

Genetic Variants in Antineutrophil Cytoplasmic Antibody-Associated Vasculitis:

A Bayesian Approach and Systematic Review

Table S1. Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) Checklist.

Section/topic	#	Checklist item	Reported on page #
TITLE			
Title	1	Identify the report as a systematic review, meta-analysis, or both.	1
ABSTRACT			
Structured summary	2	Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number.	3-4
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known.	5-6
Objectives	4	Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS).	5-6
METHODS			
Protocol and registration	5	Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number.	7-8
Eligibility criteria	6	Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale.	7-8
Information sources	7	Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched.	7-8
Search	8	Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated.	7-8
Study selection	9	State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis).	7-8 (Figure1)
Data collection process	10	Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data from investigators.	7-8
Data items	11	List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made.	Tables and Supplementary

			Tables
Risk of bias in individual studies	12	Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis.	N/A
Summary measures	13	State the principal summary measures (e.g., risk ratio, difference in means).	7-8
Synthesis of results	14	Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I ²) for each meta-analysis.	7-8

Section/topic	#	Checklist item	Reported on page #
Risk of bias across studies	15	Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies).	Tables and Supplementary Tables
Additional analyses	16	Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified.	N/A
RESULTS			
Study selection	17	Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram.	Figure 1
Study characteristics	18	For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations.	Tables and Supplementary Tables
Risk of bias within studies	19	Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12).	N/A
Results of individual studies	20	For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot.	9–11, Tables,
Synthesis of results	21	Present results of each meta-analysis done, including confidence intervals and measures of consistency.	9–11. Tables,
Risk of bias across studies	22	Present results of any assessment of risk of bias across studies (see Item 15).	Tables and Supplementary Tables
Additional analysis	23	Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see Item 16]).	N/A
DISCUSSION			
Summary of evidence	24	Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers).	12-16
Limitations	25	Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias).	15-16

Conclusions	26	Provide a general interpretation of the results in the context of other evidence, and implications for future research.	12-16
FUNDING			
Funding	27	Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review.	16

Equation S1. Calculation of False Positive Report Probability (FPRP) and Bayesian False Discovery Probability (BFDP)

Estimation of False Positive Report Probability (FPRP), which is defined as “the probability of no true association between a gene variant and disease (null hypothesis)” for a statistically significant association was calculated following methods created by Wacholder et al. FPRP is calculated with the observed p-value, statistical power of the test, and prior probability that a molecular association is real. In this review, we calculated FPRP at two levels of assumed prior probabilities, which were 10^{-3} for a candidate gene variant and 10^{-6} for a random SNP. Thus, readers could judge by themselves about the supporting evidence for a given locus. Statistical power to detect an OR of 1.2 and 1.5 were used for FPRP at both prior probabilities. Though Wacholder et al. suggested estimating statistical power based on the ability to detect an OR of 1.5 (or its reciprocal $1/1.5 = 0.67$) for OR less than 1.0, we found this estimate might be too conservative, so we decided to present results for both OR of 1.5 and 1.2 (or its reciprocal $1/1.2 = 0.83$), which is the median reported OR in our review. FPRP value can be obtained using the following equation:

$$\text{FPRP} = \frac{\alpha(1 - \pi)}{\alpha(1 - \pi) + (1 - \beta)\pi} \quad (1)$$

where π is the prior probability, α is the lowest level of significance at which a test is noteworthy ($\alpha = 0.05$), and $(1 - \beta)$ is the statistical power obtained using the following equation:

$$1 - \beta = \varphi\left\{\frac{[\log(OR_A/OR_O)]}{\sigma}\right\} - Z_{\alpha/2} \quad (2)$$

where φ is the cumulative distribution function of the standard normal distribution, and $Z_{\alpha/2}$ is the $\alpha/2$ point of the standard cumulative normal distribution. For the actual computation of FPRP, σ and $Z_{\alpha/2}$ are replaced by the standard error of the log-odds ratio estimates and the two-sided p-value point of the standard normal distribution. Computed FPRP for significant associations are summarized in Tables 1–4. All FPRP computations were performed using the Excel spreadsheet provided by Wacholder et al., and associations with FPRP <0.2 were considered noteworthy as recommended by the authors.

Moreover, we also computed the Bayesian false discovery probability (BFDP) values for the above significant associations using methods created by Wakefield. Unlike FPRP, BFDP is calculated using the following equation:

$$\text{BFDP} = \frac{ABF \times PO}{ABF \times PO + 1} \quad (3)$$

where PO is the prior odds of the null hypothesis and is equal to $\pi_0 / (1 - \pi_0)$ wherein π_0 is the prior probability of the null, and ABF is the approximate Bayes factor computed using odds ratio and standard error. One of the differences between BFDP and FPRP is the independence of BFDP from a statistical power. Its approximation is based on a logistic regression model instead of standard normal distribution.

Even though Wakefield advocates that BFDP is superior to FPRP with its straightforward and sound methodological derivation, Wakefield admits that the overall behavior of BFDP and FPRP is similar. FPRP produces posterior null estimates smaller than those produced by BFDP because the FPRP is essentially the lower bound on the posterior probability corresponding to the observed estimates [1]. Noteworthy genetic variants identified by our analysis are given in Tables 1–4, and more noteworthy genetic variants were derived from BFDP than from FPRP. Similar to the

FPRP computation, BFDP estimation was computed for both prior probabilities of 10^{-3} and 10^{-6} and is shown in Tables 1–4. All BFDP computations were also performed using the Excel spreadsheet provided by Wakefield (<http://faculty.washington.edu/jonno/cv.html>).

Table S2. List of publications included in this re-analysis [1-7].

No.	Title	Journal publication	Author	Year	Type
1	Association of granulomatosis with polyangiitis (Wegener's) with HLA-DPB1*04 and SEMA6A gene variants: evidence from genome-wide analysis	Arthritis Rheum.	Xie G, et al.	2013	GWAS
2	Identification of Functional and Expression Polymorphisms Associated With Risk for Antineutrophil Cytoplasmic Autoantibody-Associated Vasculitis	Arthritis Rheumatol.	Merkel PA, et al.	2017	GWAS
3	CTLA-4 and TNF- α promoter-308 A/G polymorphisms and ANCA-associated vasculitis susceptibility: a meta-analysis	Mol Biol Rep.	Lee YH, et al.	2012	Meta-analysis
4	Genetic variants in ANCA-associated vasculitis: a meta-analysis	Ann Rheum Dis.	Rahmattulla C, et al.	2016	Meta-analysis
5	Meta-Analysis of Associations Between Interleukin-10 Polymorphisms and Susceptibility to Vasculitis	Immunol Invest.	Jung JH, et al.	2015	Meta-analysis
6	Meta-analysis of genetic polymorphisms in granulomatosis with polyangiitis (Wegener's) reveals shared susceptibility loci with rheumatoid arthritis	Arthritis Rheum.	Chung SA, et al.	2012	Meta-analysis
7	The protein tyrosine phosphatase nonreceptor 22 C1858T polymorphism and vasculitis: a meta-analysis	Mol Biol Rep.	Lee YH, et al.	2012	Meta-analysis

Table S3. Meta-analysis results of observational studies, gene variants with statistical significance (p-value < 0.05) for each clinical diagnosis (AAV, GPA, MPA). Summary of genetic variants with FPRP, BFDP values, and noteworthy genetic variants are given in bold.

Gene/Variant	Minor allele/ Comparison	OR (95% CI)	p-value for meta- analysis	Publications (n)	Diagnosis (clinical subtypes)	No. of Cases/Controls	I² (%)	I² (P)	Egger's P-value	Power OR 1.2	Power OR 1.5	FPRP Values at Prior probability				BFDP 0.001	BFDP 0.000001	Author, Year
												OR 1.2		OR 1.5				
												0.001	0.000001	0.001	0.000001			
CD226 rs763361	T	1.14 (1.07 – 1.21)	<0.001	3	AAV	2422/17898	0	0.444	0.792	0.954	1.000	0.017	0.945	0.016	0.942	0.437	0.999	Rahmattulla, et al. 2016

CLTA-4 rs231775	G	1.16 (1.06 – 1.28)	0.002	3	AAV	1002/6179	60	0.080	0.080	0.750	1.000	0.806	1.000	0.757	1.000	0.986	1.000	[4] Rahmattulla, et al. 2016
CTLA-4 rs3087243 (CT60)	A	0.81 (0.75 – 0.87)	<0.001	3	AAV	2015/7855	25	0.262	0.122	0.218	1.000	0.000	0.033	0.000	0.007	0.001	0.347	[4] Rahmattulla, et al. 2016
CTLA-4	(AT)₈₆	0.54 (0.43 – 0.67)	<0.001	4	AAV	303/543	89	<0.001	0.946	0.000	0.028	0.348	0.998	0.001	0.437	0.010	0.913	[4] Rahmattulla, et al. 2016
CTLA-4 rs231775	GG vs. GA+AA	1.785 (1.275 – 2.499)	0.001	2	AAV	324/817	0	0.419		0.430	0.682	0.999	1.000	0.999	1.000	0.999	1.000	Lee, et al. 2012 [3]
CTLA-4 rs231775	GG+GA vs. AA	1.369 (1.045 – 1.793)	0.022	2	AAV	324/817	56	0.128		0.169	0.747	0.993	1.000	0.968	1.000	0.997	1.000	Lee, et al. 2012 [3]
CTLA-4 rs231775	GG vs. AA	1.984 (1.366 – 2.881)	3.17E-04	2	AAV	324/817	0	0.937		0.004	0.071	0.987	1.000	0.818	0.998	0.978	1.000	Lee, et al. 2012 [3]
CTLA-4 rs231775	G vs. A	1.382 (1.147 – 1.664)	0.001	2	AAV	324/817	0	0.484		0.068	0.806	0.904	0.999	0.441	0.988	0.951	1.000	Lee, et al. 2012 [3]
CTLA-4 rs3087243 (CT60)	AA vs. AG+GG	0.720 (0.591 – 0.877)	0.001	2	AAV	797/9669	10.9	0.289		0.073	0.778	0.937	0.999	0.585	0.993	0.969	1.000	Lee, et al. 2012 [3]
CTLA-4 rs3087243 (CT60)	AA+AG vs. GG	0.725 (0.538 – 0.977)	0.035	2	AAV	797/9669	63.5	0.098		0.180	0.709	0.995	1.000	0.980	1.000	0.997	1.000	Lee, et al. 2012 [3]
CTLA-4 rs3087243 (CT60)	AA vs. GG	0.693 (0.512 – 0.796)	6.39E-05	2	AAV	797/9669	57.7	0.124		0.005	0.708	0.045	0.824	0.000	0.029	0.018	0.948	Lee, et al. 2012 [3]
CTLA-4 rs3087243 (CT60)	A vs. G	0.769 (0.619 – 0.955)	0.017	2	AAV	797/9669	67.1	0.081		0.234	0.902	0.987	1.000	0.951	0.999	0.996	1.000	Lee, et al. 2012 [3]
FCGR2A rs 1801274	C	0.90 (0.82 – 0.99)	0.028	6	AAV	1239/6209	0	0.834	0.788	0.943	1.000	0.970	1.000	0.968	1.000	0.998	1.000	Rahmattulla, et al. 2016
HLA-B5	-	0.59 (0.38 – 0.92)	0.019	2	AAV	335/6573	0	0.432	NA	0.064	0.295	0.997	1.000	0.985	1.000	0.997	1.000	[4] Rahmattulla, et al. 2016
HLA-B8	-	1.48 (1.04 – 2.11)	0.028	6	AAV	475/7855	47	0.096	0.063	0.123	0.530	0.996	1.000	0.983	1.000	0.998	1.000	[4] Rahmattulla, et al. 2016
HLA-DPA1 rs9277341	C	0.35 (0.30 – 0.40)	<0.001	2	AAV	1032/2200	54	0.116	0.215	NA	NA	NA	NA	NA	NA	0.000	0.000	[4] Rahmattulla, et al. 2016
HLA-DPB1*0301	-	0.38 (0.21 – 0.69)	0.002	5	AAV	1154/1337	78	<0.001	0.938	0.005	0.032	0.997	1.000	0.979	1.000	0.996	1.000	[4] Rahmattulla, et al. 2016
HLA-DPB1*0401	-	1.99 (1.44 – 2.74)	<0.001	5	AAV	1154/1337	84	<0.001	0.738	0.001	0.042	0.962	1.000	0.373	0.998	0.870	1.000	[4] Rahmattulla, et al. 2016
HLA-DPB2 rs3130215	A	1.40 (1.29 – 1.52)	<0.001	3	AAV	1417/7249	99	<0.001	0.446	0.000	0.950	0.000	0.000	0.000	0.000	0.000	0.000	[4] Rahmattulla, et al. 2016
HLA-DPQ1*0303	-	1.82 (1.09 – 3.03)	0.021	3	AAV	176/218	17	0.301	0.916	0.055	0.229	0.997	1.000	0.989	1.000	0.998	1.000	[4] Rahmattulla, et al. 2016
HLA-DR6	-	0.50 (0.27 – 0.95)	0.033	5	AAV	487/6222	55	0.062	0.997	0.059	0.190	0.998	1.000	0.994	1.000	0.998	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB1*1101	-	1.89 (1.15 – 3.08)	0.011	2	AAV	268/465	0	0.487	NA	0.034	0.177	0.997	1.000	0.984	1.000	0.997	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB1*1201	-	0.37 (0.15 – 0.91)	0.031	2	AAV	216/465	0	0.491	NA	0.039	0.100	0.999	1.000	0.997	1.000	0.999	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB1*13	-	0.47 (0.32 – 0.70)	<0.001	4	AAV	233/833	0	0.504	0.884	0.002	0.043	0.988	1.000	0.826	1.000	0.977	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB1*14	-	1.91 (1.07 – 3.42)	0.029	4	AAV	322/862	0	0.728	0.700	0.059	0.208	0.998	1.000	0.993	1.000	0.998	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB1*15	-	1.86 (1.39 – 2.50)	<0.001	3	AAV	236/633	69	0.021	0.347	0.002	0.077	0.955	1.000	0.336	0.998	0.871	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB1*1501	-	1.68 (1.20 – 2.34)	0.002	2	AAV	216/465	0	0.925	NA	0.023	0.251	0.989	1.000	0.895	1.000	0.989	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB3	-	0.62 (0.49 – 0.79)	<0.001	4	AAV	260/1845	68	0.024	0.689	0.008	0.279	0.929	1.000	0.283	0.997	0.888	1.000	[4] Rahmattulla, et al. 2016
HLA-DRB4	-	1.69 (1.36 – 2.10)	<0.001	4	AAV	260/1845	61	0.055	0.533	0.001	0.141	0.686	1.000	0.015	0.940	0.259	0.997	[4] Rahmattulla, et al. 2016
HSD17B8 rs421446	C	0.40 (0.34 – 0.48)	<0.001	2	AAV	738/1872	0	0.620	NA	NA	NA	NA	NA	NA	NA	0.000	0.000	[4] Rahmattulla, et al. 2016
IRF5 rs10954213	G	0.77 (0.70 – 0.83)	<0.001	3	AAV	1535/6977	99	<0.001	0.948	0.019	1.000	0.000	0.000	0.000	0.000	0.000	0.001	[4] Lee, et al. 2012 [7]
PTPN22 rs2476601	T vs. C	1.415 (1.228 – 1.630)	1.59E-06	3	AAV	1184/10459	0	0.393	0.481	0.011	0.791	0.119	0.931	0.002	0.160	0.091	0.990	Rahmattulla, et al. 2016
PTPN22 rs2476601	A	1.39 (1.24 – 1.56)	<0.001	4	AAV	2099/8678	0	0.693	0.500	0.006	0.902	0.004	0.780	0.000	0.024	0.002	0.654	[4] Rahmattulla, et al. 2016
RING1/RXRb rs213213	A	1.71 (1.57 – 1.86)	<0.001	3	AAV	1414/7238	73	0.026	0.187	NA	NA	NA	NA	NA	NA	0.000	0.000	[4] Rahmattulla, et al. 2016
RXRb rs6531	C	1.63 (1.50 – 1.77)	<0.001	3	AAV	1557/6955	96	<0.001	0.292	NA	NA	NA	NA	NA	NA	0.000	0.000	[4] Rahmattulla, et al. 2016
RXRb rs9277935	T	0.44 (0.37 – 0.50)	<0.001	3	AAV	1417/7233	73	0.025	0.393	NA	NA	NA	NA	NA	NA	0.000	0.000	[4] Rahmattulla, et al. 2016
SERPINA 1	S allele	1.30 (1.03 – 1.63)	0.025	5	AAV	1474/5762	0	0.464	0.547	0.244	0.892	0.989	1.000	0.963	1.000	0.997	1.000	Rahmattulla, et al. 2016

SERPINA 1	Z allele	2.94 (2.22 – 3.88)	<0.001	8	AAV	3662/8581	41	0.092	0.078	0.000	0.000	0.173	0.995	0.000	0.025	0.000	0.005	Rahmattulla, et al. 2016 [4]
STAT4 rs 7574865	T	1.11 (1.01 – 1.22)	0.029	3	AAV	1520/6956	3	0.357	0.590	0.947	1.000	0.970	1.000	0.968	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs 352139	T	1.11 (1.00 – 1.23)	0.041	1	AAV	1289/1898	0	0.756	NA	0.932	1.000	0.980	1.000	0.979	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs 352140	T	1.13 (1.02 – 1.25)	0.018	1	AAV	1289/1898	0	0.432	NA	0.878	1.000	0.952	1.000	0.946	1.000	0.997	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352162	T	1.58 (1.43 – 1.75)	<0.001	1	AAV	1289/1898	96	<0.001	NA	NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
PTPN22 rs2476601	T vs. C	2.042 (1.534 – 2.719)	1.02E-06	2	ANCA(+) GPA	-	0	0.989	NA	0.000	0.017	0.882	0.999	0.056	0.855	0.375	0.998	Lee, et al. 2012 [7]
BACH2 rs11755527	G vs. C	1.14 (1.01 – 1.28)	0.03	2	GPA	880/1969				0.807	1.000	0.971	1.000	0.964	1.000	0.997	1.000	Chung, et al. 2012 [6]
CD226 rs763361	T	1.19 (1.11 – 1.28)	<0.001	3	GPA	2021/17898	72.2	0.006		0.589	1.000	0.005	0.832	0.003	0.745	0.124	0.993	Rahmattulla, et al. 2016 [4]
CD40 rs4810485	T vs. G/A	0.81 (0.70 – 0.92)	0.002	2	GPA	880/1969				0.331	0.999	0.781	0.997	0.542	0.992	0.965	1.000	Chung, et al. 2012 [6]
CLTA-4 rs3087243	A	0.80 (0.73 – 0.87)	<0.001	3	GPA	1561/7855	38.7	0.180		0.170	1.000	0.001	0.521	0.000	0.156	0.011	0.915	Rahmattulla, et al. 2016 [4]
CTLA-4	(AT) ₈₆	0.44 (0.34 – 0.57)	<0.001	3	GPA	210/432	86.5	0.001		0.000	0.001	0.434	0.999	0.001	0.381	0.002	0.670	Rahmattulla, et al. 2016 [4]
CTLA-4	(AT) ₈₆ vs. xx	0.402 (0.184 – 0.875)	0.022	3	GPA	251/420	81.6	<0.001		0.033	0.101	0.998	1.000	0.995	1.000	0.998	1.000	Lee, et al. 2012 [3]
CTLA-4	(AT) ₈₆ /(AT) ₈₆ vs. (AT) ₈₆ /xx+xx/xx	0.376 (0.156 – 0.908)	0.030	3	GPA	251/420	80.0	0.007		0.038	0.101	0.999	1.000	0.997	1.000	0.999	1.000	Lee, et al. 2012 [3]
CTLA-4	(AT) ₈₆ /(AT) ₈₆ +(AT) ₈₆ /xx vs. xx/xx	0.428 (0.221 – 0.827)	0.012	3	GPA	251/420	70.9	0.032		0.024	0.094	0.998	1.000	0.992	1.000	0.998	1.000	Lee, et al. 2012 [3]
CTLA-4 rs231735	G vs. T	0.82 (0.73 – 0.92)	0.001	2	GPA	880/1969				0.392	1.000	0.649	0.995	0.420	0.986	0.949	1.000	Chung, et al. 2012 [6]
CTLA-4 rs3087243 (CT60)	A vs. G	0.79 (0.70 – 0.89)	9.83E-05	2	GPA	880/1969				0.190	0.997	0.358	0.982	0.096	0.914	0.779	1.000	Chung, et al. 2012 [6]
HLA-A11	-	0.61 (0.41 – 0.90)	0.014	5	GPA	380/7702	51.4	0.084		0.058	0.327	0.995	1.000	0.975	1.000	0.997	1.000	Rahmattulla, et al. 2016 [4]
HLA-B35	-	0.62 (0.44 – 0.89)	0.010	4	GPA	349/7095	0.0	0.894		0.054	0.347	0.994	1.000	0.965	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
HLA-B62	-	2.27 (1.05 – 4.90)	0.036	2	GPA	57/1172	0.0	0.927		0.052	0.146	0.999	1.000	0.996	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPA1 rs9277341	C	0.35 (0.30 – 0.41)	<0.001	2	GPA	1032/2200	54.8	0.109		NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0101	-	0.17 (0.05 – 0.63)	0.008	1	GPA	148/89	-	-		0.009	0.020	0.999	1.000	0.997	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0201	-	0.67 (0.45 – 0.99)	0.042	2	GPA	283/458	40.0	0.197		0.137	0.510	0.997	1.000	0.989	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0301	-	0.23 (0.16 – 0.32)	<0.001	3	GPA	774/918	61.7	0.050		NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0401	-	2.89 (2.50 – 3.35)	<0.001	3	GPA	774/918	67.5	0.026		NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
HLA-DR2	-	1.36 (1.08 – 1.72)	0.010	4	GPA	301/6132	71.1	0.016		0.148	0.793	0.986	1.000	0.928	1.000	0.994	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR4	-	1.32 (1.09 – 1.60)	0.004	7	GPA	425/6424	0.0	0.461		0.166	0.904	0.966	1.000	0.838	1.000	0.989	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR6	-	0.45 (0.33 – 0.62)	<0.001	4	GPA	301/6132	59.8	0.058		0.000	0.008	0.927	1.000	0.114	0.992	0.511	0.999	Rahmattulla, et al. 2016 [4]
HLA-DRB1*12	-	4.06 (1.27 – 12.99)	0.018	2	GPA	83/142	0.0	0.553		0.020	0.047	0.999	1.000	0.997	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB1*1202	-	2.92 (1.37 – 6.23)	0.005	1	GPA	45/200	-	-		0.011	0.042	0.998	1.000	0.992	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
IDIN rs9585056	C vs. T	0.85 (0.74 – 0.98)	0.03	2	GPA	880/1969				0.607	1.000	0.976	1.000	0.962	1.000	0.997	1.000	Chung, et al. 2012 [6]
IL-10 rs1800896	C vs. T	0.729 (0.547 - 0.971)	0.031	2	GPA	164/225	0	-	0.381	0.180	0.729	0.994	1.000	0.977	1.000	0.997	1.000	Jung, et al. 2015 [5]
IL27 rs4788084	T vs. C	1.18 (1.05 – 1.33)	0.006	2	GPA	880/1969				0.608	1.000	0.917	0.999	0.870	0.999	0.992	1.000	Chung, et al. 2012 [6]
IL27, others rs151181	C vs. T	1.18 (1.05 – 1.34)	0.007	2	GPA	880/1969				0.602	1.000	0.947	0.999	0.915	0.999	0.994	1.000	Chung, et al. 2012 [6]
IL2RA rs706778	T vs. C	1.13 (1.00 – 1.27)	0.05	2	GPA	880/1969				0.843	1.000	0.979	1.000	0.976	1.000	0.998	1.000	Chung, et al. 2012 [6]
IRF5 rs10954213	G	0.66 (0.59 – 0.74)	<0.001	2	GPA	1021/6267	99.1	0.000		0.000	0.432	0.000	0.033	0.000	0.000	0.000	0.000	Rahmattulla, et al. 2016 [4]
JAK2 rs10758669	C vs. T/A	1.14 (1.01 – 1.29)	0.03	2	GPA	880/1969				0.792	1.000	0.979	1.000	0.974	1.000	0.998	1.000	Chung, et al. 2012 [6]
LEPR rs8179183	C	0.72 (0.60 – 0.86)	<0.001	1	GPA	682/1326	0.0	0.968		0.053	0.802	0.844	1.000	0.266	0.997	0.910	1.000	Rahmattulla, et al. 2016 [4]

NKX2-3 rs11190140	T vs. C	0.86 (0.77 – 0.97)	0.01	2	GPA	880/1969			0.696	1.000	0.953	1.000	0.933	0.999	0.995	1.000	Chung, et al. 2012 [6]
NKX2-3 rs6584283	T vs. C	0.86 (0.76 – 0.96)	0.009	2	GPA	880/1969			0.713	1.000	0.910	0.999	0.878	0.999	0.992	1.000	Chung, et al. 2012 [6]
PARK7, DJ-1 rs3766606	T vs. G	0.80 (0.70 – 0.92)	0.005	2	GPA	880/1969			0.283	0.995	0.861	0.998	0.638	0.994	0.975	1.000	Chung, et al. 2012 [6]
PARK7, TNFRSF9 rs12727642	A vs. C	0.81 (0.69 – 0.95)	0.01	2	GPA	880/1969			0.363	0.992	0.963	1.000	0.906	0.999	0.993	1.000	Chung, et al. 2012 [6]
PHRF1, KIAA1542 rs4963128	T vs. C	0.87 (0.77 – 0.99)	0.03	2	GPA	880/1969			0.743	1.000	0.979	1.000	0.972	1.000	0.998	1.000	Chung, et al. 2012 [6]
PTPN22 rs2476601	A	1.43 (1.26 – 1.62)	<0.001	4	GPA	1616/8678	0.0	0.411	0.003	0.774	0.006	0.867	0.000	0.024	0.002	0.649	Rahmattulla, et al. 2016 [4]
PTPN22 rs2476601	T vs. C	1.829 (1.377 – 2.431)	3.09E-05	2	GPA	-	0	0.804	0.002	0.086	0.945	0.999	0.271	0.974	0.841	1.000	Lee, et al. 2012 [7]
PTPN22 rs2476601	T vs. C	1.35 (1.12 – 1.62)	0.002	2	GPA	880/1969			0.103	0.871	0.924	0.999	0.590	0.993	0.970	1.000	Chung, et al. 2012 [6]
RASGRP1 rs17574546	C vs. A	1.18 (1.02 – 1.36)	0.03	2	GPA	880/1969			0.592	1.000	0.974	1.000	0.957	1.000	0.997	1.000	Chung, et al. 2012 [6]
RING1/RXRB rs213213	A	1.91 (1.73 – 2.10)	<0.001	3	GPA	1132/7238	0.0	0.551	NA	NA	NA	NA	NA	NA			Rahmattulla, et al. 2016 [4]
RXRB rs6531	C	1.70 (1.55 – 1.86)	<0.001	3	GPA	1211/6955	96.5	0.000	NA	NA	NA	NA	NA	NA			Rahmattulla, et al. 2016 [4]
RXRB rs9277935	T	0.37 (0.31 – 0.43)	<0.001	3	GPA	1135/7233	0.0	0.798	NA	NA	NA	NA	NA	NA			Rahmattulla, et al. 2016 [4]
SERPINA 1	S allele	1.72 (1.12 – 2.66)	0.014	2	GPA	484/1079	0.0	0.588	0.053	0.269	0.996	1.000	0.982	1.000	0.997	1.000	Rahmattulla, et al. 2016 [4]
SERPINA 1	Z allele	2.40 (1.73 - 3.33)	<0.001	4	GPA	972/2636	0.0	0.763	0.000	0.002	0.906	1.000	0.062	0.985	0.282	0.997	Rahmattulla, et al. 2016 [4]
TLR9 rs352139	T	1.18 (1.06 – 1.32)	0.003	1	GPA	919/1898	0.0	0.366	0.616	1.000	0.861	1.000	0.792	1.000	0.987	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352140	T	1.20 (1.07 – 1.35)	0.001	1	GPA	919/1898	39.7	0.198	0.500	1.000	0.828	1.000	0.707	1.000	0.981	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352162	T	1.20 (1.07 – 1.34)	0.001	1	GPA	919/1898	56.9	0.128	0.500	1.000	0.706	1.000	0.546	0.999	0.966	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs5743836	G	0.83 (0.70 – 0.99)	0.037	1	GPA	919/1898	70.5	0.066	0.482	0.993	0.988	1.000	0.975	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
FCGR3B	NA1	1.52 (1.03 – 2.25)	0.035	2	MPA	75/200	0.0	0.774	0.119	0.474	0.997	1.000	0.987	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-A11	-	2.97 (1.19 – 7.41)	0.020	1	MPA	23/405	-	-	0.026	0.072	0.999	1.000	0.996	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-A26	-	2.49 (1.00 – 6.18)	0.049	1	MPA	23/405	-	-	0.058	0.137	0.999	1.000	0.997	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB2 rs3130215	A	1.33(1.06 – 1.66)	0.013	1	MPA	156/5366	-	-	0.182	0.856	0.985	1.000	0.932	1.000	0.994	1.000	Rahmattulla, et al. 2016 [4]
HLA-DQB1*0303	-	2.11 (1.14 – 3.90)	0.018	1	MPA	50/77	-	-	0.036	0.138	0.998	1.000	0.992	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR6	-	0.29 (0.09 – 0.92)	0.035	1	MPA	30/5442	-	-	0.037	0.079	0.999	1.000	0.998	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB1*1101	-	2.57 (1.56 – 4.23)	<0.001	2	MPA	223/465	0.0	0.885	0.001	0.017	0.993	1.000	0.923	1.000	0.988	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB1*1501	-	1.65 (1.14 – 2.38)	0.007	2	MPA	157/465	0.0	0.805	0.044	0.305	0.994	1.000	0.960	1.000	0.995	1.000	Rahmattulla, et al. 2016 [4]
IRF5 rs10954213	G	1.22 (1.03 – 1.44)	0.018	2	MPA	333/6075	0.0	0.406	0.423	0.993	0.978	1.000	0.950	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
PTPN22 rs2476601	A	1.42 (1.06 – 1.89)	0.018	2	MPA	258/6310	0.0	0.641	0.124	0.646	0.992	1.000	0.962	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
RXRB rs6531	C	1.38 (1.15 – 1.66)	0.001	1	MPA	262/5251	-	-	0.069	0.812	0.901	1.000	0.438	0.999	0.950	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352139	T	0.68 (0.52 – 0.87)	0.003	1	MPA	153/1898	86.6	0.006	0.053	0.563	0.976	1.000	0.793	1.000	0.984	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352140	T	0.71 (0.55 – 0.91)	0.006	1	MPA	153/1898	71.4	0.062	0.103	0.691	0.985	1.000	0.908	1.000	0.993	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352162	T	0.74 (0.58 – 0.95)	0.020	1	MPA	153/1898	88.0	0.004	0.176	0.794	0.990	1.000	0.958	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs5743836	G	1.78 (1.32 – 2.39)	<0.001	1	MPA	153/1898	0.0	0.927	0.004	0.127	0.966	1.000	0.496	0.999	0.932	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0301	-	0.47 (0.29 – 0.75)	0.001	2	EGPA	167/829	72.1	0.028	0.008	0.071	0.995	1.000	0.956	1.000	0.994	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR4	-	1.70 (1.23 – 2.34)	0.001	4	EGPA	176/6246	0.0	0.820	0.016	0.221	0.986	1.000	0.837	1.000	0.984	1.000	Rahmattulla, et al. 2016 [4]

HLA-DR6	-	0.19 (0.04 – 0.95)	0.043	2	EGPA	26/5555	0.0	0.724		0.036	0.063	0.999	1.000	0.999	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR7	-	1.71 (1.24 – 2.37)	0.001	3	EGPA	164/804	58.0	0.093		0.017	0.216	0.987	1.000	0.855	1.000	0.986	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR8	-	3.08 (1.75 – 5.41)	<0.001	2	EGPA	114/5811	91.2	0.001		0.001	0.006	0.994	1.000	0.936	1.000	0.989	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB1*13	-	0.40 (0.24 – 0.68)	0.001	2	EGPA	150/691	29.2	0.235		0.003	0.030	0.995	1.000	0.960	1.000	0.993	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB3	-	0.58 (0.45 – 0.76)	<0.001	2	EGPA	150/691	0.0	0.653		0.004	0.156	0.948	1.000	0.333	0.998	0.890	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB4	-	2.06 (1.57 – 2.69)	<0.001	2	EGPA	150/691	0.4	0.316		0.000	0.010	0.754	1.000	0.011	0.918	0.089	0.990	Rahmattulla, et al. 2016 [4]
IL-10 rs1800896	G	0.68 (0.50 – 0.92)	0.012	1	EGPA	103/507	-	-		0.094	0.551	0.992	1.000	0.957	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
LEPR rs8179183	C	1.41 (1.10 – 1.81)	0.007	1	EGPA	196/1327	-	-		0.103	0.686	0.986	1.000	0.911	1.000	0.993	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352162	T	1.28 (1.05 – 1.57)	0.015	1	EGPA	217/1898	0.0	0.410		0.268	0.936	0.985	1.000	0.950	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]

Table S4. Meta-analysis results of observational studies, gene variants with statistical significance (p-value < 0.05) for each serologic diagnosis (MPO-ANCA, PR3-ANCA). Summary of genetic variants with FPRP, BFDP values, and noteworthy genetic variants are given in bold.

Gene/Variant	Minor allele/ Comparison	OR (95% CI)	p-value for meta- analysis	Publications (n)	Diagnosis (serologic subtypes)	No. of Cases/Controls	I² (%)	I² (P)	Egger's P-value	Power OR 1.2	Power OR 1.5	FPRP Values at Prior probability				BFDP 0.001	BFDP 0.000001	Author, Year
												OR 1.2		OR 1.5				
												0.001	0.000001	0.001	0.000001			
CTLA-4	(AT) ₁₂₂	3.69 (1.40 – 9.71)	0.008	2	MPO-ANCA	92/311	0.0	0.326		0.011	0.034	0.999	1.000	0.996	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
FCGR2A rs1801274	C	0.80 (0.67 – 0.95)	0.011	4	MPO-ANCA	844/5969	58.7	0.064		0.321	0.981	0.971	1.000	0.918	1.000	0.994	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB2 rs3130215	A	1.27 (1.02 – 1.58)	0.032	1	MPO-ANCA	167/5366	-	-		0.305	0.932	0.991	1.000	0.972	1.000	0.997	1.000	Rahmattulla, et al. 2016 [4]
HLA-DQB1*0303	-	1.91 (1.12 – 3.26)	0.017	2	MPO-ANCA	72/127	0.0	0.535		0.044	0.188	0.998	1.000	0.989	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR4	-	2.51 (1.46 – 4.32)	0.001	2	MPO-ANCA	69/202	57.0	0.127		0.004	0.032	0.996	1.000	0.966	1.000	0.994	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR9	-	1.83 (1.29 – 2.60)	0.001	3	MPO-ANCA	175/1116	0.0	0.631		0.009	0.134	0.988	1.000	0.848	1.000	0.983	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB1*1501	-	2.03 (1.26 – 3.29)	0.004	2	MPO-ANCA	89/465	0.0	0.398		0.016	0.110	0.996	1.000	0.974	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB1*16	-	3.55 (1.02 – 12.38)	0.047	1	MPO-ANCA	51/491	0.0	0.658		0.044	0.088	0.999	1.000	0.998	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
PTPN22 rs2476601	A	1.47 (1.08 – 2.00)	0.014	2	MPO-ANCA	183/6310	73.6	0.052		0.098	0.551	0.993	1.000	0.963	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
RXRB rs6531	C	1.21 (1.00 – 1.46)	0.046	1	MPO-ANCA	264/5251	-	-		0.465	0.988	0.990	1.000	0.979	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
SERPINA 1	Z allele	2.01 (1.04 - 3.87)	0.037	1	MPO-ANCA	166/805	-	-		0.061	0.191	0.998	1.000	0.995	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
SERPINA 1	Z allele	3.13 (1.21 – 8.13)	0.019	2	MPO-ANCA	78/2510	26.7	0.243		0.025	0.065	0.999	1.000	0.997	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
STAT4 rs7574865	T	1.24 (1.05 – 1.46)	0.009	2	MPO-ANCA	908/6076	64.0	0.095		0.347	0.989	0.966	1.000	0.909	1.000	0.993	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352139	T	0.78 (0.63 – 0.96)	0.017	1	MPO-ANCA	NR/NR	37.4	0.206		0.266	0.931	0.986	1.000	0.953	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352140	T	0.75 (0.62 – 0.91)	0.004	1	MPO-ANCA	NR/NR	0.0	0.471		0.143	0.884	0.961	1.000	0.800	1.000	0.986	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352162	T	0.79 (0.65 – 0.97)	0.028	1	MPO-ANCA	NR/NR	0.0	0.402		0.305	0.947	0.988	1.000	0.963	1.000	0.997	1.000	Rahmattulla, et al. 2016 [4]
CD226 rs763361	T	1.22 (1.09 – 1.36)	<0.001	2	PR3-ANCA	764/6592	86.6	0.006		0.383	1.000	0.465	0.999	0.250	0.997	0.905	1.000	Rahmattulla, et al. 2016 [4]
CLTA-4 rs3087243	A	0.81 (0.71 – 0.93)	0.003	1	PR3-ANCA	478/5257	-	-		0.344	0.997	0.890	1.000	0.737	1.000	0.983	1.000	Rahmattulla, et al. 2016 [4]

CTLA-4	(AT) ₁₀₄	0.42 (0.22 – 0.79)	0.007	1	PR3-ANCA	62/200	-	-	0.017	0.076	0.998	1.000	0.989	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-B55	-	7.35 (2.33 – 23.14)	0.001	1	PR3-ANCA	16/472	-	-	0.001	0.003	0.999	1.000	0.995	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPA1 rs9277341	C	0.27 (0.22 – 0.33)	<0.001	1	PR3-ANCA	578/1820	-	-	NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0101	-	0.45 (0.20 – 0.99)	0.048	2	PR3-ANCA	183/139	74.5	0.048	0.063	0.164	0.999	1.000	0.997	1.000	0.999	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0201	-	0.44 (0.21 – 0.91)	0.027	1	PR3-ANCA	148/89	-	-	0.042	0.131	0.998	1.000	0.995	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0301	-	0.19 (0.09 – 0.39)	<0.001	2	PR3-ANCA	183/139	90.8	0.001	0.000	0.000	0.995	1.000	0.951	1.000	0.990	1.000	Rahmattulla, et al. 2016 [4]
HLA-DPB1*0401	-	3.93 (2.75 – 5.62)	<0.001	2	PR3-ANCA	183/139	0.0	0.960	0.000	0.000	0.615	0.999	0.001	0.495	0.000	0.170	Rahmattulla, et al. 2016 [4]
HLA-DPB2 rs3130215	A	0.65 (0.55 – 0.77)	<0.001	1	PR3-ANCA	326/5366	-	-	0.002	0.385	0.235	0.997	0.002	0.618	0.062	0.985	Rahmattulla, et al. 2016 [4]
HLA-DR1	-	0.57 (0.38 – 0.86)	0.008	3	PR3-ANCA	157/560	0.0	0.506	0.035	0.228	0.995	1.000	0.970	1.000	0.996	1.000	Rahmattulla, et al. 2016 [4]
HLA-DR9	-	3.03 (1.40 – 6.56)	0.005	1	PR3-ANCA	16/472	-	-	0.009	0.037	0.998	1.000	0.992	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
HLA-DRB1*15	-	2.82 (2.00 – 3.96)	<0.001	2	PR3-ANCA	131/582	84.0	0.002	0.000	0.000	0.842	1.000	0.016	0.942	0.040	0.977	Rahmattulla, et al. 2016 [4]
PTPN22 rs2476601	A	1.42 (1.14 – 1.77)	0.002	2	PR3-ANCA	419/6310	13.2	0.283	0.067	0.687	0.964	1.000	0.725	1.000	0.980	1.000	Rahmattulla, et al. 2016 [4]
RING1/RXRB rs213213	A	2.06 (1.75 – 2.41)	<0.001	1	PR3-ANCA	326/5366	-	-	NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
RXRB rs6531	C	2.19 (1.92 – 2.51)	<0.001	1	PR3-ANCA	478/5251	-	-	NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
RXRB rs9277935	T	0.24 (0.17 – 0.33)	<0.001	1	PR3-ANCA	326/5350	-	-	NA	NA	NA	NA	NA	NA	0.000	0.000	Rahmattulla, et al. 2016 [4]
SERPINA 1	S allele	1.92 (1.12 – 3.29)	0.017	3	PR3-ANCA	145/3836	86.4	0.001	0.044	0.184	0.998	1.000	0.990	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]
SERPINA 1	Z allele	2.58 (1.57 – 4.25)	<0.001	1	PR3-ANCA	322/805	-	-	0.001	0.017	0.993	1.000	0.922	1.000	0.988	1.000	Rahmattulla, et al. 2016 [4]
SERPINA 1	Z allele	3.53 (2.28 – 5.49)	<0.001	5	PR3-ANCA	280/4788	21.3	0.279	0.000	0.000	0.963	1.000	0.229	0.997	0.512	0.999	Rahmattulla, et al. 2016 [4]
TLR9 rs352139	T	1.23 (1.09 – 1.40)	0.001	1	PR3-ANCA	NR/NR	0.0	0.910	0.354	0.999	0.829	1.000	0.633	0.999	0.974	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352140	T	1.28 (1.12 – 1.45)	0.018	1	PR3-ANCA	NR/NR	0.0	0.782	0.155	0.994	0.402	0.999	0.095	0.991	0.778	1.000	Rahmattulla, et al. 2016 [4]
TLR9 rs352162	T	1.30 (1.14 – 1.47)	<0.001	1	PR3-ANCA	NR/NR	0.0	0.503	0.101	0.989	0.221	0.996	0.028	0.967	0.532	0.999	Rahmattulla, et al. 2016 [4]
TLR9 rs5743836	G	0.83 (0.70 – 1.00)	0.045	1	PR3-ANCA	NR/NR	81.9	0.019	0.483	0.989	0.990	1.000	0.981	1.000	0.998	1.000	Rahmattulla, et al. 2016 [4]

Table S5. Results of meta analyses (combined analysis) with genome-wide association studies and replication cohort. Noteworthy genetic variants with satisfied FPRP and BFDP values are given in bold.

Gene/Variant	Comparison	OR (95% CI)	p-value	Diagnosis (clinical/serologic subtypes)	Ethnicity	No. of Cases/Controls	Power OR 1.2	Power OR 1.5	FPRP Values at Prior probability				BFDP 0.001	BFDP 0.000001	Author, Year
									OR 1.2		OR 1.5				
									0.001	0.000001	0.001	0.000001			
SNPs statistically significant (P<5.00E-08)															
HLA-DPA1 rs9277341	T vs. C	2.44 (2.21 – 2.69)	6.09E-71	AAV	Caucasian	1986/4723	NA	NA	NA	NA	NA	NA	0.000	0.000	Merkel, et al. 2017 [2]
HLA-DPB1 rs1042169	G vs. A	2.82 (2.54 – 3.13)	1.12E-84	AAV	Caucasian	1986/4723	NA	NA	NA	NA	NA	NA	0.000	0.000	Merkel, et al. 2017 [2]
HLA-DPB1 rs141530233	A del	2.99 (2.69 – 3.33)	1.13E-89	AAV	Caucasian	1986/4723	NA	NA	NA	NA	NA	NA	0.000	0.000	Merkel, et al. 2017 [2]
HLA-DQA1 rs35242582	A vs. G	1.60 (1.46 – 1.76)	6.34E-23	AAV	Caucasian	1986/4723	NA	NA	NA	NA	NA	NA	0.000	0.000	Merkel, et al. 2017 [2]
HLA-DQB1 rs1049072	A vs. G	1.40 (1.28 – 1.53)	6.46E-13	AAV	Caucasian	1986/4723	0.000	0.936	0.000	0.000	0.000	0.000	0.000	0.000	Merkel, et al. 2017 [2]
PRTN3 rs62132293	G vs. C	1.29 (1.19 – 1.39)	8.60E-11	AAV	Caucasian	1986/4723	0.029	1.000	0.000	0.000	0.000	0.000	0.000	0.002	Merkel, et al. 2017 [2]
PTPN22 rs6679677	A vs. C	1.40 (1.25 – 1.57)	1.88E-08	AAV	Caucasian	1986/4723	0.004	0.881	0.002	0.172	0.000	0.001	0.001	0.447	Merkel, et al. 2017 [2]

SERPINA1 rs28929474	T vs. C	2.18 (1.75 – 2.71)	3.09E-12	AAV	Caucasian	1986/4723	0.000	0.000	0.056	0.855	0.000	0.001	0.000	0.010	Merkel, et al. 2017 [2]
HLA-DPA1 rs9277341	C vs. T	0.33 (0.28 – 0.39)	2.18E-39	GPA	Caucasian	750/1820	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB1 rs9277554	T vs. C	0.24 (0.20 – 0.30)	1.92E-50	GPA	Caucasian	750/1820	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
SEMA6A rs26595	C vs. T	0.74 (0.67 – 0.82)	2.09E-08	GPA	Caucasian	987/2731	0.012	0.977	0.001	0.071	0.000	0.001	0.001	0.423	Xie, et al. 2013 [1]
HLA-DQA2 rs3998159	C vs. A	2.72 (2.24 – 3.22)	5.24E-25	MPO-ANCA	Caucasian	378/4723	NA	NA	NA	NA	NA	NA	0.000	0.000	Merkel, et al. 2017 [2]
HLA-DQA2 rs7454108	C vs. T	2.73 (2.25 – 3.24)	5.03E-25	MPO-ANCA	Caucasian	378/4723	NA	NA	NA	NA	NA	NA	0.000	0.000	Merkel, et al. 2017 [2]
HLA-DQB1 rs1049072	A vs. G	2.37 (2.01 – 2.78)	2.13E-24	MPO-ANCA	Caucasian	378/4723	NA	NA	NA	NA	NA	NA	0.000	0.000	Merkel, et al. 2017 [2]
SNPs with statistically borderline significance (5.00E-08≤P<0.05)															
PTPN22(R620W) rs2476601	A vs. G	1.36 (1.21 – 1.53)	1.86E-07	AAV	Caucasian	1986/4723	0.019	0.948	0.016	0.625	0.000	0.032	0.020	0.953	Merkel, et al. 2017 [2]
C3orf58 rs1512779	C vs. A	0.89 (0.79 – 0.99)	0.026	GPA	Caucasian	987/2731	0.887	1.000	0.973	1.000	0.970	1.000	0.998	1.000	Xie, et al. 2013 [1]
CCDC86 rs595018	A vs. G	1.46 (1.27 – 1.69)	1.60E-07	GPA	Caucasian	1986/4723	0.004	0.641	0.084	0.902	0.001	0.058	0.033	0.971	Xie, et al. 2013 [1]
COBL rs1949829	T vs. C	1.78 (1.42 – 2.24)	4.19E-07	GPA	Caucasian	1986/4723	0.000	0.072	0.694	0.996	0.012	0.549	0.177	0.995	Xie, et al. 2013 [1]
CTNNB1 rs9842536	T vs. C	1.17 (1.04 – 1.33)	9.70E-03	GPA	Caucasian	987/2731	0.651	1.000	0.962	1.000	0.942	0.999	0.996	1.000	Xie, et al. 2013 [1]
DCTD rs4862110	C vs. T	1.44 (1.24 – 1.67)	2.14E-06	GPA	Caucasian	1986/4723	0.008	0.705	0.151	0.947	0.002	0.167	0.092	0.990	Xie, et al. 2013 [1]
DOK4 rs6023640	T vs. G	1.29 (1.14 – 1.45)	2.73E-05	GPA	Caucasian	987/2731	0.113	0.994	0.148	0.946	0.019	0.664	0.445	0.999	Xie, et al. 2013 [1]
FLJ34870 rs7585252	G vs. A	1.26 (1.13 – 1.40)	1.74E-05	GPA	Caucasian	987/2731	0.182	0.999	0.086	0.904	0.017	0.632	0.408	0.999	Xie, et al. 2013 [1]
GRIA1 rs10515687	T vs. C	1.35 (1.15 – 1.59)	3.01E-04	GPA	Caucasian	987/2731	0.079	0.897	0.804	0.998	0.266	0.973	0.912	1.000	Xie, et al. 2013 [1]
OPCML rs4937787	C vs. A	0.82 (0.69 – 0.96)	0.016	GPA	Caucasian	987/2731	0.421	0.995	0.970	1.000	0.932	0.999	0.995	1.000	Xie, et al. 2013 [1]
PAEP rs705669	G vs. A	0.77 (0.68 – 0.87)	2.52E-05	GPA	Caucasian	987/2731	0.102	0.990	0.210	0.964	0.027	0.733	0.520	0.999	Xie, et al. 2013 [1]
RSPO4 rs6140836	C vs. T	0.75 (0.63 – 0.89)	7.09E-04	GPA	Caucasian	987/2731	0.114	0.911	0.896	0.999	0.519	0.991	0.962	1.000	Xie, et al. 2013 [1]
WSCD1 rs7503953	A vs. C	1.50 (1.29 – 1.76)	1.93E-07	GPA	Caucasian	1986/4723	0.003	0.500	0.176	0.955	0.001	0.117	0.058	0.984	Xie, et al. 2013 [1]
HLA-DQB1 rs1049072	A vs. G	1.17 (1.06 – 1.31)	3.82E-03	PR3-ANCA	Caucasian	1361/4723	0.670	1.000	0.906	0.999	0.866	0.998	0.992	1.000	Merkel, et al. 2017 [2]

Table S6. Re-analysis of the SNPs discovered in genome-wide association studies of patients with GPA. Xie, et al. only provided GPA SNPs with ORs and 95% CIs.

Gene/Variant	Comparison	OR (95% CI)	P-value	Diagnosis (clinical/serologic subtypes)	Ethnicity	No. of Cases/Controls	Power OR 1.2	Power OR 1.5	FPRP Values at Prior probability				BFDP 0.001	BFDP 0.000001	Author, Year
									OR 1.2		OR 1.5				
									0.001	0.000001	0.001	0.000001			
SNPs with P-value <5.00E-08															
HLA-DOA rs3130604	G vs. A	1.67 (1.39-2.02)	4.39E-08	GPA	Caucasian	459/1503	0.000	0.134	0.277	0.997	0.001	0.487	0.025	0.962	Xie, et al. 2013 [1]
HLA-DOA rs763469	A vs. G	1.70 (1.41-2.04)	1.46E-08	GPA	Caucasian	459/1503	0.000	0.089	0.114	0.992	0.000	0.116	0.003	0.764	Xie, et al. 2013 [1]
HLA-DPA1 rs2395309	G vs. A	0.27 (0.20-0.36)	2.15E-19	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPA1 rs3077	C vs. T	0.27 (0.20-0.36)	2.68E-19	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPA1 rs2301226	T vs. C	0.48 (0.36-0.62)	4.85E-08	GPA	Caucasian	459/1503	0.000	0.006	0.613	0.999	0.003	0.762	0.023	0.959	Xie, et al. 2013 [1]
HLA-DPA1 rs9277341	C vs. T	0.30 (0.25-0.38)	1.84E-30	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB1 rs987870	C vs. T	0.26 (0.19-0.37)	6.09E-16	GPA	Caucasian	459/1503	0.000	0.000	0.597	0.999	0.001	0.462	0.000	0.155	Xie, et al. 2013 [1]
HLA-DPB1 rs9277535	G vs. A	0.24 (0.19-0.32)	2.12E-28	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB1 rs9277554	T vs. C	0.22 (0.17-0.28)	4.88E-38	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB1 rs9277565	T vs. C	0.24 (0.18-0.32)	1.91E-24	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB1 rs2281389	C vs. T	0.24 (0.18-0.34)	1.69E-20	GPA	Caucasian	459/1503	0.000	0.000	0.458	0.999	0.000	0.187	0.000	0.013	Xie, et al. 2013 [1]
HLA-DPB1 rs3128917	G vs. T	0.22 (0.17-0.29)	4.92E-33	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB1 rs3117222	A vs. G	0.22 (0.17-0.29)	3.05E-33	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB2 rs2064478	A vs. G	0.22 (0.17-0.30)	4.29E-29	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB2 rs3130215	A vs. G	2.42 (2.08-2.82)	2.37E-30	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB2 rs3117230	C vs. T	0.22 (0.17-0.30)	4.29E-29	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB2 rs1883414	T vs. C	0.53 (0.44-0.64)	1.13E-11	GPA	Caucasian	459/1503	0.000	0.009	0.031	0.970	0.000	0.005	0.000	0.039	Xie, et al. 2013 [1]
HLA-DPB2 rs4713607	A vs. G	0.60 (0.52-0.70)	6.70E-11	GPA	Caucasian	459/1503	0.000	0.090	0.006	0.849	0.000	0.001	0.000	0.027	Xie, et al. 2013 [1]
HLA-DPB2 rs3129274	G vs. A	1.56 (1.34-1.82)	1.35E-08	GPA	Caucasian	459/1503	0.000	0.309	0.036	0.974	0.000	0.048	0.002	0.708	Xie, et al. 2013 [1]
HLA-DPB2 rs3117016	T vs. C	0.48 (0.41-0.57)	1.09E-17	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HLA-DPB2 rs3117008	T vs. C	0.60 (0.51-0.70)	4.90E-11	GPA	Caucasian	459/1503	0.000	0.090	0.006	0.849	0.000	0.001	0.000	0.027	Xie, et al. 2013 [1]
HLA-DPB2 rs3117004	C vs. T	0.57 (0.48-0.68)	1.90E-10	GPA	Caucasian	459/1503	0.000	0.041	0.034	0.972	0.000	0.010	0.000	0.161	Xie, et al. 2013 [1]
HLA-DPB2 rs6901221	C vs. A	0.42 (0.32-0.55)	6.08E-11	GPA	Caucasian	459/1503	0.000	0.000	0.475	0.999	0.001	0.423	0.002	0.651	Xie, et al. 2013 [1]
COL11A2 rs986521	C vs. T	1.85 (1.57-2.16)	2.91E-14	GPA	Caucasian	459/1503	0.000	0.004	0.000	0.246	0.000	0.000	0.000	0.000	Xie, et al. 2013 [1]
COL11A2 rs2855430	T vs. C	0.33 (0.24-0.45)	3.28E-13	GPA	Caucasian	459/1503	0.000	0.000	0.505	0.999	0.001	0.357	0.000	0.237	Xie, et al. 2013 [1]
COL11A2 rs2855425	C vs. T	1.80 (1.54-2.11)	7.77E-14	GPA	Caucasian	459/1503	0.000	0.012	0.001	0.594	0.000	0.000	0.000	0.000	Xie, et al. 2013 [1]
COL11A2 rs2855459	T vs. C	0.32 (0.23-0.44)	2.14E-13	GPA	Caucasian	459/1503	0.000	0.000	0.548	0.999	0.001	0.427	0.000	0.287	Xie, et al. 2013 [1]
RXRβ rs6531	C vs. T	1.80 (1.54-2.11)	8.48E-14	GPA	Caucasian	459/1503	0.000	0.012	0.001	0.594	0.000	0.000	0.000	0.000	Xie, et al. 2013 [1]
HSD17B8 rs439205	T vs. C	0.31 (0.24-0.39)	3.51E-23	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
HSD17B8 rs421446	C vs. T	0.39 (0.31-0.48)	8.90E-20	GPA	Caucasian	459/1503	NA	NA	NA	NA	NA	NA	0.000	0.000	Xie, et al. 2013 [1]
RING1 rs213213	A vs. G	1.83 (1.57-2.14)	6.98E-15	GPA	Caucasian	459/1503	0.000	0.006	0.001	0.375	0.000	0.000	0.000	0.000	Xie, et al. 2013 [1]

RING1 rs213212	G vs. T	1.85 (1.58-2.17)	7.63E-15	GPA	Caucasian	459/1503	0.000	0.005	0.001	0.439	0.000	0.000	0.000	0.000	Xie, et al. 2013 [1]
COBL rs1949829	T vs. C	2.19 (1.68-2.86)	3.58E-09	GPA	Caucasian	459/1503	0.000	0.003	0.632	0.999	0.003	0.759	0.017	0.946	Xie, et al. 2013 [1]
CCDC86 rs595018	A vs. G	1.61 (1.36-1.90)	2.74E-08	GPA	Caucasian	459/1503	0.000	0.201	0.064	0.986	0.000	0.080	0.003	0.764	Xie, et al. 2013 [1]
WSCD1 rs7503953	A vs. C	1.72 (1.44-2.06)	1.39E-09	GPA	Caucasian	459/1503	0.000	0.068	0.076	0.988	0.000	0.053	0.001	0.555	Xie, et al. 2013 [1]
SNPs reported non-significant (5.00E-08≤P<1.00E-04)															
TCEB3 rs2076346	C vs. T	1.46 (1.24-1.73)	8.62E-06	GPA	Caucasian	459/1503	0.012	0.623	0.512	0.999	0.019	0.952	0.433	0.999	Xie, et al. 2013 [1]
DAB1 rs264036	C vs. T	0.72 (0.62-0.85)	9.82E-05	GPA	Caucasian	459/1503	0.042	0.818	0.713	1.000	0.113	0.992	0.807	1.000	Xie, et al. 2013 [1]
DAB1 rs542873	T vs. C	1.37 (1.18-1.59)	4.70E-05	GPA	Caucasian	459/1503	0.041	0.884	0.457	0.999	0.037	0.975	0.601	0.999	Xie, et al. 2013 [1]
DAB1 rs197644	G vs. A	1.37 (1.18-1.59)	3.89E-05	GPA	Caucasian	459/1503	0.041	0.884	0.457	0.999	0.037	0.975	0.601	0.999	Xie, et al. 2013 [1]
LPHN2 rs11579502	C vs. T	1.56 (1.28-1.90)	9.43E-06	GPA	Caucasian	459/1503	0.005	0.348	0.684	1.000	0.027	0.966	0.458	0.999	Xie, et al. 2013 [1]
SCYL1BP1 rs16863343	C vs. T	2.18 (1.46-3.24)	8.15E-05	GPA	Caucasian	459/1503	0.002	0.032	0.987	1.000	0.782	1.000	0.970	1.000	Xie, et al. 2013 [1]
NCKAP5 rs1134119	C vs. T	1.79 (1.38-2.32)	8.96E-06	GPA	Caucasian	459/1503	0.001	0.091	0.896	1.000	0.106	0.992	0.658	0.999	Xie, et al. 2013 [1]
NCKAP5 rs7585252	G vs. A	1.35 (1.16-1.57)	9.69E-05	GPA	Caucasian	459/1503	0.063	0.914	0.607	0.999	0.096	0.991	0.785	1.000	Xie, et al. 2013 [1]
NEK10 rs1579900	T vs. G	1.51 (1.24-1.85)	3.97E-05	GPA	Caucasian	459/1503	0.013	0.474	0.840	1.000	0.128	0.993	0.800	1.000	Xie, et al. 2013 [1]
CTNNB1 rs9842536	T vs. C	1.46 (1.23-1.74)	1.63E-05	GPA	Caucasian	459/1503	0.014	0.619	0.624	0.999	0.037	0.974	0.575	0.999	Xie, et al. 2013 [1]
C3orf58 rs1512779	C vs. A	0.72 (0.61-0.84)	2.86E-05	GPA	Caucasian	459/1503	0.032	0.836	0.484	0.999	0.034	0.972	0.579	0.999	Xie, et al. 2013 [1]
PLSCR4 rs7628805	A vs. C	1.41 (1.18-1.67)	9.72E-05	GPA	Caucasian	459/1503	0.031	0.763	0.691	1.000	0.083	0.989	0.754	1.000	Xie, et al. 2013 [1]
ST6GAL1 rs10513807	G vs. A	0.71 (0.61-0.83)	9.49E-06	GPA	Caucasian	459/1503	0.022	0.785	0.436	0.999	0.021	0.956	0.471	0.999	Xie, et al. 2013 [1]
KIAA0746 rs4269167	T vs. C	0.73 (0.63-0.86)	7.72E-05	GPA	Caucasian	459/1503	0.057	0.861	0.747	1.000	0.163	0.995	0.858	1.000	Xie, et al. 2013 [1]
DCTD rs4862110	C vs. T	1.63 (1.36-1.94)	5.00E-08	GPA	Caucasian	459/1503	0.000	0.175	0.118	0.993	0.000	0.178	0.007	0.878	Xie, et al. 2013 [1]
OSMR rs357291	C vs. A	0.72 (0.62-0.84)	2.81E-05	GPA	Caucasian	459/1503	0.032	0.836	0.484	0.999	0.034	0.972	0.579	0.999	Xie, et al. 2013 [1]
SEMA6A rs26595	C vs. T	0.74 (0.63-0.86)	9.58E-05	GPA	Caucasian	459/1503	0.061	0.913	0.586	0.999	0.086	0.989	0.766	1.000	Xie, et al. 2013 [1]
GRIA1 rs10515687	T vs. C	1.56 (1.25-1.94)	8.11E-05	GPA	Caucasian	459/1503	0.009	0.362	0.874	1.000	0.150	0.994	0.811	1.000	Xie, et al. 2013 [1]
WWC1 rs3853242	G vs. A	0.74 (0.63-0.86)	8.55E-05	GPA	Caucasian	459/1503	0.061	0.913	0.586	0.999	0.086	0.989	0.766	1.000	Xie, et al. 2013 [1]
ERGIC1 rs1564259	A vs. G	0.69 (0.58-0.83)	7.19E-05	GPA	Caucasian	459/1503	0.023	0.642	0.785	1.000	0.114	0.992	0.797	1.000	Xie, et al. 2013 [1]
ERGIC1 rs1006721	C vs. T	0.69 (0.58-0.83)	6.22E-05	GPA	Caucasian	459/1503	0.023	0.642	0.785	1.000	0.114	0.992	0.797	1.000	Xie, et al. 2013 [1]
OFCC1 rs9358619	A vs. G	1.45 (1.21-1.74)	4.90E-05	GPA	Caucasian	459/1503	0.021	0.642	0.756	1.000	0.092	0.990	0.762	1.000	Xie, et al. 2013 [1]
HLA-DMA rs3135029	A vs. C	1.61 (1.28-2.02)	4.55E-05	GPA	Caucasian	459/1503	0.006	0.270	0.875	1.000	0.125	0.993	0.764	1.000	Xie, et al. 2013 [1]
BRD2 rs3130597	T vs. C	1.60 (1.28-2.02)	4.80E-05	GPA	Caucasian	459/1503	0.008	0.294	0.909	1.000	0.209	0.996	0.850	1.000	Xie, et al. 2013 [1]
HLA-DOA rs176248	T vs. C	0.70 (0.58-0.83)	8.16E-05	GPA	Caucasian	459/1503	0.022	0.713	0.644	0.999	0.054	0.983	0.668	1.000	Xie, et al. 2013 [1]
HLA-DOA rs206762	C vs. T	1.36 (1.17-1.58)	5.92E-05	GPA	Caucasian	459/1503	0.051	0.900	0.534	0.999	0.061	0.985	0.703	1.000	Xie, et al. 2013 [1]
HLA-DOA rs429916	A vs. C	0.37 (0.25-0.56)	4.11E-07	GPA	Caucasian	459/1503	0.000	0.003	0.977	1.000	0.490	0.999	0.862	1.000	Xie, et al. 2013 [1]
HLA-DOA rs9296068	G vs. T	0.68 (0.58-0.81)	7.49E-06	GPA	Caucasian	459/1503	0.011	0.588	0.578	0.999	0.026	0.964	0.491	0.999	Xie, et al. 2013 [1]
HLA-DPB1 rs3130192	T vs. C	1.60 (1.27-2.02)	7.51E-05	GPA	Caucasian	459/1503	0.008	0.294	0.909	1.000	0.209	0.996	0.850	1.000	Xie, et al. 2013 [1]
HLA-DPB2 rs1810472	G vs. A	0.65 (0.54-0.77)	1.06E-06	GPA	Caucasian	459/1503	0.002	0.385	0.235	0.997	0.002	0.618	0.062	0.985	Xie, et al. 2013 [1]
HLA-DPB2 rs3117035	A vs. G	0.72 (0.61-0.84)	2.50E-05	GPA	Caucasian	459/1503	0.032	0.836	0.484	0.999	0.034	0.972	0.579	0.999	Xie, et al. 2013 [1]
COL11A2 rs2235498	T vs. C	0.67 (0.55-0.81)	3.86E-05	GPA	Caucasian	459/1503	0.012	0.521	0.744	1.000	0.063	0.985	0.678	1.000	Xie, et al. 2013 [1]
COL11A2 rs9368758	A vs. G	0.44 (0.30-0.65)	3.28E-05	GPA	Caucasian	459/1503	0.001	0.018	0.982	1.000	0.669	1.000	0.946	1.000	Xie, et al. 2013 [1]
COL11A2 rs2269346	A vs. G	0.44 (0.30-0.66)	3.64E-05	GPA	Caucasian	459/1503	0.001	0.022	0.986	1.000	0.764	1.000	0.965	1.000	Xie, et al. 2013 [1]
WDR46 rs3130257	T vs. C	1.63 (1.32-2.01)	5.61E-06	GPA	Caucasian	459/1503	0.002	0.218	0.700	1.000	0.022	0.957	0.365	0.998	Xie, et al. 2013 [1]
DAXX rs211474	T vs. C	0.71 (0.60-0.84)	6.37E-05	GPA	Caucasian	459/1503	0.031	0.769	0.679	1.000	0.078	0.988	0.744	1.000	Xie, et al. 2013 [1]
KIFC1 rs211452	C vs. T	0.65 (0.55-0.76)	1.98E-07	GPA	Caucasian	459/1503	0.001	0.375	0.067	0.986	0.000	0.150	0.008	0.895	Xie, et al. 2013 [1]
SYNGAP1 rs211456	A vs. C	0.72 (0.61-0.84)	3.57E-05	GPA	Caucasian	459/1503	0.032	0.836	0.484	0.999	0.034	0.972	0.579	0.999	Xie, et al. 2013 [1]
SYNGAP1 rs2247385	G vs. A	0.69 (0.59-0.81)	5.14E-06	GPA	Caucasian	459/1503	0.011	0.663	0.353	0.998	0.009	0.896	0.271	0.997	Xie, et al. 2013 [1]
FLJ43752 rs210120	G vs. A	0.72 (0.62-0.84)	2.58E-05	GPA	Caucasian	459/1503	0.032	0.836	0.484	0.999	0.034	0.972	0.579	0.999	Xie, et al. 2013 [1]
BCKDHB rs515347	G vs. A	1.70 (1.32-2.18)	3.13E-05	GPA	Caucasian	459/1503	0.003	0.162	0.905	1.000	0.151	0.994	0.769	1.000	Xie, et al. 2013 [1]
TCBA1 rs6924068	G vs. A	1.40 (1.20-1.63)	1.37E-05	GPA	Caucasian	459/1503	0.023	0.813	0.382	0.998	0.018	0.947	0.429	0.999	Xie, et al. 2013 [1]
MAGI2 rs3779312	A vs. G	1.50 (1.26-1.78)	5.26E-06	GPA	Caucasian	459/1503	0.005	0.500	0.392	0.998	0.007	0.873	0.214	0.996	Xie, et al. 2013 [1]
CUTL1 rs1734729	T vs. C	1.41 (1.20-1.67)	4.54E-05	GPA	Caucasian	459/1503	0.031	0.763	0.691	1.000	0.083	0.989	0.754	1.000	Xie, et al. 2013 [1]
DDP6 rs4726422	G vs. A	0.74 (0.63-0.86)	7.74E-05	GPA	Caucasian	459/1503	0.061	0.913	0.586	0.999	0.086	0.989	0.766	1.000	Xie, et al. 2013 [1]
LOC441376 rs3019885	G vs. T	1.44 (1.24-1.67)	1.90E-06	GPA	Caucasian	459/1503	0.008	0.705	0.151	0.994	0.002	0.667	0.092	0.990	Xie, et al. 2013 [1]
SLC30A8 rs1793729	C vs. T	0.68 (0.57-0.80)	5.68E-06	GPA	Caucasian	459/1503	0.007	0.594	0.317	0.998	0.006	0.847	0.194	0.996	Xie, et al. 2013 [1]
SLC30A8 rs1695715	T vs. C	0.69 (0.58-0.82)	1.57E-05	GPA	Caucasian	459/1503	0.016	0.652	0.610	0.999	0.037	0.975	0.582	0.999	Xie, et al. 2013 [1]
KCNK9 rs2447406	T vs. C	1.58 (1.27-1.97)	3.25E-05	GPA	Caucasian	459/1503	0.007	0.322	0.869	1.000	0.130	0.993	0.781	1.000	Xie, et al. 2013 [1]
C9orf66 rs584922	T vs. C	0.70 (0.60-0.82)	1.30E-05	GPA	Caucasian	459/1503	0.015	0.727	0.392	0.998	0.013	0.932	0.365	0.998	Xie, et al. 2013 [1]
C9orf93 rs1341740	T vs. C	1.52 (1.23-1.87)	9.73E-05	GPA	Caucasian	459/1503	0.013	0.450	0.855	1.000	0.142	0.994	0.814	1.000	Xie, et al. 2013 [1]
LRRN6C rs10491888	G vs. A	1.54 (1.25-1.91)	5.75E-05	GPA	Caucasian	459/1503	0.012	0.405	0.880	1.000	0.173	0.995	0.837	1.000	Xie, et al. 2013 [1]
PAEP rs705669	G vs. A	0.69 (0.57-0.83)	8.53E-05	GPA	Caucasian	459/1503	0.023	0.642	0.785	1.000	0.114	0.992	0.797	1.000	Xie, et al. 2013 [1]
NEUROG3 rs731573	T vs. C	1.44 (1.20-1.72)	9.40E-05	GPA	Caucasian	459/1503	0.022	0.674	0.722	1.000	0.079	0.988	0.738	1.000	Xie, et al. 2013 [1]
PTEN rs7084813	A vs. G	0.59 (0.46-0.76)	2.79E-05	GPA	Caucasian	459/1503	0.004	0.172	0.922	1.000	0.204	0.996	0.824	1.000	Xie, et al. 2013 [1]
OPCML rs4937787	C vs. A	0.60 (0.46-0.77)	5.75E-05	GPA	Caucasian	459/1503	0.005	0.204	0.924	1.000	0.227	0.997	0.847	1.000	Xie, et al. 2013 [1]
TMPO rs2216021	C vs. T	1.36 (1.17-1.57)	6.14E-05	GPA	Caucasian	459/1503	0.044	0.909	0.382	0.998	0.029	0.967	0.544	0.999	Xie, et al. 2013 [1]
TMPO rs2011247	C vs. T	0.73 (0.63-0.85)	4.84E-05	GPA	Caucasian	459/1503	0.044	0.879	0.534	0.999	0.054	0.983	0.680	1.000	Xie, et al. 2013 [1]
FGF9 rs2031421	T vs. G	1.44 (1.21-1.72)	4.01E-05	GPA	Caucasian	459/1503	0.022	0.674	0.722	1.000	0.079	0.988	0.738	1.000	Xie, et al. 2013 [1]

RSPO4 rs6140836	C vs. T	0.58 (0.44-0.76)	7.26E-05	GPA	Caucasian	459/1503	0.004	0.156	0.948	1.000	0.333	0.998	0.890	1.000	Xie, et al. 2013 [1]
DOK5 rs6023640	T vs. G	1.40 (1.18-1.66)	8.98E-05	GPA	Caucasian	459/1503	0.038	0.786	0.740	1.000	0.121	0.993	0.815	1.000	Xie, et al. 2013 [1]
PDE9A rs2269127	A vs. G	1.65 (1.36-2.01)	4.06E-07	GPA	Caucasian	459/1503	0.001	0.172	0.457	0.999	0.004	0.793	0.094	0.990	Xie, et al. 2013 [1]

Table S7. These gene sets were computed in gene ontology enrichment analysis and protein-protein interaction network analysis. This gene set includes noteworthy variants from meta-analyses and statistically significant GWAS SNPs.

From :

- Noteworthy variants from [Association of granulomatosis with polyangiitis (Wegener's) with HLA-DPB1*04 and SEMA6A gene variants: evidence from genome-wide analysis, Xie G, et al. 2013. Supplementary data (GPA)]
- Statistically significant GWAS SNPs from [Identification of Functional and Expression Polymorphisms Associated With Risk for Antineutrophil Cytoplasmic Autoantibody-Associated Vasculitis, Merkel PA, et al. 2017]
- Noteworthy variants from all the included meta-analyses studies in this review

ANCA-associated vasculitis		Granulomatous polyangiitis (GPA)		PR3-ANCA		MPO-ANCA	
Gene	SNP ID	Gene	SNP ID	Gene	SNP ID	Gene	SNP ID
AGER	rs2070600	BCKDHB	rs515347	BRD2	rs206762	BTNL2	rs3793127
CD226	rs763361	C3orf58	rs1512779	COL11A2	Affx-52341735	C6orf10	rs6910071
CFB	rs541862	C9orf66	rs584922	COL11A2	rs2071025	HLA-DQA2	rs3998159
COL11A2	Affx-52341735	C9orf93	rs1341740	COL11A2	rs2254287	HLA-DQA2	rs7454108
COL11A2	rs2076310	CCDC86	rs595018	COL11A2	rs2257126	HLA-DQA2	rs9275184
COL11A2	rs2254287	CD226	rs763361	COL11A2	rs2294479	HLA-DQB1	rs1049072
COL11A2	rs2257126	CTLA-4	rs3087243	COL11A2	rs2744512	HLA-DQB1	rs1130399

COL11A2	rs2294479	COBL	rs1949829	COL11A2	rs2855425	HLA-DRA	rs2395163
COL11A2	rs2855425	COL11A2	rs2235498	COL11A2	rs2855437	HLA-DRA	rs2395175
COL11A2	rs2855437	COL11A2	rs2855425	COL11A2	rs2855442	HLA-DRB1	rs28366302
COL11A2	rs2855442	COL11A2	rs2855430	COL11A2	rs2855448	HLA-DRB1	rs34252386
COL11A2	rs2855448	COL11A2	rs2855459	COL11A2	rs2855459	HLA-DRB1	rs35445101
COL11A2	rs2855459	COL11A2	rs986521	COL11A2	rs3116994	HLA-DRB1	rs660895
COL11A2	rs3116994	CTLA-4	(AT) ₈₆	COL11A2	rs3116999	HLA-DRB1	rs9271824
COL11A2	rs3116999	CTNNB1	rs9842536	COL11A2	rs3129207	HLA-DRB1	rs9271897
COL11A2	rs3129207	CUTL1	rs1734729	COL11A2	rs3129234	HLA-DRB1	rs9272105
COL11A2	rs3129267	DAB1	rs197644	COL11A2	rs3129252	HLA-DRB5	rs2395185
COL11A2	rs3129270	DAB1	rs264036	COL11A2	rs3129258	HLA-DRB5	rs9268923
COL11A2	rs3130161	DAB1	rs542873	COL11A2	rs3129264	OR2W1	rs34892006
COL11A2	rs726599	DAXX	rs211474	COL11A2	rs3129267	TAP2	rs115360810
COL11A2	rs9277935	DCTD	rs4862110	COL11A2	rs3129270		
COL11A2	rs9368758	DOK4	rs6023640	COL11A2	rs3130161		
COL11A2	rs986521	DPP6	rs4726422	COL11A2	rs726599		
CTLA-4	(AT) ₈₆	ERGIC1	rs1006721	COL11A2	rs756440		
CTLA-4	rs3087243 (CT60)	ERGIC1	rs1564259	COL11A2	rs9277935		

HLA-DOA	rs17214533	FGF9	rs2031421	COL11A2	rs9368758
HLA-DOA	rs2858458	FLJ34870 (NCKAP5)	rs7585252	COL11A2	rs986521
HLA-DOA	rs3097669	FLJ43752 (LINC00336)	rs210120	DAXX	rs211449
HLA-DOA	rs3129304	GRIA1	rs10515687	EHMT2	rs486416
HLA-DOA	rs3130176	HLA-DMA	rs3135029	EHMT2	rs605203
HLA-DOA	rs3130604	HLA-DOA	rs176248	HLA-C	rs2524040
HLA-DOA	rs6936620	HLA-DOA	rs206762	HLA-C	rs3873386
HLA-DOA	rs7634469	HLA-DOA	rs3130604	HLA-C	rs9468925
HLA-DOA	rs9296068	HLA-DOA	rs763469	HLA-DOA	rs17214533
HLA-DPA1	Affx-28512796	HLA-DOA	rs9296068	HLA-DOA	rs2858458
HLA-DPA1	Affx-28512827	HLA-DPA1	rs2301226	HLA-DOA	rs3097648
HLA-DPA1	rs10214910	HLA-DPA1	rs2395309	HLA-DOA	rs3097669
HLA-DPA1	rs1042190	HLA-DPA1	rs3077	HLA-DOA	rs3129304
HLA-DPA1	rs1042434	HLA-DPA1	rs9277341	HLA-DOA	rs3130176
HLA-DPA1	rs1126543	HLA-DPB1	rs2281389	HLA-DOA	rs3130604
HLA-DPA1	rs1126769	HLA-DPB1	rs3117222	HLA-DOA	rs423639
HLA-DPA1	rs1431399	HLA-DPB1	rs3128917	HLA-DOA	rs429916
HLA-DPA1	rs2308911	HLA-DPB1	rs9277535	HLA-DOA	rs763469

HLA-DPA1	rs3077	HLA-DPB1	rs9277554	HLA-DPA1	Affx-28512796
HLA-DPA1	rs9277341	HLA-DPB1	rs9277565	HLA-DPA1	Affx-28512827
HLA-DPA1	rs987870	HLA-DPB1	rs987870	HLA-DPA1	rs10214910
HLA-DPB1	rs1042151	HLA-DPB2	rs1810472	HLA-DPA1	rs1042190
HLA-DPB1	rs1042153	HLA-DPB2	rs1883414	HLA-DPA1	rs1042434
HLA-DPB1	rs1042169	HLA-DPB2	rs2064478	HLA-DPA1	rs1126543
HLA-DPB1	rs1042335	HLA-DPB2	rs3117004	HLA-DPA1	rs1126769
HLA-DPB1	rs1071597	HLA-DPB2	rs3117008	HLA-DPA1	rs1431399
HLA-DPB1	rs1126513	HLA-DPB2	rs3117016	HLA-DPA1	rs2308911
HLA-DPB1	rs141530233	HLA-DPB2	rs3117035	HLA-DPA1	rs3077
HLA-DPB1	rs1431403	HLA-DPB2	rs3117230	HLA-DPA1	rs9277341
HLA-DPB1	rs2064474	HLA-DPB2	rs3129274	HLA-DPA1	rs987870
HLA-DPB1	rs2064476	HLA-DPB2	rs3130215	HLA-DPB1	Affx-28513472
HLA-DPB1	rs2064478	HLA-DPB2	rs4713607	HLA-DPB1	rs1042151
HLA-DPB1	rs2068204	HLA-DPB2	rs6901221	HLA-DPB1	rs1042153
HLA-DPB1	rs2071352	HSD17B8	rs421446	HLA-DPB1	rs1042169
HLA-DPB1	rs2144014	HSD17B8	rs439205	HLA-DPB1	rs1042335
HLA-DPB1	rs2179920	IRF5	rs10954213	HLA-DPB1	rs1071597

HLA-DPB1	rs2281389	KCNK9	rs2447406	HLA-DPB1	rs1126513
HLA-DPB1	rs2395314	KIAA0746	rs4269167	HLA-DPB1	rs141530233
HLA-DPB1	rs3097671	KIFC1	rs211452	HLA-DPB1	rs1431403
HLA-DPB1	rs3117223	LOC441376	rs3019885	HLA-DPB1	rs2064474
HLA-DPB1	rs3117230	LPHN2	rs11579502	HLA-DPB1	rs2064476
HLA-DPB1	rs3117231	LRRN6C	rs10491888	HLA-DPB1	rs2064478
HLA-DPB1	rs3128917	MAGI2	rs3779312	HLA-DPB1	rs2068204
HLA-DPB1	rs3128927	NCKAP5	rs1134119	HLA-DPB1	rs2071352
HLA-DPB1	rs3130190	NCKAP5	rs7585252	HLA-DPB1	rs2144014
HLA-DPB1	rs31328921	NEK10	rs1579900	HLA-DPB1	rs2179920
HLA-DPB1	rs3135024	NEUROG3	rs731573	HLA-DPB1	rs2281389
HLA-DPB1	rs7772134	OFCC1	rs9358619	HLA-DPB1	rs2281390
HLA-DPB1	rs910320	OSMR	rs357291	HLA-DPB1	rs2395314
HLA-DPB1	rs9271897	PAEP	rs705669	HLA-DPB1	rs3097671
HLA-DPB1	rs9277341	PDE9A	rs2269127	HLA-DPB1	rs3117223
HLA-DPB1	rs9277410	PLSCR4	rs7628805	HLA-DPB1	rs3117230
HLA-DPB1	rs9277424	PTPN22	rs2476601	HLA-DPB1	rs3117231
HLA-DPB1	rs9277464	RING1	rs213212	HLA-DPB1	rs3128917

HLA-DPB1	rs9277471	RING1	rs213213	HLA-DPB1	rs3128921
HLA-DPB1	rs9277489	RXRB	rs6531	HLA-DPB1	rs3128927
HLA-DPB1	rs9277498	RXRB	rs9277935	HLA-DPB1	rs3130190
HLA-DPB1	rs9277514	SEMA6A	rs26595	HLA-DPB1	rs3135024
HLA-DPB1	rs9277535	SERPINA 1	Z allele	HLA-DPB1	rs7772134
HLA-DPB1	rs9277546	SLC30A8	rs1695715	HLA-DPB1	rs910320
HLA-DPB1	rs9277554	SLC30A8	rs1793729	HLA-DPB1	rs9277410
HLA-DPB1	rs9277567	ST6GAL1	rs10513807	HLA-DPB1	rs9277424
HLA-DPB2	rs1810472	SYNGAP1	rs211456	HLA-DPB1	rs9277464
HLA-DPB2	rs1883414	SYNGAP1	rs2247385	HLA-DPB1	rs9277471
HLA-DPB2	rs3117008	TCBA1	rs6924068	HLA-DPB1	rs9277489
HLA-DPB2	rs3117016	TCEB3	rs2076346	HLA-DPB1	rs9277498
HLA-DPB2	rs3129274	TMPO	rs2011247	HLA-DPB1	rs9277514
HLA-DPB2	rs3129294	TMPO	rs2216021	HLA-DPB1	rs9277535
HLA-DPB2	rs3130215	WDR46	rs3130257	HLA-DPB1	rs9277546
HLA-DQA1	rs17612576	WSCD1	rs7503953	HLA-DPB1	rs9277554
HLA-DQA1	rs17843619	WWC1	rs3853242	HLA-DPB1	rs9277567
HLA-DQA1	rs199556640			HLA-DPB1	rs9380343

HLA-DQA1	rs28584179
HLA-DQA1	rs35242582
HLA-DQA1	rs9272116
HLA-DQA1	rs9272346
HLA-DQA1	rs9273088
HLA-DQA1	rs9273215
HLA-DQB1	rs1049072
HLA-DQB1	rs1063355
HLA-DQB1	rs1130399
HLA-DQB1	rs9274552
HLA-DRA	rs2395175
HLA-DRB1	rs116518618
HLA-DRB1	rs660895
HLA-DRB1	rs9271824
HLA-DRB1	rs9272105
HLA-DRB4	-
HSD17B8	rs421446
HSD17B8	rs459205

HLA-DPB1*0401	
HLA-DPB2	rs1810472
HLA-DPB2	rs1883414
HLA-DPB2	rs3117008
HLA-DPB2	rs3117016
HLA-DPB2	rs3117034
HLA-DPB2	rs3129274
HLA-DPB2	rs3129294
HLA-DPB2	rs3130215
HLA-DQA1	rs28584179
HLA-DQA1	rs35242582
HLA-DRB1	rs116518618
HLA-DRB1*15	
HSD17B8	rs421446
HSD17B8	rs439205
MICA	rs1882
MICA	rs2596530
MUC22	rs3094672

IRF5	rs10954213
MCCD1	rs3132454
MICA	rs1882
MICA	rs2256183
MICA	rs2596530
MICA	rs75549913
NOTCH4	rs3096702
NOTCH4	rs3134926
NOTCH4	rs382259
PRTN3	rs62132293
PTPN22	(R620W) rs2476601
PTPN22	rs6679677
RING1	rs213194
RING1	rs213209
RING1	rs213210
RING1	rs213212
RING1	rs213213
RING1	rs439121

PRTN3	rs62132293
RING1	rs213194
RING1	rs213209
RING1	rs213210
RING1	rs213212
RING1	rs213213
RING1	rs439121
RING1	rs9277946
RXRB	rs2076310
RXRB	rs6531
RXRB	rs9277935
SERPINA 1	Z allele
SERPINA1	rs28929474
TLR9	rs352140
TLR9	rs352162
WDR46	rs3130257

RING1	rs9277946
RING1/RXRB	rs213213
RXRB	rs2076310
RXRB	rs6531
RXRB	rs9277935
SERPINA 1	Z allele
SERPINA1	rs28929474
SKIV2L	rs429608
SKIV2L	rs43899
TLR9	rs352162

Figure S1. The Venn diagram including all patients with AAV and those with GPA and the respective target antigens with the noteworthy SNPs from our FPRP and BFDP analyses.

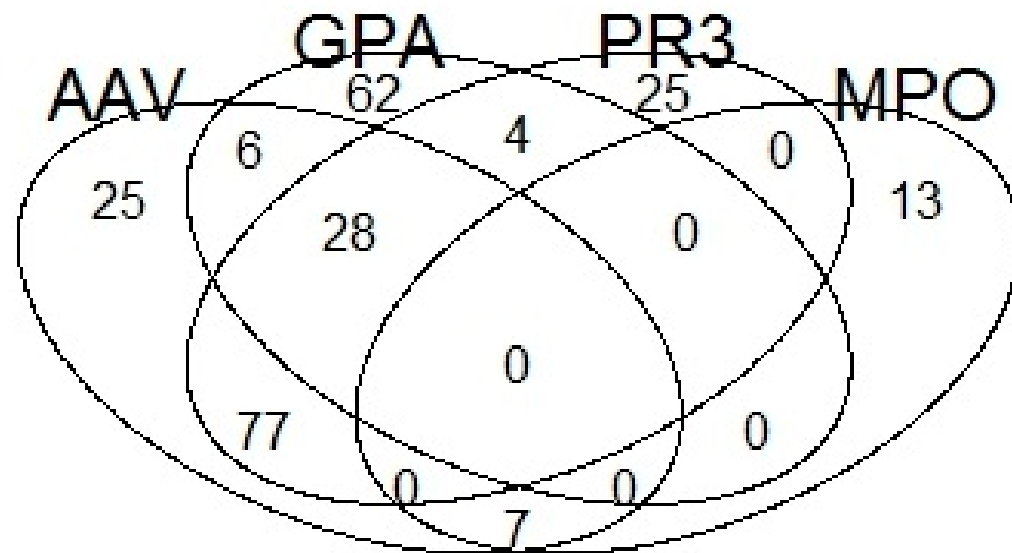
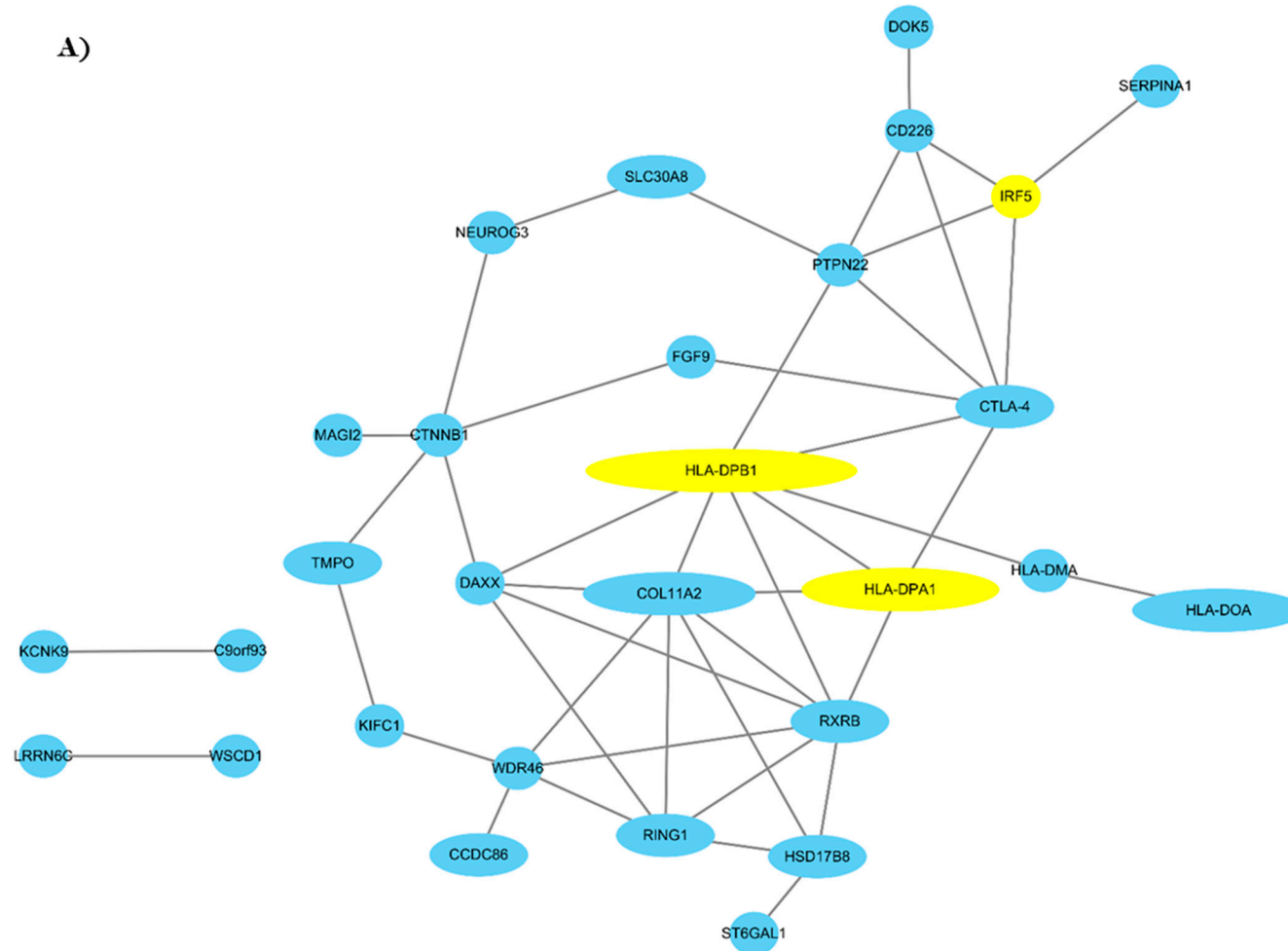


Figure S2. Protein–protein interaction network of GPA (A) and ANCA-associated vasculitis (B). Genes are weighted according to the number of SNPs of each gene. The gene set comprises the GWAS discovered SNP genes as well as noteworthy SNP genes from meta-analyses of observational studies and GWAS meta-analyses. Borderline SNPs ($5.0 \times 10^{-8} < p < 0.05$) from GWASs that were noteworthy in our analysis were also included. The yellow nodes represent the genes associated with interferon-gamma-mediated signaling pathway.



B)

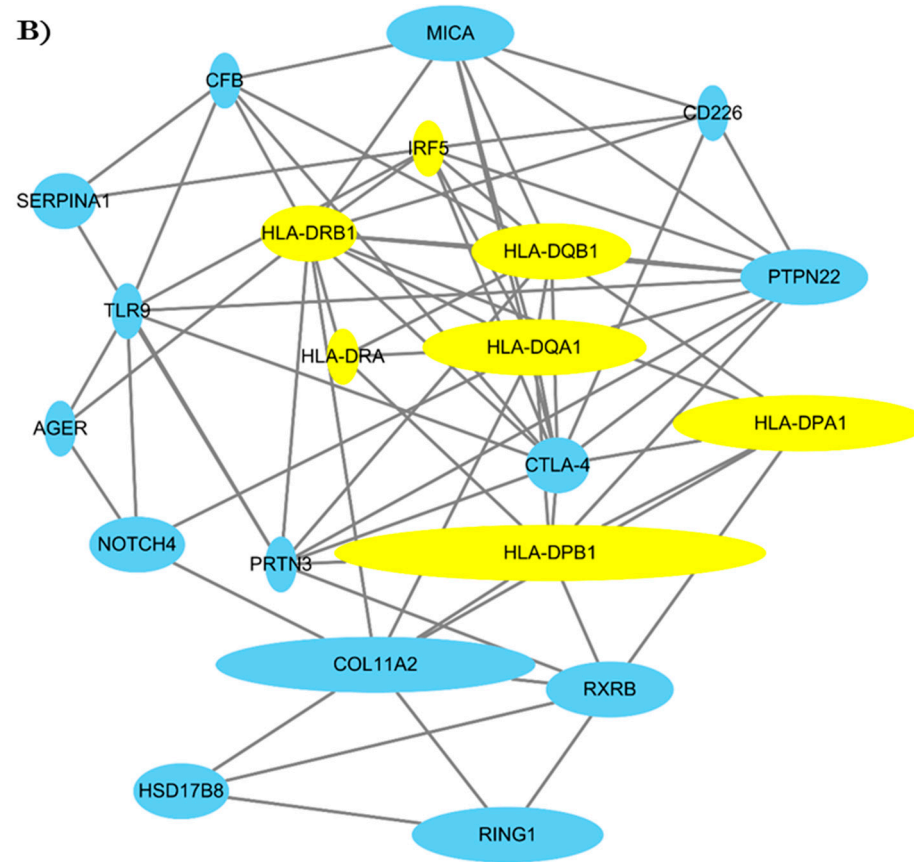
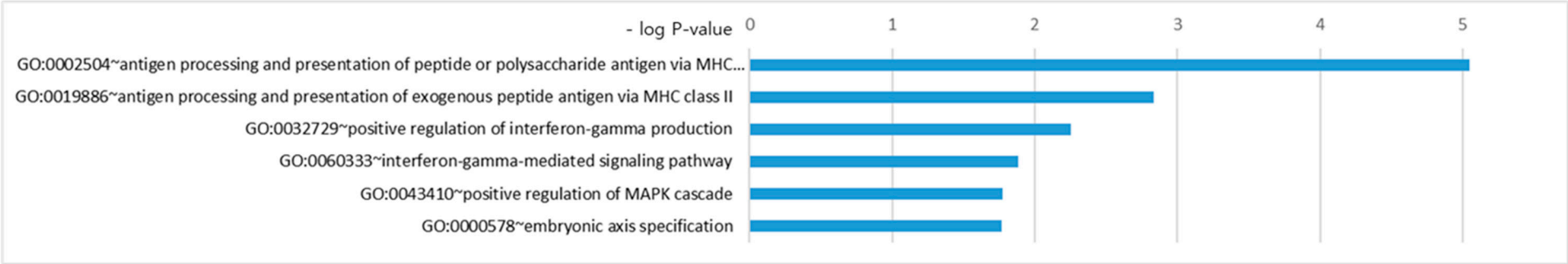
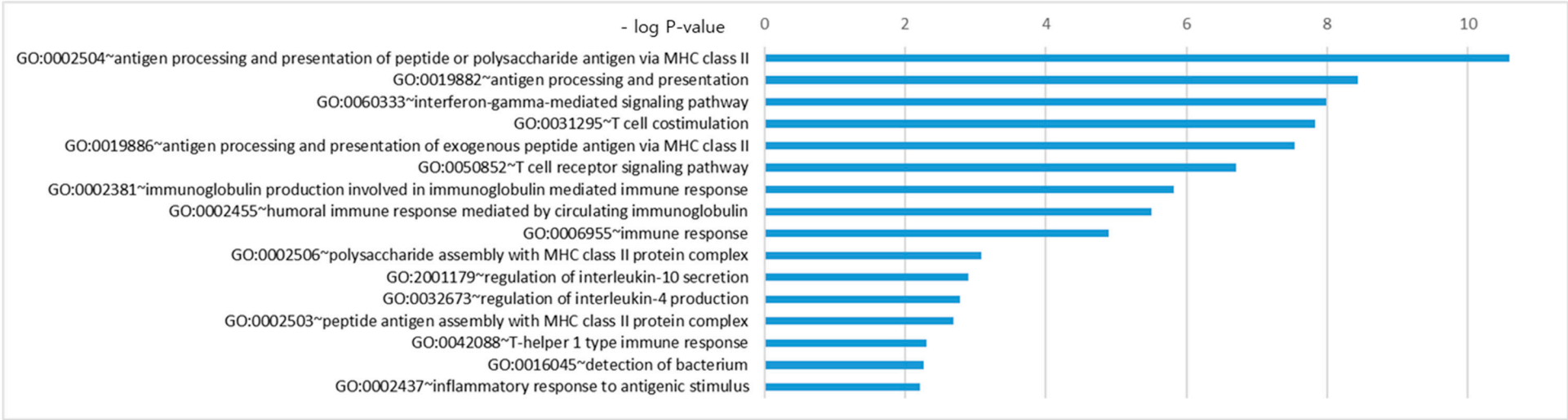


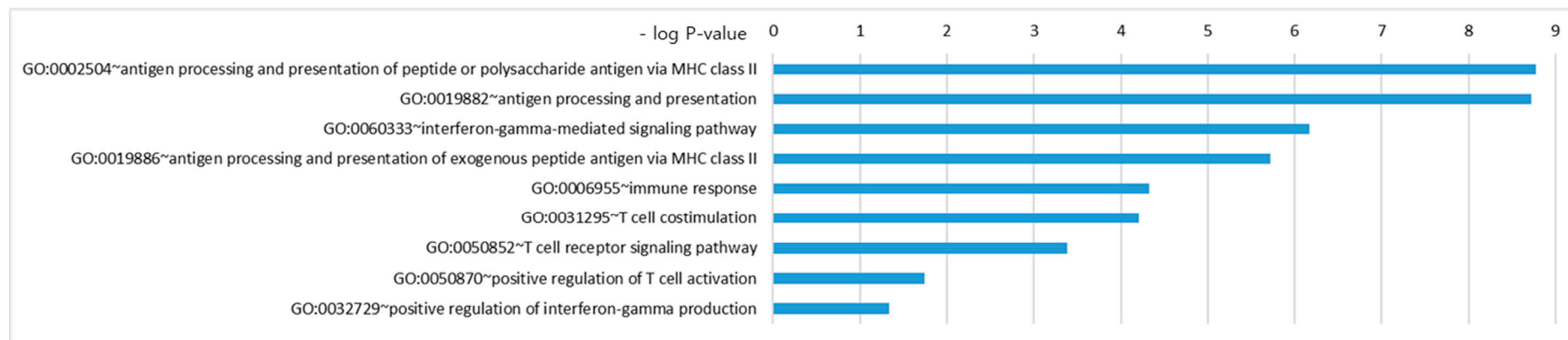
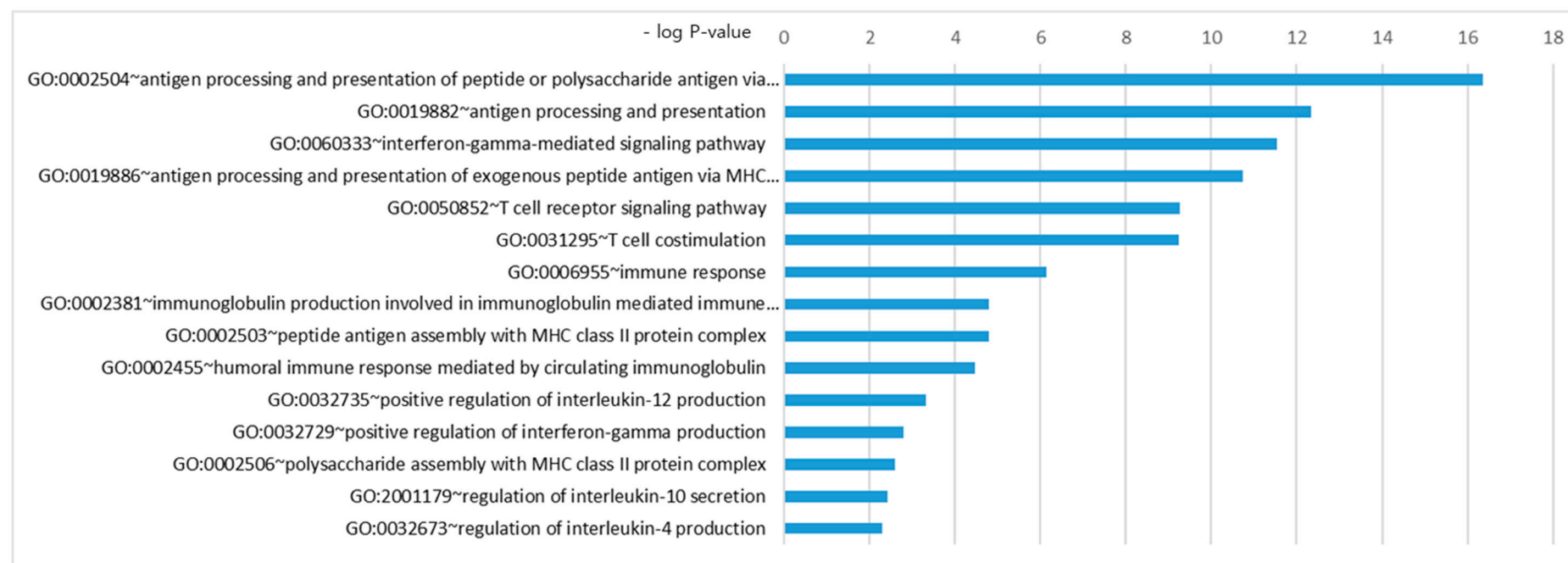
Figure S3. Gene ontology enrichment analysis of GPA (A), MPO-ANCA vasculitis (B), PR3-ANCA vasculitis (C), and ANCA-associated vasculitis (D). The gene set comprised the GWAS discovered SNP genes as well as noteworthy SNP genes identified in meta-analyses of observational studies and GWAS meta-analyses. Borderline SNPs ($5.0 \times 10^{-8} < p < 0.05$) from GWASs that were noteworthy were also included.

A



B



C**D**

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