

SUPPLEMENTARY INFORMATION

Recapitulation of Candidate Systemic Lupus Erythematosus-Associated Variants in Koreans

Ki-Sung Kwon^{1,2}, Hae-Young Cho^{1,2}, Yeun-Jun Chung^{1,2*}

¹Department of Microbiology, College of Medicine, The Catholic University of Korea, Seoul 06591, Korea,

²Integrated Research Center for Genome Polymorphism, College of Medicine,
The Catholic University of Korea, Seoul 06591, Korea

Supplementary Table 1. SNPs identified to be associated with SLE in a previous GWAS^a but not replicated in the Korean population

SNP	Gene	SNP effect	Minor allele frequency in East Asians
rs1801274	<i>FCGR2A</i>	Missense variant	0.28
rs2286672	<i>PLD2</i>	Missense variant	0.42
rs887369	<i>CXorf21</i>	Synonymous variant	0.06
rs9782955	<i>LYST</i>	Intron	0.12
rs3794060	<i>NADSYN1</i>	Intron	0.38
rs34572943	<i>ITGAM</i>	Intron	0.01
rs2941509	<i>IKZF3</i>	Intron	0.00

SNP, single-nucleotide polymorphism; SLE, systemic lupus erythematosus; GWAS, genomewide association studies.

^aSource: Bentham J, Morris DL, Cunninghame Graham DS, Pinder CL, Tomblason P, Behrens TW, *et al.* Genetic association analyses implicate aberrant regulation of innate and adaptive immunity genes in the pathogenesis of systemic lupus erythematosus. *Nat Genet* 2015;47:1457-1464.