In Silico Genotyping: Determining Genotypes in Pedigrees by Inference

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Supplementary Table 1. Detailed Comparisons of Simulated Data

Family Structures and Individuals Genotyped at Candidate SNP	Missing Genotypes			Power				Relative Efficiency versus*…	
	% of Total	% Inferred	Error Rate	Simulated H^2*	Observed Genotypes	Inferred Genotypes	All Genotypes	Alternative Design A*	Alternative Design B*
CEPH Pedigrees In Table 1 of main manuscript	46.4	82.4	0.4	0.5	0.0	83.9	97.1	NA	NA
10 3-generation pedigrees with 8 offspring each									
… grandparents and parents genotyped	57.1	82.4	0.4	0.5	0.0	74.1	92.2	NA	NA
… grandparents, parents and one child genotyped	50.0	99.2	0.7	0.5	0.0	91.2	92.2	NA	NA
100 3-generation pedigrees with 8 offspring each									
… grandparents and parents genotyped	57.1	82.4	0.4	0.05	0.3	44.3	82.2	5.13	1.78
… grandparents, parents and one child genotyped	50.0	99.2	0.7	0.05	1.3	70.8	82.2	3.87	1.93
500 nuclear families with 3 offspring each									
… parents and one child genotyped	40.0	94.6	1.1	0.05	4.7	62.1	82.7	2.40	1.37
… parents and two children genotyped	20.0	96.9	0.6	0.05	40.8	77.4	82.7	1.41	1.18
500 nuclear families with 2 offspring each									
…parents and one child genotyped	25.0	94.7	1.0	0.05	4.5	27.3	41.2	1.70	1.14

- see "relative efficiency calculation" section for description of Design A and Design B.