SUPPLEMENTARY MATERIAL

SUPPLEMENTARY NOTE:

SUPPLEMENTARY FIGURES:

SUPPLEMENTARY TABLES:

a. Member of the Japanese Research Committee on Idiopathic Osteonecrosis of the Femoral Head

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b. Acknowledgement

We appreciate the contribution of following colleagues in the Japanese Research Committee on Idiopathic Osteonecrosis of the Femoral Head.
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[11]Kyushu University Hospital
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[24]Tobata General Hospital
[25]The First Department of Internal Medicine, University of Occupational and Environmental Health, Japan
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[27]Kyoto interdisciplinary institute hospital of community medicine
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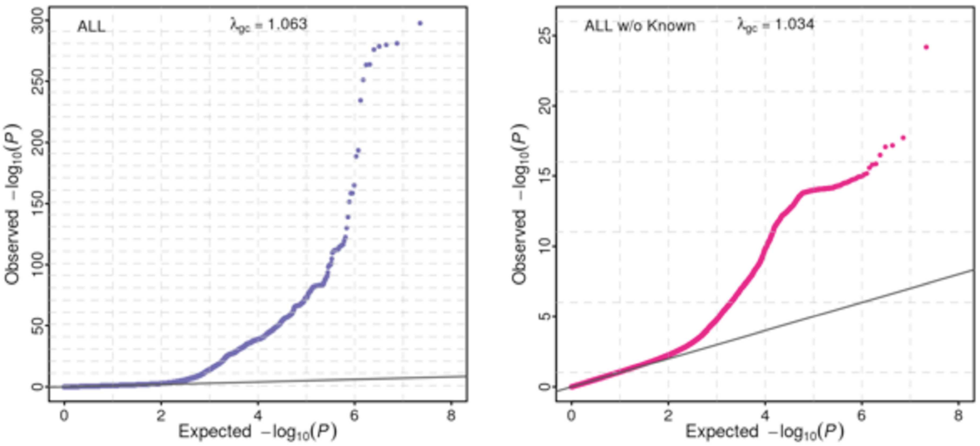
[29]Tonan hospital, Department of orhopaedic surgery
[30]Department of Orthopaedic Surgery, Osaka City University Graduate School of Medicine
[31]Orthopedis and Joint Surgery Center, Kurume Univ. Medical Center
[32]Department of Orthopaedic Surgery, Mie University Graduate School
[33]Department of Orthopaedic Surgery, Kanazawa Medical University
[34]Department of Orthopaedic Surgery, National Hospital Organization Kure Medical Center and Chugoku Cancer Center

c. Web resources

The software used has been described in details in Online Methods section. Software and resources included:
Pre-phasing: SHAPEITv2/v2.3, https://mathgen.stats.ox.ac.uk/genetics_software/shapeit
Pre-phasing: Eagle v2, https://data.broadinstitute.org/alkesgroup/Eagle/
Imputation: minimac3/4, Michigan Imputation Server, https://imputationserver.sph.umich.edu
Imputation: IMPUTEv2/v4, https://jmarchini.org/impute-4/
Association: EPACTSv3.3 (EMMAX), https://github.com/statgen/EPACTS
Association: Plinkv1.9, https://www.cog-genomics.org/plink/
Association: SNPTESTv2.5, https://mathgen.stats.ox.ac.uk/genetics_software/snptest
Meta-analysis: metal, https://genome.sph.umich.edu/wiki/METAL
Conditional analysis: GCTAv1.9, https://cnsgenomics.com/software/gcta/#Overview
Bayesian statistical fine-mapping, FINEMAP v1.4, http://www.christianbenner.com
Visualization: LocusZoom, https://genome.sph.umich.edu/wiki/LocusZoom_Standalone
Heritability estimation: LDSC, https://github.com/bulik/ldsc

Supplementary Figure 1 | Quantile-quantile (QQ) plots of the meta-analysis association *P* values for all variants (left) and the variants outside of known SLE loci (right). X-axis is the minus $\log_{10}$-transformed expected *P* values while the y-axis is the minus $\log_{10}$-transformed observed *P* values in the meta-analysis. The genomic control inflation factor (λ_{gc}) is shown in the top of each figure.



Supplementary Figure 2 | Regional association plots for the 113 SLE genomic loci. Each circle represents a variant that is plotted with its minus $\log_{10}$-transformed association *P* value and chromosomal position. Recombination rates are estimated from the International HapMap Project data, and gene annotations are taken from the hg19 UCSC Genome Browser. The SLE loci were numbered based on chromosomal position as from "region 1" to "region 113". The first 85 loci (such as region 1, region 6, and region 7) display single lead variants as purple diamonds. The other non-lead variants were colored by r^2 values with the lead variant (estimated from 7,021 unrelated Chinese controls). The following remaining 28 loci with multiple distinct association signals (such as region 2, region 3, and region 4) highlight variants associated with the first, second, third, and fourth distinct signals in red, blue, green, and purple, respectively. The lead variant for each distinct association signal were represented as diamond. For *HLA* (region 41) and 7q11.23 (region 50), we show regional plots using the most significant single variants.

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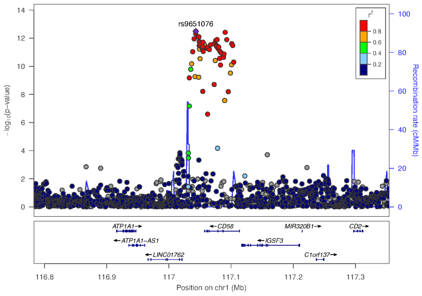

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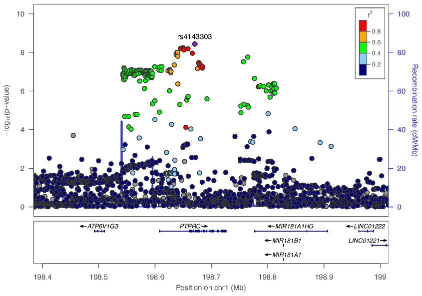

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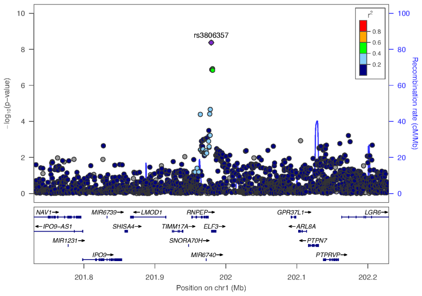

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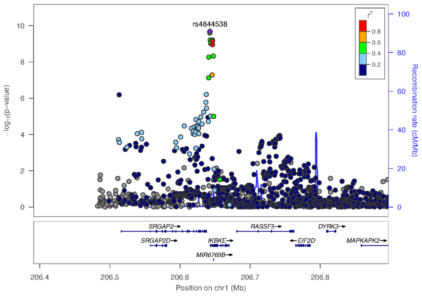

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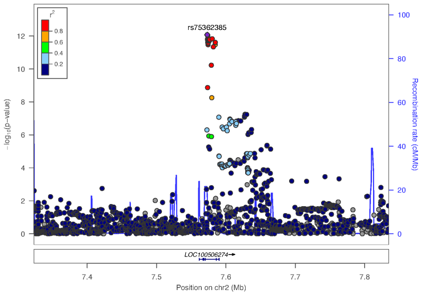

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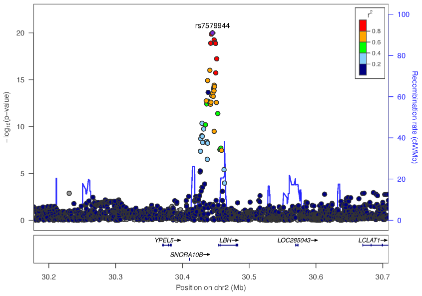

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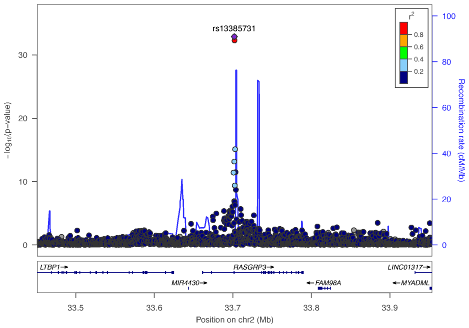

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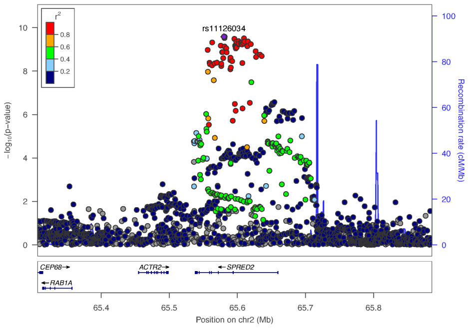

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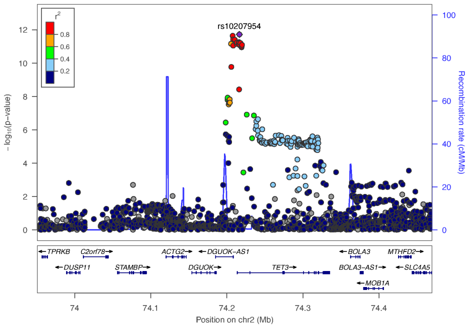

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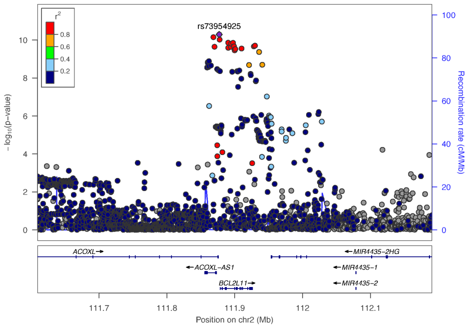

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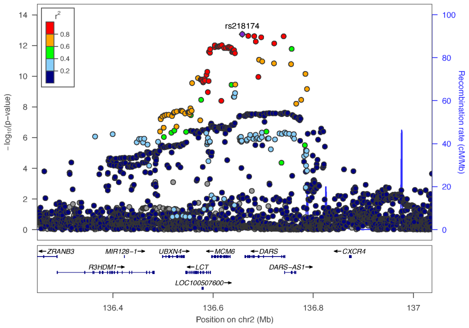

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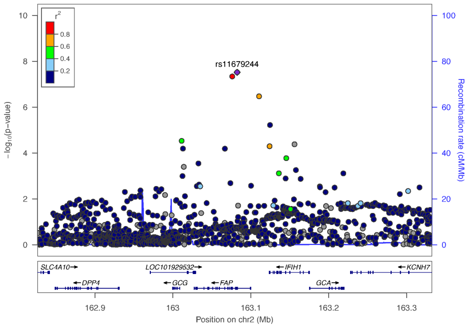

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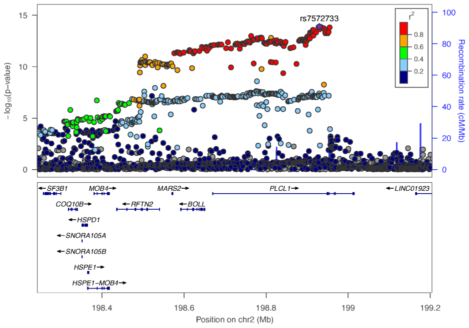

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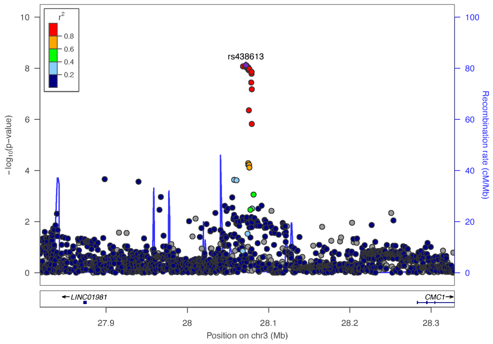

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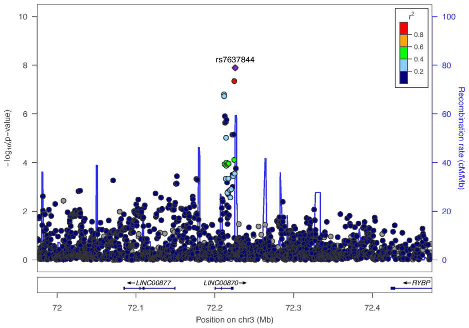

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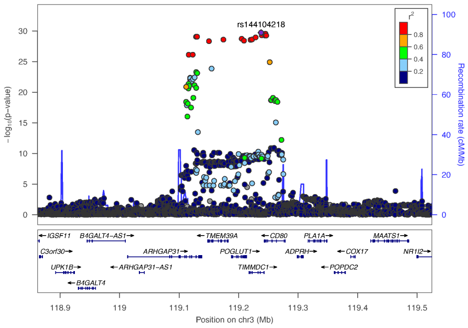

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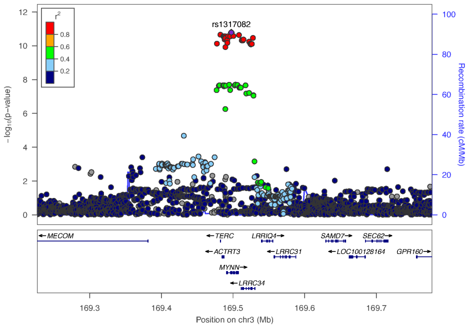

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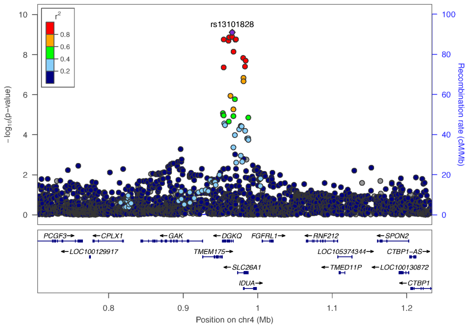

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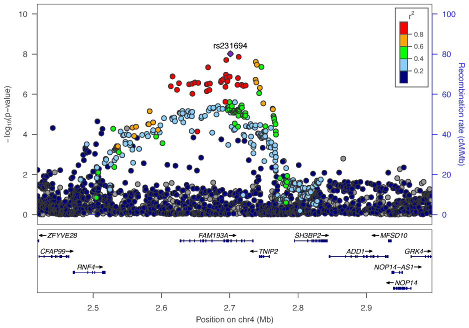

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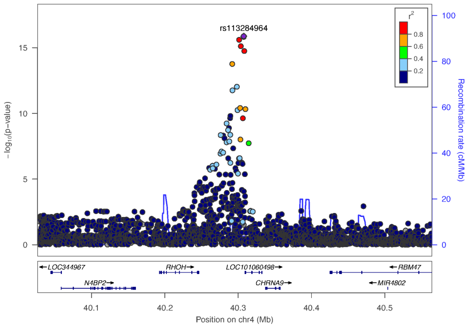

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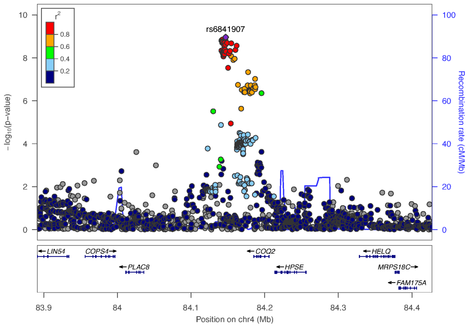

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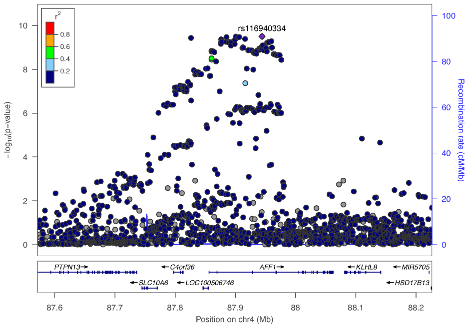

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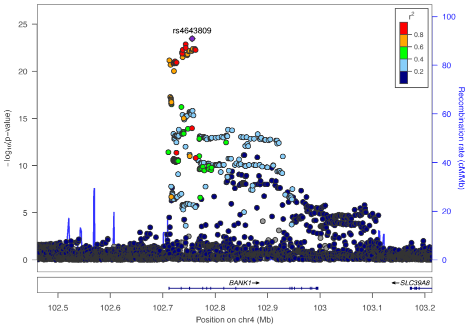

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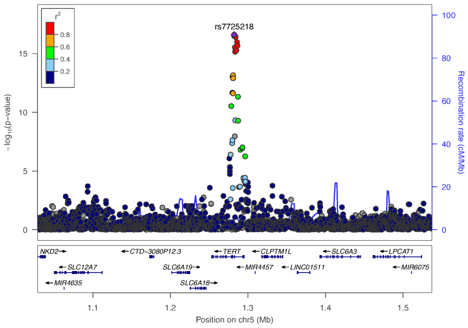

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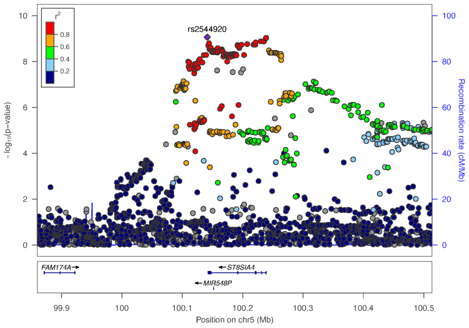

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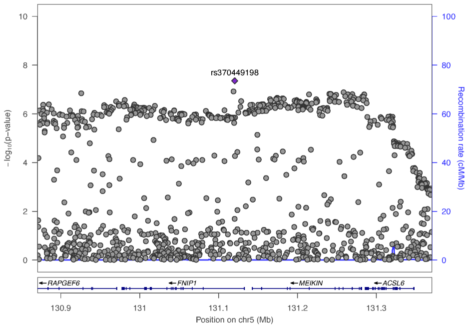

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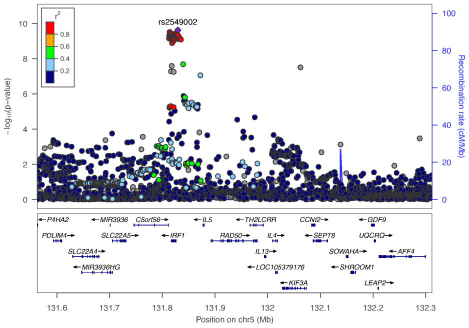

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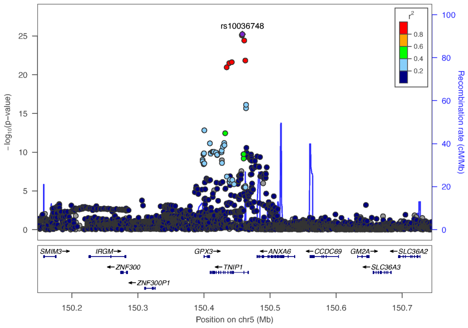

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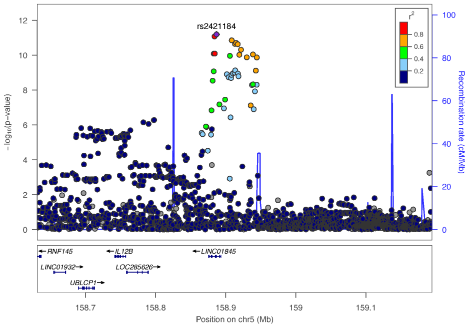

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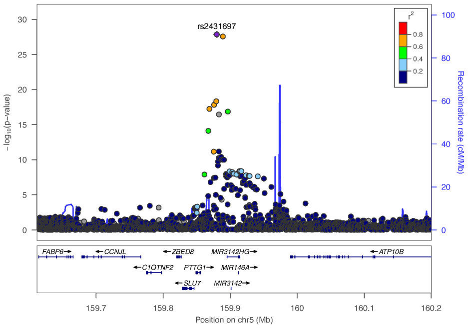

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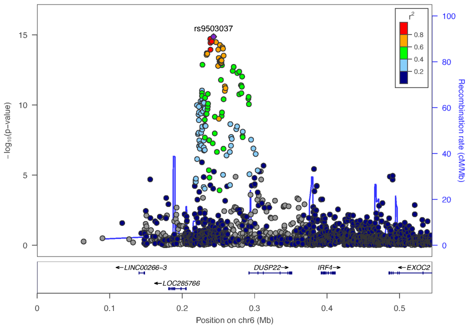

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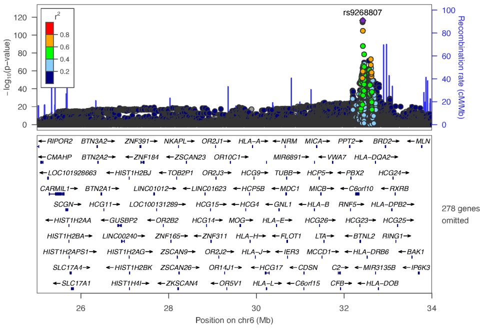

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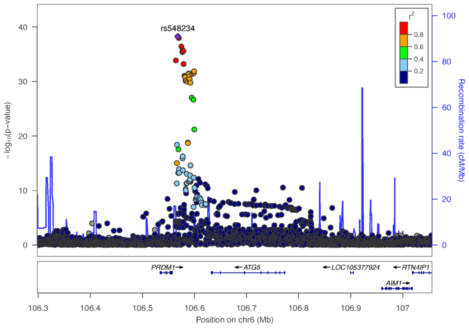

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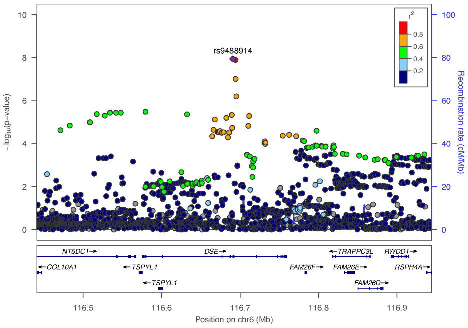

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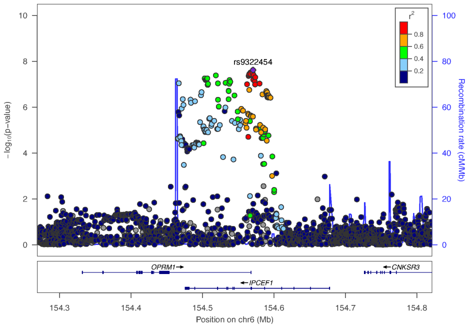

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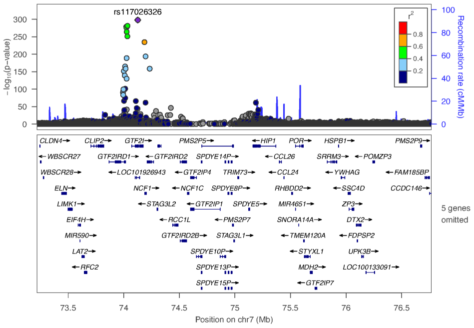

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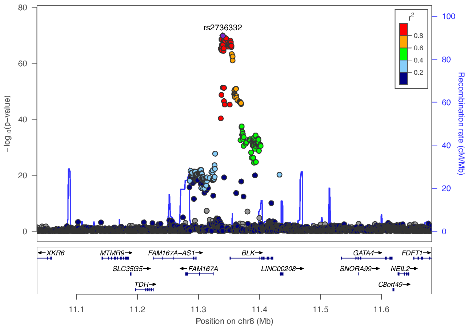

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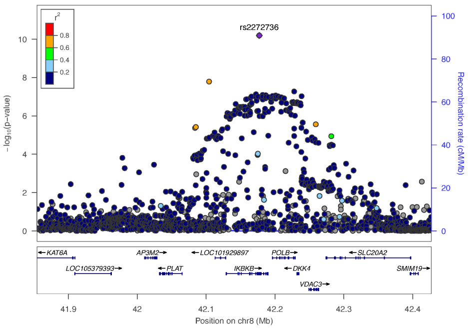

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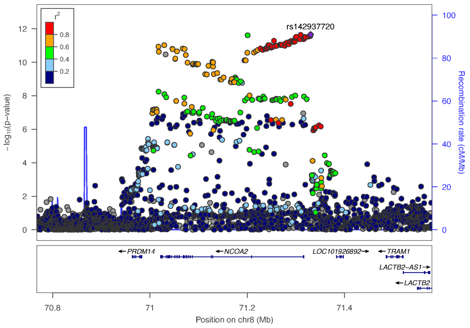

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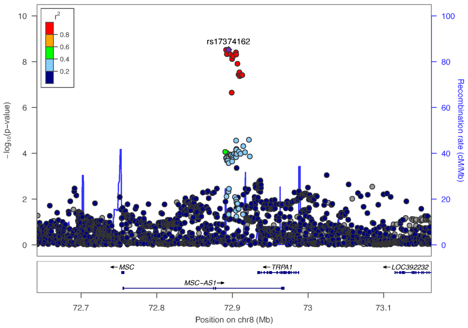

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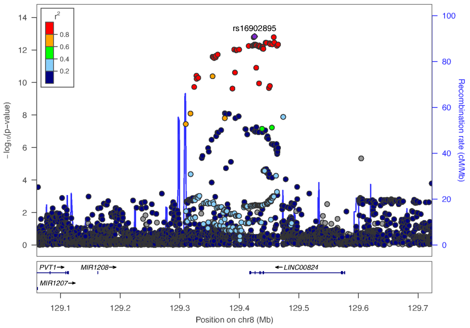

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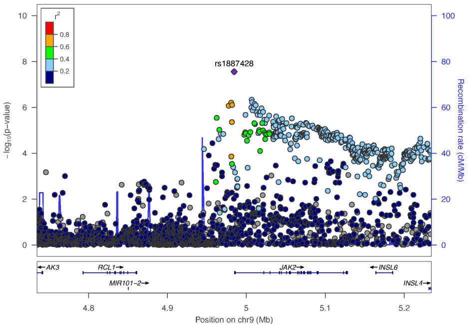

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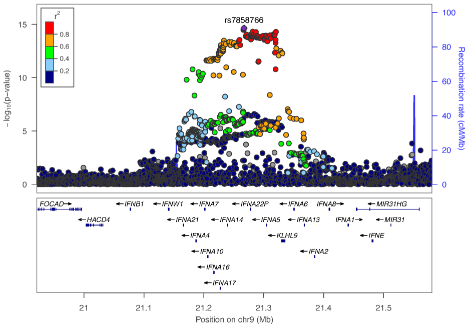

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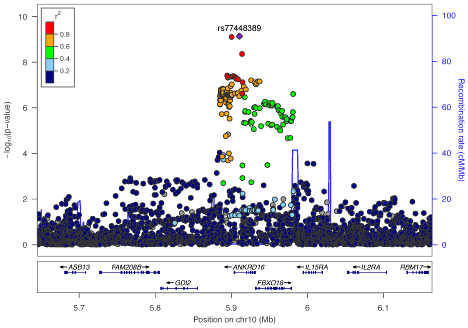

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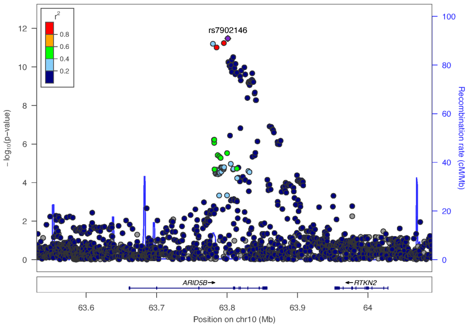

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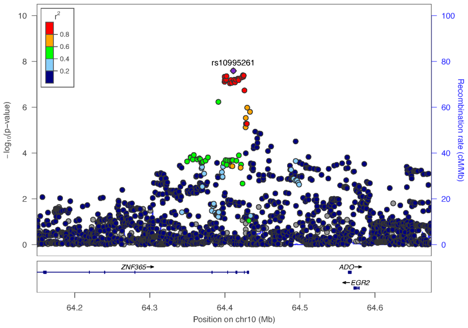

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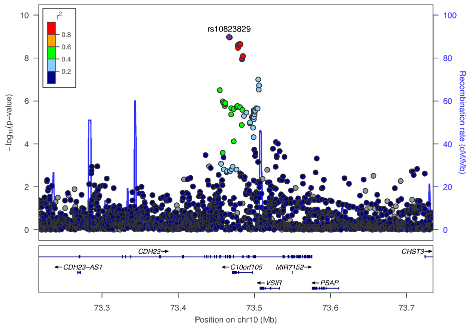

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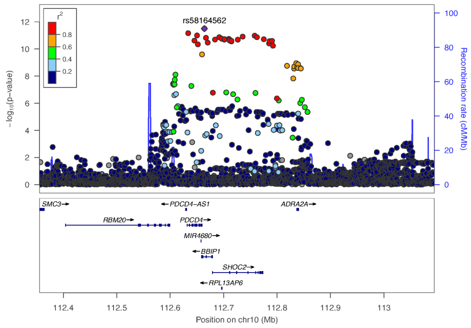

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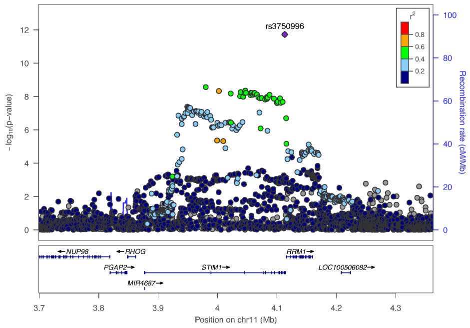

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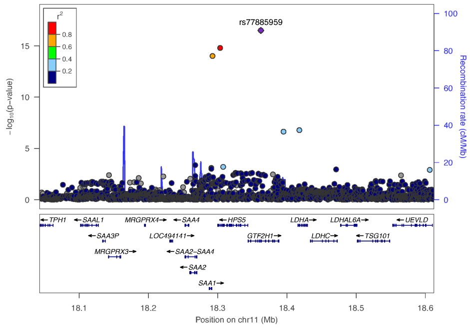

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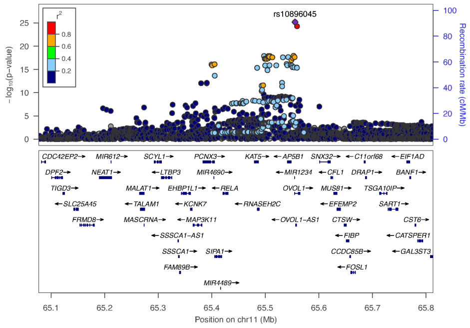

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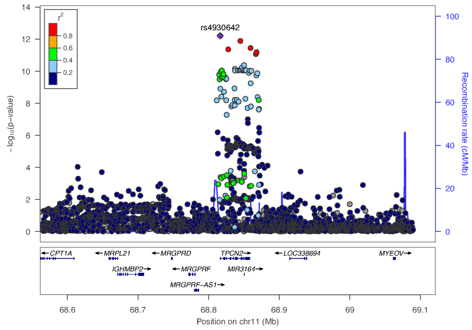

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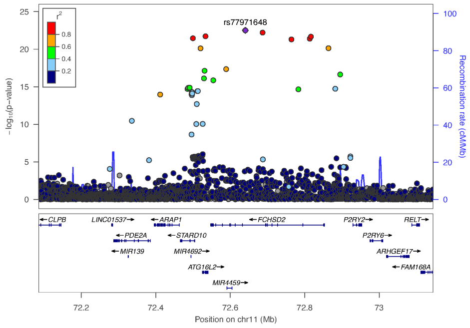

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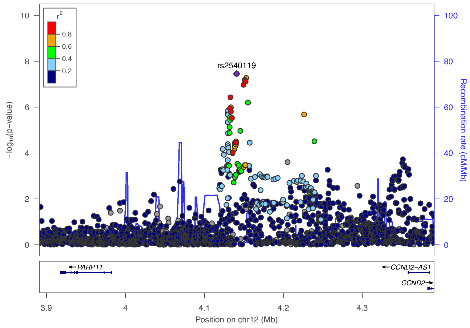

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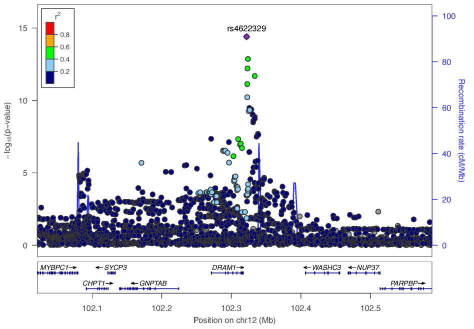

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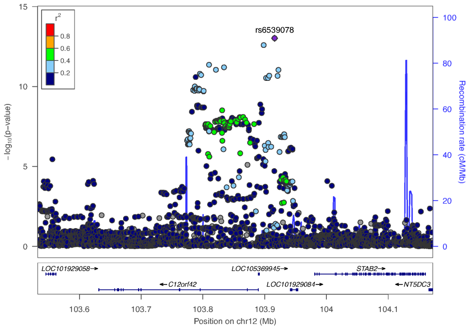

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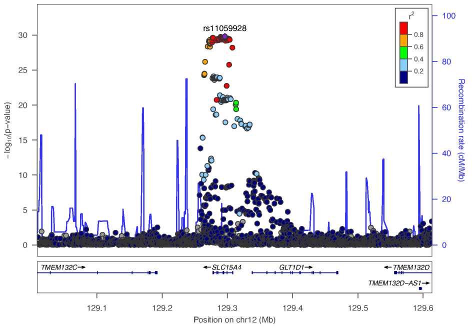

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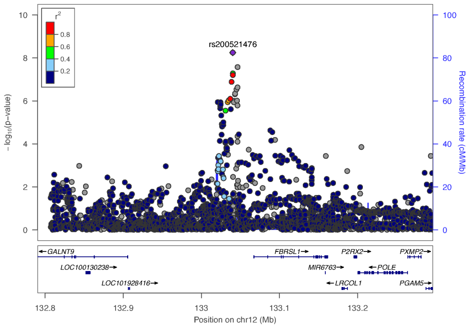

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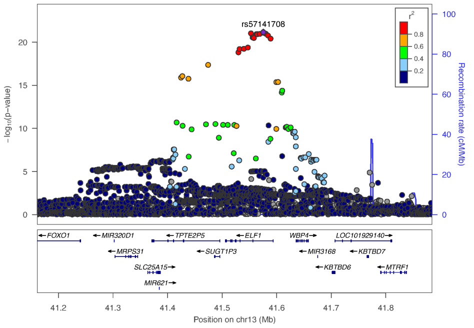

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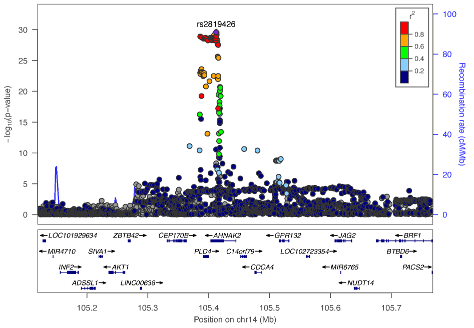

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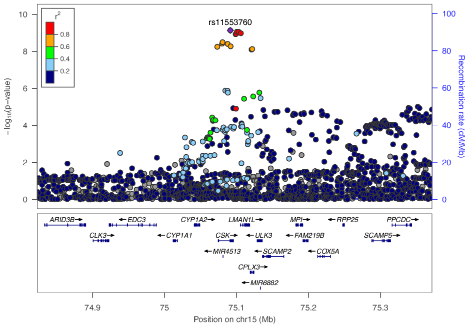

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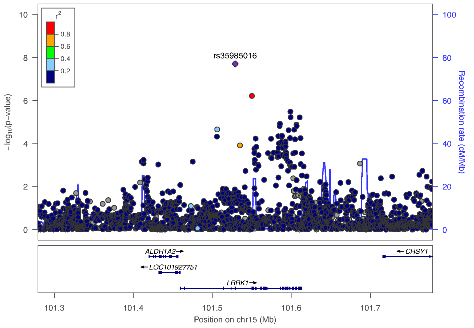

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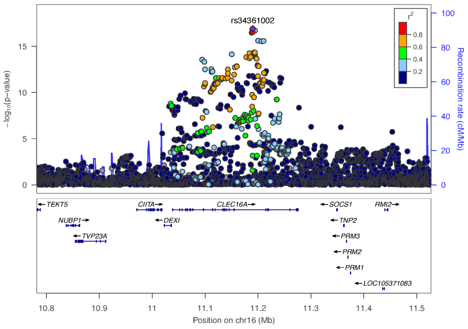

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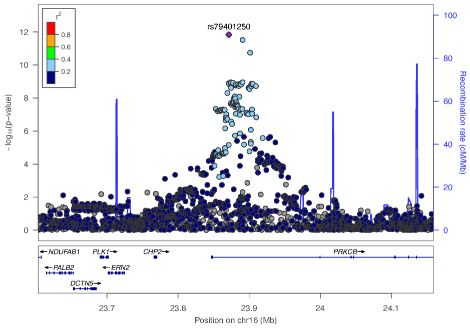

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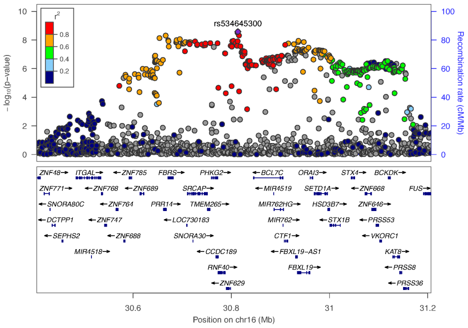

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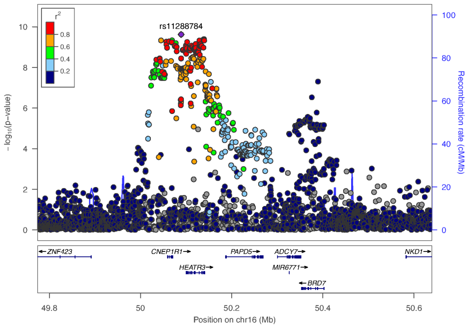

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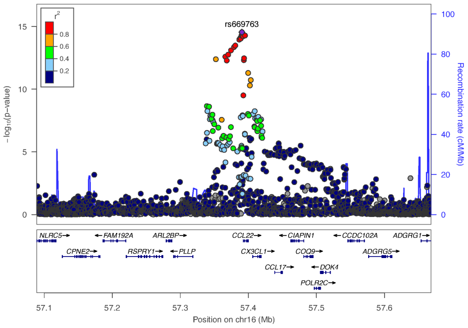

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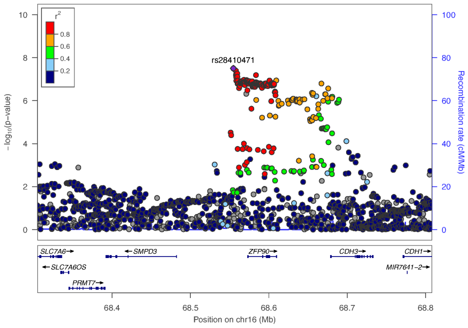
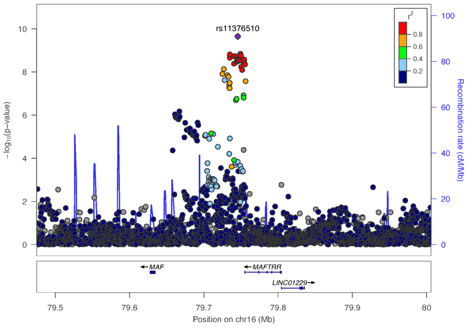
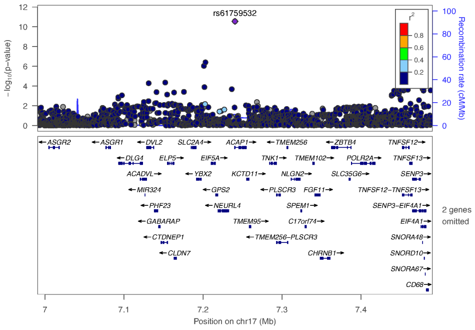


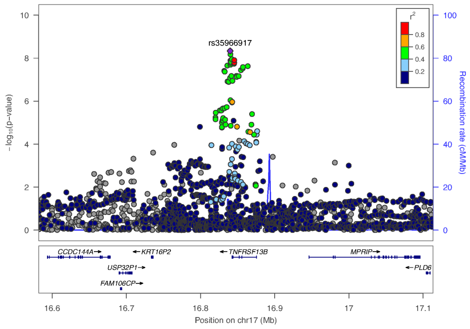
region 93: rs11376510



region 95: rs61759532



region 96: rs35966917



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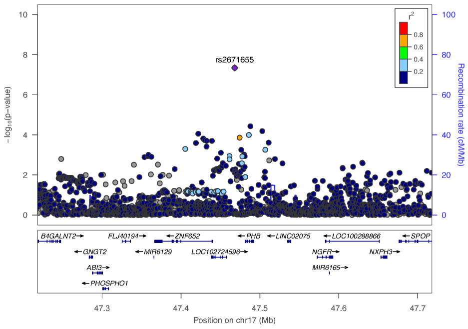

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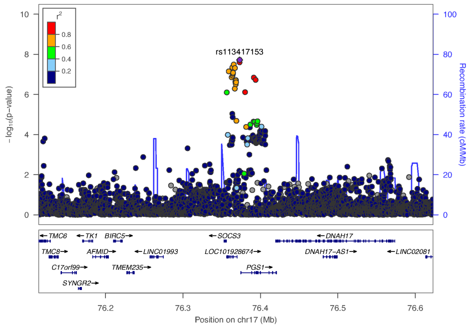

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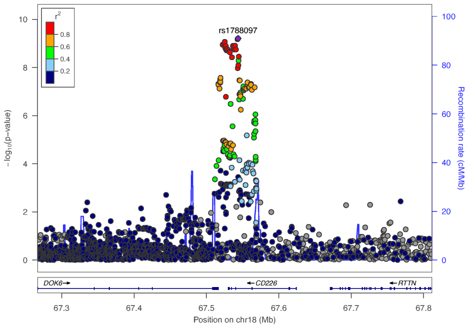

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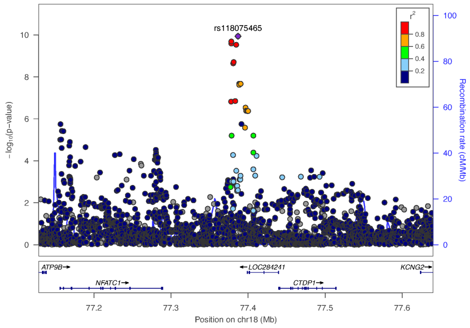

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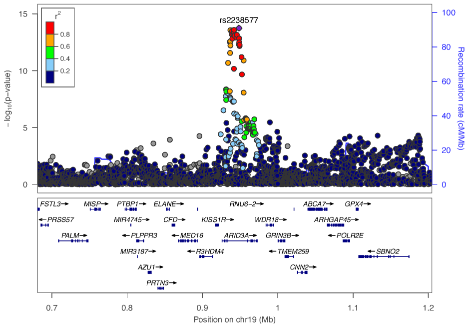

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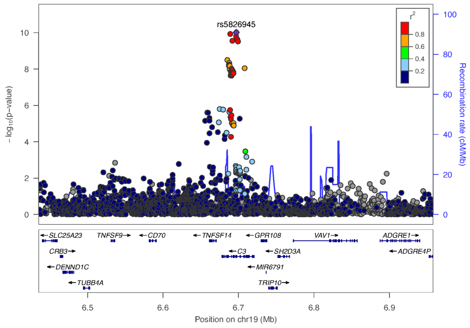

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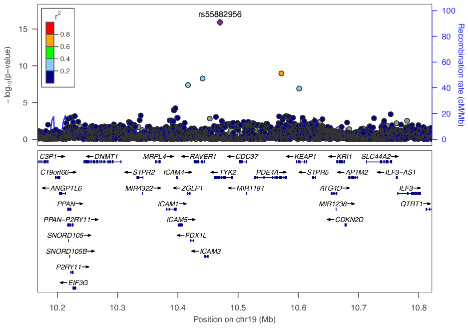

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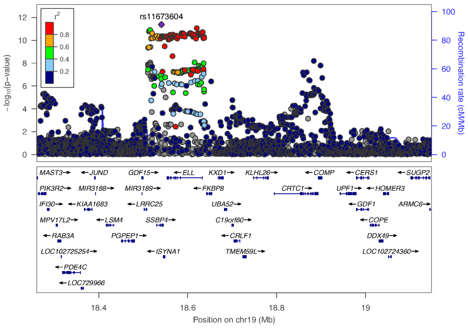

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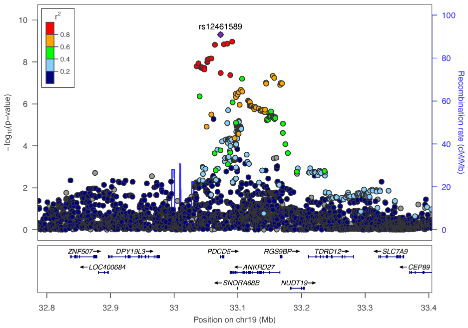
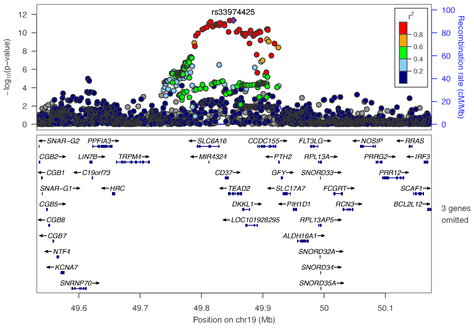


region 106: rs33974425



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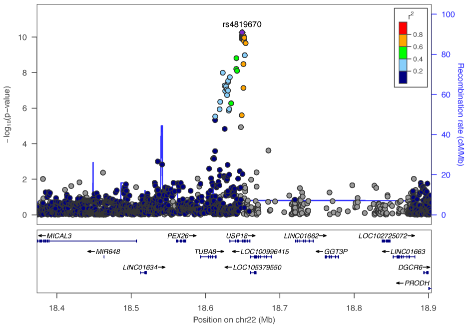
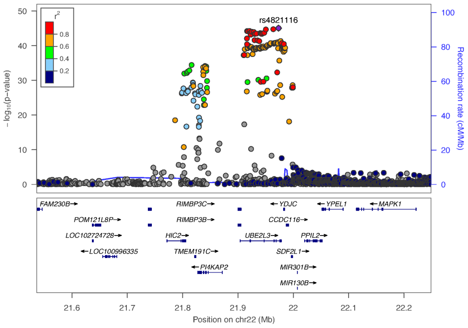
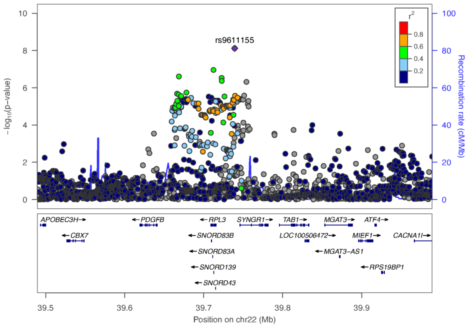


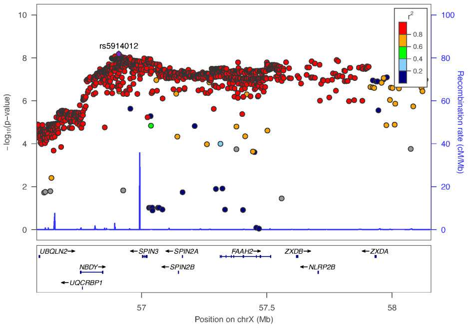
region 109: rs4821116



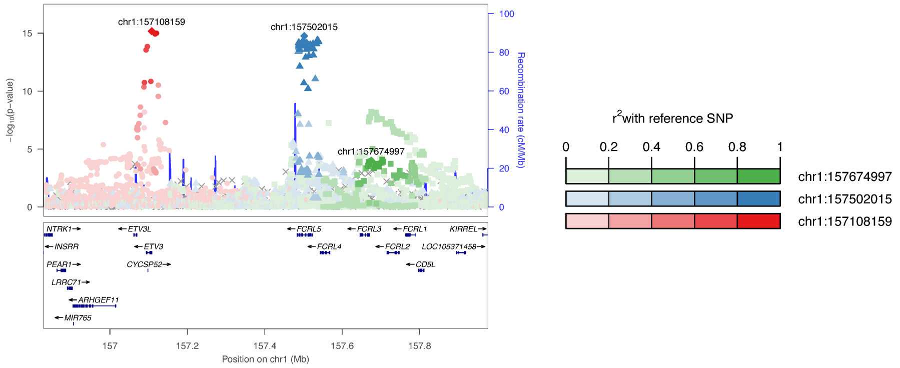
region 110: rs9611155



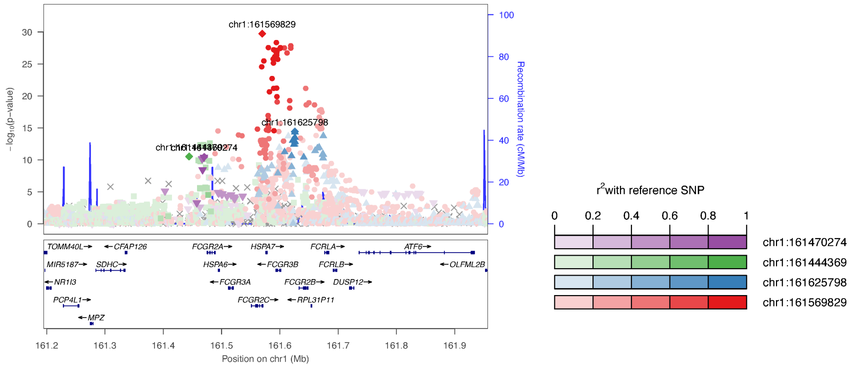
region 112: rs5914012



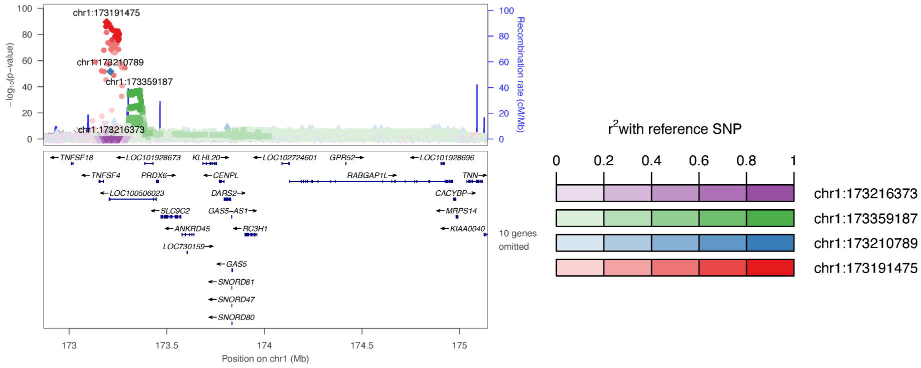
region 2: rs116785379 (1:157108159:G:C), rs112806509(1:157502015:AT:A), and rs2317230(1:157674997:G:T)



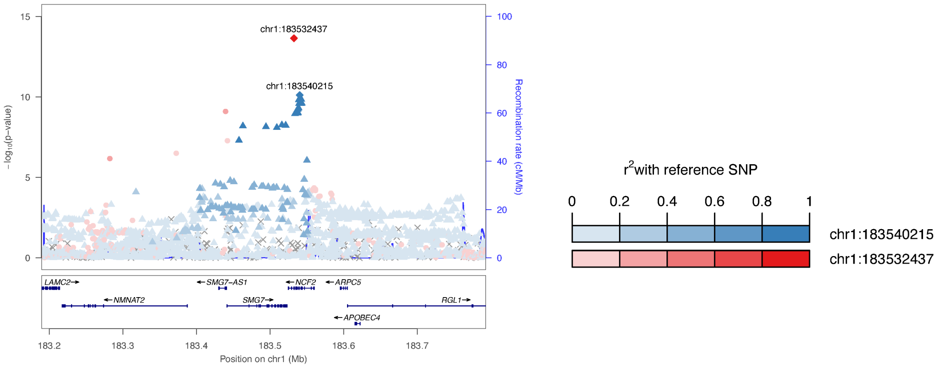
region 3: rs12120358(1:161444369:A:T), rs111994823(1:161470274:T:C), rs76107698(1:161569829:G:C), and rs75773410(1:161625798:A:G)



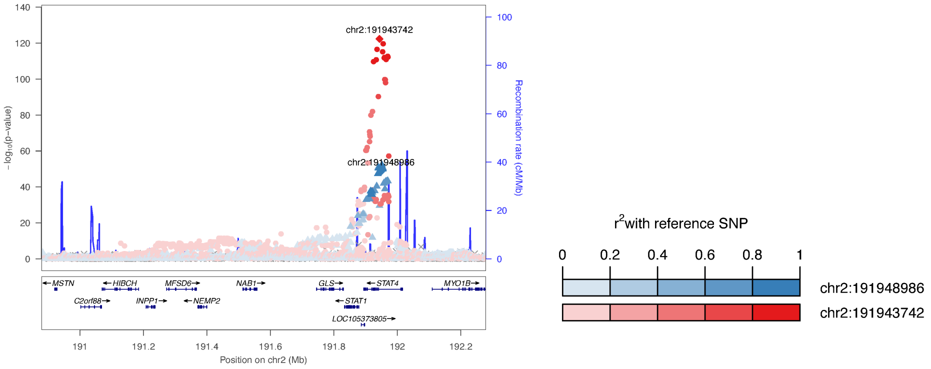
region 4: rs2205960 (1:173191475:G:T), rs117278480 (1:173210789:A:G), rs844646 (1:173216373:A:G), and rs2039982 (1:173359187:C:T)



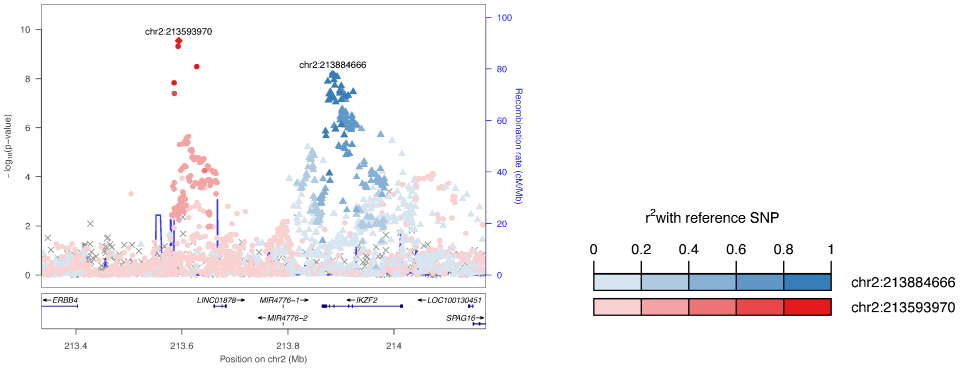
region 5: rs13306575 (1:183532437:G:A) and rs66977652 (1:183540215:TA:T)



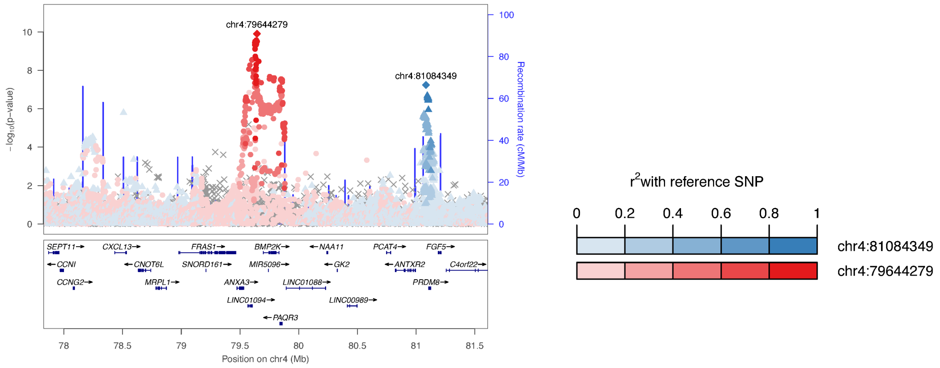
region 17: rs11889341 (2:191943742:C:T) and rs71030321 (2:191948986:T:TA)



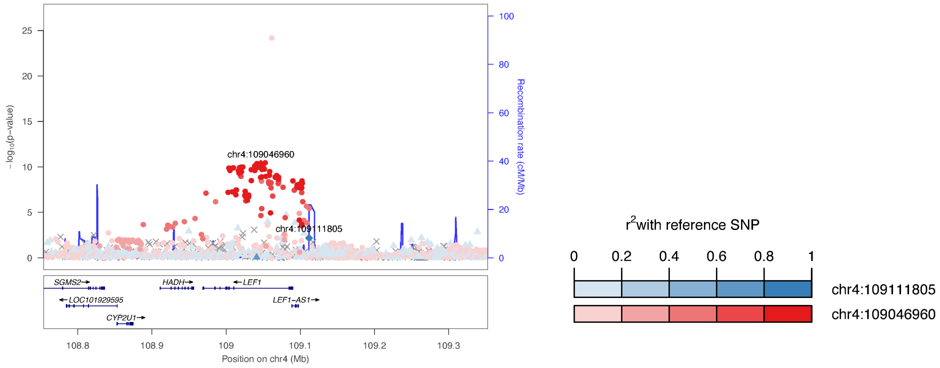
region 19: rs7565158 (2:213593970:G:T) and rs2371790 (2:213884666:A:G)



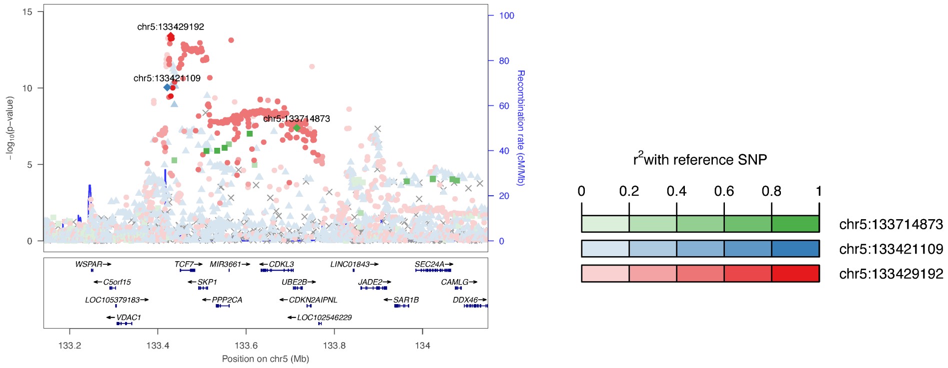
region 27: rs6533951 (4:79644279:A:G) and rs2867700 (4:81084349:A:G)



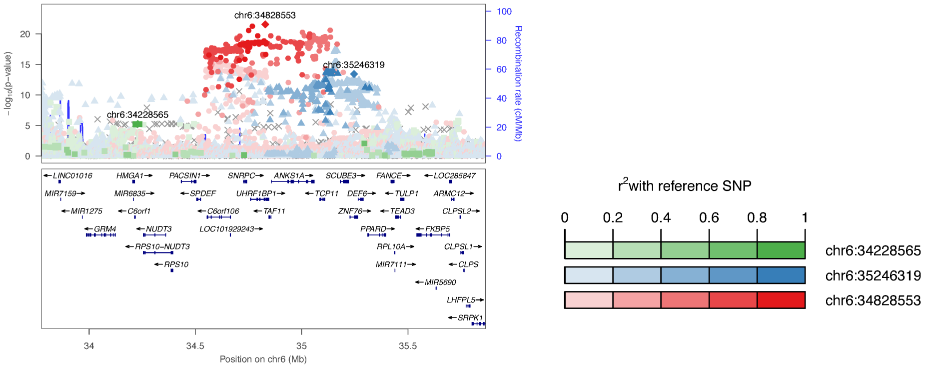
region 31: rs956237 (4:109046960:G:A) and rs57634688 (4:109111805:C:T)



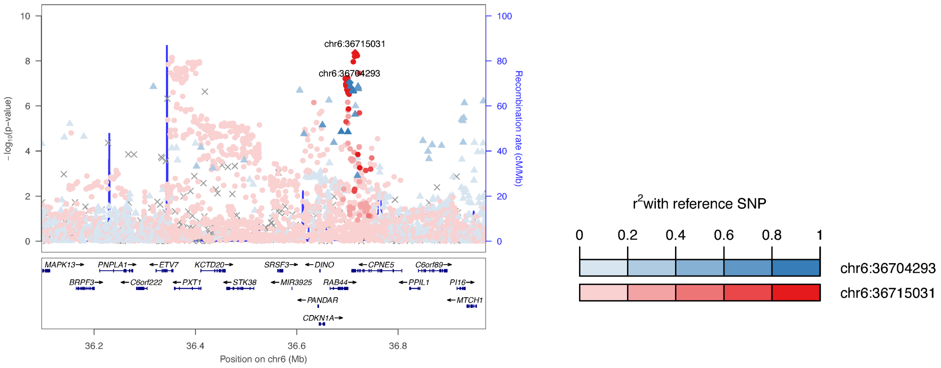
region 36: rs115267018 (5:133421109:G:C), rs6874758 (5:133429192:G:C), and rs138305363 (5:133714873:A:G)



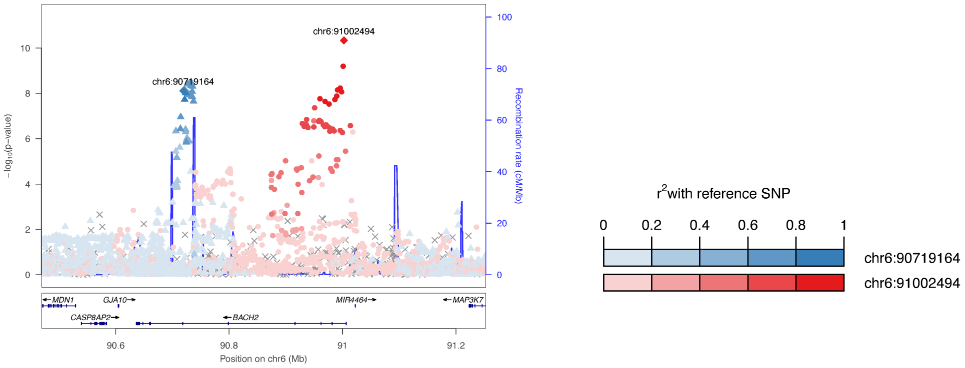
region 42: rs111658701 (6:34228565:T:C), rs6457796 (6:34828553:T:C), and rs10484578 (6:35246319:A:G)



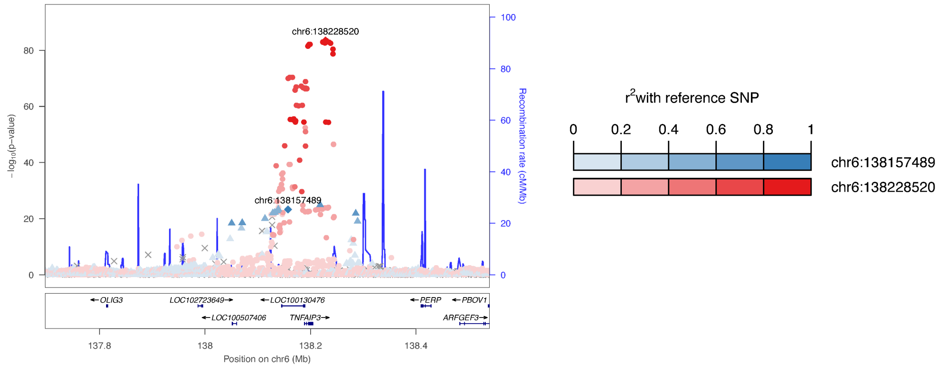
region 43: rs56285849 (6:36704293:T:C) and rs34868004 (6:36715031:C:CA)



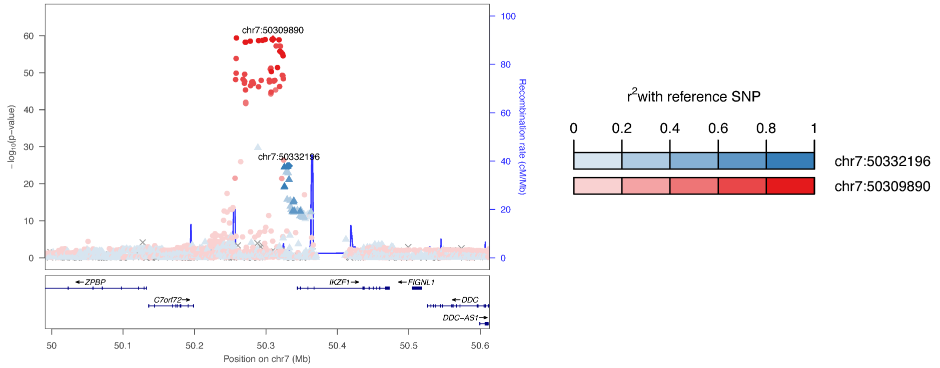
region 44: rs3857496 (6:90719164:T:C) and rs597325 (6:91002494:A:G)



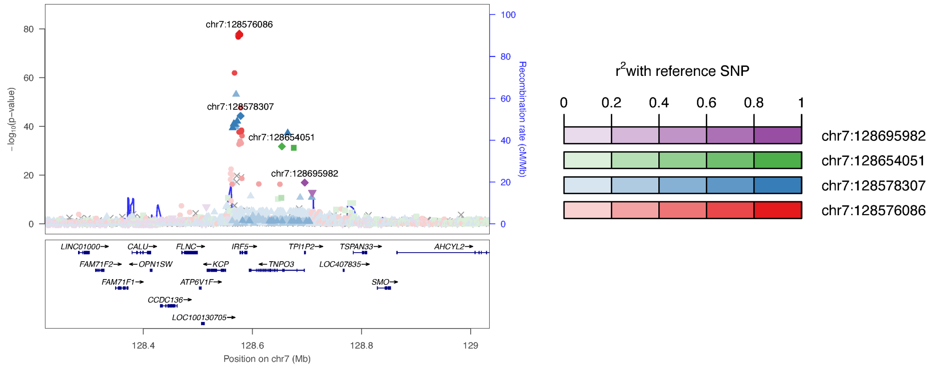
region 47: rs75163761 (6:138157489:C:T) and rs9494894 (6:138228520:T:C)



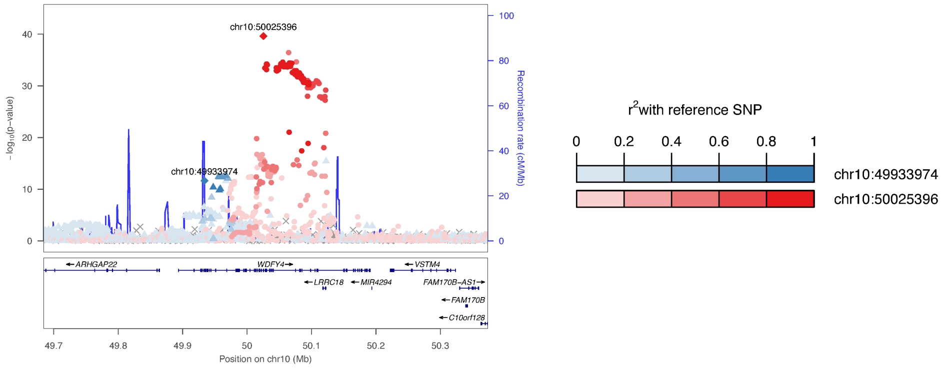
region 49: rs62447171 (7:50309890:G:A) and rs10239000 (7:50332196:A:G)



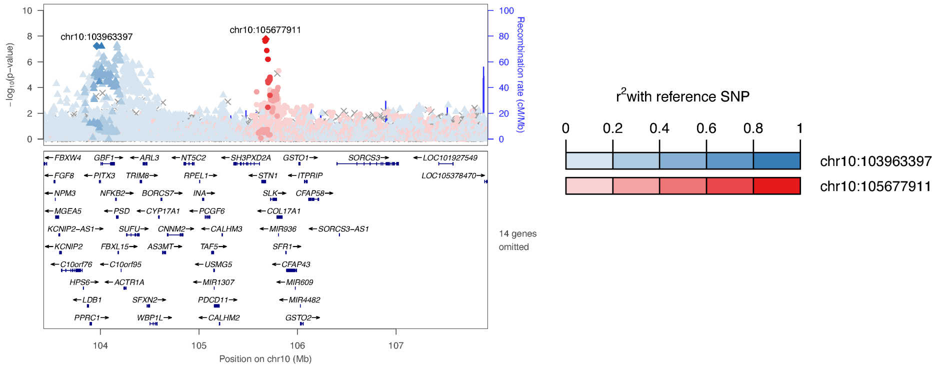
region 51: rs3757387 (7:128576086:T:C),rs41298401 (7:128578307:C:G),rs78724056 (7:128654051:G:T), and rs28364822 (7:128695982:T:A)



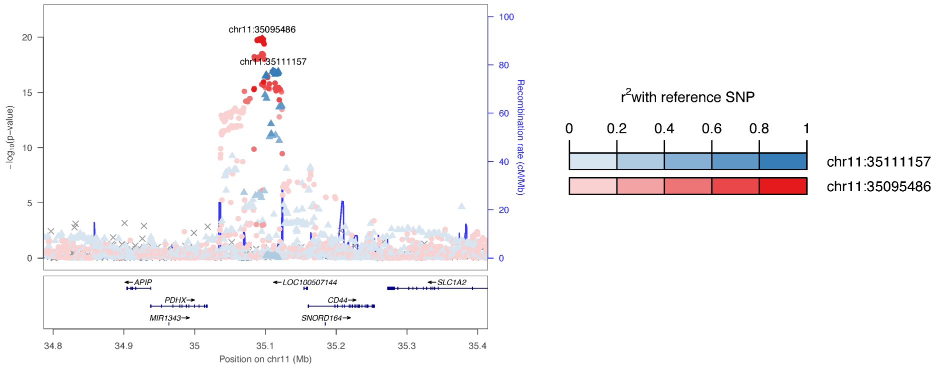
region 60: rs7072606 (10:49933974:T:C) and rs7097397 (10:50025396:G:A)



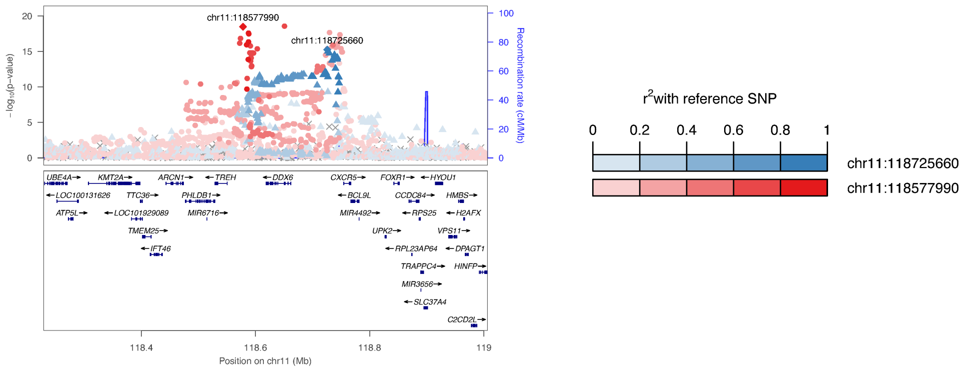
region 64: rs11599734 (10:103963397:C:G) and rs111447985 (10:105677911:C:A)



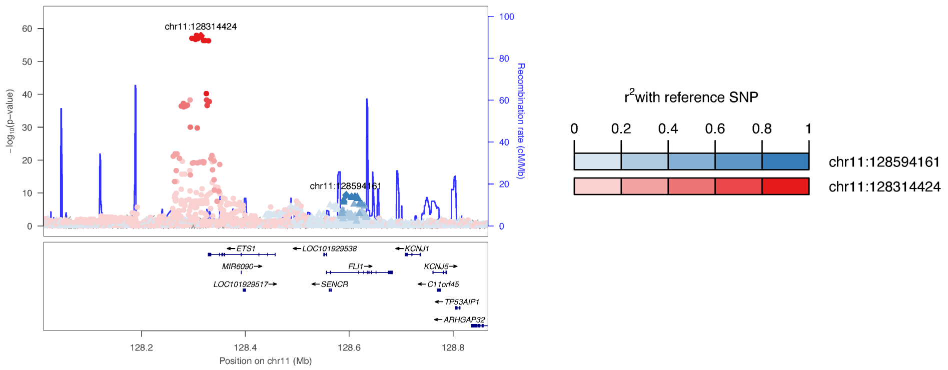
region 68: rs2732540 (11:35095486:A:G) and rs11032994 (11:35111157:G:A)



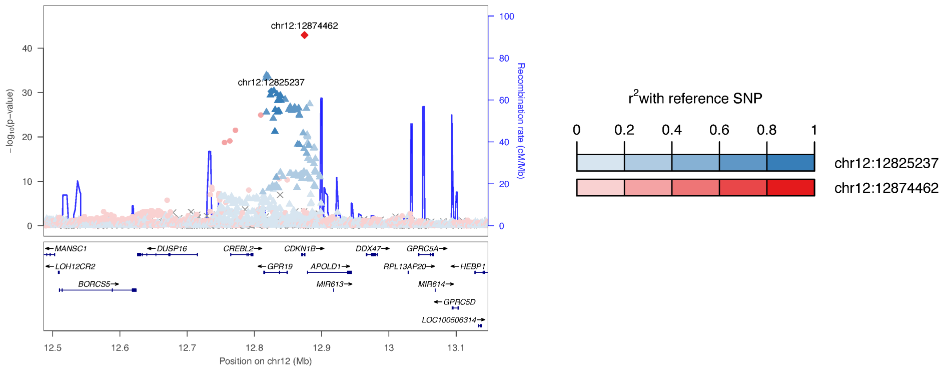
region 72: rs480958 (11:118577990:G:A) and rs4936441 (11:118725660:C:G)



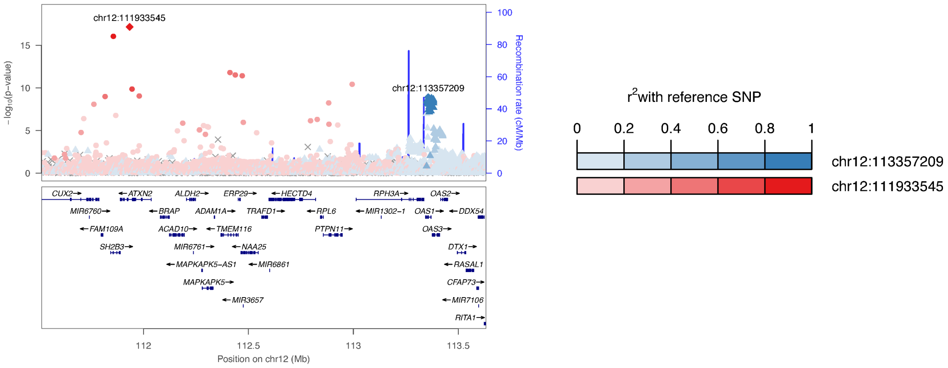
region 73: rs11501246 (11:128314424:A:G) and rs684150 (11:128594161:C:T)



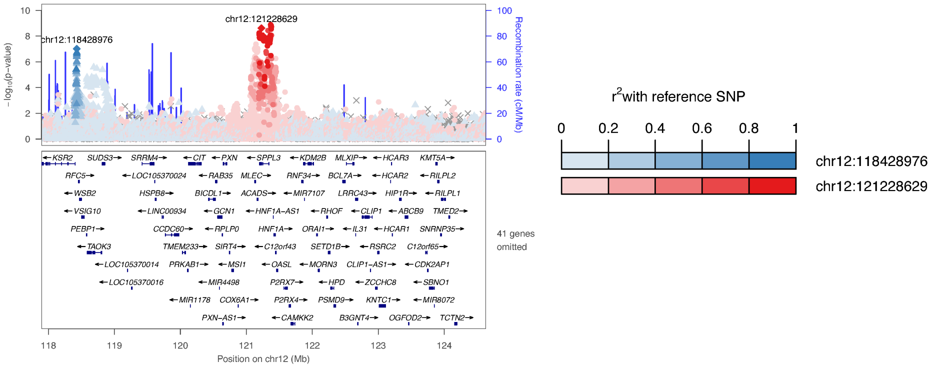
region 75: rs10845602 (12:12825237:A:G) and rs4251697 (12:12874462:G:A)



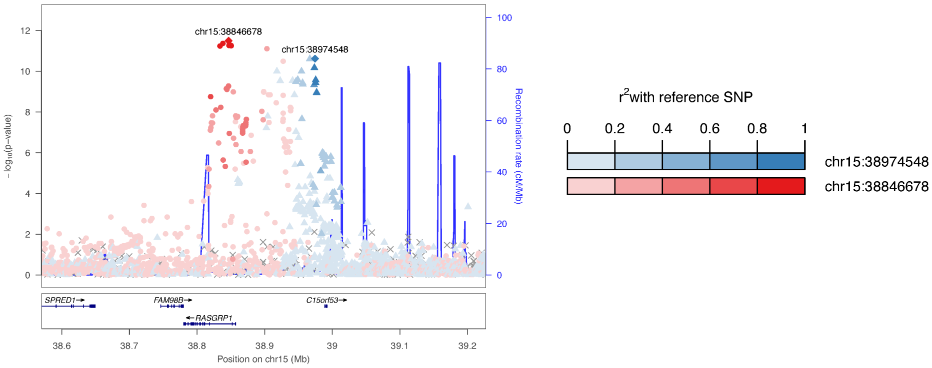
region 78: rs77465633 (12:111933545:C:A) and rs1131476 (12:113357209:G:A)



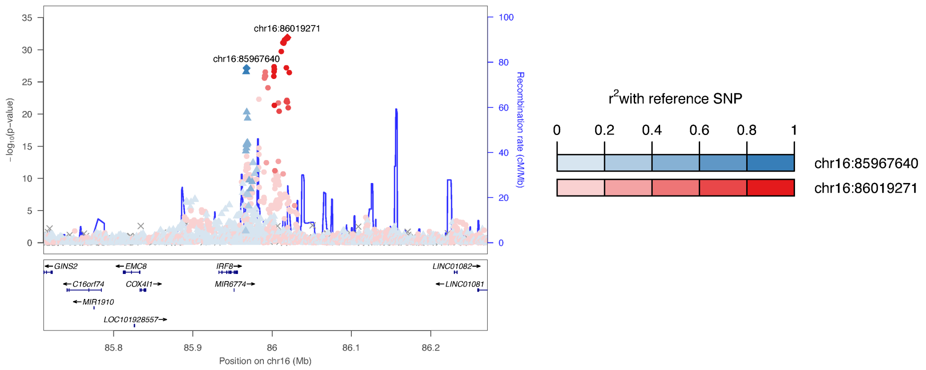
region 79: rs7139263 (12:118428976:G:A) and rs35743748 (12:121228629:C:CT)



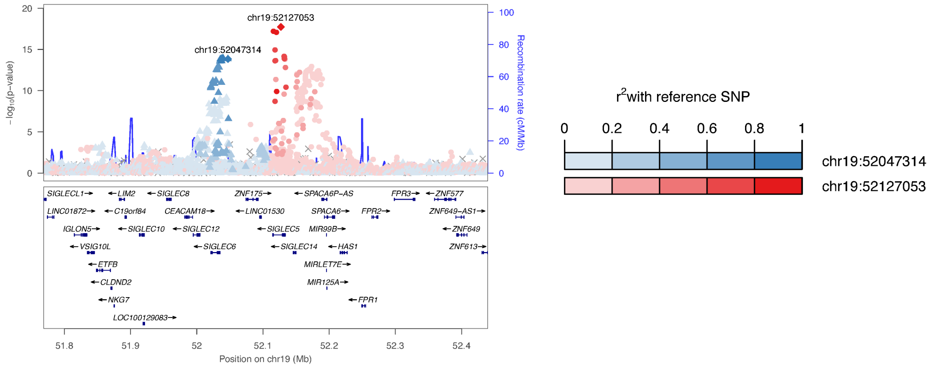
region 84: rs7170151 (15:38846678:C:T) and rs12900640 (15:38974548:A:C)



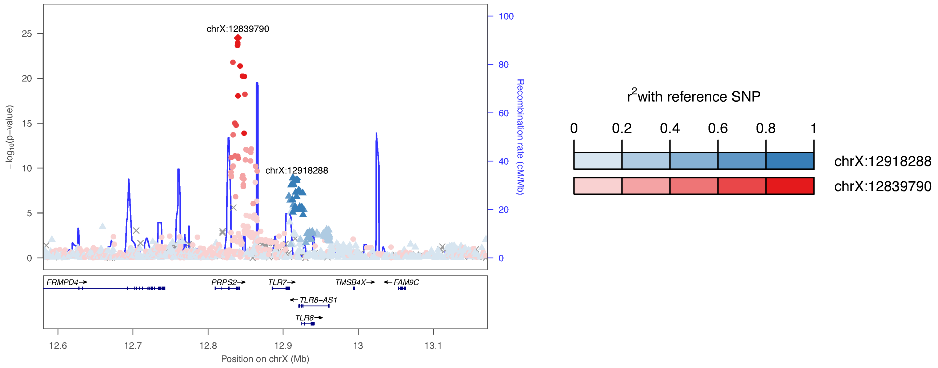
region 94: rs447632 (16:85967640:A:G) and rs11117432 (16:86019271:G:A)



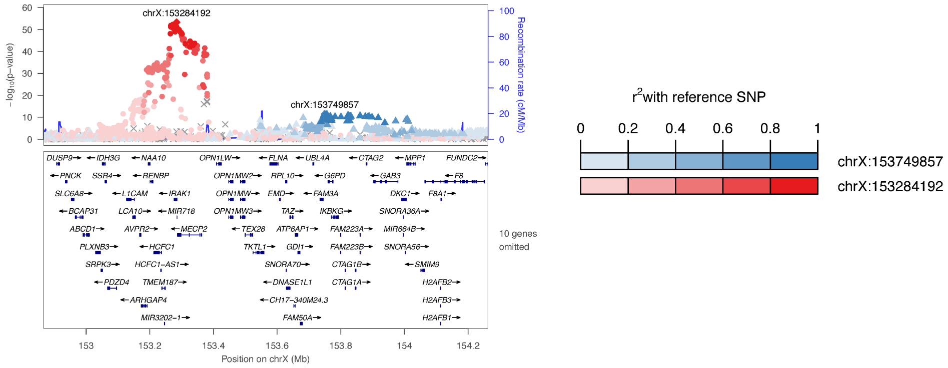
region 107: rs3794986 (19:52047314:G:T) and rs4801882 (19:52127053:G:A)



region 111: rs6641111 (X:12839790:C:G) and rs4830478 (X:12918288:G:A)



region 113: rs1059702 (X:153284192:A:G) and rs5945199 (X:153749857:G:A)



Supplementary Table 1 | Characteristics of the eight studies used in this meta-analysis

Cohort	Country	Cases	Controls	Published	SLE Criteria	Genotype Array	Pre-phasing	Genotype Imputation	Association Model	Association Tool	Number of Variants	λ_{gc}
Hong Kong	China	612	2193	PMID: 27399966	1997ACR criteria	Illumina Human610-quad BeadChip	SHAPEIT2	IMPUTE2, 1KGP3	logistic	SNPTEST	9,786,691	1.029
dataset1	Japan	1,177	140,256	New	diagnosed by collagen disease physician	IlluminaOmniExpressExome, IlluminaOmniExpress, IlluminaHumanExome	Eagle2.4.1	minimac4, 1KGP3+WGS(Japanese7k)	logistic	PLINK2.0	10,049,723	1.044
dataset2	Japan	889	3,376	PMID: 22291604	1997ACR criteria	case: Illumina HumanHap610-Quad Genotyping BeadChips control: Illumina HumanHap550v3 Genotyping BeadChips	Eagle2.4.1	minimac4, 1KGP3+WGS(Japanese7k)	logistic	PLINK2.0	9,945,421	1.029
dataset3	Japan	469	2,145	PMID: 30679154	1997ACR criteria	Illumina Human Core Exome	Eagle2.4.1	minimac4, 1KGP3+WGS(Japanese7k)	logistic	PLINK2.0	9,713,631	1.067
KOR#1	South Korea	1877	32820	New	1997ACR criteria	KoreanChip (Korean Biobank Array; Sci Rep. 2019;9(1):1382)	Eagle2	IMPUTE4, 1KGP phase3 + Korean WGS (n=397)	b.wald (cov: PC1 to 4 & sex)	EPACTS	10,934,114	1.046
KOR#2	South Korea	358	4195	PMID: 25533202	1997ACR criteria	Illumina 1M HumanOmni Array	Eagle2	IMPUTE4, 1KGP phase3 + Korean WGS (n=397)	b.wald (cov: PC1 to 4 & sex)	EPACTS	10,758,370	1.016
CHN1	China	1020	2917	PMID: 19838193	1997ACR criteria	Illumina Human610-quad BeadChip	Eagle2.4.1	Michigan Imputation Server, 1KGP phase3	EMMAX	EPACTS	8,842,696	0.981
CHN2	China	6975	7091	New	1997ACR criteria	Infinium® Global Screening Array	Eagle2.4.1	Michigan Imputation Server, 1KGP phase3	EMMAX	EPACTS	9,315,470	0.951

ACR: American College of Rheumatology. 1KGP3: 1000 Genomes Project phase 3; WGS: whole genome sequencing; Number of Variants: number of variants after filtering by minor allele frequency≥0.5%; RSQR or INFO: the genotype imputation quality scores in IMPUTE2/4 and Minimac4≥0.3; HWE: Hardy-Weinberg Equilibrium p-values in controls>1×10^{-6}; **λ_{gc}**: genomic inflation factor calculated in each data set by removing genetic variants within known SLE loci.

Supplementary Table 2 | Association results for the lead variants within the 113 genomic loci

Region	CHR	Position	SNP	EA	NEA	EAF	OR	SE	P	I^2	P_{het}	N	Nearest gene
1	1	117,043,302	rs9651076	A	G	0.431	1.117	0.015	3.26E-13	10.7	3.47E-01	208,370	CD58
2	1	157,108,159	rs116785379	C	G	0.107	1.211	0.024	6.68E-16	43.7	1.14E-01	208,370	ETV3
3	1	161,569,829	rs76107698	C	G	0.254	0.788	0.021	1.85E-30	0.0	7.62E-01	208,370	FCGR2C
4	1	173,191,475	rs2205960	T	G	0.265	1.368	0.016	3.16E-90	75.9	9.16E-04	208,370	LOC100506023
5	1	183,532,437	rs13306575	A	G	0.047	1.311	0.035	2.28E-14	43.7	1.14E-01	208,370	NCF2
6	1	198,670,469	rs4143303	A	G	0.140	0.880	0.022	3.70E-09	36.1	1.66E-01	208,370	PTPRC
7	1	201,979,455	rs3806357	A	G	0.251	1.106	0.017	4.25E-09	0.0	6.72E-01	208,370	ELF3
8	1	206,642,720	rs4844538	A	T	0.713	1.109	0.016	2.11E-10	0.0	8.45E-01	208,370	IKBKE
9	2	7,573,079	rs75362385	T	G	0.321	0.887	0.017	8.40E-13	68.3	7.52E-03	208,370	LOC100506274
10	2	30,445,026	rs7579944	T	C	0.620	0.876	0.014	1.02E-20	10.6	3.48E-01	208,370	LBH
11	2	33,701,890	rs13385731	T	C	0.860	1.287	0.021	1.29E-33	36.5	1.64E-01	208,370	RASGRP3
12	2	65,580,221	rs11126034	T	C	0.225	1.121	0.018	2.60E-10	30.5	2.07E-01	208,370	SPRED2
13	2	74,216,515	rs10207954	A	T	0.823	1.145	0.019	1.91E-12	70.3	4.81E-03	208,370	TET3
14	2	111,877,174	rs73954925	C	G	0.878	1.169	0.024	5.11E-11	56.4	4.27E-02	208,370	BCL2L11
15	2	136,658,345	rs218174	A	G	0.379	1.121	0.015	1.83E-13	0.0	9.96E-01	208,370	DARS
16	2	163,082,395	rs11679244	A	C	0.153	1.119	0.020	3.04E-08	0.0	6.32E-01	208,370	FAP
17	2	191,943,742	rs11889341	T	C	0.348	1.407	0.014	4.64E-123	91.7	1.07E-11	208,370	STAT4
18	2	198,929,806	rs7572733	T	C	0.260	1.143	0.017	1.25E-14	0.0	6.47E-01	208,370	PLCL1
19	2	213,593,970	rs7565158	T	G	0.450	1.096	0.015	2.88E-10	0.0	4.23E-01	208,370	ERBB4
20	3	28,072,086	rs438613	T	C	0.588	0.920	0.014	7.52E-09	69.4	5.87E-03	208,370	CMC1
21	3	72,225,916	rs7637844	A	C	0.871	0.877	0.023	1.28E-08	0.0	9.06E-01	208,370	LINC00870
22	3	119,237,726	rs144104218	A	AAAAC	0.310	0.833	0.016	1.89E-30	45.0	1.05E-01	208,370	TIMMDC1
23	3	169,497,585	rs1317082	A	G	0.430	1.102	0.014	1.62E-11	58.5	3.40E-02	208,370	MYNN
24	4	965,720	rs13101828	A	G	0.610	0.910	0.015	7.78E-10	0.0	7.55E-01	208,370	DGKQ
25	4	2,700,844	rs231694	T	C	0.380	1.111	0.018	9.71E-09	23.7	2.69E-01	57,253	FAM193A
26	4	40,307,587	rs113284964	G	GCTTC	0.371	1.134	0.015	1.35E-16	67.2	9.45E-03	208,370	LINC02265
27	4	79,644,279	rs6533951	A	G	0.350	1.111	0.016	1.25E-10	61.4	2.38E-02	208,370	LINC01094
28	4	84,146,996	rs6841907	T	C	0.729	0.906	0.016	1.10E-09	43.5	1.15E-01	208,370	COQ2
29	4	87,944,252	rs116940334	T	G	0.119	0.833	0.029	3.15E-10	0.0	4.37E-01	208,370	AFF1
30	4	102,756,099	rs4643809	T	C	0.305	0.846	0.016	3.53E-24	74.7	1.40E-03	208,370	BANK1
31	4	109,061,618	rs58107865	C	G	0.227	0.802	0.021	6.57E-25	1.1	4.09E-01	208,370	LEF1
32	5	1,282,414	rs7725218	A	G	0.391	1.132	0.015	2.47E-17	61.5	2.35E-02	208,370	TERT
33	5	100,141,374	rs2544920	A	T	0.226	1.122	0.019	8.74E-10	19.6	2.85E-01	208,370	ST8SIA4

34	5	131,120,338	rs370449198	A	AC	0.922	0.721	0.060	4.41E-08	0.0	4.08E-01	187,562	FNIP1
35	5	131,829,578	rs2549002	A	C	0.682	0.905	0.016	2.40E-10	20.6	2.79E-01	208,370	IRF1
36	5	133,429,192	rs6874758	C	G	0.073	1.238	0.028	3.88E-14	0.0	5.56E-01	208,370	TCF7
37	5	150,458,146	rs10036748	T	C	0.760	1.194	0.017	5.98E-26	0.0	9.47E-01	208,370	TNIP1
38	5	158,886,939	rs2421184	A	G	0.497	1.106	0.015	6.43E-12	41.2	1.31E-01	208,370	LINC01845
39	5	159,879,978	rs2431697	T	C	0.833	1.241	0.019	1.39E-28	63.5	1.77E-02	208,370	MIR3142
40	6	243,302	rs9503037	A	G	0.693	0.881	0.016	1.36E-15	42.3	1.23E-01	208,370	LOC285766
41	6	32,423,915	rs9268807	C	G	0.208	1.604	0.021	4.90E-117	61.9	2.23E-02	204,105	HLA
42	6	34,828,553	rs6457796	T	C	0.864	0.808	0.022	2.68E-22	63.7	1.71E-02	208,370	UHRF1BP1
43	6	36,715,031	rs34868004	CA	C	0.225	1.104	0.017	4.46E-09	40.7	1.34E-01	208,370	CPNE5
44	6	91,002,494	rs597325	A	G	0.548	0.906	0.015	4.60E-11	55.9	4.51E-02	208,370	BACH2
45	6	106,568,034	rs548234	T	C	0.705	0.819	0.015	5.54E-39	20.5	2.79E-01	208,370	PRDM1
46	6	116,690,849	rs9488914	T	C	0.920	0.862	0.026	1.14E-08	65.3	1.31E-02	208,370	DSE
47	6	138,230,038	rs148314165	G	GT	0.059	1.711	0.028	3.48E-84	72.7	2.61E-03	208,370	TNFAIP3
48	6	154,570,651	rs9322454	A	G	0.659	1.090	0.015	2.42E-08	0.0	4.30E-01	208,370	IPCEF1
49	7	50,258,479	rs4598207	A	T	0.705	1.333	0.018	4.12E-60	65.1	1.36E-02	208,370	C7orf72
50	7	74,126,034	rs117026326	T	C	0.175	2.137	0.021	2.20E-298	97.1	2.20E-28	201,819	LOC101926943
51	7	128,576,086	rs3757387	T	C	0.863	0.693	0.020	8.73E-79	68.3	7.58E-03	208,370	IRF5
52	8	11,339,965	rs2736332	C	G	0.734	1.360	0.017	1.57E-70	59.3	3.10E-02	208,370	BLK
53	8	42,177,163	rs2272736	A	G	0.105	0.819	0.030	6.37E-11	0.0	6.80E-01	208,370	IKBKB
54	8	71,330,166	rs142937720	A	AAGTGGCC	0.383	0.894	0.016	2.27E-12	67.9	8.12E-03	208,370	NCOA2
55	8	72,894,959	rs17374162	A	G	0.411	0.917	0.015	3.02E-09	35.7	1.69E-01	208,370	MSC-AS1
56	8	129,425,593	rs16902895	A	G	0.678	1.122	0.016	1.48E-13	0.0	8.01E-01	208,370	LINC00824
57	9	4,984,530	rs1887428	C	G	0.664	0.915	0.016	2.80E-08	59.6	3.00E-02	208,370	JAK2
58	9	21,267,087	rs7858766	T	C	0.538	1.139	0.016	2.25E-15	0.0	8.25E-01	208,370	IFNA22P
59	10	5,910,746	rs77448389	A	G	0.913	0.855	0.025	7.30E-10	0.0	5.84E-01	208,370	ANKRD16
60	10	50,025,396	rs7097397	A	G	0.651	0.810	0.016	2.23E-40	77.7	4.34E-04	208,370	WDFY4
61	10	63,801,030	rs7902146	T	C	0.691	0.900	0.015	3.34E-12	0.0	7.85E-01	208,370	ARID5B
62	10	64,411,288	rs10995261	T	C	0.240	0.909	0.017	2.57E-08	43.9	1.13E-01	208,370	ZNF365
63	10	73,466,709	rs10823829	T	C	0.718	0.910	0.016	1.05E-09	0.0	7.71E-01	208,370	CDH23
64	10	105,677,911	rs111447985	A	C	0.073	1.172	0.028	1.72E-08	0.0	5.26E-01	208,370	STN1
65	10	112,664,114	rs58164562	T	C	0.748	0.892	0.016	3.14E-12	33.3	1.86E-01	208,370	BBIP1
66	11	4,113,200	rs3750996	A	G	0.834	1.167	0.022	1.89E-12	0.0	5.22E-01	208,370	STIM1
67	11	18,362,382	rs77885959	T	G	0.978	1.694	0.062	3.16E-17	0.0	5.11E-01	204,433	GTF2H1
68	11	35,093,029	rs2785198	A	G	0.776	1.181	0.018	1.30E-20	0.0	8.62E-01	208,370	LOC100507144
69	11	65,555,524	rs10896045	A	G	0.551	1.168	0.015	6.59E-26	51.2	6.83E-02	208,370	OVOL1

70	11	68,816,370	rs4930642	A	G	0.252	1.145	0.019	6.16E-13	22.1	2.68E-01	208,370	TPCN2
71	11	72,640,480	rs77971648	T	C	0.909	1.291	0.026	3.16E-23	38.4	1.50E-01	208,370	FCHSD2
72	11	118,650,823	rs377392985	CAAAAAAAAA	C	0.341	1.161	0.017	2.86E-19	36.8	1.61E-01	208,370	DDX6
73	11	128,305,871	rs9736939	A	G	0.381	1.265	0.015	1.23E-58	71.7	3.36E-03	208,370	ETS1
74	12	4,140,876	rs2540119	T	C	0.544	1.086	0.015	3.51E-08	44.9	1.06E-01	208,370	PARP11
75	12	12,874,462	rs4251697	A	G	0.097	0.637	0.033	1.17E-43	79.1	2.20E-04	208,370	CDKN1B
76	12	102,321,935	rs4622329	A	G	0.561	1.119	0.014	4.00E-15	9.9	3.53E-01	208,370	DRAM1
77	12	103,916,080	rs6539078	T	C	0.591	0.894	0.015	9.49E-14	0.0	9.16E-01	208,370	LOC105369945
78	12	111,933,545	rs77465633	A	C	0.068	1.340	0.034	6.99E-18	4.9	3.85E-01	208,370	ATXN2
79	12	121,368,518	rs3999421	A	T	0.506	0.910	0.016	1.29E-09	47.3	9.13E-02	208,370	XLOC_009911
80	12	129,296,103	rs11059928	A	T	0.786	0.823	0.017	1.61E-30	55.7	4.62E-02	208,370	SLC15A4
81	12	133,040,182	rs200521476	G	GCATCAC	0.812	0.875	0.023	5.66E-09	26.7	2.35E-01	208,370	FBRSL1
82	13	41,575,391	rs57141708	A	G	0.224	1.183	0.018	6.84E-22	72.1	3.01E-03	208,370	ELF1
83	14	105,412,259	rs2819426	C	G	0.331	0.824	0.017	2.51E-30	51.1	6.89E-02	208,370	AHNAK2
84	15	38,846,678	rs7170151	T	C	0.563	1.107	0.015	3.20E-12	0.0	4.33E-01	208,370	RASGRP1
85	15	75,091,247	rs11553760	T	C	0.235	1.111	0.017	7.32E-10	0.0	5.80E-01	208,370	CSK
86	15	101,529,012	rs35985016	A	G	0.930	0.843	0.030	1.95E-08	0.0	8.97E-01	204,433	LRRK1
87	16	11,190,034	rs34361002	T	TAA	0.624	1.140	0.015	1.24E-17	34.6	1.77E-01	208,370	CLEC16A
88	16	23,871,457	rs79401250	T	G	0.819	1.172	0.022	1.48E-12	0.0	6.11E-01	208,370	PRKCB
89	16	30,813,454	rs534645300	A	AT	0.930	0.814	0.035	2.68E-09	34.7	1.76E-01	208,370	ZNF629
90	16	50,089,207	rs11288784	G	GT	0.365	0.902	0.016	2.38E-10	0.0	6.64E-01	208,370	HEATR3
91	16	57,390,478	rs669763	C	G	0.521	1.123	0.015	2.89E-15	11.9	3.39E-01	208,370	CCL22
92	16	68,554,755	rs28410471	A	T	0.181	1.128	0.022	3.14E-08	24.5	2.51E-01	208,370	ZFP90
93	16	79,745,672	rs11376510	G	GT	0.737	0.898	0.017	2.23E-10	0.0	7.19E-01	208,370	MAFTRR
94	16	86,019,271	rs11117432	A	G	0.088	0.728	0.027	1.27E-32	58.4	3.44E-02	208,370	IRF8
95	17	7,240,391	rs61759532	T	C	0.076	1.235	0.032	2.79E-11	24.9	2.47E-01	208,370	ACAP1
96	17	16,839,901	rs35966917	A	G	0.423	0.914	0.015	4.66E-09	0.0	5.99E-01	208,370	TNFRSF13B
97	17	47,468,020	rs2671655	T	C	0.651	1.087	0.015	4.60E-08	0.0	7.56E-01	208,370	LOC102724596
98	17	76,373,179	rs113417153	T	C	0.193	0.893	0.020	1.90E-08	2.1	4.03E-01	208,370	PGS1
99	18	67,543,688	rs1788097	T	C	0.392	1.096	0.015	6.28E-10	17.9	2.98E-01	208,370	CD226
100	18	77,386,912	rs118075465	A	G	0.147	1.140	0.020	1.16E-10	0.0	5.43E-01	208,370	LOC284241
101	19	948,532	rs2238577	T	C	0.455	0.885	0.016	1.83E-14	60.8	2.57E-02	208,370	ARID3A
102	19	6,697,088	rs5826945	A	T	0.929	0.836	0.028	9.67E-11	50.0	7.54E-02	208,370	C3

103	19	10,469,919	rs55882956	A	G	0.029	0.674	0.048	1.23E-16	21.6	2.71E-01	208,370	TYK2
104	19	18,540,988	rs11673604	T	C	0.759	1.144	0.019	4.21E-12	0.0	8.65E-01	208,370	SSBP4
105	19	33,072,768	rs12461589	T	C	0.248	0.898	0.017	5.00E-10	0.0	5.10E-01	208,370	PDCD5
106	19	49,851,746	rs33974425	CCAGCTGCAT	C	0.702	1.120	0.016	4.40E-12	42.6	1.21E-01	208,370	TEAD2
107	19	52,127,053	rs4801882	A	G	0.532	0.882	0.014	1.86E-18	57.2	3.95E-02	208,370	SIGLEC5
108	22	18,649,356	rs4819670	T	C	0.210	1.151	0.022	5.53E-11	0.0	6.50E-01	208,370	USP18
109	22	21,973,319	rs4821116	T	C	0.380	1.240	0.015	8.86E-46	29.8	2.12E-01	208,370	UBE2L3
110	22	39,739,187	rs9611155	T	C	0.761	1.137	0.022	7.66E-09	0.0	4.96E-01	208,370	SYNGR1
111	X	12,839,790	rs6641111	C	G	0.694	1.191	0.017	3.27E-25	0.0	6.45E-01	208,360	PRPS2
112	X	56,908,702	rs5914012	T	C	0.353	1.104	0.017	6.65E-09	0.0	6.45E-01	208,360	NBDY
113	X	153,284,192	rs1059702	A	G	0.783	1.356	0.020	5.89E-54	22.3	2.66E-01	208,360	IRAK1

Region: region index ID; CHR: chromosome; Position: position in base pair in genome build 19; SNP: Single nucleotide polymorphism; EA: effective allele; NEA: non-effective allele; EAF: effective allele frequency; OR: odds ratio; SE: standard error for odds ratio; I^2: heterogeneity I^2 statistics at scale of 0-100%; P_{het}: P-values for chi-squared test of heterogeneity; N: study sample size.

Supplementary Table 3 | Comparison of minor allele frequencies between East Asians and Europeans for the lead variants and their strong LD proxies within the 46 novel loci

Region	Lead Variants							LD Proxy Variants						
	CHR	Position	REF	ALT	OR	MAF_{EAS}	MAF_{NFE}	Position	REF	ALT	MAF_{EAS}	MAF_{NFE}	Statistical Power	Effect N
1	1	117043302	A	G	1.117	0.426	0.106	117032783	G	A	0.361	0.492	1.00	50,072
2	1	157108159	G	C	1.211	0.090	0.018	157114851	T	C	0.215	0.173	1.00	50,072
7	1	201979455	G	A	1.106	0.263	0.079	201977827	G	T	0.491	0.449	1.00	50,072
9	2	7573079	G	T	0.887	0.379	0.058	7572607	T	A	0.456	0.432	1.00	50,072
14	2	111877174	C	G	0.856	0.125	0.061	111862303	T	C	0.302	0.474	1.00	50,072
18	2	198929806	C	T	1.143	0.206	0.479	198898344	A	T	0.208	0.497	1.00	50,072
20	3	28072086	T	C	1.087	0.459	0.476	28075985	T	C	0.459	0.477	1.00	50,072
21	3	72225916	A	C	1.140	0.118	0.156	72214334	C	G	0.280	0.344	1.00	50,072
25	4	2700844	T	C	1.111	0.345	0.261	2700844	T	C	0.345	0.261	1.00	50,072
26	4	40307587	G	GCTTC	1.134	0.385	0.324	40279534	G	A	0.345	0.499	1.00	50,072
27	4	79644279	A	G	1.111	0.311	0.403	79637446	G	A	0.498	0.472	1.00	50,072
28	4	84146996	T	C	1.104	0.277	0.297	84146727	T	C	0.438	0.485	1.00	50,072
31	**4**	**109061618**	**G**	**C**	**0.802**	**0.249**	**0.003**	**109061618**	**G**	**C**	**0.249**	**0.003**	**0.05**	**50,072**
34	5	131120338	A	AC	1.387	0.010	0.001	131231536	C	A	0.413	0.497	1.00	50,072
35	5	131829578	C	A	1.105	0.358	0.334	131905734	C	CT	0.149	0.493	1.00	50,072
40	6	243302	A	G	1.136	0.312	0.145	256959	G	A	0.433	0.495	1.00	50,072
43	6	36715031	C	CA	1.104	0.244	0.373	36699347	G	A	0.392	0.498	1.00	50,072
46	6	116690849	C	T	1.159	0.074	0.382	116598853	A	G	0.063	0.495	1.00	50,072
48	6	154570651	G	A	0.917	0.325	0.087	154583379	T	C	0.297	0.498	1.00	50,072
54	8	71330166	AAGTGGCC	A	0.894	0.400	0.102	71344432	T	C	0.287	0.497	1.00	50,072
55	8	72894959	G	A	0.917	0.406	0.230	72920538	T	C	0.366	0.480	1.00	50,072
56	8	129425593	A	G	0.892	0.290	0.034	129445863	G	GAT	0.328	0.435	1.00	50,072
58	9	21267087	T	C	0.878	0.462	0.386	21235442	C	G	0.357	0.478	1.00	50,072
59	10	5910746	A	G	1.170	0.099	0.037	5914653	A	G	0.203	0.495	1.00	50,072
62	10	64411288	C	T	0.909	0.253	0.143	64431973	CT	C	0.430	0.433	1.00	50,072
63	10	73466709	T	C	1.099	0.276	0.029	73500155	C	T	0.453	0.245	1.00	50,072
64	10	105677911	C	A	1.172	0.068	0.002	105690267	G	A	0.209	0.410	1.00	50,072
65	10	112664114	T	C	1.121	0.230	0.058	112607783	TAAGA	T	0.412	0.290	1.00	50,072
66	11	4113200	A	G	0.857	0.217	0.000	4032665	A	G	0.372	0.496	1.00	50,072
67	**11**	**18362382**	**T**	**G**	**0.590**	**0.017**	**0.000**	**18292586**	**C**	**G**	**0.016**	**0.000**	**0.03**	**50,072**
74	12	4140876	T	C	0.921	0.466	0.223	4221407	C	T	0.081	0.480	1.00	50,072
77	12	103916080	T	C	1.119	0.394	0.176	103809931	C	G	0.324	0.488	1.00	50,072
79	12	121368518	A	T	1.099	0.476	0.408	121344515	T	C	0.473	0.496	1.00	50,072

81	12	133040182	GCATCAC	G	1.143	0.091	0.257	133063768	G	A	0.130	0.493	1.00	50,072
86	15	101529012	A	G	1.186	0.034	0.001	101506285	T	C	0.014	0.038	1.00	50,072
90	16	50089207	GT	G	0.902	0.374	0.198	50273547	C	T	0.321	0.482	1.00	50,072
93	16	79745672	G	GT	1.113	0.274	0.322	79738917	C	T	0.328	0.497	1.00	50,072
95	17	7240391	C	T	1.235	0.098	0.227	7221385	G	A	0.056	0.431	1.00	50,072
97	17	47468020	C	T	0.920	0.303	0.060	47372764	C	T	0.226	0.344	1.00	50,072
98	17	76373179	C	T	0.893	0.207	0.062	76383671	C	T	0.425	0.491	1.00	50,072
100	18	77386912	G	A	1.140	0.155	0.034	77381300	C	T	0.156	0.493	1.00	50,072
101	19	948532	C	T	0.885	0.497	0.144	930874	C	T	0.440	0.411	1.00	50,072
102	19	6697088	A	T	1.196	0.434	0.477	6721640	A	C	0.180	0.499	1.00	50,072
105	19	33072768	C	T	0.898	0.237	0.002	33040205	T	A	0.448	0.493	1.00	50,072
106	19	49851746	CCAGCTGCAT	C	0.893	0.330	0.261	49755490	T	C	0.357	0.499	1.00	50,072
108	22	18649356	T	C	1.15	0.16	0.36	18634776	C	G	0.30	0.40	1.00	50,072

Lead Variant: the variant with lowest association p-value within each of the 46 novel SLE loci; LD Proxy Variant: the variant that has highest minor allele frequency in gnomAD v3 non-Finnish Europeans among all variants having strong linkage disequilibrium r^2 ($r^2 \geq 0.2$) with lead variant in either East Asians or Europeans; Region: index ID for genomic regions; CHR: chromosome; Position: position base pair in genome build 19; REF: reference allele; ALT: alternative allele; MAF_{EAS}: minor allele frequency in East Asians from gnomAD v3 database; MAF_{NFE}: minor allele frequency in non-Finnish Europeans from gnomAD v3 database; Statistical Power: statistical power in non-Finnish Europeans for LD proxy variant using the same effect size and study sample size as current study; Effect N: effective sample size used for estimating statistical power in Europeans. The two loci in bold denote the ones in which both the lead variants and the LD proxy variants have at least ten fold higher minor allele frequencies in East Asians and whose statistical power is below 10% in European of similar sample size.

Supplementary Table 4 | LD between newly-identified and known missense variants at the same genes

Gene	Reported	Population	Current	MAF		Pairwise LD r^2	
				EAS	EUR	EAS	EUR
TYK2	rs2304256	EUR	rs55882956	0.03	0	0.028	0.000
NCF2	rs17849502	EUR/AFR	rs13306575	0.04	0	rs17849502 is monomorphic in EAS	rs13306575 is monomorphic in EUR
	rs35937854	EUR/AFR	rs13306575	0.04	0	rs35937854 is monomorphic in EAS	rs13306575 is monomorphic in EUR
	rs17849501	EUR/AFR	rs13306575	0.04	0	rs17849501 is monomorphic in EAS	rs13306575 is monomorphic in EUR
	rs2274064	EUR/AFR/HIS/EAS	rs13306575	0.35	0.47	0.024	rs13306575 is monomorphic in EUR
	rs17849502	EUR/AFR	rs66977652	0.34	0.47	rs17849502 is monomorphic in EAS	rs66977652 is not available in EUR
	rs35937854	EUR/AFR	rs66977652	0.34	0.47	rs35937854 is monomorphic in EAS	rs66977652 is not available in EUR
	rs17849501	EUR/AFR	rs66977652	0.34	0.47	rs17849501 is monomorphic in EAS	rs66977652 is not available in EUR
	rs2274064	EUR/AFR/HIS/EAS	rs66977652	0.35	0.47	0.894	0.992
OAS1	rs1051042	EAS	rs1131476	0.22	0.34	1.000	1.000
AHNAK2	rs4465542	EAS	rs2819426	0.28	0.23	0.779	0.310
IRAK1	rs1059702	EAS	rs1059702	0.2	0.14	1.000	1.000
WDFY4	rs7097397	EAS	rs7072606	0.19	0.08	0.021	0.034
	rs7097397	EAS	rs7097397	0.33	0.39	1.000	1.000

Reported: the missense variants reported previously; Population: population (Europeans: EUR; Africans: AFR; East Asians: EAS; Hispanic: HIS) in which the missense variant was originally reported, EUR: European; Current: the missense variants identified in current meta-analysis: MAF: minor allele frequency for the newly identified missense variant in East Asians (EAS) and Europeans (EUR) of 1000 Genomes Project; Pairwise LD r^2: the LD r^2 between the newly-identified missense variants and previously known missense variant within the same gene in 1000 Genomes Project East Asian (EAS) or European (EUR) samples.

Supplementary Table 5 | Association results for the index variants of the 233 distinct signals within the 113 genomic loci

Region	Novel	Lead rsID	rsID	CHR	Position	EA	NEA	EAF	Unconditional			Conditional			N
									OR	SE	P	OR	SE	P	
1	NOVEL	rs9651076	rs9651076	1	117,043,302	A	G	0.431	1.117	0.015	3.26E-13	1.117	0.015	3.63E-13	208,370
2	NOVEL	rs116785379	rs116785379	1	157,108,159	C	G	0.107	1.211	0.024	6.68E-16	1.204	0.024	4.76E-15	208,370
2	NOVEL	rs116785379	rs112806509	1	157,502,015	A	AT	0.097	0.812	0.026	1.76E-15	0.785	0.027	1.51E-19	208,370
2	NOVEL	rs116785379	rs2317230	1	157,674,997	T	G	0.392	1.061	0.015	9.86E-05	1.102	0.016	5.15E-10	208,370
3	KNOWN	rs76107698	rs12120358	1	161,444,369	A	T	0.893	0.842	0.026	2.96E-11	0.851	0.026	4.89E-10	208,370
3	KNOWN	rs76107698	rs111994823	1	161,470,274	T	C	0.964	1.409	0.052	3.41E-11	1.427	0.052	6.42E-12	208,370
3	KNOWN	rs76107698	rs76107698	1	161,569,829	C	G	0.254	0.788	0.021	1.85E-30	0.799	0.021	1.39E-26	208,370
3	KNOWN	rs76107698	rs75773410	1	161,625,798	A	G	0.923	0.774	0.033	3.84E-15	0.802	0.033	1.81E-11	208,370
4	KNOWN	rs2205960	rs2205960	1	173,191,475	T	G	0.265	1.368	0.016	3.16E-90	1.361	0.017	7.45E-71	208,370
4	KNOWN	rs2205960	rs117278480	1	173,210,789	A	G	0.913	0.649	0.028	2.23E-52	0.802	0.030	4.43E-13	208,370
4	KNOWN	rs2205960	rs844646	1	173,216,373	A	G	0.824	1.000	0.019	9.94E-01	0.864	0.020	7.90E-14	208,370
4	KNOWN	rs2205960	rs2039982	1	173,359,187	T	C	0.656	1.242	0.017	1.85E-37	1.253	0.017	2.80E-39	208,370
5	KNOWN	rs13306575	rs13306575	1	183,532,437	A	G	0.047	1.311	0.035	2.28E-14	1.357	0.036	1.48E-17	208,370
5	KNOWN	rs13306575	rs66977652	1	183,540,215	T	TA	0.623	0.907	0.015	7.76E-11	0.892	0.015	5.01E-14	208,370
6	KNOWN	rs4143303	rs4143303	1	198,670,469	A	G	0.140	0.880	0.022	3.70E-09	0.880	0.022	2.79E-09	208,370
7	NOVEL	rs3806357	rs3806357	1	201,979,455	A	G	0.251	1.106	0.017	4.25E-09	1.106	0.017	4.40E-09	208,370
8	KNOWN	rs4844538	rs4844538	1	206,642,720	A	T	0.713	1.109	0.016	2.11E-10	1.108	0.016	3.09E-10	208,370
9	NOVEL	rs75362385	rs75362385	2	7,573,079	T	G	0.321	0.887	0.017	8.40E-13	0.887	0.017	8.08E-13	208,370
10	KNOWN	rs7579944	rs7579944	2	30,445,026	T	C	0.620	0.876	0.014	1.02E-20	0.877	0.014	2.29E-20	208,370
11	KNOWN	rs13385731	rs13385731	2	33,701,890	T	C	0.860	1.287	0.021	1.29E-33	1.285	0.021	3.79E-33	208,370
12	KNOWN	rs11126034	rs11684155	2	65,581,300	T	C	0.775	0.892	0.018	2.61E-10	0.893	0.018	3.24E-10	208,370
13	KNOWN	rs10207954	rs10207954	2	74,216,515	A	T	0.823	1.145	0.019	1.91E-12	1.144	0.019	2.56E-12	208,370
14	NOVEL	rs73954925	rs73954925	2	111,877,174	C	G	0.878	1.169	0.024	5.11E-11	1.169	0.024	4.79E-11	208,370
15	KNOWN	rs218174	rs218174	2	136,658,345	A	G	0.379	1.121	0.015	1.83E-13	1.121	0.016	1.92E-13	208,370
16	KNOWN	rs11679244	rs11679244	2	163,082,395	A	C	0.153	1.119	0.020	3.04E-08	1.119	0.020	3.22E-08	208,370
17	KNOWN	rs11889341	rs11889341	2	191,943,742	T	C	0.348	1.407	0.014	4.64E-123	1.367	0.015	2.65E-99	208,370
17	KNOWN	rs11889341	rs71403211	2	191,948,986	T	TA	0.884	1.462	0.026	3.16E-49	1.323	0.026	1.81E-26	208,370
18	NOVEL	rs7572733	rs11684176	2	198,954,774	T	C	0.250	1.146	0.018	1.50E-14	1.148	0.018	1.02E-14	208,370
19	KNOWN	rs7565158	rs7565158	2	213,593,970	T	G	0.450	1.096	0.015	2.88E-10	1.098	0.015	1.13E-10	208,370
19	KNOWN	rs7565158	rs2371790	2	213,884,666	A	G	0.224	1.107	0.018	6.48E-09	1.110	0.018	2.41E-09	208,370
20	NOVEL	rs438613	rs438613	3	28,072,086	T	C	0.588	0.920	0.014	7.52E-09	0.920	0.014	6.99E-09	208,370
21	NOVEL	rs7637844	rs7637844	3	72,225,916	A	C	0.871	0.877	0.023	1.28E-08	0.877	0.023	1.25E-08	208,370
22	KNOWN	rs144104218	rs144104218	3	119,237,726	A	AAAAC	0.310	0.833	0.016	1.89E-30	0.833	0.016	1.32E-30	208,370
23	KNOWN	rs1317082	rs1317082	3	169,497,585	A	G	0.430	1.102	0.014	1.62E-11	1.102	0.014	1.71E-11	208,370
24	KNOWN	rs13101828	rs13101828	4	965,720	A	G	0.610	0.910	0.015	7.78E-10	0.909	0.015	5.63E-10	208,370
25	NOVEL	rs231694	rs231694	4	2,700,844	T	C	0.380	1.111	0.018	9.71E-09	1.112	0.018	8.02E-09	57,253
26	NOVEL	rs113284964	rs113284964	4	40,307,587	G	GCTTC	0.371	1.134	0.015	1.35E-16	1.134	0.015	1.51E-16	208,370
27	NOVEL	rs6533951	rs6533951	4	79,644,279	A	G	0.350	1.111	0.016	1.25E-10	1.110	0.016	1.71E-10	208,370

27	NOVEL	rs6533951	rs2867700	4	81,084,349	A	G	0.833	1.113	0.020	5.83E-08	1.115	0.020	3.70E-08	208,370
28	NOVEL	rs6841907	rs11099582	4	84,142,744	A	G	0.266	1.103	0.016	1.40E-09	1.103	0.016	1.10E-09	208,370
29	KNOWN	rs116940334	rs144261754	4	87,904,688	T	TAAAA	0.290	0.899	0.017	3.45E-10	0.897	0.017	1.54E-10	208,370
30	KNOWN	rs4643809	rs4643809	4	102,756,099	T	C	0.305	0.846	0.016	3.53E-24	0.844	0.016	4.69E-25	208,370
31	NOVEL	rs58107865	rs956237	4	109,046,960	A	G	0.320	1.107	0.015	4.47E-11	1.151	0.017	4.47E-17	208,370
31	NOVEL	rs58107865	rs57634688	4	109,111,805	T	C	0.366	1.044	0.016	6.55E-03	1.109	0.017	1.50E-09	208,370
32	KNOWN	rs7725218	rs7725218	5	1,282,414	A	G	0.391	1.132	0.015	2.47E-17	1.132	0.015	2.57E-17	208,370
33	KNOWN	rs2544920	rs2544920	5	100,141,374	A	T	0.226	1.122	0.019	8.74E-10	1.122	0.019	8.66E-10	208,370
34	NOVEL	rs370449198	rs370449198	5	131,120,338	A	AC	0.922	0.721	0.060	4.41E-08	-	-	-	187,562
35	NOVEL	rs2549002	rs2549002	5	131,829,578	A	C	0.682	0.905	0.016	2.40E-10	0.908	0.016	8.61E-10	208,370
36	KNOWN	rs6874758	rs115267018	5	133,421,109	C	G	0.134	0.850	0.025	9.08E-11	0.865	0.025	8.29E-09	208,370
36	KNOWN	rs6874758	rs6874758	5	133,429,192	C	G	0.073	1.238	0.028	3.88E-14	1.217	0.028	4.22E-12	208,370
36	KNOWN	rs6874758	rs138305363	5	133,714,873	A	G	0.980	0.622	0.087	4.07E-08	0.623	0.087	4.49E-08	183,009
37	KNOWN	rs10036748	rs10036748	5	150,458,146	T	C	0.760	1.194	0.017	5.98E-26	1.194	0.017	6.08E-26	208,370
38	KNOWN	rs2421184	rs2421184	5	158,886,939	A	G	0.497	1.106	0.015	6.43E-12	1.105	0.015	8.42E-12	208,370
39	KNOWN	rs2431697	rs2431697	5	159,879,978	T	C	0.833	1.241	0.019	1.39E-28	1.239	0.020	3.76E-28	208,370
40	NOVEL	rs9503037	rs9503037	6	243,302	A	G	0.693	0.881	0.016	1.36E-15	0.881	0.016	1.32E-15	208,370
41	KNOWN	rs9268807	rs79774308	6	25,411,022	A	G	0.960	1.452	0.060	5.76E-10	1.630	0.061	7.51E-16	205,565
41	KNOWN	rs9268807	rs9295676	6	25,928,376	T	G	0.598	1.105	0.015	7.94E-11	1.097	0.016	6.67E-09	208,370
41	KNOWN	rs9268807	rs77285596	6	28,410,143	T	G	0.917	1.362	0.034	2.20E-19	1.646	0.042	3.71E-32	208,370
41	KNOWN	rs9268807	rs1033568	6	29,257,967	A	G	0.429	1.081	0.016	1.34E-06	1.106	0.017	1.36E-09	208,370
41	KNOWN	rs9268807	rs111508444	6	29,603,512	A	G	0.945	1.522	0.047	2.41E-19	1.559	0.052	9.30E-18	208,370
41	KNOWN	rs9268807	rs75460055	6	29,889,250	T	C	0.039	1.020	0.064	7.61E-01	0.470	0.087	4.92E-18	60,058
41	KNOWN	rs9268807	rs534723171	6	29,909,823	T	G	0.061	0.996	0.057	9.41E-01	2.735	0.088	1.55E-30	199,552
41	KNOWN	rs9268807	rs2523968	6	29,939,148	A	T	0.429	1.058	0.017	8.11E-04	1.132	0.018	4.23E-12	204,105
41	KNOWN	rs9268807	rs1264585	6	30,285,650	A	T	0.233	1.074	0.021	7.13E-04	1.206	0.025	1.17E-13	204,105
41	KNOWN	rs9268807	rs3131933	6	30,933,864	T	C	0.808	0.922	0.019	2.07E-05	0.891	0.020	6.65E-09	204,105
41	KNOWN	rs9268807	rs566731348	6	30,994,889	A	G	0.951	1.889	0.092	3.65E-12	1.779	0.092	3.63E-10	43,187
41	KNOWN	rs9268807	rs75881311	6	31,102,273	A	T	0.082	1.064	0.032	5.14E-02	1.279	0.034	2.54E-13	57,253
41	KNOWN	rs9268807	rs112262437	6	31,247,406	C	G	0.994	1.204	0.130	1.53E-01	6.006	0.165	1.90E-27	18,003
41	KNOWN	rs9268807	rs111743557	6	31,299,497	T	TTG	0.888	0.869	0.034	3.79E-05	0.729	0.036	2.10E-18	204,105
41	KNOWN	rs9268807	rs2523483	6	31,353,792	T	G	0.939	1.214	0.046	2.11E-05	4.665	0.067	2.83E-117	204,105
41	KNOWN	rs9268807	rs28359827	6	31,360,643	A	AT	0.077	1.024	0.038	5.34E-01	2.916	0.060	1.94E-71	60,058
41	KNOWN	rs9268807	rs2516465	6	31,414,906	T	G	0.095	1.105	0.040	1.30E-02	2.113	0.051	5.93E-48	190,039
41	KNOWN	rs9268807	rs4458721	6	31,415,852	T	C	0.249	1.181	0.026	2.73E-10	1.226	0.029	2.66E-12	48,606
41	KNOWN	rs9268807	rs2263318	6	31,432,006	A	G	0.059	0.597	0.057	1.05E-19	0.315	0.081	4.29E-46	187,234
41	KNOWN	rs9268807	rs2256974	6	31,555,392	A	C	0.375	0.842	0.017	2.23E-25	0.850	0.019	2.36E-18	204,105
41	KNOWN	rs9268807	rs542914466	6	31,581,037	A	G	0.009	1.099	0.165	5.68E-01	18.321	0.227	1.54E-37	39,250
41	KNOWN	rs9268807	rs3115674	6	31,799,076	T	G	0.983	0.652	0.075	1.43E-08	0.639	0.076	4.52E-09	204,105
41	KNOWN	rs9268807	rs117217736	6	31,808,728	T	C	0.991	0.479	0.103	1.06E-12	0.164	0.138	3.36E-39	183,297
41	KNOWN	rs9268807	rs554383943	6	31,975,258	C	G	0.986	3.634	0.176	2.47E-13	12.668	0.207	1.24E-34	158,113
41	KNOWN	rs9268807	rs200283861	6	31,994,723	A	G	0.277	1.203	0.019	2.51E-23	1.154	0.020	1.36E-12	204,105
41	KNOWN	rs9268807	rs113720465	6	32,005,355	A	G	0.052	0.849	0.053	2.00E-03	0.447	0.071	5.71E-30	201,300

41	KNOWN	rs9268807	rs7774739	6	32,009,301	A	G	0.993	0.848	0.108	1.24E-01	0.483	0.113	1.33E-10	60,058
41	KNOWN	rs9268807	rs146280229	6	32,017,607	C	G	0.007	1.448	0.086	1.59E-05	1.815	0.088	9.56E-12	201,300
41	KNOWN	rs9268807	rs565981183	6	32,111,023	CA	C	0.876	1.192	0.026	1.23E-11	1.261	0.028	3.59E-16	204,105
41	KNOWN	rs9268807	rs9281714	6	32,254,259	T	TTTTATATATATATATA	0.974	1.419	0.073	1.82E-06	1.658	0.074	1.08E-11	57,253
41	KNOWN	rs9268807	rs145396511	6	32,299,458	T	C	0.989	1.251	0.076	3.41E-03	1.574	0.077	4.63E-09	204,105
41	KNOWN	rs9268807	rs368529276	6	32,321,473	A	G	0.961	2.522	0.103	3.52E-19	5.109	0.127	9.70E-38	183,297
41	KNOWN	rs9268807	rs146003878	6	32,357,239	A	T	0.016	0.925	0.070	2.63E-01	1.678	0.079	4.54E-11	204,105
41	KNOWN	rs9268807	rs9268486	6	32,368,560	T	C	0.248	0.936	0.022	3.03E-03	1.384	0.030	7.90E-27	57,253
41	KNOWN	rs9268807	rs574027387	6	32,379,313	A	ACACAC	0.673	0.973	0.028	3.20E-01	1.376	0.032	3.25E-23	25,361
41	KNOWN	rs9268807	rs9268807	6	32,423,915	C	G	0.208	1.604	0.021	4.90E-117	1.667	0.028	9.79E-73	204,105
41	KNOWN	rs9268807	rs9268989	6	32,435,549	A	G	0.378	0.856	0.021	6.49E-14	0.549	0.037	1.83E-59	60,058
41	KNOWN	rs9268807	rs9269029	6	32,437,544	A	C	0.176	0.866	0.026	2.33E-08	5.664	0.057	1.82E-205	60,058
41	KNOWN	rs9268807	rs34452045	6	32,442,118	G	GC	0.145	0.694	0.031	3.39E-31	0.549	0.039	1.97E-54	204,105
41	KNOWN	rs9268807	6:32449301:T:<INS:ME:ALU>	6	32,449,301	<INS:ME:ALU>	T	0.128	0.616	0.038	7.84E-37	0.595	0.043	8.46E-34	62,672
41	KNOWN	rs9268807	rs9269207	6	32,449,896	T	C	0.622	0.754	0.019	6.00E-48	0.376	0.046	4.36E-101	204,105
41	KNOWN	rs9268807	rs9269233	6	32,451,762	A	C	0.230	1.170	0.024	3.40E-11	0.676	0.034	5.68E-30	60,058
41	KNOWN	rs9268807	rs9270371	6	32,558,190	T	G	0.306	0.886	0.026	4.04E-06	0.521	0.036	4.05E-75	200,168
41	KNOWN	rs9268807	rs2647078	6	32,566,096	C	G	0.806	0.803	0.023	8.51E-21	0.208	0.047	7.63E-244	204,105
41	KNOWN	rs9268807	rs1966002	6	32,581,684	T	G	0.454	1.337	0.025	8.43E-31	1.722	0.033	6.75E-60	57,253
41	KNOWN	rs9268807	rs116352702	6	32,594,661	A	G	0.954	0.752	0.066	1.38E-05	0.543	0.071	7.62E-18	56,121
41	KNOWN	rs9268807	rs9273190	6	32,613,418	A	T	0.364	1.026	0.025	2.89E-01	1.790	0.037	1.10E-54	200,168
41	KNOWN	rs9268807	rs140780894	6	32,625,384	T	G	0.224	1.086	0.029	4.23E-03	1.410	0.038	3.72E-19	200,168
41	KNOWN	rs9268807	rs9274384	6	32,632,635	A	C	0.727	1.065	0.023	6.22E-03	1.415	0.030	5.26E-31	200,168
41	KNOWN	rs9268807	rs189311301	6	32,655,916	C	G	0.991	2.233	0.127	2.92E-10	2.486	0.129	1.85E-12	201,300
41	KNOWN	rs9268807	rs34723256	6	32,658,694	A	T	0.059	1.064	0.038	9.82E-02	2.282	0.047	3.59E-68	60,058
41	KNOWN	rs9268807	rs113523948	6	32,663,158	C	G	0.063	0.819	0.055	3.02E-04	0.578	0.058	3.16E-21	204,105
41	KNOWN	rs9268807	rs36030018	6	32,667,964	C	G	0.109	0.944	0.029	4.46E-02	1.586	0.037	2.55E-36	204,105
41	KNOWN	rs9268807	rs17206287	6	32,674,725	A	G	0.858	1.200	0.026	2.04E-12	1.501	0.037	2.02E-27	66,937
41	KNOWN	rs9268807	rs3135461	6	32,680,122	A	G	0.841	0.726	0.024	1.88E-39	0.711	0.031	1.93E-27	62,672
41	KNOWN	rs9268807	rs9275599	6	32,682,429	T	C	0.032	0.919	0.051	9.77E-02	1.585	0.056	1.97E-16	204,105
41	KNOWN	rs9268807	rs11426605	6	32,708,364	T	TA	0.966	0.902	0.051	4.26E-02	0.648	0.055	2.52E-15	57,253
41	KNOWN	rs9268807	rs7753017	6	32,727,325	A	G	0.237	0.745	0.021	5.33E-43	0.804	0.026	5.99E-17	204,105
41	KNOWN	rs9268807	rs574879686	6	32,749,489	A	G	0.018	0.701	0.073	1.11E-06	0.635	0.075	1.16E-09	204,105
41	KNOWN	rs9268807	rs144227975	6	32,777,915	CTTT	C	0.665	0.995	0.017	7.83E-01	0.864	0.019	4.42E-15	204,105
41	KNOWN	rs9268807	rs115910061	6	33,044,015	T	G	0.059	0.721	0.047	4.82E-12	0.655	0.049	2.98E-18	208,370
41	KNOWN	rs9268807	rs1431403	6	33,047,031	T	C	0.390	0.848	0.017	1.14E-22	0.816	0.018	5.30E-29	208,370
41	KNOWN	rs9268807	rs3846852	6	33,413,007	A	G	0.016	1.364	0.067	3.58E-06	1.515	0.068	1.23E-09	57,253
41	KNOWN	rs9268807	rs554962164	6	33,955,501	A	C	0.982	1.964	0.134	5.18E-07	2.241	0.135	2.11E-09	187,562

42	KNOWN	rs6457796	rs111658701	6	34,228,565	T	C	0.949	1.356	0.067	5.58E-06	1.489	0.068	3.93E-09	187,562
42	KNOWN	rs6457796	rs6457796	6	34,828,553	T	C	0.864	0.808	0.022	2.68E-22	0.808	0.023	6.31E-21	208,370
42	KNOWN	rs6457796	rs10484578	6	35,246,319	A	G	0.628	1.131	0.016	3.73E-14	1.108	0.017	8.26E-10	208,370
43	NOVEL	rs34868004	rs56285849	6	36,704,293	T	C	0.956	1.350	0.056	9.19E-08	1.425	0.057	3.77E-10	205,565
43	NOVEL	rs34868004	rs34868004	6	36,715,031	CA	C	0.225	1.104	0.017	4.46E-09	1.116	0.017	1.04E-10	208,370
44	KNOWN	rs597325	rs3857496	6	90,719,164	T	C	0.814	1.116	0.019	7.66E-09	1.116	0.019	8.73E-09	208,370
44	KNOWN	rs597325	rs597325	6	91,002,494	A	G	0.548	0.906	0.015	4.60E-11	0.907	0.015	4.80E-11	208,370
45	KNOWN	rs548234	rs548234	6	106,568,034	T	C	0.705	0.819	0.015	5.54E-39	0.819	0.015	6.54E-39	208,370
46	NOVEL	rs9488914	rs9488914	6	116,690,849	T	C	0.920	0.862	0.026	1.14E-08	0.862	0.026	1.10E-08	208,370
47	KNOWN	rs148314165	rs75163761	6	138,157,489	T	C	0.042	1.631	0.048	5.23E-24	1.484	0.049	5.38E-16	187,562
47	KNOWN	rs148314165	rs9494894	6	138,228,520	T	C	0.941	0.586	0.027	3.48E-84	0.600	0.028	1.98E-76	208,370
48	NOVEL	rs9322454	rs9322454	6	154,570,651	A	G	0.659	1.090	0.015	2.42E-08	1.090	0.015	2.26E-08	208,370
49	KNOWN	rs4598207	rs62447171	7	50,309,890	A	G	0.292	0.767	0.016	8.97E-60	0.790	0.017	1.49E-43	208,370
49	KNOWN	rs4598207	rs10239000	7	50,332,196	A	G	0.242	1.189	0.017	1.51E-25	1.107	0.017	4.46E-09	208,370
50	KNOWN	rs117026326	rs10716716	7	73,607,942	G	GT	0.159	1.151	0.023	8.49E-10	1.198	0.023	3.32E-15	208,370
50	KNOWN	rs117026326	rs372942110	7	73,629,019	T	TAATATATATA	0.008	2.294	0.142	5.62E-09	2.278	0.143	8.02E-09	47,452
50	KNOWN	rs117026326	rs78290495	7	73,697,541	T	C	0.965	0.799	0.047	2.00E-06	0.760	0.047	6.96E-09	204,433
50	KNOWN	rs117026326	rs530634980	7	73,910,241	T	C	0.016	2.016	0.081	5.10E-18	1.900	0.081	2.81E-15	199,014
50	KNOWN	rs117026326	rs13244581	7	73,995,034	C	G	0.092	0.667	0.044	1.59E-20	0.690	0.044	3.45E-17	201,819
50	KNOWN	rs117026326	rs116991837	7	74,003,710	A	G	0.016	2.654	0.124	3.82E-15	2.803	0.125	1.26E-16	183,488
50	KNOWN	rs117026326	rs150724213	7	74,020,343	A	G	0.010	3.882	0.171	2.51E-15	2.628	0.172	2.00E-08	18,619
50	KNOWN	rs117026326	rs7800325	7	74,032,651	T	C	0.826	0.449	0.022	1.04E-280	0.686	0.031	2.19E-33	204,433
50	KNOWN	rs117026326	rs67955681	7	74,039,668	T	TA	0.157	0.849	0.026	3.68E-10	0.793	0.028	1.32E-16	208,370
50	KNOWN	rs117026326	rs68008267	7	74,087,465	T	C	0.025	1.406	0.049	2.65E-12	1.360	0.052	3.81E-09	204,433
50	KNOWN	rs117026326	rs79171842	7	74,098,622	A	T	0.990	0.405	0.091	3.02E-23	0.400	0.094	1.57E-22	190,367
50	KNOWN	rs117026326	rs143176121	7	74,108,439	T	C	0.980	0.292	0.071	1.58E-66	0.574	0.074	6.92E-14	204,433
50	KNOWN	rs117026326	rs117026326	7	74,126,034	T	C	0.175	2.137	0.021	2.20E-298	1.490	0.028	1.27E-45	201,819
50	KNOWN	rs117026326	rs587680541	7	74,195,634	T	TC	0.014	4.140	0.085	4.24E-62	2.296	0.088	5.46E-21	197,554
50	KNOWN	rs117026326	rs199789198	7	74,196,185	A	C	0.073	3.098	0.038	2.57E-194	1.493	0.045	3.87E-19	201,819
50	KNOWN	rs117026326	rs587621258	7	75,079,055	A	G	0.008	1.854	0.119	2.27E-07	2.082	0.120	9.41E-10	56,121
50	KNOWN	rs117026326	rs794368	7	75,185,985	A	G	0.567	1.185	0.016	1.54E-26	1.111	0.016	4.52E-11	208,370
50	KNOWN	rs117026326	rs77009341	7	75,188,681	C	G	0.037	2.089	0.044	6.39E-62	1.962	0.045	2.98E-51	208,370
50	KNOWN	rs117026326	rs118048475	7	75,257,371	T	C	0.975	1.186	0.086	4.63E-02	2.302	0.106	3.68E-15	187,562
50	KNOWN	rs117026326	rs4573208	7	75,278,547	A	G	0.149	1.173	0.020	1.53E-15	1.149	0.020	3.83E-12	208,370
50	KNOWN	rs117026326	rs146063533	7	75,321,461	T	C	0.028	1.612	0.059	9.44E-16	2.149	0.074	3.11E-25	187,562
51	KNOWN	rs3757387	rs3757387	7	128,576,086	T	C	0.863	0.693	0.020	8.73E-79	0.758	0.021	2.13E-39	208,370
51	KNOWN	rs3757387	rs41298401	7	128,578,307	C	G	0.785	1.294	0.018	5.04E-45	1.219	0.019	3.91E-26	208,370
51	KNOWN	rs3757387	rs78724056	7	128,654,051	T	G	0.039	1.596	0.039	1.69E-32	1.279	0.042	3.78E-09	208,370
51	KNOWN	rs3757387	rs28364822	7	128,695,982	A	T	0.028	1.672	0.060	1.19E-17	1.664	0.060	2.86E-17	187,562
52	KNOWN	rs2736332	rs2736332	8	11,339,965	C	G	0.734	1.360	0.017	1.57E-70	1.359	0.017	2.14E-70	208,370
53	KNOWN	rs2272736	rs117627999	8	42,104,240	T	C	0.083	0.827	0.034	1.62E-08	0.827	0.034	1.64E-08	208,370
54	NOVEL	rs142937720	rs11347613	8	71,309,696	G	GA	0.368	0.888	0.017	2.34E-12	0.887	0.017	1.60E-12	208,370

55	NOVEL	rs17374162	rs10111413	8	72,891,748	A	G	0.415	0.918	0.014	3.05E-09	0.917	0.014	1.95E-09	208,370
56	NOVEL	rs16902895	rs16902895	8	129,425,593	A	G	0.678	1.122	0.016	1.48E-13	1.122	0.016	1.31E-13	208,370
57	KNOWN	rs1887428	rs1887428	9	4,984,530	C	G	0.664	0.915	0.016	2.80E-08	0.915	0.016	3.03E-08	208,370
58	NOVEL	rs7858766	rs7858766	9	21,267,087	T	C	0.538	1.139	0.016	2.25E-15	1.139	0.016	1.96E-15	208,370
59	NOVEL	rs77448389	rs77448389	10	5,910,746	A	G	0.913	0.855	0.025	7.30E-10	0.855	0.025	7.05E-10	208,370
60	KNOWN	rs7097397	rs7072606	10	49,933,974	T	C	0.809	0.884	0.018	2.22E-12	0.856	0.018	1.63E-18	208,370
60	KNOWN	rs7097397	rs7097397	10	50,025,396	A	G	0.651	0.810	0.016	2.23E-40	0.796	0.016	2.21E-46	208,370
61	KNOWN	rs7902146	rs7902146	10	63,801,030	T	C	0.691	0.900	0.015	3.34E-12	0.899	0.015	1.72E-12	208,370
62	NOVEL	rs10995261	rs10995254	10	64,401,836	T	G	0.707	1.092	0.016	4.47E-08	1.096	0.016	1.37E-08	208,370
63	NOVEL	rs10823829	rs10823829	10	73,466,709	T	C	0.718	0.910	0.016	1.05E-09	0.911	0.016	2.02E-09	208,370
64	NOVEL	rs111447985	rs11599734	10	103,963,397	C	G	0.479	0.918	0.016	5.89E-08	0.917	0.016	3.53E-08	208,370
64	NOVEL	rs111447985	rs111447985	10	105,677,911	A	C	0.073	1.172	0.028	1.72E-08	1.176	0.028	9.86E-09	208,370
65	NOVEL	rs58164562	rs58164562	10	112,664,114	T	C	0.748	0.892	0.016	3.14E-12	0.891	0.016	2.37E-12	208,370
66	NOVEL	rs3750996	rs3750996	11	4,113,200	A	G	0.834	1.167	0.022	1.89E-12	1.167	0.022	1.86E-12	208,370
67	NOVEL	rs77885959	rs77885959	11	18,362,382	T	G	0.978	1.694	0.062	3.16E-17	1.694	0.063	3.41E-17	204,433
68	KNOWN	rs2785198	rs2732540	11	35,095,486	A	G	0.224	0.847	0.018	1.30E-20	0.874	0.019	4.17E-13	208,370
68	KNOWN	rs2785198	rs11032994	11	35,111,157	A	G	0.256	1.147	0.016	1.12E-17	1.110	0.017	3.55E-10	208,370
69	KNOWN	rs10896045	rs10896045	11	65,555,524	A	G	0.551	1.168	0.015	6.59E-26	1.171	0.015	7.96E-27	208,370
70	KNOWN	rs4930642	rs4930642	11	68,816,370	A	G	0.252	1.145	0.019	6.16E-13	1.146	0.019	4.08E-13	208,370
71	KNOWN	rs77971648	rs77971648	11	72,640,480	T	C	0.909	1.291	0.026	3.16E-23	1.293	0.026	1.39E-23	208,370
72	KNOWN	rs377392985	rs480958	11	118,577,990	A	G	0.624	0.871	0.015	3.42E-19	0.890	0.016	1.51E-13	208,370
72	KNOWN	rs377392985	rs4936441	11	118,725,660	C	G	0.137	0.823	0.024	5.71E-16	0.858	0.025	4.65E-10	208,370
73	KNOWN	rs9736939	rs11501246	11	128,314,424	A	G	0.623	0.791	0.015	1.58E-58	0.793	0.015	1.08E-57	208,370
73	KNOWN	rs9736939	rs684150	11	128,594,161	T	C	0.381	0.914	0.014	4.32E-10	0.912	0.015	1.87E-10	208,370
74	NOVEL	rs2540119	rs2540119	12	4,140,876	T	C	0.544	1.086	0.015	3.51E-08	1.088	0.015	1.90E-08	208,370
75	KNOWN	rs4251697	rs10845602	12	12,825,237	A	G	0.710	1.210	0.016	5.77E-31	1.140	0.017	7.07E-14	208,370
75	KNOWN	rs4251697	rs4251697	12	12,874,462	A	G	0.097	0.637	0.033	1.17E-43	0.693	0.035	2.05E-26	208,370
76	KNOWN	rs4622329	rs4622329	12	102,321,935	A	G	0.561	1.119	0.014	4.00E-15	1.123	0.014	7.88E-16	208,370
77	NOVEL	rs6539078	rs6539078	12	103,916,080	T	C	0.591	0.894	0.015	9.49E-14	0.893	0.015	4.68E-14	208,370
78	KNOWN	rs77465633	rs77465633	12	111,933,545	A	C	0.068	1.340	0.034	6.99E-18	1.362	0.034	1.04E-19	208,370
78	KNOWN	rs77465633	rs1131476	12	113,357,209	A	G	0.756	1.110	0.017	1.25E-09	1.120	0.017	4.84E-11	208,370
79	NOVEL	rs3999421	rs7139263	12	118,428,976	A	G	0.510	1.083	0.015	9.82E-08	1.086	0.015	3.38E-08	208,370
79	NOVEL	rs3999421	rs35743748	12	121,228,629	CT	C	0.444	1.101	0.016	2.45E-09	1.101	0.016	2.55E-09	208,370
80	KNOWN	rs11059928	rs11059928	12	129,296,103	A	T	0.786	0.823	0.017	1.61E-30	0.823	0.017	2.28E-30	208,370
81	NOVEL	rs200521476	rs200521476	12	133,040,182	G	GCATCAC	0.812	0.875	0.023	5.66E-09	-	-	-	208,370
82	KNOWN	rs57141708	rs57141708	13	41,575,391	A	G	0.224	1.183	0.018	6.84E-22	1.183	0.018	6.52E-22	208,370
83	KNOWN	rs2819426	rs2819426	14	105,412,259	C	G	0.331	0.824	0.017	2.51E-30	0.824	0.017	3.57E-30	208,370
84	KNOWN	rs7170151	rs7170151	15	38,846,678	T	C	0.563	1.107	0.015	3.20E-12	1.093	0.015	2.22E-09	208,370
84	KNOWN	rs7170151	rs12900640	15	38,974,548	A	C	0.464	1.101	0.014	2.42E-11	1.085	0.015	1.90E-08	208,370
85	KNOWN	rs11553760	rs11553760	15	75,091,247	T	C	0.235	1.111	0.017	7.32E-10	1.111	0.017	7.67E-10	208,370
86	NOVEL	rs35985016	rs35985016	15	101,529,012	A	G	0.930	0.843	0.030	1.95E-08	0.843	0.030	1.95E-08	204,433
87	KNOWN	rs34361002	rs34361002	16	11,190,034	T	TAA	0.624	1.140	0.015	1.24E-17	1.140	0.015	1.33E-17	208,370
88	KNOWN	rs79401250	rs79401250	16	23,871,457	T	G	0.819	1.172	0.022	1.48E-12	1.171	0.023	2.06E-12	208,370

89	KNOWN	rs534645300	rs534645300	16	30,813,454	A	AT	0.930	0.814	0.035	2.68E-09	0.815	0.035	3.28E-09	208,370
90	NOVEL	rs11288784	rs11288784	16	50,089,207	G	GT	0.365	0.902	0.016	2.38E-10	0.901	0.016	1.40E-10	208,370
91	KNOWN	rs669763	rs669763	16	57,390,478	C	G	0.521	1.123	0.015	2.89E-15	1.124	0.015	1.91E-15	208,370
92	KNOWN	rs28410471	rs28410471	16	68,554,755	A	T	0.181	1.128	0.022	3.14E-08	1.128	0.022	3.09E-08	208,370
93	NOVEL	rs11376510	rs11376510	16	79,745,672	G	GT	0.737	0.898	0.017	2.23E-10	0.899	0.017	2.84E-10	208,370
94	KNOWN	rs11117432	rs447632	16	85,967,640	A	G	0.495	0.851	0.015	7.23E-28	0.870	0.015	1.61E-20	208,370
94	KNOWN	rs11117432	rs11117432	16	86,019,271	A	G	0.088	0.728	0.027	1.27E-32	0.759	0.027	2.42E-24	208,370
95	NOVEL	rs61759532	rs61759532	17	7,240,391	T	C	0.076	1.235	0.032	2.79E-11	1.230	0.032	6.22E-11	208,370
96	KNOWN	rs35966917	rs35966917	17	16,839,901	A	G	0.423	0.914	0.015	4.66E-09	0.916	0.015	1.04E-08	208,370
97	NOVEL	rs2671655	rs2671655	17	47,468,020	T	C	0.651	1.087	0.015	4.60E-08	1.087	0.015	4.60E-08	208,370
98	NOVEL	rs113417153	rs113417153	17	76,373,179	T	C	0.193	0.893	0.020	1.90E-08	0.893	0.020	1.91E-08	208,370
99	KNOWN	rs1788097	rs1788097	18	67,543,688	T	C	0.392	1.096	0.015	6.28E-10	1.093	0.015	1.90E-09	208,370
100	NOVEL	rs118075465	rs118075465	18	77,386,912	A	G	0.147	1.140	0.020	1.16E-10	1.136	0.020	3.23E-10	208,370
101	NOVEL	rs2238577	rs10414086	19	937,136	T	C	0.374	0.885	0.016	2.75E-14	0.883	0.016	1.29E-14	208,370
102	NOVEL	rs5826945	rs11085192	19	6,689,065	T	C	0.927	0.840	0.027	1.18E-10	0.838	0.027	6.07E-11	208,370
103	KNOWN	rs55882956	rs55882956	19	10,469,919	A	G	0.029	0.674	0.048	1.23E-16	0.668	0.048	2.55E-17	208,370
104	KNOWN	rs11673604	rs11673604	19	18,540,988	T	C	0.759	1.144	0.019	4.21E-12	1.144	0.019	3.02E-12	208,370
105	NOVEL	rs12461589	rs12461589	19	33,072,768	T	C	0.248	0.898	0.017	5.00E-10	0.898	0.017	5.42E-10	208,370
106	NOVEL	rs33974425	rs8108669	19	49,845,895	T	C	0.299	0.893	0.016	4.68E-12	0.892	0.016	1.99E-12	208,370
107	KNOWN	rs4801882	rs3794986	19	52,047,314	T	G	0.428	0.890	0.015	1.46E-14	0.894	0.015	1.74E-13	208,370
107	KNOWN	rs4801882	rs4801882	19	52,127,053	A	G	0.532	0.882	0.014	1.86E-18	0.888	0.014	1.59E-16	208,370
108	NOVEL	rs4819670	rs4819670	22	18,649,356	T	C	0.210	1.151	0.022	5.53E-11	1.155	0.022	2.17E-11	208,370
109	KNOWN	rs4821116	rs5754344	22	21,963,786	A	G	0.622	0.805	0.015	1.81E-45	0.804	0.015	6.20E-46	208,370
110	KNOWN	rs9611155	rs9611155	22	39,739,187	T	C	0.761	1.137	0.022	7.66E-09	1.137	0.022	7.33E-09	208,370
111	KNOWN	rs6641111	rs6641111	23	12,839,790	C	G	0.694	1.191	0.017	3.27E-25	1.190	0.017	4.40E-25	208,360
111	KNOWN	rs6641111	rs4830478	23	12,918,288	A	G	0.797	1.136	0.021	1.91E-09	1.135	0.021	3.11E-09	205,555
112	KNOWN	rs5914012	rs5914012	23	56,908,702	T	C	0.353	1.104	0.017	6.65E-09	1.104	0.017	6.65E-09	208,360
113	KNOWN	rs1059702	rs1059702	23	153,284,192	A	G	0.783	1.356	0.020	5.89E-54	1.352	0.020	1.07E-52	208,360
113	KNOWN	rs1059702	rs5945199	23	153,749,857	A	G	0.104	0.778	0.036	2.90E-12	0.789	0.036	4.44E-11	202,941

Region: index ID for the genomic locus; Novel: index of the novelty for the genomic locus; Lead rsID: dbSNP rsID for the lead variant within the genomic locus; rsID: dbSNP ID for index variant of the association distinct signal; CHR: chromosome; Position: position in base pair in genome build 19; EA: effective allele; NEA: non-effective allele; EAF: effective allele frequency; OR: odds ratio in the association study; SE: standard error of odds ratio in the association study; P: p-value in the association study; N: study sample size.

Supplementary Table 6 | Putative causal variants with high posterior probability (PiP ≥ 0.1) or with highest PiP within 95% credible sets for 57 genomic loci

Region	Novel	Signal SNP	Credible Set ID	Credible Set Size	Causal SNP	SNP PiP	Nearest Gene	Consequence
1	NOVEL	rs9651076	1	31	rs9651076	0.1422	CD58	intergenic
1	NOVEL	rs9651076	1	31	rs10801908	0.1201	CD58	intronic
2	NOVEL	rs112806509	1	72	rs112806509	0.0667	FCRL5	intronic
2	NOVEL	rs116785379	2	3	rs116785379	0.4422	ETV3	UTR5
2	NOVEL	rs116785379	2	3	rs80237341	0.2680	ETV3	intergenic
2	NOVEL	rs116785379	2	3	rs77868288	0.2491	ETV3	intergenic
2	NOVEL	rs2317230	3	18	rs2317230	0.2005	FCRL3	intergenic
5	KNOWN	rs13306575	1	1	rs13306575	1.0000	NCF2	exonic
5	KNOWN	rs66977652	2	16	rs66977652	0.1757	NCF2	intronic
6	KNOWN	rs4143303	1	106	rs4143303	0.0920	PTPRC	intronic
7	NOVEL	rs3806357	1	4	rs3806357	0.8728	ELF3-AS1	ncRNA_exonic
8	KNOWN	rs4844538	1	8	rs4844538	0.2773	IKBKE	upstream
8	KNOWN	rs4844538	1	8	rs6540432	0.2276	IKBKE	intergenic
9	NOVEL	rs75362385	1	22	rs75362385	0.0947	LOC100506274	ncRNA_intronic
11	KNOWN	rs13385731	1	2	rs13385731	0.7957	RASGRP3	intronic
11	KNOWN	rs13385731	1	2	rs13425999	0.2043	RASGRP3	intronic
12	KNOWN	rs11684155	1	42	rs11126034	0.0513	SPRED2	intronic
13	KNOWN	rs10207954	1	18	rs10207954	0.1346	TET3	intronic
13	KNOWN	rs10207954	1	18	rs2421690	0.1124	DGUOK-AS1	ncRNA_intronic
13	KNOWN	rs10207954	1	18	rs141389817	0.1106	DGUOK-AS1	ncRNA_intronic
15	KNOWN	rs218174	1	31	rs218174	0.1204	DARS	intergenic
16	KNOWN	rs11679244	1	3	rs11679244	0.5623	FAP	intronic
16	KNOWN	rs11679244	1	3	rs2075302	0.3764	FAP	intronic
18	NOVEL	rs11684176	1	106	rs7572733	0.0577	PLCL1	intronic
19	KNOWN	rs7565158	1	3	rs7565158	0.6258	LINC01878	intergenic
19	KNOWN	rs7565158	1	3	rs12612794	0.3117	LINC01878	intergenic
19	KNOWN	rs2371790	2	29	rs2371790	0.1120	IKZF2	intronic
19	KNOWN	rs2371790	2	29	rs12694291	0.1038	IKZF2	intronic
20	NOVEL	rs438613	1	13	rs438613	0.0985	LINC01980	intergenic
21	NOVEL	rs7637844	1	4	rs7637844	0.6651	LINC00870	intergenic
21	NOVEL	rs7637844	1	4	rs11707718	0.1976	LINC00870	intergenic
23	KNOWN	rs1317082	1	24	rs1317082	0.0833	MYNN	intronic
24	KNOWN	rs13101828	1	9	rs13101828	0.2102	DGKQ	intronic
24	KNOWN	rs13101828	1	9	rs11724804	0.1255	DGKQ	intronic
24	KNOWN	rs13101828	1	9	rs62294486	0.1228	DGKQ	intronic

24	KNOWN	rs13101828	1	9	rs1377586	0.1181	DGKQ	exonic
25	NOVEL	rs231694	1	35	rs231694	0.2060	FAM193A	intronic
25	NOVEL	rs231694	1	35	rs529432	0.1464	FAM193A	intronic
25	NOVEL	rs231694	1	35	rs231708	0.1037	FAM193A	intronic
26	NOVEL	rs113284964	1	4	rs113284964	0.3720	LINC02265	intergenic
26	NOVEL	rs113284964	1	4	rs13136820	0.3298	LINC02265	intergenic
26	NOVEL	rs113284964	1	4	rs11736377	0.1991	LINC02265	intergenic
32	KNOWN	rs7725218	1	6	rs7725218	0.3410	TERT	intronic
32	KNOWN	rs7725218	1	6	rs7726159	0.2658	TERT	intronic
32	KNOWN	rs7725218	1	6	rs4449583	0.2132	TERT	intronic
33	KNOWN	rs2544920	1	88	rs2544920	0.0388	ST8SIA4	intergenic
35	NOVEL	rs2549002	1	54	rs2549002	0.0379	IRF1	intergenic
37	KNOWN	rs10036748	1	4	rs10036748	0.3873	TNIP1	intronic
37	KNOWN	rs10036748	1	4	rs7708392	0.2806	TNIP1	intronic
37	KNOWN	rs10036748	1	4	rs6889239	0.2712	TNIP1	intronic
38	NOVEL	rs2421184	1	12	rs2421184	0.2607	LINC01845	ncRNA_intronic
38	NOVEL	rs2421184	1	12	rs4921502	0.1990	LINC01845	ncRNA_intronic
38	NOVEL	rs2421184	1	12	rs6556425	0.1212	LINC01845	intergenic
39	KNOWN	rs2431697	1	2	rs2431697	0.6581	MIR3142HG	intergenic
39	KNOWN	rs2431697	1	2	rs2431700	0.3419	MIR3142HG	intergenic
40	NOVEL	rs9503037	1	18	rs9503037	0.2160	LOC285766	intergenic
40	NOVEL	rs9503037	1	18	rs9503029	0.1504	LOC285766	intergenic
44	KNOWN	rs597325	1	3	rs597325	0.8673	BACH2	intronic
44	KNOWN	rs3857496	2	16	rs12664550	0.1013	BACH2	intronic
46	NOVEL	rs9488914	1	3	rs9488914	0.4760	DSE	intronic
46	NOVEL	rs9488914	1	3	rs9387400	0.4271	DSE	intronic
55	NOVEL	rs10111413	1	11	rs17374162	0.1580	MSC-AS1	ncRNA_intronic
55	NOVEL	rs10111413	1	11	rs10111413	0.1565	MSC-AS1	ncRNA_intronic
55	NOVEL	rs10111413	1	11	rs1036963	0.1219	MSC-AS1	ncRNA_intronic
55	NOVEL	rs10111413	1	11	rs7004602	0.1030	MSC-AS1	ncRNA_intronic
55	NOVEL	rs10111413	1	11	rs10090715	0.1008	MSC-AS1	ncRNA_intronic
56	NOVEL	rs16902895	1	35	rs16902895	0.0778	LINC00824	ncRNA_intronic
57	KNOWN	rs1887428	1	169	rs1887428	0.4455	JAK2	upstream
58	NOVEL	rs7858766	1	73	rs7858766	0.0549	IFNA22P	intergenic
62	NOVEL	rs10995254	1	21	rs10995261	0.0958	ZNF365	intronic
63	NOVEL	rs10823829	1	11	rs10823829	0.1980	CDH23	exonic
63	NOVEL	rs10823829	1	11	rs7912167	0.1923	CDH23	intronic
65	NOVEL	rs58164562	1	23	rs58164562	0.1813	BBIP1	intronic
66	NOVEL	rs3750996	1	1	rs3750996	0.9893	STIM1	UTR3
67	NOVEL	rs77885959	1	1	rs77885959	0.9764	GTF2H1	intronic
71	KNOWN	rs77971648	1	6	rs77971648	0.4840	FCHSD2	intronic

71	KNOWN	rs77971648	1	6	rs11235622	0.2456	FCHSD2	intronic
73	KNOWN	rs11501246	1	11	rs9736939	0.1745	ETS1	intergenic
73	KNOWN	rs11501246	1	11	rs11501246	0.1399	ETS1	intergenic
73	KNOWN	rs11501246	1	11	rs9736922	0.1399	ETS1	intergenic
73	KNOWN	rs11501246	1	11	rs61909064	0.1049	ETS1	intergenic
73	KNOWN	rs11501246	1	11	rs61909063	0.1009	ETS1	intergenic
73	KNOWN	rs684150	2	11	rs684150	0.4529	FLI1	intronic
73	KNOWN	rs684150	2	11	rs587862	0.1306	FLI1	intronic
73	KNOWN	rs684150	2	11	rs615671	0.1158	FLI1	intronic
74	NOVEL	rs2540119	1	11	rs2540119	0.2871	PARP11	intergenic
74	NOVEL	rs2540119	1	11	rs10848975	0.1913	PARP11	intergenic
74	NOVEL	rs2540119	1	11	rs9788147	0.1582	PARP11	intergenic
74	NOVEL	rs2540119	1	11	rs11062982	0.1362	PARP11	intergenic
76	KNOWN	rs4622329	1	1	rs4622329	0.9604	DRAM1	intergenic
78	KNOWN	rs77465633	1	2	rs77465633	0.9338	ATXN2	intronic
78	KNOWN	rs1131476	2	115	rs1131476	0.0239	OAS1	exonic
84	KNOWN	rs7170151	1	10	rs7170151	0.1836	RASGRP1	intronic
84	KNOWN	rs7170151	1	10	rs4924273	0.1813	RASGRP1	intronic
84	KNOWN	rs7170151	1	10	rs8035957	0.1260	RASGRP1	intronic
84	KNOWN	rs7170151	1	10	rs11348849	0.1013	RASGRP1	intronic
84	KNOWN	rs12900640	2	9	rs12900640	0.5383	C15orf53	intergenic
84	KNOWN	rs12900640	2	9	rs145489243	0.1285	C15orf53	intergenic
86	NOVEL	rs35985016	1	2	rs35985016	0.9295	LRRK1	exonic
88	KNOWN	rs79401250	1	3	rs79401250	0.6229	PRKCB	intronic
88	KNOWN	rs79401250	1	3	rs4592664	0.3026	PRKCB	intronic
91	KNOWN	rs669763	1	9	rs669763	0.2347	CCL22	intergenic
91	KNOWN	rs669763	1	9	rs223886	0.1287	CCL22	intergenic
91	KNOWN	rs669763	1	9	rs598366	0.1278	CCL22	intronic
91	KNOWN	rs669763	1	9	rs223887	0.1221	CCL22	intergenic
91	KNOWN	rs669763	1	9	rs223889	0.1108	CCL22	upstream
93	NOVEL	rs11376510	1	30	rs11376510	0.2451	MAFTRR	intergenic
95	NOVEL	rs61759532	1	1	rs61759532	0.9999	ACAP1	intronic
96	KNOWN	rs35966917	1	22	rs35966917	0.1572	TNFRSF13B	intergenic
96	KNOWN	rs35966917	1	22	rs66516966	0.1105	TNFRSF13B	intergenic
97	NOVEL	rs2671655	1	1	rs2671655	0.9900	LOC102724596	intergenic
98	NOVEL	rs113417153	1	18	rs113417153	0.1655	PGS1	intergenic
98	NOVEL	rs113417153	1	18	rs72899798	0.1313	PGS1	intergenic
98	NOVEL	rs113417153	1	18	rs72911373	0.1260	PGS1	intergenic
99	KNOWN	rs1788097	1	22	rs1788097	0.1007	CD226	intronic
100	NOVEL	rs118075465	1	5	rs118075465	0.3197	LOC284241	intergenic
100	NOVEL	rs118075465	1	5	rs62096783	0.1825	LOC284241	intergenic

100	NOVEL	rs118075465	1	5	rs62096781	0.1784	LOC284241	intergenic
100	NOVEL	rs118075465	1	5	rs62096782	0.1460	LOC284241	intergenic
100	NOVEL	rs118075465	1	5	rs2363126	0.1285	LOC284241	intergenic
101	NOVEL	rs10414086	1	15	rs2238577	0.1668	ARID3A	intronic
101	NOVEL	rs10414086	1	15	rs10411830	0.1182	ARID3A	intronic
101	NOVEL	rs10414086	1	15	rs10414086	0.1115	ARID3A	intronic
108	NOVEL	rs4819670	1	19	rs4819670	0.0897	USP18	intronic
112	KNOWN	rs5914012	1	815	rs5914012	0.0050	NBDY	intergenic

This table only contains the putative causal variants with SNP posterior probability larger than 0.1 and the putative causal variants with highest SNP posterior probability for each locus. Region: index ID for the genomic locus; Novel: index of the novelty for the genomic locus; Signal SNP: the rsID for all the index variants of distinct association signals. The rsIDs are separated by semicolon; Credible Set ID: index ID for the 95% credible set of causal variants; Credible Set Size: number of putative causal variants in the 95% credible set; Causal SNP: candidate putative causal variant ID; SNP PiP: posterior probability for the candidate variant to be true causal variant; Consequence: functional consequence of the candidate putative causal variant on the nearest gene.

Supplementary Table 7 | Genetic correlation between SLE and 98 complex diseases/traits in Biobank Japan

Trait	r_g	se	P-value	h^2_{SNP}	h^2_{SNP} se	N	FDR
Rheumatiod arthritis	0.4365	0.0752	6.38E-09	0.0147	0.0032	212453	6.25E-07
Albumin/globulin ratio	-0.2417	0.0567	2.04E-05	0.0947	0.0108	98626	1.98E-03
Non-albumin protein	0.2376	0.0573	3.35E-05	0.098	0.0114	98538	3.22E-03
Graves' disease	0.3183	0.0822	1.00E-04	0.0142	0.0029	212453	9.50E-03
Total protein	0.1706	0.0504	7.00E-04	0.0816	0.0074	113509	6.58E-02
Zinc sulfate turbidity test	0.3907	0.1379	4.60E-03	0.0874	0.0388	12303	4.28E-01
Interventricular septum thickness	-0.0038	0.1031	9.70E-01	0.0577	0.0275	19318	0.9703
Drug eruption	0.5256	0.806	5.14E-01	0.0008	0.0021	210081	1
Epilepsy	0.2767	0.1799	1.24E-01	0.0024	0.0021	212453	1
Cirrhosis	0.2063	0.2017	3.06E-01	0.0025	0.0023	212453	1
Chronic obstructive pulmonary disease	0.1505	0.0794	5.80E-02	0.0119	0.0028	204907	1
pulmonary tuberculosis	0.1272	0.1341	3.43E-01	0.0029	0.0019	212453	1
Chronic heart failure	0.1066	0.0759	1.60E-01	0.0115	0.0025	212453	1
Lactate dehydrogenase	0.0879	0.0647	1.74E-01	0.0334	0.0052	126319	1
Aspartate aminotransferase	0.0845	0.046	6.61E-02	0.07	0.0089	134154	1
Asthma	0.0753	0.0566	1.84E-01	0.0224	0.0031	209808	1
Osteoporosis	0.0753	0.0856	3.79E-01	0.0084	0.0023	212453	1
Alkaline phosphatase	0.0694	0.043	1.07E-01	0.0964	0.0282	105030	1
Hemoglobin	0.0637	0.0496	1.99E-01	0.07	0.0068	108769	1
Activated partial thromboplastin time	0.0626	0.0833	4.53E-01	0.0545	0.017	37767	1
Cerebral aneurysm	0.0612	0.071	3.89E-01	0.0155	0.0029	195203	1
Red blood cell count	0.0529	0.0446	2.35E-01	0.1225	0.0128	108794	1
Cervical cancer	0.0515	0.1034	6.19E-01	0.0123	0.0047	90336	1
Hematocrit	0.0486	0.0467	2.99E-01	0.0757	0.0072	108757	1
Myocardial infarction	0.0473	0.0382	2.16E-01	0.0566	0.0079	212453	1
Relative wall thickness	0.0448	0.0799	5.75E-01	0.0918	0.0272	19311	1
C-reactive protein	0.0443	0.1158	7.02E-01	0.0221	0.0092	75391	1
Esophageal cancer	0.0343	0.0653	5.99E-01	0.0129	0.0049	197045	1
Mean corpuscular hemoglobin concentration	0.0331	0.0511	5.17E-01	0.0563	0.0103	108728	1
Adult Height	0.0295	0.0235	2.09E-01	0.3563	0.0193	159148	1
Serum creatinine	0.0284	0.0394	4.72E-01	0.1051	0.0099	142097	1

Pancreatic cancer	0.0196	0.16	9.03E-01	0.002	0.0025	196187	1
Arrhythmia	0.0194	0.0447	6.64E-01	0.0311	0.0058	212453	1
Pulse pressure	0.0178	0.049	7.17E-01	0.0534	0.0051	136249	1
Type2 diabetes	0.0169	0.0322	5.99E-01	0.1061	0.0088	210865	1
Posterior wall thickness	0.0142	0.072	8.44E-01	0.1068	0.0262	19373	1
Systolic blood pressure	0.0116	0.0394	7.68E-01	0.0792	0.0074	136597	1
Arteriosclerosis obliterans	0.0105	0.0617	8.66E-01	0.0162	0.0025	212453	1
Low-density-lipoprotein cholesterol	0.01	0.0697	8.86E-01	0.0623	0.0183	72866	1
Mean arterial pressure	0.0095	0.04	8.13E-01	0.0754	0.0075	136482	1
Body mass index	0.0094	0.0303	3.11E-01	0.1708	0.0085	158284	1
Diastolic blood pressure	0.0044	0.0431	9.19E-01	0.0628	0.0064	136615	1
Estimated glomerular filtration rate	-0.0062	0.0395	8.75E-01	0.1008	0.0094	143658	1
Left ventricular internal dimension in systole	-0.0063	0.0674	9.26E-01	0.1503	0.0247	19586	1
Creatine kinase	-0.0068	0.0427	8.74E-01	0.1016	0.0105	106080	1
Nephrotic syndrome	-0.0074	0.1475	9.60E-01	0.0031	0.0023	212453	1
Stable angina	-0.0086	0.0579	8.81E-01	0.0262	0.0031	212453	1
Chloride	-0.0094	0.0509	8.53E-01	0.0593	0.0071	126402	1
Alanine aminotransferase	-0.0103	0.0452	8.20E-01	0.0637	0.0085	134182	1
Total cholesterol	-0.0122	0.0588	8.36E-01	0.0542	0.0117	128305	1
Uterine fibroid	-0.0131	0.0815	8.73E-01	0.0231	0.0055	100964	1
Cataract	-0.0132	0.0923	8.86E-01	0.0071	0.0023	212453	1
Eosinophil count	-0.0133	0.0651	8.38E-01	0.0861	0.0145	62076	1
Mean corpuscular hemoglobin	-0.015	0.0433	7.29E-01	0.1645	0.0243	108054	1
γ-glutamyl transferase	-0.0157	0.0503	7.54E-01	0.1172	0.0215	118309	1
Gastric cancer	-0.0176	0.0756	8.16E-01	0.0123	0.0031	202308	1
Total bilirubin	-0.0197	0.0537	7.13E-01	0.06	0.0188	110207	1
Basophil count	-0.0236	0.0639	7.12E-01	0.0694	0.0171	62076	1
High-density-lipoprotein cholesterol	-0.0248	0.0577	6.68E-01	0.1131	0.0362	70657	1
Blood urea nitrogen	-0.0261	0.0446	5.59E-01	0.0758	0.0077	139818	1
Triglyceride	-0.0262	0.0384	4.96E-01	0.1242	0.0332	105597	1
Mean corpuscular volume	-0.0263	0.0451	5.59E-01	0.185	0.0259	108256	1
Potassium	-0.0279	0.0475	5.57E-01	0.0544	0.0079	132938	1
cerebral infarction	-0.0287	0.0633	6.50E-01	0.0168	0.0028	210054	1
Ejection fraction	-0.0287	0.0869	7.41E-01	0.0866	0.0242	19516	1
Platelet count	-0.0309	0.0429	4.72E-01	0.1593	0.0219	108208	1

Prothrombin time	-0.0328	0.0704	6.42E-01	0.0599	0.0236	58110	1
Atopic dermatitis	-0.0347	0.0888	6.96E-01	0.0119	0.0026	212036	1
Chronic hepatitis C	-0.0349	0.1	7.28E-01	0.0077	0.0023	212453	1
Left ventricular mass	-0.0356	0.0695	6.09E-01	0.1515	0.0274	19076	1
Calcium	-0.0379	0.0675	5.75E-01	0.0531	0.0105	71701	1
Unstable angina	-0.0387	0.0647	5.49E-01	0.0151	0.0025	212453	1
Glaucoma	-0.0429	0.0684	5.31E-01	0.0139	0.0025	212453	1
Neutrophil count	-0.0439	0.0517	3.97E-01	0.1216	0.0147	62076	1
Left ventricular mass index	-0.047	0.0832	5.72E-01	0.1159	0.0274	17837	1
Blood sugar	-0.0534	0.0599	3.73E-01	0.0511	0.0089	93146	1
Left ventricular internal dimension in diastole	-0.059	0.0704	4.02E-01	0.1476	0.0239	19676	1
Colorectal cancer	-0.061	0.0792	4.41E-01	0.0144	0.0026	202807	1
White blood cell count	-0.0616	0.0448	1.69E-01	0.1074	0.0104	107964	1
Fractional shortening	-0.0641	0.0882	4.68E-01	0.0794	0.022	19580	1
Sodium	-0.0715	0.05	1.53E-01	0.0563	0.0067	127304	1
Pollinosis	-0.0719	0.0889	4.19E-01	0.0073	0.0023	212453	1
Phosphorus	-0.0736	0.0779	3.45E-01	0.0497	0.0126	42793	1
Uric acid	-0.0764	0.0376	4.22E-02	0.1643	0.0502	109029	1
Lung cancer	-0.0873	0.1079	4.18E-01	0.0048	0.0023	212453	1
Monocyte count	-0.0948	0.061	1.20E-01	0.092	0.0121	62076	1
Lymphocyte count	-0.1041	0.0532	5.04E-02	0.0855	0.0107	62076	1
Urolithiasis	-0.115	0.0596	5.35E-02	0.0187	0.0032	212453	1
Keloid	-0.1166	0.0867	1.79E-01	0.0084	0.0022	212453	1
Endometrial cancer	-0.1169	0.1303	3.70E-01	0.0085	0.0049	90730	1
Prostate cancer	-0.1208	0.0569	3.38E-02	0.0461	0.0069	109347	1
Fibrinogen	-0.1227	0.186	5.10E-01	0.0235	0.0248	18348	1
Albumin	-0.1261	0.055	2.20E-02	0.0623	0.0072	102223	1
Hemoglobin A1c	-0.1403	0.0553	1.12E-02	0.1102	0.0194	42790	1
breast cancer	-0.142	0.0687	3.89E-02	0.0273	0.0056	95283	1
Chronic hepatitis B	-0.1649	0.107	1.23E-01	0.0055	0.0023	212453	1
Hepatic cancer	-0.2594	0.2805	3.55E-01	0.0015	0.0024	197611	1
Ovarian cancer	-0.2892	0.3235	3.71E-01	0.0028	0.0046	90451	1

r_g: genetic correlation estimation in LD score regression; se: standard error of r_g estimation; h^2_{SNP} and h^2_{SNP} se: SNP-based heritability estimation for trait and its standard error; N: study sample size for trait; FDR: Benjamini-Hochberg false discovery rate.