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Patient information

The post quality control (QC) United States (US) cohort comprised 222 US RF-positive polyarticular JIA patients and 4408 US controls. Clinics enrolling at least 5 JIA patients for Cincinnati-based studies (listed in order of number contributed) were located in Cincinnati, OH; Atlanta, GA; Columbus, OH; Little Rock, AR; Long Island, NY; Charlotte, NC; Cleveland, OH; Chicago, IL; Dover, DE; Nashville, TN; Philadelphia, PA; Milwaukee, WI; Toledo, OH; Charleston, SC; and Indianapolis, IN. Additional DNA from JIA cases collected independently by investigators in Salt Lake City, UT, Dallas, TX, Kansas City, MO and Boston, MA or enrolled as part of the Trial of Early Aggressive Therapy in Juvenile Idiopathic Arthritis (TREAT) study (clinical trials identifier NCT00443430) were made available for genotyping in Cincinnati.

The US controls were derived from four sources: healthy children without known major health conditions recruited from the geographical area served by Cincinnati Children's Hospital Medical Center (CCHMC) and healthy adults collected at CCHMC. Healthy adult controls from Utah screened for autoimmune diseases and all were included in the replication cohort of previous GWAS studies[1;2]. Healthy adult controls collected at the Oklahoma Medical Research Foundation; and healthy US adult controls from the Genotype and Phenotype registry (www.gapregistry.org) and the NIDDK IBD Genetics Consortium. Healthy controls from the Oklahoma Medical Research Foundation (OMRF) were provided by the Lupus Family Registry and Repository (LFRR)[3] and the Oklahoma Immune Cohort (OIC). Each individual completed the Connective Tissue Disease Screening Questionnaire (CSQ)[4] and individuals with a "probable" systemic rheumatic disease were excluded. Each individual was enrolled into these studies after appropriate written consent and IRB approval by the OMRF and the University of Oklahoma Health Sciences Center. Healthy controls were also provided from the University of Minnesota SLE sibship collection[5] and these subjects were enrolled after appropriate written consent and IRB approval by the University of Minnesota. The US collections and their use in genetic studies have been approved by the Institutional Review Board of CCHMC and each collaborating center.

The post QC United Kingdom (UK) cohort comprised 94 RF-positive polyarticular JIA patients from five sources: The British Society for Paediatric and Adolescent Rheumatology (BSPAR) National Repository of JIA; a cohort of UK patients with long-standing JIA, described previously[6]; a cohort collected as part of the Childhood Arthritis Prospective Study (CAPS), a prospective inception cohort study of JIA cases from 5 centers across UK[7]; a cohort of children recruited for the SPARKS-CHARM (Childhood Arthritis Response to Medication) study, who fulfil ILAR criteria for JIA and are about to start new disease-modifying medication for active arthritis[8] and an ongoing collection of UK cases, the UK JIA Genetics Consortium (UKJIAGC). JIA cases were classified according to ILAR criteria[9]. There

is overlap in the JIA cases used in this study and in previous UK candidate gene studies of JIA[10-13]. All UK JIA cases were recruited with ethical approval and provided informed consent [North-West Multi-Centre Research Ethics Committee (MREC 99/8/84), the University of Manchester Committee on the Ethics of Research on Human Beings and National Research Ethics Service (NRES 02/8/104)]. The UK controls comprised the shared UK 1958 Birth cohort and UK Blood Services Common Controls. The collection was established as part of the WTCCC[14].

The post QC German cohort comprised 1 German RF-positive polyarticular JIA patient and 480 controls. These cases have already been included as a replication cohort in a genome-wide association study and previously described. These patients were recruited from the German Center for Rheumatology in Children and Adolescents, Garmisch-Partenkirchen; the Department of Pediatrics, University of Tübingen; Children's Rheumatology Unit Sendenhorst, Germany; and the Department of Pediatrics, University of Prague, Czech Republic. JIA was determined retrospectively by chart review. German population-based control samples were prepared from cord blood obtained from healthy newborns in the Survey of Neonates in Pomerania (SNiP) consortium[15]. The respective Institutional Review Boards approved the collection of these samples and participation in this study.

The post QC Norwegian cohort comprised 13 Norwegian RF-positive polyarticular JIA patients and 945 controls. The patient cohort comprised consecutive cases of JIA from two defined geographical areas in Norway with disease onset from 2000-2012 and with available DNA samples. The study was an extended part of the Nordic JIA Study, a prospective, multicentre cohort study initiated by NoSPeR (Nordic Study group of Pediatric Rheumatology) as previously described[16]. The cohort aimed to be as close to population-based as possible, as centres participated only if they were able to include all children diagnosed with JIA in their catchment area. Approval from medical and health research ethical committees and data authorities were granted and informed consent obtained from parents and/or children according to national regulations. The Norwegian controls were from the second (1995-1997) or third (2006-2008) waves of the population-based Nord-Trøndelag Health Study (HUNT) (www.ntnu.edu/hunt). They were a random selection of participants who had answered "no" to questions of whether they had ever been given a diagnosis of rheumatoid arthritis or ankylosing spondylitis. All HUNT participants gave written, informed consent. The study was approved by the Regional Committee for Medical and Health Research Ethics, Central Norway, the Norwegian Data Inspectorate, and the Norwegian Department of Health.

The post QC Canadian Cohort comprised 10 Canadian RF-positive polyarticular JIA patients. The BBOP study (Biologically Based Outcome Predictors in JIA) is a multi-center inception cohort of

prospectively collected children with new onset JIA recruited from 11 Canadian Pediatric Rheumatology Programs. Children were included in the study if they satisfied the ILAR classification criteria, were within six months of disease onset, and were treatment-naïve for medications except for non-steroidal anti-inflammatory agents. Peripheral blood and saliva samples were collected and processed as per standardized protocol at enrolment and transported to the central biobank (The Hospital for Sick Children (SickKids), Toronto, ON). Informed consent for participation was obtained from parents and informed consent or assent was obtained from patients as applicable. The study was approved by the Research Ethics Board at each participating site.

Supplementary Table 1 Samples used in the wGRS analyses

	Cases	Controls
RF-positive polyarticular JIA	Total 340	Total 10147
	UK=94	UK=4337*
	US=222	US=4386
	Germany=1	Germany=480
	Norway=13	Norway=945
	Canada=10	
Early-onset RA (16-29 yrs)	UK=370	UK=4338[#]
Later-onset RA (≥70 yrs)	UK=259	UK=4338[#]

*These 4337 UK controls are unique compared to the [#]4338 used in the RA analysis.

Supplementary Table 2 Association results in RF-positive polyarticular JIA of the 27 non-HLA SNPs most strongly associated with RF-negative polyarticular and oligoarticular JIA

SNP	Chr	Position	Gene Region	RF-poJIA minor allele	RF-poJIA risk allele	reference allele	MAF RF-poJIA	MAF controls	MAF RF+pJIA	RF-poJIA OR	RF-poJIA CI	best p-value RF+pJIA	Model	RF+pJIA OR	RF+pJIA CI
rs4648881	1	25197155	*RUNX3*	G	G	G	0.47	0.49	0.51	1.16	1.1-1.23	0.91	add	1.01	0.87-1.18
rs6679677	**1**	**114303808**	***PTPN22***	**A**	**A**	**A**	**0.14**	**0.10**	**0.15**	**1.59**	**1.45-1.73**	**1.21E-06**	**dom**	**1.83**	**1.43-2.33**
rs11265608	1	154364140	*ATP8B2 | IL6R*	A	A	A	0.12	0.10	0.12	1.28	1.16-1.4	0.17	add	1.18	0.93-1.49
rs6740838	2	100813499	*AFF3 | LONRF2*	A	A	A	0.43	0.39	0.42	1.25	1.14-1.37	0.20	add	1.11	0.95-1.29
rs10174238	2	191973034	*STAT4*	G	G	G	0.28	0.23	0.27	1.29	1.2-1.37	0.08	add	1.17	0.98-1.39
rs79893749	**3**	**46253650**	***CCR1 | CCR3***	**A**	**G**	**A**	**0.12**	**0.15**	**0.11**	**0.79**	**0.72-0.86**	**0.009**	**add**	**0.72**	**0.56-0.92**
rs4688013	3	119229486	*TIMMDC1 | CD80*	A	A	A	0.22	0.19	0.17	1.20	1.12-1.29	0.16	add	0.86	0.7-1.06
rs1479924	4	123387600	*IL2 | IL21*	G	A	G	0.24	0.29	0.29	0.80	0.74-0.85	0.91	add	1.01	0.85-1.2
rs71624119	**5**	**55440730**	***ANKRD55***	**A**	**G**	**A**	**0.20**	**0.25**	**0.19**	**0.78**	**0.73-0.84**	**0.003**	**add**	**0.74**	**0.61-0.9**
rs27290	5	96350088	*ERAP2 | LNPEP*	G	G	G	0.47	0.44	0.43	1.32	1.2-1.45	0.98	add	1.00	0.86-1.16
rs4705862	5	131813219	*C5orf56 | IRF1*	T	A	T	0.39	0.44	0.43	0.84	0.79-0.89	0.78	add	0.98	0.84-1.14
rs7808122	7	22798080	*IL6*	A	A	A	0.48	0.44	0.41	1.18	1.11-1.25	0.46	add	0.94	0.81-1.1
rs10280937	7	28182306	*JAZF1*	G	G	G	0.13	0.11	0.11	1.25	1.14-1.37	0.82	add	0.97	0.76-1.24
rs7909519	10	6089841	*IL2RA*	C	A	C	0.08	0.11	0.08	0.72	0.64-0.8	0.08	add	0.78	0.6-1.03
rs7069750	10	90762376	*FAS*	C	C	C	0.48	0.44	0.43	1.18	1.11-1.25	0.74	add	0.97	0.83-1.14
rs4755450	11	36363575	*PRR5L*	A	G	A	0.31	0.35	0.33	0.85	0.8-0.91	0.37	add	0.93	0.79-1.09
rs2364480	12	6495275	*LTBR*	C	C	C	0.28	0.25	0.24	1.20	1.12-1.28	0.31	add	0.91	0.76-1.09
rs3184504	**12**	**111884608**	***SH2B3 | ATXN2***	**A**	**A**	**A**	**0.54**	**0.49**	**0.53**	**1.20**	**1.13-1.27**	**0.01**	**add**	**1.22**	**1.04-1.42**
rs7993214	13	40350912	*COG6*	A	G	A	0.31	0.35	0.32	0.84	0.79-0.9	0.23	add	0.91	0.77-1.07
rs34132030	13	43056036	*13q14*	A	A	A	0.32	0.29	0.31	1.18	1.11-1.26	0.13	add	1.14	0.96-1.34
rs12434551	14	69253364	*ZFP36L1*	A	T	A	0.43	0.47	0.45	0.85	0.8-0.9	0.30	add	0.92	0.79-1.07
rs66718203	**16**	**11428643**	***PRM1 | RMI2***	**C**	**G**	**C**	**0.14**	**0.18**	**0.14**	**0.81**	**0.74-0.88**	**0.006**	**add**	**0.73**	**0.58-0.91**

rs2847293	18	12782448	*PTPN2*	A	A	A	0.20	0.17	0.18	1.31	1.22-1.4	0.32	add	1.11	0.91-1.36
rs34536443	**19**	**10463118**	***TYK2***	**G**	**C**	**G**	**0.03**	**0.05**	**0.02**	**0.56**	**0.47-0.67**	**0.01**	**add**	**0.53**	**0.33-0.88**
rs9979383	21	36715761	*RUNX1*	G	A	G	0.33	0.37	0.39	0.78	0.72-0.85	0.37	add	1.07	0.92-1.26
rs2266959	22	21922904	*UBE2L3*	A	A	A	0.22	0.19	0.21	1.24	1.15-1.33	0.41	add	1.08	0.9-1.31
rs2284033	22	37534034	*IL2RB*	A	G	A	0.39	0.44	0.43	0.84	0.79-0.89	0.70	add	0.97	0.83-1.13

RF-poJIA=RF-negative polyarticular and oligoarticular JIA, RF+pJIA=RF-positive polyarticular JIA, Chr=chromosome, SNP=single nucleotide polymorphism, MAF=minor allele frequency, dom=dominant, add=additive, OR=odds ratio, CI=confidence interval. Regions with p-value <0.05 are highlighted in bold.

Supplementary Table 3 Association results in RF-positive polyarticular JIA of the 44 non-HLA SNPs most strongly associated with RA

SNP	Chr	Position	Gene region	RA risk allele	RF+ pJIA ref allele	MAF RF+ pJIA	MAF controls	RA OR	RF+ pJIA best pvalue	Model	OR	CI
rs2843401	**1**	**2517993**	***MMEL1***	**A**	**A**	**0.27**	**0.33**	**0.87**	**5.05E-04**	**add**	**0.74**	**0.62-0.87**
rs2240336	**1**	**17546989**	***PADI4***	**A**	**A**	**0.38**	**0.42**	**0.88**	**1.96E-02**	**add**	**0.83**	**0.71-0.97**
rs883220	1	38389458	*POU3F1*	A	A	0.24	0.25	0.89	6.05E-01	add	0.95	0.8-1.14
rs2476601	**1**	**114179091**	***PTPN22***	**A**	**A**	**0.15**	**0.1**	**1.78**	**1.30E-06**	**dom**	**1.83**	**1.43-2.33**
rs798000	1	117082219	*CD2*	G	G	0.33	0.32	1.11	3.85E-01	add	1.07	0.91-1.26
rs8192284	**1**	**152693594**	***IL6R***	**C**	**C**	**0.36**	**0.41**	**0.9**	**1.68E-02**	**add**	**0.82**	**0.7-0.97**
rs10494360	1	159742374	*FCGR2A*	G	A	0.11	0.12	1.14	2.48E-01	add	0.86	0.67-1.11
rs2014863	1	197076224	*PTPRC*	C	G	0.38	0.37	1.09	4.77E-01	add	1.06	0.9-1.24
rs34695944	2	60978354	*REL*	G	G	0.37	0.37	1.13	4.30E-01	add	1.07	0.91-1.25
rs6546146	2	65409828	*SPRED2*	A	A	0.37	0.37	0.9	7.49E-01	add	0.97	0.83-1.14
rs10209110	2	100039124	*AFF3*	A	A	0.49	0.5	0.9	6.46E-01	add	0.96	0.83-1.12
rs13426947	2	191641499	*STAT4*	A	A	0.22	0.19	1.15	9.22E-02	add	1.17	0.97-1.42
rs11571302	**2**	**204451179**	***CTLA4***	**A**	**A**	**0.43**	**0.47**	**0.89**	**2.41E-02**	**add**	**0.84**	**0.72-0.98**
rs1980422	**2**	**204318641**	***CD28***	**G**	**G**	**0.27**	**0.23**	**1.12**	**2.36E-02**	**add**	**1.22**	**1.03-1.45**
rs35677470	3	58158676	*DNASE1L3*	A	A	0.08	0.08	1.19	9.51E-01	add	1.01	0.76-1.35
rs932036	**4**	**25699960**	***RBPJ***	**A**	**T**	**0.33**	**0.3**	**1.14**	**4.29E-02**	**add**	**1.18**	**1.01-1.39**
rs78560100	4	123260921	*IL2-IL21*	C	C	0.08	0.07	1.13	3.94E-01	add	1.13	0.85-1.5
rs71624119	**5**	**55476487**	***ANKRD55***	**A**	**A**	**0.19**	**0.24**	**0.81**	**2.91E-03**	**add**	**0.74**	**0.61-0.9**
rs39984	5	102625191	*GIN1*	A	A	0.29	0.32	0.88	1.15E-01	add	0.87	0.73-1.03
rs6911690	6	106577656	*PRDM1*	G	G	0.11	0.11	0.87	8.16E-01	add	0.97	0.76-1.24
rs6920220	**6**	**138048197**	***TNFAIP3***	**A**	**A**	**0.25**	**0.22**	**1.2**	**4.42E-03**	**add**	**1.29**	**1.08-1.54**
rs629326	6	159416701	*TAGAP*	C	C	0.4	0.41	0.9	4.65E-01	add	0.94	0.81-1.1
rs59466457	**6**	**167457744**	***CCR6***	**A**	**A**	**0.51**	**0.44**	**1.15**	**4.37E-04**	**add**	**1.32**	**1.13-1.54**
rs3807306	**7**	**128367916**	***IRF5***	**C**	**A**	**0.56**	**0.49**	**0.89**	**6.46E-04**	**add**	**1.31**	**1.12-1.53**

rs4840565	**8**	**11382954**	***BLK***	**G**	**G**	**0.34**	**0.27**	**1.1**	**5.31E-04**	**add**	**1.33**	**1.13-1.57**
rs2812378	9	34700260	*CCL21*	G	G	0.38	0.34	1.15	5.87E-02	add	1.16	0.99-1.36
rs10739580	9	122735103	*TRAF1*	G	G	0.35	0.35	1.12	8.86E-01	add	1.01	0.86-1.19
rs10795791	**10**	**6148346**	***IL2RA***	**G**	**G**	**0.46**	**0.41**	**1.09**	**2.02E-02**	**add**	**1.2**	**1.03-1.4**
rs947474	10	6430456	*PRKCQ*	G	G	0.18	0.19	0.9	9.14E-01	add	0.99	0.81-1.2
rs2275806	**10**	**8135346**	***GATA3***	**G**	**G**	**0.48**	**0.43**	**1.11**	**2.36E-02**	**add**	**1.19**	**1.02-1.39**
rs12764378	10	63470010	*ARID5B*	A	A	0.25	0.22	1.14	1.06E-01	add	1.16	0.97-1.38
rs570676	11	36448767	*TRAF6*	A	A	0.38	0.39	0.93	4.80E-01	add	0.94	0.81-1.11
rs595158	11	60666157	*CD5*	C	A	0.51	0.5	1.09	6.51E-01	add	1.04	0.89-1.21
rs4938573	**11**	**118247052**	***DDX6***	**G**	**G**	**0.15**	**0.19**	**0.87**	**3.44E-03**	**add**	**0.72**	**0.58-0.9**
rs8043085	15	36615432	*RASGRP1*	A	A	0.23	0.24	1.17	3.67E-01	add	0.92	0.77-1.1
rs8026898	**15**	**67778471**	***TLE3***	**A**	**A**	**0.31**	**0.27**	**1.17**	**2.09E-02**	**add**	**1.22**	**1.03-1.44**
rs13330176	16	84576588	*IRF8*	A	A	0.27	0.23	1.15	7.74E-02	add	1.17	0.98-1.39
rs12936409	17	35297175	*IKZF3*	A	A	0.48	0.47	1.1	2.54E-01	add	1.09	0.94-1.28
rs34536443	**19**	**10324118**	***TYK2***	**G**	**G**	**0.02**	**0.05**	**0.62**	**1.36E-02**	**add**	**0.53**	**0.33-0.88**
rs6032662	20	44167717	*CD40*	G	G	0.23	0.25	0.86	4.28E-01	add	0.93	0.77-1.12
rs2834512	21	34833469	*RCAN1*	A	A	0.11	0.12	0.86	2.58E-01	add	0.87	0.68-1.11
rs9979383	21	35637631	*RUNX1*	G	G	0.39	0.37	0.9	3.71E-01	add	1.07	0.92-1.26
rs3218251	**22**	**35875451**	***IL2RB***	**A**	**A**	**0.29**	**0.26**	**1.13**	**3.88E-02**	**add**	**1.19**	**1.01-1.41**
rs13397*	**23**	**153248248**	***IRAK1***	**A**	**A**	**0.18**	**0.12**	**1.27**	**1.49E-02**	**add**	**1.37**	

This list does not include *HLA* and *KIF5A* region, the latter is a deletion polymorphism and not analysed in this study.

RF-poJIA=RF-negative polyarticular and oligoarticular JIA, RF+pJIA=RF-positive polyarticular JIA, Chr=chromosome, SNP=single nucleotide polymorphism, MAF=minor allele frequency, dom=dominant, add=additive, OR=odds ratio, CI=confidence interval.

* MAF for this SNP is for females only. The p-value and OR are from the meta-analysis of females and male cohorts. Regions with p-value <0.05 are highlighted in bold.

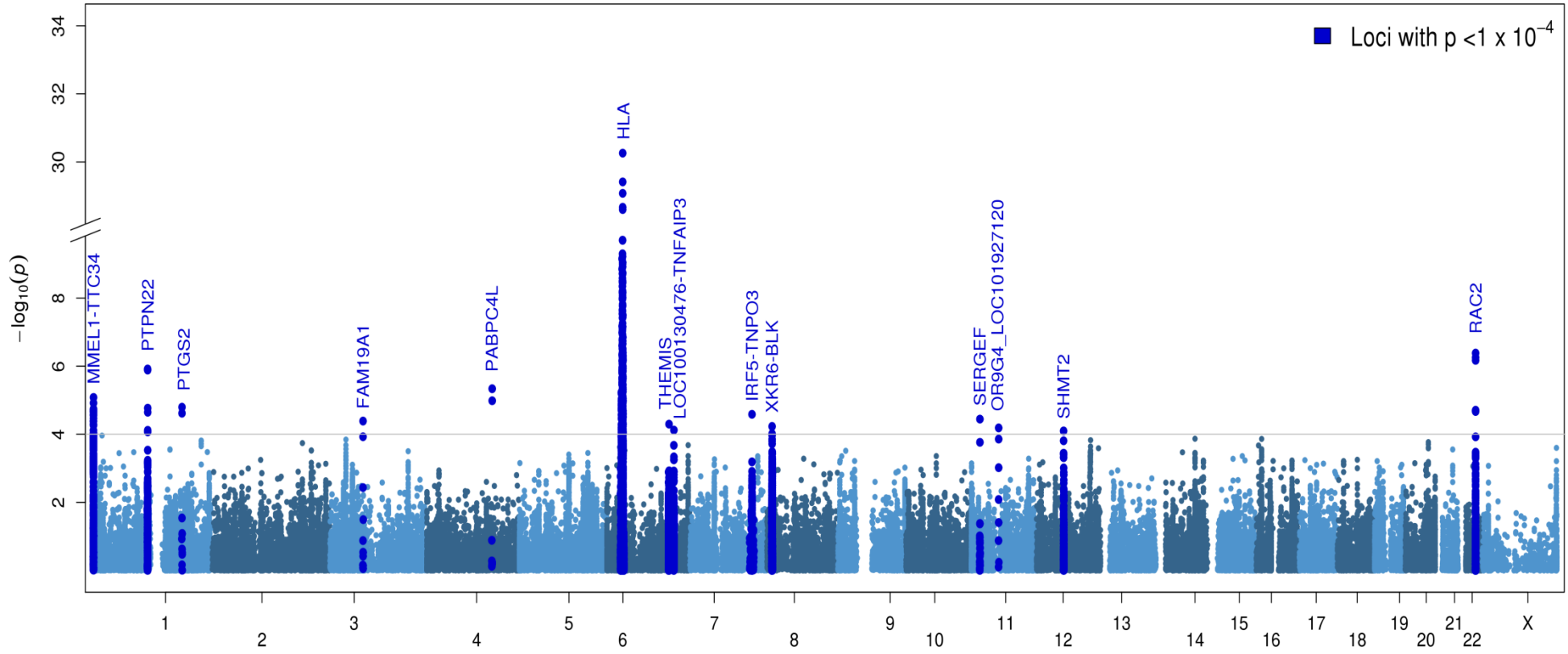
Supplementary Table 4 Most significant associations in RF-positive polyarticular JIA

Gene Region	Most Significant SNP	Chr	Position[a]	Ref. Allele	RAF Cases	RAF Controls	*P* value	Model	OR (95% CI)	SNP Location
MMEL1-TTC34	rs7526311	1	2697298	T	0.50	0.43	1.21×10^{-5}	Dominant	1.81 (1.39-2.35)	INTERGENIC
PTPN22	rs6679677	1	114303808	A	0.15	0.10	1.21×10^{-6}	Dominant	1.83 (1.43-2.33)	INTERGENIC
PTGS2	rs6681231	1	186659859	C	0.22	0.16	1.60×10^{-5}	Additive	1.51 (1.25-1.81)	INTERGENIC
PTGS2	rs20432[b]	1	186646323	C	0.21	0.15	7.13×10^{-6}	Additive	1.63 (1.32-2.02)	INTRON
FAM19A1	rs7617075	3	68240106	T	0.14	0.20	4.09×10^{-5}	Dominant	0.59 (0.46-0.76)	INTRON
PABPC4L	rs970036	4	135040295	G	0.47	0.43	4.59×10^{-6}	Recessive	1.78 (1.39-2.28)	INTERGENIC
THEMIS	rs62425513	6	128077738	T	0.22	0.16	5.03×10^{-5}	Additive	1.47 (1.22-1.78)	INTRON
LOC100130476-TNFAIP3	rs610366	6	138139694	G	0.09	0.15	7.52×10^{-5}	Dominant	0.56 (0.42-0.75)	INTERGENIC
IRF5-TNPO3	rs4731531	7	128562647	A	0.54	0.46	2.60×10^{-5}	Additive	1.39 (1.19-1.62)	INTERGENIC
XKR6 - BLK	rs9657519	8	10945439	A	0.56	0.49	5.89×10^{-5}	Recessive	1.60 (1.27-2.02)	INTRON (XKR6)
SERGEF	rs2158395	11	17828930	G	0.27	0.35	3.59×10^{-5}	Additive	0.70 (0.59-0.83)	INTRON
SERGEF	rs4757590[b]	11	17822569	C	0.26	0.34	2.23×10^{-5}	Additive	0.70 (0.60-0.83)	INTRON
OR9G4-LOC101927120	rs11228824	11	56634316	A	0.24	0.19	6.50×10^{-5}	Additive	1.45 (1.21-1.73)	INTERGENIC
SHMT2	rs2229717	12	57627074	T	0.06	0.03	7.98×10^{-5}	Dominant	1.99 (1.42-2.81)	SYNONYMOUS CODING
SHMT2	rs28365862[b]	12	57623363	G	0.07	0.04	3.92×10^{-5}	Additive	2.38 (1.58-3.61)	INTERGENIC
RAC2	rs9610687	22	37642869	A	0.25	0.34	4.14×10^{-7}	Dominant	0.57 (0.45-0.71)	INTERGENIC

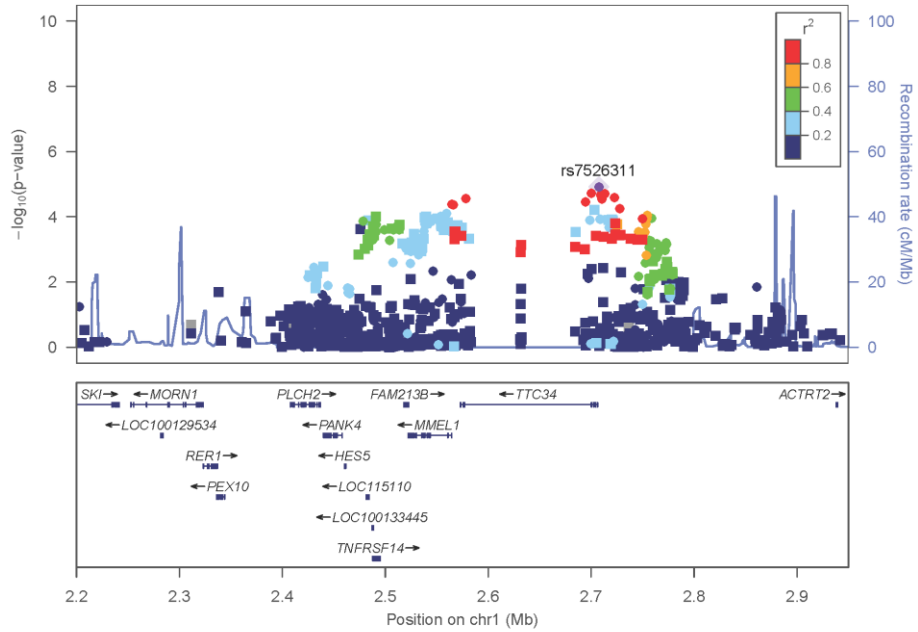
Chr., chromosome; Ref., reference; RAF, reference allele frequency; OR, odds ratio; CI, confidence interval; FDR, false discovery rate.

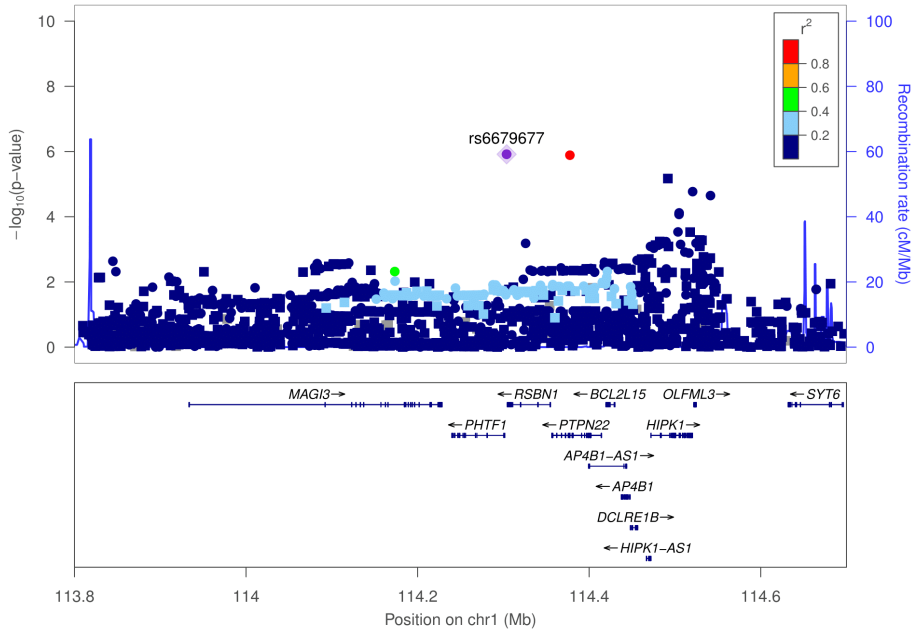
[a]Coordinates are based on the GRCh37 assembly. [b]Imputed SNP results are included when the imputed [b]SNP had a better imputed *P* value than the most significant directly genotyped SNP in the region.

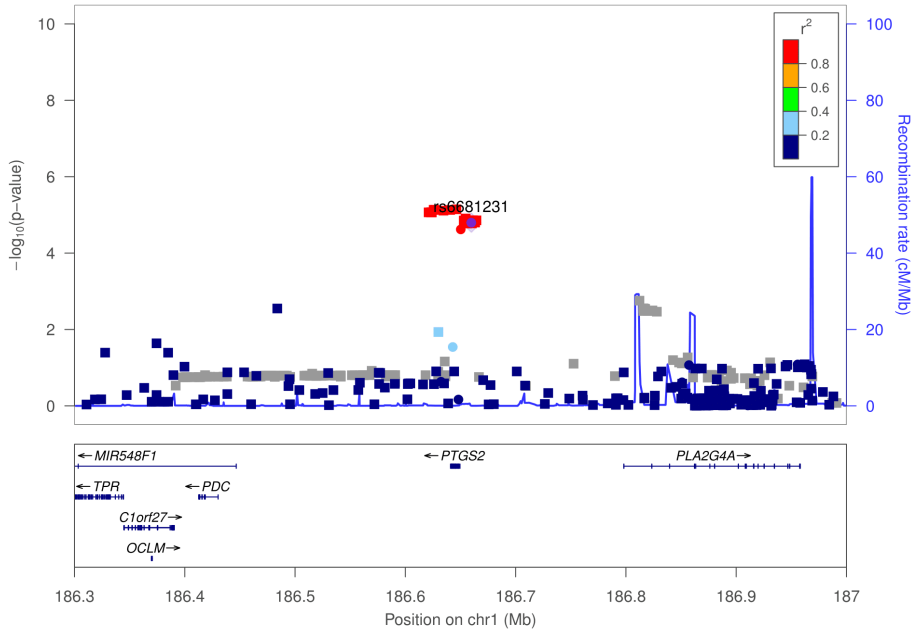
Supplementary Figure 1 Manhattan plot of association statistics for RF-positive polyarticular JIA risk loci

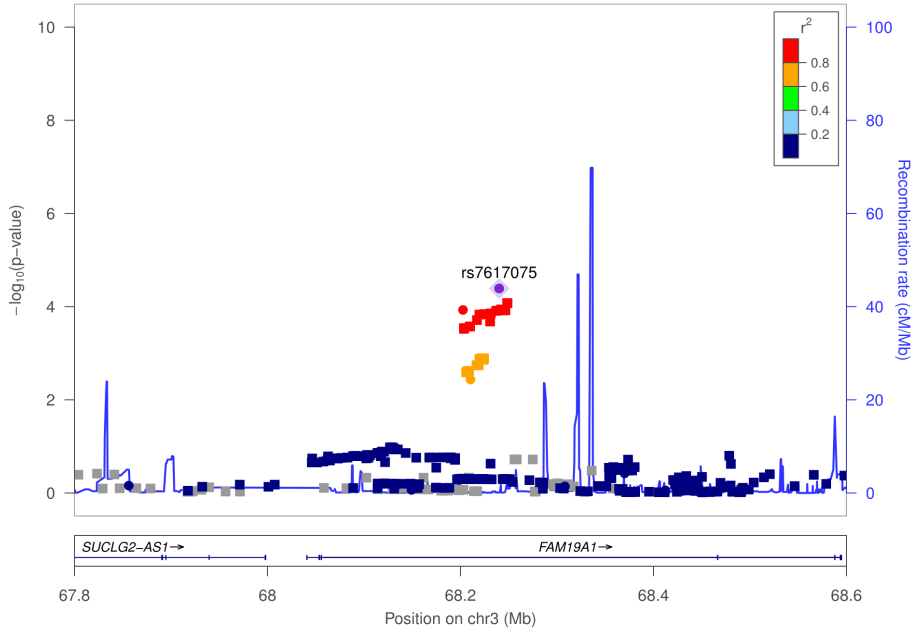


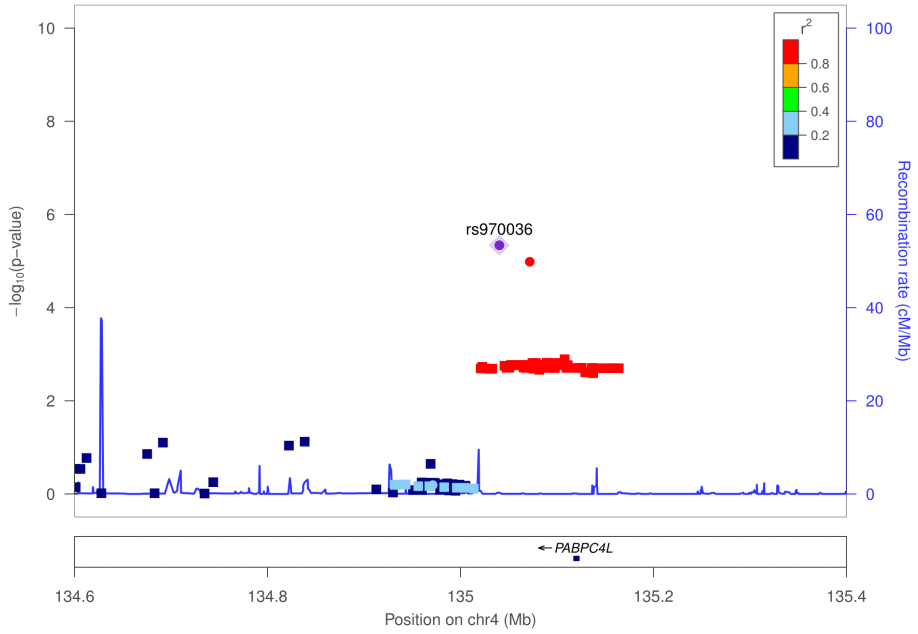
Supplementary Figure 2 Regional association plots for the most significant associations in RF-positive polyarticular JIA

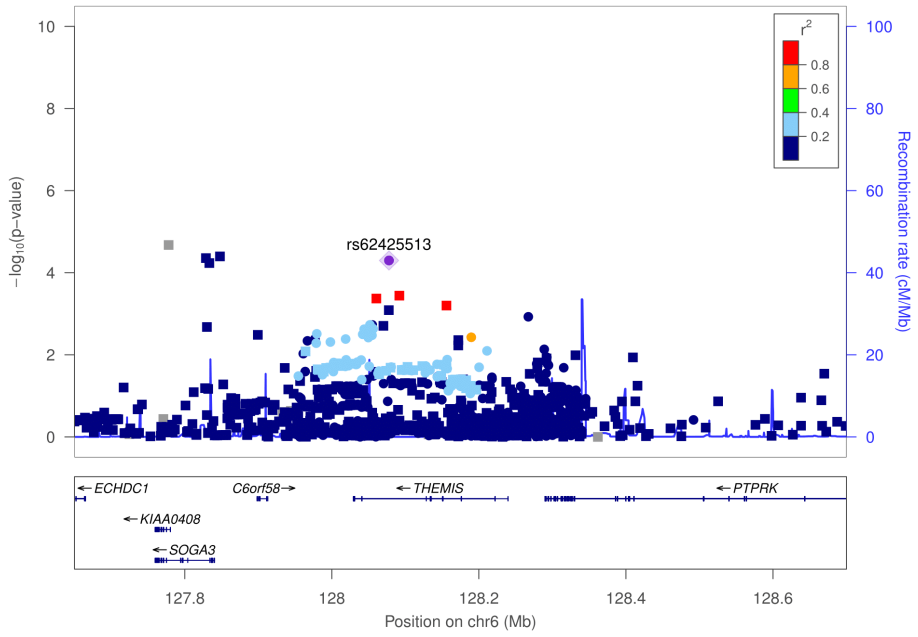


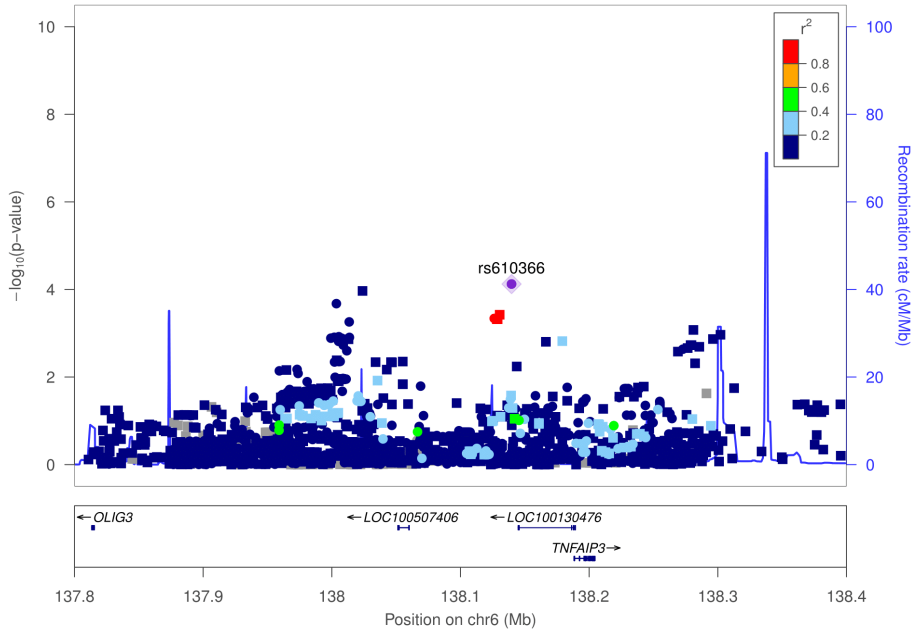


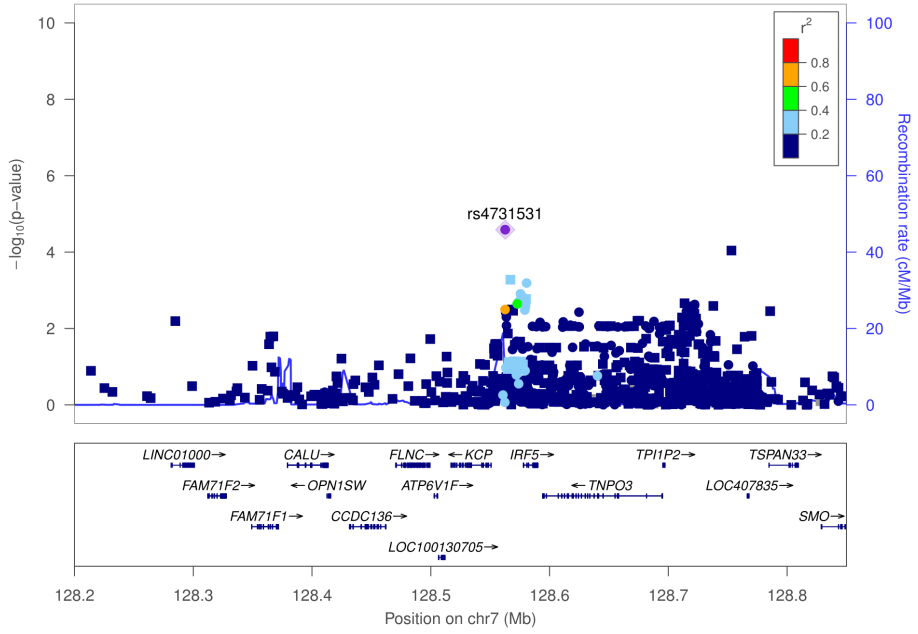

rs6681231
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
MIR548F1
PTGS2
PLA2G4A
TPR
PDC
C1orf27
OCLM
Position on chr1 (Mb)

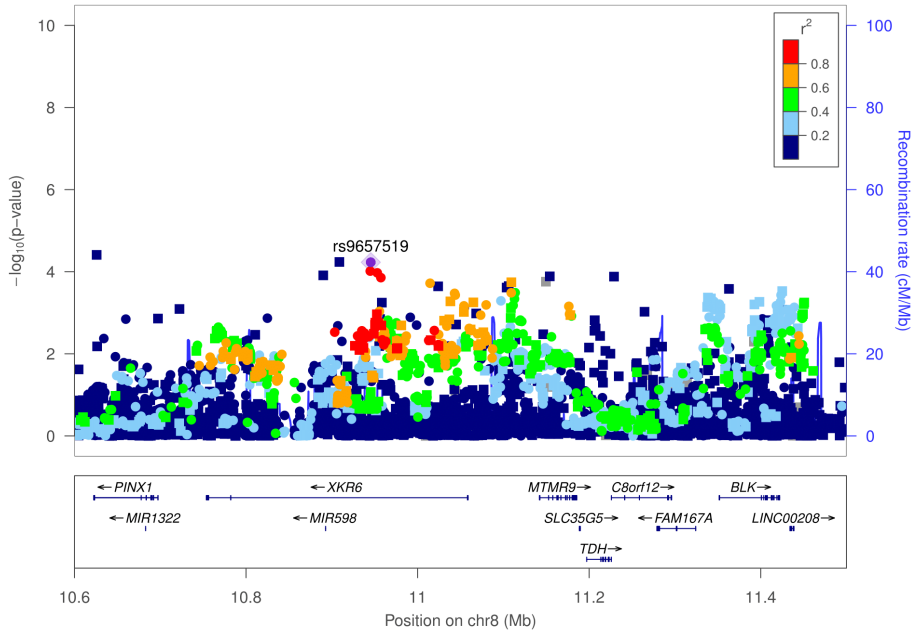

rs7617075
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SUCLG2−AS1
FAM19A1
Position on chr3 (Mb)

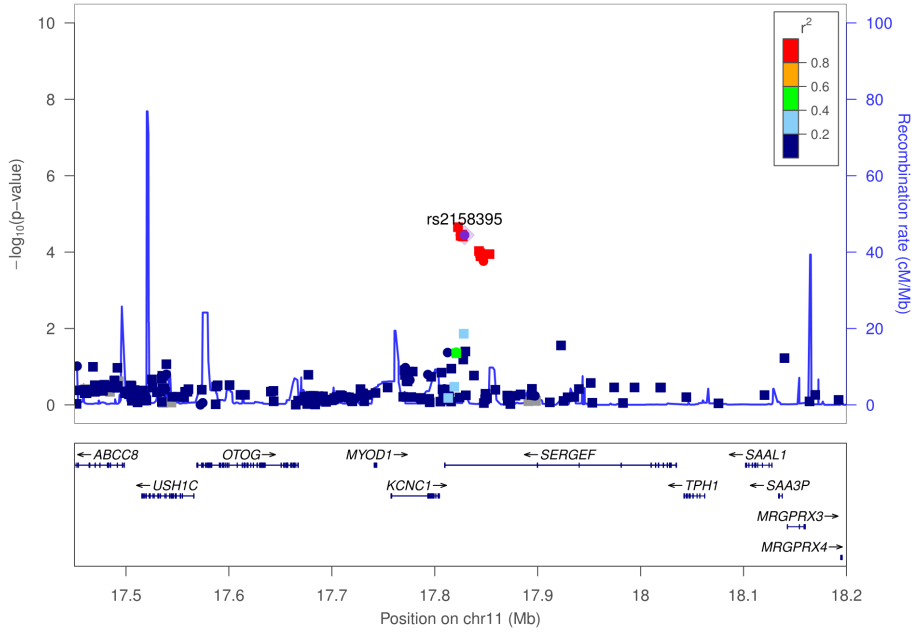

rs970036
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
PABPC4L
134.6
134.8
135
135.2
135.4
Position on chr4 (Mb)

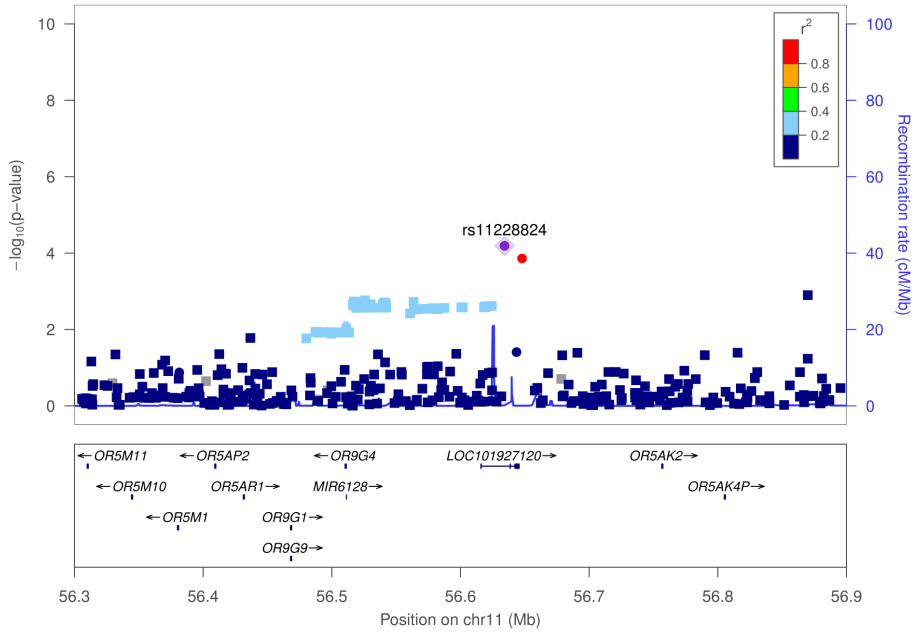

rs62425513
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ECHDC1
C6orf58
THEMIS
PTPRK
KIAA0408
SOGA3
127.8
128
128.2
128.4
128.6
Position on chr6 (Mb)

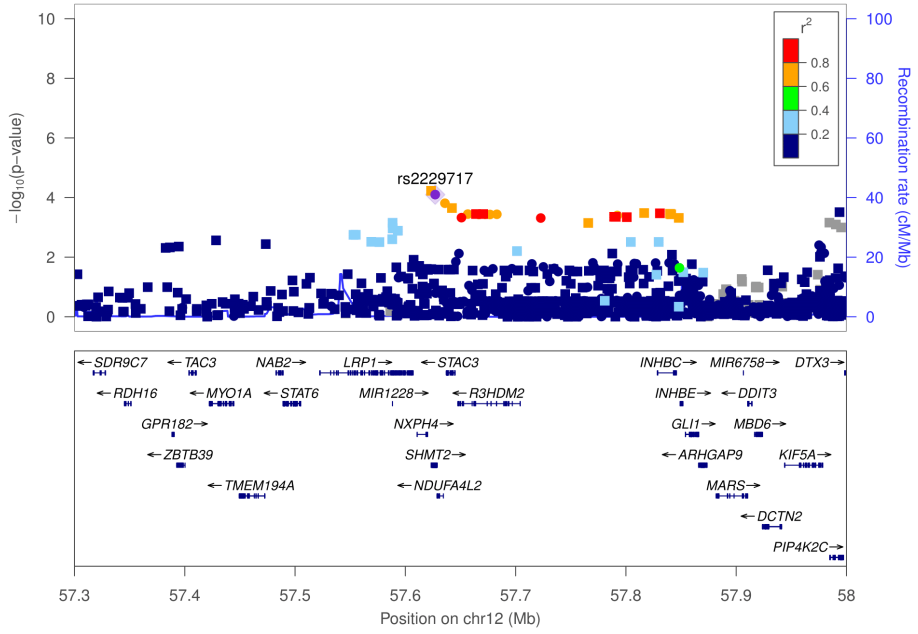

rs610366
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
OLIG3
LOC100507406
LOC100130476
TNFAIP3
Position on chr6 (Mb)

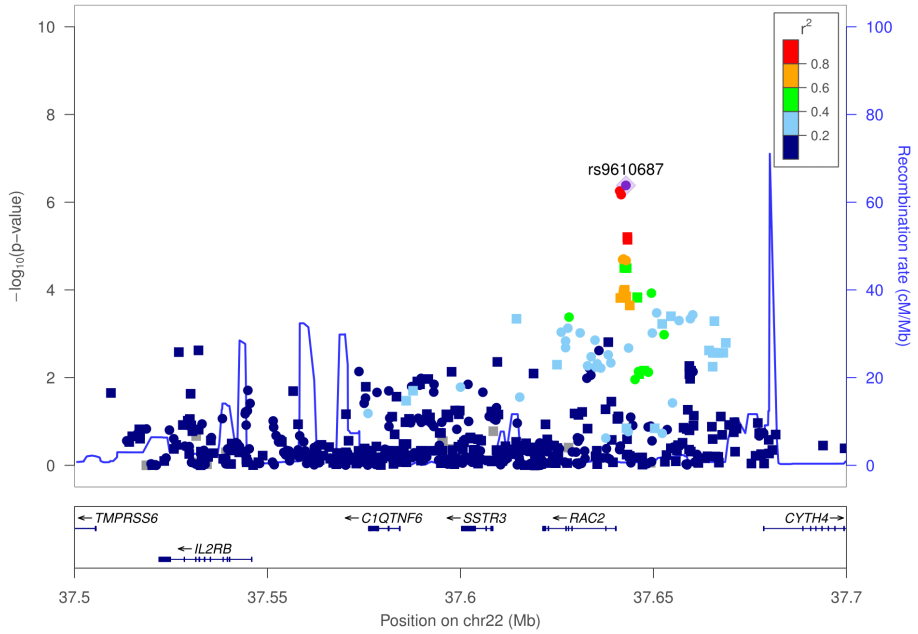

rs4731531
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
LINC01000
CALU
FLNC
KCP
IRF5
TPI1P2
TSPAN33
FAM71F2
OPN1SW
ATP6V1F
TNPO3
LOC407835
FAM71F1
CCDC136
SMO
LOC100130705
Position on chr7 (Mb)


rs9657519
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
PINX1
XKR6
MTMR9
C8orf12
BLK
MIR1322
MIR598
SLC35G5
FAM167A
LINC00208
TDH
Position on chr8 (Mb)


rs2158395
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
ABCC8
OTOG
MYOD1
SERGEF
SAAL1
USH1C
KCNC1
TPH1
SAA3P
MRGPRX3
MRGPRX4
Position on chr11 (Mb)


rs11228824
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
OR5M11
OR5AP2
OR9G4
LOC101927120
OR5AK2
OR5M10
OR5AR1
MIR6128
OR5AK4P
OR5M1
OR9G1
OR9G9
Position on chr11 (Mb)


rs2229717
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
SDR9C7
TAC3
NAB2
LRP1
STAC3
INHBC
MIR6758
DTX3
RDH16
MYO1A
STAT6
MIR1228
R3HDM2
INHBE
DDIT3
GPR182
NXPH4
GLI1
MBD6
ZBTB39
SHMT2
ARHGAP9
KIF5A
TMEM194A
NDUFA4L2
MARS
DCTN2
PIP4K2C
Position on chr12 (Mb)



Regional association plots, generated using LocusZoom, for the 13 regions associated with JIA ($P<1 \times 10^{-4}$) on the left x axis is the –log10 p-value for the SNPs across the region, on the right x axis is the recombination rate across the region and on the y axis is the chromosomal position (Mb). Coordinates are based on the NCBI37 assembly. The SNPs that are genotyped are represented by circles, the SNPs that are imputed by squares. The dots/squares are coloured according to LD (r^2) with the top SNP.

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