

Supplementary Table 1. Association of *LCE3C_LCE3B-del* genotypes with psoriasis.

Dataset	Status	<i>LCE3C_LCE3B-del/LCE3C_LCE3B-del</i>	<i>LCE3C_LCE3B-del/Intact</i>	Intact/Intact	OR ^a (95%CI)	P-value
Spain	Control	107 (28.0)	206 (53.9)	69 (18.1)	1.56 (1.19-2.08)	0.001428
	Psoriasis	66 (37.5)	95 (54.0)	15 (8.5)		
Italy	Control	159 (35.3)	198 (44.0)	93 (20.7)	1.28 (1.06-1.54)	0.007877
	Psoriasis	186 (41.3)	201 (44.7)	63 (14.0)		
France	Control	73 (44.5)	65 (39.6)	26 (15.9)	1.27 (0.91-1.75)	0.155320
	Psoriasis	68 (48.2)	60 (40.6)	13 (9.2)		
Netherlands	Control	102 (36.4)	130 (46.4)	48 (17.1)	1.49 (1.14-1.96)	0.003253
	Psoriasis	95 (46.6)	91 (44.6)	18 (8.8)		
Germany	Control	391 (41.8)	433 (46.3)	112 (12.0)	1.30 (1.15-1.50)	3.329e-05
	Psoriasis	678 (50.5)	543 (40.5)	121 (9.0)		
UK	Control	460 (45.1)	450 (44.1)	111 (10.9)	1.16 (1.02-1.33)	0.02847
	Psoriasis	454 (48.2)	415 (44.1)	72 (7.7)		
Ireland	Control	463 (48.9)	385 (40.7)	99 (10.5)	1.06 (0.89-1.28)	0.4655
	Psoriasis	195 (49.7)	164 (41.8)	33 (8.4)		
Finland	Control	150 (44.8)	136 (40.6)	49 (14.6)	1.33 (0.99-1.79)	0.05466
	Psoriasis	72 (53.3)	50 (37.0)	13 (9.6)		
US CA	Control	113 (38.4)	152 (51.7)	29 (9.9)	1.41 (1.12-1.75)	0.002496
	Psoriasis	292 (49.0)	263 (44.1)	41 (6.9)		
US MI	Control	809 (42.3)	860 (45.0)	244 (12.8)	1.10 (1.00-1.21)	0.05790
	Psoriasis	936 (44.1)	963 (45.4)	224 (10.6)		
Overall	Control	2827 (42.0)	3015 (44.9)	880 (13.1)	1.20 (1.15-1.28) ^b	1.42e-13 ^b
	Psoriasis	3042 (46.8)	2845 (43.8)	613 (9.4)		
Japan	Control	187 (34.8)	257 (47.9)	93 (17.3)	1.18 (0.99-1.39)	0.06578
	Psoriasis	216 (39.3)	257 (46.7)	77 (14.0)		
Mongolia	Control	44 (26.2)	78 (46.4)	46 (27.4)	2.04 (1.41-2.94)	9.38e-05
	Psoriasis	44 (44.0)	46 (46.0)	10 (10.0)		
China	Control	624 (32.9)	926 (48.8)	347 (18.3)	1.28 (1.16-1.41)	1.41e-07
	Psoriasis	781 (39.1)	956 (47.9)	258 (12.9)		

^aORs and P-values are derived from the log-additive model, with homozygotes for the deleted allele (*LCE3C_LCE3B-del*) at higher risk for psoriasis. Overall values for the European ancestry populations adjusted by population according to a logistic model in which population was introduced as a confounding variable (based on fixed effects model^b and a random effects model^c) after no significant evidence of heterogeneity based on allelic frequencies was detected by population.

Supplementary Table 2. Association of rs4112788 genotypes with psoriasis.

Dataset	Status	C/C (%)	C/T (%)	T/T (%)	OR ^a (95%CI)	P-value
Spain	Control	117 (30.6)	193 (50.5)	72 (18.8)	1.61 (1.23-2.13)	4.92e-04
	Psoriasis	72 (41.1)	89 (50.9)	14 (8.0)		
Italy	Control	155 (34.8)	200 (44.8)	91 (20.4)	1.37 (1.14-1.64)	0.00101
	Psoriasis	189 (42.1)	205 (45.7)	55 (12.2)		
France	Control	76 (45.8)	64 (38.6)	26 (15.7)	1.27 (0.91-1.75)	0.15532
	Psoriasis	71 (49.7)	60 (42.0)	12 (8.4)		
Netherlands	Control	102 (36.7)	129 (46.4)	47 (16.9)	1.47 (1.12-1.92)	0.00461
	Psoriasis	94 (46.5)	90 (44.6)	18 (8.9)		
Germany	Control	368 (41.4)	415 (46.7)	106 (11.9)	1.22 (1.08-1.39)	0.00208
	Psoriasis	616 (47.3)	567 (43.6)	118 (9.1)		
UK	Control	437 (44.5)	429 (43.7)	115 (11.7)	1.12 (0.98-1.28)	0.08620
	Psoriasis	472 (46.8)	446 (44.2)	90 (8.9)		
Ireland	Control	466 (48.0)	403 (41.5)	101 (10.4)	1.18 (0.99-1.41)	0.06980
	Psoriasis	222 (51.4)	180 (41.7)	30 (6.9)		
Finland	Control	149 (45.2)	135 (40.9)	46 (13.9)	1.33 (0.98-1.79)	0.06015
	Psoriasis	71 (54.6)	46 (35.4)	13 (10.0)		
US-CA	Control	115 (38.9)	149 (50.3)	32 (10.8)	1.41 (1.14-1.75)	0.00229
	Psoriasis	286 (48.6)	263 (44.7)	40 (6.8)		
US- MI	Control	811 (42.6)	850 (44.7)	241 (12.7)	1.10 (1.00-1.21)	0.05152
	Psoriasis	940 (44.6)	948 (45.0)	221 (10.5)		
Overall	Control	2795 (42.1)	2967 (44.7)	878 (13.2)	1.20 (1.15-1.27) ^b	1.81e-12 ^b
	Psoriasis	3033 (46.4)	2894 (44.3)	611 (9.3)		
China	Control	625 (33.1)	923 (48.9)	339 (18.0)	1.35 (1.22-1.47)	3.62e-10
	Psoriasis	794 (40.2)	955 (48.4)	224 (11.4)		

^aORs and P-values are derived from the log-additive model, with homozygotes C/C at higher risk for psoriasis. Overall values for the European ancestry populations were adjusted by population according to a logistic model in which population was introduced as a confounding variable (based on a fixed effects model^b and a random effects model^c) after no significant evidence of heterogeneity based on allelic frequencies was detected by population.

Supplementary Table 3. Genetic interaction analysis between rs130076 in *PSORS1* and *LCE3C_LCE3B-del* and its tag SNP.

Dataset	rs130076			Group	Epistasis ^a rs4112788-rs130076			<i>LCE3C_LCE3B</i> -rs130076		
	C/C (- group) vs. C/T+T/T (+group)	OR	95%CI		P-value	OR	95%CI	P-value	OR	95%CI
Spain	3.40	2.34-4.94	7.783 e-11	+	1.90	1.22-2.96	0.0829	1.71	1.09-2.68	0.23312
				-	1.14	0.78-1.66		1.19	0.81-1.75	
Italy	2.05	1.56-2.69	2.372 e-07	+	1.14	0.85-1.54	0.1606	1.06	0.79-1.43	0.128
				-	1.51	1.17-1.95		1.44	1.11-1.85	
Germany	4.37	3.65-5.22	7.59 e-62	+	1.26	1.03-1.54	0.4822	1.33	1.09-1.33	0.52565
				-	1.39	1.15-1.69		1.22	1.01-1.47	
France	5.58	3.41-9.12	7.081 e-13	+	1.55	0.93-2.52	0.55451	1.64	0.96-2.54	0.27597
				-	1.25	0.72-2.17		1.10	0.64-1.88	
Ireland	1.91	1.51-2.42	4.541 e-08	+	1.12	0.89-1.40	0.7500	1.03	0.82-1.29	0.68030
				-	1.19	0.88-1.59		1.11	0.82-1.50	
Finland	2.50	1.65-3.80	1.444 e-05	+	1.25	0.81-1.94	0.750	1.21	0.78-1.87	0.756
				-	1.39	0.89-2.16		1.34	0.89-2.14	
US-CA	2.72	1.97-3.74	4.209 e-10	+	1.24	0.84-1.83	0.8889	1.10	0.74-1.63	0.345
				-	1.28	0.93-1.77		1.41	1.02-1.95	
China	18.73	15.9-22.0	<2e-16	+	1.40	1.19-1.65	0.467	1.27	1.08-1.49	0.7102
				-	1.28	1.07-1.53		1.33	1.12-1.59	

OR and 95% CI interval for psoriasis of rs130076 under a dominant model of heritability for allele T, which is referred as positive (+) group: C/T+T/T; negative (-) group: C/C. ^aEpistasis analysis performed by logistic regression models which included an interaction term, (rs4112788-rs130076 or *LCE3C_LCE3B*-rs130076); P-values and OR are derived from the log-likelihood ratio test between the model including both additive effects plus the interaction term against the model that only includes additive effects. Overall values for European ancestry populations are not presented since the Woolf-test on homogeneity of OR based on allelic frequencies of rs130076 showed statistical significant heterogeneity among them (P = 1.851e-08).

Supplementary Table 4. Association of rs130076 in the *PSORS1* locus in individuals from different populations.

Dataset	Status (alleles)	rs130076 C (%)	rs130076 T (%)	HWE	OR (95%CI) T vs. C	P-value
Spain	Control	651 (85.2)	113 (14.8)	0.54	2.58 (1.91-3.49)	6.82e-10
	Psoriasis	243 (69.0)	109 (31)	0.05		
Italy	Control	718 (81.0)	168 (19.0)	0.54	1.79 (1.43-2.24)	3.56e-07
	Psoriasis	595 (70.5)	249 (29.5)	0.41		
Germany	Control	1478 (80.6)	356 (19.4)	0.83	3.01 (2.62-3.46)	<2e-16
	Psoriasis	1537 (58.0)	1115 (42.0)	4.19e-09		
France	Control	277 (82.4)	59 (17.6)	0.30	3.52 (2.44-5.09)	1.88e-11
	Psoriasis	160 (57.1)	120 (42.9)	0.06		
Ireland	Control	1368 (70.4)	574 (29.5)	1	1.55 (1.31-1.83)	3.50e-07
	Psoriasis	524 (60.6)	340 (39.4)	0.02		
Finland	Control	533 (82.3)	115 (17.7)	0.45	2.02 (1.45-2.82)	3.26e-05
	Psoriasis	181 (69.6)	79 (30.4)	0.30		
US-CA	Control	362 (80.8)	86 (19.2)	0.40	2.25 (1.72-2.93)	1.95e-09
	Psoriasis	759 (65.2)	405 (34.8)	0.006		
China	Control	3317 (89.0)	409 (11.0)	0.72	6.43 (5.70-7.25)	<2e-16
	Psoriasis	2178 (55.8)	1726 (44.2)	2.9e-153		

Overall values for European ancestry populations are not presented since the Woolf-test on homogeneity of odds ratios based on allelic frequencies of rs130076 showed statistical significant heterogeneity among them (P = 1.851e-08).