Supplementary Table 6. Korean replication data for the 140 loci identified in the Caucasian GWAS studies on Crohn's disease

Locus				Immunochip					Validation					Combined
Nearby Gene	SNP	Chr.	Position	Risk allele	RAF in control	OR	95% CI	*P* value	Risk allele	RAF in control	OR	95% CI	*P* value	*P* cmh*
(RNASET2)	rs1819333§	6q27	167,373,547	T	0.40	1.21	(1.02-1.43)	2.55E-02	T	0.37	1.35	(1.19-1.54)	7.44E-06	1.08E-06
(ZNF365)	rs224143†§¶	10q21	64,477,836	G	0.60	1.36	(1.15-1.60)	3.31E-04	G	0.59	1.37	(1.20-1.56)	3.24E-06	2.20E-09
(NKX2-3)	rs4409764§¶	10q24	101,284,237	T	0.46	1.24	(1.05-1.47)	1.18E-02	T	0.45	1.39	(1.22-1.59)	7.40E-07	7.93E-08
PRKCB	rs7404095§	16p11	23,864,590	C	0.56	1.28	(1.08-1.51)	3.80E-03	C	0.58	1.26	(1.11-1.44)	4.35E-04	4.49E-06
(IKZF3)	rs12946510	17q21	37,912,377	T	0.32	1.20	(1.20-1.01)	4.16E-02	C	0.66	1.03	(0.90-1.17)	7.07E-01	3.41E-01
DNMT3B	rs4911259†	20q11	31,376,282	T	0.09	1.49	(1.12-1.98)	5.68E-03	T	0.10	1.07	(0.87-1.32)	5.36E-01	2.80E-02
(CD40)	rs1569723†	20q12	44,742,064	C	0.34	1.21	(1.02-1.44)	2.89E-02	C	0.36	1.11	(0.97-1.26)	1.36E-01	1.19E-02

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

**P* cmh was calculated by Cochran-Mantel-Haenszel (CMH) test statistic (1 d.f.).

†Imputed SNPs.

§These SNPs passed the Bonferroni correction following the validation.

¶These SNPs have reached the genome-wide significance *P* value in the immunochip+validation set.