Supplementary Table 8. Mendelian randomization random-effects inverse-variance weighted method results without Slope-Hunter correction: Genetics of Ischemic Stroke Functional Outcome, National Institutes of Health Stroke Scale-adjusted

Protein	Estimate	Lower CI	Upper CI	*P*	FDR	OR	OR lower CI	OR upper CI
CASP-8	-0.762	-1.350	-0.174	0.011	0.022	0.467	0.259	0.841
MCP-3	0.338	-0.217	0.893	0.232	0.232	1.402	0.805	2.442
HGF	-1.669	-2.863	-0.475	0.006	0.022	0.188	0.057	0.622
S100A12	1.166	0.033	2.299	0.044	0.059	3.208	1.033	9.961

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

Supplementary Table 9. Mendelian randomization random-effects inverse-variance weighted method results: Genetics of Ischemic Stroke Functional Outcome, Slope-Hunter-corrected

Protein	Estimate	Lower CI	Upper CI	*P*	FDR	OR	OR lower CI	OR upper CI
CASP-8	-0.580	-1.098	-0.062	0.028	0.093	0.560	0.334	0.940
CCL25	-0.115	-0.337	0.106	0.308	0.513	0.891	0.714	1.112
MCP-3	0.517	-0.101	1.134	0.101	0.253	1.676	0.904	3.109
DNER	0.220	-0.296	0.735	0.403	0.576	1.246	0.744	2.086
HGF	-1.938	-2.880	-0.996	5.5E-05	0.0006	0.144	0.056	0.369
S100A12	1.104	0.277	1.932	0.009	0.045	3.017	1.319	6.900
SIRT2	-0.125	-1.084	0.835	0.799	0.886	0.883	0.338	2.305
TRAIL	0.171	-0.406	0.749	0.561	0.701	1.187	0.666	2.114
TRANCE	0.538	-0.479	1.555	0.300	0.513	1.713	0.619	4.735
TNFSF14	-0.055	-0.807	0.697	0.886	0.886	0.946	0.446	2.007

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