

Supplemental Data

Multilocus Bayesian Meta-Analysis

of Gene-Disease Associations

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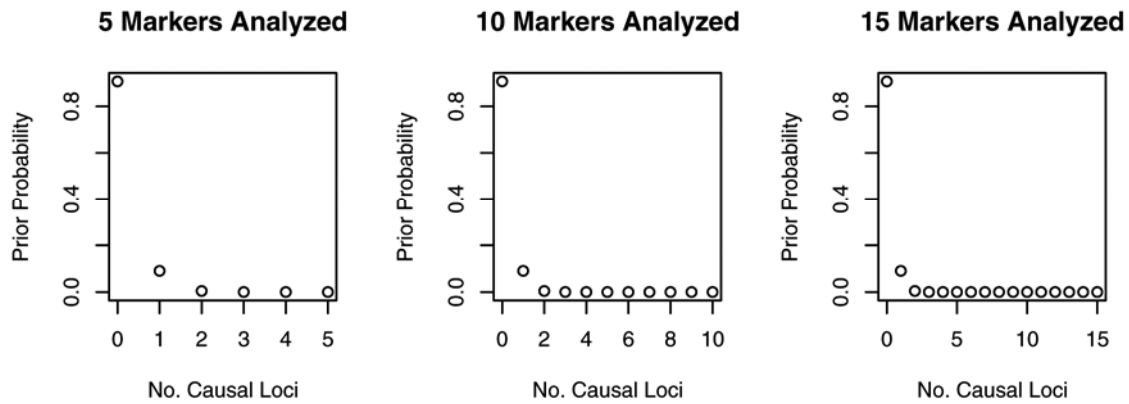


Figure S1. Model space priors used for the Bayesian multi-locus analysis. Poisson(0.05) distributions were used, truncated to the number of markers analyzed. Plots show the prior probabilities for the number of causal loci.

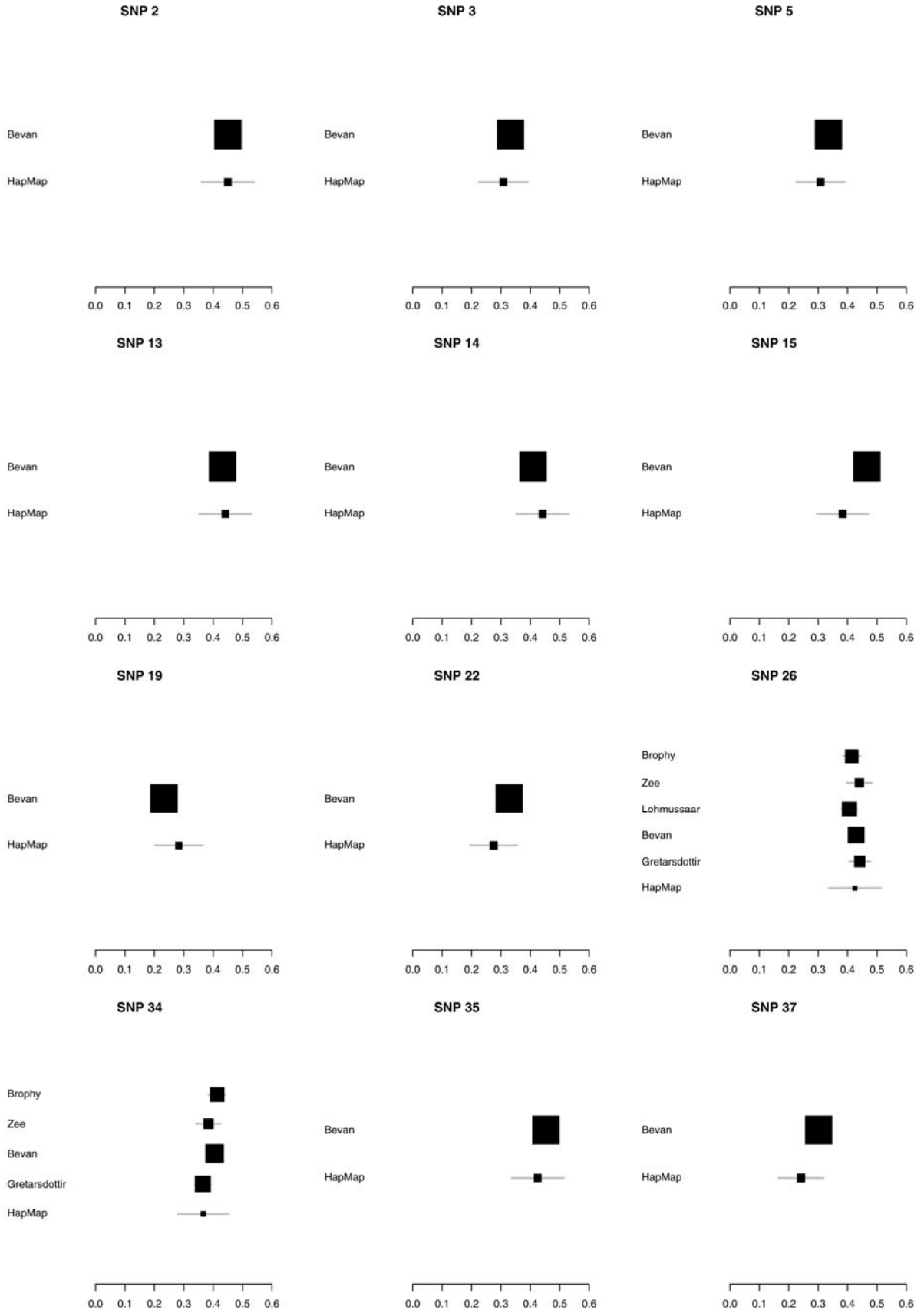


Figure S2. Study reported MAFs For SNPs 2 to 37. 95% CIs were calculated using a binomial normal approximation. SNPs are indicated by their deCODE numbers.

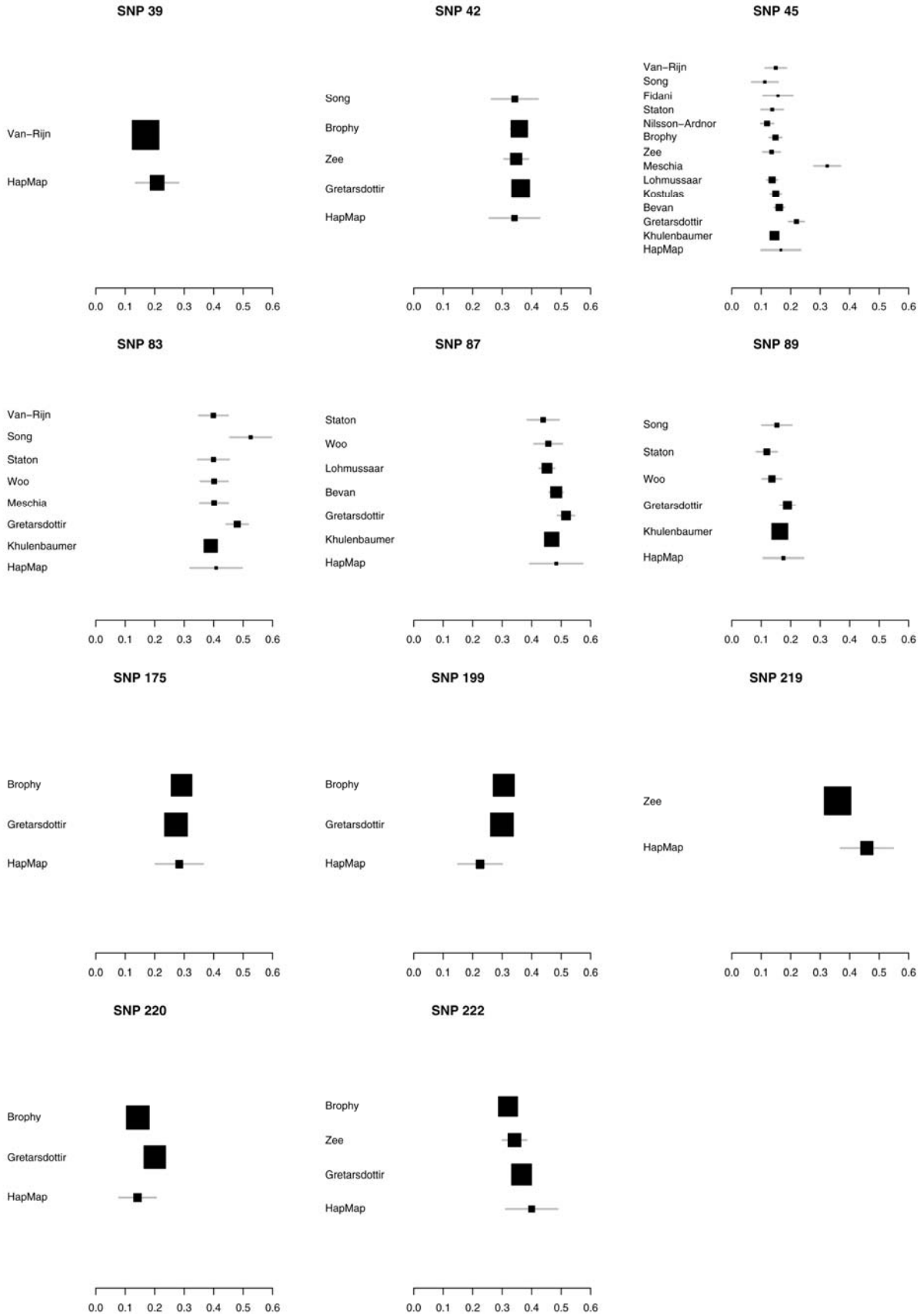


Figure S3. Study reported Minor Allele Frequencies For SNPs 39 to 222. 95% CIs were calculated using a binomial normal approximation. SNPs are indicated by their deCODE numbers.

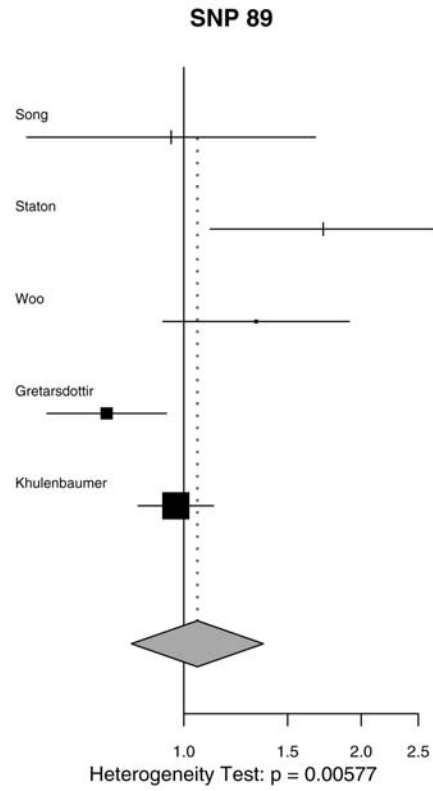
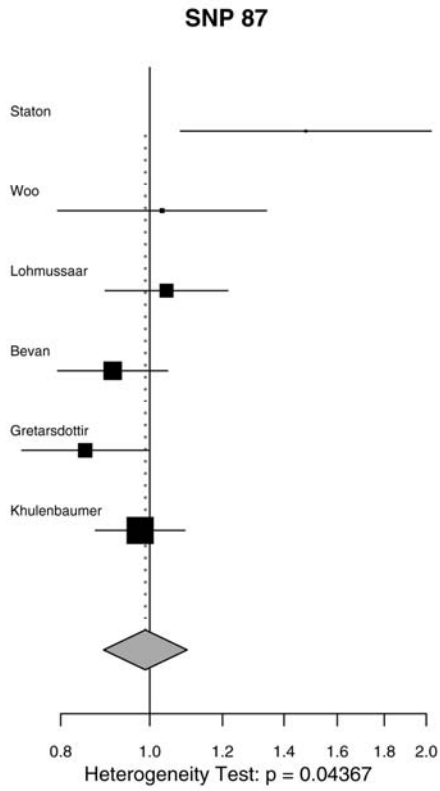
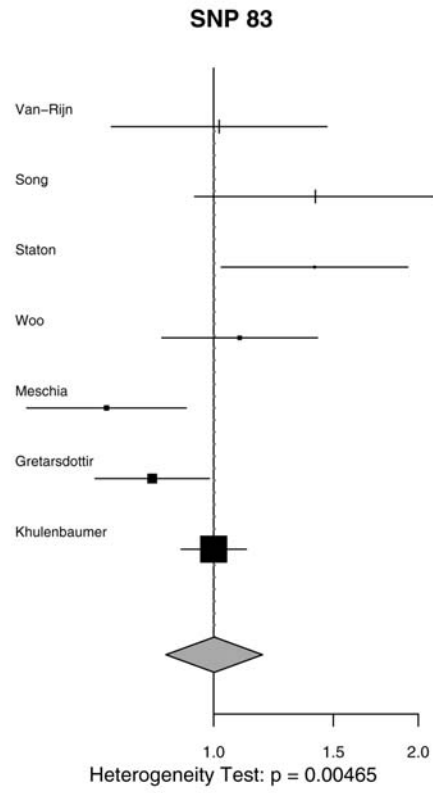
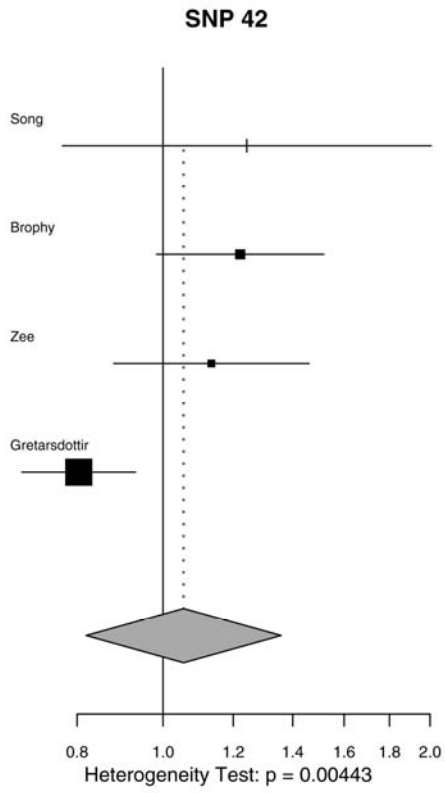


Figure S4. Reported Additive OR Forest Plots For SNPs 42, 83, 87, 89. Significant heterogeneity in reported ORs was found for these SNPs (Dersimonian and Laird p-values are given). The pooled estimates were calculated from univariate random effects Meta-analyses. For each OR, 95% confidence intervals are given.

	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5
Mean Allele F _q	0.37	0.14	0.16	0.16	0.46
True OR	1	1.5	1	1	1
Prop Sig ^a	0.05	1.00	1.00	0.90	0.05
Mean OR (SE)	0.98(0.01)	1.52(0.02)	1.29(0.01)	1.32(0.03)	0.98(0.01)
Mean CI length	0.18	0.47	0.18	0.49	0.17

Table S1. Average Results From Single-SNP Meta-Analyses of Simulated Data Replicates. Results are means (SE) of the OR estimate over 20 analyses of replicate data sets simulated under identical conditions. ^aProportion of replicates in which SNP is significant at the %5 level.

	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	σ_{Hap}
Mean Allele Fq	0.37	0.14	0.16	0.16	0.46	-
True OR	1	1.5	1	1	1	-
Mean Post Prob (SE)	0.02(0.07)	1(0.01)	0.03(0.06)	0.03(0.05)	0.09(0.25)	1.00(0)
Mean OR (SE)	1.00(< 0.01)	1.49(0.07)	1.00(< 0.01)	1.00(< 0.01)	0.99(0.04)	0.13(0.03) ^a
Mean BCI length	0.01	0.35	0.05	0.06	0.02	0.12
Mean OR pres (SE) ^b	1.01(0.05)	1.49(0.07)	0.98(0.11)	1.02(0.13)	1.00(0.06)	0.13(0.03) ^a
Mean BCI length pres ^b	0.08	0.34	0.23	0.32	0.12	0.12

Table S2. Average Results From Bayesian Multi-SNP Meta-Analyses of Simulated Data Replicates. Results are means (SE) of estimators over 20 analyses of replicate data sets simulated under identical conditions. In each analysis OR estimates were taken as the median of the posterior sample. ^aThese are point estimates of σ_{Hap} and therefore are not ORs. ^bCalculated conditional on SNP being included in a model.

	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	σ_{Hap}
Mean Allele Fq	0.37	0.43	0.44	0.44	0.46	-
True OR	1	1	1	1	1	-
Mean Post Prob (SE)	0.03(0.08)	0.02(0.03)	0.02(0.02)	0.02(0.02)	0.02(0.05)	1.00(0)
Mean OR (SE)	1.00(0.01)	1.00(< 0.01)	1.00(< 0.01)	1.00(< 0.01)	1.00(< 0.01)	0.11(0.03) ^a
Mean BCI length	0.01	0.01	0.01	< 0.01	0.01	0.11
Mean OR pres (SE) ^b	1.01(0.03)	1.00(0.04)	1.00(0.03)	1.00(0.03)	1.00(0.03)	0.11(0.03) ^a
Mean BCI length pres ^b	0.09	0.11	0.10	0.10	0.10	0.11

Table S3. Average Results From Bayesian Multi-SNP Meta-Analyses of Simulated Data Replicates. Results are means (SE) of estimators over 200 analyses of replicate data sets simulated under identical conditions. In each analysis OR estimates were taken as the median of the posterior sample. ^aThese are point estimates of σ_{Hap} and therefore are not ORs. ^bCalculated conditional on SNP being included in a model.

Study	Cases	Controls	Country	Year	SNPs		
					Typed	Reported	Analysed
Van-Rijn	89	192	Netherlands	2005	3	3	3
Song	94	99	USA	2006	23	23	5
Fidani	97	102	Greece	2007	1	1	1
Staton	151	164	Australia	2006	6	6	5
Nilsson-Ardnor	222	447	Sweden	2005	3	3	2
Brophy	248	560	USA	2006	13	13	9
Woo	250	219	USA	2006	5	5	3
Zee	259	259	USA	2006	9	9	7
Meschia	279	210	USA	2005	5	4	2
Lohmussaar	639	736	Germany	2005	12	2	2
Kostulas	685	751	Sweden	2007	2	2	2
Bevan	737	928	UK	2005	19	19	14
Gretarsdottir ^a	988	652	Iceland	2003	261	4	14
Kuhlenbaumer ^b	1159	1564	Germany	2006	6	0	4

Table S4. Study Characteristics. ^aData not included in the original publication were obtained from Brophy and Bevan. ^bData not included in the original publication were obtained from Bevan.

Excluded Study	Exc. Cases	Exc. Controls	Country	SNPs Analysed	Null Post %	Gene BF ^a
Staton	151	164	Australia	5	91.5	0.89
Meschia	279	210	USA	2	82.5	2.01
Gretarsdottir	988	652	Iceland	2	87.9	1.31
All But Biggest 5	1689	2252	-	-	86.2	1.52

Table S5. Sensitivity Analysis Of Block 2. ^aBayes Factor against the null model.