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Supplemental Data

Combined Analysis of Genome-wide Association Studies for Crohn's Disease and Psoriasis Identifies Seven Shared Susceptibility Loci

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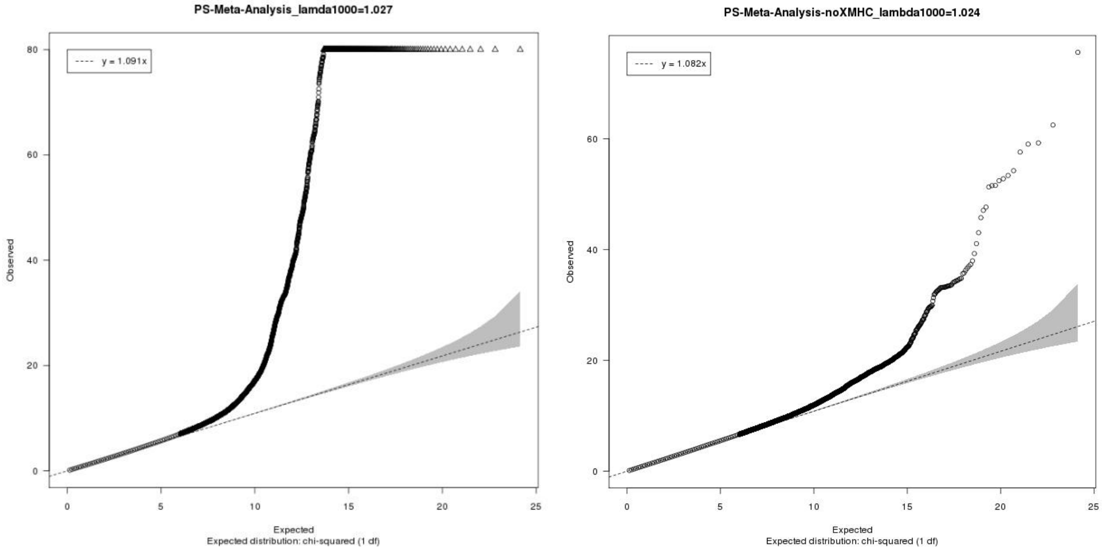
(A)



(B)

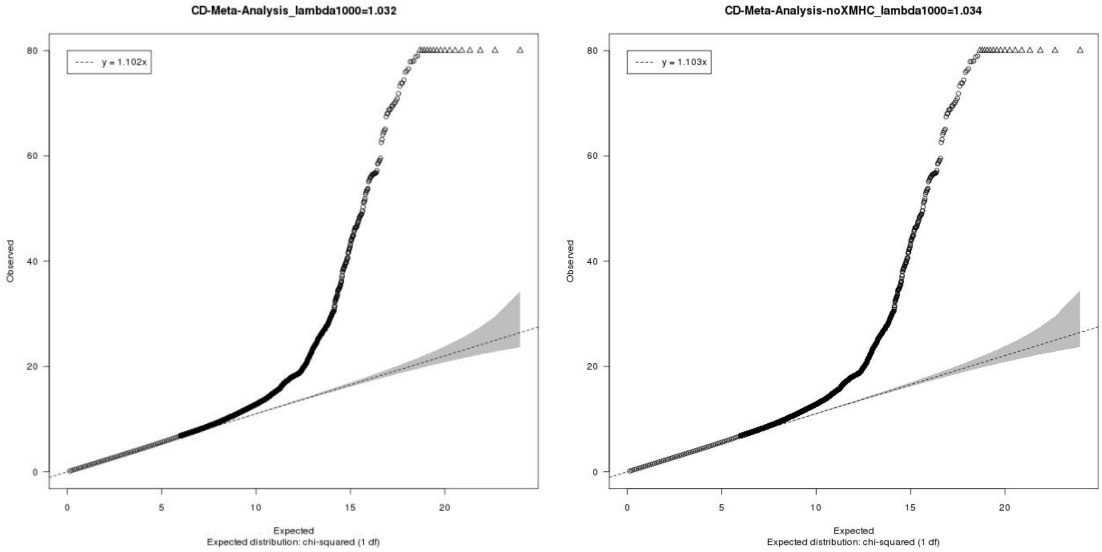


Figure S1. Quantile-Quantile Plots for the Discovery Panels A and B

Only markers that passed the quality criteria were used for plotting. The 2.5th and 97.5th centiles of the distribution under random sampling and the null hypothesis form the 95% concentration band. (A) genome-wide meta-analysis on PS (panel A); first plot of the association test statistics was calculated under inclusion of all SNPs within the extended HLA region (Chr6:25-34Mb), λ_{1000}=1.027. Second plot was calculated under exclusion of all SNPs within the extended HLA region, λ_{1000}=1.024. (B) genome-wide meta-analysis on CD (panel

B); first plot of the association test statistics was calculated under inclusion of all SNPs within the extended HLA region (Chr6:25-34Mb), λ_{1000}=1.032. Second plot was calculated under exclusion of all SNPs within the extended HLA region, λ_{1000}=1.034.

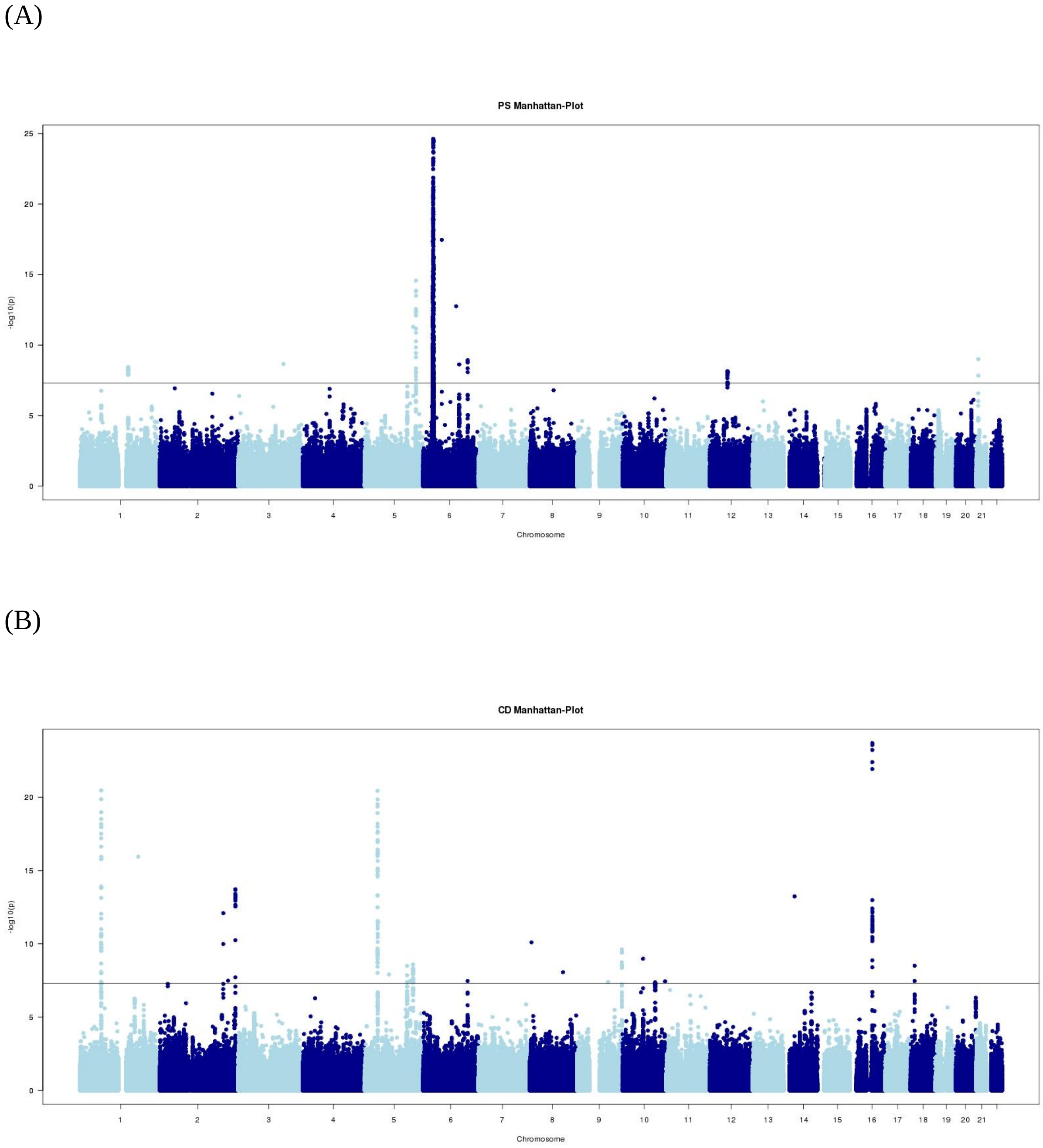


Figure S2. Results of the Genome-Wide Meta-Analysis in Discovery Panels A and B

For each marker,–$\log_{10}P$ for phenotypic association is depicted with regard to the physical location of that marker ("Manhattan plot"). Only markers that passed the quality criteria were used for plotting. Black horizontal line indicates a genome-wide significance threshold of 5×10^{-8}. (A): PS (panel A); Association signals from the extended HLA region (Chr6:25-34Mb) were truncated at the 1×10^{-25} level. (B): CD (panel B).

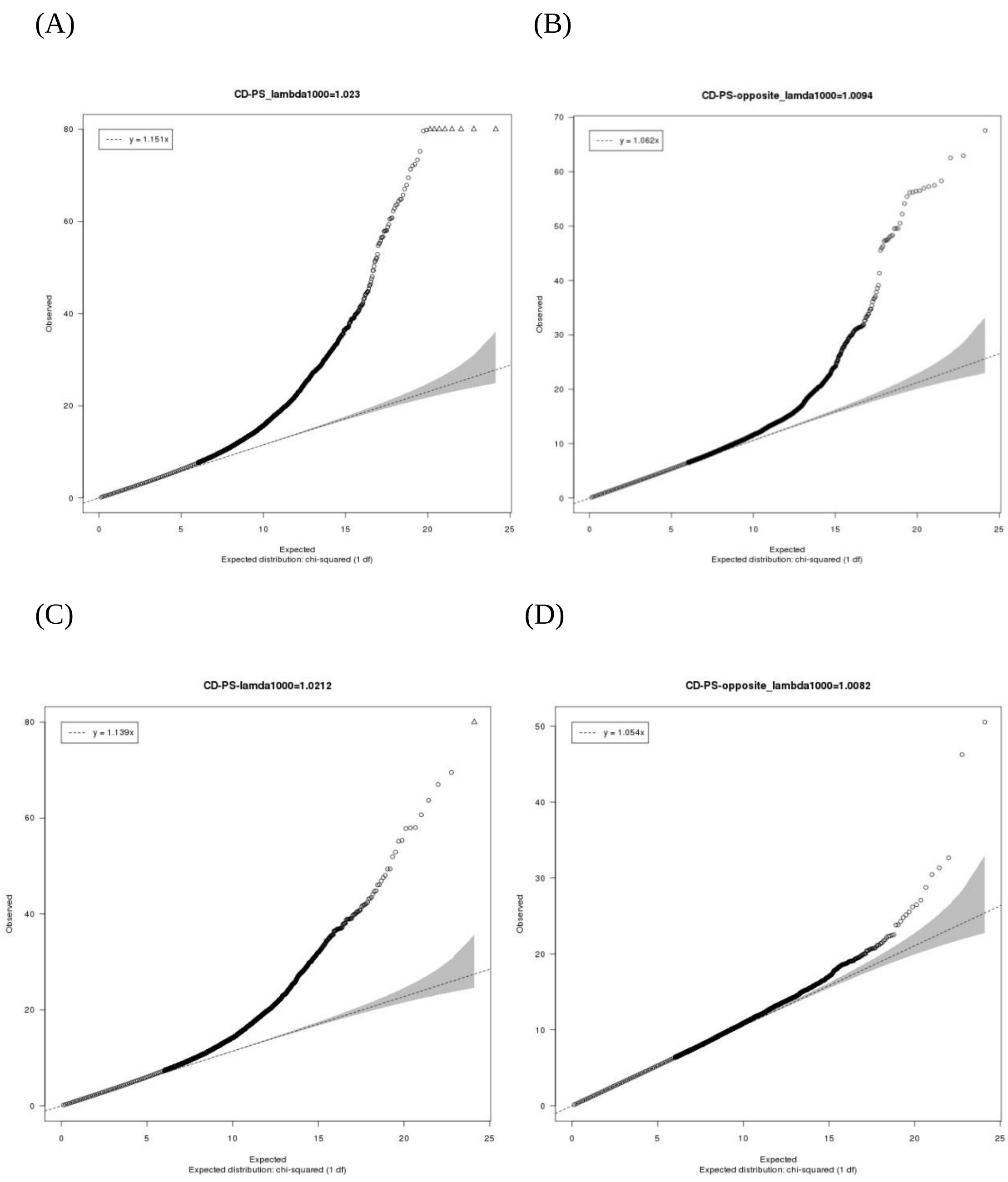
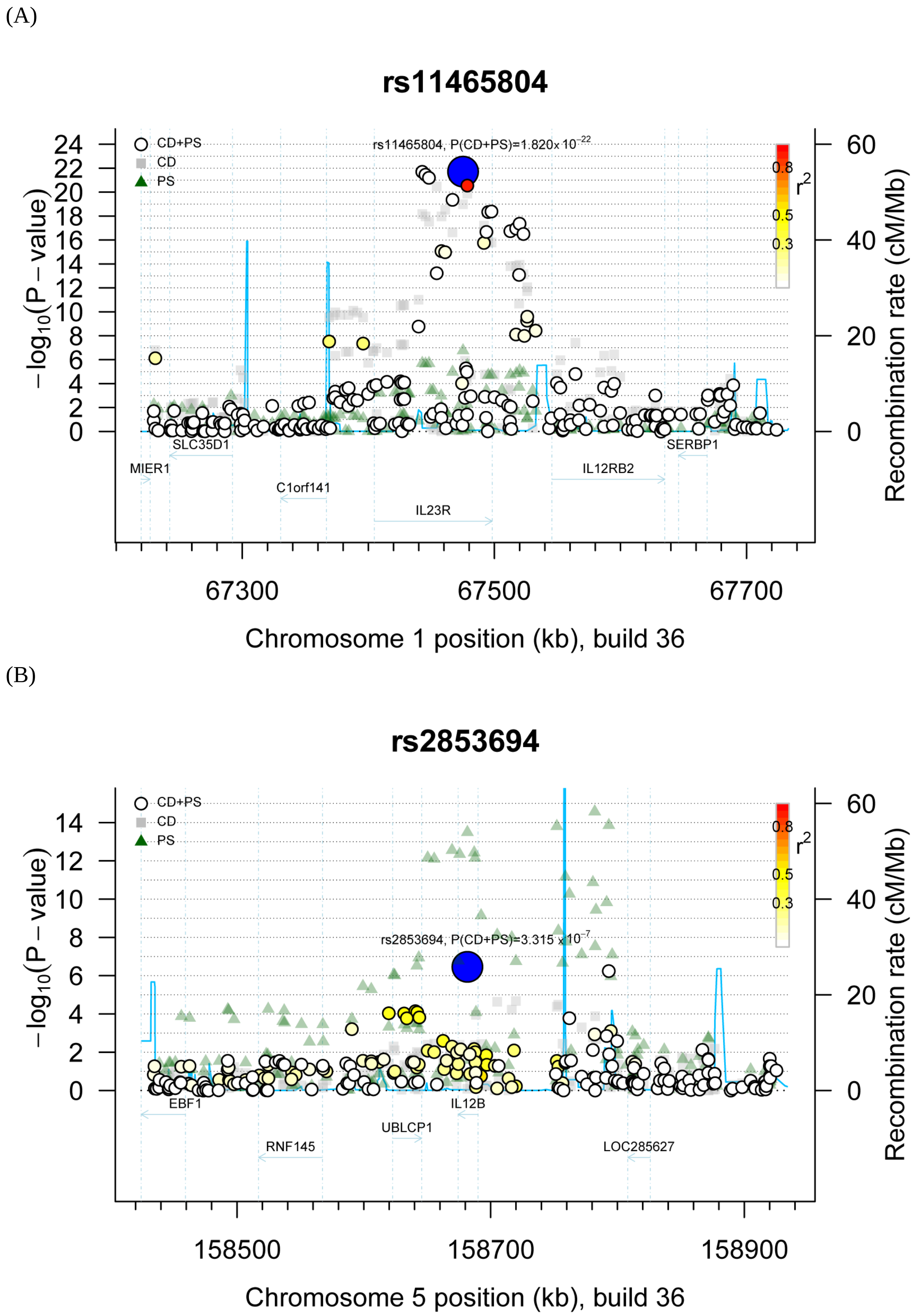
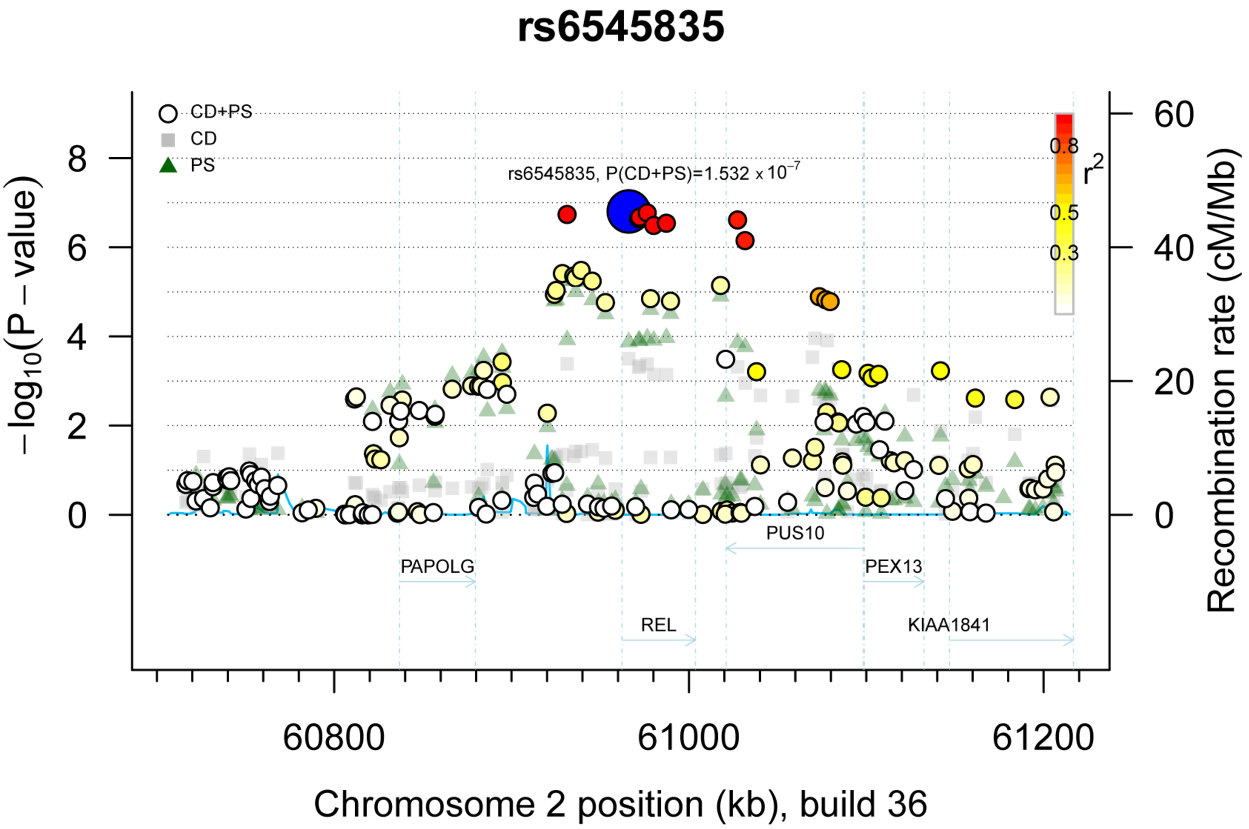


Figure S3. Quantile-quantile (Q-Q) plots for the combined–phenotype analysis (panels A and B)

(A): Same-effect meta-analysis; λ_{1000}=1.023. (B): Opposite-direction meta-analysis; λ_{1000}=1.009. (C): Same-effect meta-analysis after excluding known associated loci for PS and CD; λ_{1000}=1.021. (D): Opposite-effect meta-analysis after excluding known associated loci for PS and CD; λ_{1000}=1.008.


(A)
rs11465804
CD+PS
CD
PS
rs11465804, P(CD+PS)=1.820x 10^-22
r^2
0.8
0.5
0.3
−log10(P − value)
24
22
20
18
16
14
12
10
8
6
4
2
0
60
40
20
0
Recombination rate (cM/Mb)
SLC35D1
MIER1
C1orf141
IL23R
IL12RB2
SERBP1
67300
67500
67700
Chromosome 1 position (kb), build 36
(B)
rs2853694
CD+PS
CD
PS
rs2853694, P(CD+PS)=3.315 x 10^-7
r^2
0.8
0.5
0.3
−log10(P − value)
14
12
10
8
6
4
2
0
60
40
20
0
Recombination rate (cM/Mb)
EBF1
IL12B
UBLCP1
RNF145
LOC285627
158500
158700
158900
Chromosome 5 position (kb), build 36

(C)


rs6545835
CD+PS
CD
PS
rs6545835, P(CD+PS)=1.532 x 10^{-7}
0.8
0.5
0.3
r^2
−log₁₀(P − value)
0
2
4
6
8
Recombination rate (cM/Mb)
0
20
40
60
PAPOLG
PUS10
PEX13
REL
KIAA1841
60800
61000
61200
Chromosome 2 position (kb), build 36

(D)

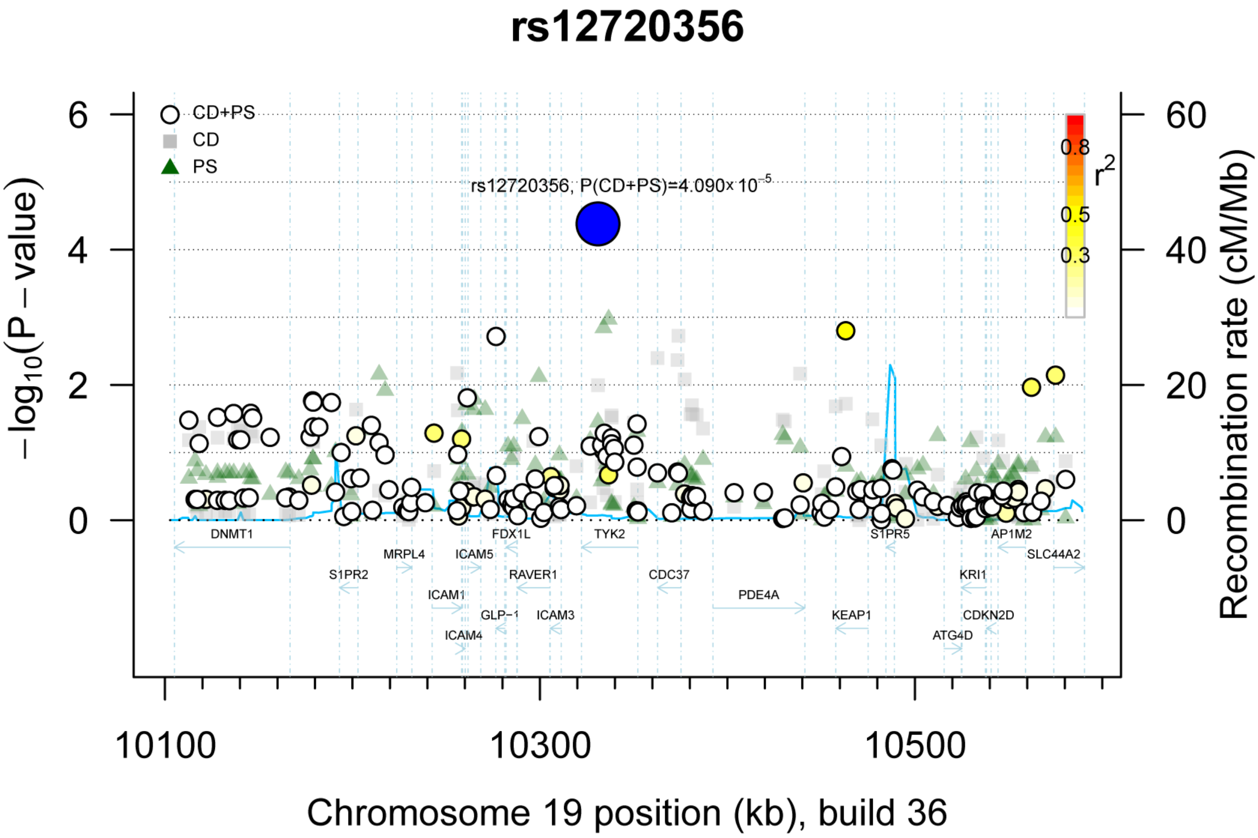
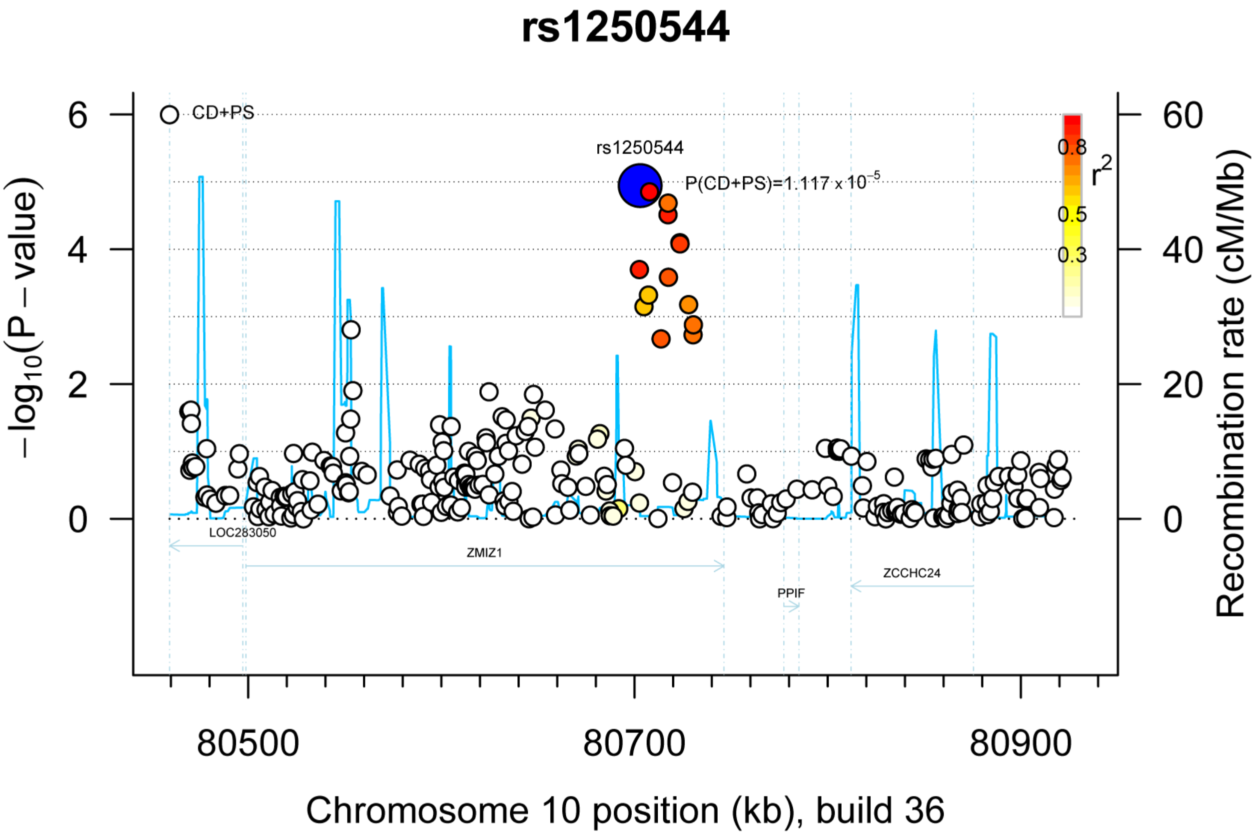

rs12720356
CD+PS
CD
PS
rs12720356, P(CD+PS)=4.090x 10^{-5}
0.8
0.5
0.3
r^2
−log₁₀(P − value)
0
2
4
6
Recombination rate (cM/Mb)
0
20
40
60
DNMT1
S1PR2
MRPL4
ICAM1
ICAM4
ICAM5
FDX1L
GLP−1
RAVER1
ICAM3
TYK2
CDC37
PDE4A
KEAP1
S1PR5
ATG4D
KRI1
CDKN2D
AP1M2
SLC44A2
10100
10300
10500
Chromosome 19 position (kb), build 36

Figure S4. Regional Association Plots of Established Risk Loci Shared between CD and PS (see also Table 1)

(A): 1p31 (*IL23R*); (B): 5p33 (*IL12B*). (C): 2p16 (*REL*). (D): 19p13 (*TYK2*). Plots (A-C) and (D) display the -$\log_{10}P$-values from the same- and opposite-direction meta-analysis of CD and PS (panels A and B, Table S1, see also Figure 1), respectively, with regard to the physical location of markers. Imputation of SNP genotypes is based on the HapMap3 reference (see Methods). Blue-filled circle: lead SNP; Other filled circles: analyzed SNPs where the fill color corresponds to the strength of linkage disequilibrium (r^2) with the lead SNP (for color coding see legend in the upper right corner of each plot); Green triangles: analyzed SNPs of the meta-analysis on PS (panel A) Gray squares: analyzed SNPs of the meta-analysis on CD (panel B) Blue line: recombination intensity (cM/Mb). Positions and gene annotations are according to NCBI's build 36 (hg18).

(A)


rs1250544
CD+PS
rs1250544
P(CD+PS)=1.117 x 10^-5
0.8
0.5
0.3
r^2
−log10(P − value)
Recombination rate (cM/Mb)
6
4
2
0
60
40
20
0
LOC283050
ZMIZ1
PPIF
ZCCHC24
80500
80700
80900
Chromosome 10 position (kb), build 36

(B)

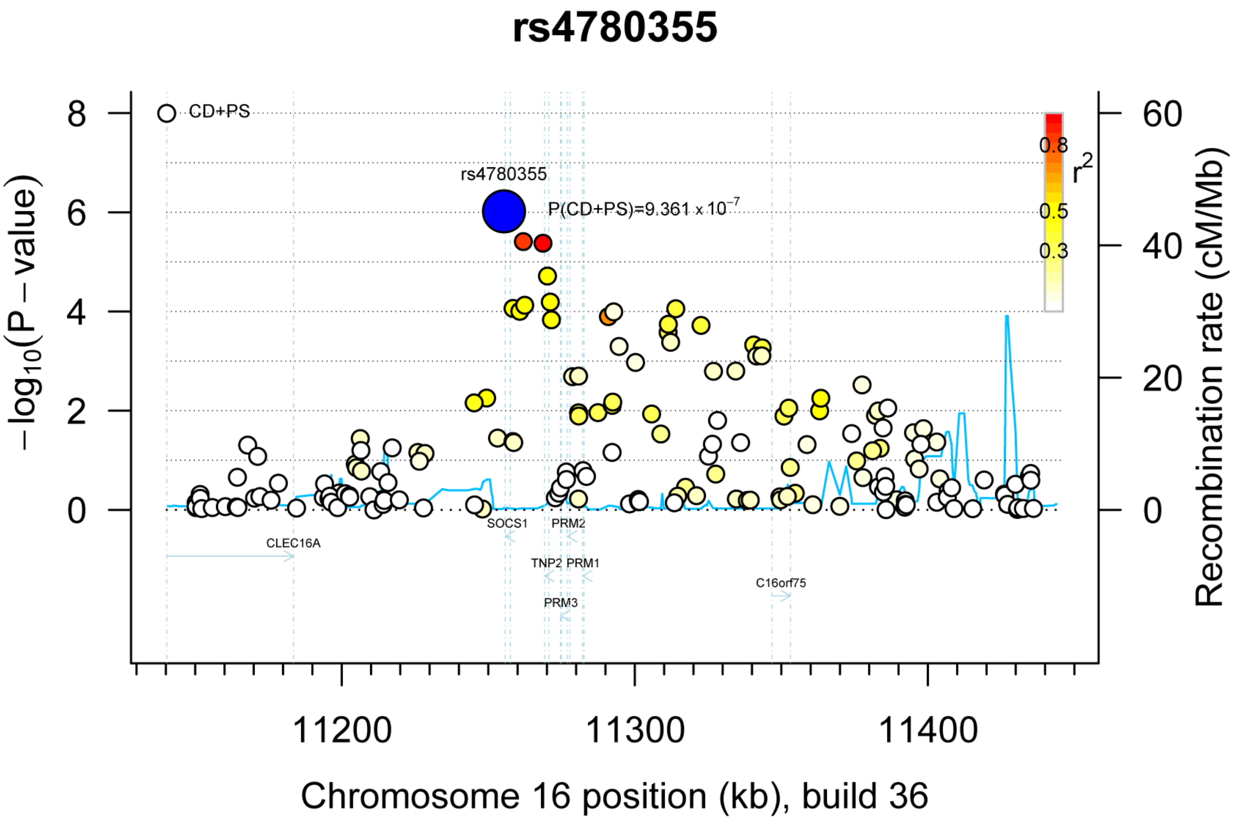

rs4780355
CD+PS
rs4780355
P(CD+PS)=9.361 x 10^-7
0.8
0.5
0.3
r^2
−log10(P − value)
Recombination rate (cM/Mb)
8
6
4
2
0
60
40
20
0
CLEC16A
SOCS1
PRM2
TNP2 PRM1
PRM3
C16orf75
11200
11300
11400
Chromosome 16 position (kb), build 36

Figure S5. Regional Association Plots of Newly Detected Risk Loci for Both CD and PS

(A): 10q22 (*ZMIZ1*); (B): 16p13 (near *SOCS1*). Shown are the -$\log_{10}P$-values from the combined-phenotype GWAS meta-analysis of CD and PS (panels A and B, Table S1, see also Figure 1) with regard to the physical location of markers. Imputation of SNP genotypes is based on the HapMap3 reference (see Methods). Blue-filled circle: lead SNP; Other filled circles: analyzed SNPs where the fill color corresponds to the strength of linkage disequilibrium (r^2) with the lead SNP (for color coding see legend in the upper right corner of each plot); Blue line: recombination intensity (cM/Mb). Positions and gene annotations are according to NCBI's build 36 (hg18).

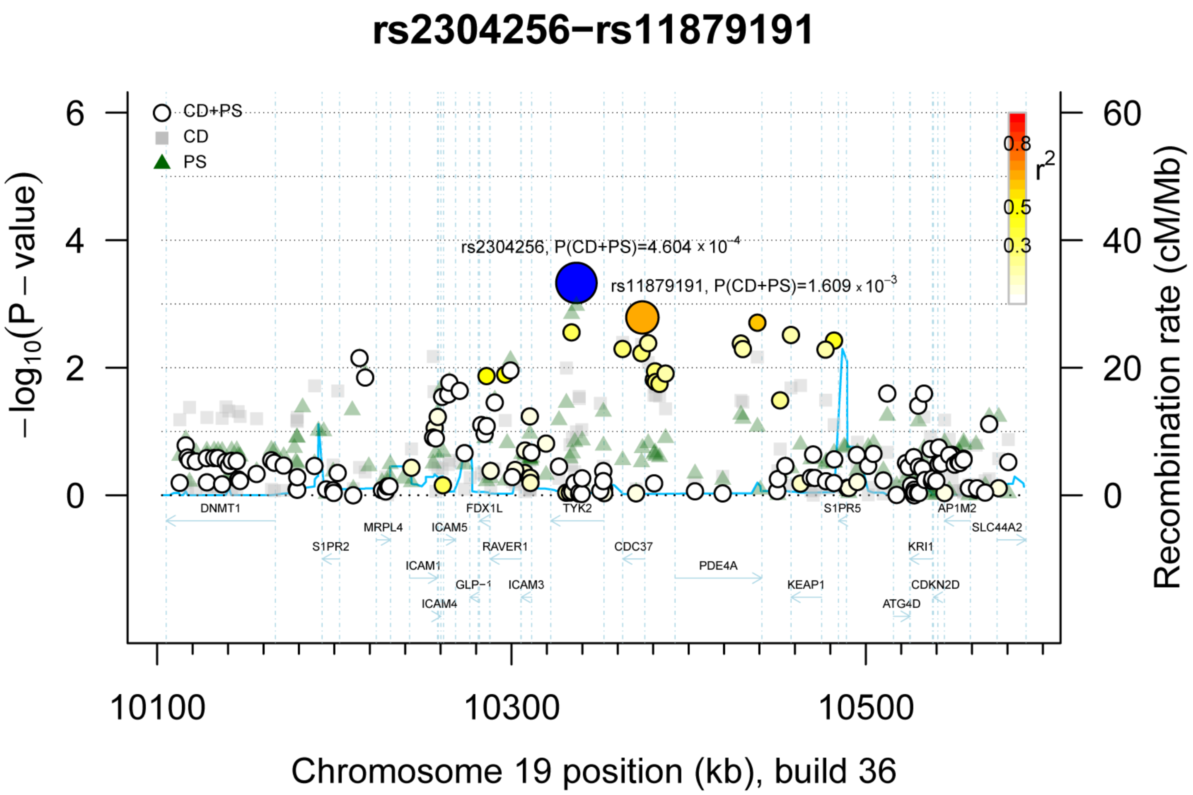


Figure S6. Regional Association Plot of the Risk Locus at 19p13 Shared between CD and PS

Shown are the -log$_{10}P$-values from the combined-phenotype GWAS meta-analysis of CD and PS (panels A and B, Table S1, see also Figure 1) considering same direction of effects with regard to the physical location of markers. Imputation of SNP genotypes is based on the HapMap3 reference (see Methods). Blue-filled circle: lead SNP; Other filled circles: analyzed SNPs where the fill color corresponds to the strength of linkage disequilibrium (r^2) with the lead SNP (for color coding see legend in the upper right corner of each plot); Green triangles: analyzed SNPs of the meta-analysis on PS (panel A) Gray squares: analyzed SNPs of the meta-analysis on CD (panel B) Blue line: recombination intensity (cM/Mb). Positions and gene annotations are according to NCBI's build 36 (hg18).

Table S1. Case/Control Panels Used in the Analysis

Panel A: Discovery panel after quality control for GWAS meta-analysis on psoriasis (PS).

Index GWAS	#Cases	#Controls	GWAS platform
Germany	469	2646	Illumina 550k, Illumina 330k, Affymetrix 6.0
United States (CASP)	757	987	Perlegen Sciences
Canada (Genizon)	1303	1322	Illumina 1M
Total	2529	4955	

Panel B: Discovery panel after quality control for GWAS meta-analysis on Crohn's disease (CD).

Index GWAS	#Cases	#Controls	GWAS platform
Germany	480	2645	Illumina550k, Illumina 300k, Affymetrix 6.0
UK (WTCCC)	1662	2860	Affymetrix 500k
Total	2142	5505	

Panel C: Replication panel after quality control for PS (*OVERLAP* approach).

Replication country	Disease	#Cases	#Controls
Germany	PS	674	1984
Estonia	PS	1126	960
United States	PS	2137	1903
United Kingdom	PS	2178	2657
Total	PS	6115	7504

Panel D: Replication panel for CD and PS after quality control (*COMBINED* approach).

Replication country	Disease	#Cases	#Controls
Germany	CD	1713	1463
Germany	PS	596	1853
Estonia	PS	413	249
Total		2722	3565

Panel E: Replication panel for CD and PS after quality control (*COMBINED* approach).

Replication country	Disease	#Cases	#Controls
Germany	CD	1672	136
Italy	CD	688	879
United Kingdom	PS	2178	2657
Total		4538	3672

Table S2. Results of same-effect analysis of the combined-phenotype (*COMBINED* approach) and of the replication in panel D (see Table S1D).

part 1

				CD+PS Discovery GWAS (4,671/10,460)		**PS GWAS (2,529/4,955)**		**CD GWAS (2,142/5,505)**		**PS Replication (1,009/2,102)**		**CD Replication (1,713/1,463)**	
Chr	**SNP**	**A1**	**Locus**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**
1	rs10489873	A	*RGS1*	7.42×10^{-06}	0.74	3.18×10^{-04}	0.73	7.51×10^{-03}	0.75	3.07×10^{-01}	1.13	1.58×10^{-01}	1.15
1	rs2208843	G	*NFASC*	5.83×10^{-05}	0.83	1.70×10^{-04}	0.77	4.71×10^{-02}	0.88	1.37×10^{-01}	0.86	2.61×10^{-01}	0.91
2	rs10184619	C	*BRE*	5.85×10^{-06}	0.88	1.53×10^{-03}	0.88	1.19×10^{-03}	0.88	9.74×10^{-01}	1.00	3.15×10^{-01}	0.95
2	rs4851527	A	*IL1R2*	2.26×10^{-05}	1.12	3.16×10^{-04}	1.15	1.59×10^{-02}	1.09	5.56×10^{-01}	0.97	1.56×10^{-01}	1.07
5	rs10053519	G	-	4.42×10^{-06}	1.14	1.09×10^{-04}	1.16	9.19×10^{-03}	1.11	9.89×10^{-01}	1.00	8.91×10^{-01}	0.99
7	rs2255323	C	*GPR85*	8.86×10^{-09}	0.80	4.13×10^{-05}	0.83	2.74×10^{-05}	0.75	3.85×10^{-01}	0.95	4.46×10^{-02}	0.89
9	rs886017	G	*RALGDS*	1.43×10^{-05}	0.88	9.31×10^{-05}	0.85	2.75×10^{-02}	0.91	8.32×10^{-01}	0.99	2.61×10^{-01}	1.06
9	rs11574906	T	*NOTCH1*	2.74×10^{-07}	1.31	1.90×10^{-03}	1.31	1.46×10^{-05}	1.59	5.45×10^{-02}	0.84	1.57×10^{-01}	0.89
10	rs7071642 [a]	A	*ZNF365*	3.41×10^{-08}	1.42	1.17×10^{-04}	1.18	7.70×10^{-05}	1.19	2.43×10^{-01}	1.08	3.22×10^{-03}	1.19
10	rs2675671	C	*CAMK2G*	3.89×10^{-06}	0.87	4.05×10^{-04}	0.87	2.74×10^{-03}	0.89	4.88×10^{-01}	0.96	3.79×10^{-01}	0.96
10	rs1250544 [a]	G	*ZMIZ1*	1.12×10^{-05}	1.14	3.85×10^{-05}	1.18	3.31×10^{-02}	1.09	1.99×10^{-04}	1.25	2.60×10^{-03}	1.17
10	rs1250550 [a]	C	*ZMIZ1*	1.52×10^{-03}	1.11	1.53×10^{-02}	1.11	4.05×10^{-02}	1.10	5.05×10^{-03}	1.19	4.75×10^{-04}	1.21
10	rs12415344	G	*SORCS1*	9.38×10^{-05}	0.41	4.93×10^{-04}	0.30	3.35×10^{-02}	0.52	4.36×10^{-01}	0.79	2.57×10^{-01}	1.42
11	rs10836477	T	*LDLRAD3*	4.12×10^{-06}	0.88	5.36×10^{-03}	0.90	2.03×10^{-04}	0.87	8.00×10^{-01}	1.02	2.73×10^{-01}	1.06
12	rs12580100	A	*IKZF4*	6.18×10^{-07}	1.29	9.24×10^{-05}	1.32	1.80×10^{-03}	1.26	2.22×10^{-01}	1.11	6.87×10^{-01}	1.03
15	rs2016902	G	*PAK6*	1.42×10^{-06}	0.38	2.88×10^{-05}	0.33	1.08×10^{-02}	0.46	5.86×10^{-01}	0.86	8.94×10^{-01}	0.95
16	rs4780355	T	*SOCS1*	9.36×10^{-07}	1.16	1.72×10^{-04}	1.18	1.47×10^{-03}	1.15	6.89×10^{-02}	1.12	4.84×10^{-06}	1.28
19	rs10405308	G	*LOC401895*	1.81×10^{-07}	0.60	6.54×10^{-04}	0.59	7.72×10^{-05}	0.60	2.29×10^{-01}	0.85	7.45×10^{-01}	0.96

part 2

				PS GWAS & Repl (3,538/7,057)		CD GWAS & Repl (3,855/6,968)		CD+PS GWAS&Repl (7,393/14,025)		
Chr	**SNP**	**A1**	**Locus**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**Status now**
1	rs10489873	A	*RGS1*	2.18×10^{-02}	0.85	4.39×10^{-01}	0.94	2.81×10^{-02}	0.89	
1	rs2208843	G	*NFASC*	8.56×10^{-05}	0.80	2.37×10^{-02}	0.89	1.54×10^{-05}	0.85	-
2	rs10184619	C	*BRE*	9.43×10^{-03}	0.92	1.54×10^{-03}	0.91	4.44×10^{-05}	0.91	-
2	rs4851527	A	*IL1R2*	7.82×10^{-03}	1.09	5.44×10^{-03}	1.09	1.20×10^{-04}	1.09	-
5	rs10053519	G	-	1.29×10^{-03}	1.11	5.02×10^{-02}	1.06	2.63×10^{-04}	1.09	-
7	rs2255323	C	*GPR85*	1.18×10^{-04}	0.86	2.02×10^{-05}	0.83	1.23×10^{-08}	0.85	-
9	rs886017	G	*RALGDS*	8.66×10^{-04}	0.90	3.20×10^{-01}	0.97	2.42×10^{-03}	0.93	-
9	rs11574906	T	*NOTCH1*	3.36×10^{-01}	1.06	1.32×10^{-01}	1.10	8.18×10^{-02}	1.14	-
10	rs7071642 [a]	A	*ZNF365*	1.19×10^{-04}	1.15	8.25×10^{-07}	1.19	5.03×10^{-10}	1.17	CD
10	rs2675671	C	*CAMK2G*	8.69×10^{-04}	0.90	3.46×10^{-03}	0.91	1.02×10^{-05}	0.91	-
10	rs1250544 [a]	G	*ZMIZ1*	3.90×10^{-08}	1.20	4.47×10^{-04}	1.12	2.66×10^{-10}	1.17	CD, PS, CDPS
10	rs1250550 [a]	C	*ZMIZ1*	3.00×10^{-04}	1.14	1.14×10^{-04}	1.15	1.26×10^{-07}	1.14	CD
10	rs12415344	G	*SORCS1*	4.29×10^{-03}	0.53	4.75×10^{-01}	0.86	1.22×10^{-02}	0.68	-
11	rs10836477	T	*LDLRAD3*	3.03×10^{-02}	0.93	2.02×10^{-02}	0.93	1.49×10^{-03}	0.93	-
12	rs12580100	A	*IKZF4*	1.58×10^{-04}	1.23	1.21×10^{-02}	1.14	9.05×10^{-06}	1.18	-
15	rs2016902	G	*PAK6*	6.21×10^{-04}	0.51	3.86×10^{-02}	0.62	7.65×10^{-05}	0.55	-
16	rs4780355	T	*SOCS1*	3.67×10^{-05}	1.16	1.01×10^{-07}	1.20	2.02×10^{-11}	1.18	-
19	rs10405308	G	*LOC401895*	1.62×10^{-03}	0.73	2.15×10^{-03}	0.76	1.14×10^{-05}	0.74	-

Chr: chromosome of marker; SNP: rs ID; A1: minor allele; Locus: one candidate gene in the region; P/OR: *P*-value and corresponding odds ratio with respect to minor allele for the combined-phenotype GWAS meta-analysis of CD and PS (panel A&B), GWAS meta-analysis of PS (panel A), GWAS meta-analysis of CD (panel B), PS replication analysis (as part of panel D), CD replication analysis (part of panel D), combined analysis of PS GWAS meta-analysis (panel A) and PS replication (part of panel D), combined analysis of CD GWAS meta-analysis (panel B) and CD replication (part of panel D), combined analysis of CD+PS GWAS meta-analysis (panel A&B) and CD+PS replication (panel D). For each panel, numbers of cases/controls are displayed in parentheses. Status now: status of association with CD and/or PS. [a] SNPs are located inside established CD risk loci with $P < 5\times10^{-8}$ [1].

Table S3. Results of opposite-effect analysis of the combined-phenotype (*COMBINED* approach) and of the replication in panel D (see Table S1D).

part 1

				CD+PS Discovery GWAS (4,671/10,460)		**PS GWAS (2,529/4,955)**		**CD GWAS (2,142/5,505)**		**PS Replication (1,009/2,102)**		**CD Replication (1,713/1,463)**	
Chr	**SNP**	**A1**	**Locus**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**P**	**OR**
1	rs7667	G	*CAPZB*	3.61×10^{-06}	1.14	3.22×10^{-04}	0.86	3.06×10^{-03}	0.89	5.39×10^{-02}	0.89	8.92×10^{-01}	0.99
3	rs1386478	A	*ZDHHC23*	6.34×10^{-07}	0.86	1.03×10^{-04}	1.19	1.53×10^{-03}	1.15	2.73×10^{-01}	1.07	9.27×10^{-01}	0.99
4	rs7677254	C	*FAT4*	1.49×10^{-05}	0.87	3.74×10^{-03}	1.16	1.21×10^{-03}	1.14	3.23×10^{-01}	1.06	6.20×10^{-01}	0.98

part 2

				PS GWAS & Repl (3,538/7,057)		**CD GWAS & Repl (3,855/6,968)**		**CD+PS GWAS&Repl (7,393/14,025)**		
Chr	**SNP**	**A1**	**Locus**	**P**	**OR**	**P**	**OR**	**P**	**OR**	**Status now**
1	rs7667	G	*CAPZB*	4.89×10^{-05}	0.87	1.38×10^{-02}	0.92	8.11×10^{-06}	0.90	-
3	rs1386478	A	*ZDHHC23*	1.33×10^{-04}	1.15	1.44×10^{-02}	1.09	7.40×10^{-06}	1.12	-
4	rs7677254	C	*FAT4*	4.89×10^{-03}	1.11	2.36×10^{-02}	1.07	6.54×10^{-05}	1.10	-

Chr: chromosome of marker; SNP: rs ID; A1: minor allele; Locus: one candidate gene in the region; P/OR: *P*-value and corresponding odds ratio with respect to minor allele for the combined-phenotype GWAS meta-analysis of CD and PS (panel A&B), GWAS meta-analysis of PS (panel A), GWAS meta-analysis of CD (panel B), PS replication analysis (as part of panel D), CD replication analysis (part of panel D), combined analysis of PS GWAS meta-analysis (panel A) and PS replication (part of panel D), combined analysis of CD GWAS meta-analysis (panel B) and CD replication (part of panel D), combined analysis of CD+PS GWAS meta-analysis (panel A&B) and CD+PS replication (panel D). For each panel, numbers of cases/controls are displayed in parentheses. Status now: status of association with CD and/or PS. For CD GWAS and CD replication data, minor and major alleles were flipped in order to calculate *P*-value (P) and odds ratio (OR) (see Methods).

Table S4. Results of *in-silico* expression quantitative trait locus (eQTL) analysis using the mRNAbySNPBrowser software [2] with significant evidence ($P_{Expression} < 1\times10^{-4}$) for differential expression.

Probe-ID	Marker	Chr	Pos	Allele	Effect	H2	LOD	P-value
227941_at	rs10181042	2	61135910	C	0.43	8.71	5.40	6.10E-007
1568658_at	rs10181042	2	61135910	C	-0.565	15.11	9.57	3.10E-011
201039_s_at	rs1250546	10	80702538	T	-0.307	4.61	4.01	1.70E-005
212124_at	rs1250546	10	80702538	T	-0.277	3.76	3.37	8.10E-005
228949_at	rs1250559	10	80723566	C	0.289	3.93	3.43	7.00E-005
221006_s_at	rs1250559	10	80723566	C	-0.296	4.13	3.43	7.00E-005
1569053_at	rs243323	16	11268703	A	-0.33	4.53	3.34	8.80E-005
241338_at	rs243323	16	11268703	A	0.328	4.48	3.45	6.60E-005
AVG_HSPA12A	rs243323	16	11268703	A	0.33	4.53	3.58	4.90E-005
221578_at	rs243323	16	11268703	A	0.344	4.96	3.55	5.30E-005
233648_at	rs243323	16	11268703	A	-0.326	4.46	3.34	8.80E-005
AVG_NRK	rs243323	16	11268703	A	0.349	5.05	3.71	3.60E-005
226456_at	rs243323	16	11268703	A	0.481	9.67	6.95	1.50E-008
227164_at	rs243323	16	11268703	A	-0.331	4.57	3.45	6.60E-005
228921_at	rs243323	16	11268703	A	0.337	4.75	3.73	3.40E-005
215170_s_at	rs243323	16	11268703	A	-0.337	4.71	3.47	6.30E-005
237383_at	rs243323	16	11268703	A	-0.351	5.13	3.68	3.80E-005
AVG_TMEM22	rs243323	16	11268703	A	-0.344	4.96	3.66	4.00E-005
1558595_at	rs243323	16	11268703	A	0.326	4.46	3.49	6.10E-005
1565567_at	rs243323	16	11268703	A	-0.349	5.11	3.72	3.50E-005
226651_at	rs243323	16	11268703	A	-0.34	4.8	3.59	4.80E-005
242819_at	rs243323	16	11268703	A	-0.337	4.73	3.37	8.10E-005
38487_at	rs243323	16	11268703	A	0.333	4.65	3.41	7.40E-005
242241_x_at	rs243323	16	11268703	A	-0.328	4.48	3.30	9.70E-005
AVG_MGC24665	rs243323	16	11268703	A	0.486	9.85	7.11	1.10E-008
223981_at	rs243323	16	11268703	A	-0.34	4.82	3.56	5.20E-005

AVG_HEL308	rs243323	16	11268703	A	-0.342	4.86	3.60	4.60E-005
241893_at	rs243323	16	11268703	A	-0.34	4.82	3.50	6.00E-005
AVG_KIAA0974	rs243323	16	11268703	A	-0.344	4.96	3.65	4.10E-005
1553900_s_at	rs243323	16	11268703	A	0.367	5.61	4.32	8.20E-006
241988_x_at	rs243323	16	11268703	A	-0.351	5.15	4.03	1.70E-005
206727_at	rs243323	16	11268703	A	0.361	5.42	3.92	2.10E-005
1565830_at	rs243323	16	11268703	A	-0.333	4.65	3.50	6.00E-005
AVG_SOX3	rs243323	16	11268703	A	0.337	4.73	3.56	5.20E-005
207155_at	rs243323	16	11268703	A	0.368	5.67	4.18	1.20E-005
236994_at	rs243323	16	11268703	A	-0.331	4.59	3.52	5.70E-005
1559494_at	rs243323	16	11268703	A	-0.324	4.4	3.29	9.90E-005
228021_at	rs243323	16	11268703	A	0.326	4.44	3.48	6.30E-005
226001_at	rs243323	16	11268703	A	-0.331	4.59	3.47	6.30E-005
236726_at	rs243323	16	11268703	A	0.328	4.48	3.33	8.90E-005
238428_at	rs243323	16	11268703	A	0.342	4.9	3.71	3.60E-005
231295_at	rs243323	16	11268703	A	0.33	4.53	3.29	9.90E-005
1556199_a_at	rs243323	16	11268703	A	0.324	4.38	3.41	7.40E-005
AVG_SNX25	rs243323	16	11268703	A	-0.365	5.55	4.01	1.70E-005
232425_at	rs243323	16	11268703	A	-0.352	5.19	3.77	3.10E-005
218829_s_at	rs243323	16	11268703	A	-0.324	4.4	3.30	9.80E-005
227408_s_at	rs243323	16	11268703	A	-0.356	5.26	3.90	2.30E-005
230570_at	rs243323	16	11268703	A	-0.347	5.05	3.66	4.10E-005
AVG_C5ORF15	rs243323	16	11268703	A	-0.333	4.63	3.39	7.70E-005
241063_at	rs243323	16	11268703	A	0.358	5.36	4.22	1.00E-005
213610_s_at	rs243323	16	11268703	A	-0.344	4.96	3.87	2.40E-005

SNPs are represented by more than one transcript. Probe-ID: probe on Affymetrix HG-U133 Plus 2.0 chip Marker: rs ID of SNP Chr: chromosome Pos: genomic position according to NCBI's build 36 (hg18). Allele: allele of effect Effect: estimate of effect size H2: heritability value LOD: logarithm of the odds score (the false discovery rate (FDR) was found to be 0.05 for a LOD score of 6.076 in [2]). P-value: probability value of lod score.

Table S5. Extract from the Catalog of Published Genome-wide association studies[3] (www.genome.gov/gwastudies, date of access Dec-01-2011) listing established disease associations for the eleven susceptibility loci shared between CD and PS.

Date Added to Catalog (since 11/25/08)	First Author/Date/ Journal/Study	Disease/Trait
1p31.3 (*IL23R*)		
04/12/11	Mells GF March 13, 2011 Nat Genet Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis.	Primary biliary cirrhosis
03/28/11	Dehghan A February 07, 2011 Circulation Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels.	C-reactive protein
03/29/11	Anderson CA February 06, 2011 Nat Genet Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47.	Ulcerative colitis
01/11/11	Franke A November 21, 2010 Nat Genet Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.	Crohn's disease
01/06/11	Sotoodehnia N November 14, 2010 Nat Genet Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction.	Ventricular conduction
12/03/10	Croteau-Chonka DC October 21, 2010 Obesity (Silver Spring) Genome-wide association study of anthropometric traits and evidence of interactions with age and study year in Filipino women.	Body mass index
12/03/10	NA	Weight
01/18/11	Strange A October 17, 2010 Nat Genet A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1.	Psoriasis
10/17/10	Waterworth DM September 23, 2010 Arterioscler Thromb Vasc Biol Genetic variants influencing circulating lipid levels and risk of coronary artery disease.	Triglycerides
09/02/10	Liu X July 18, 2010 Nat Genet Genome-wide meta-analyses identify three loci associated with primary biliary cirrhosis.	Primary biliary cirrhosis
08/30/10	Mizuki N July 11, 2010 Nat Genet Genome-wide association studies identify IL23R-IL12RB2 and IL10 as Beh╟⊏et's disease susceptibility loci.	Behcet's disease
08/18/10	Remmers EF July 11, 2010 Nat Genet Genome-wide association study identifies variants in the MHC class I, IL10, and IL23R-IL12RB2 regions associated with Beh╟⊏et's disease.	Behcet's disease
07/12/10	McGovern DP June 22, 2010 Hum Mol Genet Fucosyltransferase 2 (FUT2) non-secretor status is associated with Crohn's disease.	Crohn's disease
04/02/10	McGovern DP March 14, 2010 Nat Genet Genome-wide association identifies multiple ulcerative colitis susceptibility loci.	Ulcerative colitis
03/29/10	Dubois PC February 28, 2010 Nat Genet Multiple common variants for celiac disease influencing immune gene expression.	Celiac disease
03/17/10	Sun Q February 22, 2010 Hum Mol Genet Genome-wide association study identifies polymorphisms in LEPR as determinants of plasma soluble leptin receptor levels.	Soluble leptin receptor levels
02/12/10	Shen L January 22, 2010 Neuroimage Whole genome association study of brain-wide imaging phenotypes for identifying quantitative trait loci in MCI and AD: A study of the ADNI cohort.	Brain imaging
02/02/10	Reveille JD January 10, 2010 Nat Genet Genome-wide association study of ankylosing spondylitis identifies non-MHC susceptibility loci.	Ankylosing spondylitis
12/11/09	Barrett JC November 15, 2009 Nat Genet Genome-wide association study of ulcerative colitis identifies three new susceptibility loci, including the HNF4A region.	Ulcerative colitis
10/16/09	Rivadeneira F October 04, 2009 Nat Genet Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies.	Bone mineral density (hip)
10/16/09	NA	Bone mineral density (spine)
07/12/09	Elliott P July 01, 2009 JAMA Genetic Loci associated with C-reactive protein levels and risk of coronary heart disease.	C-reactive protein
06/21/09	Hirschfield GM May 20, 2009 N Engl J Med Primary biliary cirrhosis associated with HLA, IL12A, and IL12RB2 variants.	Primary biliary cirrhosis
06/01/09	Barrett JC May 10, 2009 Nat Genet Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes.	Type 1 diabetes
02/06/09	Nair RP January 25, 2009 Nat Genet Genome-wide scan reveals association of psoriasis with IL-23 and NF-kappaB pathways.	Psoriasis
01/21/09	Silverberg MS January 04, 2009 Nat Genet Ulcerative colitis-risk loci on chromosomes 1p36 and 12q15 found by genome-wide association study.	Ulcerative colitis
01/12/09	Aulchenko YS December 07, 2008 Nat Genet Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts.	Cholesterol, total
01/12/09	NA	LDL cholesterol
01/12/09	NA	Triglycerides
01/12/09	Kathiresan S December 07, 2008 Nat Genet Common variants at 30 loci contribute to polygenic dyslipidemia.	Triglycerides
01/12/09	Sabatti C December 07, 2008 Nat Genet Genome-wide association analysis of metabolic traits in a birth cohort from a founder population.	Metabolic traits
11/25/08	Kugathasan S August 31, 2008 Nat Genet Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease.	Inflammatory bowel disease
11/25/08	Barrett JC June 29, 2008 Nat Genet Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease.	Crohn's disease
11/25/08	Ridker PM April 24, 2008 Am J Hum Genet Loci related to metabolic-syndrome pathways including LEPR,HNF1A, IL6R, and GCKR associate with plasma C-reactive protein: the Women's Genome Health Study.	C-reactive protein
11/25/08	Kathiresan S January 13, 2008 Nat Genet Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans.	Triglycerides
11/25/08	Willer CJ January 13, 2008 Nat Genet Newly identified loci that influence lipid concentrations and risk of coronary artery disease.	Triglycerides
11/25/08	Levy D September 19, 2007 BMC Med Genet Framingham Heart Study 100K Project: genome-wide associations for blood pressure and arterial stiffness.	Blood pressure
11/25/08	Vasan RS September 19, 2007 BMC Med Genet Genome-wide association of echocardiographic dimensions, brachial artery endothelial function and treadmill exercise responses in the Framingham Heart Study.	Echocardiographic traits

11/25/08	Raelson JV September 05, 2007 Proc Natl Acad Sci U S A Genome-wide association study for Crohn's disease in the Quebec Founder Population identifies multiple validated disease loci.	Crohn's disease
11/25/08	WTCCC June 07, 2007 Nature Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls.	Crohn's disease
11/25/08	Rioux JD April 15, 2007 Nat Genet Genome-wide association study identifies new susceptibility loci for Crohn disease and implicates autophagy in disease pathogenesis.	Crohn's disease
11/25/08	Libioulle C March 05, 2007 PLoS Genet Novel Crohn disease locus identified by genome-wide association maps to a gene desert on 5p13.1 and modulates expression of PTGER4.	Crohn's disease
11/25/08	Duerr RH October 26, 2006 Science A genome-wide association study identifies IL23R as an inflammatory bowel disease gene.	Inflammatory bowel disease

2p16.1 (*REL*)

05/26/11	Shaw SY April 21, 2011 Circ Cardiovasc Genet Genetic and clinical correlates of early-outgrowth colony-forming units.	Monocyte early outgrowth colony forming units
05/02/11	Cha PC April 03, 2011 Nat Genet A genome-wide association study identifies three loci associated with susceptibility to uterine fibroids.	Uterine fibroids
04/04/11	Bhatnagar P February 17, 2011 J Hum Genet Genome-wide association study identifies genetic variants influencing F-cell levels in sickle-cell patients.	F-cell distribution
03/29/11	Anderson CA February 06, 2011 Nat Genet Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47.	Ulcerative colitis
03/18/11	Festen EA January 27, 2011 PLoS Genet A meta-analysis of genome-wide association scans identifies IL18RAP, PTPN2, TAGAP, and PUS10 as shared risk loci for Crohn's disease and celiac disease.	Crohn's disease and Celiac disease
01/08/11	Elks CE November 21, 2010 Nat Genet Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies.	Menarche (age at onset)
01/11/11	Franke A November 21, 2010 Nat Genet Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.	Crohn's disease
01/03/11	Enciso-Mora V October 31, 2010 Nat Genet A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3).	Hodgkin's lymphoma
01/18/11	Strange A October 17, 2010 Nat Genet A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1.	Psoriasis
12/01/10	Stuart PE October 17, 2010 Nat Genet Genome-wide association analysis identifies three psoriasis susceptibility loci.	Psoriasis
11/17/10	Speliotes EK October 10, 2010 Nat Genet Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index.	Body mass index
07/12/10	Voight BF June 27, 2010 Nat Genet Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis.	Type 2 diabetes
06/13/10	Stahl EA May 09, 2010 Nat Genet Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci.	Rheumatoid arthritis
05/11/10	Liu JZ April 01, 2010 Twin Res Hum Genet Genome-wide association study of height and body mass index in Australian twin families.	Height
04/02/10	McGovern DP March 14, 2010 Nat Genet Genome-wide association identifies multiple ulcerative colitis susceptibility loci.	Ulcerative colitis
04/06/10	Adkins DE March 02, 2010 Mol Psychiatry Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs.	Response to antipsychotic treatment
03/29/10	Dubois PC February 28, 2010 Nat Genet Multiple common variants for celiac disease influencing immune gene expression.	Celiac disease
03/25/10	Okada Y February 26, 2010 Hum Mol Genet A genome-wide association study in 19 633 Japanese subjects identified LHX3-QSOX2 and IGF1 as adult height loci.	Height
01/19/10	Fellay J December 24, 2009 PLoS Genet Common genetic variation and the control of HIV-1 in humans.	HIV-1 control
12/28/09	Nuinoon M November 19, 2009 Hum Genet A genome-wide association identified the common genetic variants influence disease severity in beta0-thalassemia/hemoglobin E.	Beta thalassemia/hemoglobin E disease
12/04/09	Kim JJ November 06, 2009 J Hum Genet Identification of 15 loci influencing height in a Korean population.	Height
11/03/09	Ganesh SK October 11, 2009 Nat Genet Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium.	Mean corpuscular volume
07/10/09	Stefansson H July 01, 2009 Nature Common variants conferring risk of schizophrenia.	Schizophrenia
07/01/09	Cotsapas C June 24, 2009 Hum Mol Genet Common body mass index-associated variants confer risk of extreme obesity.	Obesity (extreme)
06/17/09	Gregersen PK June 07, 2009 Nat Genet REL, encoding a member of the NF-kappaB family of transcription factors, is a newly defined risk locus for rheumatoid arthritis.	Rheumatoid arthritis
06/04/09	Landers JE May 18, 2009 Proc Natl Acad Sci U S A Reduced expression of the Kinesin-Associated Protein 3 (KIFAP3) gene increases survival in sporadic amyotrophic lateral sclerosis.	Amyotrophic lateral sclerosis
05/05/09	Cho YS April 26, 2009 Nat Genet A large-scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits.	Height
11/25/08	Gudbjartsson DF April 06, 2008 Nat Genet Many sequence variants affecting diversity of adult human height.	Height
11/25/08	Weedon MN April 06, 2008 Nat Genet Genome-wide association analysis identifies 20 loci that influence adult height.	Height
11/25/08	Murabito JM September 19, 2007 BMC Med Genet A genome-wide association study of breast and prostate cancer in the NHLBI's Framingham Heart Study.	Breast cancer
11/25/08	Menzel S September 02, 2007 Nat Genet A QTL influencing F cell production maps to a gene encoding a zinc-finger protein on chromosome 2p15.	F-cell distribution

5q33.3 (*IL12B*)

04/07/11	Chung SA March 03, 2011 PLoS Genet Differential genetic associations for systemic lupus erythematosus based on anti-dsDNA autoantibody production.	Systemic lupus erythematosus
04/07/11	Alliey-Rodriguez N March 02, 2011 Psychiatr Genet Genome-wide association study of personality traits in bipolar patients.	Personality dimensions
03/29/11	Anderson CA February 06, 2011 Nat Genet Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47.	Ulcerative colitis
12/01/10	Ellinghaus E October 17, 2010 Nat Genet Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2.	Psoriasis
11/30/10	Huffmeier U October 17, 2010 Nat Genet Common variants at TRAF3IP2 are associated with susceptibility to psoriatic arthritis and psoriasis.	Psoriatic arthritis
01/18/11	Strange A October 17, 2010 Nat Genet A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1.	Psoriasis
10/29/10	Wang KS October 01, 2010 Schizophr Res A genome-wide meta-analysis identifies novel loci associated with schizophrenia and bipolar disorder.	Bipolar disorder and schizophrenia

07/12/10	McGovern DP June 22, 2010 Hum Mol Genet Fucosyltransferase 2 (FUT2) non-secretor status is associated with Crohn's disease.	Crohn's disease
01/13/10	Hancock DB December 13, 2009 Nat Genet Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function.	Pulmonary function
10/30/09	Soranzo N October 11, 2009 Nat Genet A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium.	Mean platelet volume
03/30/09	Polasek O February 01, 2009 Croat Med J Genome-wide association study of anthropometric traits in Korcula Island, Croatia.	Anthropometric traits
02/06/09	Nair RP January 25, 2009 Nat Genet Genome-wide scan reveals association of psoriasis with IL-23 and NF-kappaB pathways.	Psoriasis
02/07/09	Zhang XJ January 25, 2009 Nat Genet Psoriasis genome-wide association study identifies susceptibility variants within LCE gene cluster at 1q21.	Psoriasis
01/12/09	Kathiresan S December 07, 2008 Nat Genet Common variants at 30 loci contribute to polygenic dyslipidemia.	LDL cholesterol
11/25/08	Barrett JC June 29, 2008 Nat Genet Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease.	Crohn's disease
11/25/08	Parkes M June 06, 2007 Nat Genet Sequence variants in the autophagy gene IRGM and multiple other replicating loci contribute to Crohn's disease susceptibility.	Crohn's disease

9p24.1 (*JAK2*)

03/29/11	Anderson CA February 06, 2011 Nat Genet Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47.	Ulcerative colitis
01/19/11	Petrovski S December 14, 2010 AIDS Common human genetic variants and HIV-1 susceptibility: a genome-wide survey in a homogeneous African population.	HIV-1 susceptibility
11/23/10	Niu N October 05, 2010 Genome Res Radiation pharmacogenomics: a genome-wide association approach to identify radiation response biomarkers using human lymphoblastoid cell lines.	Radiation response
10/14/10	Moffatt MF September 23, 2010 N Engl J Med A large-scale, consortium-based genomewide association study of asthma.	Asthma
07/16/10	Eriksson N June 24, 2010 PLoS Genet Web-based, participant-driven studies yield novel genetic associations for common traits.	Common traits (Other)
06/22/10	Johnson AD June 06, 2010 Nat Genet Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists.	Platelet aggregation
04/02/10	McGovern DP March 14, 2010 Nat Genet Genome-wide association identifies multiple ulcerative colitis susceptibility loci.	Ulcerative colitis
03/17/10	Tsai FJ February 19, 2010 PLoS Genet A genome-wide association study identifies susceptibility variants for type 2 diabetes in Han Chinese.	Type 2 diabetes
12/14/09	Asano K November 15, 2009 Nat Genet A genome-wide association study identifies three new susceptibility loci for ulcerative colitis in the Japanese population.	Ulcerative colitis
11/03/09	Ganesh SK October 11, 2009 Nat Genet Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium.	Mean corpuscular hemoglobin
11/03/09	NA	Mean corpuscular volume
10/30/09	Soranzo N October 11, 2009 Nat Genet A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium.	Hematological parameters
03/31/09	Kilpivaara O March 15, 2009 Nat Genet A germline JAK2 SNP is associated with predisposition to the development of JAK2(V617F)-positive myeloproliferative neoplasms.	Myeloproliferative neoplasms
12/09/08	Anney RJ October 24, 2008 Am J Med Genet B Neuropsychiatr Genet Conduct disorder and ADHD: evaluation of conduct problems as a categorical and quantitative trait in the international multicentre ADHD genetics study.	Attention deficit hyperactivity disorder and conduct disorder
11/25/08	Schormair B July 27, 2008 Nat Genet PTPRD (protein tyrosine phosphatase receptor type delta) is associated with restless legs syndrome.	Restless legs syndrome
11/25/08	Barrett JC June 29, 2008 Nat Genet Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease.	Crohn's disease

10q22.3 (*ZMIZ1*)

01/11/11	Franke A November 21, 2010 Nat Genet Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.	Crohn's disease
10/16/10	Lango Allen H September 29, 2010 Nature Hundreds of variants clustered in genomic loci and biological pathways affect human height.	Height
06/22/10	Quan C June 06, 2010 Nat Genet Genome-wide association study for vitiligo identifies susceptibility loci at 6q27 and the MHC.	Vitiligo
06/02/10	Turnbull C May 09, 2010 Nat Genet Genome-wide association study identifies five new breast cancer susceptibility loci.	Breast cancer
05/23/10	Morrison AC April 17, 2010 Circ Cardiovasc Genet Genomic variation associated with mortality among adults of European and African ancestry with heart failure: the cohorts for heart and aging research in genomic epidemiology consortium.	Mortality among heart failure patients
03/29/10	Dubois PC February 28, 2010 Nat Genet Multiple common variants for celiac disease influencing immune gene expression.	Celiac disease
12/10/09	Imielinski M November 15, 2009 Nat Genet Common variants at five new loci associated with early-onset inflammatory bowel disease.	Inflammatory bowel disease (early onset)
06/29/09	De Jager PL June 14, 2009 Nat Genet Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci.	Multiple sclerosis
12/09/08	Sonuga-Barke EJ October 07, 2008 Am J Med Genet B Neuropsychiatr Genet Does parental expressed emotion moderate genetic effects in ADHD? An exploration using a genome wide association scan.	Conduct disorder (interaction)
11/25/08	Ferreira MA August 17, 2008 Nat Genet Collaborative genome-wide association analysis supports a role for ANK3 and CACNA1C in bipolar disorder.	Bipolar disorder

11q13.1 (*PRDX5*)

04/12/11	Mells GF March 13, 2011 Nat Genet Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis.	Primary biliary cirrhosis
01/11/11	Franke A November 21, 2010 Nat Genet Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.	Crohn's disease
10/15/10	Yang Q September 30, 2010 Circ Cardiovasc Genet Multiple genetic loci influence serum urate levels and their relationship with gout and cardiovascular disease risk factors.	Serum urate
10/16/10	Lango Allen H September 29, 2010 Nature Hundreds of variants clustered in genomic loci and biological pathways affect human height.	Height
09/24/10	Chalasani N August 10, 2010 Gastroenterology Genome-wide association study identifies variants associated with histologic features of nonalcoholic Fatty liver disease.	Non-alcoholic fatty liver disease histology (lobular)
08/12/10	Petukhova L July 01, 2010 Nature Genome-wide association study in alopecia areata implicates both innate and adaptive immunity.	Alopecia areata

07/12/10	Ramdas WD June 10, 2010 PLoS Genet A genome-wide association study of optic disc parameters.	Vertical cup-disc ratio
05/05/10	Kottgen A April 11, 2010 Nat Genet New loci associated with kidney function and chronic kidney disease.	Chronic kidney disease
06/22/09	Kolz M June 05, 2009 PLoS Genet Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations.	Serum uric acid
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16p13.13 (*SOCS1*)

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17q21.2 (*STAT3*)

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11/25/08	Barrett JC June 29, 2008 Nat Genet Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease.	Crohn's disease

19p13.2 (*TYK2*)

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04/13/11	Grassi MA March 26, 2011 Hum Mol Genet Genome-wide meta-analysis for severe diabetic retinopathy.	Diabetic retinopathy
04/11/11	Schunkert H March 06, 2011 Nat Genet Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease.	Coronary heart disease
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01/08/11	Elks CE November 21, 2010 Nat Genet Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies.	Menarche (age at onset)
01/11/11	Franke A November 21, 2010 Nat Genet Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.	Crohn's disease
01/18/11	Strange A October 17, 2010 Nat Genet A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1.	Psoriasis
10/16/10	Lango Allen H September 29, 2010 Nature Hundreds of variants clustered in genomic loci and biological pathways affect human height.	Height
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01/12/09	Aulchenko YS December 07, 2008 Nat Genet Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts.	Cholesterol, total
01/12/09	NA	LDL cholesterol
01/12/09	Kathiresan S December 07, 2008 Nat Genet Common variants at 30 loci contribute to polygenic dyslipidemia.	HDL cholesterol
01/12/09	NA	LDL cholesterol
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11/25/08	Pare G July 04, 2008 PLoS Genet Novel association of ABO histo-blood group antigen with soluble ICAM-1: results of a genome-wide association study of 6,578 women.	Soluble ICAM-1
11/25/08	Melzer D May 09, 2008 PLoS Genet A genome-wide association study identifies protein quantitative trait loci (pQTLs).	Protein quantitative trait loci
11/25/08	Gudbjartsson DF April 06, 2008 Nat Genet Many sequence variants affecting diversity of adult human height.	Height
11/25/08	Kathiresan S January 13, 2008 Nat Genet Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans.	LDL cholesterol
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19q13.33 (*FUT2*)		
05/26/11	Zhai G April 14, 2011 PLoS Genet Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms.	Serum dehydroepiandrosterone sulphate levels
04/12/11	Mells GF March 13, 2011 Nat Genet Genome-wide association study identifies 12 new susceptibility loci for primary biliary cirrhosis.	Primary biliary cirrhosis
01/13/11	Gudmundsson J December 15, 2010 Sci Transl Med Genetic correction of PSA values using sequence variants associated with PSA levels.	Serum prostate-specific antigen levels
01/11/11	Franke A November 21, 2010 Nat Genet Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.	Crohn's disease
12/16/10	Ikram MK October 28, 2010 PLoS Genet Four novel Loci (19q13, 6q24, 12q24, and 5q14) influence the microcirculation in vivo.	Retinal vascular caliber
09/02/10	Liu X July 18, 2010 Nat Genet Genome-wide meta-analyses identify three loci associated with primary biliary cirrhosis.	Primary biliary cirrhosis
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04/15/10	Kamatani Y February 07, 2010 Nat Genet Genome-wide association study of hematological and biochemical traits in a Japanese population.	Hematological and biochemical traits
04/01/09	Tanaka T March 18, 2009 Am J Hum Genet Genome-wide association study of vitamin B6, vitamin B12, folate, and homocysteine blood concentrations.	Folate pathway vitamin levels
02/26/09	Otowa T January 23, 2009 J Hum Genet Genome-wide association study of panic disorder in the Japanese population.	Panic disorder
12/09/08	Bertram L October 29, 2008 Am J Hum Genet Genome-wide association analysis reveals putative Alzheimer's disease susceptibility loci in addition to APOE.	Alzheimer's disease
11/25/08	Hazra A September 07, 2008 Nat Genet Common variants of FUT2 are associated with plasma vitamin B12 levels.	Plasma level of vitamin B12
11/25/08	Eeles RA February 10, 2008 Nat Genet Multiple newly identified loci associated with prostate cancer susceptibility.	Prostate cancer
22q11.21 (*YDJC*)		
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04/06/11	Zhernakova A February 24, 2011 PLoS Genet Meta-analysis of genome-wide association studies in celiac disease and rheumatoid arthritis identifies fourteen non-HLA shared loci.	Celiac disease and Rheumatoid arthritis
01/11/11	Franke A November 21, 2010 Nat Genet Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.	Crohn's disease
03/29/10	Dubois PC February 28, 2010 Nat Genet Multiple common variants for celiac disease influencing immune gene expression.	Celiac disease
04/15/10	Kamatani Y February 07, 2010 Nat Genet Genome-wide association study of hematological and biochemical traits in a Japanese population.	Hematological and biochemical traits
11/09/09	Han JW October 18, 2009 Nat Genet Genome-wide association study in a Chinese Han population identifies nine new susceptibility loci for systemic lupus erythematosus.	Systemic lupus erythematosus

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