**SUPPLEMENTARY MATERIAL**

Figure S1: GTExPortal showing *tight junction protein 2* (*TJP2*) transcript expression in Whole Blood PBMCs and skin epidermis. **A:** *TJP2* Transcripts Per Million (TPM) expression levels in human tissues. Expression level in skin much higher than in blood. **B:** SNP rs7872806 minor allele "A" significant association with higher *TJP2* expression in 670 PBMC samples (Whole Blood) but not in Sun- or Non-sun exposed skin. (GTExPortal, available at https://gtexportal.org/).
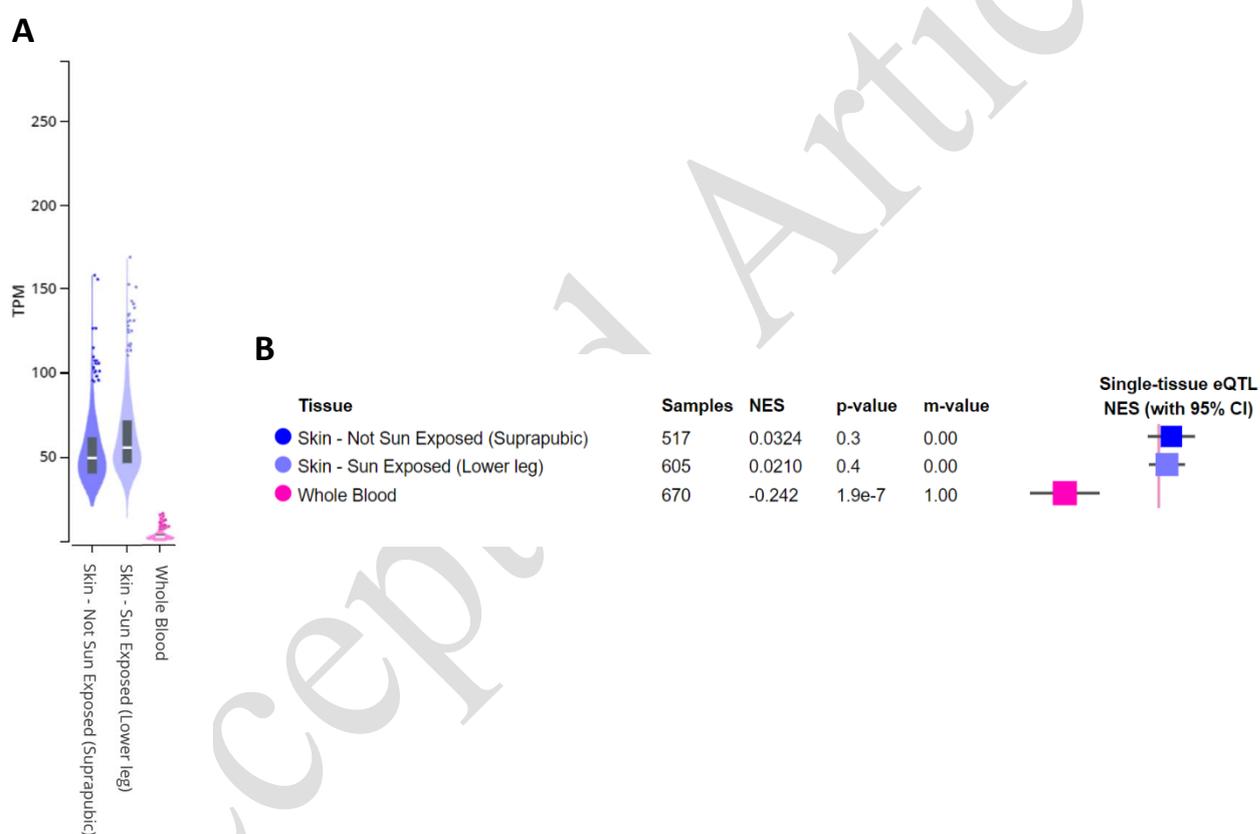
Figure S2: Overall *tight junction protein 2* (*TJP2*) transcripts expression measured as fragments per Kilobase of transcript per Million mapped reads (FPKM) in Skin biopsies obtained from individuals without AD (Non-AD), at non-lesional sites of individuals with AD (Non-lesional AD) or at lesional sites of individuals with AD (Lesional AD) retrieved from (https://www.ncbi.nlm.nih.gov/sites/GDSbrowser/). ANOVA significance *p* threshold not met. **A:** Plager *et al.*, 2007, **B:** De Benedetto *et al.*, 2011, **C:** Suárez-Fariñas *et al.*, 2011.
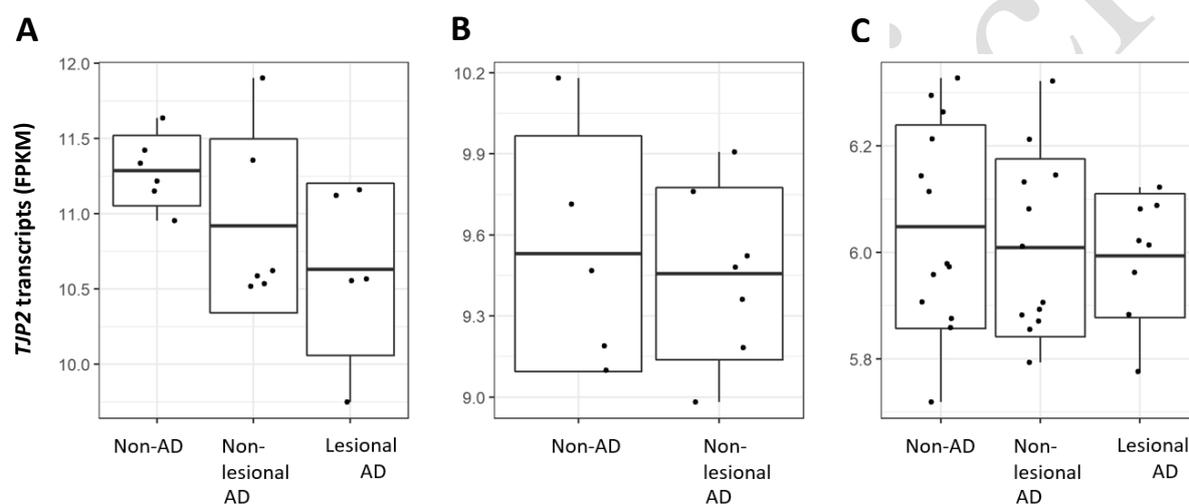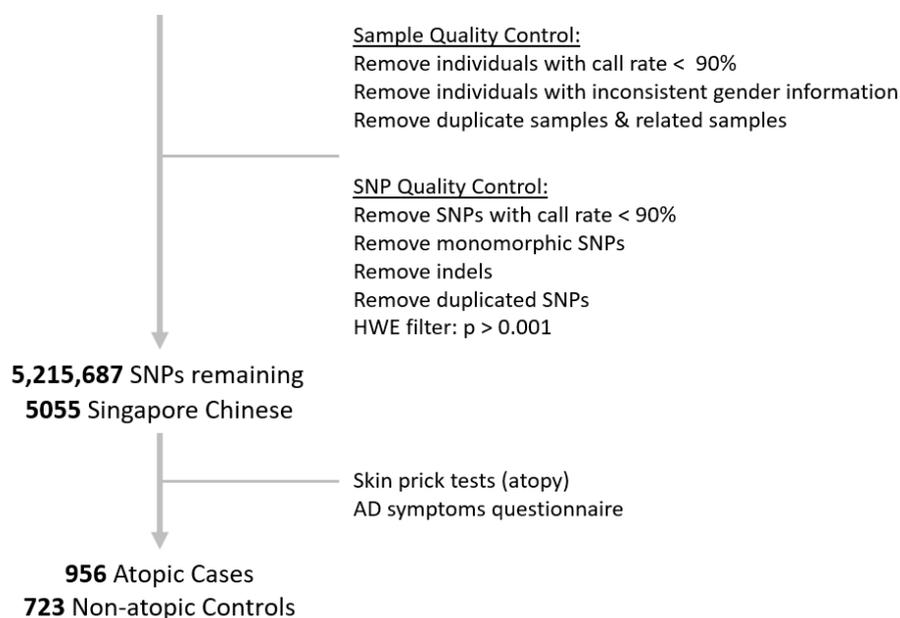
Figure S3: Transcript expression shown as quantile normalised fragments per Kilobase of transcript per Million mapped reads (FPKM) in PBMCs of 575 Singapore and Malaysia Chinese grouped according to high or low *tight junction protein 2* (*TJP2*) expression level split by median. *** indicates T-test *p* <0.001. **A:** Higher *activator protein 1* (*AP-1*) transcript expression level significantly associated with lower *TJP2* expression. **B:** Higher *cyclin D1* (*CD1*) transcript expression level significantly associated with lower *TJP2*.
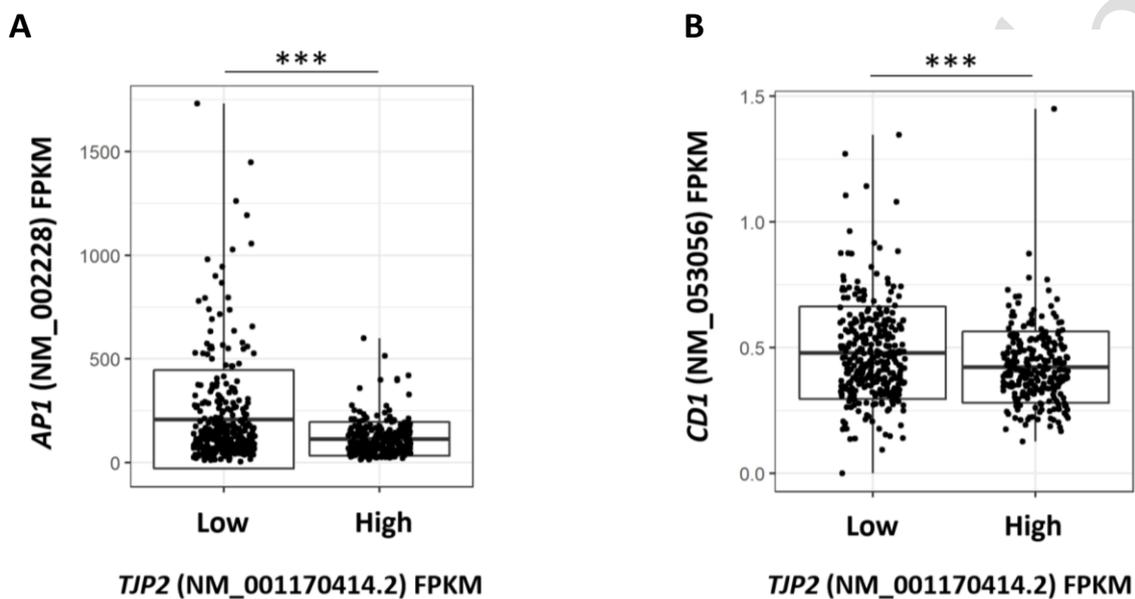
Figure S4: GWAS data preprocessing pipeline. Table shows number of single nucleotide polymorphisms (SNPs) obtained before and after imputation for each genotyping array. Sample and SNP quality control steps are described. HWE filter: Hardy-weinberg equilibrium filter.

Cohort	Number of SNPs		Platform used
	Before imputation	Imputed	
1	787,143	11,023,756	Infinium OmniZhongHua-8 v1.3 BeadChip platform
2	460,183	7,108,825	Illumina HumanHap 550 k BeadChip, version 3
3	1,671,665	8,677,992	Infinium Omni 2.5 Exome
4	759,993	8,359,859	Infinium Global Screening Array
Merged SNPs	-	5,229,035	-

Sample Quality Control:
Remove individuals with call rate < 90%
Remove individuals with inconsistent gender information
Remove duplicate samples & related samples

SNP Quality Control:
Remove SNPs with call rate < 90%
Remove monomorphic SNPs
Remove indels
Remove duplicated SNPs
HWE filter: $p > 0.001$

5,215,687 SNPs remaining
5055 Singapore Chinese

Skin prick tests (atopy)
AD symptoms questionnaire

956 Atopic Cases
723 Non-atopic Controls

Figure S5: Principal component analysis Scree Plot illustrating the proportion of explained variance for each principal component of the GWAS data. Arrows indicate the 'elbow' points at the 6th and 10th components. The first 10 principal components explained 61.1% of variance and hence were used to adjust for the GWAS data.