Supplementary Table 4. Results of the replication study for the loci identified in the Immunochip with CD in Koreans

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*
GPR35	rs3749172§¶	2q37	241,570,249	A	0.28	1.44	(1.20-1.72)	5.57E-05	A	0.27	1.50	(1.29-1.74)	7.31E-08	5.30E-11
(UBE2D3)	rs75323844†	4q24	103,774,293	T	0.52	1.42	(1.19-1.69)	8.51E-05	-	-	-	-	-	-
(PREP)	rs73771645†	6q22	106,016,785	T	0.02	3.13	(1.77-5.54)	3.90E-05	T	0.09	1.02	(0.82-1.28)	8.62E-01	4.99E-02
DDC	rs3807563	7p12	50,566,390	C	0.70	1.48	(1.23-1.78)	3.77E-05	T	0.22	1.18	(1.01-1.37)	3.21E-02	3.71E-01
(JAK2)	rs10758669	9p24	4,981,602	C	0.29	1.45	(1.21-1.74)	4.02E-05	C	0.33	1.00	(0.88-1.14)	9.82E-01	1.05E-02
PRKCQ	rs587198	10p15	6,531,149	C	0.42	1.51	(1.27-1.79)	2.28E-06	C	0.49	1.02	(0.89-1.16)	8.12E-01	2.47E-03
REEP3	rs16918645	10q21	65,346,300	A	0.75	1.49	(1.22-1.81)	7.43E-05	A	0.79	1.07	(0.91-1.25)	4.40E-01	2.12E-03
ZMIZ1	rs1250569¶	10q22	81,045,207	T	0.47	1.51	(1.28-1.79)	1.41E-06	T	0.48	1.19	(1.05-1.35)	6.45E-03	3.05E-07
PTDSS2	rs77910374‡	11p15	453,313	T	0.80	1.52	(1.22-1.90)	1.81E-04	T	0.82	1.06	(0.89-1.25)	5.27E-01	6.22E-03
FCHSD2	rs12294037	11q13	72,807,631	T	0.39	1.42	(1.19-1.68)	6.31E-05	T	0.42	1.20	(1.05-1.36)	5.50E-03	3.28E-06
PICALM	rs585820†	11q14	85,696,670	G	0.22	1.51	(1.24-1.84)	3.94E-05	A	0.57	1.07	(0.97-1.18)	1.93E-01	3.67E-01
USP6	rs28645497†	17p13	5,042,241	A	0.46	1.42	(1.19-1.69)	9.49E-05	A	0.53	1.08	(0.95-1.23)	2.52E-01	1.37E-03
PTPN2	rs514000§¶	18p11	12,854,072	C	0.30	1.43	(1.20-1.70)	4.94E-05	C	0.34	1.27	(1.11-1.44)	4.13E-04	9.00E-08
(NRIP1, USP25)	rs2823256‡§¶	21q11	16,784,706	G	0.69	1.38	(1.14-1.66)	7.01E-04	G	0.70	1.35	(1.16-1.56)	6.45E-05	2.49E-07
APP	rs72635015†	21q21	27,451,908	A	0.15	1.59	(1.27-1.99)	4.95E-05	T	0.80	1.02	(0.87-1.20)	7.69E-01	2.86E-02
UBE2L3	rs2256609	22q11	21,925,017	G	0.32	1.47	(1.22-1.76)	2.89E-05	G	0.34	1.12	(0.98-1.28)	1.09E-01	1.54E-04
UBE2L3	rs5754217	22q11	21,939,675	T	0.41	1.42	(1.20-1.68)	5.52E-05	T	0.42	1.13	(0.99-1.28)	6.95E-02	1.10E-04

Note: Chr, chromosome; CI, confidence interval; OR, odds ratio; RAF, risk allele frequency.

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

†Imputed SNPs.

‡The proxy of imputed SNPs with $P < 10^{-4}$, rs58761034 (r^2=0.77, D'=0.91) and rs200642633 (r^2=0.91, D'=0.96), respectively.

§These SNPs passed the Bonferroni correction following the validation.

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