

Table S1. Evaluation of the independent effects in the multivariable analysis of 20 xMHC SNPs potentially associated with childhood BCP-ALL (p-value < 0.01 in the singles SNP analysis).

SNP	Position	Minor allele	Test ^a	Model							
				SNP + covariates		SNP + rs7747023 + covariates		SNP + rs3130785 + covariates		SNP + rs9296068 + covariates	
				OR (95% CI) ^b	p-value	OR (95% CI) ^b	p-value	OR (95% CI) ^b	p-value	OR (95% CI) ^b	p-value
Region A											
rs3118361	29006266	A	dom	1.45 (1.11-1.89)	6.4x10 ⁻³	1.42 (1.09-1.85)	0.010	1.50 (1.14-1.95)	3.2x10 ⁻³	1.34 (1.03-1.76)	0.032
rs2032502	29009544	A	dom	0.70 (0.53-0.91)	7.5x10 ⁻³	0.88 (0.61-1.28)	0.513	0.70 (0.53-0.91)	8.1x10 ⁻³	0.70 (0.53-0.91)	7.6x10 ⁻³
rs4947256	29029919	A	add	0.72 (0.57-0.91)	6.7x10 ⁻³	0.90 (0.63-1.27)	0.532	0.72 (0.57-0.92)	8.1x10 ⁻³	0.72 (0.56-0.91)	6.4x10 ⁻³
rs7747023 ^c	29133659	G	add	0.73 (0.60-0.89)	1.7x10 ⁻³	NA	NA	0.73 (0.60-0.89)	1.6x10 ⁻³	0.73 (0.60-0.88)	1.4x10 ⁻³
rs9348821	29155182	G	add	0.74 (0.61-0.89)	1.9x10 ⁻³	1.03 (0.14-7.79)	0.977	0.73 (0.60-0.89)	1.7x10 ⁻³	0.73 (0.60-0.89)	1.6x10 ⁻³
rs1883329	29285081	A	dom	1.34 (1.09-1.66)	6.7x10 ⁻³	1.24 (0.99-1.54)	0.060	1.34 (1.08-1.65)	7.7x10 ⁻³	1.33 (1.08-1.65)	8.6x10 ⁻³
Region B											
rs17281677	30730438	A	add	1.76 (1.15-2.70)	9.0x10 ⁻³	1.71 (1.12-2.63)	0.013	1.39 (0.87-2.22)	0.173	1.82 (1.19-2.80)	6.1x10 ⁻³
rs3130666	30848139	A	add	1.80 (1.22-2.66)	3.3x10 ⁻³	1.78 (1.20-2.64)	4.0x10 ⁻³	1.46 (0.94-2.26)	0.095	1.85 (1.24-2.74)	2.4x10 ⁻³
rs3130785 ^c	30904717	A	add	1.45 (1.16-1.82)	1.3x10 ⁻³	1.46 (1.16-1.83)	1.2x10 ⁻³	NA	NA	1.46 (1.16-1.83)	1.2x10 ⁻³
rs1632856	31079715	A	add	0.80 (0.68-0.95)	9.9x10 ⁻³	0.79 (0.67-0.94)	7.9x10 ⁻³	0.83 (0.70-0.99)	0.038	0.78 (0.66-0.93)	4.7x10 ⁻³
rs2156875	31425326	A	rec	0.70 (0.54-0.91)	7.6x10 ⁻³	0.69 (0.53-0.90)	5.8x10 ⁻³	0.75 (0.57-0.97)	0.031	0.67 (0.52-0.88)	3.6x10 ⁻³
rs2848716	31495946	G	rec	0.37 (0.18-0.76)	6.2x10 ⁻³	0.37 (0.18-0.75)	5.7x10 ⁻³	0.40 (0.20-0.81)	0.011	0.37 (0.18-0.76)	6.2x10 ⁻³
rs2524279	31500885	G	add	0.73 (0.58-0.92)	8.0x10 ⁻³	0.73 (0.58-0.92)	7.4x10 ⁻³	0.74 (0.58-0.93)	0.010	0.73 (0.58-0.92)	8.3x10 ⁻³
Region C											
rs9296068 ^c	33096673	C	add	1.37 (1.17-1.61)	1.2x10 ⁻⁴	1.38 (1.17-1.62)	1.0x10 ⁻⁴	1.38 (1.17-1.62)	1.2x10 ⁻⁴	NA	NA
rs406477	33113622	G	rec	2.03 (1.21-3.42)	7.7x10 ⁻³	2.10 (1.24-3.54)	5.7x10 ⁻³	1.92 (1.14-3.24)	0.015	1.70 (1.00-2.87)	0.052
rs213220	33310618	G	dom	0.69 (0.54-0.88)	2.4x10 ⁻³	0.69 (0.54-0.87)	2.1x10 ⁻³	0.69 (0.54-0.88)	2.6x10 ⁻³	0.76 (0.60-0.98)	0.032
rs213226	33317288	G	rec	1.39 (1.09-1.78)	8.4x10 ⁻³	1.40 (1.09-1.79)	8.3x10 ⁻³	1.39 (1.08-1.78)	9.4x10 ⁻³	1.27 (0.99-1.64)	0.064
rs213203 ^d	33346382	A	het	0.68 (0.55-0.84)	3.6x10 ⁻⁴	0.69 (0.56-0.85)	6.0x10 ⁻⁴	0.68 (0.55-0.84)	4.0x10 ⁻⁴	0.68 (0.55-0.84)	4.0x10 ⁻⁴
rs210179	33593214	A	rec	1.43 (1.11-1.85)	6.3x10 ⁻³	1.45 (1.12-1.87)	4.7x10 ⁻³	1.42 (1.10-1.83)	7.8x10 ⁻³	1.35 (1.04-1.75)	0.022
rs9469473	33610865	G	add	1.42 (1.13-1.78)	2.9x10 ⁻³	1.41 (1.12-1.78)	3.0x10 ⁻³	1.44 (1.15-1.82)	1.7x10 ⁻³	1.31 (1.04-1.65)	0.023

Abbreviations: CI, confidence interval; NA, not applicable; OR, odds ratio; SNP, single nucleotide polymorphism; xMHC, extended major histocompatibility complex

^aThe genetic model of inheritance assumed in the logistic regression model and corresponding to the presented results. Abbreviations: add, log-additive; dom, dominant; rec, recessive; het, heterozygotes versus homozygotes

^bORs and 95% CI for each SNP were derived using logistic regression assuming the indicated genetic model of inheritance and adjusting for child's age, sex, race/ethnicity (non-Hispanic white versus Hispanic), and additionally for either rs7747023, rs3130785, or rs9296068 as specified in the table.

^cThe 20 SNPs showing a p-value of less than 0.01 in the single SNP analysis appeared to spatially cluster within 1 of 3 regions of the xMHC. Each SNP was adjusted for rs7747023, rs3130785, and rs9296068, the SNP with strongest p-value within each region, to evaluate the independence of effects.

^dEvaluation of the genetic model of inheritance indicated a significant deviation from the log-additive model with an effect associated with heterozygotes. ORs and 95% CI were estimated for heterozygous genotypes compared to homozygous genotypes.