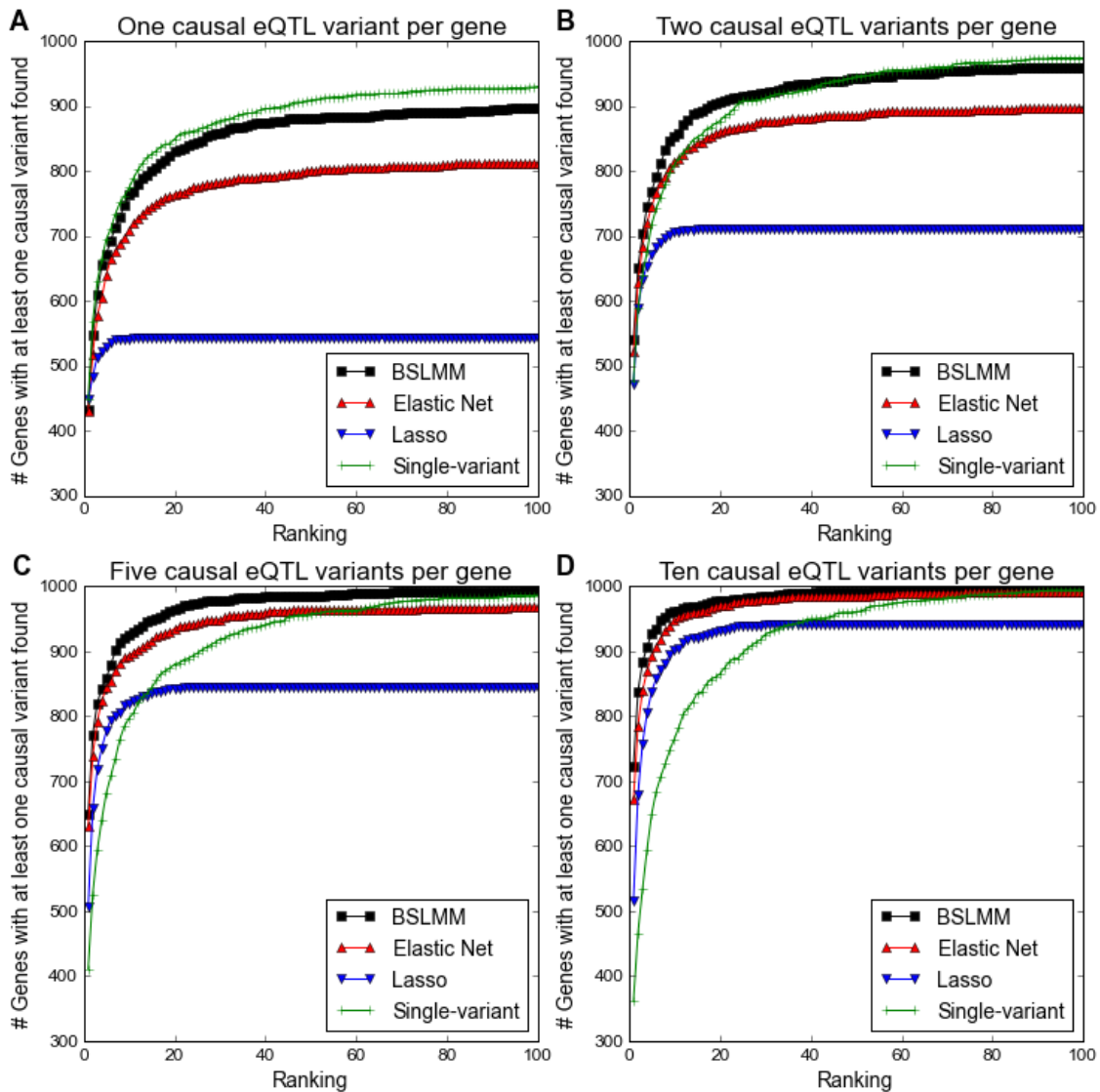
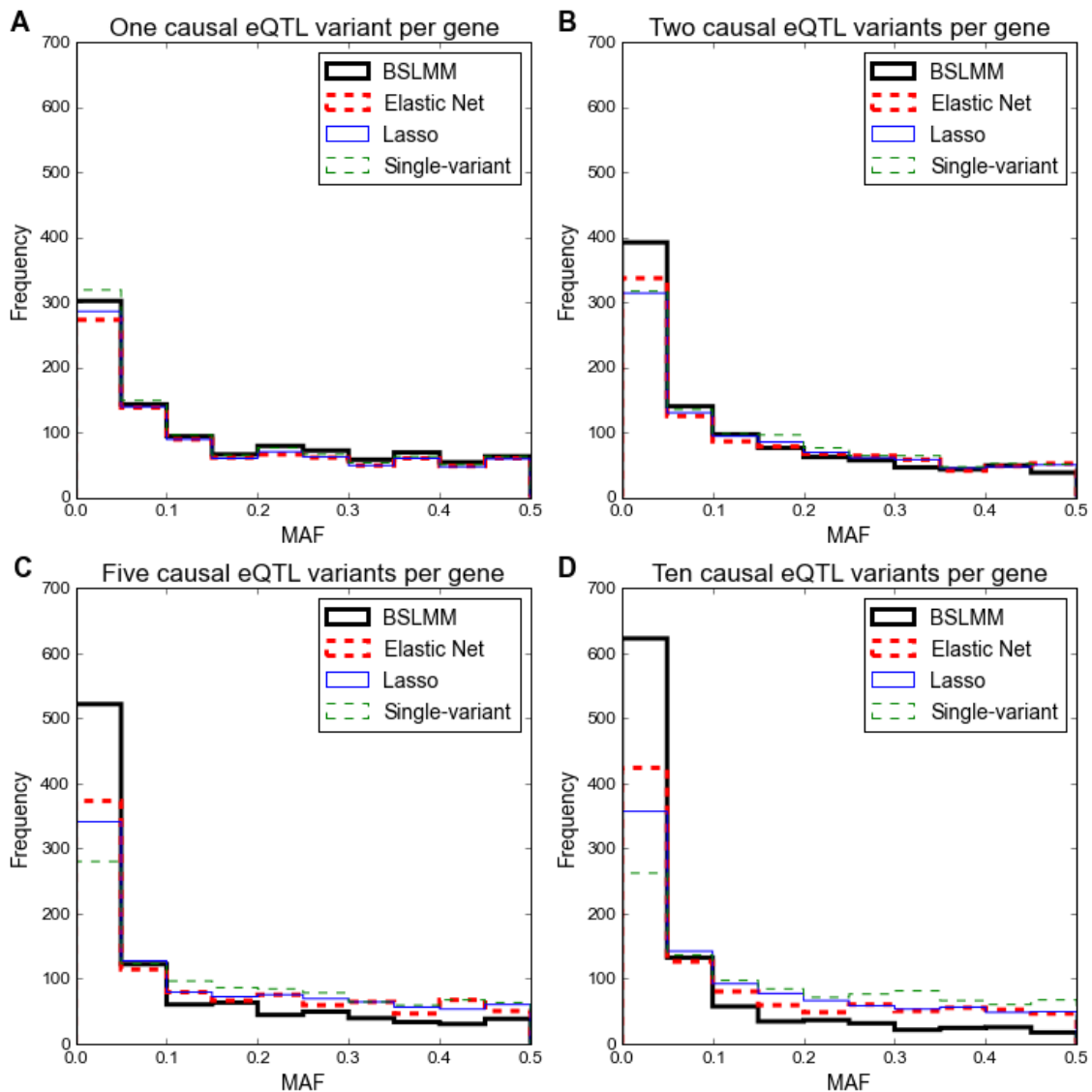


1 Supplementary Figures



2
 3 **Figure S1. The number of genes with at least one causal eQTL variant found from**
 4 **the simulation data of 503 samples with 60% heritability.** The x-axis shows the
 5 ranking cutoff and the y-axis shows the number of genes with at least one causal eQTL
 6 variant found at the ranking cutoff. (A) One causal eQTL variant per gene. (B) Two
 7 causal eQTL variants per gene. (C) Five causal eQTL variants per gene. (D) Ten causal
 8 eQTL variants per gene.

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3 **Figure S2. Minor allele frequency of eQTL SNPs identified with each method.**

4 The x-axis shows minor allele frequency (MAF) and the y-axis shows the number of top

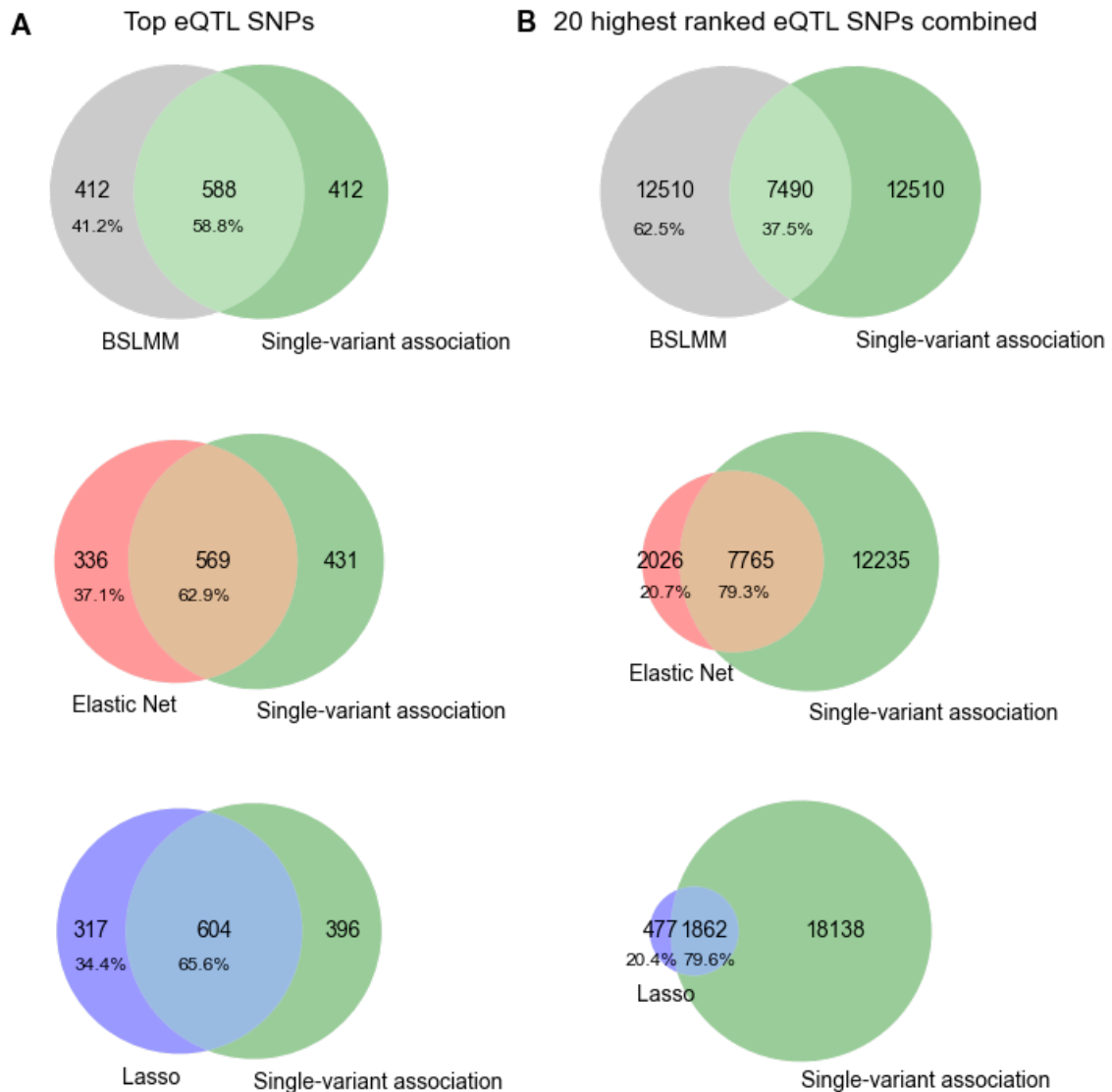
5 eQTL SNPs within the specified MAF bin identified by each method. (A) One causal

6 eQTL variant per gene. (B) Two causal eQTL variants per gene. (C) Five causal eQTL

7 variants per gene. (D) Ten causal eQTL variants per gene.

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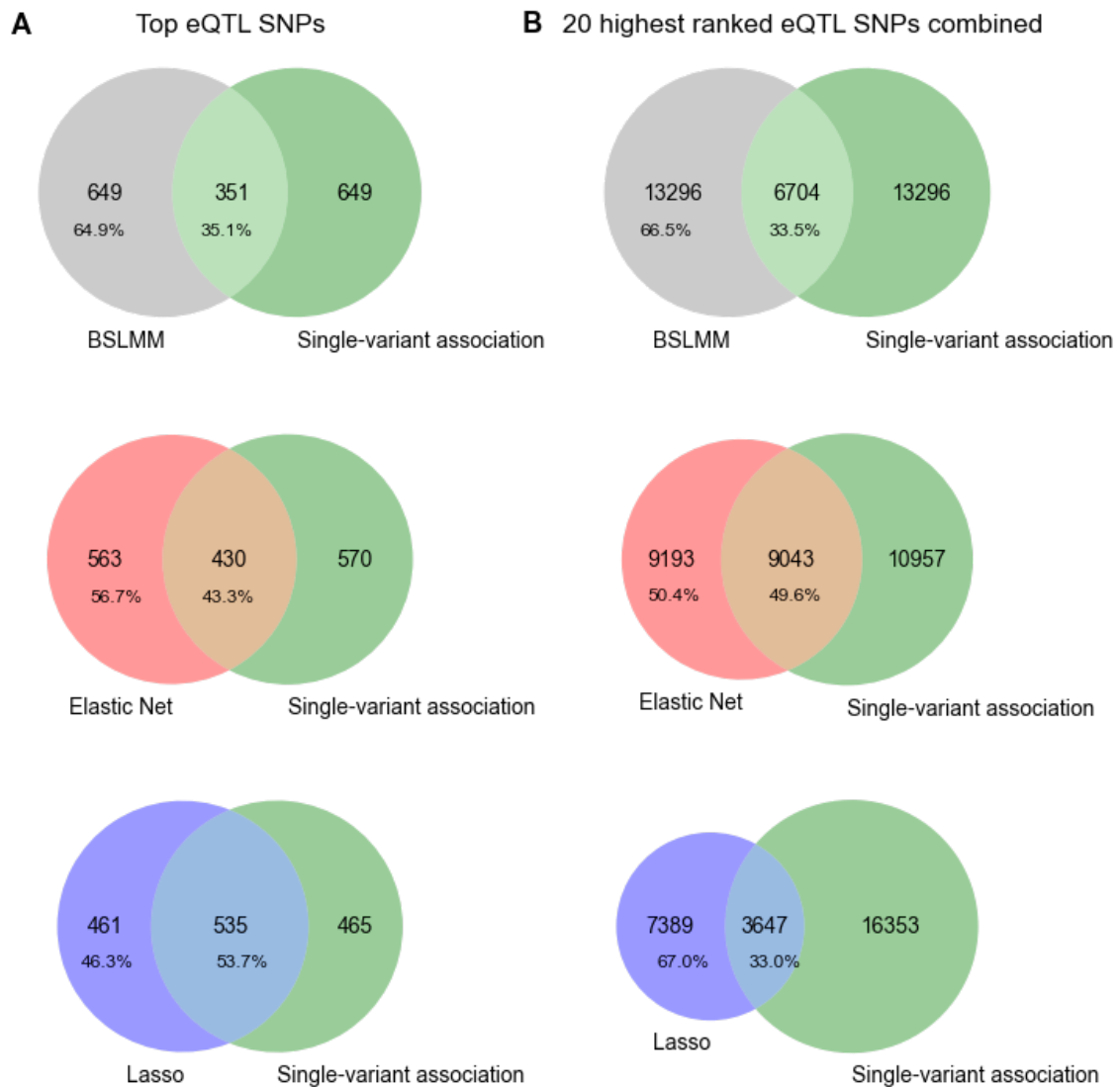
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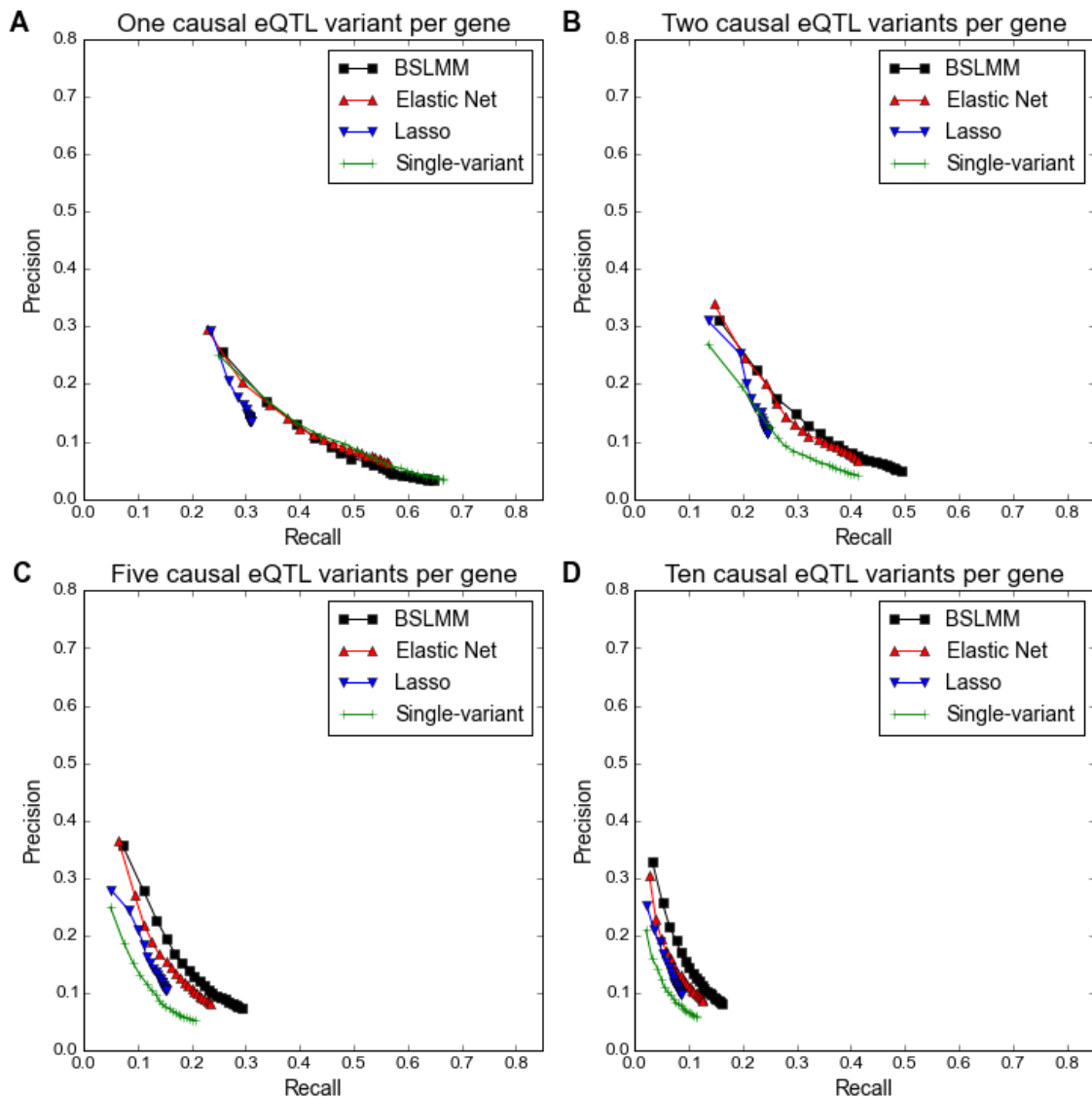
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3 **Figure S3. Overlap of the identified eQTL variants from the simulation data of 503**4 **samples with 60% heritability and one causal variant per gene. (A) Overlap of the**5 **top eQTL SNPs between each sparse polygenic model (top: BSLMM, middle: Elastic**6 **Net, bottom: Lasso) and single-variant association analysis. (B) Overlap of the 20**7 **highest ranked eQTL SNPs combined between each sparse polygenic model (top:**8 **BSLMM, middle: Elastic Net, bottom: Lasso) and single-variant association analysis.**9 **The percentages shown indicate the fraction of eQTL SNPs identified by the sparse**10 **polygenic model that overlap with those identified by single-variant association**11 **analysis.**

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 2 **Figure S4. Overlap of the identified eQTL variants from the simulation data of 503**
 3 **samples with 60% heritability and five causal variants per gene.** (A) Overlap of the
 4 top eQTL SNPs between each sparse polygenic model (top: BSLMM, middle: Elastic
 5 Net, bottom: Lasso) and single-variant association analysis. (B) Overlap of the 20
 6 highest ranked eQTL SNPs combined between each sparse polygenic model (top:
 7 BSLMM, middle: Elastic Net, bottom: Lasso) and single-variant association analysis.
 8 The percentages shown indicate the fraction of eQTL SNPs identified by the sparse
 9 polygenic model that overlap with those identified by single-variant association
 10 analysis.



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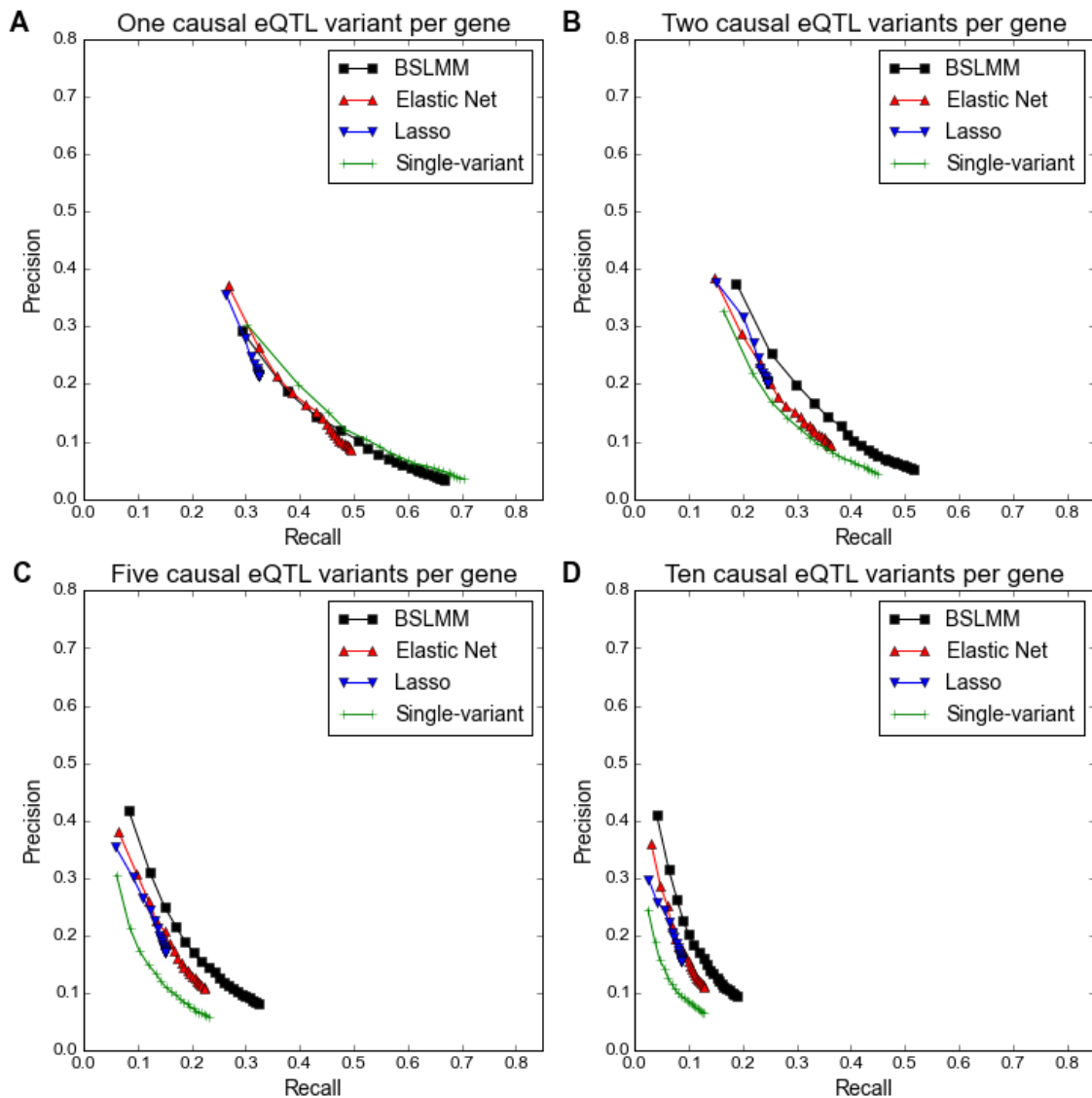
2 **Figure S5. Prediction performance for identifying causal eQTL variants from the**3 **simulation data of 100 samples with 60% heritability.** The x-axis shows recall and

4 the y-axis shows precision for the 20 highest ranked SNPs of 1,000 randomly selected

5 genes. (A) One causal eQTL variant per gene. (B) Two causal eQTL variants per gene.

6 (C) Five causal eQTL variants per gene. (D) Ten causal eQTL variants per gene.

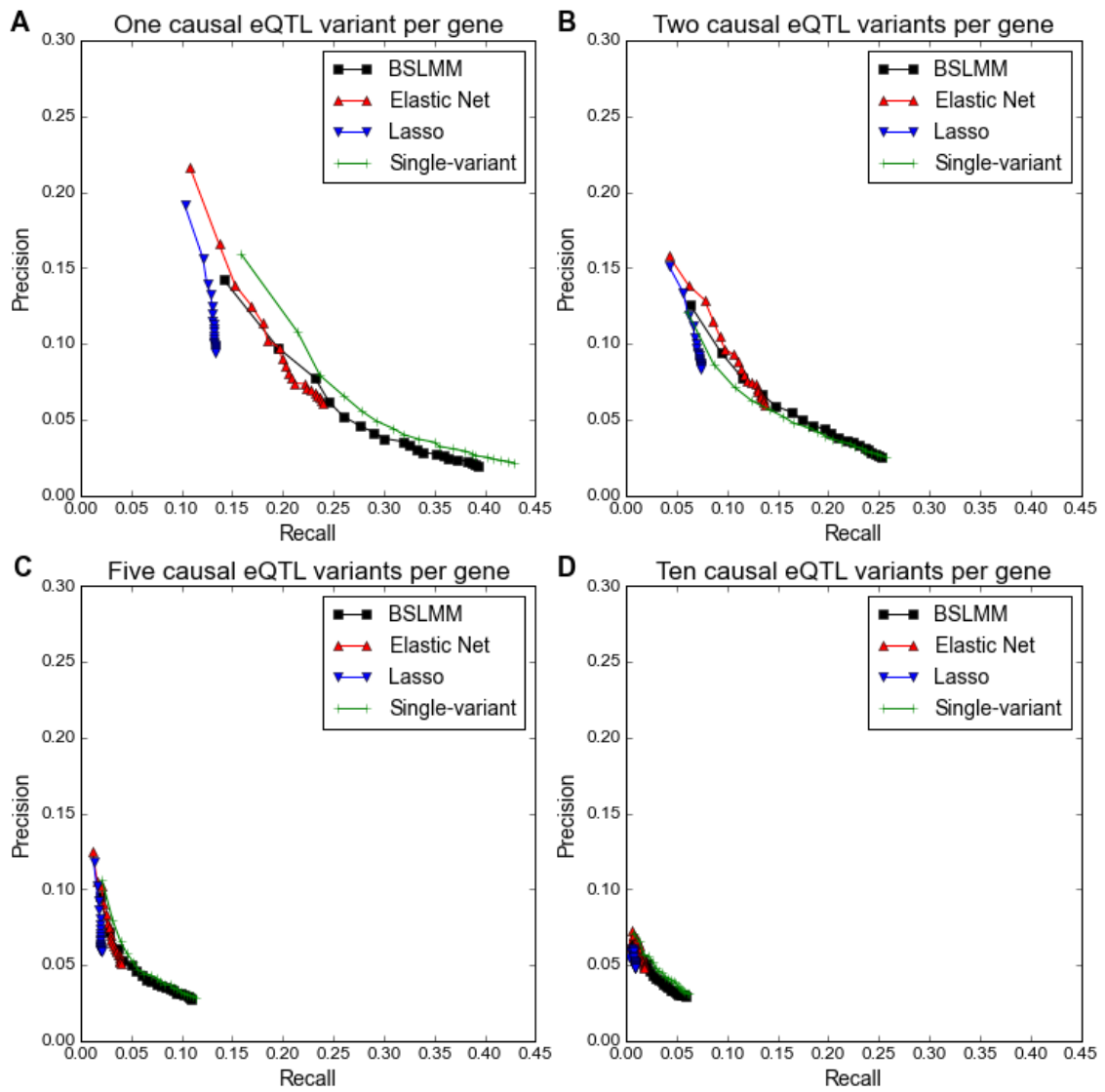
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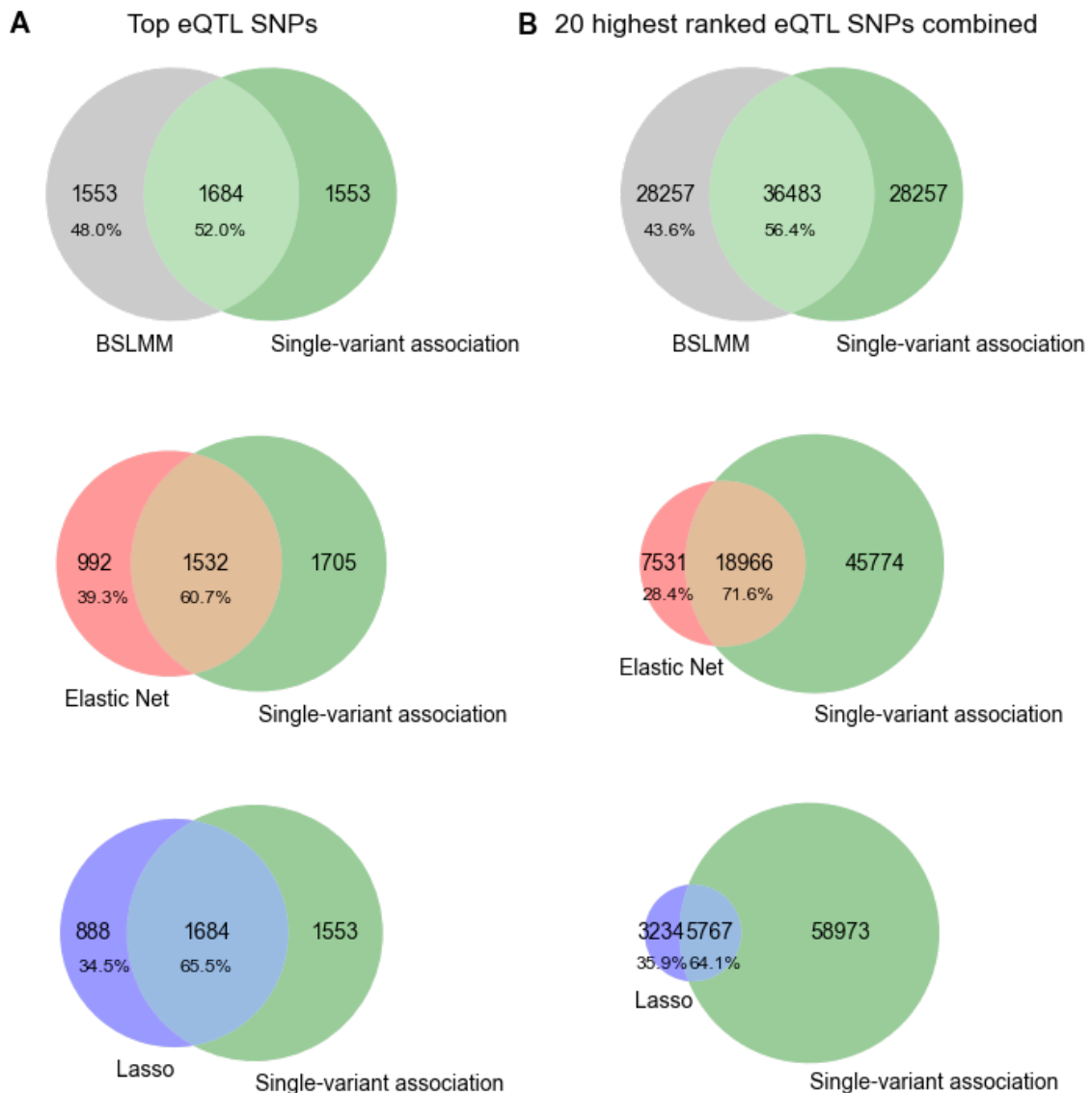
2 **Figure S6. Prediction performance for identifying causal eQTL variants from the**
 3 **simulation data of 503 samples with 20% heritability.** The x-axis shows recall and
 4 the y-axis shows precision for the 20 highest ranked SNPs of 1,000 randomly selected
 5 genes. (A) One causal eQTL variant per gene. (B) Two causal eQTL variants per gene.
 6 (C) Five causal eQTL variants per gene. (D) Ten causal eQTL variants per gene.

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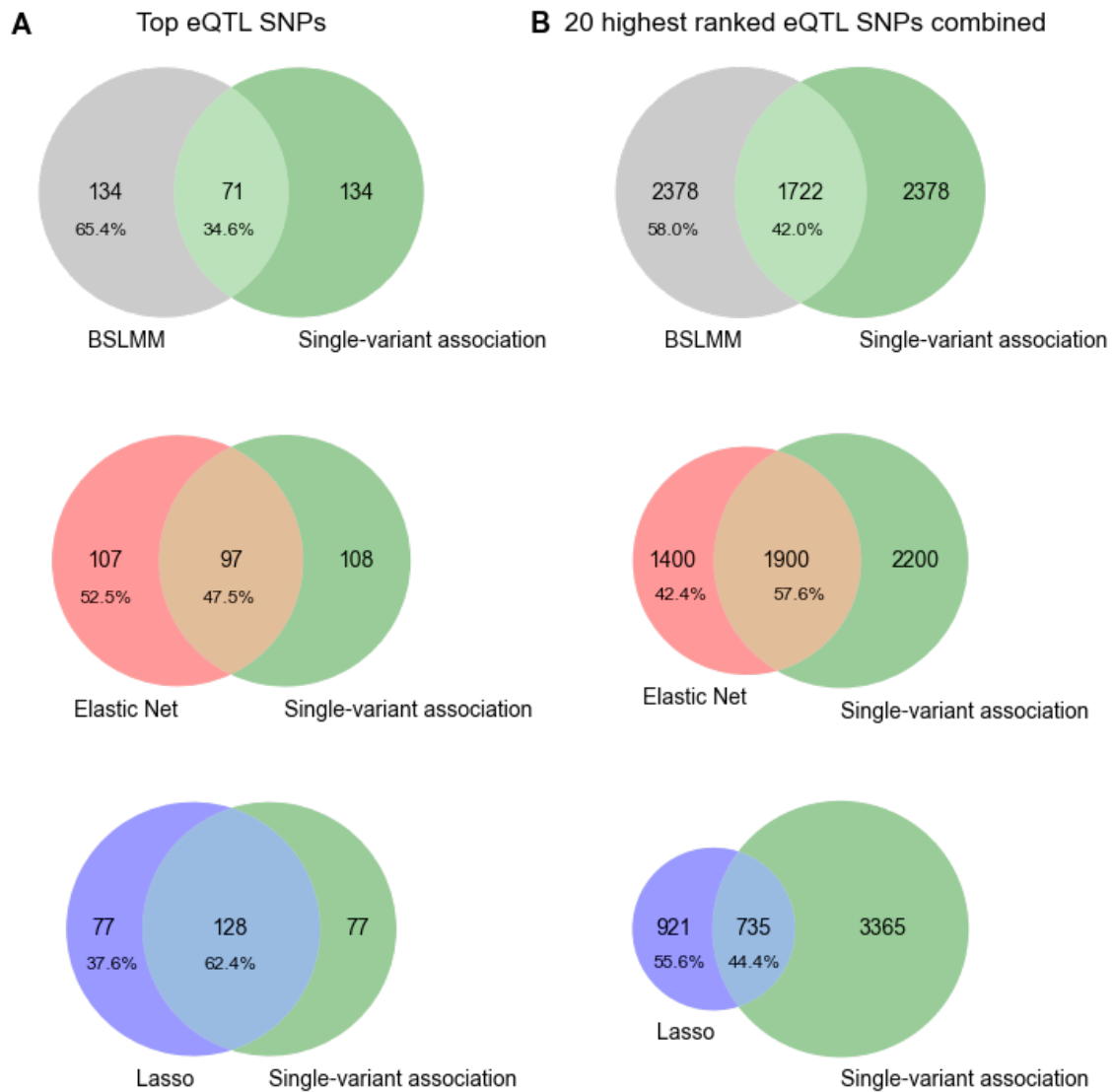
2 **Figure S7. Prediction performance for identifying causal eQTL variants from the**
 3 **simulation data of 100 samples with 20% heritability.** The x-axis shows recall and
 4 the y-axis shows precision for the 20 highest ranked SNPs of 1,000 randomly selected
 5 genes. (A) One causal eQTL variant per gene. (B) Two causal eQTL variants per gene.
 6 (C) Five causal eQTL variants per gene. (D) Ten causal eQTL variants per gene.



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2 **Figure S8. Overlap of eQTL variants of eGenes with one independent eQTL.** A)
3 Overlap of the top eQTL SNPs between BSLMM and single-variant association
4 analysis (top), Elastic Net and single-variant association analysis (middle), and Lasso
5 and single-variant association analysis (bottom). (B) Overlap of the 20 highest ranked
6 eQTL SNPs combined between BSLMM and single-variant association analysis (top),
7 Elastic Net and single-variant association analysis (middle), and Lasso and single-
8 variant association analysis (bottom). The percentages shown indicate the fraction of
9 eQTL SNPs identified by the sparse polygenic model that overlap with those identified
10 by single-variant association analysis.

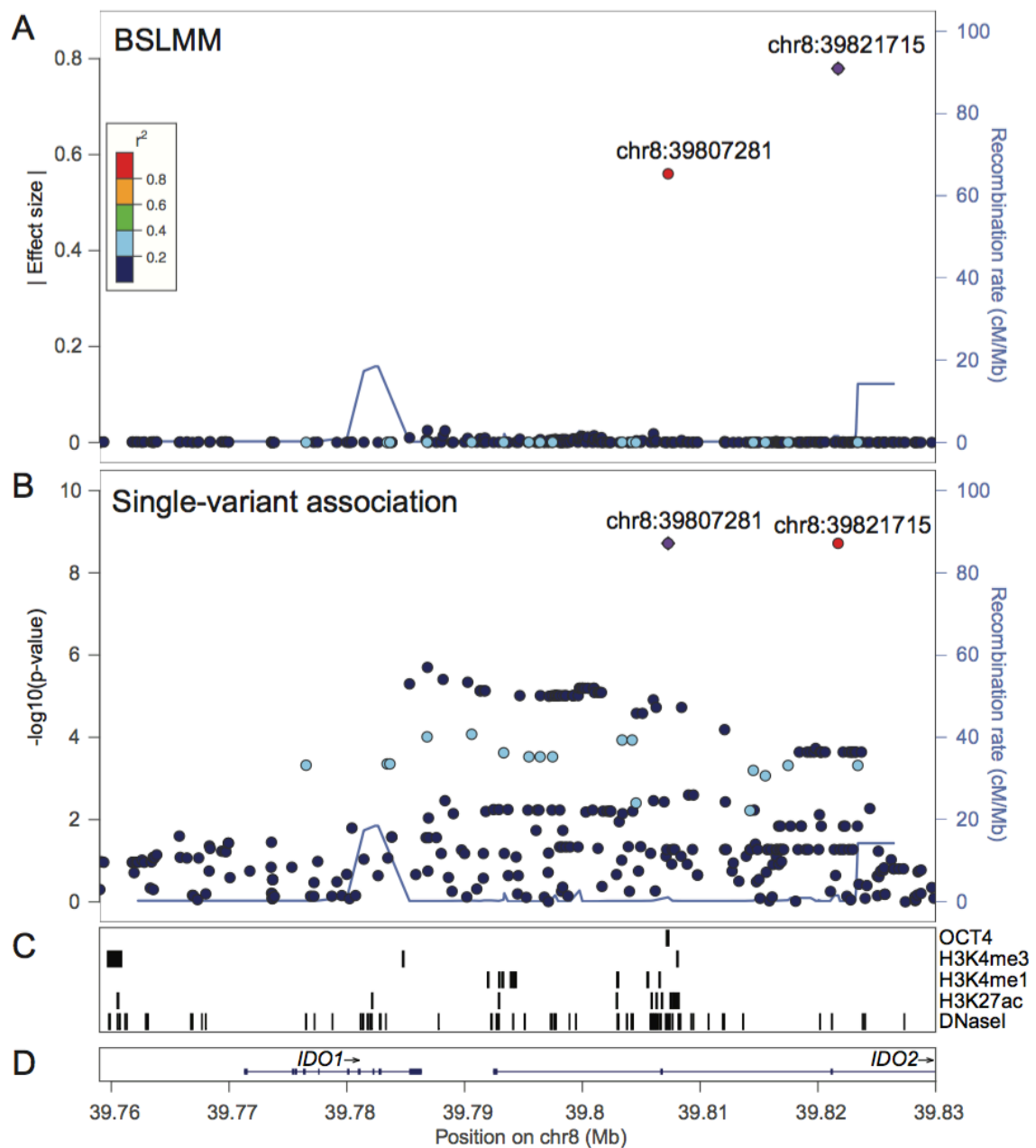
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2 **Figure S9. Overlap of eQTL variants of eGenes with more than one independent**
3 **eQTLs.** (A) Overlap of the top eQTL SNPs between BSLMM and single-variant
4 association analysis (top), Elastic Net and single-variant association analysis (middle),
5 and Lasso and single-variant association analysis (bottom). (B) Overlap of the 20
6 highest eQTL SNPs combined between BSLMM and single-variant association analysis
7 (top), Elastic Net and single-variant association analysis (middle), and Lasso and single-
8 variant association analysis (bottom). The percentages shown indicate the fraction of
9 eQTL SNPs identified by the sparse polygenic model that overlap with those identified
10 by single-variant association analysis.

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2 **Figure S10. eQTL variants identified as associated with *IDO1* expression.** Variants
3 are color-coded based on the strength of LD with the most highly associated eQTL
4 (purple diamond). (A) BSLMM identified two eQTL SNPs as the most highly ranked
5 eQTL variants, located on chr8:39807281 and chr8:39821715, which were also
6 identified as significant by single-variant association analysis. (C) Genomic regions
7 annotated with H1-hESC OCT4, iPSC histone marks (H3K4me3, H3K4me1, and
8 H3K27ac), and iPSC DNase I hypersensitive sites (DHSs). (D) Genomic coordinates of
9 *IDO1* and surrounding genes are based on hg19.