Reported PsO / PsA Association	**HLA Allele**	**HERV SNP (Major Allele/Minor Allele: Risk Allele)**				
		rs114780460 (G/A:G)	**rs3134774 (A/G:G)**	**rs9264082 (A/G:A)**	**rs3132531 (G/A:A)**	**rs3134775 (T/G:G)**
Risk	B*27 (r^2)	**0.07**	**0**	**0.05**	**0.03**	**0**
	B*27 (D')	0.35	0.11	0.38	0.82	0.1
	B*27 (+) Haplotypes	(+)G=3.4; (+)A=2.5	(+)G=3.1; (+)A=2.8	(+)G=2.8; (+)A=3.1	(+)G=5.3; (+)A=0.4	(+)G=3.0; (+)T=2.8
	B*27 (-) Haplotypes	(-)G=83.2; (-)A=10.5	(-)G=43.3; (-)A=50.8	(-)G=12.4; (-)A=81.6	(-)G=52.3; (-)A=42	(-)G=43.5; (-)T=50.7
Risk	B*38 (r^2)	**0.01**	**0.04**	**0.01**	**0.03**	**0.05**
	B*38 (D')	1	0.86	1	0.7	0.86
	B*38 (+) Haplotypes	(+)G=6.4; (+)A=0	(+)G=0.4; (+)A=6.0	(+)G=0; (+)A=6.4	(+)G=5.6; (+)A=0.8	(+)G=0.4; (+)T=6
	B*38 (-) Haplotypes	(-)G=86.1; (-)A=8.0	(-)G=46; (-)A=47.7	(-)G=15.2; (-)A=78.4	(-)G=51.9; (-)A=41.7	(-)G=46.1; (-)T=47.4
Risk	B*39 (r^2)	**0**	**0.02**	**0**	**0.02**	**0.03**
	B*39 (D')	1	1	0.46	1	1
	B*39 (+) Haplotypes	(+)G=2.7; (+)A=0	(+)G=0; (+)A=2.7	(+)G=0.2; (+)A=2.5	(+)G=2.7; (+)A=0	(+)G=0; (+)T=2.8
	B*39 (-) Haplotypes	(-)G=86.8; (-)A=10.5	(-)G=46.4; (-)A=50.9	(-)G=15; (-)A=82.3	(-)G=54.8; (-)A=42.5	(-)G=46.5; (-)T=50.7
Protective	B*40 (r^2)	**0**	**0.02**	**0**	**0.03**	**0.02**
	B*40 (D')	0.25	0.79	0.53	1	0.8
	B*40 (+) Haplotypes	(+)G=3.8; (+)A=0.3	(+)G=0.4; (+)A=3.7	(+)G=0.3; (+)A=3.8	(+)G=4.1; (+)A=0	(+)G=0.4; (+)T=3.8
	B*40 (-) Haplotypes	(-)G=85.8; (-)A=10.1	(-)G=46; (-)A=49.9	(-)G=14.9; (-)A=81	(-)G=53.4; (-)A=42.5	(-)G=46.1; (-)T=49.7
Risk	B*57 (r^2)	**0.02**	**0.16**	**0.03**	**0.19**	**0.16**
	B*57 (D')	1	0.9	1	0.92	0.9
	B*57 (+) Haplotypes	(+)G=14.3; (+)A=0	(+)G=13.6; (+)A=0.8	(+)G=0; (+)A=14.3	(+)G=0.7; (+)A=13.7	(+)G=13.5; (+)T=0.8
	B*57 (-) Haplotypes	(-)G=75.2; (-)A=10.5	(-)G=32.8; (-)A=52.9	(-)G=15.2; (-)A=70.5	(-)G=56.8; (-)A=28.8	(-)G=33; (-)T=52.7
Risk	C*06 (r^2)	**0.05**	**0.4**	**0.07**	**0.46**	**0.39**
	C*06 (D')	1	0.92	1	0.93	0.92
	C*06 (+) Haplotypes	(+)G=29.2; (+)A=0	(+)G=28; (+)A=1.2	(+)G=0; (+)A=29.2	(+)G=1.1; (+)A=15.1	(+)G=27.9; (+)T=1.2
	C*06 (-) Haplotypes	(-)G=60.6; (-)A=10.2	(-)G=18.8; (-)A=52	(-)G=15; (-)A=55.8	(-)G=55.8; (-)A=27.9	(-)G=19.1; (-)T=51.8
Risk	C*12 (r^2)	**0.01**	**0.08**	**0.02**	**0.05**	**0.08**
	C*12 (D')	1	1	1	0.85	1
	C*12 (+) Haplotypes	(+)G=8.6; (+)A=0	(+)G=0; (+)A=8.6	(+)G=0; (+)A=8.6	(+)G=8; (+)A=0.6	(+)G=0; (+)T=8.7
	C*12 (-) Haplotypes	(-)G=81.3; (-)A=10.2	(-)G=46.8; (-)A=44.7	(-)G=15; (-)A=76.4	(-)G=48.9; (-)A=42.5	(-)G=46.9; (-)T=44.4

Table S1. Linkage disequilibrium between HERV-K dUTPase SNPs and HLA alleles previously reported to be associated with psoriasis or psoriatic arthritis. For each pair of HLA and HERV alleles, r^2 values, D' values, and haplotype frequencies are shown. C*06 and B*57 show moderate LD with the HERV SNPs (max r^2=0.46 and 0.19, respectively), and thus are adjusted for in the association analysis of HERV SNPs with psoriasis. The other HLA alleles show lower LD with HERV SNPs (all r^2<0.09) and are unlikely to serve as confounders. Although in some instances D' is close to or equal to 1 for B*27, B*38, B*39, B*40, and C*12 (meaning the HLA allele exclusively associates with a particular HERV allele), in all of these cases the HLA allele occurs on less than 10% of the total haplotypes carrying that HERV allele and is thus unlikely to drive the association of the HERV allele with psoriasis. Highlighted cells indicate instances where an HLA risk allele predominantly lies on a haplotype with a protective HERV allele, or vice versa. In these situations, the HLA allele cannot serve as a confounder for the HERV association. Data is from 256 Caucasian individuals with HERV alleles sequenced and HLA typing performed by sequence-specific oligonucleotide probe (SSOP).

	Domain 3 Domain 4 Domain 5
	117 155 158 166
Peptide	G V I D S D Y N G E I Q I V I S T S V P W K A E P G E C I A Q L L I V P Y V **G/R** M G **K/R** V K L N K Q E **D/G** L E A Q
P01	I V I S T S V P W K A E P
P02	T S V P W K A E P G E C I
P03	W K A E P G E C I A Q L L
P04	P G E C I A Q L L I V P Y
P05-A	I A Q L L I V P Y V **G** M G
P05-B	I A Q L L I V P Y V **R** M G
P06-A	L I V P Y V **G** M G **K** V K L
P06-B*	L I V P Y V **G** M G **R** V K L
P06-C	L I V P Y V **R** M G **K** V K L
P06-D	L I V P Y V **R** M G **R** V K L
P07-A	Y V **G** M G **K** V K L N K Q E
P07-B*	Y V **G** M G **R** V K L N K Q E
P07-C	Y V **R** M G **K** V K L N K Q E
P07-D	Y V **R** M G **R** V K L N K Q E
P08-A	G **K** V K L N K Q E **D** L E A
P08-B*	G **K** V K L N K Q E **G** L E A
P08-C*	G **R** V K L N K Q E **D** L E A
P08-D*	G **R** V K L N K Q E **G** L E A
P09-A	L N K Q E **D** L E A Q
P09-B*	L N K Q E **G** L E A Q

Figure S1. PSORS1 HERV-K dUTPase peptide sequences used for ELISPOT assays. Boxes indicate the location of dUTPase domains. Amino acid positions are shown above the peptide sequence. Peptides corresponding to psoriasis-risk haplotypes are noted with an asterisk (*).

		Media	P01	P02	P03	P04	P05-A	P05-B	P06-A	P06-B*	P06-C	P06-D	P07-A	P07-B*	P07-C	P07-D	P08-A	P08-B*	P08-C*	P08-D*	P09-A	P09-B*	CEF	PHA
Psoriasis	PSOR01	3	**95**	15	20	**295**	**70**	40	40	**50**	35	**60**	45	45	30	35	0	35	0	**50**	0	**100**	**2865**	**2810**
	PSOR02	0.5	5	0	5	**230**	5	10	5	0	0	0	0	0	0	5	0	0	5	10	10	0	20	**960**
	PSOR03	0.5	0	0	0	**80**	0	20	5	0	15	0	0	0	0	0	0	5	0	0	0	0	40	**565**
	PSOR04	0.5	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	10	0	0	**2475**	**2245**
	PSOR05	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**145**	**1820**
	PSOR06	4	0	0	0	20	0	0	10	0	0	0	0	0	0	0	0	0	0	5	0	0	**75**	**655**
	PSOR07	0	20	0	5	**50**	5	5	5	10	0	0	10	5	10	5	0	15	10	0	0	5	10	**2125**
	PSOR08	1	0	0	0	35	0	5	5	0	0	0	0	0	0	0	0	0	0	0	0	0	10	**405**
	PSOR09	1.5	15	0	0	**90**	0	0	0	0	30	0	0	0	0	0	0	0	0	15	0	0	**100**	**1555**
	PSOR10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	**515**
	PSOR11	0.5	10	0	0	10	5	0	0	5	0	0	20	0	10	15	0	0	0	0	0	10	10	**625**
	PSOR12	1	0	0	0	0	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0	0	**55**	**2215**
	PSOR13	0.5	0	0	0	10	5	0	5	0	0	0	0	0	5	0	0	0	0	0	0	0	0	**1465**
Healthy	CTRL01	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	40	**1455**
	CTRL02	5	0	0	30	45	10	0	0	0	0	0	0	0	0	5	0	0	0	25	0	10	**225**	**2395**
	CTRL03	1	0	15	0	0	10	0	10	0	20	5	0	0	0	0	0	5	25	0	25	10	**520**	**3295**
	CTRL04	1.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**65**	**2125**
	CTRL05	0.5	5	10	25	35	10	**65**	45	30	30	0	**50**	35	0	15	20	5	35	30	10	40	**305**	**1575**
	CTRL06	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**915**	**2135**
	CTRL07	2.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**660**	**3150**
	CTRL08	0	5	15	15	35	5	0	5	5	10	5	5	5	5	5	10	5	0	5	25	10	**1145**	**1200**
	CTRL09	0.5	0	0	0	0	0	0	0	0	5	0	0	15	0	15	0	0	10	0	5	0	**190**	**370**
	CTRL10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**310**
	CTRL11	4	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0	0	10	0	0	0	**315**	**2680**

Table S2. Peripheral blood mononuclear cell reactivity against HERV-K dUTPase peptides using a gamma-interferon ELISPOT assay. Positive peptide reactivity, shown in highlighted cells, is defined as reaction > 50 SFU/10^6 PBMC. Media without addition of peptide was used as a negative control, while phytohemagglutinin (PHA) and a peptide pool from cytomegalovirus, Epstein-Barr virus, and influenza virus (CEF) were used as positive controls.