LMO1 gene polymorphisms contribute to decreased neuroblastoma susceptibility in a Southern Chinese population

Supplementary Materials

Supplementary Table S1: SNPs captured by the four GWAS identified SNPs as predicted by SNPinfo (http://snpinfo.niehs.nih.gov/) software

rs[a]	Chr	Allele	LDsnp	Pop/LD	TFBS	Splicing (ESE or ESS)	miRNA (miRanda)	nsSNP	Reg Potential	Conservation	Nearby Gene	Distance (bp)	Allele	Asian	CHB
rs10840002	11	A/G	rs10840002|rs4758051	1|CHB/0.825	—	—	—	—	0.103058	0	RIC3||LMO1	−52454||−2831	A	0.5	0.47
rs110419	11	A/G	rs110419	1	—	—	—	—	0	0	LMO1	6996|32553	A	0.634	0.53
rs110420	11	C/T	rs110419	CHB/1.000	—	—	—	—	0	0	LMO1	7192|32357	T	0.491	0.545
rs204926	11	G/A	rs110419	CHB/0.607	—	—	—	—	0	0	LMO1	9249|30300	G	0.64	0.628
rs204928	11	G/A	rs110419	CHB/0.906	—	—	—	—	0	0.001	LMO1	8576|30973	A	0.614	0.568
rs3750952	11	G/C	rs110419	CHB/0.780	—	Y	—	—	0.524312	1	LMO1	6064|33485	G	0.632	0.614
rs4758317	11	A/C	rs110419	CHB/0.976	—	—	—	—	0	0	LMO1	4954|34595	A	0.394	0.464
rs204937	11	T/C	rs204938	CHB/0.804	—	—	—	—	0.232693	0	LMO1	35081||4468	T	0.844	0.851
rs204938	11	T/C	rs204938	1	—	—	—	—	0.278185	0	LMO1	32340||7209	C	0.211	0.179
rs2061037	11	A/G	rs204938	CHB/0.676	—	—	—	—	0	0	LMO1	20772||8777	G	0.833	0.827
rs484161	11	C/T	rs204938	CHB/0.648	—	—	—	—	0.373993	0	LMO1	18668||20881	T	0.18	0.202
rs10840000	11	C/G	rs4758051|rs10840002	CHB/0.950|CHB/0.756	—	—	—	—	0.106824	0	RIC3||LMO1	−49541||−5744	C	0.506	0.571
rs4758050	11	C/G	rs4758051|rs10840002	CHB/1.000|CHB/0.829	—	—	—	—	0.067678	0	RIC3||LMO1	−47973||−7312	G	0.534	0.478
rs4758051	11	A/G	rs4758051|rs10840002	1|CHB/0.825	—	—	—	—	0	0	RIC3||LMO1	−48067||−7218	G	0.528	0.518

SNP, single nucleotide polymorphism; GWAS, genome-wide association study; LD, linkage disequilibrium; TFBS, transcription factor binding sites; ESE, exon *splicing* enhancer; ESS, exon *splicing* silencer; CHB, Han Chinese in Beijing, China

[a]The rs in bold were discovered by previous genome-wide association study.