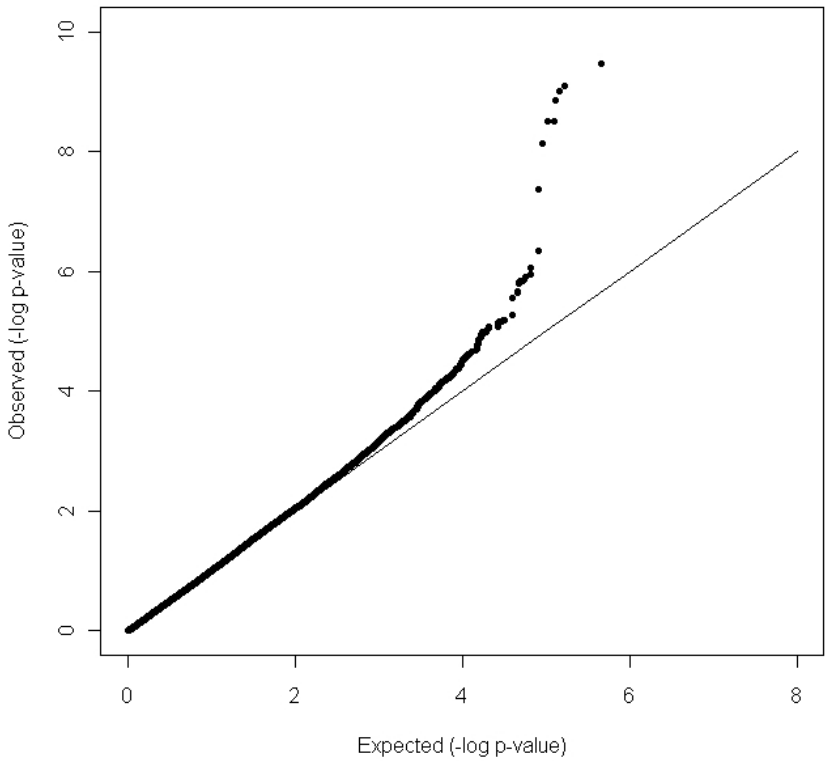
Supplementary Table 1. Summary results for top 22 markers reaching a statistical significance of $P < 5.0 \times 10^{-6}$ in the discovery phase.

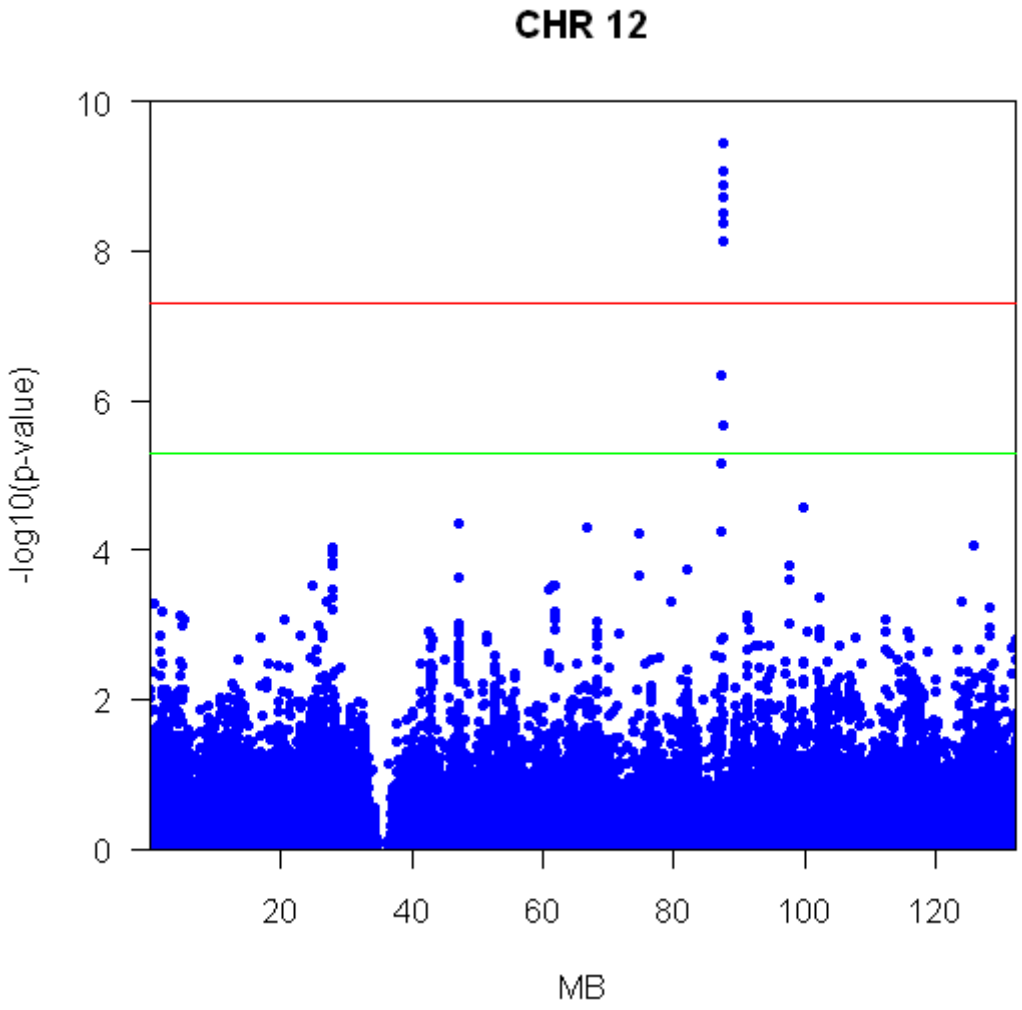
Marker[a]	Allele Major/Minor (Risk)	Chromosome	MAF Controls	MAF Cases	P-value[b]	OR (95% CI) Per allele	OR (95% CI) Heterozygote[c]	OR (95% CI) Homozygote[d]
rs4474514	A/G (A)	12	0.198	0.089	3.54×10^{-10}	0.41 (0.30-0.56)	0.43 (0.30-0.61)	0.12 (0.03-0.50)
rs3782181	T/G (T)	12	0.202	0.094	8.38×10^{-10}	0.42 (0.31-0.57)	0.42 (0.30-0.60)	0.18 (0.05-0.58)
rs3782179	A/G (A)	12	0.199	0.092	1.35×10^{-9}	0.42 (0.31-0.58)	0.43 (0.30-0.60)	0.18 (0.06-0.58)
rs11104952	C/A (C)	12	0.198	0.092	1.90×10^{-9}	0.43 (0.31-0.58)	0.43 (0.30-0.61)	0.18 (0.06-0.58)
rs1472899	T/C (T)	12	0.199	0.095	3.09×10^{-9}	0.43 (0.32-0.58)	0.43 (0.30-0.60)	0.19 (0.06-0.63)
rs1352947	A/G (A)	12	0.183	0.083	4.24×10^{-9}	0.42 (0.30-0.58)	0.41 (0.28-0.59)	0.22 (0.07-0.70)
rs995030	C/T (C)	12	0.172	0.076	7.47×10^{-9}	0.42 (0.30-0.58)	0.43 (0.29-0.62)	0.15 (0.04-0.61)
rs3770112	C/T (T)	2	0.314	0.450	4.93×10^{-8}	1.77 (1.44-2.18)	2.70 (1.94-3.76)	2.62 (1.66-4.14)
rs7486184	C/T (C)	12	0.192	0.103	4.56×10^{-7}	0.50 (0.37-0.67)	0.52 (0.37-0.72)	0.20 (0.06-0.65)
rs2524594	G/A (G)	23	0.170	0.055	8.91×10^{-7}	0.53 (0.40-0.71)	0.28[e] (0.16-0.50)	
rs1549383	G/A (A)	2	0.303	0.418	1.01×10^{-6}	1.65 (1.35-2.02)	1.77 (1.32-2.39)	2.61 (1.71-4.00)
rs6534637	G/T (T)	4	0.449	0.572	1.06×10^{-6}	1.73 (1.40-2.14)	4.52 (2.85-7.16)	3.95 (2.36-6.62)
rs7236484	T/A (A)	18	0.089	0.160	1.61×10^{-6}	1.96 (1.47-2.62)	1.63 (1.17-2.27)	13.3 (3.61-48.7)
rs6897876	C/T (C)	5	0.459	0.345	1.77×10^{-6}	0.63 (0.52-0.77)	0.78 (0.58-1.04)	0.34 (0.21-0.53)
rs3755353	G/A (A)	2	0.364	0.483	1.77×10^{-6}	1.79 (1.44-2.23)	3.38 (2.35-4.86)	2.64 (1.59-4.37)
rs7774545	A/G (G)	6	0.284	0.397	1.83×10^{-6}	1.66 (1.35-2.04)	1.92 (1.42-2.60)	2.46 (1.56-3.89)
rs6961928	C/T (T)	7	0.417	0.539	1.83×10^{-6}	1.74 (1.40-2.16)	3.30 (2.20-4.95)	3.23 (1.99-5.24)
rs12521013	G/T (G)	5	0.478	0.363	1.99×10^{-6}	0.63 (0.52-0.76)	0.82 (0.61-1.10)	0.33 (0.21-0.51)
rs26939101	A/C (A)	12	0.160	0.083	2.16×10^{-6}	0.48 (0.34-0.66)	0.48 (0.33-0.69)	0.22 (0.05-0.95)
rs4324715	T/C (T)	5	0.514	0.398	2.72×10^{-6}	0.63 (0.52-0.77)	0.89 (0.65-1.21)	0.34 (0.22-0.53)
rs2965606	T/A (A)	7	0.265	0.373	4.78×10^{-6}	1.61 (1.31-1.98)	1.64 (1.22-2.22)	2.55 (1.63-4.00)
rs17031166	C/G (G)	2	0.300	0.405	4.98×10^{-6}	1.60 (1.31-1.96)	1.67 (1.24-2.24)	2.49 (1.62-3.83)

[a]dbSNP rsnumber. [b]Difference in allele frequency determined by Fisher's Exact test. [c]OR for heterozygous carriage of minor allele compared to homozygous carriage of major allele. [d]OR for homozygous carriage of minor allele compared to homozygous carriage of major allele. [e]OR for hemizygous carriage of the minor allele compared to carriage of the major allele.

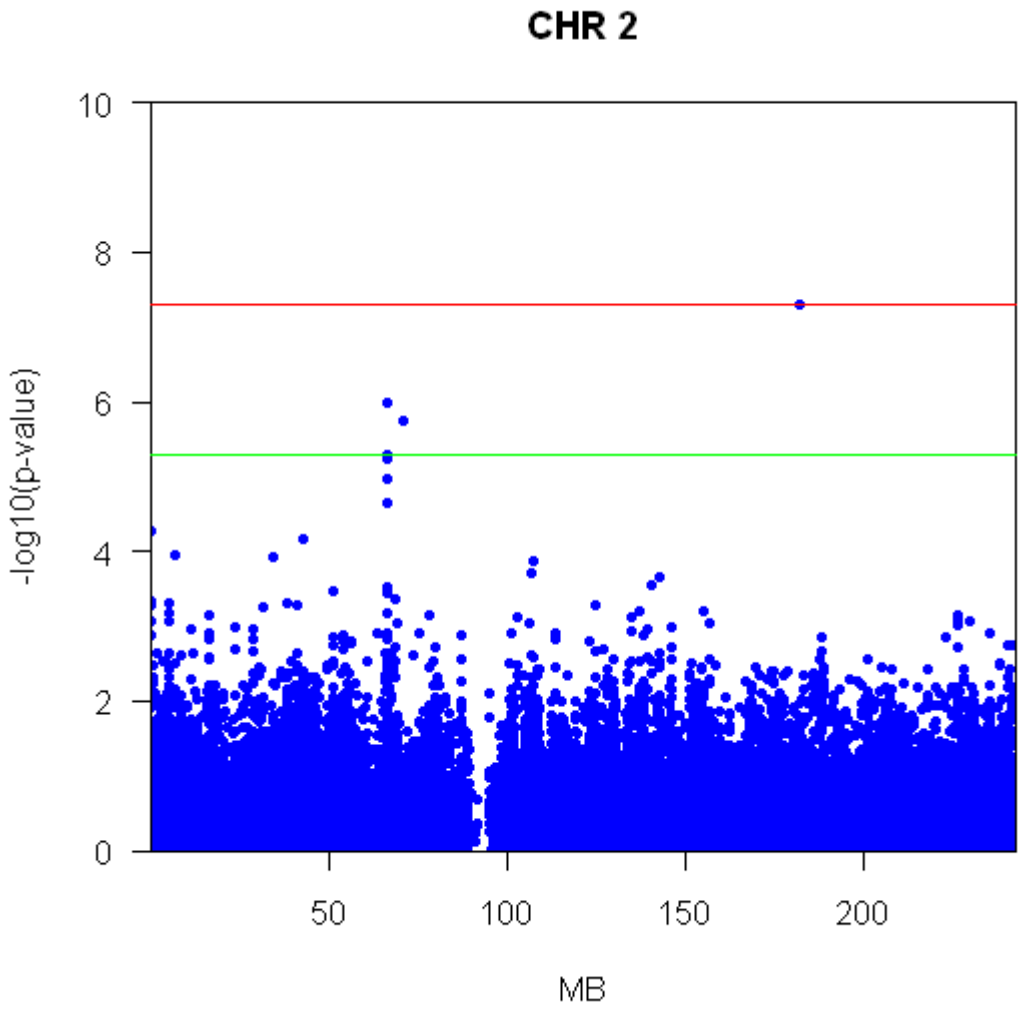
Supplemental Figure 1. Quantile-quantile plot of chi-squared test statistics for testing differences in the observed versus expected SNP allele frequencies for the 611,254 markers meeting quality control criteria.



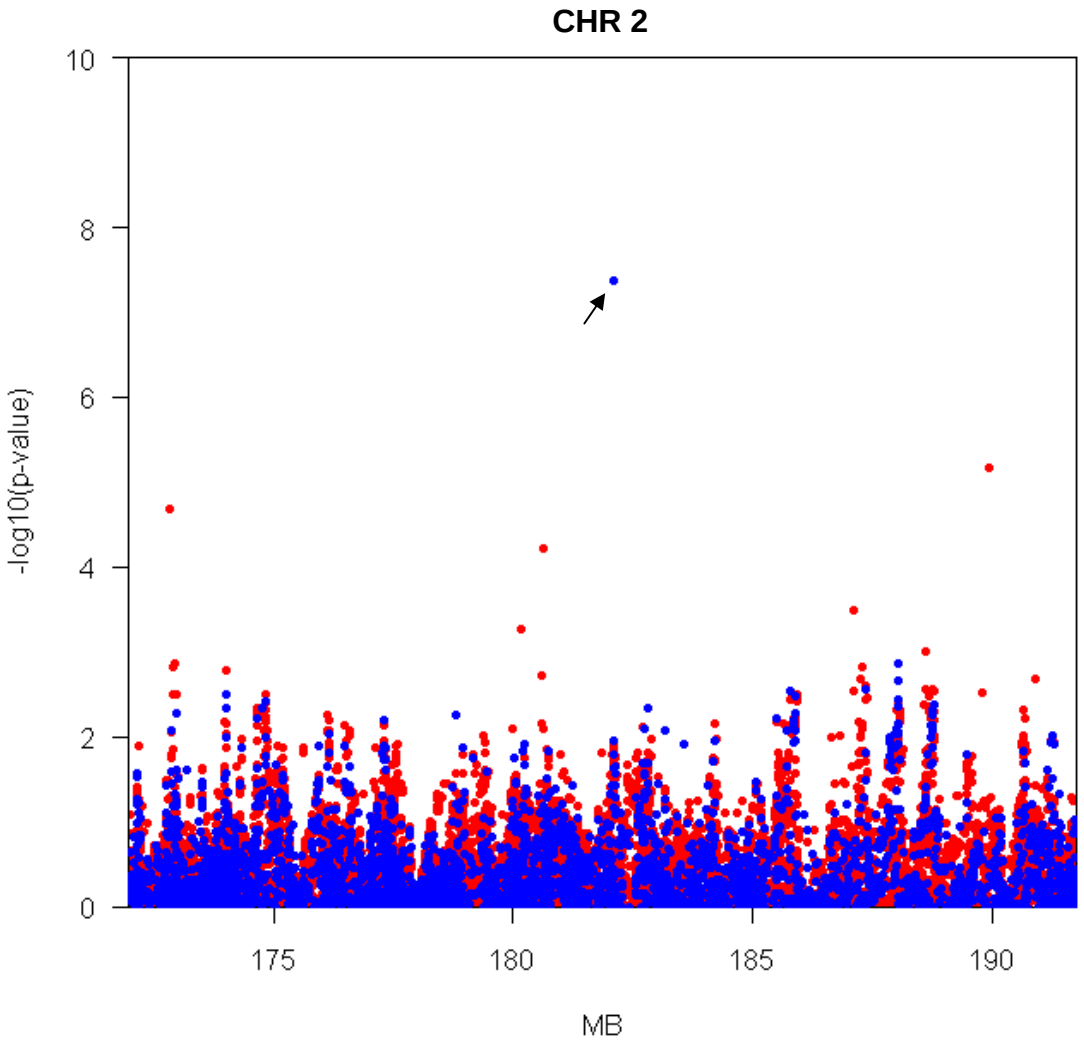
Supplemental Figure 2. Signal plot for chromosome 12.
Red line indicates genome wide significance of $P < 5.0 \times 10^{-8}$; green line indicates genome-wide significance of $P < 5.0 \times 10^{-6}$.



Supplemental Figure 3a. Signal plot for chromosome 2.
Red line indicates genome wide significance of $P < 5.0 \times 10^{-8}$; green line indicates genome-wide significance of $P < 5.0 \times 10^{-6}$.



Supplemental Figure 3b. Imputed results for the region ±10MB from rs3770112 (indicated with an arrow) on chromosome 2 using data from the discovery phase. Marker associations for the discovery phase were determined using PLINK, and the -log10 of the *P* values are shown in blue. Imputed marker associations were determined using SNPTEST, and the -log10 of the *P* values are shown in red. The correlation of -log10 of the *P* values determined from PLINK and SNPTEST for the common set of markers is 0.94.



Supplemental Figure 4. Signal plot for chromosome 5.
Red line indicates genome wide significance of $P < 5.0 \times 10^{-8}$; green line indicates genome-wide significance of $P < 5.0 \times 10^{-6}$.