American Journal of Human Genetics, Volume *92*

Supplemental Information

Refinement in Localization and Identification of Gene Regions Associated with Crohn Disease

Heather Elding, Winston Lau, Dallas M. Swallow, and Nikolas Maniatis

Supplemental Inventory

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Table S1. Whole-Genome Association Statistics and Closest Gene to the Estimated Location of the Causal Agent $\hat{S}$ for the Previously Reported 71 LD Intervals

Chr	Reported LD Interval (Mb)	Interval Span (Mb)	WTCCC $\hat{S}$	WTCCC P-value	NIDDK $\hat{S}$	NIDDK P-value	Gene region (WTCCC/NIDDK If different)
1p36.23	7.74 - 7.97	0.23	-	-	7,801.1	$2.2\text{x}10^{-05}$	*CAMTA1*[a]
1p31.3	67.36 - 67.77	0.41	67,684.8	$2.1\text{x}10^{-11}$	67,707.3	$3.0\text{x}10^{-10}$	*IL23R*[a]
1p13.2	113.95 - 114.62	0.67	114,560.3	$1.4\text{x}10^{-03}$	114,108.3	$5.0\text{x}10^{-03}$	*OLFML3/MAGI3*[a]
1q22	154.97 - 156.13	1.16	-	-	-	-	-
1q23.3	160.69 - 162.47	1.78	160,887.0	$2.6\text{x}10^{-03}$	160,837.3	$5.8\text{x}10^{-03}$	*ITLN2/CD244*
1q25.1	172.66 - 172.95	0.29	172,891.9	$3.6\text{x}10^{-13}$	-	-	*TNFSF18*
1q31.3	197.32 - 197.95	0.63	197,786.1	$1.2\text{x}10^{-04}$	-	-	*DENND1B*
1q32.1	200.85 - 201.06	0.21	200,877.3	$3.0\text{x}10^{-14}$	200,957.2	$1.5\text{x}10^{-02}$	*C1orf106*[a]*/KIF21B*[a]
1q32.1	206.80 - 207.03	0.23	-	-	-	-	-
2p23.3	25.45 - 25.60	0.15	25,389.2	$3.5\text{x}10^{-02}$	-	-	*POMC*[a]
2p23.3	27.39 - 27.86	0.47	27,697.4	$5.4\text{x}10^{-04}$	27,619.3	$2.3\text{x}10^{-11}$	***IFT172*[a]*/PPM1G*[a]**
2p21	43.45 - 43.95	0.50	43,840.8	$2.0\text{x}10^{-05}$	43,581.0	$1.1\text{x}10^{-02}$	*THADA*[a]
2p15	60.92 - 61.89	0.97	61,395.5	$1.9\text{x}10^{-05}$	-	-	*C2orf74*
2q12.1	102.80 - 103.30	0.50	103,059.8	$1.8\text{x}10^{-08}$	102,951.7	$1.7\text{x}10^{-05}$	*IL18RAPa/IL1RL1*[a]
2q33.1	198.14 - 198.96	0.82	198,957.7	$1.6\text{x}10^{-02}$	198,205.8	$1.1\text{x}10^{-03}$	*PLCL1a/ANKRD44*
2q37.1	231.05 - 231.23	0.18	231,109.3	$2.8\text{x}10^{-05}$	-	-	*SP140*[a]
2q37.1	234.15 - 234.57	0.42	234,144.8	$5.6\text{x}10^{-25}$	234,171.9	$2.2\text{x}10^{-09}$	*ATG16L1*[a]
3p24.3	18.60 - 18.88	0.28	18,707.0	$5.3\text{x}10^{-03}$	18,629.1	$2.6\text{x}10^{-05}$	*SATB1*
3p21.31	48.18 - 51.75	3.57	49,743.9	$1.7\text{x}10^{-31}$	48,818.0	$3.3\text{x}10^{-19}$	*RNF123a/PRKAR2A*[a]
5p13.1	39.84 - 40.96	1.12	40,447.1	$6.0\text{x}10^{-51}$	40,288.0	$2.7\text{x}10^{-07}$	*PTGER4*
5q13.2	72.45 - 72.58	0.13	72,465.4	$5.8\text{x}10^{-03}$	-	-	*TMEM174*
5q15	96.08 - 96.42	0.34	96,372.2	$1.3\text{x}10^{-08}$	-	-	*LNPEP*
5q31.1	129.38 - 132.02	2.64	131,748.2	$2.7\text{x}10^{-22}$	131,631.4	$8.9\text{x}10^{-07}$	*C5orf56*[a]*/SLC22A4*[a]
5q31.3	141.41 - 141.64	0.23	141,480.3	$1.3\text{x}10^{-02}$	-	-	*NDFIP1*
5q33.1	150.03 - 150.40	0.37	150,230.7	$3.6\text{x}10^{-09}$	-	-	*IRGM*
5q33.3	158.50 - 158.95	0.45	158,825.7	$5.6\text{x}10^{-06}$	158,826.0	$3.5\text{x}10^{-02}$	*IL12B*
5q35.2	173.22 - 173.54	0.32	-	-	173,417.9	$6.7\text{x}10^{-03}$	*C5orf47*[a]
6p25.2	3.41 - 3.47	0.06	3,417.6	$1.5\text{x}10^{-07}$	-	-	*SLC22A23*[a]
6p22.3	20.49 - 21.14	0.65	20,559.3	$4.3\text{x}10^{-03}$	20,433.1	$2.8\text{x}10^{-03}$	*CDKAL1a/E2F3*[a]
6p21.32	31.38 - 32.87	1.49	32,720.6	$1.2\text{x}10^{-27}$	32,193.4	$1.6\text{x}10^{-07}$	*HLA-DQB2*
6q15	90.80 - 91.08	0.28	-	-	-	-	-
6q21	106.39 - 106.56	0.17	-	-	106,421.7	$4.0\text{x}10^{-02}$	*PRDM1*
6q25.3	159.34 - 159.54	0.20	159,539.7	$1.2\text{x}10^{-03}$	-	-	*FNDC1*
6q27	167.34 - 167.55	0.21	167,441.4	$3.3\text{x}10^{-09}$	167,355.9	$8.5\text{x}10^{-03}$	*FGFR1OP*[a]*/RNASET2*[a]
7p12.2	50.25 - 50.33	0.08	50,255.3	$9.4\text{x}10^{-04}$	-	-	*C7orf72*
8q24.13	126.47 - 126.58	0.11	126,544.1	$4.5\text{x}10^{-05}$	-	-	*TRIB1*
8q24.21	129.49 - 129.60	0.11	129,567.2	$1.3\text{x}10^{-04}$	129,570.7	$2.9\text{x}10^{-03}$	***Intergenic***
9p24.1	4.94 - 5.30	0.36	5,274.6	$1.4\text{x}10^{-04}$	5,270.3	$5.4\text{x}10^{-03}$	***RLN2***
9q32	117.43 - 117.70	0.27	117,555.6	$3.9\text{x}10^{-04}$	-	-	*TNFSF15*
9q34.3	139.13 - 139.42	0.29	139,280.8	$2.3\text{x}10^{-05}$	139,299.7	$2.6\text{x}10^{-03}$	*SNAPC4*[a]*/SDCCAG3*[a]
10p15.1	6.03 - 6.17	0.14	6,189.9	$3.6\text{x}10^{-03}$	6,165.5	$1.2\text{x}10^{-08}$	*PFKFB3*[a]*/RBM17*
10p11.21	35.18 - 35.90	0.72	35,554.8	$3.4\text{x}10^{-29}$	-	-	*CCNY*[a]
10q21.1	59.83 - 60.14	0.31	59,892.8	$9.3\text{x}10^{-09}$	59,893.1	$1.6\text{x}10^{-02}$	*IPMK*
10q21.2	64.30 - 64.76	0.46	64,448.3	$1.2\text{x}10^{-18}$	-	-	*ZNF365*
10q22.3	81.00 - 81.10	0.10	-	-	81,019.8	$1.5\text{x}10^{-02}$	*ZMIZ1*[a]
10q24.2	101.27 - 101.34	0.07	101,324.7	$1.2\text{x}10^{-32}$	101,274.6	$2.3\text{x}10^{-02}$	*NKX2-3*

Table S1 continued

Chr	Reported LD Interval (Mb)	Interval Span (Mb)	WTCCC $\hat{S}$	WTCCC P-value	NIDDK $\hat{S}$	NIDDK P-value	Gene region (WTCCC/NIDDK If different)
11q12.2	61.52 - 61.68	0.16	61,680.2	$3.4x10^{-02}$	-	-	*RAB3IL1*[a]
11q13.1	63.82 - 64.29	0.47	64,027.0	$5.8x10^{-03}$	64,137.4	$3.2x10^{-02}$	*PLCB3*[a]*/RPS6KA4*[a]
11q13.5	76.02 - 76.36	0.34	76,304.4	$4.4x10^{-10}$	-	-	*C11orf30*
12q12	40.13 - 41.02	0.89	40,598.3	$3.0x10^{-02}$	40,368.0	$1.7x10^{-03}$	*LRRK2/SLC2A13*[a]
13q14.11	42.82 - 43.10	0.28	43,022.6	$1.3x10^{-07}$	-	-	*TNFSF11*
13q14.11	44.23 - 44.64	0.41	44,491.1	$6.6x10^{-12}$	44,607.7	$3.0x10^{-02}$	*LACC1/LINC00284*
14q24.1	69.16 - 69.32	0.16	69,199.5	$4.1x10^{-02}$	-	-	*ZFP36L1*
14q31.3	88.21 - 88.64	0.43	88,364.3	$6.2x10^{-05}$	88,216.2	$5.1x10^{-03}$	*GALC*
15q22.33	67.41 - 67.48	0.07	67,410.8	$1.5x10^{-02}$	-	-	*SMAD3*[a]
16p11.2	28.29 - 29.03	0.74	-	-	28,940.3	$4.5x10^{-02}$	*CD19*
16q12.1	50.46 - 50.85	0.39	50,803.2	$2.6x10^{-15}$	50,803.2	$1.1x10^{-09}$	*NOD2*[a]
			50,846.3	$1.6x10^{-13}$	50,846.5	$4.1x10^{-04}$	*CYLD*
17q12	32.49 - 32.68	0.19	-	-	32,634.2	$4.1x10^{-02}$	***CCL8***
17q12	37.37 - 38.26	0.89	37,985.9	$1.1x10^{-03}$	37,888.9	$4.2x10^{-05}$	*IKZF3*[a]*/MIEN1*
17q21.2	40.32 - 41.00	0.68	40,501.5	$2.0x10^{-18}$	-	-	*STAT3*[a]
18p11.21	12.74 - 12.93	0.19	12,875.2	$2.9x10^{-12}$	-	-	*PTPN2*[a]
19p13.3	1.09 - 1.18	0.09	1,127.7	$2.0x10^{-02}$	-	-	*SBNO2*[a]
19p13.2	10.40 - 10.64	0.24	10,560.9	$1.3x10^{-02}$	-	-	*PDE4A*[a]
19q13.11	33.73 - 33.78	0.05	-	-	-	-	-
19q13.33	49.09 - 49.28	0.19	-	-	49,212.0	$3.6x10^{-04}$	*FUT2*
20q13.33	62.18 - 62.48	0.30	62,327.9	$2.3x10^{-04}$	-	-	*RTEL1-TNFRSF6B*[a]
21q12.1	16.70 - 16.85	0.15	16,841.4	$4.4x10^{-07}$	-	-	*USP25*
21q11.21	21.81 - 22.06	0.25	-	-	-	-	-
21q22.3	45.59 - 45.70	0.11	45,609.1	$5.5x10^{-06}$	-	-	*ICOSLG*
22q12.2	29.90 - 30.67	0.77	30,228.8	$8.0x10^{-07}$	-	-	*ASCC2*[a]
22q13.1	39.67 - 39.81	0.14	-	-	39,686.8	$1.1x10^{-02}$	*RPL3*

bold denotes that the signal is replicated using the data stratified according to Non Jewish Ileal and extra-ileal inflammation; we give the closest gene (up to 300kb) to the $\hat{S}$; [a]at least one of the estimated locations $\hat{S}$ is located within the identified gene. When $\hat{S}$ is not within the gene then we give the closest gene (up to 300kb) to the $\hat{S}$. All locations in kb are in NCBI 37.

Table S2: Whole-Genome Association Statistics and the Closest Gene to the Estimated Location of the Causal Agent for the 78 Gene-Regions that Passed Our Genome-Wide Significance Threshold 1x10^{-5} with $\hat{S}$ Locations of 150kb or Less between the 2 Data Sets

Chr	WTCCC $\hat{S}$	NIDDK $\hat{S}$	Gene region (WTCCC/NIDDK if different)	Meta-P-value
1p31.3	61,982.8	61,938.8	*NFIA*[b]	1.4x10^{-07}
1p31.3	64,095.1	64,005.9	***PGM1a/EFCAB7a***[b]	1.1x10^{-08}
1q21.3	151,788.8	151,837.4	*RORC*[a]*/THEM4*	1.2x10^{-09}
1q42.2	233,765.3	233,835.4	***KCNK1***[ab]	5.3x10^{-08}
1q43	236,709.1	236,684.6	***LGALS8***[a]	2.8x10^{-07}
1q43	236,862.0	236,805.4	***ACTN2***[a]***/HEATR1***	1.3x10^{-10}
2p25.2	6,394.6	6,425.5	*LOC400940*	5.1x10^{-09}
2p24.2	16,442.2	16,452.4	***FAM49A***	5.6x10^{-06}
2p23.3	25,247.9	25,138.3	*DNAJC27-AS1*[a]*/ADCY3*[a]	8.7x10^{-18}
2p13.1	74,616.6	74,659.7	*DCTN1*[a]*/RTKN*[ab]	4.9x10^{-22}
2q14.1	117,951.4	117,821.6	***Intergenic***	3.3x10^{-06}
2q24.3	168,944.1	168,810.8	*STK39*[a]	3.3x10^{-07}
2q32.1	185,889.2	185,791.4	*ZNF804A*[a]	7.4x10^{-09}
2q34	212,427.1	212,442.8	*ERBB4*[a]	3.1x10^{-06}
3p22.3	36,213.9	36,097.7	*STAC/ARPP21*	2.6x10^{-09}
3p22.2	37,598.6	37,602.5	***ITGA9***[a]	6.2x10^{-09}
3q11.2	96,376.9	96,304.5	***EPHA6***[b]	6.6x10^{-09}
3q12.1	99,338.2	99,330.9	*COL8A1*	1.2x10^{-07}
4p12-11	48,197.8	48,342.9	*TEC*[a]*/SLAIN2*	3.4x10^{-15}
4q12	54,551.5	54,668.6	*LNX1/RPL21P44*[b]	2.7x10^{-06}
4q12	55,260.5	55,241.3	***PDGFRA***[b]	2.9x10^{-09}
4q25	110,193.1	110,128.2	***COL25A1***[ab]	6.8x10-^{06}
4q35.1	186,241.5	186,267.1	*SNX25*[a]	5.2x10^{-08}
5q22.2	112,590.6	112,572.4	***MCC***[ab]	8.5x10^{-06}
5q23.2	126,822.9	126,898.0	*MEGF10/PRRC1*[b]	5.5x10^{-10}
6p22.3	24,443.8	24,457.3	***GPLD1***[a]	4.0x10^{-07}
6p22.1	29,605.2	29,575.4	*GABBR1*[a]	5.5x10^{-06}
6q12	65,246.8	65,244.5	*EYS*[a]	1.6x10^{-07}
6q25.3	159,670.8	159,794.4	*FNDC1*[a]	1.5x10^{-08}
6q27	166,505.9	166,501.1	*T*[b]	7.0x10^{-07}
7p21.1	20,044.2	19,975.1	***MACC1/TMEM196***	1.9x10^{-07}
7p15.3	24,175.9	24,271.9	*NPY*[b]	3.9x10^{-07}
7p14.1	41,898.3	41,939.6	***INHBA-AS1/GLI3***	2.1x10^{-06}
7q21.11	80,401.5	80,470.9	*SEMA3C*[a]	4.8x10^{-06}
7q31.31	120,409.2	120,337.3	*TSPAN12/KCND2*[a]	8.7x10^{-06}
7q31.33	125,266.9	125,219.7	***Intergenic***[b]	3.7x10^{-10}

Table S2 continued

Chr	WTCCC $\hat{S}$	NIDDK $\hat{S}$	Gene region (WTCCC/NIDDK if different)	Meta-P-value
7q32.3	131,467.2	131,394.6	*PODXL*[b]	7.8x10^{-07}
8p22	17,632.9	17,635.3	*MTUS1*[a]	5.5x10^{-07}
8q12.1	57,504.1	57,507.6	*LOC100507632*	5.2x10^{-06}
8q21.13	80,385.0	80,277.0	*STMN2*[b]	1.3x10^{-12}
8q21.13	83,670.2	83,786.5	***intergenic***	1.9x10^{-08}
8q22.3	104,465.6	104,363.8	*DCAF13/FZD6*[b]	4.4x10^{-06}
8q23.3	114,908.3	114,815.4	***intergenic***[b]	4.9x10^{-11}
9p24.3	396.8	468.1	*DOCK8*[ab]	2.6x10^{-07}
10p12.1	25,571.8	25,686.6	***GPR158***[ab]	1.5x10^{-09}
10q21.1	61,019.5	61,135.2	***FAM13C***[a]	2.2x10^{-06}
10q21.2	63,604.2	63,553.3	*ARID5B/C10orf107*	7.3x10^{-09}
10q22.2	75,697.5	75,698.5	***PLAU***[b]	2.6x10^{-13}
10q22.3	79,392.4	79,247.9	*KCNMA1*[a]	2.5x10^{-06}
10q25.1	111,613.9	111,622.3	*XPNPEP1*	1.8x10^{-06}
10q25.3	115,370.8	115,381.2	***NRAP***[a]	1.0x10^{-05}
11p15.4	5,785.5	5,836.4	*OR52N4/OR52N2*[b]	3.3x10^{-10}
11p14.1	27,827.8	27,790.8	*BDNF*	8.2x10^{-07}
11q12.1	56,626.0	56,625.0	***OR9G4***	1.0x10^{-05}
11q24.2	126,774.5	126,749.9	***KIRREL3***[a]	1.1x10^{-06}
12p11.22	28,744.2	28,741.7	*CCDC91*[b]	1.1x10^{-06}
12q12	44,676.8	44,823.7	***TMEM117***[ab]	2.4x10^{-06}
12q22	92,998.8	93,090.8	***C12orf74***[b]	7.6x10^{-09}
12q23.1	101,350.2	101,350.1	***ANO4***[a]	9.3x10^{-06}
13q14.3	52,081.3	52,078.0	***MIR4703***	8.9x10^{-08}
14q21.1	39,671.6	39,601.9	*PNN/GEMIN2*[ab]	6.4x10^{-07}
14q31.1	80,015.5	80,139.6	***NRXN3***[ab]	7.6x10^{-07}
15q13.3	31,839.1	31,737.8	*OTUD7A*[a]	1.0x10^{-08}
15q14	34,414.0	34,291.8	*PGBD4/CHRM5*[a]	8.9x10^{-06}
16p13.3	7,262.9	7,200.6	*RBFOX1*[b]	1.0x10^{-05}
16p13.3	7,272.8	7,391.8	***RBFOX1***[a]	3.6x10^{-06}
16q12.1	50,417.0	50,417.2	*BRD7*	2.0x10^{-08}
16q22.1	67,464.1	67,422.7	***HSD11B2***[b]	7.5x10^{-08}
16q24.1	85,982.3	85,958.0	***IRF8***	1.5x10^{-08}
17q25.1	73,344.9	73,411.5	*GRB2*[a]*/MIR3678*	4.3x10^{-14}
18q11.2	19,677.2	19,620.4	*GATA6*	2.6x10^{-07}
18q12.3	40,517.4	40,666.0	***RIT2***[ab]	6.0x10^{-18}
18q21.1	44,940.9	44,800.7	*IER3IP1*[b]	7.8x10^{-06}
20p12.3	7,901.0	7,878.5	*HAO1*[ab]	1.4x10^{-07}
20q12	37,960.3	38,106.0	*LOC339568*	3.9x10^{-06}

Table S2 continued

Chr	WTCCC $\hat{S}$	NIDDK $\hat{S}$	Gene region (WTCCC/NIDDK if different)	Meta-P-value
20q13.12	44,741.5	44,672.0	***CD40/SLC12A5***[ab]	$7.7x10^{-08}$
22q12.3	37,325.9	37,349.3	*CSF2RB*[a]*/LOC1005006241*	$2.6x10^{-08}$
Xq28	147,228.4	147,114.7	*FMR1NB*	$4.4x10^{-07}$

bold denotes that the signal is replicated using the data stratified according to Non Jewish Ileal and extra-ileal inflammation; [a]at least one of the estimated locations $\hat{S}$ is located within the identified gene; [b]the signal is significant in the Pooled NIDDK data as well as the stratified Non Jewish Ileal and extra-ileal dataset. When $\hat{S}$ is not within the gene then we give the closest gene (up to 300kb) to the $\hat{S}$. All locations in kb are in NCBI 37.

Table S3: Whole-Genome Association Statistics and the Closest Gene to the Estimated Location of the Causal Agent for the 56 Gene-Regions with p Values 10^{-3}-10^{-5} and with $\hat{S}$ Locations of 80 kb or Less between the 2 Data Sets

Chr	WTCCC $\hat{S}$	NIDDK $\hat{S}$	Gene region (WTCCC/NIDDK if different)	Meta-P-value
1p34.1	45,764.3	45,764.4	*LOC400752*	3.6x10^{-04}
1p32.2	58,535.6	58,575.4	*DAB1*[a]	2.7x10^{-04}
1p31.3	68,056.4	68,072.2	***GADD45A***	2.9x10^{-05}
1p31.1	83,125.7	83054.7	***intergenic***	1.4x10^{-04}
1q31.3	194,273.4	194,332.3	*intergenic*[b]	2.2x10^{-04}
1q32.1	204,129.7	204,143.0	*REN*[a]	3.4x10^{-04}
1q42.12	225,508.2	225,554.8	*DNAH14*[a]	3.0x10^{-05}
1q42.12	226,248.8	226,249.4	***H3F3A***[b]	9.1x10^{-04}
2p14	67,869.6	67,871.1	*ETAA1*[b]	2.1x10^{-05}
2q11.2	102,625.1	102,625.1	*IL1R2*[a]	4.9x10^{-04}
2q31.1	170,038.8	170,037.2	***LRP2***[a]	8.4x10^{-04}
2q36.3	226,258.2	226,258.4	*NYAP2*	1.2x10^{-05}
3p14.3	55,192.0	55,115.1	*CACNA2D3*	5.7x10^{-05}
3p12.3	77,377.2	77,377.3	*ROBO2*[a]	8.2x10^{-04}
3q13.2	112,181.4	112,184.1	*BTLA*[a]	2.9x10^{-05}
3q24	148,459.5	148,419.7	*AGTR1*[a]	2.1x10^{-04}
4p15.33	13,075.6	13,050.3	*HSP90AB2*[b]	1.5x10^{-04}
4q13.2	67,799.9	67,792.9	***intergenic***	8.2x10^{-04}
4q27	121,797.6	121872.1	*PRDM5*[a]	2.1x10^{-05}
5p14.3	23,042.2	23,002.6	***CDH12***	3.9x10^{-05}
5q21.1	100,970.9	100,970.8	***intergenic***	6.0x10^{-04}
5q33.3	156,594.7	156,627.7	*FAM71B/ITK*[ab]	8.2x10^{-05}
6p22.3	21,462.0	21,467.8	*SOX4*	5.6x10^{-04}
6q21	107,433.4	107,473.5	*BEND3*[a]	3.6x10^{-05}
6q21	113,971.2	113,977.4	*MARCKS*	7.1x10^{-05}
6q22.31	125,214.4	125,215.3	*STL*[b]	3.0x10^{-04}
6q23.3	137,546.9	137,565.2	*IFNGR1*	3.5x10^{-04}
6q25.3	156,152.9	156,190.7	*intergenic*	1.9x10^{-04}
6q25.3	158,344.5	158,365.2	*SNX9*[ab]	3.1x10^{-04}
7p21.1	20,286.7	20,301.2	***MACC1***	5.5x10^{-05}
7p14.3	34,739.3	34,757.7	***NPSR1***[a]	3.2x10^{-04}
7q31.32	122,995.2	122,993.0	***IQUB***[b]	1.6x10^{-04}
7q34	142,653.2	142,650.9	*KEL*[a]	1.1x10^{-04}
8q24.22	134,050.4	134,063.7	*SLA*[a]	1.5x10^{-04}
9q21.13	74,603.0	74678.4	*C9orf85/C9orf57*	7.7x10^{-4}
9q21.2	80,206.6	80,206.7	***GNA14***[ab]	2.7x10^{-04}
9q33.1	121,364.8	121,365.0	***intergenic***	5.1x10^{-04}

Table S3 continued

Chr	WTCCC $\hat{S}$	NIDDK $\hat{S}$	Gene region (WTCCC/NIDDK if different)	Meta-P-value
10q23.31	90,787.7	90,787.7	*FAS*[b]	2.7x10^{-04}
11p15.5	1,539.0	1,539.0	*MOB2*[a]	2.1x10^{-04}
11p15.3	12,387.3	12,331.6	***MICALCL***[a]	5.1x10^{-05}
12q14.3	67,645.2	67,640.5	***CAND1***	6.9x10^{-04}
12q21.32	89,154.8	89,148.0	*KITLG*[b]	5.7x10^{-05}
12q24.32	126,746.8	126,753.9	*LOC100128554*[b]	9.9x10^{-04}
13q12.13	27,389.5	27,391.1	***GPR12***	1.3x10^{-04}
13q13.3	36,090.9	36,159.4	*NBEA*[a]	2.7x10^{-04}
13q31.3	90,018.8	90,018.6	***intergenic***	7.5x10^{-04}
13q31.3	90,206.6	90,176.3	***intergenic***	6.9x10^{-04}
14q31.1	82,444.3	82,452.3	*intergenic*[b]	5.4x10^{-05}
15q21.2	50,193.4	50,171.3	***ATP8B4***[a]	8.8x10^{-04}
16q21	61,777.3	61,777.1	*CDH8*[a]	1.4x10^{-05}
16q23.1	76,295.6	76,275.6	*CNTNAP4*	9.1x10^{-04}
16q23.1	78,458.5	78,410.4	*WWOX*[ab]	6.6x10^{-04}
20p21.1	15,802.7	15,876.4	*MACROD2*[a]	7.1x10^{-04}
21q22.2	41,532.5	41,513.2	*DSCAM*[a]	7.3x10^{-04}
22q12.3	35,540.3	35,540.4	*ISX*[b]	2.8x10^{-04}
Xq23	115,981.3	115,966.6	***intergenic***	7.3x10^{-05}

bold denotes that the signal is replicated using the data stratified according to Non Jewish Ileal and extra-ileal inflammation; [a]at least one of the estimated locations $\hat{S}$ is located within the identified gene; [b]the signal is significant in the Pooled NIDDK data as well as the stratified Non Jewish Ileal and extra-ileal dataset. When $\hat{S}$ is not within the gene then we give the closest gene (up to 300kb) to the $\hat{S}$. All locations in kb are in NCBI 37.

Table S4. GO Analysis for the Genes in Tables S1, S2, and S3

GO-ID	**Corrected P-value**	**x**	**n**	**GO ID Description**	**Genes in test set**
4871	9.6 x10^{-06}	48	2128	Signal transducer activity	*GNA14,IL1R2,CD244,ERBB4,GRB2,GABBR1,CCL8,RORC,SLA,OR52N2,AGTR1,PLCL1,PLCB3,OR52N4,CSF2RB,SEMA3C,ROBO2,STK39,NPSR1,FAS,IFNGR1,TEC,GPR158,IL18RAP,IL23R,PTGER4,NRXN3,IL1RL1,SNX25,NDFIP1,SMAD3,OR9G4,ACTN2,CD40,STAT3,FZD6,BTLA,ITGA9,CHRM5,TNFSF11,EPHA6,CD19,NPY,PDGFRA,MCC,IL12B,LRP2,GPR12*
4872	1.8 x10^{-03}	35	1686	Receptor activity	*IL1R2,CD244,ERBB4,GABBR1,RORC,OR52N2,AGTR1,OR52N4,CSF2RB,SEMA3C,ROBO2,NPSR1,FAS,IFNGR1,TEC,GPR158,IL18RAP,IL23R,PTGER4,NRXN3,IL1RL1,OR9G4,CD40,FZD6,BTLA,ITGA9,CHRM5,EPHA6,TNFSF11,NPY,PDGFRA,MCC,IL12B,LRP2,GPR12*
5515	1.9 x10^{-03}	111	8119	Protein binding	*ADCY3,TNFSF15,TNFSF18,LNX1,PNN,AGTR1,BDNF,PRKAR2A,DAB1,GATA6,PDE4A,RLN2,STK39,ROBO2,FAS,WWOX,DSCAM,MAGI3,KCND2,STMN2,ACTN2,CD40,DCTN1,SP140,FGFR1OP,PRDM5,PDGFRA,LRRK2,IL1R2,SNX9,CAMTA1,ERBB4,MOB2,PFKFB3,GRB2,KEL,ITLN2,SOX4,CCL8,CCDC91,POMC,T,RPL3,TEC,ITK,IKZF3,IL1RL1,PTPN2,PODXL,NDFIP1,SMAD3,HEATR1,DOCK8,BTLA,EPHA6,TNFSF11,NPY,MARCKS,RIT2,ATG16L1,E2F3,GABBR1,NBEA,GLI3,SLA,LNPEP,NOD2,PLCB3,CCNY,BRD7,SLC22A4,SEMA3C,CSF2RB,IFNGR1,KIRREL3,KCNMA1,CNTNAP4,RAB3IL1,COL25A1,ZMIZ1,CAND1,MCC,IL12B,GADD45A,ICOSLG,CD244,KITLG,RTKN,ZNF365,MACC1,TRIB1,ZFP36L1,CYLD,RNF123,REN,GEMIN2,SLC12A5,SNX25,XPNPEP1,STAT3,FZD6,MICALCL,ANKRD44,RPS6KA4,CD19,NRAP,IRF8,IFT172,LRP2,NFIA,RBM17*
6928	2.0 x10^{-03}	15	474	Cellular component movement	*NRXN3,ARID5B,PODXL,KITLG,GLI3,STAT3,AGTR1,BDNF,DAB1,TNFSF11,NPY,SEMA3C,ROBO2,IL12B,NKX2-3*
50896	2.2 x10^{-03}	59	3631	Response to stimulus	*ADCY3,TNFSF15,GABBR1,TNFSF18,AGTR1,NOD2,BDNF,PRKAR2A,STAC,GATA6,PDE4A,SEMA3C,STK39,ROBO2,FAS,IFNGR1,DSCAM,KCNMA1,SATB1,IL18RAP,PTGER4,C11ORF30,IRGM,CD40,SP140,HAO1,PDGFRA,HSD11B2,IL12B,LRRK2,GADD45A,ICOSLG,IL1R2,SBNO2,ERBB4,GRB2,CCL8,TRIB1,OR52N2,PLCL1,OR52N4,REN,NKX2-3,TEC,ITK,IL23R,IL1RL1,PTPN2,SMAD3,OR9G4,KCNK1,STAT3,CD19,EYS,TNFSF11,NPY,IRF8,ATG16L1,PLAU*
16020	2.5 x10^{-03}	100	7251	Membrane	*ADCY3,GNA14,TNFSF15,MEGF10,TNFSF18,PNN,AGTR1,PRKAR2A,DAB1,PDE4A,C2ORF74,STK39,ROBO2,NPSR1,FAS,MTUS1,DSCAM,MAGI3,KCND2,STMN2,SLC22A23,ACTN2,CD40,PDGFRA,LRRK2,IL1R2,SLC2A13,SNX9,ERBB4,GRB2,KEL,CCDC91,OR52N2,OR52N4,TMEM196,ITK,GPR158,IL23R,IL1RL1,PODXL,NDFIP1,SMAD3,KCNK1,CACNA2D3,BTLA,ITGA9,TMEM117,EPHA6,TNFSF11,MARCKS,RIT2,ATG16L1,PLAU,IER3IP1,GABBR1,NBEA,LNPEP,TSPAN12,NOD2,PLCB3,TMEM174,CCNY,SLC22A4,SEMA3C,CSF2RB,ANO4,IFNGR1,ATP8B4,KIRREL3,KCNMA1,IL18RAP,CNTNAP4,PTGER4,FMR1NB,NRXN3,IRGM,COL25A1,CHRM5,MCC,IL12B,THEM4,GPR12,ICOSLG,C9ORF57,CD244,KITLG,CDKAL1,CDH8,CYLD,REN,FUT2,SLC12A5,OR9G4,STAT3,FZD6,CDH12,CD19,NRAP,LRP2,NFIA*
7610	3.2 x10^{-03}	14	466	Behavior	*ADCY3,KCNMA1,CCL8,STAT3,AGTR1,PLCL1,BDNF,TNFSF11,NPY,REN,ROBO2,PLAU,DSCAM,TEC*
32501	1.3 x10^{-02}	64	4373	Multicellular organismal process	*ADCY3,GABBR1,GLI3,AGTR1,TSPAN12,NOD2,BDNF,OLFML3,DAB1,GATA6,SLC22A4,CSF2RB,SEMA3C,ROBO2,IFNGR1,WWOX,KIRREL3,DSCAM,KCNMA1,SATB1,KCND2,NRXN3,STMN2,ARID5B,ACTN2,CD40,DCTN1,CHRM5,ZMIZ1,PDGFRA,HSD11B2,PRDM1,IL12B,LRRK2,ERBB4,GRB2,KEL,KITLG,SOX4,POMC,ZFP36L1,OR52N2,T,OR52N4,REN,COL8A1,NKX23,TEC,IKZF3,PODXL,SLC12A5,SMAD3,OR9G4,STAT3,FZD6,MICALCL,EYS,TNFSF11,NPY,IRF8,IFT172,RIT2,LRP2,PLAU*
30154	1.4 x10^{-02}	30	1666	Cell differentiation	*GRB2,GABBR1,KITLG,SOX4,GLI3,ZFP36L1,T,BDNF,DAB1,GATA6,REN,SEMA3C,ROBO2,WWOX,NKX23,DSCAM,KCNMA1,SATB1,STMN2,NRXN3,SMAD3,STAT3,MICALCL,TNFSF11,ZMIZ1,IRF8,PDGFRA,CAND1,IL12B,PRDM1*
50789	1.4 x10^{-02}	88	6550	Regulation of biological process	*ISX,ADCY3,GNA14,E2F3,GABBR1,TNFSF15,RORC,GLI3,TNFSF18,SLA,PNN,TSPAN12,AGTR1,BDNF,NOD2,PRKAR2A,DAB1,STAC,GATA6,PDE4A,CCNY,BRD7,CSF2RB,ROBO2,STK39,FAS,IFNGR1,WWOX,DSCAM,KCNMA1,SATB1,IL18RAP,PTGER4,CNTNAP4,STMN2,C11ORF30,ARID5B,SNAPC4,ACTN2,CD40,PPM1G,CHRM5,ASCC2,ZMIZ1,FGFR1OP,PRDM5,PDGFRA,MCC,CAND1,PRDM1,IL12B,LRRK2,GADD45A,ICOSLG,CD244,SBNO2,ERBB4,GRB2,ITLN2,KITLG,CCL8,SOX4,RTKN,POMC,MACC1,TRIB1,ZFP36L1,T,CYLD,REN,TEC,NKX2-3,ITK,IKZF3,IL1RL1,PODXL,NDFIP1,SMAD3,STAT3,BTLA,TNFSF11,CD19,RPS6KA4,NPY,IRF8,RIT2,NFIA,PLAU*
9986	1.5 x10^{-02}	10	340	Cell surface	*KCNMA1,BTLA,CD244,NOD2,KCND2,CD19,IL1RL1,ROBO2,CD40,PLAU*

Table S4 continued

GO-ID	**Corrected P-value**	**x**	**n**	**GO ID Description**	**Genes in test set**
5488	1.5 x10^{-02}	147	12360	Binding	*ADCY3,GNA14,TNFSF15,RORC,TNFSF18,LNX1,PNN,AGTR1,BDNF,PRKAR2A,DAB1,STAC,GATA6,PDE4A,RLN2,STK39,ROBO2,NPSR1,FAS,WWOX,DSCAM,SATB1,MAGI3,KCND2,STMN2,ACTN2,CD40,DCTN1,SP140,FGFR1OP,PRDM5,PGM1,PDGFRA,HSD11B2,PRDM1,LRRK2,IL1R2,SNX9,CAMTA1,EFCAB7,ARPP21, MOB2,ERBB4,PFKFB3,DNAH14,GRB2,KEL,ITLN2,SOX4,CCL8,CCDC91,POMC,T,GALC,RPL3,OTUD7A,TEC,NKX2-3,ITK,IKZF3,PTPN2,IL1RL1,PODXL,NDFIP1,SMAD3,LGALS8,HEATR1,DOCK8,CACNA2D3,BTLA,TNFSF11,EPHA6,NPY,H3F3A,MARCKS,RIT2,ATG16L1,ISX,E2F3,GABBR1,NBEA,GLI3,THADA,SLA,LNPEP,PLCB3,NOD2,CCNY,BRD7,SLC22A4,CSF2RB,SEMA3C,IPMK,IFNGR1,KIRREL3,ATP8B4,KCNMA1,CNTNAP4, NRXN3,ARID5B,IRGM,SNAPC4,RAB3IL1,COL25A1,HAO1,PPM1G,CHRM5,ZMIZ1,MCC,CAND1,IL12B,GADD45A,ICOSLG,CD244,KITLG,RTKN,ZNF365, CDKAL1,MACC1,TRIB1,CDH8,ZFP36L1,CYLD,PLCL1,RNF123,REN,RNASET2,KIF21B,ZNF804A,GEMIN2,SLC12A5,SNX25,XPNPEP1,STAT3,FZD6,CDH12, MICALCL,ANKRD44,CD19,RPS6KA4,EYS,NRAP,IRF8,IFT172,LRP2,NFIA,RBM17*
7275	1.5 x10^{-02}	46	2970	Multicellular organismal development	*ERBB4,GRB2,KEL,GABBR1,KITLG,SOX4,GLI3,ZFP36L1,TSPAN12,T,AGTR1,BDNF,OLFML3,DAB1,GATA6,REN,SEMA3C,ROBO2,COL8A1,WWOX,KIRREL3, TEC,DSCAM,NKX23,KCNMA1,SATB1,IKZF3,NRXN3,STMN2,ARID5B,PODXL,SMAD3,DCTN1,STAT3,FZD6,MICALCL,TNFSF11,ZMIZ1,IRF8,IFT172,PDGFRA, PRDM1,IL12B,LRRK2,LRP2,PLAU*
9987	1.5 x10^{-02}	117	9366	Cellular process	*ADCY3,GNA14,TNFSF15,MEGF10,TNFSF18,LNX1,PNN,AGTR1,BDNF,PRKAR2A,DAB1,STAC,GATA6,PDE4A,STK39,ROBO2,FAS,WWOX,DSCAM,SATB1, MAGI3,KCND2,C11ORF30,STMN2,SLC22A23,ACTN2,CD40,DCTN1,FGFR1OP,PRDM5,PGM1,PDGFRA,HSD11B2,PRDM1,LRRK2,SLC2A13,SNX9,ERBB4, PFKFB3,DNAH14,GRB2,SOX4,CCL8,POMC,T,RPL3,GALC,NKX23,TEC,ITK,PTPN2,PODXL,NDFIP1,SMAD3,HEATR1,ITGA9,EPHA6,TNFSF11,NPY,H3F3A, RIT2,ATG16L1,E2F3,GPLD1,GABBR1,GLI3,SLA,LNPEP,DCAF13,PLCB3,CCNY,SLC22A4,SEMA3C,ATP8B4,KCNMA1,CNTNAP4,NRXN3,SNAPC4,IRGM, ARID5B,HAO1,PPM1G,CHRM5,ZMIZ1,CAND1,IL12B,USP25,GADD45A,ICOSLG,GPR12,SBNO2,KITLG,RTKN,CDKAL1,TRIB1,CDH8,ZFP36L1,CYLD,REN, RNASET2,FUT2,COL8A1,KIF21B,GEMIN2,SLC12A5,SNX25,XPNPEP1,STAT3,CDH12,MICALCL,RPS6KA4,NRAP,IRF8,IFT172,LRP2,NFIA,RBM17*
7154	1.9 x10^{-02}	17	812	Cell communication	*KCNMA1,SNX9,KCND2,NRXN3,GRB2,SLC12A5,SNX25,CCL8,POMC,TNFSF18,LNPEP,CHRM5,BDNF,NPY,ROBO2,RIT2,ATG16L1*
5623	2.5 x10^{-02}	170	15040	Cell	*ADCY3,GNA14,TNFSF15,RORC,MEGF10,TNFSF18,LNX1,PNN,AGTR1,BDNF,FAM49A,PRKAR2A,DAB1,STAC,GATA6,PDE4A,C2ORF74,STK39,ROBO2,NPSR1, FAS,MTUS1,WWOX,DSCAM,SATB1,MAGI3,KCND2,STMN2,C11ORF30,SLC22A23,ACTN2,CD40,SP140,DCTN1,FGFR1OP,PGM1,PRDM5,PDGFRA,HSD11B2, PRDM1,LRRK2,CAMTA1,SNX9,SLC2A13,IL1R2,ARPP21,MOB2,ERBB4,GRB2,PFKFB3,DNAH14,KEL,SOX4,CCDC91,PRRC1,POMC,OR52N2,T,OR52N4,GALC, RPL3,OTUD7A,TMEM196,TEC,NKX23,ITK,GPR158,IKZF3,IL23R,PTPN2,IL1RL1,PODXL,NDFIP1,SMAD3,LGALS8,HEATR1,CACNA2D3,KCNK1,BTLA,ITGA9, TMEM117,TNFSF11,EPHA6,NPY,H3F3A,MARCKS,RIT2,ATG16L1,PLAU,ISX,E2F3,IER3IP1,GABBR1,NBEA,GLI3,SLA,LNPEP,DCAF13,TSPAN12,PLCB3,NOD2, TMEM174,CCNY,SLC22A4,BRD7,CSF2RB,SEMA3C,ETAA1,ANO4,IPMK,IFNGR1,KIRREL3,ATP8B4,KCNMA1,IL18RAP,PTGER4,CNTNAP4,NRXN3,FMR1NB, ARID5B,IRGM,SNAPC4,COL25A1,HAO1,PPM1G,CHRM5,ZMIZ1,SDCCAG3,MCC,CAND1,IL12B,THEM4,USP25,GADD45A,ICOSLG,GPR12,CD244,C9ORF57, KITLG,RTKN,ZNF365,CDKAL1,MACC1,TRIB1,CDH8,ZFP36L1,CYLD,PLCL1,RNF123,REN,FAM71B,FUT2,KIF21B,ZNF804A,GEMIN2,SLC12A5,OR9G4, XPNPEP1,STAT3,FZD6,CDH12,MICALCL,CD19,RPS6KA4,NRAP,IRF8,IFT172,LRP2,NFIA,RBM17*
30528	4.6 x10^{-02}	25	1507	Transcription regulator activity	*ISX,CAMTA1,E2F3,SBNO2,RORC,SOX4,GLI3,ZFP36L1,T,GATA6,NKX23,TEC,SATB1,IKZF3,SNAPC4,ARID5B,SMAD3,ACTN2,STAT3,SP140,PRDM5,IRF8,CAND1,PRDM1,NFIA*
5575	4.6 x10^{-02}	180	16370	Cellular component	*ADCY3,GNA14,TNFSF15,RORC,MEGF10,TNFSF18,LNX1,PNN,AGTR1,BDNF,FAM49A,PRKAR2A,OLFML3,DAB1,STAC,GATA6,PDE4A,RLN2,C2ORF74, ROBO2,STK39,NPSR1,FAS,MTUS1,WWOX,DSCAM,SATB1,MAGI3,KCND2,STMN2,C11ORF30,SLC22A23,ACTN2,CD40,SP140,DCTN1,FGFR1OP,PGM1, PRDM5,PDGFRA,HSD11B2,PRDM1,LRRK2,CAMTA1,SNX9,SLC2A13,IL1R2,ARPP21,MOB2,ERBB4,GRB2,PFKFB3,DNAH14,KEL,ITLN2,CCL8,SOX4,CCDC91, PRRC1,POMC,OR52N2,T,OR52N4,GALC,RPL3,OTUD7A,TMEM196,TEC,NKX23,ITK,GPR158,IKZF3,IL23R,PTPN2,IL1RL1,PODXL,NDFIP1,SMAD3,LGALS8, HEATR1,CACNA2D3,KCNK1,BTLA,ITGA9,TMEM117,TNFSF11,EPHA6,NPY,H3F3A,MARCKS,RIT2,ATG16L1,PLAU,ISX,E2F3,IER3IP1,GABBR1,GPLD1,NBEA, GLI3,SLA,LNPEP,DCAF13,TSPAN12,PLCB3,NOD2,TMEM174,CCNY,SLC22A4,BRD7,CSF2RB,SEMA3C,ETAA1,ANO4,IPMK,IFNGR1,KIRREL3,ATP8B4, KCNMA1,IL18RAP,PTGER4,CNTNAP4,NRXN3,FMR1NB,ARID5B,IRGM,SNAPC4,COL25A1,HAO1,PPM1G,CHRM5,ZMIZ1,SDCCAG3,MCC,CAND1,IL12B, THEM4,USP25,GADD45A,ICOSLG,GPR12,CD244,SBNO2,C9ORF57,KITLG,RTKN,ZNF365,CDKAL1,MACC1,TRIB1,CDH8,ZFP36L1,CYLD,PLCL1,RNF123,REN, RNASET2,FNDC1,FAM71B,FUT2,COL8A1,KIF21B,ZNF804A,GEMIN2,SLC12A5,OR9G4,XPNPEP1,STAT3,FZD6,CDH12,MICALCL,CD19,RPS6KA4,EYS,NRAP, IRF8,IFT172,LRP2,NFIA,RBM17*

x is the number of genes annotated to a certain GO class; **n** is the number of genes in the reference set annotated to a certain GO class