

additional smaller association signals at *VWF* and six other loci (20). However, the total variance in plasma VWF explained by all of the significant loci in this study was estimated at only 12.8%, notably less than the heritability estimates of 32–75% previously reported in literature.

To identify additional quantitative trait loci (QTL) for VWF antigen variation and to minimize the impact of age and illness-related environmental factors, we studied two independent healthy young cohorts, the Genes and Blood-Clotting Study (GABC, $n = 1,152$) and the Trinity Student Study (TSS, $n = 2,310$) (21–23). In addition to confirming the association signals at *ABO* and *VWF*, linkage analysis identified a previously unidentified QTL on chromosome 2 (Chr2) that was undetected in our GWAS or previous studies. This locus explains 19.2% of additional plasma VWF variance and suggests that the use of cohorts with family structure can identify missing genetic determinants for other complex traits with similar allelic architecture.

Results

Study Cohorts. Table 1 displays demographic information for the two study cohorts. The median age of participants was 21 y (Q1:19, Q3:23) for the GABC cohort and 22 y (Q1:21, Q3:24) for the TSS. Although the TSS cohort was 100% ethnically Irish, the GABC cohort was of mixed ancestry, consistent with the University of Michigan student population from which participants were recruited (24). Genotyping data identified 81.5% (940 of 1,152) of the GABC cohort as European ancestry, in close agreement with self-report. Of the 502 GABC families (1,152 individuals) who passed genotyping quality control, 13 were singletons, 366 were pairs, and 94, 22, 5, and 2 were comprised of 3, 4, 5, and 6 members, respectively. In the TSS cohort, 2,310 participants were successfully genotyped, including 71 sibling pairs and one sibling trio, for a total of 145 full siblings.

VWF Antigen Levels. *SI Appendix, Fig. S1* displays the distribution of untransformed VWF antigen levels. The median VWF levels were 108.1 IU/dL and 108.4 IU/dL for the GABC and TSS cohorts, respectively (Table 1). The 5th and 95th percentiles of the distribution spanned a 3.4-fold difference, from 54.3 IU/dL to 187.1 IU/dL (GABC), and 3.2-fold difference, from 59.1 IU/dL to 187.2 IU/dL (TSS). There was no significant difference in the distributions of VWF levels between GABC and TSS (Kolmogorov–Smirnov test, $P = 0.16$). Although 23% were regular tobacco smokers (4.8% GABC, 32% TSS) based on self-report and confirmed with serum cotinine levels (TSS only), there was no significant difference in the distribution of VWF levels between smokers and nonsmokers (Kolmogorov–Smirnov test, $P = 0.40$). Narrow sense heritability (h^2) of the VWF antigen level in the combined GABC and TSS dataset was first estimated by using the known sibship relationships, yielding an intraclass correlation-based upper-bound estimate of 64.5%. This finding is consistent with the estimates derived from the genome-wide genotyping data for all individuals: 66.3% using MERLIN, and 64.9% using GCTA (*Materials and Methods*) (25, 26).

Association Studies, GABC Cohort. In the GABC dataset, 38 SNPs were significantly associated with VWF antigen level ($P < 5.0E-8$) after adjustment for age, sex, and population structure (*SI Appendix, Fig. S2A*). All 38 SNPs reside in a 300-kb region on Chr 9q34, with 31 of 38 located within the *ABO* gene (*SI Appendix, Fig. S2B*), consistent with the association signal for *ABO* reported in a previous meta-analysis (20). The G allele of the top SNP, rs687289, was associated with decreased VWF antigen level and tags the O allele of *ABO* ($\beta = -0.36 \pm 0.022$ IU/dL per allele in an additive model, $P = 1.7E-52$) (*SI Appendix, Table S1*), consistent with the known association between type O blood group and the shorter half-life of VWF. The lowest P value outside of the 9q34-associated region was $1.5E-7$, not reaching genome-wide significance. The Q-Q plot (*SI Appendix, Fig. S2C*) of observed versus expected $-\log_{10}(P$ value) demonstrates a large deviation from expectation as a result of the significant signals at the *ABO* locus (in red) and a slight signal inflation, possibly because of family structure. As the initial analysis treated all samples as unrelated, we applied multiple approaches to examine the impact of sample relatedness. These approaches include GWAF (genome-wide association analyses with family data) and EMMAX (*Materials and Methods*), the former using a linear mixed effect model and the latter using a variance components-based model. Log-scatter pair-wise comparisons (*SI Appendix, Fig. S2D and E*) and Q-Q plot comparisons (*SI Appendix, Fig. S2F and G*) showed that results obtained by considering relatedness were highly similar to those not considering relatedness. We therefore proceeded to use the original results (assuming unrelated samples) in the meta-analysis below.

Association Studies, TSS Cohort. The TSS cohort revealed two significantly associated regions (*SI Appendix, Fig. S3A*), with 31 SNPs overlapping the *ABO* locus (*SI Appendix, Fig. S3B*) and 10 SNPs overlapping the *VWF* gene (*SI Appendix, Fig. S3C*). The Q-Q plot (*SI Appendix, Fig. S3D*) of observed versus expected $-\log_{10}(P$ value) exhibits a large deviation from expectation as a result of the significant signals at the *ABO* and *VWF* loci. The association statistics for the lead SNPs are shown in *SI Appendix, Table S2*. The top *ABO* SNP in TSS, rs687289, was the same as the top *ABO* SNP in GABC, and demonstrated a similar effect size for the G allele ($\beta = -0.33 \pm 0.016$, $P = 3.7E-89$). In the *VWF* region, the highest associated SNP was rs1063856 ($\beta = -0.12 \pm 0.015$, $P = 8.5E-14$). This SNP did not reach genome-wide significance in GABC ($\beta = 0.095 \pm 0.024$, $P = 1.1E-4$) likely because of the latter's 2.4-fold smaller sample size compared with TSS.

Meta-Analysis of GABC and TSS. Seventy-three SNPs were significantly associated ($P < 5.0E-8$) with VWF level in the meta-analysis of GABC and TSS (Fig. 1 and Table 2). These SNPs collectively explained ~18.7% of the VWF level variation in an analysis using GCTA (a tool for genome-wide complex trait analysis). Of the 73 SNPs, 58 were in the associated region surrounding the *ABO* gene (including *ADAMTS13*) (*SI Appendix, Fig. S4A*), with the remaining 15 overlapping the *VWF* locus (*SI Appendix, Fig. S4B*). The strongest signal outside of the *ABO* and

Table 1. Characteristics of study participants

Cohort	GABC	TSS
Subject counts, n	1,152	2,310
Age, y (Q1, Q3)	21 (19, 23)	22 (21, 24)
Female (%)	721 (63)	1,310 (59)
Weight, lb (Q1, Q3)	145 (125, 165)	148 (133, 167)
Body mass index, kg/m ² (Q1, Q3)	22.5 (20.7, 25.0)	22.6 (21.0, 24.4)
Current smoker, n /total cohort (%)	55/1,152 (4.8)	737/2,299 (32.1)
Sibship size, (n sibships)	2 (366); 3 (94); 4 (22); 5 (5); 6 (2)	2 (71); 3 (1)
VWF, IU/dL (Q1, Q3)	108.1 (78.3, 129.7)	108.4 (79.3, 128.2)

Median values for age, weight, body mass index, and VWF levels are reported with quartiles in parentheses.

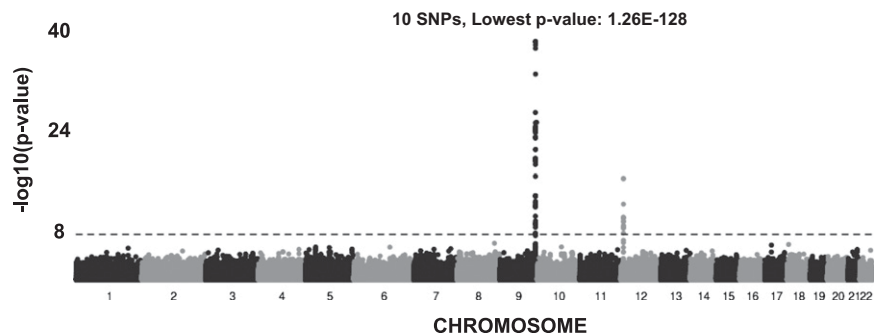


Fig. 1. GABC and TSS association meta-analysis (~724 K SNPs) using age-, sex-, and principal component-adjusted VWF values. Genome-wide $-\log_{10}(P$ value) plot. The horizontal line marks the $5E-08$ threshold of genome-wide significance.

VWF loci had a P value of $1.3E-6$, not reaching genome-wide significance.

Thirty-nine of the 73 significant SNPs in the meta-analysis were not significant in the GABC cohort, whereas 12 of the 73 were not significant in TSS. However, the allelic effect sizes and directions of the top SNPs in each cohort showed excellent agreement (*SI Appendix, Fig. S5*). R^2 values were 0.95 and 0.90 for the β -values of the top 38 GABC and top 49 TSS SNPs, respectively, suggesting that the apparent difference in significance levels are mainly due to sample size differences.

Conditional Analysis. To screen for potential secondary signals masked by the strong primary signal at *ABO*, the top SNP, rs687289, was introduced as a covariate in a conditional association analysis in the joint set of GABC and TSS cohorts (*SI Appendix, Fig. S6 A and D*). A new signal emerged at chromosome 9 in the *ABO* locus, with rs8176704 as the lead SNP ($P = 4.1E-34$), which was not significant in the original test ($P = 0.18$) (*SI Appendix, Fig. S6 B and C*). The A allele of rs8176704 tags the A2 allele of *ABO* and is associated with a decrease in VWF levels ($\beta = -0.34$), consistent with the hypomorphic effect of the A2 allele. The significant SNPs in the *ADAMTS13* locus in the meta-analysis were no longer significant in the conditional analysis, suggesting that the *ADAMTS13* signal may be because of its linkage disequilibrium with *ABO*. No other new significant genome-wide signals were detected in the conditional analysis.

ABO Haplotype Effects. Four major ABO SNP haplotypes, tagged by three ABO SNPs: rs8176704, rs8176749, and rs687289 (27), determine the majority of the ABO blood group serotypes (A1, A2, B, and O). We investigated their association with VWF antigen levels. Using the haplotypes inferred from genotype data we

deduced each subject's most likely ABO serotypes. The overall ABO blood group allele frequencies were similar to those reported in the Atherosclerosis Risk in Communities Study (ARIC) (28) and Framingham Heart Study (FHS) (29) cohort (Table 3), and were in concordance with the expected frequencies in populations with European ancestry (30). As expected, the A1 and B alleles were positively and significantly associated with the VWF antigen levels ($\beta = 0.36$ and $P = 3.5E-98$; $\beta = 0.36$ and $P = 7.2E-50$, respectively) and O and A2 alleles were negatively associated, but only the O allele was significant ($\beta = -0.34$ and $P = 2.3E-138$; $\beta = -0.038$ and $P = 0.18$, respectively).

Focused Analysis at the VWF Locus. The second significant region in the TSS cohort and in the meta-analysis was the *VWF* locus. The lead SNP in the meta-analysis was rs1063856 ($P = 5.5E-16$), a coding nonsynonymous SNP at the *VWF* gene. It is in strong linkage disequilibrium (LD) with the second highly associated SNP, rs1063857 ($r^2 = 1.00$, $P = 6.5E-16$), a coding synonymous SNP. Although this region was not significant in the GABC cohort, a power analysis using the Genetic Power Calculator (31) showed that given the effect size of $\beta = 0.012$, as seen in TSS, and given the sample size of GABC, the power to detect this VWF signal was only 38.4% in GABC.

Similar to the haplotype analysis at *ABO*, we extended the association analysis at *VWF* to haplotypes using the combined set of GABC and TSS. From the genotype data for the 71 available *VWF* SNPs we constructed a haplotype map of the *VWF* gene using Haploview and identified 12 LD blocks (*SI Appendix, Fig. S7*). Of the 15 most highly associated SNPs in the meta-analysis, 11 reside in block 6, two reside in block 7 (the top two SNPs), and the remaining two reside in block 8. These three blocks span exons 14–22, which encode the D', D2, and D3 domains of VWF

Table 2. Top meta-analysis SNPs

Meta-analysis						GABC			TSS		
Chr	SNP	Position*	Allele [†]	P value [‡]	Closest gene	Freq	β (SE)	P value [§]	Freq	β (SE)	P value [§]
9	rs687289	135126927	T	1.3E-128	<i>ABO</i>	0.643	0.36 (0.022)	1.6E-52	0.751	0.33 (0.016)	3.7E-89
9	rs11244079	135174347	A	4.4E-36	<i>LOC653163</i>	0.949	0.33 (0.055)	4.6E-09	0.937	0.35 (0.030)	3.9E-31
9	rs4962153	135313575	A	1.9E-31	<i>ADAMTS13</i>	0.839	0.208 (0.032)	1.6E-10	0.894	0.25 (0.024)	1.2E-24
9	rs11244035	135071140	T	1.9E-25	<i>OBP2B</i>	0.885	0.27 (0.039)	3.2E-12	0.915	0.23 (0.027)	3.4E-17
9	rs45618736	137580983	A	4.6E-24	<i>OBP2A</i>	0.890	0.26 (0.040)	1.3E-10	0.918	0.24 (0.029)	5.4E-17
9	rs28602591	135236487	T	3.3E-20	<i>C9orf96</i>	0.886	0.19 (0.038)	5.7E-07	0.928	0.24 (0.029)	4.8E-16
12	rs1063856	6023795	A	4.9E-16	<i>VWF</i>	0.360	-0.095 (0.024)	1.1E-04	0.395	-0.12 (0.015)	8.5E-14
9	rs4507838	135092020	A	1.54E-13	<i>LOC286310</i>	0.875	0.081 (0.036)	0.025	0.867	0.17 (0.022)	4.8E-14
9	rs554710	135171669	T	4.7E-12	<i>SURF6</i>	0.281	0.14 (0.027)	1.5E-07	0.286	0.088 (0.017)	1.8E-07
9	rs11655	135197664	A	1.9E-09	<i>SURF5</i>	0.885	-0.16 (0.037)	3.2E-05	0.885	-0.11 (0.024)	1.8E-06

Genome-wide significant (P value $< 5.0E-8$) SNPs in GABC+TSS meta-analysis and individual cohorts, sorted by P value, with respect to their relationship to the nearest gene.

*Positions are in National Center for Biotechnology Information Build 36 coordinates.

[†]Tested allele.

[‡]Meta-analysis P value.

[§]Cohort specific P value.

Table 3. ABO haplotype association

ABO-allele	Haplotype*	Allele/haplotype frequencies			GABC+TSS haplotype association	
		ARIC	FHS	GABC + TSS	β	<i>P</i> value
O	GGC	0.650	0.673	0.720	-0.34	2.3E-138
A1	AGC	0.209	0.196	0.155	0.36	3.5E-98
B	AGT	0.0730	0.0770	0.0722	0.36	7.2E-50
A2	AAC	0.0680	0.0540	0.0531	-0.038	1.8E-01

ABO-alleles, tagging haplotypes, and inferred frequencies in the FHS, ARIC, and GABC+TSS cohorts, and association results in GABC+TSS.

*rs687289, rs8176704, rs8176749.

and contain the VWF propeptide and factor VIII binding domains. Haplotype association tests of these blocks yielded *P* values of 8.8E-3, 6.3E-7, and 7.9E-3 for the most frequent haplotypes in block 6, block 7, and block 8, respectively.

Linkage Analysis. To scan for linkage signals for plasma VWF levels we analyzed the genotype data of siblings from the GABC and TSS cohorts, for a total of 561 sibships and 1,284 individuals. Linkage LOD scores from an initial scan using the unpruned dataset of ~760 K SNP were likely inflated (*SI Appendix, Fig. S84*), because of strong LD between many SNPs and missing parental genotypes (32). This explanation was supported by the reduced significance levels observed in a revised scan using an LD pruned dataset (1 SNP/Mb, $r^2 < 0.001$, 2.7 K SNPs) (*SI Appendix, Fig. S8B*).

To incorporate data-derived LD patterns, we applied the LD-modeling algorithm in MERLIN (25) to define independent LD clusters and conducted linkage analysis using inferred haplotype frequencies within clusters (*Materials and Methods*). First, markers were organized into clusters using an LD criterion of $r^2 = 0.001$. This process produced ~37 K nearly independent clusters; and the linkage analysis on each yielded its LOD score and *P* value. The per-cluster LOD scores (Fig. 2) revealed a strong linkage signal (peak LOD ~5.3) crossing the centromere of Chr2 (2q12-2p13), as well as a strong signal on Chr9 (9q34, peak LOD ~2.9). The latter region contains the *ABO* gene.

We evaluated the genome-wide significance of the linkage results with a locus-counting approach proposed by Wiltshire et al. (33) comparing the observed LOD scores of the top independent regions of linkage (IRLs) with the null distributions of LOD scores for their corresponding equal-ranked IRLs over 1,000 simulated datasets with randomized phenotypes. The IRLs were defined as the 40-cM interval around the location of the maximum LOD score. This analysis showed that the three highest IRLs in our study had higher LOD scores than the 95th percentile of their respective equal-ranked LOD score null distributions (*SI Appendix, Fig. S9A*). The highest signal, at ~82.4 Mb on Chr2, had a LOD score of 5.27 (original MERLIN *P* value = 4.2E-7; simulation-based empirical *P* value = 0.0015) (Fig. 2, and *SI Appendix, Fig. S9A*). The second strongest signal,

at ~135.3 Mb on chromosome 9, had a LOD score of 2.87 ($P = 1.4E-4$; empirical $P = 0.048$) (Fig. 2 and *SI Appendix, Fig. S9A*). The third strongest signal was at ~104.46 Mb on Chr2, with a LOD score of 2.687 ($P = 2.2E-4$; empirical $P = 0.020$) (Fig. 2 and *SI Appendix, Fig. S9A*).

The analysis above used a fixed width (± 20 cM) to define IRL boundaries. An alternative approach is to apply a LOD score cutoff, such as one unit below the maxima. This LOD-based approach yielded an overlapping interval for the first and third significant IRLs, suggesting that the two intervals may be part of the same linkage region. The combined linkage region spans 34 Mb on 2q12-2p13 (positions 74.98 Mb–108.95 Mb), crossing over the centromere (*SI Appendix, Fig. S9B*). Using the same LOD score cutoff, the second top significant IRL spans 790 Kb on 9q34 (positions 135.03 Mb–135.82 Mb) and includes the *ABO* locus (*SI Appendix, Fig. S9C*).

By using GCTA we estimated that the LOD score-based linkage intervals on Chr2 and 9 explained 19.2% and 24.5% of the variation in the VWF levels, respectively. Furthermore, by expanding from the core region on 2q12–2p13, we found that the variance explained changed minimally beyond the 34-Mb core interval, increasing from 19.2–19.7% when expanded to 48 cM, suggesting that the 34-Mb interval contains the majority of the linkage signal.

Focused Analysis in the Chr2 Linkage Region. For the Chr2 linkage region (74.98 Mb–108.95 Mb), the phased genotype data defined 886 haplotype blocks, containing 4,074 distinct haplotypes with frequency >1% in our study (*SI Appendix, SI Methods*). We performed haplotype-based association tests for VWF levels in each block. None of the tests reached region-wide significance ($P < 5.6E-5$) (*SI Appendix, Fig. S10A*), and few blocks produced substantially smaller haplotype-based *P* values than single-SNP *P* values in the same block (*SI Appendix, Fig. S10B*). Thus, these results did not provide clear evidence of association to common haplotypes that could explain the linkage signal in Chr2.

Next, we screened for sets of at least three SNPs with different LD structures between high-VWF and low-VWF individuals in the GABC cohort and identified six SNP sets in the linkage interval (*SI Appendix, SI Methods*). We performed association tests using the long-range haplotypes formed by these SNP sets and

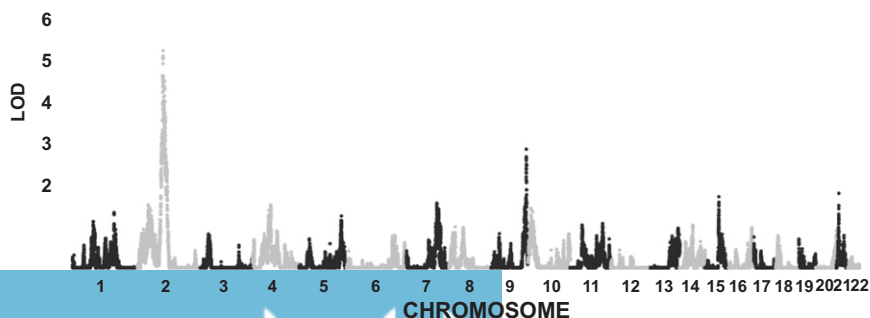


Fig. 2. Linkage analysis results for GABC+TSS using the age-, sex-, and principal component-adjusted VWF values. Genome-wide LOD Scores for 37 K “clusters,” defined in MERLIN to model the LD among SNPs (*Materials and Methods*).

discovered two sets with P values smaller than 0.001 (*SI Appendix, Table S3*). Simulation results showed that these two sets reached an empirical significance level of 0.05. The first set (empirical $P = 0.006$) was anchored by the index SNP rs6547231 (association $P = 5.8E-4$) and spanned a 987-kb interval from 78.963 Mb to 79.951 Mb. The second set (empirical $P = 0.002$), anchored by the index SNP rs7566719 (association $P = 3.3E-4$), covered an ~973-kb interval from 76.240 Mb to 77.214 Mb.

Discussion

Our association analysis of VWF variation in healthy young subjects identified two major signals at the *ABO* and *VWF* loci, confirming results from a previously published meta-analysis. Taking advantage of the sibling structure of our cohorts, we also identified a unique QTL on Chr2, which was undetected in previous studies (15, 20, 34, 35).

With a total sample size of 3,250, our GWAS was underpowered to detect the several smaller-effect loci identified in the larger CHARGE (Cohorts for Heart and Aging Research in Genome Epidemiology) consortium meta-analysis ($n = 17,596$). However, the total variation explained by the genetic loci identified in our GWAS analysis (18.7%) was notably larger than that explained by the similar analysis in the CHARGE study (12.8%). The young age and healthy status of our subjects may have increased the contribution of the heritable components of VWF levels by limiting the impact of known environmental effects on VWF levels, including age and common illnesses, such as diabetes and heart disease. For example, contrary to studies in older cohorts (36, 37), we found no associations between smoking and VWF levels in this study, suggesting that the previously observed association may be a proxy for vascular disease related to chronic smoking. Consistent with this notion, the estimated heritability of VWF variation of ~65% from our study is at the upper end of the range previously reported (13–15).

The strongest association signals in our analysis were at the *ABO* locus. *ABO* haplotype analysis confirmed that SNPs tagging the O and A2 alleles were associated with lower VWF levels, but those tagging the B and A1 alleles were associated with higher VWF levels. Thus, the association signals at *ABO* are consistent with known alteration of VWF levels through specific *ABO* glycosylation patterns. Although we were able to detect the association of the A2 allele (minor allele frequency 0.05) after a conditional analysis, we were unable to detect several other less common alleles at *ABO* (30), likely because of their lower allele frequencies. The significantly associated SNPs at the *VWF* locus tag three of seven haplotype blocks, consistent with a similar analysis of the ARIC cohort (38, 39). Although the causative SNPs are not yet at this point, they likely act via alterations in VWF biosynthesis, secretion, or clearance from plasma (40).

Previous studies have reported significant single-gene associations between plasma VWF levels and variants at the *FUT2* locus (41, 42) lipoprotein receptor-related protein (*LRP1*) (43), angiotensin-converting enzyme (*ACE*) (44), and arginine vasopressin 2 receptor (*AVPR2*) (45). None of these loci were detected in our analysis or in the CHARGE GWAS (20), although the low minor allele frequency for the *LRP1* variant (<2%) and X-chromosomal location of *AVPR2* limited the power for their detection.

In addition to GWAS, the sibling structure of our GABC and TSS cohorts enabled linkage analysis, which identified a highly significant unique QTL on Chr2. The effect size of this locus on VWF variation (19.2% variance explained) was comparable to the effect of the *ABO* locus (24.5%). Variants in this linkage interval were not detected in our GWAS analysis of the same subjects, nor were they detected in the CHARGE study (20). A previously reported linkage analysis in 21 families (the GAIT study) only identified significant linkage at the *ABO* locus (LOD = 3.46). Although a peak with LOD = 1.65 was reported on Chr2 (2q33.2), it did not overlap with the Chr2 peak in our study (15).

The linkage peak on Chr2 spans ~34 Mb and contains over 100 annotated genes, with plausible candidates for altering plasma

VWF including several glycosyltransferases, sialyltransferases, and SNARE complex proteins potentially involved in protein secretion. Conventional haplotype-based analyses revealed no region-wide significant association in the Chr2 linkage region. However, analysis of differences in LD structure between high- and low-VWF individuals (*SI Appendix, SI Methods*) identified two ~1-Mb intervals that might harbor rare causal variants contributing to the linkage signal. The first region contained seven RefSeq genes (*REG3G, REG1B, REG1A, REG1P, REG3A, CTNNA2, MIR4264*) and the second region one RefSeq gene, *LRRTM4*. Although none of the genes play an obvious role in VWF biology, these regions represent targets for future study.

We estimate that variants in the Chr2 linkage interval alter steady-state VWF level with a magnitude similar to *ABO* (20–30%). Therefore, detection as a Mendelian bleeding disorder similar to VWD (VWF levels reduced by >50%) would be unlikely. However, this locus, together with *ABO* blood group, could represent an important modifier of VWD severity and penetrance, as well as the thrombosis risk associated with elevated VWF. Identification of the underlying gene and its mechanism of action could also lead to improved treatment for VWD and venous thromboembolic disease.

Mendelian genes for complex traits, such as type 2 diabetes, are often undetected by GWAS (46, 47). However, mutations at these loci are generally very rare and contribute only a small part of the overall population variance for that trait. The large contribution of the Chr2 locus to plasma VWF variation, comparable to the effect of *ABO* but undetectable even by a well-powered GWAS, is surprising and not readily explained by known mechanisms of VWF homeostasis. We hypothesize that this locus may contain a critical VWF regulatory gene harboring rare causal variants in a situation analogous to allelic heterogeneity, thus having reduced power of detection in association tests. However, these variants might have sufficiently large effect size in each individual family and accrued linkage signals across families, thus contributing to the observed Chr2 linkage results. A similar pattern of a strong linkage signal without corresponding evidence for association was recently reported for a QTL for cystic fibrosis disease severity (48). Additionally, in silico experiments predict the presence rare variants detected by linkage that contribute to variation in complex genetic traits (49). Taken together, these findings suggest that similar loci could explain a significant portion of the “missing heritability” for other complex genetic traits.

Materials and Methods

Genes and Blood-Clotting Study. A cohort of healthy siblings was recruited from the University of Michigan, Ann Arbor, between June 26, 2006 and January 30, 2009. Participants were between the ages of 14 and 35 y, and had at least one eligible healthy sibling. Subjects who indicated that they were pregnant, had a known bleeding or blood-clotting disorder, or any illness requiring regular medical care were excluded. All participants provided informed consent by a process that was previously described (22). Subjects completed an online phenotyping survey and donated a blood sample for DNA extraction and plasma biochemical phenotyping. Details of the sample collection, genotyping, and data-cleaning process for the GABC cohort are described in *SI Appendix*.

Trinity Student Study. A cohort of 2,524 healthy, ethnically Irish individuals, attending the University of Dublin, Trinity College, with ages between 18 and 28 y, was recruited over one academic year in 2003–2004 (21, 23). Ethical approval was obtained from the Dublin Federated Hospitals Research Ethics Committee, which is affiliated with the Trinity College, and reviewed by the Office of Human Subjects Research at the National Institutes of Health. Written informed consent was obtained from participants before recruitment. Details of the sample collection, genotyping, and data-cleaning process are described in *SI Appendix*.

VWF Antigen Level. VWF antigen levels were measured in both the GABC and TSS cohorts using a custom AlphaLISA (Perkin-Elmer) assay. For further details on this assay, refer to *SI Appendix*.

Phenotype Data Processing. Consistent with previous studies (12, 20), the raw VWF antigen level distribution in our cohorts was not normal. Therefore, the antigen-level distribution was normalized by log transformation. The associations of smoking with raw VWF level distribution were analyzed with Kolmogorov-Smirnov tests. The effects of age, sex, and population structure on the VWF antigen levels were determined by separate single-factor linear regression analysis. *SI Appendix* provides further details of phenotype data processing.

Heritability of VWF Antigen Levels. For the combined set of GABC and TSS, the sib-pair intraclass correlation coefficient (ICC) was calculated using the log-transformed, age-, sex-, and PC3-adjusted values in GABC, and age- and sex-adjusted values in TSS. As there were sibships with more than two members, we randomly sampled two sibs from each family, calculated ICC, and repeated the process 500 times to obtain the average ICC. The upper-bound of the narrow sense heritability (h^2) was estimated by multiplying the average ICC by 2. In addition to the pedigree-based estimate described above, independent estimates were also calculated using the genotype

and phenotype data in MERLIN-REGRESS and GCTA using all individuals (25, 26).

Computational Analyses. A detailed description of the computational methods used to assess population substructure, association analysis, meta-analysis, linkage analysis, variance-explained calculations, and haplotype-based association analysis are provided in *SI Appendix*.

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