Supplementary Materials

Patients
Peripheral blood samples were obtained from atopic march (AM) and atopic dermatitis (AD) patients. This study was reviewed and approved by the Chung-Ang University Hospital Institutional Review Board. All groups were diagnosed with AD and AM by a dermatologist. Total immunoglobulin E was measured by ImmunoCAP-FEIA test in the patient’s serum (Supplementary Table 1).

Whole-exome sequencing processing and alignment
Sequence reads in FASTQ format were mapped to the human assembly UCSC hg19 using the Burrows-Wheeler Aligner (BWA, v0.7.7) with “mem” and seed value parameters “-k 45” to create SAM files with correct mate pair information. The read group tag included the sample name. Picard (v1.92) was then used to convert the SAM files to compressed BAM files and then to sort the BAM files by chromosome coordinate. The Genome Analysis Toolkit (v2.3.9Lite) was used to locally realign the BAM files at intervals corresponding to potential insertion/deletion (indel) alignment errors. Insertions and deletions were identified with Mutect and a GATK Somatic Indel Detector, respectively. Single-nucleotide variants and indels were annotated using snpEff (v3.6c) to classify variants as synonymous, non-synonymous, missense, frameshift point mutations, or frameshift indels.