

Supplementary Table S1. Diseases are associated with Diethylhexyl Phthalate or its descendants, while Reference Count > 5 was used as cut-odd criterion. (CTD - <https://ctdbase.org>)

#	Disease name	Inference score	Reference count
1	Arthritis, Rheumatoid	74.14	34
2	HIV Infections	33.12	11
3	Diabetes Mellitus, Type 1	25.32	19
4	Asthma	19.58	53
5	Lymphoma, Large B-Cell, Diffuse	16.43	8
6	Autoimmune Diseases	16.17	17
7	Multiple Sclerosis	13.45	13
8	Dermatitis, Allergic Contact	12.45	12
9	Respiratory Hypersensitivity	10.99	8
10	Hypersensitivity	9.37	15
11	Lupus Erythematosus, Systemic	8.78	18
12	Precursor Cell Lymphoblastic Leukemia-Lymphoma	7.84	13
13	Immunologic Deficiency Syndromes	7.48	9
14	Leukemia, Lymphocytic, Chronic, B-Cell	7.25	10
15	Burkitt Lymphoma	6.11	5
16	Glomerulonephritis, IGA	6.05	7
17	Cryopyrin-Associated Periodic Syndromes	5.36	6
18	Lymphoma, Mantle-Cell	5.29	5
19	Precursor T-Cell Lymphoblastic Leukemia-Lymphoma	5.28	9
20	Dermatitis, Atopic	5.19	13
21	Common Variable Immunodeficiency	5.09	5
22	Mevalonate Kinase Deficiency	4.44	8
23	Multiple Myeloma	4.29	17
24	IMMUNODEFICIENCY-CENTROMERIC INSTABILITY-FACIAL ANOMALIES SYNDROME 1	4.13	6
25	Ataxia Telangiectasia	3.41	6
26	Angioedemas, Hereditary	3.31	7
27	Encephalomyelitis, Autoimmune, Experimental	3.24	10
28	Urticaria	3.15	7
29	Lymphoma	3.09	8
30	Rhinitis, Allergic	3.01	5
31	Hodgkin Disease	2.51	12
32	Lymphoma, Non-Hodgkin	2	9

Supplementary Table S2. Gene-Phenotype Relationships of *FCGR2A*, *IL10* and *IRF5*. (OMIM - <http://www.omim.org>)

Gene	Phenotype	Phenotype number
<i>FCGR2A</i>	{Lupus nephritis, susceptibility to}	152700
	{Malaria, severe, susceptibility to}	611162
	{Pseudomonas aeruginosa, susceptibility to chronic infection by, in cystic fibrosis}	219700
<i>IL10</i>	{Graft-versus-host disease, protection against}	614395
	{HIV-1, susceptibility to}	609423
	{Rheumatoid arthritis, progression of}	180300
<i>IRF5</i>	{Inflammatory bowel disease 14}	612245
	{Systemic lupus erythematosus, susceptibility to, 10}	612251

Supplementary Table S3. Functions of the three intersecting genes, while $P < 0.05$ was used as cut-odd criterion. (GeneMANIA - <http://genemania.org/>)

#	Function	FDR	Genes in network
1	response to type I interferon	6.33E-08	7
2	cellular response to type I interferon	6.33E-08	7
3	cellular response to interferon-gamma	3.88316E-06	6
4	receptor signaling pathway via STAT	3.98617E-05	6
5	response to interferon-gamma	3.98617E-05	6
6	interferon-alpha production	4.94182E-05	4
7	regulation of interferon-alpha production	4.94182E-05	4
8	positive regulation of receptor signaling pathway via STAT	0.000278132	4
9	receptor signaling pathway via JAK-STAT	0.000438946	5
10	regulation of receptor signaling pathway via JAK-STAT	0.003197879	4
11	regulation of receptor signaling pathway via STAT	0.004805696	4
12	positive regulation of type I interferon production	0.010427851	3
13	regulation of cytokine secretion	0.010427851	3
14	regulation of type I interferon production	0.010427851	4
15	type I interferon production	0.011757103	4
16	regulation of interferon-beta production	0.014054377	3
17	cytokine secretion	0.014319046	3
18	interferon-beta production	0.015750258	3
19	Fc receptor signaling pathway	0.044216246	4