Supplementary Table 13. Mendelian randomization random-effects inverse-variance weighted method results without Slope-Hunter correction: Genetics of Ischemic Stroke Functional Outcome

Protein	Estimate	Lower CI	Upper CI	*P*	FDR	OR	OR lower CI	OR upper CI
CASP-8	-0.511	-1.027	0.006	0.053	0.066	0.600	0.358	1.006
HGF	-1.625	-2.546	-0.704	0.001	0.003	0.197	0.078	0.495
S100A12	0.820	-0.055	1.696	0.066	0.066	2.271	0.947	5.450

CI, confidence interval; FDR, false discovery rate; OR, odds ratio.

Supplementary Table 14. Comparison of Mendelian randomization methods used in the present publication and those used by Xu et al.

	Angerfors et al. (present study)	Xu et al.[17]
Source of genetic instrument selection	UKB-PPP[2]	SCALLOP consortium[18]
Thresholds for selecting SNPs		
P-value	$P<0.001$	$P<5\times10^{-8}$
LD clumping	$r^2<0.01$	$r^2<0.3$
cis- or *trans*-pQTL	Only *cis*-variants	Both *cis*- and *trans*-variants
Outcome GWAS data	Primary GISCOME[4] analysis, i.e., mRS score 0–2 vs. 3–6 (n=6,021)	Secondary GISCOME[4] analysis, on a subgroup of cases that could be dichotomized as mRS score 0–1 vs. 2–6 (n=4,363)
Adjustment for stroke severity (NIHSS score)	Yes	Unclear
Adjustment for collider bias	Yes, Slope-Hunter using summary statistics from the GIGASTROKE[10] GWAS	No

SNP, single nucleotide polymorphism; LD, linkage disequilibrium; pQTL, protein quantitative trait loci; GWAS, Genome-Wide Association Study; NIHSS, National Institutes of Health Stroke Scale; UKB-PPP, UK Biobank Pharma Proteomics Project; GISCOME, Genetics of Ischemic Stroke Functional Outcome; mRS, modified Ranking Scale.