

# **Causal Links Between Gut Microbiomes and Risk of Different Subtypes of Epilepsy: A Mendelian Randomization Study**

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## Supplemental Figures

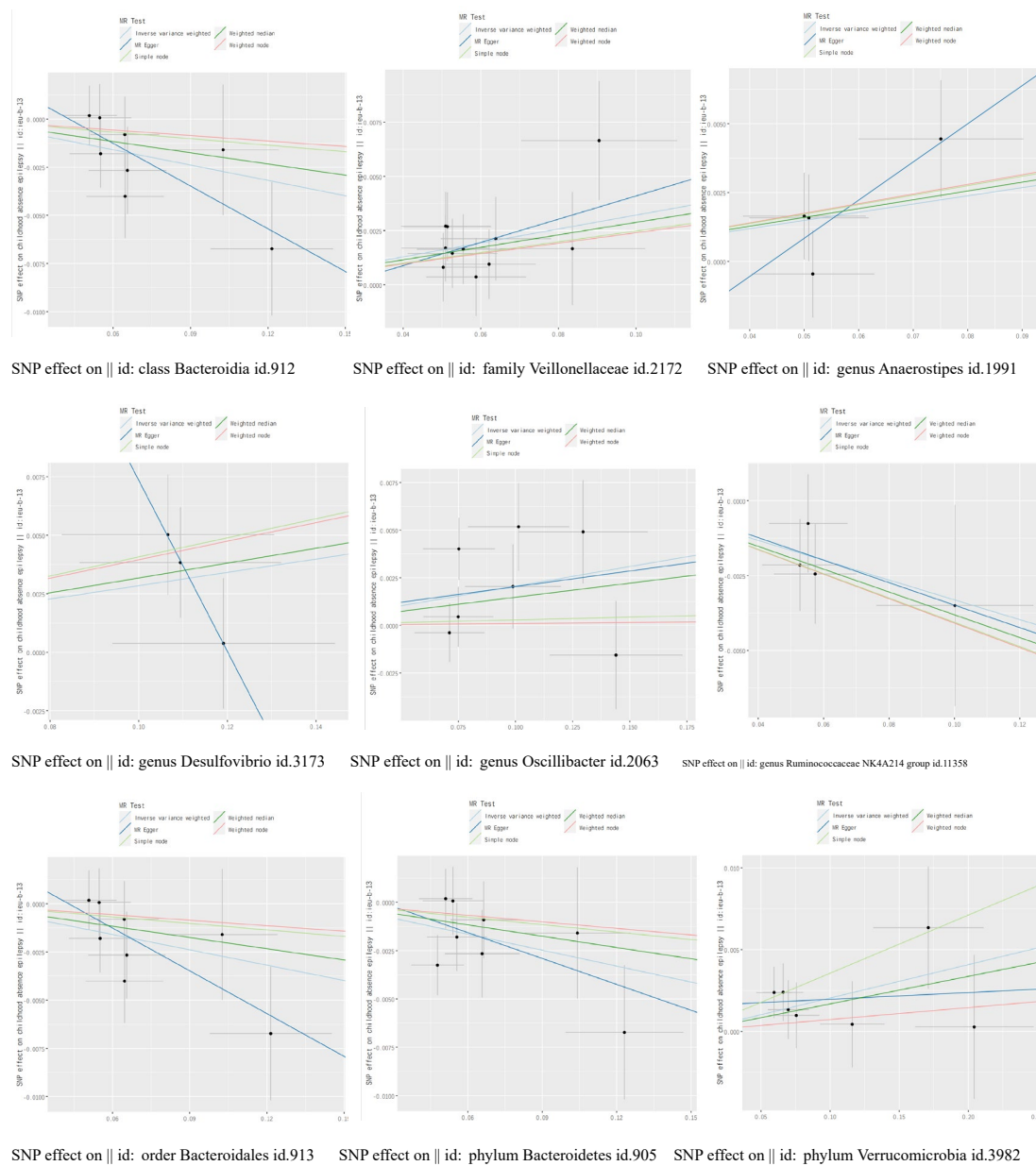
**Supplementary Figure S1.** Scatter plot of MR results. (A) scatter plot of genetic correlations of 9 GM taxa and CAE using different MR methods; (B) scatter plot of genetic correlations of 10 GM taxa and JAE using different MR methods; (C) scatter plot of genetic correlations of 5 GM taxa and FE using different MR methods; (D) scatter plot of genetic correlations of 6 GM taxa and GE using different MR methods.

**Supplementary Figure S2.** Leave-one-out analysis for subtypes of epilepsy (A) 9 GM taxa on CAE, (B) 10 GM taxa on GAE, (C) 5 GM taxa on FE and (D) 6 GM taxa on GE

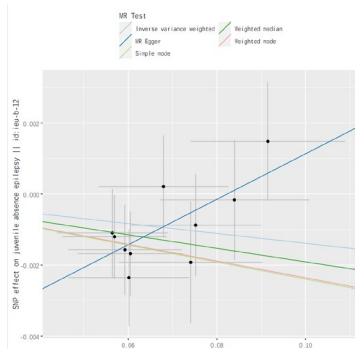
**Supplementary Figure S3:** PPI network of significant GM's SNPs mapped genes. Genes are represented by circular nodes, and their interactions are represented by edges. The size of the dots represents the Betweenness Centrality score, with high Betweenness Centrality scores being large and low scoring dots being small, and each of the bacteria related genes is represented by different colors. (A) PPI network of five significant GM's SNPs mapped genes of FE. (B) PPI network of six significant GM's SNPs mapped genes of GE. (C) PPI network of nine significant GM's SNPs mapped genes of CAE. (D) PPI network of ten significant GM's SNPs mapped genes of JAE.

**Supplementary Figure S1.** Scatter plot of MR results. (A) scatter plot of genetic correlations of 9 GM taxa and CAE using different MR methods. (B) scatter plot of genetic correlations of 10 GM taxa and JAE using different MR methods.(C) scatter plot of genetic correlations of 5 GM taxa and FE using different MR methods.(D) scatter plot of genetic correlations of 6 GM taxa and GE using different MR methods

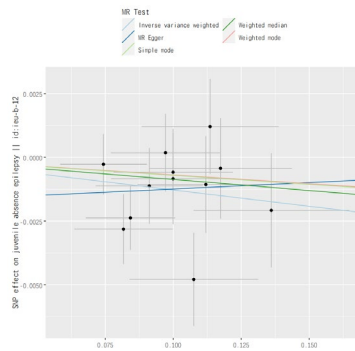
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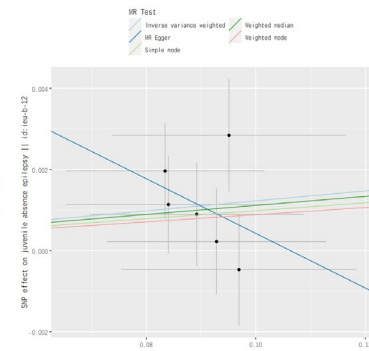
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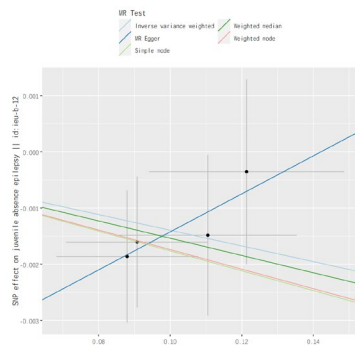
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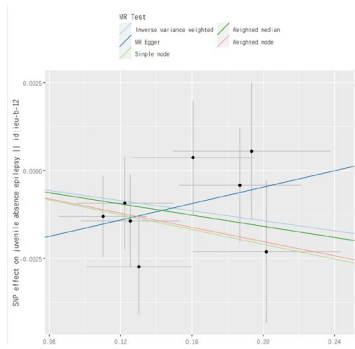
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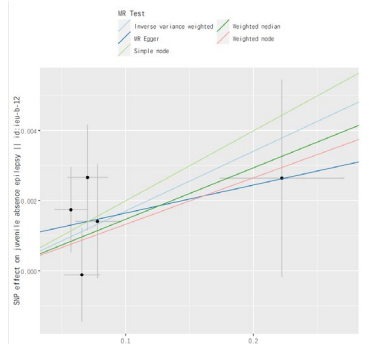
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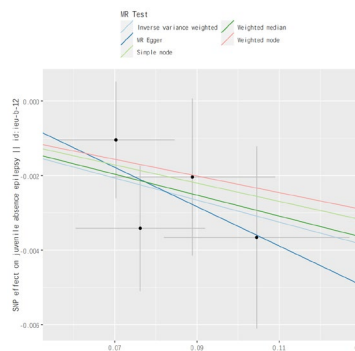
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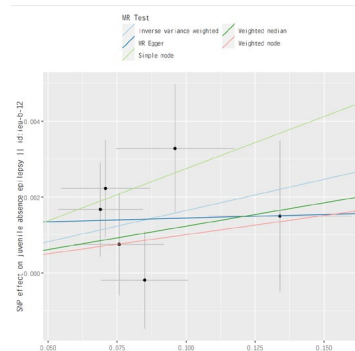
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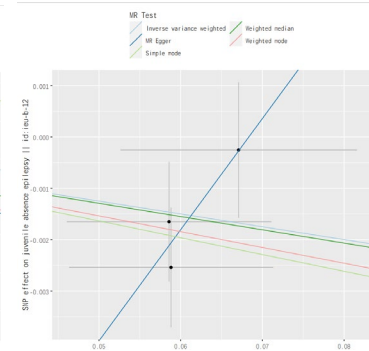
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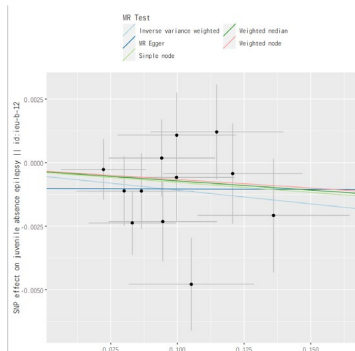
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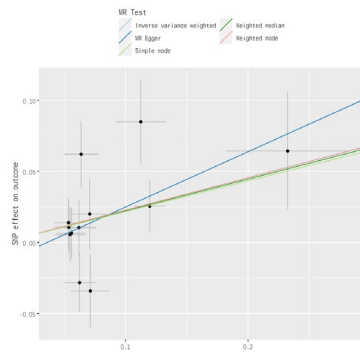


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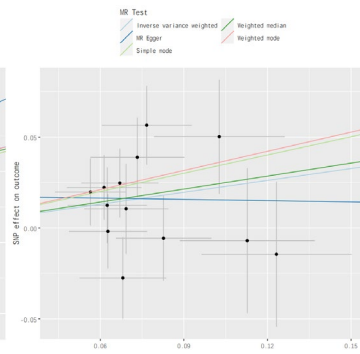


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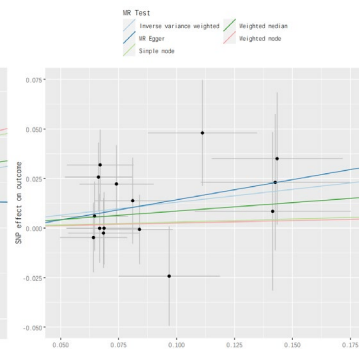
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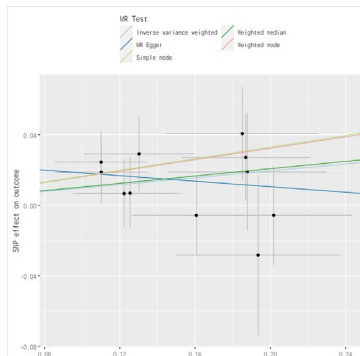
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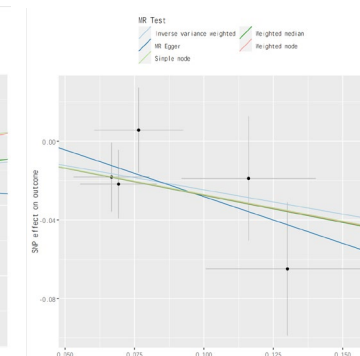
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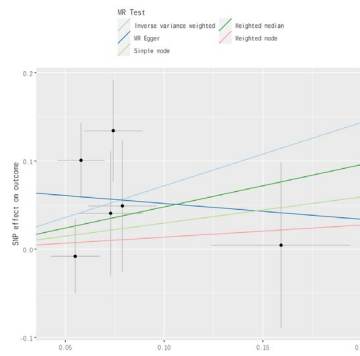


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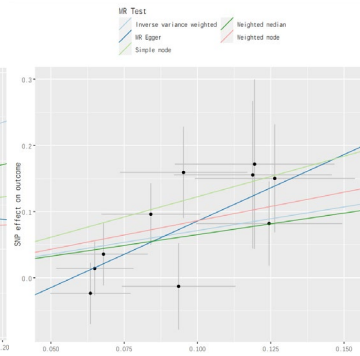


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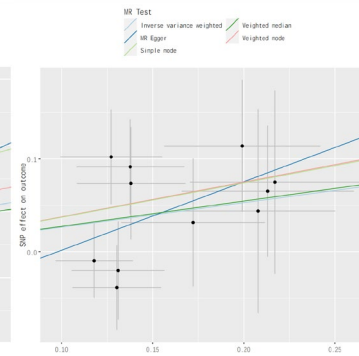
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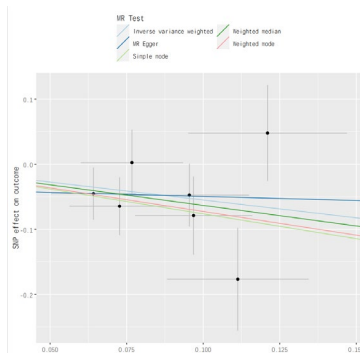
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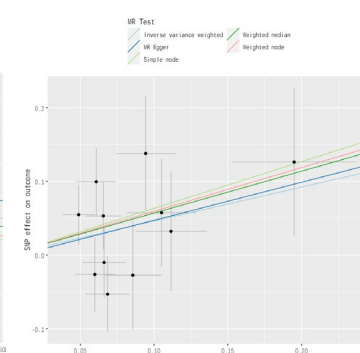
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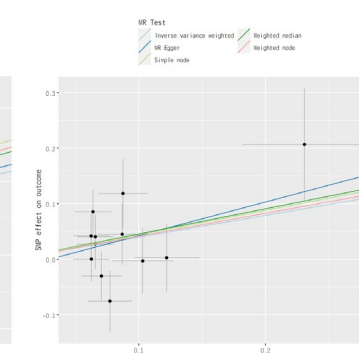
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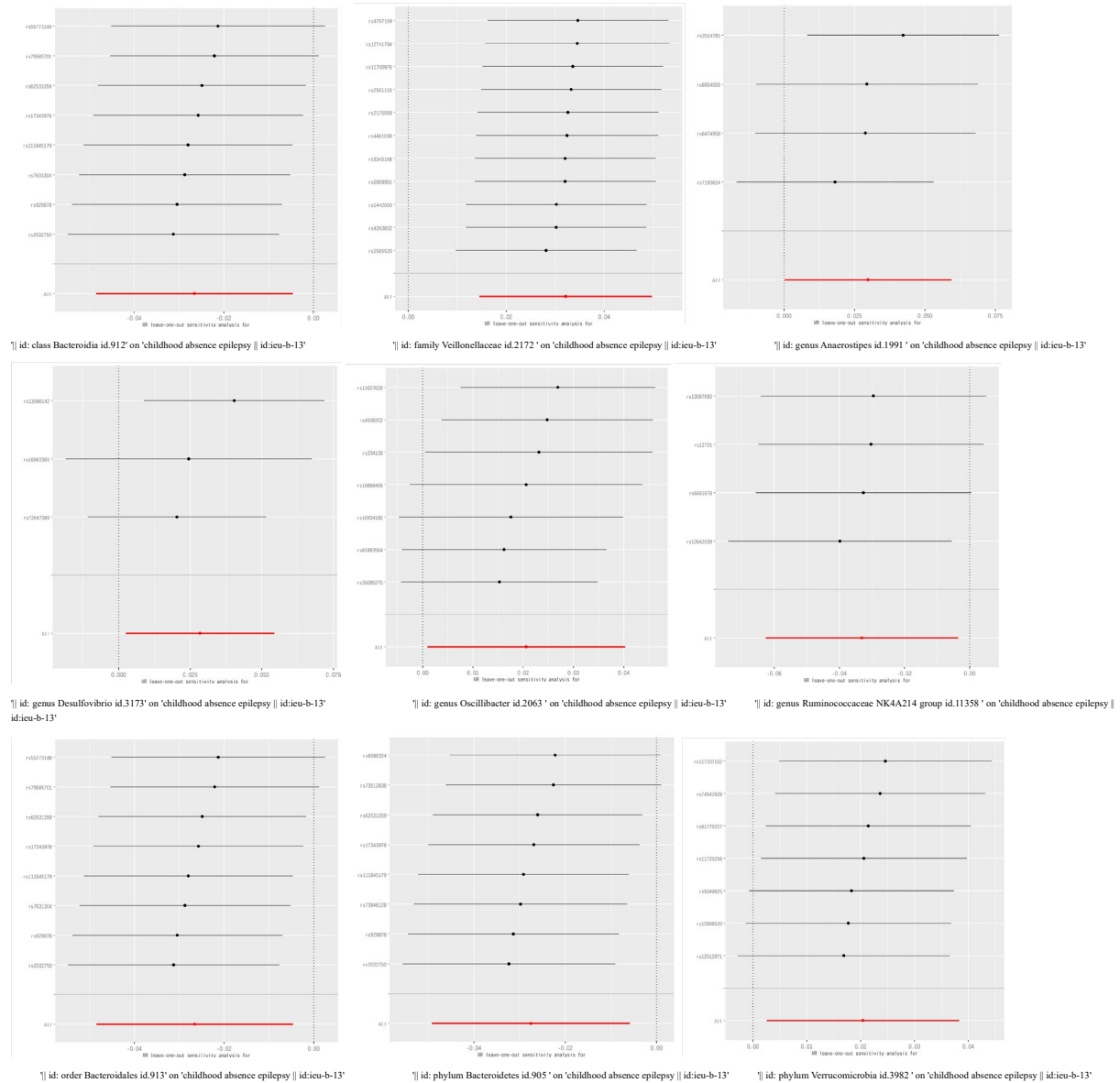
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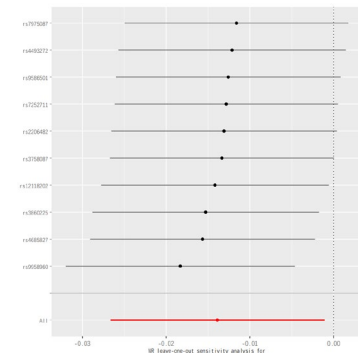
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# Supplementary Figure S2. Leave-one-out analysis for (A) 9 GM taxa on CAE, (B) 10 GM taxa on GAE, (C) 5 GM taxa on FE and (D) 6 GM taxa on GE

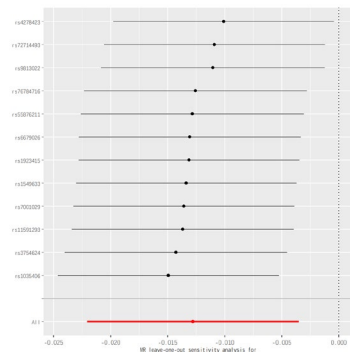
## A. CAE



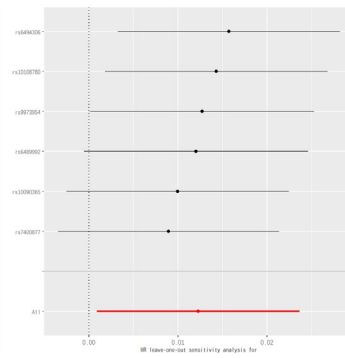
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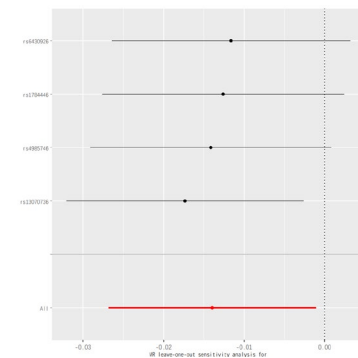
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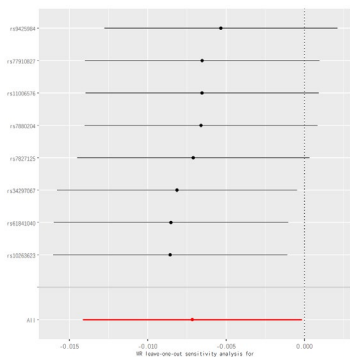
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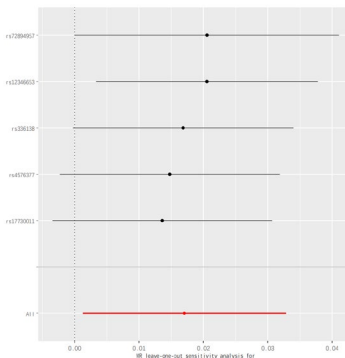
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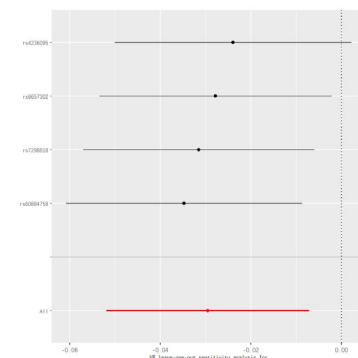
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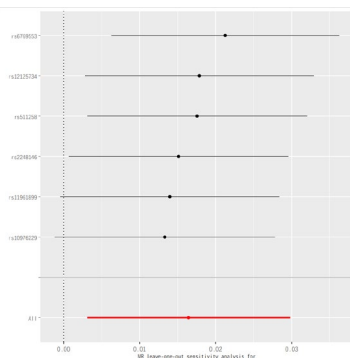
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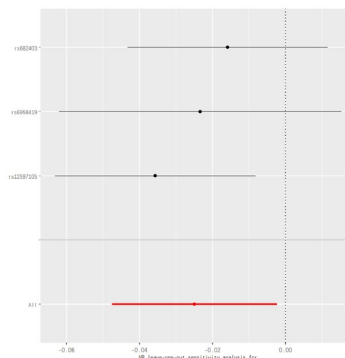
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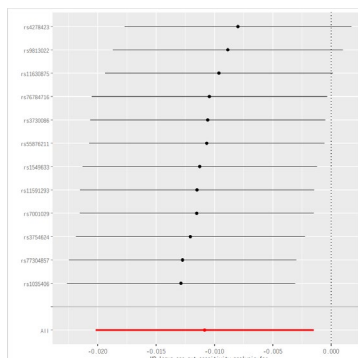
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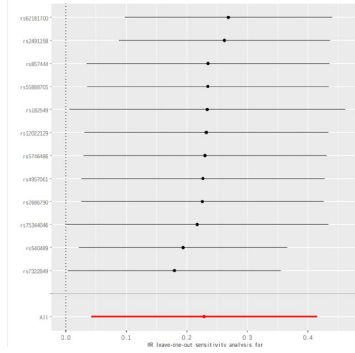
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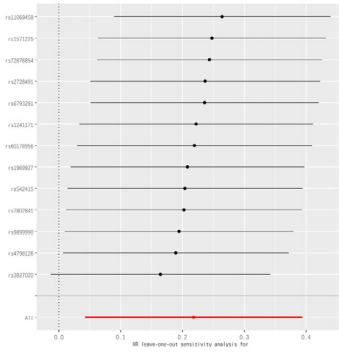
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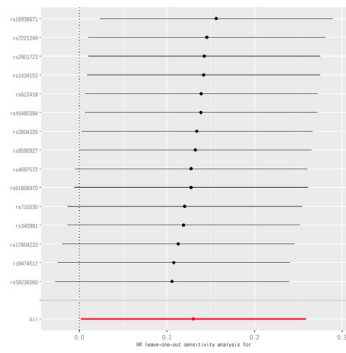
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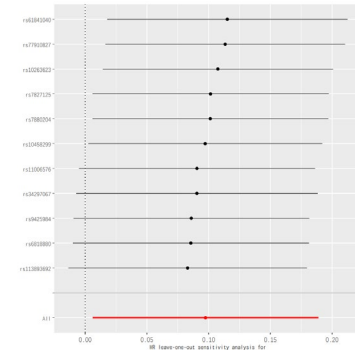
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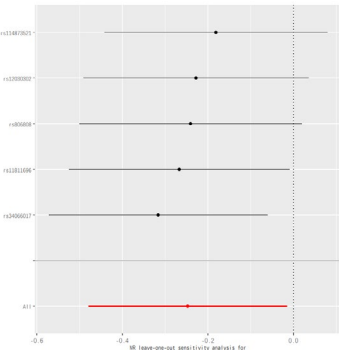
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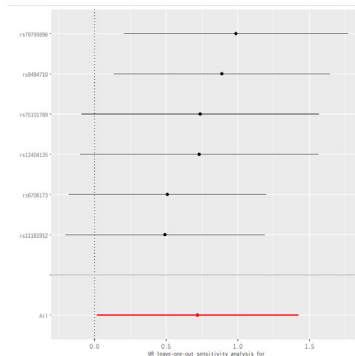


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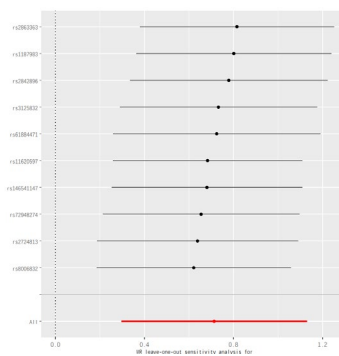


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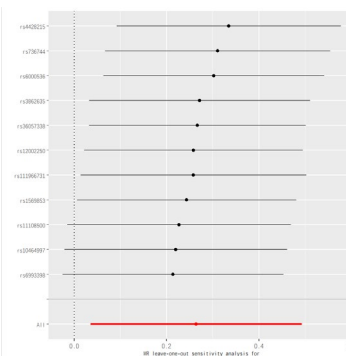
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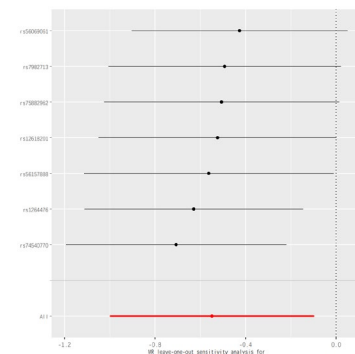
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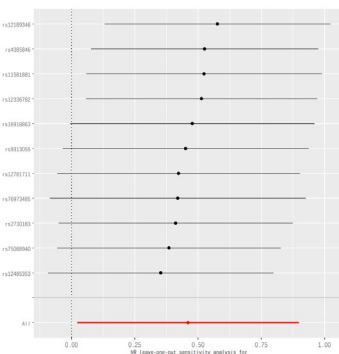
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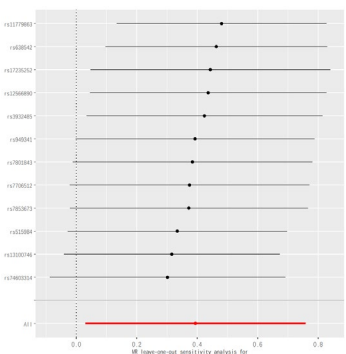
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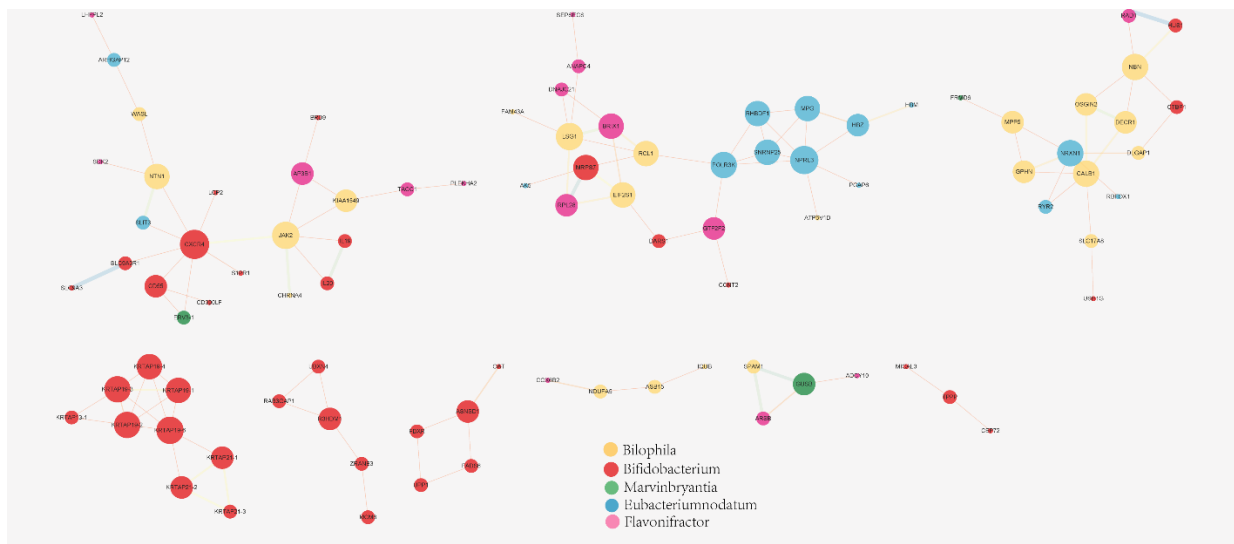
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**Supplementary Figure S3:** PPI network of significant GM's SNPs mapped genes. Genes are represented by circular nodes, and their interactions are represented by edges. The size of the dots represents the Betweenness Centrality score, with high Betweenness Centrality scores being large and low scoring dots being small, and each of the bacteria related genes is represented by different colors. (A) PPI network of five significant GM's SNPs mapped genes of FE. (B) PPI network of six significant GM's SNPs mapped genes of GE. (C) PPI network of nine significant GM's SNPs mapped genes of CAE. (D) PPI network of ten significant GM's SNPs mapped genes of JAE.



(A) PPI network of five significant GM's SNPs mapped genes of FE.



