRC	BLOC1S6	0.900
YIPF6	HIP1R	0.900
NECAP1	NAPA	0.900
TPD52L1	OCRL	0.900
SNX9	AP2S1	0.900
BLOC1S1	SH3GL2	0.900
TGOLN2	TXNDC5	0.900
PICALM	SNX5	0.900
AP1S3	DTNBP1	0.900
HIP1R	BLOC1S6	0.900
TPD52L1	AP1M1	0.900
BLOC1S1	TGOLN2	0.900
SNX9	NAPA	0.900
SNX2	DTNBP1	0.900
TPD52L1	TXNDC5	0.900
DTNBP1	NAPA	0.900
BLOC1S1	DNM2	0.900
BLOC1S1	ARF1	0.900
TBC1D8B	DTNBP1	0.900

	AP4B1	
node1	**node2**	**score**
AP1S1	PIK3C2A	0.900
SNX9	AP1S1	0.900
TPD52L1	RAB5C	0.900
AP1S3	TFRC	0.900
AP1S3	BLOC1S6	0.900
NECAP1	CPD	0.900
BLOC1S1	TBC1D8B	0.900
DNAJC6	SNX5	0.900
BLOC1S1	AP1M1	0.900
PUM1	SNX5	0.900
ARRB1	VAMP7	0.900
ARRB1	NECAP1	0.900
DNAJC6	BLOC1S6	0.900
TPD52L1	YIPF6	0.900
TPD52L1	AP3B1	0.900
SNX5	DTNBP1	0.900
TFRC	AP1S2	0.900
NECAP1	BLOC1S6	0.900
AP4E1	HSPA8	0.900
BLOC1S1	AP1B1	0.900
DTNBP1	AP4E1	0.900
AP1M1	DTNBP1	0.900
ARRB1	AP4E1	0.900
AP1S1	BLOC1S6	0.900
AP3S1	PIK3C2A	0.900
BLOC1S1	CPD	0.900
SNX5	NECAP1	0.900
AP1S3	AP1S2	0.900
BLOC1S1	OCRL	0.900
TXNDC5	NECAP1	0.900
BLOC1S1	AP1G1	0.900

	AP4B1	
node1	**node2**	**score**
NAPA	BLOC1S6	0.900
TPD52L1	AP4B1	0.900
SH3GL2	SNX5	0.900
YIPF6	DNAJC6	0.900
DTNBP1	AP1M2	0.900
YIPF6	SNX9	0.900
YIPF6	TXNDC5	0.900
BLOC1S1	SNX5	0.900
AP1S3	TBC1D8B	0.900
BLOC1S1	PICALM	0.900
NECAP1	PIK3C2A	0.900
IGF2R	AP3S1	0.900
ITSN2	HSPA8	0.900
ARRB1	TXNDC5	0.900
TGOLN2	NAPA	0.900
TFRC	AP4E1	0.900
TBC1D8B	AP3S1	0.900
TFRC	AP3S1	0.900
SNX9	DTNBP1	0.900
ARRB1	AP1S3	0.900
TPD52L1	DTNBP1	0.900
ARRB1	BLOC1S6	0.900
YIPF6	DTNBP1	0.900
TPD52L1	AP1G1	0.900
TPD52L1	AP3S1	0.900
SH3GL2	AP3S1	0.900
AP2A2	IGF2R	0.900
SNX9	AP1S2	0.900
YIPF6	TFRC	0.900
BLOC1S1	TXNDC5	0.900
PICALM	TXNDC5	0.900

	AP4B1	
node1	**node2**	**score**
GAK	BLOC1S6	0.900
TGOLN2	ITSN1	0.900
TBC1D8B	AP1S1	0.900
CLINT1	CPD	0.900
TPD52L1	TBC1D8B	0.900
AP1S3	PIK3C2A	0.900
ITSN1	IGF2R	0.900
SNX9	CPD	0.900
BLOC1S1	SNX9	0.900
TXNDC5	BLOC1S6	0.900
TPD52L1	SNX5	0.900
DTNBP1	AP1S1	0.900
DTNBP1	HSPA8	0.900
SH3GL2	TBC1D8B	0.900
TPD52L1	HIP1R	0.900
TGOLN2	AP3S1	0.900
SNX5	GAK	0.900
DTNBP1	AP1S2	0.900
TGOLN2	AP1S3	0.900
BLOC1S1	HIP1R	0.900
ARRB1	AP1S1	0.900
ARRB1	AP1S2	0.900
YIPF6	SNX5	0.900
YIPF6	SH3GL2	0.900
HSPA8	BLOC1S6	0.900
YIPF6	DNM2	0.900
AP1S3	SH3GL2	0.900
CLINT1	YIPF6	0.900
AP1M2	BLOC1S6	0.900
ARRB1	AP3S1	0.900
BLOC1S1	ARRB1	0.900

AP4B1		
node1	**node2**	**score**
SH3GL2	TXNDC5	0.900
AP1S2	CPD	0.900
YIPF6	ARRB1	0.900
TGOLN2	AP2A1	0.900
TXNDC5	CPD	0.900
HIP1R	CPD	0.900
SNX9	AP2A1	0.900
OCRL	CPD	0.900
BLOC1S1	AP1M2	0.900
OCRL	BLOC1S6	0.900
TFRC	AP2S1	0.900
ARRB1	DTNBP1	0.900
SNX9	BLOC1S6	0.900
BLOC1S1	TPD52L1	0.900
BLOC1S1	AP4E1	0.900
TPD52L1	DNAJC6	0.900
TPD52L1	BLOC1S6	0.900
AP1S3	SNX9	0.900
BLOC1S1	YIPF6	0.900
SH3GL2	IGF2R	0.900
TPD52L1	AP1S3	0.900
TPD52L1	AP1S1	0.900
TPD52L1	SH3GL2	0.900
TGOLN2	AP1B1	0.900
BLOC1S1	DNAJC6	0.900
AP1S2	PIK3C2A	0.900
AP1M1	BLOC1S6	0.900
BLOC1S1	PIK3C2A	0.900
TPD52L1	CLINT1	0.900
ARRB1	AP2S1	0.900
BLOC1S1	NAPA	0.900

HIPK1		
node1	**node2**	**score**
GATA4	NKX2-5	0.996
NPPA	NKX2-5	0.977
HIPK1	TP53	0.975
NPPA	GATA4	0.949
HIPK1	NKX2-5	0.933
HIPK1	GATA4	0.905
NPPA	HIPK1	0.900

RSBN1		
node1	**node2**	**score**
SPATA12	RSBN1	0.535
C7orf26	RSBN1	0.479
LEMD3	RSBN1	0.410
PRKACA	RSBN1	0.407

HIBCH1		
node1	**node2**	**score**
ACAT1	EHHADH	0.999
HADHA	ACAT1	0.999
ACACA	ACACB	0.999
HADH	ECHS1	0.998
ACADM	EHHADH	0.997
ACADM	HADHA	0.996
HADHA	ACADVL	0.996
HADH	ACAT1	0.994
ACADVL	EHHADH	0.994
HIBCH	HIBADH	0.992
ACACA	ACAT1	0.991
ACACB	ACAT1	0.990
HADHA	EHHADH	0.990
ACADM	ACAT1	0.988
ACADM	ECHS1	0.982
ECHS1	ACADVL	0.978
HADH	EHHADH	0.977
HADH	HIBCH	0.977
HADHA	ECHS1	0.974
ACADM	HADH	0.974
HADH	HADHA	0.974
ECHS1	EHHADH	0.971
HIBCH	EHHADH	0.969
HADHA	HIBCH	0.968
ACACA	EHHADH	0.964
HADHA	ACACB	0.963
ACACB	EHHADH	0.962
HADHA	ACACA	0.961
HIBCH	ACADVL	0.944
HIBADH	EHHADH	0.943
ECHS1	HIBCH	0.930

HIBCH1

node1	node2	score
ECHS1	ACACB	0.915
ACADM	HIBCH	0.913
ECHS1	ACAT1	0.913
ACADM	ACACB	0.912
ACADM	ACACA	0.911
ECHS1	ACACA	0.909
ACADVL	ACACB	0.909
ACADVL	ACACA	0.907
HADH	HIBADH	0.905
HIBCH	ACACB	0.903
HIBCH	ACACA	0.903
HIBCH	ACAT1	0.901

NAB1

node1	node2	score
NAB1	EGR1	0.860
EGR4	NAB1	0.782
EGR4	BCKDHB	0.764
NAB1	BCKDHB	0.732
NAB1	EGR3	0.727
BCKDHB	EGR3	0.700

GLS

node1	node2	score
CPS1	CAD	0.999
GFPT1	CAD	0.998
CAD	GFPT2	0.996
CAD	PPAT	0.994
GAD1	GLUL	0.983
GLUL	GAD2	0.983
GLUL	CAD	0.979
CPS1	GLUL	0.976
GLS	GLUL	0.976
GLUL	GLUD1	0.974
GLUD2	GAD2	0.955
GAD1	GLUD2	0.955
CAD	GAD2	0.954
GAD1	CAD	0.954
GLUD2	GLUL	0.952
CPS1	GLUD1	0.949
GLUD1	GAD2	0.948
GAD1	GLUD1	0.948
CPS1	GLUD2	0.947
GLS	GLUD1	0.945
GLS	GGT1	0.944
GAD1	GAD2	0.943
GFPT1	GLUL	0.942
GLUL	PPAT	0.940
GAD1	GLS	0.940
GLUL	ALDH4A1	0.938
ALDH4A1	GLUD1	0.936
GLUD2	ALDH4A1	0.935
GLS	GAD2	0.934
GLS	CAD	0.934
GLS	PPAT	0.933

GLS

node1	node2	score
ALDH4A1	GAD2	0.929
GLUL	GFPT2	0.929
GAD1	ALDH4A1	0.928
CPS1	GLS	0.928
GFPT1	GLS	0.925
GLUD2	GLS	0.923
GAD2	GGT1	0.922
GAD1	GGT1	0.921
GLS	GFPT2	0.920
GLUD2	GLUD1	0.919
GLS	ALDH4A1	0.918
GFPT1	PPAT	0.913
PPAT	GFPT2	0.913

PXK		
node1	**node2**	**score**
PHRF1	PXK	0.780
PHRF1	FAM167A	0.709
PXK	FAM167A	0.704

DGKQ		
node1	**node2**	**score**
DGAT1	MOGAT3	0.994
MOGAT1	DGAT1	0.991
DGAT1	DGAT2	0.991
DGAT1	MOGAT2	0.991
AGPAT1	MBOAT2	0.980
PNPLA2	DGAT1	0.977
AGPAT2	MBOAT2	0.975
LIPF	PNLIP	0.972
CDS1	AGPAT5	0.971
AGPAT4	CDS1	0.971
CEL	PNLIP	0.968
LCLAT1	CDS1	0.968
CDS2	LCLAT1	0.967
CDS2	AGPAT5	0.966
PNPLA2	DGAT2	0.965
CDS2	AGPAT3	0.965
AGPAT2	CDS1	0.965
CDS2	AGPAT4	0.965
CDS2	AGPAT2	0.963
CDS1	AGPAT3	0.963
AGPAT1	CDS1	0.962
CDS2	AGPAT1	0.961
CDS2	PLD2	0.956
CDS1	PLD2	0.956
PLD1	CDS1	0.956
PNPLA2	LPL	0.956
CDS2	PLD1	0.956
CEPT1	PLD1	0.955
LIPF	MOGAT3	0.948
MOGAT1	LIPF	0.948
LIPF	DGAT2	0.948
LIPF	MOGAT2	0.948
CEL	PNLIPRP1	0.946
PLD1	CHPT1	0.946
CEPT1	PLD2	0.945
DGKQ	PLCB2	0.945
PLD2	CHPT1	0.944
PLCB3	DGKQ	0.944
MBOAT2	PLD2	0.944
DGAT2	PNPLA3	0.943
PLCB4	DGKQ	0.943
PLCB1	DGKQ	0.943
AGPAT1	MBOAT1	0.942
CEL	LPL	0.940
AGPAT1	LCLAT1	0.939
AGPAT2	MBOAT1	0.938
PLCG2	PLCG1	0.938
DGAT1	PNPLA3	0.938
CEPT1	MBOAT2	0.937
AGPAT4	MBOAT2	0.936
DGKQ	PLCE1	0.934
PLD2	EPT1	0.933
PLD1	EPT1	0.933
AGPAT2	LCLAT1	0.932
AGPAT1	AGPAT3	0.932
PLD3	PLD2	0.932
DGKQ	PLD2	0.932
PLCD1	DGKQ	0.931
MBOAT2	EPT1	0.931
AGPAT1	AGPAT4	0.931
AGPAT1	AGPAT5	0.930
CEL	LIPG	0.929
PLCD3	DGKQ	0.928
LPL	PNPLA3	0.928
PLCB1	PLCG1	0.928
MBOAT2	AGPAT5	0.927
PLCD4	DGKQ	0.927
AGPAT2	AGPAT3	0.926
AGPAT2	PLD2	0.926
CEPT1	MBOAT1	0.926
PLD1	MBOAT2	0.926
PLD3	PLD1	0.926
MBOAT1	EPT1	0.926
AGPAT2	AGPAT4	0.925
LIPF	DGAT1	0.925
PLD1	MBOAT1	0.925
PLD4	PLD2	0.925
MBOAT1	PLD2	0.925
PLD1	AGPAT4	0.924
PLD1	AGPAT5	0.924
AGPAT1	PLD2	0.924
PNLIP	DGAT1	0.924
PLCG2	PLCB2	0.923
PLCB2	PLCG1	0.923
MOGAT3	MOGAT2	0.922
AGPAT2	AGPAT5	0.922
PLCG2	PLCB1	0.921
AGPAT3	PLD2	0.921
AGPAT4	PLD2	0.921
MBOAT2	CDS1	0.921
AGPAT2	PLD1	0.920
PLD1	AGPAT3	0.920
LCLAT1	PLD2	0.919

DGKQ		
node1	**node2**	**score**
PLD1	AGPAT1	0.919
MOGAT3	PNPLA3	0.919
AGPAT5	PLD2	0.919
MBOAT2	AGPAT3	0.919
PLD1	LCLAT1	0.919
PNPLA3	MOGAT2	0.919
CDS2	MBOAT2	0.918
PLCD1	PLCG1	0.918
PLCE1	PLCG1	0.917
PNLIP	MOGAT3	0.917
PNLIP	MOGAT2	0.917
PNLIP	PNPLA2	0.917
PLCB3	PLCG1	0.916
PNLIP	LIPG	0.916
PLCG2	PLCB3	0.916
PLCG2	PLCE1	0.916
PNLIP	DGAT2	0.916
PNLIPRP1	LPL	0.916
MOGAT1	PNPLA3	0.915
PNLIP	LPL	0.915
PLCB4	PLCG1	0.914
DGAT1	LIPC	0.914
PLCD1	PLCG2	0.914
PLCG2	PLCB4	0.914
LIPF	LIPC	0.914
PNPLA2	MOGAT2	0.914
CEPT1	EPT1	0.914
PLD4	PLD1	0.913
MOGAT1	PNPLA2	0.913
PLCG2	PLCD3	0.913
PLCD3	PLCG1	0.913

DGKQ		
node1	**node2**	**score**
MBOAT1	CDS1	0.913
PLCB3	PLCE1	0.913
PLCD4	PLCG2	0.913
PLCD1	PLCB3	0.912
EPT1	CHPT1	0.912
LIPC	DGAT2	0.912
PLCD4	PLCG1	0.912
MOGAT1	PNLIPRP1	0.911
PNLIPRP1	PNPLA3	0.911
PNPLA2	LIPG	0.911
PNLIP	LIPC	0.911
MOGAT1	LPL	0.911
LPL	MOGAT2	0.911
MBOAT2	DGKQ	0.910
LIPF	PNPLA3	0.910
CEL	LIPC	0.910
PLCD1	PLCE1	0.910
PLD1	DGKQ	0.910
PNLIP	PNLIPRP1	0.910
LIPC	PNPLA3	0.910
PLCD3	PLCE1	0.909
PLCE1	PLCB2	0.909
PNPLA2	LIPC	0.909
PLCD1	PLCB1	0.909
DGKQ	PLCG1	0.909
PLCB1	PLCE1	0.909
PLD4	PLD3	0.909
LIPF	PNPLA2	0.909
LIPF	LPL	0.909
CDS2	DGKQ	0.909
LPL	MOGAT3	0.909

DGKQ		
node1	**node2**	**score**
CEL	PNPLA2	0.909
CDS1	DGKQ	0.909
DGKQ	PLCZ1	0.909
PLD1	PLD2	0.909
PNLIPRP1	DGAT2	0.909
LCLAT1	MBOAT2	0.908
MOGAT1	LIPC	0.908
PLCB4	PLCE1	0.908
CDS2	MBOAT1	0.908
LIPF	CEL	0.908
PNPLA2	PNPLA3	0.908
PLCD1	PLCB2	0.908
LPL	LIPC	0.907
PLCB1	PLCD3	0.907
AGPAT2	DGKQ	0.907
PNLIPRP1	PNPLA2	0.907
AGPAT1	DGKQ	0.907
PLCD4	PLCE1	0.907
PLCD4	PLCB4	0.907
PLCB1	PLCB2	0.907
PNLIP	PNPLA3	0.906
PLCB3	PLCZ1	0.906
PLCD4	PLCB2	0.906
CEL	DGAT1	0.906
PNLIPRP1	DGAT1	0.906
PLCD4	PLCB1	0.906
DGKQ	DGAT2	0.906
PLCD3	PLCB3	0.906
LIPF	LIPG	0.906
LIPC	LIPG	0.906
CEL	PNPLA3	0.905

DGKQ		
node1	**node2**	**score**
PLCD1	PLCB4	0.905
PLCD4	PLCD3	0.905
AGPAT5	DGKQ	0.905
PNPLA2	DGKQ	0.905
PLCB4	PLCB3	0.905
MBOAT1	LCLAT1	0.905
MOGAT1	MOGAT3	0.905
PLCB3	PLCB2	0.904
MOGAT1	DGAT2	0.904
PLCB4	PLCD3	0.904
PLCD1	PLCD3	0.904
LIPG	PNPLA3	0.904
PNPLA2	MOGAT3	0.904
PLCD4	PLCB3	0.904
DGAT2	MOGAT2	0.904
PLCD1	PLCD4	0.904
PLCZ1	PLCG1	0.904
PNLIPRP1	MOGAT2	0.904
PLCB4	PLCB2	0.904
PLD3	MBOAT2	0.904
PLCB1	PLCB4	0.904
LCLAT1	DGKQ	0.903
AGPAT4	DGKQ	0.903
LPL	LIPG	0.903
PLD3	AGPAT1	0.903
CEPT1	DGKQ	0.903
PNLIPRP1	LIPC	0.903
PLCB4	PLCZ1	0.903
AGPAT3	DGKQ	0.903
DGAT1	LIPG	0.903
DGAT2	MOGAT3	0.903

DGKQ		
node1	**node2**	**score**
LIPG	DGAT2	0.903
PLD3	CHPT1	0.903
DGAT1	DGKQ	0.903
LIPF	PNLIPRP1	0.903
PLCG2	PLCZ1	0.902
PLCZ1	PLCE1	0.902
PLCG2	DGKQ	0.902
PLCD3	PLCB2	0.902
PLCZ1	PLCB2	0.902
PLCB1	PLCZ1	0.902
PLCD4	PLCZ1	0.902
PLCD1	PLCZ1	0.902
PNLIPRP1	LIPG	0.902
PNLIPRP3	PNLIPRP1	0.901
DGKQ	MOGAT2	0.901
PLD3	MBOAT1	0.901
CEL	MOGAT2	0.901
PLD3	EPT1	0.901
LIPF	DGKQ	0.901
PLD4	CEPT1	0.901
DGKQ	MOGAT3	0.901
PLD4	LCLAT1	0.901
CEL	DGAT2	0.901
DGKQ	EPT1	0.901
PLD3	AGPAT4	0.901
LPL	DGKQ	0.901
DGKQ	LIPG	0.901
PLD3	LCLAT1	0.901
MOGAT1	DGKQ	0.901
MOGAT1	CEL	0.901
PLCB1	PLCB3	0.901

DGKQ		
node1	**node2**	**score**
PLCD3	PLCZ1	0.901
CEPT1	PLD3	0.901
PLD4	MBOAT1	0.901
CDS2	PLD3	0.901
PLD4	CHPT1	0.901
PNLIPRP3	LIPC	0.901
PLD4	MBOAT2	0.901
LIPC	MOGAT3	0.901
CEL	MOGAT3	0.901
PLD4	EPT1	0.901
DGKQ	CHPT1	0.901
LIPC	MOGAT2	0.901
PLD4	AGPAT2	0.900
CEL	DGKQ	0.900
PNLIPRP3	PNPLA2	0.900
MOGAT1	PNLIPRP3	0.900
PNLIPRP3	LPL	0.900
PLD4	DGKQ	0.900
MOGAT1	PNLIP	0.900
PLD3	AGPAT3	0.900
PLD3	DGKQ	0.900
PNLIPRP3	DGKQ	0.900
PLD4	AGPAT4	0.900
PLD4	CDS1	0.900
PNLIPRP3	PNPLA3	0.900
LIPC	DGKQ	0.900
LIPF	PNLIPRP3	0.900
PNLIPRP3	DGAT1	0.900
PLD3	AGPAT5	0.900
PNLIPRP3	LIPG	0.900
PNLIPRP3	MOGAT3	0.900

DGKQ		
node1	**node2**	**score**
PNLIP	DGKQ	0.900
DGKQ	PNPLA3	0.900
CEPT1	CHPT1	0.900
PNLIPRP3	PNLIP	0.900
PNLIPRP1	DGKQ	0.900
CEL	PNLIPRP3	0.900
AGPAT2	PLD3	0.900
CDS2	PLD4	0.900
PLD4	AGPAT3	0.900
PLD3	CDS1	0.900
MOGAT1	LIPG	0.900
PNLIPRP1	MOGAT3	0.900
LIPG	MOGAT2	0.900
PLD4	AGPAT5	0.900
LIPG	MOGAT3	0.900
PNLIPRP3	DGAT2	0.900
PLD4	AGPAT1	0.900
MBOAT1	DGKQ	0.900
PNLIPRP3	MOGAT2	0.900

TN1P		
node1	**node2**	**score**
TNIP1	TNFAIP3	0.980

	IRF5	
node1	**node2**	**score**
TP53	CREBBP	0.998
B2M	HLA-G	0.998
OAS1	MX1	0.997
MX1	IFIT1	0.997
ISG15	IFIT1	0.997
B2M	HLA-C	0.997
MX1	ISG15	0.997
IFIT1	OAS2	0.996
IRF9	STAT2	0.996
MX1	OAS2	0.996
ISG15	IFIT3	0.996
OAS1	IFIT1	0.996
RSAD2	IFIT1	0.995
MX1	OASL	0.995
IFIT1	OAS3	0.995
IFIT1	OASL	0.995
MX1	RSAD2	0.995
ISG15	IFIT2	0.995
IFIT3	OASL	0.995
MX1	OAS3	0.994
OAS1	ISG15	0.994
MX1	IRF7	0.994
RSAD2	ISG15	0.994
IFIT2	IFIT3	0.994
IFIT3	IFIT1	0.994
OAS1	IFIT3	0.993
ISG15	IRF7	0.993
RELA	CREBBP	0.993
MX1	IFI27	0.993
MX1	IFIT3	0.993
ISG15	OASL	0.993
OAS2	MX2	0.993
IFIT3	OAS2	0.993
JUN	TP53	0.992
ISG15	IFI27	0.992
IFIT3	OAS3	0.992
ISG15	OAS3	0.992
ISG15	OAS2	0.992
TP53	KAT2B	0.992
IRF3	CREBBP	0.992
MX1	IRF9	0.992
OAS1	MX2	0.992
IFIT2	OASL	0.992
ISG15	ISG20	0.992
IRF9	ISG15	0.992
IFIT1	MX2	0.992
RSAD2	IFIT2	0.991
HLA-DPB1	HLA-DQA2	0.991
IFIT1	IRF7	0.991
MX1	IFIT2	0.991
RSAD2	IFIT3	0.991
OAS1	RSAD2	0.991
OAS2	IRF7	0.991
MX2	OAS3	0.990
KAT2B	CREBBP	0.990
RSAD2	IRF7	0.990
OAS1	IRF7	0.990
RSAD2	OAS2	0.990
IFI35	IRF7	0.990
IFNB1	IRF3	0.990
IFIT3	IRF7	0.989
RSAD2	OASL	0.989
IFIT2	OAS2	0.989
IFI35	IFIT3	0.989
IFIT2	IFIT1	0.988
IRF7	OASL	0.988
OAS1	IFIT2	0.988
MX1	IFITM1	0.987
RSAD2	OAS3	0.987
IFI35	ISG15	0.987
MX2	OASL	0.986
IRF7	OAS3	0.986
IFI35	MX1	0.986
ISG15	MX2	0.986
IRF9	IFIT1	0.985
RSAD2	MX2	0.985
IFI35	OAS1	0.985
TRAF6	IRF7	0.985
IFIT2	OAS3	0.984
IFIT3	MX2	0.984
IFI35	IFIT1	0.984
MX2	IRF7	0.984
IFIT1	IFI27	0.984
IFI35	OASL	0.983
ISG15	IFITM1	0.983
IFIT1	IRF3	0.983
OAS1	IFI27	0.983
IFNB1	IRF7	0.983
RELA	JUN	0.983
IFI35	OAS2	0.982
IRF9	IFIT3	0.982
STAT2	IRF3	0.982
IRF7	STAT2	0.981
IFI35	OAS3	0.981
HLA-G	HLA-DRB1	0.981
RSAD2	IFI27	0.980
IFIT2	IRF7	0.980
IRF9	IFIT2	0.979
ISG15	BST2	0.979
IFIT3	IFI27	0.979
IFI35	IRF9	0.979
OAS1	IRF9	0.978
MX1	MX2	0.978
MX1	IRF3	0.978
MX1	ISG20	0.978
MX1	STAT2	0.977
IRF7	ISG20	0.976
RNASEL	OASL	0.975
IFI35	RSAD2	0.975
IFIT2	ISG20	0.975
IRF9	IRF7	0.975
IFI35	IFITM1	0.974
IRF7	BST2	0.974
IFIT2	MX2	0.974
GBP1	IRF1	0.974
IFI27	OASL	0.974
OAS2	IFI27	0.974
ISG15	STAT2	0.974
JUN	CREBBP	0.974
IFIT2	STAT2	0.974
JUN	KAT2B	0.973
IRF9	ISG20	0.973
IRF9	OAS2	0.973
MX1	BST2	0.973

IRF5		
node1	**node2**	**score**
IFIT1	ISG20	0.973
OAS2	IFITM1	0.973
RSAD2	IRF3	0.973
IFI35	MX2	0.973
RELA	ICAM1	0.972
IFITM3	IFITM1	0.972
STAT2	IRF1	0.972
STAT2	ISG20	0.971
IRF9	RSAD2	0.971
IFI27	OAS3	0.971
IFIT1	IFITM1	0.971
HLA-DQA2	HLA-DRB1	0.971
IFITM1	IFI27	0.971
ISG15	IRF3	0.970
JUN	IRF3	0.970
RNASEL	OAS3	0.970
ISG20	OASL	0.970
IFI35	BST2	0.970
CIITA	IRF1	0.969
KAT2B	IRF1	0.969
IFIT3	IFITM1	0.968
ICAM1	IRF1	0.968
IFIT3	IRF1	0.968
RSAD2	IRF1	0.968
IRF7	KAT2B	0.968
OAS1	OAS3	0.967
OAS2	STAT2	0.967
RELA	KAT2B	0.967
IFI35	IFIT2	0.966
GBP1	OAS2	0.966
RELA	IRF5	0.966
IFIT1	STAT2	0.966
RSAD2	ISG20	0.965
IFIT3	ISG20	0.965
IRF9	IFITM1	0.965
IRF2	IFNB1	0.965
OAS1	GBP1	0.964
IFIT2	IRF3	0.964
IFI35	IFI27	0.964
OAS1	IFITM1	0.964
RELA	IRF3	0.964
IRF9	GBP1	0.964
IRF3	ISG20	0.964
IRF7	TRIM21	0.963
IFITM1	ISG20	0.963
OAS1	RNASEL	0.963
OAS1	ISG20	0.963
GBP1	IRF7	0.963
IFITM3	ISG15	0.963
IFITM1	BST2	0.963
IRF9	IFI27	0.963
IFI35	ISG20	0.962
IFITM1	IRF7	0.962
ISG20	IRF1	0.962
IFITM1	STAT2	0.962
RSAD2	BST2	0.962
ISG15	TRIM25	0.961
RNASEL	IRF3	0.961
RELA	IRF1	0.961
IFNB1	STAT2	0.961
IFNB1	IRF1	0.961
IRF9	OAS3	0.960
IFITM1	OASL	0.960
GBP1	OAS3	0.960
MX2	ISG20	0.960
IRF9	MX2	0.960
OAS2	ISG20	0.960
IFI35	IFITM3	0.960
MX2	IFITM1	0.960
IRF7	IFI27	0.960
IFIT2	IFI27	0.960
ISG15	IRF1	0.959
MX2	BST2	0.959
OAS1	BST2	0.959
OAS1	STAT2	0.959
IFI35	STAT2	0.959
IRF9	IRF1	0.959
IFIT2	IRF1	0.958
IFIT3	STAT2	0.958
ACTB	KAT2B	0.958
IRF9	OASL	0.958
MX1	RNASEL	0.957
IFIT2	IFITM1	0.957
IRF2	STAT2	0.957
STAT2	CREBBP	0.957
RNASEL	OAS2	0.957
MX1	IRF1	0.957
ISG15	RNASEL	0.957
OAS2	BST2	0.956
IFIT1	RNASEL	0.956
IFITM3	MX1	0.955
OASL	TRIM21	0.955
RELA	TRAF6	0.955
MX2	STAT2	0.955
IRF5	TP53	0.955
IRF9	IFNB1	0.955
RSAD2	STAT2	0.954
IRF7	IRF3	0.954
RSAD2	IFITM1	0.953
IFIT1	BST2	0.953
JUN	ACTB	0.953
CREBBP	IRF1	0.953
BST2	IRF1	0.953
IFI27	BST2	0.952
RNASEL	IRF7	0.952
IFIT2	RNASEL	0.952
IRF3	TRIM21	0.952
IFITM3	IFIT3	0.952
HLA-DRB1	TRIM21	0.951
RNASEL	ISG20	0.951
IFITM1	OAS3	0.951
RNASEL	STAT2	0.951
IRF2	KAT2B	0.951
GBP1	OASL	0.950
ISG20	IFI27	0.949
OAS2	TRIM21	0.949
IFITM3	IFIT1	0.949
RNASEL	IRF1	0.949
OAS1	TRIM21	0.949
IRF2	ISG15	0.949
IFIT1	IRF1	0.949
IRF7	CREBBP	0.949
IFI35	IRF1	0.948
IFITM3	RSAD2	0.948

IRF5		
node1	**node2**	**score**
IFITM3	IFI27	0.948
JUN	IRF1	0.948
IRF2	ISG20	0.947
IRF5	TRIM21	0.947
RELA	IRF2	0.947
IRF5	IRF3	0.946
MX2	IFI27	0.946
TRIM25	IRF3	0.946
IFIT3	BST2	0.946
HLA-C	HLA-DQA2	0.946
JUN	HMGB1	0.946
IFITM3	IFIT2	0.945
ISG20	OAS3	0.945
IFNB1	IRF5	0.945
IRF9	RNASEL	0.944
IRF2	IRF1	0.944
STAT2	OASL	0.944
IRF9	TRIM21	0.944
STAT2	OAS3	0.944
ISG20	BST2	0.944
OAS1	IFITM3	0.944
FCGR1A	ICAM1	0.943
RELA	HMGB1	0.943
IFITM3	IRF9	0.943
SP100	OAS2	0.943
MX2	IRF1	0.942
TRIM21	OAS3	0.942
IRF9	CREBBP	0.942
IFITM3	IRF7	0.942
IRF5	STAT2	0.942
IFITM3	OAS3	0.941
IFNB1	JUN	0.941
IFIT3	RNASEL	0.941
OAS1	IRF3	0.941
IRF2	CIITA	0.941
OAS1	IRF1	0.941
HMGB1	CREBBP	0.941
IRF7	IRF1	0.941
RSAD2	RNASEL	0.941
IRF9	BST2	0.940
SP100	TRIM21	0.940
JUN	IRF7	0.940
OAS2	IRF3	0.940
HMGB1	IRF3	0.940
IRF7	TRIM25	0.940
ISG15	IRF5	0.940
IFITM3	BST2	0.939
SP100	TP53	0.939
IFITM3	STAT2	0.939
IFITM3	OAS2	0.939
RNASEL	MX2	0.938
IFIT3	IRF3	0.938
MX2	IRF3	0.938
IRF2	IFIT2	0.938
OAS2	IRF1	0.938
IFITM3	ISG20	0.938
IFNB1	CREBBP	0.937
HLA-DQA2	HLA-G	0.937
BST2	OAS3	0.937
IRF5	CREBBP	0.937
B2M	ICAM1	0.937
IFIT1	IRF5	0.937
IRF2	RNASEL	0.937
IRF4	STAT2	0.936
TRAF6	TP53	0.936
OASL	BST2	0.936
IRF4	CIITA	0.936
RELA	IRF7	0.936
OAS1	SP100	0.936
STAT2	IFI27	0.936
MX1	IRF2	0.935
B2M	CD44	0.935
SP100	IRF7	0.934
IFITM3	OASL	0.934
SP100	CREBBP	0.934
IFITM3	MX2	0.934
STAT2	BST2	0.934
MX1	IRF5	0.934
RNASEL	BST2	0.934
IRF4	ISG15	0.933
OASL	IRF1	0.933
HLA-DPB1	HLA-DRB1	0.933
IRF5	TRAF6	0.933
IFIT2	BST2	0.933
B2M	JUN	0.933
HLA-DRB1	CIITA	0.933
IFITM1	IRF1	0.933
IRF3	ICAM1	0.933
IRF3	BST2	0.933
CD44	FCGR1A	0.932
TRAF6	TRIM25	0.932
HLA-DRB1	IRF5	0.932
SP100	OAS3	0.932
IRF2	GBP1	0.932
SP100	OASL	0.932
HLA-C	ICAM1	0.931
IFIT2	IRF5	0.931
IRF3	OASL	0.931
IRF5	KAT2B	0.931
IRF2	IFIT1	0.931
CIITA	ICAM1	0.931
IRF5	ISG20	0.931
RELA	IFNB1	0.931
GBP1	IRF3	0.931
IRF5	IRF7	0.930
GBP1	TRIM21	0.930
IRF9	CIITA	0.930
B2M	IRF1	0.930
IRF9	TRIM25	0.929
ACTB	CREBBP	0.929
IFIT1	TRIM25	0.929
OAS1	IRF5	0.929
MX1	TRIM25	0.928
IFITM3	IRF1	0.928
HLA-DPB1	CIITA	0.928
RELA	IRF4	0.928
PTAFR	ICAM1	0.928
IRF7	ICAM1	0.928
IRF2	CREBBP	0.927
IRF4	ISG20	0.927
IRF2	MX2	0.927
IFI27	IRF1	0.927
HLA-G	ICAM1	0.927
IRF2	IFIT3	0.927

IRF5		
node1	**node2**	**score**
IRF2	RSAD2	0.927
IFNB1	ACTB	0.927
JUN	IRF6	0.927
ACTB	HMGB1	0.927
IRF2	JUN	0.927
IRF3	OAS3	0.927
IRF4	JUN	0.927
IRF7	CIITA	0.927
IFITM3	IRF3	0.927
HLA-C	HLA-DRB1	0.926
RELA	ACTB	0.926
IRF6	SP100	0.926
HLA-C	CIITA	0.926
IRF3	IRF1	0.926
HLA-G	CIITA	0.926
CD44	IRF2	0.925
B2M	OAS1	0.925
IFITM1	IRF3	0.925
GBP1	CIITA	0.925
HLA-DPB1	CD44	0.925
CD44	IRF4	0.924
IRF9	SP100	0.924
CIITA	IRF3	0.924
B2M	CIITA	0.924
SP100	IRF3	0.924
IRF9	IRF3	0.924
HMGB1	KAT2B	0.924
RNASEL	IRF5	0.924
IFITM3	RNASEL	0.924
IRF2	OAS2	0.924
IRF9	IRF2	0.924
B2M	IRF9	0.924
ACTB	IRF3	0.924
IRF5	OAS2	0.923
B2M	GBP1	0.923
IRF4	IFIT2	0.923
IFNB1	KAT2B	0.923
IFNB1	IRF6	0.923
IRF4	IRF5	0.923
HLA-DPB1	HLA-C	0.923
TRIM21	IRF1	0.923
TRIM25	IRF1	0.923
CD44	IRF6	0.923
HLA-DPB1	ICAM1	0.922
IFI35	IRF3	0.922
IRF4	IFNB1	0.922
IRF5	CIITA	0.922
IRF2	SP100	0.922
FCGR1A	IRF1	0.922
IRF2	IRF7	0.922
IFNB1	HMGB1	0.922
CD44	IRF1	0.922
CD44	HLA-G	0.922
IRF1	OAS3	0.921
B2M	OAS2	0.921
RNASEL	IFI27	0.921
IRF6	HMGB1	0.921
IFIT3	IRF5	0.921
B2M	TRIM25	0.921
JUN	IRF5	0.921
HLA-DQA2	CIITA	0.921
OAS1	IRF2	0.921
HLA-G	IRF5	0.921
MX2	TRIM25	0.920
GBP1	FCGR1A	0.920
HLA-DRB1	ICAM1	0.920
IRF5	IRF1	0.920
IRF3	KAT2B	0.920
IRF4	IFIT1	0.920
SP100	IRF1	0.920
RNASEL	IFITM1	0.920
HLA-C	IRF1	0.919
IRF2	HMGB1	0.919
IRF2	IRF3	0.919
IRF9	ICAM1	0.919
IRF4	ACTB	0.919
IRF3	IFI27	0.919
OAS1	HLA-DRB1	0.919
FCGR1A	IRF7	0.919
GBP1	SP100	0.918
OAS1	HLA-DQA2	0.918
SP100	TRIM25	0.918
IRF4	IRF1	0.918
MX1	IRF4	0.918
CD44	IRF9	0.918
IRF5	OASL	0.918
IRF5	SP100	0.918
IRF5	OAS3	0.918
IRF2	IFI27	0.918
TRIM25	OASL	0.918
CD44	CIITA	0.917
IRF4	ICAM1	0.917
IFI35	IRF2	0.917
ACTB	IRF1	0.917
IRF2	IFITM1	0.917
IRF2	ICAM1	0.917
B2M	IRF7	0.917
GBP1	ICAM1	0.917
HLA-DQA2	IRF5	0.916
B2M	FCGR1A	0.916
ACTB	IRF7	0.916
IRF5	PTAFR	0.916
B2M	IRF2	0.916
CD44	SP100	0.916
IFITM3	IRF2	0.916
CD44	IRF7	0.916
HLA-C	IRF7	0.916
IRF9	IRF5	0.916
IRF5	ICAM1	0.916
HLA-C	IRF5	0.916
IRF2	HLA-C	0.915
IRF4	IRF7	0.915
HLA-C	HLA-G	0.915
CD44	IRF3	0.915
ACTB	IRF5	0.915
IRF4	GBP1	0.915
IRF2	TRIM25	0.915
IRF6	IRF5	0.915
IRF2	OASL	0.915
IRF5	BST2	0.915
IRF2	IRF4	0.915
HMGB1	IRF7	0.915
IRF4	FCGR1A	0.915
B2M	TRIM21	0.915

IRF5

node1	node2	score
CD44	HLA-DRB1	0.915
IRF5	MX2	0.915
IRF5	IFI27	0.914
CD44	HLA-C	0.914
GBP1	TRIM25	0.914
FCGR1A	IRF5	0.914
IFI35	RNASEL	0.914
HLA-G	IRF1	0.914
RSAD2	IRF5	0.914
IFI35	IRF5	0.914
B2M	OAS3	0.914
B2M	OASL	0.914
HLA-C	BST2	0.914
ISG15	IRF6	0.914
FCGR1A	CIITA	0.913
GBP1	IRF5	0.913
IRF4	IFIT3	0.913
HMGB1	IRF1	0.913
B2M	IRF4	0.913
IRF4	CREBBP	0.913
FCGR1A	HLA-G	0.913
IRF5	IFITM1	0.913
OAS2	TRIM25	0.913
ICAM1	TRIM21	0.913
B2M	HLA-DRB1	0.913
IRF2	IRF5	0.913
IFITM3	IRF4	0.912
HLA-DQA2	ICAM1	0.912
HLA-DPB1	IRF5	0.912
OAS1	TRIM25	0.912
IRF2	TRIM21	0.912

IRF5

node1	node2	score
IRF2	OAS3	0.912
IRF9	HLA-C	0.912
IRF2	BST2	0.912
IRF4	OAS2	0.912
IRF4	IRF3	0.912
IFI35	IRF4	0.912
IRF4	BST2	0.911
B2M	IRF6	0.911
IFITM3	IRF5	0.911
HLA-C	FCGR1A	0.911
IRF5	HMGB1	0.911
IRF4	HLA-DQA2	0.911
IRF6	ICAM1	0.911
HLA-DPB1	TRIM21	0.911
FCGR1A	TRIM21	0.911
IRF6	IRF7	0.911
CD44	HLA-DQA2	0.911
FCGR1A	IRF3	0.911
FCGR1A	ACTB	0.911
IRF5	TRIM25	0.911
HLA-C	IFI27	0.910
B2M	IRF3	0.910
HLA-DRB1	IRF3	0.910
HLA-DPB1	OAS1	0.910
HLA-C	IRF3	0.910
RSAD2	IRF4	0.910
IRF6	ACTB	0.910
B2M	IRF5	0.910
IRF4	RNASEL	0.910
B2M	HLA-DPB1	0.910
CD44	IRF5	0.910

IRF5

node1	node2	score
CD44	PTAFR	0.910
IRF4	MX2	0.910
B2M	HLA-DQA2	0.909
HLA-DPB1	HLA-G	0.909
HLA-DQA2	OAS3	0.909
IRF6	IRF1	0.909
FCGR1A	OAS2	0.909
IRF4	IFITM1	0.909
MX1	HLA-C	0.909
HLA-DQA2	GBP1	0.908
OAS1	ICAM1	0.908
IRF4	SP100	0.908
IRF6	STAT2	0.908
RELA	IRF6	0.908
ISG15	HLA-C	0.908
OAS1	IRF4	0.908
FCGR1A	HLA-DRB1	0.908
FCGR1A	PTAFR	0.908
IRF9	IRF4	0.908
HLA-DPB1	GBP1	0.908
HLA-DQA2	IRF7	0.908
MX1	IRF6	0.908
HLA-C	STAT2	0.908
HLA-DPB1	IRF4	0.908
HLA-C	ISG20	0.908
IRF2	IRF6	0.908
CD44	TP53	0.908
GBP1	HLA-DRB1	0.907
OAS1	CIITA	0.907
OAS1	IRF6	0.907
IFIT1	IRF6	0.907

IRF5

node1	node2	score
HLA-G	IRF7	0.907
IRF3	PTAFR	0.907
OAS2	ICAM1	0.907
HLA-DRB1	OASL	0.907
IRF4	KAT2B	0.907
OAS1	HLA-C	0.907
IRF4	OAS3	0.907
HLA-DRB1	OAS2	0.907
HLA-DPB1	IRF1	0.907
IRF6	ISG20	0.907
GBP1	HLA-G	0.906
IRF6	OASL	0.906
IRF4	HLA-DRB1	0.906
IRF6	OAS3	0.906
CIITA	PTAFR	0.906
IRF6	IRF3	0.906
IRF6	OAS2	0.906
IRF7	PTAFR	0.906
HLA-C	IFITM1	0.906
OAS1	FCGR1A	0.906
OAS2	CIITA	0.906
HLA-DRB1	IRF1	0.906
ICAM1	OASL	0.906
FCGR1A	OASL	0.906
HLA-C	GBP1	0.906
IRF4	IFI27	0.905
HLA-DPB1	OAS3	0.905
HLA-C	MX2	0.905
IRF9	HLA-G	0.905
HLA-DPB1	OASL	0.905
CD44	OAS2	0.905

IRF5		
node1	**node2**	**score**
IRF2	ACTB	0.905
HLA-C	IFIT1	0.905
HLA-C	OAS3	0.905
IFIT2	IRF6	0.905
HLA-DPB1	OAS2	0.905
HLA-DQA2	OASL	0.905
FCGR1A	OAS3	0.905
MX1	HLA-G	0.905
OAS1	HLA-G	0.905
IRF4	TRIM21	0.905
HLA-DRB1	OAS3	0.905
IRF6	CREBBP	0.905
HLA-G	BST2	0.905
IFI35	HLA-C	0.904
ISG15	HLA-G	0.904
CD44	GBP1	0.904
IRF2	FCGR1A	0.904
HLA-DQA2	IRF1	0.904
FCGR1A	IRF6	0.904
IRF9	HLA-DQA2	0.904
CD44	OAS1	0.904
OAS2	PTAFR	0.904
HLA-G	IFITM1	0.904
IRF9	IRF6	0.904
IRF4	IRF6	0.904
SP100	ICAM1	0.904
TRIM25	OAS3	0.904
IRF4	OASL	0.904
HLA-G	TRIM21	0.903
HLA-G	OAS3	0.903
HLA-DRB1	SP100	0.903
PTAFR	IRF1	0.903
HLA-C	OAS2	0.903
HLA-G	OAS2	0.903
IRF6	KAT2B	0.903
IFIT3	IRF6	0.903
CIITA	OAS3	0.903
HLA-DQA2	TRIM21	0.903
HLA-G	OASL	0.903
HLA-G	IFI27	0.903
IFI35	HLA-G	0.903
FCGR1A	TRIM25	0.903
IFIT3	HLA-G	0.903
HLA-C	OASL	0.903
HLA-G	MX2	0.903
CD44	TRIM21	0.902
HLA-DPB1	FCGR1A	0.902
HLA-G	ISG20	0.902
CIITA	TRIM21	0.902
HLA-C	IFIT2	0.902
IRF6	MX2	0.902
IRF2	HLA-DRB1	0.902
IRF4	HMGB1	0.902
TRIM25	CIITA	0.902
HLA-DQA2	OAS2	0.902
IFIT1	HLA-G	0.902
HLA-C	TRIM21	0.902
CD44	OASL	0.901
HLA-DPB1	IRF9	0.901
HLA-G	STAT2	0.901
HLA-DPB1	IRF6	0.901
ICAM1	OAS3	0.901
HLA-G	IRF3	0.901
B2M	SP100	0.901
FCGR1A	SP100	0.901
HLA-DQA2	IRF3	0.901
CIITA	OASL	0.901
RSAD2	HLA-G	0.901
TRIM25	ICAM1	0.901
RSAD2	HLA-C	0.901
IRF4	HLA-G	0.901
RNASEL	IRF6	0.901
IRF6	HLA-DRB1	0.901
HLA-DQA2	FCGR1A	0.901
HLA-DQA2	IRF6	0.901
HLA-DRB1	IRF7	0.901
HLA-C	IFIT3	0.901
IRF6	IFITM1	0.901
IRF2	HLA-G	0.901
IRF6	CIITA	0.901
IRF6	TRIM25	0.901
HLA-DPB1	IRF7	0.901
SP100	CIITA	0.901
IRF6	BST2	0.900
IFI35	IRF6	0.900
PTAFR	TRIM21	0.900
RSAD2	IRF6	0.900
HLA-DPB1	IRF3	0.900
IRF4	PTAFR	0.900
IRF9	FCGR1A	0.900
IRF2	HLA-DQA2	0.900
HLA-C	PTAFR	0.900
HLA-G	TRIM25	0.900
HLA-G	SP100	0.900
TRIM25	PTAFR	0.900
IFITM3	IRF6	0.900
IRF6	TRIM21	0.900
B2M	PTAFR	0.900
HLA-C	RNASEL	0.900
PTAFR	OASL	0.900
IRF9	PTAFR	0.900
PTAFR	OAS3	0.900
IRF2	PTAFR	0.900
HLA-G	PTAFR	0.900
HLA-DPB1	PTAFR	0.900
HLA-DPB1	TRIM25	0.900
IRF6	IFI27	0.900
SP100	PTAFR	0.900
CD44	TRIM25	0.900
CD44	OAS3	0.900
IFITM3	HLA-G	0.900
GBP1	IRF6	0.900
IRF9	HLA-DRB1	0.900
IRF6	HLA-G	0.900
HLA-DQA2	SP100	0.900
HLA-DPB1	IRF2	0.900
IRF4	HLA-C	0.900
OAS1	PTAFR	0.900
HLA-DQA2	PTAFR	0.900
HLA-DPB1	SP100	0.900
IFITM3	HLA-C	0.900
HLA-C	SP100	0.900
HLA-DQA2	TRIM25	0.900
HLA-DRB1	PTAFR	0.900

IRF5

node1	node2	score
HLA-C	TRIM25	0.900
IRF6	PTAFR	0.900
IFIT2	HLA-G	0.900
GBP1	PTAFR	0.900
IRF4	TRIM25	0.900
RNASEL	HLA-G	0.900
HLA-C	IRF6	0.900
HLA-DRB1	TRIM25	0.900

FAM167A

node1	node2	score
FAM167A	BLK	0.862
PHRF1	PXK	0.780
FAM167A	MTMR9	0.758
FAM167A	MTMR7	0.730
PHRF1	FAM167A	0.709
PXK	FAM167A	0.704

BLK

node1	node2	score
EFNA1	EPHA2	0.999
EFNA1	EPHA4	0.999
EGFR	EGF	0.999
EFNA1	EPHA1	0.999
PTK2B	PXN	0.999
EFNA5	EPHA4	0.999
EPHA2	EFNA5	0.999
EFNA1	EPHA5	0.998
EPHA3	EFNA5	0.998
EFNA5	EPHA5	0.997
EPHB1	EFNB1	0.997
EFNA5	EPHA1	0.997
EPHB2	EFNB1	0.997
EPHA7	EFNA5	0.997
EPHA1	EFNB1	0.997
EPHA6	EFNA1	0.997
EPHA7	EFNA1	0.997
EPHB2	EFNA5	0.996
SRC	PXN	0.995
EGFR	CBL	0.995
EPHA4	EFNB1	0.995
BCAR1	SRC	0.995
EPHB1	EFNA1	0.994
SRC	EGF	0.994
EPHB1	EFNA5	0.994
SRC	STAT3	0.993
EGFR	STAT3	0.992
EFNA1	EPHA3	0.992
BCAR1	FYN	0.991
BCAR1	PXN	0.991
EPHA3	EFNB1	0.991

BLK

node1	node2	score
EPHA7	EFNB1	0.990
EPHA2	EFNB1	0.990
BCAR1	PTK2B	0.990
PDGFB	PDGFRB	0.989
EPHA5	EFNB1	0.988
EPHB2	EFNA1	0.988
EPHA6	EFNB1	0.987
PXN	CSK	0.986
EGFR	PLCG1	0.986
PDGFRB	PLCG1	0.985
EPHA6	EFNA5	0.985
FYN	CBL	0.984
LCK	STAT3	0.984
EGF	STAT3	0.984
CD79B	CD79A	0.983
EPHA4	NGEF	0.983
EPHA2	EPHA1	0.982
RASA1	DOK1	0.982
FYN	PXN	0.982
SRC	CBL	0.982
SYK	CBL	0.981
LYN	STAT3	0.981
SRC	EFNB1	0.980
STAT3	PDGFRB	0.980
ZAP70	CBL	0.979
LCK	CBL	0.978
SRC	DOK1	0.978
SYK	VAV2	0.978
LYN	BCAR1	0.977
LYN	CBL	0.977
LCK	PXN	0.977

	BLK	
node1	**node2**	**score**
PTPN13	EFNB1	0.976
HCK	CBL	0.975
CBL	PLCG1	0.975
LYN	CD79B	0.975
DOK1	CSK	0.974
MLLT4	SRC	0.974
LYN	DAPP1	0.973
LCK	ZAP70	0.973
DAPP1	PLCG2	0.972
DAPP1	SRC	0.971
LCK	RASA1	0.971
LCK	PLCG1	0.971
FYN	SNCA	0.970
HCK	PLCG1	0.969
EPHB1	PXN	0.969
LYN	SYK	0.969
SYK	PLCG2	0.968
ZAP70	CSK	0.967
PLCG2	EGFR	0.967
RASA1	EGF	0.966
CD79B	SYK	0.966
PTPN13	SRC	0.966
SYK	CD79A	0.966
BCAR1	CBL	0.966
FGR	DOK1	0.965
FYN	PRKCD	0.965
SRC	PTK2B	0.965
HCK	PXN	0.965
FYN	STAT3	0.965
EPHA6	SRC	0.964
HCK	FGR	0.964

	BLK	
node1	**node2**	**score**
EGF	PXN	0.964
ITK	LCK	0.964
CBL	PDGFRB	0.963
DAPP1	LCK	0.963
EGF	PDGFRB	0.962
ITK	CBL	0.962
EGFR	PXN	0.962
FYN	PTK2B	0.962
FGR	CBL	0.962
LYN	CD79A	0.962
EGF	CBL	0.961
SYK	FGR	0.961
FYN	EGF	0.961
LCK	EFNB1	0.960
FYN	ZAP70	0.960
FYN	PLCG1	0.960
PDGFB	EGF	0.960
LYN	PLCG2	0.960
HCK	STAT3	0.960
SYK	LCK	0.959
LYN	PLCG1	0.959
BCAR1	CSK	0.959
ZAP70	PLCG1	0.958
ITK	PLCG1	0.958
DAPP1	SYK	0.958
SRC	EFNA5	0.958
BCAR1	LCK	0.958
SYK	PLCG1	0.957
SYK	SRC	0.957
STAT3	MAPK14	0.957
SYK	FYN	0.957

	BLK	
node1	**node2**	**score**
ITK	FYN	0.956
CD79B	BLK	0.956
FYN	DOK1	0.956
SRC	NGEF	0.956
BLK	CD79A	0.956
SRC	EGFR	0.956
EGFR	RASA1	0.956
BCAR1	HCK	0.955
EPHA1	NGEF	0.955
SRC	PLCG1	0.955
SRC	RASA1	0.955
LCK	DOK1	0.955
EGF	CSK	0.955
FYN	EPHA4	0.955
FGR	PXN	0.953
SRC	PDGFRB	0.953
EPHA6	FYN	0.953
PLCG2	SRC	0.953
PRKCD	STAT3	0.952
HCK	EGFR	0.952
EPHB2	SRC	0.952
LYN	DOK1	0.952
SRC	PRKCD	0.952
FGR	STAT3	0.951
BCAR1	FGR	0.951
ABL1	PLCG1	0.951
PTPN13	EPHB1	0.951
SYK	PTK2B	0.951
LYN	EGFR	0.950
LCK	PTK2B	0.950
EPHA6	FGR	0.950

	BLK	
node1	**node2**	**score**
PTK2B	EGFR	0.950
EFNA1	SRC	0.950
LYN	PTK2B	0.950
EPHA2	CBL	0.949
PLCG2	ZAP70	0.949
FYN	PDGFRB	0.949
FYN	CD79A	0.949
FYN	EFNB1	0.949
LYN	PRKCD	0.948
SRC	CSK	0.948
LCK	EGF	0.948
HCK	PLCG2	0.948
EPHB2	RASA1	0.948
RASA1	CSK	0.948
RASA1	PDGFRB	0.947
CD79B	FYN	0.947
LYN	PXN	0.947
HCK	SYK	0.947
SRC	EPHA4	0.947
SRC	PDGFB	0.947
LYN	EGF	0.947
EGF	PLCG1	0.947
SRC	EPHA3	0.946
SRC	SNCA	0.946
LYN	MAPK14	0.946
PLCG2	FYN	0.946
FYN	CSK	0.946
ITK	ZAP70	0.945
ITK	PLCG2	0.945
LCK	CSK	0.945
FYN	EPHA3	0.945

	BLK	
node1	**node2**	**score**
FYN	EFNA5	0.945
STAT3	BLK	0.944
SRC	MAPK14	0.944
EFNA1	NGEF	0.943
CBL	BLK	0.943
S1PR1	PDGFRB	0.943
EFNA1	FYN	0.943
LCK	PRKCD	0.943
EPHB2	VAV2	0.943
PLCG2	LCK	0.942
ABL1	PDGFB	0.942
VAV2	FYN	0.942
ITK	SRC	0.942
LYN	CSK	0.942
PTPN13	EPHB2	0.941
VAV2	SRC	0.941
SLA	FGR	0.941
LCK	MAPK14	0.940
ABL1	SRC	0.940
SLA	HCK	0.940
FYN	MAPK14	0.940
SYK	MAPK14	0.940
FGR	CSK	0.940
EPHB2	ABL1	0.939
PTK2B	PRKCD	0.939
PLCG2	PLCG1	0.938
PLCG2	BLK	0.938
HCK	RASA1	0.938
HCK	CSK	0.938
SYK	SNCA	0.938
HCK	EGF	0.938

	BLK	
node1	**node2**	**score**
LYN	RASA1	0.938
SNCA	PRKCD	0.938
ABL1	CBL	0.937
FGR	PTK2B	0.937
HCK	MAPK14	0.936
SRC	MAPK11	0.936
PTPN13	FYN	0.936
HCK	ABL1	0.936
DAPP1	PLCG1	0.936
LCK	MAPK11	0.936
EPHA5	NGEF	0.936
EPHA2	NGEF	0.935
ABL1	MAPK14	0.935
EFNA1	LCK	0.935
BCAR1	PDGFRB	0.935
VAV2	LCK	0.935
HCK	DOK1	0.935
FGR	SNCA	0.935
LCK	EFNA5	0.935
LYN	LCK	0.935
HCK	SRC	0.935
FGR	MAPK14	0.935
LYN	SRC	0.935
LYN	EFNB1	0.935
SRC	FYN	0.935
LYN	MAPK11	0.935
LYN	EFNA5	0.934
FGR	EGFR	0.934
LYN	SNCA	0.934
FGR	SRC	0.934
EGFR	PDGFRB	0.934

	BLK	
node1	**node2**	**score**
FYN	MAPK11	0.933
HCK	EFNA5	0.933
BLK	MAPK14	0.933
FGR	EGF	0.933
ITK	SYK	0.932
BCAR1	SYK	0.932
EPHA7	NGEF	0.932
HCK	EFNB1	0.932
ABL1	EPHA3	0.932
FYN	EGFR	0.931
FGR	EFNB1	0.931
FGR	EFNA1	0.931
ABL1	MAPK11	0.931
SYK	MAPK11	0.931
BLK	EFNB1	0.931
LYN	EFNA1	0.931
PDGFB	STAT3	0.931
EGFR	CSK	0.931
FGR	EFNA5	0.931
HCK	EFNA1	0.931
EFNA1	BLK	0.931
EFNA5	BLK	0.931
EPHA7	EPHA2	0.931
SRC	S1PR1	0.931
HCK	MAPK11	0.930
EPHB1	FYN	0.930
MAPK11	MAPK14	0.930
FGR	PLCG2	0.930
FGR	MAPK11	0.930
BCAR1	EPHA2	0.930
EPHA2	SRC	0.929

	BLK	
node1	**node2**	**score**
EPHA3	NGEF	0.929
ABL1	PDGFRB	0.929
EFNA5	NGEF	0.929
MAPK11	BLK	0.929
SRC	ZAP70	0.928
LYN	VAV2	0.927
PTPN13	LCK	0.927
EFNA1	PDGFRB	0.927
EPHA1	CBL	0.927
FGR	ZAP70	0.927
LYN	ZAP70	0.927
EPHA7	EPHA3	0.926
EPHA6	NGEF	0.926
HCK	ZAP70	0.926
CD79B	PLCG2	0.925
SRC	EPHA1	0.925
FYN	RASA1	0.925
LYN	HCK	0.925
EPHB1	SRC	0.924
FYN	EPHA1	0.924
EGFR	BLK	0.923
VAV2	EPHA1	0.923
EPHB2	FYN	0.923
SLA	FYN	0.923
PLCG2	CBL	0.923
LYN	PTPN13	0.923
FYN	NGEF	0.923
EPHB1	FGR	0.922
FGR	PLCG1	0.922
VAV2	EPHA4	0.922
EPHA2	FYN	0.922

BLK		
node1	**node2**	**score**
SRC	EPHA5	0.922
ITK	FGR	0.922
LCK	EGFR	0.921
EPHA7	SRC	0.921
PRKCD	PLCG1	0.921
PLCG2	CD79A	0.921
EPHA7	FYN	0.921
FYN	EPHA5	0.921
FGR	PDGFB	0.920
FGR	EPHA3	0.920
EFNA1	CBL	0.920
PTPN13	FGR	0.920
FGR	EPHA5	0.920
EPHB2	FGR	0.920
LYN	SLA	0.919
SYK	BLK	0.919
LYN	FGR	0.919
LYN	PDGFB	0.919
EPHA4	PLCG1	0.919
FGR	EPHA4	0.919
FGR	EPHA2	0.919
FGR	EPHA7	0.919
FGR	EPHA1	0.919
ITK	VAV2	0.919
HCK	PTK2B	0.919
PTPN13	BLK	0.918
VAV2	EPHA2	0.918
PDGFB	S1PR1	0.918
FYN	PDGFB	0.918
LYN	EPHA4	0.918
EPHA4	CBL	0.918
PTPN13	HCK	0.918
EFNA1	EFNB1	0.918
EPHB1	EPHA4	0.918
ZAP70	BLK	0.917
VAV2	EFNA1	0.917
LYN	EPHB1	0.917
SRC	TDGF1	0.917
HCK	NGEF	0.917
DAPP1	FYN	0.917
LCK	S1PR1	0.917
FYN	S1PR1	0.916
CD79A	CSK	0.916
FGR	PRKCD	0.916
DAPP1	CBL	0.916
EPHA2	EPHA4	0.916
EPHB2	EPHA4	0.916
ABL1	FYN	0.915
BCAR1	EFNA1	0.915
PDGFB	PLCG1	0.915
PXN	EFNB1	0.915
EPHB1	RASA1	0.915
RASA1	BLK	0.915
MLLT4	FYN	0.915
EPHA3	CBL	0.915
EPHB1	VAV2	0.915
RASA1	EFNB1	0.915
PLCG2	PRKCD	0.915
FGR	PDGFRB	0.914
FGR	S1PR1	0.914
LCK	PDGFB	0.914
MLLT4	LCK	0.914
LCK	PDGFRB	0.913
BLK	PLCG1	0.913
EFNA5	EFNB1	0.913
HCK	PRKCD	0.913
PTK2B	MAPK14	0.913
EPHA6	VAV2	0.913
EPHA1	EPHA5	0.913
SNCA	LCK	0.913
EPHA4	EPHA1	0.913
EPHA3	EPHA1	0.912
LYN	PDGFRB	0.912
BCAR1	PDGFB	0.912
LYN	EPHA1	0.912
BLK	PXN	0.912
EPHA2	LCK	0.912
LYN	EPHA2	0.912
EPHB1	HCK	0.912
PTK2B	BLK	0.911
LCK	EPHA1	0.911
LCK	EPHA3	0.911
EPHB2	EPHA1	0.911
CBL	CD79A	0.911
FGR	VAV2	0.911
PRKCD	BLK	0.911
VAV2	EPHA3	0.911
HCK	PDGFB	0.911
LYN	EPHA3	0.911
HCK	EPHA2	0.911
FGR	RASA1	0.911
EPHB1	EPHA1	0.911
LYN	EPHB2	0.911
EPHB2	EPHA3	0.910
VAV2	EFNB1	0.910
HCK	EPHA1	0.910
HCK	EPHA3	0.910
EPHB2	EPHA5	0.910
LCK	EPHA4	0.910
LYN	FYN	0.910
EPHB1	EPHA3	0.910
LYN	EPHA5	0.910
EPHB1	EPHA5	0.910
EGF	BLK	0.910
EPHB2	LCK	0.910
PDGFB	RASA1	0.910
EPHA2	EPHA5	0.910
LYN	ITK	0.910
EPHA2	EPHA3	0.910
HCK	S1PR1	0.910
EPHB1	LCK	0.910
PDGFB	CBL	0.910
HCK	EPHB2	0.910
EPHA7	EPHA1	0.910
EPHA4	BLK	0.909
HCK	EPHA5	0.909
EPHB1	BLK	0.909
HCK	EPHA4	0.909
EPHA5	BLK	0.909
EPHB2	EPHA2	0.909
HCK	EPHA7	0.909
EPHA7	BLK	0.909
VAV2	EPHA7	0.909
HCK	PDGFRB	0.909

BLK		
node1	**node2**	**score**
EPHA7	LCK	0.909
EPHA6	LCK	0.909
LYN	EPHA6	0.909
EPHA3	BLK	0.909
EPHA6	HCK	0.909
VAV2	PLCG1	0.909
LYN	EPHA7	0.909
LCK	EPHA5	0.909
EPHB2	BLK	0.909
EPHA2	BLK	0.909
EPHA1	BLK	0.909
EPHA6	BLK	0.909
BLK	CSK	0.908
ITK	HCK	0.908
PRKCD	RASA1	0.908
CD79B	CSK	0.908
EPHB1	EPHA2	0.908
ABL1	EPHA4	0.908
FGR	NGEF	0.908
MLLT4	PDGFRB	0.908
HCK	VAV2	0.908
CD79B	PLCG1	0.908
SLA	SRC	0.908
HCK	SNCA	0.908
LCK	NGEF	0.908
DAPP1	BLK	0.907
VAV2	EPHA5	0.907
VAV2	CD79A	0.907
DAPP1	CD79B	0.907
SLA	LCK	0.907
VAV2	PLCG2	0.907
EFNA1	EFNA5	0.907
LCK	BLK	0.907
PDGFRB	DOK1	0.907
ABL1	EPHA5	0.906
FYN	LCK	0.906
FGR	ABL1	0.906
MLLT4	HCK	0.906
NGEF	BLK	0.906
LYN	MLLT4	0.906
LYN	NGEF	0.906
EPHB1	ABL1	0.906
LYN	S1PR1	0.906
CD79B	CBL	0.906
BCAR1	BLK	0.905
HCK	FYN	0.905
SYK	ZAP70	0.905
S1PR1	BLK	0.905
LYN	ABL1	0.905
SRC	LCK	0.905
PLCG1	CD79A	0.905
EPHA6	EPHA1	0.905
DAPP1	HCK	0.905
DAPP1	CD79A	0.905
MLLT4	FGR	0.904
ABL1	LCK	0.904
RASA1	CD79A	0.904
PDGFB	BLK	0.904
BCAR1	PRKCD	0.904
FGR	FYN	0.904
SRC	BLK	0.903
VAV2	EFNA5	0.903
EFNA5	PLCG1	0.903
LCK	TDGF1	0.903
EPHA7	EPHA4	0.903
DAPP1	FGR	0.903
FGR	LCK	0.903
EPHA7	EPHA5	0.903
MLLT4	BLK	0.903
EPHA4	EPHA5	0.903
FYN	BLK	0.903
LYN	TDGF1	0.902
VAV2	BLK	0.902
HCK	TDGF1	0.902
FYN	TDGF1	0.902
SLA	BLK	0.902
EPHA6	EPHA2	0.902
TDGF1	BLK	0.902
LYN	BLK	0.902
EPHA6	EPHA7	0.902
EPHA6	EPHA5	0.902
FGR	TDGF1	0.902
PDGFRB	BLK	0.902
SNCA	BLK	0.902
CD79B	DOK1	0.902
EPHB1	EPHA6	0.901
EPHA6	EPHB2	0.901
EPHA6	EPHA3	0.901
ABL1	BLK	0.901
HCK	LCK	0.901
EPHB1	EPHA7	0.901
BLK	DOK1	0.901
EPHB2	EPHA7	0.901
S1PR1	PLCG1	0.901
FGR	BLK	0.901
EPHA3	EPHA5	0.901
EPHA3	EPHA4	0.901
EPHA6	EPHA4	0.901
ITK	BLK	0.901
DOK1	CD79A	0.901
EPHB1	EPHB2	0.900
PDGFB	DOK1	0.900
CD79B	VAV2	0.900
MLLT4	PDGFB	0.900
HCK	BLK	0.900
CD79B	RASA1	0.900

TMEM80		
node1	**node2**	**score**
TMEM171	TMEM218	0.714
TMEM171	TMEM80	0.651
TMEM171	CDKL5	0.564
TMEM171	TCTN1	0.546
TMEM218	ADCY3	0.539
TMEM171	ADCY3	0.538
TCTN1	TMEM218	0.533
TMEM80	CDKL5	0.487
TCTN1	ADCY3	0.468
TMEM80	TMEM218	0.449
TMEM80	ADCY3	0.441
TMEM80	FAM71E1	0.424
CDKL5	ADCY3	0.422
TCTN1	TMEM80	0.400

TYK2		
node1	**node2**	**score**
JAK3	STAT5A	0.998
JAK1	STAT5A	0.998
IFNAR1	TYK2	0.998
PIK3R1	PIK3CA	0.998
IL6R	IL6	0.998
JAK1	STAT5B	0.998
JAK3	STAT5B	0.998
JAK1	STAT6	0.997
IFNA2	IFNAR1	0.997
IRF9	STAT1	0.996
IRF9	STAT2	0.996
FOS	MAPK1	0.996
NFKB1	NFKBIA	0.996
JAK3	STAT6	0.996
IL6ST	IL6	0.996
STAT3	IL6	0.995
JAK1	STAT3	0.995
STAT5A	TYK2	0.995
IFNG	IL2	0.995
STAT5B	TYK2	0.995
IFNAR2	IFNAR1	0.995
JAK1	IL10RA	0.994
STAT1	JAK1	0.994
STAT1	TYK2	0.994
STAT2	TYK2	0.994
IFNB1	IFNAR1	0.993
FOS	MAPK3	0.993
STAT6	IL4	0.993
PIK3CB	PIK3R1	0.993
IL6ST	LIF	0.992
IFNA2	IFNAR2	0.992

TYK2		
node1	**node2**	**score**
SOCS3	STAT3	0.992
JAK1	STAT2	0.992
IL6ST	SOCS3	0.991
IL6	NFKB1	0.991
STAT3	MAPK1	0.991
JAK3	STAT3	0.990
JAK1	SOCS3	0.990
IL6R	IL6ST	0.990
STAT1	IFNAR1	0.989
JAK3	SOCS3	0.989
PTPN11	MAPK3	0.989
IL6R	STAT3	0.989
SOCS3	IL6	0.989
PIK3CD	PIK3R1	0.989
LIFR	OSM	0.989
STAT5A	IL2	0.988
STAT6	TYK2	0.988
CTF1	LIFR	0.988
FOS	IL2	0.988
STAT3	PIK3CA	0.988
STAT1	IL6	0.988
STAT5B	IL2	0.988
IL12RB1	IL23A	0.987
STAT2	IFNAR1	0.986
STAT1	SOCS3	0.986
TYK2	STAT3	0.986
STAT1	SOCS1	0.986
JAK1	SOCS1	0.986
PIK3CG	PIK3R1	0.985
JAK1	PTPN11	0.985
IL6	MAPK1	0.985

TYK2		
node1	**node2**	**score**
CNTF	LIFR	0.985
LIFR	LIF	0.985
SOCS1	TYK2	0.985
PIK3CG	PTPN11	0.985
FOS	IL6	0.985
STAT1	IFNG	0.984
STAT3	MAPK3	0.984
IFNA2	IFNG	0.984
IL12RB1	IL12RB2	0.984
SOCS3	STAT5B	0.983
JAK3	IL2	0.983
JAK3	STAT1	0.982
IFNG	IL23A	0.982
STAT1	PTPN11	0.982
IFNA17	IFNG	0.982
STAT3	IL23A	0.982
JAK1	IFNAR1	0.981
IL12RB1	IL4	0.981
IL4	IL12B	0.981
IL6	IL23A	0.981
IL6ST	IL11	0.981
IL6ST	STAT3	0.980
IL12B	IL23A	0.980
PTPN1	TYK2	0.980
SOCS1	IFNAR1	0.980
JAK1	IL4	0.980
IL2	MAPK1	0.979
IL12RB1	IL12B	0.979
IL6	IL12B	0.979
IL6ST	OSM	0.979
IL4	IL2	0.979

TYK2

node1	node2	score
IL12RB1	STAT4	0.979
PTPN11	PIK3CB	0.978
MAPK3	MAPK1	0.978
PTPN11	PIK3CA	0.978
PTPN11	MAPK1	0.978
JAK3	IL4	0.978
IL12B	IFNG	0.978
JAK1	PIK3CA	0.978
STAT5A	IL4	0.978
STAT5B	IL4	0.978
JAK3	PTPN6	0.978
JAK1	IL2	0.977
MAPK3	IL6	0.977
IL6	IL4	0.977
IFNA2	STAT2	0.976
STAT4	IL2	0.976
PIK3CD	IL2	0.976
MAPK3	NFKB1	0.976
IFNA17	IFNAR1	0.976
PIK3CB	IL2	0.976
STAT1	MAPK1	0.975
NFKB1	MAPK1	0.975
PIK3CA	NFKB1	0.975
PIK3CA	IL2	0.975
SOCS1	STAT6	0.975
FOS	IL4	0.975
IL12RB2	IL12B	0.975
PTPN1	JAK1	0.975
STAT5A	MAPK1	0.975
JAK1	PIK3CB	0.975
SOCS1	IL4	0.974
STAT5B	MAPK1	0.973
JAK3	IL6	0.973
PTPN11	SOCS3	0.973
JAK3	PTPN11	0.973
CBL	PIK3CA	0.973
PTPN11	CBL	0.973
PIK3CD	JAK1	0.973
PTPN11	IL2	0.972
PIK3R1	STAT3	0.972
SOCS1	IFNG	0.972
STAT4	IL12RB2	0.972
PIK3CB	CBL	0.971
IRF9	IFNAR1	0.971
IL6R	SOCS3	0.971
SOCS1	STAT3	0.971
PTPN11	IL6	0.971
CTF1	LIF	0.971
IL6R	JAK1	0.971
SOCS3	TYK2	0.971
STAT5A	SOCS3	0.970
IFNB1	STAT1	0.970
TYK2	IL4	0.970
STAT3	IL2	0.969
TYK2	PIK3CA	0.969
JAK1	IL6	0.969
STAT5A	SOCS1	0.969
STAT4	TYK2	0.969
SOCS1	STAT5B	0.969
IRF9	TYK2	0.969
JAK3	SOCS1	0.969
STAT1	STAT2	0.968
STAT5A	STAT3	0.968
SOCS1	IL2	0.968
CNTF	IL6ST	0.967
IL4	IFNG	0.967
IFNB1	TYK2	0.967
IFNG	MAPK1	0.967
STAT1	STAT5A	0.967
SOCS3	IL2	0.967
STAT1	IL2	0.967
STAT1	IFNAR2	0.966
IL6	IFNG	0.966
PTPN6	JAK1	0.966
IL6	IL2	0.966
IRF9	JAK1	0.965
STAT1	MAPK3	0.965
PTPN6	TYK2	0.965
PTPN1	STAT5B	0.964
PTPN1	STAT5A	0.964
STAT4	IFNG	0.964
TYK2	IL11	0.964
PTPN11	IL6ST	0.964
PIK3CG	CBL	0.964
IL12RB2	IL4	0.963
STAT4	IL12B	0.963
STAT3	IFNG	0.963
IFNAR2	STAT2	0.963
JAK1	IL6ST	0.962
IL6R	PTPN11	0.962
IFNAR2	JAK1	0.962
MAPK3	IL2	0.961
TYK2	IL6	0.961
IRF9	IFNAR2	0.961
STAT1	IL12B	0.961
STAT3	IL10RA	0.961
IFNB1	STAT2	0.961
NFKBIA	MAPK1	0.960
STAT1	STAT3	0.960
PTPN6	PIK3CG	0.960
PTPN11	TYK2	0.959
JAK1	PIK3R1	0.959
IFNAR2	TYK2	0.959
STAT6	IL12B	0.959
STAT1	IL6ST	0.959
PIK3CD	CBL	0.958
PIK3CA	IL4	0.958
PTPN6	PIK3CB	0.958
IFNB1	FOS	0.958
MAPK3	NFKBIA	0.958
PIK3R1	CBL	0.958
IFNB1	SOCS3	0.958
PIK3CD	PTPN11	0.957
JAK3	PIK3R1	0.957
STAT3	IL12B	0.957
STAT4	JAK1	0.957
IL12RB1	STAT1	0.957
JAK1	IL28RA	0.956
STAT1	IL23A	0.956
SOCS1	STAT2	0.956
STAT4	IL23A	0.956
NOS2	NFKBIA	0.956
IRF9	IFNB1	0.955
JAK1	OSM	0.955

TYK2		
node1	**node2**	**score**
JAK3	PIK3CD	0.955
IL6ST	CTF1	0.955
PIK3CA	NFKBIA	0.955
STAT1	IL10RA	0.954
PIK3CG	JAK1	0.954
FOS	STAT5B	0.954
STAT5A	FOS	0.954
TYK2	IL10RA	0.954
IFNB1	IFNAR2	0.954
SOCS3	IL23A	0.950
JAK3	PIK3CA	0.953
TYK2	CBL	0.952
JAK1	LIF	0.952
IL6R	CNTF	0.952
PTPN11	PIK3R1	0.952
PIK3R1	TYK2	0.952
STAT5B	STAT3	0.952
IFNA17	STAT2	0.952
IL6R	STAT1	0.951
IL12RB1	IL6	0.951
IL12RB1	STAT6	0.951
IL4	IL10RA	0.951
JAK3	PIK3CB	0.951
IL6ST	TYK2	0.951
SOCS3	IFNAR1	0.951
TYK2	IL12RB2	0.950
SOCS3	IL23A	0.950
IFNA17	IRF9	0.950
JAK1	IFNG	0.950
IRF9	IFNA2	0.950
IL6ST	LIFR	0.949

TYK2		
node1	**node2**	**score**
STAT5A	IFNG	0.949
MAPK3	IFNG	0.948
CNTF	JAK1	0.948
IL12RB1	TYK2	0.948
IL12RB1	STAT3	0.948
IFNA2	TYK2	0.948
TYK2	IL2	0.948
JAK1	MAPK1	0.948
IFNA2	JAK1	0.947
PIK3CG	MAPK1	0.947
PIK3CA	MAPK1	0.947
TYK2	OSM	0.947
IL12RB1	IFNG	0.947
FOS	IFNG	0.947
IL12RB2	IFNG	0.947
JAK1	IL11	0.946
PTPN1	PIK3CA	0.946
TYK2	NFKB1	0.946
PIK3CB	MAPK1	0.946
IFNB1	JAK1	0.945
JAK1	LIFR	0.945
SOCS3	IFNG	0.944
IFNAR1	IFNG	0.944
FOS	TYK2	0.944
PTPN6	IFNAR1	0.944
PIK3CD	PIK3CG	0.943
TYK2	IFNG	0.943
IL12B	NFKB1	0.943
PIK3CA	IFNG	0.943
PIK3CD	MAPK1	0.942
PTPN6	PIK3R1	0.942

TYK2		
node1	**node2**	**score**
TYK2	LIF	0.942
PTPN1	IFNAR1	0.942
IL6R	TYK2	0.942
IL23A	NFKB1	0.941
IFNA17	TYK2	0.941
TYK2	IL23A	0.941
STAT1	STAT5B	0.941
STAT5A	IL23A	0.941
JAK3	JAK1	0.941
IFNA17	IFNAR2	0.941
CBL	IL2	0.941
CNTF	TYK2	0.941
IFNA17	JAK1	0.941
STAT5B	IL10RA	0.941
JAK1	MAPK3	0.941
STAT4	STAT3	0.940
IL12RB1	STAT5A	0.940
TYK2	MAPK3	0.940
TYK2	MAPK1	0.940
STAT5A	IL12B	0.940
NOS2	TYK2	0.939
PIK3CB	TYK2	0.939
IFNB1	SOCS1	0.939
STAT1	IL12RB2	0.939
PIK3CG	TYK2	0.939
PIK3CD	TYK2	0.939
STAT5A	STAT5B	0.938
IFNAR2	IFNG	0.938
PIK3R1	NFKBIA	0.938
STAT3	IL12RB2	0.938
JAK3	MAPK1	0.938

TYK2		
node1	**node2**	**score**
JAK1	TYK2	0.938
IL6R	OSM	0.938
JAK1	CTF1	0.938
JAK3	MAPK3	0.938
JAK3	TYK2	0.938
JAK3	IL6R	0.938
STAT5A	IL10RA	0.937
PTPN11	IFNAR1	0.937
SOCS3	IL12B	0.937
PIK3CB	MAPK3	0.936
PIK3CG	MAPK3	0.936
PTPN11	STAT2	0.936
PIK3CD	MAPK3	0.936
PTPN6	PTPN11	0.935
TYK2	NFKBIA	0.935
PIK3CA	MAPK3	0.935
JAK3	STAT4	0.935
TYK2	IL12B	0.934
IL6R	MAPK3	0.934
IL28RA	TYK2	0.934
IL6R	MAPK1	0.934
TYK2	LIFR	0.934
NOS2	IL23A	0.934
IFNA2	SOCS1	0.933
CTF1	TYK2	0.933
PTPN6	MAPK1	0.933
SOCS1	CBL	0.931
IFNA2	SOCS3	0.931
IL12RB1	SOCS1	0.930
NOS2	IL12B	0.930
JAK1	CBL	0.930

TYK2		
node1	**node2**	**score**
JAK3	STAT2	0.930
STAT5A	IL6ST	0.930
PIK3CA	IL23A	0.929
IL12RB1	SOCS3	0.929
IFNA17	SOCS1	0.929
PTPN6	IL2	0.929
IFNA17	IFNB1	0.929
IL6R	IL11	0.929
PIK3CG	PIK3CA	0.929
PTPN6	MAPK3	0.929
IL12RB1	IL2	0.928
IL11	LIFR	0.928
IL6ST	IFNG	0.928
STAT6	IL12RB2	0.928
PTPN11	IFNG	0.927
CBL	IL6	0.927
IRF9	STAT3	0.926
SOCS3	CBL	0.926
PIK3R1	IL4	0.926
STAT4	NFKB1	0.926
IL6	OSM	0.926
PIK3R1	NFKB1	0.925
SOCS3	SOCS1	0.925
IL23A	NFKBIA	0.924
PTPN6	STAT2	0.924
CBL	IL4	0.924
IFNA17	SOCS3	0.924
IL6ST	IL12RB2	0.924
PTPN1	STAT2	0.923
IL12B	NFKBIA	0.923
FOS	IL12B	0.922

TYK2		
node1	**node2**	**score**
JAK3	CBL	0.922
SOCS1	IL12B	0.922
PIK3CG	PIK3CB	0.922
STAT4	IL6ST	0.921
IL6ST	IL2	0.921
PIK3R1	IL2	0.920
IL12RB2	IL23A	0.920
IL12RB1	NFKB1	0.919
IL6ST	STAT2	0.919
IFNA17	PTPN6	0.918
STAT5A	IL12RB2	0.918
PTPN6	IFNG	0.918
IL12RB1	NOS2	0.918
PTPN6	IFNA2	0.918
PIK3R1	IFNG	0.917
FOS	IL12RB2	0.916
PTPN6	IFNB1	0.916
IL12RB1	FOS	0.916
IRF9	FOS	0.915
IFNA17	PTPN1	0.915
PTPN1	PIK3R1	0.915
IFNA2	PTPN1	0.915
CBL	IFNG	0.914
IFNB1	PTPN1	0.914
IFNB1	IFNA2	0.914
SOCS1	IL12RB2	0.913
PIK3CB	PIK3CA	0.913
IFNA2	PTPN11	0.913
LIFR	IL6	0.912
PTPN1	IFNG	0.911
IL6R	IL2	0.911

TYK2		
node1	**node2**	**score**
IL6R	IL4	0.911
IFNA17	PTPN11	0.911
IL6R	CTF1	0.910
IL6R	CBL	0.910
PIK3CA	IL12B	0.910
IFNB1	PTPN11	0.909
IL12RB1	PIK3CA	0.907
JAK3	PIK3CG	0.906
PIK3CD	PIK3CA	0.905
NOS2	IL12RB2	0.905
JAK3	IL28RA	0.903
PIK3R1	IL12B	0.903
PIK3CD	PIK3CB	0.902
IL12RB1	NFKBIA	0.901
IFNA2	IL28RA	0.901
IL6	IL10RA	0.901
PIK3R1	IL23A	0.901
IL12RB1	PIK3R1	0.900
IFNA17	IFNA2	0.900

TMED1		
node1	**node2**	**score**
IL1RL1	TMED1	0.771
TMED10	TMED1	0.703

ALDH16A1

node1	node2	score
ACACA	ACACB	0.999
ACACA	ACLY	0.999
ACACB	ACLY	0.999
HADHA	EHHADH	0.990
ACACA	EHHADH	0.964
HADHA	ACACB	0.963
ACACB	EHHADH	0.962
HADHA	ACACA	0.961
EHHADH	AGXT2	0.952
ABAT	EHHADH	0.950
DERA	ALDH16A1	0.944
ABAT	AGXT2	0.921
GLDC	AGXT2	0.906
ACLY	EHHADH	0.881
HADHA	ACLY	0.873
ALDH16A1	SPG21	0.866
ALDH16A1	EHHADH	0.777
HADHA	ALDH16A1	0.777
GLDC	ALDH16A1	0.761
ALDH16A1	ACLY	0.751
ACLY	UMPS	0.745
AGXT2L2	ALDH16A1	0.737
ALDH16A1	AGXT2	0.737
ALDH16A1	ABAT	0.737
AGXT2L1	ALDH16A1	0.737
ACACA	UMPS	0.733
ACACB	UMPS	0.733
GLDC	ACLY	0.732
DERA	ACLY	0.718
ACACA	ALDH16A1	0.712
ACACB	ALDH16A1	0.712

ALDH16A1

node1	node2	score
ALDH16A1	UMPS	0.703
ADHFE1	ALDH16A1	0.701

UBE2L3

node1	node2	score
UBA52	RPS27A	0.999
CUL1	RBX1	0.999
CUL1	SKP1	0.999
SKP1	RBX1	0.999
UBE2D2	UBE2V1	0.998
UBE2D2	ANAPC11	0.998
CUL2	RBX1	0.998
UBA52	HACE1	0.997
UBE2V2	RNF4	0.996
UBA52	UBC	0.996
UBA52	UBB	0.996
UBA52	UBE2D2	0.995
UBE2L3	WWP1	0.995
UBE2D2	UBA1	0.995
UBA52	UBA6	0.995
NEDD4	RPS27A	0.994
UBE2D2	RPS27A	0.994
UBA52	UBA1	0.994
UBA52	UBE2L3	0.994
UBE2V2	UBE2L3	0.993
ARIH2	UBE2L3	0.993
UBA52	HERC3	0.993
ANAPC11	SKP1	0.993
UBA52	UBA7	0.992
UBA52	UBA3	0.992
UBE2D2	UBC	0.991
NEDD4L	UBE2D2	0.991
UBE2D2	UBA6	0.991
CUL2	SKP1	0.991
UBA52	HERC5	0.990
UBE2D2	STUB1	0.990

UBE2L3

node1	node2	score
HERC1	UBA52	0.990
UBE2V2	UBE2D2	0.990
UBA52	UBE3A	0.990
UBA52	HERC2	0.990
UBA52	HERC4	0.990
UBA52	HERC6	0.990
UBA52	PJA1	0.989
UBA52	NEDD4	0.989
UBA1	RPS27A	0.989
UBA52	NEDD4L	0.989
UBA52	SMURF2	0.989
UBA52	TRIP12	0.988
UBE2D2	UBB	0.988
UBA52	SMURF1	0.988
UBA52	ITCH	0.988
UBE3A	UBE2L3	0.988
UBA52	HUWE1	0.988
UBE2L3	UBA1	0.987
TRIP12	UBOX5	0.987
UBC	UBB	0.987
UBA52	KIAA0317	0.987
UBA52	HECW2	0.987
UBE2D2	UBA7	0.987
UBA52	UBE3C	0.987
UBA52	WWP1	0.987
UBC	TRIP12	0.986
UBE2D2	NEDD4	0.986
UBE2L3	RNF19A	0.986
UBA7	RPS27A	0.986
UBE2D2	RBX1	0.985
UBE2L3	HACE1	0.985

UBE2L3		
node1	**node2**	**score**
ANAPC11	CUL1	0.985
UBA6	RPS27A	0.985
ANAPC11	RBX1	0.984
UBC	UBA1	0.984
UBE2D2	HUWE1	0.984
UBC	CUL1	0.984
UBE2D2	UBE3A	0.983
UBA3	CUL1	0.982
SUMO1	RNF4	0.982
CUL7	RBX1	0.982
UBE2D2	RNF4	0.981
RPS27A	SMURF2	0.981
UBB	TRIP12	0.981
UBA1	CUL1	0.981
CUL2	ANAPC11	0.981
UBE2D2	CBL	0.981
UBA6	UBB	0.980
UBE2V1	RNF4	0.980
CUL7	SKP1	0.980
UBE2D2	ITCH	0.980
UBE2D2	SKP1	0.980
UBE2D2	UBE2L3	0.979
UBC	UBA6	0.979
NEDD4L	NEDD4	0.979
HERC5	HERC6	0.979
UBE2D2	PJA1	0.979
UBE2D2	CUL1	0.979
UBA7	HERC5	0.978
UBE2L3	UBA7	0.978
UBC	UBE2V1	0.978
NEDD4	UBC	0.978
UBB	RPS27A	0.978
UBB	HACE1	0.978
RPS27A	HACE1	0.978
UBC	HACE1	0.977
UBE2V2	UBC	0.977
UBE2L3	RNF144B	0.977
NEDD4L	UBC	0.977
UBC	RPS27A	0.976
UBE2D2	SMURF2	0.976
UBA1	UBB	0.976
UBE2V2	UBE2V1	0.976
NEDD4L	RPS27A	0.976
UBA52	CUL1	0.975
UBE2D2	WWP1	0.975
CUL1	UBB	0.975
UBE2L3	UBA6	0.975
UBE2L3	RBX1	0.975
UBE2D2	UBE3C	0.975
UBE2L3	STUB1	0.974
UBA3	RBX1	0.974
UBE2L3	UBE2V1	0.974
NEDD4	UBE2L3	0.974
RNF19B	UBE2L3	0.973
NEDD4	UBB	0.973
UBE2D2	UBA3	0.973
UBE2D2	SMURF1	0.973
NEDD4L	UBE2L3	0.973
ARIH1	UBE2L3	0.973
ITCH	UBC	0.973
UBC	SKP1	0.972
UBA52	STUB1	0.972
CUL1	RPS27A	0.972
SMURF1	RPS27A	0.972
UBC	UBE3C	0.972
CUL2	UBA52	0.971
SUMO1	UBC	0.971
UBB	SMURF2	0.971
CUL7	UBA3	0.971
RPS27A	HUWE1	0.971
ANAPC11	UBC	0.971
UBE3A	UBC	0.971
UBC	SMURF2	0.970
ITCH	UBB	0.970
RBCK1	UBE2L3	0.970
UBE2V2	STUB1	0.970
UBE2D2	RBCK1	0.970
ITCH	RPS27A	0.970
UBC	UBE2L3	0.970
RPS27A	WWP1	0.970
ITCH	UBE2L3	0.969
UBC	WWP1	0.969
UBE2L3	HERC3	0.969
ANAPC11	UBB	0.969
UBE2L3	SMURF2	0.969
CUL2	UBC	0.969
UBE2L3	UBE3C	0.969
HERC4	UBE2L3	0.968
UBR1	TRIP12	0.968
UBC	UBA7	0.968
UBA7	UBB	0.968
SUMO1	UBE2L3	0.968
UBE2L3	RPS27A	0.968
CUL2	UBA3	0.967
UBE2D2	UBR1	0.967
UBC	HERC2	0.967
UBC	HERC3	0.967
UBA3	UBC	0.966
UBA3	SKP1	0.966
UBB	SKP1	0.966
UBC	STUB1	0.966
UBE2L3	HERC6	0.966
UBA1	HUWE1	0.966
CUL7	UBE2D2	0.966
SUMO1	UBA1	0.966
PARK2	UBE2L3	0.966
UBE2D2	HACE1	0.965
UBA3	UBB	0.965
TRIP12	HACE1	0.964
SMURF1	UBE2L3	0.964
UBE2L3	UBB	0.963
RPS27A	SKP1	0.963
UBB	STUB1	0.963
UBC	HUWE1	0.963
UBB	HUWE1	0.963
UBE2L3	HUWE1	0.963
UBC	RBX1	0.963
HERC4	UBC	0.963
UBA52	UBOX5	0.963
UBE2L3	SKP1	0.963
NEDD4L	UBB	0.962
UBC	UBOX5	0.962
UBE2D2	TRIP12	0.962
UBE2V2	UBB	0.962

UBE2L3		
node1	**node2**	**score**
UBB	UBOX5	0.962
UBE2D2	HERC4	0.962
UBA7	CUL1	0.961
UBB	RBX1	0.961
SMURF1	UBC	0.961
RPS27A	HECW2	0.961
UBA52	SKP1	0.961
UBE2L3	HECW2	0.961
UBA52	SUMO1	0.960
KIAA0317	UBC	0.960
TRIP12	RBX1	0.960
KIAA0317	TRIP12	0.960
PARK2	STUB1	0.960
UBE3A	UBB	0.960
CUL1	UBA6	0.960
UBA3	UBE2L3	0.960
UBA1	SKP1	0.960
PJA1	UBE2L3	0.959
CUL2	HACE1	0.959
UBE2V1	UBB	0.959
NEDD4	CUL1	0.959
UBE2V1	STUB1	0.959
UBE2L3	CBL	0.959
CUL1	HACE1	0.959
KIAA0317	UBE2L3	0.959
UBE2V2	RPS27A	0.958
SMURF1	UBB	0.958
UBE2D2	HERC2	0.958
UBE2V1	RPS27A	0.958
UBE2L3	TRIP12	0.958
UBE2L3	RNF4	0.958

UBE2L3		
node1	**node2**	**score**
UBE3A	UBA1	0.957
UBE3C	UBR1	0.957
TRIP12	HUWE1	0.957
UBE2V2	UBA52	0.957
UBA1	RBX1	0.957
UBA6	TRIP12	0.955
UBC	CBL	0.955
SUMO1	UBB	0.955
NEDD4	RBX1	0.954
UBB	WWP1	0.954
UBE2D2	PARK2	0.954
UBC	HECW2	0.954
CUL1	TRIP12	0.954
UBE2L3	HERC5	0.954
CUL2	UBE2D2	0.954
UBB	HECW2	0.954
ANAPC11	UBE2L3	0.953
NEDD4	SKP1	0.953
CUL2	RPS27A	0.953
UBE2L3	UBOX5	0.953
UBA1	UBR1	0.953
UBE3C	UBB	0.953
UBA52	UBE2V1	0.953
UBC	HERC5	0.952
UBA1	HACE1	0.952
UBA7	HERC6	0.952
UBA52	RBX1	0.952
HERC1	UBE2L3	0.952
UBE3C	TRIP12	0.952
CUL2	UBB	0.952
UBE2L3	CUL1	0.952

UBE2L3		
node1	**node2**	**score**
RPS27A	HERC2	0.951
RPS27A	HERC5	0.951
HERC4	UBB	0.951
UBB	HERC5	0.951
HERC1	UBC	0.951
UBB	HERC3	0.951
UBB	HERC2	0.951
HERC4	RPS27A	0.951
RPS27A	HERC3	0.951
HERC1	UBB	0.951
HERC1	RPS27A	0.951
UBC	HERC6	0.951
RPS27A	HERC6	0.951
UBB	HERC6	0.951
CUL2	CUL7	0.950
UBE2L3	HERC2	0.950
UBE2D2	HERC6	0.950
UBE3A	CUL1	0.950
HERC1	UBE2D2	0.950
UBA1	TRIP12	0.950
UBE2D2	HERC5	0.950
TRIP12	SKP1	0.950
UBE2L3	UBR1	0.950
UBE2D2	HERC3	0.950
UBE3A	RPS27A	0.950
UBE3A	HERC2	0.949
NEDD4	UBA7	0.949
UBE3A	SKP1	0.949
CUL2	UBE3A	0.949
PARK2	UBC	0.949
UBA7	TRIP12	0.949

UBE2L3		
node1	**node2**	**score**
UBA3	RPS27A	0.948
UBA1	STUB1	0.948
UBE3A	RBX1	0.947
CUL7	UBE2L3	0.947
UBA52	ANAPC11	0.947
CUL1	HUWE1	0.947
PARK2	CUL1	0.947
HERC2	RBX1	0.947
CUL1	HERC2	0.947
UBE3C	UBOX5	0.946
SUMO1	RPS27A	0.946
CUL2	UBE2L3	0.946
NEDD4L	UBA1	0.945
RPS27A	RBX1	0.945
KIAA0317	UBR1	0.945
UBE2D2	UBOX5	0.944
UBE2D2	KIAA0317	0.944
RPS27A	UBOX5	0.944
PARK2	UBB	0.944
PJA1	UBC	0.944
CUL2	UBA1	0.944
CUL1	HERC3	0.944
HERC6	HERC3	0.943
CUL1	HERC5	0.943
NEDD4	TRIP12	0.943
UBE3A	UBR1	0.943
UBA7	HERC3	0.943
ITCH	TRIP12	0.943
CUL1	HERC6	0.942
UBA7	SKP1	0.942
HERC4	CUL1	0.942

UBE2L3		
node1	**node2**	**score**
UBE3A	UBA6	0.942
HERC1	UBOX5	0.942
CUL2	HERC4	0.941
CUL2	HERC2	0.941
UBC	UBR1	0.941
CUL2	HERC1	0.941
CUL2	HERC5	0.941
CUL2	HERC6	0.941
HERC1	CUL1	0.941
CUL2	HERC3	0.941
UBE3A	ANAPC11	0.941
HERC3	UBOX5	0.940
HERC2	UBOX5	0.940
KIAA0317	RPS27A	0.940
UBA7	RBX1	0.940
HERC5	UBOX5	0.940
UBC	RNF4	0.940
HERC6	UBOX5	0.940
HERC4	UBOX5	0.940
UBE2V1	UBA1	0.940
TRIP12	WWP1	0.940
NEDD4	UBA1	0.940
UBR1	HUWE1	0.939
UBA6	SKP1	0.939
RBCK1	UBC	0.939
UBE2D2	HECW2	0.939
UBA7	UBR1	0.939
UBA1	UBE3C	0.938
PJA1	UBOX5	0.938
HERC4	HERC6	0.938
NEDD4L	TRIP12	0.938

UBE2L3		
node1	**node2**	**score**
TRIP12	RPS27A	0.938
TRIP12	HECW2	0.938
HERC1	HERC3	0.938
UBA6	UBR1	0.938
ITCH	NEDD4	0.938
UBE2V2	UBE3C	0.938
SMURF1	TRIP12	0.937
NEDD4L	SKP1	0.937
PARK2	UBE2V1	0.937
UBE3A	UBA3	0.937
HERC1	HERC2	0.937
NEDD4	WWP1	0.937
UBA7	UBE3C	0.936
UBOX5	RBX1	0.936
UBE2V2	SUMO1	0.936
PJA1	UBB	0.936
SUMO1	RBX1	0.936
ANAPC11	TRIP12	0.936
KIAA0317	UBB	0.936
TRIP12	SMURF2	0.936
UBR1	HACE1	0.936
NEDD4L	CUL1	0.936
UBE3C	RPS27A	0.936
PARK2	RNF19A	0.936
SMURF1	SMURF2	0.935
PJA1	RPS27A	0.935
PJA1	ANAPC11	0.935
ARIH2	UBC	0.935
CUL1	SMURF2	0.935
UBA6	RBX1	0.934
CUL7	CUL1	0.934

UBE2L3		
node1	**node2**	**score**
HERC4	UBR1	0.934
HERC3	HERC2	0.934
UBE2D2	RNF19A	0.934
HERC1	UBR1	0.934
NEDD4L	WWP1	0.934
SMURF1	CUL1	0.934
HERC5	STUB1	0.934
NEDD4	SMURF2	0.934
UBB	UBR1	0.934
UBA6	UBE3C	0.934
KIAA0317	CUL1	0.933
UBE3A	STUB1	0.933
ITCH	UBA6	0.933
UBE2D2	ARIH2	0.933
STUB1	UBOX5	0.933
UBE3A	SUMO1	0.933
ITCH	UBR1	0.933
NEDD4L	ITCH	0.933
UBE2V2	UBA1	0.932
NEDD4	UBOX5	0.932
UBE3A	UBA7	0.932
UBR1	SKP1	0.932
UBA1	UBOX5	0.932
UBE3A	UBOX5	0.932
UBE3A	PARK2	0.932
ITCH	CUL1	0.931
ANAPC11	HERC5	0.931
UBE2V1	SKP1	0.931
ANAPC11	HERC6	0.931
HERC4	TRIP12	0.931
HERC5	RBX1	0.931

UBE2L3		
node1	**node2**	**score**
ITCH	UBE3C	0.931
HERC1	RBX1	0.931
HERC1	ANAPC11	0.931
CUL1	UBOX5	0.931
HERC6	RBX1	0.931
HERC4	UBA6	0.931
NEDD4	UBR1	0.931
HERC3	RBX1	0.931
UBE2V2	SKP1	0.931
PARK2	RBCK1	0.931
ANAPC11	HERC3	0.931
ANAPC11	HERC2	0.931
HERC4	ANAPC11	0.931
UBE2V2	RBX1	0.931
UBA3	ANAPC11	0.931
HERC4	RBX1	0.931
PJA1	HACE1	0.930
SKP1	STUB1	0.930
HUWE1	RBX1	0.930
UBE3A	UBE3C	0.930
CUL2	NEDD4	0.930
ITCH	UBA1	0.930
UBE3A	UBE2V1	0.930
UBA3	HACE1	0.930
CUL1	UBE3C	0.930
NEDD4	UBA6	0.930
UBA7	HACE1	0.930
UBA6	UBOX5	0.930
HACE1	UBOX5	0.930
UBE2V2	NEDD4L	0.930
UBA6	HACE1	0.930

UBE2L3		
node1	**node2**	**score**
NEDD4L	UBOX5	0.930
CUL1	WWP1	0.930
UBA7	UBOX5	0.930
CUL7	ANAPC11	0.930
NEDD4L	RBX1	0.929
UBE2V2	UBA3	0.929
HERC1	HERC4	0.929
HERC1	UBE3A	0.929
TRIP12	HERC3	0.929
ANAPC11	RPS27A	0.929
CUL1	STUB1	0.929
ITCH	RBX1	0.929
HERC4	UBE3C	0.929
KIAA0317	UBE3C	0.929
NEDD4L	STUB1	0.928
NEDD4	UBE3C	0.928
UBE2V2	UBE3A	0.928
STUB1	RBX1	0.928
UBE2V2	UBA7	0.928
UBE3C	WWP1	0.928
WWP1	UBOX5	0.928
UBE3A	TRIP12	0.928
CUL2	UBA7	0.928
PJA1	RBX1	0.928
HACE1	RBX1	0.928
UBE3C	HERC3	0.928
UBR1	UBOX5	0.927
RPS27A	STUB1	0.927
CUL1	UBR1	0.927
NEDD4L	UBE3C	0.926
UBA3	HERC2	0.926

UBE2L3		
node1	**node2**	**score**
CUL2	NEDD4L	0.926
CUL2	UBA6	0.926
HECW2	UBOX5	0.926
KIAA0317	UBOX5	0.926
SMURF1	UBOX5	0.926
ITCH	KIAA0317	0.926
HUWE1	UBOX5	0.926
UBB	CBL	0.926
HERC4	ITCH	0.926
ITCH	UBOX5	0.926
SMURF2	UBOX5	0.926
ANAPC11	UBOX5	0.926
HERC4	UBA3	0.925
PJA1	TRIP12	0.925
UBA6	HERC5	0.925
UBE3A	RNF4	0.925
UBR1	HERC3	0.925
NEDD4L	UBA7	0.925
UBE2V1	UBOX5	0.925
TRIP12	STUB1	0.925
PJA1	UBA1	0.924
UBA1	SMURF2	0.924
SMURF2	SKP1	0.924
HERC4	UBA1	0.924
KIAA0317	RBX1	0.924
NEDD4L	UBR1	0.924
UBA1	WWP1	0.924
PARK2	RPS27A	0.923
UBA6	HUWE1	0.923
PJA1	UBE2V1	0.923
UBA1	HERC5	0.923

UBE2L3		
node1	**node2**	**score**
PARK2	UBA1	0.923
UBE3A	RNF19A	0.923
UBE2V1	UBA7	0.923
HERC1	ITCH	0.923
HERC4	HACE1	0.923
PARK2	WWP1	0.923
RPS27A	CBL	0.923
ITCH	SKP1	0.922
PJA1	HUWE1	0.922
HUWE1	SKP1	0.922
UBE3C	SMURF2	0.922
UBR1	HERC2	0.922
ANAPC11	UBA1	0.922
UBA52	CBL	0.922
UBE3A	WWP1	0.922
UBE2V1	RBX1	0.922
UBE2D2	RNF144B	0.922
HERC3	HACE1	0.922
NEDD4	STUB1	0.922
SMURF1	UBA1	0.922
HERC2	SKP1	0.921
CUL7	HERC2	0.921
HERC4	KIAA0317	0.921
CUL2	WWP1	0.921
UBE2D2	RNF19B	0.921
UBE2V2	NEDD4	0.921
HERC1	TRIP12	0.921
CUL7	UBA1	0.921
WWP1	SKP1	0.921
KIAA0317	HERC3	0.921
SMURF2	RBX1	0.921

UBE2L3		
node1	**node2**	**score**
HERC4	UBA7	0.920
SMURF1	UBE3C	0.920
NEDD4L	UBE3A	0.920
TRIP12	HERC5	0.920
SMURF1	RBX1	0.920
UBE3A	PJA1	0.920
CUL2	HUWE1	0.920
TRIP12	HERC6	0.920
UBA3	TRIP12	0.920
UBR1	WWP1	0.920
PARK2	UBA6	0.920
UBE3A	NEDD4	0.920
UBE3C	HERC5	0.920
UBE3A	ARIH2	0.920
CUL2	SMURF1	0.920
CUL2	SMURF2	0.920
HERC4	HERC3	0.920
NEDD4L	UBA6	0.920
UBA3	UBA1	0.920
HERC4	HERC2	0.920
UBE3C	HERC6	0.920
SMURF1	SKP1	0.920
UBE2V1	CUL1	0.920
WWP1	RBX1	0.920
HERC1	UBA3	0.919
UBA1	RNF4	0.919
UBE3A	ITCH	0.919
PJA1	NEDD4	0.919
HERC5	HERC3	0.919
ITCH	UBA3	0.919
SMURF1	STUB1	0.919

UBE2L3		
node1	**node2**	**score**
UBR1	HERC6	0.919
CUL7	UBC	0.919
NEDD4L	ANAPC11	0.919
ANAPC11	NEDD4	0.919
RNF4	TRIP12	0.919
UBR1	HERC5	0.919
ANAPC11	UBR1	0.919
UBE3C	HECW2	0.919
UBE2V2	CUL1	0.919
UBA3	HERC3	0.919
ANAPC11	HACE1	0.918
UBA3	UBR1	0.918
NEDD4	UBE2V1	0.918
ANAPC11	STUB1	0.918
SKP1	UBOX5	0.918
UBE2V2	WWP1	0.918
UBE2V2	ANAPC11	0.918
HUWE1	STUB1	0.918
RNF19A	UBR1	0.918
PARK2	SKP1	0.918
UBA1	HECW2	0.918
ARIH2	RBX1	0.918
NEDD4	HERC5	0.918
UBA52	UBR1	0.918
CUL2	UBOX5	0.918
CUL2	ITCH	0.918
UBA6	WWP1	0.918
CUL2	UBE3C	0.918
ITCH	WWP1	0.918
UBA3	HERC5	0.918
NEDD4	HERC3	0.917

UBE2L3		
node1	**node2**	**score**
HERC4	PJA1	0.917
CUL2	KIAA0317	0.917
SMURF1	UBA7	0.917
UBA7	RNF4	0.917
PJA1	HERC6	0.917
HERC1	KIAA0317	0.917
HERC1	HACE1	0.917
RBCK1	UBE2V1	0.917
HACE1	HERC2	0.917
HERC6	HACE1	0.917
PJA1	HERC5	0.917
HERC1	PJA1	0.917
CUL1	HECW2	0.917
PJA1	HERC3	0.917
SMURF1	UBA6	0.917
UBA6	HERC6	0.917
UBE2V2	UBA6	0.917
CUL2	CUL1	0.917
PJA1	UBR1	0.917
NEDD4L	UBE2V1	0.917
PJA1	HERC2	0.917
HERC5	HACE1	0.917
PARK2	RBX1	0.916
PJA1	SMURF1	0.916
UBA3	UBA6	0.916
HERC4	NEDD4	0.916
NEDD4L	UBA3	0.916
UBE3A	HERC3	0.916
ITCH	UBA7	0.916
HERC4	RNF19A	0.916
PARK2	NEDD4	0.916

UBE2L3		
node1	**node2**	**score**
PJA1	SMURF2	0.916
CUL2	HECW2	0.916
PJA1	UBA7	0.916
WWP1	HACE1	0.916
NEDD4	HACE1	0.916
KIAA0317	NEDD4	0.916
UBE3C	HACE1	0.916
UBE3C	RBX1	0.916
UBE2V2	PJA1	0.916
CUL2	TRIP12	0.916
UBA1	HERC2	0.916
ANAPC11	SMURF2	0.916
UBA3	NEDD4	0.916
PJA1	UBA6	0.916
NEDD4	RNF19A	0.916
ITCH	STUB1	0.916
UBA3	HERC6	0.915
UBA7	SMURF2	0.915
UBA1	HERC3	0.915
RNF19A	STUB1	0.915
RNF19A	TRIP12	0.915
UBA1	HERC6	0.915
WWP1	STUB1	0.915
SMURF2	STUB1	0.915
NEDD4L	HACE1	0.915
UBA6	SMURF2	0.915
UBA6	HERC2	0.915
HACE1	SKP1	0.915
UBR1	SMURF2	0.915
UBE3C	HUWE1	0.915
ARIH2	UBE2V1	0.915

UBE2L3		
node1	**node2**	**score**
SMURF1	HACE1	0.915
CUL7	UBE3A	0.915
UBA6	HERC3	0.915
HACE1	HECW2	0.915
UBA7	HUWE1	0.915
UBA3	UBE3C	0.915
HACE1	SMURF2	0.915
HERC3	SKP1	0.915
UBA3	KIAA0317	0.915
HERC1	RNF19A	0.915
UBA3	WWP1	0.915
ITCH	HACE1	0.915
UBA7	WWP1	0.915
UBA3	UBE2V1	0.915
UBE2V1	UBE3C	0.914
HERC1	STUB1	0.914
HUWE1	HECW2	0.914
HERC1	NEDD4	0.914
KIAA0317	WWP1	0.914
UBA3	HUWE1	0.914
UBR1	HECW2	0.914
SMURF1	UBR1	0.914
ANAPC11	UBE2V1	0.914
UBR1	RPS27A	0.914
HERC5	HERC2	0.914
UBR1	RBX1	0.914
ITCH	RNF19A	0.914
KIAA0317	HUWE1	0.914
ARIH2	SKP1	0.913
HERC6	HECW2	0.913
RNF4	UBA6	0.913

UBE2L3		
node1	**node2**	**score**
UBE3C	STUB1	0.913
UBA3	SMURF2	0.913
HERC1	UBA7	0.913
ITCH	UBE2V1	0.913
HERC4	WWP1	0.913
UBA3	HECW2	0.913
HERC3	HECW2	0.913
WWP1	HUWE1	0.913
HERC5	HECW2	0.913
RNF4	UBR1	0.913
ARIH2	RBCK1	0.913
UBA7	HERC2	0.913
HERC4	HECW2	0.913
UBA6	HECW2	0.913
UBA3	UBA7	0.913
UBE2V1	UBA6	0.913
HERC1	UBA1	0.913
NEDD4	HUWE1	0.913
RNF19B	HERC5	0.913
HERC1	UBA6	0.913
ITCH	RNF144B	0.913
UBA52	PARK2	0.912
HERC6	SKP1	0.912
UBE3C	SKP1	0.912
HERC5	SKP1	0.912
ARIH2	UBR1	0.912
CUL7	PARK2	0.912
ARIH2	RNF4	0.912
HACE1	STUB1	0.912
RNF4	RBX1	0.912
CUL2	UBR1	0.912

UBE2L3		
node1	**node2**	**score**
RNF19B	UBC	0.912
HERC4	RNF144B	0.912
HERC4	SKP1	0.912
UBE3A	SMURF2	0.912
CUL2	STUB1	0.912
RBCK1	UBA1	0.912
RNF19A	RNF4	0.912
HERC1	UBE3C	0.912
ARIH2	UBOX5	0.912
PJA1	CUL1	0.912
UBR1	STUB1	0.912
HERC4	HERC5	0.912
HERC1	SKP1	0.912
UBE3A	HACE1	0.912
HERC6	HERC2	0.912
UBE3A	RBCK1	0.912
UBE2V2	UBR1	0.911
UBE2V2	UBOX5	0.911
UBA3	UBOX5	0.911
HERC1	HERC6	0.911
PJA1	KIAA0317	0.911
NEDD4L	HUWE1	0.911
NEDD4L	KIAA0317	0.911
RBCK1	SKP1	0.911
KIAA0317	UBA1	0.911
RNF19A	UBA7	0.911
ANAPC11	HUWE1	0.911
RBCK1	RNF19A	0.911
UBE3A	SMURF1	0.911
UBA7	HECW2	0.911
HUWE1	RNF144B	0.911

UBE2L3		
node1	**node2**	**score**
WWP1	HERC3	0.911
ITCH	HERC3	0.911
HERC4	RNF19B	0.911
ITCH	RBCK1	0.911
ANAPC11	WWP1	0.911
PJA1	STUB1	0.911
CUL2	ARIH2	0.911
HERC1	HERC5	0.911
KIAA0317	HECW2	0.911
RNF19A	HUWE1	0.911
UBE3A	HUWE1	0.910
RNF19A	HERC3	0.910
NEDD4L	HERC3	0.910
RNF4	SKP1	0.910
WWP1	RNF144B	0.910
CUL7	WWP1	0.910
CUL7	HUWE1	0.910
RNF19A	UBA1	0.910
RNF4	UBE3C	0.910
NEDD4	HECW2	0.910
RNF19B	SKP1	0.910
ITCH	HUWE1	0.910
ARIH2	HERC3	0.910
SMURF1	KIAA0317	0.910
RBCK1	UBB	0.910
RNF19A	SKP1	0.910
CUL2	UBE2V1	0.910
KIAA0317	UBA6	0.910
KIAA0317	UBA7	0.910
PJA1	WWP1	0.910
UBE3C	HERC2	0.910

UBE2L3		
node1	**node2**	**score**
HECW2	RBX1	0.910
ANAPC11	UBE3C	0.910
RNF4	STUB1	0.910
RBCK1	RNF4	0.910
UBE3A	HERC4	0.910
HUWE1	SMURF2	0.910
KIAA0317	SMURF2	0.910
UBE2V2	TRIP12	0.909
ARIH1	HERC5	0.909
NEDD4L	PJA1	0.909
CUL1	RNF144B	0.909
HERC1	WWP1	0.909
NEDD4L	HERC4	0.909
UBE3A	HECW2	0.909
UBA52	RBCK1	0.909
RBCK1	RPS27A	0.909
PJA1	SKP1	0.909
SMURF1	UBA3	0.909
PARK2	UBA7	0.909
RNF19A	UBA6	0.909
ITCH	ANAPC11	0.909
HERC1	ARIH2	0.909
RBCK1	CUL1	0.909
ANAPC11	KIAA0317	0.909
ITCH	PJA1	0.909
PJA1	UBE3C	0.909
SMURF1	ANAPC11	0.909
KIAA0317	RNF19A	0.909
PJA1	HECW2	0.909
KIAA0317	HACE1	0.908
KIAA0317	RNF4	0.908

UBE2L3		
node1	**node2**	**score**
ARIH2	HERC2	0.908
CUL7	NEDD4	0.908
SMURF1	HUWE1	0.908
UBE2V2	ITCH	0.908
NEDD4L	HERC5	0.908
RNF19A	CUL1	0.908
HERC1	RNF4	0.908
WWP1	SMURF2	0.908
ARIH2	CUL1	0.908
CUL7	RNF4	0.908
RBCK1	UBOX5	0.908
CUL7	SMURF1	0.908
RBCK1	NEDD4	0.908
RBCK1	UBA6	0.908
RBCK1	UBA7	0.908
PARK2	ANAPC11	0.908
HACE1	HUWE1	0.908
UBA3	RNF19A	0.908
RNF4	RNF144B	0.908
HERC3	HUWE1	0.908
HERC6	HUWE1	0.908
RNF19A	WWP1	0.908
UBE3A	KIAA0317	0.908
CUL2	RNF4	0.908
UBA3	ARIH2	0.908
RNF19A	UBE3C	0.908
NEDD4L	PARK2	0.908
ANAPC11	HECW2	0.908
ARIH2	WWP1	0.908
KIAA0317	SKP1	0.908
ARIH2	RNF19A	0.908

UBE2L3		
node1	**node2**	**score**
UBA3	RNF4	0.908
CUL1	RNF4	0.908
HERC5	HUWE1	0.908
UBE2V2	HERC2	0.908
RNF19B	RNF4	0.908
CUL2	PJA1	0.908
UBE2V1	HUWE1	0.908
PARK2	ARIH2	0.907
WWP1	HERC6	0.907
RNF4	HERC3	0.907
ARIH2	NEDD4	0.907
HECW2	SKP1	0.907
NEDD4L	SMURF1	0.907
ARIH2	KIAA0317	0.907
SMURF1	WWP1	0.907
RNF19B	HERC6	0.907
ANAPC11	RBCK1	0.907
UBE3A	HERC5	0.907
SUMO1	HERC2	0.907
ITCH	RNF19B	0.907
SMURF1	NEDD4	0.907
RNF19B	HERC3	0.907
ITCH	HERC2	0.907
UBE2V2	HERC5	0.907
RNF19A	UBE2V1	0.907
RNF19B	KIAA0317	0.907
RNF4	UBOX5	0.907
KIAA0317	HERC2	0.907
PARK2	UBOX5	0.907
WWP1	HERC5	0.907
HERC1	RBCK1	0.907

UBE2L3		
node1	**node2**	**score**
HERC4	RNF4	0.907
PARK2	HUWE1	0.907
KIAA0317	UBE2V1	0.907
SMURF1	UBE2V1	0.907
HERC4	ARIH2	0.907
PARK2	RNF144B	0.907
HERC3	RNF144B	0.907
RNF19A	UBB	0.907
NEDD4	RNF4	0.907
RNF144B	SKP1	0.906
HERC4	STUB1	0.906
RNF19B	HACE1	0.906
WWP1	HECW2	0.906
SMURF1	HERC6	0.906
HERC6	STUB1	0.906
UBA7	STUB1	0.906
HACE1	RNF144B	0.906
CUL2	RNF144B	0.906
HERC2	STUB1	0.906
ARIH2	UBA1	0.906
NEDD4	RNF144B	0.906
ANAPC11	UBA6	0.906
ARIH2	STUB1	0.906
HERC3	STUB1	0.906
UBE2V2	HERC4	0.906
SMURF1	HERC5	0.906
PJA1	UBA3	0.906
ITCH	HERC5	0.906
NEDD4L	SMURF2	0.906
UBE2V2	HACE1	0.906
HERC1	RNF144B	0.906

UBE2L3		
node1	**node2**	**score**
UBE2V1	TRIP12	0.906
ARIH2	TRIP12	0.906
HERC6	SMURF2	0.906
NEDD4	HERC6	0.906
ARIH2	UBE3C	0.906
ARIH2	HACE1	0.906
UBA1	UBA6	0.906
RNF19B	PARK2	0.906
UBE2V1	HACE1	0.906
HERC4	HUWE1	0.906
NEDD4L	RNF4	0.906
KIAA0317	RNF144B	0.906
ITCH	RNF4	0.906
RBCK1	HACE1	0.906
CUL7	HACE1	0.906
UBC	RNF19A	0.906
HERC5	SMURF2	0.906
PJA1	ARIH2	0.906
ANAPC11	UBA7	0.906
RNF19A	HACE1	0.906
UBE3A	RNF144B	0.906
ITCH	HERC6	0.906
HERC3	SMURF2	0.905
NEDD4L	HECW2	0.905
UBE2V1	HERC2	0.905
CUL7	UBR1	0.905
RNF19B	CUL1	0.905
HERC4	PARK2	0.905
NEDD4	HERC2	0.905
UBE2V1	HERC3	0.905
HERC4	SMURF2	0.905

	UBE2L3	
node1	**node2**	**score**
KIAA0317	HERC6	0.905
CUL7	UBOX5	0.905
RNF19B	UBOX5	0.905
CUL2	RNF19A	0.905
CUL7	UBA7	0.905
KIAA0317	HERC5	0.905
RNF19A	UBOX5	0.905
HERC4	UBE2V1	0.905
HERC1	UBE2V1	0.905
ANAPC11	ARIH2	0.905
UBE2V2	HUWE1	0.905
KIAA0317	STUB1	0.905
UBE2V1	UBR1	0.905
ARIH2	RNF144B	0.905
ITCH	ARIH2	0.905
UBE2V1	HERC5	0.905
NEDD4L	HERC6	0.905
UBE2V1	HERC6	0.905
CUL2	RBCK1	0.905
RNF19B	UBR1	0.905
ARIH2	UBA6	0.905
RBCK1	RBX1	0.905
UBR1	RNF144B	0.905
RNF4	HUWE1	0.905
CUL2	UBE2V2	0.905
UBA6	STUB1	0.905
UBE2V2	HERC6	0.905
RBCK1	STUB1	0.905
UBE2V2	HERC3	0.905
UBA52	RNF19A	0.905
CUL2	RNF19B	0.905

	UBE2L3	
node1	**node2**	**score**
UBE2V2	SMURF2	0.905
RNF144B	UBOX5	0.905
NEDD4L	RNF19A	0.905
ITCH	SMURF1	0.905
SMURF1	HERC3	0.905
RNF19B	UBA6	0.905
SMURF1	HERC2	0.905
UBE2V2	HERC1	0.905
HERC4	SMURF1	0.905
UBA52	RNF4	0.905
ITCH	SMURF2	0.905
ITCH	HECW2	0.904
CUL7	HERC5	0.904
UBE2V2	HECW2	0.904
SMURF2	HERC2	0.904
UBA3	STUB1	0.904
TRIP12	HERC2	0.904
RNF19B	SMURF1	0.904
RBCK1	HERC5	0.904
ARIH2	HERC6	0.904
HUWE1	HERC2	0.904
HERC1	HUWE1	0.904
RBCK1	HERC3	0.904
HERC5	RNF144B	0.904
RNF19B	HERC2	0.904
CUL7	RBCK1	0.904
RNF19A	HERC2	0.904
CUL7	HERC1	0.904
UBA7	UBA6	0.904
HERC6	RNF144B	0.904
RBCK1	HERC6	0.904

	UBE2L3	
node1	**node2**	**score**
HERC1	SMURF1	0.904
UBE2V2	KIAA0317	0.904
RNF4	UBB	0.904
HERC2	RNF144B	0.904
UBE3A	HERC6	0.904
HERC1	NEDD4L	0.904
SMURF2	HECW2	0.904
WWP1	HERC2	0.904
RNF19B	RNF19A	0.904
PJA1	RNF4	0.904
NEDD4L	HERC2	0.904
CUL7	HERC4	0.904
CUL7	UBA6	0.904
HERC2	HECW2	0.904
UBE2V2	SMURF1	0.904
UBE2V1	HECW2	0.904
UBE2V1	SMURF2	0.904
ARIH2	HERC5	0.904
UBE2V1	WWP1	0.904
HERC4	RBCK1	0.904
RBCK1	HERC2	0.904
HERC1	RNF19B	0.904
UBE2V2	ARIH2	0.904
HERC1	SMURF2	0.904
CUL7	HERC3	0.904
RNF19A	HERC6	0.904
RNF19A	HERC5	0.904
HECW2	STUB1	0.904
HERC1	HECW2	0.904
CUL7	HERC6	0.904
ANAPC11	RNF19A	0.904

	UBE2L3	
node1	**node2**	**score**
ARIH2	SMURF2	0.904
CUL7	UBE3C	0.903
ARIH2	UBB	0.903
RNF19B	ANAPC11	0.903
PJA1	RBCK1	0.903
RNF19B	RBX1	0.903
PARK2	HERC3	0.903
ARIH2	RPS27A	0.903
RNF19B	WWP1	0.903
RNF19A	RBX1	0.903
HERC1	PARK2	0.903
PARK2	SMURF2	0.903
RBCK1	UBE3C	0.903
UBA52	ARIH2	0.903
RNF19B	RNF144B	0.903
PARK2	HERC2	0.903
ITCH	PARK2	0.903
RNF19B	RBCK1	0.903
RNF19A	HECW2	0.903
PARK2	HERC6	0.903
RNF4	HERC2	0.903
SMURF1	HECW2	0.903
PARK2	HERC5	0.903
RNF19B	ARIH2	0.903
CUL2	PARK2	0.903
SMURF2	RNF144B	0.903
RNF19B	HUWE1	0.903
RNF19A	RPS27A	0.903
ANAPC11	RNF144B	0.903
RNF144B	RBX1	0.903
CUL7	NEDD4L	0.902

UBE2L3		
node1	**node2**	**score**
RNF4	WWP1	0.902
RBCK1	UBR1	0.902
CUL7	KIAA0317	0.902
UBA52	RNF19B	0.902
CUL7	STUB1	0.902
NEDD4L	RNF144B	0.902
RBCK1	RNF144B	0.902
RNF4	HERC6	0.902
ARIH2	HUWE1	0.902
RBCK1	HUWE1	0.902
RNF19B	UBB	0.902
CUL7	UBA52	0.902
KIAA0317	RBCK1	0.902
NEDD4L	ARIH2	0.902
RNF4	HERC5	0.902
PARK2	HACE1	0.902
PARK2	UBA3	0.902
RNF19B	STUB1	0.902
RNF19A	RNF144B	0.902
RNF19B	NEDD4	0.902
RNF144B	STUB1	0.902
UBA1	UBA7	0.902
UBA52	RNF144B	0.902
CUL7	SMURF2	0.901
UBC	RNF144B	0.901
RNF19B	SMURF2	0.901
CUL7	HECW2	0.901
RNF19B	UBE3C	0.901
RNF19B	UBA3	0.901
TRIP12	RNF144B	0.901
RNF4	HACE1	0.901

UBE2L3		
node1	**node2**	**score**
RNF19B	HECW2	0.901
RPS27A	RNF144B	0.901
UBA3	RNF144B	0.901
HECW2	RNF144B	0.901
CUL7	ARIH2	0.901
PARK2	SMURF1	0.901
NEDD4L	RNF19B	0.901
UBE2V2	PARK2	0.901
RNF19B	TRIP12	0.901
UBA7	RNF144B	0.901
PARK2	PJA1	0.901
CUL7	ITCH	0.901
RNF4	HECW2	0.901
RNF4	SMURF2	0.901
RBCK1	SMURF2	0.901
RNF19B	UBA7	0.901
RNF19B	PJA1	0.901
PJA1	RNF144B	0.901
UBA3	RBCK1	0.901
PJA1	RNF19A	0.901
RNF19B	RPS27A	0.901
RNF19B	UBA1	0.901
UBA1	RNF144B	0.901
PARK2	UBR1	0.901
SMURF1	ARIH2	0.901
SMURF1	RNF144B	0.901
UBB	RNF144B	0.901
RBCK1	TRIP12	0.901
ARIH2	HECW2	0.901
ARIH2	UBA7	0.901
ANAPC11	RNF4	0.901

UBE2L3		
node1	**node2**	**score**
UBE3A	RNF19B	0.901
RNF19A	SMURF2	0.901
SMURF1	RNF19A	0.901
RBCK1	WWP1	0.901
NEDD4L	RBCK1	0.901
CUL7	RPS27A	0.901
UBA6	RNF144B	0.901
CUL7	TRIP12	0.901
CUL7	PJA1	0.901
PARK2	RNF4	0.901
RBCK1	HECW2	0.901
SMURF1	RBCK1	0.901
SMURF1	RNF4	0.901
CUL7	UBB	0.901
UBE3C	RNF144B	0.901
PARK2	UBE3C	0.900
UBE2V2	RNF144B	0.900
UBE2V2	RNF19B	0.900
CUL7	UBE2V1	0.900
UBE2V1	RNF144B	0.900
UBE2V2	RBCK1	0.900
PARK2	KIAA0317	0.900
CUL7	UBE2V2	0.900
RNF4	RPS27A	0.900
CUL7	RNF19B	0.900
UBE2V2	RNF19A	0.900
CUL7	RNF19A	0.900
PARK2	HECW2	0.900
CUL7	RNF144B	0.900
PARK2	TRIP12	0.900
RNF19B	UBE2V1	0.900

Table S7. Gene-products associated in the meta-analysis and their related drugs and targets at any phase of drug development.

Gene product	Drug	Target	Max phase	Molecule type
IL12RB2	MARAVIROC	CCR5	Phase IV	Small molecule
	VICRIVIROC	CCR5	Phase III	Small molecule
	PRO-140	CCR5	Phase II	Antibody
	CENICRIVIROC	CCR5	Phase II	Small molecule
	AZD5672	CCR5	Phase II	Small molecule
	INCB-9471	CCR5	Phase II	Small molecule
	PF-04634817	CCR5	Phase II	Small molecule
	USTEKINUMAB	IL12A	Phase IV	Antibody
	BRIAKINUMAB	IL12B	Phase III	Antibody
	CANAKINUMAB	IL1B	Phase IV	Antibody
	RILONACEPT	IL1B	Phase IV	Protein
	GEVOKIZUMAB	IL1B	Phase III	Antibody
	ANAKINRA	IL1R1	Phase IV	Protein
	AMG-108	IL1R1	Phase II	Antibody
	GUSELKUMAB	IL23A	Phase III	Antibody
	TILDRAKIZUMAB	IL23A	Phase II	Antibody
	RUXOLITINIB	JAK2	Phase IV	Small molecule
	TOFACITINIB	JAK2	Phase IV	Small molecule
	BARICITINIB	JAK2	Phase III	Small molecule
	PEFICITINIB	JAK2	Phase III	Small molecule
	FEDRATINIB	JAK2	Phase III	Small molecule
	LESTAURTINIB	JAK2	Phase III	Small molecule
	PACRITINIB	JAK2	Phase III	Small molecule
	AT-9283	JAK2	Phase II	Small molecule
	BMS-911543	JAK2	Phase II	Small molecule
	AZD-1480	JAK2	Phase II	Small molecule
	AC-430	JAK2	Phase I	Small molecule
	TG-02	JAK2	Phase I	Small molecule
	XL-019	JAK2	Phase I	Small molecule
	PAZOPANIB	LCK	Phase IV	Small molecule
	DASATINIB	LCK	Phase IV	Small molecule
	ILORASERTIB	LCK	Phase II	Small molecule
	XL-228	LCK	Phase I	Small molecule
	Cerdulatinib	TYK2	Phase II	Small molecule
PTPN22	TEPLIZUMAB	CD3E	Phase III	Antibody
	OTELIXIZUMAB	CD3E	Phase III	Antibody
	VISILIZUMAB	CD3E	Phase III	Antibody
	ERTUMAXOMAB	CD3E	Phase II	Antibody
	BLINATUMOMAB	CD3G	Phase IV	Antibody
	MUROMONAB-CD3	CD3G	Phase IV	Antibody
	NI-0401	CD3G	Phase II	Antibody
	IBALIZUMAB	CD4	Phase III	Antibody
	ZANOLIMUMAB	CD4	Phase III	Antibody
	TREGALIZUMAB	CD4	Phase II	Antibody
	PAZOPANIB	LCK	Phase IV	Small molecule
	DASATINIB	LCK	Phase IV	Small molecule
	ILORASERTIB	LCK	Phase II	Small molecule
	XL-228	LCK	Phase I	Small molecule
RSBN1	GSK-690693	PRKACA	Phase I	Small molecule
GLS	CARGLUMIC ACID	CPS1	Phase IV	Small molecule
	AZATHIOPRINE	PPAT	Phase IV	Small molecule
	MERCAPTOPURINE	PPAT	Phase IV	Small molecule
IRF5	BI-505	ICAM1	Phase II	Antibody
FAM167A	DASATINIB	BLK	Phase IV	Small molecule
	ILORASERTIB	BLK	Phase II	Small molecule
	XL-228	BLK	Phase I	Small molecule
BLK	IMATINIB	ABL1	Phase IV	Small molecule
	PONATINIB	ABL1	Phase IV	Small molecule
	NILOTINIB	ABL1	Phase IV	Small molecule

Table S7. Continues

Gene product	Drug	Target	Max phase	Molecule type
BLK	Flumatinib	ABL1	Phase III	Small molecule
	BAFETINIB	ABL1	Phase II	Small molecule
	AT-9283	ABL1	Phase II	Small molecule
	REBASTINIB	ABL1	Phase II	Small molecule
	KW-2449	ABL1	Phase I	Small molecule
	ABL-001	ABL1	Phase I	Small molecule
	OSIMERTINIB	EGFR	Phase IV	Small molecule
	ERLOTINIB	EGFR	Phase IV	Small molecule
	NECITUMUMAB	EGFR	Phase IV	Antibody
	GEFITINIB	EGFR	Phase IV	Small molecule
	PANITUMUMAB	EGFR	Phase IV	Antibody
	AFATINIB	EGFR	Phase IV	Small molecule
	CETUXIMAB	EGFR	Phase IV	Antibody
	LAPATINIB	EGFR	Phase IV	Small molecule
	ROCILETINIB	EGFR	Phase III	Small molecule
	DACOMITINIB	EGFR	Phase III	Small molecule
	BRIGATINIB	EGFR	Phase III	Small molecule
	ZALUTUMUMAB	EGFR	Phase III	Antibody
	NERATINIB	EGFR	Phase III	Small molecule
	Poziotinib	EGFR	Phase II	Small molecule
	BMS-690514	EGFR	Phase II	Small molecule
	TESEVATINIB	EGFR	Phase II	Small molecule
	VARLITINIB	EGFR	Phase II	Small molecule
	MAB-425	EGFR	Phase II	Antibody
	EGF816	EGFR	Phase II	Small molecule
	AEE-788	EGFR	Phase II	Small molecule
	HM-61713	EGFR	Phase I	Small molecule
	Pyrotinib	EGFR	Phase I	Small molecule
	MP-412	EGFR	Phase I	Small molecule
	AC-480	EGFR	Phase I	Small molecule
	Epitinib	EGFR	Phase I	Small molecule
	TAK-285	EGFR	Phase I	Small molecule
	CEP-32496	EGFR	Phase I	Small molecule
	CUDC-101	EGFR	Phase I	Small molecule
	Theliatinib	EGFR	Phase I	Small molecule
	VANDETANIB	EPHA1	Phase IV	Small molecule
	DASATINIB	FYN	Phase IV	Small molecule
	ILORASERTIB	HCK	Phase II	Small molecule
	PAZOPANIB	ITK	Phase IV	Small molecule
	REGORAFENIB	MAPK11	Phase IV	Small molecule
	LOSMAPIMOD	MAPK11	Phase III	Small molecule
	PF-03715455	MAPK14	Phase II	Small molecule
	TALMAPIMOD	MAPK14	Phase II	Small molecule
	SEMAPIMOD	MAPK14	Phase II	Small molecule
	VX-745	MAPK14	Phase II	Small molecule
	PH-797804	MAPK14	Phase II	Small molecule
	BMS-582949	MAPK14	Phase II	Small molecule
	PG-760564	MAPK14	Phase II	Small molecule
	DILMAPIMOD	MAPK14	Phase II	Small molecule
	FX-005	MAPK14	Phase II	Small molecule
	LY-3007113	MAPK14	Phase I	Small molecule
	AZD-7624	MAPK14	Phase I	Small molecule
	PEGPLERANIB SODIUM	PDGFB	Phase III	Unknown
	SUNITINIB	PDGFRB	Phase IV	Small molecule
	SORAFENIB	PDGFRB	Phase IV	Small molecule
	NINTEDANIB	PDGFRB	Phase IV	Small molecule
	BECAPLERMIN	PDGFRB	Phase IV	Protein
	Masitinib	PDGFRB	Phase III	Small molecule
	CEDIRANIB	PDGFRB	Phase III	Small molecule
	QUIZARTINIB	PDGFRB	Phase III	Small molecule

Table S7. Continues

Gene product	Drug	Target	Max phase	Molecule type
BLK	DOVITINIB	PDGFRB	Phase III	Small molecule
	Orantinib	PDGFRB	Phase III	Small molecule
	VATALANIB	PDGFRB	Phase III	Small molecule
	MOTESANIB	PDGFRB	Phase III	Small molecule
	CRENOLANIB	PDGFRB	Phase III	Small molecule
	LINIFANIB	PDGFRB	Phase III	Small molecule
	Anlotinib	PDGFRB	Phase II	Small molecule
	XL-820	PDGFRB	Phase II	Small molecule
	Famitinib	PDGFRB	Phase II	Small molecule
	SU-014813	PDGFRB	Phase II	Small molecule
	FORETINIB	PDGFRB	Phase II	Small molecule
	TANDUTINIB	PDGFRB	Phase II	Small molecule
	JI-101	PDGFRB	Phase II	Small molecule
	X-82	PDGFRB	Phase II	Small molecule
	CM-082	PDGFRB	Phase I	Small molecule
	TAK-593	PDGFRB	Phase I	Small molecule
	RG-1530	PDGFRB	Phase I	Small molecule
	MIDOSTAURIN	PRKCD	Phase III	Small molecule
	UCN-01	PRKCD	Phase II	Small molecule
	SOTRASTAURIN	PRKCD	Phase II	Small molecule
	DELCASERTIB	PRKCD	Phase II	Protein
	GSK-690693	PRKCD	Phase I	Small molecule
	DEFACTINIB	PTK2B	Phase II	Small molecule
	FINGOLIMOD	S1PR1	Phase IV	Small molecule
	Siponimod	S1PR1	Phase III	Small molecule
	KRP203	S1PR1	Phase II	Small molecule
	PONESIMOD	S1PR1	Phase II	Small molecule
	APD334	S1PR1	Phase I	Small molecule
	AMISELIMOD	S1PR1	Phase	Small molecule
	BOSUTINIB	SRC	Phase IV	Small molecule
	SARACATINIB	SRC	Phase III	Small molecule
	KX2-391	SRC	Phase II	Small molecule
	XL-228	SRC	Phase I	Small molecule
	FOSTAMATINIB	SYK	Phase III	Small molecule
	R-333	SYK	Phase II	Small molecule
	R-343	SYK	Phase II	Small molecule
	ENTOSPLETINIB	SYK	Phase II	Small molecule
	Cerdulatinib	SYK	Phase II	Small molecule
	HMPL-523	SYK	Phase I	Small molecule
	TAK-659	SYK	Phase I	Small molecule
TYK2	PEGINTERFERON BETA-1A	IFNAR1	Phase IV	Protein
	PEGINTERFERON ALFA-2B	IFNAR1	Phase IV	Protein
	INTERFERON BETA-1A	IFNAR1	Phase IV	Protein
	INTERFERON BETA-1B	IFNAR1	Phase IV	Protein
	PEGINTERFERON ALFA-2A	IFNAR1	Phase IV	Protein
	INTERFERON ALFA-2B	IFNAR1	Phase IV	Protein
	IDELALISIB	PIK3CD	Phase IV	Small molecule
	RUXOLITINIB	JAK1	Phase IV	Small molecule
	TOFACITINIB	JAK1	Phase IV	Small molecule
	USTEKINUMAB	IL12B	Phase IV	Antibody
	TOCILIZUMAB	IL6R	Phase IV	Antibody
	SILTUXIMAB	IL6	Phase IV	Antibody
	INTERFERON ALFA-2A	IFNAR1	Phase IV	Protein
	INTERFERON ALFA-N3	IFNAR1	Phase IV	Protein
	INTERFERON ALFACON-1	IFNAR1	Phase IV	Protein
	BARICITINIB	JAK1	Phase III	Small molecule
	BRIAKINUMAB	IL12B	Phase III	Antibody
	SARILUMAB	IL6R	Phase III	Antibody
	PEFICITINIB	JAK1	Phase III	Small molecule
	DUVELISIB	PIK3CD	Phase III	Small molecule

Table S7. Continues

Gene product	Drug	Target	Max phase	Molecule type
TYK2	GUSELKUMAB	IL23A	Phase III	Antibody
	SIRUKUMAB	IL6	Phase III	Antibody
	BUPARLISIB	PIK3CA	Phase III	Small molecule
	TASELISIB	PIK3CB	Phase III	Small molecule
	ALBINTERFERON ALFA-2B	IFNAR1	Phase III	Protein
	COPANLISIB	PIK3CA	Phase II	Small molecule
	FILGOTINIB	JAK1	Phase II	Small molecule
	TILDRAKIZUMAB	IL23A	Phase II	Antibody
	OLOKIZUMAB	IL6	Phase II	Antibody
	PF-04691502	PIK3CB	Phase II	Small molecule
	DACTOLISIB	PIK3CA	Phase II	Small molecule
	LY-3023414	PIK3CA	Phase II	Small molecule
	Alpelisib	PIK3CA	Phase II	Small molecule
	APITOLISIB	PIK3CA	Phase II	Small molecule
	GEDATOLISIB	PIK3CA	Phase II	Small molecule
	SOLCITINIB	JAK1	Phase II	Small molecule
	INCB-047986	JAK1	Phase II	Small molecule
	CLAZAKIZUMAB	IL6	Phase II	Antibody
	DECERNOTINIB	JAK3	Phase II	Small molecule
	R-333	JAK3	Phase II	Small molecule
	PF-04236921	IL6	Phase II	Antibody
	AT-9283	JAK3	Phase II	Small molecule
	PILARALISIB	PIK3CA	Phase II	Small molecule
	BGT-226	PIK3CA	Phase II	Small molecule
	ZSTK-474	PIK3CA	Phase II	Small molecule
	PICTILISIB	PIK3CB	Phase II	Small molecule
	Cerdulatinib	JAK1	Phase II	Small molecule
	TGR-1202	PIK3CD	Phase I	Small molecule
	GSK-2636771	PIK3CB	Phase I	Small molecule
	SF-1126	PIK3CA	Phase I	Small molecule
	PF-04965842	JAK1	Phase I	Small molecule
	AMG-319	PIK3CD	Phase I	Small molecule
	GSK-2269557	PIK3CD	Phase I	Small molecule
	INCB-40093	PIK3CD	Phase I	Small molecule
	GSK-1059615	PIK3CA	Phase I	Small molecule
	Panulisib	PIK3CA	Phase I	Small molecule
	PA-799	PIK3CA	Phase I	Small molecule
	WX-037	PIK3CB	Phase I	Small molecule
	SAR-260301	PIK3CB	Phase I	Small molecule
	BAY-1082439	PIK3CB	Phase I	Small molecule
	OMIPALISIB	PIK3CB	Phase I	Small molecule
	MK-8353	MAPK1	Phase I	Small molecule
	GDC-0994	MAPK1	Phase I	Small molecule
	VS-5584	PIK3CA	Phase I	Small molecule
	PKI-179	PIK3CA	Phase I	Small molecule
	MLN-1117	PIK3CA	Phase I	Small molecule
	ME-401	PIK3CD	Phase I	Small molecule
	CAL-263	PIK3CG	Phase I	Small molecule
	RP-6530	PIK3CG	Phase I	Small molecule
UBE2L3	PEVONEDISTAT	UBA3	Phase II	Small molecule

Table S8. Different drugs currently indicated or at any phases of drug development according to the OpenTargets Platform for SSc, SLE, RA and IIM.

Drug	Type	Activity	Indicated for
RITUXIMAB	Antibody	antagonist	SSc, SLE, RA, IIM
METHOTREXATE	Small molecule	antagonist	SSc, SLE, RA, IIM
TOFACITINIB	Small molecule	antagonist	SSc, SLE, RA, IIM
TOCILIZUMAB	Antibody	antagonist	SSc, RA, IIM
BELIMUMAB	Antibody	antagonist	SSc, SLE, IIM
METHYLPREDNISOLONE	Small molecule	agonist	SSc, SLE, IIM
SIROLIMUS	Small molecule	antagonist	SSc, SLE, IIM
TACROLIMUS	Small molecule	antagonist	SSc, SLE, RA
ATORVASTATIN	Small molecule	antagonist	SSc, SLE, RA
CORTICOTROPIN	Protein	agonist	SLE, RA, IIM
CORTICOTROPIN, REPOSITORY	Protein	agonist	SLE, RA, IIM
ABATACEPT	Protein	antagonist	SLE, RA, IIM
ETANERCEPT	Protein	antagonist	SLE, RA, IIM
ROSUVASTATIN	Small molecule	antagonist	SSc, SLE
FILGRASTIM	Protein	agonist	SSc, SLE
MYCOPHENOLATE MOFETIL	Small molecule	antagonist	SSc, SLE
FLUDARABINE PHOSPHATE	Small molecule	antagonist	SSc, SLE
MYCOPHENOLIC ACID	Small molecule	antagonist	SSc, SLE
HYDROXYCHLOROQUINE	Small molecule	antagonist	SLE, RA
DIPHENHYDRAMINE	Small molecule	antagonist	SLE, RA
LEFLUNOMIDE	Small molecule	antagonist	SLE, RA
MELOXICAM	Small molecule	antagonist	SLE, RA
PIOGLITAZONE	Small molecule	agonist	SLE, RA
PREDNISONE	Small molecule	agonist	SLE, IIM
ANAKINRA	Protein	antagonist	RA, IIM
INFLIXIMAB	Antibody	antagonist	RA, IIM
BOSENTAN	Small molecule	antagonist	SSc
MACITENTAN	Small molecule	antagonist	SSc
NINTEDANIB	Small molecule	antagonist	SSc
SILDENAFIL	Small molecule	antagonist	SSc
BOTULINUM TOXIN TYPE B	Unknown	antagonist	SSc
IMATINIB	Small molecule	antagonist	SSc

RA: Rheumatoid Arthritis; SLE: Systemic Lupus Erythematosus; SSc: Systemic Sclerosis; IIM: idiopathic inflammatory myopathies

All were curated from Clinical Trials information

Table S8. Continues

Drug	**Type**	**Activity**	**Indicated for**
NILOTINIB	Small molecule	antagonist	SSc
PLERIXAFOR	Small molecule	agonist	SSc
POMALIDOMIDE	Small molecule	antagonist	SSc
RIOCIGUAT	Small molecule	agonist	SSc
TADALAFIL	Small molecule	antagonist	SSc
TREPROSTINIL	Small molecule	agonist	SSc
BUSPIRONE	Small molecule	agonist	SSc
AZATHIOPRINE	Small molecule	antagonist	SLE
ESTROGENS, CONJUGATED	Small molecule	agonist	SLE
IBANDRONIC ACID	Small molecule	antagonist	SLE
LENALIDOMIDE	Small molecule	antagonist	SLE
METFORMIN	Small molecule	antagonist	SLE
THALIDOMIDE	Small molecule	antagonist	SLE
ANIFROLUMAB	Antibody	antagonist	SLE
BLISIBIMOD	Protein	antagonist	SLE
EPRATUZUMAB	Antibody	antagonist	SLE
ACETAMINOPHEN	Small molecule	antagonist	SLE
ASPIRIN	Small molecule	antagonist	SLE
ATACICEPT	Protein	antagonist	SLE
BARICITINIB	Small molecule	antagonist	SLE
CALCITRIOL	Small molecule	agonist	SLE
CHOLECALCIFEROL	Small molecule	agonist	SLE
CYTARABINE	Small molecule	antagonist	SLE
DAPIROLIZUMAB PEGOL	Antibody	antagonist	SLE
DOXYCYCLINE	Small molecule	antagonist	SLE
FULVESTRANT	Small molecule	antagonist	SLE
LULIZUMAB PEGOL	Antibody	antagonist	SLE
PF-04236921	Antibody	antagonist	SLE
PRAVASTATIN	Small molecule	antagonist	SLE
R-333	Small molecule	antagonist	SLE
RAMIPRIL	Small molecule	antagonist	SLE
USTEKINUMAB	Antibody	antagonist	SLE
AMISELIMOD	Small molecule	up_or_down	SLE

RA: Rheumatoid Arthritis; SLE: Systemic Lupus Erythematosus; SSc: Systemic Sclerosis; IIM: idiopathic inflammatory myopathies

All were curated from Clinical Trials information

Table S8. Continues

Drug	Type	Activity	Indicated for
APREMILAST	Small molecule	antagonist	SLE
BIIB059	Antibody	antagonist	SLE
CLOPIDOGREL	Small molecule	antagonist	SLE
MSC-2364447	Small molecule	antagonist	SLE
OMALIZUMAB	Antibody	antagonist	SLE
SIMVASTATIN	Small molecule	antagonist	SLE
SOLCITINIB	Small molecule	antagonist	SLE
VENETOCLAX	Small molecule	antagonist	SLE
ADALIMUMAB	Antibody	antagonist	RA
BAZEDOXIFENE	Small molecule	up_or_down	RA
BETAMETHASONE	Small molecule	agonist	RA
CELECOXIB	Small molecule	antagonist	RA
CERTOLIZUMAB PEGOL	Antibody	antagonist	RA
DENOSUMAB	Antibody	antagonist	RA
DICLOFENAC	Small molecule	antagonist	RA
ETORICOXIB	Small molecule	antagonist	RA
FENTANYL	Small molecule	agonist	RA
GOLIMUMAB	Antibody	antagonist	RA
IBUPROFEN	Small molecule	antagonist	RA
METHYLPREDNISOLONE HEMISUCCINATE	Small molecule	agonist	RA
MILNACIPRAN	Small molecule	antagonist	RA
NAPROXEN	Small molecule	antagonist	RA
OMEPRAZOLE	Small molecule	antagonist	RA
ROFECOXIB	Small molecule	antagonist	RA
SULFASALAZINE	Small molecule	antagonist	RA
TERIPARATIDE	Protein	agonist	RA
TICAGRELOR	Small molecule	antagonist	RA
TRAMADOL	Small molecule	agonist	RA
VALDECOXIB	Small molecule	antagonist	RA
MISOPROSTOL	Small molecule	agonist	RA
NITROGLYCERIN	Small molecule	agonist	RA
OLOKIZUMAB	Antibody	antagonist	RA
SECUKINUMAB	Antibody	antagonist	RA

RA: Rheumatoid Arthritis; SLE: Systemic Lupus Erythematosus; SSc: Systemic Sclerosis; IIM: idiopathic inflammatory myopathies

All were curated from Clinical Trials information

Table S8. Continues

Drug	Type	Activity	Indicated for
TABALUMAB	Antibody	antagonist	RA
BIMAGRUMAB	Antibody	antagonist	IIM
CYCLOSPORINE	Protein	up_or_down	IIM
ALEMTUZUMAB	Antibody	antagonist	IIM
ECULIZUMAB	Antibody	antagonist	IIM
METHIMAZOLE	Small molecule	antagonist	IIM
SIPONIMOD	Small molecule	agonist	IIM
NATALIZUMAB	Antibody	antagonist	IIM

RA: Rheumatoid Arthritis; SLE: Systemic Lupus Erythematosus; SSc: Systemic Sclerosis; IIM: idiopathic inflammatory myopathies

All were curated from Clinical Trials information

Table S9. Drug target enrichment analysis

	Systemic Sclerosis	**Systemic Lupus Erythematosus**	**Rheumatoid Arthritis**	**Idiopathic inflammatory myopathies**
Number of related gene-products[a]	608	630	413	632
Number of related gene-products & drug targets[b]	23	13	0	7
Number of unrelated gene-products & drug targets[c]	73	146	89	25
Number of unrelated gene-products & no drug targets[d]	20,012	20,012	20,012	20,012
Exact Fisher's test *p* -value	1.41×10^{-18}	2.85×10^{-04}	0.00	4.62×10^{-06}

[a] Target genes from the eQTL analysis and their protein-protein interaction network.

[b] Target genes from the eQTL analysis and their protein-protein interaction network that are drug target for any of the analyzed disease.

[c] Gene-products that are drug target for any of the analyzed disease but that are not related in our study samples.

[d] Gene-products that are not related in our study samples neither drug target for any of the analyzed disease.