Supplemental Table 1: Frequency distribution of selected variables for Wilms' tumor cases and cancer-free controls.

| Variables	Cases (n=145)		Controls (n=531)		P^{a}
	No.	%	No.	%	
Age range, month	1-132		0.07-156		0.725
Mean ± SD	26.17 ± 21.48		29.73 ± 24.86		
≤18	66	45.52	233	43.88	
>18	79	54.48	298	56.12	
Gender					0.956
Female	64	44.14	233	43.88	
Male	81	55.86	298	56.12	
Clinical stages					
I	4	2.76			
II	49	33.79			
III	50	34.48			
IV	33	22.76			
NA	9	6.21			

SD, standard deviation; NA, not available.

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

Supplemental Table 2: Potential functions of the three selected *NEFL* polymorphisms as predicted by SNPinfo online software (https://snpinfo.niehs.nih.gov/snpinfo/snpfunc.html).

rs	Chromosome	Allele	TFBS	miRNA (miRanda)	Allele	Asian	CHB
rs11994014	8	A/G	--	--	G	0.649	0.613
rs2979704	8	C/T	Y	Y	T	0.605	0.614
rs1059111	8	T/A	Y	Y	A	0.606	0.567

TFBS, transcription factor binding sites; CHB, Han Chinese in Beijing, China.
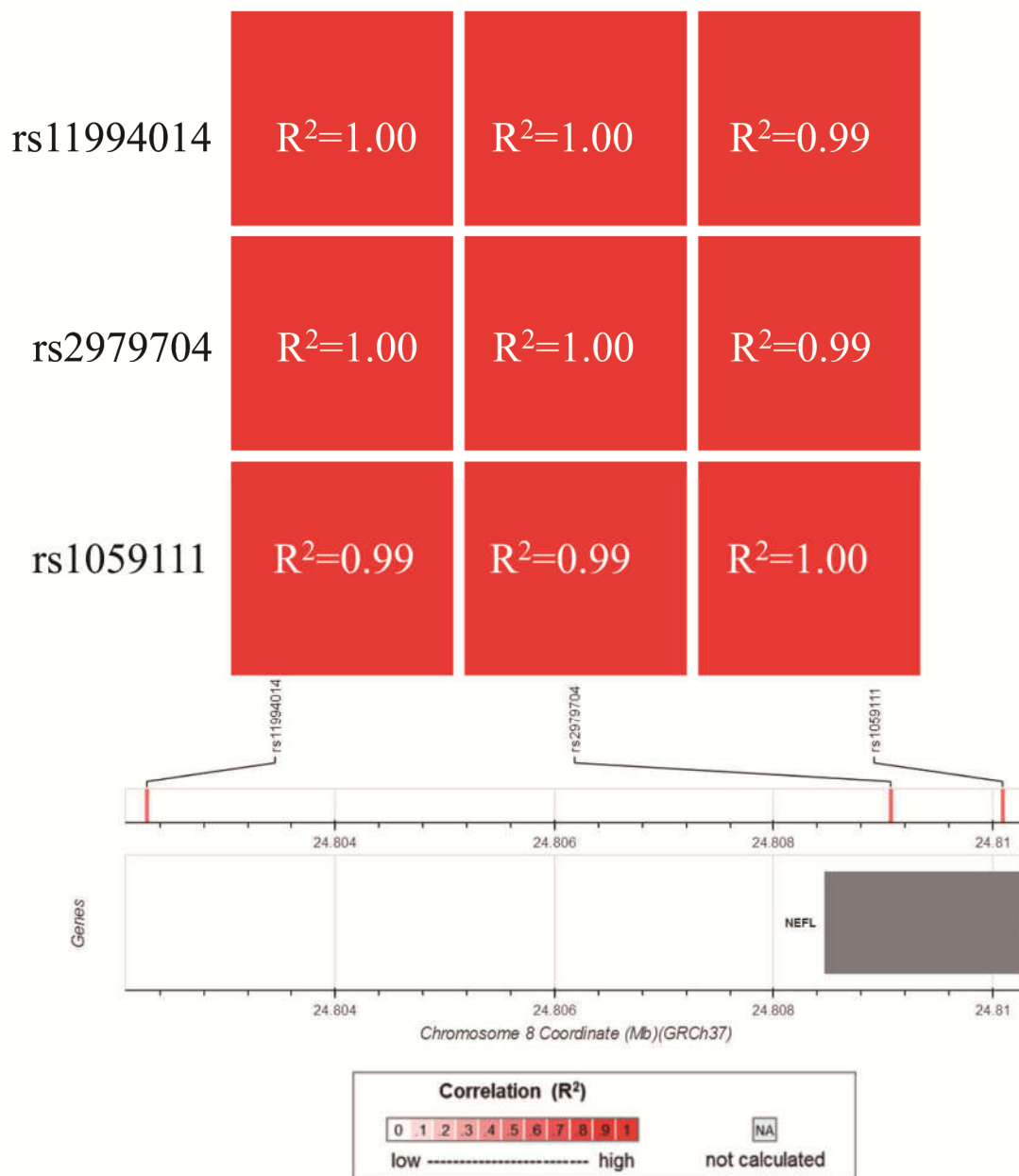
Supplemental Figure 1: Linkage disequilibrium analysis for the three selected polymorphisms in *NEFL* gene in Han Chinese population consisted of CHB (Han Chinese in Beijing, China) and CHS (Southern Han Chinese) subjects using data from LDlink online software (https://ldlink.nci.nih.gov/?tab=ldmatrix).