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Supplemental Data

PSORS2 is Due to Mutations in *CARD14*

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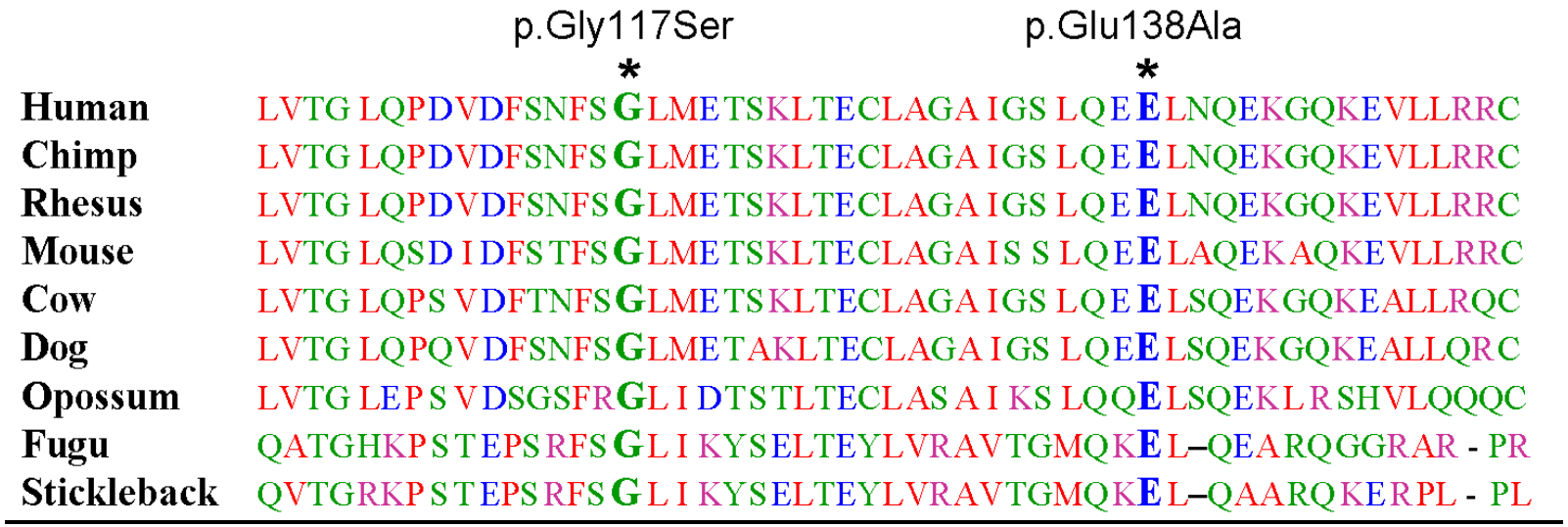

Figure S1. Conservation of the Amino Acids Altered in the Familial Forms of Psoriasis and the Pustular Psoriasis Case

Alignment of CARD14 protein sequence are shown for the indicated species. Sequences were downloaded from the UCSC Genome Browser[1] and aligned with ClustalW2.[2; 3] Altered amino acids are in bold and marked with asterisks. The genome builds used for each species were as follows: human (hg19), chimp (panTro2), rhesus (rheMac2), mouse (mm9), cow (bosTau4), dog (canFam2), opossum (monDom5), fugu (fr2), stickleback (gasAcu1), medaka (oryLat2).

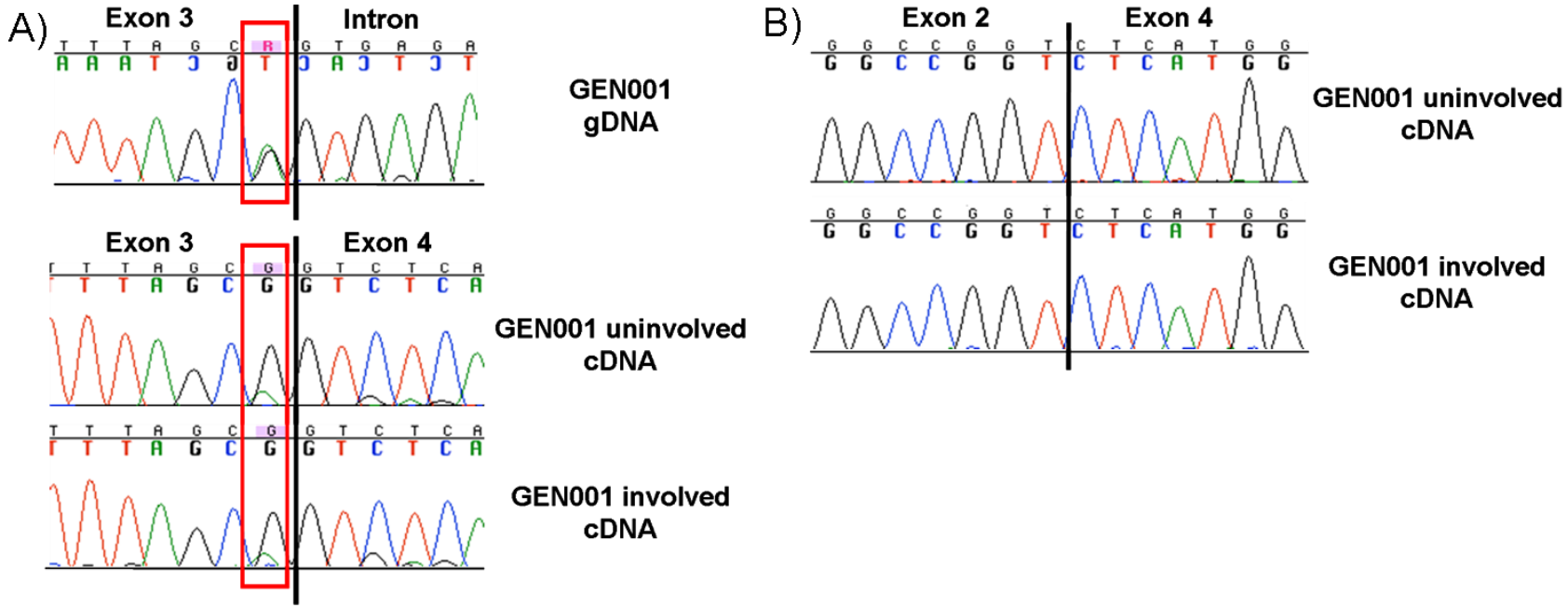

Figure S2. Sequencing of Skin-Derived cDNA from an Affected Member of Family PS1 Confirms Low-Level, In-Frame Expression of the Mutant c.349A Allele and Reveals an Isoform with Splicing Directly from Exons 2 to 4

Genomic DNA and RNA were isolated from the blood and skin (involved and uninvolved), respectively, of an affected member of family PS1 (GEN001). cDNA was isolated from RNA samples, and cDNA or genomic DNA were subjected to PCR-based sequencing with oligonucleotide primers from exon 2 and 4 of *CARD14* after purification following agarose gel electrophoresis where two PCR products had been observed (575bp and 303bp).

(A) Chromatogram obtained after sequencing the 575bp fragment revealed that the mutant to check for expression of the c.349G>A allele, (present in ~ 50% of genomic DNA fragments), was detected at lower level in cDNA from skin mutation. The mutant allele is shown to be expressed at a low level in skin on the basis of the ratios of the "G" to "A" alleles.

(B) Chromatogram obtained after sequencing the 303bp fragment revealed skipping of exon 3peak heights of the mutant allele in sequencing traces obtained in both directions.

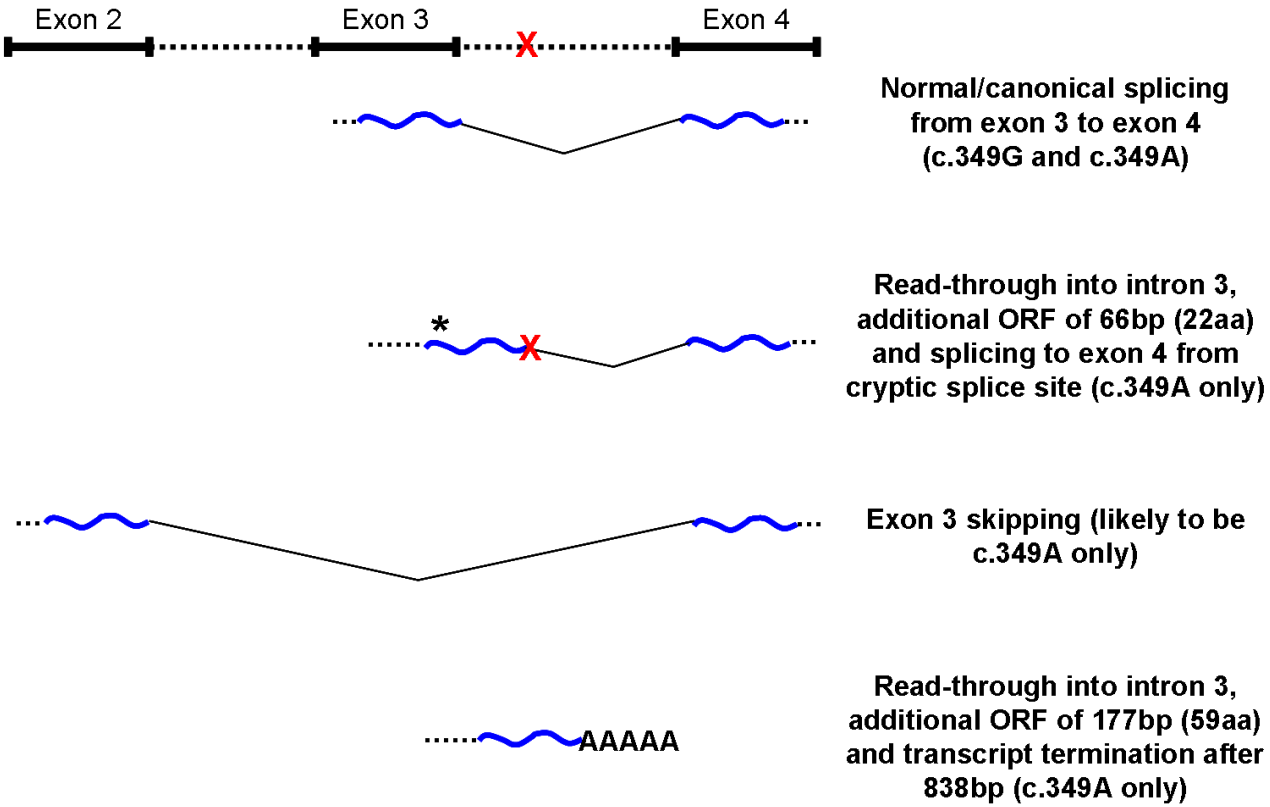

Figure S3. Schematic of Different RNA Species from the Exon 2-4 Region of *CARD14* Identified in Healthy Controls and Psoriatic Skin (Classic and GEN001) with RNA-Seq

RNA sequencing was performed with RNA from involved and uninvolved skin of GEN001. RNA was also isolated from skin biopsies of healthy controls (n=3) and matched pairs of involved and uninvolved skin from individuals with classical psoriasis (n=3 pairs). RNA libraries were generated according to manufacturer's specifications with the Illumina mRNA Sequencing kit. RNA libraries were subjected to paired-end sequencing on an Illumina HiSeq2000 for 101 cycles. Sequenced reads were aligned to the human hg19 reference genome with TopHap v1.3.2.[4; 5] Transcript assembly was performed with Cufflinks v.1.1.0.[6] Results from the exon 2-4 region of *CARD14* are presented**.** Exons 2, 3, and 4 are represented by the bold lines, introns are represented by dotted lines and "X" represents the intronic cryptic splice site predicted by *in vitro* minigene assays with the family PS1 (c.349G>A) mutation.. Supplementary Table 3 provides the percent and number of contigs for each species. *Contig variant predicted by minigene assay. ORF – open reading frame, bp – base pairs, aa – amino acids.

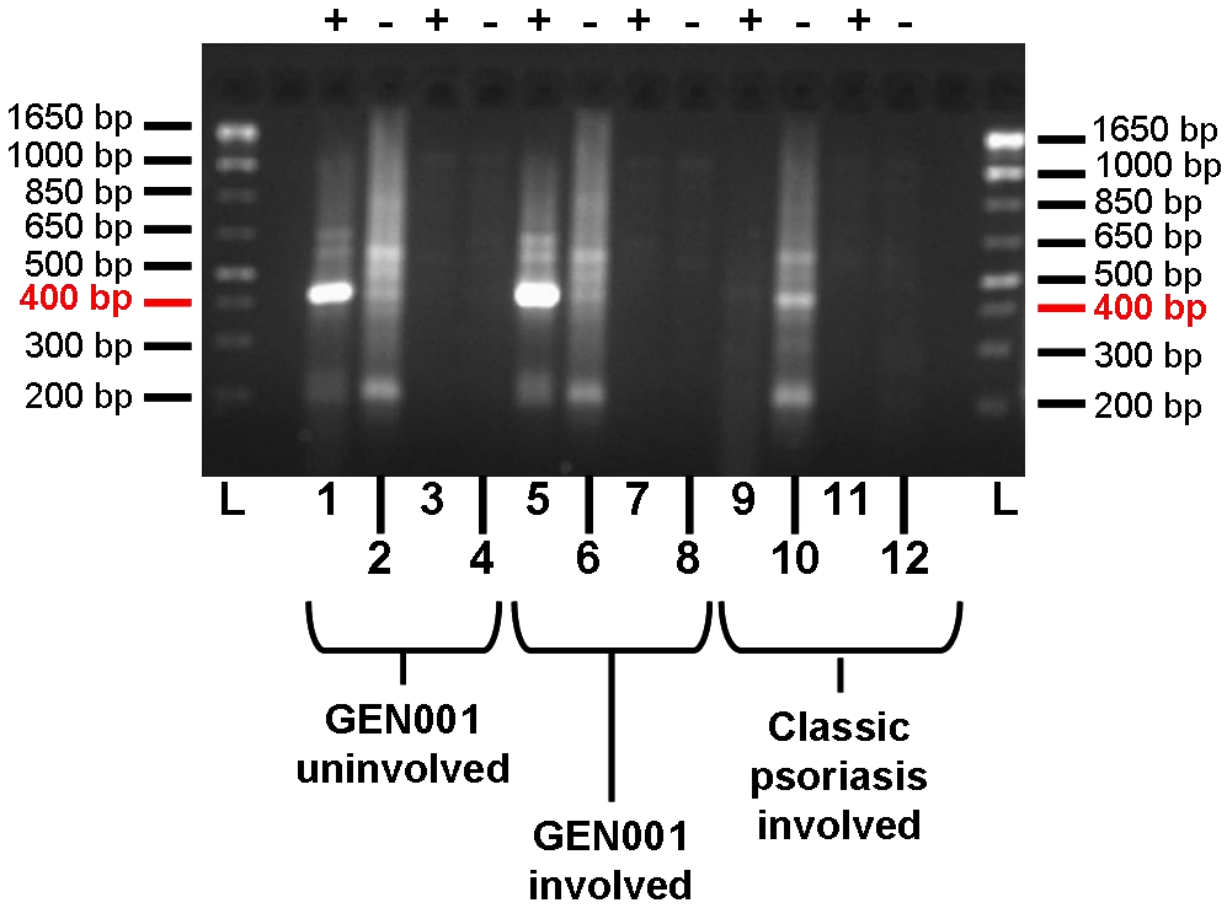

Figure S4. *CARD14* Transcripts of the Isoform with the 838 bp Intronic Sequence Insertion after Exon 3 Are Transcribed from the Same Strand as *CARD14*

cDNA was generated either with oligonucleotides that would prime the sense strand of *CARD14* mRNA (5'-AGCTGGACGAGGAGGAGGT-3') or the antisense strand (5'-CCTAAGAGCTGAGGCTGGGC-3'). Following amplification of cDNA with the same antisense primer and a nested sense primer (5'-CTGCAGCCTGATGTTGACTT-3'), a cDNA product of the predicted size of 409bp was only detected when RNA from GEN001 uninvolved or involved skin was used with *CARD14* mRNA primed for cDNA preparation in the sense direction (lanes 1 and 5). No specific product was detected with an oligonucleotide used to prime the antisense strand of CARD14 mRNA (lanes 2 and 6). Moreover, the novel CARD14 isoform was only seen with RNA from an individual from family PS1 (GEN001). No specific PCR product was seen when RNA from involved skin of classic psoriasis was subjected to cDNA preparation with either oligonucleotide (lanes 9 [sense] and 10 [antisense]). Negative controls for reverse transcriptase (RT) are shown in lanes 3, 4, 7, 8, 11, and 12. (All reagents except RT were used in the adjacent experiments). The strand of cDNA used for each PCR reaction is indicated by the "+" and "-" symbols above the image of the gel. The size, in base pairs (bp), of the ladder bands is indicated to the left and right. Lane numbers are listed below the gel, and the lanes corresponding to GEN001 uninvolved, GEN001 involved, and the classic psoriasis sample are indicated. L – ladder (1 Kb Plus DNA ladder from Invitrogen).

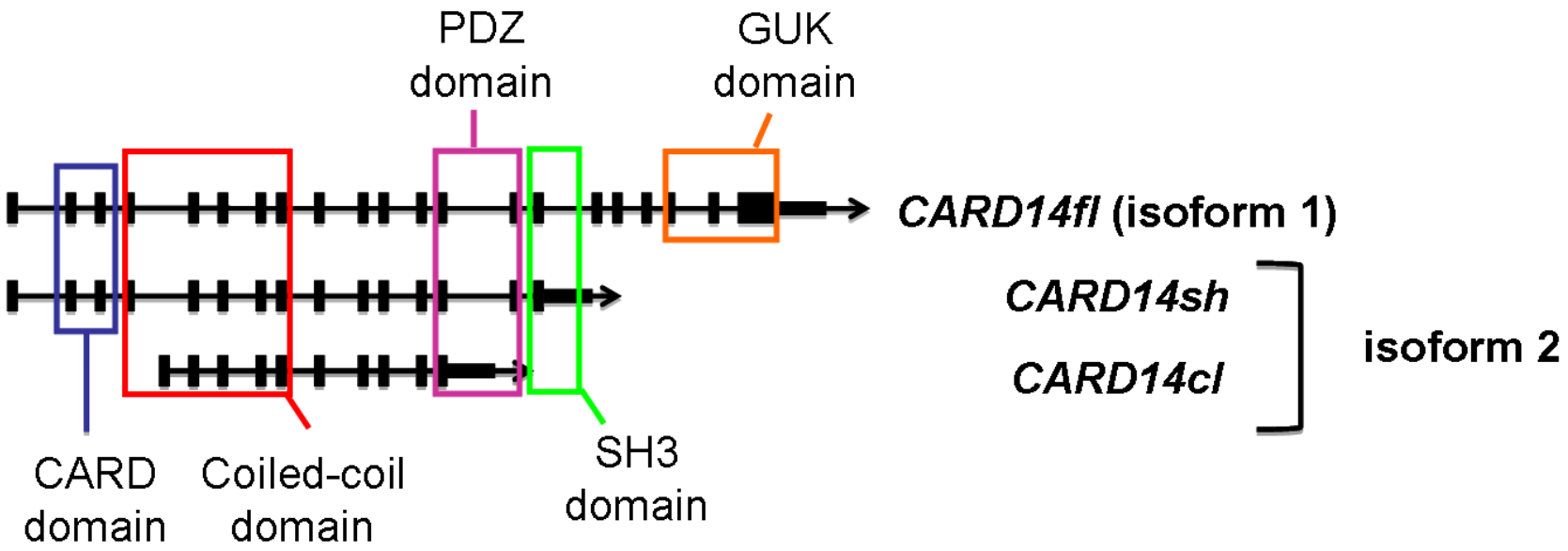

Figure S5. CARD14 Isoforms

There are several described isoforms of *CARD14* which differ in their N- and C-termini. They are represented below. *CARD14fl* is the full-length isoform. In the main article text, we discuss two other isoforms: *CARD14sh*, and *CARD14cl*. Black boxes represent exons. The major protein domains are highlighted.

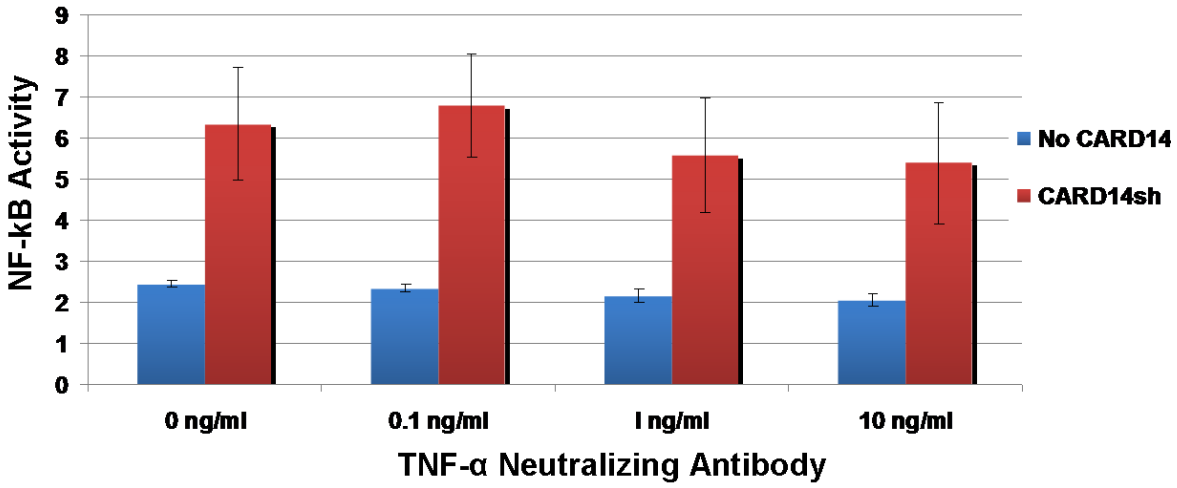

Figure S6. Effect of TNF-α Neutralization

HEK 293 cells were transfected with luciferase reporter vectors for NF-kB activation with or without *CARD14sh*. Cells were then treated with the indicated amounts of TNF-α neutralizing antibody, and relative luciferase activity was measured to determine NF-kB activity. All values were first normalized to *Renilla* expression, then adjusted relative to background levels of pTAL-Luc (see Methods). Error bars represent standard deviation of replicates.

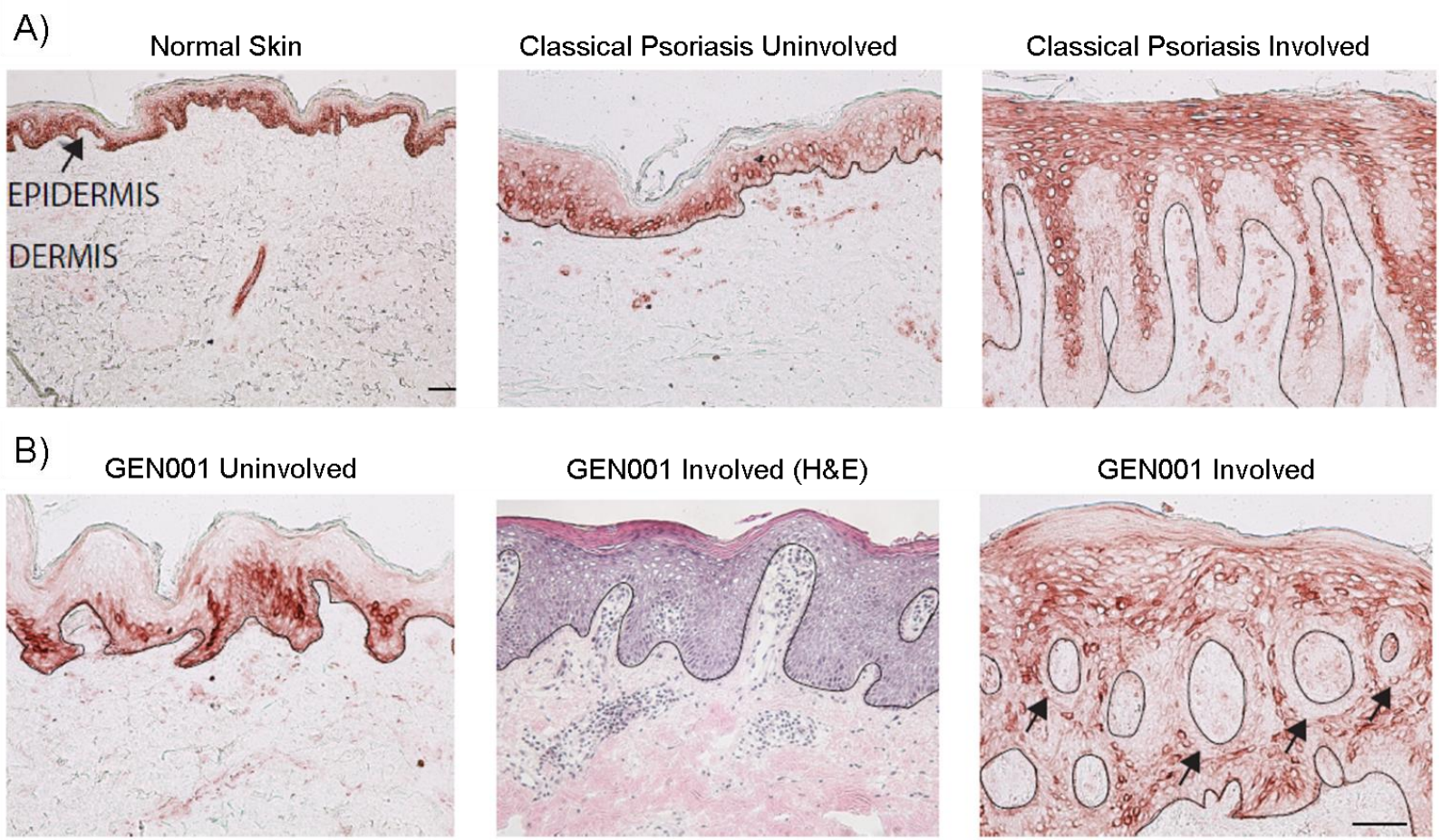

Figure S7. Distribution of CARD14 Protein in Normal and Psoriatic Skin, at Higher Magnification

Representative images for normal and psoriatic (uninvolved and involved) skin labeled with a polyclonal antibody to the internal coiled-coil domain of CARD14 that is shared by all known isoforms, and haematoxylin and eosin (H&E).

(A) Normal skin and classical psoriasis (Ps) uninvolved and involved.

(B) GEN001- PS1 affected uninvolved and involved. Black line denotes dermo-epidermal junction, with epidermis above and dermis below, lesional skin cut on cross section with dermis evident as islands projecting upwards into epidermis (identified by black arrows). GEN001 involved H&E is shown to aid orientation of GEN001 lesional tissue. Size bar 100μm.

Table S1. Results of Exome- and Targeted-Capture/NextGen Sequencing

Sample	Platform	Type of Seq.	# Cycles	# Raw Reads	Gb Raw Reads	# Aligned Reads	% Aligned	Gb Aligned Reads	% Reads On-Target	Fold Enrichment
PS1-001	Exome	SE	36	31,124,328	1.12	15,355,557	49.34	0.55	NA	NA
PS1-001	Exome	PE	76	29,396,568	4.47	10,750,515	36.57	1.63	79.00	79.32
PS1-008	Exome	PE	76	31,371,825	4.77	27,108,593	86.41	4.12	88.61	109.50
PS1-014	Exome	PE	76	28,228,119	4.29	19,896,288	70.48	3.02	8.98	9.70
PS1-026	Exome	PE	76	28,913,202	4.39	25,215,994	87.21	3.83	88.70	118.30
Affected pool	Targeted	PE	76	32,985,821	5.014	12,985,204	39.37	1.97	36.42	326.70
Unaffected pool	Targeted	PE	76	31,048,657	4.72	13,429,978	43.25	2.041	35.94	322.30

Exome sequencing was performed on DNA from four affected members of family PS1 (PS1-001, PS1-008, PS1-014, and PS1-026). Genomic capture of the entire linkage region was performed with pools of DNAs from 14 affected and 8 unaffected individuals from family PS1. Single-end (SE) or paired-end (PE) sequencing was performed. Aligned reads are those that map to the hg19 reference genome. On-target reads are aligned reads that overlap the targeting "baits" used by the capture platforms. Fold enrichment is defined as the ratio of observed on-target reads to the number expected if the distribution of reads was random.

Table S2. Mutations at PSORS2 (D17S784-qter) Detected by Exome and Targeted Capture

Gene	Detected by Exome Capture	Detected by Targeted Capture	cDNA Change	Protein Change	Genomic Location (hg19)	Confirmed by Sanger Sequencing	Segregation with Disease
CARD14	Yes	Yes	c.349G>A	p.Gly117Ser	chr17: 78,156,589	Yes	Yes
SLC26A11	Yes	Yes	c.365A>G	p.Tyr122Cys	chr17: 78,196,584	Yes	Yes
c17orf89	No	Yes	c.416C>T	None. 3'UTR	chr17: 79,215,019	Yes	No
c17orf55	No	Yes	c.2199G>A	None. 3'UTR	chr17: 79,277,395	Yes	Yes
NARF	No	Yes	c.1276A>G	p.Glu378Gly	chr17: 80,445,942	No	NA

Known polymorphisms (SNPs found in dbSNP130 and eight previously exome-sequenced HapMap individuals)[7] were removed. Five alterations remained that were detected by at least one of the two capture platforms. All were potentially deleterious mutations, and all but one were confirmed with Sanger sequencing. All members of family PS1 were also sequenced for these variants and only the mutations in *CARD14* (c.349G>A/:p.Gly117Ser) and *SLC26A11* (c.365A>G/:p.Tyr122Cys) segregated with disease.

Table S3. Number and Percentage of Different CARD14 Isoforms Due to Altered Splicing at the Exon 2–4 Region of *CARD14* in Normal and Psoriatic Skin (Classic and GEN001) Identified with RNA-Seq and PCR-Based Cloning and Sequencing of cDNA

	RNA-Seq			PCR-Based Cloning
	GEN001 Involved	**Classic Psoriasis Involved**	**Normal**	**GEN001 Involved**
Total number of contigs in region (based on 83 reads)	100% (34)	100% (14)	100% (7)	100% (44)
Canonical splicing (c.349G)	47% (16)	100% (14)	100% (7)	61.4% (27)
Canonical splicing (c.349A)	12% (4)	0% (0)	0% (0)	6.8% (3)
Splicing at minigene predicted site	9% (3)	0% (0)	0% (0)	4.5% (2)
Splicing from exon 2 to 4	17% (6)	0% (0)	0% (0)	27.3% (12)
Termination within intron 3 after 838bp (59 amino acids after exon 3 and a 3'UTR of 661bp)	15% (5)	0% (0)	0% (0)	NA

RNA was obtained from involved skin of an affected member of family PS1 (GEN001), the skin of healthy controls (normal) and involved skin of individuals with "classic" psoriasis. RNA-Seq and PCR-based cDNA cloning of samples were performed and analyzed as described in Methods. The region included for "Total number of contigs in region" is chr17:78,155,410-78,157,750. That includes the 3' end (39bp) of exon 2, all of exon 3, all of intron 3, and the 5' end of exon 4 (39bp). Contigs splicing correctly from exon 2-3 and purely exonic or intronic reads (i.e. those without evidence of splicing) were excluded from this count. Contig locations are also diagrammed in Supplementary Figure 3. For each isoform, the percentage of total RNA contigs is listed (number in parentheses). NA – not applicable.

Table S4. Expression of *CARD14* Isoforms in Various Tissues

Tissue/Cell Line	Jordan et al.	Scudiero et al.[8]
Hematopoietic/Leukocytes	--	SH
Hematopoietic/Jurkat	FL,SH	FL,SH
Hematopoietic/LBL cell line	FL,SH	--
Hematopoietic/Raji cell line	--	SH
Hematopoietic/THP1 cell line	--	SH
Hematopoietic/THP1+TZD cell line	--	SH
Skin	FL,SH,CL	--
Skin/HaCaT cell line	FL,SH	--
Skin/HEK001 cell line	FL,SH,CL	--
Thymus	FL,CL	--
Trachea	FL,SH	--
Bronchus/NHBE cell line	--	FL,SH
Bronchus/SAEC cell line	--	FL,SH
Cervix	FL,SH	--
Cervix/Hela cell line	--	FL,SH,CL
Colon	FL	--
Colon/cecum	--	--
Colon/HT29 cell line	--	SH
Colon/HT29+TNFa cell line	--	SH
Lung/NCI-H596 cell line	--	FL,CL
Lung	FL	--
Lung/SHP77 cell line	--	FL,SH
Placenta	FL,SH,CL	--

With qRT-PCR, we assayed for the presence of three *CARD14* isoforms (*CARD14fl*, *CARD14sh*, *CARD14cl*) in various human tissues using previously described primers.[8] These results are summarized below. All isoforms were expressed in skin and placenta although *CARD14sh* was the most abundant. *CARD14* isoforms were also expressed in several hematopoetic and epithelial-derived cell lines such as those of bronchus, cervix, colon and lung. *CARD14cl* had a very limited pattern of expression outside of skin and placenta. We also compare our results (Jordan et al.) with those of Scudiero et al.,[8] wherein the primers to differentiate these isoforms were initially described. FL – *CARD14fl*, SH – *CARD14sh*, CL – *CARD14cl*, -- Not interrogated.

Table S5. Changes in Transcript Levels of Key Psoriasis Genes in Different Psoriatic Skin Samples, Keratinocyte Transfectants, and a Keratinocyte Cell Line from Family PS1 after TNF-α Stimulation

		Skin Biopsies			Keratinocyte Transfectants			Immortalized Keratinocyte Lines		
Gene	**Cytoband**	**FC PP/NN**	**FC PS1-PP/ NN**	**FC Pust-PP/ NN**	**FC CARD14sh / Control**	**FC G117S/ CARD14sh**	**FC E138A/ CARD14sh**	**FC K1-1 tx/no-tx**	**FC K1-20 tx/no-tx**	**FC K5-14 tx/no-tx**
IL36G	2q13d	20.90	25.38	20.28	1.12	1.44	1.46	3.22	1.95	3.38
CCL20	2q36.3c	7.20	35.48	30.75	1.13	1.34	1.90	1.13	1.70	1.41
IL8	4q13.3d	3.56	2.49	24.72	1.36	2.10	2.41	1.05	2.61	1.32
SOD2	6q25.3f	3.23	3.43	6.17	1.12	1.39	1.78	5.45	1.84	5.75

Expression profiling was performed by interrogating Illumina bead arrays with RNA from normal skin from a healthy control (NN), skin from classic psoriasis (PP), involved skin from family PS1 (c.349G>A/p.Gly117Ser, PS1-PP) and involved skin from the individual with pustular psoriasis with the c.413A>C/p.Glu138Ala mutation (Pust-PP). RNA from HEK001 immortalized keratinocytes transfected with wildtype or mutant (c.349G>A/p.Gly117Ser [G117S] or c.413A>C/p.Glu138Ala [E138A]) CARD14*sh* was also profiled. RNA from an immortalized keratinocyte cell lines from uninvolved skin of affected members of family PS1 (K1-1 and K1-20) were profiled with and without stimulation by TNF-α. For comparison, an immortalized keratinocyte line from affected skin of a classic psoriasis case, K5-14, was also profiled with and without stimulation by TNF-α. Fold changes (FC) are shown for the indicated comparisons. NA – not applicable, IL36G – interleukin 36, gamma, CCL20 – chemokine (C-C motif) ligand 20, IL8 – interleukin 8, SOD2 – superoxide dismutase 2, mitochondrial.

Table 6. Transcriptomes of Involved Skin from Classic Psoriasis, Family PS1, and the Pustular Psoriasis Case Exhibit Similar Differences Relative to Normal Skin

Gene	Chr	Cytoband	FC PP/NN	FC GEN001 /NN	FC Pust./NN
PI3	20	20q13.12b	162.85	204.77	199.63
DEFB4	8	8p23.1e	138.48	108.46	226.27
S100A7	1	1q21.3c	125.67	129.95	156.98
S100A7A	1	1q21.3c	106.62	113.21	118.88
SPRR2A	1	1q21.3c	99.65	96.66	112.76
LOC728454	8	8p23.1f	98.74	88.14	133.81
SPRR2F	1	1q21.3c	91.70	97.68	109.29
SERPINB4	18	18q21.33b	88.18	94.90	127.58
SPRR2B	1	1q21.3c	76.41	81.75	67.41
SPRR2C	1	1q21.3c	60.87	68.60	71.70
S100A9	1	1q21.3c	48.19	48.15	44.82
SERPINB3	18	18q21.33b	39.63	41.77	48.76
LCE3A	1	1q21.3b	36.17	41.93	31.86
S100A8	1	1q21.3c	35.75	35.58	35.58
TCN1	11	11q12.1d	31.41	23.13	54.35
SPRR2D	1	1q21.3c	28.82	29.03	33.37
AKR1B10	7	7q33b	27.20	27.15	38.11
IL1F9	2	2q13d	20.90	25.38	20.28
LOC729252	17	17p11.2f	17.47	6.01	36.50
LOC400578	17	17p11.2h	17.39	7.34	34.76
LCE3D	1	1q21.3b	16.28	20.15	16.85
C10ORF99	10	10q23.1c	16.12	9.75	20.57
MGC102966	17	17p11.2c	15.97	6.52	21.81
LOC400578	17	17p11.2h	14.15	6.26	19.48
KRT6C	12	12q13.13d	13.33	7.68	27.01
KRT16	17	17q21.2b	13.25	5.35	19.40
DEFB103B	8	8p23.1e	12.75	9.86	14.23
LCE3E	1	1q21.3b	12.11	17.87	11.32
LCN2	9	9q34.11b	11.68	16.27	19.66
DEFB103B	8	8p23.1e	10.40	6.65	12.37
KYNU	2	2q22.2a	10.18	13.62	21.02
PLA2G4D	15	15q15.1d	9.26	15.47	7.37
FABP5	8	8q21.13b	9.24	12.45	11.36
OAS2	12	12q24.13b	8.92	12.37	4.53
SERPINB3	18	18q21.33b	8.89	15.95	31.68

SPRR1B	1	1q21.3c	8.59	5.47	9.86
TMPRSS11D	4	4q13.2b	8.49	10.38	12.92
CHI3L2	1	1p13.3a	8.39	12.00	6.22
IFI27	14	14q32.13a	8.12	9.42	4.42
SPRR2E	1	1q21.3c	8.09	8.26	6.03
CCL20	2	2q36.3c	7.20	35.48	30.75
HAL	12	12q23.1a	7.13	13.36	1.73
IGFL1	19	19q13.32b	6.90	4.02	3.09
KRT6B	12	12q13.13d	6.73	2.24	7.20
KRT6B	12	12q13.13d	6.67	2.05	7.83
GJB2	13	13q12.11a	6.58	5.93	6.42
ATP12A	13	13q12.12b	6.33	10.44	2.04
SPRR2G	1	1q21.3c	6.23	5.69	5.72
TGM1	14	14q12a	6.16	5.62	4.51
IL1F5	2	2q13d	6.02	6.99	5.06
KRT16	17	17q21.2b	5.89	2.18	7.62
FABP5L2	13	13q14.3d	5.72	6.56	6.64
LOC387934	13	13q22.1a	5.66	8.63	12.85
IFI6	1	1p35.3b	5.60	5.17	3.87
HPSE	4	4q21.23a	5.47	7.94	3.56
FLJ16165	19	19q13.2a	5.35	5.64	3.80
HERC6	4	4q22.1b	5.26	6.62	2.16
KRT6A	12	12q13.13d	5.18	5.14	4.52
TEX101	19	19q13.31a	5.15	4.76	2.41
KLK6	19	19q13.33d	5.14	5.37	7.45
AKR1B15	7	7q33b	5.11	5.63	10.04
ECGF1	22	22q13.33b	5.03	5.39	5.88
MX1	21	21q22.3a	5.02	6.04	2.91
ZC3H12A	1	1p34.3c	5.02	4.01	4.64
UPP1	7	7p12.3b	5.01	4.09	5.45
SPRR2E	1	1q21.3c	5.01	4.84	4.96
LOC642956	15	15q25.3a	4.99	4.22	4.15
ARSF	X	Xp22.33b	4.98	6.48	2.68
CARHSP1	16	16p13.2b	4.97	3.62	4.66
CSTA	3	3q21.1a	4.96	6.71	5.43
LOC440731	1	1q42.2a	4.95	4.44	6.53
RPL29	3	3p21.1e	4.84	3.74	3.88
FGFBP1	4	4p15.32d	4.83	3.62	6.40
EPSTI1	13	13q14.11c-q14.11d	4.80	6.06	3.75
S100A2	1	1q21.3c	4.77	2.35	4.87

GJB6	13	13q12.11b	4.75	6.00	12.99
CDC20	1	1p34.2a	4.60	3.17	3.01
NAMPT	7	7q22.2c	4.60	4.30	4.89
IFI6	1	1p35.3b	4.56	5.08	1.66
PRSS27	16	16p13.3d	4.56	3.84	6.38
OASL	12	12q24.31a	4.51	4.82	2.52
SLC16A10	6	6q21h	4.47	8.08	2.15
S100A12	1	1q21.3c	4.41	5.08	11.98
KYNU	2	2q22.2a	4.39	5.46	7.20
ISG15	1	1p36.33b	4.25	5.30	2.72
RPL29	3	3p21.1e	4.20	3.21	3.22
POL3S	16	16p11.2c	4.17	1.20	1.68
DSC2	18	18q12.1d	4.17	2.76	6.12
ACPP	3	3q22.1c	4.16	8.78	1.82
RGS20	8	8q11.23d	4.15	4.89	3.22
KIAA0101	15	15q22.31a	4.13	3.15	4.22
FABP5L2	13	13q14.3d	4.12	4.54	5.13
FABP5	8	8q21.13b	4.11	3.50	3.81
CNFN	19	19q13.2c	4.07	4.00	3.44
GJB6	13	13q12.11b	4.05	3.67	7.25
RPL14	3	3p22.1c	4.04	2.21	12.52
KLK9	19	19q13.33d	4.02	4.42	3.60
SPRR1A	1	1q21.3c	4.00	4.83	3.74
PARP9	3	3q21.1a	3.92	4.50	2.38
HAL	12	12q23.1a	3.91	7.83	1.22
ARG1	6	6q23.2a	3.90	5.54	2.17
CCNB2	15	15q22.2a	3.88	4.39	4.16
PITX1	5	5q31.1e	3.86	3.35	6.76
SERPINB13	18	18q21.33b	3.83	4.38	3.30
SAMD9	7	7q21.2b	3.80	5.24	5.79
STAT1	2	2q32.2b	3.80	5.92	4.95
LOC650517	17	17q11.2	3.80	2.76	6.38
ADAP2	17	17q11.2c	3.79	3.28	2.40
LOC643150	10	10q33.2	3.74	3.17	1.55
PDZK1IP1	1	1p33d	3.73	3.61	3.74
IFI44L	1	1p31.1e	3.73	4.75	3.02
A2ML1	12	12p13.31b	3.71	4.56	2.45
GM2A	5	5q33.1d	3.71	5.25	6.23
TOP2A	17	17q21.2a	3.70	4.63	4.78
STAT1	2	2q32.2b	3.69	5.09	3.32
LRG1	19	19p13.3d	3.57	5.00	2.36

KLK13	19	19q13.33d	3.57	3.26	7.42
LAMP3	3	3q27.1a	3.56	4.91	2.87
SLC5A1	22	22q12.3a	3.56	5.30	1.96
IL8	4	4q13.3d	3.56	2.49	24.72
ALOX12B	17	17p13.1c	3.56	3.48	2.31
FAM43A	3	3q29d	3.50	4.00	3.29
IRF7	11	11p15.5d	3.49	3.72	2.77
FUT3	19	19p13.3b	3.48	2.60	1.85
ATP10B	5	5q34a	3.46	4.43	1.72
XAF1	17	17p13.2a	3.46	4.78	1.29
OAS3	12	12q24.13b	3.45	3.93	2.71
CCBP2	3	3p22.1a	3.44	3.09	2.51
PTTG3P	8	8q13.1b	3.44	3.25	5.29
AAK1	2	2p14a	3.43	2.19	4.26
AQP3	9	9p13.3e	3.41	2.20	1.16
C9ORF169	9	9q34.3	3.41	4.22	2.57
NP	14	14q11.2b	3.41	3.48	4.56
GBP1	1	1p22.2c	3.38	4.21	7.25
GRHL3	1	1p36.11d	3.37	5.19	2.84
CXCL10	4	4q21.1a	3.35	8.31	15.57
RDH16	12	12q13.3a	3.35	4.08	2.59
MPZL2	11	11q23.3d	3.33	2.86	3.95
OAS1	12	12q24.13b	3.31	2.76	2.28
PRIC285	20	20q13.33e	3.28	3.45	1.69
CDH3	16	16q22.1c	3.27	1.45	4.31
KLK10	19	19q13.33d	3.27	2.79	4.99
PLA2G4E	15	15q15.1d	3.27	3.79	2.18
ABCA12	2	2q35a	3.26	3.82	1.64
C18ORF45	18	18q11.2b	3.25	2.45	1.19
CD24	Y	Yq11.222	3.24	3.69	3.42
CDC45L	22	22q11.21c	3.23	2.72	2.11
SOD2	6	6q25.3f	3.23	3.43	6.17
F12	5	5q35.3a	3.23	1.96	2.40
UNC93A	6	6q27c	3.22	3.96	0.80
OAS1	12	12q24.13b	3.22	4.13	0.81
SLC7A5	16	16q24.2b	3.21	1.78	2.74
PGM2	4	4p14d	3.20	2.92	2.85
GDPD3	16	16p11.2d	3.20	3.72	1.17
OAS1	12	12q24.13b	3.17	3.39	2.25
PTTG1	5	5q33.3d	3.12	2.81	3.15
IFI44	1	1p31.1e	3.08	5.14	2.46

INA	10	10q24.33a	3.05	2.91	1.96
PLA2G3	22	22q12.2c	3.05	2.82	1.99
EHF	11	11p13c-p13b	3.04	4.18	3.53
CCL22	16	16q13c	3.02	2.72	1.69
CEP55	10	10q23.33b	3.02	3.22	2.96
TYMP	22	22q13.33b	3.01	2.27	2.41
NCALD	8	8q22.3b	0.33	0.45	0.52
AQP5	12	12q13.13a	0.33	0.31	0.39
LOC643719	19	19q13.11c	0.33	0.50	1.97
AXL	19	19q13.2c	0.33	0.34	0.49
FOXC1	6	6p25.3a	0.33	0.53	0.56
KRTAP9-4	17	17q21.2a	0.33	0.32	0.57
TGFBR3	1	1p22.2a-p22.1e	0.33	0.44	0.51
LTBP4	19	19q13.2b	0.33	0.28	0.40
ATP6V1B1	2	2p13.3c	0.33	0.44	0.52
KRTAP17-1	17	17q21.2b	0.33	0.29	3.30
MUC1	1	1q22a	0.33	1.28	0.19
CLDN23	8	8p23.1d	0.33	0.32	0.54
LAMC3	9	9q34.13a	0.33	0.29	0.38
LCE1E	1	1q21.3b	0.33	0.31	0.18
DAB2	5	5p13.1c	0.33	0.34	0.48
ANGPTL2	9	9q33.3b	0.33	0.28	0.57
C10ORF116	10	10q23.2a	0.32	0.38	0.59
COL6A1	21	21q22.3f	0.32	0.25	0.42
LPAR1	9	9q31.3b	0.32	0.47	0.39
FADS2	11	11q12.2b	0.32	0.48	0.29
LHFP	13	13q13.3e	0.32	0.33	0.73
CRIP1	14	14q32.33d	0.32	0.30	0.34
ELANE	19	19p13.3i	0.32	0.45	0.35
SGCE	7	7q21.3b	0.32	0.35	0.63
KAZALD1	10	10q24.31a	0.32	0.39	0.34
CST6	11	11q13.1d	0.32	0.67	0.16
PDGFRA	4	4q12c	0.32	0.36	0.54
ISLR	15	15q24.1b	0.32	0.33	0.49
GSTM3	1	1p13.3b	0.32	0.40	0.39
KRT34	17	17q21.2b	0.32	0.28	1.64
DBN1	5	5q35.3a	0.32	0.35	0.42
HSPB6	19	19q13.12a	0.32	0.37	0.49
CAMK2N1	1	1p36.12b	0.31	0.32	0.71
CTNNBIP1	1	1p36.22d	0.31	0.26	0.22

SEPP1	5	5p12c	0.31	0.66	0.96
CTSF	11	11q13.1e	0.31	0.30	0.43
COL5A1	9	9q34.3a	0.31	0.22	0.34
SCGB2A2	11	11q12.3a	0.31	0.28	1.15
KRTAP4-5	17	17q21.2a	0.31	0.33	1.04
TPM1	15	15q22.2b	0.31	0.44	0.48
COX7A1	19	19q13.12b	0.31	0.28	0.58
MEG3	14	14q32.2b	0.31	0.37	0.31
ACOX2	3	3p14.3a	0.31	0.68	0.35
KRTAP26-1	21	21q22.11a	0.31	0.32	1.78
MSMB	10	10q11.23b	0.31	0.52	0.40
FCGRT	19	19q13.33b	0.31	0.32	0.59
TPM1	15	15q22.2b	0.31	0.47	0.44
SORBS1	10	10q23.33d	0.31	0.34	0.48
EBF1	5	5q33.3c	0.31	0.35	0.63
PMP22	17	17p12a	0.31	0.34	0.57
GSTM1	1	1p13.3b	0.30	0.32	0.23
LOC728946	17		0.30	0.27	0.39
HSD11B1	1	1q32.2b	0.30	0.50	0.27
DPYSL3	5	5q32e	0.30	0.44	0.47
ZNF807	19	19q13.11c	0.30	0.46	1.45
RARRES2	7	7q36.1c	0.30	0.29	0.93
EFEMP2	11	11q13.1d	0.30	0.31	0.49
SPRR4	1	1q21.3c	0.30	0.71	0.35
TNMD	X	Xq22.1b	0.29	0.34	0.65
LGALS1	22	22q13.1a	0.29	0.29	0.52
TPSB2	16	16p13.3e	0.29	0.21	0.65
SLIT3	5	5q35.1a-q35.1b	0.29	0.27	0.53
LOC100132535	9	9q34.11b	0.29	0.40	0.34
LOC730743	17	17q21.2	0.29	0.29	0.57
KRT85	12	12q13.13d	0.29	0.25	2.82
CGNL1	15	15q21.3d	0.29	0.53	0.56
CCL15	17	17q12b	0.29	0.36	0.45
ACACB	12	12q24.11a-q24.11b	0.29	0.39	0.65
MAMDC2	9	9q21.11b-q21.11c	0.29	0.41	0.80
COL1A1	17	17q21.33a	0.29	0.18	0.30
TPR	1	1q31.1a	0.29	0.32	0.28
GALNTL1	14	14q24.1d-q24.1e	0.29	0.27	0.37

LOC728946	17		0.29	0.30	0.68
ABI3BP	3	3q12.2a-q12.2b	0.29	0.49	0.59
SERPING1	11	11q12.1a	0.29	0.30	0.67
RNASE4	14	14q11.2b	0.28	0.30	0.48
CILP	15	15q22.31b	0.28	0.31	1.01
SFRP2	4	4q31.3d	0.28	0.28	0.39
FZD4	11	11q14.2a	0.28	0.34	0.54
LOC728255	17	17q21.2a	0.28	0.27	0.52
KRTAP2-1	17	17q21.2a	0.28	0.31	0.70
PDGFRB	5	5q33.1c	0.28	0.31	0.45
KRTAP11-1	21	21q22.11a	0.28	0.24	2.60
HBA1	16	16p13.3f	0.28	0.20	1.36
COL1A2	7	7q21.3a	0.28	0.32	0.43
F10	13	13q34c	0.28	0.31	0.43
LOC126767	1	1p36.21d	0.28	1.37	0.14
COL6A2	21	21q22.3f	0.28	0.19	0.31
RNASE1	14	14q11.2b	0.28	0.34	1.26
TAGLN	11	11q23.3b	0.27	0.22	0.54
ELOVL3	10	10q24.32b	0.27	0.95	0.16
DCN	12	12q21.33c	0.27	0.45	0.46
HS.388347	10	10q26.11	0.27	0.41	0.44
OLFML1	11	11p15.4b	0.27	0.31	0.43
CPZ	4	4p16.1c	0.27	0.36	0.42
TIMP2	17	17q25.3b-q25.3c	0.27	0.33	0.37
RHOBTB3	5	5q15c-q15d	0.27	0.30	0.33
LCE1A	1	1q21.3b	0.27	0.32	0.10
PPP1R1B	17	17q12c	0.27	0.25	0.65
MSX1	4	4p16.2a	0.27	0.27	0.48
C1QTNF1	17	17q25.3c	0.26	0.26	0.71
CRYAB	11	11q23.1b	0.26	0.20	0.33
CTSK	1	1q21.2c	0.26	0.44	0.50
ACSBG1	15	15q25.1a	0.26	0.90	0.09
SERPINA12	14	14q32.13a	0.26	0.32	0.08
LCE1D	1	1q21.3b	0.26	0.28	0.11
CPA3	3	3q24f	0.26	0.28	0.62
FBLN5	14	14q32.12a	0.26	0.28	0.46
MGST1	12	12p12.3d	0.26	0.49	0.24
MYADM	19	19q13.41b	0.25	0.24	0.35
TPSAB1	16	16p13.3e	0.25	0.17	0.39
FGL2	7	7q11.23g	0.25	0.35	0.64

PPAP2B	1	1p32.2c	0.25	0.45	0.72
KRT86	12	12q13.13d	0.25	0.26	1.85
ITM2A	X	Xq21.1b	0.25	0.35	0.42
FGFBP2	4	4p15.32d	0.25	0.40	0.34
COL6A2	21	21q22.3f	0.25	0.15	0.32
RNASE4	14	14q11.2b	0.25	0.37	0.62
FADS1	11	11q12.2b	0.24	1.23	0.20
TPSAB1	16	16p13.3e	0.24	0.17	0.61
PAMR1	11	11p13b-p13a	0.24	0.25	0.18
AWAT2	X	Xq13.1b	0.24	0.76	0.14
EFEMP1	2	2p16.1d	0.24	0.19	0.41
AEBP1	7	7p13d	0.24	0.27	0.47
CYBRD1	2	2q31.1c	0.24	0.41	0.52
HRASLS3	11	11q12.3b-q13.1a	0.24	0.25	0.88
ECM2	9	9q22.31a-q22.31b	0.24	0.35	0.64
GSTM2	1	1p13.3b	0.24	0.26	0.15
IGFBP5	2	2q35c	0.24	0.71	0.71
CCL14	17	17q12b	0.23	0.35	0.49
KRT81	12	12q13.13d	0.23	0.25	1.14
CTSG	14	14q12a	0.23	0.23	0.22
SPARC	5	5q33.1d	0.23	0.31	0.49
KRTAP9-4	17	17q21.2a	0.23	0.23	1.54
PCOLCE	7	7q22.1c	0.23	0.20	0.36
FSTL1	3	3q13.33b	0.22	0.27	0.48
PPAP2B	1	1p32.2c	0.22	0.29	0.47
GAL	11	11q13.2b	0.22	1.17	0.16
KRTAP4-7	17	17q21.2	0.22	0.24	1.24
MGST1	12	12p12.3d	0.22	0.68	0.25
PLIN	15	15q26.1b	0.22	0.20	0.58
KRTAP9-8	17	17q21.2a	0.22	0.19	0.69
CYBRD1	2	2q31.1c	0.22	0.39	0.52
COL12A1	6	6q13c-q14.1a	0.22	0.25	0.41
SVEP1	9	9q31.3b	0.22	0.29	0.58
GSN	9	9q33.2a	0.22	0.26	0.31
PCOLCE2	3	3q23d	0.22	0.22	0.76
PIP	7	7q34f	0.21	0.69	0.64
SCGB1D2	11	11q12.3a	0.21	0.14	0.82
PALM	19	19p13.3j-p13.3i	0.21	0.23	0.32
CD34	1	1q32.2a	0.21	0.29	0.51

MFAP4	17	17p11.2e	0.21	0.31	0.44
LUM	12	12q21.33c	0.21	0.24	0.92
PODN	1	1p32.3c	0.21	0.31	0.60
LOC399888	11	11p11.2b	0.20	0.27	0.23
KRTAP9-3	17	17q21.2a	0.20	0.23	1.76
KRT77	12	12q13.13d	0.20	0.30	0.21
FBLN2	3	3p25.1b	0.20	0.22	0.48
COL1A2	7	7q21.3a	0.20	0.23	0.32
CXCL12	10	10q11.21c	0.20	0.20	0.49
FBLN1	22	22q13.31c	0.19	0.32	0.35
CTHRC1	8	8q22.3c	0.19	0.32	0.68
CFH	1	1q31.3c	0.19	0.32	0.63
TIMP3	22	22q12.3a	0.19	0.21	0.32
MGP	12	12p12.3e	0.19	0.36	0.78
OLFML3	1	1p13.2b	0.19	0.20	0.32
CFH	1	1q31.3c	0.19	0.32	0.53
TSPAN8	12	12q21.1a	0.18	0.33	0.47
HLA-DRB5	6	6p21.32b	0.18	0.17	0.21
CFD	19	19p13.3i	0.17	0.29	0.51
MGP	12	12p12.3e	0.17	0.33	0.86
CXCL12	10	10q11.21c	0.17	0.26	0.51
CFH	1	1q31.3c	0.17	0.28	0.63
FHL1	X	Xq26.3b	0.16	0.18	0.39
IGFBP5	2	2q35c	0.16	0.41	0.45
FBLN2	3	3p25.1b	0.16	0.20	0.34
APOD	3	3q29e	0.16	0.25	0.42
IL1F7	2	2q13d	0.16	0.15	0.04
C5ORF46	5	5q33.1a	0.15	0.26	0.13
IGFBP6	12	12q13.13e	0.15	0.19	0.22
CD248	11	11q13.1e	0.14	0.15	0.19
CD34	1	1q32.2a	0.14	0.15	0.36
IL1F7	2	2q13d	0.14	0.11	0.05
PLAC9	10	10q22.3f	0.13	0.17	0.23
ADH1A	4	4q23b	0.13	0.16	0.91
DCN	12	12q21.33c	0.13	0.19	0.27
DCN	12	12q21.33c	0.13	0.30	0.61
H19	11	11p15.5b	0.13	0.11	0.24
MFAP5	12	12p13.31b	0.13	0.19	0.53
FBLN1	22	22q13.31c	0.13	0.11	0.14
FBLN1	22	22q13.31c	0.12	0.15	0.21
PDGFRL	8	8p22b	0.12	0.18	0.41

LCE5A	1	1q21.3b	0.12	0.09	0.06
THRSP	11	11q14.1a	0.11	0.81	0.13
PI16	6	6p21.2c	0.11	0.25	0.46
CLEC3B	3	3p21.31k	0.11	0.16	0.27
CILP	15	15q22.31b	0.11	0.11	0.72
KIAA1881	19	19p13.3	0.10	0.11	0.47
FABP7	6	6q22.31c	0.10	0.14	0.06
SCARA5	8	8p21.1e-p21.1d	0.09	0.14	0.18
WISP2	20	20q13.12a	0.08	0.11	0.07
MT4	16	16q13b	0.07	0.06	0.31
CIDEC	3	3p25.3c	0.06	0.05	1.17
FABP4	8	8q21.13b	0.06	0.07	1.18

Global expression profiling was performed on involved skin from classic psoriatic skin, an affected member of family PS1 (individual GEN001), and the child with pustular psoriasis, individual 2192, who carried the *de novo* CARD14 mutation (pust.). Normal skin was also profiled. This table provides fold changes of transcripts that most strongly differentiate classic psoriasis from normal skin, and compares them with those of GEN001 (PS1) and 2192 (Pust.). Chr – chromosome, FC – fold change in transcript level, PP/NN – involved skin versus normal skin.

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