

**ONLINE REPOSITORY****Human Atopic Dermatitis Complicated by Eczema Herpeticum is Associated  
with Abnormalities in Gamma Interferon Response**

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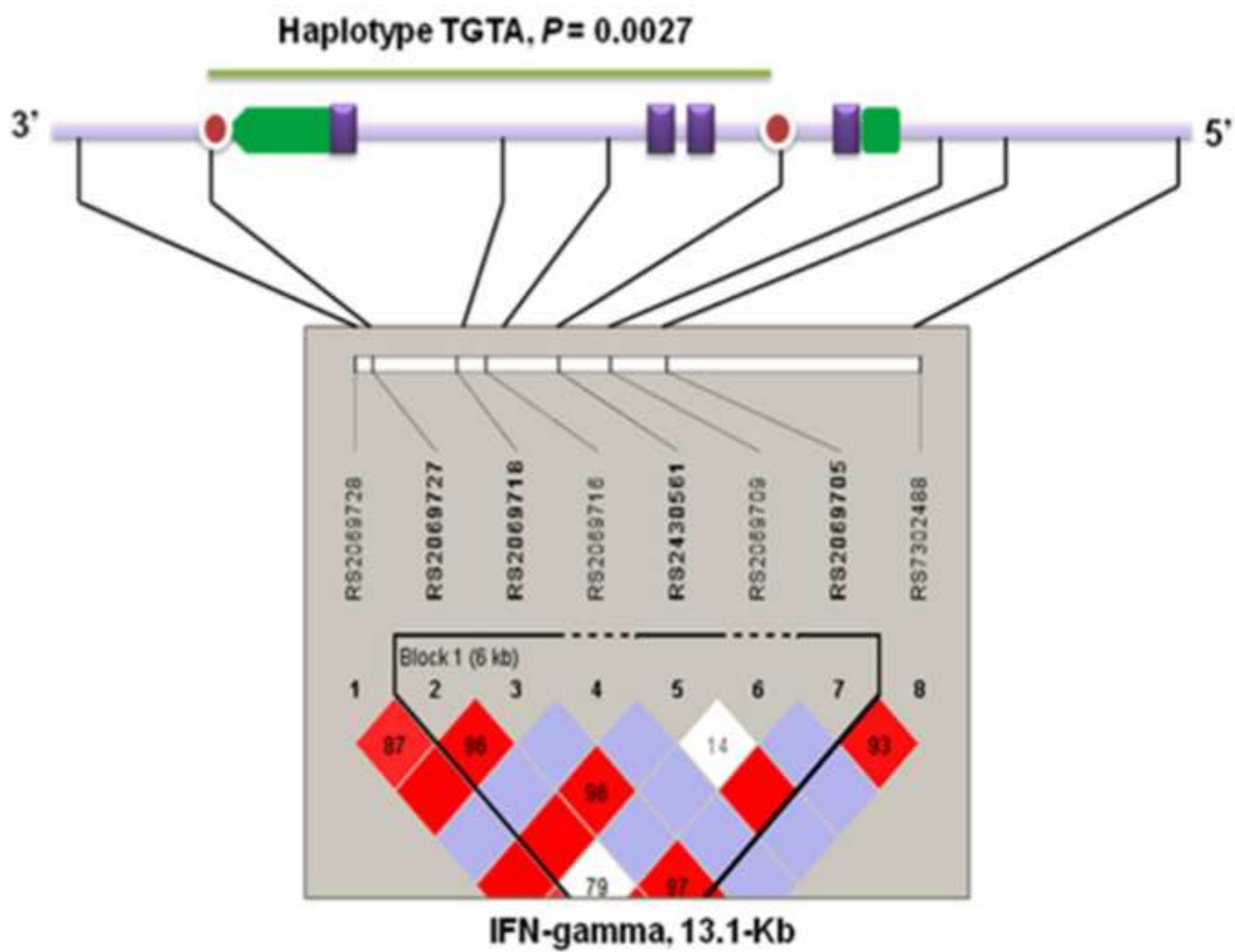
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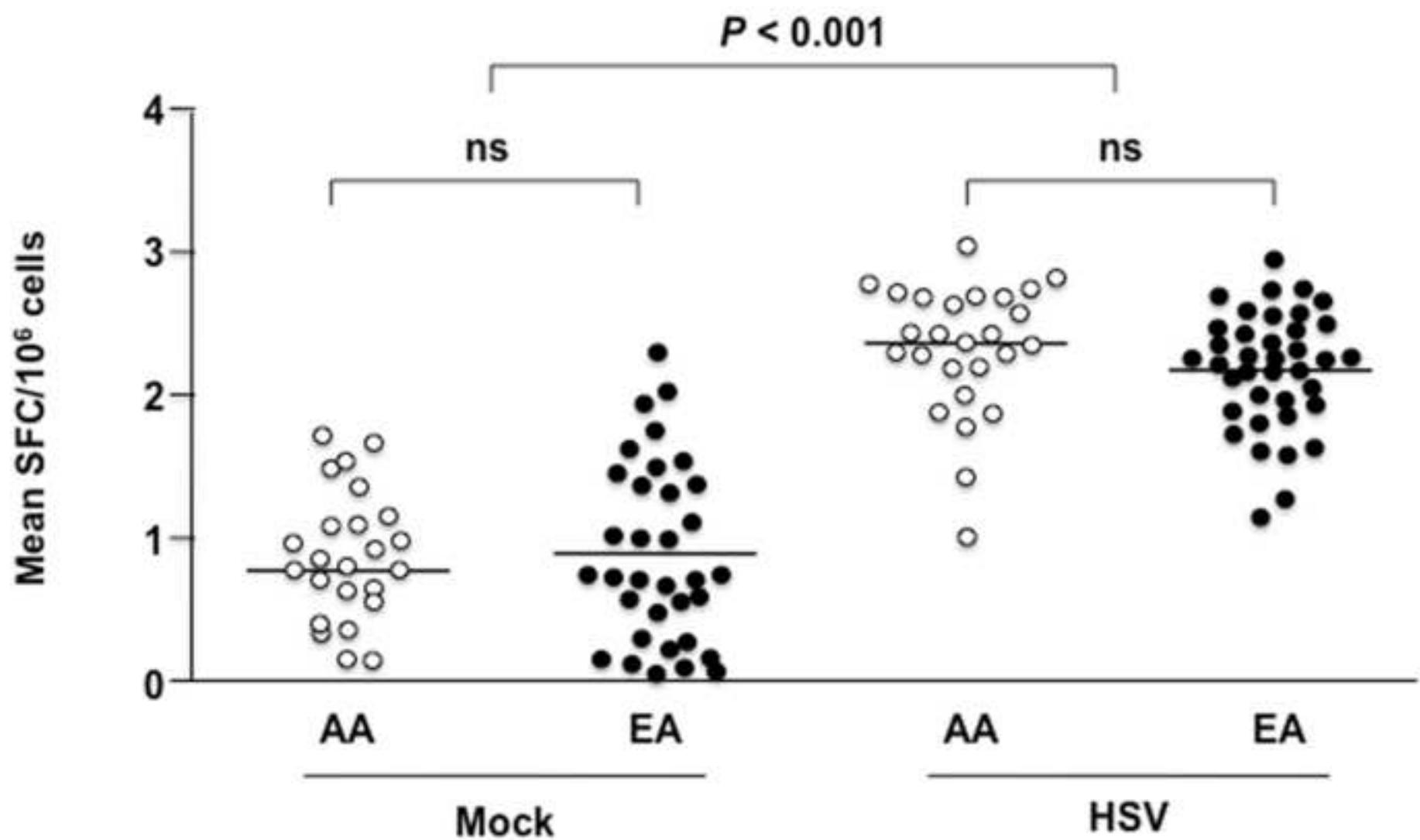
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**SUPPLEMENTAL FIGURES**

**FIG E1.** Gene structure and LD estimation for 8 *IFNG* SNPs in a European American population. The top panel is the *IFNG* structure containing 4 exons (in purple) spanning a region of 13.1 kb. (Filled circles represent the SNPs associated with IFN $\gamma$  production). Diamonds without a number correspond to D'=1; shading represents LD with a red to white gradient reflecting higher to lower D' values

**FIG E2.** Mean levels of the log<sub>10</sub>-transformed SFC/10<sup>6</sup> cells in mock- and HSV-treated PBMCs from European Americans (EA) and African Americans (AA).





**TABLE EI.** Clinical characteristics of participants in cell mediated immunity studies

		<b>ADEH+</b>	<b>ADEH-</b>	<b>NA</b>
Age (yrs)	<b>N</b>	<b>24</b>	<b>20</b>	<b>20</b>
	Mean SD	21.65 (15.42)	42.3 (10.35)	40.55 (10.50)
	Median	17.7	44.3	38.25
	(Min, Max)	(1.62,59.2)	(22.2, 54.7)	(27.3, 56)
Female	N (%)	11 (45.8%)	15 (75.0%)	12 (60.0%)
Male	N (%)	13 (54.2%)	5 (25.0%)	9 (45.0%)
African American	N (%)	5 (20.8%)	10 (50.0%)	11 (55.0%)
Caucasian	N (%)	19 (79.2%)	10 (50.0%)	9 (45.0%)

**TABLE EII.** Clinical characteristics of participants in genetics association studies of *IFNG* SNPs

<b>Characteristic</b>	<b>European American</b>		
	<b>ADEH+</b>	<b>ADEH-</b>	<b>NA</b>
Sample size	112	166	157
Males; N (%)	58 (53.7%)	49 (29.7%)	63 (40.1%)
Age; mean (SD)	22.9 (22.1)	38.4 (14.6)	36.5 (13.2)
Total IgE, Mean* (95% CI)	2,083 (1399-3100)	366.7 (261-516)	55.5 (44-69)
EASI, Mean† (95% CI)	7.4 (6.0-9.1)	3.5 (2.9-4.3)	ND

The following abbreviations are used: ADEH-, atopic dermatitis without eczema herpeticum; ADEH+, atopic dermatitis with eczema herpeticum; EASI, Eczema area and severity index; and ND, not done.

\*Geometric mean serum levels of total IgE.

†EASI determined by the percentage of eczema area on a 7-point ordinal scale: 0 = <10%; 1 = 10%-29%; 3 = 30%-49%; 4 = 50%-69%; 5 = 70%-89%; and 6 = 90%-100%.

and *IFNGR1* in the European American healthy controls (n=157).

**TABLE EIII.** SNP position, allele, role and minor allele frequency (MAF) of *IFNG* and *IFNGR1* in the European American NA controls (n=157)

SNP	SNP position	Distance from previous SNP	Alleles	Location	Minor allele frequency
<b><u>IFNG (chr12q14)</u></b>					
rs7302488	66847146		G/T	Promoter	0.23
rs2069705	66841278	5868	C/T	Promoter	0.36
rs2069709	66839970	1308	G/T	Promoter	0.02
rs2430561	66838787	1183	A/T	Intron	0.36
rs2069716	66837082	1705	A/G	Intron	0.05
rs2069718	66836429	653	C/T	Intron	0.48
rs2069727	66834490	1939	A/G	Downstream	0.34
rs2069728	66834051	439	A/G	Downstream	0.15
<b><u>IFNGR1(chr6q23.3)</u></b>					
rs2234711	137582213		C/T	Promoter	0.44
rs7749390	137582063	150	A/G	Intron (boundary)	0.44
rs10457655	137581503	560	A/G	Intron	0.23
rs9376269	137581198	305	C/G	Intron	0.20
rs1327475	137578148	3050	C/T	Intron	0.14
rs3799488	137561473	16675	C/T	Intron (boundary)	0.07