

TABLE S1
Leave-one-out imputation error rates

Category	SNP Quality	Confidence			Total
		High confidence	Medium confidence	Low confidence	
Mouse HapMap SNPs only		0.33%	7.18%	21.3%	1.66%
	fully resequenced	(46.3%)	(3.08%)	(2.25%)	(51.7%)
	mostly resequenced	0.47%	4.16%	16.8%	2.35%
		(25.0%)	(4.09%)	(2.73%)	(31.8%)
	poorly resequenced	0.87%	4.21%	15.7%	5.31%
		(9.35%)	(2.86%)	(4.29%)	(16.5%)
		0.44%	4.74%	16.8%	2.48%
	Total	(80.7%)	(8.91%)	(10.0%)	(100%)
Mouse HapMap SNPs + gap-filling SNPs		0.27%	5.82%	18.9%	1.63%
	fully resequenced	(45.6%)	(3.14%)	(2.85%)	(51.7%)
	mostly resequenced	0.39%	3.79%	16.2%	2.30%
		(25.0%)	(3.77%)	(3.04%)	(31.8%)
	poorly resequenced	0.76%	3.97%	15.8%	5.23%
		(9.35%)	(2.71%)	(4.32%)	(16.5%)
		0.37%	4.50%	16.8%	2.44%
	Total	(80.2%)	(9.62%)	(10.0%)	(100%)

Leave-one-out imputation error rates of 12 resequenced classical inbred strains using mouse HapMap SNPs only, and combining mouse HapMap SNPs and gap-filling NIEHS/Perlegen SNPs. The fraction of imputed genotypes in each category is shown within a parenthesis.