Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47

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1. Supplementary Table 1 – Index GWAS studies included in the meta-analysis.
2. Supplementary Table 2 – Country of origin of samples used in the follow-up experiment.
3. Supplementary Table 3a – Cohort specific results for all SNPs listed in Table 1 and Table 2.
4. Supplementary Table 3b – Cohort specific results for all SNPs included in follow-up phase, but failed our thresholds for follow-up.
5. Supplementary Table 4 – Subphenotype analyses at new ulcerative colitis risk loci.
6. Supplementary Table 5 – Ulcerative colitis risk variants correlated with eQTL.
7. Supplementary Table 6 – Ulcerative colitis risk variants correlated (r^2>0.5) with non-synonymous and splice-site disrupting SNPs.
8. Supplementary Table 7 – Summary of candidate genes mapping from *in silico* analysis on the 47 UC loci.
9. Supplementary Table 8 – Results from the functional enrichment analysis across all loci associated with UC susceptibility.
10. Supplementary Table 9 – Results from the International IBD Genetics Consortium CD and UC meta-analyses for the 99 loci reported for association in CD and/or UC.
11. Supplementary Figure 1 – Quantile-Quantile plots of observed vs expected chi-square statistics for the nine constituent genome-wide scans and the meta-analysis.
12. Supplementary Figure 2 – Locus wide association plots for all 47 UC loci, generated using SNAP.
13. Supplementary Figure 3 – Enrichment of biological functions for genes located in the associated UC risk loci.

Supplementary Table 1. Index GWAS studies included in the meta-analysis. Samples sizes are given post quality control.

The Cedars Sinai cohort was split into Jewish (253 cases and 323 controls) and non-Jewish (470 cases and 2,557 controls) for imputation and analysis. The NIDDK cohort was split into Jewish (98 cases and 451 controls), Northern-European descent (776 cases and 1,505 controls) and Southern-European descent (103 cases and 166 controls), as determined by self-reported Jewish descent and principal component analysis.

Index GWAS	Ulcerative Colitis cases	Population controls	Genotyping platform
Cedars-Sinai	723	2,880	Illumina HumanCNV370
German	1,036	1,694	Affymetrix SNP array 5.0 Affymetrix SNP array 6.0
CHOPSTICKS	643	6,197	Illumina HumanHap550
NIDDK	977	2122	Illumina HumanHap300 Illumina HumanHap550
Swedish	948	1,408	Illumina HumanHap550
WTCCC	2,360	5,417	Affymetrix SNP array 6.0
TOTAL	6,687	19,718	

Supplementary Table 2. Country of origin of samples used in the follow-up experiment.

Country	Ulcerative Colitis cases	Population controls	Genotyping platform
Australia	1,139	1,891	Sequenom iPlex
Belgium	1,001	1,634	Sequenom iPlex
Denmark	169	720	Sequenom iPlex
France	127	158	SNPlex
Germany	1,176	2,083	Sequenom iPlex
Italy	1,485	968	Sequenom iPlex
Lithuania	387	970	SNPlex/Taqman
New Zealand	470	455	Sequenom iPlex
Norwegian	268	282	Affymetrix SNP array 5.0
The Netherlands	750	786	Sequenom iPlex
Sweden	369	706	Sequenom iPlex
United Kingdom	2,095	1,850	Sequenom iPlex
United States	192	414	Sequenom iPlex
TOTAL	9,628	12,917	

Supplementary Table 3a. **Cohort specific results for all SNPs listed in Table 1 and Table 2.**
*****SNP selected for follow-up was not the most associated SNP in the final version of the GWAS meta-analysis. FU is risk allele frequency in controls. For GWAS, we included proportional weight given to the study, calculated from empirical variance in the imputed data. Number of cases and controls are respectively given for each component.

This supplementary table is available for download as an Excel file.

Supplementary Table 3b. **Cohort specific results for all SNPs included in follow-up phase, but failed our thresholds for follow-up.**
*****SNP selected for follow-up was not the most associated SNP in the final version of the GWAS meta-analysis. FU is risk allele frequency in controls. For GWAS, we included proportional weight given to the study, calculated from empirical variance in the imputed data.

This supplementary table is available for download as an Excel file.

Supplementary Table 4. **Subphenotype analyses at new ulcerative colitis risk loci.**
Disease location was defined using the Montreal classification system. Surgical intervention is defined as acute severe or medically refractory disease. Individuals receiving colectomy for dysplasia or malignancy were excluded. Cochran-Mantel-Haenszel tests were conducted stratifying by cohort and the Bonferroni significance threshold (0.05/87:P<5.75×10^{-4}) was adopted. Subphenotype data from the Australian, German (Pittsburgh centre), Italian, Dutch, NIDDK, Norwegian, New Zealand, Swedish and WTCCC replication cohorts were included in the analysis.

			P-value		
			E1vsE2E3	E1E2vsE3	Surgical intervention
rs734999	1p36	2.39 - 2.80	6.70E-01	9.94E-01	2.14E-01
rs35675666	1p36	7.83 - 8.13	5.66E-01	9.15E-01	6.88E-01
rs7524102	1p36	22.54 - 22.61	6.07E-01	2.78E-03	9.68E-01
rs7554511	1q32	199.06 - 199.33	NA	NA	NA
rs2310173	2q11	101.66 - 102.13	6.07E-01	2.50E-01	3.07E-02
rs11676348	2q35	218.58 - 218.97	2.62E-01	1.53E-01	9.21E-01
rs267939	5p15	10.72 - 10.90	9.37E-01	9.64E-01	6.62E-02
rs3194051	5p13	35.83 - 36.07	5.09E-01	5.52E-01	8.02E-01
rs6451493*	5p13	40.32 - 40.85	8.20E-01	7.53E-01	6.75E-01
rs254560	5q31	134.41 - 134.53	4.19E-01	5.18E-01	3.86E-01
rs6871626	5q33	158.46 - 158.86	1.66E-01	8.60E-02	5.69E-01
rs943072	6p21	43.88 - 43.92	5.39E-01	7.41E-01	1.41E-01
rs6911490	6q21	106.51 - 106.67	3.96E-01	2.44E-01	4.83E-02
rs6920220	6q23	137.88 - 138.17	4.78E-01	7.46E-01	6.22E-01
rs798502	7p22	2.70 - 2.90	1.57E-01	6.06E-01	8.08E-01
rs4728142	7q32	128.33-128.56	8.96E-01	8.42E-01	8.44E-01
rs10758669	9p24	4.93 - 5.28	8.55E-01	1.15E-01	8.64E-01
rs4246905	9q32	116.48 - 116.74	6.51E-01	2.32E-01	1.68E-01
rs10781499	9q34	138.27 - 138.55	1.55E-03	1.95E-02	7.73E-03
rs12261843	10p11	35.22 - 35.94	5.19E-01	5.29E-01	4.20E-01
rs907611	11q15	1.82 - 1.93	3.08E-01	1.28E-01	6.18E-01
rs2155219	11q13	75.72 - 76.02	4.75E-01	2.59E-01	1.91E-01
rs678170	11q23	113.76 - 114.08	8.63E-01	3.53E-01	8.15E-01
rs17085007	13q12	26.39 - 26.46	4.81E-01	8.74E-02	1.79E-01
rs941823	13q13	39.90 - 39.95	4.24E-01	6.95E-01	2.70E-01
rs16940202	16q24	84.53 - 84.58	9.55E-01	9.12E-02	1.69E-01
rs2297441	20q13	61.66 - 61.98	9.25E-01	6.53E-01	5.97E-01
rs1297265	21q11	15.62 - 15.77	3.30E-01	5.46E-01	2.64E-01
rs2838519	21q22	44.41 - 44.52	NA	NA	NA

Supplementary Table 5. Ulcerative colitis risk variants correlated with eQTL.

SNP	Chr	SNP Position (bp)	Probe center position (bp)	Illumina ArrayAddressID	Expression dataset	Gene	eQTL p-value
Loci that achieved genome-wide significance (P-value<5.0x10-8) in this study							
rs734999	1	2503076	2482955	6520725	HT-12 + Ref-8v2	*TNFRSF14*	1.04E-23
rs734999	1	2503076	2533115	2070246	HT-12 + Ref-8v2	*MMEL1*	1.25E-15
rs734999	1	2503076	2412221	650452	HT-12	*PLCH2*	1.04E-04
rs734999	1	2503076	2510429	6250338	Ref-8v2	*C1orf93*	1.24E-04
rs11676348	2	218718391	218737887	3440669	HT-12 + Ref-8v2	*IL8RA*	1.28E-30
rs11676348	2	218718391	218962428	780465	HT-12 + Ref-8v2	*SLC11A1*	9.39E-14
rs11676348	2	218718391	218704605	2900327	HT-12	*IL8RB*	1.07E-10
rs11676348	2	218718391	218838153	2940068	HT-12 + Ref-8v2	*AAMP*	2.04E-10
rs11676348	2	218718391	218704605	2710437	Ref-8v2	*IL8RB*	4.66E-09
rs11676348	2	218718391	218838153	5560079	HT-12	*AAMP*	2.74E-08
rs11676348	2	218718391	218808721	7160327	HT-12 + Ref-8v2	*ARPC2*	1.60E-04
rs2310173	2	102030060	101993025	1740451	HT-12 + Ref-8v2	*IL1R2*	1.53E-04
rs267939	5	10805315	10773346	2710491	HT-12	*DAP*	2.59E-12
rs267939	5	10805315	10773346	3460201	Ref-8v2	*DAP*	3.52E-06
rs3194051	5	35912031	35902713	3830349	HT-12	*IL7R*	3.74E-03
rs798502	7	2756406	2792378	670082	HT-12	*GNA12*	1.13E-26
rs798502	7	2756406	2792378	4070259	HT-12	*GNA12*	2.19E-06
rs798502	7	2756406	2792378	7150465	HT-12 + Ref-8v2	*GNA12*	5.15E-05
rs4728142	7	128361203	128371275	2230431	HT-12 + Ref-8v2	*IRF5*	1,31E-87
rs4728142	7	128361203	128371275	4260373	HT-12 + Ref-8v2	*IRF5*	1,30E-85
rs4728142	7	128361203	128432309	3360241	HT-12 + Ref-8v2	*TNPO3*	2,40E-35
rs4728142	7	128361203	128432309	6650730	Ref-8v2	*TNPO3*	3,98E-05
rs10781499	9	138386226	138380104	3060494	HT-12 + Ref-8v2	*CARD9*	3.08E-112
rs10781499	9	138386226	138448486	3370255	HT-12 + Ref-8v2	*INPP5E*	7.84E-71
rs10781499	9	138386226	138420539	60706	HT-12	*SDCCAG3*	5.08E-09
rs10781499	9	138386226	138460826	2600343	HT-12	*INPP5E///SEC16A*	4.38E-06
rs10781499	9	138386226	138420539	7040553	HT-12 + Ref-8v2	*SDCCAG3*	1.84E-03
rs10781499	9	138386226	138401461	2070195	HT-12 + Ref-8v2	*SNAPC4*	2.27E-03
rs4246905	9	116593070	116718768	1240209	HT-12 + Ref-8v2	*TNFSF8*	1.77E-13
rs12261843	10	35594060	35738408	5310605	HT-12	*CCNY*	9.20E-04
rs907611	11	1830648	1850422	5720192	Ref-8v2	*LSP1*	1.12E-03
rs907611	11	1830648	1850422	4180068	HT-12	*LSP1*	3.45E-03
rs2297441	20	61798026	61841706	6420450	HT-12	*SLC2A4RG*	7.91E-41
rs2297441	20	61798026	61748369	4260379	Ref-8v2	*STMN3*	2.27E-09
rs2297441	20	61798026	61866501	7040521	HT-12 + Ref-8v2	*SLC2A4RG/ZBTB46*	2.15E-03
rs2297441	20	61798026	61831773	5490390	HT-12 + Ref-8v2	*ZGPAT*	2.54E-03

SNP	Chr	SNP Position (bp)	Probe center position (bp)	Illumina ArrayAddressID	Expression dataset	Gene	eQTL p-value
Loci that achieved genome-wide significance (P-value<5x10-8) in previous studies							
rs1801274	1	159746369	159907075	6650341	HT-12 + Ref-8v2	*FCGR2B*	9.55E-09
rs1801274	1	159746369	159907075	2480717	HT-12	*FCGR2B*	1.65E-05
rs1801274	1	159746369	159748914	450762	HT-12	*FCGR2A*	2.44E-04
rs1801274	1	159746369	159907075	7550215	HT-12	*FCGR2B*	7.12E-04
rs1801274	1	159746369	159761982	160092	HT-12 + Ref-8v2	*HSPA6*	3.83E-03
rs1801274	1	159746369	159802528	1710553	HT-12 + Ref-8v2	*HSPA6*	5.33E-03
rs9822268	3	49694733	49819298	2850202	HT-12 + Ref-8v2	*UBA7*	3,88E-43
rs9822268	3	49694733	49694969	450475	HT-12 + Ref-8v2	*MST1/APEH*	6,76E-09
rs9822268	3	49694733	49728648	6020228	HT-12 + Ref-8v2	*RNF123/AMIGO3/GMPPB*	1,22E-03
rs11739663	5	647083	508370	4730682	HT-12 + Ref-8v2	*EXOC3*	3.76E-04
rs9268853	6	32537621	32768214	780403	HT-12	*HLA-DQA1/HLA-DQA2*	2.91E-37
rs9268853	6	32537621	32599600	6370315	HT-12 + Ref-8v2	*HLA-DRB5*	9.24E-30
rs9268853	6	32537621	32518213	2570564	HT-12	*HLA-DRA*	1.18E-12
rs9268853	6	32537621	32660052	5260484	HT-12 + Ref-8v2	*HLA-DRB1*	2.07E-08
rs9268853	6	32537621	32627630	2070608	HT-12	*HLA-DRB5/HLA-DRB1*	5.04E-08
rs6499188	16	67232289	67144627	5900286	HT-12 + Ref-8v2	*ZFP90*	2,63E-117
rs2872507	17	35294289	35321401	6270615	HT-12 + Ref-8v2	*GSDMB*	2.72E-189
rs2872507	17	35294289	35321401	5390608	HT-12	*GSDMB*	1.26E-77
rs2872507	17	35294289	35334101	1500112	HT-12 + Ref-8v2	*ORMDL3*	3.97E-68
rs2872507	17	35294289	35224345	6380411	HT-12	*IKZF3*	1.53E-11
rs2872507	17	35294289	35084188	2000441	HT-12 + Ref-8v2	*PNMT/PERLD1*	2.10E-10
rs6017342	20	42498442	42571209	7380139	Ref-8v2	*SERINC3*	8.92E-05
rs2838519	21	44439451	44444959	150484	HT-12	-	1.04E-03
rs5771069	22	48777607	48741943	2190452	HT-12 + Ref-8v2	*PIM3*	1.42E-11
rs5771069	22	48777607	48956068	4070300	HT-12 + Ref-8v2	*PANX2*	1.01E-07

Supplementary Table 6. Ulcerative colitis risk variants correlated (r^2>0.5) with non-synonymous and splice-site disrupting SNPs.
Data taken from 1000 Genomes Project March 2010 release (ftp://ftp.sanger.ac.uk/pub/1000genomes/REL-1005/QCALL/).

Lead SNP				Non-synonymous/Splice SNP					
CHR	dbSNP ID	POS (dbSNP 130)	RAF	dbSNP ID	POS (dbSNP 130)	Distance to lead SNP (bp)	r^2	Gene	Amino acid substitution
1p36	rs734999	2503076	C - 0.531	rs3748816	2516606	13530	0.55	*MMEL1*	M518T
1p36	rs35675666	7944560	G - 0.829	rs13306061	7836032	108528	0.52	*UTS2*	R16Q
1p36	rs35675666	7944560	G - 0.829	rs34305100	7835616	108944	0.52	*UTS2*	I12T
5p13	rs3194051	35912031	G - 0.267		SAME			*IL7R*	I356V
7p22	rs798502	2756406	A - 0.710	rs798488	2769048	12642	0.87	*GNA12*	M1V
7p22	rs798502	2756406	A - 0.710	rs2644275	2820536	64130	0.55	*GNA12*	T23I
9q32	rs4246905	116593070	C - 0.715		SAME			*TNFSF15*	H3R
9q34	rs10781499	138386226	A - 0.425	rs4077515	138386317	91	1.00	*CARD9*	S12N
9q34	rs10781499	138386226	A - 0.425	rs3812571	138395115	8889	0.69	*SNAPC4*	H799Q
20q13	rs2297441	61798026	A - 0.768	rs3208008	61796554	1472	1.00	*RTEL1*	Q1042H
20q13	rs2297441	61798026	A - 0.768	rs2257440	61798711	685	0.95	*RTEL1*	R1352C
1p31	rs11209026	67478546	G - 0.935		SAME			IL23R	R381Q
1q23	rs1801274	159746369	A - 0.506		SAME			FCGR2A	H167R
3p21	rs3197999	49696536	A - 0.298		SAME			*MST1*	R689C
3p21	rs3197999	49696536	A - 0.298	rs34762726	49664214	32322	0.90	*BSN*	A741T
6p21	rs9268853	32537621	T - 0.661	rs2076523	32478813	58808	0.57	*BTNL2*	K196E
6p21	rs9268853	32537621	T - 0.661	rs34624872	32656606	118985	0.54	*HLA-DRB1*	R220W
6p21	rs9268853	32537621	T - 0.661	rs1059352	32657503	119882	0.56	*HLA-DRB1*	G154A
6p21	rs9268853	32537621	T - 0.661	rs29029549	32659906	122285	0.68	*HLA-DRB1*	H110Y
6p21	rs9268853	32537621	T - 0.661	rs1047989	32713235	175614	0.53	*HLA-DQA1*	L8M
6p21	rs9268853	32537621	T - 0.661	rs1142333	32717242	179621	0.52	*HLA-DQA1*	R87T
6p21	rs9268853	32537621	T - 0.661	rs1064944	32717277	179656	0.54	*HLA-DQA1*	M99L/V
6p21	rs9268853	32537621	T - 0.661	rs2308891	32717987	180366	0.55	*HLA-DQA1*	Q198K/E
6p21	rs9268853	32537621	T - 0.661	rs9272774	32718233	180612	0.58	*HLA-DQA1*	SPLICE
17q12	rs2872507	35294289	A - 0.462	rs11557467	35282160	12129	0.84	*ZPBP2*	S151I
17q12	rs2872507	35294289	A - 0.462	rs2305480	35315722	21433	1.00	*GSDMB*	P243S
17q12	rs2872507	35294289	A - 0.462	rs2305479	35315743	21454	0.91	*GSDMB*	G282R
17q12	rs2872507	35294289	A - 0.462	rs11078928	35317995	23706	1.00	*GSDMB*	SPLICE
22q13	rs5771069	48777607	G - 0.505		SAME			*IL17REL*	L333P
22q13	rs5771069	48777607	G - 0.505	rs9617090	48781321	3714	0.80	*IL17REL*	G70R

Supplementary Table 7. **Summary of candidate genes mapping from *in silico* analysis on the 47 UC loci.**
GRAIL results, based on HapMap release 21, are presented if a gene had a P<0.01 and resides within the association boundaries. eQTL analyses were based on the Dubois *et al.* dataset[11] (see **Online Methods**). Positional candidate denotes the gene in which the SNP resides. Regional association plots are shown in **Supplementary Figure 2** and study-specific results are shown in **Supplementary Table 3a**. **Supplementary Tables 4 and 5** contain detailed eQTL and non-synonymous SNP results, respectively.

This supplementary table is available for download as an Excel file.

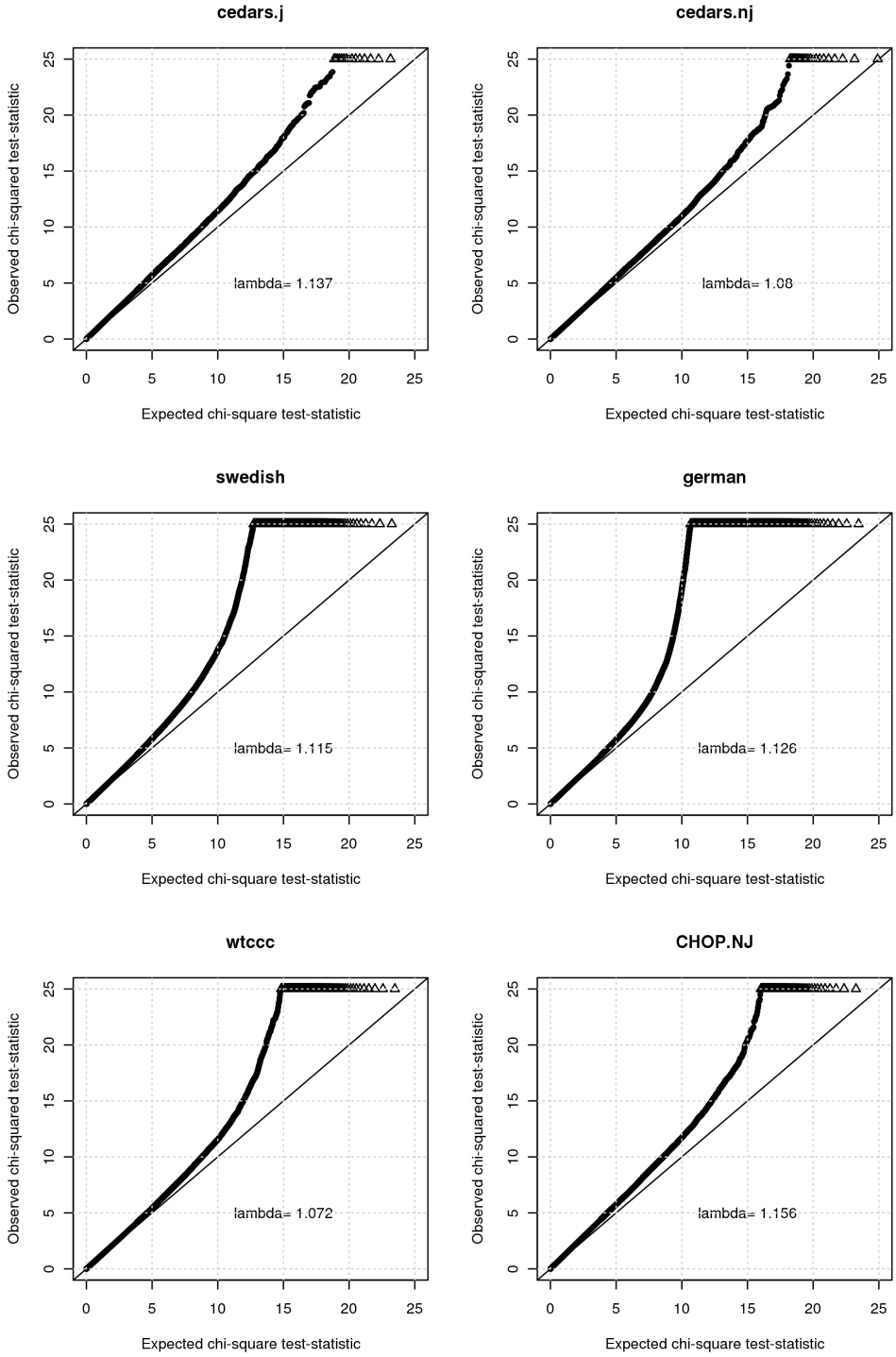
Supplementary Table 8. Results from a functional enrichment analysis across all loci associated with UC susceptibility
(see **Supplementary Figure 3**).

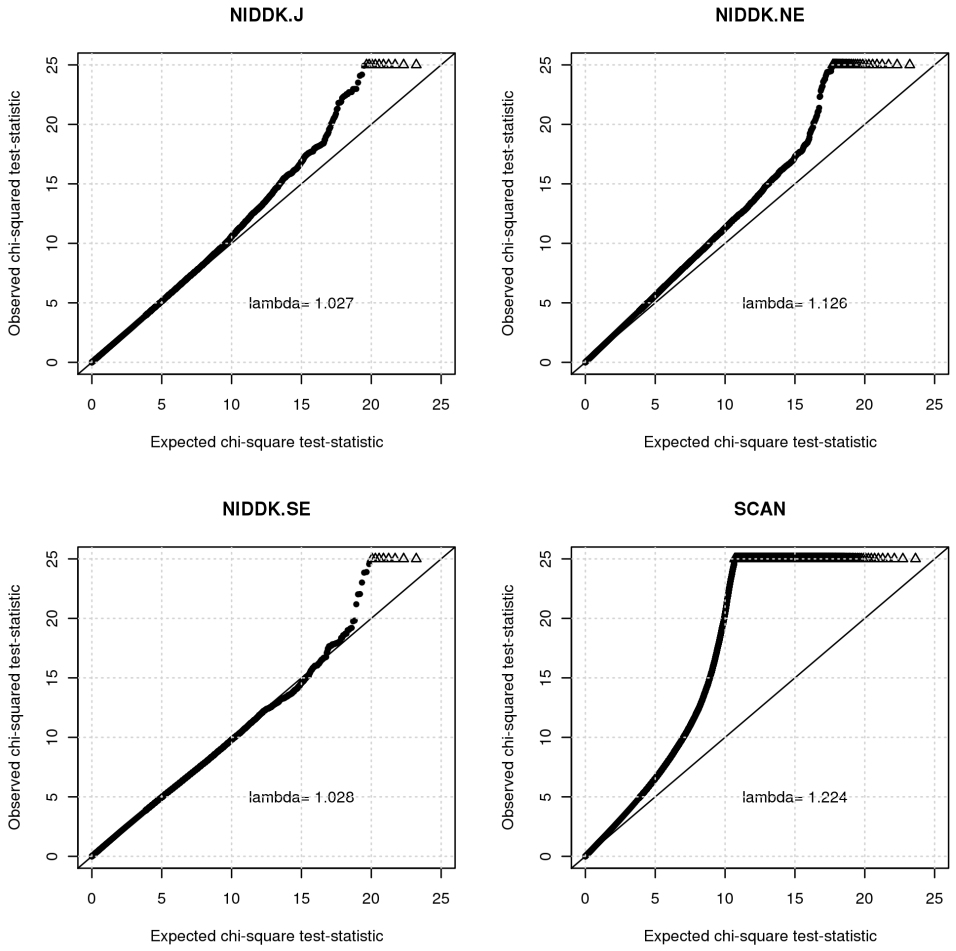
Annotated gene sets (featured in enrichment network map)	p	Candidate genes
MSigDB|HSA04060_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	2.91E-10	*CSF3, IFNG, IL10, IL12B, IL19, IL1R1, IL1R2, IL2, IL20, IL21, IL22, IL23R, IL26, IL7R, TNFRSF14, TNFRSF6B, TNFRSF9, TNFSF15, TNFSF8*
GO_MF|IgG binding	4.72E-09	*FCGR2A, FCGR2B, FCGR3A, FCGR3B, FCGR2C*
GO_MF|cytokine activity	4.21E-08	*TNFSF8, CSF3, IFNG, IL2, IL10, IL12B, TNFSF15, IL19, IL20, IL22, IL26, IL21*
MSigDB|HSA04630_JAK_STAT_SIGNALING_PATHWAY	6.79E-08	*CSF3, IFNG, IL10, IL12B, IL19, IL2, IL20, IL21, IL22, IL23R, IL26, IL7R, JAK2*
MSigDB|INFLAMPATHWAY	3.43E-05	*CSF3, IFNG, IL10, IL12B, IL2*
MSigDB|IL18PATHWAY	4.47E-05	*IFNG, IL12B, IL2*
Pnthr_BP|macrophage activation	5.32E-05	*FCGR3B, IL12B, TNFRSF9, IFNG, FCGR2A, FCGR2B, AAMP, IL20, TNFRSF14, IL10, FCGR3A, IL19, TNFSF15*
GO_BP|positive regulation of activated T cell proliferation	1.06E-04	*IL2, IL12B, ICOSLG*
MSigDB|CYTOKINEPATHWAY	1.21E-04	*IFNG, IL10, IL12B, IL2*
MSigDB|ST_INTERFERON_GAMMA_PATHWAY	1.82E-04	*IFNG, JAK2, PLA2G2A*
Pnthr_BP|response to stimulus	3.45E-04	*FCGR3B, NR1D1, IL23R, IL12B, XPO1, TNFRSF9, ICOSLG, IFNG, GPR35, IL2, PNKD, ADAD1, FCGR2A, SLC11A1, CRKRS, MAPKAPK2, PRKAA1, IL8RB, REL, PARK7, FCGR2B, AAMP, CSF3, IL1R1, AHSA2, IL20, TNFRSF14, CREM, IRF5, IL10, FCGR3A, IL19, TNFSF15, JAK2, HSPA6*
Pnthr_BP|natural killer cell activation	3.52E-04	*FCGR3B, IL12B, IFNG, FCGR2A, FCGR2B, FCGR3A, TNFSF15*
GO_BP|positive regulation of cytokine secretion	3.89E-04	*IL10, TNFSF15, IL26*
Pnthr_BP|immune response	3.98E-04	*FCGR3B, IL12B, IL23R, XPO1, TNFRSF9, ADAD1, IFNG, FCGR2A, IL8RB, FCGR2B, REL, IL20, CSF3, TNFRSF14, IRF5, IL10, FCGR3A, IL19, TNFSF15*
MSigDB|NO2IL12PATHWAY	9.32E-04	*IFNG, IL12B, JAK2*
Pnthr_BP|B cell mediated immunity	1.03E-03	*FCGR3B, IL23R, XPO1, TNFRSF9, FCGR2A, REL, FCGR2B, TNFRSF14, FCGR3A, TNFSF15*
GO_BP|positive regulation of cell adhesion	1.09E-03	*ERBB2, IFNG, IL12B*
MSigDB|TH1TH2PATHWAY	1.37E-03	*IFNG, IL12B, IL2*
MSigDB|41BBPATHWAY	1.62E-03	*IFNG, IL2, TNFRSF9*
MSigDB|DCPATHWAY	2.57E-03	*IFNG, IL10, IL12B*
MSigDB|IL12PATHWAY	2.95E-03	*IFNG, IL12B, JAK2*
MSigDB|NKTPATHWAY	5.93E-03	*IFNG, IL12B, IL2*
Pnthr_BP|response to interferon-gamma	8.50E-03	*IL12B, IFNG, ADAD1, IRF5, TNFSF15*
MSigDB|HSA04940_TYPE_I_DIABETES_MELLITUS	1.94E-02	*IFNG, IL12B, IL2*
Pnthr_BP|cell-cell signaling	2.62E-02	*ERBB2, NOTCH1, CACNA1S, UTS2, INSL4, IL12B, NR1D1, IL23R, SMPD3, TNFRSF9, IFNG, GPR25, IL2, MAPKAPK2, CRELD2, IL20, CSF3, GPSM1, TNFRSF14, IL10, IL19, TNFSF15, JAK2*
MSigDB|CALCINEURIN_NF_AT_SIGNALING	3.41E-02	*FCGR3A, IFNG, IL10, IL2*

Supplementary Table 9. **Results from the International IBD Genetics Consortium CD and UC meta-analyses for the 99 loci reported for association in CD and/or UC.**
All 99 loci reported as reaching $P < 5\times10^{-8}$ in either CD and/or UC (follow-up included, data not shown here) are listed. From those loci, 71 are reported in CD and 47 are reported in UC, including an overlap of 19 loci reported in both studies. The overlapping loci between both diseases are those with overlapping physical intervals. For those 19 loci showing association signal at genome-wide significance in both CD and UC, the best index SNP in each scan is provided if these differ. The r^2 and D' between the two index SNPs is listed under the CD SNP. FU gives the allele frequency in controls while LB95 and UB95 respectively gives lower and upper bound of the 95% confidence interval on OR.

This supplementary table is available for download as an Excel file.

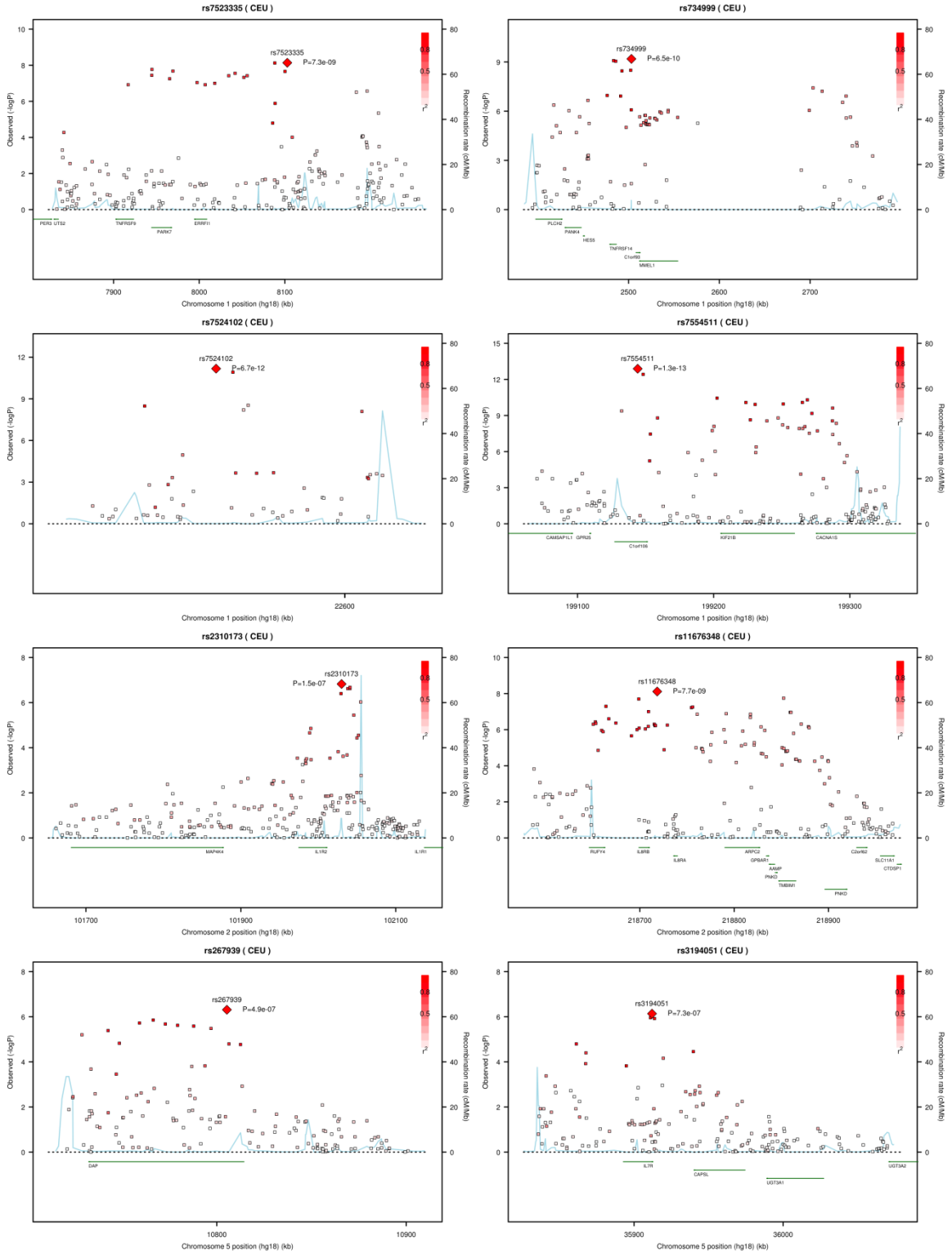
Supplementary Figure 1. Quantile-Quantile plots of observed vs. expected chi-square statistics for the nine constituent genome-wide scans and the meta-analysis (SCAN). For a detailed description of the GWAS cohorts see **Supplementary Table 1**. SNPs with an observed test-statistic greater than 25 are represented by triangles at the top of each plot.

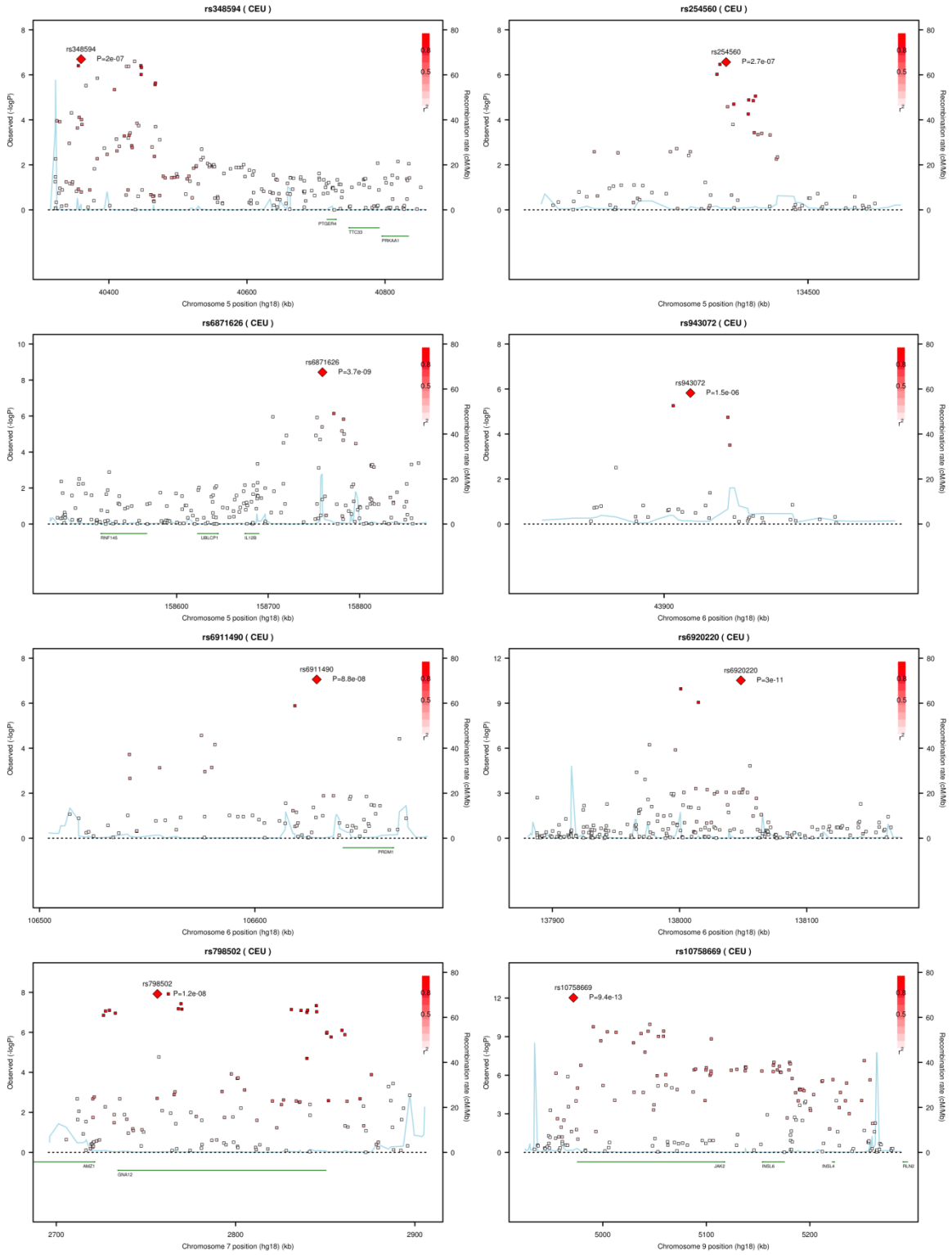


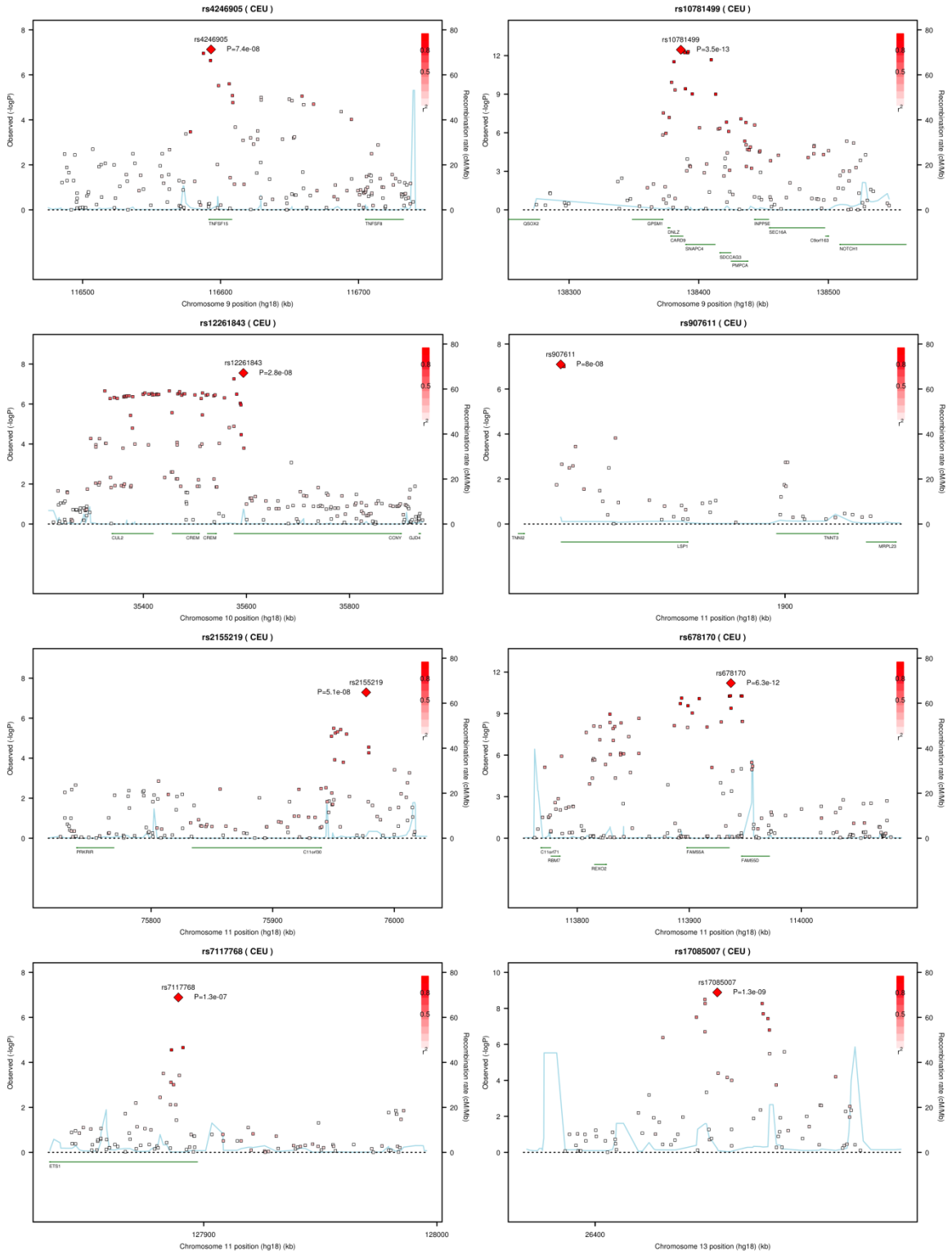

NIDDK.J
lambda= 1.027
NIDDK.NE
lambda= 1.126
NIDDK.SE
lambda= 1.028
SCAN
lambda= 1.224
Observed chi-squared test-statistic
Expected chi-square test-statistic
0
5
10
15
20
25

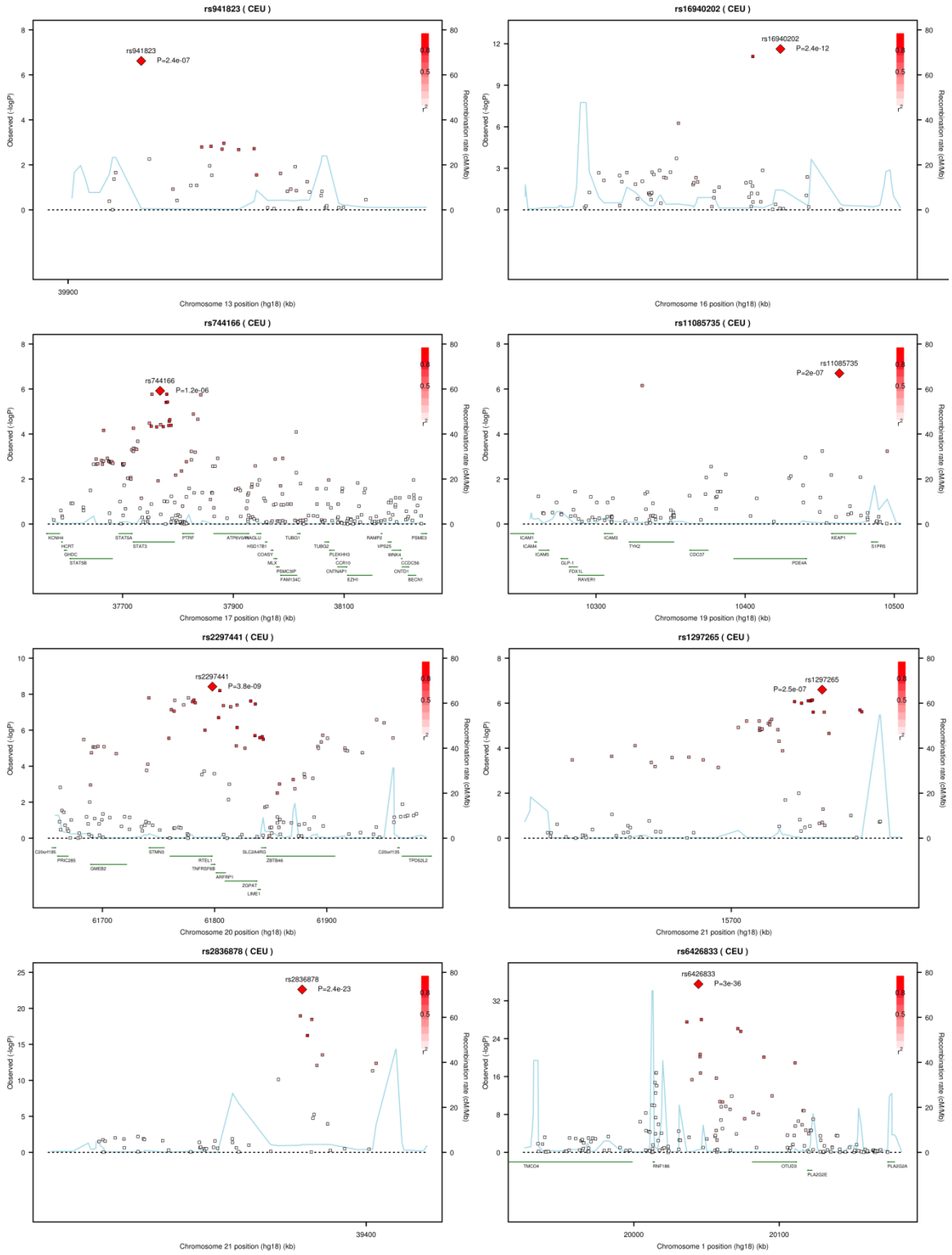
Supplementary Figure 2. Locus wide association plots for all 47 UC loci, generated using SNAP[39].

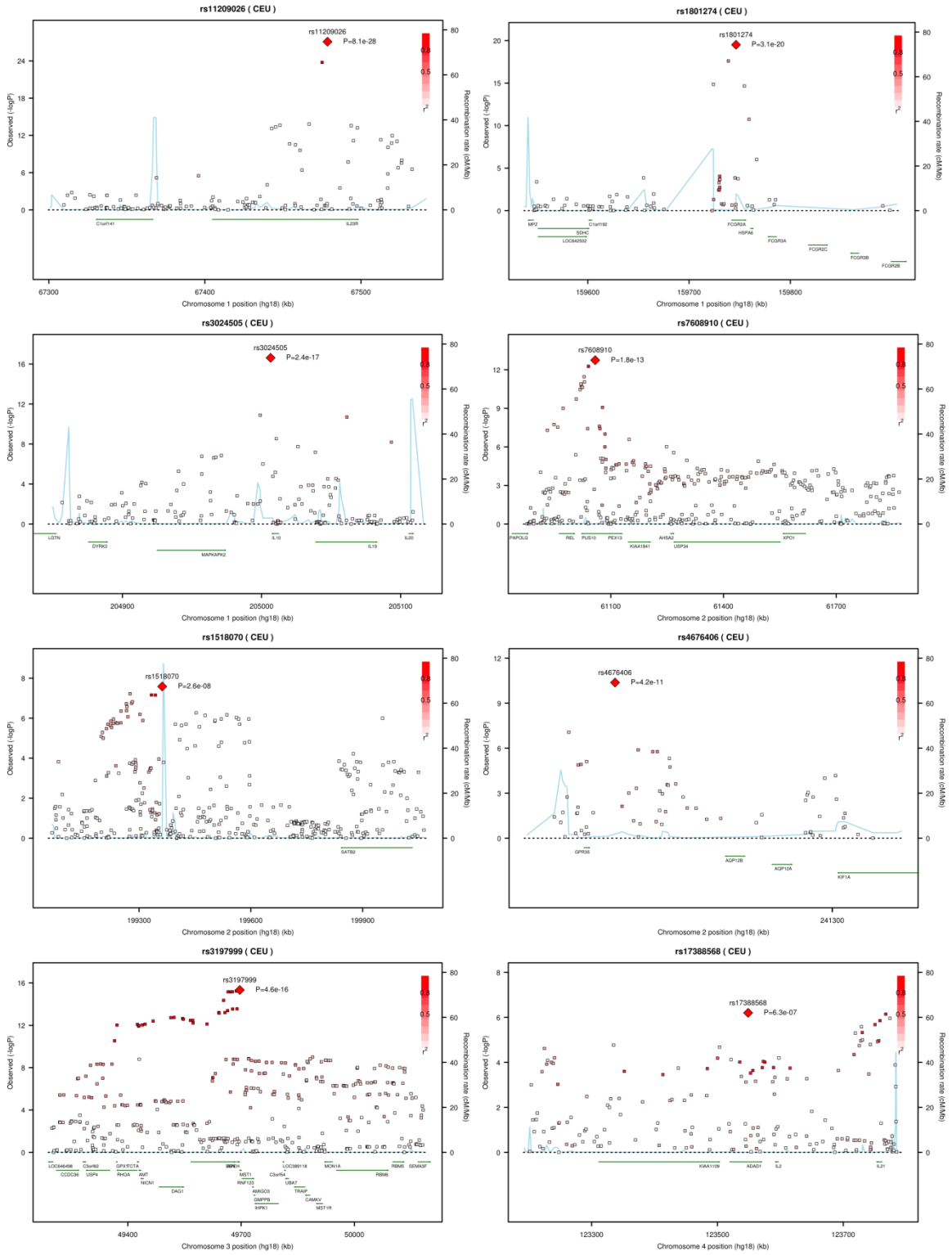
Where the locus is greater than 1Mb we show 500Kb either side of the most associated SNP. P-values are given for the meta-analysis only.

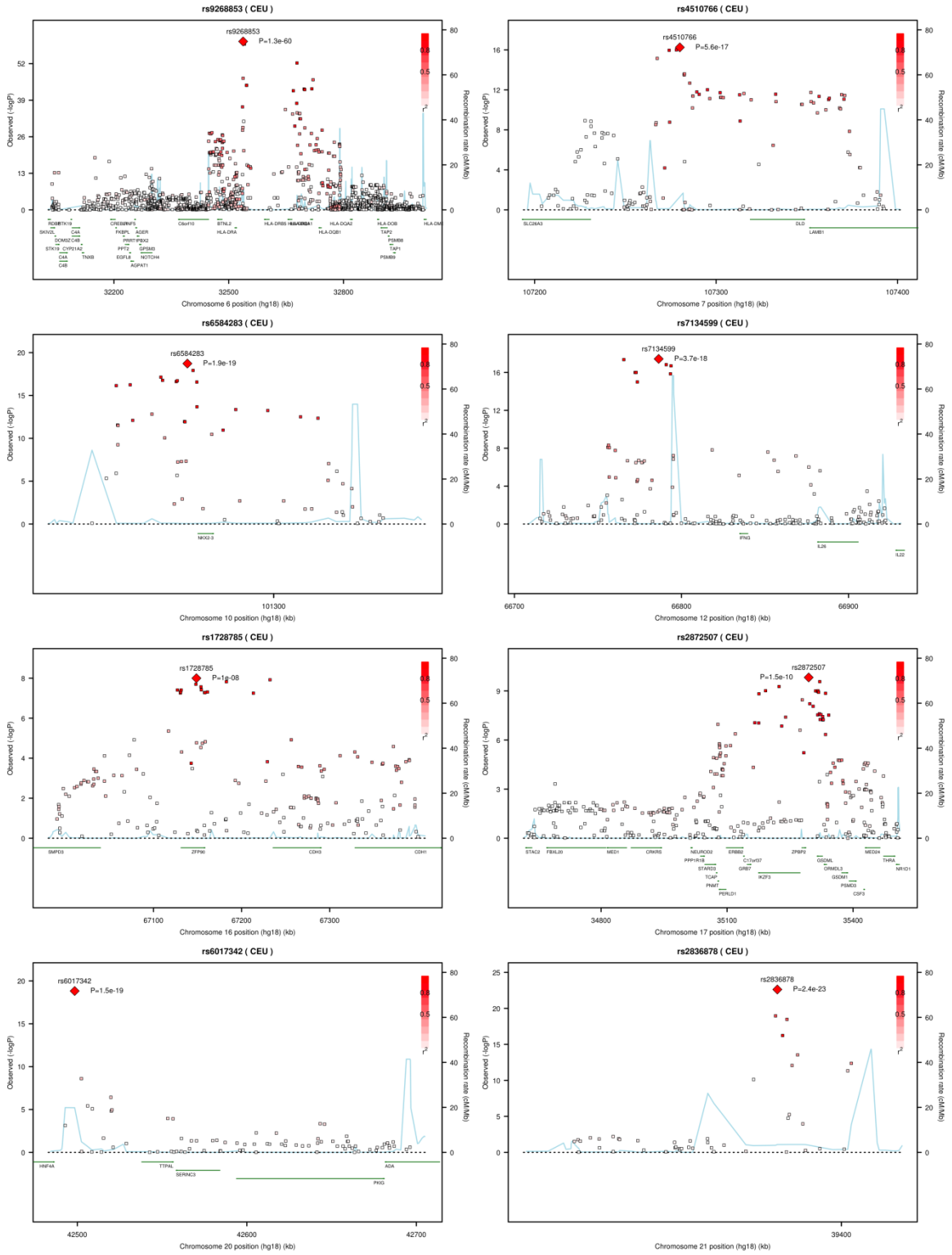


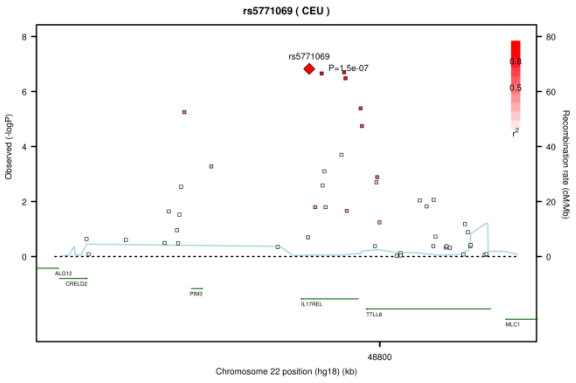

rs348594 (CEU)
rs348594
P=2e-07
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 5 position (hg18) (kb)
rs254560 (CEU)
rs254560
P=2.7e-07
rs6871626 (CEU)
rs6871626
P=3.7e-09
rs943072 (CEU)
rs943072
P=1.5e-06
Chromosome 6 position (hg18) (kb)
rs6911490 (CEU)
rs6911490
P=8.8e-08
rs6920220 (CEU)
rs6920220
P=3e-11
rs798502 (CEU)
rs798502
P=1.2e-08
Chromosome 7 position (hg18) (kb)
rs10758669 (CEU)
rs10758669
P=9.4e-13
Chromosome 9 position (hg18) (kb)

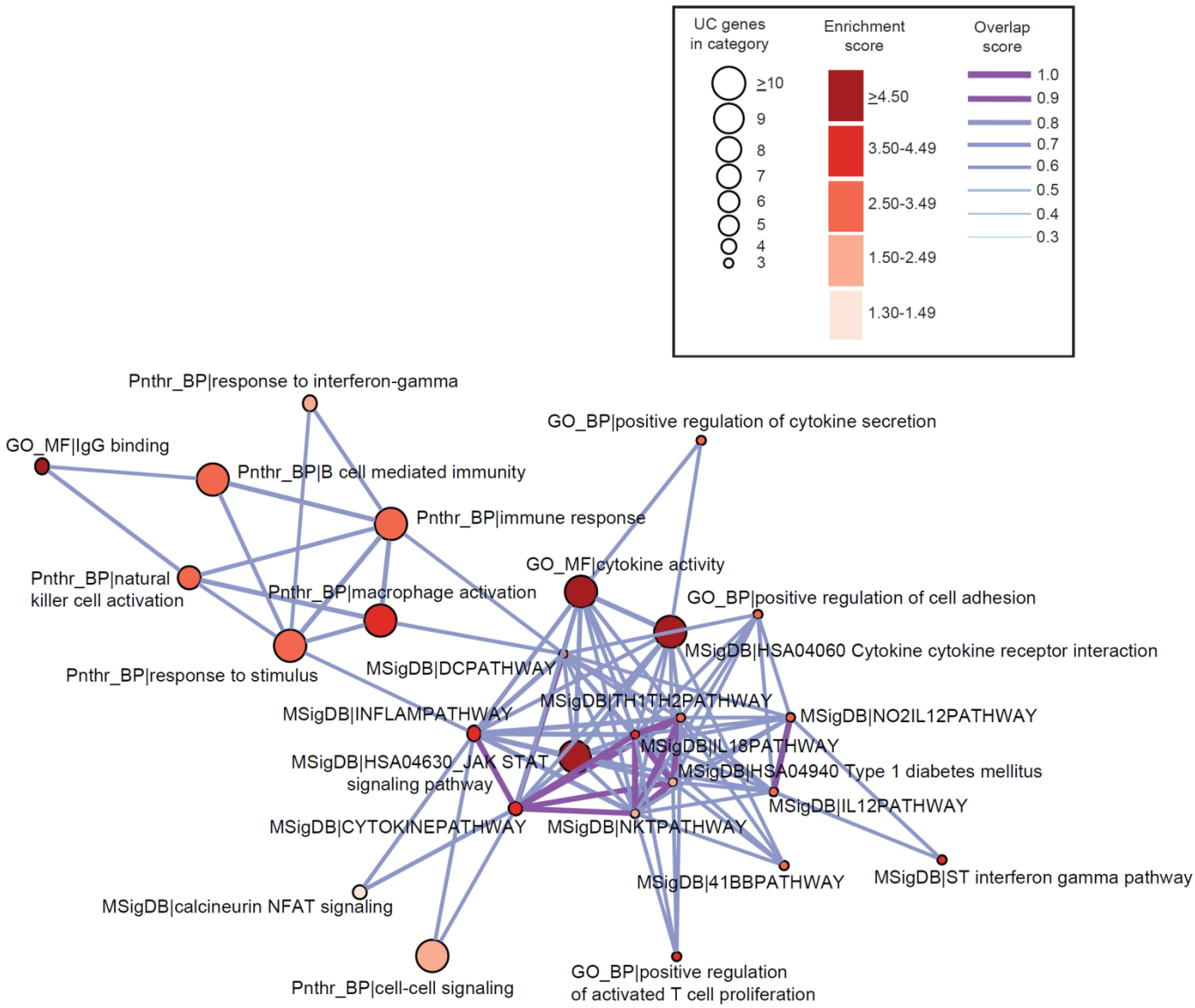

rs4246905 (CEU)
rs4246905
P=7.4e-08
rs10781499 (CEU)
rs10781499
P=3.5e-13
rs12261843 (CEU)
rs12261843
P=2.8e-08
rs907611 (CEU)
rs907611
P=8e-08
rs2155219 (CEU)
rs2155219
P=5.1e-08
rs678170 (CEU)
rs678170
P=6.3e-12
rs7117768 (CEU)
rs7117768
P=1.3e-07
rs17085007 (CEU)
rs17085007
P=1.3e-09
Observed (-logP)
Conditional (-logP)
Recombination rate (cM/Mb)
Chromosome 9 position (hg18) (kb)
Chromosome 10 position (hg18) (kb)
Chromosome 11 position (hg18) (kb)
Chromosome 13 position (hg18) (kb)


rs941823 (CEU)
rs941823
P=2.4e-07
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 13 position (hg18) (kb)
rs16940202 (CEU)
rs16940202
P=2.4e-12
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 16 position (hg18) (kb)
rs744166 (CEU)
rs744166
P=1.2e-06
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 17 position (hg18) (kb)
rs11085735 (CEU)
rs11085735
P=2e-07
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 19 position (hg18) (kb)
rs2297441 (CEU)
rs2297441
P=3.8e-09
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 20 position (hg18) (kb)
rs1297265 (CEU)
rs1297265
P=2.5e-07
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 21 position (hg18) (kb)
rs2836878 (CEU)
rs2836878
P=2.4e-23
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 21 position (hg18) (kb)
rs6426833 (CEU)
rs6426833
P=3e-36
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 1 position (hg18) (kb)


rs11209026 (CEU)
rs11209026
P=8.1e-28
rs1801274 (CEU)
rs1801274
P=3.1e-20
rs3024505 (CEU)
rs3024505
P=2.4e-17
rs7608910 (CEU)
rs7608910
P=1.8e-13
rs1518070 (CEU)
rs1518070
P=2.6e-08
rs4676406 (CEU)
rs4676406
P=4.2e-11
rs3197999 (CEU)
rs3197999
P=4.6e-16
rs17388568 (CEU)
rs17388568
P=6.3e-07
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 1 position (hg18) (kb)
Chromosome 2 position (hg18) (kb)
Chromosome 3 position (hg18) (kb)
Chromosome 4 position (hg18) (kb)


rs9268853 (CEU)
rs9268853
P=1.3e-60
Observed (-logP)
Recombination rate (cM/Mb)
Chromosome 6 position (hg18) (kb)
rs4510766 (CEU)
rs4510766
P=5.6e-17
Chromosome 7 position (hg18) (kb)
rs6584283 (CEU)
rs6584283
P=1.9e-19
Chromosome 10 position (hg18) (kb)
rs7134599 (CEU)
rs7134599
P=3.7e-18
Chromosome 12 position (hg18) (kb)
rs1728785 (CEU)
rs1728785
P=1e-08
Chromosome 16 position (hg18) (kb)
rs2872507 (CEU)
rs2872507
P=1.5e-10
Chromosome 17 position (hg18) (kb)
rs6017342 (CEU)
rs6017342
P=1.5e-19
Chromosome 20 position (hg18) (kb)
rs2836878 (CEU)
rs2836878
P=2.4e-23
Chromosome 21 position (hg18) (kb)


rs5771069 (CEU)
rs5771069
P=1.5e-07
Observed (-logP)
Recombination rate (cM/Mb)
r²
ALG12
CRELD2
PIM3
IL17REL
TTLL8
MLC1
48800
Chromosome 22 position (hg18) (kb)



Supplementary Figure 3. Enrichment of biological functions for genes located in the associated UC risk loci.

This visual map abstracts the extent of mutual overlap between gene sets and identifies a cluster of strongly connected gene sets that are enriched among genes in UC-associated regions. Nodes denote enriched gene sets or "annotation terms/categories" (assembled from GO-BP, GO-MF, Panther-BP, Panther-MF, Panther-pathways, MSigDB collection of canonical pathways which includes KEGG, BioCarta, STKE, Genmapp). Node size corresponds to the number of UC genes in each gene set (Please see Supplementary Table 8 for list of UC genes in the annotated gene sets). Node color denotes the gene set enrichment score (-Log10 (p-value)). Please refer to graphical legend (boxed) in figure. All gene sets shown are significantly enriched ($p<0.05$). The extent of mutually overlapping genes between gene sets is represented by thickness & color intensity of edges connecting nodes. The overlap score is the average of the Jaccard and Overlap coefficients. Strongly connected network components were identified using Tarjan's algorithm. With this representation, we have observed a strong enrichment signal for cytokine signaling / *JAK-STAT* / immune response-associated processes and pathways for the set of genes in the UC-associated regions.