Supplementary Information

Genome-wide association study in a Korean population identifies six novel susceptibility loci for rheumatoid arthritis

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Supplementary Table 1 | **Genes prioritized by FUMA gene mapping**

Gene	Position mapping		eQTL mapping		Chromatin interaction mapping	
	No. of SNPs	minGwas P	No. of SNP	Tissue	Mapping	Tissue
PADI3	14	1.20E-07	0	NA	No	NA
MIR3972	11	1.12E-06	0	NA	No	NA
PADI4	180	4.02E-16	187	T CD4 naive:T CD4 naive activated:T CD8 naive:Monocyte classical:Monocyte non classical:T CD4 naive TREG:Whole Blood:Lung:Spleen	Yes	Spleen
AC004824.2	120	4.02E-16	0	NA	No	NA
KCNJ10	0	1.30E-09	0	NA	Yes	GM12878
IGSF8	0	1.30E-09	0	NA	Yes	GM12878
PEA15	0	1.30E-09	0	NA	Yes	GM12878
AL121987.1	0	1.30E-09	0	NA	Yes	GM12878
RP11-574F21.2	0	1.30E-09	0	NA	Yes	GM12878
VANGL2	1	7.08E-09	0	NA	No	NA
SLAMF6	5	1.30E-09	0	NA	Yes	Spleen:GM12878
AL138930.1	1	6.65E-06	0	NA	No	NA
CD84	0	1.30E-09	0	NA	Yes	Spleen:GM12878
SLAMF1	0	1.30E-09	0	NA	Yes	GM12878
CD48	0	1.30E-09	0	NA	Yes	GM12878
SLAMF7	0	1.30E-09	0	NA	Yes	GM12878
LY9	0	1.30E-09	0	NA	Yes	GM12878
ITLN1	0	1.30E-09	0	NA	Yes	GM12878
RP11-544M22.13	0	1.30E-09	0	NA	Yes	GM12878
TSTD1	0	1.30E-09	0	NA	Yes	GM12878
USF1	0	1.30E-09	0	NA	Yes	GM12878
ARHGAP30	0	1.30E-09	0	NA	Yes	GM12878
STAT1	0	2.54E-12	0	NA	Yes	GM12878
AC067945.2	0	2.54E-12	0	NA	Yes	GM12878
STAT4	25	1.66E-13	0	NA	Yes	GM12878
CXCL13	1	1.86E-09	0	NA	No	NA
RP5-1120P11.1	0	2.90E-10	0	NA	Yes	Spleen:GM12878
RP5-1120P11.3	0	2.90E-10	0	NA	Yes	Spleen:GM12878
HSP90AB1	2	9.05E-10	0	NA	No	NA
SLC35B2	9	6.03E-10	0	NA	No	NA
MIR4647	2	9.05E-10	0	NA	No	NA
NFKBIE	14	2.90E-10	0	NA	No	NA
TMEM151B	37	2.90E-10	2	T CD4 naive TREG	No	NA
RP11-444E17.6	37	2.90E-10	0	NA	No	NA
TCTE1	22	2.90E-10	2	Small Intestine Terminal Ileum	No	NA
AARS2	19	1.67E-08	0	NA	Yes	Spleen
SPATS1	0	2.93E-08	0	NA	Yes	Spleen
IL20RA	0	3.26E-07	0	NA	Yes	GM12878
RP11-356I2.4	34	3.29E-10	0	NA	Yes	GM12878
TNFAIP3	21	3.29E-10	0	NA	Yes	GM12878
RPS6KA2	0	1.36E-13	364	T CD8 naive activated:Monocyte classical:NK:Whole Blood	No	NA
RP11-514O12.4	49	1.18E-11	0	NA	Yes	GM12878
RPS6KA2-AS1	0	2.59E-11	306	T CD4 naive activated:T CD8 naive	No	NA
RNASET2	55	1.36E-13	406	scRNA eQTLs/T CD4:scRNA eQTLs/PBMC:B cell naive:T CD4 naive:T CD4 naive activated:T CD8 naive:T CD8 naive activated:Monocyte classical:NK:T CD4 TFH:T CD4 TH1:T CD4 TH17:T CD4 TH1 17:T CD4 TH2:T CD4 memory TREG:T CD4 naive TREG:Cells EBV-transformed lymphocytes:Whole Blood:Lung:Small Intestine Terminal Ileum:Spleen	Yes	GM12878
RP1-167A14.2	152	1.18E-11	302	Cells EBV-transformed lymphocytes:Whole Blood	Yes	GM12878
MIR3939	58	1.18E-11	225	T CD4 TFH:T CD4 memory TREG	Yes	GM12878
FGFR1OP	187	1.36E-13	204	Whole Blood:Lung	Yes	GM12878
CCR6	45	1.36E-13	166	T CD4 TFH:T CD4 TH17:T CD4 TH1 17:Whole Blood:Spleen	Yes	GM12878
GPR31	0	2.03E-09	1	T CD4 naive	No	NA
EIF4H	1	6.32E-07	0	NA	Yes	GM12878

RFC2	1	NA	0	NA	No	NA
RNU6-1070P	1	NA	0	NA	No	NA
GTF2IRD1	15	1.26E-20	0	NA	No	NA
RNA5SP233	1	NA	0	NA	No	NA
AC004851.1	3	6.32E-07	0	NA	No	NA
RP5-1186P10.2	7	1.26E-20	0	NA	No	NA
GTF2I	1	2.45E-19	0	NA	No	NA
NCF1	2	1.67E-11	0	NA	No	NA
GTF2IRD2	1	2.24E-08	0	NA	No	NA
GTF2IRD2B	2	NA	0	NA	No	NA
ARID5B	4	2.39E-12	0	NA	Yes	Spleen:GM12878
RTKN2	0	2.39E-12	0	NA	Yes	GM12878
WEE1	0	1.28E-09	0	NA	Yes	Spleen:GM12878
snoU13	0	1.28E-09	0	NA	Yes	Spleen:GM12878
SWAP70	31	4.48E-10	9	Lung:Spleen	Yes	GM12878
RP11-540A21.2	14	4.48E-10	0	NA	No	NA
SBF2-AS1	31	4.48E-10	0	NA	No	NA
SBF2	21	1.51E-08	0	NA	No	NA
RP11-351I24.1	0	1.28E-09	0	NA	Yes	Spleen:GM12878
ADM	0	1.28E-09	0	NA	Yes	Spleen:GM12878
AMPD3	0	1.28E-09	0	NA	Yes	Spleen:GM12878
SH2B3	1	3.89E-09	0	NA	No	NA
ATXN2	1	3.78E-09	0	NA	No	NA
AC002395.1	1	3.78E-09	0	NA	No	NA
TMEM116	2	7.94E-08	0	NA	No	NA
ERP29	1	1.20E-07	0	NA	No	NA
NAA25	1	1.20E-07	0	NA	No	NA
MIR3657	1	1.20E-07	0	NA	No	NA
NFKBIA	9	5.28E-09	0	NA	No	NA
RP11-317N8.3	0	5.28E-09	2	T CD4 TH17	No	NA
CTD-2325P2.4	0	5.23E-06	0	NA	Yes	Lung:Spleen:GM12878
ZFP36L1	0	5.23E-06	0	NA	Yes	GM12878
LINC00638	0	3.76E-15	9	Cells EBV-transformed lymphocytes:Whole Blood:Lung:Spleen	No	NA
CTD-3051D23.1	0	8.80E-09	1	Whole Blood	No	NA
CEP170B	0	8.80E-09	1	Whole Blood	No	NA
CTD-3051D23.3	0	1.52E-12	0	NA	Yes	Spleen
PLD4	44	2.36E-16	49	Whole Blood:Spleen	Yes	Spleen
AHNAK2	68	2.36E-16	40	Lung	No	NA
C14orf79	0	2.36E-16	51	Lung	No	NA
GPR132	0	1.26E-10	1	Lung	No	NA
FAM98B	0	6.66E-10	0	NA	Yes	GM12878
RASGRP1	10	6.66E-10	8	B cell naive:Cells EBV-transformed lymphocytes:Spleen	Yes	GM12878
RP11-275I4.1	3	9.50E-10	0	NA	No	NA
LINC00158	9	6.36E-09	0	NA	No	NA
MIR155HG	0	9.88E-08	0	NA	Yes	GM12878
MRPL39	0	9.88E-08	0	NA	Yes	GM12878
JAM2	0	9.88E-08	0	NA	Yes	GM12878
ATP5J	0	9.88E-08	0	NA	Yes	GM12878
GABPA	0	9.88E-08	0	NA	Yes	GM12878
APP	0	9.88E-08	0	NA	Yes	GM12878
AP000230.1	0	9.88E-08	0	NA	Yes	GM12878
RP3-508I15.21	0	1.83E-08	1	T CD4 TH17	No	NA
APOBEC3D	0	9.16E-06	1	T CD4 TH17	No	NA
RPL3	7	6.80E-08	1	Lung	No	NA
SNORD83B	3	1.37E-04	0	NA	No	NA
SNORD83A	3	1.37E-04	0	NA	No	NA
SNORD43	6	1.37E-04	0	NA	No	NA
SYNGR1	18	4.12E-09	32	scRNA eQTLs/NK:scRNA eQTLs/PBMC:T CD4 naive:T CD8 naive:T CD8 naive activated:Monocyte classical:NK:T CD4 TFH:T CD4 TH1:T CD4 TH17:T CD4 TH1 17:T CD4 TH2:T CD4 memory TREG:T CD4 naive TREG:Cells EBV-transformed lymphocytes:Whole Blood:Lung:Small Intestine Terminal Ileum:Spleen	No	NA
TAB1	8	1.27E-08	0	NA	Yes	Spleen:GM12878
MGAT3	0	1.27E-08	3	B cell naive:Whole Blood	Yes	GM12878

ATF4	0	1.27E-08	0	NA	Yes	Spleen:GM12878
FAM58A	0	4.89E-10	5	T CD4 TH2	No	NA
PDZD4	0	4.89E-10	39	T CD4 naive:T CD4 naive activated:Whole Blood	No	NA
RENBP	2	1.33E-06	0	NA	No	NA
HCFC1	3	1.32E-06	0	NA	No	NA
TMEM187	4	4.89E-10	44	Monocyte classical:Monocyte non classical:Whole Blood:Lung:Small Intestine Terminal Ileum:Spleen	No	NA
MIR3202-1	4	7.23E-07	0	NA	No	NA
IRAK1	16	4.89E-10	0	NA	Yes	Spleen
MIR718	11	4.89E-10	0	NA	Yes	Spleen
MECP2	40	4.89E-10	18	Lung	Yes	GM12878
PLXNA3	0	7.19E-10	17	Whole Blood:Lung	No	NA
FAM3A	0	5.31E-10	14	Lung	No	NA

minGwasP, minimum Meta-GWAS *P* value of SNP(s) used in prioritizing the gene; Tissues, tissues with significant eQTL associations or chromatin interactions; NA, not available.

Supplementary Table 2 | **MAGMA gene set analysis results**

Gene set	Number of genes	Beta	Standardized beta	Standard error	*P* value*
CD40 signaling (up)[†]	91	0.699	0.047	0.092	1.62E-14
Histone citrullination[‡]	4	3.946	0.056	0.559	8.60E-13
Protein arginine deiminase activity[‡]	4	3.946	0.056	0.559	8.60E-13
IL21 mediated signaling pathway[‡]	8	1.696	0.034	0.293	3.66E-09
IL21 signaling[†]	10	1.698	0.038	0.294	3.72E-09
Lymphocyte activation[‡]	630	0.188	0.033	0.035	4.53E-08
B cell activation[‡]	236	0.289	0.031	0.056	1.56E-07
Lymphocyte differentiation[‡]	340	0.244	0.032	0.048	1.86E-07
T cell differentiation[‡]	229	0.296	0.032	0.059	3.21E-07
CD40 pathway[†]	29	0.734	0.028	0.148	3.70E-07
PKC pathway[†]	7	1.656	0.031	0.336	4.10E-07
Plasmacytoma (up)[†]	245	0.267	0.03	0.055	6.41E-07
Regulation of mast cell chemotaxis[‡]	7	1.782	0.033	0.368	6.69E-07
Positive regulation of interferon gamma secretion[‡]	8	1.831	0.037	0.382	8.43E-07
Leukocyte cell-cell adhesion[‡]	310	0.238	0.029	0.051	1.54E-06
ESR1 targets not via AKT1 (down)[†]	89	0.461	0.031	0.1	1.79E-06
Negative regulation of lipid localization[‡]	40	0.699	0.031	0.152	2.00E-06
alpha beta T cell activation[‡]	131	0.359	0.029	0.078	2.12E-06
Cancer copy number (up)[†]	320	0.226	0.028	0.049	2.26E-06
Positive regulation of cell activation[‡]	307	0.228	0.028	0.05	2.90E-06

*The Bonferroni-corrected significance threshold was defined at 0.05/15481.

[†] Curated gene sets

[‡] Gene ontology terms

Supplementary Table 3 | Genetic associations in RA loci in Korean and European populations

					Frequency[‡]		This study		Europeans		
Gene	Variant	Chr	Position[*]	EA/NEA	KOR	EUR	OR (95% CI)[‡]	*P*	OR (95% CI)[‡]	*P*	P_{het}[§]
Known variants											
PADI4	rs2301888	1	17672730	A/G	0.584	0.345	0.82 (0.78–0.86)	2.2E-15	0.90 (0.87–0.93)	5.5E-09	1.5E-03
STAT4	rs11889341	2	191943742	T/C	0.303	0.235	1.22 (1.15–1.28)	2.9E-13	1.12 (1.09–1.16)	1.4E-12	8.1E-03
PLD4-AHNAK2	rs2582532	14	105392837	T/C	0.291	0.010	0.81 (0.77–0.86)	4.5E-13	1.08 (0.83–1.39)	5.9E-01	4.0E-02
CCR6	rs1571878	6	167540842	T/C	0.554	0.552	0.83 (0.79–0.88)	6.8E-13	0.88 (0.86–0.91)	2.4E-18	4.8E-02
ARID5B	rs71508903	10	63779871	T/C	0.217	0.213	1.24 (1.17–1.32)	2.4E-12	1.15 (1.11–1.20)	3.3E-15	3.8E-02
TNFAIP3	rs17264332	6	138005515	G/A	0.000[¶]	0.218	NA	NA	1.17 (1.13–1.21)	4.1E-20	NA
	rs7752903	6	138227364	T/G	0.942	0.967	0.74 (0.67–0.81)	3.0E-10	0.71 (0.66–0.76)	1.7E-20	5.2E-01
NFKBIE	rs2233424	6	44233921	T/C	0.215	0.043	1.20 (1.13–1.27)	6.0E-10	1.33 (1.20–1.47)	3.3E-08	7.5E-02
RASGRP1	rs8032939	15	38834033	T/C	0.408	0.742	0.86 (0.81–0.90)	9.5E-10	0.88 (0.85–0.92)	3.2E-14	2.7E-01
IRAK1	rs5987194	X	153301467	C/G	0.745	0.136	1.19 (1.13–1.26)	1.0E-09	1.16 (1.12–1.21)	2.8E-12	4.6E-01
SYNGR1	rs909685	22	39747671	A/T	0.847	0.305	1.23 (1.14–1.32)	5.3E-08	1.11 (1.08–1.15)	6.4E-12	1.5E-02
UBE2L3-YDJC	rs11089637	22	21979096	T/C	0.579	0.837	0.88 (0.84–0.92)	3.7E-07	0.91 (0.87–0.95)	2.0E-07	3.3E-01
BLK	rs2736337	8	11341880	T/C	0.277	0.747	0.86 (0.81–0.91)	3.9E-07	0.92 (0.89–0.95)	7.6E-08	6.5E-02
RAD51B	rs1950897	14	68760141	T/C	0.852	0.715	1.20 (1.12–1.29)	8.3E-07	1.09 (1.06–1.12)	5.0E-08	1.5E-02
CLNK	rs13142500	4	10727357	T/C	0.423	0.545	0.88 (0.84–0.93)	1.5E-06	0.91 (0.87–0.95)	2.4E-06	4.1E-01
UBASH3A	rs1893592	21	43855067	A/C	0.754	0.722	1.15 (1.08–1.22)	2.4E-06	1.11 (1.07–1.15)	9.8E-09	3.1E-01
COG6	rs9603616	13	40368069	T/C	0.254	0.335	0.87 (0.82–0.92)	3.3E-06	0.90 (0.87–0.93)	2.8E-11	3.3E-01
RTKN2	rs6479800	10	64036881	C/G	0.077	0.233	1.22 (1.12–1.33)	1.1E-05	1.08 (1.04–1.13)	1.4E-04	1.5E-02
AFF3	rs9653442	2	100825367	T/C	0.567	0.532	0.90 (0.85–0.94)	1.2E-05	0.89 (0.87–0.92)	9.8E-15	8.8E-01
CTLA4	rs3087243	2	204738919	A/G	0.167	0.440	0.86 (0.80–0.92)	1.2E-05	0.87 (0.85–0.89)	3.6E-22	7.7E-01
ANKRD55	rs7731626	5	55444683	A/G	0.089	0.359	0.81 (0.74–0.89)	1.2E-05	0.83 (0.80–0.86)	8.2E-23	7.1E-01
WDFY4	rs2671692	10	50097819	A/G	0.329	0.635	1.12 (1.06–1.18)	1.7E-05	1.06 (1.03–1.09)	2.6E-05	6.4E-02
IL6R	rs2228145	1	154426970	A/C	0.567	0.605	1.11 (1.06–1.17)	1.8E-05	1.07 (1.04–1.10)	4.8E-06	1.6E-01
P2RY10	chrX:78464616	X	78464616	A/C	0.463	0.010	1.10 (1.05–1.15)	9.3E-05	1.16 (0.77–1.74)	4.6E-01	8.0E-01
EOMES	rs3806624	3	27764623	A/G	0.185	0.537	0.88 (0.83–0.94)	1.7E-04	0.93 (0.90–0.96)	2.8E-08	2.0E-01
GATA3	rs3824660	10	8104722	T/C	0.614	0.605	0.91 (0.86–0.96)	1.8E-04	0.91 (0.88–0.94)	2.7E-09	9.9E-01
ETS1	rs73013527	11	128496952	T/C	0.276	0.497	0.90 (0.85–0.95)	2.5E-04	0.93 (0.90–0.95)	1.0E-06	3.5E-01
LBH	rs10175798	2	30449594	A/G	0.375	0.625	1.10 (1.04–1.15)	3.1E-04	1.09 (1.06–1.12)	4.2E-08	8.4E-01
CD83	chr6:14103212	6	14103212	T/C	0.151	0.053	1.13 (1.05–1.20)	4.2E-04	1.10 (1.02–1.18)	1.3E-02	6.4E-01
SPRED2	rs1858037	2	65598300	A/T	0.811	0.342	0.90 (0.84–0.95)	4.3E-04	0.92 (0.89–0.95)	2.0E-09	5.1E-01
ETV7	rs2234067	6	36355654	A/C	0.038	0.128	0.78 (0.68–0.90)	5.0E-04	0.88 (0.84–0.92)	4.1E-08	1.1E-01
CD40	rs4239702	20	44749251	T/C	0.345	0.272	0.91 (0.87–0.96)	5.9E-04	0.88 (0.85–0.90)	1.1E-16	2.1E-01
IRF5	chr7:128580042	7	128580042	A/G	0.771	0.535	0.91 (0.86–0.96)	8.3E-04	0.89 (0.87–0.92)	4.1E-12	6.1E-01
PTPN2	rs8083786	18	12881361	A/G	0.667	0.837	0.92 (0.87–0.97)	9.5E-04	0.89 (0.86–0.93)	8.4E-09	3.9E-01
TXNDC11	rs4780401	16	11839326	T/G	0.474	0.593	1.09 (1.03–1.15)	9.8E-04	1.09 (1.06–1.13)	8.7E-09	9.7E-01
ARAP1	rs11605042	11	72411664	A/G	0.397	0.488	0.92 (0.88–0.97)	1.4E-03	0.95 (0.92–0.99)	1.4E-02	3.0E-01
FCGR2B	chr1:161644258	1	161644258	C/G	0.238	0.000[¶]	1.11 (1.04–1.18)	1.5E-03	NA	NA	NA
CEP57	rs4409785	11	95311422	T/C	0.925	0.825	0.87 (0.80–0.95)	2.0E-03	0.89 (0.86–0.93)	3.6E-09	6.0E-01
FCGR2A	rs72717009	1	161405053	T/C	0.031	0.120	0.79 (0.68–0.92)	2.9E-03	1.12 (1.07–1.18)	5.2E-07	2.6E-05
MED1	rs1877030	17	37740161	T/C	0.248	0.157	0.92 (0.87–0.97)	3.4E-03	0.92 (0.88–0.95)	1.3E-05	1.0E+00
CDK6	rs4272	7	92236829	A/G	0.894	0.785	0.89 (0.82–0.96)	3.6E-03	0.91 (0.88–0.94)	1.2E-08	6.2E-01
PRKCH	rs3783782	14	61940675	A/G	0.228	0.010	1.09 (1.03–1.15)	4.9E-03	1.12 (0.96–1.31)	1.4E-01	7.2E-01
TNFRSF14-MMEL1	chr1:2523811	1	2523811	A/G	0.459	0.295	0.94 (0.89–0.98)	7.9E-03	0.91 (0.88–0.94)	4.8E-09	3.3E-01
FCRL3	rs2317230	1	157674997	T/G	0.395	0.433	1.07 (1.02–1.12)	8.1E-03	1.06 (1.03–1.09)	1.9E-04	7.6E-01

IL3-CSF2	rs657075	5	131430118	A/G	0.283	0.100	1.08 (1.02–1.13)	8.1E-03	1.07 (1.02–1.13)	1.1E-02	9.0E-01
IKZF3-CSF3	chr17:38031857	17	38031857	T/G	0.726	0.537	0.93 (0.88–0.98)	8.2E-03	0.92 (0.89–0.94)	6.0E-10	6.7E-01
RUNX1-LOC100506403	rs8133843	21	36738242	A/G	0.535	0.625	1.07 (1.02–1.12)	1.1E-02	1.09 (1.06–1.12)	2.0E-08	4.5E-01
ZNF438	rs793108	10	31415106	T/C	0.473	0.505	1.06 (1.01–1.12)	1.2E-02	1.07 (1.04–1.10)	6.1E-07	8.5E-01
ACOXL	rs6732565	2	111607832	A/G	0.597	0.625	1.07 (1.01–1.12)	1.3E-02	1.10 (1.07–1.14)	9.4E-09	3.0E-01
CD28	rs1980422	2	204610396	T/C	0.916	0.757	0.90 (0.82–0.98)	1.3E-02	0.88 (0.85–0.92)	1.9E-13	7.6E-01
CDK2	rs773125	12	56394954	A/G	0.788	0.605	1.08 (1.02–1.15)	1.3E-02	1.09 (1.06–1.12)	2.1E-08	7.9E-01
CD226	rs2469434	18	67544046	T/C	0.604	0.587	0.94 (0.89–0.99)	1.7E-02	0.95 (0.93–0.98)	6.7E-04	6.8E-01
IRF8	rs13330176	16	86019087	A/T	0.396	0.235	1.07 (1.01–1.13)	1.7E-02	1.12 (1.08–1.17)	9.0E-09	1.5E-01
MTF1-INPP5B	rs28411352	1	38278579	T/C	0.243	0.258	1.07 (1.01–1.13)	2.1E-02	1.10 (1.07–1.14)	5.9E-09	3.8E-01
TAGAP	rs2451258	6	159506600	T/C	0.961	0.648	1.16 (1.02–1.33)	2.4E-02	1.10 (1.07–1.13)	1.6E-10	4.1E-01
CCL19-CCL21	rs11574914	9	34710338	A/G	0.060	0.338	1.12 (1.01–1.24)	2.5E-02	1.13 (1.10–1.17)	1.8E-15	8.7E-01
ATG5	rs9372120	6	106667535	T/G	0.963	0.795	0.87 (0.77–0.98)	2.6E-02	0.91 (0.88–0.94)	3.8E-08	5.0E-01
PPIL4	rs9373594	6	149834574	T/C	0.401[¶]	0.850	NA	NA	1.07 (1.02–1.12)	6.5E-03	NA
	rs1474640[†]	6	149813940	C/G	0.296	0.843[¶]	1.06 (1.01–1.12)	2.6E-02	1.08 (1.02–1.13)	1.1E-02	7.4E-01
IFNGR2	rs73194058	21	34764288	A/C	0.510	0.125	0.95 (0.90–0.99)	2.9E-02	0.88 (0.85–0.93)	2.6E-08	4.6E-02
IL2RA	rs706778	10	6098949	T/C	0.608	0.408	1.06 (1.00–1.11)	3.3E-02	1.12 (1.09–1.15)	4.6E-15	4.2E-02
C5orf30	rs2561477	5	102608924	A/G	0.256	0.315	0.94 (0.89–1.00)	3.9E-02	0.90 (0.88–0.93)	2.2E-11	1.6E-01
C1QBP	rs72634030	17	5272580	A/C	0.649	0.070	1.06 (1.00–1.11)	4.1E-02	1.12 (1.06–1.19)	2.9E-05	1.4E-01
TRAF1-C5	rs10985070	9	123636121	A/C	0.492	0.575	0.95 (0.91–1.00)	4.5E-02	0.92 (0.89–0.94)	4.2E-09	2.1E-01
ANXA3	rs10028001	4	79502972	A/T	0.589	0.628	0.95 (0.91–1.00)	5.8E-02	0.98 (0.94–1.02)	2.7E-01	3.8E-01
LOC145837	rs8026898	15	69991417	A/G	0.074	0.275	1.09 (1.00–1.19)	6.4E-02	1.15 (1.12–1.19)	5.9E-18	2.7E-01
TNFRSF9	rs227163	1	7961206	T/C	0.691	0.580	0.95 (0.90–1.00)	6.7E-02	1.00 (0.97–1.03)	9.3E-01	1.1E-01
CXCR5	rs10790268	11	118729391	A/G	0.125	0.205	0.93 (0.86–1.01)	7.0E-02	0.85 (0.82–0.89)	1.4E-17	4.5E-02
PLCL2	rs4452313	3	17047032	A/T	0.459	0.705	0.96 (0.91–1.00)	7.5E-02	0.90 (0.87–0.93)	5.2E-11	4.5E-02
IRF4	rs9378815	6	426155	C/G	0.334	0.663	1.04 (0.99–1.10)	1.2E-01	1.09 (1.06–1.13)	1.4E-07	2.0E-01
SFTPD	rs726288	10	81706973	T/C	0.212	0.030	1.04 (0.98–1.11)	1.5E-01	0.96 (0.86–1.07)	4.1E-01	1.7E-01
PVT1	rs1516971	8	129542100	T/C	0.963	0.873	1.09 (0.96–1.24)	2.0E-01	1.16 (1.11–1.21)	3.2E-11	3.8E-01
B3GNT2	rs13385025	2	62461120	A/G	0.202	0.122	1.03 (0.97–1.10)	3.1E-01	1.08 (1.02–1.15)	1.0E-02	3.0E-01
LOC339442	rs12140275	1	38633879	A/T	0.989	0.755	1.13 (0.88–1.46)	3.4E-01	1.11 (1.08–1.15)	4.4E-09	8.8E-01
PRKCQ	rs947474	10	6390450	A/G	0.908	0.815	1.04 (0.95–1.13)	4.1E-01	1.12 (1.08–1.16)	3.3E-10	9.8E-02
REL	rs34695944	2	61124850	T/C	0.978	0.632	1.06 (0.90–1.26)	4.8E-01	0.88 (0.86–0.91)	3.7E-16	3.8E-02
TPD52	rs998731	8	81095395	T/C	0.804	0.443	1.02 (0.96–1.09)	4.9E-01	1.09 (1.06–1.12)	6.6E-09	6.6E-02
LOC100506023	rs2105325	1	173349725	A/C	0.073	0.252	0.97 (0.88–1.07)	5.5E-01	0.89 (0.87–0.92)	3.3E-11	1.0E-01
RCAN1	chr21:35928240	21	35928240	T/C	0.020	0.117	0.95 (0.79–1.14)	5.8E-01	0.89 (0.85–0.93)	7.1E-07	5.1E-01
GRHL2	rs678347	8	102463602	A/G	0.199	0.725	0.99 (0.93–1.05)	6.3E-01	0.91 (0.88–0.94)	7.3E-09	2.4E-02
CDK4	rs1633360	12	58108052	T/C	0.271	0.585	1.01 (0.96–1.07)	6.9E-01	1.08 (1.05–1.11)	7.1E-08	3.6E-02
JAZF1	rs67250450	7	28174986	T/C	0.016	0.793	1.03 (0.85–1.25)	7.5E-01	1.11 (1.08–1.15)	2.6E-09	4.5E-01
TEC	rs2664035	4	48220839	A/G	0.266	0.405	1.01 (0.95–1.07)	7.9E-01	1.08 (1.05–1.11)	3.3E-08	3.0E-02
LY9-CD244	rs4656942	1	160831048	A/G	0.308	0.230	0.99 (0.94–1.05)	8.1E-01	0.99 (0.96–1.02)	4.8E-01	9.2E-01
CD2	rs624988	1	117263790	T/C	0.463	0.405	0.99 (0.95–1.04)	8.2E-01	1.09 (1.06–1.12)	8.0E-10	1.3E-03
ICOSLG-AIRE	rs2236668	21	45650009	T/C	0.836	0.285	1.00 (0.93–1.07)	9.0E-01	0.93 (0.90–0.97)	4.6E-05	1.1E-01
IL2RB	rs3218251	22	37545505	A/T	0.080	0.273	1.01 (0.92–1.10)	9.1E-01	1.08 (1.05–1.12)	5.7E-06	1.5E-01
TRAF6-RAG1/2	rs331463	11	36501787	A/T	0.064	0.147	1.00 (0.90–1.10)	9.9E-01	0.89 (0.86–0.93)	1.1E-07	4.0E-02
C4orf52	rs11933540	4	26120001	T/C	0.993	0.683	0.73 (0.52–1.04)	7.9E-02	0.87 (0.84–0.90)	9.5E-17	3.4E-01
SH2B3-PTPN11	rs10774624	12	111833788	A/G	0.994	0.497	0.89 (0.55–1.45)	6.4E-01	0.92 (0.89–0.95)	6.9E-09	9.0E-01
PTPN22	rs2476601	1	114377568	A/G	0.000[¶]	0.108	NA	NA	1.80 (1.73–1.88)	8.9E-170	NA
IL2-IL21	rs45475795	4	123399491	G/A	0.000[¶]	0.072	NA	NA	1.14 (1.08–1.20)	3.5E-06	NA
10p14	rs12413578	10	9049253	C/T	0.970[¶]	0.902	NA	NA	1.20 (1.12–1.29)	7.5E-08	NA

PTPRC	rs17668708	1	198640488	C/T	1.000[¶]	0.895	NA	NA	1.12 (1.06–1.18)	1.8E-05	NA
CFLAR-CASP8	rs6715284	2	202154397	G/C	0.040[¶]	0.103	NA	NA	1.15 (1.10–1.20)	2.5E-09	NA
DNASE1L3-ABHD6-PXK	rs73081554	3	58302935	T/C	0.000[¶]	0.072	NA	NA	1.18 (1.11–1.25)	4.7E-08	NA
IL20RB	rs9826828	3	136402060	A/G	0.000[¶]	0.020	NA	NA	1.44 (1.28–1.61)	8.7E-10	NA
CD5	rs508970	11	60906450	A/G	0.000[¶]	0.493	NA	NA	1.07 (1.04–1.10)	2.7E-06	NA
FADS1-FADS2-FADS3	rs968567	11	61595564	C/T	1.000[¶]	0.833	NA	NA	1.12 (1.08–1.17)	1.8E-08	NA
ATM	chr11:107967350	11	107967350	A/G	NA	0.923	NA	NA	1.21 (1.13–1.29)	1.1E-08	NA
TYK2	rs34536443	19	10463118	G/C	1.000[¶]	0.956	NA	NA	1.46 (1.33–1.60)	4.6E-16	NA
ILF3	chr19:10771941	19	10771941	C/T	NA	0.973	NA	NA	1.47 (1.30–1.67)	8.8E-10	NA
Novel variants											
SLAMF6	rs148363003	1	160443973	T/C	0.980	1.000[¶]	0.62 (0.53–0.72)	5.1E-10	NA	NA	NA
CXCL13	rs117605225	4	78508197	T/G	0.955	1.000[¶]	1.54 (1.34–1.77)	1.9E-09	NA	NA	NA
SWAP70	rs360136	11	9773517	A/C	0.423	0.586[¶]	1.17 (1.11–1.23)	4.5E-10	1.06 (1.02–1.10)	3.2E-03	2.0E-03
NFKBIA	rs111597524	14	35861800	T/C	0.274	0.045[¶]	1.18 (1.12–1.24)	5.3E-09	0.97 (0.89–1.04)	3.7E-01	6.4E-05
ZFP36L1	rs194757	14	69213851	A/G	0.338	0.327[¶]	0.86 (0.82–0.91)	2.4E-08	0.95 (0.92–0.98)	1.4E-03	1.6E-03
LINC00158	rs1547233	21	26769507	T/C	0.292	0.137[¶]	1.17 (1.11–1.24)	6.4E-09	1.02 (0.96–1.07)	5.7E-01	3.6E-04

The lead SNPs in non-MHC 100 RA loci and their European association statistics in previous trans-ancestral RA GWAS by Okada *et al* (*Nature*. 2014;506(7488):376-81) were retrieved.

*based on hg19

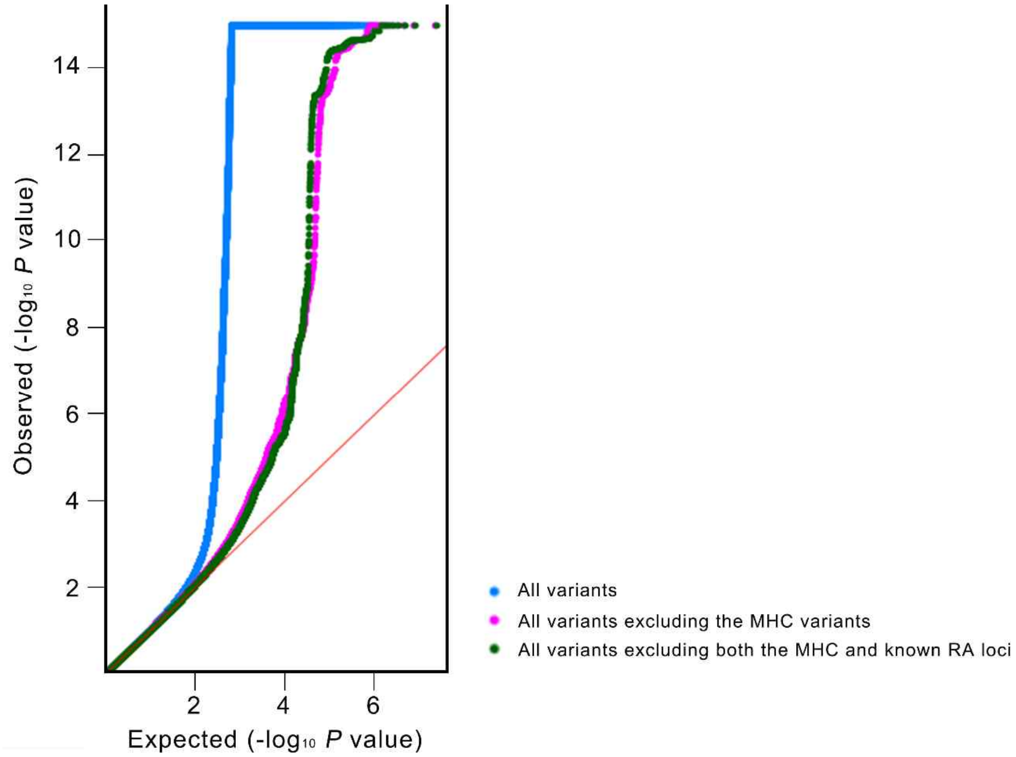
[†] Proxy variants in LD with lead variants (r^2>0.8 in the 1KGP Europeans). Proxy variants were listed when lead variants were absent in the Korean study.

[‡] Frequencies, odds ratios, and confidence intervals for effect alleles

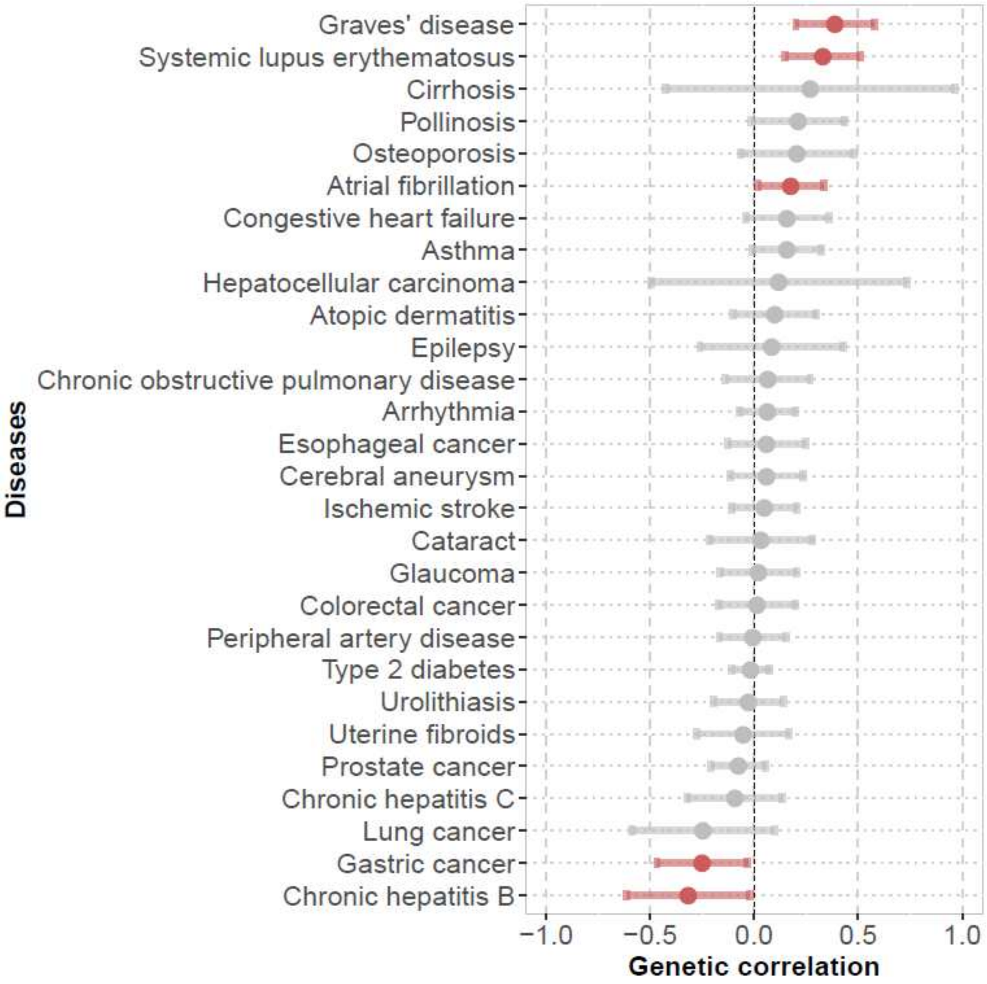
[§] *P* values for cross-cohort association heterogeneity (P_{Het}) were calculated by Cochrane's Q tests.

[¶] Effect allele frequency was retrieved from the 1KGP phase 3 data of East Asians or Europeans (https://www.ncbi.nlm.nih.gov/snp/).

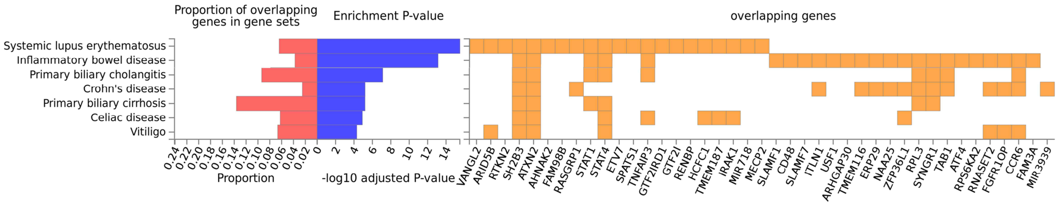
Chr, chromosome; Pos, Position; EA, effect allele; NEA, non-effect allele; KOR, Korean; EUR, European; OR, odds ratio; CI, confidence interval; NA, not available.



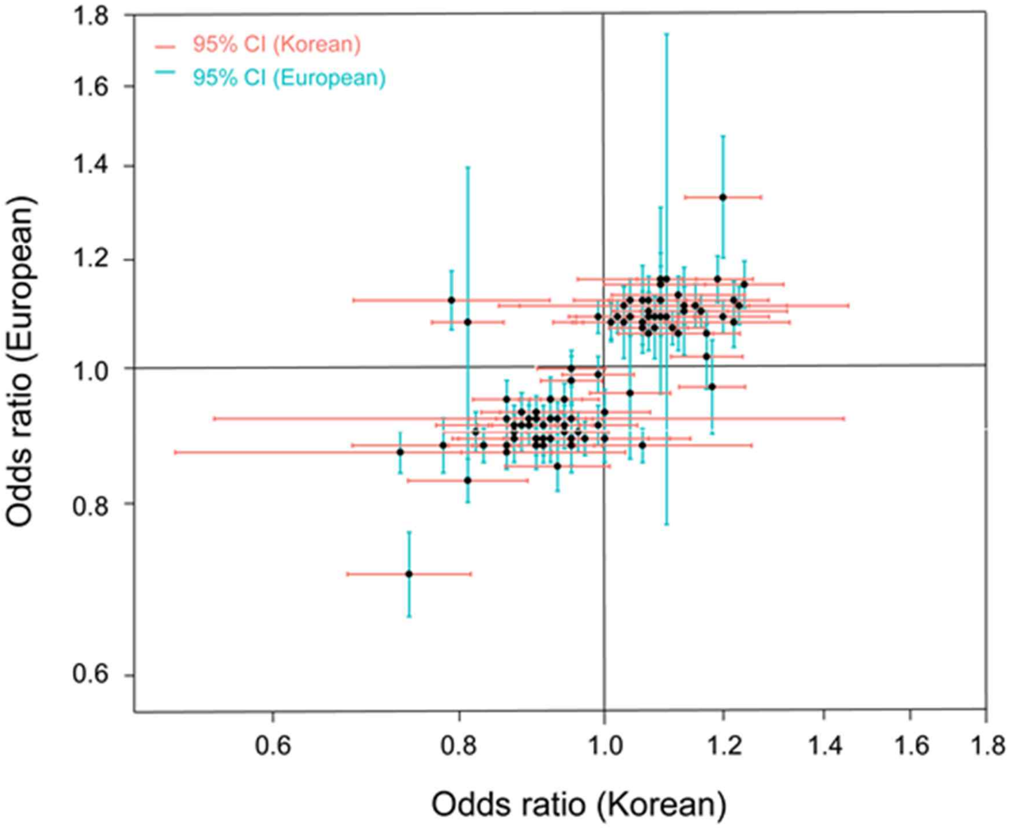
Supplementary Figure 1 | Quantile-quantile plot for a meta-analysis result. Quantile-quantile plots were generated using the RA association P_{meta} values for all variants (blue), all variants excluding the MHC variants (magenta), and all variants excluding both the MHC and known non-MHC RA loci (green) in a meta-analysis.



Supplementary Figure 2 | Genetic correlations between RA and other 28 traits. Genome-wide associations in RA have a positive correlation with those in three disease including Graves' disease, systemic lupus erythematosus, and atrial fibrillation, while a negative correlation was found with chronic hepatitis B infection and gastric cancer. Data points indicate the correlation coefficient *r* and error bars represent the 95% confidence intervals.



Supplementary Figure 3 | Significant co-occurrence of the prioritized RA-relevant genes in the susceptibility loci of other diseases. The prioritized RA-relevant genes were significantly more in the susceptibility loci of seven diseases at the false discovery rate threshold of 5% in one-sided Fisher's exact tests.



Supplementary Figure 4 | Odds ratios of RA variants in Korean and European populations. Odds ratios of 91 RA variants listed in Supplementary Table 3 were available in both Korean and European populations. Odds ratios (black dots) of the RA variants were plotted in the logarithmic axis. The error bars represent 95% confidence intervals in Koreans (green) and Europeans (red). A correlation coefficient for odds ratios in two population was estimated to be 0.76.