ASPRV1	Primer sequence 5' - 3'	Reporter 1 probe (VIC)	Reporter 2 probe (FAM)
c.220 G>A p.V74I	F: CGCCGACACTGCTCTGT R: CTGCTGCTCTCCTCTGGAA	TTGGCGTGGGTTGC	TGGCGTGGATTGC
c.259 G>A p.G87R	F: GTTCCAGAGGAGAGCAGCAG R: ACGACATTGGCCCCATCAAAA	CCGCTCCCGGCCAT	TCCGCTCCTGGCCAT
c.559 G>A p.V187I	F: CCCTCCTGAAGGCCTTTGG R: AGCCCTTACCCATGCTGTTG	CCCAAAGAGATCGTCTTT	CCAAAGAGATCATCTTT
c.728 T>C p.V243A	F: CACCCTGCAGCCCTTTGA R: CACCGCTGTATCCCAGACA	CCACCTTTACCACATTC	ACCTTTGCCACATTC
c.998 C>T p.S333F	F: GGTCCCTGGAAGATGAGTTTGAC R: GCTCCTGCCGCCCTT	AGGACCCCTCCTCAGAAG	AGGACCCCTTCTCAGAAG

Supplementary Table 1. Primer and probe sequences of custom-designed Taqman® SNP genotyping assays for the *ASPRV1* mutations V74I, G87R, V187I, V243A and S333F.

For genotyping, 10ng of genomic DNA was amplified in a 10µl reaction volume using Type-it Fast SNP Probe PCR master mix (Qiagen), 0.9µM of each primer, 0.2 µM of each probe and ran on a 7900HT Fast Real-Time PCR system (Applied Biosystems) using the manufacturer's recommended cycling conditions of 95°C for 10 minutes followed by 40 cycles of 92°C for 15 sec and 60°C for 1 minute.

	Irish atopic eczema cases	Irish population controls		Scottish dry skin cases	Scottish population controls
Genotype					
AA	84	95		38	17
AG	228	216		80	54
GG	130	147		49	29
Total number	442	458		167	100
chi-square p value	0.415			0.479	
odds ratio (95% CI)	0.98 (0.81 to 1.18)			0.90 (0.63 to 1.28)	

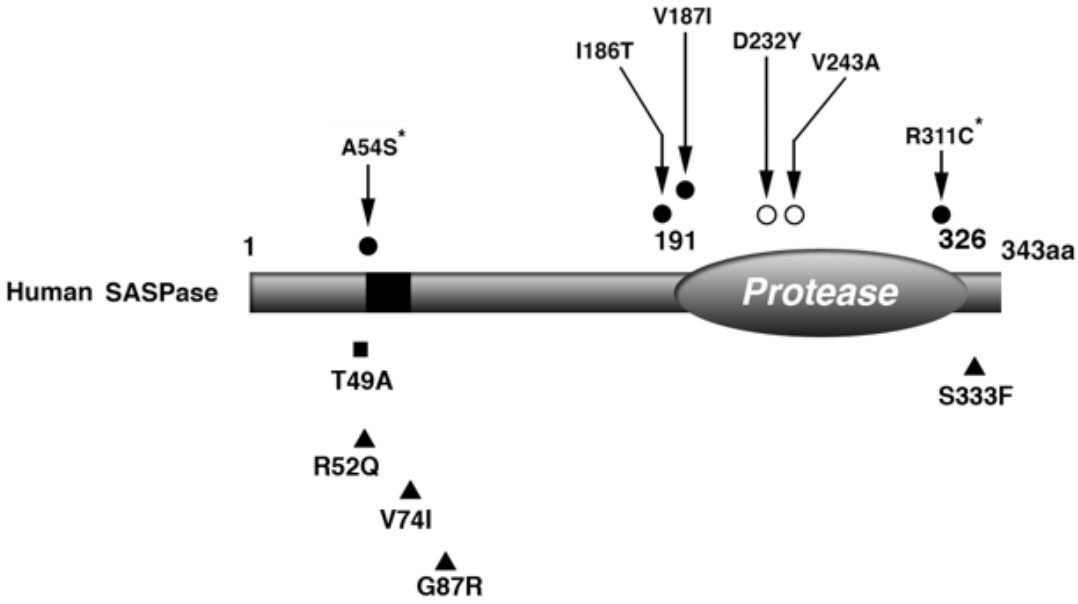
Supplementary Table 2. Results of SNP genotyping and statistical analyses of case-control studies to investigate the association of *ASPRV1* mutation T49A with atopic eczema and clinically dry skin.

The *ASPRV1* mutation T49A (rs3796097) was screened using a Taqman® validated SNP genotyping assay (assay ID c_11540993_10, Applied Biosystems). 10ng of genomic DNA was amplified in a 10µl reaction volume using Type-it Fast SNP Probe PCR master mix (Qiagen), 0.9µM of each primer, 0.2 µM of each probe and ran on a 7900HT Fast Real-Time PCR system (Applied Biosystems) using the manufacturer's recommended cycling conditions. Chi-square and logistic regression analyses were performed using the statistical analysis package Stata (StataCorp LP, College Station, TX); CI, confidence interval.

	***FLG* wild-type Irish atopic eczema cases**	***FLG* wild-type Irish population controls**		***FLG* wild-type Scottish dry skin cases**	***FLG* wild-type Scottish population controls**
Genotype					
AA	52	81		19	16
AG	150	190		45	47
GG	77	132		36	25
Total number	279	403		100	88
chi-square p value	0.217			0.467	
odds ratio (95% CI)	0.93 (0.75 to 1.15)			1.15 (0.79 to 1.73)	

Supplementary Table 3. Results of SNP genotyping and statistical analyses of case-control studies to investigate the association of *ASPRV1* mutation T49A with atopic eczema and clinically dry skin in *FLG* wild-type individuals.

FLG null mutations (R501X, 2282del4, R2447X and S3247X) were screened as previously reported (Kezic *et al.* 2011) and only those individuals with *FLG* wild-type results for each of these four mutations were included in this sub-group analysis. Chi-square and logistic regression analyses were performed using the statistical analysis package Stata (StataCorp LP, College Station, TX); CI, confidence interval.



Supplementary Figure 1. Schematic representation of the human SASPase protein (based on Matsui *et al*, 2011). The protease active site is located between amino acid residues 191 to 326 and a putative transmembrane sequence is found between amino acid residues 57 to 75. Arrows denote the *ASPRV1* mutations previously identified in atopic eczema patients (filled circles; asterisks indicate mutations identified in the same patient) and controls (open circles). Arrowheads denote the *ASPRV1* missense mutations identified in the discovery cohorts in this study. The position of the T49A mutation is indicated by a filled box.