SUPPLEMENTARY MATERIALS

Supplementary Methods

As previously described (Chen et al., 2012), we used HLA*IMP to impute to four-digit resolution HLA class I alleles (-A, -B, and -C) and HLA class II alleles (-DQA1, -DQB1, and -DRB1) of two GWAS cohorts: the WTCCC cohort of 2,178 psoriasis cases and 5,175 controls (Strange et al., 2010) and the GAIN cohort of 1,368 psoriasis cases and 1,348 controls (Nair et al., 2009). We previously confirmed the accuracy of imputation by comparing results to directly genotyped patients and found a concordance rate of 97.4% (Chen et al., 2012). The principal components of ancestry were determined using EIGENSTRAT. Conditional and stepwise logistic regression was performed using the 'condition' function in PLINK to determine whether independent effects existed. Multivariate logistic regression was performed in R software package (http://www.r-project.org/).

Table S1. HLA Class I allele-specific binding scores of LILRB1 and LILRB2 for viral load controlled determined via univariate model, from (Bashirova et al., 2014)

HLA Class I Allele	Binding Score LILRB1	Binding Score LILRB2
A*01:01	0.36	0.55
A*02:01	0.11	0.60
A*02:03	0.17	0.38
A*02:06	0.28	0.52
A*03:01	0.41	0.51
A*11:01	0.48	0.48
A*11:02	0.63	0.80
A*23:01	0.38	0.51
A*24:02	0.43	0.55
A*24:03	0.41	0.98
A*25:01	0.11	0.56
A*26:01	0.11	0.67
A*29:01	0.18	0.56
A*29:02	0.13	0.53
A*30:01	0.56	0.75
A*30:02	0.21	0.40
A*31:01	0.24	0.48
A*32:01	0.10	0.58
A*33:01	0.07	0.58
A*33:03	0.12	0.66
A*34:01	0.14	0.57
A*34:02	0.26	0.50
A*36:01	0.20	0.40
A*43:01	0.07	0.39
A*66:01	0.26	0.75
A*66:02	0.20	0.53
A*68:01	0.13	0.43
A*68:02	0.11	0.43
A*69:01	0.18	0.65
A*74:01/2	0.04	0.53
A*80:01	0.12	0.56
B*07:02	0.22	0.56
B*08:01	0.38	0.57
B*13:01	0.12	0.50
B*13:02	0.18	0.38
B*14:01	0.27	0.40
B*14:02	0.21	0.21
B*15:01	0.31	0.44
B*15:02	0.37	0.29
B*15:03	0.35	0.49

B*15:10	**0.22**	**0.20**
B*15:11	**0.27**	**0.47**
B*15:12	**0.39**	**0.38**
B*15:13	**0.19**	**0.37**
B*15:16	**0.27**	**0.31**
B*18:01	**0.40**	**0.66**
B*27:05	**0.27**	**0.14**
B*27:08	**0.49**	**0.30**
B*35:01	**0.36**	**0.41**
B*38:01	**0.30**	**0.39**
B*39:01	**0.35**	**0.32**
B*40:01	**0.18**	**0.40**
B*40:02	**0.23**	**0.33**
B*40:06	**0.24**	**0.51**
B*41:01	**0.39**	**0.39**
B*42:01	**0.42**	**0.38**
B*44:02	**0.19**	**0.36**
B*44:03	**0.19**	**0.16**
B*45:01	**0.45**	**0.54**
B*46:01	**0.31**	**0.57**
B*48:01	**0.14**	**0.52**
B*49:01	**0.06**	**0.24**
B*50:01	**0.26**	**0.32**
B*51:01	**0.18**	**0.46**
B*51:02	**0.23**	**0.33**
B*52:01	**0.10**	**0.54**
B*53:01	**0.36**	**0.47**
B*54:01	**0.25**	**0.26**
B*55:01	**0.21**	**0.52**
B*56:01	**0.25**	**0.27**
B*57:01	**0.07**	**0.09**
B*57:03	**0.26**	**0.25**
B*58:01	**0.03**	**0.12**
B*59:01	**0.18**	**0.37**
B*67:01	**0.47**	**0.41**
B*73:01	**0.33**	**0.53**
B*78:01	**0.34**	**0.72**
B*81:01	**0.32**	**0.50**
B*82:01	**0.36**	**0.41**
C*01:02	**0.04**	**0.39**
C*02:02	**0.19**	**0.54**
C*03:02	**0.13**	**0.29**
C*03:03	**0.20**	**0.30**
C*03:04	**0.39**	**0.37**
C*04:01	**0.04**	**0.18**

C*05:01	**0.24**	**0.49**
C*06:02	**0.31**	**0.76**
C*07:02	**0.15**	**0.62**
C*08:01	**0.22**	**0.36**
C*12:03	**0.21**	**0.54**
C*14:02	**0.16**	**0.5**
C*15:02	**0.36**	**0.45**
C*16:01	**0.14**	**0.50**
C*17:01	**0.08**	**0.27**
C*18:02	**0.29**	**0.61**

Table S2. *LILRB2* mRNA is significantly overexpressed in psoriasis lesional skin compared to healthy skin.

Gene	Probe ID	Adjusted P Value	Fold Change (Psoriasis lesional (n=58) vs. healthy skin (n=64))
LILRB2	210146_x_at	3.84E-10	2.39
LILRB2	207697_x_at	1.04E-09	2.20
Source: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE13355			

Figure S1. Using FACS-sorted keratinocytes, myeloid dendritic cells, and T lymphocytes from the skin of healthy human subjects, we found that LILRB2 mRNA is significantly expressed in cutaneous dendritic cells compared to negligible expression in keratinocytes, T cells, and bulk skin cells.