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**Genome-wide association trans-ethnic meta-analyses identifies novel associations
regulating coagulation Factor VIII and von Willebrand Factor plasma levels**

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Short title: Genetic regulation of FVIII and VWF

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ABSTRACT

Background: Factor VIII (FVIII) and its carrier protein von Willebrand factor (VWF) are associated with risk of arterial and venous thrombosis and with hemorrhagic disorders. We aimed to identify and functionally test novel genetic associations regulating plasma FVIII and VWF.

Methods: We meta-analyzed genome-wide association results from 46,354 individuals of European, African, East Asian, and Hispanic ancestry. All studies performed linear regression analysis using an additive genetic model and associated approximately 35 million imputed variants with natural-log transformed phenotype levels. *In vitro* gene silencing in cultured endothelial cells was performed for candidate genes to provide additional evidence on association and function. Two-sample Mendelian randomization (MR) analyses were applied to test the causal role of FVIII and VWF plasma levels on the risk of arterial and venous thrombotic events.

Results: We identified 13 novel genome-wide significant ($p \leq 2.5 \times 10^{-8}$) associations; 7 with FVIII levels (*FCHO2/TMEM171/TNPO1*, *HLA*, *SOX17/RP1*, *LINC00583/NFIB*, *RAB5C-KAT2A*, *RPL3/TAB1/SYNGR1*, and *ARSA*) and 11 with VWF levels (*PDHB/PXK/KCTD6*, *SLC39A8*, *FCHO2/TMEM171/TNPO1*, *HLA*, *GIMAP7/GIMAP4*, *OR13C5/NIPSNAP*, *DAB2IP*, *C2CD4B*, *RAB5C-KAT2A*, *TAB1/SYNGR1*, and *ARSA*), beyond 10 previously reported associations with these phenotypes. Functional validation provided further evidence of association for all loci on VWF except *ARSA* and *DAB2IP*. MR suggested causal effects of plasma FVIII activity levels on venous thrombosis and coronary artery disease risk and plasma VWF levels on ischemic stroke risk.

Conclusions: The meta-analysis identified 13 novel genetic loci regulating FVIII and VWF plasma levels, 10 of which we validated functionally. We provide some evidence for a causal role of these proteins in thrombotic events.

Keywords: Genetic, Association Studies, GWAS, Cardiovascular Disease, Risk Factors, FVIII, VWF

CLINICAL PERSPECTIVE

What is new?

- Plasma coagulation factor VIII (FVIII) and von Willebrand factor (VWF) concentrations are associated with risk of cardiovascular disease, but the factors that control their levels are not fully understood.
- Using a multi-ethnic meta-analysis of genome wide association studies, we identified 7 genome-wide significant novel associations for FVIII and 11 for VWF.

What are the clinical implications?

- We evaluated the effect of genetic variants with coronary artery disease, ischemic stroke, and venous thrombosis through Mendelian randomization analyses and found evidence of a causal effect of FVIII activity levels on venous thrombosis and coronary artery disease risk, and a causal effect of plasma VWF levels on stroke risk.
- Our findings suggest that FVIII and VWF may be potential therapeutic targets to prevent thrombotic events.

INTRODUCTION

Factor VIII (FVIII) and its carrier protein von Willebrand factor (VWF) regulate hemostasis and thrombosis, and higher plasma levels of these factors have been associated with risk of arterial and venous thrombosis, while lower levels are associated with hemorrhagic disorders¹⁻⁴ and with reduced risk of thrombotic events⁵. Previously published genetic association studies have investigated the contribution of nucleotide variation to plasma levels of these factors using genome-wide and exome-wide markers⁶⁻⁸. These studies identified and replicated 8 genetic loci associated with plasma VWF levels (*STXBP5*, *SCARA5*, *ABO*, *STAB2*, *STX2*, *VWF*, *TCN2* and *CLEC4M*), 5 of which were also associated with FVIII levels (*STXBP5*, *SCARA5*, *ABO*, *STAB2*, and *VWF*). These discoveries have broadened our understanding of the regulation of hemostasis through follow-up functional investigations^{9, 10}.

The causal effect of these factors on bleeding is well-established, since severe FVIII and VWF deficiencies lead to bleeding disorders hemophilia A and von Willebrand disease, respectively. While it is currently unclear whether FVIII and VWF levels causally influence the risk of thrombotic diseases, some genetic and observational evidence point towards an effect of these proteins on thrombotic disease. Genetic variants in *F8* gene and in 3 VWF-associated genes (*ABO*, *STXBP5* and *VWF*) are robustly associated with risk of venous thrombosis but no causal association has been established¹¹⁻¹³.

The aim of this investigation was to identify new genetic associations that influence plasma levels of FVIII and VWF by expanding the size and ancestral diversity of the discovery sample from previous genome-wide association studies (GWAS) and by improving coverage of the

genome through the use of *1000 Genomes* imputed data and the inclusion of chromosome X variants¹⁴. For discoveries that reached genome-wide significance, we conducted first-pass functional characterization of the candidate loci both to provide additional evidence of association and to better understand the biology regulating plasma levels of these coagulation phenotypes. Last, by applying our genetic findings as instrument variables, we characterized the causal effect of plasma FVIII and VWF levels on clinical cardiovascular (CV) events using Mendelian randomization (MR) analyses.

METHODS

Due to patient confidentiality agreements and to comply with the study participants consent, the original data and study materials cannot be made available to other researchers for purposes of reproducing the results or replicating the procedure. Analytic methods will be made available upon request, and summary statistics have been made publicly available through dbGaP.

Study Design and Participating Cohorts

This project was organized within the Cohorts of Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Hemostasis Working Group¹⁵. We meta-analyzed phenotype-genotype associations of low-frequency and common (minor allele frequency [MAF] > 0.01) variants in 32,610 individuals from 9 studies with FVIII levels, and in 46,354 individuals from 18 studies with VWF levels. A total of 20 studies contributed to one or both of the analyses; these included participants of European (EUR), African (AFR), East Asian (ASI), and Hispanic (HIS) ancestry. Descriptions and ancestry composition of participating cohorts are found in Supplementary Table S1. All studies were approved by appropriate institutional review

committees and all participants gave written informed consent for themselves and their minor children for the use of their DNA.

Study-Level Methods

Genotype Calling and Quality Control

All participating cohorts performed genotyping using commercial genotyping platforms available from Illumina or Affymetrix. Each study performed genotyping quality control checks and imputed the approximately 35 million polymorphic autosomal and X-chromosome variants described in the *1000 Genomes* population phase 1 version 3 for each participant using available imputation methods¹⁶. Variant calling and quality control procedures for each cohort are described in Supplementary Table S1.

Statistical Analyses

Association Analyses

Plasma FVIII activity or VWF antigen levels were measured in all participants and reported in % or IU/ml*100 units. Participants with plasma FVIII or VWF levels (or activity levels) 3-standard-deviations above or below the population mean were removed, as were individuals on anticoagulation therapy. Natural-log transformed FVIII activity and VWF antigen levels (% or IU/ml*100 units) were analyzed separately within each study. Study-specific regression analyses using an additive model of inheritance were performed for imputed variant dosages and phenotype levels, adjusting for sex, age, study design variables, and population substructure using principal components. All analyses were stratified by ancestry and then meta-analyzed. X-

chromosome variants were additionally stratified by sex, with dosage values for males coded as 0/2.

Quality Control

Study-specific findings were uploaded centrally and a quality control (QC) pipeline of all individual studies prior to meta-analysis was conducted using the EasyQC software package¹⁷. Variants with beta or standard errors (SE) values > 5 or imputation values < 0.3 were excluded from the analysis. Estimated minor allele counts (eMAC) calculated for all SNPs were a function of allele frequency, total number of samples per cohort, and imputation quality; values <10 were excluded from analysis. Alleles were harmonized according to *1000 Genomes phase1 version3* reference panel and duplicated SNPs or SNPs that had inconsistencies with the reference were excluded.

Meta, Trans-Ethnic, and Multi-Phenotype Discovery Analyses

Meta-analyses were performed in METAL within each ancestry group using a fixed-effects inverse-variance weighted approach then combined in a trans-ethnic analysis using the same method¹⁸. The trans-ethnic analyses are presented as discovery results and we used the ancestry-specific analyses to inform and interpret these signals. An association was considered genome-wide statistically significant at p-value < 2.5×10^{-8} to correct for the low-frequency variants that were not included in the initial generation of GWAS¹⁹ and only variants that passed QC in at least 3 cohorts were reported. Variants with MAF below 1% were filtered out after the meta-analyses. A genomic control coefficient was computed for each discovery cohort and was used to correct for cryptic relatedness. Finally, a locus was defined as +/- 1Mb from the SNP with the

lowest p-value, and the SNP with the lowest p-value was selected to represent the locus. Multi-phenotype methods are described in Supplementary Methods.

Functional Characterization of Candidate Loci through Gene Silencing

In the absence of replication cohorts, we conducted first-pass functional characterization of the candidate loci to provide additional evidence of association. For each genome-wide significant locus, we selected candidate genes that could be responsible for the observed associations. Selection was based on proximity to the most associated SNPs in each region, information from public databases on putative effect of the SNPs in terms of regulation of expression and function of nearby genes, and hypothesis for a biological mechanism to regulate VWF/FVIII. This selection process identified 1 to 3 candidate genes for each associated locus. To screen for functionality, human umbilical vein endothelial cells (HUVEC; Life Line Cell Technology) were plated on collagen coated 96-well plates and transfected with siRNA (Silencer Select, ThermoFisher Scientific) directed against the candidate genes using the transfection reagent oligofectamine (ThermoFisher Scientific). Cells were cultured for 4 days after transfection, and media was then replaced with control media or media containing 10 μ M of histamine for 30 minutes, to stimulate an inflammatory response. The FVIII and VWF in the media was measured by an ELISA using antibodies from Fitzgerald Industries and had detection ranges of 0.003-0.21 IU/ml for the FVIII assay and 0.5-120 ng/ul for the VWF assay. Every experiment was repeated 4 times and results are expressed as the mean \pm standard deviation (SD) of relative expression compared with a negative control (transfected with scramble siRNA).

Follow-up Genetic Analyses

Conditional Analyses

To identify additional independent genetic signals at the associated loci, we used an approximate method implemented in GCTA for conditional and joint analysis using meta-analysis summary statistics²⁰. We used best-guess imputation for variants with imputation quality >0.3 in 8,481 European-ancestry individuals from the Framingham Heart Study (FHS) as the reference panel. A description of the FHS is given in the Supplementary Methods. In order to prevent spurious conditional associations arising from a discrepancy between linkage disequilibrium in our GWAS and the reference panel, we also performed the conditional analysis on the results of the European-ancestry meta-analysis as a sensitivity analysis, since different genetic variants showed the strongest association in the trans-ethnic analysis compared with the European-only analysis.

Mendelian Randomization

For the sentinel variant in each locus in FVIII and VWF analyses, we conducted *in silico* lookups for the associations of each individual variant with 3 major CV events: coronary artery disease (CAD) in the CARDIOGRAMplusC4D Consortium^{21, 22}, ischemic stroke (IS) in the MEGASTROKE analysis within the International Stroke Genetics Consortium²³, and venous thromboembolism (VTE) in the International Network on Venous Thrombosis (INVENT) Consortium¹¹. We conducted 2-sample Mendelian Randomization (MR) analyses to detect any potential causal effects of plasma FVIII and VWF levels on each CV outcome, separately. We used summary statistics to generate 1 causal estimate per significant locus as the ratio of the variant's association with disease to the variant's association with the exposure, and estimates were then meta-analyzed using an inverse-variance weighted approach as our primary MR estimate, known as the inverse-variance weighted (IVW) estimate²⁴. Additional methods to avoid

bias due to heterogeneity, and the final variants composing the instrumental variables are further described in Supplementary Methods and in Supplementary Tables S2, S3, and S4. Since FVIII plasma levels are largely determined by VWF plasma levels owing to VWF's carrier role for FVIII in plasma, essentially all genetic predictors of plasma VWF levels are also predictors of FVIII plasma levels. The inverse, however is not true, and a small subset of variants predict FVIII plasma levels without predicting VWF levels. To investigate the independent causal role of FVIII plasma levels from that of VWF plasma levels on CVD events, we applied a multivariable MR (MVMR) approach where we adjusted for VWF variants effects in the estimate of causal association between FVIII and CVD outcomes²⁵.

RESULTS

FVIII, VWF, and Multi-phenotype Meta-Analyses

Agnostic Discovery

Data used for FVIII meta-analysis was available from 25,897 European (EA), 4,500 African (AA), 773 East or Indian Asian (EAA, IAA), and 1,440 Hispanic (HA) participants. Trans-ethnic meta-analysis for FVIII resulted 13,887,196 variants passing all filters, and identified 1,431 variants that reached genome-wide statistical significance at 11 loci. Data used for VWF was available from 42,379 EA, 3,700 AA, and 275 HA participants. Meta-analysis for VWF resulted in 10,537,485 variants passing all filters, and identified 2,453 genome-wide significant variants at 17 loci (Figures 1A-B). European-specific meta-analysis identified one significant variant at one additional locus. Analysis using combined FVIII and VWF phenotypes (see Supplementary Methods) identified 2,828 variants reaching genome-wide significance at 2 additional loci, which were not identified in single-phenotype analyses.

Table 1 shows the genetic discovery results for the FVIII, VWF, and combined FVIII-VWF phenotypes. Overall, 23 unique loci were identified. Among these, 13 were new associations not previously reported. Among the newly identified loci, 7 were associated with FVIII levels (*FCHO2/TMEM171/TNPO1*, *HLA*, *SOX17/RP1*, *LINC00583/NFIB*, *RAB5C/KAT2A*, *RPL3/TAB1/SYNGR1/PDGB*, and *ARSA*) and 11 were associated with VWF levels (*PDHB/PXK/KCTD6*, *SLC39A8*, *FCHO2/TMEM171/TNPO1*, *HLA*, *GIMAP7/GIMAP4*, *OR13C5/NIPSNAP*, *DAB2IP*, *C2CD4B*, *RAB5C/KAT2A*, *RPL3/TAB1/SYNGR1/PDGB*, and *ARSA*). Supplementary Figures S1a-n shows regional plots for the novel loci plotted for the 2 phenotypes. The lowest MAF for the index variant was 0.02 while the effect size per allele ranged from 0.015 to 0.032 (in log transformed units) for FVIII levels and from 0.014 to 0.060 for VWF levels.

Among the 23 genome-wide significant findings, 10 loci were previously reported to be associated with plasma levels of FVIII or VWF or both: *STXBP5*, *SCARA5*, *ABO*, *ST3GAL4*, *STAB2*, *STX2*, *VWF*, *TCN2*, *CLEC4M*, and *TMLHE-F8 region*.

Conditional Analyses and Variant Characterization

In follow-up analyses, we conditioned on sentinel variants to determine if secondary independent genome-wide significant signals were present. Results and additional independent variants are summarized in Table 2 along with findings from *in silico* investigations of the putative functional variant, and in Supplementary Tables S5 and S6. *SCARA5*, *ABO*, *VWF* and *STAB2* were predicted to have more than one independent signal both for FVIII and VWF analyses (details in

Supplementary Methods and in Supplementary Tables S5 and S6), some of which are in agreement with previous publications⁶. Among the independently associated variants within the *ABO* locus, SNPs rs10901252 and rs687621 perfectly discriminate B and O blood groups from A, and rs8176685 can reasonably capture information to tag A1/A2 (r^2 0.59/ D' 0.99 with the tag SNP), confirming that ABO blood groups are essential determinants of VWF and FVIII plasma levels.

Variance Explained

Overall, the top variants for these loci (including the strongest independent associated variants in each locus that reached genome-wide significance after conditional analyses) explain 17% of the phenotypic variance for FVIII and 21.3% of the variance for VWF. *ABO* locus was by far the strongest determinant, alone explaining 13.6% and 16.2% of these variances, respectively.

Functional Analyses

We silenced 21 genes across 12 loci to assess the *in vitro* impact on FVIII and VWF secretion (Figures 2a-b). These include the main candidate genes identified by proximity (Table 1). Our results suggest that 10 of the 12 candidate loci had one or more genes that changed VWF levels in media under basal and/or histamine-stimulated conditions. Specifically, silencing *PDHB*, *SLC39A8*, *TMEM171*, *TNPO1*, *HLA-C*, *GIMAP7*, *NIPSNAP3A*, *NIPSNAP3B*, *C2CD4B*, and *SYNGR1* increased VWF release into media under basal conditions whereas *ST3GAL4* silencing decreased VWF secretion. When cells were stimulated with histamine, silencing *TMEM171*, *TNPO1*, *HLA-C*, *SNIPSNAP3A* (but not *SNIPSNAP3B*), *C2CD4B*, *KAT2A*, and *TAB1* increased VWF release in the media, and *RAB5C* decreased VWF secretion (Table 1; Figures 2a-b). For

the experiments on the 5 genes that were only shown to be associated with FVIII levels (*LINC00583*, *NFIB*, *SOX17*, *RPI* and *TMLHE-F8*), we could not find detectable levels of FVIII in media from treated HUVEC cells, and therefore the experiments were inconclusive.

Mendelian Randomization Analyses and Cardiovascular Events

Figure 3 show forest plots representing the results from MR analyses. We first analyzed FVIII and VWF individually using the IVW estimates that included the sentinel variant in each locus (after exclusion of variants with pleiotropic effects, see Supplementary Tables S2, S3, and S4). Both VWF and FVIII plasma levels showed a significant causal effect on CAD, IS and VTE risk. For CAD, the ORs associated with a per SD change in natural log-transformed FVIII and VWF were (OR(CI₉₅) = 1.15 (1.05, 1.27) and 1.14 (1.05, 1.23), respectively. For IS, the ORs(CI₉₅) were 1.28 (1.14, 1.43) and 1.19 (1.10, 1.29), respectively. For VTE, the ORs(CI₉₅) were 2.75 (2.14, 3.55) and 2.31 (1.89, 2.81), respectively. Sensitivity analyses using both MR-Egger regression and weighted median estimates support the IVW estimates and no significant pleiotropic effect was evident after exclusion of the pleiotropic loci (Figure 3, Supplementary Table S3, Supplementary Figures S2a-c).

We then performed MVMR analyses of the FVIII phenotype to identify causal effects of FVIII activity levels independent of VWF levels. For VTE and CAD outcomes, adjustment of FVIII results by the effect of VWF, the ORs were modestly attenuated (20% and 16% respectively) compared with the unadjusted estimates and confidence intervals widened. For IS, however, adjustment of FVIII results by the effect of VWF resulted in an 86% attenuation of the OR(CI₉₅)

to 0.88 (0.51, 1.51). We could not demonstrate a causal association of VWF levels with VTE and CAD independent of FVIII levels.

Of note, both the *ABO* and *HLA* loci were excluded from the instrumental variables for the MR analyses due to evidence of pleiotropic effects shown in the heterogeneity tests (Supplementary Table S3). When we estimated causal effects using *ABO* alone as an instrument, estimates of causal effects were essentially the same across phenotypes and outcomes: OR(CI₉₅) 2.57 (2.47-2.67) for FVIII and VTE; OR(CI₉₅) 2.28 (2.18-2.38) for VWF and VTE; OR(CI₉₅) 1.10 (1.06-1.14) for FVIII and IS; OR(CI₉₅) 1.09 (1.05-1.13) for VWF and IS; OR(CI₉₅) 1.10 (1.06-1.14) for FVIII and CAD; and OR(CI₉₅) 1.08 (1.04-1.12) for VWF and CAD.

DISCUSSION

In the present study, we meta-analyzed data from more than 36,000 individuals with FVIII levels and more than 46,000 with VWF and identified 13 novel loci, 7 of which associated with FVIII plasma levels and 11 associated with VWF levels. Overall, new discoveries yielded an additional 6.2% and 8.1% proportion of variance explained for FVIII and VWF respectively from previous estimations⁸, and suggest that a great proportion of the genetic variance is explained by common variation. Further, we presented experimental evidence of biological function on VWF regulation for 14 of these genes from gene silencing *in vitro*: *PDHB*, *SLC39A8*, *TMEM171*, *TNPO1*, *HLA-C*, *GIMAP7*, *NIPSNAP3A and B*, *ST3GAL4*, *C2CD4B*, *RAB5C*, *KAT2A*, *TAB1*, *SYNGR1*. Last, we provide evidence in support of a causal role of FVIII levels on VTE and CAD events and of VWF levels on IS events.

Characterization of the Novel Loci Regulating FVIII and VWF

As expected for traits with strong genetic correlation, most of the newly associated loci regulate both FVIII and VWF levels in blood. Our results show that most of the highest-signal independent variants associated with these traits were located in introns or non-coding regions, although a substantial proportion were in strong LD ($R^2 > 0.8$) with mutations causing missense or frameshift mutations in the nearby genes (Table 2 and Supplementary Table S7). We also explored eQTL associations using publicly available data and we conducted pathway analyses for the novel loci. See Supplementary Methods and Supplementary Tables S8-S13 for this information.

For most loci, several genes were identified within the associated region, and we selected 1 or more genes for further characterization using *in vitro* cell models. Based on our initial functional characterization, 1 or more plausible culprit genes regulating VWF secretion could be isolated at most loci. Interestingly, several candidate genes that showed a clear change in VWF levels upon silencing have been shown to participate in vesicle trafficking and exocytosis, as well as intracellular signaling and inflammatory response. The most relevant functional genes are described below and summarized in Supplementary Figure S3.

VWF Biogenesis, Vesicle Trafficking and Secretion

ST3GAL4 is a Golgi transferase that catalyzes transfer of sialic acids in VWF glycan branches that are essential to its biogenesis, adhesive activity and clearance²⁶. It also has a role in clearance of desialylated platelets with effects on platelet homeostasis. Genetic variants in *ST3GAL4* locus have been associated with total cholesterol, LDL cholesterol,

alkaline phosphatase, increased platelet aggregation, fibrinogen, CRP, and CAD (see further details and references in Supplementary Table S7). Our functional analyses showed a substantial reduction of VWF release upon *ST3GAL4* silencing, which strengthens the evidence of this gene as a novel VWF regulator in basal conditions.

SYNGR1 (*Synaptogryn-1*) encodes an integral membrane protein associated with presynaptic vesicles in neuronal cells. Several commonalities have been described between the exocytic machinery that drives vesicle trafficking and membrane fusion in endothelial cells and synaptic machinery found in neurons^{27, 28}, which suggest that SYNGR1 could have a role in vesicle trafficking and exocytosis of VWF from the Weibel-Palade bodies. Genetic variation in this locus has also been associated with IgG glycosylation, rheumatoid arthritis, and inflammatory bowel disease/Crohn's disease, the last 2 consistent with an effect of deregulation of interleukin and inflammatory signaling pathways.

NIPSNAP3A and *NIPSNAP3B* were selected as the main biologically plausible genes for locus on chromosome 9, and results from the functional study show evidence of significant upregulated levels of VWF upon silencing of either gene. Again, a reported role of these genes in vesicular trafficking²⁹ suggest that these genes could be important in Weibel-Palade formation and exocytosis of VWF, both in basal conditions and under inflammatory stimuli.

Among the 2 new loci found in the trans-ethnic multi-phenotype analysis, *RAB5C* is particularly interesting. It is a member of the Rab protein family, thought to ensure fidelity in the process of docking and fusion of vesicles with their correct acceptor compartment³⁰,

which may be relevant to the process of fusion of Weibel-Palate vesicles to release VWF in endothelial cells. *RAB5C* silencing caused a significant decrease of VWF release in media of endothelial cells upon stimulation with histamine.

Our *in vitro* cell work showed a significantly increased VWF secretion upon *PDHB* silencing. *PDHB* codes for a subunit of the pyruvate dehydrogenase complex, which converts pyruvate to acetyl-CoA in the mitochondrion. We speculate that it is possible that the metabolism of endothelial cells regulates vesicle trafficking and exocytosis of VWF, meaning that the exocytosis process is dependent on the energetic status of the endothelial cell. Genetic variation in this locus has also been associated with total cholesterol, SLE, and RA.

Intracellular Signaling and Inflammatory Response

TAB1 silencing increased VWF released in media in our *in vitro* functional analyses, whereas no effect could be seen for *PDGFB*, a gene that has been implicated in CAD and VTE risk. TAB1 is a regulatory protein that acts as a mediator of several intracellular signaling pathways, especially those mediated by TGF- β , WNT-1 and interleukin-1 which suggest it might have a role mediating VWF release upon certain cellular stimuli.

Similarly, silencing *C2CD4B* gene in cultured endothelial cells resulted in strong upregulation of VWF release both in basal and under stimulus conditions. Allelic variants in this gene have also been associated with fasting glucose homeostasis and type 2 diabetes. Transcripts of this gene are predominantly found in the nuclear compartment of endothelial

cells, and a possible role in regulation of transcription that might increase vascular permeability in acute inflammation has been suggested³¹. Similarly, *TNPO1* codes for a nuclear receptor (Transportin-1³²) which mediates nuclear import of several proteins, which could also suggest a role in regulation of transcription under certain circumstances.

DAB2IP is involved in several relevant cell-signaling pathways in response to inflammation, innate immune response, and cell growth inhibition, apoptosis, cell survival, angiogenesis, cell migration and maturation in endothelial cells, and genetic variation in this gene has been associated with abdominal aortic aneurysm and heart rate. Despite the strong genetic signal in our data, functional confirmation could not be achieved for *DAB2IP* in our secretion experiment so additional investigative work is needed.

GIMAP7 showed a significant increase of VWF release upon silencing. GTPases of immunity-associated proteins (GIMAPs) are regulators of lymphocyte survival and homeostasis³³ although limited data have been published regarding the function of these proteins.

Finally, although it did not reach genome-wide significance in the trans-ethnic meta-analysis, we found a single locus that close to *SLC39A8* and that was genome-wide significant in our meta-analysis VWF associations in European-ancestry samples. This gene, which encodes a zinc transporter that functions in the cellular import of zinc at the onset of inflammation, has also been associated with blood pressure, high-density lipoprotein (HDL)

cholesterol levels and BMI. Our functional work also suggested a strong effect on VWF levels in media from endothelial cells *in vitro* upon *SLC39A8* silencing.

Although further functional characterization of these genes is needed to fully characterize the role of all the investigated genes in VWF regulation, our results demonstrate that these studies are a valid tool to elucidate functional genes coming from genetic associations, and to shed light into the most relevant biological pathways implicated in the regulation of the phenotype under study.

Mendelian Randomization and Clinical Implications

Our results provide insights into the causal role of FVIII and VWF in 3 CV events, which are the leading causes of deaths globally.

Biological and genetic evidence indicate that circulating FVIII levels are mainly determined by levels of VWF³⁴. In the present study, we calculated the genetic correlation between VWF and FVIII based on the genome-wide association results from European-descent individuals (see Supplementary Methods) and found that the proportion of shared heritability of between these 2 phenotypes is 83.5%. This result is strengthened by the overlapping findings found in the individual GWAS, and suggests that, with some exceptions, the genetic pathways that regulate VWF levels indirectly regulate FVIII levels. Given the role of VWF regulating FVIII, we used 3 loci that were uniquely associated with FVIII independent of VWF and pursued conditional analyses that adjusted for the effect of VWF plasma levels to test the causal effect of FVIII on CV events. For IS, we found no evidence of a causal effect of FVIII independent of the VWF

effect, which suggests that VWF biology may causally contribute to IS risk. For VTE and CAD, however, we found evidence supporting a causal effect of FVIII independent of the VWF effect. As there were no genetic loci that independently associated with VWF levels and not FVIII levels, we could not adjust the VWF analyses for FVIII. Nonetheless, given the similarities in the magnitude of the VWF-adjusted FVIII causal ORs with the VWF causal ORs for VTE and CAD, our data suggest that the VWF causal association for VTE and CAD may be driven primarily by the biologic effect of FVIII, although this hypothesis could not be tested.

The results of the MR analyses suggest that both FVIII and VWF may be reasonable targets for the prevention or intervention of CAD and VTE while VWF may be a reasonable target for IS. Indeed over the past decade this line of thinking and research has been pursued and these molecules are currently under investigation as pharmaceutical targets for the prevention of thrombotic events³⁵⁻³⁸. In this paper, we report on 23 unique genetic loci associated with plasma levels of FVIII and/or VWF, of which 13 are newly reported associations. These discoveries may offer new targets in the development of pharmaceutical agonistics or antagonists that may modulate thrombotic risk.

Strengths and Limitations

A major strength of the study was the relatively large sample size and the use of a denser imputation panel than was used in past discovery efforts. With this approach, we had hoped to identify uncommon associated variants but the MAF of the variants in the newly associated loci were relatively common, with just 1 variant having an MAF of less than 0.10. Our study design did not identify new associations marked by rare variation. Increasing the number of study

participants to increase statistical power or improving the quality of the imputation from genotyping arrays may help to identify uncommon or rare variants associated with the outcomes. Some of the novel findings may be false positives, as we did not have access to independent populations to replicate our discoveries. Replication is required to validate genetic associations, especially for those close to the threshold for statistical significance. To offset this limitation, we conducted functional validation by silencing candidate genes and measuring VWF release; we view this functional work as a strength of the study. We were able to test only the regulation of VWF expression and not the regulation of VWF clearance by macrophages³⁹. Nor were we able to test other mechanisms that regulates synthesis in megakaryocytes but not endothelial cells. Further, the need for a particular cellular stimulus that cannot be mimicked by histamine stimulation for the effect to be produced would be missed by our approach. Finally, it could be that the effect of some genetic associations can only be seen through overexpression rather than silencing of the gene. We attempted to also measure FVIII release but levels were too low so new models are required to validate the impact the candidate genes on FVIII levels; this is a limitation of our approach. All functional work was done *in vitro*, which carries limitations relative to *in vivo* investigations. The strong genetic co-regulation of both FVIII and VWF levels allowed us to conduct multi-phenotypes analyses and increase statistical power for discovery. Our MR approach using improved instrumental variants allows to establish for the first time a causal relationship between VWF and FVIII and several CV events. With only 3 loci associated with FVIII alone, the power of the VWF-adjusted MR analyses for FVIII and CV events was limited and we could not investigate the association of VWF on CV events independent of FVIII. There is a degree of overlap between our sample and the sample from consortia providing CV

events GWAS data, which might create some bias in MR analyses⁴⁰; this is a limitation of our work.

CONCLUSIONS

We found 13 novel genetic loci with modest contributions to plasma levels of FVIII and/or VWF. Our discovery approach including first-pass functional validation has provided relevant information on the best candidate gene at the novel loci. Finally, MR analyses provided some evidence implicating FVIII plasma levels in the risk of CAD and VTE, and VWF plasma levels in the risk of IS. In summary, our work has identified novel loci regulating proteins essential for hemostasis and coagulation. These findings may provide genetic tools for therapeutic and preventive strategies and may be useful to identify new biologic pathways upon which to intervene to reduce the burden of arterial and venous outcomes.

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REFERENCES:

1. Folsom AR. Hemostatic risk factors for atherothrombotic disease: an epidemiologic view. *Thromb Haemost.* 2001;86:366-373.
2. Koster T, Blann AD, Briet E, Vandenbroucke JP and Rosendaal FR. Role of clotting factor VIII in effect of von Willebrand factor on occurrence of deep-vein thrombosis. *Lancet.* 1995;345:152-155.
3. Smith A, Patterson C, Yarnell J, Rumley A, Ben-Shlomo Y and Lowe G. Which hemostatic markers add to the predictive value of conventional risk factors for coronary heart disease and ischemic stroke? The Caerphilly Study. *Circulation.* 2005;112:3080-3087.
4. Spiel AO, Gilbert JC and Jilma B. von Willebrand factor in cardiovascular disease: focus on acute coronary syndromes. *Circulation.* 2008;117:1449-1459.
5. Seaman CD, Yabes J, Comer DM and Ragni MV. Does deficiency of von Willebrand factor protect against cardiovascular disease? Analysis of a national discharge register. *J Thromb Haemost.* 2015;13:1999-2003.
6. Huffman JE, de Vries PS, Morrison AC, Sabater-Lleal M, Kacprowski T, Auer PL, Brody JA, Chasman DI, Chen MH, Guo X, Lin LA, Marioni RE, Muller-Nurasyid M, Yanek LR, Pankratz N, Grove ML, de Maat MP, Cushman M, Wiggins KL, Qi L, Sennblad B, Harris SE, Polasek O, Riess H, Rivadeneira F, Rose LM, Goel A, Taylor KD, Teumer A, Uitterlinden AG, Vaidya D, Yao J, Tang W, Levy D, Waldenberger M, Becker DM, Folsom AR, Giulianini F, Greinacher A, Hofman A, Huang CC, Kooperberg C, Silveira A, Starr JM, Strauch K, Strawbridge RJ, Wright AF, McKnight B, Franco OH, Zakai N, Mathias RA, Psaty BM, Ridker PM, Tofler GH, Volker U, Watkins H, Fornage M, Hamsten A, Deary IJ, Boerwinkle E, Koenig W, Rotter JI, Hayward C, Dehghan A, Reiner AP, O'Donnell CJ and Smith NL. Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood.* 2015;126:e19-29.
7. Johnsen JM, Auer PL, Morrison AC, Jiao S, Wei P, Haessler J, Fox K, McGee SR, Smith JD, Carlson CS, Smith N, Boerwinkle E, Kooperberg C, Nickerson DA, Rich SS, Green D,

Peters U, Cushman M, Reiner AP and Project NES. Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. *Blood*. 2013;122:590-597.

8. Smith NL, Chen MH, Dehghan A, Strachan DP, Basu S, Soranzo N, Hayward C, Rudan I, Sabater-Lleal M, Bis JC, de Maat MP, Rumley A, Kong X, Yang Q, Williams FM, Vitart V, Campbell H, Malarstig A, Wiggins KL, Van Duijn CM, McArdle WL, Pankow JS, Johnson AD, Silveira A, McKnight B, Uitterlinden AG, Wellcome Trust Case Control C, Aleksic N, Meigs JB, Peters A, Koenig W, Cushman M, Kathiresan S, Rotter JI, Bovill EG, Hofman A, Boerwinkle E, Tofler GH, Peden JF, Psaty BM, Leebek F, Folsom AR, Larson MG, Spector TD, Wright AF, Wilson JF, Hamsten A, Lumley T, Witteman JC, Tang W and O'Donnell CJ. Novel associations of multiple genetic loci with plasma levels of factor VII, factor VIII, and von Willebrand factor: The CHARGE (Cohorts for Heart and Aging Research in Genome Epidemiology) Consortium. *Circulation*. 2010;121:1382-1392.

9. Zhu Q, Yamakuchi M, Ture S, de la Luz Garcia-Hernandez M, Ko KA, Modjeski KL, LoMonaco MB, Johnson AD, O'Donnell CJ, Takai Y, Morrell CN and Lowenstein CJ. Syntaxin-binding protein STXBP5 inhibits endothelial exocytosis and promotes platelet secretion. *J Clin Invest*. 2014;124:4503-4516.

10. Rydz N, Swystun LL, Notley C, Paterson AD, Riches JJ, Sponagle K, Boonyawat B, Montgomery RR, James PD and Lillicrap D. The C-type lectin receptor CLEC4M binds, internalizes, and clears von Willebrand factor and contributes to the variation in plasma von Willebrand factor levels. *Blood*. 2013;121:5228-5237.

11. Germain M, Chasman DI, de Haan H, Tang W, Lindstrom S, Weng LC, de Andrade M, de Visser MC, Wiggins KL, Suchon P, Saut N, Smadja DM, Le Gal G, van Hylckama Vlieg A, Di Narzo A, Hao K, Nelson CP, Rocanin-Arjo A, Folkersen L, Monajemi R, Rose LM, Brody JA, Slagboom E, Aissi D, Gagnon F, Deleuze JF, Deloukas P, Tzourio C, Dartigues JF, Berr C, Taylor KD, Civelek M, Eriksson P, Cardiogenics C, Psaty BM, Houwing-Duitermaat J, Goodall

AH, Cambien F, Kraft P, Amouyel P, Samani NJ, Basu S, Ridker PM, Rosendaal FR, Kabrhel C, Folsom AR, Heit J, Reitsma PH, Tregouet DA, Smith NL and Morange PE. Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. *Am J Hum Genet.* 2015;96:532-542.

12. Hinds DA, Buil A, Ziemek D, Martinez-Perez A, Malik R, Folkersen L, Germain M, Malarstig A, Brown A, Soria JM, Dichgans M, Bing N, Franco-Cereceda A, Souto JC, Dermitzakis ET, Hamsten A, Worrall BB, Tung JY, Metastroke Consortium, Invent Consortium and Sabater-Lleal M. Genome-wide association analysis of self-reported events in 6135 individuals and 252 827 controls identifies 8 loci associated with thrombosis. *Hum Mol Genet.* 2016;25:1867-1874.

13. Smith NL, Rice KM, Bovill EG, Cushman M, Bis JC, McKnight B, Lumley T, Glazer NL, van Hylckama Vlieg A, Tang W, Dehghan A, Strachan DP, O'Donnell CJ, Rotter JI, Heckbert SR, Psaty BM and Rosendaal FR. Genetic variation associated with plasma von Willebrand factor levels and the risk of incident venous thrombosis. *Blood.* 2011;117:6007-6011.

14. de Vries PS, Sabater-Lleal M, Chasman DI, Trompet S, Ahluwalia TS, Teumer A, Kleber ME, Chen MH, Wang JJ, Attia JR, Marioni RE, Steri M, Weng LC, Pool R, Grossmann V, Brody JA, Venturini C, Tanaka T, Rose LM, Oldmeadow C, Mazur J, Basu S, Franberg M, Yang Q, Ligthart S, Hottenga JJ, Rumley A, Mulas A, de Craen AJ, Grotevendt A, Taylor KD, Delgado GE, Kifley A, Lopez LM, Berentzen TL, Mangino M, Bandinelli S, Morrison AC, Hamsten A, Tofler G, de Maat MP, Draisma HH, Lowe GD, Zoledziowska M, Sattar N, Lackner KJ, Volker U, McKnight B, Huang J, Holliday EG, McEvoy MA, Starr JM, Hysi PG, Hernandez DG, Guan W, Rivadeneira F, McArdle WL, Slagboom PE, Zeller T, Psaty BM, Uitterlinden AG, de Geus EJ, Stott DJ, Binder H, Hofman A, Franco OH, Rotter JI, Ferrucci L, Spector TD, Deary IJ, Marz W, Greinacher A, Wild PS, Cucca F, Boomsma DI, Watkins H, Tang W, Ridker PM, Jukema JW, Scott RJ, Mitchell P, Hansen T, O'Donnell CJ, Smith NL, Strachan DP and Dehghan A.

Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. *PLoS One*. 2017;12:e0167742.

15. Psaty BM, O'Donnell CJ, Gudnason V, Lunetta KL, Folsom AR, Rotter JI, Uitterlinden AG, Harris TB, Witteman JC, Boerwinkle E and Consortium C. Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: Design of prospective meta-analyses of genome-wide association studies from 5 cohorts. *Circ Cardiovasc Genet*. 2009;2:73-80.

16. 1000 Genomes Project Consortium, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT and McVean GA. An integrated map of genetic variation from 1,092 human genomes. *Nature*. 2012;491:56-65.

17. Winkler TW, Day FR, Croteau-Chonka DC, Wood AR, Locke AE, Magi R, Ferreira T, Fall T, Graff M, Justice AE, Luan J, Gustafsson S, Randall JC, Vedantam S, Workalemahu T, Kilpelainen TO, Scherag A, Esko T, Kutalik Z, Heid IM, Loos RJ and Genetic Investigation of Anthropometric Traits C. Quality control and conduct of genome-wide association meta-analyses. *Nat Protoc*. 2014;9:1192-1212.

18. Willer CJ, Li Y and Abecasis GR. METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics*. 2010;26:2190-2191.

19. Fadista J, Manning AK, Florez JC and Groop L. The (in)famous GWAS P-value threshold revisited and updated for low-frequency variants. *Eur J Hum Genet*. 2016;24:1202-5.

20. Yang J, Lee SH, Goddard ME and Visscher PM. GCTA: a tool for genome-wide complex trait analysis. *Am J Hum Genet*. 2011;88:76-82.

21. Nikpay M, Goel A, Won HH, Hall LM, Willenborg C, Kanoni S, Saleheen D, Kyriakou T, Nelson CP, Hopewell JC, Webb TR, Zeng L, Dehghan A, Alver M, Armasu SM, Auro K, Bjornes A, Chasman DI, Chen S, Ford I, Franceschini N, Gieger C, Grace C, Gustafsson S, Huang J, Hwang SJ, Kim YK, Kleber ME, Lau KW, Lu X, Lu Y, Lyytikainen LP, Mihailov E, Morrison AC, Pervjakova N, Qu L, Rose LM, Salfati E, Saxena R, Scholz M, Smith AV, Tikkanen E,

Uitterlinden A, Yang X, Zhang W, Zhao W, de Andrade M, de Vries PS, van Zuydam NR, Anand SS, Bertram L, Beutner F, Dedoussis G, Frossard P, Gauguier D, Goodall AH, Gottesman O, Haber M, Han BG, Huang J, Jalilzadeh S, Kessler T, Konig IR, Lannfelt L, Lieb W, Lind L, Lindgren CM, Lokki ML, Magnusson PK, Mallick NH, Mehra N, Meitinger T, Memon FU, Morris AP, Nieminen MS, Pedersen NL, Peters A, Rallidis LS, Rasheed A, Samuel M, Shah SH, Sinisalo J, Stirrups KE, Trompet S, Wang L, Zaman KS, Ardissino D, Boerwinkle E, Borecki IB, Bottinger EP, Buring JE, Chambers JC, Collins R, Cupples LA, Danesh J, Demuth I, Elosua R, Epstein SE, Esko T, Feitosa MF, Franco OH, Franzosi MG, Granger CB, Gu D, Gudnason V, Hall AS, Hamsten A, Harris TB, Hazen SL, Hengstenberg C, Hofman A, Ingelsson E, Iribarren C, Jukema JW, Karhunen PJ, Kim BJ, Kooner JS, Kullo IJ, Lehtimaki T, Loos RJF, Melander O, Metspalu A, Marz W, Palmer CN, Perola M, Quertermous T, Rader DJ, Ridker PM, Ripatti S, Roberts R, Salomaa V, Sanghera DK, Schwartz SM, Seedorf U, Stewart AF, Stott DJ, Thiery J, Zalloua PA, O'Donnell CJ, Reilly MP, Assimes TL, Thompson JR, Erdmann J, Clarke R, Watkins H, Kathiresan S, McPherson R, Deloukas P, Schunkert H, Samani NJ and Farrall M. A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nat Genet.* 2015;47:1121-1130.

22. Loley C, Alver M, Assimes TL, Bjornes A, Goel A, Gustafsson S, Hernesniemi J, Hopewell JC, Kanoni S, Kleber ME, Lau KW, Lu Y, Lyytikainen LP, Nelson CP, Nikpay M, Qu L, Salfati E, Scholz M, Tukiainen T, Willenborg C, Won HH, Zeng L, Zhang W, Anand SS, Beutner F, Bottinger EP, Clarke R, Dedoussis G, Do R, Esko T, Eskola M, Farrall M, Gauguier D, Giedraitis V, Granger CB, Hall AS, Hamsten A, Hazen SL, Huang J, Kahonen M, Kyriakou T, Laaksonen R, Lind L, Lindgren C, Magnusson PK, Marouli E, Mihailov E, Morris AP, Nikus K, Pedersen N, Rallidis L, Salomaa V, Shah SH, Stewart AF, Thompson JR, Zalloua PA, Chambers JC, Collins R, Ingelsson E, Iribarren C, Karhunen PJ, Kooner JS, Lehtimaki T, Loos RJ, Marz W, McPherson R, Metspalu A, Reilly MP, Ripatti S, Sanghera DK, Thiery J, Watkins H, Deloukas P, Kathiresan S, Samani NJ, Schunkert H, Erdmann J and Konig IR. No

Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. *Scientific reports*. 2016;6:35278.

23. Malik R, Chauhan G, Traylor M, Sargurupremraj M, Okada Y, Mishra A, Rutten-Jacobs L, Giese AK, van der Laan SW, Gretarsdottir S, Anderson CD, Chong M, Adams HHH, Ago T, Almgren P, Amouyel P, Ay H, Bartz TM, Benavente OR, Bevan S, Boncoraglio GB, Brown RD, Jr., Butterworth AS, Carrera C, Carty CL, Chasman DI, Chen WM, Cole JW, Correa A, Cotlarciuc I, Cruchaga C, Danesh J, de Bakker PIW, DeStefano AL, den Hoed M, Duan Q, Engelter ST, Falcone GJ, Gottesman RF, Grewal RP, Gudnason V, Gustafsson S, Haessler J, Harris TB, Hassan A, Havulinna AS, Heckbert SR, Holliday EG, Howard G, Hsu FC, Hyacinth HI, Ikram MA, Ingelsson E, Irvin MR, Jian X, Jimenez-Conde J, Johnson JA, Jukema JW, Kanai M, Keene KL, Kissela BM, Kleindorfer DO, Kooperberg C, Kubo M, Lange LA, Langefeld CD, Langenberg C, Launer LJ, Lee JM, Lemmens R, Leys D, Lewis CM, Lin WY, Lindgren AG, Lorentzen E, Magnusson PK, Maguire J, Manichaikul A, McArdle PF, Meschia JF, Mitchell BD, Mosley TH, Nalls MA, Ninomiya T, O'Donnell MJ, Psaty BM, Pulit SL, Rannikmae K, Reiner AP, Rexrode KM, Rice K, Rich SS, Ridker PM, Rost NS, Rothwell PM, Rotter JI, Rundek T, Sacco RL, Sakaue S, Sale MM, Salomaa V, Sapkota BR, Schmidt R, Schmidt CO, Schminke U, Sharma P, Slowik A, Sudlow CLM, Tanislav C, Tatlisumak T, Taylor KD, Thijs VNS, Thorleifsson G, Thorsteinsdottir U, Tiedt S, Trompet S, Tzourio C, van Duijn CM, Walters M, Wareham NJ, Wassertheil-Smoller S, Wilson JG, Wiggins KL, Yang Q, Yusuf S, Bis JC, Pastinen T, Ruusalepp A, Schadt EE, Koplev S, Bjorkegren JLM, Codoni V, Civelek M, Smith NL, Tregouet DA, Christophersen IE, Roselli C, Lubitz SA, Ellinor PT, Tai ES, Kooner JS, Kato N, He J, van der Harst P, Elliott P, Chambers JC, Takeuchi F, Johnson AD, Sanghera DK, Melander O, Jern C, Strbian D, Fernandez-Cadenas I, Longstreth WT, Jr., Rolfs A, Hata J, Woo D, Rosand J, Pare G, Hopewell JC, Saleheen D, Stefansson K, Worrall BB, Kittner SJ, Seshadri S, Fornage M, Markus HS, Howson JMM, Kamatani Y, Debette S, Dichgans M, Malik R, Chauhan G, Traylor M, Sargurupremraj M, Okada Y, Mishra A, Rutten-Jacobs L, Giese AK, van

der Laan SW, Gretarsdottir S, Anderson CD, Chong M, Adams HHH, Ago T, Almgren P, Amouyel P, Ay H, Bartz TM, Benavente OR, Bevan S, Boncoraglio GB, Brown RD, Jr., Butterworth AS, Carrera C, Carty CL, Chasman DI, Chen WM, Cole JW, Correa A, Cotlarciuc I, Cruchaga C, Danesh J, de Bakker PIW, DeStefano AL, Hoed MD, Duan Q, Engelter ST, Falcone GJ, Gottesman RF, Grewal RP, Gudnason V, Gustafsson S, Haessler J, Harris TB, Hassan A, Havulinna AS, Heckbert SR, Holliday EG, Howard G, Hsu FC, Hyacinth HI, Ikram MA, Ingelsson E, Irvin MR, Jian X, Jimenez-Conde J, Johnson JA, Jukema JW, Kanai M, Keene KL, Kissela BM, Kleindorfer DO, Kooperberg C, Kubo M, Lange LA, Langefeld CD, Langenberg C, Launer LJ, Lee JM, Lemmens R, Leys D, Lewis CM, Lin WY, Lindgren AG, Lorentzen E, Magnusson PK, Maguire J, Manichaikul A, McArdle PF, Meschia JF, Mitchell BD, Mosley TH, Nalls MA, Ninomiya T, O'Donnell MJ, Psaty BM, Pulit SL, Rannikmae K, Reiner AP, Rexrode KM, Rice K, Rich SS, Ridker PM, Rost NS, Rothwell PM, Rotter JI, Rundek T, Sacco RL, Sakaue S, Sale MM, Salomaa V, Sapkota BR, Schmidt R, Schmidt CO, Schminke U, Sharma P, Slowik A, Sudlow CLM, Tanislav C, Tatlisumak T, Taylor KD, Thijs VNS, Thorleifsson G, Thorsteinsdottir U, Tiedt S, Trompet S, Tzourio C, van Duijn CM, Walters M, Wareham NJ, Wassertheil-Smoller S, Wilson JG, Wiggins KL, Yang Q, Yusuf S, Amin N, Aparicio HS, Arnett DK, Attia J, Beiser AS, Berr C, Buring JE, Bustamante M, Caso V, Cheng YC, Choi SH, Chowhan A, Cullell N, Dartigues JF, Delavaran H, Delgado P, Dorr M, Engstrom G, Ford I, Gurpreet WS, Hamsten A, Heitsch L, Hozawa A, Ibanez L, Ilinca A, Ingelsson M, Iwasaki M, Jackson RD, Jood K, Jousilahti P, Kaffashian S, Kalra L, Kamouchi M, Kitazono T, Kjartansson O, Kloss M, Koudstaal PJ, Krupinski J, Labovitz DL, Laurie CC, Levi CR, Li L, Lind L, Lindgren CM, Lioutas V, Liu YM, Lopez OL, Makoto H, Martinez-Majander N, Matsuda K, Minegishi N, Montaner J, Morris AP, Muino E, Muller-Nurasyid M, Norrving B, Ogishima S, Parati EA, Peddareddygari LR, Pedersen NL, Pera J, Perola M, Pezzini A, Pileggi S, Rabionet R, Riba-Llena I, Ribases M, Romero JR, Roquer J, Rudd AG, Sarin AP, Sarju R, Sarnowski C, Sasaki M, Satizabal CL, Satoh M, Sattar N, Sawada N, Sibolt G, Sigurdsson A, Smith A, Sobue K,

Soriano-Tarraga C, Stanne T, Stine OC, Stott DJ, Strauch K, Takai T, Tanaka H, Tanno K, Teumer A, Tomppo L, Torres-Aguila NP, Touze E, Tsugane S, Uitterlinden AG, Valdimarsson EM, van der Lee SJ, Volzke H, Wakai K, Weir D, Williams SR, Wolfe CDA, Wong Q, Xu H, Yamaji T, Sanghera DK, Melander O, Jern C, Strbian D, Fernandez-Cadenas I, Longstreth WT, Jr., Rolfs A, Hata J, Woo D, Rosand J, Pare G, Hopewell JC, Saleheen D, Stefansson K, Worrall BB, Kittner SJ, Seshadri S, Fornage M, Markus HS, Howson JMM, Kamatani Y, Debette S, Dichgans M, Consortium AF, Cohorts for H, Aging Research in Genomic Epidemiology C, International Genomics of Blood Pressure C, Consortium I, Starnet, BioBank Japan Cooperative Hospital G, Consortium C, Consortium E-C, Consortium EP-I, International Stroke Genetics C, Consortium M, Neurology Working Group of the CC, Network NSG, Study UKYLD, Consortium M and Consortium M. Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nat Genet.* 2018;50:524-537.

24. Burgess S, Bowden J, Fall T, Ingelsson E and Thompson SG. Sensitivity Analyses for Robust Causal Inference from Mendelian Randomization Analyses with Multiple Genetic Variants. *Epidemiology.* 2017;28:30-42.

25. Do R, Willer CJ, Schmidt EM, Sengupta S, Gao C, Peloso GM, Gustafsson S, Kanoni S, Ganna A, Chen J, Buchkovich ML, Mora S, Beckmann JS, Bragg-Gresham JL, Chang HY, Demirkan A, Den Hertog HM, Donnelly LA, Ehret GB, Esko T, Feitosa MF, Ferreira T, Fischer K, Fontanillas P, Fraser RM, Freitag DF, Gurdasani D, Heikkila K, Hypponen E, Isaacs A, Jackson AU, Johansson A, Johnson T, Kaakinen M, Kettunen J, Kleber ME, Li X, Luan J, Lytikainen LP, Magnusson PK, Mangino M, Mihailov E, Montasser ME, Muller-Nurasyid M, Nolte IM, O'Connell JR, Palmer CD, Perola M, Petersen AK, Sanna S, Saxena R, Service SK, Shah S, Shungin D, Sidore C, Song C, Strawbridge RJ, Surakka I, Tanaka T, Teslovich TM, Thorleifsson G, Van den Herik EG, Voight BF, Volcik KA, Waite LL, Wong A, Wu Y, Zhang W, Absher D, Asiki G, Barroso I, Been LF, Bolton JL, Bonnycastle LL, Brambilla P, Burnett MS, Cesana G, Dimitriou M, Doney AS, Doring A, Elliott P, Epstein SE, Eyjolfsson GI, Gigante B,

Goodarzi MO, Grallert H, Gravito ML, Groves CJ, Hallmans G, Hartikainen AL, Hayward C, Hernandez D, Hicks AA, Holm H, Hung YJ, Illig T, Jones MR, Kaleebu P, Kastelein JJ, Khaw KT, Kim E, Klopp N, Komulainen P, Kumari M, Langenberg C, Lehtimaki T, Lin SY, Lindstrom J, Loos RJ, Mach F, McArdle WL, Meisinger C, Mitchell BD, Muller G, Nagaraja R, Narisu N, Nieminen TV, Nsubuga RN, Olafsson I, Ong KK, Palotie A, Papamarkou T, Pomilla C, Pouta A, Rader DJ, Reilly MP, Ridker PM, Rivadeneira F, Rudan I, Ruukonen A, Samani N, Scharnagl H, Seeley J, Silander K, Stancakova A, Stirrups K, Swift AJ, Tirit L, Uitterlinden AG, van Pelt LJ, Vedantam S, Wainwright N, Wijmenga C, Wild SH, Willemsen G, Wilsgaard T, Wilson JF, Young EH, Zhao JH, Adair LS, Arveiler D, Assimes TL, Bandinelli S, Bennett F, Bochud M, Boehm BO, Boomsma DI, Borecki IB, Bornstein SR, Bovet P, Burnier M, Campbell H, Chakravarti A, Chambers JC, Chen YD, Collins FS, Cooper RS, Danesh J, Dedoussis G, de Faire U, Feranil AB, Ferrieres J, Ferrucci L, Freimer NB, Gieger C, Groop LC, Gudnason V, Gyllenstein U, Hamsten A, Harris TB, Hingorani A, Hirschhorn JN, Hofman A, Hovingh GK, Hsiung CA, Humphries SE, Hunt SC, Hveem K, Iribarren C, Jarvelin MR, Jula A, Kahonen M, Kaprio J, Kesaniemi A, Kivimaki M, Kooner JS, Koudstaal PJ, Krauss RM, Kuh D, Kuusisto J, Kyvik KO, Laakso M, Lakka TA, Lind L, Lindgren CM, Martin NG, Marz W, McCarthy MI, McKenzie CA, Meneton P, Metspalu A, Moilanen L, Morris AD, Munroe PB, Njolstad I, Pedersen NL, Power C, Pramstaller PP, Price JF, Psaty BM, Quertermous T, Rauramaa R, Saleheen D, Salomaa V, Sanghera DK, Saramies J, Schwarz PE, Sheu WH, Shuldiner AR, Siegbahn A, Spector TD, Stefansson K, Strachan DP, Tayo BO, Tremoli E, Tuomilehto J, Uusitupa M, van Duijn CM, Vollenweider P, Wallentin L, Wareham NJ, Whitfield JB, Wolfenbittel BH, Altshuler D, Ordovas JM, Boerwinkle E, Palmer CN, Thorsteinsdottir U, Chasman DI, Rotter JI, Franks PW, Ripatti S, Cupples LA, Sandhu MS, Rich SS, Boehnke M, Deloukas P, Mohlke KL, Ingelsson E, Abecasis GR, Daly MJ, Neale BM and Kathiresan S. Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nat Genet.* 2013;45:1345-1352.

26. Song J, Xue C, Preisser JS, Cramer DW, Houck KL, Liu G, Folsom AR, Couper D, Yu F and Dong JF. Association of Single Nucleotide Polymorphisms in the ST3GAL4 Gene with VWF Antigen and Factor VIII Activity. *PLoS One*. 2016;11:e0160757.
27. Sudhof TC. The synaptic vesicle cycle: a cascade of protein-protein interactions. *Nature*. 1995;375:645-653.
28. Lowenstein CJ, Morrell CN and Yamakuchi M. Regulation of Weibel-Palade body exocytosis. *Trends in cardiovascular medicine*. 2005;15:302-308.
29. Buechler C, Bodzioch M, Bared SM, Sigruener A, Boettcher A, Lapicka-Bodzioch K, Aslanidis C, Duong CQ, Grandl M, Langmann T, Dembinska-Kiec A and Schmitz G. Expression pattern and raft association of NIPSNAP3 and NIPSNAP4, highly homologous proteins encoded by genes in close proximity to the ATP-binding cassette transporter A1. *Genomics*. 2004;83:1116-1124.
30. Han HJ, Sudo K, Inazawa J and Nakamura Y. Isolation and mapping of a human gene (RABL) encoding a small GTP-binding protein homologous to the Ras-related RAB gene. *Cytogenetics and cell genetics*. 1996;73:137-139.
31. Warton K, Foster NC, Gold WA and Stanley KK. A novel gene family induced by acute inflammation in endothelial cells. *Gene*. 2004;342:85-95.
32. Twyffels L, Gueydan C and Kruys V. Transportin-1 and Transportin-2: protein nuclear import and beyond. *FEBS Lett*. 2014;588:1857-1868.
33. Krucken J, Schroetel RM, Muller IU, Saidani N, Marinovski P, Benten WP, Stamm O and Wunderlich F. Comparative analysis of the human gimap gene cluster encoding a novel GTPase family. *Gene*. 2004;341:291-304.
34. Lacroix-Desmazes S, Repesse Y, Kaveri SV and Dasgupta S. The role of VWF in the immunogenicity of FVIII. *Thromb Res*. 2008;122 Suppl 2:S3-6.
35. De Meyer SF, De Maeyer B, Deckmyn H and Vanhoorelbeke K. Von Willebrand factor: drug and drug target. *Cardiovascular & hematological disorders drug targets*. 2009;9:9-20.

36. De Meyer SF, Stoll G, Wagner DD and Kleinschnitz C. von Willebrand factor: an emerging target in stroke therapy. *Stroke*. 2012;43:599-606.
37. Gragnano F, Sperlongano S, Golia E, Natale F, Bianchi R, Crisci M, Fimiani F, Pariggiano I, Diana V, Carbone A, Cesaro A, Concilio C, Limongelli G, Russo M and Calabro P. The Role of von Willebrand Factor in Vascular Inflammation: From Pathogenesis to Targeted Therapy. *Mediators Inflamm*. 2017;2017:5620314.
38. Mannucci PM. Platelet/von Willebrand factor inhibitors to the rescue of ischemic stroke. *Arterioscler Thromb Vasc Biol*. 2010;30:1882-1884.
39. O'Sullivan JM, Aguila S, McRae E, Ward SE, Rawley O, Fallon PG, Brophy TM, Preston RJ, Brady L, Sheils O, Chion A and O'Donnell JS. N-linked glycan truncation causes enhanced clearance of plasma-derived von Willebrand factor. *J Thromb Haemost*. 2016;14:2446-2457.
40. Burgess S, Davies NM and Thompson SG. Bias due to participant overlap in two-sample Mendelian randomization. *Genet Epidemiol*. 2016;40:597-608.

Table 1: Main association results for FVIII and VWF trans-ethnic GWAS meta-analysis.

rsID	Effect Allele	Other Allele	Freq FVIII	N FVIII	Beta FVIII	P FVIII	Freq VWF	N VWF	Beta VWF	P VWF	Closest Gene(s)	Association	vWF Release at Baseline (B) and upon Stimulation (S) for Candidate Loci
rs55954186	a	g	0.36	35,513	0.011	2.2E-05	0.37	46,229	0.015	5.2E-09	<i>PDHB, PXX, KCTD6</i>	New	<i>PDHB</i> (B=↑**; S=ns), <i>PXX</i> (B=ns; S=ns), <i>KCTD6</i> (B=ns; S=ns)
rs6855246	a	g	0.93	35,513	0.003	0.672	0.92	46,068	-0.034	8.68E-10	<i>SLC39A8</i> †	New	<i>SLC39A8</i> (B=↑**)
rs548630	a	c	0.49	36,286	0.016	2.1E-10	0.47	46,137	-0.018	1.2E-12	<i>FCHO2, TMEM171, TNPO1</i>	New	<i>FCHO</i> (B=ns; S=ns), <i>TMEM171</i> (B=↑***; S=↑*), <i>TNPO1</i> (B=↑***; S=↑**)
rs9390460	t	c	0.47	36,286	0.019	2.2E-15	0.46	46,212	-0.033	5.6E-42	<i>STXBP5</i>	Known	-
rs9271597 ‡	a	t	0.41	28,203	0.015	1.4E-08	0.41	31,364	-0.012	2.1E-04	<i>HLA region</i>	New	<i>HLA-C</i> (B=↑**; S=↑***)
rs7788962	a	g	0.62	33,773	0.010	2.3E-04	0.61	46,231	-0.014	7.3E-09	<i>GIMAP7, GIMAP4</i>	New	<i>GIMAP7</i> (B=↑***; S=ns), <i>GIMAP4</i> (B=ns; S=ns)
rs4276643	t	c	0.66	36,286	0.023	1.3E-19	0.67	44,168	-0.029	8.8E-28	<i>SCARA5</i>	Known	-
rs10102164	a	g	0.19	36,286	0.019	2.4E-09	0.20	46,230	0.009	2.9E-03	<i>SOX17, RPI</i>	New	Too little FVIII released by endothelial cells to be detected <i>in vitro</i>
rs6479259	t	c	0.73	28,535	0.021	1.1E-03	0.73	24,987	-0.056	1.5E-08	<i>OR13C5, NIPSNAP</i> §	New	<i>NIPSNAP3A</i> (B=↑*; S=↑**), <i>NIPSNAP3B</i> (B=↑*; S=ns)
rs10985344	a	g	0.25	36,286	0.011	7.5E-05	0.25	46,178	0.017	3.5E-09	<i>DAB2IP</i>	New	<i>DAB2IP</i> (B=ns; S=ns)
rs687289	a	g	0.36	36,286	0.145	1.9E-770	0.33	46,231	0.197	5.0E-1443	<i>ABO</i>	Known	-
9:13930481: ID	d	i	0.85	22,480	0.032	2.7E-10	0.85	29,409	-0.003	4.4E-01	<i>LINC00583, NFIB</i>	New	Too little FVIII released by endothelial cells to be detected <i>in vitro</i>
rs35458154	a	g	0.03	33,871	0.048	3.1E-08	0.03	44,020	0.060	3.0E-12	<i>ST3GAL4</i>	Known	<i>ST3GAL4</i> (B=↓**; S=ns)
rs4981022	a	g	0.69	36,286	0.025	3.0E-20	0.69	46,232	0.035	6.6E-41	<i>STAB2</i>	Known	-
rs4759787	a	c	0.40	36,286	0.011	1.1E-05	0.37	46,180	0.023	7.7E-20	<i>STX2</i>	Known	-
rs2238109	a	t	0.39	36,286	0.026	3.5E-24	0.38	46,232	0.050	1.8E-89	<i>VWF</i>	Known	-
rs4904820	a	g	0.49	36,286	0.014	1.8E-08	0.47	46,232	0.022	6.0E-19	<i>TCN2</i>	Known	-
rs6494314	t	c	0.18	36,286	0.007	2.4E-02	0.17	46,232	-0.018	1.1E-08	<i>C2CD4B</i>	New	<i>C2CD4B</i> (B=↑*; S=↑**)
rs1869365			Significant in combined multiphenotype analysis							<5.0E-8	<i>RAB5C, KAT2A</i>	New	<i>RAB5C</i> (B=ns; S=↓*), <i>KAT2A</i> (B=ns; S=↑**)
rs2277998	a	g	0.30	33,097	0.010	4.4E-04	0.30	45,566	-0.022	6.5E-16	<i>CLEC4M</i>	Known	-
rs5750823 #	t	c	0.70	36,286	0.013	1.5E-06	0.72	46,230	-0.020	6.0E-14	<i>RPL3, TAB1, SYNGR1, PDGB</i>	New	<i>TAB1</i> (B=ns; S=↑**), <i>SYNGR1</i> (B=↑*; S=ns), <i>PDGFB</i> (B=ns; S=ns)
rs9616897			Significant in combined multiphenotype analysis							<5.0E-8	<i>ARSA</i>	New	<i>ARSA</i> (B=ns; S=ns)
rs150926226 ¶	c	g	0.62	20,537	0.017	3.3E-09	0.65	28,685	-0.005	7.0E-02	<i>TMLHE, F8</i>	Known	Too little FVIII released by endothelial cells to be detected <i>in vitro</i>

Footnotes: “Freq” refers to the allele frequency of the effect allele. “B” = baseline; “S” = stimulated; “ns” = not significant; *p-value<0.05; **p-value<0.01; ***p-value<0.001.

Beta and Frequency refer always to the Effect_allele, and they are expressed as natural-log transformed values from the original units (reported in % or IU/ml*100 units).

†SLC39A8 was found in vWF meta-analysis of EA only (N=42,145).

‡ Although not in LD with this variant, a low-frequency variant 665Kb upstream rs9271597 was found significantly associated to vWF levels (rs80082277; p=1x10-8) and we consider it within the HLA region; thus, we pursued this gene for further functional validation.

§Olfactory receptor family was not considered for further functional validation for its low expression in the relevant tissues (mainly artery and whole blood).
|| The *ST3GAL4* locus was new at the time of analyses, although reported in a recent candidate gene study lacking replication (PMID: 27584569).
The highest associated SNP in this locus for FVIII is rs137631 ($p=9.5 \times 10^{-9}$), located close to **RPL3 gene**, 112Kb downstream TAB1/SYNGR1 locus and in low LD with rs5750823 ($R^2=0.14$)
¶ Chromosome X variant for VWF only available for EU samples (N=28.685).

Table 2: Characteristics of all associated independent variants after conditional analyses.

MarkerName	rsID	Closest Gene(s)	variant position	putative functional	EUR-only	TRANS-ethnic	Top Meta variant	LD† (r2)	LD* (D')		
					Original P-value	Conditional P-value	Original P-value	Conditional P-value			
FVIII (n=29,573 EUR; n=36,286 TRANS)											
5:72406659	rs548630	TNPO1; FCHO2; TMEM171	9.5 kb 5' TMEM171		5.14E-10	3.96E-10	2.10E-10	2.06E-10	5:72406659	Top variant	Top variant
6:147701217	rs9390461	STXBP5	intronic	rs1039084, missense	2.74E-13	4.06E-13	1.73E-14	-	6:147703299	0.98	1.00
6:147703299	rs9399599	STXBP5	intronic	rs1039084, missense	3.73E-13	-	1.41E-15	4.70E-16	6:147703299	Top variant	Top variant
8:27778148	rs55829013	SCARA5	intronic		3.39E-10	8.54E-10	5.81E-10	-	8:27805815	0.51	0.77
8:27823832	rs11780263	SCARA5	intronic		3.41E-17	6.96E-17	1.39E-19	-	8:27805815	0.10	0.98
8:27805815	rs7816579	SCARA5	intronic	SiPhy conserved	5.32E-16	-	6.52E-21	4.07E-21	8:27805815	Top variant	Top variant
8:55421614	rs10102164	SOX17; RP1	intergenic		1.66E-07	-	2.38E-09	2.44E-09	8:55421614	Top variant	Top variant
9:13930481:ID	rs35468074	LINC00583	intronic		1.74E-10	1.24E-10	2.66E-10	3.10E-10	9:13930481:ID	Top variant	Top variant
9:136116662	rs11793768	ABO	14 Kb 3' ABO		3.74E-13	1.29E-62	2.16E-13	-	9:136132908:ID	0.08	0.72
9:136137065	rs687621	ABO	intronic		1.18E-647	p<1E-320	6.85E-778	-	9:136132908:ID	0.89	0.98
9:135976698	rs35108384	ABO	intronic		4.58E-12	-	2.24E-12	6.53E-12	9:136132908:ID	0.00	0.14
9:136114000	rs78490142	ABO	17 kb 3' ABO		1.12E-03	-	6.53E-05	1.48E-13	9:136132908:ID	0.01	1.00
9:136132908:ID	rs8176719	ABO	intronic	SiPhy conserved	1.62E-307	-	3.52E-403	p<1E-320	9:136132908:ID	Top variant	Top variant
9:136178821	rs574237	ABO	intergenic		2.89E-29	-	6.94E-38	5.38E-26	9:136132908:ID	0.01	0.18
9:136181539	rs551924	ABO	intergenic		2.81E-48	-	9.21E-75	2.20E-63	9:136132908:ID	0.00	0.14
9:136207218	rs607900	ABO	intergenic	rs116779216, missense SURF1	6.86E-03	-	3.21E-15	1.85E-13	9:136132908:ID	0.00	0.19
9:136255149	rs62575992	ABO	intergenic		3.46E-42	-	8.45E-45	1.83E-26	9:136132908:ID	0.02	0.80
9:136344853	rs3124758	ABO	intergenic		2.71E-21	-	1.74E-18	5.88E-15	9:136132908:ID	0.00	0.14
12:6062894	rs57040304	VWF	intronic	rs7962217, missense, SiPhy cons	1.51E-15	1.22E-14	7.71E-12	-	12:6160614	0.00	0.09

12:6160614	rs7135039	VWF	intronic	rs1063856, missense	3.00E-19	7.02E-18	2.32E-24	7.21E-20	12:6160614	Top variant	Top variant
12:6070845	rs12423482	VWF	intronic	rs7962217, missense, SiPhy cons	2.49E-15	-	2.92E-18	1.57E-17	12:6160614	0.00	0.15
12:6160146	rs11064010	VWF	intronic		8.36E-07	-	2.41E-11	2.51E-09	12:6160614	0.01	0.33
12:104000319	rs1070073	STAB2	intronic		1.07E-13	5.04E-13	2.25E-14	-	12:104149874	0.00	0.16
12:104147207	rs3751198	STAB2	intronic		2.16E-17	5.91E-17	5.88E-18	-	12:104149874	0.70	0.98
12:104000470	rs2723889	STAB2	intronic		1.08E-13	-	2.14E-14	1.21E-14	12:104149874	0.00	0.16
12:104149874	rs4981022	STAB2	intronic		1.16E-17	-	2.95E-20	4.47E-21	12:104149874	Top variant	Top variant
14:92268531	rs10498631	TC2N	intronic		6.69E-09	8.63E-09	2.30E-08	-	14:92302972	0.54	0.82
14:92302972	rs58204830	TC2N	intronic		2.57E-08	-	6.28E-09	7.03E-09	14:92302972	Top variant	Top variant
22:39717706	rs137631	RPL3	1.3Kb 5' of RPL3		2.35E-07	-	9.48E-09	1.34E-08	22:39717706	Top variant	Top variant
X:154721357	rs150926226	TMLHE,F8				‡	3.25E-09	‡	X:154721357	-	-

VWF (n=42,256 EUR; n=46,232 TRANS)

3:58383174	rs55692656	PXK; KCTD6; PDHB	intronic PXK	rs56384862, missense PXK; rs34579268 missense PXK; rs200687616 frameshift PDHB	6.48E-09	1.01E-08	3.33E-08	-	3:58436476	0.94	1.00
3:58436476	rs55954186	PXK; KCTD6; PDHB	17 kb 3' of PXK	rs56384862, missense PXK; rs34579268 missense PXK; rs200687616 frameshift PDHB	8.72E-09	-	5.20E-09	8.06E-09	3:58436476	Top variant	Top variant
5:72403453	rs7733340	TNPO1; FCHO2; TMEM171	intergenic		5.80E-13	1.52E-12	3.40E-12	-	5:72406659	0.93	0.99
5:72406659	rs548630	TNPO1; FCHO2; TMEM171	9.5 kb 5' TMEM171		1.33E-12	-	1.22E-12	6.19E-13	5:72406659	Top variant	Top variant
6:31192766	rs9263993	HLA region	intergenic		8.54E-09	3.50E-09	1.69E-07	-	6:31925848	0.00	0.63
6:31941629	rs116420479	HLA region	intronic STK19		3.10E-08	1.49E-08	1.02E-08	-	6:31925848	0.94	0.98

6:31158633	rs9263861	HLA region	intergenic		3.08E-08	-	3.25E-08	8.64E-09	6:31925848	0.00	1.00
6:31906828	rs78593564	HLA region	intronic C2		3.15E-08	-	1.03E-08	2.76E-09	6:31925848	1.00	1.00
6:147694334	rs9390460	STXBP5	intronic	rs1039084, missense	6.32E-38	1.67E-38	5.58E-42	1.27E-42	6:147694334	Top variant	Top variant
7:150296496	rs13230842	GIMAP7; GIMAP4	intergenic		2.06E-08	1.96E-08	2.95E-08	-	7:150227227	0.18	0.97
7:150227227	rs7788962	GIMAP7; GIMAP4	9.1Kb 3' of GIMAP7		6.29E-08	-	7.30E-09	1.36E-08	7:150227227	Top variant	Top variant
8:27803599	rs4276643	SCARA5	intronic		5.77E-27	1.19E-29	8.77E-28	7.69E-31	8:27803599	Top variant	Top variant
8:27815481	rs62496810	SCARA5	intronic		3.74E-08	4.38E-11	4.98E-08	6.04E-11	8:27803599	0.02	1
9:124416940	rs10985344	DAB2IP	intronic		4.11E-09	3.76E-09	3.47E-09	-	9:124416940	Top variant	Top variant
9:124421965	rs4837886	DAB2IP	intronic		3.84E-09	-	4.43E-09	3.94E-09	9:124416940	0.79	0.97
9:135919501	rs138796740	ABO	intergenic		2.61E-08	7.06E-11	3.59E-08	-	9:136132908:ID	0.00	0.15
9:136128546	rs7857390	ABO	2.5Kb 3' of ABO		p<1E-320	7.81E-294	2.15E-393	-	9:136132908:ID	0.36	1
9:136145414:ID	rs202001822	ABO	intronic		5.90E-78	1.46E-39	2.26E-80	-	9:136132908:ID	0.10	1
9:136147553	rs660340	ABO	intronic		p<1E-320	p<1E-320	1.11E-492	-	9:136132908:ID	0.33	0.87
9:136177394	rs656105	ABO	intergenic		1.20E-66	2.62E-129	4.23E-73	-	9:136132908:ID	0.02	0.19
9:136128000	rs10901252	ABO	3.1 Kb 3' of ABO	rs8176747, missense; rs8176746, missense; rs8176743 missense	1.78E-291	-	2.61E-351	p<1E-320	9:136132908:ID	0.16	0.99
9:136130677	rs62641786	ABO	3'UTR		2.79E-96	-	2.59E-106	8.85E-30	9:136132908:ID	0.03	0.91
9:136138765:ID	rs8176685	ABO	intronic		p<1E-320	-	5.95E-507	p<1E-320	9:136132908:ID	0.31	1
9:136316367	rs28680325	ABO	intronic ADAMTS13		1.04E-09	-	2.88E-10	1.12E-09	9:136132908:ID	0.01	0.25
11:126296825	rs35458154	ST3GAL4	intronic		6.35E-12	8.31E-12	2.96E-12	2.42E-12	11:126296825	Top variant	Top variant
12:6157394	rs2283335	VWF	intronic	rs1063856, missense	6.48E-83	5.55E-79	2.08E-89	-	12:6153967	1	1
12:6160146	rs11064010	VWF	intronic		1.60E-27	8.75E-22	7.90E-27	2.40E-21	12:6153967	0.01	0.30
12:6225931	rs112814955	VWF	intronic		1.43E-42	3.14E-49	9.02E-43	4.00E-50	12:6153967	0.01	0.34
12:6153967	rs2238109	VWF	intronic	rs1063856, missense	1.37E-82	-	1.77E-89	3.41E-87	12:6153967	Top variant	Top variant
12:104000319	rs1070073	STAB2	intronic		2.28E-36	8.23E-31	2.03E-36	6.72E-32	12:104149874	0.00	0.16
12:104007418	rs11111679	STAB2	intronic		2.31E-14	4.79E-10	1.22E-14	1.60E-10	12:104149874	0.00	0.02
12:104127353	rs73192004	STAB2	intronic	rs17034433, missense	2.29E-08	2.33E-08	5.09E-09	6.57E-09	12:104149874	0.01	0.53

12:104149874	rs4981022	STAB2	intronic		5.44E-37	4.69E-41	6.57E-41	8.65E-45	12:104149874	Top variant	Top variant
12:131287011	rs6486599	STX2	intronic	rs17564, missense	4.23E-18	1.92E-18	1.14E-18	-	12:131290180	1.00	1
12:131290180	rs4759787	STX2	intronic	rs17564, missense	4.45E-18	-	7.73E-20	3.84E-20	12:131290180	Top variant	Top variant
14:92290744	rs10498632	TCN2	intronic		2.58E-18	4.74E-18	5.00E-18	-	14:92318935	0.53	0.99
14:92318935	rs4904820	TCN2	intronic		8.30E-18	-	6.04E-19	2.40E-19	14:92318935	Top variant	Top variant
15:62455019	rs6494314	C2CD4B	700bp 3' of gene	rs8040712, missense	9.63E-08	-	1.14E-08	1.30E-08	15:62455019	Top variant	Top variant
19:7831628	rs2277998	CLEC4M	missense	rs2277998, missense	2.02E-15	7.30E-16	6.47E-16	1.74E-15	19:7831628	Top variant	Top variant
22:39790191	rs2413590	PFGFB; SYNGR1; TAB1	5.6Kb of TAB1		3.96E-12	4.44E-12	2.02E-12	-	22:39829973	0.75	0.94
22:39829973	rs5750823	PFGFB; SYNGR1; TAB1	intronic TAB1		2.98E-11	-	5.95E-14	7.58E-14	22:39829973	Top variant	Top variant

Footnotes: †LD with top variant in the region, calculated using FHS data. ‡Primary SNP was not well imputed in FHS and no other SNPs in the region

achieved genome-wide significance in conditional analyses. “slct pJ” = joint p-value from GCTA “slct”. “Original p-value” = p-value from discovery meta-analysis. The putative functional column indicates the best candidate variant in high linkage disequilibrium with the associated variant ($R^2 > 0.8$) that has been identified *in silico* as the best candidate variant to have an impact on the adjacent gene/s. No functional work was performed in known genes, and these are symbolized by “-” in the last column.

Figure Legends

Figure 1A: Manhattan plot for the trans-ethnic analyses FVIII. Representation of genome-wide results. Loci named by closest gene. In black, novel associations.

Figure 1B: Manhattan plot for the trans-ethnic analyses VWF. Representation of genome-wide results. Loci named by closest gene. In black, novel associations.

Figure 2A. Silencing candidate genes changes basal release of VWF.

HUVEC cells were transfected with siRNA against selected genes for 4 days, the media was changed, cells were cultured for 30 min, and VWF was measured in the supernatant via ELISA. $n = 4 \pm \text{S.D.}$ * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. All results are relative to VWF release after transfection with a scrambled control siRNA, which is set as reference (100%).

Figure 2B. Silencing candidate genes changes stimulated release of VWF.

HUVEC cells were transfected with siRNA against selected genes for 4 days, the media was changed, cells were stimulated with histamine 10 μM for 30 min, and VWF was measured in the supernatant by an ELISA. $n = 4 \pm \text{S.D.}$ * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. All results are relative to VWF release after transfection with a scrambled control siRNA, which is set as reference (100%).

Figure 3. Mendelian Randomization results. Results show OR (95% confidential interval) per every higher standard deviation change in FVIII (Figure 3A) and VWF. (Figure 3B). CAD

(Coronary Artery Disease), IVW(inverse-variance weighted method), IVW.adjusted (IVW FVIII adjusted for the effects of VWF).