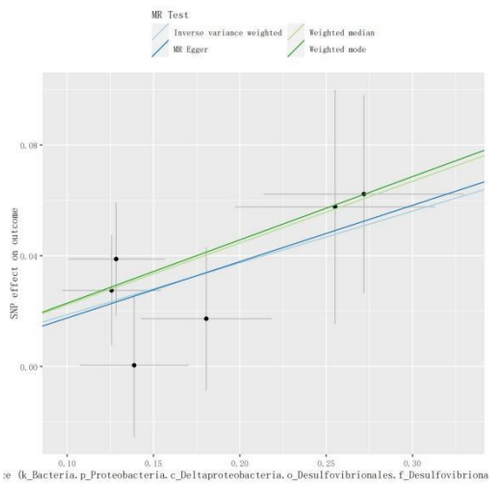
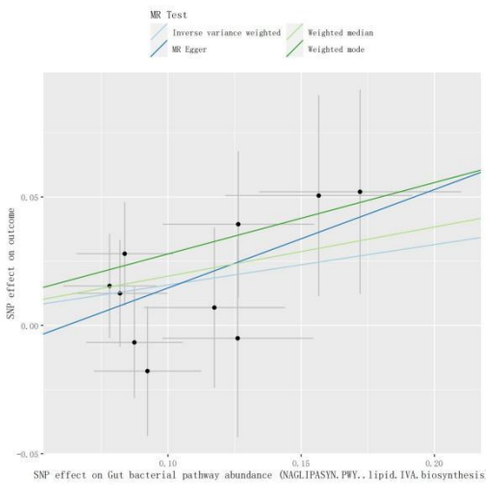
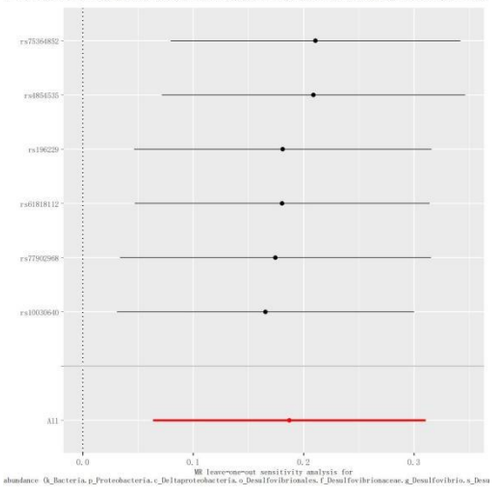
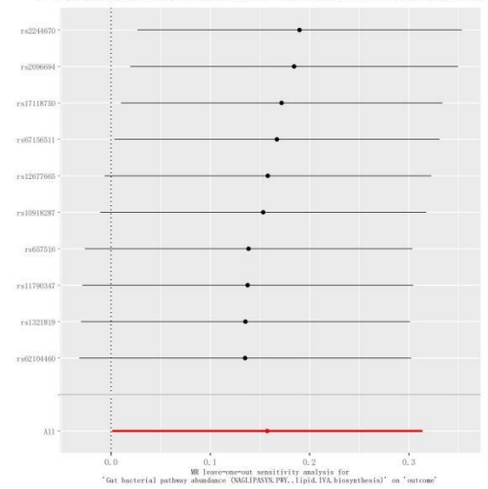
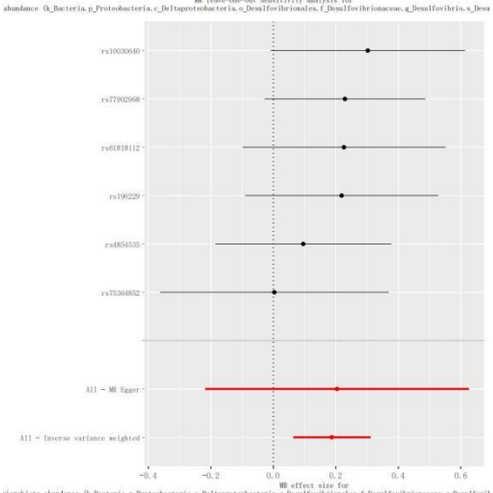
Supplementary Figure S1. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Gut microbiota on AD

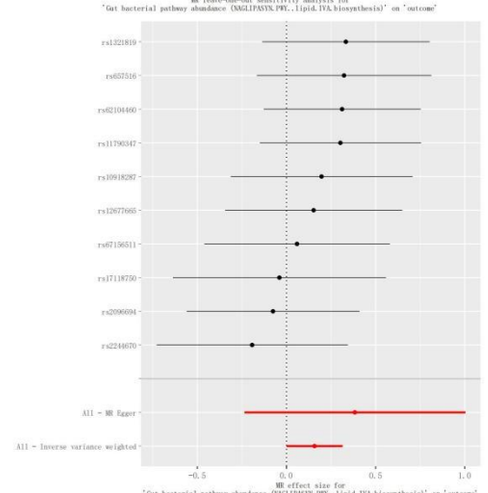


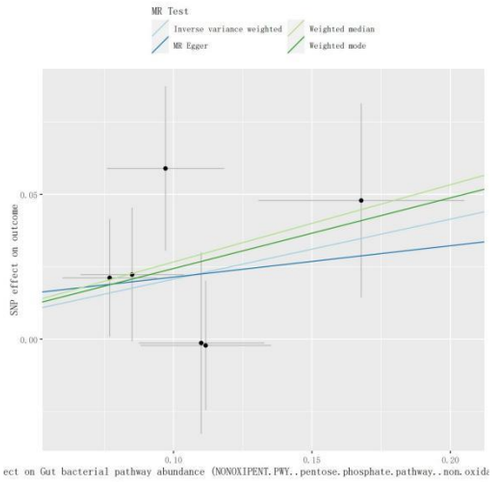




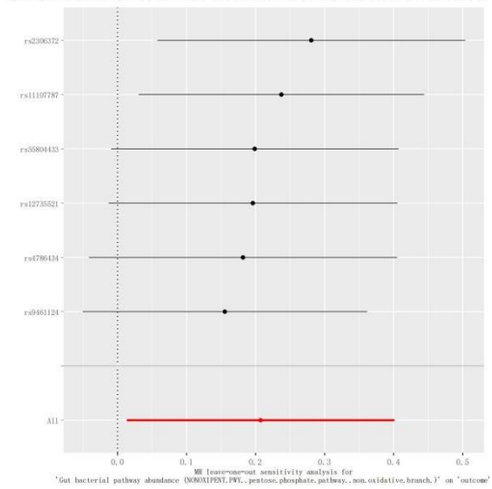


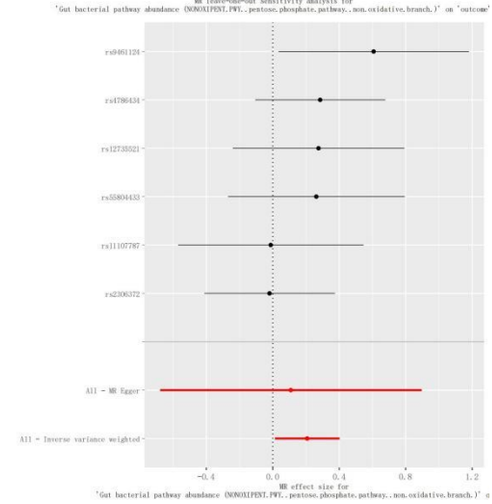


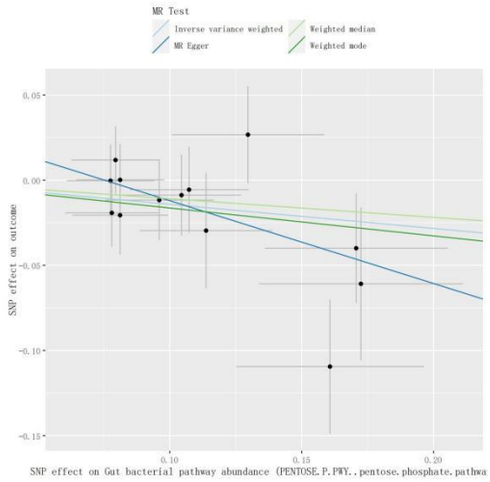




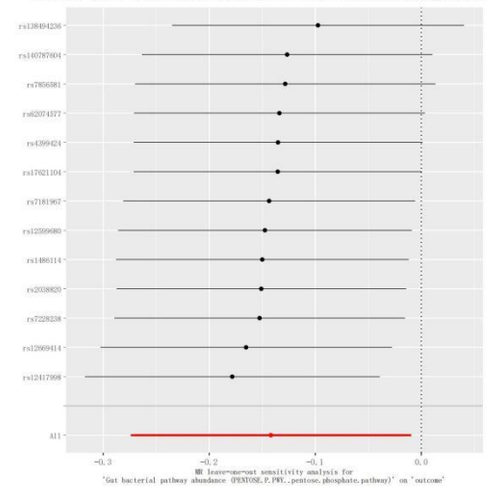
ect on Gut bacterial pathway abundance (NONOXIPENT.PWY..pentose.phosphate.pathway..non.oxida

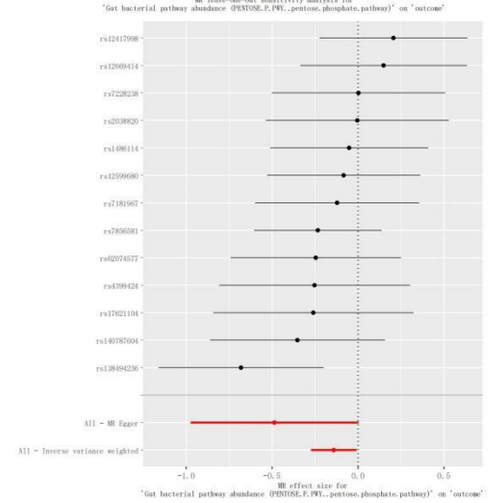


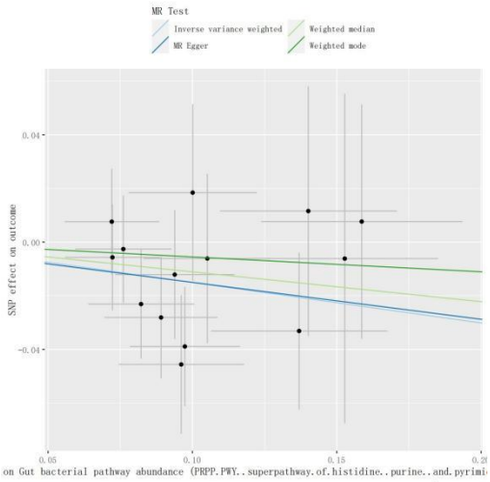


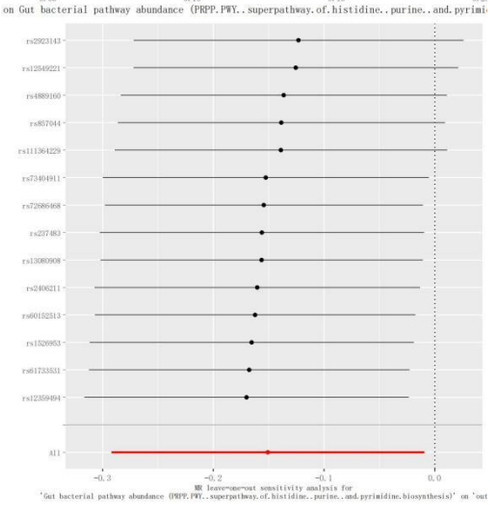


SNP effect on Gut bacterial pathway abundance (PENTOSE.P.PWY..pentose.phosphate.pathwa






MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.04
0.00
−0.04
0.05
0.10
0.15
on Gut bacterial pathway abundance (PRPP.PWY..superpathway.of.histidine..purine..and.pyrimi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rs61733531
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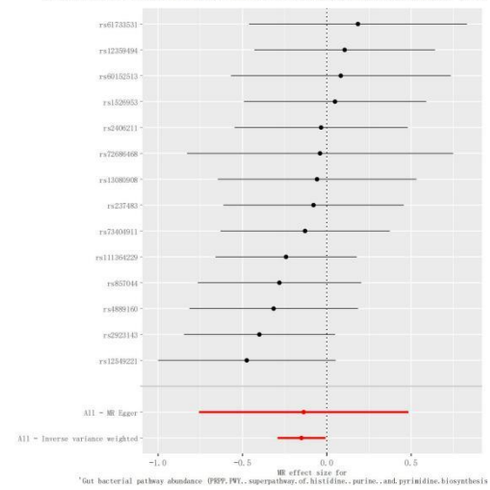
All
−0.3
−0.2
−0.1
0.0
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PRPP.PWY..superpathway.of.histidine..purine..and.pyrimidine.biosynthesis)' on 'out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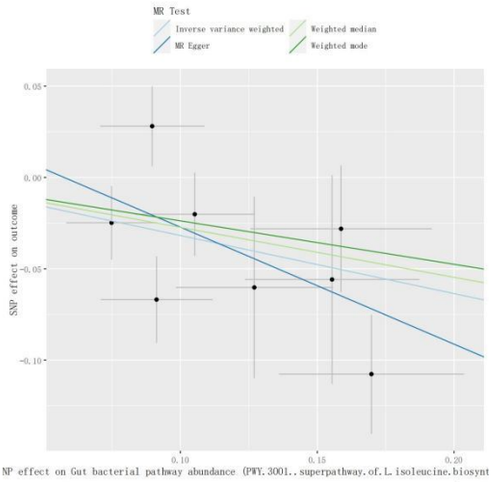
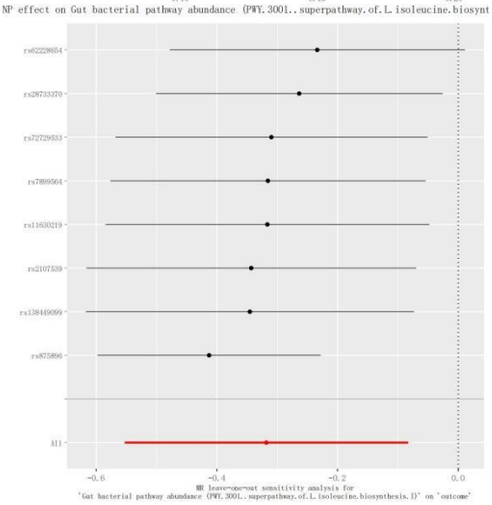
rs4889160
rs2923143
rs12549221
All - MR Egger
All - Inverse variance weighted
−1.0
−0.5
0.0
0.5
MR effect size for
'Gut bacterial pathway abundance (PRPP.PWY..superpathway.of.histidine..purine..and.pyrimidine.biosynthesis


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.05
0.00
−0.05
−0.10
0.10
0.15
0.20
NP effect on Gut bacterial pathway abundance (PWY.3001..superpathway.of.L.isoleucine.biosynt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All
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MR leave-one-out sensitivity analysis for
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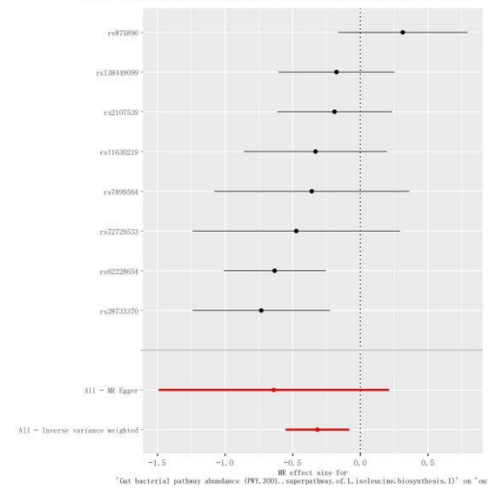
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All - MR Egger
All - Inverse variance weighted
−1.5
−1.0
−0.5
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0.5
MR effect size for
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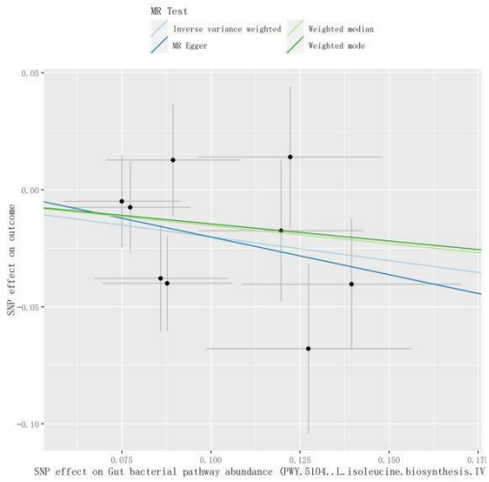
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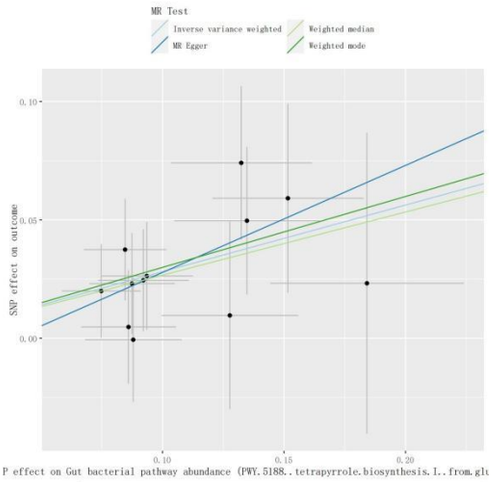
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Gut bacterial pathway abundance (PWY.5104..L.isoleucine.biosynthesis.IV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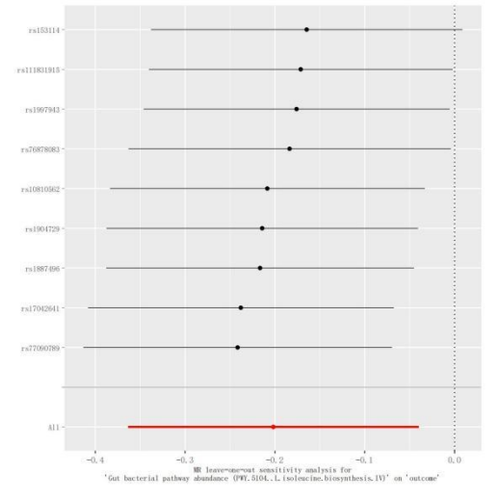
Weighted median
Weighted mode
SNP effect on outcome
P effect on Gut bacterial pathway abundance (PWY.5188..tetrapyrrole.biosynthesis.I..from.glu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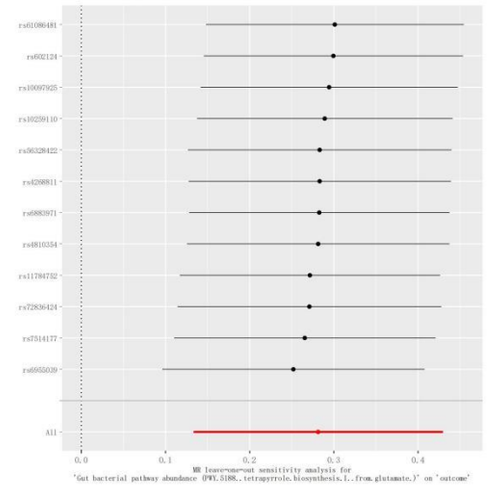
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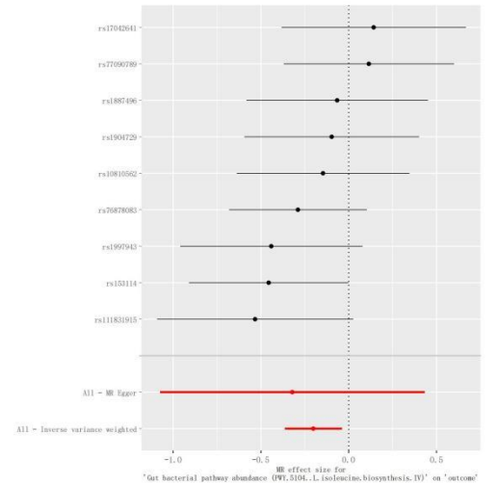
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All - Inverse variance weighted
MR effect size for
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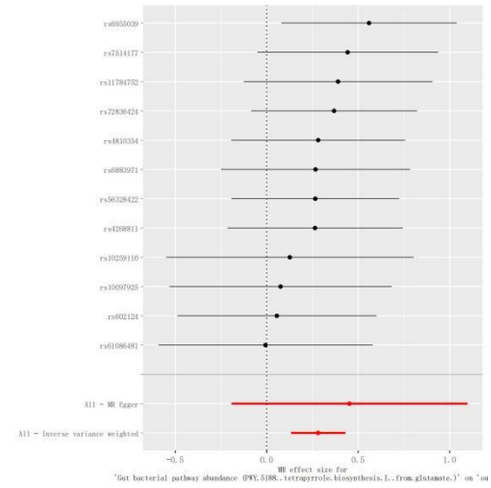
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All - MR Egger
All - Inverse variance weighted
MR effect size for
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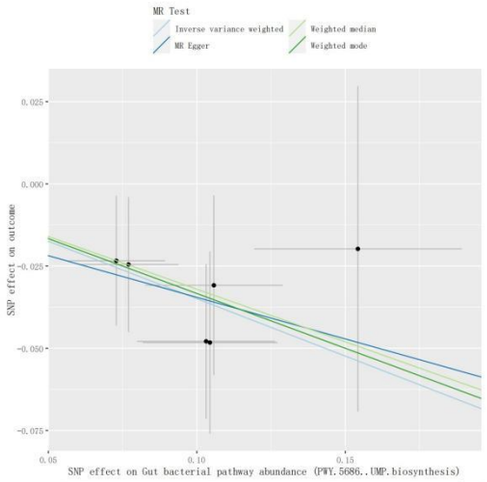
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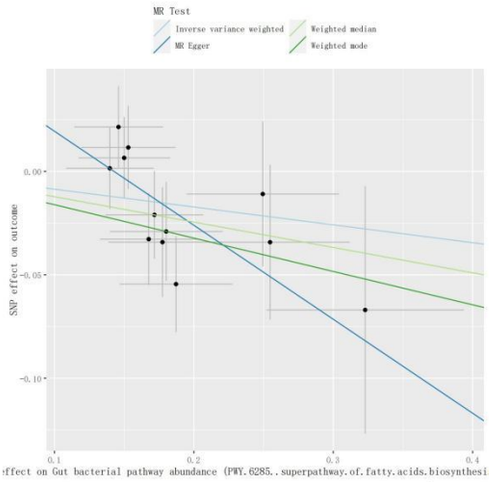
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Gut bacterial pathway abundance (PWY.5686..UMP.biosynthesis)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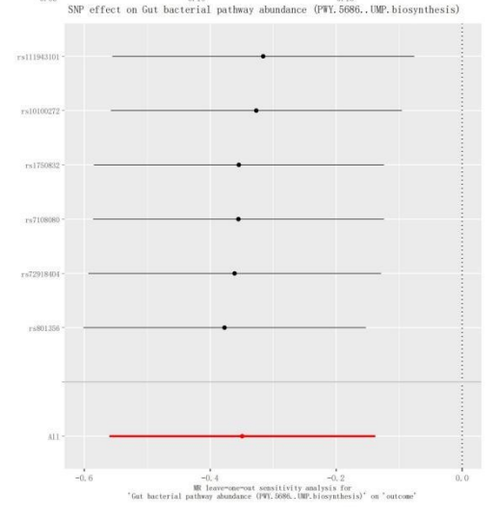
Weighted mode
SNP effect on outcome
effect on Gut bacterial pathway abundance (PWY.6285..superpathway.of.fatty.acids.biosynthesi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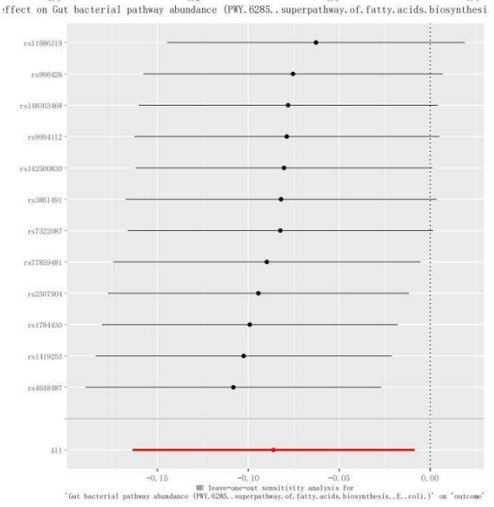
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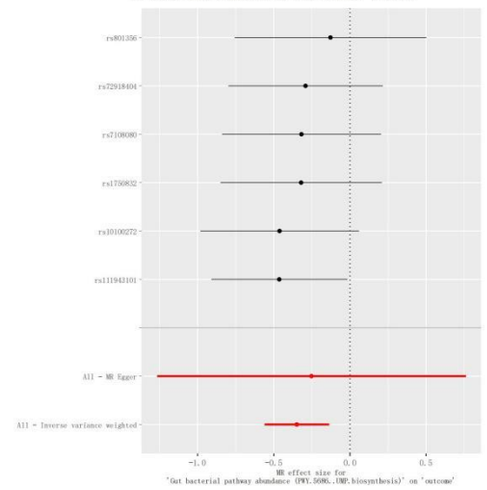
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MR effect size for
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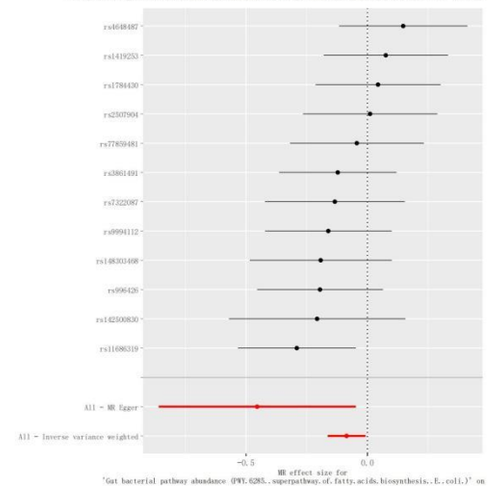
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MR effect size for
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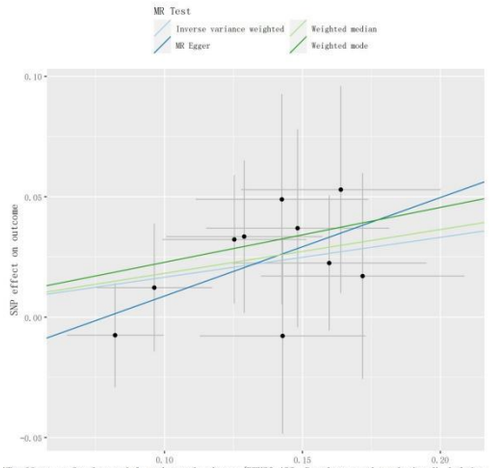
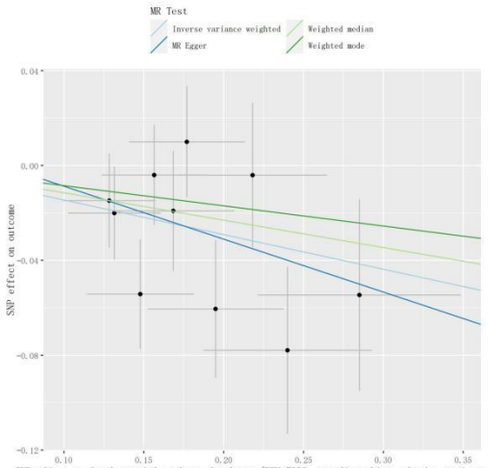
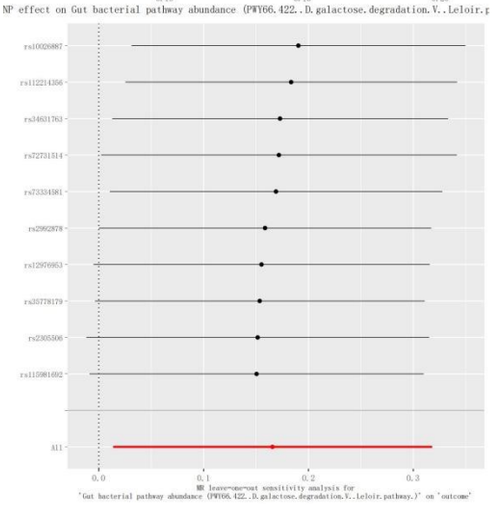


NP effect on Gut bacterial pathway abundance (PWY66.422..D.galactose.degradation.V..Leloir.p



SNP effect on Gut bacterial pathway abundance (PWY.7392..taxadiene.biosynthesis..engineer



MR leave-one-out sensitivity analysis for
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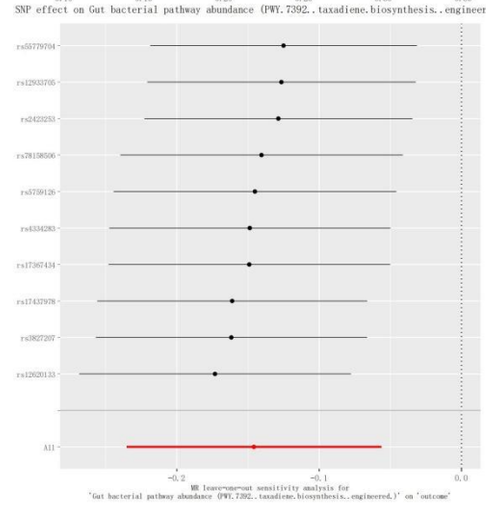

MR leave-one-out sensitivity analysis for
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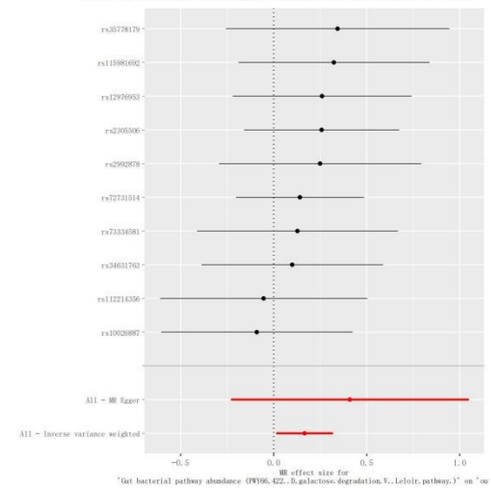

MR effect size for
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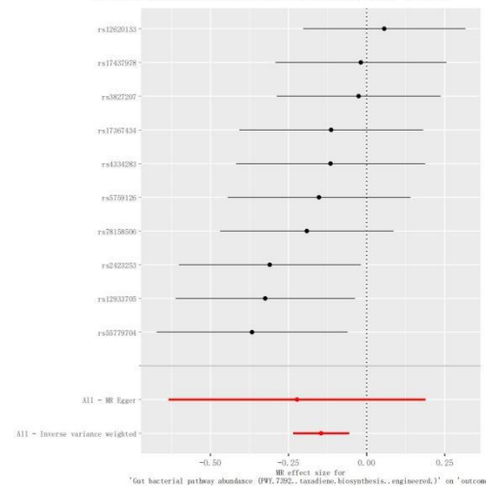

MR effect size for
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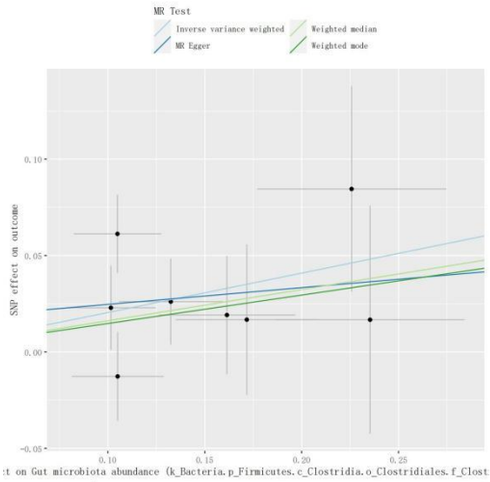
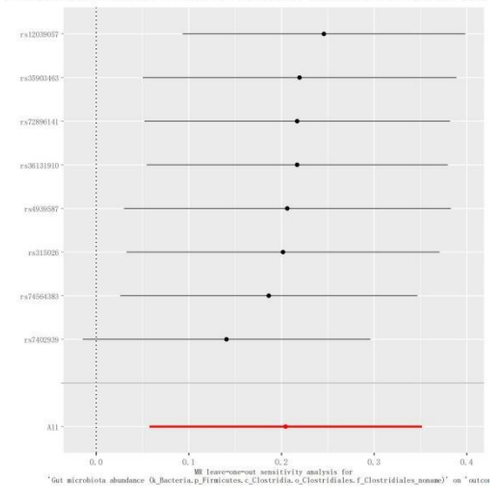


:t on Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clost



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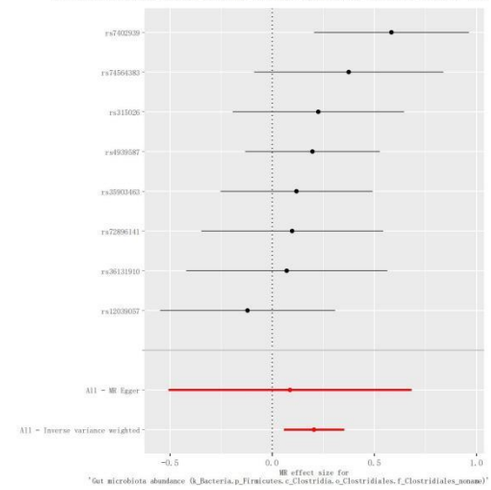
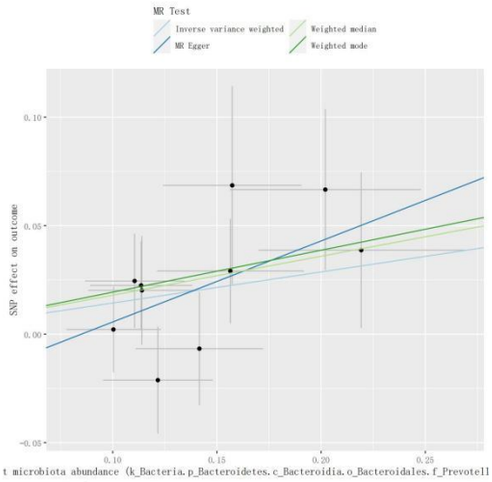
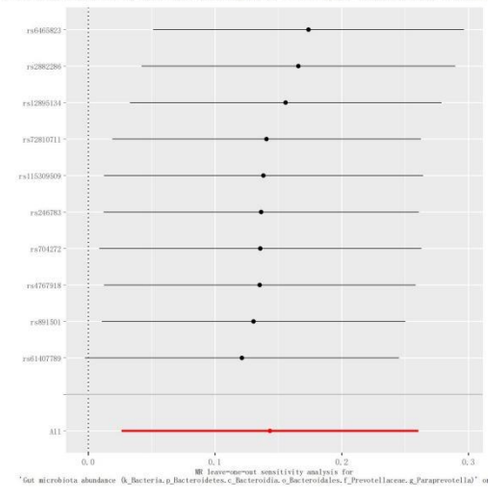


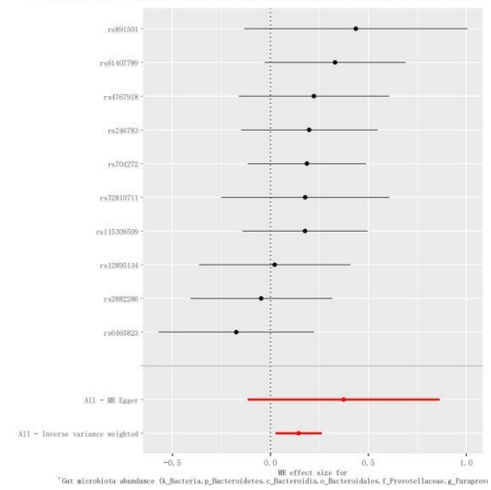
'Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clostridiales_noname)'



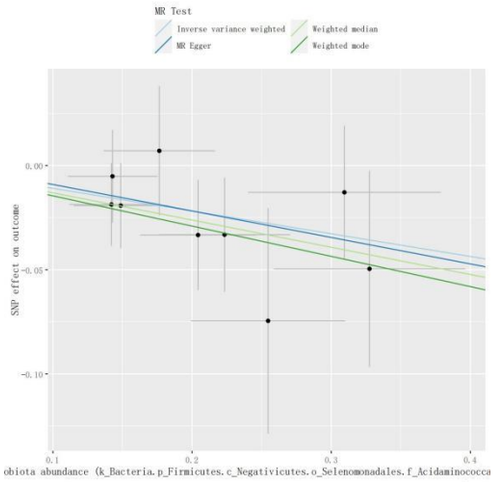
t microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Prevotell



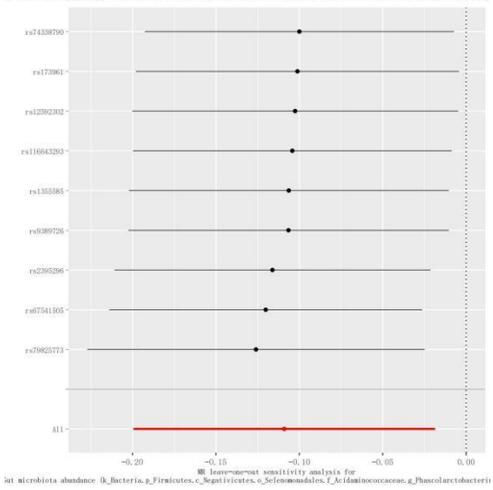
'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae.g_Paraprevotella)' o



'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae.g_Paraprev

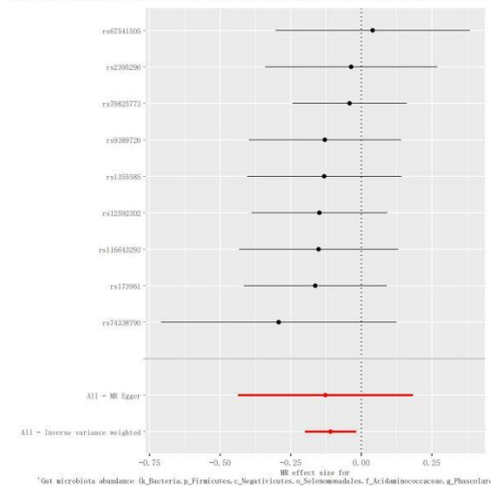


obiota abundance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococca



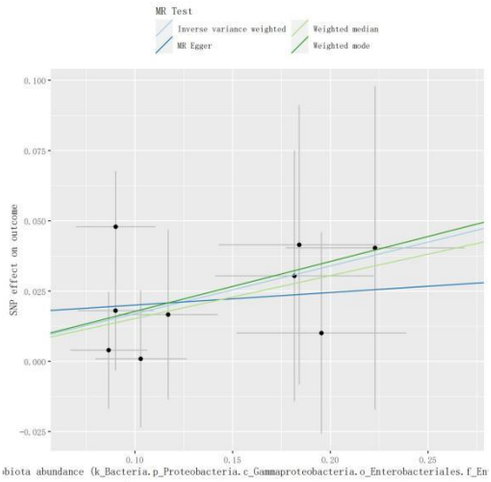
MR leave-one-out sensitivity analysis for

iut microbiota abundance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococcaceae.g_Phascolarctobacteri



MR effect size for

'Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococcaceae.g_Phascolarc



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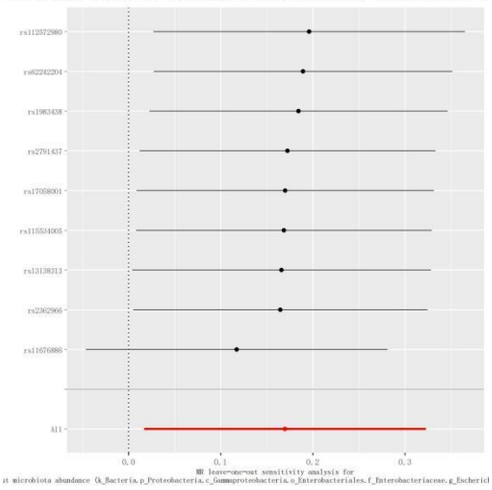
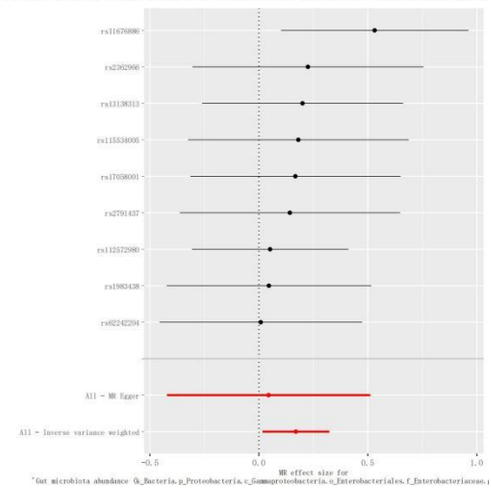


MR leave-one-out sensitivity analysis for

it microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Escherich



MR effect size for

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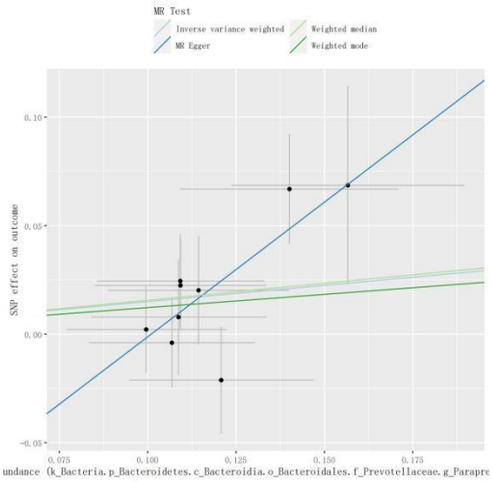
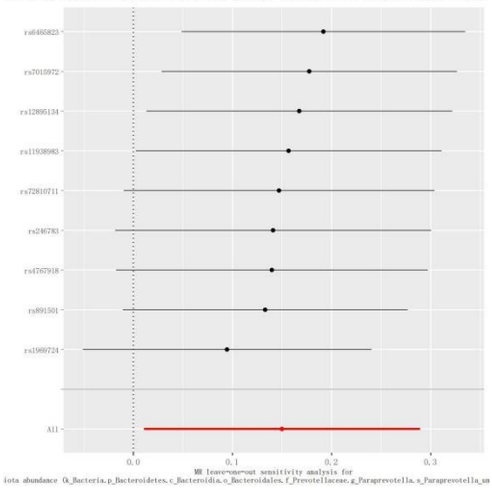
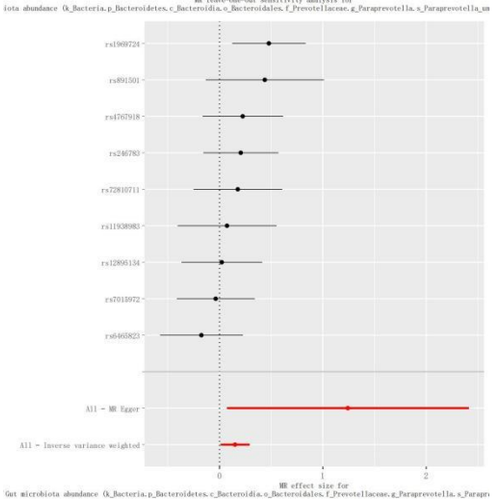


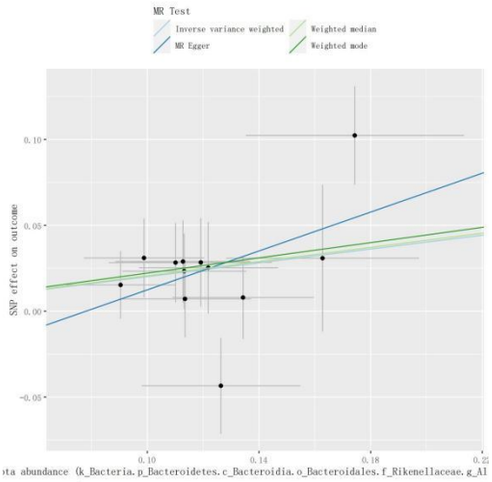
undance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae.g_Parapre



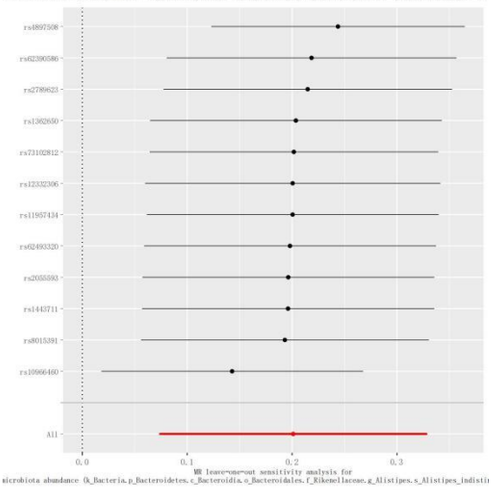
iota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae.g_Paraprevotella.s_Paraprevotella_un



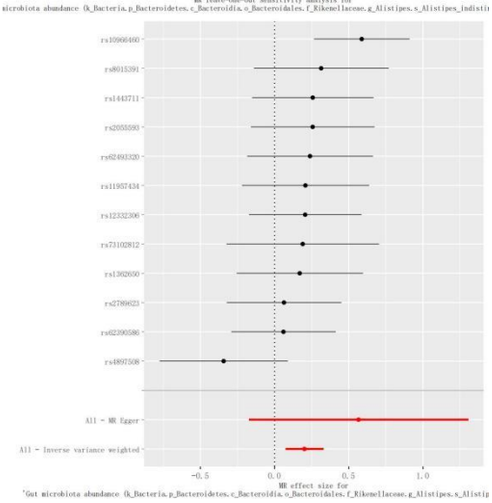
Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Prevotellaceae.g_Paraprevotella.s_Paraprev



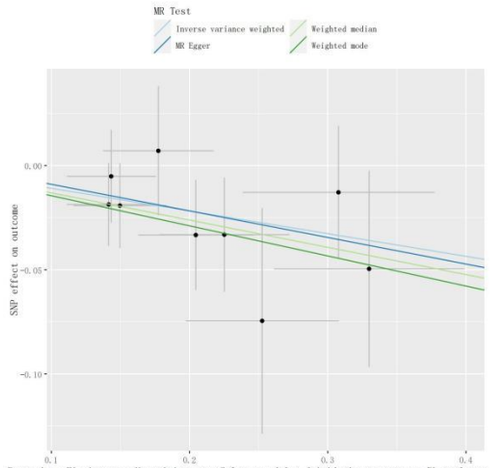
ta abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_Al



microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_Alistipes.s_Alistipes_indistii



'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_Alistipes.s_Alistip



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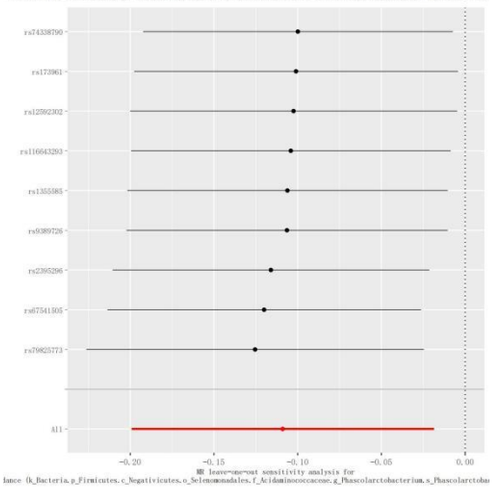
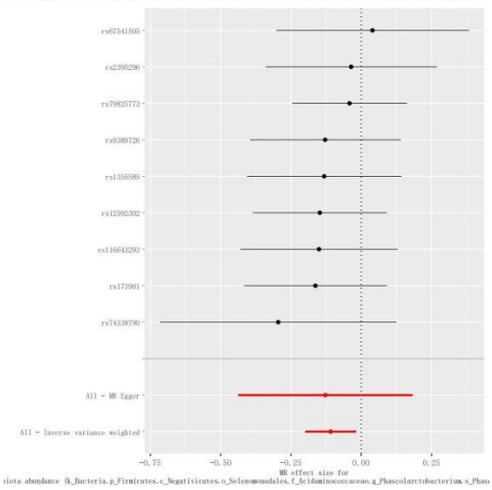


lance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococcaceae.g_Phascolarctobacterium.s_Phascolarctoba

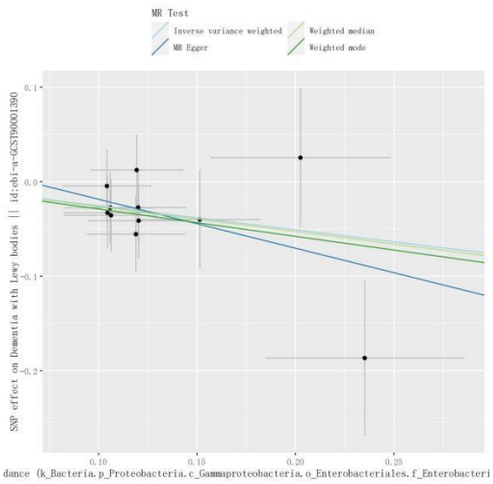
MR leave-one-out sensitivity analysis for

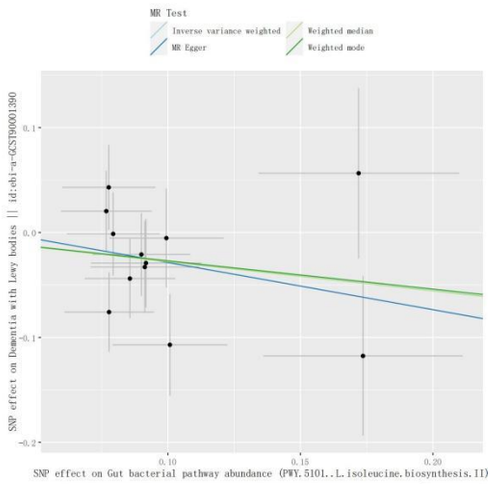


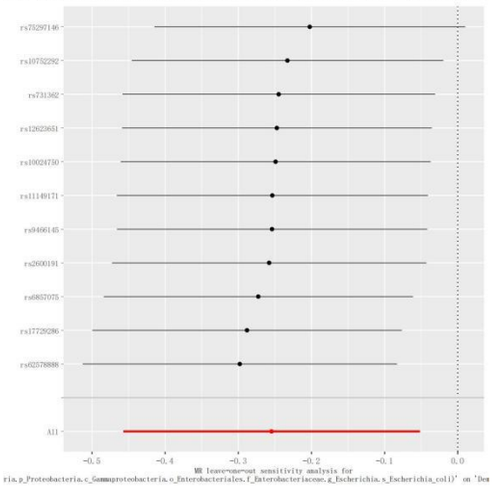
MR effect size for

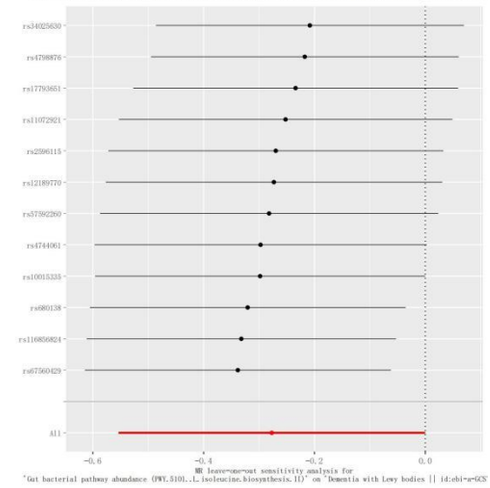
biota abundance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococcaceae.g_Phascolarctobacterium.s_Phasc

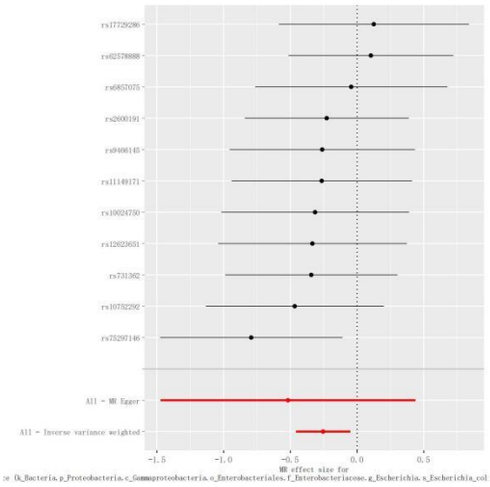
Supplementary Figure S2. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Gut microbiota on DLB

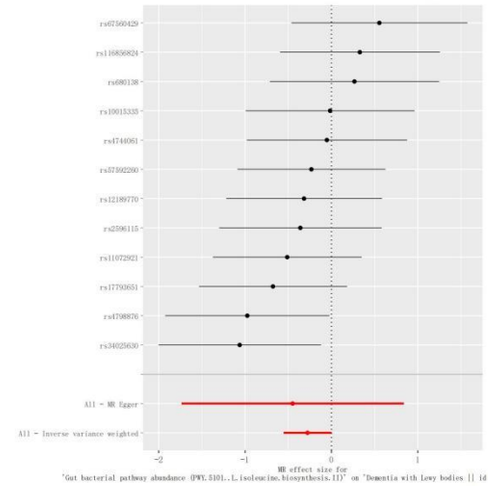


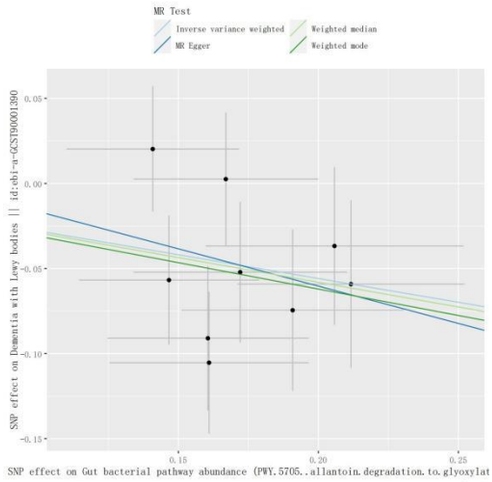




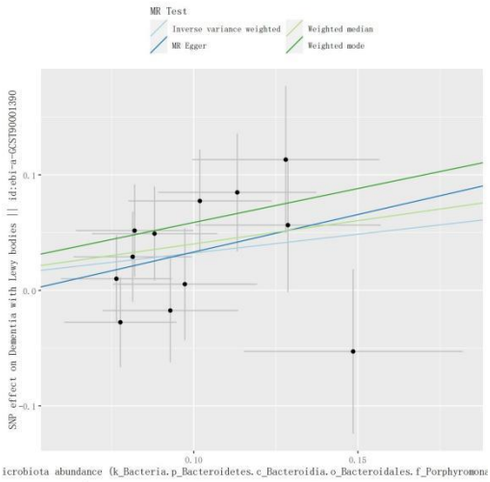




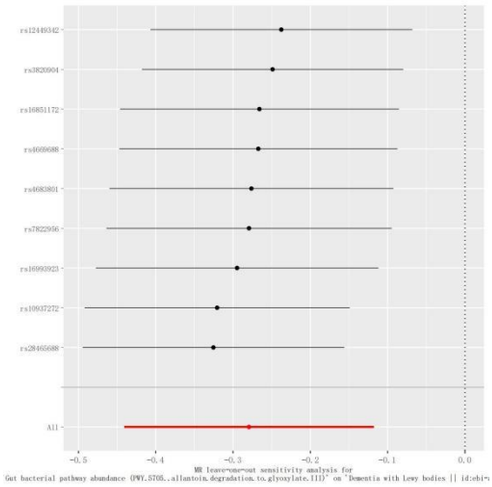




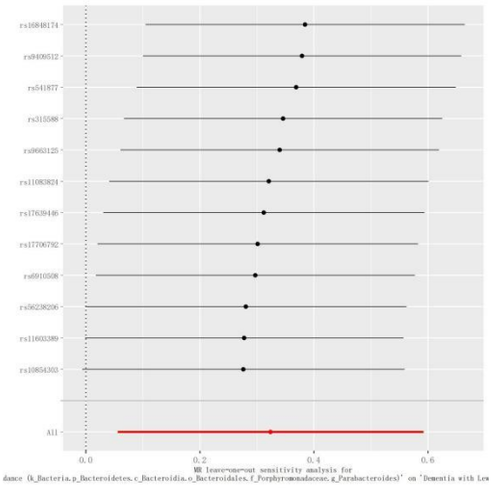
SNP effect on Gut bacterial pathway abundance (PWY.5705..allantoin.degradation.to.glyoxylat



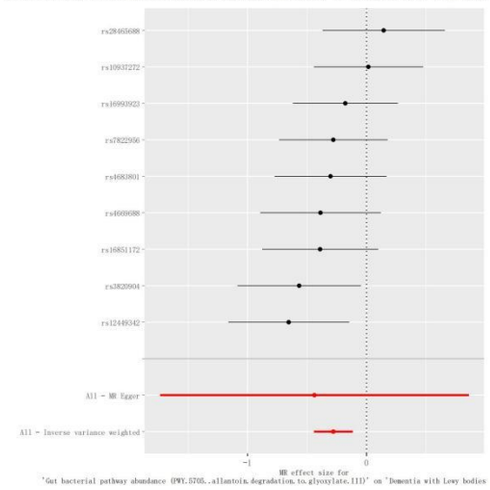
icrobiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromona



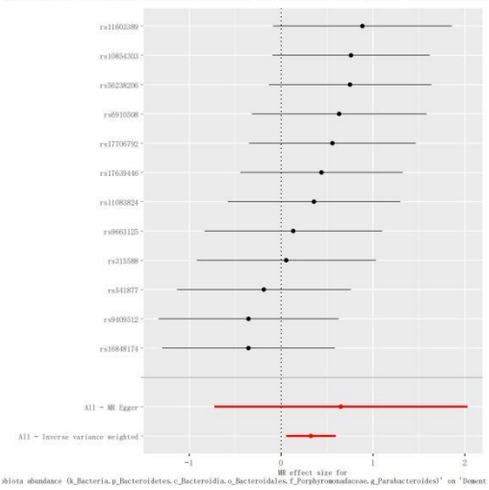
Gut bacterial pathway abundance (PWY.5705..allantoin.degradation.to.glyoxylate.III)' on 'Dementia with Lewy bodies || id:ebi-a



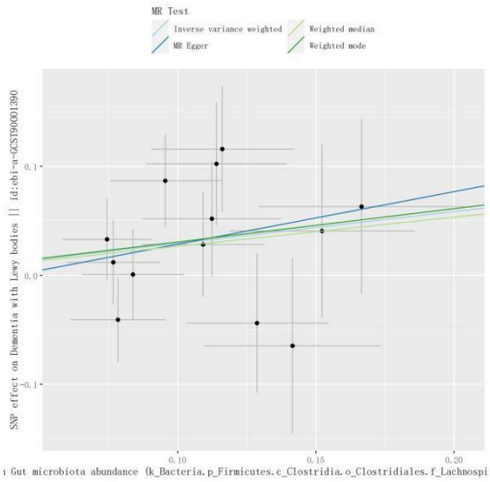
dance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae.g_Parabacteroides)' on 'Dementia with Lew



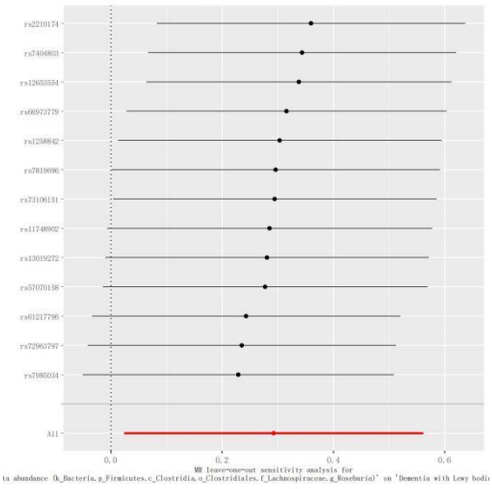
'Gut bacterial pathway abundance (PWY.5705..allantoin.degradation.to.glyoxylate.III)' on 'Dementia with Lewy bodies'



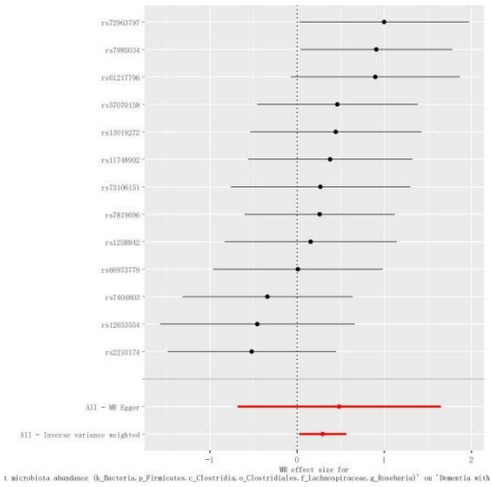
biota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Porphyromonadaceae.g_Parabacteroides)' on 'Dement



ı Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospi

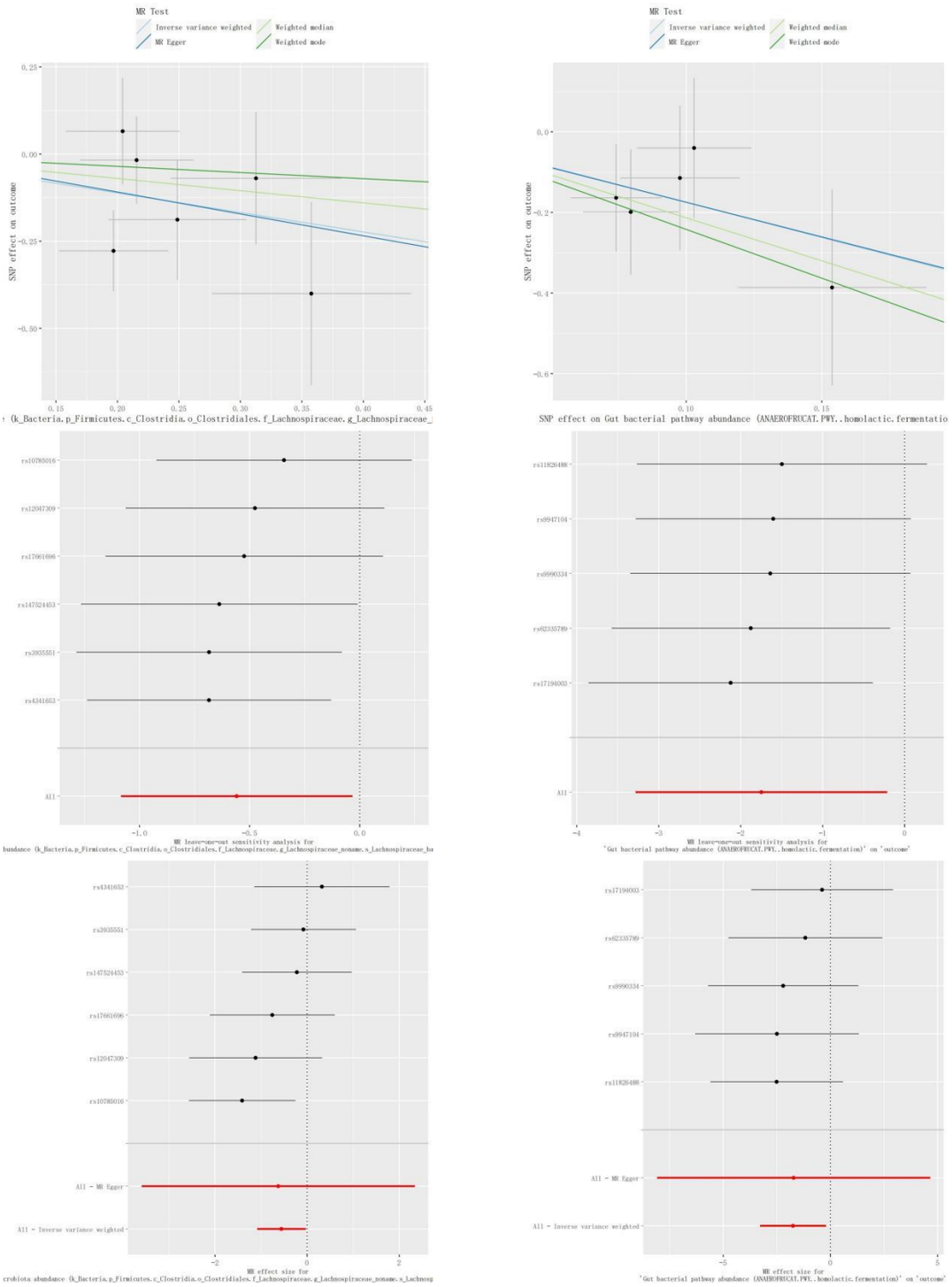


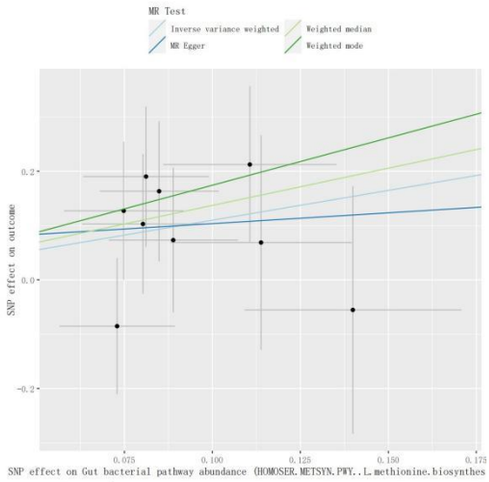
MR leave-one-out sensitivity analysis for
ta abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g_Roseburia)' on 'Dementia with Lewy bodi

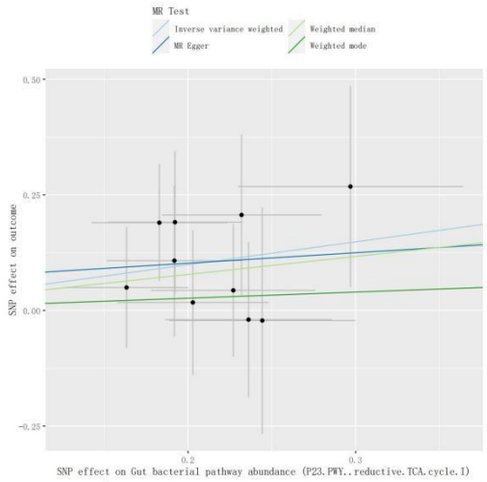


MR effect size for
t microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Lachnospiraceae.g_Roseburia)' on 'Dementia with

Supplementary Figure S3. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Gut microbiota on FTD




MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.2
0.0
−0.2
0.075
0.100
0.125
0.150
0.175
SNP effect on Gut bacterial pathway abundance (HOMOSER.METSYN.PWY..L.methionine.biosynthes


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
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0.25
0.00
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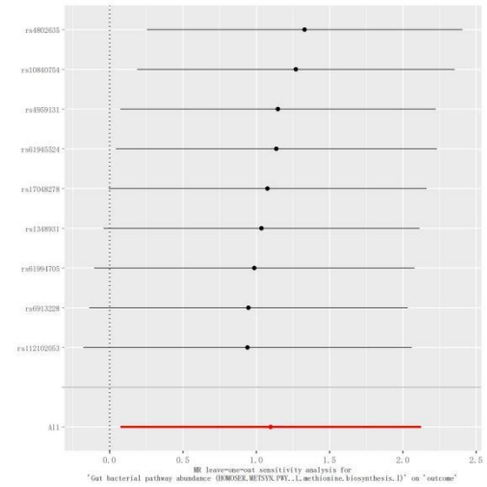
0.3
SNP effect on Gut bacterial pathway abundance (P23.PWY..reductive.TCA.cycle.I)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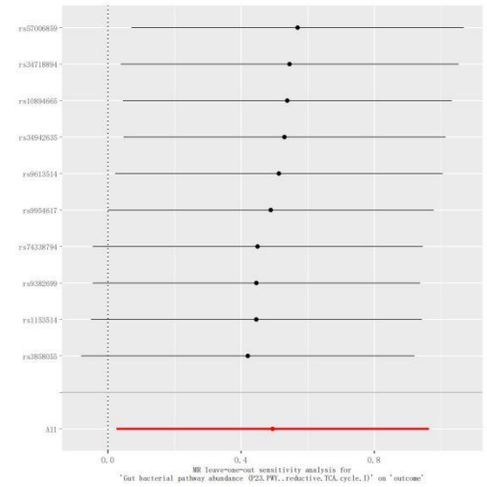
rs112102053
All
0.0
0.5
1.0
1.5
2.0
2.5
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (HOMOSER.METSYN.PWY..L.methionine.biosynthesis.I)' on 'outcome'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rs74338794
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rs1153514
rs3858055
All
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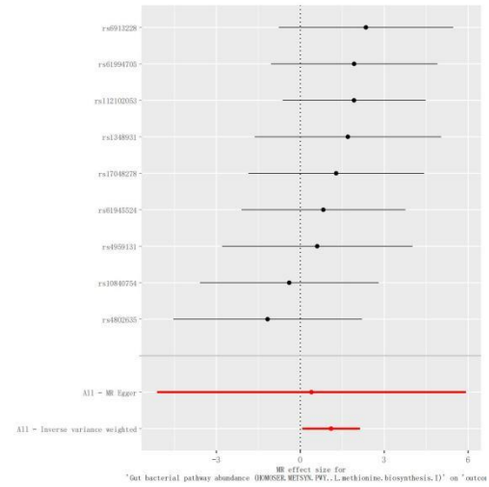
0.4
0.8
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (P23.PWY..reductive.TCA.cycle.I)' on 'outcome'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rs4959131
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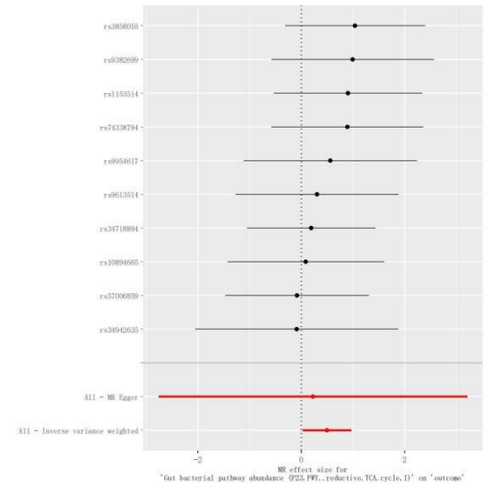
rs4802635
All - MR Egger
All - Inverse variance weighted
−3
0
3
6
MR effect size for
'Gut bacterial pathway abundance (HOMOSER.METSYN.PWY..L.methionine.biosynthesis.I)' on 'outcom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All - MR Egger
All - Inverse variance weighted
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MR effect size for
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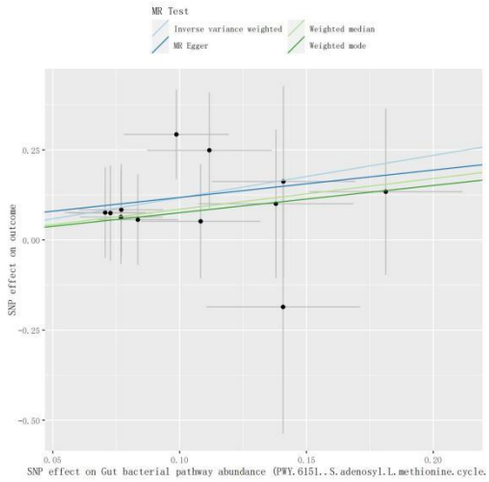
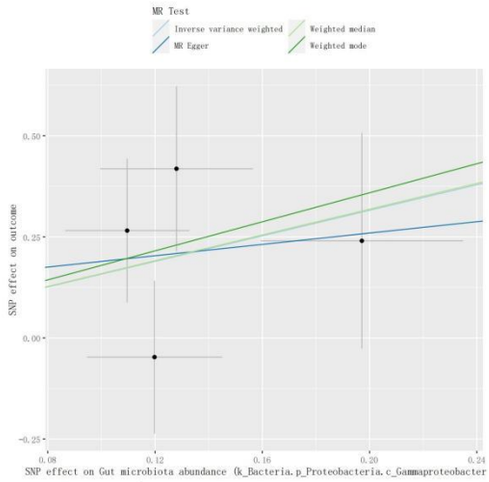
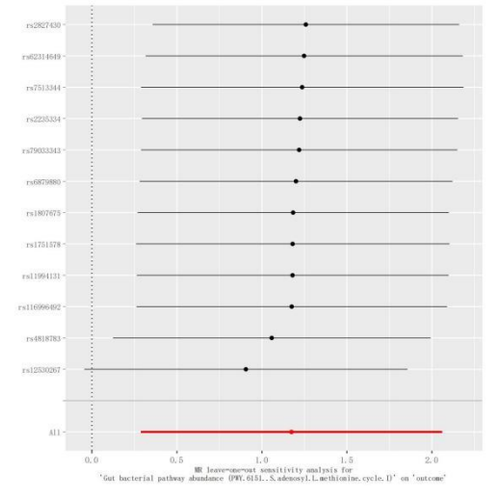

MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Gut bacterial pathway abundance (PWY.6151..S.adenosyl.L.methionine.cycle.


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Gut microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacter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MR leave-one-out sensitivity analysis for
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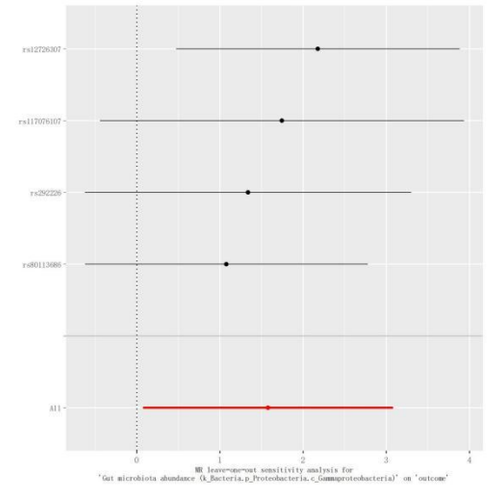
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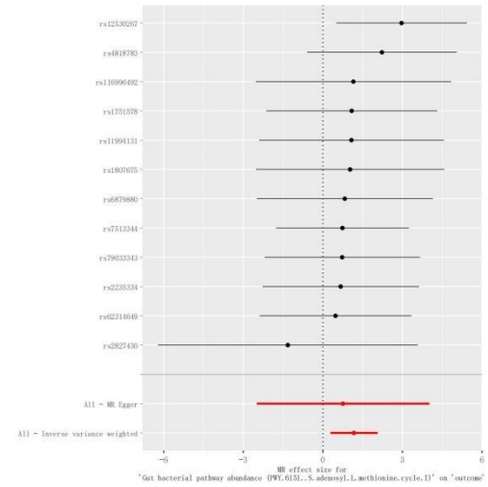
MR leave-one-out sensitivity analysis for
'Gut microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria)' on 'outcome'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rs62314649
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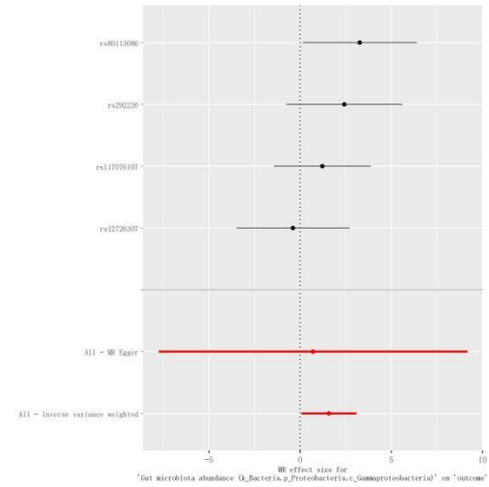
All - MR Egger
All - Inverse variance weighted
MR effect size for
'Gut bacterial pathway abundance (PWY.6151..S.adenosyl.L.methionine.cycle.1)' on 'outcome'


rs80113686
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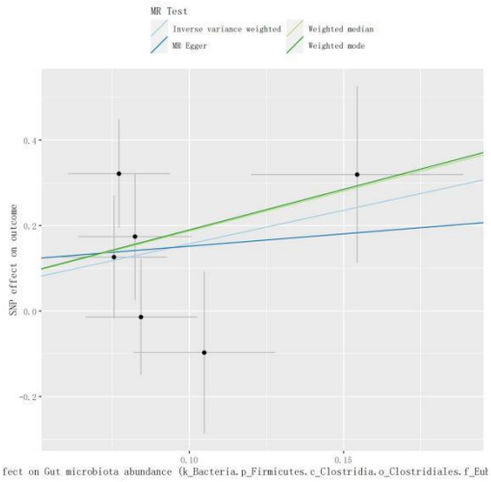
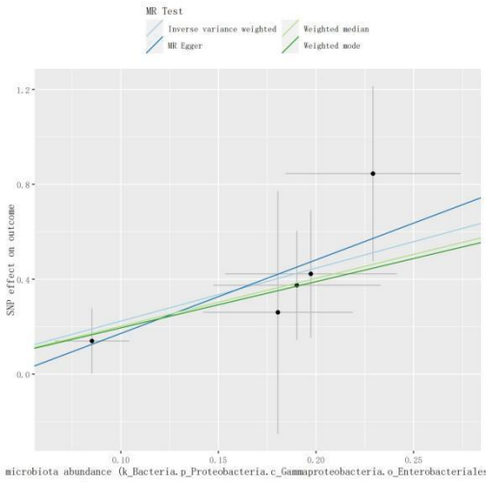
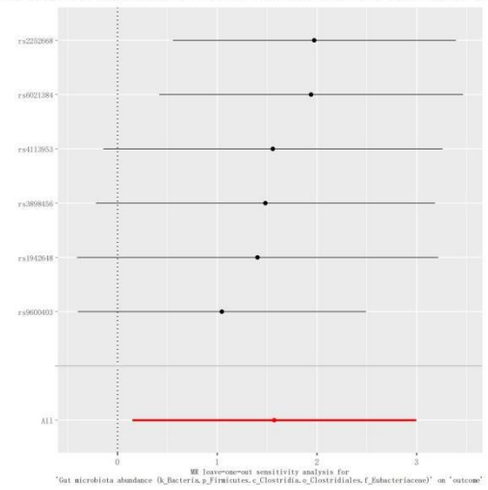
All - Inverse variance weighted
MR effect size for
'Gut microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria)' on 'outcome'

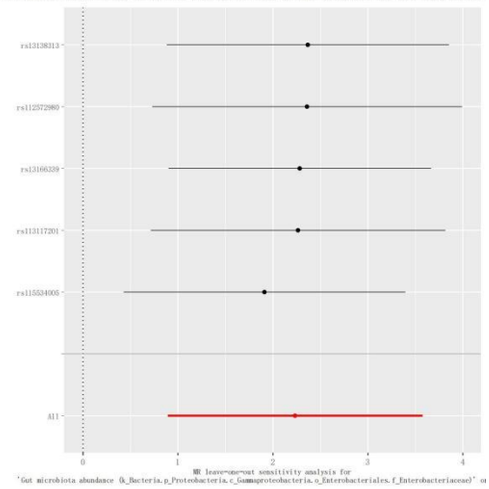


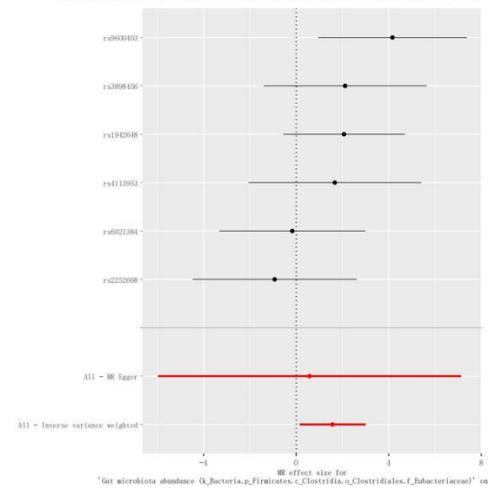


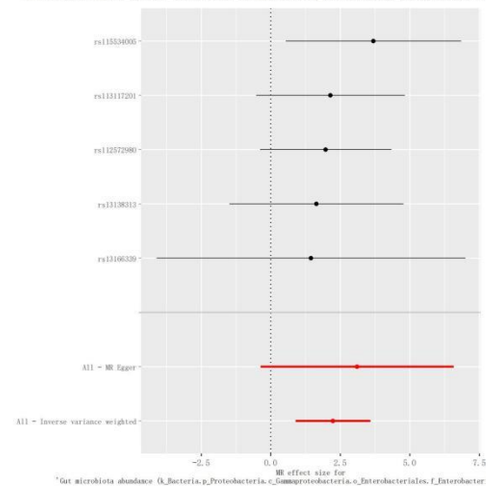
fect on Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eub

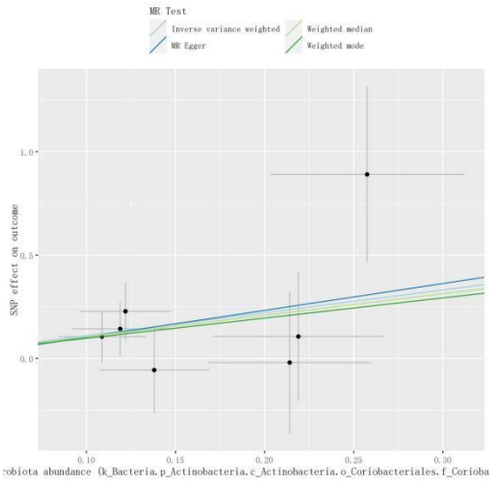
microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales

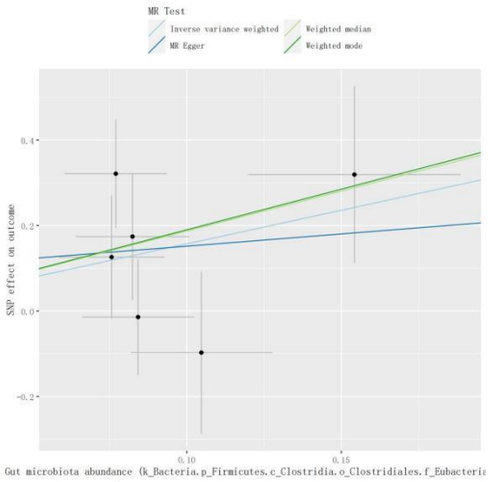






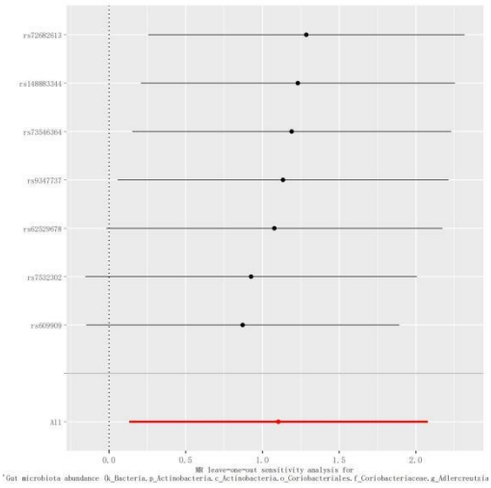


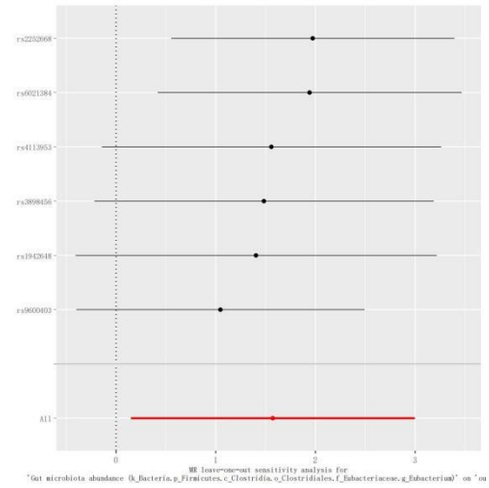




obiota abundance (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Coriobacteriales.f_Corioba

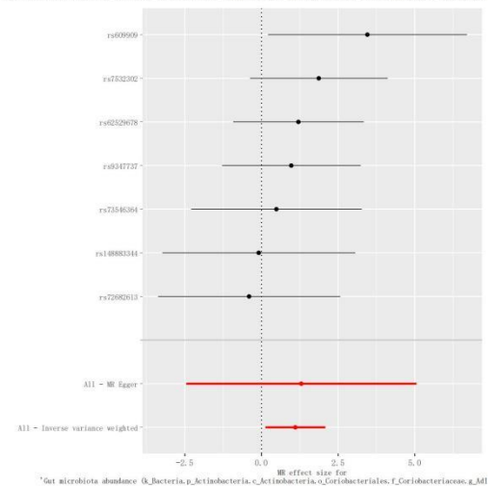
Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteria

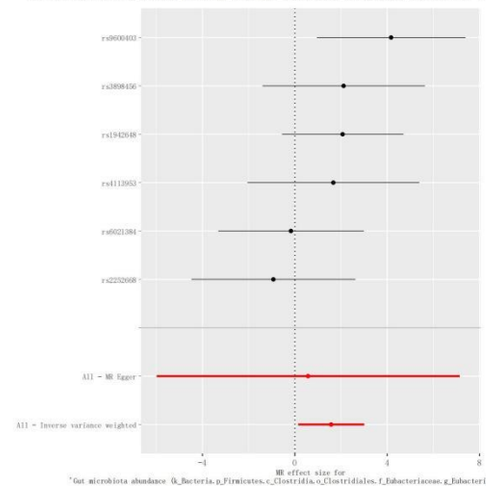




MR leave-one-out sensitivity analysis for
'Gut microbiota abundance (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Coriobacteriales.f_Coriobacteriaceae.g_Adlercreutzia

MR leave-one-out sensitivity analysis for
'Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae.g_Eubacterium)' on 'ou





MR effect size for
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MR effect size for
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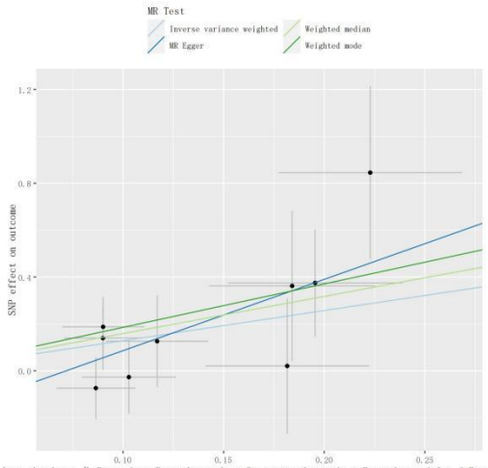

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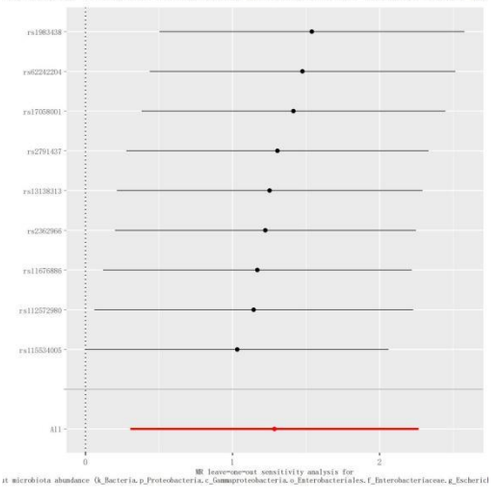
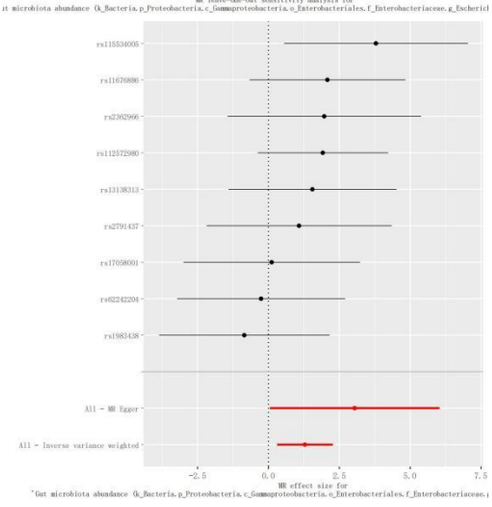
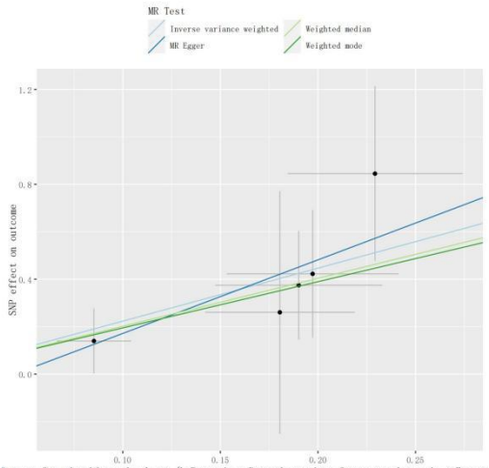
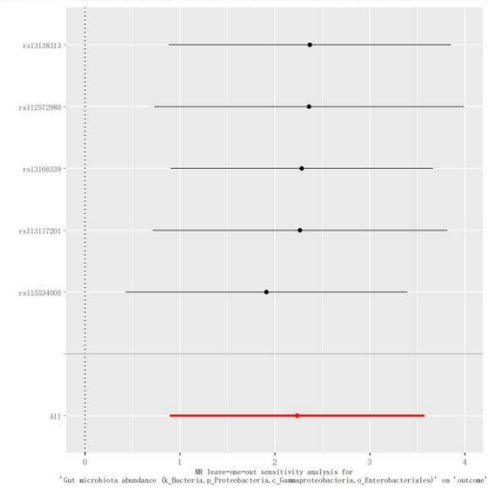




'Gut microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Escherich



fect on Gut microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Entero



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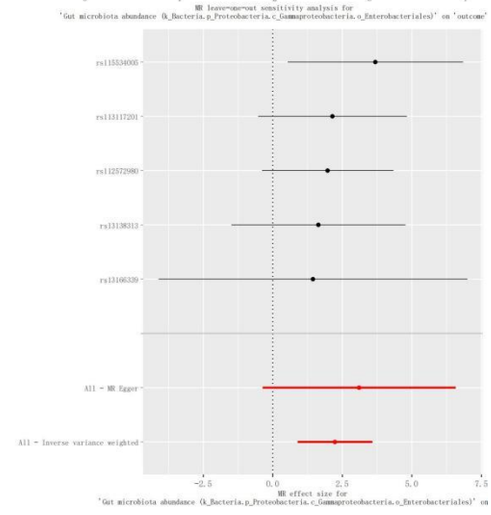

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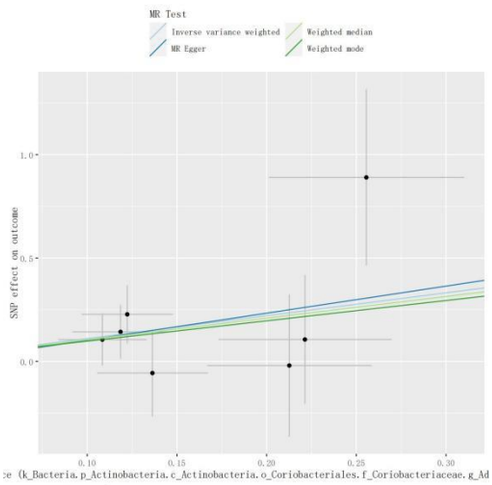
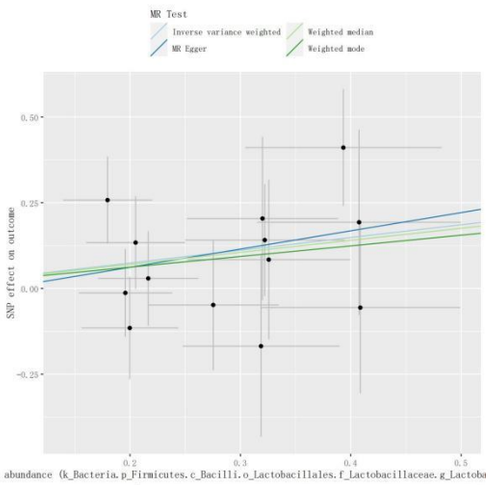
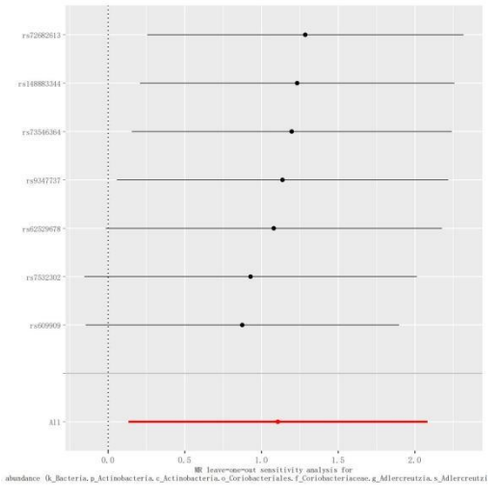
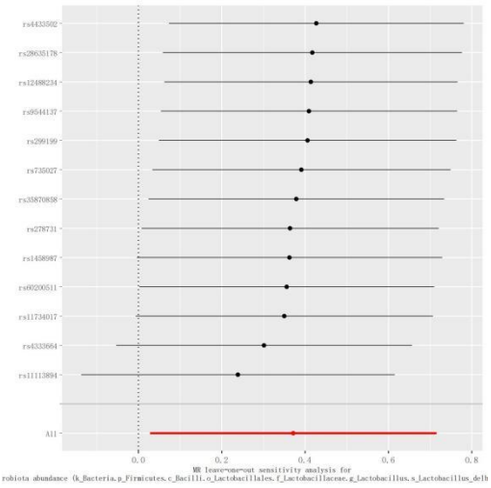




ce (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Coriobacteriales.f_Coriobacteriaceae.g_Ad

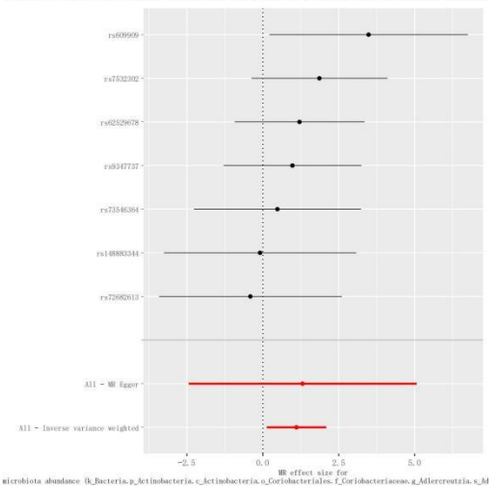
abundance (k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactoba

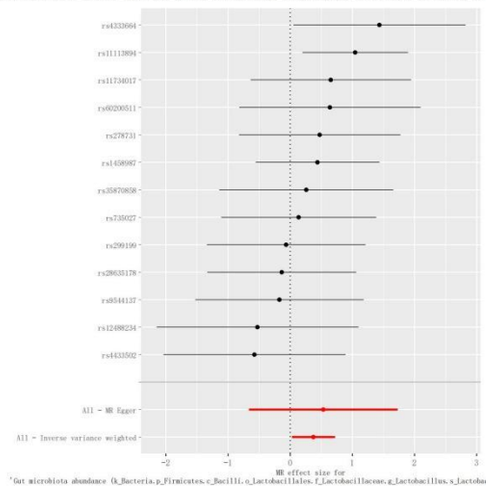




abundance (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Coriobacteriales.f_Coriobacteriaceae.g_Adlercreutzi

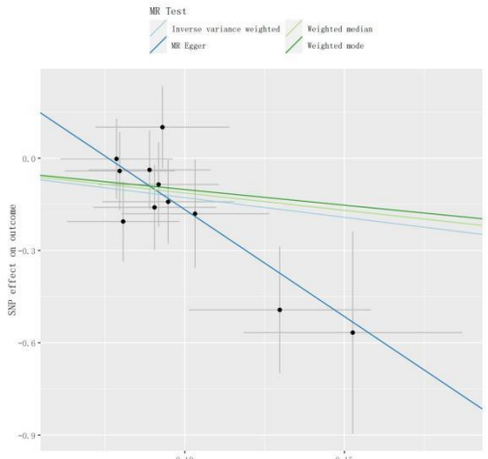
robiota abundance (k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactobacillus.s_Lactobacillus_delb

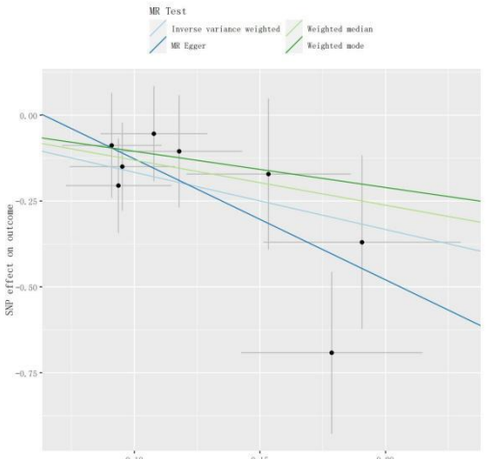




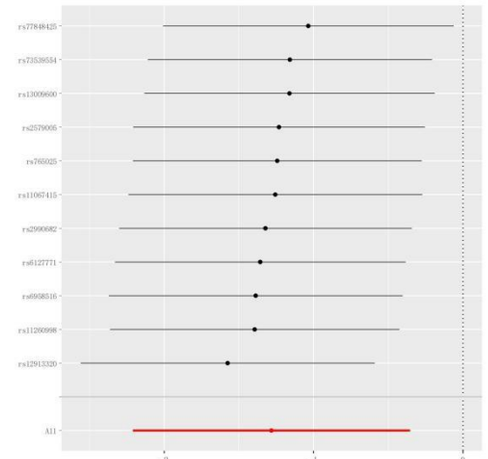
microbiota abundance (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Coriobacteriales.f_Coriobacteriaceae.g_Adlercreutzia.s_Ad

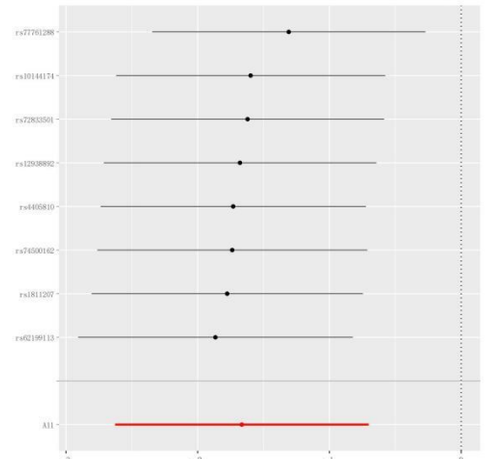
'Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacillaceae.g_Lactobacillus.s_Lactoba



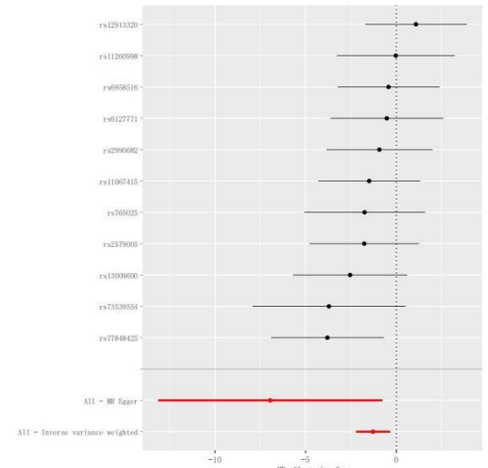


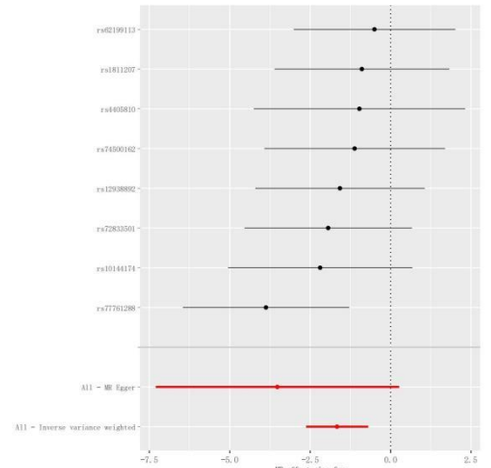
ce (k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrion abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacter





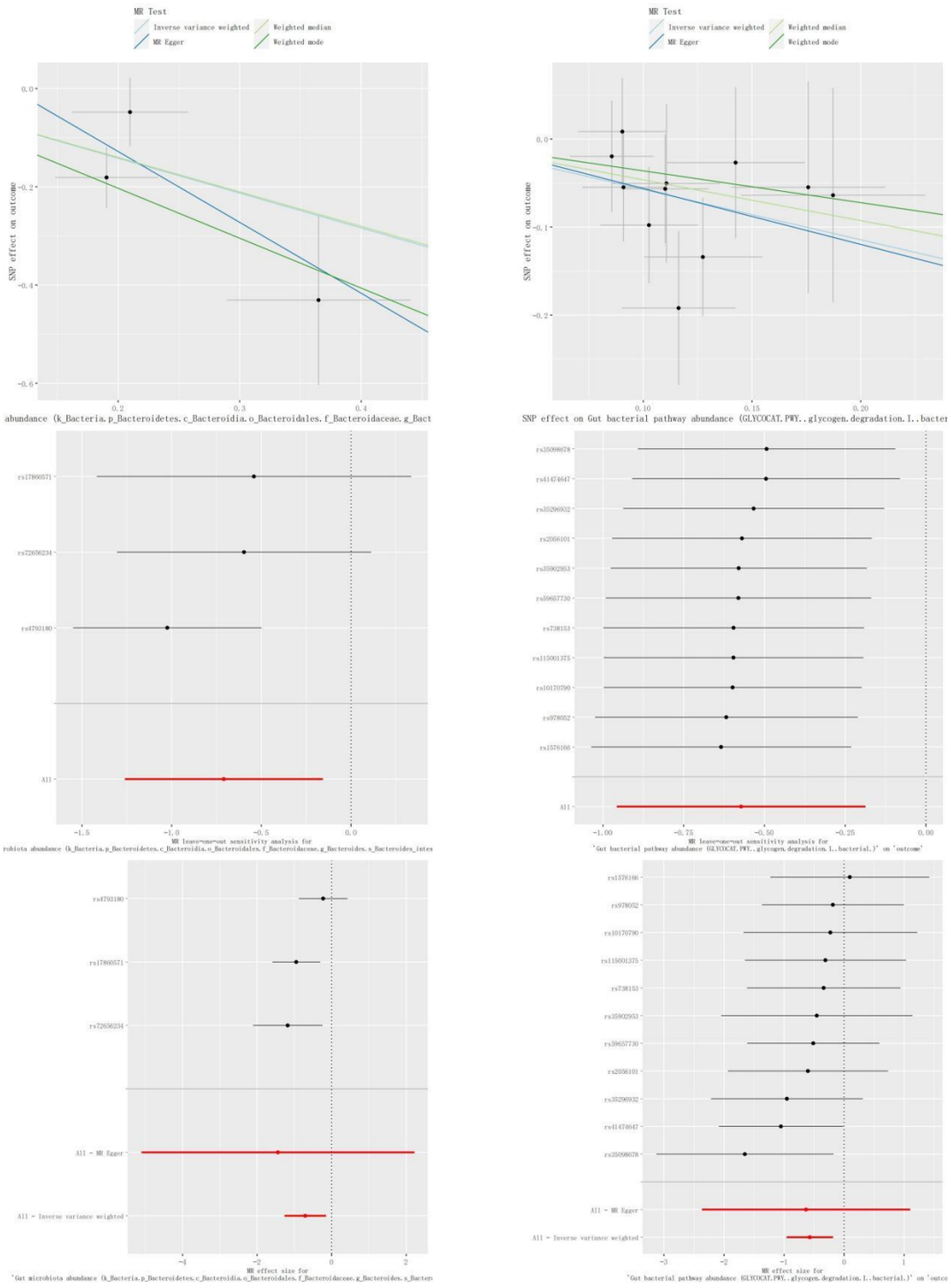
abundance (k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae.g_Bilophila.s_Bilophibiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacteroides_thetaio

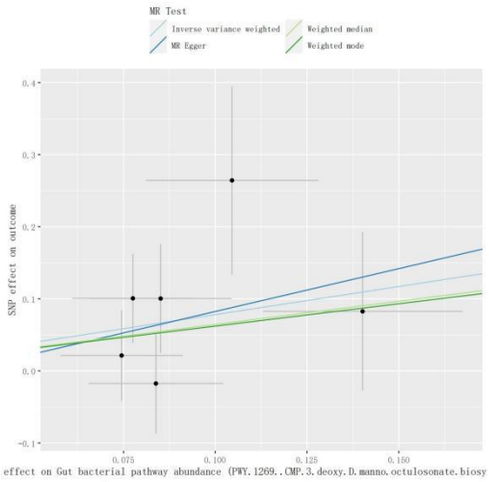


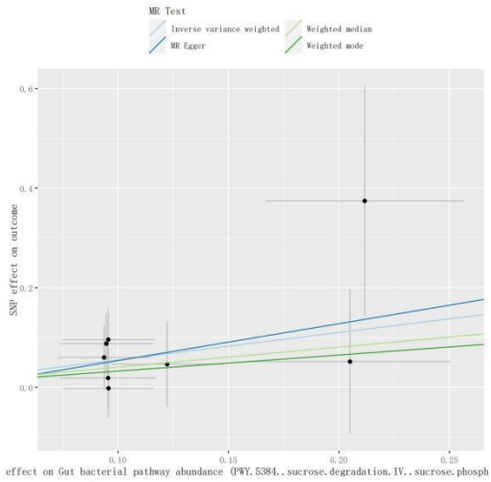


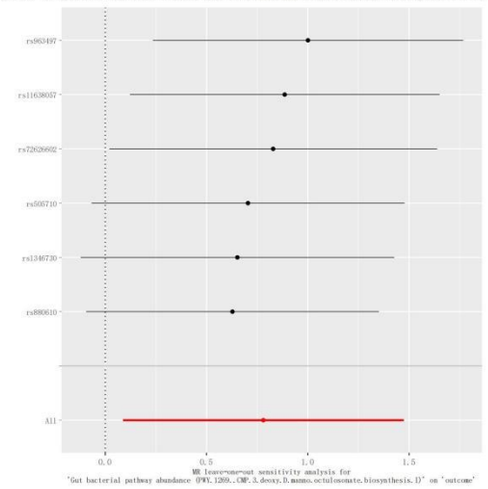
microbiota abundance (k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria.o_Desulfovibrionales.f_Desulfovibrionaceae.g_Bilophila)'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacteroi

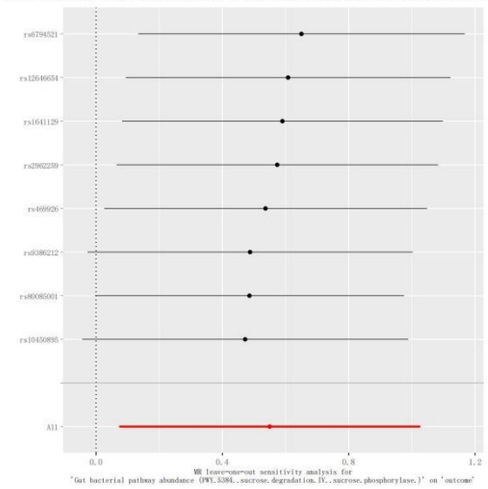
Supplementary Figure S4. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Gut microbiota on PDD

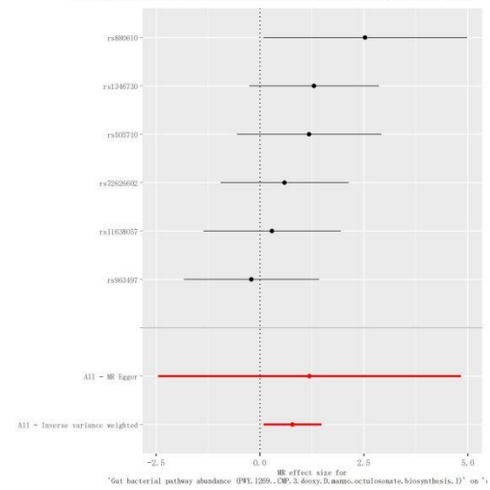


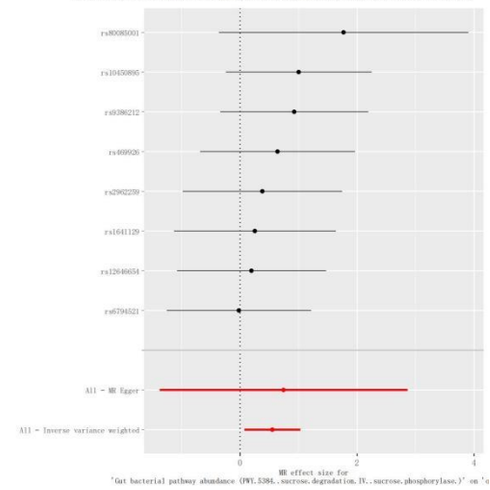

MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.4
0.3
0.2
0.1
0.0
-0.1
0.075
0.100
0.125
0.150
effect on Gut bacterial pathway abundance (PWY.1269..CMP.3.deoxy.D.manno.octulosonate.biosy


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.6
0.4
0.2
0.0
0.10
0.15
0.20
0.25
effect on Gut bacterial pathway abundance (PWY.5384..sucrose.degradation.IV..sucrose.phosph


rs963497
rs11638057
rs72626602
rs503710
rs1346730
rs880610
All
0.0
0.5
1.0
1.5
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PWY.1269..CMP.3.deoxy.D.manno.octulosonate.biosynthesis.I)' on 'outcome'


rs6794521
rs12646654
rs1641129
rs2962259
rs469926
rs9386212
rs80085001
rs10450895
All
0.0
0.4
0.8
1.2
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PWY.5384..sucrose.degradation.IV..sucrose.phosphorylase.)' on 'outcome'


rs880610
rs1346730
rs503710
rs72626602
rs11638057
rs963497
All - MR Egger
All - Inverse variance weighted
-2.5
0.0
2.5
5.0
MR effect size for
'Gut bacterial pathway abundance (PWY.1269..CMP.3.deoxy.D.manno.octulosonate.biosynthesis.I)' on '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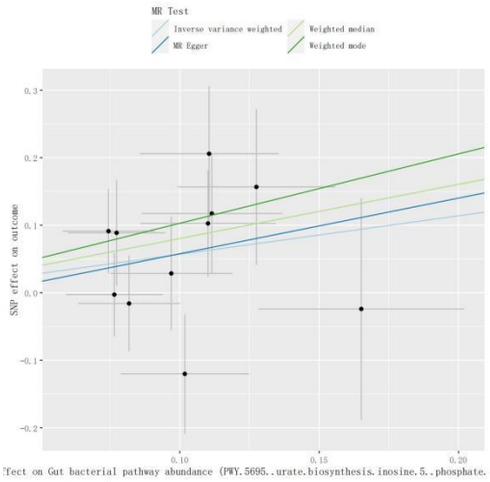
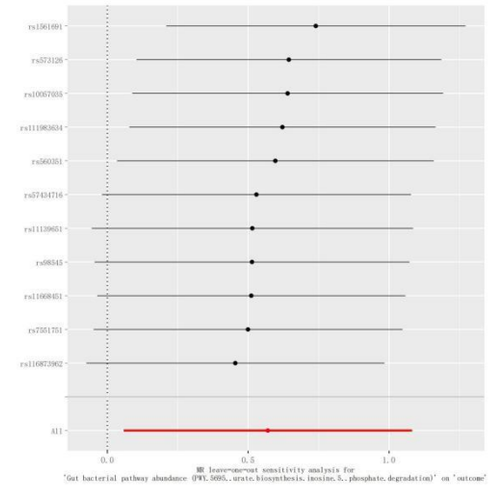
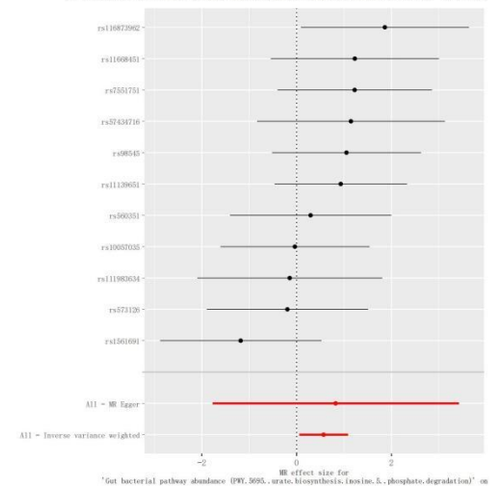
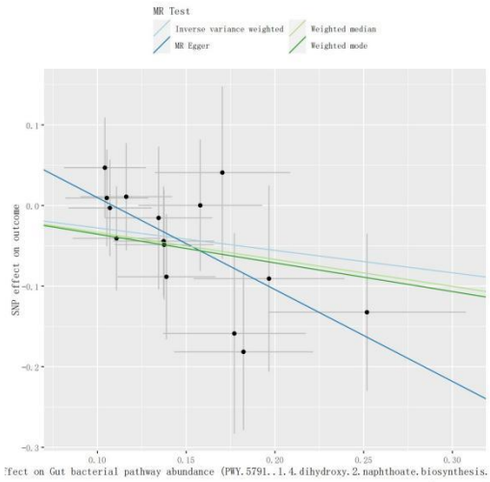
rs12646654
rs6794521
All - MR Egger
All - Inverse variance weighted
0
2
4
MR effect size for
'Gut bacterial pathway abundance (PWY.5384..sucrose.degradation.IV..sucrose.phosphorylase.)' on '



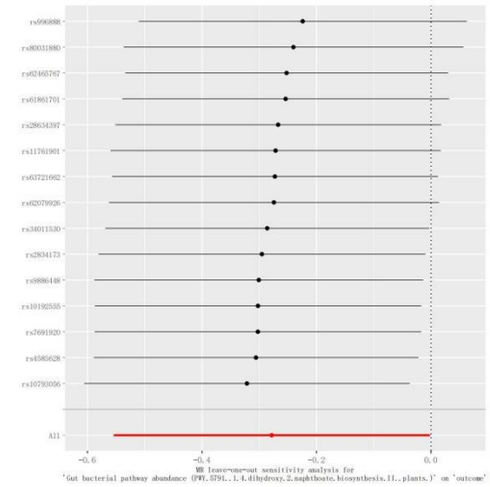
Effect on Gut bacterial pathway abundance (PWY.5695..urate.biosynthesis.inosine.5..phosphate.

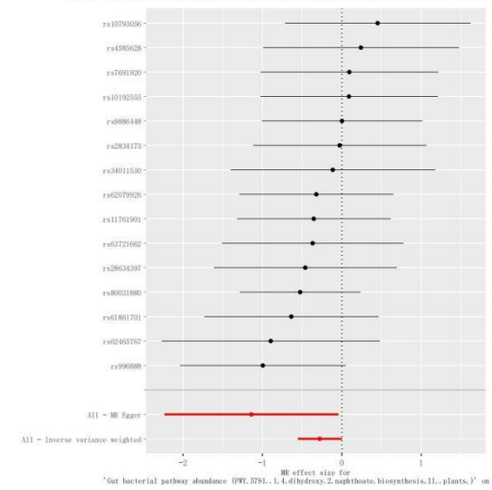


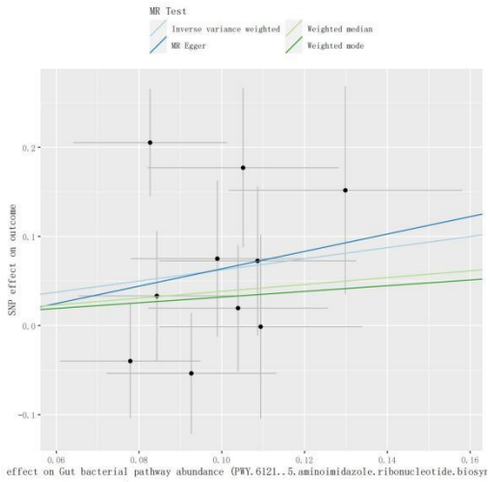




Effect on Gut bacterial pathway abundance (PWY.5791..1.4.dihydroxy.2.naphthoate.biosynthesis.







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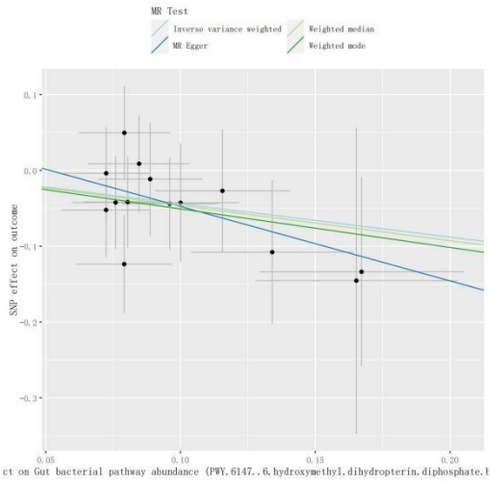
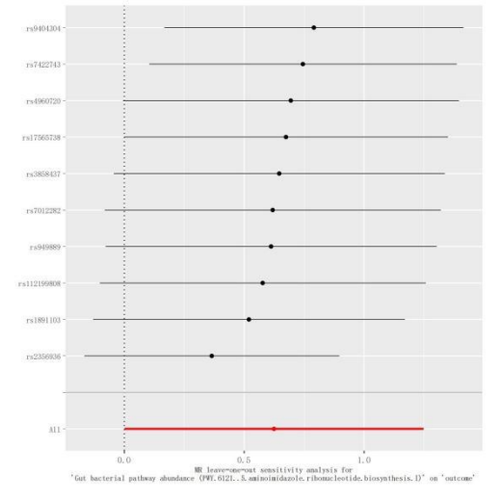
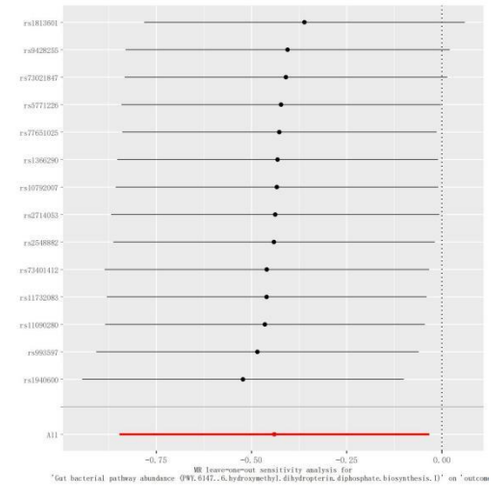
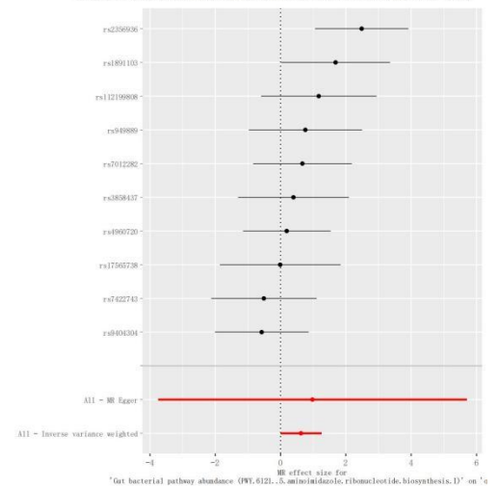
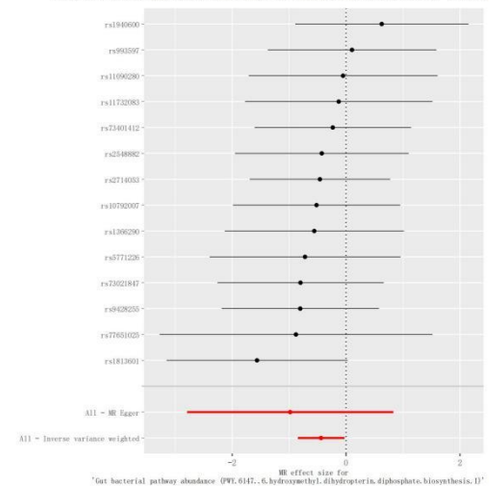


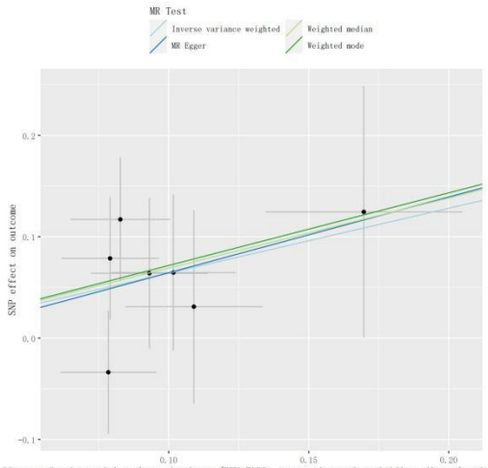
ct on Gut bacterial pathway abundance (PWY.6147..6.hydroxymethyl.dihydropterin.diphosphate.b



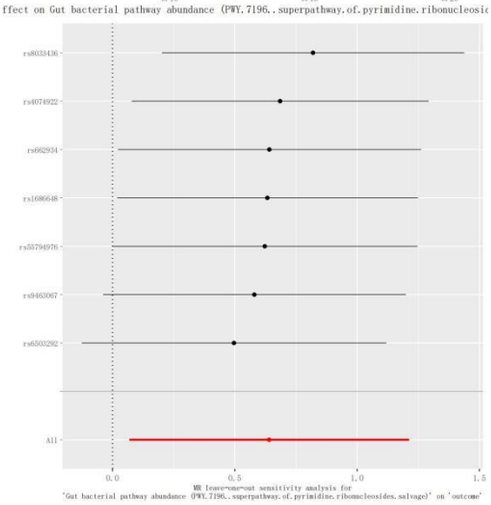




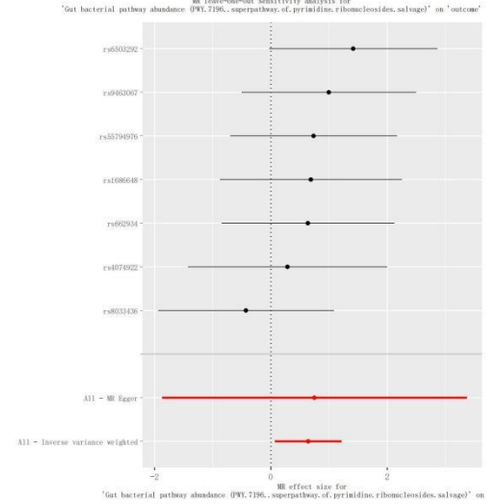




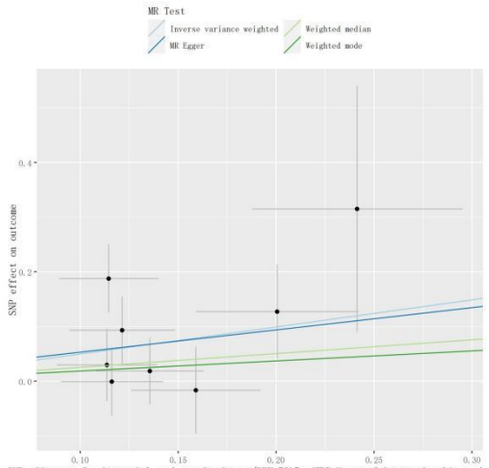
ffect on Gut bacterial pathway abundance (PWY.7196..superpathway.of.pyrimidine.ribonucleosic



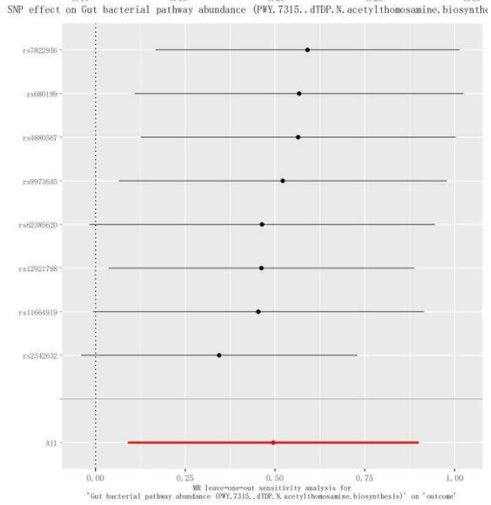
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PWY.7196..superpathway.of.pyrimidine.ribonucleosides.salvage)' on 'outcome'



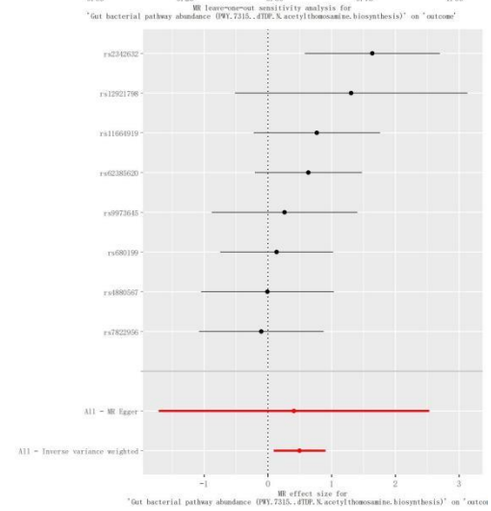
MR effect size for
'Gut bacterial pathway abundance (PWY.7196..superpathway.of.pyrimidine.ribonucleosides.salvage)' on



SNP effect on Gut bacterial pathway abundance (PWY.7315..dTDP.N.acetylthomosamine.biosynthe



MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PWY.7315..dTDP.N.acetylthomosamine.biosynthesis)' on 'outcome'



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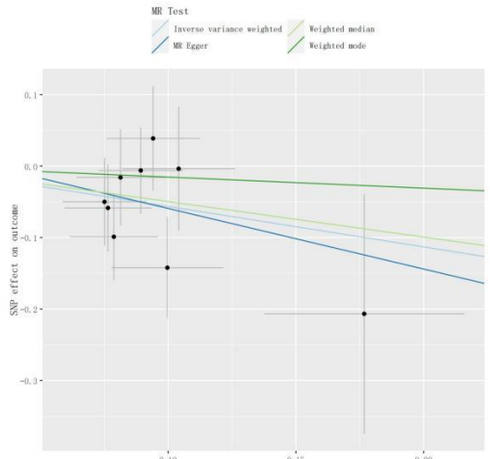

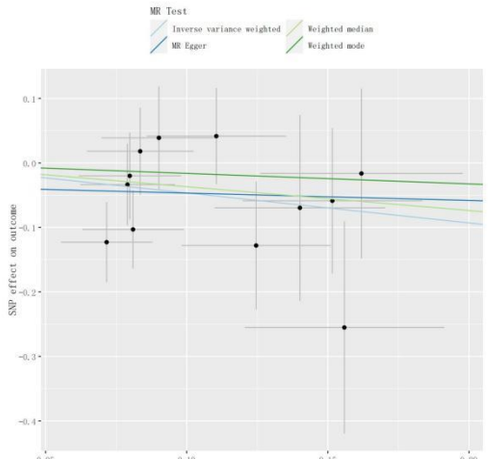

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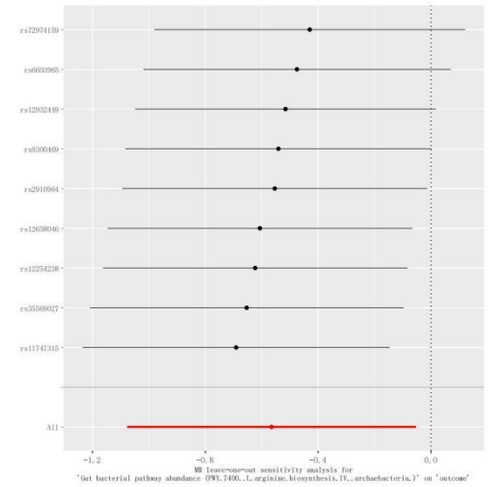
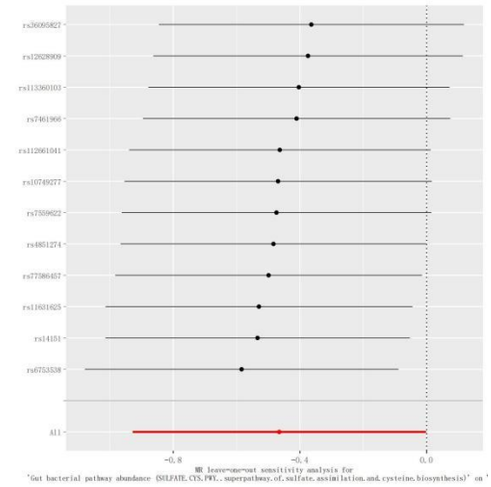
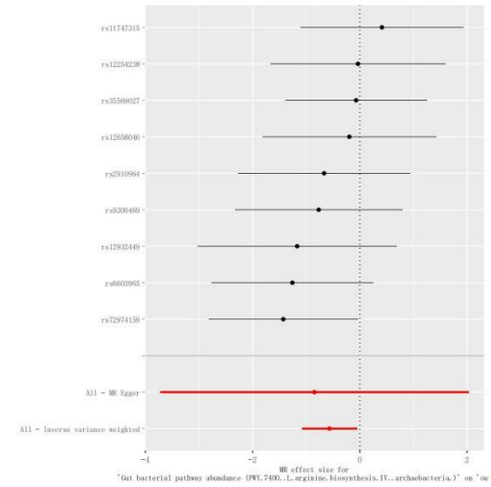
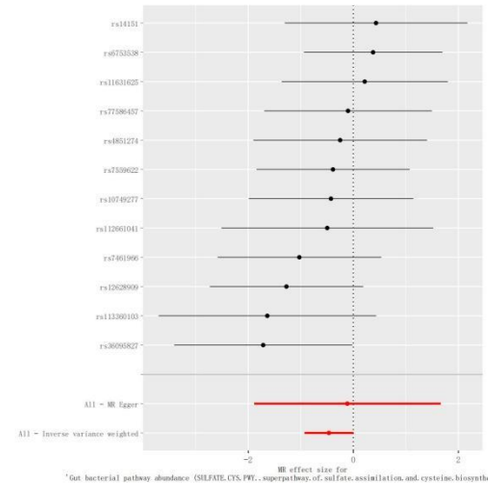
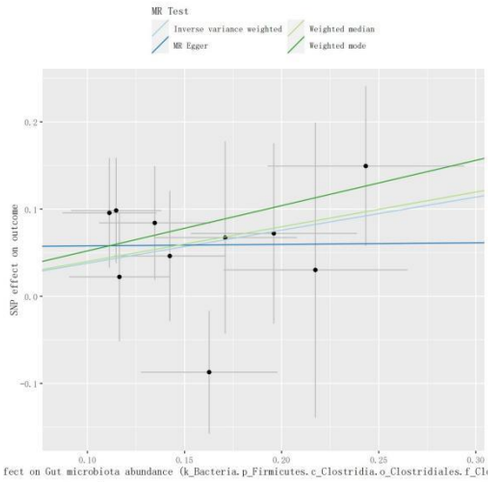
Gut bacterial pathway abundance (SULFATE.CYS.PWY..superpathway.of.sulfate.assimilation.and.c



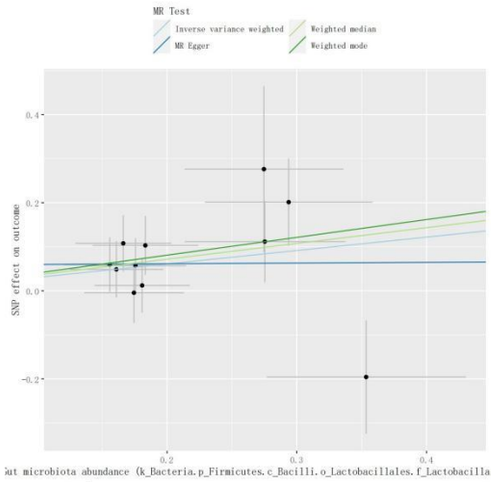




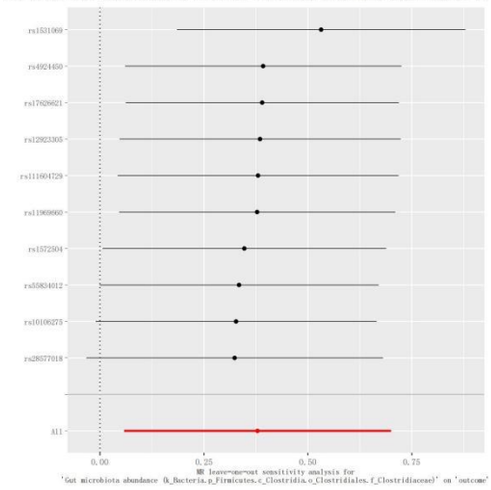


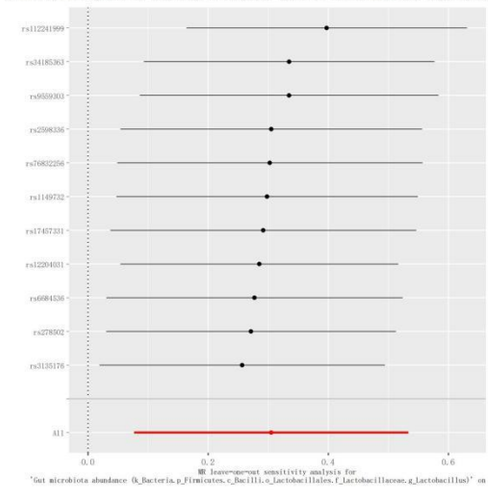


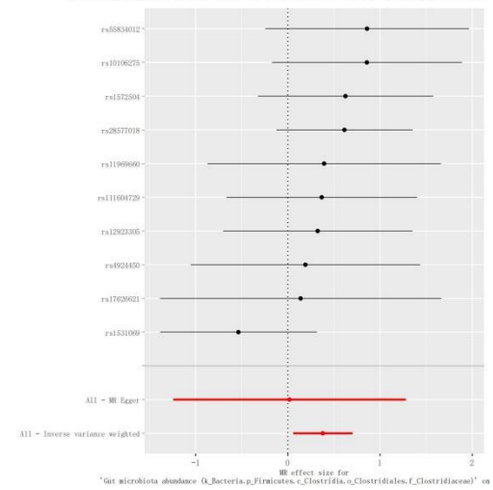
fect on Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Clo

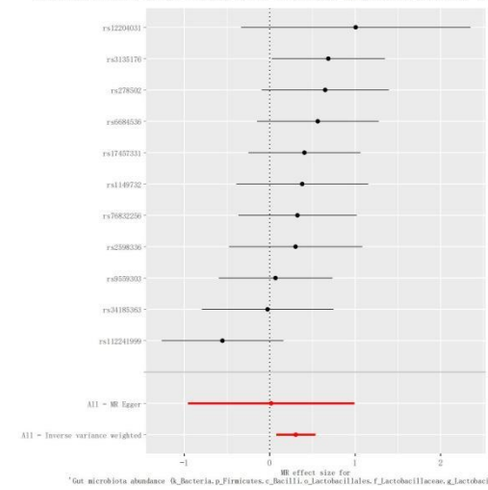


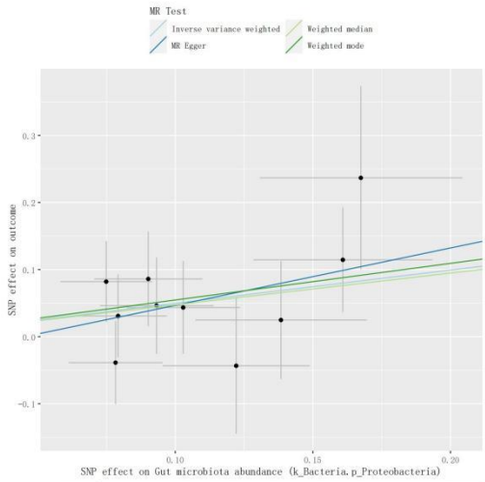
ut microbiota abundance (k_Bacteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Lactobacilla

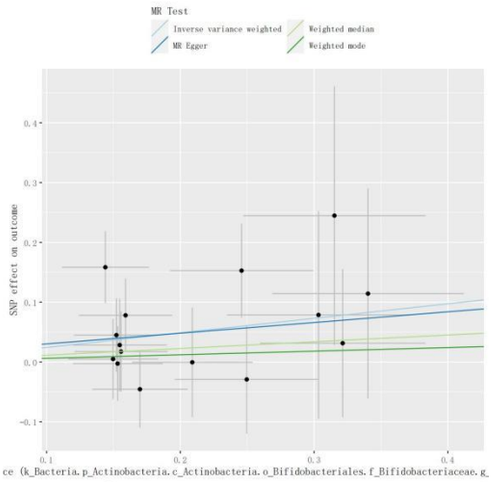


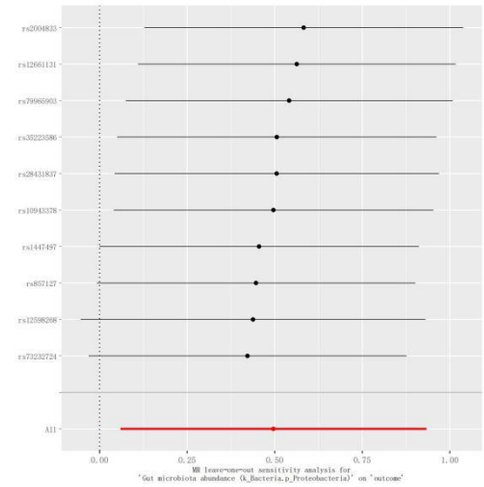







MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Gut microbiota abundance (k_Bacteria.p_Proteobacteria)


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
ce (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Bifidobacteriales.f_Bifidobacteriaceae.g_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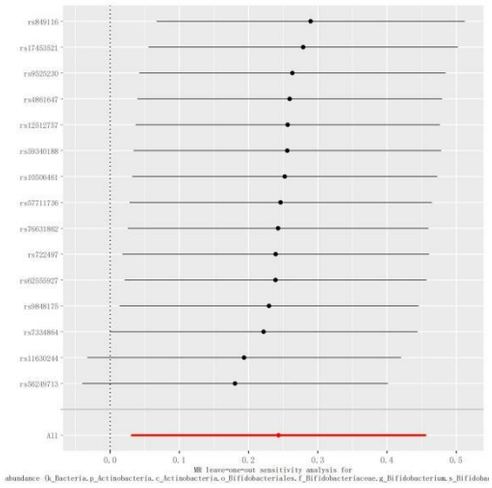
MR leave-one-out sensitivity analysis for
'Gut microbiota abundance (k_Bacteria.p_Proteobacteria)' on 'outcome'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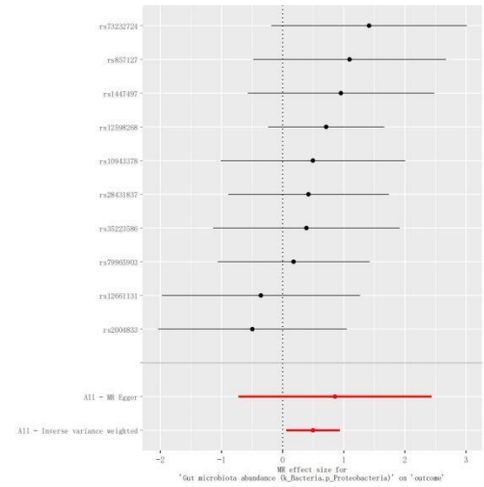
rs9848175
rs7334864
rs11630244
rs56249713
All
MR leave-one-out sensitivity analysis for
abundance (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.s_Bifidobac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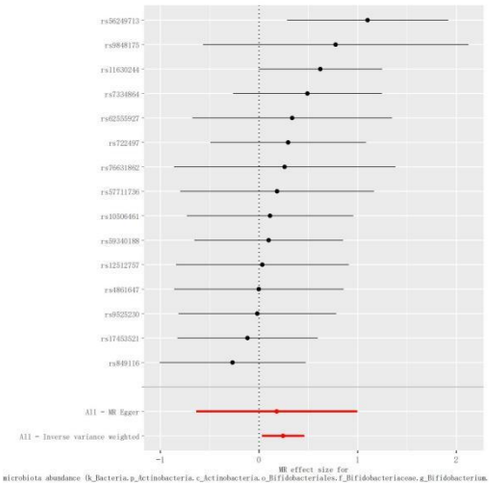
All - MR Egger
All - Inverse variance weighted
MR effect size for
'Gut microbiota abundance (k_Bacteria.p_Proteobacteria)' on 'outcome'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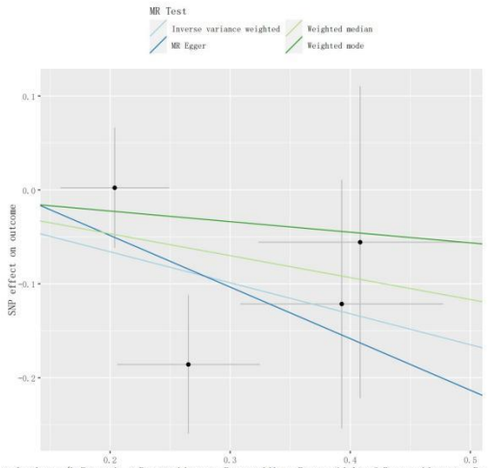
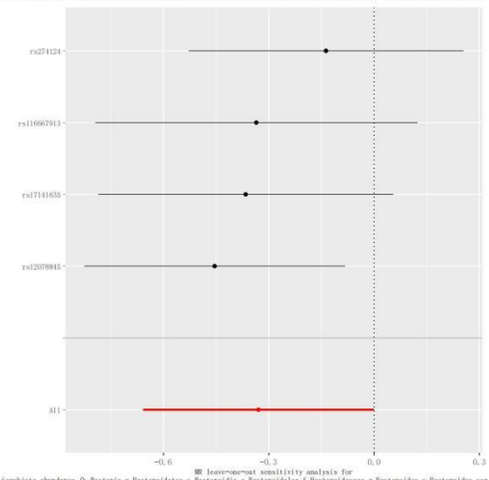
rs12512757
rs4861647
rs9525230
rs17453521
rs849116
All - MR Egger
All - Inverse variance weighted
MR effect size for
microbiota abundance (k_Bacteria.p_Actinobacteria.c_Actinobacteria.o_Bifidobacteriales.f_Bifidobacteriaceae.g_Bifidobacterium.



a abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bac



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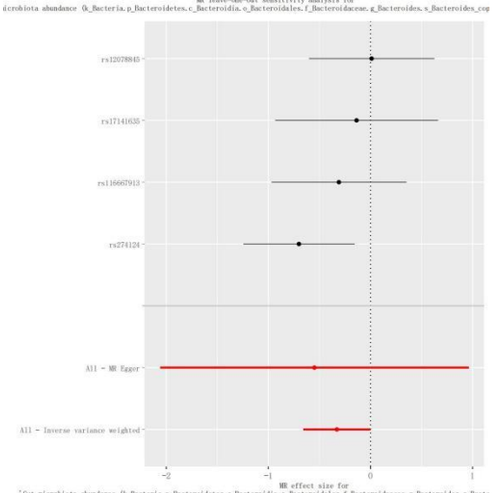
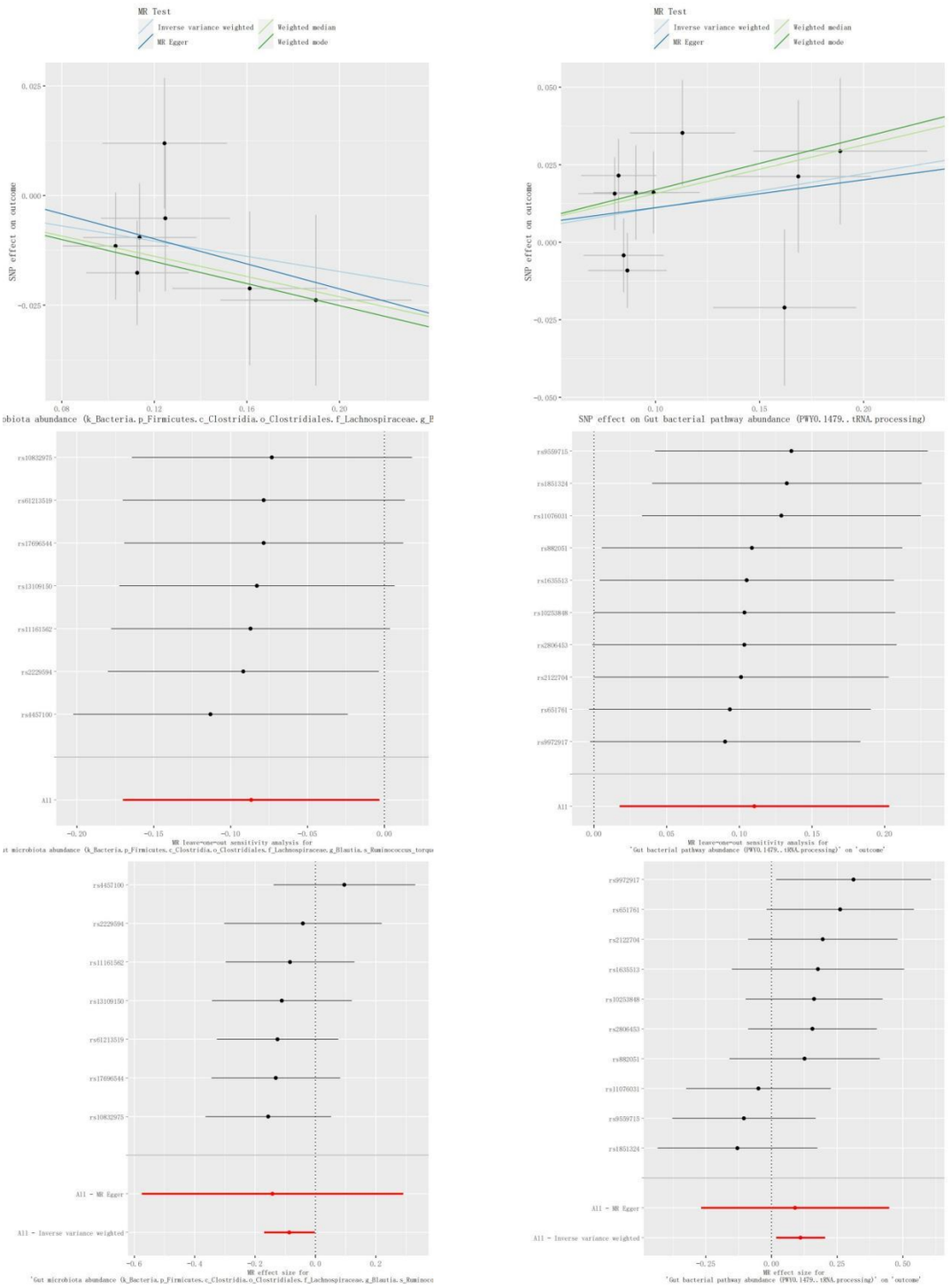
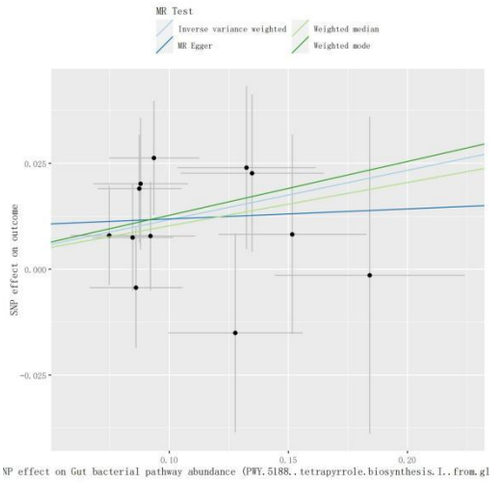
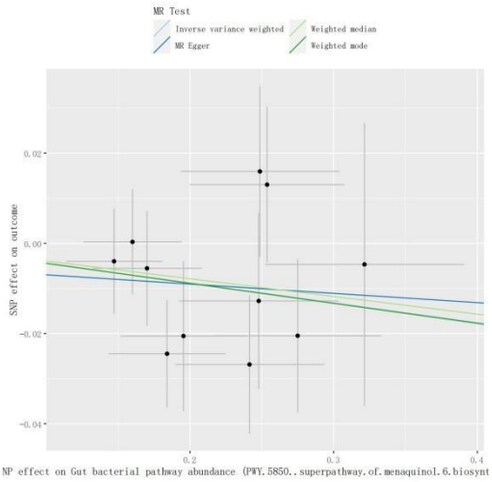


"Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacte

Supplementary Figure S5. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Gut microbiota on VD




MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.025
0.000
−0.025
0.10
0.15
0.20
NP effect on Gut bacterial pathway abundance (PWY.5188..tetrapyrrole.biosynthesis.I..from.gl


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.02
0.00
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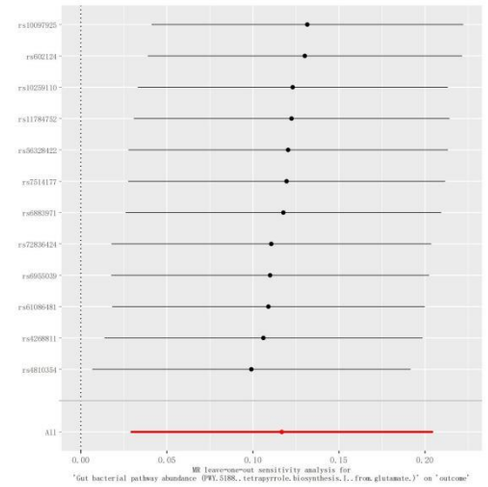
−0.04
0.2
0.3
0.4
NP effect on Gut bacterial pathway abundance (PWY.5850..superpathway.of.menaquinol.6.biosynt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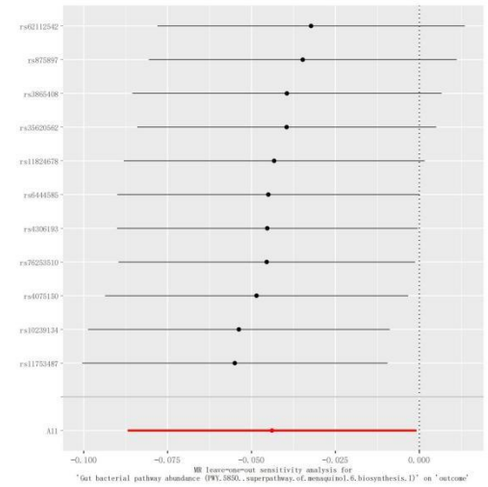
rs4810354
All
0.00
0.05
0.10
0.15
0.20
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PWY.5188..tetrapyrrole.biosynthesis.I..from.glutamate.)' on 'outcome'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rs4075150
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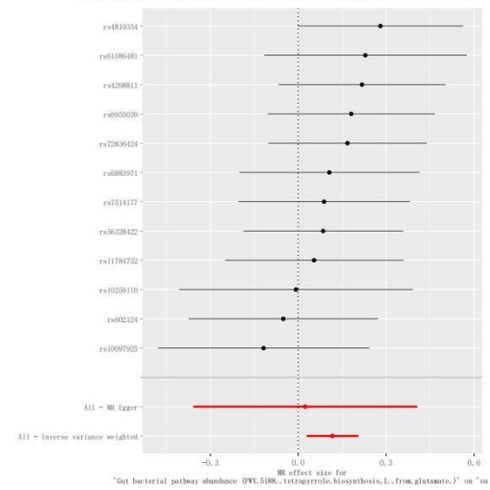
rs11753487
All
−0.100
−0.075
−0.050
−0.025
0.000
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PWY.5850..superpathway.of.menaquinol.6.biosynthesis.I)' on 'outcome'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All - MR Egger
All - Inverse variance weighted
−0.3
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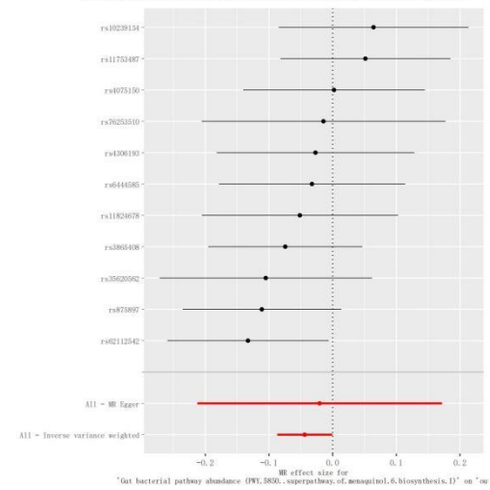
0.6
MR effect size for
'Gut bacterial pathway abundance (PWY.5188..tetrapyrrole.biosynthesis.I..from.glutamate.)' on 'ou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All - MR Egger
All - Inverse variance weighted
−0.2
−0.1
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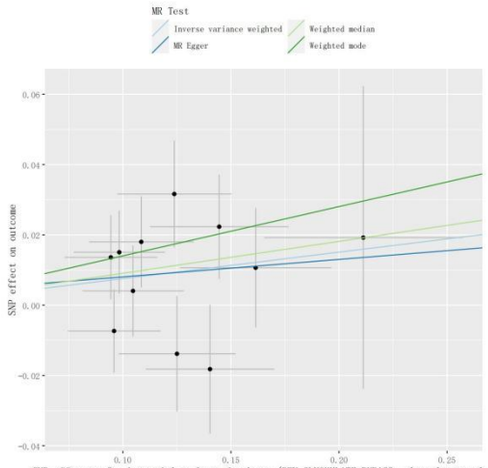
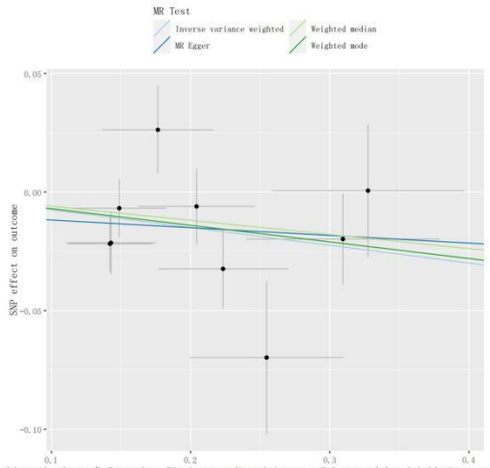
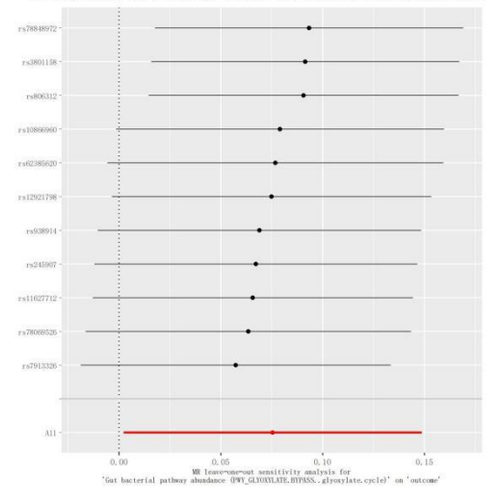
0.1
0.2
MR effect size for
'Gut bacterial pathway abundance (PWY.5850..superpathway.of.menaquinol.6.biosynthesis.I)' on 'ou


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Gut bacterial pathway abundance (PWY_GLYOXYLATE.BYPASS..glyoxylate.cycle


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
obiota abundance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococca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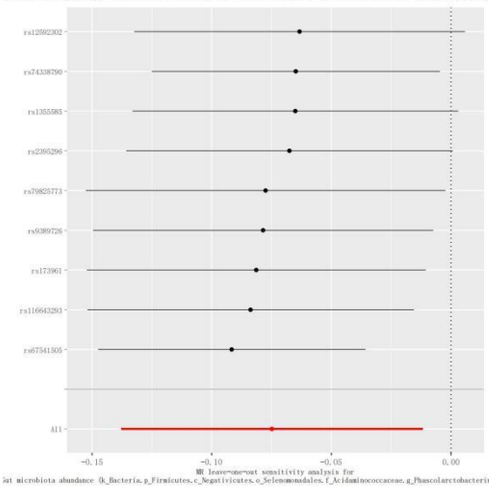
MR leave-one-out sensitivity analysis for
'Gut bacterial pathway abundance (PWY_GLYOXYLATE.BYPASS..glyoxylate.cycle)' on 'outcome'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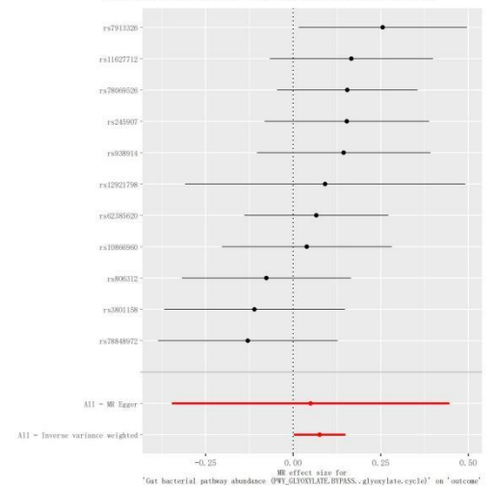
All
MR leave-one-out sensitivity analysis for
ut microbiota abundance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococcaceae.g_Phascolarctobacteriu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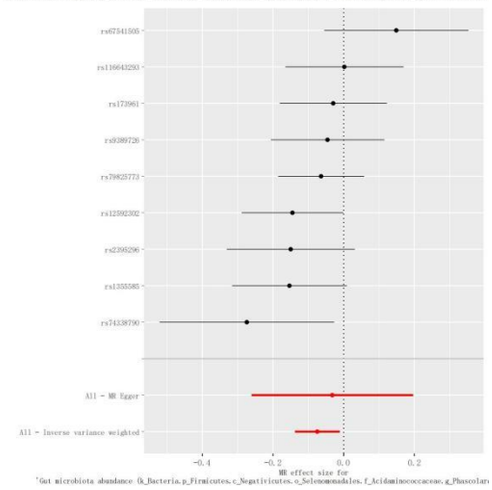
All - MR Egger
All - Inverse variance weighted
MR effect size for
'Gut bacterial pathway abundance (PWY_GLYOXYLATE.BYPASS..glyoxylate.cycle)' on 'outcome'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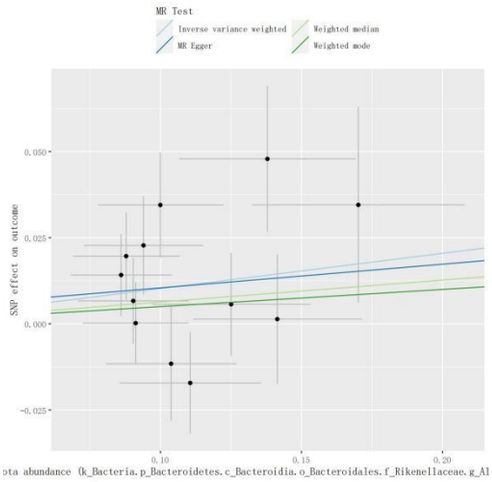
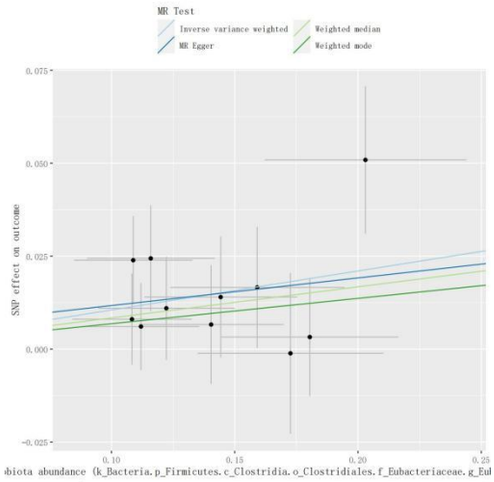
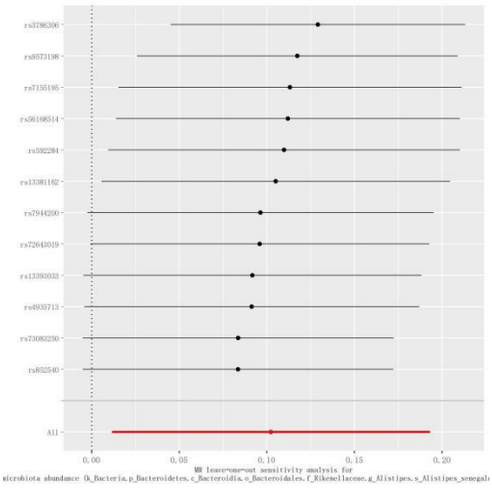
All - MR Egger
All - Inverse variance weighted
MR effect size for
'Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Negativicutes.o_Selenomonadales.f_Acidaminococcaceae.g_Phascolar



ota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_Al



biota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae.g_Eub



MR leave-one-out sensitivity analysis for
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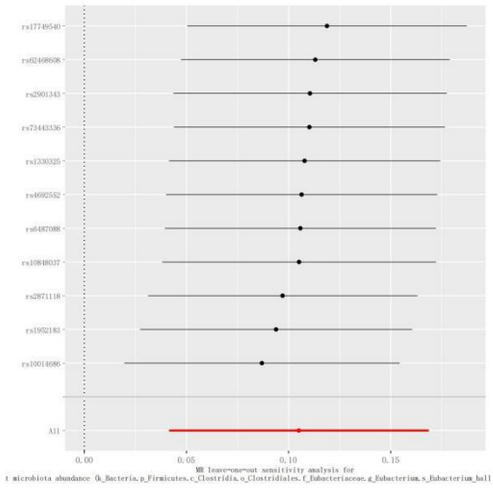
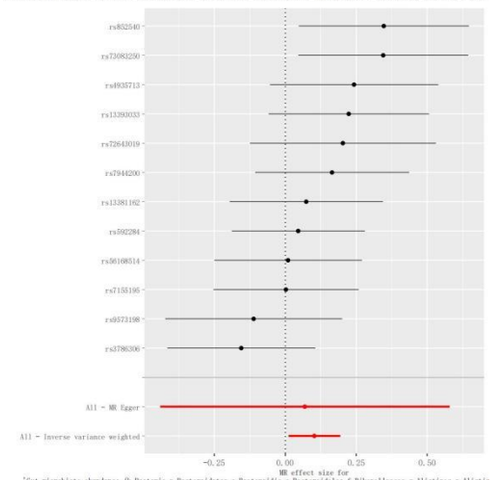
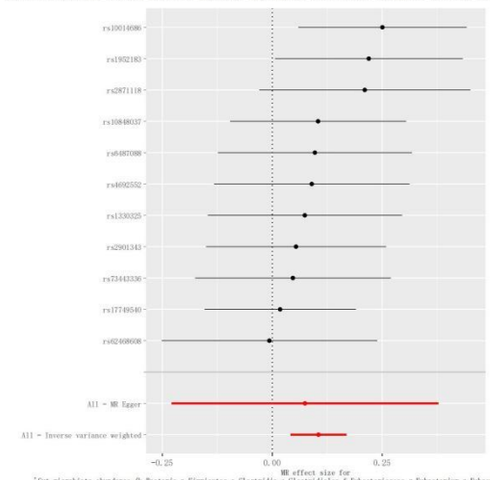


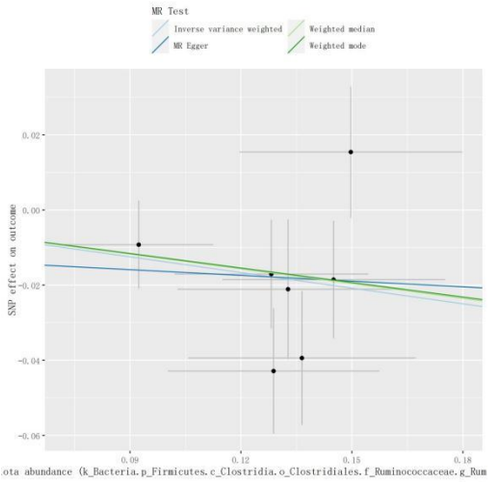
MR leave-one-out sensitivity analysis for
t microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae.g_Eubacterium.s_Eubacterium_hall

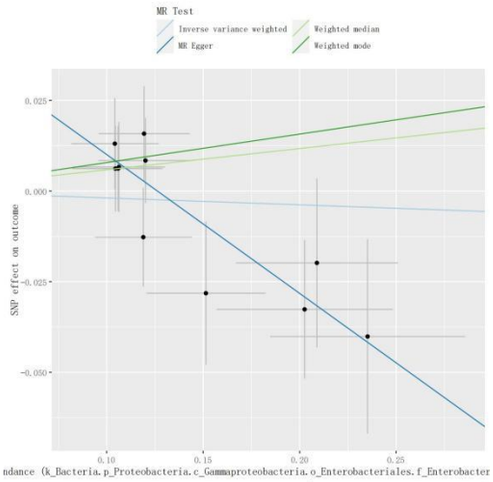


MR effect size for
'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Rikenellaceae.g_Alistipes.s_Alistig



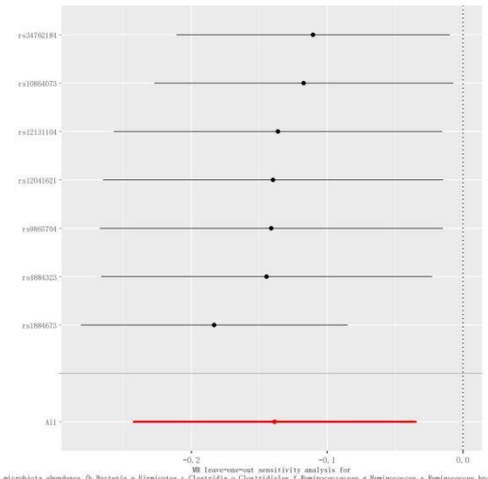
MR effect size for
'Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Eubacteriaceae.g_Eubacterium.s_Eubac



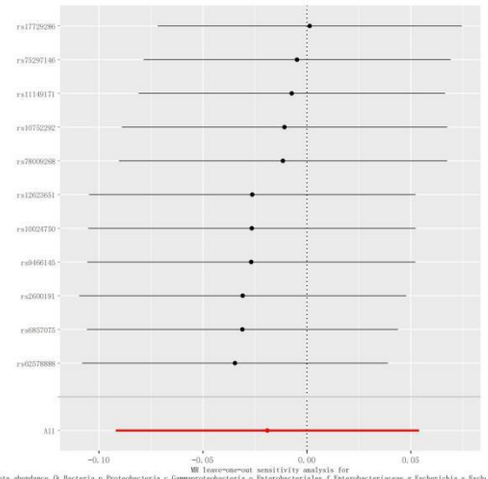


ota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Rum

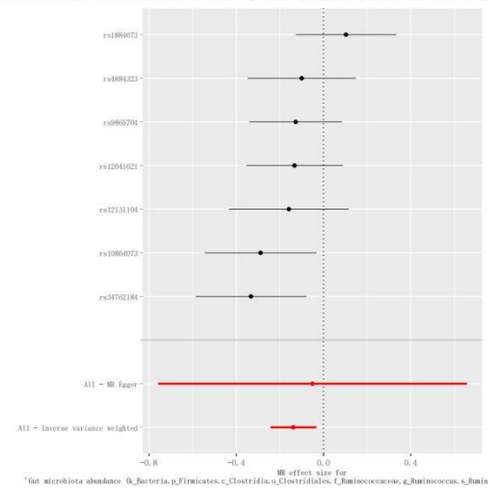
ndance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacter



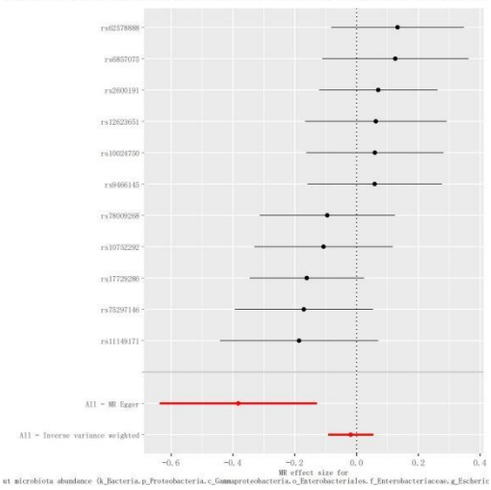
microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Ruminococcus.s_Ruminococcus_bro



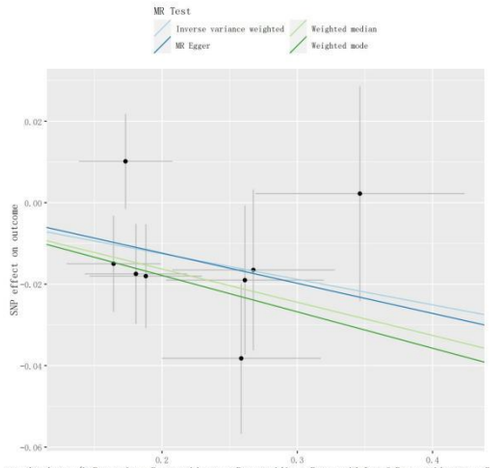
ota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Escherichia.s_Esch



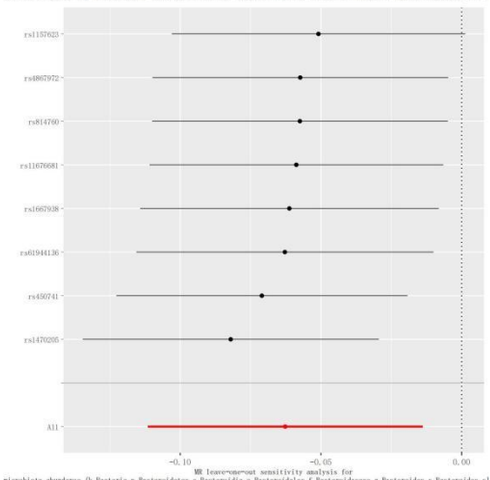
'Gut microbiota abundance (k_Bacteria.p_Firmicutes.c_Clostridia.o_Clostridiales.f_Ruminococcaceae.g_Ruminococcus.s_Rumin



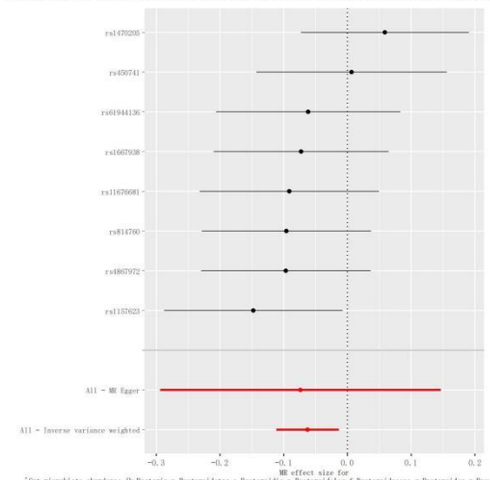
ut microbiota abundance (k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Enterobacteriales.f_Enterobacteriaceae.g_Escheric



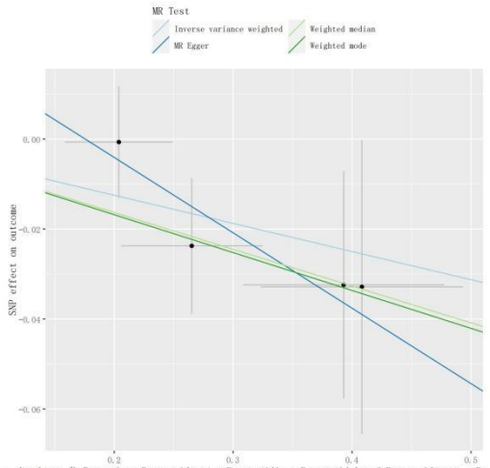
ota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_E



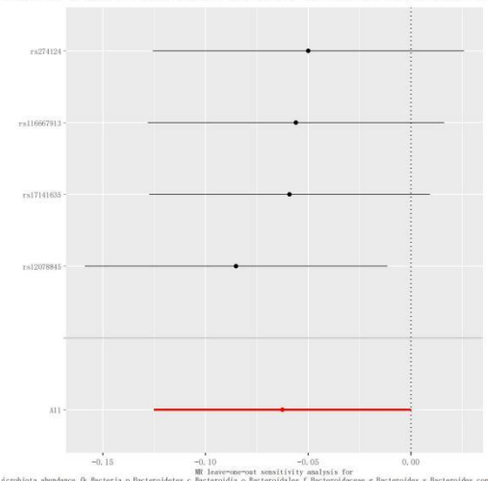
MR leave-one-out sensitivity analysis for
microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacteroides_cl



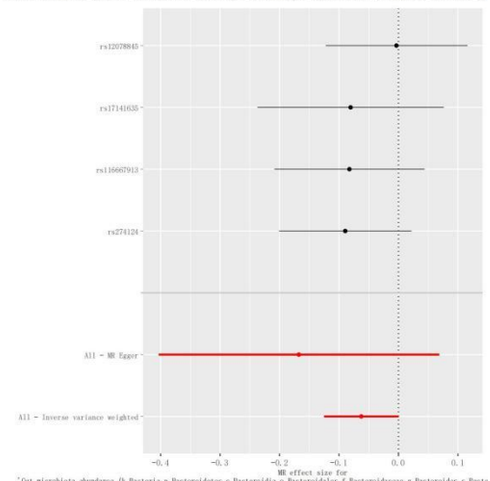
MR effect size for
'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bac



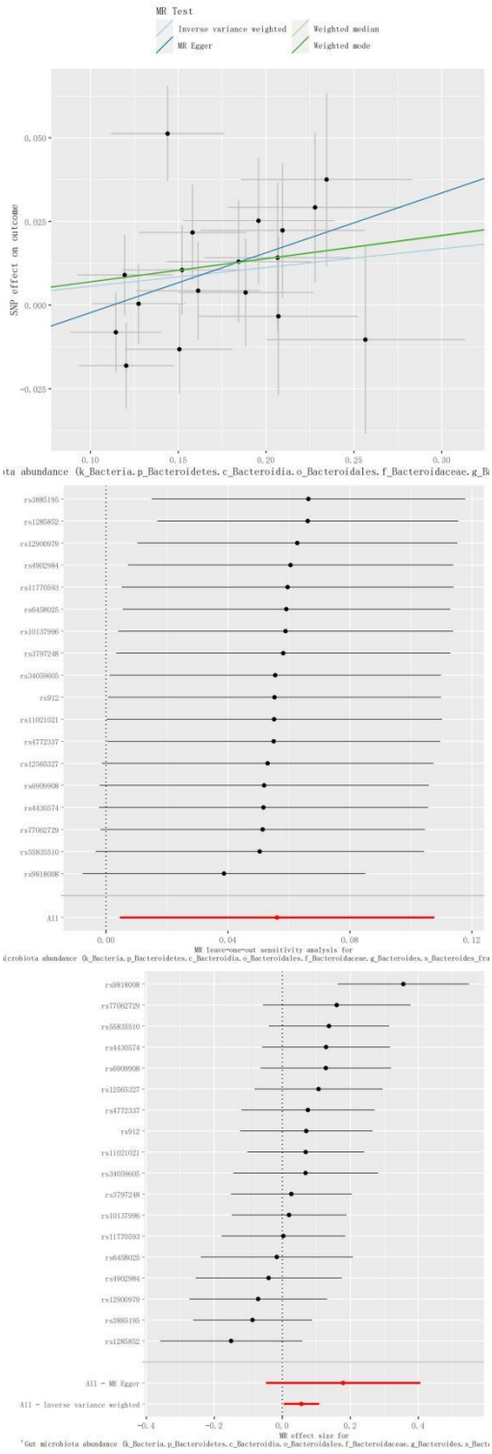
a abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Ba



MR leave-one-out sensitivity analysis for
crobiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacteroides_cop



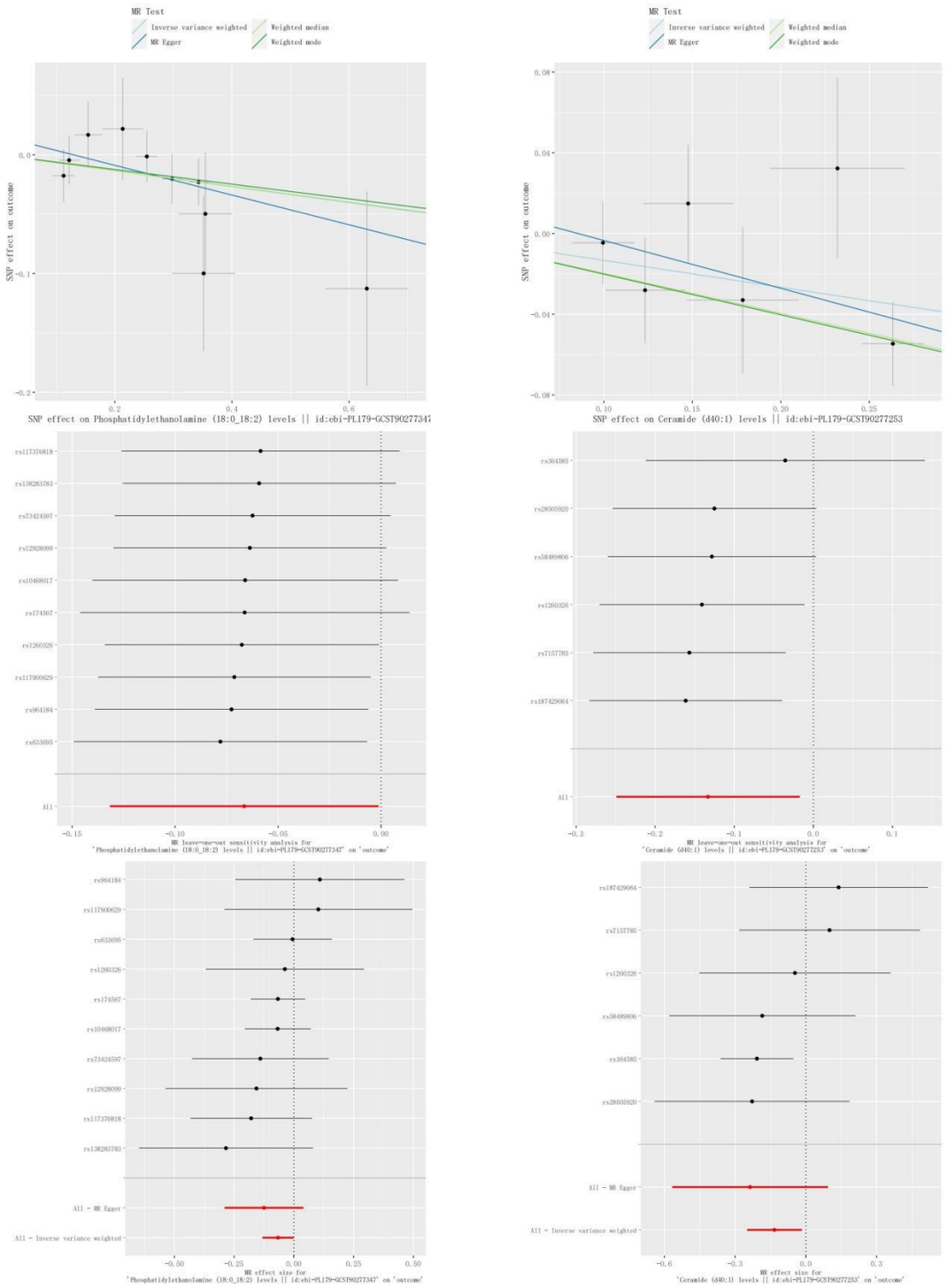
ME effect size for
'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacte

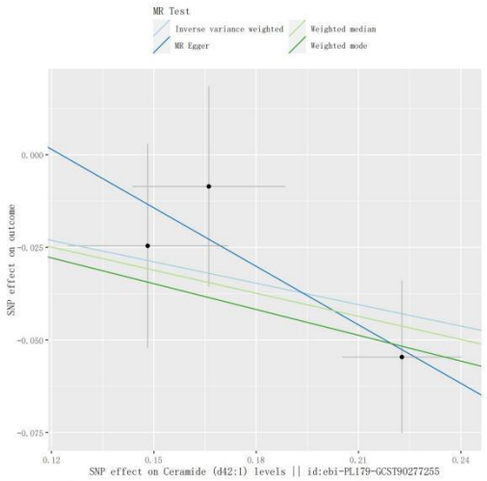

MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.050
0.025
0.000
−0.025
0.10
0.15
0.20
0.25
0.30
ota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Ba

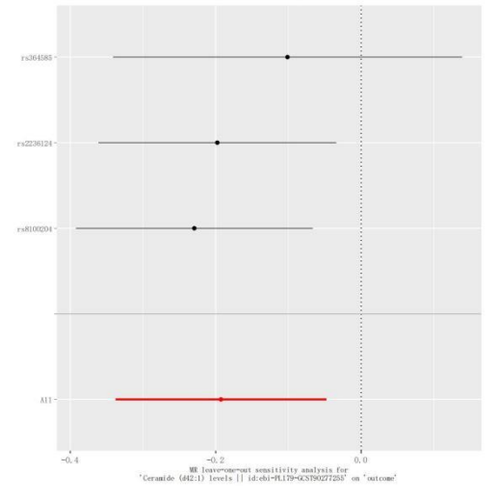
rs3885195
rs1285852
rs12900979
rs4902984
rs11770593
rs6458025
rs10137996
rs3797248
rs34059605
rs912
rs11021021
rs4772337
rs12565327
rs6909908
rs4430574
rs77082729
rs55835510
rs9818008
All
0.00
0.04
0.08
0.12
MR leave-one-out sensitivity analysis for
icrobiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacteroides_fra

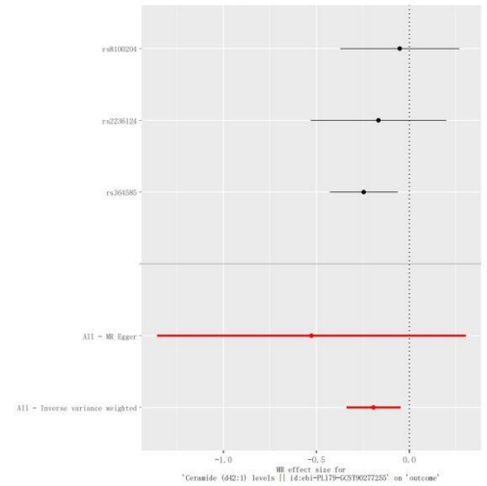
rs9818008
rs77082729
rs55835510
rs4430574
rs6909908
rs12565327
rs4772337
rs912
rs11021021
rs34059605
rs3797248
rs10137996
rs11770593
rs6458025
rs4902984
rs12900979
rs3885195
rs1285852
All - MR Egger
All - Inverse variance weighted
−0.4
−0.2
0.0
0.2
0.4
MR effect size for
'Gut microbiota abundance (k_Bacteria.p_Bacteroidetes.c_Bacteroidia.o_Bacteroidales.f_Bacteroidaceae.g_Bacteroides.s_Bacte

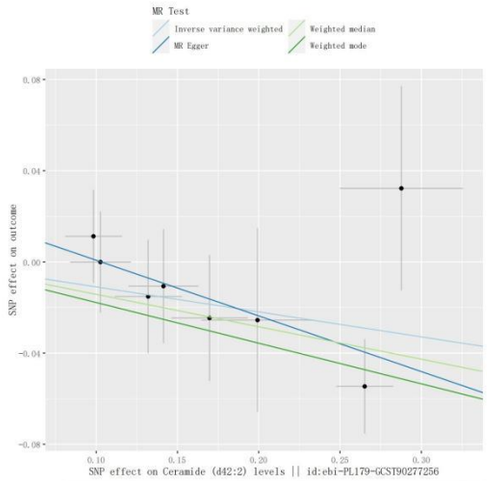
Supplementary Figure S6. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Plasma lipidome on AD

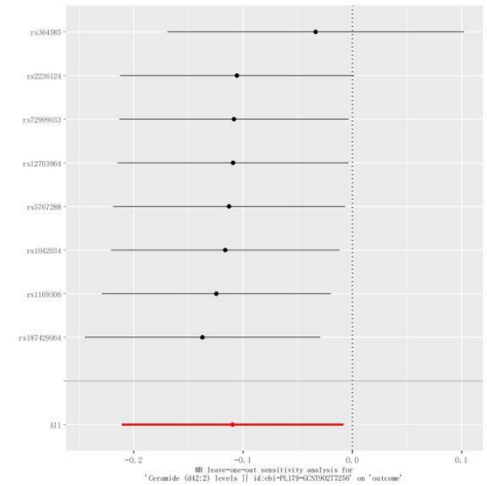


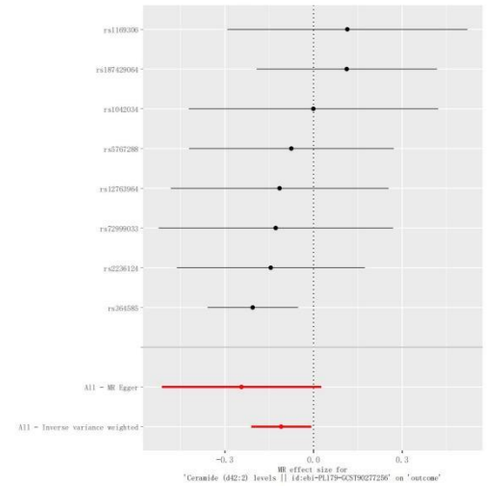

MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.000
−0.025
−0.050
−0.075
0.12
0.15
0.18
0.21
0.24
SNP effect on Ceramide (d42:1) levels || id:ebi-PL179-GCST90277255

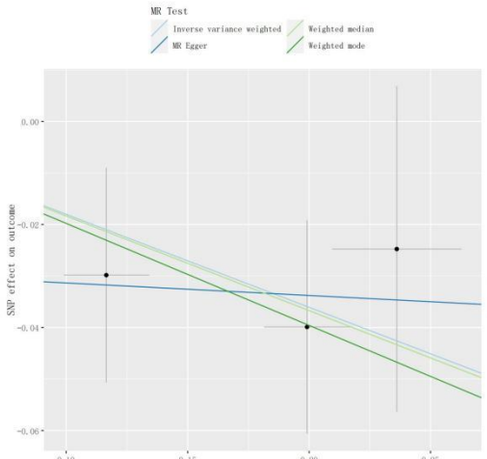

rs364585
rs2236124
rs8100204
All
−0.4
−0.2
0.0
MR leave-one-out sensitivity analysis for
'Ceramide (d42:1) levels || id:ebi-PL179-GCST90277255' on 'outcome'

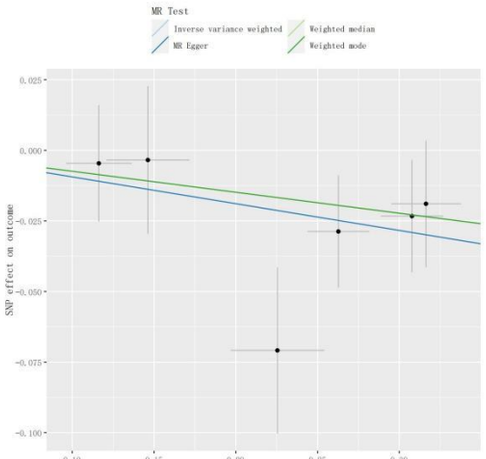

rs8100204
rs2236124
rs364585
All - MR Egger
All - Inverse variance weighted
−1.0
−0.5
0.0
MR effect size for
'Ceramide (d42:1) levels || id:ebi-PL179-GCST90277255' on 'outcome'

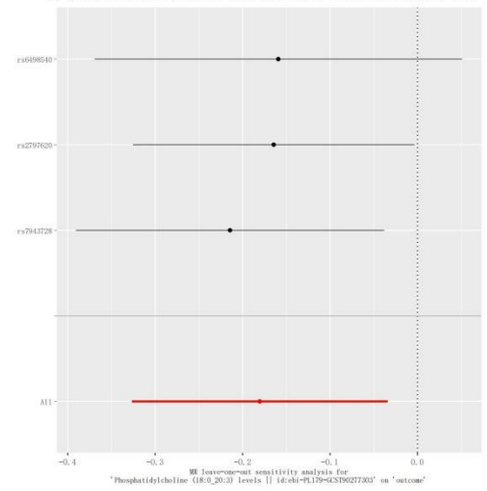

MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.08
0.04
0.00
−0.04
−0.08
0.10
0.15
0.20
0.25
0.30
SNP effect on Ceramide (d42:2) levels || id:ebi-PL179-GCST90277256

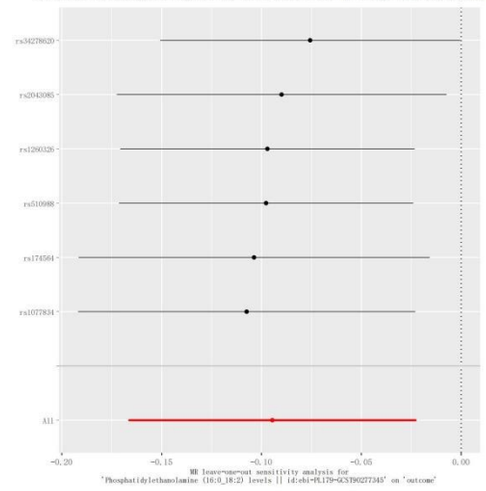

rs364585
rs2236124
rs72999033
rs12763964
rs5767288
rs1042034
rs1169306
rs187429064
All
−0.2
−0.1
0.0
0.1
MR leave-one-out sensitivity analysis for
'Ceramide (d42:2) levels || id:ebi-PL179-GCST90277256' on 'outcome'

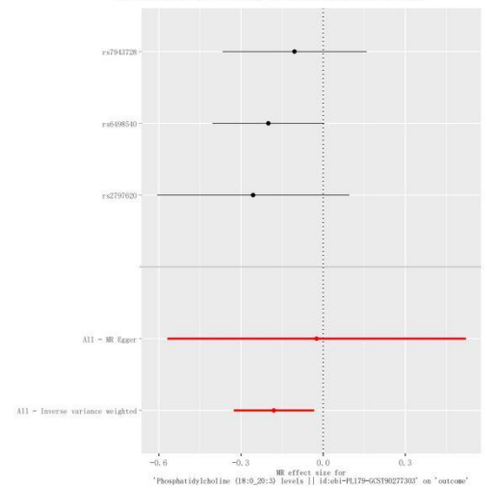

rs1169306
rs187429064
rs1042034
rs5767288
rs12763964
rs72999033
rs2236124
rs364585
All - MR Egger
All - Inverse variance weighted
−0.3
0.0
0.3
MR effect size for
'Ceramide (d42:2) levels || id:ebi-PL179-GCST90277256' on 'outcome'

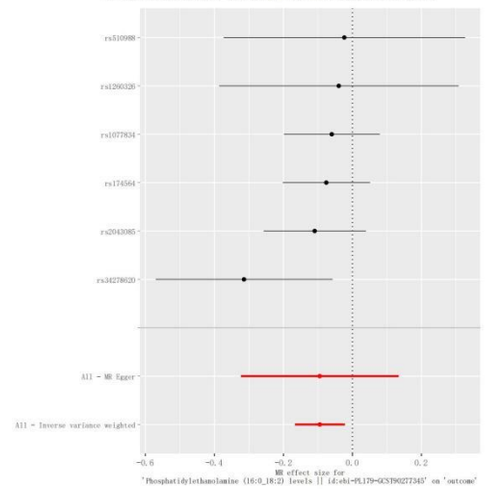

MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Phosphatidylcholine (18:0_20:3) levels || id:ebi-PL179-GCST90277303


MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
SNP effect on Phosphatidylethanolamine (16:0_18:2) levels || id:ebi-PL179-GCST9027734

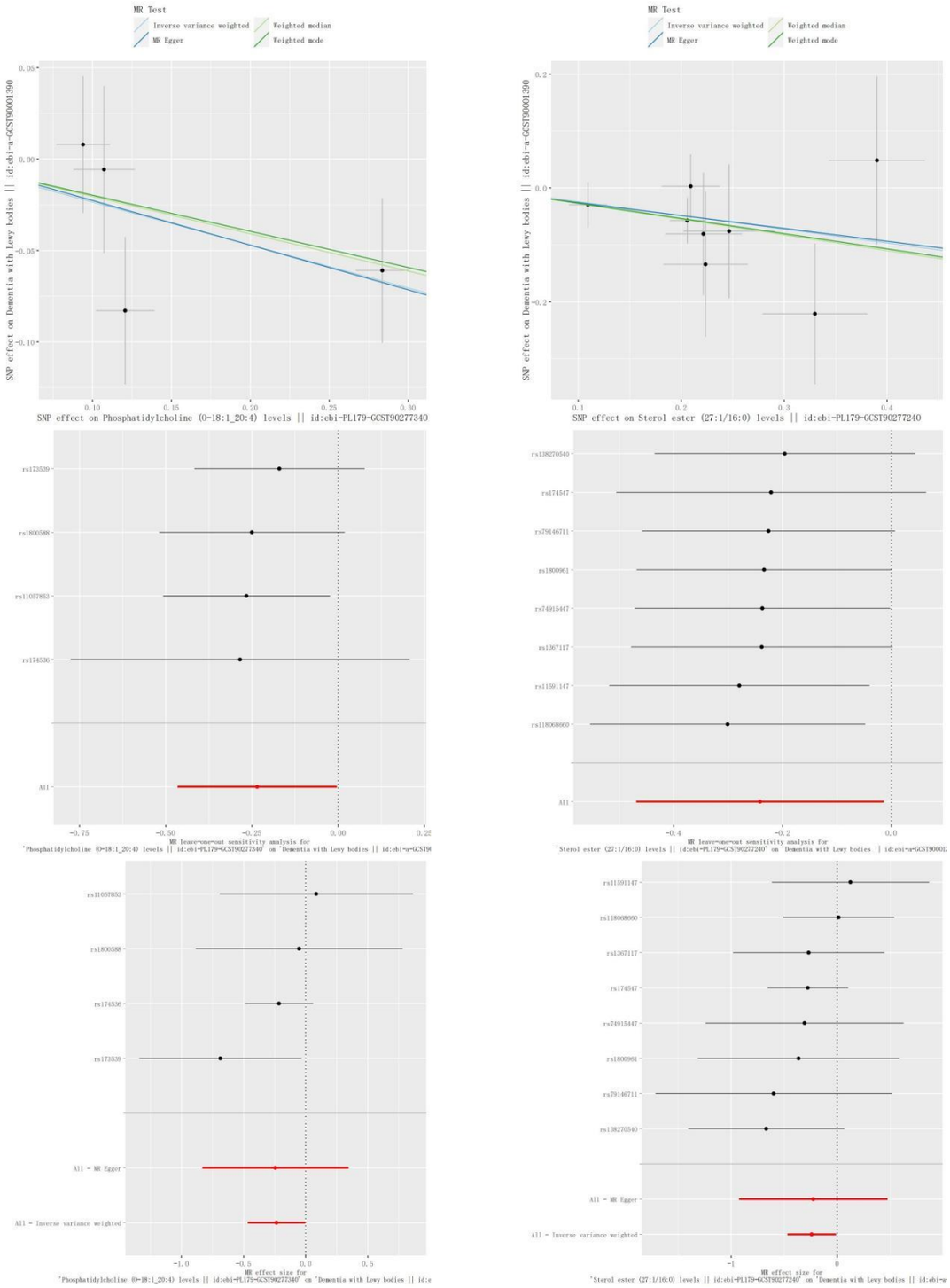

rs6498540
rs2797620
rs7943728
All
MR leave-one-out sensitivity analysis for
'Phosphatidylcholine (18:0_20:3) levels || id:ebi-PL179-GCST90277303' on 'outcome'

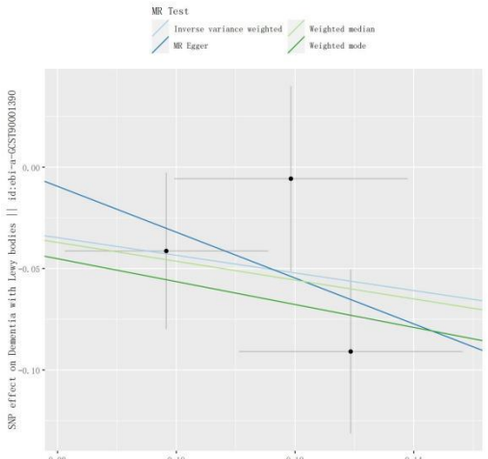

rs34278620
rs2043085
rs1260326
rs510988
rs174564
rs1077834
All
MR leave-one-out sensitivity analysis for
'Phosphatidylethanolamine (16:0_18:2) levels || id:ebi-PL179-GCST90277345' on 'outcome'

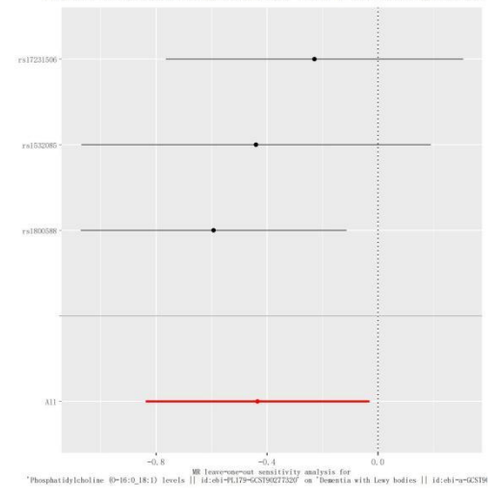

rs7943728
rs6498540
rs2797620
All - MR Egger
All - Inverse variance weighted
MR effect size for
'Phosphatidylcholine (18:0_20:3) levels || id:ebi-PL179-GCST90277303' on 'outcome'

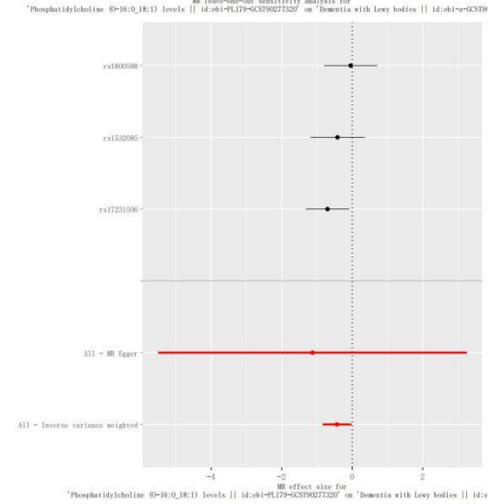

rs510988
rs1260326
rs1077834
rs174564
rs2043085
rs34278620
All - MR Egger
All - Inverse variance weighted
MR effect size for
'Phosphatidylethanolamine (16:0_18:2) levels || id:ebi-PL179-GCST90277345' on 'outcome'

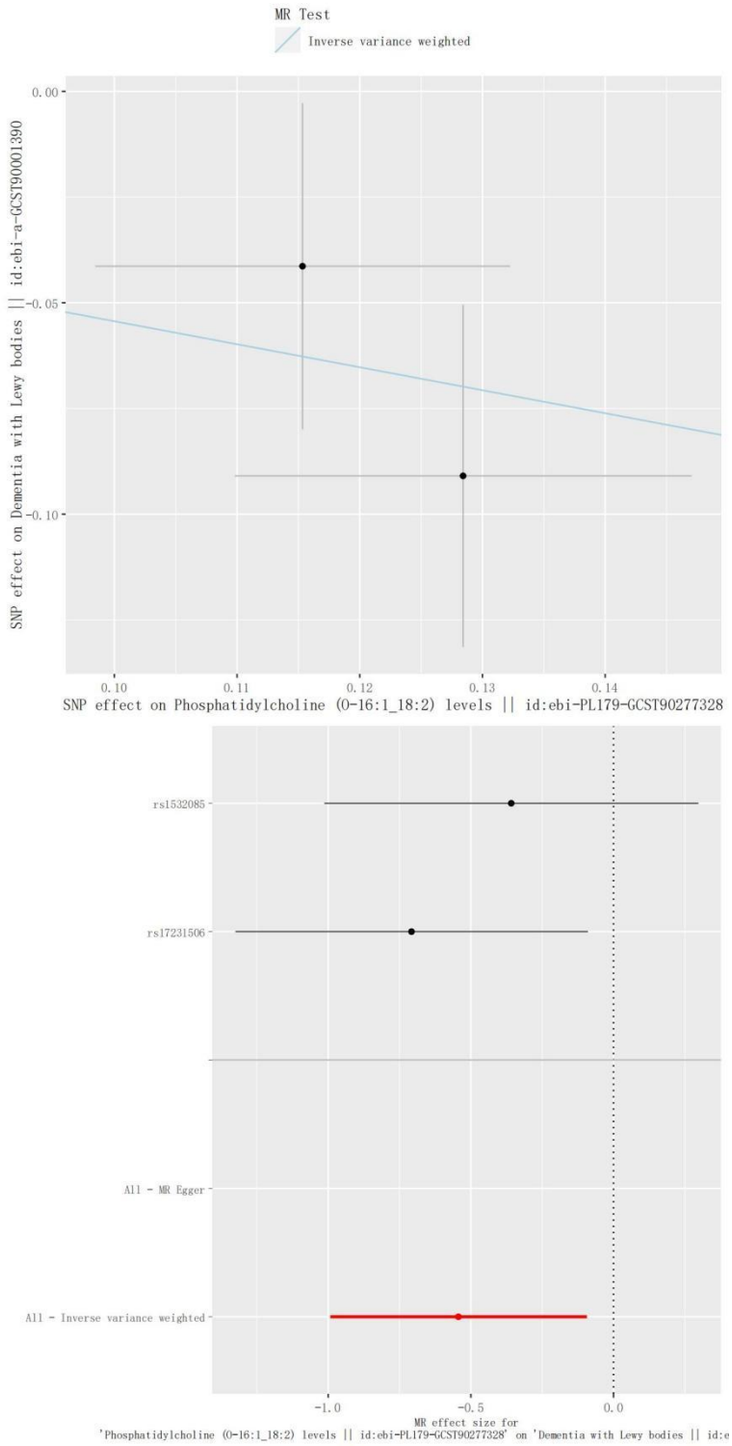
Supplementary Figure S7. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Plasma lipidome on DLB



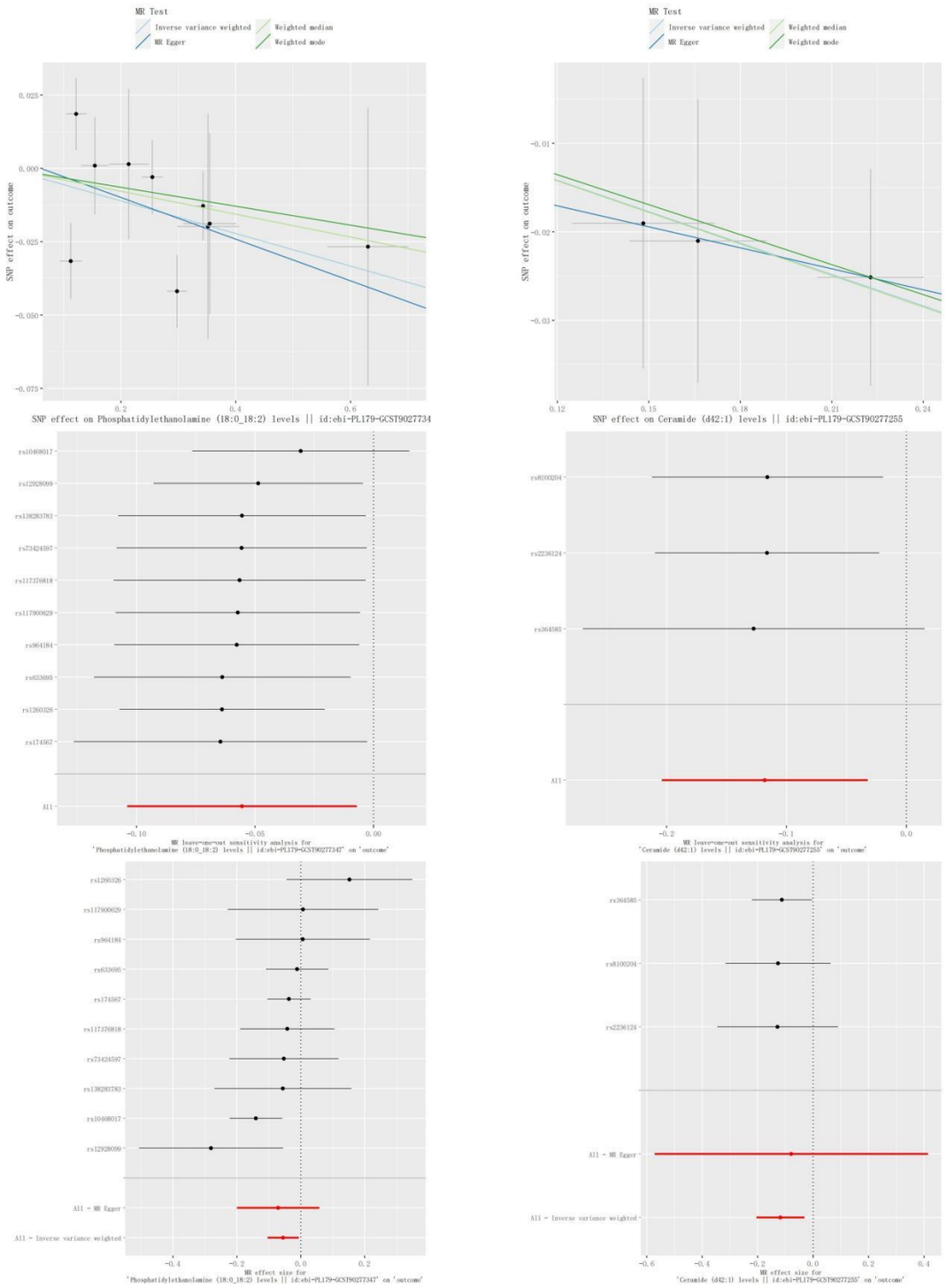

MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on Dementia with Lewy bodies || id:ebi-a-GCST90001390
0.00
-0.05
-0.10
0.08
0.10
0.12
0.14
SNP effect on Phosphatidylcholine (O-16:0_18:1) levels || id:ebi-PL179-GCST90277320

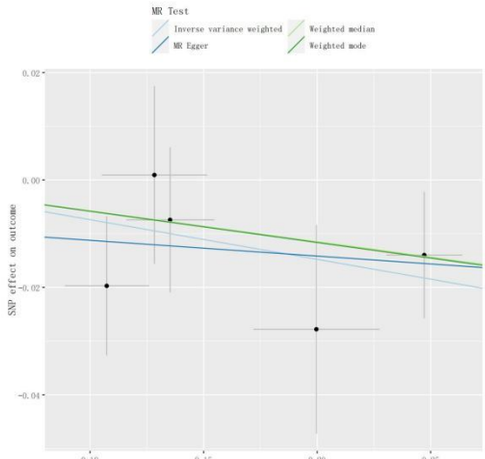

rs17231506
rs1532085
rs1800588
All
-0.8
-0.4
0.0
MR leave-one-out sensitivity analysis for
'Phosphatidylcholine (O-16:0_18:1) levels || id:ebi-PL179-GCST90277320' on 'Dementia with Lewy bodies || id:ebi-a-GCST9

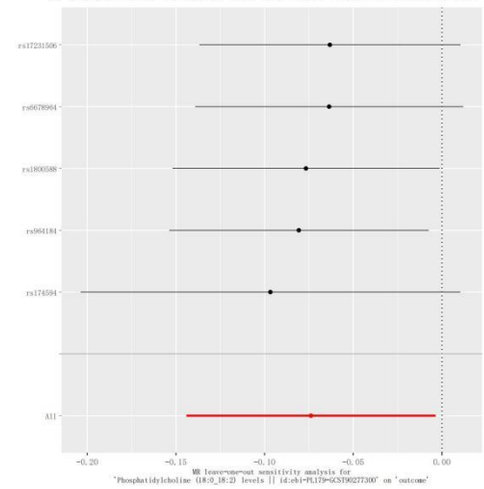

rs1800588
rs1532085
rs17231506
All - MR Egger
All - Inverse variance weighted
-4
-2
0
2
MR effect size for
'Phosphatidylcholine (O-16:0_18:1) levels || id:ebi-PL179-GCST90277320' on 'Dementia with Lewy bodies || id:e

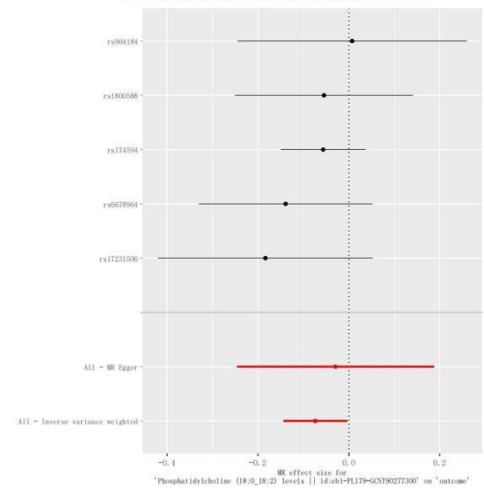

MR Test
Inverse variance weighted
0.00
−0.05
−0.10
SNP effect on Dementia with Lewy bodies || id:ebi-a-GCST90001390
0.10
0.11
0.12
0.13
0.14
SNP effect on Phosphatidylcholine (0-16:1_18:2) levels || id:ebi-PL179-GCST90277328
rs1532085
rs17231506
All - MR Egger
All - Inverse variance weighted
−1.0
−0.5
0.0
MR effect size for
'Phosphatidylcholine (0-16:1_18:2) levels || id:ebi-PL179-GCST90277328' on 'Dementia with Lewy bodies || id:e

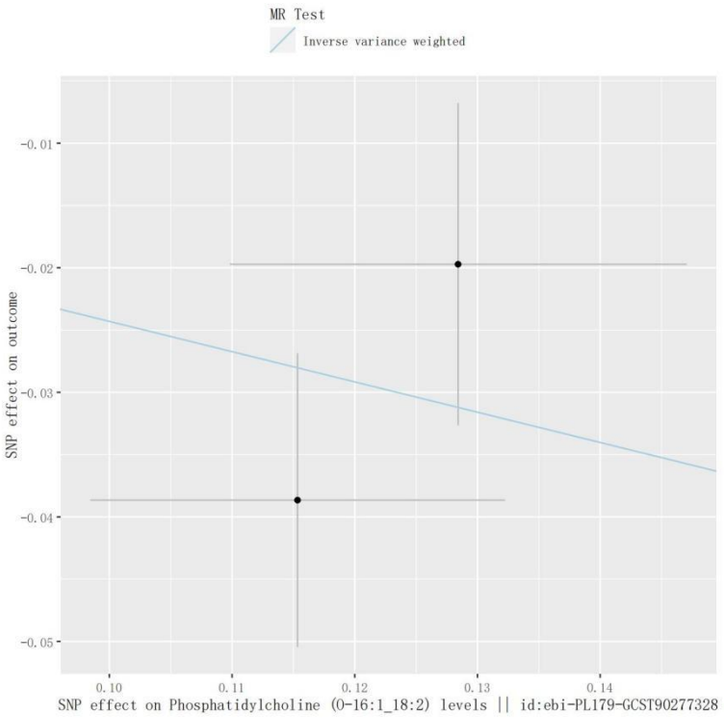
Supplementary Figure S8. Scatter plots, MR leave-one-out sensitivity analysis and Forest plots for Plasma lipidome on VD

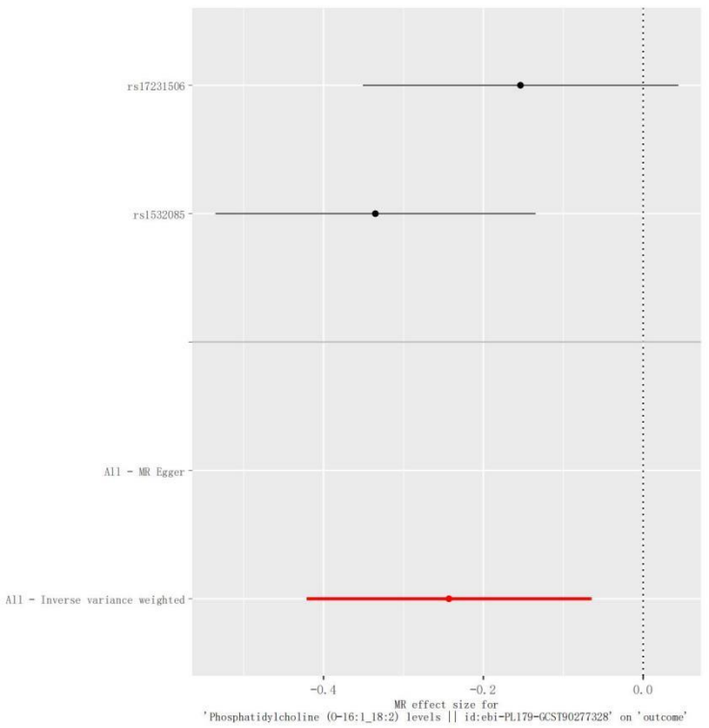



MR Test
Inverse variance weighted
MR Egger
Weighted median
Weighted mode
SNP effect on outcome
0.02
0.00
−0.02
−0.04
0.10
0.15
0.20
0.25
SNP effect on Phosphatidylcholine (18:0_18:2) levels || id:ebi-PL179-GCST90277300


rs17231506
rs6678964
rs1800588
rs964184
rs174594
All
−0.20
−0.15
−0.10
−0.05
0.00
MR leave-one-out sensitivity analysis for
'Phosphatidylcholine (18:0_18:2) levels || id:ebi-PL179-GCST90277300' on 'outcome'


rs964184
rs1800588
rs174594
rs6678964
rs17231506
All - MR Egger
All - Inverse variance weighted
−0.4
−0.2
0.0
0.2
MR effect size for
'Phosphatidylcholine (18:0_18:2) levels || id:ebi-PL179-GCST90277300' on 'outcome'


MR Test
Inverse variance weighted
SNP effect on outcome
-0.01
-0.02
-0.03
-0.04
-0.05
0.10
0.11
0.12
0.13
0.14
SNP effect on Phosphatidylcholine (O-16:1_18:2) levels || id:ebi-PL179-GCST90277328


rs17231506
rs1532085
All - MR Egger
All - Inverse variance weighted
-0.4
-0.2
0.0
MR effect size for
'Phosphatidylcholine (O-16:1_18:2) levels || id:ebi-PL179-GCST90277328' on 'outcome'