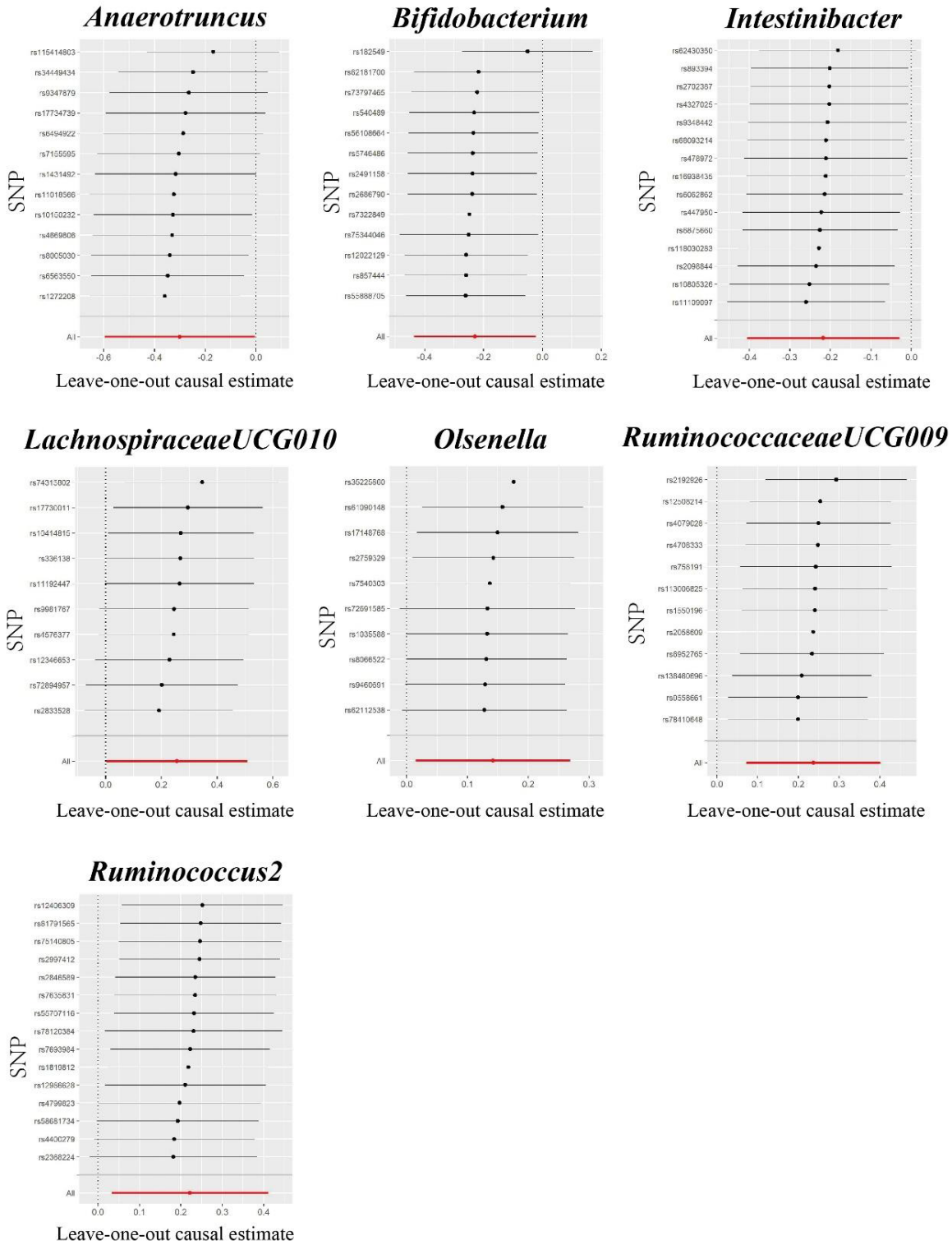
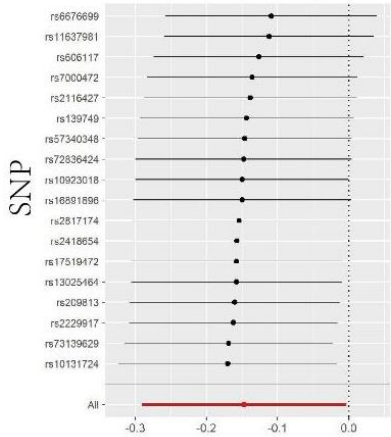


SUPPLEMENTARY FIGURES



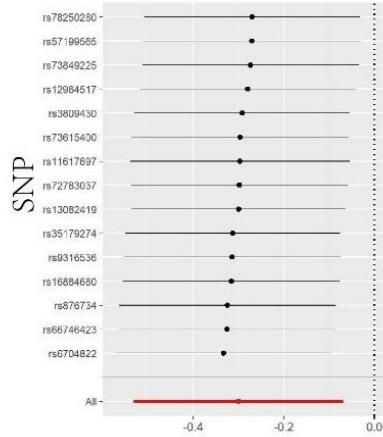
Supplementary Figure 1. Leave-one-out plots for the causal association between gut microbiota and GH in forward MR analyses.

***Eubacterium
(ruminantium group)***



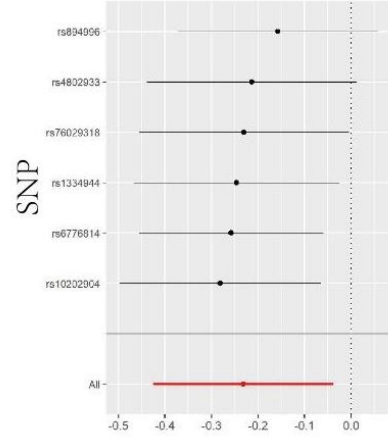
Leave-one-out causal estimate

***Eubacterium
(ventriosum group)***



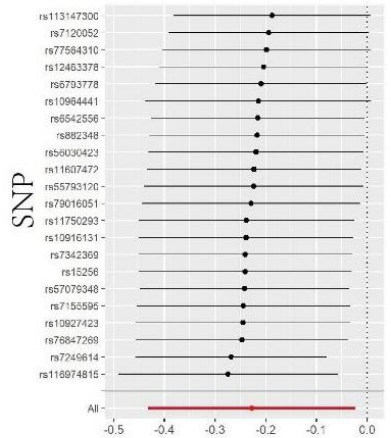
Leave-one-out causal estimate

Methanobrevibacter



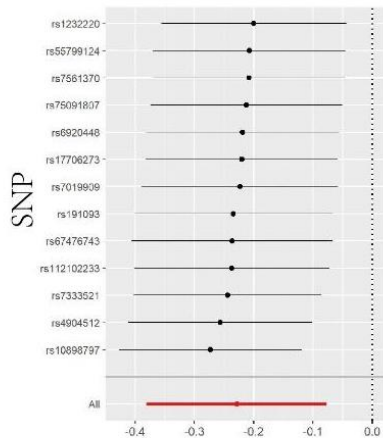
Leave-one-out causal estimate

RuminococcaceaeUCG002



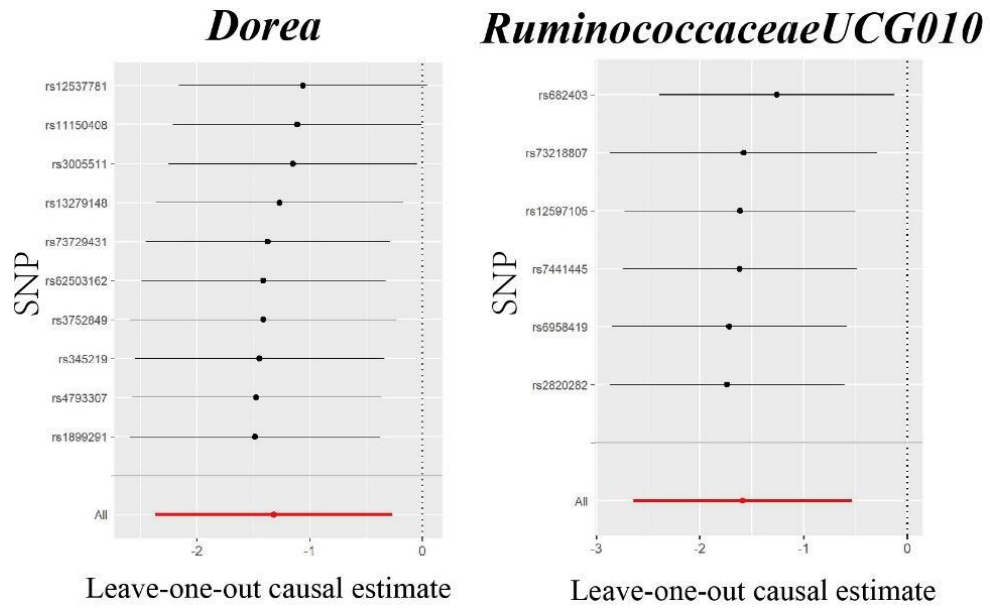
Leave-one-out causal estimate

Tyzzerella3

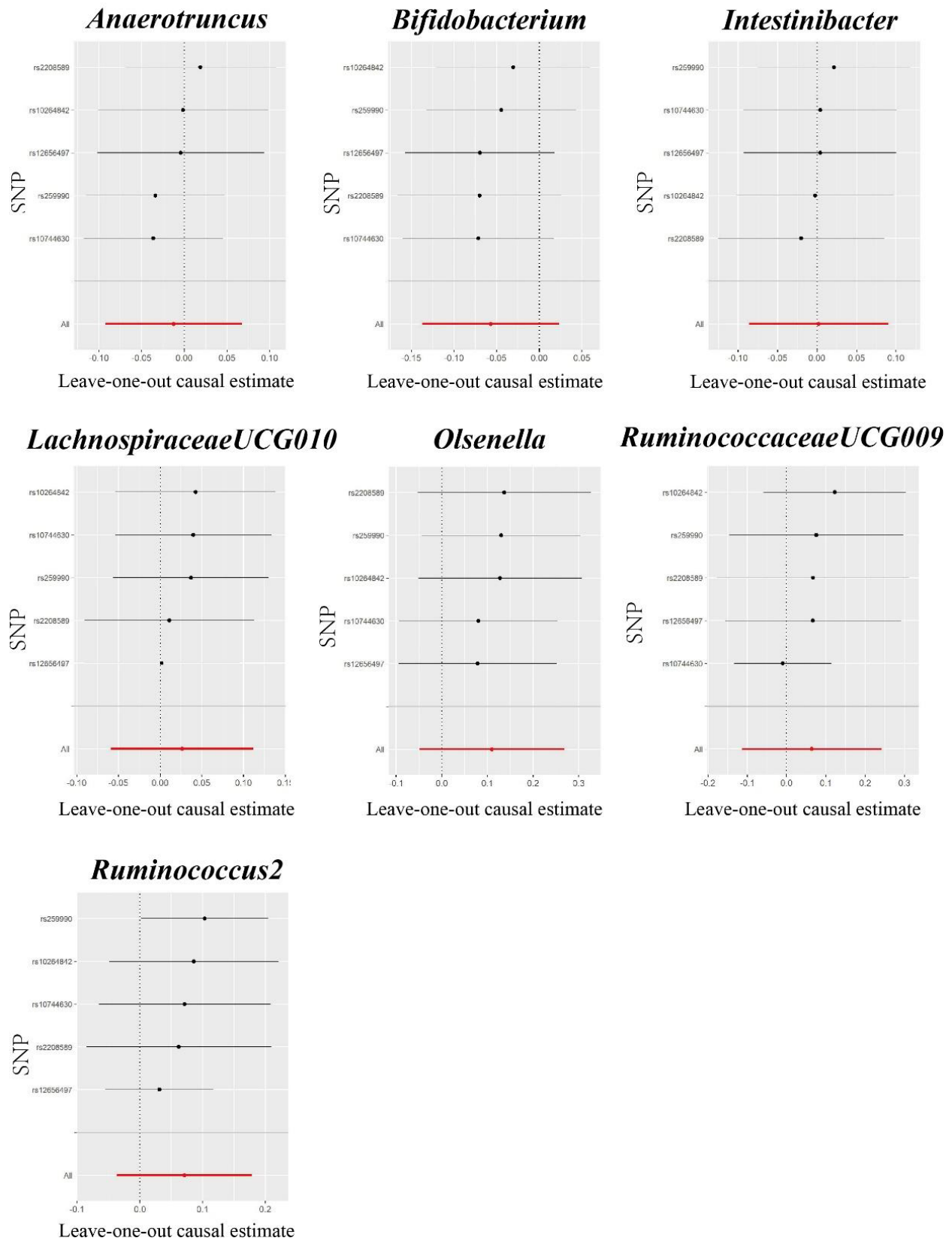


Leave-one-out causal estimate

Supplementary Figure 2. Leave-one-out plots for the causal association between gut microbiota and PE in forward MR analyses.

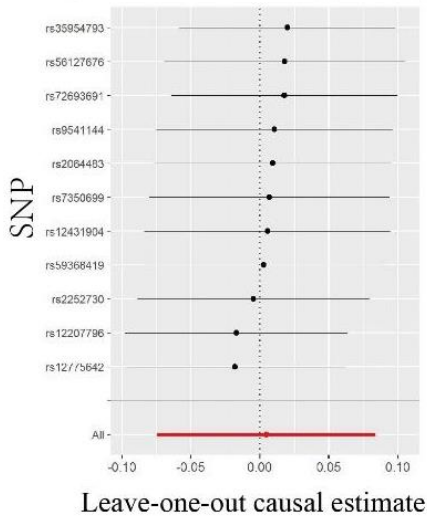


Supplementary Figure 3. Leave-one-out plots for the causal association between gut microbiota and eclampsia in forward MR analyses.

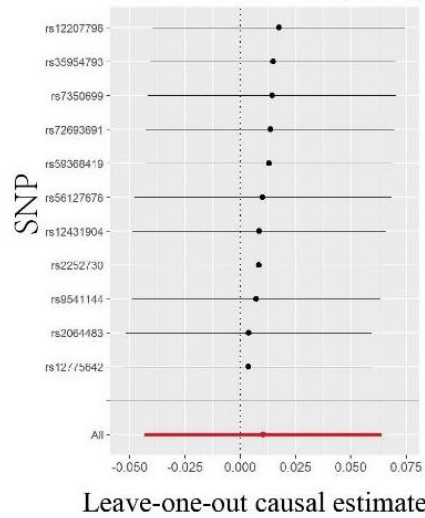


Supplementary Figure 4. Leave-one-out plots for the causal association between gut microbiota and GH in reverse MR analyses.

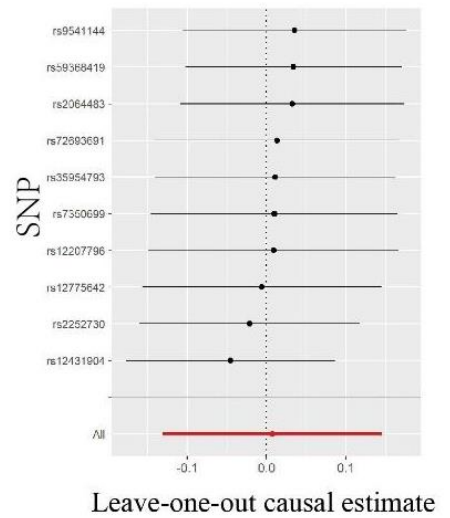
***Eubacterium
(ruminantium group)***



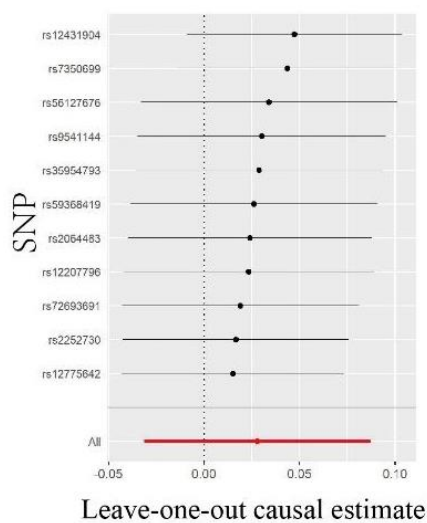
***Eubacterium
(ventriosum group)***



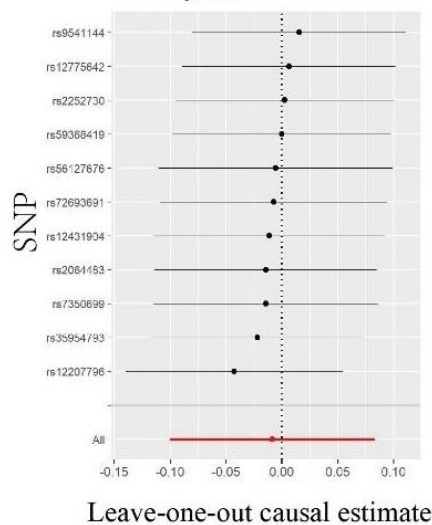
Methanobrevibacter



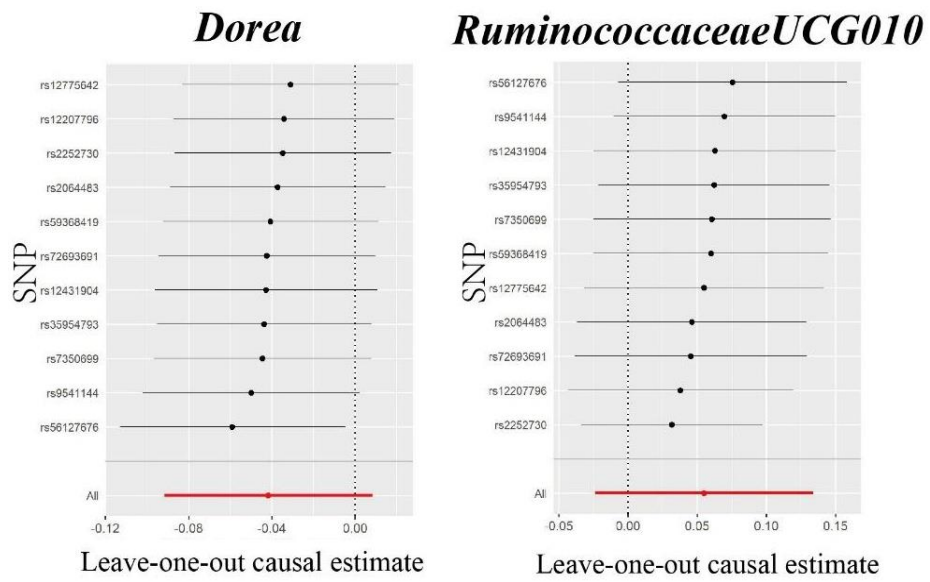
RuminococcaceaeUCG002



Tyzzzeria3



Supplementary Figure 5. Leave-one-out plots for the causal association between gut microbiota and PE in reverse MR analyses.



Supplementary Figure 6. Leave-one-out plots for the causal association between gut microbiota and eclampsia in reverse MR analyses.