Supplementary Table 1. Summary of SNP and sample quality control for each genotype array used in Phase 1 and 2

	Phase 1			Phase 2a	Phase 2b	
	OmniExpressExome	**CoreExome**	**Immunochip**	**PromiSERA Sequencing**	**1M-Duo-v3**	**Omni1-Quad-v1-0**
Genotyped SNPs	964193	547644	196524	NA	1199187	1140419
Failed	88939	26265	10051	NA	64730	1900001
MAF<1%	248861	237203	49334	NA	154023	162448
Final SNP Total for imputation	626393	284176	137139	NA	980434	787970
SNPs with MAF>5% & INFO>0.8 post imputation	**5707255**	**5690412**	**926912**	**NA**	**5742906**	**5689816**
Genotyped Samples	1152	694	560	449[a]	263	2023
Call rate	7	3	10	NA	0	15
Gender	18	0	2	NA	0	5
IBD (Relatedness/Duplicate samples)	18	3	4	NA	0	34
PCA (Non-European ancestry)	109	101	20	1	18	69
non-MTX	83	110	261	0	152	1808
High dose steroid	0	0	102	0	0	0
Incomplete clinical data	146	24	9	20	8	0
Final Sample Total	**823**	**453**	**148**	**429**	**85**	**92**

[a] Samples sequenced, not genotyped

Supplementary Table 2. Summary of the Methotrexate metabolism candidate genes selection

Gene	cytoband	Pathway	Full name	Position Start (bp)	Position End (bp)	SNPs Tested
MTHFR	1p36.22	Folate metabolism	methylenetetrahydrofolate reductase (NAD(P)H)	11845787	11866160	69
AMPD1	1p13.2	Adenosine metabolism	adenosine A3 receptor	112025970	112106597	217
ADORA3	1p13.2	Adenosine signalling	adenosine monophosphate deaminase 1	115215719	115238239	43
ADORA1	1q32.1	Adenosine signalling	adenosine A1 receptor	203096836	203136533	76
MTR	1q43	Homocysteine metabolism	5-methyltetrahydrofolate-homocysteine methyltransferase	236958581	237067281	185
ATIC	2q35	Adenosine accumulation	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	216176679	216214496	107
PPAT	4q12	De novo purine synthesis	phosphoribosyl pyrophosphate amidotransferase	57259528	57301802	80
ABCG2	4q22.1	MTX transport	ATP-binding cassette, sub-family G (WHITE), member 2	89011416	89152474	329
MTRR	5p15.31	Homocysteine metabolism	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	7869217	7901237	80
DHFR	5q14.1	Folate metabolism	dihydrofolate reductase	79922045	79950800	140
TPMT	6p22.3	Purine metabolism	thiopurine S-methyltransferase	18128542	18155374	52
SLC29A1	6p21.1	Adenosine transport	solute carrier family 29 (nucleoside transporters), member 1	44187242	44201888	17
NT5E	6q14.3	Adenosine metabolism	5'-nucleotidase, ecto (CD73)	86159302	86205509	48
ABCB1	7q21.12	MTX transport	ATP-binding cassette, sub-family B (MDR/TAP), member 1	87133179	87342639	215
GGH	8q12.3	MTX metabolism	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	63927638	63951610	84
FPGS	9q34.11	MTX metabolism	folylpolyglutamate synthase	130565154	130576556	7
ADK	10q22.2	Adenosine metabolism	adenosine kinase	75910943	76469061	643
ABCC2	10q24.2	MTX transport	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	101542463	101611662	100
MTHFD1	14q23.2	Folate metabolism	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	64854759	64926725	115
MTHFS	15q25.1	Folate metabolism	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	80135889	80189627	117
ADORA2B	17p12	Adenosine signalling	adenosine A2b receptor	15848231	15879210	10
SHMT1	17p11.2	Folate metabolism	serine hydroxymethyltransferase 1 (soluble)	18231187	18266856	91
TYMS	18p11.32	Folate metabolism	thymidylate synthetase	657604	673499	64
ITPA	20p13	Purine metabolism	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	3189514	3204516	63
ADA	20q13.12	Adenosine accumulation	adenosine deaminase	43248163	43280376	41
GART	21q22.11	Adenosine accumulation	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	34876238	34915198	40
CBS	21q22.3	Homocysteine metabolism	cystathionine-beta-synthase	44473301	44496472	68
SLC19A1	21q22.3	MTX transport	solute carrier family 19 (folate transporter), member 1	46934629	46962385	56
ADORA2A	22q11.23	Adenosine signalling	adenosine A2a receptor	24823530	24838325	11

Supplementary Table 3. Mean baseline and follow-up measures for each of the 4 traits by study

				Mean (SD) clinical measurement															
				DAS28				SJC28				TJC28				CRP			
Study	**Origin**	**Genotype Array**	**N**	**Baseline**		**Follow-up**		**Baseline**		**Follow-up**		**Baseline**		**Follow-up**		**Baseline**		**Follow-up**	
Phase 1																			
YEAR	UK	OmniExpressExome-8v1-2	343	5.0	(1.2)	3.8	(1.4)	8.7	(6.7)	3.6	(4.6)	10.8	(7.8)	6.9	(7.8)	30.7	(39.4)	15.2	(23.6)
TEAR[a]	US	OmniExpressExome-8v1-2	117	5.6	(1.0)	4.0	(1.4)	12.4	(5.8)	5.7	(5.5)	13.7	(6.8)	6.5	(6.8)				
SWEFOT	Sweden	OmniExpressExome-8v1-2	325	5.1	(0.9)	3.6	(1.2)	10.6	(5.2)	4.7	(4.8)	9.4	(6.0)	4.5	(4.9)	34.9	(39.4)	15.4	(23.4)
Netherlands	Netherlands	OmniExpressExome-8v1-2	38	4.6	(1.2)	3.5	(1.2)	7.9	(5.6)	3.7	(3.8)	10.3	(7.4)	6.0	(6.3)	15.9	(22.1)	6.0	(8.3)
RAMS	UK	CoreExome-24-v1-0	274	4.4	(1.2)	3.4	(1.1)	7.5	(6.1)	3.1	(4.1)	9.5	(7.8)	5.3	(6.0)	14.4	(21.7)	8.9	(14.3)
IDEA	UK	CoreExome-24-v1-0	29	4.9	(1.3)	3.0	(1.2)	6.8	(4.7)	1.7	(2.7)	11.3	(7.5)	3.7	(6.0)	32.4	(48.1)	7.5	(11.3)
IACON	UK	CoreExome-24-v1-0	128	4.3	(1.3)	3.0	(1.2)	5.6	(5.4)	1.6	(2.5)	8.3	(7.4)	3.6	(5.2)	18.7	(25.3)	10.9	(17.5)
EMPIRE	UK	CoreExome-24-v1-0	22	4.2	(0.9)	2.9	(1.2)	3.2	(4.6)	1.2	(1.9)	8.6	(5.5)	4.7	(5.1)	15.5	(20.8)	8.1	(21.5)
CARDERA Trials[a]	UK	Immunochip	148	5.8	(1.1)	4.4	(1.3)	10.4	(6.5)	6.4	(7.0)	13.6	(7.6)	7.0	(6.7)				
Phase 2a																			
PromiSERA	UK	Sequencing at mean depth 0.5x	429	4.8	(1.2)	3.2	(1.2)	7.6	(5.5)	2.3	(3.6)	9.5	(7.2)	4.2	(5.4)	30.3	(39.4)	10.5	(17.4)
Phase 2b																			
AMBITION	International	1M-Duo-v3	85	6.0	(0.8)	4.3	(1.4)	14.1	(5.3)	7.1	(6.4)	17.3	(6.8)	9.3	(8.0)	34.8	(39.7)	13.9	(22.8)
MabThera Trials	International	Omni1-Quad-v1-0	32	5.7	(0.9)	3.7	(1.5)	11.5	(4.6)	4.7	(5.4)	15.0	(6.8)	6.4	(7.6)	28.9	(26.7)	9.4	(11.6)
Ocrelizumab Trials	International	Omni1-Quad-v1-0	60	6.0	(0.9)	4.0	(1.2)	13.3	(5.8)	5.0	(4.0)	16.9	(6.6)	6.2	(6.0)	34.3	(28.1)	16.0	(21.0)

[a] CRP not available, DAS28 calculated using ESR

Supplementary Table 4. Phase 1 and 2 results for all regions followed-up in the DAS28 analysis.

Regions were followed up if they included one SNP with P<1x10-5 and at least one other SNP within 200kb with P<5x10-5

The SNPs in bold on chromosome 10:80706139-81146643 were included because they reached P<1e-4 in Cobb et al (14) and P<0.01 in Phase 1

			Phase 1				Phase 2a				Phase 2b		
Marker	**Chr**	**Position**	**Effect Allele**	**β**	**SE**	**P**	**Effect Allele**	**β**	**SE**	**P**	**β**	**SE**	**P**
RS1370894:81083861:C:T	3	81083861	C	0.121	0.035	6.65E-04	C	0.037	0.061	5.50E-01	0.099	0.100	3.23E-01
RS2639268:81086662:T:G	3	81086662	T	0.121	0.035	6.05E-04	T	0.036	0.061	5.58E-01	0.101	0.100	3.13E-01
RS2639280:81096365:G:A	3	81096365	G	0.119	0.035	8.01E-04	G	0.036	0.062	5.64E-01	0.099	0.100	3.23E-01
RS1370890:81097039:G:A	3	81097039	G	0.121	0.035	6.11E-04	G	0.037	0.061	5.52E-01	0.099	0.100	3.23E-01
RS2578338:81108432:T:A	3	81108432	T	0.118	0.035	8.89E-04	T	0.007	0.062	9.10E-01	0.046	0.102	6.51E-01
RS2639286:81109090:A:G	3	81109090	A	0.118	0.035	9.03E-04	A	0.008	0.062	9.04E-01	0.046	0.102	6.51E-01
RS2578334:81110304:A:C	3	81110304	A	0.179	0.038	2.93E-06	A	0.063	0.066	3.39E-01	0.113	0.109	3.02E-01
RS2639210:81113949:T:C	3	81113949	T	0.178	0.038	3.12E-06	T	0.050	0.066	4.47E-01	0.109	0.110	3.21E-01
RS2639209:81115005:A:G	3	81115005	A	0.156	0.035	6.27E-06	G	0.015	0.060	7.97E-01	-0.151	0.101	1.34E-01
RS2578332:81115254:G:A	3	81115254	G	0.169	0.044	1.14E-04	G	0.053	0.080	5.06E-01	0.172	0.113	1.29E-01
RS2639208:81115534:A:G	3	81115534	G	-0.131	0.035	1.50E-04	G	0.012	0.060	8.35E-01	0.029	0.102	7.73E-01
RS2639207:81115535:A:G	3	81115535	A	0.170	0.044	1.12E-04	A	0.061	0.080	4.50E-01	0.171	0.113	1.29E-01
RS2639206:81115721:A:T	3	81115721	T	0.170	0.044	1.12E-04	T				0.171	0.113	1.29E-01
RS2639206:81115721:A:G	3	81115721	A	0.170	0.044	1.12E-04	A				0.171	0.113	1.29E-01
RS1837228:81117005:G:T	3	81117005	G	0.171	0.044	9.61E-05	G	0.047	0.080	5.56E-01	0.171	0.113	1.31E-01
RS1837229:81117203:G:A	3	81117203	G	0.170	0.044	1.05E-04	G	0.055	0.080	4.89E-01	0.171	0.113	1.30E-01
RS2639205:81118364:C:G	3	81118364	C	0.170	0.044	1.07E-04	C	0.048	0.080	5.46E-01	0.171	0.113	1.30E-01
RS2578330:81118422:T:C	3	81118422	T	0.170	0.044	1.05E-04	T	0.055	0.080	4.89E-01	0.171	0.113	1.30E-01
RS6775210:81118507:C:G	3	81118507	G	0.170	0.044	1.05E-04	G	0.055	0.080	4.89E-01	0.171	0.113	1.30E-01
RS2578329:81119052:T:C	3	81119052	T	0.169	0.044	1.13E-04	T	0.061	0.080	4.49E-01	0.171	0.113	1.29E-01
RS1470008:81119293:C:T	3	81119293	C	0.170	0.044	1.07E-04	C	0.054	0.081	5.07E-01	0.171	0.113	1.30E-01
RS2578328:81119759:C:T	3	81119759	C	0.170	0.044	1.05E-04	C	0.054	0.081	5.07E-01	0.171	0.113	1.30E-01
RS13072710:81120509:G:A	3	81120509	A	0.170	0.044	1.02E-04	A	0.054	0.081	5.08E-01	0.171	0.113	1.30E-01
RS1438555:81120546:A:G	3	81120546	A	0.170	0.044	1.07E-04	A	0.046	0.081	5.66E-01	0.171	0.113	1.30E-01
RS2639204:81121223:A:C	3	81121223	A	0.170	0.044	1.05E-04	A	0.054	0.081	5.07E-01	0.171	0.113	1.30E-01
RS2639203:81121707:A:C	3	81121707	A	0.170	0.044	1.05E-04	A	0.054	0.081	5.07E-01	0.171	0.113	1.30E-01
RS2639202:81121744:C:T	3	81121744	C	0.157	0.035	5.58E-06	T	0.021	0.060	7.32E-01	-0.151	0.101	1.35E-01
RS2578327:81121868:A:C	3	81121868	A	0.170	0.044	1.08E-04	A	0.047	0.081	5.64E-01	0.171	0.113	1.31E-01
RS13096435:81124363:A:G	3	81124363	G	0.170	0.044	1.07E-04	G	0.054	0.081	5.08E-01	0.171	0.113	1.30E-01
RS9879857:81124414:A:G	3	81124414	A	0.170	0.044	1.06E-04	A	0.054	0.081	5.07E-01	0.171	0.113	1.30E-01
RS4589960:81124547:T:A	3	81124547	T	0.170	0.044	1.06E-04	T	0.054	0.081	5.07E-01	0.171	0.113	1.30E-01
RS28514668:81124813:T:C	3	81124813	T	0.158	0.035	5.26E-06	C				-0.151	0.101	1.36E-01
RS2888400:81124819:C:A	3	81124819	A	-0.143	0.038	2.05E-04	A	0.014	0.065	8.32E-01	-0.039	0.115	7.32E-01
RS2372751:81124821:C:A	3	81124821	C	0.172	0.037	2.85E-06	A	0.018	0.062	7.70E-01	-0.128	0.107	2.31E-01
RS28503842:81124823:C:A	3	81124823	A	-0.143	0.038	2.05E-04	A	0.014	0.065	8.36E-01	-0.039	0.115	7.32E-01
RS2639229:81125424:G:T	3	81125424	G	0.170	0.044	1.04E-04	G	0.054	0.081	5.07E-01	0.171	0.113	1.30E-01
RS2639228:81126108:G:A	3	81126108	G	0.170	0.044	1.06E-04	G	0.042	0.081	6.00E-01	0.171	0.113	1.30E-01
RS2639227:81126562:C:T	3	81126562	C	0.170	0.044	1.04E-04	C	0.042	0.081	6.00E-01	0.171	0.113	1.30E-01
RS2578325:81126872:A:G	3	81126872	A	0.170	0.044	1.06E-04	A	0.050	0.081	5.40E-01	0.171	0.113	1.30E-01
RS2639225:81127127:C:T	3	81127127	C	0.159	0.035	4.48E-06	T	0.016	0.060	7.92E-01	-0.150	0.101	1.38E-01
RS9830652:81127652:G:A	3	81127652	G	-0.133	0.035	1.22E-04	G	0.012	0.060	8.43E-01	0.036	0.102	7.21E-01
RS34401600:125764421:G:T	5	125764421	T	-0.174	0.044	7.44E-05	T	-0.004	0.073	9.57E-01	0.008	0.105	9.36E-01
RS71586093:125766357:C:A	5	125766357	A	-0.160	0.043	2.30E-04	A	0.018	0.073	8.07E-01	0.030	0.106	7.76E-01
RS4639225:125767116:T:C	5	125767116	C	-0.146	0.038	1.03E-04	C	-0.009	0.064	8.86E-01	0.095	0.101	3.49E-01
RS73783699:125768251:C:T	5	125768251	T	-0.159	0.043	2.05E-04	T	0.031	0.073	6.65E-01	0.033	0.105	7.54E-01
RS34299555:125768530:A:G	5	125768530	G	-0.164	0.043	1.18E-04	G	0.031	0.073	6.67E-01	0.034	0.105	7.45E-01
RS34781836:125768899:G:A	5	125768899	A	-0.165	0.043	1.17E-04	A	0.030	0.073	6.84E-01	0.037	0.105	7.26E-01
RS71586094:125770184:C:T	5	125770184	T	-0.170	0.043	6.87E-05	T	0.040	0.073	5.86E-01	0.037	0.105	7.22E-01
RS58840038:125773164:A:T	5	125773164	T	-0.168	0.038	7.96E-06	T	-0.037	0.065	5.71E-01	0.035	0.100	7.28E-01
RS35171120:125775936:G:A	5	125775936	A	-0.169	0.042	6.55E-05	A	0.033	0.072	6.49E-01	0.028	0.105	7.94E-01
RS6866739:125776486:G:A	5	125776486	A	-0.168	0.042	6.82E-05	A	0.033	0.072	6.44E-01	0.026	0.105	8.01E-01
RS11744511:125779180:A:C	5	125779180	C	-0.162	0.037	1.50E-05	C	-0.040	0.064	5.38E-01	0.063	0.101	5.34E-01
RS74784837:21957280:G:A	6	21957280	A	-0.379	0.110	5.98E-04	A	-0.180	0.197	3.63E-01	0.271	0.269	3.13E-01

RS62402542:21978679:T:C	6	21978679	C	-0.206	0.052	7.49E-05	C	0.099	0.093	2.89E-01	0.092	0.132	4.86E-01
RS10806941:21981157:A:C	6	21981157	A	-0.237	0.053	7.99E-06	A	0.103	0.100	3.07E-01	0.109	0.141	4.40E-01
RS6903359:21986214:C:T	6	21986214	C	-0.235	0.052	7.40E-06	C	0.073	0.099	4.59E-01	0.105	0.138	4.50E-01
RS2026708:21986895:A:G	6	21986895	G	-0.231	0.052	9.12E-06	G	0.067	0.099	4.98E-01	0.101	0.138	4.64E-01
RS6909264:21987116:C:A	6	21987116	C	-0.177	0.041	1.50E-05	C	-0.135	0.072	6.01E-02	0.168	0.110	1.28E-01
RS6480912:80706139:C:T	10	80706139	T	-0.131	0.051	9.73E-03	T				0.268	0.139	5.41E-02
RS12412788:80711556:T:A	10	80711556	A	-0.132	0.051	9.59E-03	A	0.179	0.086	3.91E-02	0.263	0.140	5.97E-02
RS74731489:80725427:C:T	10	80725427	T	-0.200	0.063	1.50E-03	T	0.128	0.112	2.53E-01	0.134	0.184	4.67E-01
RS60526605:80732355:C:T	10	80732355	T	-0.150	0.055	6.55E-03	T	0.173	0.088	5.01E-02	0.335	0.146	2.21E-02
RS11002762:80737512:G:C	10	80737512	C	-0.146	0.055	8.36E-03	C	0.147	0.088	9.38E-02	0.382	0.147	9.45E-03
RS11002764:80741205:C:T	10	80741205	T	-0.137	0.053	9.97E-03	T	0.134	0.084	1.13E-01	0.338	0.140	1.60E-02
RS12761567:80799476:A:G	10	80799476	G	-0.151	0.055	6.12E-03	G	0.056	0.088	5.24E-01	-0.009	0.143	9.51E-01
RS7087678:80827506:T:G	10	80827506	G	-0.179	0.069	9.46E-03	G	-0.105	0.109	3.36E-01	0.089	0.160	5.76E-01
RS2297923:80827990:C:T	10	80827990	T	-0.183	0.068	7.24E-03	T	-0.108	0.109	3.22E-01	0.083	0.160	6.02E-01
RS12264256:80828816:C:G	10	80828816	G	-0.207	0.080	9.79E-03	G	-0.048	0.122	6.97E-01	-0.057	0.176	7.47E-01
RS1115287:80829386:C:G	10	80829386	G	-0.209	0.080	9.28E-03	G	-0.043	0.122	7.24E-01	-0.053	0.176	7.63E-01
RS55883128:80829908:G:C	10	80829908	C	-0.211	0.080	8.83E-03	C	0.042	0.122	7.29E-01			
RS1337983:80832022:C:T	10	80832022	T	-0.216	0.081	7.30E-03	T	0.044	0.122	7.22E-01			
RS4641401:80832147:G:A	10	80832147	A	-0.217	0.081	7.27E-03	A	0.044	0.122	7.22E-01			
RS66870634:80832289:C:T	10	80832289	T	-0.216	0.079	6.20E-03	T	-0.039	0.121	7.45E-01	-0.068	0.180	7.07E-01
RS7067958:80832381:A:G	10	80832381	G	-0.224	0.080	4.97E-03	G	-0.042	0.121	7.31E-01	-0.065	0.180	7.18E-01
RS7086247:80832464:T:C	10	80832464	C	-0.217	0.081	7.12E-03	C	0.044	0.122	7.22E-01			
RS35439188:80833380:G:A	10	80833380	A	-0.217	0.081	7.14E-03	A	0.044	0.122	7.22E-01			
RS703988:80937265:C:G	10	80937265	C	0.122	0.036	6.16E-04	C				0.039	0.103	7.07E-01
RS703987:80939219:G:C	10	80939219	G	0.127	0.034	2.38E-04	G	0.056	0.059	3.44E-01	0.075	0.102	4.61E-01
RS703986:80940565:G:C	10	80940565	G	0.130	0.034	1.53E-04	G	0.055	0.059	3.53E-01	0.079	0.102	4.37E-01
RS697240:80940804:T:C	10	80940804	T	0.130	0.034	1.49E-04	T	0.059	0.059	3.18E-01	0.078	0.102	4.42E-01
RS810517:80942620:C:T	10	80942620	T	-0.099	0.033	2.75E-03	T	-0.074	0.061	2.26E-01	-0.050	0.099	6.10E-01
RS12571751:80942631:A:G	10	80942631	G	-0.102	0.033	2.17E-03	G	-0.074	0.061	2.26E-01	-0.050	0.099	6.09E-01
RS703981:80942855:G:C	10	80942855	C	-0.100	0.033	2.35E-03	C	-0.072	0.061	2.36E-01	-0.066	0.098	4.97E-01
RS703980:80943841:G:A	10	80943841	A	-0.101	0.033	2.33E-03	A	-0.072	0.061	2.39E-01	-0.066	0.098	4.97E-01
RS703979:80944095:T:C	10	80944095	T	0.129	0.033	1.10E-04	T	0.048	0.058	4.10E-01	0.078	0.100	4.34E-01
RS703978:80944147:C:G	10	80944147	C	0.131	0.033	9.44E-05	C	0.049	0.058	3.96E-01	0.068	0.101	5.00E-01
RS703977:80944230:T:G	10	80944230	G	-0.101	0.033	2.31E-03	G	-0.072	0.061	2.36E-01	-0.066	0.098	4.97E-01
RS703976:80945964:C:G	10	80945964	G	-0.101	0.033	2.18E-03	G	-0.070	0.061	2.47E-01	-0.066	0.098	4.97E-01
RS697239:80947438:T:C	10	80947438	C	-0.100	0.033	2.52E-03	C	-0.071	0.061	2.45E-01	-0.065	0.098	5.07E-01
RS697238:80947668:T:G	10	80947668	T	0.128	0.033	1.18E-04	T	0.050	0.058	3.87E-01	0.107	0.099	2.81E-01
RS703975:80947777:T:G	10	80947777	G	-0.099	0.033	2.67E-03	G	-0.062	0.061	3.11E-01	-0.065	0.098	5.07E-01
RS703973:80948883:T:A	10	80948883	T	0.123	0.034	2.80E-04	T	0.065	0.059	2.71E-01	0.089	0.100	3.70E-01
RS748179:80949874:G:C	10	80949874	G	0.123	0.034	2.97E-04	G	0.063	0.059	2.84E-01	0.089	0.100	3.70E-01
RS703972:80952826:G:C	10	80952826	C	-0.096	0.033	3.79E-03	C	-0.054	0.061	3.73E-01	-0.068	0.097	4.83E-01
RS703971:80953123:G:C	10	80953123	G	0.123	0.034	2.98E-04	G	0.064	0.059	2.79E-01	0.088	0.100	3.79E-01
RS703970:80953136:A:C	10	80953136	A	0.124	0.033	1.77E-04	A	0.044	0.058	4.47E-01	0.081	0.098	4.08E-01
RS703969:80953393:G:C	10	80953393	G	0.123	0.033	2.09E-04	G	0.044	0.058	4.47E-01	0.081	0.098	4.07E-01
RS703968:80953436:C:G	10	80953436	C	0.123	0.034	3.02E-04	C	0.071	0.059	2.32E-01	0.090	0.100	3.69E-01
RS703967:80953451:A:C	10	80953451	C	-0.096	0.033	3.82E-03	C	-0.055	0.061	3.67E-01	-0.068	0.097	4.85E-01
RS697237:80954686:G:A	10	80954686	A	0.135	0.045	2.88E-03	A	0.076	0.058	1.95E-01	0.088	0.095	3.54E-01
RS1613299:80954785:C:T	10	80954785	T	0.124	0.045	5.74E-03	T	0.074	0.060	2.17E-01	0.105	0.101	3.00E-01
RS703965:80955067:C:T	10	80955067	T	0.123	0.033	1.53E-04	T	0.071	0.059	2.26E-01	0.082	0.096	3.94E-01
RS1250562:80958588:C:T	10	80958588	T	0.125	0.035	3.68E-04	T	0.027	0.059	6.44E-01	0.123	0.103	2.29E-01
RS2802370:80960884:G:A	10	80960884	A	0.085	0.033	9.57E-03	G	-0.005	0.059	9.34E-01	-0.008	0.097	9.31E-01
RS1250575:80963546:G:A	10	80963546	A	0.086	0.033	9.44E-03	G	-0.009	0.058	8.75E-01	-0.008	0.097	9.31E-01
RS1250576:80964796:A:C	10	80964796	C	0.107	0.034	1.90E-03	C	0.026	0.058	6.60E-01	0.062	0.101	5.37E-01
RS942794:80965109:T:C	10	80965109	C	0.086	0.033	9.58E-03	T	-0.006	0.059	9.24E-01	-0.009	0.097	9.29E-01
RS942796:80967220:C:T	10	80967220	T	0.097	0.034	3.98E-03	T	0.033	0.059	5.77E-01	0.052	0.097	5.97E-01
RS2802361:80971640:G:C	10	80971640	C	0.100	0.034	3.87E-03	C	0.028	0.059	6.30E-01	0.081	0.100	4.18E-01
RS2764817:80972653:C:G	10	80972653	G	0.099	0.034	4.18E-03	G	0.028	0.059	6.37E-01	0.084	0.099	3.98E-01
RS11002873:80974782:C:T	10	80974782	T	-0.180	0.062	3.84E-03	T	0.084	0.128	5.13E-01	0.155	0.183	3.96E-01
RS11002877:80978240:A:T	10	80978240	T	-0.164	0.060	6.25E-03	T	0.085	0.127	5.05E-01	0.154	0.183	4.02E-01

RS2802363:80988837:A:G	10	80988837	G	0.098	0.034	4.43E-03	G	0.029	0.059	6.27E-01	0.067	0.099	5.02E-01
RS56351363:81146401:C:T	10	81146401	T	-0.175	0.064	5.95E-03	T	0.041	0.100	6.82E-01	-0.324	0.180	7.18E-02
RS56696174:81146643:C:T	10	81146643	T	-0.176	0.063	5.52E-03	T	0.041	0.100	6.87E-01	-0.325	0.179	6.99E-02
RS981168:84547861:G:T	10	84547861	T	-0.144	0.035	3.34E-05	T	0.057	0.060	3.42E-01	-0.101	0.103	3.27E-01
RS2065537:84555444:G:A	10	84555444	A	-0.143	0.034	3.22E-05	A	0.051	0.060	3.93E-01	-0.092	0.102	3.72E-01
RS1333213:84557534:T:C	10	84557534	C	-0.145	0.034	2.51E-05	C	0.047	0.059	4.25E-01	-0.090	0.102	3.78E-01
RS1333214:84557575:A:G	10	84557575	G	-0.142	0.034	3.84E-05	G	0.050	0.059	4.05E-01	-0.090	0.102	3.78E-01
RS7100577:84558219:G:C	10	84558219	C	-0.143	0.034	3.43E-05	C	0.049	0.060	4.15E-01	-0.090	0.102	3.78E-01
RS1390408:84559575:T:C	10	84559575	C	-0.144	0.034	2.89E-05	C	0.050	0.059	4.05E-01	-0.091	0.102	3.77E-01
RS7911153:84561597:A:T	10	84561597	T	-0.142	0.034	4.02E-05	T	0.048	0.060	4.17E-01	-0.091	0.102	3.75E-01
RS11196013:84562714:A:G	10	84562714	G	-0.140	0.035	5.13E-05	G	0.049	0.060	4.06E-01	-0.092	0.102	3.65E-01
RS2483307:84564127:G:A	10	84564127	G	0.181	0.035	2.16E-07	G	-0.055	0.060	3.53E-01	0.046	0.099	6.39E-01
RS501376:84570188:G:T	10	84570188	T	-0.162	0.035	3.48E-06	T	0.068	0.058	2.42E-01	-0.071	0.096	4.59E-01
RS342389:84581485:T:C	10	84581485	T	0.129	0.037	5.57E-04	T	-0.074	0.059	2.08E-01	0.175	0.104	9.29E-02
RS4488143:84596866:C:T	10	84596866	C	0.178	0.035	3.19E-07	T	0.083	0.057	1.52E-01	-0.076	0.096	4.25E-01
RS485907:84599583:T:A	10	84599583	A	-0.178	0.035	2.92E-07	A	0.084	0.057	1.44E-01	-0.074	0.096	4.36E-01
RS539088:84609007:T:C	10	84609007	T	0.145	0.038	1.16E-04	T	-0.104	0.059	7.95E-02	0.197	0.100	4.75E-02
RS168201:84610081:G:A	10	84610081	G	0.184	0.035	9.85E-08	G	-0.096	0.057	9.13E-02	0.080	0.092	3.82E-01
RS474496:84614384:C:A	10	84614384	C	0.143	0.037	1.37E-04	C	-0.100	0.059	8.99E-02	0.176	0.100	7.86E-02
RS560083:84614844:T:C	10	84614844	T	0.139	0.037	1.72E-04	T	-0.117	0.059	4.66E-02	0.193	0.095	4.28E-02
RS2453684:84623024:T:C	10	84623024	T	0.123	0.037	9.40E-04	T	-0.093	0.058	1.14E-01	0.170	0.097	7.99E-02
RS2453683:84623035:G:C	10	84623035	G	0.124	0.037	8.39E-04	G	-0.097	0.058	9.44E-02	0.190	0.096	4.71E-02
RS568271:84631585:G:T	10	84631585	G	0.163	0.035	2.91E-06	T	0.076	0.057	1.83E-01	-0.092	0.091	3.16E-01
RS563749:84632070:C:A	10	84632070	C	0.162	0.035	3.48E-06	A	0.075	0.057	1.88E-01	-0.101	0.091	2.65E-01
RS533042:84637229:A:G	10	84637229	A	0.162	0.035	3.00E-06	G	0.067	0.057	2.38E-01	-0.092	0.091	3.12E-01
RS474541:84637580:A:G	10	84637580	A	0.163	0.035	2.98E-06	G	0.067	0.057	2.38E-01	-0.092	0.091	3.13E-01
RS2483297:84639403:C:T	10	84639403	C	0.162	0.035	3.05E-06	T	0.067	0.057	2.39E-01	-0.092	0.091	3.13E-01
RS2475793:84639649:T:C	10	84639649	T	0.162	0.035	3.33E-06	C	0.067	0.057	2.37E-01	-0.091	0.091	3.22E-01
RS574409:84640120:G:A	10	84640120	G	0.162	0.035	3.05E-06	A	0.065	0.057	2.53E-01	-0.093	0.091	3.11E-01
RS526353:84642326:A:T	10	84642326	A	0.161	0.035	3.82E-06	T	0.069	0.057	2.25E-01	-0.104	0.091	2.51E-01
RS580333:84643651:G:A	10	84643651	G	0.162	0.035	3.28E-06	A	0.062	0.057	2.74E-01	-0.096	0.091	2.89E-01
RS11196336:84647395:C:G	10	84647395	G	-0.154	0.044	5.35E-04	G	-0.056	0.077	4.74E-01	-0.022	0.107	8.35E-01
RS4326733:84650672:T:C	10	84650672	C	-0.167	0.047	3.61E-04	C	-0.056	0.083	4.99E-01	-0.033	0.115	7.76E-01
RS2483299:84652722:G:A	10	84652722	A	-0.176	0.035	6.36E-07	A	0.076	0.061	2.16E-01	-0.094	0.095	3.23E-01
RS4509701:84653310:G:A	10	84653310	A	-0.172	0.036	1.53E-06	A	0.066	0.064	2.99E-01	-0.073	0.098	4.54E-01
RS4034740:84653311:G:A	10	84653311	A	-0.172	0.036	1.53E-06	A	0.066	0.064	2.99E-01	-0.073	0.098	4.54E-01
RS2483302:84653390:A:G	10	84653390	G	-0.175	0.035	6.51E-07	G	0.066	0.061	2.77E-01	-0.093	0.095	3.28E-01
RS2475795:84654626:G:A	10	84654626	A	-0.172	0.036	1.43E-06	A	0.069	0.064	2.79E-01	-0.072	0.098	4.59E-01
RS2483303:84661277:G:A	10	84661277	A	-0.167	0.035	1.79E-06	A	0.072	0.061	2.36E-01	-0.062	0.094	5.10E-01
RS12256472:84668708:C:A	10	84668708	A	-0.125	0.037	7.57E-04	A	0.048	0.066	4.68E-01	-0.095	0.099	3.37E-01
RS2483305:84673213:G:C	10	84673213	C	-0.168	0.035	1.78E-06	C	0.058	0.060	3.33E-01	-0.061	0.094	5.14E-01
RS4275560:84818271:C:T	10	84818271	T	-0.159	0.048	7.95E-04	T	0.078	0.072	2.80E-01	0.052	0.136	7.04E-01
RS11081085:4009054:G:T	18	4009054	T	-0.169	0.043	7.98E-05	T	0.110	0.075	1.42E-01	-0.046	0.115	6.89E-01
RS11081086:4009163:G:A	18	4009163	A	-0.166	0.043	1.03E-04	A	0.122	0.076	1.08E-01	-0.046	0.115	6.87E-01
RS9961339:4009380:T:C	18	4009380	C	-0.177	0.042	2.42E-05	C	0.105	0.074	1.59E-01	-0.040	0.114	7.25E-01
RS62083651:4010087:C:T	18	4010087	T	-0.171	0.043	6.52E-05	T	0.111	0.075	1.41E-01	-0.035	0.115	7.58E-01
RS4561560:4010307:A:G	18	4010307	G	-0.172	0.043	6.34E-05	G	0.107	0.075	1.56E-01	-0.034	0.115	7.67E-01
RS6417026:4010420:A:G	18	4010420	G	-0.181	0.042	1.99E-05	G	0.089	0.074	2.28E-01	-0.033	0.115	7.71E-01
RS6506154:4010493:A:T	18	4010493	T	-0.172	0.043	6.45E-05	T	0.107	0.075	1.59E-01	-0.033	0.115	7.75E-01
RS11081087:4011061:T:A	18	4011061	A	-0.179	0.043	2.73E-05	A	0.089	0.074	2.28E-01	-0.027	0.116	8.17E-01
RS11081088:4011538:T:C	18	4011538	C	-0.178	0.043	2.95E-05	C	0.090	0.074	2.22E-01	-0.024	0.116	8.35E-01
RS11081089:4011564:C:T	18	4011564	T	-0.165	0.044	1.52E-04	T	0.114	0.077	1.39E-01	-0.022	0.117	8.49E-01
RS112922208:4011714:C:T	18	4011714	T	-0.165	0.044	1.53E-04	T	0.112	0.077	1.45E-01	-0.022	0.117	8.52E-01
RS7245170:4012085:A:G	18	4012085	G	-0.170	0.043	7.70E-05	G	0.105	0.073	1.50E-01	-0.011	0.117	9.27E-01
RS7230434:4012132:T:C	18	4012132	C	-0.174	0.043	4.98E-05	C	0.094	0.074	2.02E-01	-0.017	0.117	8.86E-01
RS57816977:4012466:T:C	18	4012466	C	-0.217	0.048	5.33E-06	C	0.124	0.076	1.04E-01	0.001	0.125	9.96E-01
RS17653931:4019781:A:T	18	4019781	T	-0.198	0.050	6.34E-05	T	0.124	0.080	1.22E-01	-0.006	0.125	9.61E-01
RS62083652:4019804:C:T	18	4019804	T	-0.201	0.050	5.18E-05	T	0.130	0.080	1.06E-01	-0.017	0.125	8.90E-01

Supplementary Table 5. Phase 1 and 2 results for all regions followed-up in the CRP analysis.

Regions were followed up if they included one SNP with P<1x10-5 and at least one other SNP within 200kb with P<5x10-5

			Phase 1				Phase 2a				Phase 2b		
Marker	**Chr**	**Position**	**Effect Allele**	**β**	**SE**	**P**	**Effect Allele**	**β**	**SE**	**P**	**β**	**SE**	**P**
RS7750348:54580930:A:G	6	54580930	G	-0.192	0.054	3.56E-04	G	-0.097	0.085	2.58E-01	-0.066	0.155	6.70E-01
RS962308:54583590:G:A	6	54583590	A	-0.192	0.054	3.70E-04	A	-0.095	0.087	2.73E-01	-0.066	0.155	6.70E-01
RS12208446:54599513:G:A	6	54599513	A	-0.177	0.047	1.58E-04	A	-0.091	0.073	2.12E-01	-0.052	0.134	7.00E-01
RS9474982:54600465:T:C	6	54600465	C	-0.177	0.047	1.58E-04	C	-0.091	0.073	2.12E-01	-0.058	0.135	6.64E-01
RS9474983:54601401:C:A	6	54601401	A	-0.177	0.047	1.58E-04	A	-0.091	0.073	2.12E-01	-0.059	0.135	6.64E-01
RS34304112:54602086:G:A	6	54602086	A	-0.191	0.054	3.96E-04	A	-0.124	0.088	1.58E-01	-0.070	0.155	6.51E-01
RS12209646:54603171:A:G	6	54603171	G	-0.178	0.047	1.57E-04	G	-0.091	0.073	2.12E-01	-0.059	0.134	6.61E-01
RS13220672:54615504:T:G	6	54615504	G	-0.178	0.047	1.46E-04	G	-0.092	0.073	2.09E-01	-0.059	0.134	6.62E-01
RS13220641:54622762:T:G	6	54622762	G	-0.192	0.054	3.91E-04	G	-0.113	0.088	2.00E-01	-0.071	0.155	6.47E-01
RS16885970:54623670:A:G	6	54623670	G	-0.193	0.054	3.59E-04	G	-0.113	0.088	2.00E-01	-0.071	0.155	6.47E-01
RS62412576:54636524:T:C	6	54636524	C	-0.257	0.056	4.82E-06	C	-0.056	0.094	5.49E-01	-0.006	0.185	9.75E-01
RS76386258:54636556:A:G	6	54636556	G	-0.257	0.056	4.87E-06	G	-0.057	0.094	5.43E-01	-0.006	0.185	9.76E-01
RS62412577:54636748:A:G	6	54636748	G	-0.255	0.056	5.75E-06	G	-0.056	0.092	5.45E-01	-0.010	0.184	9.58E-01
RS77914035:54641812:A:G	6	54641812	G	-0.199	0.052	1.22E-04	G	-0.090	0.084	2.82E-01	-0.062	0.160	6.97E-01
RS62412578:54648365:T:C	6	54648365	C	-0.260	0.056	3.58E-06	C	-0.054	0.093	5.66E-01	0.014	0.185	9.42E-01
RS62412580:54650151:C:A	6	54650151	A	-0.260	0.056	3.58E-06	A	-0.054	0.093	5.66E-01	0.013	0.185	9.44E-01
RS75253686:54651352:G:A	6	54651352	A	-0.248	0.055	7.74E-06	A	-0.055	0.090	5.39E-01	-0.001	0.173	9.98E-01
RS79244342:54660244:C:G	6	54660244	G	-0.261	0.056	3.31E-06	G	-0.054	0.093	5.66E-01	0.016	0.181	9.28E-01
RS62412597:54664045:C:A	6	54664045	A	-0.259	0.056	3.88E-06	A	-0.054	0.094	5.61E-01	0.025	0.179	8.90E-01
RS12661022:54669411:A:G	6	54669411	G	-0.260	0.056	3.42E-06	G	-0.036	0.093	7.01E-01	0.030	0.181	8.67E-01
RS73430625:54670334:C:T	6	54670334	T	-0.258	0.056	4.01E-06	T	-0.035	0.093	7.06E-01	0.024	0.179	8.93E-01
RS62412600:54676773:G:T	6	54676773	T	-0.249	0.055	6.58E-06	T	-0.043	0.091	6.35E-01	0.003	0.167	9.83E-01
RS114338885:54678631:T:C	6	54678631	C	-0.247	0.055	7.18E-06	C	-0.043	0.091	6.39E-01	0.005	0.167	9.77E-01
RS201873829:54687626:T:C	6	54687626	C	-0.249	0.055	6.57E-06	C				0.031	0.172	8.59E-01
RS62412603:54689249:G:A	6	54689249	A	-0.255	0.056	4.66E-06	A	-0.035	0.093	7.06E-01	0.012	0.184	9.49E-01
RS9464141:54690036:T:C	6	54690036	C	-0.213	0.051	2.72E-05	C	-0.074	0.085	3.84E-01	0.063	0.156	6.87E-01
RS62412629:54699299:C:T	6	54699299	T	-0.270	0.081	8.69E-04	T	0.130	0.133	3.30E-01			
RS62412630:54699618:T:C	6	54699618	C	-0.269	0.081	8.71E-04	C	0.130	0.133	3.30E-01			
RS62412631:54699667:C:G	6	54699667	G	-0.269	0.081	8.70E-04	G	0.130	0.133	3.30E-01			
RS62412632:54701539:C:G	6	54701539	G	-0.269	0.081	8.71E-04	G	0.130	0.133	3.30E-01			
RS9396000:54706583:A:G	6	54706583	G	-0.273	0.082	8.30E-04	G	0.103	0.136	4.49E-01			
RS62412635:54707084:G:A	6	54707084	A	-0.273	0.082	8.33E-04	A	0.103	0.136	4.49E-01			
RS9357819:54708077:T:G	6	54708077	G	-0.273	0.082	8.30E-04	G	0.104	0.137	4.48E-01			
RS17682328:54710076:G:A	6	54710076	A	-0.275	0.081	7.31E-04	A	0.107	0.136	4.34E-01			
RS17749547:54710440:A:T	6	54710440	T	-0.273	0.082	8.36E-04	T	0.104	0.137	4.48E-01			
RS62412645:54711088:A:G	6	54711088	G	-0.273	0.082	8.37E-04	G	0.104	0.137	4.47E-01			
RS62412646:54711321:G:A	6	54711321	A	-0.273	0.082	8.35E-04	A	0.069	0.139	6.21E-01			
RS62412648:54711859:G:A	6	54711859	A	-0.272	0.081	8.57E-04	A	0.101	0.136	4.55E-01			
RS62412649:54711898:C:T	6	54711898	T	-0.272	0.081	8.55E-04	T	0.102	0.136	4.55E-01			
RS79634348:54714430:T:C	6	54714430	C	-0.272	0.081	8.51E-04	C	0.090	0.139	5.16E-01			
RS17682340:54721939:G:A	6	54721939	A	-0.271	0.082	8.74E-04	A	0.047	0.139	7.36E-01			
RS144480824:95954225:C:T	9	95954225	T	0.555	0.148	1.70E-04	T	0.268	0.270	3.22E-01			
RS138159152:96004987:A:C	9	96004987	C	0.525	0.138	1.37E-04	C	-0.015	0.202	9.41E-01			
RS7866300:96027767:T:C	9	96027767	C	0.177	0.045	9.27E-05	C	-0.017	0.073	8.16E-01	0.223	0.125	7.38E-02
RS116057316:96031223:C:A	9	96031223	A	0.478	0.139	5.70E-04	A	0.070	0.211	7.40E-01			
RS7875384:96032719:G:A	9	96032719	G	0.179	0.045	6.79E-05	G	-0.015	0.073	8.41E-01	0.157	0.118	1.82E-01
RS4743907:96035015:C:A	9	96035015	C	0.179	0.045	6.79E-05	C	-0.015	0.073	8.40E-01	0.157	0.118	1.82E-01
RS10821103:96035614:T:C	9	96035614	T	0.179	0.045	6.78E-05	T	-0.015	0.073	8.41E-01	0.157	0.118	1.82E-01
RS4744213:96038524:G:T	9	96038524	G	0.179	0.045	6.79E-05	G	-0.015	0.073	8.41E-01	0.158	0.118	1.81E-01
RS7023262:96042061:A:G	9	96042061	A	0.179	0.045	6.64E-05	A	-0.015	0.073	8.41E-01	0.159	0.118	1.78E-01
RS1931364:96047452:T:C	9	96047452	T	0.183	0.045	4.85E-05	T	-0.029	0.073	6.89E-01	0.158	0.118	1.81E-01
RS1889339:96053928:G:A	9	96053928	G	0.191	0.042	5.66E-06	G	-0.061	0.069	3.81E-01	0.166	0.112	1.40E-01
RS145271912:96059669:C:T	9	96059669	T	0.537	0.143	1.80E-04	T	0.124	0.236	5.99E-01			

Supplementary Table 6. Phase 1 and 2 results for all regions followed-up in the SJC28 analysis.

Regions were followed up if they included one SNP with P<1x10-5 and at least one other SNP within 200kb with P<5x10-5

			Phase 1				Phase 2a				Phase 2b		
Marker	**Chr**	**Position**	**Effect Allele**	**β**	**SE**	**P**	**Effect Allele**	**β**	**SE**	**P**	**β**	**SE**	**P**
RS71652597:	1	95441429	T	0.179	0.048	2.02E-04	T	-0.125	0.082	1.29E-01	-0.236	0.145	1.05E-01
RS11805382:	1	95467107	C	0.157	0.043	3.01E-04	C	-0.137	0.070	5.06E-02	-0.219	0.128	8.69E-02
RS11586384:	1	95471741	A	0.154	0.043	3.58E-04	A	-0.137	0.069	4.92E-02	-0.216	0.127	8.90E-02
RS12739445:	1	95472638	C	0.154	0.043	3.57E-04	C				-0.216	0.127	8.92E-02
RS11589700:	1	95473441	T	0.154	0.043	3.58E-04	T	-0.147	0.070	3.78E-02	-0.214	0.127	9.16E-02
RS35512410:	1	95509771	T	0.197	0.050	8.88E-05	T	-0.154	0.091	9.26E-02	-0.232	0.151	1.25E-01
RS12724474:	1	95511833	T	0.152	0.043	4.18E-04	T	-0.146	0.070	3.68E-02	-0.215	0.127	8.98E-02
RS12753842:	1	95515325	C	0.152	0.043	3.88E-04	C	-0.146	0.070	3.64E-02	-0.215	0.127	9.05E-02
RS35051418:	1	95526961	C	0.152	0.043	3.89E-04	C	-0.146	0.070	3.72E-02	-0.215	0.127	9.06E-02
RS12751061:	1	95530591	T	0.151	0.043	4.31E-04	T	-0.142	0.071	4.49E-02	-0.215	0.127	8.98E-02
RS79375907:	1	95539561	T	0.151	0.043	4.41E-04	T	-0.141	0.071	4.69E-02	-0.215	0.127	8.97E-02
RS34254763:	1	95540961	C	0.151	0.043	4.44E-04	C	-0.149	0.071	3.59E-02	-0.215	0.127	8.96E-02
RS11582082:	1	95594697	G	0.163	0.043	1.59E-04	G	-0.121	0.068	7.61E-02	-0.216	0.127	8.83E-02
RS12753865:	1	95595953	C	0.188	0.046	3.96E-05	C	-0.142	0.073	5.30E-02	-0.290	0.137	3.46E-02
RS35466718:	1	95597124	G	0.185	0.046	5.14E-05	G	-0.141	0.073	5.24E-02	-0.294	0.137	3.18E-02
RS35961290:	1	95597575	C	0.186	0.046	4.56E-05	C	-0.139	0.072	5.38E-02	-0.293	0.137	3.24E-02
RS71654410:	1	95599964	A	0.185	0.046	4.90E-05	A	-0.141	0.073	5.23E-02	-0.296	0.137	3.04E-02
RS35575248:	1	95600822	C	0.185	0.046	4.63E-05	C	-0.139	0.072	5.38E-02	-0.295	0.137	3.09E-02
RS71654411:	1	95601022	G	0.185	0.046	4.63E-05	G	-0.139	0.072	5.37E-02	-0.295	0.137	3.08E-02
RS34136988:	1	95601076	A	0.185	0.046	4.64E-05	A	-0.139	0.072	5.37E-02	-0.295	0.137	3.07E-02
RS71654412:	1	95601693	T	0.185	0.046	4.94E-05	T	-0.141	0.073	5.23E-02	-0.297	0.137	2.97E-02
RS34100681:	1	95603056	G	0.185	0.046	4.98E-05	G	-0.141	0.073	5.27E-02	-0.298	0.137	2.91E-02
RS35917978:	1	95603988	C	0.185	0.046	4.99E-05	C	-0.141	0.073	5.27E-02	-0.298	0.136	2.88E-02
RS34790705:	1	95604370	C	0.184	0.046	5.32E-05	C	-0.141	0.073	5.27E-02	-0.298	0.136	2.87E-02
RS11352565:	1	95604674	C	0.182	0.045	5.67E-05	C	-0.140	0.072	5.22E-02	-0.305	0.136	2.51E-02
RS35949014:	1	95604835	G	0.185	0.045	4.72E-05	G	-0.139	0.072	5.41E-02	-0.297	0.136	2.93E-02
RS10047154:	1	95605075	T	0.185	0.045	4.73E-05	T	-0.139	0.072	5.41E-02	-0.297	0.136	2.92E-02
RS35098538:	1	95605446	G	0.185	0.045	4.74E-05	G	-0.139	0.072	5.41E-02	-0.297	0.136	2.90E-02
RS35013306:	1	95605772	A	0.185	0.045	4.74E-05	A	-0.139	0.072	5.41E-02	-0.297	0.136	2.89E-02
RS77817666:	1	95606052	A	0.185	0.045	4.76E-05	A	-0.139	0.072	5.41E-02	-0.297	0.136	2.88E-02
RS78629196:	1	95606070	G	0.185	0.045	4.75E-05	G	-0.139	0.072	5.41E-02	-0.297	0.136	2.88E-02
RS13376185:	1	95606278	T	0.185	0.045	4.76E-05	T	-0.139	0.072	5.41E-02	-0.298	0.136	2.88E-02
RS13375406:	1	95606305	C	0.185	0.045	4.75E-05	C	-0.139	0.072	5.41E-02	-0.298	0.136	2.88E-02
RS13376187:	1	95606370	T	0.185	0.045	4.76E-05	T	-0.137	0.072	5.79E-02	-0.298	0.136	2.87E-02
RS71654413:	1	95607088	T	0.185	0.046	5.08E-05	T	-0.137	0.073	5.99E-02	-0.299	0.136	2.78E-02
RS12742928:	1	95608395	C	0.184	0.046	5.50E-05	C	-0.137	0.073	5.96E-02	-0.300	0.136	2.69E-02
RS34537407:	1	95610253	G	0.184	0.045	5.36E-05	G	-0.137	0.073	5.99E-02	-0.300	0.135	2.62E-02
RS34203531:	1	95612022	T	0.180	0.045	7.67E-05	T	-0.138	0.072	5.77E-02	-0.306	0.135	2.37E-02
RS36101683:	1	95612246	A	0.183	0.045	5.50E-05	A	-0.137	0.073	5.97E-02	-0.300	0.135	2.61E-02
RS79662819:	1	95619804	T	0.202	0.048	2.93E-05	T	-0.096	0.082	2.43E-01	-0.306	0.139	2.73E-02
RS35143903:	1	95622527	T	0.188	0.045	3.09E-05	T	-0.063	0.072	3.82E-01	-0.281	0.142	4.82E-02
RS77507976:	1	95625787	C	0.196	0.045	1.56E-05	C	-0.062	0.072	3.89E-01	-0.270	0.142	5.71E-02
RS14598837:	1	95626509	T	0.196	0.045	1.59E-05	T	-0.062	0.072	3.89E-01	-0.270	0.142	5.72E-02
RS7555236:9	1	95631314	A	0.194	0.045	1.76E-05	A				-0.269	0.142	5.85E-02
RS60929805:	1	95646386	T	0.194	0.045	1.76E-05	T	-0.062	0.072	3.89E-01	-0.269	0.142	5.81E-02
RS9659908:9	1	95656127	T	0.195	0.045	1.73E-05	T	-0.060	0.072	4.04E-01	-0.269	0.142	5.81E-02
RS12749053:	1	95660556	G	0.195	0.045	1.67E-05	G	-0.059	0.072	4.13E-01	-0.269	0.142	5.81E-02
RS34037437:	1	95660921	G	0.195	0.045	1.65E-05	G	-0.059	0.072	4.13E-01	-0.269	0.142	5.81E-02
RS76064624:	1	95661033	G	0.196	0.045	1.59E-05	G	-0.060	0.073	4.11E-01	-0.269	0.142	5.81E-02
RS71654417:	1	95661200	A	0.196	0.045	1.59E-05	A	-0.060	0.073	4.11E-01	-0.269	0.142	5.81E-02
RS71654418:	1	95662658	T	0.197	0.045	1.50E-05	T	-0.060	0.073	4.11E-01	-0.269	0.142	5.81E-02
RS71654419:	1	95664497	G	0.199	0.046	1.23E-05	G	-0.060	0.073	4.11E-01	-0.270	0.142	5.81E-02
RS1927043:9	1	95667251	G	0.128	0.039	9.09E-04	G	-0.047	0.056	4.02E-01	-0.225	0.122	6.44E-02
RS35179427:	1	95670888	A	0.210	0.047	7.77E-06	A	-0.052	0.075	4.88E-01	-0.246	0.148	9.72E-02
RS933107:95	1	95672229	C	0.199	0.046	1.26E-05	C	-0.059	0.071	4.12E-01	-0.268	0.142	5.94E-02
RS11165339:	1	95674064	T	0.200	0.046	1.37E-05	T	-0.051	0.072	4.85E-01	-0.268	0.142	5.93E-02
RS14667272	1	95676957	C	0.201	0.046	1.33E-05	C	-0.048	0.073	5.08E-01	-0.304	0.146	3.70E-02
RS14783573	1	95681001	G	0.201	0.046	1.28E-05	G	-0.052	0.074	4.81E-01	-0.276	0.144	5.60E-02
RS12755552:	1	95685026	G	0.202	0.046	9.49E-06	G	-0.060	0.073	4.07E-01	-0.275	0.144	5.65E-02
RS10747468:	1	95686291	T	0.201	0.046	1.04E-05	T	-0.060	0.071	4.03E-01	-0.274	0.144	5.79E-02
RS6678964:9	1	95694268	A	0.198	0.046	1.67E-05	A	-0.051	0.072	4.85E-01	-0.274	0.144	5.75E-02
RS6671200:9	1	95697529	A	0.198	0.046	1.73E-05	A	-0.051	0.072	4.85E-01	-0.273	0.144	5.87E-02
RS34396223:	1	95697828	T	0.200	0.046	1.50E-05	T	-0.053	0.074	4.77E-01	-0.276	0.144	5.60E-02
RS62625008:	1	95702582	G	0.204	0.046	1.01E-05	G	-0.053	0.074	4.77E-01	-0.276	0.144	5.60E-02
RS35403759:	1	95702890	T	0.204	0.046	9.95E-06	T	-0.053	0.074	4.77E-01	-0.276	0.144	5.60E-02
RS640527:95	1	95705615	G	0.204	0.046	9.77E-06	G	-0.051	0.072	4.85E-01	-0.274	0.144	5.73E-02
RS259359:95	1	95709039	A	0.205	0.046	9.42E-06	A	-0.051	0.072	4.85E-01	-0.273	0.144	5.87E-02

RS259357:95	1	95711478	G	0.205	0.046	9.13E-06	G	-0.051	0.073	4.82E-01	-0.274	0.144	5.74E-02
RS259354:95	1	95718205	T	0.205	0.046	9.17E-06	T	-0.051	0.073	4.82E-01	-0.275	0.144	5.74E-02
RS259352:95	1	95720137	A	0.205	0.046	9.20E-06	A	-0.051	0.073	4.82E-01	-0.275	0.145	5.74E-02
RS259350:95	1	95724831	G	0.205	0.046	9.32E-06	G	-0.051	0.073	4.82E-01	-0.275	0.145	5.73E-02
RS259346:95	1	95728746	A	0.205	0.046	9.46E-06	A	-0.051	0.073	4.82E-01	-0.276	0.145	5.71E-02
RS259345:95	1	95729649	A	0.209	0.047	8.38E-06	A	-0.050	0.073	4.93E-01	-0.276	0.146	5.95E-02
RS75200920:	1	95733196	C	0.206	0.046	8.99E-06	C	-0.054	0.075	4.67E-01	-0.282	0.147	5.50E-02
RS259338:95	1	95738307	G	0.202	0.047	1.47E-05	G	-0.051	0.073	4.81E-01	-0.273	0.147	6.27E-02
RS259334:95	1	95739701	C	0.201	0.047	1.69E-05	C	-0.052	0.073	4.80E-01	-0.269	0.146	6.61E-02
RS34266846:	1	95739748	A	0.202	0.047	1.58E-05	A	-0.048	0.075	5.19E-01	-0.270	0.146	6.47E-02
RS2196344:1	2	138027117	G	0.104	0.030	5.61E-04	G	-0.028	0.046	5.43E-01	0.070	0.086	4.19E-01
RS1453301:1	2	138080695	A	0.155	0.034	7.05E-06	A	-0.050	0.057	3.85E-01	-0.026	0.098	7.88E-01
RS115073210	2	138087826	T	0.141	0.035	5.52E-05	T	-0.049	0.057	3.89E-01	0.004	0.100	9.65E-01
RS2375460:1	2	138124934	G	0.153	0.035	9.46E-06	G	-0.046	0.056	4.17E-01	0.040	0.100	6.90E-01
RS76965865:	2	138136163	T	0.148	0.035	2.18E-05	T	-0.043	0.057	4.54E-01	0.035	0.101	7.32E-01
RS192385684	2	138148956	A	0.151	0.035	1.53E-05	A	-0.050	0.058	3.91E-01	0.058	0.103	5.76E-01
RS78109372:	2	138200698	T	0.148	0.035	2.69E-05	T	-0.018	0.057	7.60E-01	0.056	0.105	5.94E-01
RS16838979:	2	138232065	G	0.129	0.034	1.41E-04	G	0.012	0.054	8.27E-01	0.071	0.100	4.80E-01
RS1584435:1	2	138237038	C	0.126	0.034	1.92E-04	C	0.013	0.055	8.15E-01	0.069	0.099	4.83E-01
RS979460:13	2	138238565	G	0.127	0.034	1.77E-04	G	0.013	0.054	8.08E-01	0.068	0.099	4.93E-01
RS6752201:1	2	138239557	G	0.128	0.034	1.66E-04	G	0.014	0.055	8.02E-01	0.074	0.100	4.59E-01
RS2375572:1	2	138239948	T	0.127	0.034	1.72E-04	T	0.013	0.054	8.08E-01	0.068	0.099	4.89E-01
RS10928610:	2	138239976	G	0.127	0.034	1.81E-04	G	0.017	0.054	7.60E-01	0.068	0.099	4.90E-01
RS4954516:1	2	138240046	C	0.124	0.034	2.44E-04	C	0.023	0.055	6.76E-01	0.069	0.098	4.85E-01
RS6738926:1	2	138241568	C	0.128	0.034	1.57E-04	C	0.012	0.054	8.22E-01	0.068	0.099	4.93E-01
RS4014249:1	2	138243218	T	0.127	0.034	1.72E-04	T	0.008	0.055	8.77E-01	0.069	0.099	4.85E-01
2:138245630	2	138245630	G	0.129	0.034	1.44E-04	G	0.015	0.054	7.89E-01	0.068	0.099	4.89E-01
RS374909224	2	138245631	C	0.129	0.034	1.44E-04	C	0.015	0.054	7.89E-01	0.068	0.099	4.89E-01
RS369566508	2	138245632	C	0.129	0.034	1.44E-04	C	0.015	0.054	7.89E-01	0.068	0.099	4.89E-01
RS4954517:1	2	138245780	A	0.128	0.034	1.54E-04	A	0.003	0.055	9.63E-01	0.070	0.099	4.78E-01
RS1448913:1	2	138248048	G	0.129	0.034	1.44E-04	G	0.013	0.055	8.19E-01	0.071	0.099	4.73E-01
RS6744179:1	2	138258902	G	0.128	0.035	2.08E-04	G	0.003	0.056	9.59E-01	0.083	0.100	4.04E-01
RS16855781:	2	138259383	T	0.128	0.035	2.06E-04	T	0.003	0.056	9.59E-01	0.083	0.100	4.04E-01
RS16838999:	2	138260747	G	0.128	0.035	2.06E-04	G	0.003	0.056	9.62E-01	0.084	0.100	3.99E-01
RS4637178:1	2	138266490	G	0.142	0.035	5.27E-05	G	-0.025	0.056	6.57E-01	0.087	0.104	3.99E-01
RS7560352:1	2	138268796	C	0.143	0.035	4.79E-05	C	-0.028	0.057	6.18E-01	0.084	0.104	4.20E-01
RS11683210:	2	138269887	C	0.143	0.035	4.67E-05	C	-0.028	0.057	6.18E-01	0.082	0.104	4.30E-01
RS6430726:1	2	138274056	C	0.140	0.035	6.45E-05	C	-0.026	0.057	6.51E-01	0.076	0.104	4.67E-01
RS16839052:	2	138281621	A	0.145	0.035	3.70E-05	A	-0.024	0.057	6.75E-01	0.072	0.103	4.84E-01
RS16839057:	2	138281867	A	0.145	0.035	3.68E-05	A	-0.024	0.057	6.76E-01	0.072	0.103	4.85E-01
RS1375359:1	2	138287342	T	0.145	0.035	3.57E-05	T	-0.025	0.057	6.59E-01	0.070	0.103	4.94E-01
RS10496772:	2	138288940	A	0.145	0.035	3.58E-05	A	-0.025	0.057	6.59E-01	0.071	0.103	4.92E-01
RS10496773:	2	138289249	C	0.145	0.035	3.44E-05	C	-0.025	0.057	6.53E-01	0.080	0.103	4.39E-01
RS79666024:	2	138289670	T	0.098	0.030	9.25E-04	T	-0.039	0.050	4.38E-01	0.032	0.093	7.32E-01
RS79051617:	2	138290556	A	0.141	0.035	5.96E-05	A	-0.025	0.057	6.56E-01	0.062	0.103	5.46E-01
RS74742572:	2	138290589	C	0.141	0.035	5.96E-05	C	-0.025	0.057	6.56E-01	0.062	0.103	5.46E-01
RS75220310:	2	138290596	C	0.141	0.035	5.96E-05	C	-0.025	0.057	6.56E-01	0.062	0.103	5.46E-01
RS75196298:	2	138290630	A	0.098	0.030	9.21E-04	A	-0.039	0.050	4.38E-01	0.034	0.094	7.20E-01
RS74857577:	2	138290712	A	0.098	0.030	9.24E-04	A	-0.039	0.050	4.38E-01	0.032	0.093	7.29E-01
RS79736465:	2	138290714	A	0.145	0.035	3.68E-05	A	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS78457542:	2	138291019	C	0.145	0.035	3.69E-05	C	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS79553067:	2	138293229	G	0.144	0.035	3.74E-05	G	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS77120039:	2	138293648	A	0.144	0.035	3.75E-05	A	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS10496775:	2	138295175	G	0.144	0.035	3.78E-05	G	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS80266107:	2	138295449	A	0.144	0.035	3.79E-05	A	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS16839083:	2	138295534	A	0.149	0.035	2.23E-05	A	-0.025	0.057	6.56E-01	0.070	0.103	5.00E-01
RS76031140:	2	138295578	A	0.144	0.035	3.80E-05	A	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS74594386:	2	138295579	G	0.144	0.035	3.80E-05	G	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS76437171:	2	138295639	G	0.144	0.035	3.80E-05	G	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS11692824:	2	138296552	G	0.144	0.035	3.82E-05	G	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS34084191:	2	138296591	G	0.144	0.035	3.82E-05	G	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS11692871:	2	138296614	C	0.144	0.035	3.82E-05	C	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS75070445:	2	138296684	C	0.144	0.035	3.82E-05	C	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS77996164:	2	138297969	C	0.101	0.030	6.25E-04	C	-0.038	0.050	4.49E-01	0.033	0.093	7.26E-01
RS77120507:	2	138297983	A	0.144	0.035	3.85E-05	A	-0.025	0.057	6.63E-01	0.071	0.103	4.92E-01
RS2084501:1	2	138298908	T	0.144	0.035	3.87E-05	T	-0.025	0.057	6.59E-01	0.071	0.103	4.93E-01
RS2122125:1	2	138299544	A	0.098	0.030	9.67E-04	A	-0.039	0.050	4.38E-01	0.033	0.093	7.21E-01
RS80078506:	2	138300565	A	0.145	0.035	3.42E-05	A	-0.025	0.057	6.60E-01	0.071	0.103	4.93E-01
RS78400336:	2	138301748	A	0.144	0.035	3.95E-05	A	-0.025	0.057	6.59E-01	0.071	0.103	4.92E-01
RS74703966:	2	138302938	T	0.144	0.035	3.98E-05	T	-0.025	0.057	6.59E-01	0.071	0.103	4.92E-01
RS1375370:1	2	138303667	A	0.144	0.035	4.20E-05	A	-0.026	0.057	6.42E-01	0.071	0.103	4.92E-01
RS77968347:	2	138304997	G	0.143	0.035	4.41E-05	G	-0.025	0.057	6.59E-01	0.071	0.103	4.92E-01

RS75267349:	2	138305359	A	0.143	0.035	4.46E-05	A	-0.021	0.057	7.07E-01	0.071	0.103	4.92E-01
RS11688551:	2	138324865	C	0.133	0.034	9.06E-05	C	-0.018	0.057	7.50E-01	0.083	0.106	4.36E-01
RS11682842:	2	138324893	T	0.133	0.034	9.22E-05	T	-0.020	0.057	7.30E-01	0.081	0.106	4.43E-01
RS73958890:	2	138326366	A	0.113	0.034	9.32E-04	A	0.018	0.058	7.51E-01	0.054	0.104	6.01E-01
RS35310070:	4	109827971	T	0.226	0.067	7.13E-04	T	-0.152	0.132	2.50E-01			
RS34333670:	4	109853029	C	0.221	0.066	8.90E-04	C	-0.088	0.119	4.59E-01			
RS35373487:	4	109856648	C	0.221	0.066	8.92E-04	C	-0.088	0.119	4.59E-01			
RS77458347:	4	109896081	T	0.183	0.041	6.68E-06	T	-0.018	0.063	7.73E-01	0.182	0.145	2.08E-01
RS74725108:	4	109897353	C	0.176	0.046	1.19E-04	C	0.006	0.066	9.23E-01	0.273	0.156	7.89E-02
RS35341926:	4	109905647	A	0.185	0.043	1.52E-05	A	-0.009	0.064	8.92E-01	0.204	0.145	1.59E-01
RS71603009:	4	109908663	T	0.185	0.048	1.30E-04	T	0.013	0.068	8.53E-01	0.169	0.183	3.55E-01
RS35576173:	4	109910567	A	0.185	0.048	1.30E-04	A	0.012	0.068	8.56E-01	0.169	0.183	3.55E-01
RS14353610:	4	109911081	G	0.288	0.069	3.19E-05	G	-0.116	0.127	3.65E-01			
RS13108583:	4	109913881	G	0.185	0.048	1.30E-04	G	0.012	0.069	8.65E-01	0.169	0.183	3.55E-01
RS13129214:	4	109914898	T	0.185	0.048	1.30E-04	T	0.009	0.069	8.99E-01	0.169	0.183	3.55E-01
RS14479919:	4	109918786	C	0.186	0.048	1.25E-04	C	0.010	0.069	8.85E-01	0.167	0.183	3.61E-01
RS37655302:	4	109921850	T	0.186	0.048	1.22E-04	T	0.012	0.069	8.65E-01	0.166	0.183	3.64E-01
RS34526674:	4	109922206	T	0.186	0.048	1.22E-04	T	0.016	0.069	8.23E-01	0.166	0.183	3.64E-01
RS36191788:	4	109922708	C	0.186	0.048	1.22E-04	C	0.013	0.068	8.53E-01	0.166	0.183	3.65E-01
RS71603011:	4	109926252	T	0.200	0.050	6.32E-05	T	0.021	0.070	7.69E-01	-0.006	0.190	9.74E-01
RS11614653:	4	109926608	G	0.288	0.068	2.12E-05	G	-0.127	0.119	2.86E-01			
RS13103995:	4	109927860	C	0.154	0.046	7.96E-04	C	0.034	0.064	5.95E-01			
RS1834354:1	4	109984359	T	0.092	0.027	8.08E-04	T	-0.011	0.045	8.17E-01	-0.104	0.083	2.11E-01
RS1834355:1	4	109984584	A	0.092	0.027	8.17E-04	A	-0.010	0.045	8.20E-01	-0.104	0.083	2.09E-01
RS11136820:	4	109985934	G	0.477	0.127	1.72E-04	G	0.356	0.231	1.23E-01			
RS3113687:1	4	109987381	C	0.090	0.027	7.06E-04	C	-0.024	0.044	5.80E-01	-0.121	0.082	1.37E-01
RS11338410:	4	110065584	C	0.435	0.126	5.77E-04	C	0.249	0.160	1.21E-01			
RS13953933:	4	110088196	T	0.404	0.110	2.42E-04	T	0.265	0.181	1.43E-01			
RS35935352:	4	155078715	T	0.289	0.060	1.49E-06	T	0.163	0.095	8.56E-02	-0.091	0.259	7.24E-01
RS71620289:	4	155079054	T	0.286	0.060	1.99E-06	T	0.166	0.095	8.21E-02	-0.048	0.265	8.57E-01
RS4432731:1	4	155080330	T	0.281	0.060	3.02E-06	T	0.166	0.095	8.22E-02	-0.026	0.271	9.23E-01
RS36123238:	4	155085107	A	0.286	0.060	2.04E-06	A	0.171	0.096	7.54E-02	0.009	0.264	9.73E-01
RS4352458:1	4	155091541	T	0.275	0.060	4.21E-06	T	0.141	0.091	1.23E-01	-0.080	0.258	7.56E-01
RS14494091:	4	155092290	T	0.256	0.053	1.43E-06	T	0.106	0.082	1.96E-01	0.109	0.217	6.16E-01
RS4624637:1	4	155094318	C	0.279	0.061	5.07E-06	C	0.151	0.093	1.05E-01	-0.050	0.263	8.48E-01
RS71620292:	4	155103222	G	0.286	0.078	2.38E-04	G	-0.408	0.134	2.54E-03			
RS34249493:	4	155250786	A	0.263	0.071	2.00E-04	A	-0.176	0.143	2.18E-01			
RS10945810:	6	162728075	C	0.090	0.027	8.64E-04	C	-0.002	0.045	9.70E-01	-0.006	0.091	9.47E-01
RS12198792:	6	162728396	C	0.123	0.026	2.43E-06	C	-0.003	0.042	9.43E-01	0.039	0.081	6.30E-01
RS4709595:1	6	162729381	G	0.124	0.026	2.08E-06	G	-0.002	0.042	9.66E-01	0.038	0.080	6.40E-01
RS12663189:	6	162730663	C	0.124	0.026	2.00E-06	C	-0.007	0.042	8.69E-01	0.038	0.080	6.35E-01
RS12214761:	6	162732259	G	-0.107	0.027	5.73E-05	G	0.046	0.043	2.91E-01	0.028	0.076	7.11E-01
RS10447369:	6	162733512	C	0.121	0.026	2.76E-06	C	-0.007	0.042	8.63E-01	0.037	0.080	6.48E-01
RS2156269:1	6	162742131	G	0.114	0.026	9.76E-06	G	-0.003	0.042	9.50E-01	0.036	0.080	6.58E-01
RS4327667:1	6	162742901	T	0.114	0.026	9.77E-06	T	-0.003	0.042	9.50E-01	0.036	0.080	6.55E-01
RS12193354:	6	162743355	G	0.114	0.026	9.89E-06	G	-0.001	0.042	9.89E-01	0.036	0.080	6.55E-01
RS12191007:	6	162745252	A	0.113	0.026	1.10E-05	A				0.030	0.081	7.08E-01
RS9458521:1	6	162745500	C	0.116	0.026	7.21E-06	C	-0.002	0.042	9.58E-01	0.037	0.080	6.45E-01
RS9458522:1	6	162745510	C	0.114	0.026	9.83E-06	C	-0.002	0.042	9.57E-01	0.037	0.080	6.45E-01
RS4708953:1	6	162746266	G	0.114	0.026	9.88E-06	G	-0.003	0.042	9.41E-01	0.037	0.080	6.43E-01
RS7769694:1	6	162746882	G	0.114	0.026	9.90E-06	G	-0.003	0.042	9.41E-01	0.038	0.080	6.40E-01
RS7776148:1	6	162747801	C	0.114	0.026	9.90E-06	C	-0.002	0.042	9.71E-01	0.038	0.080	6.33E-01
RS9458523:1	6	162748045	A	0.114	0.026	9.95E-06	A	-0.003	0.042	9.41E-01	0.039	0.080	6.29E-01
RS9458524:1	6	162748555	C	0.114	0.026	9.69E-06	C	-0.003	0.042	9.43E-01	0.034	0.081	6.74E-01
RS9347620:1	6	162750092	T	-0.097	0.028	5.20E-04	T	0.047	0.045	3.03E-01	-0.010	0.085	9.03E-01
RS9347621:1	6	162750426	T	-0.096	0.028	5.96E-04	T	0.048	0.045	2.94E-01	-0.011	0.084	8.93E-01
RS12205467:	6	162751769	C	-0.090	0.026	6.61E-04	C	0.038	0.043	3.78E-01	0.041	0.078	5.98E-01
RS4544885:1	6	162754606	A	-0.103	0.028	2.54E-04	A	0.041	0.045	3.68E-01	0.000	0.085	9.97E-01
RS6911138:1	6	162757723	T	-0.104	0.028	2.29E-04	T	0.037	0.045	4.07E-01	0.003	0.085	9.68E-01
RS7383674:1	6	162760045	C	-0.095	0.027	4.40E-04	C	0.041	0.043	3.40E-01	0.054	0.076	4.77E-01
RS6455810:1	6	162765089	T	-0.094	0.027	4.85E-04	T	0.042	0.043	3.23E-01	0.064	0.077	4.05E-01
RS7786536:4	7	4227904	A	0.097	0.029	8.19E-04	A	-0.028	0.047	5.51E-01	-0.042	0.087	6.32E-01
RS1806470:4	7	4242376	T	0.102	0.031	9.61E-04	T	-0.029	0.049	5.61E-01	-0.079	0.090	3.81E-01
RS10230864:	7	4242729	T	0.096	0.029	9.26E-04	T	-0.023	0.048	6.30E-01	-0.055	0.087	5.26E-01
RS12666923:	7	4242744	T	0.096	0.029	9.26E-04	T	-0.023	0.048	6.30E-01	-0.055	0.087	5.26E-01
RS10259400:	7	4242787	C	0.096	0.029	9.26E-04	C	-0.023	0.048	6.30E-01	-0.055	0.087	5.26E-01
RS7783622:4	7	4242925	G	0.096	0.029	9.53E-04	G	-0.023	0.048	6.29E-01	-0.056	0.087	5.18E-01
RS7801236:4	7	4242946	T	0.096	0.029	9.54E-04	T	-0.023	0.048	6.29E-01	-0.056	0.087	5.18E-01
RS7800149:4	7	4242963	A	0.096	0.029	9.54E-04	A	-0.024	0.049	6.26E-01	-0.056	0.087	5.18E-01
RS7787800:4	7	4243083	C	0.096	0.029	9.30E-04	C	-0.024	0.049	6.27E-01	-0.055	0.087	5.26E-01
RS7801698:4	7	4243264	G	0.096	0.029	9.34E-04	G	-0.024	0.049	6.27E-01	-0.055	0.087	5.26E-01
RS17134550:	7	4243418	T	0.096	0.029	9.36E-04	T	-0.024	0.049	6.27E-01	-0.055	0.087	5.27E-01

RS17134554:	7	4243578	A	0.096	0.029	9.37E-04	A	-0.024	0.049	6.27E-01	-0.055	0.087	5.27E-01
RS17134563:	7	4243685	T	0.096	0.029	9.31E-04	T	-0.024	0.049	6.23E-01	-0.055	0.087	5.30E-01
RS17134567:	7	4243758	T	0.096	0.029	9.25E-04	T	-0.023	0.049	6.36E-01	-0.055	0.087	5.27E-01
RS28629320:	7	4244138	T	0.097	0.029	8.86E-04	T	-0.024	0.049	6.27E-01	-0.055	0.087	5.27E-01
RS10236427:	7	4379718	T	0.128	0.033	1.23E-04	T	0.080	0.055	1.45E-01	0.104	0.110	3.41E-01
RS56980976:	7	4391937	C	0.097	0.028	5.25E-04	C	0.019	0.045	6.70E-01	0.110	0.089	2.15E-01
RS7793011:4	7	4392351	G	0.098	0.028	4.46E-04	G	0.019	0.045	6.70E-01	0.111	0.089	2.11E-01
RS4723665:4	7	4392868	G	0.098	0.028	4.45E-04	G	0.019	0.045	6.70E-01	0.112	0.089	2.08E-01
RS61454646:	7	4393978	C	0.100	0.028	3.38E-04	C	0.019	0.045	6.76E-01	0.114	0.089	2.00E-01
RS11129942:	7	4397160	T	0.136	0.037	2.50E-04	T	0.061	0.057	2.82E-01	0.270	0.109	1.34E-02
RS7787822:4	7	4397297	T	0.123	0.037	8.60E-04	T	0.046	0.057	4.23E-01	0.278	0.107	9.07E-03
RS17134719:	7	4397459	G	0.125	0.037	7.01E-04	G	0.022	0.058	7.01E-01	0.279	0.107	8.90E-03
RS12668386:	7	4398505	T	0.121	0.037	9.80E-04	T	0.048	0.059	4.12E-01	0.267	0.107	1.23E-02
RS58549091:	7	4398714	C	0.126	0.037	6.23E-04	C	0.050	0.059	3.96E-01	0.271	0.106	1.09E-02
RS2057892:4	7	4399101	G	0.100	0.028	3.18E-04	G	0.029	0.044	5.14E-01	0.092	0.089	3.01E-01
RS7458131:4	7	4399366	G	0.102	0.028	2.57E-04	G	0.029	0.044	5.14E-01	0.094	0.089	2.88E-01
RS5021676:4	7	4399481	T	0.100	0.028	3.17E-04	T	0.029	0.044	5.14E-01	0.092	0.089	3.01E-01
RS5021675:4	7	4399557	G	0.102	0.028	2.59E-04	G	0.029	0.044	5.14E-01	0.094	0.089	2.88E-01
RS5021674:4	7	4399614	T	0.100	0.028	3.17E-04	T	0.030	0.044	4.96E-01	0.092	0.089	3.01E-01
RS5021673:4	7	4399638	G	0.100	0.028	3.29E-04	G	0.030	0.044	4.98E-01	0.095	0.089	2.85E-01
RS5021672:4	7	4399743	C	0.102	0.028	2.37E-04	C	0.030	0.044	4.94E-01	0.094	0.089	2.88E-01
RS5021671:4	7	4399800	G	0.102	0.028	2.59E-04	G	0.030	0.044	4.96E-01	0.094	0.089	2.88E-01
RS7802793:4	7	4400139	G	0.102	0.028	2.62E-04	G	0.030	0.044	4.96E-01	0.095	0.089	2.86E-01
RS73051240:	7	4400400	C	0.103	0.028	2.11E-04	C	0.029	0.044	5.09E-01	0.094	0.089	2.91E-01
RS73051242:	7	4400401	A	0.101	0.028	2.98E-04	A	0.030	0.044	4.97E-01	0.092	0.089	3.01E-01
RS4723681:4	7	4400493	C	0.102	0.028	2.58E-04	C	0.030	0.044	4.96E-01	0.094	0.089	2.88E-01
RS4723682:4	7	4400669	C	0.102	0.028	2.31E-04	C	0.030	0.044	5.00E-01	0.092	0.088	2.95E-01
RS4723684:4	7	4400850	G	0.102	0.028	2.23E-04	G	0.033	0.044	4.64E-01	0.091	0.088	3.00E-01
RS4723685:4	7	4400870	A	0.101	0.028	2.76E-04	A	0.033	0.044	4.64E-01	0.088	0.088	3.15E-01
RS4723687:4	7	4400977	T	0.101	0.028	2.75E-04	T	0.033	0.044	4.63E-01	0.088	0.088	3.13E-01
RS11773381:	7	4401128	T	0.101	0.028	2.75E-04	T	0.033	0.044	4.63E-01	0.088	0.088	3.14E-01
RS11764685:	7	4401349	C	0.123	0.037	8.57E-04	C	0.049	0.058	4.00E-01	0.262	0.106	1.37E-02
RS11767003:	7	4401503	A	0.101	0.028	2.75E-04	A	0.033	0.044	4.63E-01	0.088	0.088	3.15E-01
RS11764749:	7	4401547	C	0.101	0.028	2.63E-04	C	0.032	0.044	4.70E-01	0.088	0.088	3.16E-01
RS11760485:	7	4401550	T	0.101	0.028	2.71E-04	T	0.033	0.044	4.63E-01	0.088	0.087	3.17E-01
RS7776529:4	7	4401820	G	0.102	0.028	2.22E-04	G	0.033	0.044	4.64E-01	0.090	0.088	3.02E-01
RS28403109:	7	4401876	A	0.101	0.028	2.84E-04	A	0.033	0.044	4.64E-01	0.087	0.088	3.19E-01
RS28629195:	7	4401934	C	0.101	0.028	2.75E-04	C	0.033	0.044	4.63E-01	0.087	0.088	3.19E-01
RS57205131:	7	4401983	G	0.101	0.028	2.76E-04	G	0.033	0.044	4.63E-01	0.087	0.088	3.21E-01
RS56098795:	7	4402225	A	0.101	0.028	2.76E-04	A	0.034	0.044	4.39E-01	0.087	0.088	3.22E-01
RS57518719:	7	4402398	A	0.101	0.028	2.76E-04	A	0.032	0.044	4.65E-01	0.087	0.088	3.22E-01
RS9655026:4	7	4402663	T	0.100	0.028	3.34E-04	T	0.032	0.044	4.66E-01	0.086	0.088	3.25E-01
RS9655027:4	7	4402672	T	0.101	0.028	2.75E-04	T	0.033	0.044	4.64E-01	0.087	0.088	3.22E-01
RS4723690:4	7	4402953	C	0.101	0.028	2.78E-04	C	0.033	0.044	4.64E-01	0.087	0.088	3.22E-01
RS73034803:	7	4403440	G	0.121	0.037	9.56E-04	G	0.048	0.059	4.10E-01	0.259	0.106	1.47E-02
RS10233780:	7	4404058	G	0.096	0.028	4.97E-04	G	0.034	0.045	4.46E-01	0.083	0.087	3.43E-01
RS11971739:	7	4405780	A	0.122	0.037	9.36E-04	A	0.047	0.058	4.18E-01	0.260	0.106	1.45E-02
RS10488360:	7	4411209	A	0.112	0.028	6.80E-05	A	0.039	0.046	4.01E-01	0.087	0.089	3.30E-01
RS11763858:	7	4411996	G	0.105	0.028	1.72E-04	G	0.034	0.046	4.59E-01	0.097	0.086	2.61E-01
RS4720258:4	7	4412359	C	0.102	0.028	2.71E-04	C	0.035	0.046	4.47E-01	0.078	0.087	3.69E-01
RS4723705:4	7	4412593	G	0.105	0.028	1.85E-04	G	0.035	0.046	4.42E-01	0.093	0.087	2.82E-01
RS56768695:	7	4412974	A	0.105	0.028	1.87E-04	A	0.035	0.046	4.53E-01	0.093	0.086	2.84E-01
RS2107841:4	7	4413163	T	0.105	0.028	1.88E-04	T	0.032	0.046	4.88E-01	0.093	0.087	2.83E-01
RS2107842:4	7	4413313	C	0.090	0.027	7.52E-04	C	0.065	0.043	1.30E-01	0.079	0.087	3.64E-01
RS6970156:4	7	4413680	T	0.104	0.028	1.91E-04	T	0.041	0.046	3.78E-01	0.093	0.087	2.83E-01
RS10247619:	7	4413725	T	0.104	0.028	1.92E-04	T	0.042	0.046	3.59E-01	0.093	0.087	2.83E-01
RS10247751:	7	4413797	T	0.104	0.028	1.92E-04	T	0.042	0.046	3.59E-01	0.093	0.087	2.83E-01
RS7789446:4	7	4413892	C	0.091	0.027	7.49E-04	C	0.065	0.043	1.31E-01	0.079	0.087	3.64E-01
RS10261602:	7	4414227	A	0.104	0.028	1.95E-04	A	0.042	0.046	3.59E-01	0.093	0.087	2.83E-01
RS12668729:	7	4414427	A	0.104	0.028	1.96E-04	A	0.042	0.046	3.59E-01	0.093	0.087	2.83E-01
RS10242817:	7	4414460	A	0.104	0.028	1.97E-04	A	0.042	0.046	3.59E-01	0.093	0.087	2.83E-01
RS9639771:4	7	4414803	G	0.089	0.027	9.40E-04	G	0.056	0.043	1.95E-01	0.079	0.087	3.64E-01
RS9639772:4	7	4414838	G	0.089	0.027	9.71E-04	G	0.054	0.043	2.13E-01	0.082	0.086	3.43E-01
RS314606:44	7	4415377	G	0.103	0.028	2.27E-04	G	0.030	0.046	5.14E-01	0.093	0.087	2.81E-01
RS314607:44	7	4415396	A	0.103	0.028	2.27E-04	A	0.030	0.046	5.14E-01	0.093	0.087	2.81E-01
RS314608:44	7	4415414	C	0.103	0.028	2.27E-04	C	0.030	0.046	5.13E-01	0.093	0.087	2.81E-01
RS314609:44	7	4415434	T	0.103	0.028	2.34E-04	T	0.030	0.046	5.17E-01	0.093	0.087	2.81E-01
RS314610:44	7	4415457	G	0.089	0.027	8.84E-04	G	0.055	0.043	1.96E-01	0.082	0.087	3.46E-01
RS314611:44	7	4415570	G	0.103	0.028	2.26E-04	G	0.031	0.046	5.04E-01	0.093	0.087	2.81E-01
RS314612:44	7	4415799	G	0.090	0.027	8.54E-04	G	0.055	0.043	2.02E-01	0.079	0.087	3.62E-01
RS415736:44	7	4415889	G	0.089	0.027	8.76E-04	G	0.053	0.043	2.17E-01	0.080	0.087	3.57E-01
RS314613:44	7	4415974	A	0.103	0.028	2.24E-04	A	0.031	0.046	5.03E-01	0.094	0.087	2.79E-01

RS314614:44	7	4416748	C	0.104	0.028	2.17E-04	C	0.032	0.046	4.84E-01	0.093	0.087	2.82E-01
RS314616:44	7	4416972	G	0.104	0.028	2.17E-04	G	0.030	0.046	5.14E-01	0.094	0.087	2.80E-01
RS314617:44	7	4416989	G	0.104	0.028	2.16E-04	G	0.030	0.046	5.14E-01	0.094	0.087	2.80E-01
RS314618:44	7	4417183	G	0.104	0.028	2.13E-04	G	0.032	0.046	4.85E-01	0.094	0.087	2.80E-01
RS314619:44	7	4417241	A	0.104	0.028	2.12E-04	A	0.044	0.046	3.42E-01	0.094	0.087	2.78E-01
RS314620:44	7	4417406	G	0.098	0.027	3.39E-04	G	0.049	0.043	2.53E-01	0.080	0.088	3.60E-01
RS314621:44	7	4417483	A	0.104	0.028	2.11E-04	A	0.032	0.046	4.84E-01	0.094	0.087	2.78E-01
RS314622:44	7	4417616	G	0.090	0.027	7.94E-04	G	0.052	0.043	2.20E-01	0.079	0.087	3.62E-01
RS314623:44	7	4417987	A	0.105	0.028	1.94E-04	A	0.035	0.046	4.51E-01	0.095	0.087	2.71E-01
RS314624:44	7	4418719	G	0.091	0.027	7.38E-04	G	0.054	0.043	2.07E-01	0.098	0.086	2.58E-01
RS314626:44	7	4419126	A	0.105	0.028	2.02E-04	A	0.034	0.046	4.59E-01	0.114	0.086	1.87E-01
RS314627:44	7	4419287	C	0.093	0.027	6.12E-04	C	0.064	0.043	1.34E-01	0.098	0.086	2.58E-01
RS314631:44	7	4421153	G	0.093	0.027	6.78E-04	G	0.063	0.043	1.39E-01	0.102	0.087	2.41E-01
RS314634:44	7	4421616	G	0.145	0.031	3.24E-06	G	0.082	0.051	1.06E-01	0.183	0.099	6.51E-02
RS314635:44	7	4421857	A	0.146	0.031	2.90E-06	A	0.082	0.051	1.08E-01	0.186	0.099	6.07E-02
RS314636:44	7	4421870	G	0.146	0.031	2.90E-06	G	0.082	0.051	1.09E-01	0.186	0.099	6.08E-02
RS314637:44	7	4421893	A	0.146	0.031	2.90E-06	A	0.082	0.051	1.08E-01	0.186	0.099	6.07E-02
RS314638:44	7	4421964	A	0.145	0.031	3.25E-06	A	0.082	0.051	1.07E-01	0.184	0.099	6.27E-02
RS314639:44	7	4421987	A	0.143	0.031	4.75E-06	A	0.082	0.051	1.07E-01	0.184	0.099	6.29E-02
RS314640:44	7	4422671	A	0.148	0.041	2.59E-04	A	0.081	0.051	1.12E-01	0.184	0.099	6.46E-02
RS314642:44	7	4423038	T	0.142	0.033	1.38E-05	T	0.085	0.052	1.00E-01	0.129	0.101	1.99E-01
RS314643:44	7	4423268	C	0.149	0.043	5.40E-04	C	0.082	0.051	1.12E-01	0.186	0.100	6.41E-02
RS314644:44	7	4423293	T	0.149	0.042	4.33E-04	T	0.083	0.051	1.07E-01	0.181	0.101	7.23E-02
RS314645:44	7	4423360	C	0.148	0.044	8.17E-04	C	0.085	0.052	1.03E-01	0.191	0.102	5.97E-02
RS666360:44	7	4423658	A	0.114	0.032	3.60E-04	A	0.041	0.049	4.04E-01	0.131	0.095	1.69E-01
RS442775:44	7	4490934	G	0.088	0.027	9.23E-04	G	0.028	0.040	4.89E-01	0.065	0.087	4.52E-01
RS12703674:	7	144974590	A	0.146	0.042	5.37E-04	A	0.017	0.049	7.30E-01	0.012	0.099	9.00E-01
RS10251260:	7	144993911	C	0.139	0.040	5.60E-04	C	0.035	0.049	4.78E-01	0.024	0.099	8.07E-01
RS11770321:	7	145024241	G	0.138	0.041	8.64E-04	G	0.033	0.049	4.98E-01	0.026	0.098	7.94E-01
RS62495649:	7	145038219	C	0.137	0.033	2.65E-05	C	0.038	0.049	4.38E-01	0.018	0.099	8.58E-01
RS7799049:1	7	145043501	T	0.143	0.041	5.63E-04	T	0.000	0.050	9.96E-01	0.017	0.099	8.62E-01
RS193464:14	7	145046518	C	0.094	0.028	6.96E-04	C	0.091	0.042	3.08E-02	-0.008	0.086	9.26E-01
RS4317490:1	7	145046520	G	0.144	0.040	3.22E-04	G	0.060	0.047	2.08E-01	0.013	0.095	8.93E-01
RS10264696:	7	145048455	G	0.144	0.040	3.28E-04	G	0.061	0.047	2.00E-01	0.012	0.095	8.97E-01
RS1158062:1	7	145049829	C	0.139	0.032	1.26E-05	C	0.065	0.048	1.75E-01	0.023	0.096	8.07E-01
RS10261772:	7	145051221	T	0.144	0.040	2.93E-04	T	0.061	0.047	2.00E-01	0.012	0.095	8.97E-01
RS41685:145	7	145051737	A	0.093	0.028	7.32E-04	A	0.079	0.042	6.09E-02	-0.012	0.086	8.86E-01
RS41684:145	7	145052219	T	0.093	0.028	7.42E-04	T	0.091	0.042	3.17E-02	-0.008	0.086	9.24E-01
RS55742011:	7	145053232	A	0.144	0.039	2.51E-04	A	0.060	0.047	2.03E-01	0.012	0.095	8.99E-01
RS41683:145	7	145055203	G	0.092	0.028	9.37E-04	G	0.087	0.042	4.04E-02	-0.002	0.086	9.85E-01
RS11379827:	7	145059089	G	0.143	0.032	9.39E-06	G	0.021	0.049	6.70E-01	0.023	0.096	8.07E-01
RS12703685:	7	145060913	G	0.143	0.032	9.52E-06	G	0.041	0.049	4.04E-01	0.023	0.096	8.08E-01
RS35532565:	7	145061738	C	0.143	0.032	9.57E-06	C	0.038	0.048	4.27E-01	0.023	0.096	8.08E-01
RS13243561:	7	145068642	C	0.142	0.032	1.04E-05	C	0.037	0.048	4.40E-01	0.023	0.096	8.13E-01
RS850326:14	7	145120062	T	0.094	0.027	3.99E-04	T	0.070	0.042	9.18E-02	-0.005	0.082	9.50E-01
RS850395:14	7	145131472	C	-0.087	0.026	9.25E-04	C	-0.060	0.042	1.50E-01	-0.043	0.085	6.16E-01
RS7254338:4	19	49717516	C	0.142	0.040	3.94E-04	C	-0.116	0.058	4.71E-02	0.016	0.122	8.99E-01
RS11630962(	19	49717796	T	0.182	0.044	3.20E-05	T	-0.142	0.059	1.70E-02	0.011	0.128	9.33E-01
RS3848547:4	19	49717875	C	0.092	0.026	4.34E-04	C	0.004	0.041	9.14E-01	0.026	0.078	7.41E-01
RS79930852:	19	49718265	T	0.179	0.044	4.16E-05	T	-0.141	0.059	1.74E-02	0.006	0.129	9.66E-01
RS11668962:	19	49718548	A	0.093	0.026	4.24E-04	A	0.000	0.041	9.92E-01	0.009	0.078	9.06E-01
RS11313600(	19	49719070	G	0.092	0.026	4.08E-04	G	0.004	0.041	9.28E-01	0.012	0.077	8.74E-01
RS79102179:	19	49719573	T	0.186	0.043	1.58E-05	T	-0.148	0.059	1.30E-02	0.004	0.126	9.75E-01
RS11527493(	19	49720501	T	0.186	0.043	1.59E-05	T	-0.148	0.059	1.30E-02	0.004	0.126	9.75E-01
RS75610145:	19	49720834	C	0.186	0.043	1.59E-05	C	-0.148	0.059	1.30E-02	0.004	0.126	9.74E-01
RS9676781:4	19	49720910	C	0.097	0.026	2.07E-04	C	0.006	0.041	8.77E-01	0.001	0.076	9.89E-01
RS73050610:	19	49721561	C	0.091	0.026	4.38E-04	C	0.007	0.041	8.67E-01	0.012	0.077	8.73E-01
RS11481138:	19	49722791	C	0.186	0.043	1.62E-05	C	-0.148	0.059	1.30E-02	0.004	0.126	9.74E-01
RS56242266:	19	49723297	C	0.097	0.026	2.16E-04	C	0.004	0.041	9.27E-01	0.001	0.076	9.88E-01
RS56162137:	19	49723531	C	0.091	0.026	4.52E-04	C	0.003	0.041	9.45E-01	0.013	0.077	8.66E-01
RS8113222:4	19	49723889	A	0.090	0.027	7.35E-04	A	0.014	0.043	7.38E-01	0.002	0.079	9.81E-01
RS8103217:4	19	49725042	G	0.091	0.026	4.73E-04	G	0.003	0.041	9.46E-01	0.012	0.077	8.72E-01
RS3848548:4	19	49725487	C	0.097	0.026	2.18E-04	C	0.004	0.041	9.28E-01	0.001	0.076	9.88E-01
RS73578334:	19	49726807	T	0.154	0.040	1.23E-04	T	-0.144	0.058	1.34E-02	0.031	0.121	7.96E-01
RS8112298:4	19	49727160	C	0.090	0.026	4.83E-04	C	0.003	0.041	9.35E-01	0.012	0.077	8.72E-01
RS8112128:4	19	49727539	A	0.186	0.043	1.51E-05	A	-0.147	0.059	1.31E-02	0.004	0.125	9.77E-01
RS3848549:4	19	49727996	A	0.091	0.026	4.63E-04	G	-0.007	0.041	8.74E-01	-0.002	0.076	9.82E-01
RS3843746:4	19	49728186	T	0.090	0.026	5.38E-04	T	0.006	0.041	8.77E-01	0.016	0.077	8.39E-01
RS11692470(	19	49728428	T	0.186	0.043	1.42E-05	T	-0.150	0.060	1.26E-02	-0.002	0.126	9.85E-01
RS8105169:4	19	49728893	C	0.090	0.026	4.88E-04	C	0.002	0.041	9.57E-01	0.012	0.077	8.73E-01
RS14101904:	19	49729741	T	0.189	0.043	1.03E-05	T	-0.150	0.059	1.17E-02	0.005	0.124	9.67E-01
RS2878571:4	19	49729853	G	0.089	0.026	5.79E-04	G	0.006	0.041	8.84E-01	0.014	0.077	8.54E-01

RS12608776:	19	49731824	G	0.180	0.042	1.50E-05	G	-0.142	0.059	1.63E-02	-0.023	0.121	8.52E-01
RS11878934:	19	49732614	C	0.151	0.039	1.30E-04	C	-0.139	0.057	1.53E-02	0.006	0.119	9.60E-01
RS61184327:	19	49733234	T	0.150	0.039	1.31E-04	T	-0.139	0.057	1.53E-02	0.004	0.118	9.70E-01
RS12610107:	19	49735062	A	0.146	0.039	1.62E-04	A	-0.143	0.057	1.29E-02	0.001	0.115	9.96E-01
RS35785122:	19	49735107	T	0.180	0.041	1.16E-05	T	-0.146	0.058	1.25E-02	-0.030	0.118	8.02E-01
RS56758737:	19	49735111	T	0.181	0.041	9.87E-06	T	-0.147	0.058	1.20E-02	-0.028	0.118	8.11E-01
RS58106112:	19	49735271	A	0.182	0.041	9.55E-06	A	-0.147	0.058	1.20E-02	-0.027	0.119	8.17E-01
RS12610169:	19	49735520	T	0.181	0.041	1.06E-05	T	-0.146	0.058	1.28E-02	-0.027	0.119	8.19E-01
RS59251910:	19	49735637	T	0.181	0.041	1.03E-05	T	-0.146	0.058	1.28E-02	-0.026	0.119	8.24E-01
RS56674801:	19	49735940	G	0.182	0.041	9.65E-06	G	-0.146	0.058	1.24E-02	-0.024	0.119	8.37E-01
RS73580436:	19	49736660	G	0.183	0.041	8.24E-06	G	-0.146	0.058	1.23E-02	-0.019	0.120	8.72E-01
RS1175812:4	19	49737476	G	0.202	0.042	1.78E-06	G	-0.140	0.059	1.78E-02	0.002	0.125	9.89E-01
RS1175813:4	19	49737486	G	0.205	0.042	1.44E-06	G	-0.149	0.059	1.23E-02	0.004	0.126	9.76E-01
RS11699647:	20	22949613	A	0.159	0.044	2.69E-04	A	0.023	0.069	7.40E-01	0.325	0.153	3.35E-02
RS926727:22	20	22997422	T	0.140	0.033	1.84E-05	T	-0.023	0.052	6.63E-01	0.250	0.102	1.43E-02
RS36011369:	20	23006996	T	0.136	0.033	3.01E-05	T	-0.001	0.053	9.88E-01	0.216	0.103	3.60E-02
RS13045080:	20	23009546	G	0.134	0.033	3.74E-05	G	0.000	0.053	9.93E-01	0.214	0.103	3.80E-02
RS11905464:	20	23012830	G	0.135	0.033	3.21E-05	G	0.000	0.052	9.93E-01	0.213	0.103	3.85E-02
RS3176123:2	20	23027413	G	0.145	0.032	7.74E-06	G	0.016	0.053	7.61E-01	0.217	0.103	3.44E-02
RS1042579:2	20	23028724	A	0.146	0.032	6.92E-06	A	0.016	0.053	7.57E-01	0.240	0.103	1.99E-02
RS2749812:2	20	23062927	A	0.127	0.036	4.55E-04	A	0.055	0.061	3.73E-01	0.139	0.113	2.21E-01
RS2836907:4	21	40504673	A	-0.109	0.028	1.39E-04	A	-0.027	0.048	5.68E-01	-0.081	0.089	3.65E-01
RS1078306:4	21	40507612	G	-0.126	0.028	5.80E-06	G	-0.055	0.046	2.38E-01	-0.061	0.091	5.00E-01
RS56113957:	21	40509103	A	-0.127	0.028	4.69E-06	A	-0.053	0.046	2.57E-01	-0.059	0.091	5.13E-01
RS2836915:4	21	40509189	T	-0.128	0.028	4.46E-06	T	-0.053	0.046	2.56E-01	-0.060	0.091	5.09E-01
RS2836917:4	21	40509990	C	-0.128	0.028	4.84E-06	C	-0.055	0.046	2.31E-01	-0.073	0.092	4.27E-01
RS2836920:4	21	40512918	G	-0.103	0.026	9.38E-05	G	-0.033	0.043	4.37E-01	0.053	0.083	5.25E-01
RS2836977:4	21	40666066	C	-0.086	0.026	8.35E-04	C	-0.024	0.042	5.70E-01	0.014	0.084	8.70E-01
RS7282624:4	21	40667040	T	-0.086	0.026	8.34E-04	T	-0.024	0.042	5.69E-01	0.014	0.084	8.69E-01
RS34038277:	21	40699847	G	-0.086	0.026	9.14E-04	G	-0.013	0.042	7.57E-01	0.029	0.087	7.41E-01

Supplementary Table 7. Phase 1 and 2 results for all regions followed-up in the TJC28 analysis.

Regions were followed up if they included one SNP with P<1x10-5 and at least one other SNP within 200kb with P<5x10-5

			Phase 1				Phase 2a				Phase 2b		
Marker	**Chr**	**Position**	**Effect Allele**	**β**	**SE**	**P**	**Effect Allele**	**β**	**SE**	**P**	**β**	**SE**	**P**
RS7733945:5	5	56738129	G	0.121	0.034	4.22E-04	G	0.058	0.057	3.10E-01	-0.053	0.096	5.81E-01
RS2408764:5	5	56789257	A	0.124	0.035	3.73E-04	A	0.093	0.056	9.77E-02	0.003	0.102	9.80E-01
RS2910488:5	5	56791669	G	0.134	0.035	1.39E-04	G	0.084	0.057	1.36E-01	0.010	0.102	9.19E-01
RS36101114:	5	56800268	A	0.186	0.042	1.11E-05	A	0.035	0.067	5.97E-01	-0.170	0.125	1.75E-01
RS13163202:	5	56800442	G	0.190	0.041	4.31E-06	G	0.045	0.065	4.88E-01	-0.170	0.125	1.73E-01
RS17687301:	5	56801671	G	0.186	0.041	5.21E-06	G	0.045	0.065	4.90E-01	-0.169	0.124	1.74E-01
RS2408817:5	5	56804544	T	0.187	0.041	5.09E-06	T	0.049	0.066	4.54E-01	-0.169	0.124	1.74E-01
RS969627:56	5	56808503	T	0.107	0.032	7.36E-04	T	0.024	0.052	6.47E-01	-0.093	0.087	2.88E-01
RS10058818:	5	56808696	G	0.175	0.037	2.43E-06	G	0.059	0.059	3.12E-01	-0.101	0.113	3.68E-01
RS2408819:5	5	56811853	G	0.188	0.041	5.21E-06	G	0.058	0.066	3.81E-01	-0.161	0.125	1.98E-01
RS7732419:5	5	56814315	A	-0.108	0.033	9.16E-04	A	0.083	0.052	1.11E-01	0.029	0.091	7.53E-01
RS7715327:5	5	56816708	A	0.185	0.041	8.21E-06	A				-0.161	0.123	1.92E-01
RS28841699:	5	56817089	T	0.189	0.041	4.83E-06	T	0.057	0.066	3.94E-01	-0.158	0.125	2.05E-01
RS13155650:	5	56817256	C	-0.108	0.033	8.93E-04	C	0.078	0.052	1.34E-01	0.027	0.091	7.63E-01
RS1820124:5	5	56817523	A	0.150	0.036	2.57E-05	A	0.075	0.057	1.91E-01	-0.107	0.100	2.86E-01
RS10067535:	5	56821804	A	0.160	0.040	6.05E-05	A	0.026	0.066	6.88E-01	-0.123	0.115	2.88E-01
RS10053917:	5	56822514	A	0.157	0.037	1.75E-05	A	0.035	0.059	5.54E-01	-0.073	0.107	4.96E-01
RS10071415:	5	56823261	A	0.160	0.040	5.51E-05	A	0.020	0.066	7.61E-01	-0.123	0.115	2.88E-01
RS16887064:	5	56827833	C	-0.116	0.033	4.85E-04	C	0.080	0.052	1.25E-01	0.015	0.094	8.70E-01
RS6894346:5	5	56828038	C	-0.116	0.033	4.85E-04	C	0.079	0.052	1.28E-01	0.015	0.094	8.70E-01
RS7737477:5	5	56828350	C	0.158	0.040	6.70E-05	C	0.019	0.065	7.66E-01	-0.124	0.116	2.83E-01
RS7737786:5	5	56828545	G	0.157	0.044	3.57E-04	G	0.033	0.074	6.52E-01	-0.126	0.136	3.51E-01
RS10513117:	5	56839119	A	0.159	0.040	6.57E-05	A	0.017	0.065	7.98E-01	-0.123	0.116	2.85E-01
RS13180282:	5	56841371	A	-0.127	0.036	4.51E-04	A	0.030	0.054	5.87E-01	0.064	0.102	5.31E-01
RS11412084:	5	56845189	C	-0.123	0.036	6.90E-04	C	0.030	0.055	5.83E-01	0.060	0.102	5.59E-01
RS55680983:	5	56849541	C	-0.116	0.034	7.78E-04	C	0.087	0.052	9.72E-02	0.020	0.095	8.33E-01
RS12521025:	5	56860922	G	0.139	0.037	1.80E-04	G	-0.011	0.062	8.56E-01	-0.134	0.108	2.13E-01
RS4385168:5	5	56861430	G	0.140	0.037	1.65E-04	G	-0.014	0.062	8.26E-01	-0.134	0.108	2.14E-01
RS10472017:	5	56865025	T	0.157	0.038	4.16E-05	T	-0.018	0.063	7.79E-01	-0.131	0.112	2.40E-01
RS10078603:	5	56865792	A	-0.127	0.034	2.20E-04	A	0.084	0.053	1.14E-01	0.012	0.096	8.97E-01
RS10461636:	5	56866507	A	-0.128	0.034	2.00E-04	A	0.086	0.053	1.05E-01	0.025	0.096	7.92E-01
RS874061:56	5	56872531	G	-0.121	0.031	1.19E-04	A	-0.043	0.049	3.86E-01	-0.063	0.090	4.87E-01
RS6885855:5	5	56873637	G	0.159	0.039	3.56E-05	G	-0.024	0.062	7.05E-01	-0.145	0.113	1.99E-01
RS10058952:	5	56873915	T	0.160	0.039	3.32E-05	T	-0.025	0.062	6.88E-01	-0.146	0.113	1.96E-01
RS10472018:	5	56878155	G	0.136	0.034	5.53E-05	G	-0.084	0.057	1.42E-01	-0.072	0.106	4.93E-01
RS12518745:	5	56881357	C	0.132	0.033	8.44E-05	C	-0.067	0.057	2.34E-01	-0.071	0.103	4.88E-01
RS17132:568	5	56881662	A	0.131	0.033	8.86E-05	A	-0.067	0.057	2.37E-01	-0.071	0.103	4.90E-01
RS17739758:	5	56885624	G	0.129	0.034	1.21E-04	G	-0.067	0.056	2.32E-01	-0.044	0.106	6.76E-01
RS13172186:	5	56887318	T	-0.115	0.033	5.73E-04	T	0.075	0.053	1.64E-01	-0.018	0.094	8.46E-01
RS13173296:	5	56888027	T	-0.115	0.033	5.79E-04	T	0.075	0.053	1.60E-01	-0.014	0.094	8.82E-01
RS10078903:	5	56890354	A	0.138	0.034	5.39E-05	A	-0.054	0.057	3.42E-01	-0.041	0.109	7.09E-01
RS12055214:	5	56890523	C	-0.112	0.033	7.74E-04	C	0.054	0.053	3.05E-01	-0.004	0.092	9.62E-01
RS12055216:	5	56890571	C	-0.112	0.033	7.78E-04	C	0.050	0.052	3.44E-01	-0.005	0.092	9.57E-01
RS929809:56	5	56891257	G	-0.118	0.033	2.71E-04	G	0.043	0.052	4.03E-01	0.009	0.090	9.19E-01
RS156015:95	5	95831193	G	-0.120	0.035	5.50E-04	G	0.089	0.055	1.05E-01	0.050	0.093	5.86E-01
RS116247586	5	95954929	G	0.267	0.075	3.89E-04	G	0.141	0.129	2.74E-01	-0.184	0.215	3.91E-01
RS115959386	5	95956231	G	0.264	0.075	4.39E-04	G	0.141	0.129	2.73E-01	-0.185	0.214	3.87E-01
RS12153685:	5	95962592	A	0.281	0.076	2.31E-04	A	0.127	0.128	3.20E-01	-0.233	0.215	2.79E-01
RS12153149:	5	95962712	T	0.312	0.080	9.45E-05	T	0.128	0.127	3.16E-01	-0.216	0.212	3.07E-01
RS114464243	5	95966720	T	0.306	0.088	5.38E-04	T	0.276	0.129	3.31E-02	-0.263	0.235	2.64E-01
RS115356569	5	95969427	G	0.306	0.088	5.38E-04	G	0.275	0.129	3.32E-02	-0.262	0.235	2.65E-01
RS78721774:	5	95972784	A	0.306	0.088	5.50E-04	A	0.276	0.129	3.28E-02	-0.261	0.235	2.66E-01
RS114613344	5	95972994	G	0.305	0.088	5.51E-04	G	0.276	0.129	3.28E-02	-0.261	0.235	2.66E-01
RS55731125:	5	95976780	A	0.276	0.063	1.07E-05	A	0.169	0.093	6.96E-02	-0.182	0.180	3.14E-01
RS56039602:	5	95981776	G	0.277	0.061	4.89E-06	G	0.166	0.091	6.98E-02	-0.076	0.174	6.61E-01
RS10515242:	5	95982675	C	0.277	0.061	4.78E-06	C	0.166	0.091	6.89E-02	-0.081	0.172	6.37E-01
RS191133734	5	95984432	C	0.279	0.066	2.78E-05	C	0.204	0.105	5.35E-02	-0.038	0.189	8.41E-01
RS116324776	5	95988572	A	0.293	0.085	5.42E-04	A	-0.039	0.136	7.74E-01			

RS11463254(	5	96004344	T	0.306	0.085	3.35E-04	T	-0.069	0.131	5.99E-01			
RS11381219(	5	96032889	A	-0.396	0.113	4.36E-04	A	0.110	0.199	5.82E-01	-0.248	0.241	3.03E-01
RS18109343(	5	96038657	T	0.496	0.146	6.63E-04	T	-0.347	0.224	1.21E-01			
RS78971950:	5	96048605	A	0.491	0.147	8.33E-04	A	-0.351	0.211	9.63E-02			
RS74784837:	6	21957280	A	-0.368	0.099	2.01E-04	A	-0.109	0.167	5.14E-01	0.304	0.243	2.11E-01
RS2149334:2	6	21977074	C	0.107	0.032	9.91E-04	C	0.149	0.052	4.39E-03	-0.054	0.083	5.15E-01
RS62402542:	6	21978679	C	-0.199	0.046	1.76E-05	C	0.021	0.079	7.89E-01	0.073	0.119	5.43E-01
RS10806941:	6	21981157	A	-0.222	0.047	2.72E-06	A	0.041	0.085	6.29E-01	0.063	0.128	6.21E-01
RS6903359:2	6	21986214	C	-0.223	0.047	1.94E-06	C	0.026	0.083	7.55E-01	0.056	0.125	6.54E-01
RS2026708:2	6	21986895	G	-0.221	0.046	1.87E-06	G	0.024	0.084	7.77E-01	0.056	0.125	6.54E-01
RS6909264:2	6	21987116	C	-0.162	0.036	8.25E-06	C	-0.114	0.061	6.07E-02	0.106	0.100	2.89E-01
RS10946494:	6	21987427	G	0.118	0.032	2.50E-04	G	0.142	0.051	5.53E-03	-0.065	0.083	4.33E-01
RS6921547:2	6	21989092	C	0.122	0.032	1.62E-04	C	0.149	0.052	3.95E-03	-0.074	0.084	3.83E-01
RS78701001:	6	22015736	G	-0.363	0.110	9.42E-04	G	0.212	0.201	2.92E-01			
RS1034138:3	6	37535292	A	0.146	0.036	4.99E-05	A	-0.077	0.054	1.54E-01	0.085	0.097	3.79E-01
RS12205241:	6	37540870	A	0.346	0.073	2.09E-06	A	-0.228	0.106	3.15E-02	-0.039	0.172	8.19E-01
RS2776898:3	6	37541111	T	0.161	0.033	9.86E-07	T	-0.111	0.050	2.75E-02	0.143	0.090	1.13E-01
RS2797775:3	6	37541515	C	0.166	0.036	3.45E-06	C	-0.071	0.053	1.80E-01	0.105	0.098	2.80E-01
RS1776438:3	6	37553497	T	0.139	0.037	2.12E-04	T	-0.106	0.056	6.14E-02	-0.029	0.112	7.95E-01
RS2776899:3	6	37555313	A	0.131	0.037	3.60E-04	A	-0.095	0.056	8.83E-02	-0.007	0.109	9.48E-01
RS2797788:3	6	37556367	G	0.132	0.037	3.31E-04	G	-0.099	0.056	7.57E-02	-0.019	0.107	8.61E-01
RS9369010:3	6	37563373	A	0.126	0.035	3.41E-04	A	-0.117	0.054	2.96E-02	-0.026	0.108	8.12E-01
RS9369011:3	6	37563752	T	0.135	0.037	2.12E-04	T	-0.100	0.056	7.52E-02	-0.028	0.113	8.07E-01
RS78645868:	6	37568921	A	0.139	0.037	1.63E-04	A	-0.093	0.056	9.82E-02	-0.020	0.110	8.53E-01
RS9366936:3	6	37569453	T	0.141	0.037	1.45E-04	T	-0.090	0.057	1.13E-01	-0.035	0.113	7.58E-01
RS11766828:	7	16498897	T	-0.111	0.033	6.83E-04	T	-0.012	0.052	8.24E-01	0.063	0.091	4.84E-01
RS2528465:1	7	16520887	C	-0.104	0.031	6.97E-04	C	-0.005	0.052	9.16E-01	0.125	0.087	1.50E-01
RS2704669:1	7	16521181	C	-0.115	0.032	3.45E-04	C	0.008	0.052	8.83E-01	0.222	0.096	2.01E-02
RS6461261:1	7	16536546	A	0.105	0.031	7.46E-04	T	-0.018	0.050	7.22E-01	0.151	0.089	8.91E-02
RS917221:16	7	16541388	A	-0.104	0.031	8.52E-04	A	-0.027	0.050	5.89E-01	0.151	0.089	8.79E-02
RS4721507:1	7	16544311	G	0.138	0.033	2.43E-05	G	0.013	0.053	8.13E-01	-0.098	0.090	2.75E-01
RS886758:16	7	16544777	T	0.139	0.032	1.95E-05	T	-0.006	0.053	9.06E-01	-0.086	0.091	3.45E-01
RS886757:16	7	16544872	G	0.138	0.032	2.06E-05	G	-0.006	0.053	9.12E-01	-0.072	0.090	4.22E-01
RS11446140:	7	16547268	T	0.145	0.032	7.50E-06	T	-0.001	0.054	9.78E-01	-0.116	0.093	2.12E-01
RS17169519:	7	16550092	C	0.119	0.031	1.58E-04	C	0.020	0.052	7.01E-01	-0.105	0.087	2.26E-01
RS17169520:	7	16550888	G	0.119	0.035	6.25E-04	G	-0.011	0.055	8.41E-01	-0.093	0.094	3.22E-01
RS55884702:	7	16552081	A	0.156	0.036	1.54E-05	A	0.015	0.058	7.92E-01	-0.141	0.099	1.56E-01
RS11772541:	7	16554248	A	0.125	0.034	2.70E-04	A	0.019	0.055	7.35E-01	-0.078	0.096	4.17E-01
RS73076743:	7	16556172	T	0.157	0.036	1.29E-05	T	0.003	0.058	9.55E-01	-0.144	0.100	1.50E-01
RS17367241:	7	16558486	T	0.120	0.035	5.44E-04	T	-0.026	0.055	6.37E-01	-0.090	0.097	3.53E-01
RS58891569:	7	16559017	T	0.118	0.035	6.40E-04	T	-0.022	0.055	6.86E-01	-0.093	0.097	3.37E-01
RS11766241:	7	16560143	C	0.118	0.035	6.63E-04	C	-0.025	0.055	6.58E-01	-0.097	0.097	3.21E-01
RS11762176:	7	16562458	C	0.119	0.035	6.04E-04	C	-0.020	0.055	7.15E-01	-0.107	0.099	2.79E-01
RS17464820:	7	16563868	G	0.120	0.035	5.44E-04	G	-0.020	0.055	7.12E-01	-0.116	0.100	2.48E-01
RS11765776:	7	16564431	G	0.120	0.035	5.24E-04	G	-0.022	0.055	6.96E-01	-0.121	0.101	2.28E-01
RS28442057:	15	55110958	T	0.143	0.032	7.89E-06	T	-0.012	0.052	8.16E-01	0.039	0.094	6.79E-01
RS35839641:	15	55112746	C	0.139	0.032	1.67E-05	C	-0.016	0.052	7.64E-01	0.044	0.096	6.44E-01
RS8027395:5	15	55112976	C	0.139	0.032	1.75E-05	C	-0.015	0.052	7.65E-01	0.043	0.096	6.49E-01
RS8026599:5	15	55113077	A	0.137	0.032	2.37E-05	A	-0.016	0.052	7.62E-01	0.043	0.096	6.50E-01
RS12922544:	16	14089420	T	0.139	0.033	3.29E-05	T	-0.032	0.050	5.26E-01	0.023	0.086	7.94E-01
RS11642211:	16	14089855	G	0.119	0.032	2.57E-04	G	-0.039	0.050	4.28E-01	0.012	0.086	8.92E-01
RS8053013:1	16	14090683	T	0.142	0.033	1.76E-05	T	-0.018	0.050	7.25E-01	0.022	0.085	7.96E-01
RS12446816:	16	14092341	G	0.150	0.033	5.14E-06	G	-0.014	0.050	7.75E-01	0.006	0.085	9.48E-01
RS17256168:	16	14098247	C	0.125	0.032	8.48E-05	C	-0.008	0.050	8.66E-01	0.002	0.083	9.80E-01
RS1651186:1	16	14113801	G	0.114	0.032	3.47E-04	G	-0.033	0.050	5.05E-01	0.039	0.086	6.53E-01
RS1651184:1	16	14115453	A	0.123	0.032	1.13E-04	A	-0.040	0.050	4.33E-01	0.020	0.086	8.13E-01
RS11137763:	17	42784441	A	0.338	0.096	4.07E-04	A	-0.017	0.143	9.05E-01	-0.790	0.366	3.07E-02
RS392407:42	17	42911757	G	0.306	0.089	6.39E-04	G	-0.065	0.146	6.59E-01	-0.267	0.317	3.99E-01
RS7213960:4	17	42923398	T	0.111	0.031	3.83E-04	T	0.053	0.049	2.85E-01	0.018	0.088	8.35E-01
RS9910260:4	17	42939170	A	0.150	0.034	7.79E-06	A	0.049	0.055	3.75E-01	0.088	0.099	3.75E-01
RS9912760:4	17	42939189	G	0.145	0.034	1.49E-05	G	0.047	0.055	3.92E-01	0.083	0.099	3.99E-01
RS7224602:4	17	42939605	T	0.150	0.034	7.82E-06	T	0.049	0.055	3.75E-01	0.084	0.099	3.94E-01
RS8077272:4	17	42941468	C	0.150	0.034	7.82E-06	C	0.049	0.055	3.75E-01	0.084	0.099	3.94E-01

RS8072901:4	17	42941517	A	0.150	0.034	7.82E-06	A	0.049	0.055	3.74E-01	0.084	0.099	3.94E-01
RS11658874:	17	42943091	T	0.150	0.034	7.82E-06	T	0.049	0.055	3.74E-01	0.084	0.099	3.94E-01
RS9899734:4	17	42944218	T	0.150	0.034	7.80E-06	T	0.049	0.055	3.74E-01	0.084	0.099	3.95E-01
RS7208122:4	17	42947087	C	0.150	0.034	7.81E-06	C	0.049	0.055	3.74E-01	0.084	0.099	3.95E-01
RS7212451:4	17	42947114	C	0.150	0.034	7.81E-06	C	0.049	0.055	3.74E-01	0.084	0.099	3.95E-01
RS9910936:4	17	42949168	T	0.152	0.034	6.70E-06	T	0.048	0.055	3.82E-01	0.084	0.099	3.96E-01
RS9915732:4	17	42949202	T	0.150	0.034	7.98E-06	T	0.048	0.055	3.82E-01	0.084	0.099	3.96E-01
RS11654183:	17	42949808	A	0.151	0.034	7.76E-06	A	0.050	0.055	3.69E-01	0.070	0.099	4.80E-01
RS7210874:4	17	42951169	G	0.146	0.034	1.32E-05	G	0.047	0.055	3.91E-01	0.085	0.099	3.91E-01
RS7214846:4	17	42951265	G	0.150	0.034	7.79E-06	G	0.049	0.055	3.74E-01	0.084	0.099	3.97E-01
RS7211720:4	17	42953991	C	0.150	0.034	7.77E-06	C	0.049	0.055	3.74E-01	0.083	0.099	4.01E-01
RS7212041:4	17	42954134	C	0.150	0.034	7.86E-06	C	0.049	0.055	3.74E-01	0.083	0.099	4.01E-01
RS11652831:	17	42955227	T	0.150	0.034	7.77E-06	T	0.049	0.055	3.74E-01	0.083	0.099	4.03E-01
RS11868767:	17	42956055	A	0.150	0.034	7.75E-06	A	0.049	0.055	3.74E-01	0.082	0.099	4.05E-01
RS7213110:4	17	42956535	G	0.150	0.034	7.76E-06	G	0.048	0.055	3.87E-01	0.082	0.099	4.07E-01
RS2289675:4	17	42957127	A	0.150	0.034	7.75E-06	A	0.048	0.055	3.87E-01	0.082	0.099	4.09E-01
RS7223598:4	17	42957631	A	0.150	0.034	7.73E-06	A	0.048	0.055	3.87E-01	0.081	0.099	4.10E-01
RS12602642:	17	42958374	A	0.139	0.033	2.51E-05	A	0.015	0.054	7.74E-01	0.087	0.097	3.67E-01
RS36120415:	17	42959491	G	0.111	0.031	3.90E-04	G	0.054	0.050	2.78E-01	0.021	0.089	8.16E-01
RS1561970:4	17	42960624	A	0.151	0.034	7.66E-06	A	0.047	0.055	3.93E-01	0.081	0.099	4.10E-01
RS1561967:4	17	42961959	C	0.150	0.034	7.83E-06	C	0.047	0.055	3.94E-01	0.088	0.099	3.71E-01
RS9896445:4	17	42965540	C	0.151	0.034	7.96E-06	C	0.047	0.055	3.89E-01	0.088	0.099	3.75E-01
RS7210042:4	17	42967295	C	0.150	0.034	8.41E-06	C	0.046	0.055	3.96E-01	0.090	0.099	3.64E-01
RS6503407:4	17	42969035	A	0.150	0.034	8.59E-06	A	0.047	0.055	3.94E-01	0.092	0.099	3.54E-01
RS9895197:4	17	42971570	T	0.150	0.034	8.91E-06	T	0.047	0.055	3.94E-01	0.094	0.100	3.44E-01
RS75707322:	17	42972122	A	0.202	0.057	3.94E-04	A	0.177	0.099	7.64E-02	0.205	0.159	1.98E-01
RS9908594:4	17	42973313	A	0.149	0.034	9.16E-06	A	0.047	0.055	3.94E-01	0.097	0.100	3.28E-01
RS12947309:	17	42974143	T	0.149	0.034	9.41E-06	T	0.047	0.055	3.94E-01	0.098	0.100	3.28E-01
RS8068761:4	17	42976114	T	0.148	0.034	1.05E-05	T	0.047	0.055	3.94E-01	0.104	0.100	2.98E-01
RS7222312:4	17	42978554	C	0.149	0.034	9.80E-06	C	0.047	0.055	3.94E-01	0.091	0.100	3.61E-01
RS8079610:4	17	42979670	A	0.149	0.034	9.33E-06	A	0.047	0.055	3.94E-01	0.090	0.100	3.68E-01
RS8079308:4	17	42980189	A	0.148	0.034	1.06E-05	A	0.048	0.055	3.83E-01	0.091	0.100	3.63E-01
RS9904512:4	17	42981104	C	0.121	0.032	1.68E-04	C	0.015	0.051	7.63E-01	0.085	0.094	3.68E-01
RS3826425:4	17	42981654	G	0.132	0.032	4.32E-05	G	0.070	0.053	1.88E-01	0.093	0.099	3.49E-01
RS3744473:4	17	42982288	G	0.149	0.034	9.54E-06	G	0.047	0.055	3.93E-01	0.091	0.100	3.63E-01
RS12222:429	17	42982729	A	0.149	0.034	8.68E-06	A	0.047	0.055	3.94E-01	0.091	0.100	3.63E-01
RS17027:429	17	42983193	G	0.149	0.034	8.98E-06	G	0.047	0.055	3.94E-01	0.091	0.100	3.62E-01
RS11558961:	17	42984687	C	0.149	0.034	8.95E-06	C	0.047	0.055	3.88E-01	0.092	0.100	3.59E-01
RS11651396:	17	42984842	A	0.149	0.034	8.95E-06	A	0.047	0.055	3.88E-01	0.092	0.100	3.59E-01
RS9915329:4	17	42985823	C	0.103	0.031	9.79E-04	C	0.050	0.050	3.25E-01	0.026	0.089	7.68E-01
RS9916491:4	17	42987524	C	0.149	0.034	8.68E-06	C	0.047	0.055	3.88E-01	0.097	0.100	3.30E-01
RS2289679:4	17	42988092	C	0.150	0.034	8.31E-06	C	0.047	0.055	3.88E-01	0.099	0.100	3.21E-01
RS3785891:4	17	42990340	T	0.123	0.032	1.07E-04	T	0.023	0.049	6.44E-01	0.110	0.092	2.29E-01
RS56986638:	17	43024776	T	0.165	0.040	3.84E-05	T	0.076	0.064	2.33E-01	0.012	0.114	9.18E-01
RS7222424:4	17	43025648	A	0.165	0.040	3.89E-05	A	0.076	0.064	2.33E-01	0.010	0.114	9.29E-01
RS9674520:4	17	43027713	T	0.164	0.040	4.02E-05	T	0.077	0.064	2.30E-01	0.013	0.114	9.10E-01
RS8068006:4	17	43028619	T	0.164	0.040	4.09E-05	T	0.077	0.064	2.31E-01	0.014	0.113	9.05E-01
RS8067703:4	17	43029158	A	0.164	0.040	4.13E-05	A	0.077	0.064	2.29E-01	0.014	0.113	8.99E-01
RS8073976:4	17	43033225	A	0.164	0.040	4.07E-05	A	0.077	0.064	2.30E-01	0.021	0.111	8.48E-01
RS3024272:4	17	43044680	A	0.134	0.039	5.88E-04	A	0.043	0.063	4.97E-01	-0.007	0.111	9.48E-01
RS79553250:	17	43049319	T	0.139	0.039	4.11E-04	T	0.045	0.063	4.75E-01	-0.011	0.111	9.22E-01
RS11362918(	17	43051948	T	0.138	0.039	4.72E-04	T	0.050	0.064	4.29E-01	-0.016	0.113	8.85E-01

Supplementary Table 8. DAS28 results for all SNPs with P<0.0001 in a genome-wide study of methotrexate response in Indian rheumatoid arthritis patients (Senapti et al.)

Effect direction is in relation to effect allele: + indicates improvement in DAS28 score/response, - indicates increase in DAS score/non-response.

					DAS28		Effect Direction		
Marker	**Chr**	**Position**	**Senapti *et al.* P-value**	**Effect Allele**	**β**	**P-value**	**Senapti *et al.***	**This Study**	**gene**
RS3820304	1	13938788	0.0007	G	0.029	4.45E-01	-	-	*PDPN*
RS12746273	1	23950177	0.001	T	0.033	4.37E-01	+	-	
RS12142410	1	30636759	0.0001	G	0.049	6.65E-01	-	-	
RS10493098	1	42261889	0.0002	C	0.032	3.64E-01	-	-	*HIVEP3*
RS332823	1	61674052	0.0008	G	0.004	9.04E-01	+	-	*NFIA*
RS855849	1	64353473	0.001	A	0.002	9.57E-01	+	-	*ROR1*
RS7511712	1	118279908	0.0005	C	-0.007	8.52E-01	+	+	
RS3754123	1	118319990	0.0002	G	-0.030	4.09E-01	+	+	*LOC100131261*
RS3754125	1	118323282	0.0002	C	-0.030	3.99E-01	+	+	
RS12128109	1	153212668	0.0008	A	0.016	6.69E-01	+	-	
RS1317986	1	159955432	0.0004	A	0.004	9.18E-01	-	-	
RS6699725	1	161703525	0.0004	T	0.067	2.10E-01	-	-	
RS3748699	1	165877751	0.0007	A	-0.031	5.35E-01	-	+	*UCK2*
RS16852868	1	165881969	0.0005	C	-0.031	5.32E-01	-	+	
RS3010141	1	195854742	0.0009	T	-0.078	6.73E-02	+	+	
RS4423076	1	203123837	0.0005	T	0.071	1.77E-01	+	-	*ADORA1*
RS6703183	1	209712889	0.0006	C	0.066	7.93E-02	+	-	
RS9424584	1	232840697	0.0001	C	-0.004	9.45E-01	-	+	
RS499370	1	238751937	0.0005	A	-0.008	8.31E-01	-	+	
RS947103	1	245766651	0.0006	A	0.025	4.82E-01	+	-	*KIF26B*
RS1437701	2	4173729	0.0006	T	0.068	5.32E-02	-	-	
RS10204428	2	20084133	0.0006	G	0.025	6.82E-01	+	-	*FLJ12334*
RS13036246	2	25532969	0.0005	C	0.025	4.62E-01	+	-	*DNMT3A*
RS6722613	2	25539357	0.0001	G	0.050	3.61E-01	+	-	*DNMT3A*
RS10208987	2	44043135	0.0003	G	0.055	3.71E-01	-	-	*ABCG5*
RS4148189	2	44047530	0.0005	T	0.095	8.22E-02	-	-	*ABCG5*
RS6705555	2	72062531	0.0005	T	0.022	5.54E-01	+	-	
RS2861609	2	78633880	0.0005	A	-0.012	8.38E-01	+	+	
RS1455390	2	78655712	0.0007	G	-0.014	8.12E-01	+	+	
RS724710	2	111907691	0.0007	T	-0.046	4.13E-01	-	+	*BCL2L11*
RS1878114	2	118355321	0.0005	C	-0.013	8.31E-01	-	+	
RS4849589	2	118356511	0.0004	T	-0.013	8.33E-01	-	+	
RS12691828	2	133530648	0.0002	G	0.042	2.44E-01	-	-	*NCKAP5*
RS12466096	2	134861399	0.0006	C	-0.008	8.47E-01	-	+	
RS6749316	2	138073500	0.0009	T	-0.045	2.00E-01	+	+	*THSD7B*
RS10206675	2	154440521	0.0007	G	-0.014	8.35E-01	-	+	
RS1401750	2	154453616	0.0009	A	-0.006	8.90E-01	-	+	
RS4335901	2	154460874	0.0009	G	-0.011	7.68E-01	-	+	
RS1519635	2	154481164	0.0004	G	-0.001	9.89E-01	-	+	
RS908919	2	154519277	0.0007	T	-0.046	2.49E-01	-	+	
RS2881873	2	154524124	0.0008	T	0.031	5.22E-01	-	-	
RS1435004	2	163657083	0.0007	A	-0.026	5.46E-01	-	+	*KCNH7*
RS13018302	2	163703613	0.0006	C	-0.058	1.46E-01	-	+	
RS3817135	2	165753118	0.0005	G	-0.002	9.46E-01	+	+	
RS16867139	2	180872427	0.0009	G	-0.045	5.91E-01	+	+	
RS10188385	2	185949889	0.0003	C	0.065	1.20E-01	+	-	
RS9288109	2	186025368	0.0005	C	0.086	2.03E-01	+	-	
RS1038361	2	186031490	0.0004	A	0.090	2.21E-01	+	-	
RS6795047	3	1933220	0.0008	T	-0.025	6.38E-01	-	+	
RS1387091	3	1988126	0.0008	G	-0.039	3.95E-01	-	+	
RS13065523	3	4274646	0.0003	T	-0.057	1.01E-01	-	+	
RS1876613	3	4282950	0.0003	C	-0.059	8.92E-02	-	+	
RS12486791	3	4325300	0.000094	C	-0.056	1.12E-01	-	+	
RS3804989	3	4728008	0.0003	G	-0.031	3.71E-01	-	+	*ITPR1*
RS6803471	3	4732040	0.0008	G	-0.040	2.48E-01	-	+	*ITPR1*
RS9311395	3	4741821	0.0005	A	-0.041	2.42E-01	-	+	*ITPR1*
RS155421	3	6464294	0.0005	T	0.008	8.21E-01	+	-	
RS7645290	3	15855531	0.0006	C	0.063	1.70E-01	+	-	*ANKRD28*
RS6764520	3	54591243	0.001	G	-0.018	6.59E-01	-	+	*CACNA2D3*
RS3772985	3	58186719	0.0003	A	-0.007	8.94E-01	-	+	*DNASE1L3*
RS1349008	3	76721413	0.001	G	-0.038	4.70E-01	-	+	*ROBO2*
RS4350947	3	121744849	0.0002	C	0.004	9.30E-01	-	-	

RS931574	3	123098965	0.0005	T	0.010	8.46E-01	-	-	*ADCY5*
RS12636883	3	132429522	0.0006	A	-0.020	8.11E-01	-	+	*NPHP3-ACAD11*
RS2369832	3	132437390	0.0008	T	-0.012	7.94E-01	-	+	*NPHP3-ACAD11*
RS3860503	3	132438301	0.0004	C	-0.014	7.52E-01	-	+	*NPHP3-ACAD11*
RS13078077	3	143853149	0.0005	G	-0.024	5.07E-01	+	+	
RS6440786	3	151510257	0.0002	G	-0.009	8.44E-01	-	+	
RS819851	3	155706888	0.0004	C	-0.117	9.36E-02	-	+	
RS7651855	3	160412175	0.000071	T	0.000	9.97E-01	-	-	
RS1378661	3	160424299	0.00008	T	0.007	8.96E-01	-	-	
RS7624766	3	160429869	4.80E-07	G	0.014	8.42E-01	-	-	
RS6793037	3	160447946	0.0002	C	0.073	3.44E-01	-	-	
RS13061243	3	165859107	0.0007	C	-0.017	6.41E-01	-	+	
RS9682469	3	168414697	0.0009	C	-0.027	4.48E-01	+	+	*EGFEM1P*
RS790003	3	194341327	0.0006	A	-0.019	5.98E-01	-	+	*TMEM44*
RS3901794	4	7149008	0.0007	T	0.042	2.39E-01	-	-	
RS11724494	4	7153642	0.0002	T	-0.057	1.13E-01	-	+	
RS6826086	4	21614663	0.0008	T	-0.110	1.90E-02	+	+	*KCNIP4*
RS10516395	4	21628375	0.0007	C	-0.087	1.20E-01	+	+	*KCNIP4*
RS13152723	4	22203707	0.0005	G	-0.014	7.48E-01	-	+	
RS4697041	4	23603378	0.0003	A	-0.011	8.69E-01	-	+	
RS880358	4	56276478	0.0009	T	-0.002	9.65E-01	+	+	*TMEM165*
RS2412664	4	56457387	0.001	A	0.008	8.56E-01	+	-	*PDCL2*
RS1355803	4	60534555	0.0002	C	0.019	6.99E-01	+	-	
RS17015234	4	90162268	0.0006	A	0.052	1.53E-01	-	-	
RS10516570	4	112478170	0.001	G	0.022	5.72E-01	-	-	
RS17051353	4	122361659	0.0003	A	-0.067	2.65E-01	-	+	
RS13110000	4	123578060	0.0007	C	0.051	3.11E-01	-	-	
RS10440412	4	126734051	0.0006	T	-0.075	9.88E-02	-	+	
RS10017061	4	130788112	0.000027	A	-0.117	5.24E-01	-	+	
RS4487360	4	130790570	0.000031	T	-0.117	5.24E-01	-	+	
RS1517955	4	137912755	0.0001	T	-0.007	8.36E-01	-	+	
RS1319034	4	154966332	0.0007	C	-0.025	5.21E-01	-	+	
RS17372382	4	154968120	0.0007	G	-0.040	2.64E-01	-	+	
RS2611215	4	166574267	0.0006	A	0.063	2.98E-01	-	-	
RS2611212	4	166574651	0.0004	A	0.087	1.98E-01	-	-	
RS17688688	4	166592304	0.0005	A	0.049	5.52E-01	-	-	
RS1976543	4	170052646	0.0008	T	-0.070	6.08E-02	-	+	*SH3RF1*
RS2660432	4	170075171	0.0004	T	-0.067	7.55E-02	-	+	*SH3RF1*
RS10004048	4	170075273	0.0006	T	-0.068	7.16E-02	-	+	*SH3RF1*
RS11133119	4	176820049	0.0004	C	-0.028	4.34E-01	+	+	*GPM6A*
RS6827227	4	178755843	0.001	T	0.016	6.46E-01	-	-	*LOC285501*
RS12188301	5	1847639	0.0009	A	-0.033	7.90E-01	-	+	
RS1370978	5	10826267	0.0009	T	-0.022	6.12E-01	-	+	
RS16894002	5	24817630	0.0003	G	-0.024	8.19E-01	-	+	
RS10078309	5	24826395	0.0009	C	-0.019	8.58E-01	-	+	
RS10070340	5	36641769	0.0009	A	0.041	3.05E-01	-	-	*SLC1A3*
RS2124948	5	52928392	0.0005	T	-0.011	7.29E-01	+	+	*NDUFS4*
RS12517465	5	52942938	0.0005	A	-0.011	7.28E-01	+	+	*NDUFS4*
RS2290697	5	52978722	0.0007	T	-0.010	7.54E-01	+	+	*NDUFS4*
RS7730112	5	77251788	0.0005	A	0.045	4.82E-01	+	-	
RS16878218	5	80212435	0.0004	G	-0.009	8.57E-01	+	+	
RS2369629	5	98524496	0.0007	T	-0.008	8.12E-01	+	+	
RS989983	5	125034613	0.0003	A	0.004	9.31E-01	+	-	
RS245047	5	149327973	0.0003	T	-0.023	5.25E-01	-	+	
RS7731137	5	154005654	0.0006	T	-0.004	9.53E-01	-	+	
RS6895949	5	163273413	0.0005	A	0.062	2.52E-01	-	-	
RS1421862	5	163276790	0.0007	G	0.049	2.52E-01	-	-	
RS10060591	5	163293601	0.0001	T	0.058	4.11E-01	-	-	
RS11749716	5	165106225	0.0009	T	0.113	3.26E-02	-	-	
RS4701077	5	178604377	0.0002	T	0.013	8.65E-01	-	-	*ADAMTS2*
RS2170616	6	2557509	0.0006	T	-0.020	7.32E-01	-	+	
RS4959684	6	2589139	0.0007	T	-0.015	6.91E-01	+	+	
RS12664620	6	6282943	0.0007	G	0.015	7.30E-01	+	-	*F13A1*
RS9296672	6	13425532	0.0008	T	0.073	7.65E-02	+	-	*GFOD1*
RS2876366	6	14577131	0.0001	A	-0.050	3.51E-01	-	+	
RS9476596	6	14582008	0.0001	C	-0.051	3.60E-01	-	+	
RS1259065	6	15001506	0.0008	C	-0.033	3.21E-01	+	+	

RS4645427	6	18531115	0.0004	A	-0.018	6.30E-01	-	+	
RS4716289	6	18582886	0.0006	A	0.029	4.44E-01	+	-	
RS11751260	6	21959437	0.0002	C	0.044	2.82E-01	-	-	*LINC00340*
RS13212670	6	21969495	0.0009	T	0.010	7.90E-01	+	-	*LINC00340*
RS2534678	6	31463963	0.0003	T	0.041	4.37E-01	-	-	
RS2534657	6	31472459	0.0006	T	0.043	4.14E-01	-	-	*MICB*
RS2854028	6	33179689	0.0005	T	0.017	6.67E-01	-	-	*RING1*
RS2237093	6	36035354	0.0006	T	0.022	6.79E-01	-	-	*MAPK14*
RS9380546	6	36060240	0.0008	A	0.026	6.43E-01	-	-	*MAPK14*
RS4395718	6	36215693	0.0009	A	-0.006	8.84E-01	+	+	*PNPLA1*
RS12200371	6	38446634	0.0003	G	-0.015	8.03E-01	-	+	*BTBD9*
RS6458085	6	38884441	0.0007	A	-0.003	9.29E-01	-	+	*LOC100131047*
RS1964743	6	83445429	0.0008	A	0.106	1.55E-03	+	-	
RS7755798	6	109637154	0.0008	T	-0.002	9.60E-01	-	+	
RS1358771	6	132451644	0.001	G	0.027	4.93E-01	+	-	
RS6570330	6	139632859	0.0001	A	0.020	5.83E-01	+	-	
RS10946113	6	158584691	0.0005	A	0.069	5.52E-01	-	-	*SERAC1*
RS9365947	6	158588702	0.0005	T	0.106	2.21E-01	-	-	*SERAC1*
RS9348087	6	158598474	0.0005	T	0.106	2.15E-01	-	-	*GTF2H5*
RS9348153	6	158643526	0.0007	T	0.135	2.51E-01	-	-	
RS9348215	6	158685709	0.0009	T	0.065	1.78E-01	-	-	
RS10155975	7	13493700	0.0004	T	0.027	6.55E-01	+	-	
RS10242586	7	13497326	0.0002	T	0.039	5.12E-01	+	-	
RS4721415	7	15236132	0.0005	A	0.018	7.55E-01	-	-	
RS7792372	7	31213561	0.0005	C	-0.034	6.23E-01	-	+	
RS7803708	7	51148028	0.001	G	0.023	6.40E-01	-	-	*COBL*
RS10488323	7	52655888	0.0006	C	-0.017	7.56E-01	+	+	
RS10282659	7	81279925	0.0003	T	-0.014	7.43E-01	-	+	
RS10242168	7	81279976	0.0003	G	-0.016	7.18E-01	-	+	
RS258704	7	81762176	0.0002	C	-0.042	2.84E-01	-	+	*CACNA2D1*
RS10954664	7	81775555	0.0002	C	0.016	6.36E-01	+	-	*CACNA2D1*
RS3808267	7	90595848	0.0005	G	-0.038	3.47E-01	-	+	*CDK14*
RS1527680	7	94534886	0.0001	G	-0.071	4.23E-01	-	+	
RS17157128	7	103538333	0.0005	G	0.016	8.11E-01	-	-	*RELN*
RS10277802	7	103562551	0.001	A	-0.117	4.50E-01	-	+	*RELN*
RS284395	7	121885177	0.0007	A	-0.010	8.13E-01	-	+	
RS284391	7	121890781	0.0007	A	-0.010	8.17E-01	-	+	
RS4726603	7	139801222	0.0004	T	-0.003	9.71E-01	-	+	*JHDM1D*
RS1062277	7	139801777	0.0004	G	-0.002	9.81E-01	-	+	*JHDM1D*
RS11486906	7	139809574	0.0004	C	-0.003	9.71E-01	-	+	*JHDM1D*
RS12539339	7	140097554	0.0009	G	-0.074	4.15E-01	+	+	*SLC37A3*
RS855679	7	149478321	0.0008	C	0.015	8.06E-01	-	-	*SSPO*
RS7776495	7	154077301	0.0009	T	-0.010	7.87E-01	+	+	*DPP6*
RS1420823	8	5225481	0.0006	C	-0.014	6.93E-01	-	+	
RS7813625	8	27159459	0.0004	C	-0.018	7.92E-01	+	+	*TRIM35*
RS327329	8	31853498	0.0009	C	0.065	2.21E-01	+	-	*NRG1*
RS1462875	8	31860194	0.0005	A	0.048	2.12E-01	+	-	*NRG1*
RS10958713	8	42180716	0.0003	T	0.027	4.66E-01	-	-	*IKBKB*
RS1608806	8	83729106	0.0008	C	-0.080	1.33E-01	+	+	
RS2449529	8	98785523	0.0001	G	-0.049	4.42E-01	-	+	
RS6470446	8	127504653	0.0005	C	-0.010	8.97E-01	+	+	
RS1339287	9	8233804	0.0008	T	-0.019	6.10E-01	+	+	
RS1768575	9	8235513	0.001	A	-0.023	6.29E-01	+	+	
RS1341740	9	15850604	0.001	T	-0.026	7.92E-01	-	+	*CCDC171*
RS1359715	9	78354076	0.0007	T	0.003	9.56E-01	-	-	
RS155531	9	82535584	0.0003	C	0.047	2.13E-01	+	-	
RS267574	9	82535883	0.0009	A	0.042	2.64E-01	+	-	
RS3739809	9	82941434	0.0004	G	-0.089	8.93E-02	+	+	
RS11138635	9	82987698	0.0004	G	-0.035	3.95E-01	+	+	
RS3927559	9	83726045	0.0009	T	-0.003	9.49E-01	-	+	
RS10980551	9	113504910	0.001	G	0.002	9.64E-01	+	-	*MUSK*
RS10121207	9	119990164	0.0001	T	-0.039	2.69E-01	-	+	*ASTN2*
RS710074	9	133967295	0.0005	C	-0.019	8.00E-01	+	+	*LAMC3*
RS1320077	10	1618731	0.0001	A	-0.025	4.84E-01	-	+	*ADARB2*
RS1901633	10	4810561	0.000014	G	0.013	7.37E-01	-	-	
RS3123078	10	51524971	0.0003	C	-0.016	6.09E-01	-	+	
RS10993994	10	51549496	0.0006	T	-0.009	8.64E-01	-	+	

RS3780944	10	73858454	0.0006	C	-0.099	1.75E-01	+	+	*ASCC1*
RS2250840	10	78910074	0.001	G	0.002	9.55E-01	+	-	*KCNMA1*
RS3852502	10	92836763	0.0006	G	-0.064	6.55E-02	+	+	
RS4570501	10	128556923	0.0002	G	-0.024	4.85E-01	+	+	*LOC728065*
RS11245203	10	128562826	0.0003	C	-0.037	3.02E-01	+	+	*LOC728065*
RS7896581	10	129673530	0.0007	T	-0.041	4.02E-01	-	+	
RS10741770	11	19397116	0.0008	A	0.031	4.08E-01	-	-	*NAV2*
RS4756731	11	42443911	0.000087	G	0.018	6.24E-01	+	-	
RS3861059	11	42450746	0.000093	T	0.016	6.47E-01	+	-	
RS2292891	11	43942186	0.001	C	0.020	8.28E-01	+	-	*LOC100507300*
RS2434484	11	43949008	0.001	G	0.036	5.87E-01	+	-	
RS7103602	11	43949511	0.0007	G	-0.014	8.75E-01	+	+	
RS4356257	11	87263827	0.0006	A	0.011	7.64E-01	-	-	
RS2126248	11	98673511	0.000071	A	0.037	7.18E-01	-	-	
RS2566389	11	98692890	0.0002	G	0.034	7.37E-01	-	-	
RS561202	11	107590335	0.0008	C	-0.033	5.92E-01	-	+	
RS1985242	11	113848273	0.0002	A	-0.002	9.55E-01	-	+	*HTR3A*
RS3901231	11	123562397	0.000033	T	-0.014	7.06E-01	-	+	
RS478951	11	125983154	0.0003	G	0.064	6.94E-02	+	-	
RS621381	11	126003326	0.0009	T	0.023	5.26E-01	+	-	
RS10791290	11	133226125	0.0006	A	0.011	8.92E-01	-	-	*OPCML*
RS3741952	12	3131206	0.0008	T	-0.031	4.68E-01	+	+	*TEAD4*
RS1529418	12	9770355	0.0002	A	0.019	7.51E-01	+	-	*LOC374443*
RS7310367	12	9786707	0.0004	G	0.013	8.31E-01	+	-	*LOC374443*
RS12833541	12	24661124	0.0002	A	0.013	8.15E-01	+	-	*SOX5*
RS10843737	12	30550521	0.0008	G	-0.053	1.42E-01	+	+	
RS1546189	12	42183510	0.0005	T	-0.041	3.55E-01	-	+	
RS297924	12	50285061	0.0006	C	-0.052	1.47E-01	+	+	*FAIM2*
RS4761981	12	51674501	0.0006	T	0.043	3.78E-01	+	-	
RS266676	12	55117176	0.0008	G	0.062	7.41E-02	-	-	
RS4024193	12	61727679	0.001	C	-0.033	3.55E-01	+	+	
RS2596741	12	95903543	0.0009	C	0.049	1.62E-01	-	-	*METAP2*
RS7962756	12	101088009	0.001	T	-0.018	7.04E-01	-	+	
RS1426434	12	115666362	0.0008	A	-0.010	8.05E-01	+	+	
RS1199742	13	21529256	0.0005	T	-0.011	8.32E-01	+	+	
RS945664	13	21534199	0.0005	A	0.010	8.87E-01	+	-	
RS17369571	13	22487625	0.0008	A	-0.047	2.76E-01	-	+	
RS2031724	13	31602261	0.0006	T	0.153	1.50E-01	+	-	
RS1329313	13	35194022	0.001	C	0.003	9.35E-01	-	-	*LINC00457*
RS1329312	13	35194226	0.0007	C	0.014	6.90E-01	-	-	*LINC00457*
RS1410949	13	35258371	0.0008	A	0.039	7.59E-01	+	-	
RS1876583	13	35269505	0.0008	C	0.027	7.69E-01	+	-	
RS9315305	13	35272349	0.0001	A	-0.048	4.10E-01	-	+	
RS9529615	13	35307066	0.0002	A	0.030	7.60E-01	+	-	
RS4143549	13	36108184	0.0003	C	0.068	5.80E-02	-	-	*NBEA*
RS928169	13	52507110	0.0004	G	0.050	1.42E-01	-	-	*ATP7B*
RS1801249	13	52515354	0.0008	A	0.046	1.78E-01	+	-	*ATP7B*
RS4943046	13	52519746	0.001	G	0.045	1.88E-01	+	-	*ATP7B*
RS732774	13	52523808	0.0006	C	0.043	2.08E-01	+	-	*ATP7B*
RS3825526	13	52531363	0.001	A	-0.062	7.28E-02	+	+	*ATP7B*
RS3825527	13	52545141	0.0008	G	-0.049	1.46E-01	+	+	*ATP7B*
RS633158	13	58620938	0.0007	C	-0.019	6.17E-01	+	+	
RS9538278	13	59612377	0.00006	G	-0.025	4.91E-01	-	+	
RS7318676	13	75664005	0.0008	C	-0.064	7.13E-02	+	+	
RS9515676	13	90716425	0.0003	C	-0.045	1.97E-01	-	+	*LINC00559*
RS342715	13	92383193	0.0005	G	0.002	9.53E-01	-	-	*GPC5*
RS11627948	14	30588110	0.0005	T	-0.016	6.59E-01	+	+	
RS11627212	14	30605415	0.000053	G	-0.016	6.51E-01	+	+	
RS720761	14	30641789	0.0002	C	0.033	3.58E-01	-	-	
RS1956461	14	30656078	0.0006	C	0.046	2.09E-01	-	-	
RS2183631	14	31958761	0.0003	C	0.026	5.09E-01	-	-	
RS1952897	14	31972097	0.0008	G	0.070	7.71E-02	-	-	
RS3945419	14	31989902	0.0007	G	0.073	6.04E-02	-	-	
RS11621047	14	33651174	0.0006	A	0.059	1.89E-01	+	-	*NPAS3*
RS900362	14	34522444	0.000079	C	0.010	7.74E-01	+	-	
RS4982133	14	34526819	0.00003	A	0.018	6.19E-01	+	-	
RS2806246	14	42755963	0.0005	A	0.008	8.47E-01	+	-	

RS11634827	15	54513878	0.0007	G	-0.044	4.27E-01	-	+	*UNC13C*
RS12101550	15	92857342	0.0009	G	-0.068	2.34E-01	+	+	
RS8043535	15	97392522	0.0006	C	0.019	6.02E-01	-	-	
RS8042199	15	97392553	0.0007	G	0.019	6.01E-01	-	-	
RS1703794	15	99613173	0.000035	C	0.006	8.87E-01	+	-	
RS1670200	15	99613245	0.0002	C	0.042	2.34E-01	-	-	
RS6497441	16	9829848	0.0009	T	-0.022	7.86E-01	+	+	
RS9925256	16	52473263	0.0009	G	-0.017	6.39E-01	-	+	*TOX3*
RS2550364	16	58228701	0.0007	C	-0.031	3.60E-01	-	+	*CSNK2A2*
RS12599067	16	76777664	0.0007	A	-0.005	9.32E-01	-	+	
RS2966099	16	81550448	0.0007	C	0.021	7.01E-01	-	-	*CMIP*
RS9891235	17	31836993	0.0005	C	-0.015	7.96E-01	+	+	*ASIC2*
RS4791201	17	63314560	0.0005	G	-0.001	9.91E-01	-	+	
RS8068707	17	63315996	0.0004	C	0.024	6.05E-01	-	-	
RS10438701	17	71395173	0.0009	G	-0.027	7.35E-01	+	+	*SDK2*
RS6565593	17	79515075	0.0005	A	0.025	4.73E-01	-	-	*C17orf70*
RS3830068	17	79622899	0.0008	C	0.051	1.87E-01	-	-	*PDE6G*
RS6506569	18	8275857	8.40E-06	C	-0.050	1.43E-01	+	+	*PTPRM*
RS11080567	18	12312075	0.0002	T	0.053	5.04E-01	-	-	*TUBB6*
RS12607321	18	12316779	0.0001	C	0.053	5.02E-01	-	-	*TUBB6*
RS7231304	18	12350505	0.0004	C	0.036	6.02E-01	-	-	*AFG3L2*
RS1945162	18	22166762	0.0004	T	0.025	5.93E-01	+	-	
RS1945166	18	22169993	0.0004	C	0.025	5.81E-01	+	-	
RS12608350	18	27828310	0.0002	T	-0.009	8.03E-01	+	+	
RS4799816	18	33384924	0.0003	C	-0.060	3.48E-01	+	+	
RS1942240	18	33387429	0.0005	C	-0.057	3.54E-01	+	+	
RS10502880	18	44770746	0.0005	C	-0.021	5.42E-01	-	+	*SKOR2*
RS12327160	18	73731308	0.0009	G	-0.040	3.26E-01	-	+	
RS1542951	18	75591259	0.000075	C	0.030	6.96E-01	+	-	
RS731723	19	12588119	0.0004	C	-0.042	5.81E-01	+	+	*ZNF709*
RS6113161	20	2171649	0.0005	G	0.112	1.72E-02	-	-	
RS6082438	20	2204811	0.00009	T	-0.005	8.86E-01	-	+	
RS6116308	20	4295353	0.0006	A	-0.054	3.07E-01	-	+	
RS2148815	20	6363480	0.001	T	-0.009	8.07E-01	+	+	
RS6085681	20	6770690	0.0009	A	-0.016	6.54E-01	+	+	
RS2650972	20	6783274	0.000032	T	0.007	8.49E-01	-	-	
RS1545	20	10386013	0.0009	A	-0.025	6.37E-01	-	+	*MKKS*
RS16991547	20	10394046	0.0009	A	-0.028	5.96E-01	-	+	*MKKS*
RS6133927	20	10406156	0.0009	G	-0.029	5.87E-01	-	+	*MKKS*
RS852105	20	17154897	0.0009	T	0.038	7.36E-01	-	-	
RS726256	20	17456843	0.0008	T	-0.004	8.96E-01	+	+	*PCSK2*
RS6080714	20	17472515	0.0002	G	-0.006	8.63E-01	-	+	
RS6028910	20	38784641	0.001	G	0.040	6.30E-01	+	-	
RS400420	20	55470340	0.0007	A	0.016	6.60E-01	-	-	
RS2249634	20	55470625	0.0004	G	0.038	2.81E-01	-	-	
RS1276434	20	55479307	0.0003	G	0.005	8.88E-01	-	-	
RS6064463	20	55480277	0.000041	C	-0.010	7.82E-01	-	+	
RS6027736	20	59260773	0.0008	C	-0.084	1.04E-01	+	+	
RS17802507	20	59269198	0.001	C	-0.081	1.19E-01	+	+	
RS11700217	20	61407407	0.001	A	-0.053	4.09E-01	-	+	*LOC100652730*
RS150760	21	27808458	0.0009	A	-0.005	8.84E-01	-	+	*LOC100996571*
RS2836544	21	39963124	0.0009	A	0.047	2.11E-01	-	-	*ERG*
RS2836565	21	39976701	0.0003	A	0.018	6.26E-01	-	-	*ERG*
RS724055	22	30675923	0.0003	A	0.006	8.62E-01	-	-	

Supplementary Table 9. DAS28 results for all SNPs with P<0.0001 in a genome-wide study of methotrexate response in European juvenile idiopathic arthritis patients (Cobb et al.)

Effect direction is in relation to effect allele: + indicates improvement in DAS28 score/response, - indicates increase in DAS score/non-response.

					DAS28		Effect Direction		
Marker	**Chr**	**Position**	**Cobb *et al.* P-value**	**Effect Allele**	**β**	**P-value**	**Cobb *et al.***	**This Study**	**gene**
RS951437	1	163033511	6.45x10-4	T	-0.027	6.27E-01	-	+	
RS951438	1	163033537	6.45x10-4	T	-0.026	6.36E-01	-	+	
RS2661319	1	163039777	7.71x10-4	T	0.045	3.71E-01	+	-	*RGS4*
RS4657400	1	165103961	4.65x10-5	C	0.057	3.17E-01	-	-	
RS2972472	3	115447624	8.52x10-4	C	-0.052	2.44E-01	+	+	
RS11707482	3	126099612	3.63x10-4	A	0.038	3.35E-01	-	-	*LOC100506907*
RS9864977	3	126101047	4.89x10-4	C	0.037	3.37E-01	-	-	*LOC100506907*
RS2270813	5	157164889	7.25x10-5	T	0.017	6.35E-01	+	-	*THG1L*
RS2270812	5	157164962	7.25x10-5	T	0.021	5.73E-01	+	-	*THG1L*
RS300195	5	162698920	7.21x10-4	T	0.014	9.06E-01	-	-	
RS1465221	7	77764253	7.34x10-4	A	0.021	7.17E-01	+	-	*MAGI2*
RS3917558	7	94932904	5.35x10-4	C	0.099	2.78E-01	-	-	*PON1*
RS3917556	7	94933189	7.96x10-4	C	0.069	5.77E-01	-	-	*PON1*
RS3917551	7	94934455	8.07x10-4	A	0.069	5.77E-01	-	-	*PON1*
RS3917548	7	94935905	7.96x10-4	G	0.052	6.27E-01	-	-	*PON1*
RS3917541	7	94937624	7.96x10-4	A	0.055	5.97E-01	-	-	*PON1*
RS2158155	7	94938176	7.96x10-4	A	0.077	5.06E-01	-	-	*PON1*
RS2299257	7	94942765	5.35x10-4	C	-0.013	7.24E-01	-	+	*PON1*
RS854556	7	94944923	9.11x10-4	T	-0.037	3.04E-01	+	+	*PON1*
RS854557	7	94945215	9.11x10-4	G	-0.036	3.23E-01	+	+	*PON1*
RS2301711	7	94945659	6.79x10-4	C	0.052	5.88E-01	-	-	*PON1*
RS854559	7	94945872	7.40x10-4	A	-0.038	3.02E-01	+	+	*PON1*
RS854561	7	94947017	9.11x10-4	T	-0.038	3.02E-01	+	+	*PON1*
RS854562	7	94947969	8.48x10-5	T	-0.026	4.84E-01	+	+	*PON1*
RS854563	7	94948009	9.11x10-4	A	-0.038	3.02E-01	+	+	*PON1*
RS3917493	7	94948028	7.96x10-4	C	0.085	4.16E-01	-	-	*PON1*
RS17611963	7	122520343	9.00x10-4	T	-0.065	4.25E-01	-	+	*CADPS2*
RS16939230	8	76939927	7.27x10-5	G	0.085	2.31E-01	-	-	
RS11988715	8	76944293	4.51x10-4	T	0.069	2.52E-01	-	-	
RS13274868	8	82921787	2.48x10-4	T	-0.022	5.77E-01	-	+	
RS4529421	8	82921979	5.73x10-4	G	-0.065	6.97E-02	-	+	
RS998249	8	82961957	4.72x10-4	T	-0.018	6.19E-01	-	+	
RS1576733	9	84141525	5.20x10-5	C	0.044	2.28E-01	-	-	
RS703979	10	80944095	7.69x10-4	T	0.129	1.10E-04	-	-	*ZMIZ1*
RS703970	10	80953136	8.26x10-5	A	0.124	1.77E-04	-	-	*ZMIZ1*
RS697237	10	80954686	7.06x10-4	A	0.135	2.88E-03	-	-	*ZMIZ1*
RS2802371	10	80961519	1.41x10-5	C	0.084	1.06E-02	-	-	*ZMIZ1*
RS1250576	10	80964796	9.28x10-5	C	0.107	1.90E-03	-	-	*ZMIZ1*
RS942796	10	80967220	3.14x10-4	T	0.097	3.98E-03	-	-	*ZMIZ1*
RS1250582	10	80973447	2.09x10-5	T	0.083	1.16E-02	-	-	*ZMIZ1*
RS1250591	10	80985374	7.29x10-5	A	-0.073	3.00E-02	+	+	*ZMIZ1*
RS17680055	11	99778206	6.17x10-4	G	0.079	5.09E-02	-	-	*CNTN5*
RS11609579	12	101843240	2.62x10-4	G	0.101	2.20E-02	-	-	
RS11110810	12	101856465	5.08x10-4	T	0.105	2.77E-02	-	-	
RS595775	13	101840684	3.46x10-4	T	-0.059	9.30E-02	-	+	*NALCN*
RS1896195	15	26770557	8.98x10-4	C	-0.003	9.38E-01	+	+	
RS4906679	15	26814773	2.45x10-4	C	0.014	7.02E-01	+	-	*GABRB3*
RS4906680	15	26816588	3.33x10-4	A	0.008	8.19E-01	+	-	*GABRB3*
RS882898	20	60320706	8.51x10-4	A	0.060	1.40E-01	+	-	*CDH4*
RS11699916	20	60326201	1.84x10-4	A	0.085	2.54E-02	+	-	*CDH4*

Supplementary Table 10. The most significant variant per locus, where the locus had a long-range chromatin interaction with a MTX metabolism candidate gene

DHS - Cell lines or tissues in which the SNP overlaps with a Dnase I hypersensitivity site

HiC GM12878 1kb res/5kb res - The list of genes whose promoter interacts with the given SNP, in order of significance. Bold genes are involved in MTX metabolism.

MARKER	CHR	BP	DHS
DAS28			
RS703987:80939219:G:C	10	80939219	CD34+_Mobilized;Monocytes-CD14+_RO01746
RS942796:80967220:C:T	10	80967220	.
RS57816977:4012466:T:C	18	4012466	.
SJC			
RS926727:22997422:C:T	20	22997422	HRCEpiC;RPTEC
RS34038277:40699847:A:G	21	40699847	.
RS2836920:40512918:T:G	21	40512918	.
RS2836915:40509189:C:T	21	40509189	A549;Adult_CD4_Th0;BE2_C;CD34+_Mobilized;CMK;FibroP;GM12892;Gliobla;H1-hESC;H7-hESC;H9ES;HAEpiC;HConF;HEEpiC;HFF;HFF-Myc;HMEC;HPDE6-E6E7;HRE;HTR8svn;HVMF;HeLa-S3;HeLa-S3+IFNa4h;HepG2;K562;MCF-7;MCF-7+Hypoxia_LacAcid; Medullo;Melano;NB4;NT2-D1;PrEC;RWPE1;SAEC;SK-N-SH_RA;Urothelia+UT189;WERI-Rb-1;WI-38+4OHTAM_20nM_72hr;iPS;pHTE;A549
TJC			
RS2776898:37541111:T:C	6	37541111	.
RS2289679:42988092:G:C	17	42988092	.

MARKER	CHR	BP	HiC GM12878 1kb res
DAS28			
RS703987:80939219:G:C	10	80939219	ZMIZ1;ZCCHC24;LINC00595;ZMIZ1-AS1;DLG5;POLR3A;LINC00856;PPIF;SFTPA1;ANXA11;C10orf54;RPS24
RS942796:80967220:C:T	10	80967220	ZMIZ1;ZMIZ1-AS1;SFTPA2;ZCCHC24;MBL1P;KCNMA1;DLG5;RPS24;LINC00856
RS57816977:4012466:T:C	18	4012466	DLGAP1-AS4;DLGAP1;DLGAP1-AS5;LINC00667;METTL4;MYL12A;TGIF1
SJC			
RS926727:22997422:C:T	20	22997422	SSTR4;THBD;LINC00656;CST9;NXT1;GZF1;NAPB;CSTL1;CST8;CST13P;CST3;LRRN4;SEC23B
RS34038277:40699847:A:G	21	40699847	BRWD1-AS1;HMGN1;WRB;BRWD1;LCA5L;SH3BGR;PSMG1;MX2;DYRK1A;ERG;LINC00114;ETS2
RS2836920:40512918:T:G	21	40512918	LINC00114;PSMG1;BRWD1;HMGN1;WRB;LCA5L;DSCR9;KCNJ6;DSCR10;ERG;ETS2
RS2836915:40509189:C:T	21	40509189	LCA5L;ERG;ETS2;PSMG1;WRB;DSCR10;LINC00114;BRWD1;RIPK4;KCNJ15
TJC			
RS2776898:37541111:T:C	6	37541111	CCDC167;MIR4462;MDGA1;BTBD9;TMEM217;FGD2;TBC1D22B;CMTR1
RS2289679:42988092:G:C	17	42988092	GFAP;CCDC103;EFTUD2;KIF18B;C1QL1;NMT1;DCAKD;HIGD1B;ACBD4;PLCD3;HEXIM1;HEXIM2;GJC1;FMNL1;DBF4B;MAP3K14;ITGA2B;MEIOC;ADAM11;MAP3K14-AS1;ARHGAP27;CCDC43;SPATA32;SPECC1;TMEM106A;ATXN7L3;GRN;GPATCH8;FZD2

MARKER	CHR	BP	HiC GM12878 5kb res
DAS28			
RS703987:80939219:G:C	10	80939219	ZMIZ1;ZMIZ1-AS1;PPIF;RPS24;LINC00856;LINC00595;POLR3A;ZCCHC24;DLG5;EIF5AL1;SFTPA2;SFTPA1;MAT1A;TSPAN14;MBL1P;SFTPD;TMEM254;PLAC9;DYDC2;KCNMA1;BMS1P21;ANXA11;DYDC1;FAM213A;SH2D4B;LDB3;ANKRD2;RGS10;FRMPD2;COL13A1; SLC29A3;CDHR1;CCSER2;OPN4;BMPR1A;STAMBPL1;IFIT2;IFIT3;KIF20B;BTAF1;CYP26A1;SORBS1;ALDH18A1;C10orf12;RRP12;ZFYVE27;CRTAC1;GOT1;DNMBP;SH3PXD2A;CFAP43;MIR609;GSTO2;ITPRIP;ADD3;MXI1;CASP7;AFAP1L2;ABLIM1;PNLIP;NANOS1;PLPP4;TACC2;PLEKHA1; PTPRE;DPYSL4;TUBGCP2;MIR3944;UPF2;C10orf10;LINC00842;ARHGAP22;WDFY4;C10orf71;ERCC6;CHAT;NCOA4;CISD1;CDK1;RUFY2;HKDC1;HK1;TACR2;TSPAN15;AIFM2;NODAL;ADAMTS14;PCBD1;C10orf105;C10orf54;CDH23;PSAP;DDIT4;MICU1;FAM149B1;USP54;PLAU;C10orf55;ADK
RS942796:80967220:C:T	10	80967220	ZMIZ1;ZMIZ1-AS1;PPIF;RPS24;LINC00595;ZCCHC24;DLG5;POLR3A;LINC00856;EIF5AL1;SFTPA2;SFTPA1;ANXA11;KCNMA1;BMS1P21;FAM213A;SH2D4B;LDB3;BEND3P3;MBL1P;SFTPD;TMEM254;PLAC9;MAT1A;DYDC2;DYDC1;TSPAN14;**ABCC2**;FAM170B-AS1;VCL;C10orf99;CDHR1;ACTA2; CPEB3;MMS19;MARVELD1;SFRP5;PYROXD2;CPN1;NEURL1;SFR1;ITPRIP;SORCS3;ABLIM1;SHTN1;MIR4681;INPP5F;SCART1;LRRC18;C10orf53;ASAH2;TET1;DDX50;HK1;TYSND1;NPFFR1;LRRC20;EIF4EBP2;TBATA;C10orf105;SEC24C
RS57816977:4012466:T:C	18	4012466	DLGAP1-AS4;DLGAP1;DLGAP1-AS3;MYL12B;DLGAP1-AS1;DLGAP1-AS5;ZBTB14;MYL12A;TGIF1;EMILIN2;LINC00667;EPB41L3;METTL4;LOC727896;LPIN2;MIR3976;AKAIN1;LINC00526;L3MBTL4;ARHGAP28;**TYMS**;TYMSOS;CBX3P2;SMCHD1;MYOM1;TMEM200C;MIR4317;LAMA1; PTPRM;MTCL1;RAB31;CEP192;MC2R;RBBP8;PIK3C3;CTIF;MYO5B;SMAD4;SERPINB8;LINC00470
SJC			
RS926727:22997422:C:T	20	22997422	SSTR4;THBD;CD93;LINC00656;NXT1;GZF1;CSTL1;NAPB;FOXA2;CST8;CST9L;CST13P;CST9;LINC00261;CST3;PAX1;LOC284788;CST11;CST4;CST2;SYNDIG1;RALGAPA2;CST1;PROKR2;LRRN4;KIZ;GGTLC1;CST7;ACSS1;VSX1;ZNF337;DEFB121;CHD6;FITM2;PLCB4;PCSK2;RRBP1;RIN2;CST5; FLJ33581;APMAP;ENTPD6;PYGB;ABHD12;GINS1;NINL;NANP;DEFB118;DEFB122;DEFB123;CCM2L;GGT7;PTPRT;MIR3194;VAPB;ZNF831;PHACTR3;CDH26;OXT;ITPA;SLC23A2;PLCB1;ANKEF1;ESF1;KIF16B;SNRPB2;OTOR;SNX5;SEC23B;LOC100130264;XRN2;NKX2-4;NKX2-2;LINC01432
RS34038277:40699847:A:G	21	40699847	BRWD1-AS1;BRWD1;HMGN1;WRB;PSMG1;LCA5L;SH3BGR;LINC00114;ETS2;MX1;MX2;KCNJ15;B3GALT5;PLAC4;C2CD2;ERG;IGSF5;BACE2;BTG3;SON;TTC3;DSCAM-IT1;UMODL1;TFF1;LTN1;BACH1;SCAF4;SYNJ1;CLDN14;DSCR3;B3GALT5-AS1;LINC00323;MIR3197;TMPRSS2;LINC00111; RIPK4;PRDM15;ABCG1;RSPH1;PKNOX1;SIK1;KRTAP10-3;ADARB1;MCM3AP;MRPL39;JAM2;APP;USP16;CCT8;MAP3K7CL;SOD1;TCP10L;C21orf59;DNAJC28;SMIM11A;KCNE1;SETD4;HLCS;DYRK1A;DSCR10;FAM3B;ZBTB21;UMODL1-AS1;TMPRSS3;WDR4;TRAPPC10;PFKL;C21orf2; ITGB2-AS1;POFUT2;COL18A1;PCBP3;MCM3AP-AS1;NRIP1;CXADR;C21orf91-OT1;N6AMT1;GRIK1-AS2;MRAP;URB1;PAXBP1;C21orf62-AS1;C21orf62;IFNAR1;GART;CRYZL1;ITSN1;ATP5O;RUNX1-IT1;RUNX1;CBR3-AS1;DOPEY2;CHAF1B;RIPPLY3;DSCR9;DSCR4
RS2836920:40512918:T:G	21	40512918	PSMG1;LINC00114;ETS2;WRB;ERG;LCA5L;BRWD1;SH3BGR;BRWD1-AS1;HMGN1;DSCR10;KCNJ15;B3GALT5;MX2;KCNJ6;B3GALT5-AS1;MIR3197;FAM3B;BACE2;C21orf59;PLAC4;LINC00479;RIPK4;C2CD2;ABCG1;KRTAP13-4;LINC00159;SNORA80A;KCNE1;RUNX1;SETD4;CBR1;TTC3; DYRK1A;DSCR4;IGSF5;DSCAM-AS1;DSCAM-IT1;DSCAM;LINC00323;MX1;TMPRSS2;ZBTB21;UMODL1;WDR4;CBS;HSF2BP;KRTAP10-8;KRTAP10-10;POFUT2;FTCD;SPATC1L;MCM3AP;HSPA13;CHODL;LINC00113;RWDD2B;LINC00189;KRTAP27-1;KRTAP6-2;SOD1;SCAF4;EVA1C;TCP10L; SYNJ1;OLIG2;OLIG1;LINC01548;IFNAR1;ITSN1;LINC00310;SMIM11A;DOPEY2;SIM2;HLCS;PIGP;DSCR9;DSCR3;DSCR8
RS2836915:40509189:C:T	21	40509189	PSMG1;LINC00114;ETS2;LCA5L;BRWD1;WRB;ERG;DSCR10;SH3BGR;HMGN1;BRWD1-AS1;PLAC4;KCNJ15;IGSF5;LINC00323;LINC00479;B3GALT5;FAM3B;MX2;RUNX1;HLCS;BACE2;TMPRSS2;RIPK4;**SLC19A1**;BTG3;GRIK1;LOC100133286;DSCR3;KCNJ6;B3GALT5-AS1;PCP4;MIR3197;C2CD2; ZBTB21;UMODL1;TRPM2;KRTAP10-7;KRTAP12-1;TSPEAR;PCBP3;PCNT;C21orf91-OT1;MAP3K7CL;GRIK1-AS1;KRTAP27-1;KRTAP6-3;HUNK;MIS18A;MRAP;EVA1C;TCP10L;SYNJ1;PAXBP1;C21orf62;ITSN1;LINC00310;KCNE1;LOC100506403;CBR3-AS1;CLDN14;SIM2;RIPPLY3;TTC3;DYRK1A;DSCR4;DSCR8
TJC			
RS2776898:37541111:T:C	6	37541111	MIR4462;CCDC167;MDGA1;CMTR1;TBC1D22B;RNF8;TMEM217;ZFAND3;BTBD9;FGD2;PIM1;PPIL1;DNAH8;MAPK14;PI16;MTCH1;GLO1;CPNE5;C6orf89;GLP1R;PNPLA1;LOC100131047;TOMM6;ANKS1A;TEAD3;BRPF3;ETV7;MIR3925;RAB44;MOCS1;NFYA;TREML4;TREML5P;NCR2;TFEB;CCND3; MIR4647;TOB2P1;HLA-F-AS1;TRIM10;RPP21;CLIC1;VARS;COL11A2;GRM4;SPDEF;SLC26A8;KCTD20;STK38;CDKN1A;SAYSD1;KCNK5;KCNK17;KIF6;TDRG1;UNC5CL;ADCY10P1;TREML1;TREML2;TREM1;MIR4641;MDFI;PGC;TRERF1;UBR2;RRP36;PTK7;CUL9;ZNF318;XPO5;POLH;VEGFA;LINC01512;TMEM63B;CAPN11;SLC29A1; TMEM151B;SPATS1;CDC5L;LRRC1;MTO1;RAET1E-AS1;IRF4;SERPINB6;LY86;RANBP9;GMNN;HIST1H3C;ZSCAN23;OR14J1;MAS1L;TRIM26;TRIM39;HLA-E;MDC1;PSORS1C3;CFB;HLA-DPB2;RGL2;C6orf1;PACSIN1;UHRF1BP1;FANCE;MIR5690;FKBP5;LOC285847;ARMC12;CLPSL1;LHFPL5;SRPK1;MAPK13;C6orf222;SRSF3
RS2289679:42988092:G:C	17	42988092	CCDC103;GFAP;EFTUD2;KIF18B;C1QL1;DCAKD;NMT1;ACBD4;HIGD1B;GJC1;ADAM11;PLCD3;HEXIM2;HEXIM1;DBF4B;FMNL1;MAP3K14;CCDC43;MEIOC;MAP3K14-AS1;ARHGAP27;SPATA32;FZD2;GPATCH8;SLC25A39;ITGA2B;ASB16;ATXN7L3;CRHR1; TMEM101;HDAC5;C17orf53;RUNDC3A;GRN;FAM171A2;SP6;CRHR1-IT1;SPPL2C;LSM12;G6PC3;UBTF;MIR4315-1;MAPT;STH;KANSL1;KPNB1;LRRC59;LLGL2;STARD3;WNK4;ETV4;MPP2;FAM215A;NAGS;ASB16-AS1;SLC4A1;PLEKHM1;HOXB3;PRAC1;TAC4;PDK2;RSAD1;CACNA1G;SNORA21;MED1;PGAP3;PSMD3;KRT13;JUP; ACLY;TTC25;NKIRAS2;RAB5C;GHDC;PTRF;COASY;CNTNAP1;EZH1;AOC2;BRCA1;LINC00854;DHX8;MEOX1;C17orf105;MPP3;CD300LG;PPY;PYY;TMUB2;WNT9B;GOSR2;MIR5089;MYL4;NPEPPS;TBX21;OSBPL7;MRPL10;SCRN2;MIR196A1;HOXB13;GIP;PHB;NGFR;NXPH3;FAM117A;KAT7;DLX4;SAMD14;EME1;MYCBPAP;EPN3;SPATA20; C17orf67;SRSF1;MRC2;RAB37;GRIN2C;UNC13D;ACOX1;CYTH1;CBX2;BAIAP2;INPP5K;TOP3A;SHMT1;SPECC1;SARM1;SUPT6H;GOSR1;MIR4733;MIR4724;RFFL;UNC45B;CCL5;PIGW;ACACA;GPR179;SRCIN1;PCGF2;ARL5C;PPP1R1B;PNMT;ERBB2;IKZF3;NR1D1;RARA;KRT26;KLHL11;CNP;ZNF385C;KAT2A;STAT3;ATP6V0A1;TUBG2; RAMP2;VPS25;COA3;BECN1;PSME3;AARSD1;RPL27;VAT1;RND2;NBR1;TMEM106A;LINC00910;MIR2117;SOST

Supplementary Table 11. Annotation of the most highly asscociated regions at P<1e-5 for each of the 4 traits analysed genome-wide

Genes: with SNP or supporting SNPs with P<5e-5 located within gene

Nearby Genes: all genes less than 20kb from the start and stop of the hit region

Chromatin interactions: show the genes with most significant long-range chromatin interactions in GM12878 with the 25 top loci

Number of SNPs in Score: shows the number of SNPs in the region used to create a regional genetic score predicting response to MTX

Genetically related traits: lists the traits whose genetic scores have absolute correlation above 0.5 with the regional genetic score for MTX response (separated by comma)

Correlations: shows the correlations between the regional genetic score and the scores for the traits in the previous column (separated by comma)

						Chromatin interactions					
Trait	**Marker**	**Chr**	**Position**	**Genes**	**Nearby Genes**	**candidate1**	**candidate2**	**candidate3**	**Number of SNPs in Score**	**Genetically related traits**	**Correlation**
DAS28	rs2372751	3	81124821	*LINC02027*		*PROS1*	*GBE1*		7		
	rs58840038	5	125773164	*GRAMD3*	*GRAMD3*	*GRAMD3*			6		
	rs6903359	6	21986214	*CASC15*	*CASC15*	*CASC15*			5		
	rs168201	10	84610081	*NRG3*	*NRG3*	*NRG3*			29		
	rs57816977	18	4012466	*DLGAP1*	*DLGAP1, DLGAP1-AS4*	*DLGAP1*			13		
$\log_e$(CRP+1)	rs79244342	6	54660244	*KRASP1*	*RNU6-1023P*	*FAM83B*			14		
	rs1889339	9	96053928	*WNK2*	*WNK2*	*NINJ1*	*WNK2*		7	FGD3_eQTL_cis	-0.52
SJC28	rs35179427	1	95670888	*RWDD3, TMEM56-RWDD3*	*ALG14, RWDD3, TMEM56, TMEM5*	*RWDD3*			62	phospholipid 16:0, phospholipid 18:0	-0.67, 0.64
	rs1453301	2	138080695	*THSD7B*	*RNA5SP105, THSD7B*	*THSD7B*			40		
	rs77458347	4	109896081	*COL25A1*	*COL25A1*	*COL25A1*			5		
	rs144940912	4	155092290			*RNF175*	*DCHS2*				
	rs12663189	6	162730663	*PARK2*	*PARK2*	*PARK2*			16		
	rs314637	7	4421893			*SDK1*			8		
	rs113798271	7	145059089			*TPK1*			6	METABOLON.32562	0.98
	rs1175813	19	49737486			*CD37*	*SLC17A7*		17		
	rs1042579	20	23028724	*THBD*	*SSTR4, THBD*	*THBD*			6	Very Low Density Lipoprotein (VLDL) particle mean diameter	0.6
	rs2836915	21	40509189			*LCA5L*	*ETS2*		5	BRWD1_eQTL_cis, HMGN1_eQTL_cis, PSMG1_eQTL_cis	0.63, 0.54, 0.54
TJC28	rs10058818	5	56808696	*LINCR-0003*		*GAPT*	*ACTBL2*		17		
	rs10515242	5	95982675		*CAST*	*CAST*	*ERAP1*		4		
	rs2026708	6	21986895	*CASC15*	*CASC15*	*CASC15*			5		
	rs2776898	6	37541111			*CCDC167*	*MDGA1*		4		
	rs114461403	7	16547268		*SOSTDC1*	*SOSTDC1*	*LRRC72*		6		
	rs28442057	15	55110958		*HNRNPA1P74, UNC13C*	*UNC13C*			82		
	rs12446816	16	14092341			*ERCC4*	*MKL2*		4		
	rs9910936	17	42949168	*CCDC103, EFTUD2, GFAP, KIF18E*	*ACBD4, C1QL1, CCDC103, DCAKD*	*EFTUD2*	*C1QL1*	*CCDC103*	53	DBF4B_eQTL_cis, EFTUD2_eQTL_cis	-0.68, 0.81

Supplementary Table 12. Phase 1 results for the most significant regions from an analysis of EULAR responders (Good and Moderate) versus non-responders.

Regions are shown if they included one SNP with P<1x10-5 and at least one other SNP within 200kb with P<5x10-5

Marker	Chr	Position	Non-responders	Responders	Effect Allele	Odds Ratio for non-response	P
RS10889647:67154496:T:A	1	67154496	413	831	A	1.49	4.82E-05
RS1408852:67155328:T:C	1	67155328	413	831	C	1.49	4.58E-05
RS682896:67186062:T:C	1	67186062	413	831	T	1.49	3.77E-05
RS269072:112593217:T:C	1	112593217	413	831	C	1.43	4.99E-05
RS655856:112594445:G:A	1	112594445	413	831	A	1.43	4.24E-05
RS543966:112594930:C:T	1	112594930	413	831	T	1.43	4.98E-05
RS269074:112596703:A:C	1	112596703	413	831	C	1.43	4.93E-05
RS1867402:112597212:T:C	1	112597212	413	831	C	1.43	4.91E-05
RS269076:112597282:C:G	1	112597282	413	831	G	1.43	4.91E-05
RS269079:112597532:A:G	1	112597532	413	831	G	1.43	4.99E-05
RS7584342:166288314:C:T	2	166288314	413	831	T	1.63	4.22E-05
RS6758348:166292513:A:C	2	166292513	413	831	C	1.64	3.60E-05
RS420914:4275016:A:G	5	4275016	413	831	A	1.77	1.22E-05
RS62343132:4275018:A:G	5	4275018	413	831	A	1.77	1.22E-05
RS63749549:4275020:A:G	5	4275020	413	831	A	1.77	1.22E-05
RS62343133:4275022:A:G	5	4275022	413	831	A	1.77	1.22E-05
RS10042800:4275024:A:G	5	4275024	413	831	A	1.77	1.22E-05
RS7703981:151944065:A:G	5	151944065	413	831	G	1.93	4.61E-05
RS17113408:151945295:A:T	5	151945295	413	831	T	1.93	4.46E-05
RS6875259:151946335:G:T	5	151946335	413	831	T	1.93	4.47E-05
RS58664268:151947234:G:A	5	151947234	413	831	A	1.93	4.46E-05
RS17113421:151947300:T:C	5	151947300	413	831	C	1.93	4.48E-05
RS6891765:151947696:G:A	5	151947696	413	831	A	1.93	4.67E-05
RS55970355:151948482:A:G	5	151948482	413	831	G	1.93	4.49E-05
RS6867859:151950297:G:T	5	151950297	413	831	T	1.92	4.76E-05
RS56091795:151954561:G:A	5	151954561	413	831	A	1.96	4.24E-05
RS61608756:151958695:G:C	5	151958695	413	831	C	1.92	4.99E-05
RS62395569:151959418:G:A	5	151959418	413	831	A	1.92	4.93E-05
RS79641272:151970619:G:C	5	151970619	413	831	C	1.96	3.51E-05
RS62395602:152002839:C:T	5	152002839	413	831	T	2.01	3.97E-05
RS17113527:152017153:A:T	5	152017153	413	831	T	1.95	4.55E-05
RS7730407:152028739:T:C	5	152028739	413	831	C	1.95	4.49E-05
RS61494452:152032374:T:C	5	152032374	413	831	C	1.95	4.49E-05
RS11953908:152033079:G:A	5	152033079	413	831	A	1.95	4.52E-05
RS146321269:152035133:C:T	5	152035133	413	831	T	1.81	3.10E-05
RS6877248:152043215:T:C	5	152043215	413	831	C	1.95	4.97E-05
RS62398677:152044579:T:C	5	152044579	413	831	C	1.95	4.72E-05
RS55641807:152047538:G:A	5	152047538	413	831	A	1.95	4.66E-05
RS56214789:152047682:G:A	5	152047682	413	831	A	1.95	4.67E-05
RS4309962:152052316:C:T	5	152052316	413	831	T	1.99	3.25E-05
RS2390595:21915464:G:A	7	21915464	413	831	A	0.68	4.24E-05
RS13308113:21917360:G:A	7	21917360	413	831	G	0.67	2.31E-05
RS10227946:78315218:G:A	7	78315218	413	831	A	0.66	2.21E-05
RS10255247:78389781:C:T	7	78389781	413	831	T	0.67	4.70E-05
RS37876:78431095:C:G	7	78431095	413	831	G	0.68	4.65E-05
RS37880:78434236:T:G	7	78434236	413	831	G	0.68	4.91E-05
RS246460:78441198:T:C	7	78441198	413	831	C	0.67	2.95E-05
RS246462:78443174:A:G	7	78443174	413	831	G	0.67	2.94E-05
RS13268737:22101593:T:C	8	22101593	413	831	C	0.65	2.67E-05
RS13249656:22113565:G:T	8	22113565	413	831	T	0.65	3.25E-05
RS12549719:22116085:A:G	8	22116085	413	831	G	0.65	3.73E-05
RS2585139:143808175:C:G	8	143808175	466	926	G	0.72	4.69E-05
RS7010768:143825951:T:G	8	143825951	466	926	T	0.71	4.65E-05
RS4567164:100206602:C:G	9	100206602	413	831	C	0.40	2.45E-06
RS6415827:100244171:G:A	9	100244171	413	831	G	0.55	4.92E-05
RS4742695:100256460:A:C	9	100256460	413	831	A	0.55	4.71E-05
RS41302651:130167338:C:T	9	130167338	466	926	T	1.46	5.65E-06
RS3824413:130167390:C:T	9	130167390	466	926	T	1.45	5.90E-06
RS3802363:130167569:T:C	9	130167569	466	926	C	1.45	5.86E-06

RS10987637:130168326:C:T	9	130168326	466	926	T	1.43	1.76E-05
RS72767909:130168873:C:T	9	130168873	466	926	T	1.45	6.05E-06
RS4075850:130169301:G:A	9	130169301	466	926	A	1.45	6.03E-06
RS6635:130169874:A:G	9	130169874	466	926	G	1.45	6.04E-06
RS3088163:130170000:A:T	9	130170000	466	926	T	1.45	6.02E-06
RS10819288:130170311:T:G	9	130170311	466	926	G	1.46	5.70E-06
RS62579723:130170806:G:A	9	130170806	466	926	A	1.45	6.01E-06
RS62579724:130170831:G:A	9	130170831	466	926	A	1.45	6.02E-06
RS142175068:130170950:T:C	9	130170950	466	926	C	1.45	6.01E-06
RS12379702:130172055:T:C	9	130172055	466	926	C	1.45	5.99E-06
RS55976691:130172469:C:T	9	130172469	466	926	T	1.45	5.98E-06
RS7866114:130173253:A:G	9	130173253	466	926	G	1.44	9.23E-06
RS10987641:130173451:G:A	9	130173451	466	926	A	1.45	5.92E-06
RS7047760:130175096:G:A	9	130175096	466	926	A	1.46	5.69E-06
RS10987644:130175933:C:T	9	130175933	466	926	T	1.46	5.85E-06
RS7035547:130178912:T:C	9	130178912	466	926	C	1.43	1.51E-05
RS62579727:130179808:A:G	9	130179808	466	926	G	1.43	1.56E-05
RS4074145:130180404:A:G	9	130180404	466	926	G	1.43	1.64E-05
RS17464948:130181886:T:C	9	130181886	466	926	T	0.69	1.72E-05
RS62579728:130182596:T:G	9	130182596	466	926	T	0.69	1.78E-05
RS6415844:130183114:T:C	9	130183114	466	926	T	0.69	1.44E-05
RS4316239:130183486:G:C	9	130183486	466	926	G	0.69	1.75E-05
RS10987648:130183790:T:C	9	130183790	466	926	T	0.69	1.45E-05
RS3924308:130185385:C:A	9	130185385	466	926	C	0.68	8.87E-06
RS7470971:130185708:A:T	9	130185708	466	926	A	0.68	1.06E-05
RS7020736:130187866:T:G	9	130187866	466	926	G	1.44	1.35E-05
RS62586845:130188796:G:A	9	130188796	466	926	A	1.44	1.27E-05
RS3923308:130197225:G:A	9	130197225	466	926	A	1.44	1.11E-05
RS10987652:130200577:C:T	9	130200577	466	926	T	1.44	1.07E-05
RS10987653:130201107:T:C	9	130201107	466	926	C	1.44	1.07E-05
RS10987654:130201206:C:T	9	130201206	466	926	T	1.44	1.07E-05
RS7869384:130201941:C:T	9	130201941	466	926	T	1.44	1.07E-05
RS7869873:130202302:C:T	9	130202302	466	926	T	1.44	1.07E-05
RS12380014:130204394:A:G	9	130204394	466	926	G	1.44	1.07E-05
RS2265816:130205517:C:T	9	130205517	466	926	T	1.44	1.07E-05
RS2248154:130206134:C:T	9	130206134	466	926	T	1.44	1.07E-05
RS2248025:130206762:C:T	9	130206762	466	926	T	1.44	1.07E-05
RS2247687:130209637:T:C	9	130209637	466	926	C	1.44	1.07E-05
RS2247682:130209700:A:C	9	130209700	466	926	C	1.44	1.07E-05
RS2491101:130215249:C:T	9	130215249	466	926	T	1.44	9.95E-06
RS2244331:130216120:G:T	9	130216120	466	926	T	1.45	9.18E-06
RS2244218:130216951:G:T	9	130216951	466	926	T	1.45	9.07E-06
RS2243509:130217050:C:G	9	130217050	466	926	G	1.45	9.15E-06
RS2798430:130220879:A:T	9	130220879	466	926	T	1.45	8.04E-06
RS2254164:130227079:T:A	9	130227079	466	926	A	1.45	8.09E-06
RS2253930:130228495:A:G	9	130228495	466	926	G	1.45	8.62E-06
RS2253898:130229262:A:G	9	130229262	466	926	G	1.45	8.62E-06
RS2253811:130229564:C:A	9	130229564	466	926	A	1.44	9.81E-06
RS2253806:130229652:A:G	9	130229652	466	926	A	0.71	4.18E-05
RS2253414:130232890:T:A	9	130232890	466	926	A	1.41	3.43E-05
RS2253411:130232909:G:C	9	130232909	466	926	C	1.41	3.43E-05
RS111988501:130233956:C:T	9	130233956	466	926	T	1.41	3.41E-05
RS62584994:130234594:G:A	9	130234594	466	926	A	1.47	1.04E-05
RS115721486:130234596:G:A	9	130234596	466	926	A	1.42	2.98E-05
RS2995822:130234634:A:G	9	130234634	466	926	G	1.42	2.36E-05
RS2250267:130236243:G:A	9	130236243	466	926	A	1.42	2.25E-05
RS2250184:130236589:C:G	9	130236589	466	926	G	1.42	2.95E-05
RS2250161:130237356:T:C	9	130237356	466	926	C	1.42	2.29E-05
RS2250021:130238122:T:C	9	130238122	466	926	C	1.42	2.28E-05
RS2250020:130238160:C:T	9	130238160	466	926	T	1.42	2.28E-05
RS2249936:130238645:C:G	9	130238645	466	926	G	1.42	2.25E-05
RS2249803:130239900:G:A	9	130239900	466	926	A	1.42	2.26E-05
RS1539568:130242109:C:T	9	130242109	466	926	T	1.42	2.25E-05

RS2246600:130243846:G:A	9	130243846	466	926	A	1.42	2.24E-05
RS7875862:130245545:G:C	9	130245545	466	926	C	1.42	2.24E-05
RS2246375:130245787:G:T	9	130245787	466	926	T	1.42	2.24E-05
RS62584996:130247355:G:T	9	130247355	466	926	T	1.42	2.27E-05
RS2243464:130248366:T:A	9	130248366	466	926	A	1.42	2.25E-05
RS2245677:130251512:G:A	9	130251512	466	926	A	1.44	1.20E-05
RS1547840:130252307:T:A	9	130252307	466	926	T	1.42	2.77E-05
RS1539564:130253931:A:G	9	130253931	466	926	G	1.42	2.35E-05
RS2249290:130255568:C:T	9	130255568	466	926	T	1.42	2.61E-05
RS2798429:130257191:G:A	9	130257191	466	926	A	1.42	2.72E-05
RS2249052:130258160:A:T	9	130258160	466	926	T	1.42	2.31E-05
RS2248725:130260788:C:T	9	130260788	466	926	T	1.43	2.00E-05
RS2488902:130261085:C:T	9	130261085	466	926	T	1.43	1.91E-05
RS62584998:130262434:G:T	9	130262434	466	926	T	1.42	2.38E-05
RS2245461:130266088:G:A	9	130266088	466	926	G	0.70	1.92E-05
RS2245445:130266399:G:A	9	130266399	466	926	G	0.70	2.88E-05
RS2244957:130271051:G:A	9	130271051	466	926	G	0.69	1.59E-05
RS2265814:130274290:T:G	9	130274290	466	926	T	0.71	4.36E-05
RS2254719:130282097:G:A	9	130282097	466	926	G	0.71	3.56E-05
RS7075325:3359961:G:A	10	3359961	466	926	A	0.71	3.91E-05
RS11595859:3360188:C:T	10	3360188	466	926	T	0.70	3.14E-05
RS12765037:3366559:T:G	10	3366559	466	926	G	0.70	3.67E-05
RS11594429:3368555:A:G	10	3368555	466	926	G	0.70	3.60E-05
RS1572539:3373163:G:C	10	3373163	466	926	C	0.71	4.02E-05
RS2297761:3377859:C:T	10	3377859	466	926	T	0.70	2.79E-05
RS12415414:3378151:T:C	10	3378151	466	926	C	0.71	4.37E-05
RS11597857:3378897:T:G	10	3378897	466	926	G	0.70	2.80E-05
RS11814386:3381890:C:T	10	3381890	466	926	T	0.70	4.21E-05
RS11251856:3381912:T:C	10	3381912	466	926	C	0.70	4.04E-05
RS11251857:3382156:A:G	10	3382156	466	926	G	0.70	3.57E-05
RS11251859:3382482:C:G	10	3382482	466	926	G	0.71	4.35E-05
RS34033143:3382723:T:G	10	3382723	466	926	G	0.70	4.12E-05
RS2924279:4863093:G:A	10	4863093	413	831	G	1.54	1.25E-05
RS2961620:4863351:C:T	10	4863351	413	831	C	1.54	1.03E-05
RS745290:30790264:T:C	10	30790264	466	926	C	1.48	2.02E-05
RS10763790:30791355:G:C	10	30791355	466	926	C	1.49	1.42E-05
RS728976:30792581:C:T	10	30792581	466	926	T	1.49	1.42E-05
RS11008075:30793299:C:G	10	30793299	466	926	G	1.49	1.16E-05
RS10763791:30794155:T:C	10	30794155	466	926	C	1.49	1.18E-05
RS57172677:30800604:T:C	10	30800604	466	926	C	1.48	2.16E-05
RS11008080:30802799:A:C	10	30802799	466	926	C	1.45	4.39E-05
RS882080:30804597:T:A	10	30804597	466	926	A	1.48	2.06E-05
RS2002695:30805480:A:G	10	30805480	466	926	G	1.48	2.12E-05
RS2009810:30806199:T:A	10	30806199	466	926	A	1.48	2.22E-05
RS12774393:30806833:G:C	10	30806833	466	926	C	1.48	2.35E-05
RS7296850:67338701:A:T	12	67338701	413	831	T	1.45	2.78E-05
RS6581724:67339018:A:G	12	67339018	413	831	G	1.45	3.03E-05
RS7966850:67340137:A:T	12	67340137	413	831	T	1.45	2.40E-05
RS7136625:67340896:T:C	12	67340896	413	831	C	1.52	2.20E-06
RS6581725:67350123:T:C	12	67350123	413	831	T	0.66	8.64E-06
RS1604843:67351176:A:G	12	67351176	413	831	A	0.66	9.42E-06
RS1354442:67351481:T:A	12	67351481	413	831	T	0.66	9.50E-06
RS10878540:67352669:C:T	12	67352669	413	831	C	0.66	9.67E-06
RS10878542:67356453:G:A	12	67356453	413	831	G	0.66	9.66E-06
RS4277193:67361657:G:A	12	67361657	413	831	G	0.66	9.73E-06
RS1604841:67362788:A:G	12	67362788	413	831	A	0.66	9.82E-06
RS2089133:67364152:T:C	12	67364152	413	831	T	0.66	9.89E-06
RS1117041:67364485:A:G	12	67364485	413	831	A	0.66	1.00E-05
RS1896092:108395223:C:T	12	108395223	413	831	C	1.62	3.70E-05
RS1896093:108395719:T:C	12	108395719	413	831	T	1.61	4.19E-05
RS1896096:108396894:C:T	12	108396894	413	831	C	1.61	4.16E-05
RS10861850:108399880:T:C	12	108399880	413	831	T	1.62	3.58E-05
RS714906:108401324:G:C	12	108401324	413	831	G	1.62	3.54E-05

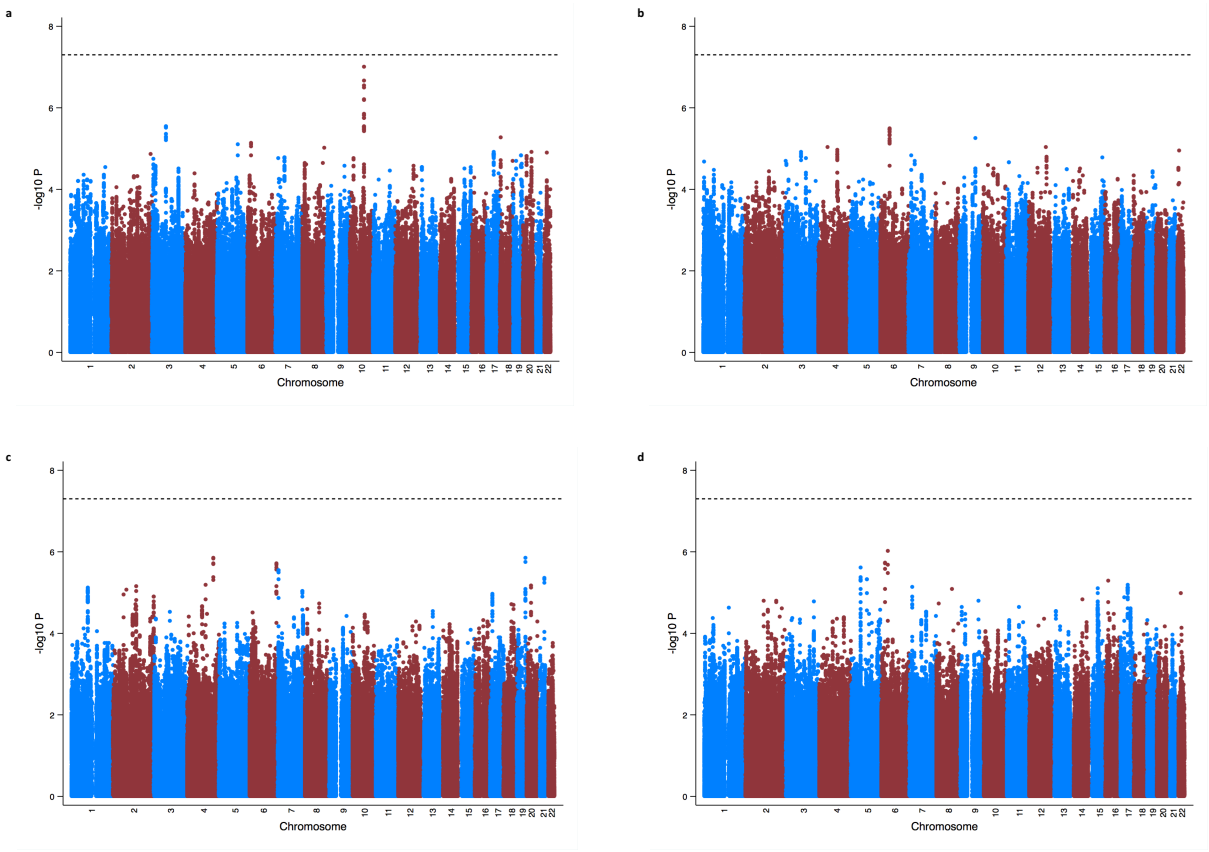
RS1896052:108402518:C:A	12	108402518	413	831	C	1.62	3.52E-05
RS6539400:108402874:C:A	12	108402874	413	831	C	1.62	3.50E-05
RS2194988:108403370:T:C	12	108403370	413	831	T	1.63	4.12E-05
RS4459358:108404076:A:T	12	108404076	413	831	A	1.62	3.42E-05
RS1896061:108408845:C:G	12	108408845	413	831	C	1.62	3.24E-05
RS1896062:108408861:T:A	12	108408861	413	831	T	1.62	3.69E-05
RS1896063:108408969:C:A	12	108408969	413	831	C	1.62	3.24E-05
RS1896065:108409623:T:G	12	108409623	413	831	T	1.62	3.68E-05
RS1896071:108410993:C:G	12	108410993	413	831	C	1.62	3.52E-05
RS1896080:108414313:C:T	12	108414313	413	831	C	1.62	3.64E-05
RS7974678:108417105:T:C	12	108417105	413	831	T	1.61	4.03E-05
RS7296801:108433529:G:C	12	108433529	413	831	G	1.61	4.53E-05
RS7305634:108465742:G:A	12	108465742	413	831	G	1.61	4.36E-05
RS4475966:108466021:T:C	12	108466021	413	831	T	1.61	4.35E-05
RS10746115:108475650:C:T	12	108475650	413	831	C	1.65	1.85E-05
RS10778607:108475893:G:T	12	108475893	413	831	G	1.64	2.40E-05
RS10778608:108476202:T:C	12	108476202	413	831	T	1.59	4.98E-05
RS1431977:3620717:G:T	17	3620717	466	926	T	0.71	3.43E-05
RS1977020:3622508:C:T	17	3622508	466	926	T	1.44	2.24E-05
RS16953429:3626816:G:A	17	3626816	466	926	A	1.43	3.68E-05
RS12943844:3631620:G:C	17	3631620	466	926	G	1.48	8.26E-06
RS55661368:19427601:C:A	17	19427601	413	831	A	0.69	3.10E-05
RS2440164:19428610:A:G	17	19428610	413	831	G	0.69	2.61E-05
RS2440165:19428719:T:C	17	19428719	413	831	C	0.69	2.61E-05
RS11870808:19429379:G:C	17	19429379	413	831	C	0.69	2.28E-05
RS8071709:19429790:A:C	17	19429790	413	831	C	0.69	4.27E-05
RS2453578:19430645:T:C	17	19430645	413	831	C	0.69	3.45E-05
RS111374932:19431959:T:C	17	19431959	413	831	C	0.69	2.48E-05
RS11871125:19432393:C:T	17	19432393	413	831	T	0.69	2.48E-05
RS2252281:19437187:T:C	17	19437187	413	831	C	0.69	3.55E-05
RS2453580:19438321:T:C	17	19438321	413	831	C	0.70	4.14E-05
RS2453581:19438560:C:T	17	19438560	413	831	T	0.69	2.81E-05
RS2453582:19439066:C:T	17	19439066	413	831	T	0.69	3.10E-05
RS894680:19440538:G:A	17	19440538	413	831	A	0.69	2.62E-05
RS2453583:19442036:A:T	17	19442036	413	831	T	0.68	1.87E-05
RS2453584:19443445:G:C	17	19443445	413	831	C	0.67	1.20E-05
RS4817650:16480898:C:T	21	16480898	413	831	T	0.64	8.26E-07
RS2823061:16481665:G:A	21	16481665	413	831	A	0.66	2.52E-06
RS4816486:16482620:A:G	21	16482620	413	831	G	0.66	3.07E-06
RS2823062:16482643:T:G	21	16482643	413	831	G	0.66	3.50E-06
RS9978683:16483454:G:A	21	16483454	413	831	A	0.66	4.33E-06
RS7282412:16484651:T:A	21	16484651	413	831	A	0.66	3.71E-06
RS2823065:16485897:C:T	21	16485897	413	831	T	0.66	7.61E-06
RS2823066:16486315:G:A	21	16486315	413	831	A	0.66	1.06E-05
RS2026849:16486626:G:A	21	16486626	413	831	A	0.66	1.30E-05

Supplementary Table 13. Phase 1 results for the most significant regions from an analysis of EULAR Good responders versus non-responders.

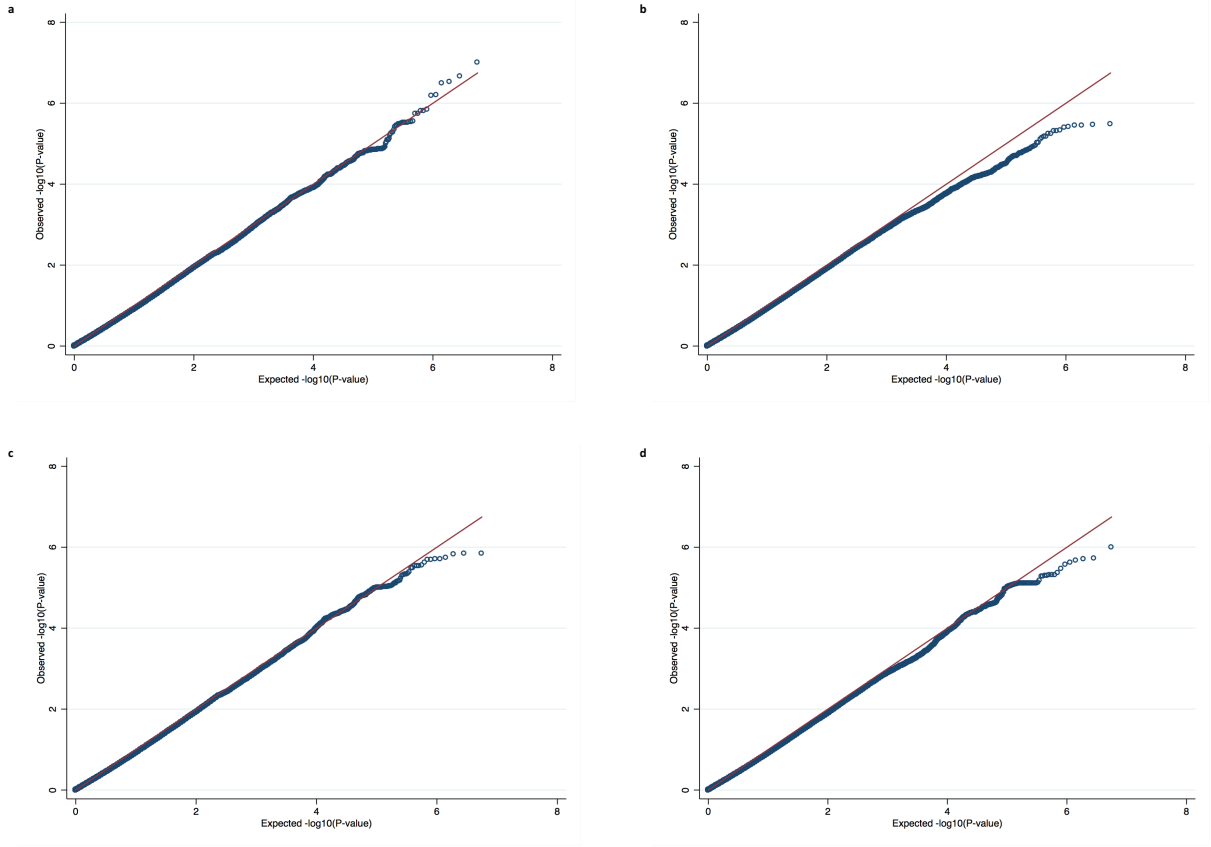
Regions are shown if they included one SNP with P<1x10-5 and at least one other SNP within 200kb with P<5x10-5

Marker	Chr	Position	Non-responders	Good Responders	Effect Allele	Odds Ratio for non-response	P
RS79944340:76866742:G:A	1	76866742	413	383	A	2.35	3.85E-06
RS11577449:76869325:T:A	1	76869325	413	383	A	2.34	4.00E-06
RS61771525:76892302:A:G	1	76892302	413	383	G	1.82	3.05E-05
RS6577247:101865870:G:T	1	101865870	413	383	G	0.37	2.87E-05
RS11164191:101866707:C:T	1	101866707	413	383	C	0.39	4.77E-05
RS4908139:101866905:G:C	1	101866905	413	383	G	0.39	4.47E-05
RS10874488:101867800:G:A	1	101867800	413	383	G	0.37	2.81E-05
RS7540539:101869322:T:A	1	101869322	413	383	T	0.37	2.79E-05
RS12128264:203575060:T:G	1	203575060	413	383	T	0.63	1.54E-05
RS12121279:203576156:G:T	1	203576156	413	383	G	0.64	2.11E-05
RS12131388:203577939:T:C	1	203577939	413	383	T	0.63	1.78E-05
RS12125553:203580111:G:T	1	203580111	413	383	G	0.64	1.90E-05
RS1970963:203586060:T:A	1	203586060	413	383	T	0.64	3.14E-05
RS7568567:151786203:C:G	2	151786203	413	383	G	1.52	4.91E-05
RS1118980:151839884:G:T	2	151839884	413	383	G	0.64	3.22E-05
RS13026509:151853097:G:C	2	151853097	413	383	G	0.64	2.52E-05
RS12987768:151872127:C:T	2	151872127	413	383	C	0.64	2.03E-05
RS12990477:151885001:G:A	2	151885001	413	383	G	0.64	3.90E-05
RS1546485:14533006:A:T	8	14533006	413	383	A	0.64	1.07E-05
RS28842205:14545161:C:T	8	14545161	413	383	C	1.52	4.62E-05
RS1510454:14553223:A:T	8	14553223	413	383	T	0.65	2.35E-05
RS6999437:14554875:T:C	8	14554875	413	383	T	1.53	3.80E-05
RS6995277:14554878:A:C	8	14554878	413	383	A	1.53	3.80E-05
RS7017742:14554992:C:T	8	14554992	413	383	C	1.53	3.81E-05
RS17321361:14555348:A:T	8	14555348	413	383	A	1.52	4.32E-05
RS2247039:14659604:C:G	8	14659604	413	383	C	0.65	1.81E-05
RS28843818:14661422:T:C	8	14661422	413	383	C	1.54	2.62E-05
RS28798118:14661423:G:C	8	14661423	413	383	C	1.54	2.62E-05
RS28877698:14661444:C:A	8	14661444	413	383	A	1.58	6.89E-06
RS28880069:14661518:C:G	8	14661518	413	383	C	0.65	1.62E-05
RS138769756:14664899:C:T	8	14664899	413	383	T	1.53	2.06E-05
RS187891412:14665482:C:A	8	14665482	413	383	A	1.56	1.09E-05
RS1031054:14668259:C:T	8	14668259	413	383	T	1.56	1.14E-05
RS2250879:14668742:G:C	8	14668742	413	383	G	0.63	5.96E-06
RS2250963:14669239:T:A	8	14669239	413	383	T	0.61	1.77E-06
RS2034005:14670877:C:G	8	14670877	413	383	C	0.63	5.67E-06
RS2251199:14671281:A:G	8	14671281	413	383	A	0.62	4.15E-06
RS2483307:84564127:G:A	10	84564127	413	383	G	1.55	2.14E-05
RS4488143:84596866:C:T	10	84596866	413	383	C	1.59	8.42E-06
RS485907:84599583:T:A	10	84599583	413	383	T	1.59	7.57E-06
RS168201:84610081:G:A	10	84610081	413	383	G	1.59	7.48E-06
RS7171524:94738563:G:C	15	94738563	413	383	G	0.59	1.72E-05
RS17629107:94740359:C:T	15	94740359	413	383	C	0.59	1.09E-05
RS6497177:94741598:T:G	15	94741598	413	383	T	0.59	1.10E-05
RS12909327:94742652:G:C	15	94742652	413	383	G	0.64	3.05E-05
RS28813744:94744876:T:C	15	94744876	413	383	T	0.58	1.35E-05
RS28397663:47328183:C:T	17	47328183	466	403	T	0.65	3.23E-05
RS34666276:47379486:T:C	17	47379486	466	403	C	0.65	4.06E-05
RS9889262:47398070:T:A	17	47398070	466	403	A	0.65	4.09E-05
RS12940887:47402807:C:T	17	47402807	466	403	T	0.65	4.09E-05
RS62076439:47404628:G:T	17	47404628	466	403	T	0.65	4.13E-05
RS35587648:47418178:G:A	17	47418178	466	403	A	0.65	3.78E-05
RS35073649:47422510:C:T	17	47422510	466	403	T	0.65	3.92E-05
RS7207729:47423740:C:T	17	47423740	466	403	T	0.65	3.82E-05
RS6504608:47424681:C:A	17	47424681	466	403	A	0.65	3.83E-05
RS57816977:4012466:T:C	18	4012466	413	383	C	0.54	1.18E-05
RS17653931:4019781:A:T	18	4019781	413	383	T	0.54	2.84E-05
RS62083652:4019804:C:T	18	4019804	413	383	T	0.53	1.86E-05
RS2335226:14949034:C:G	19	14949034	413	383	G	0.61	2.75E-05
RS10413393:14950428:C:A	19	14950428	413	383	A	0.62	4.96E-05

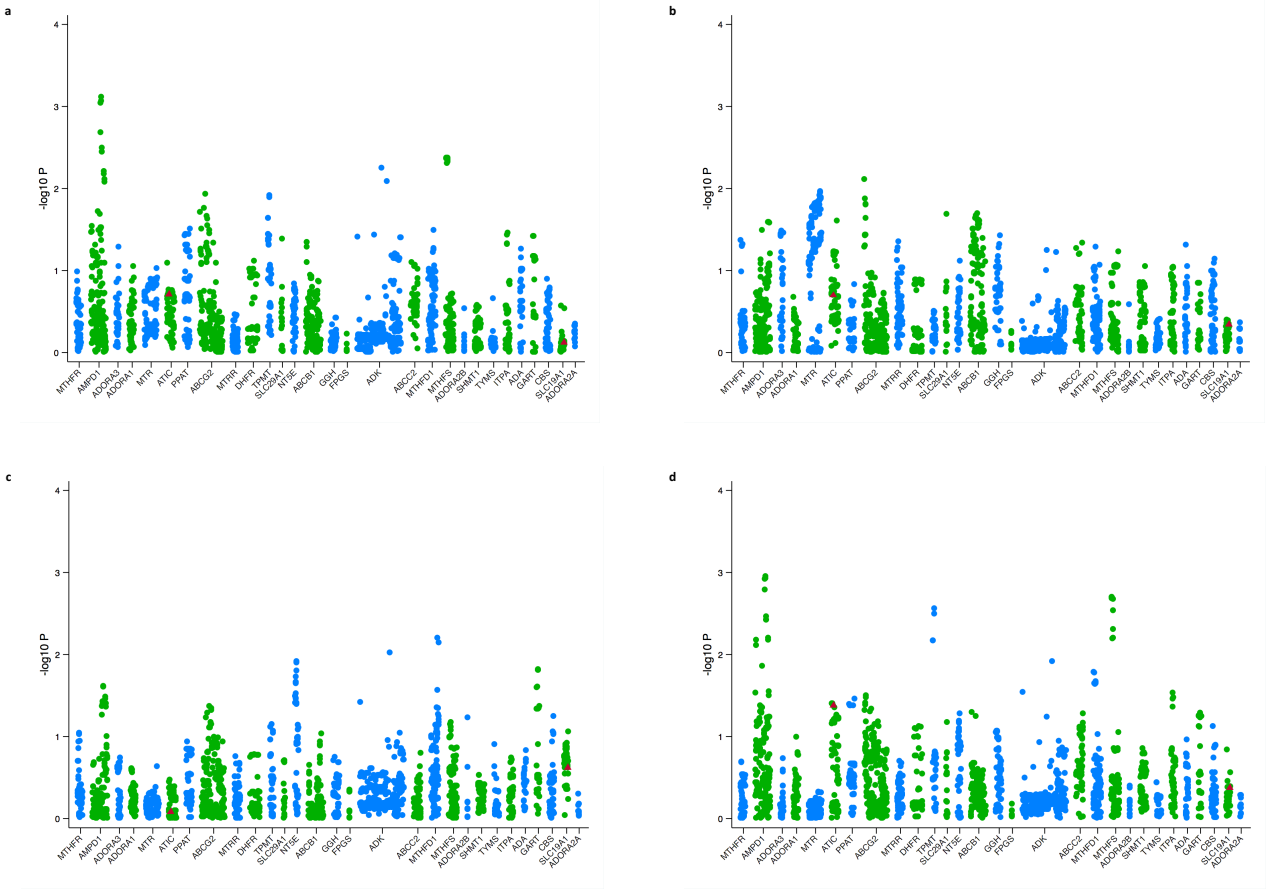
Supplementary Figure 1. Manhattan plots of the genome-wide association analyses for DAS28 (a), CRP (b), SJC28 (c) and TJC28 (d). The dashed line indicates the P-value for 5 x 10^{-8}.



Supplementary Figure 2. QQ-plots of the genome-wide association analyses for DAS28 (a), CRP (b), SJC28 (c) and TJC28 (d).



Supplementary Figure 3. Results for methotrexate metabolism candidate genes for DAS28 (a), CRP (b), SJC28 (c) and TJC28 (d). Genes are plotted in chromosome-basepair order
SNPs previously associated in more than one study, rs2372536 in *ATIC* and rs1051266 in *SLC19A1*, are indicated by a red triangle.



Appendix I

MATURA Consortium

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CARDERA

CARDERA Genetics Cohort

CARDERA-1 Trial

Choy EH, Smith CM, Farewell V, Walker D, Hassell A, Chau L, Scott DL

CARDERA-2 Trial

Scott IC, Ibrahim F, Simpson G, Kowalczyk A, White-Alao B, Hassell A, Plant M, Richards S, Walker D, Scott DL.

CARDERA-1 and 2 Genetics Cohort

Scott IC, Lewis CM, Cope AP, Steer S, Spain S.

Appendix II

PAMERA Consortium

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