

**Supplemental Table 1.** Frequency distribution of selected characteristics in cases and controls

Variables	Cases (n=469)		Controls (n=998)		<i>P</i> <sup>a</sup>
	No.	%	No.	%	
Age range, month	0.00-132.00		0.03-156.00		0.263
Mean ± SD	34.07±27.60		32.89±27.43		
≤18	169	36.03	390	39.08	
>18	300	63.97	608	60.92	
Gender					0.911
Female	196	41.79	414	41.48	
Male	273	58.21	584	58.52	
INSS stages					
I	133	28.42	/	/	
II	100	21.37	/	/	
III	69	14.74	/	/	
IV	147	31.41	/	/	
4s	11	2.35	/	/	
NA	8	1.71	/	/	
Sites of origin					
Adrenal gland	162	34.54	/	/	
Retroperitoneal region	138	29.42	/	/	
Mediastinum	121	25.80	/	/	
Other region	40	8.53	/	/	
NA	8	1.71	/	/	

SD, standard deviation; NA, not available.

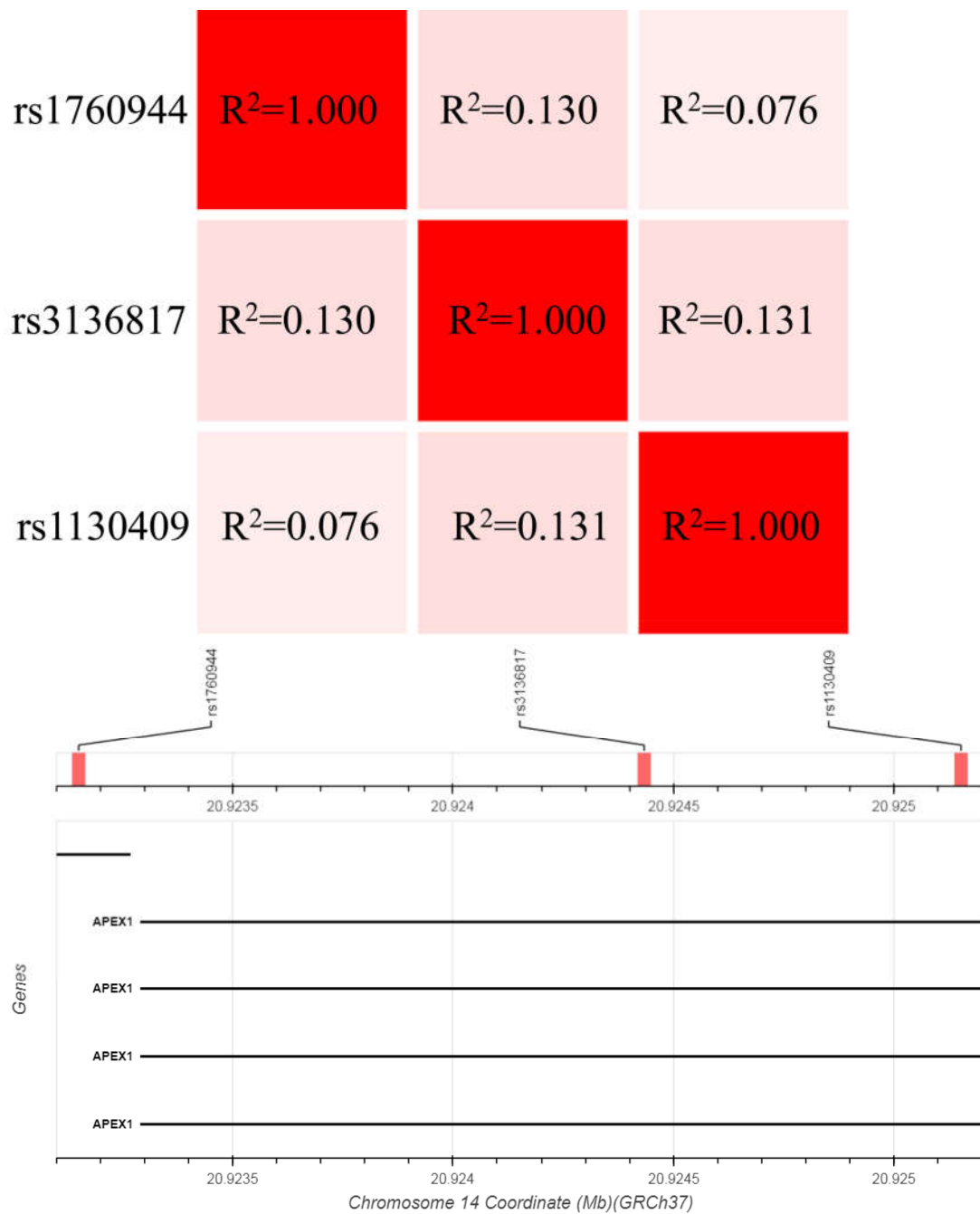
<sup>a</sup> Two-sided  $\chi^2$  test for distributions between neuroblastoma cases and cancer-free controls.

**Supplemental Table 2.** Association between *APEXI* gene polymorphisms and neuroblastoma risk (Divided subjects)

Genotype	Guangdong province				Henan province				Shaanxi province			
	Cases (N=275)	Controls (N=531)	AOR (95% CI) <sup>a</sup>	P <sup>a</sup>	Cases (N=118)	Controls (N=281) <sup>b</sup>	AOR (95% CI) <sup>a</sup>	P <sup>a</sup>	Cases (N=76)	Controls (N=186)	AOR (95% CI) <sup>a</sup>	P <sup>a</sup>
rs1130409 T>G												
TT	108 (39.27)	210 (39.55)	1.00		37 (31.36)	77 (27.50)	1.00		30 (39.47)	53 (28.49)	1.00	
TG	129 (46.91)	227 (42.75)	1.10 (0.80-1.51)	0.547	56 (47.46)	152 (54.29)	0.77 (0.46-1.26)	0.296	31 (40.79)	88 (47.31)	0.62 (0.34-1.15)	0.129
GG	38 (13.82)	94 (17.70)	0.78 (0.50-1.22)	0.282	25 (21.19)	51 (18.21)	0.97 (0.52-1.81)	0.912	15 (19.74)	45 (24.19)	0.59 (0.28-1.22)	0.154
Additive			0.93 (0.76-1.14)	0.486			0.96 (0.70-1.31)	0.779			0.75 (0.52-1.08)	0.120
Dominant	167 (60.73)	321 (60.45)	1.01 (0.75-1.36)	0.952	81 (68.64)	203 (72.50)	0.82 (0.51-1.31)	0.401	46 (60.53)	133 (71.51)	0.61 (0.35-1.07)	0.085
Recessive	237 (86.18)	437 (82.30)	0.74 (0.50-1.12)	0.157	93 (78.81)	229 (81.79)	1.14 (0.66-1.97)	0.633	61 (80.26)	141 (75.81)	0.76 (0.40-1.47)	0.420
rs1760944 T>G												
TT	101 (36.73)	186 (35.03)	1.00		34 (28.81)	93 (33.21)	1.00		20 (26.32)	55 (29.57)	1.00	
TG	128 (46.55)	245 (46.14)	0.96 (0.70-1.33)	0.816	62 (52.54)	125 (44.64)	1.38 (0.84-2.27)	0.210	40 (52.63)	100 (53.76)	1.11 (0.59-2.09)	0.748
GG	46 (16.73)	100 (18.83)	0.85 (0.56-1.31)	0.462	22 (18.64)	62 (22.14)	0.99 (0.53-1.85)	0.970	16 (21.05)	31 (16.67)	1.43 (0.65-3.15)	0.380
Additive			0.93 (0.76-1.14)	0.489			1.03 (0.76-1.39)	0.863			1.19 (0.80-1.76)	0.398
Dominant	174 (63.27)	345 (64.97)	0.93 (0.69-1.26)	0.642	84 (71.19)	187 (66.79)	1.25 (0.78-2.00)	0.358	56 (73.68)	131 (70.43)	1.19 (0.65-2.16)	0.581
Recessive	229 (83.27)	431 (81.17)	0.87 (0.59-1.28)	0.482	96 (81.36)	218 (77.86)	0.81 (0.47-1.40)	0.456	60 (78.95)	155 (83.33)	1.33 (0.68-2.61)	0.404
rs3136817 T>C												
TT	232 (84.36)	443 (83.43)	1.00		97 (82.20)	230 (82.14)	1.00		67 (88.16)	142 (76.34)	1.00	
TC	40 (14.55)	85 (16.01)	0.90 (0.60-1.35)	0.600	18 (15.25)	47 (16.79)	0.90 (0.50-1.63)	0.729	9 (11.84)	40 (21.51)	0.48 (0.22-1.05)	0.065
CC	3 (1.09)	3 (0.56)	1.87 (0.37-9.34)	0.448	3 (2.54)	3 (1.07)	2.33 (0.46-11.78)	0.308	0 (0.00)	4 (2.15)	/	/
Additive			0.97 (0.67-1.41)	0.872			1.07 (0.65-1.75)	0.792			0.43 (0.21-0.91)	0.026
Dominant	43 (15.64)	88 (16.57)	0.93 (0.62-1.38)	0.720	21 (17.80)	50 (17.86)	0.99 (0.56-1.74)	0.962	9 (11.84)	44 (23.66)	0.44 (0.20-0.94)	0.035
Recessive	272 (98.91)	528 (99.44)	1.90 (0.38-9.49)	0.436	115 (97.46)	277 (98.93)	2.37 (0.47-11.96)	0.297	76 (100.00)	182 (97.85)	/	/
Combined effect of protective genotypes <sup>c</sup>												
0	184 (66.91)	337 (63.47)	1.00		75 (63.56)	160 (57.14)	1.00		46 (60.53)	101 (54.30)	1.00	
1-3	91 (33.09)	194 (36.53)	0.87 (0.64-1.18)	0.358	43 (36.44)	120 (42.86)	0.75 (0.48-1.17)	0.203	30 (39.47)	85 (45.70)	0.78 (0.45-1.33)	0.357

AOR, adjusted odds ratio; CI, confidence interval.

<sup>a</sup> Adjusted for age and gender.<sup>b</sup> One was failed in genotyping.<sup>c</sup> Protective genotypes were rs1130409 GG, rs1760944 GG and rs3136817 TC/TT derived from combined subjects.



**Supplemental Figure 1.** Linkage disequilibrium analysis for the three selected polymorphisms in *APEX1* gene in Han Chinese population consisting of CHS (Southern Han Chinese) and CHB (Han Chinese in Beijing, China) subjects using data from LDlink online software (<https://ldlink.nci.nih.gov/?tab=ldmatrix>).