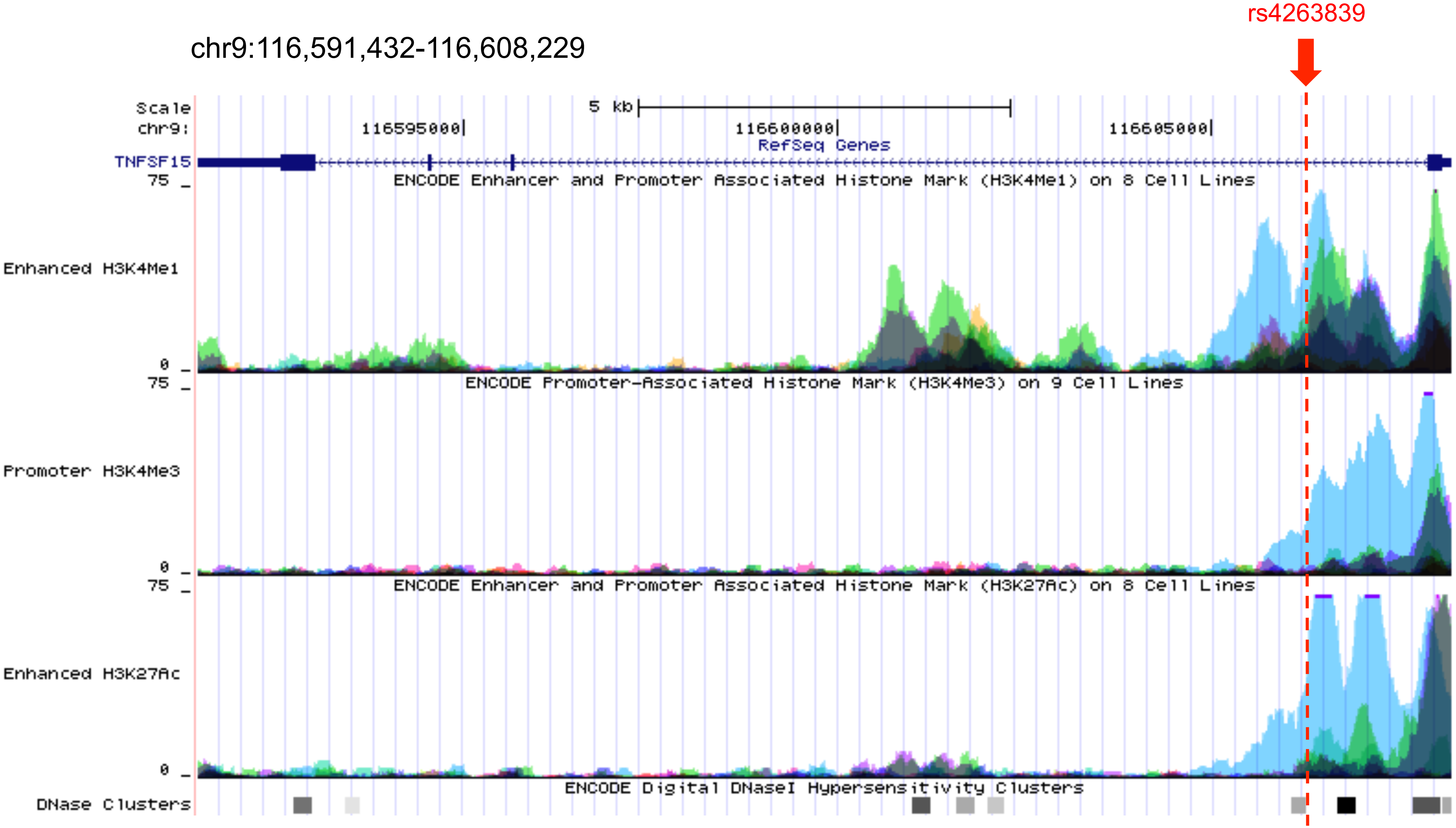
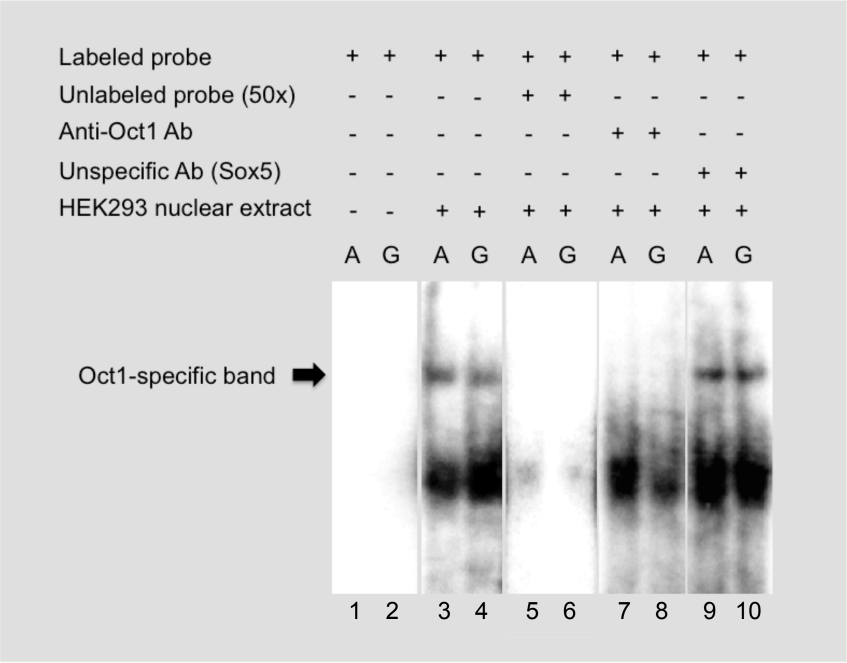


Supplementary Figure 1. Summary of ENCODE data for the TNFSF15 locus. The UCSC Human Genome Browser (http://genome.ucsc.edu) was used to produce a graphical representation of histone (H3K4Me1 and H3K4Me3), acetylation (H3K27Ac) and DNase hypersensitive (DNase clusters) marks influencing chromatin accessibility, which is associated with enhancers, promoters, and DNA regions of active transcription. Genomic coordinates of the region shown are reported in the top left corner, and the position of the rs4263839 SNP along the TNFSF15 gene is indicated by a red arrow and a vertical dashed line. See http://www.genome.gov/10005107 for a detailed description of the ENCODE project; ENCODE data can be accessed via http://genome.ucsc.edu/ENCODE.



Supplementary Figure 2. Analysis of *TNFSF15* rs4263839 SNP by Electrophoretic Mobility Shift Assay (EMSA). Oligonucleotide duplexes corresponding to the alleles (A and G) at the rs4263839 polymorphism were labeled with ^{32}P-ATP and incubated with nuclear extracts from HEK293 cells in the presence or absence of unlabeled probes, and specific antibodies as indicated. Specificity of binding (as from lanes 3 and 4) was confirmed by running duplexes alone (lanes 1 and 2), in combination with excess cold competitor (lanes 4 and 5), and by supershift analysis with an antibody directed vs human Oct-1 (lanes 7 and 8). No supershift (band still present) was observed with an unspecific antibody directed vs human Sox5 (lanes 9 and 10). Overall, no different EMSA pattern was observed for the two alleles in any of the tested conditions.

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Filename: Zucchelli_Supplementary_Tables_1-4.pdf

Supplementary Table 1. Association of Crohn's disease risk loci with irritable bowel syndrome (IBS)

Marker ID	Chr	Nearest Gene	SNP	Risk allele	Total sample		Sweden		USA	
					P	**OR (95%CI)**	**P**	**OR (95%CI)**	**P**	**OR (95%CI)**
rs2476601	1p13	PTPN22	G/a	G	0.55	1.08 (0.85-1.35)	0.33	1.15 (0.87-1.52)	0.73	0.93 (0.63-1.38)
rs11465804	1p31	IL23R	T/g	T	0.75	0.94 (0.68-1.30)	0.071	1.49 (0.95-2.34)	*0.0060*	0.45 (0.25-0.83)
rs2274910	1q23	ITLN1	C/t	C	0.48	1.05 (0.91-1.22)	0.97	1.00 (0.83-1.21)	0.26	1.15 (0.90-1.47)
rs9286879	1q24	TNFSF18	A/g	G	0.73	1.03 (0.87-1.21)	0.73	1.04 (0.84-1.28)	0.94	0.99 (0.75-1.30)
rs11584383	1q32	C1orf81	T/c	T	0.19	1.10 (0.95-1.27)	0.43	1.08 (0.89-1.29)	0.33	1.14 (0.88-1.46)
rs3828309	2q37	ATG16L1	G/a	G	0.99	1.00 (0.87-1.15)	0.59	0.95 (0.80-1.13)	0.54	1.08 (0.85-1.35)
rs3197999	3p21	MST1	G/a	A	0.54	1.05 (0.90-1.22)	0.43	1.08 (0.89-1.31)	0.92	1.01 (0.78-1.31)
rs4613763	5p13	PTGER4	T/c	C	0.27	0.90 (0.74-1.09)	0.12	0.82 (0.64-1.05)	0.64	1.08 (0.77-1.51)
rs2188962	5q31	C5orf56	C/t	T	0.96	1.00 (0.86-1.15)	0.26	0.90 (0.75-1.08)	0.16	1.18 (0.93-1.50)
rs10045431	5q33	IL12B	C/a	C	0.30	1.09 (0.93-1.28)	0.52	1.06 (0.88-1.29)	0.42	1.11 (0.85-1.44)
rs11747270	5q33	IRGM	A/g	G	0.89	1.02 (0.78-1.34)	0.061	1.40 (0.99-1.98)	0.051	0.66 (0.44-1.00)
rs6908425	6p22	CDKAL1	C/t	C	0.55	0.95 (0.80-1.13)	0.38	0.91 (0.74-1.12)	0.92	1.01 (0.76-1.35)
rs7746082	6q21	PRDM1	G/c	C	0.71	1.03 (0.88-1.21)	0.24	0.89 (0.72-1.08)	*0.031*	1.34 (1.02-1.75)
rs2301436	6q27	CCR6	C/t	T	0.089	0.88 (0.76-1.02)	0.28	0.90 (0.74-1.09)	0.20	0.86 (0.68-1.08)
rs1456893	7p12	IKZF1	A/g	A	0.90	0.99 (0.85-1.16)	0.36	1.10 (0.90-1.34)	0.15	0.83 (0.64-1.07)
rs1551398	8q24	TRIB1	A/g	A	0.36	1.08 (0.93-1.25)	0.21	1.12 (0.93-1.35)	0.92	1.01 (0.80-1.28)
rs10758669	9p24	JAK2	A/c	C	0.79	0.98 (0.85-1.14)	0.55	0.95 (0.79-1.13)	0.75	1.04 (0.81-1.33)
rs4263839	9q32	TNFSF15	G/a	G	***2.2E-05***	1.37 (1.19-1.58)	*0.0033*	1.32 (1.10-1.58)	*0.0027*	1.45 (1.14-1.85)
rs17582416	10p11	CUL2	T/g	G	0.95	1.00 (0.86-1.15)	0.97	1.00 (0.83-1.19)	0.80	0.97 (0.76-1.24)
rs10995271	10q21	ZNF365	G/c	C	0.89	1.01 (0.87-1.17)	0.68	0.96 (0.80-1.15)	0.42	1.11 (0.86-1.42)
rs11190140	10q24	NKX2-3	C/t	T	0.55	0.96 (0.83-1.10)	0.91	0.99 (0.83-1.18)	0.36	0.90 (0.71-1.13)
rs7927894	11q13	C11orf30	C/t	T	0.79	0.98 (0.85-1.14)	0.96	1.00 (0.83-1.21)	0.63	0.94 (0.74-1.20)
rs11175593	12q12	LRRK2	C/t	T	0.12	0.64 (0.36-1.13)	0.89	0.94 (0.42-2.14)	0.059	0.48 (0.23-1.02)
rs3764147	13q14	C13orf31	A/g	G	0.22	0.90 (0.75-1.07)	0.11	0.83 (0.66-1.05)	0.94	1.01 (0.77-1.33)
rs2066844	16q12	NOD2	C/t	T	-	- -	-	- -	0.92	0.97 (0.53-1.79)
rs2066847	16q12	NOD2	DEL/c	C	-	- -	0.14	0.57 (0.27-1.21)	-	- -
rs2872507	17q12	ORMDL3	G/a	A	0.82	0.98 (0.85-1.13)	0.88	0.99 (0.83-1.18)	0.84	0.98 (0.77-1.24)
rs744166	17q21	STAT3	A/g	A	0.13	1.11 (0.97-1.27)	0.10	1.16 (0.97-1.39)	0.76	1.04 (0.82-1.32)
rs2542151	18p11	PTPN2	T/g	G	0.77	1.03 (0.85-1.25)	0.52	1.08 (0.85-1.39)	0.67	0.94 (0.69-1.27)
rs1736135	21q21	USP25	T/c	T	0.082	1.14 (0.98-1.32)	0.082	1.16 (0.98-1.38)	0.54	1.08 (0.85-1.35)
rs762421	21q22	ICOSLG	A/g	G	0.27	1.08 (0.94-1.25)	0.98	1.00 (0.83-1.19)	0.069	1.24 (0.98-1.58)

Lower case indicates minor allele at each SNP. Significant P values are reported in italics, with those withstanding Bonferroni correction for multiple tests also in bold type.

Supplementary Table 2. Association of Crohn's disease risk loci with constipation-predominant irritable bowel syndrome (IBS-C)

Marker ID	**Chr**	**Nearest Gene**	**SNP**	**Risk allele**	**Total sample**		**Sweden**		**USA**	
					P	**OR (95%CI)**	**P**	**OR (95%CI)**	**P**	**OR (95%CI)**
rs2476601	1p13	PTPN22	G/a	G	0.91	0.98 (0.70-1.36)	0.81	1.05 (0.67-1.65)	0.68	0.90 (0.55-1.47)
rs11465804	1p31	IL23R	T/g	T	0.16	0.71 (0.45-1.14)	0.56	0.83 (0.45-1.53)	0.19	0.53 (0.24-1.18)
rs2274910	1q23	ITLN1	C/t	C	0.14	1.19 (0.94-1.50)	0.27	1.19 (0.87-1.63)	0.30	1.19 (0.85-1.66)
rs9286879	1q24	TNFSF18	A/g	G	0.98	1.00 (0.78-1.29)	0.90	1.02 (0.72-1.45)	0.96	0.99 (0.69-1.42)
rs11584383	1q32	C1orf81	T/c	T	0.38	1.11 (0.88-1.41)	0.98	1.00 (0.72-1.39)	0.19	1.25 (0.89-1.75)
rs3828309	2q37	ATG16L1	G/a	G	0.46	1.09 (0.88-1.35)	0.72	0.94 (0.70-1.26)	0.14	1.27 (0.93-1.73)
rs3197999	3p21	MST1	G/a	A	0.14	1.19 (0.95-1.49)	0.11	1.29 (0.95-1.76)	0.67	1.07 (0.77-1.50)
rs4613763	5p13	PTGER4	T/c	C	0.34	0.86 (0.63-1.17)	0.42	0.84 (0.55-1.29)	0.53	0.87 (0.56-1.36)
rs2188962	5q31	C5orf56	C/t	T	0.54	1.07 (0.86-1.33)	1.00	1.00 (0.74-1.36)	0.37	1.15 (0.84-1.57)
rs10045431	5q33	IL12B	C/a	C	0.15	1.19 (0.93-1.52)	0.55	1.11 (0.79-1.56)	0.14	1.30 (0.92-1.84)
rs11747270	5q33	IRGM	A/g	G	0.98	1.01 (0.67-1.51)	0.16	1.52 (0.87-2.68)	0.22	0.71 (0.41-1.24)
rs6908425	6p22	CDKAL1	C/t	C	0.75	1.04 (0.80-1.36)	0.76	1.06 (0.74-1.54)	0.88	1.03 (0.70-1.51)
rs7746082	6q21	PRDM1	G/c	C	0.94	0.99 (0.78-1.26)	0.31	0.84 (0.59-1.19)	0.39	1.16 (0.82-1.63)
rs2301436	6q27	CCR6	C/t	T	0.67	1.05 (0.84-1.31)	0.80	1.04 (0.75-1.45)	0.75	0.95 (0.70-1.29)
rs1456893	7p12	IKZF1	A/g	A	0.35	0.89 (0.71-1.12)	0.79	1.04 (0.75-1.44)	0.10	0.76 (0.54-1.06)
rs1551398	8q24	TRIB1	A/g	A	0.16	1.18 (0.93-1.48)	0.29	1.19 (0.86-1.64)	0.40	1.15 (0.83-1.59)
rs10758669	9p24	JAK2	A/c	C	0.26	0.88 (0.71-1.10)	*0.038*	0.72 (0.52-0.99)	0.61	1.09 (0.79-1.48)
rs4263839	9q32	TNFSF15	G/a	G	***8.7E-07***	1.79 (1.41-2.26)	*0.0010*	1.72 (1.23-2.41)	*1.9E-04*	1.85 (1.33-2.57)
rs17582416	10p11	CUL2	T/g	G	0.99	1.00 (0.80-1.24)	0.94	1.01 (0.75-1.37)	0.94	0.99 (0.72-1.35)
rs10995271	10q21	ZNF365	G/c	C	0.87	0.98 (0.79-1.23)	0.60	0.92 (0.68-1.25)	0.71	1.07 (0.76-1.48)
rs11190140	10q24	NKX2-3	C/t	T	0.11	0.84 (0.68-1.04)	0.13	0.79 (0.59-1.07)	0.49	0.90 (0.66-1.22)
rs7927894	11q13	C11orf30	C/t	T	0.96	1.01 (0.80-1.26)	0.60	0.92 (0.67-1.26)	0.56	1.10 (0.80-1.51)
rs11175593	12q12	LRRK2	C/t	T	0.089	0.48 (0.19-1.18)	0.78	0.40 (0.05-3.13)	0.16	0.49 (0.18-1.38)
rs3764147	13q14	C13orf31	A/g	G	0.75	0.96 (0.74-1.24)	0.51	0.88 (0.59-1.30)	0.89	1.03 (0.72-1.46)
rs2066844	16q12	NOD2	C/t	T	-	- -	-	- -	0.70	1.16 (0.54-2.52)
rs2066847	16q12	NOD2	DEL/c	C	-	- -	0.33	0.48 (0.11-2.09)	-	- -
rs2872507	17q12	ORMDL3	G/a	A	0.51	0.93 (0.75-1.15)	0.69	1.06 (0.79-1.43)	0.15	0.80 (0.58-1.09)
rs744166	17q21	STAT3	A/g	A	0.96	1.01 (0.81-1.25)	0.86	0.97 (0.73-1.29)	0.78	1.04 (0.76-1.42)
rs2542151	18p11	PTPN2	T/g	G	0.30	0.85 (0.63-1.16)	0.95	1.01 (0.66-1.56)	0.13	0.72 (0.47-1.11)
rs1736135	21q21	USP25	T/c	T	0.22	1.14 (0.93-1.39)	0.21	1.20 (0.90-1.61)	0.64	1.08 (0.79-1.46)
rs762421	21q22	ICOSLG	A/g	G	0.68	1.05 (0.84-1.30)	0.66	0.93 (0.69-1.27)	0.29	1.18 (0.87-1.61)

Lower case indicates minor allele at each SNP. Significant P values are reported in italics, with those withstanding Bonferroni correction for multiple tests also in bold type.

Supplementary Table3. Association of Crohn's disease risk loci with diarrhea-predominant irritable bowel syndrome (IBS-D)

Marker ID	Chr	Nearest Gene	SNP	Risk allele	Total sample		Sweden		USA	
					P	OR (95%CI)	P	OR (95%CI)	P	OR (95%CI)
rs2476601	1p13	PTPN22	G/a	G	0.74	1.05 (0.78-1.43)	0.38	1.20 (0.79-1.83)	0.62	0.88 (0.56-1.40)
rs11465804	1p31	IL23R	T/g	T	0.91	0.97 (0.63-1.51)	*0.0053*	3.13 (1.22-8.01)	*0.0086*	0.42 (0.22-0.82)
rs2274910	1q23	ITLN1	C/t	C	0.46	1.08 (0.88-1.32)	0.60	0.93 (0.71-1.21)	0.12	1.27 (0.93-1.71)
rs9286879	1q24	TNFSF18	A/g	G	0.58	1.07 (0.85-1.34)	0.37	1.15 (0.85-1.55)	0.57	0.91 (0.65-1.27)
rs11584383	1q32	C1orf81	T/c	T	0.17	1.15 (0.93-1.41)	0.57	1.09 (0.82-1.44)	0.25	1.19 (0.88-1.62)
rs3828309	2q37	ATG16L1	G/a	G	0.48	0.93 (0.77-1.14)	0.59	0.93 (0.71-1.21)	0.65	0.93 (0.71-1.22)
rs3197999	3p21	MST1	G/a	A	0.54	1.07 (0.87-1.32)	0.48	1.11 (0.83-1.47)	0.81	1.04 (0.76-1.42)
rs4613763	5p13	PTGER4	T/c	C	0.82	0.97 (0.75-1.26)	0.58	0.90 (0.63-1.30)	0.57	1.12 (0.76-1.65)
rs2188962	5q31	C5orf56	C/t	T	0.51	1.07 (0.88-1.30)	0.68	0.95 (0.72-1.24)	0.13	1.26 (0.94-1.69)
rs10045431	5q33	IL12B	C/a	C	0.96	0.99 (0.80-1.23)	0.73	0.95 (0.71-1.27)	0.85	1.03 (0.75-1.42)
rs11747270	5q33	IRGM	A/g	G	0.62	0.91 (0.62-1.33)	0.28	1.33 (0.80-2.22)	0.11	0.66 (0.39-1.12)
rs6908425	6p22	CDKAL1	C/t	C	*0.038*	0.78 (0.62-0.98)	*0.021*	0.69 (0.51-0.95)	0.54	0.89 (0.63-1.26)
rs7746082	6q21	PRDM1	G/c	C	0.33	1.11 (0.90-1.38)	0.53	0.91 (0.67-1.22)	*0.039*	1.40 (1.02-1.92)
rs2301436	6q27	CCR6	C/t	T	*0.0019*	0.72 (0.58-0.89)	*0.014*	0.68 (0.50-0.93)	0.069	1.30 (0.98-1.72)
rs1456893	7p12	IKZF1	A/g	A	0.71	0.96 (0.78-1.19)	0.47	1.11 (0.83-1.48)	0.16	0.79 (0.58-1.09)
rs1551398	8q24	TRIB1	A/g	A	0.78	0.97 (0.79-1.19)	0.47	1.11 (0.83-1.48)	0.42	0.88 (0.67-1.17)
rs10758669	9p24	JAK2	A/c	C	0.70	0.96 (0.79-1.17)	0.65	0.94 (0.72-1.23)	0.74	0.95 (0.71-1.28)
rs4263839	9q32	TNFSF15	G/a	G	0.038	1.23 (1.01-1.51)	0.34	1.15 (0.87-1.52)	0.072	1.32 (0.97-1.78)
rs17582416	10p11	CUL2	T/g	G	0.98	1.00 (0.82-1.22)	0.94	1.01 (0.77-1.32)	0.74	0.95 (0.71-1.27)
rs10995271	10q21	ZNF365	G/c	C	0.61	1.05 (0.86-1.29)	0.93	1.01 (0.77-1.32)	0.54	1.10 (0.82-1.48)
rs11190140	10q24	NKX2-3	C/t	T	0.47	0.93 (0.77-1.13)	0.46	0.91 (0.70-1.18)	0.70	0.95 (0.71-1.26)
rs7927894	11q13	C11orf30	C/t	T	0.35	0.91 (0.74-1.11)	0.65	0.94 (0.72-1.23)	0.35	0.87 (0.64-1.17)
rs11175593	12q12	LRRK2	C/t	T	0.41	0.74 (0.36-1.53)	0.83	1.14 (0.36-3.57)	0.30	0.63 (0.26-1.55)
rs3764147	13q14	C13orf31	A/g	G	0.56	0.93 (0.74-1.18)	0.14	0.77 (0.54-1.10)	0.44	1.14 (0.82-1.58)
rs2066844	16q12	NOD2	C/t	T	-	- -	-	- -	0.99	1.00 (0.48-2.07)
rs2066847	16q12	NOD2	DEL/c	C	-	- -	0.33	0.54 (0.16-1.86)	-	- -
rs2872507	17q12	ORMDL3	G/a	A	0.82	0.98 (0.81-1.19)	0.45	0.90 (0.70-1.17)	0.55	1.09 (0.82-1.45)
rs744166	17q21	STAT3	A/g	A	0.39	1.09 (0.90-1.31)	0.57	1.08 (0.83-1.39)	0.50	1.10 (0.83-1.46)
rs2542151	18p11	PTPN2	T/g	G	0.31	1.14 (0.88-1.48)	0.17	1.28 (0.90-1.82)	0.86	0.97 (0.67-1.40)
rs1736135	21q21	USP25	T/c	T	0.064	1.20 (0.99-1.47)	0.052	1.30 (1.00-1.69)	0.53	1.10 (0.83-1.46)
rs762421	21q22	ICOSLG	A/g	G	0.30	1.11 (0.91-1.35)	0.91	1.02 (0.78-1.32)	0.23	1.19 (0.89-1.59)

Lower case indicates minor allele at each SNP. Significant P values are reported in italics, with those withstanding Bonferroni correction for multiple tests also in bold type.

Supplementary Table 4. Association of Crohn's disease risk loci with alternating irritable bowel syndrome (IBS-A)

Marker ID	Chr	Nearest Gene	SNP	Risk allele	Total sample		Sweden		USA	
					P	**OR (95%CI)**	**P**	**OR (95%CI)**	**P**	**OR (95%CI)**
rs2476601	1p13	PTPN22	G/a	G	0.38	1.15 (0.83-1.59)	0.36	1.19 (0.81-1.74)	0.87	1.05 (0.56-1.97)
rs11465804	1p31	IL23R	T/g	T	0.77	1.08 (0.66-1.76)	0.11	1.64 (0.86-3.12)	0.037	0.37 (0.15-0.93)
rs2274910	1q23	ITLN1	C/t	C	0.54	0.93 (0.76-1.14)	0.63	0.94 (0.74-1.21)	0.69	0.93 (0.64-1.35)
rs9286879	1q24	TNFSF18	A/g	G	0.88	0.98 (0.78-1.24)	0.45	0.90 (0.67-1.20)	0.41	1.19 (0.79-1.80)
rs11584383	1q32	C1orf81	T/c	T	0.67	1.04 (0.85-1.28)	0.38	1.12 (0.86-1.46)	0.59	0.90 (0.62-1.31)
rs3828309	2q37	ATG16L1	G/a	G	0.87	1.02 (0.83-1.26)	0.63	1.06 (0.83-1.36)	0.67	0.93 (0.64-1.34)
rs3197999	3p21	MST1	G/a	A	0.19	0.86 (0.69-1.08)	0.36	0.88 (0.67-1.15)	0.34	0.81 (0.53-1.24)
rs4613763	5p13	PTGER4	T/c	C	0.27	0.85 (0.64-1.13)	0.087	0.74 (0.52-1.05)	0.54	1.17 (0.71-1.93)
rs2188962	5q31	C5orf56	C/t	T	0.22	0.88 (0.71-1.08)	0.061	0.79 (0.61-1.01)	0.52	1.14 (0.77-1.68)
rs10045431	5q33	IL12B	C/a	C	0.20	1.16 (0.93-1.46)	0.27	1.16 (0.88-1.53)	0.51	1.15 (0.76-1.73)
rs11747270	5q33	IRGM	A/g	G	0.55	1.12 (0.77-1.65)	0.26	1.32 (0.83-2.11)	0.60	0.84 (0.43-1.62)
rs6908425	6p22	CDKAL1	C/t	C	0.41	1.11 (0.86-1.43)	0.35	1.15 (0.85-1.55)	0.96	1.01 (0.63-1.62)
rs7746082	6q21	PRDM1	G/c	C	0.77	1.03 (0.83-1.30)	0.61	0.93 (0.71-1.22)	0.19	1.32 (0.88-1.97)
rs2301436	6q27	CCR6	C/t	T	0.48	0.93 (0.75-1.15)	0.95	1.01 (0.77-1.32)	0.21	1.27 (0.88-1.83)
rs1456893	7p12	IKZF1	A/g	A	0.81	1.03 (0.82-1.30)	0.33	1.14 (0.87-1.49)	0.28	0.79 (0.53-1.20)
rs1551398	8q24	TRIB1	A/g	A	0.46	1.09 (0.88-1.35)	0.60	1.08 (0.83-1.40)	0.56	1.12 (0.76-1.67)
rs10758669	9p24	JAK2	A/c	C	0.42	1.09 (0.89-1.33)	0.55	1.08 (0.84-1.37)	0.56	1.12 (0.76-1.64)
rs4263839	9q32	TNFSF15	G/a	G	*0.015*	1.30 (1.05-1.60)	*0.045*	1.30 (1.00-1.69)	0.17	1.30 (0.89-1.89)
rs17582416	10p11	CUL2	T/g	G	0.57	0.94 (0.77-1.16)	0.99	1.00 (0.78-1.27)	0.29	0.81 (0.55-1.20)
rs10995271	10q21	ZNF365	G/c	C	0.79	1.03 (0.83-1.27)	0.53	0.92 (0.72-1.18)	0.12	1.37 (0.92-2.05)
rs11190140	10q24	NKX2-3	C/t	T	0.95	0.99 (0.81-1.21)	0.33	1.13 (0.89-1.43)	0.10	0.73 (0.51-1.06)
rs7927894	11q13	C11orf30	C/t	T	0.57	0.94 (0.77-1.16)	0.79	1.03 (0.81-1.32)	0.15	0.76 (0.52-1.11)
rs11175593	12q12	LRRK2	C/t	T	0.47	0.74 (0.33-1.70)	0.81	1.21 (0.43-3.42)	0.15	0.38 (0.09-1.67)
rs3764147	13q14	C13orf31	A/g	G	0.12	0.82 (0.64-1.06)	0.35	0.86 (0.63-1.18)	0.19	0.74 (0.47-1.16)
rs2066844	16q12	NOD2	C/t	T	-	- -	-	- -	0.082	0.27 (0.06-1.18)
rs2066847	16q12	NOD2	DEL/c	C	-	- -	0.46	0.69 (0.26-1.84)	-	- -
rs2872507	17q12	ORMDL3	G/a	A	0.71	1.04 (0.85-1.27)	0.49	1.09 (0.86-1.38)	0.73	0.94 (0.66-1.34)
rs744166	17q21	STAT3	A/g	A	*0.021*	1.27 (1.03-1.55)	*0.011*	1.37 (1.08-1.75)	0.78	1.05 (0.73-1.52)
rs2542151	18p11	PTPN2	T/g	G	0.56	1.08 (0.83-1.42)	0.96	0.99 (0.70-1.40)	0.31	1.25 (0.81-1.93)
rs1736135	21q21	USP25	T/c	T	0.37	1.10 (0.90-1.34)	0.87	1.02 (0.81-1.28)	0.16	1.32 (0.90-1.92)
rs762421	21q22	ICOSLG	A/g	G	0.70	1.04 (0.85-1.27)	0.72	0.96 (0.75-1.22)	0.21	1.27 (0.88-1.84)

Lower case indicates minor allele at each SNP. Significant P values are reported in italics, with those withstanding Bonferroni correction for multiple tests also in bold type.