Tables:

Table 1: Demographic features, clinical laboratory test results and the prevalence of conventional risk factors for ischemic stroke patients and controls in the study population.

Parameter	Patients (n=239)	Control (n=130)	*P*	OR (%95 CI)
Age	65.6±13.5	64.2±12.2	0.067[a]	
Male, n (%)	133 (55.6)	63 (51.5)	0.186[b]	1.334 (0.870-2.048)
Hypertension, n (%)	160 (66.9)	49 (37.7)	0.000[b]	3.35 (2.144-5.227)
Diabetes mellitus, n (%)	77 (32.2)	20 (15.4)	0.000[b]	2.614(1.511-4.523)
Smokers, n (%)	65 (27.2)	16 (12.3)	0.001[b]	2.662(1.467-4.829)
Obesity, n (%)	53 (22.2)	8 (6.2)	0.000[b]	4.191(1928-9.113)
Total cholesterol (mmol/L)	4.76 ±1.34	4.70±1.28	0.679[c]	
Triglycerides (mmol/L)	1.54 ±0.75	1.44±0.60	0.195[c]	
HDL-cholesterol (mmol/L)	1.08±0.31	1.20±0.31	0.001[c]	
LDL-cholesterol (mmol/L)	2.85±1.17	2.76±0.04	0.499[c]	

For age, given values are median (quartiles) other values are either number of subjects, percentage, or mean ± SD
[a]Mann-Whitney U test is applied
[b]Chi-square test is applied
[c]Independent Samples T-test is applied

Table 2: Distributions of genotypes and allele frequencies for single nucleotide polymorphisms, C419A (rs4925) of the *GSTO1* gene and A424G (rs156697) of the *GSTO2* gene.

Genotypes/Alleles	Patients n=239, (%)	Controls n=130, (%)	OR (95%CI)	P
GSTO1 C419A				
CC	101 (42.3)	62 (47.7)	1.245[a]	0.315[a]
CA	105 (43.9)	47 (36.2)	(0.811-1.914)	
AA	33 (13.8)	21 (16.1)		
C	0.642	0.658	1.071[b]	0.675[b]
A	0.358	0.342	(0.779-1.47)	
GSTO2 A424G				
AA	97 (40.6)	50 (38.5)	0.915[c]	0.691[c]
AG	107 (44.8)	55 (42.3)	(0.591-1.146)	
GG	35 (14.6)	25 (19.2)		
A	0.630	0.596	0.868[d]	0.370[d]
G	0.370	0.404	(0.637-1.183)	

[a] CA+AA versus CC, [b] A versus C
[c]AG+GG versus AA, [d]G versus A

Table 3: Distribution of the double combined haplotypes for C419A (rs4925) of the *GSTO1* gene and A424G (rs156697) of the *GSTO2* gene.

Combined haplotypes	Patients n=239, (%)	Controls n=130, (%)	OR	P
CCAA	83 (34.7)	42 (32.3)	1.115	0.639
CCAG	18 (7.5)	20 (15.4)	0.448	**0.017**
CCGG	2 (0.8)	1 (0.8)	1.089	1
CAAA	13 (5.4)	6 (4.6)	1.189	0.732
CAAG	79 (33.1)	31 (23.8)	1.577	0.064
CAGG	12 (5.0)	9 (6.5)	0.710	0.451
AAAA	2 (0.8)	2 (1.5)	0.540	0.543
AAAG	9 (3.8)	4 (3.1)	1.232	0.732
AAGG	21 (8.8)	15 (11.5)	0.739	0.395

Table 4: Stratification of diabetic/non-diabetic and smoker/non-smoker groups according to different *GSTO1* and *GSTO2* genotypes and stroke-control status.

Genotypes		Diabetic (n=97)	Non-diabetic (n=272)	OR	*P*	Smoker (n=81)	Non-smoker (n=288)	OR	*P*
All	Stroke	77	162	2.614	0.000	65	174	2.662	0.001
	Control	20	110			16	114		
GSTO1 C419A									
CC	Stroke	30	71	1.760[b]	0.142	25	76	1.937[d]	0.118
	Control	12	50			9	53		
CA+AA	Stroke	47	91	3.873[b]	0.000	40	98	3.556[d]	0.002
	Control	8	60			7	61		
GSTO2 A424G									
AA	Stroke	31	66	2.465[b]	0.037	28	69	2.130[d]	0.085
	Control	8	42			8	42		
AG+GG	Stroke	46	96	2.715[b]	0.004	37	105	3.171[d]	0.004
	Control	12	68			8	72		

[b] OR calculated against non diabetic, [d] OR calculated against non-smoker, [e] Fisher Exact Test is Applied

Table 5: Logistic regression analysis results of conventional risk factors, lipid parameters, and *GSTO1* and *GSTO2* genotypes on ischemic stroke

Parameters	OR	95%CI	*P*
Hypertension	3.043	1.840-5.031	0.000
Smoking	3.258	1.658-6.500	0.001
Obesity	2.593	1.129-5.956	0.025
HDL-cholesterol	0.270	0.111-0.654	0.004

Table 6: Comparison of the wild-type and variant allele frequencies of the *GSTO1* and *GSTO2* genes in different populations of control groups.

Population	Number of sample	Wild allele (C)	Variant allele (A)	Reference
Turkish	**130**	**0.658**	**0.342**	**This Study**
Turkish	214	0.689	0.311	Ada et al. 2013
	194	0.915	0.085	Takeshita et al. 2009

Population	Number of sample	Wild allele (A)	Variant allele (G)	Reference
	251	0.817	0.183	Chung et al. 2011
Taiwanese	764	0.834	0.166	Hsu et al. 2011
	184	0.818	0.182	Chung et al. 2009
German	280	0.680	0.320	Kölsch et al. 2004
American	727	0.655	0.345	Ozturk et al. 2005
Serbian	130	0.637	0.363	Stamenkovic et al. 2013
Chinese	215	0.853	0.137	Fu et al. 2008
Italian	157	0.876	0.124	Capurso et al. 2010
Population	**Number of sample**	**Wild allele (A)**	**Variant allele (G)**	**Reference**
Turkish	**130**	**0.596**	**0.404**	**This Study**
Turkish	194	0.781	0.219	Takeshita et al. 2009
Taiwanese	251	0.741	0.259	Chung et al. 2011
	764	0.753	0.247	Hsu et al. 2011
Brazil	222	0.626	0.374	Morari et al. 2006
American	732	0.695	0.305	Ozturk et al. 2005
Serbia	124	0.669	0.331	Stamenkovic et al. 2013
Japanese	369	0.726	0.274	Kiyohara et al. 2010
	102	0.784	0.216	Takeshita et al. 2009
Thai	151	0.770	0.230	Chariyalertsak et al. 2009
Iranian	134	0.630	0.370	Masoudi et al. 2009