Supplementary Table 7. The percentage of genetic variance explained by 13 SNPs identified in Korean Crohn's disease

				Alleles		RAF					
Chr	SNP	Position	Gene(s)	Risk	Non-risk	Case	Control	OR	95% CI	P_{trend}	Additive genetic variance explained
1p31	rs76418789	67,648,596	*IL23R*	G	A	0.96	0.94	1.68	(1.14-2.47)	8.20E-03	0.19%
2q37	rs3749172	241,570,249	*GPR35*	A	C	0.36	0.28	1.44	(1.20-1.72)	5.57E-05	0.35%
6p21	rs10947261	32,373,232	*BTNL2*	T	G	0.36	0.29	1.40	(1.17-1.68)	2.38E-04	0.30%
6p21	rs9271366	32,586,854	*(HLA-DRB1, HLA-DQA1)*	A	G	0.94	0.89	1.96	(1.46-2.64)	5.34E-06	0.55%
6p21	rs751728	33,764,033	*MLN*	T	C	0.78	0.74	1.26	(1.04-1.53)	1.80E-02	0.13%
6q27	rs2149085	167,371,110	*(RNASET2)*	T	C	0.44	0.40	1.20	(1.02-1.42)	3.20E-02	0.10%
9q32	rs6478108	117,558,703	*TNFSF15*	T	C	0.71	0.51	2.48	(2.06-2.97)	1.15E-23	2.54%
10q21	rs224143	64,477,836	*(ZNF365)*	G	A	0.67	0.60	1.36	(1.15-1.60)	3.31E-04	0.29%
10q22	rs1250569	81,045,207	*ZMIZ1*	T	C	0.57	0.47	1.51	(1.28-1.79)	1.41E-06	0.54%
10q24	rs4409764	101,284,237	*(NKX2-3)*	T	G	0.51	0.46	1.24	(1.05-1.47)	1.18E-02	0.15%
11q13	rs11235667	72,863,697	*(ATG16L2, FCHSD2)*	G	A	0.13	0.09	1.54	(1.17-2.03)	2.10E-03	0.20%
18p11	rs514000	12,854,072	*PTPN2*	C	T	0.39	0.30	1.43	(1.20-1.70)	4.94E-05	0.35%
21q11	rs2823256	16,784,706	*(NRIP1, USP25)*	G	A	0.75	0.69	1.38	(1.14-1.66)	7.01E-04	0.28%

Note: Chr, chromosome; CI, confidence interval; OR, odds ratio; Position, chromosome position (hg19); RAF, risk allele frequency.