

## Supplementary Data

**New Variants including *ARG1* polymorphisms associated with C-reactive protein levels**

**identified by genome-wide association and pathway analysis**

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### Supplementary Tables

**Table S1.** Characteristics of the subjects in stage 1 and 2 data.

	<b>Stage 1</b>	<b>Stage 2</b>
N	7626	903
Age (years)*	52.5±8.6	41.8±8.6
Male (%)	3586(47.0)	518 (57.4)
BMI (kg/m <sup>2</sup> )*	24.6±3.1	23.7±3.2
Smoker (%)	25.6	45.1
Drinker (%)	53.3	82.9
Pulse rate*	63.6±7.4	65.1±9.6
CRP(mg/dL)*	0.2±0.45	0.1±0.12

\*Mean ± SD

**Table S2.** SNP loci associated with serum CRP levels in the stage 1 data.

SNP*	Locus	Nearest Gene	Position**	Minor allele	MAF	Median CRP level (mg/dL)			Type***	Effect Size	SE	P
						11	12	22				
rs7553007	1q23.2	<i>CRP</i>	157965173	G	0.369	0.17	0.15	0.13	genotyped	0.182	0.023	7.34E-16
rs1205	1q23.2	<i>CRP</i>	157948857	C	0.364	0.17	0.15	0.13	imputed	0.181	0.023	2.21E-15
rs2808629	1q23.2	<i>CRP</i>	157943420	G	0.363	0.17	0.15	0.13	imputed	0.181	0.023	2.50E-15
rs2794520	1q23.2	<i>CRP</i>	157945440	C	0.364	0.17	0.15	0.13	imputed	0.181	0.023	2.82E-15
rs2808628	1q23.2	<i>CRP</i>	157942635	G	0.360	0.17	0.15	0.13	imputed	0.182	0.023	3.43E-15
rs876537	1q23.2	<i>CRP</i>	157941557	C	0.359	0.17	0.15	0.13	imputed	0.182	0.023	3.61E-15
rs2027471	1q23.2	<i>CRP</i>	157956012	T	0.344	0.17	0.15	0.13	imputed	0.171	0.023	2.30E-13
rs1341665	1q23.2	<i>CRP</i>	157958183	G	0.344	0.17	0.15	0.13	imputed	0.17	0.023	2.98E-13
rs16842599	1q23.2	<i>CRP</i>	157964099	C	0.140	0.18	0.16	0.13	imputed	0.199	0.031	2.39E-10
rs16842559	1q23.2	<i>CRP</i>	157942795	C	0.140	0.18	0.16	0.13	imputed	0.199	0.031	2.54E-10
rs16842568	1q23.2	<i>CRP</i>	157942844	G	0.140	0.18	0.16	0.13	imputed	0.199	0.031	2.54E-10
rs12081480	1q23.2	<i>CRP</i>	157973614	G	0.140	0.18	0.16	0.13	imputed	0.199	0.032	2.96E-10
rs12081252	1q23.2	<i>CRP</i>	157973137	C	0.140	0.18	0.16	0.13	imputed	0.198	0.031	3.28E-10
rs12068753	1q23.2	<i>CRP</i>	157959161	A	0.140	0.18	0.16	0.13	genotyped	0.197	0.031	3.41E-10
rs12081264	1q23.2	<i>CRP</i>	157973184	C	0.140	0.18	0.16	0.13	imputed	0.197	0.031	3.81E-10
rs3093075	1q23.2	<i>CRP</i>	157946537	T	0.145	0.19	0.16	0.13	imputed	0.190	0.031	8.66E-10
rs3093077	1q23.2	<i>CRP</i>	157946260	C	0.145	0.19	0.16	0.13	genotyped	0.190	0.031	9.30E-10
rs16842502	1q23.2	<i>CRP</i>	157920487	A	0.140	0.18	0.16	0.13	imputed	0.184	0.032	7.80E-09
rs2794526	1q23.2	<i>CRP</i>	157892102	A	0.125	0.18	0.16	0.14	imputed	0.172	0.033	1.79E-07

rs4275453	1q23.2	<i>CRP</i>	157974671	C	0.255	0.17	0.15	0.13	imputed	0.132	0.025	2.06E-07
rs1446976	1q23.2	<i>CRP</i>	157895818	G	0.125	0.18	0.16	0.14	imputed	0.170	0.033	2.32E-07
rs1446975	1q23.2	<i>CRP</i>	157895966	C	0.125	0.18	0.16	0.14	imputed	0.170	0.033	2.32E-07
rs1891186	1q23.2	<i>CRP</i>	157895645	G	0.126	0.18	0.16	0.13	imputed	0.170	0.033	2.34E-07
rs1891187	1q23.2	<i>CRP</i>	157895677	A	0.125	0.18	0.16	0.13	imputed	0.170	0.033	2.34E-07
rs12087465	1q23.2	<i>CRP</i>	157891923	A	0.109	0.17	0.16	0.14	imputed	0.178	0.035	4.17E-07
rs2794500	1q23.2	<i>CRP</i>	157901645	T	0.125	0.18	0.16	0.13	genotyped	0.162	0.033	7.94E-07
rs1841972	5q23.2	<i>SNCAIP</i>	121824037	G	0.226	0.15	0.14	0.14	genotyped	0.121	0.026	4.87E-06
rs10478555	5q23.2	<i>SNCAIP</i>	121809430	T	0.222	0.15	0.14	0.14	imputed	0.121	0.027	6.78E-06
rs12517578	5q21.3	<i>EFNA5</i>	106008730	G	0.355	0.12	0.14	0.14	genotyped	-0.102	0.023	6.98E-06
rs2608951	6q23.2	<i>ARG1</i>	131825473	G	0.120	0.13	0.13	0.14	genotyped	-0.174	0.033	1.96E-07
rs9483280	6q23.2	<i>ARG1</i>	131798329	G	0.115	0.13	0.13	0.14	imputed	-0.177	0.034	2.02E-07
rs9402328	6q23.2	<i>ARG1</i>	131798744	C	0.115	0.13	0.13	0.14	imputed	-0.177	0.034	2.02E-07
rs2143779	6q23.2	<i>ARG1</i>	131800478	T	0.115	0.13	0.13	0.14	imputed	-0.177	0.034	2.05E-07
rs9492976	6q23.2	<i>ARG1</i>	131797691	A	0.115	0.13	0.13	0.14	imputed	-0.177	0.034	2.06E-07
rs2179771	6q23.2	<i>ARG1</i>	131796623	C	0.115	0.13	0.13	0.14	imputed	-0.177	0.034	2.14E-07
rs9375813	6q23.2	<i>ARG1</i>	131798940	A	0.115	0.13	0.13	0.14	genotyped	-0.177	0.034	2.30E-07
rs9483281	6q23.2	<i>ARG1</i>	131806872	A	0.115	0.13	0.13	0.14	imputed	-0.176	0.034	2.31E-07
rs2608928	6q23.2	<i>ARG1</i>	131833564	A	0.119	0.13	0.13	0.14	imputed	-0.173	0.034	2.54E-07
rs2491204	6q23.2	<i>ARG1</i>	131839097	T	0.119	0.13	0.13	0.14	imputed	-0.173	0.034	2.69E-07
rs9321294	6q23.2	<i>ARG1</i>	131837250	T	0.119	0.13	0.13	0.14	imputed	-0.173	0.034	2.75E-07
rs2608927	6q23.2	<i>ARG1</i>	131835736	T	0.119	0.13	0.13	0.14	imputed	-0.172	0.034	2.80E-07

rs6904726	6q23.2	<i>ARG1</i>	131810390	A	0.115	0.13	0.13	0.14	imputed	-0.174	0.034	3.26E-07
rs6904733	6q23.2	<i>ARG1</i>	131810402	T	0.115	0.13	0.13	0.14	imputed	-0.174	0.034	3.26E-07
rs6927792	6q23.2	<i>ARG1</i>	131810800	C	0.115	0.13	0.13	0.14	imputed	-0.174	0.034	3.26E-07
rs2608935	6q23.2	<i>ARG1</i>	131831429	A	0.117	0.13	0.13	0.14	genotyped	-0.171	0.034	3.68E-07
rs9492992	6q23.2	<i>ARG1</i>	131844120	T	0.151	0.13	0.13	0.14	genotyped	-0.15	0.03	6.88E-07
rs9493000	6q23.2	<i>ARG1</i>	131850284	C	0.150	0.13	0.13	0.14	imputed	-0.149	0.03	8.41E-07
rs7740929	6q23.2	<i>ARG1</i>	131850315	G	0.150	0.13	0.13	0.14	imputed	-0.149	0.03	8.41E-07
rs3861462	6q23.2	<i>ARG1</i>	131851129	C	0.150	0.13	0.13	0.14	imputed	-0.148	0.03	1.04E-06
rs2608913	6q23.2	<i>ARG1</i>	131911954	C	0.309	0.14	0.13	0.14	imputed	-0.11	0.024	3.76E-06
rs2807272	6q23.2	<i>ARG1</i>	131832938	T	0.109	0.14	0.13	0.14	imputed	-0.157	0.035	6.30E-06
rs2608917	6q23.2	<i>ARG1</i>	131913649	G	0.312	0.14	0.13	0.14	imputed	-0.107	0.024	6.93E-06
rs2807273	6q23.2	<i>ARG1</i>	131834214	G	0.109	0.14	0.13	0.14	imputed	-0.156	0.035	7.10E-06
rs2446213	6q23.2	<i>ARG1</i>	131915724	C	0.312	0.14	0.14	0.14	genotyped	-0.106	0.024	7.55E-06
rs2491209	6q23.2	<i>ARG1</i>	131822823	A	0.110	0.14	0.13	0.14	imputed	-0.158	0.035	7.82E-06
rs2608919	6q23.2	<i>ARG1</i>	131915028	T	0.312	0.14	0.14	0.14	imputed	-0.106	0.024	7.89E-06
rs2608921	6q23.2	<i>ARG1</i>	131915428	T	0.312	0.14	0.14	0.14	imputed	-0.106	0.024	7.89E-06
rs2608915	6q23.2	<i>ARG1</i>	131913007	G	0.312	0.14	0.14	0.14	imputed	-0.106	0.024	7.93E-06
rs2608916	6q23.2	<i>ARG1</i>	131913298	G	0.312	0.14	0.14	0.14	imputed	-0.106	0.024	7.93E-06
rs2608918	6q23.2	<i>ARG1</i>	131914585	T	0.312	0.14	0.14	0.14	imputed	-0.106	0.024	7.93E-06
rs2608912	6q23.2	<i>ARG1</i>	131911476	C	0.312	0.14	0.14	0.14	genotyped	-0.106	0.024	7.94E-06
rs2608914	6q23.2	<i>ARG1</i>	131912304	A	0.312	0.14	0.14	0.14	imputed	-0.106	0.024	7.94E-06
rs2608982	6q23.2	<i>ARG1</i>	131917893	T	0.312	0.14	0.14	0.14	imputed	-0.105	0.024	8.52E-06

rs2781650	6q23.2	<i>ARG1</i>	131918414	G	0.312	0.14	0.14	0.14	imputed	-0.105	0.024	8.52E-06
rs2781651	6q23.2	<i>ARG1</i>	131918636	G	0.312	0.14	0.14	0.14	imputed	-0.105	0.024	8.52E-06
rs2749933	6q23.2	<i>ARG1</i>	131918926	T	0.312	0.14	0.14	0.14	imputed	-0.105	0.024	8.52E-06
rs2608976	6q23.2	<i>ARG1</i>	131919868	C	0.312	0.14	0.14	0.14	imputed	-0.105	0.024	8.52E-06
rs4443525	6q23.2	<i>ARG1</i>	131839960	A	0.109	0.14	0.13	0.14	imputed	-0.155	0.035	8.64E-06
rs2608940	6q23.2	<i>ARG1</i>	131840624	T	0.109	0.14	0.13	0.14	imputed	-0.155	0.035	8.64E-06
rs2062375	8q24.12	<i>TNFRSF11B</i>	120046973	G	0.271	0.16	0.15	0.13	imputed	0.113	0.025	5.22E-06
rs9969672	8q24.12	<i>TNFRSF11B</i>	120075261	T	0.268	0.15	0.15	0.13	imputed	0.113	0.025	6.29E-06
rs7014574	8q24.12	<i>TNFRSF11B</i>	120046258	C	0.268	0.15	0.15	0.13	genotyped	0.111	0.025	6.78E-06
rs11992136	8q24.12	<i>TNFRSF11B</i>	120072908	C	0.268	0.15	0.15	0.13	imputed	0.113	0.025	6.92E-06
rs2062377	8q24.12	<i>TNFRSF11B</i>	120076601	T	0.271	0.15	0.15	0.13	imputed	0.11	0.025	9.85E-06
rs796126	10p11.22	<i>ARHGAP12</i>	32008765	T	0.364	0.13	0.14	0.15	genotyped	-0.109	0.023	1.76E-06
rs796127	10p11.22	<i>ARHGAP12</i>	32008735	T	0.364	0.13	0.14	0.15	genotyped	-0.109	0.023	1.95E-06
rs2488384	10p11.22	<i>ARHGAP12</i>	32013773	T	0.371	0.13	0.14	0.15	imputed	-0.11	0.023	2.20E-06
rs1775437	10p11.22	<i>ARHGAP12</i>	32004232	T	0.359	0.13	0.14	0.15	imputed	-0.108	0.023	2.35E-06
rs796130	10p11.22	<i>ARHGAP12</i>	32006513	G	0.360	0.13	0.14	0.15	genotyped	-0.107	0.023	2.97E-06
rs796082	10p11.22	<i>ZEB1</i>	31960297	G	0.360	0.13	0.14	0.15	imputed	-0.102	0.023	9.24E-06
rs1169310	12q24.31	<i>HNFI1A</i>	119923816	G	0.443	0.16	0.14	0.13	imputed	0.121	0.022	4.95E-08
rs1169306	12q24.31	<i>HNFI1A</i>	119922694	C	0.444	0.16	0.14	0.13	imputed	0.121	0.022	5.15E-08
rs735396	12q24.31	<i>HNFI1A</i>	119923227	T	0.444	0.16	0.14	0.13	imputed	0.121	0.022	5.34E-08
rs2464195	12q24.31	<i>HNFI1A</i>	119919858	G	0.444	0.16	0.14	0.13	imputed	0.121	0.022	5.83E-08
rs1169313	12q24.31	<i>CI2orf43</i>	119927053	T	0.446	0.16	0.14	0.13	genotyped	0.119	0.022	6.66E-08

rs2259816	12q24.31	<i>HNF1A</i>	119919970	G	0.446	0.16	0.14	0.13	genotyped	0.119	0.022	7.10E-08
rs2259820	12q24.31	<i>HNF1A</i>	119919725	C	0.446	0.16	0.14	0.13	imputed	0.119	0.022	8.58E-08
rs2464196	12q24.31	<i>HNF1A</i>	119919810	G	0.446	0.16	0.14	0.13	imputed	0.119	0.022	8.58E-08
rs2393791	12q24.31	<i>HNF1A</i>	119908339	C	0.480	0.12	0.14	0.16	genotyped	-0.118	0.022	8.89E-08
rs7310409	12q24.31	<i>HNF1A</i>	119909244	A	0.479	0.12	0.14	0.16	imputed	-0.116	0.022	1.38E-07
rs2393775	12q24.31	<i>HNF1A</i>	119908957	G	0.482	0.12	0.14	0.16	imputed	-0.116	0.022	1.75E-07
rs1182933	12q24.31	<i>CI2orf43</i>	119939005	C	0.452	0.16	0.14	0.13	imputed	0.114	0.022	4.05E-07
rs2708101	12q24.31	<i>OASL</i>	119972015	C	0.482	0.16	0.14	0.13	genotyped	0.106	0.022	1.36E-06
rs1920792	12q24.31	<i>HNF1A</i>	119888967	C	0.468	0.16	0.14	0.13	imputed	0.099	0.022	6.35E-06
rs7305618	12q24.31	<i>HNF1A</i>	119887315	T	0.468	0.16	0.14	0.13	imputed	0.099	0.022	6.86E-06
rs1169303	12q24.31	<i>HNF1A</i>	119920759	A	0.245	0.17	0.14	0.13	imputed	0.114	0.026	9.47E-06
rs7953249	12q24.31	<i>HNF1A</i>	119888107	A	0.469	0.16	0.14	0.13	genotyped	0.097	0.022	9.85E-06
rs17596685	13q14.11	<i>TNFSF11</i>	42015201	T	0.352	0.13	0.14	0.14	genotyped	-0.102	0.023	6.69E-06

\*98 SNP loci with unadjusted  $P$  value  $< 10^{-5}$  were presented; \*\* Positions of the SNPs were based on NCBI human genome build 36.3 (hg18);

\*\*\* Type indicates if a SNP is genotype or imputed; Chr, chromosome; MAF, minor allele frequency; CRP, C-reactive protein; SE, standard error;

**Table S3.** SNP loci associated with serum CRP levels in the stage 2 data and meta-analysis.

SNP*	Nearest gene	Locus	Position	Minor allele	Stage 2		Meta-analysis		Q	I <sup>2</sup>
					$\beta$ (SE)	P	$\beta$	P		
rs7553007	<i>CRP</i>	1q23.2	157965173	G	0.099 (0.042)	1.93E-02	0.164	1.72E-16	0.085	66.23
rs1205	<i>CRP</i>	1q23.2	157948857	C	0.099 (0.043)	2.07E-02	0.163	5.09E-16	0.093	64.63
rs2808629	<i>CRP</i>	1q23.2	157943420	G	0.098 (0.043)	2.30E-02	0.163	6.64E-16	0.088	65.72
rs2794520	<i>CRP</i>	1q23.2	157945440	C	0.098 (0.043)	2.30E-02	0.162	7.39E-16	0.089	65.52
rs2808628	<i>CRP</i>	1q23.2	157942635	G	0.100 (0.043)	2.00E-02	0.164	7.50E-16	0.097	63.73
rs876537	<i>CRP</i>	1q23.2	157941557	C	0.094 (0.043)	3.17E-02	0.163	1.49E-15	0.072	69.15
rs1341665	<i>CRP</i>	1q23.2	157958183	G	0.103 (0.043)	1.72E-02	0.155	3.76E-14	0.176	45.42
rs2027471	<i>CRP</i>	1q23.2	157956012	T	0.100 (0.043)	2.12E-02	0.155	3.92E-14	0.151	51.52
rs16842599	<i>CRP</i>	1q23.2	157964099	C	0.182 (0.058)	1.78E-03	0.195	1.55E-12	0.791	0
rs12081480	<i>CRP</i>	1q23.2	157973614	G	0.182 (0.058)	1.80E-03	0.195	1.90E-12	0.795	0
rs16842559	<i>CRP</i>	1q23.2	157942795	C	0.179 (0.058)	2.17E-03	0.194	1.99E-12	0.758	0
rs16842568	<i>CRP</i>	1q23.2	157942844	G	0.179 (0.058)	2.17E-03	0.194	1.99E-12	0.758	0
rs12081252	<i>CRP</i>	1q23.2	157973137	C	0.182 (0.058)	1.78E-03	0.194	2.10E-12	0.805	0
rs12068753	<i>CRP</i>	1q23.2	157959161	A	0.182 (0.058)	1.78E-03	0.194	2.18E-12	0.813	0
rs12081264	<i>CRP</i>	1q23.2	157973184	C	0.182 (0.058)	1.78E-03	0.194	2.42E-12	0.813	0
rs3093075	<i>CRP</i>	1q23.2	157946537	T	0.167 (0.058)	3.76E-03	0.185	1.15E-11	0.728	0
rs3093077	<i>CRP</i>	1q23.2	157946260	C	0.168 (0.057)	3.57E-03	0.185	1.18E-11	0.736	0
rs16842502	<i>CRP</i>	1q23.2	157920487	A	0.171 (0.058)	3.57E-03	0.181	9.62E-11	0.841	0
rs4275453	<i>CRP</i>	1q23.2	157974671	C	0.124 (0.046)	7.90E-03	0.130	5.26E-09	0.871	0
rs12517578	<i>EFNA5</i>	5q21.3	106008730	G	-0.005 (0.044)	9.10E-01	-0.082	5.21E-05	0.048	74.34
rs1841972	<i>SNCAIP</i>	5q23.2	121824037	G	-0.025 (0.049)	6.04E-01	0.088	1.61E-04	0.008	85.63
rs10478555	<i>SNCAIP</i>	5q23.2	121809430	T	-0.021 (0.049)	6.76E-01	0.088	1.77E-04	0.011	84.39

rs9375813	<i>ARG1</i>	6q23.2	131798940	A	-0.132 (0.063)	3.73E-02	-0.167	2.85E-08	0.538	0
rs9483280	<i>ARG1</i>	6q23.2	131798329	G	-0.127 (0.063)	4.40E-02	-0.166	3.08E-08	0.486	0
rs9402328	<i>ARG1</i>	6q23.2	131798744	C	-0.127 (0.063)	4.40E-02	-0.166	3.08E-08	0.486	0
rs9492976	<i>ARG1</i>	6q23.2	131797691	A	-0.127 (0.063)	4.40E-02	-0.166	3.13E-08	0.486	0
rs2143779	<i>ARG1</i>	6q23.2	131800478	T	-0.125 (0.063)	4.73E-02	-0.165	3.41E-08	0.467	0
rs2179771	<i>ARG1</i>	6q23.2	131796623	C	-0.124 (0.063)	4.92E-02	-0.165	3.72E-08	0.465	0
rs9483281	<i>ARG1</i>	6q23.2	131806872	A	-0.117 (0.063)	6.35E-02	-0.163	5.35E-08	0.406	0
rs2608951	<i>ARG1</i>	6q23.2	131825473	G	-0.110 (0.062)	7.74E-02	-0.159	5.79E-08	0.361	0
rs2608928	<i>ARG1</i>	6q23.2	131833564	A	-0.114 (0.062)	6.76E-02	-0.160	6.27E-08	0.406	0
rs2608935	<i>ARG1</i>	6q23.2	131831429	A	-0.122 (0.063)	5.32E-02	-0.160	6.56E-08	0.490	0
rs9321294	<i>ARG1</i>	6q23.2	131837250	T	-0.114 (0.062)	6.76E-02	-0.159	6.70E-08	0.410	0
rs2491204	<i>ARG1</i>	6q23.2	131839097	T	-0.114 (0.062)	6.95E-02	-0.159	6.73E-08	0.404	0
rs2608927	<i>ARG1</i>	6q23.2	131835736	T	-0.114 (0.062)	6.76E-02	-0.159	6.85E-08	0.411	0
rs6904726	<i>ARG1</i>	6q23.2	131810390	A	-0.111 (0.063)	7.81E-02	-0.160	9.44E-08	0.380	0
rs6904733	<i>ARG1</i>	6q23.2	131810402	T	-0.111 (0.063)	7.87E-02	-0.160	9.54E-08	0.379	0
rs6927792	<i>ARG1</i>	6q23.2	131810800	C	-0.111 (0.063)	7.87E-02	-0.160	9.54E-08	0.379	0
rs2807272	<i>ARG1</i>	6q23.2	131832938	T	-0.117 (0.064)	6.95E-02	-0.148	1.30E-06	0.576	0
rs2807273	<i>ARG1</i>	6q23.2	131834214	G	-0.117 (0.064)	6.95E-02	-0.147	1.45E-06	0.584	0
rs4443525	<i>ARG1</i>	6q23.2	131839960	A	-0.116 (0.064)	7.14E-02	-0.146	1.79E-06	0.591	0
rs2608940	<i>ARG1</i>	6q23.2	131840624	T	-0.116 (0.064)	7.14E-02	-0.146	1.79E-06	0.591	0
rs2491209	<i>ARG1</i>	6q23.2	131822823	A	-0.093 (0.066)	1.58E-01	-0.144	4.01E-06	0.387	0
rs3861462	<i>ARG1</i>	6q23.2	131851129	C	-0.034 (0.058)	5.57E-01	-0.124	4.06E-06	0.083	66.84
rs9493000	<i>ARG1</i>	6q23.2	131850284	C	-0.027 (0.058)	6.43E-01	-0.123	4.56E-06	0.060	71.66
rs7740929	<i>ARG1</i>	6q23.2	131850315	G	-0.027 (0.058)	6.43E-01	-0.123	4.56E-06	0.060	71.66
rs9492992	<i>ARG1</i>	6q23.2	131844120	T	-0.002 (0.057)	9.74E-01	-0.118	1.05E-05	0.022	81.07
rs2608913	<i>ARG1</i>	6q23.2	131911954	C	-0.019 (0.043)	6.64E-01	-0.089	2.00E-05	0.063	70.98



rs2446213	<i>ARG1</i>	6q23.2	131915724	C	-0.012 (0.043)	7.75E-01	-0.084	4.75E-05	0.057	72.4
rs2608917	<i>ARG1</i>	6q23.2	131913649	G	-0.011 (0.043)	8.04E-01	-0.084	4.76E-05	0.052	73.55
rs2608919	<i>ARG1</i>	6q23.2	131915028	T	-0.012 (0.043)	7.75E-01	-0.084	4.91E-05	0.058	72.28
rs2608921	<i>ARG1</i>	6q23.2	131915428	T	-0.012 (0.043)	7.75E-01	-0.084	4.91E-05	0.058	72.28
rs2608915	<i>ARG1</i>	6q23.2	131913007	G	-0.012 (0.043)	7.80E-01	-0.084	4.96E-05	0.057	72.39
rs2608916	<i>ARG1</i>	6q23.2	131913298	G	-0.012 (0.043)	7.80E-01	-0.084	4.96E-05	0.057	72.39
rs2608918	<i>ARG1</i>	6q23.2	131914585	T	-0.012 (0.043)	7.80E-01	-0.084	4.96E-05	0.057	72.39
rs2608912	<i>ARG1</i>	6q23.2	131911476	C	-0.012 (0.043)	7.84E-01	-0.084	5.10E-05	0.057	72.5
rs2608914	<i>ARG1</i>	6q23.2	131912304	A	-0.012 (0.043)	7.84E-01	-0.084	5.10E-05	0.057	72.5
rs2608982	<i>ARG1</i>	6q23.2	131917893	T	-0.012 (0.043)	7.75E-01	-0.084	5.23E-05	0.059	72.04
rs2781650	<i>ARG1</i>	6q23.2	131918414	G	-0.012 (0.043)	7.75E-01	-0.084	5.23E-05	0.059	72.04
rs2781651	<i>ARG1</i>	6q23.2	131918636	G	-0.012 (0.043)	7.75E-01	-0.084	5.23E-05	0.059	72.04
rs2749933	<i>ARG1</i>	6q23.2	131918926	T	-0.012 (0.043)	7.75E-01	-0.084	5.23E-05	0.059	72.04
rs2608976	<i>ARG1</i>	6q23.2	131919868	C	-0.012 (0.043)	7.75E-01	-0.084	5.23E-05	0.059	72.04
rs2062375	<i>TNFRSF11B</i>	8q24.12	120046973	G	0.012 (0.045)	7.87E-01	0.089	3.77E-05	0.049	74.25
rs9969672	<i>TNFRSF11B</i>	8q24.12	120075261	T	0.014 (0.045)	7.56E-01	0.090	4.17E-05	0.053	73.25
rs11992136	<i>TNFRSF11B</i>	8q24.12	120072908	C	0.015 (0.045)	7.44E-01	0.089	4.35E-05	0.056	72.61
rs7014574	<i>TNFRSF11B</i>	8q24.12	120046258	C	0.007 (0.044)	8.74E-01	0.087	6.06E-05	0.040	76.29
rs2062377	<i>TNFRSF11B</i>	8q24.12	120076601	T	0.004 (0.045)	9.34E-01	0.085	9.39E-05	0.038	76.9
rs796127	<i>ARHGAP12</i>	10p11.22	32008735	T	-0.041 (0.042)	3.22E-01	-0.093	3.23E-06	0.158	49.89
rs796126	<i>ARHGAP12</i>	10p11.22	32008765	T	-0.040 (0.042)	3.43E-01	-0.093	3.26E-06	0.146	52.73
rs1775437	<i>ARHGAP12</i>	10p11.22	32004232	T	-0.038 (0.042)	3.59E-01	-0.092	4.50E-06	0.143	53.44
rs2488384	<i>ARHGAP12</i>	10p11.22	32013773	T	-0.035 (0.043)	4.15E-01	-0.093	5.31E-06	0.123	57.97
rs796130	<i>ARHGAP12</i>	10p11.22	32006513	G	-0.038 (0.042)	3.64E-01	-0.091	5.64E-06	0.149	51.94
rs796082	<i>ZEB1</i>	10p11.22	31960297	G	-0.018 (0.043)	6.72E-01	-0.083	3.91E-05	0.085	66.36
rs2393791	<i>HNF1A</i>	12q24.31	119908339	C	-0.138 (0.041)	8.28E-04	-0.122	2.90E-10	0.665	0

rs7310409	<i>HNFI1A</i>	12q24.31	119909244	A	-0.138 (0.041)	7.79E-04	-0.121	4.35E-10	0.641	0
rs2393775	<i>HNFI1A</i>	12q24.31	119908957	G	-0.137 (0.042)	1.08E-03	-0.120	7.51E-10	0.647	0
rs1169313	<i>C12orf43</i>	12q24.31	119927053	T	0.109 (0.041)	7.96E-03	0.117	1.72E-09	0.828	0
rs1169310	<i>HNFI1A</i>	12q24.31	119923816	G	0.104 (0.041)	1.08E-02	0.117	1.75E-09	0.716	0
rs1169306	<i>HNFI1A</i>	12q24.31	119922694	C	0.104 (0.041)	1.08E-02	0.117	1.84E-09	0.719	0
rs735396	<i>HNFI1A</i>	12q24.31	119923227	T	0.104 (0.041)	1.08E-02	0.117	1.91E-09	0.721	0
rs2464195	<i>HNFI1A</i>	12q24.31	119919858	G	0.104 (0.041)	1.08E-02	0.117	2.09E-09	0.726	0
rs2259816	<i>HNFI1A</i>	12q24.31	119919970	G	0.104 (0.041)	1.04E-02	0.116	2.45E-09	0.751	0
rs2259820	<i>HNFI1A</i>	12q24.31	119919725	C	0.097 (0.041)	1.79E-02	0.114	5.13E-09	0.630	0
rs2464196	<i>HNFI1A</i>	12q24.31	119919810	G	0.097 (0.041)	1.79E-02	0.114	5.13E-09	0.630	0
rs1182933	<i>C12orf43</i>	12q24.31	119939005	C	0.093 (0.042)	2.72E-02	0.109	3.44E-08	0.656	0
rs1920792	<i>HNFI1A</i>	12q24.31	119888967	C	0.118 (0.040)	3.56E-03	0.103	8.12E-08	0.680	0
rs7305618	<i>HNFI1A</i>	12q24.31	119887315	T	0.118 (0.040)	3.56E-03	0.103	8.79E-08	0.675	0
rs2708101	<i>OASL</i>	12q24.31	119972015	C	0.091 (0.041)	2.51E-02	0.103	1.03E-07	0.750	0
rs7953249	<i>HNFI1A</i>	12q24.31	119888107	A	0.118 (0.040)	3.53E-03	0.102	1.27E-07	0.645	0
rs1169303	<i>HNFI1A</i>	12q24.31	119920759	A	0.095 (0.046)	3.79E-02	0.110	1.04E-06	0.726	0
rs17596685	<i>TNFSF11</i>	13q14.11	42015201	T	-0.059 (0.043)	1.74E-01	-0.093	3.74E-06	0.378	0

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\*Among the 98 SNP loci with unadjusted  $P$  value  $< 10^{-5}$  in stage 1 result, 92 available SNPs in stage 2 data were presented

**Table S4.** *P*-values and LD values of neighboring SNPs of the rs9375813 in the *ARG1* locus.

L1	L2	Gene	BP	BETA	SE	P-value *	D'	$r^2$
rs9375813	rs17596690	<i>ARG1</i>	131794917	-0.152	0.035	1.42E-05	0.963	0.874
rs9375813	rs2179771	<i>ARG1</i>	131796623	-0.177	0.034	2.14E-07	1	0.999
rs9375813	rs9492976	<i>ARG1</i>	131797691	-0.177	0.034	2.06E-07	1	0.999
rs9375813	rs9483280	<i>ARG1</i>	131798329	-0.177	0.034	2.02E-07	1	0.999
rs9375813	rs9402328	<i>ARG1</i>	131798744	-0.177	0.034	2.02E-07	1	0.999
rs9375813	rs2143779	<i>ARG1</i>	131800478	-0.177	0.034	2.05E-07	1	0.999
rs9375813	rs2608903	<i>ARG1</i>	131805071	-0.076	0.024	1.35E-03	0.998	0.260
rs9375813	rs9483281	<i>ARG1</i>	131806872	-0.176	0.034	2.31E-07	0.999	0.999
rs9375813	rs6904726	<i>ARG1</i>	131810390	-0.174	0.034	3.26E-07	0.999	0.999
rs9375813	rs6904733	<i>ARG1</i>	131810402	-0.174	0.034	3.26E-07	0.999	0.999
rs9375813	rs6927792	<i>ARG1</i>	131810800	-0.174	0.034	3.26E-07	0.999	0.999
rs9375813	rs2491209	<i>ARG1</i>	131822823	-0.158	0.035	7.82E-06	0.988	0.923
rs9375813	rs2608951	<i>ARG1</i>	131825473	-0.174	0.033	1.96E-07	0.996	0.951
rs9375813	rs2608935	<i>ARG1</i>	131831429	-0.171	0.034	3.68E-07	0.995	0.940
rs9375813	rs2807272	<i>ARG1</i>	131832938	-0.157	0.035	6.30E-06	0.969	0.903
rs9375813	rs2608928	<i>ARG1</i>	131833564	-0.173	0.034	2.54E-07	0.997	0.960
rs9375813	rs2807273	<i>ARG1</i>	131834214	-0.156	0.035	7.10E-06	0.968	0.903
rs9375813	rs2608927	<i>ARG1</i>	131835736	-0.172	0.034	2.80E-07	0.997	0.959
rs9375813	rs9321294	<i>ARG1</i>	131837250	-0.173	0.034	2.75E-07	0.997	0.959
rs9375813	rs2491204	<i>ARG1</i>	131839097	-0.173	0.034	2.69E-07	0.997	0.958
rs9375813	rs4443525	<i>ARG1</i>	131839960	-0.155	0.035	8.64E-06	0.968	0.902
rs9375813	rs2608940	<i>ARG1</i>	131840624	-0.155	0.035	8.64E-06	0.968	0.902

**Table S5.** Associations of the previously reported CRP-related loci.

SNP	Chr	Position* (bp)	Nearest Gene	MAF	Type**	Minor allele	Effect Size	P	Reference
rs6700896	1	65862370	<i>LEPR</i>	0.11	imputed	C	-0.017	0.6171	Elliot et al, 2009
rs1805096	1	65874845	<i>LEPR</i>	0.11	genotyped	G	-0.017	0.6164	Reiner et al, 2012
rs1892534	1	65878532	<i>LEPR</i>	0.11	genotyped	C	-0.018	0.6002	Ridker et al, 2008
rs2186245	1	65890652	<i>LEPR</i>	0.24	imputed	C	-0.018	0.4948	Ridker et al, 2008
rs12022410	1	65926521	<i>LEPR</i>	0.09	imputed	A	-0.051	0.1911	Ridker et al, 2008
rs2211651	1	65928609	<i>LEPR</i>	0.11	imputed	G	-0.015	0.6609	Ridker et al, 2008
rs2889195	1	65929318	<i>LEPR</i>	0.11	genotyped	C	-0.012	0.7178	Ridker et al, 2008
rs4291477	1	65963663	<i>PDE4B</i>	0.17	genotyped	G	-0.029	0.3151	Ridker et al, 2008
rs4537545	1	152685503	<i>IL6R</i>	0.44	genotyped	T	-0.056	0.0112	Elliot et al, 2009
rs4129267	1	152692888	<i>IL6R</i>	0.44	imputed	T	-0.059	0.0089	Ridker et al, 2008
rs8192284	1	152693594	<i>IL6R</i>	0.44	imputed	C	-0.059	0.0087	Ridker et al, 2008; Okada et al, 2011
rs12093699	1	157914612	<i>CRP</i>	0.06	imputed	A	0.147	0.0017	Ridker et al, 2008
rs876537	1	157941557	<i>CRP</i>	0.36	imputed	C	0.182	3.61E-15	Wu et al, 2012
rs2794520	1	157945440	<i>CRP</i>	0.36	imputed	C	0.181	2.82E-15	Ridker et al, 2008
rs3093075	1	157946537	<i>CRP</i>	0.15	imputed	T	0.190	8.66E-10	Ridker et al, 2008
rs1205	1	157948857	<i>CRP</i>	0.36	imputed	C	0.181	2.21E-15	Ridker et al, 2008
rs1417938	1	157950810	<i>CRP</i>	0.07	imputed	A	0.169	9.89E-05	Ridker et al, 2008

rs2027471	1	157956012	<i>CRP</i>	0.34	imputed	T	0.171	2.30E-13	Ridker et al, 2008
rs3116656	1	157958996	<i>CRP</i>	0.07	imputed	G	0.182	1.58E-05	Ridker et al, 2008
rs12068753	1	157959161	<i>CRP</i>	0.14	genotyped	A	0.197	3.41E-10	Ridker et al, 2008
rs3116653	1	157963534	<i>CRP</i>	0.08	imputed	C	0.173	2.98E-05	Ridker et al, 2008
rs3116651	1	157965109	<i>CRP</i>	0.08	genotyped	T	0.171	3.44E-05	Ridker et al, 2008
rs7553007	1	157965173	<i>CRP</i>	0.37	genotyped	G	0.182	7.34E-16	Ridker et al, 2008; Elliot et al, 2009; Reiner et al, 2012
rs780094	2	27594741	<i>GCKR</i>	0.46	genotyped	C	-0.059	0.0067	Ridker et al, 2008
rs1260333	2	27602128	<i>GCKR</i>	0.46	imputed	G	-0.062	0.0054	Ridker et al, 2008
rs2097677	7	22699364	<i>IL6</i>	0.24	imputed	A	0.091	0.0004	Okada et al, 2011
rs10778213	12	102019281	<i>ASCLI</i>	0.17	imputed	T	0.055	0.0607	Ridker et al, 2008
rs7305618	12	119887315	<i>HNFI1A</i>	0.47	imputed	T	0.099	6.86E-06	Wu et al, 2012
rs7953249	12	119888107	<i>HNFI1A</i>	0.47	genotyped	A	0.097	9.85E-06	Ridker et al, 2008
rs7310409	12	119909244	<i>HNFI1A</i>	0.48	imputed	A	-0.116	1.38E-07	Ridker et al, 2008; Okada et al, 2011
rs2464196	12	119919810	<i>HNFI1A</i>	0.45	imputed	G	0.119	8.58E-08	Ridker et al, 2008
rs2259816	12	119919970	<i>HNFI1A</i>	0.45	genotyped	G	0.119	7.10E-08	Reiner et al, 2012
rs1169307	12	119922765	<i>HNFI1A</i>	0.10	imputed	T	0.131	0.0003	Ridker et al, 2008
rs735396	12	119923227	<i>HNFI1A</i>	0.44	imputed	T	0.121	5.34E-08	Ridker et al, 2008
rs4420638	19	50114786	<i>APOE-CI-CII cluster</i>	0.11	genotyped	G	-0.098	0.0040	Elliot et al, 2009; Okada et al, 2011

\*Position is based on NCBI human genome build 36.3 (hg18)

\*\*Type indicates if a SNP is genotype or imputed; Chr, Chromosome; MAF, minor allele frequency

**Table S6. Re-prioritized genetic variants list after GWAS.**

SNPs	Chr	Position	GWAS P-value	Final Weight	Before Re-prioritization	After Re-prioritization
rs7553007	1	157965173	7.34E-16	5.40E-16	1	1
rs1205	1	157948857	2.21E-15	2.27E-15	2	2
rs2794520	1	157945440	2.82E-15	2.49E-15	4	3
rs2808629	1	157943420	2.50E-15	3.27E-15	3	4
rs2808628	1	157942635	3.43E-15	4.48E-15	5	5
rs876537	1	157941557	3.61E-15	4.72E-15	6	6
rs2027471	1	157956012	2.30E-13	3.01E-13	7	7
rs1341665	1	157958183	2.98E-13	3.89E-13	8	8
rs16842599	1	157964099	2.39E-10	2.46E-10	9	9
rs12081480	1	157973614	2.96E-10	3.05E-10	12	10
rs16842568	1	157942844	2.54E-10	3.32E-10	10	11
rs16842559	1	157942795	2.54E-10	3.32E-10	11	12
rs12081252	1	157973137	3.28E-10	3.38E-10	13	13
rs12081264	1	157973184	3.81E-10	3.92E-10	15	14
rs12068753	1	157959161	3.41E-10	4.46E-10	14	15
<b>rs2608912</b>	<b>6</b>	<b>131911476</b>	<b>7.94E-06</b>	<b>7.22E-10</b>	<b>87</b>	<b>16</b>
<b>rs2608976</b>	<b>6</b>	<b>131919868</b>	<b>8.52E-06</b>	<b>7.62E-10</b>	<b>88</b>	<b>17</b>
rs3093075	1	157946537	8.66E-10	1.13E-09	16	18
<b>rs2608921</b>	<b>6</b>	<b>131915428</b>	<b>7.89E-06</b>	<b>1.21E-09</b>	<b>81</b>	<b>19</b>
rs3093077	1	157946260	9.30E-10	1.22E-09	17	20
rs16842502	1	157920487	7.80E-09	1.02E-08	18	21
rs1169310	12	119923816	4.95E-08	5.10E-08	19	22
rs1169306	12	119922694	5.15E-08	5.30E-08	20	23
rs735396	12	119923227	5.34E-08	5.50E-08	21	24
rs2464195	12	119919858	5.83E-08	6.00E-08	22	25
rs1169313	12	119927053	6.66E-08	6.86E-08	23	26
rs2259816	12	119919970	7.10E-08	7.31E-08	24	27
rs2464196	12	119919810	8.58E-08	8.83E-08	25	28
rs2259820	12	119919725	8.58E-08	8.83E-08	26	29
rs2393791	12	119908339	8.89E-08	9.15E-08	27	30
rs7310409	12	119909244	1.38E-07	1.42E-07	28	31
rs2393775	12	119908957	1.75E-07	1.80E-07	29	32
rs1891187	1	157895677	2.34E-07	2.07E-07	42	33
rs4275453	1	157974671	2.06E-07	2.12E-07	36	34
rs1446976	1	157895818	2.32E-07	2.13E-07	41	35
rs1891186	1	157895645	2.34E-07	2.32E-07	43	36
rs2794526	1	157892102	1.79E-07	2.34E-07	30	37
rs2608951	6	131825473	1.96E-07	2.56E-07	31	38
rs9402328	6	131798744	2.02E-07	2.64E-07	32	39
rs9483280	6	131798329	2.02E-07	2.64E-07	33	40
rs2143779	6	131800478	2.05E-07	2.68E-07	34	41
rs9492976	6	131797691	2.06E-07	2.69E-07	35	42
rs2179771	6	131796623	2.14E-07	2.80E-07	37	43
rs9375813	6	131798940	2.30E-07	3.01E-07	38	44
rs9483281	6	131806872	2.31E-07	3.02E-07	39	45
rs1446975	1	157895966	2.32E-07	3.03E-07	40	46

rs2608928	6	131833564	2.54E-07	3.32E-07	44	47
rs2491204	6	131839097	2.69E-07	3.52E-07	45	48
rs9321294	6	131837250	2.75E-07	3.59E-07	46	49
rs2608927	6	131835736	2.80E-07	3.66E-07	47	50
rs1182933	12	119939005	4.05E-07	4.17E-07	52	51
rs6927792	6	131810800	3.26E-07	4.26E-07	48	52
rs6904733	6	131810402	3.26E-07	4.26E-07	49	53
rs6904726	6	131810390	3.26E-07	4.26E-07	50	54
rs2608935	6	131831429	3.68E-07	4.81E-07	51	55
rs12087465	1	157891923	4.17E-07	5.45E-07	53	56
rs9492992	6	131844120	6.88E-07	8.99E-07	54	57
rs2794500	1	157901645	7.94E-07	1.04E-06	55	58
rs7740929	6	131850315	8.41E-07	1.10E-06	56	59
rs9493000	6	131850284	8.41E-07	1.10E-06	57	60
rs3861462	6	131851129	1.04E-06	1.36E-06	58	61
rs2708101	12	119972015	1.36E-06	1.40E-06	59	62
rs796126	10	32008765	1.76E-06	2.30E-06	60	63
rs796127	10	32008735	1.95E-06	2.55E-06	61	64
rs2488384	10	32013773	2.20E-06	2.88E-06	62	65
rs1775437	10	32004232	2.35E-06	3.07E-06	63	66
rs2608913	6	131911954	3.76E-06	3.87E-06	65	67
rs796130	10	32006513	2.97E-06	3.88E-06	64	68
rs1841972	5	121824037	4.87E-06	6.36E-06	66	69
rs1920792	12	119888967	6.35E-06	6.54E-06	70	70
rs2062375	8	120046973	5.22E-06	6.82E-06	67	71
rs7305618	12	119887315	6.86E-06	7.06E-06	74	72
rs2608917	6	131913649	6.93E-06	7.14E-06	76	73
rs17596685	13	42015201	6.69E-06	7.47E-06	71	74
rs2446213	6	131915724	7.55E-06	7.77E-06	79	75
rs2608919	6	131915028	7.89E-06	8.12E-06	82	76
rs2608918	6	131914585	7.93E-06	8.17E-06	83	77
rs2608916	6	131913298	7.93E-06	8.17E-06	84	78
rs2608915	6	131913007	7.93E-06	8.17E-06	85	79
rs2608914	6	131912304	7.94E-06	8.18E-06	86	80
rs9969672	8	120075261	6.29E-06	8.22E-06	68	81
rs2807272	6	131832938	6.30E-06	8.23E-06	69	82
rs2749933	6	131918926	8.52E-06	8.77E-06	89	83
rs2781651	6	131918636	8.52E-06	8.77E-06	90	84
rs2781650	6	131918414	8.52E-06	8.77E-06	91	85
rs2608982	6	131917893	8.52E-06	8.77E-06	92	86
rs7014574	8	120046258	6.78E-06	8.86E-06	72	87
rs10478555	5	121809430	6.78E-06	8.86E-06	73	88
rs11992136	8	120072908	6.92E-06	9.04E-06	75	89
rs12517578	5	106008730	6.98E-06	9.12E-06	77	90
rs2807273	6	131834214	7.10E-06	9.28E-06	78	91
rs1169303	12	119920759	9.47E-06	9.75E-06	96	92
rs7953249	12	119888107	9.85E-06	1.01E-05	98	93
rs2491209	6	131822823	7.82E-06	1.02E-05	80	94
rs2608940	6	131840624	8.64E-06	1.13E-05	93	95
rs4443525	6	131839960	8.64E-06	1.13E-05	94	96

rs796082	10	31960297	9.24E-06	1.21E-05	95	97
rs2062377	8	120076601	9.85E-06	1.29E-05	97	98
rs1978838	5	106008311	1.01E-05	1.32E-05	99	99
rs7010267	8	120015837	1.05E-05	1.37E-05	100	100

**Bold characters represent three SNPs, rs2608912, rs2608976, rs2608921, whose ranking of significance levels became highly elevated after SNP prioritization from 87th, 88th and 81th to 16th, 17th and 19th, respectively.**



**Table S7.** Associations of the top significant SNP polymorphisms on cardiovascular disease traits based on the whole KARE samples (7,626 samples).

Disease Trait	N <sup>¶</sup>	Chr	SNP	Position	Minor Allele	P*	OR <sup>†</sup>	SE	L95 <sup>‡</sup>	U95 <sup>§</sup>
Myocardial infarction	55	1	rs7553007	157965173	G	0.1566	1.31	0.19	0.90	1.92
		6	rs9375813	131798940	A	0.3262	0.71	0.35	0.36	1.41
		12	rs2393791	119908339	C	0.3223	1.21	0.19	0.83	1.77
Coronary artery disease	65	1	rs7553007	157965173	G	0.9496	1.01	0.18	0.71	1.45
		6	rs9375813	131798940	A	0.3253	0.73	0.32	0.39	1.36
		12	rs2393791	119908339	C	0.1322	0.76	0.18	0.54	1.09
Hypertension	1115	1	rs7553007	157965173	G	0.6138	1.03	0.05	0.93	1.13
		<b>6</b>	<b>rs9375813</b>	<b>131798940</b>	<b>A</b>	<b>0.0440</b>	<b>0.86</b>	<b>0.08</b>	<b>0.74</b>	<b>1.00</b>
		12	rs2393791	119908339	C	0.5570	0.97	0.05	0.89	1.07

¶N : Number of case samples

\*P: Age and gender adjusted logistic regression was performed based on the above phenotype.

†OR: Estimated odds ratio for minor allele

‡L95: Lower bound of 95% confidence interval for odds ratio

§U95: Upper bound of 95% confidence interval for odds ratio

**Table S8.** Genes mapped with variant in adaptive immune response.

<b>Gene Name</b>	<b>Variant</b>	<b>Functional Class*</b>	<b><math>-\log_{10}(P\text{-value})^{**}</math></b>
<i>CRP</i>	rs7553007	-	15.134
<i>EXO1</i>	rs1418761	-	3.079
<i>TLR4</i>	rs2244872	-	2.409
<i>C9</i>	rs2738238	-	2.407
<i>CTSC</i>	rs217090	-	2.363
<i>SYK</i>	rs2613310	-	2.281
<i>CD46</i>	rs7144	-	2.121
<i>PRKCD</i>	rs13084863	-	2
<i>IL12B</i>	rs6896881	-	1.965
<i>TXK</i>	rs10938521	-	1.85
<i>C8B</i>	rs599857	-	1.803
<i>CR1</i>	rs677066	-	1.797
<i>MSH2</i>	rs6708696	-	1.744
<i>PIK3CD</i>	rs4240896	-	1.734
<i>RIPK2</i>	rs2665636	-	1.726
<i>PIK3CG</i>	rs7804699	-	1.718
<i>CADM1</i>	rs693246	-	1.692
<i>C5</i>	rs2159777	-	1.648
<i>IFNG</i>	rs4244065	-	1.614
<i>RAB27A</i>	rs9920114	-	1.608
<i>IFNB1</i>	rs4977657	-	1.551
<i>JAM3</i>	rs661820	-	1.535
<i>LIG4</i>	rs16971751	-	1.53
<i>ITK</i>	rs25856	-	1.527
<i>MEF2C</i>	rs4521516	-	1.496
<i>KLHL6</i>	rs7618957	-	1.418
<i>C7</i>	rs2455307	-	1.411
<i>CR2</i>	rs7527218	-	1.408
<i>HSPD1</i>	rs13386066	-	1.407
<i>MBL2</i>	rs12262251	-	1.401
<i>VEGFA</i>	rs4714696	-	1.386
<i>RORC</i>	rs3828057	-	1.368
<i>POU2F2</i>	rs11883412	-	1.355
<i>GCNT3</i>	rs6494120	-	1.351

<i>LYST</i>	rs12038267	-	1.332
<i>SERPING1</i>	rs2729358	-	1.326
<i>ZAP70</i>	rs2290127	-	1.323
<i>CLU</i>	rs1316801	-	1.305
<i>C3</i>	rs11569538	-	1.303
<i>MLH1</i>	rs1540354	-	1.232
<i>IL18</i>	rs360729	-	1.207
<i>EXOSC3</i>	rs10814621	-	1.156
<i>CTSH</i>	rs12438191	-	1.126
<i>FAS</i>	rs17378702	-	1.107
<i>BCL6</i>	rs873205	-	1.04
<i>TNFSF4</i>	rs16845607	-	1.03
<i>CXCL13</i>	rs1500498	-	0.973
<i>IL4</i>	rs2243283	-	0.962
<i>CTSS</i>	rs12568757	-	0.922
<i>C8A</i>	rs635833	-	0.888
<i>C6</i>	rs3805716	-	0.874
<i>NBN</i>	rs1805793	-	0.858
<i>LEF1</i>	rs11097978	-	0.827
<i>NOD2</i>	rs1981760	-	0.819
<i>DLG1</i>	rs768858	-	0.811
<i>C4BPA</i>	rs10746451	-	0.758
<i>TNFRSF11A</i>	rs3744929	-	0.725
<i>CD55</i>	rs2940252	-	0.723
<i>C2</i>	rs9267673	-	0.717
<i>C1RL</i>	rs744141	-	0.691
<i>AICDA</i>	rs4883169	-	0.683
<i>XRCC4</i>	rs6894425	-	0.677
<i>HLA-DRB1</i>	rs615672	-	0.63
<i>CFI</i>	rs4698788	-	0.621
<i>MASP2</i>	rs7556039	-	0.618
<i>TGFB1</i>	rs2241716	-	0.616
<i>FCER1G</i>	rs4489574	-	0.609
<i>SWAP70</i>	rs10770049	-	0.593
<i>UNC13D</i>	rs8067076	-	0.592
<i>C1S</i>	rs7306673	-	0.568
<i>CD74</i>	rs2569094	-	0.565

<i>LY9</i>	rs4656932	-	0.539
<i>BCL3</i>	rs8100239	-	0.529
<i>INPP5D</i>	rs3935584	-	0.526
<i>BCL10</i>	rs11161585	-	0.502
<i>CRTAM</i>	rs7126620	-	0.419
<i>MSH6</i>	rs17036815	-	0.398
<i>HLA-DQB1</i>	rs35120848	-	0.344
<i>C1QA</i>	rs158762	-	0.337
<i>TLR6</i>	rs3775073	-	0.334
<i>CD8A</i>	rs1515950	-	0.307
<i>C3AR1</i>	rs10846450	-	0.28
<i>SLC11A1</i>	rs13062	-	0.267
<i>ADAM17</i>	rs10929587	-	0.264
<i>MYD88</i>	rs7744	-	0.232
<i>SLA2</i>	rs221308	-	0.224
<i>HLA-DMA</i>	rs1050391	-	0.221
<i>ZP3</i>	rs1019096	-	0.207
<i>NFKB2</i>	rs11574851	-	0.194
<i>C1QB</i>	rs629409	-	0.181
<i>C4BPB</i>	rs8942	-	0.137
<i>STAT6</i>	rs12368672	-	0.129
<i>CTSL1</i>	rs2274611	-	0.059

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\*Functional class, SNPs that may alter protein, gene expression or the role of protein in context of pathway

\*\* $-\log_{10}(P)$  for SNP in discovery phase of this GWAS

**Table S9.** Genes mapped with variant in leukocyte mediated immunity.

<b>Gene Name</b>	<b>Variant</b>	<b>Functional Class</b>	<b>-log<sub>10</sub>( P-value)</b>
<i>CRP</i>	rs7553007	-	15.134
<i>IL6</i>	rs2961312	-	3.197
<i>EXO1</i>	rs1418761	-	3.079
<i>TLR4</i>	rs2244872	-	2.409
<i>C9</i>	rs2738238	-	2.407
<i>CTSC</i>	rs217090	-	2.363
<i>CLEC2A</i>	rs7957464	-	2.361
<i>CPLX2</i>	rs2443541	-	2.313
<i>CD46</i>	rs7144	-	2.121
<i>PRKCD</i>	rs13084863	-	2
<i>IL6R</i>	rs4537545	-	1.952
<i>C8B</i>	rs599857	-	1.803
<i>CR1</i>	rs677066	-	1.797
<i>MSH2</i>	rs6708696	-	1.744
<i>PIK3CD</i>	rs4240896	-	1.734
<i>PIK3CG</i>	rs7804699	-	1.718
<i>CADM1</i>	rs693246	-	1.692
<i>YWHAZ</i>	rs1470764	-	1.688
<i>C5</i>	rs2159777	-	1.648
<i>RAB27A</i>	rs9920114	-	1.608
<i>LIG4</i>	rs16971751	-	1.53
<i>C7</i>	rs2455307	-	1.411
<i>MYO1F</i>	rs12462590	-	1.41
<i>CR2</i>	rs7527218	-	1.408
<i>HSPD1</i>	rs13386066	-	1.407
<i>MBL2</i>	rs12262251	-	1.401
<i>ANXA3</i>	rs6855458	-	1.376
<i>POU2F2</i>	rs11883412	-	1.355
<i>GCNT3</i>	rs6494120	-	1.351
<i>LYST</i>	rs12038267	-	1.332
<i>SERPING1</i>	rs2729358	-	1.326
<i>CLU</i>	rs1316801	-	1.305
<i>C3</i>	rs11569538	-	1.303

<i>MLL5</i>	rs10274607	-	1.254
<i>MLH1</i>	rs1540354	-	1.232
<i>EXOSC3</i>	rs10814621	-	1.156
<i>DBH</i>	rs3025425	-	1.137
<i>CTSH</i>	rs12438191	-	1.126
<i>FAS</i>	rs17378702	-	1.107
<i>TUBB</i>	rs8233	-	1.094
<i>SERPINB9</i>	rs318486	-	1.077
<i>TNFSF4</i>	rs16845607	-	1.03
<i>CTSG</i>	rs17257069	-	0.994
<i>IL4</i>	rs2243283	-	0.962
<i>C8A</i>	rs635833	-	0.888
<i>ADORA3</i>	rs2798564	-	0.874
<i>C6</i>	rs3805716	-	0.874
<i>NBN</i>	rs1805793	-	0.858
<i>NOD2</i>	rs1981760	-	0.819
<i>DLG1</i>	rs768858	-	0.811
<i>STXBP3</i>	rs11102337	-	0.773
<i>C4BPA</i>	rs10746451	-	0.758
<i>CD55</i>	rs2940252	-	0.723
<i>C2</i>	rs9267673	-	0.717
<i>PLA2G1B</i>	rs2522136	-	0.709
<i>C1RL</i>	rs744141	-	0.691
<i>AICDA</i>	rs4883169	-	0.683
<i>XRCC4</i>	rs6894425	-	0.677
<i>SLAMF7</i>	rs17378627	-	0.667
<i>HLA-DRB1</i>	rs615672	-	0.63
<i>CFI</i>	rs4698788	-	0.621
<i>MASP2</i>	rs7556039	-	0.618
<i>FCER1G</i>	rs4489574	-	0.609
<i>SWAP70</i>	rs10770049	-	0.593
<i>UNC13D</i>	rs8067076	-	0.592
<i>C1S</i>	rs7306673	-	0.568
<i>CD74</i>	rs2569094	-	0.565
<i>LY9</i>	rs4656932	-	0.539
<i>BCL3</i>	rs8100239	-	0.529
<i>INPP5D</i>	rs3935584	-	0.526

<i>BCL10</i>	rs11161585	-	0.502
<i>CRTAM</i>	rs7126620	-	0.419
<i>MSH6</i>	rs17036815	-	0.398
<i>LYN</i>	rs16922296	-	0.385
<i>ACE</i>	rs4351	-	0.358
<i>HLA-DQB1</i>	rs35120848	-	0.344
<i>CIQA</i>	rs158762	-	0.337
<i>CD8A</i>	rs1515950	-	0.307
<i>LAT</i>	rs9924619	-	0.305
<i>CEBPG</i>	rs17530508	-	0.299
<i>SLC11A1</i>	rs13062	-	0.267
<i>ADAM17</i>	rs10929587	-	0.264
<i>MYD88</i>	rs7744	-	0.232
<i>SLA2</i>	rs221308	-	0.224
<i>HLA-DMA</i>	rs1050391	-	0.221
<i>ZP3</i>	rs1019096	-	0.207
<i>CIQB</i>	rs629409	-	0.181
<i>C4BPB</i>	rs8942	-	0.137

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**Table S10.** Genes mapped with variant in photoreceptor outer segment.

<b>Gene Name</b>	<b>Variant</b>	<b>Functional Class</b>	<b><math>-\log_{10}(P\text{-value})</math></b>
<i>HNF1A</i>	rs2259816	-	7.149
<i>RAPGEF4</i>	rs1530591	-	2.877
<i>MAK</i>	rs478791	-	2.799
<i>RP1</i>	rs9650182	-	2.289
<i>MYRIP</i>	rs17759069	-	2.145
<i>PROM1</i>	rs12152560	-	2.032
<i>GNAT3</i>	rs10954212	-	1.987
<i>PCDH15</i>	rs11003592	-	1.972
<i>RP1L1</i>	rs4427133	-	1.627
<i>RAB27A</i>	rs9920114	-	1.608
<i>PTPRK</i>	rs41514350	-	1.501
<i>CNGA1</i>	rs7694104	-	1.454
<i>GNB1</i>	rs2272908	-	1.401
<i>TULP1</i>	rs3777746	-	1.341
<i>CNGB3</i>	rs11988618	-	1.229
<i>MYO5A</i>	rs1693523	-	1.214
<i>RHO</i>	rs2855552	-	0.958
<i>PDC</i>	rs11803944	-	0.804
<i>CNGA3</i>	rs4851131	-	0.791
<i>CDHR1</i>	rs10509491	-	0.765
<i>INHA</i>	rs753974	-	0.558
<i>PTGS1</i>	rs1234909	-	0.454
<i>MYO7A</i>	rs3781695	-	0.452
<i>C2orf71</i>	rs17744052	-	0.432
<i>MERTK</i>	rs13016143	-	0.348
<i>IQCB1</i>	rs4311252	-	0.184
<i>PPEF2</i>	rs13434876	-	0.122



**Table S11.** Genes mapped with variant in cell surface binding.

<b>Gene Name</b>	<b>Variant</b>	<b>Functional class</b>	<b><math>-\log_{10}(P\text{-value})</math></b>
<i>CRP</i>	rs7553007	-	15.134
<i>PCSK6</i>	rs1947942	-	2.162
<i>CD36</i>	rs17260734	-	2.045
<i>PRB3</i>	rs1834856	-	2.022
<i>THBS1</i>	rs2618162	-	1.644
<i>SFTPD</i>	rs2181204	-	1.551
<i>STAB2</i>	rs1866297	-	1.527
<i>AIMP1</i>	rs16999761	-	1.524
<i>SELP</i>	rs3917843	-	1.465
<i>SELPLG</i>	rs11114011	-	1.441
<i>HSPD1</i>	rs13386066	-	1.407
<i>MBL2</i>	rs12262251	-	1.401
<i>VEGFA</i>	rs4714696	-	1.386
<i>PDGFC</i>	rs2343116	-	1.376
<i>BPI</i>	rs7273966	-	1.322
<i>ANXA5</i>	rs4833753	-	1.32
<i>SPN</i>	rs1364182	-	1.3
<i>F3</i>	rs10782985	-	1.287
<i>APOH</i>	rs2873966	-	1.269
<i>AGGF1</i>	rs3762982	-	1.194
<i>APOA4</i>	rs1263173	-	1.038
<i>TLR2</i>	rs11938228	-	0.908
<i>ATP5A1</i>	rs9955008	-	0.881
<i>LBP</i>	rs2232596	-	0.753
<i>PLA2G1B</i>	rs2522136	-	0.709
<i>HBEGF</i>	rs2237077	-	0.631
<i>CD1D</i>	rs400214	-	0.631
<i>CD48</i>	rs352683	-	0.619
<i>TGFB1</i>	rs2241716	-	0.616
<i>CD2</i>	rs797999	-	0.603
<i>ADIPOQ</i>	rs6773957	-	0.518
<i>DAG1</i>	rs1050088	-	0.338

<i>PLG</i>	rs2144723	-	0.285
<i>PGLYRP1</i>	rs1861790	-	0.256
<i>PDGFB</i>	rs17000920	-	0.161
<i>FGB</i>	rs2059503	-	0.15
<i>HRG</i>	rs16861013	-	0.148
<i>SPACA3</i>	rs28906	-	0.141
<i>ALB</i>	rs16849267	-	0.13
<i>LILRB2</i>	rs4022330	-	0.121
<i>SERPINF2</i>	rs4790285	-	0.048

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**Table S12.** Genes mapped with variant in cholesterol binding

<b>Gene Name</b>	<b>Variant</b>	<b>Functional</b>	<b>Class</b>	<b><math>-\log_{10}(P\text{-value})</math></b>
<i>CRP</i>	rs7553007	-		15.134
<i>ABCA1</i>	rs4260948	-		2.749
<i>SOAT1</i>	rs425858	-		2.07
<i>PTCH1</i>	rs7862599	-		1.801
<i>ABCG1</i>	rs2839482	-		1.776
<i>PMP2</i>	rs6995156	-		1.41
<i>APOA2</i>	rs5085	-		1.139
<i>NR1H3</i>	rs7118396	-		0.74
<i>CYP11A1</i>	rs7174179	-		0.612
<i>CAVI</i>	rs1049334	-		0.557
<i>NPC2</i>	rs2358785	-		0.482
<i>APOC3</i>	rs2071523	-		0.389
<i>SOAT2</i>	rs12809590	-		0.323
<i>TSPO2</i>	rs9369260	-		0.315
<i>STARD3</i>	rs11869286	-		0.273
<i>CETP</i>	rs1800775	-		0.194
<i>STAR</i>	rs16887217	-		0.109
<i>IHH</i>	rs10208728	-		0.031

**Table S13.** Genes mapped with variant in bacterial cell surface binding

<b>Gene Name</b>	<b>Variant</b>	<b>Functional Class</b>	<b>P-value</b>
<i>CRP</i>	rs7553007	-	15.134
<i>CD36</i>	rs17260734	-	2.045
<i>PRB3</i>	rs1834856	-	2.022
<i>SFTPD</i>	rs2181204	-	1.551
<i>STAB2</i>	rs1866297	-	1.527
<i>SELPLG</i>	rs11114011	-	1.441
<i>MBL2</i>	rs12262251	-	1.401
<i>BPI</i>	rs7273966	-	1.322
<i>SPN</i>	rs1364182	-	1.3
<i>TLR2</i>	rs11938228	-	0.908
<i>LBP</i>	rs2232596	-	0.753
<i>DAG1</i>	rs1050088	-	0.338
<i>PGLYRP1</i>	rs1861790	-	0.256
<i>SPACA3</i>	rs28906	-	0.141

**Table 14.** Pathway analysis results of GSA-SNP software

set name	gene count	set size	z-score	p-value	corrected p-value	FDR
low-density lipoprotein particle binding	12	13	10.65696	0	0	<0.001
lipoprotein particle binding	20	21	9.056942	0	0	<0.001
protein-lipid complex binding	20	21	9.056942	0	0	<0.001
opsonization	7	7	7.509131	3.00E-14	4.84E-11	<0.001
negative regulation of lipid storage	14	14	7.456615	4.42E-14	5.71E-11	<0.001
bacterial cell surface binding	16	17	7.360872	9.16E-14	9.86E-11	<0.001
quaternary ammonium group binding	15	15	7.349194	1.00E-13	9.23E-11	<0.001
negative regulation of macrophage derived foam cell differentiation	13	13	7.251112	2.06E-13	1.66E-10	<0.001
regulation of lipid storage	30	31	6.647502	1.49E-11	1.07E-08	<0.001
humoral immune response mediated by circulating immunoglobulin	31	165	6.461015	5.20E-11	3.36E-08	<0.001
response to lead ion	13	14	6.119311	4.70E-10	2.76E-07	<0.001
complement activation, classical pathway	26	160	6.087637	5.73E-10	3.08E-07	<0.001
regulation of macrophage derived foam cell differentiation	27	27	6.064354	6.62E-10	3.29E-07	<0.001
humoral immune response	72	220	5.744094	4.62E-09	2.13E-06	<0.001
cholesterol binding	20	23	5.468741	2.27E-08	9.76E-06	<0.001
alcohol binding	39	42	5.385632	3.61E-08	1.46E-05	<0.001
sterol binding	27	30	5.211166	9.38E-08	3.57E-05	<0.001
presynaptic membrane	43	47	5.137044	1.40E-07	5.01E-05	<0.001
complement activation	33	174	4.856848	5.96E-07	2.03E-04	<0.001

interferon-gamma-mediated signaling pathway	58	69	4.723106	1.16E-06	3.75E-04	<0.001
regulation of bone resorption	24	26	4.606352	2.05E-06	6.30E-04	<0.001
regulation of inclusion body assembly	5	5	4.585766	2.26E-06	6.64E-04	<0.001
neuron cell-cell adhesion	12	12	4.54256	2.78E-06	7.80E-04	<0.001
regulation of axonogenesis	89	97	4.521542	3.07E-06	8.26E-04	<0.001
cell adhesion molecule binding	50	52	4.519113	3.10E-06	8.02E-04	<0.001
bone resorption	18	18	4.490447	3.55E-06	8.83E-04	<0.001
cellular response to interferon-gamma	73	84	4.472573	3.86E-06	9.25E-04	<0.001
immunoglobulin mediated immune response	57	194	4.468101	3.95E-06	9.10E-04	<0.001
bone remodeling	29	31	4.441771	4.46E-06	9.94E-04	<0.001
adherens junction organization	41	42	4.421697	4.90E-06	0.001054	<0.001
lymphocyte mediated immunity	78	216	4.38258	5.86E-06	0.001222	<0.001
B cell mediated immunity	59	196	4.368199	6.26E-06	0.001264	<0.001
ion gated channel activity	21	21	4.362452	6.43E-06	0.001259	<0.001
sarcoplasm	46	53	4.361622	6.46E-06	0.001226	<0.001
neuron recognition	26	28	4.348114	6.87E-06	0.001267	<0.001
Ras guanyl-nucleotide exchange factor activity	88	93	4.341321	7.08E-06	0.001271	<0.001
oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	6	7	4.339601	7.14E-06	0.001246	<0.001
sensory perception of pain	47	50	4.286067	9.09E-06	0.001546	<0.001
regulation of gene expression by genetic imprinting	10	14	4.285719	9.11E-06	0.001509	<0.001
renal absorption	10	12	4.276583	9.49E-06	0.001533	<0.001
regulation of bone remodeling	27	29	4.244055	1.10E-05	0.001729	<0.001

renal system process	61	65	4.172091	1.51E-05	0.002321	<0.001
homophilic cell adhesion	89	142	4.133757	1.78E-05	0.002681	<0.001
regulation of ion transmembrane transporter activity	87	92	4.129602	1.82E-05	0.002668	<0.001
Rac GTPase activator activity	13	14	4.070027	2.35E-05	0.003374	<0.001
positive regulation of developmental growth	37	40	4.052437	2.53E-05	0.003559	<0.001
cell surface binding	49	54	4.022512	2.88E-05	0.003957	<0.001
regulation of ion transmembrane transport	99	104	4.004745	3.10E-05	0.004178	<0.001
regulation of developmental growth	88	95	3.995403	3.23E-05	0.004257	<0.001
genetic imprinting	14	18	3.977398	3.48E-05	0.004501	<0.001
protein activation cascade	51	194	3.973328	3.54E-05	0.004489	<0.001
sarcoplasmic reticulum	43	49	3.962999	3.70E-05	0.004597	<0.001
positive regulation of vascular endothelial growth factor receptor signaling pathway	15	16	3.951533	3.88E-05	0.004732	<0.001
M band	12	12	3.931123	4.23E-05	0.005057	<0.001
regulation of transmembrane transporter activity	91	97	3.913258	4.55E-05	0.005348	<0.001
activation of transmembrane receptor protein tyrosine kinase activity	9	10	3.902895	4.75E-05	0.005482	<0.001
regulation of calcium-mediated signaling	28	31	3.890484	5.00E-05	0.005669	<0.001
reverse cholesterol transport	15	17	3.887109	5.07E-05	0.005649	<0.001
positive regulation of calcium-mediated signaling	21	23	3.851229	5.88E-05	0.006434	<0.001
sprouting angiogenesis	31	33	3.843308	6.07E-05	0.006535	<0.001
regulation of protein tyrosine kinase activity	40	46	3.823879	6.57E-05	0.006956	<0.001

positive regulation of transcription initiation from RNA polymerase II promoter	5	6	3.821247	6.64E-05	0.006917	<0.001
sialyltransferase activity	20	21	3.815319	6.80E-05	0.006973	<0.001
response to interferon-gamma	88	99	3.815148	6.81E-05	0.006869	<0.001
regulation of kidney size	5	5	3.785822	7.66E-05	0.007613	<0.001
steroid binding	61	73	3.750922	8.81E-05	0.008622	<0.001
positive regulation of bone resorption	10	12	3.713883	1.02E-04	0.00984	<0.001
positive regulation of bone remodeling	10	12	3.713883	1.02E-04	0.009695	<0.001
collagen fibril organization	36	36	3.704467	1.06E-04	0.009916	<0.001
glomerulus development	42	44	3.624851	1.45E-04	0.013341	<0.001
adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	91	228	3.615305	1.50E-04	0.013648	<0.001
calcium-activated potassium channel activity	17	17	3.611891	1.52E-04	0.013637	<0.001
phagocytosis	62	68	3.609953	1.53E-04	0.013551	<0.001
calcium channel activity	88	92	3.589673	1.66E-04	0.014452	<0.001
regulation of calcium ion transport via voltage-gated calcium channel activity	46	47	3.578154	1.73E-04	0.014902	<0.001
regulation of tissue remodeling	37	40	3.553349	1.90E-04	0.016165	<0.001
tissue homeostasis	78	85	3.532565	2.06E-04	0.017264	<0.001
embryonic limb morphogenesis	89	104	3.529207	2.08E-04	0.01726	<0.001
embryonic appendage morphogenesis	89	104	3.529207	2.08E-04	0.017042	<0.001
regulation of homotypic cell-cell adhesion	13	14	3.515712	2.19E-04	0.017707	<0.001
photoreceptor outer segment	32	33	3.507113	2.26E-04	0.018064	<0.001



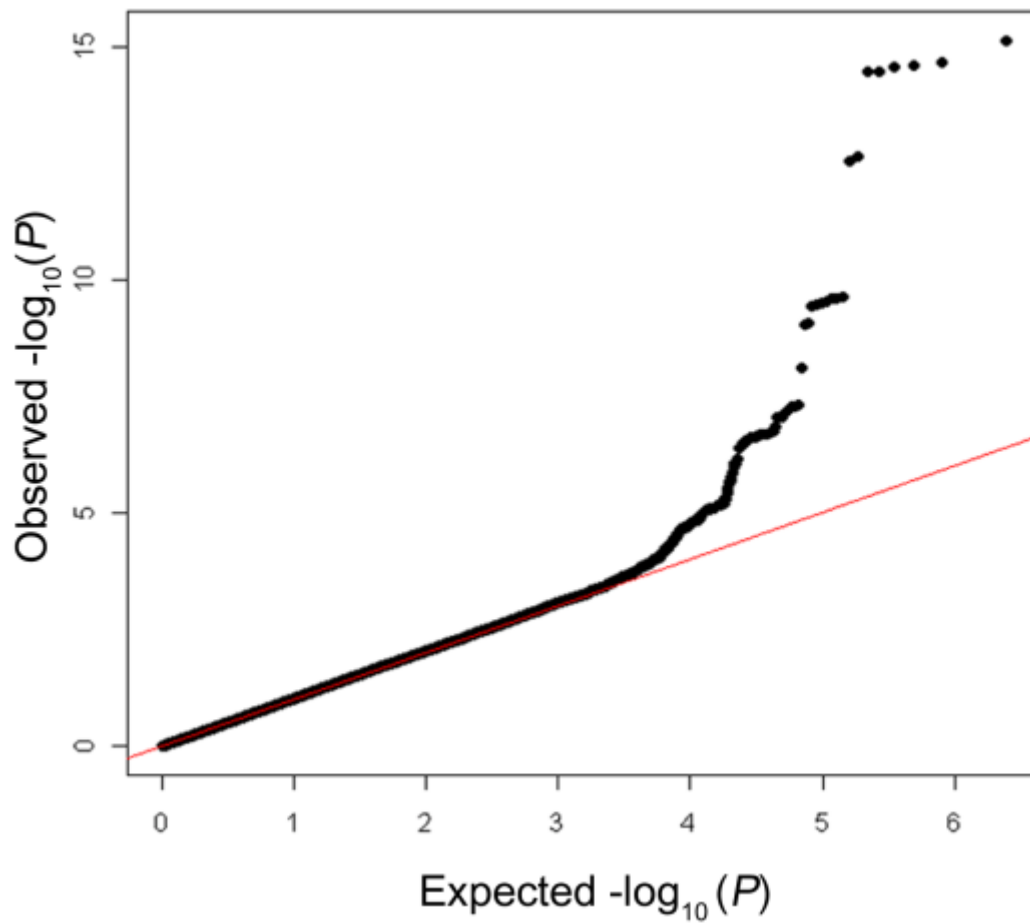
MHC protein complex	33	46	3.496108	2.36E-04	0.018596	<0.001
regulation of platelet activation	21	22	3.482246	2.49E-04	0.01935	<0.001
acute inflammatory response	54	61	3.478179	2.52E-04	0.019412	<0.001
response to caffeine	12	12	3.47671	2.54E-04	0.019289	<0.001
cyclic-nucleotide phosphodiesterase activity	24	27	3.4661	2.64E-04	0.019833	<0.001
transmembrane receptor protein kinase activity	76	83	3.456761	2.73E-04	0.020297	<0.001
positive regulation of transporter activity	28	30	3.451965	2.78E-04	0.020427	<0.001
sensory perception of temperature stimulus	7	8	3.444503	2.86E-04	0.020763	<0.001
3,5-cyclic-nucleotide phosphodiesterase activity	23	26	3.443682	2.87E-04	0.020595	<0.001
cytosolic calcium ion transport	35	38	3.443463	2.87E-04	0.020385	<0.001
epithelial cell proliferation	45	50	3.433255	2.98E-04	0.020938	<0.001
Rho guanyl-nucleotide exchange factor activity	71	75	3.431285	3.00E-04	0.020864	<0.001
voltage-gated sodium channel complex	13	14	3.407591	3.28E-04	0.02252	<0.001
sodium channel complex	13	14	3.407591	3.28E-04	0.022283	<0.001
positive regulation of cell-substrate adhesion	48	51	3.386791	3.54E-04	0.023793	<0.001
sterol transport	38	41	3.376995	3.66E-04	0.024402	<0.001
cholesterol transport	38	41	3.376995	3.66E-04	0.024153	<0.001
acute-phase response	37	42	3.360967	3.88E-04	0.025341	<0.001
regulation of lipase activity	97	107	3.358244	3.92E-04	0.025336	<0.001
excretion	48	50	3.329992	4.34E-04	0.027774	<0.001
positive regulation of ERK1 and ERK2 cascade	77	83	3.328859	4.36E-04	0.027614	<0.001

regulation of synapse structure and activity	47	49	3.323742	4.44E-04	0.027853	<0.001
protein phosphatase type 2A complex	16	19	3.313376	4.61E-04	0.028628	<0.001
cAMP metabolic process	31	32	3.304465	4.76E-04	0.029272	<0.001
regulation of dendrite development	55	57	3.301381	4.81E-04	0.029317	<0.001
heparan sulfate proteoglycan metabolic process	18	21	3.299158	4.85E-04	0.029274	<0.001
phosphoric diester hydrolase activity	91	98	3.297083	4.88E-04	0.029218	<0.001
calcium ion transport into cytosol	34	37	3.290452	5.00E-04	0.029641	<0.001
positive regulation of ion transmembrane transporter activity	22	23	3.287474	5.05E-04	0.029684	<0.001
positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	7	7	3.281417	5.16E-04	0.030056	<0.001
negative regulation of phosphorylation	81	85	3.279335	5.20E-04	0.030008	<0.001
voltage-gated sodium channel activity	14	15	3.26874	5.40E-04	0.030879	<0.001
MHC class II receptor activity	8	11	3.25891	5.59E-04	0.031688	<0.001
integrin-mediated signaling pathway	70	72	3.256359	5.64E-04	0.031696	<0.001
positive regulation of cell growth	78	87	3.247585	5.82E-04	0.032408	<0.001

**Table S15.** Combined *P* value estimation for ICSNPathway and GSA-SNP by Fisher Stastatics

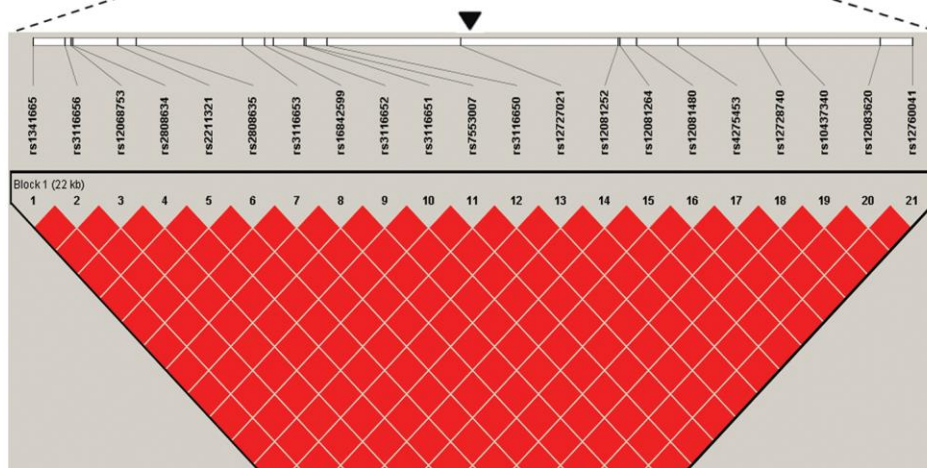
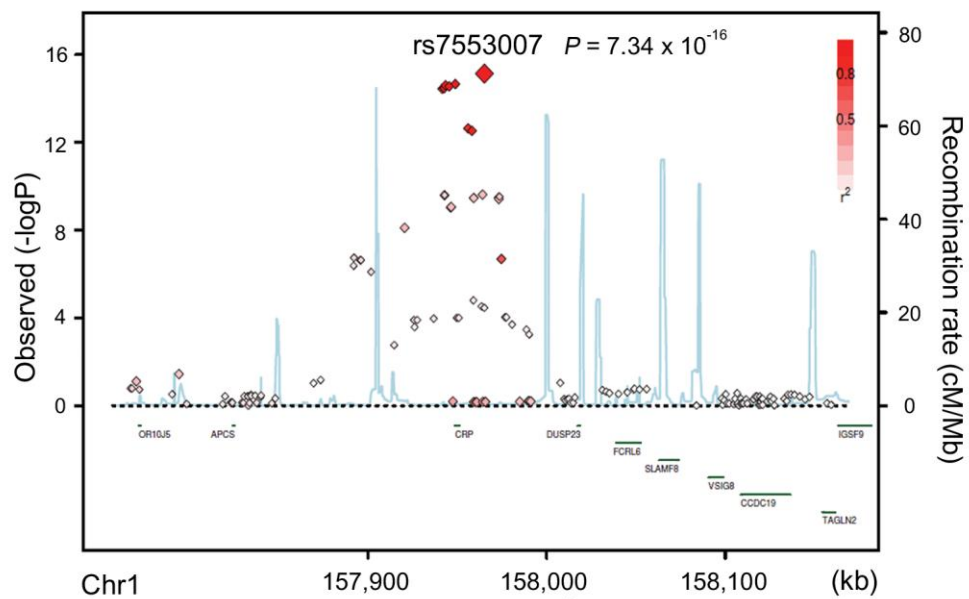
Candidate pathway	Description	ICSNPathway		GSA-SNP		Combined P value by Fisher's method
		Nominal <i>P</i>	FDR	<i>P</i>	FDR	
GO:0001750	Photoreceptor outer segment	< 0.001	< 0.001	2.26E-04	< 0.001	3.68E-06
GO:0043498	Cell surface binding	< 0.001	< 0.001	2.88E-05	< 0.001	5.3E-07
GO:0015485	Cholesterol binding	< 0.001	< 0.001	2.27E-08	< 0.001	< 0.001
GO:0051635	Bacterial cell surface binding	< 0.001	< 0.001	9.16E-14	< 0.001	< 0.001

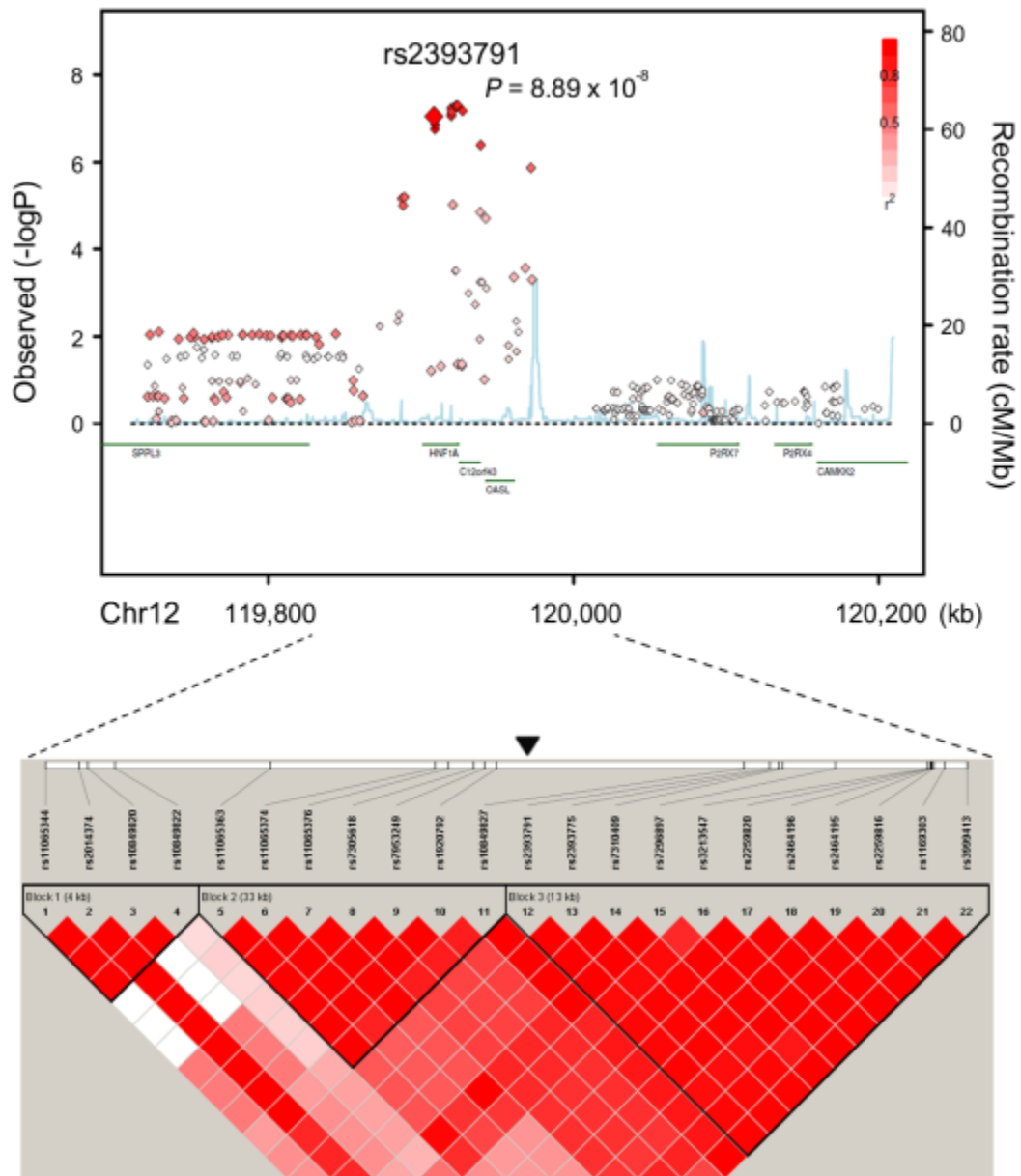
## Supplementary Figures



**Figure S1.** A Quantile–Quantile plot of  $P$ -values in the GWAS for serum CRP levels (stage 1). The horizontal axis indicates the expected  $-\log_{10}(P)$ -values. The vertical axis indicates the observed  $-\log_{10}(P)$ -values). The red line represents  $y=x$ .

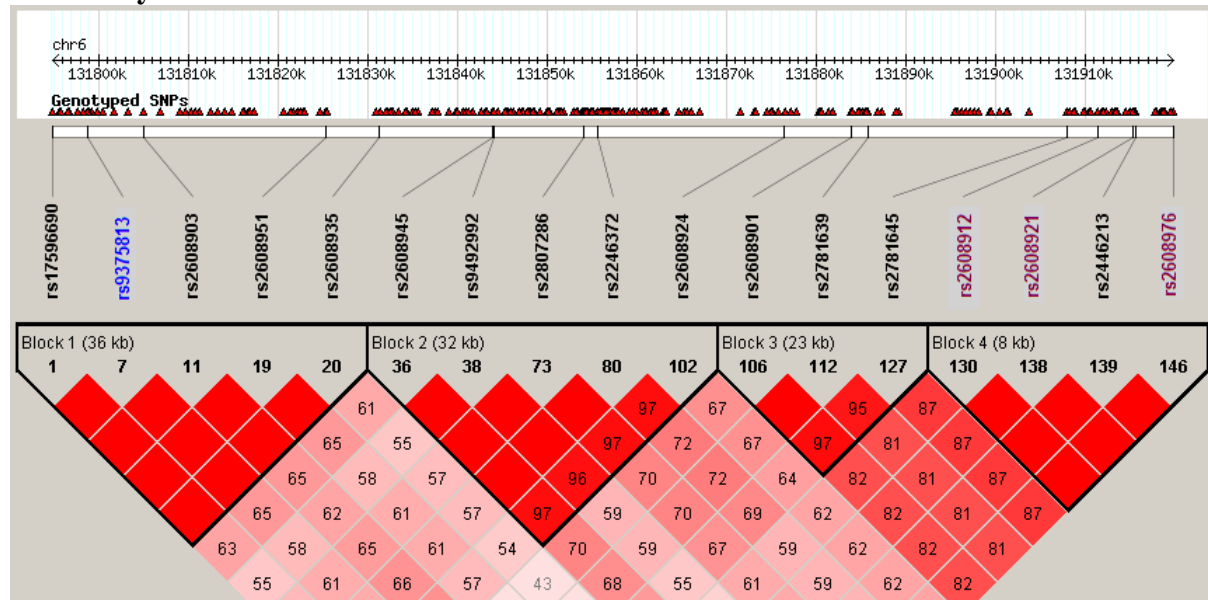
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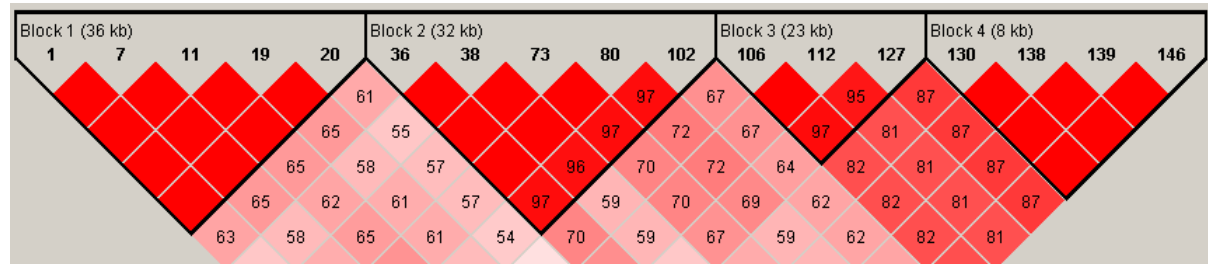
**B**

**Figure S2.** (A) Stage 1 data showing a regional association (upper panel) and linkage disequilibrium (LD; lower panel) plots of the *CRP* locus around rs7553007. Arrow head represents rs7553007. (B) Stage 1 data showing a regional association (upper panel) and linkage disequilibrium (LD; lower panel) plots of the *HNF1A* locus around rs2393791. Arrow head represents rs2393791.

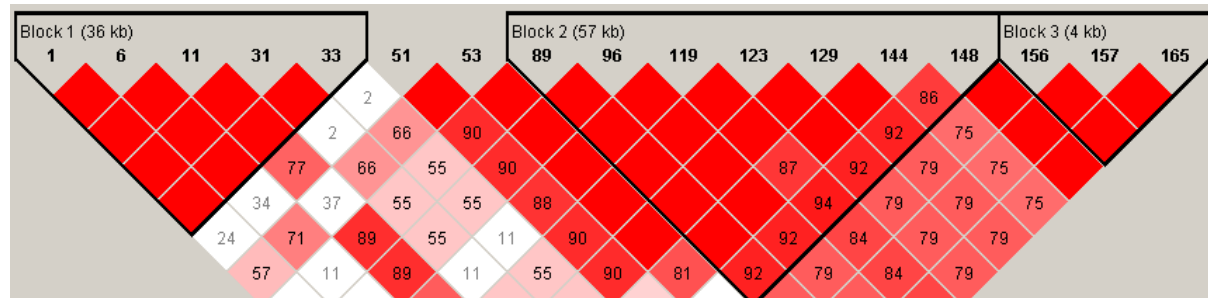
## This study



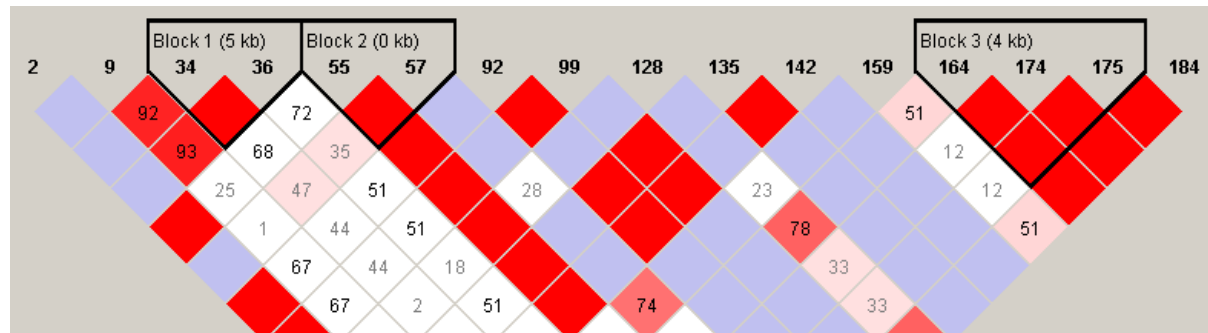
## CHB+JPT



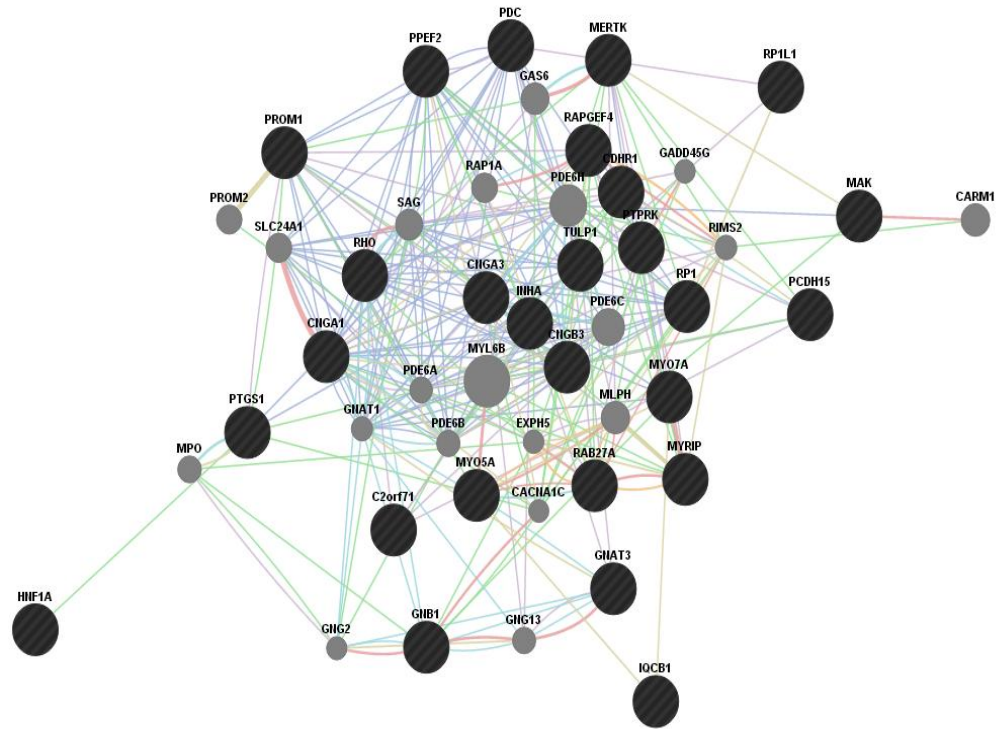
## CEU



## YRI

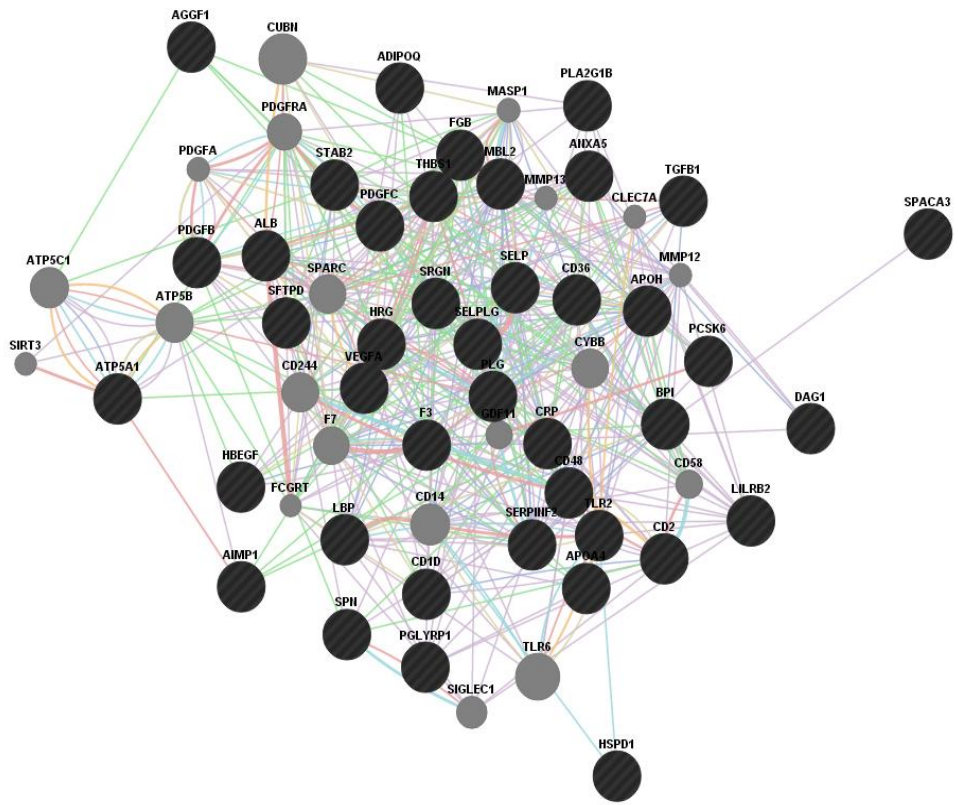


**Figure S3.** Pairwise linkage disequilibrium (LD) between the selected SNPs in *ARG1* locus around rs9375813. LD plots for Korea population were drawn using the genotype data from the present study, whereas LD plots for Japanese, Chinese, Europeans and Africans were made from genotype data from HapMap Stage 2. Blue ID indicates the most significant SNP. Purple ID indicates the SNPs whose rank got elevated after re-prioritization.

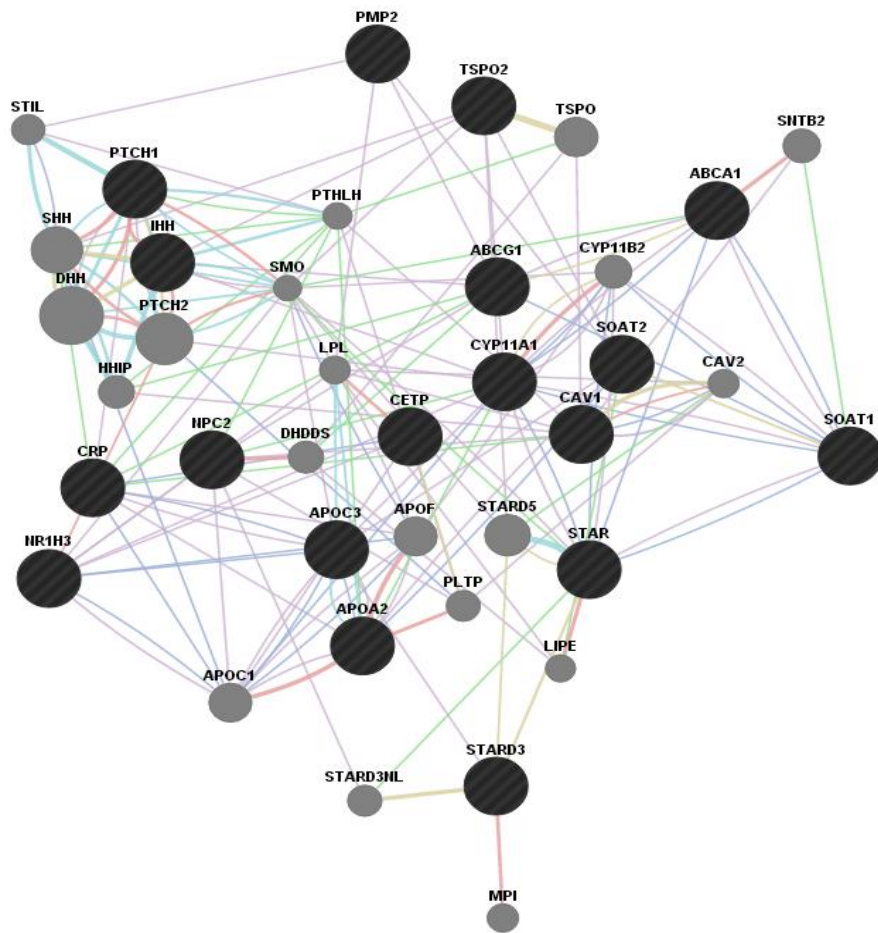


**Figure S4.** Gene network of photoreceptor outer segment pathway by GeneMANIA analysis. Using the genes identified from pathway analysis, GeneMANIA network analysis was performed. Query genes are depicted as black nodes and discovered genes are depicted as gray nodes. Edges show different interactions among genes; purple indicates for co-expression; light-blue indicates for pathway; dark yellow indicates for shared protein domains; red indicates for physical interactions; dark blue indicates for co-localization; green indicates for genetic interactions. Node sizes are determined according to their weight in the network.

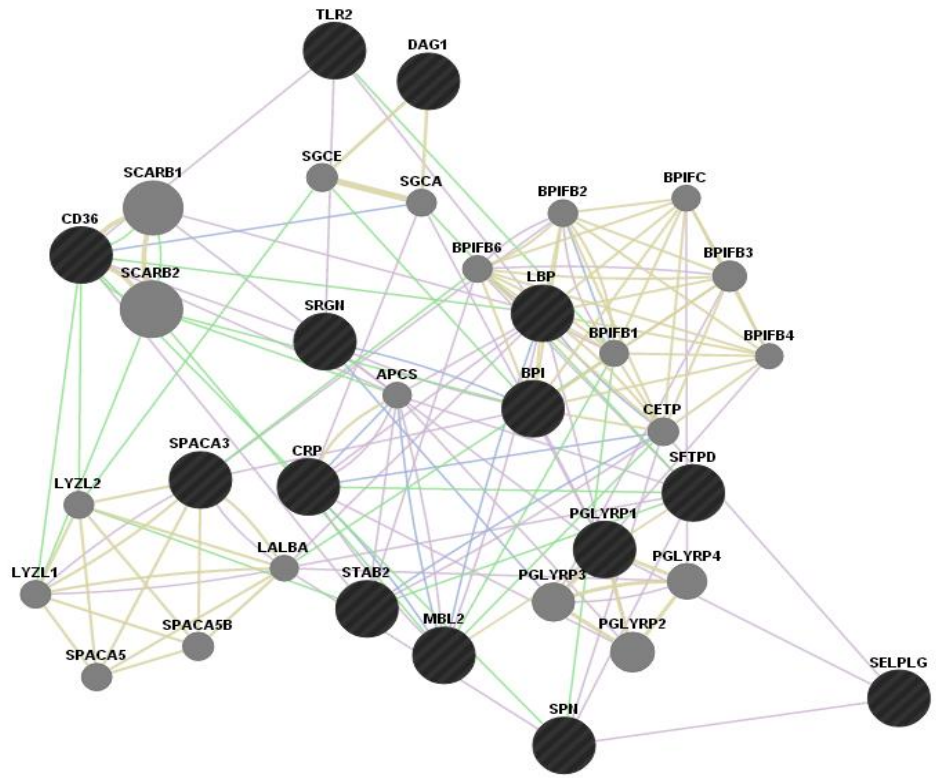




**Figure S5.** Gene network of cell surface binding pathway by GeneMANIA.



**Figure S6.** Gene network of cholesterol binding pathway by GeneMANIA.



**Figure S7.** Gene network of bacterial cell surface binding pathway by GeneMANIA.