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Identification of immune-relevant factors conferring sarcoidosis genetic risk

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At a Glance Commentary

Sarcoidosis is a complex granulomatous disease with unknown etiology. There is a considerable genetic contribution, however only a small fraction of the estimated heritability is explained, with variants in HLA region conferring the largest effects.

The study successfully identified four novel genetic risk loci for sarcoidosis and refined the association signal in the HLA-region to three independent signals. Our results are supportive of the hypothesis that sarcoidosis partly shares a genetic background with other immune-related diseases. Thus, our findings may inspire a revised classification of clinical disease manifestations and subphenotypes. Our results further implicate a role of genetic factors in many aspects of sarcoidosis pathogenesis, especially in IL23/Th17-signaling, and may provide hypotheses on novel therapeutic targets.

This article has an online data supplement, which is accessible from this issue's table of content online at “www.atsjournals.org".

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Abstract:

Rationale and Objectives: To define further genetic risk loci for sarcoidosis, we used the Immunochip for a candidate gene association study of immune-associated loci. **Methods**: Altogether the study population comprised over 19,000 individuals. In a two-stage design, 1726 German sarcoidosis cases and 5482 controls were genotyped for 128,705 SNPs using the Illumina Immunochip for the screening step. The remaining 3955 cases, 7514 controls and 684 parents of affected offspring were used for validation and replication of 44 candidate and 2 established risk SNPs. **Measurements and Main Results**: Four novel susceptibility loci were identified with genome-wide significance in the European case-control populations, located on chromosomes 12q24.12 (rs653178; *ATXN2/SH2B3*), 5q33.3 (rs4921492; *IL12B*), 4q24 (rs223498; *MANBA/NFKB1*) and 2q33.2 (rs6748088; *FAM117B*). We further defined three independent association signals in the HLA-region with genome-wide significance, peaking in the *BTNL2* promoter region (rs5007259), at *HLA-B* (rs4143332/HLA-B*0801) and at *HLA-DPB1* (rs9277542), and found another novel independent signal near *IL23R* (rs12069782) on chromosome 1p31.3. **Conclusions**: Functional predictions and protein network analyses suggest a prominent role of the drug-targetable IL23/Th17-signaling pathway in the genetic etiology of sarcoidosis. Our findings reveal a substantial genetic overlap of sarcoidosis with diverse immune-mediated inflammatory disorders, which could be of relevance for the clinical application of modern therapeutics.

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Introduction

Sarcoidosis is a complex inflammatory disease of mainly the lung with an unknown etiology that affects mostly young adults (20-40 years) [1]. It is characterized by heterogeneous clinical manifestations with diverse organ involvement and disease course. Previous genome-wide association studies (GWAS) as well as candidate gene-driven investigations identified a number of genetic risk loci for sarcoidosis like *BTNL2* [2-4], *ANXA11* [5-8], a locus on chromosome 11q13.1 [9] and, most consistently, several loci in the *HLA* region on chromosome *6p21* [10]. Some risk loci are shared for sarcoidosis and other inflammatory or autoimmune conditions, e.g. allelic variation of SNP rs11209026 (Arg381Gln) in the *IL23R* gene locus predisposes, among others, to sarcoidosis, inflammatory bowel disease, psoriasis and ankylosing spondylitis [11-15]. Given the large overlap of the genetic risk maps of complex inflammatory and autoimmune diseases, the Immunochip array was designed for genotyping a comprehensive set of known immune-associated variants and for fine-mapping a subset of 186 selected risk loci [16,17]. This array was successfully used before to identify novel and shared risk loci for various complex immune-related diseases [18-24]. We employed the Immunochip to screen 1,726 German sarcoidosis patients and 5,482 healthy controls for novel sarcoidosis risk loci, followed by replication in four independent European collections (4605 cases and 12,673 controls) and another three populations for replication and subphenotype analysis (**Table 1**).

Materials and Methods

Patient and control subjects

The study sample comprised 5681 sarcoidosis cases, all of which were diagnosed according to international standards [25], 12996 controls and 684 parents of affected offspring. Analyses were performed in eight independent panels (A, B-I, B-II, C-I, C-II, D, E and F; **Table 1**). A detailed description and definition of the study sample including sarcoidosis subphenotypes is given as **Supplementary information.**

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Immunochip genotyping and quality control

DNA samples of panel A were genotyped using the Immunochip, comprising a total of 196,524 SNP assays [17]. Quality control excluded 67,819 SNPs and 143 individuals from analysis. Principal component analysis revealed no population stratification in the remaining samples and no population outliers were detected. Unless described differently, genotype data of panels B, C and E and F were generated using Sequenom® Mass-ARRAY iPlex (Sequenom, Inc., San Diego, USA) [26] and Taqman® technology (Applied Biosystems, Foster City, USA). In every analysis step, SNPs that had > 5% missing data (call rate (CR) ≥ 95%), a minor allele frequency < 1% and exact Hardy-Weinberg equilibrium $P < 10^{-4}$ were excluded. The controls of panel C-III were genotyped using the Illumina Immunochip custom array (The Genome Institute, Singapore). Genotyping for panel D was performed at the OMRF using the Illumina Immunochip. See **Supplementary information** for further details.

Statistical analysis and SNP selection

Data filtering and any statistical analysis of genotype data was carried out using PLINK v.1.07, applying logistic regression model throughout all case-control analysis, including conditional analysis using an allelic model for genotype coding [27]. Most promising SNPS (excluding *ANXA11* and HLA SNPs) were selected for follow-up and joint analysis upon ranking top with their p value ($p < 10^{-4}$) in the association analysis and a positive visual inspection of regional plots. The study design is visualized in the **Supplementary information**. HLA-haplotypes were imputed using HLA*IMP:02 with default parameters [28]. All statistical test used in this study and methods applied for in-silico analyses are described in the **Supplementary information**.

Results

After applying conservative and established quality filters to panel A, 1726 sarcoidosis cases, 5482 controls and 128,705 SNPs were included in the analysis of this dataset (**Table 1** and Methods section) and analyzed by a logistic regression analysis. The 44 most promising SNPs were selected based on ranked p values as described in the Methods section and investigated in a joint analysis of all available European case-control panels A, B-I, B-II, C-I and C-II (total of 4605 cases and 12,673 controls; **Table 1**). This approach led to the identification of four novel susceptibility loci for sarcoidosis in Europeans with genome-wide significant association signals (**Table 2**; **Figure 1**). For the respective lead variants, the effect sizes did not differ significantly between the investigated populations as assessed by the Breslow-Day test.

Novel non-HLA risk loci with genome-wide significance

SNP marker rs653178 on chromosome 12q24.12 was associated with the smallest p value in the joint analysis ($p = 1.64 \times 10^{-10}$; OR [95% CI] = 1.19 [1.14-1.27]). The potentially causative non-synonymous variant rs3184504 in the SH2B adaptor protein 3 (*SH2B3*) locus was in high LD with the lead SNP rs653178 and strongly associated in panel A ($r^2 = 0.87$; $p = 3.42 \times 10^{-6}$; OR [95% CI] = 0.83 [0.77-0.90]). For rs653178, a subphenotype-differential effect was observed for Löfgren syndrome in panel B-II ($p = 6.75 \times 10^{-3}$; OR [95% CI] = 1.97 [1.20-3.24]). Complete results for the subphenotype analysis are given in **Table S1**.

Second, in the chromosome 5q33.3 region upstream of *IL12B*, SNP rs4921492 yielded a genome-wide significant result ($p = 2.14 \times 10^{-9}$; OR [95% CI] = 1.20 [1.13-1.27]) for sarcoidosis. Concerning subphenotypes, this marker associated with nominal significance with the involvement of the central nervous system in panel F ($p = 0.035$; OR [95% CI] = 1.51 [1.03-2.23]). See **Table S2** for complete subphenotype results. Besides the lead SNP rs4921492, five markers that are in high LD with it are strongly associated with sarcoidosis **(Table S3)**. One of those, namely SNP rs12651787 ($p = 9.59 \times 10^{-6}$; OR [95% CI] = 1.20 [1.10-1.29]) is in high LD with rs1422877 ($r^2 = 0.97$), which is predicted to reside in an NF-kappa-B binding site and to confer allele-specific binding probabilities for the transcription factor RelA.

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Third, SNP rs223498 located on chromosome 4q24 near *NFKB1* showed a significant association in the joint analysis ($p = 1.28 \times 10^{-9}$; OR [95% CI] = 1.19 [1.12-1.26]). In panel A, a neighboring SNP (rs227375) was associated with the same effect size (OR [95% CI] = 1.19 [1.10-1.29]), but did not represent an independent signal as investigated by conditional regression analysis (data not shown). The region was sparsely covered with markers on the Immunochip (17 SNPs in a region of +-250 kb around the lead SNP). According to previous GWAS data [9], the association signal may extend beyond *MANBA* and *NFKB1* (**Figure S1 A**). For rs223498, none of the investigated sarcoidosis subphenotypes was associated significantly (**Table S4**).

Fourth, in the *FAM117B* gene region on chromosome 2q33.2, marker rs6748088 displayed a significant p value in the joint analysis ($p = 2.10 \times 10^{-8}$; OR [95% CI] = 1.18 [1.11-1.25]). Only four markers were located in the +/-500 kb-region around the lead SNP. Consulting previous GWAS data [9] did not allow the restriction of the association signal to a specific gene encoded in the region, but suggests a second independent signal in the genomic region (**Figure S1 B**). Conditional regression analysis in this dataset suggests an independent signal, represented by rs17469010 ($p = 0.002$; OR [95% CI] = 1.68 [1.21-2.33]). Subphenotype analysis did not reveal any significant differential effects for this marker (**Table S5**).

The complete results for the 44 selected SNPs, including p values for the Breslow-Day test, are listed in **Tables S6 and S7**. None of the four novel risk variants showed a significant association in the African-American sample (panel D). Power calculations revealed limited power to replicate the findings in panel D (rs653178: 14.6%; rs4921492: 42.7%; rs223498: 26.1%); rs6748088: 21.4%). In the German trio panel E, one of the newly identified risk SNPs (rs4921492) showed nominal significance ($p = 0.039$; OR [95% CI] = 1.27 [1.01-1.59]; **Table S8**). The statistical power to detect the three remaining association signals in panel E was low with 17.6% (rs653178), 14.0% (rs223498 and rs6748088), respectively.

Candidates and secondary signals

One SNP in the *TYK2* gene region, rs34536443, was associated with nearly genome-wide significance in the joint analysis of the European case-control panels ($p = 5.48 \times 10^{-8}$;

OR [95% CI] = 0.64 [0.55-0.76]; **Table S3**) and showed the same trend in the German trio panel E ($p = 0.086$; OR = 0.55 [0.27-1.10]; **Table S4**). It causes an amino acid change in the TYK2 protein (Pro1104Ala) and has therefore a high potential to be functionally relevant. No data were available for this SNP for the African-American sample (panel D). Subphenotype analysis in panel F suggests an association with fibrosis compared to non-fibrotic patients ($p = 0.01$; OR [95% CI] = 4.59 [1.33-15.76]; allele frequency $(AF)_{fibrotic} = 0.06$; $AF_{non\text{-}fibr} = 0.01$).

Further, two SNPs in the known sarcoidosis risk locus *IL23R* on chromosome 1p31.3 were associated with genome-wide significance in panel A (rs12069782: $p = 4.20 \times 10^{-8}$; OR [95% CI] = 1.30 [1.18-1.43] and rs12090164: $p = 4.51 \times 10^{-8}$; OR [95% CI] = 1.30 [1.18-1.42]; **Tables S6 and S7**), of which rs12090164 was omitted from follow-up due to complete LD ($r^2 = 1$). Subphenotype analysis did not reveale any subphenotype-differential effects (**Table S9**). Conditional regression analysis showed that the association signal of rs12069782 was independent of the association previously reported [11,29]. See the **Supplementary information** for details. The lead SNP rs12069782 was subjected to replication in the European case-control populations (panels B-I, B-II, C-I and C-II). In this analysis the ORs ranged from 1.03 to 1.46, with $p = 3.07 \times 10^{-10}$ (OR [95% CI] = 1.24 [1.16-1.33]) in the joint analysis of panels A, B, and C (**Tables S6 and S7**). However, the association was not confirmed in the African-American panel D (power = 68.3%) or the German trio panel E (power = 14.7%; **Table S8**).

Risk variants in the HLA-region

The combined analysis of single markers in the HLA-region and imputed classical HLA alleles in panel A revealed that a total of 1172 associated markers of the extended HLA-region (chr6: 25-35 Mb; $p < 5.0 \times 10^{-8}$), comprising three independent association signals. See **Supplementary data** for complete results.

The BTNL2 region

The strongest association in the HLA region was represented by marker rs5007259 in the *BTNL2* promoter region ($p = 1.55 \times 10^{-35}$; OR [95% CI] = 0.60 [0.55-0.65]; **Figure 2**). In a recently published association study comprising panel D (samples of African-American (AA) origin) and additional sarcoidosis patients and controls of European-American (EA) origin [30], marker rs5007259 was associated with nominal significance in both subsets ($p_{AA} = 3.80 \times 10^{-3}$; $p_{EA} = 7.05 \times 10^{-7}$). See **Table S10** for complete results on overlapping signals in the HLA-region. Subphenotype analysis of rs5007259 revealed a nominally significant association with Löfgren syndrome, with OR ranging from 0.37 to 0.52. Complete results for the subphenotype analysis of this marker are given in **Table S11**.

The *BTNL2* region was densely covered by the Immunochip, allowing fine-mapping of the major signal to the putative promoter region of *BTNL2* (**Figure S2**). The previously reported functional splice site variant rs2076530 was significantly associated (panel A; $p = 9.64 \times 10^{-25}$; OR [95% CI] = 0.65 [0.60-0.70]), however no longer significant after including the allelic dosage for rs5007259 as a covariate, i.e. conditioning on rs5007259 ($p_{cond} = 0.097$). In contrast, the association of rs5007259 remained highly significant ($p_{cond} = 5.00 \times 10^{-13}$). According to FuncPred, the most strongly associated variants in the promoter region are predicted to reside in transcription factor (TF) binding sites.

Analysis of HLA-haplotypes using logistic regression analysis revealed a significant association of HLA-DRB1-haplotypes (*0101: $p = 1.42 \times 10^{-18}$; OR [95% CI] = 0.48 [0.41-0.57] and *0301: $p = 4.99 \times 10^{-19}$; OR [95%] = 1.65 [1.48-1.84]) with sarcoidosis, a finding which has most consistently been reported (reviewed in [31]). HLA-DRB1*0301 was associated also in the small sample of patients with Löfgren syndrome ($p = 2.25 \times 10^{-13}$; OR [95% CI] = 4.20 [2.86-6.86]), confirming previous findings [32]. The *BTNL2* SNPs rs5007259 remained significantly associated after conditioning on HLA-DRB1*0101 ($p = 1.63 \times 10^{-23}$; OR [95% CI] = 0.65 [0.60-0.71]) and HLA-DRB1*0301 ($p = 5.63 \times 10^{-25}$; OR [95% CI] = 0.64 [0.59-0.70]) in our study population. Vice versa, the association of both haplotypes was diminished by conditioning on rs5007259 ($p = 2.29 \times 10^{-8}$; OR [95% CI] = 0.61 [0.52-0.73] and $p = 5.43 \times 10^{-7}$; OR [95% CI] = 1.34 [1.20-1.51]).

HLA-B and HLA-DPB1

When conditioning all markers and the imputed haplotypes in the HLA-region on rs5007259, marker rs4143332 that is located upstream of *HLA-B* yielded the smallest p value ($p_{cond} = 7.73 \times 10^{-18}$; OR [95% CI] = 1.64 [1.47-1.84]; **Figure 2**). The most significantly associated haplotype HLA-B*0801 showed an association signal of similar strength ($p_{cond} = 2.56 \times 10^{-17}$; OR [95% CI] = 1.63 [1.45-1.82]). Subphenotype analysis of rs4143332 revealed a significant difference in allele frequency between patients affected by acute and chronic sarcoidosis (OR ≤ 2.21), and an even stronger differential effect for Löfgren syndrome (OR ≤ 2.85). See **Table S12** for complete results of the subphenotype analysis for this marker.

Conditioning on both rs5007259 and rs4143332 revealed a third independent association signal with genome-wide significance in the HLA-region that is represented by SNP rs9277542 ($p_{cond} = 1.13 \times 10^{-10}$; OR [95% CI] = 1.32 [1.21-1.44]; **Figure 2**). In panel F, this marker displayed a differential effect for skin involvement ($p = 7.13 \times 10^{-3}$; OR [95% CI] = 0.62 [0.44-0.88]). The complete results for the subphenotype association analysis are given in **Table S13**. Marker rs9277542 is located in the 3´-UTR of *HLA-DPB1*. None of the surrounding highly associated markers confer an amino acid change in the encoded protein, but functional predictions suggest a role in expression regulation via allele-specific miRNA binding (**Table S14**) and alternative splicing according to SNPinfo [33]. See the **Supplementary information** and **Data File S1** for the results of imputed HLA-haplotype analysis, subphenotype analysis and complete information on the association of HLA-haplotypes. Association signals of established sarcoidosis risk variants are given in the **Supplementary information**.

Protein network analysis

A network analysis of potentially affected gene products was performed using STRING [34]. Proteins that were included in the analysis were selected based on the association and *in silico*-analysis presented in this manuscript (i.e. BTNL2, HLA-DPB1, HLA-B, MICA, ANXA11, IL23R, SH2B3, CRIP1, IL12B, MANBA, NFKB1 and FAM117B) or were previously described or hypothesized as potentially affected (i.e. TNF, HLA-DRB1, HLA-DQB1, OS9, CYP27B1,

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KCNK4, CCDC88B and RAB23). The analysis identified one prominent protein network, comprising key molecules of the IL12/IL23 signaling pathways (**Figure 3**).

Sharing of risk loci and cumulative heritability

Our study demonstrated a considerable sharing pattern of sarcoidosis susceptibility factors, especially of the IL23/IL12 signaling pathway with other disorders and phenotypes, such as ankylosing spondylitis, inflammatory bowel disease and psoriasis (*IL23R*, *IL12B* and *TYK2*), rheumatoid arthritis (*IL23R* and *TYK2*) and multiple sclerosis (*IL12B* and *TYK2*; reviewed in [17]). However, the exact association patterns are not identical for these conditions as illustrated in a comparison of the *IL12B* and *IL23R* signal for sarcoidosis, psoriasis and Crohn´s disease [35] **(Figure S3**). Sequential conditional logistic regression analysis, calculation of LD and test for epistasis proved the independence of the eleven sarcoidosis risk variants located in the *BTNL2, HLA-B, HLA-DPB1, ANXA11, IL23R, ATXN2, IL12B, MANBA, FAM117B,* chromosome 11q13.1 and *RAB23* regions (**Figure S4**). However, assuming a prevalence of 40/100,000, the cumulative heritability of the respective eleven lead variants was estimated to be only 2.78% (**Table S15)**.

Discussion

In our study, we successfully screened the largest sarcoidosis case-control study population to date for novel risk factors and identified chromosomes 12q24.12 (*ATXN2/SH2B3*), 5q33.3 (near *IL12B*), 4q24 (*MANBA/NFKB1*) and 2q33.2 (*FAM117B*) as susceptibility regions for sarcoidosis in the investigated European samples. We further found a novel, independent association signal on chromosome 1p31.3 (*IL23R*). Due to the extraordinary sample size and the applied level of significance, our findings are highly reliable to represent true genetic risk factors for sarcoidosis in Europeans. However, the analysis of the associated markers in an African-American sarcoidosis population was not successful, which could have power (<68% throughout all tests), genetic and functional reasons. This discrepancy points out the need for explicit trans-ancestry association studies to get insight into the genetic architecture of sarcoidosis across populations of diverse ancestry. Analysis of sarcoidosis subphenotypes revealed several findings with nominal significance. However, due to the large numbers of test, the majority of these results would not remain significant after correction for multiple testing and thus have to be investigated in independent samples for validation. Therefore these findings are not discussed in detail here.

The identified sarcoidosis susceptibility loci harbor genetic variants that may be functionally relevant in the context of sarcoidosis pathogenesis, affecting either known or novel players: First, variant rs3184504 on chromosome 12q24.12 induces an amino acid change (R262W) in the SH2B3 protein, an intriguing candidate. SH2B3 is involved in B-cell proliferation [36] and the endothelial response to TNF [37] and has not yet been implicated in sarcoidosis pathogenesis. The rs3184504*A risk allele is associated with stronger activation of the NOD2 recognition pathway in response to lipopolysaccharide and muramyl dipeptide, suggesting SH2B3 may play a role in protection against bacterial infection [38]. Second, among the associated markers in the chromosome 5q33.3 region, SNP rs1422877 confers allele-specific binding probabilities for the transcription factor RelA, which could influence the expression of neighboring genes, e.g. of the *IL12B* gene that encodes the p40 subunit of the IL12 and the IL23 receptors. Third, the lead SNP in the chromosome 1p31.3 region is located in the putative promoter region of the *IL23R* gene and might therefore influence *IL23R* expression. Fourth, the associated variants on chromosome 2q33.2 could affect the expression of many genes, among them BMPR2, which is involved in the regulation of inflammatory processes in the lung [39] and has been suggested as a core mediator in sarcoidosis pathogenesis in comparison to idiopathic pulmonary fibrosis [40]. Fifth, allelic variation of the candidate risk SNP rs34536443 (*TYK2* Pro1104Ala) is known to influence Th2 lymphocyte polarization [41]. The risk allele “C” reduces TYK2 activity in T lymphocytes and shifts the cytokine secretion towards a Th2 cytokine profile. This shift is also observed in severe sarcoidosis with progressing pulmonary fibrosis [42]. Strikingly, the rare rs34536443-C allele is strongly associated with fibrosis among sarcoidosis patients in panel F. Due to the large effect size (OR = 4.6), this finding provides potential for clinical application as a marker for high risk patients, given a successful independent replication. Functional hypotheses on risk variants in the remaining novel susceptibility regions are given in the **Supplementary information**. Since the identification of genetic defects and deranged pathways does not necessarily imply a direct link to immunopathogenesis or therapy, further experimental work is necessary to assess these above

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mentioned hypotheses and to clarify the potential role of the associated variants in the specific molecular processes in sarcoidosis pathogenesis and whether they represent useful targets in a therapeutic approach.

A network analysis of the potentially affected gene products defined in this study identified one prominent protein network, comprising key molecules of the IL12/IL23 signaling pathway (reviewed in [17]). From these data, we hypothesize that the IL12/Th1 and IL23/Th17 signaling pathways could be affected by the described risk alleles. Both, Th1 and Th17 cells are present in granulomas of sarcoidosis patients and are known to play a crucial role in disease process [43,44]. This is in line with emerging reports on the role of Th17 T cells in sarcoidosis and confirms Th1 cells as well-established players in disease pathogenesis [44,45].

Of note, the two loci *IL12B* and *IL23R* are shared risk loci for sarcoidosis, the skin disease psoriasis and the granulomatous Crohn´s disease, yet with differing association patterns. Given a more detailed genetic investigation, this information could be of value, since targeting the IL12/IL23 signaling pathway using the p40 antibody ustekinumab is approved in psoriasis treatment and also seems promising in the therapy of severe Crohn´s disease [46,47]. However, for sarcoidosis no such positive effect was observed [48]. Since genetic data were not incorporated in this ustekinumab trial in sarcoidosis, we hypothesize that genetic information might aid the identification of a subset of sarcoidosis patients that may have a higher chance to respond to the treatment, alike reported for a variant in the *TNF* locus and anti-TNF treatment [49]. Functional and clinical studies would be necessary to evaluate the usefulness of ustekinumab in such a genetically defined subcohort.

The HLA-region has long been known and is most consistently reported to be associated with sarcoidosis. Our group had reported the association of *BTNL2* and suggested the splice variant rs2076530 as the underlying risk factor before [2]. Since then, this association has been replicated in other European and non-European populations [4,50-55]. However, in this study the most strongly associated variants were located in the *BTNL2* promoter region and are predicted to reside in transcription factor (TF) binding sites. They may therefore influence expression of *BTNL2* by altering TF binding. Thus, this result may point to a different underlying mechanism, while it confirms BTNL2 as a risk factor for sarcoidosis.

The second independent signal in the HLA-region peaked near HLA-B with the common haplotype HLA-B*0801 showing the strongest effect, with lead SNP rs4143332 being significantly associated with acute sarcoidosis and Löfgren syndrome, which is in line with previous findings [56,57]. It is part of the so-called "8.1 ancestral haplotype" (HLA A*0101: Cw*0701: B*0801: DRB1*0301: DQA1*0501: DQB1*0201), which is common in Europeans and includes a large number of genes related to the immune system. The 8.1 ancestral haplotype has been repeatedly reported in the context of sarcoidosis susceptibility and progression [56,57] and is associated with several other immune-related diseases [58], for example systemic lupus erythematosus and primary sclerosing cholangitis [21,59].

The third signal in the HLA-region is located in the 5´-UTR region of *HLA-DPB1.* This gene encodes a subunit of the HLA-DP receptor that plays a central role in the immune system by presenting peptides derived from extracellular proteins. *HLA-DPB1* genotypes had been linked to sarcoidosis before [60-63] and the Glu69 variant (rs1042140) is known to be associated with chronic beryllium disease, a phenocopy of sarcoidosis [64]. In our study population, none of the Glu69 containing haplotypes were associated with genome-wide significance (data not shown). Instead, this is the first report that locates this association at *HLA-DPB1* to the 5´-UTR region of the gene, where the associated markers are predicted to affect miRNA binding and alternative splicing. See the **Supplementary information** for further functional hypotheses on associated variants. Overall, the genetic findings reported here are highly reliable, setting a most solid ground for subsequent experimental validation.

Altogether based on our study and previous findings, we defined eleven sarcoidosis risk loci (*BTNL2, HLA-B, HLA-DPB1, ANXA11, IL23R, SH2B3/ATXN2, IL12B, NFKB1/MANBA, FAM177B,* chromosome 11q13.1 and *RAB23*). However, the cumulative heritability of the eleven lead variants was estimated to be only 2.78%. This means that additional genetic risk factors for sarcoidosis remain to be discovered, which may include common variants with even smaller effects or risk alleles with lower frequencies, which were not targeted with the SNP selection strategy applied in this study. The detected loci show a considerable sharing pattern with other disorders and phenotypes. This overlap is supportive of the hypothesis that sarcoidosis shares a common genetic background with other immune-related diseases. Thus, our findings

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may inspire a revised classification of clinical disease manifestations and subphenotypes and may provide hypotheses for novel therapeutic targets.

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Figure legends:

Fig. 1: Association signals of newly discovered sarcoidosis risk regions in panel A that showed genome-wide significance in the joint analysis of the European case-control panels A, B-I, B-II, C-I and C-II on (**a**) chromosome 12q24.12 (lead SNP rs653178, non-synonymous SNP rs3184504) and (**b**) 5q33.3 (lead SNP rs4921492), (**c**) 4q24 (lead SNP rs223498) and (**d**) 2q33.2 (lead SNP rs6748088) . The respective lead SNPs are marked by blue diamonds. The strength of LD (r^2) between the lead SNP and surrounding markers and the recombination rate is given according to according to 1000 Genomes data (phase I - release March 2012) and is indicated by red to yellow coloring and the light blue line, respectively. Positions shown are according to NCBI's build 37(hg19).

Fig. 2. Association signals with genome-wide significance in the screening panel A: (**a**) BTNL2 (rs5007259), (**b**) HLA-B (rs414332), (**c**) HLA-DRB1 (rs9267488) and (**d**) IL23R (rs12069782). For (b) and (c) the depicted p values are derived from the sequential conditional regression analysis, conditioned on SNP rs5007259 (b) and on rs5007259 and rs414332 (c). See Figure 1 for descriptions.

Fig. 3: Protein interaction network, which was generated using STRING based on i) co-expression of the respective transcripts, ii) experiments and iii) information from (in parts) curated pathway databases, applying a confidence score > 0.7. Colored nodes represent proteins that are or may be affected by sarcoidosis risk variants.

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Tables:

Table 1: Study populations; the number of individuals is given after (and before) quality control.

Panel	**Descent**	**Number of cases**	**% male**	**Mean age in 2014 (years) [SD]**	**Number of controls**	**% male**	**Mean age in 2014 (years) [SD]**
A	European (Germany)	1726 (1869)	39 (40)	62.9 [11.6]	5482 (5600)	51 (51)	57.2 [12.6]
B-I	European (Germany)	573 (585)	49 (49)	55.7 [12.6]	3327 (3500)	47 (47)	48.7 [14.9]
B-II	European (Germany)	266 (307)	46 (45)	61.0 [13.7]	266 (285)	50 (50)	58.3 [17.7]
C-I	European (Czech Republic)	256 (267)	45 (46)	56.2 [13.1]	305 (330)	42 (43)	45.6 [9.6]
C-II	European (Sweden)	817 (1121)	57 (58)	54.1 [12.4]	2040	28	53.6 [11.2]
D	African-American (USA)	781	26	47.9 [15.2]	876	22	38.9 [10.2]
E	European (Germany)	342*	43	52.5 [7.2]**	-	-	-
F	European (Serbia)	920 (920)	47	53.3 [11.4]	-	-	-

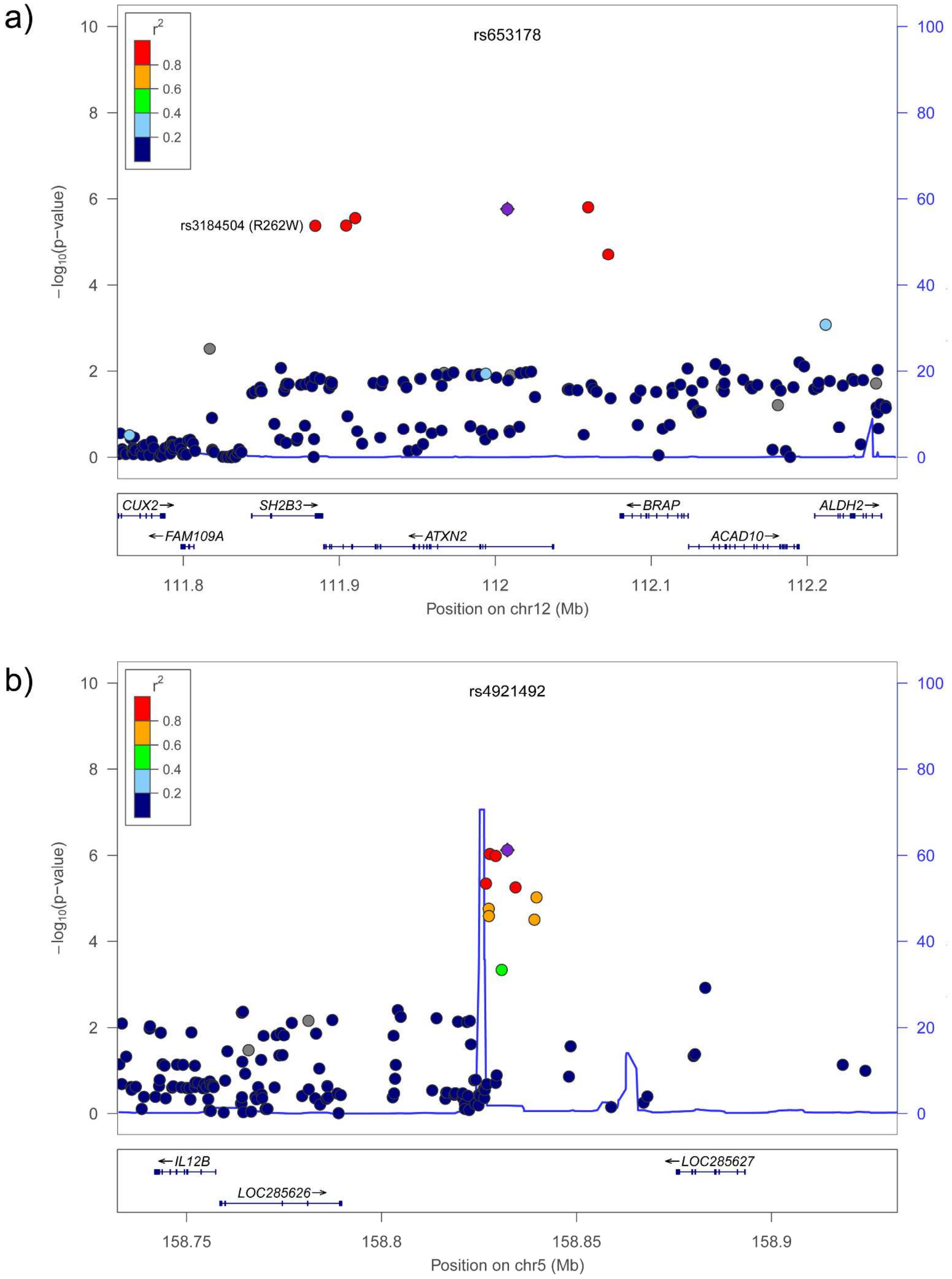
*number of trios (two parents with one affected offspring) **given for the affected offspring

Table 2: Association results for newly discovered sarcoidosis risk variants. The position of the respective lead variant is given according to human genome build 19. Odds Ratios (OR) refer to allele 1 (A1), and P values are presented for the logistic regression model using an allelic model for genotype coding. The threshold for genome-wide significance ($p < 5 \times 10^{-8}$) in the Cochran-Mantel-Haenzel test (P CMH) was applied to define a true association.

	dbSNP ID	**rs653178**	**rs4921492**	**rs223498**	**rs6748088**
	Chr	12	5	4	2
	Position	112,007,756	158,832,277	103,651,962	203,264,771
	Candidate genes	*ATXN2, SH2B3*	*IL12B*	*NFKB, MANBA*	*FAM117B*
	A1	G	A	C	C
	A2	A	C	A	T
Panel A	**AF**$_{cases}$	0.55	0.39	0.51	0.34
	AF$_{controls}$	0.5	0.34	0.47	0.31
	P value	1.36×10^{-6}	7.56×10^{-7}	6.68×10^{-6}	4.30E-04
	OR [95% CI]	1.21 [1.12-1.30]	1.22 [1.13-1.32]	1.19 [1.10-1.29]	1.16 [1.07-1.26]
Panel B-I	**AF**$_{cases}$	0.54	0.39	0.52	0.35
	AF$_{controls}$	0.49	0.35	0.48	0.30
	P value	8.06×10^{-3}	0.019	0.012	1.34E-04
	OR [95% CI]	1.19 [1.05-1.34]	1.17 [1.03-1.33]	1.18 [1.04-1.33]	1.29 [1.13-1.48]
Panel B-II	**AF**$_{cases}$	0.54	0.4	0.5	0.37
	AF$_{controls}$	0.51	0.33	0.48	0.31
	P value	ns	0.039	ns	0.048
	OR [95% CI]	1.13 [0.89-1.44]	1.33 [1.04-1.71]	1.08 [0.85-1.38]	1.29 [1.00-1.67]
Panel C-I	**AF**$_{cases}$	0.58	0.38	0.44	0.36
	AF$_{controls}$	0.48	0.36	0.49	0.32
	P value	8.94×10^{-4}	ns	ns	ns
	OR [95% CI]	1.49 [1.18-1.89]	1.11 [0.87-1.41]	0.82 [0.64-1.03]	1.20 [0.94-1.54]
Panel C-II	**AF**$_{cases}$	0.50	0.38	0.54	0.32
	AF$_{controls}$	0.48	0.35	0.48	0.30
	P value	ns	ns	1.08×10^{-5}	ns
	OR [95% CI]	1.12 [0.99-1.26]	1.14 [0.94-1.39]	1.30 [1.16-1.46]	1.10 [0.95-1.27]
Joint analysis	**P CMH**	1.64×10^{-10}	2.14×10^{-9}	1.28×10^{-9}	2.10×10^{-8}
	OR [95% CI]	1.19 [1.14-1.27]	1.20 [1.13-1.27]	1.19 [1.12-1.26]	1.18 [1.11-1.25]

Figures

Figure 1



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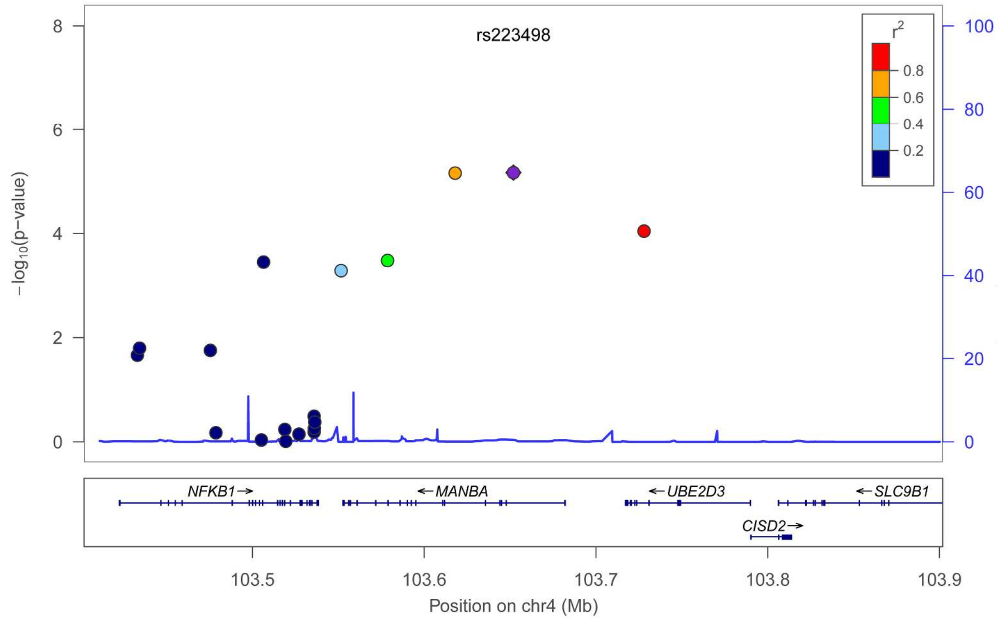
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40
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80
100
NFKB1→
←MANBA
←UBE2D3
←SLC9B1
CISD2→
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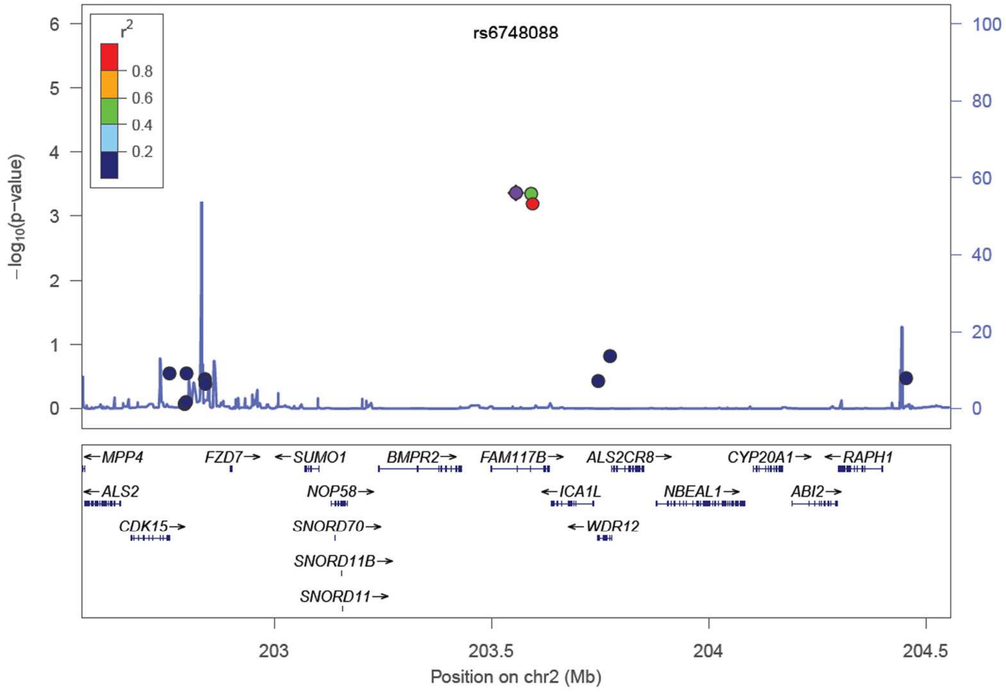
103.6
103.7
103.8
103.9
Position on chr4 (Mb)

d)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←ALS2
NOP58→
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NBEAL1→
ABI2→
CDK15→
SNORD70→
←WDR12
SNORD11B→
SNORD11→
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Position on chr2 (Mb)

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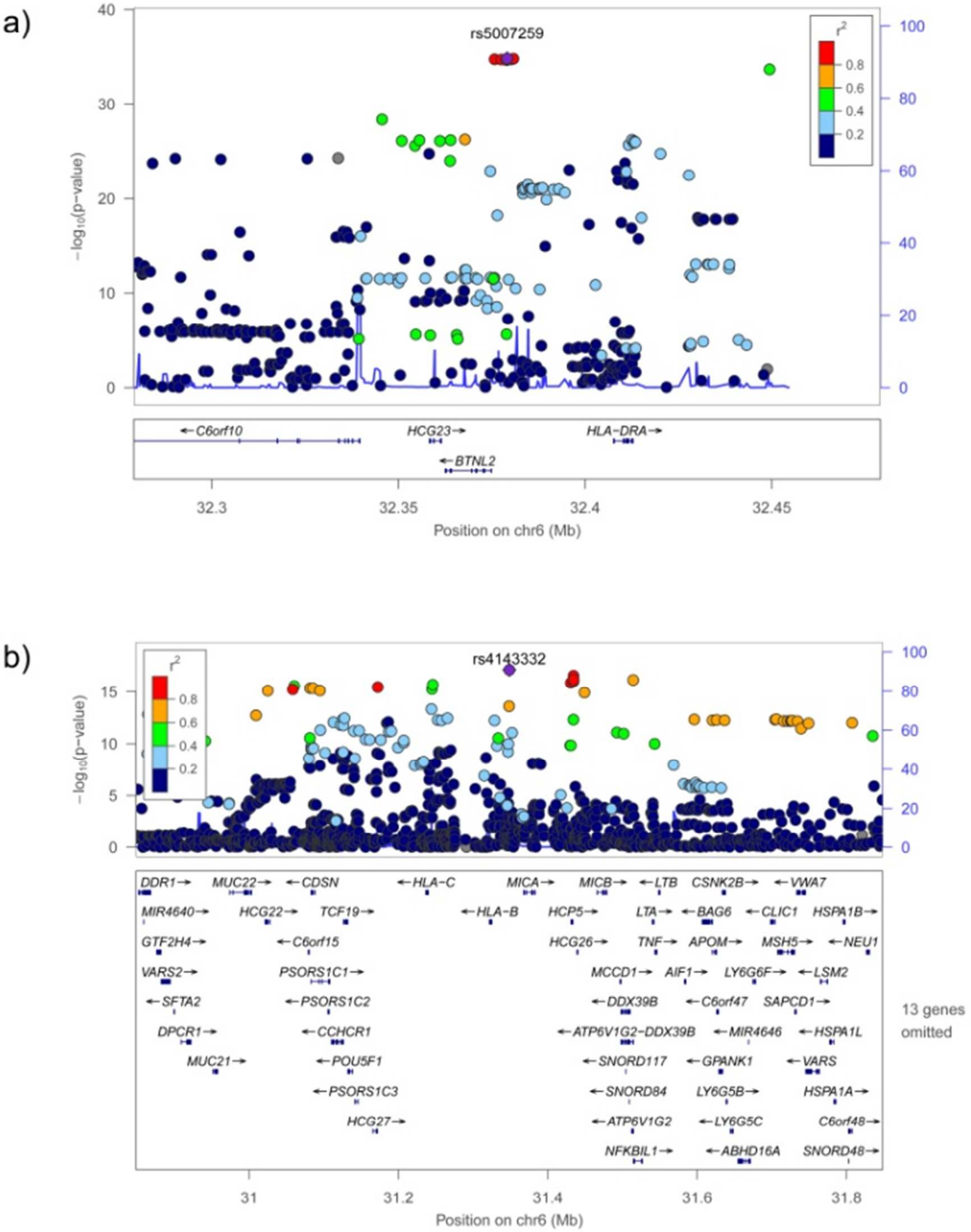
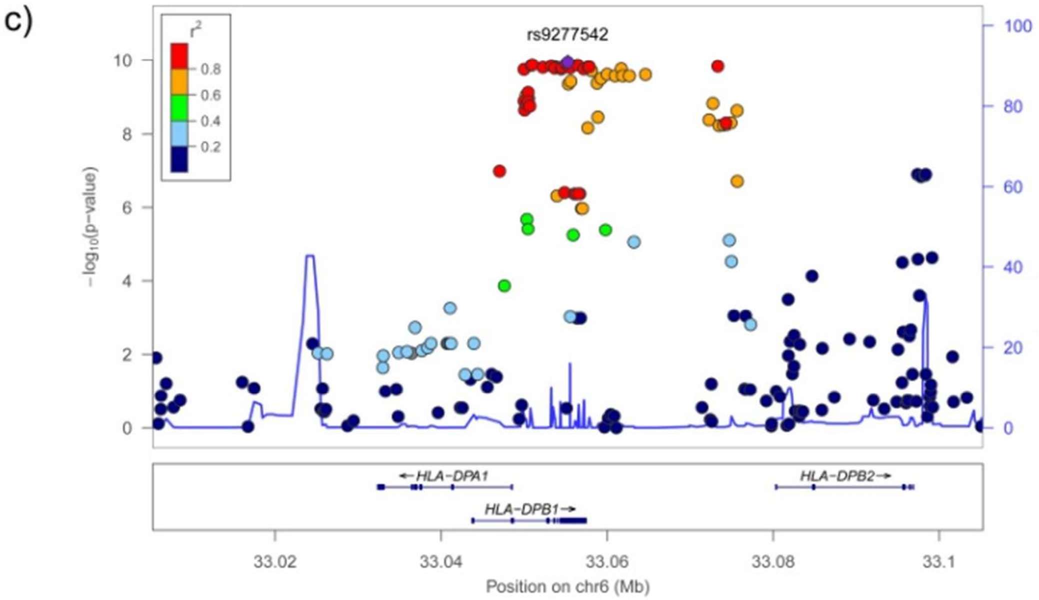
Figure 2




c)
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0
20
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60
80
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HLA−DPB2
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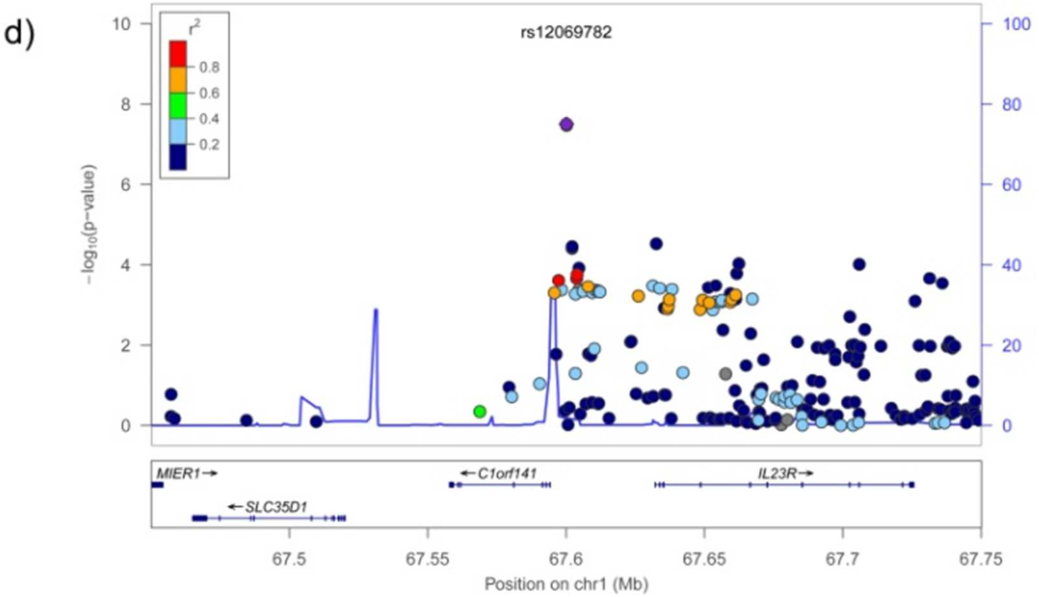
33.04
33.06
33.08
33.1
Position on chr6 (Mb)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C1orf141
IL23R
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67.55
67.6
67.65
67.7
67.75
Position on chr1 (Mb)

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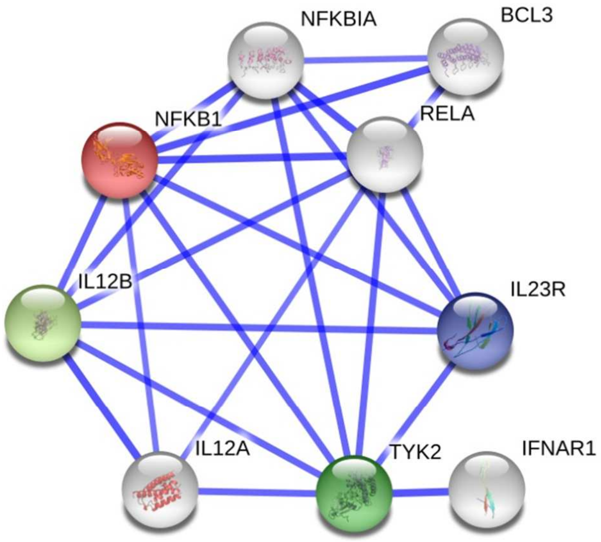
Figure 3



Identification of immune-relevant factors conferring sarcoidosis genetic risk

ONLINE SUPPLEMENTARY MATERIALS

Contents

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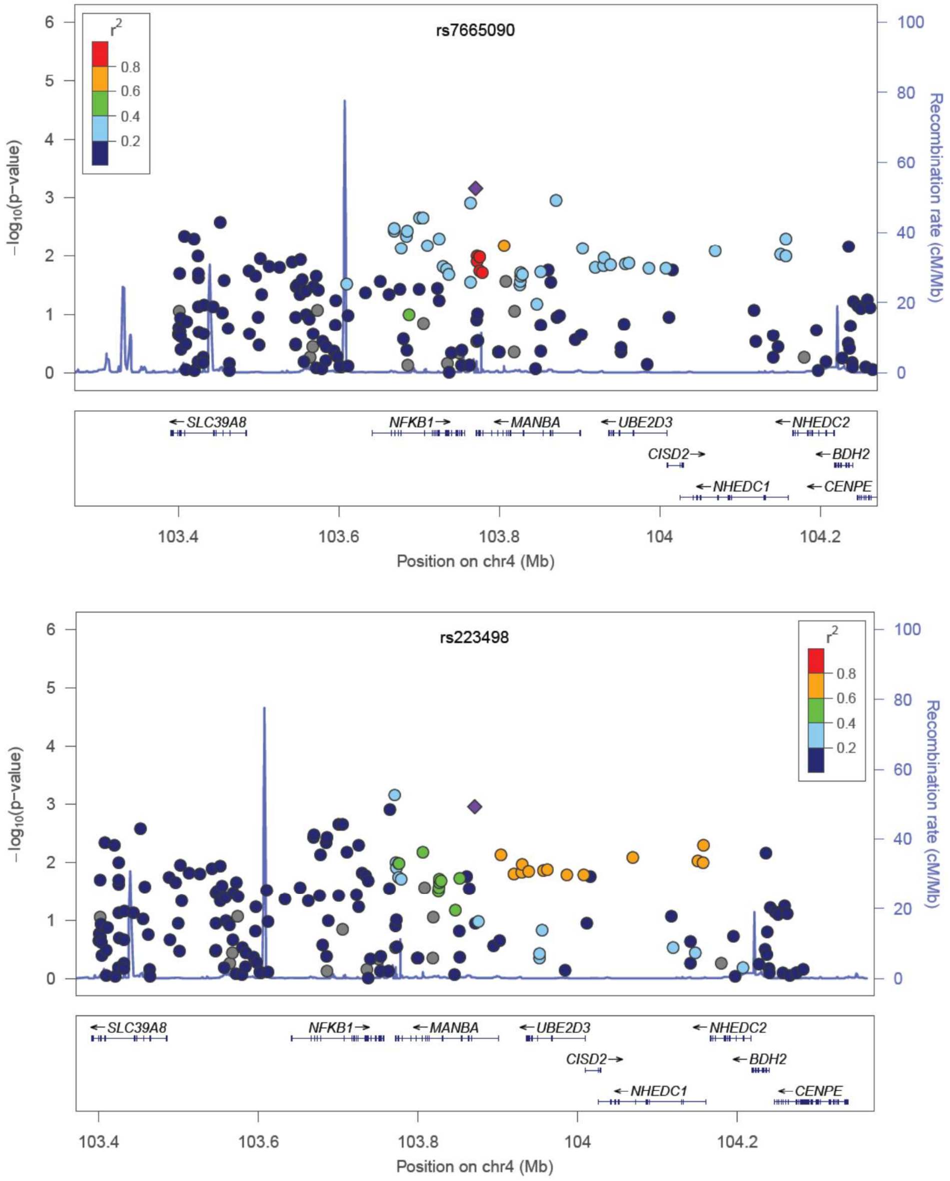
Figure S1: Association signal in the extended MANBA and FAM117B region

A: Association signals from a previously published GWAS using the Affymetrix 6.0 Human Gene Chip and imputation [1]. Chromosomal positions are given according to human genome build 18. The lead SNP is named on top of the plots and the respective signal is marked by a purple diamond. **B:** Association signals from a previously published GWAS using the Affymetrix 6.0 Human Gene Chip [2]. Chromosomal positions are given according to human genome build 19.

A



B

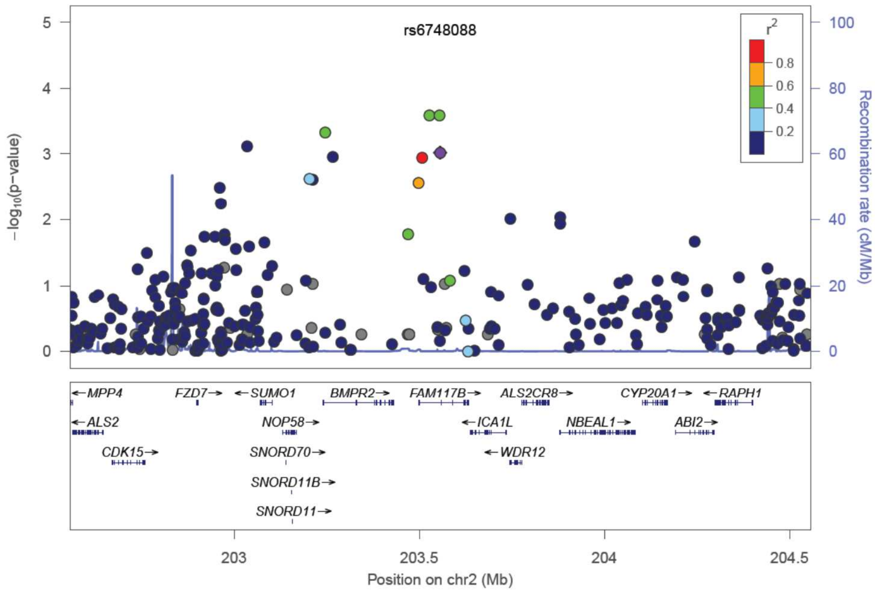

rs6748088
r²
0.8
0.6
0.4
0.2
5
4
3
2
1
0
−log10(p−value)
100
80
60
40
20
0
Recombination rate (cM/Mb)
←MPP4
FZD7→
←SUMO1
BMPR2→
FAM117B→
ALS2CR8→
CYP20A1→
←RAPH1
←ALS2
NOP58→
←ICA1L
NBEAL1→
ABI2→
CDK15→
SNORD70→
←WDR12
SNORD11B→
SNORD11→
203
203.5
204
204.5
Position on chr2 (Mb)

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Figure S2: Association signal in the *BTNL2* gene region

The lead SNP (rs5007259) is marked by a red diamond, and the splicing SNP rs2076530 is depicted in orange.

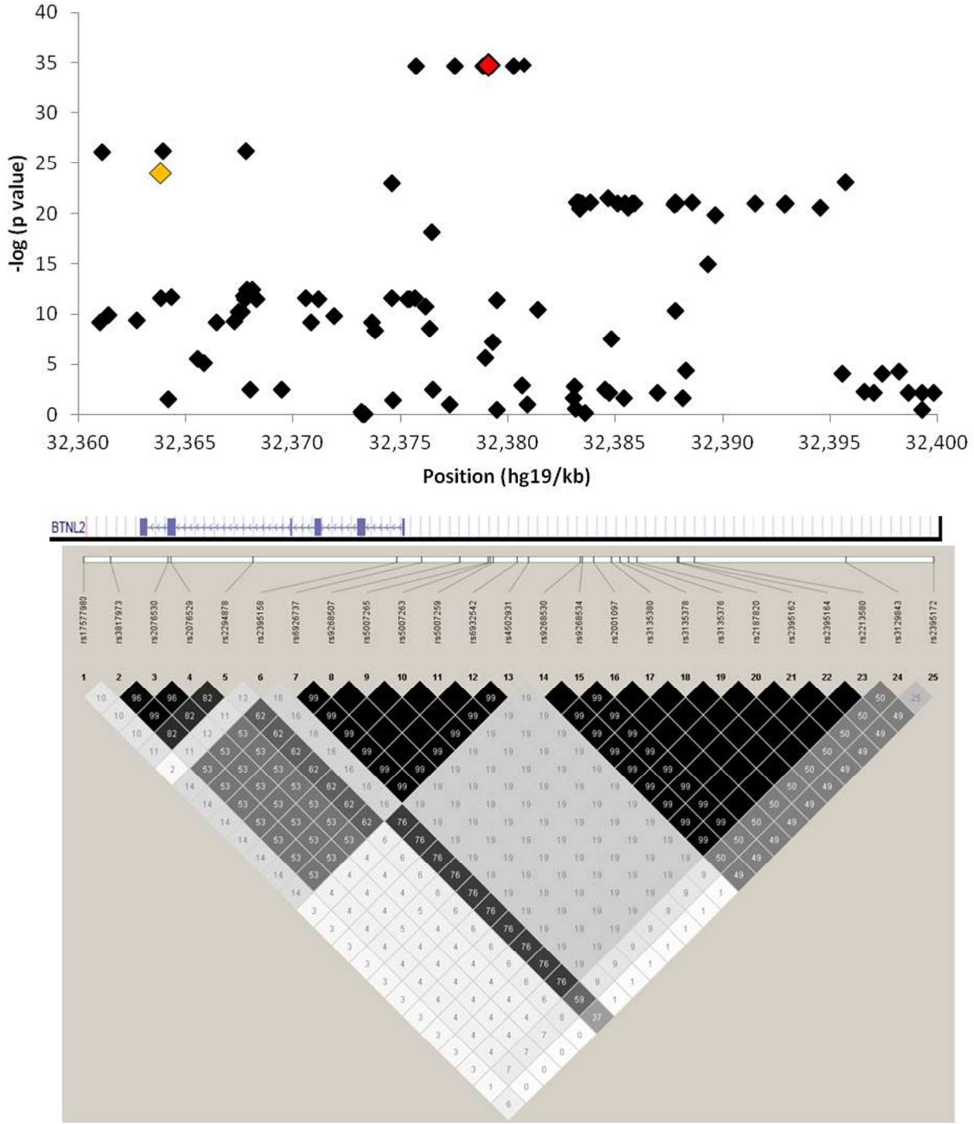

Figure S3: Comparison of signals in the associated *IL23R* and *IL12B* loci between sarcoidosis, Crohn´s disease and psoriasis

Results for Crohn´s disease (CD) and psoriasis (PS) are included in prior studies [3,4], and are derived from the analysis of 1773 German CD, 615 German PS patients and the controls of panel A (n =5482). Odds ratios are shown for SNPs that display a p value < 0.05 in the association analysis (except plot a): p < 0.1 for PS) and an OR > 1.15 or an OR < 0.87, respectively. The lead SNP reported here are marked by a black line and box.

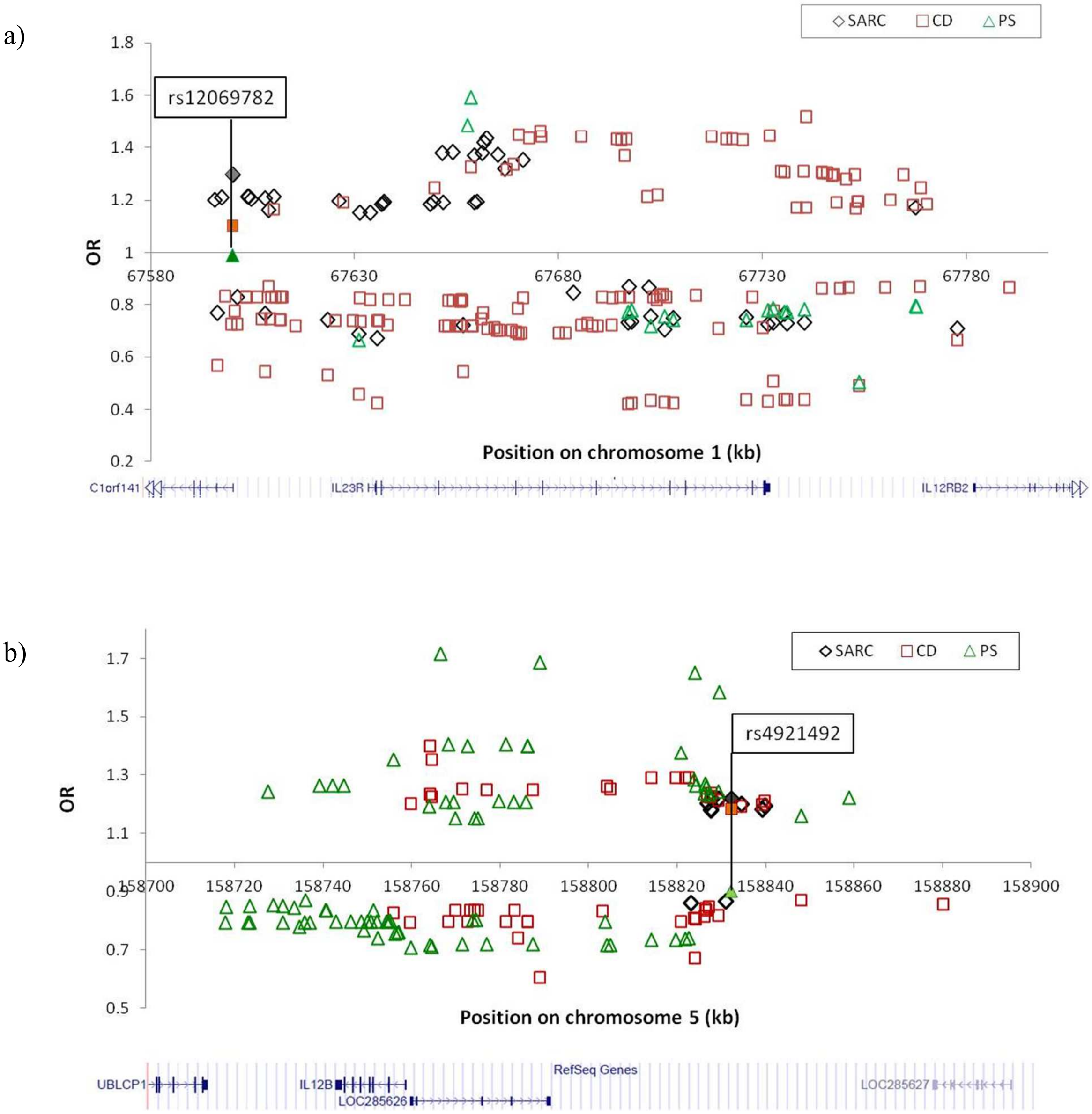

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Figure S4: LD (r²) between confirmed sarcoidosis risk loci in panel A

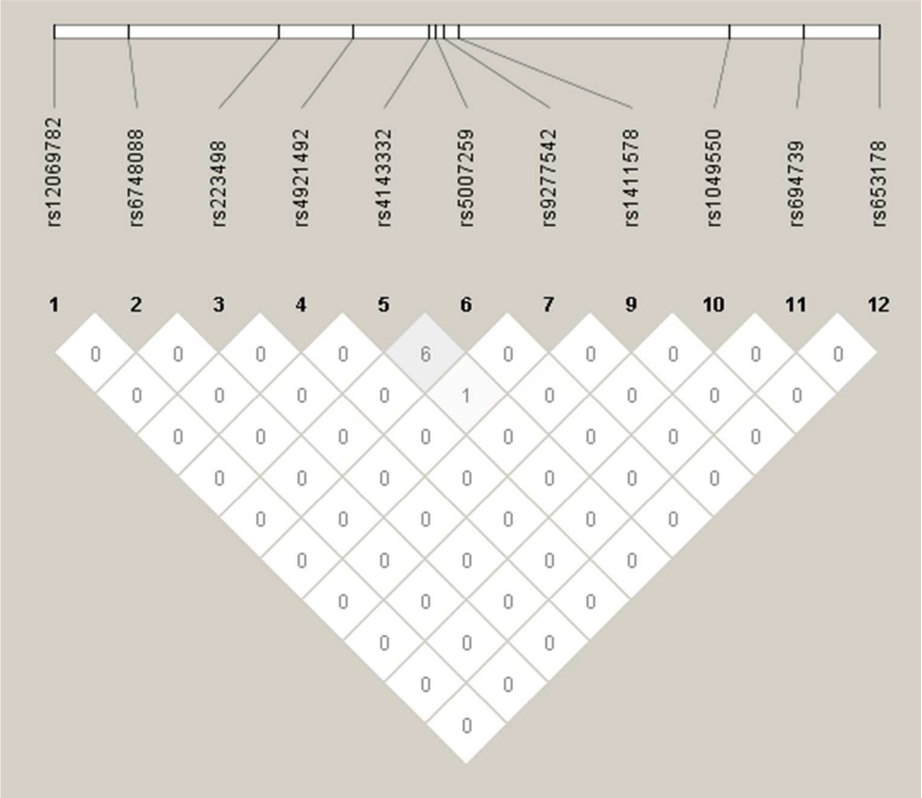

Table S1: Results of the subphenotype analysis for marker rs653178 (*ATXN2/SH2B3*)

Abbreviations: allele frequency (AF); subphenotype (SPT); p value (P): odds ratio (OR); lower 95% confidence interval (L95); upper 95% confidence interval (U95). P values < 0.05 are marked in red.

Panel	Allele	AF controls	N controls	subphenotype	N SPT	AF (panel E: T/A)	P	OR	L95	U95	N non-SPT	AF non-SPT	P	OR	L95	U95
A	T	0.50	5482	acute	566	0.45	8.06E-04	0.81	0.72	0.92	1025	0.45	7.96E-01	0.98	1.14	0.85
A	T	0.50	5482	chronic	1025	0.45	**7.80E-05**	0.83	0.75	0.91	566	0.45	7.96E-01	1.02	0.88	1.18
A	T	0.50	5482	Löfgren	64	0.45	2.90E-01	0.83	0.58	1.18	401	0.45	9.14E-01	0.98	0.67	1.42
A	T	0.50	5482	eye	33	0.45	4.60E-01	0.83	0.51	1.35	-	-	-	-	-	-
A	T	0.50	5482	skin	66	0.47	4.86E-01	0.89	0.63	1.25	1519	0.45	7.10E-01	1.07	0.75	1.52
B-I	C	0.49	3278	acute	187	0.55	1.23E-02	1.31	1.06	1.61	374	0.53	5.28E-01	1.08	0.84	1.39
B-I	C	0.49	3278	chronic	374	0.53	1.61E-02	1.21	1.04	1.41	187	0.55	5.28E-01	0.92	1.18	0.72
B-I	C	0.49	3278	Löfgren	57	0.55	1.65E-01	1.30	0.90	1.89	-	-	-	-	-	-
B-I	C	0.49	3278	eye	44	0.60	3.17E-02	1.60	1.04	2.45	-	-	-	-	-	-
B-II	T	0.49	285	acute	50	0.49	9.90E-01	1.00	0.66	1.54	185	0.43	3.04E-01	1.26	1.96	0.81
B-II	T	0.49	285	chronic	185	0.43	8.85E-02	0.80	0.61	1.04	50	0.49	3.04E-01	0.79	0.51	1.24
B-II	T	0.49	285	Löfgren	38	0.59	9.26E-02	1.52	0.93	2.46	211	0.42	6.75E-03	1.97	1.20	3.24
B-II	T	0.49	285	skin	22	0.50	8.92E-01	1.04	0.57	1.93	213	0.45	5.32E-01	1.22	0.66	2.27
C-I	T	0.53	330	acute	20	0.47	4.97E-01	0.80	1.53	0.41	40	0.43	6.90E-01	1.17	2.56	0.54
C-I	T	0.53	330	bones,muscle,joints	19	0.44	3.15E-01	0.71	0.36	1.39	-	-	-	-	-	-
C-I	T	0.53	330	chronic	40	0.43	1.12E-01	0.68	1.10	0.42	20	0.47	6.90E-01	0.85	0.39	1.86
C-I	T	0.53	330	extra pulmonary	65	0.47	2.03E-01	0.78	0.54	1.14	65	0.52	3.83E-01	0.80	0.49	1.31
C-I	T	0.53	330	liver	21	0.52	9.35E-01	0.97	0.52	1.82	-	-	-	-	-	-
C-I	T	0.53	330	Löfgren	46	0.46	1.83E-01	0.74	0.48	1.15	191	0.41	4.00E-01	1.22	0.77	1.94
C-I	T	0.53	330	persistent	110	0.41	2.55E-03	0.62	0.45	0.85	88	0.48	1.99E-01	0.77	0.51	1.15
C-I	T	0.53	330	resolving	88	0.48	2.11E-01	0.81	0.58	1.13	110	0.41	1.99E-01	1.30	1.95	0.87

C-I	T	0.53	330	skin	40	0.44	1.15E-01	0.68	0.43	1.10	-	-	-	-	-	-
D	C	0.07	784	eye	163	0.06	4.32E-01	0.82	0.49	1.36	327	0.07	4.40E-01	0.80	0.46	1.41
D	C	0.07	784	liver	115	0.05	3.24E-01	0.72	0.38	1.38	375	0.08	3.22E-01	0.71	0.36	1.40
D	C	0.07	784	extra pulmonary	446	0.08	7.73E-01	1.05	0.76	1.45	121	0.06	3.98E-01	1.29	0.71	2.33
D	C	0.07	784	skin	222	0.08	4.04E-01	1.19	0.79	1.77	274	0.06	1.35E-01	1.48	0.89	2.46
E	C	-	-	acute	94	34/45	2.16E-01	0.76	0.48	1.18	-	-	-	-	-	-
E	C	-	-	chronic	212	100/101	9.44E-01	0.99	0.75	1.31	-	-	-	-	-	-
F	T	-	-	chronic	435	0.45	-	-	-	-	484	0.46	4.98E-01	0.94	0.78	1.13
F	T	-	-	persistent	535	0.45	-	-	-	-	382	0.46	8.23E-01	0.98	0.81	1.18
F	T	-	-	skin	113	0.49	-	-	-	-	807	0.45	3.66E-01	1.14	0.86	1.52
F	T	-	-	cardiac	34	0.42	-	-	-	-	886	0.46	5.88E-01	0.87	0.53	1.43
F	T	-	-	CNS	56	0.41	-	-	-	-	864	0.46	3.12E-01	0.82	0.56	1.21
F	T	-	-	fibrosis	25	0.40	-	-	-	-	883	0.46	4.31E-01	0.79	0.45	1.41
F	T	-	-	eye	113	0.47	-	-	-	-	807	0.46	7.10E-01	1.06	0.80	1.40
F	T	-	-	extra pulmonary	229	0.46	-	-	-	-	685	0.46	9.39E-01	0.99	0.80	1.23

Table S2: Results of the subphenotype analysis for marker rs4921492 (*IL12B*)

Abbreviations and description: See Table S1.

Panel	Allele	AF controls	N controls	subphenotype	N SPT	AF (panel E: T/A)	P	OR	L95	U95	N non-SPT	AF non-SPT	P	OR	L95	U95
A	A	0.34	5482	acute	566	0.38	1.66E-02	1.17	1.03	1.32	1025	0.40	3.33E-01	0.93	1.08	0.80
A	A	0.34	5482	chronic	1025	0.40	**3.84E-06**	1.26	1.14	1.38	566	0.38	3.33E-01	1.08	0.93	1.25
A	A	0.34	5482	Löfgren	64	0.39	2.63E-01	1.23	0.86	1.75	401	0.41	7.20E-01	0.93	0.64	1.36
A	A	0.34	5482	eye	33	0.36	7.30E-01	1.09	0.66	1.81	-	-	-	-	-	-
A	A	0.34	5482	skin	66	0.33	6.72E-01	0.92	0.64	1.33	1519	0.39	1.40E-01	0.76	0.52	1.10
B-I	A	0.35	3278	acute	187	0.40	5.71E-02	1.23	0.99	1.52	374	0.38	5.22E-01	1.09	1.40	0.84
B-I	A	0.35	3278	chronic	374	0.38	1.23E-01	1.13	0.97	1.33	187	0.40	5.22E-01	0.92	0.71	1.19
B-I	A	0.35	3278	Löfgren	57	0.42	1.12E-01	1.35	0.93	1.97	-	-	-	-	-	-
B-I	A	0.35	3278	eye	44	0.38	6.17E-01	1.12	0.72	1.73	-	-	-	-	-	-
B-II	A	0.33	285	acute	50	0.41	1.37E-01	1.39	0.90	2.15	185	0.38	3.84E-01	1.12	1.75	0.71
B-II	A	0.33	285	chronic	185	0.38	1.15E-01	1.25	0.95	1.64	50	0.41	3.84E-01	0.90	0.57	1.41
B-II	A	0.33	285	Löfgren	38	0.37	5.44E-01	1.17	0.71	1.92	211	0.39	6.81E-01	0.90	0.54	1.49
B-II	A	0.33	285	skin	22	0.36	6.82E-01	1.14	0.60	2.17	213	0.40	6.69E-01	0.87	0.46	1.66
C-I	A	0.34	330	acute	20	0.48	9.06E-02	1.73	0.91	3.28	40	0.30	5.95E-02	2.11	4.62	0.96
C-I	A	0.34	330	bones,muscle,joints	19	0.34	9.86E-01	0.99	0.50	1.98	-	-	-	-	-	-
C-I	A	0.34	330	chronic	40	0.30	4.38E-01	0.82	0.49	1.36	20	0.48	5.95E-02	0.47	0.22	1.04
C-I	A	0.34	330	extra pulmonary	65	0.39	2.87E-01	1.23	0.84	1.82	65	0.36	6.29E-01	1.13	0.68	1.88
C-I	A	0.34	330	liver	21	0.40	4.19E-01	1.30	0.69	2.46	-	-	-	-	-	-
C-I	A	0.34	330	Löfgren	46	0.39	3.67E-01	1.23	0.78	1.92	191	0.38	9.09E-01	1.03	0.64	1.64
C-I	A	0.34	330	persistent	110	0.37	4.31E-01	1.14	0.83	1.56	88	0.36	7.62E-01	1.07	0.71	1.61
C-I	A	0.34	330	resolving	88	0.36	7.20E-01	1.07	0.75	1.51	110	0.37	7.62E-01	0.94	1.42	0.62
C-I	A	0.34	330	skin	40	0.45	6.01E-02	1.56	0.98	2.50	-	-	-	-	-	-

D	A	0.32	784	eye	163	0.35	2.83E-01	1.15	0.89	1.48	327	0.34	7.81E-01	1.04	0.78	1.40
D	A	0.32	784	liver	115	0.34	6.02E-01	1.08	0.80	1.46	375	0.35	8.90E-01	0.98	0.70	1.37
D	A	0.32	784	extra pulmonary	446	0.34	2.61E-01	1.11	0.93	1.32	121	0.34	9.89E-01	1.00	0.73	1.37
D	A	0.32	784	skin	222	0.34	4.24E-01	1.10	0.88	1.37	274	0.35	7.30E-01	0.95	0.72	1.26
E	C	-	-	acute	94	53/48	6.19E-01	1.10	0.75	1.63	-	-	-	-	-	-
E	C	-	-	chronic	212	100/75	5.88E-02	1.33	0.99	1.80	-	-	-	-	-	-
F	A	-	-	chronic	435	0.44	-	-	-	-	484	0.41	1.48E-01	1.15	0.95	1.39
F	A	-	-	persistent	535	0.43	-	-	-	-	382	0.41	3.31E-01	1.10	0.91	1.33
F	A	-	-	skin	113	0.41	-	-	-	-	807	0.42	7.71E-01	0.96	0.72	1.28
F	A	-	-	cardiac	34	0.35	-	-	-	-	886	0.42	2.18E-01	0.72	0.43	1.21
F	A	-	-	CNS	56	0.52	-	-	-	-	864	0.42	3.49E-02	1.51	1.03	2.23
F	A	-	-	fibrosis	25	0.44	-	-	-	-	883	0.42	7.70E-01	1.09	0.62	1.92
F	A	-	-	eye	113	0.43	-	-	-	-	807	0.42	8.65E-01	1.03	0.77	1.36
F	A	-	-	extra pulmonary	229	0.44	-	-	-	-	685	0.42	4.59E-01	1.09	0.87	1.35

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Table S3: Results for SNPs in the associated region on chromosome 5q33.3 (*IL12B*) region

Results are shown for the 6 SNPs most strongly associated SNPs, i.e. smallest p value, in the 5q33.3 region. Odds ratios (OR) refer to Allele 1 (A1); further abbreviations: 95 % confidence intervals for OR (95 % CI); Linkage disequilibrium (LD).

SNP	Position hg19	A1	P	OR [95% CI]	LD with rs4921492 (r^2)
rs4921492	158,832,277	A	7.56E-07	1.22 [1.13-1.32]	-
rs56167332	158,827,769	A	9.30E-07	1.22 [1.13-1.32]	0.86
rs755374	158,829,294	A	1.03E-06	1.22 [1.13-1.32]	0.90
rs6871626	158,826,792	T	4.60E-06	1.21 [1.11-1.30]	0.85
rs60689680	158,834,367	T	5.63E-06	1.20 [1.11-1.30]	0.85
rs12651787	158,839,745	C	9.59E-06	1.20 [1.10-1.29]	0.80

Table S4: Results of the subphenotype analysis for marker rs223498 (*MANBA/NFKB1*)

Abbreviations and description: See Table S1.

panel	Allele	MAF controls	N controls	subphenotype	N SPT	MAF (panel E: T/A)	P	OR	L95	U95	N non-SPT	MAF non-SPT	P	OR	L95	U95
A	C	0.47	5482	acute	566	0.52	4.48E-04	1.25	1.10	1.41	1025	0.50	2.24E-01	1.09	1.27	0.95
A	C	0.47	5482	chronic	1025	0.50	7.34E-03	1.14	1.04	1.25	566	0.52	2.24E-01	0.91	0.79	1.06
A	C	0.47	5482	Löfgren	64	0.53	1.56E-01	1.29	0.91	1.83	401	0.48	2.47E-01	1.25	0.86	1.81
A	C	0.47	5482	eye	33	0.47	9.94E-01	1.00	0.61	1.64	-	-	-	-	-	-
A	C	0.47	5482	skin	66	0.52	2.83E-01	1.21	0.86	1.70	1519	0.51	8.47E-01	1.04	0.73	1.47
B-I	C	0.49	3278	acute	187	0.51	3.51E-01	1.11	0.90	1.36	374	0.53	5.48E-01	0.93	0.72	1.19
B-I	C	0.49	3278	chronic	374	0.53	2.38E-02	1.19	1.02	1.39	187	0.51	5.48E-01	1.08	1.39	0.84
B-I	C	0.49	3278	Löfgren	57	0.52	5.03E-01	1.14	0.78	1.64	-	-	-	-	-	-

B-I	C	0.49	3278	eye	44	0.52	4.92E-01	1.16	0.76	1.77	-	-	-	-	-	-
B-II	C	0.48	285	acute	50	0.43	3.78E-01	0.82	0.52	1.28	185	0.44	9.14E-01	0.97	1.57	0.61
B-II	C	0.48	285	chronic	185	0.44	2.06E-01	0.84	0.64	1.10	50	0.43	9.14E-01	1.03	0.64	1.65
B-II	C	0.48	285	Löfgren	38	0.34	3.15E-02	0.55	0.32	0.95	211	0.44	1.45E-01	0.66	0.37	1.16
B-II	C	0.48	285	skin	22	0.40	3.14E-01	0.72	0.37	1.38	213	0.43	6.94E-01	0.88	0.45	1.70
C-I	C	0.49	330	acute	20	0.47	7.74E-01	0.90	0.43	1.87	40	0.53	5.59E-01	0.77	1.84	0.32
C-I	C	0.49	330	bones,muscle,joints	19	0.47	7.74E-01	0.90	0.43	1.87	-	-	-	-	-	-
C-I	C	0.49	330	chronic	40	0.53	5.65E-01	1.16	0.69	1.95	20	0.47	5.59E-01	1.30	0.54	3.09
C-I	C	0.49	330	extra pulmonary	65	0.49	9.77E-01	0.99	0.68	1.46	65	0.47	7.47E-01	1.09	0.65	1.84
C-I	C	0.49	330	liver	21	0.48	8.21E-01	0.93	0.49	1.76	-	-	-	-	-	-
C-I	C	0.49	330	Löfgren	46	0.50	9.12E-01	1.03	0.64	1.64	191	0.44	3.69E-01	1.25	0.77	2.03
C-I	C	0.49	330	persistent	110	0.46	4.22E-01	0.88	0.64	1.21	88	0.46	9.25E-01	1.02	0.67	1.54
C-I	C	0.49	330	resolving	88	0.46	4.02E-01	0.86	0.61	1.22	110	0.46	9.25E-01	0.98	1.48	0.65
C-I	C	0.49	330	skin	40	0.46	5.65E-01	0.86	0.53	1.42	-	-	-	-	-	-
D	A	0.17	784	eye	163	0.20	4.19E-01	1.13	0.84	1.53	327	0.20	9.74E-01	0.99	0.71	1.39
D	A	0.17	784	liver	115	0.20	2.94E-01	1.21	0.85	1.72	375	0.19	6.69E-01	1.09	0.74	1.59
D	A	0.17	784	extra pulmonary	446	0.19	4.07E-01	1.09	0.89	1.35	121	0.24	1.51E-01	0.78	0.55	1.10
D	A	0.17	784	skin	222	0.18	7.85E-01	1.04	0.79	1.37	274	0.21	3.24E-01	0.85	0.62	1.17
E	C	-	-	acute	94	46/50	6.83E-01	0.92	0.62	1.37	-	-	-	-	-	-
E	C	-	-	chronic	212	98/83	2.65E-01	1.18	0.88	1.58	-	-	-	-	-	-
F	A	-	-	chronic	435	0.49	-	-	-	-	484	0.50	7.87E-01	0.97	0.81	1.17
F	A	-	-	persistent	535	0.49	-	-	-	-	382	0.50	6.33E-01	0.95	0.79	1.15
F	A	-	-	skin	113	0.51	-	-	-	-	807	0.49	5.16E-01	1.10	0.83	1.47
F	A	-	-	cardiac	34	0.58	-	-	-	-	886	0.49	1.67E-01	1.43	0.86	2.36
F	A	-	-	CNS	56	0.53	-	-	-	-	864	0.49	4.61E-01	1.16	0.79	1.70
F	A	-	-	fibrosis	25	0.48	-	-	-	-	883	0.49	8.32E-01	0.94	0.52	1.69
F	A	-	-	eye	113	0.50	-	-	-	-	807	0.49	9.47E-01	1.01	0.76	1.34
F	A	-	-	extra pulmonary	229	0.50	-	-	-	-	685	0.49	7.02E-01	1.04	0.84	1.30

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Table S5: Results of the subphenotype analysis for marker rs6748088 (*FAM117B*)

Abbreviations and description: See Table S1.

panel	Allele	MAF controls	N controls	subphenotype	N SPT	MAF (panel E: T/A)	P	OR	L95	U95	N non-SPT	MAF non-SPT	P	OR	L95	U95
A	G	0.31	5482	acute	566	0.35	1.12E-02	1.18	1.04	1.34	1025	0.34	6.39E-01	1.04	1.21	0.89
A	G	0.31	5482	chronic	1025	0.34	1.07E-02	1.14	1.03	1.26	566	0.35	6.39E-01	0.96	0.83	1.12
A	G	0.31	5482	Löfgren	64	0.34	4.06E-01	1.17	0.81	1.69	401	0.33	8.57E-01	1.04	0.70	1.53
A	G	0.31	5482	eye	33	0.35	4.95E-01	1.19	0.72	1.98	-	-	-	-	-	-
A	G	0.31	5482	skin	66	0.38	8.75E-02	1.36	0.95	1.94	1519	0.34	3.41E-01	1.19	0.83	1.71
B-I	G	0.30	3278	acute	187	0.34	5.75E-02	1.24	0.99	1.54	374	0.35	7.52E-01	0.96	1.25	0.74
B-I	G	0.30	3278	chronic	374	0.35	1.73E-03	1.29	1.10	1.52	187	0.34	7.52E-01	1.04	0.80	1.36
B-I	G	0.30	3278	Löfgren	57	0.35	2.18E-01	1.28	0.87	1.88	-	-	-	-	-	-
B-I	G	0.30	3278	eye	44	0.32	6.76E-01	1.10	0.70	1.73	-	-	-	-	-	-
B-II	G	0.31	285	acute	50	0.39	1.14E-01	1.42	0.92	2.21	185	0.36	5.40E-01	1.15	1.82	0.73
B-II	G	0.31	285	chronic	185	0.36	1.35E-01	1.24	0.94	1.63	50	0.39	5.40E-01	0.87	0.55	1.37
B-II	G	0.31	285	Löfgren	38	0.37	3.03E-01	1.30	0.79	2.14	211	0.36	8.59E-01	1.05	0.63	1.74
B-II	G	0.31	285	skin	22	0.41	1.73E-01	1.54	0.82	2.89	213	0.36	4.92E-01	1.25	0.66	2.35
C-I	G	0.32	330	acute	20	0.33	8.61E-01	1.07	0.52	2.18	40	0.33	9.30E-01	1.04	2.40	0.45
C-I	G	0.32	330	chronic	40	0.33	9.19E-01	1.03	0.62	1.69	20	0.33	9.30E-01	0.96	0.42	2.22
C-I	G	0.32	330	Löfgren	46	0.29	5.61E-01	0.87	0.53	1.41	191	0.37	1.69E-01	0.70	0.43	1.16
C-I	G	0.32	330	skin	40	0.30	7.68E-01	0.92	0.55	1.55	-	-	-	-	-	-
C-I	G	0.32	330	persistent	110	0.35	4.05E-01	1.15	0.83	1.59	88	0.39	4.20E-01	0.84	0.56	1.28
C-I	G	0.32	330	resolving	88	0.39	8.44E-02	1.36	0.96	1.93	110	0.35	4.20E-01	1.18	1.79	0.78
C-I	G	0.32	330	bones,muscle,joints	19	0.29	7.58E-01	0.89	0.42	1.89	-	-	-	-	-	-
C-I	G	0.32	330	extra pulmonary	65	0.34	6.72E-01	1.09	0.73	1.63	65	0.36	7.61E-01	0.92	0.54	1.57
C-I	G	0.32	330	liver	21	0.29	6.50E-01	0.85	0.43	1.70	-	-	-	-	-	-

D	G	0.11	784	eye	163	0.11	9.52E-01	0.99	0.68	1.44	327	0.09	5.13E-01	1.16	0.75	1.79
D	G	0.11	784	liver	115	0.10	5.94E-01	0.88	0.55	1.41	375	0.10	9.65E-01	0.99	0.60	1.63
D	G	0.11	784	extra pulmonary	446	0.11	6.19E-01	0.94	0.72	1.22	121	0.09	5.01E-01	1.18	0.73	1.90
D	G	0.11	784	skin	222	0.09	1.89E-01	0.79	0.55	1.13	274	0.11	2.69E-01	0.79	0.52	1.20
E	G	-	-	acute	94	44/36	3.71E-01	1.22	0.79	1.90	-	-	-	-	-	-
E	G	-	-	chronic	212	70/96	4.36E-02	0.73	0.54	0.99	-	-	-	-	-	-
F	G	-	-	chronic	435	0.38	-	-	-	-	484	0.37	6.05E-01	1.05	0.87	1.27
F	G	-	-	persistent	535	0.37	-	-	-	-	382	0.38	8.88E-01	0.99	0.81	1.20
F	G	-	-	skin	113	0.34	-	-	-	-	807	0.38	2.55E-01	0.84	0.62	1.13
F	G	-	-	cardiac	34	0.43	-	-	-	-	886	0.37	3.86E-01	1.24	0.76	2.03
F	G	-	-	CNS	56	0.34	-	-	-	-	864	0.38	3.70E-01	0.83	0.55	1.25
F	G	-	-	fibrosis	25	0.42	-	-	-	-	883	0.37	5.04E-01	1.21	0.69	2.15
F	G	-	-	eye	113	0.34	-	-	-	-	807	0.38	2.28E-01	0.83	0.62	1.12
F	G	-	-	extra pulmonary	229	0.36	-	-	-	-	685	0.38	4.60E-01	0.92	0.74	1.15

Table S6: Results in the German study panels A, B-I and B-II.

Results are shown for the 46 SNP that were investigated in the meta-analysis of panel A,B and C, comprising 44 novel candidate SNPs and 2 known risk SNPs. SNPs with a genome-wide significant result in the meta-analysis are high-lighted in green. P values for the chi square test are shown, odds ratios (OR) refer to Allele 1 (A1); further abbreviations: Chromosome (Chr); 95 % confidence intervals for OR (95 % CI).

					Panel A		Panel B-I		Panel B-II	
Chr	**dbSNP ID**	**Position (hg19)**	**A1**	**A2**	**P value**	**OR [95 % CI]**	**P value**	**OR [95 % CI]**	**P value**	**OR [95 % CI]**
1	rs12731471	7,904,699	T	C	6.49E-04	1.23 [1.09-1.39]	3.88E-01	1.10 [0.89-1.35]	4.78E-01	1.15 [0.20-0.78]
1	rs12072552	32,177,704	C	A	8.17E-04	0.88 [0.81-0.95]	6.08E-01	0.97 [0.85-1.10]	1.87E-01	1.18 [0.12-0.92]
1	rs12069782	67,600,101	C	T	4.20E-08	1.30 [1.18-1.43]	2.73E-01	1.09 [0.93-1.28]	1.36E-02	1.46 [0.15-1.08]
1	rs41283516	114,443,343	A	C	3.17E-04	1.37 [1.15-1.63]	7.50E-02	0.73 [0.52-1.03]	NA	NA
1	rs11810143	161,480,649	G	A	5.37E-04	1.22 [1.09-1.36]	2.18E-01	0.89 [0.73-1.07]	6.33E-01	0.91 [0.19-0.63]
1	rs926474	172,901,724	G	A	1.07E-05	1.19 [1.10-1.29]	8.68E-01	1.01 [0.89-1.15]	3.72E-03	1.44 [0.13-1.13]
2	rs7599598	97,351,840	G	A	2.36E-04	0.86 [0.80-0.93]	1.78E-02	1.17 [1.03-1.32]	8.66E-01	0.98 [0.12-0.77]
2	rs2314398	97,413,488	G	C	7.77E-05	0.85 [0.78-0.92]	5.24E-02	1.14 [1.00-1.30]	8.42E-01	1.03 [0.13-0.79]
2	rs34365371	102,843,349	G	C	6.95E-04	1.68 [1.24-2.27]	4.47E-02	1.57 [1.01-2.46]	4.25E-01	1.59 [0.59-0.50]
2	rs6748088†	203,556,526	C	T	4.30E-04	1.16 [1.07-1.26]	1.34E-04	1.29 [1.13-1.48]	4.78E-02	1.29 [0.13-1.00]
2	rs76210392	204,804,214	A	G	6.80E-04	0.58 [0.42-0.80]	2.38E-01	0.72 [0.41-1.25]	9.76E-01	1.01 [0.44-0.43]
2	rs3948463	231,036,860	A	G	1.95E-05	1.32 [1.16-1.50]	8.01E-01	1.03 [0.82-1.28]	3.59E-01	1.22 [0.22-0.80]
2	rs2303542	231,150,806	T	C	1.79E-07	1.23 [1.14-1.33]	8.33E-01	1.01 [0.89-1.15]	4.55E-01	1.10 [0.12-0.86]
2	rs933957	231,177,904	G	A	2.42E-06	1.22 [1.12-1.33]	1.65E-02	1.19 [1.03-1.36]	8.55E-01	0.98 [0.14-0.75]
2	rs10178603	234,206,610	G	A	6.09E-04	0.87 [0.81-0.94]	4.19E-01	0.95 [0.84-1.08]	6.76E-01	1.05 [0.12-0.83]
3	rs9880099	136,255,776	G	A	2.83E-04	1.63 [1.25-2.13]	4.02E-01	0.81 [0.50-1.32]	4.74E-01	1.38 [0.45-0.57]

4	rs17211702	102,977,140	C	T	7.95E-04	0.87 [0.81-0.95]	9.07E-01	0.99 [0.87-1.13]	3.26E-01	1.14 [0.13-0.88]
4	rs223498	103,651,962	C	A	6.68E-06	1.19 [1.10-1.29]	1.17E-02	1.18 [1.04-1.33]	5.14E-01	1.08 [0.12-0.85]
5	rs4921492	158,832,277	A	C	7.56E-07	1.22 [1.13-1.32]	1.92E-02	1.17 [1.03-1.33]	2.42E-02	1.33 [0.13-1.04]
6	rs1411578#	57,054,843	G	C	7.11E-04	1.19 [1.08-1.32]	1.93E-02	1.22 [1.03-1.45]	9.78E-01	1.00 [0.17-0.71]
7	rs16869462	97,758,335	A	G	9.36E-05	1.33 [1.15-1.53]	2.38E-01	1.15 [0.91-1.45]	5.91E-01	1.13 [0.22-0.73]
7	rs7786877	100,214,015	G	A	1.08E-04	1.19 [1.09-1.29]	4.53E-01	1.06 [0.91-1.22]	2.10E-01	0.84 [0.14-0.64]
8	rs72666877	79,720,613	T	C	5.52E-04	1.22 [1.09-1.37]	7.29E-01	1.04 [0.85-1.26]	3.61E-01	1.19 [0.19-0.82]
9	rs9409609	94,339,510	A	G	1.73E-04	1.21 [1.09-1.33]	1.27E-01	0.88 [0.74-1.04]	1.63E-01	1.25 [0.16-0.91]
9	rs77584282	123,672,383	T	C	1.62E-06	1.43 [1.24-1.66]	3.57E-02	1.29 [1.02-1.63]	4.70E-01	0.84 [0.24-0.52]
9	rs79972325	139,267,838	T	C	4.02E-05	1.72 [1.33-2.24]	8.50E-01	1.04 [0.70-1.54]	7.79E-01	1.12 [0.40-0.51]
10	rs1248990	29,025,678	A	C	3.07E-05	0.80 [0.71-0.89]	8.69E-01	0.99 [0.83-1.17]	4.77E-01	0.89 [0.17-0.64]
11	rs694739*	64,097,233	C	T	3.33E-06	0.83 [0.76-0.90]	3.06E-02	0.87 [0.76-0.99]	2.06E-04	0.62 [0.13-0.48]
11	rs12418080	114,467,655	A	G	9.25E-04	0.85 [0.77-0.94]	3.83E-05	1.36 [1.17-1.57]	3.42E-01	0.87 [0.15-0.65]
11	rs45460493	118,455,465	A	G	2.24E-04	1.62 [1.25-2.10]	1.17E-01	1.36 [0.92-2.02]	3.89E-01	1.40 [0.39-0.65]
11	rs2434936	129,619,287	A	G	8.05E-04	1.15 [1.06-1.24]	5.68E-01	1.04 [0.91-1.19]	8.63E-01	1.02 [0.13-0.80]
12	rs2364480	6,495,275	C	A	6.09E-04	1.17 [1.07-1.28]	8.48E-01	1.01 [0.88-1.17]	8.72E-01	0.98 [0.14-0.74]
12	rs10877030	58,256,714	G	T	3.38E-04	0.86 [0.79-0.93]	2.81E-01	0.93 [0.81-1.06]	5.24E-01	0.92 [0.13-0.71]
12	rs653178	112,007,756	G	A	1.36E-06	1.21 [1.12-1.30]	8.06E-03	1.19 [1.05-1.34]	3.15E-01	1.13 [0.12-1.44]
13	rs6490812	24,203,027	T	C	7.18E-04	0.86 [0.80-0.94]	1.30E-01	0.90 [0.78-1.03]	4.07E-01	1.12 [0.13-0.86]
13	rs9512257	27,114,324	C	A	7.05E-05	0.85 [0.79-0.92]	2.36E-02	1.16 [1.02-1.31]	3.89E-01	0.90 [0.12-0.71]
14	rs2246695	62,008,065	G	A	2.49E-05	0.80 [0.72-0.89]	9.41E-01	0.99 [0.84-1.17]	5.83E-01	1.09 [0.16-0.80]
15	rs12594231	32,176,304	C	T	1.55E-05	1.18 [1.10-1.28]	6.07E-01	1.03 [0.91-1.17]	8.14E-01	0.97 [0.12-0.76]
15	rs8040456	59,356,103	G	A	1.44E-05	1.21 [1.11-1.32]	5.21E-01	1.05 [0.91-1.21]	5.95E-01	1.08 [0.14-0.82]
16	rs34817272	11,333,849	C	T	6.03E-06	1.20 [1.11-1.30]	2.23E-01	1.09 [0.95-1.24]	5.70E-01	1.08 [0.13-0.84]

17	rs117542454	40,724,638	A	G	3.81E-04	1.56 [1.22-2.00]	1.62E-01	1.33 [0.89-1.97]	4.91E-01	1.35 [0.43-0.58]
18	rs2847260	12,775,591	G	A	6.24E-04	1.19 [1.08-1.32]	6.33E-03	1.26 [1.07-1.49]	1.06E-01	1.30 [0.16-0.94]
19	rs34536443	10,463,118	C	G	5.95E-06	0.60 [0.48-0.75]	9.25E-02	0.71 [0.48-1.06]	5.77E-01	0.84 [0.31-0.46]
19	rs439401	45,414,451	T	C	3.33E-04	1.16 [1.07-1.25]	3.41E-01	0.94 [0.82-1.07]	7.74E-01	1.04 [0.13-0.81]
21	rs61735800	43,329,572	C	T	5.39E-04	0.71 [0.59-0.86]	1.02E-01	0.78 [0.57-1.05]	3.40E-01	1.30 [0.28-0.76]
22	rs17728461	30,598,552	G	C	7.39E-04	1.15 [1.06-1.25]	5.72E-03	0.82 [0.72-0.95]	7.93E-01	1.04 [0.13-0.80]

previously established susceptibility locus on chromosome 6p12.1 [5]

* previously established susceptibility locus on chromosome 11q13.1 [1]

† previously suggested susceptibility locus on chromosome 2q33.2 [2]

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Table S7: Results in the Czech and Swedish study panels C-I, C-II and in the joint analysis

Results are shown for the 46 SNP that were investigated in the meta-analysis of panel A,B and C, comprising 44 novel candidate SNPs and 2 known risk SNPs. For the meta-analysis, P values Cochran-Mantel-Haenzel test (P CMH) and from the Breslow-Day test for homogeneous effects in the meta-analysis (P BD) are given. SNPs with a genome-wide significant result in the meta-analysis are highlighted in green, and the respective significant P value is highlighted in red, significant results in BD test ($p < 0.05/46 = 0.001$) are highlighted in yellow. For Panels C-I and C-II p values for the chi square test are shown (P value) and odds ratios (OR) refer to Allele 1 (A1); further abbreviations: Chromosome (Chr); 95 % confidence intervals for OR (95 % CI).

					Panel C-I		Panel C-II		Joint analysis Panels A,B,C		
Chr	**dbSNP ID**	**Position (hg19)**	**A1**	**A2**	**P value**	**OR [95 % CI]**	**P value**	**OR [95 % CI]**	**P CMH**	**OR [95% CI]**	**P BD**
1	rs12731471	7,904,699	T	C	6.28E-01	1.11 [0.73-1.68]	2.82E-01	1.16 [0.89-1.50]	2.94E-04	1.18 [1.08-1.30]	8.95E-01
1	rs12072552	32,177,704	C	A	4.42E-01	0.91 [0.72-1.15]	1.74E-02	1.15 [1.03-1.29]	3.23E-01	0.97 [0.92-1.03]	9.94E-04
1	rs12069782	67,600,101	C	T	8.29E-01	1.03 [0.78-1.37]	3.48E-03	1.25 [1.08-1.46]	3.07E-10	1.24 [1.16-1.33]	1.92E-01
1	rs41283516	114,443,343	A	C	5.51E-01	1.20 [0.66-2.16]	2.52E-01	0.74 [0.44-1.24]	3.13E-01	1.08 [0.93-1.24]	2.53E-07
1	rs11810143	161,480,649	G	A	6.27E-01	0.92 [0.64-1.30]	7.65E-01	0.97 [0.81-1.17]	1.19E-01	1.07 [0.98-1.16]	2.30E-02
1	rs926474	172,901,724	G	A	4.74E-01	1.09 [0.86-1.39]	3.74E-01	0.92 [0.76-1.11]	6.05E-05	1.13 [1.06-1.20]	1.15E-02
2	rs7599598	97,351,840	G	A	2.79E-01	1.14 [0.90-1.45]	6.50E-01	0.97 [0.87-1.09]	1.14E-01	0.96 [0.91-1.01]	1.18E-03
2	rs2314398	97,413,488	G	C	3.03E-01	1.15 [0.88-1.49]	8.65E-01	0.99 [0.88-1.12]	7.48E-02	0.95 [0.90-1.01]	1.54E-03
2	rs34365371	102,843,349	G	C	9.91E-01	0.99 [0.30-3.27]	3.93E-01	0.81 [0.49-1.32]	2.85E-03	1.38 [1.12-1.72]	1.40E-01
2	rs6748088†	203,556,526	C	T	1.47E-01	1.20 [0.94-1.54]	1.33E-01	1.10 [0.97-1.25]	2.10E-08	1.18 [1.11-1.25]	4.46E-01
2	rs76210392	204,804,214	A	G	3.78E-01	0.68 [0.28-1.62]	8.52E-01	1.08 [0.49-2.38]	8.12E-04	0.66 [0.52-0.85]	5.27E-01
2	rs3948463	231,036,860	A	G	9.83E-01	1.00 [0.67-1.50]	3.49E-01	0.90 [0.72-1.12]	3.28E-03	1.15 [1.05-1.26]	2.92E-02

2	rs2303542	231,150,806	T	C	6.42E-01	1.06 [0.84-1.34]	2.47E-01	1.07 [0.95-1.21]	4.56E-06	1.14 [1.08-1.20]	8.04E-02
2	rs933957	231,177,904	G	A	7.84E-01	1.04 [0.81-1.33]	2.76E-02	1.16 [1.02-1.32]	6.94E-08	1.18 [1.11-1.25]	4.46E-01
2	rs10178603	234,206,610	G	A	5.70E-01	1.07 [0.85-1.35]	3.29E-01	0.94 [0.84-1.06]	3.76E-02	0.94 [0.89-1.00]	4.89E-02
3	rs9880099	136,255,776	G	A	3.80E-01	1.60 [0.55-4.65]	5.86E-01	0.81 [0.39-1.72]	1.27E-02	1.31 [1.06-1.61]	8.56E-02
4	rs17211702	102,977,140	C	T	6.95E-01	1.05 [0.82-1.34]	2.82E-01	0.93 [0.82-1.06]	8.68E-03	0.93 [0.88-0.98]	1.53E-01
4	rs223498	103,651,962	C	A	9.20E-02	0.82 [0.64-1.03]	1.08E-05	1.30 [1.16-1.46]	1.28E-09	1.19 [1.12-1.26]	7.32E-03
5	rs4921492	158,832,277	A	C	4.13E-01	1.11 [0.87-1.41]	1.76E-01	1.14 [0.94-1.39]	2.14E-09	1.20 [1.13-1.27]	7.92E-01
6	rs1411578#	57,054,843	G	C	8.83E-02	1.33 [0.96-1.85]	3.04E-01	1.14 [0.89-1.45]	1.25E-05	1.19 [1.10-1.28]	7.81E-01
7	rs16869462	97,758,335	A	G	6.28E-02	1.50 [0.98-2.31]	1.80E-01	1.16 [0.93-1.43]	1.03E-05	1.25 [1.13-1.38]	6.25E-01
7	rs7786877	100,214,015	G	A	3.08E-01	0.87 [0.66-1.14]	7.87E-02	0.89 [0.77-1.01]	8.77E-02	1.06 [0.99-1.12]	1.15E-03
8	rs72666877	79,720,613	T	C	1.89E-01	0.79 [0.55-1.13]	4.43E-02	0.81 [0.65-0.99]	9.03E-02	1.08 [0.99-1.17]	3.89E-03
9	rs9409609	94,339,510	A	G	7.13E-01	1.06 [0.78-1.44]	5.27E-01	0.95 [0.82-1.11]	3.88E-02	1.08 [1.00-1.15]	6.40E-03
9	rs77584282	123,672,383	T	C	6.08E-01	1.16 [0.67-2.01]	9.95E-01	1.00 [0.79-1.27]	2.53E-05	1.25 [1.13-1.39]	4.77E-02
9	rs79972325	139,267,838	T	C	6.48E-01	0.82 [0.35-1.93]	2.40E-01	1.29 [0.84-1.98]	8.75E-04	1.36 [1.14-1.64]	1.59E-01
10	rs1248990	29,025,678	A	C	9.93E-01	1.00 [0.75-1.33]	2.84E-02	0.84 [0.71-0.98]	3.13E-05	0.85 [0.79-0.92]	2.24E-01
11	rs694739*	64,097,233	C	T	1.57E-02	0.74 [0.57-0.94]	2.58E-08	0.70 [0.62-0.79]	3.41E-16	0.79 [0.75-0.84]	3.40E-02
11	rs12418080	114,467,655	A	G	8.33E-01	1.03 [0.77-1.38]	1.84E-01	0.90 [0.78-1.05]	1.80E-01	0.96 [0.89-1.02]	6.69E-06
11	rs45460493	118,455,465	A	G	3.89E-01	0.65 [0.24-1.76]	1.79E-01	1.50 [0.83-2.73]	8.01E-05	1.47 [1.21-1.78]	4.85E-01
11	rs2434936	129,619,287	A	G	9.93E-01	1.00 [0.78-1.28]	2.89E-01	0.94 [0.83-1.06]	3.19E-02	1.06 [1.01-1.13]	9.03E-02
12	rs2364480	6,495,275	C	A	6.64E-01	0.94 [0.70-1.25]	4.31E-02	1.14 [1.00-1.30]	9.35E-04	1.11 [1.04-1.18]	2.85E-01
12	rs10877030	58,256,714	G	T	3.78E-01	0.89 [0.69-1.15]	2.66E-02	0.87 [0.77-0.98]	1.25E-05	0.88 [0.83-0.93]	9.04E-01
12	rs653178	112,007,756	G	A	8.94E-04	1.49 [1.18-1.89]	6.42E-02	1.12 [0.99-1.26]	1.64E-10	1.19 [1.14-1.27]	2.89E-01
13	rs6490812	24,203,027	T	C	9.73E-01	1.01 [0.77-1.31]	5.90E-02	0.89 [0.78-1.01]	1.95E-04	0.89 [0.84-0.95]	3.84E-01
13	rs9512257	27,114,324	C	A	6.86E-01	1.05 [0.83-1.33]	9.67E-01	1.00 [0.89-1.12]	5.06E-02	0.95 [0.90-1.00]	1.19E-03
14	rs2246695	62,008,065	G	A	6.15E-01	1.09 [0.78-1.53]	3.93E-01	1.11 [0.87-1.41]	6.25E-03	0.90 [0.83-0.97]	1.72E-02
15	rs12594231	32,176,304	C	T	8.29E-01	0.97 [0.77-1.23]	5.23E-02	0.89 [0.79-1.00]	1.85E-02	1.07 [1.01-1.13]	1.75E-03
15	rs8040456	59,356,103	G	A	3.50E-01	0.88 [0.67-1.15]	1.34E-02	0.84 [0.73-0.96]	3.55E-02	1.07 [1.00-1.14]	2.24E-04
16	rs34817272	11,333,849	C	T	1.38E-01	0.83 [0.65-1.06]	7.31E-01	1.02 [0.91-1.15]	2.62E-04	1.11 [1.05-1.17]	2.47E-02

17	rs117542454	40,724,638	A	G	5.63E-01	0.75 [0.29-1.96]	4.86E-01	1.33 [0.60-2.97]	2.87E-04	1.43 [1.18-1.73]	6.51E-01
18	rs2847260	12,775,591	G	A	7.50E-01	0.95 [0.67-1.33]	7.32E-03	1.23 [1.06-1.44]	2.82E-07	1.21 [1.12-1.30]	6.33E-01
19	rs34536443	10,463,118	C	G	7.27E-02	0.51 [0.24-1.08]	3.66E-02	0.69 [0.49-0.98]	5.48E-08	0.64 [0.55-0.76]	7.39E-01
19	rs439401	45,414,451	T	C	5.41E-01	0.93 [0.73-1.18]	7.93E-01	0.98 [0.87-1.11]	5.38E-02	1.06 [1.00-1.12]	3.27E-02
21	rs61735800	43,329,572	C	T	6.33E-01	1.15 [0.64-2.07]	3.75E-01	0.82 [0.54-1.26]	9.41E-04	0.79 [0.68-0.91]	1.89E-01
22	rs17728461	30,598,552	G	C	7.49E-01	0.96 [0.75-1.23]	8.57E-01	0.98 [0.81-1.19]	9.98E-05	0.88 [0.83-0.94]	3.79E-01

previously established susceptibility locus on chromosome 6p12.1 [5]

* previously established susceptibility locus on chromosome 11q13.1 [1]

† previously suggested susceptibility locus on chromosome 2q33.2 [2]

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Table S8: Results in the African-American study panel D and in the German trios (panel E)

Results are shown for six SNPs, which were associated with genome-wide significance in the joint analysis of the European panels A-C, including five novel and one known susceptibility variant. For panel D, P values from the regression analysis are given, and results of the transmission disequilibrium test are shown for Panel E. Odds ratios (OR) refer to Allele 1 (A1); further abbreviations: Chromosome (Chr); 95 % confidence intervals for OR (95 % CI).

					Panel D		Panel E	
Chr	**dbSNP ID**	**Position (hg19)**	**A1**	**A2**	**P value**	**OR [95 % CI]**	**P value**	**OR [95 % CI]**
1	rs12069782	67,600,101	C	T	6.44E-01	0.96 [0.82-1.13]	2.43E-01	0.84 [0.63-1.12]
2	rs6748088†	203,556,526	C	T	6.97E-01	0.96 [0.77-1.19]	2.77E-01	0.88 [0.69-1.11]
4	rs223498	103,651,962	C	A	4.21E-01	1.08 [0.90-1.29]	3.04E-01	1.13 [0.90-1.41]
5	rs4921492	158,832,277	A	C	4.59E-01	1.06 [0.91-1.23]	3.90E-02	1.27 [1.01-1.59]
11	rs694739*	64,097,233	C	T	4.70E-01	0.90 [0.67-1.20]	4.14E-03	0.72 [0.57-0.90]
12	rs653178	112,007,756	G	A	6.93E-01	0.95 [0.72-1.25]	5.01E-01	1.08 [0.86-1.35]

* previously established susceptibility locus on chromosome 11q13.1 [1]

† previously suggested susceptibility locus on chromosome 2q33.2 [2]

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Table S9: Results of the subphenotype analysis for marker rs12069782 (*IL23R*) in panel F

Abbreviations and description: See Table S1.

panel	Allele	MAF controls	N controls	subphenotype	N SPT	MAF (panel E: T/A)	P	OR	L95	U95	N non-SPT	MAF non-SPT	P	OR	L95	U95
A	C	0.18	5482	acute	566	0.21	1.53E-02	1.20	1.04	1.40	1025	0.23	1.92E-01	0.89	1.06	0.75
A	C	0.18	5482	chronic	1025	0.23	**1.52E-07**	1.35	1.21	1.52	566	0.21	1.92E-01	1.12	0.94	1.34
A	C	0.18	5482	Löfgren	64	0.18	9.33E-01	0.98	0.62	1.54	401	0.22	3.86E-01	0.81	0.51	1.30
A	C	0.18	5482	eye	33	0.24	2.10E-01	1.43	0.81	2.52	-	-	-	-	-	-
A	C	0.18	5482	skin	66	0.21	3.83E-01	1.21	0.79	1.83	1519	0.22	7.45E-01	0.93	0.61	1.43
B-I	C	0.18	3278	acute	187	0.19	7.80E-01	1.04	0.79	1.36	374	0.19	7.40E-01	0.95	1.30	0.69
B-I	C	0.18	3278	chronic	374	0.19	3.49E-01	1.10	0.90	1.33	187	0.19	7.40E-01	1.06	0.77	1.45
B-I	C	0.18	3278	Löfgren	57	0.21	3.97E-01	1.22	0.77	1.92	-	-	-	-	-	-
B-I	C	0.18	3278	eye	44	0.19	7.45E-01	1.09	0.64	1.86	-	-	-	-	-	-
B-II	C	0.17	285	acute	50	0.27	1.57E-02	1.83	1.12	2.99	185	0.22	3.09E-01	1.30	2.15	0.78
B-II	C	0.17	285	chronic	185	0.22	4.25E-02	1.41	1.01	1.96	50	0.27	3.09E-01	0.77	0.46	1.28
B-II	C	0.17	285	Löfgren	38	0.28	2.19E-02	1.89	1.09	3.26	211	0.22	2.44E-01	1.39	0.80	2.42
B-II	C	0.17	285	skin	22	0.34	4.21E-03	2.55	1.32	4.95	213	0.22	6.57E-02	1.85	0.95	3.60
C-I	C	0.21	330	acute	20	0.20	8.31E-01	0.92	0.41	2.03	40	0.33	1.52E-01	0.52	1.28	0.21
C-I	C	0.21	330	chronic	40	0.33	2.54E-02	1.77	1.07	2.92	20	0.20	1.52E-01	1.93	0.78	4.76
C-I	C	0.21	330	Löfgren	46	0.24	5.88E-01	1.15	0.69	1.93	191	0.23	8.16E-01	1.07	0.62	1.82
C-I	C	0.21	330	skin	40	0.21	9.71E-01	0.99	0.56	1.75	-	-	-	-	-	-
C-I	C	0.21	330	persistent	110	0.24	4.10E-01	1.16	0.81	1.67	88	0.23	7.50E-01	1.08	0.68	1.72
C-I	C	0.21	330	resolving	88	0.23	7.11E-01	1.08	0.72	1.61	110	0.24	7.50E-01	0.93	1.48	0.58
C-I	C	0.21	330	bones,muscle,joints	19	0.24	7.42E-01	1.14	0.53	2.46	-	-	-	-	-	-
C-I	C	0.21	330	extra pulmonary	65	0.20	7.16E-01	0.92	0.57	1.46	65	0.24	4.20E-01	0.78	0.43	1.42
C-I	C	0.21	330	liver	21	0.31	1.49E-01	1.64	0.83	3.25	-	-	-	-	-	-
D	C	0.22	784	eye	163	0.17	2.09E-02	0.70	0.51	0.95	327	0.22	2.58E-02	0.67	0.47	0.95

D	C	0.22	784	liver	115	0.20	2.43E-01	0.81	0.58	1.15	375	0.21	8.26E-01	0.96	0.65	1.41
D	C	0.22	784	extra pulmonary	446	0.20	1.30E-01	0.86	0.70	1.05	121	0.27	1.72E-02	0.66	0.47	0.93
D	C	0.22	784	skin	222	0.18	8.02E-02	0.79	0.61	1.03	274	0.22	1.26E-01	0.78	0.56	1.07
E	C	-	-	acute	94	19/38	1.19E-02	0.50	0.29	0.87	-	-	-	-	-	-
E	C	-	-	chronic	212	55/53	8.47E-01	1.04	0.71	1.51	-	-	-	-	-	-
F	C	-	-	chronic	435	0.21	-	-	-	-	484	0.21	9.30E-01	0.99	0.79	1.24
F	C	-	-	persistent	535	0.22	-	-	-	-	382	0.21	6.09E-01	1.06	0.84	1.34
F	C	-	-	skin	113	0.25	-	-	-	-	807	0.21	1.77E-01	1.26	0.90	1.76
F	C	-	-	cardiac	34	0.23	-	-	-	-	886	0.21	7.61E-01	1.10	0.61	1.97
F	C	-	-	CNS	56	0.20	-	-	-	-	864	0.21	8.22E-01	0.95	0.58	1.53
F	C	-	-	fibrosis	25	0.21	-	-	-	-	883	0.21	9.49E-01	0.98	0.48	1.98
F	C	-	-	eye	113	0.23	-	-	-	-	807	0.21	5.10E-01	1.12	0.80	1.57
F	C	-	-	extra pulmonary	229	0.22	-	-	-	-	685	0.21	6.19E-01	1.07	0.82	1.39

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Table S10: Comparison of HLA-signals

Results for SNPs in the HLA-region, which are genome-wide significant in the German panel A (GER), and which are included in a recently published US-American GWAS comprising individuals of European (EA) and African-American (AA) origin [6]. Results with genome-wide significance ($p < 5 \times 10^{-8}$) are highlighted in red. P values conditioned (cond) on rs5007259 (*lead SNP of German panel A), rs2227139 († lead SNP in the AA dataset) and rs1964995 (ǂ SNP with genome-wide significance in EA dataset); ns: p value > 0.05.

dbSNP ID	Position (hg19)	Left gene	Gene	Right gene	P GER	P GER cond rs5007259	P GER cond rs2227139	P GER cond rs1964995	P AA	P EA
rs9268145	32,257,284	NOTCH4	-	C6orf10	4.47E-09	ns	2.11E-02	ns	6.13E-06	2.47E-05
rs6910071	32,282,854	NOTCH4	C6orf10	HNRNPA1P2	4.15E-09	ns	1.94E-02	ns	4.67E-06	3.50E-05
rs28361060	32,303,848	HNRNPA1P2	C6orf10	BTNL2	4.81E-09	ns	2.08E-02	ns	4.67E-06	3.65E-05
rs9268362	32,333,341	HNRNPA1P2	C6orf10	BTNL2	2.53E-09	ns	1.56E-02	ns	4.67E-06	3.14E-05
rs2395153	32,345,595	C6orf10	-	BTNL2	4.24E-29	1.43E-02	1.03E-11	1.68E-04	4.78E-05	2.12E-06
rs2294878	32,367,795	C6orf10	BTNL2	HLA-DRA	5.44E-27	ns	8.90E-14	4.98E-06	3.31E-04	4.43E-07
rs6926737	32,375,745	BTNL2	-	HLA-DRA	1.83E-35	-	9.07E-17	1.36E-06	6.06E-03	2.96E-07
rs9268507	32,377,539	BTNL2	-	HLA-DRA	2.00E-35	-	1.05E-16	1.42E-06	3.80E-03	7.05E-07
rs5007265	32,378,866	BTNL2	-	HLA-DRA	2.00E-35	-	1.05E-16	1.42E-06	3.80E-03	7.05E-07
rs5007263	32,378,982	BTNL2	-	HLA-DRA	2.23E-35	-	1.09E-16	1.42E-06	3.80E-03	7.05E-07
rs5007259*	32,379,101	BTNL2	-	HLA-DRA	1.55E-35	-	8.48E-17	1.34E-06	3.80E-03	7.05E-07
rs6932542	32,380,262	BTNL2	-	HLA-DRA	1.88E-35	-	1.10E-16	1.42E-06	3.48E-03	7.05E-07
rs4502931	32,380,782	BTNL2	-	HLA-DRA	1.60E-35	-	1.01E-16	1.23E-06	3.80E-03	7.05E-07
rs8084	32,411,035	BTNL2	HLA-DRA	HLA-DRB9	1.28E-23	4.05E-07	ns	9.34E-05	3.69E-11	1.21E-03
rs7192	32,411,646	BTNL2	HLA-DRA	HLA-DRB9	2.06E-26	6.24E-07	-	3.10E-04	1.40E-11	1.26E-04
rs7195	32,412,539	BTNL2	HLA-DRA	HLA-DRB9	5.99E-27	3.62E-07	-	2.12E-04	1.40E-11	1.26E-04
rs2213586	32,413,094	HLA-DRA	-	HLA-DRB9	1.27E-26	6.70E-07	-	3.55E-04	1.40E-11	1.26E-04

rs2213585	32,413,150	HLA-DRA	-	HLA-DRB9	8.22E-27	6.31E-07	-	3.32E-04	1.40E-11	1.26E-04
rs2227139†	32,413,459	HLA-DRA	-	HLA-DRB9	1.04E-26	-	-	3.11E-04	9.15E-12	1.26E-04
rs3129890	32,414,273	HLA-DRA	-	HLA-DRB9	1.79E-16	1.41E-06	ns	6.40E-03	1.13E-10	2.88E-01
rs7754768	32,420,179	HLA-DRA	-	HLA-DRB9	1.74E-25	2.17E-05	ns	4.05E-03	6.29E-07	1.13E-04
rs1964995‡	32,449,411	HLA-DRB9	-	HLA-DRB5	2.13E-34	-	5.13E-14	-	1.62E-06	3.61E-08
rs477515	32,569,691	HLA-DRB1	-	HLA-DQA1	7.72E-12	ns	1.13E-02	1.59E-03	1.66E-06	4.53E-04
rs502771	32,578,970	HLA-DRB1	-	HLA-DQA1	1.00E-23	8.51E-07	2.39E-23	1.36E-07	3.46E-08	1.64E-03

Table S11: Results of the subphenotype analysis for marker rs5007259 (*BTNL2*) in panel F

Abbreviations and description: See Table 1.

Panel	Allele	AF controls	N controls	Subphenotype	N SPT	AF (panel E: T/A)	P	OR	L95	U95	N non-SPT	AF non-SPT	P	OR	L95	U95
A	G	0.48	5482	acute	566	0.33	**1.36E-24**	0.51	0.45	0.58	1025	0.38	1.84E-03	0.78	0.91	0.67
A	G	0.48	5482	chronic	1025	0.38	**4.34E-18**	0.65	0.59	0.72	566	0.33	1.84E-03	1.28	1.09	1.49
A	G	0.48	5482	Löfgren	64	0.26	**3.31E-07**	0.37	0.25	0.55	401	0.38	1.05E-02	0.58	0.38	0.88
A	G	0.48	5482	eye	33	0.50	8.03E-01	1.06	0.66	1.73	-	-	-	-	-	-
A	G	0.48	5482	skin	66	0.48	9.95E-01	1.00	0.71	1.41	1519	0.36	3.04E-03	1.69	1.19	2.39
B-I	G	0.49	3278	acute	187	0.37	**2.40E-06**	0.60	0.48	0.74	374	0.36	8.92E-01	1.02	1.32	0.79
B-I	G	0.49	3278	chronic	374	0.36	**2.47E-11**	0.59	0.50	0.69	187	0.37	8.92E-01	0.98	0.76	1.27
B-I	G	0.49	3278	Löfgren	57	0.32	2.91E-04	0.49	0.33	0.72	-	-	-	-	-	-
B-I	G	0.49	3278	eye	44	0.50	9.12E-01	1.02	0.67	1.56	-	-	-	-	-	-
B-II	G	0.48	285	acute	50	0.38	6.87E-02	0.66	0.42	1.03	185	0.45	2.52E-01	0.76	1.21	0.48
B-II	G	0.48	285	chronic	185	0.45	2.87E-01	0.87	0.67	1.13	50	0.38	2.52E-01	1.31	0.82	2.08
B-II	G	0.48	285	Löfgren	38	0.37	7.47E-02	0.63	0.38	1.05	211	0.45	2.05E-01	0.71	0.42	1.20

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B-II	G	0.48	285	skin	22	0.39	2.11E-01	0.67	0.36	1.26	213	0.44	5.27E-01	0.81	0.43	1.54
C-I	G	0.48	330	acute	20	0.33	5.20E-02	0.52	0.26	1.02	40	0.43	2.90E-01	0.65	1.44	0.29
C-I	G	0.48	330	bones,muscle,joints	19	0.50	8.39E-01	1.07	0.56	2.06	-	-	-	-	-	-
C-I	G	0.48	330	chronic	40	0.43	3.26E-01	0.79	0.49	1.26	20	0.33	2.90E-01	1.54	0.69	3.40
C-I	G	0.48	330	extra pulmonary	65	0.38	2.68E-02	0.65	0.44	0.95	65	0.36	7.97E-01	1.07	0.65	1.77
C-I	G	0.48	330	liver	21	0.36	1.13E-01	0.59	0.31	1.14	-	-	-	-	-	-
C-I	G	0.48	330	Löfgren	46	0.33	4.71E-03	0.52	0.33	0.82	191	0.37	4.28E-01	0.82	0.51	1.33
C-I	G	0.48	330	persistent	110	0.40	3.14E-02	0.71	0.52	0.97	88	0.35	3.41E-01	1.22	0.81	1.84
C-I	G	0.48	330	resolving	88	0.35	1.99E-03	0.58	0.41	0.82	110	0.40	3.41E-01	0.82	1.24	0.54
C-I	G	0.48	330	skin	40	0.35	2.44E-02	0.58	0.35	0.94	-	-	-	-	-	-
D	A	0.37	784	eye	163	0.43	5.67E-02	1.26	0.99	1.61	327	0.48	8.71E-02	0.78	0.59	1.04
D	A	0.37	784	liver	115	0.49	4.17E-04	1.66	1.25	2.20	375	0.46	5.32E-01	1.10	0.81	1.51
D	A	0.37	784	extra pulmonary	446	0.46	**3.25E-05**	1.42	1.21	1.68	121	0.47	6.48E-01	0.93	0.69	1.25
D	A	0.37	784	skin	222	0.44	1.08E-02	1.32	1.07	1.63	274	0.48	1.44E-01	0.82	0.63	1.07
E	G	-	-	acute	94	34/46	1.80E-01	0.74	0.47	1.15	-	-	-	-	-	-
E	G	-	-	chronic	212	79/116	8.06E-03	0.68	0.51	0.91	-	-	-	-	-	-
F	G	-	-	chronic	435	0.35	-	-	-	-	484	0.29	1.81E-02	1.27	1.04	1.55
F	G	-	-	persistent	535	0.32	-	-	-	-	382	0.32	1.00E+00	1.00	0.82	1.22
F	G	-	-	skin	113	0.35	-	-	-	-	807	0.31	3.14E-01	1.17	0.87	1.57
F	G	-	-	cardiac	34	0.41	-	-	-	-	886	0.32	1.09E-01	1.50	0.91	2.48
F	G	-	-	CNS	56	0.31	-	-	-	-	864	0.32	9.26E-01	0.98	0.65	1.49
F	G	-	-	fibrosis	25	0.35	-	-	-	-	883	0.32	5.86E-01	1.18	0.65	2.15
F	G	-	-	eye	113	0.34	-	-	-	-	807	0.32	4.54E-01	1.12	0.83	1.51
F	G	-	-	extra pulmonary	229	0.34	-	-	-	-	685	0.31	4.13E-01	1.10	0.88	1.38

Table S12: Results of the subphenotype analysis for marker rs4143332 (*HLA-B*) in panel F

Abbreviations and description: See Table 1. The given P values are not conditioned on rs5007259.

Panel	Allele	AF controls	N controls	Subphenotype	N SPT	AF (panel E: T/U)	P	OR	L95	U95	N non-SPT	AF non-SPT	P	OR	L95	U95
A	A	0.11	5482	acute	566	0.24	3.03E-38	2.59	2.23	3.00	1025	0.15	1.43E-10	1.81	2.17	1.51
A	A	0.11	5482	chronic	1025	0.15	1.60E-07	1.43	1.25	1.64	566	0.24	1.43E-10	0.55	0.46	0.66
A	A	0.11	5482	Löfgren	64	0.32	6.41E-14	3.82	2.62	5.56	401	0.14	3.82E-07	2.85	1.88	4.33
A	A	0.11	5482	eye	33	0.08	3.77E-01	0.66	0.27	1.66	-	-	-	-	-	-
A	A	0.11	5482	skin	66	0.20	1.53E-03	1.99	1.29	3.07	1519	0.19	7.36E-01	1.08	0.70	1.67
B-I	A	0.08	3278	acute	187	0.21	1.04E-17	3.06	2.34	3.99	374	0.13	7.27E-04	1.76	2.45	1.26
B-I	A	0.08	3278	chronic	374	0.13	2.81E-06	1.74	1.37	2.19	187	0.21	7.27E-04	0.57	0.41	0.79
B-I	A	0.08	3278	Löfgren	57	0.25	1.44E-10	3.80	2.45	5.88	-	-	-	-	-	-
B-I	A	0.08	3278	eye	44	0.15	2.27E-02	1.97	1.09	3.58	-	-	-	-	-	-
B-II	A	0.10	285	acute	50	0.19	8.57E-03	2.16	1.20	3.87	185	0.13	9.79E-02	1.66	3.03	0.91
B-II	A	0.10	285	chronic	185	0.13	2.19E-01	1.30	0.85	1.98	50	0.19	9.79E-02	0.60	0.33	1.10
B-II	A	0.10	285	Löfgren	38	0.22	2.69E-03	2.58	1.36	4.88	211	0.12	2.35E-02	2.09	1.09	3.99
B-II	A	0.10	285	skin	22	0.21	1.97E-02	2.48	1.13	5.46	213	0.14	1.65E-01	1.74	0.79	3.84
C-I	A	0.11	330	acute	20	0.15	4.29E-01	1.44	0.58	3.54	40	0.16	8.60E-01	0.91	2.60	0.32
C-I	A	0.11	330	bones,muscle,joints	19	0.13	6.72E-01	1.23	0.47	3.26	-	-	-	-	-	-
C-I	A	0.11	330	chronic	40	0.16	1.60E-01	1.58	0.83	3.00	20	0.15	8.60E-01	1.10	0.38	3.15
C-I	A	0.11	330	extra pulmonary	65	0.18	3.08E-02	1.75	1.05	2.92	65	0.18	1.00E+00	1.00	0.53	1.89
C-I	A	0.11	330	liver	21	0.21	3.94E-02	2.22	1.02	4.83	-	-	-	-	-	-
C-I	A	0.11	330	Löfgren	46	0.20	1.71E-02	1.98	1.12	3.50	191	0.16	4.18E-01	1.27	0.71	2.28
C-I	A	0.11	330	persistent	110	0.16	3.41E-02	1.59	1.03	2.46	88	0.17	8.56E-01	0.95	0.56	1.62
C-I	A	0.11	330	resolving	88	0.17	2.82E-02	1.67	1.05	2.66	110	0.16	8.56E-01	1.05	1.79	0.62
C-I	A	0.11	330	skin	40	0.19	4.09E-02	1.88	1.02	3.47	-	-	-	-	-	-
D	A	0.03955	784	eye	163	0.02	1.39E-01	0.57	0.27	1.20	327	0.05	4.18E-02	0.43	0.19	0.97
D	A	0.03955	784	liver	115	0.05	5.10E-01	1.24	0.65	2.35	375	0.04	3.68E-01	1.40	0.68	2.88
D	A	0.03955	784	extra pulmonary	446	0.04	7.23E-01	0.93	0.61	1.41	121	0.05	4.95E-01	0.79	0.39	1.57

D	A	0.03955	784	skin	222	0.04	7.06E-01	0.90	0.52	1.55	274	0.05	5.09E-01	0.80	0.42	1.54
E	A	-	-	acute	94	11/15	4.33E-01	0.73	0.34	1.60	-	-	-	-	-	-
E	A	-	-	chronic	212	22/36	6.60E-02	0.61	0.36	1.04	-	-	-	-	-	-
F	A	-	-	acute	484	0.21	-	-	-	-	435	0.11	4.30E-09	2.21	2.89	1.69
F	A	-	-	chronic	435	0.11	-	-	-	-	484	0.21	4.30E-09	0.45	0.35	0.59
F	A	-	-	persistent	535	0.13	-	-	-	-	382	0.19	2.97E-04	0.63	0.49	0.81
F	A	-	-	skin	113	0.10	-	-	-	-	807	0.17	8.88E-03	0.54	0.34	0.86
F	A	-	-	cardiac	34	0.12	-	-	-	-	886	0.16	3.50E-01	0.70	0.33	1.48
F	A	-	-	CNS	56	0.10	-	-	-	-	864	0.16	7.25E-02	0.56	0.30	1.06
F	A	-	-	fibrosis	25	0.08	-	-	-	-	883	0.16	1.23E-01	0.45	0.16	1.27
F	A	-	-	eye	113	0.10	-	-	-	-	807	0.17	1.00E-02	0.55	0.35	0.87
F	A	-	-	extra pulmonary	229	0.11	-	-	-	-	685	0.17	1.38E-03	0.59	0.42	0.82

Table S13: Results of the subphenotype analysis for marker rs9277542 (*HLA-DPB1*) in panel F

Abbreviations and description: See Table 1. The given P values are not conditioned on rs5007259 and/or rs4143332.

Panel	Allele	MAF controls	N controls	Subphenotype	N SPT	AF (panel E: T/A)	P	OR	L95	U95	N non-SPT	AF non-SPT	P	OR	L95	U95
A	G	0.29	5482	acute	566	0.36	1.36E-07	1.41	1.24	1.60	1025	0.35	6.42E-01	1.04	1.21	0.89
A	G	0.29	5482	chronic	1025	0.35	1.31E-09	1.36	1.23	1.50	566	0.36	6.42E-01	0.96	0.83	1.12
A	G	0.29	5482	Löfgren	64	0.37	4.23E-02	1.45	1.01	2.08	401	0.34	5.98E-01	1.11	0.75	1.63
A	G	0.29	5482	eye	33	0.32	5.59E-01	1.17	0.69	1.96	-	-	-	-	-	-
A	G	0.29	5482	skin	66	0.30	8.02E-01	1.05	0.72	1.53	1519	0.36	1.27E-01	0.74	0.51	1.09
B-I	G	0.27	3278	acute	187	0.36	4.50E-04	1.48	1.19	1.85	374	0.37	7.72E-01	0.96	1.25	0.74
B-I	G	0.27	3278	chronic	374	0.37	1.03E-07	1.54	1.31	1.81	187	0.36	7.72E-01	1.04	0.80	1.35
B-I	G	0.27	3278	Löfgren	57	0.32	2.58E-01	1.26	0.84	1.88	-	-	-	-	-	-
B-I	G	0.27	3278	eye	44	0.33	2.81E-01	1.28	0.81	2.02	-	-	-	-	-	-
B-II	G	0.29	285	acute	50	0.28	8.33E-01	0.95	0.58	1.55	185	0.32	3.83E-01	0.80	1.32	0.48
B-II	G	0.29	285	chronic	185	0.32	2.40E-01	1.19	0.89	1.58	50	0.28	3.83E-01	1.25	0.76	2.07
B-II	G	0.29	285	Löfgren	38	0.31	7.47E-01	1.09	0.64	1.86	211	0.33	7.40E-01	0.91	0.53	1.57
B-II	G	0.29	285	skin	22	0.36	2.83E-01	1.42	0.75	2.69	213	0.31	4.54E-01	1.28	0.67	2.45
C-I	G	0.26	330	acute	20	0.40	4.95E-02	1.91	0.99	3.69	40	0.31	3.41E-01	1.47	3.23	0.67
C-I	G	0.26	330	bones,muscle,joints	19	0.53	3.16E-04	3.19	1.65	6.17	-	-	-	-	-	-
C-I	G	0.26	330	chronic	40	0.31	3.01E-01	1.30	0.79	2.16	20	0.40	3.41E-01	0.68	0.31	1.50
C-I	G	0.26	330	extra pulmonary	65	0.35	4.05E-02	1.52	1.02	2.27	65	0.29	3.25E-01	1.30	0.77	2.20
C-I	G	0.26	330	liver	21	0.26	9.61E-01	1.02	0.50	2.07	-	-	-	-	-	-
C-I	G	0.26	330	Löfgren	46	0.28	6.22E-01	1.13	0.69	1.84	191	0.28	9.70E-01	0.99	0.60	1.64
C-I	G	0.26	330	persistent	110	0.30	2.77E-01	1.21	0.86	1.70	88	0.26	4.86E-01	1.17	0.75	1.83
C-I	G	0.26	330	resolving	88	0.26	8.75E-01	1.03	0.71	1.51	110	0.30	4.86E-01	0.85	1.33	0.55
C-I	G	0.26	330	skin	40	0.36	4.79E-02	1.63	1.00	2.66	-	-	-	-	-	-
D	A	0.42	784	eye	163	0.44	7.82E-01	1.04	0.81	1.32	327	0.39	1.74E-01	1.22	0.92	1.63

D	A	0.42	784	liver	115	0.37	1.15E-01	0.79	0.59	1.06	375	0.41	2.83E-01	0.84	0.60	1.16
D	A	0.42	784	extra pulmonary	446	0.42	4.80E-01	0.94	0.80	1.11	121	0.39	3.92E-01	1.14	0.84	1.55
D	A	0.42	784	skin	222	0.40	2.65E-01	0.88	0.71	1.10	274	0.41	6.83E-01	0.95	0.72	1.24
E	G	-	-	acute	94	44/34	2.58E-01	1.29	0.83	2.03	-	-	-	-	-	-
E	G	-	-	chronic	212	93/76	1.91E-01	1.22	0.90	1.66	-	-	-	-	-	-
F	G	-	-	chronic	435	0.27	-	-	-	-	484	0.29	3.02E-01	0.90	0.73	1.10
F	G	-	-	persistent	535	0.26	-	-	-	-	382	0.30	5.17E-02	0.81	0.66	1.00
F	G	-	-	skin	113	0.20	-	-	-	-	807	0.29	7.13E-03	0.62	0.44	0.88
F	G	-	-	cardiac	34	0.21	-	-	-	-	886	0.28	2.21E-01	0.69	0.38	1.26
F	G	-	-	CNS	56	0.24	-	-	-	-	864	0.28	3.14E-01	0.79	0.50	1.25
F	G	-	-	fibrosis	25	0.20	-	-	-	-	883	0.28	2.77E-01	0.67	0.32	1.39
F	G	-	-	eye	113	0.22	-	-	-	-	807	0.29	5.99E-02	0.72	0.51	1.02
F	G	-	-	extra pulmonary	229	0.25	-	-	-	-	685	0.29	1.40E-01	0.83	0.65	1.06

Table S14: Predicted allele-specific miRNA binding sites for associated SNPs in the *HLA-DPB1* gene region using miRanda with default parameters.

The position of the respective allele is highlighted in red.

SNP	Allele	Position	Forward Sequence	miRNA
rs1042544	G	15	aGTCAGTTTCTATCGTTCTGCTc	hsa-miR-16
rs9277533	C	19	gtataATGGGGCCTGTTACA	hsa-miR-194
rs9277533	T	16	taaTGGGGCCTGTTATACAT	hsa-miR-568
rs9277534	A	5	GACCACTATTCTTAACTATTCAA	hsa-miR-153
rs9277534	A	17	atttATGTCTCAGACCACTATTCT	hsa-miR-219-2-3p
rs929	G	15	tgAGGGTTTTAGTAGACA	hsa-miR-934

Table S15: Heritability explained by 11 confirmed or genome-wide significant sarcoidosis risk loci.

The odds ratio (OR) is given for the respective risk allele. See supplementary methods for details.

Chr	dbSNP ID	Position hg19	Locus	OR	Heritability
6	rs5007259	32,379,101	BTNL2	1.66	0.0095
6	rs4143332	31,348,365	HLA-B	1.90	0.0037
10	rs1049550	81,926,702	ANXA11	1.32	0.0028
11	rs671976*	64,046,029	11q13.1	1.31	0.0028
6	rs9277542	33,055,247	HLA-DPB1	1.37	0.0024
1	rs12069782	67,600,101	IL23R	1.31	0.0016
12	rs653178	112,007,756	ATXN2	1.19	0.0012
5	rs4921492	158,832,277	IL12B	1.20	0.0012
4	rs223498	103,651,962	MANBA	1.19	0.0012
2	rs6748088	203,264,771	FAM117B	1.18	0.0009
6	rs1411578	57,054,843	Rab23	1.19	0.0006
Cumulative heritability					0.0278

*OR taken from [1]

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Supplementary information

The study sample

The screening panel A comprised 1869 sarcoidosis cases that were analyzed and described in previous studies [7,8] and 5600 control subjects, including 2573 control individuals from Popgen [9], 1500 controls from the Heinz Nixdorf RECALL (HNR) study [10], 998 adults from the KORA Study Augsburg (Collaborative Health Research in the Region of Augsburg) [11], 314 control individuals of South German origin and part of the control population of the Munich recruited from the Bavarian Red Cross, and 215 control individuals recruited from the Charité - Universitätsmedizin Berlin. The patients of panel A are in parts further classified as being affected by Löfgren´s syndrome (n = 64), or by an acute (n = 566) or chronic (n = 1025) course of the disease, as described in detail previously [12]. In panel B-I, genotypes of 585 German sarcoidosis patients were compared to those of 3500 healthy individuals from the EMIL study [13] (n = 2574) and from the KORA study Augsburg [11] (n = 926). Panel B-II comprised 307 sarcoidosis patients and 285 controls from a sample described elsewhere [14]. Panel C-I consists of 267 sarcoidosis cases and 330 controls from the Czech Republic and substantially overlaps with the sample described elsewhere [15]. For subphenotype analysis, panel C-I was extended by n=43 Czech patients recruited at the Prague General Hospital and Thomayer Hospital for the GenPhenReSa Consortium. The Swedish cohort (panel C-II) comprised 1121 sarcoidosis cases described elsewhere [16], and 2041 controls from Swedish Epidemiological Investigation of Rheumatoid Arthritis (EIRA) study [17]. Panel D comprised of 789 cases and 1122 controls taken from an extensive cohort of African-American (AA) sarcoidosis patients and controls assembled from the ACCESS Group [18], the SAGA collection [19], the Henry Ford Health System in Detroit, Michigan [20], the Lupus Family Registry and Repository (LFRR) - Oklahoma Medical Research Foundation (OMRF) [21], and the Rheumatic Disease Research Core Center (RDRCC) - OMRF. Each sample collection site received the IRB approval to recruit samples. All of the AA ImmunoChip samples were processed and genotyped at the OMRF under the auspice of the OMRF IRB. Panel E consists of 342 German trios, comprising both parents and one offspring affected by sarcoidosis described previously [12]. Panel F consists of 920 sarcoidosis patients of Serbian origin that were recruited and deeply phenotyped at the University Hospital of Pulmonology at the Clinical Center of Serbia for the GenPhenReSa Consortium. All cases were diagnosed according to international

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standards [22]. The large majority of the patients have been in follow-up without a need to revise the diagnosis, e.g. a change of the diagnosis to chronic beryllium disease. The frequency of misdiagnoses is therefore negligible.

Sarcoidosis subphenotypes

For panels A, B-I, B-II, C-I, D, E and F information of subphenotypes were and compiled retrospectively according to current standards [22,23]. On this basis the following rough subphenotype definitions were introduced for the subphenotype analysis in this study: intensive symptoms from the beginning (“acute”), chronic onset with a subtle symptoms in the beginning (“chronic”), duration more than two years receiving constant therapy (“persistent”), free of symptoms within two years without medication or receiving medication once (“resolving”), organ involvement as named (“skin”, “eye”, “liver”, “CNS”, “cardiac”, “bones,muscle,joints” meaning bones or muscle or joints), hilar lymphadenopathy and erythema nodosum or arthritis (“Löfgren syndrome”), any organs involved apart from the lung (“extra pulmonary involvement”) and patients with radiographic signs of pulmonary fibrosis (“fibrosis”).

The GenPhenReSa Consortium

The members of the GenPhenReSa Consortium are listed in the following table:

Institution	City, Nation	Primary Investigator	Coworker
University Hospital Freiburg	Freiburg, D	J. Müller-Quernheim	A. Prasse
Evangelische Lungenklinik Berlin Buch	Berlin, D	C. Grohé	-
Gemeinschaftskrankenhaus Havelhöhe	Berlin, D	C. Grah	-
Ruhrlandklinik	Essen, D	U. Costabel	F. Bonella
Department of Medicine II, University Medical Center	Bonn, D	S. Pabst	-
Universities of Giessen and Marburg Lung Center (UGMLC)	Giessen, D	A. Günther	Benjamin Löh
Department of Pneumology, University Medical Center Leipzig	Leipzig, D	H. Wirtz	-
Department of Pneumology, University Medical Center Regensburg	Regensburg, D	M. Pfeifer	-
Pneumologische Praxis, Neuruppin	Neuruppin, D	Weihrich	-
Medical Hospital, Research Center	Borstel. D	K.I. Gaede	P. Zabel

Borstel			
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Respiratory Diseases and Lung Transplant Unit, Clinical and Specialist Medicine Dept,AOUS,Siena University, Siena, Italy	Siena, Italy	P. Rottoli	E. Bargagli C. Olivieri
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IRCCS San Matteo Hospital Foundation - Pneumology Unit, Pavia	Pavia, Italy	Z. Kadija	F. Mariani
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Academic Respiratory unit, School of Clinical Sciences, University of Bristol	Bristol, UK	A. B. Millar	-
Aintree Chest Centre, University Hospital Aintree Lower Lane	Liverpool,UK	L. Spencer	Sarah Agnew
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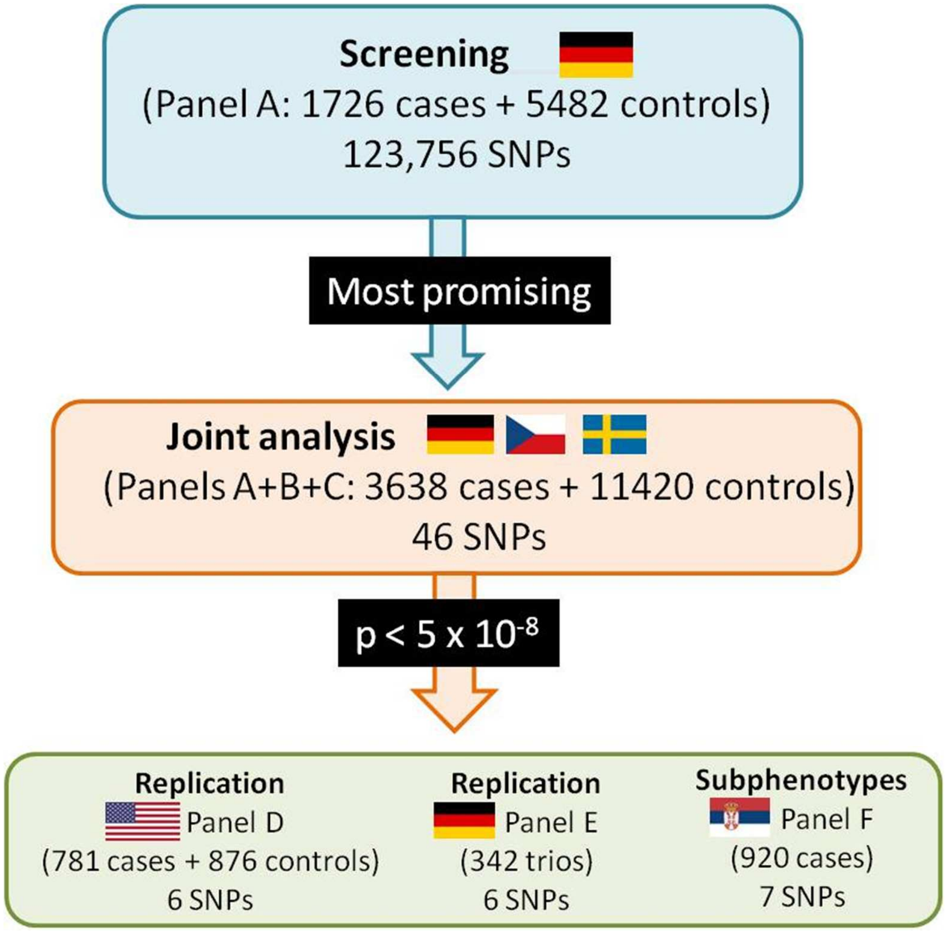
Study design

Panel A was used for screening approx. 120.000 SNPs for association with sarcoidosis. Based on the results of the screening step, 46 SNPs were selected as most promising candidates and were investigated in the remaining European case-control panels B and C. Panels A, B and C were analyzed together ("joint analysis") in order asses significane of the findings. Analysis of panel D approaches the replication of the significant findings in an non-European population of African ancestry, while panle E constitutes of sarcoidosis trios allowing family-based association analysis. Panel F was employed to assess subphenotype-specific effects in a deeply phenotyped European population.



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Further information on Immunochip genotyping and quality control

The Immunochip is a BeadChip developed for highly multiplexed SNP genotyping of complex DNA. Data of panel A were analyzed using Illumina's GenomeStudio Genotyping Module. The NCBI build 36 (hg18) map was used (Illumina manifest file Immuno_BeadChip_ 11419691_B.bpm) and normalized probe intensities were extracted for all samples passing standard laboratory QC thresholds. Genotype calling was performed with the GenomeStudio GenTrain 2.0 algorithm (Illumina's GenomeStudio data analysis software) and the custom generated cluster file of Trynka *et al.* (based on an initial clustering of 2,000 UK samples and subsequent manual readjustment of cluster positions) [24].

SNPs that had >5% missing data, a minor allele frequency <1% or deviated from Hardy-Weinberg equilibrium (exact $P<10^{-4}$ in controls) per sample study were excluded using the PLINK software version 1.07 [25]. Samples with >3% missing data were excluded. For robust relatedness testing (IBS/IBD estimation) and population structure analysis, we generated a pruned subset of 23,535 SNPs excluding X- and Y-chromosomes, SNPs in LD (leaving no pairs with $r^2>0.2$), and 11 high-LD regions as described by Price *et al.* [26]. Pair-wise percentage IBD values were computed using PLINK. By definition, Z0: P(IBD=0), Z1: P(IBD=1), Z2: P(IBD=2), Z0+Z1+Z2=1, and PI_HAT: P(IBD=2) + 0.5 * P(IBD=1) (proportion IBD). One individual (the one showing greater missingness) from each pair with PI_HAT>0.1875 (which is halfway between expected IBD for third- and second degree relatives) was removed ($n_{\text{Samples}}=84$). “Extreme outliers” were detected by comparing the distribution of the IBS values for each individual with the combined IBS distribution of the entire study population. Individuals less related to the entire study 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, the individual was removed from the population ($n_{\text{Samples}}=68$). One outlier individual with an average marker heterozygosity of ±5 s.d. away from the sample mean was excluded. The remaining individuals were tested for population stratification using the principal components stratification method, as implemented in EIGENSTART [27]. A small excerpt of the Immunuochip dataset of panel A, namely 12 SNPs in the sialic acid acetylesterase (*SIAE*) locus, was analyzed in a previous study [29].

Genotyping for panel D was performed at the OMRF using the Illumina Immunochip. SNPs had to meet the following quality control criteria for inclusion: well-defined cluster plots by

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visual inspections, call rate >95%, minor allele frequency >0.01, Hardy-Weinberg proportion test P > 1 x 10-3 in controls, and case-control differences in missingness P > 0.001. Samples were removed from analysis if they were a duplicate of another sample, presented cryptic relatedness in the independent datasets (the proportion of alleles shared identical by descent >0.25), displayed low call rates (<90%), exhibited extreme heterozygosity (>5 standard deviations from the mean), demonstrated either outlying principal component values of population membership calculated by EIGENSOFT 3.0 [27], or revealed discrepancies between reported gender and genetic data. The final ImmunoChip datasets contained 123,756 SNPs (781 cases and 876 controls, 379 males and 1,278 females) that passed our quality control measures.

Details on statistical analysis

Sequential conditional regression analysis was used for analysis of HLA-haplotypes and –SNPs as implemented in PLINK, i.e. a logistic regression analysis with the allelic dosage of the respective SNP as a covariate. The transmission disequilibrium test (TDT) was used for family-based association analysis in panel E [28]. The Cochran-Mantel-Haenszel test for 2x2xK stratified tables was used testing for association across populations (joint analysis), and the Breslow-Day test was used to assess homogeneity of ORs in the different populations, applying a significance threshold of $p = 0.01$. Power calculations were performed using the “PS power and sample size” software, for a detection p value of 0.05 and complete LD between the respective SNP and the causative variant ($r^2 = 1$) [29]. For power calculations in the African-American panel D allele frequencies were estimated from this specific study population. Power calculations for the TDT applied to panel E were performed using G*Power [30]. Association analysis of panel D was performed using logistic regression assuming an additive genetic model and adjusted for gender and the first three principal components. Any SNP positions are given according to GRCh37/hg19, unless described differently. Estimation of the cumulative heritability explained by risk markers were performed using the method described by So *et al.* (https://sites.google.com/site/honcheongso/software/varexp) [31], assuming a prevalence of 40/100,000.

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Methods for in-silico analyses

For prediction of the putative functional consequences of associated SNPs, including effects on transcription factor and miRNA binding, splicing and damaging properties, the FuncPred tool of the NIEHS SNPinfo web server was used [32], including predictions using Polyphen [33] and ESPERR [34]. Information on amino acid changes was retrieved from dbSNP via the UCSC genome database [35]. Information on variants in LD with risk markers were retrieved using SNAP based on CEU 1000 Genomes Pilot 1 dataset [36], a maximum distance of 500 Mb and a LD threshold of $r^2 \geq 0.8$. The eQTL browser was used to retrieve information on potential allele-specific expression patterns from diverse cell lines and tissues (http://eqtl.uchicago.edu/cgi-bin/gbrowse/eqtl/). Network analysis was conducted using STRING version 8.0 based on public available protein interaction data, without using information based on textmining and positional neighborhood [37]. Proteins that were included in the analysis were selected based on the association and *in silico*-analysis presented in this manuscript (i.e. BTNL2, HLA-DPB1, HLA-B, MICA, ANXA11, IL23R, SH2B3, CRIP1, IL12B, MANBA, NFKB1 and FAM117B), or were previously described or hypothesized as potentially affected (i.e. TNF, HLA-DRB1, HLA-DQB1, OS9, CYP27B1, KCNK4, CCDC88B and RAB23). Transcription factor binding prediction was performed using PROMO version 3.0.2 [38] based on the TRANSFAC database version 8.3. A systematic search for DNase hypersenitive sites that overlap with the genomic location of highly associated SNPs was carried out on the basis of ENCODE DNase clusters including 124 cell lines [39].

Association signal in the IL23R region

Conditional regression analysis showed that newly identified susceptibility marker rs12069782 represents an independent and novel sarcoidosis risk variant in the *IL23R* gene region, independent of the association previously reported [12,40]. Of three known risk markers that were represented in the dataset, rs11465804 and rs11209026 (Arg381Gln) were associated with nominal significance in study panel A ($p = 1.96 \times 10^{-3}$; OR [95% CI] = 0.76 [0.63-0.90] and $p = 9.54 \times 10^{-5}$; OR [95% CI] = 0.71 [0.59-0.84]), also after conditioning on rs12069782 ($p = 2.14 \times 10^{-3}$ and $p = 1.88 \times 10^{-4}$, respectively). Vice versa, rs12069782 remained significant after conditioning on rs11465804 and rs11209026 ($p = 3.97 \times 10^{-8}$ and $p = 6.65 \times 10^{-8}$).

Replication of HLA signals

Marker rs2227139 near *HLA-DRA* and rs1964995 near *HLA-DRB5*, which were associated with sarcoidosis in African-Americans and European Americans, respectively [6], were confirmed with nominal significance with and without conditioning on the top three HLA signals (**Table S5**; rs2227139: $p = 1.04 \times 10^{-26}$, OR = 1.53; rs1964995: $p = 2.13 \times 10^{-34}$, OR = 0.59). Interestingly, conditioning on rs1964995 diminished the association of the HLA lead SNP rs5007259 to nominal significance ($p = 1.34 \times 10^{-6}$). The same was true vice versa, suggesting that that these two SNPs may not represent independent signals.

Neither rs4143332 nor rs9277542 were represented in the recently published US-American GWAS on sarcoidosis [6]. The HLA-DPB1*0101 haplotype, which had been described as a risk haplotype for sarcoidosis before in an African-American population [41], was associated with nominal significance (p = 0.020; OR = 1.17) after conditioning on rs5007259 and rs4143332.

Analysis of imputed HLA-haplotype alleles

Imputation and association analysis of classical HLA-alleles alone showed genome-wide significance for *HLA-B*, *HLA-C*, *HLA-DPB1*, *HLA-DQA*, *HLA-DQB*, *HLA-DRB*, *HLA-DRB3* and *HLA-DRB4* haplotypes, with the most significant signal obtained for HLA-B*0801 ($p = 1.33 \times 10^{-29}$).

Subphenotype-specific analysis of markers in the HLA-region in panel A

In the analysis of HLA-haplotypes and SNPs in acute sarcoidosis patients compared to controls, an additional signal was detected peaking at marker rs3129843 ($p = 6.40 \times 10^{-45}$; OR [95% CI] = 3.81 [2.71-3.73]), which is located between the *BTNL2* and the *HLA-DRA* gene locus. This signals stretched over an approximately 13 kb-region, harboring *C6ORF10*, *BTNL2* and *HLA-DRA*. The smallest p value of all haplotypes was observed for HLA-DRB1*0301 ($p = 1.48 \times 10^{-41}$; OR [95% CI] = 2.91[2.49-3.40]). This association disappeared after conditioning on rs3129843 ($p_{cond} = 0.152$; OR [95% CI] = 1.40[0.88-2.20]. In the very small sub-sample of patients with Löfgren syndrome (n = 64) this haplotype was strongly associated ($p = 2.25 \times 10^{-15}$; OR [95 CI] = 4.20 [2.86-6.16]). This is in line with prior reports that link carriership of this haplotype to disease resolution among patients with Löfgren syndrome [42]. However, the smallest p value and the strongest effect in the analysis of the Löfgren sample was seen for rs1794282 ($p = 1.75 \times 10^{-15}$; OR [95% CI] = 4.84 [3.29-7.15]).

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When conditioning all markers in the HLA-region on rs3129843 in the acute sample, the smallest p value was obtained for SNP rs5007259 in the *BTNL2* gene region, which represents the lead signal in the overall sarcoidosis analysis.

The chronic subphenotype shows a similar association pattern as the overall sarcoidosis phenotype with the major association signal represented by rs5007259 ($p = 7.37 \times 10^{-18}$; OR [95% CI] = 0.65 [0.59-0.72]). The lowest p values among the analyzed haplotypes were displayed by HLA-DQB1*0501 ($p = 2.01 \times 10^{-15}$; OR [95% CI] = 0.46 [0.38-0.55]) and HLA-DRB1*0101 ($p = 2.17 \times 10^{-15}$; OR [95% CI] = 0.41 [0.33-0.51]). The strongest signal after conditioning on rs5007259 was located in the *HLA-DPB1* gene region (rs3128921; $p = 3.86 \times 10^{-11}$; OR [95% CI] = 1.42 [1.28-1.57]). The two haplotypes remain significantly associated, however with reduced effect sizes (HLA-DQB1*0501: $p = 7.17 \times 10^{-09}$; OR [95% CI] = 0.55 [0.45-0.67]) and HLA-DRB1*0101: $p = 1.60 \times 10^{-09}$; OR [95% CI] = 0.50 [0.40-0.62]).

Association signals of known risk loci in study panel A

Three SNP markers in the *ANXA11* locus (rs1953600, rs2573346 and rs1049550) were associated with genome-wide significance and thereby directly confirmed this region as susceptibility locus for the disease. The association of the risk variants rs1411578 and rs1040461 (both *RAB23*; $p = 7.11 \times 10^{-4}$ and $p = 2.21 \times 10^{-3}$, respectively) in panel A confirmed previous findings [5]. Marker rs1411578 was further investigated in panels B and C, displaying nominal significance in the meta-analysis of panels A, B and C ($p = 1.86 \times 10^{-5}$; OR = 1.18). Further, risk SNP rs694739, located on chromosome 11q13.1 [1], was associated with $p = 3.33 \times 10^{-6}$ in panel A and with genome-wide significance in the meta-analysis of panels A, B and C ($p = 1.14 \times 10^{-16}$; OR = 0.79). The *OS9* lead SNP rs1050045 was associated with borderline significance in panel A (p = 0.057) [2].

Additional information and functional hypotheses on associated variants and genes

Chromosome 12q24.12: Variant rs3184504 induces an amino acid change (R262W) in the SH2B3 protein, an intriguing candidate. SH2B3 is involved in B-cell proliferation [43] and the endothelial response to TNF [44] and has not yet been implicated in sarcoidosis pathogenesis. A recent functional investigation revealed that carriers of the SH2B3 rs3184504*A risk allele showed stronger activation of the NOD2 recognition pathway in response to lipopolysaccharide and muramyl dipeptide, suggesting SH2B3 may play a role in protection against bacterial infection [45]. The lead SNP of this region (rs653178) has further been described as a trans-eQTL in circulating monocytes, an important cell type in sarcoidosis pathogenesis, influencing cystein-rich intestinal protein 1 (CRIP1) expression [46]. CRIP1 is associated with the acute-phase immune response [47] and is also expressed in human airway epithelial cells [48]. In mice, CRIP1 over-expression impacted host defense by skewing towards a Th2 phenotype [49].

Chromosome 4q24: As one candidate for a causal variant, SNP rs223498 resides in a DNase hypersensitive site observed in HeLa cells. According to the TRANScription FACtor (TRANSFAC) database [50], the rs223498 risk allele C introduces a binding site for the transcription factor GATA6, which is highly expressed in lung tissue [51]. GATA6 has been reported to be involved in a number of diseases and phenotypes of the lung, e.g. pulmonary arterial hypertension and lung adenocarcinoma metastasis [52,53], yet not in sarcoidosis.

Chromosome 2q33.2: The lead SNP of the 2q33.2 region (rs6748088) had been suggested as a risk variant for sarcoidosis in a previous GWAS from our group, reporting similar effect sizes [2]. However due to the smaller sample size in that study, no significant result had been obtained. The region harbors 15 candidate genes, all of which could be affected by the known, or yet to be discovered, associated variants. Whether the suggested second independent signal in the region is a true finding, remains to be investigated. The lead SNP identified in our study (rs6748088) was proposed to influence FAM117B expression in circulation monocytes [54], which is expressed in human immune cells. A further reasonable candidate encoded in this region is BMPR2, which is involved in the regulation of inflammatory processes in the lung [55] and has been suggested as a core mediator in sarcoidosis pathogenesis in comparison to idiopathic pulmonary fibrosis [56].

Chromosome 19p13.2: Allelic variation of the candidate risk SNP rs34536443 (*TYK2* Pro1104Ala) is known to influence Th2 lymphocyte polarization [57]. The risk allele “C” reduces TYK2 activity in T lymphocytes and shifts the cytokine secretion towards a Th2 cytokine profile. This shift is also observed in severe sarcoidosis with progressing pulmonary fibrosis [58] and reflected by a strong association of rare rs34536443-C allele with fibrosis among sarcoidosis patients ($p = 0.008$; OR [95% CI] = 4.59 [1.33-15.76]).

BTNL2*:* In mice, BTNL2 has been shown to control mucosal inflammation by promoting FOXP3 expression and thereby the development of regulatory T cells [59], while in human

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CD4+ T cells from bronchoalveolar lavage fluid of sarcoidosis patients FOXP3 expression is reduced [60]. We hypothesize that in a genetically susceptible individual deregulated BTNL2 expression might result in the impaired function and abundance of regulatory T cells described for sarcoidosis [61-63]. Since *FOXP3* mRNA expression was reported to be elevated in peripheral blood after treatment with prednisone, it might be possible that genetic variation in the BTNL2 locus also influences the response to this common treatment of sarcoidosis.

Additional supplementary data:

File S1: Results from the logistic and sequential conditional regression analysis of HLA-haplotypes and SNP markers

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Data file S1: Results from the logistic and sequential conditional regression analysis of HLA-haplotypes and SNP markers

Haplotypes were imputed from SNP genotype data using HLA*IMP and frequencies were analyzed using logistic regression analysis. Results are given for all SNPs and haplotypes with a genome-wide significant p value in the logistic regression analysis (P). Extended models include the allelic dosage for rs5007259 and rs4143332 as covariates (P cond). Nominal significant p values > 5.0×10^{-8} are printed in grey. Results for the lead signals are highlighted in green, i.e. rs5007259 (#872), rs4143332 (#579) and rs9277542 (#1133).

#	dbSNP ID/ haplotype	Position hg19	OR	P	P cond rs5007259	P cond rs5007259, rs4143332
1	A*0101	-	1.36	5.01E-10	5.04E-06	4.51E-01
2	B*0801	-	1.88	5.94E-30	2.56E-17	NA
3	B*3501	-	0.50	2.46E-12	4.72E-09	9.89E-08
4	C*0401	-	0.63	2.17E-10	4.97E-07	3.45E-05
5	C*0701	-	1.71	4.57E-26	1.51E-16	5.35E-02
6	DPB1*0101	-	1.44	6.38E-09	2.68E-06	1.98E-02
7	DQA*0101	-	0.72	4.50E-08	3.33E-02	7.53E-02
8	DQA*0501	-	1.60	2.40E-18	6.64E-08	8.46E-01
9	DQB*0201	-	1.65	3.79E-19	3.65E-07	2.69E-01
10	DQB*0501	-	0.53	5.11E-18	5.49E-07	1.04E-06
11	DRB1*0101	-	0.48	1.42E-18	2.29E-08	4.30E-08
12	DRB1*0301	-	1.65	4.99E-19	5.43E-07	2.10E-01
13	DRB3*9101	-	1.64	3.16E-22	1.65E-07	7.79E-01
14	DRB3*9901	-	1.49	9.12E-24	1.73E-04	6.42E-02
15	DRB4*9101	-	0.70	2.30E-12	5.29E-01	5.36E-01
16	DRB4*9901	-	0.70	1.30E-13	7.40E-01	7.00E-01
17	rs13195040	27,413,924	1.46	2.55E-09	3.17E-05	3.98E-01
18	rs10484399	27,534,528	1.45	3.86E-09	2.95E-05	3.75E-01
19	rs17693963	27,710,165	1.40	4.48E-08	2.19E-04	2.19E-01
20	rs200484	27,775,674	1.38	4.08E-08	1.00E-04	4.01E-01
21	rs34706883	27,805,255	1.42	2.01E-08	8.71E-05	2.20E-01
22	rs13212651	27,806,985	1.42	1.85E-08	8.25E-05	2.26E-01
23	rs13194781	27,815,639	1.42	1.82E-08	7.93E-05	2.25E-01
24	rs13199772	27,834,085	1.43	1.61E-08	7.33E-05	2.34E-01
25	rs13218875	27,884,012	1.43	1.53E-08	1.26E-04	1.07E-01
26	rs156743	27,967,089	1.36	4.08E-08	8.07E-05	5.67E-01
27	rs149990	27,998,258	1.36	4.40E-08	9.06E-05	5.44E-01

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28	rs13197574	28,060,239	1.44	5.11E-09	6.43E-05	1.30E-01
29	rs13205911	28,124,114	1.44	5.32E-09	6.68E-05	1.26E-01
30	rs9393908	28,190,830	1.35	3.70E-08	1.61E-04	5.25E-01
31	rs9366717	28,191,057	1.35	3.98E-08	1.61E-04	5.25E-01
32	rs9380069	28,203,300	1.35	4.80E-08	1.83E-04	5.01E-01
33	rs13211507	28,257,377	1.46	1.32E-09	2.32E-05	1.99E-01
34	rs853685	28,288,785	1.34	2.34E-08	1.72E-05	8.39E-01
35	rs853676	28,299,687	1.34	2.65E-08	2.04E-05	8.66E-01
36	rs13213152	28,349,698	1.49	1.93E-10	8.38E-06	2.66E-01
37	rs2232423	28,366,151	1.49	1.93E-10	8.38E-06	2.66E-01
38	rs13194504	28,630,691	1.50	6.39E-11	3.79E-06	3.18E-01
39	rs6908726	28,671,343	1.51	6.77E-12	2.70E-07	7.79E-01
40	rs9468413	28,689,672	1.40	6.20E-10	4.18E-07	5.86E-01
41	rs9393929	28,696,063	1.51	9.34E-12	3.48E-07	7.30E-01
42	rs6456834	28,700,352	1.39	1.06E-09	6.40E-07	6.58E-01
43	rs1233579	28,712,663	1.51	1.52E-11	1.43E-06	3.47E-01
44	rs9257136	28,723,841	1.51	1.95E-11	1.64E-06	3.36E-01
45	rs1233599	28,731,188	1.52	1.21E-11	1.12E-06	3.83E-01
46	rs1233604	28,734,676	1.52	1.09E-11	1.12E-06	3.84E-01
47	rs1311918	28,753,646	1.52	1.21E-11	1.12E-06	3.83E-01
48	rs7767099	28,768,698	1.52	1.14E-11	1.06E-06	3.89E-01
49	rs3131343	28,775,564	1.51	1.78E-11	1.46E-06	3.52E-01
50	rs4324798	28,776,117	1.51	1.82E-11	1.48E-06	3.52E-01
51	rs3118357	28,802,149	1.52	1.52E-11	1.39E-06	3.53E-01
52	rs9257248	28,803,291	1.52	1.39E-11	1.29E-06	3.65E-01
53	rs3132389	28,831,021	1.52	1.01E-11	1.02E-06	4.07E-01
54	rs3132390	28,832,788	1.51	5.05E-12	2.03E-07	8.06E-01
55	rs3132392	28,838,629	1.52	1.39E-11	1.29E-06	3.65E-01
56	rs3135309	28,855,805	1.51	1.67E-11	1.25E-06	3.75E-01
57	rs2230683	28,891,176	1.52	1.09E-11	8.69E-07	4.30E-01
58	rs3118361	28,898,287	1.53	8.28E-12	1.10E-06	4.40E-01
59	rs3130895	28,905,791	1.52	1.10E-11	1.07E-06	3.86E-01
60	rs3130845	28,923,367	1.52	1.56E-11	1.35E-06	3.55E-01
61	rs3130837	28,948,092	1.52	1.29E-11	1.17E-06	3.69E-01
62	rs3130888	28,949,960	1.51	2.26E-11	1.49E-06	3.55E-01
63	rs3130893	28,980,707	1.50	2.78E-11	1.61E-06	3.27E-01
64	rs3117143	29,031,142	1.51	1.93E-11	1.48E-06	3.26E-01
65	rs3129788	29,057,639	1.51	2.17E-11	1.60E-06	3.18E-01
66	rs3130773	29,095,908	1.50	3.65E-11	2.33E-06	2.78E-01
67	rs3129171	29,155,749	1.30	1.47E-08	3.86E-06	3.01E-01
68	rs3116830	29,167,575	1.50	3.43E-11	2.36E-06	2.66E-01
69	rs3117326	29,240,378	1.51	2.43E-11	1.93E-06	2.83E-01
70	rs3130834	29,248,149	1.51	2.25E-11	1.81E-06	2.97E-01
71	rs3117425	29,260,431	1.53	2.85E-12	3.36E-07	5.85E-01
72	rs3117439	29,266,483	1.52	1.02E-11	9.21E-07	3.73E-01
73	rs3117427	29,274,136	1.50	3.08E-11	1.93E-06	3.06E-01

74	rs9257793	29,335,154	1.49	7.79E-12	1.24E-07	9.66E-01
75	rs9257800	29,340,743	1.52	7.03E-12	9.75E-07	2.49E-01
76	rs3749971	29,342,775	1.47	2.06E-10	7.12E-06	1.69E-01
77	rs9257803	29,344,395	1.44	2.03E-10	9.06E-07	6.74E-01
78	rs9257805	29,346,329	1.42	5.69E-10	1.95E-06	6.21E-01
79	rs9257809	29,356,331	1.48	1.33E-10	7.78E-06	8.36E-02
80	rs442694	29,356,687	1.49	8.16E-11	6.69E-06	8.33E-02
81	rs429479	29,372,323	1.45	5.84E-10	1.19E-05	8.88E-02
82	rs1535039	29,411,432	1.51	1.68E-11	2.37E-06	1.37E-01
83	rs2746149	29,435,355	1.51	7.39E-12	1.07E-06	2.14E-01
84	rs2746150	29,442,701	1.51	1.19E-11	1.83E-06	1.60E-01
85	rs1233491	29,461,730	1.51	1.68E-11	2.24E-06	1.41E-01
86	rs1233489	29,463,043	1.50	2.19E-11	2.61E-06	1.25E-01
87	rs1233480	29,477,414	1.46	1.04E-10	1.76E-06	2.77E-01
88	rs404240	29,523,957	1.51	8.59E-12	1.77E-06	1.18E-01
89	rs1235162	29,537,224	1.54	2.76E-13	3.20E-07	1.50E-01
90	rs1233396	29,546,799	1.53	8.45E-14	1.32E-08	8.59E-01
91	rs926552	29,548,089	1.52	1.30E-13	2.18E-08	7.40E-01
92	rs29218	29,607,429	1.29	1.75E-08	4.97E-05	8.79E-01
93	rs3129073	29,615,822	1.30	8.15E-09	4.64E-05	8.30E-01
94	rs375984	29,644,502	1.28	1.85E-08	2.38E-05	8.12E-01
95	rs2535238	29,645,038	1.28	1.88E-08	2.38E-05	8.18E-01
96	rs2747421	29,645,118	1.28	1.88E-08	2.38E-05	8.18E-01
97	rs3117301	29,654,700	1.27	4.92E-08	7.47E-05	9.19E-01
98	rs1610601	29,700,183	1.28	1.67E-08	4.32E-05	8.89E-01
99	rs1633063	29,726,046	1.29	7.23E-09	2.67E-05	8.06E-01
100	rs1633005	29,764,472	1.34	6.94E-10	2.08E-06	8.17E-01
101	rs1610682	29,801,324	1.28	2.47E-08	3.38E-05	9.78E-01
102	rs1611133	29,809,382	1.28	2.06E-08	2.91E-05	9.32E-01
103	rs2734986	29,818,568	1.35	1.04E-09	8.93E-06	3.66E-01
104	rs2734974	29,833,779	1.29	2.15E-08	1.80E-05	9.76E-01
105	rs1611635	29,836,463	1.36	7.46E-10	7.07E-06	3.88E-01
106	rs2524005	29,899,677	1.31	4.93E-09	3.95E-06	8.97E-01
107	rs3132685	29,945,949	1.54	3.24E-15	2.14E-08	6.24E-01
108	rs356971	29,979,797	1.36	4.71E-10	1.58E-06	7.25E-01
109	rs3129012	29,988,642	1.34	1.97E-09	4.61E-06	5.31E-01
110	rs259926	29,991,867	1.35	5.44E-10	1.97E-06	6.78E-01
111	rs8321	30,032,522	1.62	7.44E-17	1.30E-09	5.57E-01
112	rs9261290	30,038,647	1.62	7.40E-17	1.30E-09	5.74E-01
113	rs1264714	30,042,209	1.36	2.53E-10	1.02E-06	8.18E-01
114	rs1264709	30,056,476	1.35	5.15E-10	1.72E-06	7.15E-01
115	rs1264706	30,063,652	1.62	5.24E-17	1.08E-09	6.09E-01
116	rs1264703	30,065,416	1.31	8.74E-10	5.22E-08	2.07E-01
117	rs1264702	30,065,575	1.32	8.03E-10	6.34E-08	2.49E-01
118	rs916570	30,066,031	1.28	1.12E-08	2.39E-07	2.34E-01
119	rs916569	30,066,097	1.31	2.25E-09	8.92E-08	2.76E-01

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120	rs1264698	30,067,177	1.31	2.18E-09	9.11E-08	2.89E-01
121	rs1264697	30,067,568	1.30	3.73E-09	1.47E-07	3.22E-01
122	rs1264696	30,067,834	1.30	4.25E-09	1.69E-07	3.35E-01
123	rs1264695	30,067,892	1.30	2.87E-09	1.24E-07	2.73E-01
124	rs1108052	30,069,795	1.30	2.87E-09	1.24E-07	2.73E-01
125	rs2072110	30,070,178	1.31	1.57E-09	6.72E-08	2.20E-01
126	rs2240071	30,070,932	1.31	1.96E-09	2.08E-07	3.81E-01
127	rs1110446	30,070,937	1.31	1.85E-09	2.05E-07	3.89E-01
128	rs2844796	30,072,511	1.30	6.69E-09	2.72E-07	4.05E-01
129	rs2248289	30,072,721	1.29	9.01E-09	3.47E-07	4.35E-01
130	rs2523992	30,075,103	1.39	8.64E-11	1.39E-06	4.29E-01
131	rs2023473	30,075,613	1.63	1.02E-17	4.04E-10	6.99E-01
132	rs2523989	30,078,275	1.47	6.54E-14	1.35E-08	9.06E-01
133	rs2239529	30,078,330	1.47	4.04E-14	9.37E-09	8.60E-01
134	rs2523988	30,079,129	1.49	8.79E-14	3.12E-08	6.12E-01
135	rs2249099	30,079,307	1.44	6.69E-13	7.96E-08	8.96E-01
136	rs2523987	30,079,993	1.49	9.78E-14	3.36E-08	5.96E-01
137	rs2517598	30,080,274	1.45	3.79E-13	5.09E-08	9.37E-01
138	rs2844793	30,080,496	1.46	1.81E-13	2.94E-08	9.93E-01
139	rs9261425	30,081,108	1.29	1.34E-10	6.54E-08	8.44E-03
140	rs2517597	30,081,189	1.49	9.06E-14	3.18E-08	5.99E-01
141	rs2523986	30,081,246	1.49	9.78E-14	3.36E-08	5.96E-01
142	rs2523985	30,081,334	1.44	5.39E-13	6.45E-08	9.25E-01
143	rs2523984	30,082,003	1.44	5.22E-13	6.14E-08	9.44E-01
144	rs2523983	30,082,221	1.48	2.39E-13	6.36E-08	5.54E-01
145	rs2245420	30,082,688	1.44	6.33E-13	7.25E-08	9.06E-01
146	rs2523981	30,083,182	1.48	2.39E-13	6.36E-08	5.54E-01
147	rs2523980	30,083,505	1.48	2.46E-13	6.49E-08	5.53E-01
148	rs2523979	30,083,515	1.49	2.26E-14	1.19E-08	8.53E-01
149	rs2523978	30,083,708	1.64	1.01E-17	4.30E-10	5.94E-01
150	rs2517596	30,083,855	1.49	1.24E-13	4.11E-08	5.81E-01
151	rs2523976	30,084,696	1.49	7.06E-14	2.69E-08	6.17E-01
152	rs1015466	30,085,916	1.47	3.35E-13	8.56E-08	5.66E-01
153	rs2517592	30,093,137	1.32	1.52E-10	3.02E-06	4.28E-01
154	rs2844790	30,094,113	1.51	3.16E-14	3.72E-08	4.86E-01
155	rs1541269	30,103,360	1.51	1.79E-14	2.20E-08	5.39E-01
156	rs2844789	30,112,795	1.63	1.02E-17	3.86E-10	6.77E-01
157	rs2517645	30,122,623	1.41	4.14E-12	1.02E-06	5.40E-01
158	rs2523735	30,122,657	1.53	2.55E-15	8.52E-09	7.79E-01
159	rs1970	30,125,543	1.62	2.00E-17	6.58E-10	5.89E-01
160	rs1573296	30,127,805	1.62	2.00E-17	6.58E-10	5.89E-01
161	rs2157678	30,128,949	1.62	2.29E-17	7.21E-10	5.56E-01
162	rs929157	30,137,209	1.47	3.44E-13	3.70E-07	3.05E-01
163	rs2523729	30,137,387	1.63	1.13E-17	4.77E-10	6.27E-01
164	rs2844785	30,147,230	1.48	1.10E-13	1.52E-07	3.89E-01
165	rs11158	30,152,467	1.64	6.00E-18	3.21E-10	6.35E-01

166	rs2106072	30,153,363	1.64	5.41E-18	2.98E-10	6.37E-01
167	rs2517622	30,155,149	1.63	1.37E-17	5.18E-10	6.18E-01
168	rs2517618	30,158,127	1.48	1.18E-13	1.61E-07	3.87E-01
169	rs2517614	30,163,955	1.37	1.63E-11	1.17E-08	4.09E-01
170	rs2523722	30,165,273	1.37	1.33E-11	9.94E-09	3.91E-01
171	rs2517613	30,165,662	1.48	1.18E-13	1.61E-07	3.87E-01
172	rs2523721	30,166,266	1.36	4.59E-11	2.83E-08	4.55E-01
173	rs2523720	30,166,886	1.48	1.18E-13	1.61E-07	3.87E-01
174	rs2523719	30,168,319	1.46	3.13E-13	3.11E-07	3.54E-01
175	rs2517612	30,169,092	1.48	9.05E-14	1.44E-07	3.96E-01
176	rs2517611	30,169,327	1.38	8.15E-12	7.12E-09	3.58E-01
177	rs2517610	30,170,280	1.36	2.86E-11	2.04E-08	4.19E-01
178	rs1117490	30,170,510	1.37	1.14E-11	9.16E-09	3.67E-01
179	rs2523716	30,170,525	1.37	1.43E-11	1.15E-08	3.79E-01
180	rs1117489	30,170,827	1.37	1.48E-11	1.19E-08	3.76E-01
181	rs2844776	30,171,827	1.37	2.31E-11	1.66E-08	4.11E-01
182	rs971570	30,172,513	1.38	8.38E-12	7.51E-09	3.55E-01
183	rs2523713	30,173,330	1.36	3.79E-11	2.87E-08	4.68E-01
184	rs2021722	30,174,131	1.37	1.29E-11	1.05E-08	3.77E-01
185	rs885912	30,174,633	1.36	3.27E-11	2.30E-08	4.21E-01
186	rs2188100	30,181,883	1.48	5.88E-14	1.09E-07	4.63E-01
187	rs885916	30,202,571	1.48	7.08E-14	1.20E-07	4.18E-01
188	rs2844777	30,206,014	1.65	1.64E-18	1.09E-10	8.43E-01
189	rs2844773	30,207,495	1.49	8.24E-15	1.24E-08	9.74E-01
190	rs2188099	30,209,918	1.49	8.24E-15	1.24E-08	9.74E-01
191	rs2022083	30,213,540	1.49	9.68E-15	1.44E-08	9.90E-01
192	rs3094078	30,224,970	1.65	2.45E-18	1.48E-10	8.17E-01
193	rs3094076	30,226,305	1.48	1.29E-14	1.54E-08	9.36E-01
194	rs9261630	30,227,915	1.47	2.12E-14	2.31E-08	9.63E-01
195	rs3129699	30,229,989	1.48	1.69E-14	1.88E-08	9.59E-01
196	rs3130398	30,230,760	1.48	1.69E-14	1.88E-08	9.59E-01
197	rs3130400	30,230,777	1.48	2.06E-14	2.19E-08	9.64E-01
198	rs3094074	30,230,930	1.48	1.69E-14	1.88E-08	9.59E-01
199	rs3094073	30,231,224	1.48	2.08E-14	2.30E-08	9.90E-01
200	rs3130401	30,231,273	1.48	1.69E-14	1.88E-08	9.59E-01
201	rs3132659	30,231,330	1.48	1.51E-14	1.73E-08	9.25E-01
202	rs3132658	30,231,666	1.48	2.30E-14	2.37E-08	9.97E-01
203	rs3094071	30,231,768	1.48	1.81E-14	1.91E-08	9.61E-01
204	rs3094070	30,231,829	1.48	1.69E-14	1.88E-08	9.59E-01
205	rs3130403	30,232,009	1.48	1.92E-14	2.07E-08	9.51E-01
206	rs3130404	30,232,250	1.48	1.85E-14	1.92E-08	9.37E-01
207	rs3094630	30,232,436	1.48	1.88E-14	1.97E-08	9.67E-01
208	rs3129701	30,232,672	1.48	1.25E-14	1.53E-08	9.19E-01
209	rs3094629	30,232,953	1.49	8.51E-15	1.05E-08	9.40E-01
210	rs3129703	30,233,558	1.48	1.69E-14	1.88E-08	9.59E-01
211	rs3130405	30,234,152	1.48	1.53E-14	1.69E-08	9.43E-01

212	rs3129831	30,234,627	1.48	1.69E-14	1.88E-08	9.59E-01
213	rs3129832	30,234,657	1.47	2.48E-14	2.49E-08	9.99E-01
214	rs3129705	30,234,721	1.48	1.38E-14	1.59E-08	9.26E-01
215	rs3129706	30,234,931	1.48	1.69E-14	1.88E-08	9.59E-01
216	rs3129707	30,235,204	1.48	1.69E-14	1.88E-08	9.59E-01
217	rs1264622	30,256,936	1.33	2.62E-09	1.75E-04	2.09E-01
218	rs1264587	30,279,074	1.32	5.20E-09	2.66E-04	1.93E-01
219	rs3130380	30,279,130	1.65	2.06E-18	1.40E-10	7.30E-01
220	rs3094628	30,285,312	1.64	3.69E-18	2.11E-10	8.12E-01
221	rs3094064	30,296,253	1.63	9.77E-18	3.42E-10	7.15E-01
222	rs3094067	30,299,245	1.65	1.66E-18	1.18E-10	7.34E-01
223	rs3129837	30,306,306	1.49	7.91E-15	9.97E-09	8.82E-01
224	rs3129840	30,307,342	1.49	8.71E-15	1.06E-08	9.13E-01
225	rs3132650	30,312,176	1.48	9.76E-15	1.17E-08	9.22E-01
226	rs3130355	30,318,327	1.65	2.13E-18	1.39E-10	7.22E-01
227	rs3130364	30,319,154	1.68	2.10E-19	2.67E-11	9.42E-01
228	rs3132649	30,321,057	1.52	3.63E-15	9.48E-10	9.18E-01
229	rs3094061	30,321,189	1.54	7.90E-16	2.84E-10	9.67E-01
230	rs3130374	30,321,336	1.53	3.02E-15	8.24E-10	9.50E-01
231	rs3094627	30,321,482	1.52	3.63E-15	9.48E-10	9.18E-01
232	rs3130375	30,321,732	1.52	3.75E-15	9.89E-10	9.17E-01
233	rs3130376	30,323,109	1.54	6.13E-16	2.28E-10	7.94E-01
234	rs3094060	30,323,110	1.55	3.58E-16	1.53E-10	7.70E-01
235	rs3130377	30,323,393	1.64	4.72E-18	3.55E-10	4.78E-01
236	rs3094624	30,326,809	1.64	3.32E-18	2.80E-10	5.21E-01
237	rs3094058	30,327,196	1.64	4.06E-18	3.29E-10	5.07E-01
238	rs3130350	30,327,839	1.64	3.69E-18	3.02E-10	5.09E-01
239	rs3094622	30,327,952	1.64	1.39E-18	1.35E-10	7.74E-01
240	rs3130351	30,328,192	1.64	4.87E-18	3.57E-10	4.78E-01
241	rs3130352	30,328,357	1.64	3.21E-18	2.64E-10	5.26E-01
242	rs3094621	30,328,753	1.64	1.54E-18	1.47E-10	7.69E-01
243	rs3094057	30,329,966	1.65	2.83E-18	2.60E-10	5.12E-01
244	rs3094056	30,330,071	1.64	4.47E-18	3.43E-10	4.77E-01
245	rs3132647	30,330,737	1.65	2.92E-18	2.40E-10	5.14E-01
246	rs3130353	30,331,216	1.64	5.07E-18	3.91E-10	4.75E-01
247	rs3094054	30,333,505	1.63	7.46E-18	6.80E-10	4.51E-01
248	rs3129809	30,335,621	1.61	1.54E-17	8.53E-10	5.79E-01
249	rs3129812	30,337,974	1.65	2.50E-18	2.35E-10	5.13E-01
250	rs3129815	30,340,528	1.64	3.50E-18	2.94E-10	4.97E-01
251	rs3132638	30,341,471	1.62	1.21E-17	7.44E-10	5.91E-01
252	rs3129817	30,342,753	1.63	1.41E-18	1.63E-10	9.61E-01
253	rs3129818	30,342,966	1.61	1.35E-17	8.02E-10	5.88E-01
254	rs3132634	30,343,272	1.64	2.22E-18	1.47E-10	7.33E-01
255	rs3129820	30,343,569	1.61	1.35E-17	8.02E-10	5.88E-01
256	rs3129821	30,344,038	1.61	1.39E-17	8.19E-10	5.73E-01
257	rs3132631	30,344,645	1.61	1.39E-17	8.38E-10	5.87E-01

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258	rs3132630	30,345,118	1.62	1.30E-17	7.90E-10	6.02E-01
259	rs3130370	30,345,294	1.61	1.62E-17	8.99E-10	5.70E-01
260	rs3129822	30,346,208	1.61	1.54E-17	8.53E-10	5.79E-01
261	rs3132627	30,346,760	1.65	2.50E-18	2.35E-10	5.13E-01
262	rs3132625	30,347,720	1.61	1.35E-17	8.02E-10	5.88E-01
263	rs71750455	30,348,460	1.62	9.45E-18	6.12E-10	6.59E-01
264	rs3130123	30,352,647	1.61	1.54E-17	9.09E-10	5.71E-01
265	rs3130126	30,353,739	1.62	1.16E-17	7.17E-10	5.99E-01
266	rs3094050	30,358,591	1.62	1.22E-17	7.75E-10	5.95E-01
267	rs3094703	30,358,957	1.62	1.21E-17	7.53E-10	6.14E-01
268	rs3094036	30,363,085	1.64	4.47E-18	3.56E-10	4.72E-01
269	rs3094034	30,363,351	1.64	4.47E-18	3.56E-10	4.72E-01
270	rs3130116	30,365,448	1.59	2.16E-16	6.78E-09	1.76E-01
271	rs11961853	30,365,629	1.47	1.30E-13	4.74E-08	5.87E-01
272	rs3132645	30,409,249	1.63	8.17E-18	7.63E-10	3.01E-01
273	rs3132616	30,416,456	1.63	6.92E-18	6.82E-10	3.10E-01
274	rs3130141	30,432,177	1.61	3.21E-17	1.89E-09	2.15E-01
275	rs3094694	30,451,904	1.42	3.83E-13	9.25E-08	9.00E-01
276	rs3094024	30,495,860	1.64	1.92E-18	4.62E-10	2.31E-01
277	rs3130247	30,515,043	1.64	1.92E-18	4.62E-10	2.31E-01
278	rs3132610	30,544,401	1.63	1.70E-18	3.95E-10	2.76E-01
279	rs9262132	30,611,350	1.65	4.61E-19	1.61E-10	3.13E-01
280	rs9262135	30,618,906	1.68	2.85E-20	2.74E-11	5.28E-01
281	rs9262143	30,652,781	1.69	9.59E-21	1.05E-11	6.69E-01
282	rs3132585	30,687,614	1.68	1.64E-20	1.85E-11	5.71E-01
283	rs3132584	30,688,427	1.45	5.62E-15	6.29E-10	2.39E-01
284	rs8233	30,692,965	1.44	7.09E-15	7.68E-10	2.55E-01
285	rs3095330	30,693,633	1.42	1.16E-13	1.55E-08	7.02E-01
286	rs3095329	30,693,816	1.44	6.90E-15	7.30E-10	2.50E-01
287	rs3094127	30,697,447	1.44	8.34E-15	8.31E-10	2.34E-01
288	rs1064627	30,698,541	1.50	1.83E-16	1.58E-10	3.67E-01
289	rs3094125	30,709,357	1.68	2.10E-20	2.20E-11	5.50E-01
290	rs3130662	30,713,808	1.49	3.53E-15	4.96E-09	7.98E-01
291	rs2535324	30,718,035	1.26	2.17E-08	2.91E-06	3.52E-01
292	rs3129973	30,721,143	1.69	1.48E-21	1.83E-12	8.13E-01
293	rs3095328	30,723,781	1.72	2.46E-22	9.11E-13	8.28E-01
294	rs3095326	30,725,841	1.70	1.11E-21	1.49E-12	8.46E-01
295	rs3095340	30,726,939	1.56	1.35E-18	1.51E-11	5.69E-01
296	rs3131036	30,728,290	1.30	1.16E-09	2.46E-05	7.74E-01
297	rs3094122	30,728,360	1.32	2.25E-10	3.64E-05	3.81E-01
298	rs3094121	30,730,960	1.29	1.22E-08	9.24E-05	2.61E-01
299	rs3094120	30,731,556	1.29	1.23E-08	9.29E-05	2.61E-01
300	rs3094117	30,737,486	1.28	3.11E-09	7.83E-06	9.06E-01
301	rs3094116	30,738,408	1.30	9.27E-10	1.47E-05	8.96E-01
302	rs3130673	30,746,519	1.68	3.72E-21	2.60E-12	8.52E-01
303	rs3129981	30,758,857	1.65	1.65E-20	6.07E-12	9.13E-01

304	rs3131050	30,760,025	1.68	2.49E-21	2.06E-12	9.02E-01
305	rs3094112	30,761,734	1.29	7.81E-09	6.21E-05	3.22E-01
306	rs3129985	30,762,542	1.68	2.49E-21	2.06E-12	9.02E-01
307	rs3131060	30,763,291	1.68	2.49E-21	2.06E-12	9.02E-01
308	rs3131064	30,763,893	1.56	8.79E-19	2.70E-12	2.17E-01
309	rs3130641	30,764,081	1.68	3.51E-21	2.61E-12	8.44E-01
310	rs1264377	30,764,907	1.49	1.00E-15	3.33E-11	6.14E-01
311	rs1264373	30,769,273	1.75	1.27E-23	1.26E-13	9.44E-01
312	rs1264372	30,769,726	1.31	8.59E-10	1.21E-05	6.73E-01
313	rs1264361	30,777,498	1.69	9.34E-22	1.09E-12	8.99E-01
314	rs886425	30,781,301	1.69	9.34E-22	1.09E-12	8.99E-01
315	rs886424	30,782,002	1.69	1.15E-21	1.29E-12	8.39E-01
316	rs886423	30,782,205	1.59	3.08E-19	6.27E-12	6.29E-01
317	rs1264353	30,787,762	1.69	9.34E-22	1.09E-12	8.99E-01
318	rs1264352	30,789,647	1.59	4.39E-19	6.87E-12	6.41E-01
319	rs1264350	30,796,545	1.58	1.11E-18	4.30E-12	8.21E-01
320	rs1264341	30,802,465	1.74	2.06E-23	3.85E-13	3.75E-01
321	rs2517582	30,808,762	0.79	5.85E-09	3.69E-05	3.84E-02
322	rs2535335	30,812,497	0.76	4.67E-11	3.00E-06	8.67E-03
323	rs2535332	30,813,249	1.73	6.33E-23	8.53E-13	3.92E-01
324	rs2517576	30,815,035	1.52	8.12E-20	7.44E-10	4.25E-01
325	rs2844664	30,815,945	0.77	2.44E-10	1.45E-06	3.74E-03
326	rs2844663	30,815,951	0.76	2.97E-11	2.37E-06	7.09E-03
327	rs2535331	30,816,270	0.76	1.14E-10	8.06E-07	2.71E-03
328	rs2844662	30,817,879	0.76	3.38E-11	2.55E-06	7.32E-03
329	rs2844659	30,824,532	1.51	9.06E-20	8.26E-10	4.31E-01
330	rs2844657	30,829,522	1.52	7.76E-20	7.45E-10	4.24E-01
331	rs2535326	30,832,063	0.76	3.80E-11	2.63E-06	7.66E-03
332	rs9262263	30,833,957	1.75	1.16E-23	2.49E-13	4.39E-01
333	rs3130657	30,837,646	0.77	4.47E-10	2.09E-06	4.75E-03
334	rs2535340	30,838,497	1.75	7.54E-24	1.79E-13	5.02E-01
335	rs2844654	30,838,688	0.77	4.47E-10	2.08E-06	4.67E-03
336	rs2535339	30,839,430	0.77	6.35E-10	2.35E-06	4.75E-03
337	rs1264334	30,844,260	0.76	4.16E-11	2.75E-06	7.67E-03
338	rs1264333	30,844,314	0.77	4.20E-10	1.96E-06	4.35E-03
339	rs1264332	30,845,563	0.77	2.89E-10	1.48E-06	3.98E-03
340	rs1264331	30,846,830	0.77	3.07E-10	1.53E-06	3.83E-03
341	rs1264327	30,850,582	0.77	3.26E-10	2.56E-06	4.62E-03
342	rs1264318	30,863,530	1.51	1.97E-19	9.24E-10	4.26E-01
343	rs886422	30,864,279	1.75	7.06E-24	1.54E-13	5.12E-01
344	rs1264312	30,872,982	1.75	7.54E-24	1.75E-13	5.11E-01
345	rs1264309	30,875,899	0.77	3.95E-10	1.80E-06	4.29E-03
346	rs886420	30,879,636	1.76	4.34E-24	1.17E-13	6.04E-01
347	rs1264308	30,879,987	1.75	6.80E-24	1.53E-13	5.12E-01
348	rs1264307	30,880,757	0.77	4.85E-10	2.06E-06	4.71E-03
349	rs1264305	30,882,277	0.76	7.09E-11	4.75E-07	1.78E-03

350	rs1264304	30,882,415	1.75	5.97E-24	1.35E-13	5.14E-01
351	rs1264303	30,882,513	0.77	3.70E-10	1.68E-06	4.13E-03
352	rs1264301	30,882,781	0.77	4.10E-10	1.82E-06	4.32E-03
353	rs1264300	30,882,856	0.77	4.03E-10	1.83E-06	4.38E-03
354	rs1264299	30,883,920	0.77	3.95E-10	1.80E-06	4.29E-03
355	rs1264298	30,884,436	0.77	3.95E-10	1.80E-06	4.29E-03
356	rs1264297	30,884,806	0.77	5.85E-10	2.66E-06	5.46E-03
357	rs9262289	30,885,686	0.77	2.73E-10	1.42E-06	3.78E-03
358	rs9262290	30,885,821	0.77	3.61E-10	1.70E-06	4.12E-03
359	rs9262293	30,886,350	0.77	3.95E-10	1.80E-06	4.29E-03
360	rs7756286	30,887,311	0.77	4.03E-10	1.81E-06	4.30E-03
361	rs7738138	30,887,344	0.77	3.95E-10	1.80E-06	4.29E-03
362	rs2249464	30,888,161	1.37	7.15E-16	2.46E-09	1.05E-03
363	rs2517467	30,889,260	1.37	7.65E-16	2.55E-09	1.07E-03
364	rs2517466	30,890,055	0.77	3.95E-10	1.80E-06	4.29E-03
365	rs2074506	30,890,483	0.77	3.92E-10	1.76E-06	4.23E-03
366	rs753725	30,890,871	1.39	7.61E-17	4.53E-10	4.33E-04
367	rs2252856	30,893,251	0.77	4.42E-10	1.94E-06	4.51E-03
368	rs2532938	30,893,831	0.77	3.95E-10	1.80E-06	4.29E-03
369	rs4678	30,893,941	1.43	1.30E-15	1.51E-08	7.59E-01
370	rs2532936	30,894,408	0.77	3.65E-10	1.72E-06	4.13E-03
371	rs2532935	30,894,573	0.77	5.63E-10	2.29E-06	5.01E-03
372	rs2532934	30,894,759	1.37	1.65E-15	4.53E-09	1.50E-03
373	rs2517462	30,896,190	0.77	3.95E-10	1.80E-06	4.29E-03
374	rs2532929	30,897,774	0.75	9.21E-12	1.58E-07	1.25E-03
375	rs2532927	30,898,434	0.77	2.17E-10	1.68E-06	3.98E-03
376	rs3131787	30,899,524	1.44	6.47E-16	8.80E-09	6.77E-01
377	rs2844651	30,900,664	1.37	2.38E-15	6.30E-09	1.70E-03
378	rs3132571	30,905,313	1.31	1.07E-11	1.14E-08	5.08E-02
379	rs3131921	30,907,335	1.55	1.29E-17	2.88E-11	6.89E-01
380	rs2844702	30,912,481	0.77	6.24E-10	3.19E-06	6.39E-03
381	rs3132581	30,913,458	1.58	1.90E-18	7.35E-12	8.44E-01
382	rs3130781	30,914,552	1.44	3.50E-16	4.23E-09	5.09E-01
383	rs3130782	30,914,843	1.51	2.40E-16	2.95E-11	5.56E-01
384	rs3094086	30,919,391	1.59	6.12E-19	2.62E-12	9.56E-01
385	rs2517449	30,919,701	0.77	6.50E-10	2.84E-06	5.98E-03
386	rs3132580	30,920,124	1.58	1.02E-18	3.97E-12	8.92E-01
387	rs2240804	30,920,890	0.77	4.16E-10	3.48E-06	5.96E-03
388	rs2532921	30,922,570	0.77	5.53E-10	2.44E-06	5.46E-03
389	rs3131934	30,931,844	1.70	1.24E-23	9.54E-14	5.35E-01
390	rs3131783	30,932,068	1.59	6.19E-20	4.75E-13	3.71E-01
391	rs2844697	30,932,309	1.30	5.95E-11	2.56E-07	1.52E-01
392	rs3095089	30,933,794	1.55	6.44E-21	9.28E-12	2.35E-01
393	rs3132579	30,940,989	1.59	5.44E-22	5.40E-11	7.16E-01
394	rs3131931	30,945,265	1.33	3.98E-11	4.70E-05	4.17E-01
395	rs2517425	30,949,670	1.31	2.15E-10	3.44E-05	6.33E-01

396	rs886403	30,957,618	1.31	2.23E-10	3.67E-05	5.83E-01
397	rs1634718	30,972,865	1.32	6.02E-11	6.53E-05	3.67E-01
398	rs1634719	30,973,165	1.29	1.79E-09	5.47E-05	6.05E-01
399	rs7755802	30,982,209	0.79	1.16E-08	1.51E-03	3.31E-01
400	rs7776233	30,984,128	0.79	2.88E-08	1.57E-03	2.55E-01
401	rs9262492	30,986,015	0.79	2.72E-08	1.50E-03	2.50E-01
402	rs2894176	30,986,038	0.79	8.12E-09	8.53E-04	2.37E-01
403	rs9262498	30,986,835	0.79	2.67E-08	1.46E-03	2.45E-01
404	rs9262499	30,987,098	0.79	1.26E-08	1.55E-03	3.36E-01
405	rs4713411	30,987,176	0.79	1.05E-08	1.44E-03	3.24E-01
406	rs7758976	30,987,786	0.79	1.08E-08	1.41E-03	3.22E-01
407	rs4713422	30,999,902	0.79	4.25E-09	3.36E-05	4.06E-02
408	rs10807077	31,001,467	0.80	3.99E-08	1.40E-04	7.22E-02
409	rs4248153	31,002,527	0.78	7.89E-10	9.79E-05	1.07E-01
410	rs2517549	31,008,598	1.29	7.86E-10	2.90E-06	8.44E-01
411	rs2517546	31,009,055	1.72	1.37E-24	1.89E-13	6.37E-01
412	rs9262564	31,009,137	1.29	7.86E-10	2.90E-06	8.44E-01
413	rs2517544	31,009,508	1.34	3.46E-11	3.01E-07	6.42E-01
414	rs2508015	31,010,200	1.27	2.94E-09	3.64E-06	6.36E-01
415	rs10947129	31,011,662	0.73	1.11E-08	4.67E-05	4.38E-03
416	rs12528584	31,011,845	0.73	1.11E-08	4.67E-05	4.38E-03
417	rs10947130	31,013,746	0.70	6.44E-09	1.18E-06	1.82E-04
418	rs10947131	31,015,936	0.70	3.78E-09	8.37E-07	1.37E-04
419	rs9295947	31,019,460	0.70	4.08E-09	8.55E-07	1.37E-04
420	rs2394427	31,019,562	0.70	4.08E-09	8.55E-07	1.37E-04
421	rs4713429	31,021,017	0.72	3.42E-10	1.37E-06	4.33E-04
422	rs9262615	31,021,161	0.75	5.82E-09	1.68E-05	3.39E-03
423	rs9262628	31,023,148	0.77	3.42E-10	9.36E-07	6.58E-03
424	rs3131788	31,024,796	1.82	1.81E-27	8.03E-16	7.62E-01
425	rs9262636	31,025,848	0.73	5.29E-10	3.10E-06	8.57E-04
426	rs2517523	31,026,434	0.77	2.81E-10	7.90E-07	5.92E-03
427	rs3906263	31,031,904	0.72	3.32E-10	8.53E-07	2.52E-04
428	rs2394423	31,032,042	0.73	5.55E-10	3.19E-06	8.74E-04
429	rs2517500	31,033,509	0.77	2.67E-10	8.01E-07	5.85E-03
430	rs2517497	31,036,783	0.77	2.85E-10	8.04E-07	5.90E-03
431	rs2523888	31,040,720	0.77	3.42E-10	8.90E-07	6.17E-03
432	rs2523882	31,042,217	0.78	2.92E-08	1.84E-06	4.85E-03
433	rs2523881	31,042,608	0.77	2.80E-10	7.88E-07	5.84E-03
434	rs2249231	31,043,232	0.77	4.35E-10	1.24E-06	7.42E-03
435	rs2905759	31,044,468	0.77	2.73E-10	7.89E-07	5.64E-03
436	rs2517474	31,046,494	0.75	2.02E-13	2.46E-06	3.41E-02
437	rs2523843	31,046,528	0.77	3.09E-10	8.76E-07	6.16E-03
438	rs2106067	31,048,263	0.77	2.36E-10	6.99E-07	5.25E-03
439	rs6941772	31,048,916	0.77	2.52E-10	7.15E-07	5.23E-03
440	rs9263473	31,050,179	0.77	2.59E-10	7.31E-07	5.49E-03
441	rs9263474	31,050,244	0.77	2.59E-10	7.31E-07	5.49E-03

442	rs2517471	31,052,098	0.77	2.83E-10	8.22E-07	5.95E-03
443	rs2535311	31,052,684	0.77	2.01E-10	6.11E-07	5.15E-03
444	rs2535304	31,054,687	0.77	1.66E-10	4.94E-07	4.16E-03
445	rs3130544	31,058,340	1.83	8.29E-28	6.01E-16	7.47E-01
446	rs2535296	31,060,219	1.69	1.67E-25	2.86E-16	4.33E-02
447	rs2233976	31,079,994	0.59	2.76E-11	1.77E-08	1.52E-06
448	rs2233974	31,080,016	1.54	4.58E-19	2.62E-09	4.88E-01
449	rs2233956	31,081,205	1.51	2.98E-17	2.84E-11	8.59E-01
450	rs1265048	31,081,409	0.76	7.28E-11	2.33E-08	4.84E-04
451	rs3094222	31,081,434	1.82	1.05E-27	4.59E-16	8.95E-01
452	rs3095298	31,082,932	1.45	2.58E-15	1.73E-10	9.82E-01
453	rs3094220	31,082,987	1.44	4.97E-15	3.38E-10	9.99E-01
454	rs3094216	31,084,048	1.44	4.60E-15	3.10E-10	9.86E-01
455	rs3130985	31,085,356	1.83	5.46E-28	4.62E-16	7.22E-01
456	rs3132550	31,086,048	1.44	3.40E-15	2.77E-10	9.83E-01
457	rs3130989	31,086,377	1.25	2.55E-08	7.29E-05	9.18E-01
458	rs3095325	31,086,997	1.25	2.28E-08	6.83E-05	9.07E-01
459	rs3095317	31,088,671	1.25	2.45E-08	7.18E-05	9.15E-01
460	rs2239520	31,088,922	1.25	2.45E-08	7.18E-05	9.15E-01
461	rs3095314	31,089,631	1.25	2.72E-08	7.67E-05	9.33E-01
462	rs3130556	31,094,636	1.35	9.23E-13	1.33E-08	4.46E-01
463	rs3130557	31,094,703	1.83	1.15E-27	7.79E-16	5.78E-01
464	rs9263708	31,095,270	1.50	6.08E-18	4.92E-12	4.69E-01
465	rs3130564	31,101,674	1.47	8.96E-16	7.68E-10	4.13E-01
466	rs130072	31,112,484	0.57	3.52E-12	2.92E-09	1.99E-07
467	rs130079	31,112,737	1.39	1.21E-13	8.71E-13	8.24E-02
468	rs130066	31,122,315	1.26	7.73E-09	7.36E-10	1.50E-02
469	rs130076	31,122,482	1.42	1.57E-14	1.57E-12	1.70E-01
470	rs3130453	31,124,849	1.24	2.38E-08	2.87E-08	1.97E-02
471	rs72856718	31,125,257	0.56	2.78E-12	2.37E-09	1.61E-07
472	rs720466	31,125,705	1.39	7.55E-14	4.32E-13	5.25E-02
473	rs720465	31,125,777	1.31	6.98E-11	6.55E-10	1.15E-01
474	rs720467	31,125,799	0.57	4.51E-12	4.01E-09	2.82E-07
475	rs3130455	31,125,978	1.42	1.78E-14	1.75E-12	1.69E-01
476	rs3095239	31,126,790	0.81	3.40E-08	1.81E-08	1.08E-02
477	rs3094187	31,126,944	0.81	4.38E-08	2.75E-08	1.31E-02
478	rs1150765	31,127,562	1.39	6.50E-14	3.56E-13	5.38E-02
479	rs6905862	31,127,602	1.25	1.44E-08	1.31E-09	1.73E-02
480	rs2073724	31,129,707	0.57	3.06E-12	2.58E-09	1.79E-07
481	rs1419881	31,130,593	1.24	2.74E-08	1.31E-09	1.15E-02
482	rs13409	31,132,140	1.25	1.57E-08	1.47E-09	1.80E-02
483	rs885952	31,139,490	1.23	1.47E-07	2.80E-08	8.11E-02
484	rs1265159	31,140,047	1.38	9.16E-13	5.89E-12	1.88E-01
485	rs885950	31,140,152	1.22	3.52E-07	4.55E-08	9.36E-02
486	rs1265158	31,140,741	1.31	5.95E-11	1.69E-07	2.14E-01
487	rs887468	31,141,523	1.32	2.94E-11	2.70E-09	2.62E-01

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488	rs3130457	31,147,194	1.38	8.36E-13	5.57E-12	2.05E-01
489	rs1265181	31,155,785	1.40	3.75E-13	3.90E-11	6.15E-01
490	rs1265178	31,161,229	1.40	3.93E-13	4.06E-11	6.15E-01
491	rs4713447	31,162,963	0.78	1.42E-09	2.73E-07	7.54E-03
492	rs9501077	31,167,512	0.78	1.43E-09	2.74E-07	7.55E-03
493	rs9366768	31,168,494	0.78	1.42E-09	2.73E-07	7.54E-03
494	rs9263870	31,170,514	0.64	5.34E-10	8.10E-08	1.02E-05
495	rs9263871	31,170,528	0.79	1.53E-08	4.33E-06	1.26E-02
496	rs9263872	31,170,608	0.78	1.32E-09	2.80E-07	7.86E-03
497	rs9263873	31,170,713	0.78	1.44E-09	2.94E-07	8.16E-03
498	rs6921948	31,171,257	0.74	6.89E-14	7.96E-10	3.58E-04
499	rs3132510	31,172,151	1.87	3.17E-28	3.62E-16	8.84E-01
500	rs2894181	31,174,527	0.74	1.10E-13	1.11E-09	4.43E-04
501	rs3132506	31,176,226	1.35	9.73E-12	4.31E-11	2.22E-01
502	rs3869109	31,184,196	1.42	1.74E-18	1.04E-12	6.46E-05
503	rs9263964	31,186,039	1.42	1.80E-18	9.73E-13	5.78E-05
504	rs9263966	31,186,230	0.64	3.49E-10	5.23E-08	7.32E-06
505	rs9263967	31,186,245	1.42	1.37E-18	8.25E-13	5.38E-05
506	rs9263969	31,186,534	0.73	2.90E-10	1.89E-08	5.42E-05
507	rs3130467	31,187,075	1.35	3.93E-12	6.81E-12	4.84E-02
508	rs3130517	31,190,303	1.35	2.88E-12	6.04E-12	5.33E-02
509	rs12662501	31,190,850	0.70	1.10E-09	5.02E-08	2.25E-05
510	rs6928399	31,195,218	0.76	8.80E-11	1.66E-06	4.40E-03
511	rs3130473	31,199,208	1.33	4.85E-11	2.34E-10	2.46E-01
512	rs2394894	31,206,920	1.34	1.57E-11	8.08E-11	2.89E-01
513	rs2394895	31,206,979	1.35	1.00E-11	4.90E-11	2.44E-01
514	rs1793891	31,221,698	1.33	2.97E-11	1.26E-08	5.14E-01
515	rs2844627	31,229,462	1.33	1.84E-11	9.85E-09	5.18E-01
516	rs2245822	31,230,800	1.34	1.00E-11	6.62E-09	5.02E-01
517	rs2248880	31,233,510	1.34	8.33E-12	5.47E-09	4.90E-01
518	rs2524094	31,240,041	1.28	2.54E-10	7.67E-05	5.83E-01
519	rs2074489	31,240,128	0.76	2.62E-09	7.50E-06	3.07E-03
520	rs2395471	31,240,692	0.76	1.24E-11	8.90E-06	3.77E-02
521	rs2249742	31,240,721	0.73	6.11E-15	3.27E-08	2.24E-03
522	rs5010528	31,241,032	0.63	1.25E-10	2.94E-07	2.29E-05
523	rs2524084	31,241,639	1.31	3.38E-11	4.54E-08	1.94E-01
524	rs3134745	31,242,762	1.37	9.25E-13	1.11E-08	7.86E-01
525	rs2524074	31,244,021	1.57	1.23E-27	4.74E-14	2.02E-04
526	rs2524069	31,244,789	1.71	1.39E-25	5.50E-16	1.31E-01
527	rs2524067	31,245,821	1.71	6.15E-26	2.13E-16	6.37E-02
528	rs9348859	31,249,977	0.75	1.25E-12	7.59E-09	2.30E-04
529	rs3873375	31,251,360	0.77	1.68E-09	4.25E-05	1.78E-02
530	rs2394963	31,251,462	0.76	6.76E-10	2.47E-05	1.27E-02
531	rs2524054	31,252,396	1.60	8.20E-28	5.29E-13	4.44E-03
532	rs9461684	31,253,444	0.63	1.81E-10	4.03E-07	3.17E-05
533	rs2853935	31,253,878	1.40	2.76E-17	6.31E-10	2.36E-03

534	rs2853933	31,254,088	1.40	4.45E-17	8.79E-10	2.79E-03
535	rs9468920	31,254,936	0.76	6.76E-10	2.47E-05	1.27E-02
536	rs9468922	31,255,286	0.75	3.03E-12	1.61E-07	1.15E-03
537	rs2853928	31,257,511	1.59	9.93E-28	5.80E-13	4.59E-03
538	rs2524040	31,257,625	1.40	4.45E-17	8.79E-10	2.79E-03
539	rs9468925	31,258,837	0.75	2.11E-12	1.39E-07	1.67E-03
540	rs2524163	31,259,579	1.40	4.45E-17	8.79E-10	2.79E-03
541	rs9468926	31,260,218	0.75	3.80E-12	1.90E-07	1.26E-03
542	rs2524156	31,260,397	1.40	4.45E-17	8.79E-10	2.79E-03
543	rs2243868	31,261,276	1.40	4.45E-17	8.79E-10	2.79E-03
544	rs3873379	31,262,169	0.76	6.76E-10	2.47E-05	1.27E-02
545	rs3873380	31,262,438	0.76	6.07E-10	2.52E-05	1.30E-02
546	rs2246954	31,265,262	1.36	4.69E-15	6.66E-08	1.11E-02
547	rs2247056	31,265,490	1.60	5.21E-28	3.57E-13	3.71E-03
548	rs3905495	31,265,539	0.76	1.29E-10	2.00E-06	5.85E-03
549	rs2853922	31,266,190	1.40	2.85E-17	6.13E-10	2.37E-03
550	rs16899205	31,266,361	0.76	5.72E-10	2.13E-05	1.16E-02
551	rs16899207	31,266,387	0.76	6.17E-10	2.24E-05	1.21E-02
552	rs2524089	31,266,522	1.40	3.12E-17	6.55E-10	2.45E-03
553	rs4543367	31,266,767	0.77	1.53E-09	4.47E-05	2.05E-02
554	rs9380240	31,268,832	0.78	2.46E-09	5.99E-05	1.01E-01
555	rs9366778	31,269,173	0.78	2.27E-09	5.77E-05	9.93E-02
556	rs9468935	31,269,553	0.76	8.76E-10	3.68E-05	1.33E-02
557	rs1960278	31,269,874	1.40	1.89E-17	4.14E-10	1.64E-03
558	rs3873386	31,273,745	0.76	1.69E-11	8.31E-07	5.10E-03
559	rs28752872	31,302,750	0.74	4.36E-14	2.22E-06	3.90E-02
560	rs2507997	31,314,781	1.38	1.20E-12	1.23E-07	3.72E-01
561	rs4540292	31,317,182	0.73	5.42E-14	2.35E-09	1.32E-04
562	rs4394275	31,318,177	0.75	1.78E-09	6.07E-06	2.87E-03
563	rs2523589	31,327,334	0.73	2.52E-15	2.55E-07	1.41E-02
564	rs2523578	31,328,542	1.60	4.50E-28	5.89E-13	7.72E-03
565	rs2523554	31,331,829	1.45	5.50E-21	1.58E-10	2.57E-03
566	rs2523544	31,333,562	1.52	2.04E-20	2.92E-11	3.31E-01
567	rs2844571	31,335,647	1.33	7.74E-12	1.59E-05	5.57E-01
568	rs2523535	31,336,250	1.30	6.72E-11	8.15E-07	4.96E-01
569	rs9295986	31,338,528	0.74	1.55E-10	1.80E-05	8.22E-03
570	rs2844546	31,344,657	1.30	8.88E-11	8.64E-05	4.37E-01
571	rs2442744	31,345,376	1.30	9.08E-11	8.92E-05	4.29E-01
572	rs2507984	31,345,596	1.30	9.08E-11	8.92E-05	4.29E-01
573	rs2442736	31,346,621	1.43	2.76E-15	6.11E-10	7.85E-01
574	rs9266636	31,347,033	0.72	2.96E-13	7.07E-05	1.60E-02
575	rs9266638	31,347,057	0.72	2.18E-13	5.73E-05	1.38E-02
576	rs3094600	31,347,144	1.45	8.78E-18	1.04E-10	7.37E-02
577	rs2244020	31,347,451	0.75	1.06E-11	4.73E-04	1.42E-01
578	rs9266669	31,348,077	1.72	2.08E-25	2.52E-14	7.32E-01
579	rs4143332	31,348,365	1.90	1.12E-30	7.73E-18	NA

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580	rs2442749	31,352,040	1.46	3.42E-19	8.89E-12	1.65E-02
581	rs2853977	31,379,304	1.41	3.87E-18	8.18E-09	7.32E-03
582	rs2256175	31,380,449	0.79	3.37E-09	1.12E-04	2.53E-01
583	rs2596530	31,387,373	1.41	3.57E-18	7.78E-09	7.12E-03
584	rs2844513	31,388,214	0.80	1.42E-08	6.54E-04	4.30E-01
585	rs2516448	31,390,410	1.41	4.68E-18	9.68E-09	8.41E-03
586	rs3128982	31,417,191	1.30	6.45E-10	8.49E-06	3.46E-01
587	rs3131621	31,425,499	1.26	2.78E-08	1.55E-04	1.64E-01
588	rs3094228	31,429,927	1.54	8.97E-20	1.43E-10	9.22E-01
589	rs3094605	31,430,694	1.87	2.78E-29	1.36E-16	2.13E-01
590	rs3099840	31,430,721	1.54	8.59E-20	1.44E-10	9.19E-01
591	rs3128987	31,434,198	1.61	1.46E-22	4.85E-13	3.98E-01
592	rs3131619	31,434,331	1.87	1.95E-29	9.87E-17	2.90E-01
593	rs3094013	31,434,366	1.89	5.68E-30	2.78E-17	2.99E-01
594	rs3131618	31,434,621	1.88	1.19E-29	6.59E-17	6.84E-01
595	rs2844503	31,442,731	0.77	8.98E-11	1.18E-05	6.30E-02
596	rs2523656	31,444,048	0.78	1.14E-08	9.73E-04	1.28E-01
597	rs2248372	31,446,466	0.78	8.25E-09	1.01E-03	1.42E-01
598	rs3099844	31,448,976	1.83	1.80E-28	1.22E-15	7.56E-01
599	rs2516412	31,462,321	1.25	3.34E-08	3.63E-04	4.22E-01
600	rs2844499	31,475,913	1.26	1.35E-08	1.42E-04	5.79E-01
601	rs2516400	31,481,105	1.26	2.66E-08	2.23E-04	5.11E-01
602	rs9469021	31,490,970	0.50	2.32E-08	3.60E-05	1.43E-04
603	rs3093988	31,492,453	1.67	3.98E-25	8.23E-12	5.51E-01
604	rs11796	31,501,212	1.27	8.89E-09	1.76E-04	6.29E-01
605	rs1055384	31,501,558	1.67	3.98E-25	1.08E-11	6.61E-01
606	rs3093974	31,506,210	1.28	2.49E-09	8.65E-05	8.26E-01
607	rs3130059	31,509,284	1.26	2.87E-08	3.67E-04	4.89E-01
608	rs3130630	31,510,933	1.26	1.61E-08	2.56E-04	5.56E-01
609	rs2071594	31,512,720	1.26	2.11E-08	3.01E-04	5.17E-01
610	rs9267488	31,514,247	1.90	1.22E-30	7.30E-17	3.32E-01
611	rs2229094	31,540,556	0.73	2.63E-11	5.37E-05	8.46E-03
612	rs1800629	31,543,031	1.62	6.52E-23	1.01E-10	8.19E-01
613	rs2857595	31,568,469	1.50	3.52E-18	1.15E-08	9.66E-01
614	rs3132451	31,582,025	1.41	1.74E-13	7.59E-07	5.84E-01
615	rs2269475	31,583,931	0.69	4.29E-09	6.87E-03	3.09E-02
616	rs3763295	31,587,938	0.69	3.42E-09	6.07E-03	2.79E-02
617	rs3115665	31,589,264	1.42	8.43E-14	1.07E-06	4.67E-01
618	rs3130070	31,591,808	1.42	8.78E-14	1.09E-06	4.58E-01
619	rs3130622	31,592,524	1.41	2.53E-13	1.53E-06	3.85E-01
620	rs3132450	31,596,138	1.84	1.38E-26	4.67E-13	5.83E-01
621	rs3130623	31,597,700	1.41	1.19E-13	6.17E-07	6.32E-01
622	rs3130626	31,598,489	1.41	2.47E-13	1.69E-06	3.91E-01
623	rs2736157	31,600,820	1.42	1.26E-13	1.34E-06	4.35E-01
624	rs3130627	31,600,851	1.42	8.03E-14	1.01E-06	4.77E-01
625	rs2242657	31,602,489	0.69	5.55E-09	7.47E-03	3.29E-02

626	rs2261033	31,603,591	0.74	1.91E-13	2.43E-05	4.51E-02
627	rs9267522	31,603,770	1.42	1.26E-13	1.37E-06	4.24E-01
628	rs3130628	31,609,272	1.41	1.98E-13	1.82E-06	3.90E-01
629	rs2077102	31,611,840	0.70	8.39E-09	9.78E-03	4.11E-02
630	rs3117583	31,619,576	1.42	1.52E-13	1.56E-06	4.09E-01
631	rs3117582	31,620,520	1.84	1.68E-26	5.67E-13	5.51E-01
632	rs3132449	31,626,013	1.84	1.56E-26	5.16E-13	5.82E-01
633	rs2242655	31,627,449	0.70	1.05E-08	1.13E-02	4.37E-02
634	rs3130618	31,632,134	1.41	2.00E-13	1.89E-06	3.84E-01
635	rs2295665	31,632,686	0.70	1.09E-08	1.12E-02	4.50E-02
636	rs9267531	31,636,742	1.83	1.77E-26	5.62E-13	5.78E-01
637	rs2280800	31,646,398	0.70	1.11E-08	1.15E-02	4.59E-02
638	rs2242653	31,675,765	0.71	6.22E-09	4.83E-03	3.17E-02
639	rs3131383	31,704,294	1.84	1.56E-26	4.91E-13	7.13E-01
640	rs3101018	31,705,864	1.84	1.36E-26	4.40E-13	7.28E-01
641	rs3749953	31,713,124	0.70	1.69E-08	3.13E-03	1.96E-02
642	rs3130484	31,715,882	1.83	2.47E-26	6.62E-13	6.69E-01
643	rs3131379	31,721,033	1.83	2.47E-26	6.62E-13	6.69E-01
644	rs3117574	31,725,230	1.83	2.47E-26	6.62E-13	6.69E-01
645	rs3131378	31,725,285	1.83	2.47E-26	6.62E-13	6.69E-01
646	rs3117575	31,726,253	1.84	2.17E-26	6.17E-13	6.76E-01
647	rs3117577	31,727,474	1.84	2.17E-26	6.17E-13	6.66E-01
648	rs6905572	31,731,881	0.70	1.18E-08	2.19E-03	1.50E-02
649	rs3115671	31,734,345	1.83	2.57E-26	6.83E-13	6.79E-01
650	rs3130490	31,739,120	1.81	4.25E-25	3.48E-12	5.85E-01
651	rs915652	31,749,142	1.83	2.76E-26	1.10E-12	6.32E-01
652	rs4711279	31,802,465	0.71	4.12E-08	5.50E-03	2.83E-02
653	rs3130679	31,807,540	1.84	2.42E-26	9.82E-13	6.55E-01
654	rs574914	31,819,376	0.73	3.00E-08	7.44E-03	4.89E-02
655	rs693906	31,835,164	1.56	6.99E-18	1.76E-11	6.79E-01
656	rs521977	31,836,827	1.46	2.51E-19	1.25E-06	2.59E-01
657	rs589428	31,848,220	1.38	7.23E-15	2.59E-05	4.43E-01
658	rs652888	31,851,234	1.33	1.85E-09	9.02E-07	4.68E-01
659	rs535586	31,860,337	1.38	8.13E-15	2.83E-05	4.63E-01
660	rs558702	31,870,326	1.83	4.64E-26	1.23E-12	7.27E-01
661	rs519417	31,878,433	1.83	5.67E-26	1.73E-12	7.50E-01
662	rs644045	31,883,957	1.42	7.28E-18	2.91E-05	3.05E-01
663	rs497309	31,892,484	1.83	8.61E-26	2.17E-12	6.86E-01
664	rs537160	31,916,400	1.42	1.42E-17	3.08E-04	6.85E-01
665	rs1270942	31,918,860	1.83	1.30E-25	2.63E-12	6.86E-01
666	rs2072633	31,919,578	1.36	1.10E-14	1.07E-04	2.01E-01
667	rs630379	31,922,254	1.43	1.79E-17	1.38E-04	8.73E-01
668	rs440454	31,927,342	1.40	1.27E-15	6.20E-04	8.60E-01
669	rs419788	31,928,799	1.40	9.51E-16	5.63E-04	8.61E-01
670	rs592229	31,930,441	1.29	7.25E-11	3.38E-03	8.06E-01
671	rs389884	31,940,897	1.83	1.21E-25	2.52E-12	7.82E-01

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672	rs389883	31,947,460	1.42	6.47E-17	1.74E-04	8.09E-01
673	rs1150758	32,028,149	1.55	2.26E-17	9.66E-08	3.27E-01
674	rs1150755	32,038,550	1.55	1.75E-17	7.09E-08	3.53E-01
675	rs7774197	32,046,275	0.58	1.57E-08	3.59E-04	1.09E-03
676	rs1150754	32,050,758	1.55	1.36E-17	6.57E-08	3.59E-01
677	rs1150753	32,059,867	1.84	9.70E-26	2.15E-12	8.22E-01
678	rs3130288	32,096,001	1.84	4.73E-26	1.45E-12	9.57E-01
679	rs204999	32,109,979	1.26	2.18E-07	1.66E-09	1.49E-01
680	rs3134952	32,113,571	1.29	7.14E-08	1.63E-08	6.36E-01
681	rs9296009	32,114,515	0.73	7.44E-09	2.42E-02	5.89E-02
682	rs3134608	32,117,971	1.30	2.10E-08	4.38E-09	4.18E-01
683	rs2269425	32,123,639	0.65	1.94E-11	1.07E-03	3.04E-03
684	rs3096697	32,134,510	1.30	2.05E-08	3.72E-09	4.05E-01
685	rs3130347	32,134,656	1.30	2.12E-08	4.09E-09	4.13E-01
686	rs3130284	32,140,487	1.30	2.23E-08	4.14E-09	4.14E-01
687	rs3131297	32,141,005	1.30	2.23E-08	4.14E-09	4.14E-01
688	rs3134947	32,145,205	1.30	2.57E-08	4.71E-09	4.33E-01
689	rs3134946	32,145,993	1.30	2.28E-08	4.35E-09	4.24E-01
690	rs3096689	32,145,999	1.30	2.35E-08	4.48E-09	4.26E-01
691	rs3134945	32,146,492	1.30	2.20E-08	4.19E-09	4.19E-01
692	rs3134944	32,146,644	1.30	2.57E-08	4.71E-09	4.33E-01
693	rs9469089	32,146,657	0.65	6.96E-12	1.80E-04	9.73E-04
694	rs3130349	32,147,696	1.36	2.46E-10	3.45E-09	5.65E-01
695	rs3134940	32,149,816	1.36	3.13E-10	4.22E-09	5.92E-01
696	rs1800625	32,152,442	1.36	2.48E-10	3.05E-09	5.89E-01
697	rs204995	32,154,285	1.34	1.53E-10	1.34E-11	3.38E-02
698	rs204994	32,154,998	1.29	3.18E-08	1.36E-08	4.14E-01
699	rs204993	32,155,581	1.23	3.79E-06	2.41E-08	3.95E-01
700	rs204992	32,156,908	1.32	4.66E-09	2.47E-09	2.75E-01
701	rs176095	32,158,319	1.32	3.69E-09	1.96E-09	2.73E-01
702	rs3134605	32,159,956	1.32	9.82E-10	2.22E-08	3.70E-01
703	rs204991	32,161,366	1.39	6.87E-12	4.15E-07	9.68E-01
704	rs204990	32,161,430	1.40	6.36E-12	3.41E-07	9.82E-01
705	rs204989	32,161,852	1.39	6.94E-12	4.37E-07	9.58E-01
706	rs2071278	32,165,444	1.44	8.85E-13	2.34E-06	3.67E-01
707	rs3134942	32,168,771	1.51	1.04E-14	2.33E-08	5.15E-01
708	rs3132935	32,171,075	1.32	1.29E-09	2.83E-08	4.13E-01
709	rs3131296	32,172,993	1.51	8.72E-15	2.07E-08	5.36E-01
710	rs3132947	32,176,782	1.33	9.06E-10	1.99E-08	3.72E-01
711	rs3132956	32,179,438	1.50	2.12E-14	3.88E-08	4.41E-01
712	rs3134796	32,189,921	1.50	2.12E-14	4.16E-08	5.05E-01
713	rs3134931	32,190,620	0.78	2.51E-08	9.38E-04	5.10E-02
714	rs434841	32,191,041	1.23	9.93E-07	1.04E-08	1.89E-02
715	rs3134930	32,191,620	1.33	3.92E-11	3.31E-03	6.21E-01
716	rs3130303	32,205,867	1.44	2.22E-12	6.76E-08	7.44E-01
717	rs6901158	32,205,942	1.44	2.70E-12	7.84E-08	7.23E-01

718	rs3130304	32,207,181	1.32	3.00E-10	1.79E-02	1.46E-01
719	rs416352	32,207,393	1.26	5.17E-09	4.47E-01	8.67E-02
720	rs424232	32,208,324	1.31	5.87E-11	2.79E-03	9.33E-01
721	rs507778	32,209,861	1.27	1.35E-09	4.31E-01	1.43E-01
722	rs412657	32,211,085	1.25	7.81E-09	6.12E-02	8.67E-01
723	rs411326	32,211,317	0.75	1.68E-09	5.86E-01	9.54E-01
724	rs6936204	32,217,092	1.40	9.50E-17	1.30E-04	2.78E-01
725	rs10223710	32,218,681	0.73	2.47E-08	4.55E-02	1.49E-01
726	rs4959089	32,219,725	0.73	2.47E-08	4.55E-02	1.49E-01
727	rs3115572	32,220,484	1.43	3.61E-19	8.49E-08	4.63E-03
728	rs12525893	32,220,577	0.73	3.28E-08	4.16E-02	1.38E-01
729	rs3130316	32,221,228	1.43	5.36E-19	1.06E-07	5.24E-03
730	rs3130320	32,223,258	1.45	7.09E-20	2.40E-07	1.01E-02
731	rs3115569	32,224,139	1.39	7.14E-13	5.14E-10	5.84E-02
732	rs3132971	32,230,256	1.82	5.92E-25	2.92E-11	9.79E-01
733	rs9268055	32,230,608	1.39	7.14E-13	5.14E-10	5.84E-02
734	rs3115563	32,233,638	1.39	7.14E-13	5.14E-10	5.84E-02
735	rs3132928	32,234,015	1.39	7.14E-13	5.14E-10	5.84E-02
736	rs3096681	32,235,177	1.39	6.57E-13	4.80E-10	5.69E-02
737	rs3132931	32,235,895	1.40	1.64E-13	2.48E-10	4.93E-02
738	rs3115560	32,236,142	1.39	8.42E-13	6.07E-10	6.22E-02
739	rs3096673	32,238,013	1.39	6.29E-13	4.60E-10	5.35E-02
740	rs3096674	32,238,219	1.41	1.29E-13	2.06E-10	4.56E-02
741	rs3132945	32,238,680	1.39	4.36E-13	3.43E-10	4.77E-02
742	rs3115557	32,239,651	1.41	1.32E-13	2.07E-10	4.66E-02
743	rs1559874	32,243,155	1.40	2.24E-13	2.54E-10	4.81E-02
744	rs3130340	32,244,627	1.39	9.29E-13	6.55E-10	6.30E-02
745	rs3115553	32,245,827	1.39	7.14E-13	5.14E-10	5.84E-02
746	rs9268125	32,252,678	1.40	2.53E-13	3.41E-10	5.69E-02
747	rs9268127	32,253,559	1.52	2.30E-17	6.61E-09	4.30E-01
748	rs9268131	32,254,452	1.40	1.64E-13	2.48E-10	4.93E-02
749	rs9268137	32,255,269	1.41	6.11E-14	1.05E-10	3.92E-02
750	rs7751896	32,255,410	1.39	9.64E-13	6.69E-10	6.77E-02
751	rs9268145	32,257,284	0.72	4.47E-09	9.56E-01	9.90E-01
752	rs17422727	32,259,923	0.69	3.89E-09	3.04E-03	1.34E-02
753	rs6935269	32,260,350	1.39	7.50E-13	5.57E-10	5.69E-02
754	rs7775397	32,261,252	1.83	4.44E-25	2.43E-11	9.64E-01
755	rs3749966	32,261,507	1.39	5.92E-13	4.27E-10	5.32E-02
756	rs6910668	32,263,458	1.52	2.57E-17	6.70E-09	4.39E-01
757	rs17422797	32,265,528	0.53	3.91E-12	4.77E-06	6.22E-06
758	rs7745174	32,266,795	1.52	2.57E-17	6.70E-09	4.39E-01
759	rs7750783	32,268,080	1.40	1.78E-13	2.71E-10	4.91E-02
760	rs6909427	32,268,701	1.39	5.40E-13	3.91E-10	5.20E-02
761	rs7775332	32,270,363	1.39	4.92E-13	3.80E-10	4.89E-02
762	rs7742654	32,271,443	1.39	4.89E-13	3.17E-10	5.17E-02
763	rs3864299	32,271,674	1.39	6.50E-13	3.63E-10	4.83E-02

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764	rs3864300	32,271,807	1.39	4.79E-13	3.14E-10	5.18E-02
765	rs12660769	32,272,310	0.66	2.28E-08	7.14E-05	4.41E-04
766	rs9268165	32,272,327	1.39	5.01E-13	3.27E-10	5.18E-02
767	rs9268166	32,272,433	1.39	4.79E-13	3.11E-10	5.14E-02
768	rs9268167	32,272,437	1.39	5.92E-13	4.27E-10	5.32E-02
769	rs6457536	32,273,765	1.39	5.25E-13	3.37E-10	5.25E-02
770	rs9268176	32,274,079	1.40	1.70E-13	2.56E-10	4.74E-02
771	rs9268177	32,274,882	1.83	4.28E-25	2.38E-11	9.64E-01
772	rs9268192	32,277,211	1.40	4.26E-13	2.87E-10	5.00E-02
773	rs9268197	32,277,934	1.40	3.11E-13	4.31E-10	5.55E-02
774	rs9268198	32,278,187	1.39	5.25E-13	3.37E-10	5.25E-02
775	rs3864302	32,278,792	1.41	1.18E-13	1.02E-10	3.07E-02
776	rs9268202	32,279,340	1.41	8.64E-14	1.24E-10	3.68E-02
777	rs6934776	32,279,816	1.40	1.64E-13	2.40E-10	4.75E-02
778	rs6939410	32,280,182	1.41	6.27E-14	1.04E-10	3.42E-02
779	rs1018434	32,281,360	1.39	1.06E-12	5.36E-10	6.66E-02
780	rs1018433	32,281,510	1.39	6.26E-13	3.73E-10	5.53E-02
781	rs1018430	32,281,688	1.39	5.09E-13	3.77E-10	5.10E-02
782	rs9268212	32,281,889	1.41	1.35E-13	2.05E-10	4.48E-02
783	rs9268215	32,282,471	1.39	5.25E-13	3.37E-10	5.25E-02
784	rs6910071	32,282,854	0.72	4.15E-09	9.66E-01	9.99E-01
785	rs6909790	32,282,979	1.39	4.76E-13	3.26E-10	5.26E-02
786	rs6915455	32,283,494	1.39	5.45E-13	3.54E-10	5.30E-02
787	rs9268219	32,284,108	1.83	1.76E-24	4.26E-11	9.29E-01
788	rs9268235	32,290,208	1.82	5.50E-25	2.85E-11	9.96E-01
789	rs521828	32,291,643	1.35	2.16E-12	4.61E-08	9.00E-02
790	rs12524063	32,297,310	0.66	1.43E-08	3.40E-05	2.67E-04
791	rs3129949	32,298,814	1.42	8.82E-15	2.07E-06	6.29E-01
792	rs1003879	32,299,592	1.29	1.58E-10	1.20E-02	9.73E-01
793	rs1003878	32,299,822	1.42	8.82E-15	2.07E-06	6.29E-01
794	rs1265757	32,302,382	1.82	6.77E-25	3.38E-11	9.75E-01
795	rs28361060	32,303,848	0.72	4.81E-09	9.45E-01	9.78E-01
796	rs9368716	32,306,090	0.79	7.57E-09	6.28E-03	3.96E-01
797	rs1033499	32,307,532	1.52	3.55E-17	8.80E-09	4.74E-01
798	rs3117137	32,309,911	1.42	1.16E-14	2.43E-06	6.55E-01
799	rs2395149	32,325,562	1.83	5.71E-25	3.13E-11	9.91E-01
800	rs3129924	32,333,299	1.51	1.18E-16	9.42E-09	4.51E-01
801	rs9268362	32,333,341	0.72	2.53E-09	9.68E-01	9.23E-01
802	rs3129925	32,333,419	1.51	1.18E-16	9.67E-09	4.52E-01
803	rs3129926	32,333,480	1.51	1.14E-16	9.20E-09	4.50E-01
804	rs12529400	32,333,650	0.66	1.31E-08	3.22E-05	2.39E-04
805	rs3129927	32,333,827	1.83	5.04E-25	2.91E-11	9.93E-01
806	rs2143462	32,335,204	1.51	3.00E-17	1.61E-09	2.39E-01
807	rs2143461	32,335,347	1.51	1.06E-16	8.77E-09	4.49E-01
808	rs3129933	32,336,161	1.52	3.55E-17	8.80E-09	4.74E-01
809	rs3129939	32,336,766	1.50	1.38E-16	1.09E-08	4.70E-01

810	rs3129943	32,338,695	1.31	7.46E-10	3.60E-05	9.51E-01
811	rs2073044	32,338,986	0.73	3.19E-10	6.17E-01	4.90E-01
812	rs2050190	32,339,076	1.31	4.68E-11	7.93E-03	7.97E-01
813	rs2050189	32,339,647	1.32	5.55E-09	1.76E-03	5.15E-01
814	rs6913309	32,339,840	0.66	9.48E-17	2.69E-01	3.91E-01
815	rs9268401	32,341,318	0.71	3.07E-12	3.50E-01	3.84E-01
816	rs9391858	32,341,398	0.57	1.04E-17	1.11E-04	1.45E-04
817	rs9268403	32,341,473	0.71	2.89E-12	3.58E-01	3.91E-01
818	rs9268428	32,344,973	0.71	3.19E-12	3.47E-01	3.80E-01
819	rs2395153	32,345,595	0.61	4.24E-29	1.43E-02	1.78E-02
820	rs8180664	32,347,490	0.71	3.07E-12	3.50E-01	3.84E-01
821	rs9268456	32,349,946	0.71	3.08E-12	3.51E-01	3.82E-01
822	rs9268457	32,350,036	0.71	7.81E-12	3.00E-01	3.31E-01
823	rs9268459	32,350,776	0.71	2.66E-12	3.49E-01	3.82E-01
824	rs4373382	32,350,868	0.63	7.60E-27	1.26E-02	5.10E-02
825	rs6930777	32,351,566	0.57	2.27E-14	3.58E-04	6.20E-04
826	rs4424066	32,354,428	0.64	2.48E-26	1.45E-02	5.73E-02
827	rs1555115	32,354,520	0.68	7.98E-10	1.84E-03	1.11E-02
828	rs9268472	32,355,605	0.63	6.61E-27	1.21E-02	4.96E-02
829	rs17423649	32,357,133	0.68	7.12E-10	1.73E-03	1.06E-02
830	rs9268474	32,357,165	0.71	2.78E-12	3.58E-01	3.92E-01
831	rs12529049	32,357,715	0.68	5.73E-10	1.39E-03	8.83E-03
832	rs3129950	32,358,201	1.83	1.73E-25	1.44E-11	7.23E-01
833	rs3117099	32,358,270	1.41	3.87E-14	3.91E-07	3.31E-01
834	rs17495592	32,358,533	0.68	9.85E-11	8.03E-04	5.48E-03
835	rs3817976	32,361,003	0.68	7.21E-10	1.82E-03	1.12E-02
836	rs3817973	32,361,111	0.63	7.79E-27	1.31E-02	5.24E-02
837	rs3817969	32,361,388	0.68	1.22E-10	9.27E-04	6.24E-03
838	rs28362678	32,362,745	0.68	3.84E-10	1.22E-03	7.21E-03
839	rs2076530	32,363,816	0.65	9.64E-25	9.72E-02	2.62E-01
840	rs9268480	32,363,844	0.71	2.57E-12	3.63E-01	3.97E-01
841	rs2076529	32,363,955	0.63	6.45E-27	1.23E-02	4.98E-02
842	rs9268481	32,364,356	0.71	2.20E-12	3.84E-01	4.18E-01
843	rs4248166	32,366,421	0.71	6.22E-10	3.95E-02	1.23E-01
844	rs2294884	32,367,259	0.71	5.01E-10	3.90E-02	1.30E-01
845	rs2294883	32,367,451	0.70	5.48E-11	2.04E-02	7.63E-02
846	rs2294882	32,367,515	0.70	6.70E-11	2.22E-02	8.45E-02
847	rs2294881	32,367,604	0.70	6.08E-11	2.13E-02	7.95E-02
848	rs2294880	32,367,722	0.71	1.50E-12	4.23E-01	4.61E-01
849	rs9268482	32,367,777	0.71	2.89E-12	3.55E-01	3.89E-01
850	rs2294878	32,367,795	0.64	5.44E-27	1.30E-01	3.41E-01
851	rs3817966	32,367,847	0.70	3.55E-13	4.89E-01	5.23E-01
852	rs3817963	32,368,087	0.70	3.55E-13	4.89E-01	5.23E-01
853	rs3817962	32,368,314	0.71	2.89E-12	3.55E-01	3.89E-01
854	rs2076525	32,370,616	0.71	2.52E-12	3.68E-01	4.08E-01
855	rs2076523	32,370,835	0.77	6.34E-10	1.08E-02	3.11E-03

856	rs2076522	32,371,179	0.71	3.38E-12	3.48E-01	3.91E-01
857	rs3793127	32,371,915	0.71	1.65E-10	6.31E-01	7.30E-01
858	rs3806156	32,373,698	0.77	6.41E-10	1.06E-02	3.06E-03
859	rs3806157	32,373,801	0.78	4.17E-09	6.13E-03	1.71E-03
860	rs2395158	32,374,595	1.65	1.15E-23	2.06E-07	7.37E-01
861	rs3763307	32,374,622	0.71	2.34E-12	3.76E-01	4.19E-01
862	rs9268494	32,375,352	0.72	3.40E-12	9.20E-02	1.10E-01
863	rs9268497	32,375,424	0.72	3.00E-12	9.61E-02	1.15E-01
864	rs9268499	32,375,695	0.71	2.45E-12	1.81E-01	2.04E-01
865	rs6926737	32,375,745	0.60	1.83E-35	NA	NA
866	rs3763311	32,376,176	0.72	1.85E-11	1.17E-01	1.36E-01
867	rs3763312	32,376,348	0.73	2.93E-09	3.92E-01	4.73E-01
868	rs3763313	32,376,471	0.60	5.94E-19	1.16E-03	1.39E-03
869	rs9268507	32,377,539	0.60	2.00E-35	NA	NA
870	rs5007265	32,378,866	0.60	2.00E-35	NA	NA
871	rs5007263	32,378,982	0.60	2.23E-35	NA	NA
872	rs5007259	32,379,101	0.60	1.55E-35	NA	NA
873	rs9268516	32,379,489	0.71	3.81E-12	3.05E-01	3.38E-01
874	rs6932542	32,380,262	0.60	1.88E-35	NA	NA
875	rs4502931	32,380,782	0.60	1.60E-35	NA	NA
876	rs9268521	32,381,374	0.71	3.24E-11	7.72E-01	8.51E-01
877	rs9268530	32,383,223	1.59	7.47E-22	9.23E-06	9.35E-01
878	rs9268534	32,383,307	1.59	7.10E-22	9.10E-06	9.32E-01
879	rs6908065	32,383,341	1.58	3.01E-21	1.78E-05	9.80E-01
880	rs6930933	32,383,410	1.58	1.06E-21	1.04E-05	9.61E-01
881	rs3135382	32,383,441	1.58	1.09E-21	1.13E-05	9.64E-01
882	rs2001097	32,383,858	1.58	8.66E-22	9.95E-06	9.42E-01
883	rs3135380	32,384,677	1.59	3.30E-22	6.33E-06	8.84E-01
884	rs9268543	32,384,801	0.71	2.88E-08	9.07E-01	6.77E-01
885	rs3135378	32,385,099	1.58	9.32E-22	1.03E-05	9.50E-01
886	rs3135376	32,385,470	1.58	9.32E-22	1.03E-05	9.50E-01
887	rs3135374	32,385,605	1.58	2.45E-21	1.35E-05	9.14E-01
888	rs3135372	32,385,782	1.58	1.05E-21	1.09E-05	9.60E-01
889	rs2187820	32,385,873	1.58	9.32E-22	1.03E-05	9.50E-01
890	rs2395161	32,387,752	1.58	1.14E-21	1.11E-05	9.60E-01
891	rs2395162	32,387,780	1.58	8.05E-22	9.22E-06	9.47E-01
892	rs2395163	32,387,809	0.70	4.13E-11	9.36E-01	8.25E-01
893	rs2395164	32,387,860	1.58	9.32E-22	1.03E-05	9.50E-01
894	rs2213580	32,388,574	1.59	7.50E-22	1.02E-05	9.10E-01
895	rs9268557	32,389,305	0.73	1.12E-15	3.77E-05	1.02E-02
896	rs3135363	32,389,648	1.47	1.30E-20	5.72E-03	9.71E-01
897	rs3135356	32,391,516	1.58	1.11E-21	9.93E-06	9.56E-01
898	rs3135353	32,392,877	1.63	1.22E-21	1.42E-06	8.13E-01
899	rs3135351	32,392,945	1.59	1.00E-21	9.72E-06	9.46E-01
900	rs2395171	32,394,537	1.58	2.40E-21	1.04E-05	9.30E-01
901	rs3129843	32,395,726	1.81	8.73E-24	2.86E-10	8.39E-01

902	rs17496307	32,401,036	0.51	5.44E-18	5.29E-07	8.86E-07
903	rs9268614	32,402,778	0.70	1.39E-11	7.49E-01	6.53E-01
904	rs3135394	32,408,497	1.79	1.11E-23	2.30E-10	9.08E-01
905	rs3135393	32,408,842	1.59	1.07E-22	9.02E-07	4.63E-01
906	rs17496549	32,409,708	0.51	3.47E-18	2.17E-07	4.13E-07
907	rs3129887	32,410,691	1.61	1.68E-24	2.21E-08	1.13E-01
908	rs8084	32,411,035	1.49	1.28E-23	4.05E-07	7.55E-04
909	rs2239806	32,411,307	1.58	2.64E-22	9.98E-07	4.63E-01
910	rs2239805	32,411,376	1.59	1.11E-22	9.29E-07	4.54E-01
911	rs7192	32,411,646	1.53	2.06E-26	6.24E-07	1.14E-03
912	rs3177928	32,412,435	0.57	1.33E-17	4.47E-05	5.55E-05
913	rs7195	32,412,539	1.54	5.99E-27	3.62E-07	7.62E-04
914	rs1051336	32,412,592	1.58	2.84E-22	1.04E-06	4.65E-01
915	rs1041885	32,412,809	1.58	3.11E-22	1.06E-06	4.67E-01
916	rs2213586	32,413,094	1.53	1.27E-26	6.70E-07	1.20E-03
917	rs2213585	32,413,150	1.53	8.22E-27	6.31E-07	1.18E-03
918	rs2227139	32,413,459	1.53	1.04E-26	5.83E-07	1.10E-03
919	rs3129890	32,414,273	1.42	1.79E-16	1.41E-06	7.57E-02
920	rs3129891	32,415,080	1.49	1.07E-18	2.60E-04	9.71E-01
921	rs7754768	32,420,179	1.52	1.74E-25	2.17E-05	5.74E-03
922	rs9268832	32,427,789	1.49	3.26E-23	3.37E-04	3.72E-02
923	rs9268835	32,428,115	0.70	1.20E-12	5.44E-01	5.51E-01
924	rs9268838	32,428,715	0.70	1.93E-12	5.90E-01	5.99E-01
925	rs9268853	32,429,643	0.70	8.86E-14	8.12E-01	7.79E-01
926	rs9268862	32,430,167	1.46	1.03E-18	1.31E-08	1.03E-02
927	rs4428528	32,430,362	1.46	1.61E-18	1.56E-08	1.09E-02
928	rs7766843	32,430,729	1.46	2.26E-18	1.91E-08	1.19E-02
929	rs7747521	32,431,105	1.46	1.58E-18	1.69E-08	1.12E-02
930	rs9268885	32,431,705	1.46	1.58E-18	1.69E-08	1.12E-02
931	rs9268923	32,432,835	0.70	9.21E-14	8.11E-01	7.74E-01
932	rs2395185	32,433,167	0.70	9.98E-14	8.26E-01	7.92E-01
933	rs9268969	32,434,349	0.70	8.97E-14	8.04E-01	7.72E-01
934	rs9268976	32,434,874	1.46	1.46E-18	1.61E-08	1.09E-02
935	rs9268977	32,434,939	1.46	1.58E-18	1.69E-08	1.12E-02
936	rs9268980	32,435,123	1.46	1.58E-18	1.69E-08	1.12E-02
937	rs9368726	32,438,542	0.71	2.51E-13	8.52E-01	8.20E-01
938	rs9269043	32,438,598	1.46	1.58E-18	1.69E-08	1.12E-02
939	rs9405108	32,438,648	0.70	9.98E-14	8.26E-01	7.92E-01
940	rs2157338	32,439,323	1.46	1.58E-18	1.69E-08	1.12E-02
941	rs2187823	32,439,508	1.46	1.46E-18	1.60E-08	1.12E-02
942	rs1964995	32,449,411	0.59	2.13E-34	1.79E-06	2.48E-06
943	rs3830135	32,548,464	0.51	1.91E-18	1.49E-07	3.00E-07
944	rs477515	32,569,691	0.72	7.72E-12	3.82E-01	3.90E-01
945	rs2858867	32,575,325	1.49	4.97E-23	9.81E-08	2.28E-03
946	rs532098	32,578,052	0.78	5.95E-10	9.80E-01	2.60E-01
947	rs5021728	32,578,653	1.52	1.31E-23	7.60E-07	3.84E-02

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948	rs502771	32,578,970	1.52	1.00E-23	8.51E-07	4.01E-02
949	rs13207945	32,579,708	0.78	6.03E-10	9.78E-01	2.59E-01
950	rs4530903	32,581,889	0.50	8.17E-19	7.80E-08	1.52E-07
951	rs642093	32,582,075	1.45	5.08E-18	7.88E-04	9.63E-01
952	rs17533167	32,590,844	0.50	1.60E-18	1.02E-07	1.96E-07
953	rs3129763	32,590,925	1.47	6.01E-19	2.67E-04	7.22E-01
954	rs9271588	32,590,953	0.66	3.76E-24	1.42E-01	2.46E-01
955	rs3104389	32,595,097	0.70	1.27E-13	6.82E-01	6.45E-01
956	rs9272219	32,602,269	1.39	1.79E-15	1.89E-05	1.75E-01
957	rs2187668	32,605,884	1.65	3.60E-19	3.80E-07	2.95E-01
958	rs9273012	32,611,641	1.39	1.79E-15	1.89E-05	1.75E-01
959	rs2854275	32,628,428	1.65	3.15E-19	3.35E-07	2.79E-01
960	rs9275141	32,651,117	0.80	3.25E-08	4.18E-01	4.50E-01
961	rs4947342	32,653,070	0.72	6.67E-11	9.21E-01	9.66E-01
962	rs3129716	32,657,436	1.65	2.96E-19	2.77E-07	3.07E-01
963	rs4642516	32,657,543	0.80	2.50E-08	3.77E-01	4.96E-01
964	rs9469220	32,658,310	0.70	8.43E-19	6.32E-05	1.52E-02
965	rs2856674	32,659,645	1.67	8.22E-20	1.39E-07	3.45E-01
966	rs9275224	32,659,878	0.73	8.82E-16	2.45E-03	1.37E-01
967	rs2858324	32,660,375	1.54	4.66E-27	4.22E-05	1.96E-02
968	rs6457617	32,663,851	0.73	2.31E-15	3.01E-03	1.51E-01
969	rs6457620	32,663,999	0.73	2.34E-15	3.01E-03	1.50E-01
970	rs2647012	32,664,458	1.55	7.59E-28	2.45E-05	1.45E-02
971	rs1794282	32,666,526	1.81	8.53E-24	1.85E-10	9.85E-01
972	rs9275332	32,666,943	0.63	4.61E-20	2.22E-03	3.46E-03
973	rs17427599	32,667,364	0.64	7.87E-17	1.79E-04	7.87E-04
974	rs9275371	32,668,296	0.63	3.15E-20	1.92E-03	3.05E-03
975	rs1612904	32,669,018	1.48	1.13E-22	5.19E-03	4.32E-01
976	rs9275390	32,669,156	0.63	4.49E-20	2.02E-03	3.19E-03
977	rs9275393	32,669,439	0.63	3.53E-20	2.00E-03	3.16E-03
978	rs9275407	32,670,037	0.63	3.72E-20	2.05E-03	3.22E-03
979	rs2856717	32,670,308	1.54	1.05E-27	3.52E-05	1.91E-02
980	rs9275425	32,670,874	0.63	1.83E-20	1.41E-03	2.28E-03
981	rs9275428	32,670,978	0.63	3.53E-20	2.00E-03	3.16E-03
982	rs13192471	32,671,103	0.58	2.21E-17	7.76E-05	1.39E-04
983	rs1794275	32,671,248	0.73	1.34E-08	1.36E-01	2.54E-01
984	rs9275439	32,671,521	0.63	3.53E-20	2.00E-03	3.16E-03
985	rs17499655	32,672,135	0.58	5.75E-17	1.03E-04	1.86E-04
986	rs9275555	32,677,088	0.62	7.76E-19	3.74E-04	5.66E-04
987	rs6932517	32,678,182	1.50	1.61E-24	2.08E-05	9.30E-03
988	rs9275578	32,679,384	0.66	1.64E-14	1.14E-02	1.45E-02
989	rs9275580	32,679,462	0.62	1.87E-19	2.83E-04	4.39E-04
990	rs9275582	32,680,070	0.62	4.92E-19	3.83E-04	5.56E-04
991	rs2858332	32,681,161	0.69	3.82E-21	1.21E-04	1.66E-02
992	rs2858331	32,681,277	0.73	5.05E-14	1.73E-04	1.70E-02
993	rs9275596	32,681,631	1.47	6.12E-22	7.25E-03	5.13E-01

994	rs3998158	32,681,992	0.62	1.86E-18	2.70E-04	4.32E-04
995	rs9275602	32,682,812	1.51	4.62E-15	2.41E-08	5.33E-01
996	rs9275652	32,685,822	1.33	1.80E-09	3.68E-04	7.00E-01
997	rs9275659	32,686,103	1.33	1.99E-09	3.84E-04	6.76E-01
998	rs9275660	32,686,196	1.33	1.76E-09	3.64E-04	6.79E-01
999	rs9275686	32,687,570	1.33	1.76E-09	3.64E-04	6.79E-01
1000	rs9461799	32,689,529	0.78	8.27E-10	3.39E-04	3.64E-02
1001	rs763026	32,691,745	1.33	1.76E-09	3.64E-04	6.79E-01
1002	rs9469246	32,692,227	0.77	2.43E-10	2.35E-04	2.90E-02
1003	rs9275936	32,692,933	1.33	2.29E-09	4.23E-04	6.50E-01
1004	rs12528892	32,693,506	0.54	9.24E-10	9.43E-05	1.28E-04
1005	rs2859113	32,697,785	1.28	3.43E-10	2.84E-03	2.74E-01
1006	rs2859112	32,698,013	0.78	1.10E-09	4.13E-04	4.15E-02
1007	rs9276171	32,698,918	1.34	3.64E-10	1.00E-04	9.62E-01
1008	rs2859100	32,699,479	0.78	1.60E-09	6.95E-04	6.01E-02
1009	rs2859078	32,702,449	1.31	7.84E-09	5.00E-04	6.40E-01
1010	rs7773149	32,706,042	1.29	1.20E-10	2.09E-03	2.40E-01
1011	rs6457644	32,706,128	0.78	5.13E-10	2.90E-04	3.99E-02
1012	rs7773955	32,706,719	0.79	1.07E-08	1.88E-03	1.11E-01
1013	rs9276370	32,707,295	1.29	1.48E-10	2.04E-03	2.30E-01
1014	rs5021448	32,707,706	1.33	8.89E-10	1.82E-04	8.53E-01
1015	rs2213567	32,711,655	1.29	1.91E-10	4.44E-03	3.72E-01
1016	rs2227127	32,711,782	0.78	5.14E-10	2.82E-04	3.32E-02
1017	rs9276430	32,712,182	1.29	1.30E-10	3.40E-03	3.23E-01
1018	rs9276431	32,712,247	1.29	2.01E-10	7.34E-03	4.67E-01
1019	rs11758312	32,716,372	1.24	4.13E-08	4.89E-03	3.49E-01
1020	rs9276490	32,718,681	1.28	5.02E-10	7.99E-03	4.80E-01
1021	rs5016066	32,718,818	1.24	3.33E-08	4.03E-03	3.15E-01
1022	rs2157327	32,719,491	1.29	1.36E-10	4.39E-03	3.73E-01
1023	rs2213572	32,719,804	1.28	3.30E-10	6.69E-03	4.60E-01
1024	rs2213571	32,719,937	1.29	1.79E-10	4.69E-03	3.88E-01
1025	rs10807113	32,722,186	1.25	2.46E-08	3.59E-03	2.99E-01
1026	rs6918223	32,722,532	1.25	2.46E-08	3.60E-03	2.99E-01
1027	rs9276555	32,722,754	1.36	1.01E-10	2.18E-04	8.04E-01
1028	rs7770024	32,723,341	1.25	2.34E-08	3.50E-03	2.96E-01
1029	rs7769979	32,723,572	1.25	2.46E-08	3.60E-03	2.99E-01
1030	rs7774452	32,723,869	1.25	2.21E-08	3.43E-03	2.92E-01
1031	rs7756516	32,723,917	1.25	2.06E-08	3.25E-03	2.86E-01
1032	rs3213489	32,724,305	1.29	2.09E-10	5.19E-03	4.06E-01
1033	rs2301271	32,725,193	1.30	5.58E-11	3.75E-03	3.54E-01
1034	rs1023449	32,727,905	1.28	2.42E-10	5.67E-03	4.24E-01
1035	rs1023448	32,728,191	1.28	2.42E-10	5.67E-03	4.24E-01
1036	rs4248169	32,728,554	1.28	2.70E-10	5.96E-03	4.33E-01
1037	rs2395256	32,728,588	1.28	3.09E-10	6.31E-03	4.41E-01
1038	rs2395258	32,728,642	1.28	2.69E-10	6.00E-03	4.33E-01
1039	rs2006165	32,728,787	1.28	2.78E-10	5.15E-03	3.96E-01

1040	rs2071551	32,729,459	1.29	1.22E-10	5.29E-03	4.21E-01
1041	rs9276584	32,730,835	1.36	1.27E-10	2.48E-04	7.75E-01
1042	rs1573649	32,731,258	0.77	2.12E-11	1.18E-03	1.16E-01
1043	rs1573646	32,731,624	0.77	1.67E-11	1.15E-03	1.15E-01
1044	rs1978029	32,731,710	0.76	7.38E-12	9.57E-04	1.05E-01
1045	rs6902723	32,731,960	0.77	6.07E-11	1.86E-03	1.50E-01
1046	rs6903130	32,732,210	0.77	2.80E-11	1.38E-03	1.27E-01
1047	rs9276586	32,732,937	0.76	9.98E-12	1.06E-03	1.08E-01
1048	rs9276598	32,733,987	0.77	4.47E-11	1.74E-03	1.38E-01
1049	rs7382794	32,734,030	0.77	3.33E-11	1.44E-03	1.22E-01
1050	rs1894412	32,734,829	0.77	3.12E-11	1.39E-03	1.28E-01
1051	rs9296043	32,736,103	0.79	1.85E-09	1.09E-03	1.02E-01
1052	rs1585891	32,736,722	0.79	1.85E-09	1.09E-03	1.02E-01
1053	rs6457658	32,737,149	0.79	1.85E-09	1.09E-03	1.02E-01
1054	rs9276607	32,737,257	1.37	4.32E-11	1.24E-04	8.92E-01
1055	rs6457661	32,737,494	0.79	1.84E-09	1.09E-03	1.02E-01
1056	rs6936428	32,739,174	0.79	9.10E-09	1.93E-03	1.40E-01
1057	rs1383264	32,739,967	1.29	1.22E-10	5.73E-04	2.22E-01
1058	rs1480383	32,740,856	1.38	2.76E-15	1.45E-05	4.32E-02
1059	rs2857209	32,741,918	0.72	1.40E-14	1.72E-03	3.19E-02
1060	rs9276612	32,742,712	1.34	2.19E-13	2.04E-05	4.17E-02
1061	rs2621412	32,743,000	0.73	3.32E-14	2.15E-03	3.82E-02
1062	rs13195441	32,743,298	0.73	7.90E-12	5.62E-02	2.06E-01
1063	rs13203429	32,744,852	0.72	5.60E-15	1.27E-03	2.50E-02
1064	rs9276644	32,745,043	1.34	2.25E-13	2.01E-05	4.35E-02
1065	rs719654	32,752,139	0.71	2.59E-12	2.71E-03	1.73E-02
1066	rs7762279	32,755,290	1.77	3.26E-21	7.87E-10	4.24E-01
1067	rs7758736	32,758,394	1.33	4.74E-09	1.21E-03	4.72E-01
1068	rs1158784	32,758,761	0.74	1.38E-10	2.72E-02	1.28E-01
1069	rs3948793	32,759,448	1.33	9.03E-13	3.26E-05	5.62E-02
1070	rs1383261	32,765,451	1.33	4.76E-13	3.98E-06	1.40E-02
1071	rs7383606	32,766,593	1.33	5.66E-13	4.07E-06	1.56E-02
1072	rs4947350	32,767,620	1.40	2.91E-13	1.48E-07	6.00E-02
1073	rs7381376	32,767,673	1.33	1.36E-12	8.77E-06	2.06E-02
1074	rs2621367	32,768,721	0.72	4.63E-14	2.28E-04	6.36E-03
1075	rs2199874	32,769,926	0.73	5.96E-13	6.23E-04	1.55E-02
1076	rs2621358	32,770,808	0.71	1.97E-14	1.58E-04	4.56E-03
1077	rs2621338	32,776,583	0.71	1.78E-14	1.44E-04	4.07E-03
1078	rs2857118	32,777,900	0.72	3.00E-14	1.59E-04	4.29E-03
1079	rs11244	32,780,723	1.30	3.86E-10	3.01E-05	1.65E-01
1080	rs2856997	32,781,776	0.76	2.41E-11	1.04E-02	2.66E-01
1081	rs2071475	32,782,387	0.70	1.39E-12	2.23E-03	1.45E-02
1082	rs2071474	32,782,582	0.71	1.50E-14	4.41E-05	1.63E-03
1083	rs2071473	32,782,605	0.71	8.54E-16	8.58E-04	1.74E-02
1084	rs2621326	32,783,896	0.75	1.66E-12	2.85E-03	1.03E-01
1085	rs2859579	32,784,073	0.71	1.54E-14	4.35E-05	1.65E-03

1086	rs2071472	32,784,620	0.71	1.72E-14	4.60E-05	1.71E-03
1087	rs2071470	32,784,753	0.71	1.30E-14	4.15E-05	1.53E-03
1088	rs1894408	32,786,833	0.80	2.01E-08	5.40E-02	4.93E-01
1089	rs1894407	32,787,036	0.79	1.74E-08	4.96E-02	4.69E-01
1090	rs2857106	32,787,570	0.73	3.07E-09	4.16E-02	1.23E-01
1091	rs2621323	32,788,707	0.74	4.68E-12	1.46E-02	1.11E-01
1092	rs2621322	32,788,712	0.74	5.92E-09	5.07E-02	1.45E-01
1093	rs2621321	32,789,480	0.74	8.79E-11	1.62E-03	2.06E-02
1094	rs2857103	32,791,299	0.75	5.81E-11	2.83E-02	1.76E-01
1095	rs2856993	32,791,403	0.74	9.83E-09	6.14E-02	1.69E-01
1096	rs2857101	32,794,676	0.74	1.57E-10	2.33E-03	2.76E-02
1097	rs241456	32,795,965	0.75	2.11E-10	3.30E-03	3.45E-02
1098	rs241455	32,796,019	0.77	1.51E-08	2.80E-02	1.63E-01
1099	rs241453	32,796,226	0.74	1.33E-10	2.43E-03	2.78E-02
1100	rs241452	32,796,346	0.75	3.69E-10	4.17E-03	4.06E-02
1101	rs241451	32,796,480	0.75	3.09E-11	2.58E-02	1.56E-01
1102	rs17034	32,796,521	0.75	2.67E-10	3.21E-03	3.42E-02
1103	rs241448	32,796,684	0.75	2.77E-10	4.10E-03	4.08E-02
1104	rs241447	32,796,750	0.75	6.47E-10	5.57E-03	5.05E-02
1105	rs241446	32,796,967	0.75	2.79E-10	3.66E-03	3.76E-02
1106	rs241445	32,797,072	0.75	2.09E-10	3.24E-03	3.42E-02
1107	rs241440	32,797,361	0.75	2.64E-10	3.24E-03	3.42E-02
1108	rs154977	32,900,018	1.34	4.05E-12	2.01E-05	5.25E-02
1109	rs1480380	32,913,246	1.70	8.23E-17	1.11E-08	5.66E-02
1110	rs9276931	32,928,984	1.67	3.07E-16	8.08E-09	3.52E-02
1111	rs9500927	32,961,361	1.48	8.51E-13	7.99E-09	8.78E-03
1112	rs429916	32,978,587	1.51	1.04E-09	4.34E-07	2.31E-02
1113	rs1431403	33,047,031	1.32	9.70E-11	1.19E-10	1.03E-07
1114	rs9277357	33,049,979	1.38	4.46E-14	7.11E-14	1.77E-10
1115	rs9277358	33,049,983	1.36	5.08E-13	7.11E-13	1.27E-09
1116	rs9277361	33,050,045	1.35	8.61E-13	1.38E-12	2.22E-09
1117	rs9277366	33,050,107	1.36	1.35E-12	1.47E-12	2.12E-09
1118	rs6899657	33,050,223	1.41	3.37E-15	2.16E-13	8.86E-10
1119	rs9277378	33,050,279	1.36	4.89E-13	8.46E-13	1.52E-09
1120	rs9277385	33,050,473	1.37	2.05E-13	3.60E-13	7.43E-10
1121	rs9277386	33,050,499	1.36	4.60E-13	7.25E-13	1.31E-09
1122	rs9277389	33,050,526	1.36	4.14E-13	6.05E-13	1.08E-09
1123	rs3097674	33,050,683	1.36	6.02E-13	1.10E-12	1.74E-09
1124	rs9277393	33,050,877	1.37	6.62E-14	4.64E-14	1.38E-10
1125	rs9277394	33,050,970	1.37	6.14E-14	4.43E-14	1.33E-10
1126	rs9277437	33,052,250	1.37	7.49E-14	5.26E-14	1.56E-10
1127	rs9277462	33,053,271	1.37	6.82E-14	4.80E-14	1.43E-10
1128	rs9277471	33,053,682	1.37	8.07E-14	5.65E-14	1.65E-10
1129	rs9277472	33,053,723	1.37	7.06E-14	4.97E-14	1.49E-10
1130	rs1042544	33,054,457	1.37	9.34E-14	6.33E-14	1.73E-10
1131	rs931	33,054,550	1.37	7.71E-14	5.40E-14	1.60E-10

1132	rs9277538	33,055,047	1.37	5.69E-14	3.96E-14	1.27E-10
1133	rs9277542	33,055,247	1.37	5.11E-14	3.53E-14	1.13E-10
1134	rs9277545	33,055,323	1.41	1.50E-15	7.38E-14	4.41E-10
1135	rs9277546	33,055,346	1.37	7.13E-14	4.66E-14	1.36E-10
1136	rs9277554	33,055,538	1.37	7.71E-14	5.40E-14	1.60E-10
1137	rs9501259	33,055,551	1.47	1.68E-09	2.01E-08	9.58E-04
1138	rs9277555	33,055,605	1.41	1.26E-15	6.01E-14	3.73E-10
1139	rs9461832	33,056,384	1.79	1.33E-14	8.02E-10	1.06E-03
1140	rs3117228	33,056,435	1.37	6.57E-14	4.58E-14	1.36E-10
1141	rs9296075	33,056,788	1.78	1.60E-14	8.97E-10	1.05E-03
1142	rs3130188	33,057,176	1.37	9.34E-14	6.33E-14	1.73E-10
1143	rs3117226	33,057,659	1.40	1.89E-14	2.15E-12	6.74E-09
1144	rs3117225	33,057,711	1.37	7.69E-14	5.18E-14	1.51E-10
1145	rs3097652	33,057,835	1.37	7.69E-14	5.18E-14	1.51E-10
1146	rs1367730	33,058,114	1.42	5.43E-16	2.69E-14	1.94E-10
1147	rs3128972	33,058,774	1.41	1.50E-15	7.09E-14	4.17E-10
1148	rs2179920	33,058,874	1.43	2.29E-15	2.47E-13	3.47E-09
1149	rs2179919	33,059,262	1.41	1.06E-15	5.07E-14	3.13E-10
1150	rs3128917	33,059,996	1.42	8.24E-16	3.99E-14	2.41E-10
1151	rs3117222	33,060,949	1.41	9.17E-16	4.55E-14	2.66E-10
1152	rs3130190	33,061,690	1.42	5.12E-16	2.68E-14	1.71E-10
1153	rs3130191	33,061,871	1.41	9.17E-16	4.55E-14	2.66E-10
1154	rs2395314	33,062,673	1.41	9.17E-16	4.55E-14	2.66E-10
1155	rs3117213	33,064,605	1.41	1.18E-15	4.36E-14	2.44E-10
1156	rs2064478	33,072,266	1.42	4.72E-15	3.35E-13	4.10E-09
1157	rs3130210	33,072,729	1.43	1.19E-15	9.42E-14	1.48E-09
1158	rs2064476	33,073,322	1.37	8.59E-14	5.49E-14	1.46E-10
1159	rs2064474	33,073,463	1.41	1.99E-14	5.27E-13	5.82E-09
1160	rs3117234	33,073,984	1.41	2.11E-14	5.70E-13	5.65E-09
1161	rs3128927	33,074,288	1.35	2.17E-12	1.26E-12	4.99E-09
1162	rs3130212	33,074,389	1.41	2.03E-14	5.39E-13	5.46E-09
1163	rs3117231	33,074,908	1.39	2.21E-14	1.67E-12	4.89E-09
1164	rs6911848	33,075,259	1.77	2.38E-14	7.50E-10	9.01E-04
1165	rs3117230	33,075,635	1.42	2.54E-15	1.67E-13	2.31E-09
1166	rs3128930	33,075,666	1.33	5.07E-11	6.57E-11	1.94E-07
1167	rs11965763	33,076,682	1.77	2.54E-14	8.00E-10	9.16E-04
1168	rs7744381	33,081,798	1.65	2.26E-13	6.95E-10	3.18E-04
1169	rs6928350	33,083,197	1.72	2.78E-13	2.89E-08	5.38E-03
1170	rs525623	33,672,603	1.48	1.83E-11	7.32E-09	1.98E-05
1171	rs16869648	33,847,345	1.69	3.97E-09	2.80E-06	4.90E-03
1172	rs6457746	33,848,232	1.66	8.43E-09	3.79E-06	5.68E-03