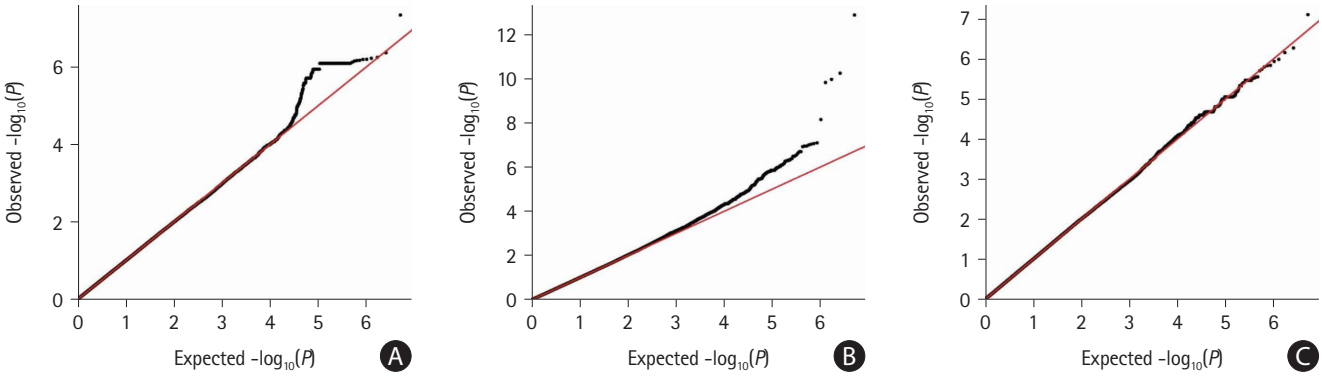
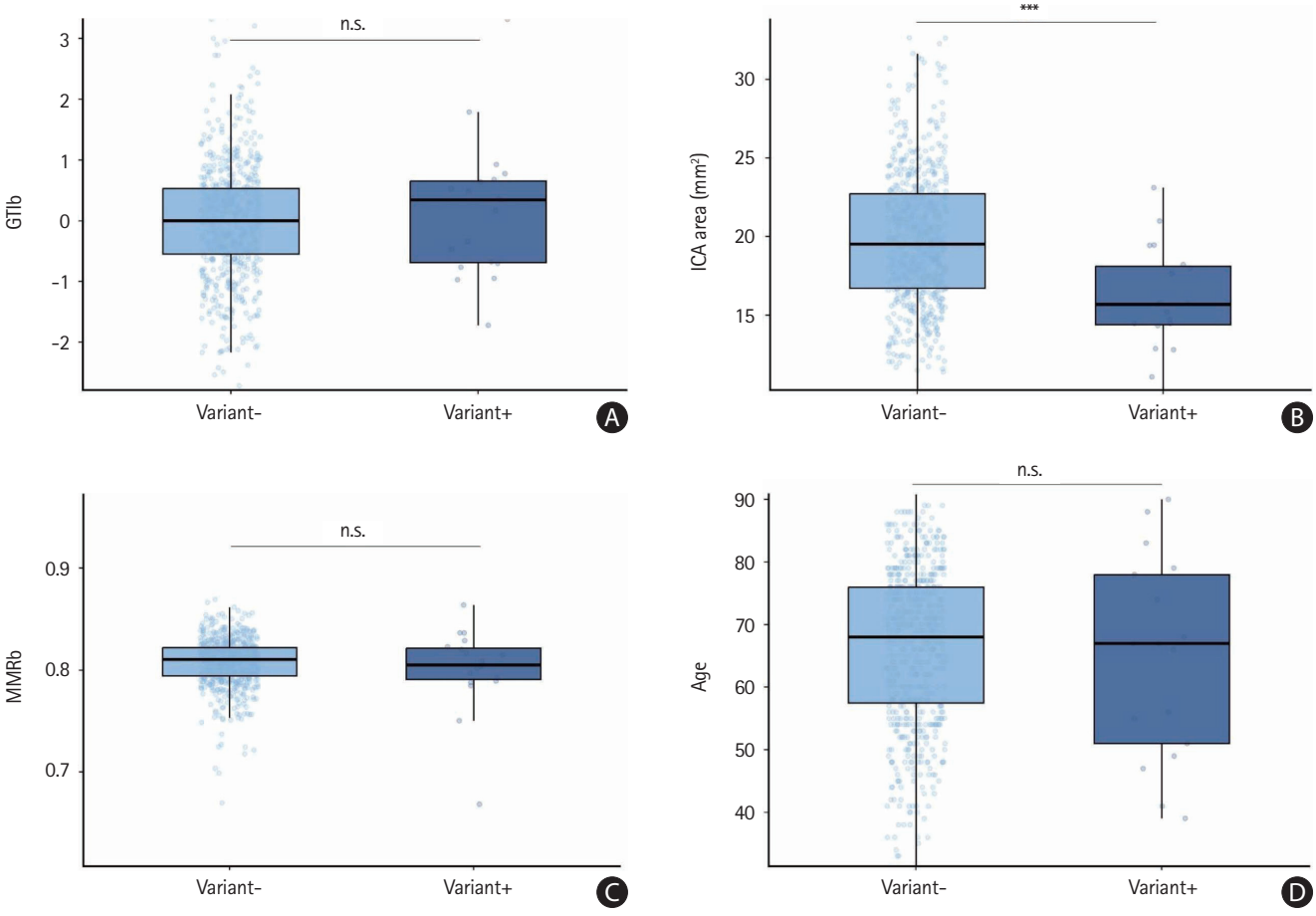


Supplementary Figure 3. Quantile–quantile plots showing the observed versus expected $-\log_{10}(P)$ distributions for the genome-wide association analyses of GTIb (A), ICA area (B), and MMRb (C). The red line indicates the null hypothesis of no association. The genomic inflation factors (λ) were 1.00 for GTIb, 0.99 for ICA area and 1.00 for MMRb, indicating no systematic inflation of test statistics. GTIb, basal global tortuosity index; ICA, internal carotid artery; MMRb, basal minimum-to-maximum diameter ratio.



Supplementary Figure 4. Validation of intracranial vessel feature distributions according to *RNF213* variant status in the KUMC cohort. Box-and-jitter plots compare the GTIb (A), ICA area (B), MMRb (C), and age (D) between variant- and variant+ groups. *RNF213* p.R4810K carriers showed smaller ICA area, consistent with the SMC cohort results. Statistical comparisons were performed using the Wilcoxon rank-sum test. n.s., not significant; GTIb, basal global tortuosity index; ICA, internal carotid artery; MMRb, basal minimum-to-maximum diameter ratio; KUMC, Korea University Medical Center; SMC, Samsung Medical Center. ***P<0.001.

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