Supplemental Information

Association of Common Genetic Variants in

Pre-microRNAs and Neuroblastoma Susceptibility:

A Two-Center Study in Chinese Children

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Table S1 Frequency distribution of selected characteristics in neuroblastoma cases and cancer-free controls

Variables	Guangdong province					Henan province				
	Cases (N=275)		Controls (N=531)		P [a]	Cases (N=118)		Controls (N=281)		P [a]
	No.	%	No.	%		No.	%	No.	%	
Age range, month	0-132		0.07-156		0.229	0-131.1		0.1-144.0		0.484
Mean ± SD	31.50±25.43		29.73±24.86			46.24±29.98		44.97±33.23		
<12	70	25.45	145	27.31		9	7.63	32	11.39	
12-60	177	64.36	313	58.95		76	64.41	179	63.70	
>60	28	10.18	73	13.75		33	27.97	70	24.91	
Gender					0.510					0.196
Female	114	41.45	233	43.88		54	45.76	109	38.79	
Male	161	58.55	298	56.12		64	54.24	172	61.21	
Clinical stages [b]										
I	54	19.64				15	12.71			
II	62	22.55				31	26.27			
III	49	17.82				19	16.10			
IV	94	34.18				49	41.53			
4s	8	2.91				3	2.54			
NA	8	2.91				1	0.85			
Sites of origin										
Adrenal gland	64	23.27				89	75.42			
Retroperitoneal region	87	31.64				/	/			
Mediastinum	90	32.73				19	16.10			
Other region	26	9.45				10	8.47			
NA	8	2.91				/	/			

SD, standard deviation; NA, not available.

[a] Two-sided χ^2 test for distributions between neuroblastoma cases and cancer-free controls.

[b] INSS criteria defined stage 4s as age <1 year old with localized primary tumor as delineated in stage I or II, with dissemination limited to liver, skin, or bone marrow.

Table S2 Logistic regression analyses on associations between selected polymorphisms and neuroblastoma risk in Chinese children (homozygous and allele comparing models)

miRNA	SNP	Allele		Case (N=393)			Control (N=812)			Homozygous (BB vs. AA)		Allele comparing (B vs. A)	
		A	B	AA	AB	BB	AA	AB	BB	AOR [a] (95% CI)	P [a]	AOR [a] (95% CI)	P [a]
miR-27a	rs895819	T	C	220	153	20	442	312	58	0.70 (0.41-1.19)	0.185	0.91 (0.75-1.11)	0.354
miR-34b/c	rs4938723	T	C	221	107	49	377	358	75	1.11 (0.75-1.66)	0.597	**0.82 (0.68-0.99)**	**0.039**
miR-137	rs1625579	T	G	343	46	3	719	90	1	6.28 (0.65-60.51)	0.112	1.18 (0.83-1.68)	0.354
miR-146a	rs2910164	C	G	142	189	60	282	397	130	0.91 (0.63-1.32)	0.621	0.95 (0.80-1.14)	0.591
miR-149	rs2292832	T	C	286	62	32	560	172	59	1.06 (0.68-1.67)	0.789	0.88 (0.70-1.11)	0.294
miR-196a2	rs11614913	T	C	107	192	94	230	399	183	1.10 (0.79-1.55)	0.566	1.05 (0.89-1.25)	0.566
miR-218	rs11134527	A	G	154	164	73	276	403	131	1.00 (0.70-1.41)	0.986	0.94 (0.79-1.12)	0.504
miR-423	rs6505162	C	A	244	132	17	522	258	31	1.16 (0.63-2.15)	0.626	1.08 (0.88-1.34)	0.436
miR-608	rs4919510	G	C	127	190	76	227	405	179	0.76 (0.54-1.08)	0.112	0.87 (0.73-1.03)	0.099

AOR, adjusted odds ratio; CI, confidence interval.

The results were in bold if the 95% CI excluded 1 or *P*<0.05.

[a] Adjusted for age and gender.

Table S3 Function of selected polymorphisms as predicted by SNPinfo (http://snpinfo.niehs.nih.gov/) software

miRNA	rs	Chr	Allele	TFBS	Splicing (ESE or ESS)	Allele	Asian	CHB
miR-27a	rs895819	19	C/T	Y	Y	T	--	0.711
miR-34b/c	rs4938723	11	C/T	Y	--	T	0.669	0.643
miR-137	rs1625579	1	T/G	--	--	T	0.947	0.940
miR-146a	rs2910164	5	C/G	Y	Y	G	0.469	0.446
miR-149	rs2292832	2	C/T	Y	Y	C	0.339	0.315
miR-196a2	rs11614913	12	C/T	Y	Y	C	0.427	0.411
miR-218	rs11134527	5	A/G	Y	--	G	0.417	0.367
miR-423	rs6505162	17	A/C	Y	Y	C	0.811	0.833
miR-608	rs4919510	10	C/G	Y	Y	C	0.491	0.488

TFBS, transcription factor binding sites; ESE, exon splicing enhancer; ESS, exon splicing silencer; CHB, Han Chinese in Beijing, China.

Table S4 Association of *miR-34b/c* rs4938723 T>C and *miR-218* rs11134527 A>G polymorphisms with neuroblastoma susceptibility

Genotype	Guangdong province				Henan province				Combined			
	Cases (N=275)	Controls (N=531)	Adjusted OR (95% CI) [a]	*P* [a]	Cases (N=118)	Controls (N=281)	Adjusted OR (95% CI) [a]	*P* [a]	Cases (N=393)	Controls (N=812)	Adjusted OR (95% CI) [a]	*P* [a]
rs4938723 T>C												
TT	147 (56.76)	244 (46.12)	1.00		74 (62.71)	133 (47.33)	1.00		221 (58.62)	377 (46.54)	1.00	
TC	80 (30.89)	236 (44.61)	**0.56 (0.41-0.78)**	**0.0005**	27 (22.88)	122 (43.42)	**0.40 (0.24-0.67)**	**0.0004**	107 (28.38)	358 (44.20)	**0.51 (0.39-0.67)**	**<0.0001**
CC	32 (12.36)	49 (9.26)	1.07 (0.65-1.75)	0.797	17 (14.41)	26 (9.25)	1.15 (0.58-2.26)	0.690	49 (13.00)	75 (9.26)	1.11 (0.75-1.66)	0.597
Additive			0.84 (0.67-1.05)	0.122			0.79 (0.57-1.10)	0.162			**0.83 (0.69-0.997)**	**0.046**
Dominant	112 (43.24)	285 (53.88)	**0.65 (0.48-0.88)**	**0.005**	44 (37.29)	148 (52.67)	**0.54 (0.35-0.83)**	**0.006**	156 (41.38)	433 (53.46)	**0.62 (0.48-0.79)**	**0.0001**
Recessive	227 (87.64)	480 (90.74)	1.36 (0.85-2.19)	0.202	101 (85.59)	255 (90.75)	1.60 (0.83-3.08)	0.162	328 (87.00)	735 (90.74)	1.46 (1.00-2.15)	0.052
T	374 (72.20)	724 (68.43)	1.00		175 (74.15)	388 (69.04)	1.00		549 (72.81)	1112 (68.64)	1.00	
C	144 (27.80)	334 (31.57)	0.83 (0.66-1.05)	0.113	61 (25.85)	174 (30.96)	0.77 (0.55-1.09)	0.141	205 (27.19)	508 (31.36)	**0.82 (0.68-0.99)**	**0.039**
rs11134527 A>G												
AA	107 (39.19)	162 (30.62)	1.00		47 (39.83)	114 (40.57)	1.00		154 (39.39)	276 (34.07)	1.00	
AG	117 (42.86)	286 (54.06)	**0.62 (0.45-0.86)**	**0.004**	47 (39.83)	117 (41.64)	0.98 (0.61-1.59)	0.940	164 (41.94)	403 (49.75)	**0.73 (0.56-0.96)**	**0.022**
GG	49 (17.95)	81 (15.31)	0.90 (0.58-1.38)	0.618	24 (20.34)	50 (17.79)	1.17 (0.65-2.12)	0.602	73 (18.67)	131 (16.17)	1.00 (0.70-1.41)	0.986
Additive			0.87 (0.70-1.08)	0.211			1.07 (0.80-1.43)	0.666			0.94 (0.79-1.12)	0.509
Dominant	166 (60.81)	367 (69.38)	**0.68 (0.50-0.93)**	**0.014**	71 (60.17)	167 (59.43)	1.04 (0.67-1.61)	0.866	237 (60.61)	534 (65.93)	0.80 (0.62-1.02)	0.073
Recessive	224 (82.05)	448 (84.69)	1.18 (0.80-1.75)	0.401	94 (79.66)	231 (82.21)	1.18 (0.69-2.04)	0.546	318 (81.33)	679 (83.83)	1.19 (0.86-1.63)	0.290
A	331 (60.62)	610 (57.66)	1.00		141 (59.75)	345 (61.39)	1.00		472 (60.36)	955 (58.95)	1.00	
G	215 (39.38)	448 (42.34)	0.88 (0.71-1.08)	0.219	95 (40.25)	217 (38.61)	1.08 (0.79-1.47)	0.645	310 (39.64)	665 (41.05)	0.94 (0.79-1.12)	0.504

OR, odds ratio; CI, confidence interval.

The results were in bold if the 95% CI excluded 1 or *P*<0.05.

[a] χ^2 test for genotype distributions between neuroblastoma patients and controls.

[b] Adjusted for age and gender.