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Supplemental Data

Simple and Efficient Analysis of Disease Association With Missing Genotype Data

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Table S1. Bias of Log Odds Ratio Estimates and Coverage Probabilities (CP) of 99% Confidence Intervals for Untyped SNPs Under Additive Models for 4 Regions of 5 SNPs on Chromosome 18 of the HapMap CEU Sample

	Odds Ratio = 1		Odds Ratio = 1.4	
	Bias	CP	Bias	CP
A	–0.004	0.989	–0.036	0.985
B	–0.001	0.992	–0.016	0.988
C	–0.003	0.990	–0.005	0.990
D	–0.002	0.991	–0.012	0.988

Note: (A) SNP 21 in the region of SNPs 20-24 with MAF of 0.40 and R_s^2 of 0.24; (B) SNP 22 in the region of SNPs 20-24 with MAF of 0.25 and R_s^2 of 0.42; (C) SNP 26 in the region of SNPs 24-28 with MAF of 0.25 and R_s^2 of 0.85; (D) SNP 65 in the region of SNPs 63-67 with MAF of 0.37 and R_s^2 of 0.62. For odds ratio of 1, one minus the coverage probability yields the type I error rate at the 1% nominal significance level.