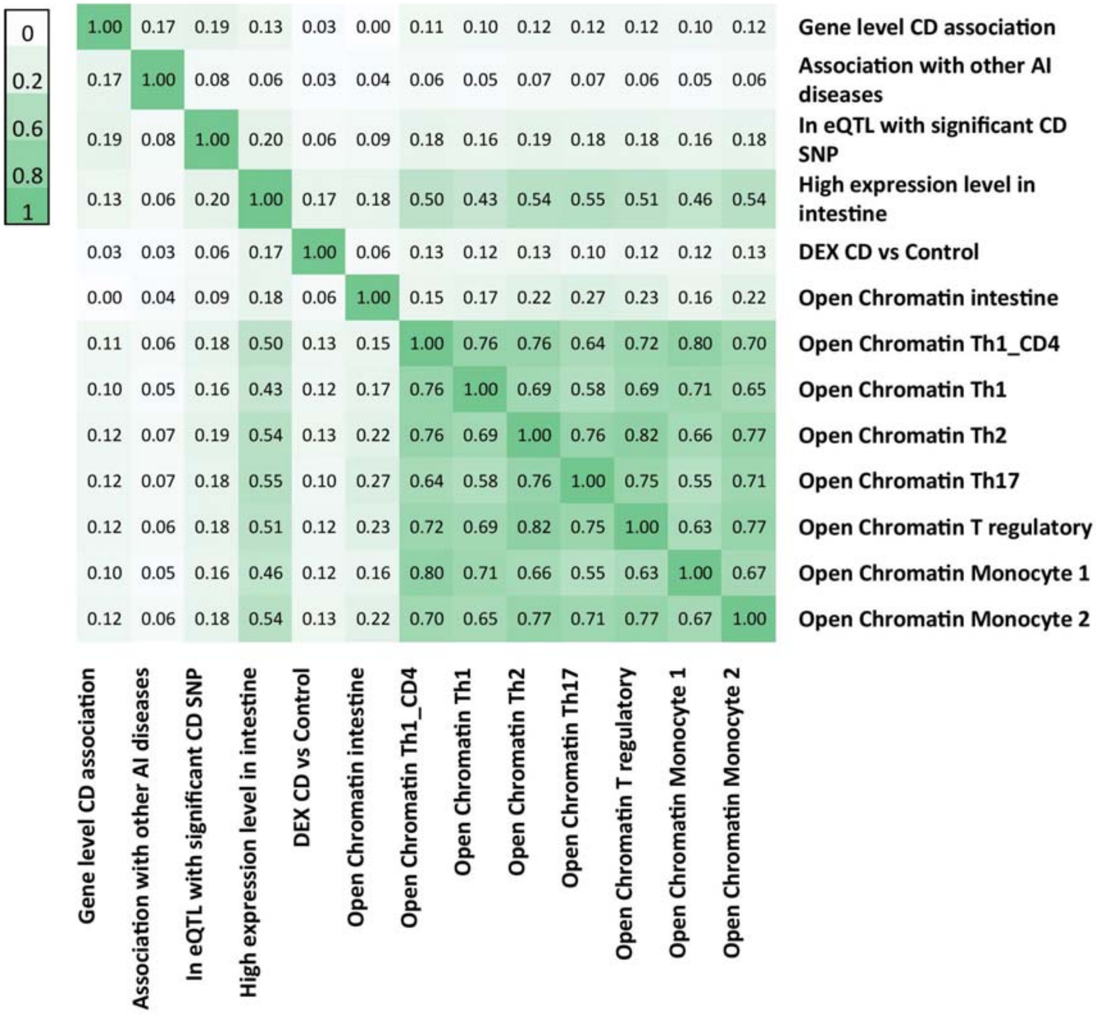
Supplementary Figure S1. Pearson correlation between each pair of gene features.



	Gene level CD association	Association with other AI diseases	In eQTL with significant CD SNP	High expression level in intestine	DEX CD vs Control	Open Chromatin intestine	Open Chromatin Th1_CD4	Open Chromatin Th1	Open Chromatin Th2	Open Chromatin Th17	Open Chromatin T regulatory	Open Chromatin Monocyte 1	Open Chromatin Monocyte 2
Gene level CD association	1.00	0.17	0.19	0.13	0.03	0.00	0.11	0.10	0.12	0.12	0.12	0.10	0.12
Association with other AI diseases	0.17	1.00	0.08	0.06	0.03	0.04	0.06	0.05	0.07	0.07	0.06	0.05	0.06
In eQTL with significant CD SNP	0.19	0.08	1.00	0.20	0.06	0.09	0.18	0.16	0.19	0.18	0.18	0.16	0.18
High expression level in intestine	0.13	0.06	0.20	1.00	0.17	0.18	0.50	0.43	0.54	0.55	0.51	0.46	0.54
DEX CD vs Control	0.03	0.03	0.06	0.17	1.00	0.06	0.13	0.12	0.13	0.10	0.12	0.12	0.13
Open Chromatin intestine	0.00	0.04	0.09	0.18	0.06	1.00	0.15	0.17	0.22	0.27	0.23	0.16	0.22
Open Chromatin Th1_CD4	0.11	0.06	0.18	0.50	0.13	0.15	1.00	0.76	0.76	0.64	0.72	0.80	0.70
Open Chromatin Th1	0.10	0.05	0.16	0.43	0.12	0.17	0.76	1.00	0.69	0.58	0.69	0.71	0.65
Open Chromatin Th2	0.12	0.07	0.19	0.54	0.13	0.22	0.76	0.69	1.00	0.76	0.82	0.66	0.77
Open Chromatin Th17	0.12	0.07	0.18	0.55	0.10	0.27	0.64	0.58	0.76	1.00	0.75	0.55	0.71
Open Chromatin T regulatory	0.12	0.06	0.18	0.51	0.12	0.23	0.72	0.69	0.82	0.75	1.00	0.63	0.77
Open Chromatin Monocyte 1	0.10	0.05	0.16	0.46	0.12	0.16	0.80	0.71	0.66	0.55	0.63	1.00	0.67
Open Chromatin Monocyte 2	0.12	0.06	0.18	0.54	0.13	0.22	0.70	0.65	0.77	0.71	0.77	0.67	1.00

Supplementary Table S1. Enrichment of gene features among CD region genes and among CD reference genes.

Gene feature	Category (N)	CD loci (#gene = 1,328)	non CD loci (#gene = 23,134)	log OR(95%CI)	p-value	CD reference (#gene = 54)	non CD reference (#gene = 24,408)	log OR(95%CI)	p-value
Gene level CD association	> 0.05 (22694)	745(56.1%)	21949(94.9%)			13(24.1%)	22681(92.9%)		
	(3E-6, 0.05] (1566)	421(31.7%)	1145(4.9%)	2.38(2.25,2.52)	3.14E-268	22(40.7%)	1544(6.3%)	3.21(2.53,3.9)	5.22E-20
	<=3E-6 (202)	162(12.2%)	40(0.2%)	4.78(4.43,5.14)	9.70E-155	19(35.2%)	183(0.7%)	5.2(4.48,5.92)	1.94E-45
Association with other AI diseases	None (23975)	1196(90.1%)	22779(98.5%)			24(44.4%)	23951(98.1%)		
	In 1 study (337)	70(5.3%)	267(1.2%)	1.61(1.34,1.88)	1.37E-31	8(14.8%)	329(1.3%)	3.19(2.38,4)	9.89E-15
	In >=2 studies (150)	62(4.7%)	88(0.4%)	2.6(2.27,2.93)	1.28E-53	22(40.7%)	128(0.5%)	5.14(4.54,5.75)	1.44E-62
In eQTL with significant CD SNP	No (21498)	1003(75.5%)	20495(88.6%)			29(53.7%)	21469(88%)		
	Yes (2964)	325(24.5%)	2639(11.4%)	0.92(0.79,1.05)	4.76E-43	25(46.3%)	2939(12%)	1.84(1.3,2.38)	1.76E-11
High expression level in intestine	No (10858)	431(32.5%)	10427(45.1%)			6(11.1%)	10852(44.5%)		
	Yes (13604)	897(67.5%)	12707(54.9%)	0.54(0.42,0.65)	5.20E-19	48(88.9%)	13556(55.5%)	1.86(1.01,2.71)	1.81E-05
Differential expression (CD vs Control)	No (22220)	1182(89%)	21038(90.9%)			43(79.6%)	22177(90.9%)		
	Yes (2242)	146(11%)	2096(9.1%)	0.21(0.04,0.39)	0.0177506	11(20.4%)	2231(9.1%)	0.93(0.27,1.6)	0.0058468
Open Chromatin Intestine	No (15061)	941(70.9%)	14120(61%)			27(50%)	15034(61.6%)		
	Yes (9401)	387(29.1%)	9014(39%)	-0.44(-0.56,-0.32)	1.18E-12	27(50%)	9374(38.4%)	0.47(-0.06,1.01)	0.0829909
Open Chromatin Th1CD4	No (6901)	187(14.1%)	6714(29%)			3(5.6%)	6898(28.3%)		
	Yes (17561)	1141(85.9%)	16420(71%)	0.91(0.76,1.07)	4.28E-30	51(94.4%)	17510(71.7%)	1.9(0.74,3.07)	0.0013735
Open Chromatin Th1	No (5205)	129(9.7%)	5076(21.9%)			1(1.9%)	5204(21.3%)		
	Yes (19257)	1199(90.3%)	18058(78.1%)	0.96(0.78,1.14)	1.69E-24	53(98.1%)	19204(78.7%)	2.66(0.69,4.64)	0.0083025
Open Chromatin Th2	No (8582)	300(22.6%)	8282(35.8%)			5(9.3%)	8577(35.1%)		
	Yes (15880)	1028(77.4%)	14852(64.2%)	0.65(0.52,0.78)	4.49E-22	49(90.7%)	15831(64.9%)	1.67(0.75,2.59)	0.0003785
Open Chromatin Th17	No (10195)	383(28.8%)	9812(42.4%)			6(11.1%)	10189(41.7%)		
	Yes (14267)	945(71.2%)	13322(57.6%)	0.6(0.48,0.72)	5.87E-22	48(88.9%)	14219(58.3%)	1.75(0.9,2.6)	5.56E-05
Open Chromatin Tregulatory	No (7681)	259(19.5%)	7422(32.1%)			2(3.7%)	7679(31.5%)		
	Yes (16781)	1069(80.5%)	15712(67.9%)	0.67(0.53,0.81)	3.48E-21	52(96.3%)	16729(68.5%)	2.48(1.07,3.89)	0.0005764
Open Chromatin Monocyte 1	No (5917)	162(12.2%)	5755(24.9%)			3(5.6%)	5914(24.2%)		
	Yes (18545)	1166(87.8%)	17379(75.1%)	0.87(0.7,1.04)	2.15E-24	51(94.4%)	18494(75.8%)	1.69(0.53,2.86)	0.0043854
Open Chromatin Monocyte 2	No (8145)	243(18.3%)	7902(34.2%)			3(5.6%)	8142(33.4%)		
	Yes (16317)	1085(81.7%)	15232(65.8%)	0.84(0.7,0.98)	3.41E-31	51(94.4%)	16266(66.6%)	2.14(0.98,3.31)	0.000314

P-values and log odds ratios (log OR) are from a logistic regression model using single gene feature as the predictor.

Supplementary Table S2. Weights of gene features in the regression model.

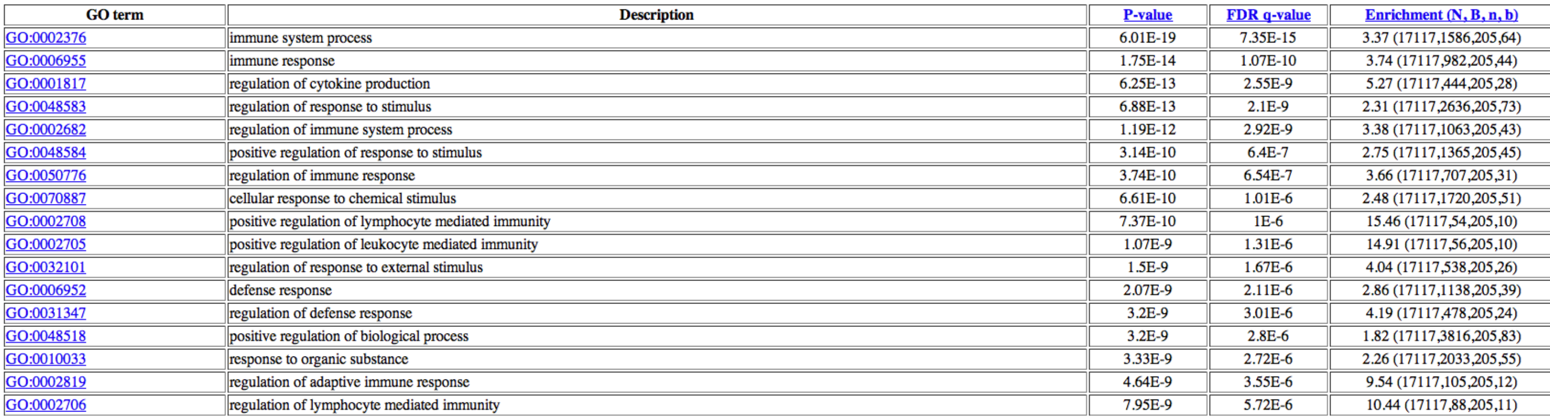
	Weight	Std.Error	P-value
(Intercept)	-8.6082	0.5351	<2e-16
Gene level CD association [0.05,3E-6)	2.3622	0.3828	6.77E-10
Gene level CD association <=3E-6	3.6612	0.443	<2e-16
Association with other AI diseases (In 1 study)	2.0311	0.4469	5.50E-06
Association with other AI diseases (In >=2 studies)	3.5127	0.3566	<2e-16
High expression level in intestine	1.0446	0.4943	0.0346
In eQTL with significant CD SNP	0.3061	0.3225	0.3426
Differential expression between CD and Control	0.313	0.3906	0.4229
Open Chromatin in Th17 cell	0.2081	0.4827	0.6663

Supplementary Table S3. Gene features and prioritization scores of human genes. Excel file available upon request.

Supplementary Table S4. Gene Ontology enrichment of genes ranked top 213 by integrative model.

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)
GO:0002376	immune system process	2.43E-33	2.98E-29	4.37 (17117,1586,205,83)
GO:0002682	regulation of immune system process	4.24E-30	2.6E-26	5.18 (17117,1063,205,66)
GO:0001817	regulation of cytokine production	6.82E-27	2.78E-23	8.09 (17117,444,205,43)
GO:0006955	immune response	8.4E-27	2.57E-23	5.10 (17117,982,205,60)
GO:0019221	cytokine-mediated signaling pathway	1.51E-26	3.7E-23	10.06 (17117,307,205,37)
GO:0050865	regulation of cell activation	2.35E-26	4.8E-23	8.77 (17117,381,205,40)
GO:0071345	cellular response to cytokine stimulus	1.3E-25	2.28E-22	8.07 (17117,424,205,41)
GO:0051249	regulation of lymphocyte activation	2.56E-25	3.92E-22	9.73 (17117,309,205,36)
GO:0034097	response to cytokine	2.9E-25	3.94E-22	7.13 (17117,515,205,44)
GO:0071346	cellular response to interferon-gamma	4.41E-25	5.4E-22	22.33 (17117,86,205,23)
GO:0050776	regulation of immune response	5.41E-25	6.01E-22	5.91 (17117,707,205,50)
GO:0002694	regulation of leukocyte activation	2.07E-24	2.11E-21	8.78 (17117,352,205,37)
GO:0034341	response to interferon-gamma	2.49E-24	2.35E-21	19.09 (17117,105,205,24)
GO:0060333	interferon-gamma-mediated signaling pathway	1.24E-23	1.08E-20	26.51 (17117,63,205,20)
GO:0050863	regulation of T cell activation	1.42E-23	1.16E-20	11.06 (17117,234,205,31)
GO:0002684	positive regulation of immune system process	4.32E-20	3.3E-17	5.60 (17117,626,205,42)
GO:0031347	regulation of defense response	8.46E-20	6.09E-17	6.46 (17117,478,205,37)
GO:0050867	positive regulation of cell activation	9.6E-20	6.52E-17	9.66 (17117,242,205,28)
GO:0050670	regulation of lymphocyte proliferation	6.54E-19	4.21E-16	12.47 (17117,154,205,23)
GO:0032944	regulation of mononuclear cell proliferation	7.6E-19	4.65E-16	12.39 (17117,155,205,23)
GO:0071310	cellular response to organic substance	7.73E-19	4.51E-16	3.51 (17117,1453,205,61)
GO:0070663	regulation of leukocyte proliferation	1.37E-18	7.63E-16	12.08 (17117,159,205,23)
GO:0002696	positive regulation of leukocyte activation	4.79E-18	2.55E-15	9.36 (17117,232,205,26)
GO:0051251	positive regulation of lymphocyte activation	7.96E-18	4.06E-15	9.75 (17117,214,205,25)
GO:0070887	cellular response to chemical stimulus	8.41E-18	4.12E-15	3.16 (17117,1720,205,65)
GO:0002819	regulation of adaptive immune response	1.97E-17	9.28E-15	15.11 (17117,105,205,19)
GO:0048583	regulation of response to stimulus	3.76E-17	1.7E-14	2.57 (17117,2636,205,81)
GO:0050870	positive regulation of T cell activation	5.44E-17	2.38E-14	11.07 (17117,166,205,22)
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	7.29E-17	3.08E-14	15.66 (17117,96,205,18)
GO:0051239	regulation of multicellular organismal process	9.13E-17	3.72E-14	2.94 (17117,1906,205,67)
GO:0048002	antigen processing and presentation of peptide antigen	1.51E-16	5.97E-14	10.56 (17117,174,205,22)
GO:0048518	positive regulation of biological process	1.62E-16	6.19E-14	2.17 (17117,3816,205,99)
GO:0010033	response to organic substance	1.63E-16	6.05E-14	2.83 (17117,2033,205,69)
GO:0032649	regulation of interferon-gamma production	1.78E-16	6.41E-14	18.82 (17117,71,205,16)
GO:0002683	negative regulation of immune system process	3.14E-16	1.1E-13	9.51 (17117,202,205,23)
GO:0002478	antigen processing and presentation of exogenous peptide antigen	4.56E-16	1.55E-13	10.82 (17117,162,205,21)
GO:0019882	antigen processing and presentation	6.68E-16	2.21E-13	9.19 (17117,209,205,23)
GO:0019884	antigen processing and presentation of exogenous antigen	1.09E-15	3.52E-13	10.38 (17117,169,205,21)
GO:0006952	defense response	1.91E-15	5.99E-13	3.60 (17117,1138,205,49)
GO:0080134	regulation of response to stress	2.3E-15	7.04E-13	4.15 (17117,846,205,42)
GO:0001819	positive regulation of cytokine production	5.34E-15	1.59E-12	7.86 (17117,255,205,24)
GO:0002706	regulation of lymphocyte mediated immunity	6.74E-15	1.96E-12	15.18 (17117,88,205,16)
GO:0032101	regulation of response to external stimulus	9.5E-15	2.7E-12	5.12 (17117,538,205,33)
GO:0002703	regulation of leukocyte mediated immunity	2.18E-14	6.06E-12	12.67 (17117,112,205,17)
GO:0002699	positive regulation of immune effector process	2.54E-14	6.9E-12	12.56 (17117,113,205,17)
GO:0042129	regulation of T cell proliferation	2.54E-14	6.75E-12	12.56 (17117,113,205,17)
GO:0050778	positive regulation of immune response	3.97E-14	1.03E-11	5.64 (17117,429,205,29)
GO:1902105	regulation of leukocyte differentiation	1.21E-13	3.09E-11	8.84 (17117,189,205,20)
GO:0048584	positive regulation of response to stimulus	1.26E-13	3.16E-11	3.12 (17117,1365,205,51)

Supplementary Table S5. Gene Ontology enrichment of genes ranked top 213 by GWAS-only model.



GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)
GO:0002376	immune system process	6.01E-19	7.35E-15	3.37 (17117,1586,205,64)
GO:0006955	immune response	1.75E-14	1.07E-10	3.74 (17117,982,205,44)
GO:0001817	regulation of cytokine production	6.25E-13	2.55E-9	5.27 (17117,444,205,28)
GO:0048583	regulation of response to stimulus	6.88E-13	2.1E-9	2.31 (17117,2636,205,73)
GO:0002682	regulation of immune system process	1.19E-12	2.92E-9	3.38 (17117,1063,205,43)
GO:0048584	positive regulation of response to stimulus	3.14E-10	6.4E-7	2.75 (17117,1365,205,45)
GO:0050776	regulation of immune response	3.74E-10	6.54E-7	3.66 (17117,707,205,31)
GO:0070887	cellular response to chemical stimulus	6.61E-10	1.01E-6	2.48 (17117,1720,205,51)
GO:0002708	positive regulation of lymphocyte mediated immunity	7.37E-10	1E-6	15.46 (17117,54,205,10)
GO:0002705	positive regulation of leukocyte mediated immunity	1.07E-9	1.31E-6	14.91 (17117,56,205,10)
GO:0032101	regulation of response to external stimulus	1.5E-9	1.67E-6	4.04 (17117,538,205,26)
GO:0006952	defense response	2.07E-9	2.11E-6	2.86 (17117,1138,205,39)
GO:0031347	regulation of defense response	3.2E-9	3.01E-6	4.19 (17117,478,205,24)
GO:0048518	positive regulation of biological process	3.2E-9	2.8E-6	1.82 (17117,3816,205,83)
GO:0010033	response to organic substance	3.33E-9	2.72E-6	2.26 (17117,2033,205,55)
GO:0002819	regulation of adaptive immune response	4.64E-9	3.55E-6	9.54 (17117,105,205,12)
GO:0002706	regulation of lymphocyte mediated immunity	7.95E-9	5.72E-6	10.44 (17117,88,205,11)

Supplementary Table S6. Effect of CD risk allele on gene expression based on eQTL information. Genes are categorized according to their differential expression in macrophage subsets.

SNP CD association p-value< 0.01 **eQTL p-value<1E-5**	**24 hour**			**Chi-squared p-value (down regulation by risk allele: genes highly expressed in M1 vs. all other genes)**
	more expressed in M2	More expressed in M1	Genes not showing high expression level in M1	0.01472
CD_risk_allele_cause_decreased_expression	39	66	2026	
CD_risk_allele_cause_increased_expression	33	31	1655	

SNP CD association p-value< 0.01 **eQTL p-value<1E-5**	**6 hour**			**Chi-squared p-value (down regulation by risk allele: genes highly expressed in M1 vs. all other genes)**
	more expressed in M2	More expressed in M1	Genes not showing high expression level in M1	0.02426
CD_risk_allele_cause_decreased_expression	24	59	2033	
CD_risk_allele_cause_increased_expression	22	28	1658	

Supplementary Table S7. Quality control of RNA-seq data showing the number of reads mapped for each sample and correlation between each sample and other samples obtained from the same tissue.

Sample group	Phenotype	Sample ID	sequencing platform	number all mapped reads	number non-PCR duplicate mapped reads	percentage non-PCR duplicate	median correlation with samples in same group (LPMC or Terminal ileal samples)	Comment
Body Map	Brain	ERR030882	HiSeq 2000; paired end; 2/lane	144597292	27770888	0.192056764		
Body Map	Breast	ERR030883	HiSeq 2000; paired end; 2/lane	149270686	19660870	0.131712867		
Body Map	Adrenal	ERR030881	HiSeq 2000; paired end; 2/lane	149835249	25254748	0.168550112		
Body Map	Adipose	ERR030880	HiSeq 2000; paired end; 2/lane	152035153	17811406	0.117153209		
Body Map	Lung	ERR030879	HiSeq 2000; paired end; 2/lane	155825625	12560122	0.0806037		
Body Map	Kidney	ERR030885	HiSeq 2000; paired end; 2/lane	158704536	16404525	0.103365193		
Body Map	WhiteBloodCell	ERR030875	HiSeq 2000; paired end; 2/lane	160622580	10669866	0.066428182		
Body Map	SkeletalMuscle	ERR030876	HiSeq 2000; paired end; 2/lane	161171838	7282803	0.045186573		
Body Map	Thyroid	ERR030872	HiSeq 2000; paired end; 2/lane	162512970	23470025	0.144419396		
Body Map	Ovary	ERR030874	HiSeq 2000; paired end; 2/lane	163083358	29927602	0.183511073		
Body Map	Prostate	ERR030877	HiSeq 2000; paired end; 2/lane	163491044	15627932	0.095588918		
Body Map	Colon	ERR030884	HiSeq 2000; paired end; 2/lane	165199634	13424423	0.08126182		
Body Map	Liver	ERR030887	HiSeq 2000; paired end; 2/lane	163589427	12163145	0.074351657		
Body Map	Testes	ERR030873	HiSeq 2000; paired end; 2/lane	164149821	24594842	0.149831671		
Body Map	LymphNode	ERR030878	HiSeq 2000; paired end; 2/lane	165421737	11575677	0.069976759		
Body Map	Heart	ERR030886	HiSeq 2000; paired end; 2/lane	169651392	21317897	0.125657071		
Brain	Brain	brain HSB130	GAIIX; single end; 1/lane	23030378	6322345	0.274521981		
Brain	Brain	brain HSB126	GAIIX; single end; 1/lane	25035136	9675488	0.386476351		
Brain	Brain	brain HSB145	GAIIX; single end; 1/lane	27313443	12312672	0.450791649		
Brain	Brain	brain HSB123	GAIIX; single end; 1/lane	29170186	13144234	0.45060508		
LPMC	CD	mRNA C1086	HiSeq 2000; paired end; 1/lane	127997897	31495369	0.246061613	0.908	
LPMC	Control	mRNA C1080	HiSeq 2000; paired end; 1/lane	160648987	31164430	0.193990828	0.935	
LPMC	Control	mRNA C1081	HiSeq 2000; paired end;	166158711	9677412	0.058241978	0.93	

			1/lane					
LPMC	CD	mRNA C1063	HiSeq 2000; paired end; 1/lane	386174706	16235078	0.04204076	0.932	
LPMC	Control	mRNA C1070	HiSeq 2000; paired end; 1/lane	388378161	18992423	0.048901882	0.928	
LPMC	CD	mRNA C1055	HiSeq 2000; paired end; 1/lane	409455084	10038159	0.024515898	0.94	
Terminal ileum RISK	CD	J1-0002	HiSeq; single end; 12/lane	4020413	1892509	0.470725023	0.734	excluded
Terminal ileum RISK	CD	J1-0001	HiSeq; single end; 12/lane	5067684	1877716	0.370527444	0.846	excluded
Terminal ileum RISK	CD	J1-0007	HiSeq; single end; 12/lane	6879094	2720321	0.395447569	0.883	excluded
Terminal ileum RISK	CD	J1-0033	HiSeq; single end; 12/lane	9791093	3588245	0.366480535	0.894	excluded
Terminal ileum RISK	CD	J1-0005	HiSeq; single end; 12/lane	14404539	789469	0.054806961	0.755	excluded
Terminal ileum RISK	Control	J1-0003	HiSeq; single end; 12/lane	10015865	3674859	0.366903807	0.916	
Terminal ileum RISK	Control	J1-0006	HiSeq; single end; 12/lane	12043698	3903584	0.32411839	0.917	
Terminal ileum RISK	CD	J1-0004	HiSeq; single end; 12/lane	12649207	6349694	0.501983563	0.954	
Terminal ileum RISK	CD	J1-0019	HiSeq; single end; 12/lane	13494731	7468961	0.553472389	0.914	
Terminal ileum RISK	Control	J1-0012	HiSeq; single end; 12/lane	13903102	6613990	0.475720454	0.95	
Terminal ileum RISK	Control	J1-0008	HiSeq; single end; 12/lane	13953919	6724103	0.481879177	0.951	
Terminal ileum RISK	Control	J1-0011	HiSeq; single end; 12/lane	14106709	6853101	0.485804379	0.953	
Terminal ileum RISK	CD	J1-0009	HiSeq; single end; 12/lane	15152683	6820545	0.450121276	0.939	
Terminal ileum RISK	Control	J1-0013	HiSeq; single end; 12/lane	15295746	8214396	0.537037945	0.961	
Terminal ileum RISK	CD	J1-0016	HiSeq; single end; 12/lane	15331812	7197167	0.469427032	0.942	
Terminal ileum RISK	Control	J1-0015	HiSeq; single end; 12/lane	15387993	7568296	0.491831261	0.951	
Terminal ileum RISK	Control	J1-0034	HiSeq; single end; 12/lane	15406183	7611892	0.494080331	0.905	
Terminal ileum RISK	Control	J1-0017	HiSeq; single end; 12/lane	15494899	8516733	0.549647532	0.957	
Terminal ileum RISK	Control	J1-0010	HiSeq; single end; 12/lane	15832105	5589446	0.353045031	0.942	
Terminal ileum RISK	Control	J1-0020	HiSeq; single end; 12/lane	16023759	8033112	0.501325064	0.956	
Terminal ileum RISK	Control	J1-0021	HiSeq; single end; 12/lane	16624694	6334337	0.381019765	0.943	
Terminal ileum	CD	J1-0014	HiSeq; single end; 12/lane	16699323	8361792	0.500726407	0.953	

RISK							
Terminal ileum RISK	CD	J1-0018	HiSeq; single end; 12/lane	16755491	7463374	0.445428546	0.955
Terminal ileum RISK	CD	J1-0026	HiSeq; single end; 12/lane	17263319	8919830	0.516692648	0.957
Terminal ileum RISK	Control	J1-0023	HiSeq; single end; 12/lane	17456274	8336624	0.477571789	0.953
Terminal ileum RISK	Control	J1-0042	HiSeq; single end; 12/lane	17567585	8756429	0.498442387	0.932
Terminal ileum RISK	Control	J1-0027	HiSeq; single end; 12/lane	18155578	10048344	0.553457676	0.946
Terminal ileum RISK	Control	J1-0029	HiSeq; single end; 12/lane	18435432	6663730	0.361463187	0.948
Terminal ileum RISK	Control	J1-0031	HiSeq; single end; 12/lane	18577527	8865190	0.477199683	0.96
Terminal ileum RISK	CD	J1-0022	HiSeq; single end; 12/lane	18661334	8417370	0.451059394	0.952
Terminal ileum RISK	CD	J1-0025	HiSeq; single end; 12/lane	18675523	8230613	0.4407166	0.949
Terminal ileum RISK	Control	J1-0024	HiSeq; single end; 12/lane	18691550	9496484	0.508062948	0.947
Terminal ileum RISK	Control	J1-0028	HiSeq; single end; 12/lane	19074152	9536868	0.499989095	0.944
Terminal ileum RISK	CD	J1-0035	HiSeq; single end; 12/lane	19135665	9413868	0.491954055	0.962
Terminal ileum RISK	CD	J1-0030	HiSeq; single end; 12/lane	19192420	9681968	0.504468327	0.961
Terminal ileum RISK	Control	J1-0037	HiSeq; single end; 12/lane	19442257	5523461	0.284095669	0.921
Terminal ileum RISK	CD	J1-0032	HiSeq; single end; 12/lane	19880586	8869453	0.446136397	0.951
Terminal ileum RISK	CD	J1-0036	HiSeq; single end; 12/lane	19959510	9704702	0.486219451	0.953
Terminal ileum RISK	CD	J1-0038	HiSeq; single end; 12/lane	20313233	9545947	0.469937356	0.961
Terminal ileum RISK	Control	J1-0041	HiSeq; single end; 12/lane	20561815	9564285	0.465147897	0.949
Terminal ileum RISK	Control	J1-0043	HiSeq; single end; 12/lane	20681616	9718008	0.469886299	0.962
Terminal ileum RISK	CD	J1-0039	HiSeq; single end; 12/lane	20737766	9443569	0.455380247	0.935
Terminal ileum RISK	Control	J1-0044	HiSeq; single end; 12/lane	20836137	9915975	0.475902755	0.944
Terminal ileum RISK	Control	J1-0040	HiSeq; single end; 12/lane	21179103	9931171	0.468913674	0.957
Terminal ileum RISK	CD	J1-0046	HiSeq; single end; 12/lane	21631343	8104513	0.374665272	0.956
Terminal ileum RISK	Control	J1-0045	HiSeq; single end; 12/lane	22917810	10360767	0.452083641	0.961
Terminal ileum	CD	J1-0048	HiSeq; single end; 12/lane	23614763	11697480	0.495346068	0.952

RISK								
Terminal ileum RISK	CD	J1-0047	HiSeq; single end; 12/lane	23718059	11623811	0.490082726	0.957	
Terminal ileum RISK	CD	J1-0049	HiSeq; single end; 12/lane	24267100	9673994	0.39864648	0.931	
Terminal ileum RISK	CD	J1-0050	HiSeq; single end; 12/lane	31918201	11412767	0.357562978	0.93	
Terminal ileum Yale	CD	Sample wz86-8	HiSeq; paired end; 6/lane	55540246	18404738	0.331376602	0.869	excluded
Terminal ileum Yale	CD	Sample wz86-3	HiSeq; paired end; 6/lane	56299734	6136117	0.10899016	0.888	excluded
Terminal ileum Yale	CD	Sample wz86-9	HiSeq; paired end; 6/lane	45884054	20807702	0.453484385	0.967	
Terminal ileum Yale	Control	Sample wz86-15	HiSeq; paired end; 6/lane	47108022	18598003	0.394794819	0.959	
Terminal ileum Yale	CD	Sample wz86-6	HiSeq; paired end; 6/lane	59451774	21960895	0.369390071	0.951	
Terminal ileum Yale	CD	Sample wz86-7	HiSeq; paired end; 6/lane	61708239	19533621	0.316548022	0.951	
Terminal ileum Yale	CD	Sample wz86-2	HiSeq; paired end; 6/lane	63841092	20741208	0.324888052	0.942	
Terminal ileum Yale	Control	Sample wz86-18	HiSeq; paired end; 6/lane	64198414	25726617	0.400736021	0.962	
Terminal ileum Yale	CD	Sample wz86-1	HiSeq; paired end; 6/lane	68832309	22149862	0.321794551	0.959	
Terminal ileum Yale	CD	Sample wz86-4	HiSeq; paired end; 6/lane	69181608	16286343	0.235414346	0.941	
Terminal ileum Yale	Control	Sample wz86-17	HiSeq; paired end; 6/lane	71059983	28386087	0.399466561	0.964	
Terminal ileum Yale	Control	Sample wz86-19	HiSeq; paired end; 6/lane	71645077	28056132	0.391598881	0.961	
Terminal ileum Yale	CD	Sample wz86-10	HiSeq; paired end; 6/lane	75708466	29754105	0.393008954	0.964	
Terminal ileum Yale	CD	Sample wz86-5	HiSeq; paired end; 6/lane	76129286	26730838	0.351124244	0.965	
Terminal ileum Yale	Control	Sample wz86-16	HiSeq; paired end; 6/lane	80399063	28455989	0.353934336	0.96	

Supplementary Table S8. List of CD reference genes.

geneID	Source	PubMed
ADAM17	Mendelian form of CD	22010916
ATG16L1	Immunochip	23128233
CARD9	Immunochip; Excess of rare variants in cases or controls	23128233; 21983784
CCR6	Modified intestinal pathology in in two mouse knockout experiments	23047555; 14515278
CD226	Immunochip	23128233
CD40	Immunochip	23128233
CD48	Immunochip	23128233
CD6	Immunochip	23128233
CEBPB	Immunochip	23128233
CREM	Immunochip	23128233
CRTC3	Immunochip	23128233
CXCL5	Immunochip	23128233
CXCR5	Immunochip	23128233
DAP	Immunochip	23128233
DOK3	Immunochip	23128233
EPO	Immunochip	23128233
FOS	Immunochip	23128233
FUT2	Immunochip; Mutation linked to differences in intestinal microbes	23128233; 23047555; 22068912
GPR35	Immunochip	23128233
GPR65	Immunochip	23128233
ICOSLG	Immunochip	23128233
IFIH1	Excess of rare variants in cases or controls	21983784
IL10	Immunochip	23128233
IL10RA	Mendelian form of CD	19890111;24216686
IL10RB	Mendelian form of CD	19890111;24216686
IL12B	Immunochip	23128233
IL18RAP	Excess of rare variants in cases or controls	21983784
IL23R	Immunochip	23128233
IRF8	Immunochip	23128233
IRGM	Immunochip; Expression level linked with autophagy of internalized bacteria	23128233; 19165925
IFNG	Immunochip	23128233
JAK2	Immunochip	23128233
LACC1	Immunochip	23128233
MAP3K8	Immunochip	23128233
NKX2-3	Immunochip	23128233
NOD2	Immunochip	23128233

PRKCB	Immunochip	23128233
PTGER4	Immunochip	23128233
PTPN22	Immunochip	23128233
RASGRP1	Immunochip	23128233
REL	Immunochip	23128233
RIPK2	Immunochip	23128233
RORC	Immunochip	23128233
SMAD3	Immunochip	23128233
SOCS1	Immunochip	23128233
SPRED2	Immunochip	23128233
STAT3	Immunochip	23128233
TAGAP	Immunochip	23128233
TNFAIP3	Immunochip	23128233
TNFSF15	Immunochip	23128233
TRAF3IP2	Immunochip	23128233
TYK2	Immunochip	23128233
UBE2L3	Immunochip;	23128233
ZNF365	Fine mapping and conditional analysis identified a single nonsynonymous SNP linked to expression of multiple genes in CD patients	23047555; 21257989