

Fig E1. Flowchart of sample QC and exclusions.

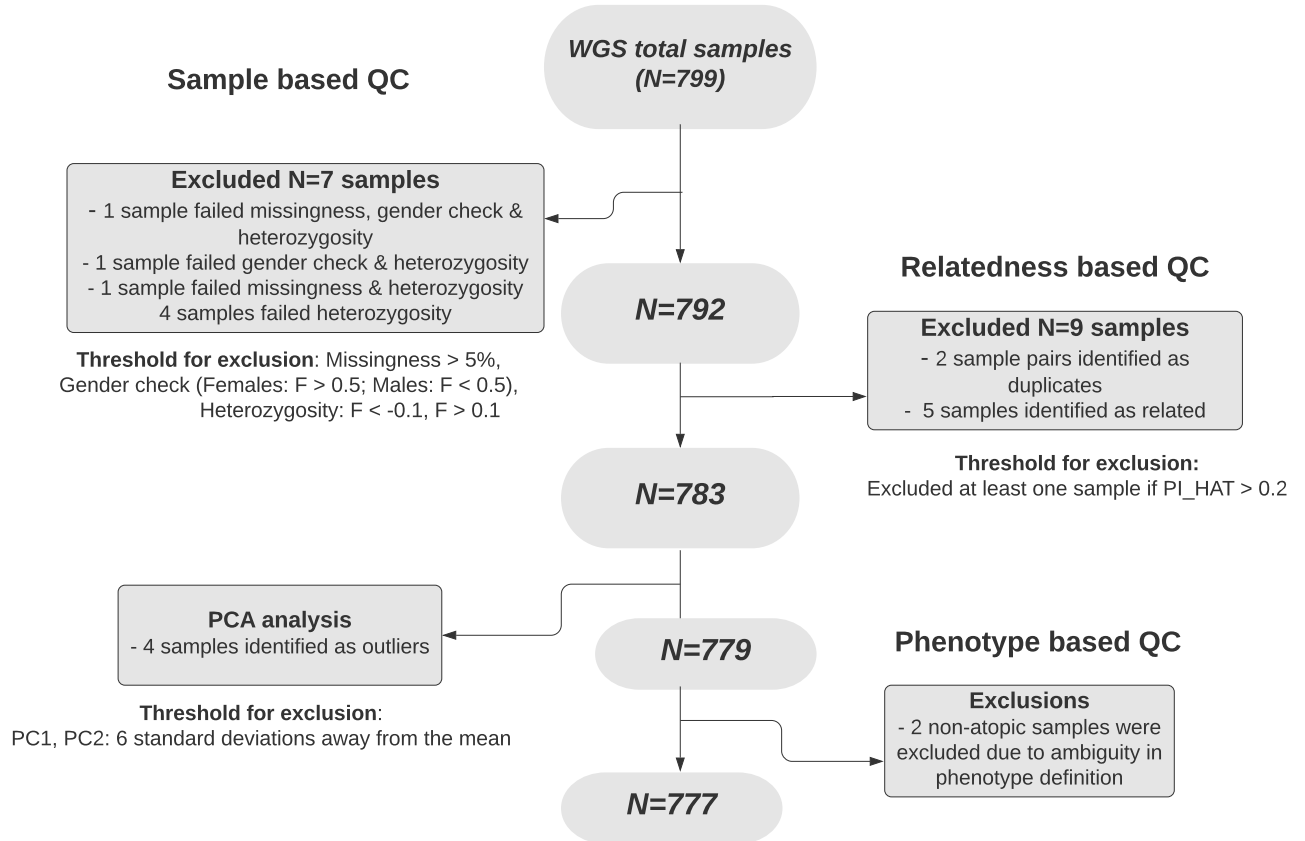


Fig E2. Scree plot of the first ten principal components generated from smart PCA

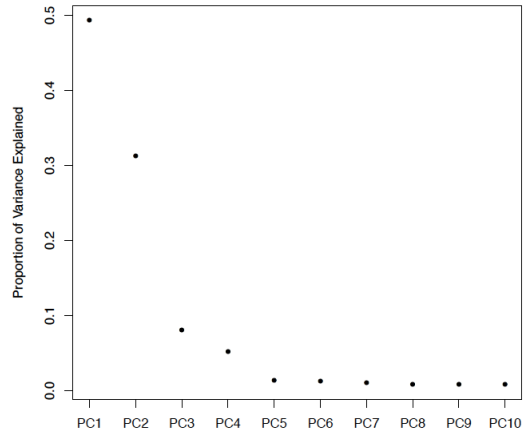


Fig E3. Scatter plots of the first five principal components colored by sequencing batch

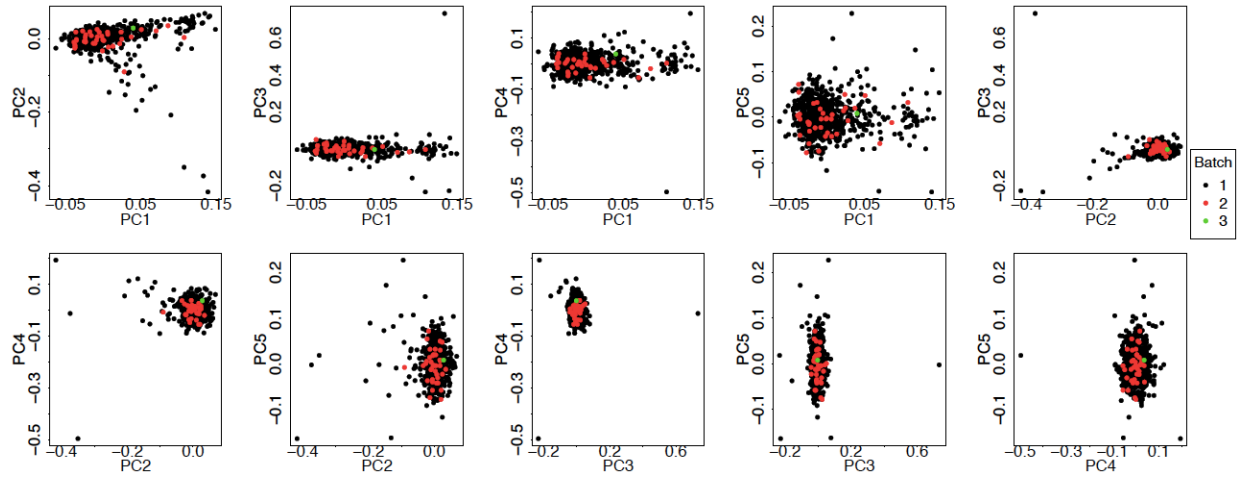


Fig E4. Genome wide gene-based tests performed to identify genes harboring damaging variants that determine eczema herpeticum. Results are presented as Q-Q plots for genome wide gene-based tests, and colored dots indicate the 8 genes moved forward to functional follow up; the genes had to meet the threshold of $p < 0001$ in the comparison of ADEH+ vs. ADEH- (left column) or ADEH+ vs. NA (middle column), but not in the comparison of ADEH- to NA (right column).

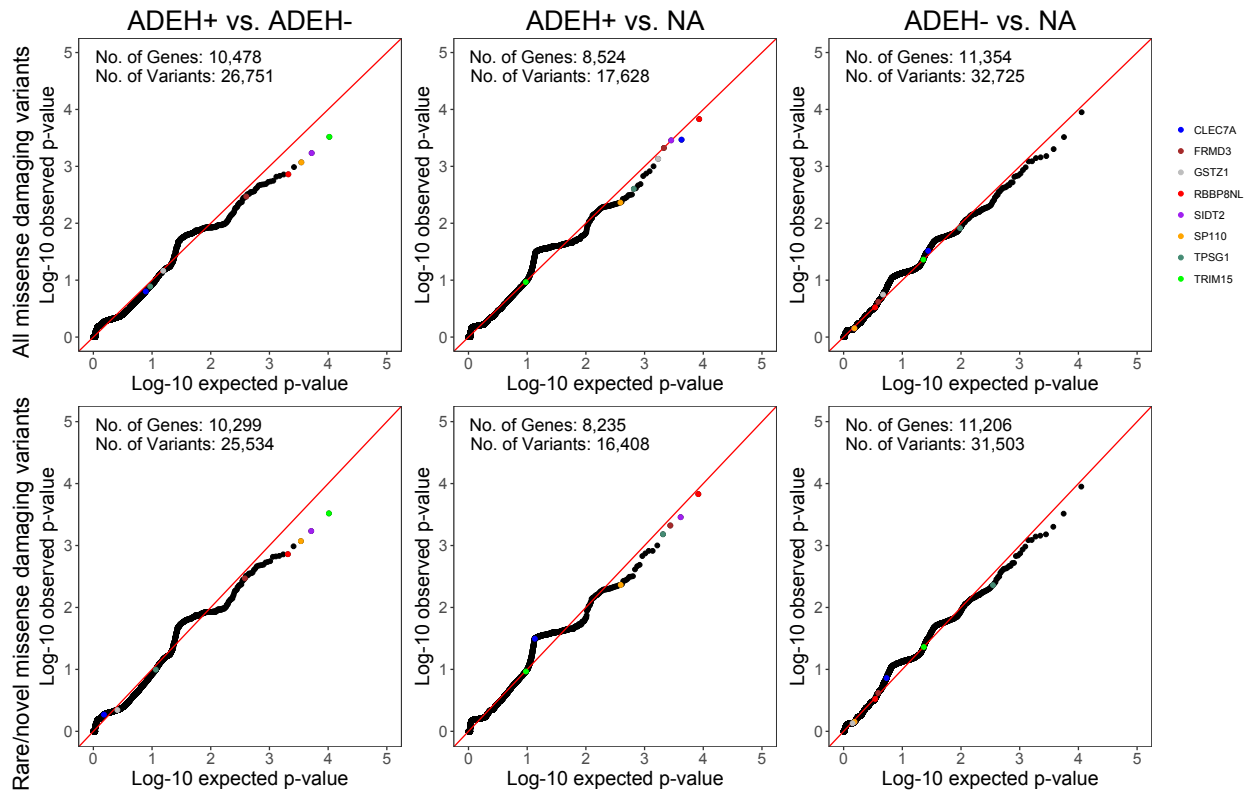


Figure E5. Gene expression of six candidate genes in NHPK in the presence and absence of HSV-1. Data are presented as mean \pm SD, n=3.

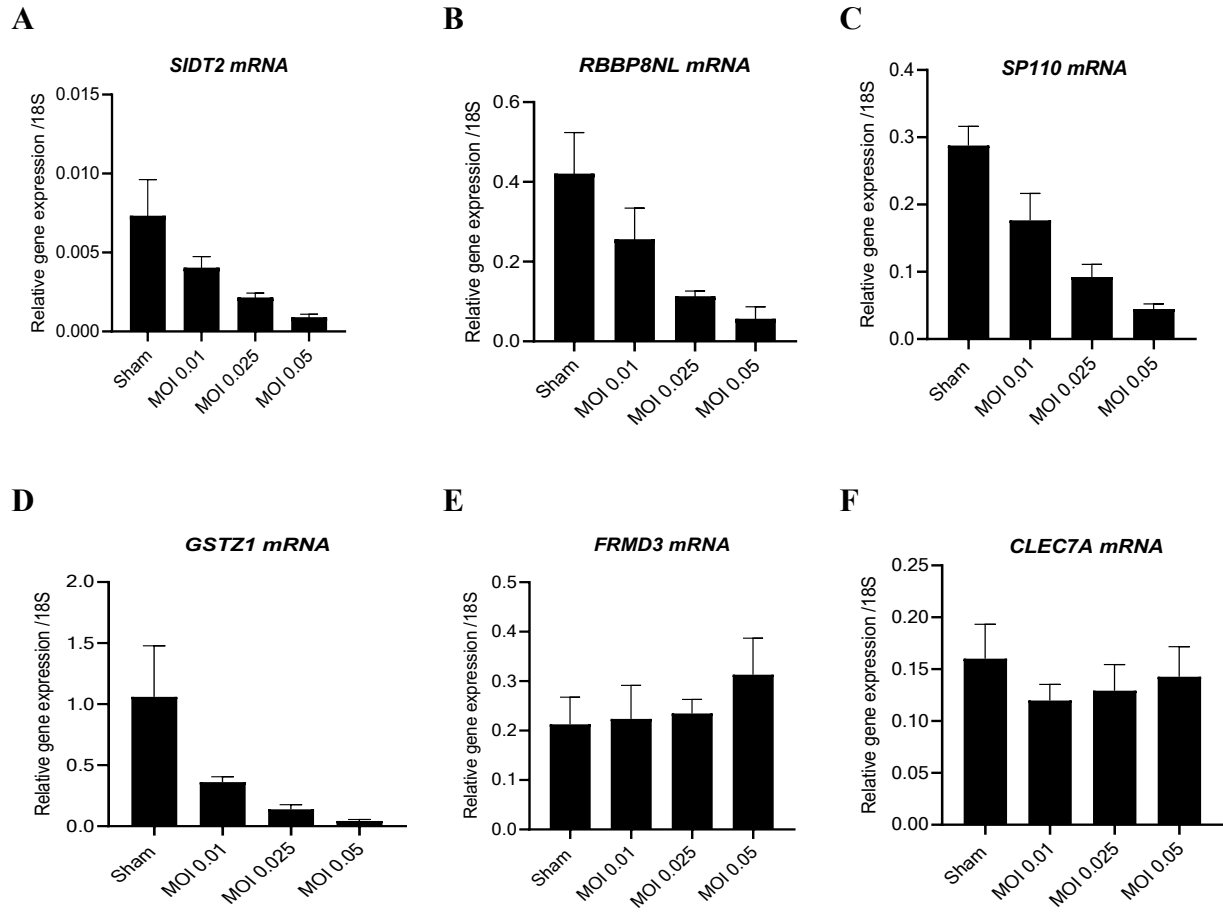


Figure E6. Gene expression of six candidate genes in NHEK treated with scrambled and specific gene siRNA in the presence and absence of HSV-1 (24 hours after infection). Data are presented as mean \pm SD, n=3.

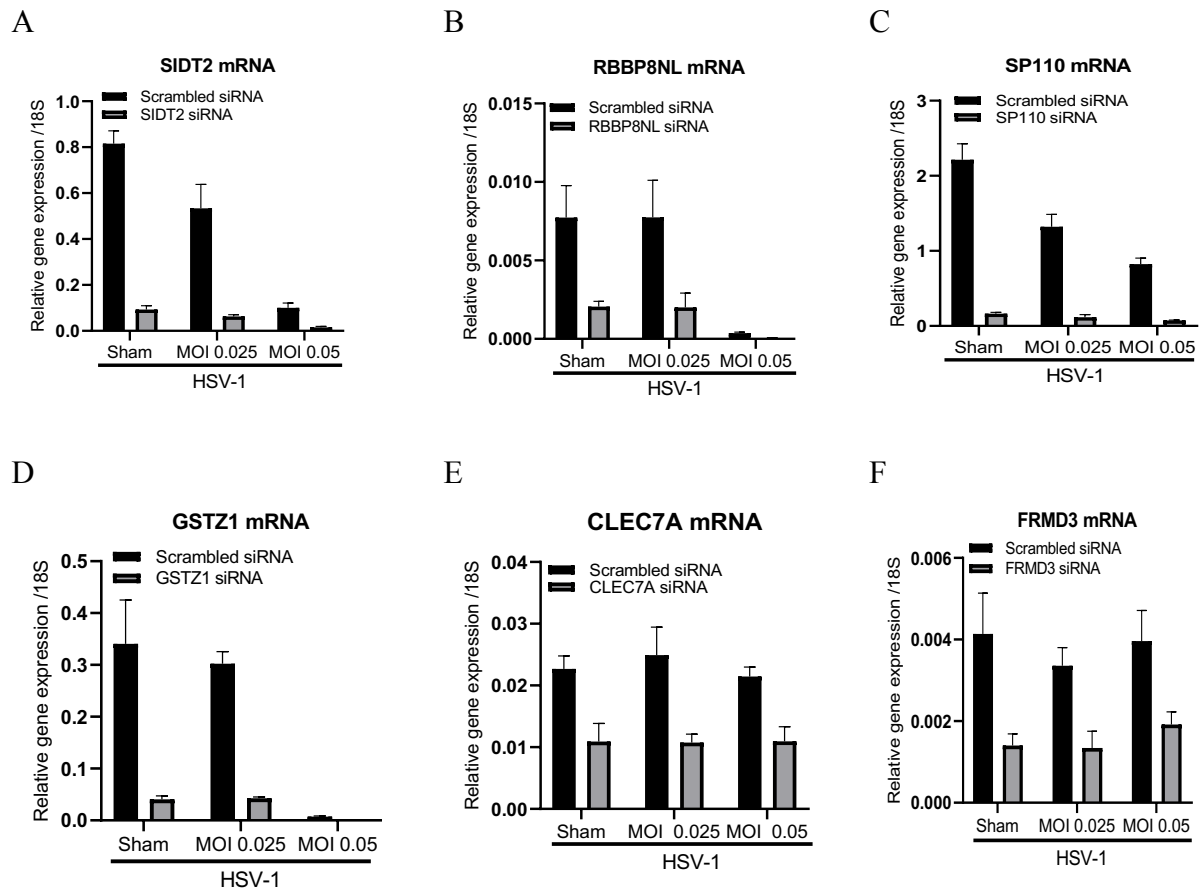


Figure E7. IFN β 1 gene expression wasn't altered in *SIDT2*- and *RBBP8NL*-silenced NHPK upon HSV-1 stimulation. (A) *SIDT2* gene expression; (B) *IFN β 1* gene expression in *SIDT2* –silenced NHPK compared to scrambled siRNA treated NHPK; (C) *RBBP8NL* gene expression; (D) *IFN β 1* gene expression in *RBBP8NL* –silenced NHPK compared to scrambled siRNA treated NHPK; Data of three independent experiments combined. Comparisons of log-transformed relative gene expression values between specific gene siRNA and scrambled siRNA under varying MOI were made using t-tests. Statistical significance is represented as ns = not significant, * $p < 0.05$ and ** $p < 0.01$.

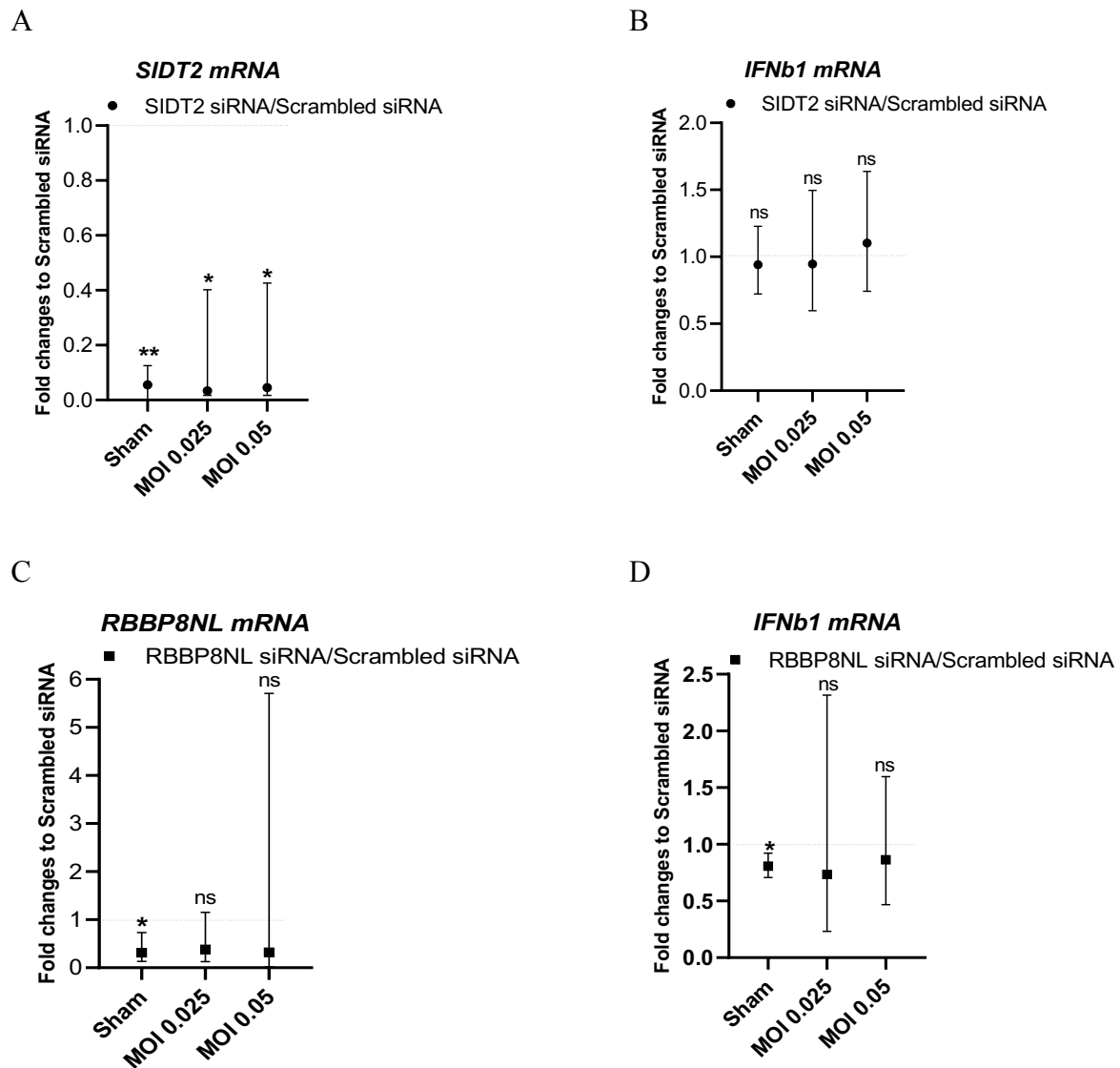


Table E1. On target siRNA sequences

Gene	ON-TARGETplus SMARTpool siRNA sequences	
SIDT2	5'-CCAAGAACGUCUCGCAGAA-3', 5'-CCAUCACCGUACAGCGCAA-3'	5'-GCAACAGGACAGAGGGCGU-3', 5'-ACAAGCGUGUUCUGCGGAA-3'
SP110	5'-GGAGAAAGAUUUCUGUUA-3', 5'-GAGGAUGGAACUUGGUUA-3'	5'-CAAUUAACCUGCGUGAAU-3', 5'-AAAGAUGACUCAACUUGUA-3'
RBBP8NL	5'-GGACAUCUCCAGUGGCCAA-3', 5'-CCAACGAGAUGAACGGGCU-3'	5'-GACCAGAGUCCGACGAACU-3', 5'-CGGCAGCAGGAGUUCGAGA-3'
CLEC7A	5'-CAGGAUAGCUGUUGUUUA-3', 5'-GAAGAUGGAUUAACUCAA-3'	5'-GGAUGAAGAUGGAUUAUACU-3', 5'-CUUCGACUCUCAAGCAAU-3'
FRMD3	5'-GGAAGUAGAUUUCGAUUA-3', 5'-GAACUAGUGUACAACCAA-3'	5'-UUUCGGAGCUCCAGCGUCA-3', 5'-CAUGAACCCUUGAAGAUUA-3'
TPSG1	5'-UGAAAGUCUCCGUGGUGGA-3', 5'-CCCUGAACUCAUCCGACUA-3'	5'-GCAGCAUCCUUCAGCCCGA-3', 5'-CGGCCUCUCCUUCUGCUA-3'
GSTZ1	5'-GCACAGCGGGCAUUAUCUG-3', 5'-GACCAUGGCUGAUCUGUGC-3'	5'-CCACUGAGCUGAGGGCCUA-3', 5'-GGCAAUUGCUGAAAGAUUC-3'
TRIM15	5'-GGGAGAAACUUACUGCGAG-3', 5'-CCCUGAAGGUGGUCCAUGA-3'	5'-GCGAGAACGAUGCCGAGUU-3', 5'-GCAGAACCACAGACGGCUU-3'
Scrambled	5'-UGGUUUACAUGUCGACUAA-3', 5'-UGGUUUACAUGUUUCUGA-3'	5'-UGGUUUACAUGUUGUGUGA-3', 5'-UGGUUUACAUGUUUCCUA-3'

Table E2. Primers used for examination of gene silencing efficiency

Gene name	Primers purchased from Applied Biosystems
<i>RBBP8NL</i>	Hs00293019_m1
<i>SIDT2</i>	Hs00211141_m1
<i>SP110</i>	Hs00893490_m1
<i>TRIM15</i>	Hs00264400_m1
<i>CLEC7A</i>	Hs01902549_S1
<i>FRMD3</i>	Hs00604157_m1
<i>TPSG1</i>	Hs01550477_g1
<i>GSTZ1</i>	Hs01041668_m1

Table E4A. Association analysis results for variants of interest focusing on variants previously identified as associated with ADEH+ .

snp147	chr:position (hg19)	PMID	MAF (ADEH+ ADEH- NA)	ADEH+ vs ADEH-	ADEH+ vs NA	ADEH- vs NA	Func.refGene	Gene.refGene	AAChange.refGene	
				OR [95% CI] P-value	OR [95% CI] P-value	OR [95% CI] P-value				
rs10058453	chr5:35880820	20466416	37.7% 32.0% 30.3%	0.73 [0.5-1.2] 0.1738	0.66 [0.4-1.1] 0.0928	0.92 [0.7-1.2] 0.5236	intergenic	IL7R; CAPSL	.	
rs10213865	chr5:35857850		33.6% 24.2% 30.3%	1.46 [0.9-2.3] 0.0941	1.07 [0.7-1.7] 0.7577	0.75 [0.6-1.0] 0.0174	intronic	IL7R	.	
rs12516866	chr5:35851261		44.9% 39.5% 44.4%	1.19 [0.8-1.8] 0.4093	0.96 [0.6-1.5] 0.8645	0.82 [0.7-1.0] 0.0790	intergenic	SPEF2; IL7R	.	
rs1389832	chr5:35858721		37.7% 32.0% 29.9%	0.73 [0.5-1.2] 0.1738	0.64 [0.4-1.1] 0.0789	0.90 [0.7-1.2] 0.4212	intronic	IL7R	.	
rs1898671	chr5:110408002		27.5% 35.9% 29.9%	0.65 [0.4-1.1] 0.0775	0.86 [0.5-1.5] 0.5797	1.34 [1.1-1.7] 0.0184	intronic	TSLP	.	
rs2416259	chr5:110419742		excluded from analysis for QC							
rs17175350		26343451	Not in our dataset							
rs372412638			Not in our dataset							
rs374787981			Not in our dataset							
rs11575936	chr6:137540425		1.02% <0.01% 0.21%	30.23 [0.6-1570.0] 0.0907	4.88 [0.2-106.3] 0.3136	0.16 [0.0-18.8] 0.3255	exonic: nonsynonymous SNV	IFNGR1	NM_000416:exon1: c.G40A:p.V14M	
rs1327475	chr6:137536455	17.4% 15.8% 16.2%	1.06 [0.6-1.9] 0.8252	1.04 [0.6-1.9] 0.8936	0.96 [0.7-1.3] 0.8068	intronic	IFNGR1	.		
rs17175322	chr6:137528119	<0.01% <0.01% 0.21%	NA	1.60 [0.0-188.1] 1.0000	0.16 [0.0-18.8] 0.3255	exonic: nonsynonymous SNV	IFNGR1	NM_000416:exon2: c.G181A:p.V61I		
rs1887415	chr6:137519238	1.02% 0.50% <0.01%	2.01 [0.4-11.7] 0.4357	14.60 [0.3-680.2] 0.1713	5.34 [0.5-61.9] 0.1804	exonic: nonsynonymous SNV	IFNGR1	NM_000416:exon7: c.T1400C:p.L467P		
rs11132242	chr4:185321941	39.8% 38.7% 39.2%	1.04 [0.7-1.6] 0.8570	1.05 [0.7-1.7] 0.8391	0.98 [0.8-1.2] 0.8935	intronic	IRF2	.		
rs1124191	chr4:185302246	30.6% 26.9% 24.0%	0.81 [0.5-1.3] 0.3676	0.69 [0.4-1.1] 0.1320	0.86 [0.7-1.1] 0.2421	ncRNA_intronic	LOC102723766	.		
rs1342852	chr4:185306117	32.6% 36.3% 37.9%	0.88 [0.6-1.4] 0.5881	0.80 [0.5-1.3] 0.3477	0.93 [0.7-1.2] 0.5153	intergenic	LOC102723766; IRF2	.		
rs17488073	chr4:185328973	12.2% 15.3% 14.5%	0.78 [0.4-1.5] 0.4448	0.83 [0.4-1.6] 0.5870	1.07 [0.8-1.5] 0.6758	intronic	IRF2	.		
rs809909	chr4:185324610	27.5% 33.2% 34.3%	1.29 [0.8-2.1] 0.2941	1.36 [0.8-2.2] 0.2332	1.06 [0.8-1.3] 0.6474	intronic	IRF2	.		

Table E4B. Association analysis results for variants of interest focusing on variants previously identified as associated with AD.

snp147	chr:position (hg19)	MAF (ADEH+ ADEH- NA)	ADEH+ vs ADEH-	ADEH+ vs NA	ADEH- vs NA	Func.refGene	Gene.refGene	
			OR [95% CI] P-value	OR [95% CI] P-value	OR [95% CI] P-value			
rs7512552	chr1:150265704	46.9% 43.0% 49.7%	0.80 [0.5-1.3] 0.3328	1.05 [0.7-1.7] 0.8218	NA	upstream	MRPS21	
rs61813875	chr1:152536650	10.2% 6.32% 1.68%	1.63 [0.8-3.3] 0.1731	6.62 [2.5-17.9] 2.0E-04	NA	intergenic	CRCT1;LCE3E	
rs6602364	chr10:6038853	45.9% 48.5% 45.7%	0.82 [0.5-1.3] 0.3671	0.75 [0.5-1.2] 0.2030	0.90 [0.7-1.1] 0.3612	intergenic	IL15RA;IL2RA	
rs2944542	chr10:64369999	32.6% 35.2% 38.8%	1.17 [0.7-1.9] 0.5033	1.39 [0.9-2.2] 0.1665	1.17 [0.9-1.5] 0.1771	intronic	ZNF365	
rs7127307	chr11:128187383	34.6% 43.3% 44.9%	0.70 [0.5-1.1] 0.1059	0.62 [0.4-1.0] 0.0473	0.94 [0.8-1.2] 0.5563	intergenic	LOC101929497;ETS1	
rs10791824	chr11:65559266	38.7% 36.3% 41.5%	0.87 [0.6-1.4] 0.5323	1.09 [0.7-1.8] 0.7229	1.25 [1.0-1.6] 0.0599	intronic	OVOL1	
rs2212434	chr11:76281593	42.8% 49.6% 42.4%	1.39 [0.9-2.2] 0.1352	1.93 [1.2-3.1] 0.0049	1.36 [1.1-1.7] 0.0078	intergenic	EMSY;LRRC32	
rs2038255	chr14:35559126	17.3% 21.3% 19.6%	0.75 [0.4-1.3] 0.3214	0.82 [0.5-1.5] 0.5012	1.11 [0.8-1.5] 0.4634	ncRNA_intronic	LOC101927178	
rs2041733	chr16:11229589	46.9% 49.8% 44.7%	1.18 [0.8-1.8] 0.4576	0.95 [0.6-1.5] 0.8334	0.81 [0.6-1.0] 0.0672	intronic	CLEC16A	
rs12951971	chr17:40528131	13.5% 11.5% 8.05%	1.16 [0.6-2.2] 0.6586	1.55 [0.8-3.0] 0.1952	1.49 [1.0-2.2] 0.0428	intronic	STAT3	
rs6419573	chr2:103027103		excluded from analysis for QC					
rs4643526	chr2:61184651	16.3% 20.2% 16.8%	0.78 [0.4-1.4] 0.3951	0.99 [0.5-1.8] 0.9838	1.29 [1.0-1.7] 0.0955	intronic	PUS10	
rs112111458	chr2:71100105	11.2% 10.9% 14.7%	1.07 [0.6-2.0] 0.8301	0.73 [0.4-1.5] 0.3856	0.70 [0.5-1.0] 0.0329	intergenic	CD207;LINC01143	
rs10199605	chr2:8495097	30.6% 30.0% 29.7%	1.00 [0.6-1.6] 0.9963	1.01 [0.6-1.6] 0.9556	1.02 [0.8-1.3] 0.8925	intergenic	LINC00299;LOC101929567	
rs4809219	chr20:62303115	20.4% 21.1% 26.1%	1.09 [0.6-1.8] 0.7552	1.46 [0.8-2.6] 0.1833	1.33 [1.0-1.7] 0.0302	ncRNA_intronic	RTEL1-TNFRSF6B	
rs1249910	chr3:112391174	39.8% 33.2% 32.6%	0.76 [0.5-1.2] 0.2214	0.73 [0.5-1.2] 0.1825	0.97 [0.8-1.2] 0.8152	intergenic	CCDC80;LOC101929694	

snp147	chr:position (hg19)	MAF (ADEH+ ADEH- NA)	ADEH+ vs ADEH-	ADEH+ vs NA	ADEH- vs NA	Func.refGene	Gene.refGene
			OR [95% CI] P-value	OR [95% CI] P-value	OR [95% CI] P-value		
rs7625909	chr3:53091164	35.7% 29.1% 33.0%	1.32 [0.8-2.1] 0.2314	1.12 [0.7-1.8] 0.6213	0.83 [0.7-1.1] 0.1335	intergenic	SFMBT1;RFT1
rs6827756(4:1232 43592)	chr4:123184411*	38.7% 38.4% 38.1%	1.02 [0.7-1.6] 0.9176	0.99 [0.6-1.6] 0.9554	0.98 [0.8-1.2] 0.8652	intronic	KIAA1109
rs12188917	chr5:131991085	23.4% 24.3% 19.4%	NA	1.35 [0.8-2.4] 0.2833	1.35 [1.0-1.8] 0.0313	ncRNA_intronic	TH2LCRR
rs10214237	chr5:35883734	33.6% 24.3% 29.8%	1.45 [0.9-2.3] 0.0971	1.10 [0.7-1.7] 0.6830	0.77 [0.6-1.0] 0.0307	intergenic	IL7R;CAPSL
rs4713555	chr6:32575524	19.3% 24.7% 26.6%	0.76 [0.5-1.3] 0.3097	0.66 [0.4-1.2] 0.1481	0.89 [0.7-1.2] 0.3850	intergenic	HLA-DRB1;HLA-DQA1
rs6473227	chr8:81285892	42.8% 40.1% 40.4%	0.90 [0.6-1.4] 0.6244	0.91 [0.6-1.4] 0.6778	1.01 [0.8-1.3] 0.9356	intergenic	MIR5708;ZBTB10
rs12730935	Not in our dataset						
rs145809981							
rs2592555							
rs2918307							
rs4312054							

* A nearby SNP (rs6827756; at 123,184,411 bp) in LD ($r^2 = 0.97$ in the 1000 Genomes Project) showed similar association ($\log_{10}(\text{Bayes factor}) = 7.21$, European fixed-effects $P = 3 \times 10^{-9}$)

Table E5: Clinical characteristics of carriers for variants enriched in recurrent ADEH+ subjects from Table III.

Gene	Variant dbSNP ID		carrier-heterozygous			carrier-homozygous				
			ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)	ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)		
SIDT2	rs142171036	N	2	4	0	-	-	-		
		Males N (%)	1 (50%)	3 (75%)	-	-	-	-		
		Age* (Yrs) mean (SD)	17.5 (19.1)	31.2 (15)	-	-	-	-		
		Total IgE (kU/L) mean (range)	17.8 (4.5-31.1)	7452 (716-23135)	-	-	-	-		
		Eosinophils mean (range)	132 (123-141)	520 (41-1250)	-	-	-	-		
		Phadiatop (kUA/L) mean (range)	0.3 (0.3-0.3)	123.2 (54.6-286)	-	-	-	-		
		EASI mean (range)	2.4 (0.3-4.4)	14.1 (0.7-28.9)	-	-	-	-		
		Rajka-Langeland score mean (SD)	5.5 (0.7)	6.2 (2.8)	-	-	-	-		
		CLEC7A	rs16910526	N	70	14	25	6	1	1
				Males N (%)	36 (51.4%)	7 (50%)	7 (28%)	3 (50%)	1 (100%)	0 (0%)
Age* (Yrs) mean (SD)	32.4 (19.8)			19.6 (17)	44.2 (14.9)	31.2 (22.2)	13	26.9		
Total IgE (kU/L) mean (range)	3992.7 (2.5-82020)			2886.8 (31.7-10412)	29.1 (3.4-89.8)	2702 (10.1-14380)	995 (995-995)	8.9 (8.9-8.9)		
Eosinophils mean (range)	329.9 (23-1356)			541.4 (41-1409)	111.6 (5-322)	400.5 (173-588)	108 (108-108)	149 (149-149)		
Phadiatop (kUA/L) mean (range)	138.9 (0.1-5632)			119.1 (0.2-726)	0.2 (0.1-0.3)	40.6 (0.2-88.1)	59.5 (59.5-59.5)	0.3 (0.3-0.3)		
EASI mean (range)	15.4 (0.4-63.9)			18.6 (0.6-55)	-	13.2 (1.9-33.7)	23 (23-23)	-		
Rajka-Langeland score mean (SD)	6.8 (1.5)			7.1 (1.8)	-	6.5 (2.1)	7 (NA)	-		

Gene	Variant dbSNP ID		carrier-heterozygous			carrier-homozygous				
			ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)	ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)		
CLEC7A	rs140318683	N	4	1	0	-	-	-		
		Males N (%)	2 (50%)	1 (100%)	-	-	-	-		
		Age* (Yrs) mean (SD)	32.2 (23.7)	8 (NA)	-	-	-	-		
		Total IgE (kU/L) mean (range)	298.2 (196-395)	65.8 (65.8-65.8)	-	-	-	-		
		Eosinophils mean (range)	352.5 (223-554)	656 (656-656)	-	-	-	-		
		Phadiatop (kUA/L) mean (range)	28.9 (14.6-55.8)	2.2 (2.2-2.2)	-	-	-	-		
		EASI mean (range)	11.8 (1.4-24.8)	14.8 (14.8-14.8)	-	-	-	-		
		Rajka-Langeland score mean (SD)	6.2 (2.1)	8 (NA)	-	-	-	-		
		GSTZ1	rs7972	N	71	12	25	4	2	2
				Males N (%)	32 (45.1%)	5 (41.7%)	6 (24%)	3 (75%)	0 (0%)	1 (50%)
Age* (Yrs) mean (SD)	24.5 (15.8)			22.1 (15.9)	38.2 (13.9)	29.2 (22)	20.5 (6.4)	48.5 (23.3)		
Total IgE (kU/L) mean (range)	2215.6 (2.6-25887)			2302.7 (14.5-9914)	11.1 (2-40)	1256 (17.2-4869)	65.2 (38.4-92)	27.4 (6.7-48.1)		
Eosinophils mean (range)	279.2 (23-2195)			445 (41-1013)	117.1 (5-391)	558.5 (42-1042)	341 (207-475)	147 (50-244)		
Phadiatop (kUA/L) mean (range)	101.8 (0.1-1416)			180.6 (7.3-1013)	0.2 (0.1-0.3)	15.8 (0.2-49.9)	11.6 (3.7-19.4)	0.2 (0.1-0.3)		
EASI mean (range)	12.8 (0.3-55.5)			12.6 (0-28.4)	-	11.8 (5-21.8)	7.9 (5.7-10.2)	-		
Rajka-Langeland score mean (SD)	6.9 (1.3)			6.8 (2.1)	-	7.2 (1.3)	6 (1.4)	-		

Gene	Variant dbSNP ID		carrier-heterozygous			carrier-homozygous				
			ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)	ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)		
TPSG1	rs61587627	N	22	3	2	-	-	-		
		Males N (%)	9 (40.9%)	1 (33.3%)	0 (0%)	-	-	-		
		Age* (Yrs) mean (SD)	28.5 (19.9)	21.7 (19)	29 (5.7)	-	-	-		
		Total IgE (kU/L) mean (range)	2361.5 (2-16421)	2406 (1911-2936)	11.2 (4.9-17.5)	-	-	-		
		Eosinophils mean (range)	279.4 (11-1419)	481.7 (88-948)	49.5 (16-83)	-	-	-		
		Phadiatop (kUA/L) mean (range)	117.7 (0.2-1127)	247.4 (7.3-689)	0.1 (0.1-0.1)	-	-	-		
		EASI mean (range)	14.5 (1.1-66.8)	12.8 (3.5-19.6)	-	-	-	-		
		Rajka-Langeland score mean (SD)	7.2 (1.3)	6.8 (1.9)	-	-	-	-		
		TPSG1	rs187607214	N	3	2	0	-	-	-
				Males N (%)	1 (33.3%)	1 (50%)	-	-	-	-
Age* (Yrs) mean (SD)	39 (17.8)			46 (22.6)	-	-	-	-		
Total IgE (kU/L) mean (range)	126.7 (3.6-372)			4024 (3535-4513)	-	-	-	-		
Eosinophils mean (range)	173.7 (62-352)			454 (138-770)	-	-	-	-		
Phadiatop (kUA/L) mean (range)	21 (0.6-41.4)			263.5 (95-432)	-	-	-	-		
EASI mean (range)	12.9 (0.5-24.2)			10.6 (4.9-16.4)	-	-	-	-		
Rajka-Langeland score mean (SD)	6 (2.6)			7 (1.4)	-	-	-	-		

Gene	Variant dbSNP ID		carrier-heterozygous			carrier-homozygous				
			ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)	ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)		
SP110	rs372023963	N	0	1	0	-	-	-		
		Males N (%)	-	0 (0%)	-	-	-	-		
		Age* (Yrs) mean (SD)	-	46 (NA)	-	-	-	-		
		Total IgE (kU/L) mean (range)	-	14.5 (14.5-14.5)	-	-	-	-		
		Eosinophils mean (range)	-	196 (196-196)	-	-	-	-		
		Phadiatop (kUA/L) mean (range)	-	NA (NA)	-	-	-	-		
		EASI mean (range)	-	0 (0-0)	-	-	-	-		
		Rajka-Langeland score mean (SD)	-	4 (NA)	-	-	-	-		
		SP110	rs768938186	N	0	1	0	-	-	-
				Males N (%)	-	0 (0%)	-	-	-	-
Age* (Yrs) mean (SD)	-			4 (NA)	-	-	-	-		
Total IgE (kU/L) mean (range)	-			1477 (1477-1477)	-	-	-	-		
Eosinophils mean (range)	-			593 (593-593)	-	-	-	-		
Phadiatop (kUA/L) mean (range)	-			90.3 (90.3-90.3)	-	-	-	-		
EASI mean (range)	-			2 (2-2)	-	-	-	-		
Rajka-Langeland score mean (SD)	-			4 (NA)	-	-	-	-		

Gene	Variant dbSNP ID		carrier-heterozygous			carrier-homozygous				
			ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)	ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)		
SP110	rs149485401	N	6	3	2	-	-	-		
		Males N (%)	4 (66.7%)	2 (66.7%)	0 (0%)	-	-	-		
		Age* (Yrs) mean (SD)	25 (12.5)	22 (19)	49.5 (9.1)	-	-	-		
		Total IgE (kU/L) mean (range)	2140.2 (198-10629)	9139 (1911-23135)	20.4 (20.4-20.4)	-	-	-		
		Eosinophils mean (range)	500.7 (221-1288)	397.3 (88-948)	175 (74-276)	-	-	-		
		Phadiatop (kUA/L) mean (range)	36 (12.3-73.2)	35.9 (7.3-54.6)	0.2 (0.1-0.3)	-	-	-		
		EASI mean (range)	13.7 (2.2-48.7)	19.4 (15.2-23.2)	-	-	-	-		
		Rajka-Langeland score mean (SD)	6.8 (1.2)	7.7 (1.5)	-	-	-	-		
		RBBP8NL	rs200738153	N	16	7	4	-	-	-
				Males N (%)	8 (50%)	2 (28.6%)	0 (0%)	-	-	-
Age* (Yrs) mean (SD)	26.1 (17.9)			19.9 (13.6)	28.1 (4)	-	-	-		
Total IgE (kU/L) mean (range)	3708.6 (17.6-15650)			4274.6 (65.8-23135)	6.6 (5-9.8)	-	-	-		
Eosinophils mean (range)	369.4 (23-1095)			391.1 (156-656)	93.5 (13-152)	-	-	-		
Phadiatop (kUA/L) mean (range)	108.2 (0.1-578)			44.8 (2.2-90.3)	0.2 (0.1-0.3)	-	-	-		
EASI mean (range)	16.5 (0.6-52.9)			13.4 (2-23.7)	-	-	-	-		
Rajka-Langeland score mean (SD)	6.9 (1.9)			6.9 (1.7)	-	-	-	-		

Gene	Variant dbSNP ID		carrier-heterozygous			carrier-homozygous				
			ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)	ADEH- (n=491)	ADEH+ (n=49)	NA (n=237)		
TRIM15	rs34823152	N	33	13	26	1	0	0		
		Males N (%)	11 (33.3%)	6 (46.2%)	7 (26.9%)	1 (100%)	-	-		
		Age* (Yrs) mean (SD)	27.9 (17.4)	21.3 (14.1)	38.1 (16.8)	54 (NA)	-	-		
		Total IgE (kU/L) mean (range)	1548.1 (5.5-12027)	3540 (14.5-23102)	18.4 (2-48.1)	4.4 (4.4-4.4)	-	-		
		Eosinophils mean (range)	339.7 (32-1396)	373.4 (108-1013)	95.7 (9-391)	42 (42-42)	-	-		
		Phadiatop (kUA/L) mean (range)	63.2 (0.2-692)	540 (0.4-4181)	0.3 (0.1-0.3)	NA	-	-		
		EASI mean (range)	12.5 (0.4-58.5)	14.5 (0-37.2)	-	15.8 (15.8-15.8)	-	-		
		Rajka-Langeland score mean (SD)	6.8 (1.3)	6.9 (2)	-	8 (NA)	-	-		
		FRMD3	rs4877747	N	22	8	7	1	0	0
				Males N (%)	14 (63.6%)	4 (50%)	2 (28.6%)	1 (100%)	-	-
Age* (Yrs) mean (SD)	32.4 (17.3)			20.9 (19.6)	35.4 (13.1)	15 (NA)	-	-		
Total IgE (kU/L) mean (range)	2488.5 (5.6-36013)			570.6 (14.4-1592)	9.9 (2.7-21.1)	551 (551-551)	-	-		
Eosinophils mean (range)	304.9 (63-782)			299.4 (22-785)	75 (32-112)	255 (255-255)	-	-		
Phadiatop (kUA/L) mean (range)	85.6 (0.1-998)			45.3 (0.4-97.3)	0.2 (0.1-0.3)	22.9 (22.9-22.9)	-	-		
EASI mean (range)	12.4 (1.6-44.9)			5.7 (0-23.7)	-	4.4 (4.4-4.4)	-	-		
Rajka-Langeland score mean (SD)	6.7 (1.8)			6 (1.5)	-	6 (NA)	-	-		