Supplementary Information for:

Genome-wide association study identifies a psoriasis susceptibility locus at *TRAF3IP2*

Eva Ellinghaus[1], David Ellinghaus[1], Philip E. Stuart[2], Rajan P. Nair[2], Sophie Debrus[3], John V. Raelson[3], Majid Belouchi[3], Hélène Fournier[3], Claudia Reinhard[3], Jun Ding[4], Yun Li[4], Trilokraj Tejasvi[2], Johann Gudjonsson[2], Stefan W. Stoll[2], John J. Voorhees[2], Sylviane Lambert[2], Stephan Weidinger[5,6], Bernadette Eberlein[5], Manfred Kunz[7], Proton Rahman[8], Dafna D. Gladman[9], Christian Gieger[10], H. Erich Wichmann[10,11,12], Tom H. Karlsen[13], Gabriele Mayr[14], Mario Albrecht[14], Dieter Kabelitz[15], Ulrich Mrowietz[6], Gonçalo R. Abecasis[4], James T. Elder[2,16], Stefan Schreiber[1], Michael Weichenthal[6,‡,*] and Andre Franke[1,‡ ,*]

[1] Institute of Clinical Molecular Biology, Christian-Albrechts-University, 24105 Kiel, Germany

[2] Department of Dermatology, University of Michigan, Ann Arbor, MI 48109, USA

[3] Genizon BioSciences, Inc., St. Laurent, QC, Canada H4T 2C7

[4] Department of Biostatistics, Center for Statistical Genetics, University of Michigan, Ann Arbor, MI 48109, USA

[5] Department of Dermatology and Allergy, Technische Universität München, 80802 Munich, Germany

[6] Department of Dermatology, University Hospital Schleswig-Holstein, Christian-Albrechts-University, 24105 Kiel, Germany

[7] Comprehensive Center for Inflammation Medicine, University of Lübeck, 23538 Lübeck, Germany

[8] Department of Medicine, Memorial University, St. John’s, Newfoundland A1C 5B8, Canada

[9] Division of Rheumatology University Toronto, Psoriatic Arthritis Program, University Health Network, Toronto, Ontario M5T 2S8, Canada

[10] Institute of Epidemiology, Helmholtz Centre Munich, German Research Center for Environmental Health, 85764 Neuherberg, Germany

[11] Institute of Medical Informatics, Biometry and Epidemiology, Ludwig-Maximilians-University, 81377 Munich, Germany

[12] Klinikum Grosshadern, 81377 Munich, Germany
[13] Medical Department, Rikshospitalet University Hospital, 0027 Oslo, Norway
[14] Max Planck Institute for Informatics, 66123 Saarbrücken, Germany
[15] Institute for Immunology, University Hospital Schleswig-Holstein, Christian-Albrechts-University, 24105 Kiel, Germany
[16] Ann Arbor Veterans Affairs Hopital, Ann Arbor, MI 48105, USA
[*] shared senior authorship

[‡] **To whom correspondence should be addressed:**
Prof. Dr. rer. nat. Andre Franke (a.franke@mucosa.de)
Institute of Clinical Molecular Biology
Christian-Albrechts-University Kiel
Schittenhelmstr. 12
D-24105 Kiel, Germany
Tel.: +49-431-597-4138
Fax.: +49-431-597-2196

Prof. Dr. med. Michael Weichenthal (MWeichenthal@dermatology.uni-kiel.de)
Department of Dermatology
University Hospital Schleswig-Holstein
Schittenhelmstr. 7,
D-24105 Kiel, Germany
Tel.: +49-431-597-1537
Fax.: +49-431-597-1606

Supplementary Figure 1. Quality control of genome-wide association data.

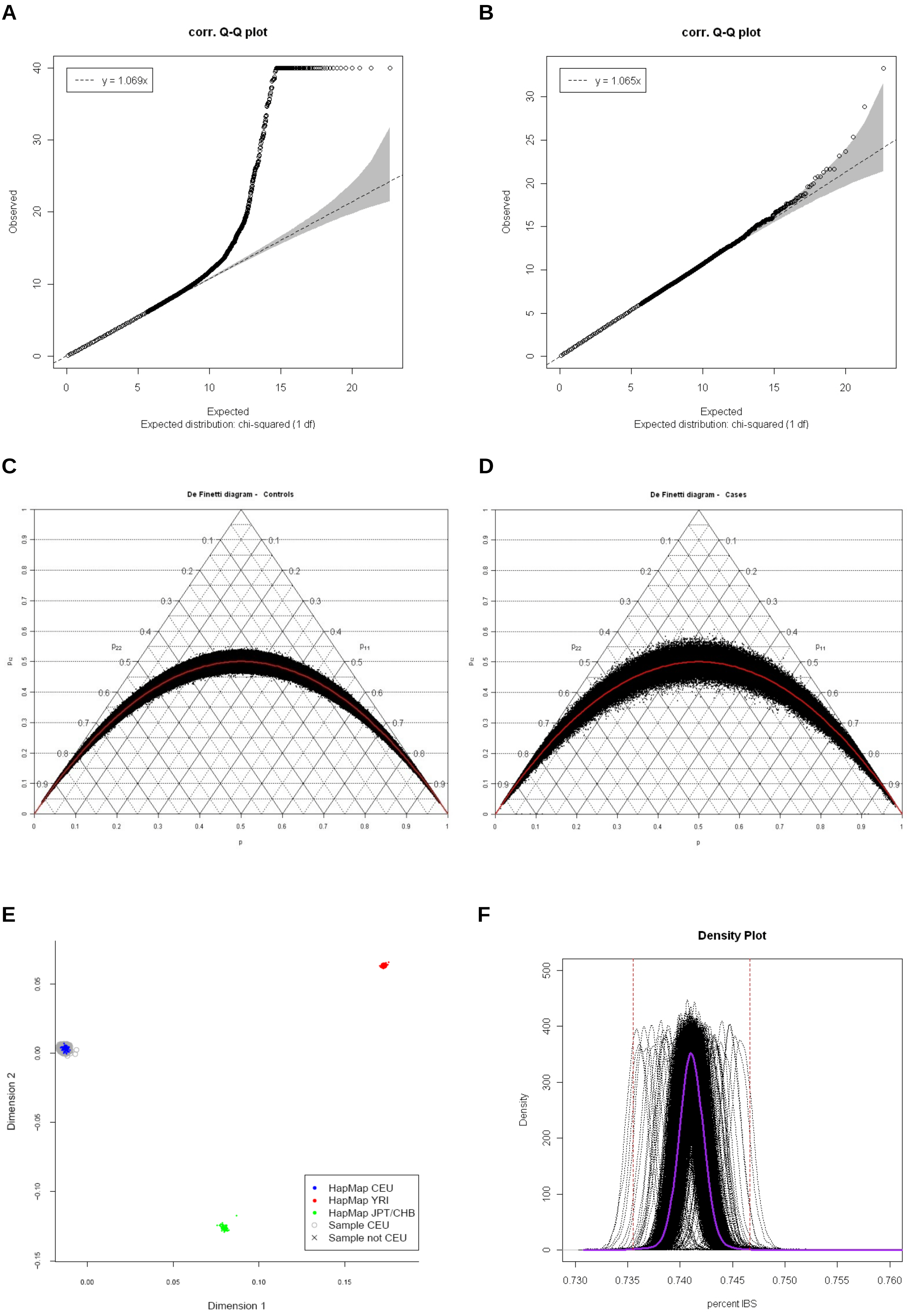
(A) To display whether the study generated more significant results than expected by chance, the quantile-quanile (Q-Q) plot of the association test statistic was calculated for all genotyped SNPs that passed quality control (n=504,742). For better scaling the Y-axis was limited to a maximum value of $\text{chi}^2=40$. 65 SNPs with a $\text{chi}^2>40$ form a “plateau” along the top. **(B)** The second plot was calculated under exclusion of all SNPs within the extended MHC region (Chr 6, 25-34 Mb: n=2,462 SNPs in interval), leaving 502,280 SNPs for plotting. The genomic inflation factor, based on median chi-squared was estimated to be $\lambda=1.065$, indicating minimal undetected population stratification or cryptic relatedness, which would result in deviation from the null across the entire distribution.

The De Finetti diagrams show genotype distributions of all quality-controlled SNPs in the control **(C)** and case **(D)** population. Any point within the de Finetti triangle corresponds to a specific combination of the three genotype frequencies p_{11}, p_{12} and p_{22} in relation to each other: The curved red line is referred to as the Hardy-Weinberg parabola and depicts the genotype distributions strictly fulfilling Hardy-Weinberg equilibrium. The black band of genotype distributions represents an area where deviation from Hardy-Weinberg is not too strong.

(E) The multidimensional scaling (MDS) plot showed genuine European ancestry for the cleaned GWAS panel A which was plotted with the three distinct HapMap sample populations (see box with legend in plot) for the first two principal components. After exclusion of 17 “outliers” (see **F**) none of the samples (denoted as grey circles) showed evidence of non-European ancestry.

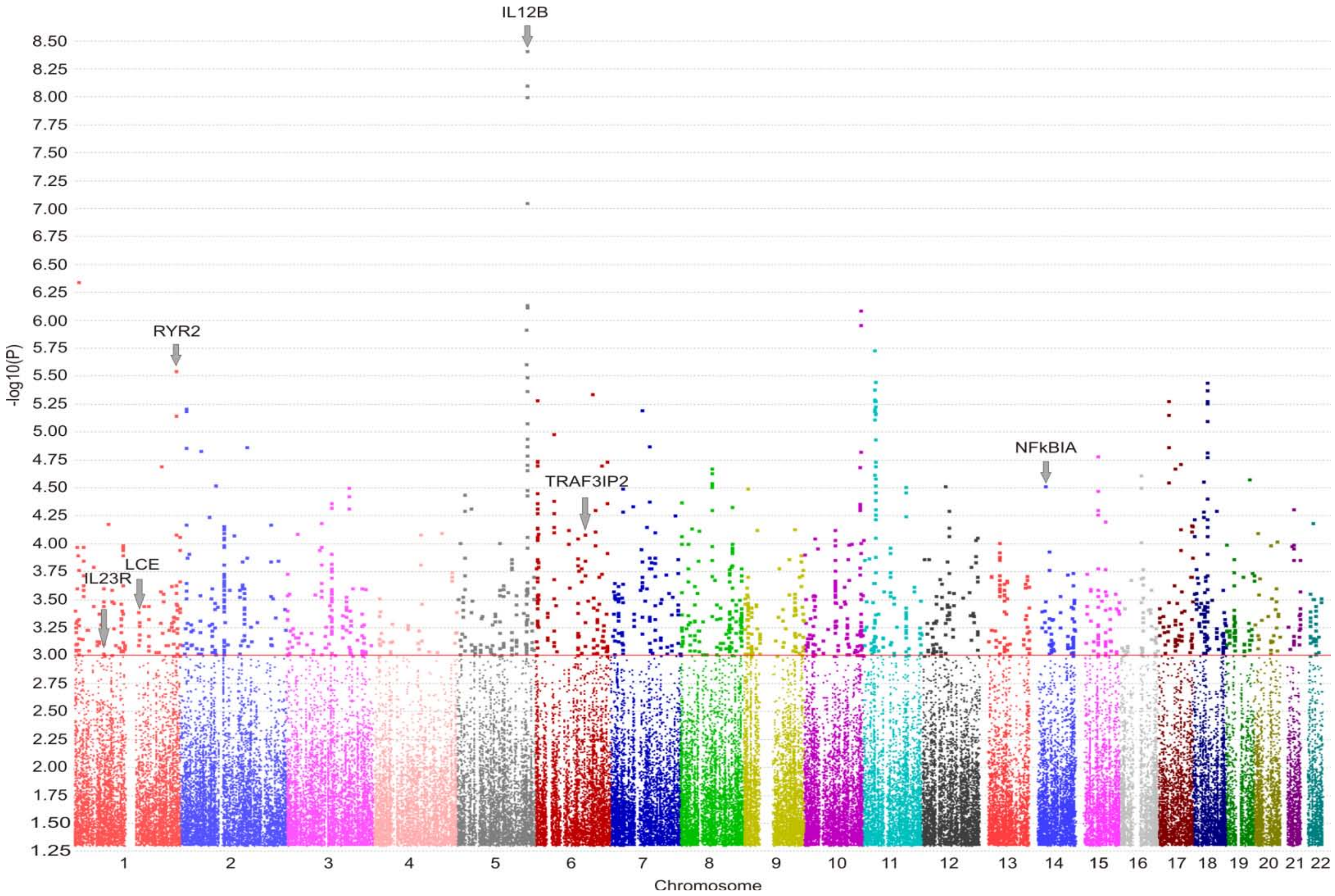
(F) Pair-wise percentage IBS (identity-by-state) values were computed, using PLINK[1] in order to detect “outliers” by comparing the distribution of the IBS values for each individual with the combined IBS distribution of the entire population. Two types of “outliers” were detected: 1) individuals less related to the entire population than expected were defined as those for whom >60% of the IBS values were smaller than the median minus three times the interquartile range (3×IQR) of the population distribution. In this case, these individuals were removed from the population; 2) individuals with a close cognate relative in the population were defined as those who had at least one observed IBS value above the median plus 3×IQR. In this case, the member of the cognate pair with the lower call rate was removed from the population. 17 non-European “outliers” and 8 related individuals were detected and hence excluded from subsequent analyses. In the final analysis, 472 cases and 1146 controls were included.

1. Purcell, S. et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* **81**, 559-75 (2007).

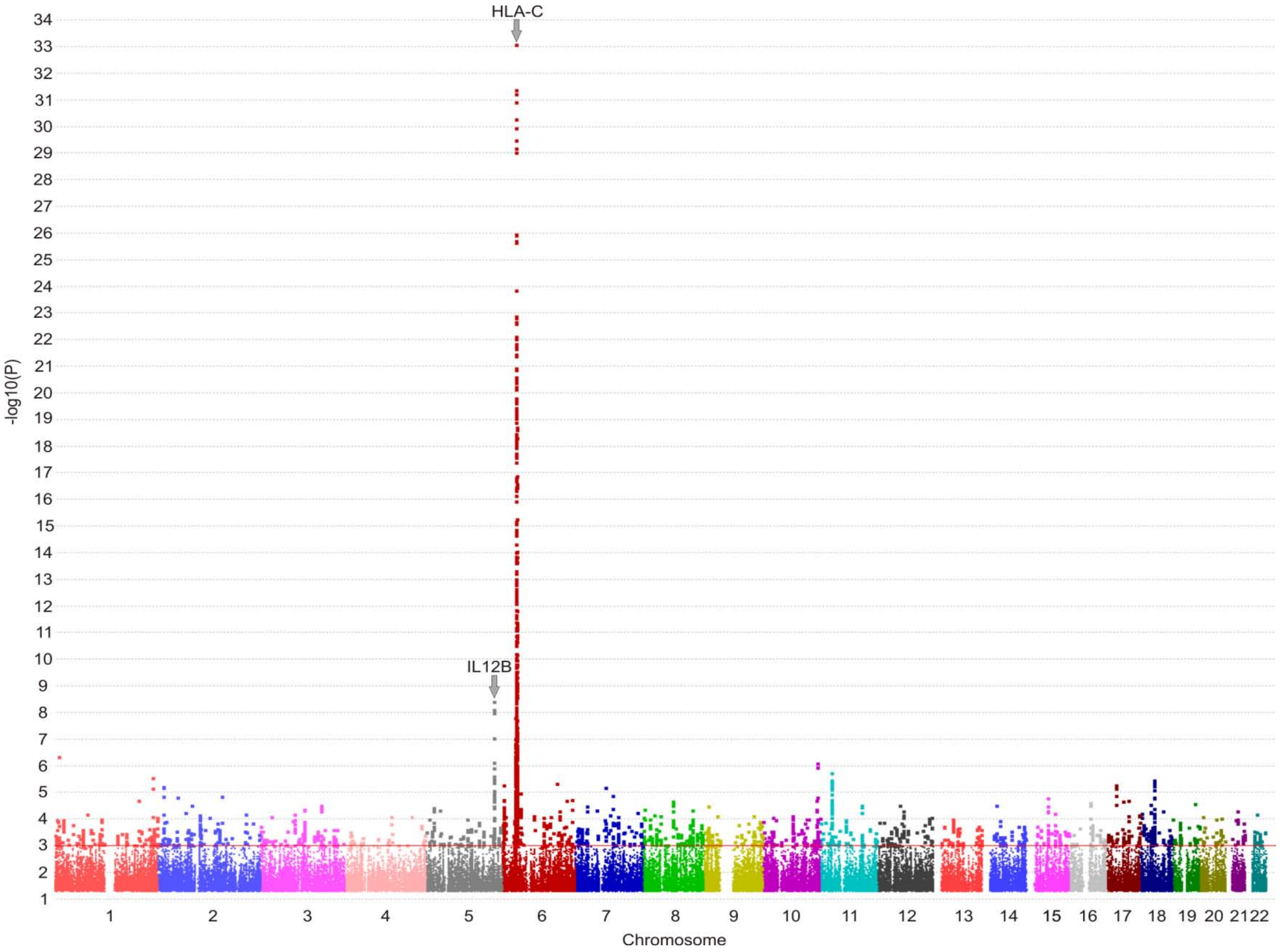

A
corr. Q-Q plot
y = 1.069x
Observed
Expected
Expected distribution: chi-squared (1 df)
B
corr. Q-Q plot
y = 1.065x
Observed
Expected
Expected distribution: chi-squared (1 df)
C
De Finetti diagram - Controls
p22
p11
p12
p
D
De Finetti diagram - Cases
p22
p11
p12
p
E
Dimension 1
Dimension 2
HapMap CEU
HapMap YRI
HapMap JPT/CHB
Sample CEU
Sample not CEU
F
Density Plot
Density
percent IBS

Supplementary Figure 2. Results of association analysis. For each SNP the negative decadic logarithm for the corresponding *P*-value of the allelic test of the genome-wide association study is shown, according to chromosome. **(A)** Only markers outside of the extended MHC that passed quality control criteria before clumping and had a *P*-value <0.05 were used for plotting (n=130,679). In addition to some of the already known loci (*IL12B*, *IL23R* and *LCE*), the novel locus *TRAF3IP2* as well as some other loci with marginal evidence for association, are highlighted by arrows. **(B)** All markers with a *P*-value<0.05 that passed quality control before clumping were used for plotting (n=134,443). The *HLA-C* locus stands out clearly from all other loci. Marker positions are in NCBI's build 36. The plot was created with Haploview 4.1.

A



B


HLA-C
IL12B
-log10(P)
34
33
32
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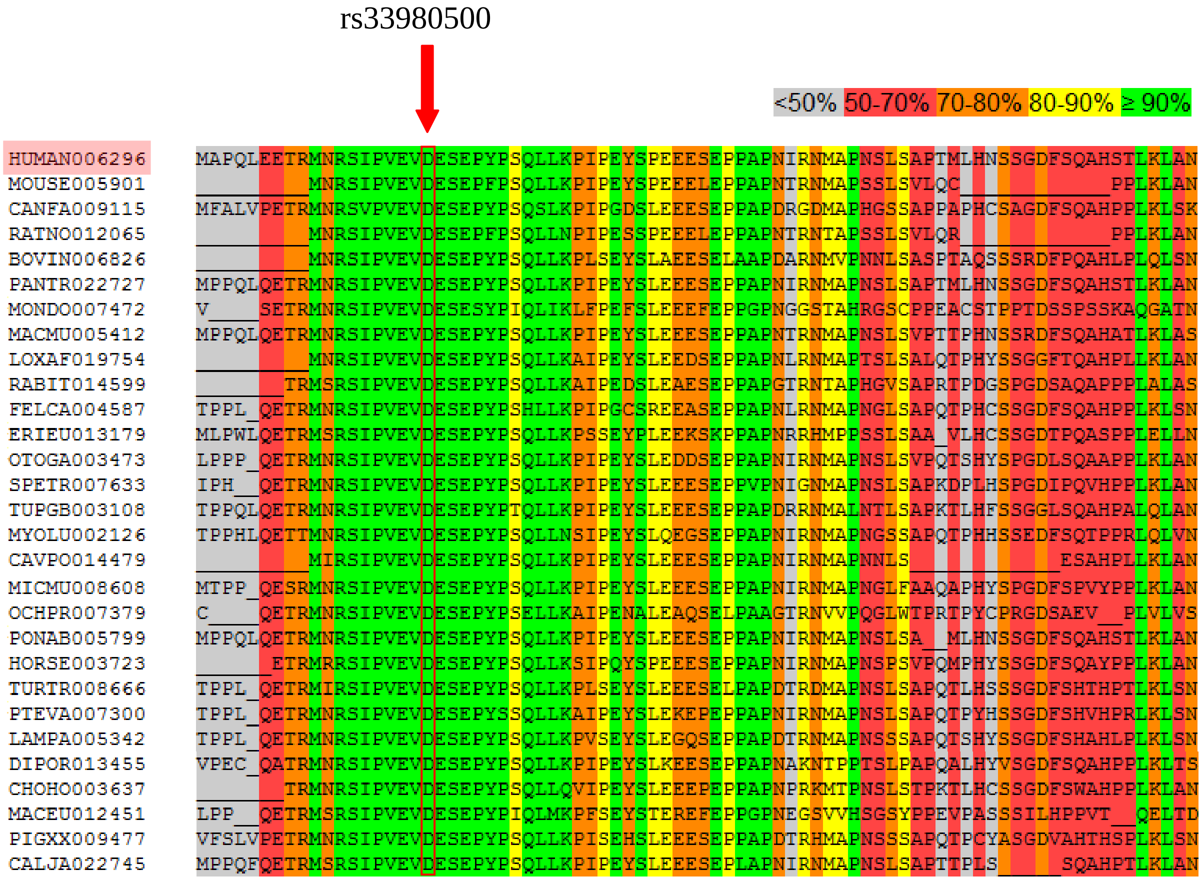
Chromosome

Supplementary Figure 3. Protein sequence alignment of TRAF3IP2. Structure-based multiple sequence alignment of the N terminal part (first 80 amino acids of the human protein) of TRAF3IP2 protein homologues (OMA Group 40491[2]). TRAF3IP2 is a 60 kDa (574 aa) polypeptide with a helix-loop-helix at the N terminus, a coiled-coil at the C terminus and two putative TNFR-associated factor (TRAF) binding sites, EEESE (residues 38-42) and EERPA (residues 333-337). Alignment positions with 80-90% or ≥90% physicochemically conserved amino acids are shaded in yellow or green, respectively. The non-synonymous SNP rs33980500 causes a mutation in the protein sequence (position highlighted by red arrow) from D (aspartic acid; negative electrical charge) to N (asparagine; nonpolar). This change in charge at a conserved position might impact the three-dimensional protein structure and hence the function of TRAF3IP2. The mutation is located in a region that is 90% conserved among the different species. The high overall conservation reflects the importance of this N-terminal part of the protein.

HUMAN006296: human; MOUSE005901: house mouse; CANFA009115: dog; RATNO012065: brown rat; BOVIN006826: cattle; PANTR022727: common chimpanzee; MONDO007472: gray short-tailed opossum; MACMU005412: rhesus macaque; LOXAF019754: african bush elephant; RABIT014599: European rabbit; FELCA004587: cat; ERIEU013179: European hedgehog; OTOGA003473: northern greater galago; SPETR007633: thirteen-lined ground squirrel; TUPGB003108: northern treeshrew; MYOLU002126: little brown bat; CAVPO014479: guinea pig; MICMU008608: gray mouse lemur; OCHPR007379: american pika; PONAB005799: Sumatran orangutan; HORSE003723: horse; TURTR008666: common bottlenose dolphin; PTEVA007300: large flying fox; LAMPA005342: guanaco; DIPOR013455: ord's kangaroo rat; CHOHO003637: Hoffmann's two-toed sloth; MACEU012451: tammar wallaby; PIGXX009477: wild boar; CALJA022745: common marmoset

2. Schneider, A., Dessimoz, C. & Gonnet, G.H. OMA Browser--exploring orthologous relations across 352 complete genomes. *Bioinformatics* **23**, 2180-2 (2007).



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HUMAN006296   MAPQLEETRMNRSIPVEVDESEPYPSQLLKPIPEYSPEEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLAN
MOUSE005901   _________MNRSIPVEVDESEPFPSQLLKPIPEYSPEEELEPPAPNTRNMAPSSLSVLQC____________PPLKLAN
CANFA009115   MFALVPETRMNRSVPVEVDESEPYPSQSLKPIPGDSLEEESEPPAPDRGDMAPHGSSAPPAPHCSAGDFSQAHPPLKLSK
RATNO012065   _________MNRSIPVEVDESEPFPSQLLNPIPESSPEEELEPPAPNTRNTAPSSLSVLQR____________PPLKLAN
BOVIN006826   _________MNRSIPVEVDESEPYPSQLLKPLSEYSLAEESELAAPDARNMVPNNLSASPTAQSSSRDFPQAHLPLQLSN
PANTR022727   MPPQLQETRMNRSIPVEVDESEPYPSQLLKPIPEYSLEEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLAN
MONDO007472   V____SETRMNRSIPVEVDESESYPIQLIKLFPEFSLEEEFEPPGPNGGSTAHRGSCPPEACSTPPTDSSPSSKAQGATN
MACMU005412   MPPQLQETRMNRSIPVEVDESEPYPSQLLKPIPEYSLEEESEPPAPNTRNMAPNSLSVPTTPHNSSRDFSQAHATLKLAS
LOXAF019754   _________MNRSIPVEVDESEPYPSQLLKAIPEYSLEEDSEPPAPNLRNMAPTSLSALQTPHYSSGGFTQAHPLLKLAN
RABIT014599   _______TRMSRSIPVEVDESEPYPSQLLKAIPEDSLEAESEPPAPGTRNTAPHGVSAPRTPDGSPGDSAQAPPPLALAS
FELCA004587   TPPL_QETRMNRSIPVEVDESEPYPSHLLKPIPGCSREEASEPPAPNLRNMAPNGLSAPQTPHCSSGDFSQAHPPLKLSN
ERIEU013179   MLPWLQETRMSRSIPVEVDESEPYPSQLLKPSSEYPLEEKSKPPAPNRRHMPPSSLSAA_VLHCSSGDTPQASPPLELLN
OTOGA003473   LPPP_QETRMNRSIPVEVDESEPYPSQLLKPIPEYSLEDDSEPPAPNIRNMAPNSLSVPQTSHYSPGDLSQAAPPLKLAN
SPETR007633   IPH__QETRMNRSIPVEVDESEPYPSQLLKPIPEYSLEEESEPPVPNIGNMAPNSLSAPKDPLHSPGDIPQVHPPLKLAN
TUPGB003108   TPPQLQETRMNRSIPVEVDESEPYPTQLLKPIPEYSLEEESEPPAPDRRNMALNTLSAPKTLHFSSGGLSQAHPALQLAN
MYOLU002126   TPPHLQETTMNRSIPVEVDESEPYPSQLLNSIPEYSLQEGSEPPAPNIRNMAPNGSSAPQTPHHSSEDFSQTPPRLQLVN
CAVPO014479   _________MIRSIPVEVDESEPYPSQLLKPIPEYSLEEESEPPAPNIRNMAPNNLS____________ESAHPLLKLAN
MICMU008608   MTPP_QESRMNRSIPVEVDESEPYPSQLLKPIPEYSLEEESEPPAPNIRNMAPNGLFAAQAPHYSPGDFSPVYPPLKLAN
OCHPR007379   C____QETRMNRSIPVEVDESEPYPSELLKAIPENALEAQSELPAAGTRNVVPQGLWTPRTPYCPRGDSAEV__PLVLVS
PONAB005799   MPPQLQETRMNRSIPVEVDESEPYPSQLLKPIPEYSLEEESEPPAPNIRNMAPNSLSA__MLHNSSGDFSQAHSTLKLAN
HORSE003723   ______ETRMRRSIPVEVDESEPYPSQLLKSIPQYSPEEESEPPAPNIRNMAPNSPSVPQMPHYSSGDFSQAYPPLKLAN
TURTR008666   TPPL_QETRMIRSIPVEVDESEPYPSQLLKPLSEYSLEEESELPAPDTRDMAPNSLSAPQTLHSSSGDFSHTHPTLKLSN
PTEVA007300   TPPL_QETRMNRSIPVEVDESEPYSSQLLKAIPEYSLEKEPEPPAPNIRNMAPNSLSAPQTPYHSSGDFSHVHPRLKLSN
LAMPA005342   TPPL_QETRMNRSIPVEVDESEPYPSQLLKPVSEYSLEGQSEPPAPDTRNMAPNSSSAPQTSHYSSGDFSHAHLPLKLSN
DIPOR013455   VPEC_QATRMNRSIPVEVDESEPYPSQLLKPIPEYSLKEESEPPAPNAKNTPPTSLPAPQALHYVSGDFSQAHPPLKLTS
CHOHO003637   _______TRMNRSIPVEVDESEPYPSQLLQVIPEYSLEEEPEPPAPNPRKMTPNSLSTPKTLHCSSGDFSWAHPPLKLAN
MACEU012451   LPP__QETRMSRSIPVEVDESEPYPIQLMKPFSEYSTEREFEPPGPNEGSVVHSGSYPPEVPASSSILHPPVT__QELTD
PIGXX009477   VFSLVPETRMNRSIPVEVDESEPYPSQLLKPISEHSLEEESEPPAPDTRHMAPNSSSAPQTPCYASGDVAHTHSPLKLSN
CALJA022745   MPPQFQETRMSRSIPVEVDESEPYPSQLLKPIPEYSLEEESEPLAPNIRNMAPNSLSAPTTPLS_____SQAHPTLKLAN
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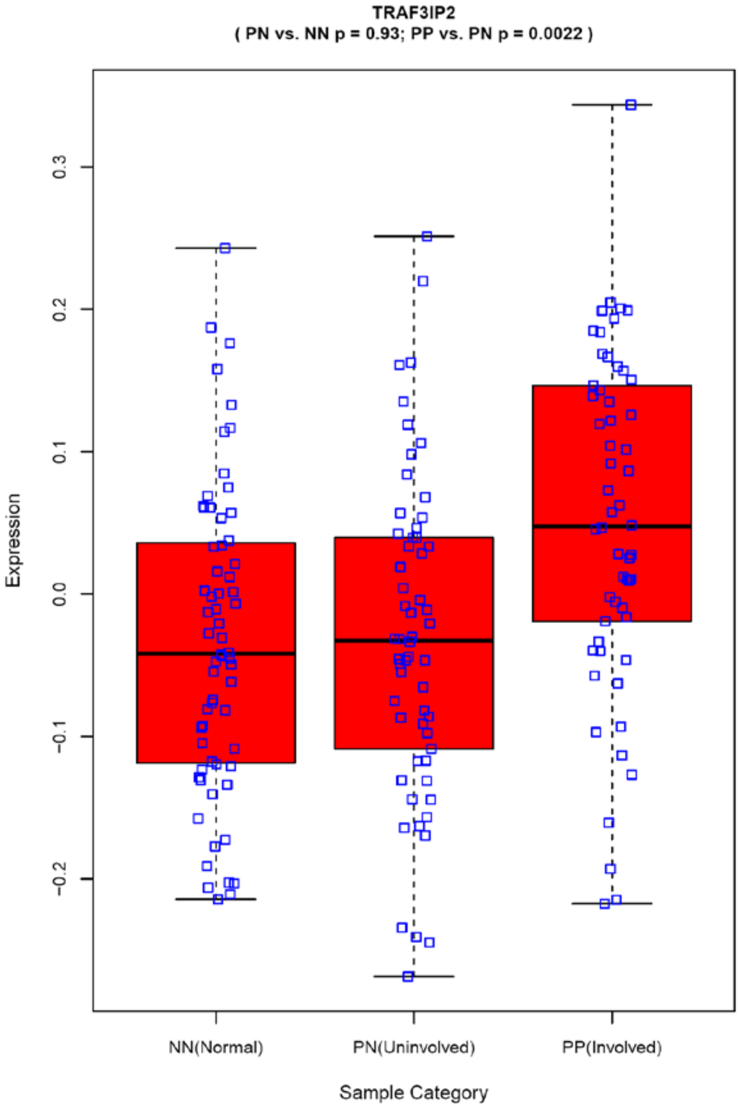
URL: http://omabrowser.org

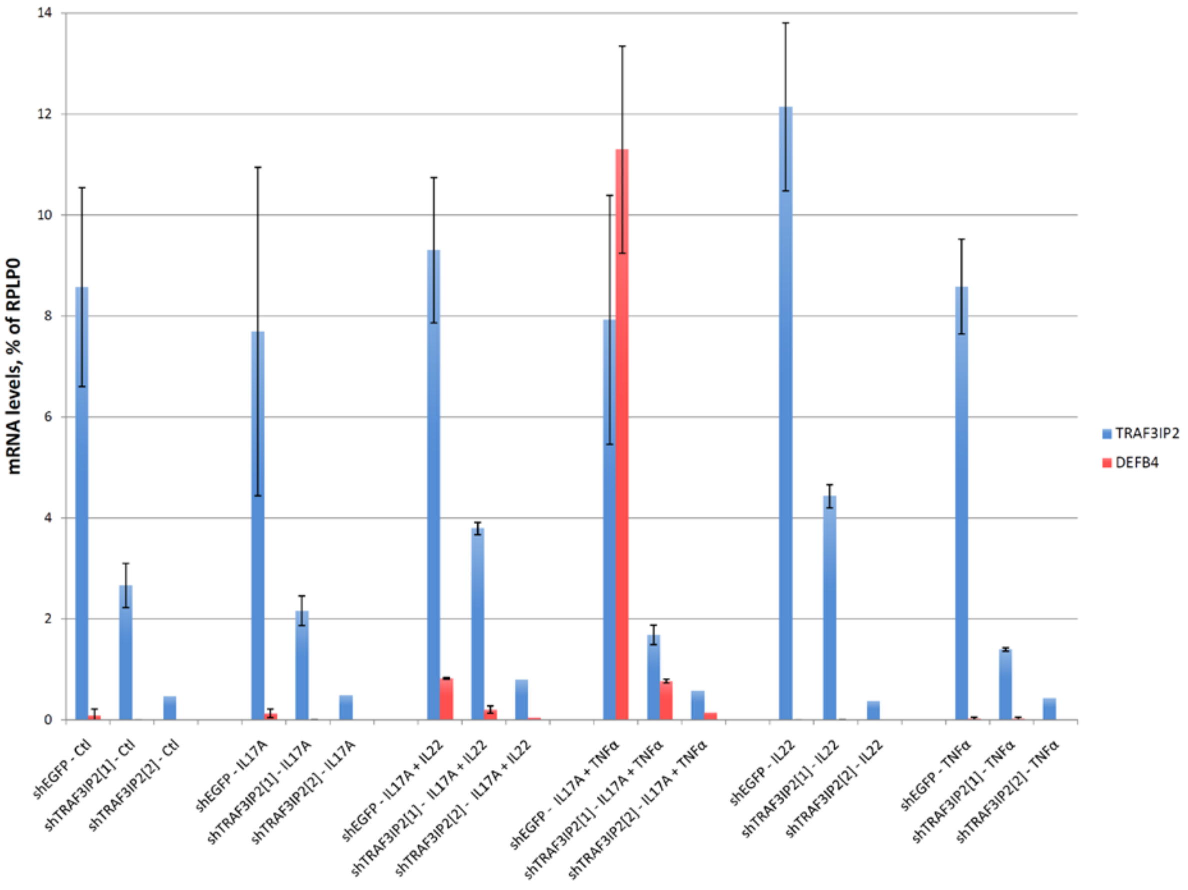
Supplementary Figure 4. Gene expression data for the *TRAF3IP2* locus. Biopsies were taken from psoriasis plaques (PP) and uninvolved skin (PN) of psoriasis patients as well as from normal skin (NN) of healthy controls. The final analysis included 53 psoriatic patients and 57 controls. Study subjects did not use any systemic anti-psoriatic treatments for two weeks prior or topical anti-psoriatic treatments for one week prior to biopsy. Samples were run on Affymetrix U133 Plus 2.0 arrays according to the manufacturer's protocol. The raw data were processed using the robust multi-chip average (RMA) method adjusting the plotted RMA expression levels for batch and gender effects[3]. The plot includes individual measurements as well as box-plots summarizing trait distribution for the transcript. A slightly altered expression level between involved and uninvolved skin of psoriasis patients could be observed for the *TRAF3IP2* locus (P=2.2×10^{-3}).

3. Gudjonsson, J.E. et al. Global gene expression analysis reveals evidence for decreased lipid biosynthesis and increased innate immunity in uninvolved psoriatic skin. *J Invest Dermatol* **129**, 2795-804 (2009).

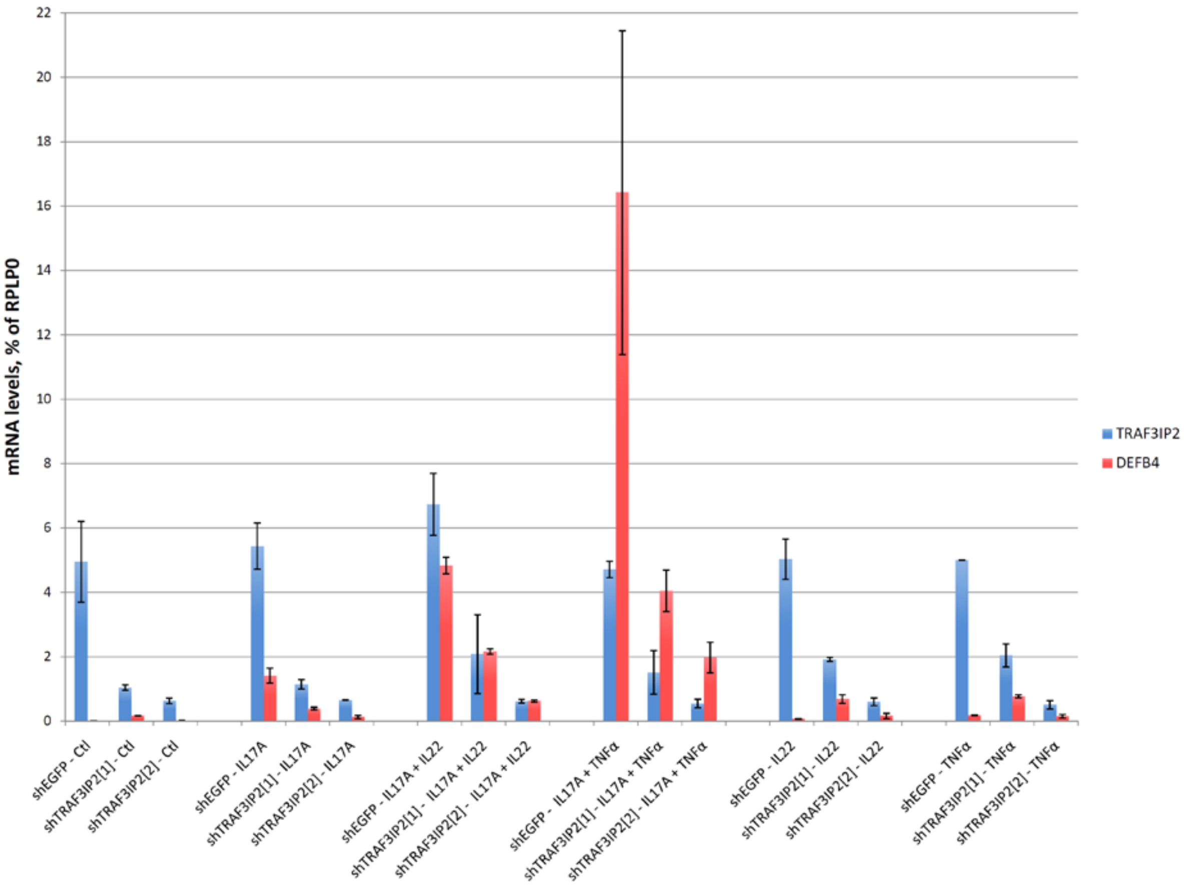


Supplementary Figure 5. *TRAF3IP2* mediated expression of β-defensin 2 in keratinocytes. We silenced *TRAF3IP2* with two different small hairpin RNAs (shRNA) against this gene in **(A)** immortalized N-TERT keratinocytes and in **(B)** normal human keratinocytes (NHK). Both shRNAs caused an unequivocal knockdown of *TRAF3IP2*. We measured the effect of different stimuli (IL-17A, IL-22, TNF-α) on *DEFB4* expression (encoding the protein β-defensin 2; hBD-2) in keratinocytes with non-silenced (shEGFP) and silenced *TRAF3IP2* (shTRAF3IP2[1] and [2]). For both cell lines, IL-17A in combination with TNF-α exclusively induced an increased expression of *DEFB4* in the control cells (shEGFP - IL-17A+TNF-α) while *DEFB4* expression was abrogated in *TRAF3IP2* silenced cells (shTRAF3IP2[1] and [2] - IL-17A+TNF α). Target gene expression was normalized to the control gene *RPLP0* and mRNA levels were expressed as percent of *RPLP0*. The error bars indicate standard deviation (s.d.).

A



B


mRNA levels, % of RPLP0
22
20
18
16
14
12
10
8
6
4
2
0
TRAF3IP2
DEFB4
shEGFP - Ctl
shTRAF3IP2[1] - Ctl
shTRAF3IP2[2] - Ctl
shEGFP - IL17A
shTRAF3IP2[1] - IL17A
shTRAF3IP2[2] - IL17A
shEGFP - IL17A + IL22
shTRAF3IP2[1] - IL17A + IL22
shTRAF3IP2[2] - IL17A + IL22
shEGFP - IL17A + TNFα
shTRAF3IP2[1] - IL17A + TNFα
shTRAF3IP2[2] - IL17A + TNFα
shEGFP - IL22
shTRAF3IP2[1] - IL22
shTRAF3IP2[2] - IL22
shEGFP - TNFα
shTRAF3IP2[1] - TNFα
shTRAF3IP2[2] - TNFα

Supplementary Table 1. Characteristics of cases/control sets used for discovery (panel A) and replication (panels B-F).

	GWAS	Replication				
	Panel A Germany	Panel B Germany	Panel C USA (CASP)	Panel D Canada (Genizon)	Panel E* University of Michigan	Panel F* Canada
controls/cases *before* QC	1161/487	1832/690	1412/1375	996/765	1661/1987	1090/1282
controls/cases *after* QC	1146/472	1824/681	1322/1303	994/762	1661/1987	1090/1282
Sex distribution; % Female						
controls	57	59	54	68	60	52
cases	47	43	51	43	54	45
Age distribution; mean age (years)						
at sampling **controls**	53±14.6	39±12.4	40±17.0	58±16.0	45±18.0	54±15.6
at sampling **cases**	44±14.4	48±16.3[a]	49±15.6	45±13.0	50±19.0	45±13.4
at onset	24±14.6	29±17.3[b]	26±14.5	26±7.5	29±17.6	29±15.2
Disease extent						
Psoriatic Arthritis; %	8	15[c]	26	18	19	67
Family Psoriasis; %	31	32[d]	55	NA	57	46
IBD; %	NA	NA	4	1	3	3

*Only genotyped for rs13210247 and rs33980500. NA: data not available. Number of samples with missing data (if above 10% of the respective fraction): a 81, b 125, c 183, d 109.

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Supplementary Table 2. Association results of replication. The top 147 SNPs were selected for follow-up from the GWAS panel A. These SNPs were genotyped in the German replication case-control panel B. With the American (CASP) and the French-Canadian (Genizon) case-control panels C and D, respectively, an *in silico* replication was performed. SNPs are ranked according to their *P*-values obtained in the initial GWAS. Positions (**Pos. (bp)**) are in NCBI's build 36. The number of cases and controls is shown in the top column of each subtable. **Chr.**: Chromosome. **A1** denotes the rarer allele, while **A2** is the more common allele in the GWAS analysis. $\mathbf{AF_{A1}}$, the allele frequency of the rarer allele, is shown for cases and for controls, respectively. In the same column, in each case below the allele frequency, the absolute genotype counts are shown **(11/12/22)**, corresponding to A1A1/A1A2/A2A2. $\boldsymbol{P_{\mathrm{CCA}}}$ denotes the *P*-value of a Pearsons's χ^2-test for alleles (one degree of freedom). ***LRP*** is the corresponding likelihood ratio *P*-value. The odds ratio (**OR**) and the 95% confidence interval (**95% CI**) are listed for carriership of the rarer allele A1. The combined *P*-value of the meta-analysis and the direction of the effect (**Direction**) are shown for the independent replication panels B to D ($\boldsymbol{P_{\mathrm{repl.}}}$) as well as for the GWAS-panel and the independent replication panels together (panels A-D; $\boldsymbol{P_{\mathrm{comb.}}}$). Significant *P*-values of the combined analysis of panels B-D ($P_{\mathrm{repl.}}<0.05$) are highlighted in bold italic. The *TRAF3IP2* lead SNP is highlighted by grey shading. For those SNPs that failed quality control in the replication, the according table cells are left blank.

				Panel A – GWAS **Germany** 472 cases 1146 controls					**Panel B** **Germany** 681cases 1824 controls		**Panel C** **CASP** 1303 cases 1322 controls		**Panel D** **Genizon** 762 cases 994 controls		**Panel B - D** **(replication only)** **Combined analysis** 2746 cases 4140 controls		**Panel A - D** **(GWAS & replication)** **Combined analysis** 3218 cases 5286 controls	
Chr Pos. (bp)	**dbSNP ID**	**Nearby genes (relative position)**	**A1 A2**	**AF$_{A1}$ (11/12/22) Case**	**AF$_{A1}$ (11/12/22) Control**	P_{CCA}	***LRP***	**OR (95% CI)**	**AF$_{A1}$ (11/12/22) Case**	**AF$_{A1}$ (11/12/22) Control**	**AF$_{A1}$ (11/12/22) Case**	**AF$_{A1}$ (11/12/22) Control**	**AF$_{A1}$ (11/12/22) Case**	**AF$_{A1}$ (11/12/22) Control**	$P_{repl.}$	**Direction**	$P_{comb.}$	**Direction**
5 158,692,478	rs2546890	*IL12B* (within gene)	G A	0.36 (61/215/196)	0.46 (244/566/336)	8.83×10^{-08}	7.17×10^{-08}	0.65 (0.56-0.76)	0.38 (88/270/211)	0.44 (364/847/578)	0.42 (–/–/–)	0.49 (–/–/–)	0.45 (151/380/230)	0.53 (279/487/228)	***9.07×10^{-15}***	---	1.29×10^{-20}	----
1 10,914,691	rs2387698	*C1orf127* (± 20 kb)	A G	0.35 (54/219/199)	0.44 (216/581/349)	4.50×10^{-07}	4.21×10^{-07}	0.67 (0.57-0.78)	0.41 (89/277/200)	0.42 (290/943/576)	—	—	0.39 (115/365/281)	0.38 (156/443/393)	0.78	-?+	3.92×10^{-03}	--?+
11 26,561,907	rs12295638	*TMEM16C* (within gene)	C T	0.14 (10/116/346)	0.09 (8/186/952)	1.84×10^{-06}	4.16×10^{-06}	1.75 (1.39-2.2)	0.08 (6/77/487)	0.09 (12/296/1476)	0.10 (12/237/1027)	0.11 (19/242/1060)	0.10 (5/140/616)	0.09 (7/175/812)	0.53	--+	0.13	+--+
1 235,345,148	rs2485558	*RYR2* (within gene)	G C	0.31 (52/194/226)	0.24 (58/423/665)	2.81×10^{-06}	4.83×10^{-06}	1.49 (1.26-1.76)	0.24 (36/207/328)	0.23 (93/628/1077)	0.23 (–/–/–)	0.21 (–/–/–)	0.26 (–/–/–)	0.24 (–/–/–)	***0.01***	+++	1.53×10^{-05}	++++
18 32,217,202	rs9963077	*FHOD3* (within gene)	C T	0.33 (51/207/214)	0.41 (202/543/401)	3.55×10^{-06}	6.53×10^{-06}	0.69 (0.59-0.81)	0.38 (94/248/230)	0.37 (238/841/719)	0.38 (–/–/–)	0.39 (–/–/–)	0.37 (–/–/–)	0.39 (–/–/–)	0.81	+--	0.025	-+--
6 127,635,257	rs1013640	*RNF146* (within gene)	A G	0.06 (1/54/417)	0.03 (0/60/1086)	4.55×10^{-06}	—	2.34 (1.61-3.39)	0.03 (0/29/545)	0.03 (2/101/1693)	—	—	0.02 (0/31/731)	0.03 (1/53/940)	0.16	-?-	0.22	+-?-
17 21,641,670	rs17052344	gene desert	A G	0.30 (41/201/230)	0.22 (53/407/686)	5.23×10^{-06}	1.11×10^{-11}	1.48 (1.25-1.76)	0.22 (33/196/343)	0.21 (77/602/1117)	0.23 (70/444/761)	0.23 (71/457/788)	0.25 (–/–/–)	0.23 (–/–/–)	0.20	+++	1.71×10^{-03}	++++
11 26,613,666	rs12577224	*TMEM16C* (within gene)	T C	0.21 (18/159/295)	0.28 (93/464/589)	5.88×10^{-06}	4.33×10^{-06}	0.66 (0.55-0.79)	0.27 (44/226/300)	0.28 (129/730/935)	0.27 (–/–/–)	0.29 (–/–/–)	0.70 (–/–/–)	0.70 (–/–/–)	0.34	---	4.68×10^{-03}	----
2 13,022,673	rs16859555	gene desert	A G	0.13 (12/96/364)	0.08 (7/161/978)	6.14×10^{-06}	4.58×10^{-05}	1.75 (1.37-2.24)	0.09 (1/96/476)	0.09 (21/292/1476)	0.10 (–/–/–)	0.10 (–/–/–)	0.10 (7/141/614)	0.11 (10/200/782)	0.75	-+-	0.09	+-+-
7 71,142,370	rs10280768	*CALN1* (within gene)	G T	0.24 (21/183/268)	0.32 (112/502/532)	6.30×10^{-06}	6.07×10^{-06}	0.67 (0.56-0.8)	0.30 (56/239/277)	0.31 (167/783/853)	0.28 (–/–/–)	0.28 (–/–/–)	0.32 (–/–/–)	0.29 (–/–/–)	0.74	--+	0.09	---+
11 26,649,543	rs7101498	*SLC5A12* (within gene)	C T	0.30 (48/187/237)	0.22 (65/385/696)	6.83×10^{-06}	1.55×10^{-05}	1.48 (1.25-1.75)	0.22 (26/193/356)	0.22 (89/603/1101)	0.32 (–/–/–)	0.31 (–/–/–)	0.31 (–/–/–)	0.30 (–/–/–)	0.15	+++	1.14×10^{-03}	++++
5 158,705,160	rs953861	*IL12B* (± 20 kb)	G A	0.23 (26/165/281)	0.17 (31/317/798)	1.60×10^{-05}	2.73×10^{-05}	1.51 (1.25-1.82)	0.22 (28/198/347)	0.18 (46/559/1217)	0.22 (–/–/–)	0.17 (–/–/–)	0.21 (29/256/477)	0.14 (24/239/731)	***6.50×10^{-14}***	+++	6.21×10^{-18}	++++
6 40,833,805	rs9380990	gene desert	T C	0.29 (41/194/237)	0.22 (62/381/703)	1.03×10^{-05}	2.60×10^{-05}	1.47 (1.24-1.74)	0.24 (35/203/337)	0.25 (108/661/1020)	0.25 (–/–/–)	0.24 (–/–/–)	0.19 (–/–/–)	0.23 (–/–/–)	0.47	-+-	0.20	+-+-
7 87,765,328	rs10263111	*STEAP4* (within gene)	C G	0.39 (72/221/179)	0.47 (256/567/323)	1.32×10^{-05}	1.62×10^{-05}	0.71 (0.61-0.83)	0.45 (118/276/174)	0.43 (328/875/582)	0.45 (–/–/–)	0.48 (–/–/–)	0.53 (–/–/–)	0.50 (–/–/–)	0.82	+-+	0.09	-+-+
15 48,159,823	rs7177318	*ATP8B4* (within gene)	A G	0.32 (53/201/218)	0.41 (192/546/408)	1.64×10^{-05}	1.98×10^{-05}	0.70 (0.6-0.83)	0.38 (79/271/216)	0.40 (288/869/632)	0.40 (–/–/–)	0.40 (–/–/–)	0.44 (146/373/243)	0.42 (166/497/331)	0.59	--+	0.018	---+
6 1,388,897	rs9501722	*FOXF2* (± 50 kb)	G A	0.48 (116/219/137)	0.40 (180/548/418)	1.82×10^{-05}	3.11×10^{-05}	1.40 (1.2-1.63)	0.42 (97/299/171)	0.43 (336/868/586)	0.42 (220/633/422)	0.44 (256/657/407)	0.42 (–/–/–)	0.43 (–/–/–)	0.10	---	0.70	+---
6 161,889,299	rs17651312	*PARK2* (within gene)	A G	0.13 (4/115/353)	0.08 (3/180/963)	1.83×10^{-05}	8.17×10^{-06}	1.69 (1.33-2.15)	0.10 (7/101/464)	0.09 (21/286/1489)	0.10 (–/–/–)	0.11 (–/–/–)	0.07 (–/–/–)	0.07 (–/–/–)	0.86	+-+	0.09	++-+
17 50,205,854	rs2958907	gene desert	C T	0.12 (8/94/370)	0.18 (33/341/772)	1.92×10^{-05}	9.12×10^{-06}	0.61 (0.49-0.77)	0.17 (20/158/396)	0.16 (35/512/1241)	0.18 (–/–/–)	0.17 (–/–/–)	0.16 (–/–/–)	0.18 (–/–/–)	0.99	++-	0.06	-++-
6 149,198,304	rs17663626	*UST* (within gene)	T C	0.14 (7/117/348)	0.09 (11/182/953)	1.98×10^{-05}	3.59×10^{-05}	1.66 (1.31-2.09)	0.10 (7/100/463)	0.10 (23/323/1446)	0.10 (19/218/1042)	0.10 (21/232/1069)	0.11 (7/156/599)	0.11 (9/200/785)	0.87	+-+	0.09	++-+
1 201,340,419	rs3898276	*MYOG* (± 20 kb)	C A	0.11 (5/94/373)	0.07 (4/142/1000)	2.01×10^{-05}	3.07×10^{-05}	1.76 (1.35-2.29)	0.08 (2/79/486)	0.07 (3/254/1535)	—	—	0.08 (5/119/638)	0.08 (5/149/840)	0.42	+?+	3.38×10^{-03}	++?+
10 125,929,581	rs10901570	gene desert	T C	0.16 (7/135/330)	0.22 (61/393/692)	2.03×10^{-05}	3.12×10^{-05}	0.65 (0.53-0.79)	0.20 (23/188/365)	0.20 (76/555/1165)	0.22 (–/–/–)	0.20 (–/–/–)	0.18 (–/–/–)	0.19 (–/–/–)	0.56	++-	0.18	-++-
17 37,799,296	rs11079043	*PTRF, STAT3* (± 10 kb)	T C	0.29 (35/204/233)	0.22 (53/398/695)	2.11×10^{-05}	7.17×10^{-08}	1.45 (1.22-1.72)	0.28 (46/239/283)	0.28 (140/722/930)	0.22 (–/–/–)	0.22 (–/–/–)	0.22 (–/–/–)	0.23 (–/–/–)	0.91	++-	0.08	+++-
16 48,151,027	rs746158	*ZNF423* (within gene)	C T	0.41 (76/233/163)	0.49 (281/560/305)	2.44×10^{-05}	4.21×10^{-07}	0.72 (0.62-0.84)	0.46 (120/288/156)	0.45 (370/860/553)	0.47 (276/658/343)	0.47 (290/669/361)	0.44 (143/387/232)	0.45 (196/508/290)	0.78	++-	0.11	-++-
18 23,678,519	rs4401120	gene desert	G C	0.18 (16/142/314)	0.25 (74/432/640)	2.75×10^{-05}	4.16×10^{-06}	0.67 (0.55-0.81)	0.25 (29/224/319)	0.24 (99/668/1030)	0.27 (–/–/–)	0.27 (–/–/–)	0.31 (–/–/–)	0.31 (–/–/–)	0.80	+++	0.11	-+++
14 34,908,987	rs2145623	*NFKBIA* (± 50 kb)	C G	0.34 (45/233/194)	0.27 (87/444/615)	3.01×10^{-05}	4.83×10^{-06}	1.41 (1.2-1.66)	0.33 (52/253/260)	0.30 (174/714/903)	0.30 (108/553/612)	0.28 (84/561/671)	0.28 (–/–/–)	0.26 (–/–/–)	***2.29×10^{-03}***	+++	5.01×10^{-06}	++++
12 53,346,493	rs7960640	*DCD* (± 20 kb)	T C	0.12 (5/105/362)	0.08 (4/165/977)	3.04×10^{-05}	6.53×10^{-06}	1.69 (1.32-2.17)	0.08 (7/87/481)	0.09 (10/295/1485)	0.10 (12/223/1038)	0.09 (9/232/1076)	0.10 (–/–/–)	0.10 (–/–/–)	0.86	-+-	0.10	+-+-

				Panel A – GWAS **Germany** 472 cases 1146 controls					**Panel B** **Germany** 681cases 1824 controls		**Panel C** **CASP** 1303 cases 1322 controls		**Panel D** **Genizon** 762 cases 994 controls		**Panel B - D** **(replication only)** **Combined analysis** 2746 cases 4140 controls		**Panel A - D** **(GWAS & replication)** **Combined analysis** 3218 cases 5286 controls	
Chr Pos. (bp)	**dbSNP ID**	**Nearby genes (relative position)**	**A1 A2**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**P_{CCA}**	***LRP***	**OR (95% CI)**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**$P_{repl.}$**	**Direction**	**$P_{comb.}$**	**Direction**
11 97,645,772	rs1941784	gene desert	A C	0.42 (82/229/161)	0.34 (127/526/493)	3.06×10^{-05}	—	1.39 (1.19-1.62)	0.39 (92/253/229)	0.38 (257/849/699)	0.37 (–/–/–)	0.39 (–/–/–)	0.41 (–/–/–)	0.41 (–/–/–)	0.52	+-+	0.22	++-+
3 141,446,665	rs4234484	*CLSTN2* (within gene)	T A	0.02 (0/21/451)	0.06 (1/126/1019)	3.10×10^{-05}	2.56×10^{-06}	0.38 (0.24-0.61)	0.03 (1/30/543)	0.03 (1/96/1706)	0.04 (–/–/–)	0.03 (–/–/–)	0.03 (1/39/694)	0.03 (1/54/927)	0.12	++-	0.67	-++-
9 9,041,277	rs324459	*PTPRD* (within gene)	A T	0.28 (35/198/239)	0.36 (153/516/477)	3.15×10^{-05}	1.11×10^{-11}	0.70 (0.6-0.83)	0.33 (64/256/251)	0.33 (199/796/807)	0.34 (–/–/–)	0.33 (–/–/–)	0.35 (–/–/–)	0.37 (–/–/–)	0.73	-+-	0.03	--+-
7 27,235,373	rs12700794	*EVX1* (± 20 kb)	A C	0.23 (20/176/276)	0.17 (36/314/796)	3.18×10^{-05}	4.33×10^{-06}	1.48 (1.23-1.79)	0.19 (15/181/371)	0.17 (54/505/1228)	0.20 (52/412/813)	0.20 (46/424/852)	0.15 (–/–/–)	0.17 (–/–/–)	0.77	++-	0.038	+++-
5 17,522,464	rs2459789	gene desert	T C	0.22 (22/168/282)	0.16 (29/314/803)	3.61×10^{-05}	4.58×10^{-05}	1.49 (1.23-1.8)	0.18 (16/176/383)	0.17 (59/505/1255)	0.20 (–/–/–)	0.19 (–/–/–)	0.21 (35/257/470)	0.21 (42/343/609)	0.56	++-	0.02	+++-
3 102,020,586	rs9879088	*ABI3BP* (within gene)	A G	0.42 (78/243/151)	0.35 (146/505/495)	4.25×10^{-05}	1.55×10^{-05}	1.38 (1.18-1.61)	0.37 (86/239/238)	0.36 (225/830/725)	0.36 (144/625/508)	0.35 (166/602/553)	0.37 (107/345/310)	0.35 (123/456/415)	0.29	+++	6.34×10^{-03}	++++
6 161,899,254	rs6901951	*PARK2* (within gene)	G A	0.18 (13/142/317)	0.12 (13/255/878)	4.25×10^{-05}	2.73×10^{-05}	1.54 (1.25-1.9)	0.16 (16/162/399)	0.16 (52/473/1278)	0.16 (31/351/891)	0.16 (33/363/921)	0.12 (–/–/–)	0.13 (–/–/–)	0.92	+--	0.09	++--
7 50,249,131	rs12669163	gene desert	C A	0.27 (37/182/253)	0.21 (43/387/716)	4.59×10^{-05}	2.60×10^{-05}	1.44 (1.21-1.71)	0.23 (31/191/346)	0.23 (102/619/1067)	—	—	0.23 (38/271/453)	0.21 (49/327/617)	0.70	-?+	0.01	+-?+
8 117,643,793	rs6988499	gene desert	C T	0.41 (83/225/164)	0.34 (142/493/511)	4.63×10^{-05}	1.62×10^{-05}	1.38 (1.18-1.61)	0.34 (66/259/247)	0.35 (207/852/739)	0.34 (144/575/555)	0.33 (156/568/596)	0.34 (–/–/–)	0.31 (–/–/–)	0.43	-++	0.01	+-++
5 31,868,376	rs12697261	*PDZD2* (within gene)	T C	0.49 (116/231/125)	0.41 (184/573/389)	4.75×10^{-05}	2.31×10^{-06}	1.37 (1.18-1.6)	0.42 (99/275/198)	0.44 (358/875/560)	0.46 (–/–/–)	0.45 (–/–/–)	0.45 (–/–/–)	0.45 (–/–/–)	0.81	-++	0.12	+-++
6 2,958,487	rs9378759	*NQO2* (within gene)	T C	0.27 (42/171/259)	0.20 (48/373/725)	4.81×10^{-05}	3.23×10^{-05}	1.44 (1.21-1.71)	0.23 (28/200/334)	0.21 (80/608/1107)	0.20 (–/–/–)	0.20 (–/–/–)	0.22 (–/–/–)	0.24 (–/–/–)	0.73	+--	0.14	++--
21 27,236,500	rs2830590	*ADAMTS5* (within gene)	C T	0.23 (23/173/276)	0.30 (100/491/555)	4.89×10^{-05}	1.98×10^{-05}	0.70 (0.58-0.83)	0.28 (40/236/293)	0.27 (125/718/962)	0.26 (87/473/709)	0.25 (88/491/733)	0.25 (–/–/–)	0.26 (–/–/–)	0.92	++-	0.06	-++-
15 48,094,708	rs2899446	*ATP8B4* (within gene)	G A	0.46 (93/247/132)	0.38 (166/541/439)	4.90×10^{-05}	3.11×10^{-05}	1.37 (1.18-1.6)	0.44 (106/299/166)	0.41 (311/855/619)	0.39 (179/625/469)	0.41 (199/664/450)	0.37 (106/344/308)	0.37 (129/474/389)	0.87	+--	0.06	++--
6 133,959,061	rs2636605	gene desert	C G	0.30 (44/199/229)	0.38 (168/535/443)	4.91×10^{-05}	8.17×10^{-06}	0.72 (0.61-0.84)	0.36 (75/239/239)	0.35 (219/826/738)	0.36 (140/592/514)	0.37 (186/579/529)	0.38 (–/–/–)	0.36 (–/–/–)	0.88	+-+	0.06	-+-+
18 53,938,048	rs4940643	*NEDD4L* (within gene)	A G	0.10 (6/84/382)	0.06 (8/123/1015)	5.00×10^{-05}	9.12×10^{-06}	1.75 (1.33-2.29)	0.08 (1/82/491)	0.08 (10/256/1520)	—	—	0.05 (4/83/675)	0.06 (7/129/858)	0.35	-?-	0.18	+-?-
7 146,170,289	rs2727632	*CNTNAP2* (within gene)	A C	0.39 (74/217/181)	0.47 (249/569/328)	5.52×10^{-05}	3.59×10^{-05}	0.73 (0.62-0.85)	0.43 (122/247/201)	0.45 (347/900/537)	0.43 (232/630/412)	0.43 (218/688/413)	0.45 (154/374/234)	0.42 (173/488/333)	0.58	-++	0.21	--++
2 65,660,531	rs1641488	gene desert	C T	0.16 (12/129/331)	0.22 (58/398/690)	5.66×10^{-05}	3.07×10^{-05}	0.67 (0.55-0.81)	0.16 (22/169/474)	0.19 (76/512/1205)	0.20 (60/364/818)	0.22 (71/386/824)	0.21 (33/235/463)	0.20 (52/297/630)	0.05	--+	4.57×10^{-04}	---+
18 2,400,483	rs11873219	gene desert	G T	0.14 (12/110/350)	0.09 (12/192/942)	5.99×10^{-05}	3.12×10^{-05}	1.60 (1.27-2.01)	0.10 (5/99/470)	0.10 (19/335/1435)	0.12 (–/–/–)	0.12 (–/–/–)	0.12 (–/–/–)	0.12 (–/–/–)	0.53	--+	0.23	+--+
15 65,481,820	rs11071951	*IQCH* (within gene)	C T	0.54 (134/239/99)	0.46 (243/570/333)	6.26×10^{-05}	3.20×10^{-05}	1.36 (1.17-1.59)	0.49 (131/284/148)	0.48 (442/824/503)	0.47 (–/–/–)	0.49 (–/–/–)	0.46 (153/393/212)	0.46 (208/491/293)	0.51	+-+	0.25	++-+
22 26,290,673	rs881459	gene desert	A G	0.45 (83/258/131)	0.37 (149/559/438)	6.45×10^{-05}	—	1.37 (1.17-1.59)	0.43 (124/328/216)	0.43 (337/853/596)	0.42 (–/–/–)	0.42 (–/–/–)	0.38 (104/349/274)	0.36 (127/452/399)	0.35	+++	9.81×10^{-03}	++++
3 78,753,263	rs17016412	*ROBO1* (within gene)	C A	0.30 (49/188/235)	0.24 (58/426/662)	6.50×10^{-05}	1.08×10^{-04}	1.41 (1.19-1.67)	0.26 (41/227/298)	0.25 (109/692/991)	0.24 (78/452/749)	0.23 (66/466/790)	0.22 (–/–/–)	0.21 (–/–/–)	0.23	+++	4.65×10^{-03}	++++
2 206,521,473	rs4675571	*FLJ20309* (± 50 kb)	G A	0.13 (9/104/359)	0.19 (48/337/761)	6.64×10^{-05}	3.71×10^{-05}	0.65 (0.52-0.8)	0.17 (18/164/383)	0.17 (47/508/1230)	0.15 (27/316/905)	0.15 (28/348/930)	0.16 (25/191/546)	0.17 (28/276/690)	0.75	++-	0.04	-+--
2 97,701,111	rs11687510	*ZAP7* (within gene)	T C	0.43 (77/250/145)	0.35 (145/521/480)	6.89×10^{-05}	4.46×10^{-05}	1.37 (1.17-1.6)	0.42 (103/263/200)	0.40 (304/831/645)	0.32 (–/–/–)	0.33 (–/–/–)	0.34 (82/356/322)	0.33 (112/440/442)	0.95	+-+	0.09	++-+
7 81,613,491	rs10954664	*CACNA2D1* (within gene)	C T	0.48 (108/236/128)	0.40 (185/556/405)	6.98×10^{-05}	8.41×10^{-05}	1.36 (1.17-1.59)	0.42 (87/299/183)	0.42 (322/860/602)	0.43 (–/–/–)	0.41 (–/–/–)	0.43 (143/368/250)	0.43 (183/484/327)	0.34	-++	9.65×10^{-03}	+-++
6 1,369,361	rs4317453	*FOXF2* (± 50 kb)	A G	0.42 (84/231/157)	0.35 (135/525/486)	7.07×10^{-05}	—	1.37 (1.17-1.6)	0.34 (64/268/239)	0.36 (239/790/757)	0.35 (162/572/540)	0.36 (170/611/537)	0.34 (84/315/334)	0.36 (116/424/441)	0.27	---	0.46	+---
6 1,363,159	rs9392288	*FOXF2* (± 50 kb)	A G	0.36 (53/232/187)	0.43 (219/557/370)	7.17×10^{-05}	5.11×10^{-05}	0.73 (0.62-0.85)	0.45 (108/293/173)	0.42 (320/858/595)	0.42 (–/–/–)	0.41 (–/–/–)	0.47 (177/367/218)	0.44 (190/491/313)	***0.018***	+++	0.69	-+++

				Panel A – GWAS **Germany** 472 cases 1146 controls					**Panel B** **Germany** 681cases 1824 controls		**Panel C** **CASP** 1303 cases 1322 controls		**Panel D** **Genizon** 762 cases 994 controls		**Panel B - D** **(replication only)** **Combined analysis** 2746 cases 4140 controls		**Panel A - D** **(GWAS & replication)** **Combined analysis** 3218 cases 5286 controls	
Chr Pos. (bp)	**dbSNP ID**	**Nearby genes (relative position)**	**A1 A2**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**P_{CCA}**	***LRP***	**OR (95% CI)**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**$P_{repl.}$**	**Direction**	**$P_{comb.}$**	**Direction**
2 97,711,518	rs6714710	*ZAP70* (within gene)	T G	0.42 (75/249/148)	0.50 (298/549/299)	7.19×10^{-05}	6.61×10^{-05}	0.73 (0.63-0.86)	0.46 (116/281/167)	0.45 (367/911/540)	0.51 (330/620/312)	0.49 (307/668/331)	0.51 (184/397/181)	0.52 (261/509/224)	0.67	++-	0.18	-++-
9 117,558,071	rs7874534	gene desert	T C	0.45 (97/231/144)	0.38 (172/519/455)	7.36×10^{-05}	1.38×10^{-04}	1.36 (1.17-1.59)	0.42 (95/285/189)	0.42 (277/936/575)	—	—	0.39 (121/350/290)	0.39 (154/474/366)	0.97	+?-	0.04	++?-
6 73,294,472	rs16882514	gene desert	C T	0.06 (0/60/412)	0.03 (0/75/1071)	7.45×10^{-05}	8.43×10^{-05}	2.00 (1.41-2.83)	0.05 (0/60/514)	0.05 (6/157/1636)	0.05 (–/–/–)	0.05 (–/–/–)	0.06 (–/–/–)	0.06 (–/–/–)	0.29	+++	7.20×10^{-03}	++++
10 69,328,657	rs10997866	*SIRT1* (within gene)	A G	0.39 (67/233/172)	0.32 (118/488/540)	7.46×10^{-05}	1.34×10^{-04}	1.37 (1.17-1.61)	0.39 (99/247/230)	0.37 (239/856/697)	0.34 (–/–/–)	0.34 (–/–/–)	0.34 (–/–/–)	0.34 (–/–/–)	0.26	+++	6.16×10^{-03}	++++
7 101,444,622	rs1060697	*CUX1* (within gene)	T C	0.16 (12/128/332)	0.22 (62/387/697)	7.84×10^{-05}	5.90×10^{-05}	0.67 (0.55-0.82)	0.17 (17/160/387)	0.20 (72/577/1136)	0.21 (–/–/–)	0.20 (–/–/–)	0.17 (23/217/522)	0.18 (39/271/684)	0.19	-+-	3.79×10^{-03}	--+-
4 156,237,223	rs7663039	gene desert	T C	0.23 (23/170/279)	0.30 (95/491/560)	7.92×10^{-05}	1.91×10^{-05}	0.70 (0.59-0.84)	0.26 (40/205/328)	0.27 (133/691/976)	—	—	0.28 (–/–/–)	0.29 (–/–/–)	0.45	-?-	6.73×10^{-03}	--?-
20 8,515,519	rs6086518	*PLCB1* (within gene)	G A	0.30 (50/189/233)	0.38 (160/546/440)	7.94×10^{-05}	1.04×10^{-04}	0.72 (0.61-0.85)	0.33 (62/251/254)	0.35 (233/792/754)	0.35 (147/606/525)	0.35 (170/576/572)	0.38 (116/352/294)	0.35 (126/453/415)	0.89	-++	0.11	--++
3 24,568,239	rs17543143	gene desert	G A	0.06 (0/61/411)	0.03 (0/77/1069)	8.03×10^{-05}	—	1.98 (1.4-2.79)	0.07 (3/74/496)	0.07 (12/242/1547)	—	—	—	—	0.44	-??	0.06	+-??
6 5,324,227	rs2432749	*FARS2* (within gene)	C T	0.45 (94/241/137)	0.38 (160/551/435)	8.09×10^{-05}	6.37×10^{-05}	1.36 (1.17-1.59)	0.42 (101/283/192)	0.44 (371/851/586)	0.42 (230/618/429)	0.42 (234/651/437)	0.41 (127/364/270)	0.43 (179/492/321)	0.12	---	0.75	+---
6 112,029,413	rs13210247	*TRAF3IP2* (within gene)	G A	0.10 (9/81/382)	0.06 (6/135/1005)	8.17×10^{-05}	2.83×10^{-04}	1.70 (1.3-2.22)	0.09 (7/90/472)	0.07 (11/228/1559)	0.91 (–/–/–)	0.93 (–/–/–)	0.09 (–/–/–)	0.07 (–/–/–)	***6.25×10^{-06}***	+++	7.31×10^{-09}	++++
4 107,603,066	rs17036750	gene desert	C T	0.05 (1/43/428)	0.02 (1/48/1097)	8.22×10^{-05}	7.45×10^{-04}	2.24 (1.48-3.37)	0.04 (0/36/542)	0.03 (2/107/1700)	0.02 (–/–/–)	0.03 (–/–/–)	0.02 (–/–/–)	0.02 (–/–/–)	0.90	+--	0.11	++--
2 120,877,872	rs12623934	gene desert	G A	0.21 (20/153/299)	0.15 (19/304/823)	8.37×10^{-05}	1.22×10^{-04}	1.48 (1.22-1.79)	0.18 (23/161/387)	0.19 (65/537/1187)	0.18 (–/–/–)	0.17 (–/–/–)	0.16 (17/216/529)	0.18 (32/298/664)	0.79	-+-	0.14	+-+-
8 3,410,499	rs13248151	*CSMD1* (within gene)	A G	0.31 (50/192/230)	0.38 (166/546/434)	8.45×10^{-05}	9.36×10^{-05}	0.72 (0.62-0.85)	0.35 (74/252/247)	0.36 (244/802/750)	0.36 (–/–/–)	0.37 (–/–/–)	0.43 (–/–/–)	0.39 (–/–/–)	0.74	--+	0.16	---+
12 127,258,873	rs10847569	gene desert	A C	0.43 (91/221/160)	0.35 (136/539/471)	8.70×10^{-05}	9.91×10^{-05}	1.36 (1.17-1.59)	0.36 (71/261/235)	0.36 (220/847/733)	0.36 (–/–/–)	0.36 (–/–/–)	0.35 (–/–/–)	0.35 (–/–/–)	0.58	+++	0.027	++++
10 22,907,844	rs2031620	*PIP4K2A* (within gene)	T C	0.42 (80/232/160)	0.34 (145/498/503)	8.89×10^{-05}	1.08×10^{-04}	1.36 (1.17-1.59)	0.38 (78/279/216)	0.36 (240/825/737)	0.39 (–/–/–)	0.39 (–/–/–)	0.37 (–/–/–)	0.35 (–/–/–)	0.11	+++	1.60×10^{-03}	++++
20 52,207,834	rs1570669	*CYP24A1* (within gene)	G A	0.30 (43/199/230)	0.37 (158/538/450)	9.48×10^{-05}	1.14×10^{-04}	0.72 (0.62-0.85)	0.35 (77/244/254)	0.36 (238/806/746)	0.36 (183/558/537)	0.33 (154/571/596)	0.36 (–/–/–)	0.37 (–/–/–)	0.59	-+-	0.22	--+-
5 6,729,931	rs1651071	*SRD5A1* (± 10 kb)	A G	0.53 (134/236/102)	0.46 (247/557/342)	9.70×10^{-05}	1.27×10^{-04}	1.35 (1.16-1.57)	0.48 (140/269/160)	0.48 (422/853/510)	0.48 (282/649/334)	0.49 (316/651/334)	0.50 (181/403/178)	0.48 (226/510/257)	0.89	+-+	0.07	++-+
10 108,036,628	rs17834272	gene desert	A G	0.35 (54/221/197)	0.28 (80/480/586)	9.86×10^{-05}	3.54×10^{-04}	1.38 (1.17-1.62)	0.32 (61/247/265)	0.28 (143/713/925)	0.30 (121/527/626)	0.31 (130/552/637)	0.32 (–/–/–)	0.32 (–/–/–)	0.17	+--	3.26×10^{-03}	++--
19 1,134,851	rs1123751	*SBNO2* (± 10 kb)	G C	0.17 (15/134/323)	0.24 (59/423/664)	1.01×10^{-04}	—	0.68 (0.56-0.83)	0.21 (19/232/378)	0.20 (86/526/1159)	—	—	0.22 (47/233/454)	0.23 (61/328/582)	0.53	+?-	0.13	-+?-
20 37,965,320	rs11086765	gene desert	G A	0.22 (24/159/289)	0.16 (27/315/804)	1.02×10^{-04}	1.14×10^{-04}	1.46 (1.2-1.76)	0.17 (16/167/386)	0.17 (73/476/1238)	0.20 (47/409/823)	0.19 (55/380/886)	0.21 (31/259/470)	0.21 (49/328/616)	0.74	-+-	0.046	+-+-
21 23,619,231	rs1459403	gene desert	C G	0.05 (1/42/429)	0.02 (2/45/1099)	1.03×10^{-04}	—	2.23 (1.47-3.37)	0.05 (14/27/533)	0.04 (2/131/1666)	—	—	0.03 (0/49/682)	0.03 (2/57/923)	0.09	+?+	4.72×10^{-04}	++?+
8 72,348,139	rs11785185	*EYA1* (within gene)	A T	0.19 (13/155/304)	0.14 (32/250/864)	1.04×10^{-04}	1.04×10^{-04}	1.49 (1.22-1.82)	0.17 (15/158/396)	0.15 (49/432/1308)	0.15 (28/317/934)	0.16 (34/358/929)	0.13 (–/–/–)	0.14 (–/–/–)	0.66	+--	0.19	++--
1 6,165,922	rs7542655	*CHD5* (± 10 kb)	G C	0.05 (2/43/427)	0.02 (1/52/1093)	1.06×10^{-04}	—	2.16 (1.45-3.22)	0.03 (0/41/529)	0.03 (0/125/1685)	—	—	—	—	0.65	-??	0.038	+-??
1 112,488,507	rs1442840	gene desert	G C	0.41 (79/229/164)	0.34 (114/548/484)	1.08×10^{-04}	9.98×10^{-05}	1.36 (1.16-1.59)	0.38 (85/262/225)	0.37 (228/873/695)	0.37 (–/–/–)	0.35	0.37 (–/–/–)	0.39 (–/–/–)	0.68	++-	0.04	+++-
10 30,824,637	rs7081639	*MAP3K8* (± 50 kb)	C T	0.30 (38/209/225)	0.37 (170/515/461)	1.10×10^{-04}	1.18×10^{-04}	0.73 (0.62-0.85)	0.36 (82/259/229)	0.37 (264/784/738)	0.36 (165/597/516)	0.36 (159/632/531)	0.36 (101/344/317)	0.38 (149/459/386)	0.49	-+-	0.02	--+-
7 69,955,663	rs7784844	gene desert	C T	0.37 (56/234/182)	0.30 (95/492/559)	1.10×10^{-04}	1.20×10^{-04}	1.37 (1.17-1.61)	0.28 (51/226/294)	0.31 (176/771/848)	0.31 (–/–/–)	0.31 (–/–/–)	0.30 (–/–/–)	0.33 (–/–/–)	***0.05***	-+-	0.94	+-+-

				Panel A – GWAS **Germany** 472 cases 1146 controls					**Panel B** **Germany** 681cases 1824 controls		**Panel C** **CASP** 1303 cases 1322 controls		**Panel D** **Genizon** 762 cases 994 controls		**Panel B - D** **(replication only)** **Combined analysis** 2746 cases 4140 controls		**Panel A - D** **(GWAS & replication)** **Combined analysis** 3218 cases 5286 controls	
Chr Pos. (bp)	**dbSNP ID**	**Nearby genes (relative position)**	**A1 A2**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**P_{CCA}**	***LRP***	**OR (95% CI)**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**$P_{repl.}$**	**Direction**	**$P_{comb.}$**	**Direction**
3 74,622,313	rs7610815	*CNTN3* (within gene)	T G	0.06 (0/54/418)	0.03 (0/66/1080)	1.12×10^{-04}	—	2.04 (1.41-2.94)	0.04 (1/47/526)	0.03 (3/105/1683)	—	—	0.03 (0/45/689)	0.03 (2/51/930)	0.09	+?+	5.43×10^{-04}	++?+
17 50,719,025	rs16955840	*HLF* (within gene)	C T	0.04 (1/40/431)	0.02 (1/44/1101)	1.13×10^{-04}	6.14×10^{-04}	2.26 (1.48-3.46)	0.04 (1/50/524)	0.04 (3/143/1657)	0.03 (–/–/–)	0.03 (–/–/–)	0.03 (–/–/–)	0.03 (–/–/–)	0.72	+-+	0.18	++-+
14 43,316,238	rs11157365	gene desert	C A	0.12 (6/101/365)	0.08 (5/166/975)	1.17×10^{-04}	1.39×10^{-04}	1.63 (1.27-2.09)	0.09 (4/92/472)	0.09 (10/312/1466)	0.10 (–/–/–)	0.10 (–/–/–)	0.10 (6/136/617)	0.11 (9/206/776)	0.22	---	0.56	+---
8 117,611,566	rs4268153	gene desert	A G	0.12 (10/97/365)	0.08 (13/158/975)	1.19×10^{-04}	1.93×10^{-04}	1.61 (1.26-2.06)	0.07 (2/69/501)	0.09 (19/301/1485)	0.08 (5/189/1083)	0.08 (7/194/1120)	0.09 (–/–/–)	0.08 (–/–/–)	0.13	--+	0.76	+--+
2 19,643,786	rs11096601	gene desert	T C	0.47 (110/228/134)	0.40 (196/528/422)	1.22×10^{-04}	2.01×10^{-04}	1.35 (1.16-1.57)	0.41 (100/270/201)	0.42 (323/895/599)	0.43 (244/615/420)	0.43 (253/622/445)	0.45 (142/396/224)	0.46 (196/519/279)	0.44	-+-	0.32	+-+-
10 748,971	rs11253337	*DIP2C* (± 50 kb)	T G	0.26 (31/184/257)	0.20 (49/359/738)	1.23×10^{-04}	1.63×10^{-04}	1.42 (1.19-1.69)	0.22 (36/178/354)	0.21 (88/560/1133)	0.24 (–/–/–)	0.23 (–/–/–)	0.23 (43/259/459)	0.22 (46/348/600)	0.14	+++	2.71×10^{-03}	++++
2 150,052,578	rs17348610	*LYPD6* (± 20 kb)	G A	0.17 (9/145/318)	0.12 (16/246/884)	1.31×10^{-04}	1.13×10^{-04}	1.50 (1.22-1.86)	0.13 (11/124/438)	0.12 (25/396/1401)	0.13 (24/281/971)	0.13 (19/293/1008)	0.11 (15/141/606)	0.12 (15/212/767)	0.87	++-	0.07	+++-
7 101,423,966	rs202159	*CUX1* (within gene)	T C	0.35 (64/202/206)	0.28 (77/491/578)	1.32×10^{-04}	1.06×10^{-04}	1.37 (1.17-1.61)	0.31 (53/249/263)	0.29 (142/782/890)	0.30 (–/–/–)	0.30 (–/–/–)	0.31 (64/345/348)	0.29 (78/426/488)	0.18	+-+	4.18×10^{-03}	++-+
11 12,032,405	rs7928952	(± 50 kb)	A C	0.24 (28/170/274)	0.18 (39/334/773)	1.34×10^{-04}	—	1.43 (1.19-1.72)	0.21 (25/177/372)	0.21 (91/575/1120)	—	—	0.19 (42/247/471)	0.18 (42/331/620)	0.65	-?+	0.017	+-?+
12 5,395,521	rs10849262	*NTF3* (± 20 kb)	A G	0.31 (46/202/224)	0.38 (159/555/432)	1.35×10^{-04}	1.47×10^{-04}	0.73 (0.62-0.86)	0.36 (83/248/238)	0.36 (238/801/757)	0.35 (163/571/545)	0.34 (152/599/569)	0.34 (88/346/328)	0.36 (138/438/418)	0.88	++-	0.13	-++-
12 15,220,937	rs12425381	*RERG* (within gene)	G C	0.27 (40/172/260)	0.21 (43/385/718)	1.36×10^{-04}	5.80×10^{-04}	1.41 (1.18-1.68)	0.24 (38/181/354)	0.23 (96/646/1053)	0.20 (58/398/822)	0.22 (79/435/808)	0.22 (–/–/–)	0.21 (–/–/–)	0.56	+-+	0.25	++-+
9 104,585,304	rs994864	gene desert	T C	0.22 (26/161/285)	0.29 (96/473/577)	1.37×10^{-04}	4.79×10^{-04}	0.71 (0.59-0.85)	0.30 (62/217/292)	0.29 (152/715/919)	0.28 (87/512/630)	0.26 (87/447/726)	0.26 (–/–/–)	0.28 (–/–/–)	0.14	++-	0.73	-++-
10 99,624,633	rs4919154	*CRTAC1* (within gene)	C T	0.42 (82/229/161)	0.49 (274/573/299)	1.37×10^{-04}	1.89×10^{-04}	0.74 (0.64-0.87)	0.46 (120/285/163)	0.48 (400/912/490)	0.46 (280/620/378)	0.47 (279/697/345)	0.50 (176/405/181)	0.50 (244/510/239)	0.22	---	5.51×10^{-03}	----
21 41,671,059	rs379839	*MX2* (within gene)	A G	0.53 (137/222/113)	0.45 (229/580/337)	1.38×10^{-04}	1.98×10^{-04}	1.34 (1.15-1.56)	0.47 (111/304/153)	0.48 (426/886/501)	—	—	0.44 (148/361/253)	0.45 (221/449/324)	0.24	-?-	0.32	+-?-
6 110,593,105	rs12191724	*WASF1* (within gene)	A G	0.07 (5/59/408)	0.12 (19/232/895)	1.40×10^{-04}	1.35×10^{-04}	0.59 (0.45-0.77)	0.11 (3/117/455)	0.10 (22/325/1477)	—	—	0.11 (14/184/564)	0.09 (20/183/791)	***0.04***	+?+	0.77	-+?+
6 1,394,120	rs2745636	gene desert	G T	0.40 (80/215/177)	0.47 (251/582/313)	1.41×10^{-04}	8.03×10^{-05}	0.74 (0.64-0.87)	0.46 (116/278/176)	0.45 (378/889/546)	0.45 (273/602/395)	0.45 (262/652/402)	0.50 (182/394/186)	0.47 (214/510/269)	0.34	+++	0.42	-+++
12 57,286,450	rs10877152	gene desert	G C	0.24 (36/157/279)	0.31 (110/494/542)	1.42×10^{-04}	1.31×10^{-04}	0.72 (0.6-0.85)	0.27 (32/230/310)	0.29 (139/754/903)	0.27 (100/473/675)	0.27 (87/530/687)	0.31 (–/–/–)	0.32 (–/–/–)	0.24	-+-	6.67×10^{-03}	--+-
2 206,519,890	rs12478185	*FLJ20309* (± 50 kb)	T C	0.06 (0/53/419)	0.10 (14/197/935)	1.43×10^{-04}	4.98×10^{-05}	0.55 (0.41-0.75)	0.09 (8/86/480)	0.08 (6/270/1543)	0.08 (–/–/–)	0.08 (–/–/–)	0.09 (7/129/625)	0.09 (5/165/824)	0.38	+-+	0.38	-+-+
2 139,925,381	rs2163585	gene desert	C T	0.40 (70/232/170)	0.47 (260/554/332)	1.43×10^{-04}	1.31×10^{-04}	0.74 (0.64-0.87)	0.44 (122/262/178)	0.44 (364/859/573)	0.47 (–/–/–)	0.46 (–/–/–)	0.48 (–/–/–)	0.48 (–/–/–)	0.50	++-	0.29	-++-
7 71,123,181	rs844788	*CALN1* (within gene)	C T	0.12 (5/106/361)	0.18 (31/342/773)	1.43×10^{-04}	2.18×10^{-04}	0.65 (0.52-0.81)	0.17 (18/167/390)	0.18 (62/519/1223)	0.16 (35/327/916)	0.16 (36/360/925)	0.18 (–/–/–)	0.17 (–/–/–)	0.81	--+	0.06	---+
7 92,759,408	rs7790676	*CCDC132* (within gene)	G A	0.06 (2/56/414)	0.11 (21/201/924)	1.44×10^{-04}	—	0.57 (0.42-0.76)	0.12 (10/126/437)	0.12 (35/367/1397)	0.11 (–/–/–)	0.11 (–/–/–)	0.11 (–/–/–)	0.12 (–/–/–)	0.79	++-	0.06	-++-
1 44,771,051	rs10890308	*RNF220* (within gene)	C T	0.45 (101/227/144)	0.38 (182/514/450)	1.59×10^{-04}	2.50×10^{-04}	1.34 (1.15-1.57)	0.38 (80/276/218)	0.40 (299/846/664)	0.40 (194/625/457)	0.39 (197/622/498)	0.36 (117/319/326)	0.39 (145/486/363)	0.37	-+-	0.40	+-+-
12 111,192,923	rs11610922	*C12orf51* (within gene)	A G	0.09 (4/72/396)	0.05 (5/106/1035)	1.60×10^{-04}	8.27×10^{-04}	1.75 (1.31-2.35)	0.06 (1/66/507)	0.06 (4/209/1575)	—	—	0.10 (–/–/–)	0.08 (–/–/–)	0.22	+?+	2.51×10^{-03}	++?+
10 125,925,994	rs7904325	gene desert	A G	0.14 (6/123/343)	0.20 (50/358/738)	1.62×10^{-04}	8.73×10^{-05}	0.67 (0.54-0.83)	0.19 (24/168/380)	0.17 (58/501/1247)	0.18 (32/385/823)	0.18 (44/381/866)	0.17 (21/210/531)	0.18 (28/299/667)	0.83	+--	0.15	-+--
6 475,476	rs6938671	*EXOC2* (within gene)	G T	0.36 (63/210/199)	0.29 (95/473/578)	1.63×10^{-04}	2.26×10^{-04}	1.36 (1.16-1.6)	0.31 (60/252/256)	0.30 (155/764/887)	0.28 (–/–/–)	0.27 (–/–/–)	0.27 (49/312/401)	0.26 (61/404/529)	0.20	+++	5.07×10^{-03}	++++
6 103,217,861	rs6571042	gene desert	T C	0.11 (8/91/373)	0.07 (8/150/988)	1.63×10^{-04}	2.77×10^{-04}	1.63 (1.26-2.1)	0.09 (5/90/479)	0.08 (14/253/1507)	0.09 (–/–/–)	0.09 (–/–/–)	0.08 (–/–/–)	0.07 (–/–/–)	0.34	+-+	0.01	++-+

				Panel A – GWAS **Germany** 472 cases 1146 controls					**Panel B** **Germany** 681cases 1824 controls		**Panel C** **CASP** 1303 cases 1322 controls		**Panel D** **Genizon** 762 cases 994 controls		**Panel B - D** **(replication only)** **Combined analysis** 2746 cases 4140 controls		**Panel A - D** **(GWAS & replication)** **Combined analysis** 3218 cases 5286 controls	
Chr **Pos. (bp)**	**dbSNP ID**	**Nearby genes (relative position)**	**A1** **A2**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	P_{CCA}	***LRP***	**OR (95% CI)**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	$P_{\text{repl.}}$	**Direction**	$P_{\text{comb.}}$	**Direction**
8 139,010,233	rs2326142	gene desert	T G	0.44 (91/234/147)	0.51 (293/589/264)	1.63×10^{-04}	2.99×10^{-04}	0.75 (0.64-0.87)	0.48 (141/267/166)	0.46 (390/883/516)	0.48 (–/–/–)	0.47 (–/–/–)	0.50 (–/–/–)	0.49 (–/–/–)	0.30	+++	0.48	-+++
9 82,740,226	rs7042779	gene desert	C G	0.05 (1/46/425)	0.02 (1/55/1090)	1.65×10^{-04}	3.51×10^{-04}	2.09 (1.41-3.09)	0.02 (2/21/546)	0.02 (2/62/1736)	0.03 (–/–/–)	0.03 (–/–/–)	0.03 (–/–/–)	0.03 (–/–/–)	0.30	++-	0.01	+++-
8 111,387,472	rs16880591	gene desert	G A	0.04 (0/36/436)	0.07 (5/158/983)	1.66×10^{-04}	8.29×10^{-05}	0.50 (0.35-0.72)	0.07 (0/83/492)	0.07 (6/225/1562)	0.07 (–/–/–)	0.07 (–/–/–)	0.06 (–/–/–)	0.06 (–/–/–)	0.32	+++	0.45	-+++
16 52,679,248	rs697769	*FTO* (within gene)	A G	0.40 (75/229/168)	0.47 (264/559/323)	1.67×10^{-04}	2.05×10^{-04}	0.74 (0.64-0.87)	0.44 (109/272/188)	0.45 (366/872/549)	0.44 (–/–/–)	0.44 (–/–/–)	0.44 (–/–/–)	0.43 (–/–/–)	0.64	--+	0.04	---+
9 137,155,534	rs647128	*OLFM1* (± 10 kb)	A G	0.40 (72/231/169)	0.47 (251/575/320)	1.70×10^{-04}	1.29×10^{-04}	0.74 (0.64-0.87)	0.47 (136/257/167)	0.44 (378/853/578)	0.47 (–/–/–)	0.46 (–/–/–)	0.44 (153/359/250)	0.43 (177/510/307)	0.16	+++	0.71	-+++
6 96,685,540	rs7742857	*FUT9* (within gene)	G T	0.29 (43/185/244)	0.35 (142/528/476)	1.73×10^{-04}	2.36×10^{-04}	0.73 (0.62-0.86)	0.36 (76/256/243)	0.35 (212/836/773)	0.35 (145/585/539)	0.35 (144/619/551)	0.33 (77/347/338)	0.34 (113/456/425)	0.98	++-	0.11	-++-
4 178,728,437	rs4690536	gene desert	A G	0.28 (42/184/246)	0.35 (132/540/474)	1.79×10^{-04}	1.91×10^{-04}	0.73 (0.62-0.86)	0.34 (67/257/252)	0.33 (193/820/797)	0.33 (–/–/–)	0.34 (–/–/–)	0.33 (69/360/332)	0.32 (102/433/458)	0.95	+-+	0.09	-+-+
19 59,186,575	rs251850	*CACNG6* (± 10 kb)	C T	0.27 (41/172/259)	0.21 (50/380/716)	1.79×10^{-04}	—	1.40 (1.17-1.66)	0.25 (49/234/379)	0.23 (101/627/1061)	—	—	0.22 (37/254/441)	0.20 (31/328/622)	0.026	+?+	1.14×10^{-04}	++?+
14 98,598,490	rs8004111	gene desert	A G	0.28 (35/191/246)	0.34 (127/532/487)	1.81×10^{-04}	1.50×10^{-04}	0.73 (0.62-0.86)	0.33 (68/235/262)	0.30 (164/761/873)	0.30 (–/–/–)	0.30 (–/–/–)	0.34 (–/–/–)	0.34 (–/–/–)	0.15	+++	0.74	-+++
3 793,135	rs17047823	gene desert	C A	0.15 (11/122/339)	0.11 (13/215/918)	1.83×10^{-04}	2.52×10^{-04}	1.52 (1.22-1.9)	0.12 (15/120/441)	0.12 (24/376/1391)	0.14 (–/–/–)	0.14 (–/–/–)	0.10 (–/–/–)	0.13 (–/–/–)	0.16	+--	0.72	++--
7 126,637,457	rs17864159	*GRM8* (within gene)	T C	0.09 (3/81/388)	0.06 (7/114/1025)	1.86×10^{-04}	3.04×10^{-04}	1.71 (1.29-2.27)	0.06 (2/69/498)	0.07 (6/223/1576)	—	—	0.05 (2/67/693)	0.05 (1/103/890)	0.57	-?-	0.14	+-?-
14 86,629,923	rs12586410	gene desert	T G	0.45 (98/230/144)	0.38 (174/520/452)	1.87×10^{-04}	1.76×10^{-04}	1.34 (1.15-1.56)	0.41 (86/296/191)	0.40 (285/880/646)	0.60 (–/–/–)	0.58 (–/–/–)	0.41 (139/352/271)	0.39 (145/486/363)	0.63	+-+	0.039	++-+
19 63,328,964	rs6510125	*ZNF329* (± 10 kb)	T C	0.28 (36/195/241)	0.22 (68/371/707)	1.89×10^{-04}	2.88×10^{-04}	1.39 (1.17-1.65)	0.24 (37/203/332)	0.23 (89/647/1081)	0.24 (68/470/741)	0.26 (80/517/725)	0.24 (41/281/440)	0.23 (51/358/585)	0.80	+-+	0.16	++-+
9 135,657,976	rs10123623	*VAV2* (within gene)	G A	0.08 (3/66/403)	0.04 (0/100/1046)	1.89×10^{-04}	1.95×10^{-04}	1.80 (1.32-2.46)	0.06 (0/68/503)	0.07 (7/222/1566)	—	—	0.06 (–/–/–)	0.05 (–/–/–)	0.98	-?+	0.05	+-?+
13 24,616,283	rs7325885	*FAM123A* (± 50 kb)	G T	0.52 (132/228/112)	0.45 (251/530/365)	1.92×10^{-04}	3.61×10^{-04}	1.33 (1.15-1.55)	0.48 (127/291/154)	0.47 (401/906/497)	0.45 (261/648/370)	0.45 (254/693/373)	0.42 (121/390/250)	0.45 (214/465/315)	0.35	+--	0.43	++--
5 174,125,915	rs1507805	*MSX2* (± 50 kb)	C T	0.25 (28/179/265)	0.19 (37/365/744)	1.95×10^{-04}	3.47×10^{-04}	1.41 (1.18-1.69)	0.20 (26/173/372)	0.20 (77/552/1158)	0.23 (72/439/740)	0.22 (68/437/801)	0.23 (–/–/–)	0.20 (–/–/–)	0.08	+++	1.30×10^{-03}	++++
18 28,336,657	rs12455882	*FAM59A* (± 50 kb)	A G	0.12 (10/96/366)	0.18 (30/344/772)	1.95×10^{-04}	7.61×10^{-05}	0.66 (0.53-0.82)	0.15 (10/148/413)	0.15 (40/469/1287)	—	—	0.22 (–/–/–)	0.20 (–/–/–)	0.48	-?+	0.18	--?+
6 143,329,978	rs1041656	*HIVEP2* (± 50 kb)	A G	0.50 (120/234/118)	0.43 (209/564/373)	1.95×10^{-04}	1.62×10^{-04}	1.33 (1.15-1.55)	0.45 (108/285/177)	0.45 (361/895/546)	0.42 (–/–/–)	0.42 (–/–/–)	0.41 (–/–/–)	0.43 (–/–/–)	0.54	---	0.28	+---
9 9,020,517	rs375118	*PTPRD* (within gene)	G C	0.10 (10/77/385)	0.15 (25/298/823)	1.95×10^{-04}	6.15×10^{-05}	0.64 (0.5-0.81)	0.09 (4/95/476)	0.11 (18/359/1420)	0.10 (8/249/1018)	0.10 (11/244/1061)	0.10 (9/145/572)	0.10 (11/192/774)	0.38	-++	0.016	--++
9 127,898,418	rs11787836	gene desert	T C	0.19 (14/145/313)	0.13 (20/268/858)	1.95×10^{-04}	1.83×10^{-04}	1.47 (1.2-1.8)	0.18 (21/165/387)	0.20 (72/585/1149)	0.20 (49/407/821)	0.21 (70/419/830)	0.16 (–/–/–)	0.16 (–/–/–)	0.06	---	0.93	+---
18 8,574,076	rs12051975	*RAB12* (± 50 kb)	G T	0.03 (0/32/440)	0.07 (3/148/995)	1.98×10^{-04}	—	0.49 (0.33-0.72)	0.08 (1/82/489)	0.05 (5/187/1609)	0.05 (–/–/–)	0.05 (–/–/–)	0.07 (1/94/638)	0.06 (6/98/879)	***1.07×10^{-03}***	+++	1.90E-01	-+++
12 40,527,536	rs11181191	gene desert	G C	0.23 (28/161/283)	0.17 (41/314/791)	2.06×10^{-04}	2.86×10^{-04}	1.42 (1.18-1.71)	0.21 (26/206/342)	0.19 (63/567/1160)	0.21 (63/408/800)	0.20 (62/410/844)	0.19 (–/–/–)	0.20 (–/–/–)	0.29	++-	0.01	+++-
16 24,229,868	rs7187560	*CACNG3* (within gene)	T C	0.39 (76/215/181)	0.46 (241/573/332)	2.09×10^{-04}	2.45×10^{-04}	0.75 (0.64-0.87)	0.45 (106/293/169)	0.42 (327/860/617)	0.45 (–/–/–)	0.44 (–/–/–)	0.56 (–/–/–)	0.56 (–/–/–)	***0.04***	+++	0.83	-+++
13 60,972,767	rs17258304	gene desert	C T	0.10 (8/82/382)	0.15 (23/307/816)	2.11×10^{-04}	2.49×10^{-04}	0.64 (0.51-0.81)	0.14 (11/151/415)	0.16 (55/456/1294)	0.14 (21/320/930)	0.14 (27/322/969)	0.17 (–/–/–)	0.15 (–/–/–)	0.79	--+	0.06	---+
6 2,966,865	rs10223660	*NQO2* (± 10 kb)	T C	0.51 (114/255/103)	0.44 (205/597/344)	2.16×10^{-04}	—	1.33 (1.14-1.55)	0.39 (80/275/200)	0.40 (245/842/591)	—	—	—	—	0.57	-??	0.06	+-??
7 71,077,743	rs12530737	*CALN1* (within gene)	C T	0.22 (24/163/285)	0.29 (98/459/589)	2.17×10^{-04}	2.66×10^{-04}	0.72 (0.6-0.85)	0.28 (50/225/294)	0.28 (150/695/945)	0.25 (–/–/–)	0.26 (–/–/–)	0.30 (69/316/377)	0.29 (88/406/499)	0.62	--+	0.04	---+

				Panel A – GWAS **Germany** 472 cases 1146 controls					**Panel B** **Germany** 681cases 1824 controls		**Panel C** **CASP** 1303 cases 1322 controls		**Panel D** **Genizon** 762 cases 994 controls		**Panel B - D** **(replication only)** **Combined analysis** 2746 cases 4140 controls		**Panel A - D** **(GWAS & replication)** **Combined analysis** 3218 cases 5286 controls	
Chr **Pos. (bp)**	**dbSNP ID**	**Nearby genes (relative position)**	**A1** **A2**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**P_{CCA}**	***LRP***	**OR (95% CI)**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**AF_{A1} (11/12/22) Case**	**AF_{A1} (11/12/22) Control**	**$P_{repl.}$**	**Direction**	**$P_{comb.}$**	**Direction**
11 24,429,664	rs10834343	*LUZP2* (± 50 kb)	A G	0.43 (84/240/148)	0.50 (283/591/272)	2.22×10^{-04}	3.22×10^{-04}	0.75 (0.64-0.87)	0.50 (151/276/148)	0.48 (426/868/488)	0.49 (–/–/–)	0.48 (–/–/–)	0.50 (–/–/–)	0.52 (–/–/–)	0.60	++-	0.26	-++-
13 102,872,067	rs9586186	gene desert	T C	0.20 (19/154/299)	0.15 (32/279/835)	2.26×10^{-04}	2.88×10^{-04}	1.44 (1.19-1.76)	0.17 (17/151/405)	0.16 (38/484/1265)	0.16 (33/329/903)	0.16 (42/334/941)	0.15 (19/180/555)	0.17 (28/279/687)	0.61	+--	0.25	++--
7 27,208,185	rs2067087	*HOXA13* (± 10 kb)	G C	0.35 (50/226/196)	0.28 (95/458/593)	2.26×10^{-04}	8.31×10^{-04}	1.36 (1.15-1.59)	0.30 (45/248/266)	0.28 (154/696/921)	0.31 (116/567/582)	0.31 (112/577/609)	0.25 (–/–/–)	0.27 (–/–/–)	0.78	++-	0.06	+++-
13 55,384,367	rs9597294	gene desert	C A	0.12 (5/99/368)	0.17 (38/310/798)	2.26×10^{-04}	1.43×10^{-04}	0.65 (0.52-0.82)	0.16 (20/140/416)	0.16 (51/486/1247)	0.15 (–/–/–)	0.16 (–/–/–)	0.13 (–/–/–)	0.14 (–/–/–)	0.17	---	4.39×10^{-03}	----
10 69,536,179	rs9919371	*MYPN* (± 10 kb)	C T	0.11 (6/89/377)	0.07 (5/146/995)	2.27×10^{-04}	3.03×10^{-04}	1.63 (1.26-2.12)	0.10 (12/95/465)	0.08 (12/266/1517)	0.07 (–/–/–)	0.07 (–/–/–)	0.07 (–/–/–)	0.06 (–/–/–)	0.05	+++	8.30×10^{-04}	++++
12 121,629,420	rs7979863	*KNTC1* (within gene)	A G	0.39 (74/226/172)	0.32 (111/521/514)	1.27×10^{-04}	8.08×10^{-05}	1.36 (1.16-1.59)	0.33 (71/240/253)	0.37 (227/869/716)	0.33 (–/–/–)	0.35 (–/–/–)	0.36 (104/336/322)	0.36 (124/461/409)	***3.00×10^{-02}***	--+	0.78	+--+
13 45,282,832	rs1529877	*LOC283514* (within gene)	C T	0.46 (100/235/137)	0.39 (170/550/426)	1.30×10^{-04}	1.32×10^{-04}	1.35 (1.16-1.57)	0.40 (86/273/203)	0.43 (327/858/583)	0.40 (–/–/–)	0.37 (–/–/–)	0.39 (109/379/274)	0.38 (148/463/383)	0.54	-++	0.027	+-++
5 96,865,773	rs6556983	gene desert	T C	0.10 (7/83/382)	0.06 (5/134/1007)	9.71×10^{-05}	1.62×10^{-04}	1.70 (1.3-2.23)	0.06 (3/64/507)	0.06 (8/219/1597)	0.06 (–/–/–)	0.07 (–/–/–)	0.07 (4/95/663)	0.07 (6/137/851)	0.27	---	0.48	+---
8 117,587,454	rs7820674	gene desert	T C	0.21 (20/160/292)	0.16 (33/291/822)	1.14×10^{-04}	1.83×10^{-04}	1.46 (1.2-1.77)	0.16 (12/161/402)	0.17 (45/538/1217)	0.17 (–/–/–)	0.18 (–/–/–)	0.19 (28/237/494)	0.17 (26/293/674)	0.63	--+	0.21	+--+
1 112,456,517	rs461311	gene desert	G T	0.16 (14/126/332)	0.22 (52/410/684)	1.02×10^{-04}	6.97×10^{-05}	0.68 (0.55-0.82)	0.22 (29/188/348)	0.21 (73/609/1103)	0.25 (–/–/–)	0.24 (–/–/–)	0.25 (43/291/428)	0.24 (51/366/577)	0.14	+++	0.72	-+++
19 16,970,436	rs4808550	*CPAMD8* (within gene)	A G	0.21 (21/155/296)	0.15 (27/300/819)	1.78×10^{-04}	2.56×10^{-04}	1.45 (1.19-1.75)	0.17 (15/166/383)	0.17 (49/526/1221)	0.19 (50/379/848)	0.17 (34/380/905)	0.19 (34/216/512)	0.19 (32/318/644)	0.48	++-	0.02	+++-
5 123,839,501	rs10067065	gene desert	C T	0.35 (50/229/193)	0.28 (94/458/594)	1.46×10^{-04}	1.86×10^{-04}	1.37 (1.16-1.61)	0.27 (38/233/302)	0.29 (157/724/922)	0.71 (–/–/–)	0.71 (–/–/–)	0.30 (75/306/381)	0.28 (94/370/530)	0.96	--+	0.11	+--+
7 154,099,909	rs916514	*DPP6* (within gene)	G A	0.09 (3/76/393)	0.14 (20/271/855)	1.37×10^{-04}	6.64×10^{-05}	0.61 (0.47-0.79)	0.09 (8/83/483)	0.11 (35/337/1447)	0.09 (–/–/–)	0.11 (–/–/–)	0.10 (9/133/619)	0.09 (7/161/826)	***0.0496***	--+	6.03×10^{-04}	---+
2 223,040,164	rs7604173	*SGPP2* (within gene)	T C	0.47 (98/245/129)	0.39 (183/539/424)	1.41×10^{-04}	1.63×10^{-04}	1.34 (1.15-1.57)	0.42 (108/265/198)	0.41 (308/856/620)	0.40 (208/594/473)	0.40 (218/623/481)	0.42 (136/365/261)	0.42 (173/488/333)	0.84	+--	0.06	++--
12 61,590,288	rs7962536	*PPM1H* (within gene)	T C	0.19 (23/135/314)	0.25 (85/408/653)	1.80×10^{-04}	2.89×10^{-04}	0.70 (0.58-0.84)	0.22 (33/192/351)	0.23 (112/614/1086)	0.21 (–/–/–)	0.22 (–/–/–)	0.21 (38/251/473)	0.22 (59/328/607)	0.22	---	6.40×10^{-03}	----
6 149,166,288	rs959131	*UST* (within gene)	C T	0.30 (40/206/226)	0.24 (68/413/665)	1.83×10^{-04}	2.14×10^{-04}	1.38 (1.17-1.63)	0.25 (35/216/322)	0.24 (103/675/1029)	0.26 (–/–/–)	0.26 (–/–/–)	0.26 (55/287/420)	0.27 (66/396/531)	0.72	++-	0.05	+++-
11 102,081,585	rs1939015	*MMP27* (within gene)	G A	0.12 (6/97/369)	0.16 (25/315/806)	1.56×10^{-03}	9.78×10^{-04}	0.69 (0.55-0.87)	0.14 (8/144/415)	0.14 (35/440/1317)	0.15 (–/–/–)	0.17 (–/–/–)	0.17 (25/213/524)	0.20 (49/296/649)	***0.026***	---	7.09×10^{-04}	----

Supplementary Table 3. eQTL analysis. SNP-expression associations were tested separately in normal skin (NN; n=57), in uninvolved skin (PN; n=53), and in involved skin (PP; n=53). For this analysis, cis-associations were tested between each transcript (i.e. probe) of *TRAF3IP2* and other proteins and the accordant two SNPs (rs13210247 and rs33980500). Specifically, we used the score test in Merlin (`fastassoc` option) to test the association. For genotyped SNPs, the number of copies of one allele was modeled. For imputed SNPs, the dosage (i.e. the expected number of copies) of one allele was modelled. After correcting for multiple testing by Bonferroni (corrected significance threshold of $\alpha=7\times10^{-4}$ [0.05/66]) no significant association could be detected. The two tested SNPs were not correlated with the expression of the corresponding genes.

SNP	Gene	Affymetrix probe	eQTL *P*-value		
			NN (Normal)	PN (Uninvolved)	(PP) Involved
rs13210247	*TRAF3IP2*	202987_at	0.14	0.07	0.63
		215411_s_at	0.66	0.31	0.21
rs33980500	*TRAF3IP2*	202987_at	0.026	0.12	0.02
		215411_s_at	0.62	0.28	0.18
	TRAF1	205599_at	0.71	0.40	0.043
		235116_at	0.55	0.045	0.11
	TRAF2	204413_at	0.088	0.16	0.12
	TRAF3	208315_x_at	0.55	0.90	0.093
		221571_at	0.23	0.32	0.24
	TRAF4	202871_at	0.89	0.97	3.13E-03
		211899_s_at	0.21	0.89	0.11
		242473_at	0.32	0.14	0.62
	TRAF5	1569861_at	0.53	0.70	7.32E-03
		204352_at	0.96	0.090	0.13
	TRAF6	205558_at	0.30	0.15	0.98
	TRAF7	223029_s_at	0.96	0.33	0.15
		223030_at	0.55	3.91E-03	0.55
		223031_s_at	0.81	0.93	0.38
	IKBKB	209341_s_at	0.13	0.13	0.52
		209342_s_at	0.25	0.12	0.90
		211027_s_at	0.52	0.22	0.29
	IKBKG	209929_s_at	0.26	0.89	0.47
		36004_at	0.98	0.17	0.82
	NFKB1	209239_at	0.74	0.73	0.16
		239876_at	0.04	0.96	0.62
	NFKB2	207535_s_at	0.90	0.85	0.59
		209636_at	0.68	0.24	0.81
		211524_at	0.76	0.99	0.89
	NFKBIA	201502_s_at	0.43	0.63	0.10
		231699_at	0.18	0.13	0.71
	NFKBIB	214062_x_at	0.14	0.83	0.53
		214448_x_at	0.30	0.60	0.64
		228388_at	0.87	0.22	0.26