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EXTENDED REPORT

Genetic variants in ANCA-associated vasculitis: a meta-analysis

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ABSTRACT

Background Genetic factors may influence the pathogenic pathways leading to antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis (AAV). We performed a meta-analysis to determine the genetic variants most likely associated with AAV and investigated whether diagnostic and serological subtypes within AAV have distinct genetic backgrounds.

Methods Studies investigating the association between genetic variants and AAV in humans were searched in PubMed, EMBASE and Web of Science. All variants investigated in at least two studies were selected. Subsequently, all studies assessing these variants were included in this meta-analysis. Additionally, data on these variants from the largest genome-wide association studies in AAV were included to increase the validity of this meta-analysis.

Results The literature search yielded 5180 articles. 62 articles investigating 140 genetic variants were included, 33 of which were associated with AAV in a meta-analysis. These genetic variants were in or near the following genes: *CD226*, *CTLA-4*, *FCGR2A*, *HLA-B*, *HLA-DP*, *HLA-DQ*, *HLA-DR*, *HSD17B8*, *IRF5*, *PTPN22*, *RING1/RXR*, *RXR*, *STAT4*, *SERPINA1* and *TLR9*. Moreover, we identified genetic distinctions between granulomatosis with polyangiitis and microscopic polyangiitis and between proteinase 3 ANCA vasculitis and myeloperoxidase ANCA vasculitis. In 76% of the genetic variants, subdivision based on ANCA serotype resulted in higher ORs than subdivision based on clinical diagnosis.

Conclusions This meta-analysis identified 33 genetic variants associated with AAV, supporting a role for alpha-1-antitrypsin, the major histocompatibility complex system, and several distinct inflammatory processes in AAV pathogenesis. Our results indicate that subdivision of AAV based on ANCA serotype has a stronger genetic basis than subdivision based on clinical diagnosis.

characteristics,^{3,4} leading to debate regarding whether these subtypes are part of a single disease spectrum or represent distinct diseases.^{5–7} To date, the prevailing concept of a single disease spectrum has resulted in similar treatment strategies in clinical trials^{8–10} and to suggestions that genetic studies should consider the subtypes together.¹¹ Evidence that these subtypes are pathogenically distinct may lead to the development of syndrome-specific therapeutic strategies.

Both environmental and genetic factors are thought to be involved in the pathogenesis of AAV.¹² Evidence for the role of genetic factors comes from differences in the prevalence of AAV between ethnic groups,¹³ familial association studies¹⁴ and genetic associations studies including the two genome-wide association studies (GWAS) performed in AAV.^{15,16}

Attempts to replicate findings of genetic association studies performed in AAV have yielded inconsistent outcomes. Small sample sizes and false-positive results arising from the low prior probabilities of genetic associations may be responsible for these inconsistencies.¹⁷ These factors are especially relevant in complex diseases such as AAV.¹⁸

The aim of this study was to determine the genetic variants associated with AAV. Therefore, we performed a meta-analysis to assess the pooled effect of all genetic variants that have been investigated in AAV in at least two studies. To increase the validity of this meta-analysis, we also included previously unpublished data from the largest GWAS performed in AAV.¹⁵ Moreover, we conducted stratified analyses based on clinical diagnosis and ANCA serotype to investigate whether these different AAV subtypes have distinct genetic backgrounds.

INTRODUCTION

Antineutrophil cytoplasmic antibody (ANCA)-associated vasculitis (AAV) is a systemic autoimmune disease in which patients often have circulating proteinase 3 (PR3)-ANCA or myeloperoxidase (MPO)-ANCA.^{1,2} The clinical syndromes within the spectrum of AAV are granulomatosis with polyangiitis (GPA), microscopic polyangiitis (MPA) and eosinophilic granulomatosis with polyangiitis.

The subtypes within AAV show significant differences in clinical and epidemiological

METHODS**Literature search and eligibility**

A comprehensive search string was carried out in collaboration with a librarian. PubMed, EMBASE and Web of Science were searched until April 2014 for studies investigating genetic variants in patients with AAV. The search strategy consisted of multiple queries combining ‘Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis’, ‘ANCA’, ‘vasculitis’, ‘Granulomatosis with Polyangiitis’, ‘Wegener’s Granulomatosis’, ‘Microscopic polyangiitis’, ‘Eosinophilic granulomatosis with polyangiitis’,



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'Churg Strauss Syndrome', 'PR3', 'MPO', 'Polymorphisms' or 'Genes'. To minimise the chance of omitting references, a second broader search was performed for genetic variants in vasculitis in general rather than AAV alone (online supplementary table S1). The specific genes and polymorphisms that resulted from the previous searches were added in a next search to minimise the chance of omitting references. To ensure maximum sensitivity, no limits, filters or language restrictions were placed on the searches.

Two observers (CR and DvH) independently reviewed the titles and abstracts of the citations retrieved by the search and read potentially relevant studies independently. Studies that compared genetic variants between patients with AAV and controls without AAV derived from the general population were eligible. Cases had to have an AAV by fulfilling either the Chapel Hill Consensus Conference criteria,¹⁹ American College of Rheumatology criteria,²⁰ European Medicines Agency algorithm,²¹ 1998 Japanese criteria proposed by the Research Committee on Intractable Vasculitides, the Ministry of Health, Labour and Welfare of Japan,²² or clinical, histological and serological criteria. Definitions of cases and controls in each included study are depicted in online supplementary table S2. All genetic variants investigated in at least two studies were included. Genetic variants investigated in multiple cohorts in one publication were also included. This was the case for genetic variants in *GHSR*,²³ *LEPR*²³ and *TLR9*.²⁴ For the included genetic variants, all genetic studies were identified to estimate the pooled effect of the genetic variant in a meta-analysis, irrespective of their p values. To increase the validity of this meta-analysis, we also included unpublished data on these genetic variants from the Lyons *et al*¹⁵ GWAS. This was possible for the genetic variants in this meta-analysis that were not human leucocyte antigen (HLA) serotypes or tandem repeats and that were genotyped in the Lyons *et al* GWAS. Moreover, we included data from the stage 1 analysis including all single-nucleotide polymorphisms (SNPs) with a p value <10⁻⁴ from the Xie *et al*¹⁶ GWAS.

Data extraction

Minor allele frequencies of the included genetic variants were extracted from included studies. Studies investigating the same genetic variant published by the same author(s) were checked for overlapping patient groups, in which case only the study with the largest patient group was included. Studies that reported insufficient data to calculate an OR were excluded.

Statistical analysis

ORs and 95% CIs were calculated at the allele level. To account for potential heterogeneity, random-effects model was performed in all analyses that included at least five studies.²⁵ Because the HLA serotypes are not completely independent from the HLA alleles, the following HLA variants were collapsed in the analyses: *HLA-DR1*, *HLA-DRB1*01* and *HLA-DRB1*0101*; *HLA-DR3* and *HLA-DRB1*03*; *HLA-DR7* and *HLA-DRB1*07*; *HLA-DR8* and *HLA-DRB1*08*; and *HLA-DR9*, *HLA-DRB1*09* and *HLA-DRB1*0901*. Collapsing other HLA variants was not possible because some studies investigated multiple, closely related, HLA variants in the same patients. If these HLA variants had been collapsed, the same patients would have been included in the same analysis multiple times, increasing their weight in the analysis and introducing a systematic error. To determine whether the disease subtypes within AAV represent parts of a single disease spectrum or distinct clinical entities, we performed pre-specified subgroup

analysis stratifying patients according to clinical diagnosis (GPA/MPA) and ANCA serotype (PR3-ANCA/MPO-ANCA and cytoplasmic (c)-ANCA/perinuclear (p)-ANCA), if enough data were available. Moreover, we performed stratified analyses based on ethnicity for all genetic variants investigated in both Caucasian and Asian patients. We assumed difference in effect estimates likely to be present in case subgroups showed significant effects in opposite directions, that is, having a protective effect in one subgroup but leading to an increased risk of AAV in the other subgroup. Heterogeneity within studies was displayed by I², which reflects the percentage of total variation across studies beyond chance.²⁶ Egger and Harbord tests were used to assess publication bias.²⁷ All of the p values presented are nominal p values and are not corrected for multiple testing. Correction for multiple testing was not performed as the strong linkage disequilibrium between variants tested in the major histocompatibility complex (MHC) region makes calculating an appropriate multiple correction factor impractical. All analyses were performed using STATA V.12 (StataCorp. 2011; Stata Statistical Software: Release 12, College Station, Texas, USA).

RESULTS

Initial search and results

Our literature search yielded 5180 articles, from which we identified 140 genetic variants published in 62 articles. All included studies were case-control studies, two of which were GWAS. These articles were published from 1978 through 2014, and the number of patients with AAV included ranged from 12 to 1445. The characteristics of all included studies are provided in online supplementary table S2. Additionally, previously unpublished data from the Lyons *et al*¹⁵ GWAS were available and included in the meta-analysis for 18 genetic variants: *CD226* rs763361, *CTLA-4* rs231775, *CTLA-4* rs3087243, *FCAR* rs16986050, *FCGR2A* rs1801274, *GHSR* rs509035, *HLA-DPB2* rs3130215, *IL-1β* rs1143634, *IL-6* rs1800795, *IL-10* rs1800896, *IRF5* rs10954213, *PTPN22* rs2476601, *RING1/RXR* rs213213, *RXR* rs6531, *RXR* rs9277935, *STAT4* rs7574865, *SERPINA1* Z allele and *TNFA* rs1800629.

Thirty-three genetic variants were significantly associated with AAV after meta-analysis (table 1 and online supplementary figure S1), and 107 genetic variants were not associated with AAV after meta-analysis (online supplementary table S3). The ORs for the significant associations after meta-analysis ranged from 0.35 to 0.81 for protective genetic variants and from 1.13 to 2.94 for the genetic variants associated with an increased risk of AAV.

AAV is associated with the Z and S alleles of *SERPINA1*

Both the S allele and Z allele of *SERPINA1* were significantly associated with AAV, with pooled ORs of 1.30 (95% CI 1.03 to 1.63) and 2.94 (95% CI 2.22 to 3.88), respectively. Subgroup analysis showed that the association with the *SERPINA1* Z allele was present in both PR3-ANCA (pooled OR 2.58 (95% CI 1.57 to 4.25)) and MPO-ANCA (pooled OR 2.01 (95% CI 1.04 to 3.87)) positive patients and in both c-ANCA (pooled OR 3.53 (95% CI 2.28 to 5.49)) and p-ANCA (pooled OR 3.13 (95% CI 1.21 to 8.13)) positive patients (see online supplementary table S4 and figure S2).

AAV is associated with genetic variants in the MHC region

Seventeen genetic variants in *HLA-B*, *HLA-DP*, *HLA-DQ* and *HLA-DR* remained significantly associated with AAV after meta-analysis (table 1). *HLA-DPA1* rs9277341 had the strongest protective effect (pooled OR 0.35 (95% CI 0.30 to 0.40)), and

Table 1 Genetic variants significantly associated with antibody-associated vasculitis (AAV) after meta-analysis

Variant by gene (minor allele)	Publications (n)	Cases (n)/controls (n)	OR (95% CI)	p Value for meta-analysis	I ² (%)	p Value for heterogeneity	p Value for funnel plot asymmetry*
<i>CD226</i> rs763361 (T)	3	2422/17898	1.14 (1.07 to 1.21)	<0.001	0	0.444	0.792
<i>CTLA-4</i> (AT) ₈₆	4	303/543	0.54 (0.43 to 0.67)	<0.001	89	<0.001	0.946
<i>CTLA-4</i> rs231775 (G)	3	1002/6179	1.16 (1.06 to 1.28)	0.002	60	0.080	0.080
<i>CTLA-4</i> rs3087243 (A)	3	2015/7855	0.81 (0.75 to 0.87)	<0.001	25	0.262	0.122
<i>FCGR2A</i> rs1801274 (C)	6	1239/6209	0.90 (0.82 to 0.99)	0.028	0	0.834	0.788
<i>HLA-B5</i>	2	335/6573	0.59 (0.38 to 0.92)	0.019	0	0.432	N/A
<i>HLA-B8</i>	6	475/7855	1.48 (1.04 to 2.11)	0.028	47	0.096	0.063
<i>HLA-DPA1</i> rs9277341 (C)	2	1032/2200	0.35 (0.30 to 0.40)	<0.001	54	0.116	0.215
<i>HLA-DPB1</i> *0301	5	1154/1337	0.38 (0.21 to 0.69)	0.002	78	<0.001	0.938
<i>HLA-DPB1</i> *0401	5	1154/1337	1.99 (1.44 to 2.74)	<0.001	84	<0.001	0.738
<i>HLA-DPB2</i> rs3130215 (A)	3	1417/7249	1.40 (1.29 to 1.52)	<0.001	99	<0.001	0.446
<i>HLA-DQB1</i> *0303	3	176/218	1.82 (1.09 to 3.03)	0.021	17	0.301	0.916
<i>HLA-DR6</i>	5	487/6222	0.50 (0.27 to 0.95)	0.033	55	0.062	0.997
<i>HLA-DRB1</i> *1101	2	268/465	1.89 (1.15 to 3.08)	0.011	0	0.487	N/A
<i>HLA-DRB1</i> *1201	2	216/465	0.37 (0.15 to 0.91)	0.031	0	0.491	N/A
<i>HLA-DRB1</i> *13	4	233/833	0.47 (0.32 to 0.70)	<0.001	0	0.504	0.884
<i>HLA-DRB1</i> *14	4	322/862	1.91 (1.07 to 3.42)	0.029	0	0.728	0.700
<i>HLA-DRB1</i> *15	3	236/633	1.86 (1.39 to 2.50)	<0.001	69	0.021	0.347
<i>HLA-DRB1</i> *1501	2	216/465	1.68 (1.20 to 2.34)	0.002	0	0.925	N/A
<i>HLA-DRB3</i>	4	260/1845	0.62 (0.49 to 0.79)	<0.001	68	0.024	0.689
<i>HLA-DRB4</i>	4	260/1845	1.69 (1.36 to 2.10)	<0.001	61	0.055	0.533
<i>HSD17B8</i> rs421446 (C)	2	738/1872	0.40 (0.34 to 0.48)	<0.001	0	0.620	N/A
<i>IRF5</i> rs10954213 (G)	3	1535/6977	0.77 (0.70 to 0.83)	<0.001	99	<0.001	0.948
<i>PTPN22</i> rs2476601 (A)	4	2099/8678	1.39 (1.24 to 1.56)	<0.001	0	0.693	0.500
<i>RING1/RXR</i> rs213213 (A)	3	1414/7238	1.71 (1.57 to 1.86)	<0.001	73	0.026	0.187
<i>RXR</i> rs6531 (C)	3	1557/6955	1.63 (1.50 to 1.77)	<0.001	96	<0.001	0.292
<i>RXR</i> rs9277935 (T)	3	1417/7233	0.44 (0.37 to 0.50)	<0.001	73	0.025	0.393
<i>SERPINA1</i> S allele	5	1474/5762	1.30 (1.03 to 1.63)	0.025	0	0.464	0.547
<i>SERPINA1</i> Z allele	8	3662/8581	2.94 (2.22 to 3.88)	<0.001	41	0.092	0.078
<i>STAT4</i> rs7574865 (T)	3	1520/6956	1.11 (1.01 to 1.22)	0.029	3	0.357	0.590
<i>TLR9</i> rs352162 (T)	1	1289/1898	1.58 (1.43 to 1.75)	<0.001	96	<0.001	N/A
<i>TLR9</i> rs352140 (T)	1	1289/1898	1.13 (1.02 to 1.25)	0.018	0	0.432	N/A
<i>TLR9</i> rs352139 (T)	1	1289/1898	1.11 (1.00 to 1.23)	0.041	0	0.756	N/A

*Harbord test for funnel plot asymmetry was performed for all genetic variants, except for *CD226* rs763361, *CTLA-4* rs3087243, and *PTPN22* rs2476601. In these cases, the Harbord test was not applicable and the Egger test was performed.

*HLA-DPB1**0401 was the strongest contributor to an increased risk of AAV (pooled OR 1.99 (95% CI 1.44 to 2.74)).

RING1/RXR rs213213, *RXR* rs6531 and *RXR* rs9277935 were also significantly associated with AAV with pooled ORs of 1.71 (95% CI 1.57 to 1.86), 1.63 (95% CI 1.50 to 1.77) and 0.44 (95% CI 0.37 to 0.50), respectively.

AAV is associated with genetic variants involved in inflammatory processes

CTLA-4 rs231775 was associated with an increased risk of AAV (pooled OR of 1.16 (95% CI 1.06 to 1.28)) while *CTLA-4* rs3087243 and *CTLA-4* (AT)₈₆ had a protective effect (pooled ORs of 0.81 (95% CI 0.75 to 0.87) and 0.54 (95% CI 0.43 to 0.67), respectively). *PTPN22* rs2476601, *CD226* rs763361 and *IRF5* rs10954213 were also significantly associated with AAV, with pooled ORs of 1.39 (95% CI 1.24 to 1.56), 1.14 (95% CI 1.07 to 1.21) and 0.77 (95% CI 0.70 to 0.83), respectively. Moreover, *TLR9* rs352162 and rs352140 were significantly associated with AAV with pooled ORs of 1.58 (95% CI 1.43 to 1.75) and 1.13 (95% CI 1.02 to 1.25), respectively.

Genetic associations differ for the different diagnostic and serological subtypes of AAV

A significant association with GPA and/or MPA was present for 25 genetic variants, and a significant association with both GPA and MPA was present for 10 genetic variants (online supplementary table S4 and figure S2). In 6 of these 10 genetic variants (60%), the associations were in opposite directions, that is, having a protective effect in one subgroup but leading to an increased risk of AAV in the other subgroup (figure 1). A significant association with PR3-ANCA and/or MPO-ANCA was present for 25 genetic variants, and a genetic association with both PR3-ANCA and MPO-ANCA was present for seven genetic variants. In four of these seven genetic variants (57%), the associations were in opposite directions, that is, having a protective effect in one subgroup but leading to an increased risk of AAV in the other subgroup (figure 1). Moreover, ORs were higher for ANCA serotype than for clinical diagnosis in 76% (16/21) of the genetic variants that were significantly associated with both clinical diagnosis and ANCA serotype.

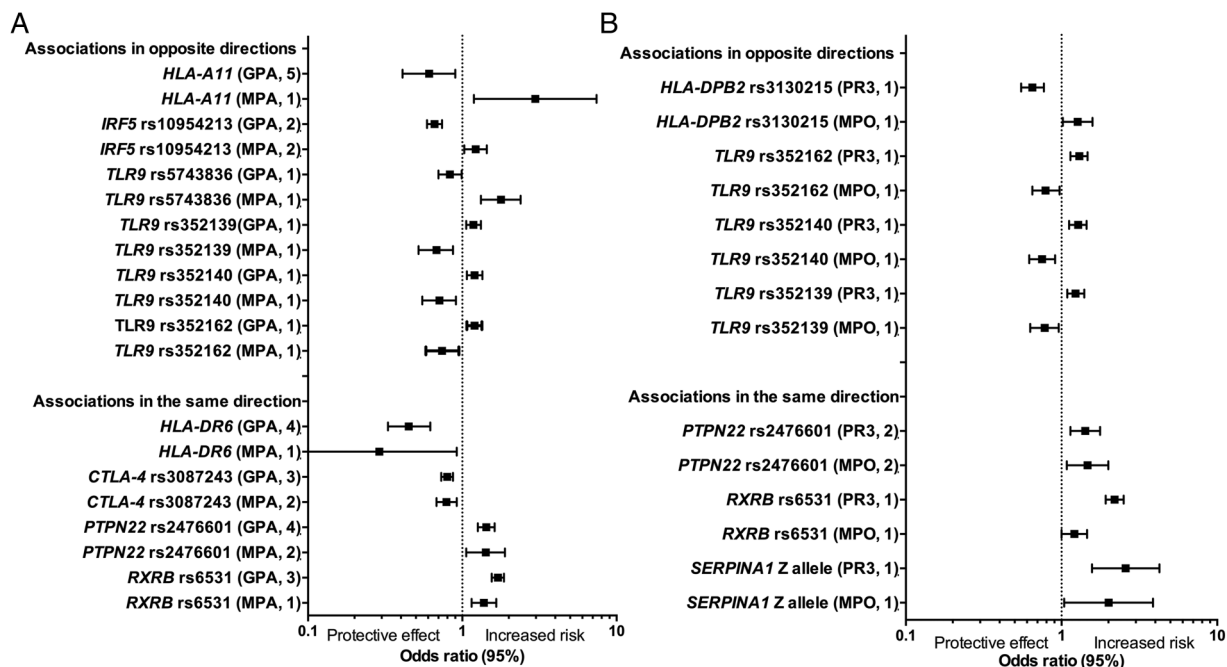


Figure 1 Subgroup analysis based on clinical diagnosis (A) and antineutrophil cytoplasmic antibody (ANCA) serotype (B), with the clinical diagnosis (A) or ANCA serotype (B) and number of included publications depicted between the parentheses. (A) In 6 of the 10 genetic variants (60%) in which there was an association with both granulomatosis with polyangiitis (GPA) and microscopic polyangiitis (MPA), the associations were in opposite directions. (B) In four of the seven genetic variants (57%) in which there was an association with both proteinase 3 (PR3)-ANCA vasculitis and myeloperoxidase (MPO)-ANCA vasculitis, the associations were in opposite directions.

Genetic associations differ for AAV patients of Caucasian and Asian origin

The results of the stratified analyses performed for 42 variants investigated in both Caucasian and Asian patients are depicted in online supplementary table S5. *CTLA-4* (AT)₈₆, *CTLA-4* (AT)₁₀₆ and *HLA-DR6* were significantly associated with AAV in the Caucasian patients but not in the Asian patients. Conversely, *HLA-B55* was significantly associated with AAV in the Asian patients but not in the Caucasian patients. Of interest, *IRF5* rs10954213 (G) was significantly associated with AAV in both the Caucasian and Asian patients; however, it had a protective effect in the Caucasian patients while it increased the risk of AAV in the Asian patients. The results of these analyses should be interpreted with caution because each analysis included only one study involving Asian patients.

Genetic variants identified by GWAS

To date, two GWAS have been performed in AAV. The first GWAS included patients with GPA and MPA and found *HLA-DP* rs3117242, *COL11A2* rs3130233, *COL11A2* rs3117016 and *SERPINA1* rs7151526 to be associated with AAV.¹⁵ Moreover, *HLA-DP* rs3117242, *ARHGAP18* rs1705767 and *SERPINA1* rs7151526 were associated with PR3-ANCA vasculitis, and *HLA-DQ* rs5000634 was associated with MPO-ANCA vasculitis. The second GWAS included only patients with GPA and found *HLA-DPB1* rs9277554 and *HL-DPA1* rs9277341 to be associated with GPA.¹⁶ *SEMA6A* rs26595 was associated with GPA at a genome-wide significance level when the results of the two cohorts that were included in this GWAS were combined. However, although *SEMA6A* rs26595 was not genotyped in the first GWAS,¹⁵ data for a large number of proxy SNPs across this locus were available, and these did not reach statistical significance (data not shown).

DISCUSSION

This meta-analysis identified 33 genetic variants, in or near 15 genes, associated with AAV. Twenty of these 33 genetic variants were present in the MHC region. This study provides the first complete and comprehensive overview including all genetic variants investigated in AAV in at least two studies. Genetic variants in or near *CD226*, *CTLA-4*, *FCGR2A*, *HLA-B*, *HLA-DP*, *HLA-DQ*, *HLA-DR*, *HSD17B8*, *IRF5*, *PTPN22*, *RING1/RXR*B, *RXR*B, *STAT4*, *SERPINA1* and *TLR9* were associated with AAV in this meta-analysis. Of interest, *FCGR2A* and *STAT4* were not associated with AAV in the individual studies, but were significantly associated with AAV after meta-analysis. Moreover, we showed genetic distinctions between the clinical diagnoses GPA and MPA and between the ANCA serotypes PR3-ANCA and MPO-ANCA. Additionally, our results confirm that subdivision of AAV based on ANCA serotype has a stronger genetic basis than subdivision based on clinical diagnosis.

A number of the genetic variants associated with AAV in this meta-analysis have also been associated with other autoimmune diseases, such as *CTLA-4* rs3087243 in rheumatoid arthritis^{28 29} and type 1 diabetes^{30 31} and *PTPN22* rs2476601 in Crohn's disease,^{32–34} Behçet's disease,³⁵ systemic lupus erythematosus^{36–38} and giant cell arteritis.^{39 40} These findings are in line with the fact that first-degree relatives of patients with AAV have an increased risk of other autoimmune diseases.^{41 42} Overlapping genetic variants may form the basis of a disturbed immune system, and together with environmental factors and other, more distinct genetic factors, form a 'bad hand of cards' that leads to the development of AAV.

The results of this meta-analysis support a role for the intricate relationship among alpha-1-antitrypsin and ANCA, the MHC system and other inflammatory processes in the pathogenesis of AAV. The association between *SERPINA1* and AAV supports the concept that ANCA are important in AAV

pathogenesis. Alpha-1-antitrypsin is coded by *SERPINA1* and is a major inhibitor of PR3. It has been hypothesised that lower levels of alpha-1-antitrypsin, resulting from the presence of the Z and S alleles of *SERPINA1*, lead to increased levels of circulating PR3 and possibly trigger the synthesis of anti-PR3-ANCA.⁴³ This hypothesis implies that the association of AAV with alpha-1-antitrypsin deficiency is restricted to PR3-ANCA-positive patients; however, in this meta-analysis, the association between the Z allele of *SERPINA1* was present in both PR3-ANCA-positive and MPO-ANCA-positive patients and in both c-ANCA-positive and p-ANCA-positive patients. Another hypothesis is that patients with AAV and alpha-1-antitrypsin deficiency have a reduced ability to bind PR3 released by previously activated neutrophils, thus promoting PR3-mediated proteolytic vessel damage.

As noted, 20 genetic variants in the MHC region were associated with AAV in this meta-analysis. We, therefore, confirm an important role for the MHC region, but because of linkage disequilibrium, were unable to determine the nature of this association, that is, whether it represents single or multiple independent associations. Both GWAS showed that the SNP association signal in the MHC region was fully accounted for by *HLA-DPB1*, dramatically diminishing the associations of other SNPs in this region.^{15 16} The results of our meta-analysis also support a role for other inflammatory processes in the pathogenesis of AAV, with the associations with *CTLA-4* and *PTPN22* suggesting a role for a threshold of activation or suppression of T cells.

The different subtypes generally grouped under the umbrella term AAV have profound differences in ANCA specificities³ and clinical outcomes.⁴ The results of this meta-analysis indicate that these different AAV subtypes also have distinct genetic backgrounds, as previously shown in a GWAS.¹⁵ Moreover, we found significant associations in opposite directions for the different AAV subgroups. Significant associations of the same SNP in opposite directions for different types of autoimmune diseases have been described before and could be indicative of different mechanisms of disease.⁴⁴ Larger studies are required to investigate this issue further in AAV.

The subdivision of AAV based on ANCA serotype had the stronger genetic basis in our meta-analysis; in 76% of the genetic variants, subdivision based on ANCA serotype resulted in higher ORs than subdivision based on clinical diagnosis. The results of these analyses should, however, be interpreted with caution because of the limited number of studies included in some of the analyses and need to be validated in other studies. Although until now the concept of a single disease spectrum has resulted in similar treatment strategies in patients with AAV, our limited results suggest that syndrome-specific therapeutics based on ANCA serotype strategies may be considered.

Our study has some limitations. First, in some of our analyses, the number of subjects or studies was limited; this limitation was especially the case in the subgroup analyses. Second, publication bias is an issue of concern in all meta-analyses. Authors might omit non-significant genetic associations and report only those associations that reach statistical significance. However, none of the tests performed to assess funnel plot asymmetry in this meta-analysis were significant. Furthermore, the studies included in this meta-analysis show heterogeneity with respect to clinical diagnosis, ANCA serotype, disease characteristics, ethnicity and study design. The clinical heterogeneity was accompanied by statistical heterogeneity for 16 of the 140 included genetic variants. However, there is no fully accepted statistical measure that precisely determines clinical

heterogeneity.²⁷ To account for heterogeneity, random-effects models were performed where possible.²⁵ Nevertheless, estimates reported in this study should be interpreted with caution, especially when statistical heterogeneity was present or when a small number of studies and/or relatively small groups of participants were included. Finally, it should be kept in mind that the genetic associations identified do not imply causality. While they provide insight into pathogenicity and suggest the involvement of certain pathways, these may not represent therapeutic targets.

In summary, this meta-analysis identified 33 genetic variants, in or near 15 genes, associated with AAV. Moreover, we showed genetic distinctions among the different AAV subtypes, supporting the concept that these subtypes may represent distinct autoimmune syndromes. These subtypes are most likely driven by ANCA serotype and not by clinical diagnosis.

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REFERENCES

- Berden A, Gocceroglu A, Jayne D, *et al.* Diagnosis and management of ANCA associated vasculitis. *BMJ* 2012;344:e26.
- Sable-Fourtassou R, Cohen P, Mahr A, *et al.* Antineutrophil cytoplasmic antibodies and the Churg-Strauss syndrome. *Ann Intern Med* 2005;143:632–8.
- Hagen EC, Daha MR, Hermans J, *et al.* Diagnostic value of standardized assays for anti-neutrophil cytoplasmic antibodies in idiopathic systemic vasculitis. EC/BCR Project for ANCA Assay Standardization. *Kidney Int* 1998;53:743–53.
- Mukhtyar C, Flossmann O, Hellmich B, *et al.* Outcomes from studies of antineutrophil cytoplasm antibody associated vasculitis: a systematic review by the European League Against Rheumatism systemic vasculitis task force. *Ann Rheum Dis* 2008;67:1004–10.
- Hogan SL, Falk RJ, Nachman PH, *et al.* Various forms of life in antineutrophil cytoplasmic antibody-associated vasculitis. *Ann Intern Med* 2006;144:377–8; author reply 8–9.
- Hoffman GS, Langford CA. Are there different forms of life in the antineutrophil cytoplasmic antibody universe? *Ann Intern Med* 2005;143:683–5.
- Linder R, Orth I, Hagen EC, *et al.* Differentiation between Wegener's granulomatosis and microscopic polyangiitis by an artificial neural network and by traditional methods. *J Rheumatol* 2011;38:1039–47.
- Jayne D, Rasmussen N, Andrassy K, *et al.* A randomized trial of maintenance therapy for vasculitis associated with antineutrophil cytoplasmic autoantibodies. *N Engl J Med* 2003;349:36–44.
- Jones RB, Tervaert JW, Hauser T, *et al.* Rituximab versus cyclophosphamide in ANCA-associated renal vasculitis. *N Engl J Med* 2010;363:211–20.
- Stone JH, Merkel PA, Spiera R, *et al.* Rituximab versus cyclophosphamide for ANCA-associated vasculitis. *N Engl J Med* 2010;363:221–32.
- Monach PA, Merkel PA. Genetics of vasculitis. *Curr Opin Rheumatol* 2010;22:157–63.
- de Lind van Wijngaarden RA, van Rijn L, Hagen EC, *et al.* Hypotheses on the etiology of antineutrophil cytoplasmic autoantibody associated vasculitis: the cause is hidden, but the result is known. *Clin J Am Soc Nephrol* 2008;3:237–52.
- Piram M, Maldini C, Mahr A. Effect of race/ethnicity on risk, presentation and course of connective tissue diseases and primary systemic vasculitides. *Curr Opin Rheumatol* 2012;24:193–200.
- Knight A, Sandin S, Asklung J. Risks and relative risks of Wegener's granulomatosis among close relatives of patients with the disease. *Arthritis Rheum* 2008;58:302–7.
- Lyons JA, Rayner TF, Trivedi S, *et al.* Genetically distinct subsets within ANCA-associated vasculitis. *N Engl J Med* 2012;367:214–23.
- Xie G, Roshandel D, Sherva R, *et al.* Association of granulomatosis with polyangiitis (Wegener's) with HLA-DPB1*04 and SEMA6A gene variants: evidence from genome-wide analysis. *Arthritis Rheum* 2013;65:2457–68.
- Ioannidis JP, Ntzani EE, Trikalinos TA, *et al.* Replication validity of genetic association studies. *Nat Genet* 2001;29:306–9.
- Wacholder S, Chanock S, Garcia-Closas M, *et al.* Assessing the probability that a positive report is false: an approach for molecular epidemiology studies. *J Natl Cancer Inst* 2004;96:434–42.
- Jennette JC, Falk RJ, Andrassy K, *et al.* Nomenclature of systemic vasculitides. Proposal of an international consensus conference. *Arthritis Rheum* 1994;37:187–92.

- 20 Leavitt RY, Fauci AS, Bloch DA, *et al.* The American College of Rheumatology 1990 criteria for the classification of Wegener's granulomatosis. *Arthritis Rheum* 1990;33:1101–7.
- 21 Watts R, Lane S, Hanslik T, *et al.* Development and validation of a consensus methodology for the classification of the ANCA-associated vasculitides and polyarteritis nodosa for epidemiological studies. *Ann Rheum Dis* 2007;66:222–7.
- 22 Tsuchiya N, Kobayashi S, Kawasaki A, *et al.* Genetic background of Japanese patients with antineutrophil cytoplasmic antibody-associated vasculitis: association of HLA-DRB1*0901 with microscopic polyangiitis. *J Rheumatol* 2003;30:1534–40.
- 23 Wiczorek S, Holle JU, Bremer JP, *et al.* Contrasting association of a non-synonymous leptin receptor gene polymorphism with Wegener's granulomatosis and Churg-Strauss syndrome. *Rheumatology (Oxford)* 2010;49:907–14.
- 24 Husmann CA, Holle JU, Moosig F, *et al.* Genetics of toll like receptor 9 in ANCA associated vasculitides. *Ann Rheum Dis* 2014;73:890–6.
- 25 Borenstein M, Hedges LV, Higgins JTH, *et al.* A basic introduction to fixed-effect and random-effects models for meta-analysis. *Res Synth Methods* 2010;1:97–111.
- 26 Higgins JP, Thompson SG, Deeks JJ, *et al.* Measuring inconsistency in meta-analyses. *BMJ* 2003;327:557–60.
- 27 Egger M, Davey Smith G, Schneider M, *et al.* Bias in meta-analysis detected by a simple, graphical test. *BMJ* 1997;315:629–34.
- 28 Kurreeman F, Liao K, Chibnik L, *et al.* Genetic basis of autoantibody positive and negative rheumatoid arthritis risk in a multi-ethnic cohort derived from electronic health records. *Am J Hum Genet* 2011;88:57–69.
- 29 Stahl EA, Raychaudhuri S, Remmers EF, *et al.* Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. *Nat Genet* 2010;42:508–14.
- 30 Barrett JC, Clayton DG, Concannon P, *et al.* Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. *Nat Genet* 2009;41:703–7.
- 31 Todd JA, Walker NM, Cooper JD, *et al.* Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. *Nat Genet* 2007;39:857–64.
- 32 Barrett JC, Hansoul S, Nicolae DL, *et al.* Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. *Nat Genet* 2008;40:955–62.
- 33 Franke A, McGovern DP, Barrett JC, *et al.* Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nat Genet* 2010;42:1118–25.
- 34 Anderson CA, Massey DC, Barrett JC, *et al.* Investigation of Crohn's disease risk loci in ulcerative colitis further defines their molecular relationship. *Gastroenterology* 2009;136:523–9.e3.
- 35 Baranathan V, Stanford MR, Vaughan RW, *et al.* The association of the PTPN22 620W polymorphism with Behcet's disease. *Ann Rheum Dis* 2007;66:1531–3.
- 36 Gateva V, Sandling JK, Hom G, *et al.* A large-scale replication study identifies TNIP1, PRDM1, JAZF1, UHRF1BP1 and IL10 as risk loci for systemic lupus erythematosus. *Nat Genet* 2009;41:1228–33.
- 37 Graham RR, Hom G, Ortmann W, *et al.* Review of recent genome-wide association scans in lupus. *J Intern Med* 2009;265:680–8.
- 38 Harley JB, Alarcon-Riquelme ME, Criswell LA, *et al.*, International Consortium for Systemic Lupus Erythematosus Genetics (SLEGEN). Genome-wide association scan in women with systemic lupus erythematosus identifies susceptibility variants in ITGAM, PXX, KIAA1542 and other loci. *Nat Genet* 2008;40:204–10.
- 39 Serrano A, Marquez A, Mackie SL, *et al.* Identification of the PTPN22 functional variant R620W as susceptibility genetic factor for giant cell arteritis. *Ann Rheum Dis* 2013;72:1882–6.
- 40 Carmona FD, Mackie SL, Martin JE, *et al.* A large-scale genetic analysis reveals a strong contribution of the HLA class II region to giant cell arteritis susceptibility. *Am J Hum Genet* 2015;96:565–80.
- 41 Hemminki K, Li X, Sundquist J, *et al.* Familial associations of rheumatoid arthritis with autoimmune diseases and related conditions. *Arthritis Rheum* 2009;60:661–8.
- 42 Knight A, Sandin S, Askling J. Increased risk of autoimmune disease in families with Wegener's granulomatosis. *J Rheumatol* 2010;37:2553–8.
- 43 Segelmark M, Elzouki AN, Wieslander J, *et al.* The PiZ gene of alpha 1-antitrypsin as a determinant of outcome in PR3-ANCA-positive vasculitis. *Kidney Int* 1995;48:844–50.
- 44 Sirota M, Schaub MA, Batzoglu S, *et al.* Autoimmune disease classification by inverse association with SNP alleles. *PLoS Genet* 2009;5:e1000792.

Online supplement

Genetic variants in ANCA-associated vasculitis: a meta-analysis

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Supplementary Table S1. Literature search strategies

Database	Search Strategy
PubMed	<p><i>Two strategies:</i></p> <p><u>1. AAV and genes</u> ("Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis"[Mesh] OR "ANCA-associated vasculitis"[all fields] OR "ANCA associated vasculitis"[all fields] OR "Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis"[all fields] OR "Pauci-Immune Vasculitis"[all fields] OR "Pauci Immune Vasculitis"[all fields] OR "Pauci-Immune Vasculitides"[all fields] OR "ANCA-Associated Vasculitides"[all fields] OR "ANCA Associated Vasculitides"[all fields] OR "ANCA-Associated Vasculitide"[all fields] OR ("ANCA"[all fields] AND vasculit*[all fields]) OR ("Anti-Neutrophil"[all fields] AND "Cytoplasmic"[all fields] AND "Antibody-Associated"[all fields] AND vasculit*[all fields]) OR "Churg-Strauss Syndrome"[all fields] OR "Churg Strauss Syndrome"[all fields] OR "Allergic Granulomatous Angiitis"[all fields] OR "Allergic Granulomatous Angiitides"[all fields] OR "Allergic Angiitis"[all fields] OR "Churg-Strauss Vasculitis"[all fields] OR "eosinophilic granulomatosis with polyangiitis"[all fields] OR ("eosinophilic"[all fields] AND "granulomatosis"[all fields] AND "polyangiitis"[all fields]) OR "Microscopic Polyangiitis"[all fields] OR "Microscopic Polyangiitides"[all fields] OR "Wegener Granulomatosis"[all fields] OR "Wegener's Granulomatosis"[all fields] OR "Wegeners Granulomatosis"[all fields] OR "granulomatosis with polyangiitis"[all fields] OR ("granulomatosis"[all fields] AND "polyangiitis"[all fields]) OR "anca"[tw] OR (("pr3"[all fields] OR "pr-3"[all fields] OR "mpo"[all fields]) AND ("Vasculitis"[mesh] OR vasculit*[all fields] OR "anca"[tw])) OR "Antibodies, Antineutrophil Cytoplasmic"[Mesh] OR "Antineutrophil Cytoplasmic Antibody"[all fields] OR "Anti-Neutrophil Cytoplasmic Antibody"[all fields] OR "Anti Neutrophil Cytoplasmic Antibody"[all fields] OR "Anti-Neutrophil Cytoplasmic Antibodies"[all fields] OR "Anti Neutrophil Cytoplasmic Antibodies"[all fields] OR "Antineutrophil Cytoplasmic Antibodies"[all fields]) AND ("genes"[mesh] OR "genes"[all fields] OR "gene"[all fields] OR "genetic"[all fields] OR "genetics"[Subheading] OR "genetics"[all fields] OR "genetics"[mesh] OR "polymorphism, genetic"[mesh] OR "polymorphism"[all fields] OR "polymorphisms"[all fields] OR "dna"[mesh] OR "dna"[all fields] OR "genome"[mesh] OR "genome"[all fields] OR "genomes"[all fields] OR "genomics"[mesh] OR "genomics"[all fields] OR "genomic"[all fields] OR "Genetic Phenomena"[mesh] OR "Genetic Structures"[Mesh])</p> <p><u>2. Vasculitis and genes (excluding AAV)</u> (("Vasculitis"[majr] OR vasculit*[ti]) AND ("genes"[majr] OR "genes"[ti] OR "gene"[ti] OR "genetic"[ti] OR "genetics"[ti] OR "genetics"[majr] OR "polymorphism, genetic"[majr] OR "polymorphism"[ti] OR "polymorphisms"[ti] OR "dna"[majr] OR "dna"[ti] OR "genome"[majr] OR "genome"[ti] OR "genomes"[ti] OR "genomics"[majr] OR "genomics"[ti] OR "genomic"[ti] OR "Genetic Phenomena"[majr] OR "Genetic</p>

	<p>Structures"[majr])) NOT (("Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis"[Mesh] OR "ANCA-associated vasculitis"[all fields] OR "ANCA associated vasculitis"[all fields] OR "Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis"[all fields] OR "Pauci-Immune Vasculitis"[all fields] OR "Pauci Immune Vasculitis"[all fields] OR "Pauci-Immune Vasculitides"[all fields] OR "ANCA-Associated Vasculitides"[all fields] OR "ANCA Associated Vasculitides"[all fields] OR "ANCA-Associated Vasculitide"[all fields] OR ("ANCA"[all fields] AND vasculit*[all fields]) OR ("Anti-Neutrophil"[all fields] AND "Cytoplasmic"[all fields] AND "Antibody-Associated"[all fields] AND vasculit*[all fields]) OR "Churg-Strauss Syndrome"[all fields] OR "Churg Strauss Syndrome"[all fields] OR "Allergic Granulomatous Angiitis"[all fields] OR "Allergic Granulomatous Angiitides"[all fields] OR "Allergic Angiitis"[all fields] OR "Churg-Strauss Vasculitis"[all fields] OR "eosinophilic granulomatosis with polyangiitis"[all fields] OR ("eosinophilic"[all fields] AND "granulomatosis"[all fields] AND "polyangiitis"[all fields]) OR "Microscopic Polyangiitis"[all fields] OR "Microscopic Polyangiitides"[all fields] OR "Wegener Granulomatosis"[all fields] OR "Wegener's Granulomatosis"[all fields] OR "Wegeners Granulomatosis"[all fields] OR "granulomatosis with polyangiitis"[all fields] OR ("granulomatosis"[all fields] AND "polyangiitis"[all fields]) OR "anca"[tw] OR ("pr3"[all fields] OR "pr-3"[all fields] OR "mpo"[all fields]) AND ("Vasculitis"[mesh] OR vasculit*[all fields] OR "anca"[tw])) OR "Antibodies, Antineutrophil Cytoplasmic"[Mesh] OR "Antineutrophil Cytoplasmic Antibody"[all fields] OR "Anti-Neutrophil Cytoplasmic Antibody"[all fields] OR "Anti Neutrophil Cytoplasmic Antibody"[all fields] OR "Anti-Neutrophil Cytoplasmic Antibodies"[all fields] OR "Anti Neutrophil Cytoplasmic Antibodies"[all fields] OR "Antineutrophil Cytoplasmic Antibodies"[all fields]) AND ("genes"[mesh] OR "genes"[all fields] OR "gene"[all fields] OR "genetic"[all fields] OR "genetics"[Subheading] OR "genetics"[all fields] OR "genetics"[mesh] OR "polymorphism, genetic"[mesh] OR "polymorphism"[all fields] OR "polymorphisms"[all fields] OR "dna"[mesh] OR "dna"[all fields] OR "genome"[mesh] OR "genome"[all fields] OR "genomes"[all fields] OR "genomics"[mesh] OR "genomics"[all fields] OR "genomic"[all fields] OR "Genetic Phenomena"[mesh] OR "Genetic Structures"[Mesh]))</p>
Embase	<p><i>Two strategies:</i></p> <p><u>1. AAV and genes</u> (ANCA associated vasculitis/ OR "ANCA-associated vasculitis".mp OR "ANCA associated vasculitis".mp OR "Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis".mp OR "Pauci-Immune Vasculitis".mp OR "Pauci Immune Vasculitis".mp OR "Pauci-Immune Vasculitides".mp OR "ANCA-Associated Vasculitides".mp OR "ANCA Associated Vasculitides".mp OR "ANCA-Associated Vasculitide".mp OR ("ANCA".mp AND vasculit*.mp) OR ("Anti-Neutrophil".mp AND "Cytoplasmic".mp AND "Antibody-Associated".mp AND vasculit*.mp) OR "Churg-Strauss Syndrome".mp OR "Churg Strauss Syndrome".mp OR "Allergic Granulomatous Angiitis".mp OR "Allergic Granulomatous Angiitides".mp OR "Allergic Angiitis".mp OR "Churg-Strauss Vasculitis".mp OR "eosinophilic</p>

	<p>granulomatosis with polyangiitis".mp OR ("eosinophilic".mp AND "granulomatosis".mp AND "polyangiitis".mp) OR "Microscopic Polyangiitis".mp OR "Microscopic Polyangiitides".mp OR "Wegener Granulomatosis".mp OR "Wegener's Granulomatosis".mp OR "Wegeners Granulomatosis".mp OR "granulomatosis with polyangiitis".mp OR ("granulomatosis".mp AND "polyangiitis".mp) OR "anca".mp OR (("pr3".mp OR "pr-3".mp OR "mpo".mp) AND (exp Vasculitis/ OR vasculit*.mp OR "anca".mp)) OR neutrophil cytoplasmic antibody/ OR "Antineutrophil Cytoplasmic Antibody".mp OR "Anti-Neutrophil Cytoplasmic Antibody".mp OR "Anti Neutrophil Cytoplasmic Antibody".mp OR "Anti-Neutrophil Cytoplasmic Antibodies".mp OR "Anti Neutrophil Cytoplasmic Antibodies".mp OR "Antineutrophil Cytoplasmic Antibodies".mp) AND (exp Gene/ OR gene.mp OR genom*.mp OR genes.mp OR exp genetic polymorphism/ OR polymorphism*.mp OR dna.mp OR exp dna/ OR exp *Heredity/)</p> <p><u>2. Vasculitis and genes (excluding AAV)</u> ((exp *Vasculitis/ OR vasculit*.ti) AND (exp *Gene/ OR gene.ti OR genom*.ti OR genes.ti OR exp *genetic polymorphism/ OR polymorphism*.ti OR dna.ti OR exp *dna/ OR exp *Heredity/)) NOT ((ANCA associated vasculitis/ OR "ANCA-associated vasculitis".mp OR "ANCA associated vasculitis".mp OR "Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis".mp OR "Pauci-Immune Vasculitis".mp OR "Pauci Immune Vasculitis".mp OR "Pauci-Immune Vasculitides".mp OR "ANCA-Associated Vasculitides".mp OR "ANCA Associated Vasculitides".mp OR "ANCA-Associated Vasculitide".mp OR ("ANCA".mp AND vasculit*.mp) OR ("Anti-Neutrophil".mp AND "Cytoplasmic".mp AND "Antibody-Associated".mp AND vasculit*.mp) OR "Churg-Strauss Syndrome".mp OR "Churg Strauss Syndrome".mp OR "Allergic Granulomatous Angiitis".mp OR "Allergic Granulomatous Angiitides".mp OR "Allergic Angiitis".mp OR "Churg-Strauss Vasculitis".mp OR "eosinophilic granulomatosis with polyangiitis".mp OR ("eosinophilic".mp AND "granulomatosis".mp AND "polyangiitis".mp) OR "Microscopic Polyangiitis".mp OR "Microscopic Polyangiitides".mp OR "Wegener Granulomatosis".mp OR "Wegener's Granulomatosis".mp OR "Wegeners Granulomatosis".mp OR "granulomatosis with polyangiitis".mp OR ("granulomatosis".mp AND "polyangiitis".mp) OR "anca".mp OR (("pr3".mp OR "pr-3".mp OR "mpo".mp) AND (exp Vasculitis/ OR vasculit*.mp OR "anca".mp)) OR neutrophil cytoplasmic antibody/ OR "Antineutrophil Cytoplasmic Antibody".mp OR "Anti-Neutrophil Cytoplasmic Antibody".mp OR "Anti Neutrophil Cytoplasmic Antibody".mp OR "Anti-Neutrophil Cytoplasmic Antibodies".mp OR "Anti Neutrophil Cytoplasmic Antibodies".mp) AND (exp Gene/ OR gene.mp OR genom*.mp OR genes.mp OR exp genetic polymorphism/ OR polymorphism*.mp OR dna.mp OR exp dna/ OR exp *Heredity/))</p>
Web of Science	<p><i>Two strategies:</i></p> <p><u>1. AAV and genes</u> TS=(("ANCA-associated vasculitis" OR "ANCA associated vasculitis" OR</p>

"Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis" OR "Pauci-Immune Vasculitis" OR "Pauci Immune Vasculitis" OR "Pauci-Immune Vasculitides" OR "ANCA-Associated Vasculitides" OR "ANCA Associated Vasculitides" OR "ANCA-Associated Vasculitide" OR ("ANCA" AND vasculit*) OR ("Anti-Neutrophil" AND "Cytoplasmic" AND "Antibody-Associated" AND vasculit*) OR "Churg-Strauss Syndrome" OR "Churg Strauss Syndrome" OR "Allergic Granulomatous Angiitis" OR "Allergic Granulomatous Angiitides" OR "Allergic Angiitis" OR "Churg-Strauss Vasculitis" OR "eosinophilic granulomatosis with polyangiitis" OR ("eosinophilic" AND "granulomatosis" AND "polyangiitis") OR "Microscopic Polyangiitis" OR "Microscopic Polyangiitides" OR "Wegener Granulomatosis" OR "Wegener's Granulomatosis" OR "Wegeners Granulomatosis" OR "granulomatosis with polyangiitis" OR ("granulomatosis" AND "polyangiitis") OR "anca" OR (("pr3" OR "pr-3" OR "mpo") AND (exp Vasculitis/ OR vasculit* OR "anca")) OR "neutrophil cytoplasmic antibody" OR "Antineutrophil Cytoplasmic Antibody" OR "Anti-Neutrophil Cytoplasmic Antibody" OR "Anti Neutrophil Cytoplasmic Antibody" OR "Anti-Neutrophil Cytoplasmic Antibodies" OR "Anti Neutrophil Cytoplasmic Antibodies" OR "Antineutrophil Cytoplasmic Antibodies") AND (gene OR genes OR genom* OR genetic* OR Polymorphism* OR dna))

2. Vasculitis and genes (excluding AAV)

(TI=((vasculit*) AND (gene OR genes OR genom* OR genetic* OR Polymorphism* OR dna))) NOT (TS(("ANCA-associated vasculitis" OR "ANCA associated vasculitis" OR "Anti-Neutrophil Cytoplasmic Antibody-Associated Vasculitis" OR "Pauci-Immune Vasculitis" OR "Pauci Immune Vasculitis" OR "Pauci-Immune Vasculitides" OR "ANCA-Associated Vasculitides" OR "ANCA Associated Vasculitides" OR "ANCA-Associated Vasculitide" OR ("ANCA" AND vasculit*) OR ("Anti-Neutrophil" AND "Cytoplasmic" AND "Antibody-Associated" AND vasculit*) OR "Churg-Strauss Syndrome" OR "Churg Strauss Syndrome" OR "Allergic Granulomatous Angiitis" OR "Allergic Granulomatous Angiitides" OR "Allergic Angiitis" OR "Churg-Strauss Vasculitis" OR "eosinophilic granulomatosis with polyangiitis" OR ("eosinophilic" AND "granulomatosis" AND "polyangiitis") OR "Microscopic Polyangiitis" OR "Microscopic Polyangiitides" OR "Wegener Granulomatosis" OR "Wegener's Granulomatosis" OR "Wegeners Granulomatosis" OR "granulomatosis with polyangiitis" OR ("granulomatosis" AND "polyangiitis") OR "anca" OR (("pr3" OR "pr-3" OR "mpo") AND (exp Vasculitis/ OR vasculit* OR "anca")) OR "neutrophil cytoplasmic antibody" OR "Antineutrophil Cytoplasmic Antibody" OR "Anti-Neutrophil Cytoplasmic Antibody" OR "Anti Neutrophil Cytoplasmic Antibody" OR "Anti-Neutrophil Cytoplasmic Antibodies" OR "Anti Neutrophil Cytoplasmic Antibodies" OR "Antineutrophil Cytoplasmic Antibodies") AND (gene OR genes OR genom* OR genetic* OR Polymorphism* OR dna)))

Supplementary Table S2. Study characteristics of the included studies

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
CD226 rs763361 (T)	Wieczorek et al. 2009 ^{1**}	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy subjects	761/1226	GPA (642), EGPA (119)	PR3-ANCA (438), MPO-ANCA (32), ANCA negative (43)	1.24 (1.11 – 1.39)
		Case-Control	UK	ACR and CHCC criteria	Geographically matched subjects from the general population	105/9337	GPA (all patients)	NR	1.17 (0.89 – 1.54)
	Chung et al. 2012 ^{2**}	Case-Control	USA	ACR criteria	Geographically matched subjects with no (family) history of autoimmune disease	424/469	GPA (all patients)	PR3-ANCA (339), MPO-ANCA (44), ANCA negative (39)	1.08 (0.90 – 1.30)
		Case-Control	Canada	ACR criteria	Geographically matched subjects with no history of autoimmune disease	456/1500	GPA (all patients)	NR	1.09 (0.94 – 1.26)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5366	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.08 (0.96 – 1.21)
CTLA-4 (AT)₈₆	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	0.18 (0.10 – 0.35)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	1.31 (0.76 – 2.25)
	Zhou et al. 2004 ⁶	Case-Control	USA	ACR criteria	Geographically and ethnically matched healthy, unrelated subjects	117/123	GPA (all patients)	PR3-ANCA (82), MPO-ANCA (5), PR3- and MPO-ANCA positive (2), ANCA negative (25)	0.38 (0.26 – 0.55)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.72 (0.51 – 1.02)
<i>CTLA-4</i> (AT)₁₀₂	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	1.71 (0.15 – 19.22)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	0.89 (0.47 – 1.68)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	1.73 (0.85 – 3.54)
<i>CTLA-4</i> (AT)₁₀₄	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	1.74 (0.96 – 3.13)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	1.15 (0.70 – 1.91)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	1.09 (0.70 – 1.59)
CTLA-4 (AT)₁₀₆	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	2.84 (0.74 – 10.91)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	0.41 (0.14 – 1.22)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	2.63 (1.09 – 6.35)
CTLA-4 (AT)₁₀₈	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	0.90 (0.42 – 1.95)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	0.89 (0.47 – 1.68)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	1.78 (1.05 – 3.03)
CTLA-4 (AT)₁₁₀	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	0.48 (0.02 9.36)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	0.25 (0.01 – 4.62)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
CTLA-4 (AT)₁₁₆	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.74 (0.34 – 1.61)
	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	1.37 (0.26 – 7.26)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	0.75 (0.03 – 18.56)
CTLA-4 (AT)₁₁₈	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.540 (0.11 – 2.62)
	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	3.44 (0.21 – 55.85)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	0.75 (0.08 – 7.33)
CTLA-4 (AT)₁₂₂	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.27 (0.06 – 1.18)
	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	10.32 (0.42 – 256.50)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	2.32 (0.57 – 9.47)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.47 (0.05 – 4.27)
CTLA-4 (AT)₁₂₄	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	14.47 (1.59 – 131.86)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	2.28 (0.14 – 36.59)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.63 (0.13 – 3.16)
CTLA-4 (AT)₁₂₆	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	4.78 (1.04 – 21.93)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	0.45 (0.05 – 3.88)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.81 (0.21 – 3.18)
CTLA-4 (AT)₁₂₈	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	1.12 (0.05 – 27.93)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	49/111	MPA (all patients)	MPO-ANCA (all patients)	6.98 (0.72 – 67.95)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
CTLA-4 rs231775 (G)	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.69 (0.22 – 2.18)
	Slot et al. 2008 ⁸	Case-Control	The Netherlands	CHCC criteria	Geographically and ethnically matched healthy subjects	104/185	GPA (50), MPA (24), EGPA (7), RLV (21)	PR3-ANCA (49), MPO-ANCA (34), PR3- and MPO-ANCA positive (2), ANCA negative (17)	1.53 (1.09 – 2.17)
	Kamesh et al. 2009 ⁹	Case-Control	UK	CHCC criteria	Ethnically matched healthy subjects with no (family) history of autoimmune disease	222/629	GPA (116), MPA (96)	NR	1.32 (1.06 – 1.65)
CTLA-4 rs3087243 (A)	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5365	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.09 (0.97 – 1.22)
	Kamesh et al. 2009 ⁹	Case-Control	UK	CHCC criteria	Ethnically matched healthy subjects with no (family) history of autoimmune disease	222/629	GPA (116), MPA (96)	NR	0.67 (0.54 – 0.83)
	Chung et al. 2012 ^{2**}	Case-Control	USA	ACR criteria	Geographically matched subjects with no (family) history of autoimmune disease	424/469	GPA (all patients)	PR3-ANCA (339), MPO-ANCA (44), ANCA negative (39)	0.80 (0.66 – 0.97)
		Case-Control	Canada	ACR criteria	Geographically matched subjects with no history of autoimmune disease	456/1500	GPA (all patients)	NR	0.78 (0.67 – 0.91)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
FCAR rs16986050 (G)	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	913/5257	GPA (565), MPA (262)	PR3-ANCA (478), MPO-ANCA (264)	0.85 (0.77 - 0.94)
	Kelley et al. 2011 ^{10**}	Case-Control	USA	ACR and CHCC criteria	Geographically matched subjects with no (family) history of autoimmune disease	445/413	GPA (all patients)	NR	0.65 (0.50 – 0.83)
		Case-Control	USA, Canada	ACR and CHCC criteria	HapMap Caucasians	190/113	GPA (all patients)	NR	0.79 (0.52 – 1.21)
FCGR2A rs1801274 (C)	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5365	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.07 (0.93 – 1.24)
	Edberg et al. 1997 ¹¹	Case-Control	USA, Chile, Germany, Canada	ACR and CHCC criteria	Ethnically matched healthy volunteers	147/149	GPA (all patients)	NR	0.85 (0.61 – 1.17)
	Dijstelbloem et al. 1999 ¹²	Case-Control	The Netherlands	ACR criteria	Ethnically matched healthy blood donors	91/154	GPA (all patients)	PR3-ANCA (all patients)	0.98 (0.68 – 1.41)
	Tse et al. 1999 ¹³	Case-Control	UK	CHCC criteria	Ethnically matched healthy subjects	107/100	GPA (48), MPA (54), EGPA (1), PAN (4)	PR3-ANCA (75), MPO-ANCA (32)	1.00 (0.68 – 1.48)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	50/303	MPA (all patients)	MPO-ANCA (all patients)	0.68 (0.37 – 1.24)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
FCGR3A rs396991 (G)	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5365	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	0.89 (0.79 – 0.99)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	1.03 (0.73 – 1.43)
	Dijstelbloem et al. 1999 ¹²	Case-Control	The Netherlands	ACR criteria	Ethnically matched healthy blood donors	91/154	GPA (all patients)	PR3-ANCA (all patients)	1.30 (0.89 – 1.91)
FCGR3B (NA1)	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	50/303	MPA (all patients)	MPO-ANCA (all patients)	0.65 (0.39 – 1.07)
	Dijstelbloem et al. 1999 ¹²	Case-Control	The Netherlands	ACR criteria	Ethnically matched healthy blood donors	91/154	GPA (all patients)	PR3-ANCA (all patients)	1.05 (0.72 – 1.53)
	Tse et al. 2000 ¹⁴	Case-Control	UK	CHCC criteria	Ethnically matched healthy subjects	101/100	GPA (45), MPA (52), EGPA (1), PAN (3)	PR3-ANCA (61), MPO-ANCA (30)	1.24 (0.8 – 1.87)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	50/303	MPA (all patients)	MPO-ANCA (all patients)	1.29 (0.82 – 2.03)
	Kelley et al. 2011 ¹⁰	Case-Control	USA	ACR and CHCC criteria	Geographically matched subjects with no (family) history of autoimmune disease	673/413	GPA (all patients)	NR	0.86 (0.72 – 1.03)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
GHSR rs509035 (A)	Wieczorek et al. 2010 ^{15**}	Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	454/820	GPA (all patients)	NR	1.22 (1.02 – 1.45)
		Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	179/516	GPA (all patients)	NR	0.94 (0.72 – 1.23)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	914/5259	GPA (565), MPA (262)	PR3-ANCA (478), MPO-ANCA (264)	1.00 (0.90 – 1.11)
GHSR rs519384 (A)	Wieczorek et al. 2010 ^{15**}	Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	449/813	GPA (all patients)	NR	1.17 (0.98 – 1.40)
		Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	179/515	GPA (all patients)	NR	1.01 (0.77 – 1.33)
GHSR rs572169 (A)	Wieczorek et al. 2010 ^{15**}	Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	442/812	GPA (all patients)	NR	1.21 (1.01 – 1.44)
		Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	178/492	GPA (all patients)	NR	0.96 (0.73 – 1.25)
HLA-AI	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	1.53 (0.81 – 2.87)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.84 (0.47 – 1.52)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.92 (0.42 – 2.03)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
HLA-A2	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.08 (0.87 – 1.35)
	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	0.78 (0.42 – 1.45)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.04 (0.62 – 1.73)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.90 (0.37 – 2.23)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.87 (0.48 – 1.58)
HLA-A3	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.98 (0.81 – 1.17)
	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	1.73 (0.90 – 3.31)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.51 (0.86 – 2.66)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.88 (0.89 – 3.98)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
<i>HLA-A9</i>	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.04 (0.84 – 1.31)
	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	1.09 (0.46 – 2.59)
	Katz et al. 1979 ²¹	Case-Control	USA	Clinical and histological criteria	Ethnically matched subjects	31/418	GPA (all patients)	NR	69.13 (3.28 – 456.19)
<i>HLA-A10</i>	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.79 (0.58 – 1.06)
	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	1.06 (0.32 – 3.48)
	Katz et al. 1979 ²¹	Case-Control	USA	Clinical and histological criteria	Ethnically matched subjects	31/418	GPA (all patients)	NR	69.13 (3.28 – 1456.19)
<i>HLA-A11</i>	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.61 (0.33 – 1.12)
	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/607	GPA (all patients)	NR	1.96 (0.81 – 4.72)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.68 (0.24 – 1.90)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.71 (0.17 – 3.03)
	Papasteriades et al. 1997 ²²	Case-Control	Greece	Histologically proven AAV	Geographically and ethnically matched healthy subjects	23/405	MPA (all patients)	NR	2.97 (1.19 – 7.41)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.43 (0.14 – 1.27)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.62 (0.39 – 0.99)
<i>HLA-A24</i>	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.91 (0.36 – 2.31)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.75 (0.34 – 1.65)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.81 (0.51 – 6.37)
<i>HLA-A25</i>	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.43 (0.33 – 6.17)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-A26	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	2.09 (0.61 – 7.16)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.68 (0.09 – 5.07)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	2.36 (1.00. – 5.60)
	Papasteriades et al. 1997 ²²	Case-Control	Greece	Histologically proven AAV	Geographically and ethnically matched healthy subjects	23/405	MPA (all patients)	NR	2.49 (1.01 – 6.18)
HLA-A28	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.39 (0.07 – 2.05)
	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	0.40 (0.02 – 6.68)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.32 (0.04 – 2.34)
HLA-A29	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.88 (0.57 – 1.38)
	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	2.11 (0.68 – 6.57)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.31 (0.04 – 2.25)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
<i>HLA-A30</i>	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.66 (0.11 – 4.04)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.68 (0.09 – 5.07)
<i>HLA-A31</i>	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	2.02 (0.18 – 22.63)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.07 (0.25 – 4.54)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.55 (0.46 – 5.24)
<i>HLA-A32</i>	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.33 (0.03 – 3.20)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	3.73 (1.24 – 11.22)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	2.07 (0.60 – 7.04)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.24 (0.03 – 2.21)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
<i>HLA-B5</i>	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	0.93 (0.28 – 3.02)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.56 (0.35 – 0.89)
<i>HLA-B7</i>	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	1.54 (0.77 – 3.08)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.74 (1.02 – 2.96)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.07 (0.52 – 2.22)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.00 (0.80 – 1.26)
<i>HLA-B8</i>	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	1.24 (0.60 – 2.56)
	Katz et al. 1979 ²¹	Case-Control	USA	Clinical and histological criteria	Ethnically matched subjects	31/418	GPA (all patients)	NR	2.30 (1.18 – 4.50)
	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	17/113	GPA (all patients)	NR	2.47 (1.01 – 6.05)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.03 (0.55 – 1.93)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	3.27 (1.02 – 10.50)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.11 (0.88 – 1.40)
HLA-B12	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	1.01 (0.47 – 2.15)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.96 (0.74 – 1.24)
HLA-B13	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	0.87 (0.12 – 6.50)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	2.09 (0.62 – 7.07)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.79 (0.21 – 3.03)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.63 (0.31 – 1.28)
HLA-B14	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/701	GPA (all patients)	NR	0.32 (0.02 – 5.24)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.51 (0.16 – 1.63)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.52 (0.25 – 9.26)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.16 (0.63 – 2.14)
HLA-B15	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.38 (0.55 – 3.43)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.98 (0.74 – 1.29)
HLA-B18	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/549	GPA (all patients)	NR	1.16 (0.35 – 3.85)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.53 (0.13 – 2.21)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.78 (0.296 – 2.072)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.75 (0.435 – 1.283)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-B27	Strimlan et al. 1978 ¹⁶	Case-Control	USA	Histologically proven AAV	Ethnically matched healthy blood donors	31/600	GPA (all patients)	NR	0.74 (0.18 – 3.093)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.60 (0.14 – 2.503)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.06 (0.00 – 1.102)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.77 (0.48 – 1.247)
HLA-B35	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	0.45 (0.11 – 1.86)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.80 (0.187 – 3.40)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.85 (0.28 – 2.62)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.81 (0.59 – 1.12)
HLA-B37	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.14 (0.01 – 2.72)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.07 (0.58 – 1.98)
HLA-B39	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.86 (0.11 – 6.51)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.33 (0.01 – 8.20)
HLA-B40	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.65 (0.52 – 5.23)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5872	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.90 (0.67 – 1.22)
HLA-B44	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.07 (0.58 – 2.00)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	2.50 (0.845 – 7.403)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	3.27 (1.02 – 10.50)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
<i>HLA-B49</i>	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	1.27 (0.30 – 5.44)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	2.02 (0.18 – 22.63)
<i>HLA-B51</i>	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.87 (0.64 – 5.49)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.61 (0.19 – 1.92)
<i>HLA-B55</i>	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	7.35 (2.33 – 23.14)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.07 (0.00 – 1.30)
<i>HLA-B57</i>	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	2.78 (1.05 – 7.32)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.00 (0.06 – 16.21)
<i>HLA-B60</i>	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	3.51 (0.99 – 12.36)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.19 (0.28 – 5.13)
HLA-B62	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/700	GPA (all patients)	NR	2.38 (0.70 – 8.12)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.71 (0.58 – 4.99)
HLA-Cw1	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.45 (0.58 – 3.58)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	52/51	GPA (all patients)	NR	0.98 (0.24 – 4.03)
HLA-Cw3	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.40 (0.65 – 3.01)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	52/51	GPA (all patients)	NR	1.32 (0.62 – 2.81)
HLA-Cw7	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.50 (0.12 – 2.10)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DPA1 rs9277341 (C)	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	52/51	GPA (all patients)	NR	1.10 (0.62 – 1.96)
	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	282/380	GPA (all patients)	ANCA+ (250), ANCA- (27)	0.38 (0.29 – 0.51)
	Xie et al. 2013 ^{25**}	Case-control (GWAS)	Canada, USA	ACR criteria	Geographically matched healthy subjects	459/1503	GPA (all patients)	c-ANCA (351)	0.30 (0.24 – 0.37)
		Case-control (GWAS)	USA	ACR criteria	Geographically matched healthy subjects	291/317	GPA (all patients)	c-ANCA (227)	0.43 (0.32 – 0.57)
HLA-DPBI*0101	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.20 (0.53 – 2.75)
HLA-DPBI*0201	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	0.17 (0.05 – 0.63)
	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	0.78 (0.49 – 1.23)
	Tsuchiya et al. 2006 ²⁸	Case-Control	Japan	Japanese 1998 criteria	Geographically matched healthy subjects	50/77	MPA (all patients)	MPO-ANCA (all patients)	0.44 (0.21 – 0.91)
	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	135/369	GPA (all patients)	ANCA+ (108), ANCA- (27)	1.38 (0.75 – 2.52)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.93 (0.57 – 1.51)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DPBI*0301	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.27 (0.56 – 2.89)
	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	0.02 (0.00 – 0.15)
	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	135/369	GPA (all patients)	ANCA+ (108), ANCA- (27)	0.28 (0.14 – 0.55)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.65 (0.38 – 1.11)
	Arning et al. 2011 ^{30**}	Case-Control	Germany	CHCC criteria	Geographically and ethnically matched healthy blood donors	482/356	GPA (389), EGPA (56), MPA (37)	NR	0.30 (0.21 – 0.44)
		Case-Control	UK	CHCC criteria	Geographically and ethnically matched healthy blood donors	193/104	GPA (102), MPA (82), EGPA (9)	NR	0.35 (0.16 – 0.77)
HLA-DPBI*0401	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.42 (0.84 – 2.38)
	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	3.91 (2.62 – 5.84)
	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	135/369	GPA (all patients)	ANCA+ (108), ANCA- (27)	2.15 (1.61 – 2.86)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	1.06 (0.78 – 1.45)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Arning et al. 2011 ^{30**}	Case-Control	Germany	CHCC criteria	Geographically and ethnically matched healthy blood donors	482/356	GPA (389), EGPA (56), MPA (37)	NR	2.34 (1.92 – 2.85)
		Case-Control	UK	CHCC criteria	Geographically and ethnically matched healthy blood donors	193/104	GPA (102), MPA (82), EGPA (9)	NR	2.02 (1.44 – 2.85)
HLA-DPBI*0402	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.82 (0.38 – 1.78)
	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	1.11 (0.65 – 1.92)
	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	135/369	GPA (all patients)	ANCA+ (108), ANCA- (27)	1.14 (0.78 – 1.68)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	1.15 (0.75 – 1.77)
HLA-DPBI*0501	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.34 (0.26 – 7.02)
	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	0.20 (0.01 – 4.93)
HLA-DPBI*0601	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	3.79 (0.19 – 74.15)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DPB1*0901	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	0.60 (0.08 – 4.29)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.52 (0.15 – 1.84)
HLA-DPB2 rs3130215 (A)	Jagiello et al. 2004 ²⁷	Case-Control	Germany	ACR and CHCC criteria, biopsy	Geographically matched subjects	148/89	GPA (all patients)	PR3-ANCA (all patients)	1.81 (0.07 – 44.73)
	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	282/380	GPA (all patients)	ANCA+ (250), ANCA- (27)	2.35 (1.88 – 2.94)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5365	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	0.88 (0.79 – 0.99)
HLA-DQB1*02	Xie et al. 2013 ²⁵	Case-control (GWAS)	Canada, USA	ACR criteria	Geographically matched healthy subjects	459/1503	GPA (all patients)	c-ANCA (351)	2.44 (2.10 – 2.84)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	0.98 (0.45 – 2.13)
HLA-DQB1*0302	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/50	GPA (all patients)	NR	0.85 (0.41 – 1.77)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.07 (0.53 – 2.20)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
HLA-DQB1*0303	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	0.94 (0.36 – 2.49)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.84 (0.27 – 2.65)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	2.97 (0.72 – 12.23)
HLA-DQB1*04	Tsuchiya et al. 2006 ²⁸	Case-Control	Japan	Japanese 1998 criteria	Geographically matched healthy subjects	50/77	MPA (all patients)	MPO-ANCA (all patients)	2.11 (1.14 – 3.90)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	1.74 (0.40 – 7.50)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/50	GPA (all patients)	NR	1.49 (0.24 – 9.08)
HLA-DQB1*0501	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.77 (0.91 – 3.42)
HLA-DQB1*0602	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	0.77 (0.32 – 1.88)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.64 (0.29 – 1.42)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	12.86 (2.65 – 62.31)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
<i>HLA-DQ7</i>	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/50	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.21 (0.70 – 2.10)
	Papasteriades et al. 1997 ²²	Case-Control	Greece	Histologically proven AAV	Geographically and ethnically matched healthy subjects	23/405	MPA (all patients)	NR	0.66 (0.34 – 1.30)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	0.43 (0.16 – 1.16)
HLA-DR1	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	2.17 (0.90 – 5.23)
	Papiha et al. 1992 ³²	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	27/105	GPA (all patients)	NR	4.37 (2.01 – 9.48)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.89 (0.44 – 1.82)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	1.12 (0.48 – 2.64)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	0.68 (0.67 – 1.75)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.56 (0.23 – 1.35)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.71 (0.43 – 1.15)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5442	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.67 (0.49 – 0.92)
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	0.53 (0.34 – 0.81)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.79 (0.28 – 2.19)
HLA-DR2	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	1.91 (0.97 – 3.75)
	Papiha et al. 1992 ³²	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	27/105	GPA (all patients)	NR	1.20 (0.56 – 2.54)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.19 (0.66 – 2.13)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DR3	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.33 (0.08 – 1.38)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5442	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.97 (0.77 – 1.22)
	Elkon et al. 1983 ²³	Case-Control	UK	Clinical, and histological, criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	1.01 (0.52 – 1.99)
	Papiha et al. 1992 ³²	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	27/105	GPA (all patients)	NR	1.41 (0.59 – 3.36)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.75 (0.43 – 1.30)
	Papasteriades et al. 1997 ²²	Case-Control	Greece	Histologically proven AAV	Geographically and ethnically matched healthy subjects	23/405	MPA (all patients)	NR	0.16 (0.02 – 1.18)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	2.54 (1.00 – 6.46)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.55 (0.53 – 4.52)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.66 (0.39 – 1.11)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DR4	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5442	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.07 (0.84 – 1.35)
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	1.30 (0.86 – 1.95)
	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	1.00 (0.52 – 1.92)
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/300	GPA (all patients)	NR	0.96 (0.50 – 1.83)
	Papiha et al. 1992 ³²	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	27/105	GPA (all patients)	NR	0.81 (0.32 – 2.07)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	1.24 (0.74 – 2.07)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	0.72 (0.27 – 1.88)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	1.25 (0.54 – 2.90)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.57 (0.61 – 4.01)
	Vaglio et al. 2007 ³⁵	Case-Control	Italy	ACR and CHCC criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	48/350	EGPA (all patients)	MPO-ANCA (18), ANCA negative (26), undetermined (4)	1.73 (0.84 – 3.57)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/341	EGPA (all patients)	NR	1.87 (1.23 – 2.82)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5442	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	1.53 (1.25 – 1.87)
	Cao et al. 2011 ^{33**}	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	0.73 (0.51 – 1.05)
		Case-Control	USA (all African Americans)	Histologically proven AAV	USA African Americans- Bethesda database	16/112	NR	PR3-ANCA (9), MPO-ANCA (4), p-ANCA (2), ANCA negative (1)	0.62 (0.08 – 5.01)
HLA-DR5	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	0.72 (0.28 – 1.85)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DR6	Papiha et al. 1992 ³²	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	27/105	GPA (all patients)	NR	0.18 (0.02 – 1.37)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.95 (0.45 – 2.01)
	Papasteriades et al. 1997 ²²	Case-Control	Greece	Histologically proven AAV	Geographically and ethnically matched healthy subjects	23/405	MPA (all patients)	NR	1.59 (0.80 – 3.15)
	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5442	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.80 (0.58 – 1.09)
	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	0.16 (0.04 – 0.70)
	Papiha et al. 1992 ³²	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	27/105	GPA (all patients)	NR	0.11 (0.01 – 1.83)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.60 (0.27 – 1.31)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.63 (0.56 – 4.77)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DR7	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5442	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.44 (0.32 – 0.59)
	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	0.512 (0.22 – 1.22)
	Papiha et al. 1992 ³²	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	27/105	GPA (all patients)	NR	0.64 (0.23 – 1.73)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	0.99 (0.40 – 2.48)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.77 (0.34 – 1.75)
	Vaglio et al. 2007 ³⁵	Case-Control	Italy	ACR and CHCC criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	48/350	EGPA (all patients)	MPO-ANCA (18), ANCA negative (26), undetermined (4)	2.42 (1.47 – 4.00)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/341	EGPA (all patients)	NR	1.58 (1.01 – 2.47)
HLA-DR8	Stassen et al. 2009 ¹⁹	Case-Control	The Netherlands	CHCC criteria	Geographically matched healthy blood donors	304/5442	GPA (241), MPA (30), EGPA (12), RVL (21)	PR3-ANCA (218), MPO-ANCA (64), other (4), ANCA negative (18)	0.96 (0.72 – 1.27)
	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	0.52 (0.22 – 1.22)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Murty et al. 1991 ¹⁷	Case-Control	Ireland, UK	Histologically proven AAV	Geographically matched healthy subjects	41/300	GPA (all patients)	NR	1.05 (0.21 – 5.14)
	Zhang et al. 1995 ²⁶	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	2.21 (0.67 – 7.32)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	1.63 (0.66 – 4.05)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	1.23 (0.31 – 4.91)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.00 (0.12 – 5.08)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	2.03 (1.01 – 4.05)
	Stassen et al. 2009 ¹⁹	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.95 (0.59 – 1.54)
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	0.76 (0.37 – 1.55)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
HLA-DR9	Elkon et al. 1983 ²³	Case-Control	UK	Clinical and histological criteria	Geographically matched subjects	46/113	GPA (17), EGPA (14), PAN (15)	NR	0.49 (0.02 – 10.21)
	Nakamaru et al. 1996 ²⁰	Case-Control	Japan	Clinical, histological, serological criteria	Geographically matched healthy subjects	16/472	GPA (all patients)	c-ANCA (all patients)	3.03 (1.40 – 6.56)
	Fujii et al. 2000 ³⁶	Case-Control	Japan	CHCC criteria	Geographically matched healthy subjects	12/472	NR	MPO-ANCA (all patients)	2.75 (1.12 – 6.76)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	0.94 (0.04 – 23.32)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.66 (0.11 – 4.04)
	Vaglio et al. 2007 ³⁵	Case-Control	Italy	ACR and CHCC criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	48/350	EGPA (all patients)	MPO-ANCA (18), ANCA negative (26), undetermined (4)	1.83 (0.20 – 16.56)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.80 (0.17 – 3.74)
	Stassen et al. 2009 ¹⁹	Case-Control	UK	CHCC criteria	Geographically matched healthy subjects	94/90	GPA (56), MPA (31), RVL (7)	PR3-ANCA (36), MPO-ANCA (19), PR3- and MPO-ANCA positive (3)	0.35 (0.11 – 1.09)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	0.75 (0.208 – 2.72)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.68 (0.43 – 1.06)
	Tsuchiya et al. 2013 ³⁷	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	116/265	MPA (96)	MPO-ANCA (all patients)	1.74 (1.18 – 2.57)
HLA-DRB1*0401	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	2.10 (0.52 – 8.50)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.58 (0.18 – 1.90)
HLA-DRB1*0403	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.95 (0.27 – 3.40)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.16 (0.02 – 1.30)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
<i>HLA-DRB1*0405</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.61 (0.30 – 1.22)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	1.13 (0.52 – 2.49)
<i>HLA-DRB1*0406</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.65 (0.19 – 2.22)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	1.84 (0.73 – 4.63)
<i>HLA-DRB1*0407</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	2.82 (0.78 – 10.14)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.44 (0.02 – 10.77)
<i>HLA-DRB1*0410</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	1.67 (0.32 – 8.69)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.44 (0.02 – 10.77)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
<i>HLA-DRB1*0802</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	1.16 (0.42 – 3.18)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.26 (0.01 – 5.47)
<i>HLA-DRB1*0803</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	1.51 (0.78 – 2.93)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	1.19 (0.61 – 2.33)
<i>HLA-DRB1*10</i>	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	1.43 (0.13 – 16.03)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	5.10 (0.24 – 107.55)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.40 (0.02 – 7.44)
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	0.75 (0.21 – 2.72)
<i>HLA-DRB1*11</i>	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	0.723 (0.26 – 2.04)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
<i>HLA-DRB1*1101</i>	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.28 (0.48 – 3.38)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.88 (0.53 – 1.48)
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	1.09 (0.66 – 1.80)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	1.75 (1.02 – 3.00)
	Tsuchiya et al. 2013 ³⁷	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	116/265	MPA (96)	MPO-ANCA (all patients)	2.79 (0.84 – 9.23)
<i>HLA-DRB1*12</i>	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	2.97 (0.721 – 2.23)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	6.31 (0.75 – 53.40)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/369	EGPA (all patients)	NR	0.57 (0.17 – 1.93)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	0.59 (0.17 – 2.06)
HLA-DRB1*1201	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.21 (0.03 – 1.60)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.46 (0.16 – 1.29)
HLA-DRB1*1202	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.37 (0.05 – 2.90)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	1.70 (0.93 – 3.13)
HLA-DRB1*13	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	0.56 (0.20 – 1.53)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.65 (0.31 – 1.38)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DRB1*1302	Vaglio et al. 2007 ³⁵	Case-Control	Italy	ACR and CHCC criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	48/350	EGPA (all patients)	MPO-ANCA (18), ANCA negative (26), undetermined (4)	0.23 (0.07 – 0.73)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/341	EGPA (all patients)	NR	0.50 (0.28 – 0.89)
	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.54 (0.24 – 1.23)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.52 (0.16 – 1.67)
HLA-DRB1*14	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	1.07 (0.27 – 4.16)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	2.02 (0.18 – 22.63)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/341	EGPA (all patients)	NR	1.83 (0.72 – 4.65)
	Cao et al. 2011 ³³	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	2.82 (1.05 – 7.59)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
<i>HLA-DRB1*1403</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	1.25 (0.34 – 4.60)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	1.32 (0.19 – 9.41)
<i>HLA-DRB1*1405</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.11 (0.01 – 1.91)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.96 (0.44 – 2.13)
<i>HLA-DRB1*15</i>	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	0.79 (0.34 – 1.83)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.13 (0.57 – 2.26)
	Cao et al. 2011 ^{33**}	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	2.72 (1.84 – 4.03)
		Case-Control	USA (all African Americans)	Histologically proven AAV	USA African Americans- Bethesda database	16/112	NR	PR3-ANCA (9), MPO-ANCA (4), p-ANCA (2), ANCA negative (1)	2.08 (0.86 – 5.03)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
<i>HLA-DRB1*1501</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	1.62 (0.79 – 3.35)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	1.69 (1.16 – 2.46)
<i>HLA-DRB1*1502</i>	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.67 (0.32 – 1.39)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.35 (0.10 – 1.27)
<i>HLA-DRB1*16</i>	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3 (all patients)	0.40 (0.02 – 7.80)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.14 (0.01 – 2.72)
	Cao et al. 2011 ^{33**}	Case-Control	USA (96 Caucasians and 41 African Americans)	Histologically proven AAV	Ethnically matched community-based control frequencies (Healthy Organ Donor- North Carolina Services)	137/379	NR	PR3-ANCA (90), MPO-ANCA (47)	1.39 (0.34 – 5.59)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
		Case-Control	USA (all African Americans)	Histologically proven AAV	USA African Americans-Bethesda database	16/112	NR	PR3-ANCA (9), MPO-ANCA (4), p-ANCA (2), ANCA negative (1)	2.42 (0.47 – 12.55)
HLA-DRB1*1602	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	64/265	GPA (3), MPA (50), EGPA (8), PAN (3)	MPO-ANCA (all patients)	0.24 (0.01 – 4.171)
	Luo et al. 2011 ³⁴	Case-Control	China	EMA algorithm	Ethnically matched healthy blood donors	152/200	GPA (45), MPA (107)	PR3-ANCA (19), MPO-ANCA (130), PR3- and MPO-ANCA positive (3)	0.12 (0.01 – 2.14)
HLA-DRB3	Spencer et al. 1992 ³⁸	Case-Control	UK	Clinical criteria	Geographically and ethnically matched subjects	59/1103	GPA (34), MPA (25)	c-ANCA (47), p-ANCA (10), ANCA negative (2)	0.29 (0.11 – 0.79)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.41 (0.76 – 2.60)
	Vaglio et al. 2007 ³⁵	Case-Control	Italy	ACR and CHCC criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	48/350	EGPA (all patients)	MPO-ANCA (18), ANCA negative (26), undetermined (4)	0.54 (0.35 – 0.84)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/341	EGPA (all patients)	NR	0.61 (0.44 – 0.86)
HLA-DRB4	Spencer et al. 1992 ³⁸	Case-Control	UK	Clinical criteria	Geographically and ethnically matched subjects	59/1103	GPA (34), MPA (25)	c-ANCA (47), p-ANCA (10), ANCA negative (2)	1.38 (0.89 – 2.13)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
HLA-DRB5	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	0.89 (0.46 – 1.72)
	Vaglio et al. 2007 ³⁵	Case-Control	Italy	ACR and CHCC criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	48/350	EGPA (all patients)	MPO-ANCA (18), ANCA negative (26), undetermined (4)	2.49 (1.58 – 3.90)
	Wieczorek et al. 2008 ²⁹	Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	102/341	EGPA (all patients)	NR	1.87 (1.34 – 2.61)
	Spencer et al. 1992 ³⁸	Case-Control	UK	Clinical criteria	Geographically and ethnically matched subjects	59/1103	GPA (34), MPA (25)	c-ANCA (47), p-ANCA (10), ANCA negative (2)	1.35 (0.69 – 2.63)
	Von Vietinghoff et al. 2006 ¹⁸	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	51/51	GPA (all patients)	NR	1.07 (0.82 – 2.18)
HSD17B8 rs421446 (C)	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	282/369	GPA (all patients)	ANCA+ (250), ANCA- (27)	0.43 (0.32 – 0.57)
IL-1β (A2)	Xie et al. 2013 ²⁵	Case-control (GWAS)	Canada, USA	ACR criteria	Geographically matched healthy subjects	459/1503	GPA (all patients)	c-ANCA (351)	0.39 (0.32 – 0.48)
	Huang et al. 2000 ⁴	Case-Control	Sweden	ACR criteria	Geographically and ethnically matched healthy subjects	32/109	GPA (all patients)	PR3-ANCA (29)	1.21 (0.55 – 2.63)
	Borgmann et al. 2003 ³⁹	Case-Control	Germany	CHCC criteria	Geographically matched healthy, unrelated subjects	109/196	NR	PR3-ANCA (79), MPO-ANCA (30)	0.89 (0.61 – 1.29)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Zhou et al. 2004 ⁶	Case-Control	USA	ACR criteria	Geographically and ethnically matched healthy, unrelated subjects	117/123	GPA (all patients)	PR3-ANCA (82), MPO-ANCA (5), PR3- and MPO-ANCA positive (2), ANCA negative (25)	1.16 (0.72 – 1.85)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	914/5259	GPA (565), MPA (262)	PR3-ANCA (478), MPO-ANCA (264)	1.00 (0.89 – 1.12)
ILIRN*1	Borgmann et al. 2003 ³⁹	Case-Control	Germany	CHCC criteria	Geographically matched healthy, unrelated subjects	109/234	NR	PR3-ANCA (79), MPO-ANCA (30)	1.12 (0.79 – 1.59)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	1.00 (0.69 – 1.44)
ILIRN*2	Borgmann et al. 2003 ³⁹	Case-Control	Germany	CHCC criteria	Geographically matched healthy, unrelated subjects	109/234	NR	PR3-ANCA (79), MPO-ANCA (30)	1.00 (0.69 – 1.43)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	1.01 (0.69 – 1.48)
ILIRN*3	Borgmann et al. 2003 ³⁹	Case-Control	Germany	CHCC criteria	Geographically matched healthy, unrelated subjects	109/234	NR	PR3-ANCA (79), MPO-ANCA (30)	0.30 (0.07 – 1.33)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	1.06 (0.35 – 3.20)
ILIRN*4	Borgmann et al. 2003 ³⁹	Case-Control	Germany	CHCC criteria	Geographically matched healthy, unrelated subjects	109/234	NR	PR3-ANCA (79), MPO-ANCA (30)	0.71 (0.03 – 17.58)

Variants	Article	Study details		Definitions		Cases / Controls	Participants (n)		OR (95% CI)
		Design	Setting	Cases	Controls		Diagnoses	ANCA serotype	Allele level
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.95 (0.09 – 10.56)
IL1RN*5	Borgmann et al. 2003 ³⁹	Case-Control	Germany	CHCC criteria	Geographically matched healthy, unrelated subjects	109/234	NR	PR3-ANCA (79), MPO-ANCA (30)	1.07 (0.10 – 11.91)
	Persson et al. 2013 ⁷	Case-Control	Sweden	ACR and CHCC criteria, EMA algorithm	Blood donors	105/200	GPA (61), MPA (44)	PR3-ANCA (62), MPO-ANCA (43)	0.63 (0.03 – 15.60)
IL-6 rs1800795 (C)	Zhou et al. 2004 ⁶	Case-Control	USA	ACR criteria	Geographically and ethnically matched healthy, unrelated subjects	117/123	GPA (all patients)	PR3-ANCA (82), MPO-ANCA (5), PR3- and MPO-ANCA positive (2), ANCA negative (25)	1.00 (0.70 – 1.44)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	1.37 (0.76 – 2.48)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	914/5259	GPA (565), MPA (262)	PR3-ANCA (478), MPO-ANCA (264)	1.04 (0.94 – 1.15)
	Husmann et al. 2014 ⁴⁰	Case-Control	Germany	EMA algorithm	Geographically matched healthy blood donors	863/1344	GPA (646), MPA (53), EGPA (164)	NR	0.95 (0.85 – 1.08)
IL-10 rs1800872 (A)	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	1.10 (0.55 – 2.12)
	Wieczorek et al. 2008 ⁴¹	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	506/507	GPA (403), EGPA (103)	ANCA+ (389), ANCA- (110)	1.00 (0.81 – 1.23)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
<i>IL-10</i> rs1800896 (G)	Murakozy et al. 2001 ⁴²	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	39/72	GPA (all patients)	NR	0.59 (0.34 – 1.03)
	Bartfai et al. 2003 ⁴³	Case-Control	Caucasian patients	ACR and CHCC criteria	Ethnically matched blood donors	161/153	GPA (125), MPA (36)	NR	0.74 (0.54 – 1.02)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	1.18 (0.67 – 2.10)
	Wieczorek et al. 2008 ⁴¹	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	506/507	GPA (403), EGPA (103)	ANCA+ (389), ANCA- (110)	0.88 (0.74 – 1.05)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5360	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.04 (0.93 – 1.17)
<i>IRF5</i> rs10954213 (G)	Wieczorek et al. 2010 ⁴⁴	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	627/902	GPA (all patients)	NR	0.31 (0.26 – 0.37)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5365	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.04 (0.93 – 1.17)
	Kawasaki et al. 2013 ⁴⁵	Case-Control	Japan	EMA algorithm	Geographically matched healthy, unrelated subjects	232/710	GPA (28), MPA (177), EGPA (15), unclassified (12)	MPO (all patients)	1.28 (1.04 – 1.58)
<i>LEPR</i> rs8179183 (C)	Wieczorek et al. 2010 ^{15***}	Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	456/818	GPA (all patients)	NR	0.72 (0.58 – 0.90)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
MPO rs2333227 (A)		Case-Control	Germany	CHCC criteria	Geographically matched healthy subjects	226/508	GPA (all patients)	NR	0.71 (0.52 – 0.97)
		Case-Control	Germany	ACR criteria	Geographically matched healthy subjects	196/1327	EGPA (all patients)	NR	1.41 (1.10 – 1.81)
	Reynolds et al. 2002 ⁴⁶	Case-Control	The Netherlands	CHCC criteria	Ethnically matched healthy subjects	142/192	GPA (96), MPA (26), EGPA (8), iRPGN (12)	PR3-ANCA (92), MPO-ANCA (50)	1.07 (0.70 – 1.63)
	Fiebeler et al. 2004 ⁴⁷	Case-Control	Germany	Clinical criteria	Geographically matched healthy subjects	119/270	GPA (63), MPA (56)	PR3-ANCA (71), MPO-ANCA (48)	0.90 (0.62 – 1.32)
PCDI rs1156882 (A)	Rajp et al. 2007 ⁴⁸	Case-Control	UK	CHCC criteria and histological criteria	Ethnically matched healthy subjects	134/150	GPA (69), MPA (65)	PR3-ANCA (91), MPO-ANCA (43)	0.92 (0.61 – 1.39)
	Slot et al. 2008 ⁸	Case-Control	The Netherlands	CHCC criteria	Geographically and ethnically matched healthy subjects	102/204	GPA (50), MPA (24), EGPA (7), RLV (21)	PR3-ANCA (49), MPO-ANCA (34), PR3- and MPO-ANCA positive (2), ANCA negative (17)	0.94 (0.52 – 1.70)
	Sakthivel et al. 2009 ⁴⁹	Case-Control	Sweden	Clinical criteria	Geographically and ethnically matched blood donors	66/275	GPA (all patients)	NR	0.78 (0.37 – 1.64)
PTPN22 rs2476601 (A)	Jagiello et al. 2005 ⁵⁰	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy subjects	199/399	GPA (all patients)	c-ANCA+ (168), p-ANCA+ (1), ANCA negative (30)	1.75 (1.23 – 2.49)
	Chung et al. 2012 ^{2**}	Case-Control	USA	ACR criteria	Geographically matched subjects with no (family) history of autoimmune disease	424/469	GPA (all patients)	PR3-ANCA (339), MPO-ANCA (44), ANCA negative (39)	1.25 (0.91 – 1.71)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
RING1/RXR B rs213213 (A)		Case-Control	Canada	ACR criteria	Geographically matched subjects with no history of autoimmune disease	456/1500	GPA (all patients)	NR	1.40 (1.11 – 1.78)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5365	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.35 (1.14 – 1.60)
	Martorana et al. 2012 ⁵¹	Case-Control	Italy	ACR and CHCC criteria	Geographically matched healthy subjects with no history of autoimmune disease	344/945	GPA (143), EGPA (99), MPA (102)	c-ANCA (126), p-ANCA (163), ANCA negative (39)	1.40 (0.97 – 2.04)
	Heckmann et al. 2008 ²⁴	Case-Control	Germany	ACR criteria	Geographically matched healthy blood donors	279/369	GPA (all patients)	ANCA+ (250), ANCA- (27)	2.13 (1.70 – 2.67)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5366	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.55 (1.38 – 1.74)
	Xie et al. 2013 ²⁵	Case-control (GWAS)	Canada, USA	ACR criteria	Geographically matched healthy subjects	459/1503	GPA (all patients)	c-ANCA (351)	1.83 (1.57 – 2.13)
RXRB rs6531 (C)	Szyld et al. 2006 ⁵²	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy subjects	187/201	GPA (all patients)	ANCA+ (151), ANCA- (36)	0.60 (0.45 – 0.80)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
RXRB rs9277935 (T)	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	911/5251	GPA (565), MPA (262)	PR3-ANCA (478), MPO-ANCA (264)	1.79 (1.61 – 1.98)
	Xie et al. 2013 ²⁵	Case-control (GWAS)	Canada, USA	ACR criteria	Geographically matched healthy subjects	459/1503	GPA (all patients)	c-ANCA (351)	1.81 (1.55 – 2.11)
	Wieczorek et al. 2009 ⁵³	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	282/380	GPA (all patients)	NR	0.39 (0.29 – 0.54)
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5350	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	0.51 (0.43 – 0.61)
	Xie et al. 2013 ²⁵	Case-control (GWAS)	Canada, USA	ACR criteria	Geographically matched healthy subjects	459/1503	GPA (all patients)	c-ANCA (351)	0.34 (0.27 – 0.44)
SERPINA1 S allele	Lhotta et al. 1994 ⁵⁴	Case-Control	Austria	ACR	Geographically matched healthy subjects	32/868	GPA (29), MPA (2), iRPGN (1)	c-ANCA (all patients)	0.69 (0.09 – 5.11)
	Griffith et al. 1996 ⁵⁵	Case-Control	UK	CHCC criteria	Geographically and ethnically matched unrelated subjects	102/2310	GPA (51), MPA (29), EGPA (9), PAN (2), iRPGN (11)	c-ANCA (70), p-ANCA (32)	1.42 (0.79 – 2.52)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
SERPINA1 Z allele	Mahr et al. 2010 ⁵⁶	Case-Control	USA	ACR criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	433/421	GPA (all patients)	PR3-ANCA (339), MPO-ANCA (44), ANCA negative (39)	1.68 (1.08 – 2.63)
	Morris et al. 2011 ⁵⁷	Case-Control	Germany (531), France (81), UK (244)	CHCC criteria	Geographically and ethnically matched healthy subjects with no (family) history of autoimmune disease	856/1505	GPA (723), MPA (133)	c-ANCA (605), p-ANCA (150), ANCA negative (54)	1.11 (0.81 – 1.51)
	Chorostowska-Wynimko et al. 2013 ⁵⁸	Case-Control	Poland	Clinical, histological, and serological criteria	Geographically matched neonates born alive	51/658	GPA (all patients)	c-ANCA (43), p-ANCA (2), ANCA negative (4)	2.61 (0.56 – 12.08)
	Lhotta et al. 1994 ⁵⁴	Case-Control	Austria	ACR criteria	Geographically matched healthy subjects	32/868	GPA (29), MPA (2), iRPGN (1)	c-ANCA (all patients)	8.76 (3.63 – 21.17)
	Griffith et al. 1996 ⁵⁵	Case-Control	UK	CHCC criteria	Geographically and ethnically matched unrelated subjects	102/2310	GPA (51), MPA (29), EGPA (9), PAN (2), iRPGN (11)	c-ANCA (70), p-ANCA (32)	2.20 (1.05 – 4.62)
	Callea et al. 1997 ⁵⁹	Case-Control	Italy	CHCC criteria	Healthy blood donors	84/200	GPA (33), MPA (28), iRPGN (23)	c-ANCA (38), p-ANCA (46)	4.90 (1.21 – 19.83)
	Borgmann et al. 2001 ⁶⁰	Case-Control	Germany	ACR and CHCC criteria	Geographically and ethnically matched healthy, unrelated subjects	97/752	GPA (all patients)	c-ANCA (all patients)	3.36 (1.45 – 7.79)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Mahr et al. 2010 ⁵⁶	Case-Control	USA	ACR criteria	Geographically matched healthy subjects with no (family) history of autoimmune disease	433/421	GPA (all patients)	PR3-ANCA (339), MPO-ANCA (44), ANCA negative (39)	1.99 (1.12 – 3.52)
	Morris et al. 2011 ⁵⁷	Case-Control	Germany (531), France (81), UK (244)	CHCC criteria	Geographically and ethnically matched healthy subjects with no (family) history of autoimmune disease	856/1505	GPA (723), MPA (133)	c-ANCA (605), p-ANCA (150), ANCA negative (54)	2.25 (1.60 – 3.18)
	Previously unpublished Lyons et al. 2012 GWAS data ^{3**}	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	562/805	GPA (391), MPA (143)	PR3-ANCA (322), MPO-ANCA (166)	2.59 (1.66 – 4.02)
		Case-control (GWAS)	Europe	EMA algorithm, supported by either serology or histology	Geographically matched subjects	1445/1062	NR	NR	4.19 (2.62 – 6.69)
	Chorostowska-Wynimko et al. 2013 ⁵⁸	Case-Control	Poland	Clinical, histological, serological criteria	Geographically matched neonates born alive	51/658	GPA (all patients)	c-ANCA (43), p-ANCA (2), ANCA negative (4)	2.19 (0.63 – 7.55)
STAT4 rs7574865 (T)	Wieczorek et al. 2010 ⁴⁴	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	612/880	GPA (all patients)	NR	1.01 (0.85 – 1.20)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
TGF-β_1 rs1800471 (C)	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5366	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.18 (1.04 – 1.35)
	Kawasaki et al. 2013 ⁴⁵	Case-Control	Japan	EMA algorithm	Geographically matched healthy, unrelated subjects	232/710	GPA (28), MPA (177), EGPA (15), unclassified (12)	MPO (all patients)	1.10 (0.89 – 1.37)
	Murakozy et al. 2001 ⁴²	Case-Control	Germany	ACR and CHCC criteria	Geographically matched healthy blood donors	39/72	GPA (all patients)	NR	2.20 (0.89 – 5.44)
	Bartfai et al. 2003 ⁴³	Case-Control	Caucasian patients	ACR and CHCC criteria	Ethnically matched blood donors	161/96	GPA (125), MPA (36)	NR	1.06 (0.52 – 2.14)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	1.86 (0.73 – 4.71)
TNFα rs1800629 (A)	Mascher et al. 1997 ⁶¹	Case-Control	Germany	ACR and CHCC criteria	Healthy blood donors	35/111	GPA (all patients)	c-ANCA (32), p-ANCA (1), ANCA negative (1)	1.54 (0.77 – 3.10)
	Zhou et al. 2004 ⁶	Case-Control	USA	ACR criteria	Geographically and ethnically matched healthy, unrelated subjects	117/123	GPA (all patients)	PR3-ANCA (82), MPO-ANCA (5), PR3- and MPO-ANCA positive (2), ANCA negative (25)	0.88 (0.52 – 1.50)
	Spriewald et al. 2005 ³¹	Case-Control	Germany	ACR and CHCC criteria	Ethnically matched healthy subjects	32/91	GPA (all patients)	PR3-ANCA (all patients)	2.22 (0.93 – 5.29)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
	Previously unpublished Lyons et al. 2012 GWAS data ³	Case-control (GWAS)	UK	EMA algorithm, supported by either serology or histology	Wellcome Trust Case Control Consortium (UK)	676/5366	GPA (394), MPA (156)	PR3-ANCA (326), MPO-ANCA (167)	1.06 (0.92 – 1.23)
<i>TNFR11</i> 196R	Tsuchiya et al. 2003 ⁵	Case-Control	Japan	CHCC and Japanese 1998 criteria	Geographically matched healthy subjects	50/262	MPA (all patients)	MPO-ANCA (all patients)	0.67 (0.31 – 1.45)
	Zhou et al. 2004 ⁶	Case-Control	USA	ACR criteria	Geographically and ethnically matched healthy, unrelated subjects	117/123	GPA (all patients)	PR3-ANCA (82), MPO-ANCA (5), PR3- and MPO-ANCA positive (2), ANCA negative (25)	1.05 (0.70 – 1.57)
<i>TLR9</i> rs352162 (T)	Husmann et al. 2014 ^{40**}	Case-Control	Germany	EMA algorithm	Geographically matched healthy blood donors	863/1344	GPA (646), MPA (53), EGPA (164)	NR	1.89 (1.67 – 2.14)
			The Netherlands, UK	EMA algorithm	Geographically and ethnically matched healthy subjects	426/554	GPA (273), MPA (100), EGPA (53)	NR	1.07 (0.90 – 1.28)
<i>TLR9</i> rs352140 (T)	Husmann et al. 2014 ^{40**}	Case-Control	Germany	EMA algorithm	Geographically matched healthy blood donors	863/1344	GPA (646), MPA (53), EGPA (164)	NR	1.16 (1.03 – 1.31)
			The Netherlands, UK	EMA algorithm	Geographically and ethnically matched healthy subjects	426/554	GPA (273), MPA (100), EGPA (53)	NR	1.06 (0.89 – 1.27)
<i>TLR9</i> rs352139 (T)	Husmann et al. 2014 ^{40**}	Case-Control	Germany	EMA algorithm	Geographically matched healthy blood donors	863/1344	GPA (646), MPA (53), EGPA (164)	NR	1.12 (0.99 – 1.27)

Variants	Article	Study details		Definitions		Participants (n)			OR (95% CI)
		Design	Setting	Cases	Controls	Cases / Controls	Diagnoses	ANCA serotype	Allele level
TLR9 rs5743836 (G)	Husmann et al. 2014 ^{40**}	Case-Control	The Netherlands, UK	EMA algorithm	Geographically and ethnically matched healthy subjects	426/554	GPA (273), MPA (100), EGPA (53)	NR	1.08 (0.91 – 1.30)
			Germany	EMA algorithm	Geographically matched healthy blood donors	863/1344	GPA (646), MPA (53), EGPA (164)	NR	0.82 (0.69 – 0.98)
			The Netherlands, UK	EMA algorithm	Geographically and ethnically matched healthy subjects	426/554	GPA (273), MPA (100), EGPA (53)	NR	1.22 (0.94 – 1.58)

ACR, American College of Rheumatology; ANCA, anti-neutrophil cytoplasm antibody; AAV, ANCA-associated vasculitis; c-ANCA, cytoplasmic ANCA; CHCC, Chapel Hill Consensus Conference; EGPA, eosinophilic granulomatosis with polyangiitis; EMA, European Medicines Agency; GPA, granulomatosis with polyangiitis; GWAS, genome-wide association study; iRPGN, idiopathic rapidly progressive glomerulonephritis; MPA, microscopic polyangiitis; MPO-ANCA, myeloperoxidase ANCA; NR, not reported; PAN, polyarteritis nodosa; p-ANCA, perinuclear ANCA; NR, not reported; RLV, renal limited vasculitis; PR3-ANCA, proteinase 3 ANCA; UK, United Kingdom; USA, United States of America. **Two cohorts described in the same publication; ***Three cohorts described in the same publication.

Supplementary Table 3. Genetic variants not associated with AAV after meta-analysis

Variant by gene (minor allele)	Publica- tions (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta- analysis	I² (%)	P value for heterogeneity	P value for funnel plot asymmetry
<i>CTLA-4</i> (AT) ₁₀₂	3	186/420	1.20 (0.75 – 1.90)	0.449	0	0.375	0.986
<i>CTLA-4</i> (AT) ₁₀₄	3	186/420	1.21 (0.92 – 1.60)	0.180	0	0.390	0.227
<i>CTLA-4</i> (AT) ₁₀₆	3	186/420	1.30 (0.74 – 2.29)	0.359	75	0.018	0.674
<i>CTLA-4</i> (AT) ₁₀₈	3	186/420	0.88 (0.50 – 1.56)	0.963	0	0.963	0.473
<i>CTLA-4</i> (AT) ₁₁₀	3	186/420	0.74 (0.34 – 1.61)	0.441	0	0.667	0.171
<i>CTLA-4</i> (AT) ₁₁₆	3	186/420	0.80 (0.27 – 2.33)	0.677	0	0.724	0.786
<i>CTLA-4</i> (AT) ₁₁₈	3	186/420	0.46 (0.16 – 1.35)	0.158	26	0.258	0.155
<i>CTLA-4</i> (AT) ₁₂₂	3	186/420	1.70 (0.62 – 4.71)	0.304	26	0.260	0.557
<i>CTLA-4</i> (AT) ₁₂₄	3	186/420	1.97 (0.73 – 5.31)	0.178	61	0.080	0.637
<i>CTLA-4</i> (AT) ₁₂₆	3	186/420	1.25 (0.53 – 2.94)	0.609	53	0.121	0.701
<i>CTLA-4</i> (AT) ₁₂₈	3	186/420	1.15 (0.47 – 2.82)	0.760	37	0.204	0.826
<i>FCAR</i> rs16986050 (G)	2	1311/5891	0.93 (0.82 – 1.05)	0.211	84	0.002	0.523
<i>FCGR3A</i> rs396991 (G)	2	141/457	1.00 (0.74 – 1.34)	0.978	79	0.030	N/A
<i>FCGR3B</i> (NA1)	4	982/970	0.96 (0.84 – 1.11)	0.590	37	0.191	0.210
<i>GHSR</i> rs509035 (A)	2	1547/6595	1.04 (0.96 – 1.14)	0.342	52	0.123	0.874
<i>GHSR</i> rs519384 (A)	1	628/1328	1.12 (0.96 – 1.30)	0.140	0	0.389	N/A
<i>GHSR</i> rs572169 (A)	1	620/1304	1.12 (0.97 – 1.30)	0.118	50	0.158	N/A
<i>HLA-A1</i>	4	427/7324	1.07 (0.89 – 1.30)	0.455	0	0.567	0.996
<i>HLA-A2</i>	5	443/7796	0.96 (0.82 – 1.12)	0.582	0	0.956	0.335
<i>HLA-A3</i>	4	427/7324	1.18 (0.97 – 1.42)	0.092	35	0.201	0.273
<i>HLA-A9</i>	3	366/6991	0.85 (0.65 – 1.13)	0.266	77	0.014	0.311

Variant by gene (minor allele)	Publica- tions (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta- analysis	I² (%)	P value for heterogeneity	P value for funnel plot asymmetry
<i>HLA-A10</i>	3	366/6991	0.79 (0.48 – 1.30)	0.356	78	0.010	0.273
<i>HLA-A11</i>	6	466/8107	0.97 (0.52 – 1.81)	0.924	65	0.013	0.273
<i>HLA-A24</i>	3	108/1223	0.94 (0.56 – 1.60)	0.830	0	0.510	0.090
<i>HLA-A25</i>	2	92/751	1.82 (0.72 – 4.58)	0.206	0	0.699	N/A
<i>HLA-A26</i>	4	131/1628	1.56 (0.89 – 2.74)	0.124	43	0.154	0.143
<i>HLA-A28</i>	3	376/6962	0.80 (0.52 – 1.23)	0.302	0	0.538	0.066
<i>HLA-A29</i>	3	123/988	0.88 (0.38 – 2.03)	0.760	42	0.178	0.801
<i>HLA-A30</i>	2	92/751	1.03 (0.25 – 4.28)	0.964	0	0.496	N/A
<i>HLA-A31</i>	3	108/1223	1.02 (0.43 – 2.44)	0.969	0	0.482	0.169
<i>HLA-A32</i>	3	108/1223	1.62 (0.74 – 3.54)	0.231	62	0.074	0.996
<i>HLA-B7</i>	4	427/7324	1.11 (0.91 – 1.35)	0.294	30	0.232	0.234
<i>HLA-B12</i>	2	335/6573	0.97 (0.76 – 1.23)	0.775	0	0.911	N/A
<i>HLA-B13</i>	4	427/7324	0.78 (0.46 – 1.34)	0.373	0	0.413	0.319
<i>HLA-B14</i>	4	427/7324	0.90 (0.54 – 1.49)	0.676	0	0.487	0.615
<i>HLA-B15</i>	2	355/5923	1.01 (0.77 – 1.31)	0.955	0	0.482	N/A
<i>HLA-B18</i>	4	427/7172	0.76 (0.50 – 1.16)	0.204	0	0.865	0.756
<i>HLA-B27</i>	4	412/7223	0.67 (0.44 – 1.02)	0.061	1	0.388	0.336
<i>HLA-B35</i>	4	412/7095	0.78 (0.58 – 1.06)	0.108	0	0.885	0.527
<i>HLA-B37</i>	2	355/5923	0.93 (0.51 – 1.70)	0.814	44	0.182	N/A
<i>HLA-B39</i>	2	67/523	0.65 (0.11 – 3.68)	0.622	0	0.619	N/A
<i>HLA-B40</i>	2	355/5923	0.94 (0.70 – 1.25)	0.652	0	0.319	N/A
<i>HLA-B44</i>	3	108/1223	1.53 (0.96 – 2.44)	0.072	46	0.157	0.225
<i>HLA-B49</i>	2	92/751	1.46 (0.43 – 4.92)	0.542	0	0.747	N/A

Variant by gene (minor allele)	Publica- tions (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta- analysis	I² (%)	P value for heterogeneity	P value for funnel plot asymmetry
<i>HLA-B51</i>	2	67/523	1.03 (0.46 – 2.32)	0.943	50	0.158	N/A
<i>HLA-B55</i>	2	67/523	1.07 (0.40 – 2.88)	0.887	93	<0.001	N/A
<i>HLA-B57</i>	2	92/751	2.37 (0.92 – 6.11)	0.075	0	0.493	N/A
<i>HLA-B60</i>	2	57/1172	1.98 (0.77 – 5.09)	0.154	20	0.263	N/A
<i>HLA-B62</i>	2	57/1172	1.95 (0.87 – 4.37)	0.107	0	0.688	N/A
<i>HLA-Cw1</i>	2	68/523	1.28 (0.59 – 2.77)	0.534	0	0.650	N/A
<i>HLA-Cw3</i>	2	68/523	1.36 (0.79 – 2.33)	0.267	0	0.907	N/A
<i>HLA-Cw7</i>	2	68/523	0.96 (0.57 – 1.62)	0.877	3	0.309	N/A
<i>HLA-DPB1*0101</i>	2	242/139	0.65 (0.34 – 1.22)	0.178	84	0.013	N/A
<i>HLA-DPB1*0201</i>	4	435/904	0.85 (0.65 – 1.12)	0.241	49	0.118	0.708
<i>HLA-DPB1*0402</i>	4	479/877	1.10 (0.87 – 1.40)	0.433	0	0.893	0.074
<i>HLA-DPB1*0501</i>	2	242/139	0.86 (0.22 – 3.33)	0.823	7	0.300	N/A
<i>HLA-DPB1*0601</i>	2	242/139	1.25 (0.28 – 5.67)	0.769	7	0.300	N/A
<i>HLA-DPB1*0901</i>	2	242/139	0.63 (0.20 – 2.01)	0.438	0	0.476	N/A
<i>HLA-DQB1*02</i>	2	83/141	0.91 (0.53 – 1.55)	0.720	0	0.796	N/A
<i>HLA-DQB1*0302</i>	2	126/141	1.03 (0.58 – 1.82)	0.931	0	0.832	N/A
<i>HLA-DQB1*04</i>	2	83/141	1.63 (0.52 – 5.11)	0.404	0	0.893	N/A
<i>HLA-DQB1*0501</i>	2	209/282	1.32 (0.79 – 2.20)	0.287	53	0.143	N/A
<i>HLA-DQB1*0602</i>	2	126/141	1.36 (0.70 – 2.64)	0.360	91	0.001	N/A
<i>HLA-DQ7</i>	3	149/546	0.82 (0.56 – 1.20)	0.302	49	0.142	0.252
<i>HLA-DR1</i>	10	1009/7105	0.93 (0.64 – 1.34)	0.684	70	<0.001	0.105
<i>HLA-DR2</i>	5	487/6222	1.10 (0.80 – 1.54)	0.554	37	0.176	0.757
<i>HLA-DR3</i>	9	816/7045	1.05 (0.81 – 1.36)	0.740	41	0.096	0.946

Variant by gene (minor allele)	Publica- tions (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta- analysis	I² (%)	P value for heterogeneity	P value for funnel plot asymmetry
<i>HLA-DR4</i>	11	914/7696	1.19 (0.95 – 1.50)	0.132	47	0.037	0.342
<i>HLA-DR5</i>	5	494/6155	0.90 (0.61 – 1.31)	0.570	32	0.206	0.965
<i>HLA-DR7</i>	7	610/6493	1.08 (0.73 – 1.60)	0.164	66	0.007	0.932
<i>HLA-DR8</i>	9	823/7157	1.10 (0.80 – 1.51)	0.552	15	0.307	0.375
<i>HLA-DR9</i>	11	1016/8204	1.16 (0.71 – 1.90)	0.560	60	0.005	0.925
<i>HLA-DRB1*0401</i>	2	216/465	0.93 (0.38 – 2.28)	0.869	48	0.167	N/A
<i>HLA-DRB1*0403</i>	2	216/465	0.49 (0.17 – 1.42)	0.190	53	0.144	N/A
<i>HLA-DRB1*0405</i>	2	216/465	0.78 (0.47 – 1.30)	0.344	27	0.242	N/A
<i>HLA-DRB1*0406</i>	2	216/465	1.22 (0.61 – 2.5)	0.580	44	0.182	N/A
<i>HLA-DRB1*0407</i>	2	216/465	1.95 (0.61 – 6.29)	0.263	13	0.283	N/A
<i>HLA-DRB1*0410</i>	2	216/465	1.17 (0.27 – 5.05)	0.832	0	0.463	N/A
<i>HLA-DRB1*0802</i>	2	216/465	0.94 (0.36 – 2.43)	0.897	0	0.359	N/A
<i>HLA-DRB1*0803</i>	2	216/465	1.33 (0.83 – 2.14)	0.236	0	0.622	N/A
<i>HLA-DRB1*10</i>	4	322/890	0.98 (0.39 – 2.46)	0.969	0	0.627	0.596
<i>HLA-DRB1*11</i>	4	322/890	0.98 (0.71 – 1.34)	0.818	0	0.818	1.000
<i>HLA-DRB1*12</i>	4	322/890	1.12 (0.60 – 2.09)	0.712	54	0.088	0.121
<i>HLA-DRB1*1302</i>	2	216/465	0.54 (0.27 – 1.05)	0.068	0	0.952	N/A
<i>HLA-DRB1*1202</i>	2	216/465	1.42 (0.81 – 2.49)	0.219	49	0.160	N/A
<i>HLA-DRB1*1403</i>	2	216/465	1.27 (0.43 – 3.76)	0.666	0	0.964	N/A
<i>HLA-DRB1*1405</i>	2	216/465	0.66 (0.32 – 1.37)	0.265	57	0.125	N/A
<i>HLA-DRB1*1502</i>	2	216/465	0.57 (0.30 – 1.07)	0.079	0	0.398	N/A
<i>HLA-DRB1*16</i>	3	236/633	0.91 (0.37 – 2.27)	0.842	15	0.315	0.436
<i>HLA-DRB1*1602</i>	2	216/465	0.17 (0.02 – 1.29)	0.086	0	0.734	N/A

Variant by gene (minor allele)	Publica- tions (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta- analysis	I ² (%)	P value for heterogeneity	P value for funnel plot asymmetry
<i>HLA-DRB5</i>	2	110/1154	1.20 (0.73 – 1.97)	0.470	0	0.643	N/A
<i>IL-1β</i> (A2)	4	1172/5687	1.00 (0.90 – 1.12)	0.995	0	0.805	0.645
<i>IL1RN</i> *1	2	214/434	1.06 (0.82 – 1.37)	0.662	0	0.659	N/A
<i>IL1RN</i> *2	2	214/434	1.00 (0.77 – 1.31)	0.980	0	0.956	N/A
<i>IL1RN</i> *3	2	214/434	0.61 (0.26 – 1.44)	0.257	45	0.176	N/A
<i>IL1RN</i> *4	2	214/434	0.85 (0.13 – 5.82)	0.872	0	0.888	N/A
<i>IL1RN</i> *5	2	214/434	0.88 (0.13 – 5.94)	0.892	0	0.796	N/A
<i>IL-6</i> rs1800795 (C)	4	1926/6817	1.01 (0.94 – 1.09)	0.793	0	0.537	0.584
<i>IL-10</i> rs1800872 (A)	2	538/598	1.01 (0.83 – 1.22)	0.963	0	0.795	N/A
<i>IL-10</i> rs1800896 (G)	5	1414/6183	0.90 (0.76 – 1.07)	0.232	55	0.063	0.285
<i>LEPR</i> rs8179183 (C)	1	878/2653	0.89 (0.77 – 1.03)	0.118	89	<0.001	0.780
<i>MPO</i> rs2333227 (A)	3	395/299	0.96 (0.76 – 1.21)	0.696	0	0.822	0.478
<i>PCD1</i> rs1156882 (A)	2	168/479	0.88 (0.55 – 1.38)	0.568	0	0.701	N/A
<i>TGF-β₁</i> rs1800471 (C)	3	232/259	1.49 (0.92 – 2.41)	0.107	0	0.401	0.220
<i>TNFα</i> rs1800629 (A)	4	860/5691	1.14 (0.88 – 1.45)	0.327	29	0.236	0.389
<i>TNFR2</i> 196R	2	167/385	0.94 (0.66 – 1.34)	0.749	0	0.317	N/A
<i>TLR9</i> rs5743836 (G)	1	1289/1898	0.93 (0.81 – 1.08)	0.343	83	0.014	N/A

Supplementary Table S4. Results of the meta-analyses stratified by diagnostic and serologic subgroups

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>CD226</i> rs763361 (T)				
GPA	3	2021/17898	1.19 (1.11 – 1.28)	<0.001
MPA	1	156/5366	1.04 (0.83 – 1.31)	0.739
EGPA	1	119/1226	1.19 (0.91 – 1.56)	0.208
PR3-ANCA	2	764/6592	1.22 (1.09 – 1.36)	<0.001
MPO-ANCA	2	199/6592	1.20 (0.99 – 1.46)	0.066
<i>CTLA-4</i> (AT) ₈₆				
GPA	3	210/432	0.44 (0.34 – 0.57)	<0.001
MPA	2	93/311	0.87 (0.60 – 1.25)	0.450
PR3-ANCA	1	62/200	0.71 (0.47 – 1.09)	0.122
MPO-ANCA	2	92/311	0.94 (0.65 – 1.35)	0.733
<i>CTLA-4</i> (AT) ₁₀₂				
GPA	2	93/309	0.94 (0.45 – 1.94)	0.856
MPA	2	93/311	0.86 (0.51 – 1.45)	0.574
PR3-ANCA	1	62/200	0.87 (0.41 – 1.87)	0.722
MPO-ANCA	2	92/311	0.69 (0.26 – 1.81)	0.456
<i>CTLA-4</i> (AT) ₁₀₄				
GPA	2	93/309	0.84 (0.55 – 1.27)	0.398
MPA	2	93/311	0.87 (0.58 – 1.29)	0.474
PR3-ANCA	1	62/200	0.42 (0.22 – 0.79)	0.007
MPO-ANCA	2	92/311	0.85 (0.57 – 1.26)	0.412
<i>CTLA-4</i> (AT) ₁₀₆				
GPA	2	93/309	1.69 (0.67 – 4.25)	0.264
MPA	2	93/311	0.64 (0.28 – 1.46)	0.287
PR3-ANCA	1	62/200	1.83 (0.60 – 5.55)	0.289
MPO-ANCA	2	92/311	0.53 (0.22 – 1.30)	0.168
<i>CTLA-4</i> (AT) ₁₀₈				
GPA	2	93/309	0.40 (0.12 – 1.35)	0.141
MPA	2	93/311	0.75 (0.36 – 1.54)	0.431
PR3-ANCA	1	62/200	0.30 (0.07 – 1.28)	0.103
MPO-ANCA	2	92/311	0.66 (0.31 – 1.41)	0.291
<i>CTLA-4</i> (AT) ₁₁₀				
GPA	2	93/309	0.55 (0.18 – 1.74)	0.311
MPA	2	93/311	0.26 (0.05 – 1.36)	0.109
PR3-ANCA	1	62/200	0.56 (0.16 – 1.94)	0.359
MPO-ANCA	2	92/311	0.26 (0.05 – 1.38)	0.113
<i>CTLA-4</i> (AT) ₁₁₆				
GPA	2	93/309	0.66 (0.17 – 2.60)	0.553
MPA	2	93/311	0.41 (0.05 – 3.38)	0.408
PR3-ANCA	1	62/200	0.21 (0.01 – 3.72)	0.288
MPO-ANCA	2	92/311	0.69 (0.12 – 3.98)	0.673
<i>CTLA-4</i> (AT) ₁₁₈				
GPA	2	93/309	0.32 (0.06 – 1.68)	0.176
MPA	2	93/311	0.31 (0.06 – 1.69)	0.175

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
PR3-ANCA	1	62/200	0.11 (0.01 – 1.81)	0.121
MPO-ANCA	2	92/311	0.44 (0.10 – 1.97)	0.283
<i>CTLA-4</i> (AT) ₁₂₂				
GPA	2	93/309	1.32 (0.26 – 6.80)	0.742
MPA	2	93/311	1.57 (0.48 – 5.19)	0.456
PR3-ANCA	1	62/200	0.35 (0.02 – 6.62)	0.487
MPO-ANCA	2	92/311	3.69 (1.40 – 9.71)	0.008
<i>CTLA-4</i> (AT) ₁₂₄				
GPA	2	93/309	1.69 (0.67 – 4.25)	0.264
MPA	2	93/311	0.64 (0.28 – 1.46)	0.287
PR3-ANCA	1	62/200	1.83 (0.60 – 5.55)	0.289
MPO-ANCA	2	92/311	0.53 (0.22 – 1.30)	0.168
<i>CTLA-4</i> (AT) ₁₂₆				
GPA	2	93/309	1.43 (0.47 – 4.35)	0.526
MPA	2	93/311	0.38 (0.08 – 2.11)	0.266
PR3-ANCA	1	62/200	0.21 (0.01 – 3.72)	0.288
MPO-ANCA	2	92/311	0.54 (0.12 – 2.46)	0.428
<i>CTLA-4</i> (AT) ₁₂₈				
GPA	2	93/309	0.39 (0.07 – 2.14)	0.278
MPA	2	93/311	1.27 (0.39 – 4.20)	0.694
PR3-ANCA	1	62/200	0.29 (0.04 – 2.25)	0.235
MPO-ANCA	2	92/311	1.29 (0.39 – 4.28)	0.674
<i>CTLA-4</i> rs231775 (G)				
GPA	2	510/5994	1.05 (0.92 – 1.20)	0.430
MPA	2	252/5994	1.17 (0.97 – 1.40)	0.100
PR3-ANCA	1	326/5365	1.00 (0.85 – 1.18)	0.983
MPO-ANCA	1	167/5365	0.96 (0.77 – 1.21)	0.747
<i>CTLA-4</i> rs3087243 (A)				
GPA	3	1561/7855	0.80 (0.73 – 0.87)	<0.001
MPA	2	358/5886	0.79 (0.68 – 0.92)	0.003
PR3-ANCA	1	478/5257	0.81 (0.71 – 0.93)	0.003
MPO-ANCA	1	264/5257	0.96 (0.80 – 1.15)	0.658
<i>FCAR</i> rs16986050 (G)				
GPA	2	1029/5891	0.92 (0.80 – 1.05)	0.214
MPA	1	394/5365	0.93 (0.69 – 1.26)	0.647
PR3-ANCA	1	326/5365	1.13 (0.93 – 1.38)	0.211
MPO-ANCA	1	167/5365	1.00 (0.75 – 1.33)	0.988
<i>FCGR2A</i> rs1801274 (C)				
GPA	5	1082/5969	0.99 (0.94 – 1.05)	0.827
MPA	4	800/5766	0.97 (0.81 – 1.15)	0.698
PR3-ANCA	4	883/5820	0.91 (0.79 – 1.03)	0.138
MPO-ANCA	4	844/5969	0.80 (0.67 – 0.95)	0.011
<i>FCGR3A</i> rs396991 (G)				
GPA	1	91/154	1.30 (0.89 – 1.91)	0.172
MPA	1	50/303	0.65 (0.39 – 1.07)	0.090
PR3-ANCA	1	91/154	1.30 (0.89 – 1.91)	0.172

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
MPO-ANCA	1	50/303	0.65 (0.39 – 1.07)	0.090
<i>FCGR3B</i> (NA1)				
GPA	3	865/667	0.93 (0.80 – 1.08)	0.343
MPA	2	75/200	1.52 (1.03 – 2.25)	0.035
PR3-ANCA	2	143/254	1.07 (0.79 – 1.45)	0.664
MPO-ANCA	2	121/403	1.19 (0.86 – 1.64)	0.287
<i>GHSR</i> rs509035 (A)				
GPA	2	1198/6595	1.05 (0.96 – 1.16)	0.292
MPA	1	262/5259	1.00 (0.82 – 1.20)	0.966
PR3-ANCA	1	478/5259	1.05 (0.91 – 1.21)	0.521
MPO-ANCA	1	264/5259	0.83 (0.68 – 1.01)	0.057
<i>HLA-A2</i>				
GPA	5	380/7796	0.96 (0.81 – 1.14)	0.633
c-ANCA	1	16/96	0.90 (0.37 – 2.23)	0.826
<i>HLA-A11</i>				
GPA	5	380/7702	0.61 (0.41 – 0.90)	0.014
MPA	1	23/405	2.97 (1.19 – 7.41)	0.020
c-ANCA	1	16/472	0.71 (0.17 – 3.03)	0.644
<i>HLA-A24</i>				
GPA	3	108/1223	0.94 (0.56 – 1.60)	0.830
c-ANCA	1	16/472	0.75 (0.34 – 1.65)	0.476
<i>HLA-A26</i>				
GPA	3	108/1223	1.24 (0.61 – 2.54)	0.550
MPA	1	23/405	2.49 (1.00 – 6.18)	0.049
c-ANCA	1	16/472	2.36 (1.00 – 5.60)	0.051
<i>HLA-A31</i>				
GPA	3	108/1223	1.02 (0.43 – 2.44)	0.969
c-ANCA	1	16/472	1.55 (0.46 – 5.24)	0.479
<i>HLA-A32</i>				
GPA	3	108/1223	1.62 (0.74 – 3.54)	0.231
c-ANCA	1	16/472	2.07 (0.61 – 7.04)	0.246
<i>HLA-B35</i>				
GPA	4	349/7095	0.62 (0.44 – 0.89)	0.010
c-ANCA	1	16/472	0.80 (0.19 – 3.40)	0.757
<i>HLA-B39</i>				
GPA	2	67/523	0.65 (0.11 – 3.68)	0.622
c-ANCA	1	16/472	0.86 (0.11 – 6.51)	0.887
<i>HLA-B44</i>				
GPA	3	108/1223	1.53 (0.96 – 2.44)	0.072
c-ANCA	1	16/472	2.50 (0.85 – 7.40)	0.098
<i>HLA-B51</i>				
GPA	2	67/523	1.03 (0.46 – 2.32)	0.943
c-ANCA	1	16/472	1.87 (0.64 – 5.49)	0.255

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>HLA-B55</i>				
GPA	2	67/523	1.07 (0.40 – 2.88)	0.887
c-ANCA	1	16/472	7.35 (2.33 – 23.14)	0.001
<i>HLA-B60</i>				
GPA	2	57/1172	1.98 (0.77 – 5.09)	0.154
c-ANCA	1	16/472	1.19 (0.28 – 5.13)	0.814
<i>HLA-B62</i>				
GPA	2	57/1172	2.27 (1.05 – 4.90)	0.036
c-ANCA	1	16/472	2.21 (0.83 – 5.91)	0.114
<i>HLA-Cw1</i>				
GPA	2	68/523	1.28 (0.59 – 2.77)	0.534
c-ANCA	1	16/472	1.45 (0.58 – 3.58)	0.426
<i>HLA-Cw3</i>				
GPA	2	68/523	1.36 (0.79 – 2.33)	0.267
c-ANCA	1	16/472	1.40 (0.65 – 3.01)	0.384
<i>HLA-Cw7</i>				
GPA	2	68/523	0.96 (0.57 – 1.62)	0.877
c-ANCA	1	16/472	0.50 (0.12 – 2.10)	0.340
<i>HLA-DPA1</i> rs9277341 (C)				
GPA	2	1032/2200	0.35 (0.30 – 0.41)	<0.001
c-ANCA	1	578/1820	0.27 (0.22 – 0.33)	<0.001
<i>HLA-DPB1*0101</i>				
GPA	1	148/89	0.17 (0.05 – 0.63)	0.008
PR3-ANCA	2	183/139	0.45 (0.20 – 0.99)	0.048
MPO-ANCA	1	22/50	1.01 (0.29 – 3.48)	0.986
<i>HLA-DPB1*0201</i>				
GPA	2	283/458	0.67 (0.45 – 0.99)	0.042
MPA	1	50/77	1.38 (0.75 – 2.52)	0.298
EGPA	1	102/369	0.93 (0.57 – 1.51)	0.759
PR3-ANCA	1	148/89	0.44 (0.21 – 0.91)	0.027
MPO-ANCA	1	50/77	1.38 (0.75 – 2.52)	0.298
<i>HLA-DPB1*0301</i>				
GPA	3	774/918	0.23 (0.16 – 0.32)	<0.001
MPA	1	119/460	0.67 (0.37 – 1.21)	0.186
EGPA	2	167/829	0.47 (0.29 – 0.75)	0.001
PR3-ANCA	2	183/139	0.19 (0.09 – 0.39)	<0.001
MPO-ANCA	1	22/50	1.71 (0.74 – 3.94)	0.210
ANCA negative	1	27/369	0.58 (0.21 – 1.65)	0.311
<i>HLA-DPB1*0401</i>				
GPA	3	774/918	2.89 (2.50 – 3.35)	<0.001
MPA	1	119/460	1.09 (0.80 – 1.49)	0.597
EGPA	2	167/829	1.08 (0.85 – 1.36)	0.548
PR3-ANCA	2	183/139	3.93 (2.75 – 5.62)	<0.001
MPO-ANCA	1	22/50	1.43 (0.67 – 3.02)	0.351
ANCA negative	1	27/369	1.26 (0.73 – 2.20)	0.407

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>HLA-DPB1*0402</i>				
GPA	2	283/458	1.13 (0.82 – 1.55)	0.439
EGPA	1	102/369	1.15 (0.75 – 1.75)	0.533
PR3-ANCA	2	183/139	1.11 (0.69 – 1.77)	0.674
MPO-ANCA	1	22/50	0.94 (0.31 – 2.85)	0.913
<i>HLA-DPB1*0501</i>				
GPA	1	148/89	0.20 (0.01 – 4.93)	0.324
PR3-ANCA	2	183/139	1.11 (0.26 – 4.76)	0.886
MPO-ANCA	1	22/50	1.14 (0.10 – 12.91)	0.916
<i>HLA-DPB1*0601</i>				
GPA	1	148/89	0.60 (0.08 – 4.29)	0.610
PR3-ANCA	2	183/139	1.12 (0.23 – 5.51)	0.887
MPO-ANCA	1	22/50	6.93 (0.28 – 173.53)	0.239
<i>HLA-DPB1*0901</i>				
GPA	1	148/89	1.81 (0.07 – 44.73)	0.716
PR3-ANCA	2	183/139	0.98 (0.27 – 3.62)	0.978
MPO-ANCA	1	22/50	0.91 (0.17 – 4.85)	0.907
<i>HLA-DPB2 rs3130215 (A)</i>				
GPA	3	1135/7249	1.37 (0.88 – 2.13)	0.160
MPA	1	156/5366	1.33(1.06 – 1.66)	0.013
PR3-ANCA	1	326/5366	0.65 (0.55 – 0.77)	<0.001
MPO-ANCA	1	167/5366	1.27 (1.02 – 1.58)	0.032
<i>HLA-DQB1*02</i>				
GPA	2	83/141	0.91 (0.53 – 1.55)	0.720
PR3-ANCA	1	32/91	0.98 (0.45 – 2.14)	0.954
<i>HLA-DQB1*0302</i>				
GPA	1	32/91	0.94 (0.36 – 2.49)	0.905
PR3-ANCA	2	67/141	1.03 (0.54 – 1.98)	0.924
MPO-ANCA	1	22/50	1.06 (0.37 – 2.99)	0.917
<i>HLA-DQB1*0303</i>				
GPA	1	32/91	2.97 (0.72 – 12.23)	0.132
MPA	1	50/77	2.11 (1.14 – 3.90)	0.018
PR3-ANCA	2	67/141	0.79 (0.31 – 2.05)	0.634
MPO-ANCA	2	72/127	1.91 (1.12 – 3.26)	0.017
<i>HLA-DQB1*04</i>				
GPA	2	83/141	1.63 (0.52 – 5.11)	0.404
PR3-ANCA	1	32/91	1.74 (0.40 – 7.50)	0.457
<i>HLA-DQB1*0501</i>				
GPA	1	32/91	0.77 (0.32 – 1.88)	0.568
PR3-ANCA	2	67/141	1.05 (0.58 – 1.91)	0.865
MPO-ANCA	1	22/50	2.05 (0.84 – 4.97)	0.113
<i>HLA-DQB1*0602</i>				
GPA	1	32/91	0.89 (0.38 – 2.05)	0.779
PR3-ANCA	2	67/141	0.80 (0.42 – 1.54)	0.504
MPO-ANCA	1	22/50	0.35 (0.08 – 1.63)	0.181

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>HLA-DQ7</i>				
GPA	1	32/91	0.43 (0.16 – 1.16)	0.095
MPA	1	23/405	0.66 (0.34 – 1.30)	0.234
PR3-ANCA	2	67/141	0.98 (0.58 – 1.66)	0.940
MPO-ANCA	1	22/50	1.26 (0.57 – 2.77)	0.569
<i>HLA-DR1</i>				
GPA	6	413/6002	0.76 (0.58 – 1.00)	0.054
MPA	4	223/6020	1.12 (0.72 – 1.74)	0.612
EGPA	3	128/5924	0.82 (0.53 – 1.26)	0.360
PR3-ANCA	3	157/560	0.57 (0.38 – 0.86)	0.008
MPO-ANCA	3	133/734	0.78 (0.49 – 1.25)	0.297
<i>HLA-DR2</i>				
GPA	4	301/6132	1.36 (1.08 – 1.72)	0.010
EGPA	1	14/113	1.40 (0.45 – 4.39)	0.561
PR3-ANCA	1	35/90	1.34 (0.63 – 2.86)	0.442
MPO-ANCA	1	22/90	1.03 (0.39 – 2.69)	0.958
c-ANCA	1	16/472	0.33 (0.08 – 1.38)	0.128
<i>HLA-DR3</i>				
GPA	5	368/5802	1.24 (1.00 – 1.56)	0.056
MPA	2	38/518	0.45 (0.17 – 1.14)	0.092
EGPA	2	116/482	0.70 (0.43 – 1.13)	0.139
PR3-ANCA	3	157/560	1.29 (0.90 – 1.86)	0.170
MPO-ANCA	2	69/469	0.85 (0.49 – 1.48)	0.574
<i>HLA-DR4</i>				
GPA	7	425/6424	1.32 (1.09 – 1.60)	0.004
MPA	2	66/5555	1.50 (0.98 – 2.30)	0.060
EGPA	4	176/6246	1.70 (1.23 – 2.34)	0.001
PR3-ANCA	3	157/560	0.98 (0.71 – 1.36)	0.917
MPO-ANCA	2	69/202	2.51 (1.46 – 4.32)	0.001
c-ANCA	1	16/472	0.72 (0.27 – 1.88)	0.498
<i>HLA-DR5</i>				
GPA	3	285/5660	0.76 (0.54 – 1.06)	0.102
MPA	1	23/405	1.59 (0.80 – 3.15)	0.182
EGPA	1	14/113	1.24 (0.34 – 4.46)	0.746
PR3-ANCA	1	35/90	0.85 (0.30 – 2.42)	0.756
MPO-ANCA	1	22/90	0.52 (0.12 – 2.38)	0.402
<i>HLA-DR6</i>				
GPA	4	301/6132	0.45 (0.33 – 0.62)	<0.001
MPA	1	30/5442	0.29 (0.09 – 0.92)	0.035
EGPA	2	26/5555	0.19 (0.04 – 0.95)	0.043
PR3-ANCA	1	35/90	0.28 (0.06 – 1.25)	0.096
MPO-ANCA	1	22/90	0.70 (0.20 – 2.51)	0.586
c-ANCA	1	16/472	1.63 (0.56 – 4.77)	0.371
<i>HLA-DR7</i>				
GPA	5	368/5802	0.92 (0.71 – 1.19)	0.508
MPA	1	15/113	0.70 (0.20 – 2.44)	0.575
EGPA	3	164/804	1.71 (1.24 – 2.37)	0.001
PR3-ANCA	1	32/91	1.00 (0.40 – 2.48)	0.991

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>HLA-DR8</i>				
GPA	5	381/6206	0.89 (0.57 – 1.39)	0.610
MPA	1	51/5442	0.31 (0.04 – 2.21)	0.242
EGPA	2	114/5811	3.08 (1.75 – 5.41)	<0.001
PR3-ANCA	3	157/560	0.68 (0.33 – 1.42)	0.308
MPO-ANCA	2	69/469	1.70 (0.80 – 3.60)	0.170
c-ANCA	1	16/472	1.63 (0.66 – 4.05)	0.291
<i>HLA-DR9</i>				
GPA	6	402/6369	0.90 (0.58 – 1.39)	0.623
MPA	3	218/578	1.14 (0.83 – 1.56)	0.423
EGPA	3	164/832	1.07 (0.33 – 3.42)	0.915
PR3-ANCA	2	122/470	0.47 (0.09 – 2.58)	0.383
MPO-ANCA	3	175/1116	1.83 (1.29 – 2.60)	0.001
c-ANCA	1	16/472	3.03 (1.40 – 6.56)	0.005
<i>HLA-DRB1*0401</i>				
GPA	1	45/200	0.49 (0.06 – 3.90)	0.499
MPA	2	157/465	1.42 (0.60 – 3.41)	0.426
MPO-ANCA	1	64/265	2.10 (0.52 – 8.50)	0.300
<i>HLA-DRB1*0403</i>				
GPA	1	45/200	0.26 (0.02 – 4.46)	0.349
MPA	2	157/465	0.48 (0.14 – 1.59)	0.227
MPO-ANCA	1	64/265	0.95 (0.27 – 3.40)	0.943
<i>HLA-DRB1*0405</i>				
GPA	1	45/200	0.15 (0.01 – 2.49)	0.184
MPA	2	157/465	0.95 (0.56 – 1.62)	0.862
MPO-ANCA	1	64/265	0.61 (0.30 – 1.22)	0.159
<i>HLA-DRB1*0406</i>				
GPA	1	45/200	2.28 (0.67 – 7.74)	0.187
MPA	2	157/465	1.31 (0.62 – 2.78)	0.483
MPO-ANCA	1	64/265	0.65 (0.19 – 2.22)	0.487
<i>HLA-DRB1*0407</i>				
GPA	1	45/200	1.47 (0.06 – 36.42)	0.813
MPA	2	157/465	1.95 (0.54 – 6.99)	0.306
MPO-ANCA	1	64/265	2.82 (0.78 – 10.14)	0.113
<i>HLA-DRB1*0410</i>				
GPA	1	45/200	1.47 (0.06 – 36.42)	0.813
MPA	2	157/465	1.53 (0.35 – 6.64)	0.569
MPO-ANCA	1	64/265	1.67 (0.32 – 8.69)	0.544
<i>HLA-DRB1*0802</i>				
GPA	1	45/200	0.88 (0.04 – 18.50)	0.935
MPA	2	157/465	0.99 (0.35 – 2.79)	0.984
MPO-ANCA	1	64/265	1.16 (0.42 – 3.18)	0.778
<i>HLA-DRB1*0803</i>				
GPA	1	45/200	1.18 (0.43 – 3.25)	0.749
MPA	2	157/465	1.25 (0.73 – 2.13)	0.413
MPO-ANCA	1	64/265	1.51 (0.78 – 2.93)	0.226

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>HLA-DRB1*10</i>				
GPA	2	83/142	2.61 (0.45 – 15.24)	0.286
EGPA	1	102/369	0.40 (0.02 – 7.44)	0.538
PR3-ANCA	2	122/470	0.59 (0.13 – 2.65)	0.487
MPO-ANCA	1	47/379	1.48 (0.32 – 6.76)	0.616
<i>HLA-DRB1*11</i>				
GPA	2	83/142	0.97 (0.49 – 1.94)	0.932
EGPA	1	102/369	0.88 (0.53 – 1.48)	0.632
PR3-ANCA	2	122/470	0.97 (0.58 – 1.62)	0.908
MPO-ANCA	1	47/379	1.10 (0.51 – 2.38)	0.805
<i>HLA-DRB1*1101</i>				
GPA	1	45/200	0.16 (0.02 – 1.21)	0.076
MPA	2	223/465	2.57 (1.56 – 4.23)	<0.001
MPO-ANCA	1	116/265	2.79 (0.84 – 9.23)	0.093
<i>HLA-DRB1*12</i>				
GPA	2	83/142	4.06 (1.27 – 12.99)	0.018
EGPA	1	102/369	0.57 (0.17 – 1.93)	0.362
PR3-ANCA	2	122/470	1.01 (0.36 – 2.81)	0.983
MPO-ANCA	1	47/379	1.16 (0.26 – 5.16)	0.850
<i>HLA-DRB1*1201</i>				
GPA	1	45/200	0.15 (0.01 – 2.49)	0.184
MPA	2	157/465	0.51 (0.21 – 1.26)	0.146
MPO-ANCA	1	64/265	0.21 (0.03 – 1.60)	0.132
<i>HLA-DRB1*1202</i>				
GPA	1	45/200	2.92 (1.37 – 6.23)	0.005
MPA	2	157/465	1.07 (0.55 – 2.09)	0.838
PR3-ANCA	1	19/200	1.63 (0.46 – 5.75)	0.449
MPO-ANCA	2	89/465	1.00 (0.38 – 2.61)	1.000
<i>HLA-DRB1*13</i>				
GPA	2	83/142	0.61 (0.34 – 1.12)	0.111
EGPA	2	150/691	0.40 (0.24 – 0.68)	0.001
PR3-ANCA	1	32/91	0.56 (0.20 – 1.53)	0.257
<i>HLA-DRB1*1302</i>				
GPA	1	45/200	0.89 (0.19 – 4.12)	0.878
MPA	2	157/465	0.46 (0.20 – 1.02)	0.055
MPO-ANCA	1	64/265	0.54 (0.24 – 1.23)	0.142
<i>HLA-DRB1*14</i>				
GPA	2	83/142	1.26 (0.40 – 4.01)	0.698
EGPA	1	102/341	1.83 (0.72 – 4.65)	0.205
PR3-ANCA	2	122/470	2.00 (0.87 – 4.56)	0.101
MPO-ANCA	1	47/379	2.04 (0.43 – 9.74)	0.372
<i>HLA-DRB1*1403</i>				
GPA	1	45/200	2.24 (0.20 – 24.93)	0.513
MPA	2	157/465	0.81 (0.21 – 3.19)	0.767
MPO-ANCA	1	64/265	1.25 (0.34 – 4.60)	0.739
<i>HLA-DRB1*1405</i>				
GPA	1	45/200	1.51 (0.53 – 4.27)	0.437

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
MPA	2	157/465	0.45 (0.18 – 1.15)	0.096
MPO-ANCA	1	64/265	0.11 (0.01 – 1.91)	0.131
<i>HLA-DRB1*15</i>				
GPA	2	83/142	0.97 (0.57 – 1.65)	0.921
PR3-ANCA	2	131/582	2.82 (2.00 – 3.96)	<0.001
MPO-ANCA	1	51/491	0.80 (0.37 – 1.73)	0.566
<i>HLA-DRB1*1501</i>				
GPA	1	45/200	1.70 (0.98 – 2.94)	0.059
MPA	2	157/465	1.65 (1.14 – 2.38)	0.007
PR3-ANCA	1	19/200	0.98 (0.40 – 2.45)	0.973
MPO-ANCA	2	89/465	2.03 (1.26 – 3.29)	0.004
<i>HLA-DRB1*1502</i>				
GPA	1	45/200	0.80 (0.18 – 3.69)	0.779
MPA	2	157/465	0.60 (0.30 – 1.21)	0.154
MPO-ANCA	1	64/265	0.67 (0.32 – 1.39)	0.279
<i>HLA-DRB1*16</i>				
GPA	2	83/142	0.23 (0.03 – 1.85)	0.166
PR3-ANCA	2	131/582	1.00 (0.29 – 3.41)	0.996
MPO-ANCA	1	51/491	3.55 (1.02 – 12.38)	0.047
<i>HLA-DRB1*1602</i>				
GPA	1	45/200	0.40 (0.02 – 7.25)	0.533
MPA	2	157/465	0.23 (0.03 – 1.72)	0.151
MPO-ANCA	1	64/265	0.24 (0.01 – 4.17)	0.327
<i>HLA-DRB3</i>				
GPA	1	51/51	1.41 (0.76 – 2.60)	0.276
EGPA	2	150/691	0.58 (0.45 – 0.76)	<0.001
<i>HLA-DRB4</i>				
GPA	1	51/51	0.89 (0.46 – 1.72)	0.738
EGPA	2	150/691	2.06 (1.57 – 2.69)	<0.001
<i>IL-1β (A2)</i>				
GPA	3	714/5491	1.07 (0.93 – 1.22)	0.336
MPA	1	262/5259	0.89 (0.72 – 1.10)	0.286
PR3-ANCA	2	557/5455	1.01 (0.87 – 1.17)	0.930
MPO-ANCA	2	294/5455	1.00 (0.82 – 1.21)	0.971
<i>IL1RN*1</i>				
GPA	1	61/200	0.88 (0.57 – 1.37)	0.573
MPA	1	105/200	1.21 (0.83 – 1.77)	0.325
PR3-ANCA	2	122/434	1.12 (0.82 – 1.54)	0.476
MPO-ANCA	2	92/434	0.98 (0.69 – 1.40)	0.916
<i>IL1RN*2</i>				
GPA	1	61/200	1.22 (0.78 – 1.92)	0.380
MPA	1	105/200	0.77 (0.52 – 1.16)	0.212
PR3-ANCA	2	122/434	0.95 (0.68 – 1.31)	0.748
MPO-ANCA	2	92/434	1.02 (0.71 – 1.47)	0.921
<i>IL1RN*3</i>				
GPA	1	61/200	0.72 (0.15 – 3.40)	0.682

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
MPA	1	105/200	1.50 (0.55 – 4.08)	0.429
PR3-ANCA	2	122/434	0.61 (0.21 – 1.76)	0.358
MPO-ANCA	2	92/434	0.71 (0.22 – 2.29)	0.571
<i>IL1RN*4</i>				
GPA	1	61/200	0.65 (0.03 – 13.64)	0.782
MPA	1	105/200	1.91 (0.27 – 13.68)	0.518
PR3-ANCA	2	122/434	0.95 (0.11 – 8.63)	0.964
MPO-ANCA	2	92/434	3.08 (0.58 – 16.42)	0.188
<i>IL1RN*5</i>				
GPA	1	61/200	1.09 (0.04 – 26.86)	0.959
MPA	1	105/200	0.63 (0.03 – 15.60)	0.779
PR3-ANCA	2	122/434	0.87 (0.10 – 7.74)	0.901
MPO-ANCA	2	92/434	2.18 (0.32 – 14.79)	0.424
<i>IL-6 rs1800795 (C)</i>				
GPA	4	1360/1558	0.99 (0.94 – 1.04)	0.750
MPA	2	315/6593	0.98 (0.84 – 1.16)	0.829
EGPA	1	426/6593	0.96 (0.76 – 1.21)	0.730
PR3-ANCA	3	NR/6694	0.98 (0.89 – 1.09)	0.751
MPO-ANCA	2	NR/6603	1.04 (0.90 – 1.20)	0.616
<i>IL-10 rs1800872 (A)</i>				
GPA	2	435/598	1.03 (0.84 – 1.27)	0.762
EGPA	1	103/507	0.89 (0.62 – 1.27)	0.512
PR3-ANCA	1	32/91	1.10 (0.55 – 2.20)	0.793
<i>IL-10 rs1800896 (G)</i>				
GPA	5	993/6183	0.95 (0.85 – 1.05)	0.293
MPA	2	192/5513	0.95 (0.78 – 1.17)	0.655
EGPA	1	103/507	0.68 (0.50 – 0.92)	0.012
PR3-ANCA	2	358/5451	1.05 (0.90 – 1.22)	0.527
MPO-ANCA	1	167/5360	0.96 (0.77 – 1.19)	0.693
<i>IRF5 rs10954213 (G)</i>				
GPA	2	1021/6267	0.66 (0.59 – 0.74)	<0.001
MPA	2	333/6075	1.22 (1.03 – 1.44)	0.018
PR3-ANCA	1	326/5365	1.09 (0.93 – 1.28)	0.293
MPO-ANCA	2	399/6075	1.12 (0.96 – 1.31)	0.142
<i>LEPR rs8179183 (C)</i>				
GPA	1	682/1326	0.72 (0.60 – 0.86)	<0.001
EGPA	1	196/1327	1.41 (1.10 – 1.81)	0.007
<i>MPO rs2333227 (A)</i>				
GPA	1	69/150	0.70 (0.41 – 1.21)	0.204
MPA	1	65/150	1.18 (0.72 – 1.93)	0.523
PR3-ANCA	3	258/549	1.00 (0.77 – 1.31)	0.977
MPO-ANCA	3	141/549	0.94 (0.68 – 1.31)	0.719
<i>PTPN22 rs2476601 (A)</i>				
GPA	4	1616/8678	1.43 (1.26 – 1.62)	<0.001
MPA	2	258/6310	1.42 (1.06 – 1.89)	0.018
EGPA	1	99/945	0.52 (0.21 – 1.29)	0.158

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
PR3-ANCA	2	419/6310	1.42 (1.14 – 1.77)	0.002
MPO-ANCA	2	183/6310	1.47 (1.08 – 2.00)	0.014
<i>RING1/RXR</i> B rs213213 (A)				
GPA	3	1132/7238	1.91 (1.73 – 2.10)	<0.001
MPA	1	156/5366	1.15 (0.90 – 1.45)	0.264
PR3-ANCA	1	326/5366	2.06 (1.75 – 2.41)	<0.001
MPO-ANCA	1	167/5366	1.05 (0.83 – 1.32)	0.687
<i>RXR</i> B rs6531 (C)				
GPA	3	1211/6955	1.70 (1.55 – 1.86)	<0.001
MPA	1	262/5251	1.38 (1.15 – 1.66)	0.001
PR3-ANCA	1	478/5251	2.19 (1.92 – 2.51)	<0.001
MPO-ANCA	1	264/5251	1.21 (1.00 – 1.46)	0.046
ANCA negative	1	36/201	1.02 (0.59 – 1.74)	0.948
<i>RXR</i> B rs9277935 (T)				
GPA	3	1135/7233	0.37 (0.31 – 0.43)	<0.001
MPA	1	156/5350	0.93 (0.70 – 1.24)	0.629
PR3-ANCA	1	326/5350	0.24 (0.17 – 0.33)	<0.001
MPO-ANCA	1	167/5350	1.18 (0.92 – 1.53)	0.193
<i>SERPINA1</i> S allele				
GPA	2	484/1079	1.72 (1.12 – 2.66)	0.014
c-ANCA	3	145/3836	1.92 (1.12 – 3.29)	0.017
<i>SERPINA1</i> Z allele				
GPA	4	972/2636	2.40 (1.73 - 3.33)	<0.001
MPA	1	143/805	1.60 (0.76 - 3.39)	0.218
PR3-ANCA	1	322/805	2.58 (1.57 - 4.25)	<0.001
MPO-ANCA	1	166/805	2.01 (1.04 - 3.87)	0.037
c-ANCA	5	280/4788	3.53 (2.28 – 5.49)	<0.001
p-ANCA	2	78/2510	3.13 (1.21 – 8.13)	0.019
<i>STAT4</i> rs7574865 (T)				
GPA	2	1288/6246	1.06 (0.94 – 1.20)	0.331
MPA	1	676/5366	1.12 (0.86 – 1.46)	0.392
PR3-ANCA	1	676/5366	1.06 (0.88 – 1.28)	0.547
MPO-ANCA	2	908/6076	1.24 (1.05 – 1.46)	0.009
<i>TGF-β₁</i> rs1800471 (C)				
GPA	3	196/259	1.52 (0.93 – 2.48)	0.096
MPA	1	36/96	1.03 (0.35 – 2.99)	0.960
PR3-ANCA	1	32/91	1.86 (0.73 – 4.71)	0.193
<i>TNFα</i> rs1800629 (A)				
GPA	4	578/5691	1.15 (0.98 – 1.35)	0.098
MPA	1	156/5366	1.13 (0.95 – 1.35)	0.182
PR3-ANCA	2	357/5457	1.21 (0.93 – 1.57)	0.149
MPO-ANCA	1	167/5366	0.88 (0.66 – 1.17)	0.375
<i>TNFR2</i> 196R				
GPA	1	177/123	1.05 (0.70 – 1.57)	0.819
MPA	1	50/262	0.67 (0.31 – 1.45)	0.313
MPO-ANCA	1	50/262	0.67 (0.31 – 1.45)	0.313

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>TLR9</i> rs352162 (T)				
GPA	1	919/1898	1.20 (1.07 – 1.34)	0.001
MPA	1	153/1898	0.74 (0.58 – 0.95)	0.020
EGPA	1	217/1898	1.28 (1.05 – 1.57)	0.015
PR3-ANCA	1	NR/NR	1.30 (1.14 – 1.47)	<0.001
MPO-ANCA	1	NR/NR	0.79 (0.65 – 0.97)	0.028
ANCA negative	1	NR/NR	1.22 (0.99 – 1.50)	0.060
<i>TLR9</i> rs352140 (T)				
GPA	1	919/1898	1.20 (1.07 – 1.35)	0.001
MPA	1	153/1898	0.71 (0.55 – 0.91)	0.006
EGPA	1	217/1898	1.17 (0.96 – 1.43)	0.129
PR3-ANCA	1	NR/NR	1.28 (1.12 – 1.45)	<0.001
MPO-ANCA	1	NR/NR	0.75 (0.62 – 0.91)	0.004
ANCA negative	1	NR/NR	1.19 (0.97 – 1.47)	0.097
<i>TLR9</i> rs352139 (T)				
GPA	1	919/1898	1.18 (1.06 – 1.32)	0.003
MPA	1	153/1898	0.68 (0.52 – 0.87)	0.003
EGPA	1	217/1898	1.21 (0.99 – 1.47)	0.057
PR3-ANCA	1	NR/NR	1.23 (1.09 – 1.40)	0.001
MPO-ANCA	1	NR/NR	0.78 (0.63 – 0.96)	0.017
ANCA negative	1	NR/NR	1.20 (0.98 – 1.47)	0.086
<i>TLR9</i> rs5743836 (G)				
GPA	1	919/1898	0.83 (0.70 – 0.99)	0.037
MPA	1	153/1898	1.78 (1.32 – 2.39)	<0.001
EGPA	1	217/1898	0.90 (0.68 – 1.21)	0.499
PR3-ANCA	1	NR/NR	0.83 (0.70 – 1.00)	0.045
MPO-ANCA	1	NR/NR	1.20 (0.91 – 1.58)	0.207
ANCA negative	1	NR/NR	0.99 (0.74 – 1.34)	0.970

Supplementary Table S5. Results of the meta-analyses stratified by ethnic subgroups

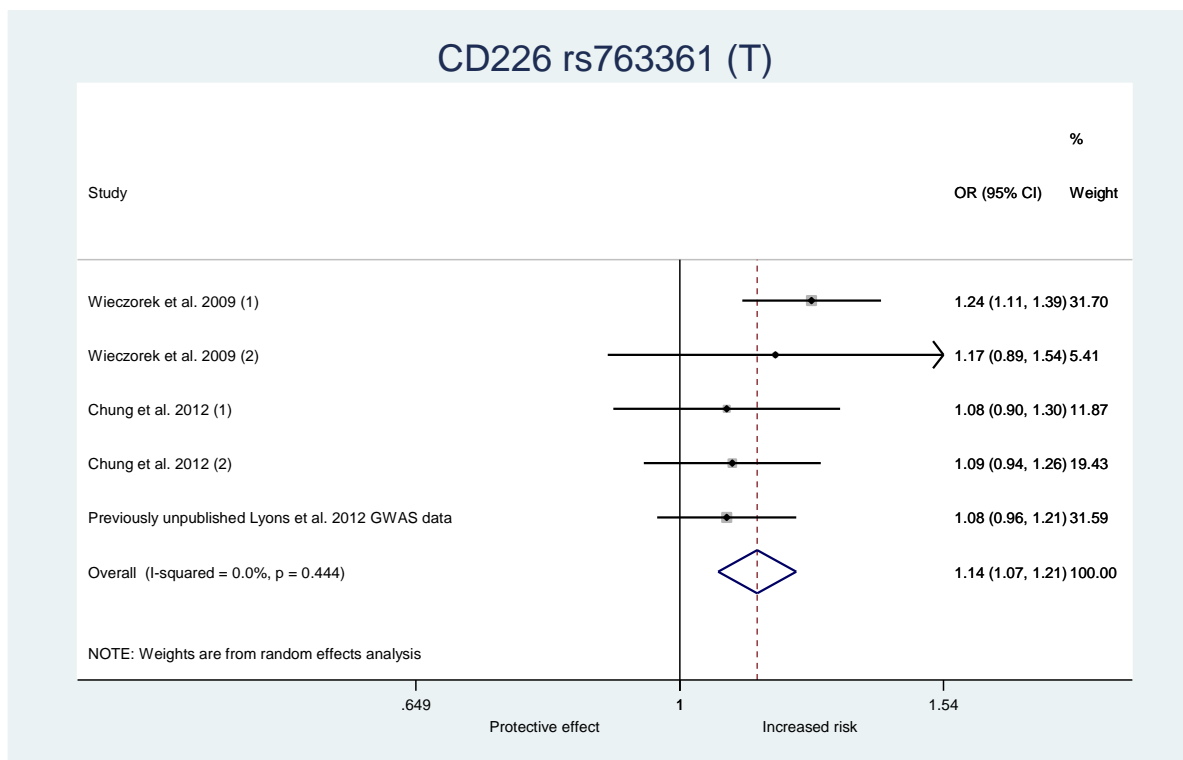
Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>CTLA-4 (AT)₈₆</i>				
Asian	1	49/111	1.31 (0.76 – 2.25)	0.333
Caucasian	3	254/432	0.46 (0.36 – 0.58)	<0.001
<i>CTLA-4 (AT)₁₀₂</i>				
Asian	1	49/111	0.89 (0.47 – 1.68)	0.714
Caucasian	2	137/309	1.73 (0.87 – 3.44)	0.117
<i>CTLA-4 (AT)₁₀₄</i>				
Asian	1	49/111	1.15 (0.70 – 1.91)	0.578
Caucasian	2	137/309	1.24 (0.88 – 1.73)	0.215
<i>CTLA-4 (AT)₁₀₆</i>				
Asian	1	49/111	0.41 (0.14 – 1.22)	0.109
Caucasian	2	137/309	2.69 (1.28 – 5.63)	0.009
<i>CTLA-4 (AT)₁₀₈</i>				
Asian	1	49/111	0.82 (0.33 – 2.02)	0.670
Caucasian	2	137/309	0.92 (0.44 – 1.92)	0.831
<i>CTLA-4 (AT)₁₁₀</i>				
Asian	1	49/111	0.25 (0.01 – 4.62)	0.349
Caucasian	2	137/309	0.84 (0.37 – 1.91)	0.679
<i>CTLA-4 (AT)₁₁₆</i>				
Asian	1	49/111	0.75 (0.03 – 18.56)	0.860
Caucasian	2	137/309	0.80 (0.26 – 2.50)	0.705
<i>CTLA-4 (AT)₁₁₈</i>				
Asian	1	49/111	0.75 (0.08 – 7.33)	0.807
Caucasian	2	137/309	0.41 (0.12 – 1.39)	0.152
<i>CTLA-4 (AT)₁₂₂</i>				
Asian	1	49/111	2.32 (0.57 – 9.45)	0.241
Caucasian	2	137/309	1.22 (0.27 – 5.49)	0.799
<i>CTLA-4 (AT)₁₂₄</i>				
Asian	1	49/111	2.28 (0.14 – 36.80)	0.562
Caucasian	2	137/309	1.94 (0.67 – 5.58)	0.222
<i>CTLA-4 (AT)₁₂₆</i>				
Asian	1	49/111	0.45 (0.05 – 3.88)	0.466
Caucasian	2	137/309	1.65 (0.63 – 4.32)	0.305
<i>CTLA-4 (AT)₁₂₈</i>				
Asian	1	49/111	6.98 (0.72 – 67.95)	0.094
Caucasian	2	137/309	0.72 (0.24 – 2.15)	0.560

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>FCGR2A</i> rs1801274 (C)				
Asian	1	50/303	0.68 (0.37 – 1.24)	0.208
Caucasian	5	1126/5969	0.91 (0.82 – 1.00)	0.043
<i>FCGR3A</i> rs396991 (G)				
Asian	1	50/303	0.65 (0.39 – 1.07)	0.090
Caucasian	1	91/154	1.30 (0.89 – 1.91)	0.172
<i>FCGR3B</i> (NA1)				
Asian	1	50/303	1.29 (0.82 – 2.03)	0.267
Caucasian	3	865/667	0.93 (0.80 – 1.08)	0.343
<i>HLA-A2</i>				
Asian	1	16/472	0.90 (0.37 – 2.23)	0.826
Caucasian	4	427/7324	0.96 (0.81 – 1.13)	0.595
<i>HLA-A11</i>				
Asian	1	16/472	0.71 (0.17 – 3.03)	0.644
Caucasian	5	450/7635	1.01 (0.50 – 2.05)	0.978
<i>HLA-A24</i>				
Asian	1	16/472	0.75 (0.34 – 1.65)	0.476
Caucasian	2	92/751	1.16 (0.57 – 2.38)	0.683
<i>HLA-A26</i>				
Asian	1	16/472	2.36 (1.00 – 5.60)	0.051
Caucasian	3	115/1156	1.21 (0.58 – 2.55)	0.612
<i>HLA-A31</i>				
Asian	1	16/472	1.55 (0.46 – 5.24)	0.479
Caucasian	2	92/751	0.73 (0.21 – 2.52)	0.613
<i>HLA-A32</i>				
Asian	1	16/472	2.07 (0.61 – 7.04)	0.246
Caucasian	2	92/751	1.41 (0.52 – 3.84)	0.500
<i>HLA-B35</i>				
Asian	1	16/472	0.80 (0.17 – 3.40)	0.757
Caucasian	3	396/6623	0.78 (0.58 – 1.06)	0.115
<i>HLA-B39</i>				
Asian	1	16/472	0.86 (0.11 – 6.51)	0.887
Caucasian	1	51/51	0.33 (0.01 – 8.20)	0.499
<i>HLA-B44</i>				
Asian	1	16/472	2.50 (0.85 – 7.40)	0.098
Caucasian	2	92/751	1.41(0.85 – 2.35)	0.188

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
<i>HLA-B51</i>				
Asian	1	16/472	1.87 (0.64 – 5.49)	0.255
Caucasian	1	51/51	0.61 (0.19 – 1.92)	0.394
<i>HLA-B55</i>				
Asian	1	16/472	7.35 (2.34 – 23.14)	0.001
Caucasian	1	51/51	0.07 (0.00 – 1.30)	0.075
<i>HLA-B60</i>				
Asian	1	16/472	1.19 (0.28 – 5.13)	0.814
Caucasian	1	41/700	3.51 (0.99 – 12.36)	0.051
<i>HLA-B62</i>				
Asian	1	16/472	1.71 (0.58 – 4.99)	0.331
Caucasian	1	41/700	2.38 (0.70 – 8.12)	0.166
<i>HLA-Cw1</i>				
Asian	1	16/472	1.45 (0.58 – 3.58)	0.426
Caucasian	1	52/51	0.98 (0.24 – 4.03)	0.978
<i>HLA-Cw3</i>				
Asian	1	16/472	1.40 (0.66 – 3.01)	0.384
Caucasian	1	52/51	1.32 (0.62 – 2.81)	0.479
<i>HLA-Cw7</i>				
Asian	1	16/472	0.50 (0.12 – 2.10)	0.340
Caucasian	1	52/51	1.10 (0.62 – 1.96)	0.735
<i>HLA-DPB1*0201</i>				
Asian	1	50/77	1.38 (0.75 – 2.52)	0.298
Caucasian	3	385/827	0.76 (0.56 – 1.03)	0.073
<i>HLA-DQB1*0303</i>				
Asian	1	50/77	2.11 (1.14 – 3.90)	0.018
Caucasian	2	126/141	1.35 (0.55 – 3.33)	0.515
<i>HLA-DR1</i>				
Asian	1	64/265	1.12 (0.48 – 2.64)	0.793
Caucasian	9	945/6840	0.91 (0.61 – 1.36)	0.651
<i>HLA-DR2</i>				
Asian	1	16/472	0.33 (0.08 – 1.38)	0.128
Caucasian	4	471/5750	1.06 (0.87 – 1.29)	0.565
<i>HLA-DR4</i>				
Asian	1	16/472	0.72 (0.27 – 1.88)	0.498
Caucasian	10	882/7262	1.23 (0.97 – 1.57)	0.088

Variant by gene	Publications (n)	Cases (n) / Controls (n)	OR (95% CI)	P value for meta-analysis
HLA-DR6				
Asian	1	16/472	1.63 (0.56 – 4.77)	0.371
Caucasian	4	471/5750	0.43 (0.30 – 0.61)	<0.001
HLA-DR8				
Asian	1	16/472	1.63 (0.66 – 4.05)	0.291
Caucasian	8	597/1483	1.05 (0.75 – 1.49)	0.768
HLA-DR9				
Asian	4	296/1409	1.67 (0.83 – 3.34)	0.148
Caucasian	7	510/1443	0.63 (0.34 – 1.19)	0.152
<i>IRF5</i> rs10954213 (G)				
Asian	1	232/710	1.28 (1.04 – 1.58)	0.022
Caucasian	2	1303/6267	0.69 (0.63 – 0.76)	<0.001
<i>STAT4</i> rs7574865 (T)				
Asian	1	232/710	1.10 (0.89 – 1.37)	0.388
Caucasian	2	1288/6246	1.11 (1.00 – 1.24)	0.044
<i>TNFR11</i> 196R				
Asian	1	50/262	0.67 (0.31 – 1.45)	0.313
Caucasian	1	117/123	1.05 (0.70 – 1.57)	0.819

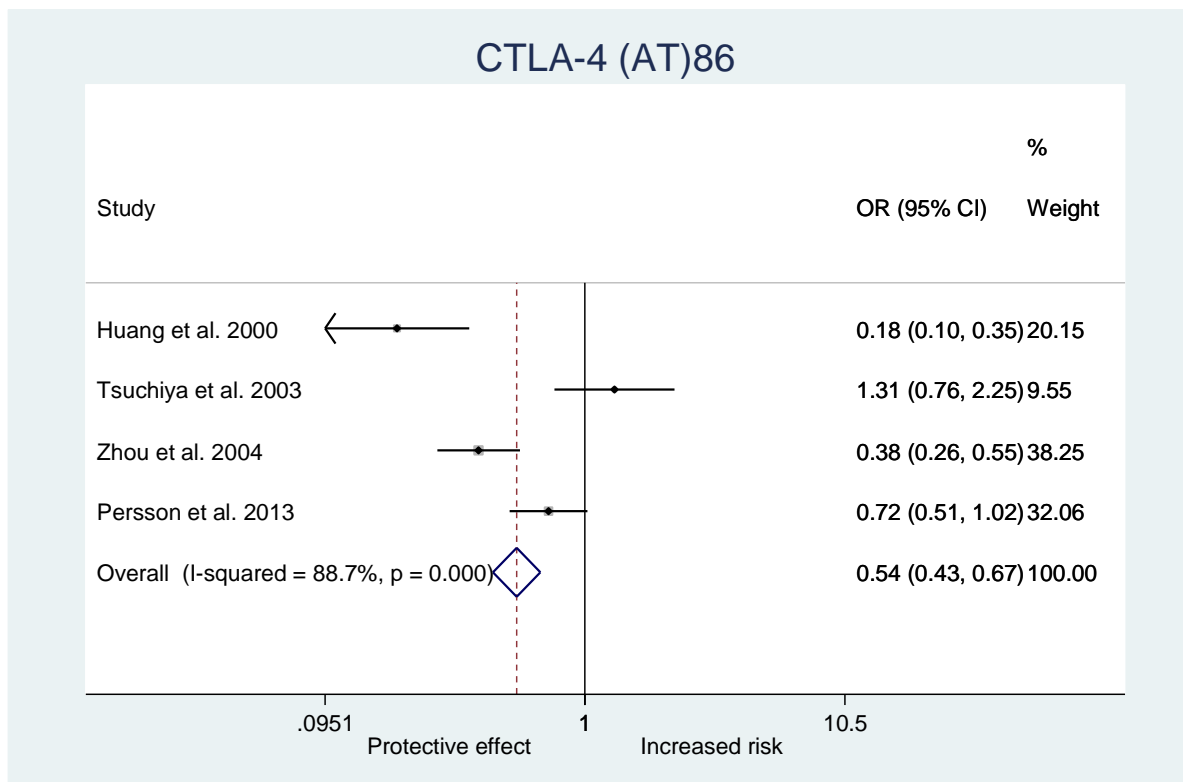
Supplementary Figure S1. Forest plots



CD226 rs763361 (T) forest plot. Harbold test: N/A, Egger test: $p=0.792$.

References

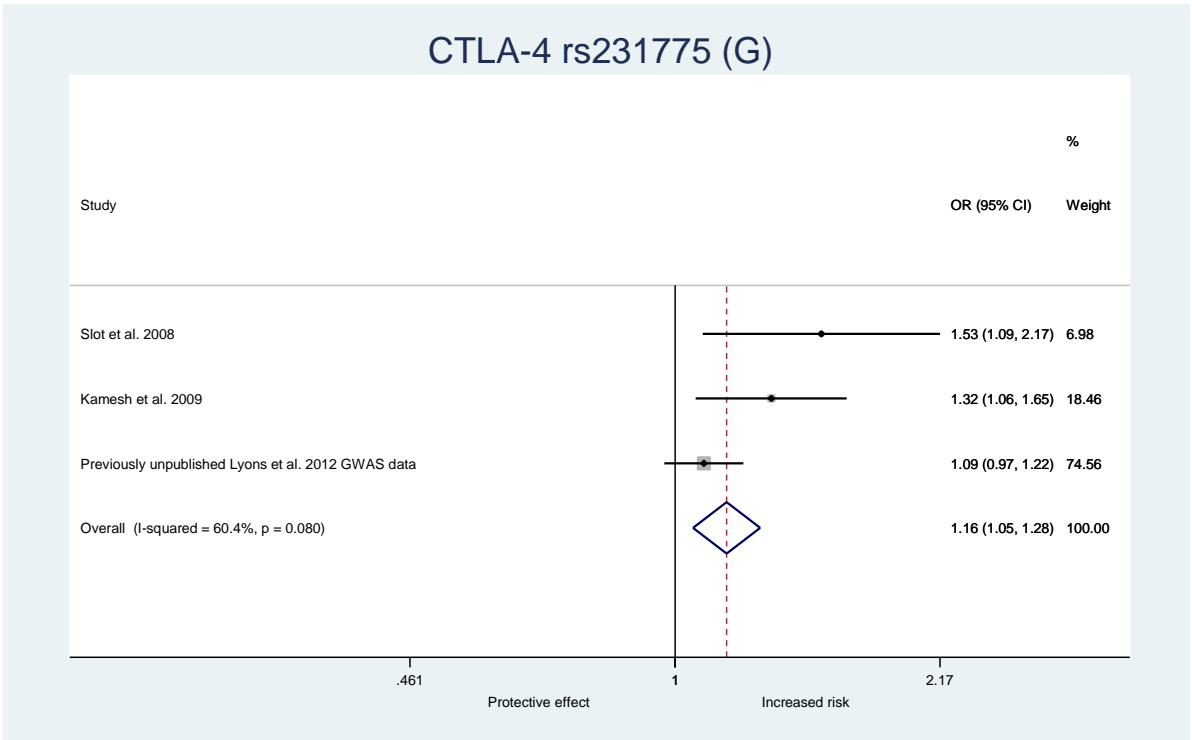
¹**, ²**, ³



CTLA-4 (AT)₈₆ forest plot. Harbold test: $p=0.946$, Egger test: $p=0.788$.

References

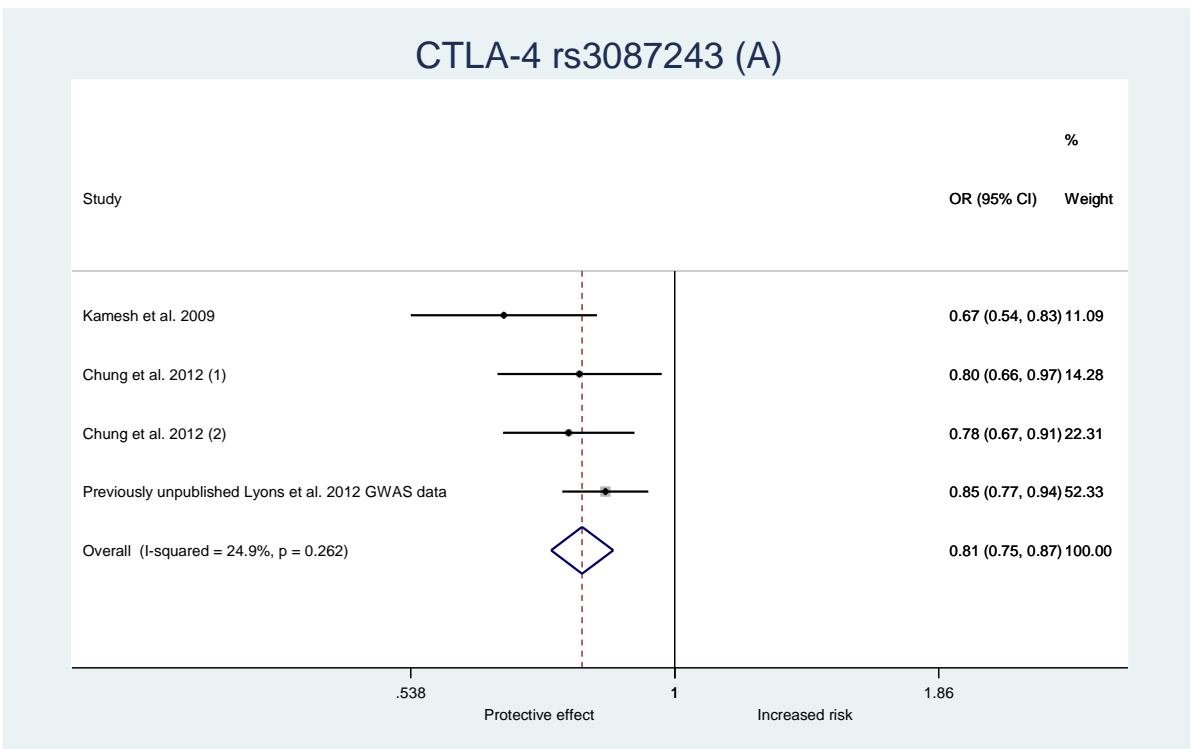
⁴, ⁵, ⁶, ⁷, , ,



CTLA-4 rs231775 (G) forest plot. Harbold test: $p=0.080$, Egger test: $p=0.081$.

References

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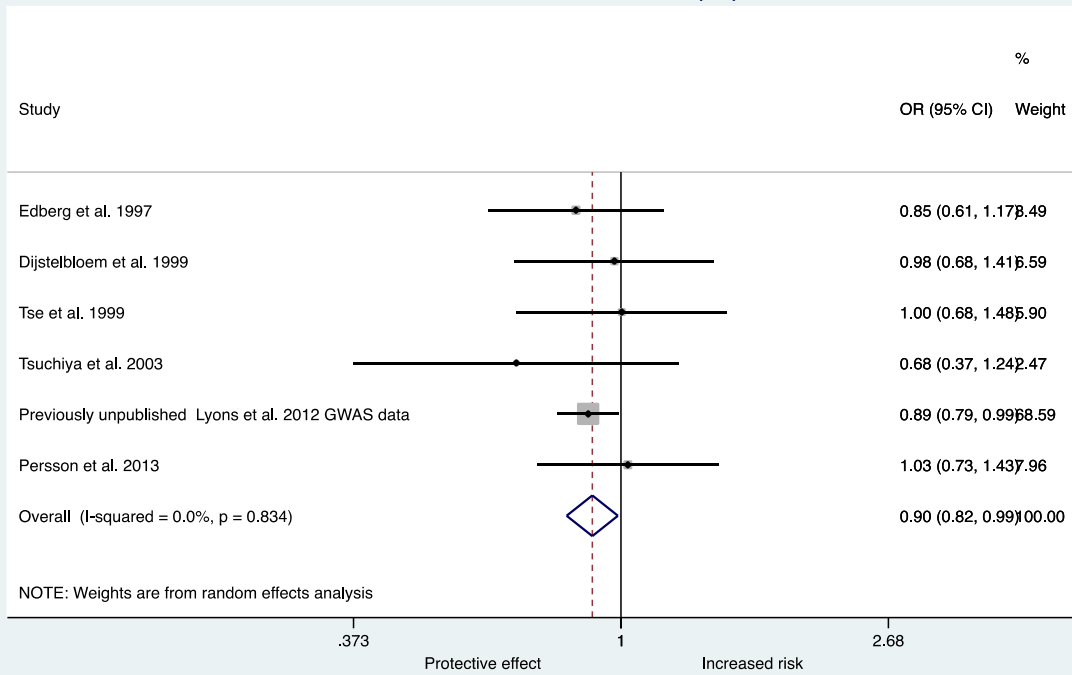


CTLA-4 rs3087243 (A) forest plot. Harbold test: N/A, Egger test: $p=0.122$.

References

9 2** 3
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FCGR2A rs1801274 (C)

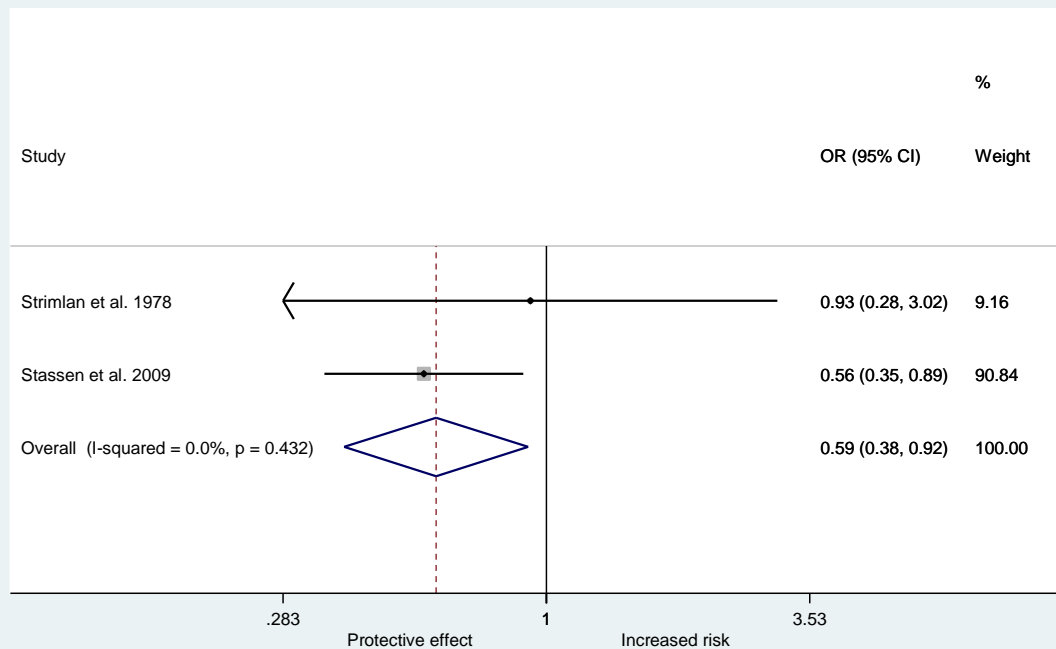


FCGR2A rs1801274 (C) forest plot. Harbold test: $p=0.788$, Egger test: $p=0.829$.

References

11 12 13 5 7 3
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HLA-B5

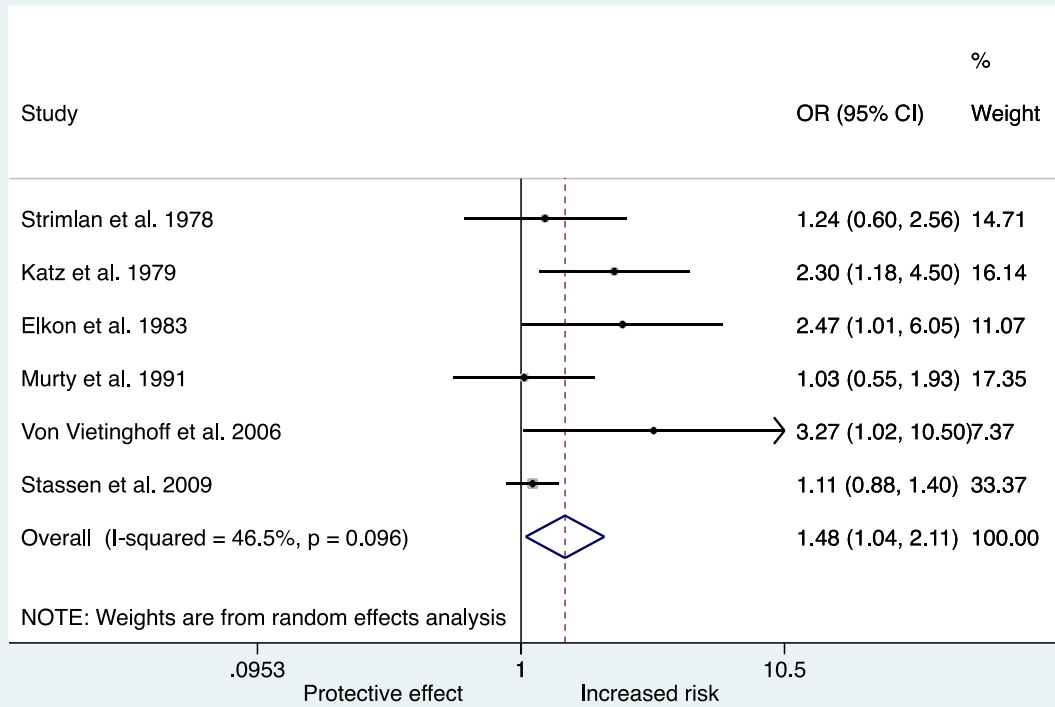


HLA-B5 forest plot. Harbold test: N/A, Egger test: N/A.

References

16 19
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HLA-B8

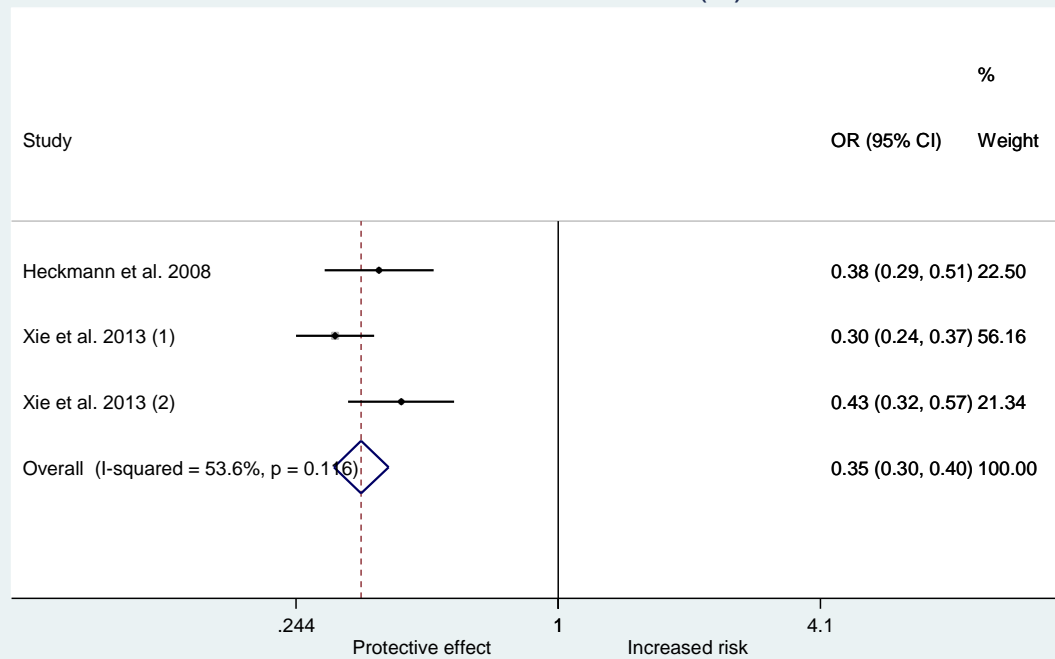


HLA-B8 forest plot. Harbold test: $p=0.063$, Egger test: $p=0.077$.

References

16 21 23 17 18 19
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HLA-DPA1 rs9277341 (C)

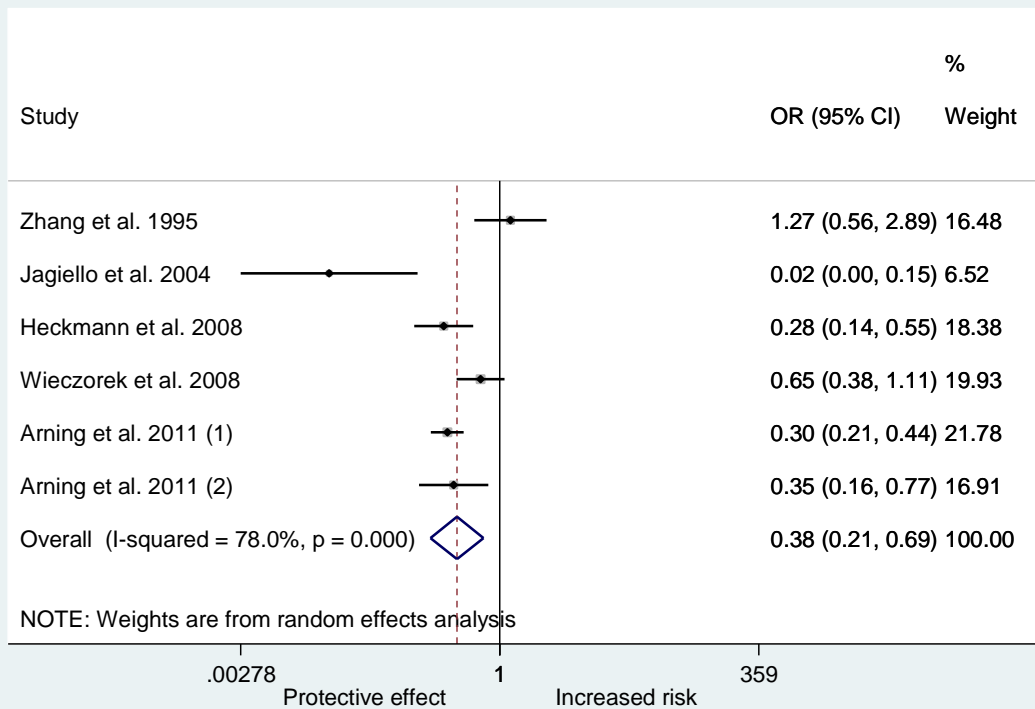


HLA-DPA1 rs9277341 (C) forest plot. Harbold test: $p=0.215$, Egger test: $p=0.219$.

References

24 25**
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HLA-DPB1*0301

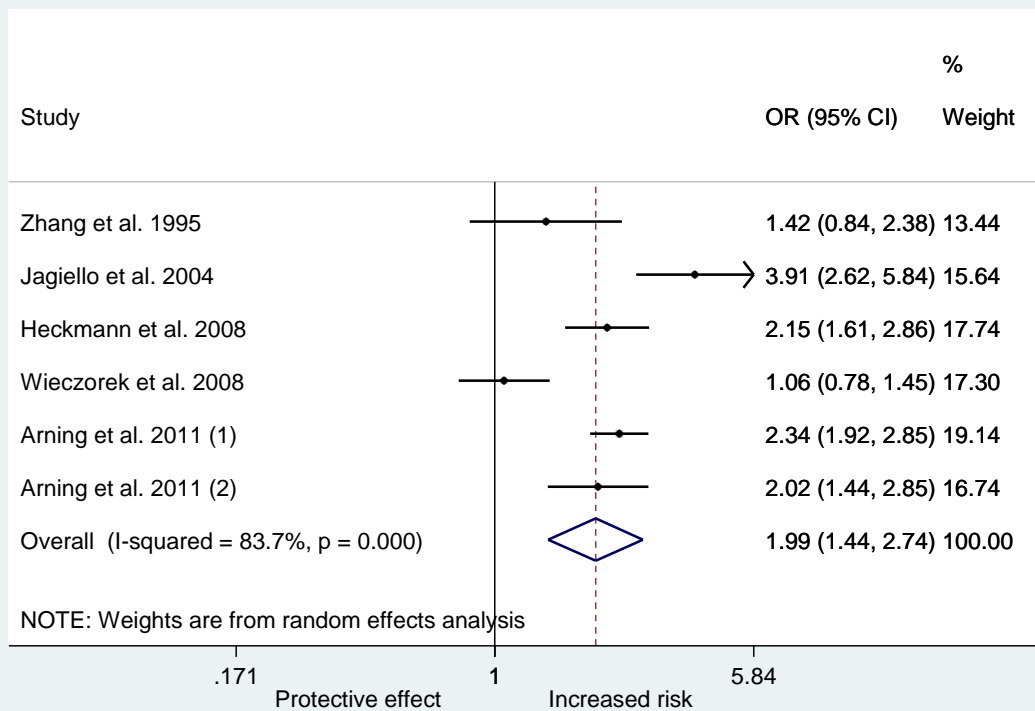


HLA-DPB1*0301 forest plot. Harbold test: $p=0.938$, Egger test: $p=0.744$.

References

²⁶, ²⁷, ²⁴, ²⁹, ³⁰**

HLA-DPB1*0401

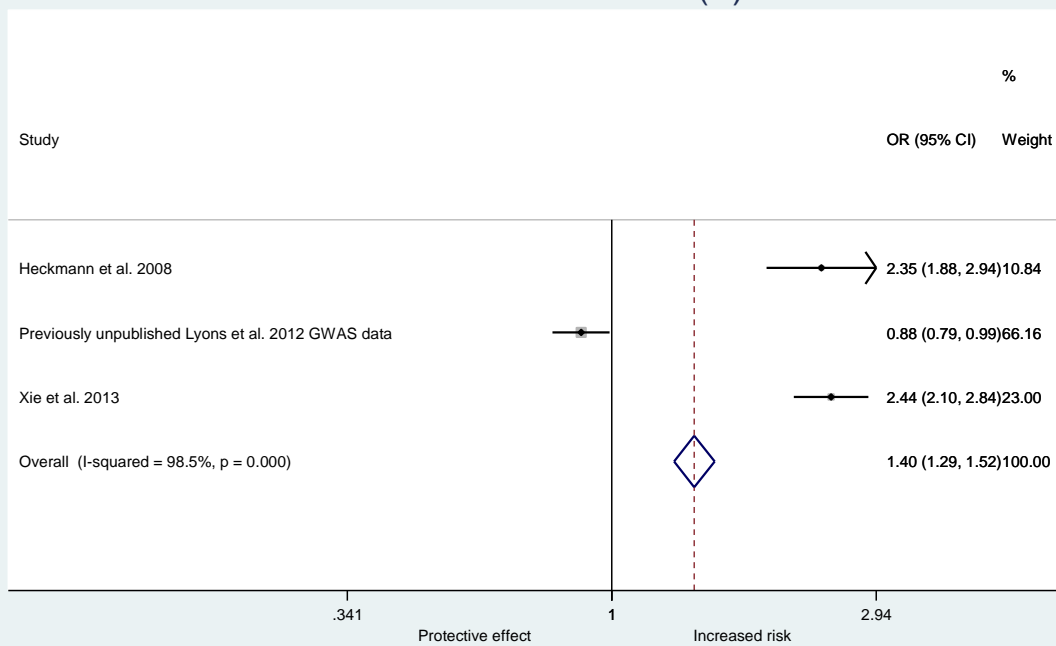


HLA-DPB1*0401 forest plot. Harbold test: $p=0.738$, Egger test: $p=0.759$.

References

²⁶, ²⁷, ²⁴, ²⁹, ³⁰**

HLA-DPB2 rs3130215 (A)

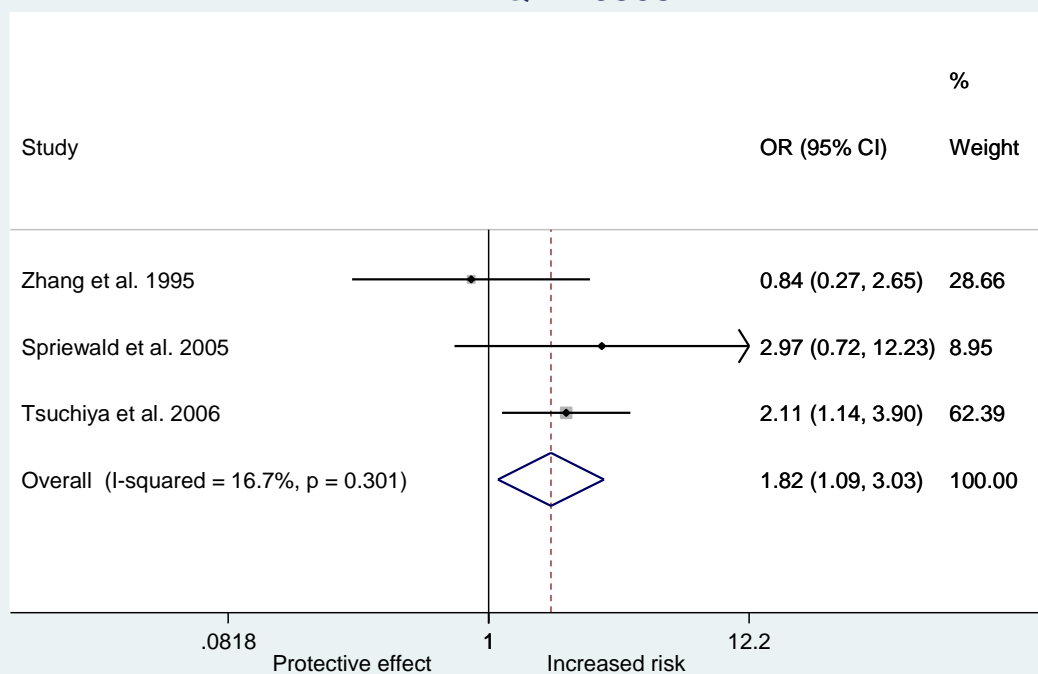


HLA-DPB2 rs3130215 (A) forest plot. Harbold test: $p=0.446$, Egger test: $p=0.431$.

References

24 3 25
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HLA-DQB1*0303

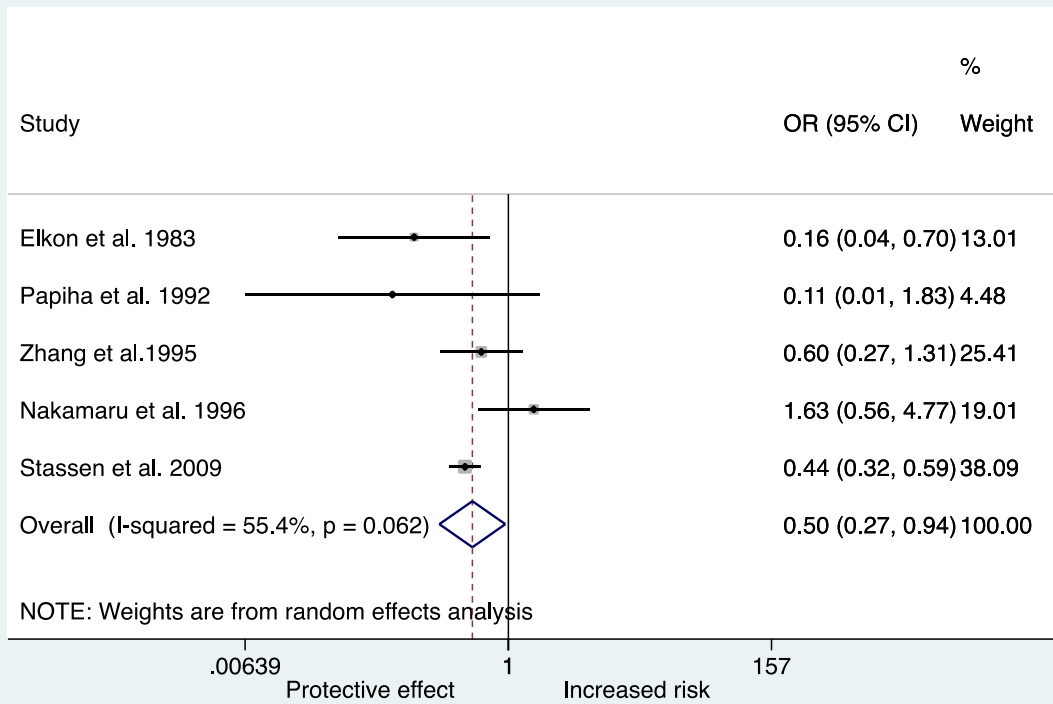


HLA-DQB1*0303 forest plot. Harbold test: $p=0.916$, Egger test: $p=0.834$.

References

26 31 28
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HLA-DR6

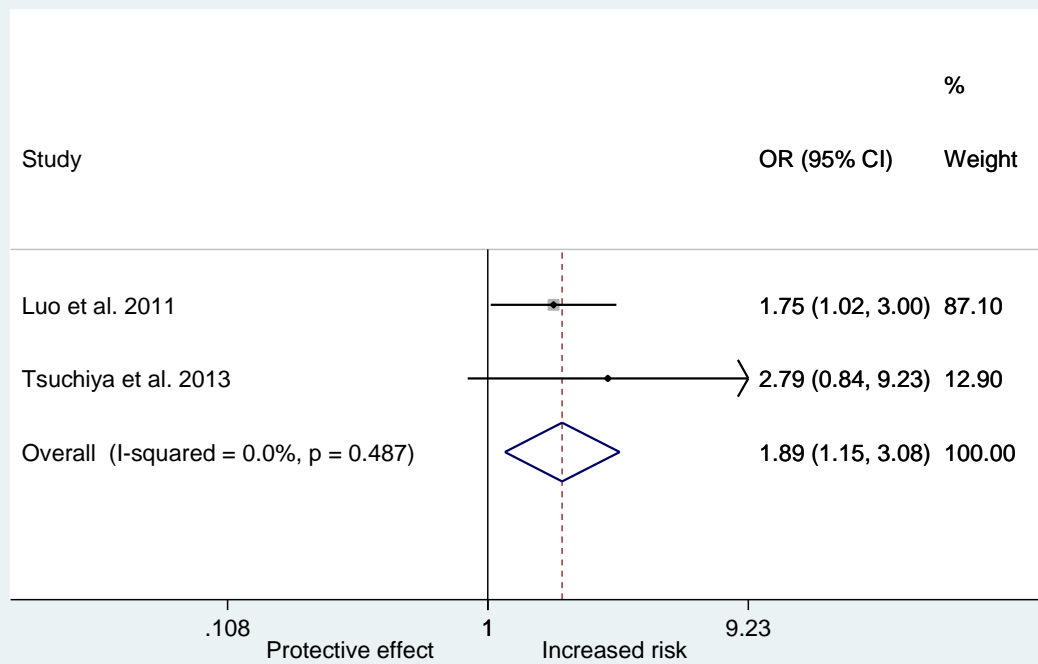


HLA-DR6 forest plot. Harbold test: $p=0.997$, Egger test: $p=0.989$.

References

23 32 26 20 19
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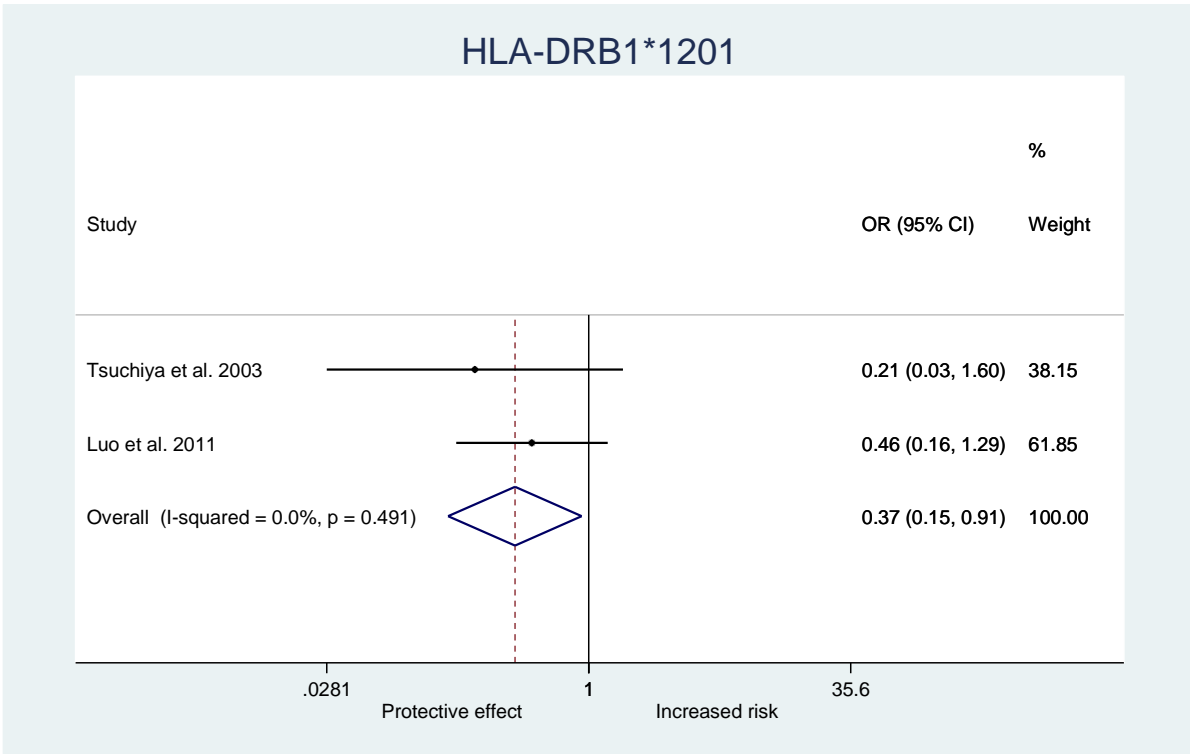
HLA-DRB1*1101



HLA-DRB1*1101 forest plot. Harbold test: N/A, Egger test: N/A.

References

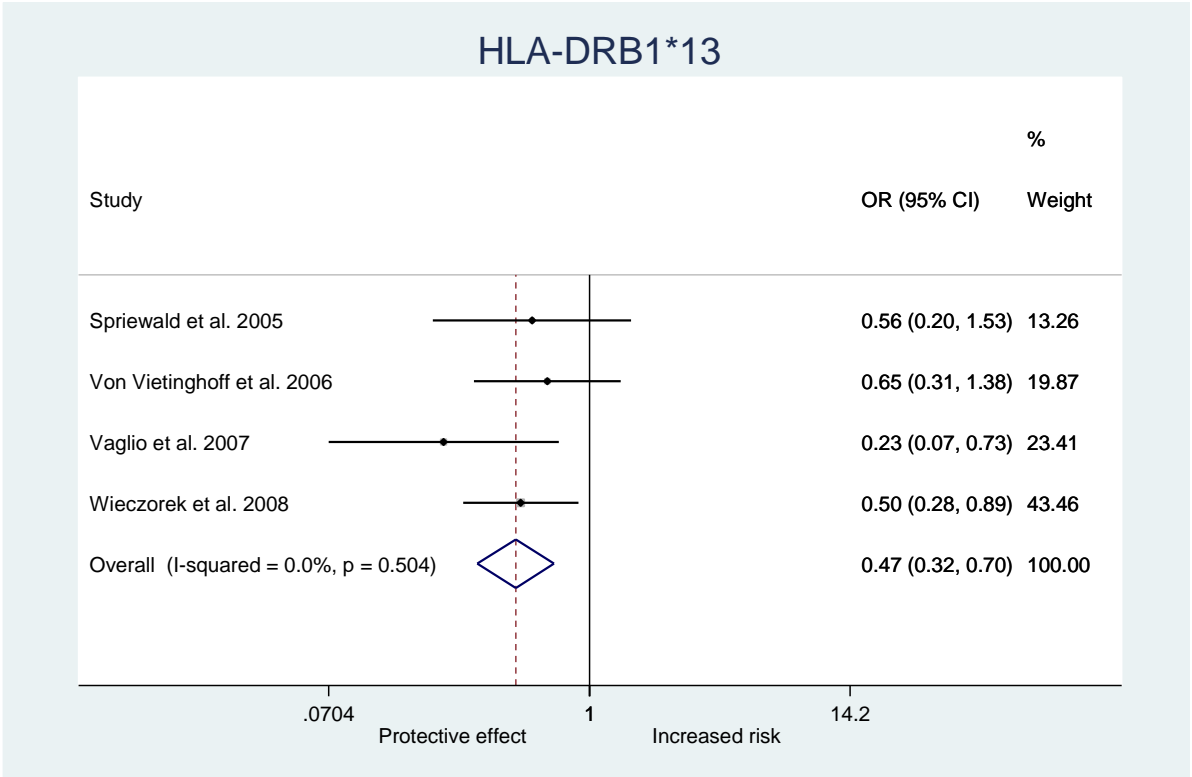
34 37
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HLA-DRB1*1201 forest plot. Harbold test: N/A, Egger test: N/A.

References

5 34
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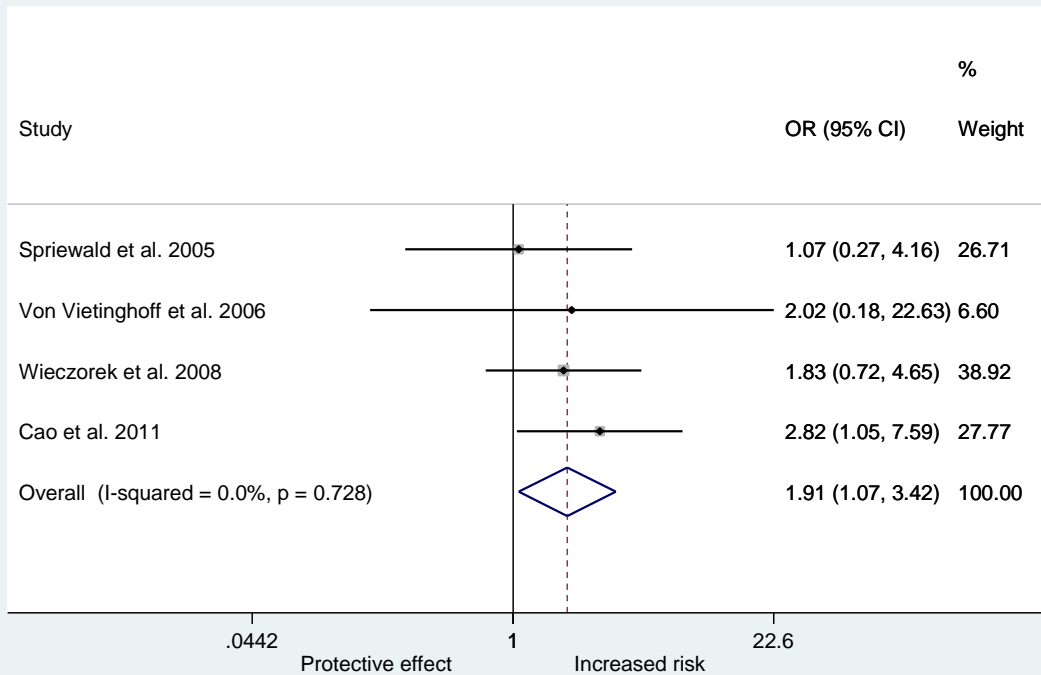


HLA-DRB1*13 forest plot. Harbold test: p=0.884, Egger test: p=0.467.

References

31 18 35 29
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HLA-DRB1*14

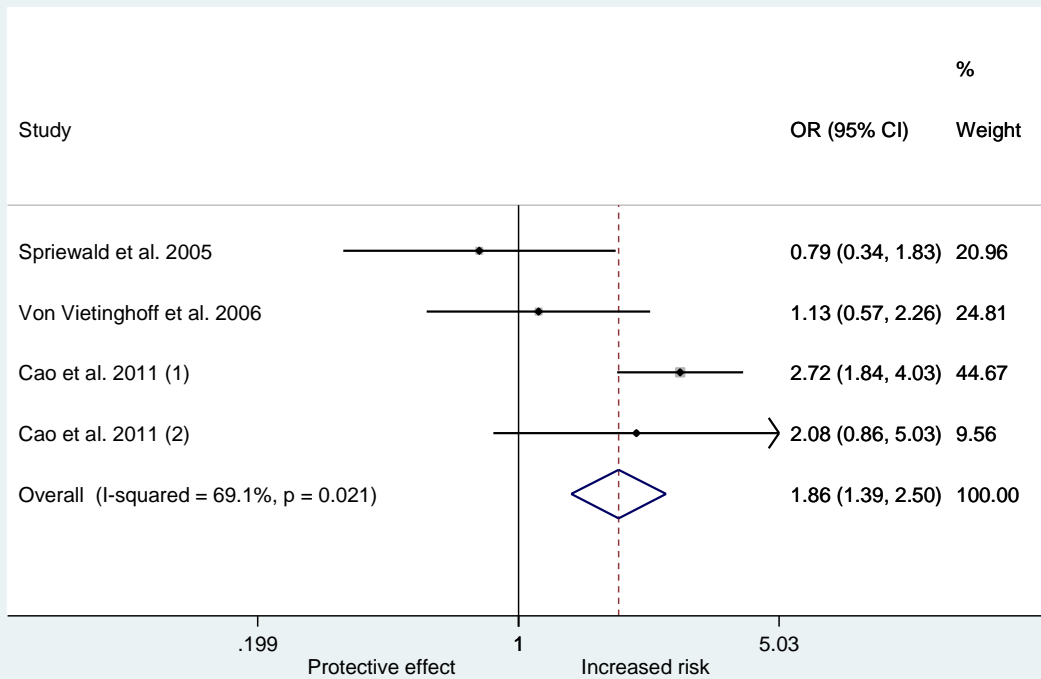


HLA-DRB1*14 forest plot. Harbold test: $p=0.700$, Egger test: $p=0.706$.

References

31 18 29 33
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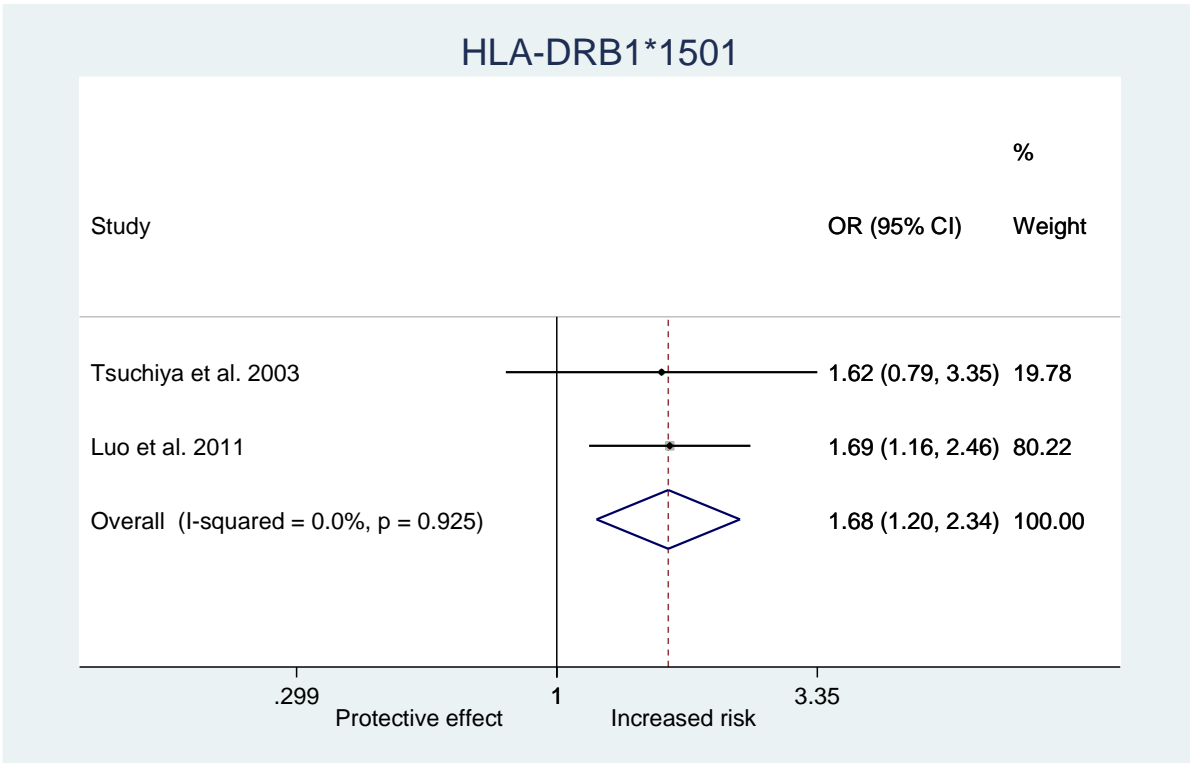
HLA-DRB1*15



HLA-DRB1*15 forest plot. Harbold test: $p=0.347$, Egger test: $p=0.214$.

References

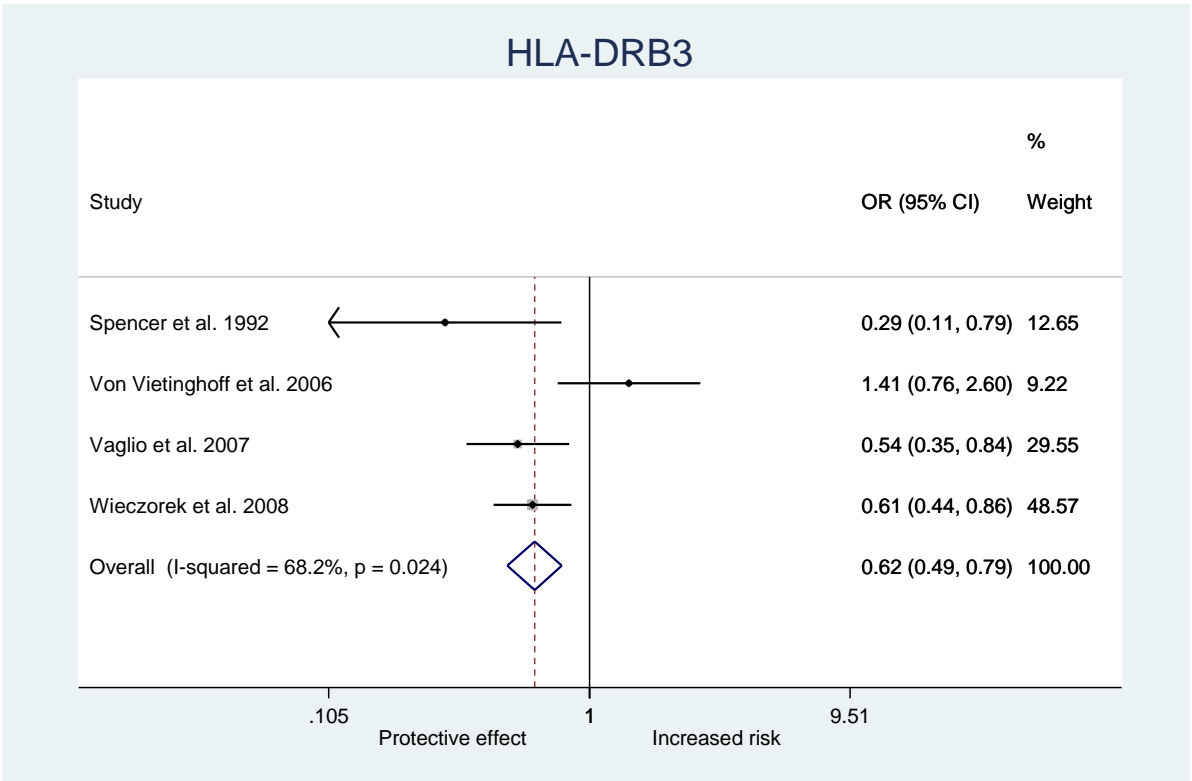
31 18 33**
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HLA-DRB1*1501 forest plot. Harbold test: N/A, Egger test: N/A.

References

5, 34,

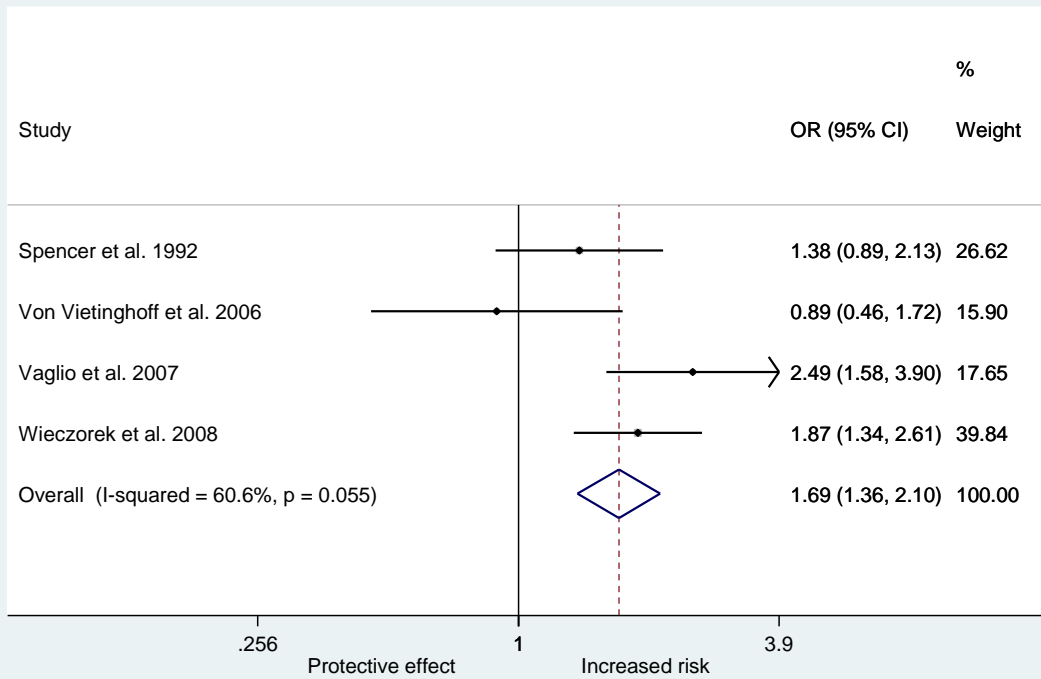


HLA-DRB3 forest plot. Harbold test: p=0.689, Egger test: p=0.958.

References

38, 18, 35, 29,

HLA-DRB4

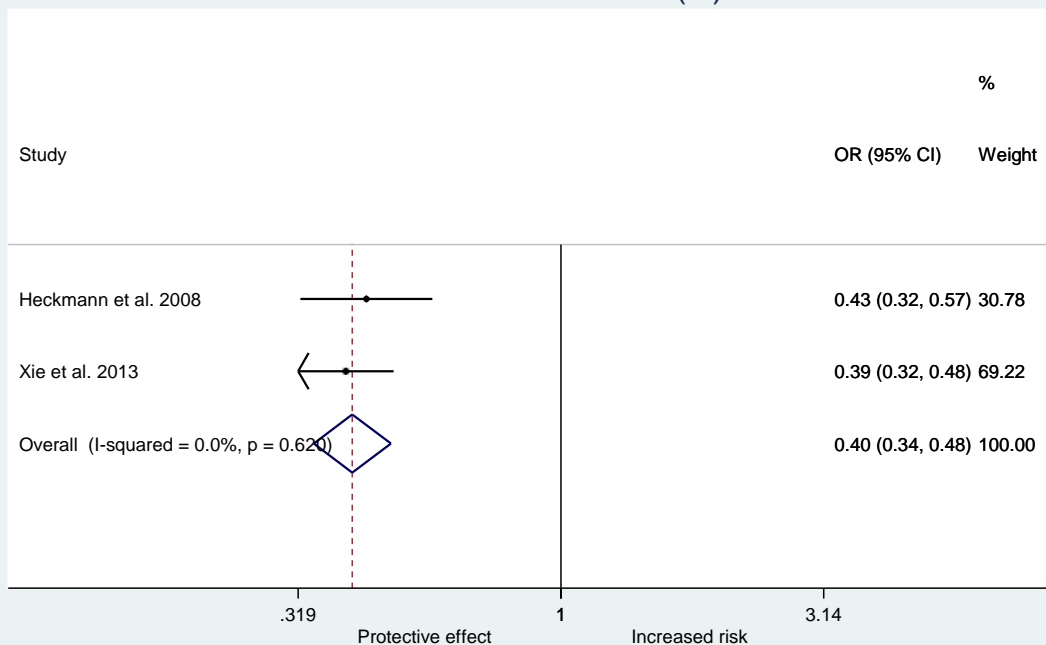


HLA-DRB4 forest plot. Harbord test: $p=0.533$, Egger test: $p=0.388$.

References

38 18 35 29
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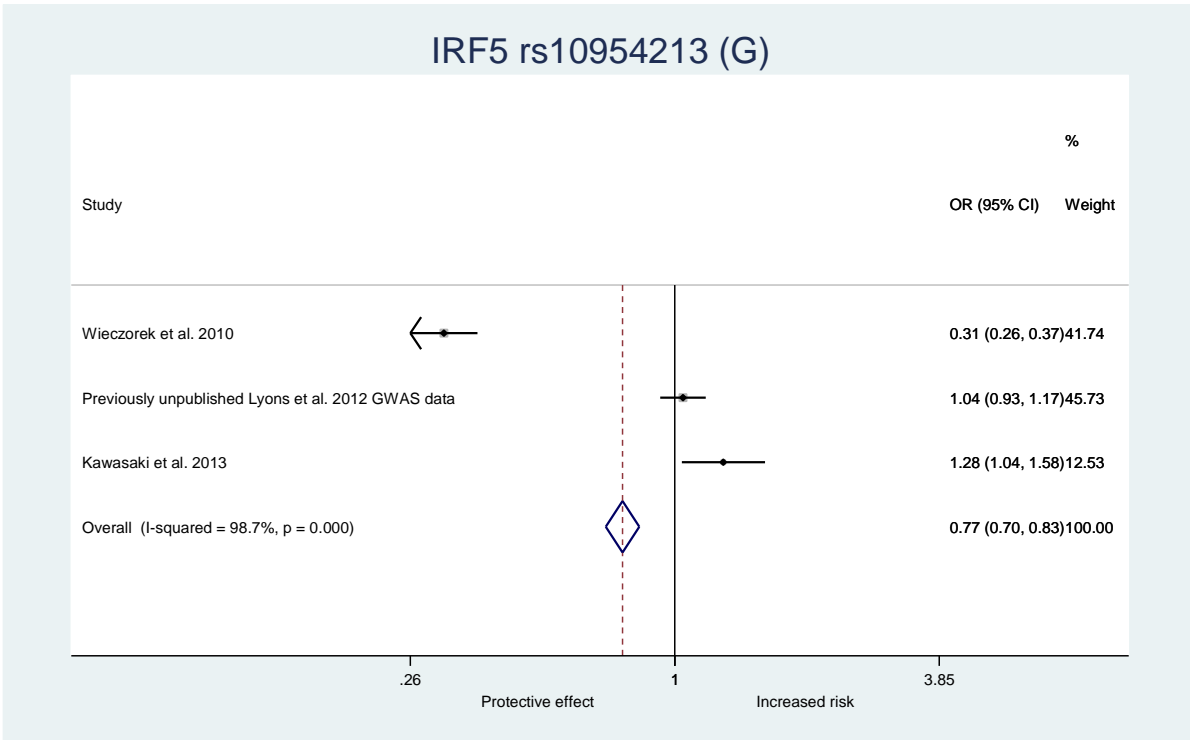
HSD17B8 rs421446 (C)



HSD17B8 rs421446 (C) forest plot. Harbord test: N/A, Egger test: N/A.

References

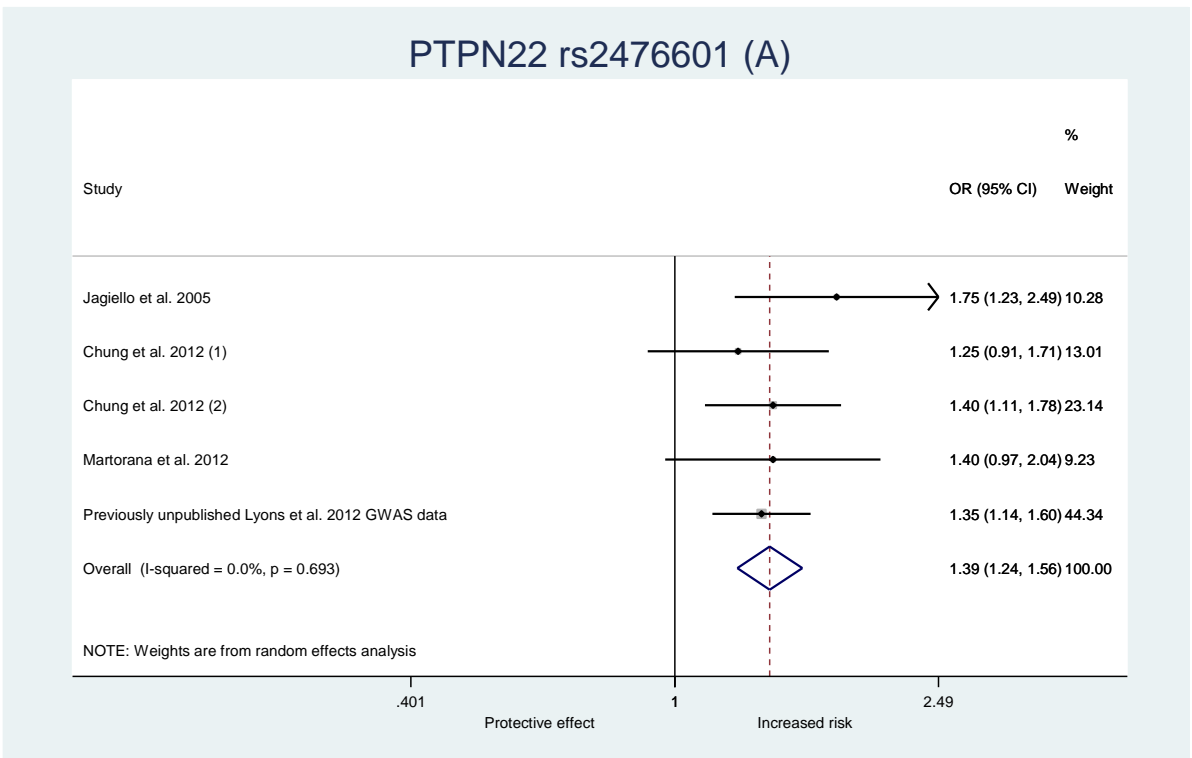
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IRF5 rs10954213 (G) forest plot. Harbold test: $p=0.948$, Egger test: $p=0.833$.

References

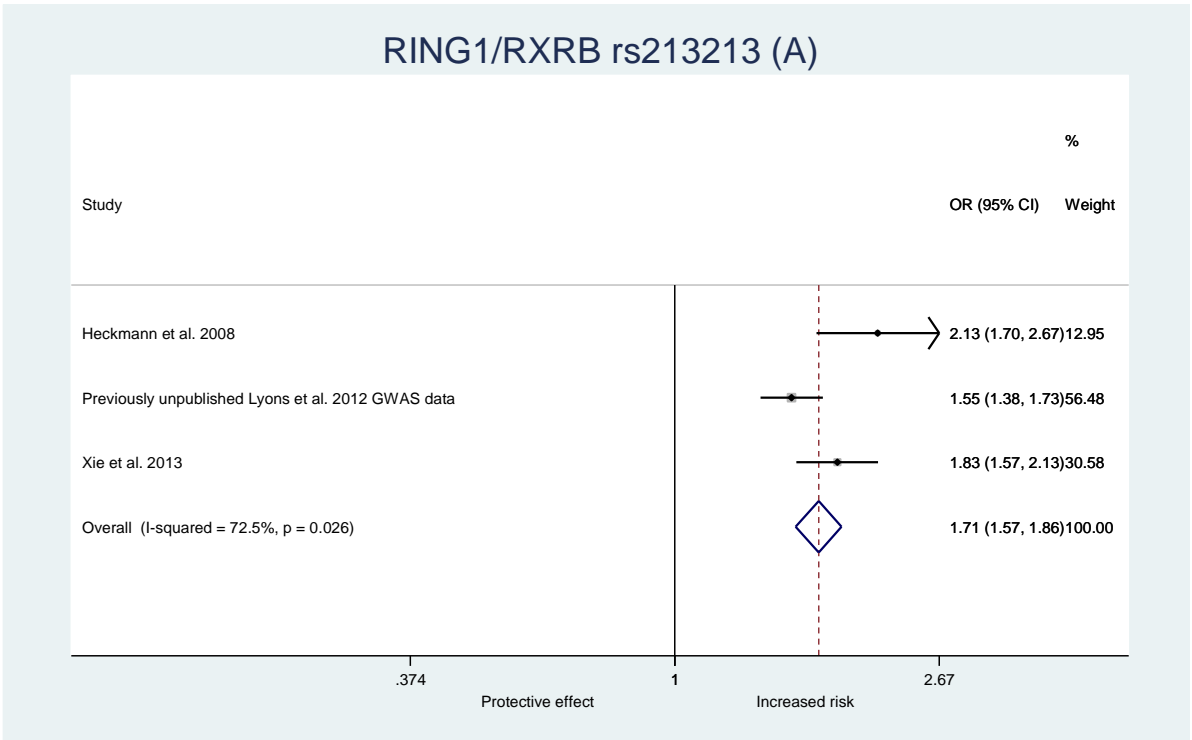
44 3 45
, ,



PTPN22 rs2476601 (A) forest plot. Harbold test: N/A, Egger test: $p=0.500$.

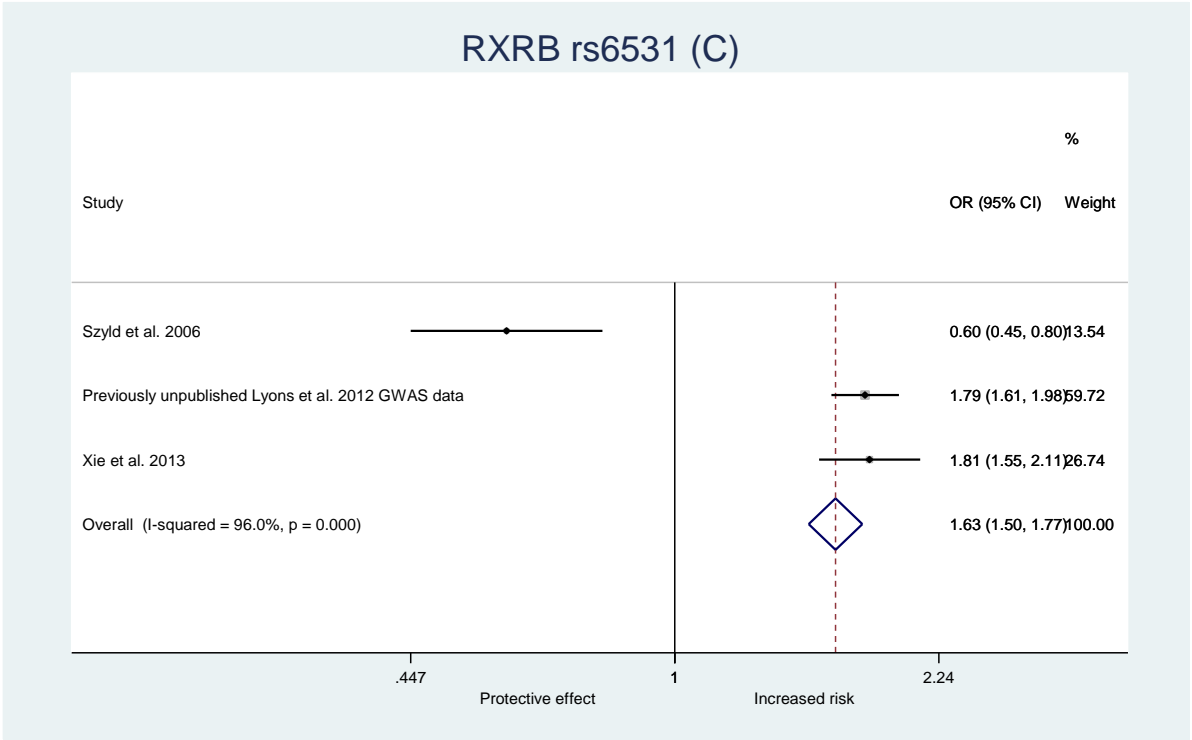
References

50 2** 51 3
, ,



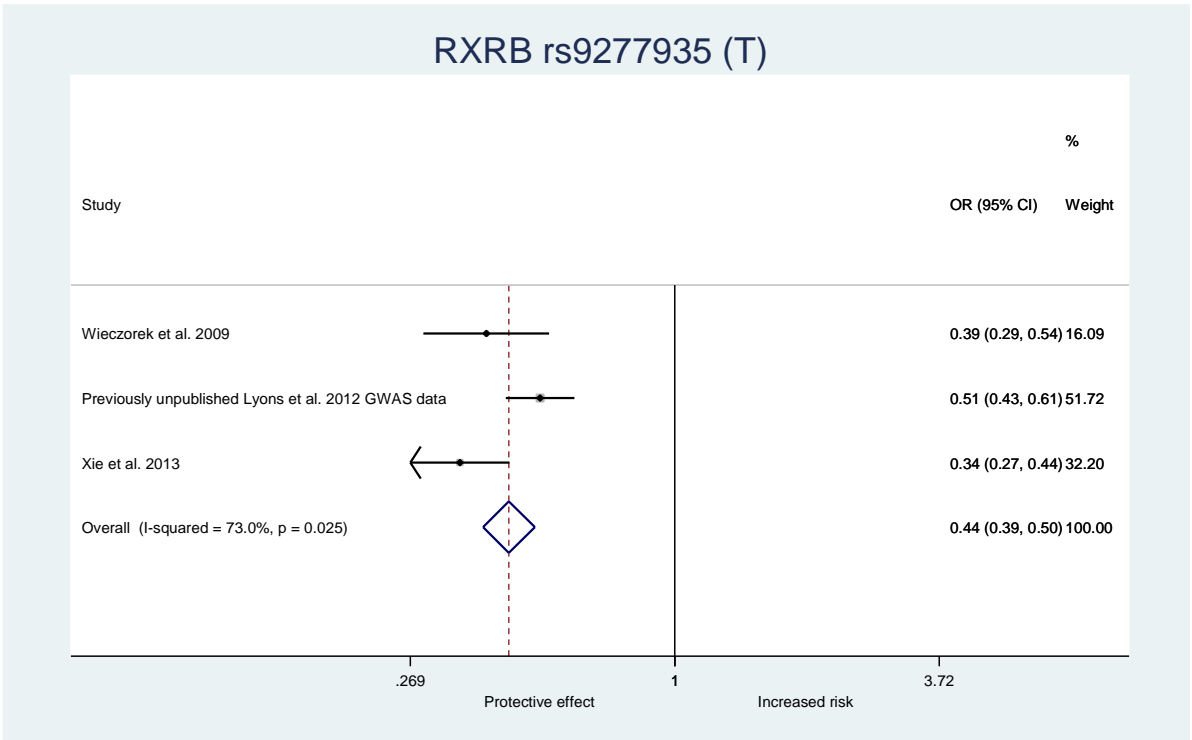
RING1/RXR_B rs213213 (A) forest plot. Harbold test: $p=0.187$, Egger test: $p=0.169$.

References
24 3 25
, ,



RXR_B rs6531 (C) forest plot. Harbold test: $p=0.292$, Egger test: $p=0.301$.

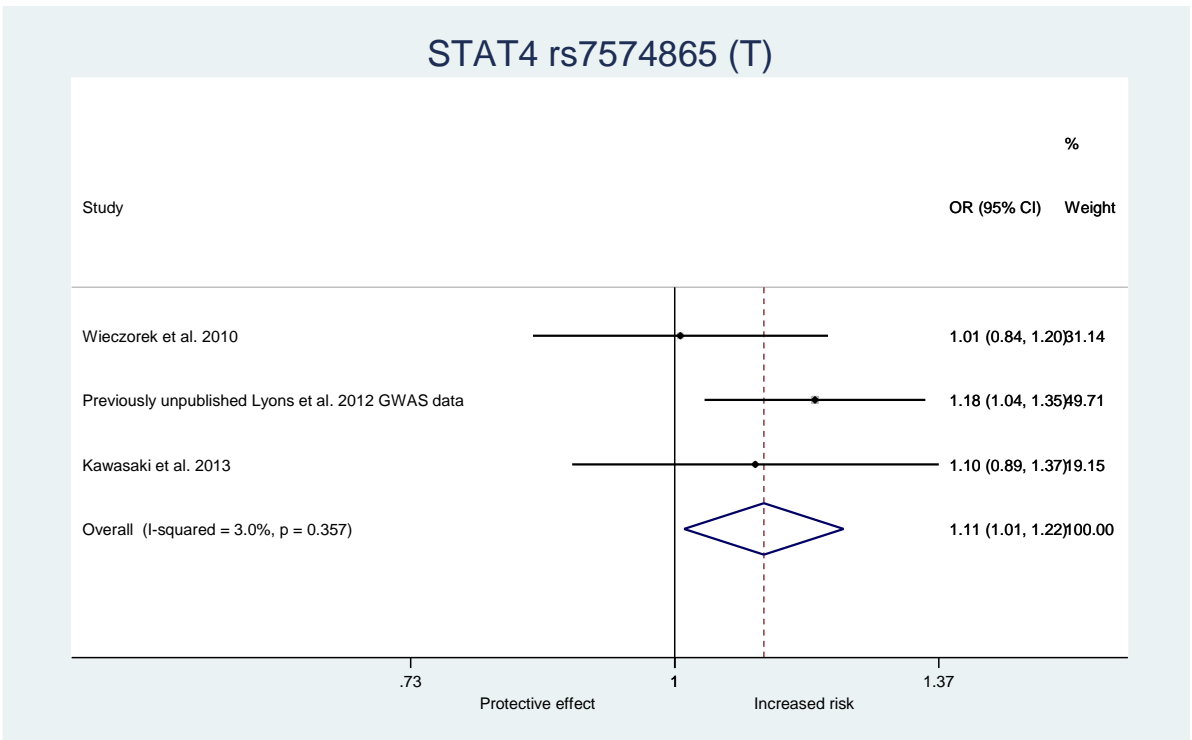
References
52 3 25
, ,



RXRB rs9277935 (T) forest plot. Harbold test: $p=0.393$, Egger test: $p=0.406$.

References

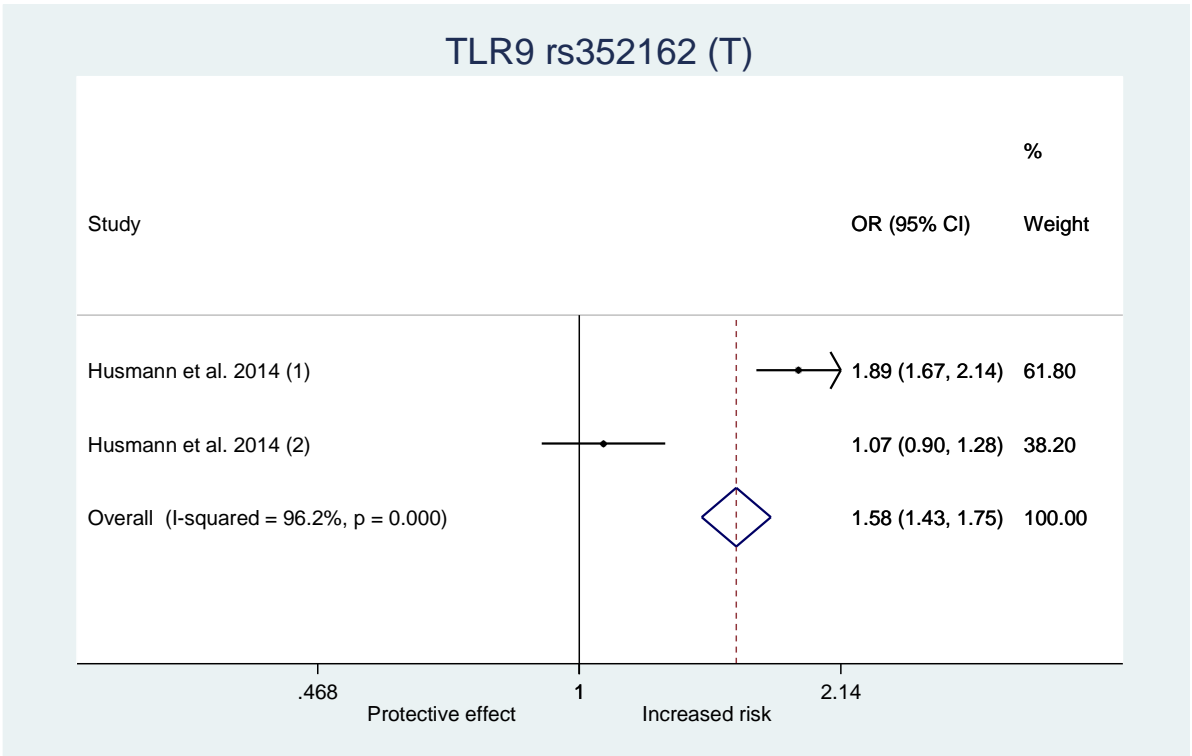
53 3 25
, ,



STAT4 rs7574865 (T) forest plot. Harbold test: $p=0.590$, Egger test: $p=0.567$.

References

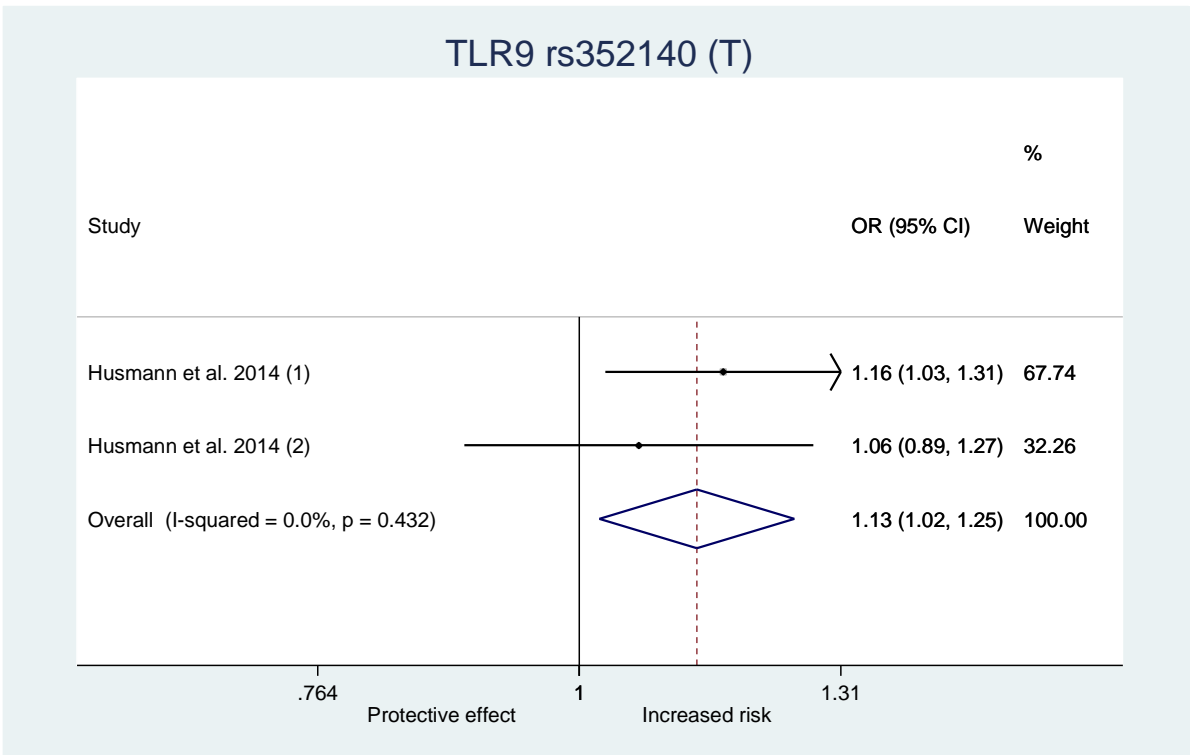
44 45 3
, ,



TLR9 rs352162 (T) forest plot. Harbold test: N/A, Egger test: N/A.

References

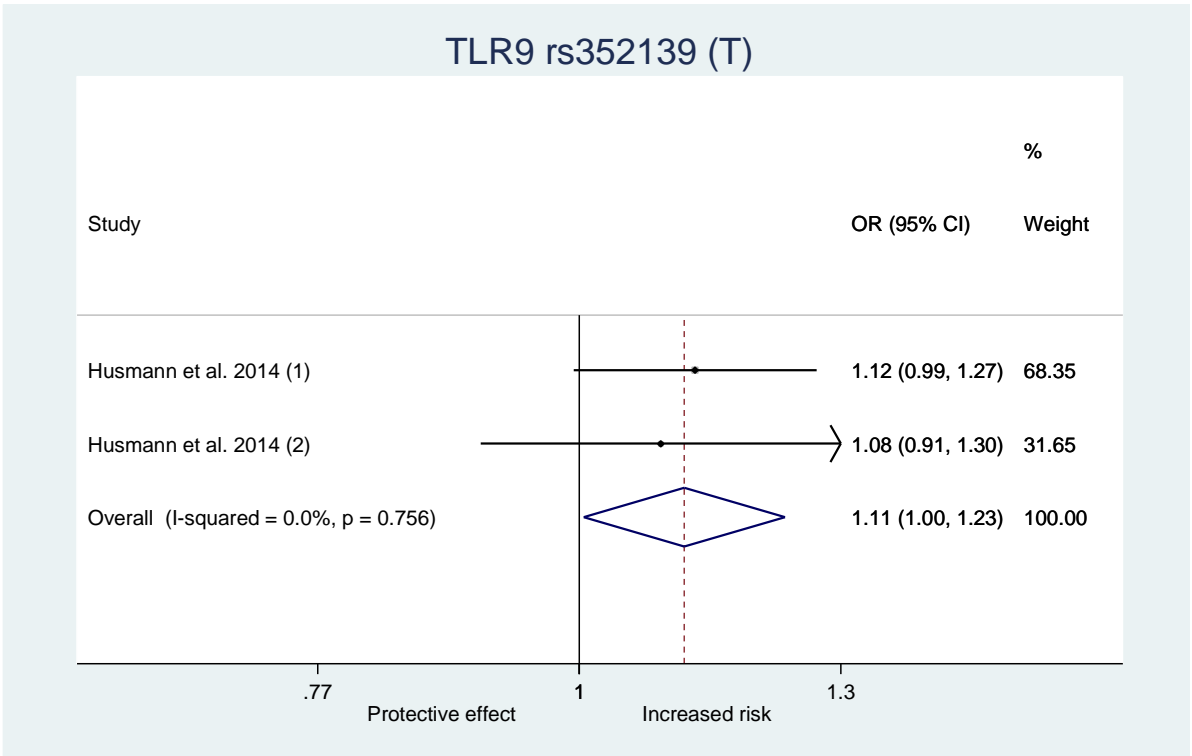
40**



TLR9 rs352140 (T) forest plot. Harbold test: N/A, Egger test: N/A.

References

40**



TLR9 rs352139 (T) forest plot. Harbold test: N/A, Egger test: N/A.

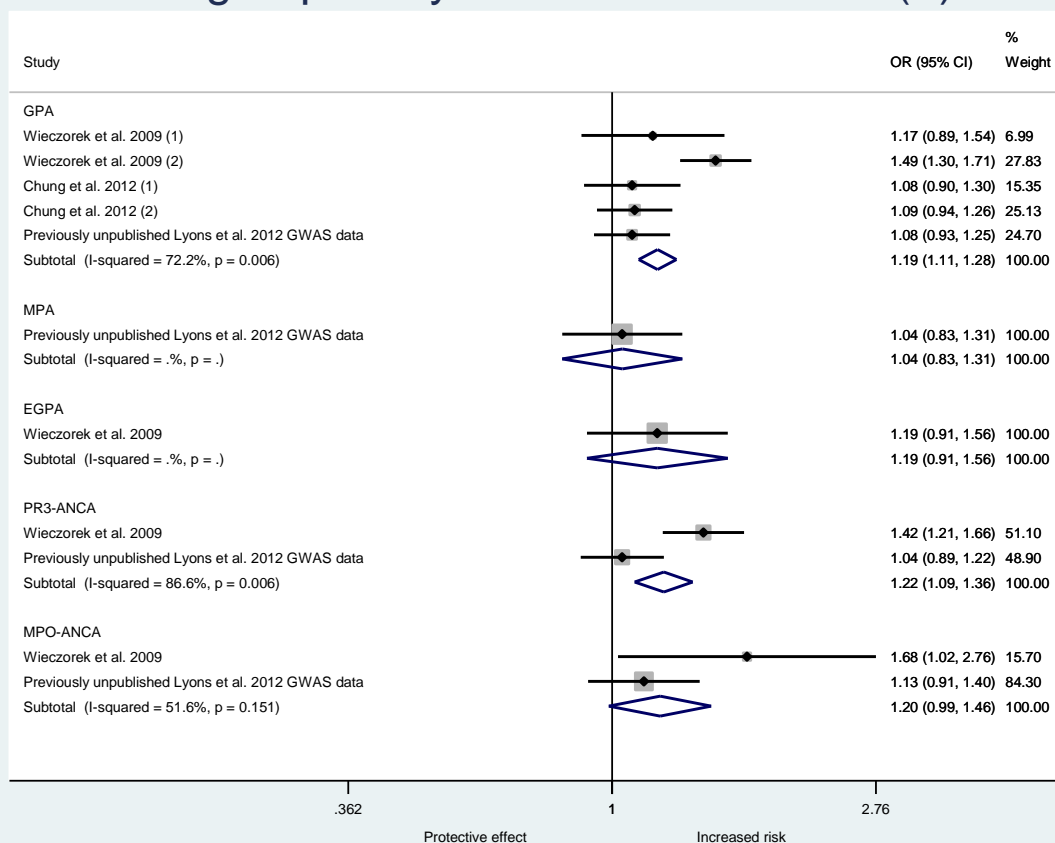
References

⁴⁰**

- **Two cohorts described in the same publication.
- ***Three cohorts described in the same publication.
- N/A, not applicable

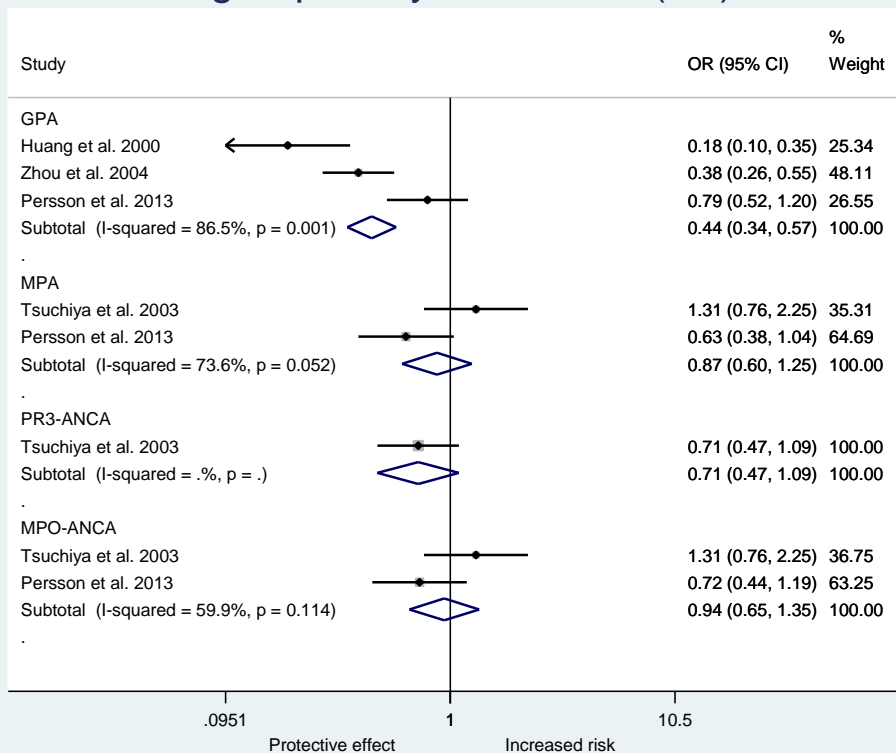
Supplementary Figure S2. Forest plots by diagnostic and serologic subgroups

Subgroup analysis CD226 rs763361 (T)



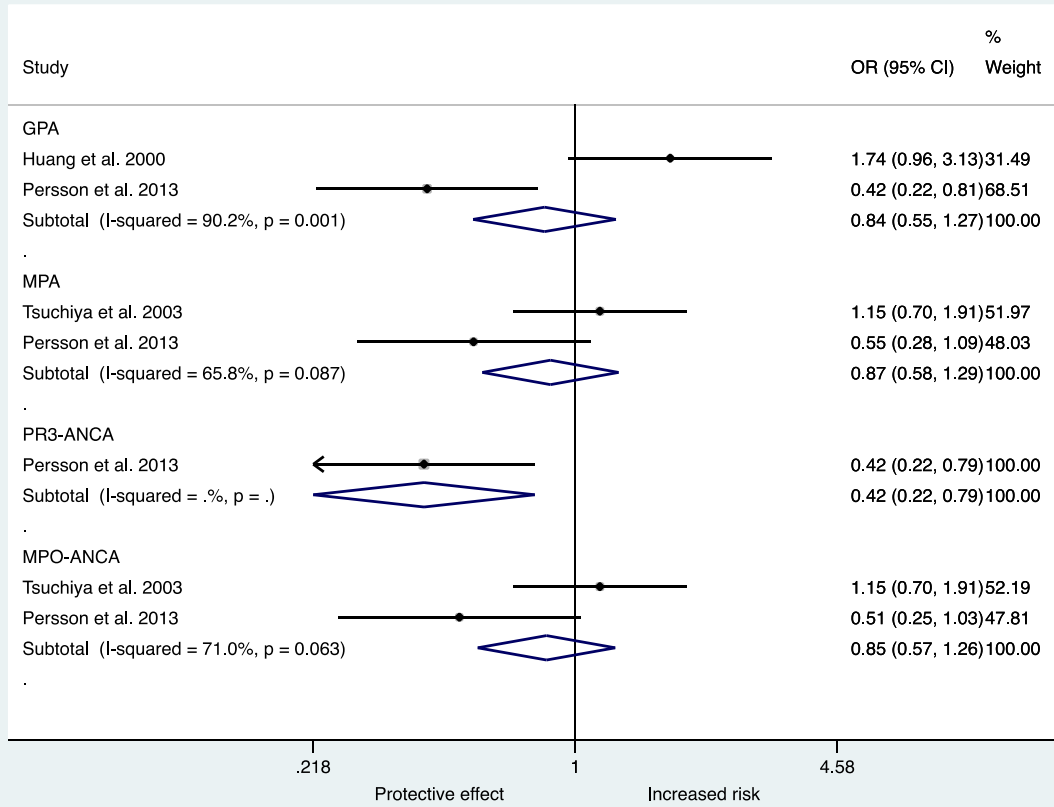
References: ¹**, ²**, ³

Subgroup analysis CTLA-4 (AT)86



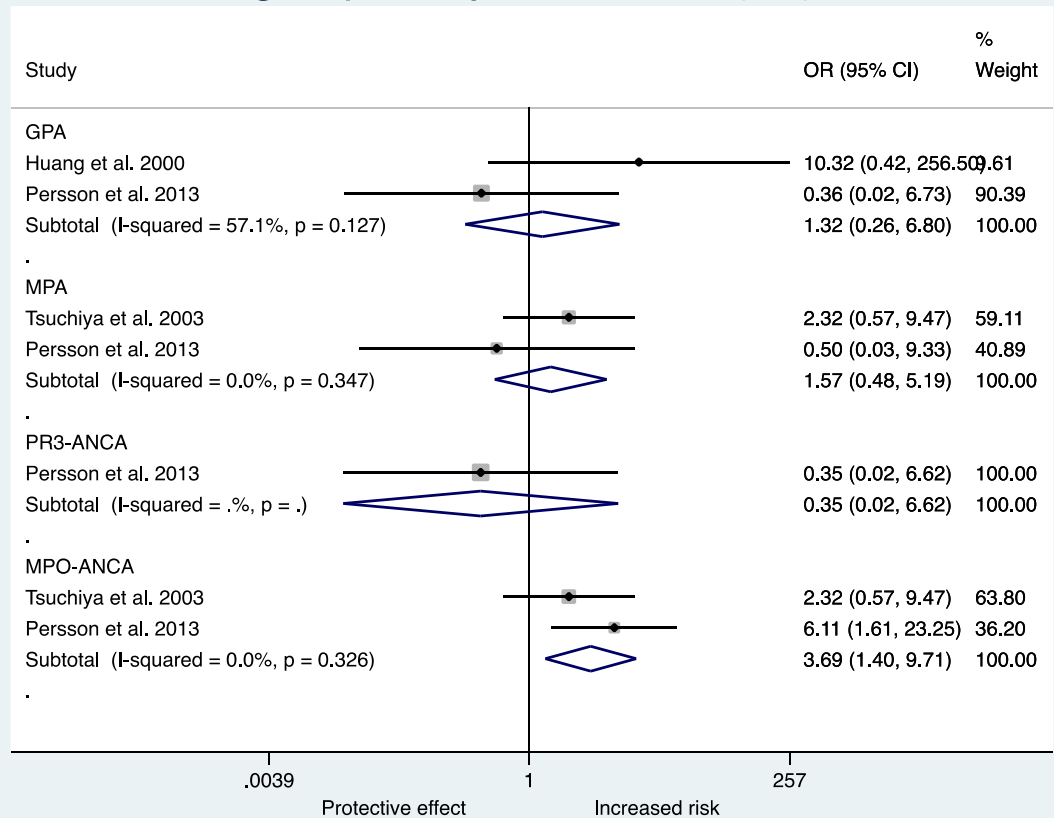
References: ⁴, ⁵, ⁶, ⁷

Subgroup analysis CTLA-4 (AT)104



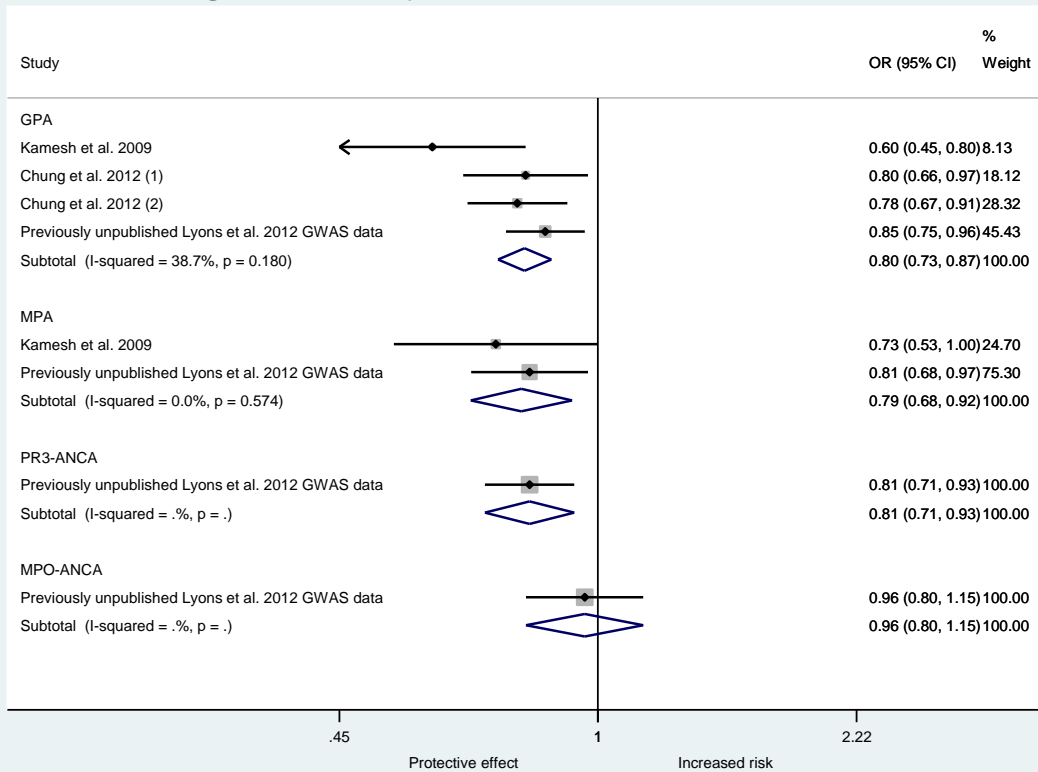
References: 4, 7, 5

Subgroup analysis CTLA-4 (AT)122



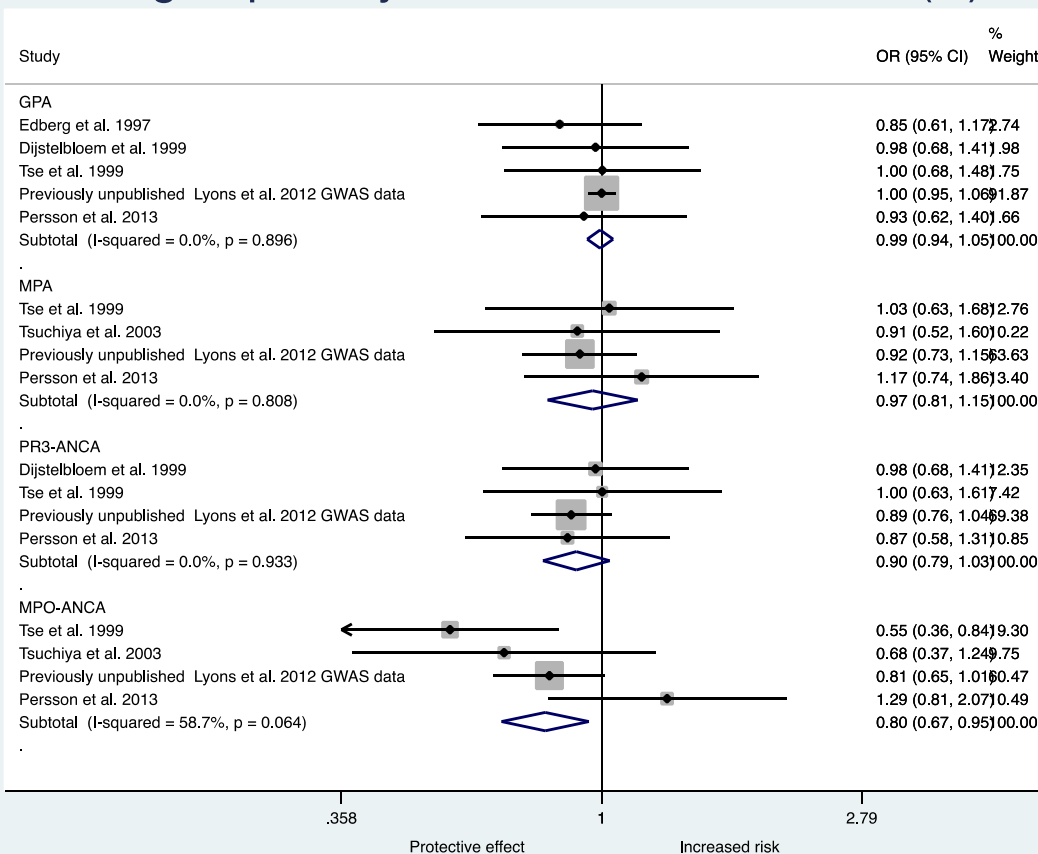
References: 4, 7, 5

Subgroup analysis CTLA-4 rs3087243 (A)



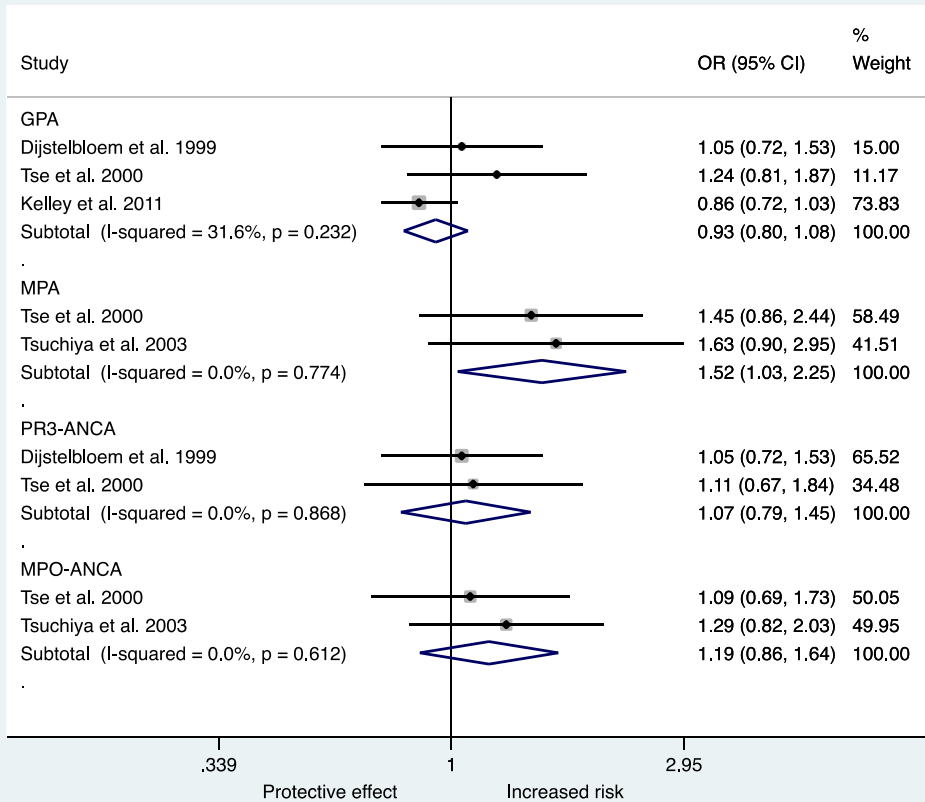
References: ⁹, ²*, ³

Subgroup analysis FCGR2A rs1801274 (C)



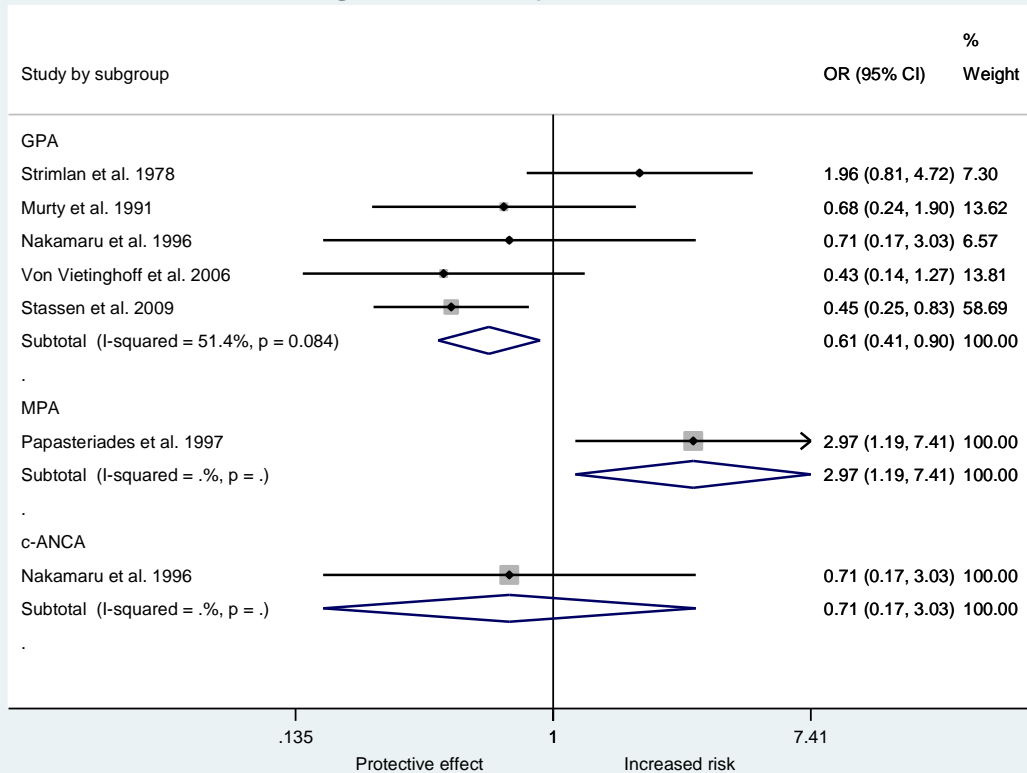
References: ¹¹, ¹², ¹³, ⁵, ⁷, ³

Subgroup analysis FCGR3B (NA1)



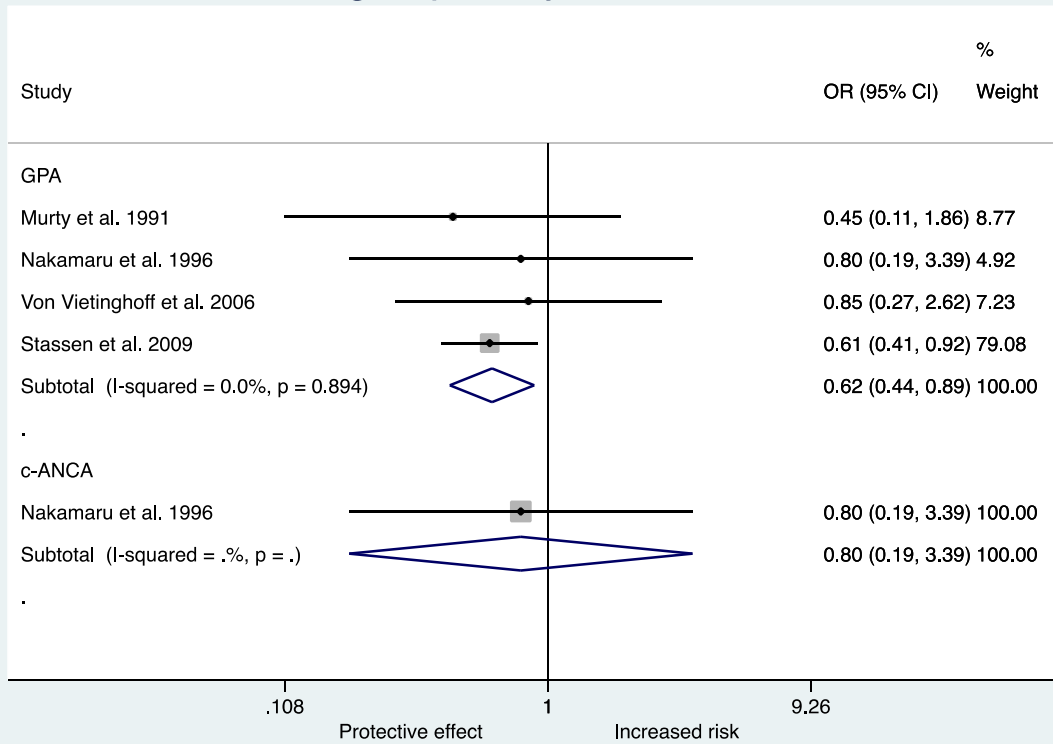
References: ^{12, 14, 10, 5}

Subgroup analysis HLA-A11



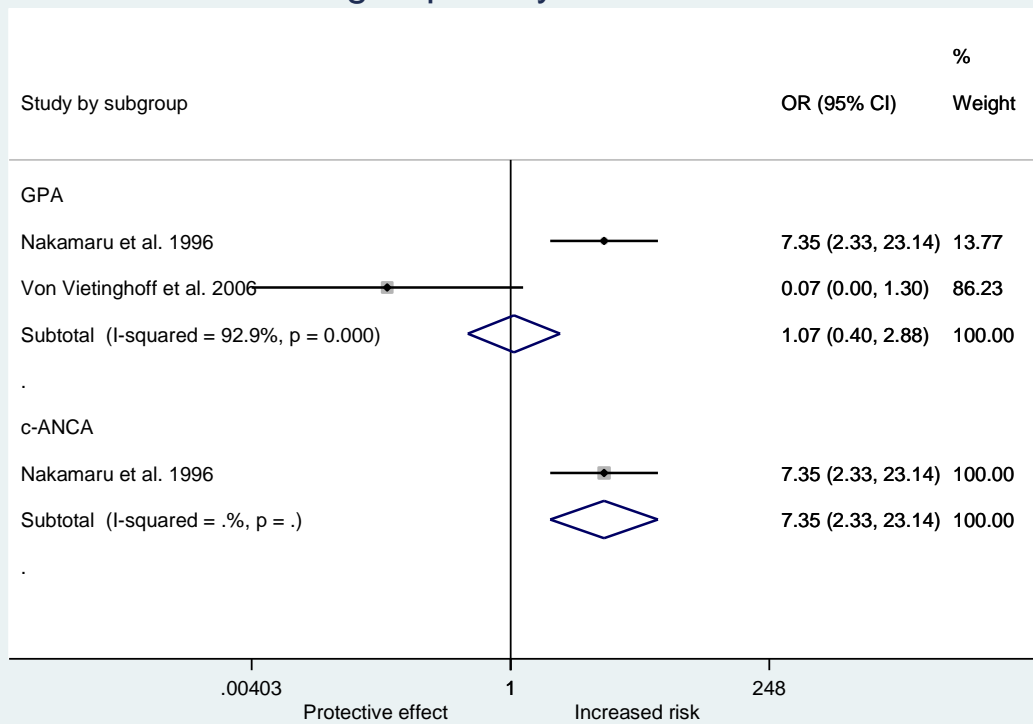
References: ^{16, 17, 20, 22, 18, 19}

Subgroup analysis HLA-B35



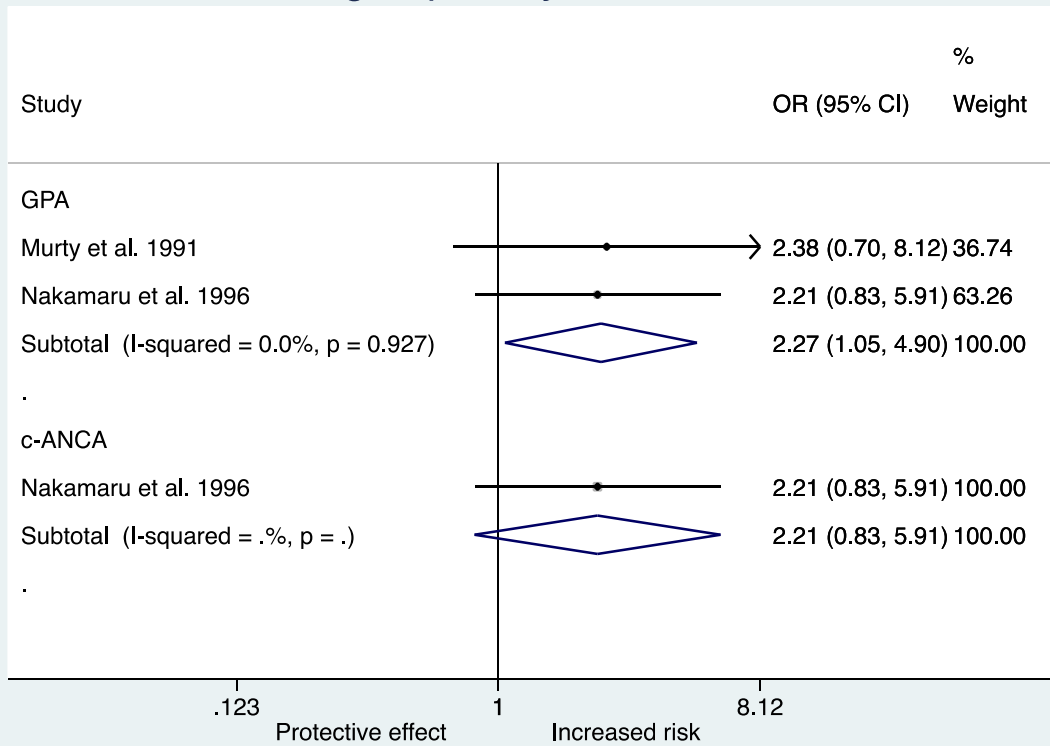
References: ^{17, 20, 18, 19}

Subgroup analysis HLA-B55



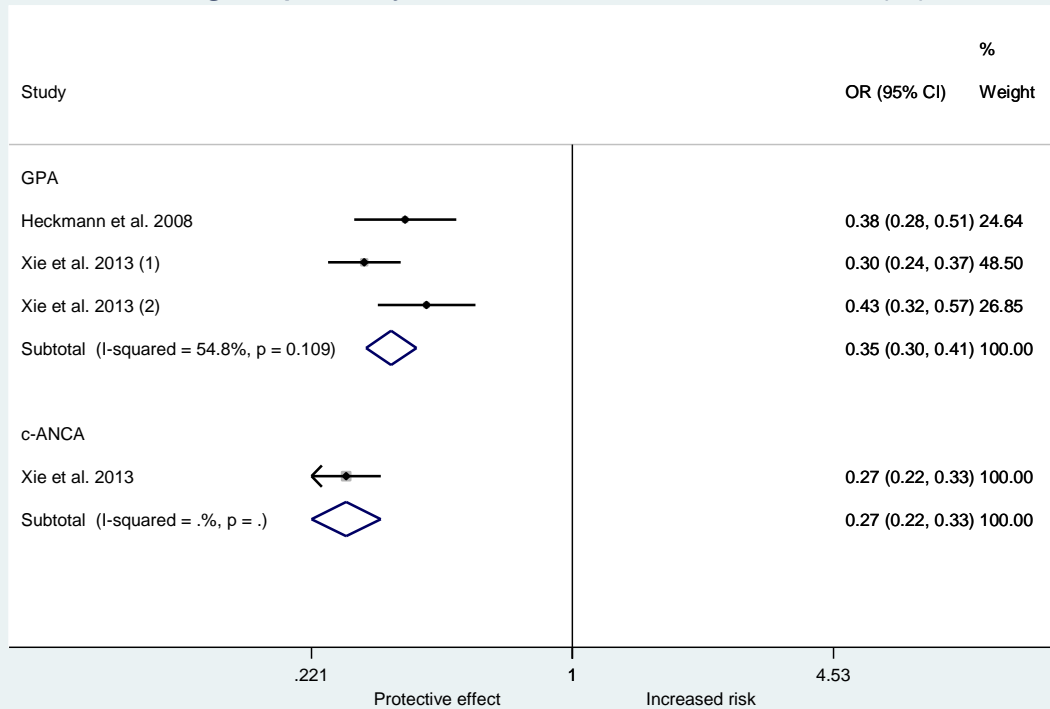
References: ^{20, 18}

Subgroup analysis HLA-B62



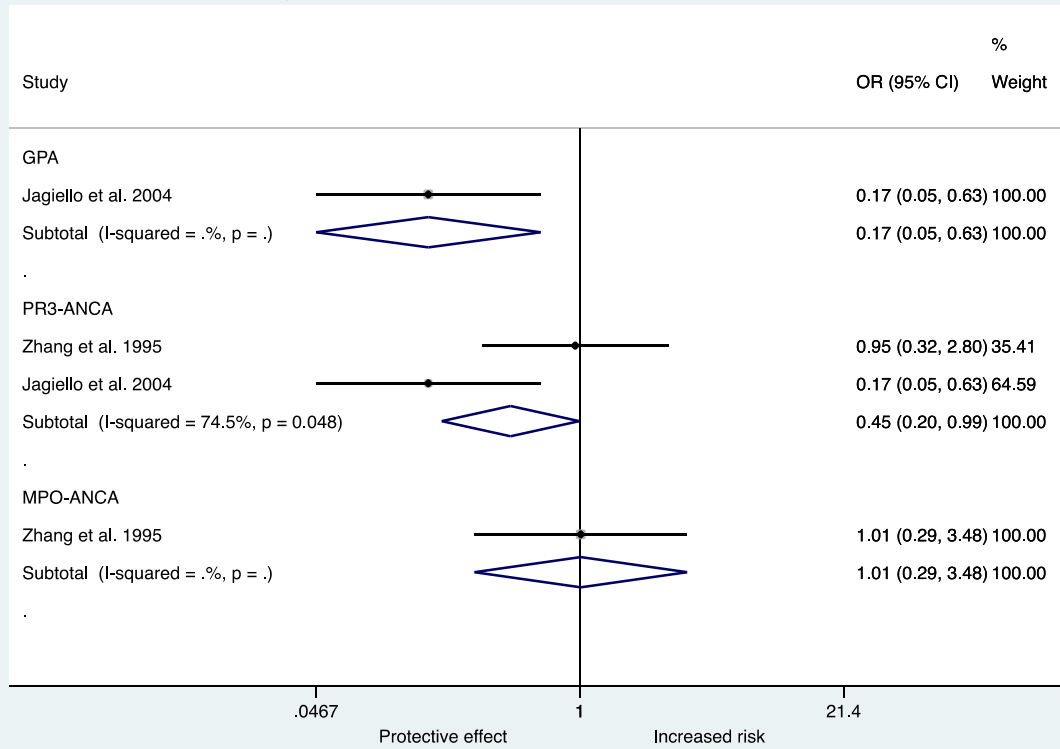
References: ¹⁷, ²⁰

Subgroup analysis HLA-DPA1 rs9277341 (C)



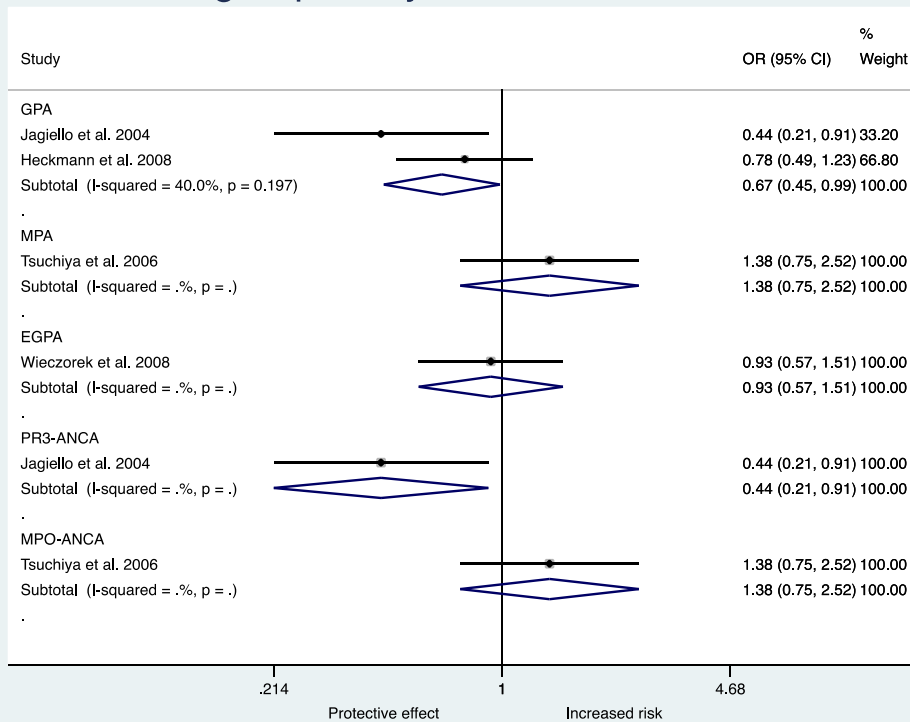
References: ²⁴, ^{25**}

Subgroup analysis HLA-DPB1*0101



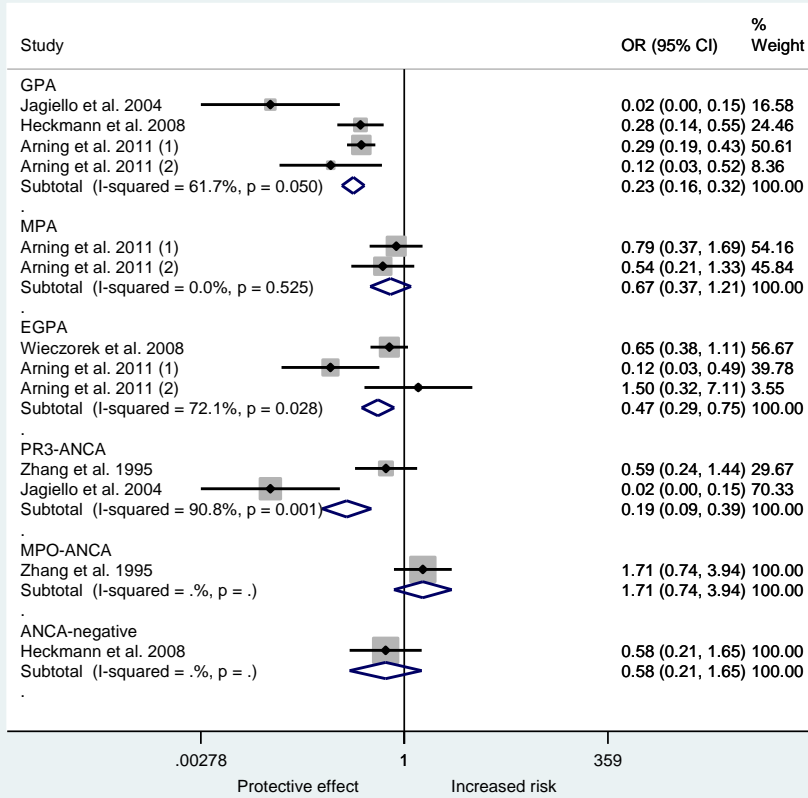
References: ²⁷, ²⁶

Subgroup analysis HLA-DPB1*0201



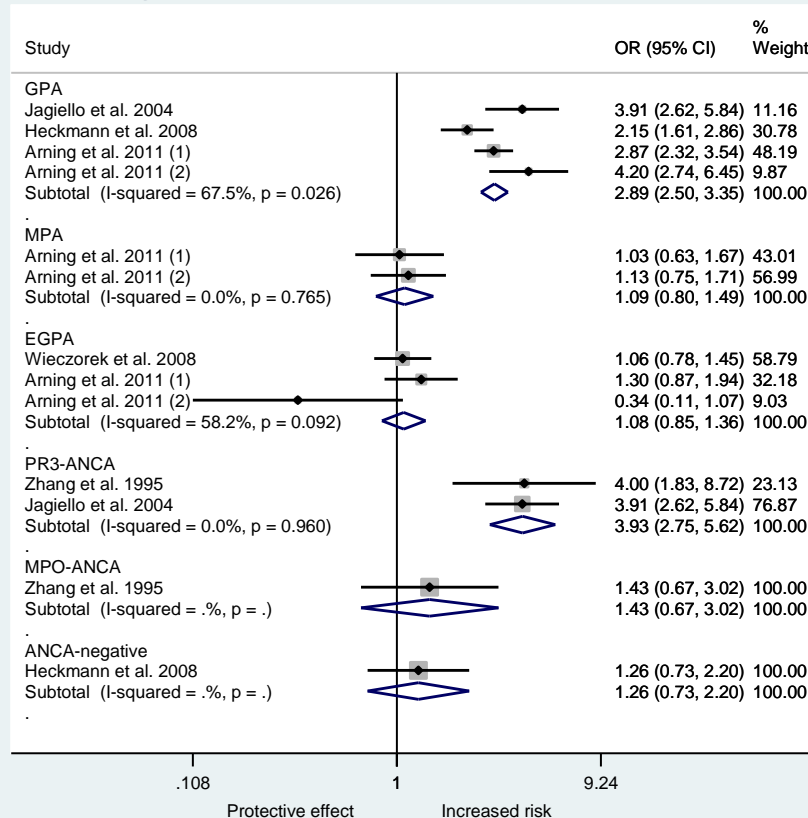
References: ²⁷, ²⁴, ²⁸, ²⁹

Subgroup analysis HLA-DPB1*0301



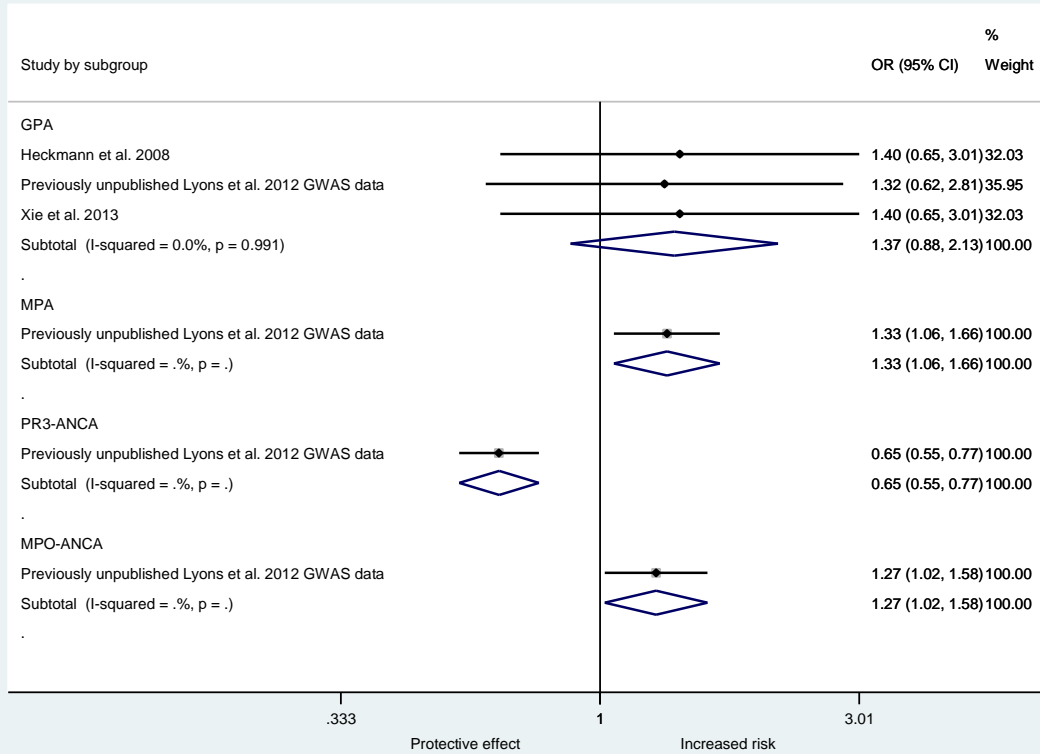
References: 26, 27, 24, 29, 30**

Subgroup analysis HLA-DPB1*0401



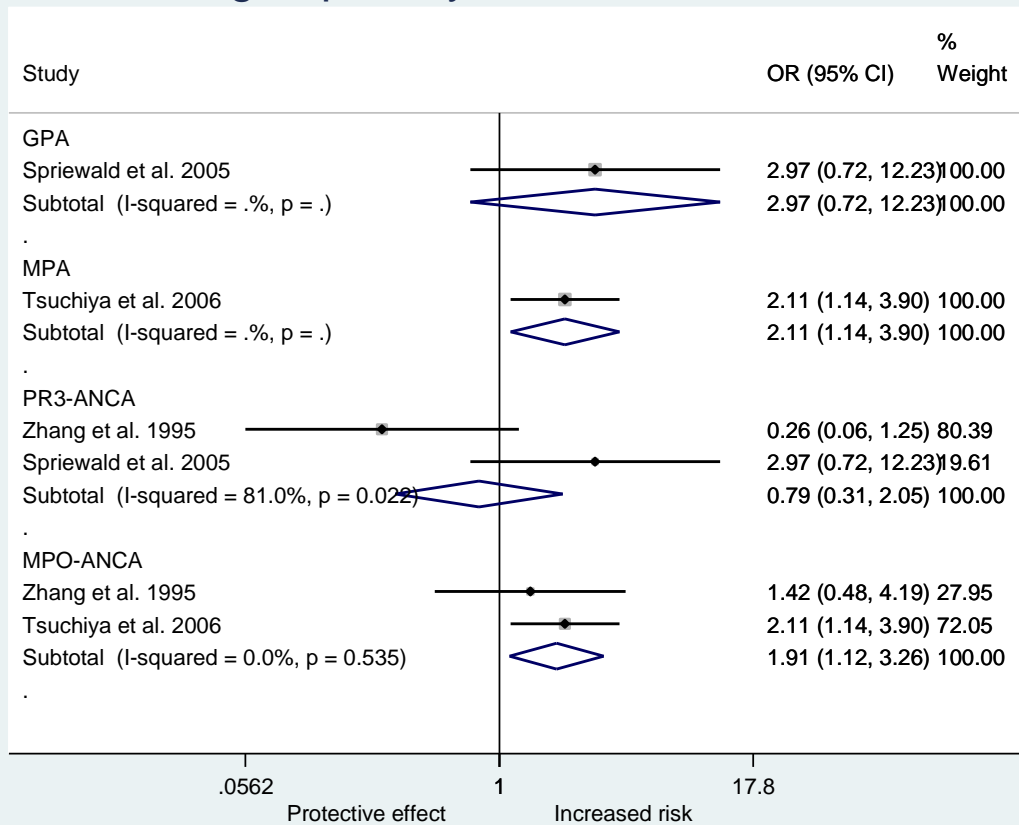
References: 26, 27, 24, 29, 30**

Subgroup analysis HLA-DPB2 rs3130215 (A)



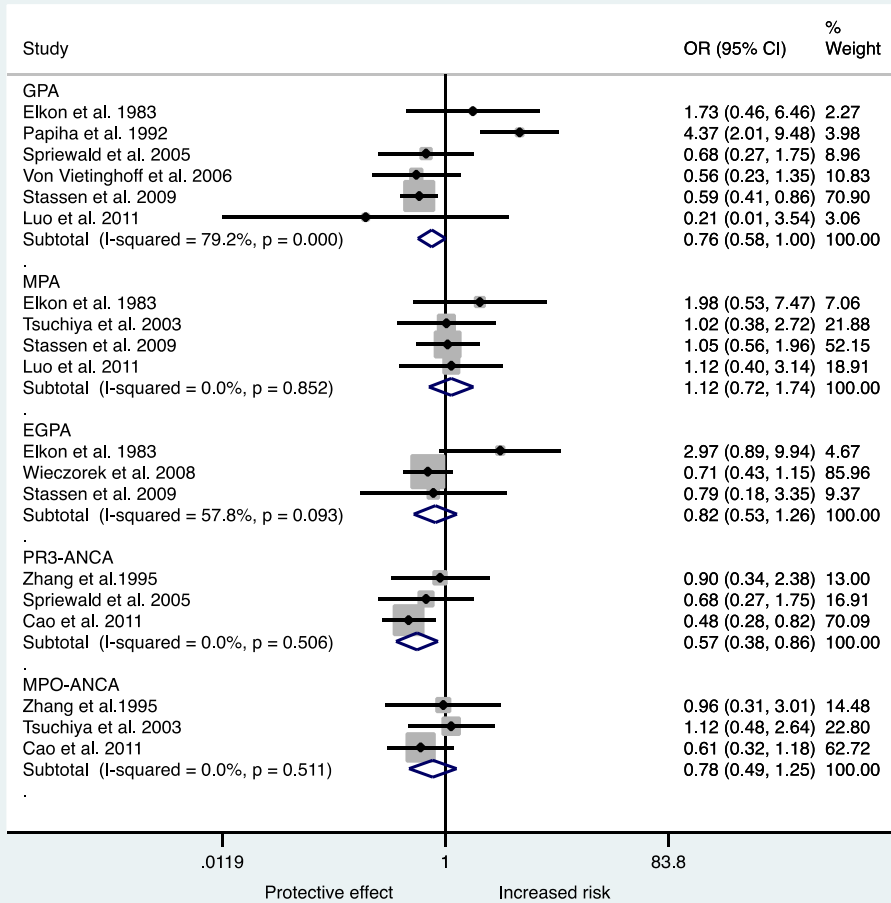
References: ^{24, 3, 25}

Subgroup analysis HLA-DQB1*0303



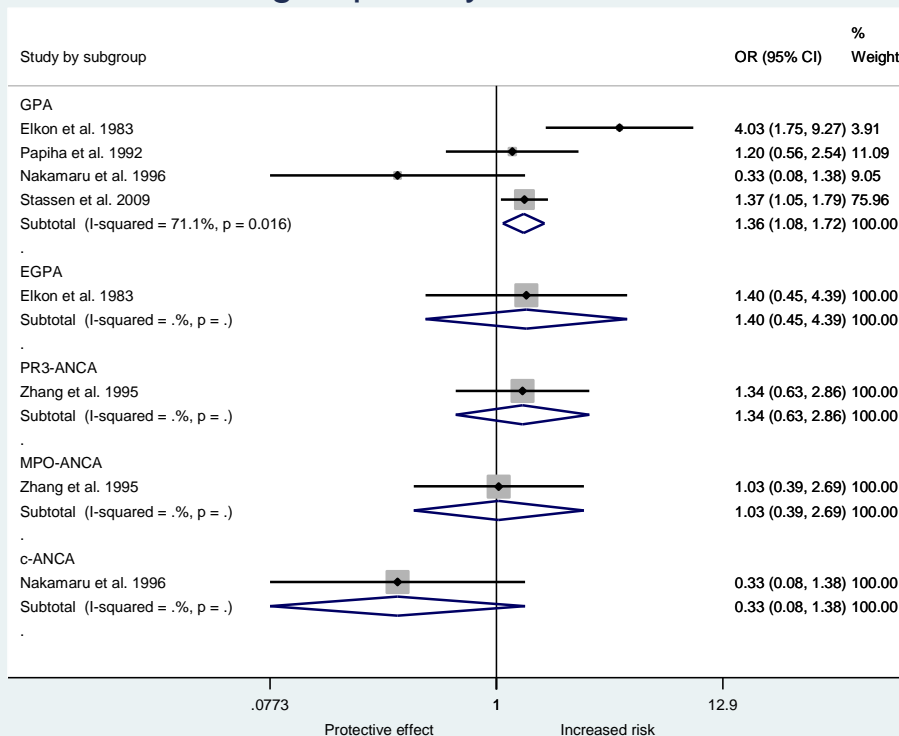
References: ^{26, 31, 28}

Subgroup analysis HLA-DR1



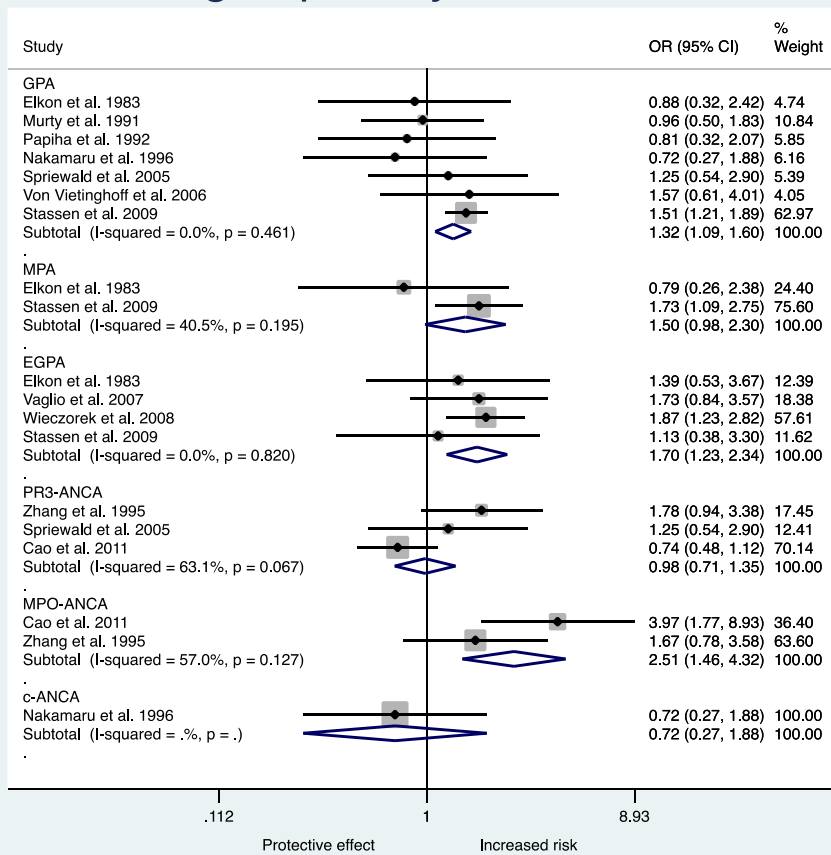
References: 23, 32, 31, 18, 19, 34, 5, 29, 26, 33

Subgroup analysis HLA-DR2



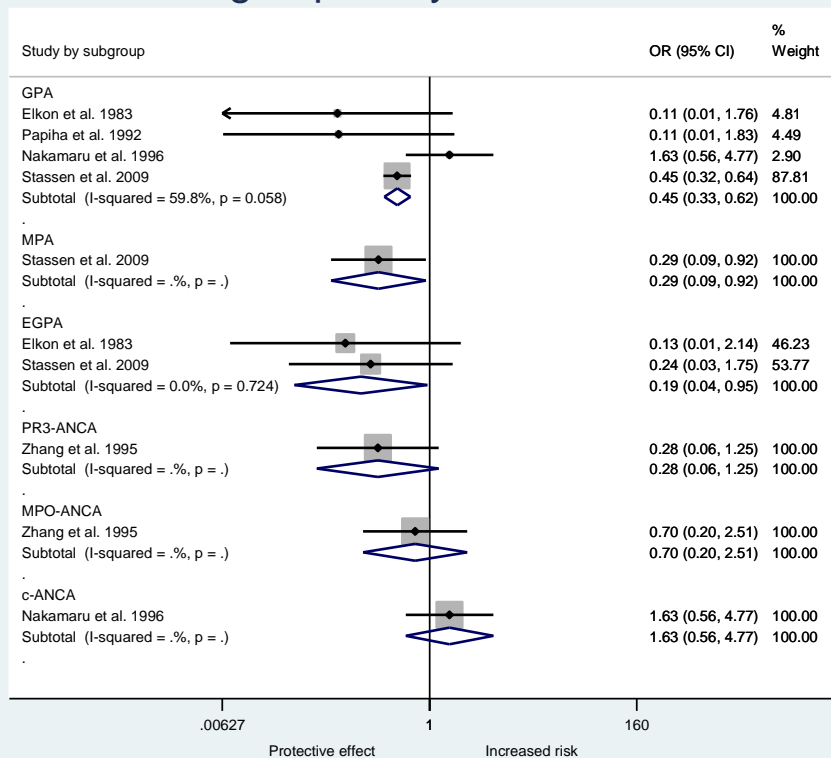
References: 23, 32, 26, 20, 19

Subgroup analysis HLA-DR4



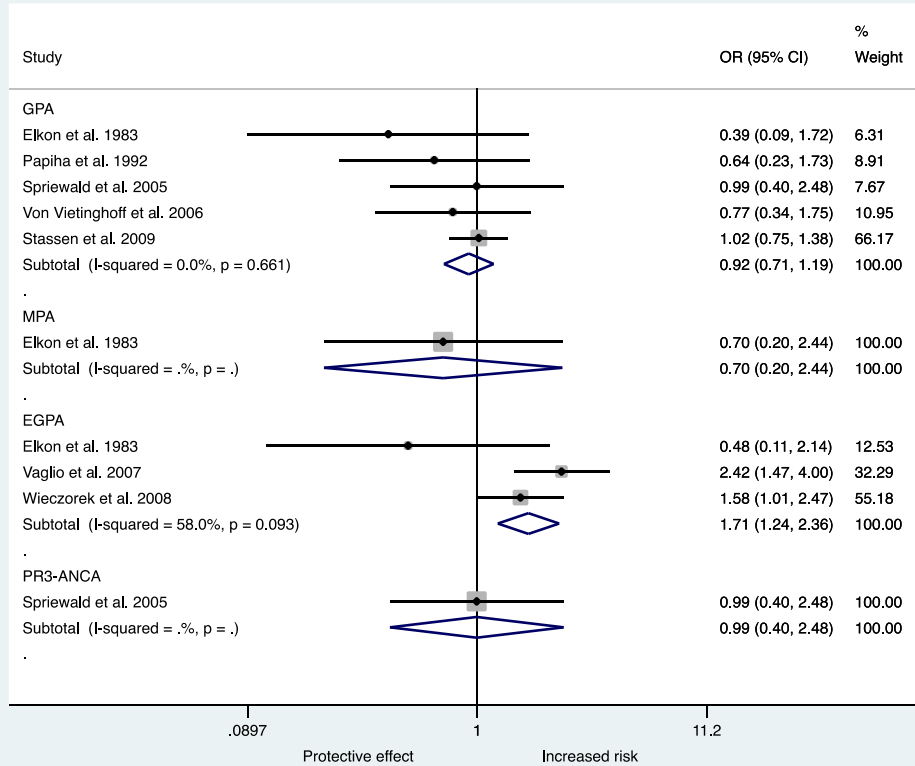
References: 23, 17, 32, 20, 31, 18, 19, 35, 29, 26, 33

Subgroup analysis HLA-DR6



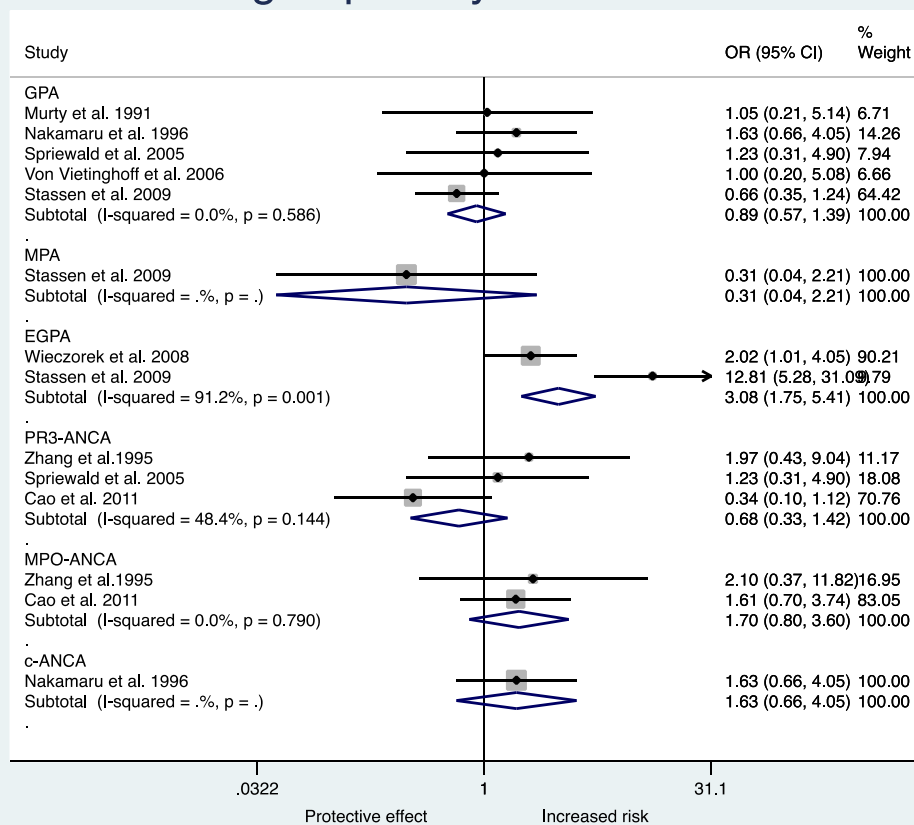
References: 23, 32, 26, 20, 19

Subgroup analysis HLA-DR7



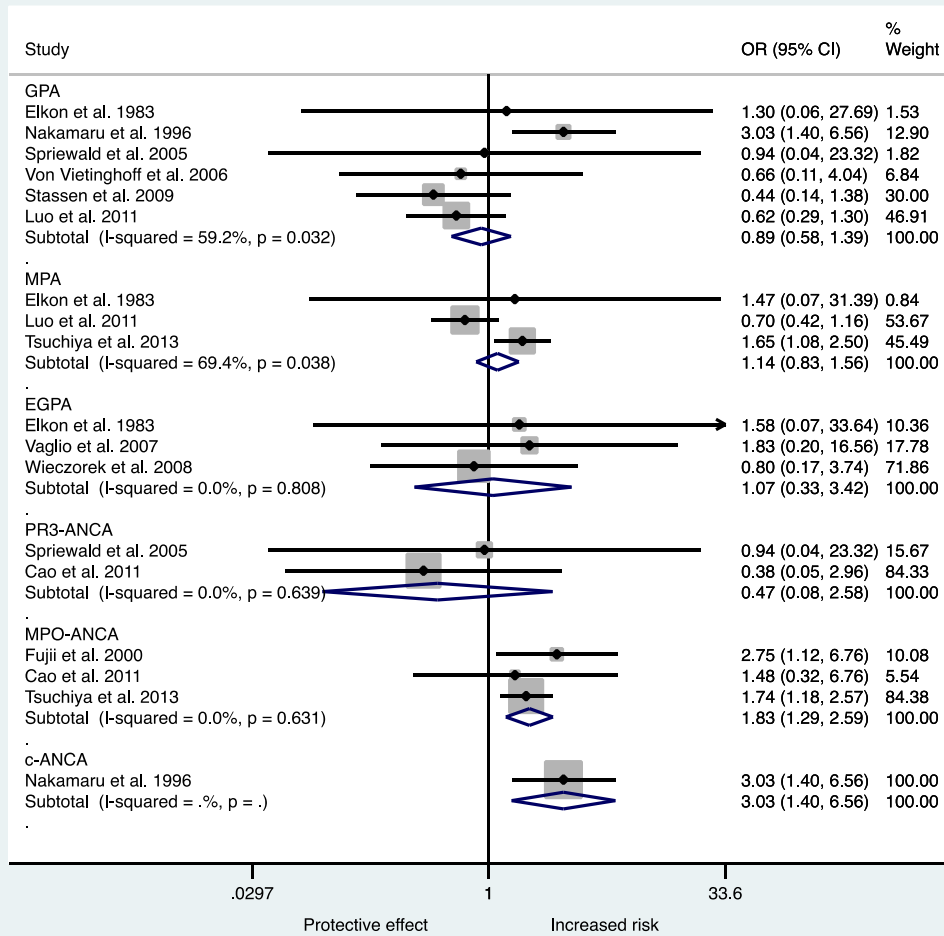
References: 23, 32, 31, 18, 19, 35, 29

Subgroup analysis HLA-DR8



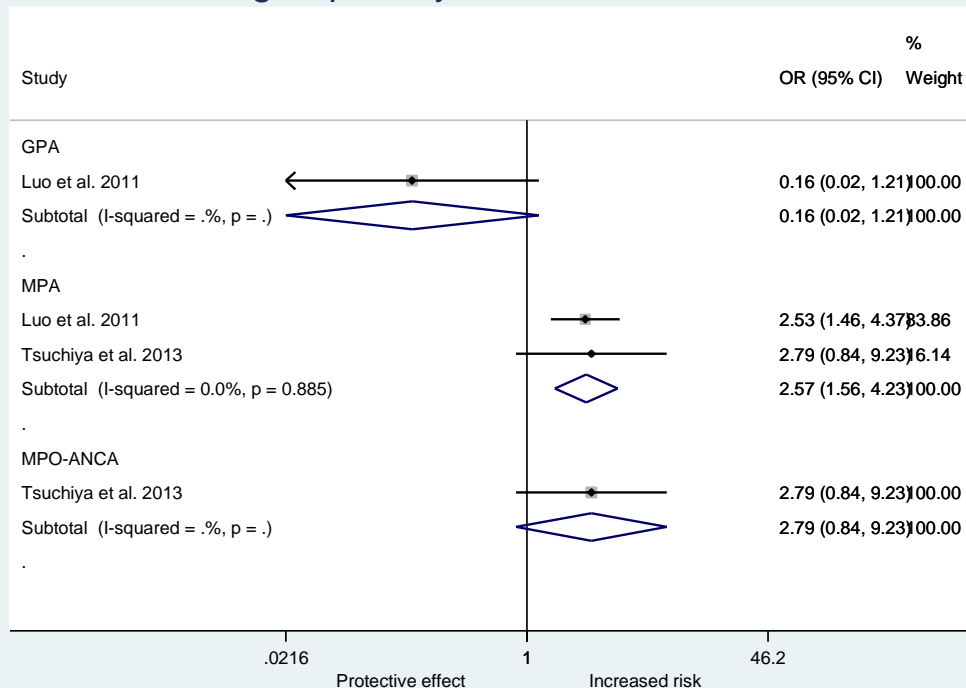
References: 17, 20, 31, 18, 19, 29, 26, 33

Subgroup analysis HLA-DR9



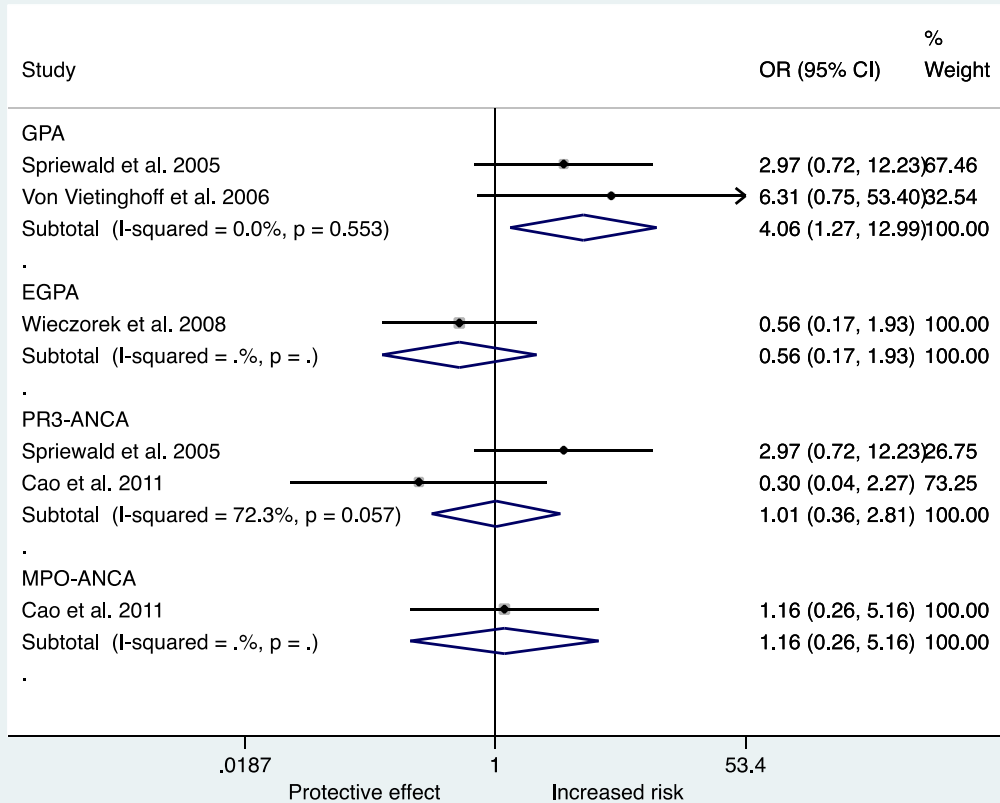
References: 23, 20, 31, 18, 19, 34, 37, 35, 29, 33, 36

Subgroup analysis HLA-DRB1*1101



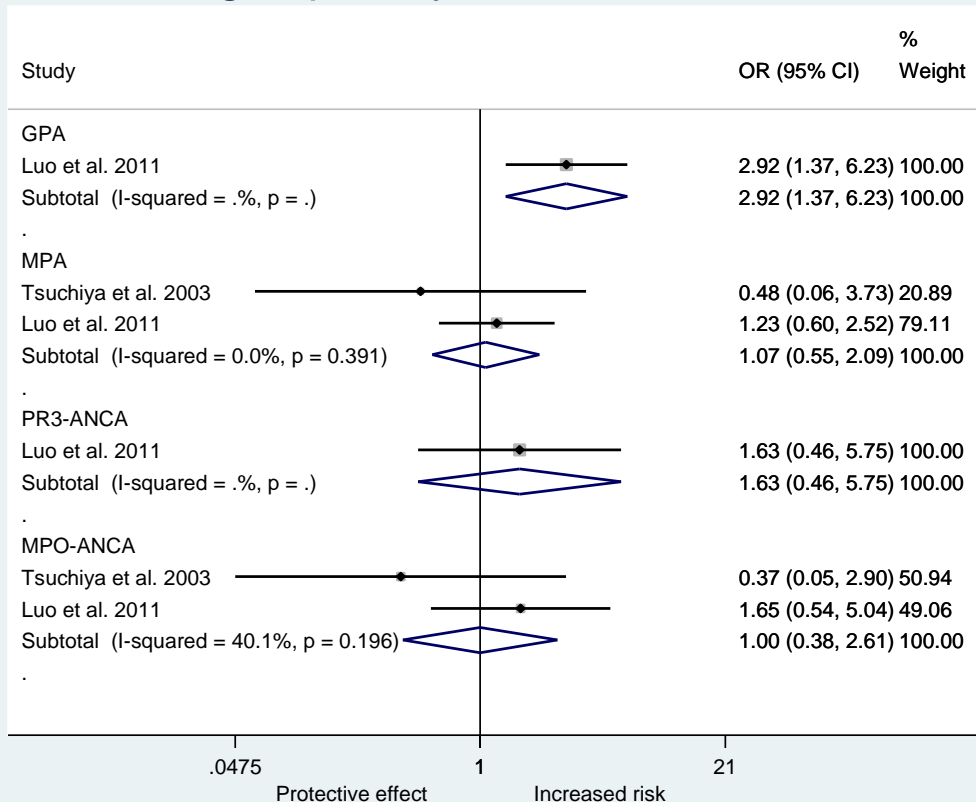
References: 34, 37

Subgroup analysis HLA-DRB1*12



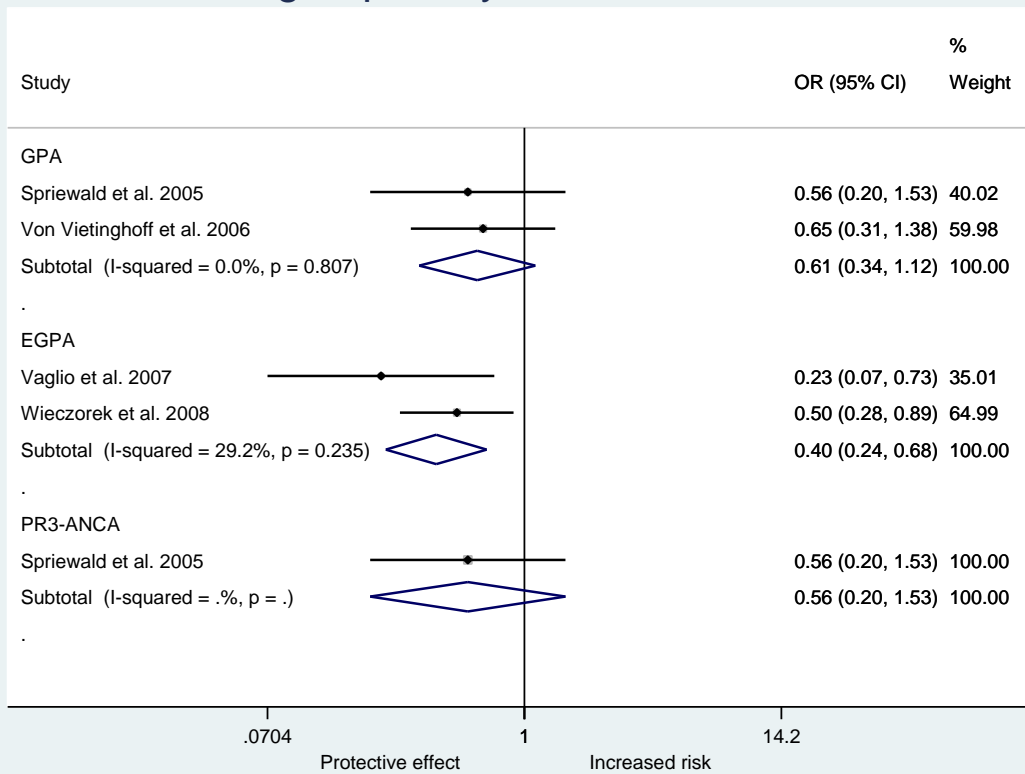
References: ^{31, 18, 29, 33}

Subgroup analysis HLA-DRB1*1202



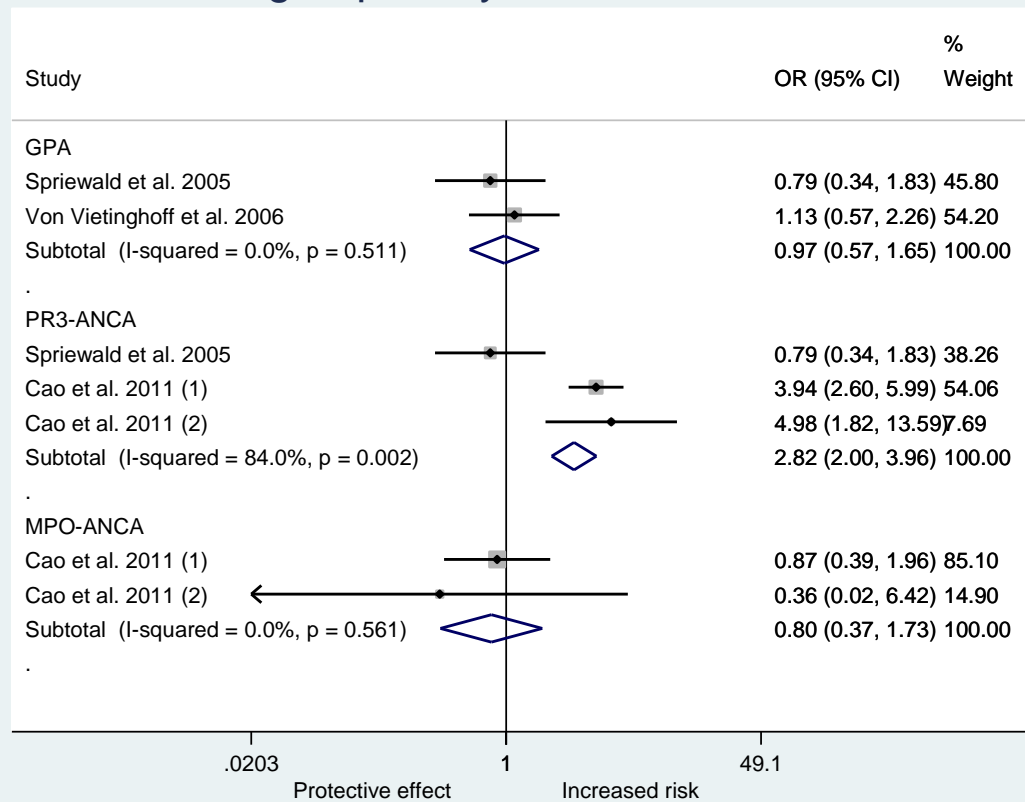
References: ^{5, 34}

Subgroup analysis HLA-DRB1*13



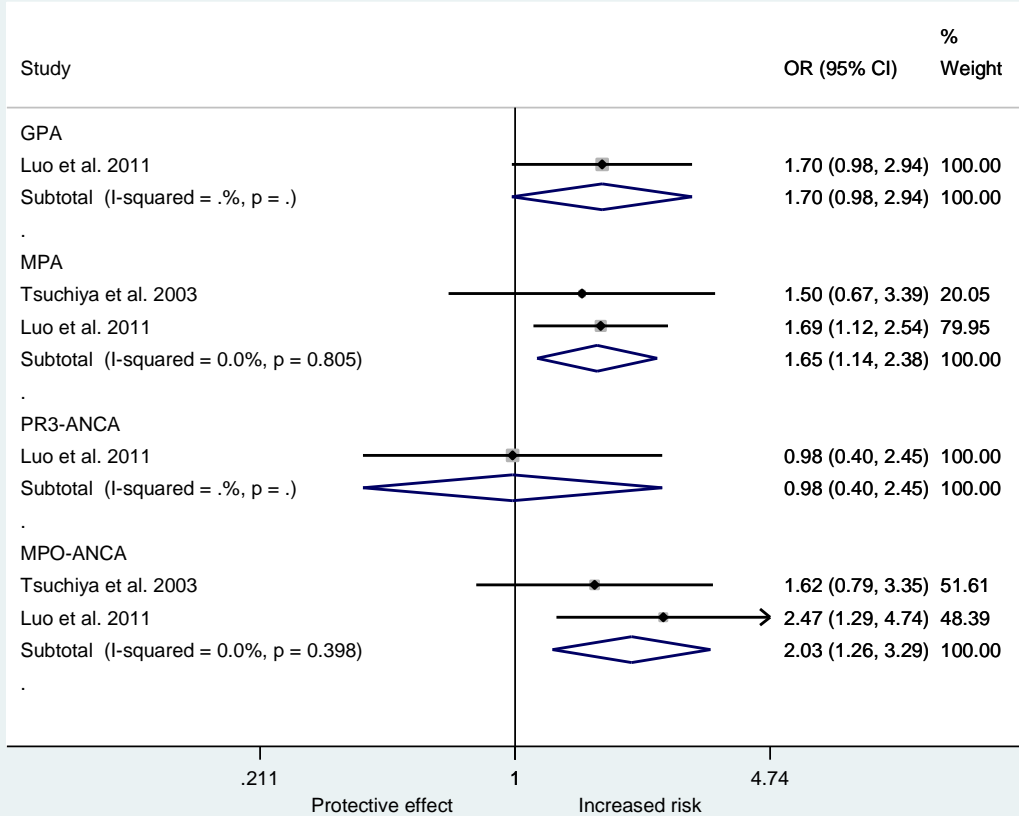
References: ³¹, ¹⁸, ³⁵, ²⁹

Subgroup analysis HLA-DRB1*15



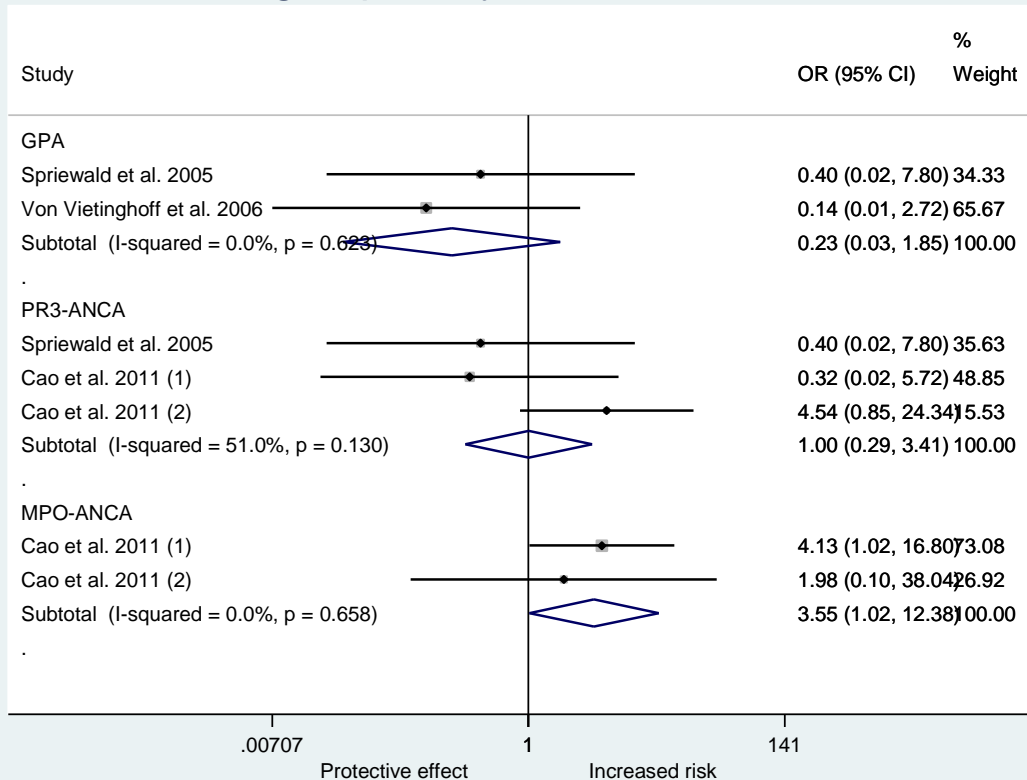
References: ³¹, ¹⁸, ³³**

Subgroup analysis HLA-DRB1*1501



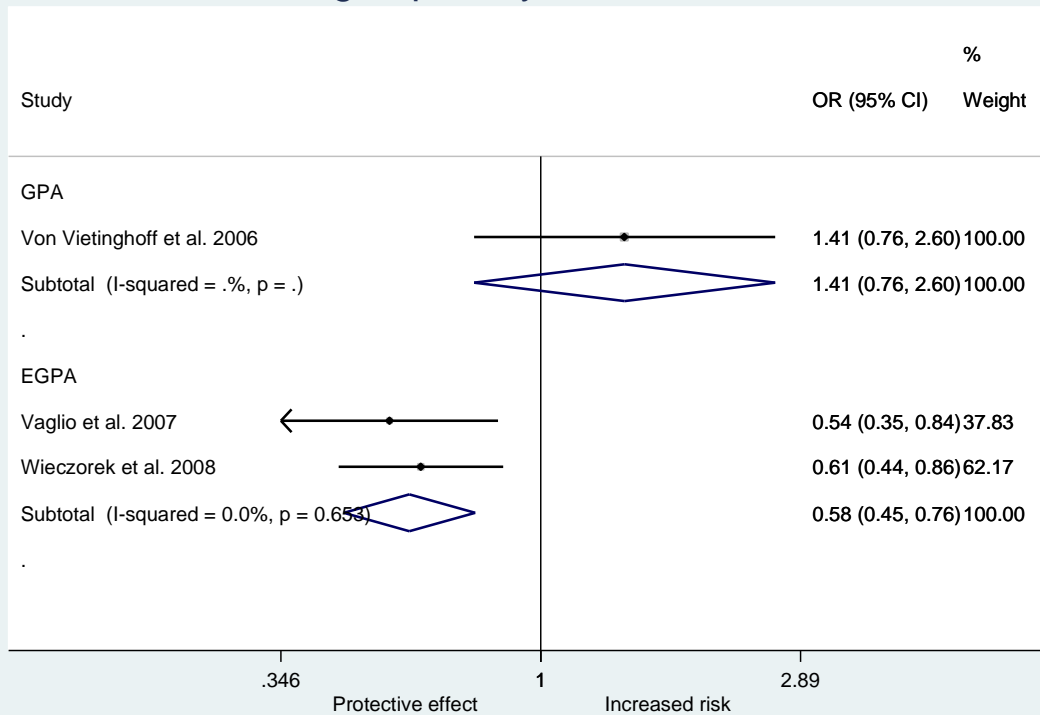
References: ⁵, ³⁴

Subgroup analysis HLA-DRB1*16



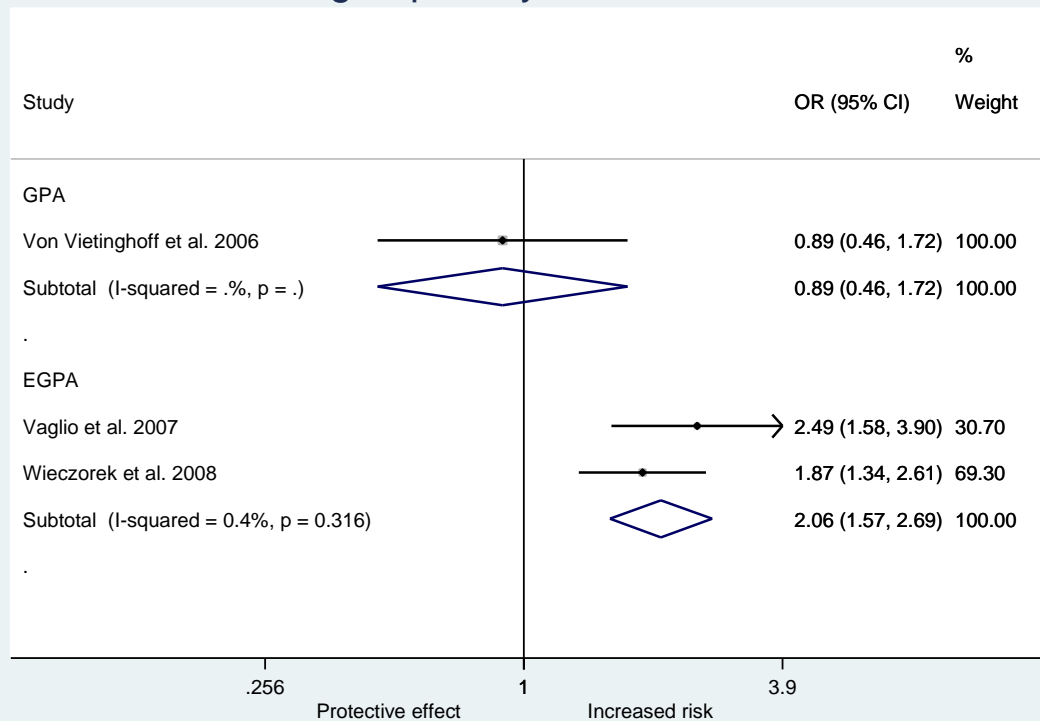
References: ³¹, ¹⁸, ^{33**}

Subgroup analysis HLA-DRB3



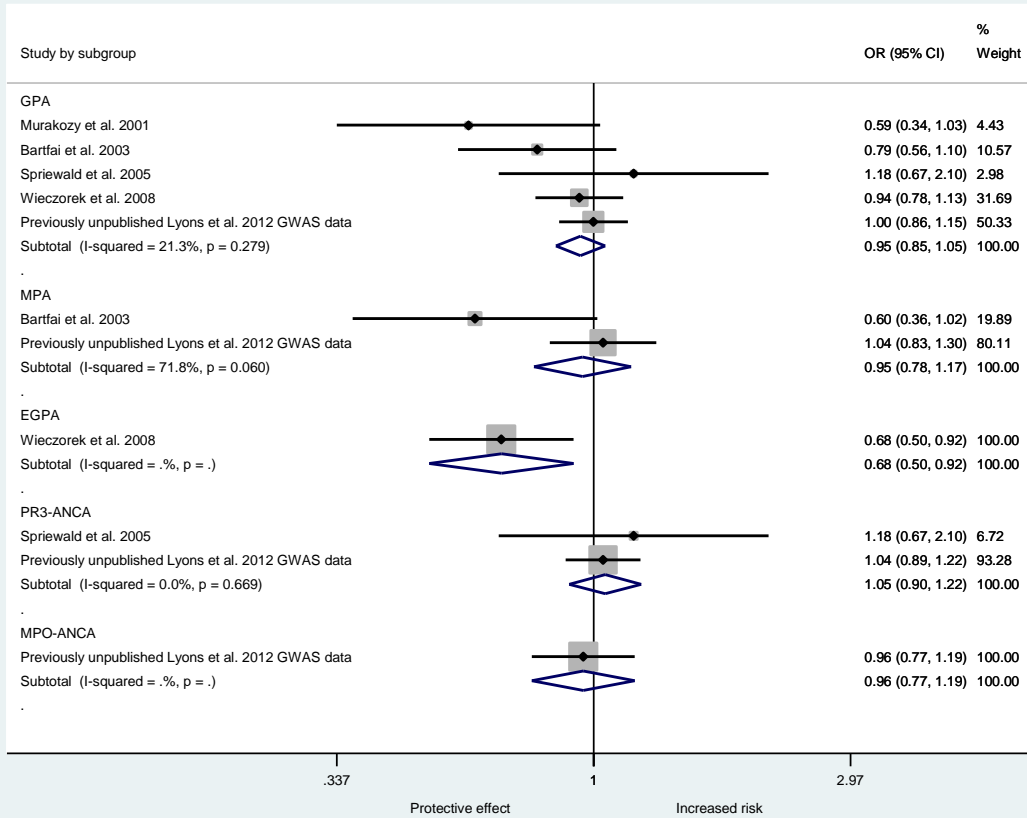
References: ^{18, 35, 29}

Subgroup analysis HLA-DRB4



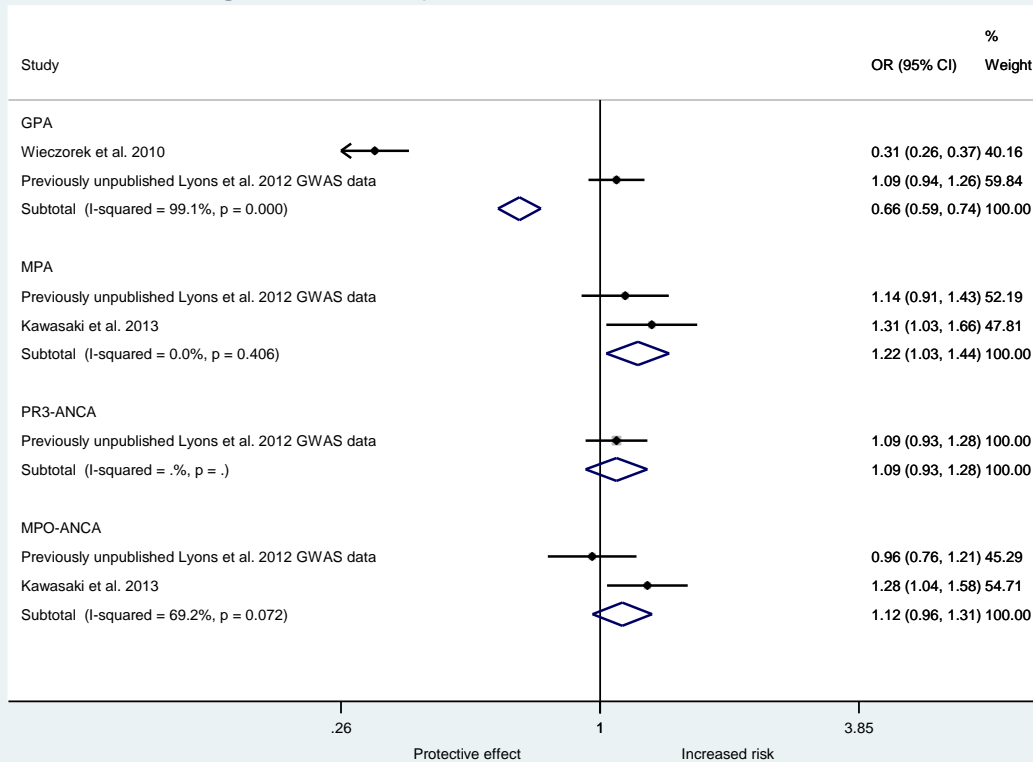
References: ^{18, 35, 29}

Subgroup analysis IL-10 rs1800896 (G)



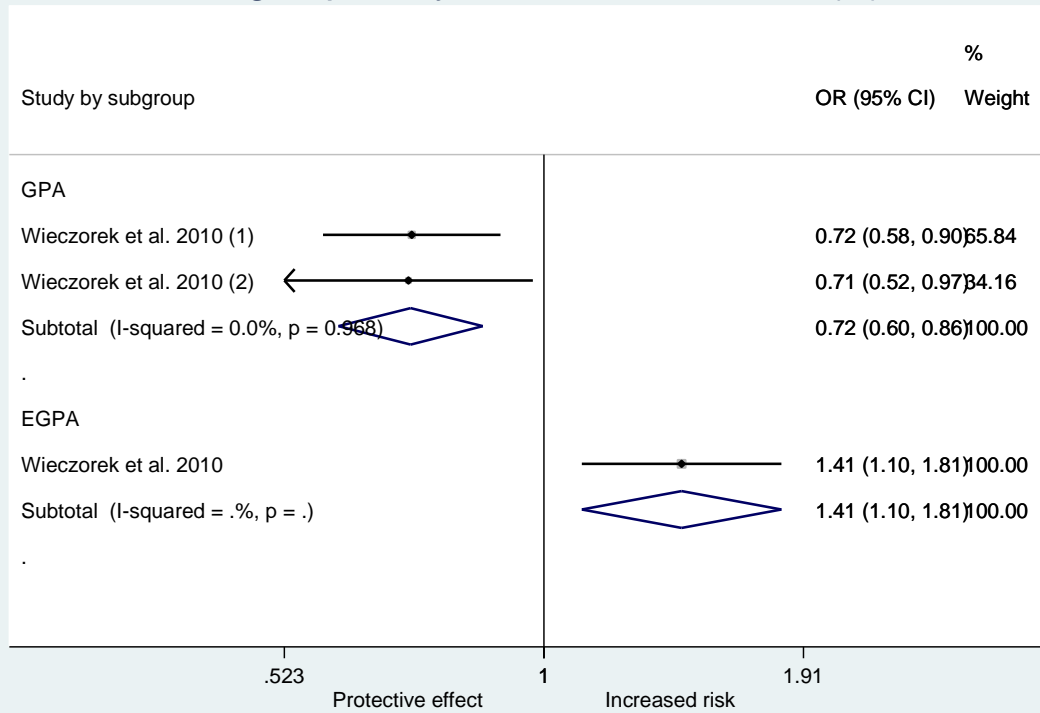
References: 42, 43, 31, 41, 3

Subgroup analysis IRF5 rs10954213 (G)



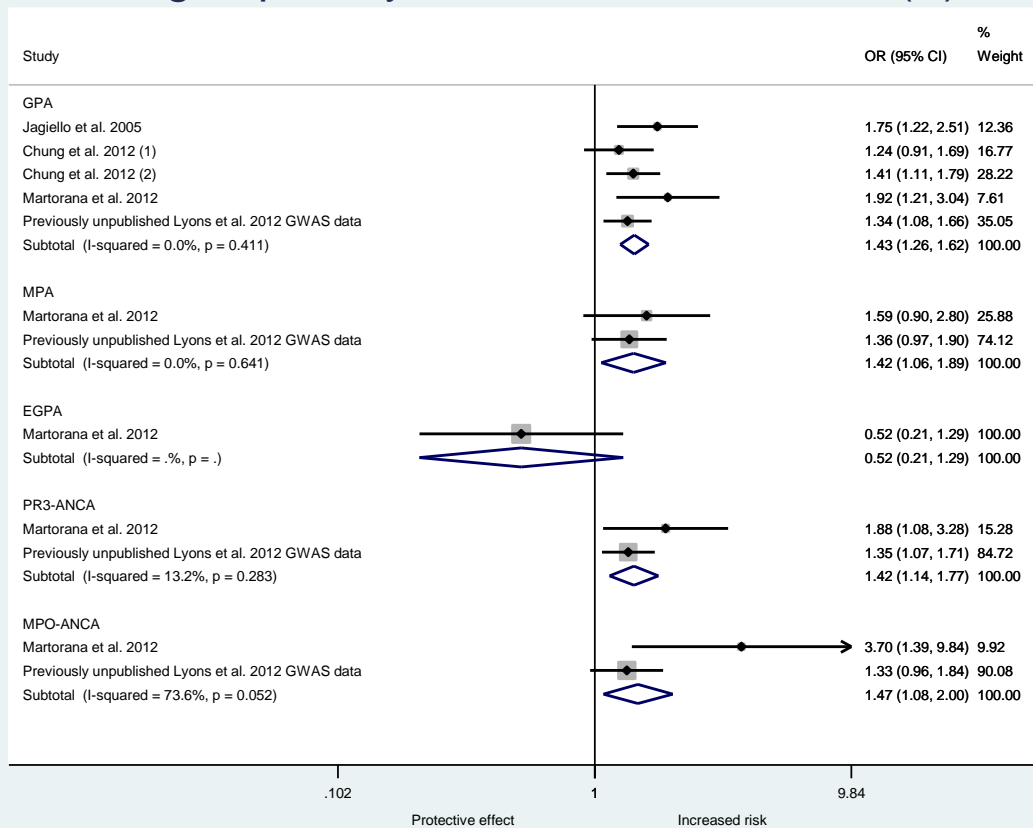
References: 44, 3, 45

Subgroup analysis LEPR rs8179183 (C)



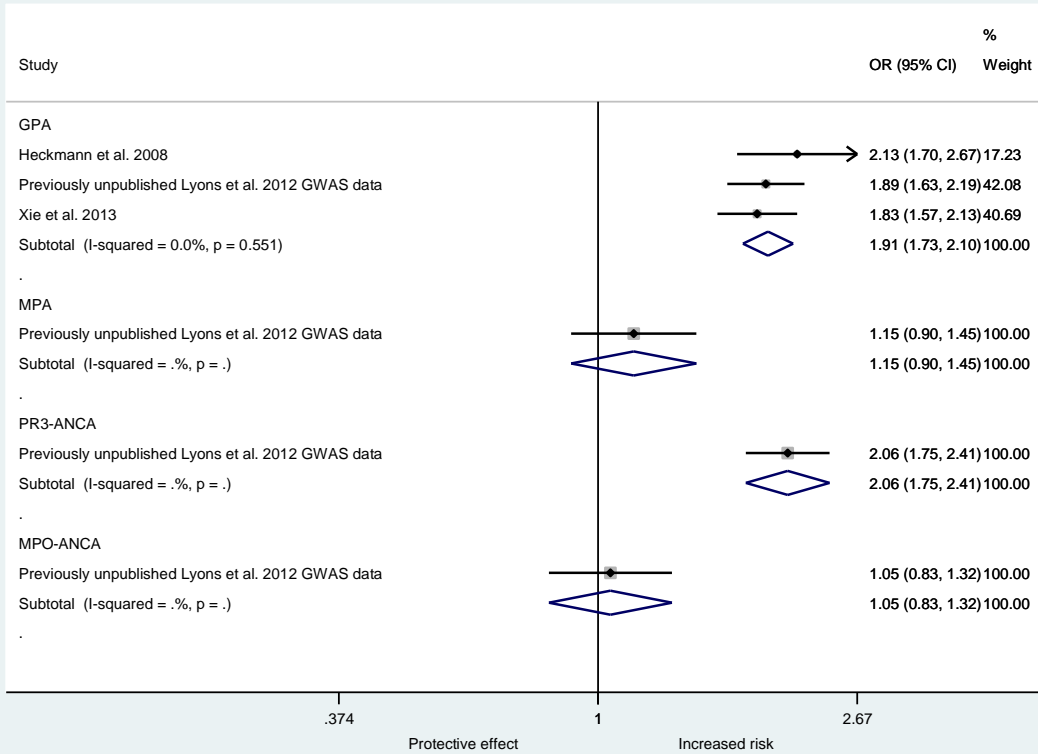
References: 15**

Subgroup analysis PTPN22 rs2476601 (A)



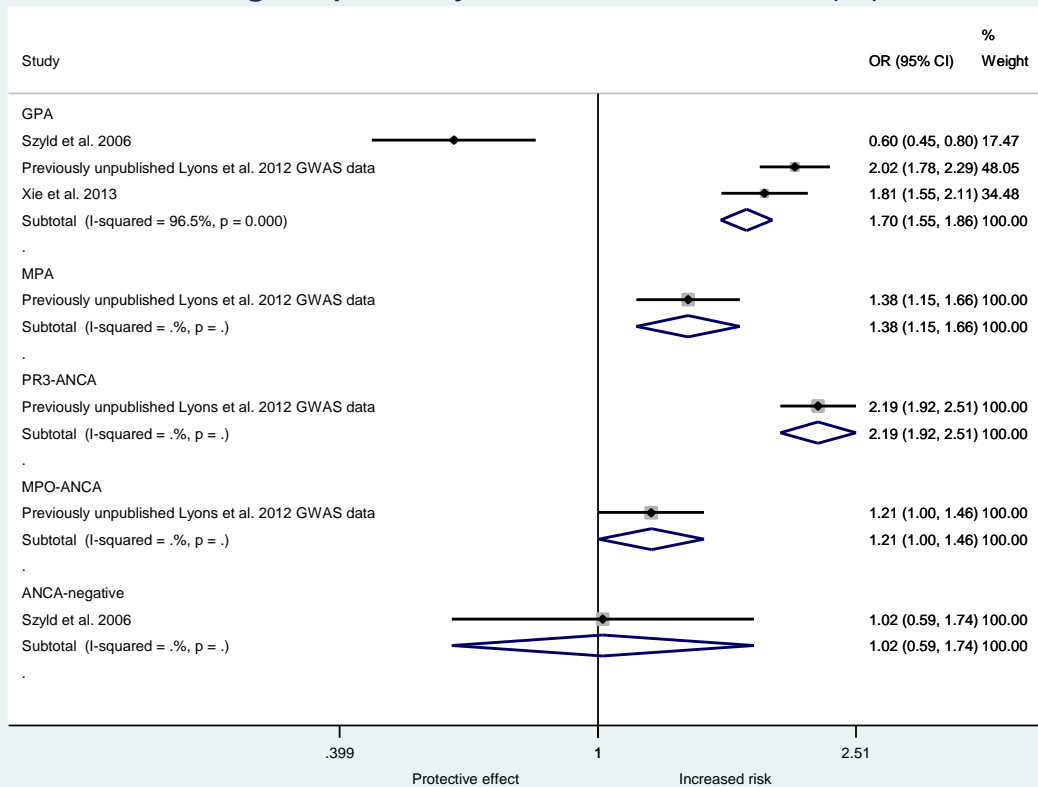
References: 50, 2**, 51, 3

Subgroup analysis RING1/RXRB rs213213 (A)



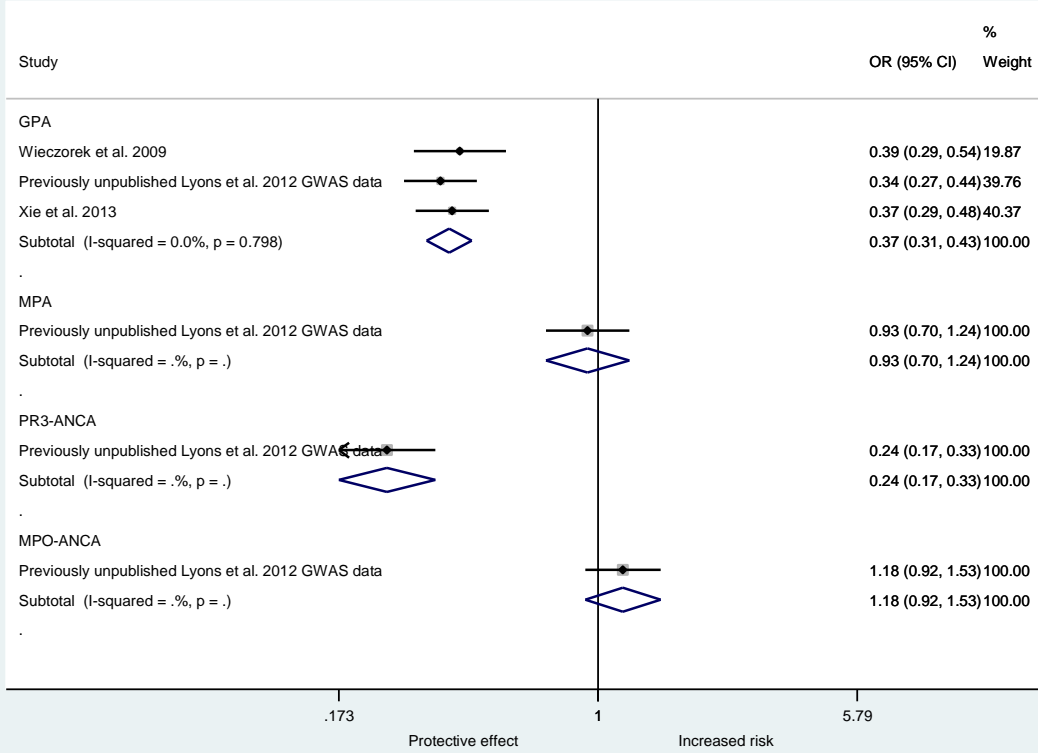
References: ²⁴, ³, ²⁵

Subgroup analysis RXRB rs6531 (C)



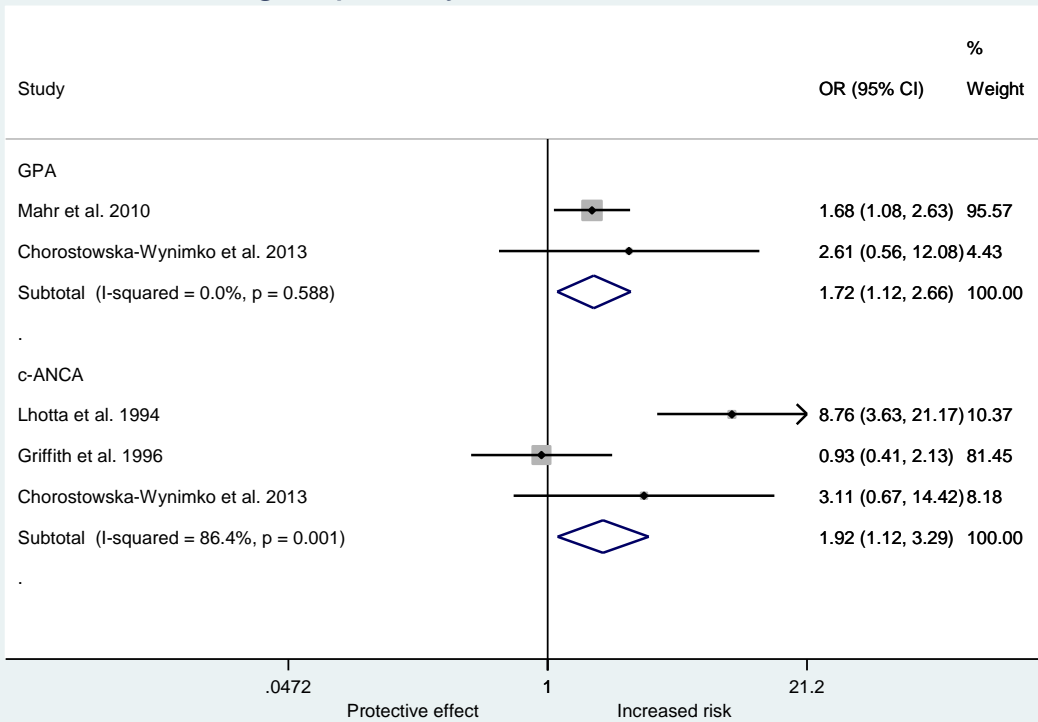
References: ⁵², ³, ²⁵

Subgroup analysis RXRB rs9277935 (T)



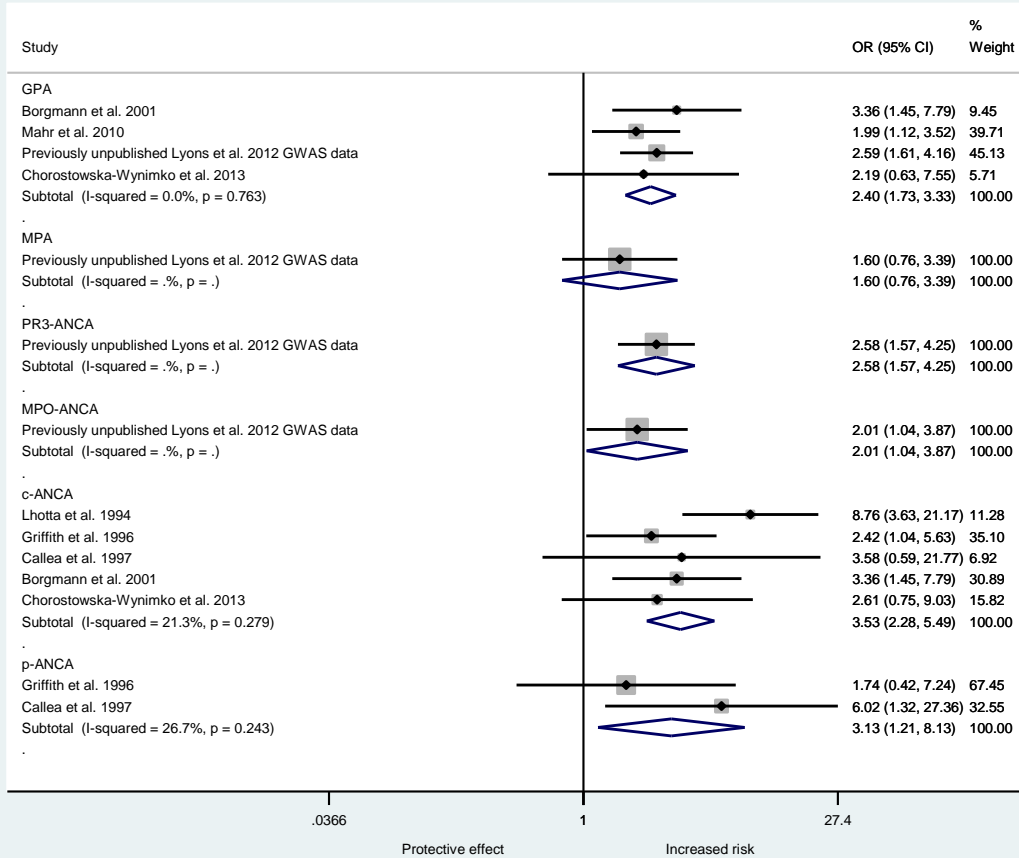
References: ^{53, 3, 25}

Subgroup analysis SERPINA1 S allele



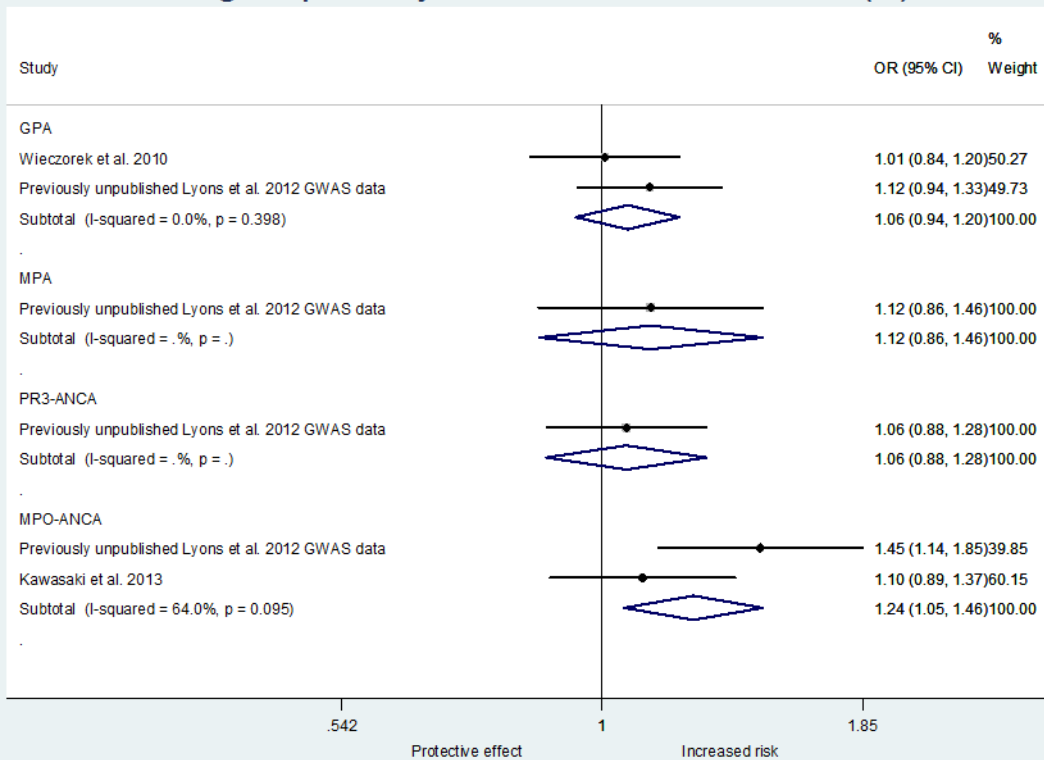
References: ^{54, 55, 56, 58}

Subgroup analysis SERPINA1 Z allele



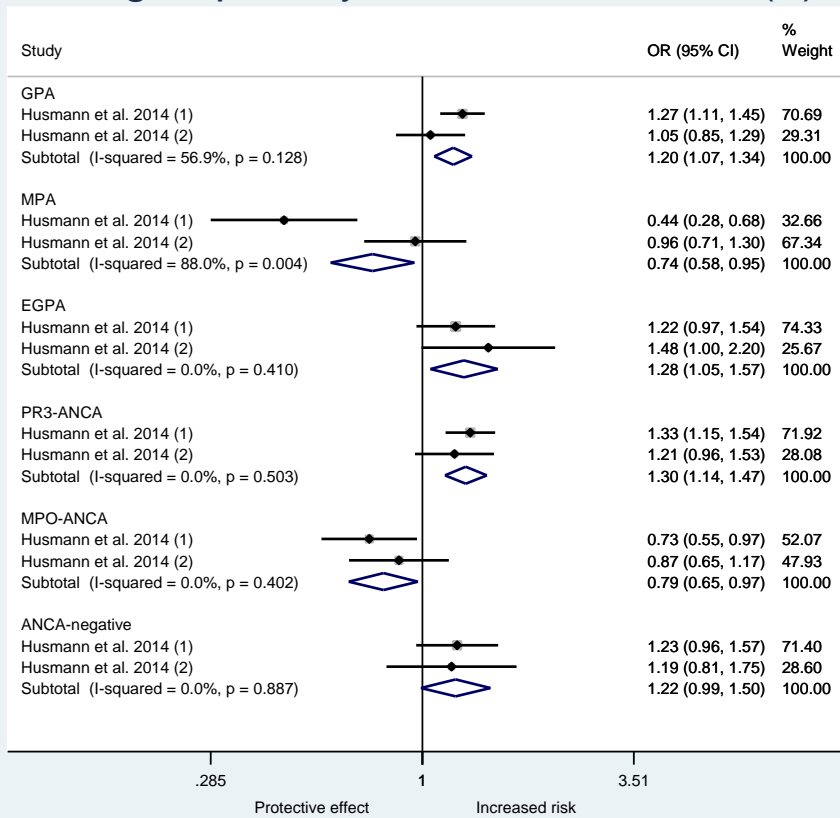
References: 54, 55, 59, 60, 56, 3, 58

Subgroup analysis STAT4 rs7574865 (T)



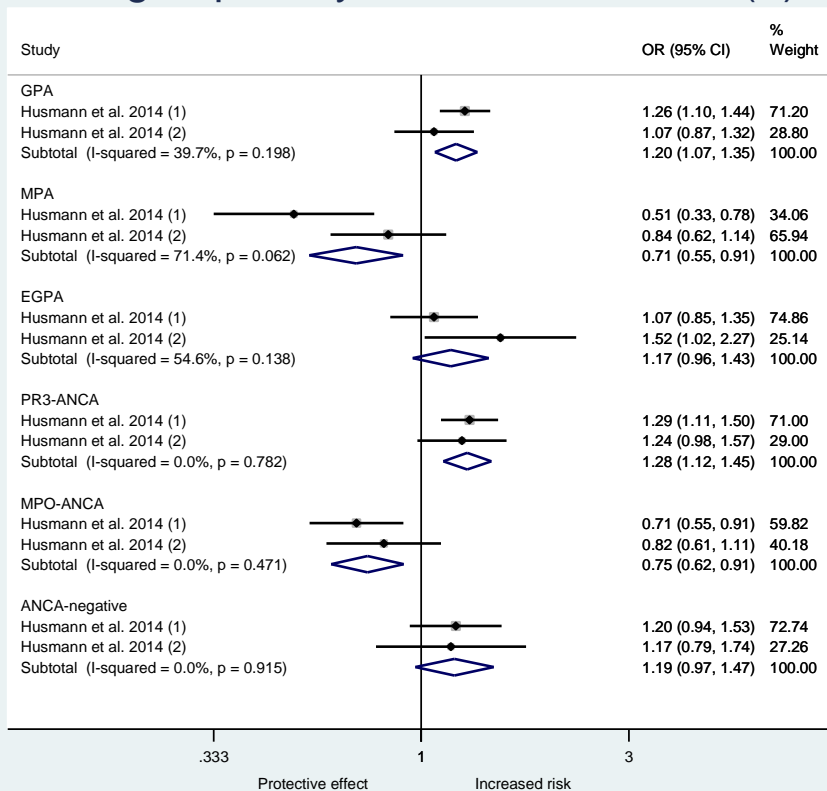
References: 44, 45

Subgroup analysis TLR9 rs352162 (T)



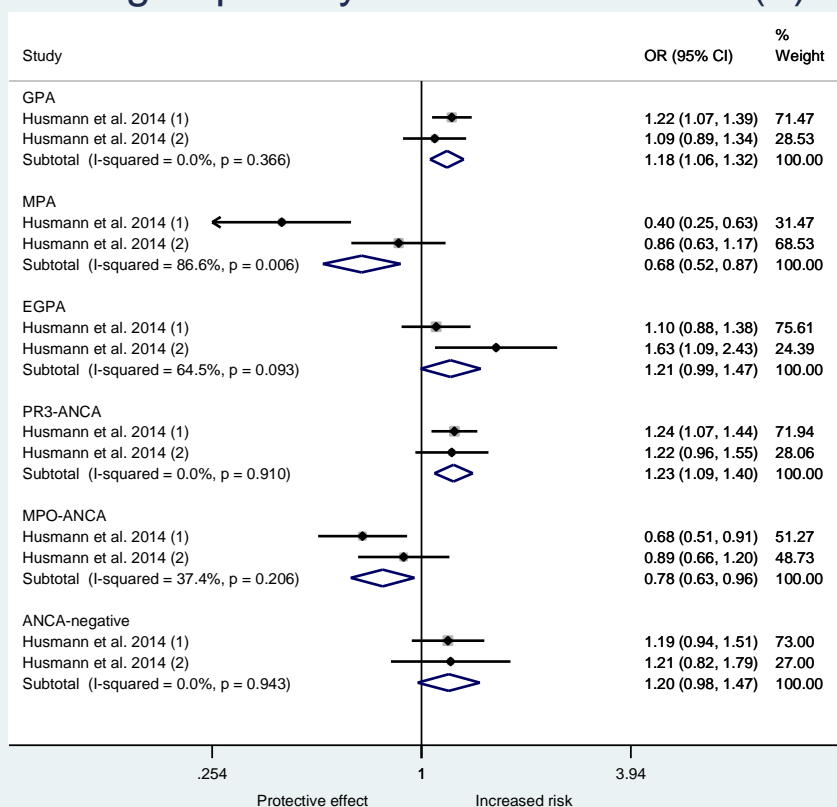
References: ⁴⁰**

Subgroup analysis TLR9 rs352140 (T)



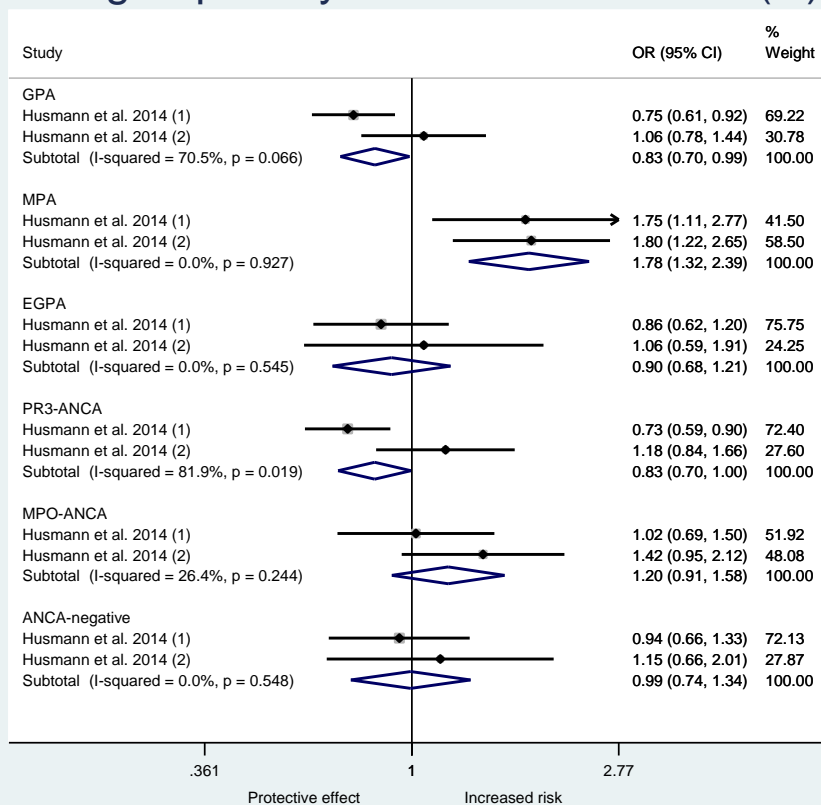
References: ⁴⁰**

Subgroup analysis TLR9 rs352139 (T)



References: 40**

Subgroup analysis TLR9 rs5743836 (G)



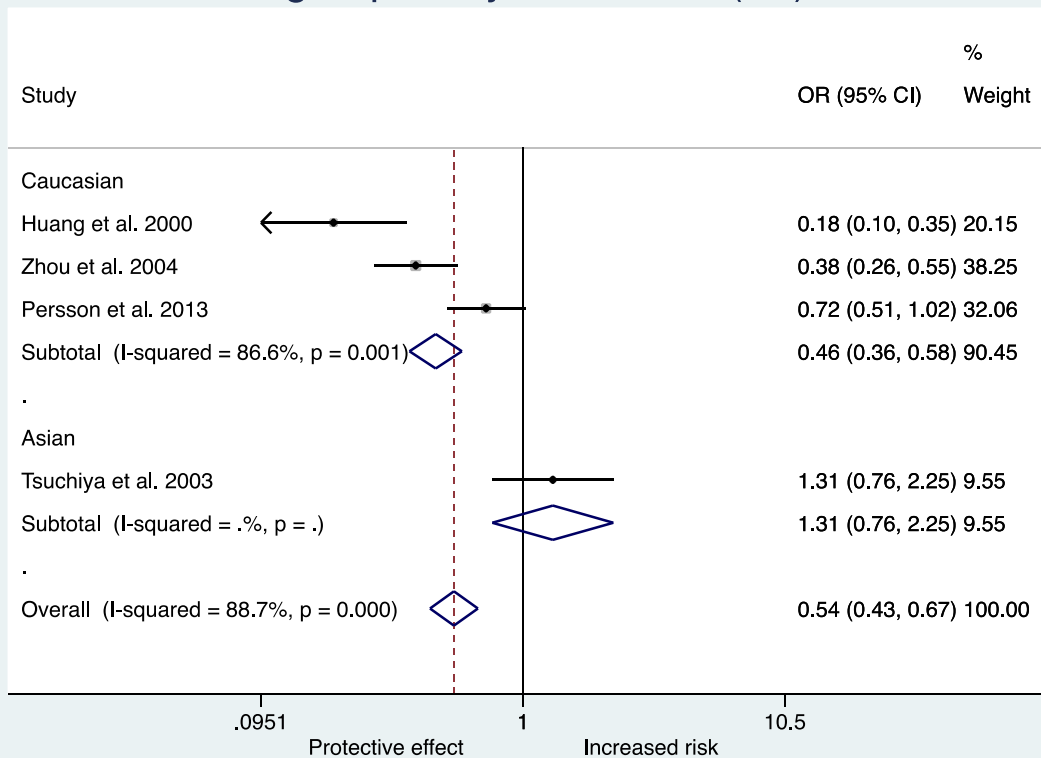
References: 40**

**Two cohorts described in the same publication.

***Three cohorts described in the same publication.

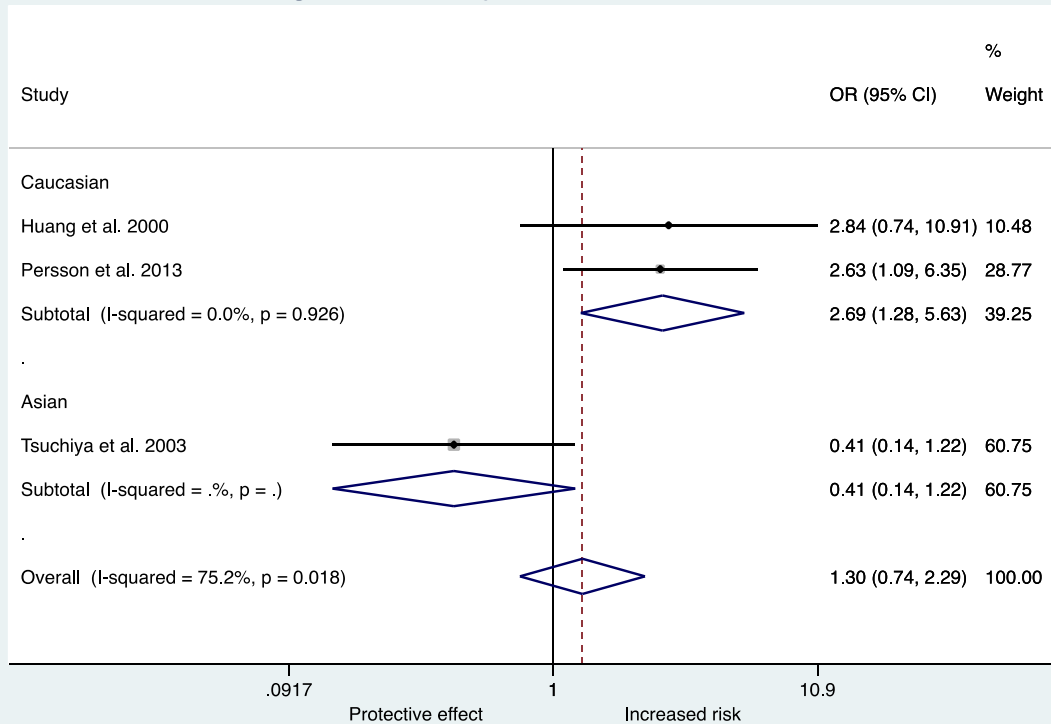
Supplementary Figure S3. Forest plots by ethnic subgroups

Subgroup analysis CTLA-4 (AT)86



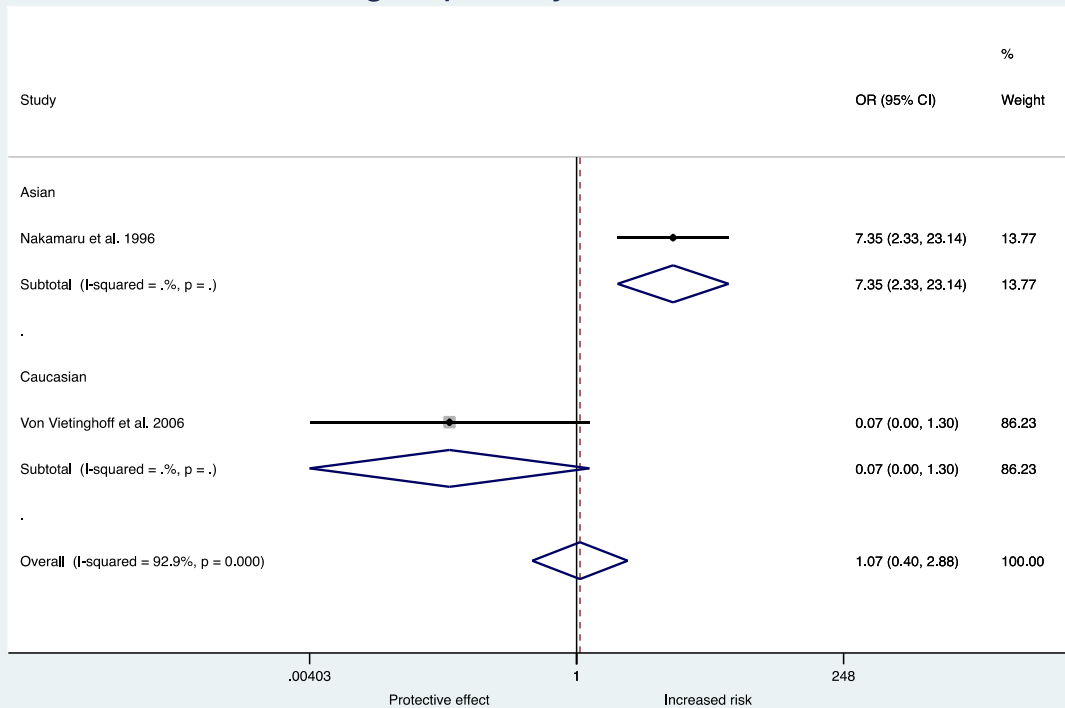
References: ⁴, ⁵, ⁶, ⁷

Subgroup analysis CTLA-4 (AT)106



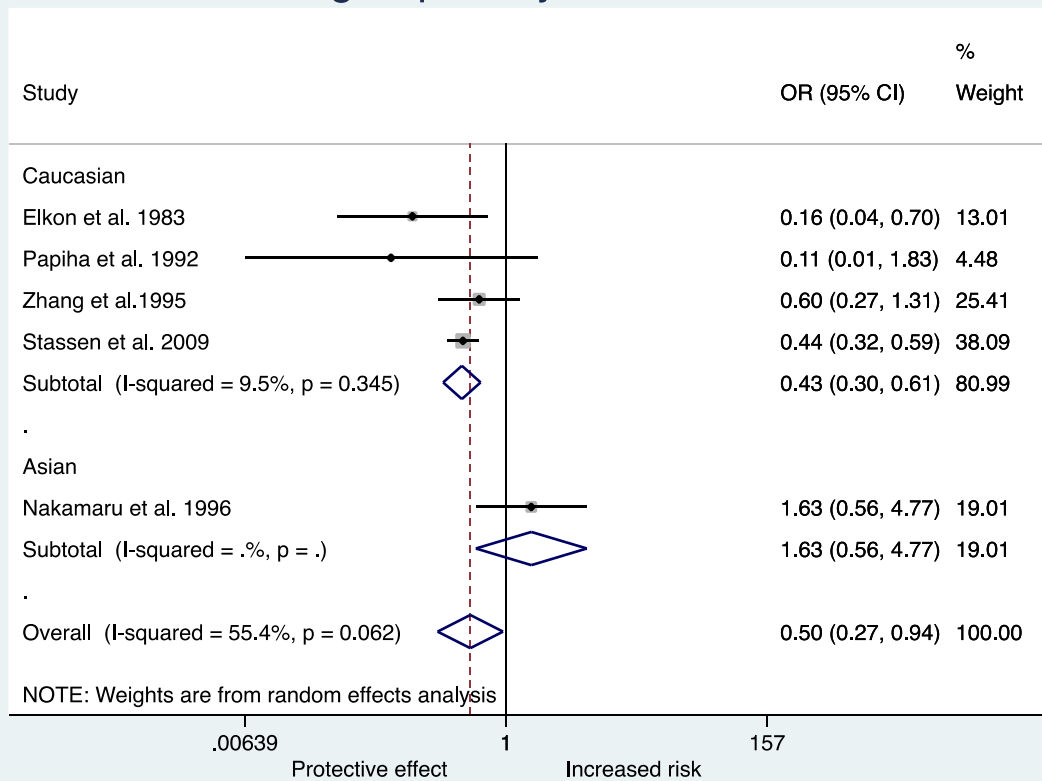
References: ⁴, ⁵, ⁷

Subgroup analysis HLA-B55



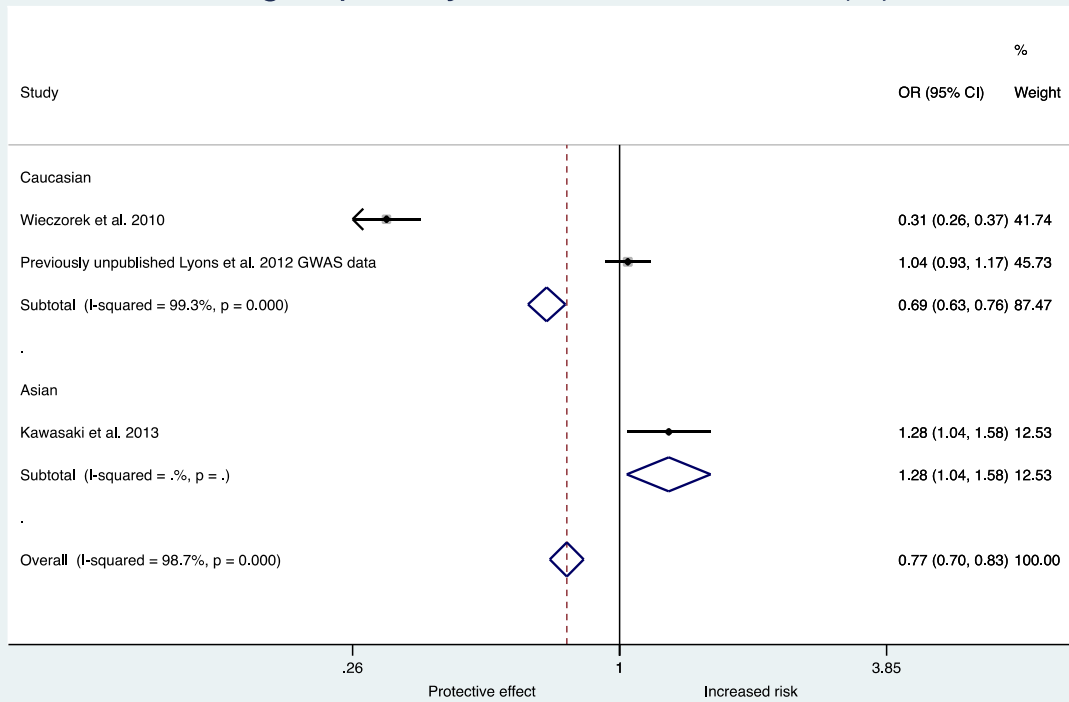
References: ^{20, 18}

Subgroup analysis HLA-DR6



References: ^{23, 32, 26, 20, 19}

Subgroup analysis IRF5 rs10954213 (G)



References: ⁴⁴, ³, ⁴⁵

References

1. Wiczorek S, Hoffjan S, Chan A, *et al.* Novel association of the CD226 (DNAM-1) Gly307Ser polymorphism in Wegener's granulomatosis and confirmation for multiple sclerosis in German patients. *Genes Immun* 2009;10:591-5.
2. Chung SA, Xie G, Roshandel D, *et al.* Meta-analysis of genetic polymorphisms in granulomatosis with polyangiitis (Wegener's) reveals shared susceptibility loci with rheumatoid arthritis. *Arthritis Rheum* 2012;64:3463-71.
3. Lyons PA, Rayner TF, Trivedi S, *et al.* Genetically distinct subsets within ANCA-associated vasculitis. *N Engl J Med* 2012;367:214-23.
4. Huang D, Giscombe R, Zhou Y, *et al.* Polymorphisms in CTLA-4 but not tumor necrosis factor-alpha or interleukin 1beta genes are associated with Wegener's granulomatosis. *J Rheumatol* 2000;27:397-401.
5. Tsuchiya N, Kobayashi S, Kawasaki A, *et al.* Genetic background of Japanese patients with antineutrophil cytoplasmic antibody-associated vasculitis: association of HLA-DRB1*0901 with microscopic polyangiitis. *J Rheumatol* 2003;30:1534-40.
6. Zhou Y, Huang D, Paris PL, *et al.* An analysis of CTLA-4 and proinflammatory cytokine genes in Wegener's granulomatosis. *Arthritis Rheum* 2004;50:2645-50.
7. Persson U, Gullstrand B, Pettersson A, *et al.* A candidate gene approach to ANCA-associated vasculitis reveals links to the C3 and CTLA-4 genes but not to the IL1-Ra and Fcgamma-RIIa genes. *Kidney Blood Press Res* 2013;37:641-8.
8. Slot MC, Sokolowska MG, Savelkoul KG, *et al.* Immunoregulatory gene polymorphisms are associated with ANCA-related vasculitis. *Clin Immunol* 2008;128:39-45.
9. Kamesh L, Heward JM, Williams JM, *et al.* CT60 and +49 polymorphisms of CTLA 4 are associated with ANCA-positive small vessel vasculitis. *Rheumatology (Oxford)* 2009;48:1502-5.
10. Kelley JM, Monach PA, Ji C, *et al.* IgA and IgG antineutrophil cytoplasmic antibody engagement of Fc receptor genetic variants influences granulomatosis with polyangiitis. *Proc Natl Acad Sci U S A* 2011;108:20736-41.
11. Edberg JC, Wainstein E, Wu J, *et al.* Analysis of FcgammaRII gene polymorphisms in Wegener's granulomatosis. *Exp Clin Immunogenet* 1997;14:183-95.
12. Dijkstra HM, Scheepers RH, Oost WW, *et al.* Fcgamma receptor polymorphisms in Wegener's granulomatosis: risk factors for disease relapse. *Arthritis Rheum* 1999;42:1823-7.
13. Tse WY, Abadeh S, McTiernan A, *et al.* No association between neutrophil FcgammaRIIIa allelic polymorphism and anti-neutrophil cytoplasmic antibody (ANCA)-positive systemic vasculitis. *Clin Exp Immunol* 1999;117:198-205.
14. Tse WY, Abadeh S, Jefferis R, *et al.* Neutrophil FcgammaRIIIb allelic polymorphism in anti-neutrophil cytoplasmic antibody (ANCA)-positive systemic vasculitis. *Clin Exp Immunol* 2000;119:574-7.
15. Wiczorek S, Holle JU, Bremer JP, *et al.* Contrasting association of a non-synonymous leptin receptor gene polymorphism with Wegener's granulomatosis and Churg-Strauss syndrome. *Rheumatology (Oxford)* 2010;49:907-14.
16. Strimlan CV, Taswell HF, Kueppers F, *et al.* HLA-A antigens of patients with Wegener's granulomatosis. *Tissue Antigens* 1978;11:129-31.
17. Murty GE, Mains BT, Middleton D, *et al.* HLA antigen frequencies and Wegener's granulomatosis. *Clin Otolaryngol Allied Sci* 1991;16:448-51.
18. von Vietinghoff S, Busjahn A, Schonemann C, *et al.* Major histocompatibility complex HLA region largely explains the genetic variance exercised on neutrophil membrane proteinase 3 expression. *J Am Soc Nephrol* 2006;17:3185-91.

19. Stassen PM, Cohen-Tervaert JW, Lems SP, *et al.* HLA-DR4, DR13(6) and the ancestral haplotype A1B8DR3 are associated with ANCA-associated vasculitis and Wegener's granulomatosis. *Rheumatology (Oxford)* 2009;48:622-5.
20. Nakamaru Y, Maguchi S, Takizawa M, *et al.* The association between human leukocyte antigens (HLA) and cytoplasmic-antineutrophil cytoplasmic antibody (cANCA)-positive Wegener's granulomatosis in a Japanese population. *Rhinology* 1996;34:163-5.
21. Katz P, Alling DW, Haynes BF, *et al.* Association of Wegener's granulomatosis with HLA-B8. *Clin Immunol Immunopathol* 1979;14:268-70.
22. Papasteriades C, Hatziyannakos D, Siakotos M, *et al.* HLA antigens in microscopic polyarteritis (MP) with renal involvement. *Dis Markers* 1997;13:117-22.
23. Elkon KB, Sutherland DC, Rees AJ, *et al.* HLA antigen frequencies in systemic vasculitis: increase in HLA-DR2 in Wegener's granulomatosis. *Arthritis Rheum* 1983;26:102-5.
24. Heckmann M, Holle JU, Arning L, *et al.* The Wegener's granulomatosis quantitative trait locus on chromosome 6p21.3 as characterised by tagSNP genotyping. *Ann Rheum Dis* 2008;67:972-9.
25. Xie G, Roshandel D, Sherva R, *et al.* Association of granulomatosis with polyangiitis (Wegener's) with HLA-DPB1*04 and SEMA6A gene variants: evidence from genome-wide analysis. *Arthritis Rheum* 2013;65:2457-68.
26. Zhang L, Jayne DR, Zhao MH, *et al.* Distribution of MHC class II alleles in primary systemic vasculitis. *Kidney Int* 1995;47:294-8.
27. Jagiello P, Gencik M, Arning L, *et al.* New genomic region for Wegener's granulomatosis as revealed by an extended association screen with 202 apoptosis-related genes. *Hum Genet* 2004;114:468-77.
28. Tsuchiya N, Kobayashi S, Hashimoto H, *et al.* Association of HLA-DRB1*0901-DQB1*0303 haplotype with microscopic polyangiitis in Japanese. *Genes Immun* 2006;7:81-4.
29. Wiczorek S, Hellmich B, Gross WL, *et al.* Associations of Churg-Strauss syndrome with the HLA-DRB1 locus, and relationship to the genetics of antineutrophil cytoplasmic antibody-associated vasculitides: comment on the article by Vaglio *et al.* *Arthritis Rheum* 2008;58:329-30.
30. Arning L, Holle JU, Harper L, *et al.* Are there specific genetic risk factors for the different forms of ANCA-associated vasculitis? *Ann Rheum Dis* 2011;70:707-8.
31. Spriewald BM, Witzke O, Wassmuth R, *et al.* Distinct tumour necrosis factor alpha, interferon gamma, interleukin 10, and cytotoxic T cell antigen 4 gene polymorphisms in disease occurrence and end stage renal disease in Wegener's granulomatosis. *Ann Rheum Dis* 2005;64:457-61.
32. Papiha SS, Murty GE, Ad'Hia A, *et al.* Association of Wegener's granulomatosis with HLA antigens and other genetic markers. *Ann Rheum Dis* 1992;51:246-8.
33. Cao Y, Schmitz JL, Yang J, *et al.* DRB1*15 allele is a risk factor for PR3-ANCA disease in African Americans. *J Am Soc Nephrol* 2011;22:1161-7.
34. Luo H, Chen M, Yang R, *et al.* The association of HLA-DRB1 alleles with antineutrophil cytoplasmic antibody-associated systemic vasculitis in Chinese patients. *Hum Immunol* 2011;72:422-5.
35. Vaglio A, Martorana D, Maggiore U, *et al.* HLA-DRB4 as a genetic risk factor for Churg-Strauss syndrome. *Arthritis Rheum* 2007;56:3159-66.
36. Fujii A, Tomizawa K, Arimura Y, *et al.* Epitope analysis of myeloperoxidase (MPO) specific anti-neutrophil cytoplasmic autoantibodies (ANCA) in MPO-ANCA-associated glomerulonephritis. *Clin Nephrol* 2000;53:242-52.
37. Tsuchiya N. Genetics of ANCA-associated vasculitis in Japan: a role for HLA-DRB1*09:01 haplotype. *Clin Exp Nephrol* 2013;17:628-30.
38. Spencer SJ, Burns A, Gaskin G, *et al.* HLA class II specificities in vasculitis with antibodies to neutrophil cytoplasmic antigens. *Kidney Int* 1992;41:1059-63.

39. Borgmann S, Endisch G, Hacker UT, *et al.* Proinflammatory genotype of interleukin-1 and interleukin-1 receptor antagonist is associated with ESRD in proteinase 3-ANCA vasculitis patients. *Am J Kidney Dis* 2003;41:933-42.
40. Husmann CA, Holle JU, Moosig F, *et al.* Genetics of toll like receptor 9 in ANCA associated vasculitides. *Ann Rheum Dis* 2014;73:890-6.
41. Wieczorek S, Hellmich B, Arning L, *et al.* Functionally relevant variations of the interleukin-10 gene associated with antineutrophil cytoplasmic antibody-negative Churg-Strauss syndrome, but not with Wegener's granulomatosis. *Arthritis Rheum* 2008;58:1839-48.
42. Murakozy G, Gaede KI, Ruprecht B, *et al.* Gene polymorphisms of immunoregulatory cytokines and angiotensin-converting enzyme in Wegener's granulomatosis. *J Mol Med (Berl)* 2001;79:665-70.
43. Bartfai Z, Gaede KI, Russell KA, *et al.* Different gender-associated genotype risks of Wegener's granulomatosis and microscopic polyangiitis. *Clin Immunol* 2003;109:330-7.
44. Wieczorek S, Holle JU, Muller S, *et al.* A functionally relevant IRF5 haplotype is associated with reduced risk to Wegener's granulomatosis. *J Mol Med (Berl)* 2010;88:413-21.
45. Kawasaki A, Inoue N, Ajimi C, *et al.* Association of IRF5 polymorphism with MPO-ANCA-positive vasculitis in a Japanese population. *Genes Immun* 2013;14:527-9.
46. Reynolds WF, Stegeman CA, Tervaert JW. -463 G/A myeloperoxidase promoter polymorphism is associated with clinical manifestations and the course of disease in MPO-ANCA-associated vasculitis. *Clin Immunol* 2002;103:154-60.
47. Fiebeler A, Borgmann S, Woywodt A, *et al.* No association of G-463A myeloperoxidase gene polymorphism with MPO-ANCA-associated vasculitis. *Nephrol Dial Transplant* 2004;19:969-71.
48. Rajp A, Adu D, Savage CO. Meta-analysis of myeloperoxidase G-463/A polymorphism in anti-neutrophil cytoplasmic autoantibody-positive vasculitis. *Clin Exp Immunol* 2007;149:251-6.
49. Sakhivel P, Giscombe R, Ramanujam R, *et al.* Polymorphisms in PDCD1 gene are not associated with Wegener's granulomatosis. *Rheumatol Int* 2009;29:1247-50.
50. Jagiello P, Aries P, Arning L, *et al.* The PTPN22 620W allele is a risk factor for Wegener's granulomatosis. *Arthritis Rheum* 2005;52:4039-43.
51. Martorana D, Maritati F, Malerba G, *et al.* PTPN22 R620W polymorphism in the ANCA-associated vasculitides. *Rheumatology (Oxford)* 2012;51:805-12.
52. Szyld P, Jagiello P, Csernok E, *et al.* On the Wegener granulomatosis associated region on chromosome 6p21.3. *BMC Med Genet* 2006;7:21.
53. Wieczorek S, Knaup S, Gross WL, *et al.* Genetic variability of RXRB, PPARA, and PPARG in Wegener's granulomatosis. *PPAR Res* 2009;2009:786781.
54. Lhotta K, Vogel W, Meisl T, *et al.* Alpha 1-antitrypsin phenotypes in patients with anti-neutrophil cytoplasmic antibody-positive vasculitis. *Clin Sci (Lond)* 1994;87:693-5.
55. Griffith ME, Lovegrove JU, Gaskin G, *et al.* C-antineutrophil cytoplasmic antibody positivity in vasculitis patients is associated with the Z allele of alpha-1-antitrypsin, and P-antineutrophil cytoplasmic antibody positivity with the S allele. *Nephrol Dial Transplant* 1996;11:438-43.
56. Mahr AD, Edberg JC, Stone JH, *et al.* Alpha(1)-antitrypsin deficiency-related alleles Z and S and the risk of Wegener's granulomatosis. *Arthritis Rheum* 2010;62:3760-7.
57. Morris H, Morgan MD, Wood AM, *et al.* ANCA-associated vasculitis is linked to carriage of the Z allele of alpha(1) antitrypsin and its polymers. *Ann Rheum Dis* 2011;70:1851-6.
58. Chorostowska-Wynimko J, Gawryluk D, Struniawski R, *et al.* Incidence of alpha-1 antitrypsin Z and S alleles in patients with granulomatosis with polyangiitis - pilot study. *PneumonolAlergolPol* 2013;81:319-22.

59. Callea F, Gregorini G, Sinico A, *et al.* alpha 1-Antitrypsin (AAT) deficiency and ANCA-positive systemic vasculitis: genetic and clinical implications. *Eur J Clin Invest* 1997;27:696-702.
60. Borgmann S, Endisch G, Urban S, *et al.* A linkage disequilibrium between genes at the serine protease inhibitor gene cluster on chromosome 14q32.1 is associated with Wegener's granulomatosis. *Clin Immunol* 2001;98:244-8.
61. Mascher B, Schmitt W, Csernok E, *et al.* Polymorphisms in the tumor necrosis factor genes in Wegener's granulomatosis. *Exp Clin Immunogenet* 1997;14:226-33.