

**Supplementary Table 1.** Log-linear, likelihood-ratio association analysis between 29 regulatory SNPs from 12 cell-cycle genes and childhood pre-B ALL.

Gene, DNA variant	Model	LR Chi2 (df)	P
<b>CCND1</b>			
rs1944129	Child vs. Null	1.2295 (2)	0.5408
	Mother vs. Null	2.1512 (2)	0.3411
rs36225395	Child vs. Null	0.4281 (2)	0.8073
	Mother vs. Null	1.7239 (2)	0.4223
<b>CDC25a</b>			
rs1903061	Child vs. Null	0.2266 (2)	0.8929
	Mother vs. Null	0.2315 (2)	0.8907
<b>CDKN1A</b>			
rs733590	Child vs. Null	2.5003 (2)	0.2865
	Mother vs. Null	2.6508 (2)	0.2657
rs762624	Child vs. Null	0.3833 (2)	0.8256
	Mother vs. Null	1.9700 (2)	0.3734
rs2395655	Child vs. Null	1.8532 (2)	0.3959
	Mother vs. Null	1.9417 (2)	0.3788
<b>CDKN1B</b>			
rs3759217	Child vs. Null	1.8690 (2)	0.3928
	Mother vs. Null	0.7517 (2)	0.6867
rs35756741	Child vs. Null	7.5044 (2)	0.0235
	Mother vs. Null	1.2860 (2)	0.5257
	Child + Mother vs. Null	8.5604 (4)	0.0731
	Child + Mother vs. Child	1.0560 (2)	0.5898
rs36228499	Child vs. Null	0.2166 (2)	0.8973
	Mother vs. Null	2.8311 (2)	0.2428
<b>CDKN2A</b>			
rs36228834	Child vs. Null	14.4130 (2)	<b>0.0007</b>
	Mother vs. Null	0.65476 (2)	0.7209
	Child + Mother vs. Null	22.5809 (4)	0.0002
	Child + Mother vs. Child	8.1678 (2)	0.0168

<b>CDKN2B</b>			
rs36229158	Child vs. Null	5.6281 (2)	0.0600
	Mother vs. Null	1.4635 (2)	0.4811
	Child + Mother vs. Null	13.2885 (4)	0.0099
	Child + Mother vs. Child	7.6604 (2)	0.0217
rs2069416 <sup>1</sup>	Child vs. Null	10.1261 (2)	<b>0.0063</b>
	Mother vs. Null	0.9204 (2)	0.6312
	Child + Mother vs. Null	12.3208 (4)	0.0152
	Child + Mother vs. Child	2.1947 (2)	0.3338
rs2069418	Child vs. Null	0.1654 (2)	0.9206
	Mother vs. Null	3.4934 (2)	0.1744
<b>E2F1</b>			
rs3213141	Child vs. Null	5.3498 (2)	0.0689
	Mother vs. Null	3.1276 (2)	0.2093
<b>HDAC1</b>			
rs1741981	Child vs. Null	4.3556 (2)	0.1133
	Mother vs. Null	0.1855 (2)	0.9114
rs36212121	Child vs. Null	3.8760 (2)	0.1440
	Mother vs. Null	0.0251 (2)	0.9875
rs36212119	Child vs. Null	0.0436 (2)	0.9784
	Mother vs. Null	1.5479 (2)	0.4612
<b>MADH3</b>			
rs36221701	Child vs. Null	0.5317 (2)	0.7666
	Mother vs. Null	1.0401 (2)	0.5945
rs36222034	Child vs. Null	5.0971 (2)	0.0782
	Mother vs. Null	5.5164 (2)	0.0634
rs11633026	Child vs. Null	0.9712 (2)	0.6153
	Mother vs. Null	0.0025 (2)	0.9987
<b>MDM2</b>			
rs1144944	Child vs. Null	1.9874 (2)	0.3702
	Mother vs. Null	0.4247 (2)	0.8087
rs3730485	Child vs. Null	0.6397 (2)	0.7263
	Mother vs. Null	0.5579 (2)	0.7566

rs937282	Child vs. Null	0.0355 (2)	0.9824
	Mother vs. Null	1.7830 (2)	0.4100
rs2279744	Child vs. Null	2.3131 (2)	0.3146
	Mother vs. Null	4.2749 (2)	0.1180
<b>RB1</b>			
rs1573601	Child vs. Null	0.1689 (2)	0.9190
	Mother vs. Null	0.2512 (2)	0.8820
<b>TGFB1</b>			
rs2317130	Child vs. Null	3.3133 (2)	0.1908
	Mother vs. Null	1.4944 (2)	0.4737
rs4803457	Child vs. Null	1.0157 (2)	0.6018
	Mother vs. Null	1.5627 (2)	0.4578
rs11466313	Child vs. Null	2.3172 (2)	0.3139
	Mother vs. Null	1.4790 (2)	0.4773
rs1800469	Child vs. Null	1.8827 (2)	0.3901
	Mother vs. Null	2.4241 (2)	0.2976

Likelihood-ratio tests were performed in a forward stepwise fashion. The most significant single-step test (Child vs. Null or Mother vs. Null) was tested against a joint effects model in a 2 degree of freedom likelihood-ratio test (Child + Mother vs. Child or Child + Mother vs. Mother). Mating symmetry (i.e. six mating-type parameters) was assumed at all loci but variants rs1144944 and rs3730485 of the *MDM2* gene, as well as *CDKN2B* rs2069416 for which MA models (nine mating-type parameters) were used to test for association. Multiple testing corrections were performed on the single-step association tests using the Benjamini-Hochberg false discovery rate (FDR) method with a type I error rate of 10%; nominal P values are shown, those in bold remain significant after FDR adjustment.

LR Chi2 indicates likelihood-ratio chi-square test; df, degrees of freedom.

<sup>1</sup>*CDKN2B* SNP rs2069416 is tri-allelic A>T,C. For analysis, individuals were grouped according to their T allele such that \*\*>\*T>TT.