Supplementary Information

Increased Risk of Psoriasis due to combined effect of HLA-Cw6 and LCE3 risk alleles in Indian population

Aditi Chandra[1], Anirudhya Lahiri[1], Swapan Senapati[2], Baidehi Basu[1], Saurabh Ghosh[1], Indranil Mukhopadhyay[1], Akhilesh Behra[3], Somenath Sarkar[4], Gobinda Chatterjee[3], Raghunath Chatterjee[1]*

[1] Human Genetics Unit, Indian Statistical Institute, 203 B. T. Road, Kolkata, India 700108

[2] Consultant Dermatologist, Uttarpara, Hooghly India 712258

[3] Department of Dermatology, SSKM Hospital, Kolkata, India

[4] Department of Dermatology, School of Tropical medicine, Kolkata, India

*Author for correspondence:

E-mail:- rchatterjee@isical.ac.in; Tel:- +91 33 2575 3243; Fax:- +91 33 2577 3049

Supplementary Tables

Table S1. Sample Summary

Sample	Population	Sample Size	Mean Age of Onset/Age (SD)	Male/Female(%)	Type1/Type2(%)
Case		705	34.96 (15.68) Range : 08-79	68/32	61.74/38.26
Control	Eastern India	738	39.24 (14.72) Range : 11-83	52.79/47.21	
Total		**1443**	**37.095**	**60.4/39.6**	

Table S2. Association of HLA-Cw6 allele with TypeI and TypeII Psoriasis

	Psoriasis		Normal
	TypeI	**TypeII**	
HLA-Cw6 Frequency	0.534247	0.34211	0.148501
P-Value	**< 2.2 x 10^{-16}**	**1.38 x 10^{-11}**	
95% CI	5.01 - 8.71	2.15 - 4.13	
Odds Ratio	6.61	2.98	

Table S3. Characteristics of the SNPs and CNV studied here

SNP ID/CNV	Chromosome	Alleles	Nearest Gene	Position from Gene	HWE (P-values)		
		Major/Minor			**All**	**Case**	**Control**
rs1886734	1	C/A	LCE3A	3' down (+4168)	0.8881	0.4981	0.443
Deletion	1	del/ins	LCE3C-3B	32.2kbp	0.0659	0.6017	0.064
rs4112788	1	G/A	LCE3D	3' down (+584bp)	0.7246	0.5593	0.3329
rs7516108	1	C/T	LCE3E	5' up (-2981bp)	0.3177	0.6526	0.0847

Table S4. LCE3 SNPs showed similar association level even after adjusting for age and sex

SNP/CNV	Nearest Gene	Genotypes	Genotype Frequency		p-value
		Major/Hetero/Minor	**Case**	**Control**	
rs1886734	LCE3A	CC/CA/AA	0.43/0.46/0.11	0.40/0.46/0.15	1.04 x 10^{-1}
Deletion	**LCE 3C-3B**	**Del-Del/Del-Ins/Ins-Ins**	**0.43/0.45/0.13**	**0.37/0.45/0.18**	**3.18 x 10^{-2}**
rs4112788	LCE3D	GG/GA/AA	0.43/0.46/0.11	0.40/0.45/0.15	1.02 x 10^{-1}
rs7516108	LCE3E	CC/CT/TT	0.38/0.48/0.14	0.36/0.46/0.19	7.92 x 10^{-2}

Table S5. Linkage pattern (with r^2 values) of LCE3 cluster

r2: Total	DELETION	rs4112788	rs7516108
rs1886734	0.806	0.971	0.610
DELETION	-	0.813	0.524
rs4112788	-	-	0.613

Table S6: TypeI (Age of Onset<=40 years) showed higher LCE3 association

SNP ID	Control	TypeI (n=438)				TypeII (n=268)			
	MAF	MAF	OR	95% CI	p-value	MAF	OR	95% CI	p-value
rs1886734	0.37	0.33	1.20	1.01- 1.43	**0.03958**	0.36	1.01	0.88-1.33	0.4605
Deletion	0.41	0.34	1.34	1.12- 1.60	**0.001075**	0.37	1.15	0.94-1.41	0.1694
rs4112788	0.37	0.33	1.21	1.02- 1.44	**0.03229**	0.36	1.07	0.87-1.31	0.5352
rs7516108	0.42	0.37	1.21	1.01- 1.43	**0.03392**	0.39	1.11	0.90-1.36	0.3187

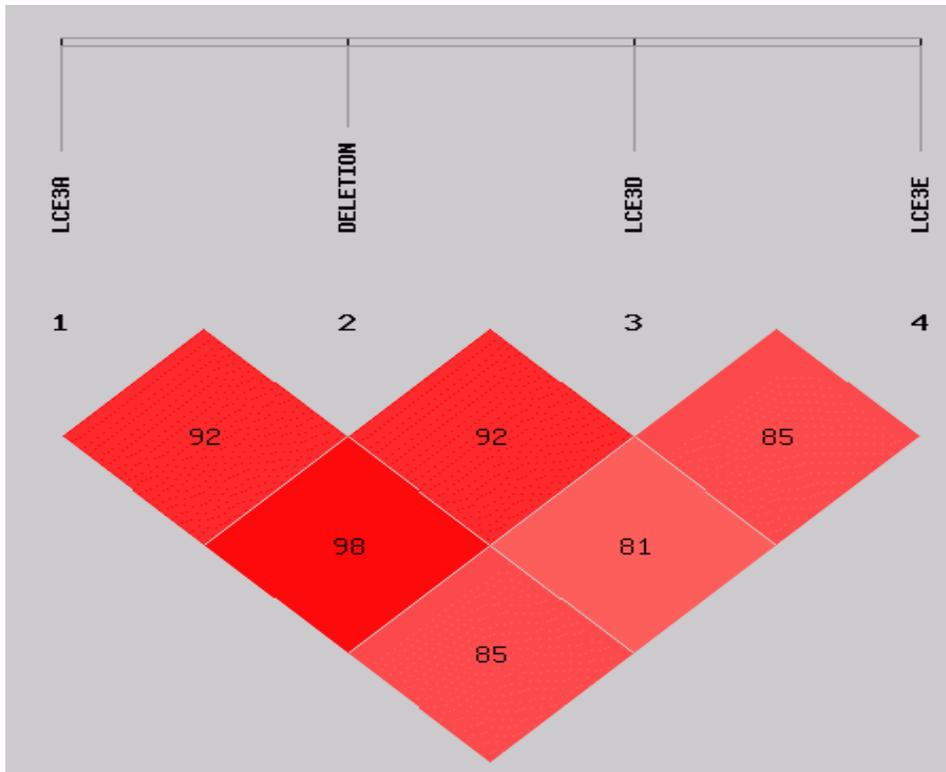## Table S7: Association model of LCE3E SNP and LCE3C-3B Deletion

		Major(1)	Minor(2)	Case(11/12/22)	Control(11/12/22)	p-value
rs7516108 (LCE3E)	Additive	C	T	269/335/97	257/329/137	0.0329
	Dominant			**604/97**	**586/137**	**0.00987**
	Recessive			269/432	257/466	0.2692
LCE3C-3B Deletion	Additive	Del	Ins	300/313/89	270/329/133	0.0064
	Dominant			**613/89**	**599/133**	**0.004069**
	Recessive			300/402	270/462	0.0237

Table S8: Association of SNPs after age and sex adjustment on stratified samples
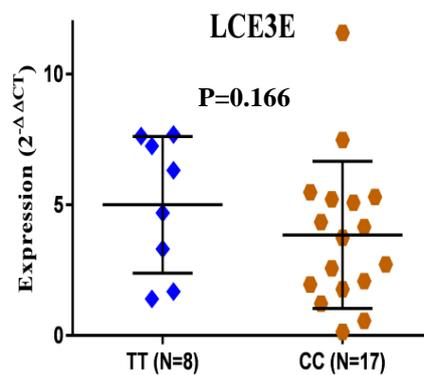
HLA-Cw6 Present			
SNP	**MAF**		
	Case	**Control**	**Adjusted p-value**
LCE3A	**0.30**	**0.46**	2.85×10^{-4}
DELETION	**0.32**	**0.49**	2.85×10^{-4}
LCE3D	**0.30**	**0.46**	2.85×10^{-4}
LCE3E	**0.36**	**0.48**	4.20×10^{-3}
HLA-Cw6 Absent			
SNP	**MAF**		
	Case	**Control**	**Adjusted p-value**
LCE3A	0.37	0.36	8.41×10^{-1}
DELETION	0.38	0.39	8.41×10^{-1}
LCE3D	0.37	0.35	8.41×10^{-1}
LCE3E	0.4	0.4	8.41×10^{-1}

Supplementary Figures

FigureS1. LD pattern (D') of LCE3 cluster. Total LCE3 cluster showed strong linkage in Indian population.

FigureS1b. Variation in expression pattern from diseased tissue with respect to genotypes of LCE3E gene.

FigureS1c. Expression pattern of LCE3D and LCE3E genes with respect to genotype and HLA-Cw6 status.