Supplementary Table 1. Genome-wide significant SNPs associated with GTIb and ICA area

Phenotype	Chromosome	SNP	Reference allele	Effect allele	Effect allele frequency	β	Standard error	T	*P*	rsID	Gene : Consequence
GTIb	17	17:78358945:A:G	G	A	0.0276	0.58	0.106	5.532	4.65×10^{-8}	rs112735431	*RNF213* : Missense Variant *RNF213-AS1* : Intron Variant
ICA area	1	1:230435170:A:G	G	A	0.0064	9.08	1.402	6.474	1.53×10^{-10}	rs117146955	
	7	7:64202191:A:G	A	G	0.0069	8.93	1.347	6.626	5.81×10^{-11}	rs186074302	
	17	17:78358945:A:G	G	A	0.0276	-5.10	0.679	-7.514	1.34×10^{-13}	rs112735431	*RNF213* : Missense Variant *RNF213-AS1* : Intron Variant
	17	17:78438765:A:G	G	A	0.0159	-5.29	0.906	-5.839	7.25×10^{-9}	rs112107108	
	17	17:78762582:C:T	C	T	0.0164	-5.78	0.885	-6.525	1.11×10^{-10}	rs138309870	*RPTOR* : Intron Variant

Genome-wide association analysis identified a single SNP (rs112735431) in the *RNF213* locus showing a significant association with GTIb. For ICA area, five SNPs surpassed the genome-wide significance threshold ($P<5\times10^{-8}$), including the *RNF213* p.R4810K variant (rs112735431) and other variants on chromosomes 1, 7, and 17. Chromosomal positions are based on the GRCh37 (hg19) reference genome. β estimates correspond to the effect allele.
SNP, single-nucleotide polymorphism; GTIb, basal global tortuosity index; ICA, internal carotid artery.

Supplementary Table 2. Baseline characteristics according to *RNF213* variant and MMD status

Variable	MMD-/variant- (n=888)	MMD-/variant+ (n=37)	MMD+/variant+ (n=14)	*P*
Age (yr)	67.5±13.2	62.7±13.6	49.9±11.7	<0.001
Female sex	330 (37.16)	15 (40.54)	8 (57.14)	0.288
Smoking status				0.533
Never smoker	512 (57.66)	21 (56.76)	7 (50.00)	
Ex-smoker	206 (23.20)	7 (18.92)	2 (14.29)	
Current smoker	170 (19.14)	9 (24.32)	5 (35.71)	
Alcohol consumption, bottle per week	0.9±2.4	1.3±2.7	0.5±0.6	0.450
Hypertension	637 (71.73)	30 (81.08)	8 (57.14)	0.227
Diabetes mellitus	292 (32.88)	10 (27.03)	3 (21.43)	0.595
Dyslipidemia	548 (61.71)	22 (59.46)	11 (78.57)	0.416
Previous stroke or TIA	205 (23.09)	8 (21.62)	5 (35.71)	0.510
Congestive heart failure	33 (3.72)	1 (2.70)	1 (7.14)	0.507
Peripheral arterial occlusive disease	13 (1.46)	2 (5.41)	1 (7.14)	0.064
Coronary artery disease	104 (11.71)	8 (21.62)	0 (0.00)	0.195
Initial NIHSS	4.2±4.8	5.1±6.5	4.5±6.1	0.921
Previous mRS	0 (0–0)	0 (0–0)	0 (0–1)	0.120
mRS at 3 months	1 (0–2)	1 (0–1)	1 (0–1)	0.207
TOAST classification				<0.001
Large artery atherosclerosis	236 (26.58)	12 (32.43)	7 (50.00)	
Cardioembolic	191 (21.51)	8 (21.62)	0 (0.00)	
Small artery occlusion	206 (23.20)	4 (10.81)	0 (0.00)	
Other	89 (10.02)	8 (21.62)	7 (50.00)	
Undetermined	166 (18.69)	5 (13.51)	0 (0.00)	

Continuous variables are presented as mean±standard deviation, and categorical variables as frequency (percentage). mRS values are presented as median (interquartile range). *P*-values were calculated using the Kruskal–Wallis test for non-normally distributed continuous variables and chi-square or Fisher's exact test for categorical variables, as appropriate.
MMD, moyamoya disease; TIA, transient ischemic attack; NIHSS, National Institutes of Health Stroke Scale; mRS, modified Rankin scale; TOAST, Trial of ORG 10172 in Acute Stroke Treatment.