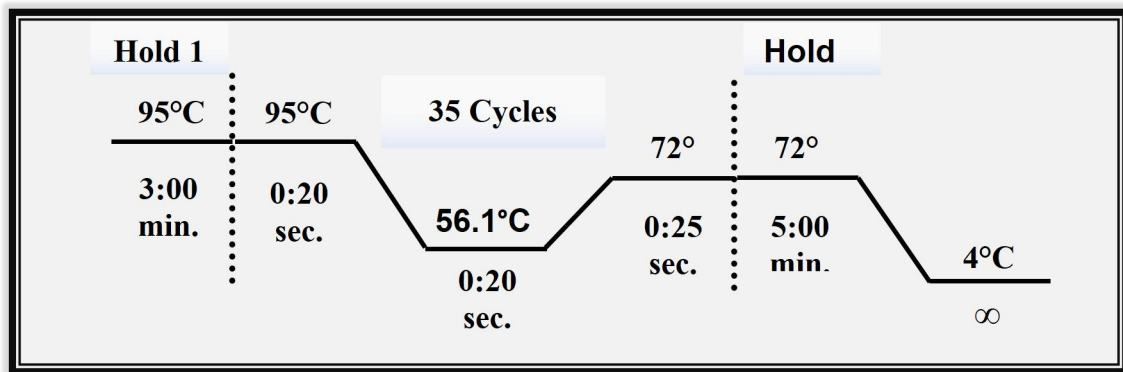
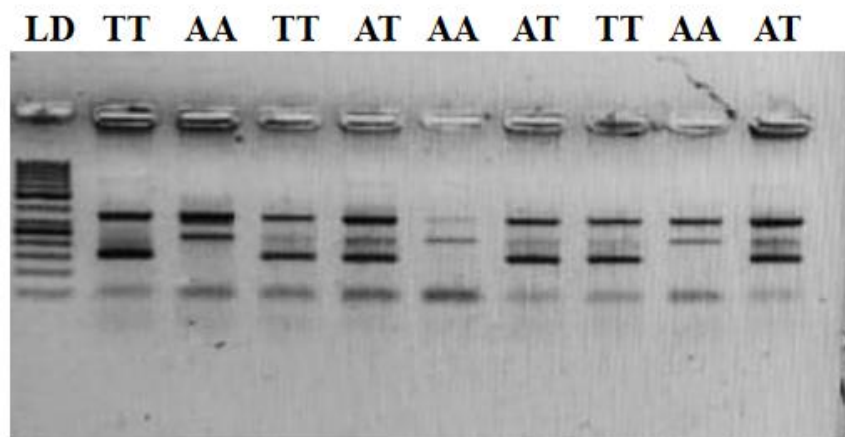


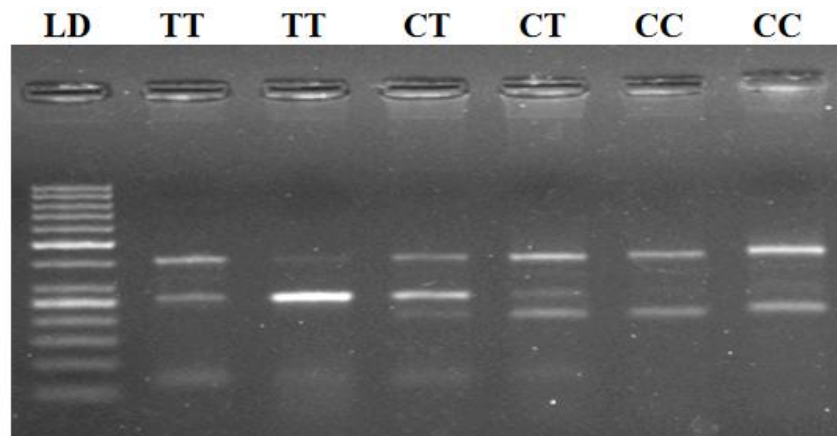
Supplementary Figure 1 Thermocycling profile for PCR of *IFI16* rs1057028.



Supplementary Figure 2 Thermocycling profile for PCR of *AIM2* rs2814770.



Supplementary Figure 3 Gel results of amplification of *IFI16* rs1057028. LD represents 50bp Ladder. Genotypes AA is represented by 253bp and 379bp amplicons, AT with 172bp, 253bp, 379bp amplicons and TT with 173bp and 379bp amplicons.



Supplementary Figure 4 Gel results of amplification of *AIM2* rs2814770. LD represents 50bp Ladder. Genotypes TT is represented by 261bp and 407bp amplicons, CT with 203bp, 261bp, 407bp amplicons and CC with 203bp and 407bp amplicons.

Supplementary Table 1 The sequence, length, T_m and product size of primer set for *IFI16* rs1057028

Sr. No	Primer	Sequence	Length	T _m
1	IFI16_rs1057028_IF (T)	CCCAGGAACAGCGTCAGCTTCTAT	24	66.9
2	IFI16_rs1057028_IR (A)	GTTGTGCTGGCCTCTGAAGGGTT	23	66.6
3	IFI16_rs1057028_OF	CTGACAATTGCCTGGAGGGATACAT	25	65.8
4	IFI16_rs1057028_OR	TGATCCCTGTAAATTATGGTGGGGAG	26	66.2

Supplementary Table 2 The sequence, length, T_m and product size of primer set for *AIM2* rs2814770

Sr. No.	Primer	Sequence	Length (bases)	T _m
1	AIM2_rs2814770_IF_(C)	GATAGGGAACACTAAGATTTACATGAC	27	63.7
2	AIM2_rs2814770_IR_(T)	TGGGTGAGAAATGATATTGGAGAAGAA	27	63.7
3	AIM2_rs2814770_OF	AGATACCCTTTCCTAGGGGAAGACA	25	62.8
4	AIM2_rs2814770_OR	ATAGGGGGAAATATGAAATCTTGAAATTAA	30	62.6

Supplementary Table 3 Product size of PCR amplification

Gene	Sr No	Allele	Product size
<i>IFI16</i> rs1057028	1	T	173bp
	2	A	253bp

	3	Two outer primer product	379bp
<i>AIM2</i> rs2814770	1	T	261bp
	2	C	203bp
	3	Two outer primer product	407bp

Supplementary Table 4 RegulomDB-based regulatory annotations for *IFI16* rs1057028 and *AIM2* rs2841770

Gene	Variant ID	Serached coordinates	Peaks	Rank	Score
<i>IFI16</i>	rs1057028	chr1:159032598-159032599	197	1f	0.55324
<i>AIM2</i>	rs2841770	chr1:159042981-159042982	196	1f	0.19549

Table 5 GTEx eQTL summary for *IFI16* rs1057028 showing tissue specific genotype-expression effects

Gene	Variant ID	Ref_Alt	Tissue	Total samples	Genotype			NES	P value
					TT	AT	AA		
eQTL									
<i>IFI16</i> (ENSG00000163565.20)	rs1057028 (chr1_159032599_T_A_b38)	T_A	Skin - Not Sun Exposed (Suprapubic)	649	46	200	403	-0.18	2.5e-10

Skin - Sun Exposed (Lower leg)	751	58	231	462	-0.14	8.8e-9
Esophagoues- Mucosa	609	43	188	383	-	0.0000055 0.079

Significant e/sQTL-tissue pairs are presented in bold. Total samples: represents the number of RNA-seq samples for which genotype data is available, NES: defined as slope of the linear regression representing eQTL effect sizes and is determined as the effect of the alternative allele (Alt) relative to the reference allele (Ref) in the human genome reference GRCh38/hg38, p-value: from a t-test that compares observed NES from single-tissue eQTL analysis to a null NES of 0. Alt: Alternative allele; Ref: Reference allele; and NES: Normalized effect size.

Supplementary Table 6 GTEx eQTL summary for *AIM2* rs2841770 showing tissue specific genotype-expression effects

Gene	Variant ID	Ref_Alt	Tissue	Total samples	Genotype			NES	P value
					TT	CT	CC		
eQTL									
<i>AIM2</i>	rs2814770	T_C	Spleen	277	13	80	184	0.29	2.2e-8
(ENSG00000163568.15)	(chr1_159042982_T_C_b38)		Whole blood	800	33	210	557	0.13	3.9e-7