

Supplementary data file S-2: Gene ontology annotation [1] of known genes for SLE, calculated using GOSTat [2]

<u>GO Term</u>	<u>Associated Genes</u>	<u>No. of genes (Total 67)</u>	<u>No. of Term- Associated Genes (Total 33972)</u>	<u>P-value</u>
<u>GO:0005515</u> Protein binding	trex1, traf6, cd44, actn4, kpna1, ppp2ca, scube1, notch4, ube2l3, tnfaip3, trim27, trim31, syk, jazf1, parvb, dnaja1, ptn, fcgr2a, ptpn22, rasgrp3, atg5, fcgr1a, ica1, tyk2, fcgr3a, rps6ka1, crp, fcgr2b, stat1, ets1, micb, tap2, stat4, pxk, lrrc18, fcgr1, bc4a, fcgr3b, pttg1, lyn, tnip1, c4b, mecp2, irak1, blk, tnfsf4, il21, spp1, itgam, il10, skiv2l	51	9005	1.15×10^{-16}
<u>GO:0002376</u> Immune system process	fcgr1a, c1qa, fcgr3a, fcgr2b, c2, traf6, ets1, micb, tap2, hla-drb2, irf8, notch4, syk, fcgr1b, c4a, fcgr3b, bank1, lyn, hla-drb3, c4b, pdcd1, c1qb, fcgr2a, tnfsf4, il21, il10	26	1386	1.59×10^{-16}
<u>GO:0006955</u> Immune response	fcgr1a, c1qa, fcgr3a, fcgr2b, c2, traf6, ets1, micb, tap2, hla-drb2, irf8, syk, fcgr1b, c4a, fcgr3b, hla-drb3, c4b, pdcd1, c1qb, fcgr2a, tnfsf4, il10	22	1189	1.52×10^{-13}
<u>GO:0019865</u> Immunoglobulin binding	fcgr1a, fcgr2a, fcgr3b, fcgr3a, fcgr2b, fcgr1b	6	16	9.05×10^{-11}
<u>GO:0032403</u> Protein complex binding	trex1, fcgr1a, fcgr3b, fcgr3a, fcgr2b, actn4, fcgr2a, syk, fcgr1b	9	101	9.17×10^{-11}
<u>GO:0019864</u> Ig G binding	fcgr1a, fcgr2a, fcgr3b, fcgr3a, fcgr2b	5	8	2.34×10^{-10}
<u>GO:0051239</u> Regulator of multicellular organismal process	c4a, c1qa, c2, c4b, traf6, c1qb, pxk, il21, spp1, syk, il10	11	277	1.04×10^{-09}
<u>GO:0048518</u>	c4a, c1qa, lyn, c4b, c2, traf6, ets1, c1qb, actn4, ppp2ca, ptn, irak1,	17	1062	2.18×10^{-09}

Positive regulation of biological process	notch4, tnfsf4, il21, syk, il10			
<u>GO:0002252</u>	c4a, c1qa, c2, c4b, traf6, c1qb, syk, il10	8	110	5.66x10 ⁻⁰⁹
Immune effector process				
<u>GO:0065007</u>	c1qa, c2, ikzf1, traf6, actn4, kpna1, ppp2ca, irf8, scube1, notch4, ube2l3, irf5, tnfaip3, trim27, syk, azf1, prdm1, c1qb, serpind1, ptn, rasgrp3, ets1, stat1, stat4, pxk, c4a, lyn, tnip1, c4b, mecp2, irak1, tnfsf4, il21, spp1, il10	35	6731	7.29x10 ⁻⁰⁹
Biological regulation				
<u>GO:0050789</u>	c1qa, c2, ikzf1, traf6, stat1, ets1, stat4, actn4, kpna1, ppp2ca, notch4, irf8, pxk, ube2l3, irf5, tnfaip3, trim27, syk, jazf1, c4a, lyn, prdm1, tnip1c4b, mecp2, c1qb, irak1, ptn, tnfsf4, il21, rasgrp3, spp1, il10	33	6140	8.18x10 ⁻⁰⁹
Regulation of biological process				
<u>GO:0002253</u>	c4a, c1qa, c2, c4b, syk, traf6, c1qb	7	71	8.28x10 ⁻⁰⁹
Activation of immune response				
<u>GO:0007243</u>	lyn, traf6, stat1, ppp2ca, stat4, blk, irak1, tnfaip3, rasgrp3, syk, il10	11	376	1.39x10 ⁻⁰⁸
Protein kinase cascade				
<u>GO:0002443</u>	c1qa, c2, c4b, syk, traf6, c1qb, il10	7	78	1.39x10 ⁻⁰⁸
Leukocyte mediated immunity				
<u>GO:0050778</u>	c4a, c1qa, c2, c4b, syk, traf6, c1qb	7	85	2.41x10 ⁻⁰⁸
Positive regulation of immune response				
<u>GO:0002684</u>	c4a, c1qa, c2, c4b, syk, traf6, c1qb	7	86	2.45x10 ⁻⁰⁸
Positive regulation of immune system process				
<u>GO:0050776</u>	c4a, c1qa, c2, c4b, syk, traf6, c1qb	7	98	5.83x10 ⁻⁰⁸
Regulation of immune response				

<u>GO:0002682</u>	c4a, c1qa, c2, c4b, syk, traf6, c1qb	7	100	6.35x10 ⁻⁰⁸
Regulation of immune system process				
<u>GO:0051240</u>	c4a, c1qa, c2, c4b, syk, traf6, c1qb	7	105	8.49x10 ⁻⁰⁸
Positive regulation of multicellular organismal process				
<u>GO:0002449</u>	c1qa, c2, c4b, traf6, c1qb, il10	6	72	3.12x10 ⁻⁰⁷
Lymphocyte mediated immunity				
<u>GO:0005886</u>	fcgr1a, or2h2, fcgr3a, fcgr2b, cd44, micb, ppp2ca, hla-drb2, scube1, notch4, pxk, trim27syk, fcgr1b, parvb, fcgr3b, lyn, hla-drb3, irak1, fcgr2a, tnfsf4, rasgrp3, itgam	23	3816	3.12x10 ⁻⁰⁷
Plasma membrane				
<u>GO:0032501</u>	or2h2, c1qa, c2, ikzf1, traf6, ets1, ppp2ca, irf8, scube1, notch4, pxk, syk, c4a, lyn, c4b, pdcd1c1qb, serpin1, ptn, ptpn22, il21, spp1, il10	23	3822	3.13x10 ⁻⁰⁷
Multicellular organismal process				
<u>GO:0006959</u>	c4a, c1qa, c2, c4b, pdcd1, c1qb	6	75	3.61x10 ⁻⁰⁷
Humoral immune response				
<u>GO:0002460</u>	c1qa, c2, c4b, traf6, c1qb, il10	6	76	3.61x10 ⁻⁰⁷
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains				
<u>GO:0002250</u>	c1qa, c2, c4b, traf6, c1qb, il10	6	76	3.61x10 ⁻⁰⁷
Adaptive immune response				
<u>GO:0002526</u>	c4a, c1qa, crp, c2, c4b, c1qb	6	79	4.39x10 ⁻⁰⁷
Acute Inflammatory response				

<u>GO:0006956</u>	c4a, c1qa, c2, c4b, c1qb	5	39	4.91×10^{-07}
Complement Activation				
<u>GO:0002541</u>	c4a, c1qa, c2, c4b, c1qb	5	39	4.91×10^{-07}
Inactivation of plasma proteins during acute inflammatory response				
<u>GO:0006952</u>	c4a, or2h2, c1qa, crp, tnip1, c2, c4b, c1qb, micb, scube1, il10	11	584	6.43×10^{-07}
Defense response				
<u>GO:0016064</u>	c1qa, c2, c4b, c1qb, il10	5	51	1.84×10^{-06}
Immunoglobulin mediated immune response				

References:

1. Camon E, Magrane M, Barrell D, et al. The Gene Ontology Annotation (GOA) Database: sharing knowledge in Uniprot with Gene Ontology. Nucleic Acids Res 2004;32(Database issue):D262-6.
2. Beissbarth T, Speed TP. GStat: find statistically overrepresented Gene Ontologies within a group of genes. Bioinformatics 2004;20(9):1464-5.