Supplementary Table 2. Sequence variants outside the HLA region associated with RA overall, in GWAS meta-analysis on study populations from six Northwestern-European countries (31,313 cases and 995,377 controls).[#]

							Sweden			Denmark			Iceland			Norway			UK			Finland			Combined		
Chr	Position	rsID*	*Close gene*	Variant annotation	EA	OA	Freq EA (%)	OR	*P*	Freq EA (%)	OR	*P*	Freq EA (%)	OR	*P*	Freq EA (%)	OR	*P*	Freq EA (%)	OR	*P*	Freq EA (%)	OR	*P*	OR	*P*	P_{het}
chr1	2800059	rs897628*	***TTC34***	missense	T	C	30.22	0.92	*1.18E-03*	29.36	0.96	*0.0296*	29.65	0.93	*0.0114*	31.91	0.88	*0.0253*	33.62	0.96	*0.063*	35.00	0.91	*4.82E-05*	**0.94**	***1.87E-10***	*0.302*
chr1	113834946	rs2476601	***PTPN22***	missense	A	G	12.08	1.57	*2.67E-49*	10.56	1.43	*1.94E-40*	13.32	1.29	*1.48E-11*	11.03	1.50	*2.56E-08*	9.65	1.28	*9.27E-18*	14.88	1.45	*7.47E-32*	**1.41**	***3.85E-144***	*0*
chr2	191094763	rs4853458	***STAT4,GLS***	intron	A	G	23.83	1.10	*1.44E-04*	21.90	1.07	*2.17E-03*	20.64	1.12	*6.97E-04*	21.99	1.04	*0.469*	22.37	1.12	*5.31E-07*	23.14	1.14	*7.25E-07*	**1.10**	***2.72E-19***	*0.424*
chr2	203874196	rs3087243	***CTLA4***	downstream gene	A	G	39.35	0.89	*1.07E-07*	41.52	0.91	*4.52E-07*	40.04	0.95	*0.0946*	40.46	0.94	*0.27*	44.80	0.95	*5.52E-03*	32.99	0.89	*8.30E-07*	**0.92**	***3.04E-19***	*0.0982*
chr3	58197909	rs35677470	***DNASE1L3***	missense	A	G	6.86	1.21	*7.69E-06*	7.86	1.12	*6.24E-04*	7.59	1.07	*0.174*	6.44	1.05	*0.651*	7.79	1.07	*0.0573*	6.11	1.06	*0.228*	**1.10**	***1.81E-08***	*0.21*
chr4	26089240	rs932036	*LINC02357*	intergenic	T	A	27.90	1.13	*1.69E-07*	28.89	1.05	*7.47E-03*	25.99	1.11	*9.98E-04*	27.05	1.13	*0.0282*	29.95	1.10	*6.80E-06*	28.37	1.08	*1.50E-03*	**1.09**	***6.65E-18***	*0.29*
chr5	56148856	rs7731626	***ANKRD55***	intron	A	G	34.86	0.87	*3.43E-09*	35.34	0.88	*7.22E-11*	39.14	0.88	*9.08E-06*	36.44	0.82	*1.47E-04*	36.69	0.88	*3.37E-10*	27.83	0.88	*5.61E-07*	**0.88**	***1.09E-39***	*0.827*
chr6	137678425	rs35926684,rs397886367	.	regulatory region	G	GA	23.61	1.15	*1.97E-08*	22.63	1.07	*1.60E-03*	20.31	1.08	*0.0244*	24.18	1.12	*0.0407*	22.69	1.08	*5.13E-04*	20.86	1.05	*0.0527*	**1.09**	***1.48E-14***	*0.19*
chr6	167127770	rs3093017	*CCR6*	intron	C	G	45.47	1.10	*5.70E-06*	45.12	1.05	*7.47E-03*	46.27	1.07	*0.0135*	45.98	1.17	*2.03E-03*	43.37	1.04	*0.07*	44.77	1.13	*1.22E-07*	**1.07**	***7.04E-15***	*0.0153*
chr7	50313596	rs10261758*	*IKZF1*	intron	G	A	33.46	1.05	*0.029*	31.17	1.04	*0.0555*	31.04	1.05	*0.104*	31.02	1.15	*0.0108*	28.82	1.12	*1.24E-08*	38.40	1.07	*0.00251*	**1.07**	***3.56E-12***	*0.0563*
chr7	128938247	rs2004640*	***IRF5***	splice donor	G	T	46.83	0.93	*5.32E-04*	48.75	0.96	*0.0142*	47.26	0.92	*1.20E-03*	46.81	0.95	*0.342*	51.20	0.93	*2.49E-04*	47.89	0.93	*5.36E-04*	**0.94**	***5.11E-13***	*0.752*
chr8	11480078	rs2409780	.	regulatory region	C	T	26.29	1.08	*1.09E-03*	27.12	1.07	*4.68E-04*	21.76	1.09	*7.07E-03*	27.72	0.92	*0.155*	25.40	1.09	*1.18E-04*	25.85	1.09	*7.34E-04*	**1.08**	***1.29E-12***	*0.153*
chr8	100265412	rs1660322*	*RNF19A*	intron	C	T	29.41	1.04	*0.11*	29.86	1.07	*4.56E-04*	30.96	1.06	*0.0478*	29.74	1.17	*2.97E-03*	31.06	1.05	*0.0164*	30.25	1.10	*8.22E-05*	**1.07**	***8.65E-11***	*0.24*
chr9	120873843	rs10985070	***PHF19,TRAF1***	upstream gene	C	A	46.73	1.08	*3.08E-04*	46.03	1.07	*2.85E-04*	44.02	1.11	*2.02E-04*	45.73	1.06	*0.261*	43.64	1.01	*0.556*	48.59	1.05	*0.0181*	**1.06**	***8.69E-10***	*0.0875*
chr10	6060794	rs3118471	***IL2RA***	intron	G	A	34.47	1.06	*0.0141*	32.25	1.09	*3.37E-06*	34.12	1.02	*0.532*	33.48	1.09	*0.108*	29.67	1.06	*4.79E-03*	36.42	1.10	*2.53E-05*	**1.07**	***1.72E-12***	*0.259*
chr10	31122426	rs1538981	.	regulatory region	C	T	43.71	0.94	*6.23E-03*	45.56	0.94	*7.51E-04*	44.49	0.97	*0.198*	44.38	0.90	*0.0413*	48.96	0.94	*7.64E-04*	40.86	0.92	*3.56E-04*	**0.94**	***9.37E-12***	*0.809*
chr11	64340005	rs479777*	*CCDC88B*	upstream gene	C	T	33.47	0.92	*2.07E-04*	34.17	0.94	*1.58E-03*	32.87	0.95	*0.0795*	33.50	0.88	*0.0144*	33.41	0.96	*0.0667*	38.45	0.93	*2.02E-03*	**0.94**	***1.38E-10***	*0.477*
chr11	118870448	rs7117261	.	regulatory region	T	C	20.03	0.92	*2.55E-03*	20.08	0.90	*8.01E-06*	17.76	0.95	*0.135*	21.28	0.79	*3.24E-04*	19.34	0.94	*0.0159*	16.61	0.91	*2.53E-03*	**0.92**	***7.63E-13***	*0.17*
chr12	111446804	rs3184504	***SH2B3***	missense	T	C	46.74	1.08	*5.65E-04*	50.60	1.06	*2.71E-03*	37.86	1.07	*0.0198*	45.38	1.19	*6.10E-04*	46.35	1.08	*4.67E-05*	40.83	1.12	*1.95E-07*	**1.08**	***1.10E-17***	*0.136*
chr13	39771329	rs7320598	*COG6*	intron	T	C	33.63	0.93	*1.27E-03*	34.29	0.91	*2.30E-07*	31.89	0.95	*0.106*	34.12	0.89	*3.27E-02*	34.46	0.94	*3.30E-03*	35.69	0.93	*1.80E-03*	**0.93**	***1.55E-14***	*0.599*
chr14	92651884	rs117068593*	***RIN3***	missense	T	C	15.65	0.95	*0.117*	17.23	0.91	*6.94E-05*	15.57	0.84	*1.98E-05*	16.41	1.01	*0.868*	18.41	0.94	*7.26E-03*	14.22	0.95	*0.141*	**0.93**	***1.93E-09***	*0.0795*
chr15	69746861	rs2117234*	.	intergenic	T	C	46.69	1.12	*4.99E-07*	46.22	1.07	*2.89E-04*	49.83	1.09	*2.83E-03*	44.97	1.10	*0.0574*	47.08	1.05	*5.26E-03*	47.64	1.07	*3.88E-03*	**1.08**	***2.71E-15***	*0.468*
chr16	85977427	rs13333054	***IRF8***	intergenic	T	C	23.08	1.07	*0.00561*	22.49	1.10	*1.58E-05*	23.15	1.02	*0.459*	23.78	1.09	*0.161*	22.70	1.07	*1.19E-03*	19.25	1.07	*0.0194*	**1.07**	***1.12E-10***	*0.671*
chr19	10352442	rs34536443	***TYK2***	missense	C	G	3.64	0.71	*2.94E-08*	4.18	0.77	*5.30E-08*	4.38	0.79	*8.11E-04*	4.51	0.69	*4.27E-03*	4.39	0.78	*9.52E-07*	3.06	0.71	*3.84E-07*	**0.75**	***2.54E-29***	*0.676*
chr19	10359299	rs12720356*	***TYK2***	missense	C	A	8.60	0.92	*0.0215*	7.84	0.92	*0.014*	5.98	0.93	*0.249*	9.06	0.82	*0.0296*	9.31	0.89	*4.52E-04*	8.25	0.87	*4.78E-04*	**0.90**	***4.31E-10***	*0.712*

[#]We performed a meta-analysis using logistic regression assuming a multiplicative model, reporting odds ratios (OR) and two-sided *P*-values (Methods and Gudbjartsson et al, 2015). Variants were split into five classes based on their genome annotation, and significance threshold based on the number of variants in each class, thereby adjusting for all 60 million variants tested (Methods). The primary signal at each genomic locus was defined as the sequence variant with the lowest Bonferroni adjusted *P*-value using the adjusted significance thresholds. Conditional analysis was performed to identify lead signals and possible secondary signals within 500 kB from index variants (excluding the HLA locus). This applied to the following marker pair: chr19:10352442 and chr19:10359299.

*Sequence variants that are not correlated (R^2<0.8) with, and significant after adjustment for, previously reported sequence variants for RA (Supplementary Table 1).

Bold indicates sequence variants that are supported by functional variant annotation, where the variant or correlated variant, R^2>0.8) are coding, associate with mRNA expression and/or plasma protein levels (summarized in Figure 2).

Abbreviations: EA: effect allele; OA: other allele; OR: odds ratio; P_{het}: a *P*-value for test of heterogeneity between the results in cohorts included in the meta-analysis.