

Supplementary Table 11. Allele combinations of *DICER*, *DROSHA*, *RAN*, and *XPO5* polymorphisms between ischemic stroke patients and control subjects by multidimensional reduction method

Haplotype	Controls (2n=806)	Cases (2n=1,170)	OR (95% CI)*	P†	P‡
<i>DICER</i> rs13078 A>T- <i>DICER</i> rs3742330 A>G- <i>DROSHA</i> rs6877842 C>G- <i>DROSHA</i> rs10719 T>C- <i>RAN</i> rs14035 C>T- <i>XPO5</i> rs11077 A>C					
A-A-C-T-C-A	207 (25.7)	301 (25.7)	1.000 (reference)		
A-A-C-T-C-C	32 (4.0)	23 (2.0)	0.645 (0.368–1.129)	0.157	0.165
A-A-C-T-T-C	9 (1.1)	3 (0.3)	0.299 (0.080–1.116)	0.079	0.095
A-A-C-C-C-C	9 (1.1)	3 (0.3)	0.299 (0.080–1.116)	0.079	0.095
A-A-C-C-T-C	0	14 (1.2)	26.02 (1.544–438.5)	0.0002	0.001
A-A-G-T-C-A	8 (1.0)	0	0.053 (0.003–0.919)	0.003	0.009
A-G-C-T-C-A	184 (22.8)	286 (24.4)	1.394 (1.088–1.786)	0.010	0.024
A-G-C-T-C-C	21 (2.6)	14 (1.2)	0.598 (0.298–1.200)	0.165	0.165
A-G-C-T-T-A	36 (4.5)	70 (6.0)	1.744 (1.130–2.693)	0.014	0.028
A-G-C-C-C-A	39 (4.8)	86 (7.4)	1.978 (1.309–2.988)	0.001	0.004
A-G-C-C-C-C	1 (0.1)	18 (1.5)	16.15 (2.140–121.8)	0.0002	0.001
A-G-G-T-C-A	6 (0.7)	19 (1.6)	2.841 (1.118–7.218)	0.024	0.038
T-G-C-T-C-A	2 (0.2)	11 (0.9)	4.934 (1.083–22.47)	0.025	0.038
<i>DICER</i> rs3742330 A>G- <i>DROSHA</i> rs6877842 C>G- <i>DROSHA</i> rs10719 T>C- <i>RAN</i> rs14035 C>T- <i>XPO5</i> rs11077 A>C					
A-C-T-C-A	220 (27.3)	321 (27.4)	1.000 (reference)		
A-C-T-C-C	34 (4.2)	23 (2.0)	0.464 (0.266–0.809)	0.007	0.011
A-C-T-T-A	74 (9.2)	70 (6.0)	0.648 (0.448–0.938)	0.023	0.031
A-C-T-T-C	11 (1.4)	3 (0.3)	0.187 (0.052–0.678)	0.006	0.011
A-C-C-T-C	0	14 (1.2)	19.89 (1.180–335.4)	0.001	0.003
A-G-T-C-A	8 (1.0)	0	0.040 (0.002–0.703)	0.001	0.003
G-C-T-C-C	22 (2.7)	15 (1.3)	0.467 (0.237–0.921)	0.037	0.042
G-C-C-C-A	39 (4.8)	88 (7.5)	1.546 (1.022–2.340)	0.043	0.043
G-C-C-C-C	1 (0.1)	20 (1.7)	13.71 (1.825–102.9)	0.0004	0.003
<i>DICER</i> rs3742330 A>G- <i>DROSHA</i> rs10719 T>C- <i>RAN</i> rs14035 C>T- <i>XPO5</i> rs11077 A>C					
A-T-C-A	230 (28.5)	323 (27.6)	1.000 (reference)		
A-T-C-C	35 (4.3)	25 (2.1)	0.509 (0.296–0.873)	0.014	0.024
A-T-T-A	77 (9.6)	79 (6.8)	0.731 (0.511–1.044)	0.099	0.099
A-T-T-C	11 (1.4)	4 (0.3)	0.259 (0.081–0.824)	0.017	0.024
A-C-C-C	12 (1.5)	4 (0.3)	0.237 (0.076–0.746)	0.010	0.023
A-C-T-C	0	14 (1.2)	20.66 (1.226–348.4)	0.001	0.004
G-T-C-C	26 (3.2)	17 (1.5)	0.466 (0.247–0.878)	0.024	0.028
G-C-C-C	0	20 (1.7)	29.21 (1.757–485.8)	<0.0001	0.0001
<i>DICER</i> rs3742330 A>G- <i>DROSHA</i> rs10719 T>C- <i>XPO5</i> rs11077 A>C					
A-T-A	308 (38.2)	403 (34.4)	1.000 (reference)		
A-T-C	44 (5.5)	28 (2.4)	0.486 (0.296–0.799)	0.004	0.010
G-T-A	233 (28.9)	390 (33.3)	1.279 (1.027–1.594)	0.029	0.048
G-T-C	28 (3.5)	22 (1.9)	0.601 (0.337–1.070)	0.104	0.104
G-C-A	65 (8.1)	121 (10.3)	1.423 (1.017–1.991)	0.045	0.056
G-C-C	3 (0.4)	20 (1.7)	5.095 (1.500–17.31)	0.004	0.010
<i>DICER</i> rs3742330 A>G- <i>XPO5</i> rs11077 A>C					
A-A	418 (51.9)	570 (48.7)	1.000 (reference)		
A-C	57 (7.1)	48 (4.1)	0.618 (0.412–0.925)	0.022	0.022
G-A	298 (37.0)	511 (43.7)	1.257 (1.039–1.522)	0.020	0.022

Values are presented as number (%).

RAN, Ran GTPase; XPO5, exportin 5; OR, odds ratio; CI, confidence interval.

*Odds ratios was calculated to reference for total frequency; †P-value calculated by chi-square test; ‡P-value calculated by false discovery rate test.