Supplementary Tables

Table S1: Credible set sizes from the three fine-mapping methods, across datasets with different genotyping or imputation strategies. The sizes of the credible sets are roughly the same across all the methods and datasets.

Method	**Mean SNPs/set**	**Median SNPs/set**	**95% quantile**
J-test LBC-1KG	5	1	16
J-test LBC-HRC	5	1	19
J-test LBC-WGS	4	1	14
BIMBAM LBC-1KG	6	2	21
BIMBAM LBC-HRC	6	2	23
BIMBAM LBC-WGS	5	1	20
BSLMM LBC-1KG	5	2.5	14
BSLMM LBC-HRC	5	2	15
BSLMM LBC-WGS	4	1	10

Table S2: The mean non-reference discordance rate (NRD) in genotypes between the whole genome sequence, and the genotyped and imputed SNPs, for all common SNPs in the genome (MAF>0.1).

Dataset	**Mean NRD for Genotyped SNPs**	**Mean NRD for Imputed SNPs**
LBC-HRC	0.4%	1.6%
LBC-1KG	0.4%	3.2%

Table S3: Fine-mapping results from 1000 replicates of three simulated traits, using two datasets. The coverage of the causal variant reaches approximately 95% in all of the cases. Demonstrating that the three fine-mapping methods work as expected under ideal conditions. Comparing the size of the sets we see that the three methods all perform generally on par with one another.1

(a) $h^2 = 0.2$

	Method	**Coverage**	**Mean SNPs/set**	Median SNPs/set	**95% quantile**
	J-Test	97%	7	1	31
$N = 3781$	BIMBAM	97%	5	2	20
	BSLMM	97%	6	2	22
	J-Test	95%	15	3	48
$N = 1366$	BIMBAM	97%	10	4	38
	BSLMM	97%	13	4	38

(b) $h^2 = 0.1$

	Method	**Coverage**	**Mean SNPs/set**	Median SNPs/set	**95% quantile**
	J-Test	97%	19	3	57
$N = 3781$	BIMBAM	97%	10	3	35
	BSLMM	97%	13	3	44
	J-Test	94%	20	7	80
$N = 1366$	BIMBAM	96%	16	7	61
	BSLMM	95%	17	8	64

(c) $h^2 = 0.05$

	Method	**Coverage**	**Mean SNPs/set**	Median SNPs/set	**95% quantile**
	J-Test	96%	19	6	78
$N = 3781$	BIMBAM	97%	14	6	50
	BSLMM	97%	15	6	61
	J-Test	96%	33	12	108
$N = 1366$	BIMBAM	97%	23	11	79
	BSLMM	97%	28	11	87