Supplementary Data

SUPPLEMENTARY TABLE S1. ASSOCIATIONS AMONG HEMORRHAGIC, ISCHEMIC STROKE, AND NORMAL CONTROLS

Gene	SNP	Strokes (n=674) vs. Controls (n=267)			Hemorrhagic (n=109) vs. Controls (n=267)			Ischemic (n=565) vs. Controls (n=267)			Hemorrhagic (n=109) vs. Ischemic (n=565)		
		MAF			MAF			MAF			MAF		
		Strokes	Controls	p-Value	Hemorrhagic	Controls	p-Value	Ischemic	Controls	p-Value	Hemorrhagic	Ischemic	p-Value
NPPB	rs198389A/G	0.132	0.125	0.367	0.115	0.125	0.613	0.136	0.125	0.197	0.115	0.136	0.489
	rs5227G/T	0.000	0.000	—	0.000	0.000	—	0.000	0.000	—	0.000	0.000	—
	rs35640285G/T	0.000	0.000	—	0.000	0.000	—	0.000	0.000	—	0.000	0.000	—
NPPA	rs61757273G/T	0.071	0.068	0.313	0.060	0.068	0.931	0.073	0.068	0.132	0.060	0.073	0.481
	rs198373A/G	0.007	0.002	0.072	0.000	0.002	—	0.008	0.002	**0.032**	0.000	0.008	—
	rs198372G/A	0.007	0.002	0.071	0.000	0.002	—	0.008	0.002	**0.032**	0.000	0.008	—
	rs5063G/A	0.094	0.099	0.625	0.096	0.099	0.880	0.093	0.099	0.617	0.096	0.093	0.913
	rs5065T/C	0.007	0.006	0.779	0.009	0.006	0.954	0.007	0.006	0.613	0.009	0.007	0.674
	rs5067A/G	0.007	0.006	0.785	0.009	0.006	0.951	0.007	0.006	0.619	0.009	0.007	0.660

Bold value indicates the statistical significance of P<0.05.

p-Values of additive model were obtained by logistic analysis adjusted for age, sex, and histories of hypertension and diabetes mellitus as covariables. MAF, minor allele frequency.

SNP, single-nucleotide polymorphism.

SUPPLEMENTARY TABLE S2. ASSOCIATIONS AMONG CARDIOEMBOLISM, LARGE-ARTERY ATHEROSCLEROSIS, AND SMALL-VESSEL OCCLUSION IN ISCHEMIC STROKE

Gene	SNP	CE (n=33) vs. LAA (n=123)			CE (n=33) vs. SVO (n=395)			LAA (n=123) vs. SVO (n=395)		
		MAF			MAF			MAF		
		CE	LAA	p-Value	CE	SVO	p-Value	LAA	SVO	p-Value
NPPB	rs198389A/G	0.156	0.135	0.459	0.156	0.133	0.444	0.135	0.133	0.986
	rs5227G/T	0.000	0.000	—	0.000	0.000	—	0.000	0.000	—
	rs35640285G/T	0.000	0.000	—	0.000	0.000	—	0.000	0.000	—
NPPA	rs61757273G/T	0.091	0.095	0.871	0.091	0.065	0.296	0.095	0.065	0.161
	rs198373A/G	0.000	0.000	—	0.000	0.010	—	0.000	0.010	—
	rs198372G/A	0.000	0.000	—	0.000	0.010	—	0.000	0.010	—
	rs5063G/A	0.076	0.111	0.578	0.076	0.090	0.802	0.111	0.090	0.397
	rs5065T/C	0.030	0.008	0.102	0.030	0.004	**0.020**	0.008	0.004	0.410
	rs5067A/G	0.030	0.008	0.101	0.030	0.004	**0.020**	0.008	0.004	0.413

Bold value indicates the statistical significance of P<0.05.

p-Values of additive model were obtained by logistic analysis adjusted for age, sex, and histories of hypertension and diabetes mellitus as covariables.

CE, cardioembolism; LAA, large-artery atherosclerosis; SVO, small-vessel occlusion.

SUPPLEMENTARY TABLE S3. IN SILICO ANALYSIS FOR POTENTIAL TRANSCRIPTIONAL REGULATION AT rs198372G/A (OR C/T) IN NPPA

SNP	Position	Allele	Binding factor	Signal sequence
rs198372G/A (or C/T)	Promoter of NPPA	G (or C)	ACF	AA**C**CAAT
			alpha-CBF	**C**C̄A̅AT
			alpha-IRP	**C̄**CAAT
			CDP	**C̄**CAAT
			CP1	**C̄**CAAT
			CP2	**C̄**CAAT
			H1TF2	**C̄**CAAT
			NF-1	**C̄**CAAT
			NF-E	**C̄**CAAT
			SRF	**C̄**CAAT
		A (or T)	Pit-1	A̅**T̲**CAATA

Signal sequences for transcriptional binding factors are predicted using the Signal Scan program (www-bimas.cit.nih.gov/molbio/signal/).

Bold and underline indicates the complementary nucleotide (C and T) for major and minor (G and A) allele of rs198372 polymorphism, respectively.