Supplementary figure S1  Schematic map of rs6933349 and cg21325723 within human major histocompatibility complex (MHC) region on the short arm of chromosome 6.
Supplementary figure S2  The association between DNA methylation (cg21325723) and ACPA-positive RA in the EIRA study.

$P$ value = 1.49E-9
Supplementary figure S3  The associations between DNA methylation level on cg21325723 and genetic variant of rs6933349 in healthy controls (A), and in ACPA-positive RA cases (B), stratified by smoking status, in the EIRA study.
Supplementary figure S4. The correlation of cg21325723 methylation on the same individual separated by 9 years from the InCHIANTI cohort.

Pearson's correlation coefficient = 0.722
Supplementary figure S5  The associations between the DNA methylation level (cg21325723) and genetic variant of rs6933349 in all individuals (A), and in never smokers or current smokers in the EIMS study.
Supplementary table S1  Linkage disequilibrium ($r^2$) between the newly identified SNP, rs6933349, and the major RA risk shared epitope (SE) alleles

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