

Table 3. Synergistic Effects between *IL12B* and HLA-B*52:01 in Each Study

Study	RERI		AP		SI	
	(95% CI)	p	(95% CI)	p	(95% CI)	p
Genome scanning	2.90 (0.60–5.20)	0.014	0.50 (0.23–0.78)	0.00034	2.57 (1.08–6.09)	0.032
Replication study	3.87 (1.70–6.05)	0.00049	0.62 (0.42–0.81)	4.7×10^{-10}	3.76 (1.51–9.32)	0.0043
Combined study	3.46 (1.90–5.02)	1.4×10^{-5}	0.58 (0.42–0.73)	1.0×10^{-12}	3.24 (1.72–6.11)	0.00028

Abbreviations are as follows: RERI, relative excess risk; AP, attributable proportion; SI, synergy index; CI, confidence interval.

analyze whether these two loci are associated with TAK and whether the interactions are observed in other populations.

Taken together, the current study identified two susceptibility genes to TAK and provided evidence of a common immunological pathway exerted by the *IL12B* region that is involved in the etiology of TAK and other autoimmune disorders and of its synergistic role with HLA in the susceptibility to TAK.

Supplemental Data

Supplemental Data include six figures and one table and can be found with this article online at <http://www.cell.com/AJHG/>.

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Web Resources

The URLs for data presented herein are as follows:

Gene Expression Omnibus (GEO), <http://www.ncbi.nlm.nih.gov/geo/>

Genevar (Gene Expression Variation), <http://www.sanger.ac.uk/resources/software/genevar/>

International HapMap Project, <http://hapmap.ncbi.nlm.nih.gov/>

Online Mendelian Inheritance in Man (OMIM), <http://www.omim.org/>

PLINK, <http://pngu.mgh.harvard.edu/~purcell/plink/>

R statistical software, <http://www.r-project.org/>

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