

Table S1 Linear regression for associations between SNPs and total IgE (n=626) and eos% (n=725) among eczema patients as analyzed by the additive model

Gene	SNP	LogIgE level		Eos%	
		β (95% CI)	P	β (95% CI)	P
<i>IL10</i>	rs1800872	-0.034 (-0.116 to 0.047)	0.411	0.06 (-0.521 to 0.640)	0.84
	rs1800896	0.077 (-0.099 to 0.254)	0.388	-1.016 (-2.200 to 0.169)	0.093
	rs3790622	-0.048 (-0.211 to 0.116)	0.569	0.448 (-0.725 to 1.621)	0.454
	rs3021094	0.006 (-0.068 to 0.080)	0.878	-0.076 (-0.585 to 0.433)	0.769
<i>TGFB1</i>	rs1800469	0.046 (-0.033 to 0.125)	0.255	0.212 (-0.327 to 0.751)	0.441
<i>IL6R</i>	rs2228145	0.014 (-0.065 to 0.092)	0.734	-0.171 (-0.699 to 0.358)	0.526
	rs6689393	-0.013 (-0.089 to 0.064)	0.742	-0.047 (-0.557 to 0.463)	0.857
	rs4845374	-0.061 (-0.181 to 0.059)	0.316	-0.119 (-0.864 to 0.625)	0.753
<i>STAT3</i>	rs4796793	0.028 (-0.051 to 0.108)	0.487	-0.120 (-0.637 to 0.396)	0.647

SNP, single-nucleotide polymorphism; IgE, immunoglobulin E; eos%, eosinophil percentage; logIgE, log-transformed total IgE; CI, confidence interval; *IL10*, interleukin-10; *TGFB1*, transforming growth factor-beta 1; *IL6R*, IL-6 receptor; *STAT3*, signal transducer and activator of transcription 3.

Table S2 Linear regression of associations between SNPs and SCORAD among 398 eczema patients

Gene	SNP	Addictive model		Dominant model		Recessive model	
		β (95% CI)	P	β (95% CI)	P	β (95% CI)	P
<i>IL10</i>	rs1800872	-2.68 (-5.92 to 0.56)	0.105	6.60 (-0.30 to 13.50)	0.061	-2.22 (-6.59 to 2.15)	0.318
	rs1800896	-1.80 (-8.60 to 4.99)	0.602	0.03 (-18.81 to 18.86)	0.998	-2.89 (-11.49 to 5.71)	0.509
	rs3790622	-3.45 (-10.24 to 3.35)	0.319	-11.25 (-48.32 to 25.83)	0.551	-4.22 (-11.34 to 2.91)	0.245
	rs3021094	0.60 (-2.47 to 3.66)	0.702	-0.13 (-5.04 to 4.77)	0.957	1.52 (-3.60 to 6.64)	0.559
<i>TGFB1</i>	rs1800469	-2.70 (-6.05 to 0.64)	0.112	3.87 (-2.47 to 10.21)	0.231	-3.18 (-7.87 to 1.50)	0.182
<i>IL6R</i>	rs2228145	2.56 (-0.70 to 5.83)	0.123	-0.33 (-6.77 to 6.11)	0.920	4.82 (0.28 to 9.36)	0.037
	rs6689393	2.07 (-1.01 to 5.15)	0.186	-1.90 (-6.93 to 3.14)	0.459	3.55 (-1.42 to 8.53)	0.161
	rs4845374	-0.68 (-5.59 to 4.24)	0.787	-7.01 (-28.66 to 14.64)	0.525	-1.19 (-6.46 to 4.08)	0.656
<i>STAT3</i>	rs4796793	2.82 (-0.35 to 5.99)	0.081	-8.35 (-14.10 to -2.60)	0.005	0.68 (-3.89 to 5.25)	0.771

SNP, single-nucleotide polymorphism; SCORAD, SCORing Atopic Dermatitis; CI, confidence interval; *IL10*, interleukin-10; *TGFB1*, transforming growth factor-beta 1; *IL6R*, IL-6 receptor; *STAT3*, signal transducer and activator of transcription 3.

Table S3 Associations between eczema and *IL10* and *IL6R* haplotypes

Gene (SNP combination)	Haplotype	Frequency		Adjusted OR	95% CI	P [†]
		Eczema	Control			
<i>IL10</i> (rs3790622_rs3021094)	GT	0.475	0.467	Reference		
	GG	0.473	0.481	1.01	0.90-1.14	0.817
	AG	0.050	0.051	0.94	0.71-1.23	0.631
<i>IL6R</i> (rs6689393_rs4845374)	AT	0.516	0.541	Reference		
	GT	0.365	0.331	1.14	1.00-1.30	0.047
	GA	0.115	0.123	0.98	0.81-1.18	0.812

[†], adjusted for age and sex. *IL10*, interleukin-10; *IL6R*, IL-6 receptor; SNP, single-nucleotide polymorphism; OR, odds ratio; CI, confidence interval.

Table S4 GMDR analysis of *FLG*, 11q13 and regulatory genes for logIgE level

Model formed by <i>IL10</i> , <i>TGFB1</i> , <i>IL6R</i> , <i>STAT3</i> , <i>FLG</i> , and 11q13 locus	CVC	TA	P [†]
rs11236802	8	0.552	0.019
rs4845374_rs11236802	3	0.551	0.033
rs1933064_rs6592651_rs11236802	6	0.570	0.007
rs4796793_rs1933064_rs6592651_rs11236802	7	0.613	<0.001
rs1800872_rs1800469_rs2228145_rs1933064_rRs11236802	4	0.564	0.019
rs3021094_rs1800469_rs2228145_rs1933064_rs6592650_rs7942382	4	0.525	0.224
rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs11236802	6	0.523	0.268
rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs6592651_rs11236802	9	0.569	0.084
rs1800872_rs3021094_rs1800469_rs6689393_rs4796793_rs1933064_rs6592650_rs6592651_rs11236802	9	0.637	0.018

Adjusted for age and gender. †, based on 5,000 permutations. GMDR, generalized multifactor dimensionality reduction; *FLG*, filaggrin; logIgE, log-transformed total IgE; IgE, immunoglobulin E; CVC, cross-validation consistency; TA, testing accuracy; *IL10*, interleukin-10; *TGFB1*, transforming growth factor-beta 1; *IL6R*, IL-6 receptor; *STAT3*, signal transducer and activator of transcription 3.

Table S5 GMDR analysis for *FLG*, 11q13 and regulatory genes for eczema diagnosis

Model formed by <i>IL10</i> , <i>TGFB1</i> , <i>IL6R</i> , <i>STAT3</i> , <i>FLG</i> , and 11q13 locus	CVC	TA	P [†]
rs7927894	7	0.510	0.377
rs1800872_rs6592650	3	0.504	0.377
rs1933064_rs6592651_rs7927894	5	0.494	0.623
rs1800872_rs2228145_rs4796793_rs6592650	2	0.493	0.989
rs1800872_rs6689393_rs1933064_rs6592650_rs11236802	5	0.508	0.828
rs3021094_rs2228145_rs4796793_rs1933064_rs6592650_rs11236802	4	0.474	0.828
rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs11236802	5	0.453	0.945
rs1800872_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs6592651_rs7942382	5	0.490	0.623
rs1800872_rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs6592651_rs11236802	3	0.409	0.989
rs1800872_rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs6592651_rs7927894_rs7942382	10	0.558	0.172
rs1800872_rs3021094_rs1800469_rs2228145_rs6689393_rs4796793_rs1933064_rs6592650_rs6592651_rs7927894_rs7942382	6	0.440	0.623
rs1800872_rs3790622_rs3021094_rs1800469_rs2228145_rs6689393_rs4796793_rs1933064_rs6592650_rs6592651_rs7927894_rs7942382	9	0.522	0.828

Adjusted for age and gender. †, based on 5,000 permutations. GMDR, generalized multifactor dimensionality reduction; *FLG*, filaggrin; logIgE, log-transformed total IgE; IgE, immunoglobulin E; CVC, cross-validation consistency; TA, testing accuracy; *IL10*, interleukin-10; *TGFB1*, transforming growth factor-beta 1; *IL6R*, IL-6 receptor; *STAT3*, signal transducer and activator of transcription 3.

Table S6 GMDR analysis for *FLG*, 11q13 and regulatory genes for atopic eczema

Model formed by <i>IL10</i> , <i>TGFB1</i> , <i>IL6R</i> , <i>STAT3</i> , <i>FLG</i> , and 11q13 locus	CVC	TA	P [†]
rs7927894	10	0.550	0.006
rs3021094_rs7927894	3	0.554	0.018
rs1800872_rs2228145_rs6592650	7	0.563	0.008
rs1800872_rs2228145_rs4796793_rs6592650	2	0.572	0.004
rs3021094_rs2228145_rs1933064_rs6592650_rs11236802	6	0.563	0.009
rs3021094_rs1800469_rs2228145_rs1933064_rs6592650_rs11236802	7	0.573	0.006
rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs11236802	9	0.516	0.326
rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs6592651_rs11236802	10	0.569	0.066
rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs6592651_rs7942382_rs11236802	5	0.528	0.312
rs1800872_rs3021094_rs1800469_rs2228145_rs4796793_rs1933064_rs6592650_rs6592651_rs7942382_rs11236802	8	0.531	0.346

Adjusted for age and gender. [†], based on 5,000 permutations. GMDR, generalized multifactor dimensionality reduction; *FLG*, filaggrin; logIgE, log-transformed total IgE; IgE, immunoglobulin E; CVC, cross-validation consistency; TA, testing accuracy; *IL10*, interleukin-10; *TGFB1*, transforming growth factor-beta 1; *IL6R*, IL-6 receptor; *STAT3*, signal transducer and activator of transcription 3.