Article:

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Table 2. Summary of the most highly associated regions at $P < 1 \times 10^{-5}$ identified in Phase 1 for each of the 4 traits analysed genome-wide.

					Phase 1				Phase 2a		Phase 2b		
Trait	**Marker**	**Chr**	**Position**	**Effect Allele**	**Allele Frequency**	**β^a (95% CI)**	**P-value**	**I^2 (%)**	**β^a (95% CI)**	**P-value**	**β^a (95% CI)**	**P-value**	**Genes^b**
DAS28	rs2372751	3	81124821	C	0.49	0.17 (0.10, 0.24)	2.8×10^{-6}	0	-0.02 (-0.14, 0.10)	0.77	0.13 (-0.08, 0.34)	0.23	*LINC02027*
	rs58840038	5	125773164	T	0.31	-0.17 (-0.24, -0.09)	8.0×10^{-6}	0	-0.04 (-0.16, 0.09)	0.57	0.03 (-0.16, 0.23)	0.73	*GRAMD3*
	rs6903359	6	21986214	C	0.13	-0.23 (-0.34, -0.13)	7.4×10^{-6}	0	0.07 (-0.12, 0.27)	0.46	0.10 (-0.17, 0.38)	0.45	*CASC15*
	rs168201	10	84610081	G	0.48	0.18 (0.12, 0.25)	9.8×10^{-8}	0	-0.10 (-0.21, 0.02)	0.091	0.08 (-0.10, 0.26)	0.38	*NRG3*
	rs57816977	18	4012466	C	0.18	-0.22 (-0.31, -0.12)	5.3×10^{-6}	0	0.12 (-0.03, 0.27)	0.10	0.00 (-0.24, 0.25)	1.00	*DLGAP1*
$\log_e$(CRP+1)	rs79244342	6	54660244	G	0.09	-0.26 (-0.37, -0.15)	3.3×10^{-6}	0	-0.05 (-0.24, 0.13)	0.57	0.02 (-0.34, 0.37)	0.93	*KRASP1*
	rs1889339	9	96053928	G	0.18	0.19 (0.11, 0.27)	5.7×10^{-6}	0	-0.06 (-0.20, 0.07)	0.38	0.17 (-0.05, 0.39)	0.14	*WNK2*
SJC28	rs35179427	1	95670888	A	0.08	0.21 (0.12, 0.30)	7.8×10^{-6}	0	-0.05 (-0.20, 0.09)	0.49	-0.25 (-0.54, 0.04)	0.10	*RWDD3* *TMEM56-RWDD3*
	rs1453301	2	138080695	A	0.16	0.15 (0.09, 0.22)	7.1×10^{-6}	0	-0.05 (-0.16, 0.06)	0.39	-0.03 (-0.22, 0.17)	0.79	*THSD7B*
	rs77458347	4	109896081	T	0.14	0.18 (0.10, 0.26)	6.7×10^{-6}	0	-0.02 (-0.14, 0.10)	0.77	0.18 (-0.10, 0.47)	0.21	*COL25A1*
	rs144940912	4	155092290	T	0.07	0.26 (0.15, 0.36)	1.4×10^{-6}	16	0.11 (-0.05, 0.27)	0.20	0.11 (-0.32, 0.53)	0.62	
	rs12663189	6	162730663	C	0.43	0.12 (0.07, 0.17)	2.0×10^{-6}	0	-0.01 (-0.09, 0.08)	0.87	0.04 (-0.12, 0.20)	0.64	*PARK2*
	rs314637	7	4421893	A	0.22	0.15 (0.08, 0.21)	2.9×10^{-6}	13	0.08 (-0.02, 0.18)	0.11	0.19 (-0.01, 0.38)	0.06	
	rs113798271	7	145059089	G	0.21	0.14 (0.08, 0.21)	9.4×10^{-6}	29	0.02 (-0.08, 0.12)	0.67	0.02 (-0.16, 0.21)	0.81	
	rs1175813	19	49737486	G	0.11	0.20 (0.12, 0.29)	1.4×10^{-6}	0	-0.15 (-0.27, -0.03)	0.012	0.00 (-0.24, 0.25)	0.98	
	rs1042579	20	23028724	A	0.23	0.15 (0.08, 0.21)	6.9×10^{-6}	0	0.02 (-0.09, 0.12)	0.76	0.24 (0.04, 0.44)	0.020	*THBD*
	rs2836915	21	40509189	T	0.31	-0.13 (-0.18, -0.07)	4.5×10^{-6}	0	-0.05 (-0.14, 0.04)	0.26	-0.06 (-0.24, 0.12)	0.51	

TJC28	rs10058818	5	56808696	G	0.21	0.17 (0.10, 0.25)	2.4×10^{-6}	8	0.06 (-0.06, 0.17)	0.31	-0.10 (-0.32, 0.12)	0.37	*LINCR-0003*
	rs10515242	5	95982675	C	0.06	0.28 (0.16, 0.40)	4.8×10^{-6}	0	0.17 (-0.01, 0.35)	0.069	-0.08 (-0.42, 0.26)	0.64	
	rs2026708	6	21986895	G	0.14	-0.22 (-0.31, -0.13)	1.9×10^{-6}	0	0.02 (-0.14, 0.19)	0.78	0.06 (-0.19, 0.30)	0.65	*CASC15*
	rs2776898	6	37541111	T	0.35	0.16 (0.10, 0.23)	9.9×10^{-7}	0	-0.11 (-0.21, -0.01)	0.027	0.14 (-0.03, 0.32)	0.11	
	rs114461403	7	16547268	T	0.33	0.15 (0.08, 0.21)	7.5×10^{-6}	0	0.00 (-0.11, 0.10)	0.98	-0.12 (-0.30, 0.07)	0.21	
	rs28442057	15	55110958	T	0.34	0.14 (0.08, 0.21)	7.9×10^{-6}	0	-0.01 (-0.11, 0.09)	0.82	0.04 (-0.15, 0.22)	0.68	
	rs12446816	16	14092341	G	0.38	0.15 (0.09, 0.21)	5.1×10^{-6}	0	-0.01 (-0.11, 0.08)	0.77	0.01 (-0.16, 0.17)	0.95	
	rs9910936	17	42949168	T	0.28	0.15 (0.09, 0.22)	6.7×10^{-6}	0	0.05 (-0.06, 0.16)	0.38	0.08 (-0.11, 0.28)	0.40	*CCDC103 EFTUD2 GFAP KIF18B*

Abbreviations: DAS28, disease activity score in 28 joints; CRP, C-reactive protein; SJC28, swollen joint count 28; TJC tender joint count 28; Chr chromosome; **β** beta; CI confidence interval; I^2 Heterogeneity statistic [a] Per-allele for change in outcome in number of standard deviations, positive values correspond to worse response. [b] SNP or supporting SNPs with $P<5x10^{-5}$ located within gene.