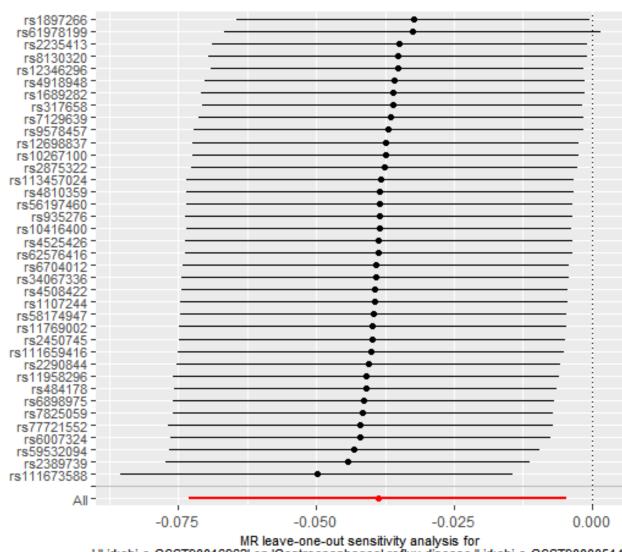
Figure 1 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Alistipes id.968) on gastroesophageal reflux disease

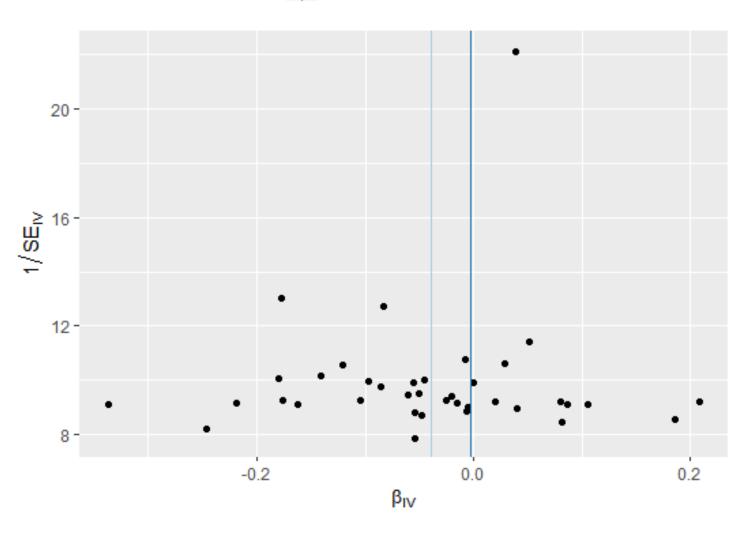


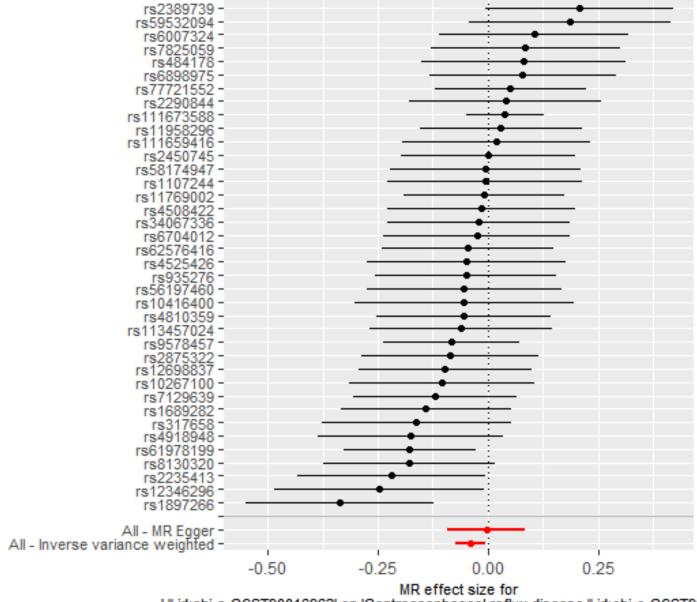
MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016962' on 'Gastroesophageal reflux disease || id:ebi-a-GCST90000514'

MR Method

Inverse variance weighted

MR Egger





" || id:ebi-a-GCST90016962" on 'Gastroesophageal reflux disease || id:ebi-a-GCST90

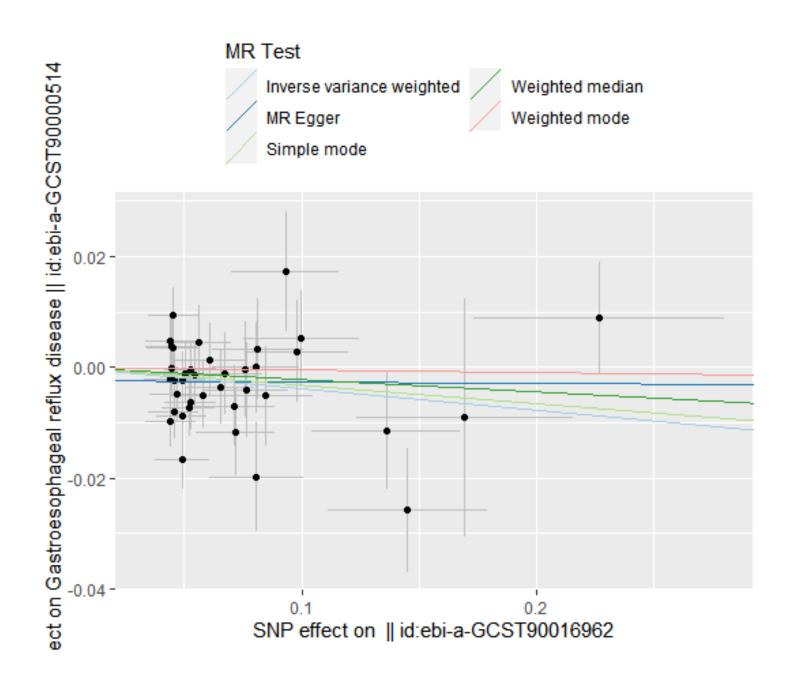
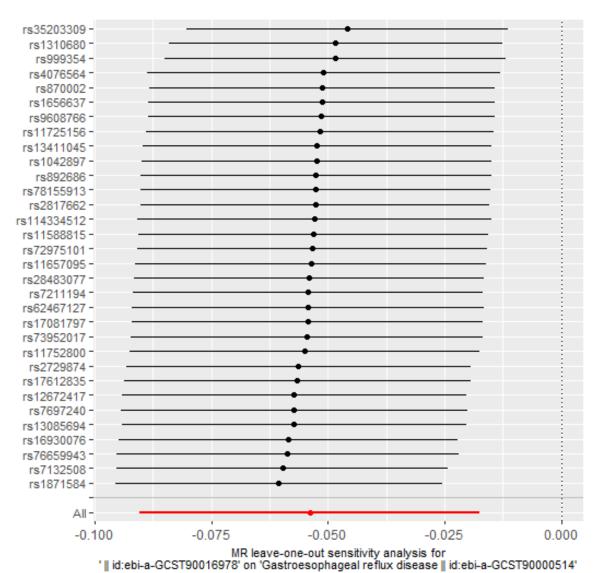


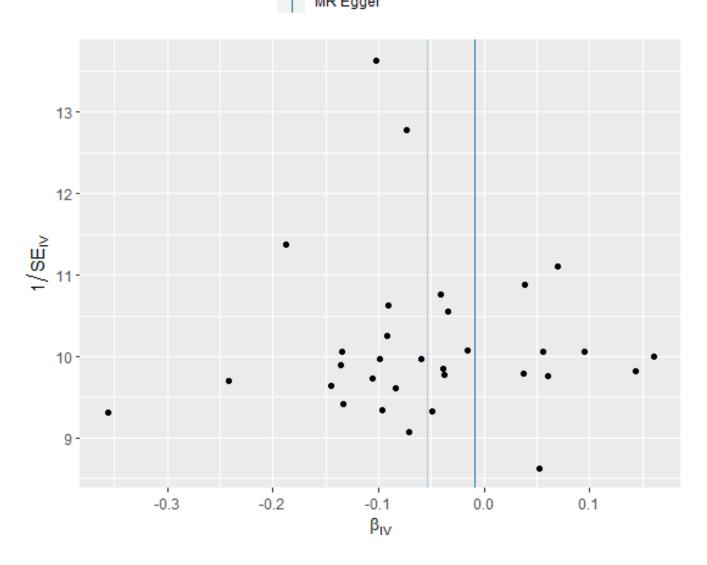
Figure 2 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Christensenellaceae R 7group id.11283) on gastroesophageal reflux disease

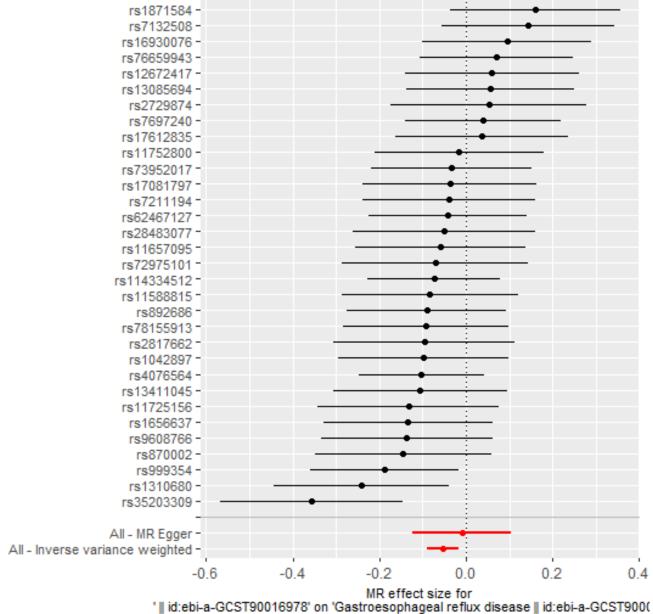


MR Method

Inverse variance weighted

MR Egger





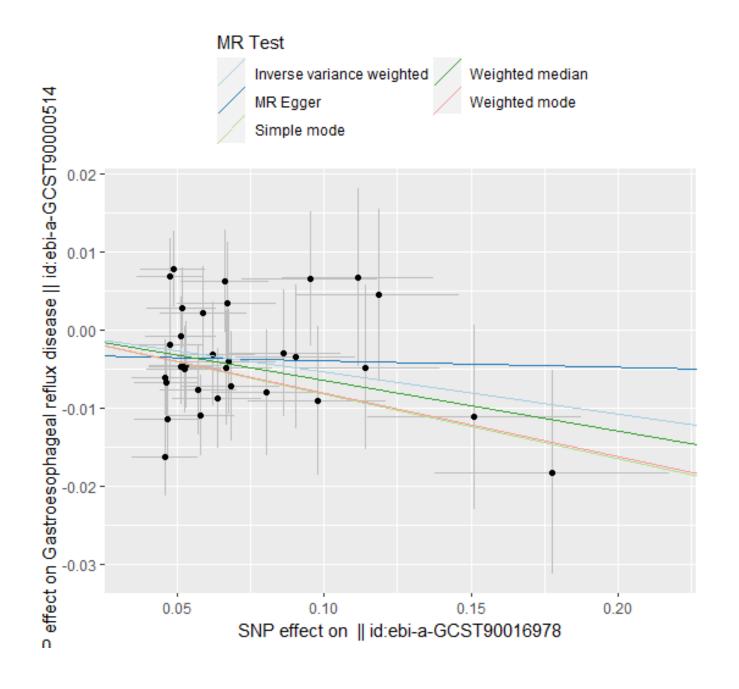
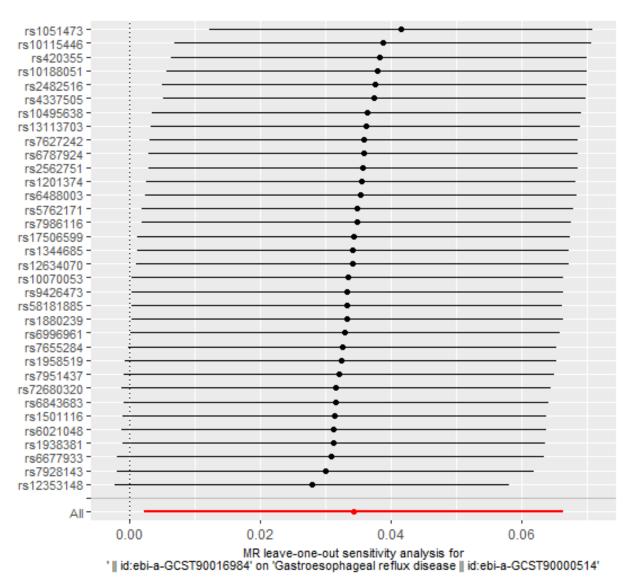


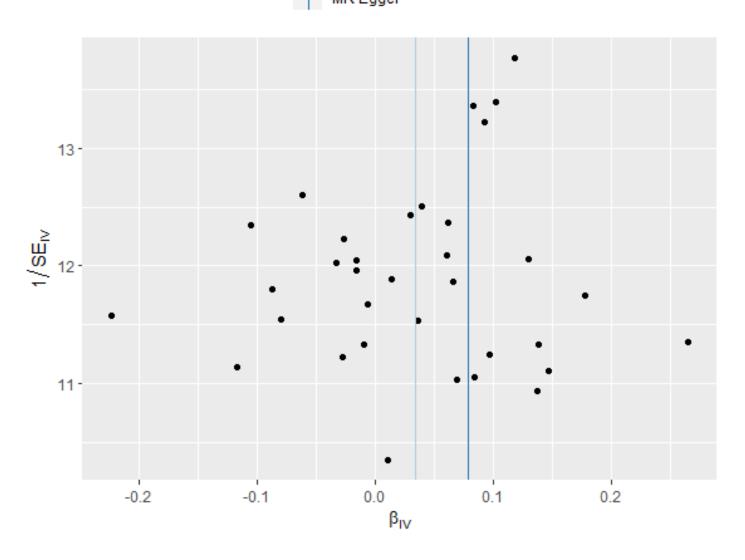
Figure 3 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Coprococcus2 id.11302) on gastroesophageal reflux disease

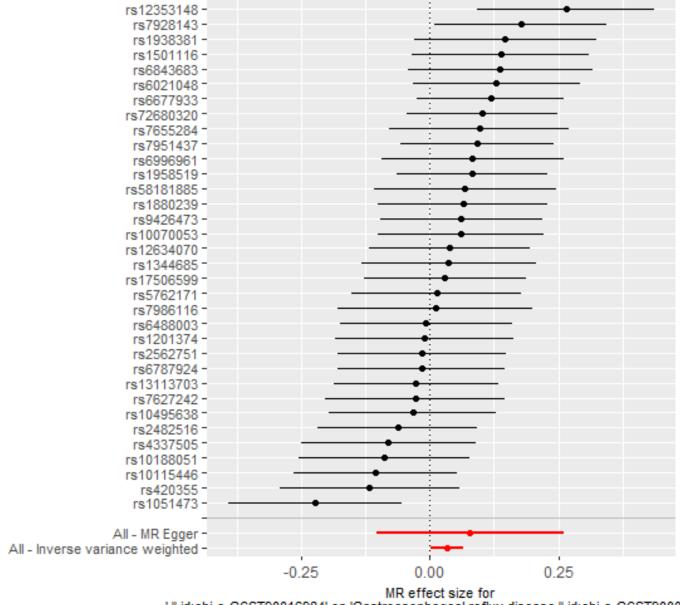


MR Method

Inverse variance weighted

MR Egger





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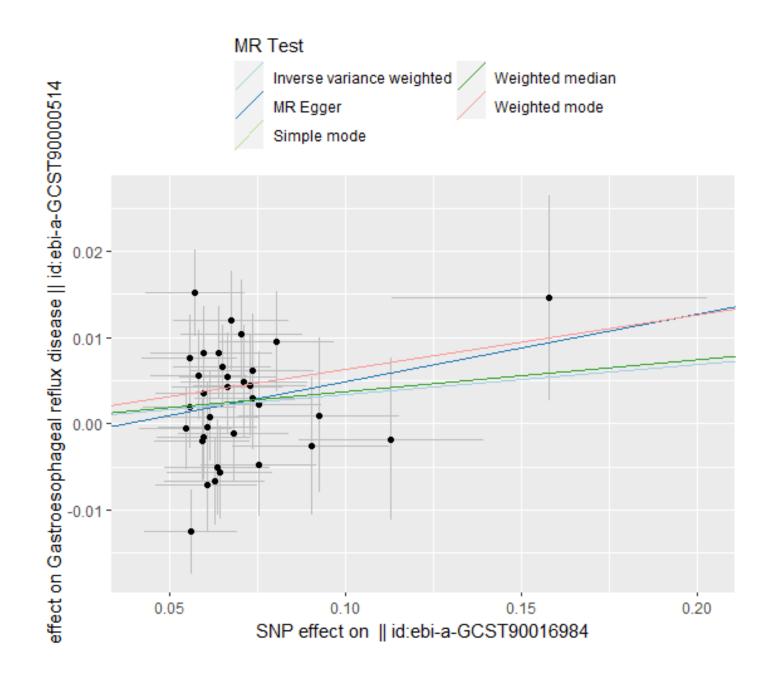
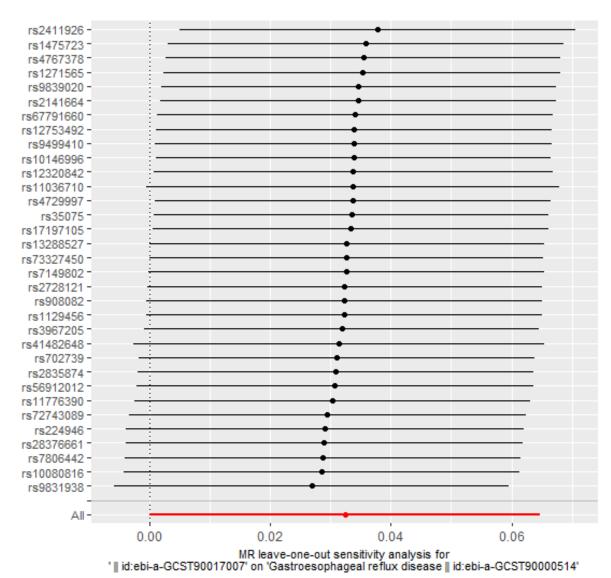


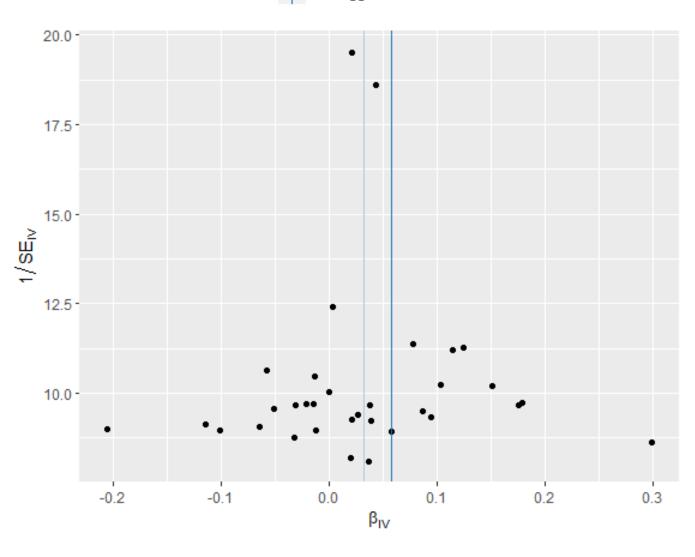
Figure 4 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Faecalibacterium id.2057) on gastroesophageal reflux disease

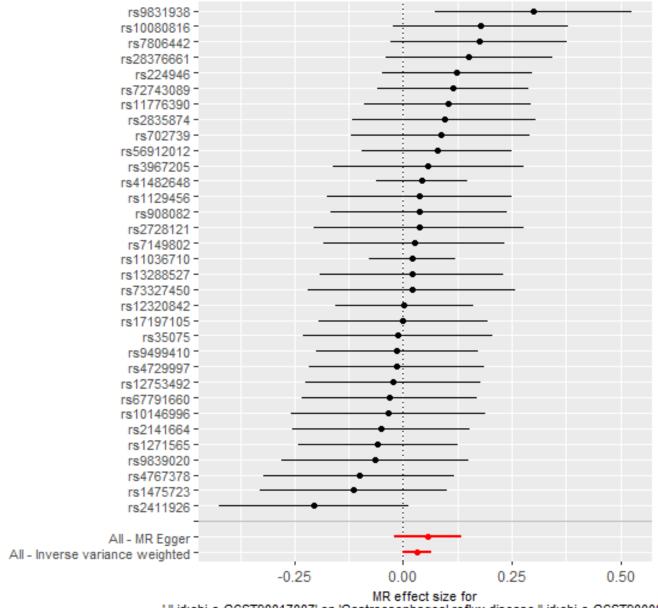


MR Method

Inverse variance weighted

MR Egger





" id:ebi-a-GCST90017007" on 'Gastroesophageal reflux disease || id:ebi-a-GCST90000

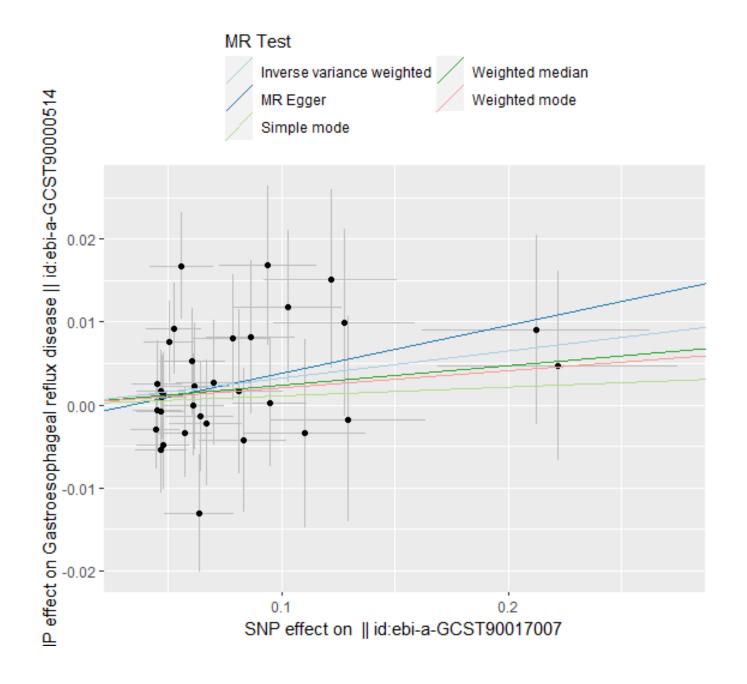
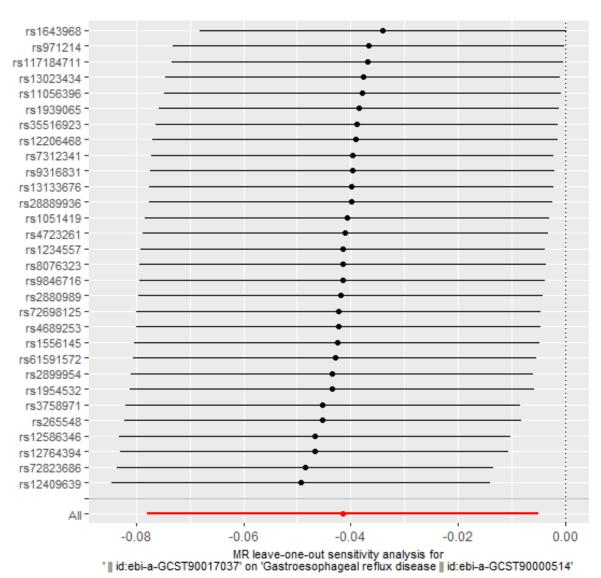


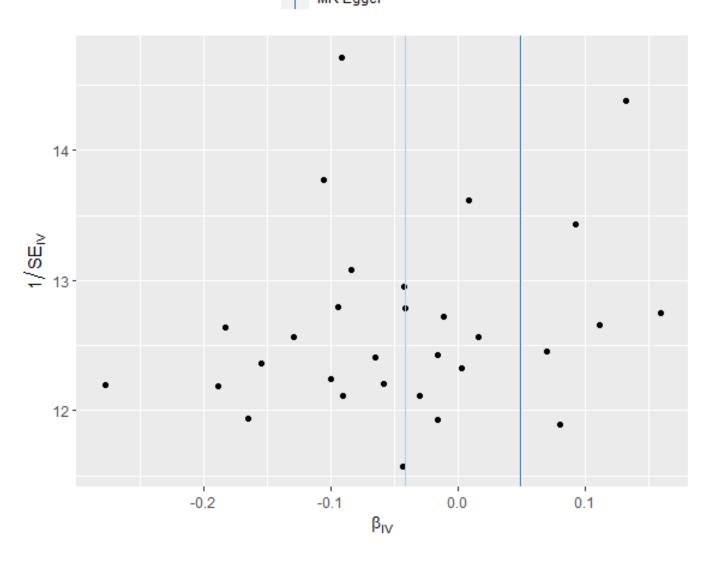
Figure 5 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Oscillospira id.2064) on gastroesophageal reflux disease

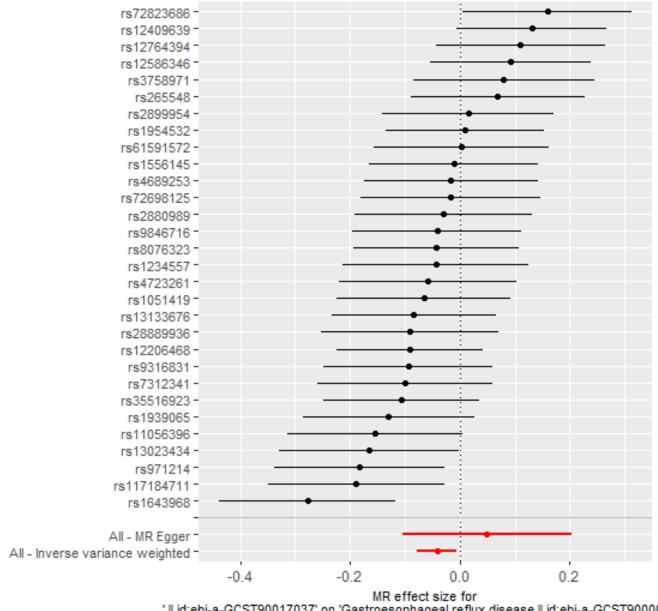


MR Method

Inverse variance weighted

MR Egger





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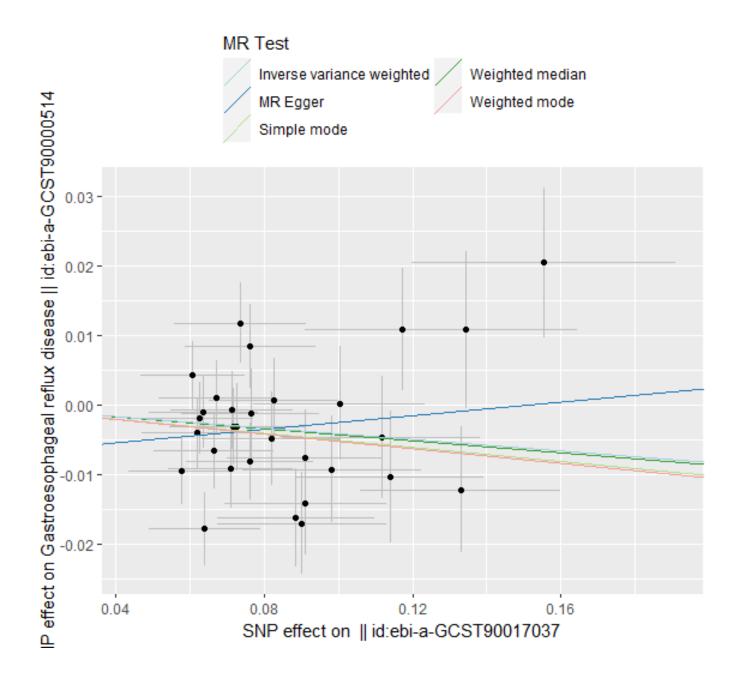
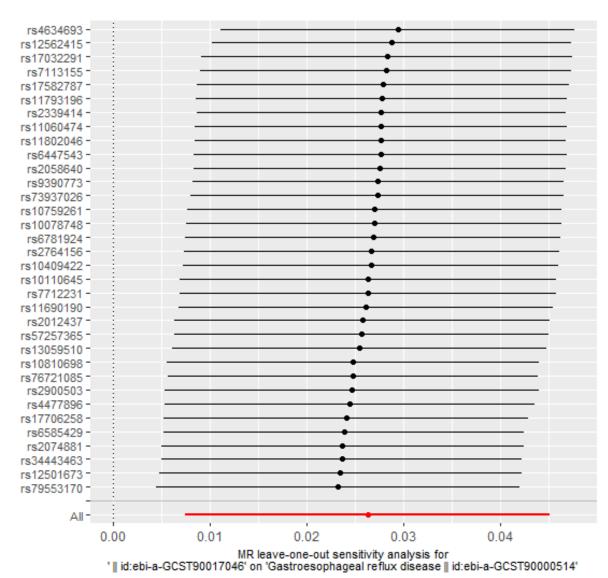


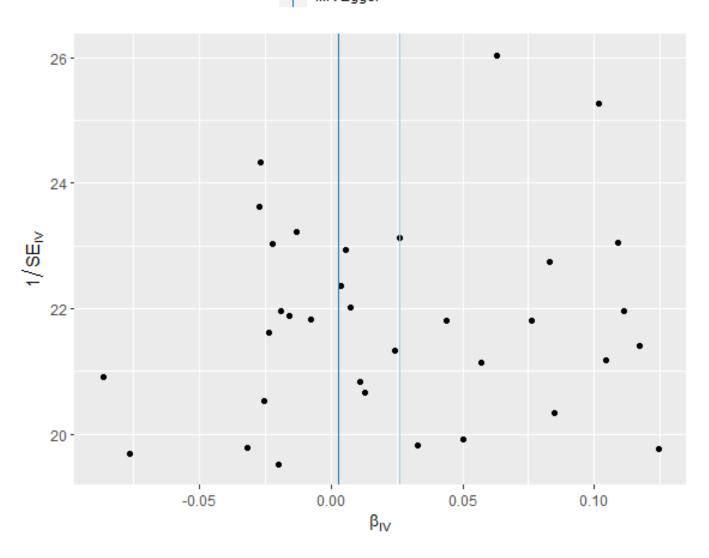
Figure 6 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Rikenellaceae RC9 gut group id.11191) on gastroesophageal reflux disease

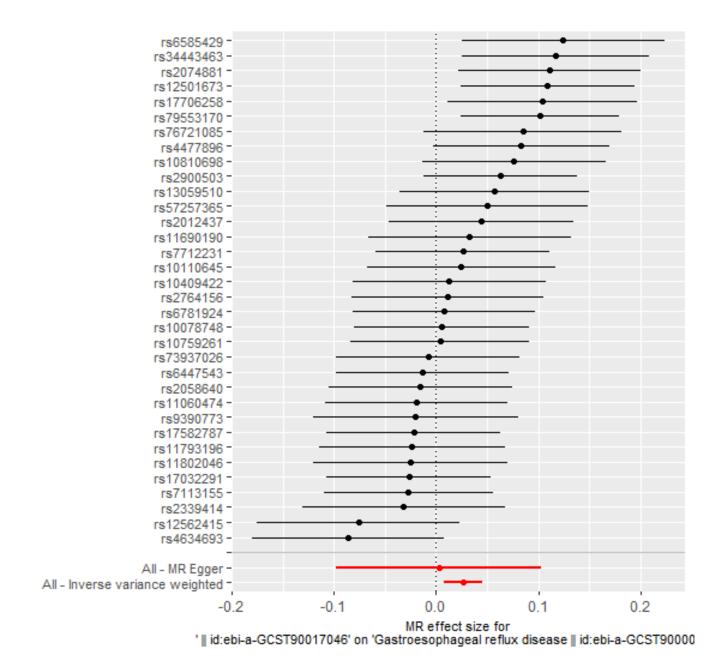


MR Method

Inverse variance weighted

MR Egger





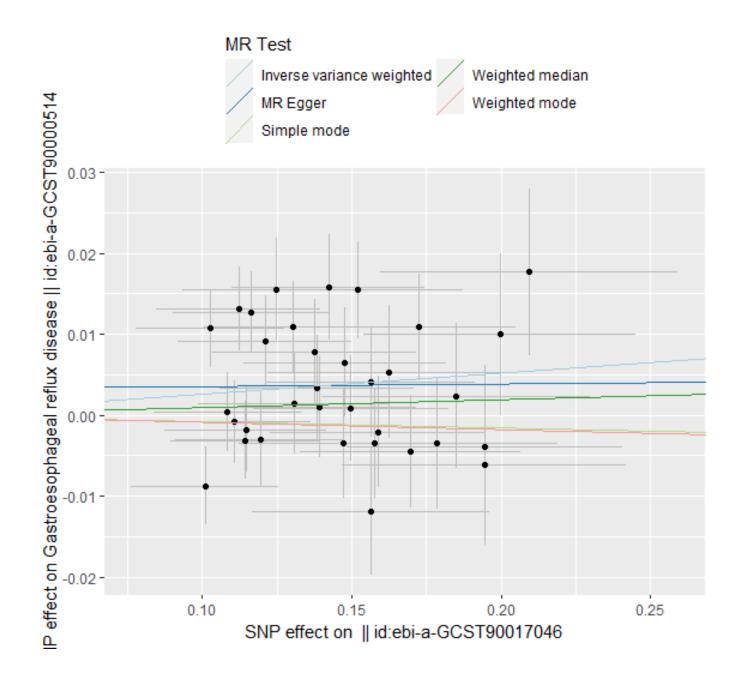
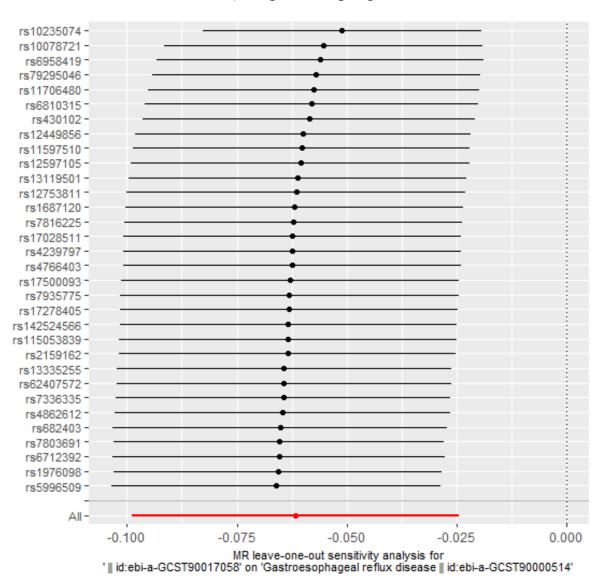


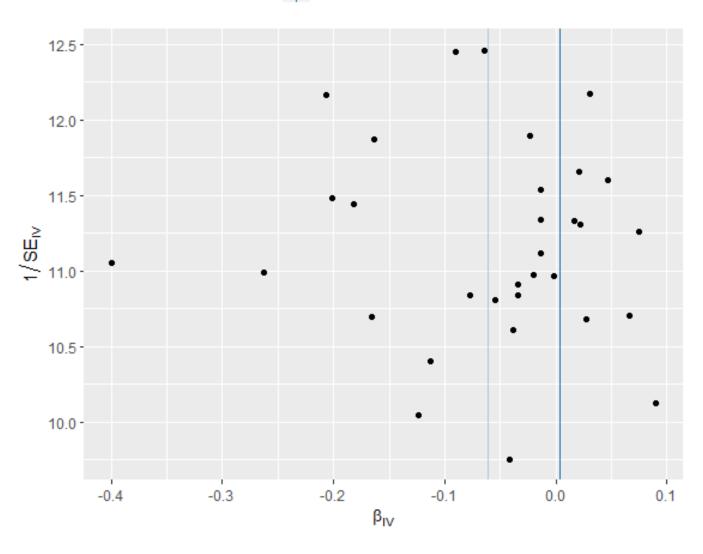
Figure 7 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG010 id.11367) on gastroesophageal reflux disease

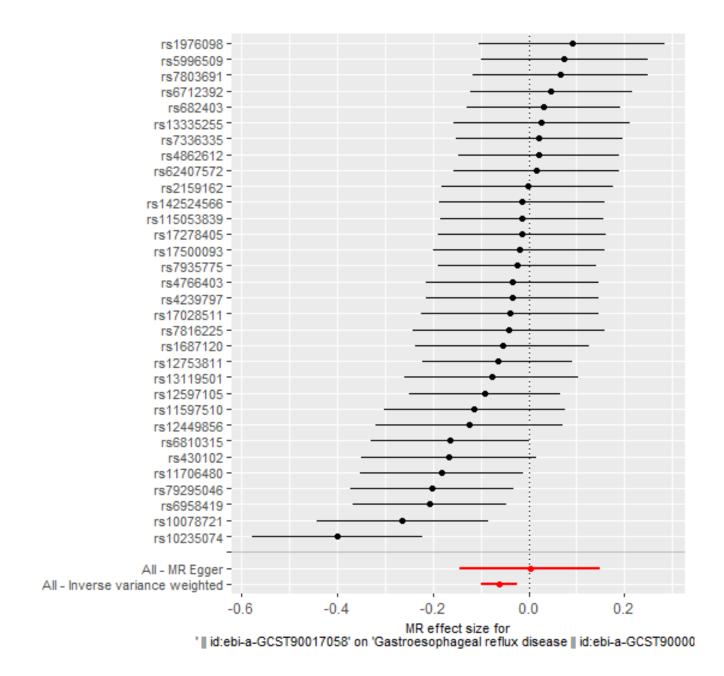


MR Method

Inverse variance weighted

MR Egger





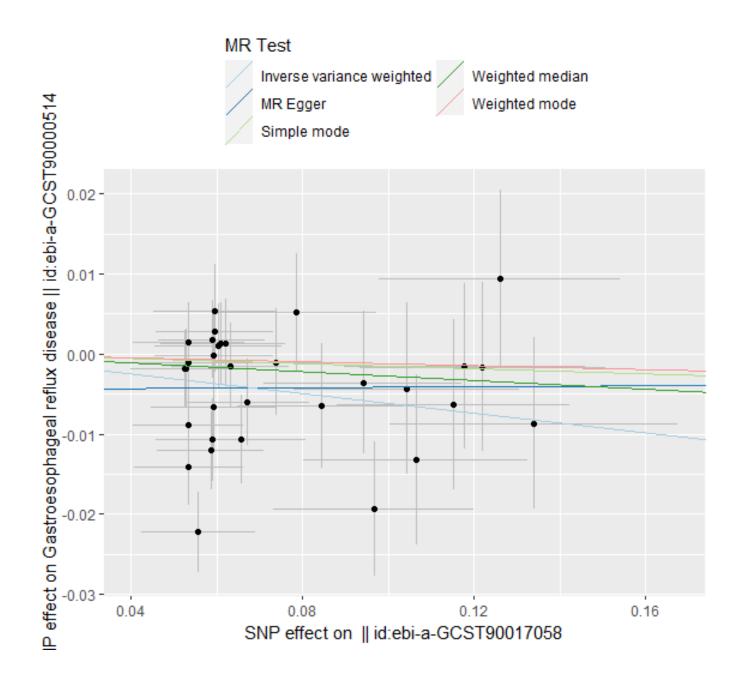
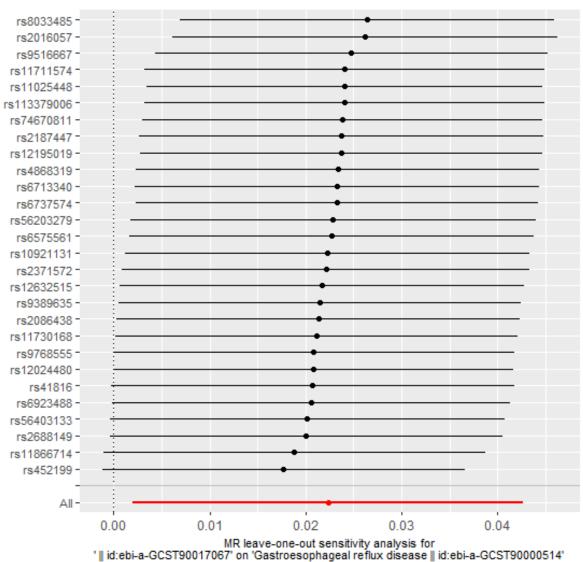


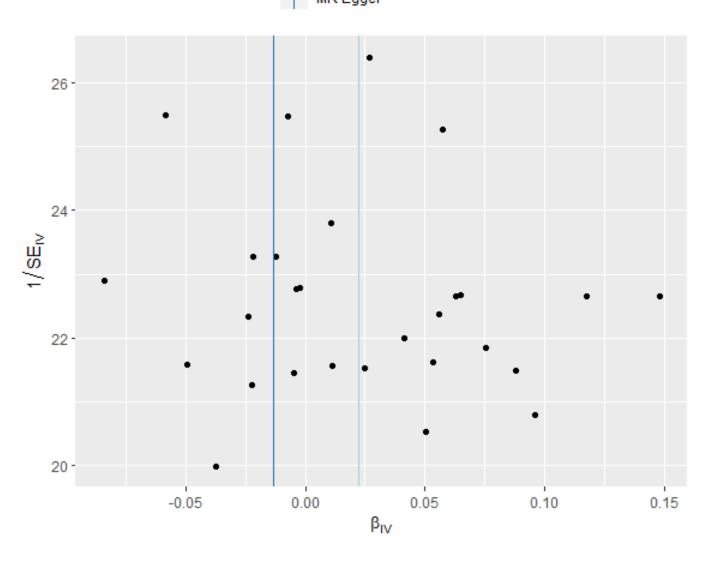
Figure 8 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Sellimonas id.14369) on gastroesophageal reflux disease

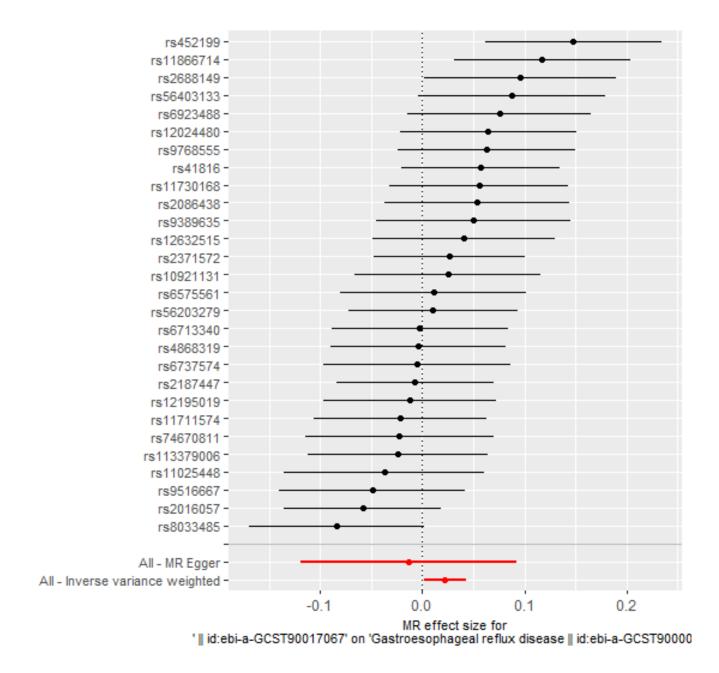


MR Method

Inverse variance weighted

MR Egger





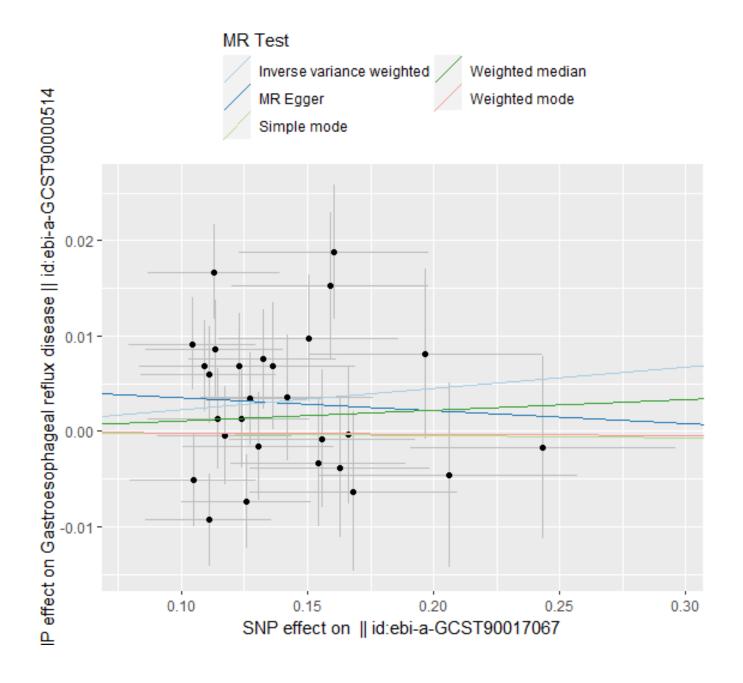
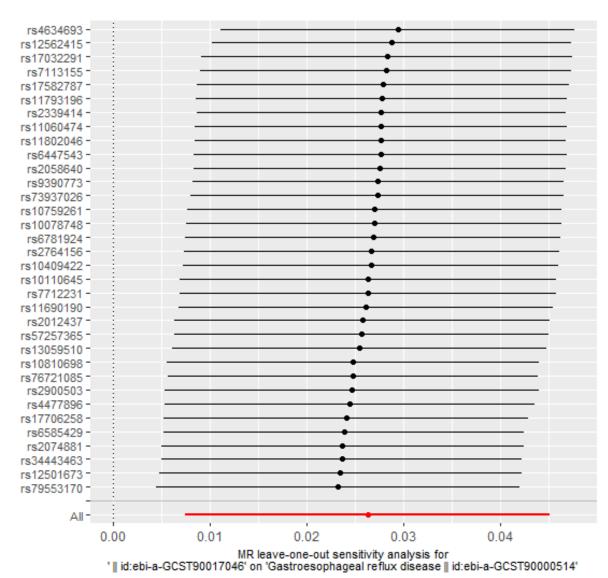


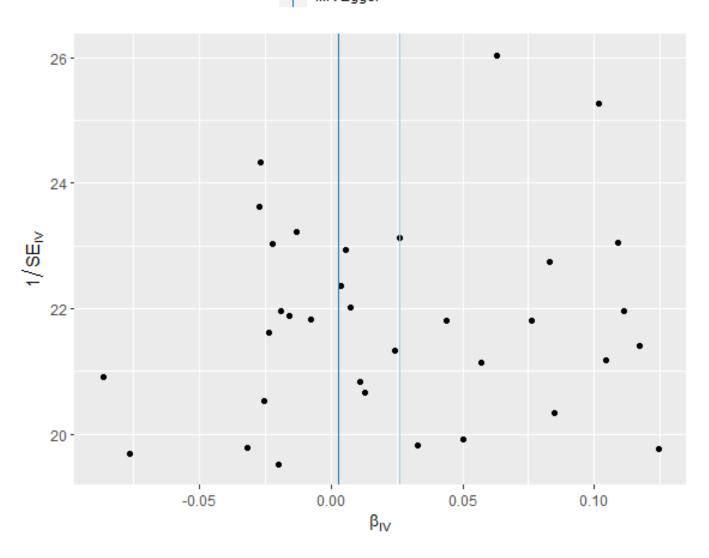
Figure 9 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Slackia id.825) on gastroesophageal reflux disease

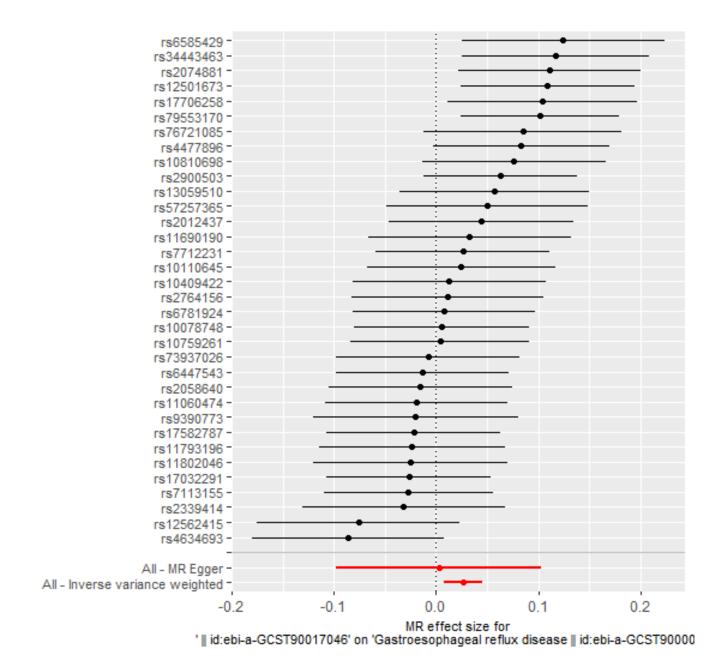


MR Method

Inverse variance weighted

MR Egger





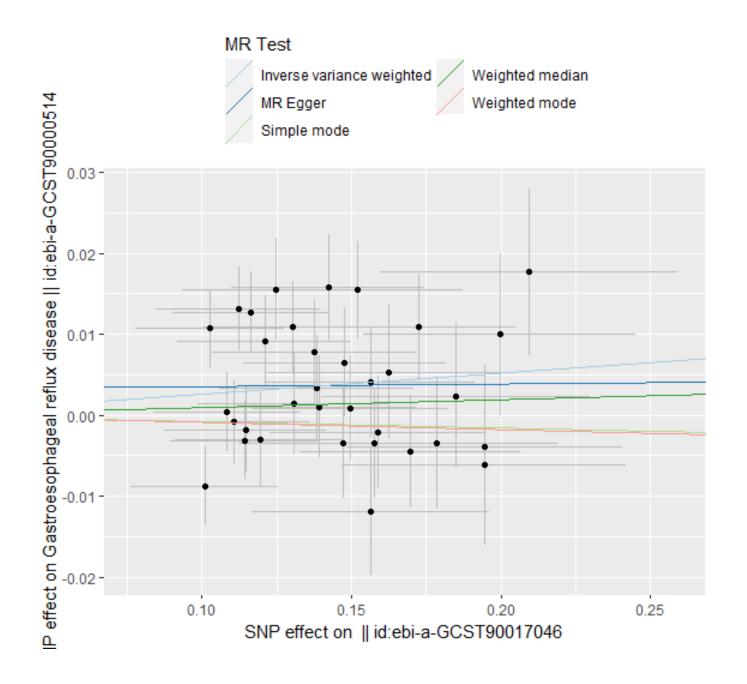
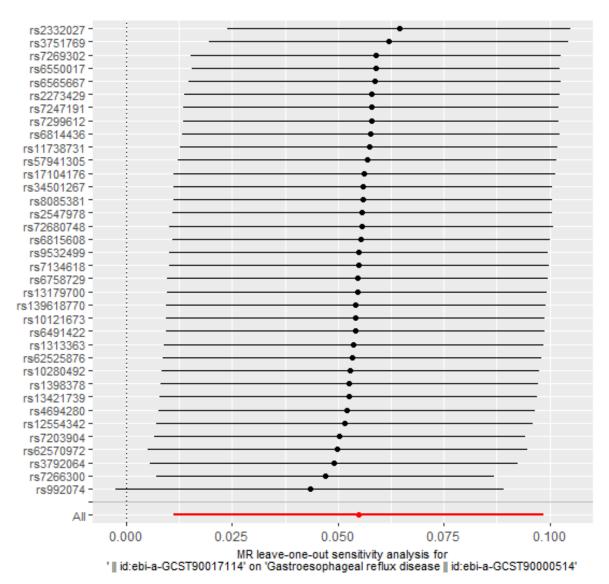


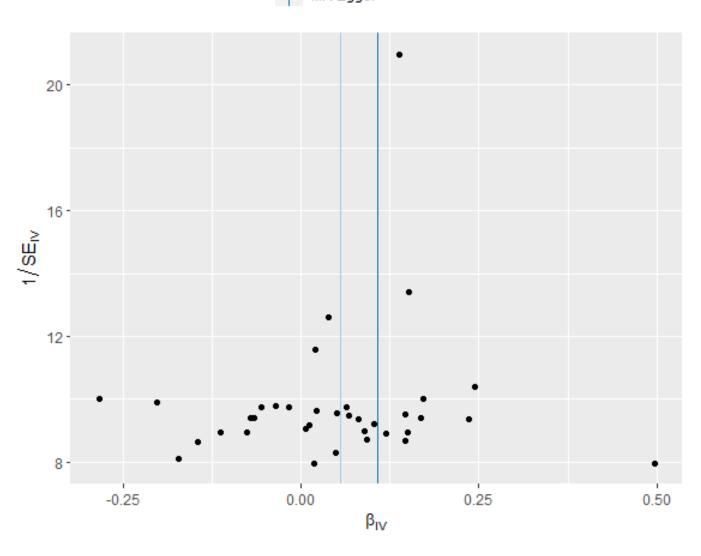
Figure 10 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Firmicutes id.1672) on gastroesophageal reflux disease

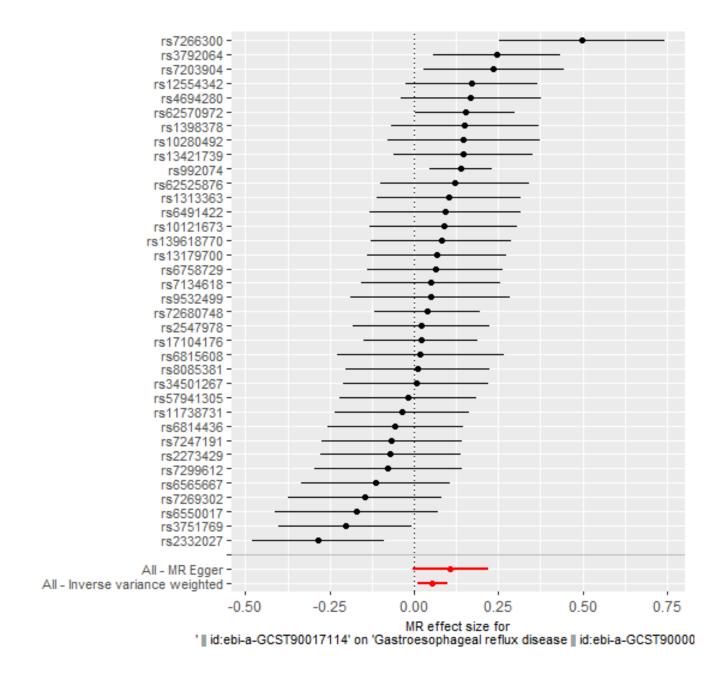


MR Method

Inverse variance weighted

MR Egger





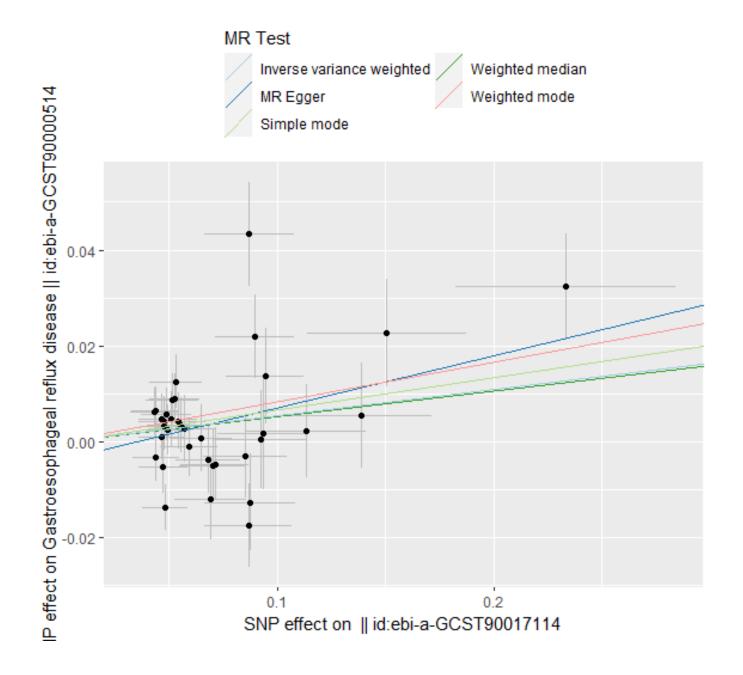
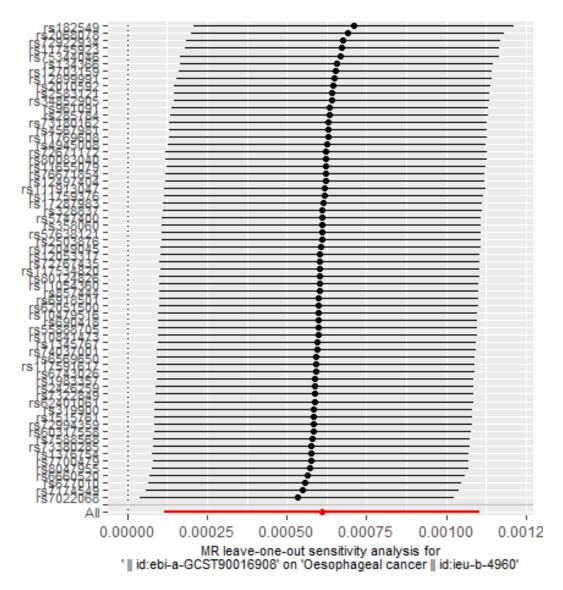


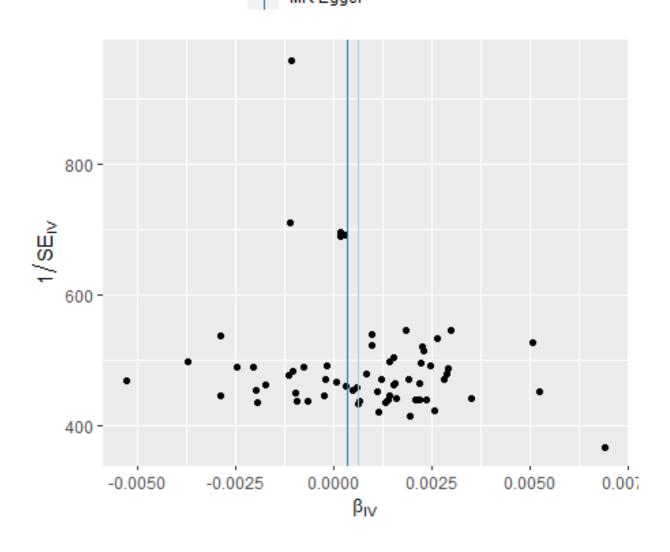
Figure 11 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Actinobacteria id.419) on oesophageal cancer

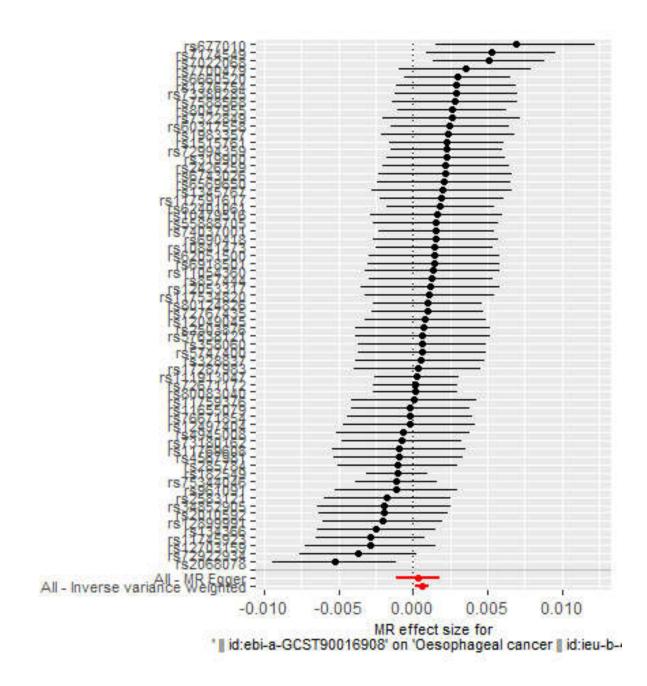


MR Method

Inverse variance weighted

MR Egger





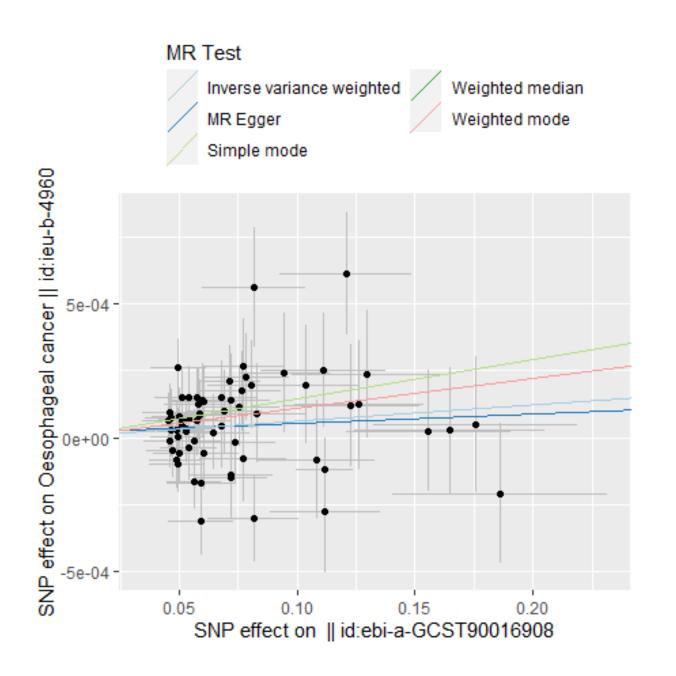
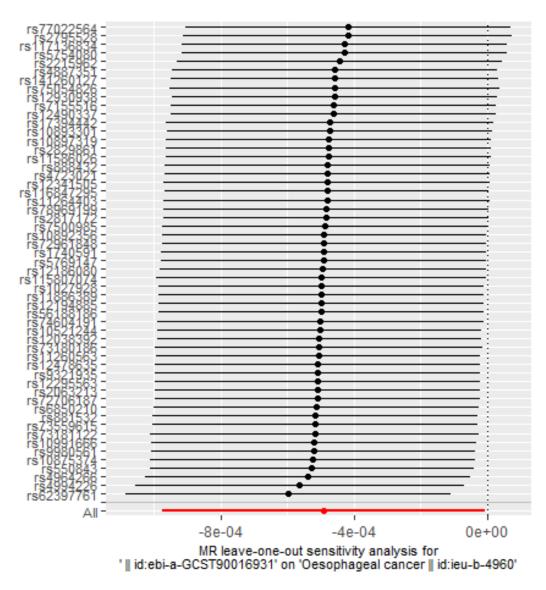
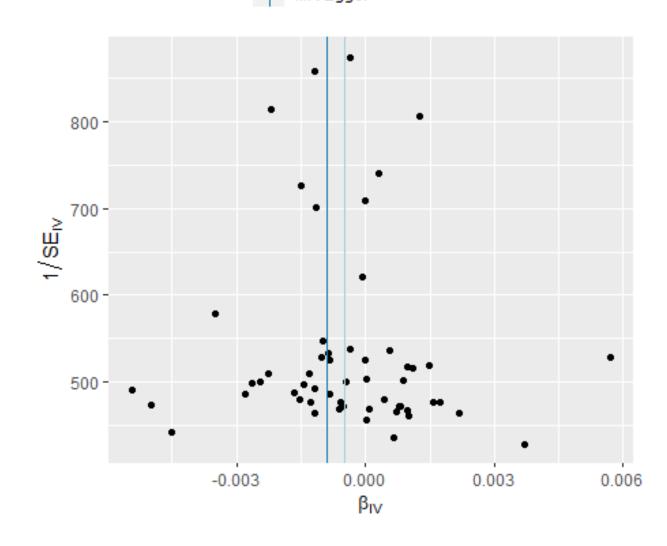
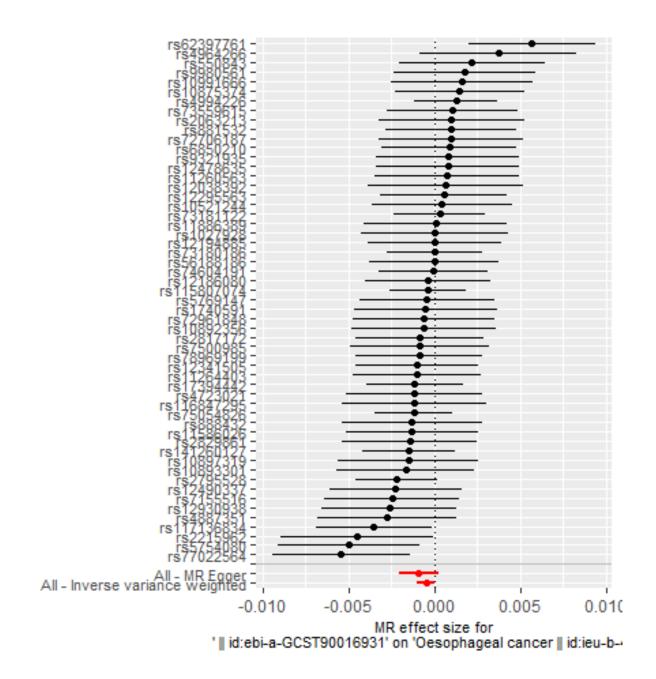


Figure 12 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Clostridiaceae1 id.1869) on oesophageal cancer



Inverse variance weighted MR Egger





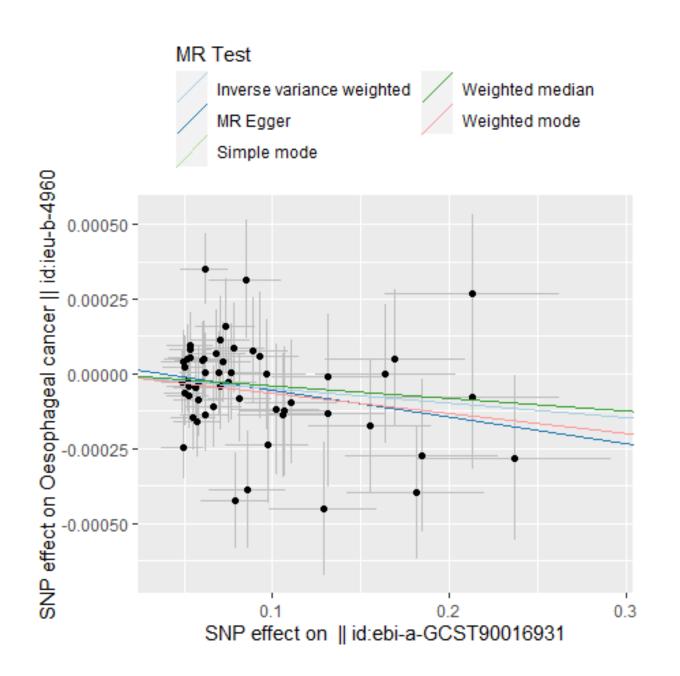
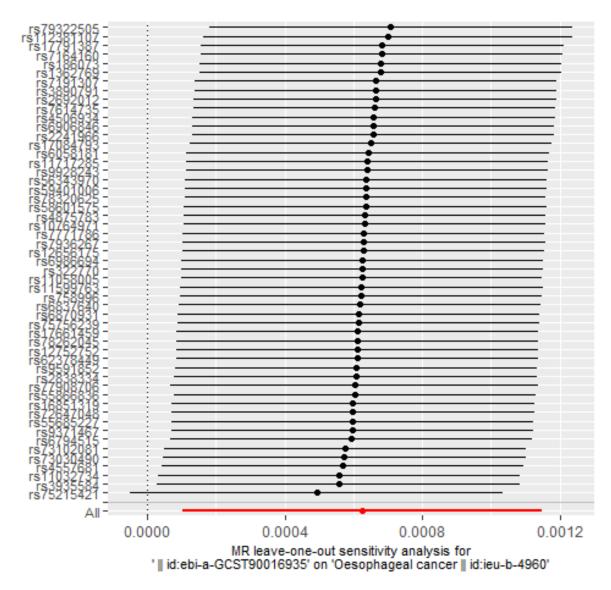
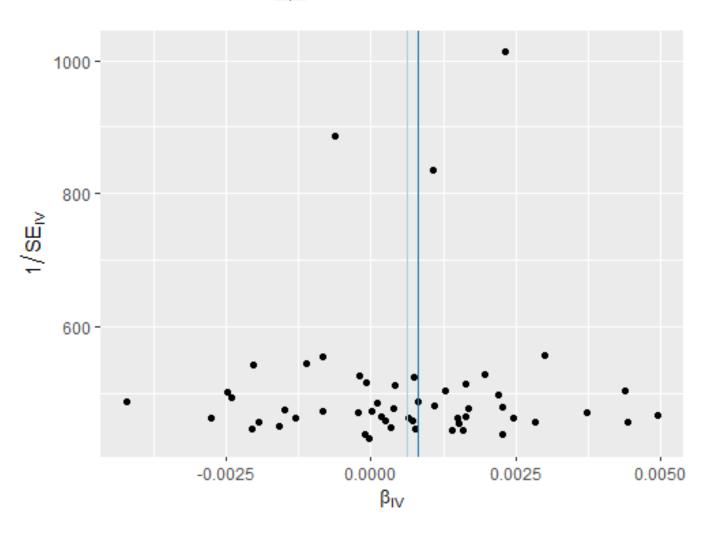


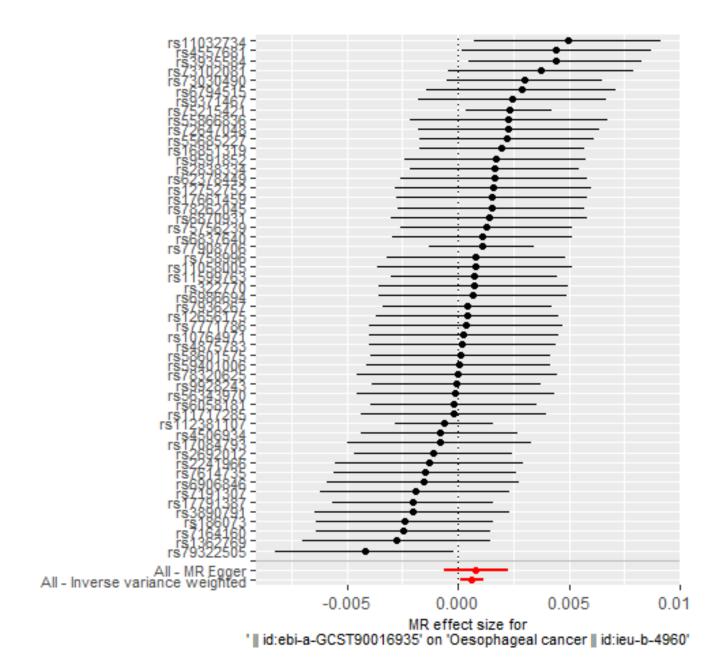
Figure 13 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Desulfovibrionaceae id.3169) on oesophageal cancer



MR Method Inverse variance weighted







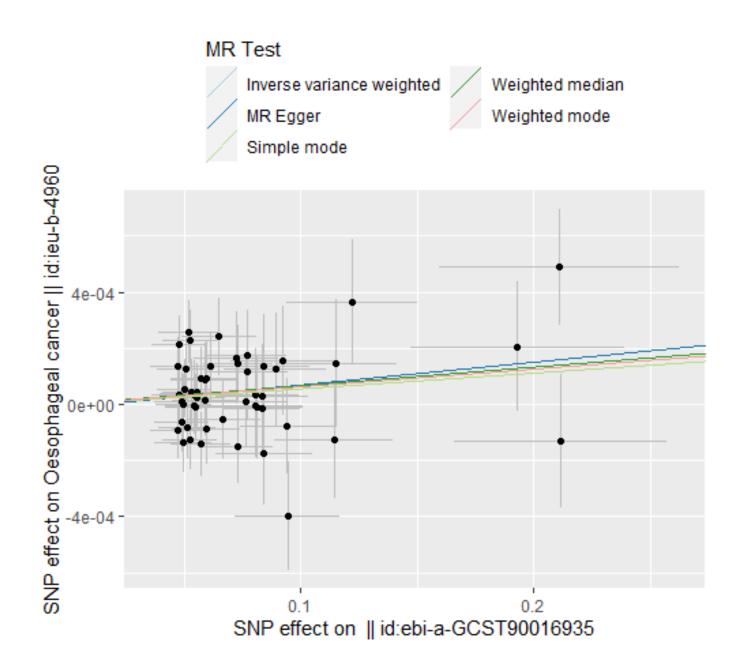
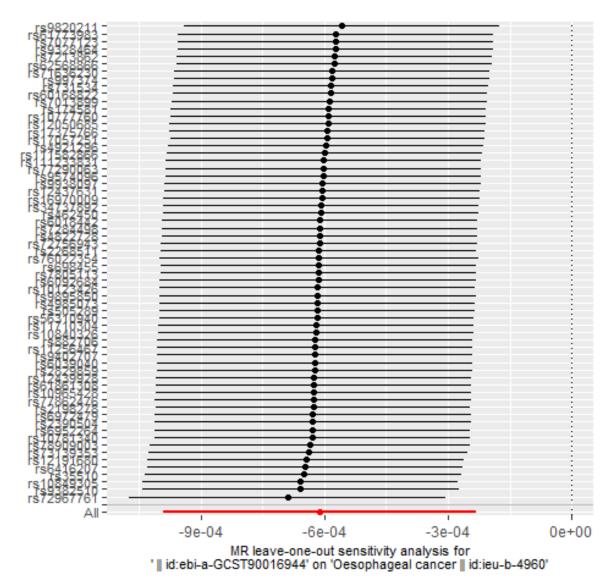
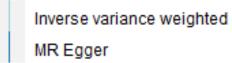
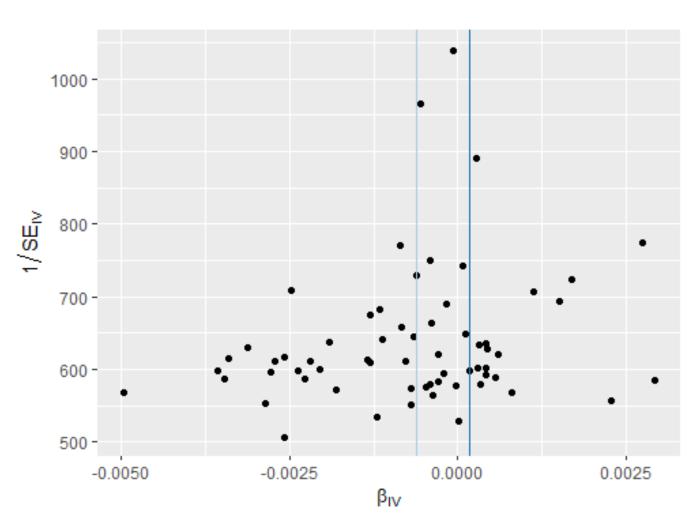
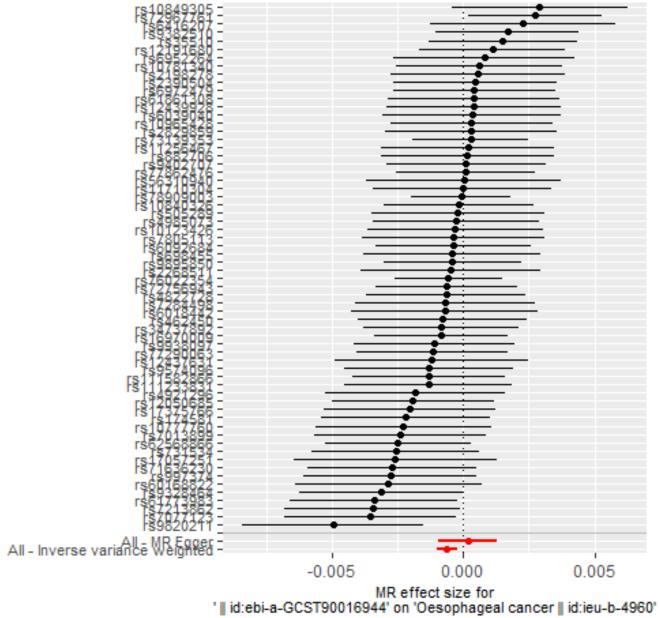


Figure 14 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Pasteurellaceae id.3689) on oesophageal cancer









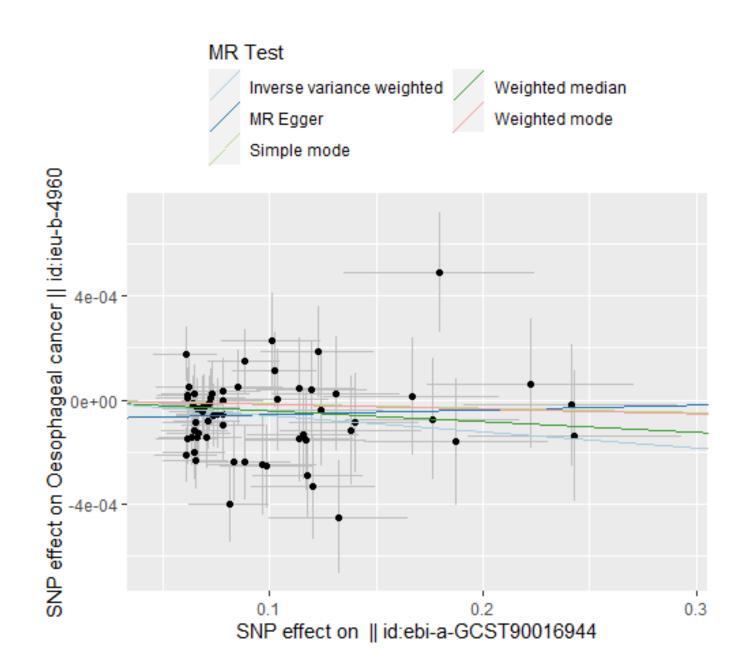
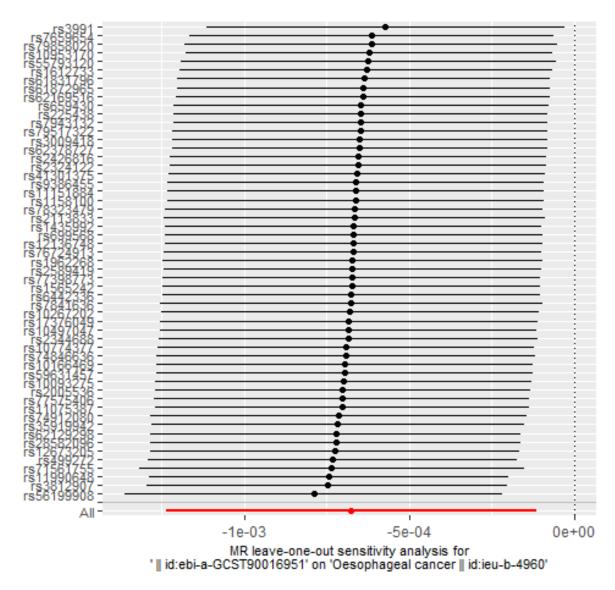
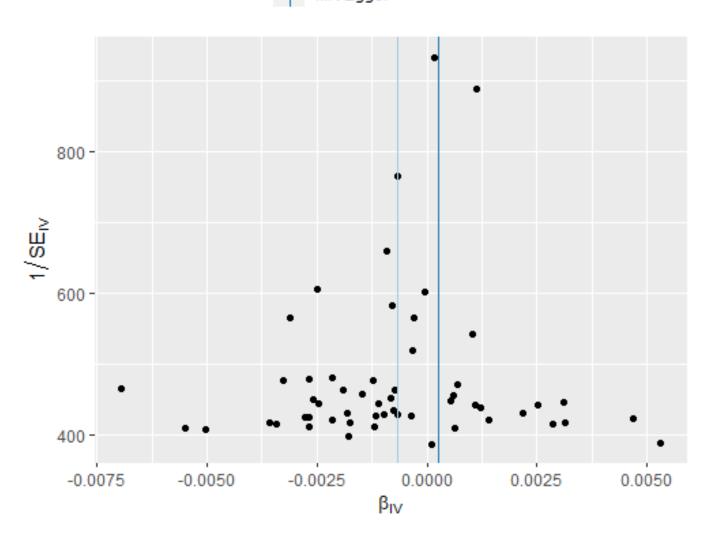
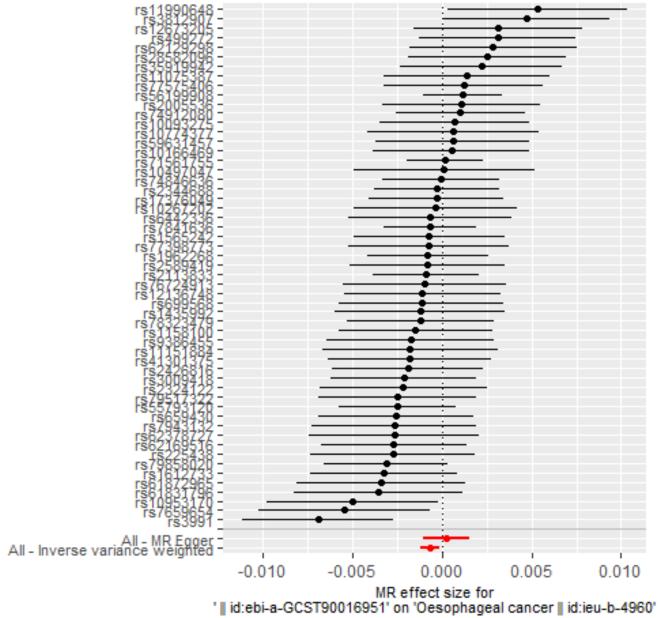


Figure 15 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Ruminococcaceae id.2050) on oesophageal cancer



Inverse variance weighted MR Egger





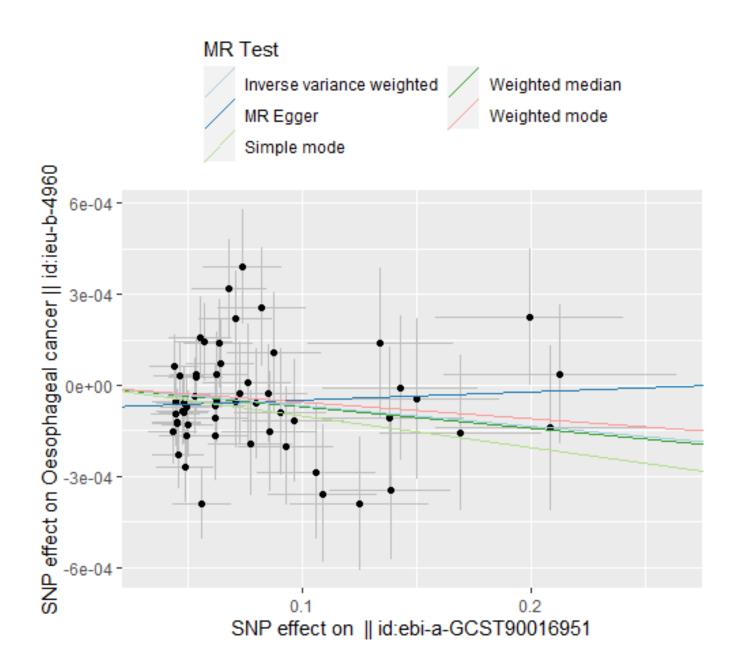
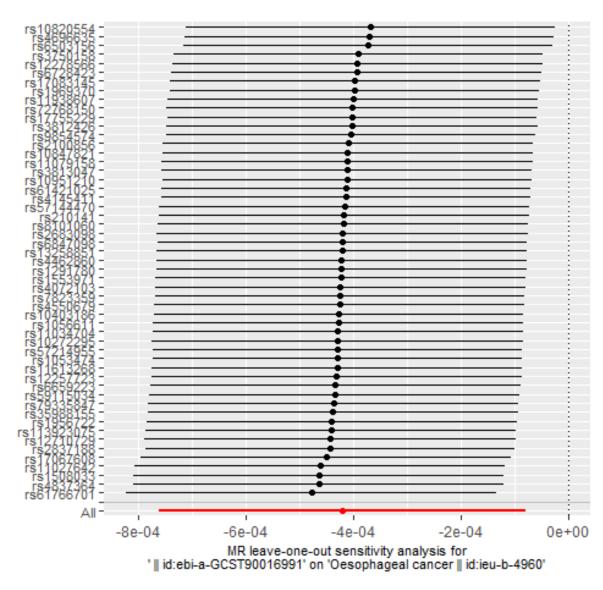
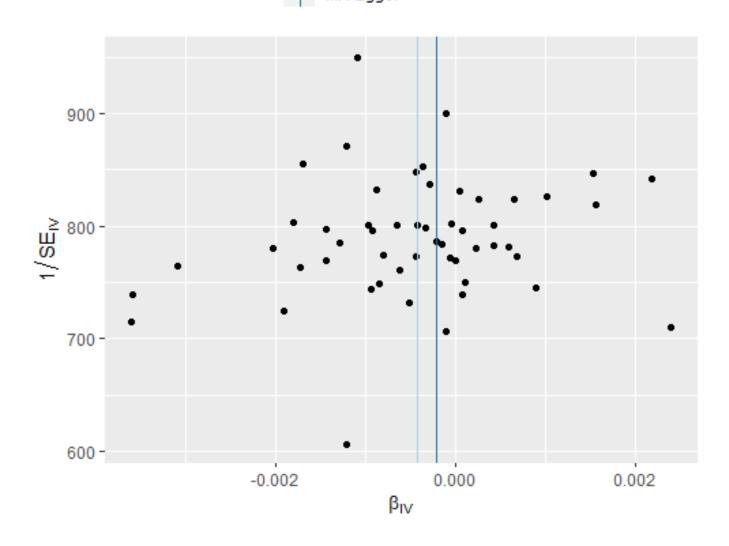
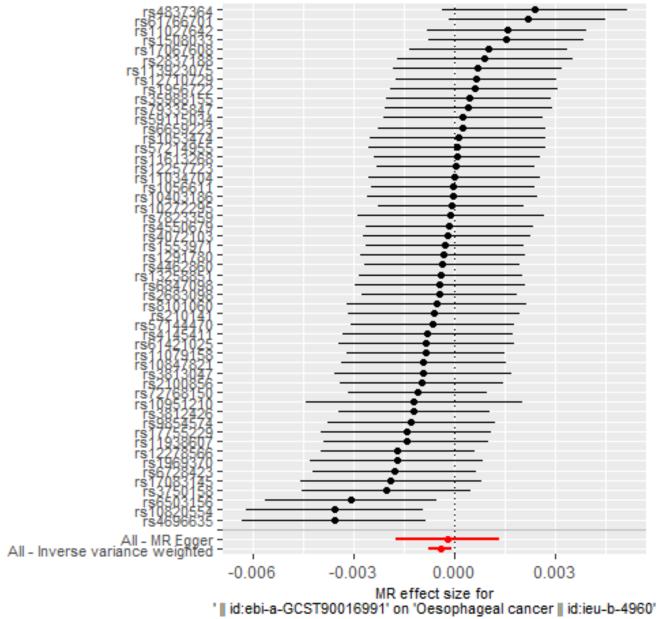


Figure 16 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eisenbergiella id.11304) on oesophageal cancer



MR Method Inverse variance weighted MR Egger





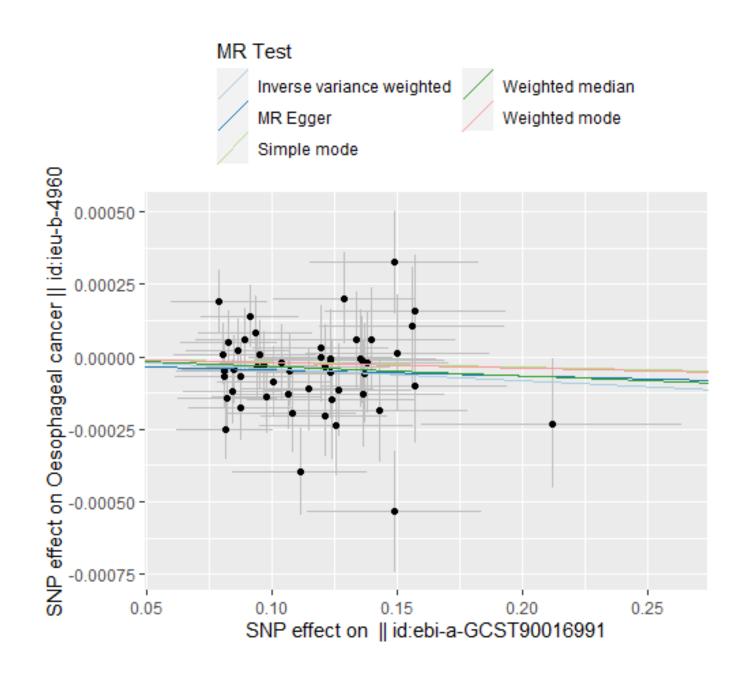
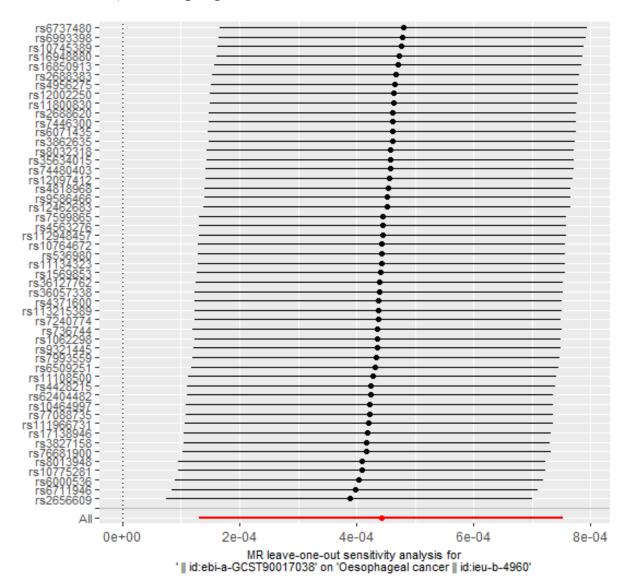
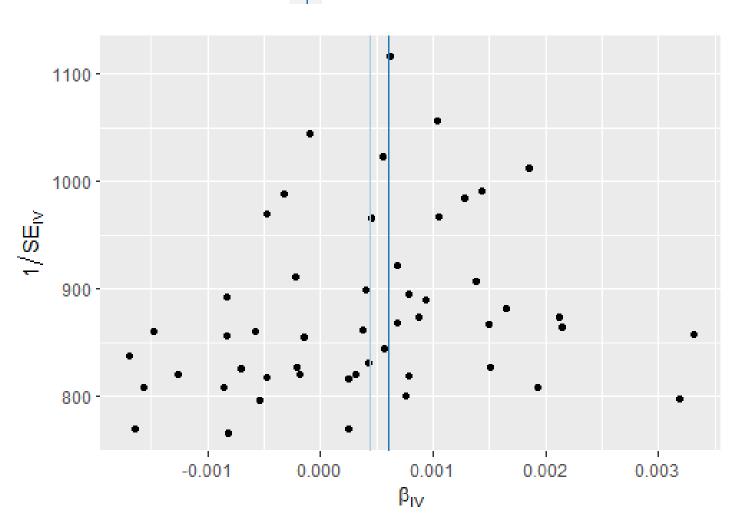
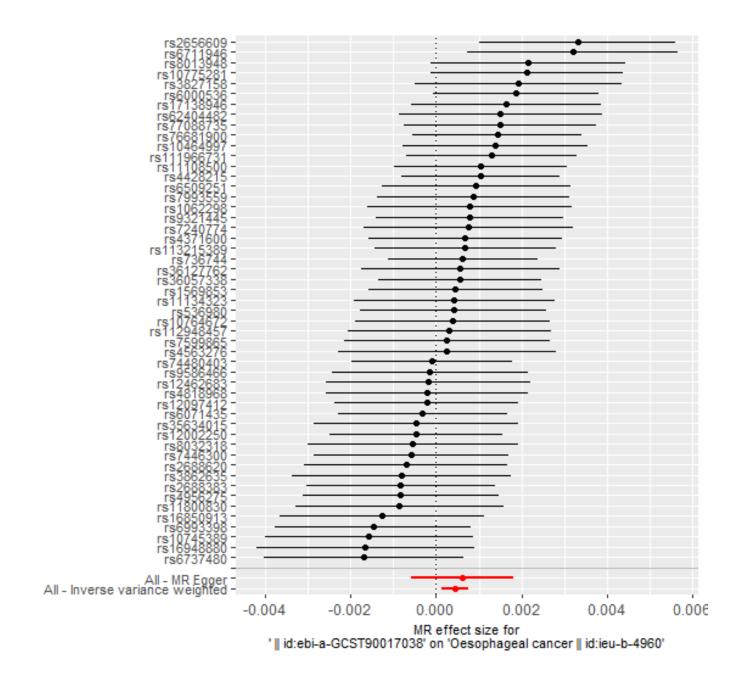


Figure 17 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Oxalobacter id.2978) on oesophageal cancer



Inverse variance weighted MR Egger







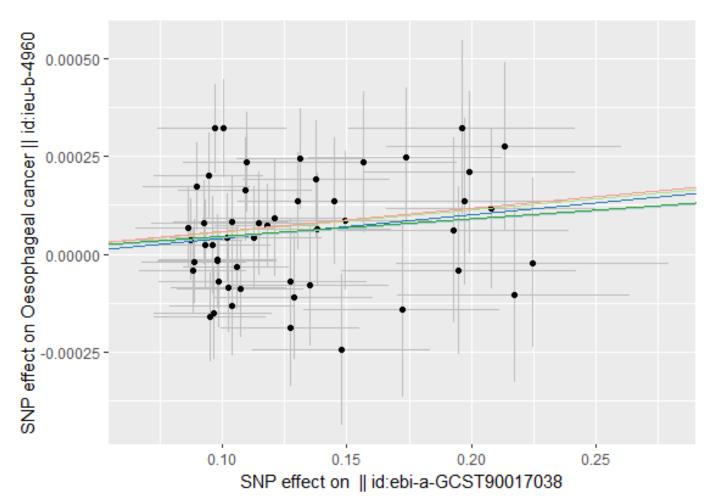
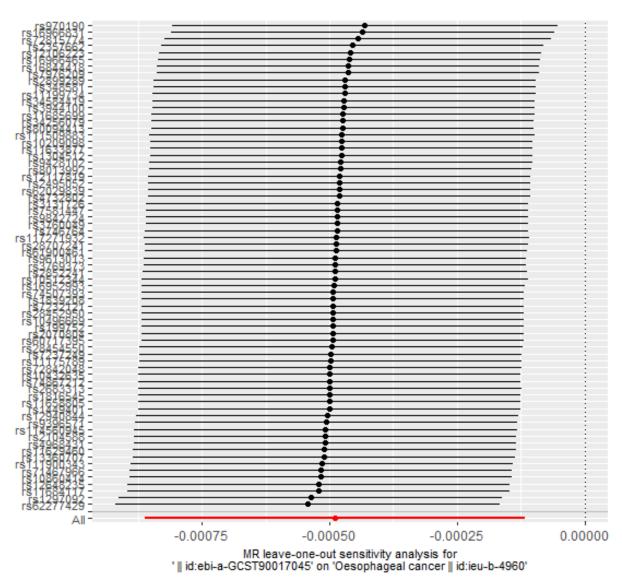
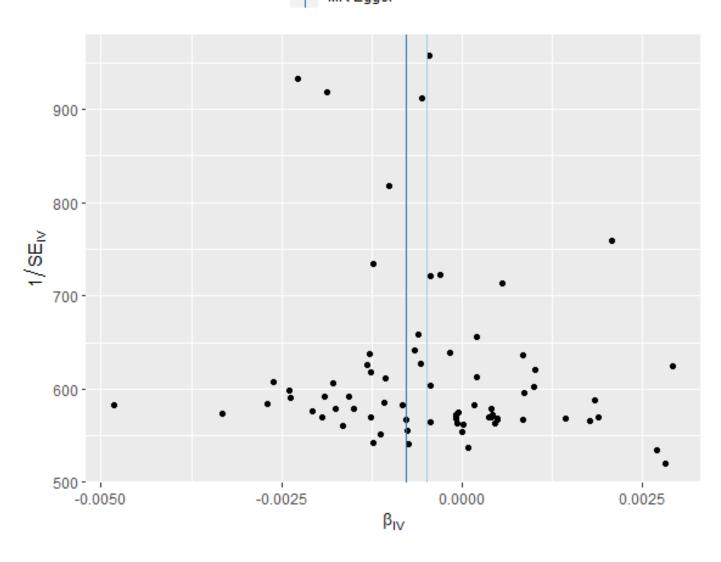
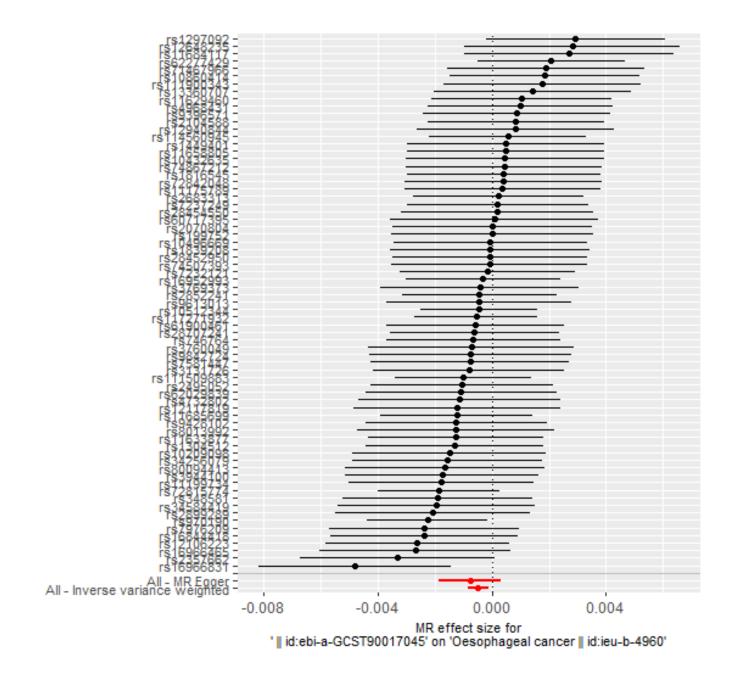


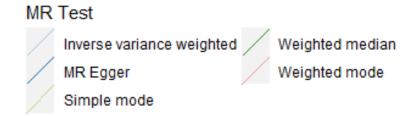
Figure 18 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Prevotella9 id.11183) on oesophageal cancer



MR Method Inverse variance weighted MR Egger







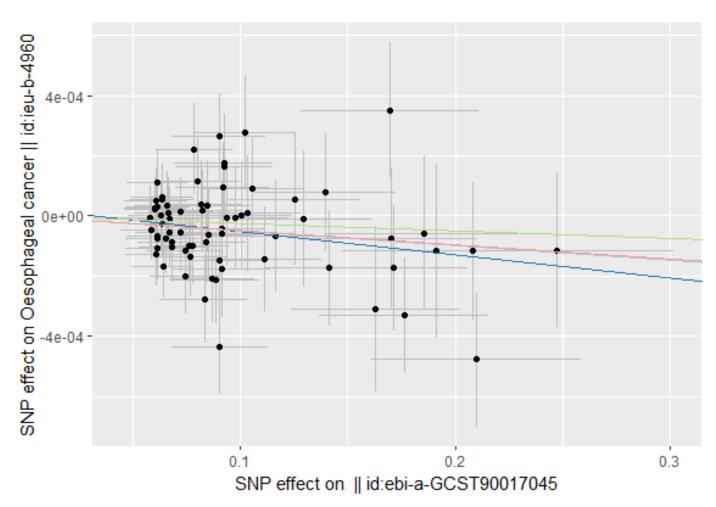
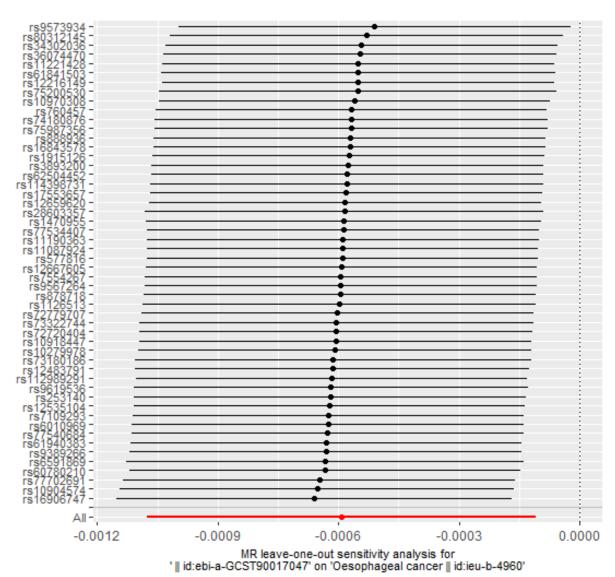
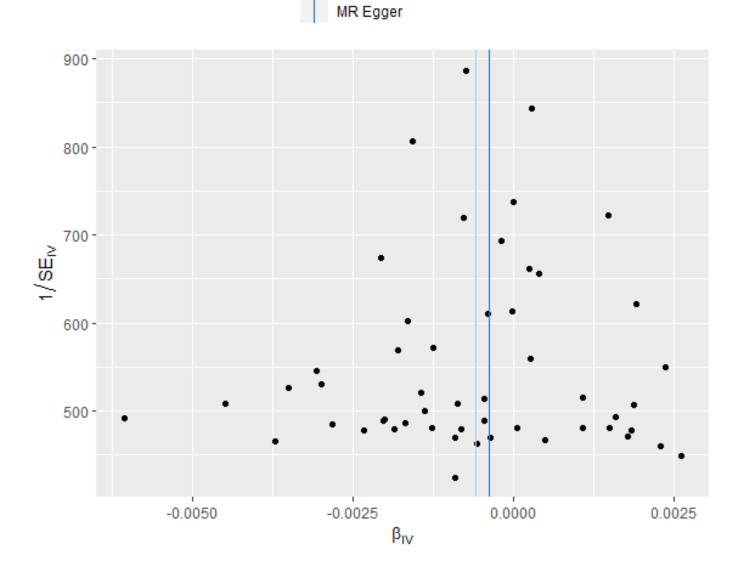
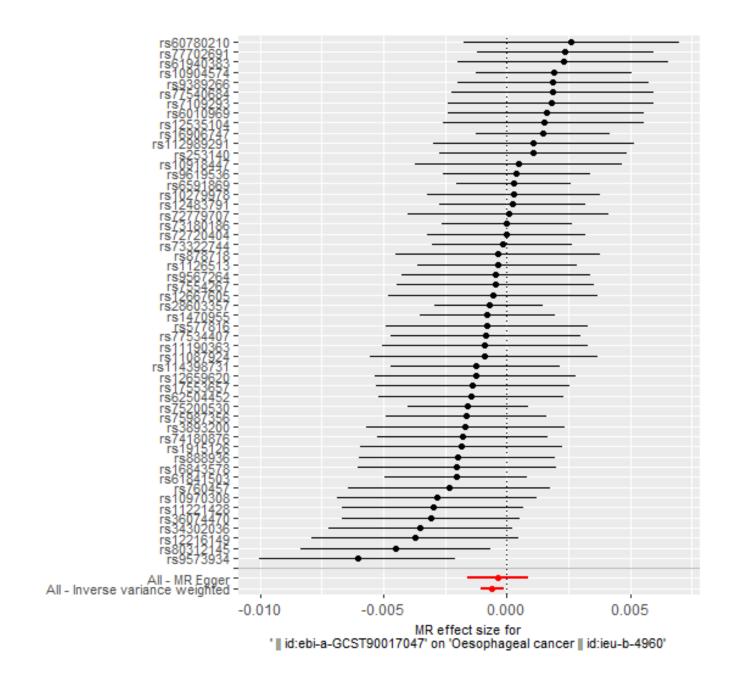


Figure 19 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Romboutsia id.11347) on oesophageal cancer



MR Method Inverse variance weighted







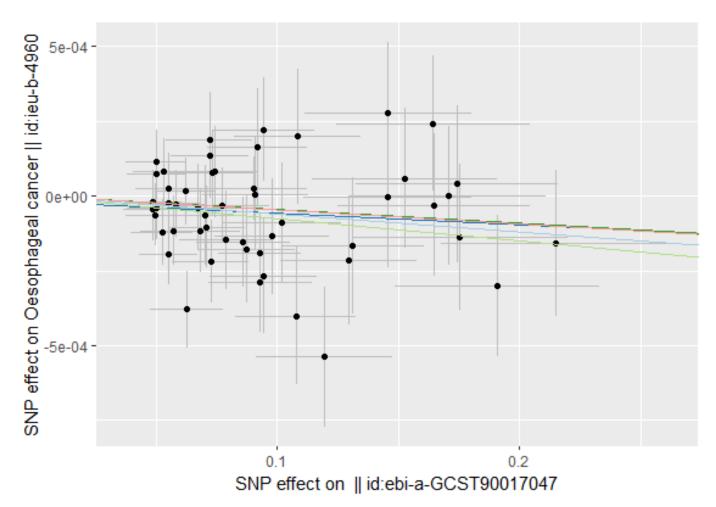
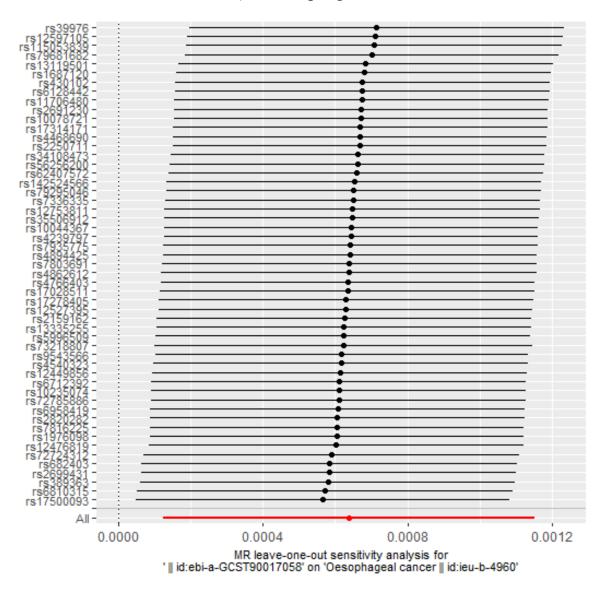
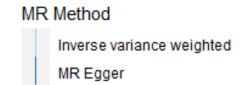
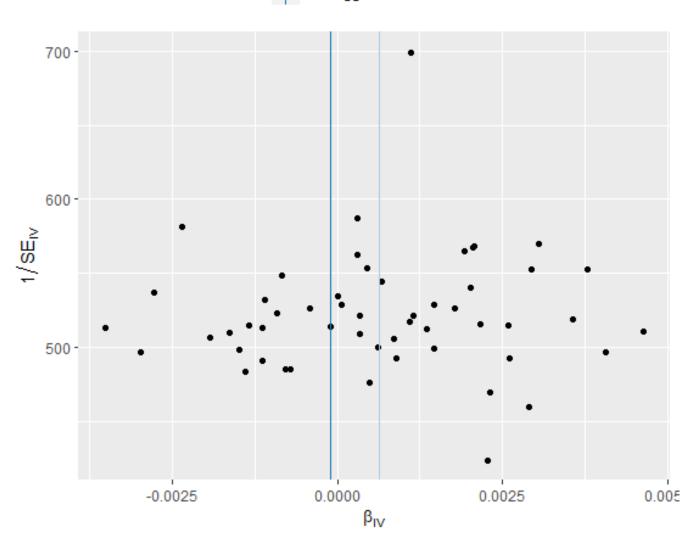
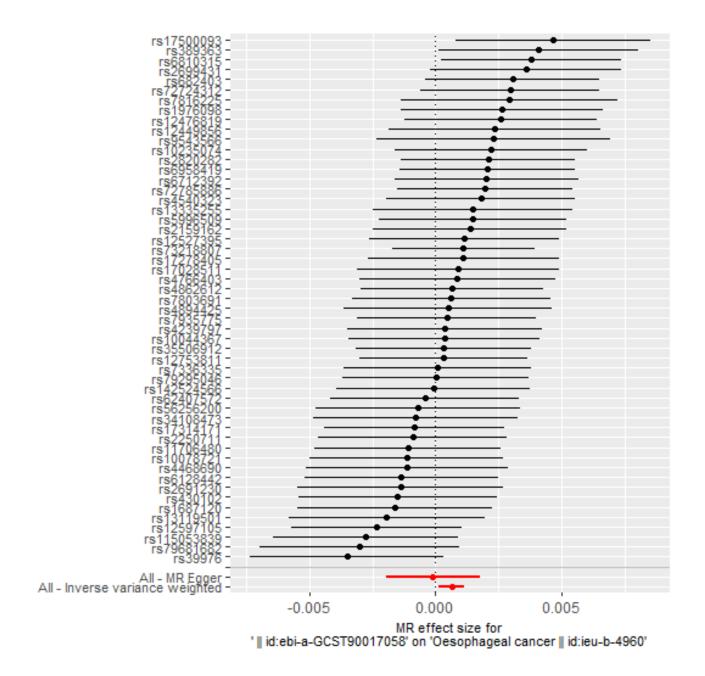


Figure 20 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG010 id.11367) on oesophageal cancer











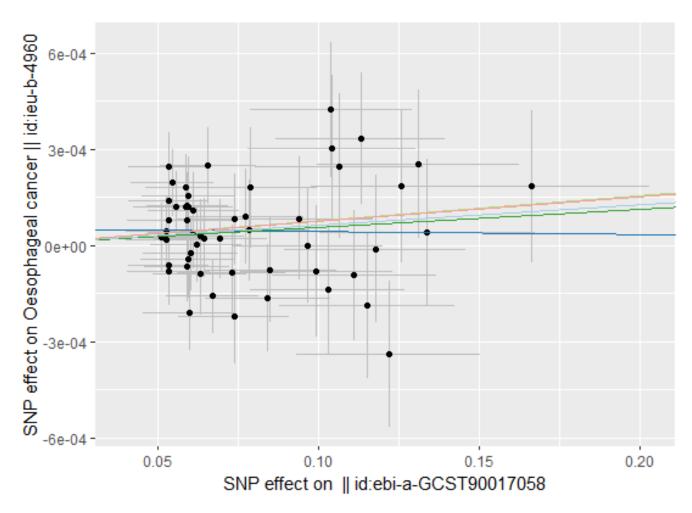
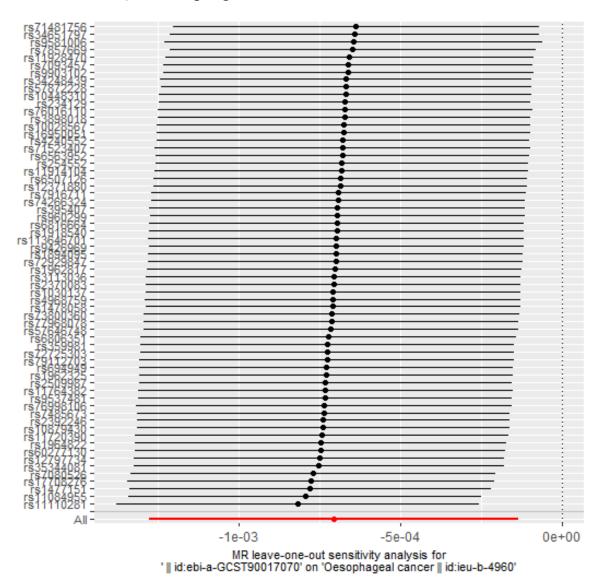


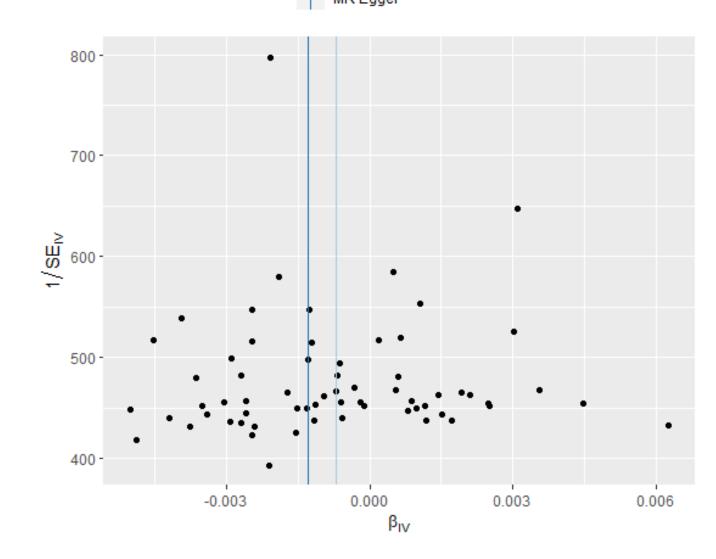
Figure 21 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Streptococcus id.1853) on oesophageal cancer

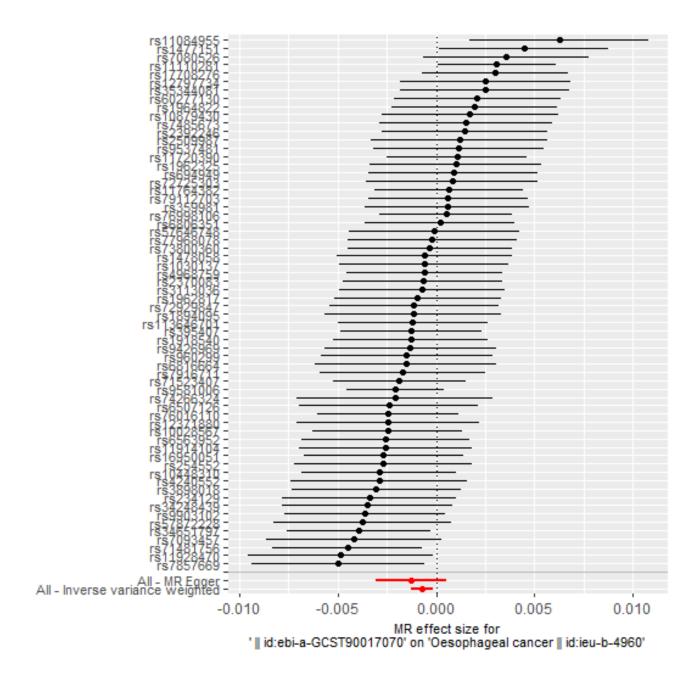


MR Method

Inverse variance weighted

MR Egger







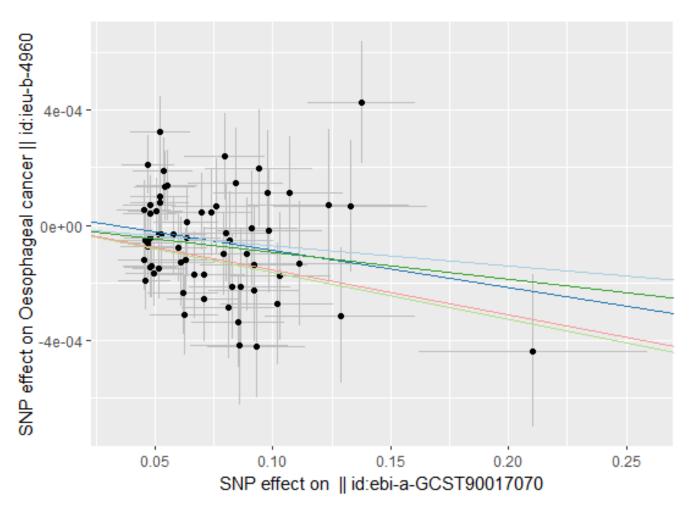
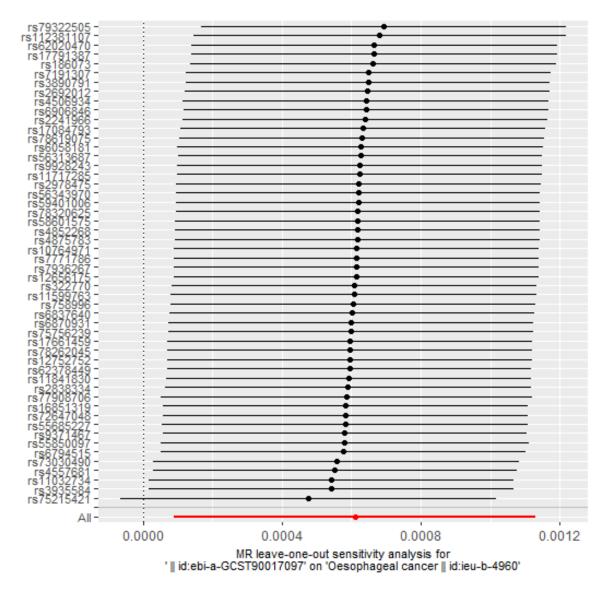


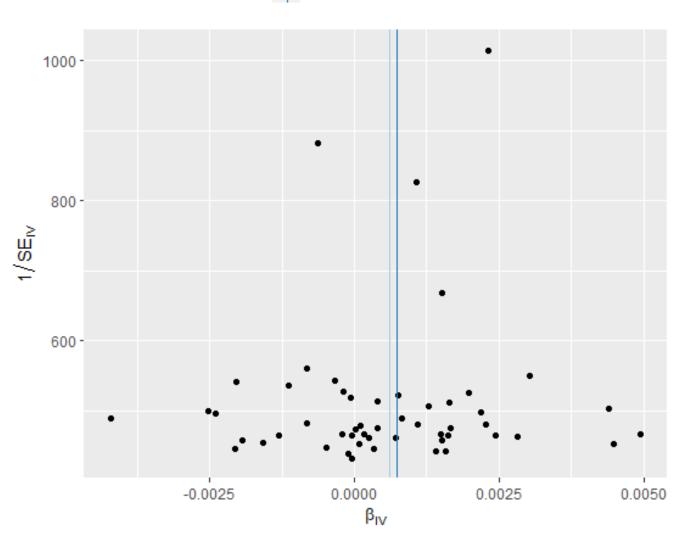
Figure 22 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Desulfovibrionales id.3156) on oesophageal cancer

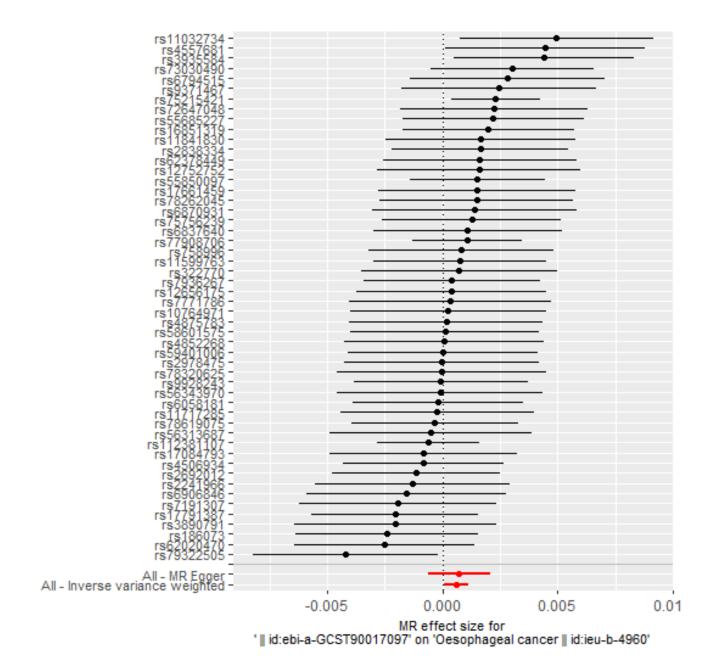


MR Method

Inverse variance weighted

MR Egger







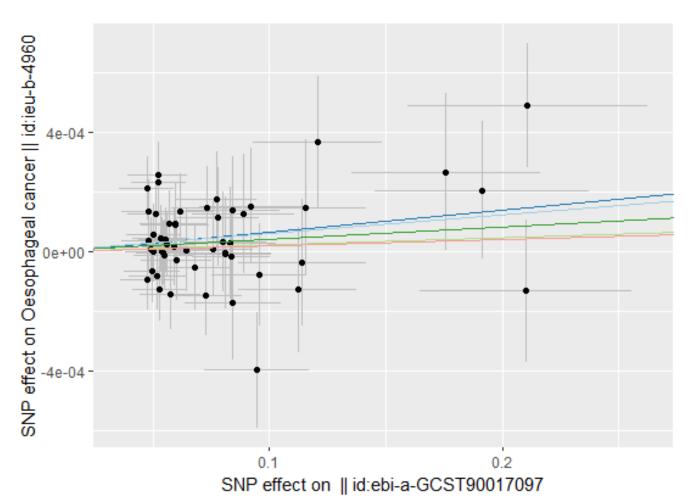
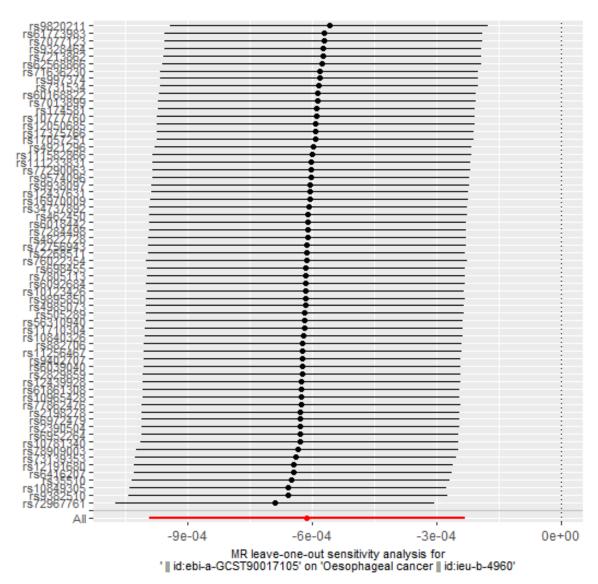
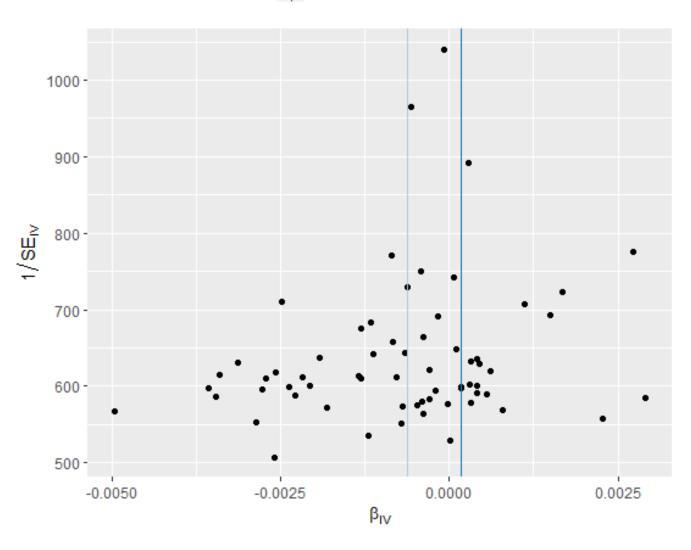


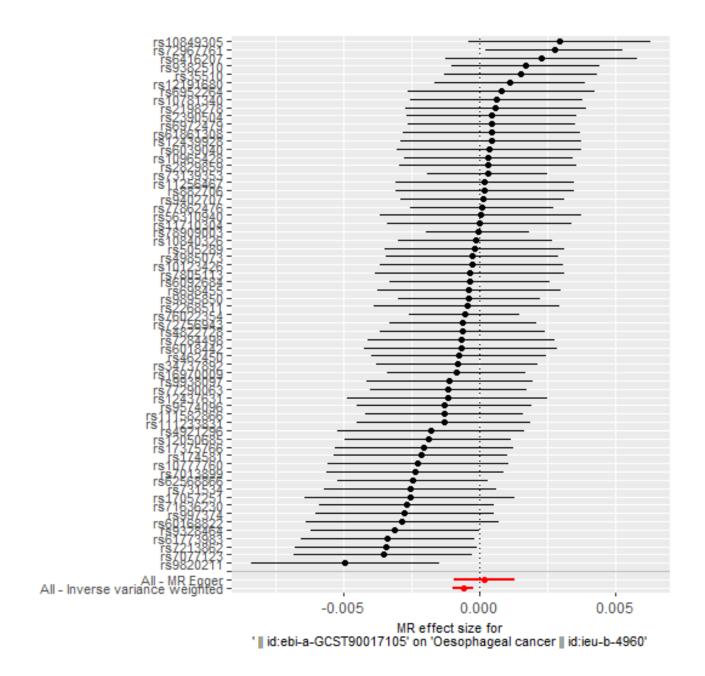
Figure 23 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Pasteurellales id.3688) on oesophageal cancer



MR Method Inverse variance weighted

MR Egger







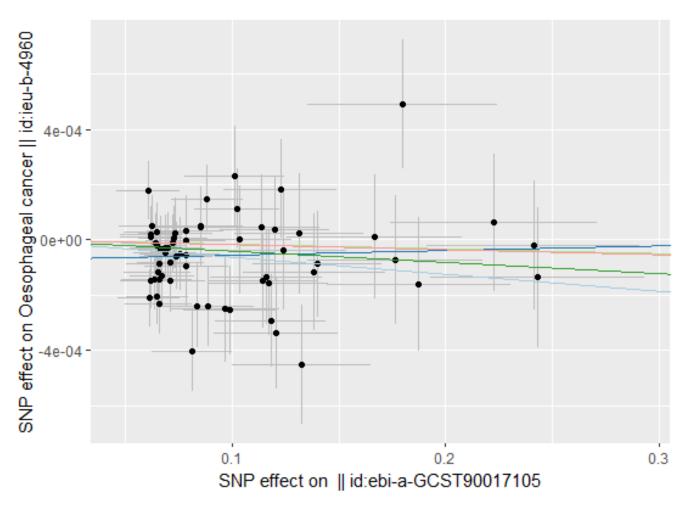
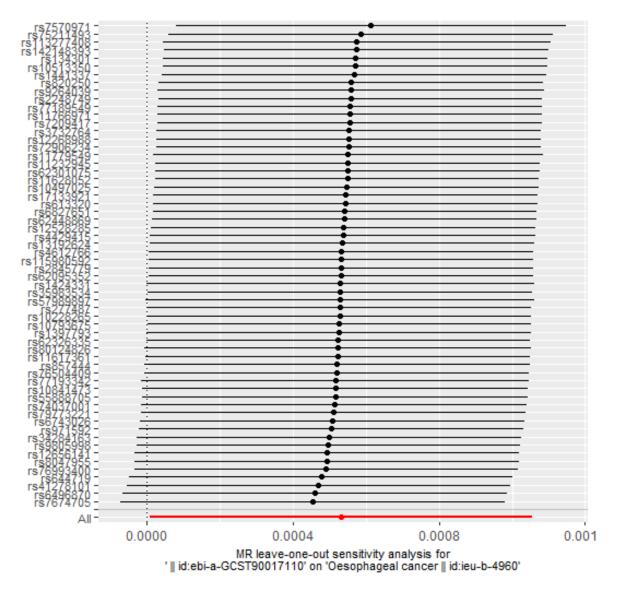


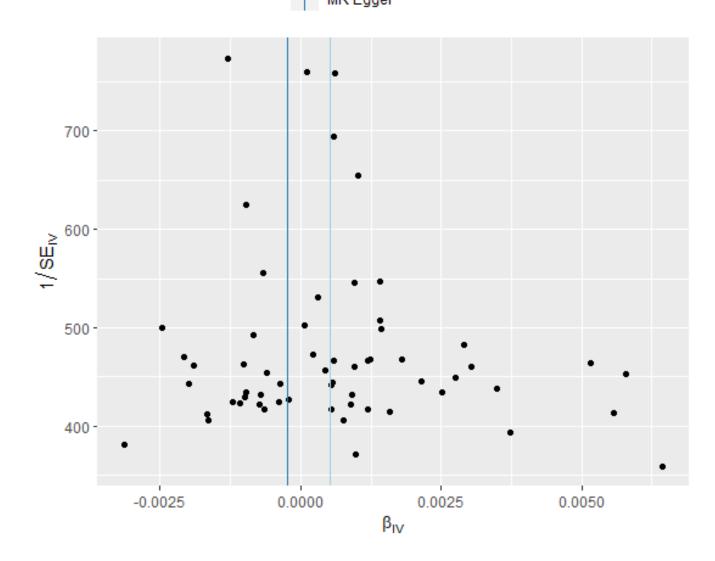
Figure 24 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Actinobacteria id.400) on oesophageal cancer

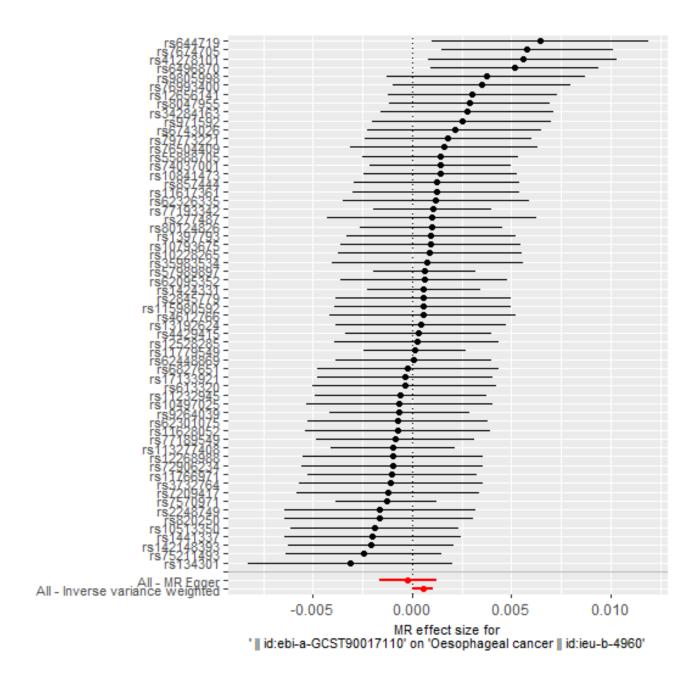


MR Method

Inverse variance weighted

MR Egger







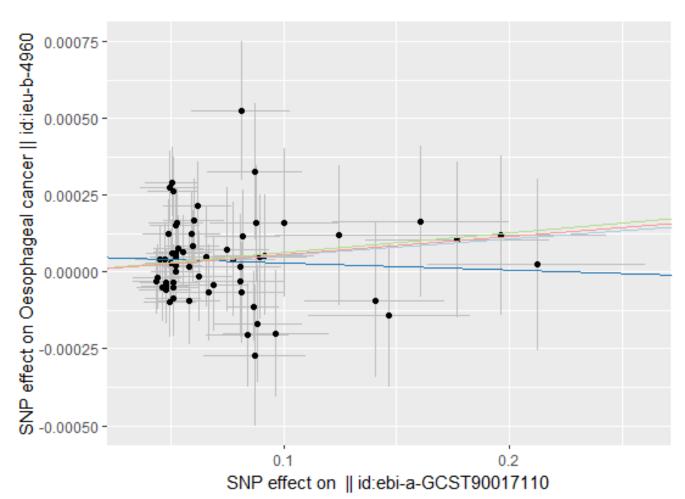
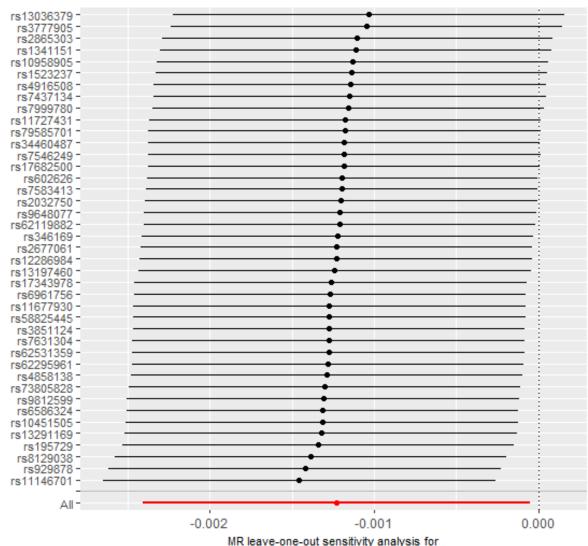
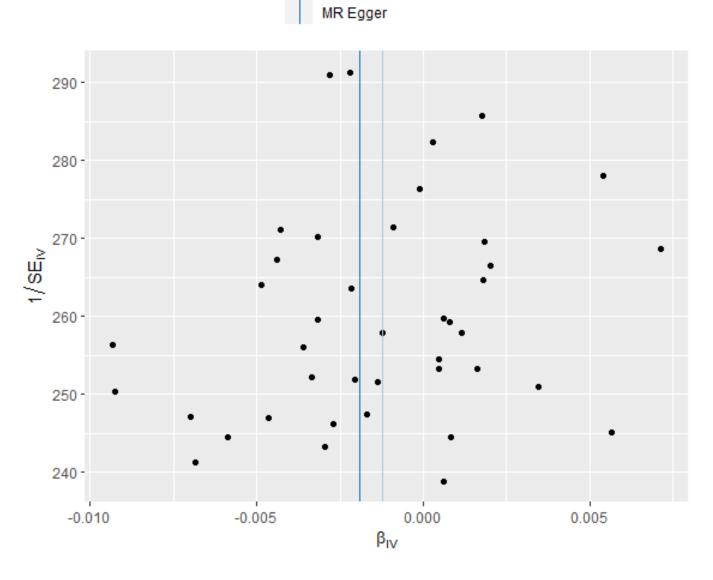


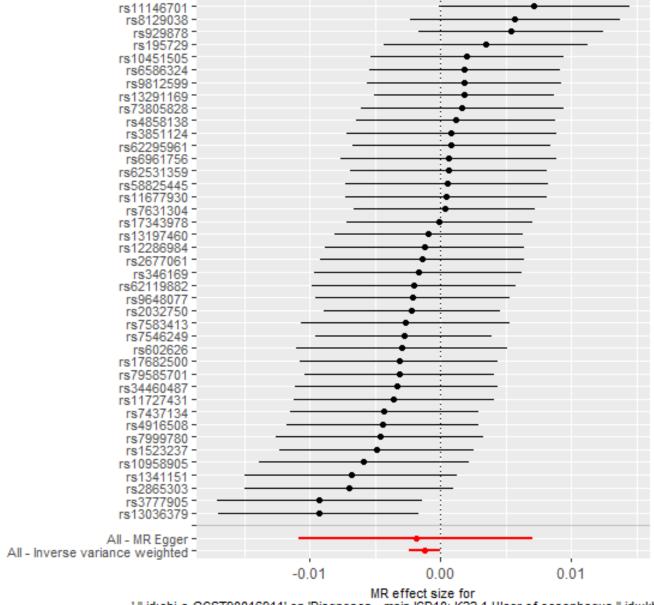
Figure 25 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Bacteroidia id.912) on ulcer of oesophagus



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016911' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus || id:ukb-b-13731'

MR Method Inverse variance weighted





" id:ebi-a-GCST90016911" on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus | id:ukb

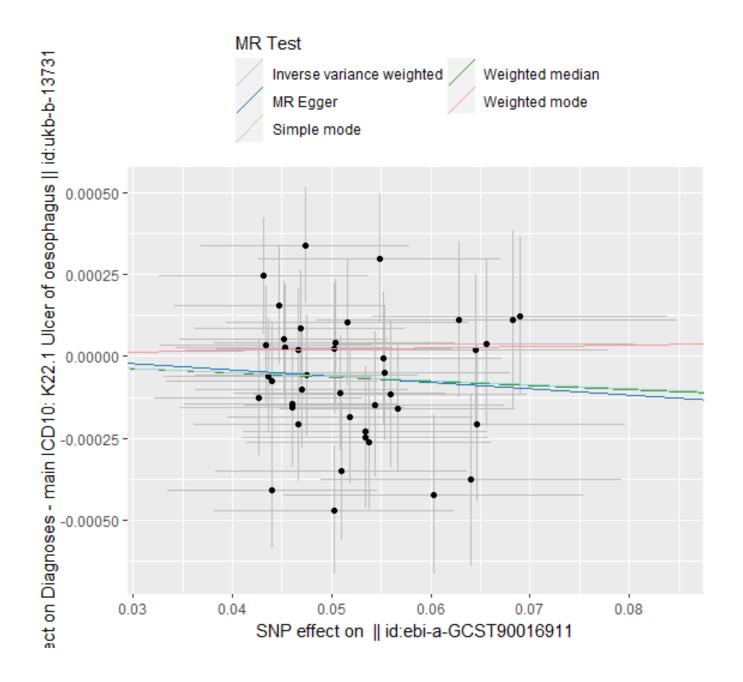
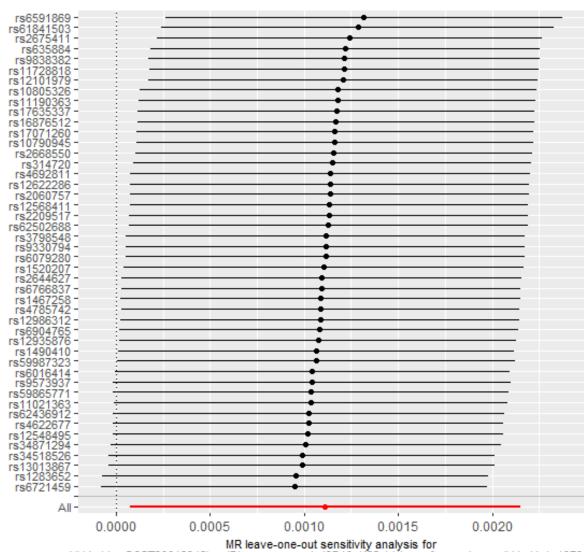
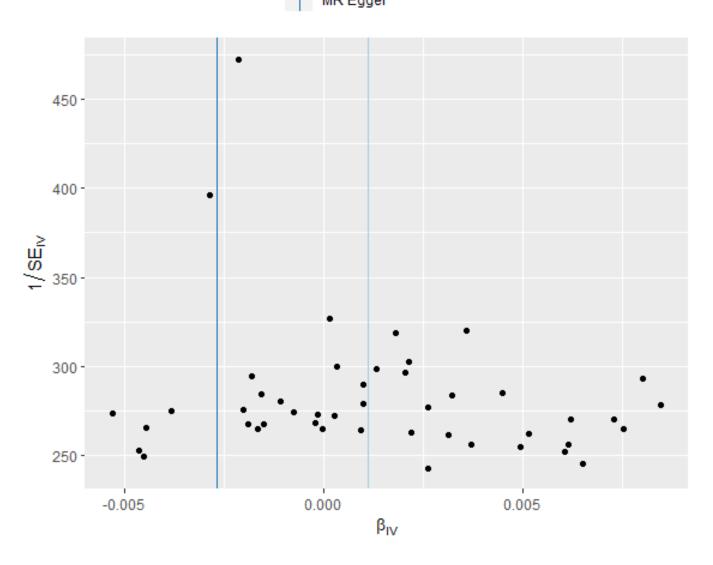


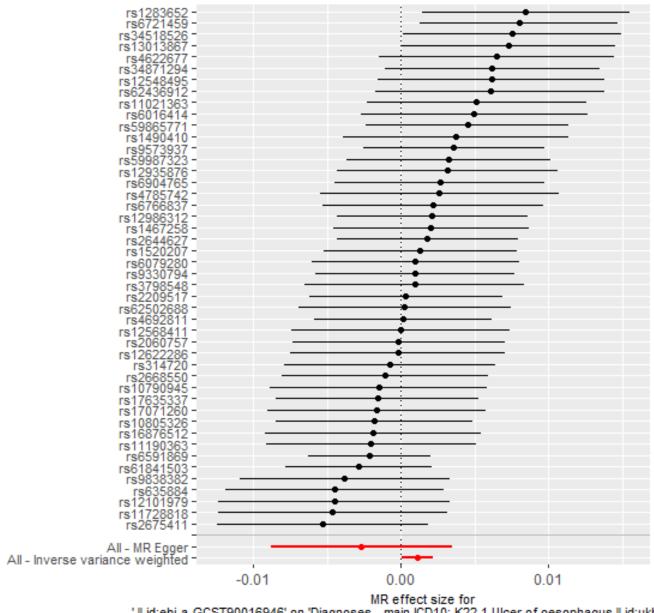
Figure 26 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Peptostreptococcaceae id.2042) on ulcer of oesophagus



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016946' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus || id:ukb-b-13731'

MR Method Inverse variance weighted MR Egger





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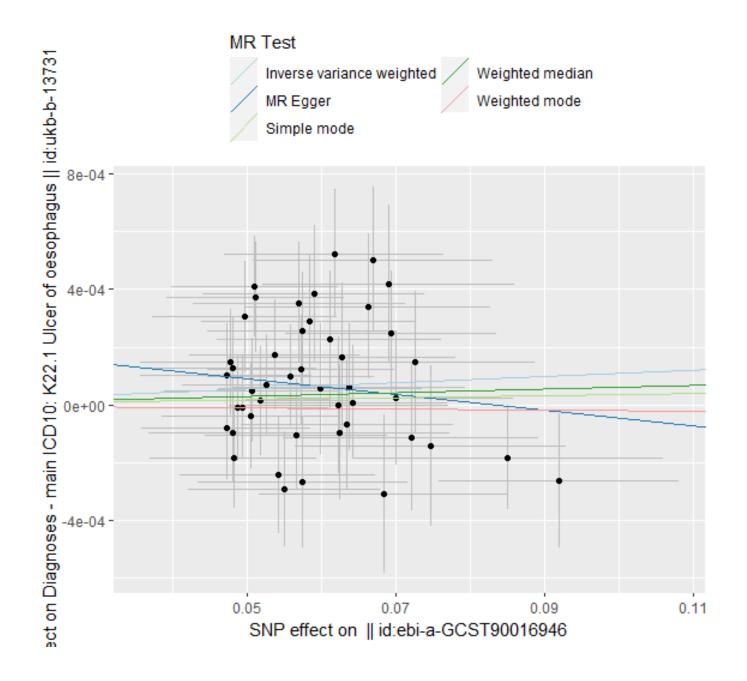
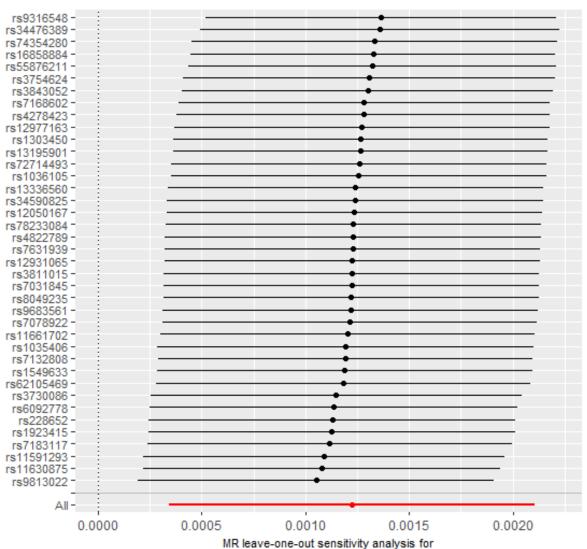


Figure 27 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Rhodospirillaceae id.2717) on ulcer of oesophagus

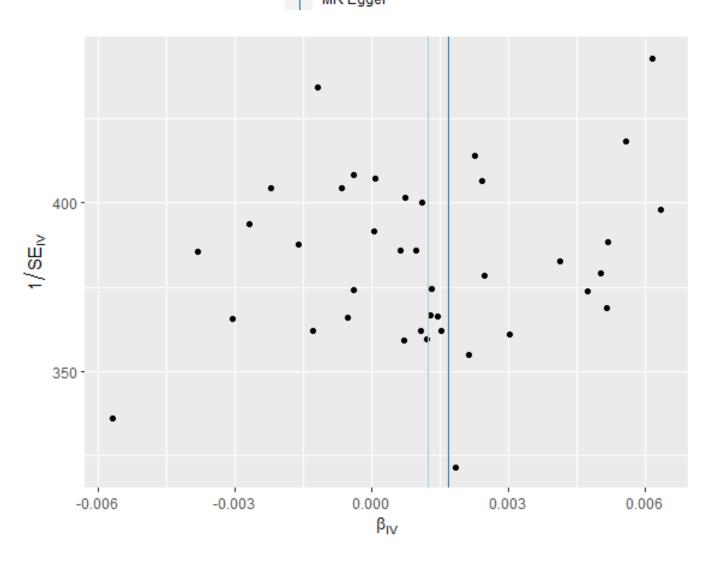


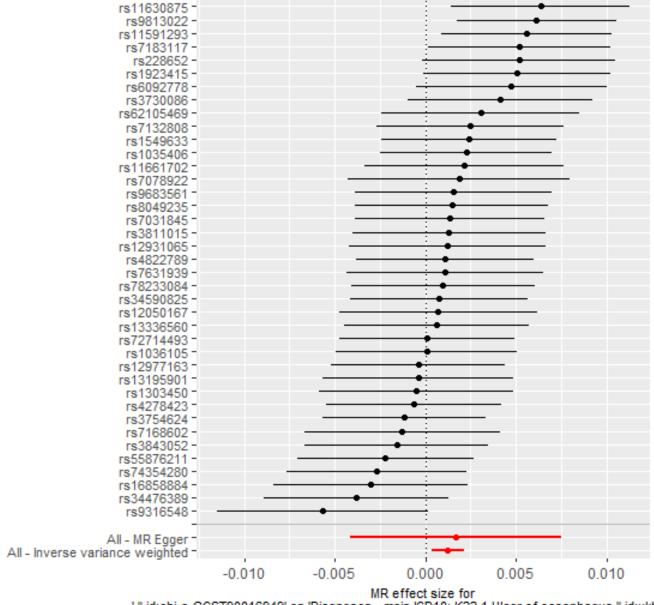
MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016949' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus || id:ukb-b-13731'

MR Method

Inverse variance weighted

MR Egger





" id:ebi-a-GCST90016949" on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus | id:ukb

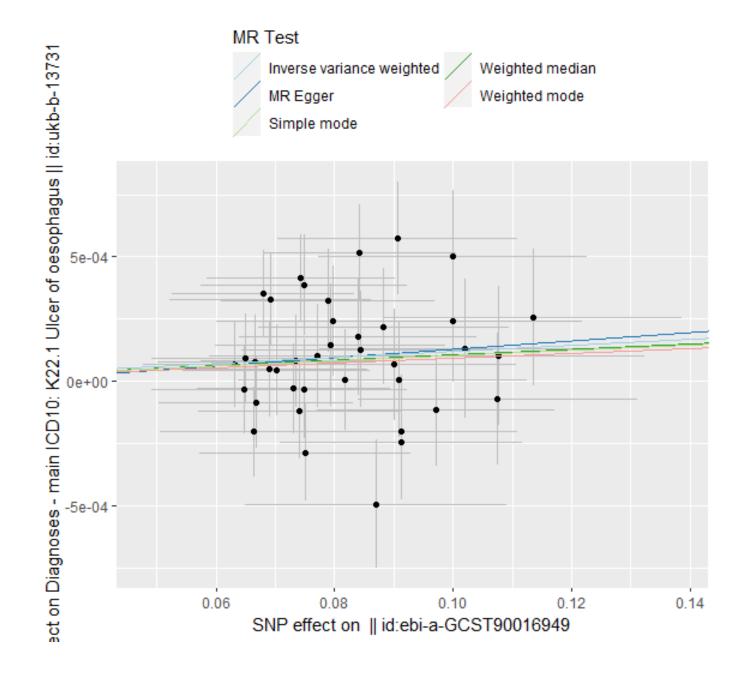
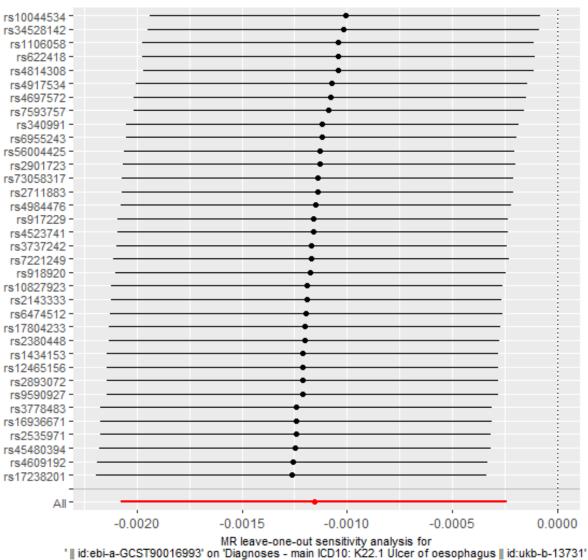
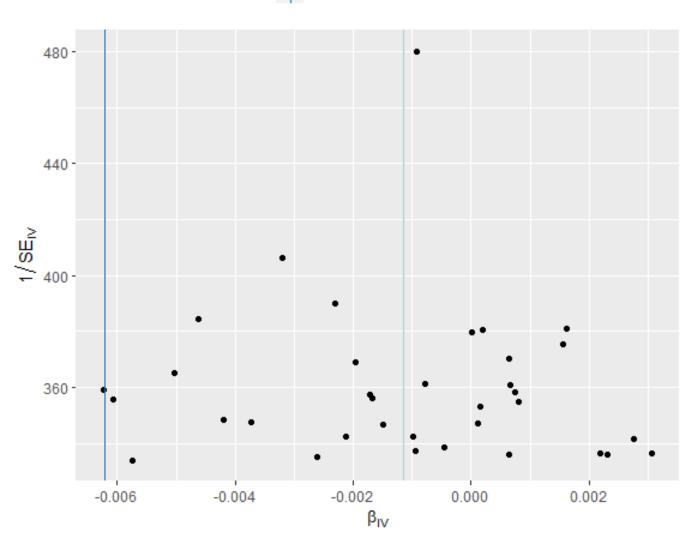


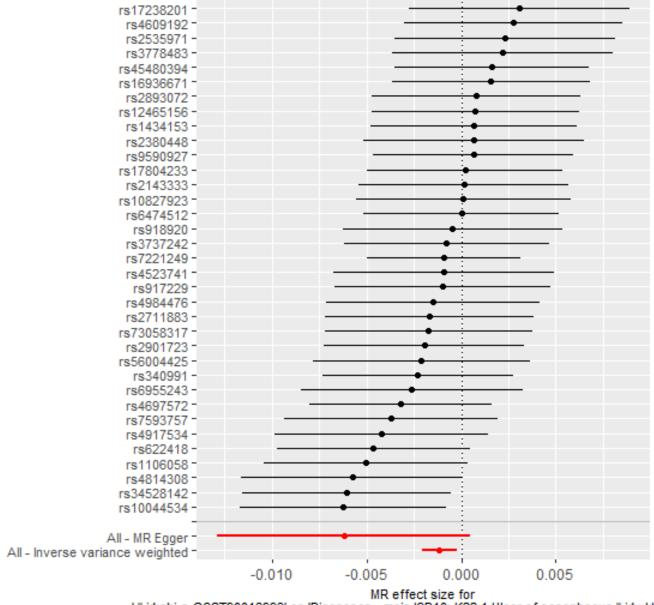
Figure 28 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Erysipelatoclostridium id.11381) on ulcer of oesophagus



MR Method Inverse variance weighted

MR Egger





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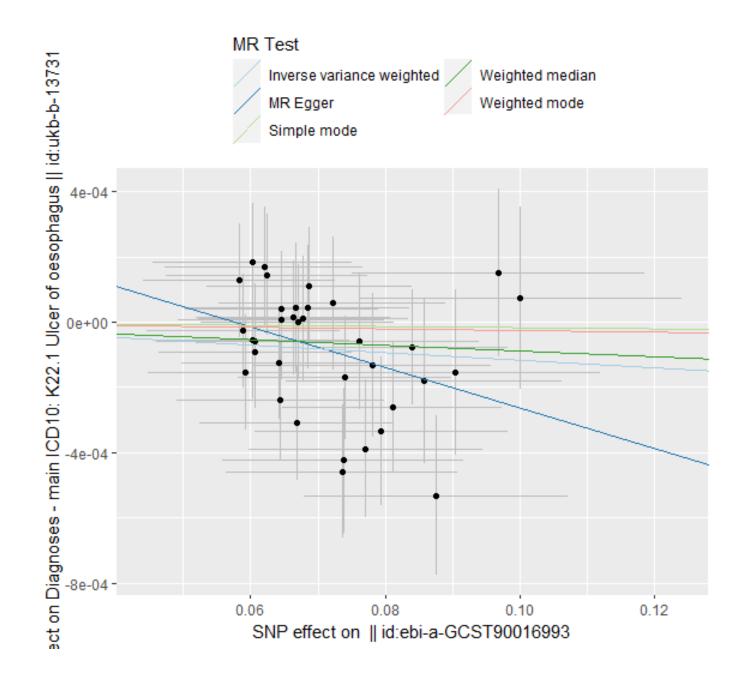
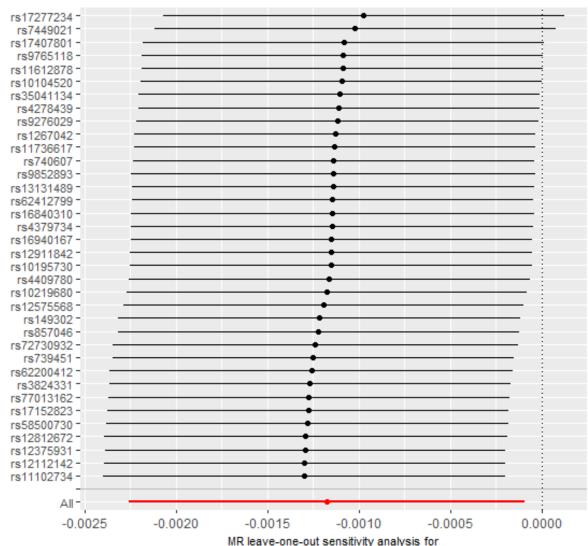


Figure 29 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Family XIII AD3011 group id.11293) on ulcer of oesophagus

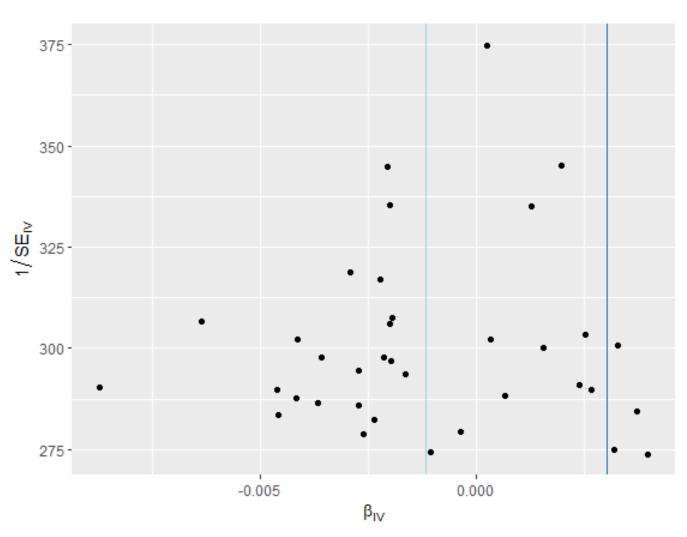


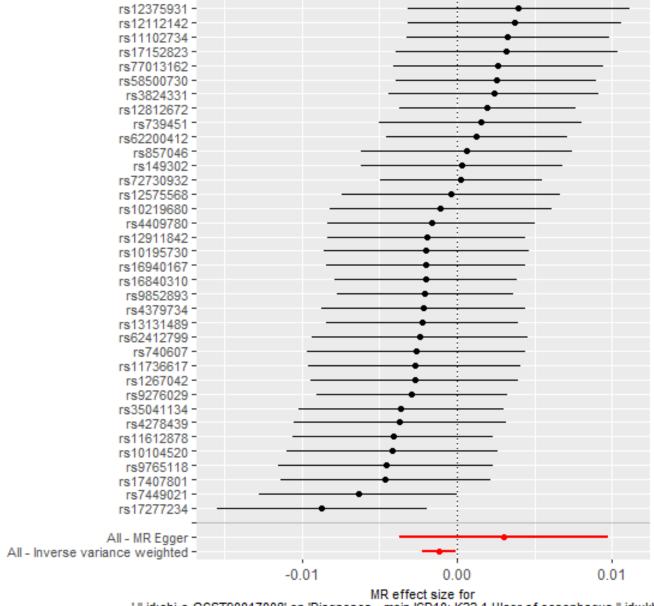
MR leave-one-out sensitivity analysis for ' ∥ id:ebi-a-GCST90017008' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus ∥ id:ukb-b-13731'

MR Method

Inverse variance weighted







" id:ebi-a-GCST90017008" on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus | id:ukb

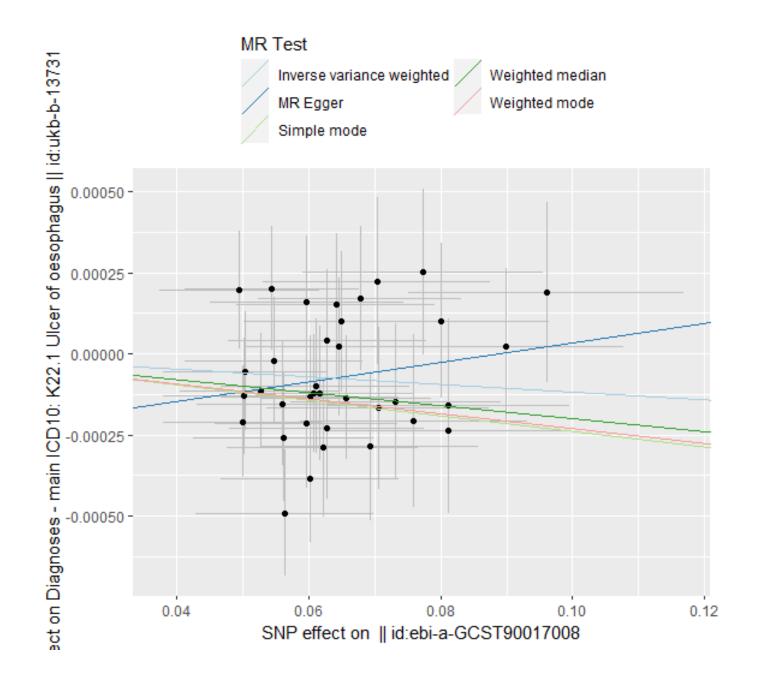
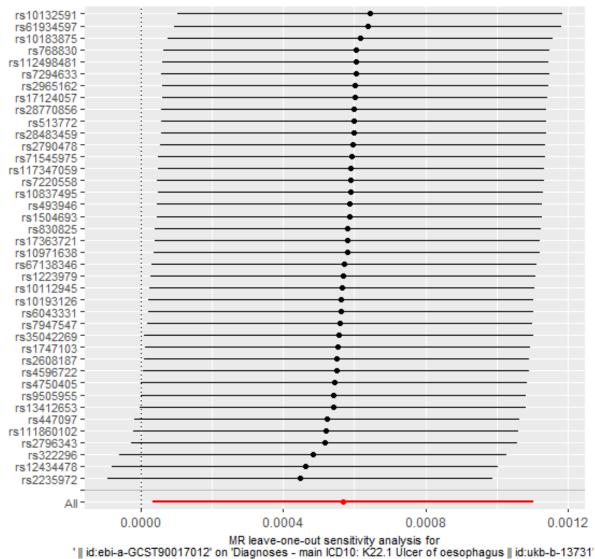


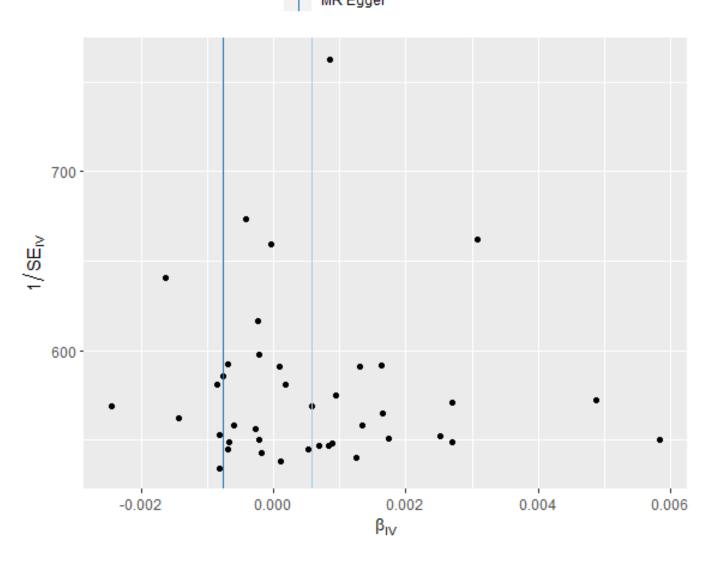
Figure 30 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Gordonibacter id.821) on ulcer of oesophagus

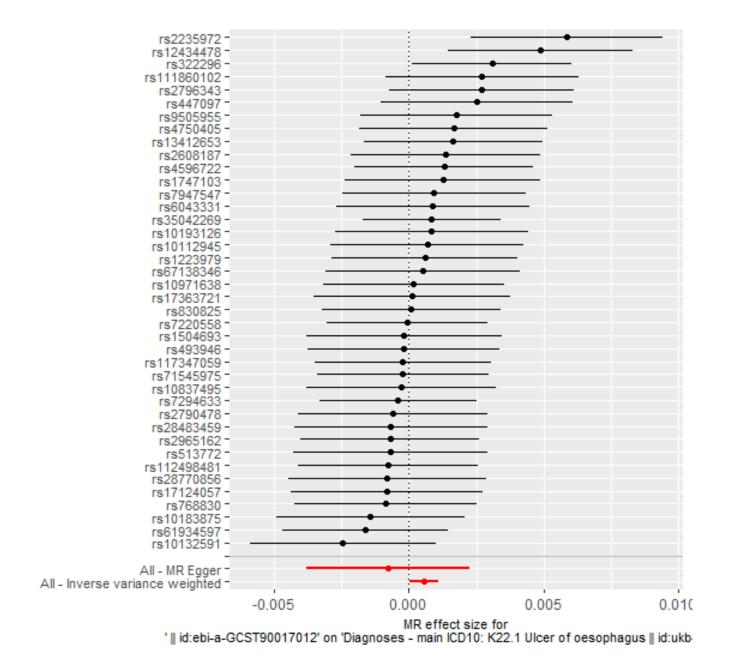


MR Method

Inverse variance weighted

MR Egger





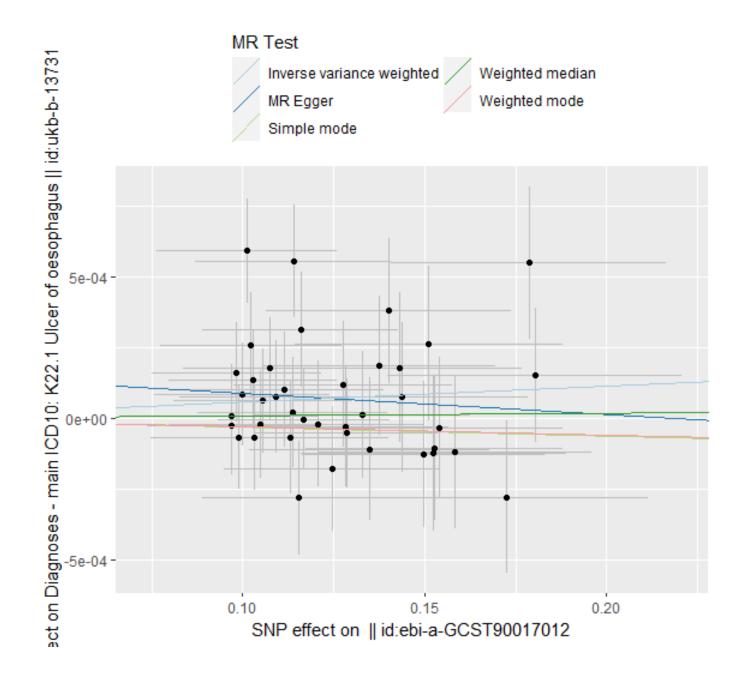
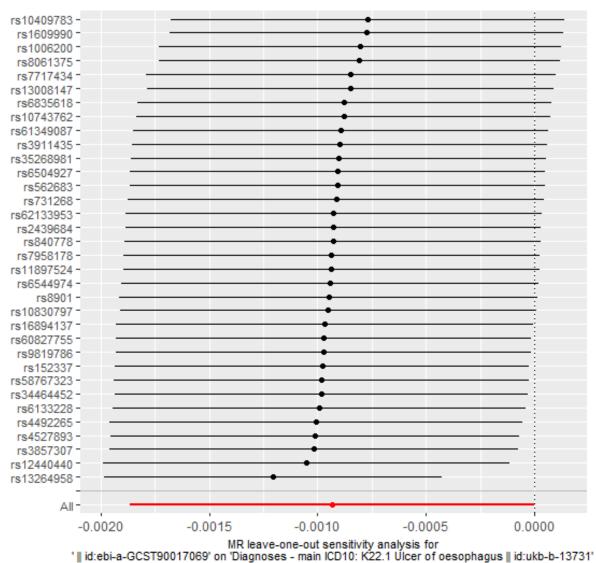
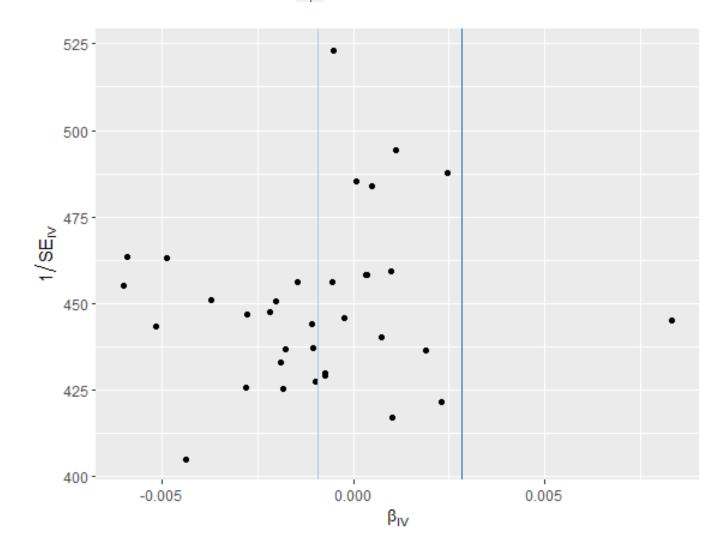


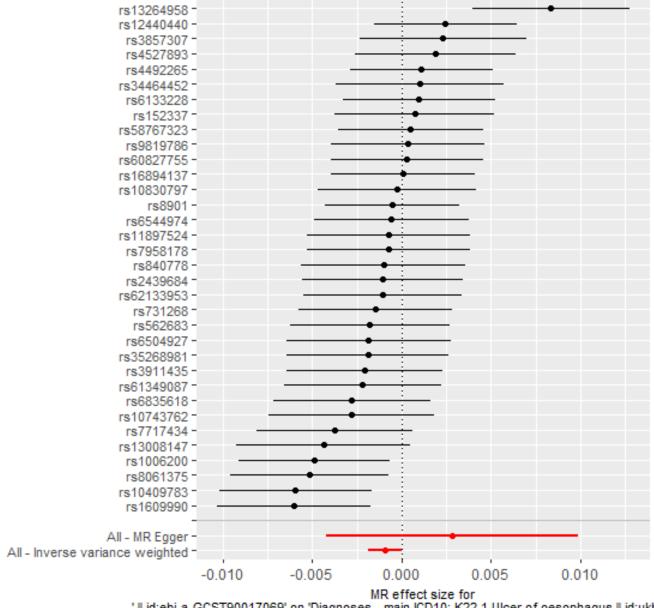
Figure 31 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Slackia id.825) on ulcer of oesophagus



MR Method Inverse variance weighted

MR Egger





" id:ebi-a-GCST90017069" on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus | id:ukb

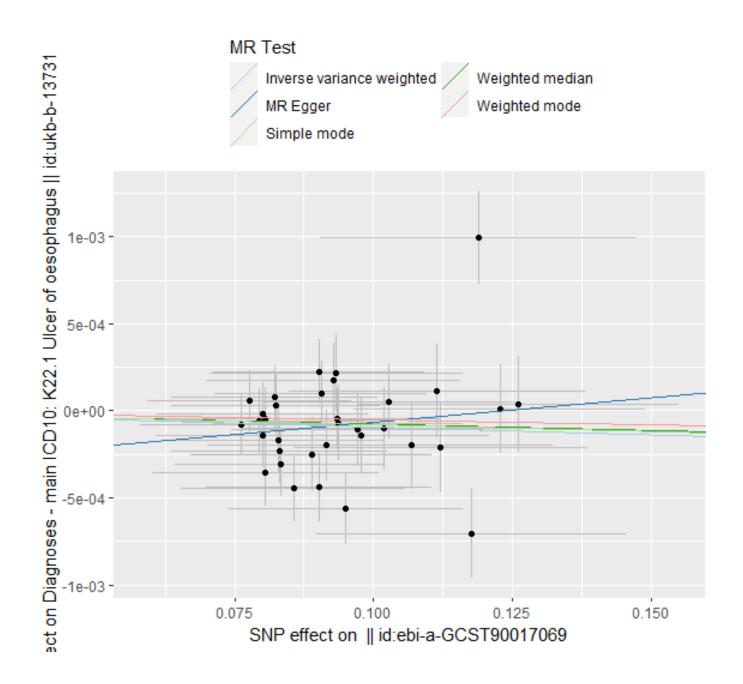
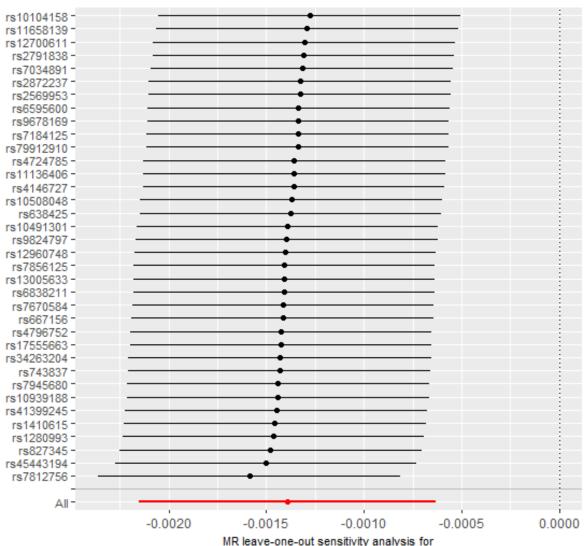


Figure 32 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Terrisporobacter id.11348) on ulcer of oesophagus

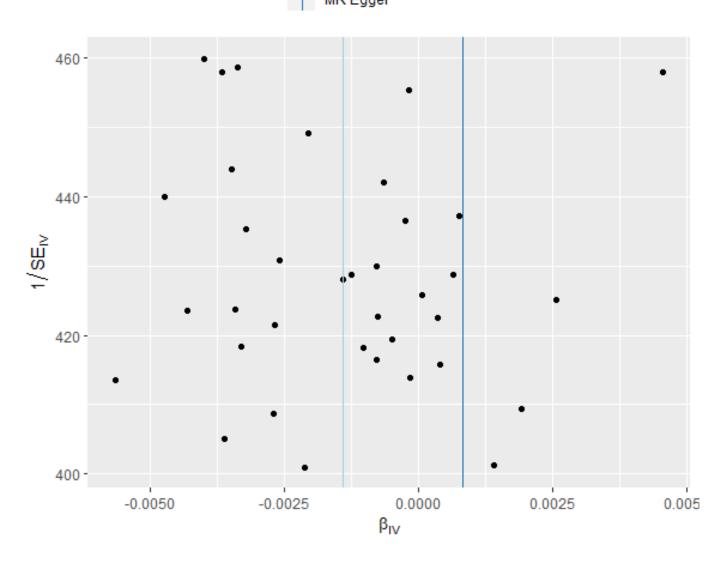


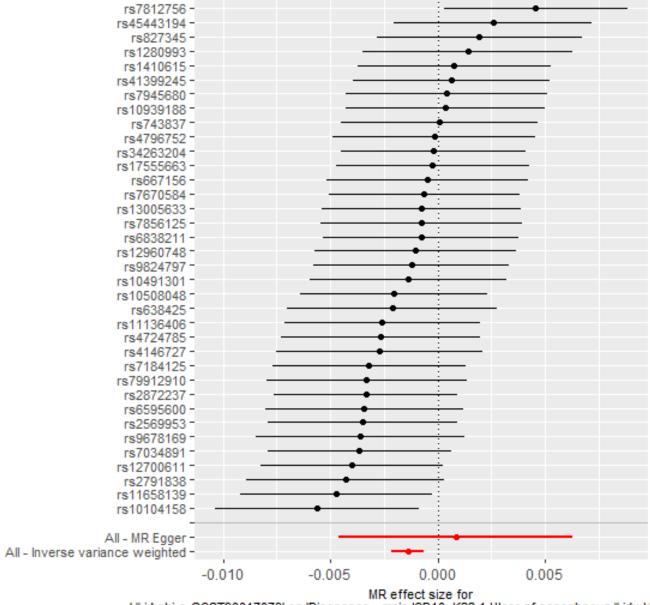
MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017073' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus || id:ukb-b-13731'

MR Method

Inverse variance weighted

MR Egger





' || id:ebi-a-GCST90017073' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus || id:ukb

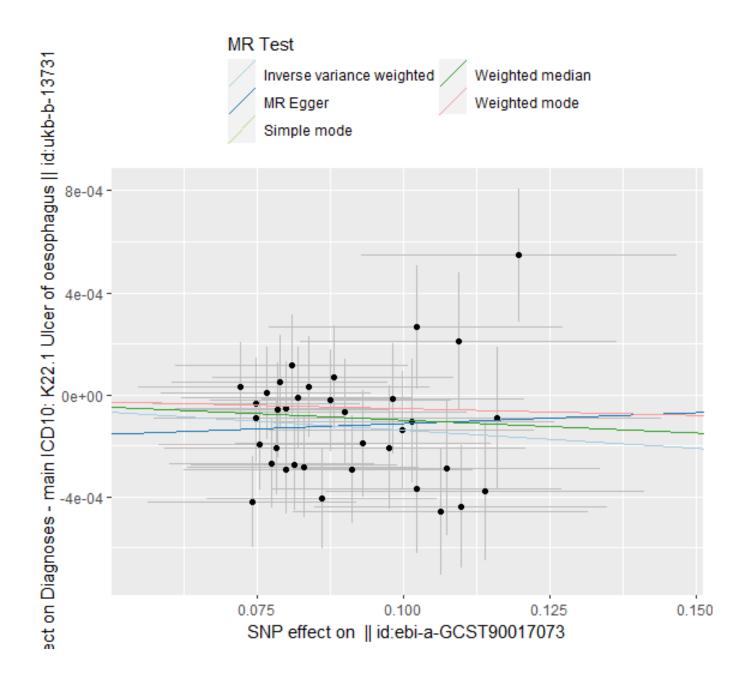
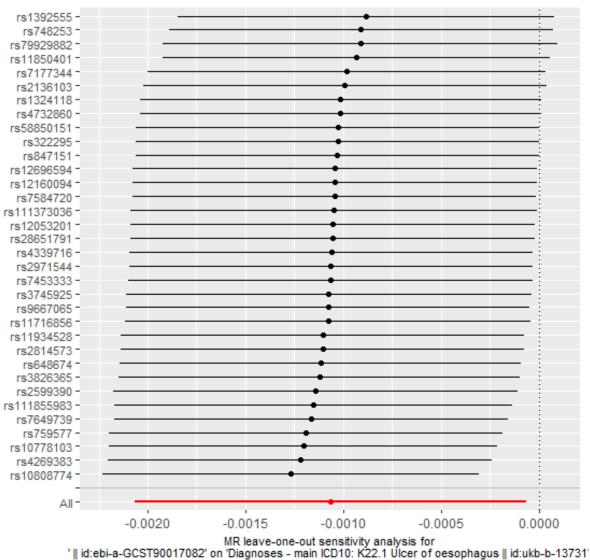
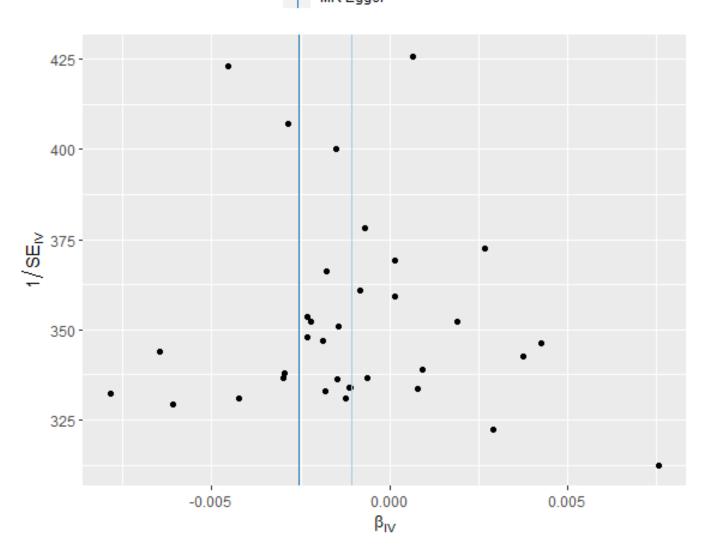


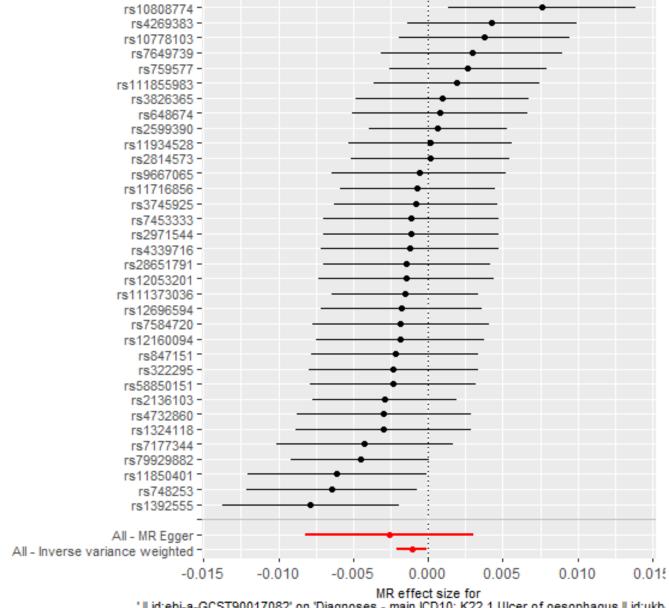
Figure 33 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.2001) on ulcer of oesophagus



MR Method

Inverse variance weighted MR Egger





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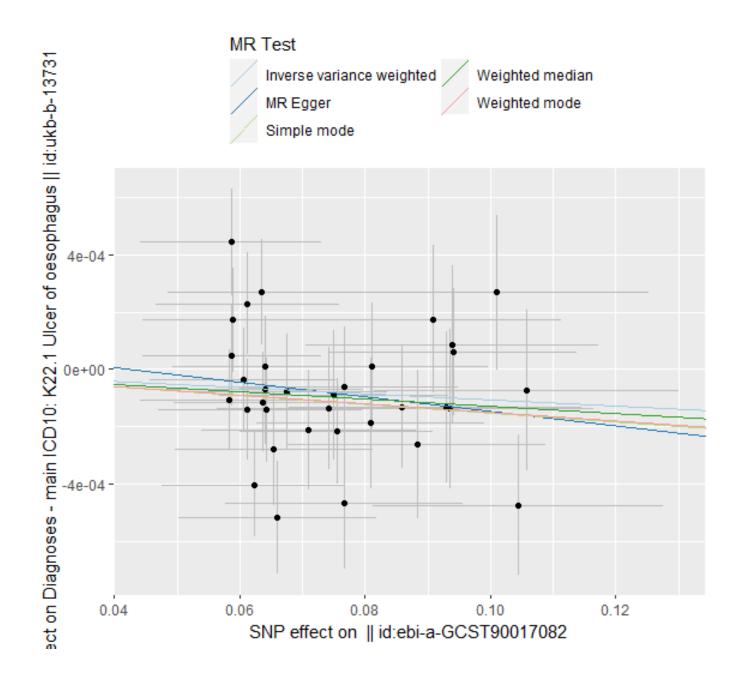
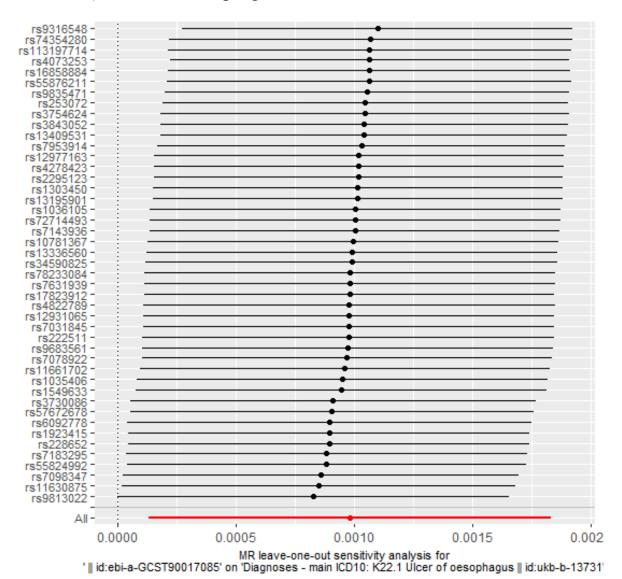


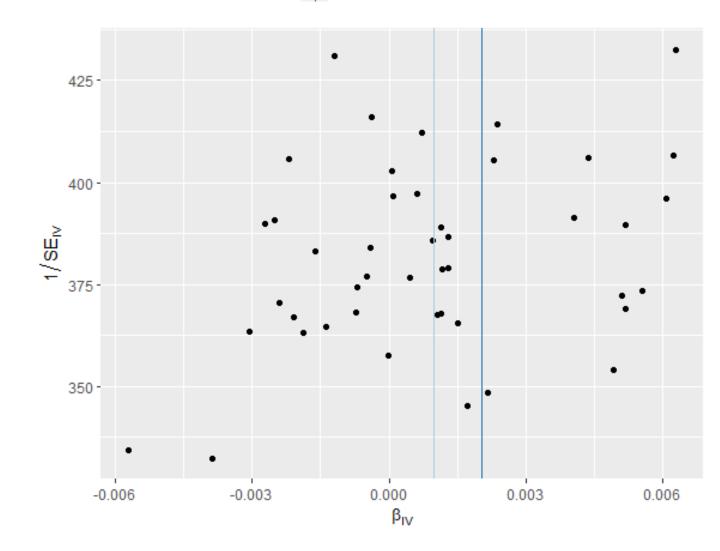
Figure 34 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.2755) on ulcer of oesophagus

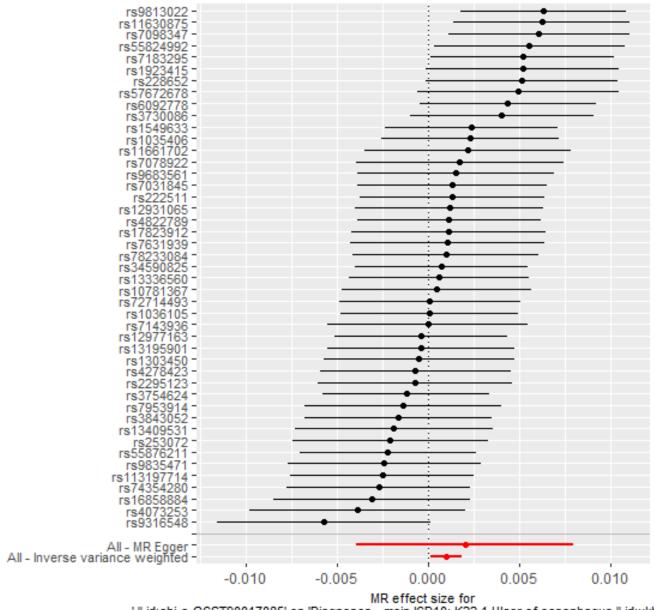


MR Method

Inverse variance weighted







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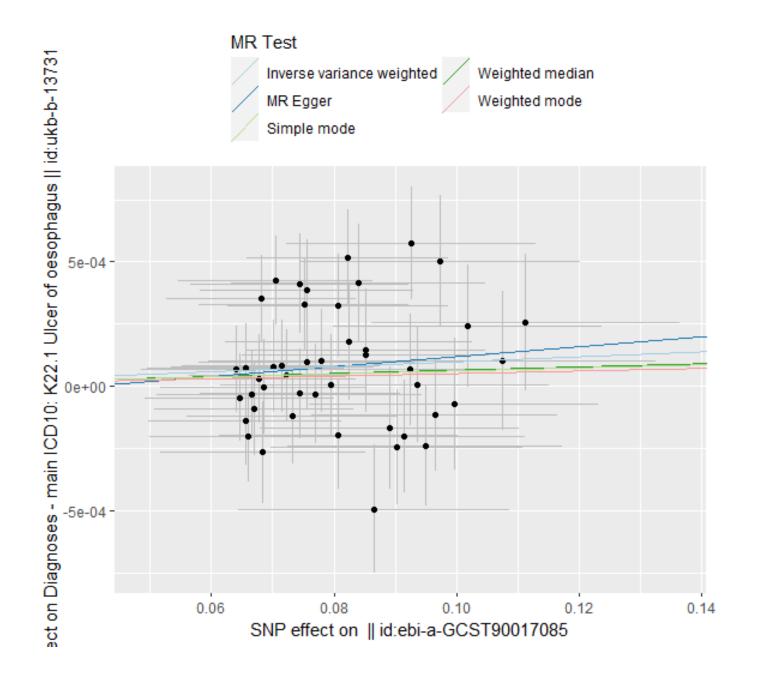
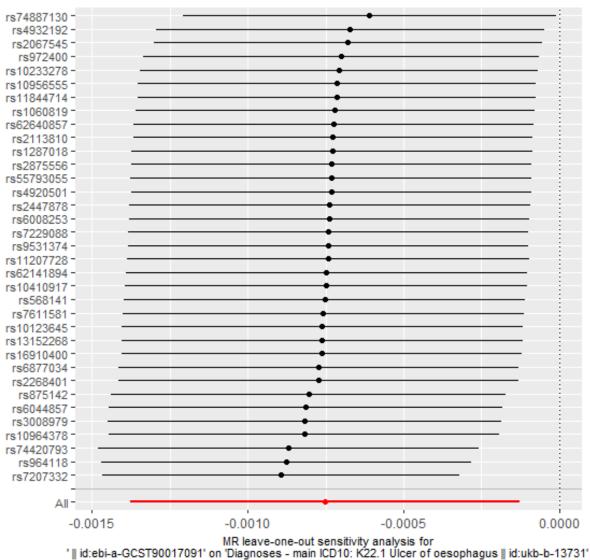


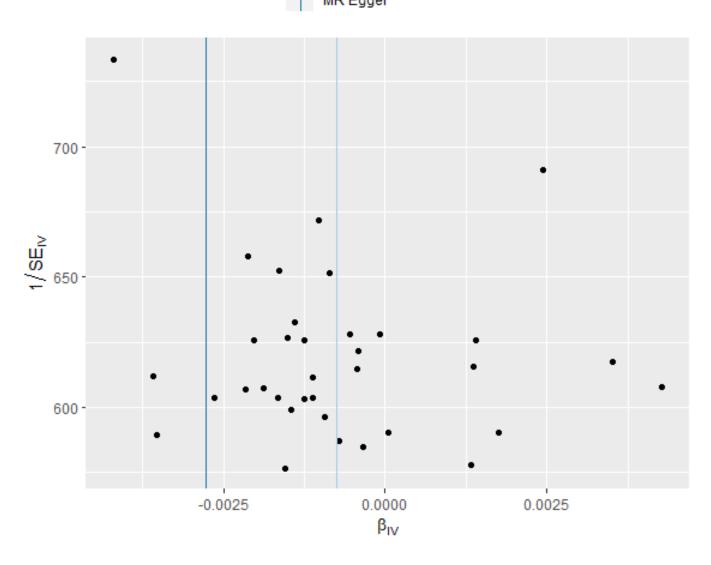
Figure 35 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Bacillales id.1674) on ulcer of oesophagus

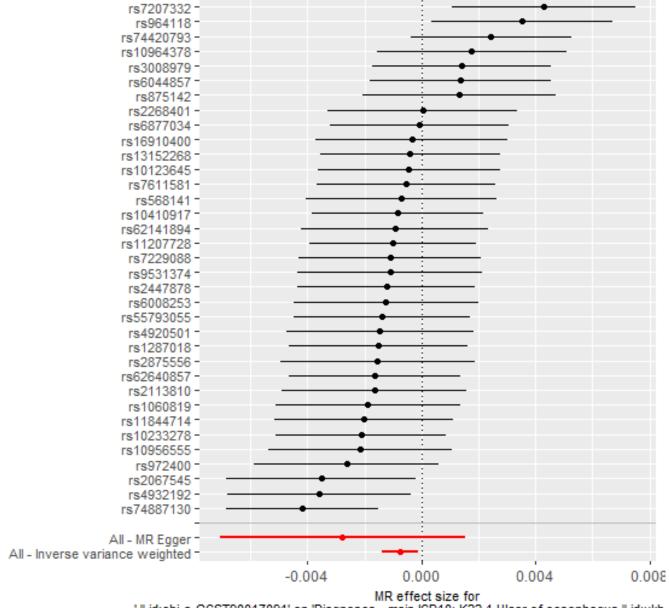


MR Method

Inverse variance weighted

MR Egger





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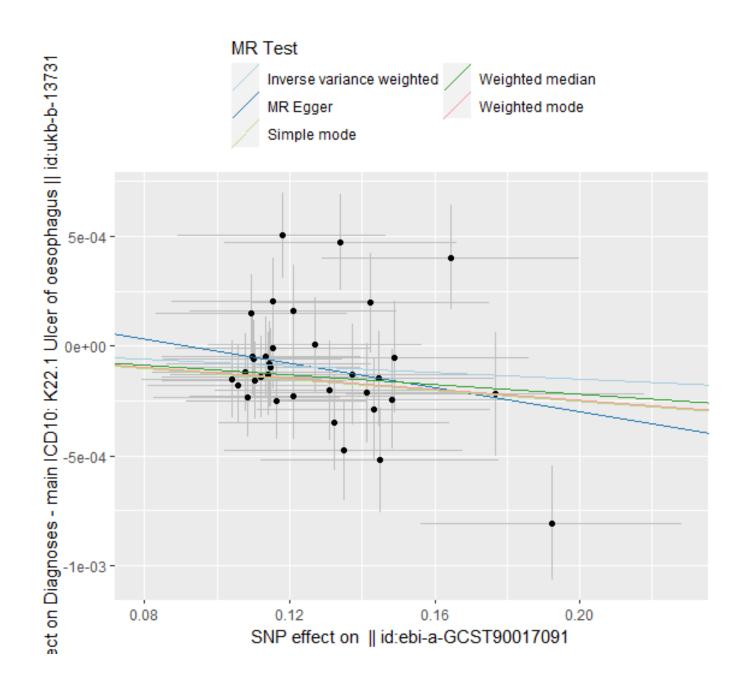
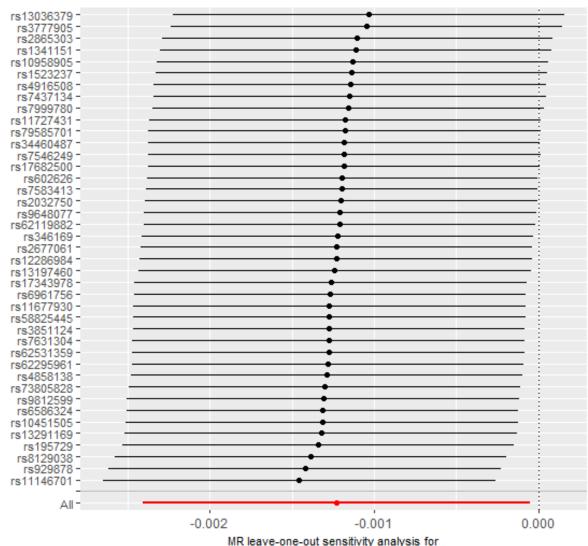
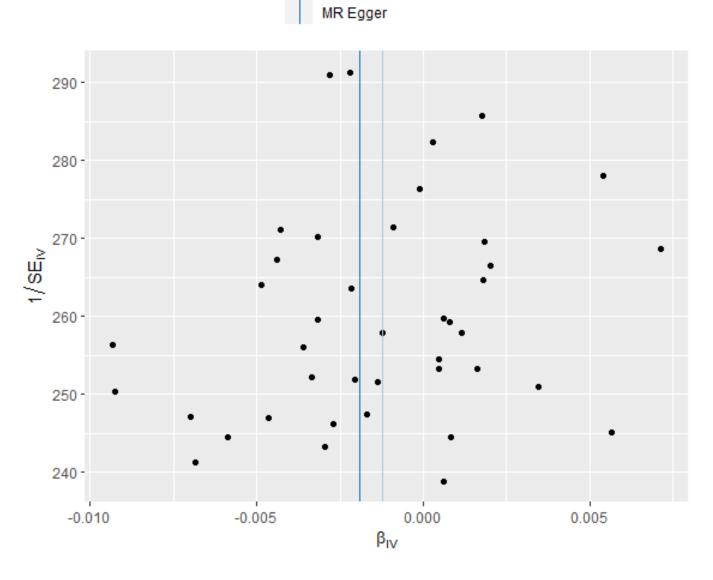


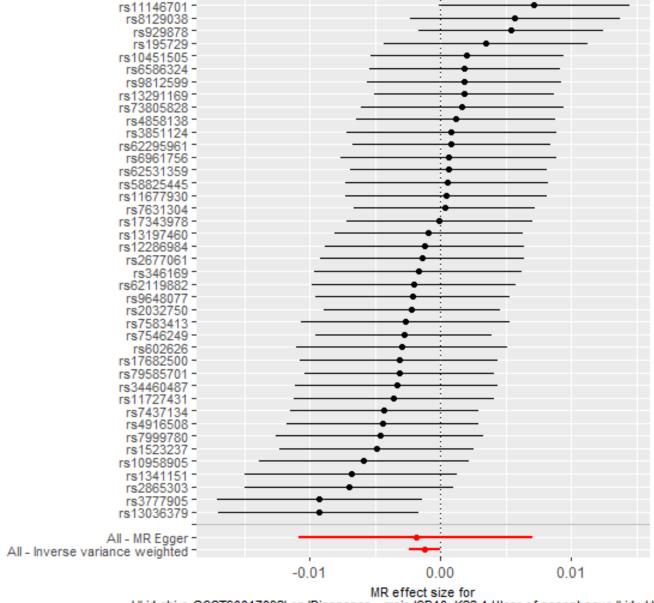
Figure 36 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Bacteroidales id.913) on ulcer of oesophagus



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017092' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus || id:ukb-b-13731'

MR Method Inverse variance weighted





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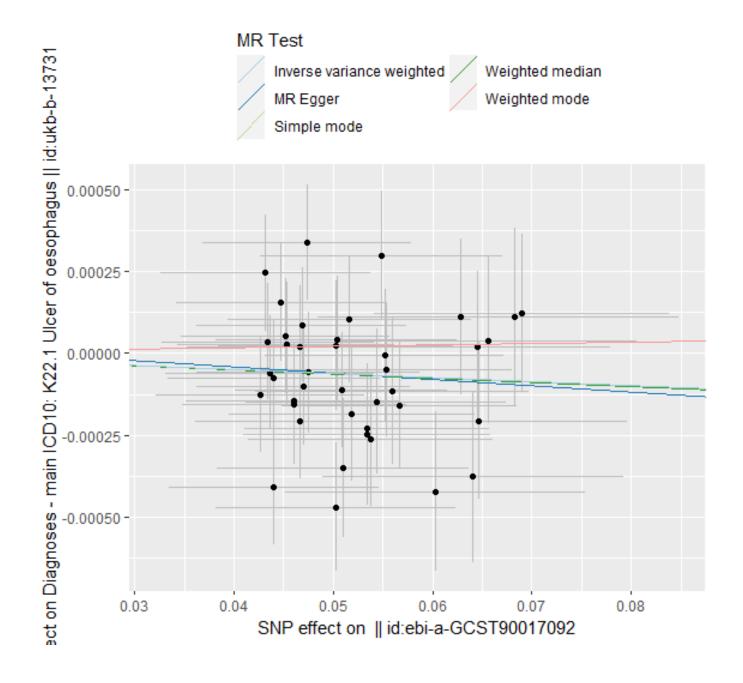
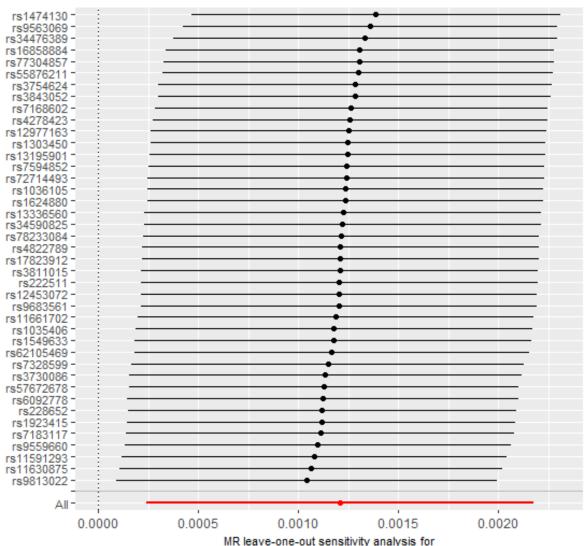


Figure 37 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Rhodospirillales id.2667) on ulcer of oesophagus

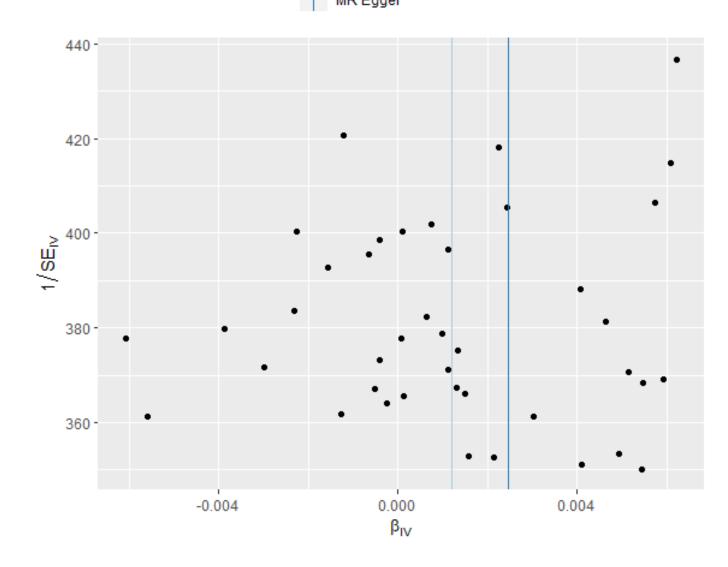


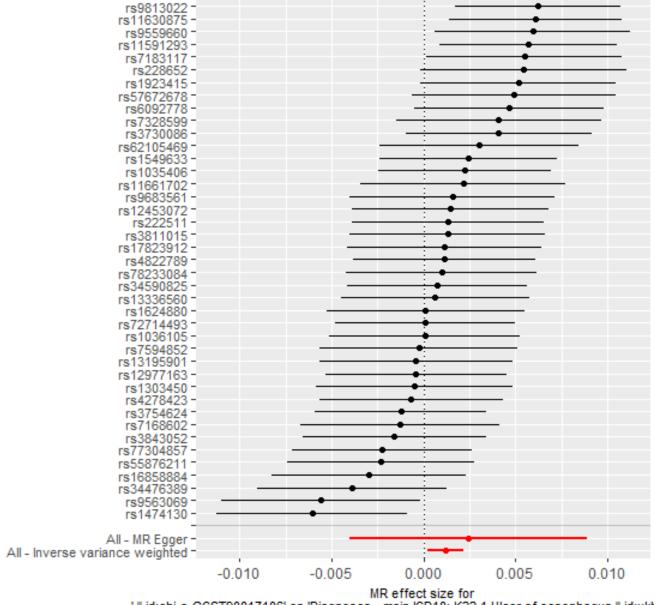
MR leave-one-out sensitivity analysis for ' ∥ id:ebi-a-GCST90017106' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus ∥ id:ukb-b-13731'

MR Method

Inverse variance weighted

MR Egger





' || id:ebi-a-GCST90017106' on 'Diagnoses - main ICD10: K22.1 Ulcer of oesophagus || id:ukb-

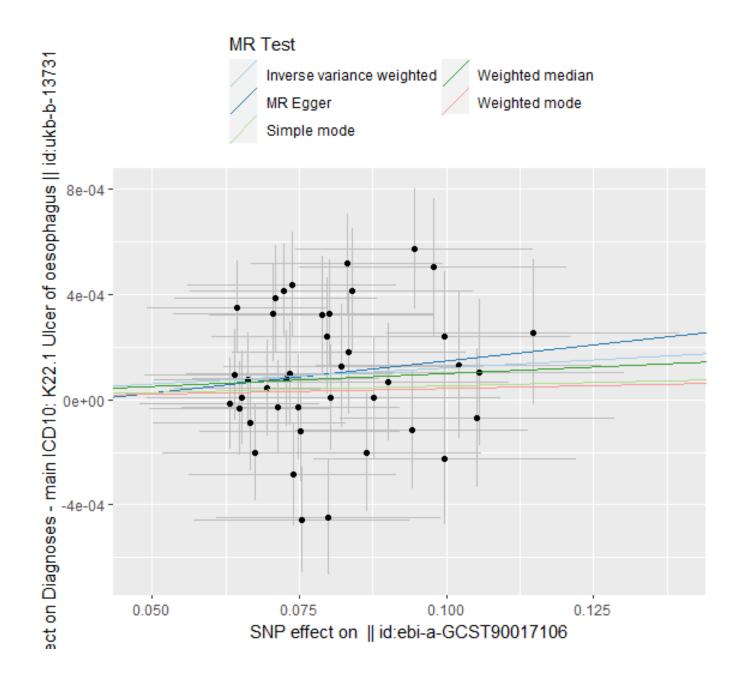
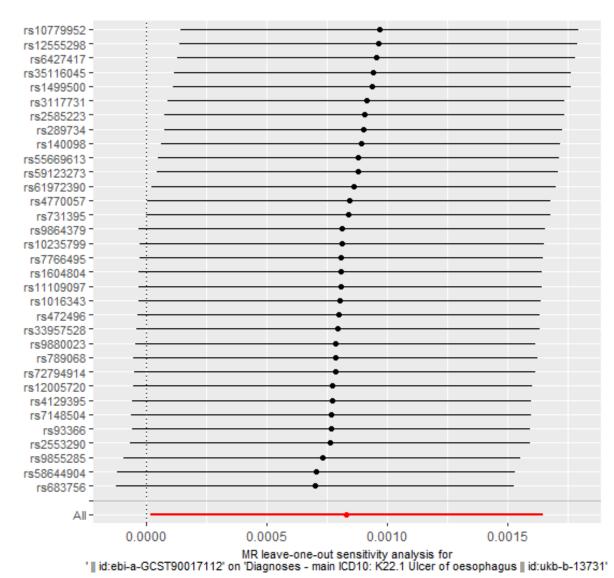


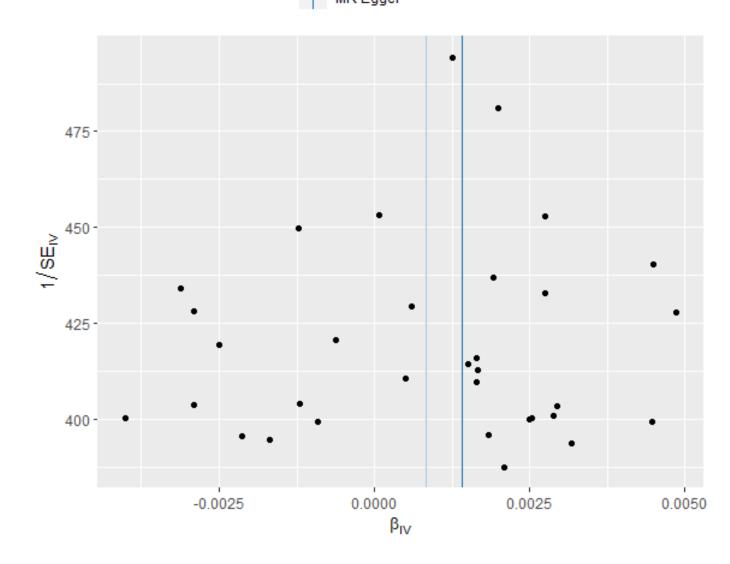
Figure 38 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Cyanobacteria id.1500) on ulcer of oesophagus

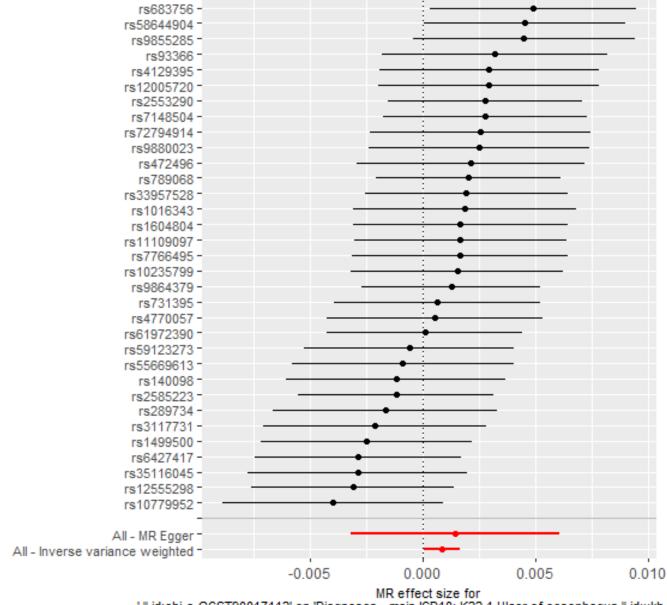


MR Method

Inverse variance weighted

MR Egger





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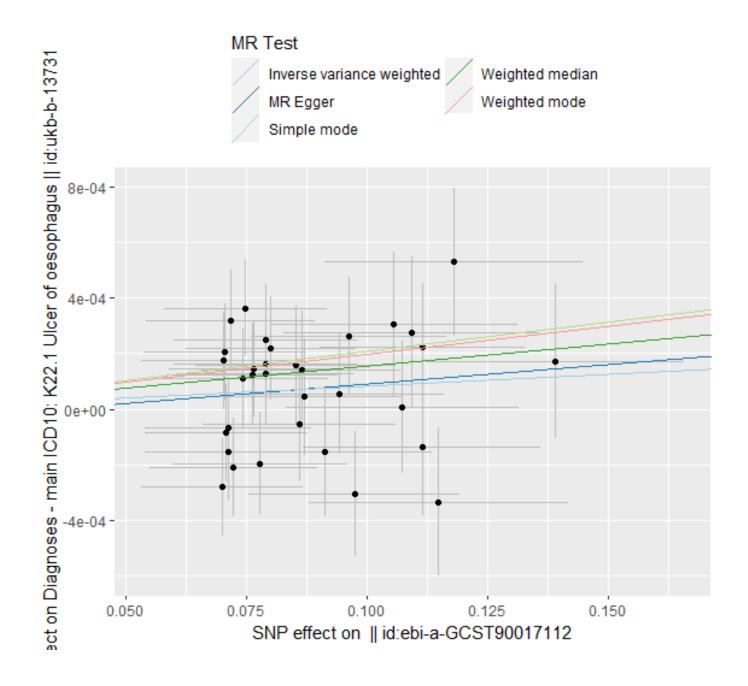
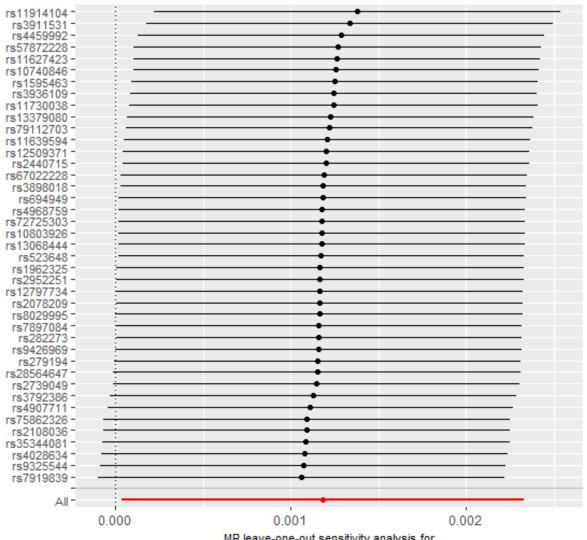


Figure 39 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Bacilli id.1673) on gastric ulcer

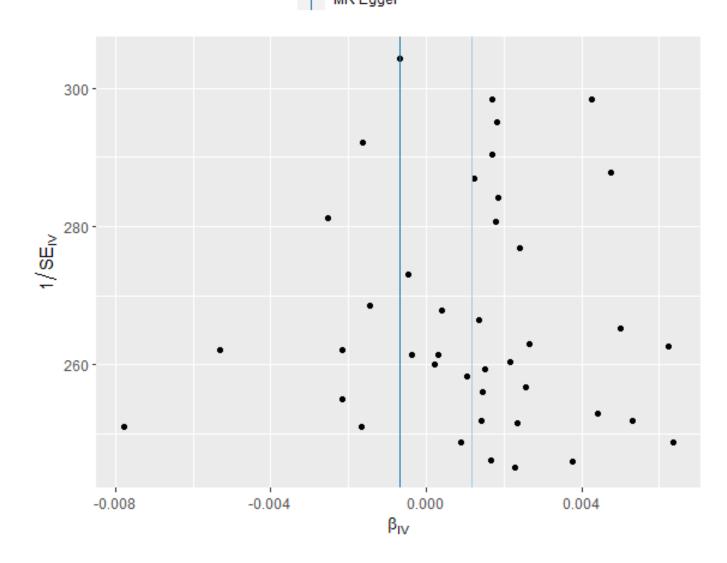


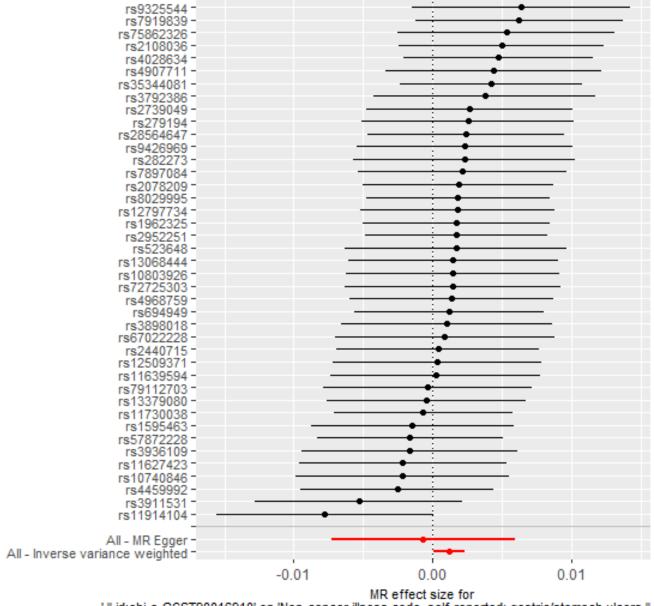
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MR Method

Inverse variance weighted

MR Egger





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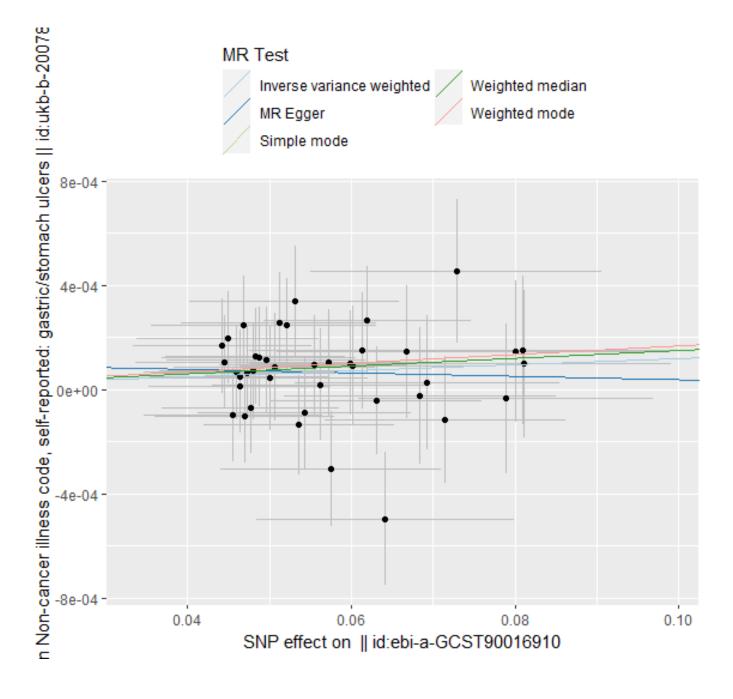
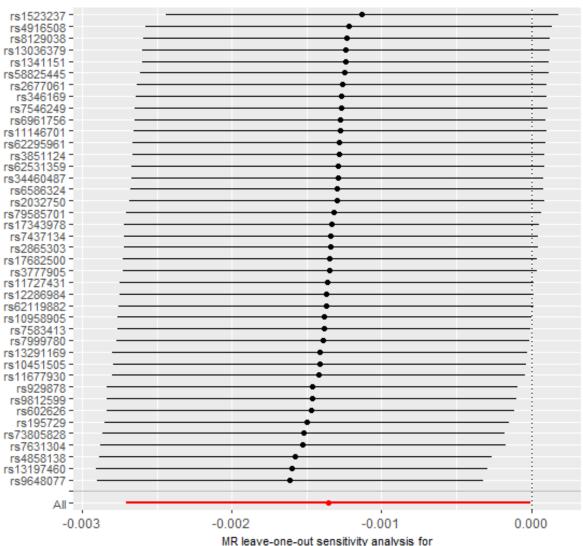


Figure 40 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Bacteroidia id.912) on gastric ulcer

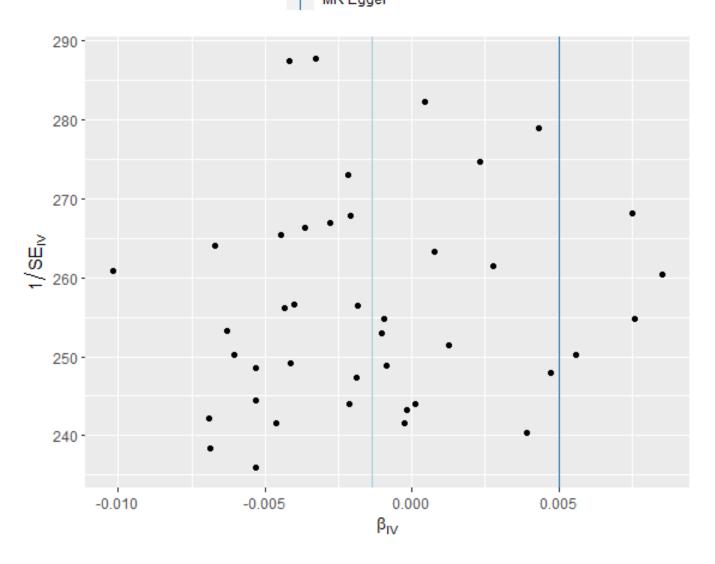


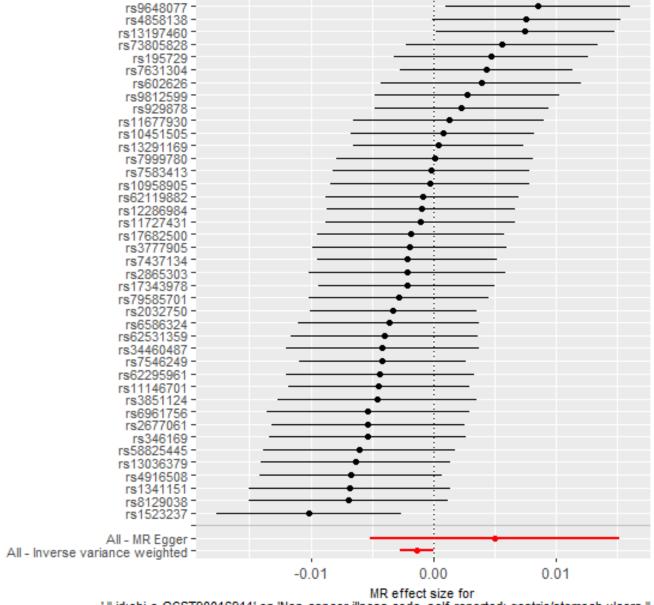
MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016911' on 'Non-cancer illness code, self-reported: gastric/stomach ulcers || id:ukb-b-20

MR Method

Inverse variance weighted

MR Egger





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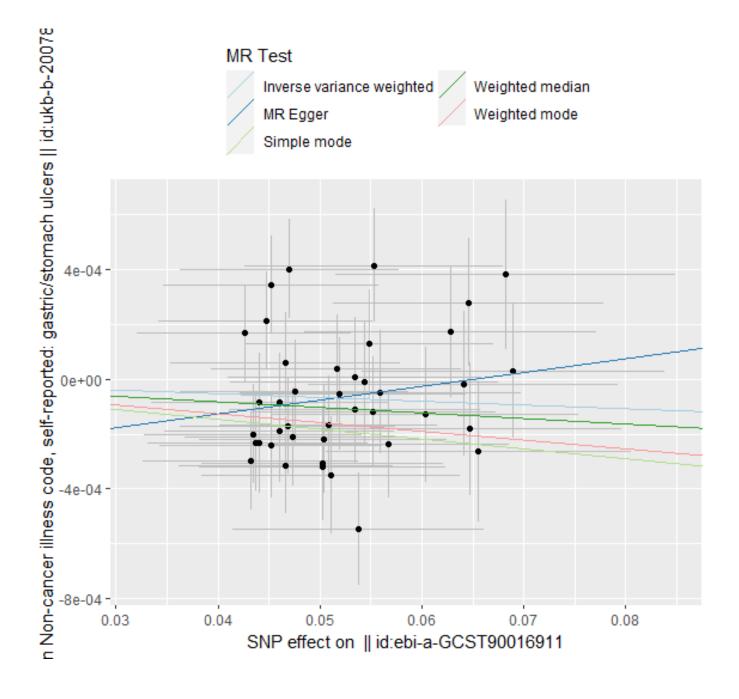
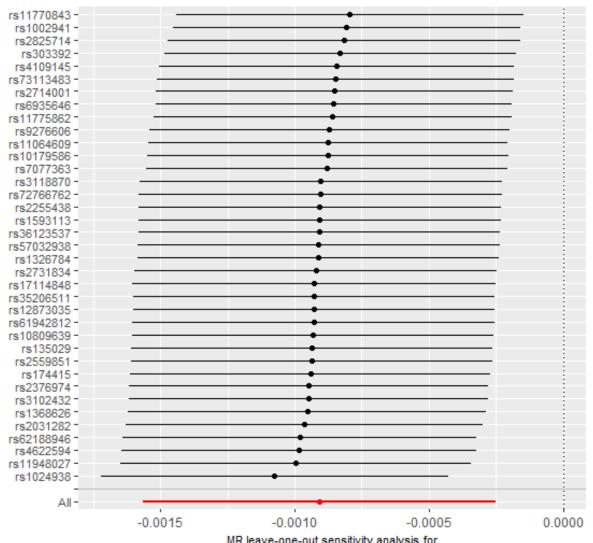


Figure 41 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Lentisphaeria id.2250) on gastric ulcer

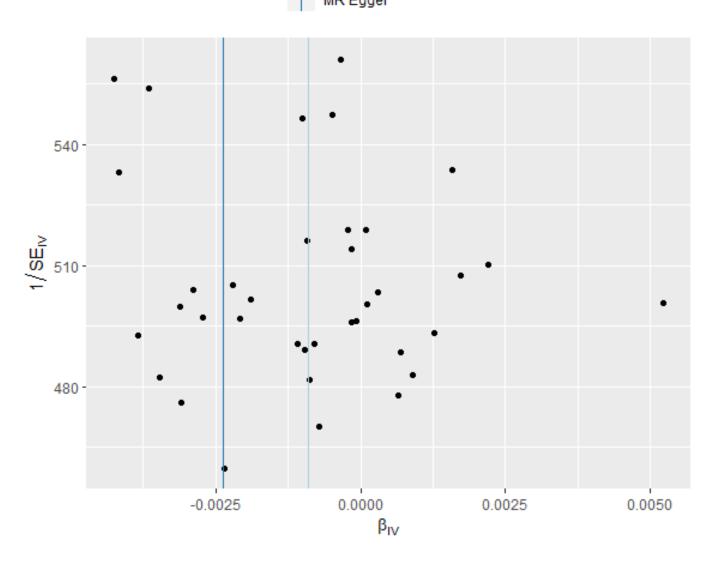


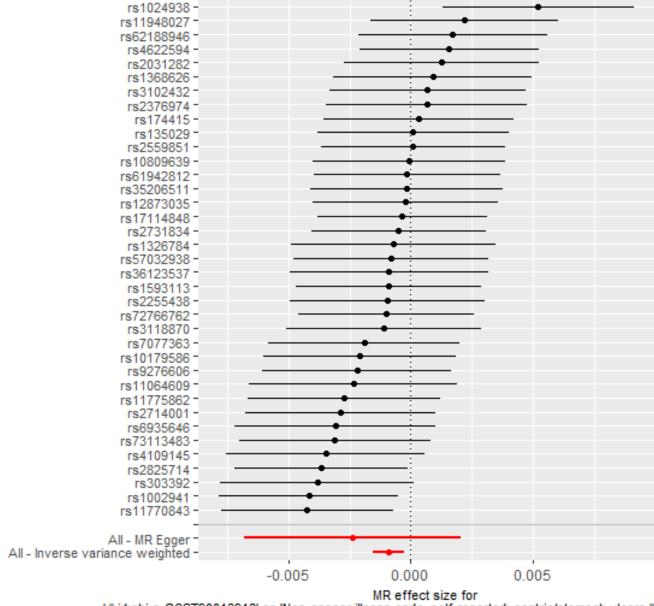
MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016918' on 'Non-cancer illness code, self-reported: gastric/stomach ulcers || id:ukb-b-2(

MR Method

Inverse variance weighted

MR Egger





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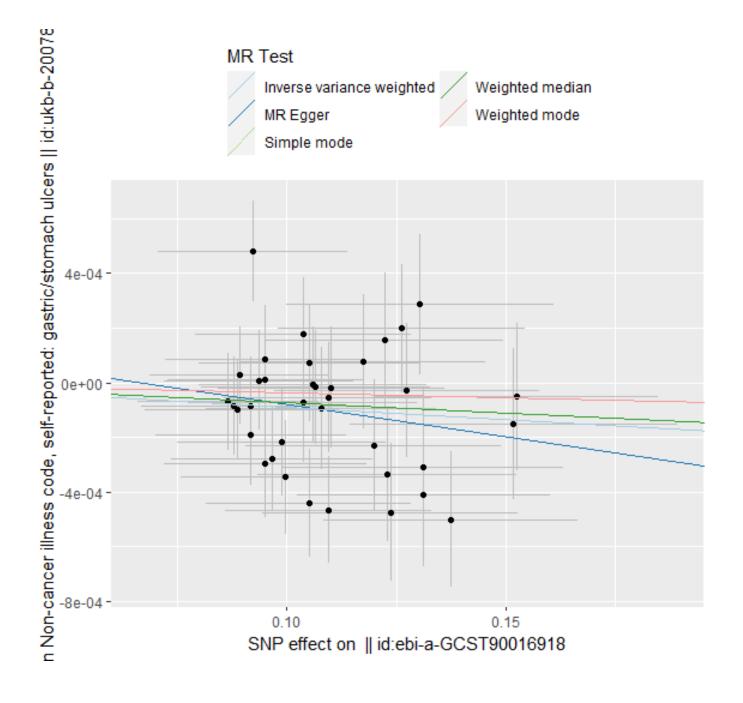
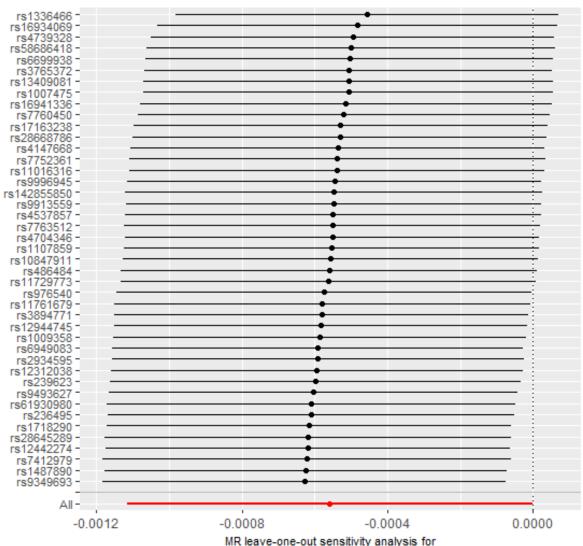


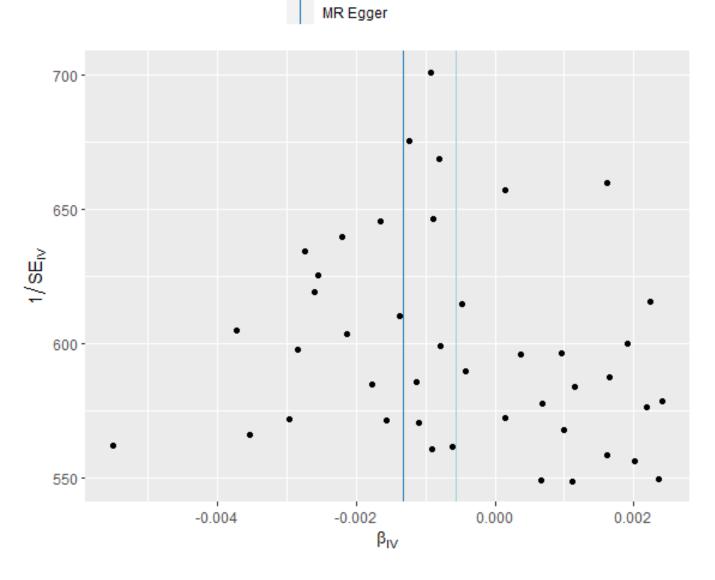
Figure 42 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Butyrivibrio id.1993) on gastric ulcer

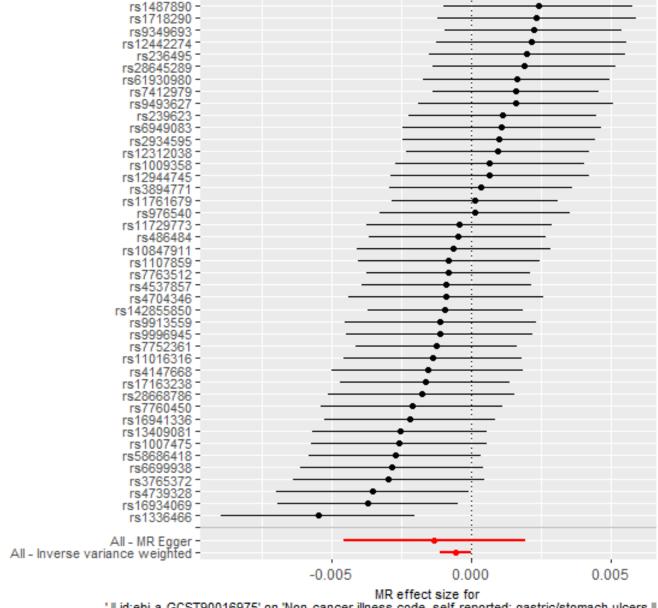


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MR Method

Inverse variance weighted





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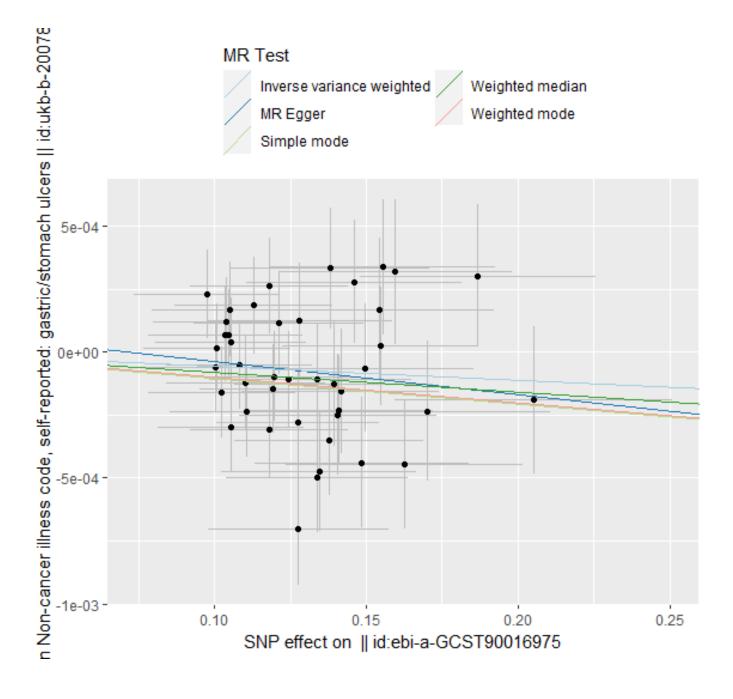
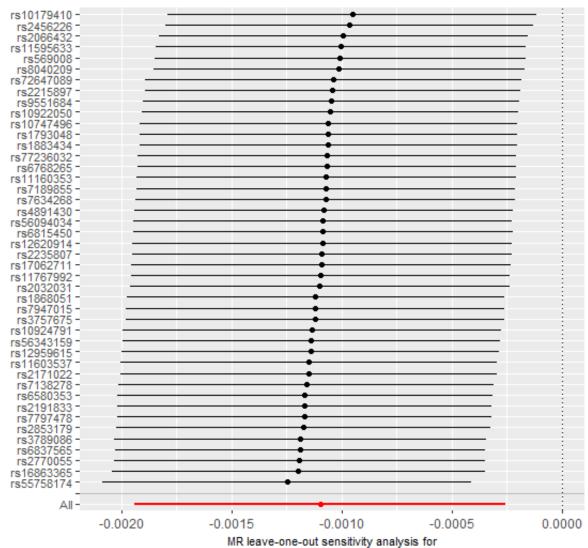
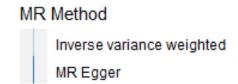
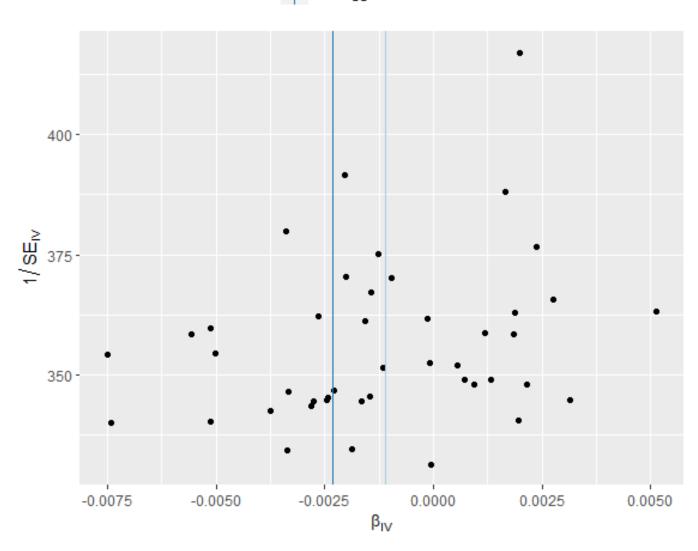


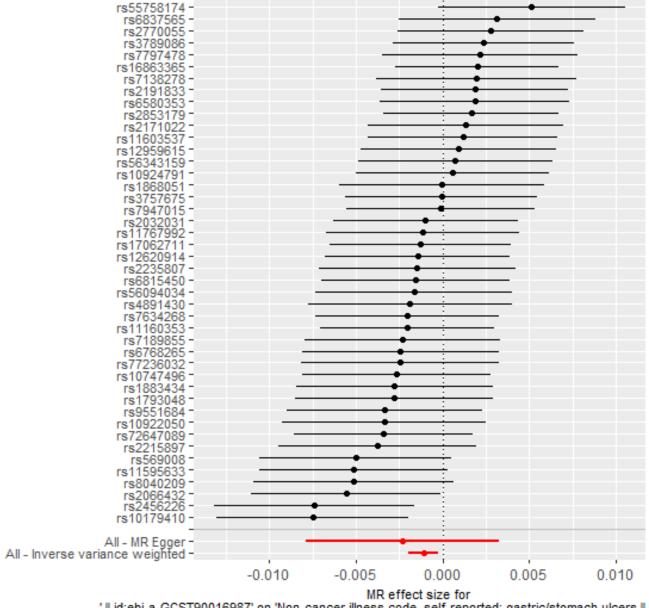
Figure 43 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Desulfovibrio id.3173) on gastric ulcer



"|| id:ebi-a-GCST90016987" on 'Non-cancer illness code, self-reported: gastric/stomach ulcers || id:ukb-b-20







" || id:ebi-a-GCST90016987" on "Non-cancer illness code, self-reported: gastric/stomach ulcers || ic

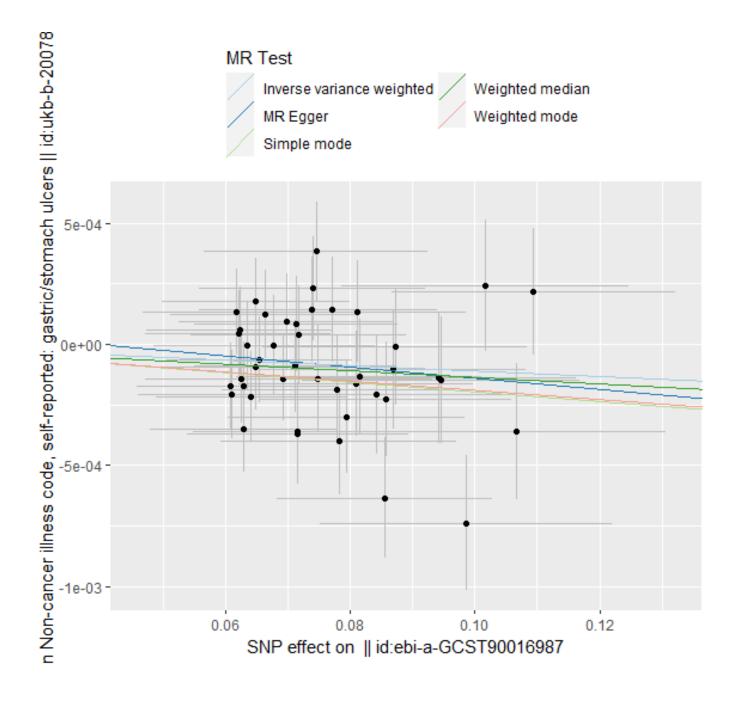
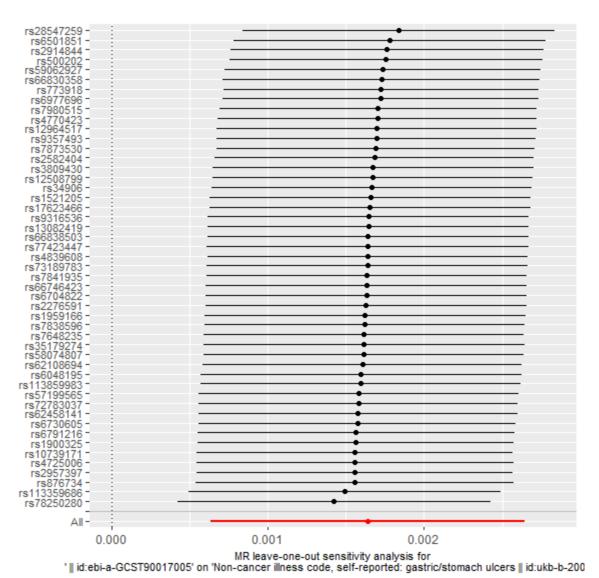


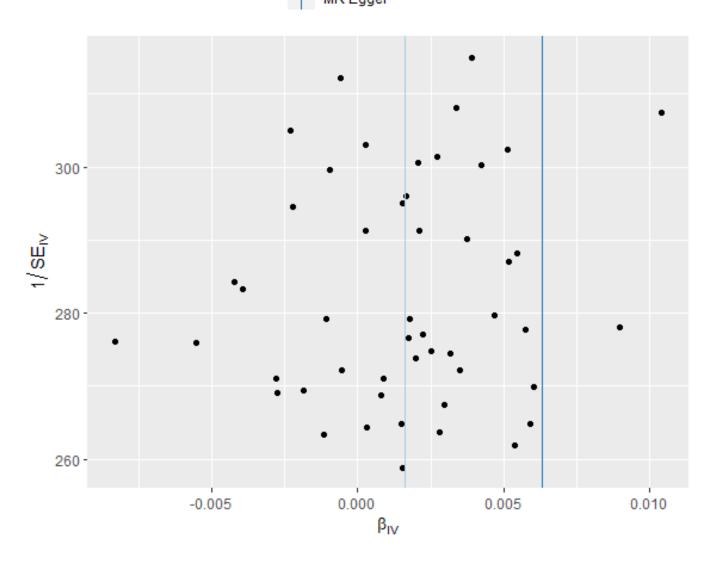
Figure 44 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium ventriosum group id.11341) on gastric ulcer

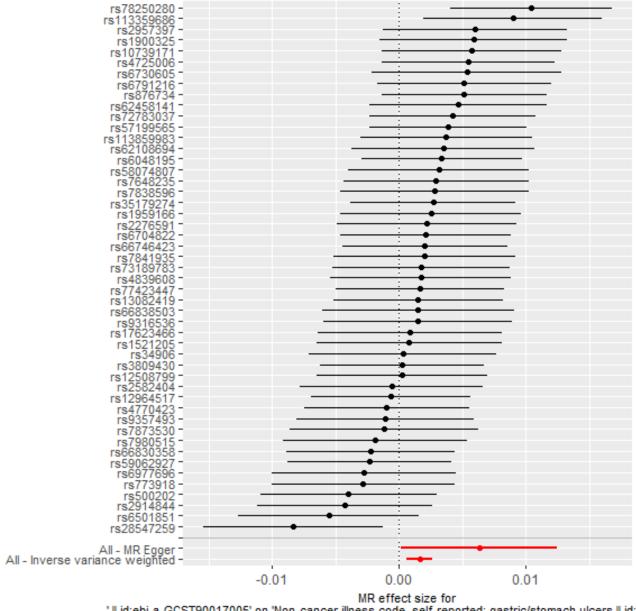


MR Method

Inverse variance weighted

MR Egger





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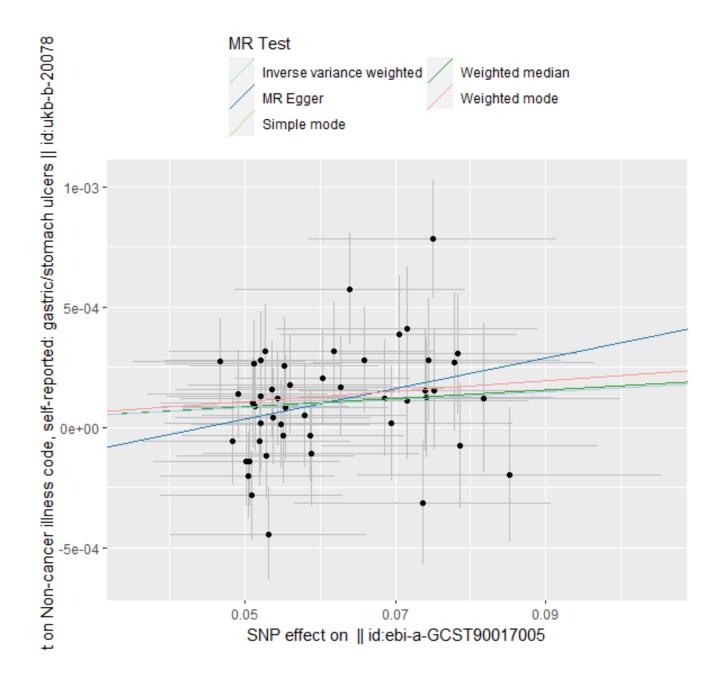
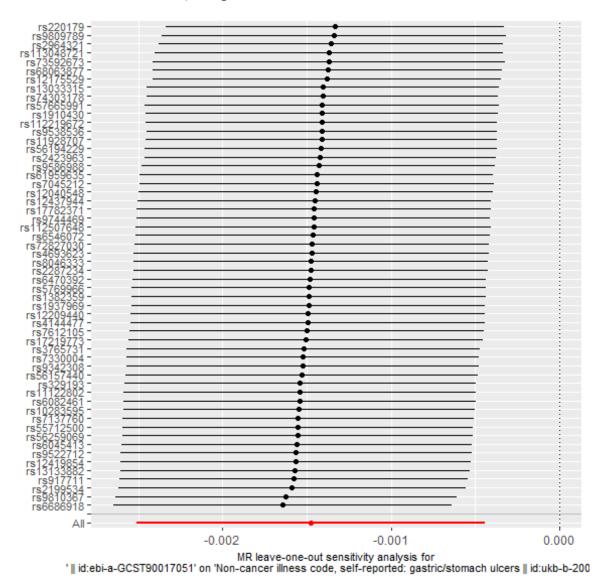
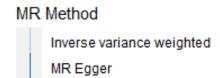
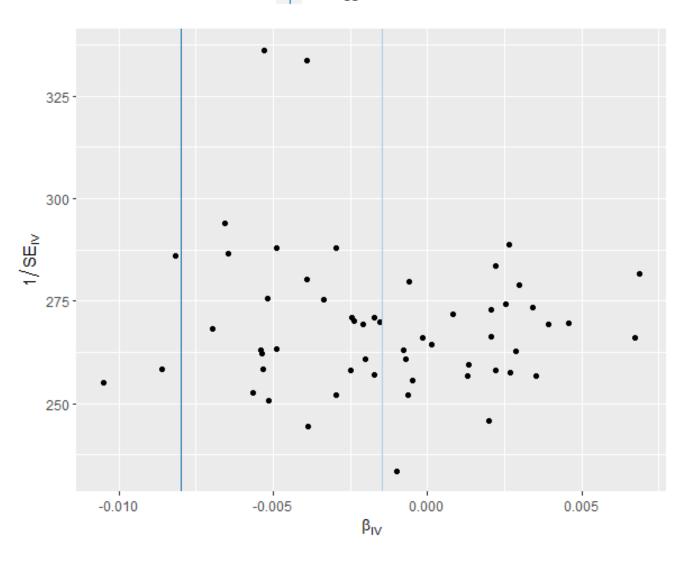
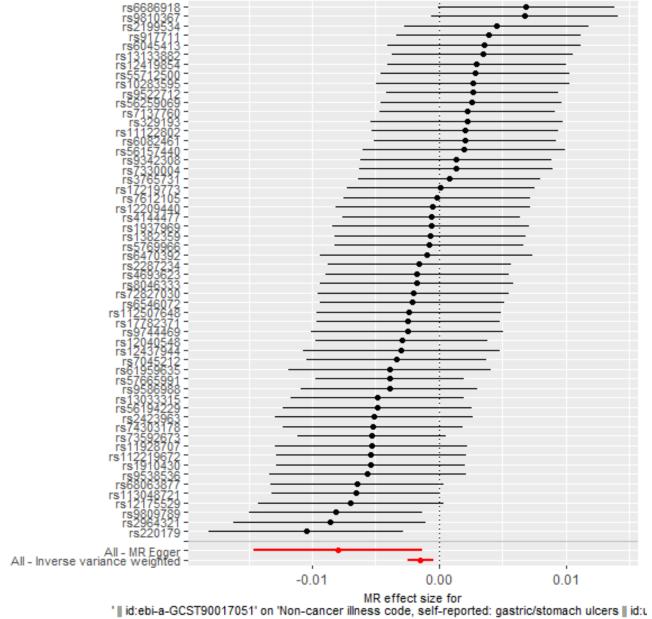


Figure 45 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminiclostridium9 id.11357) on gastric ulcer









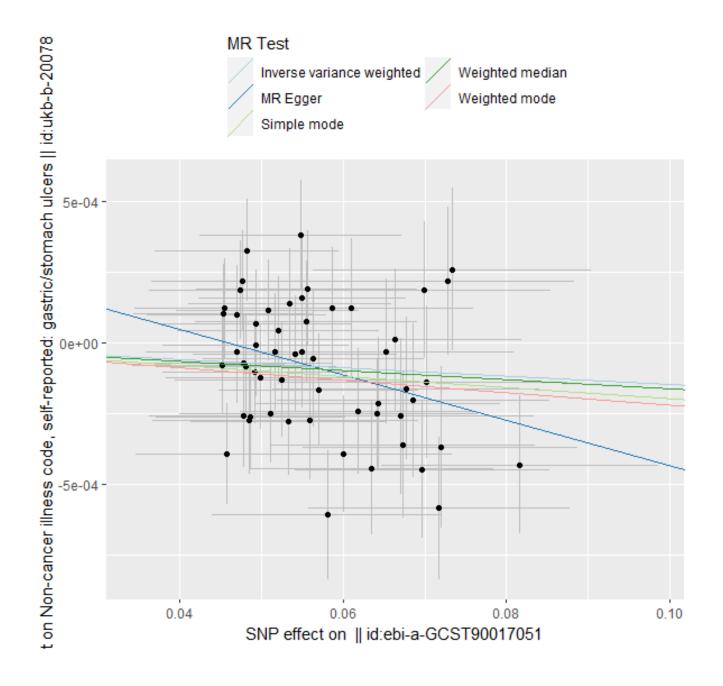
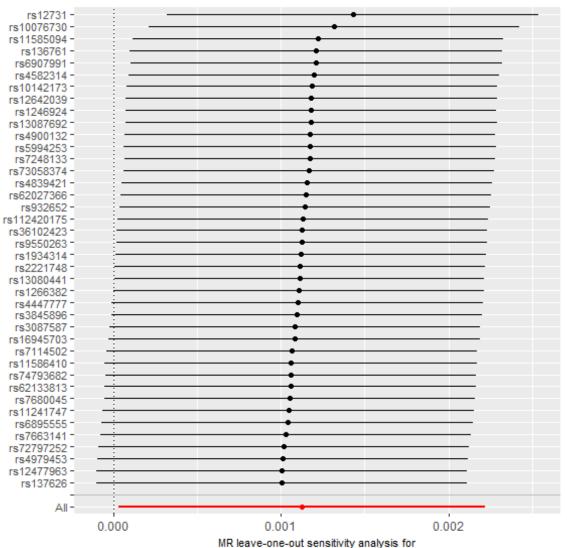
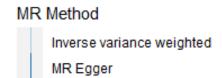
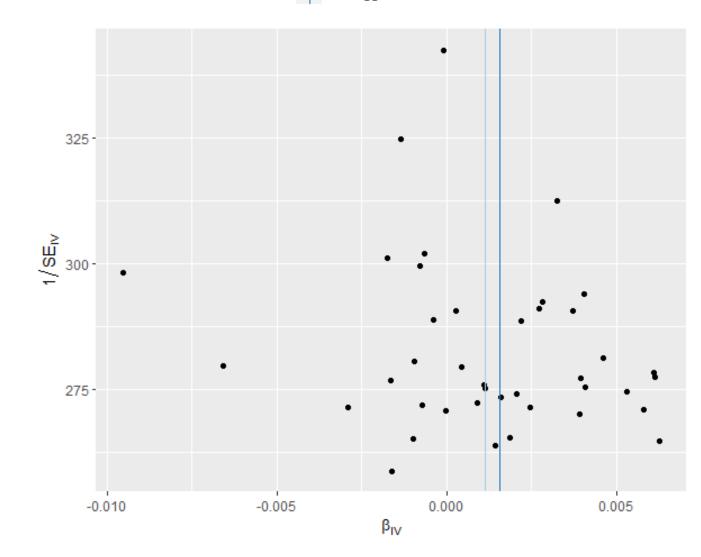


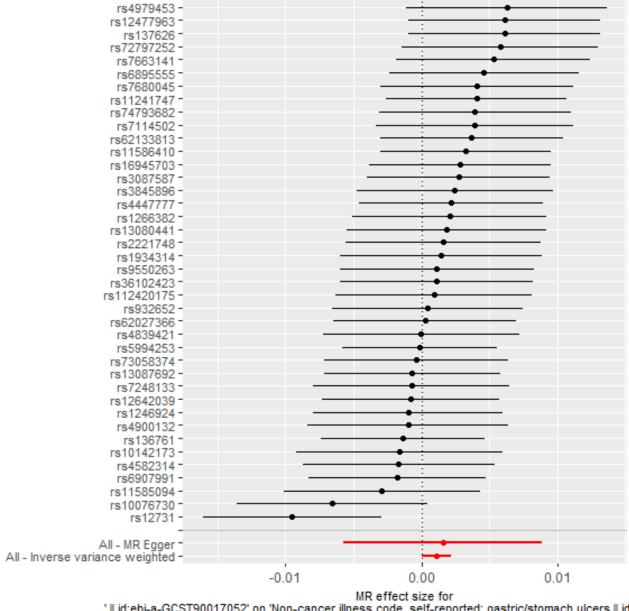
Figure 46 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae NK4A214 group id.11358) on gastric ulcer



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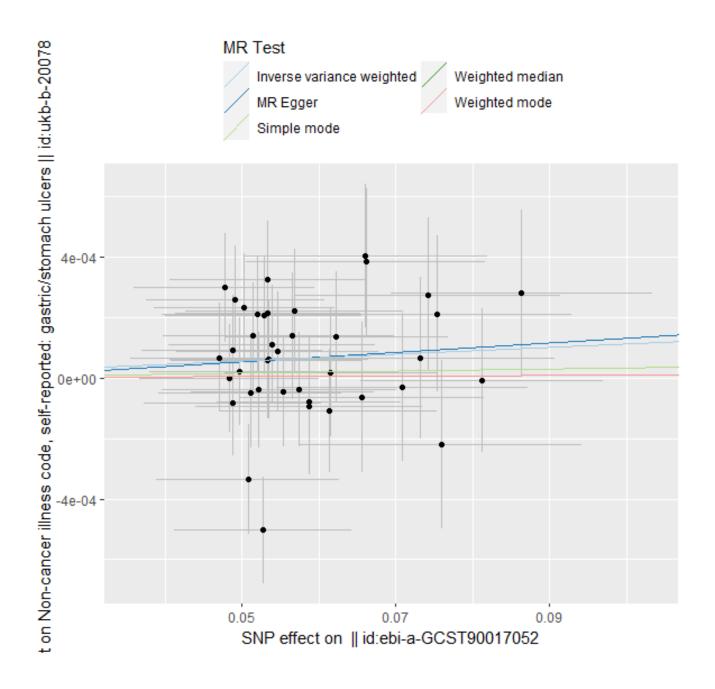
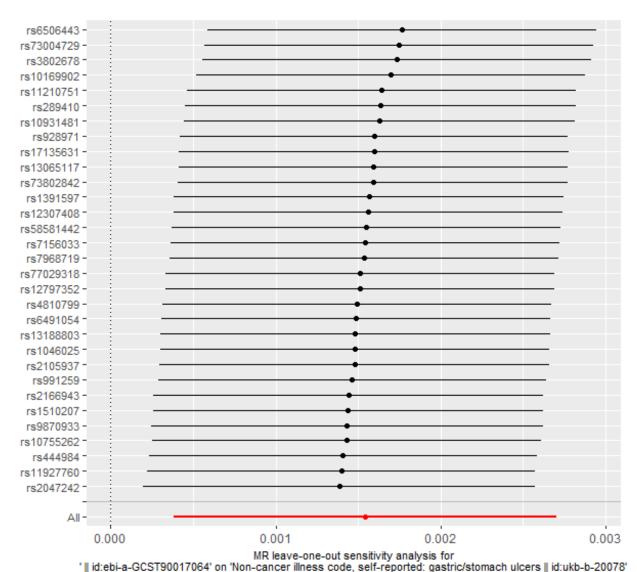


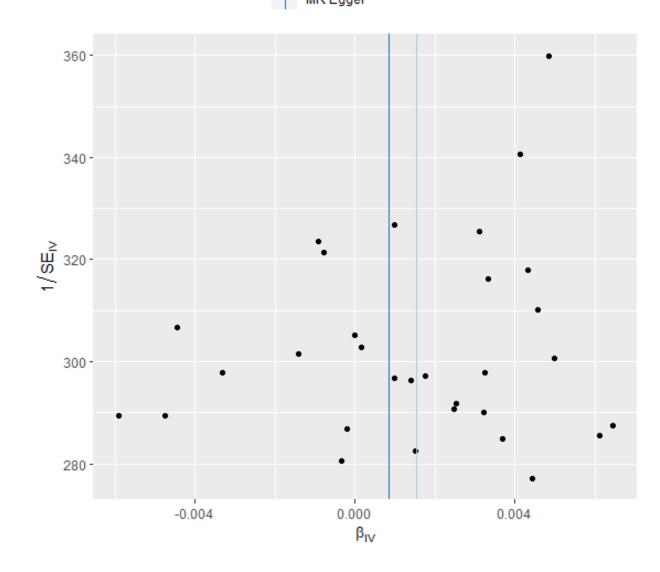
Figure 47 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcus gauvreauii group id.11342) on gastric ulcer

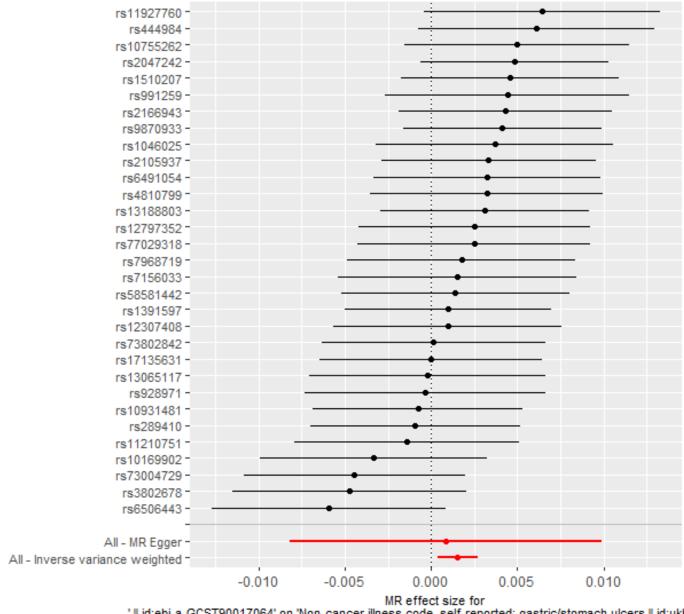


MR Method

Inverse variance weighted

MR Egger





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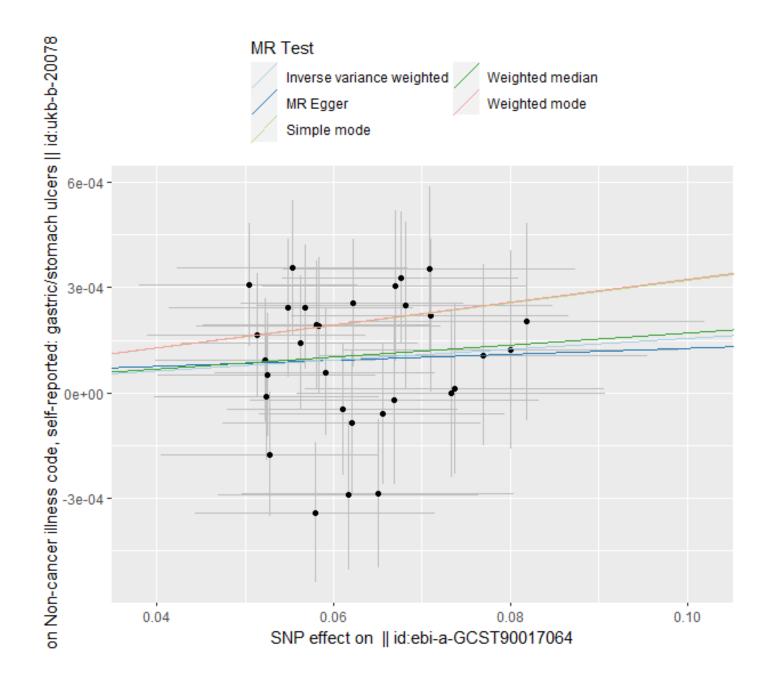
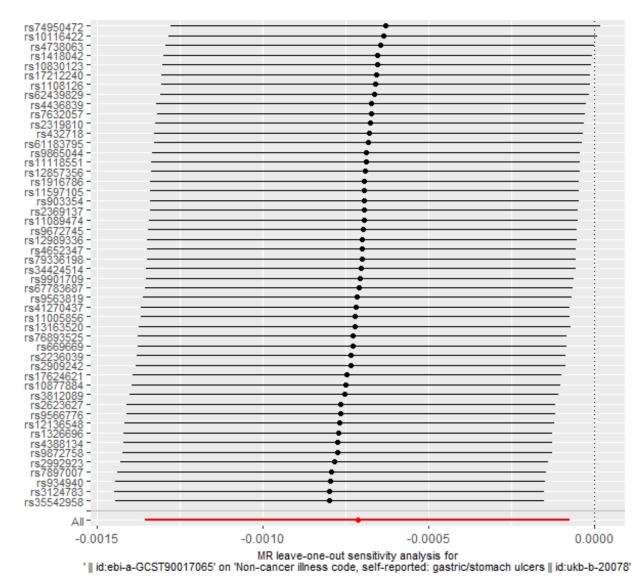
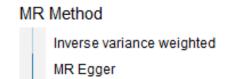
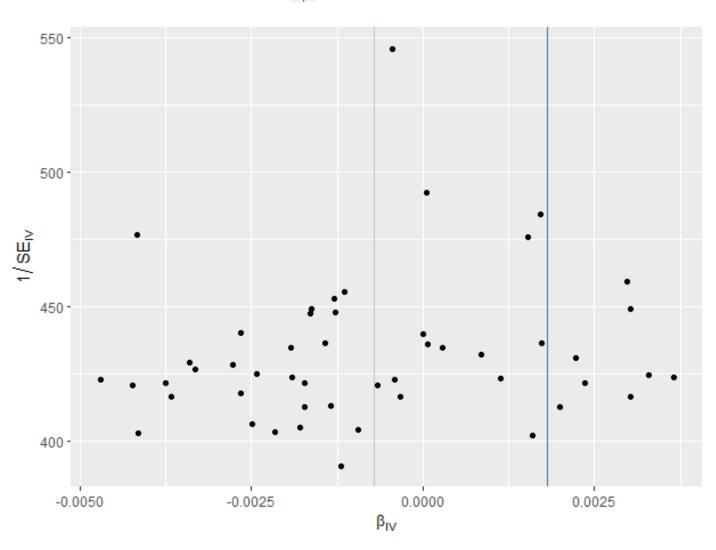
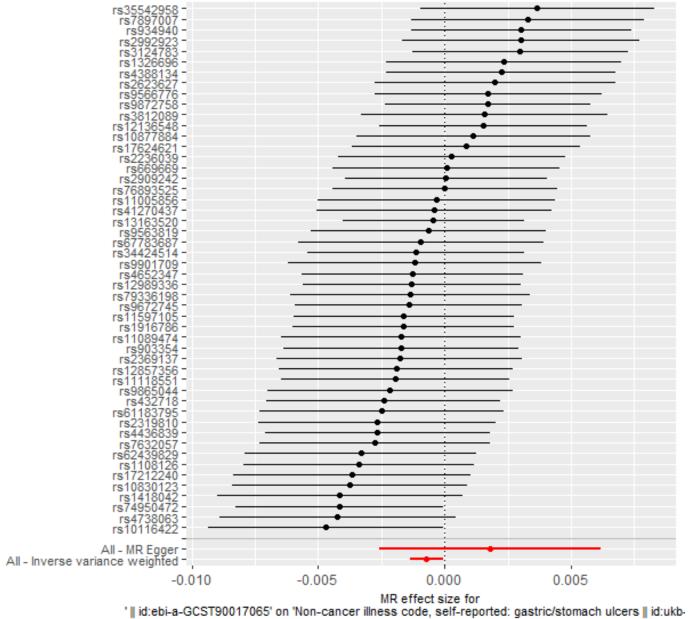


Figure 48 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcus gnavus group id.14376) on gastric ulcer









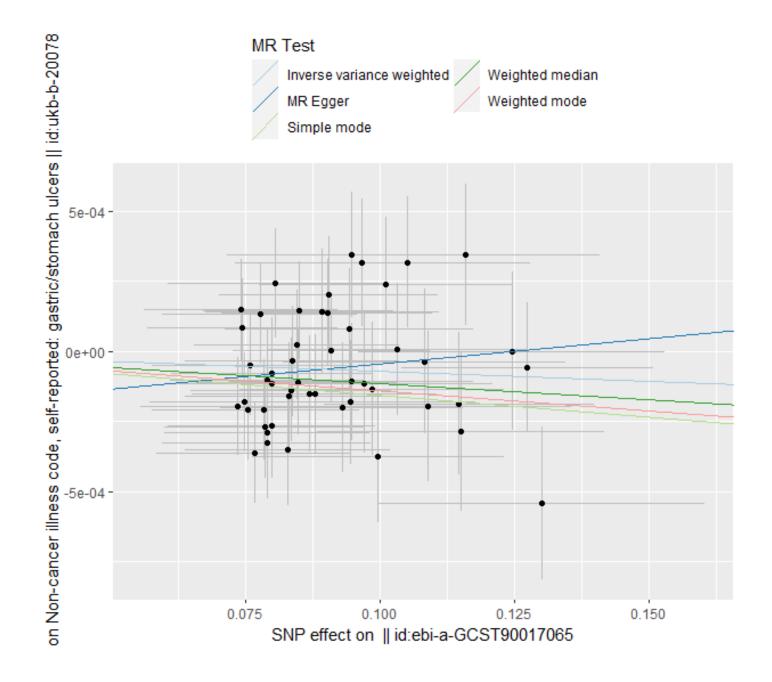
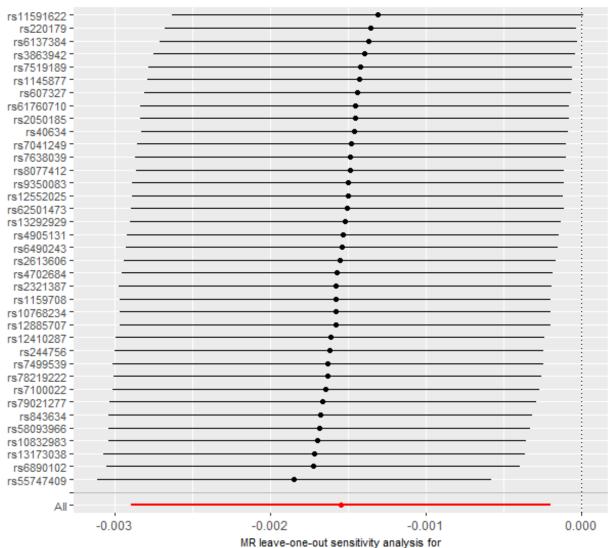
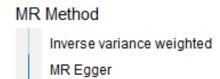
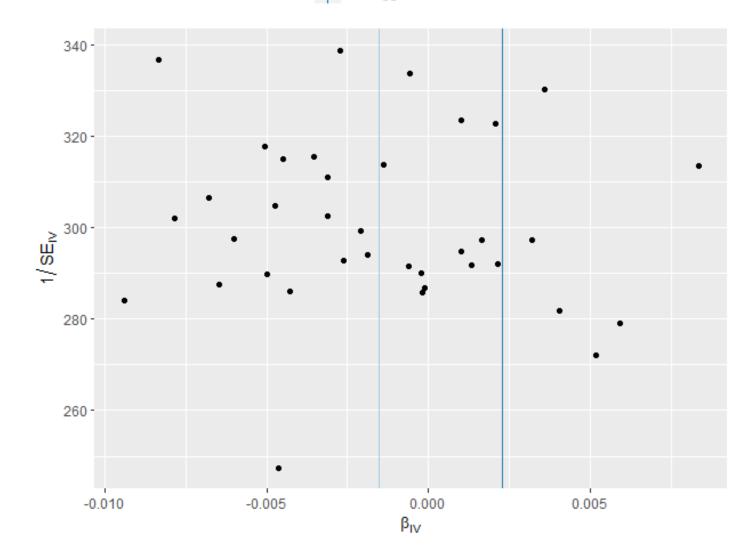


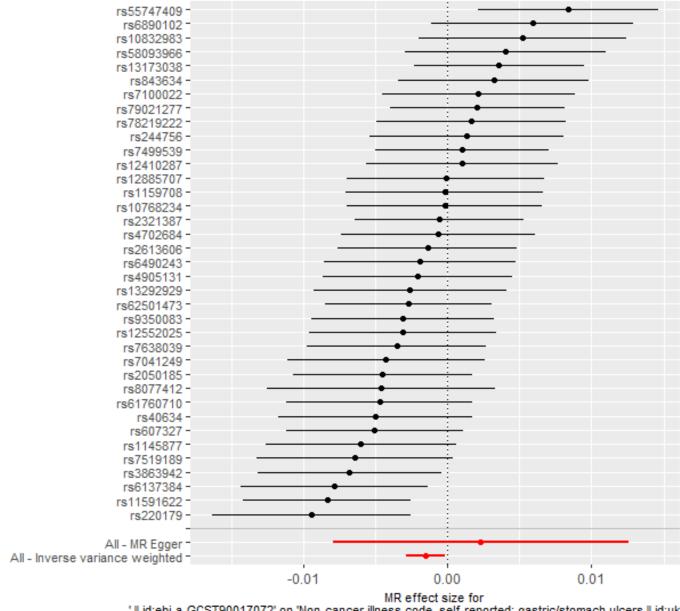
Figure 49 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Sutterella id.2896) on gastric ulcer



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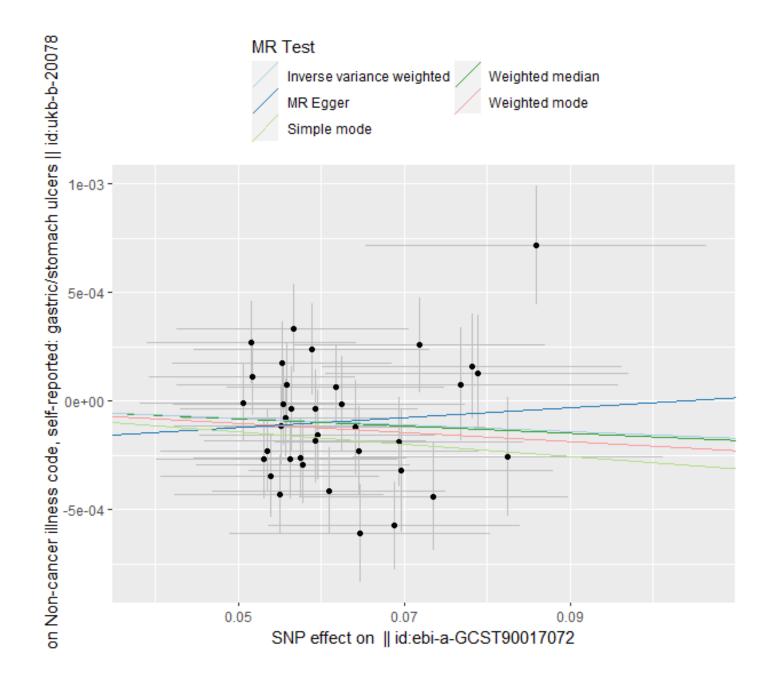
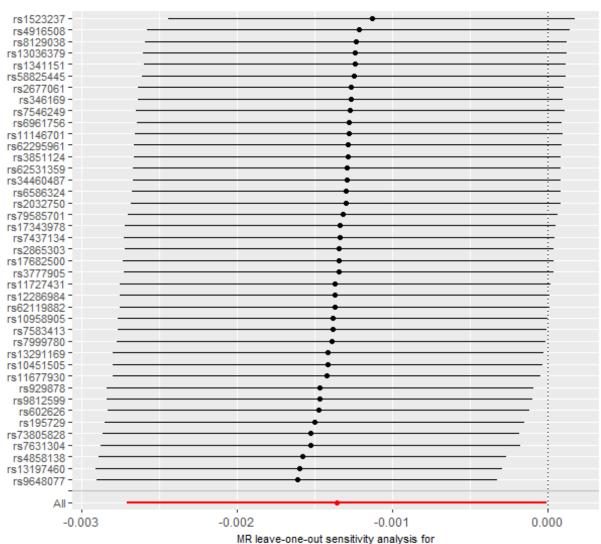


Figure 50 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Bacteroidales id.913) on gastric ulcer

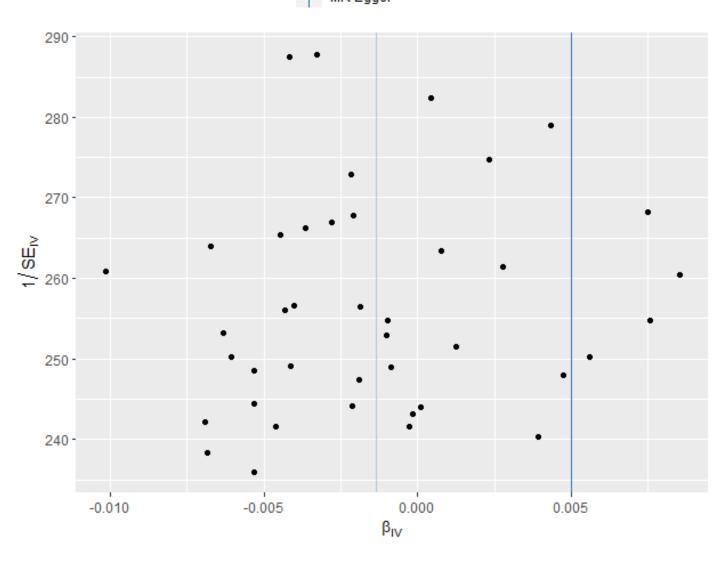


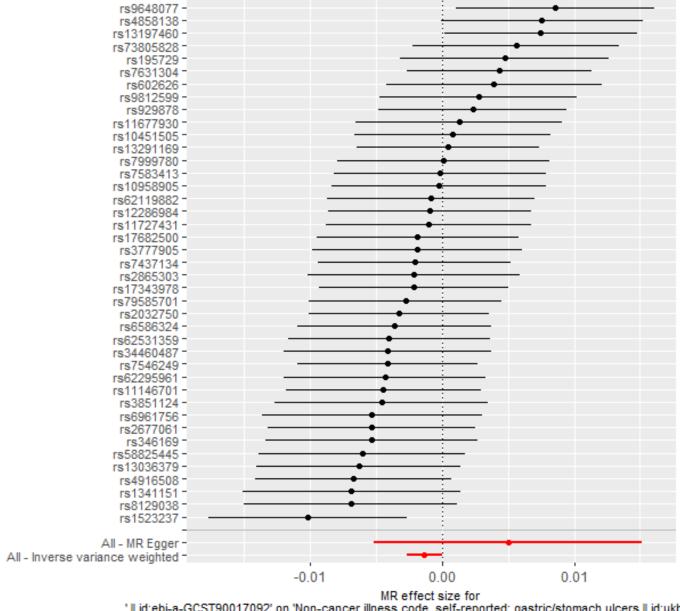
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MR Method

Inverse variance weighted

MR Egger





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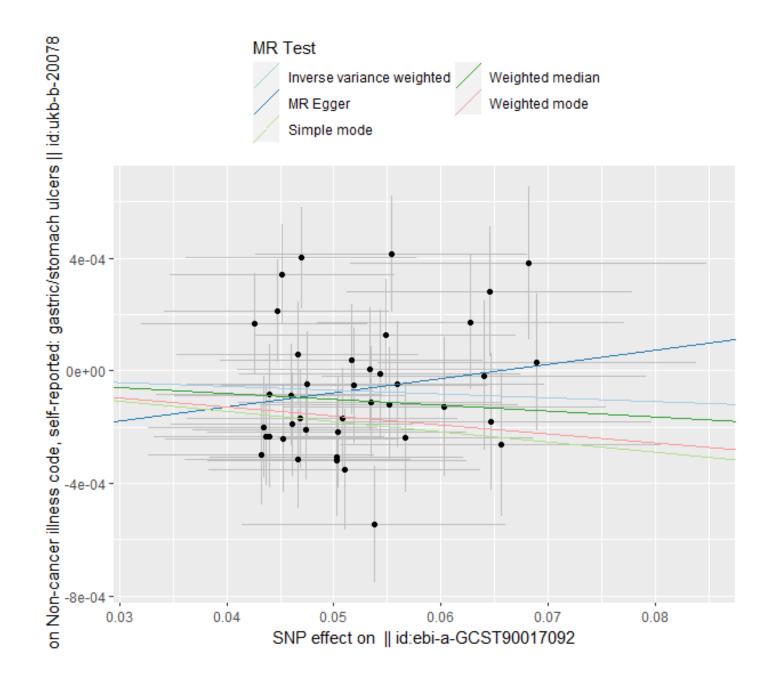
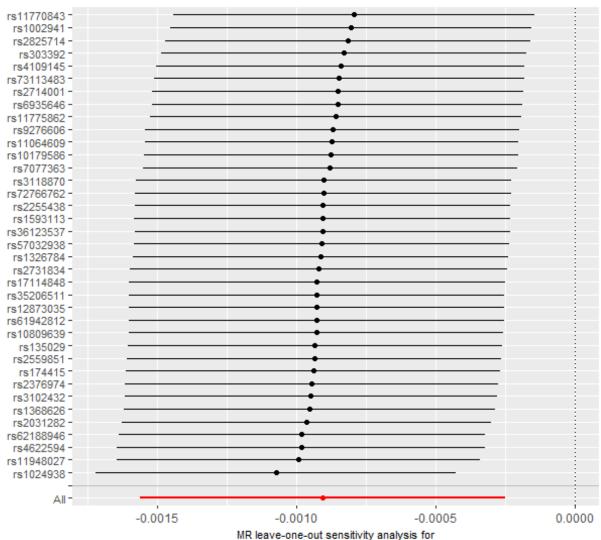


Figure 51 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Victivallales id.2254) on gastric ulcer

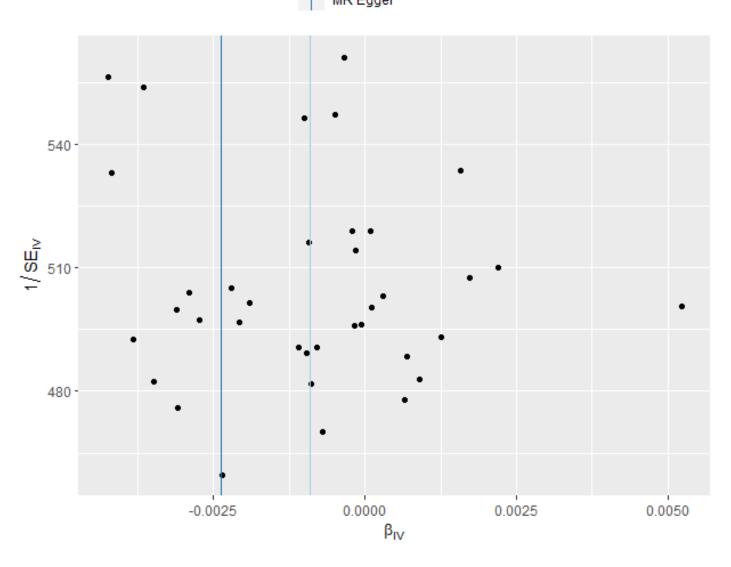


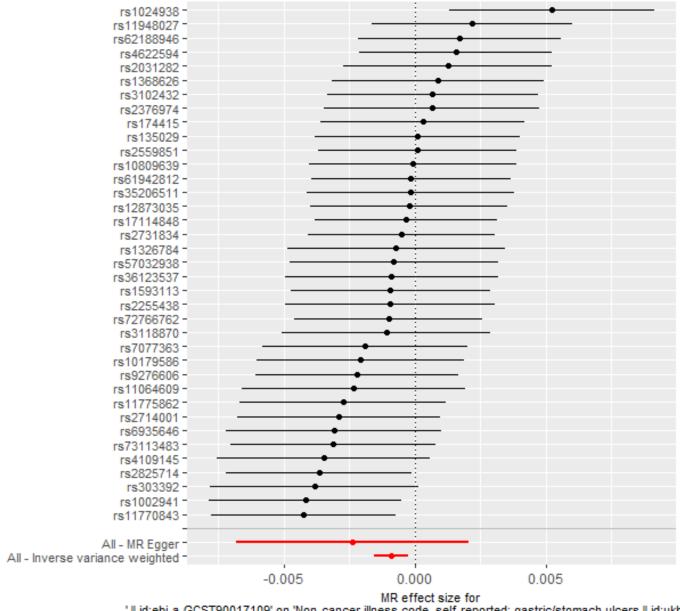
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MR Method

Inverse variance weighted

MR Egger





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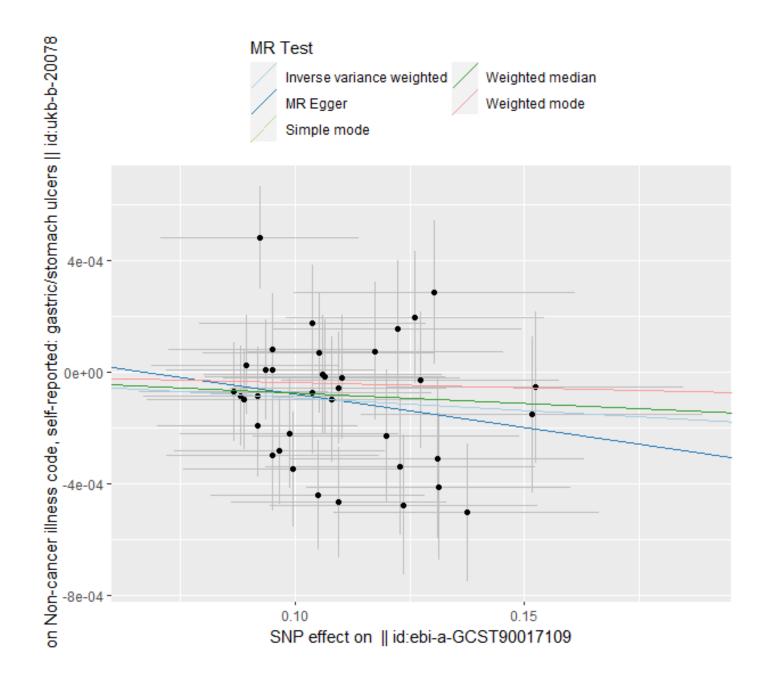
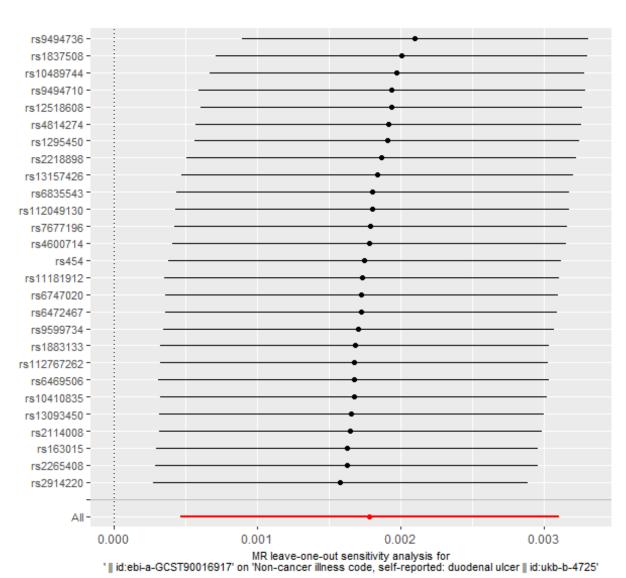


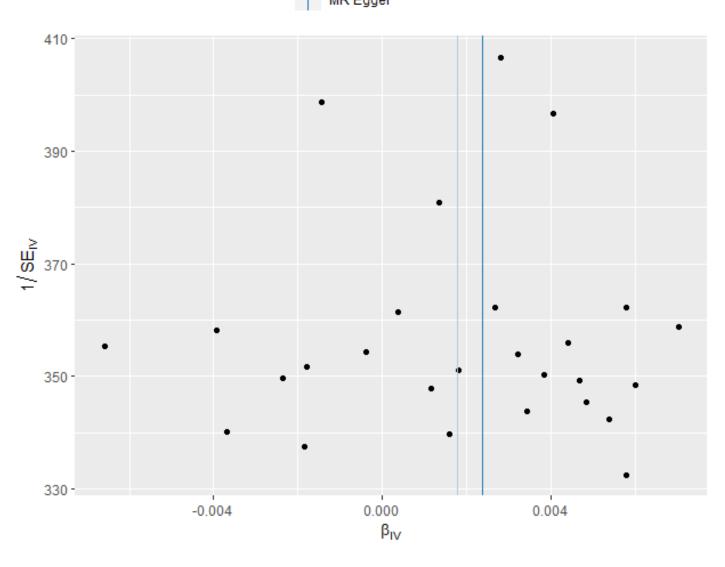
Figure 52 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Gammaproteobacteria id.3303) on duodenal ulcer

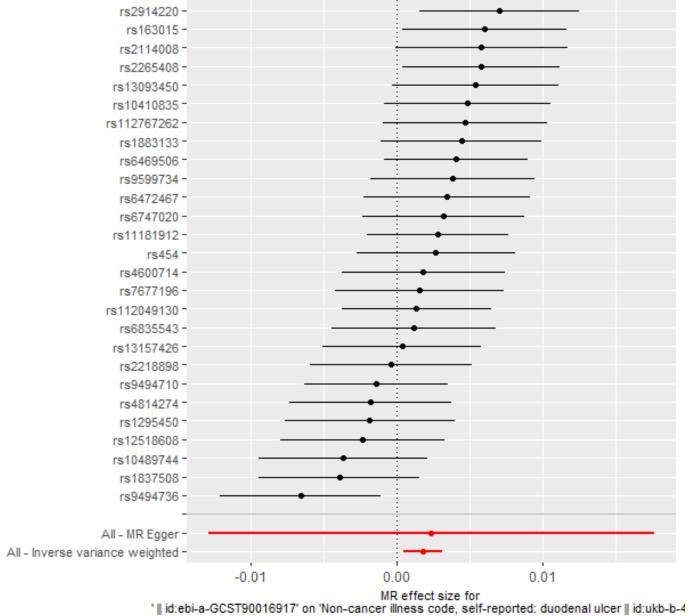


MR Method

Inverse variance weighted

MR Egger





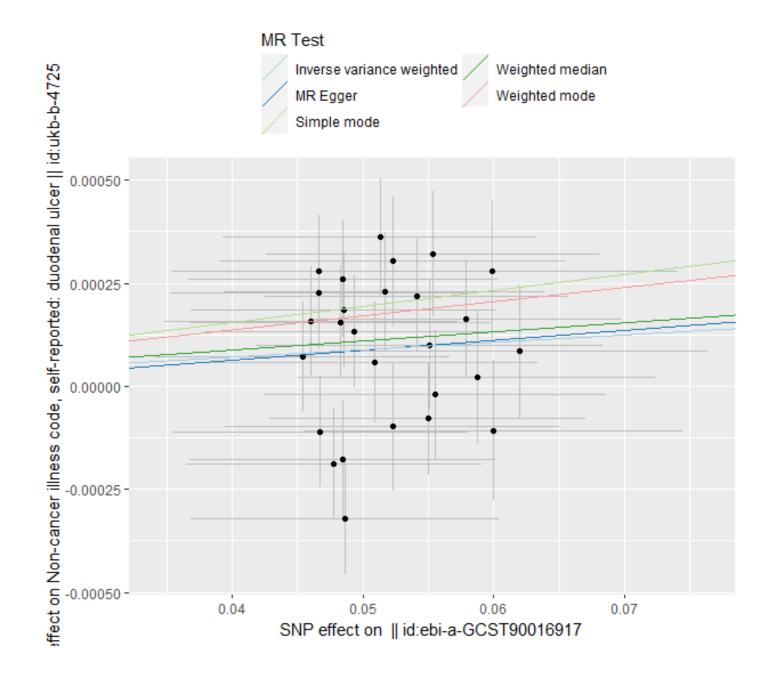
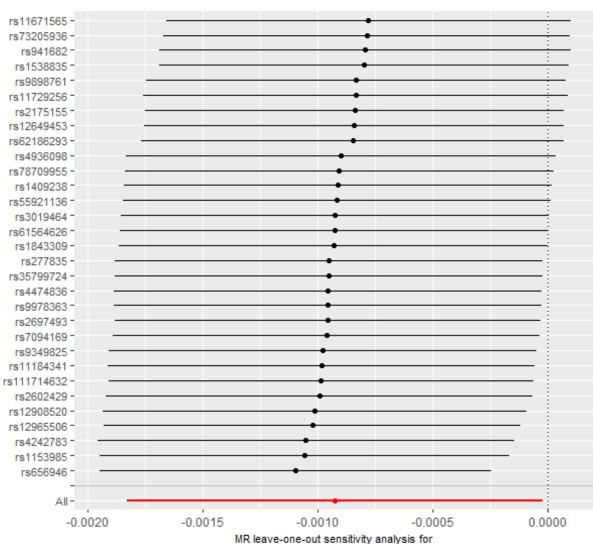
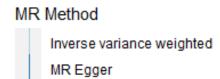
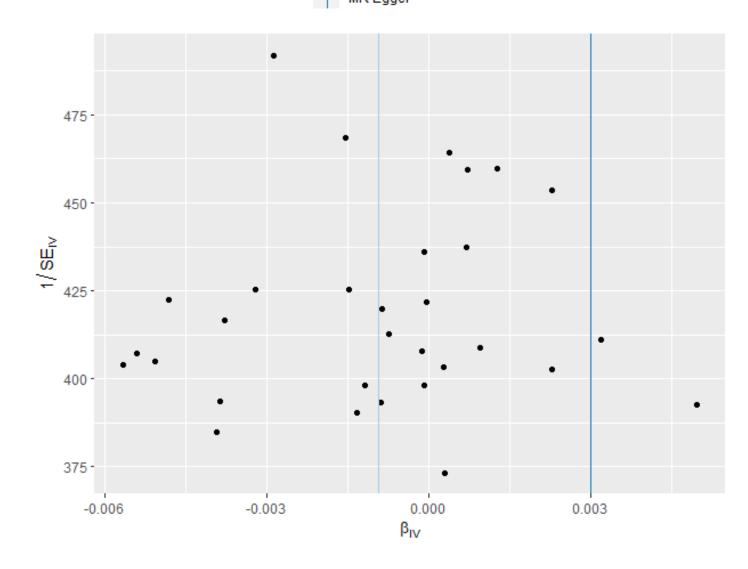


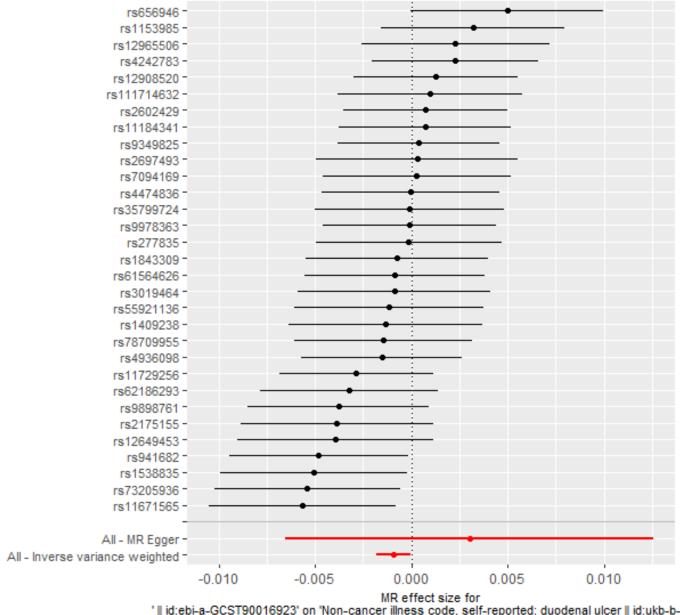
Figure 53 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Verrucomicrobiae id.4029) on duodenal ulcer



| id:ebi-a-GCST90016923' on 'Non-cancer illness code, self-reported: duodenal ulcer || id:ukb-b-4725'







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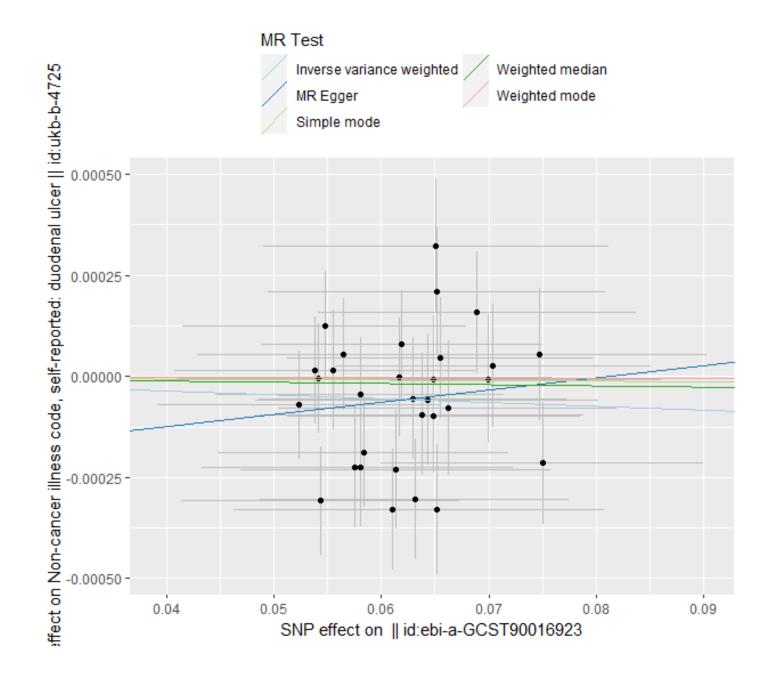
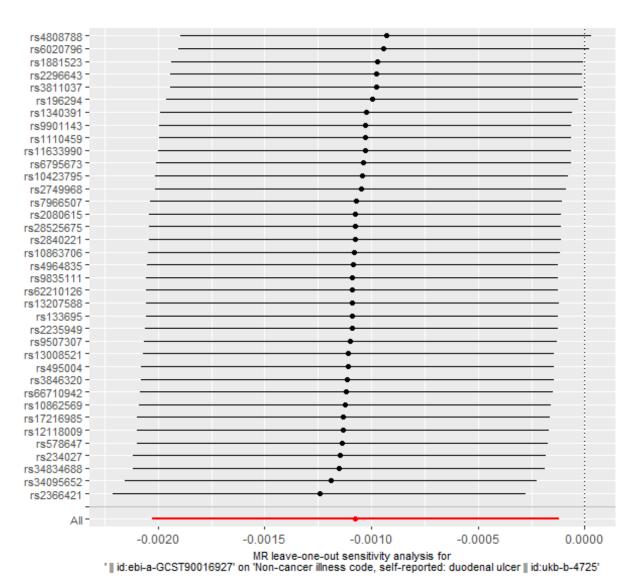
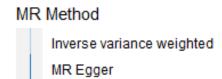
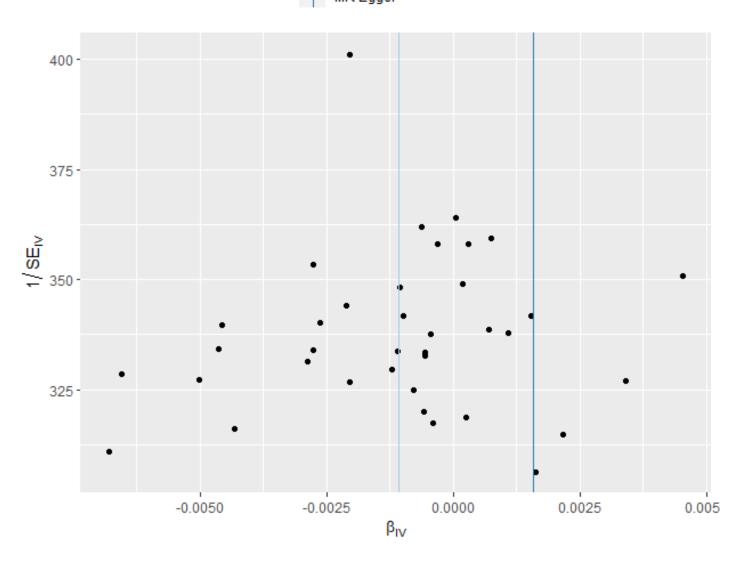
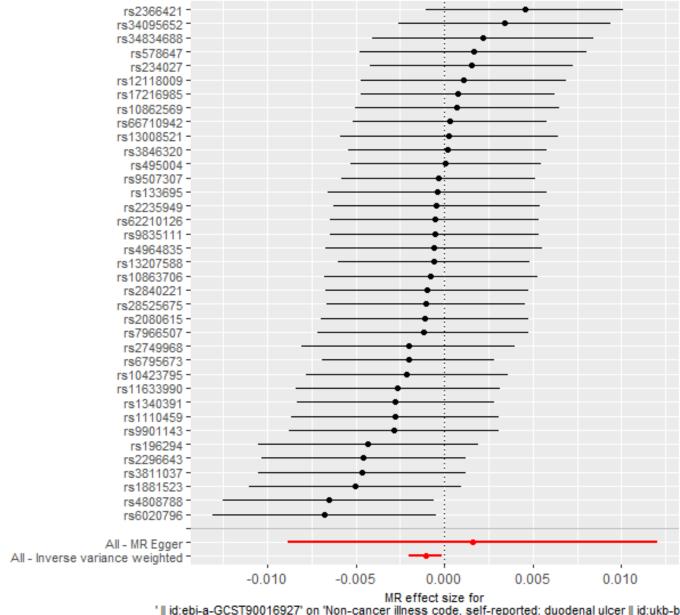


Figure 54 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Bacteroidaceae id.917) on duodenal ulcer









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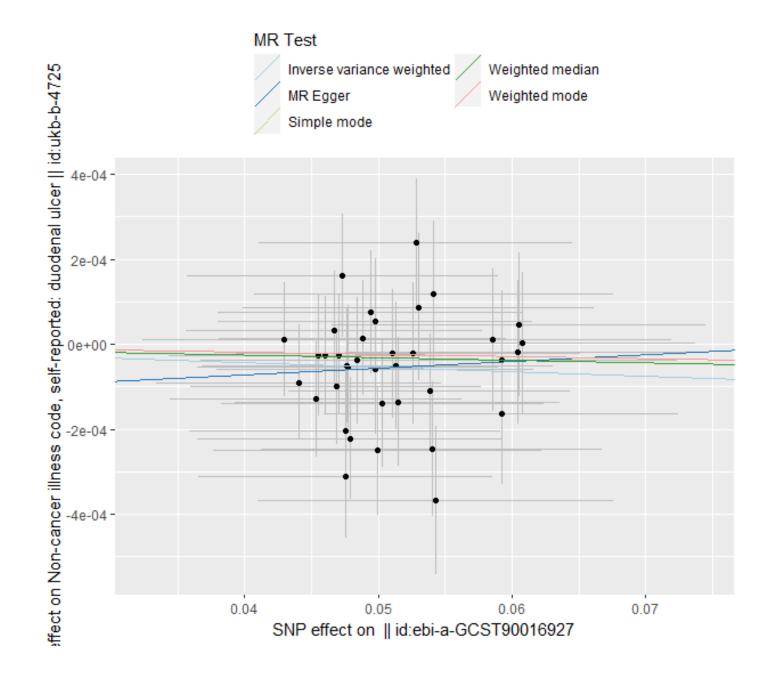
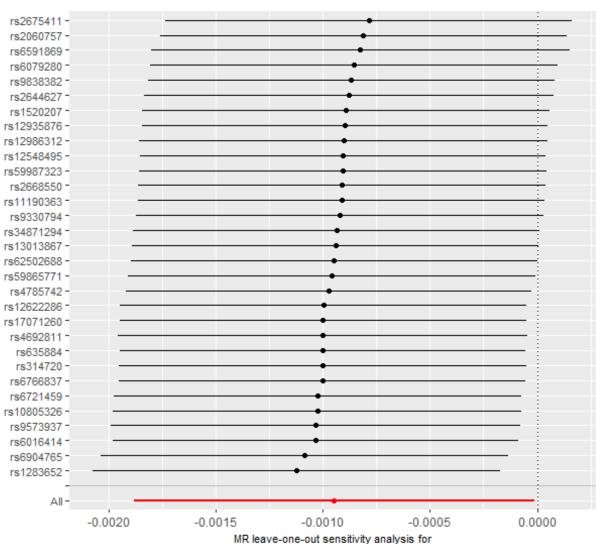
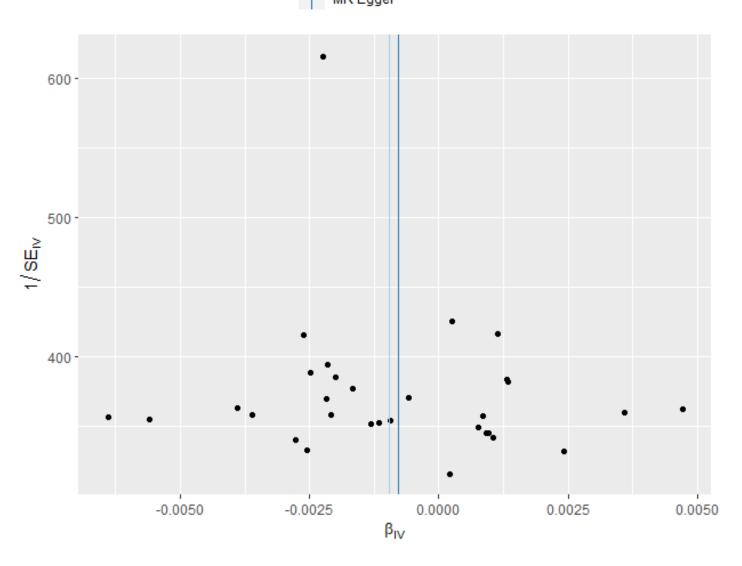


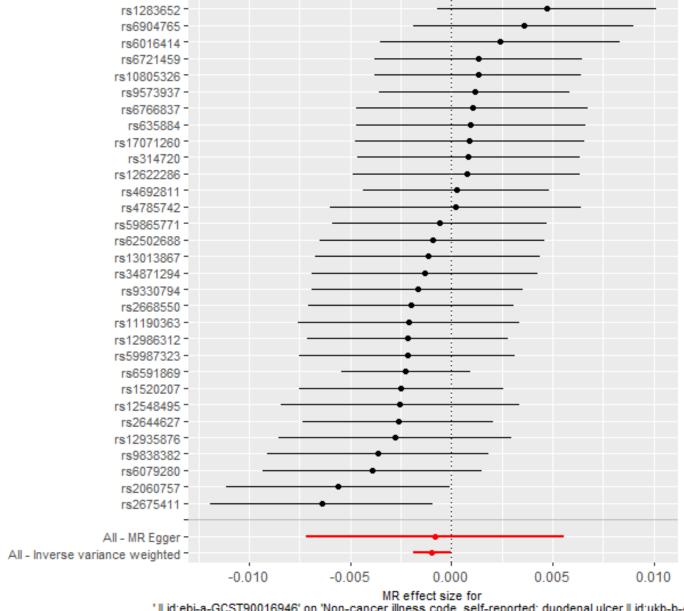
Figure 55 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Peptostreptococcaceae id.2042) on duodenal ulcer



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MR Method
Inverse variance weighted
MR Egger





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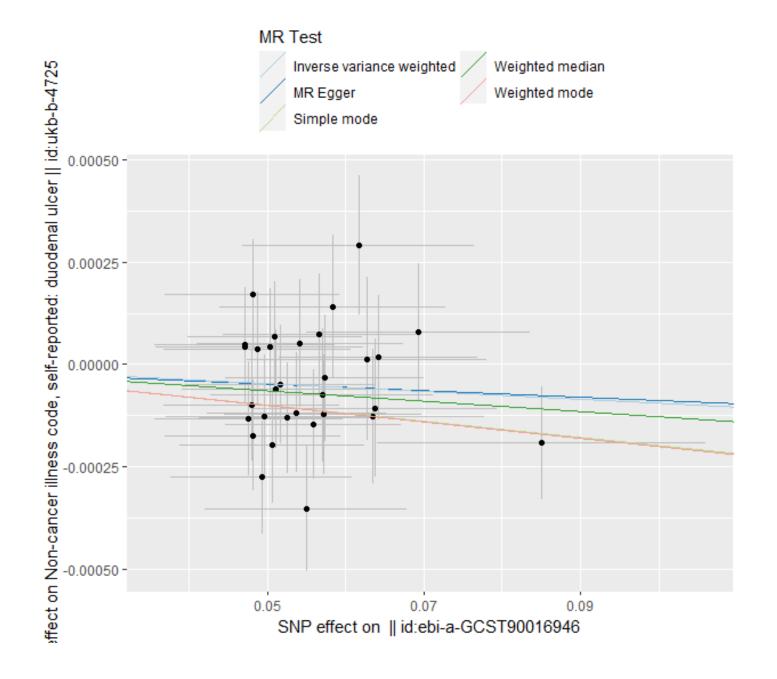
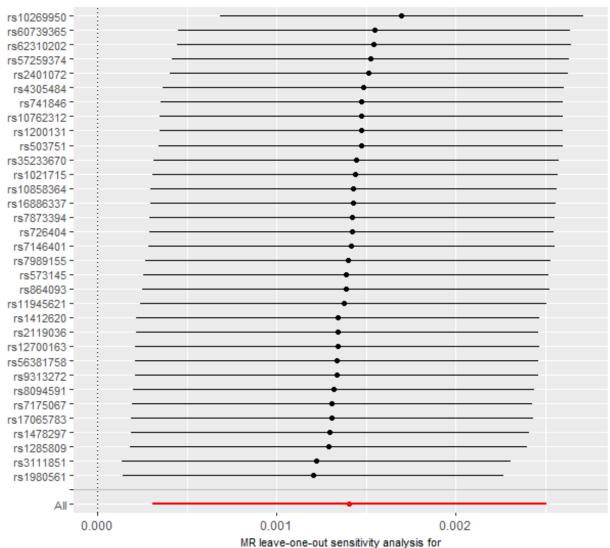


Figure 56 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Porphyromonadaceae id.943) on duodenal ulcer

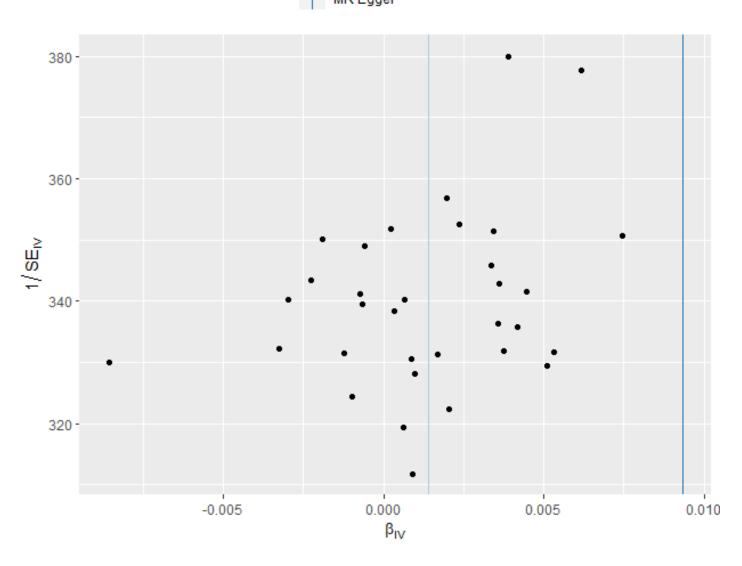


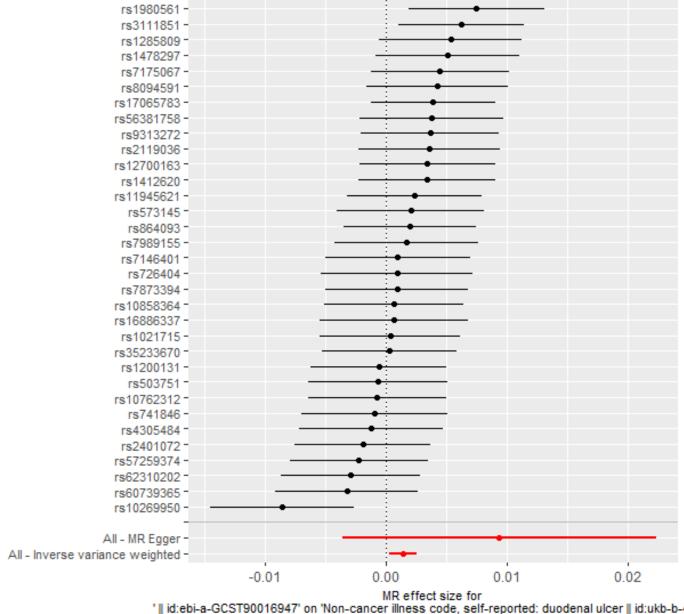
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MR Method

Inverse variance weighted

MR Egger





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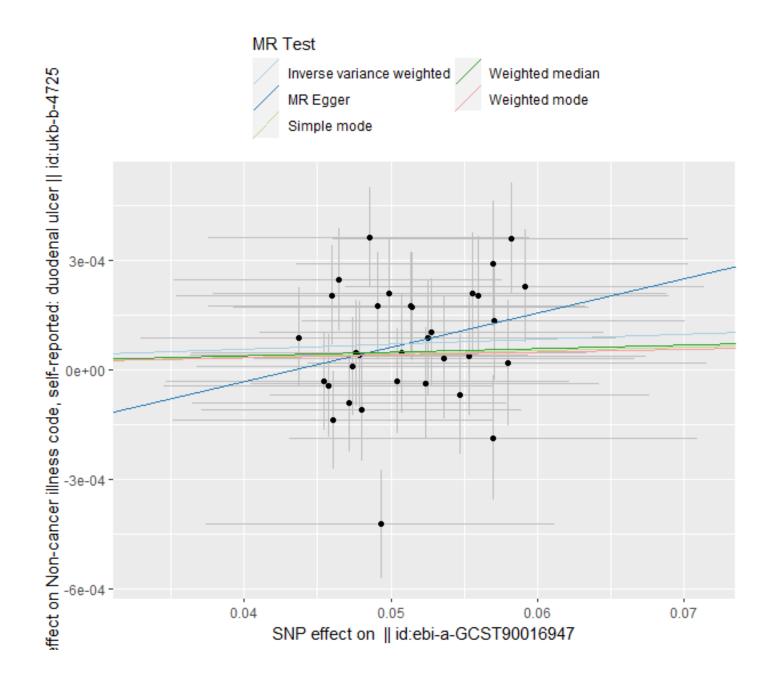
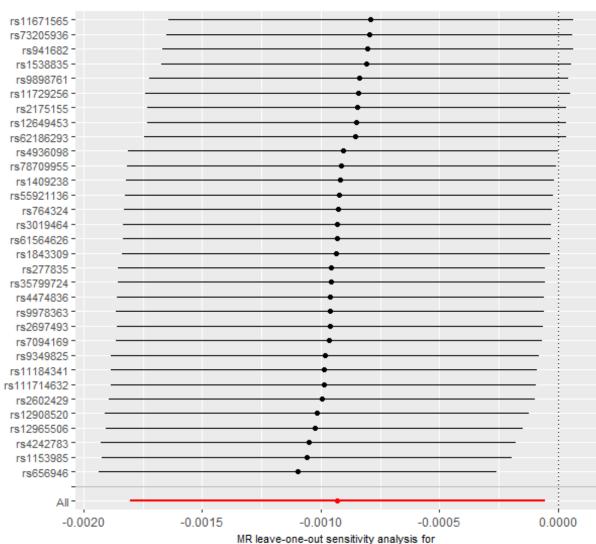


Figure 57 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Verrucomicrobiaceae id.4036) on duodenal ulcer

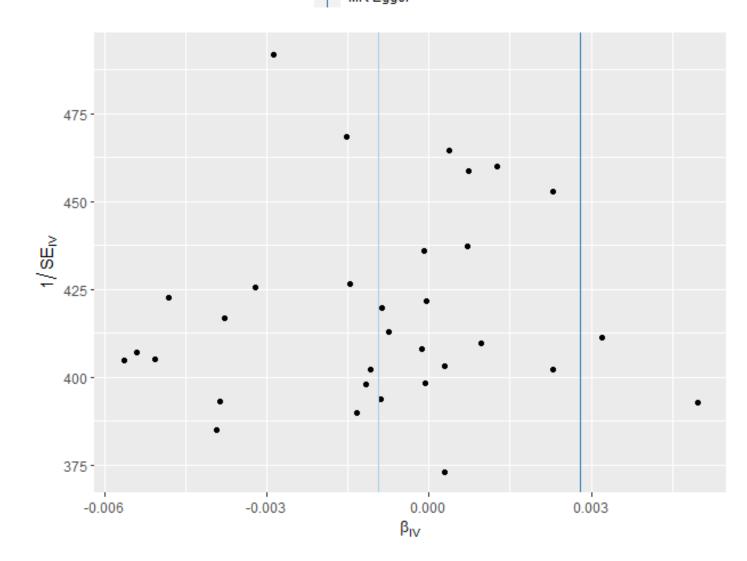


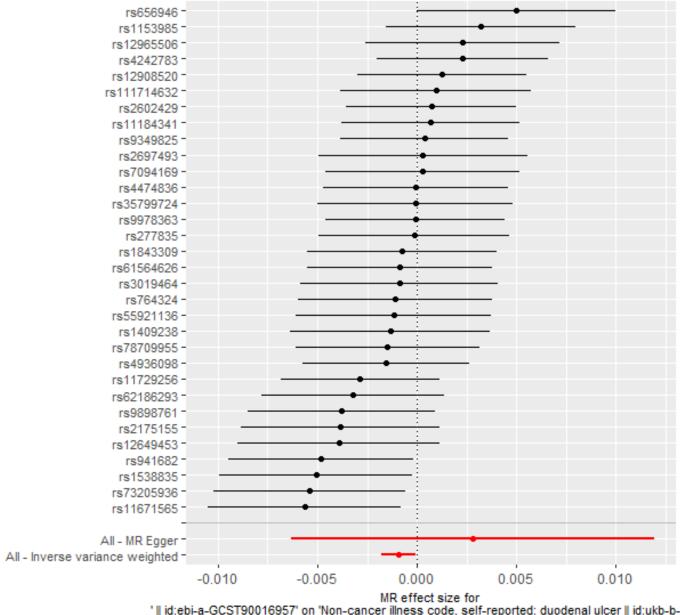
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MR Method

Inverse variance weighted

MR Egger





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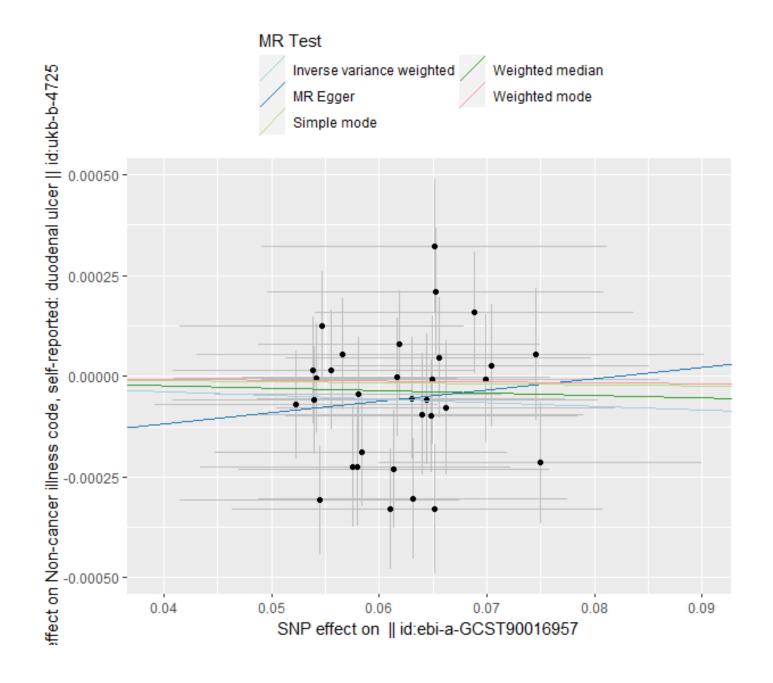
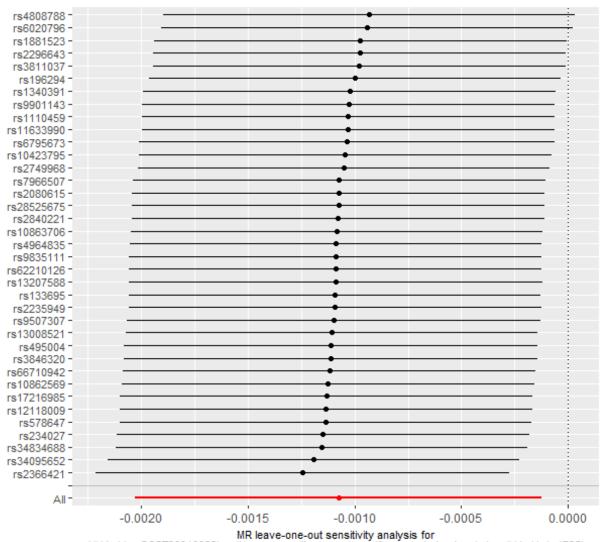


Figure 58 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Bacteroides id.918) on duodenal ulcer

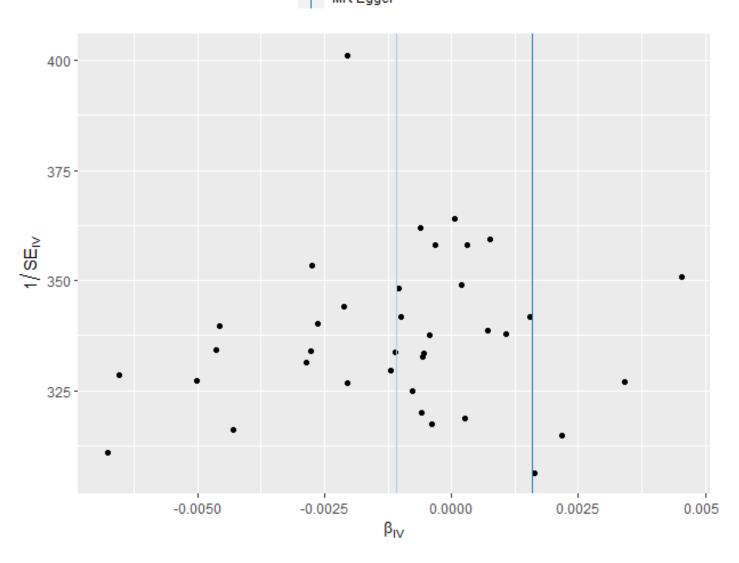


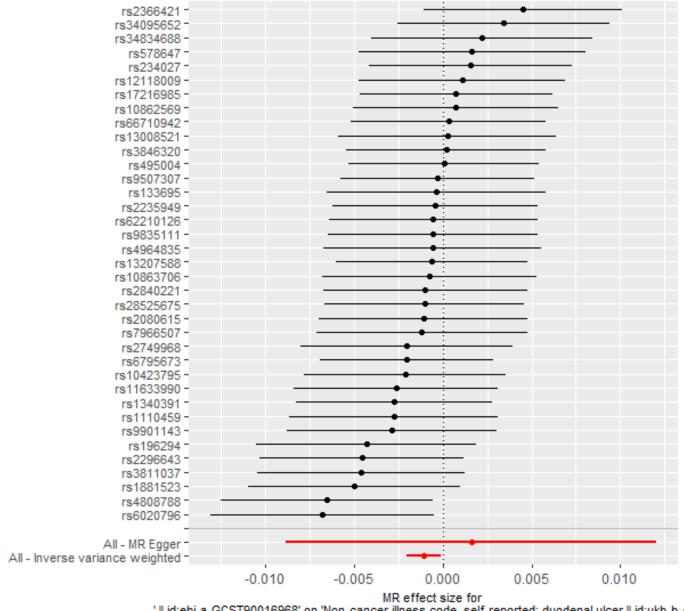
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MR Method

Inverse variance weighted

MR Egger





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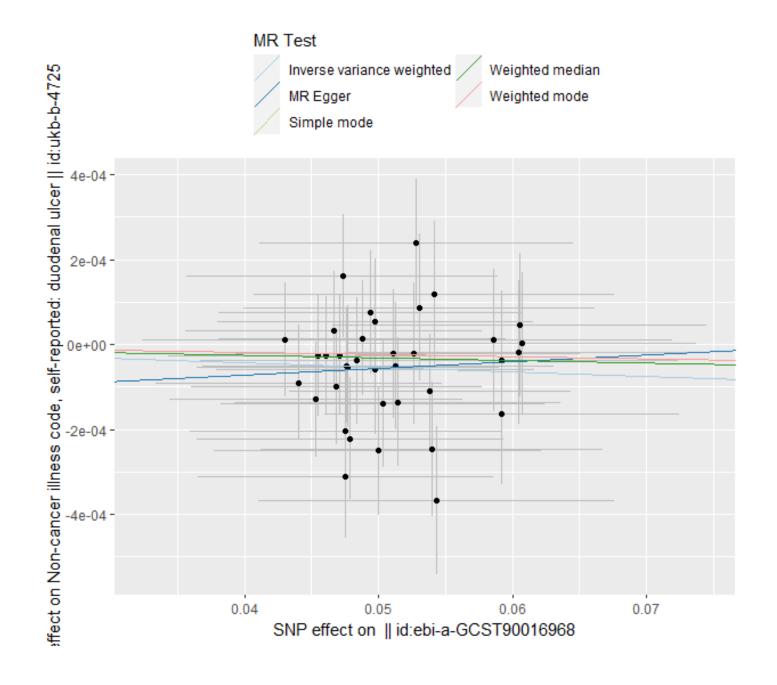
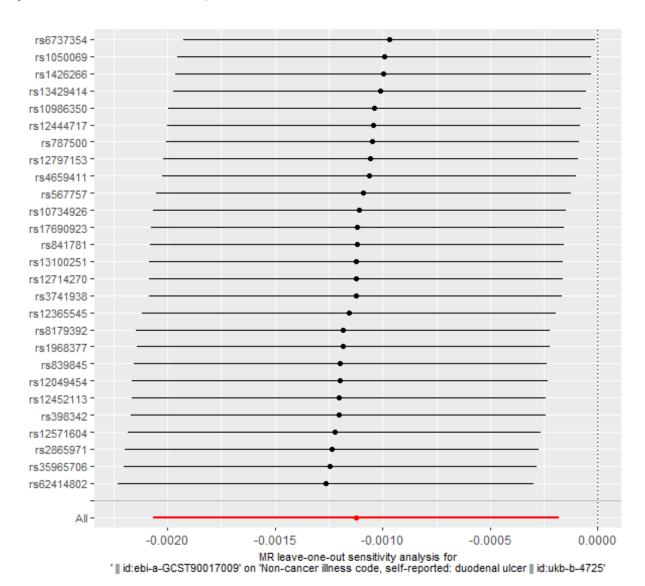


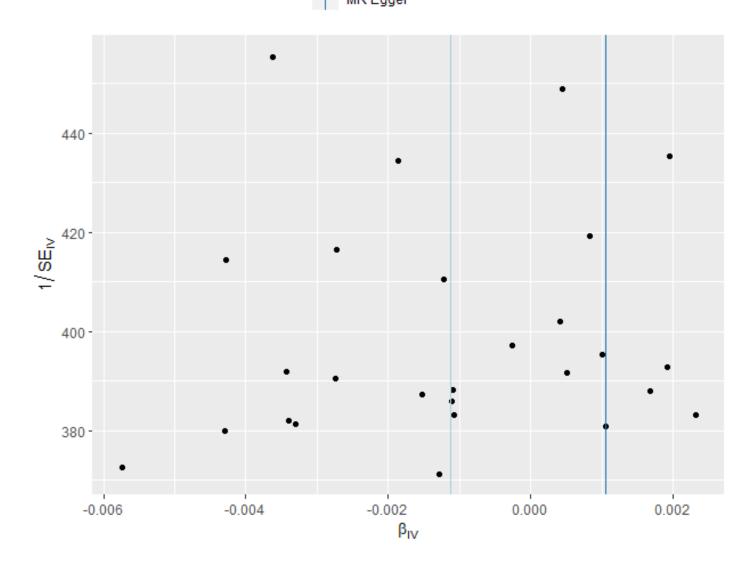
Figure 59 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Family XIII UCG001 id.11294) on duodenal ulcer

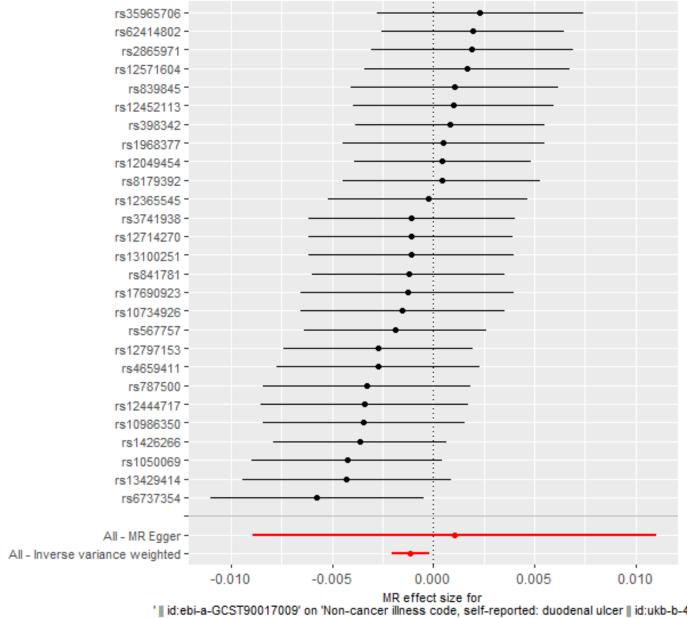


MR Method

Inverse variance weighted

MR Egger





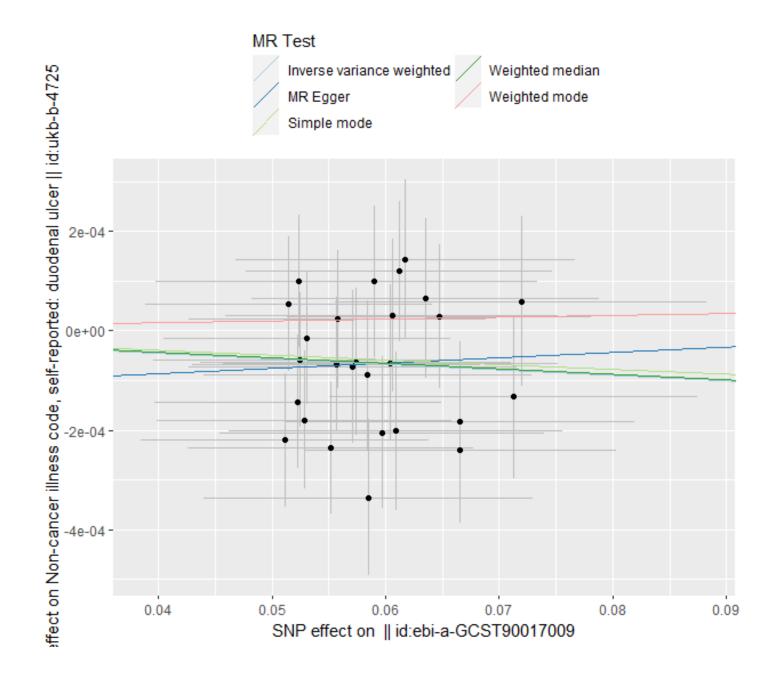
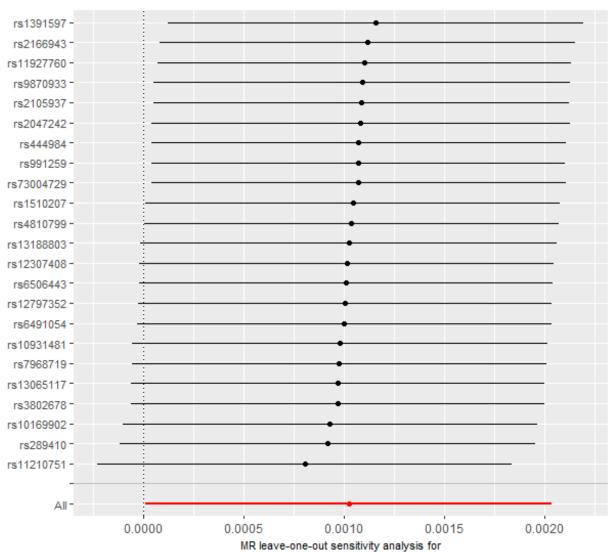
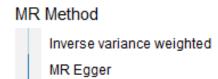
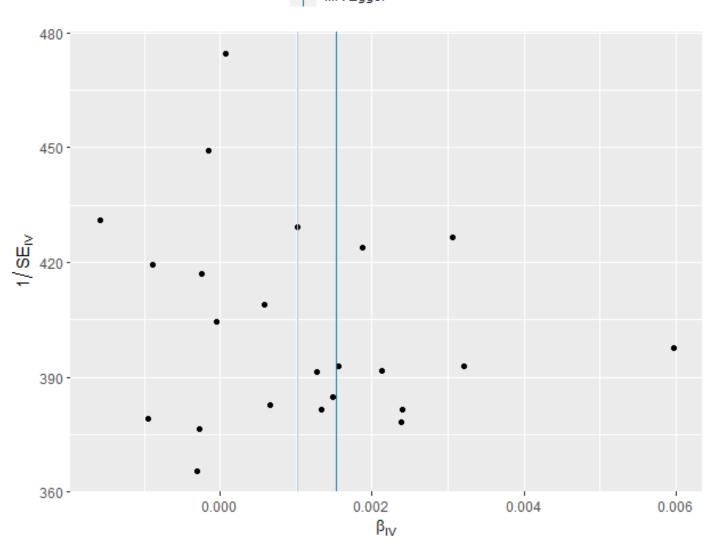


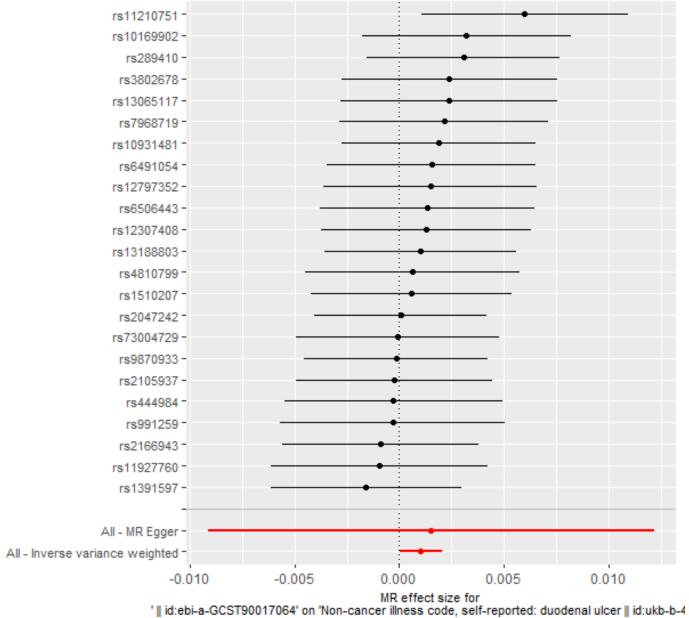
Figure 60 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcus gauvreauii group id.11342) on duodenal ulcer



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017064' on 'Non-cancer illness code, self-reported: duodenal ulcer || id:ukb-b-4725'







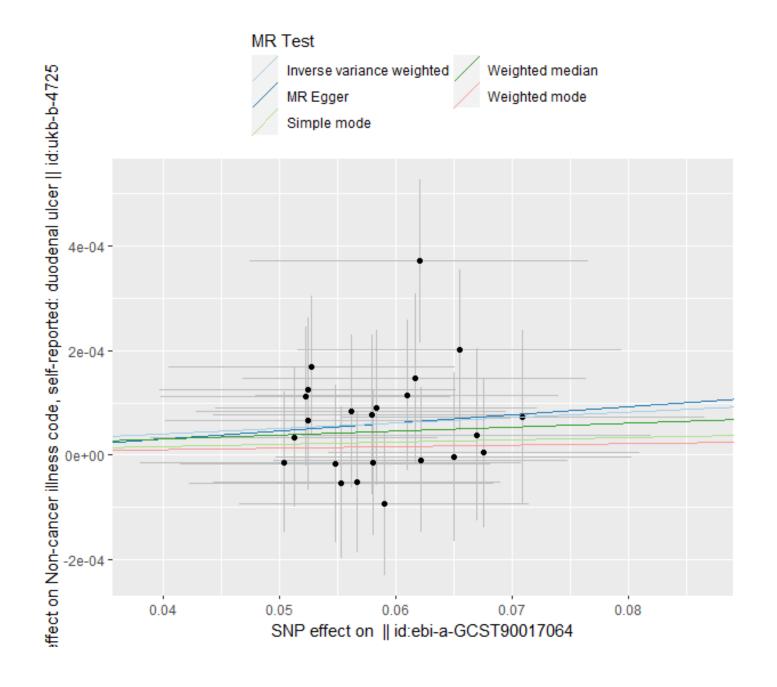
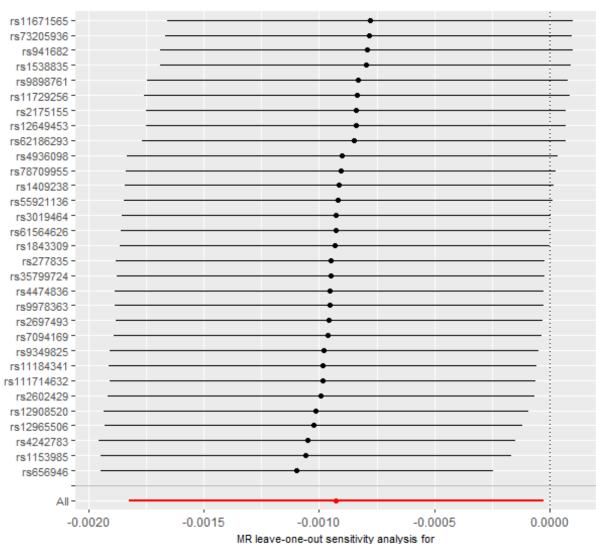


Figure 61 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Verrucomicrobiales id.4030) on duodenal ulcer

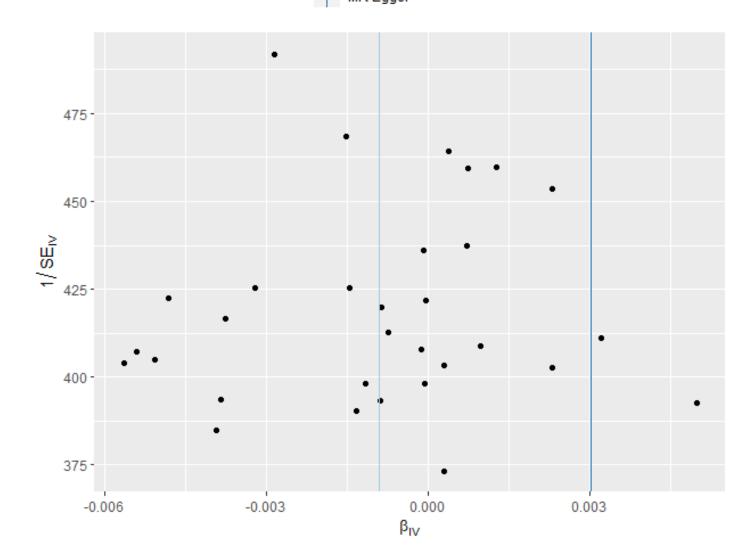


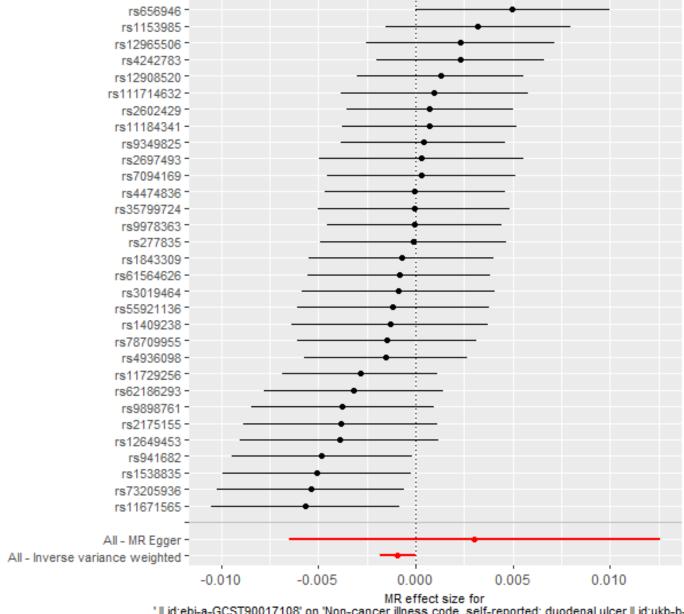
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MR Method

Inverse variance weighted

MR Egger





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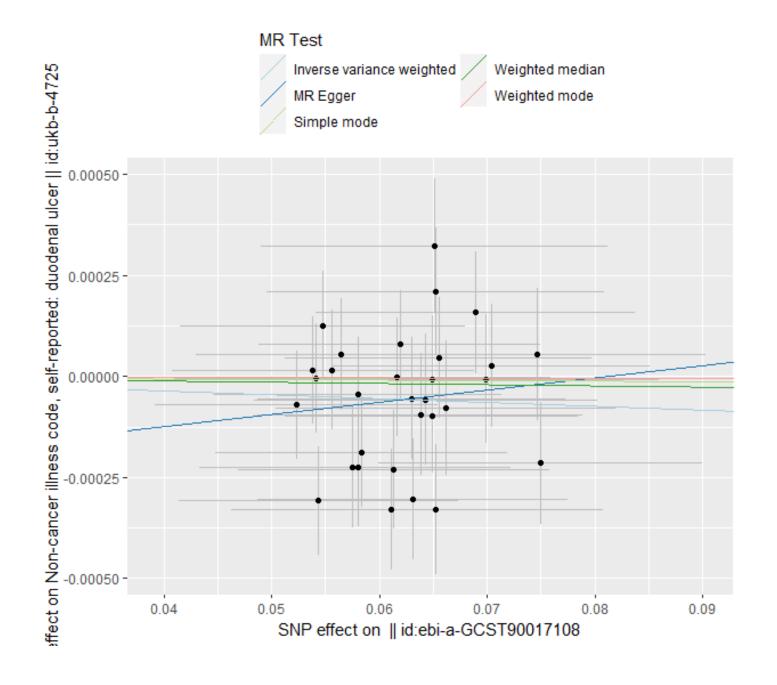
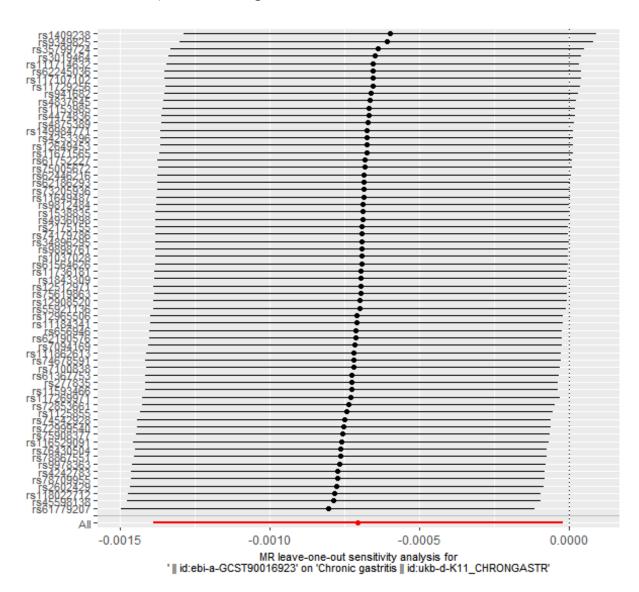


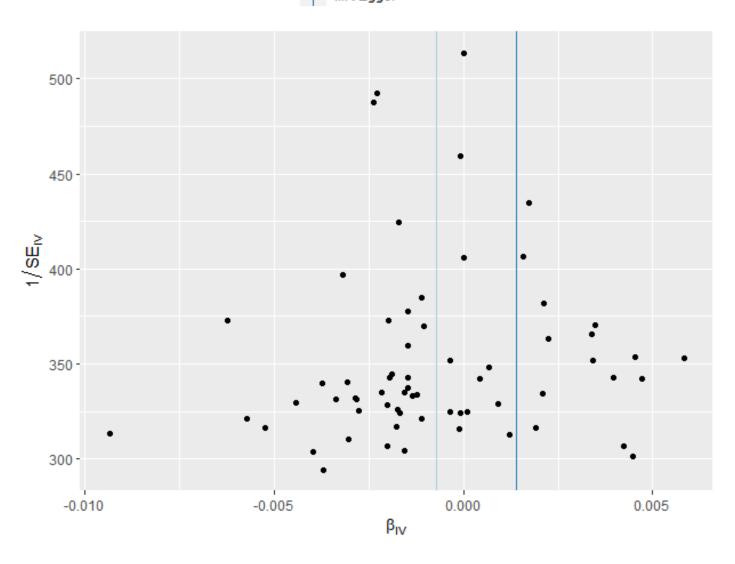
Figure 62 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Verrucomicrobiae id.4029) on chronic gastritis

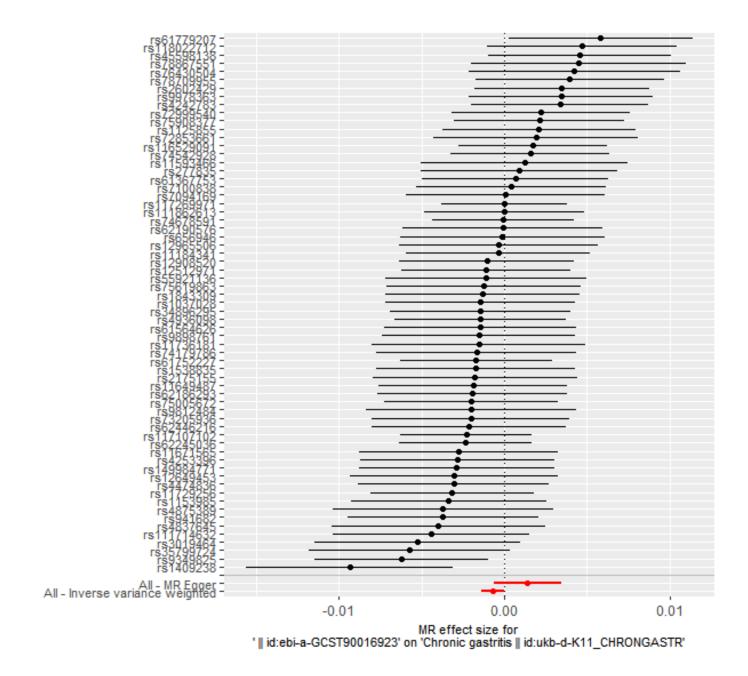


MR Method

Inverse variance weighted

MR Egger





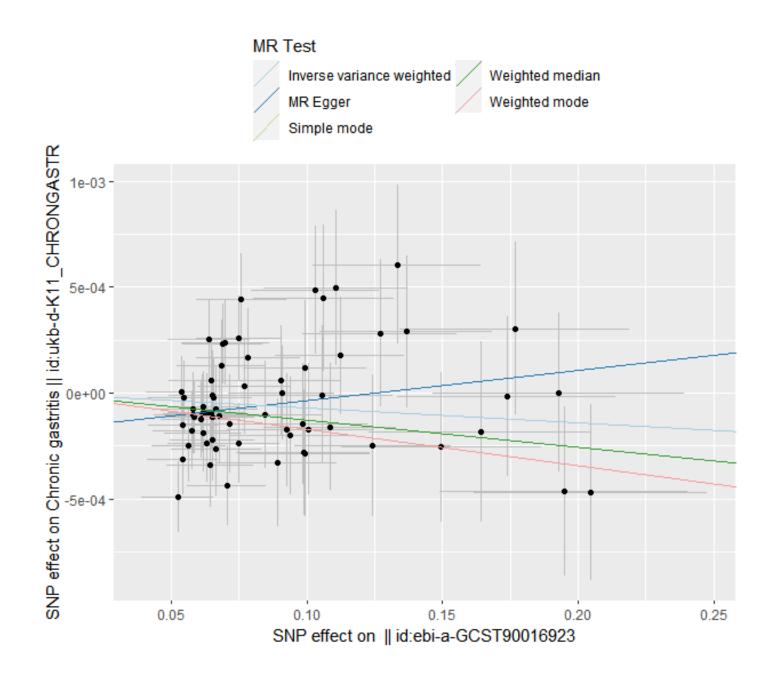
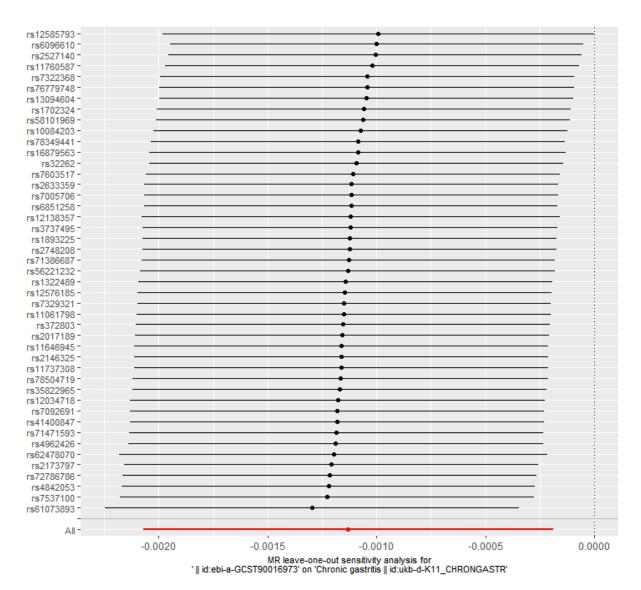
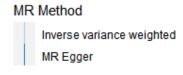
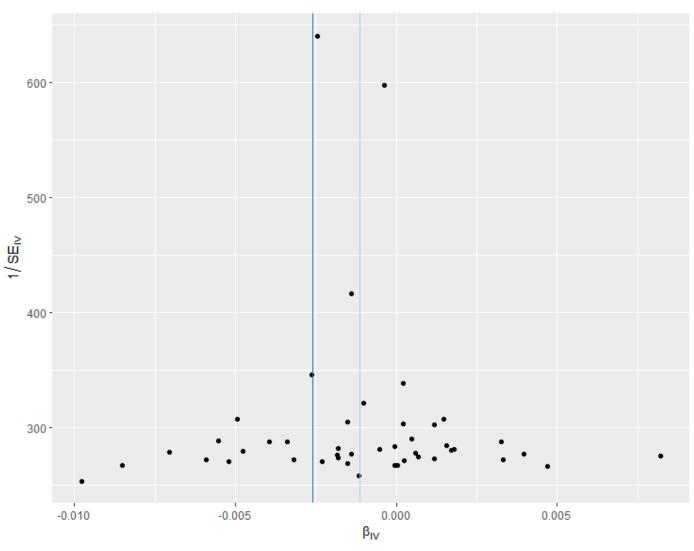
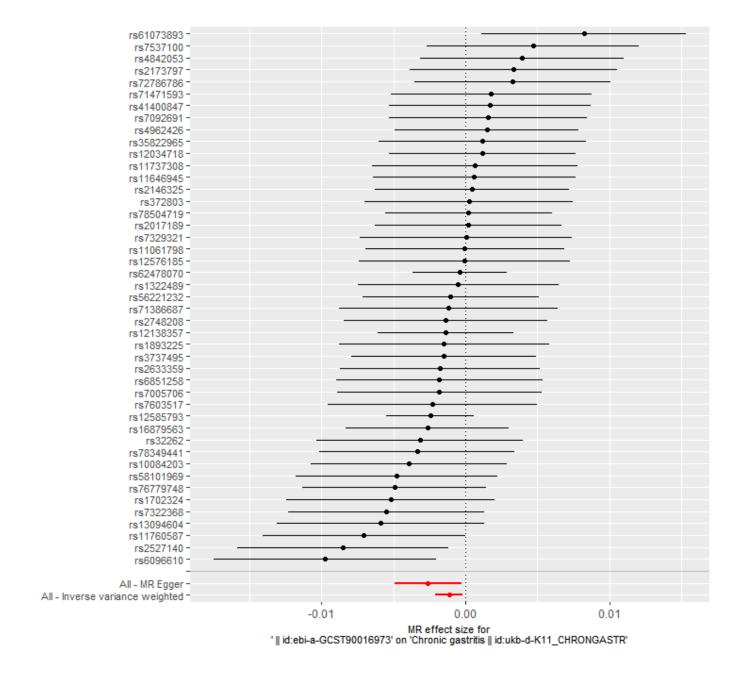


Figure 63 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Butyricicoccus id.2055) on chronic gastritis









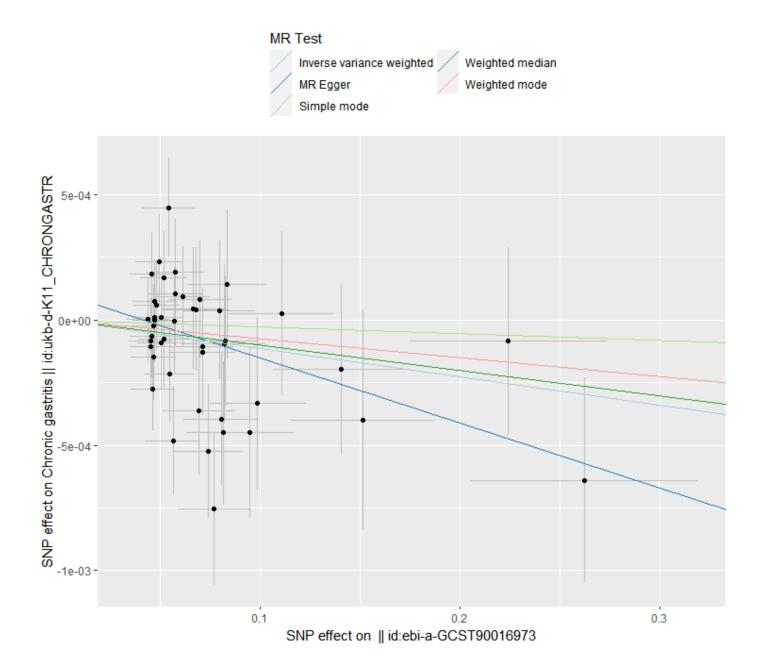
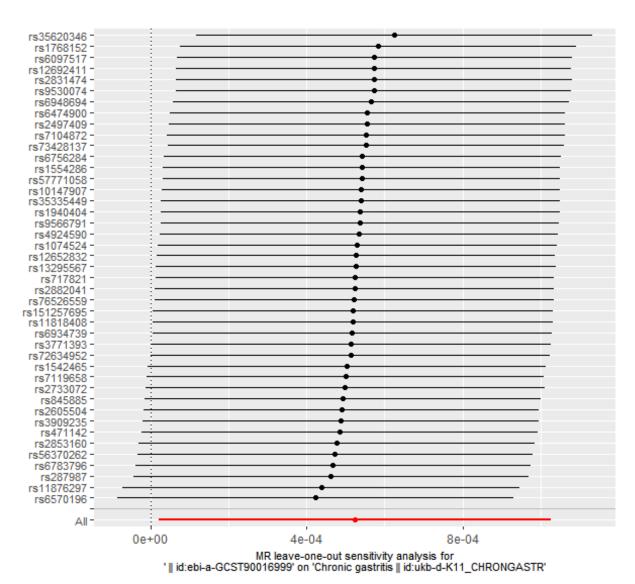
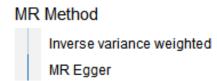
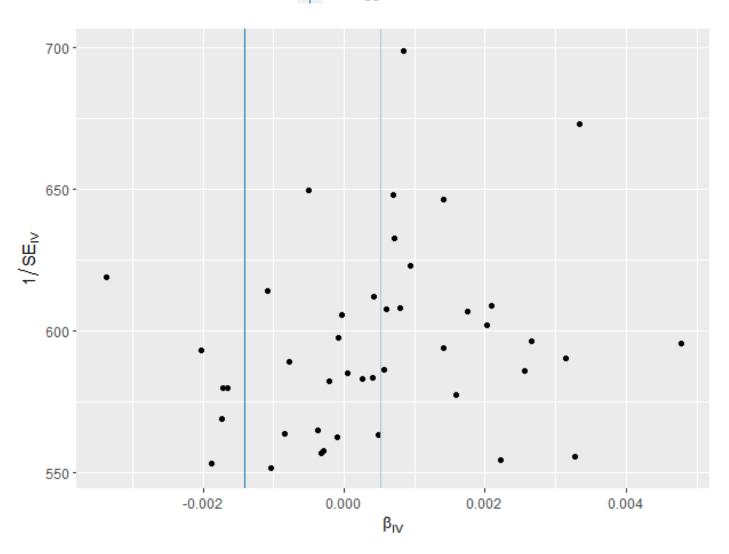
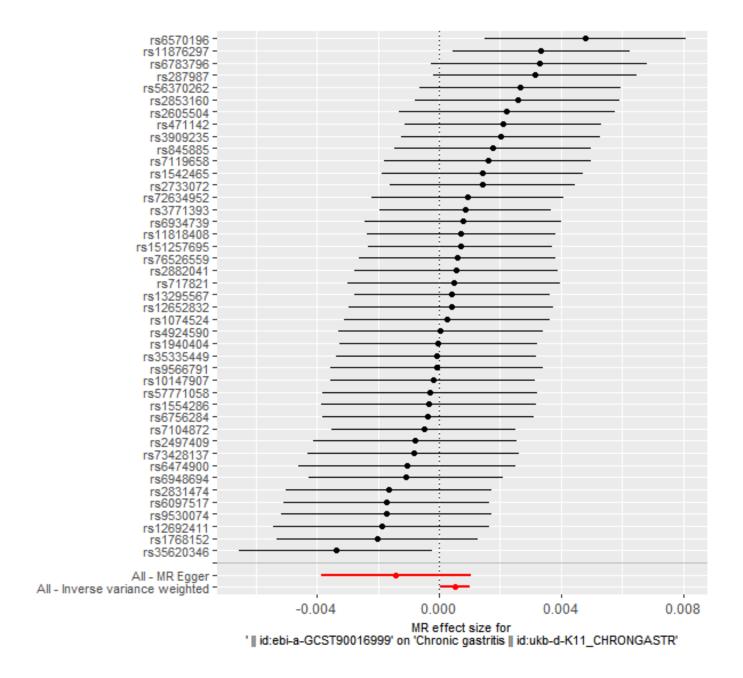


Figure 64 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium fissicatena group id.14373) on chronic gastritis









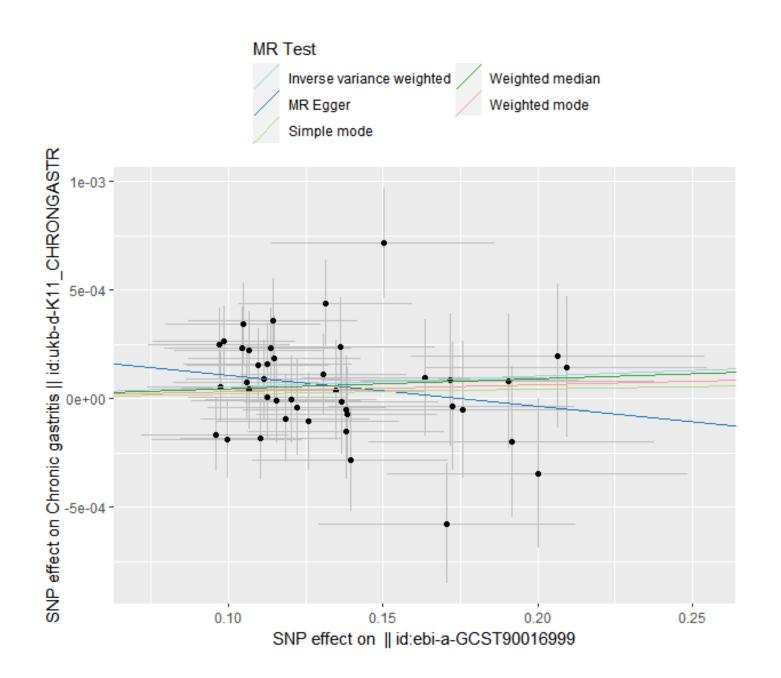
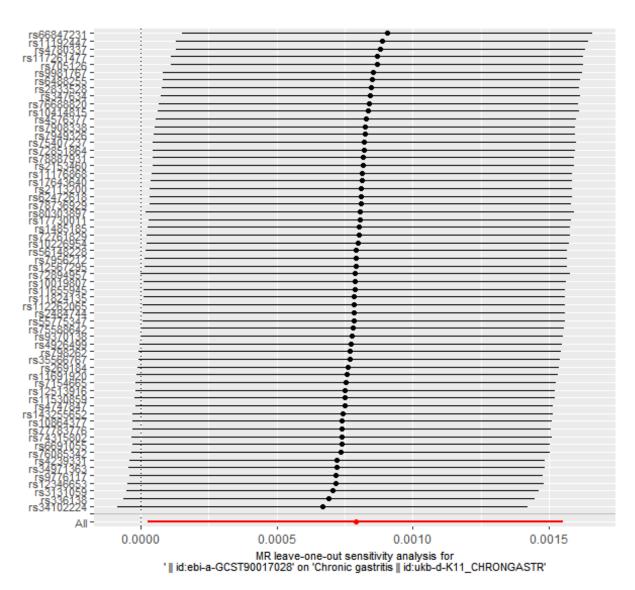


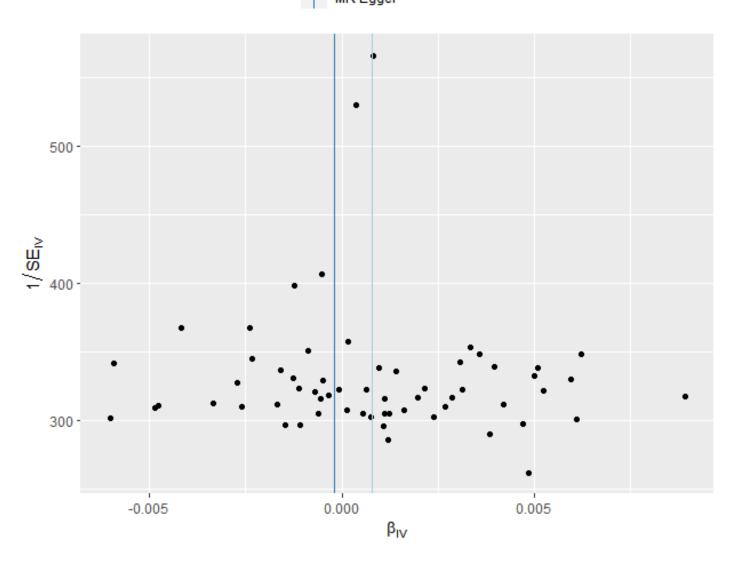
Figure 65 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lachnospiraceae UCG010 id.11330) on chronic gastritis

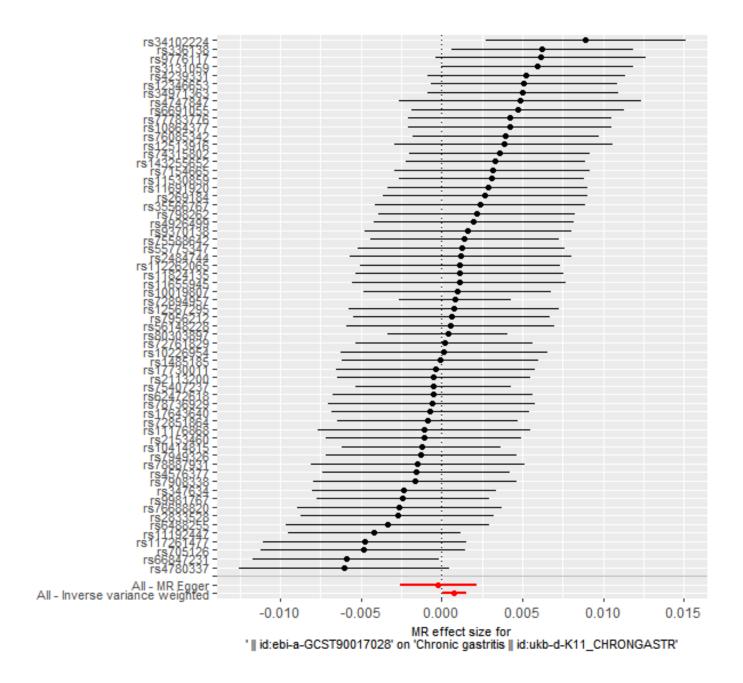


MR Method

Inverse variance weighted

MR Egger





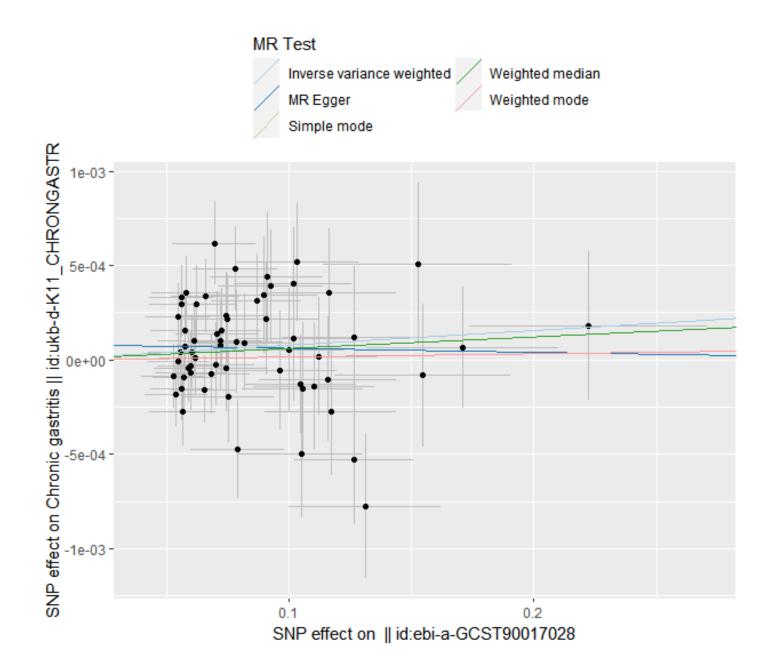
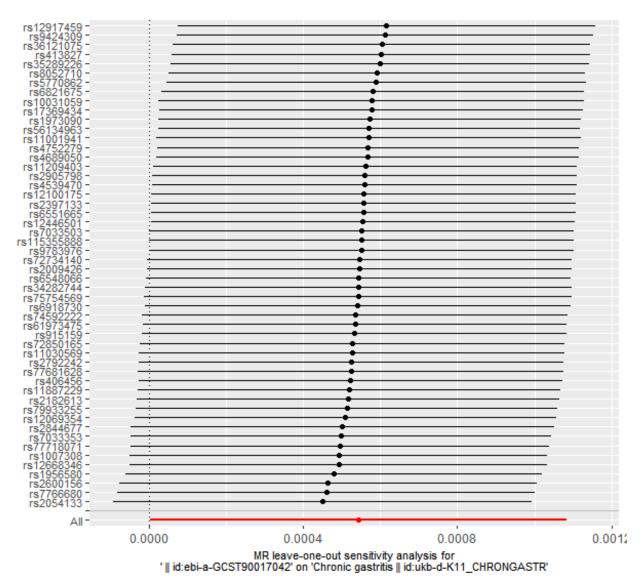
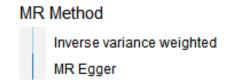
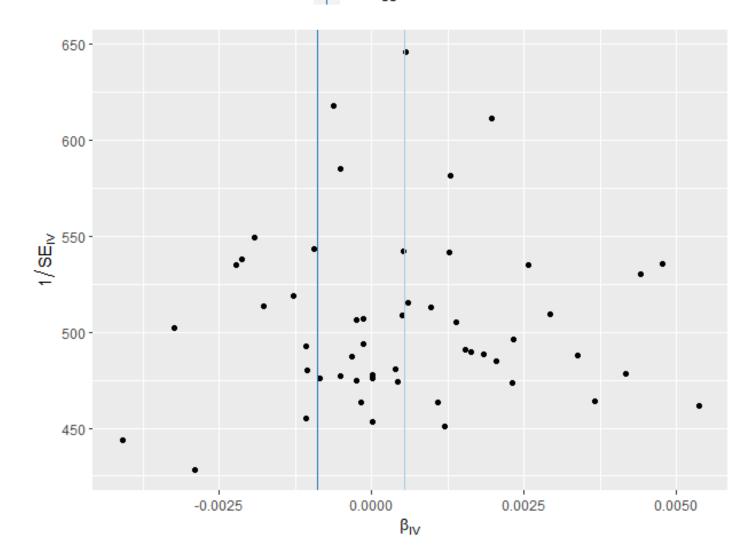
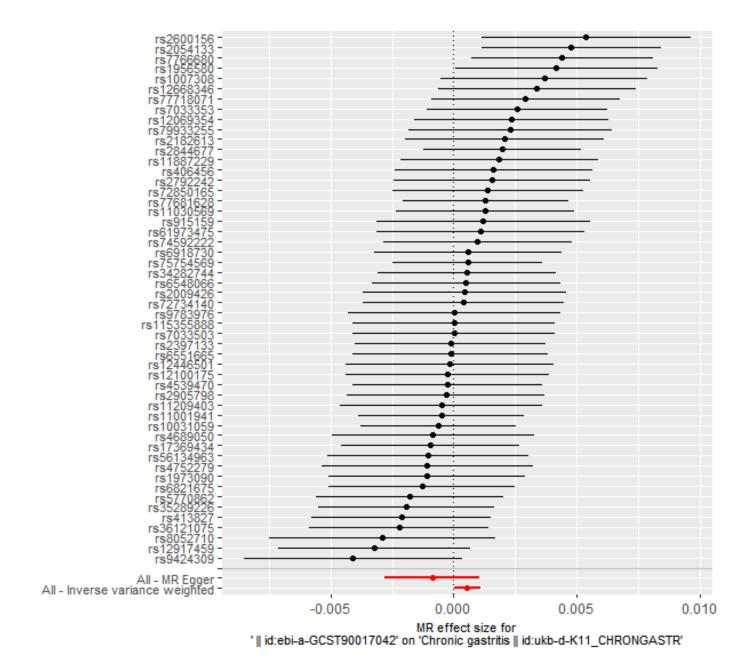


Figure 66 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Peptococcus id.2037) on chronic gastritis









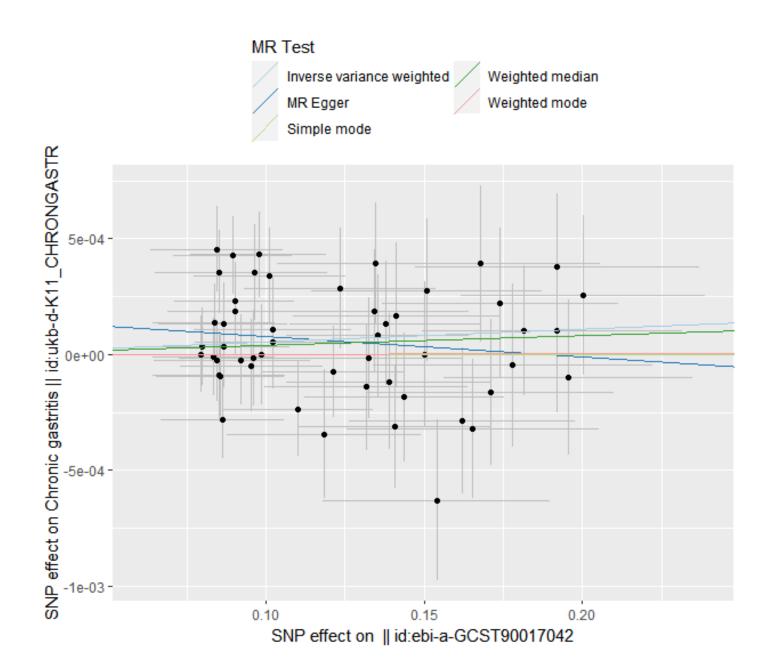
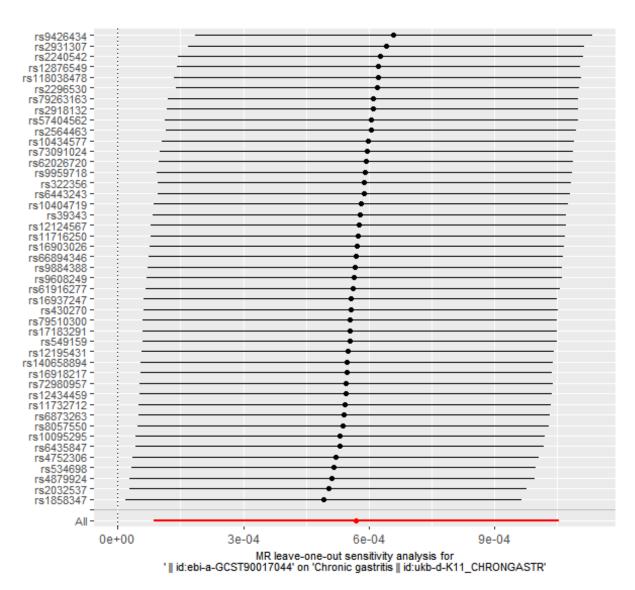
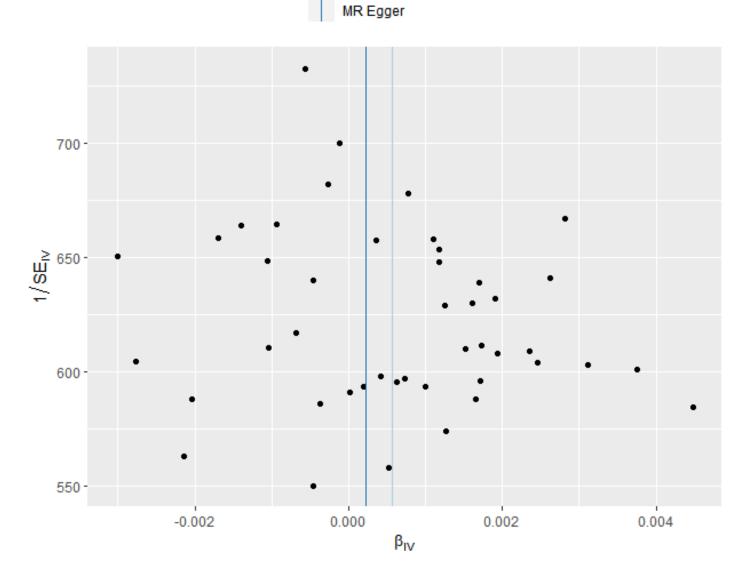


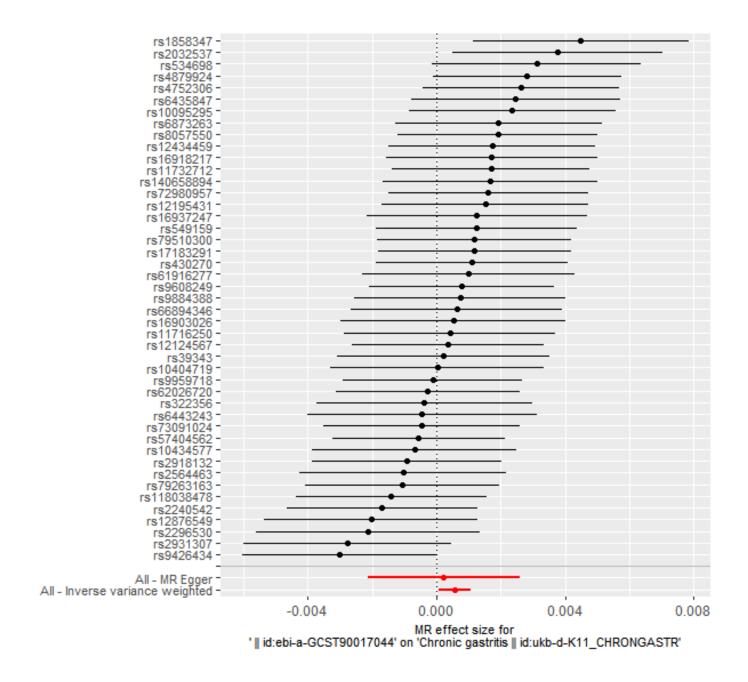
Figure 67 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Prevotella7 id.11182) on chronic gastritis



MR Method

Inverse variance weighted





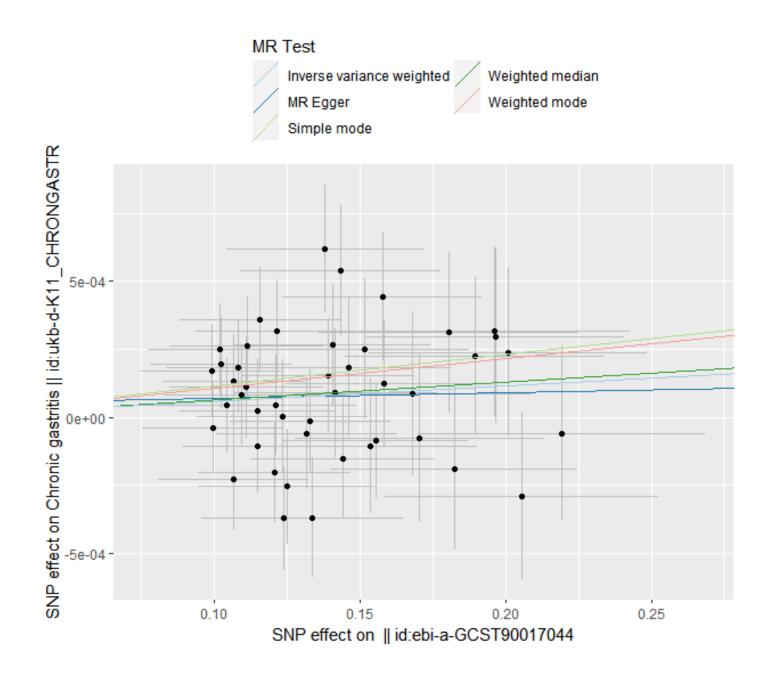
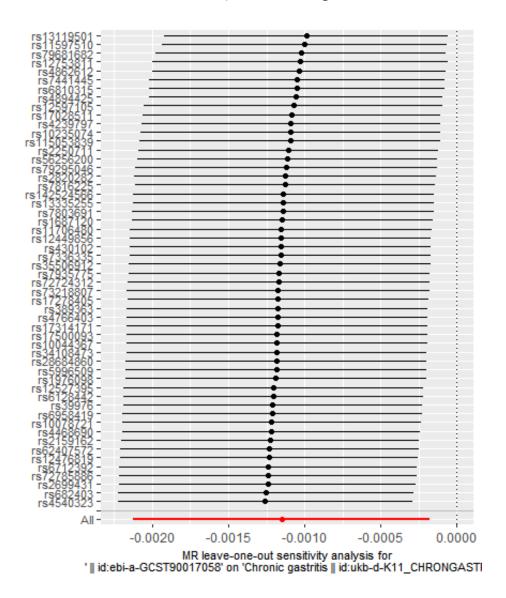


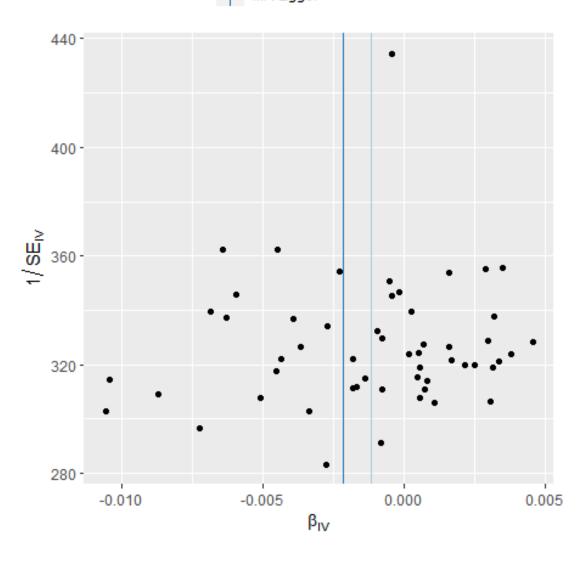
Figure 68 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG010 id.11367) on chronic gastritis

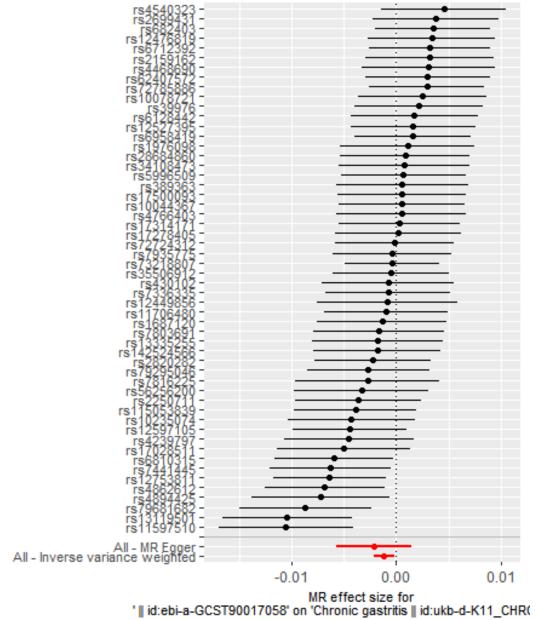


MR Method

Inverse variance weighted

MR Egger





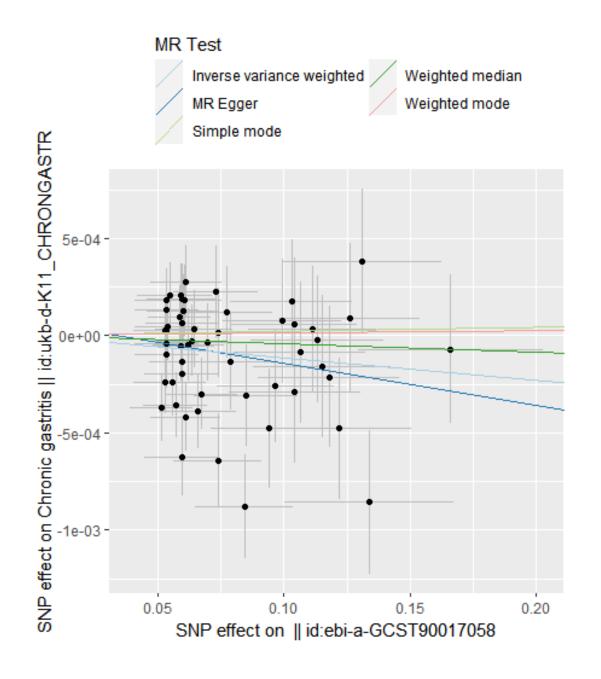
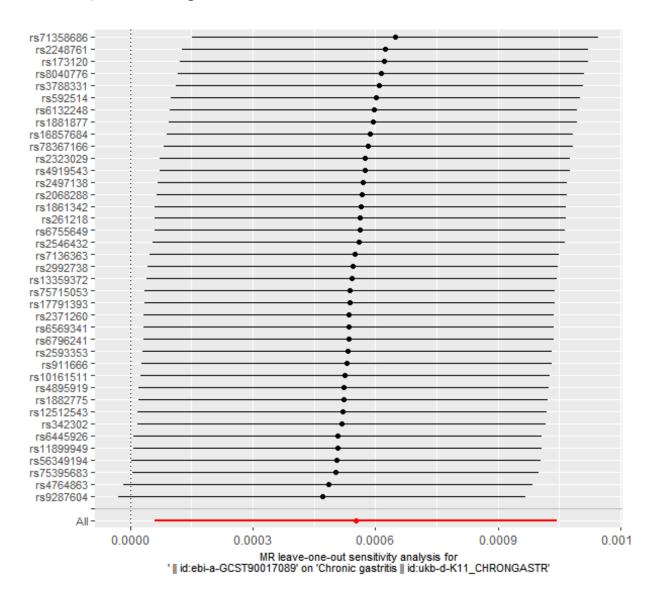


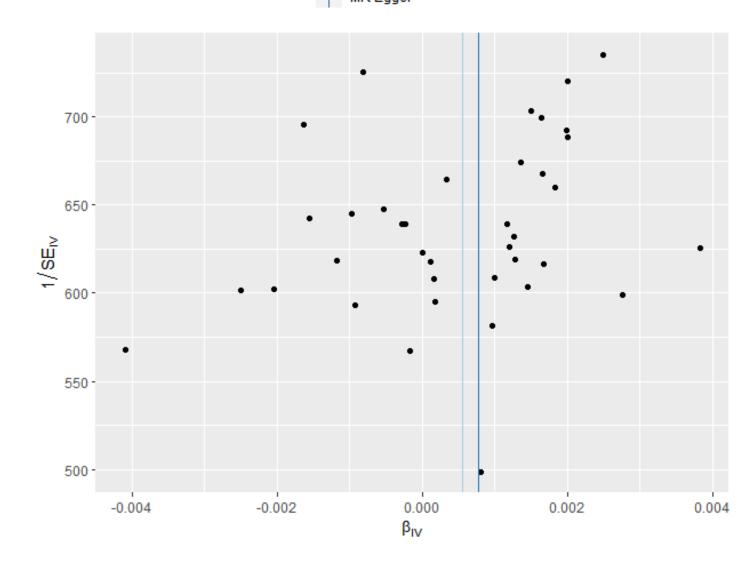
Figure 69 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Victivallis id.2256) on chronic gastritis

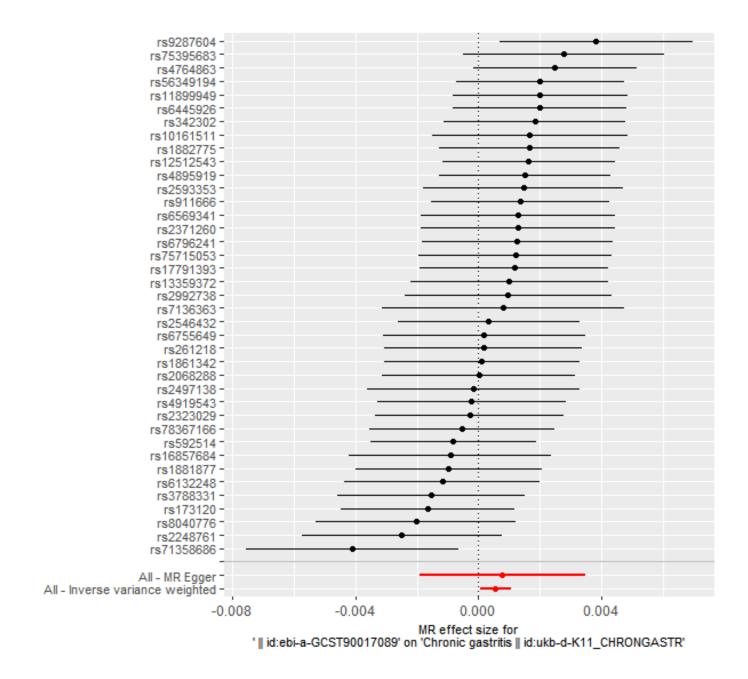


MR Method

Inverse variance weighted

MR Egger





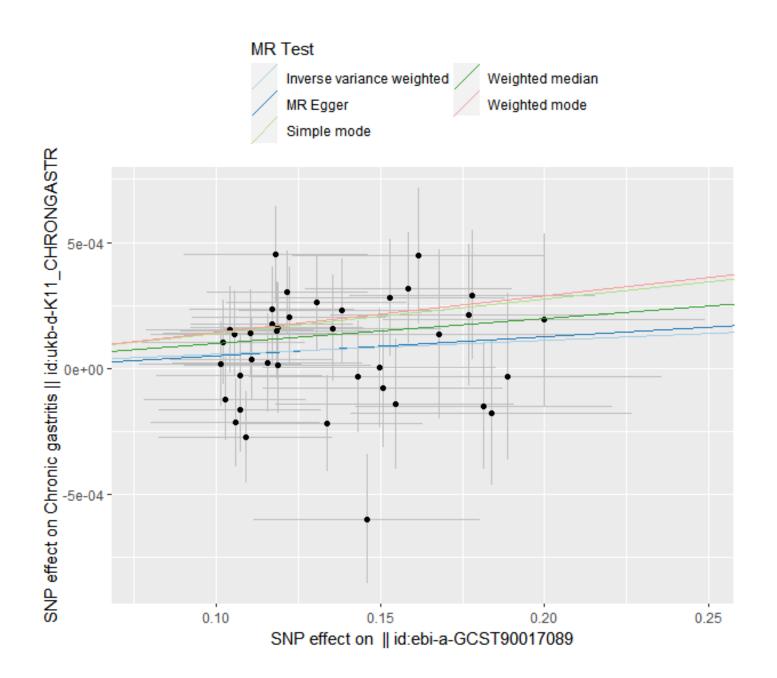
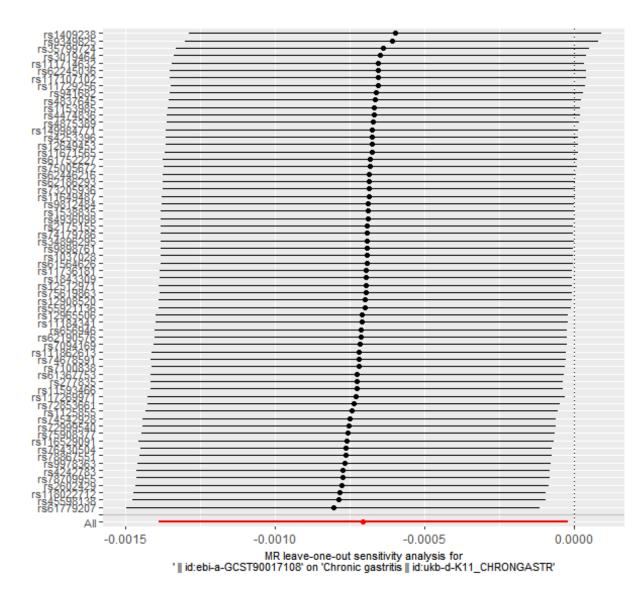


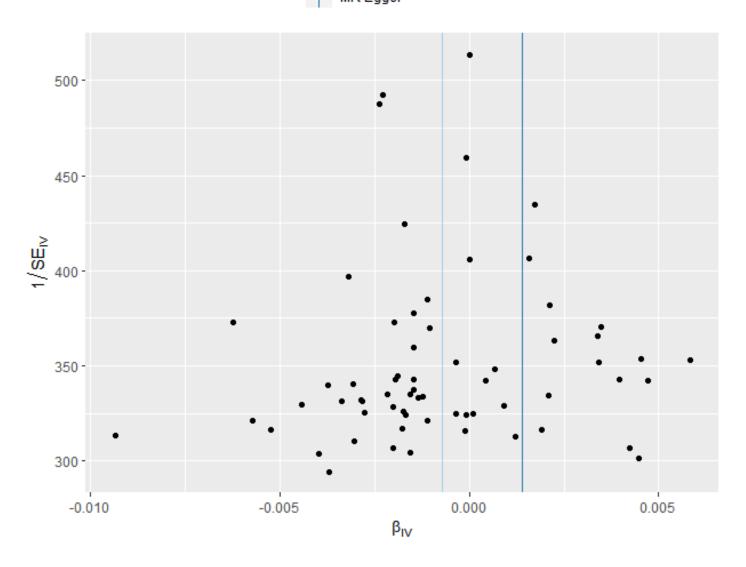
Figure 70 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Verrucomicrobiales id.4030) on chronic gastritis

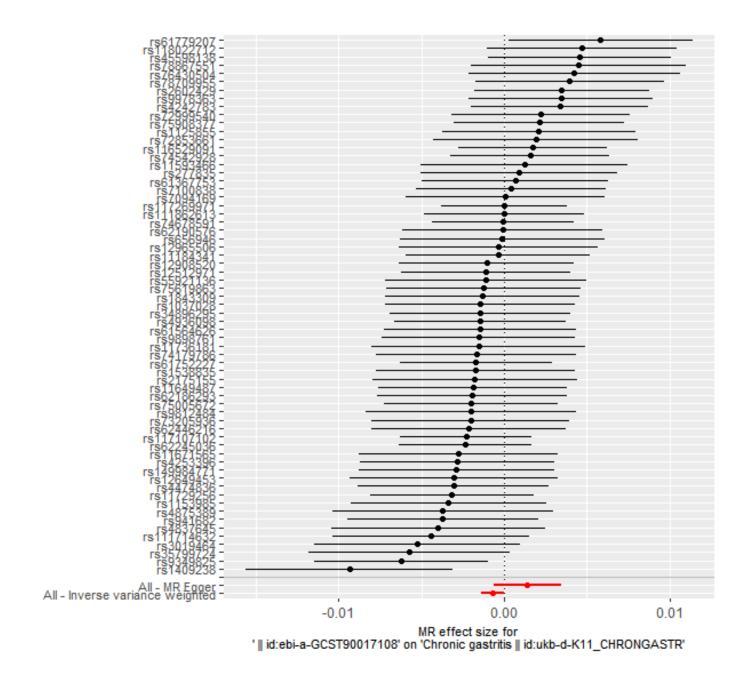


MR Method

Inverse variance weighted

MR Egger





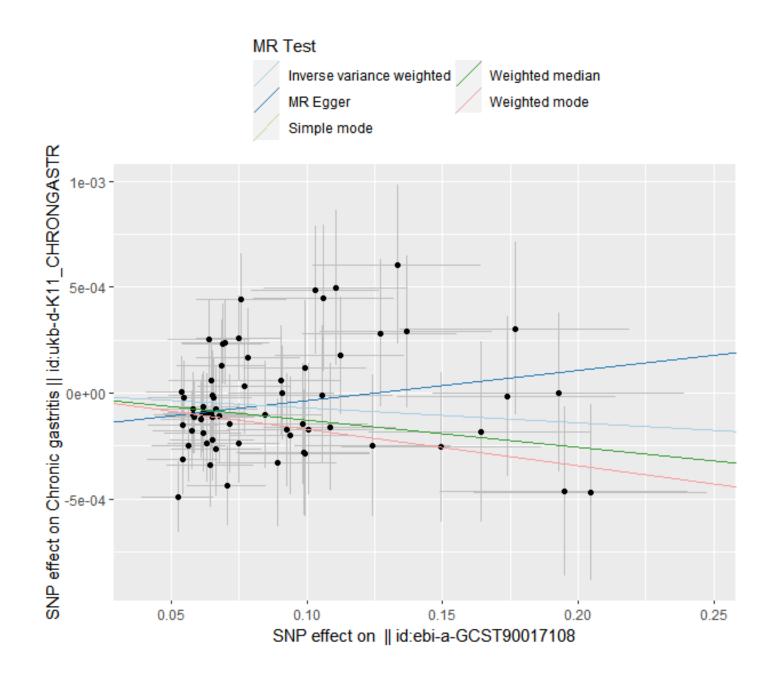
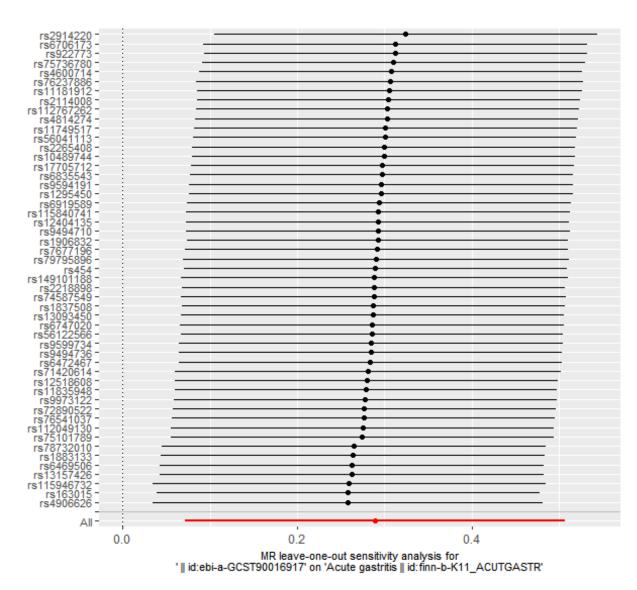


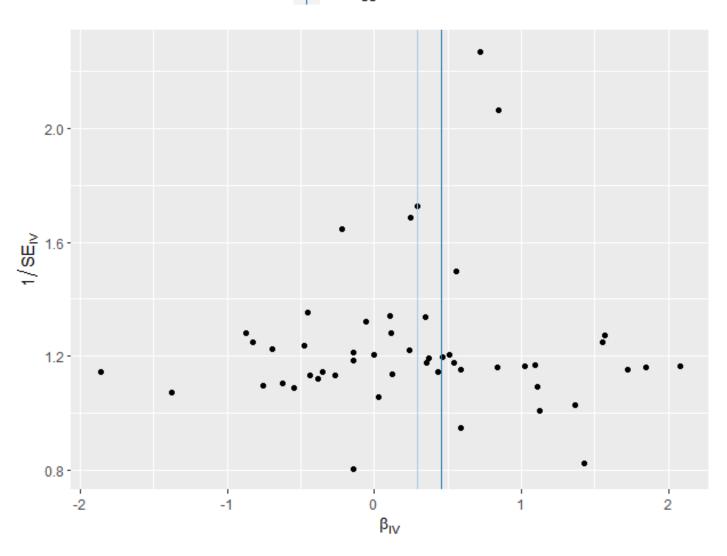
Figure 71 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Gammaproteobacteria id.3303) on acute gastritis

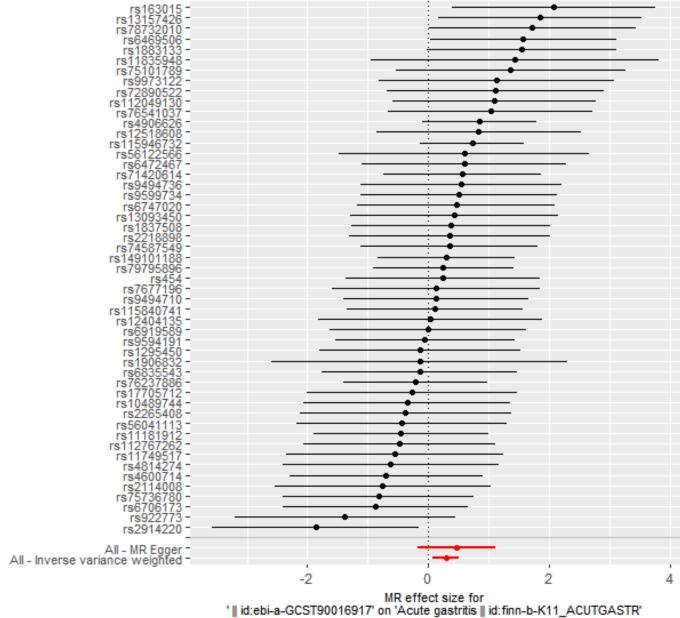


MR Method

Inverse variance weighted

MR Egger







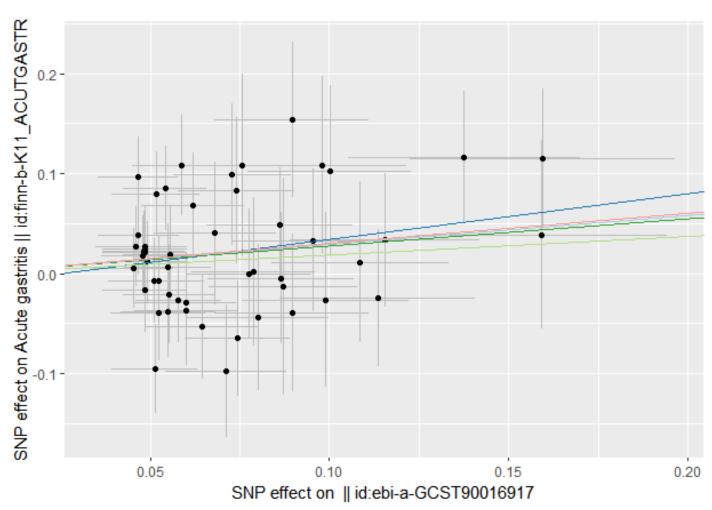
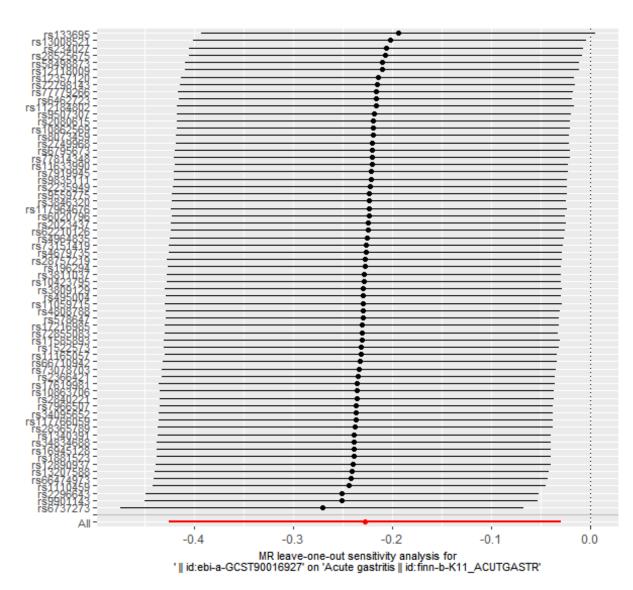
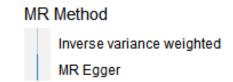
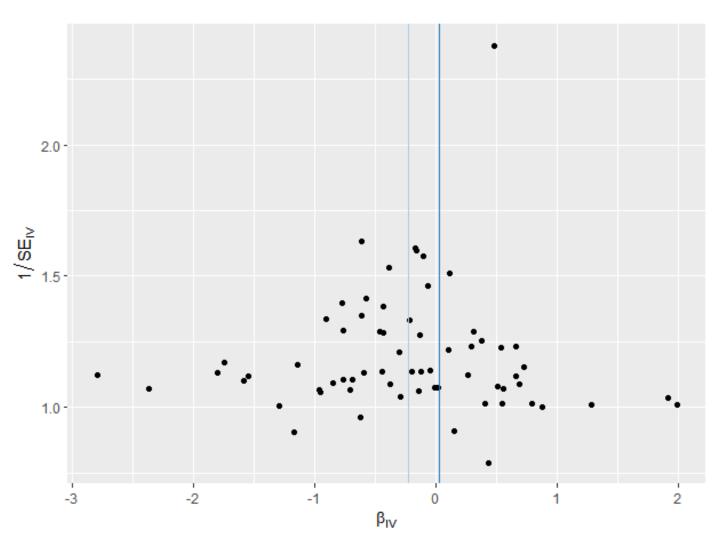
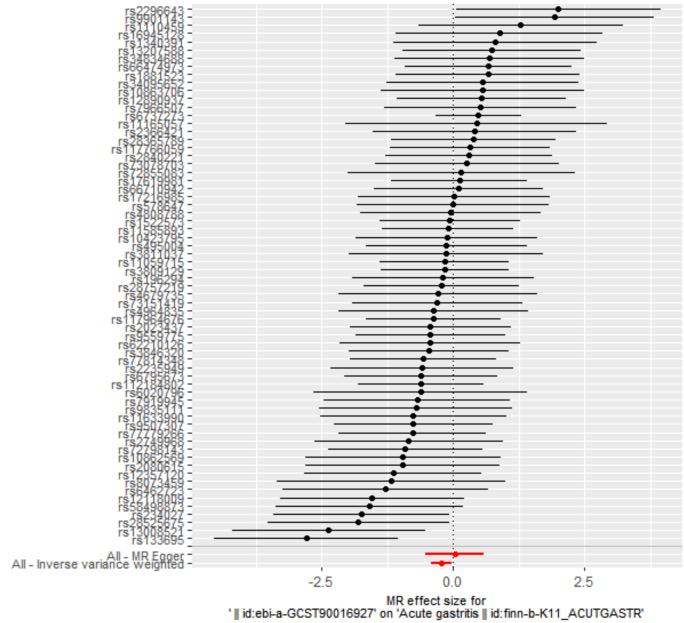


Figure 72 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Bacteroidaceae id.917) on acute gastritis











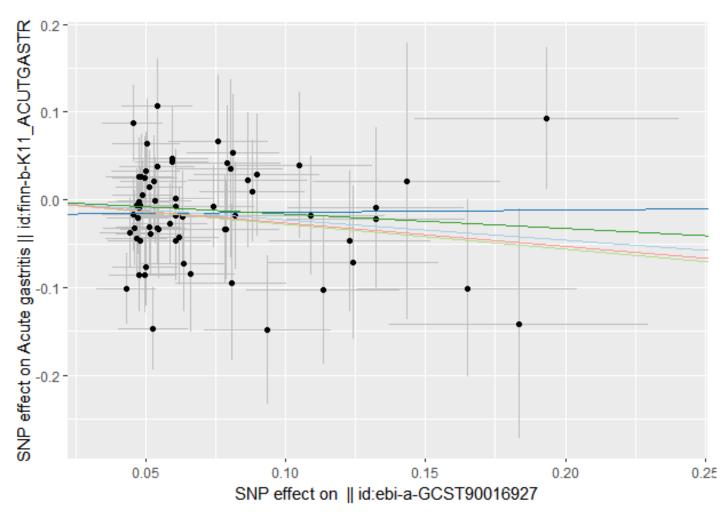
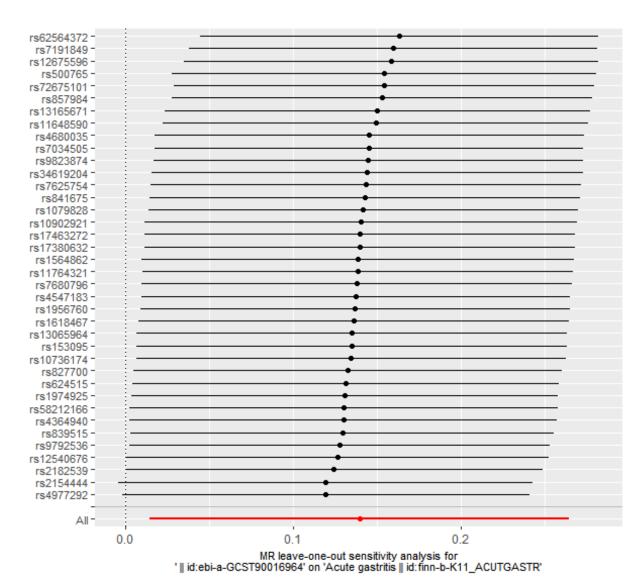
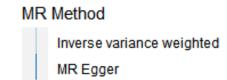
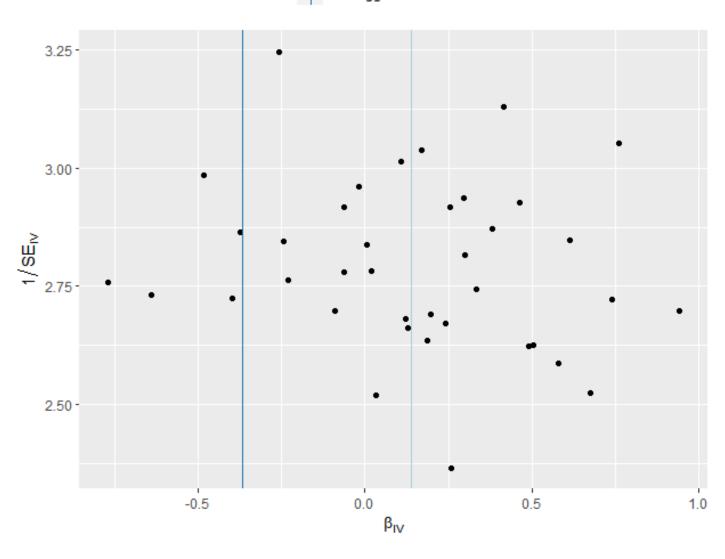
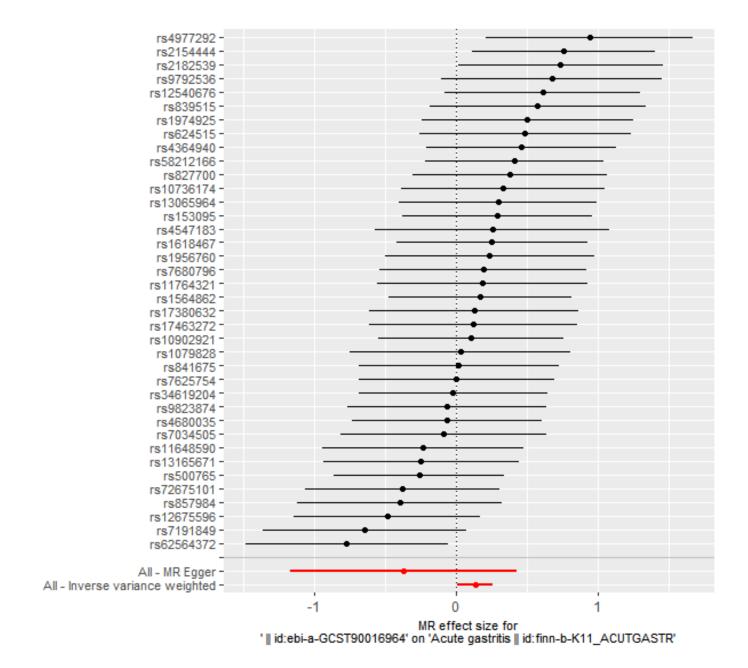


Figure 73 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Alloprevotella id.961) on acute gastritis











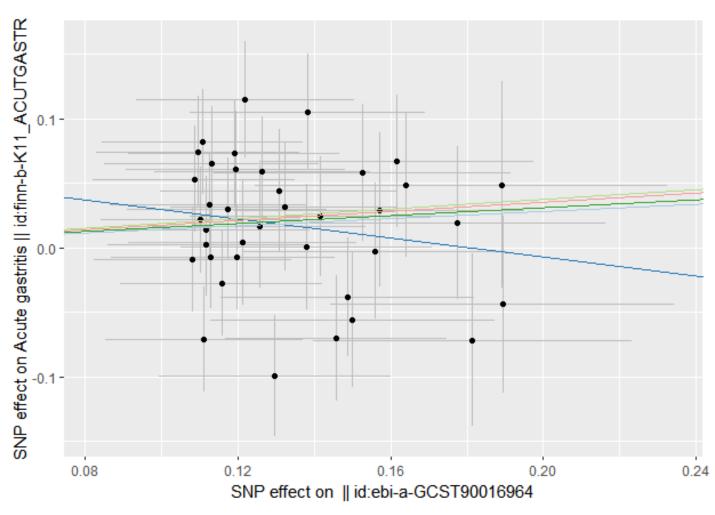
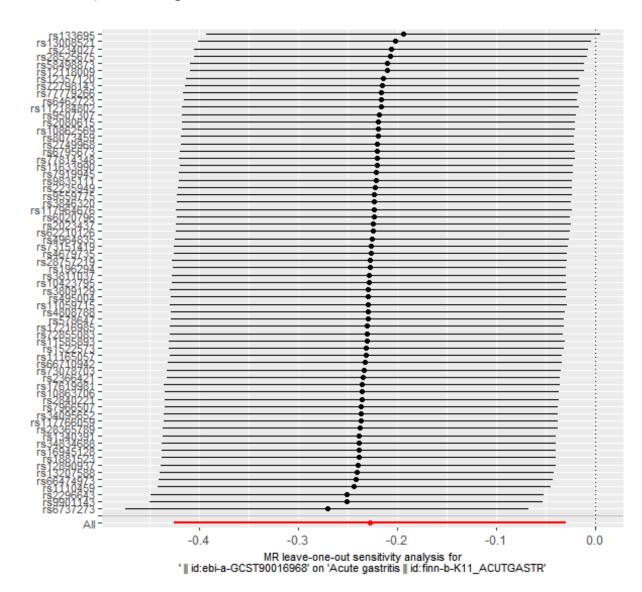
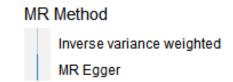
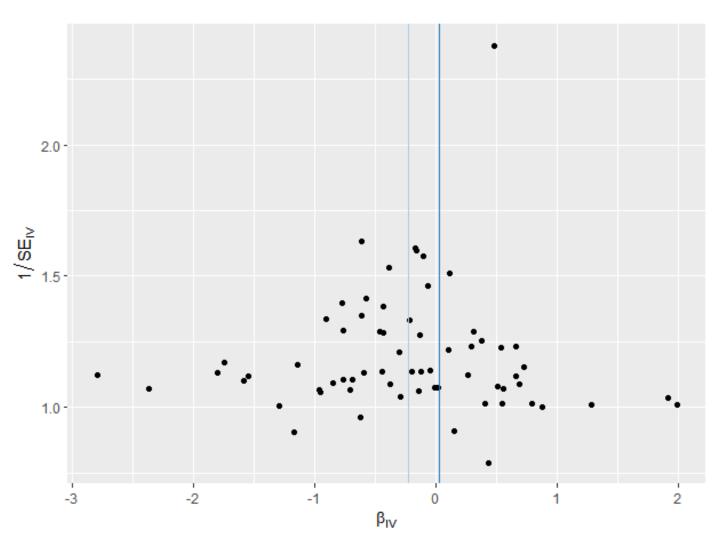
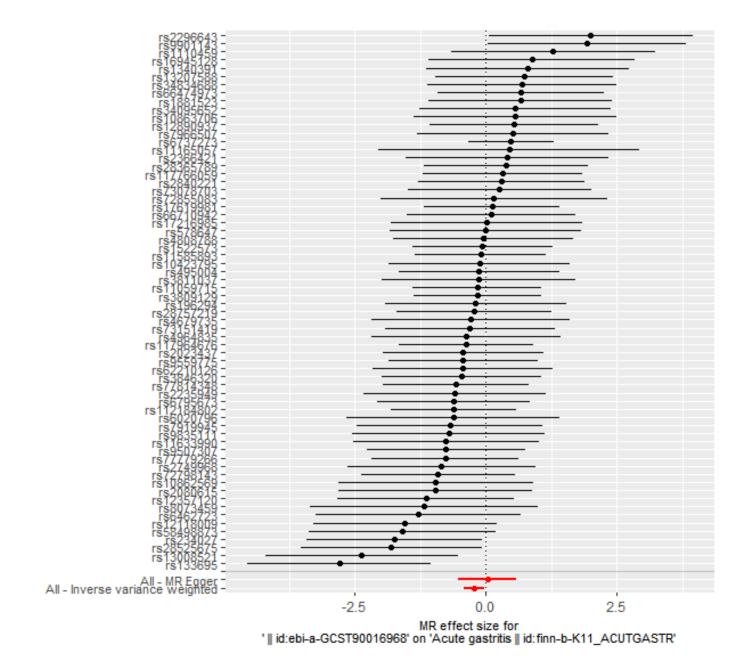


Figure 74 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Bacteroides id.918) on acute gastritis











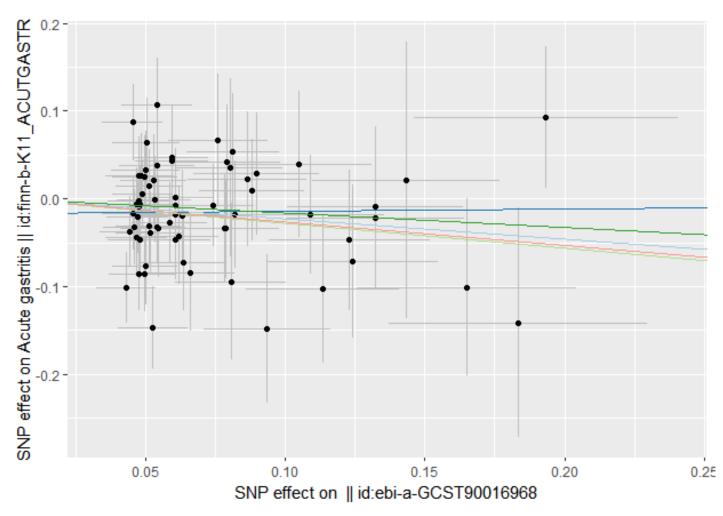
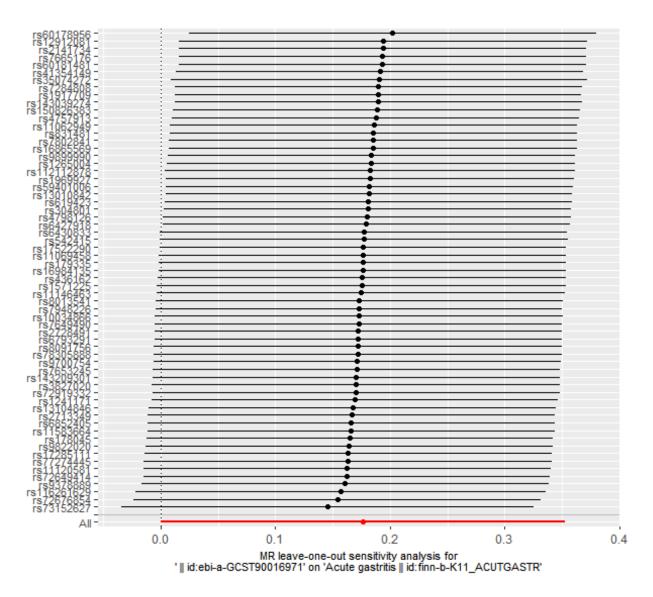


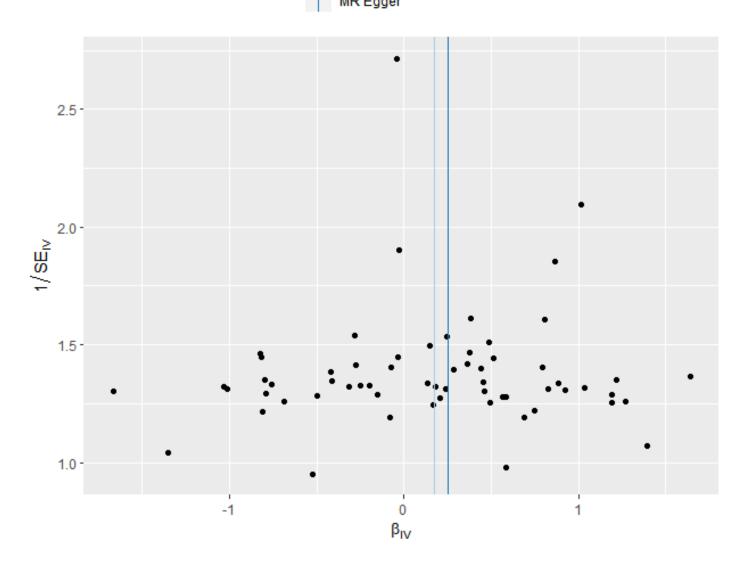
Figure 75 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Bilophila id.3170) on acute gastritis

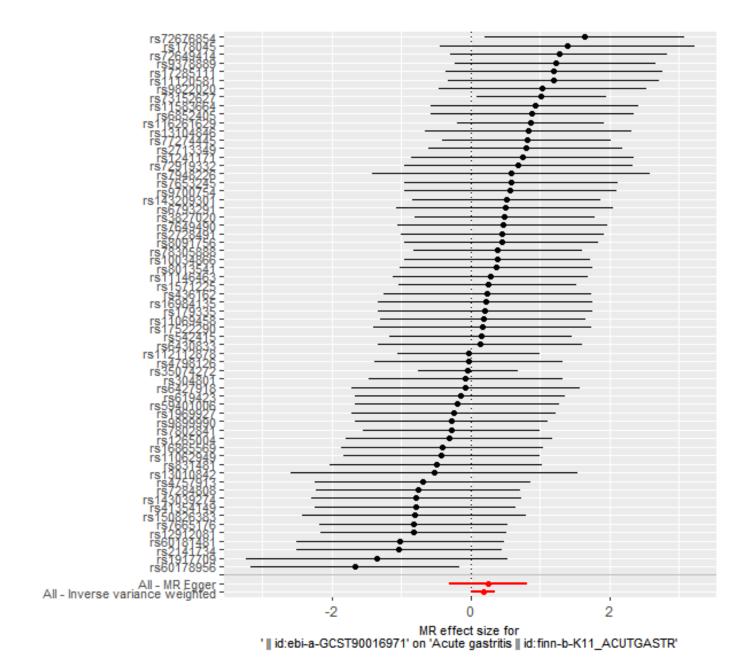


MR Method

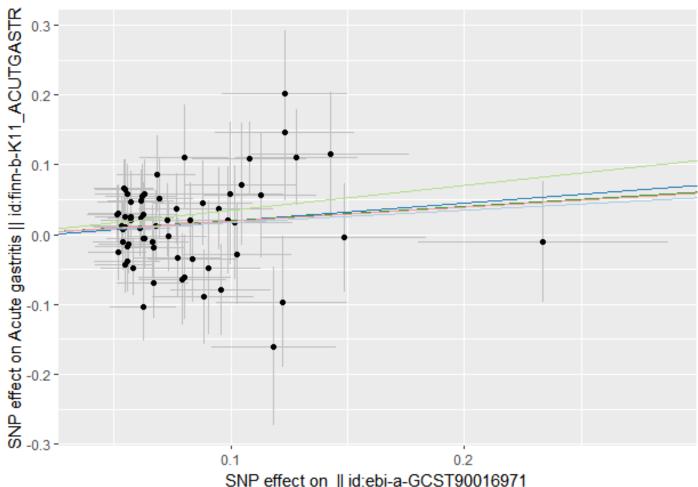
Inverse variance weighted

MR Egger



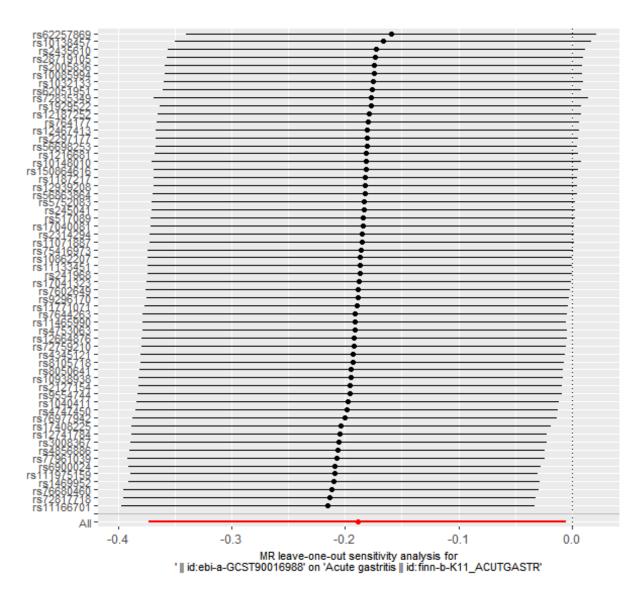






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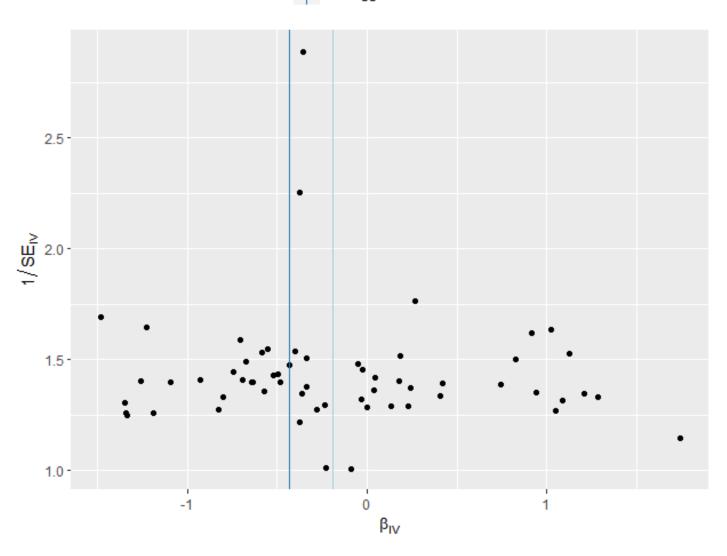
Figure 76 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Dialister id.2183) on acute gastritis

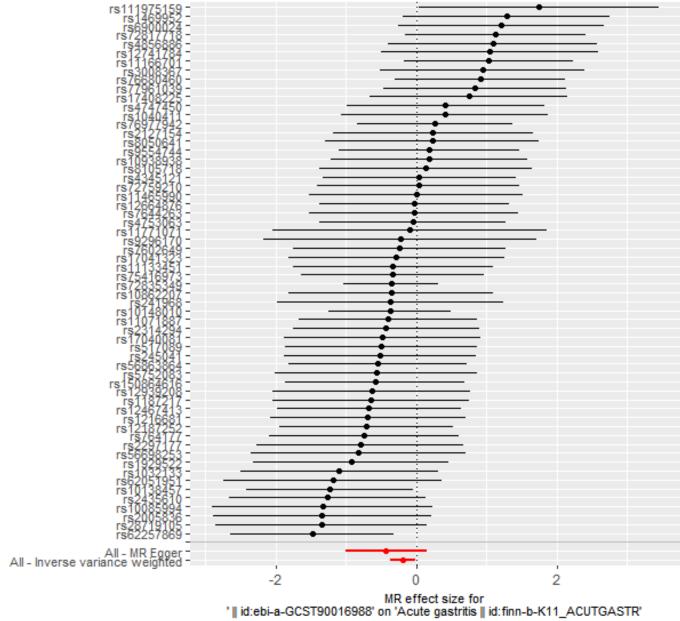


MR Method

Inverse variance weighted

MR Egger







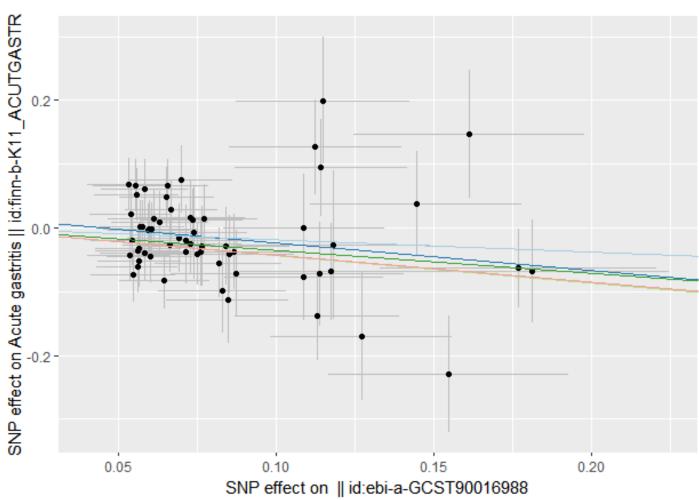
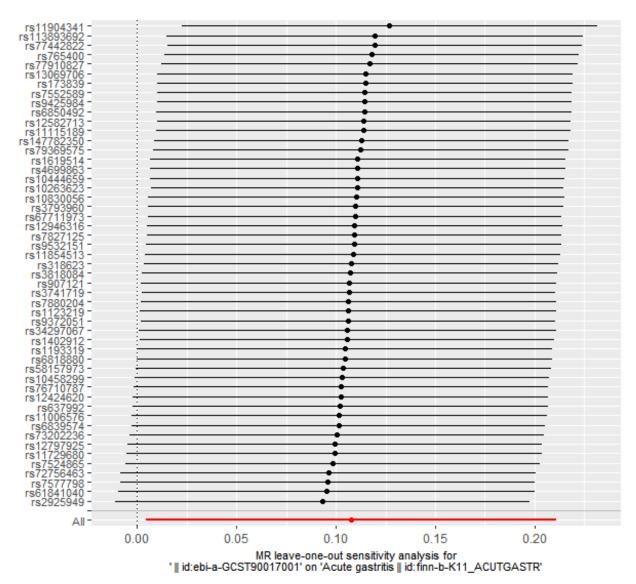


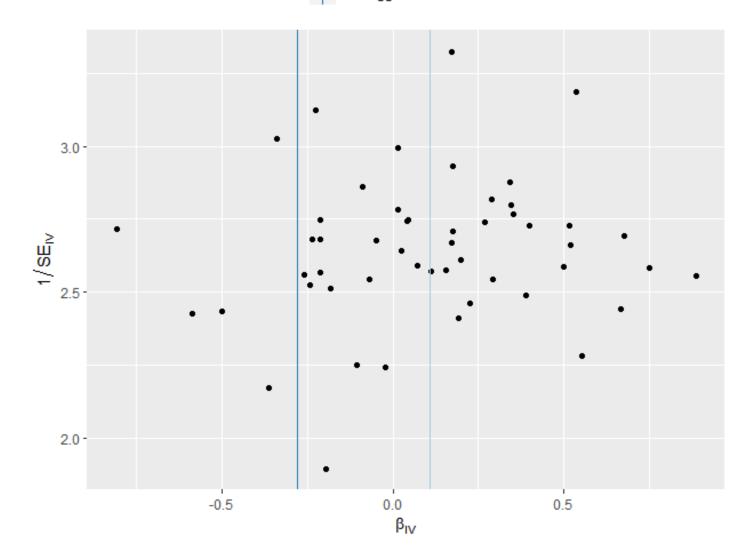
Figure 77 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium nodatum group id.11297) on acute gastritis

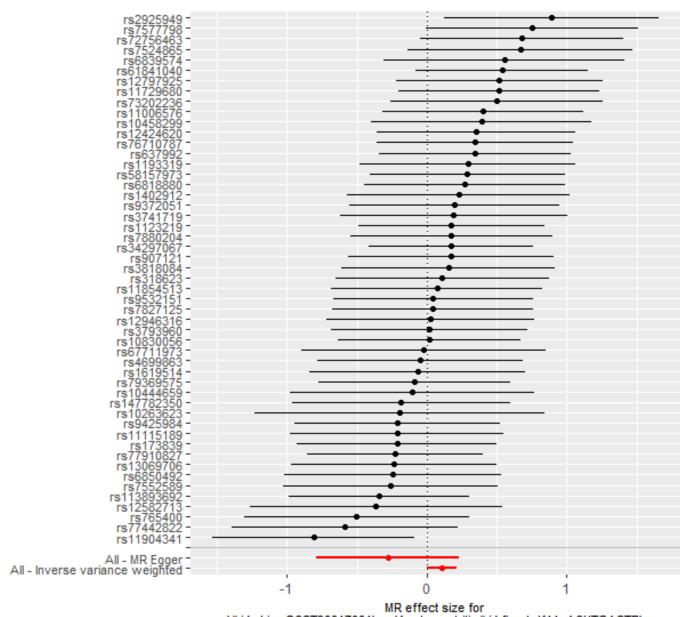


MR Method

Inverse variance weighted

MR Egger





MR effect size for
' || id:ebi-a-GCST90017001' on 'Acute gastritis || id:finn-b-K11_ACUTGASTR'



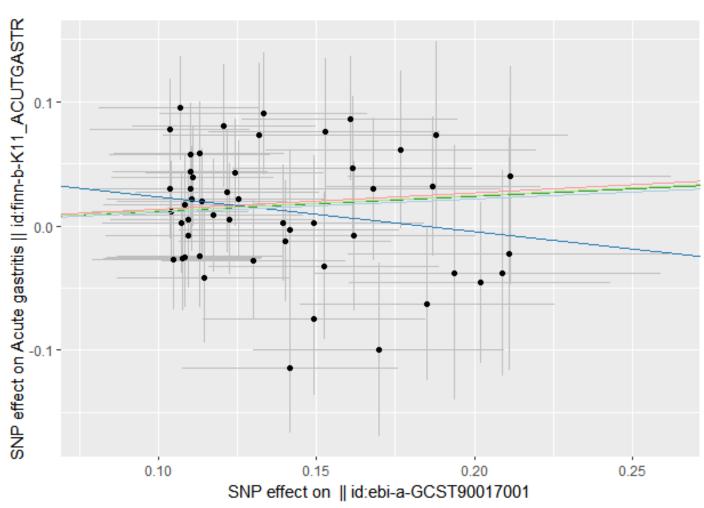
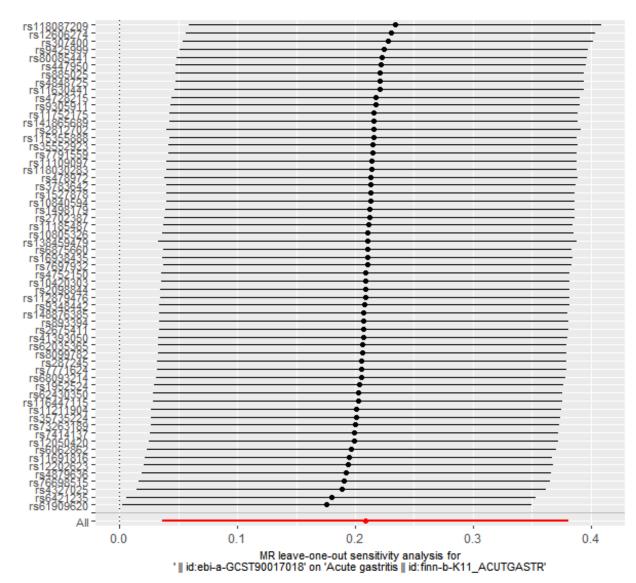
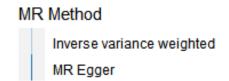
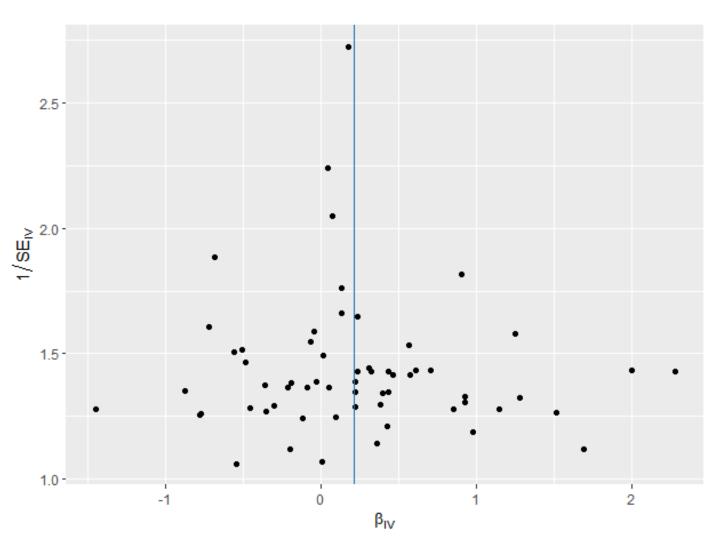
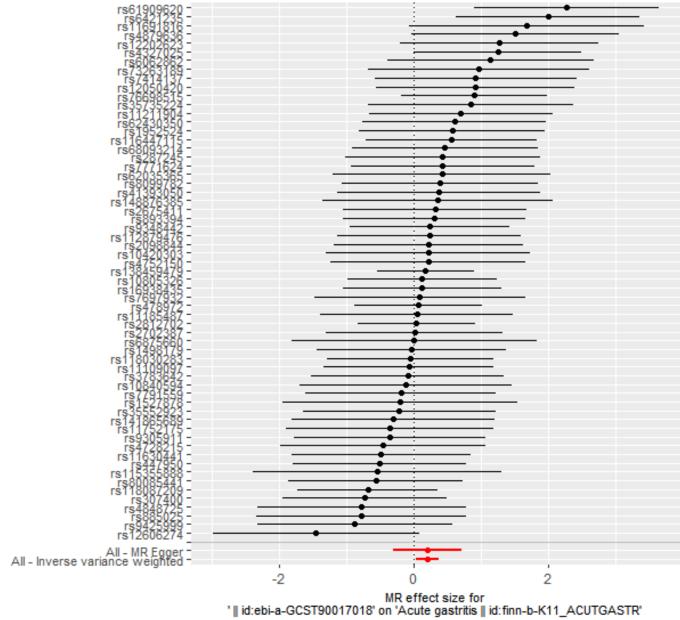


Figure 78 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Intestinibacter id.11345) on acute gastritis

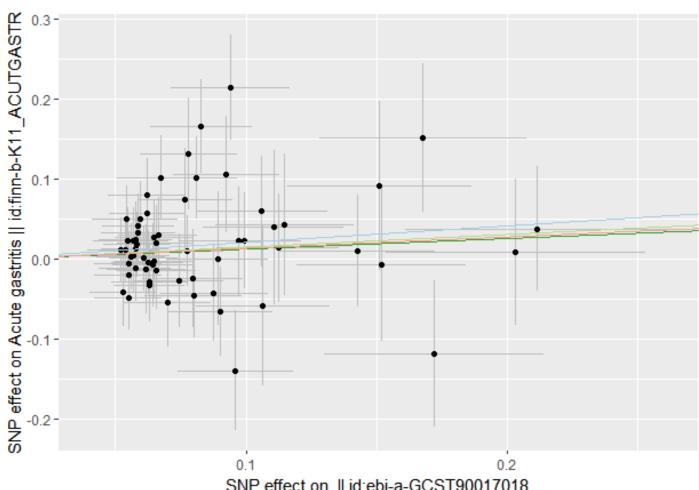






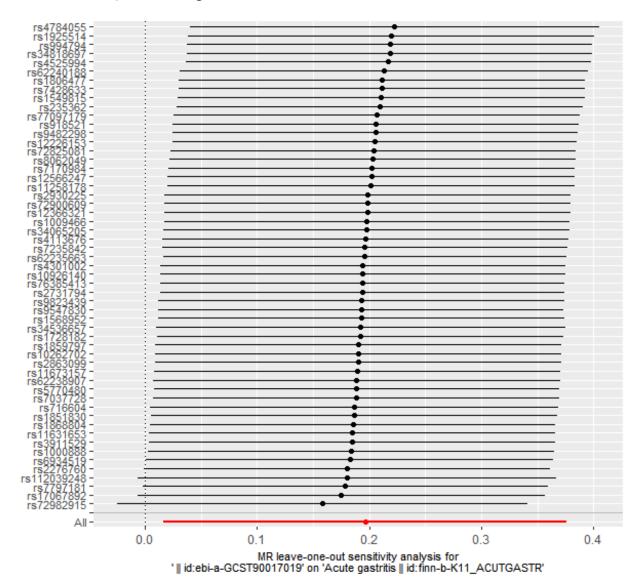


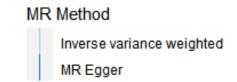


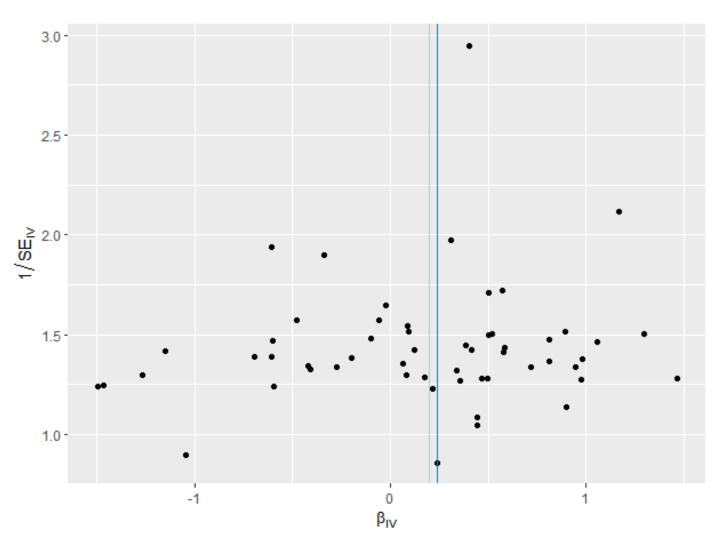


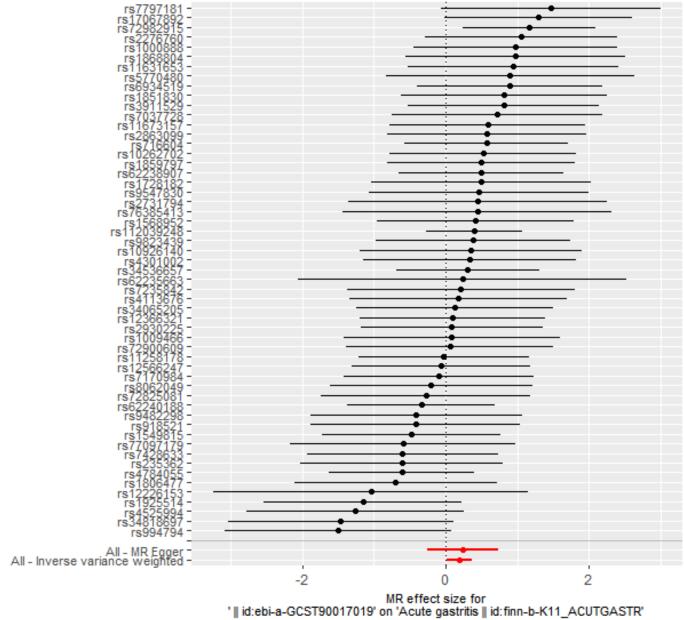
SNP effect on || id:ebi-a-GCST90017018

Figure 79 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Intestinimonas id.2062) on acute gastritis











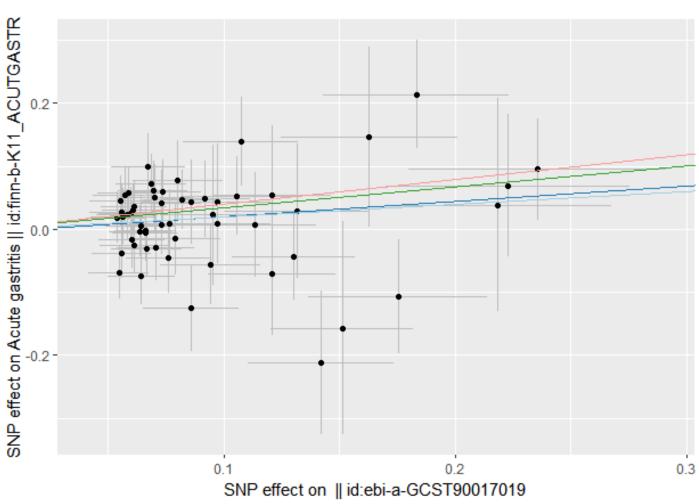
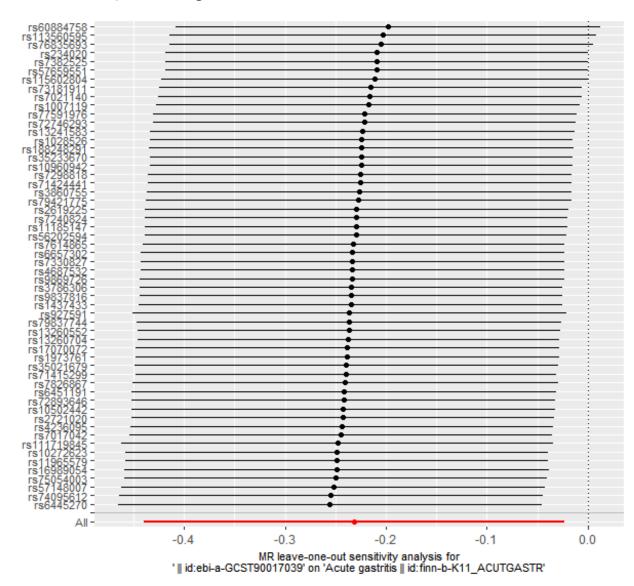
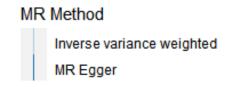
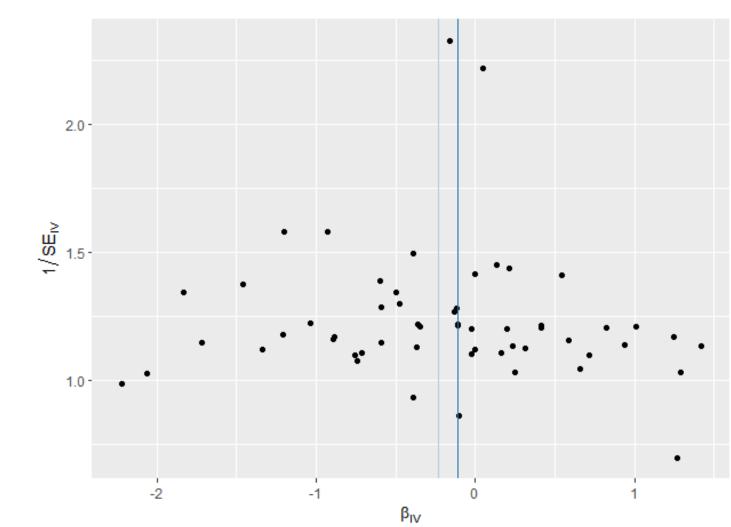
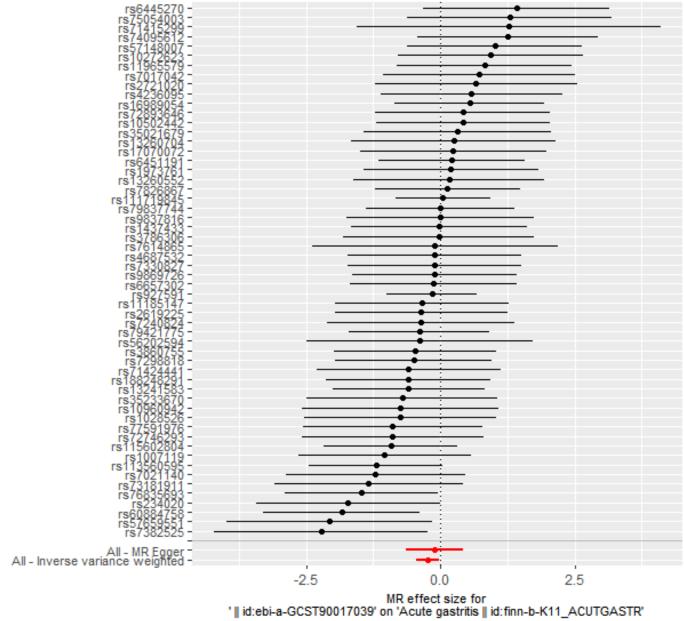


Figure 80 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Parabacteroides id.954) on acute gastritis











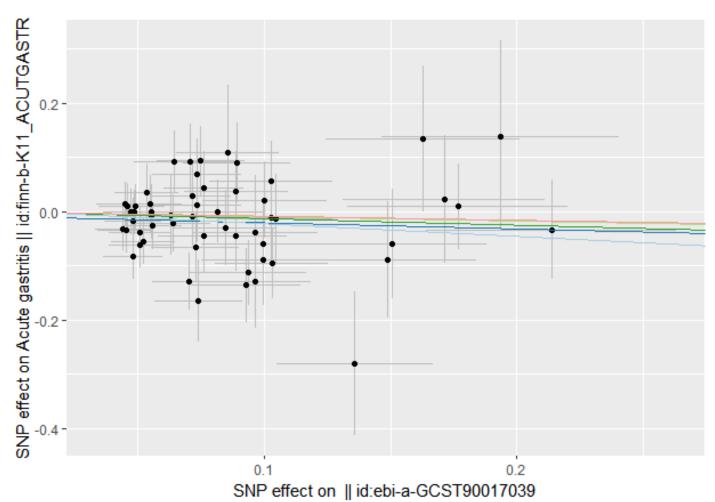
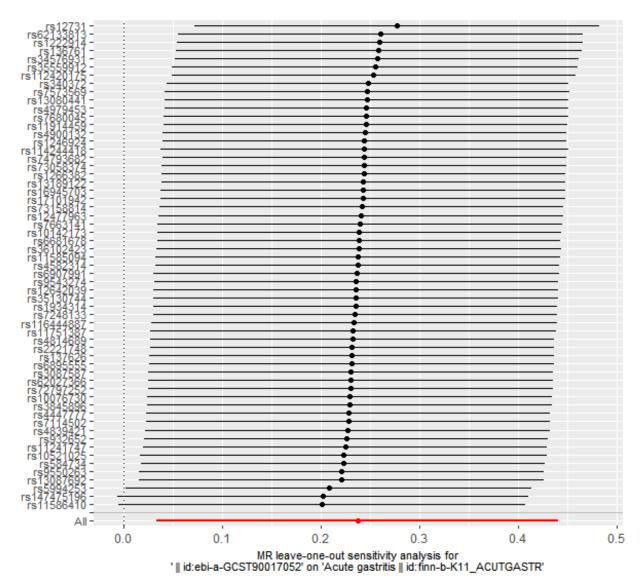
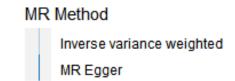
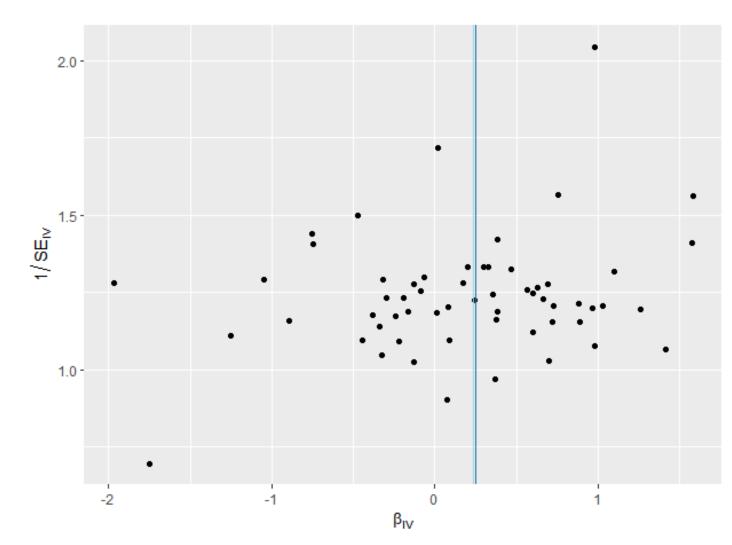
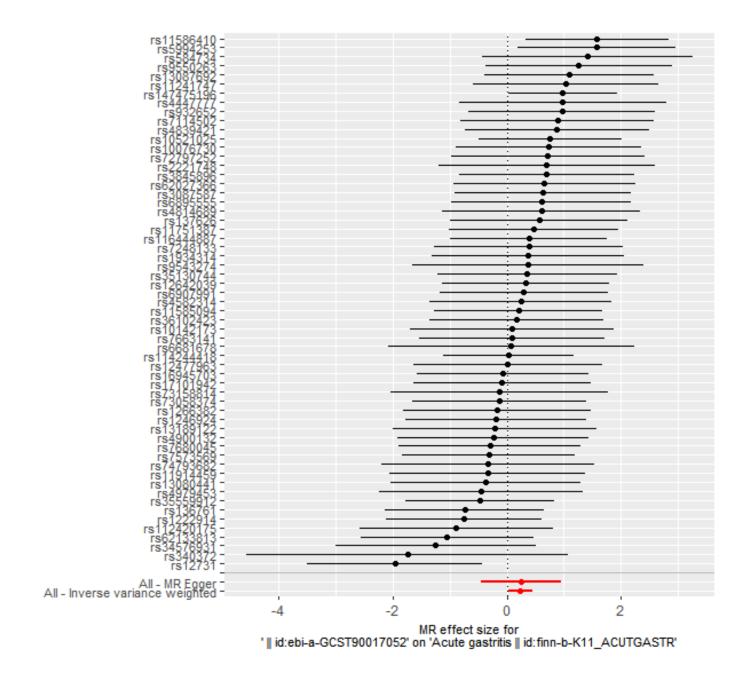


Figure 81 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae NK4A214 group id.11358) on acute gastritis











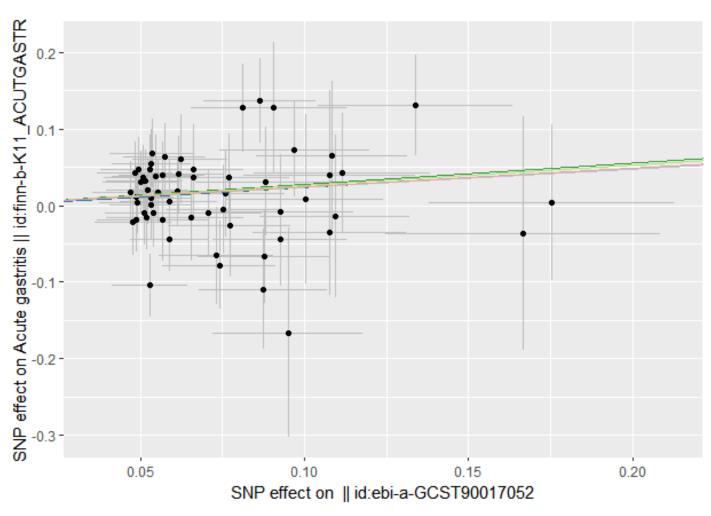
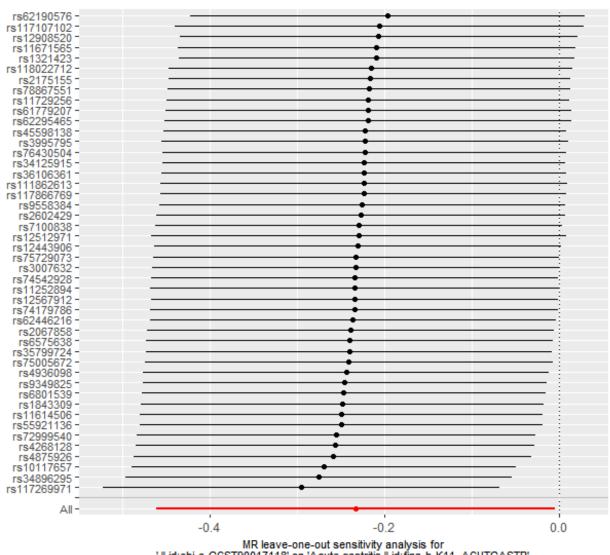
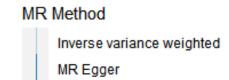
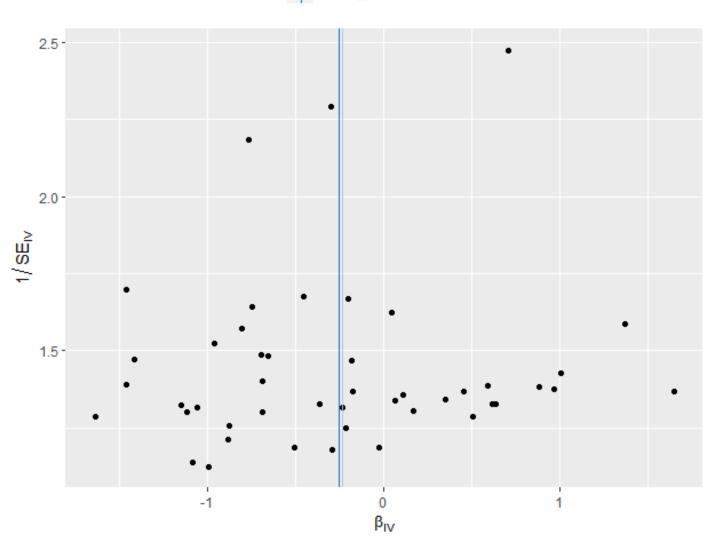


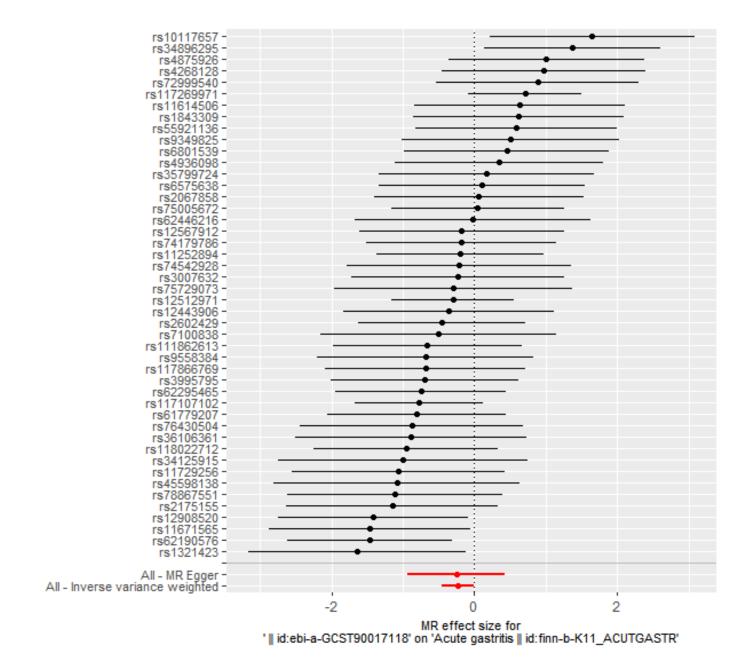
Figure 82 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Verrucomicrobia id.3982) on acute gastritis

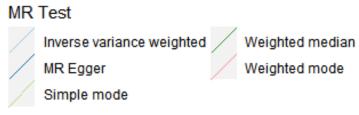


MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017118' on 'Acute gastritis || id:finn-b-K11_ACUTGASTR'









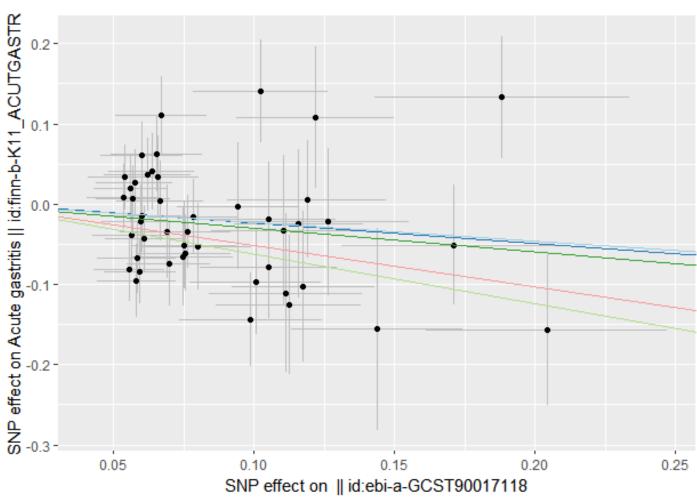
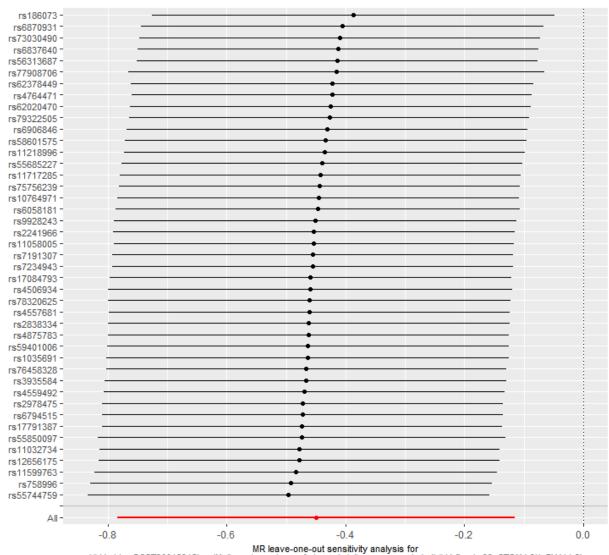
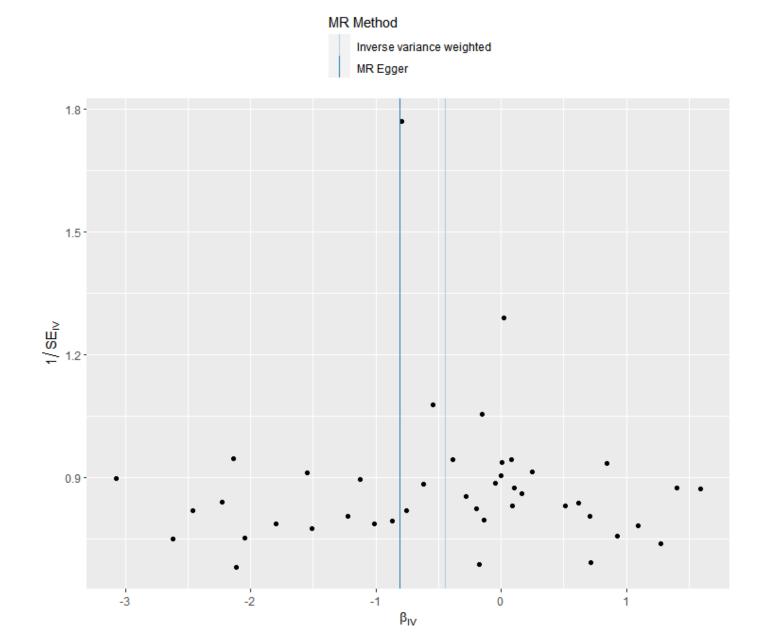
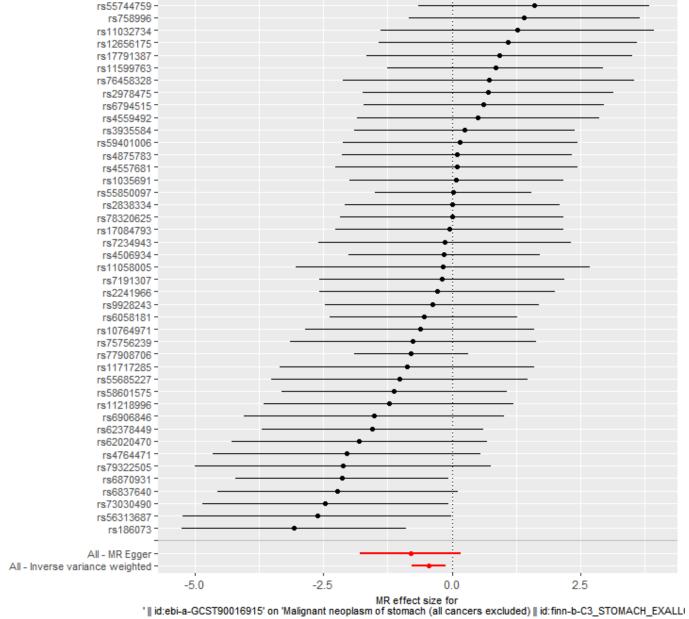


Figure 83 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Deltaproteobacteria id.3087) on gastric cancer



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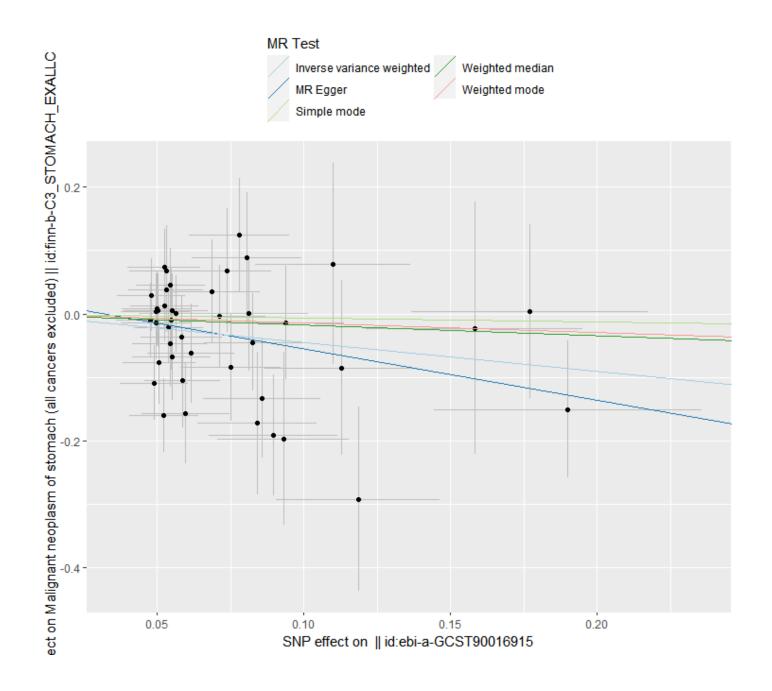
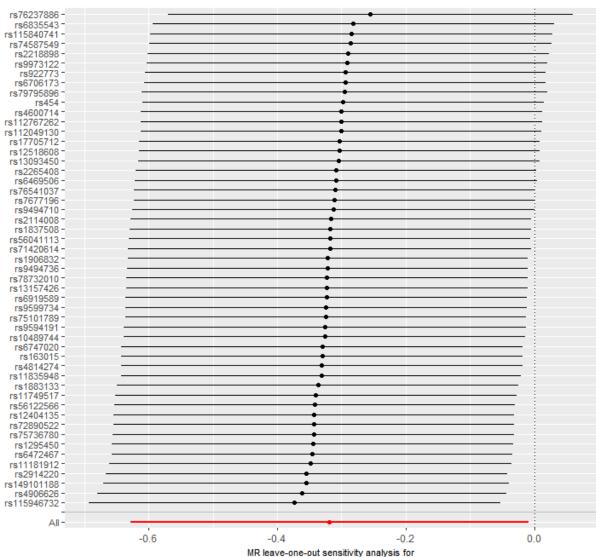
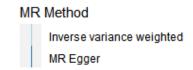
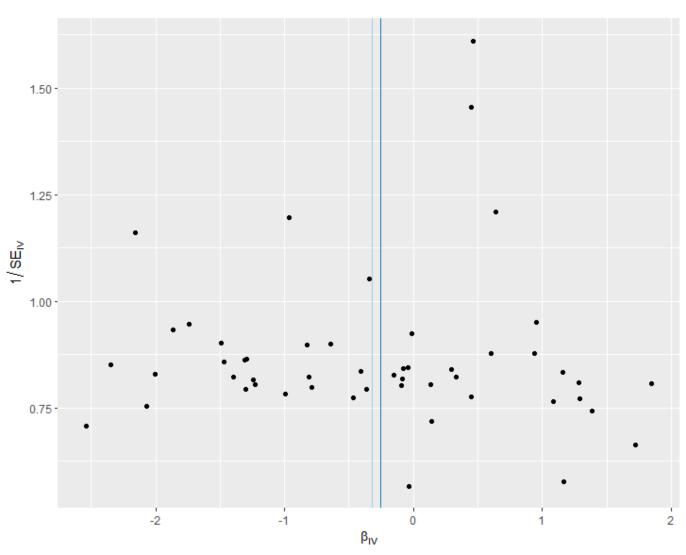


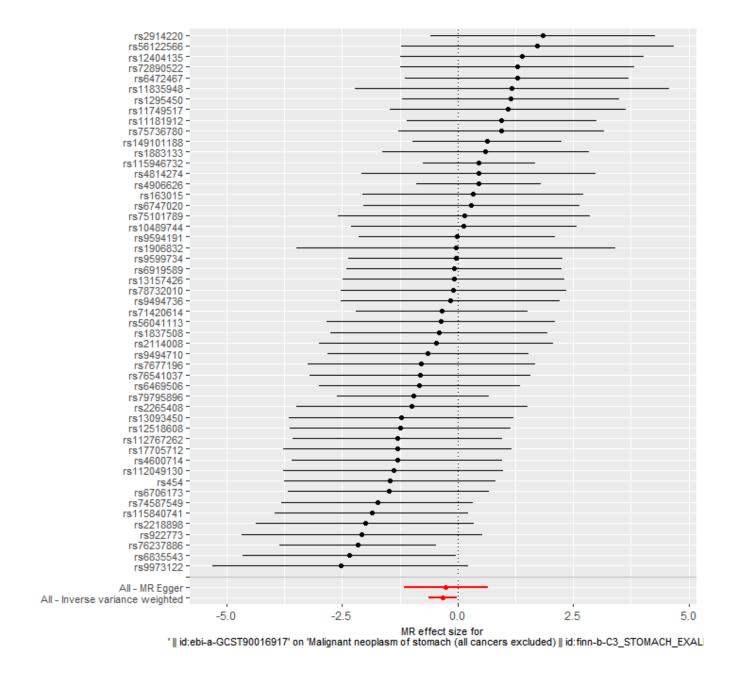
Figure 84 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Gammaproteobacteria id.3303) on gastric cancer



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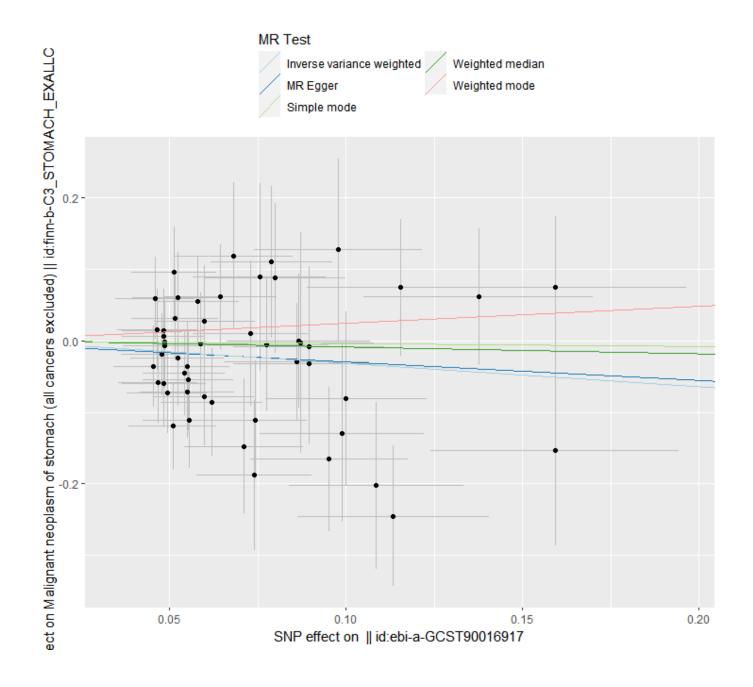
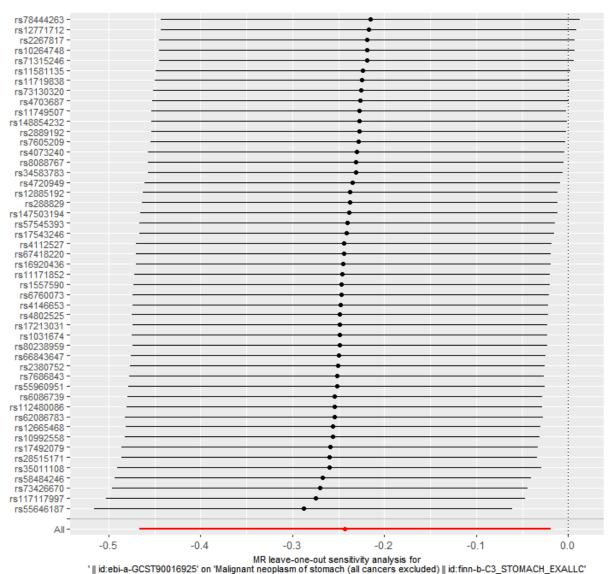
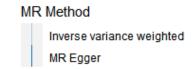
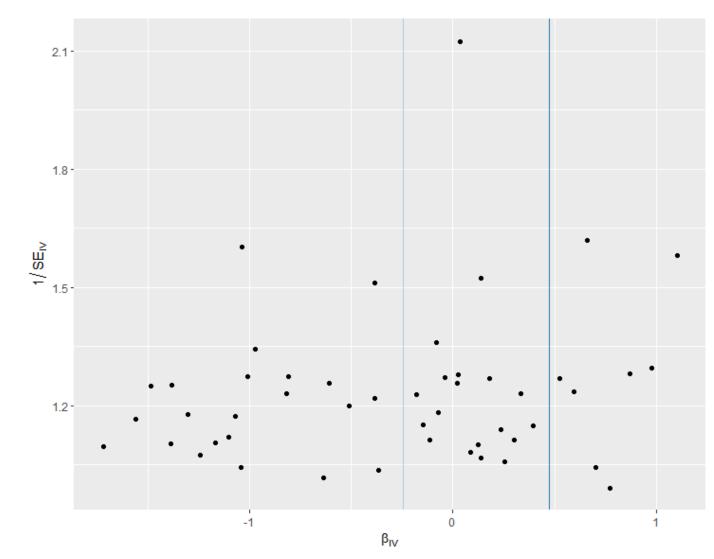
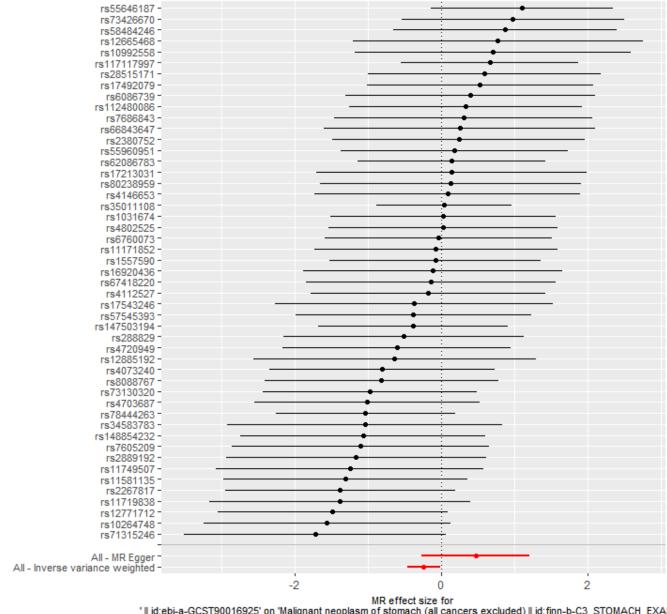


Figure 85 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Actinomycetaceae id.421) on gastric cancer









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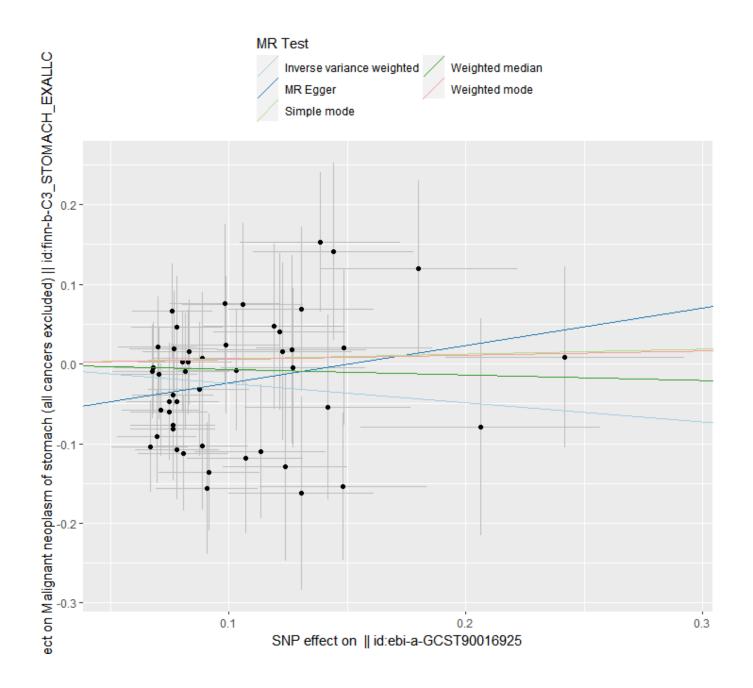
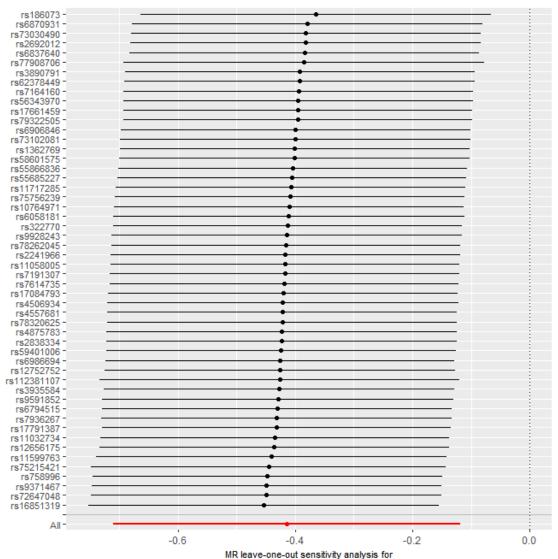
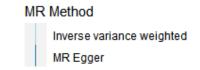
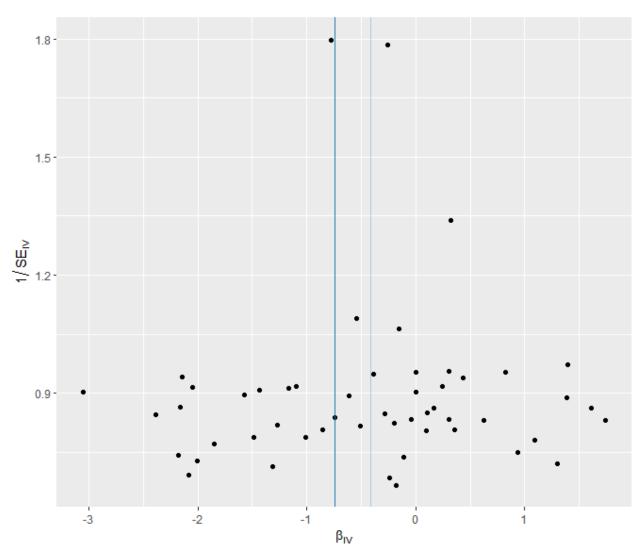


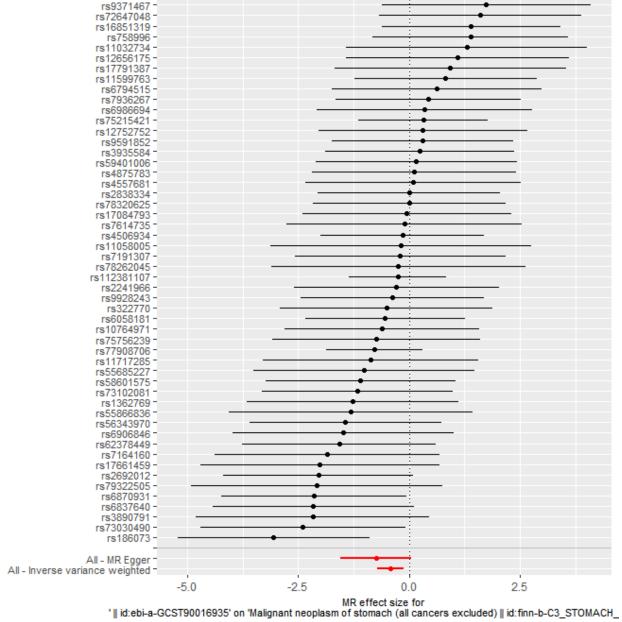
Figure 86 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Desulfovibrionaceae id.3169) on gastric cancer



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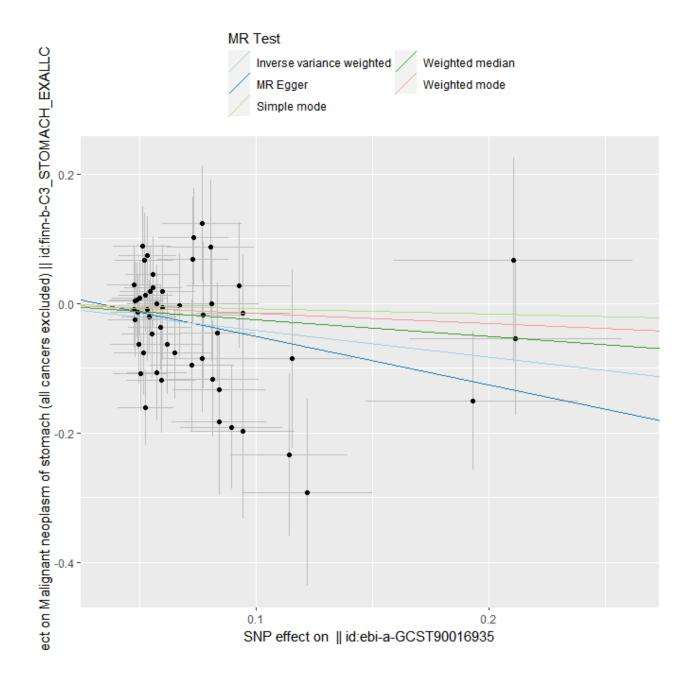
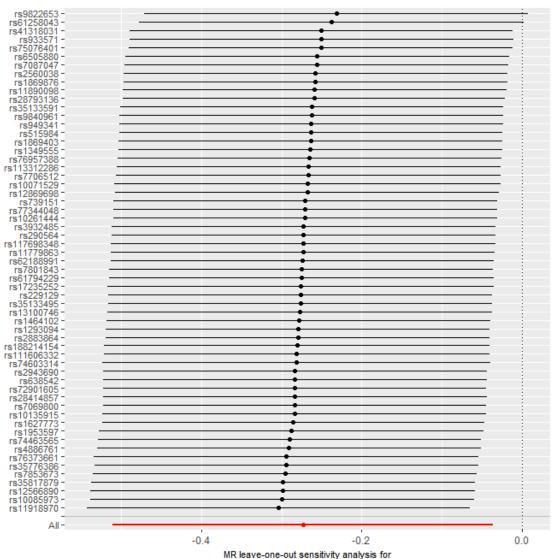
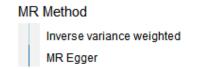
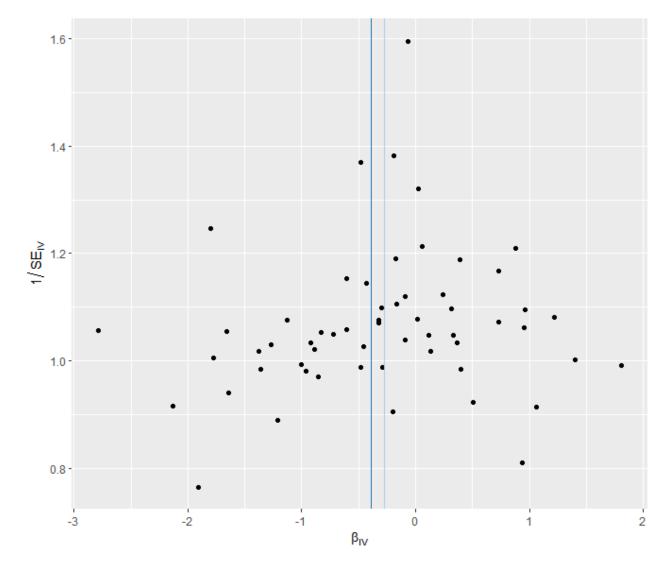


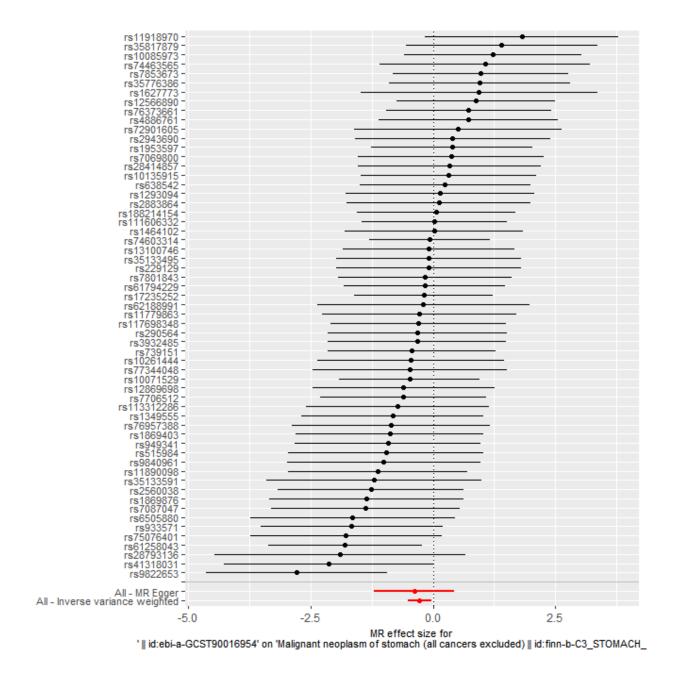
Figure 87 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown family id.1000005471) on gastric cancer



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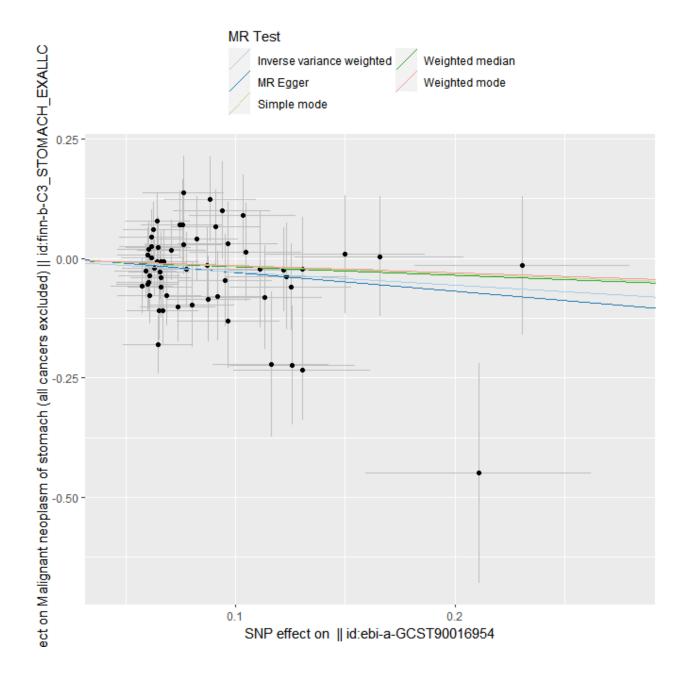
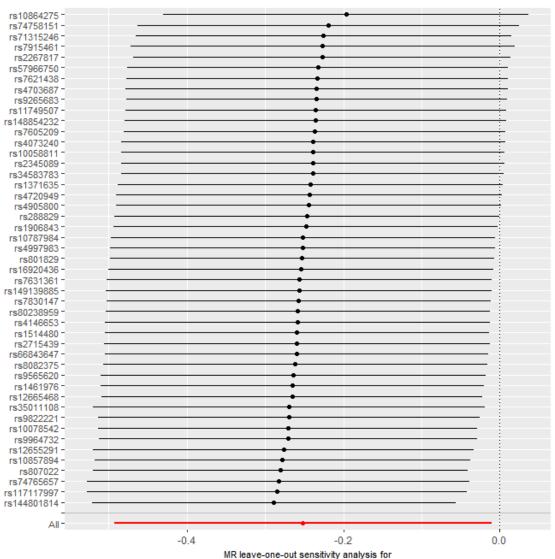
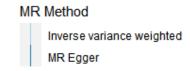
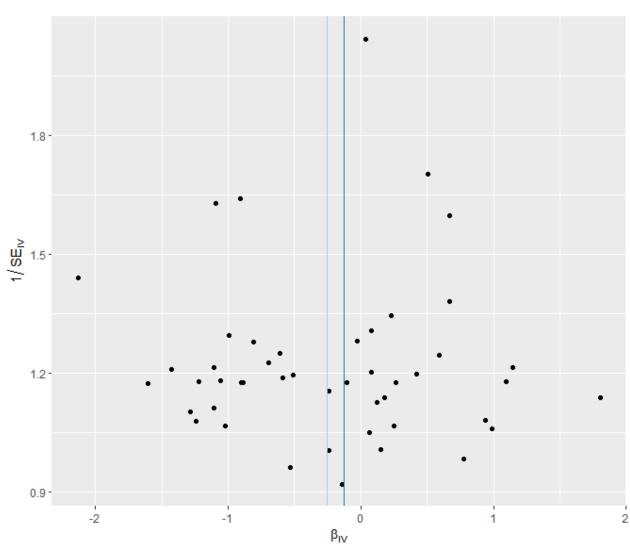


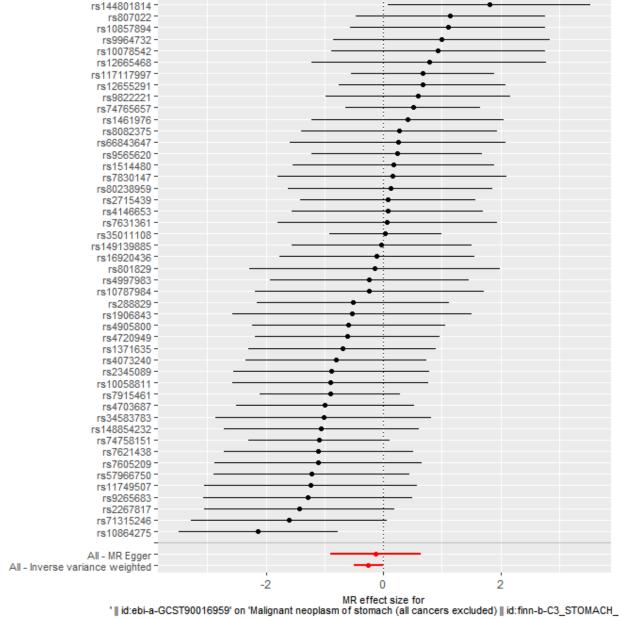
Figure 88 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Actinomyces id.423) on gastric cancer



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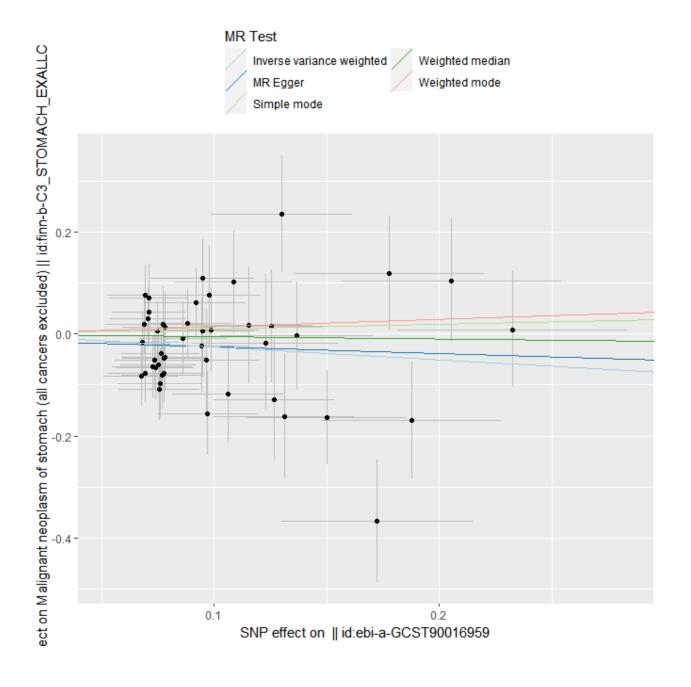
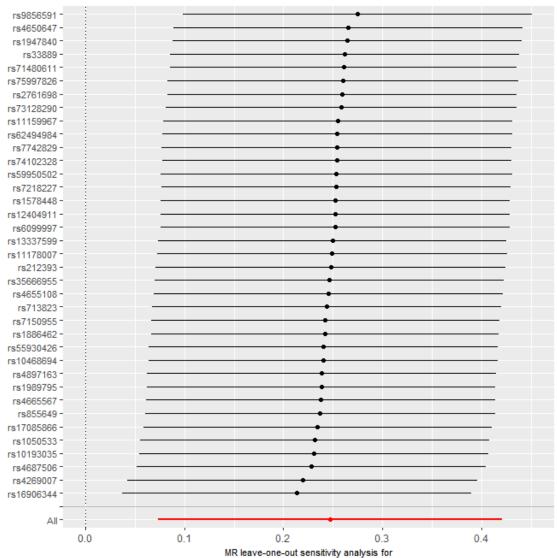
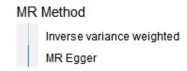
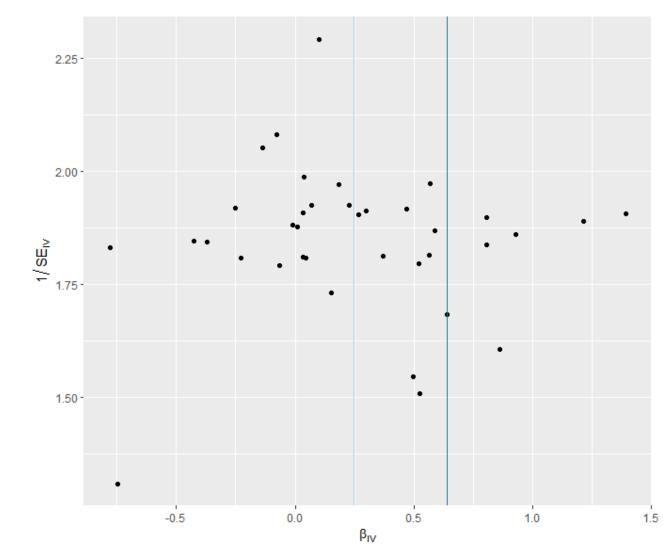


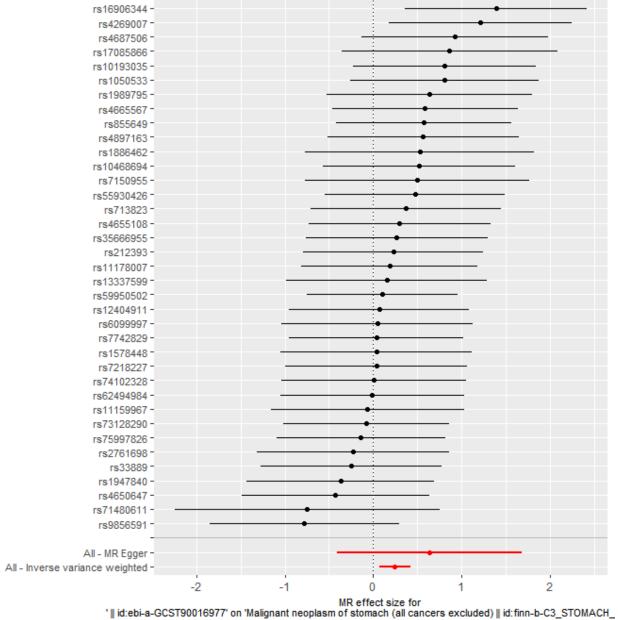
Figure 89 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Catenibacterium id.2153) on gastric cancer



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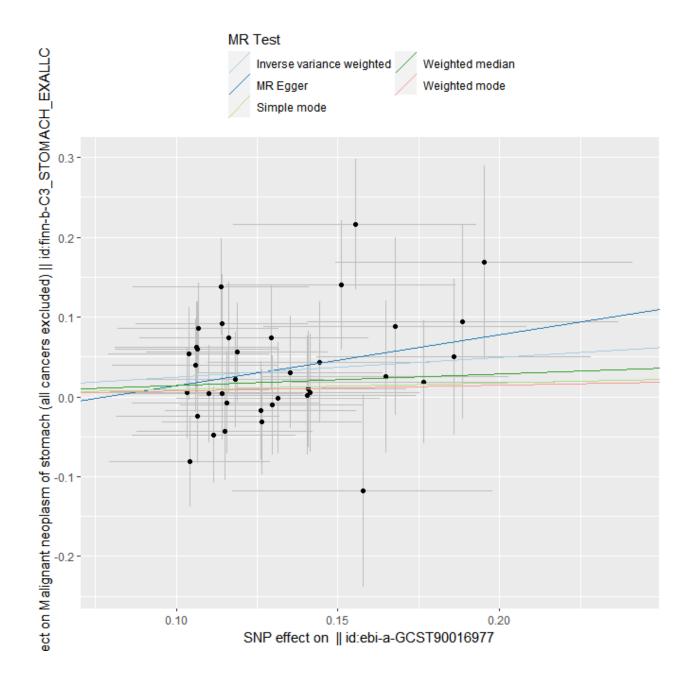
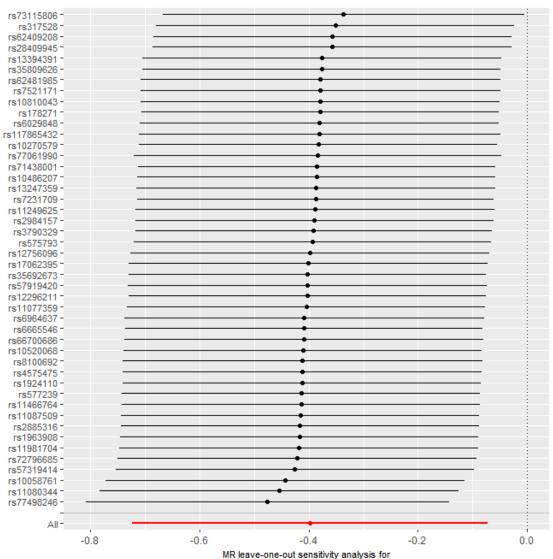
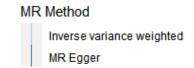
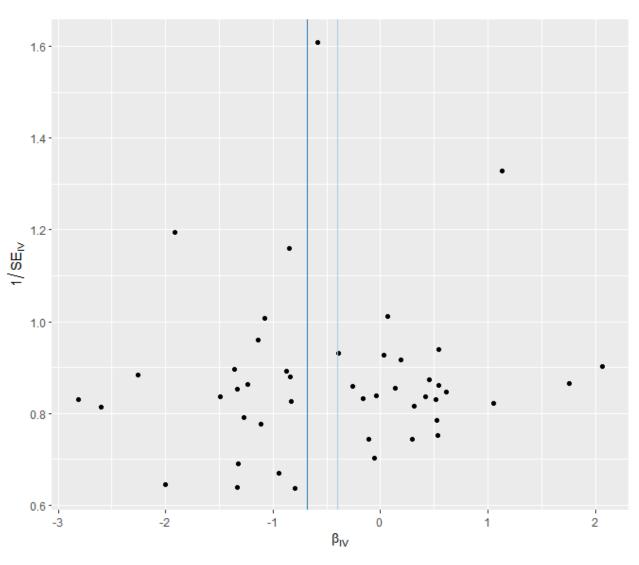


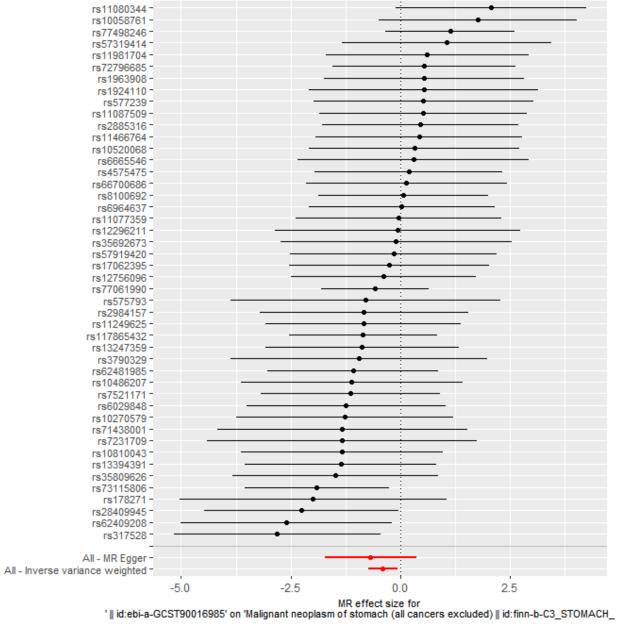
Figure 90 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Coprococcus3 id.11303) on gastric cancer



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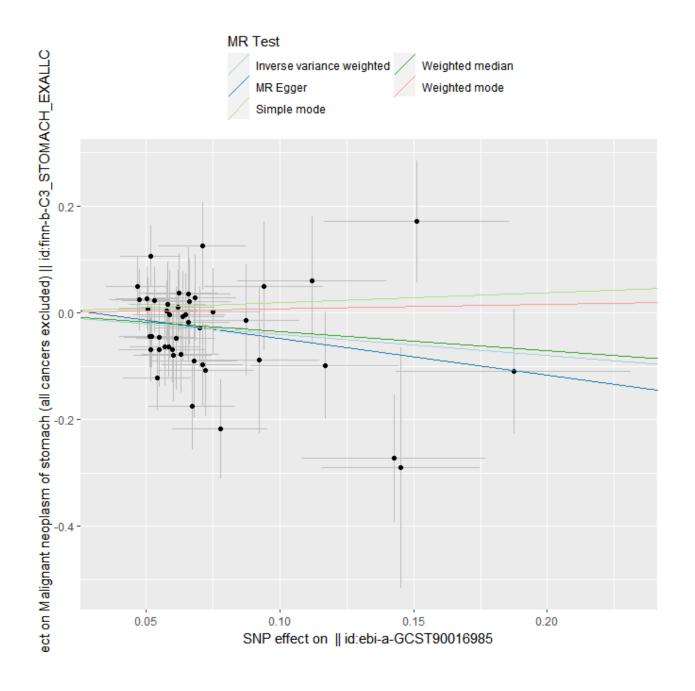
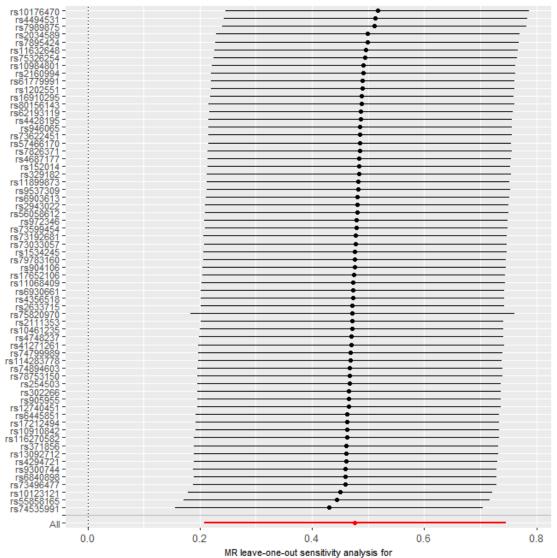
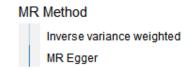
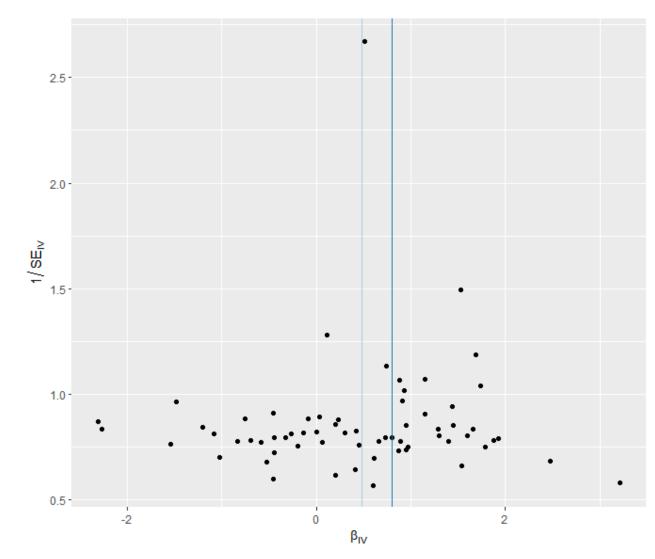


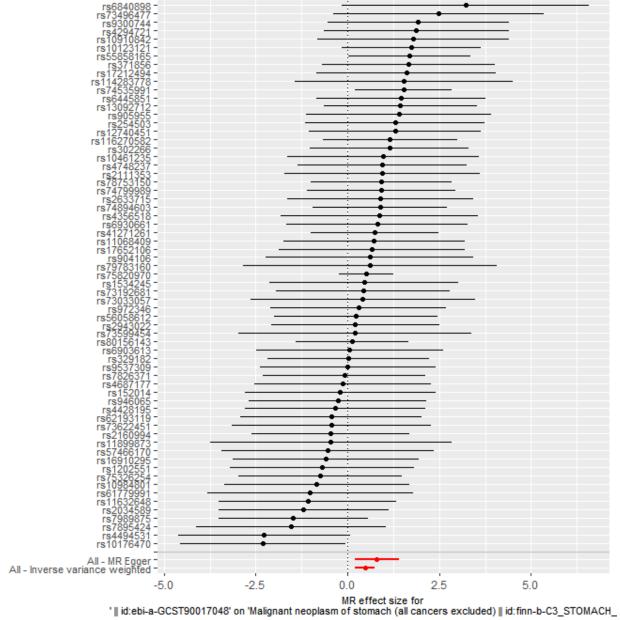
Figure 91 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Roseburia id.2012) on gastric cancer



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017048' on 'Malignant neoplasm of stomach (all cancers excluded) || id:finn-b-C3_STOMACH_EXALLC'







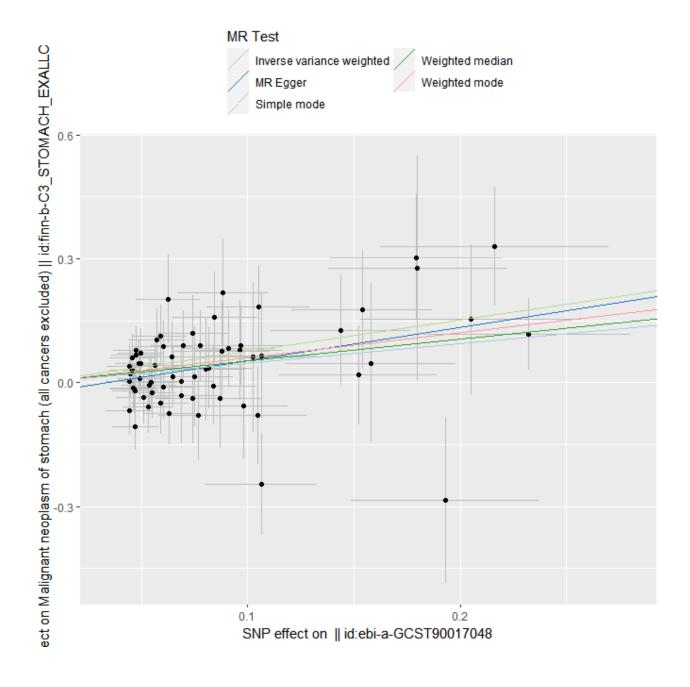
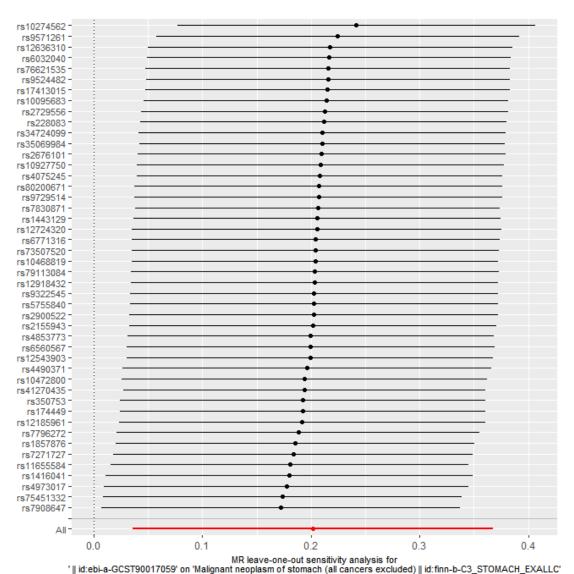
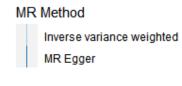
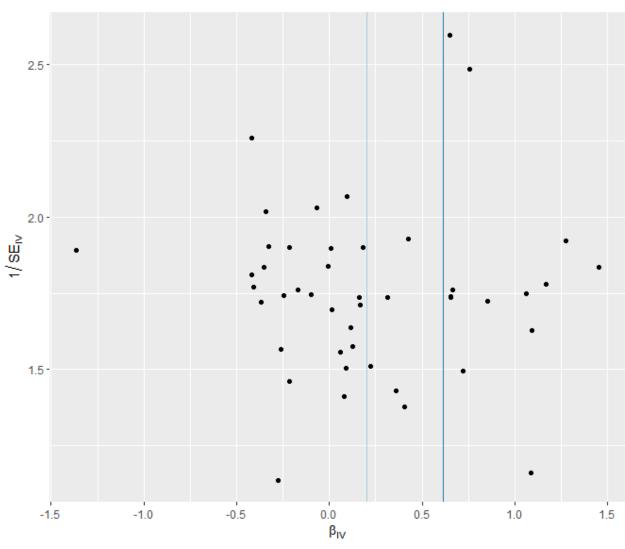
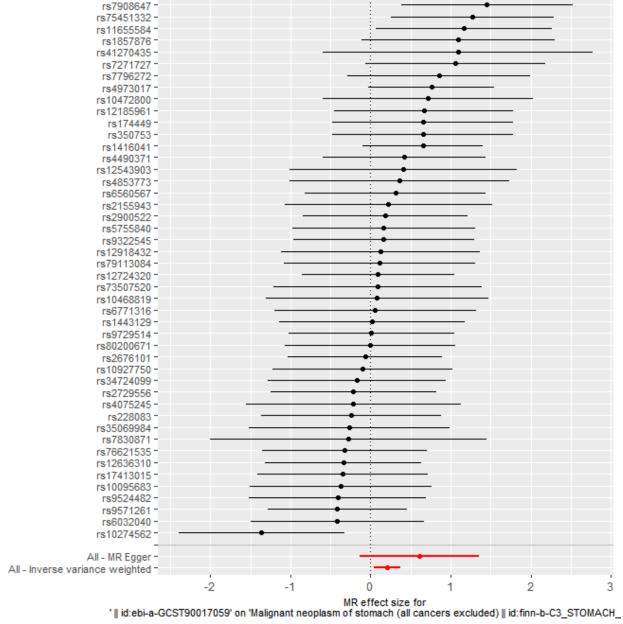


Figure 92 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG011 id.11368) on gastric cancer









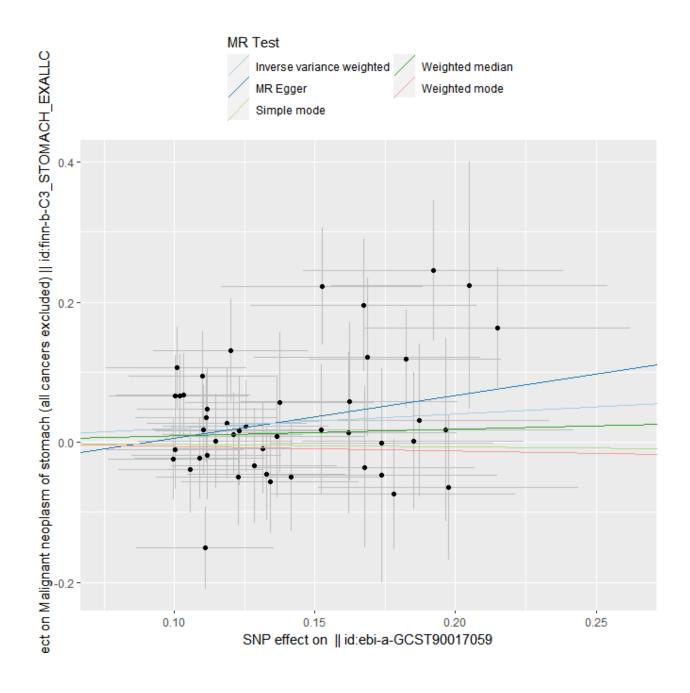
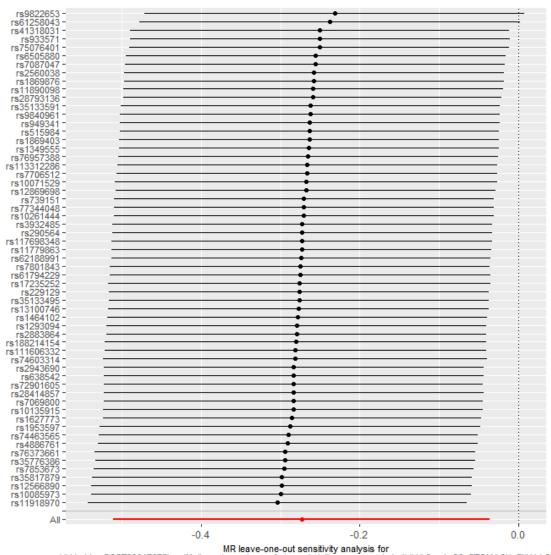
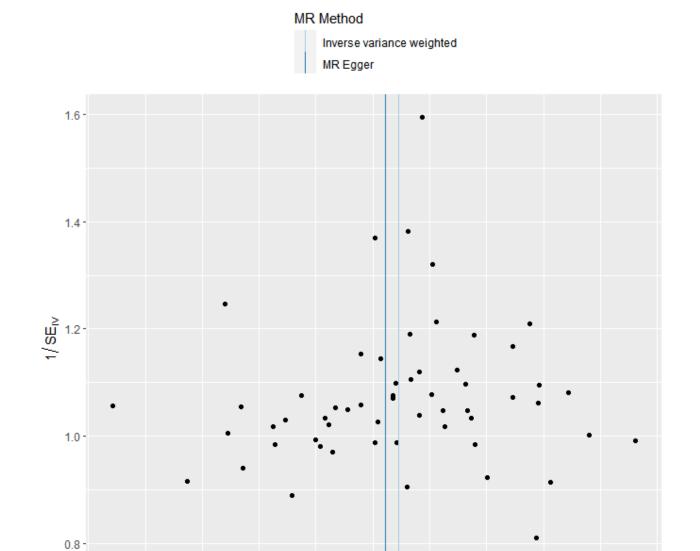


Figure 93 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.1000005472) on gastric cancer



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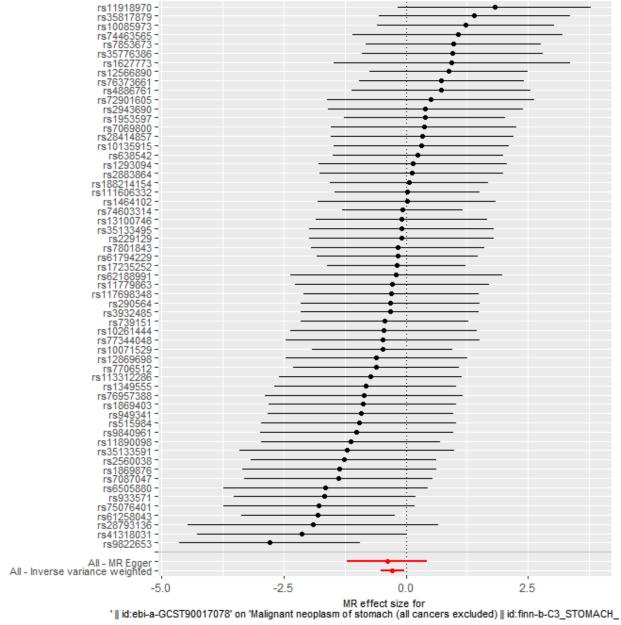
-1

0

 β_{IV}

-3

-2



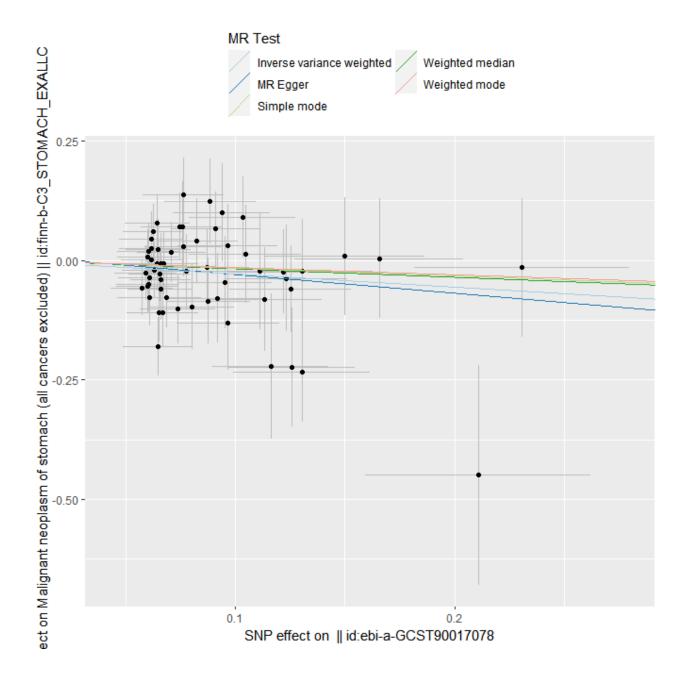
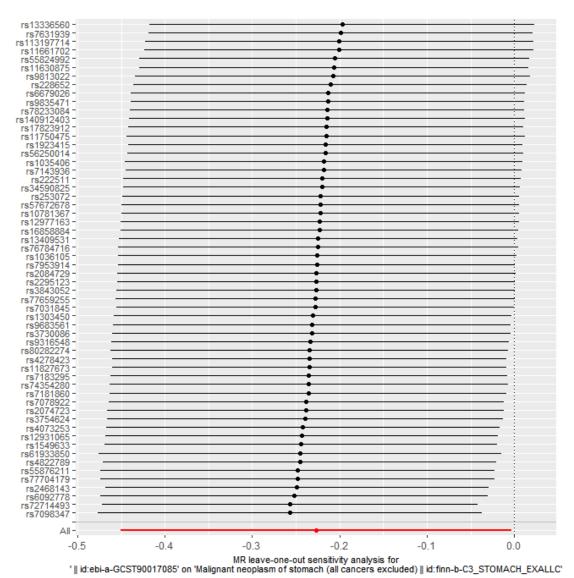
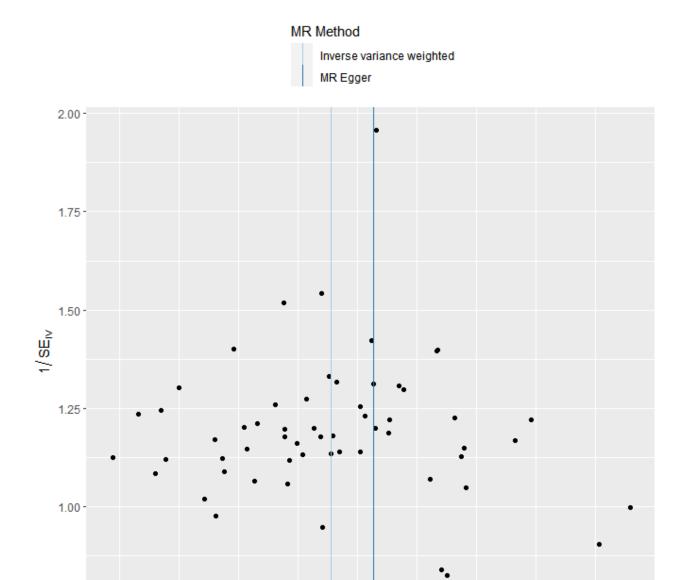


Figure 94 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.2755) on gastric cancer



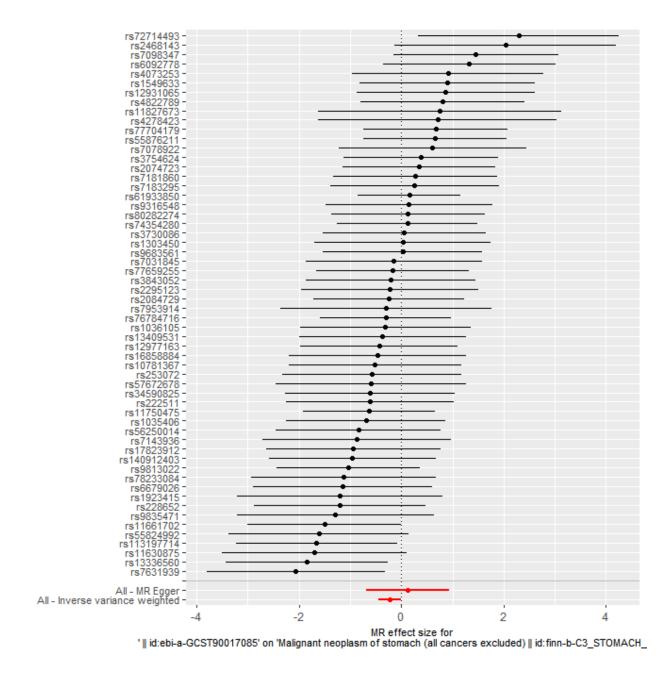


 β_{IV}

2

-2

-1



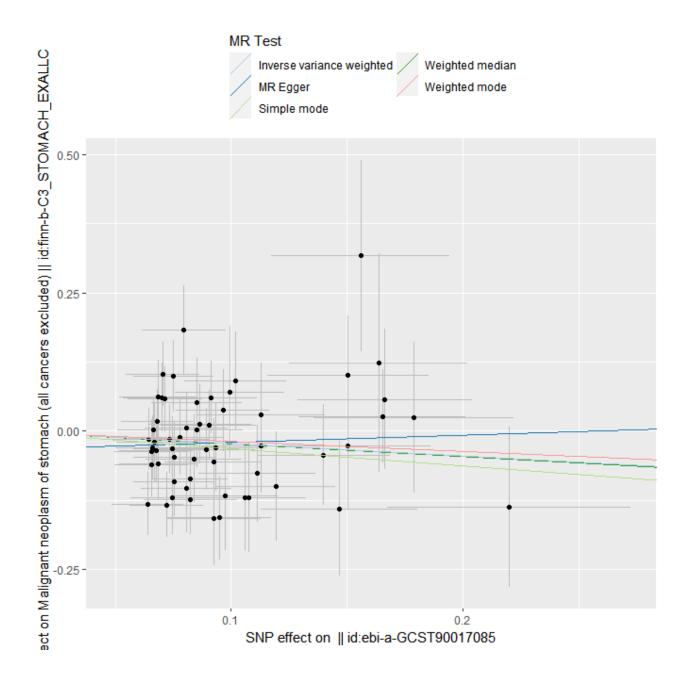
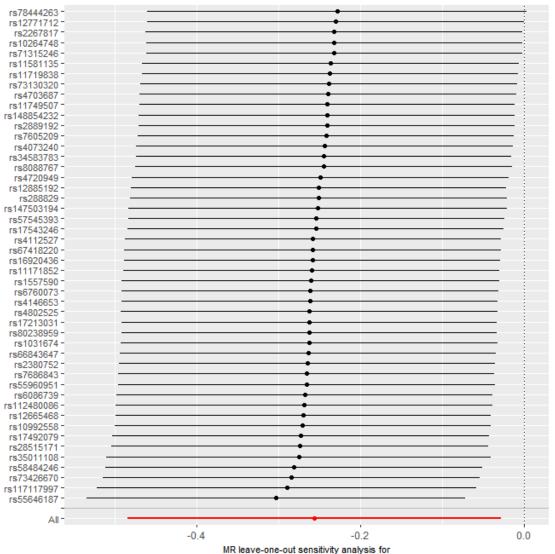
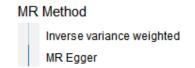
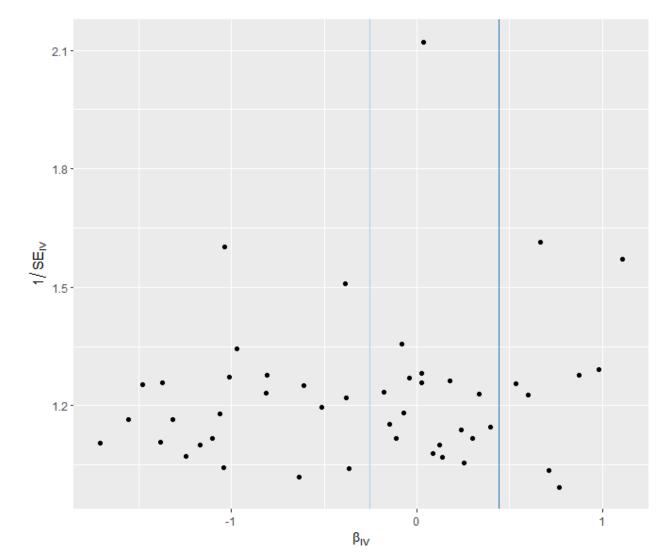


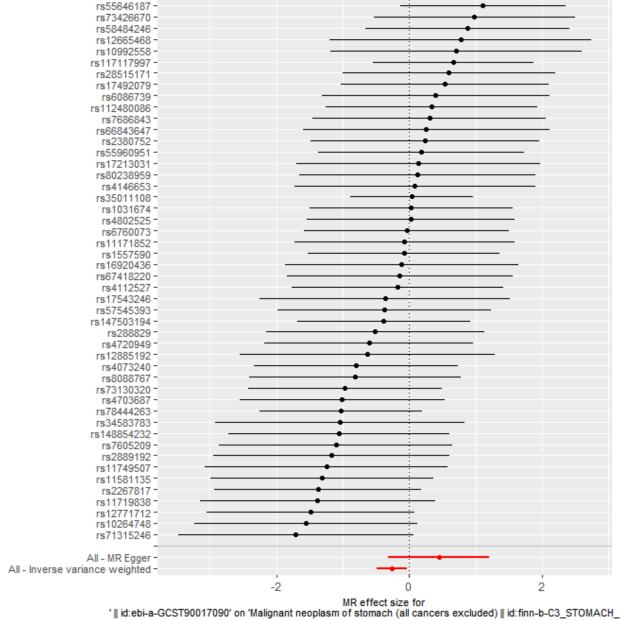
Figure 95 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Actinomycetales id.420) on gastric cancer



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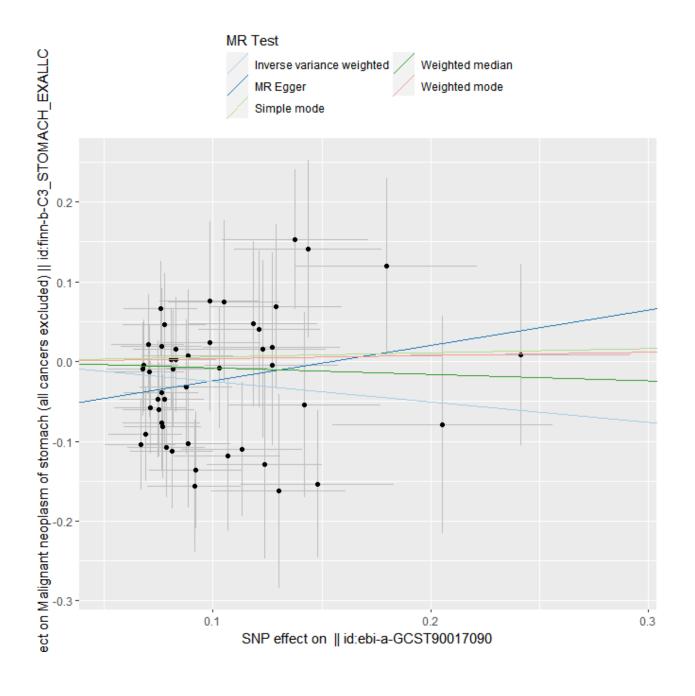
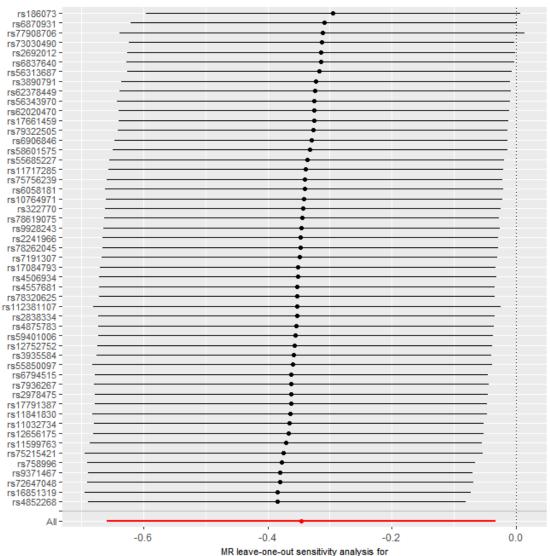
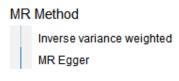
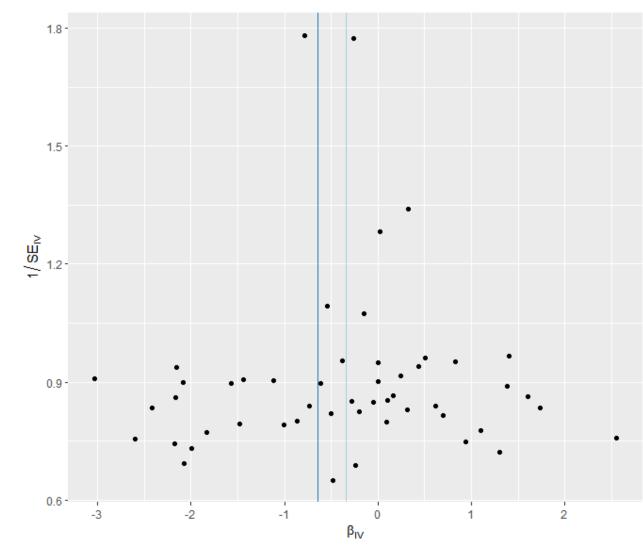


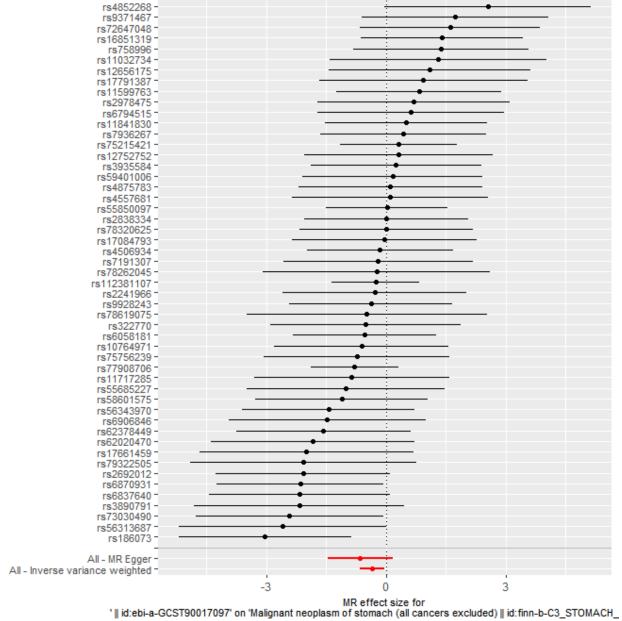
Figure 96 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Desulfovibrionales id.3156) on gastric cancer



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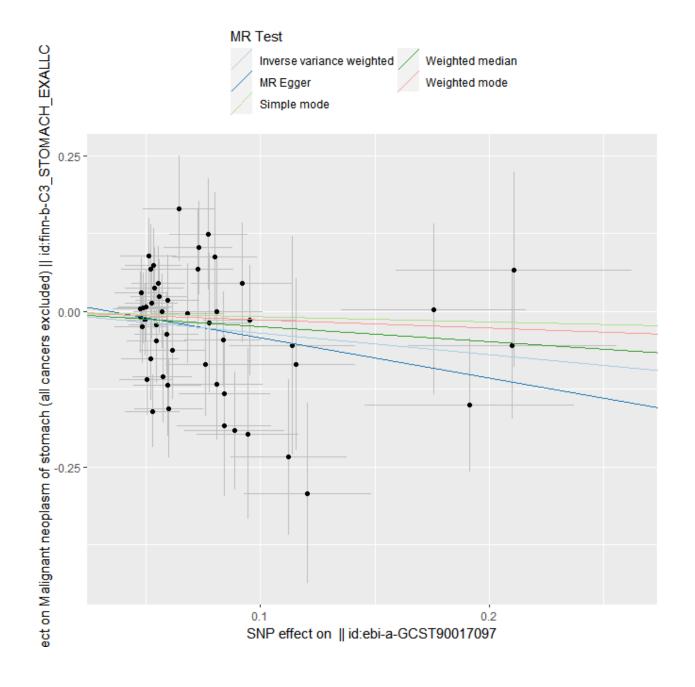
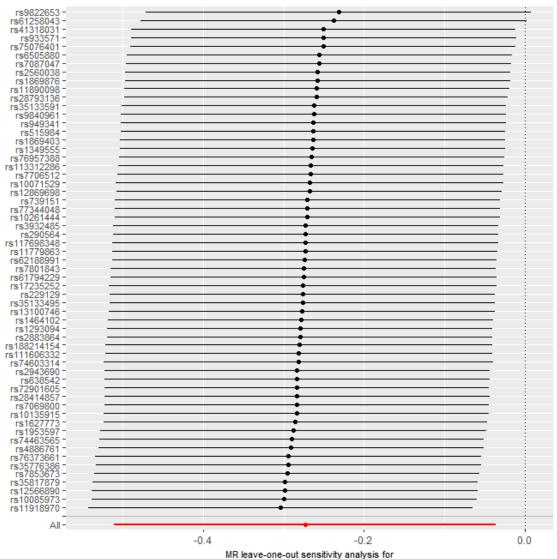
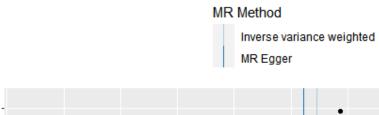
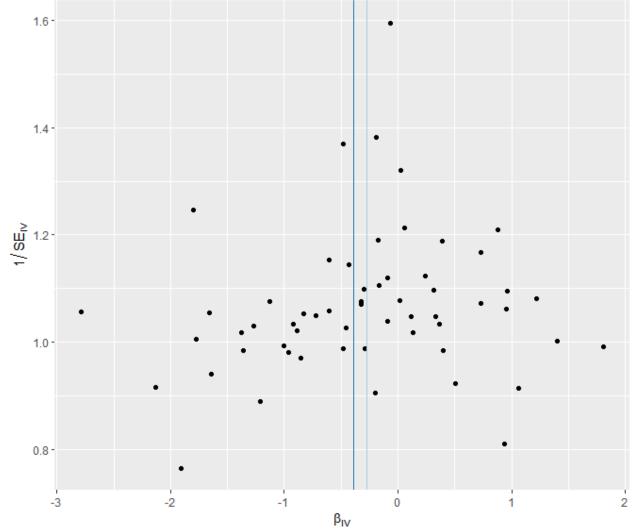


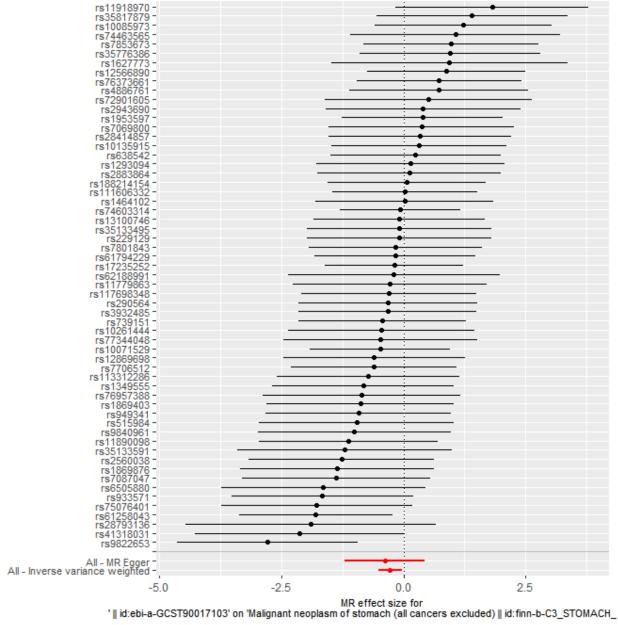
Figure 97 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Mollicutes RF9 id.11579) on gastric cancer



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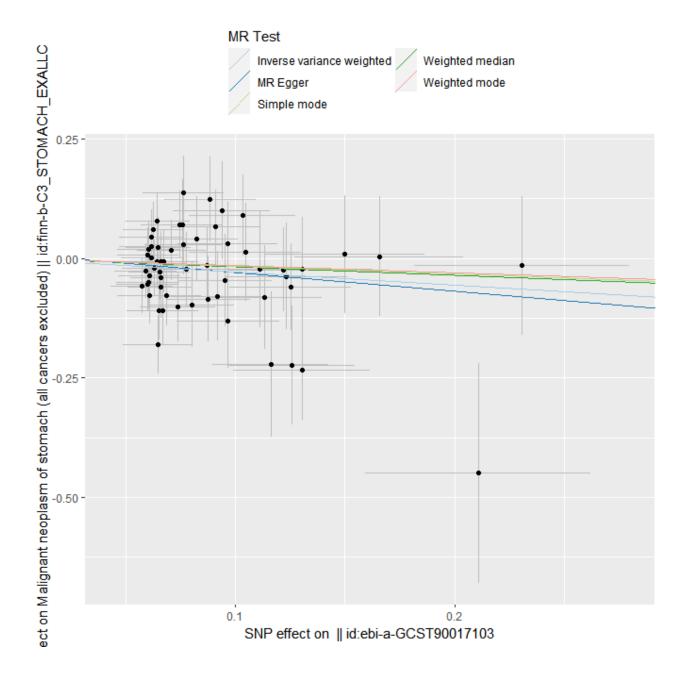
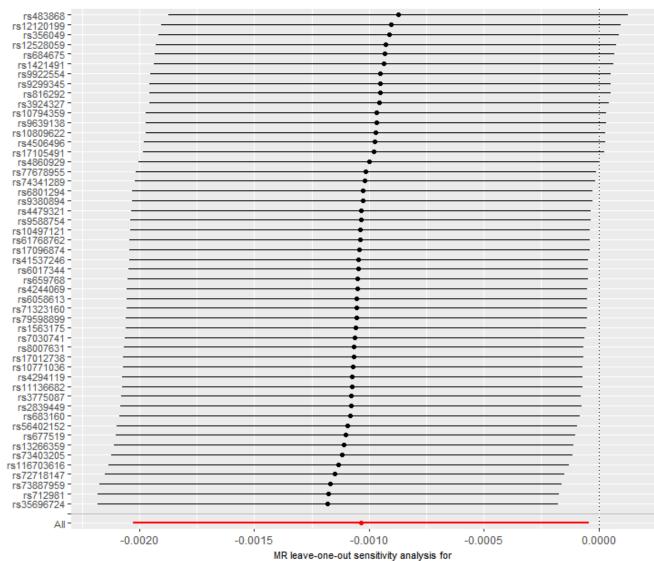
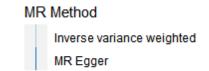
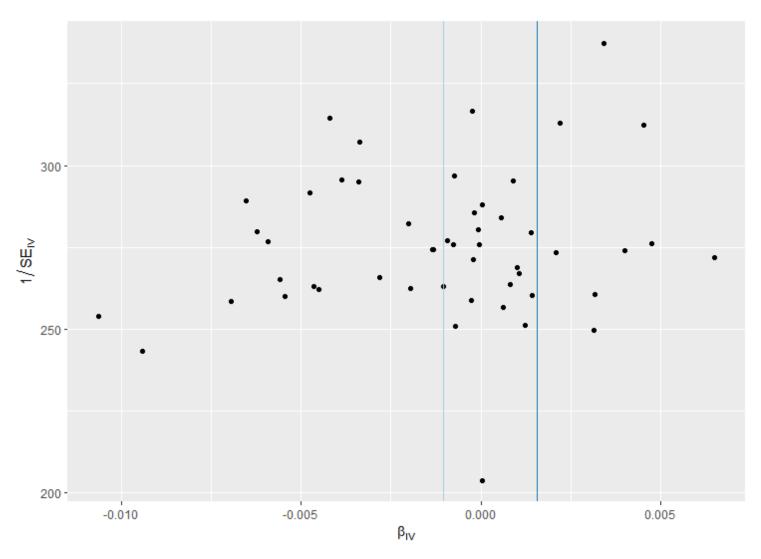


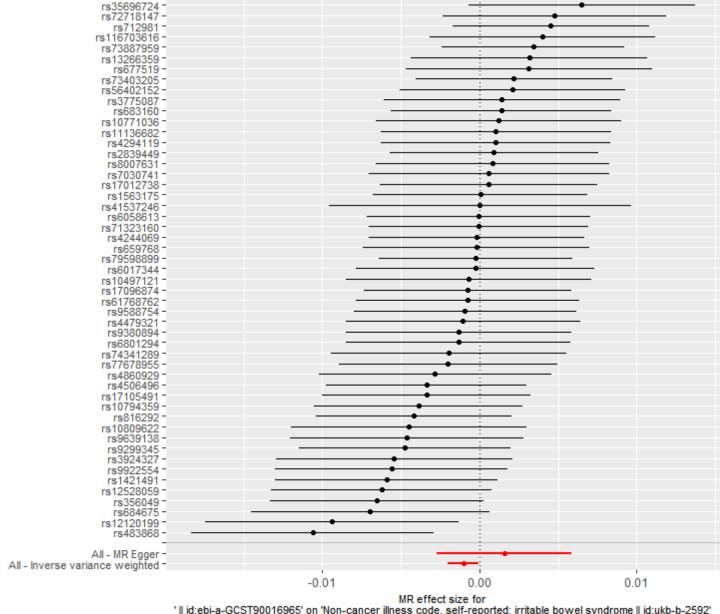
Figure 98 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Anaerofilum id.2053) on irritable bowel syndrome



' || id:ebi-a-GCST90016965' on 'Non-cancer illness code, self-reported: irritable bowel syndrome || id:ukb-b-2592'







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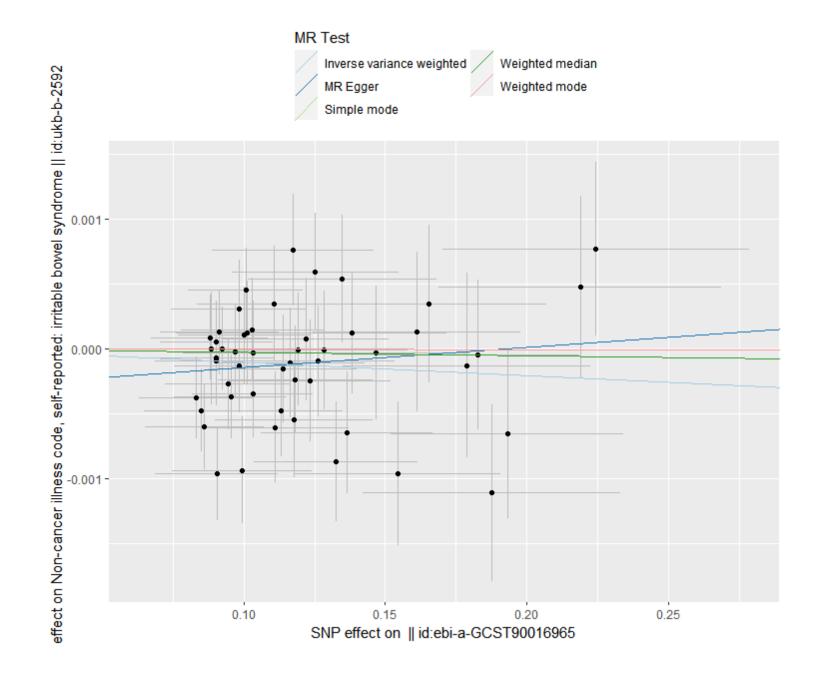
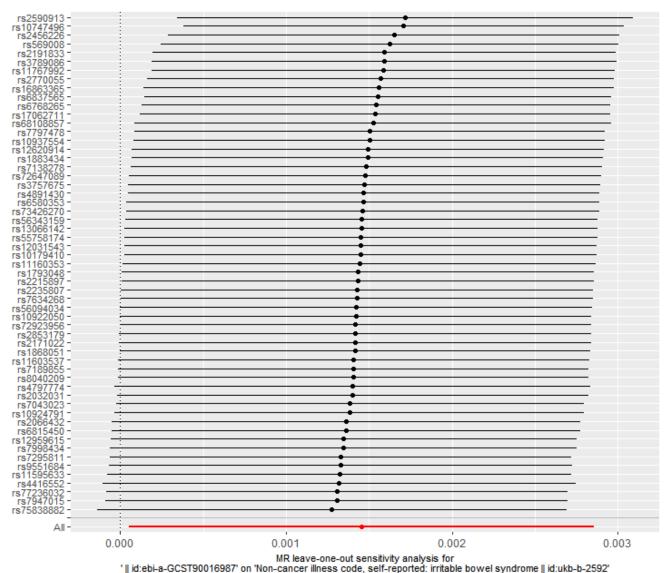
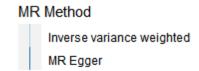
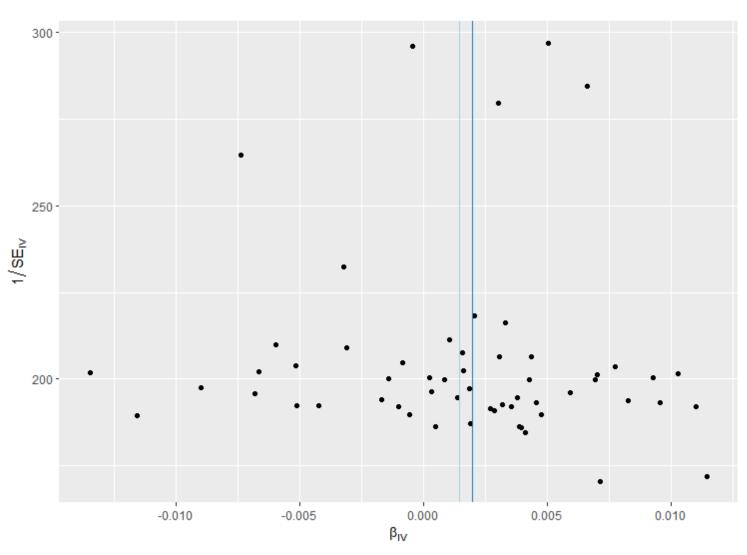
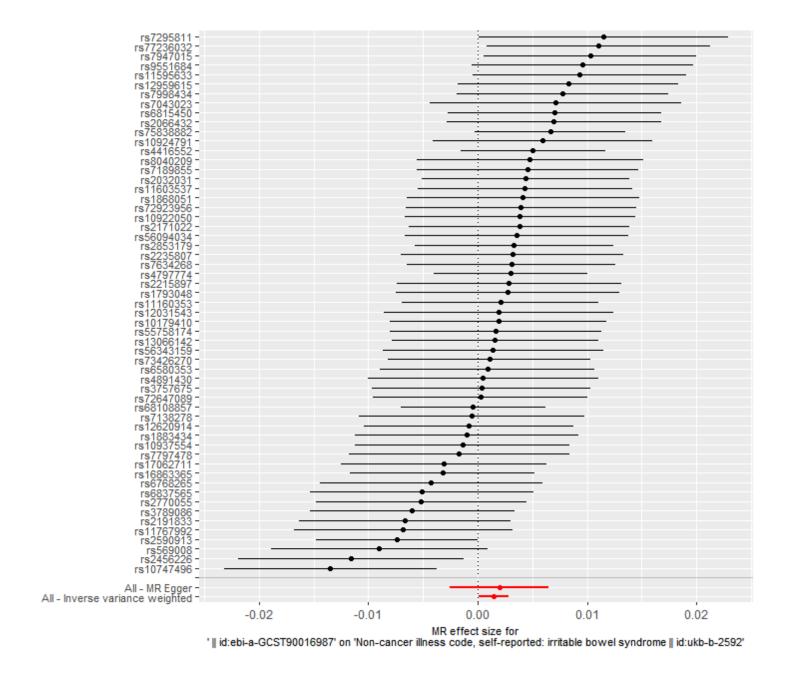


Figure 99 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Desulfovibrio id.3173) on irritable bowel syndrome









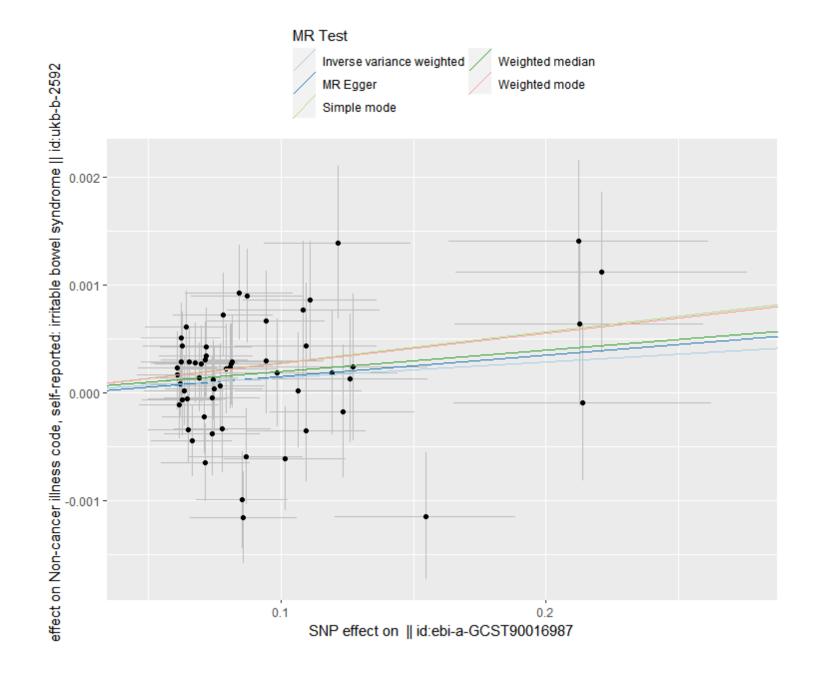
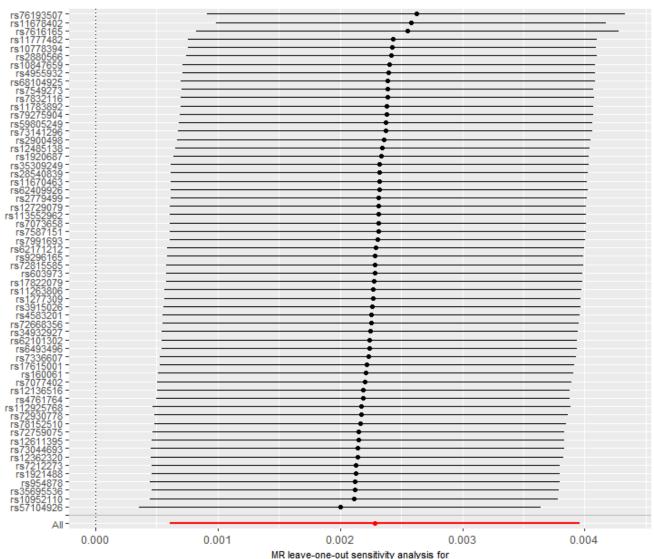
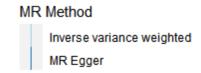
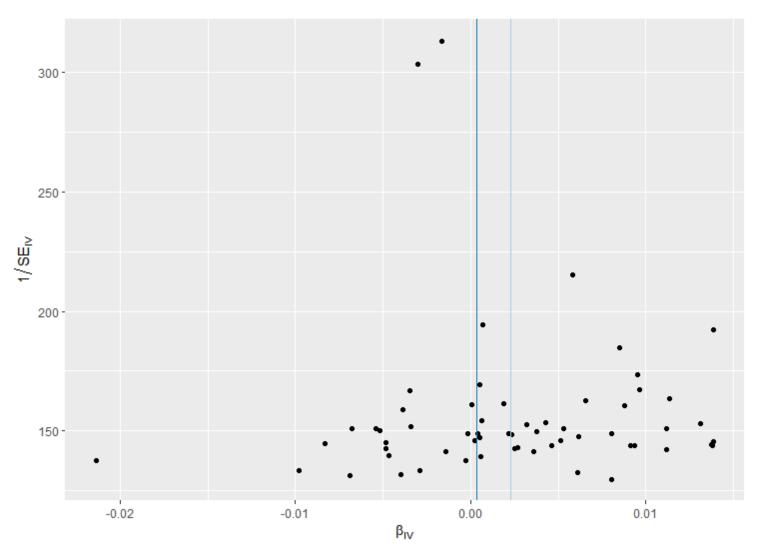


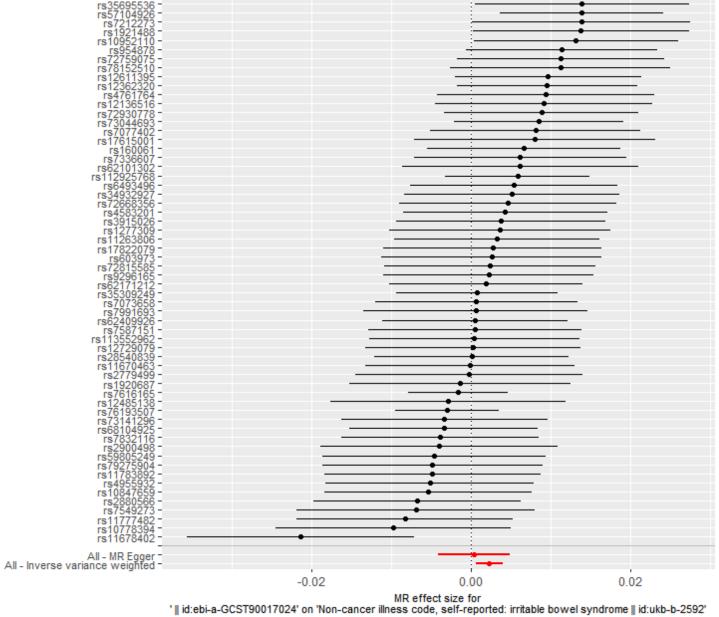
Figure 100 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lachnospiraceae NK4A136 group id.11319) on irritable bowel syndrome



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017024' on 'Non-cancer illness code, self-reported: irritable bowel syndrome || id:ukb-b-2592'







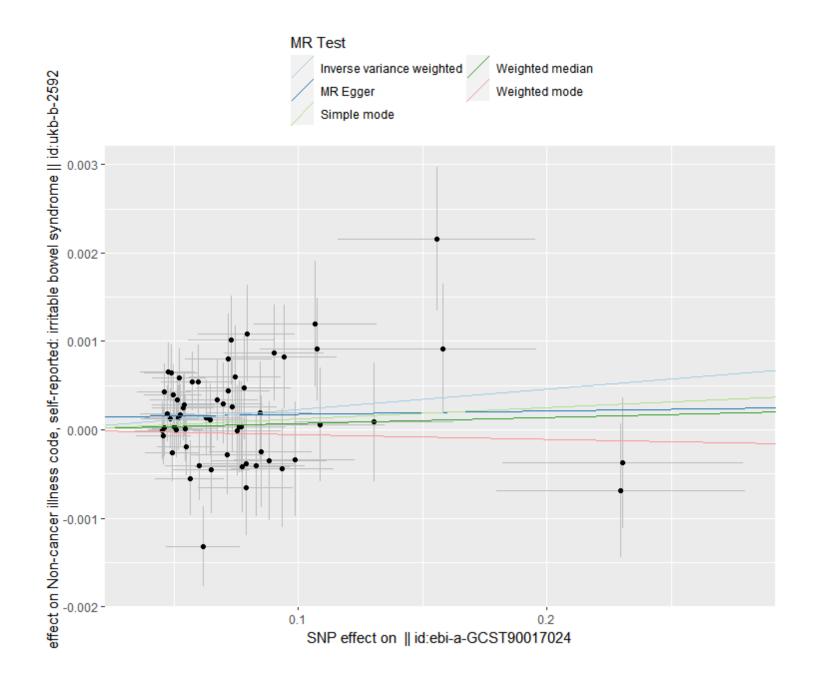
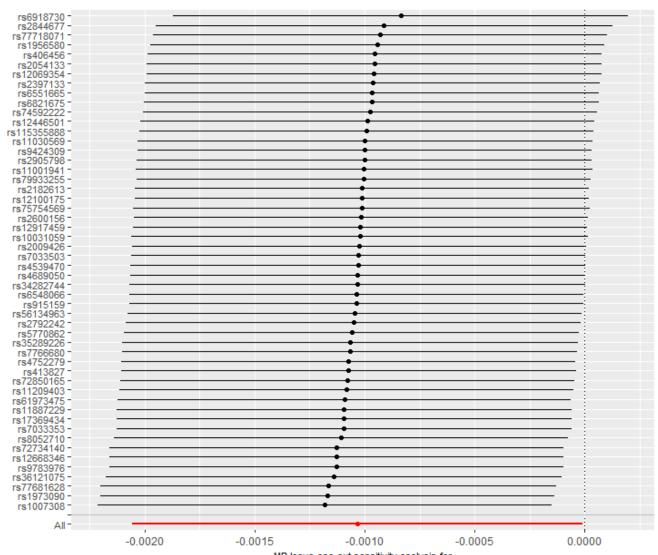
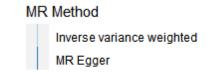
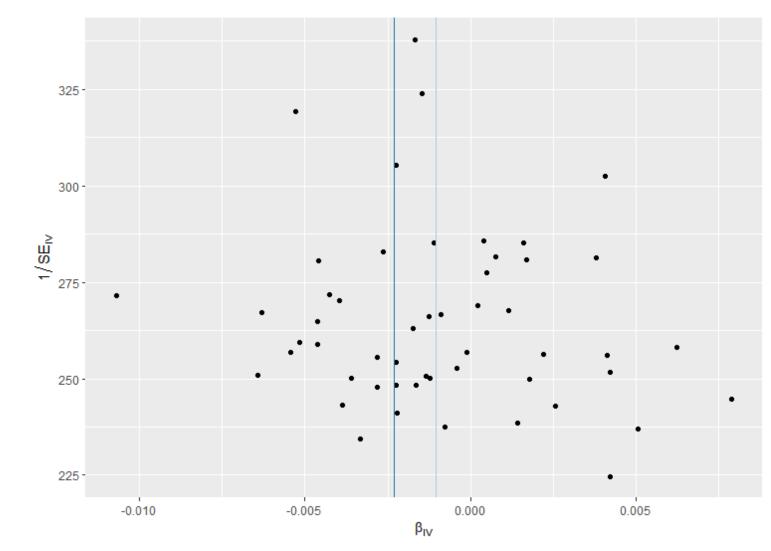


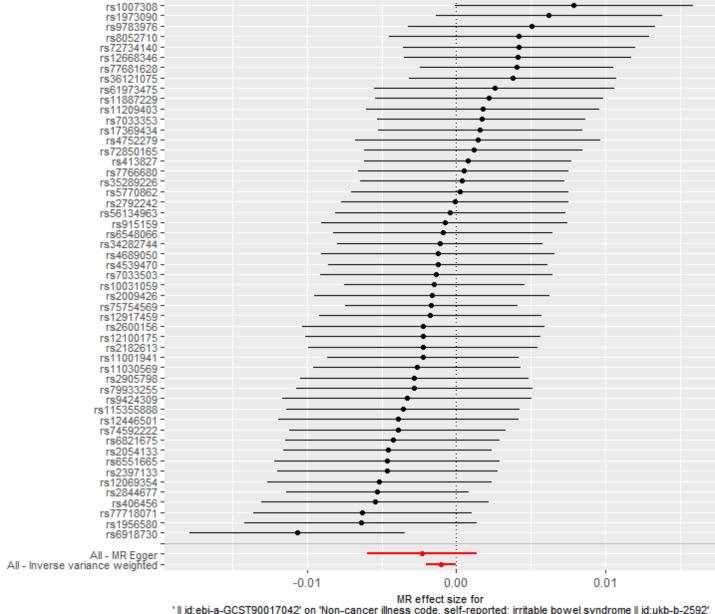
Figure 101 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Peptococcus id.2037) on irritable bowel syndrome



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017042' on 'Non-cancer illness code, self-reported: irritable bowel syndrome || id:ukb-b-2592'







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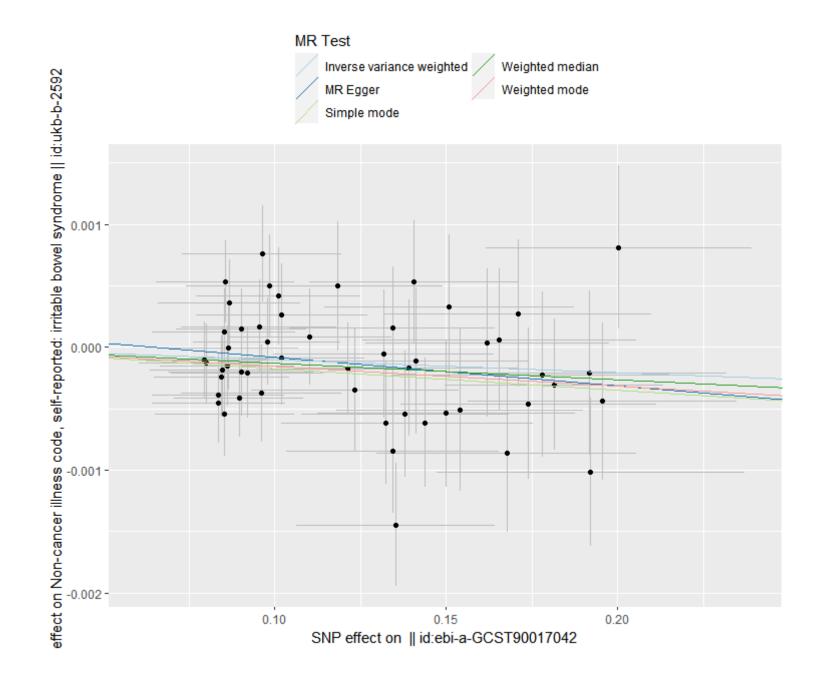
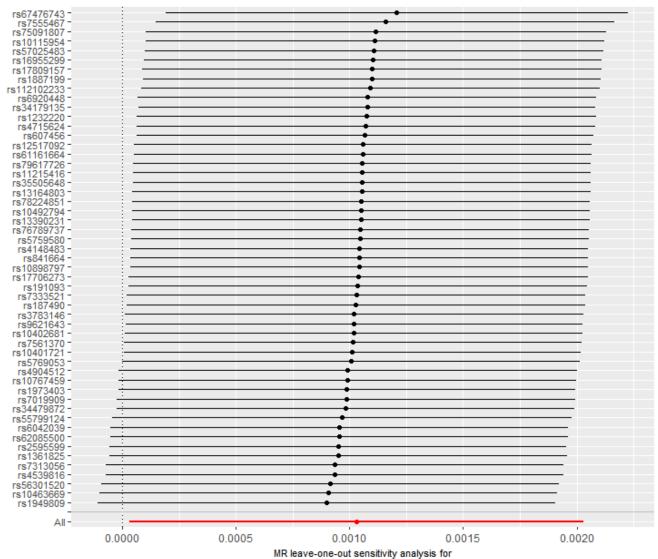
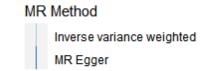
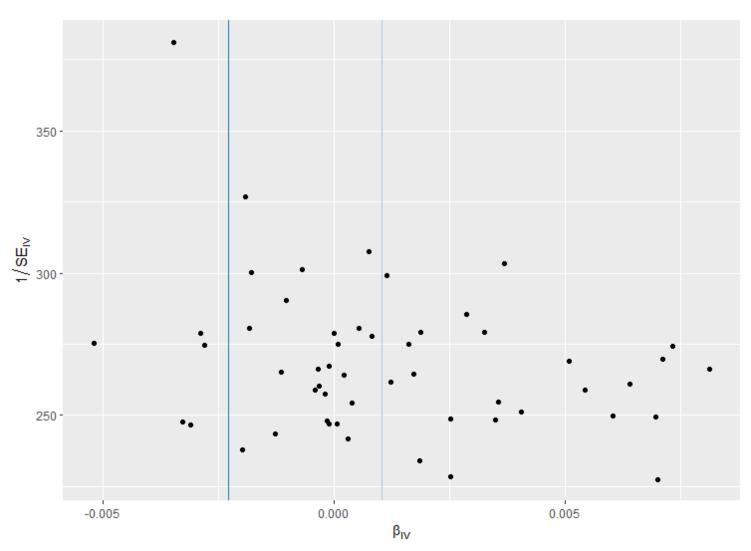


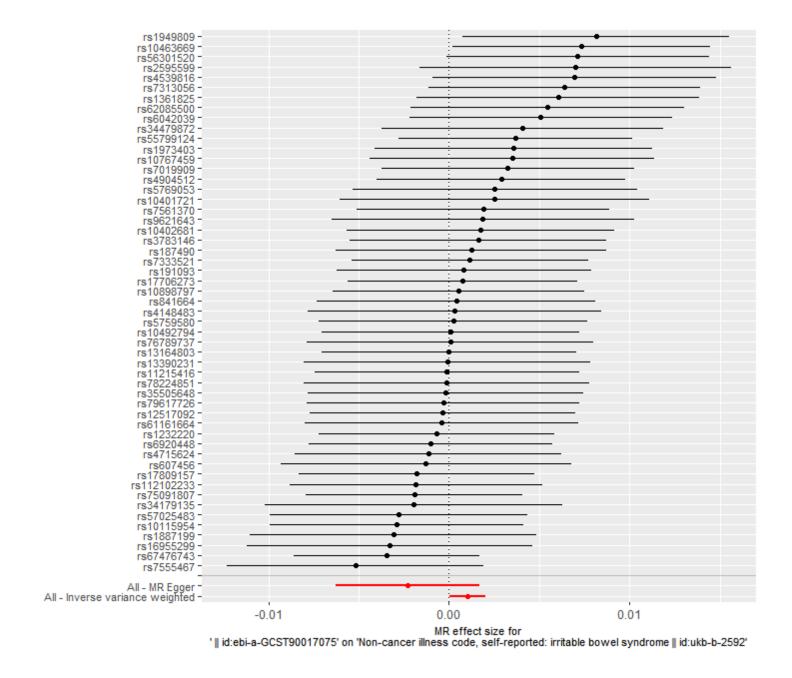
Figure 102 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Tyzzerella3 id.11335) on irritable bowel syndrome



leave-one-out sensitivity analysis for
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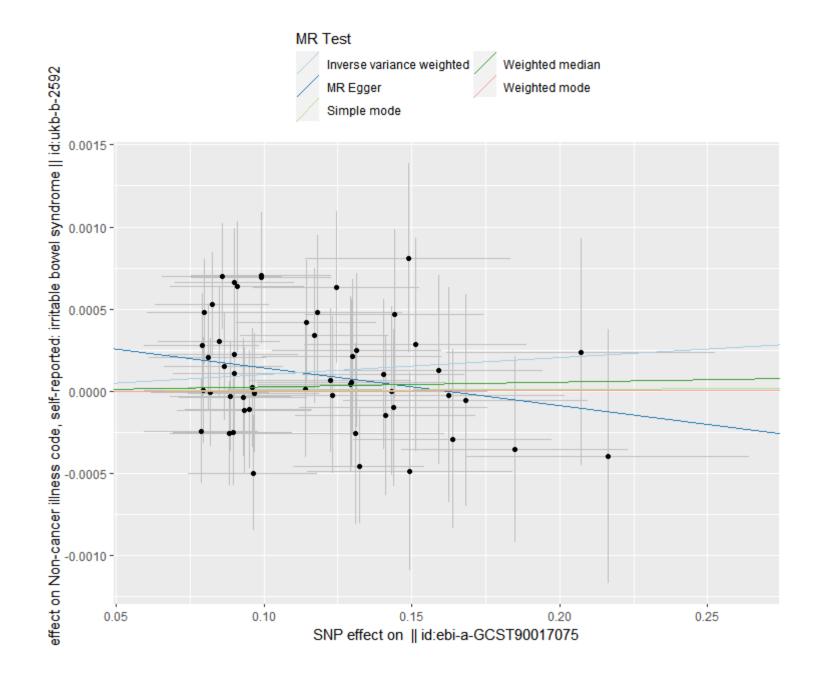
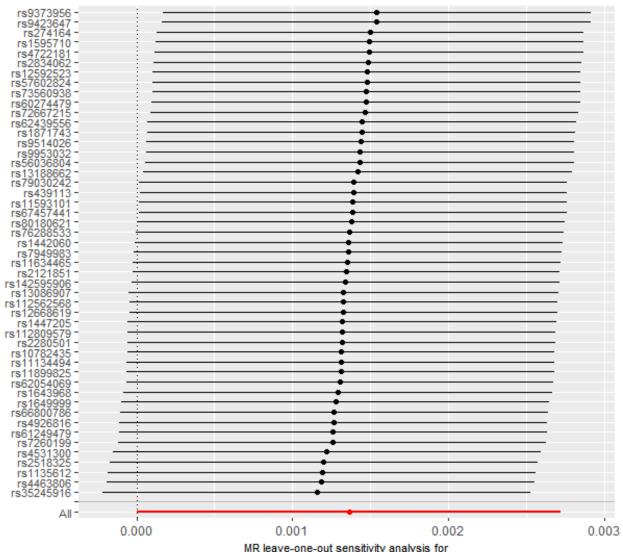


Figure 103 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Negativicutes id.2164) on diverticular disease

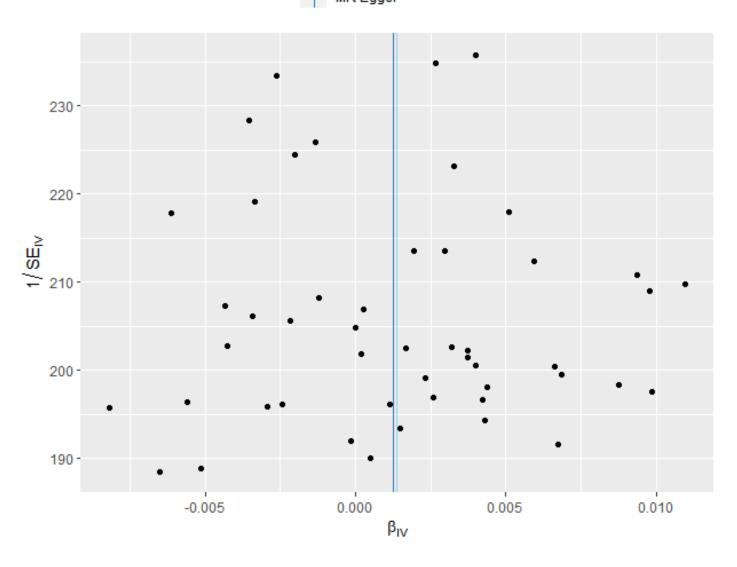


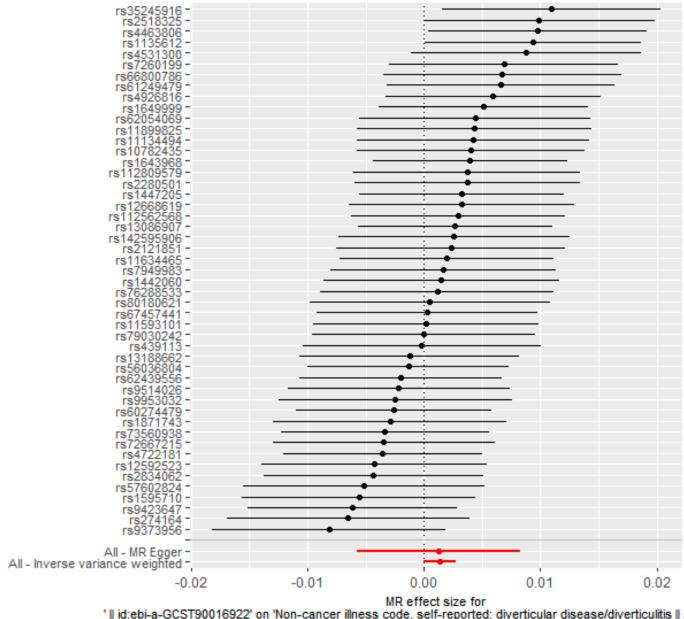
MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016922' on 'Non-cancer illness code, self-reported: diverticular disease/diverticulitis || id:ukb-b-14

MR Method

Inverse variance weighted

MR Egger





" || id:ebi-a-GCST90016922" on "Non-cancer illness code, self-reported: diverticular disease/diverticulitis || id

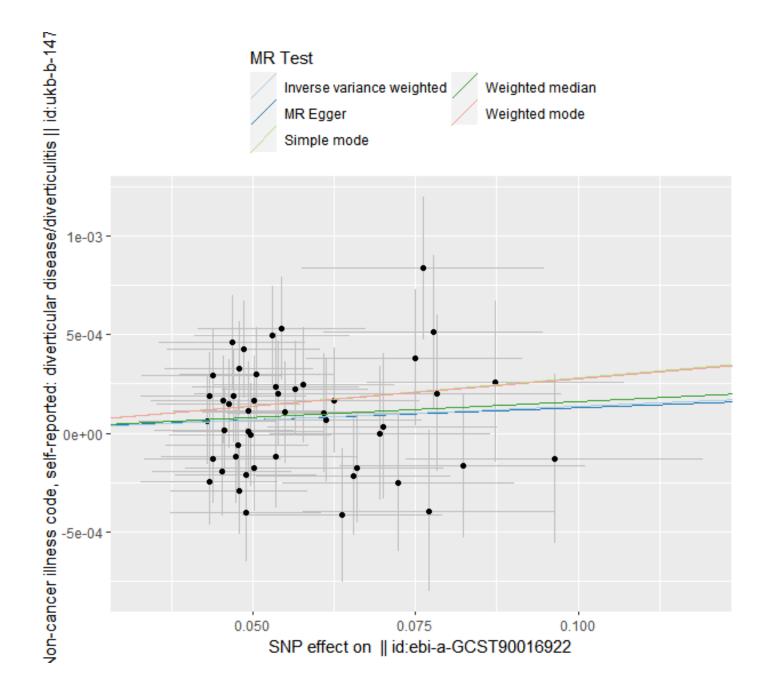
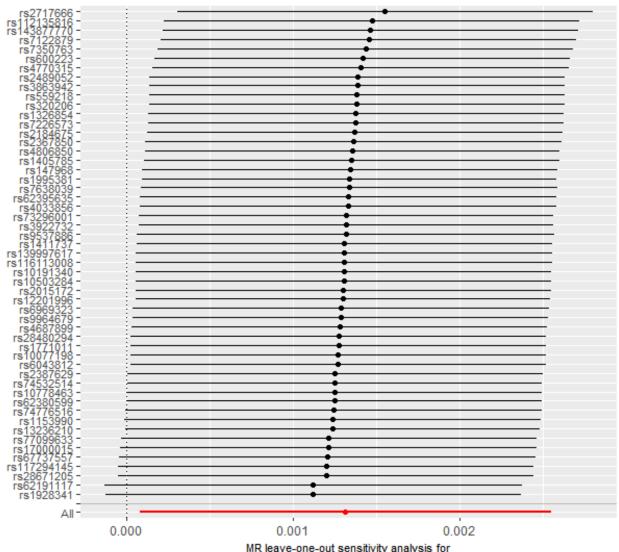


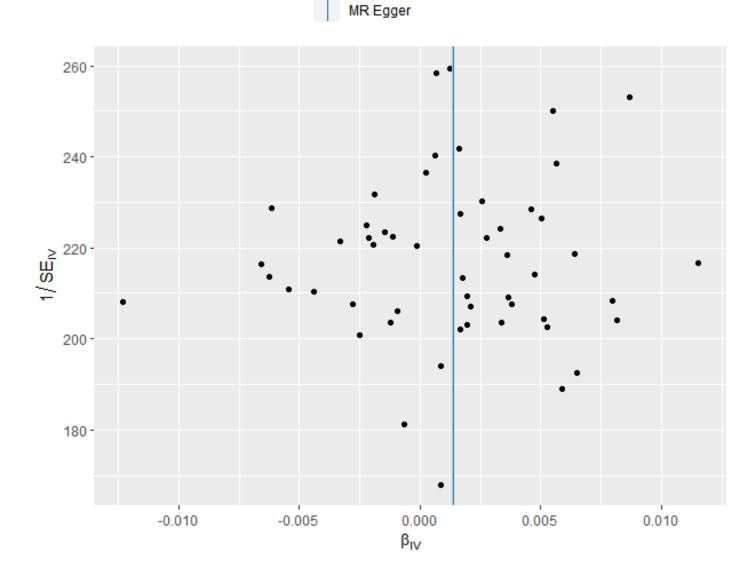
Figure 104 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Alcaligenaceae id.2875) on diverticular disease

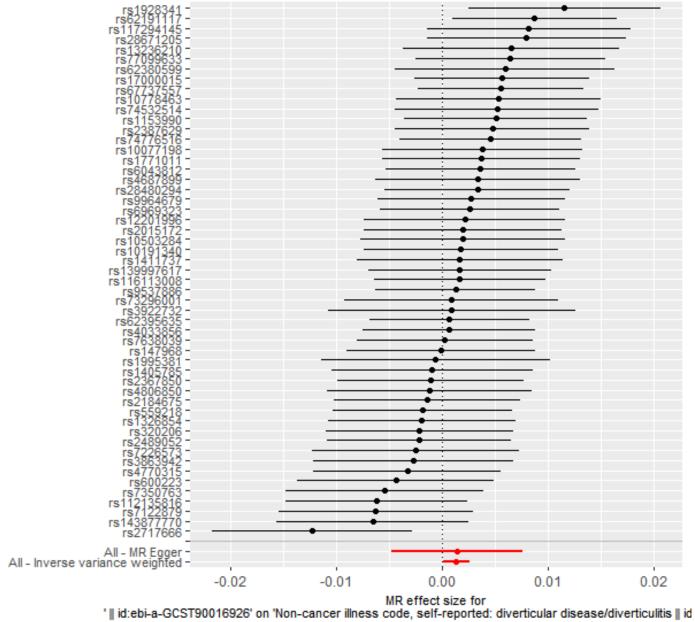


MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016926' on 'Non-cancer illness code, self-reported: diverticular disease/diverticulitis || id:ukb-b-14

MR Method

Inverse variance weighted





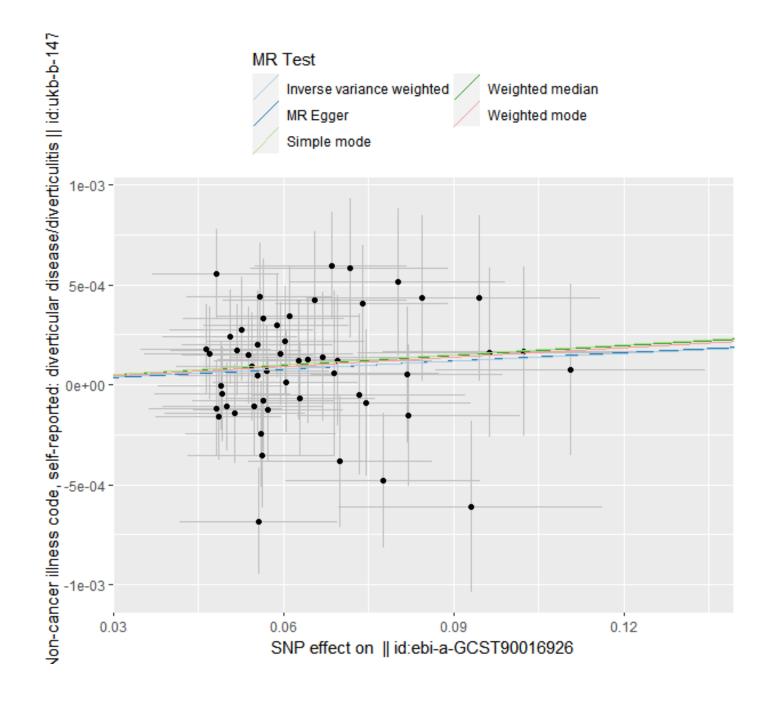
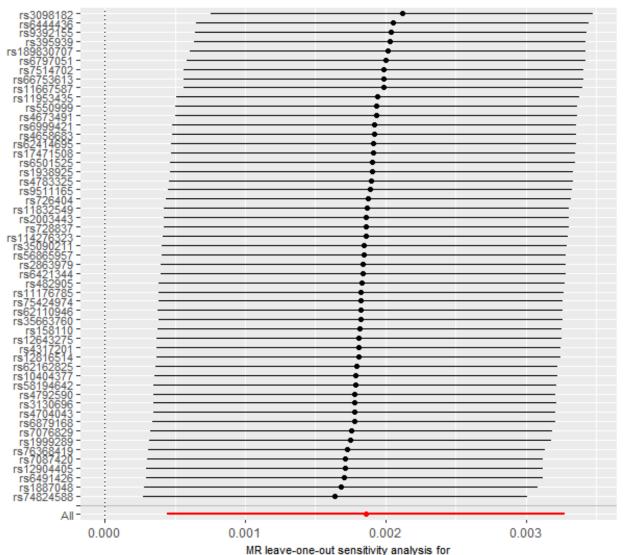
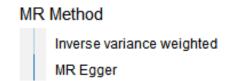
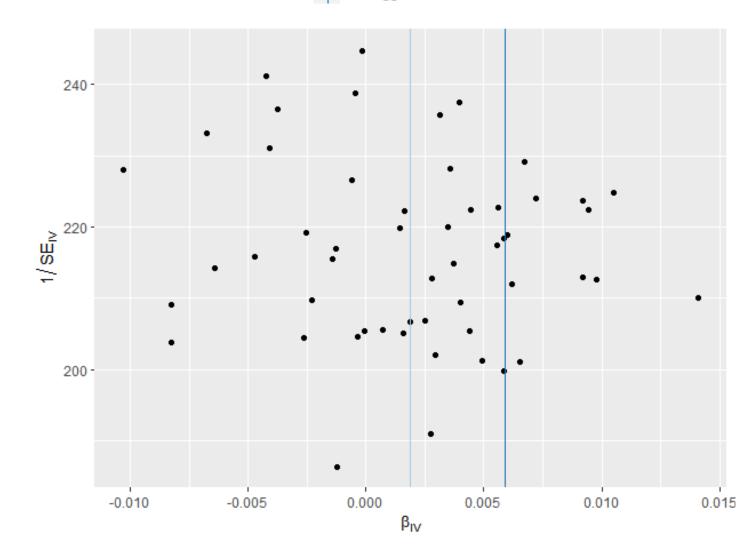


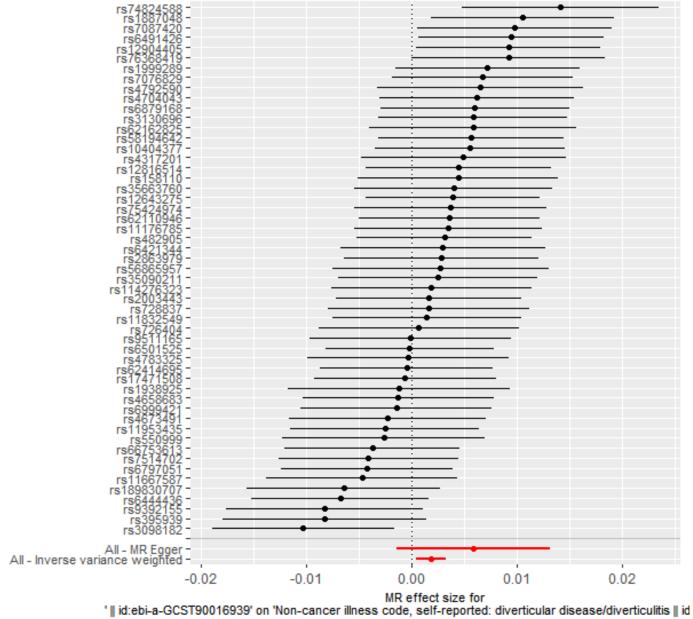
Figure 105 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Family XIII id.1957) on diverticular disease



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016939' on 'Non-cancer illness code, self-reported: diverticular disease/diverticulitis || id:ukb-b-14







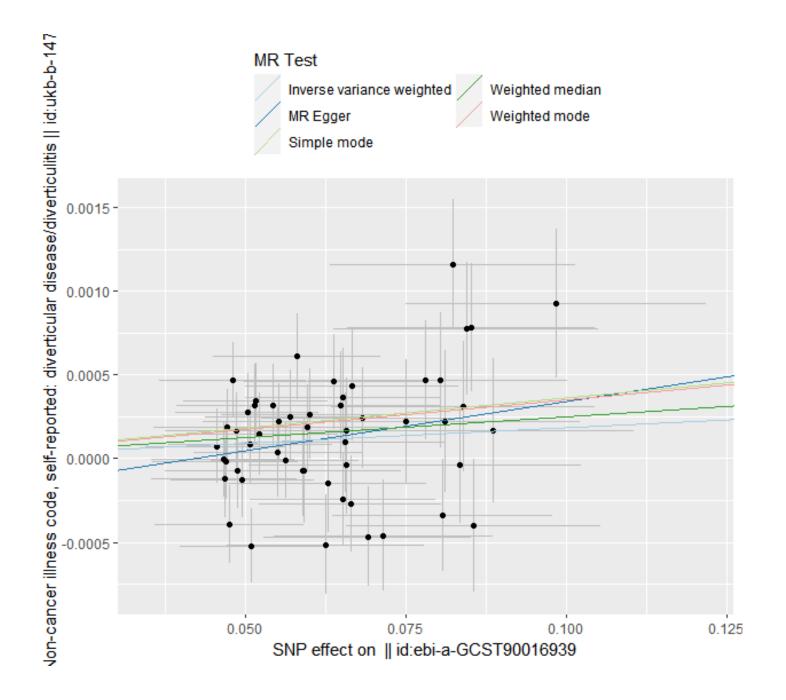
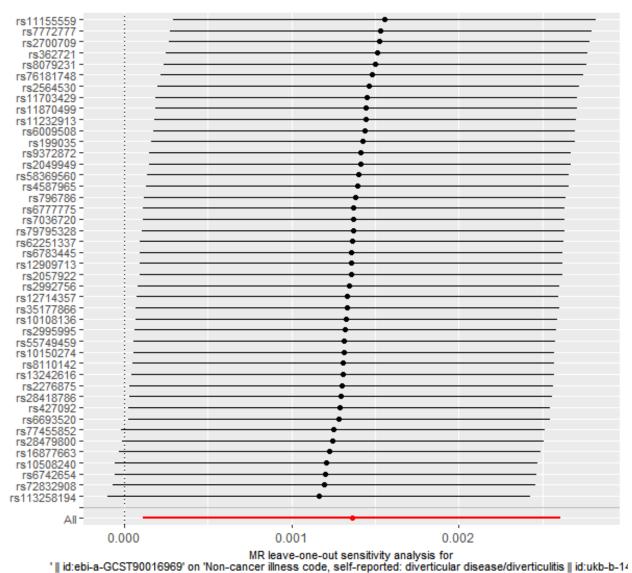


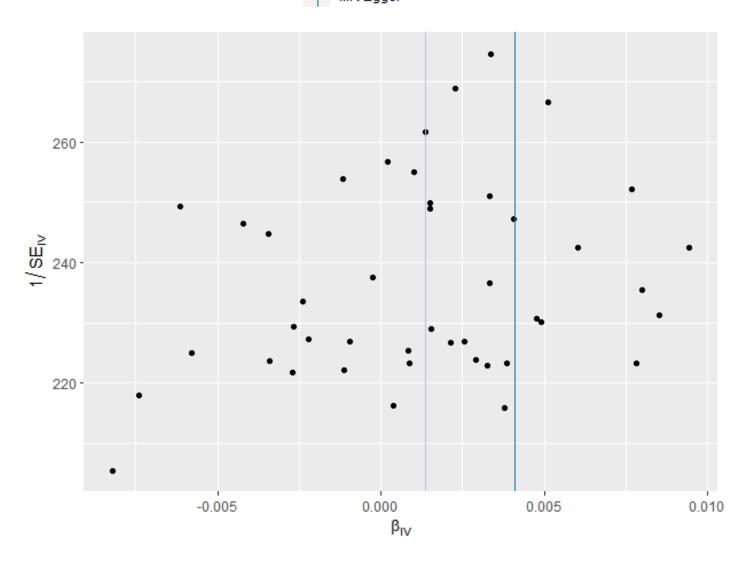
Figure 106 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Barnesiella id.944) on diverticular disease

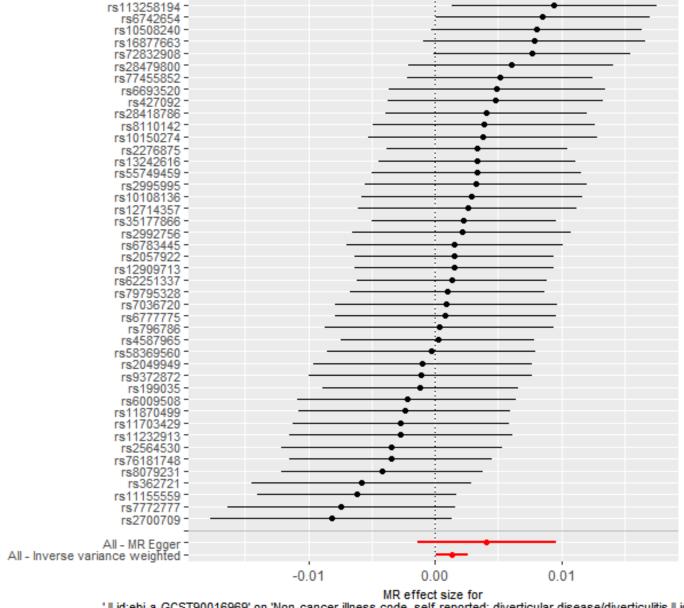


MR Method

Inverse variance weighted

MR Egger





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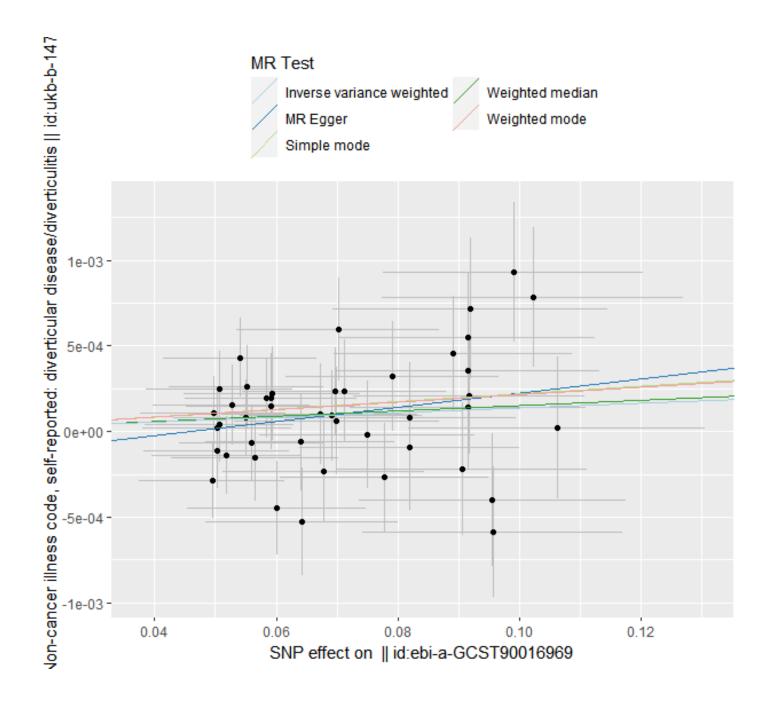
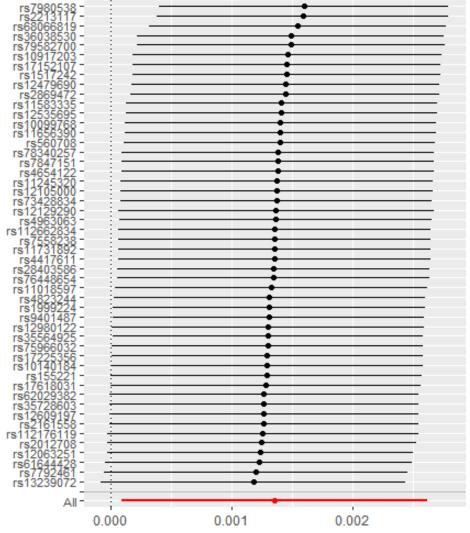
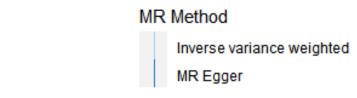
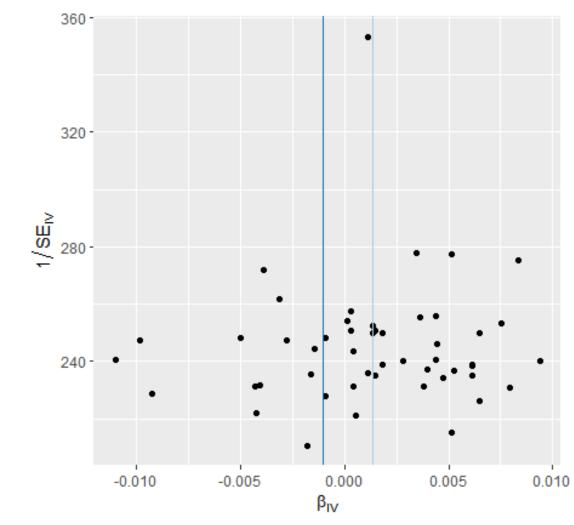


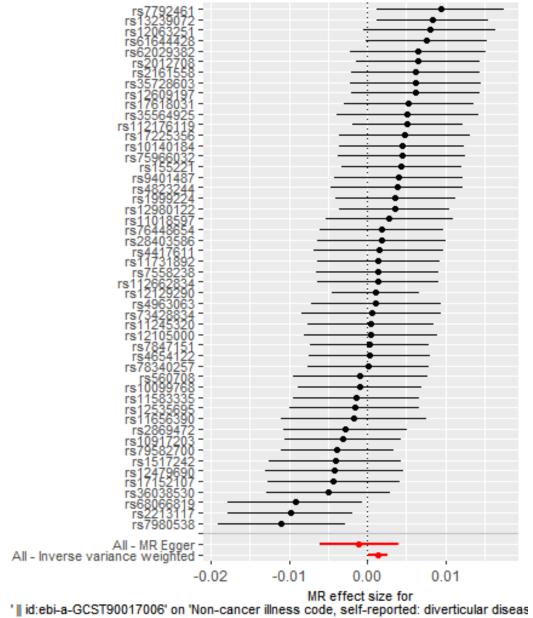
Figure 107 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium xylanophilum group id.14375) on diverticular disease



MR leave-one-out sensitivity analysis for :ebi-a-GCST90017006' on 'Non-cancer illness code, self-reported: diverticular disease/divertic







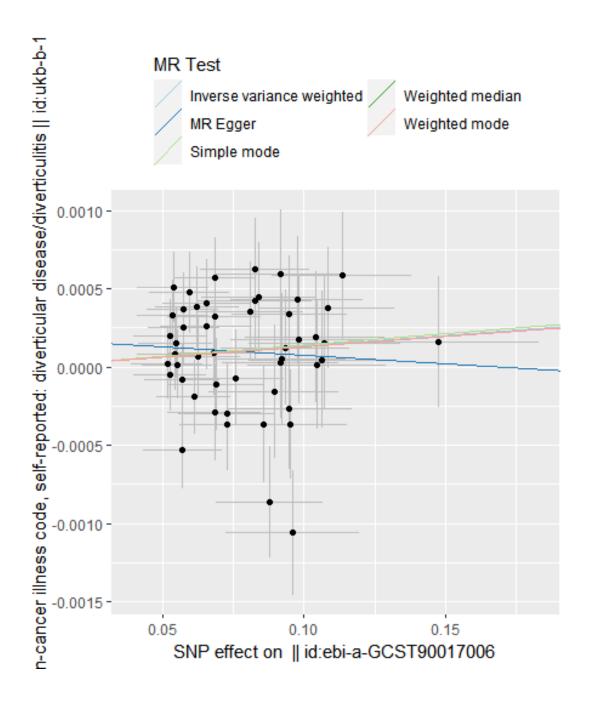
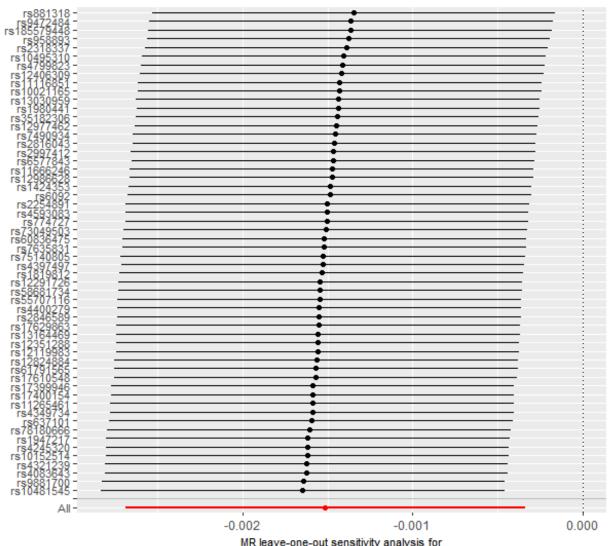


Figure 108 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcus2 id.11374) on diverticular disease

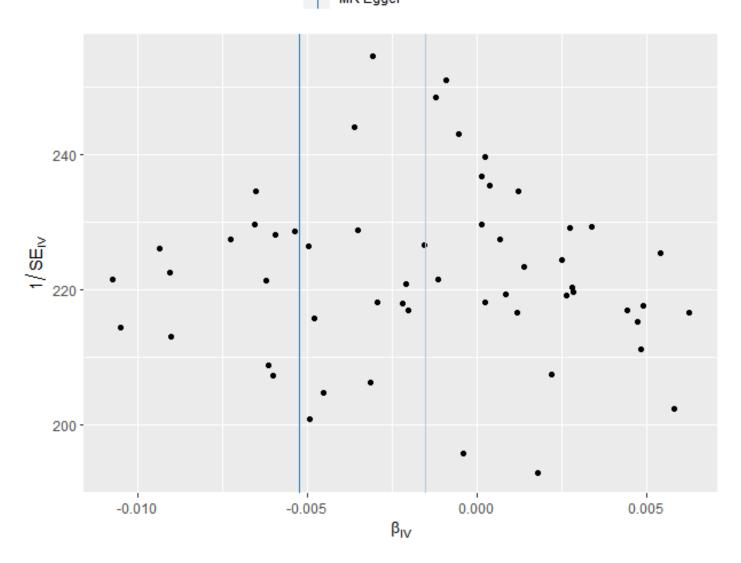


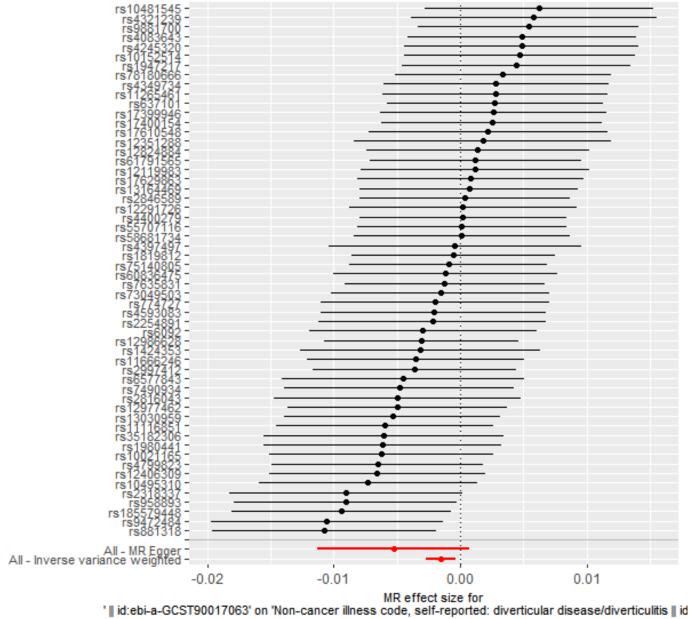
MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017063' on 'Non-cancer illness code, self-reported: diverticular disease/diverticulitis || id:ukb-b-14

MR Method

Inverse variance weighted

MR Egger





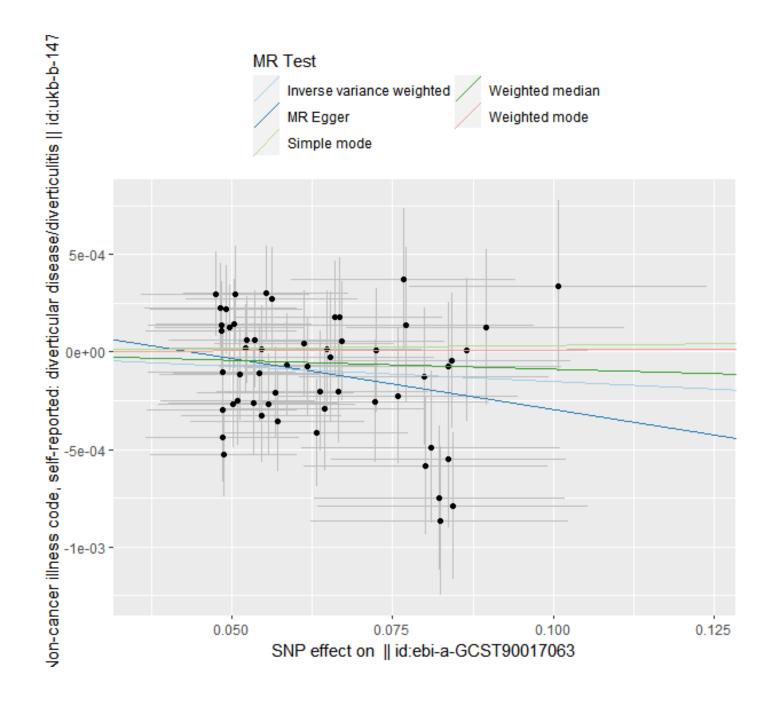
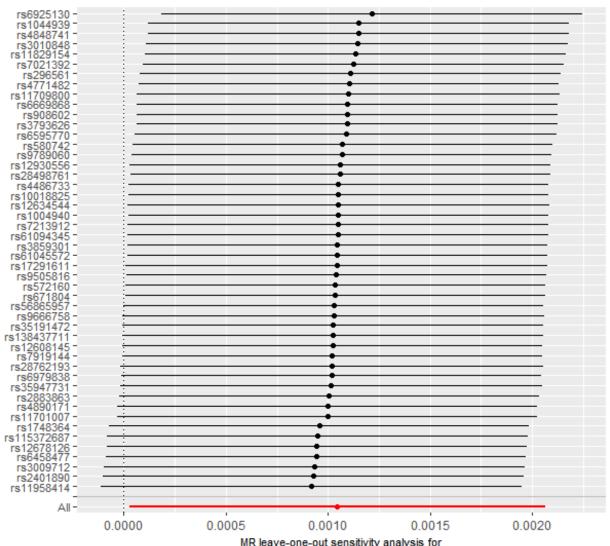
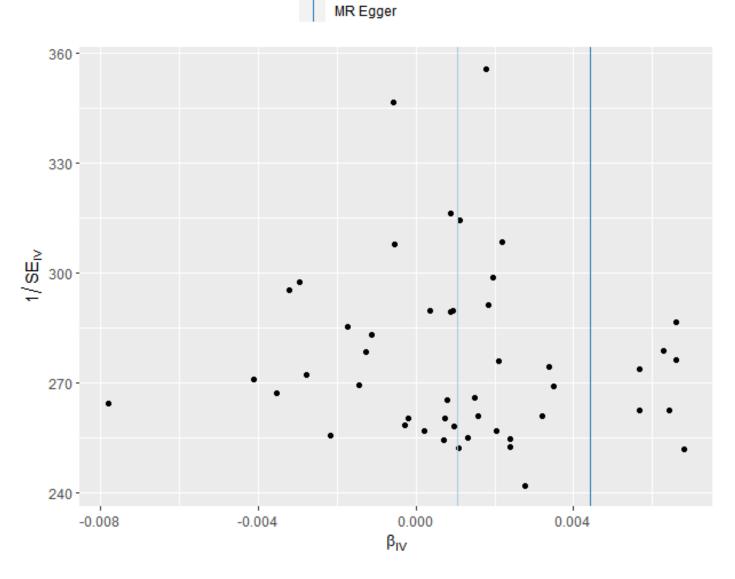


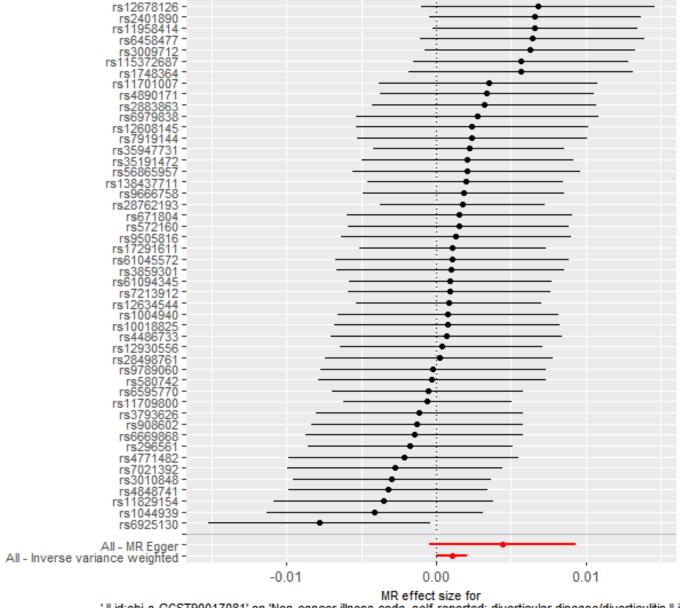
Figure 109 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.1868) on diverticular disease



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90017081' on 'Non-cancer illness code, self-reported: diverticular disease/diverticulitis || id:ukb-b-14

MR Method Inverse variance weighted





" id:ebi-a-GCST90017081" on "Non-cancer illness code, self-reported: diverticular disease/diverticulitis || id

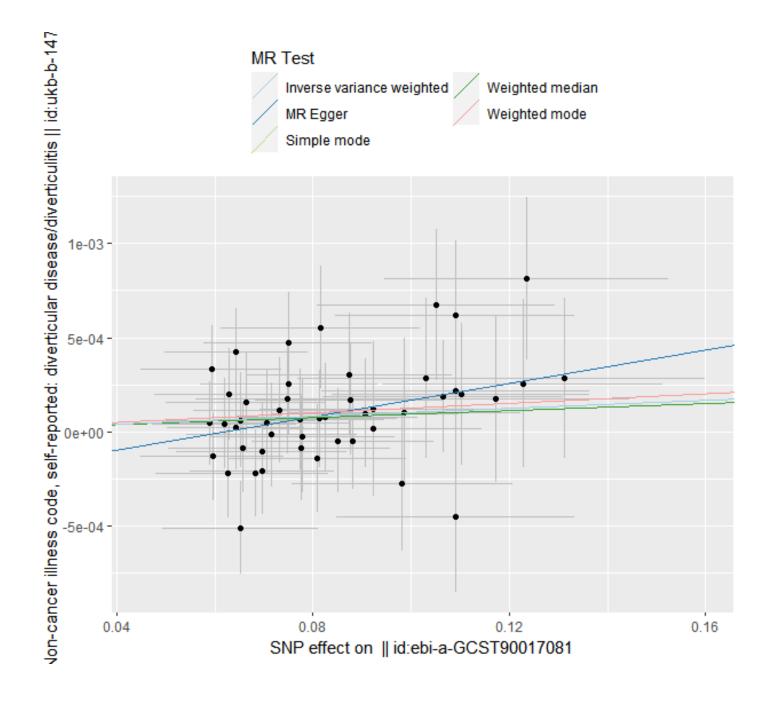
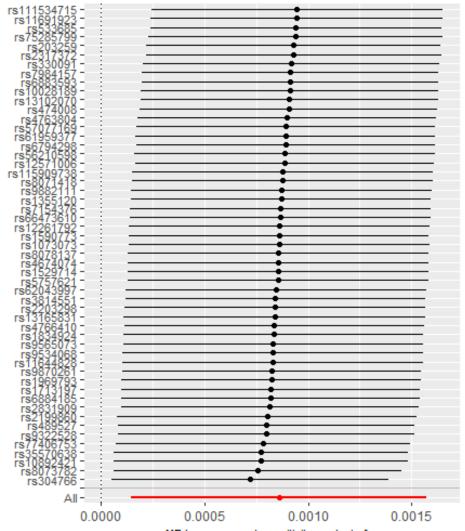


Figure 110 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.959) on diverticular disease

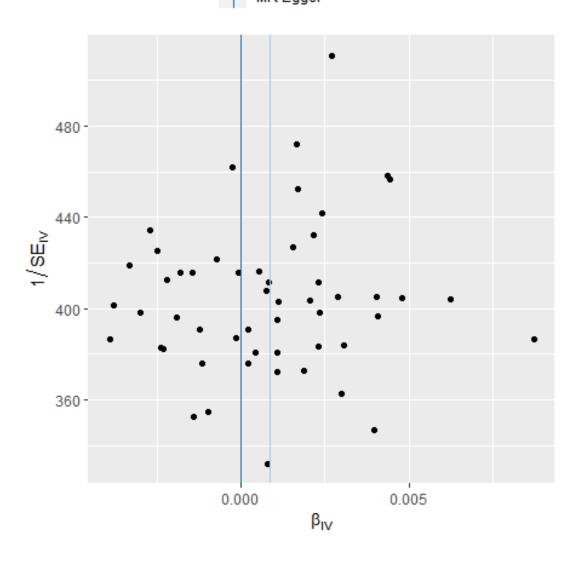


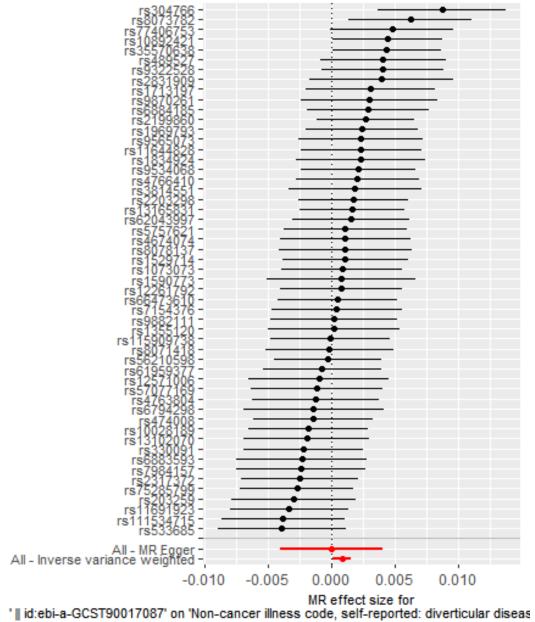
MR leave-one-out sensitivity analysis for :ebi-a-GCST90017087' on 'Non-cancer illness code, self-reported: diverticular disease/divertic

MR Method

Inverse variance weighted

MR Egger





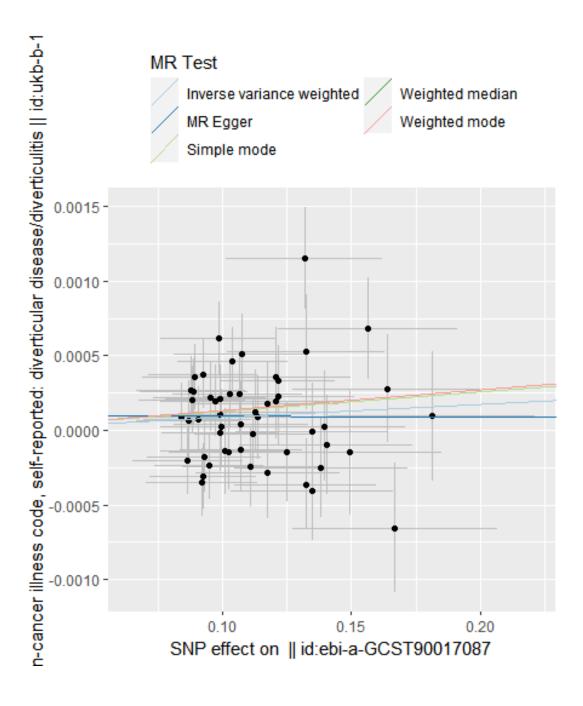
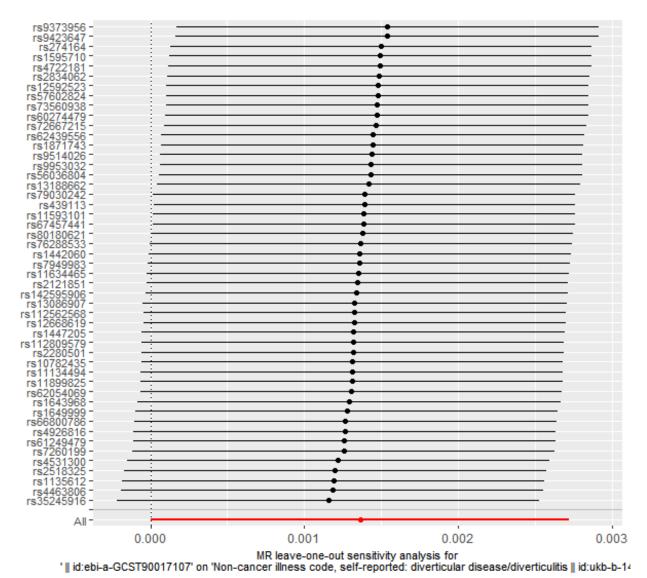


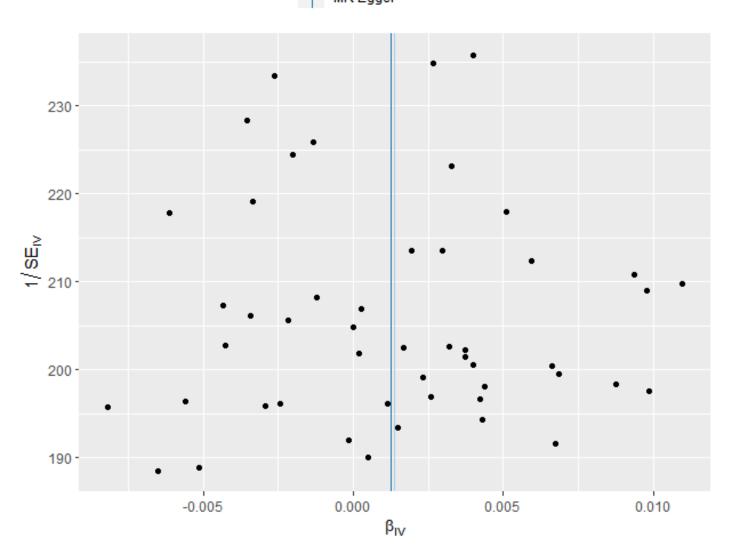
Figure 111 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Selenomonadales id.2165) on diverticular disease

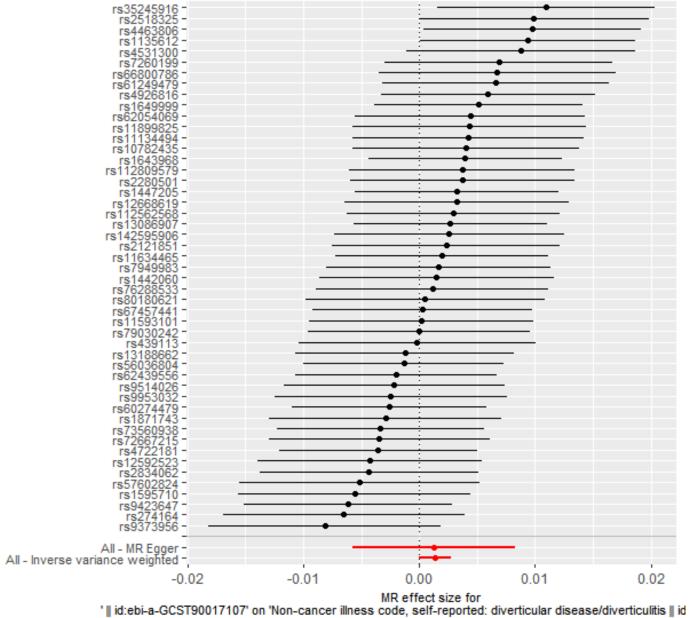


MR Method

Inverse variance weighted

MR Egger





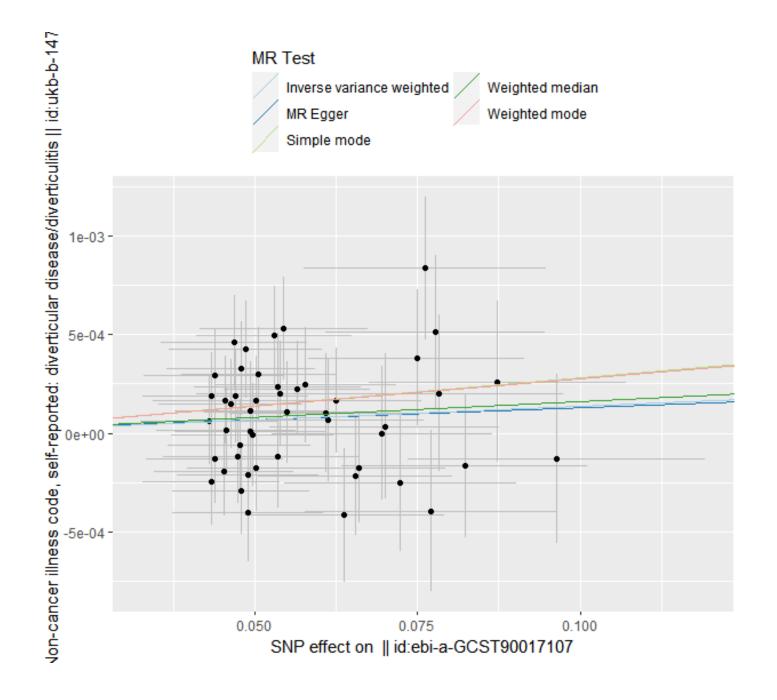
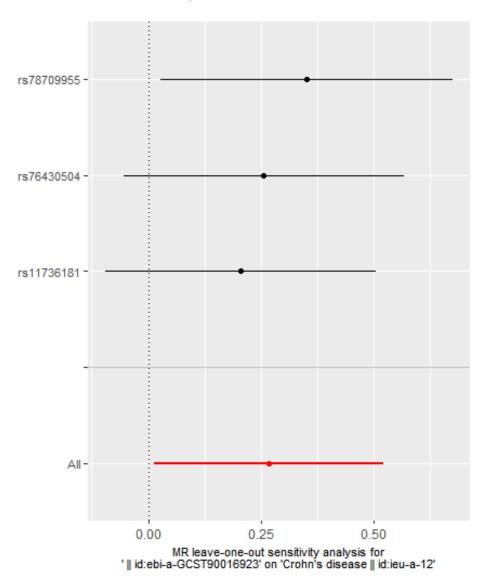


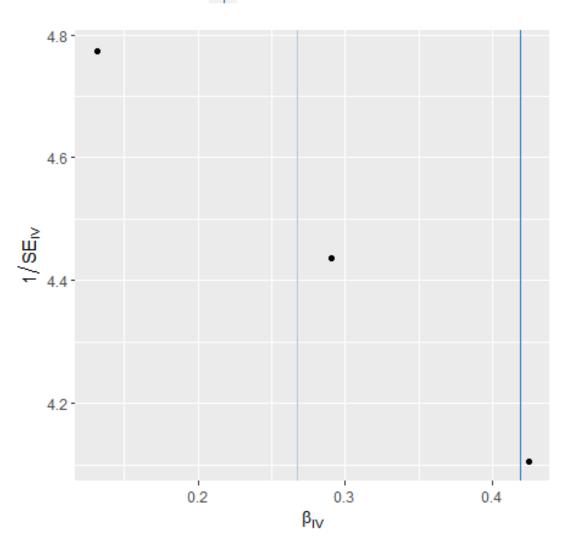
Figure 112 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Verrucomicrobiae id.4029) on crohn's disease

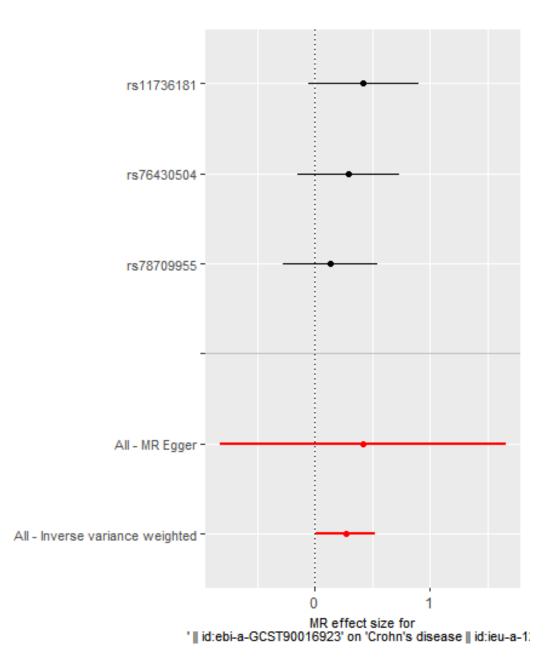


MR Method

Inverse variance weighted

MR Egger





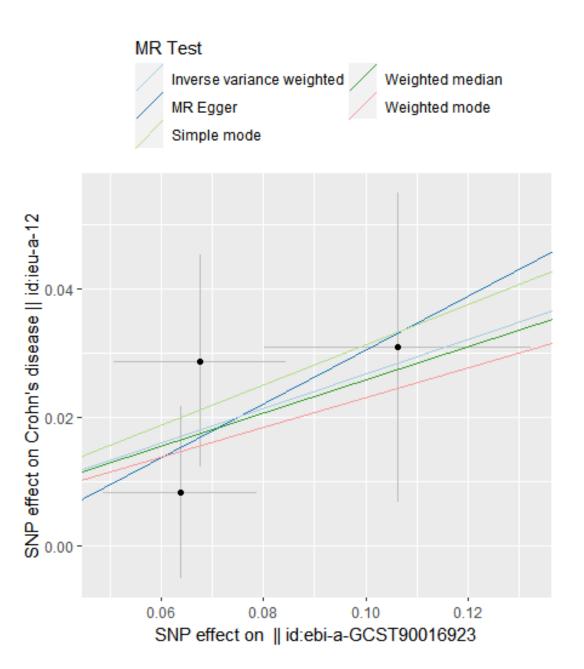
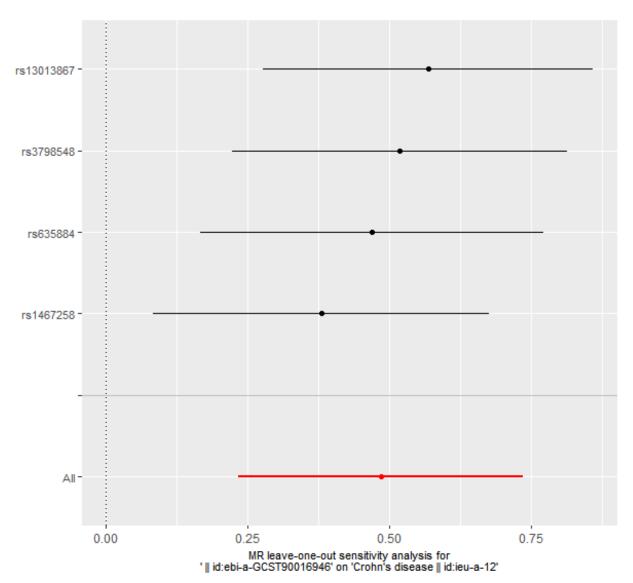


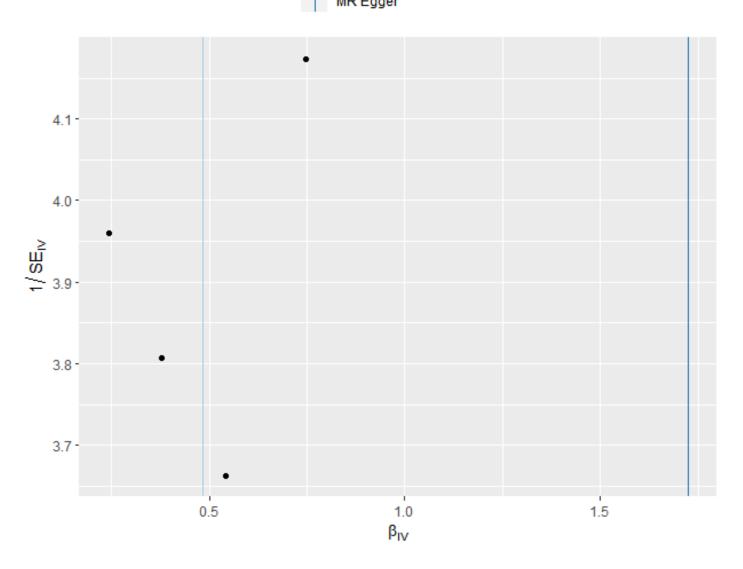
Figure 113 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Peptostreptococcaceae id.2042) on crohn's disease

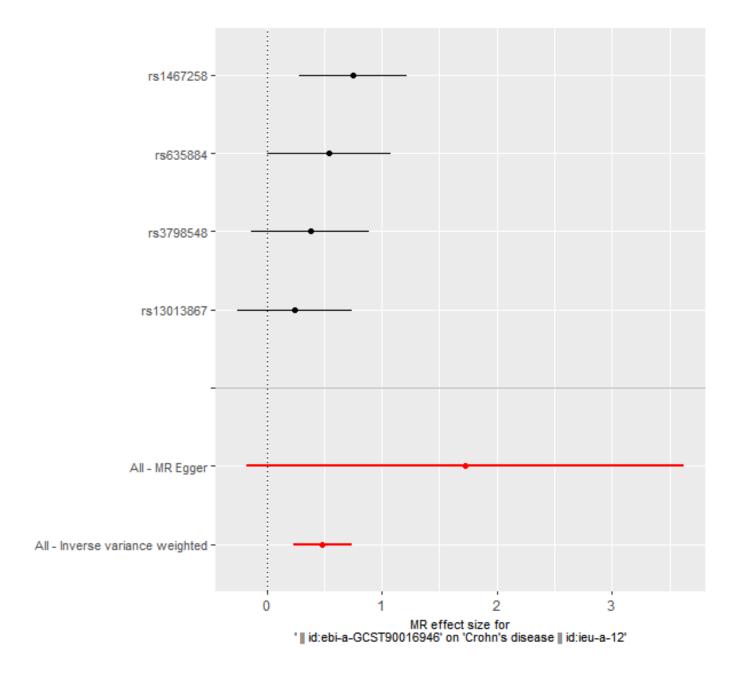


MR Method

Inverse variance weighted

MR Egger





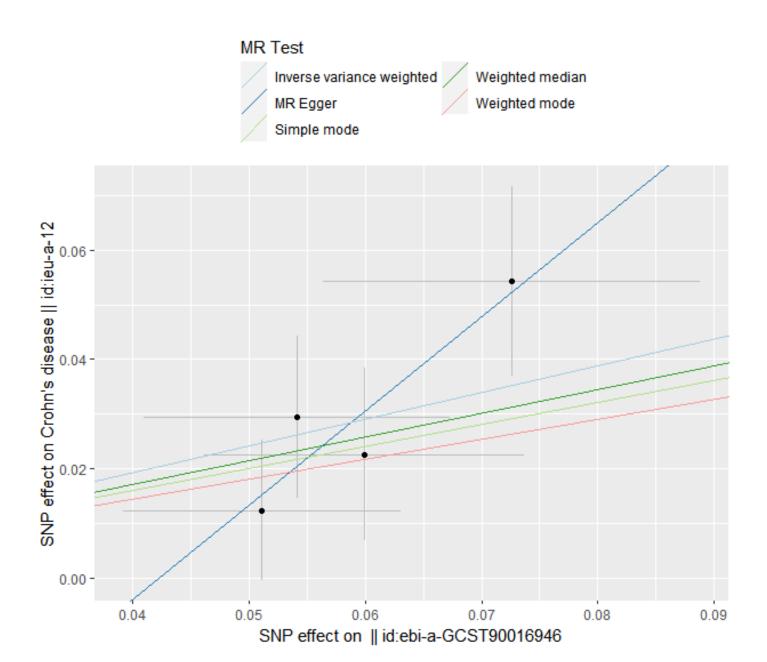
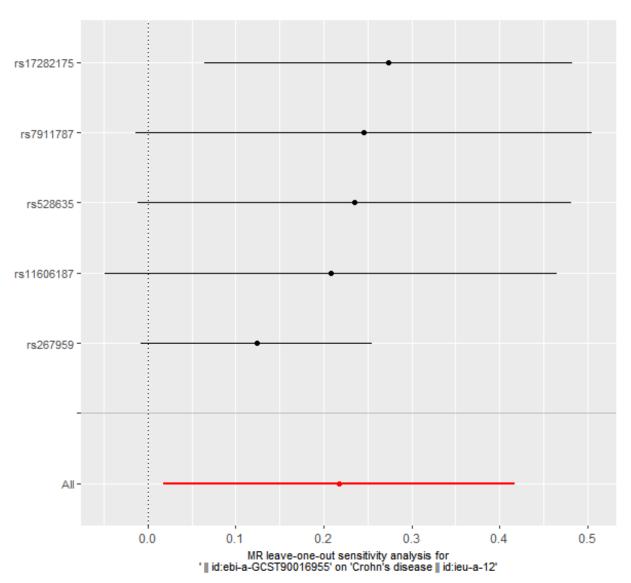
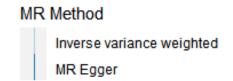
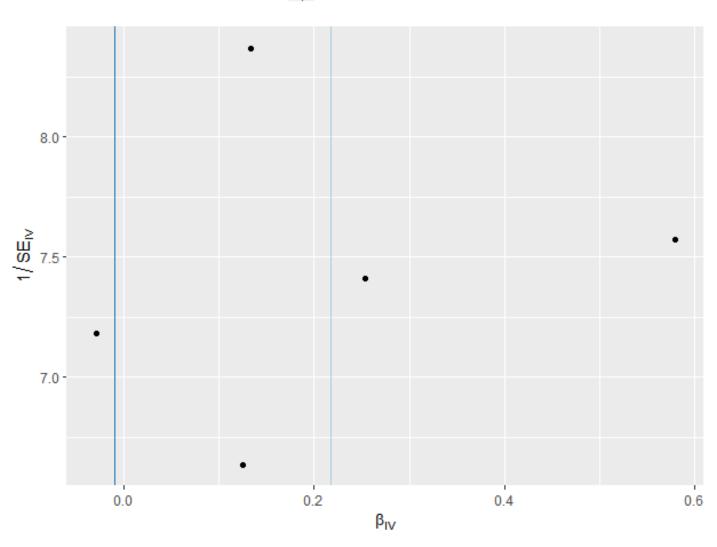
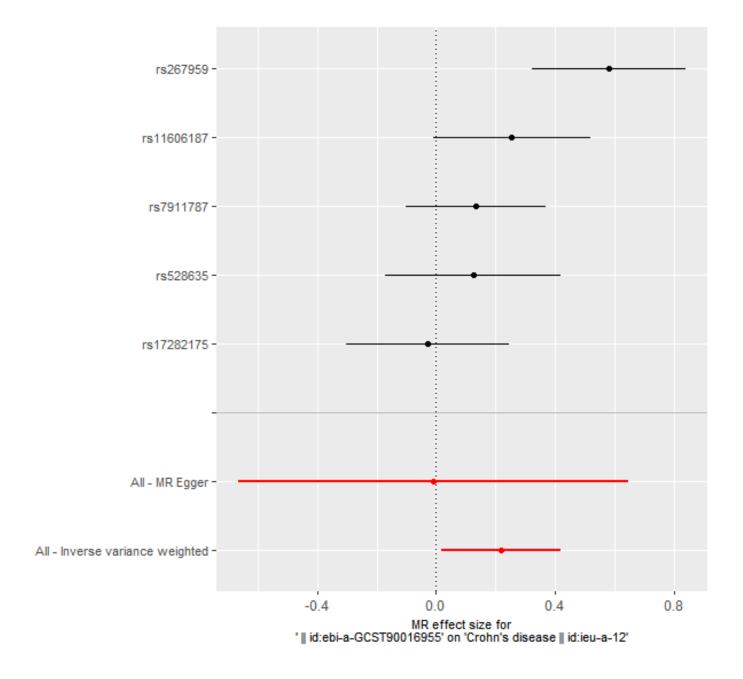


Figure 114 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown family id.1000006161) on crohn's disease









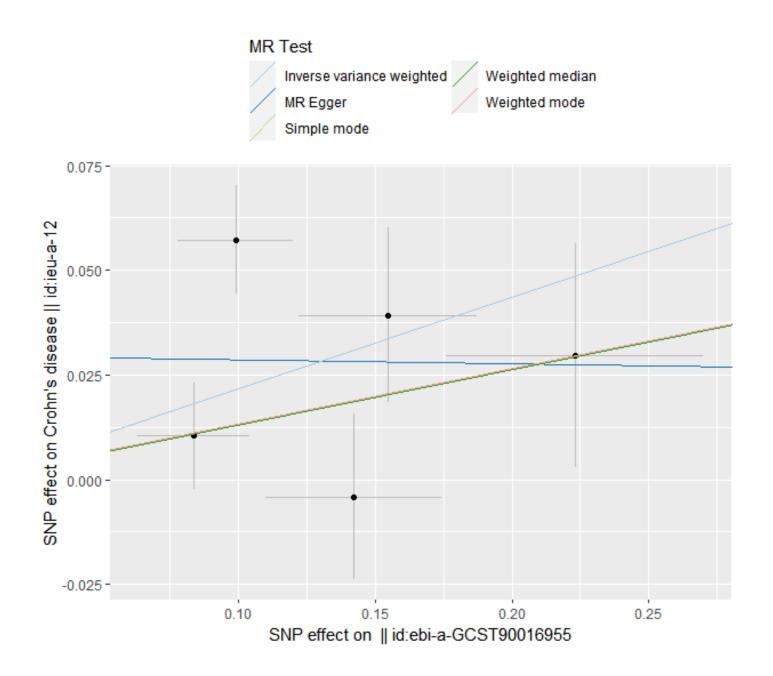
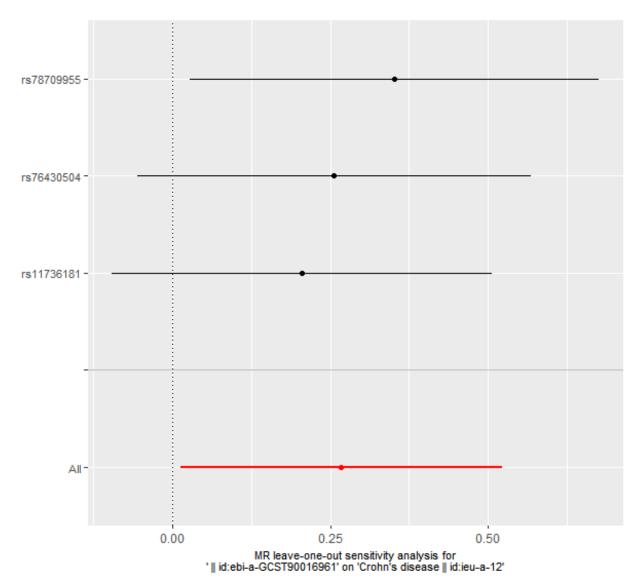
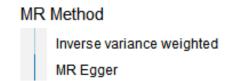
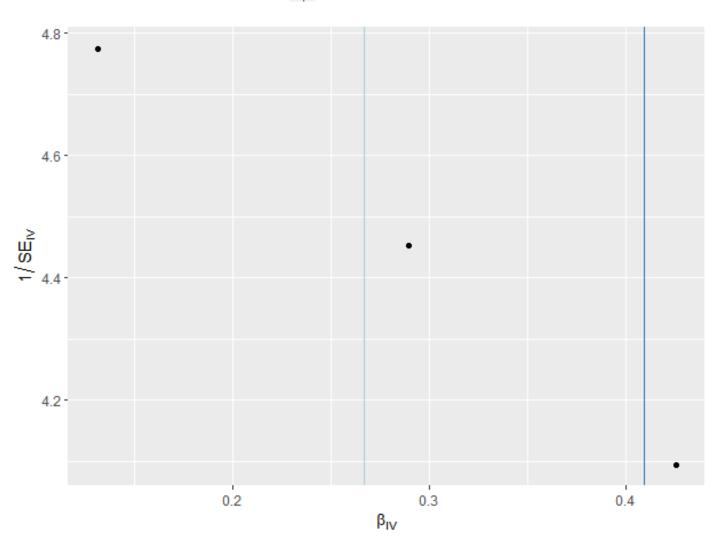
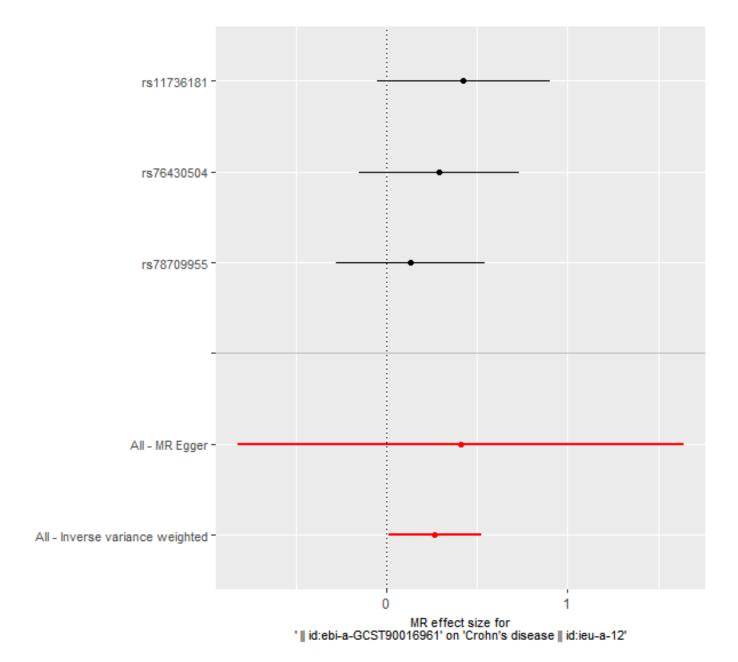


Figure 115 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Akkermansia id.4037) on crohn's disease









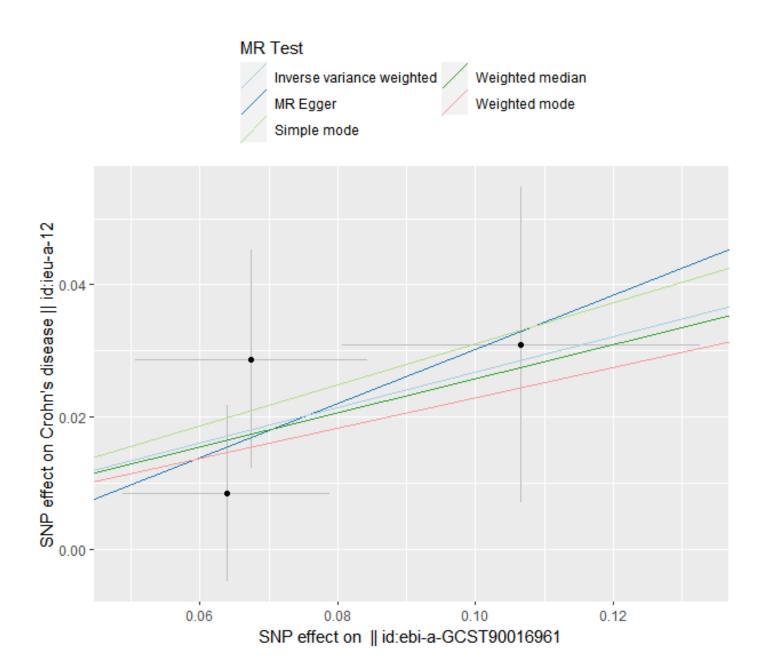
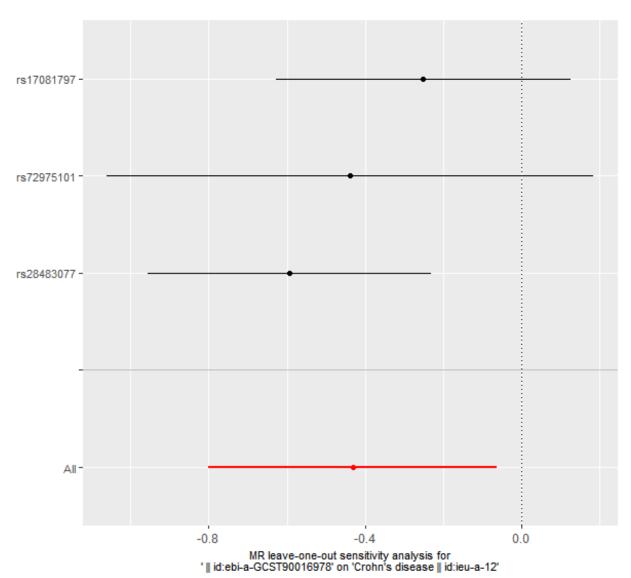


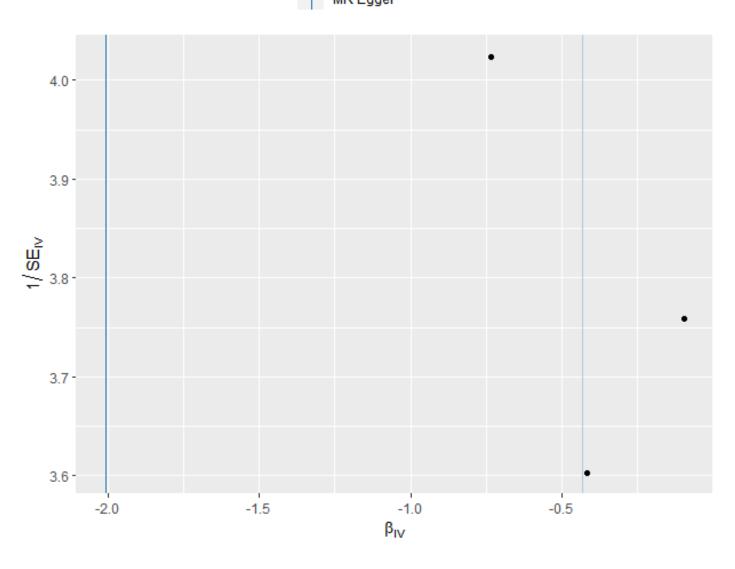
Figure 116 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Christensenellaceae R 7group id.11283) on crohn's disease

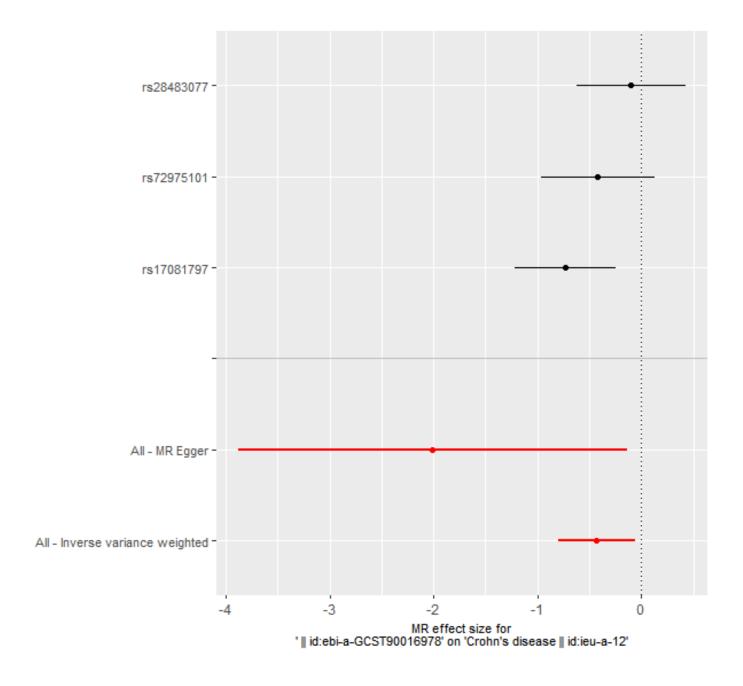


MR Method

Inverse variance weighted

MR Egger





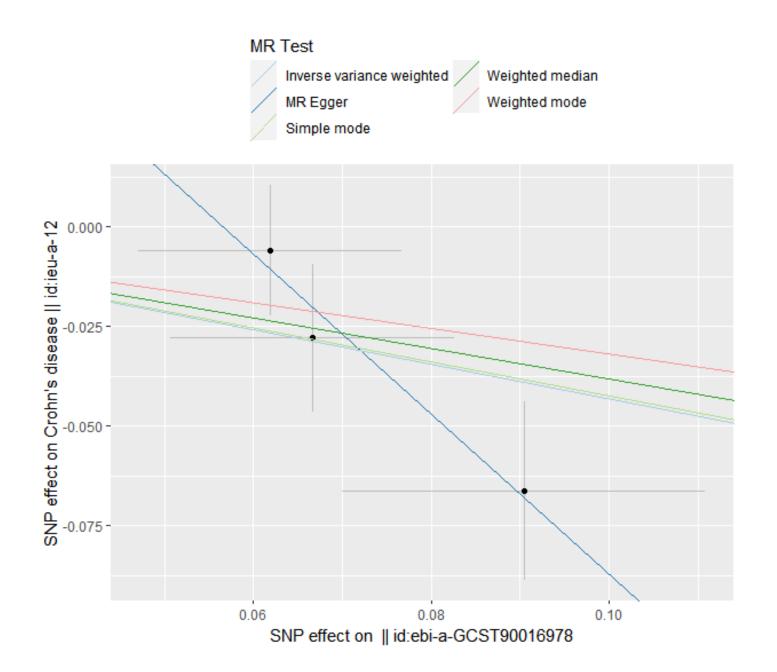
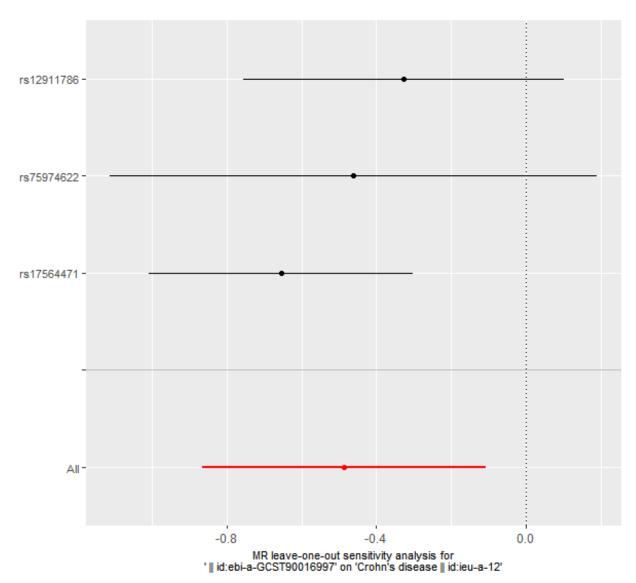
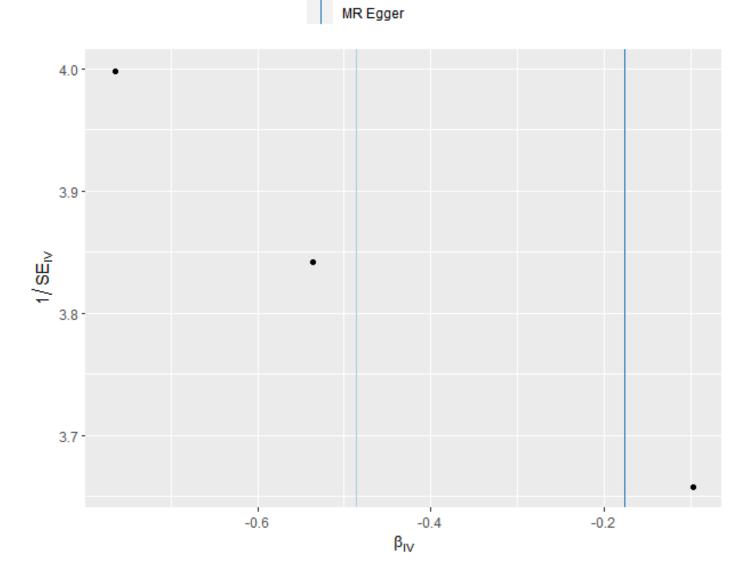


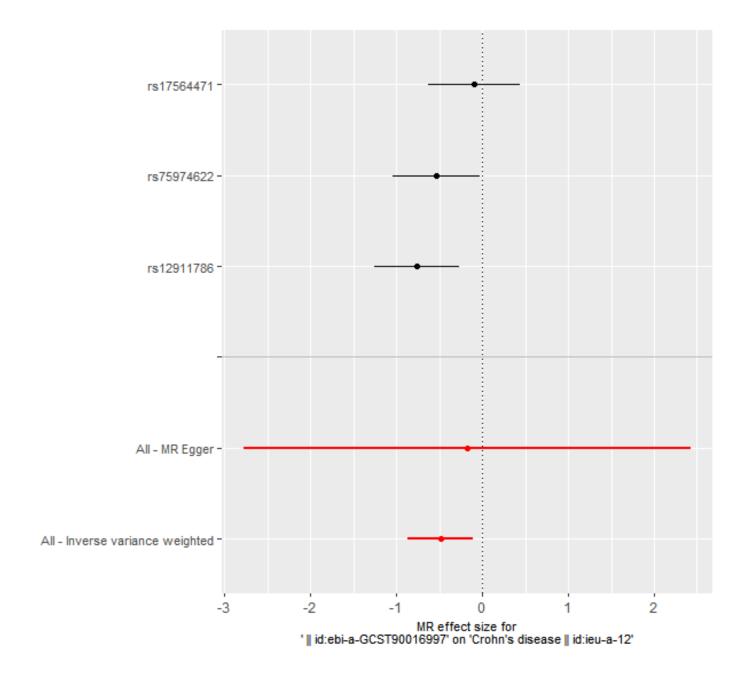
Figure 117 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium coprostanoligenes group id.11375) on crohn's disease



MR Method

Inverse variance weighted





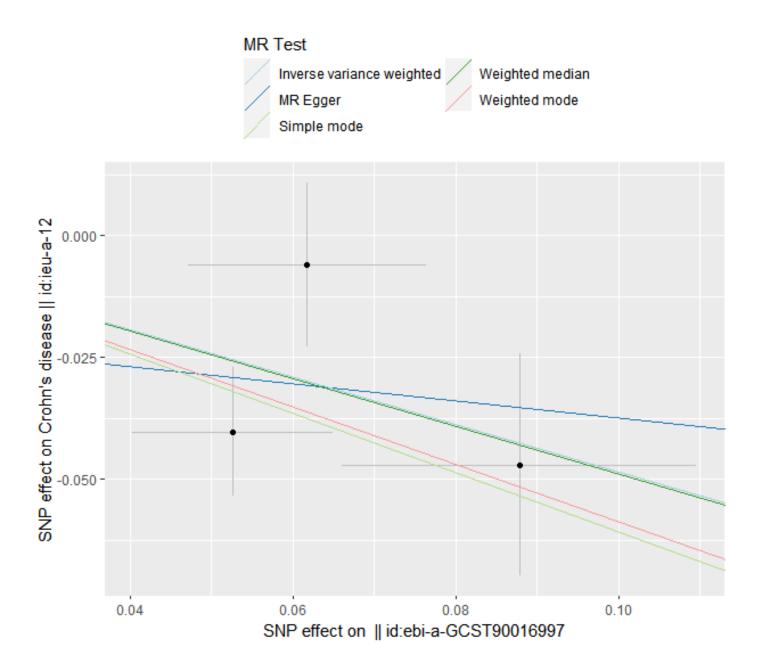
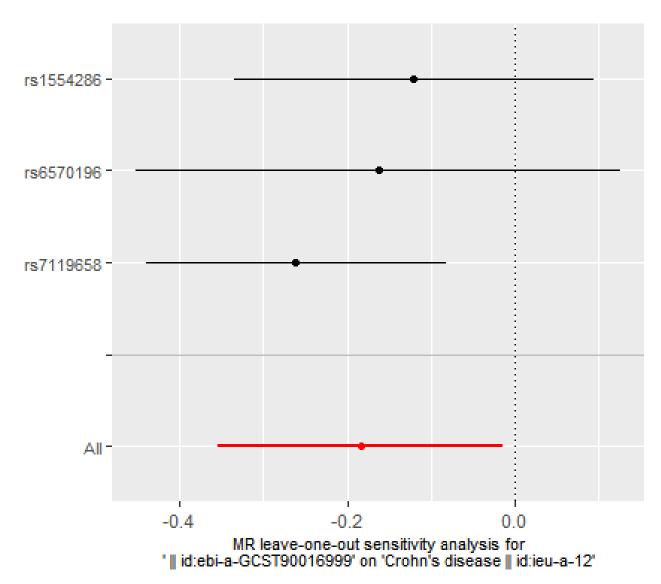
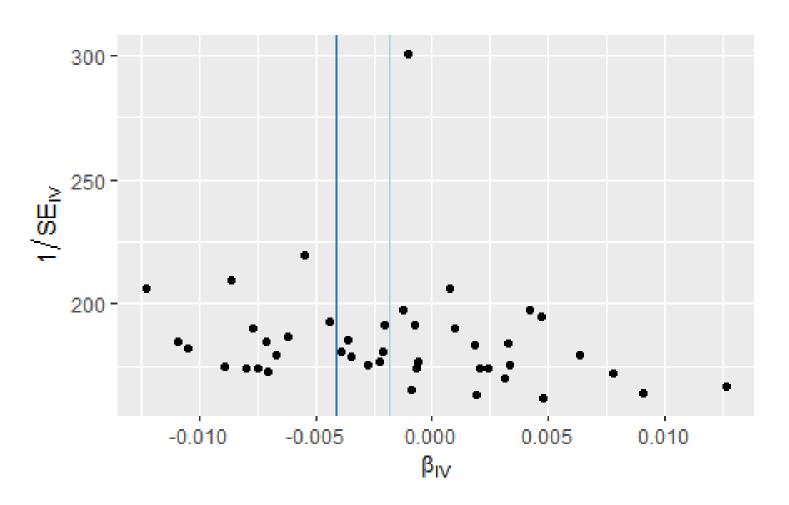


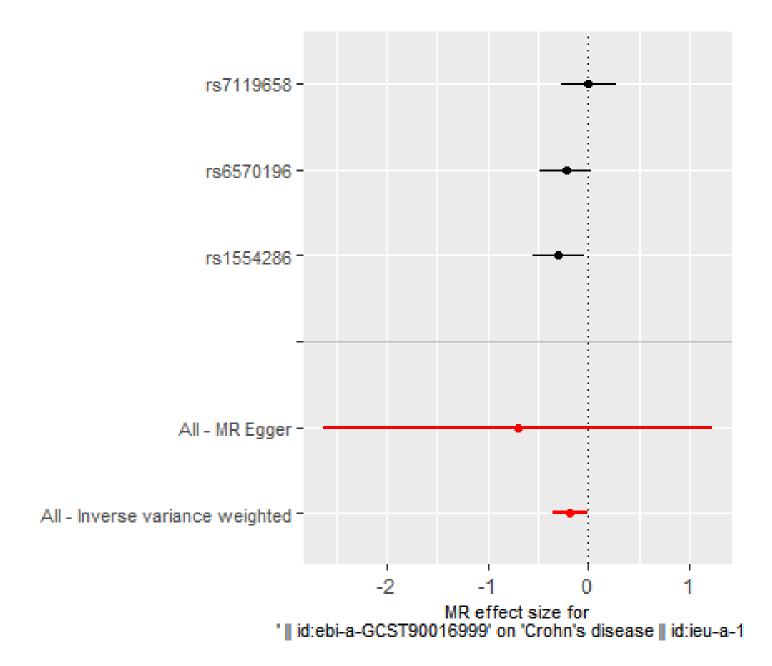
Figure 118 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium fissicatena group id.14373) on crohn's disease



MR Method

Inverse variance weighted MR Egger





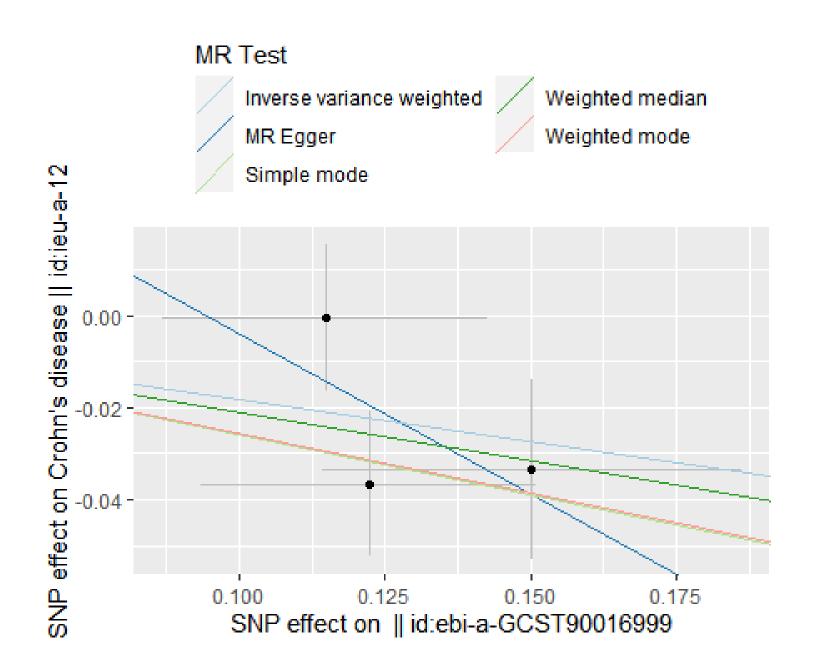
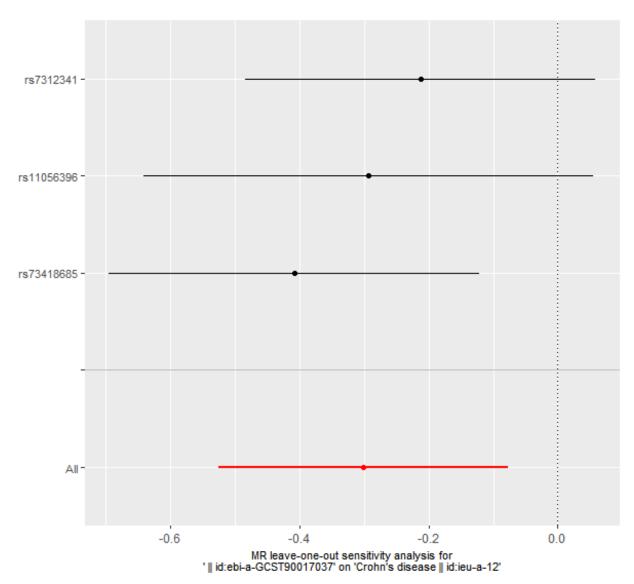


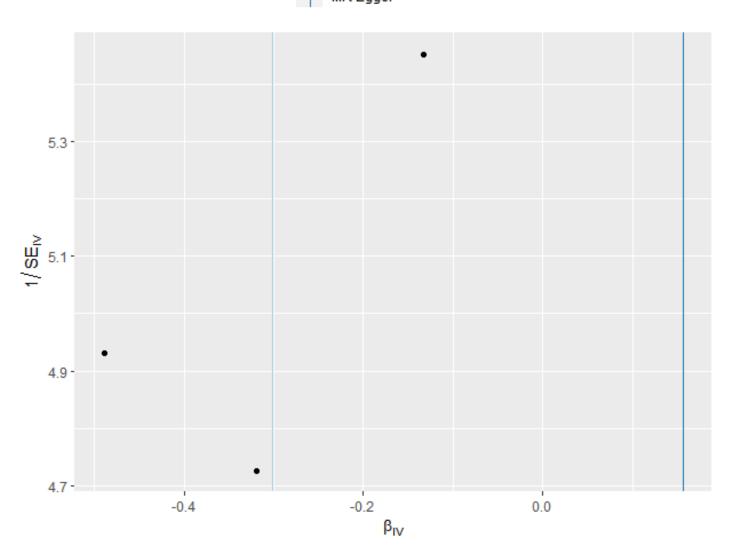
Figure 119 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Oscillospira id.2064) on crohn's disease

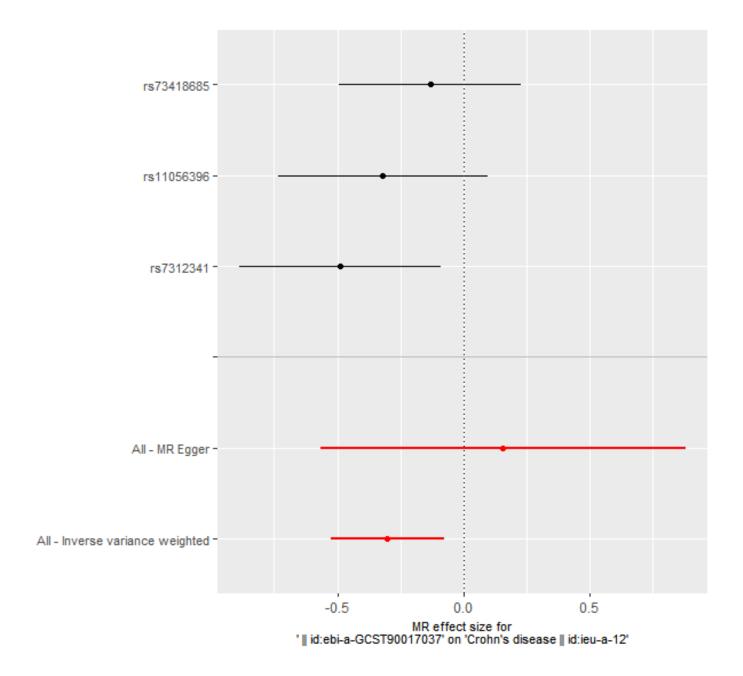


MR Method

Inverse variance weighted

MR Egger





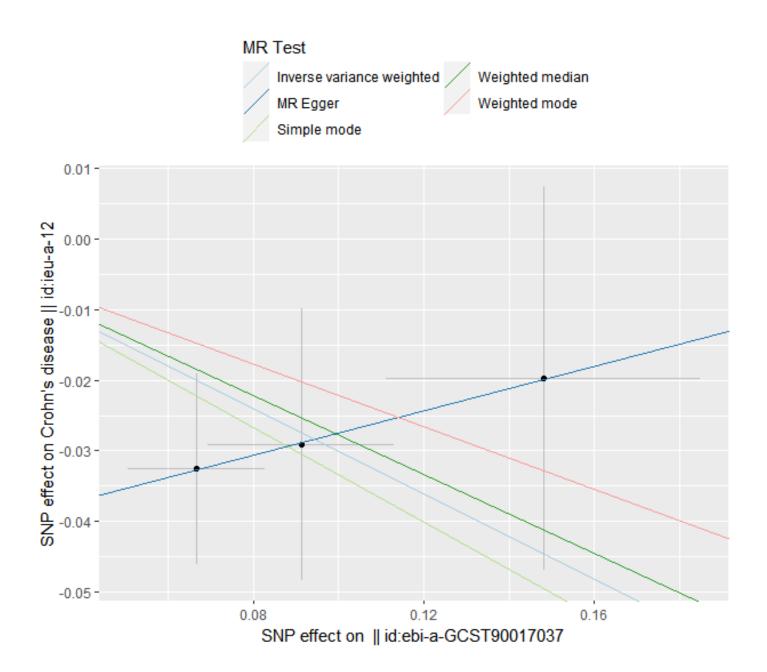
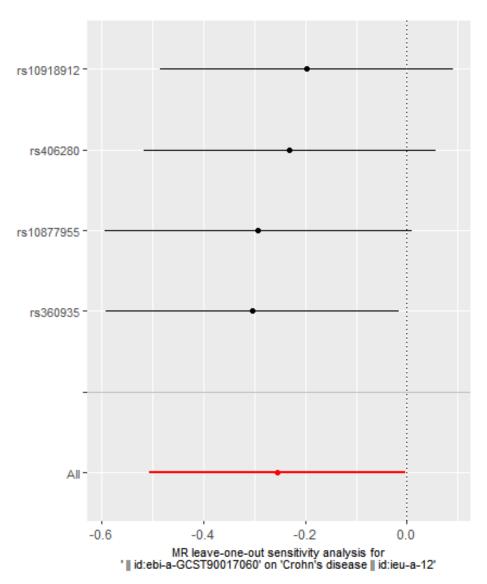
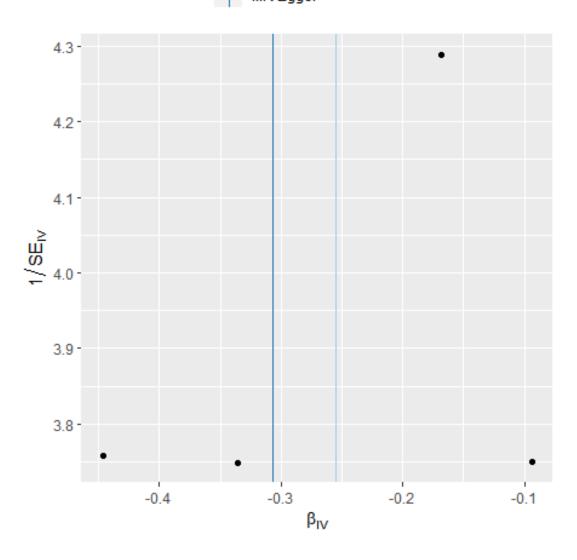


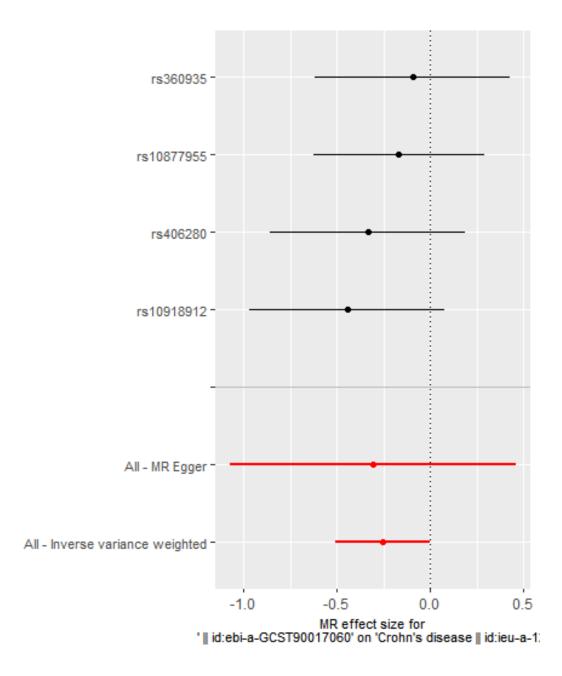
Figure 120 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG013 id.11370) on crohn's disease



MR Method

Inverse variance weighted MR Egger





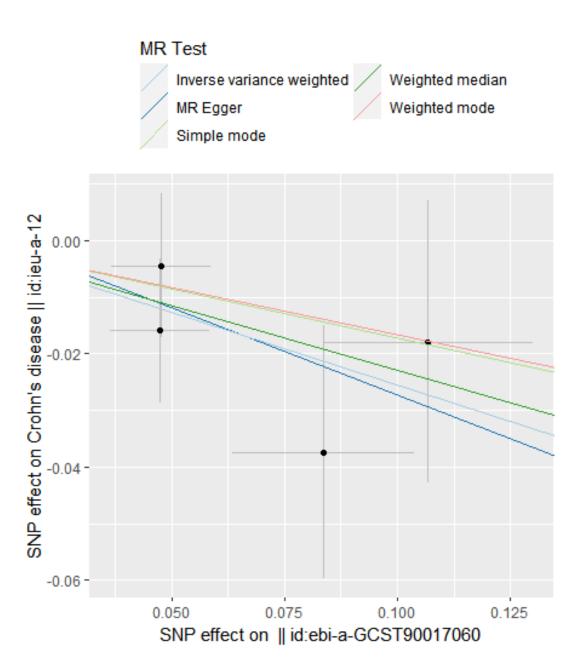
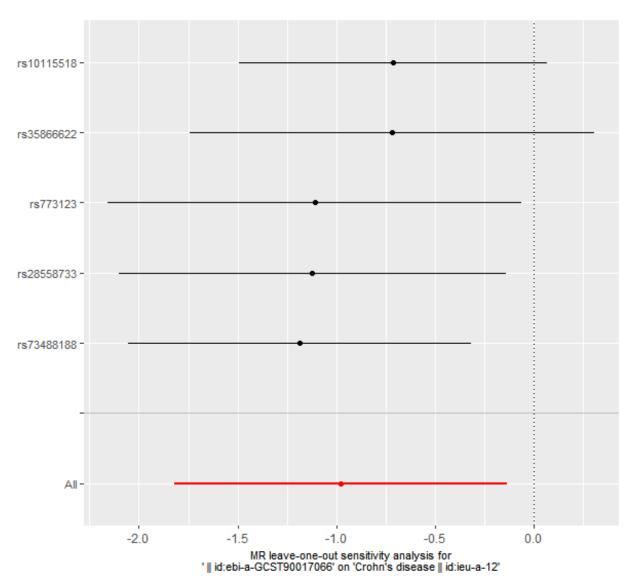


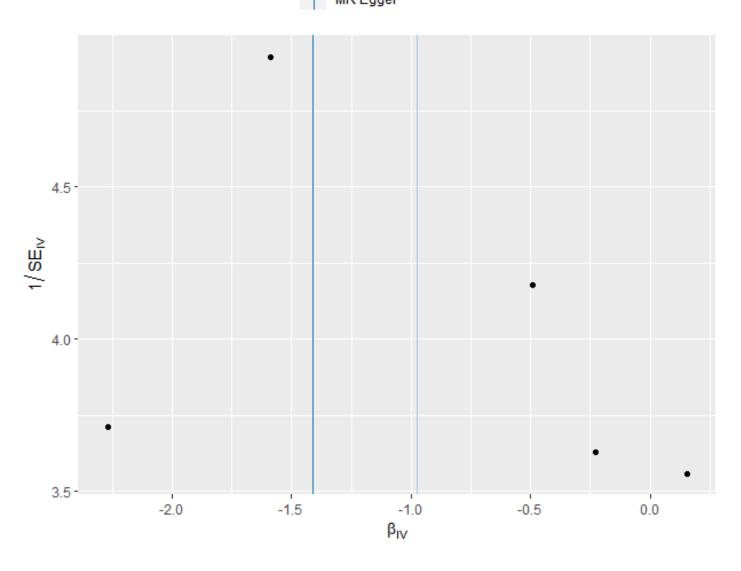
Figure 121 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcus torques group id.14377) on crohn's disease

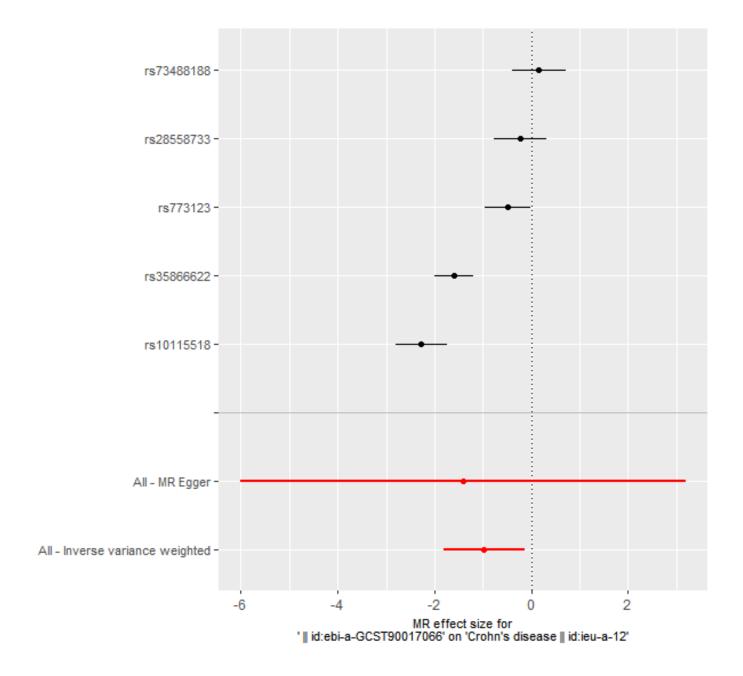


MR Method

Inverse variance weighted

MR Egger





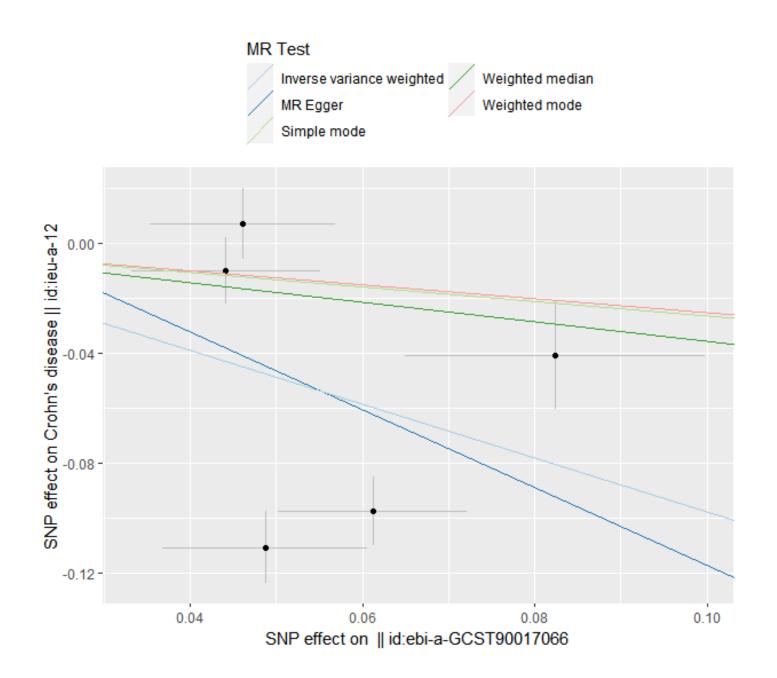
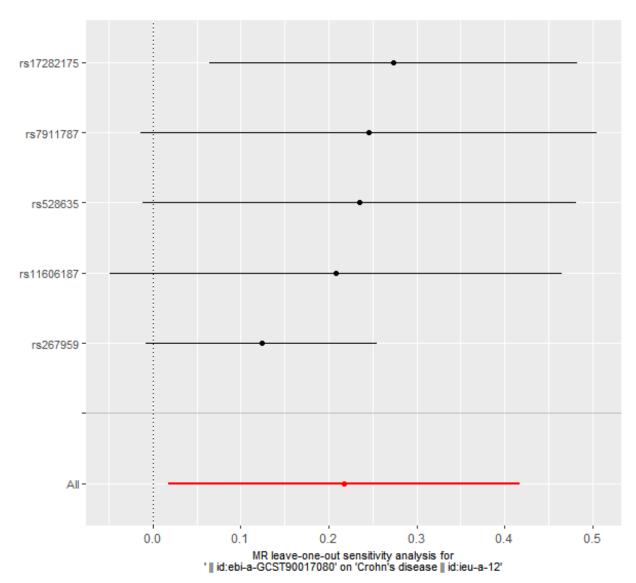
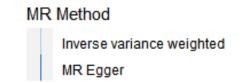
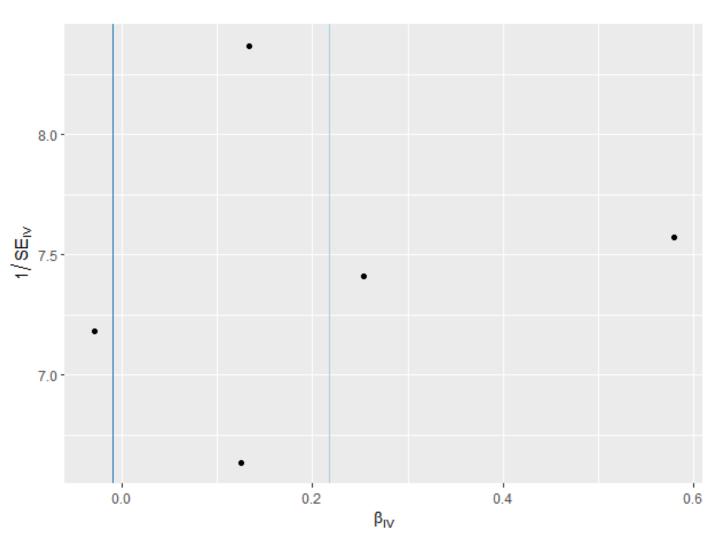
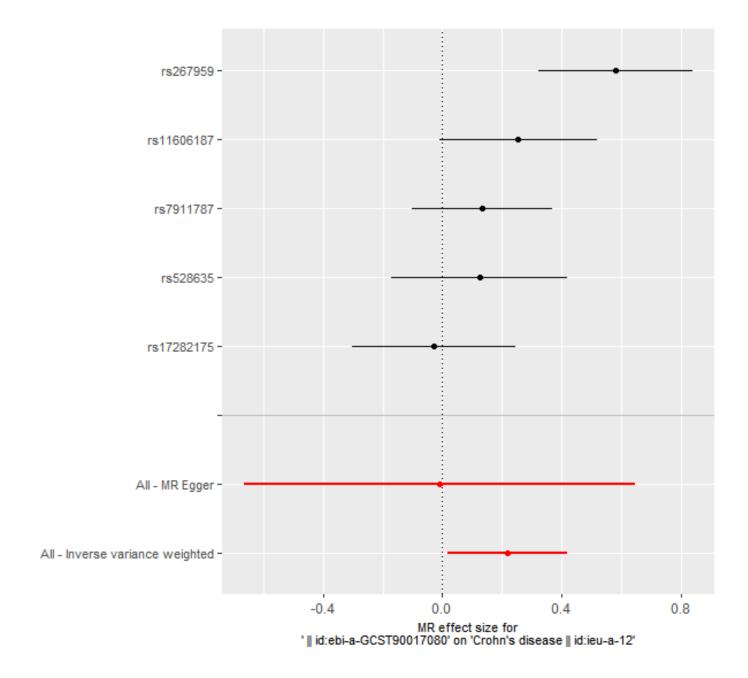


Figure 122 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.1000006162) on crohn's disease









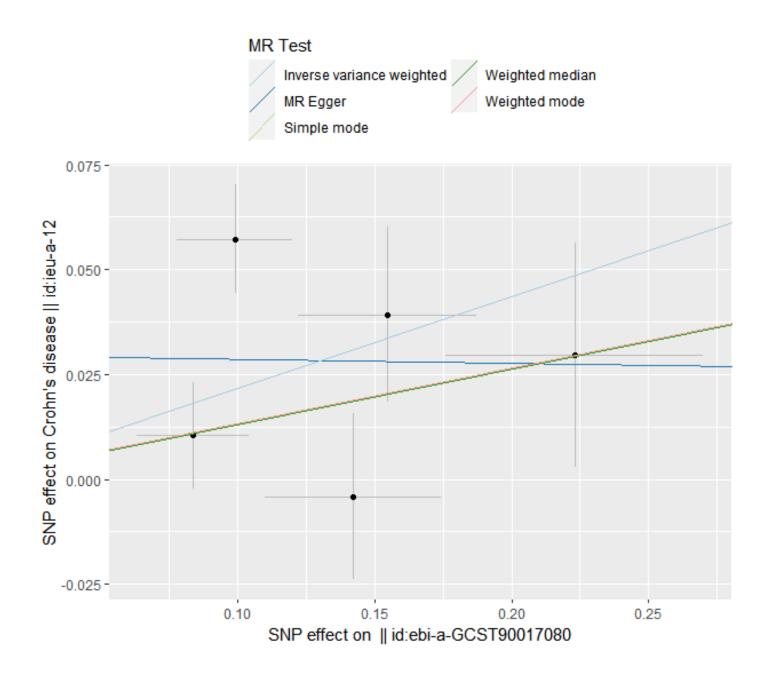
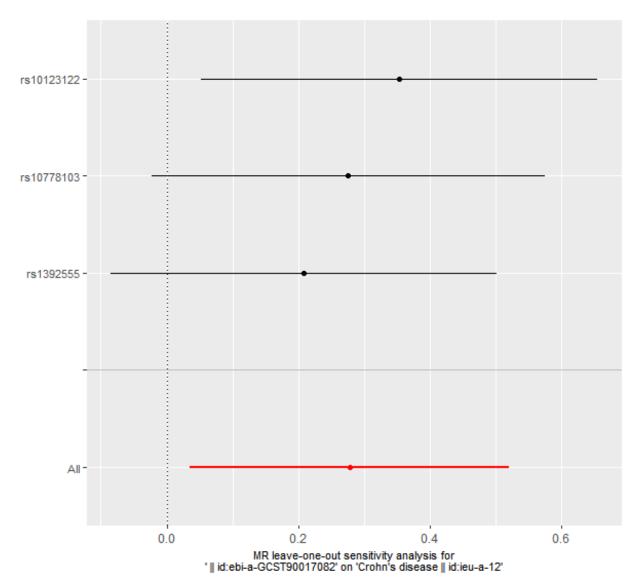


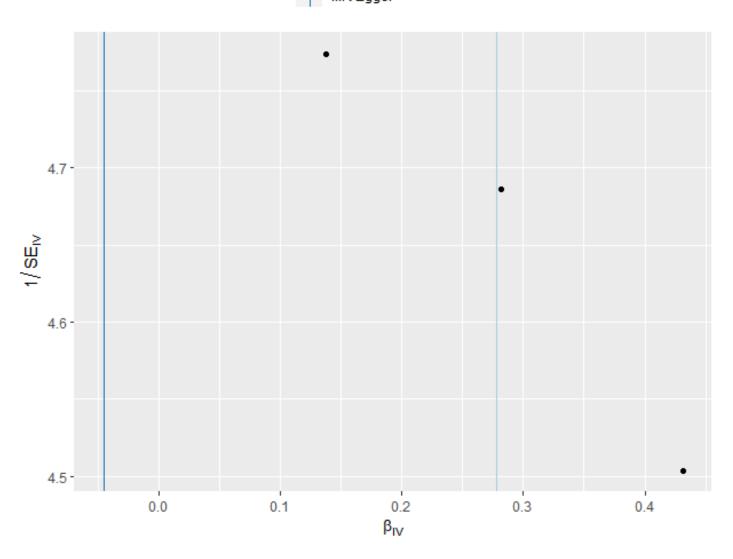
Figure 123 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.2001) on crohn's disease

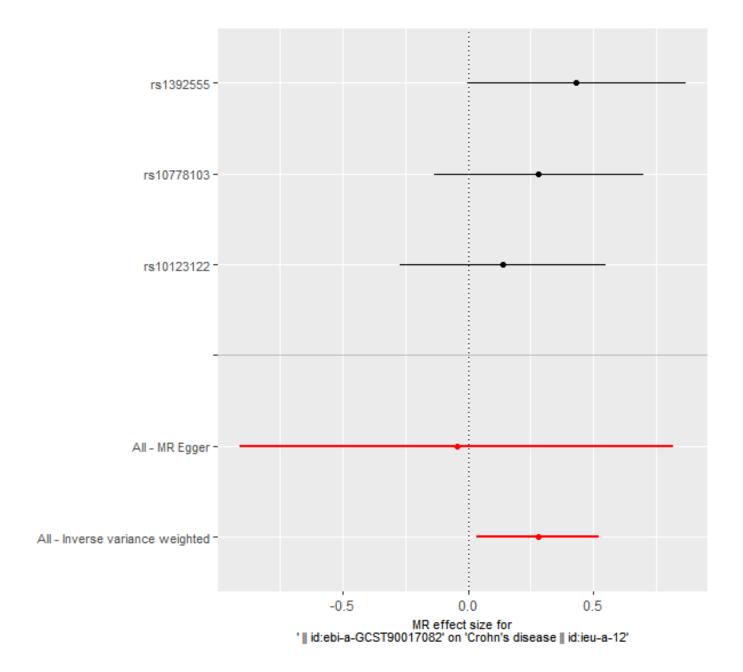


MR Method

Inverse variance weighted

MR Egger





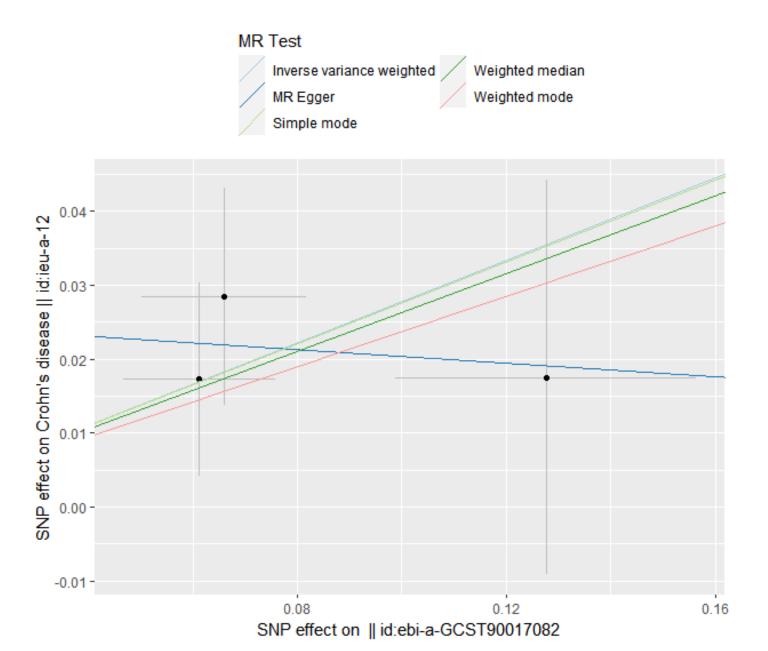
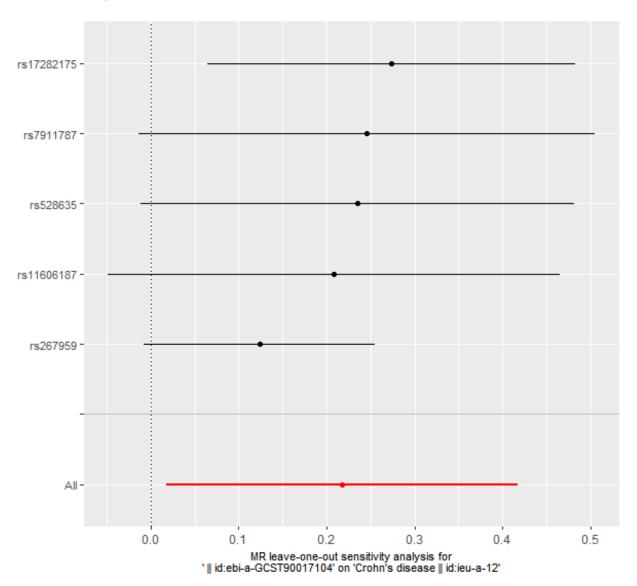
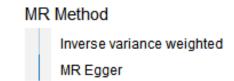
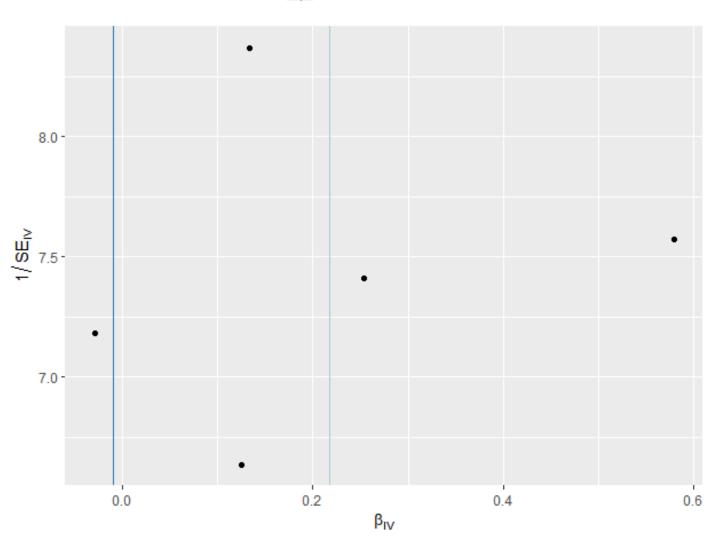
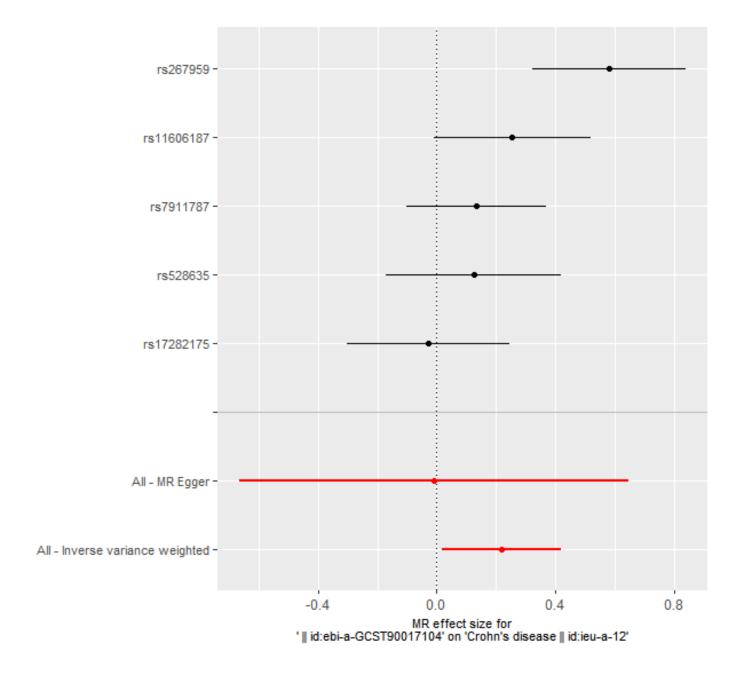


Figure 124 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order NB1n id.3953) on crohn's disease









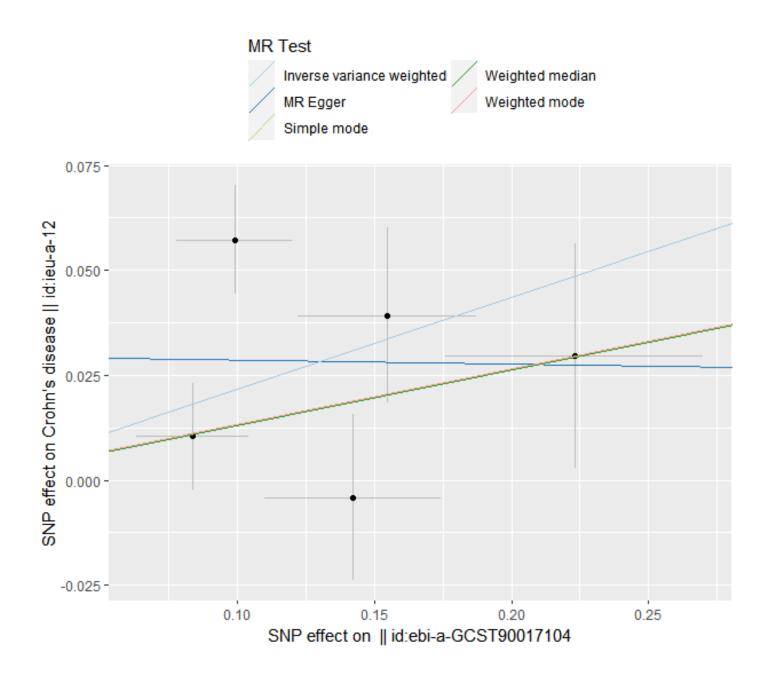
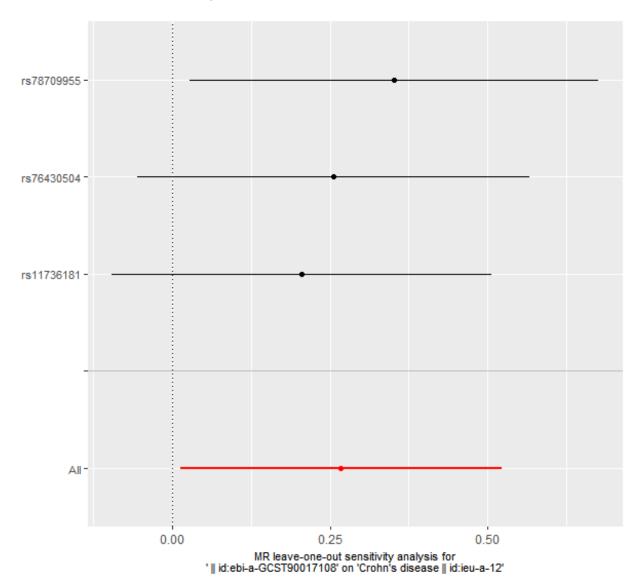
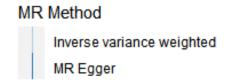
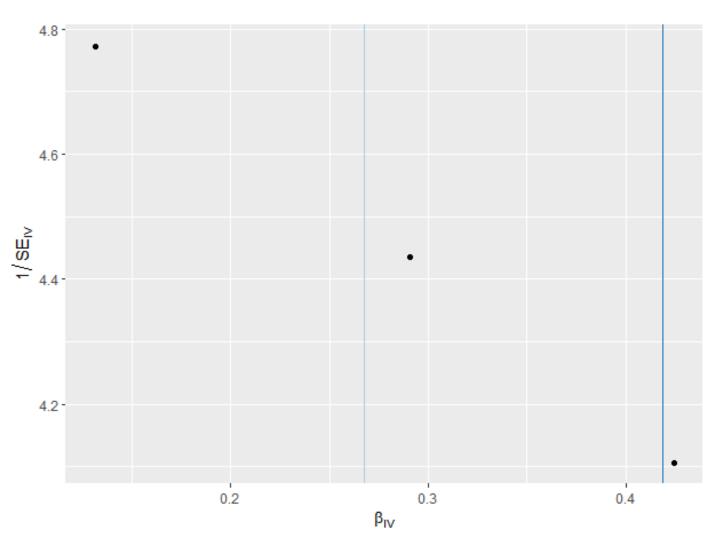
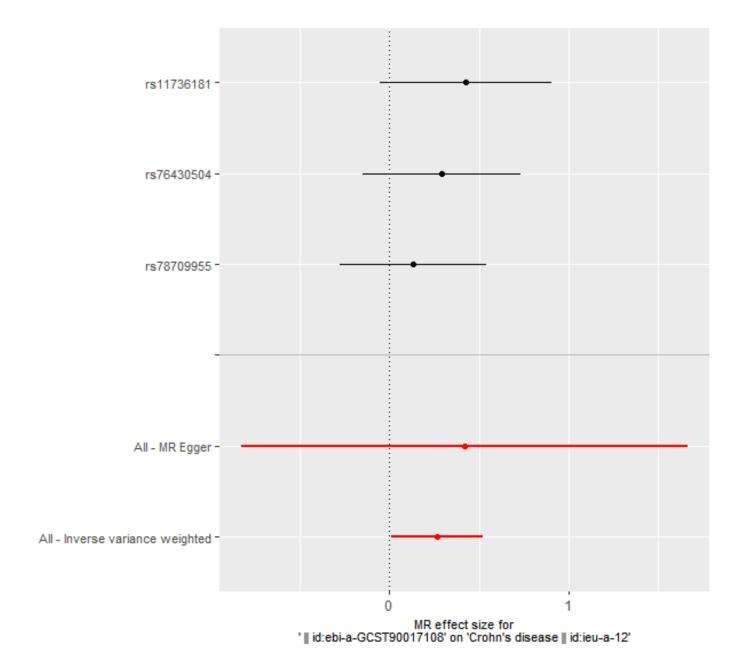


Figure 125 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Verrucomicrobiales id.4030) on crohn's disease









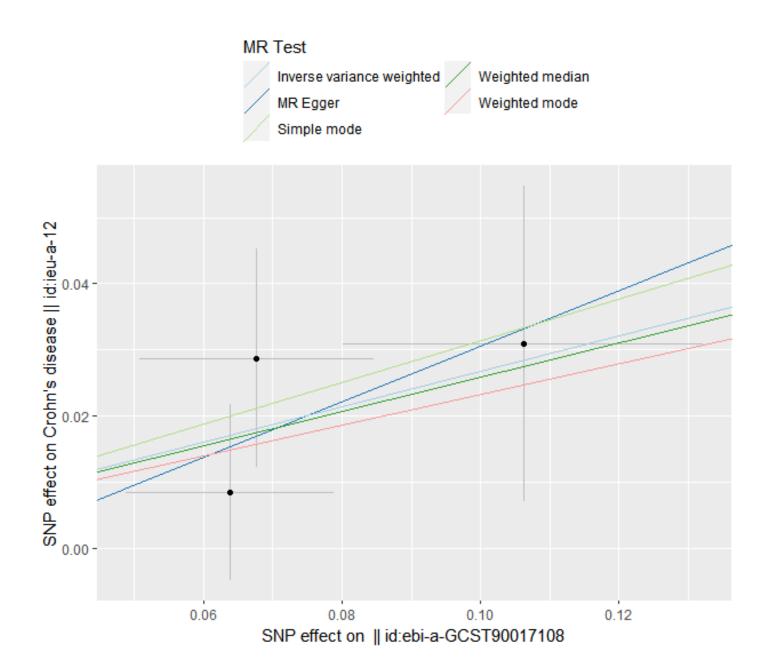
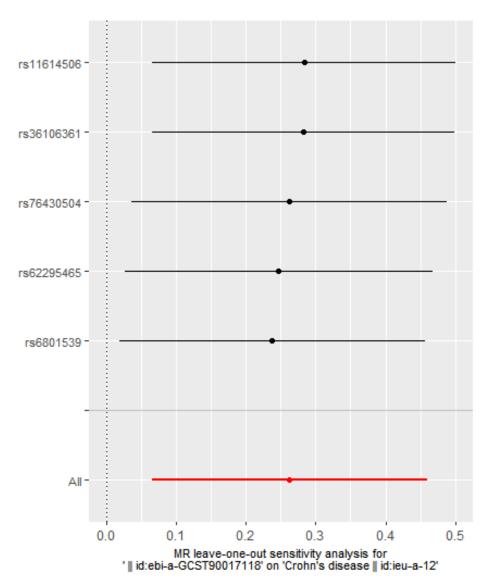


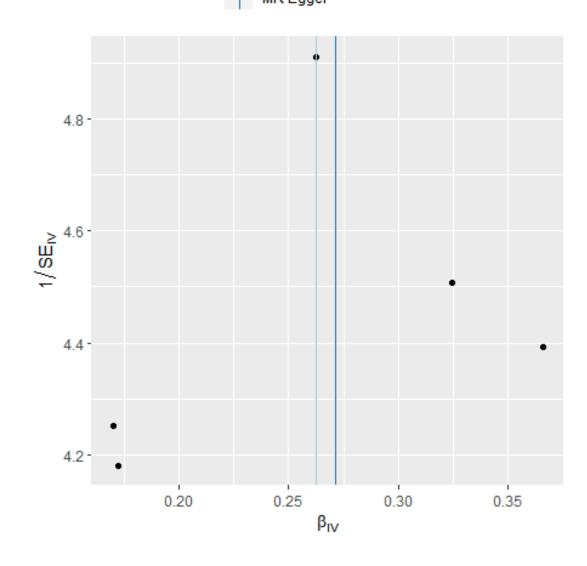
Figure 126 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Verrucomicrobia id.3982) on crohn's disease

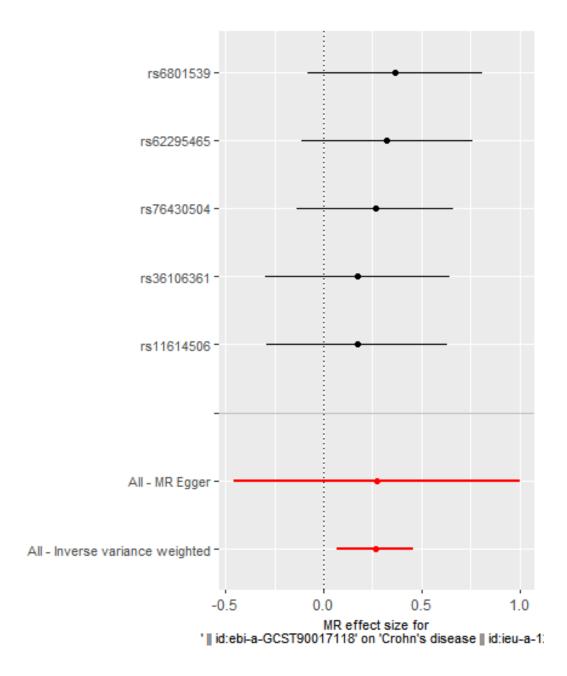


MR Method

Inverse variance weighted

MR Egger





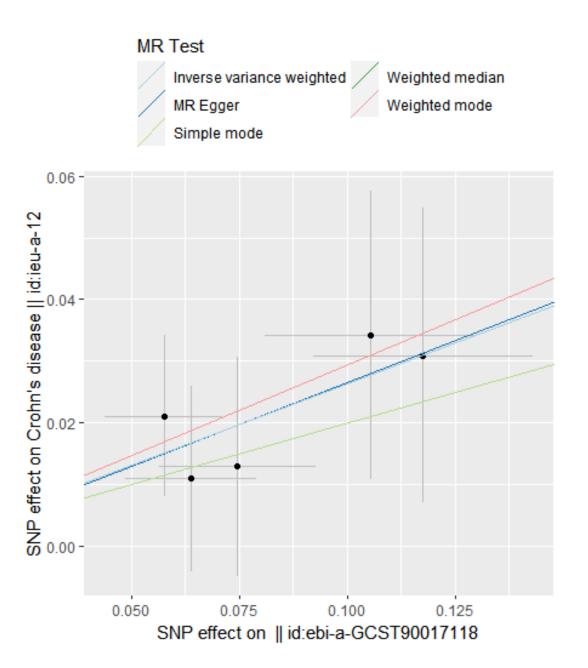
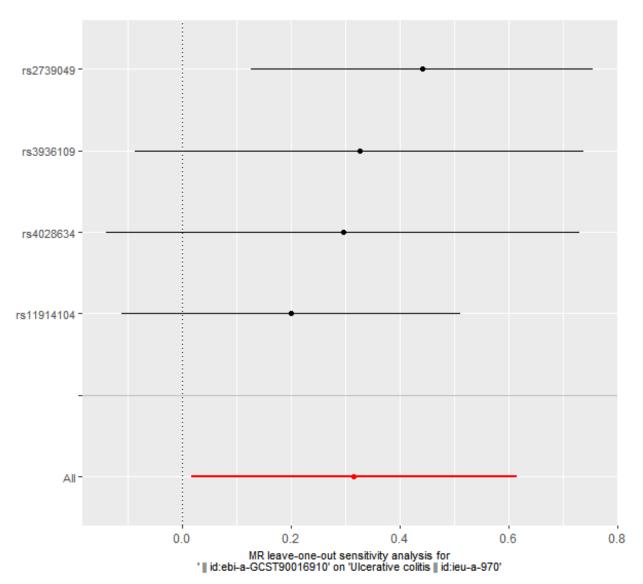


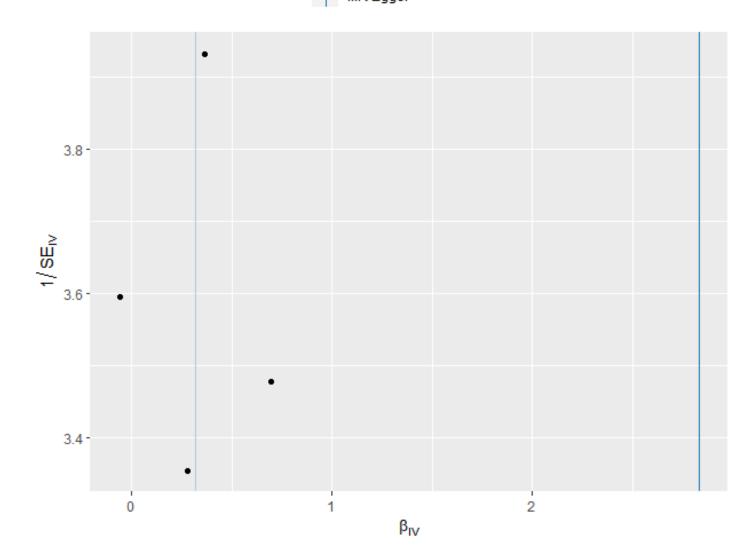
Figure 127 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Bacilli id.1673) on ulcerative colitis

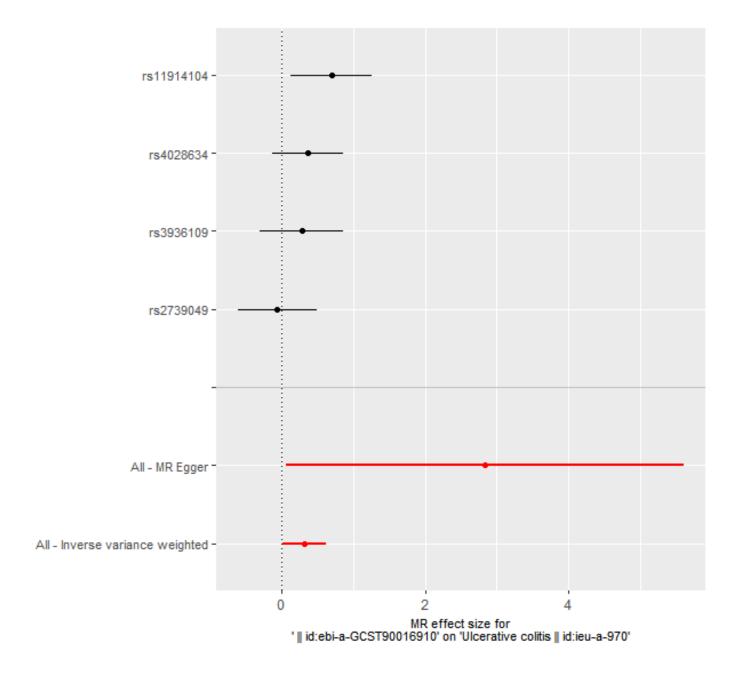


MR Method

Inverse variance weighted

MR Egger







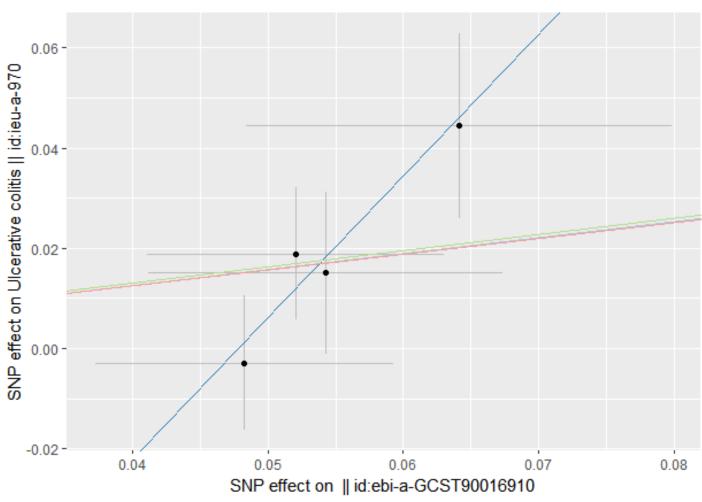
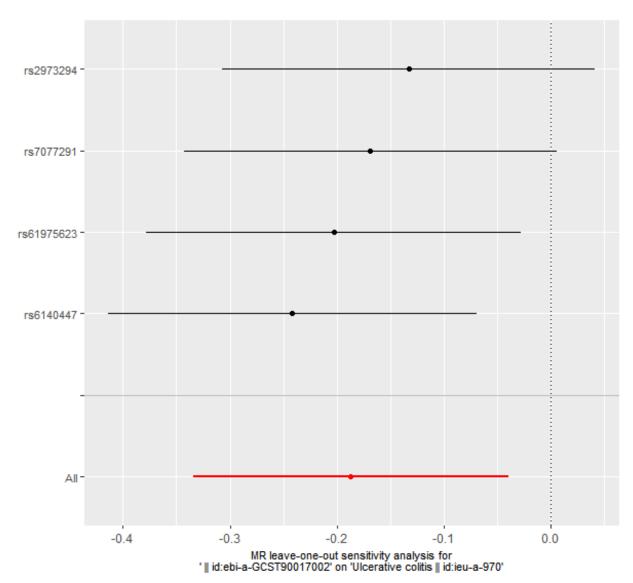


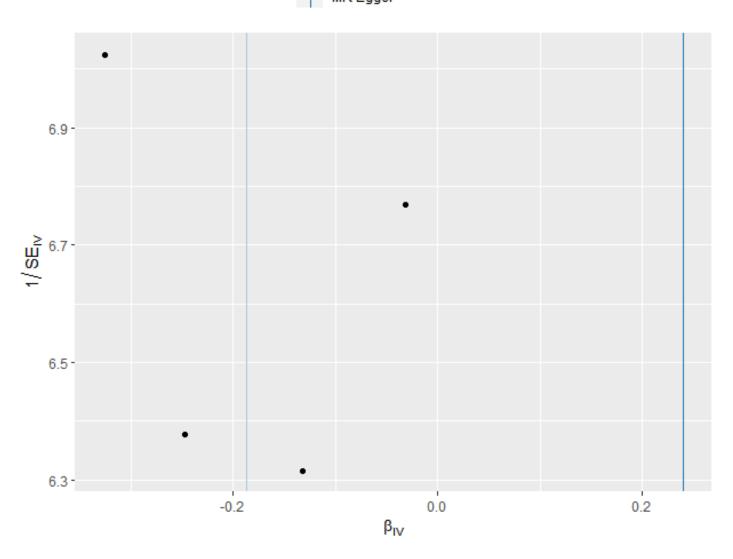
Figure 128 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium oxidoreducens group id.11339) on ulcerative colitis

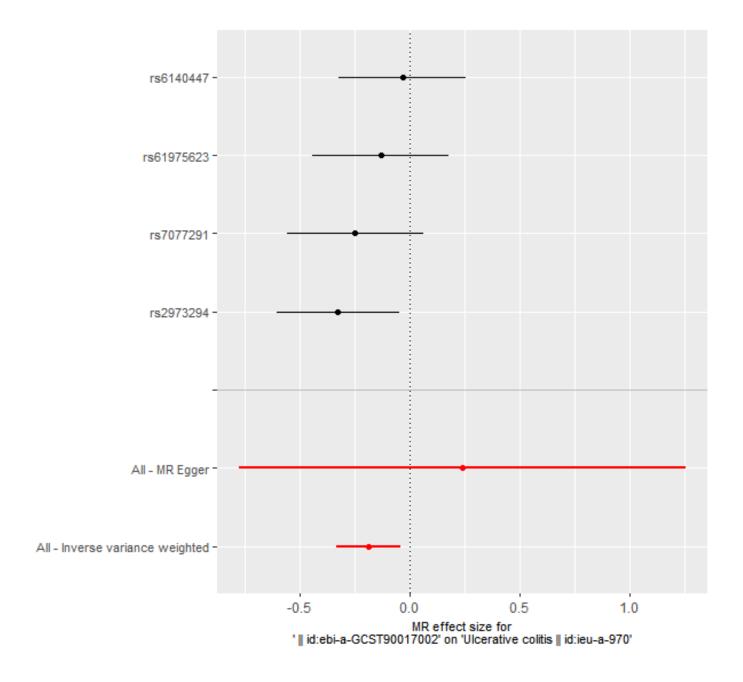


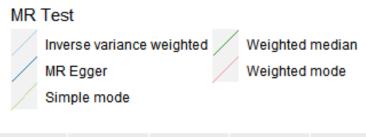
MR Method

Inverse variance weighted

MR Egger







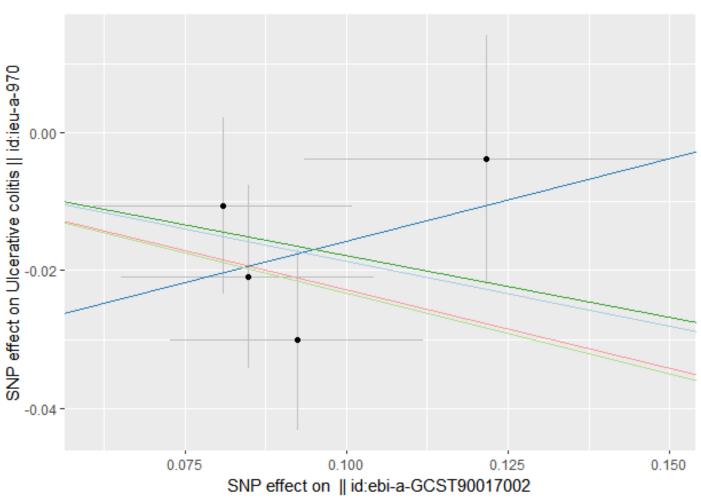
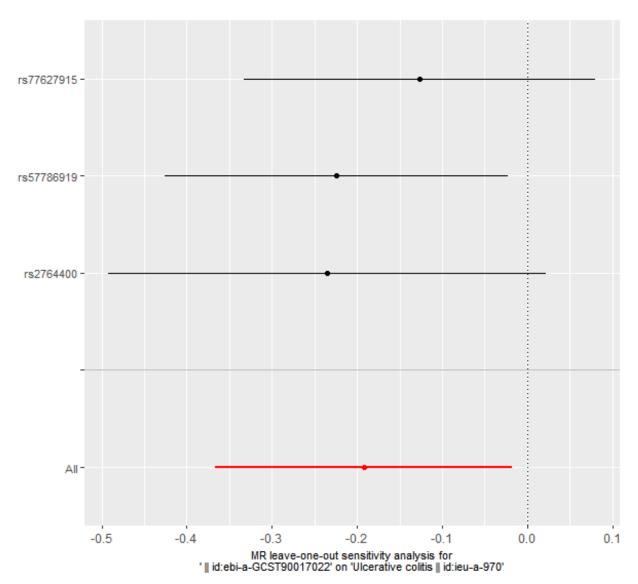
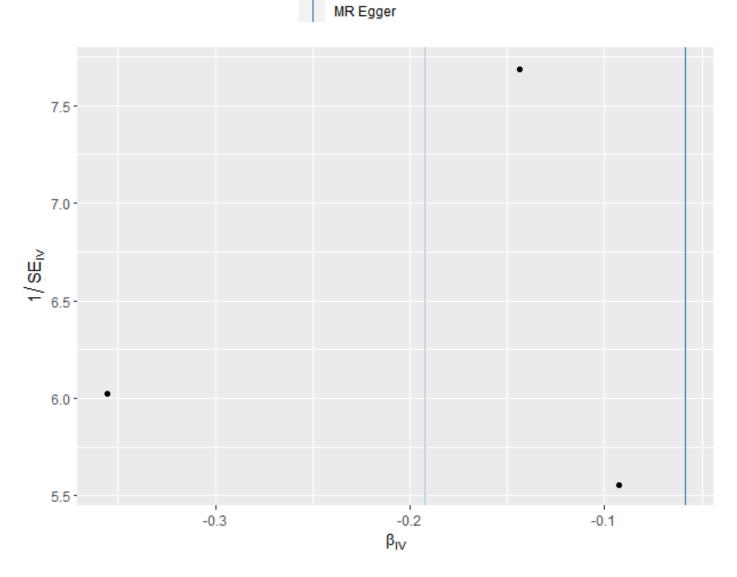


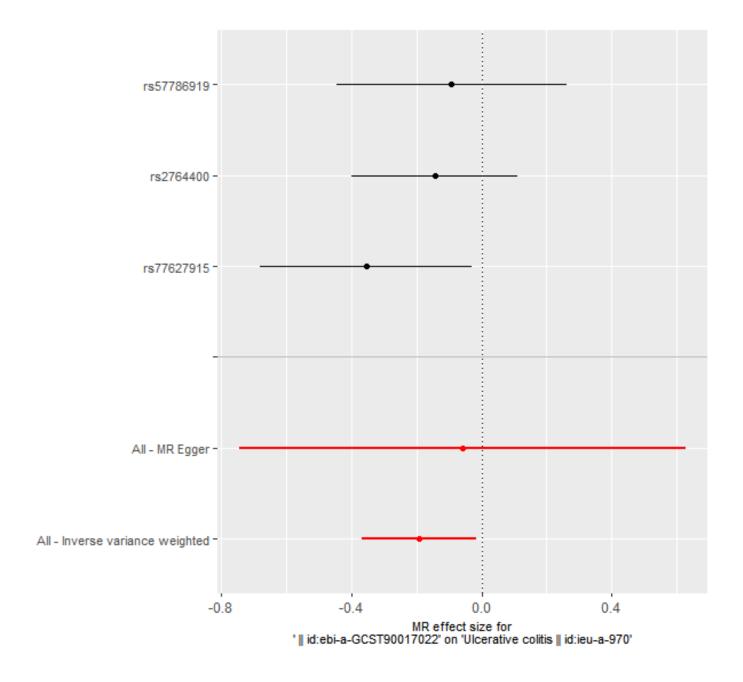
Figure 129 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lachnospiraceae NC2004 group id.11316) on ulcerative colitis

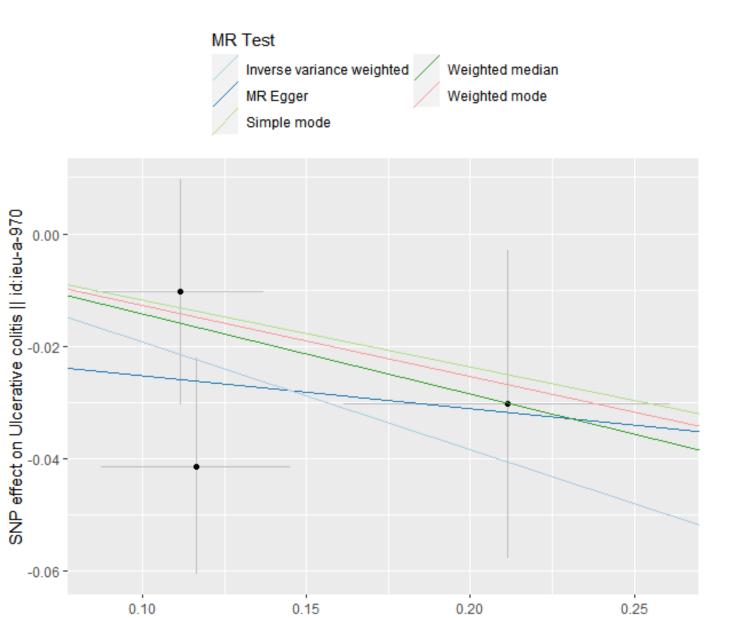


MR Method

Inverse variance weighted

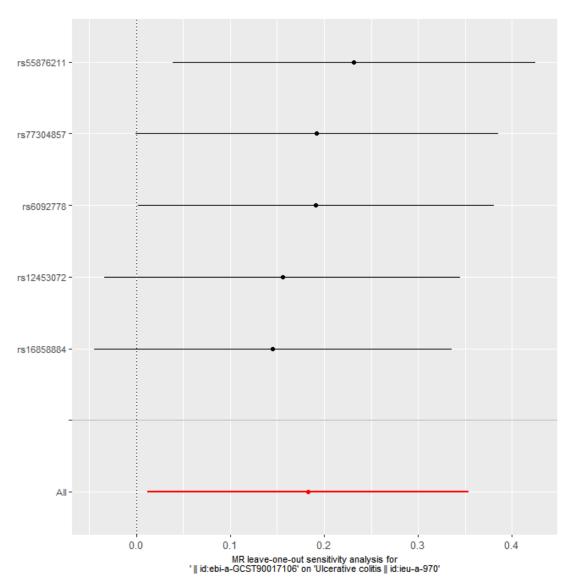


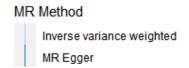


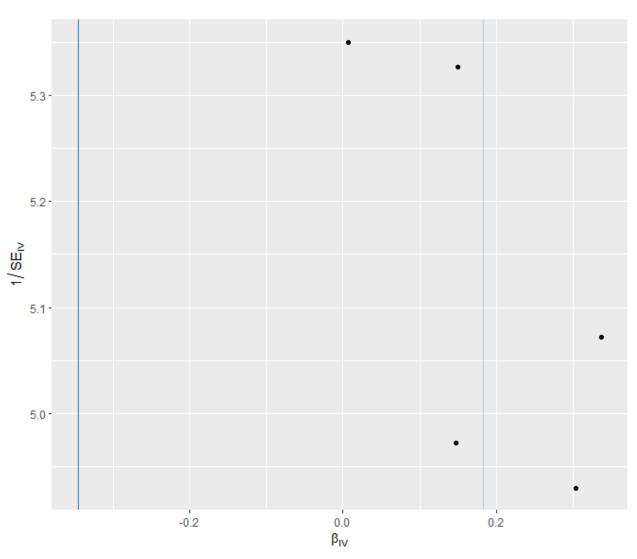


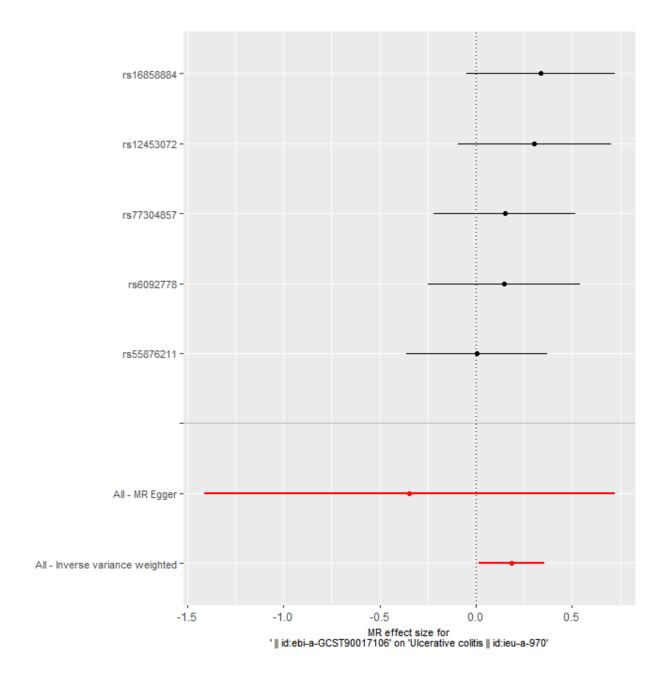
SNP effect on || id:ebi-a-GCST90017022

Figure 130 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Rhodospirillales id.2667) on ulcerative colitis









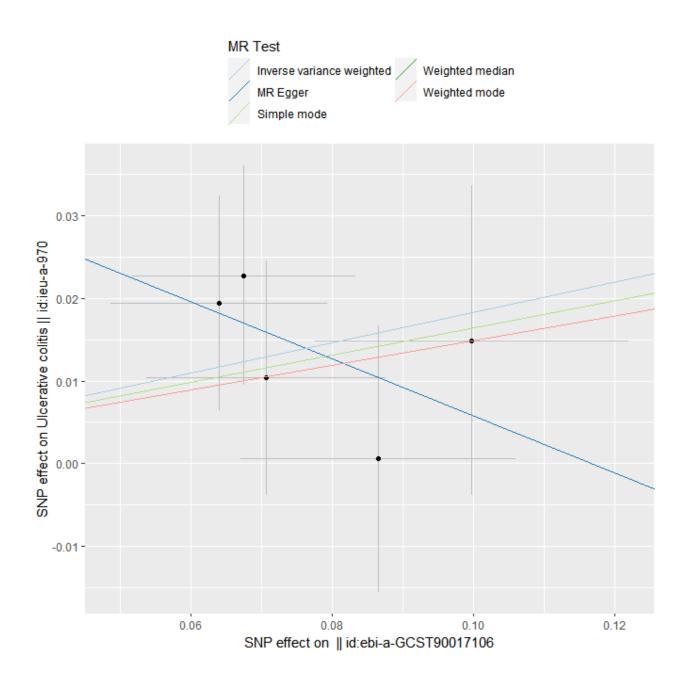
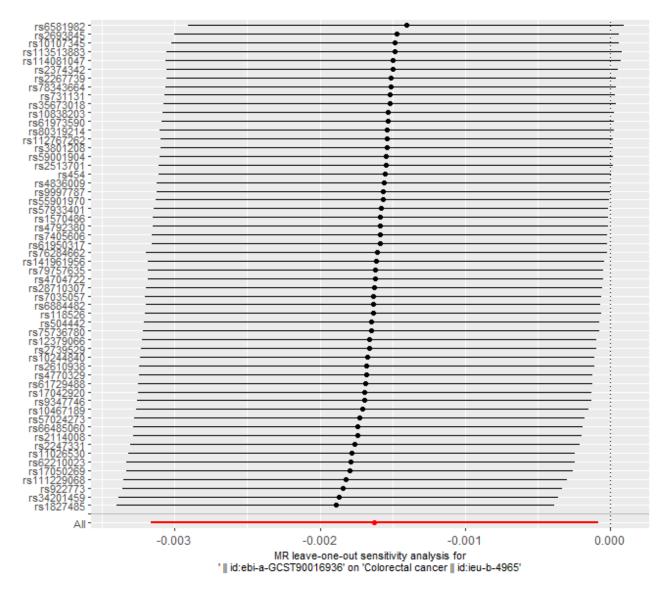
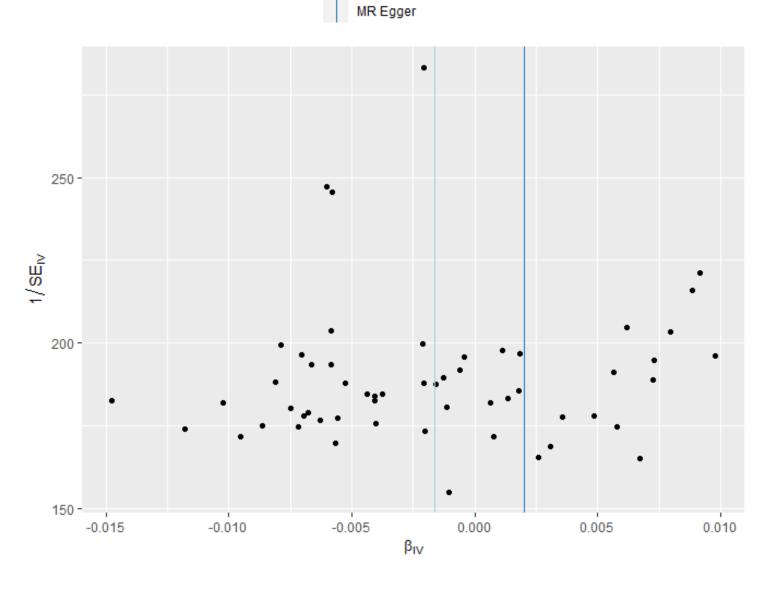


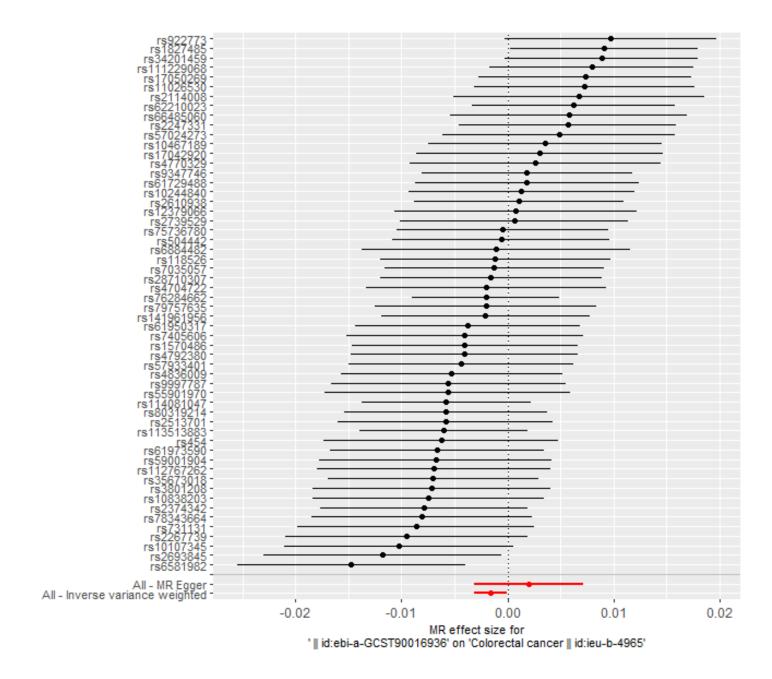
Figure 131 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Enterobacteriaceae id.3469) on colorectal cancer



MR Method

Inverse variance weighted







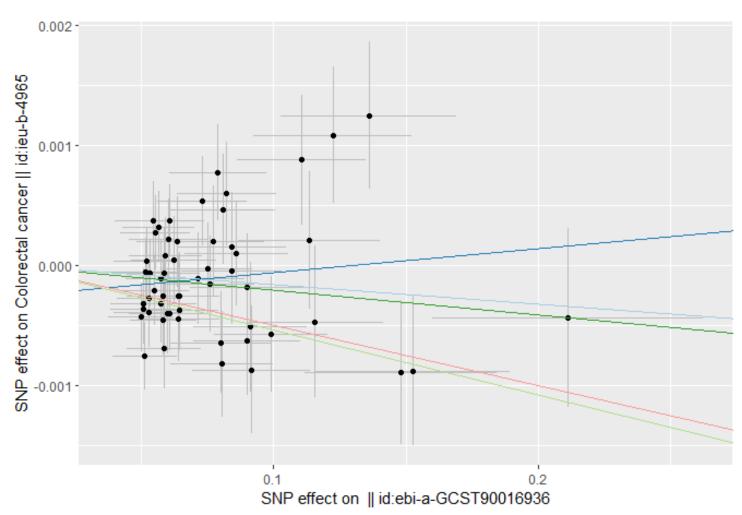
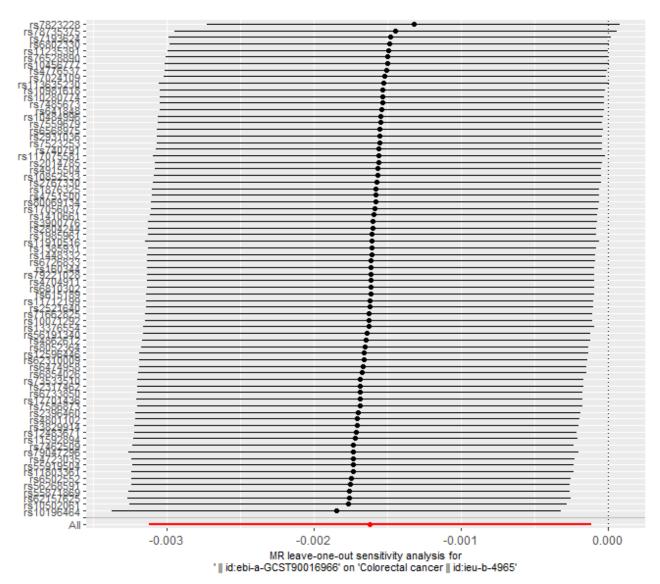
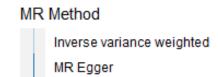
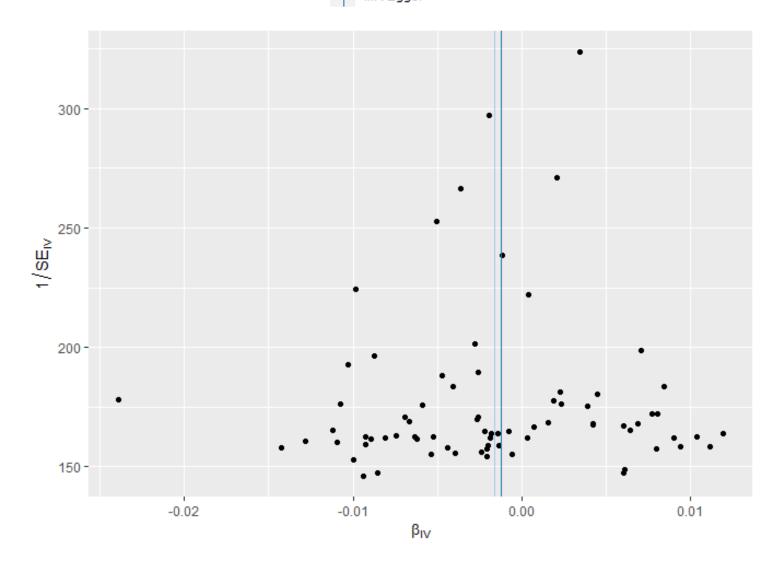
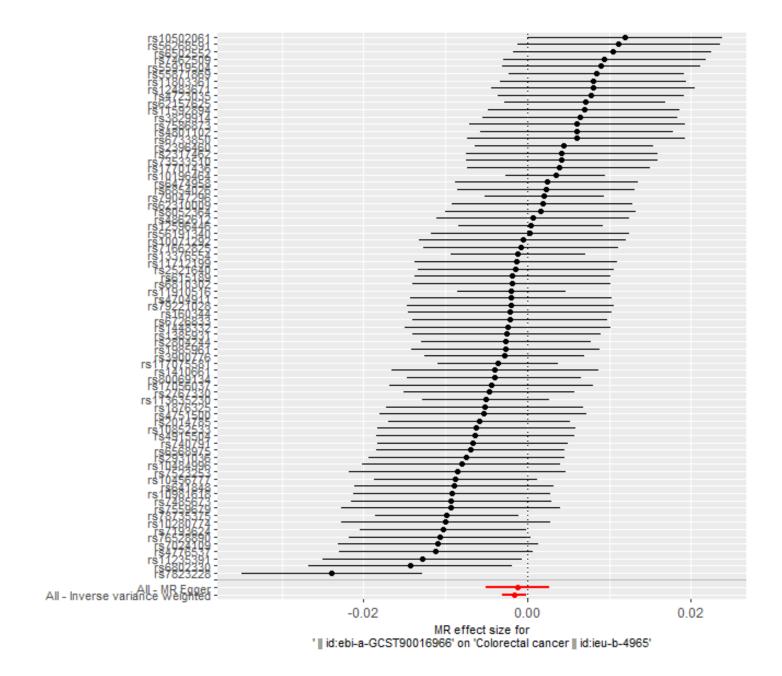


Figure 132 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Anaerostipes id.1991) on colorectal cancer











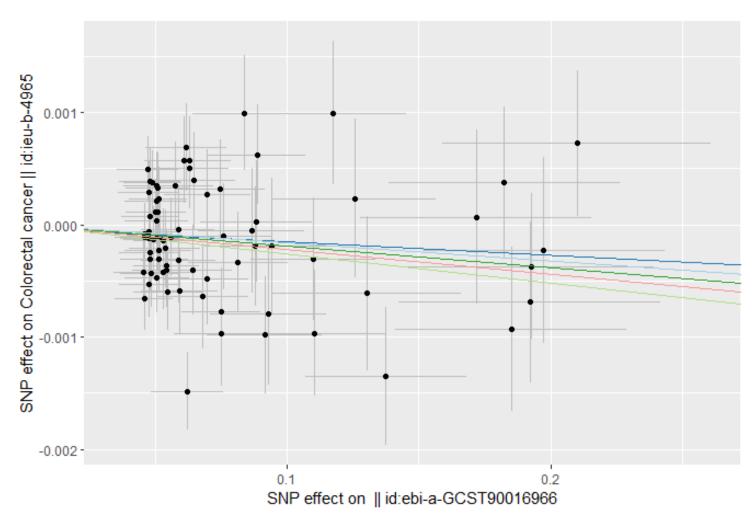
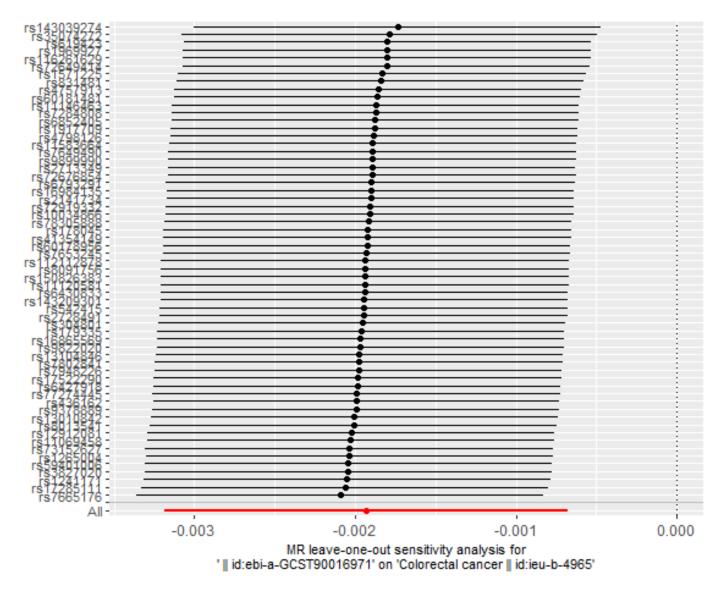
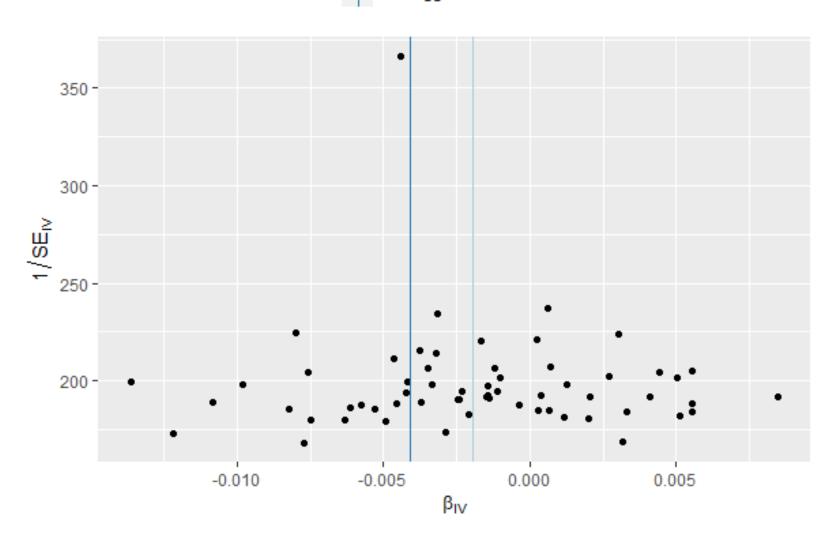


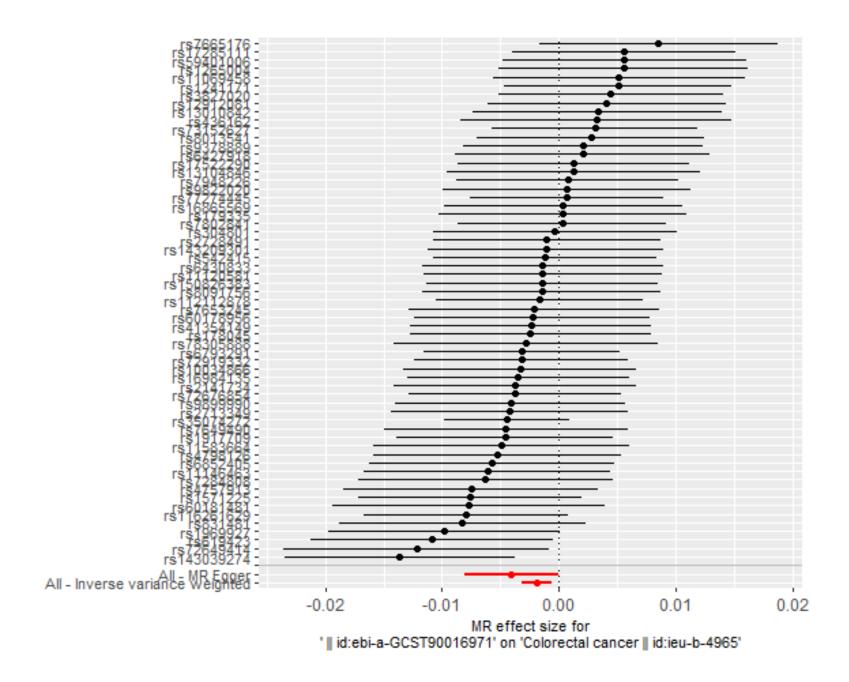
Figure 133 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Bilophila id.3170) on colorectal cancer



MR Method

Inverse variance weighted MR Egger







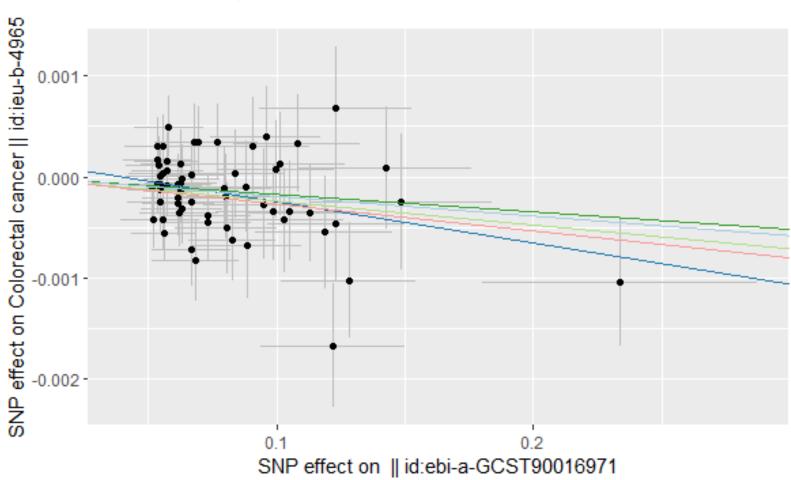
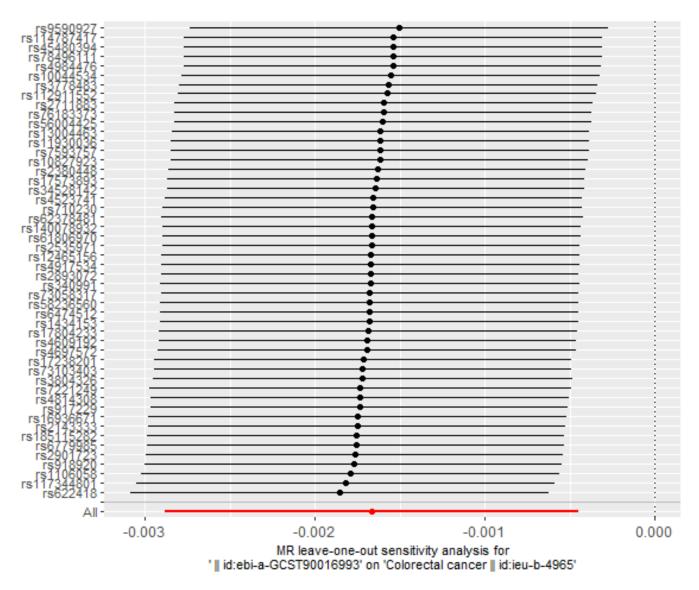
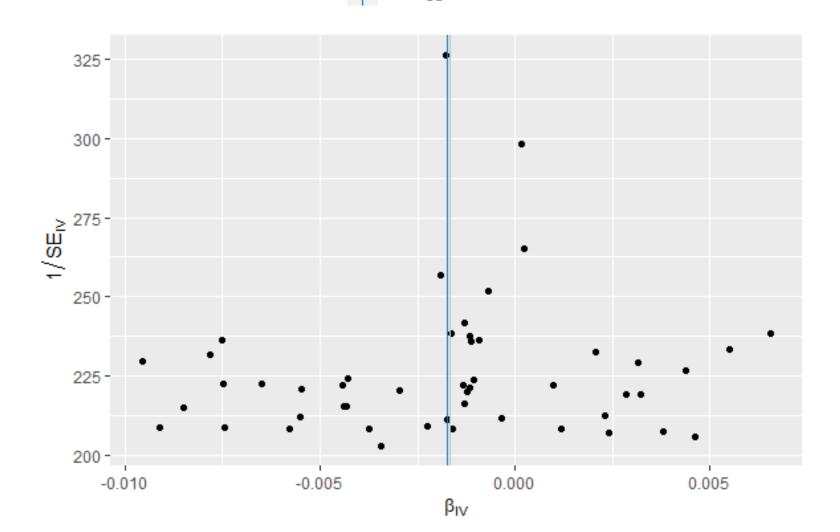
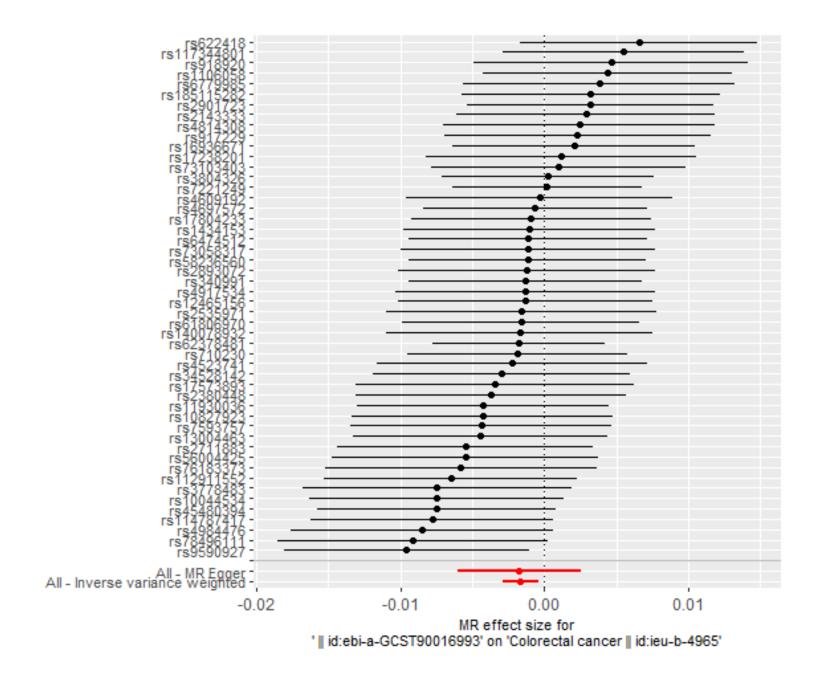


Figure 134 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Erysipelatoclostridium id.11381) on colorectal cancer



MR Method Inverse variance weighted MR Egger







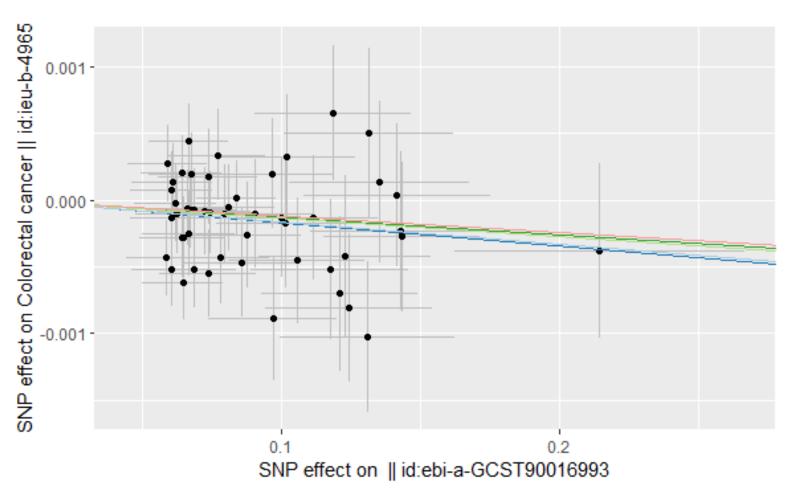
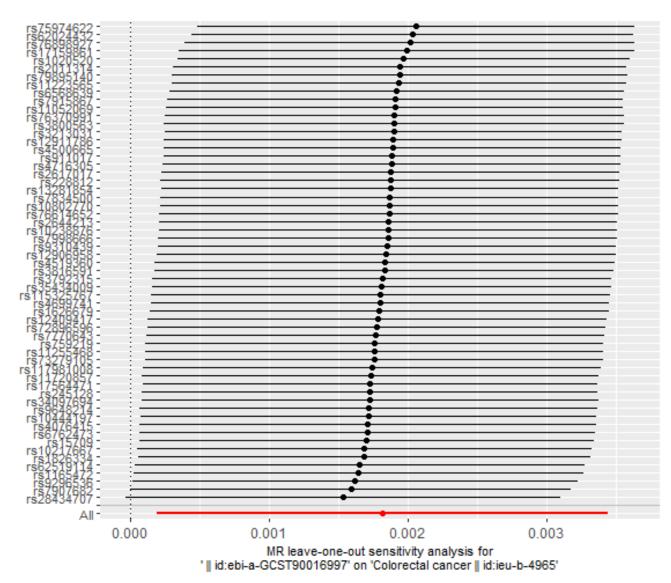
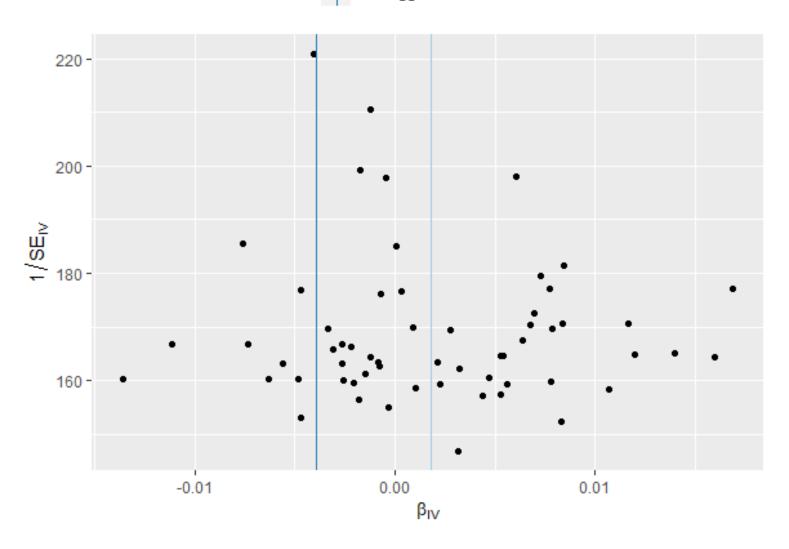


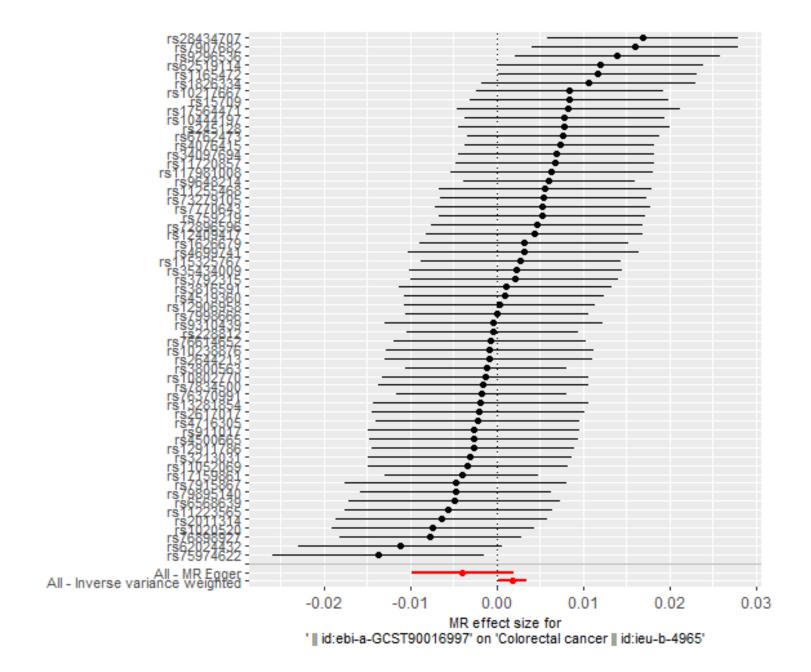
Figure 135 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium coprostanoligenes group id.11375) on colorectal cancer



MR Method

Inverse variance weighted MR Egger







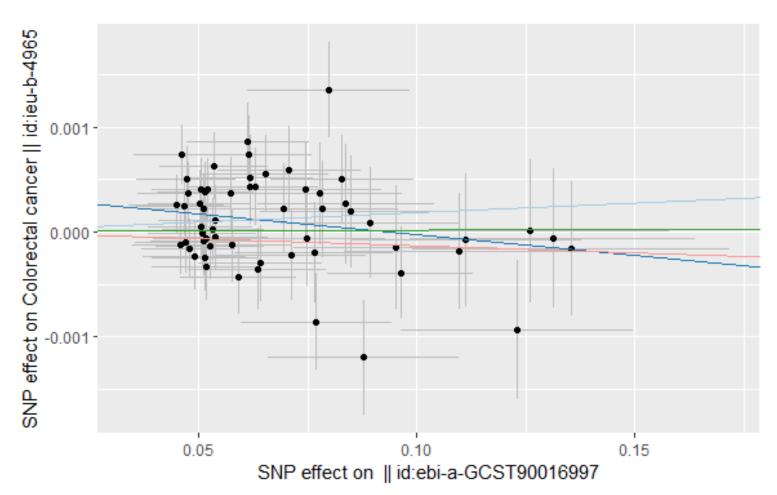
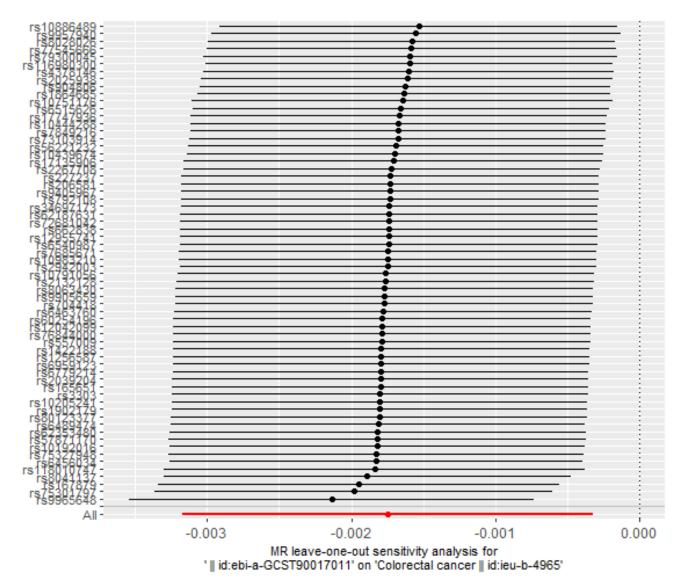
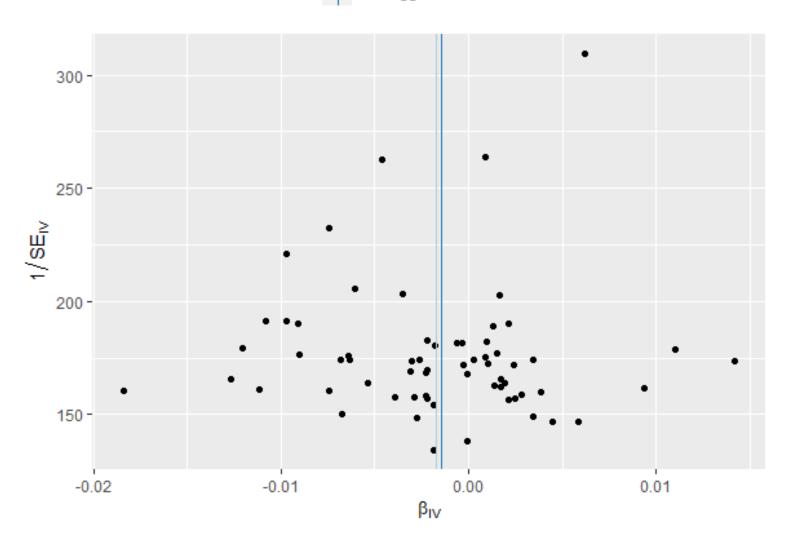


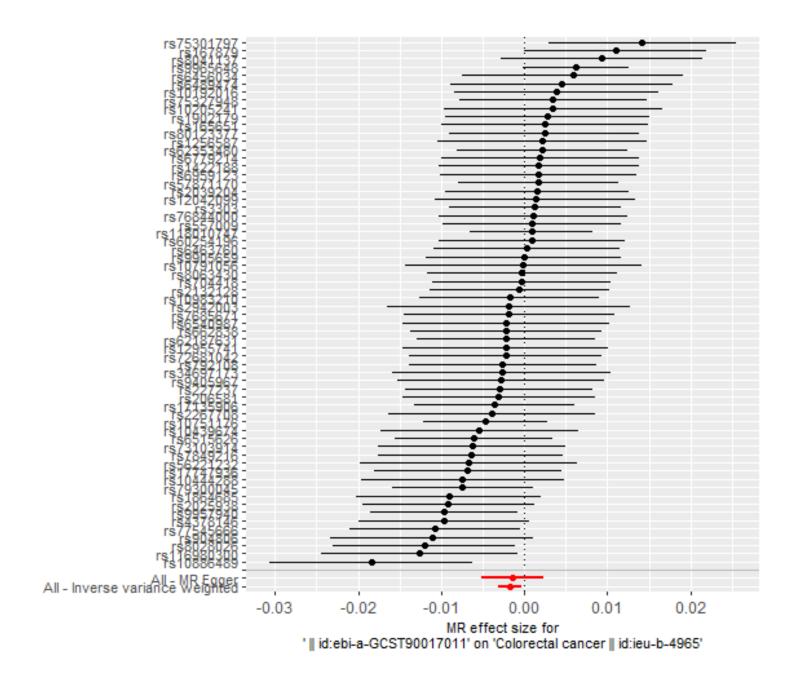
Figure 136 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Fusicatenibacter id.11305) on colorectal cancer



MR Method

Inverse variance weighted MR Egger







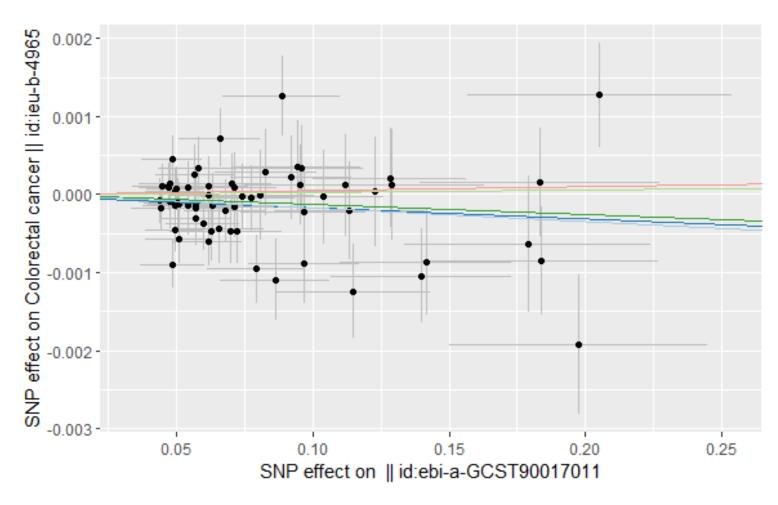
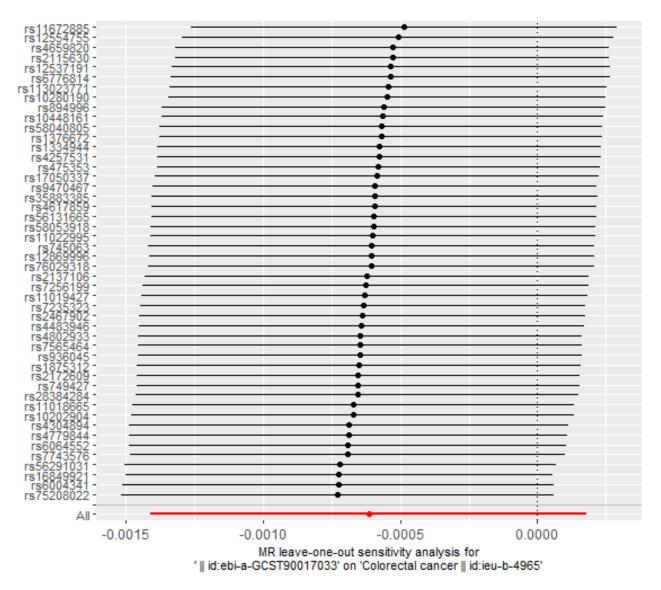
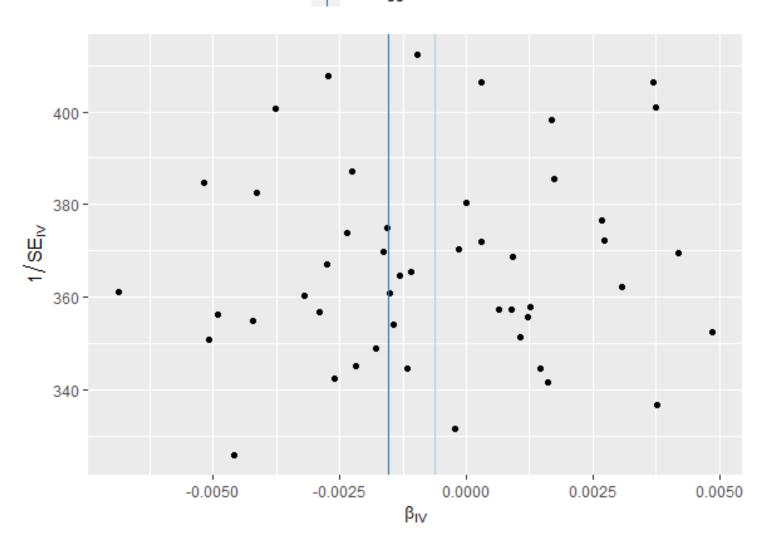


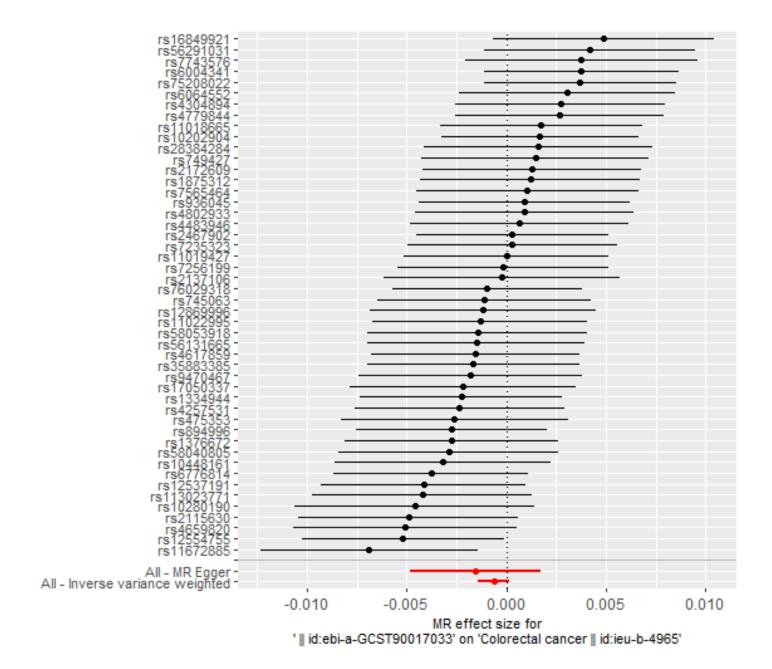
Figure 137 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Methanobrevibacter id.123) on colorectal cancer



MR Method

Inverse variance weighted MR Egger







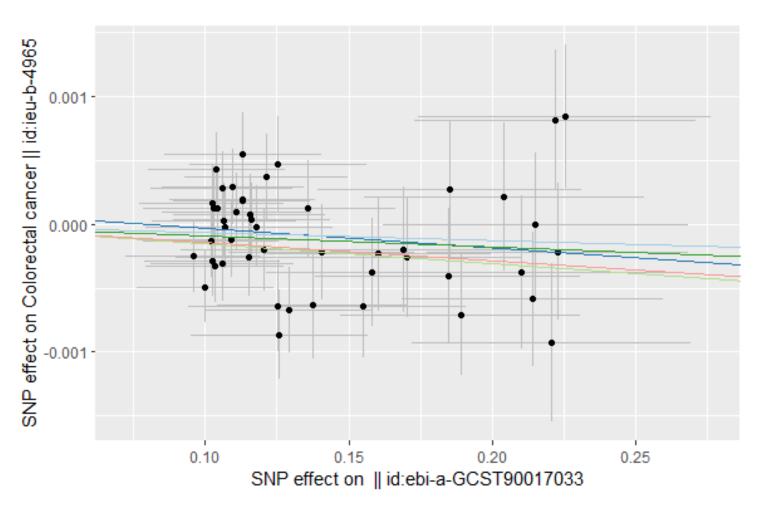
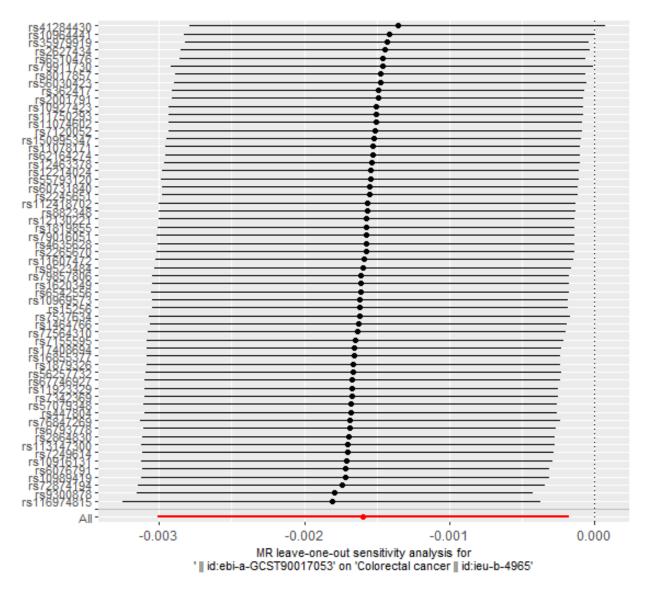
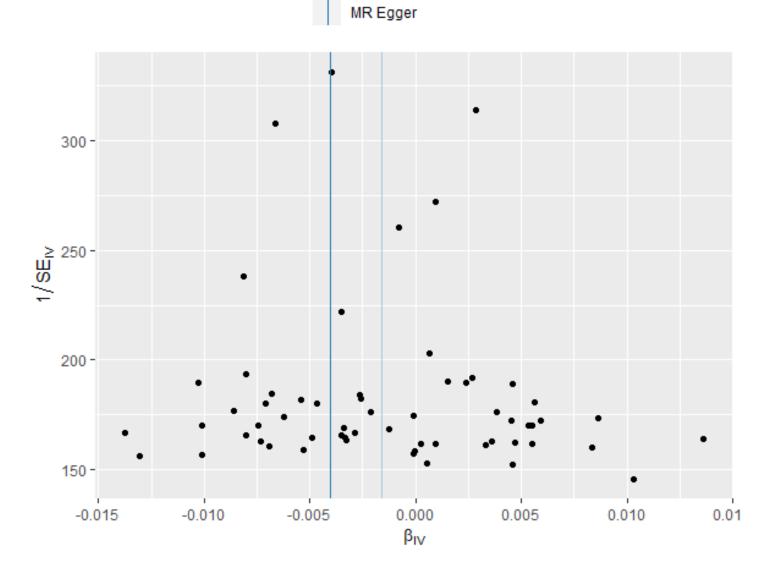


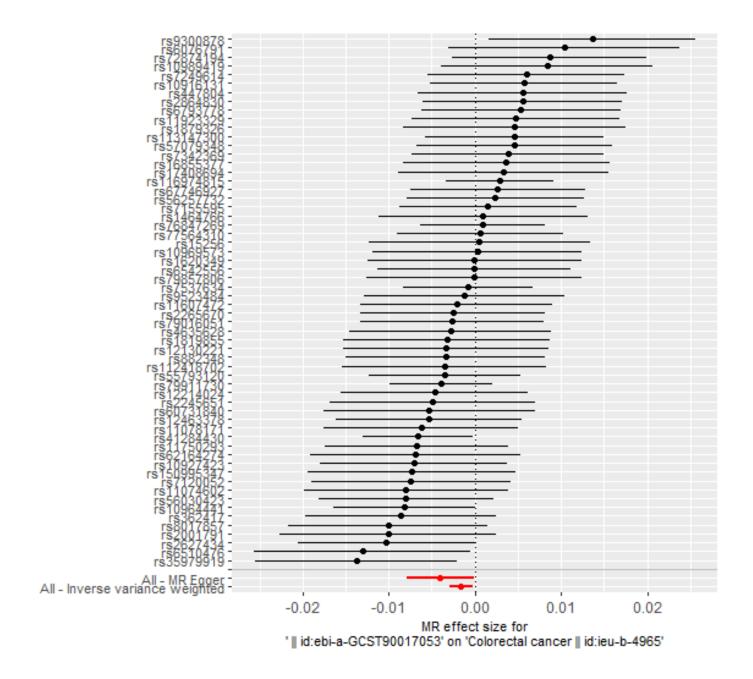
Figure 138 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG002 id.11360) on colorectal cancer

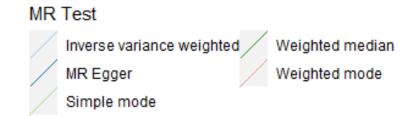


MR Method

Inverse variance weighted







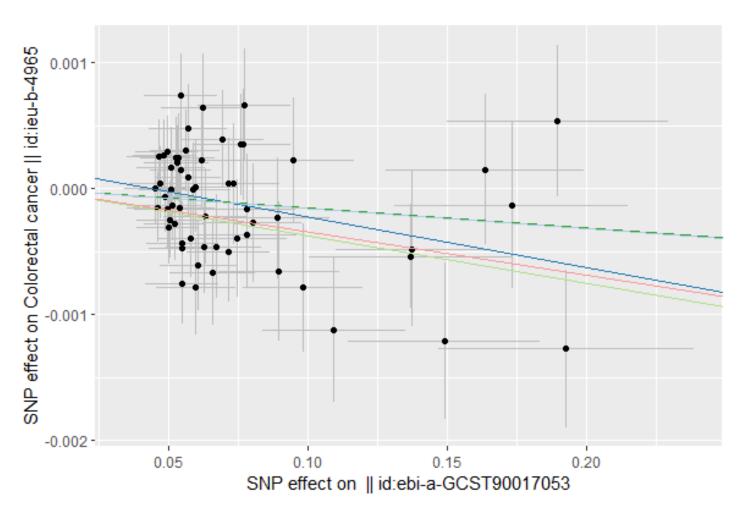
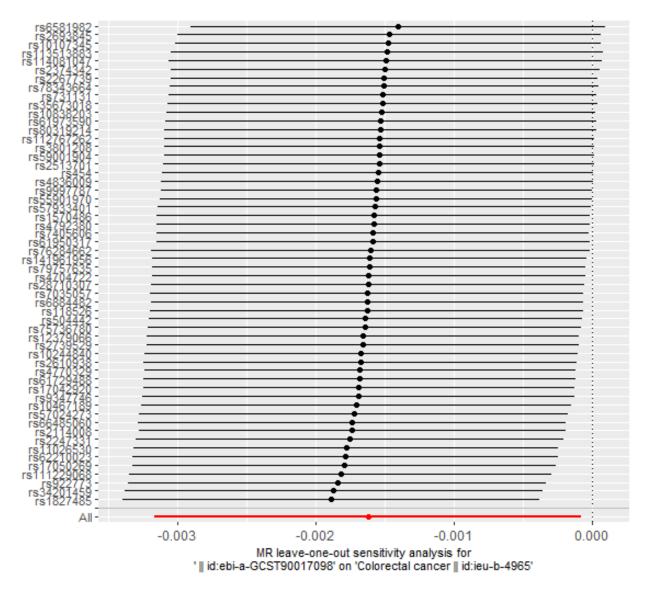
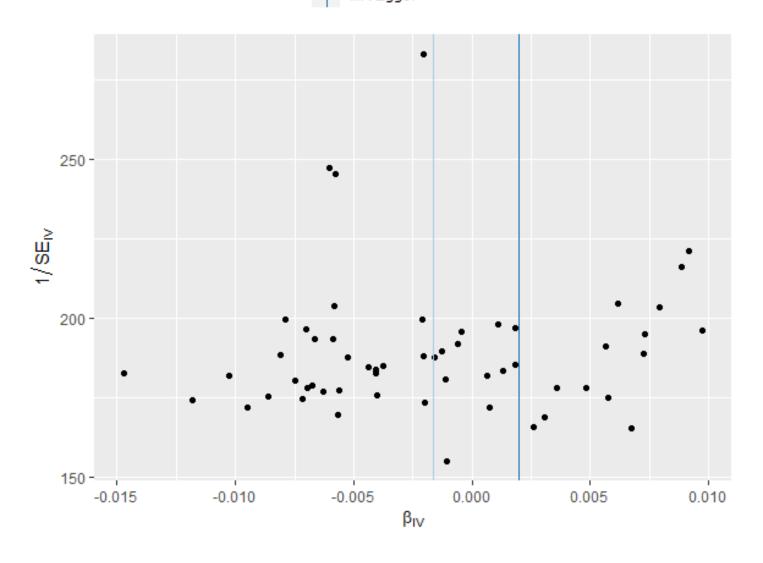


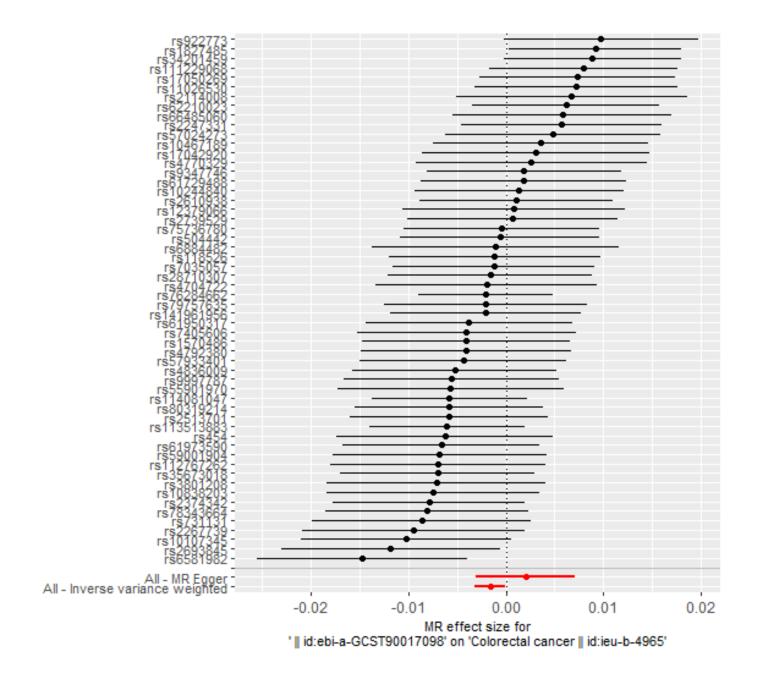
Figure 139 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Enterobacteriales id.3468) on colorectal cancer



MR Method

Inverse variance weighted MR Egger







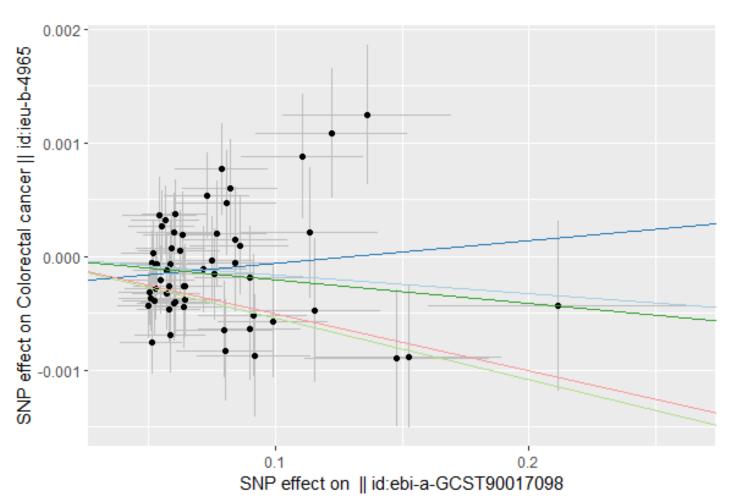
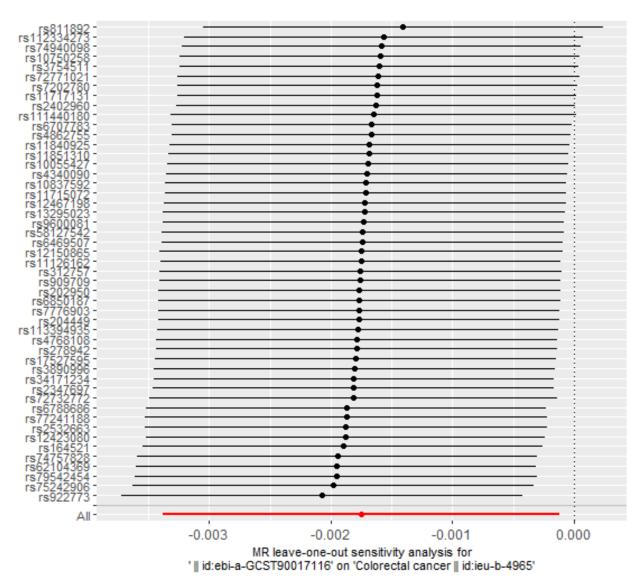
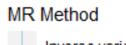


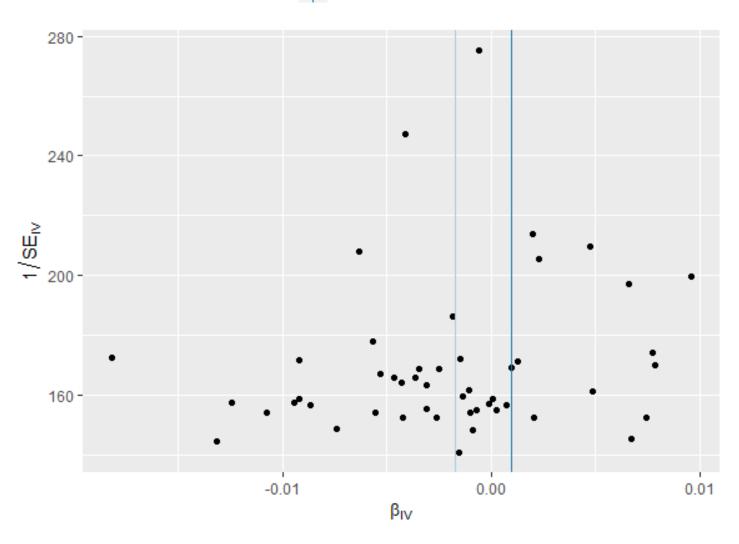
Figure 140 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Proteobacteria id.2375) on colorectal cancer

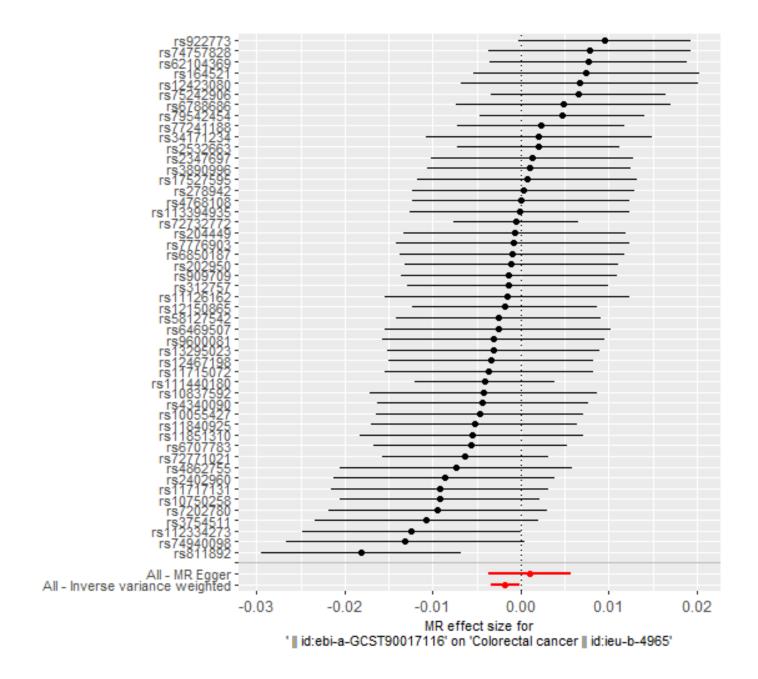


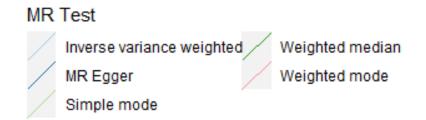


Inverse variance weighted

MR Egger







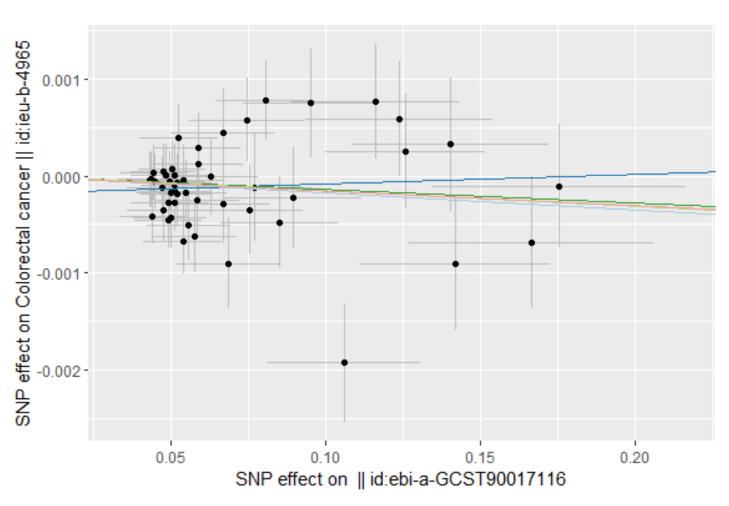
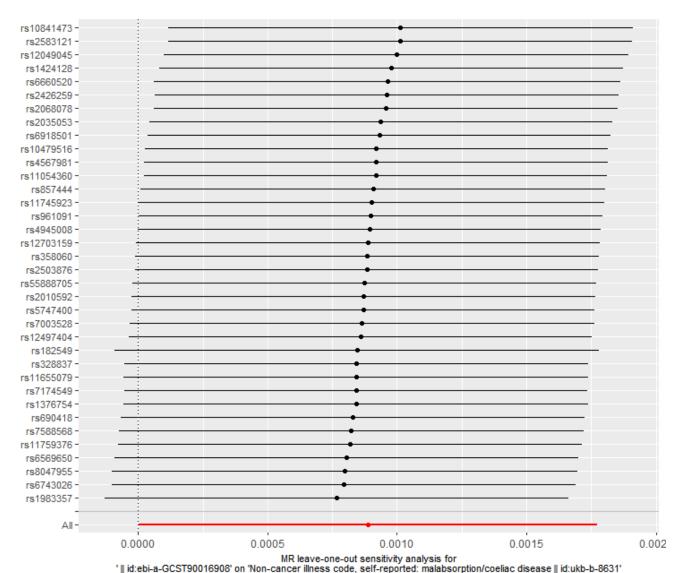
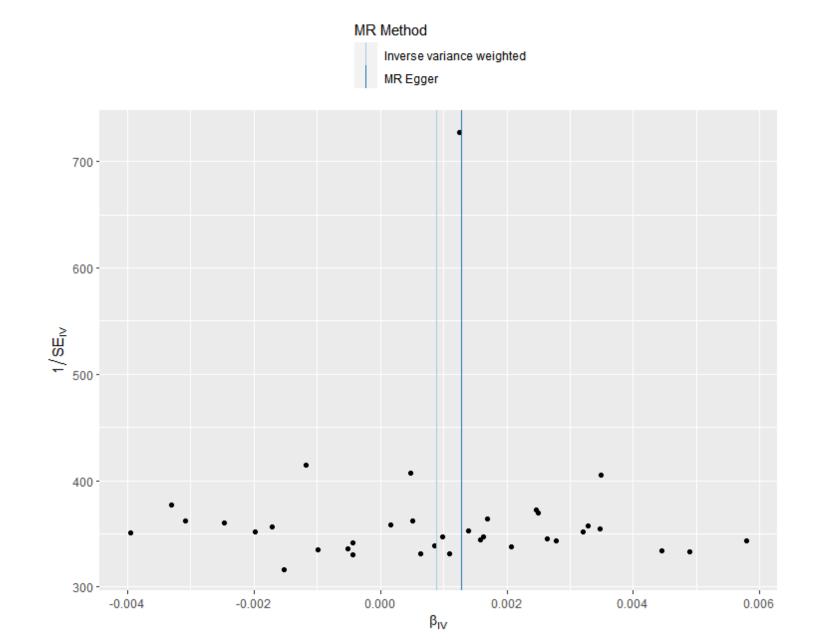
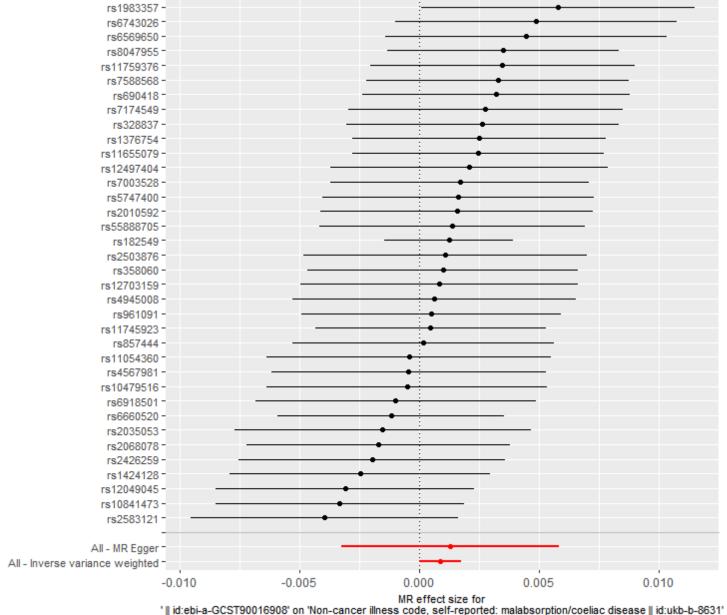


Figure 141 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Actinobacteria id.419) on coeliac disease







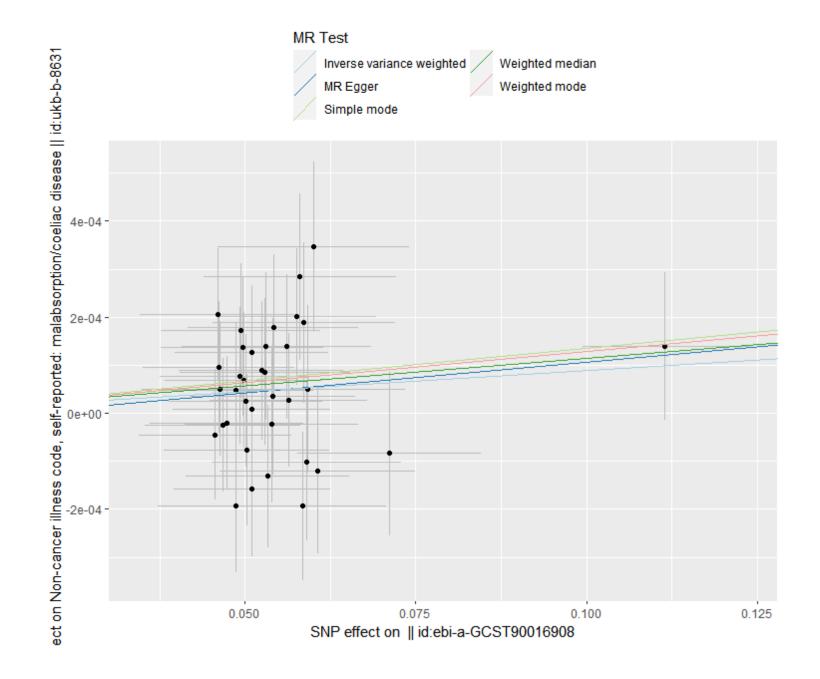
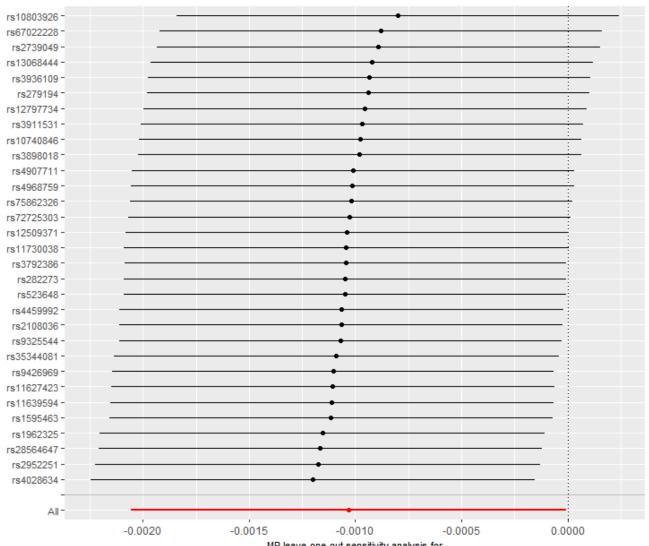
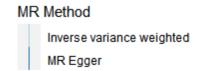
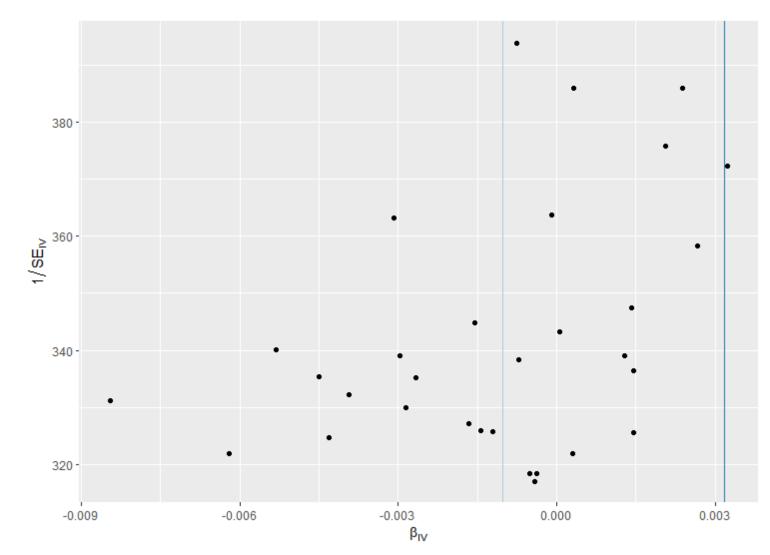


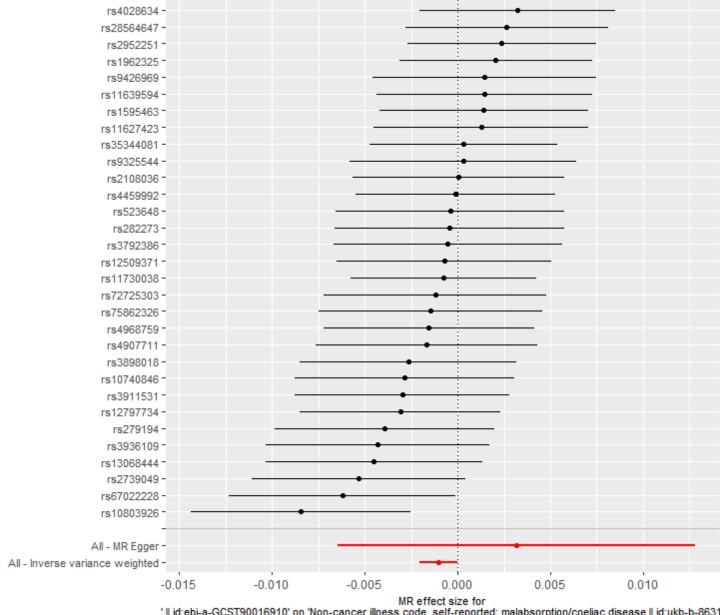
Figure 142 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Bacilli id.1673) on coeliac disease



MR leave-one-out sensitivity analysis for ' || id:ebi-a-GCST90016910' on 'Non-cancer illness code, self-reported: malabsorption/coeliac disease || id:ukb-b-8631'







" || id:ebi-a-GCST90016910" on "Non-cancer illness code, self-reported: malabsorption/coeliac disease || id:ukb-b-8631"

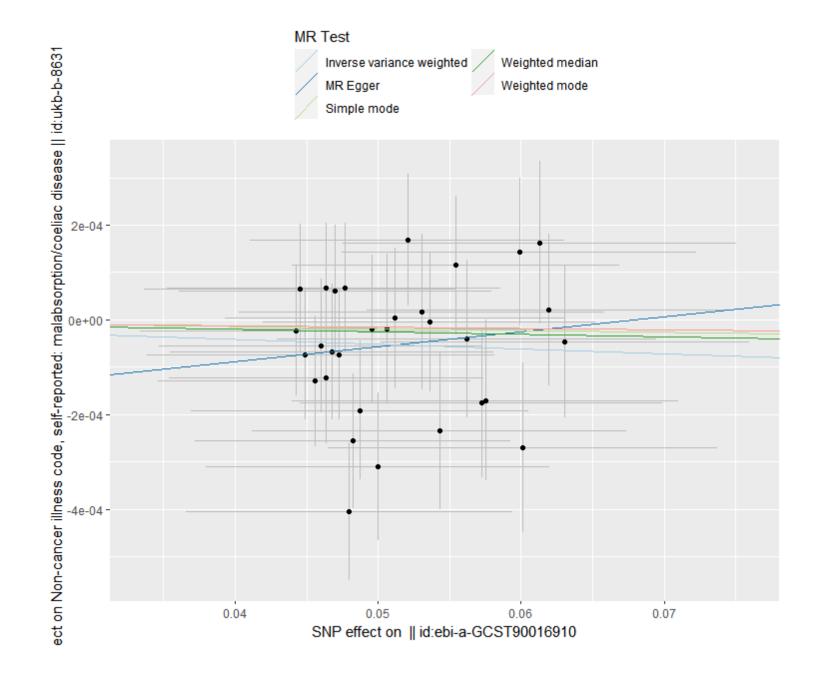
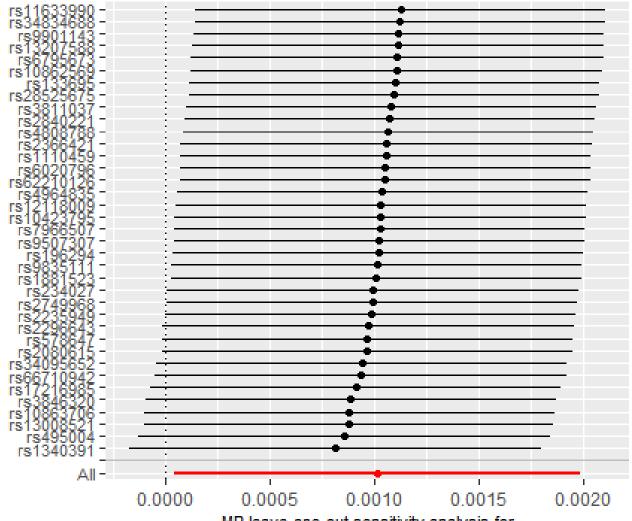


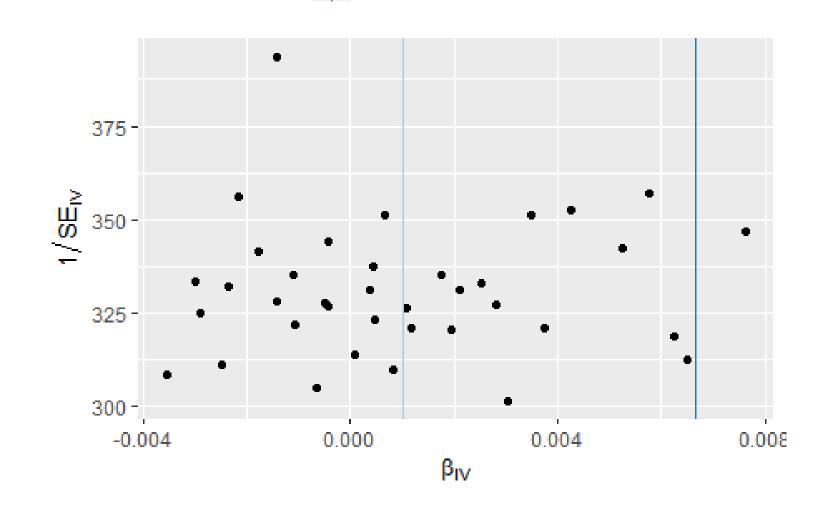
Figure 143 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Bacteroidaceae id.917) on coeliac disease

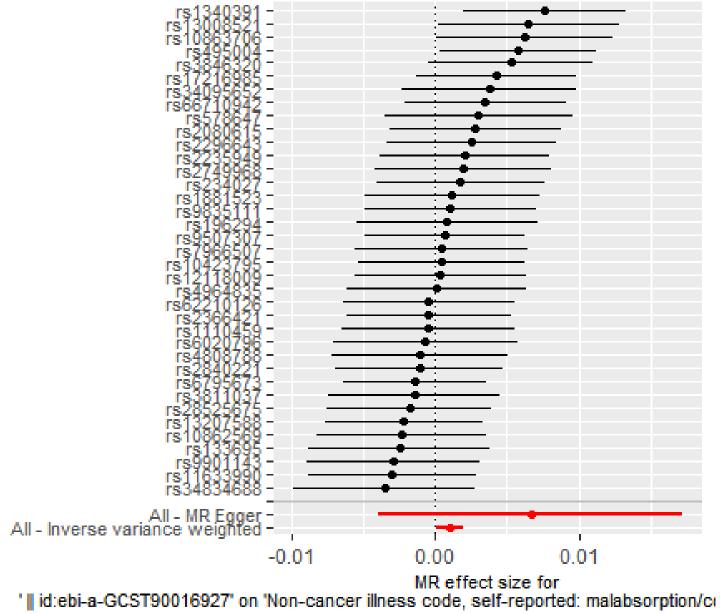


MR leave-one-out sensitivity analysis for diebi-a-GCST90016927' on 'Non-cancer illness code, self-reported: malabsorption/coeliac disc

MR Method

Inverse variance weighted MR Egger





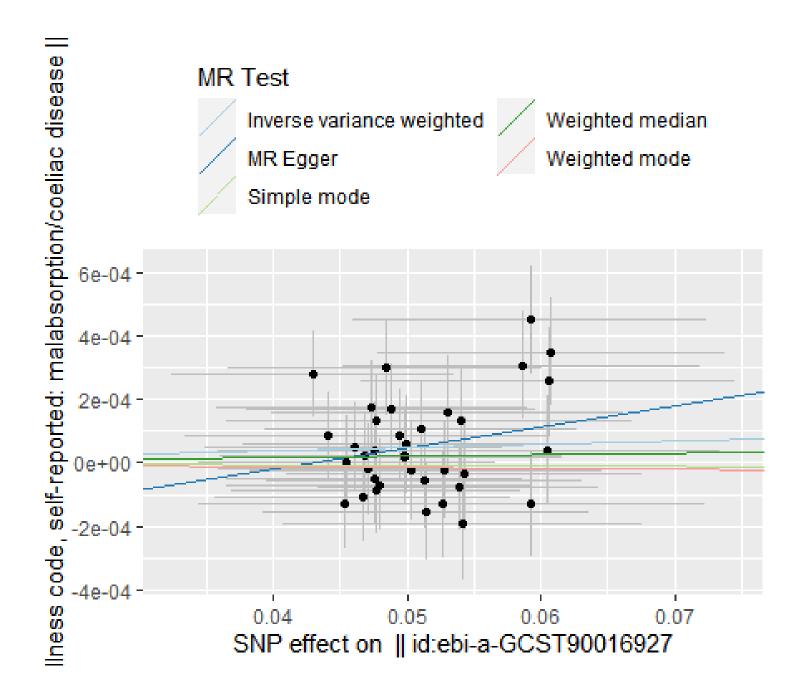
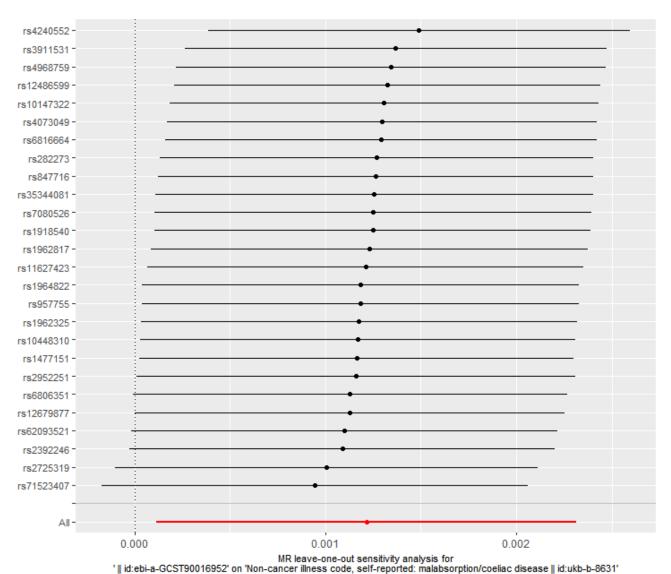
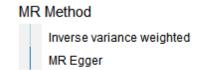
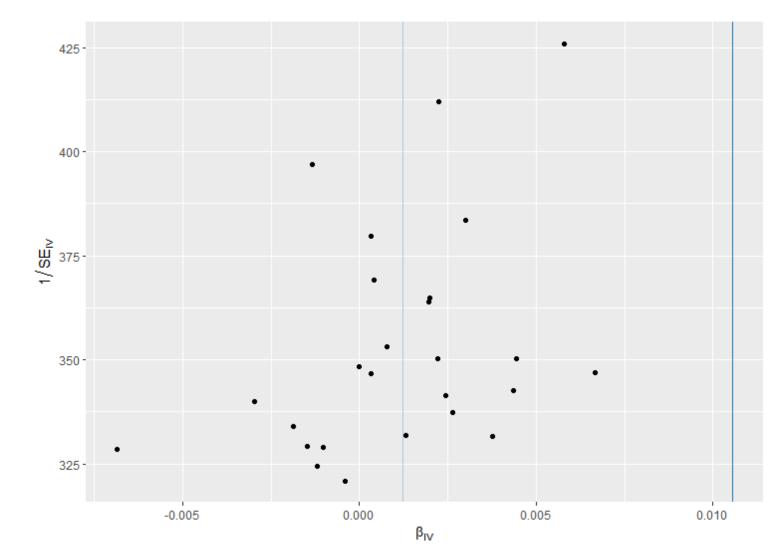
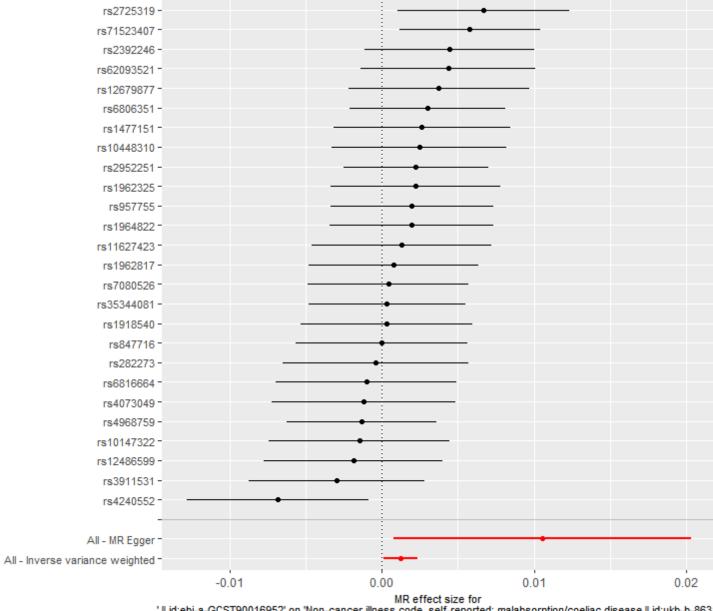


Figure 144 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Streptococcaceae id.1850) on coeliac disease









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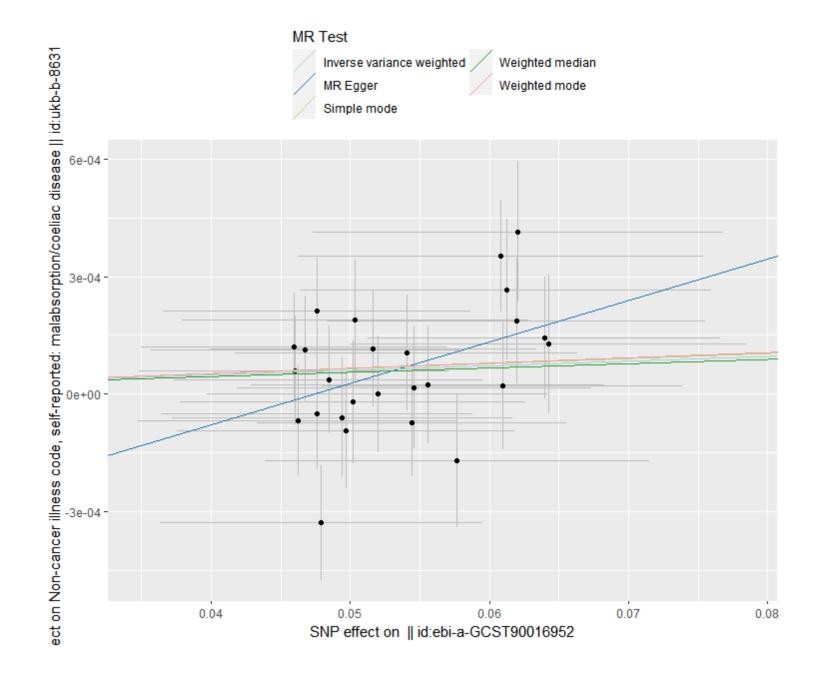
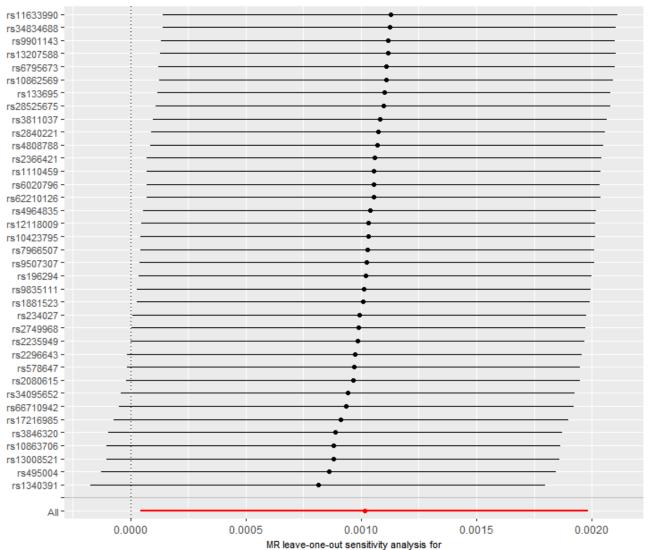
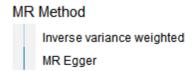
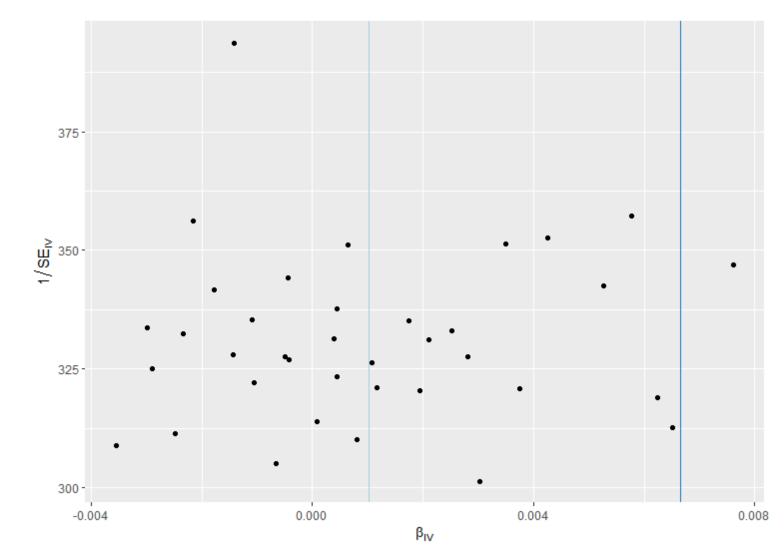


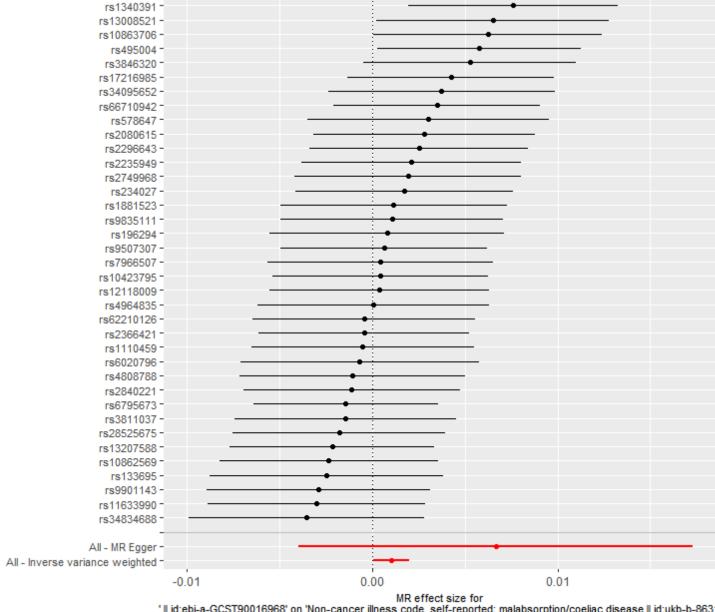
Figure 145 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Bacteroides id.918) on coeliac disease



with leave-one-out sensitivity analysis for '∥ id:ebi-a-GCST90016968' on 'Non-cancer illness code, self-reported: malabsorption/coeliac disease ∥ id:ukb-b-8631'







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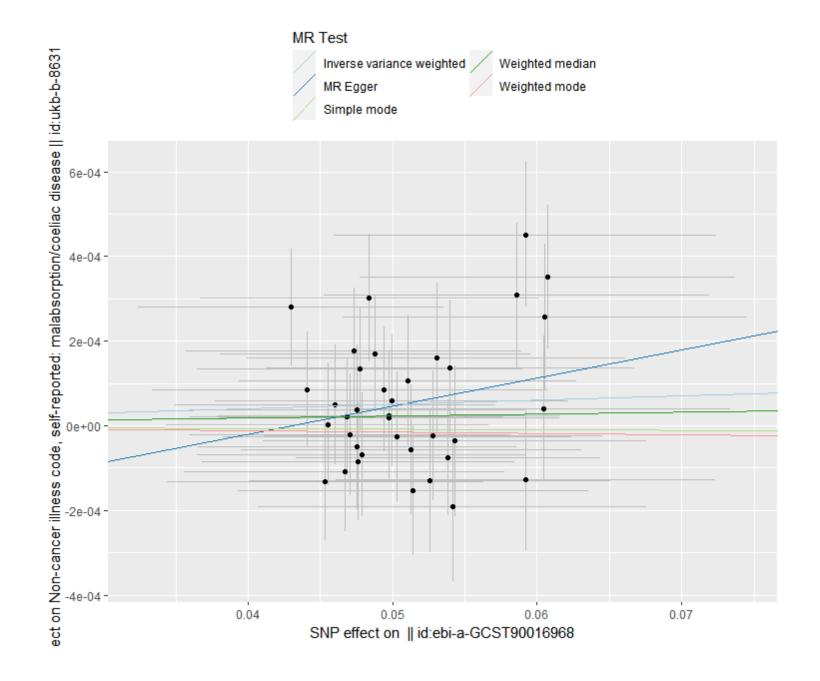
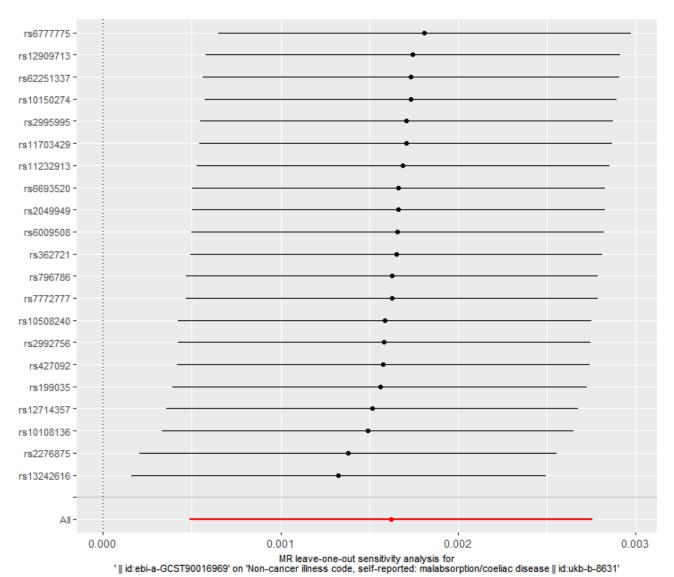
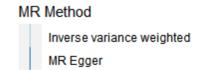
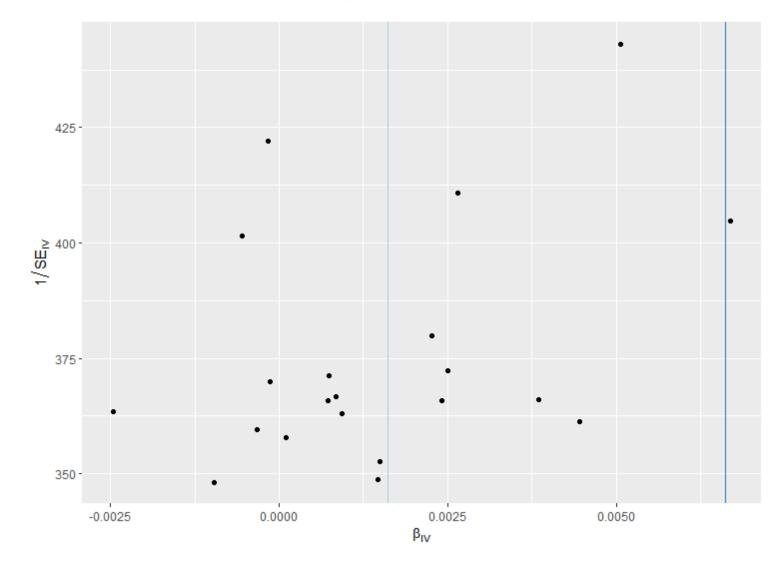
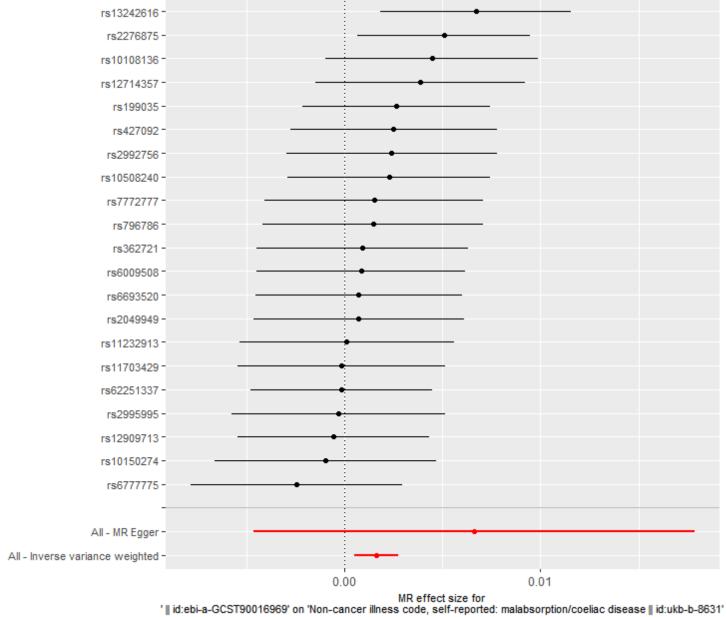


Figure 146 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Barnesiella id.944) on coeliac disease









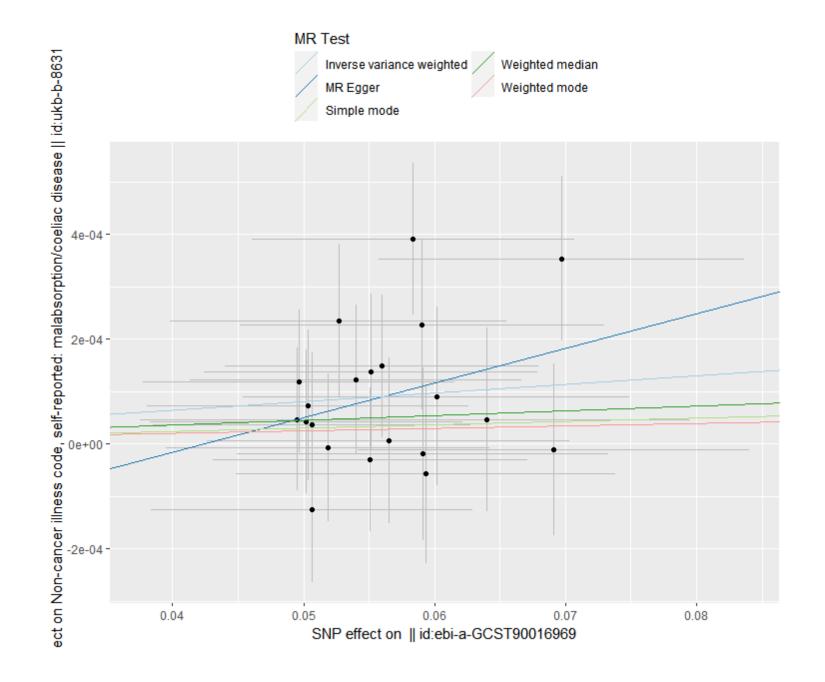
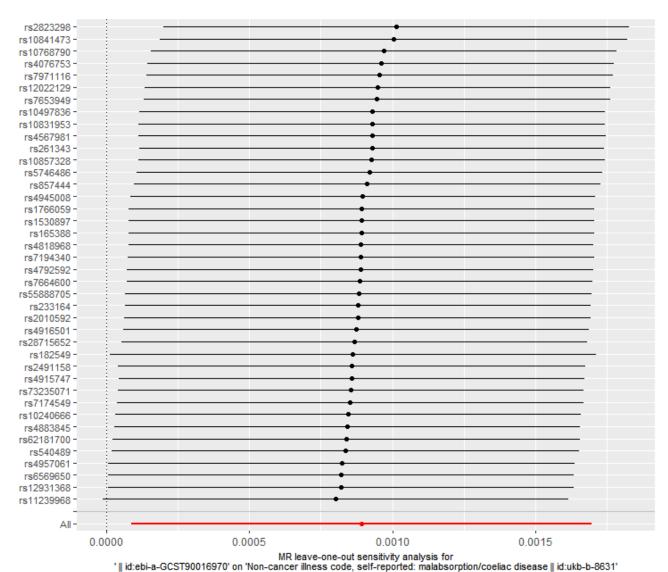
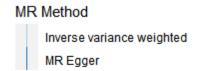
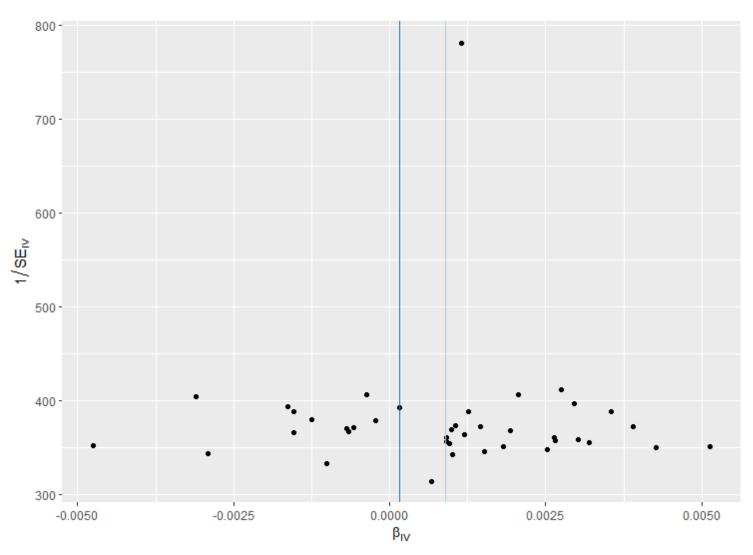
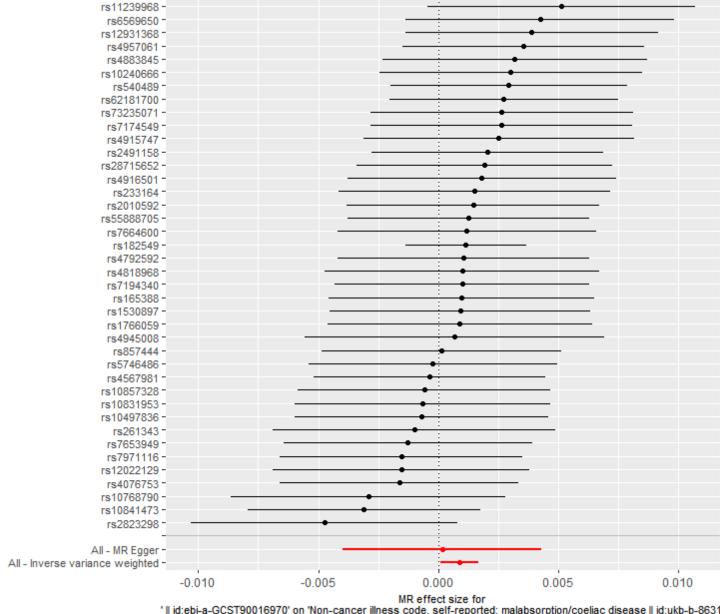


Figure 147 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Bifidobacterium id.436) on coeliac disease









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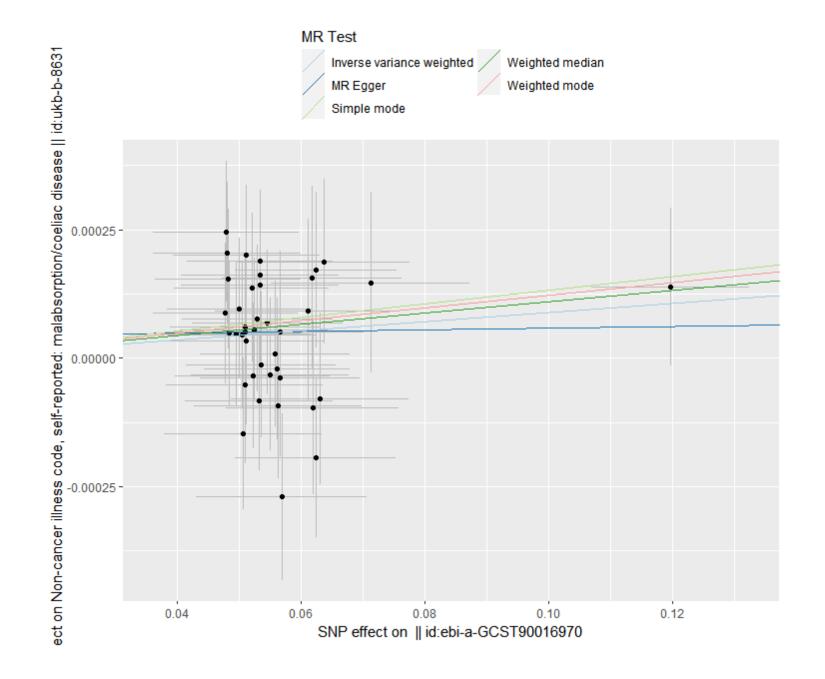
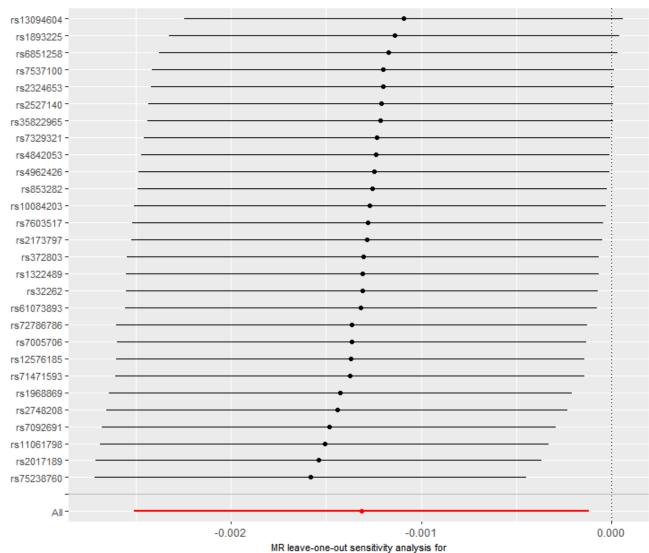
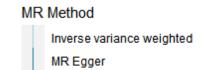
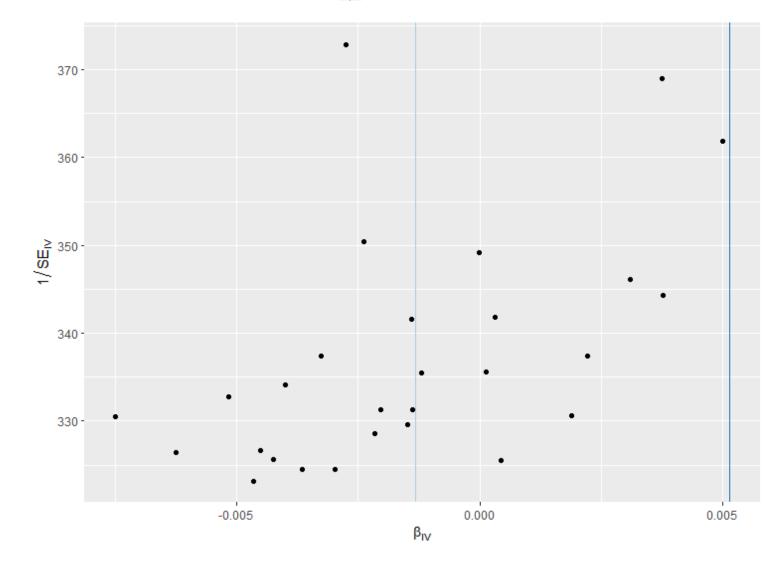


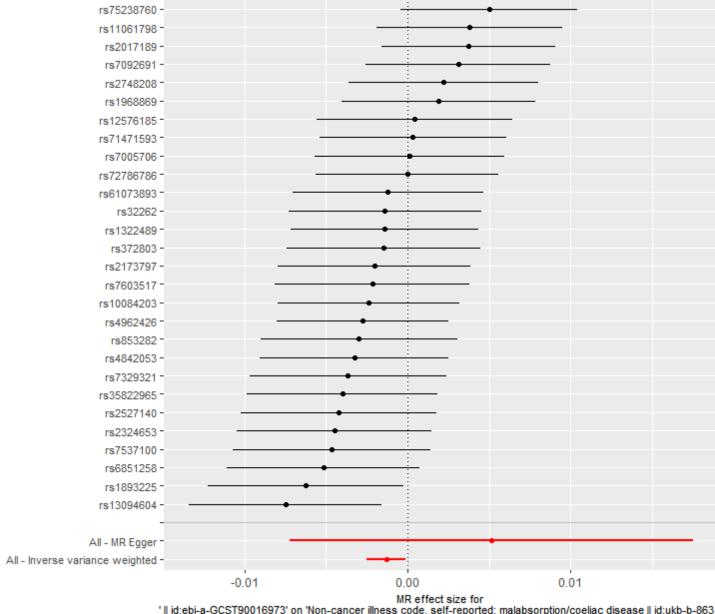
Figure 148 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Butyricicoccus id.2055) on coeliac disease



MR leave-one-out sensitivity analysis for
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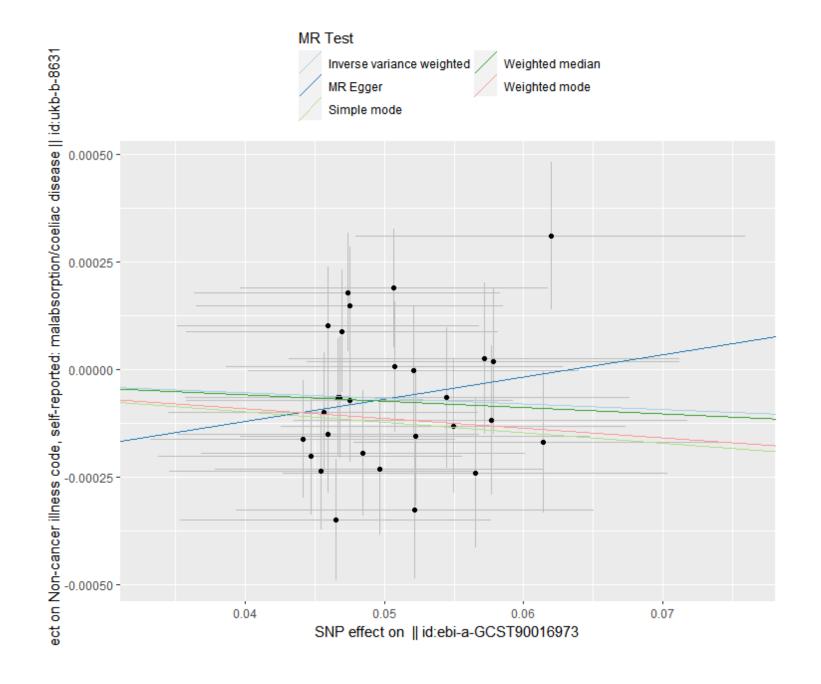
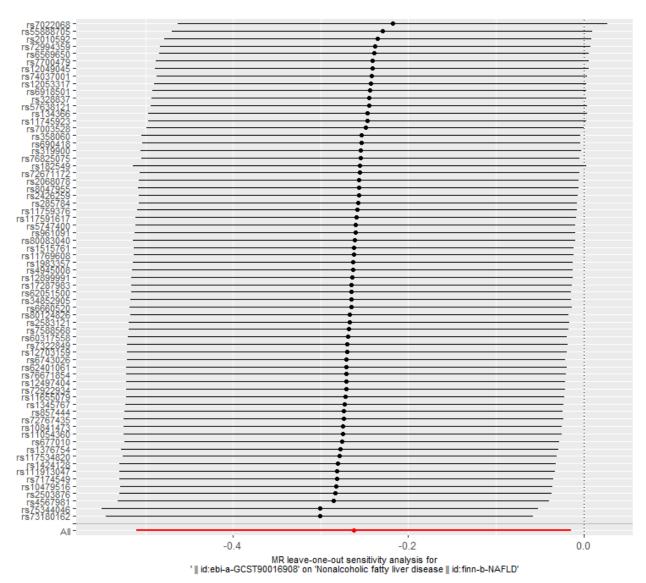
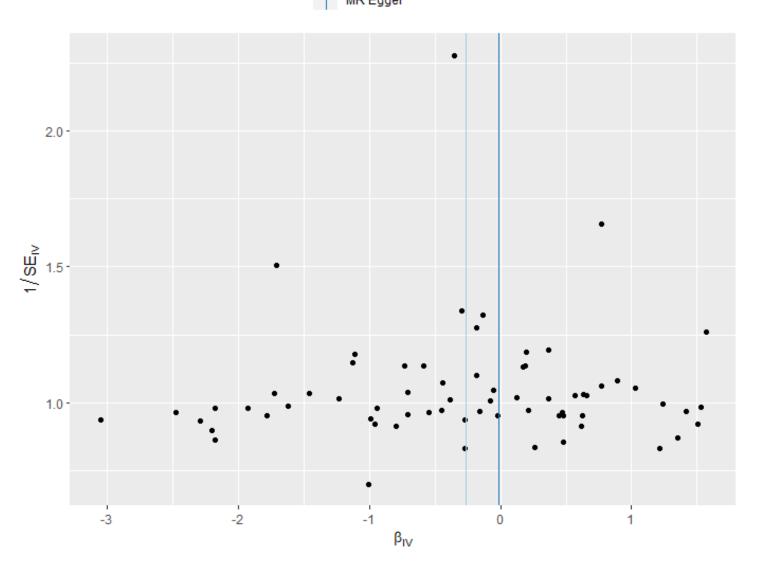


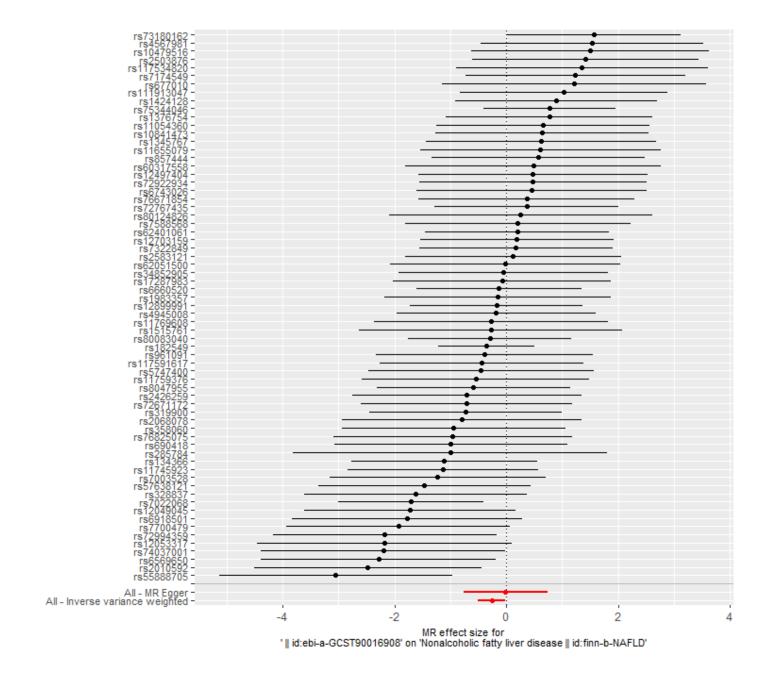
Figure 149 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Actinobacteria id.419) on nonalcoholic fatty liver disease





Inverse variance weighted MR Egger





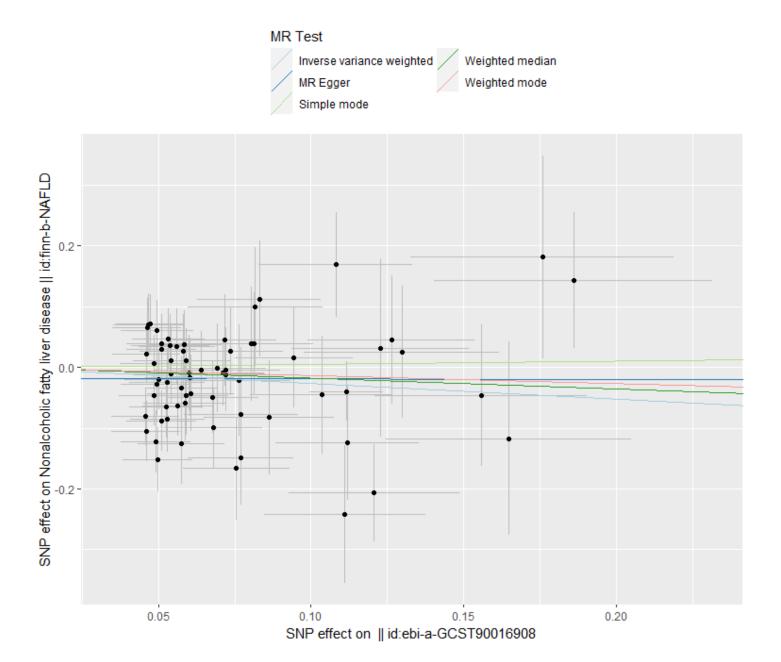
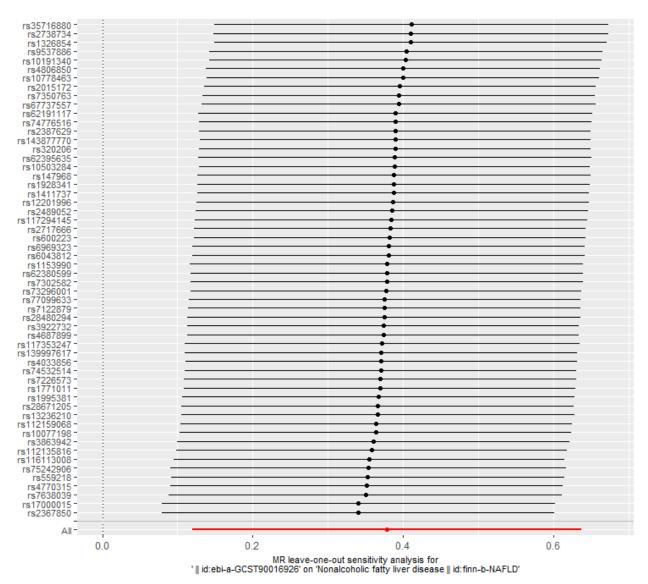
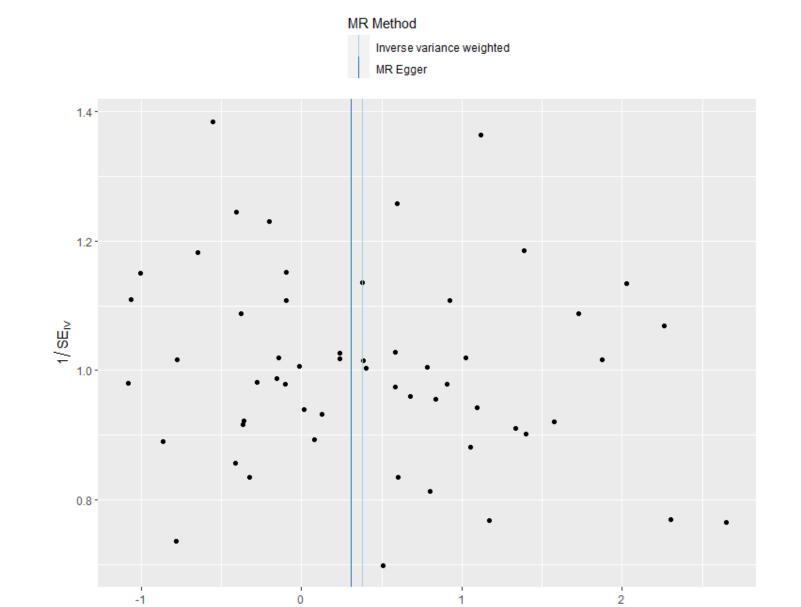
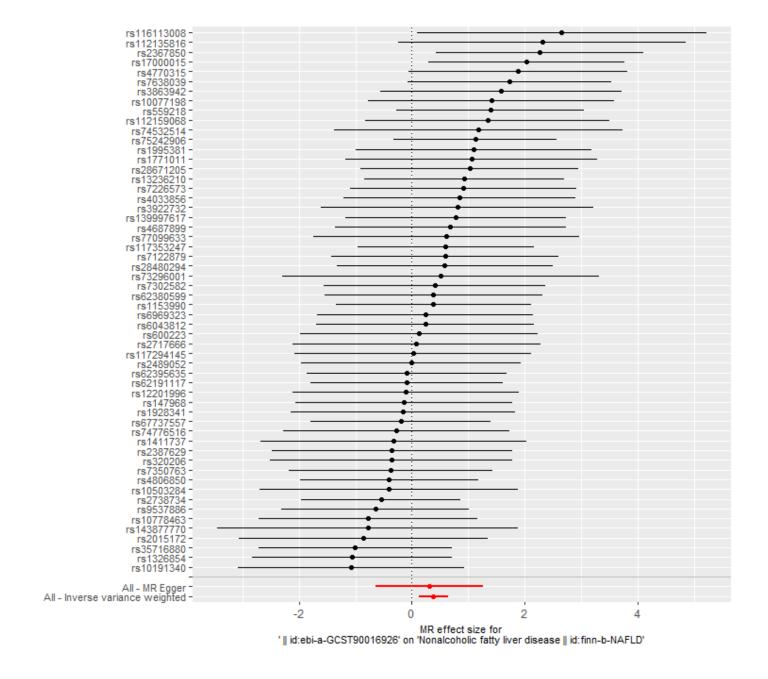


Figure 150 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Alcaligenaceae id.2875) on nonalcoholic fatty liver disease





 β_{IV}





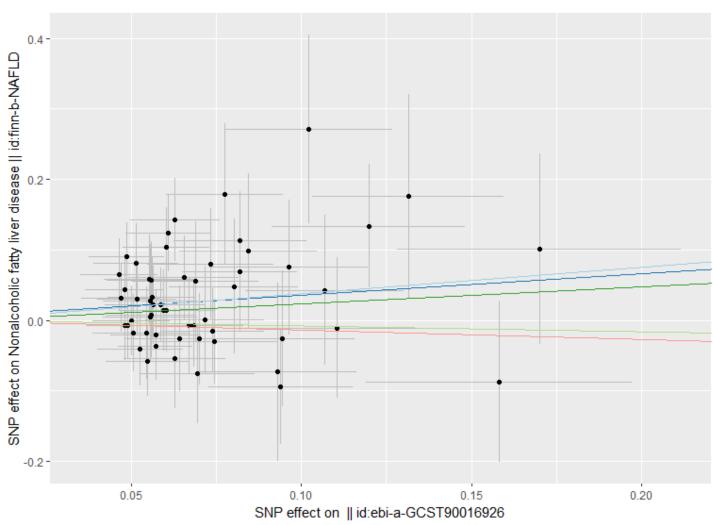
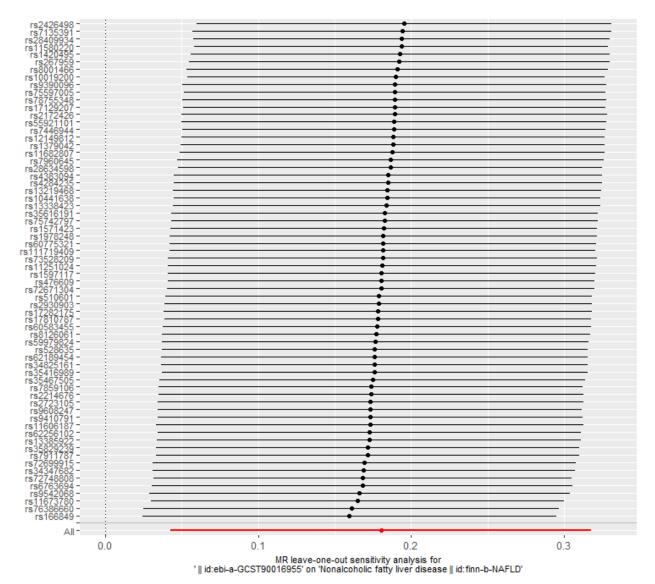
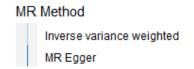
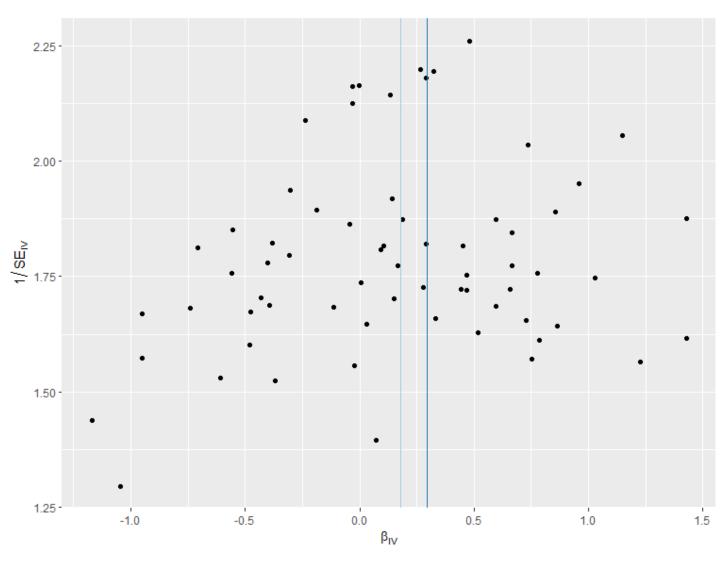
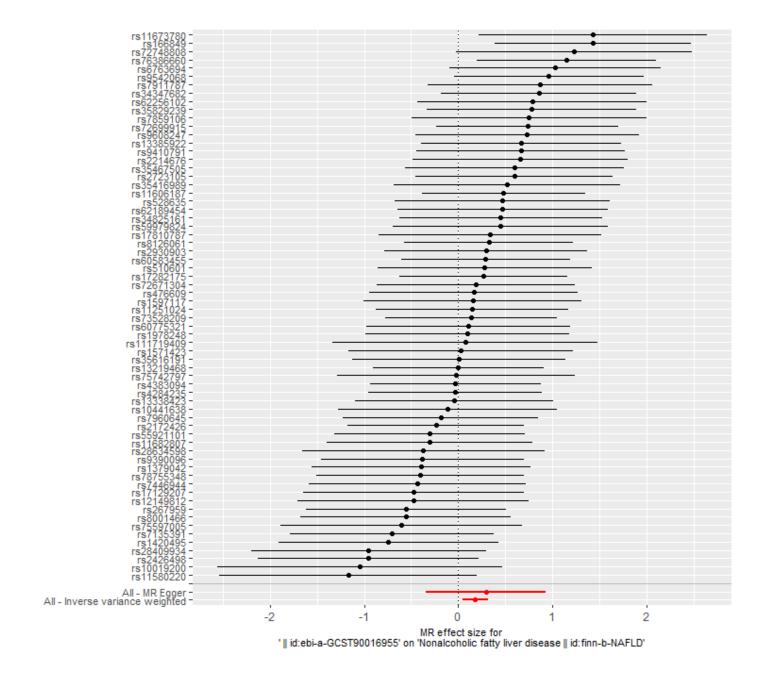


Figure 151 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown family id.1000006161) on nonalcoholic fatty liver disease









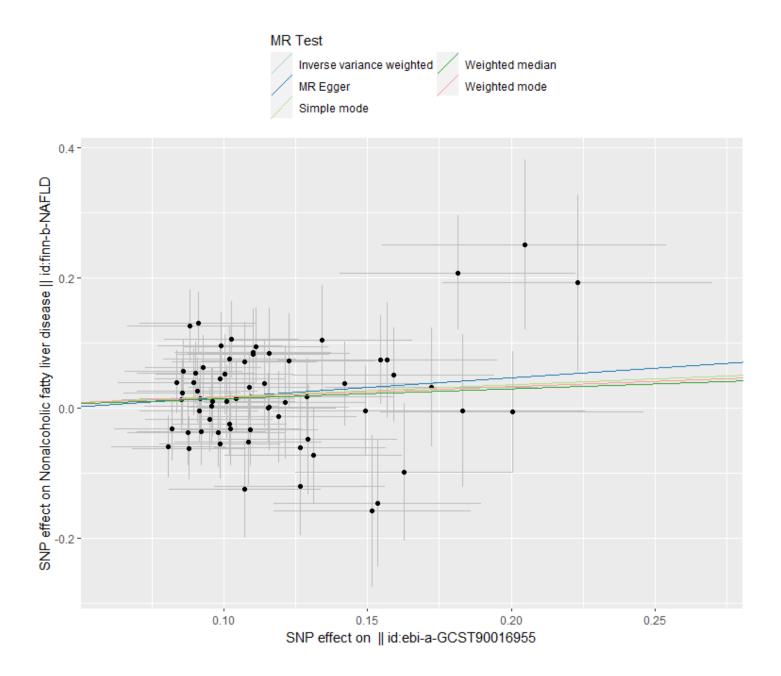
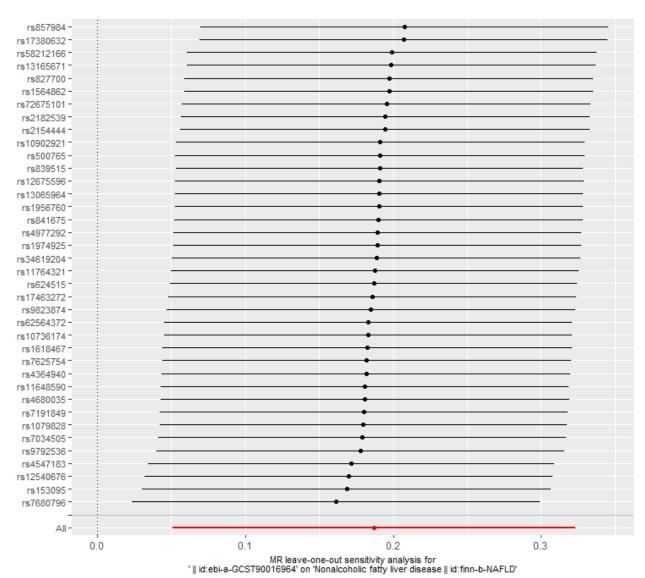
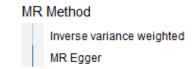
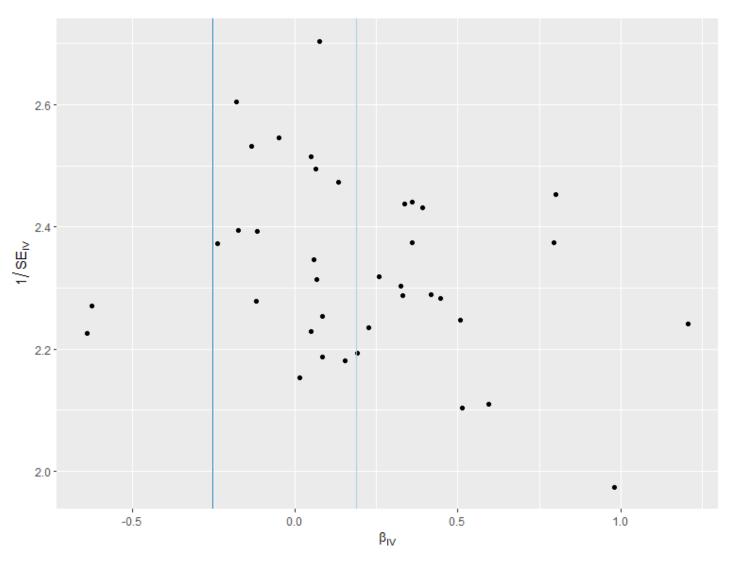
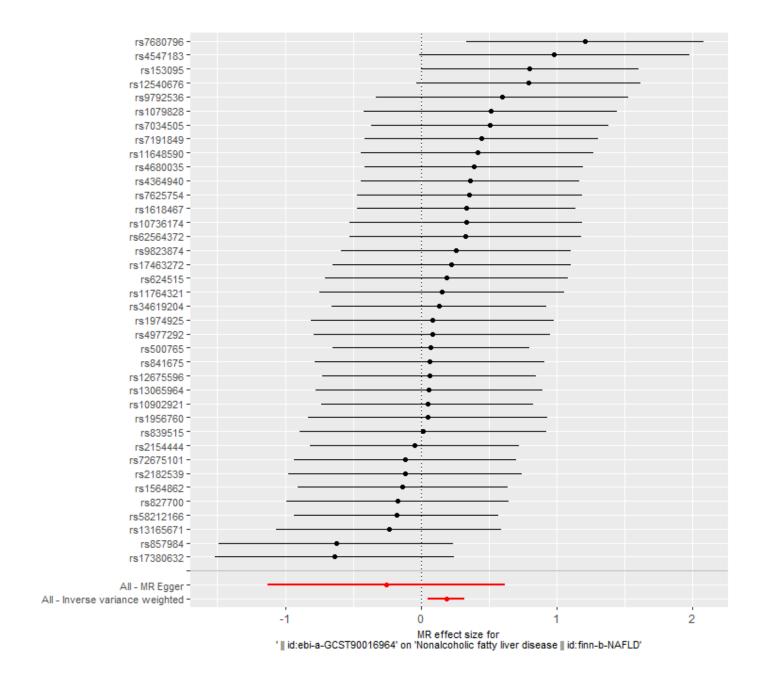


Figure 152 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Alloprevotella id.961) on nonalcoholic fatty liver disease











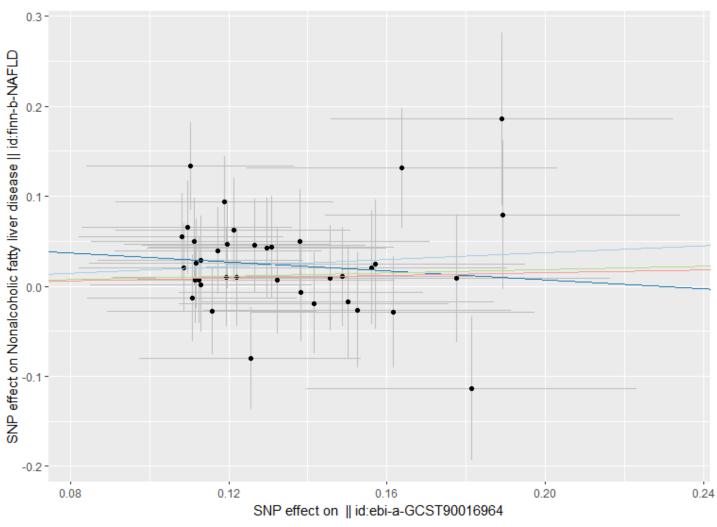
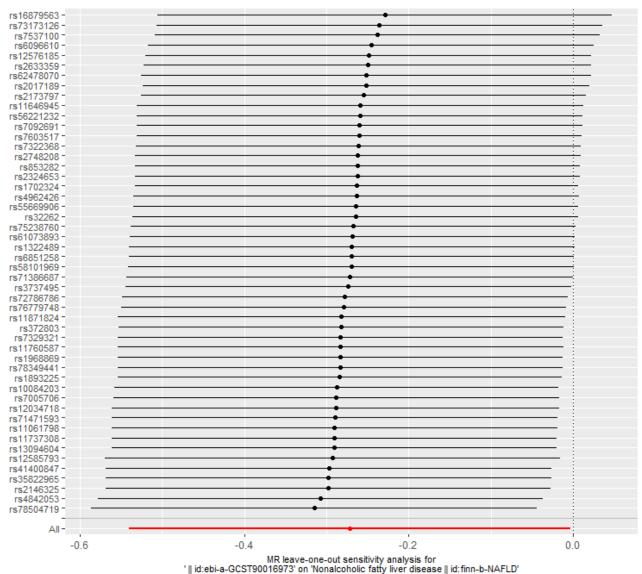
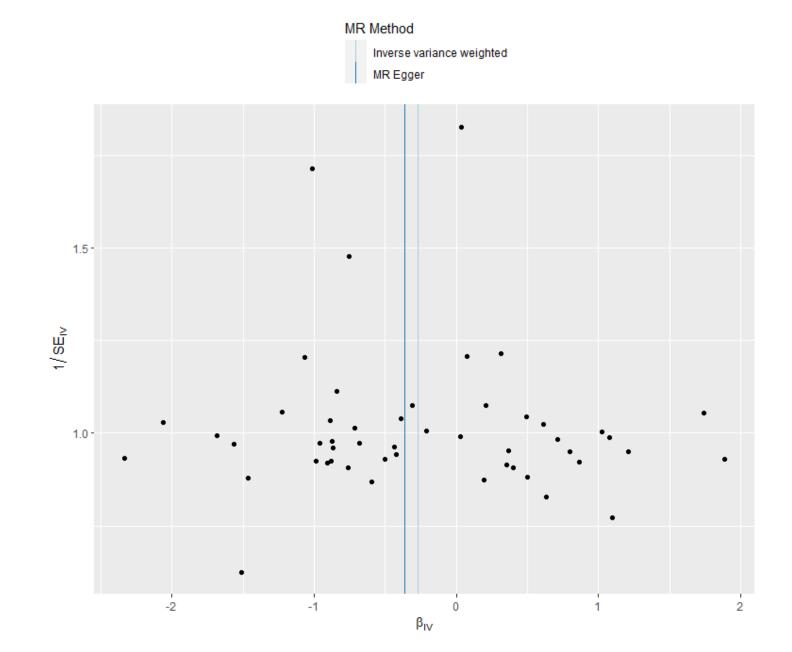
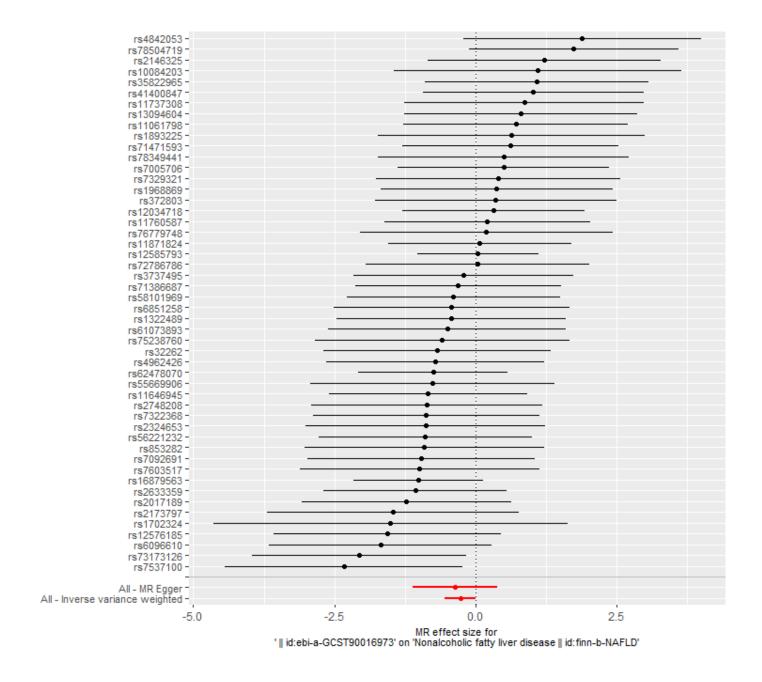


Figure 153 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Butyricicoccus id.2055) on nonalcoholic fatty liver disease







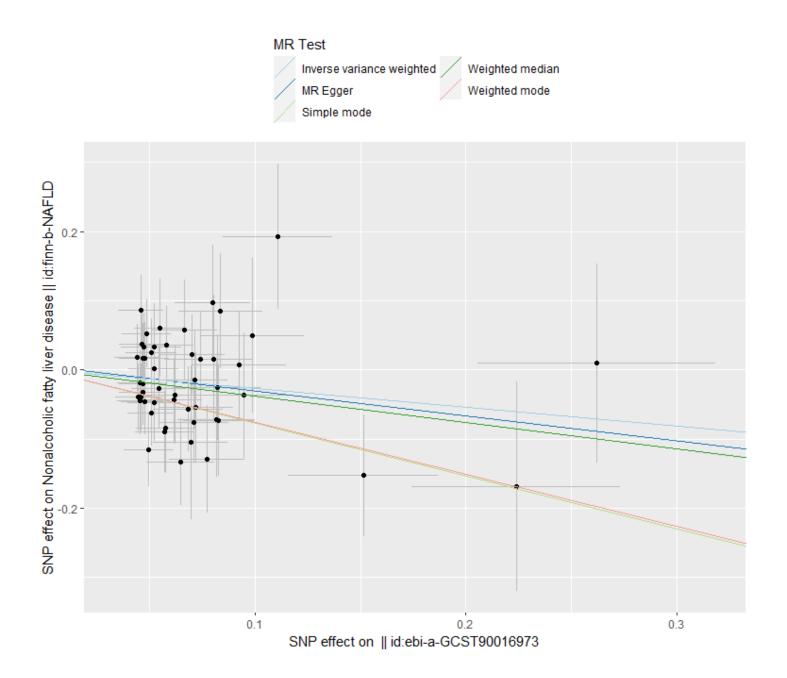
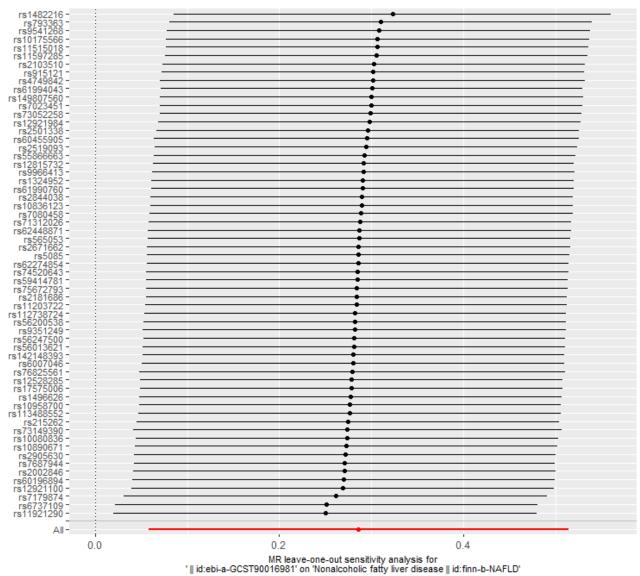
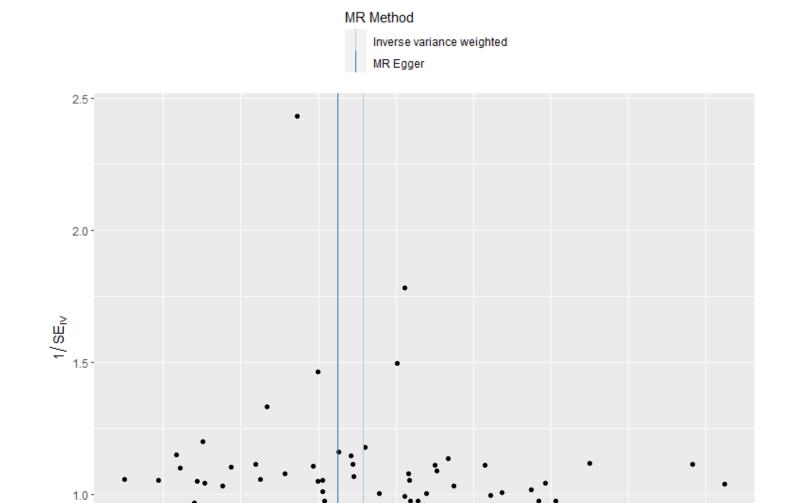


Figure 154 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Collinsella id.815) on nonalcoholic fatty liver disease



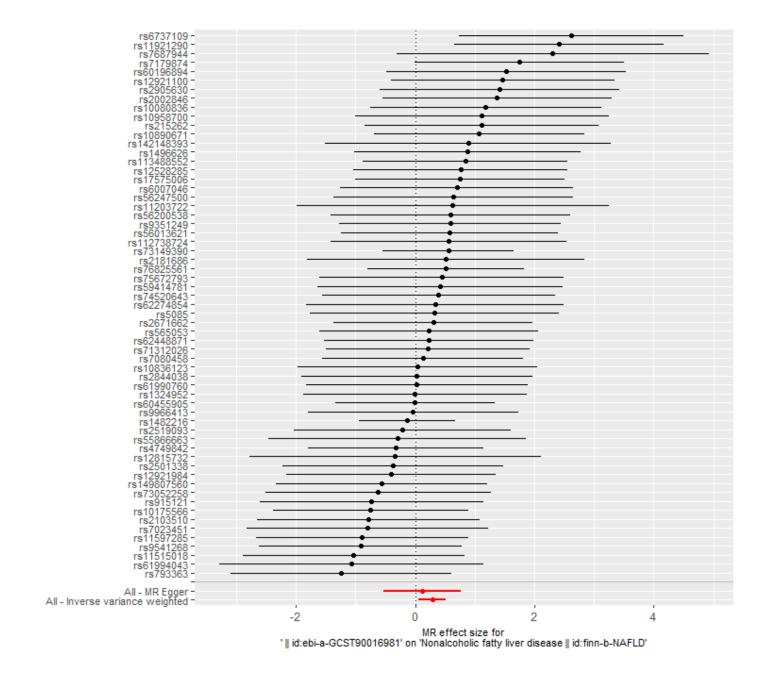


 β_{IV}

2

0

-1



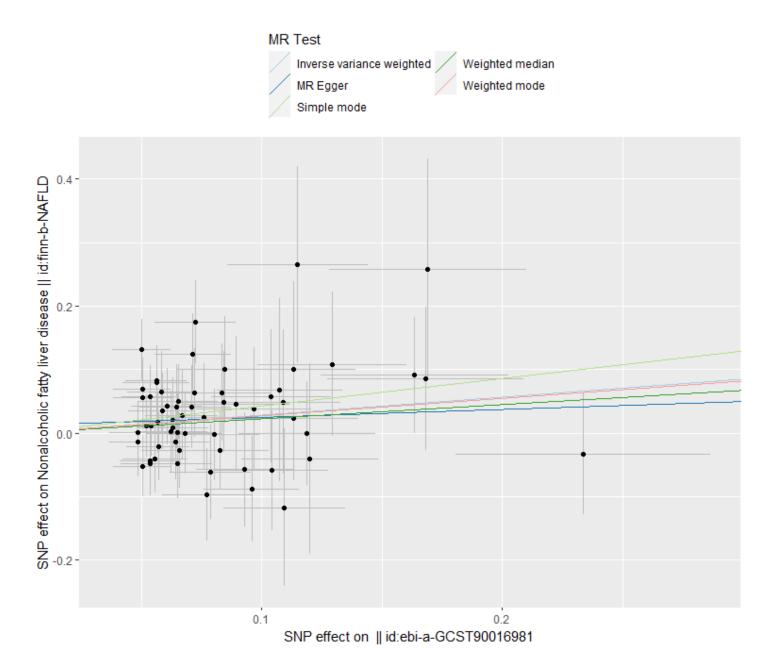
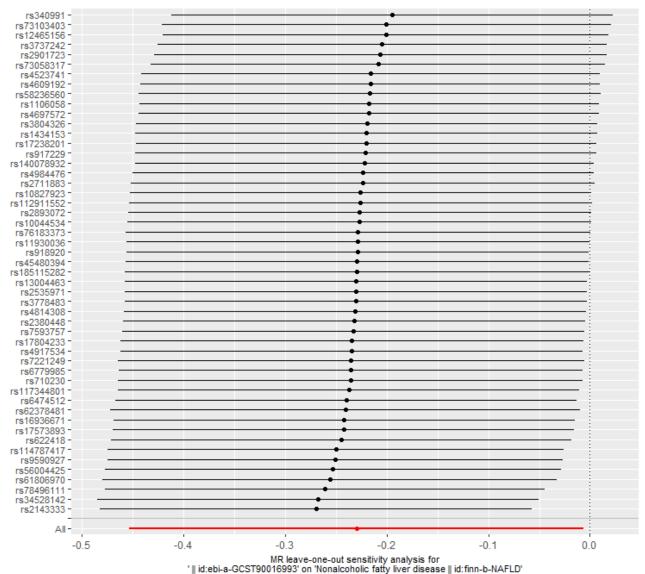
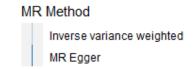
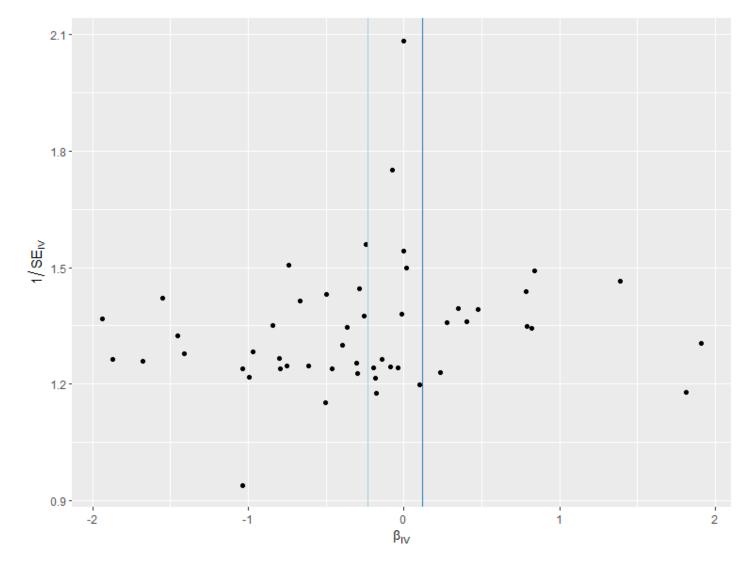
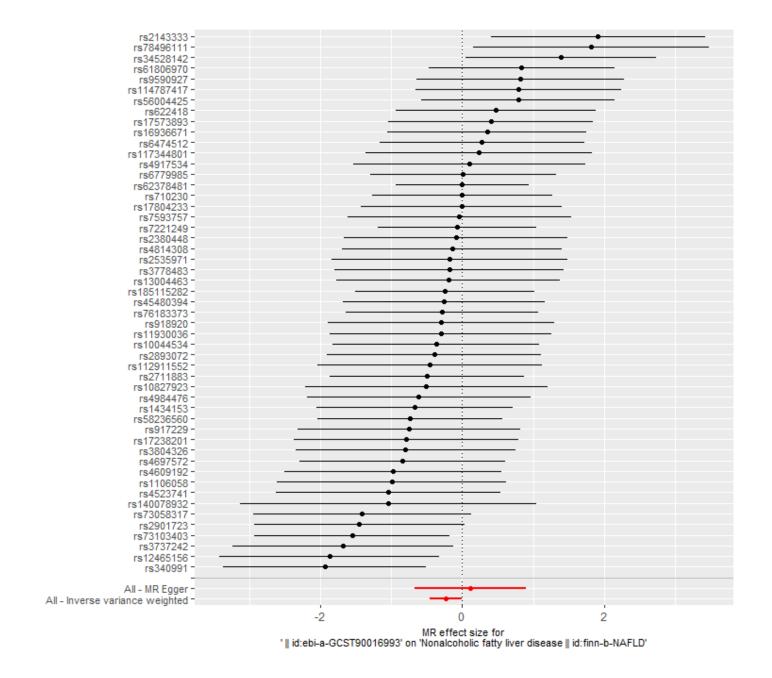


Figure 155 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Erysipelatoclostridium id.11381) on nonalcoholic fatty liver disease











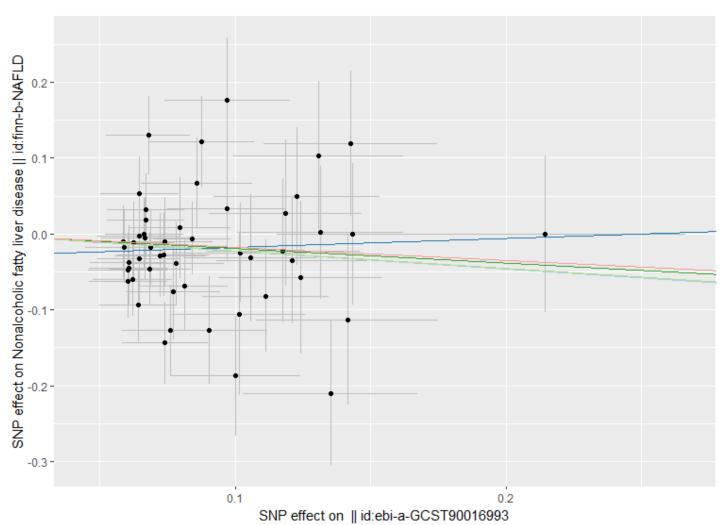
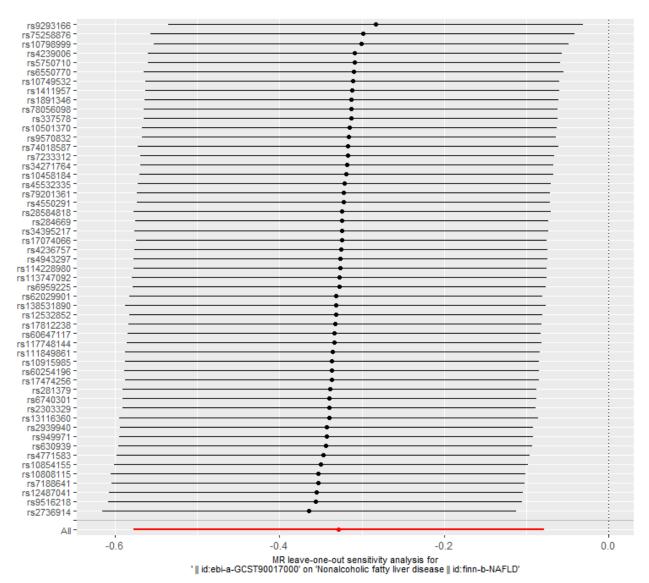
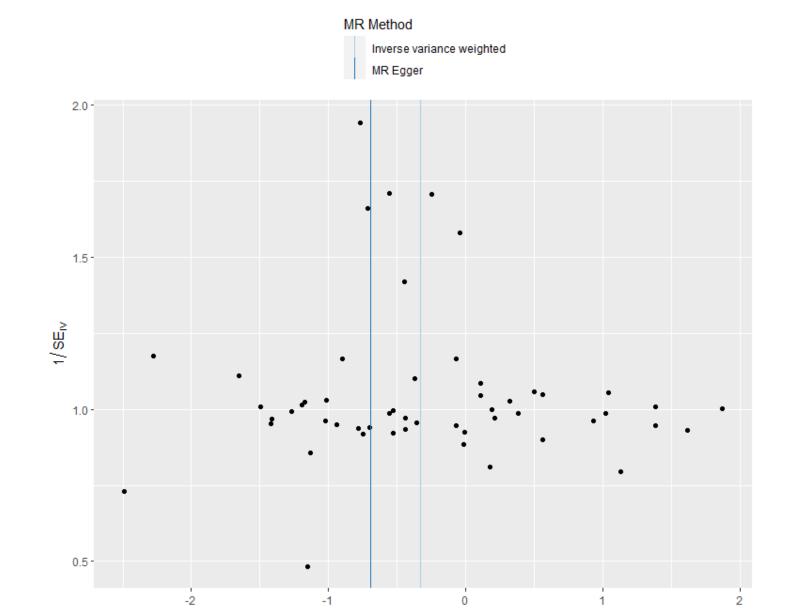
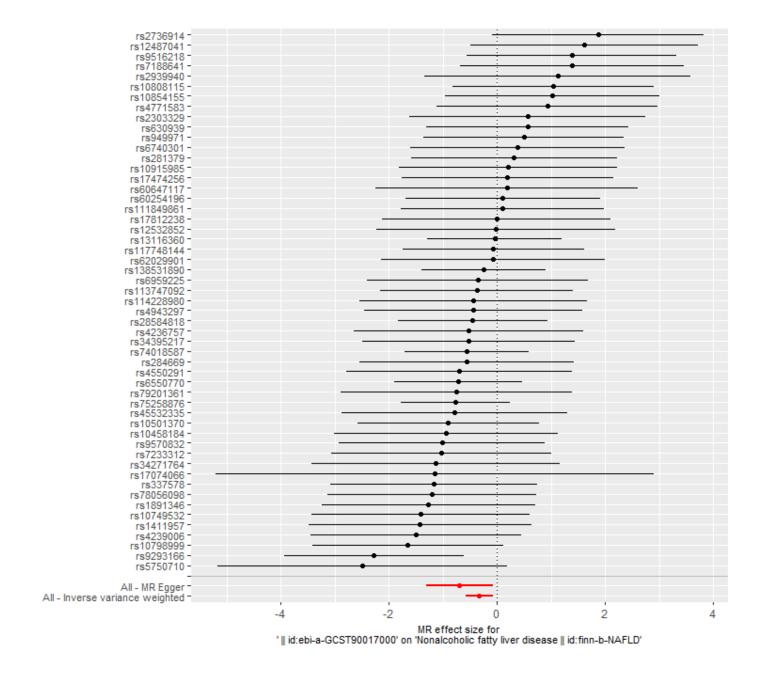


Figure 156 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium hallii group id.11338) on nonalcoholic fatty liver disease





 β_{IV}



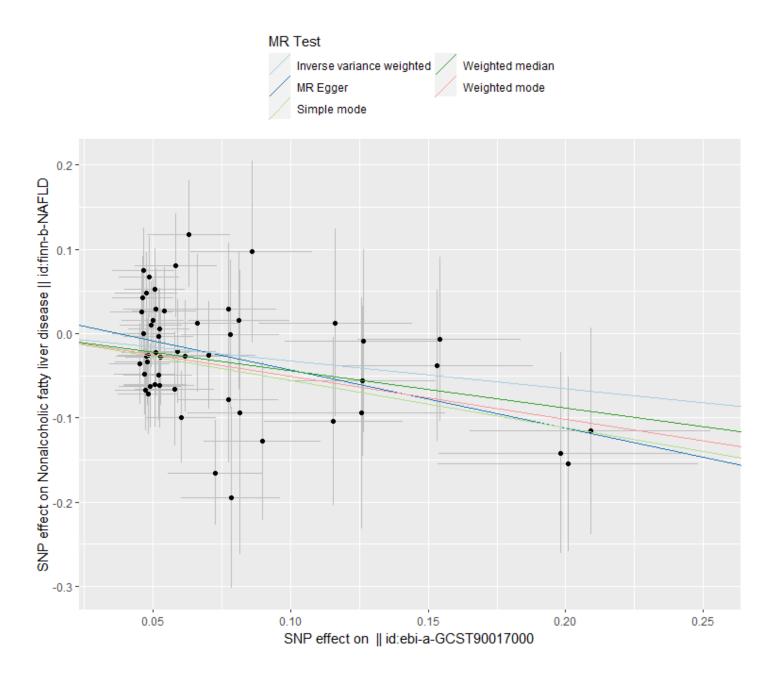
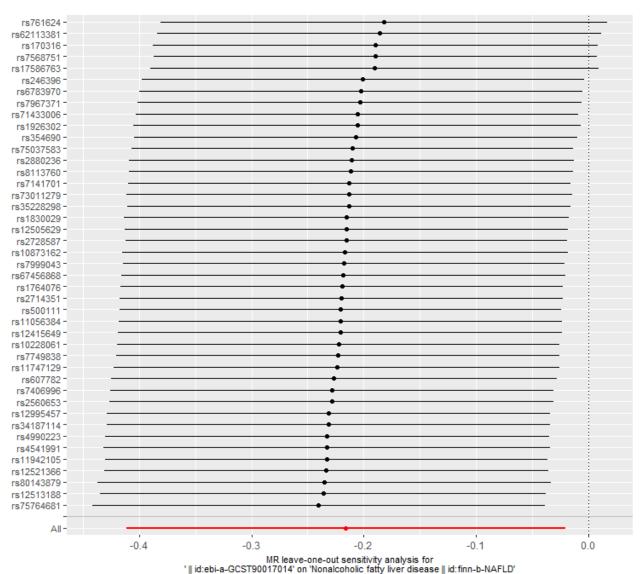
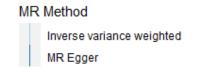
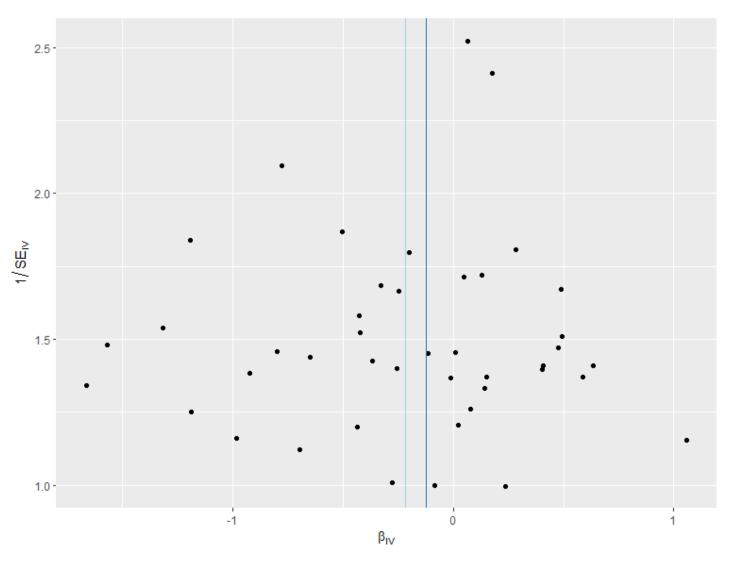
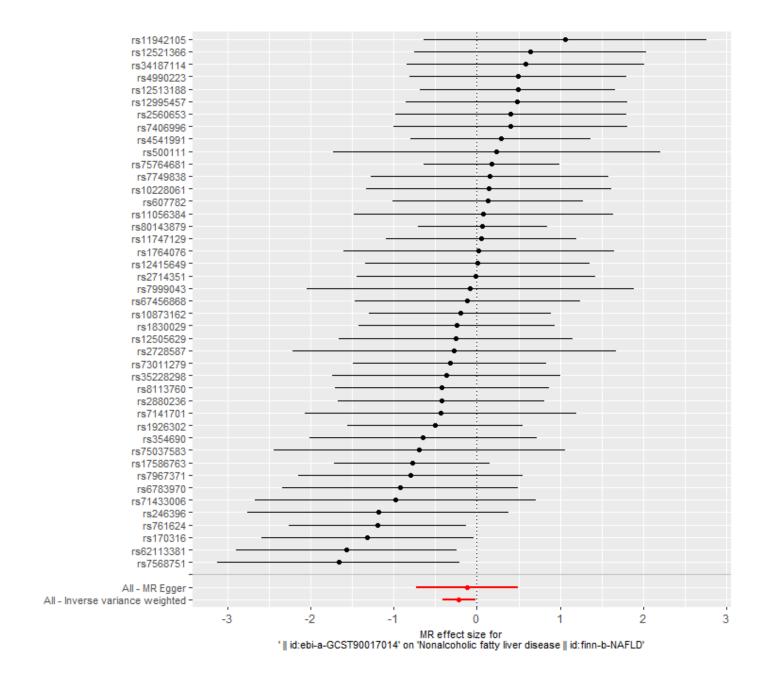


Figure 157 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Holdemanella id.11393) on nonalcoholic fatty liver disease











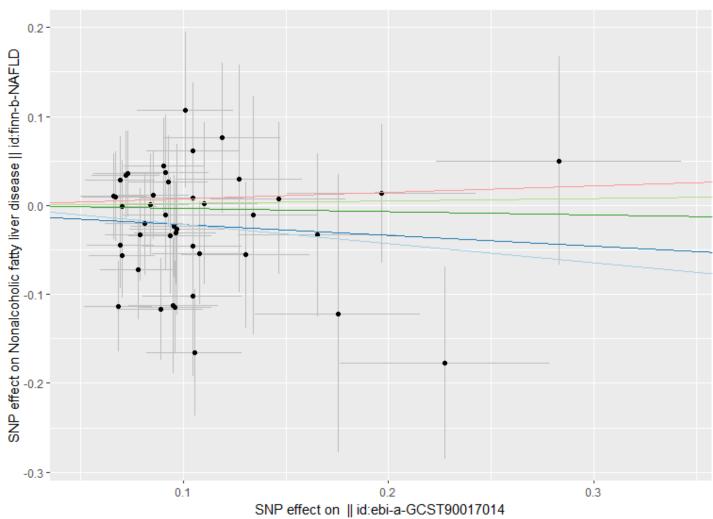
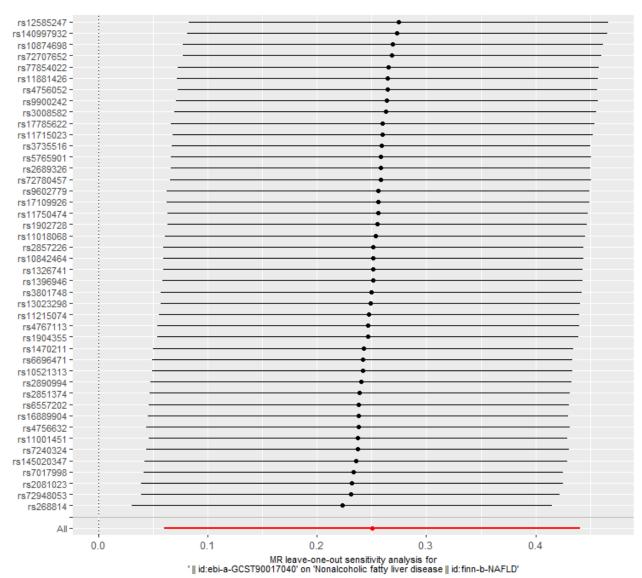
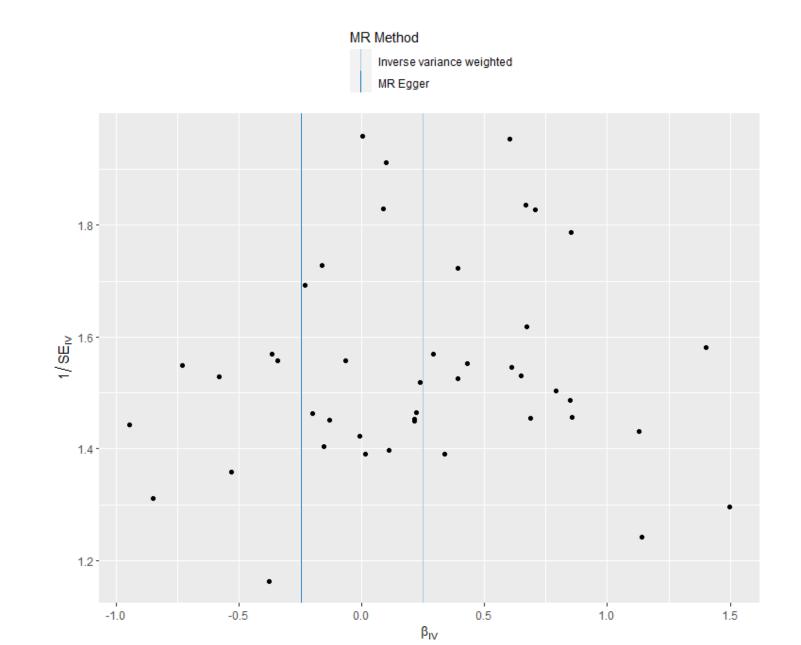
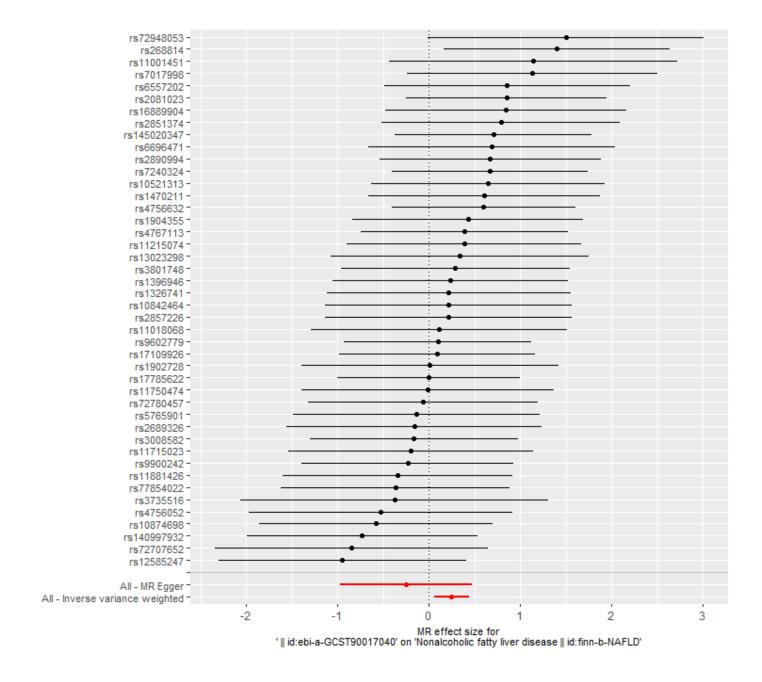
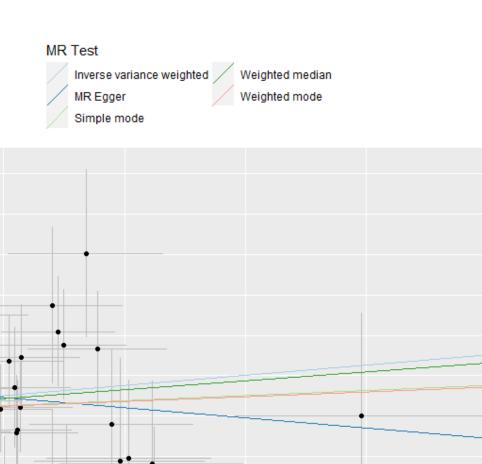


Figure 158 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Paraprevotella id.962) on nonalcoholic fatty liver disease









0.2

SNP effect on || id:ebi-a-GCST90017040

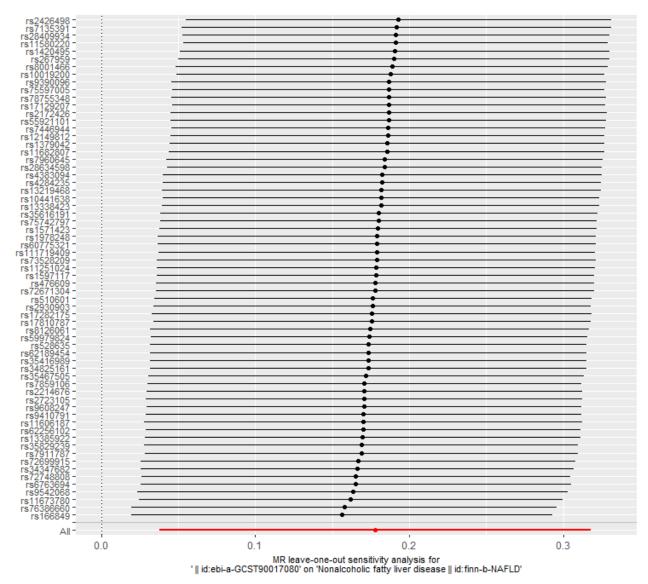
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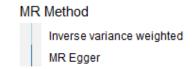
0.3 -

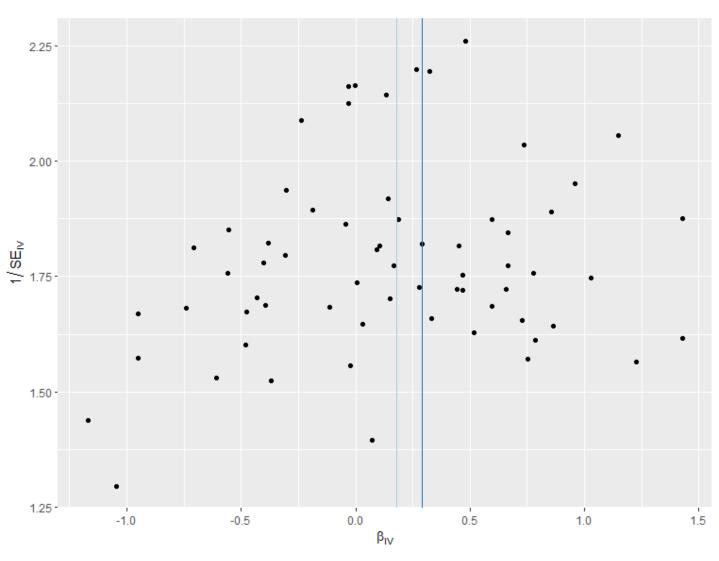
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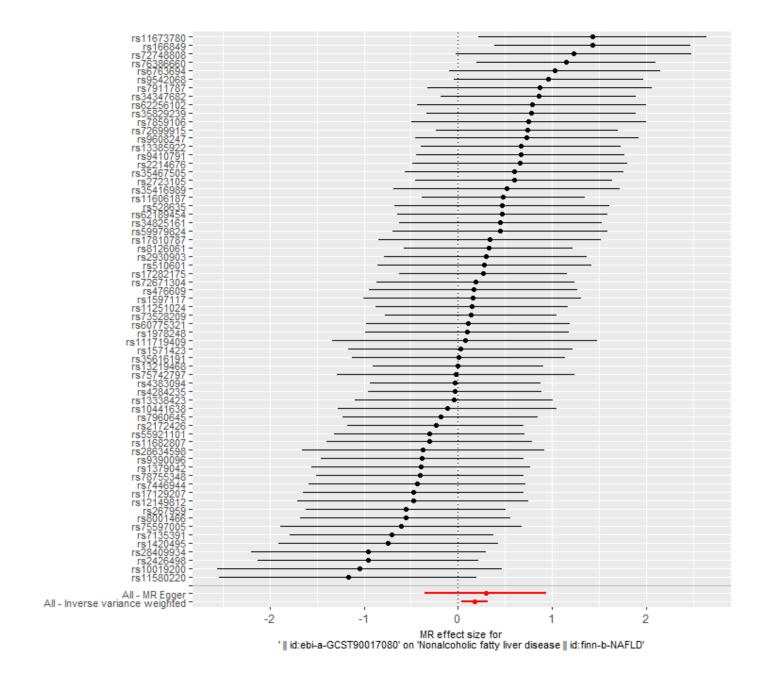
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Figure 159 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.1000006162) on nonalcoholic fatty liver disease









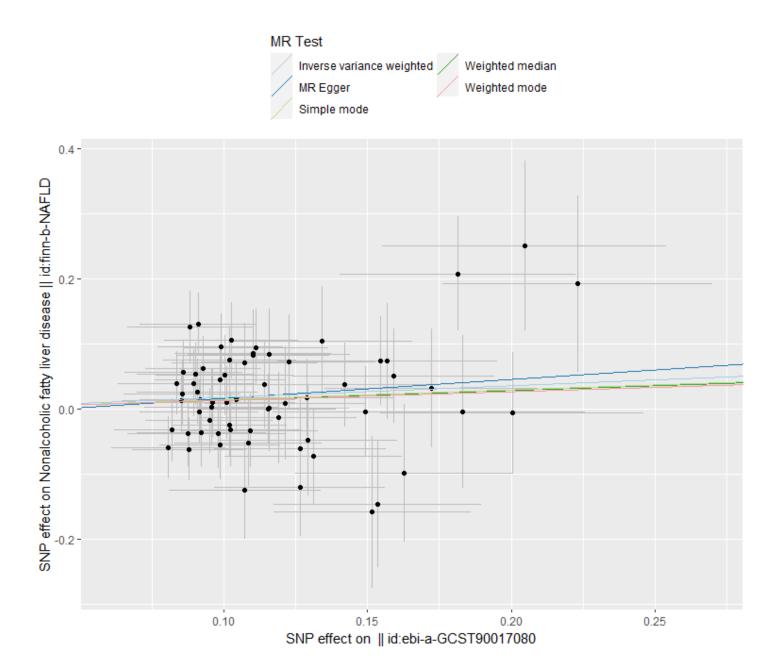
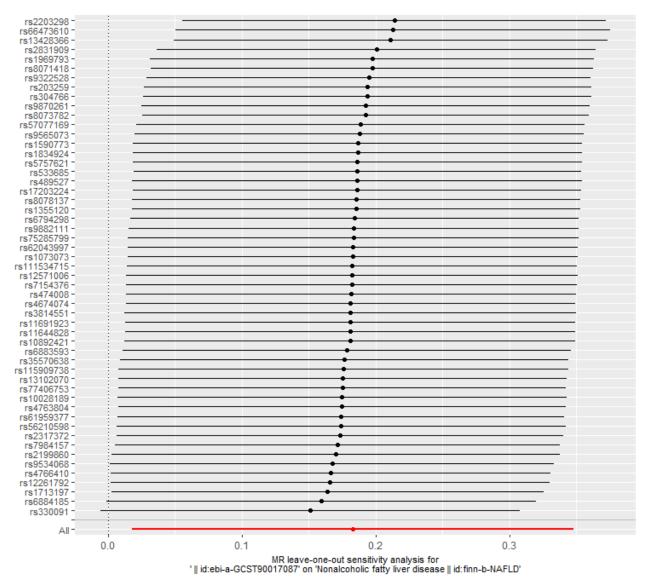
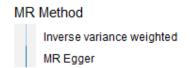
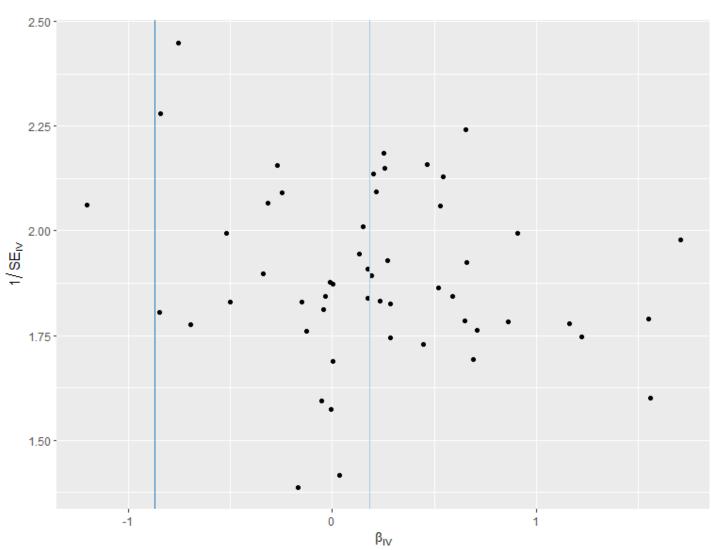
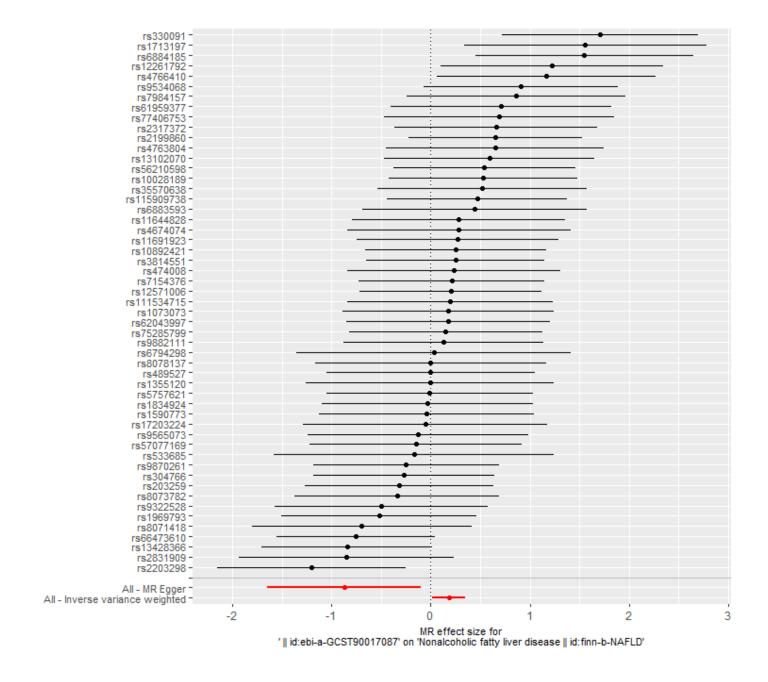


Figure 160 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.959) on nonalcoholic fatty liver disease









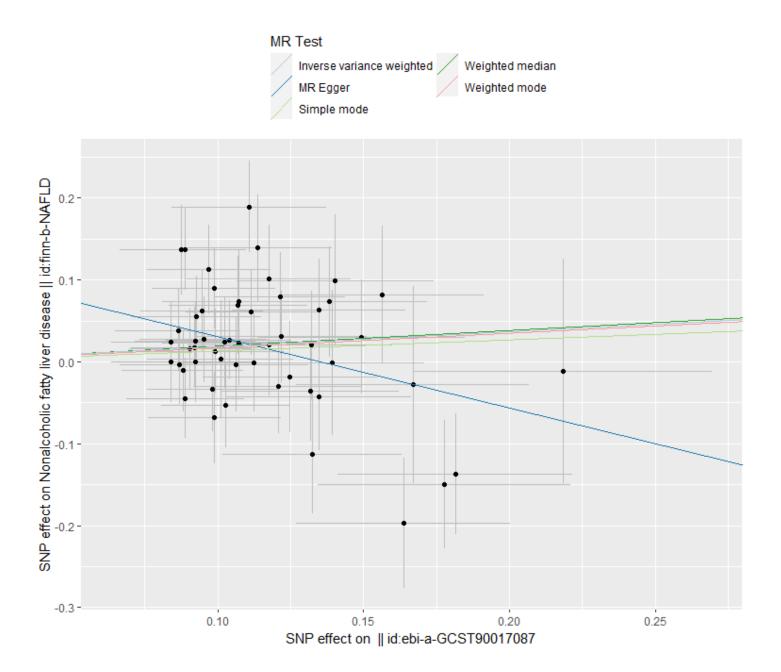
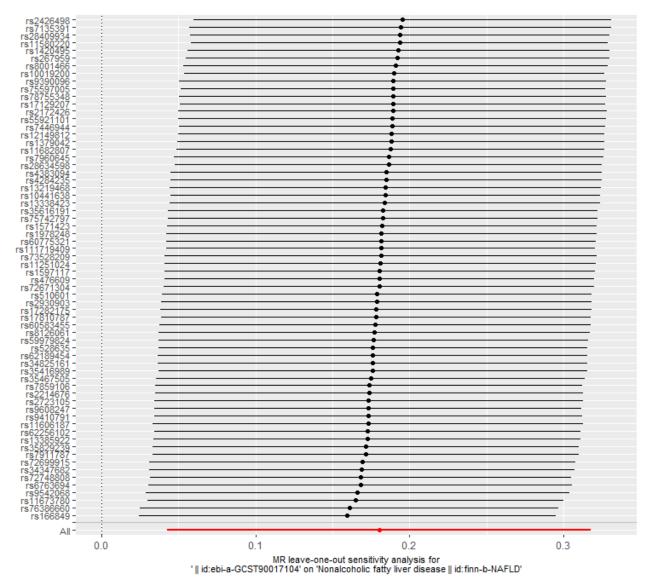
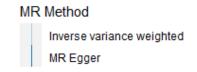
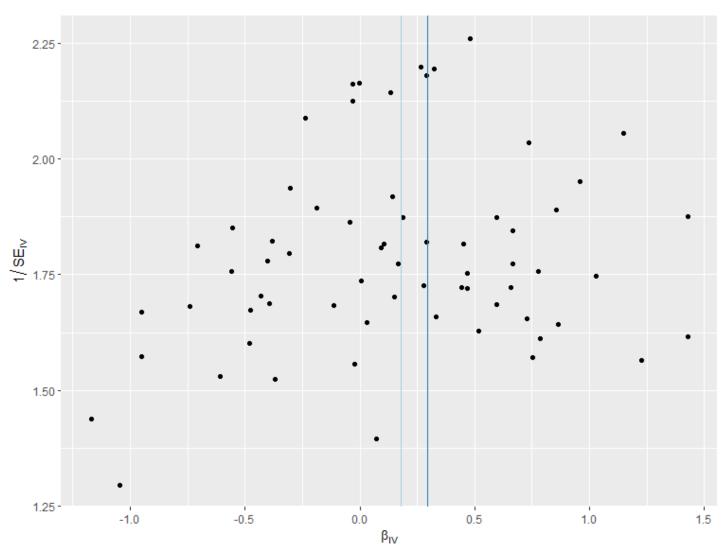
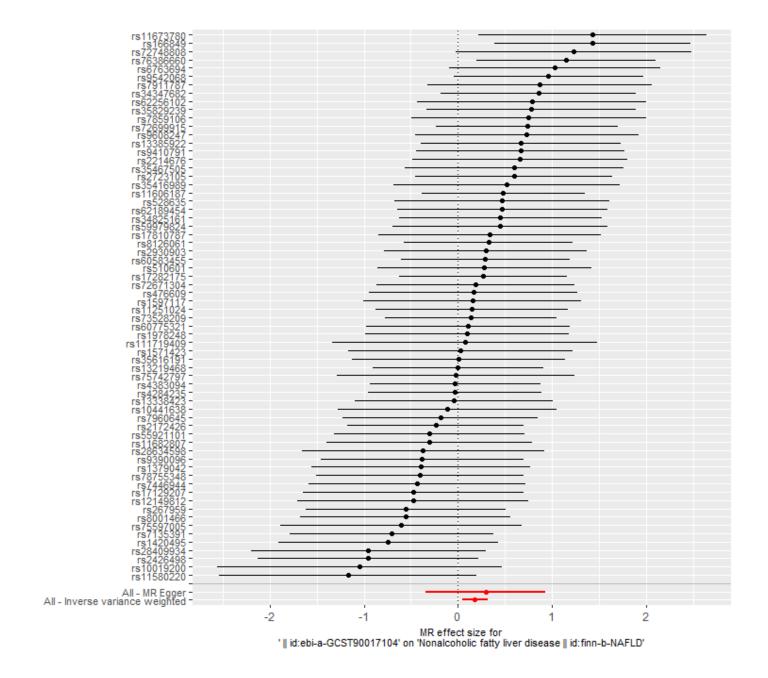


Figure 161 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order NB1n id.3953) on nonalcoholic fatty liver disease









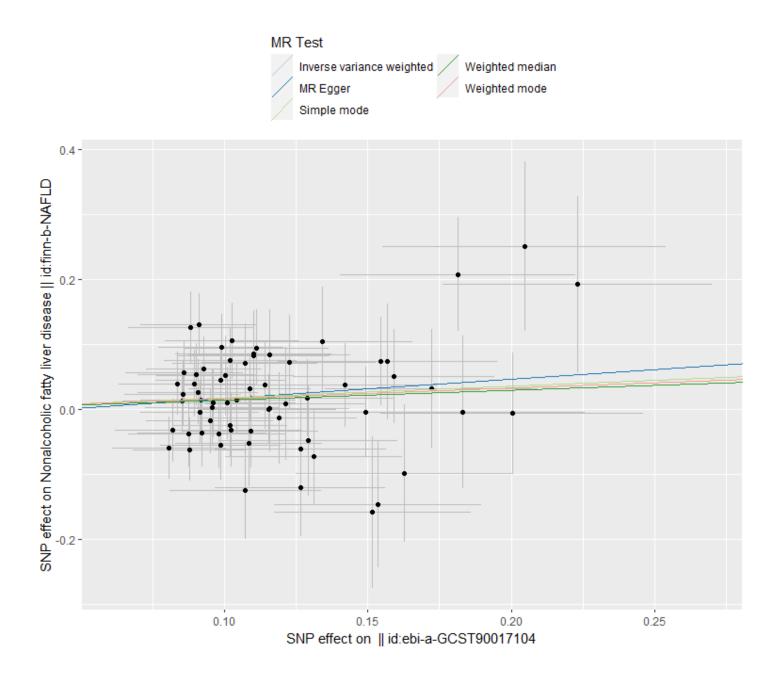
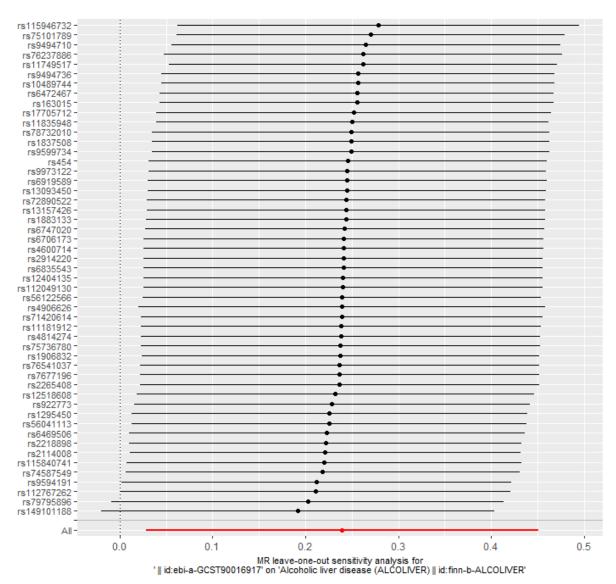
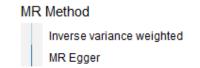
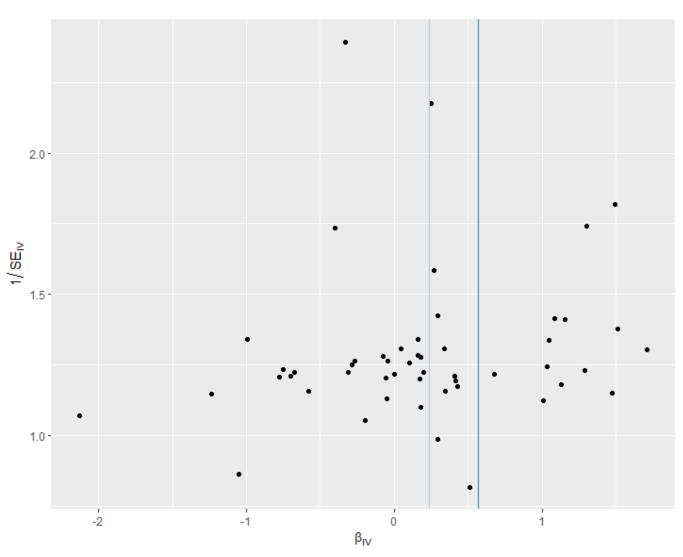
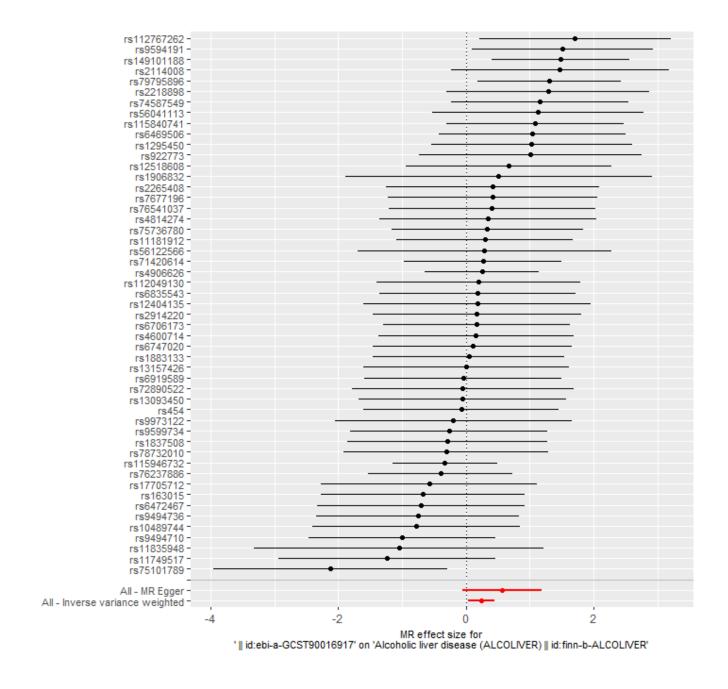


Figure 162 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Gammaproteobacteria id.3303) on alcoholic liver disease









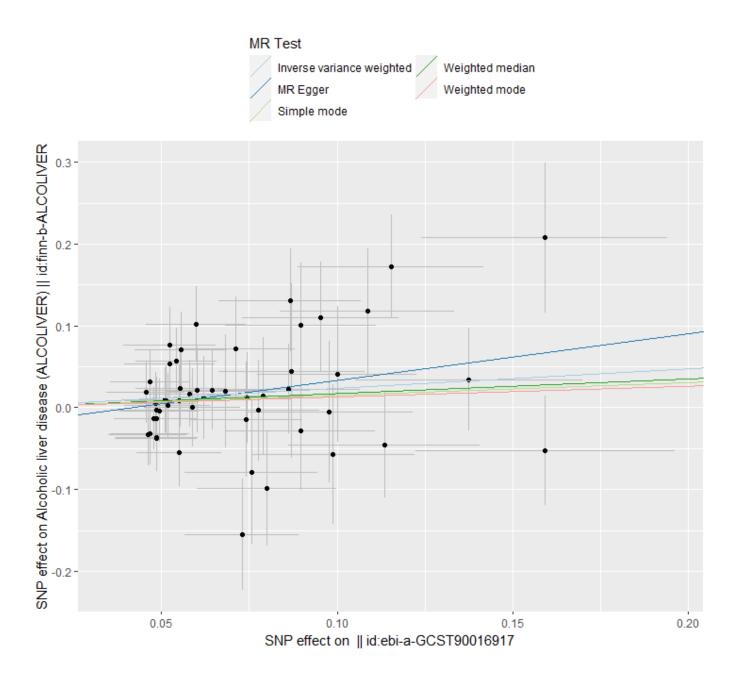
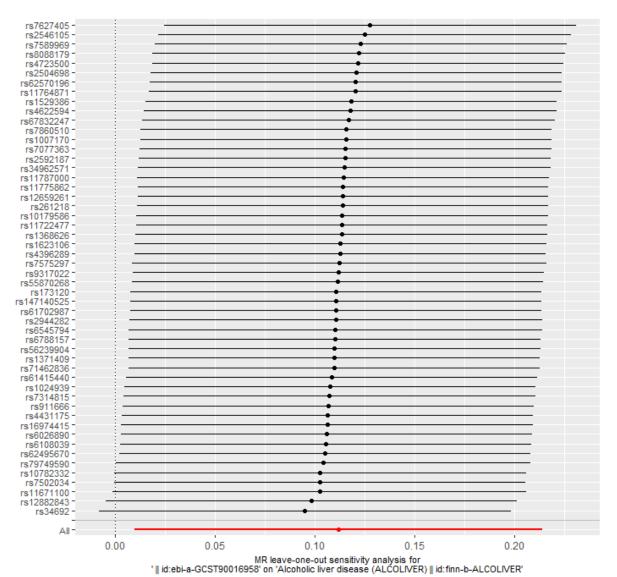
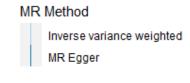
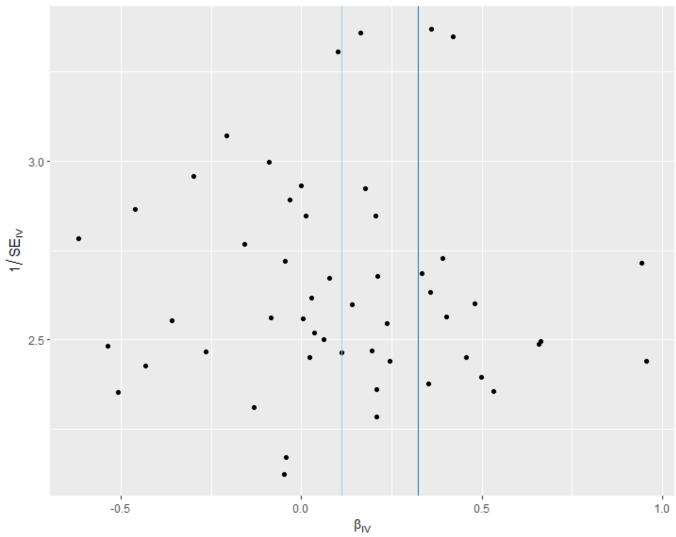
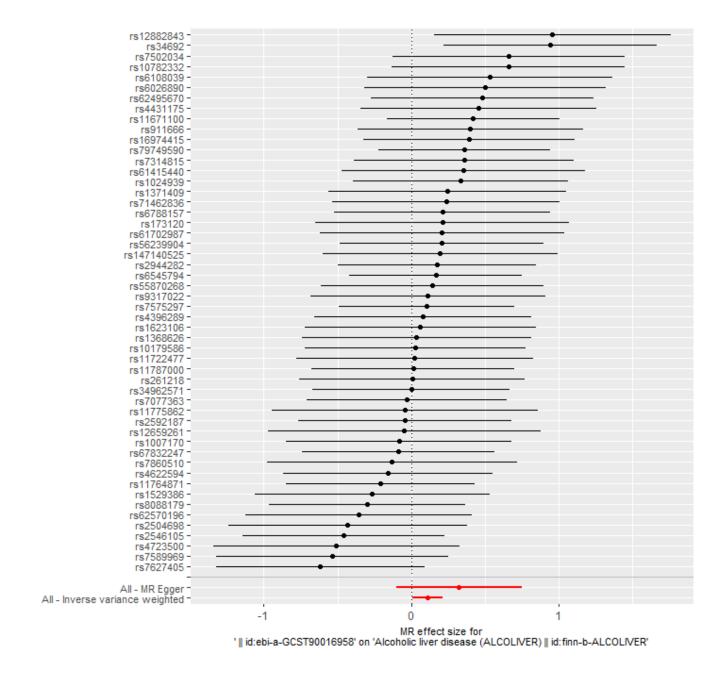


Figure 163 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Victivallaceae id.2255) on alcoholic liver disease









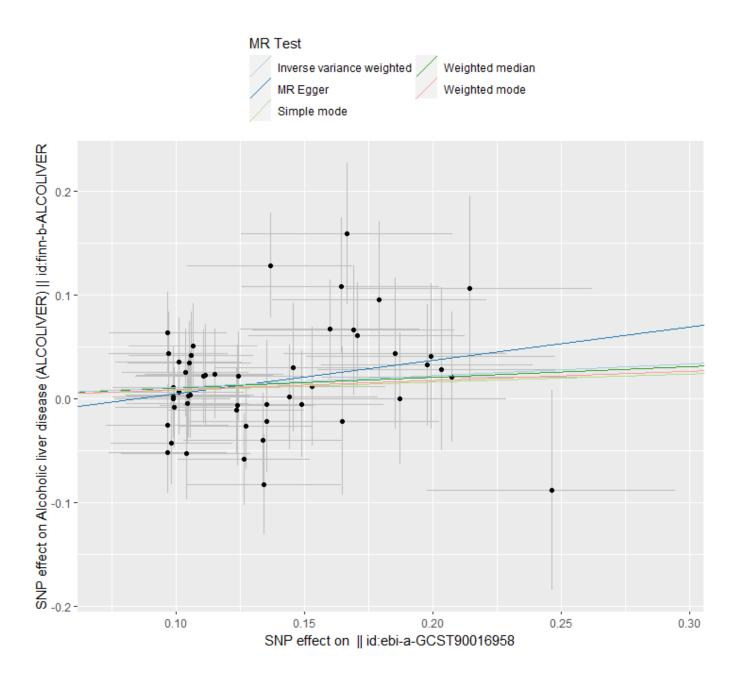
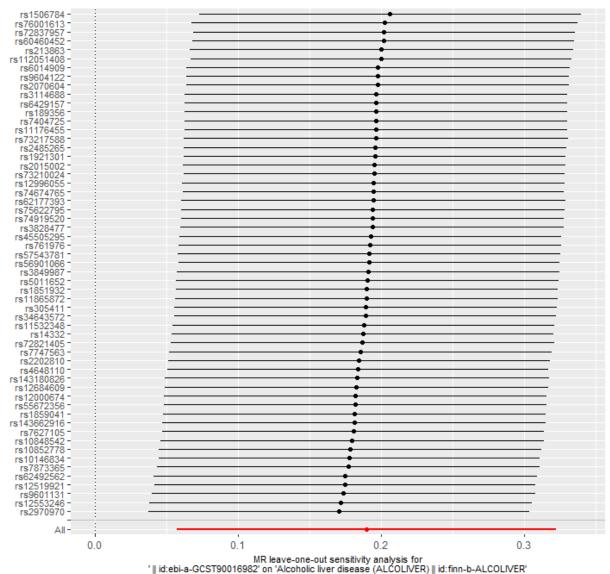
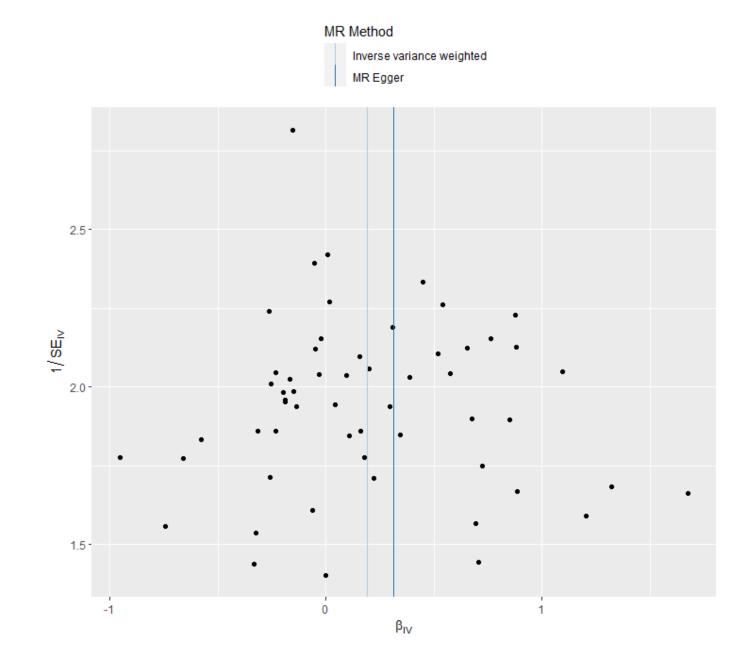
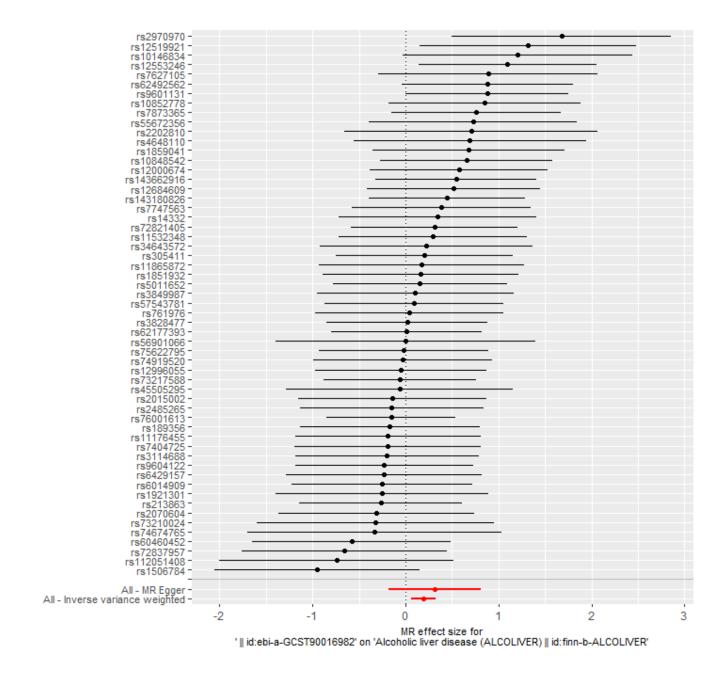


Figure 164 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Coprobacter id.949) on alcoholic liver disease







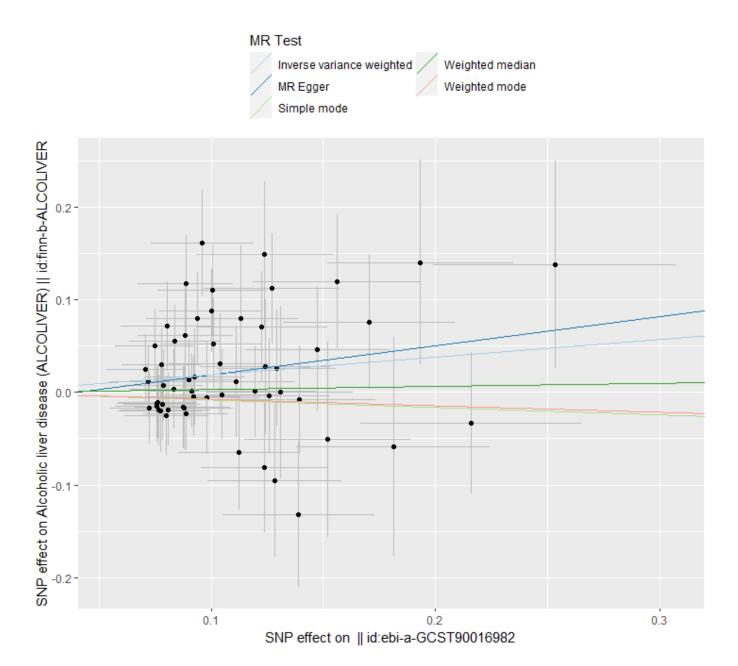
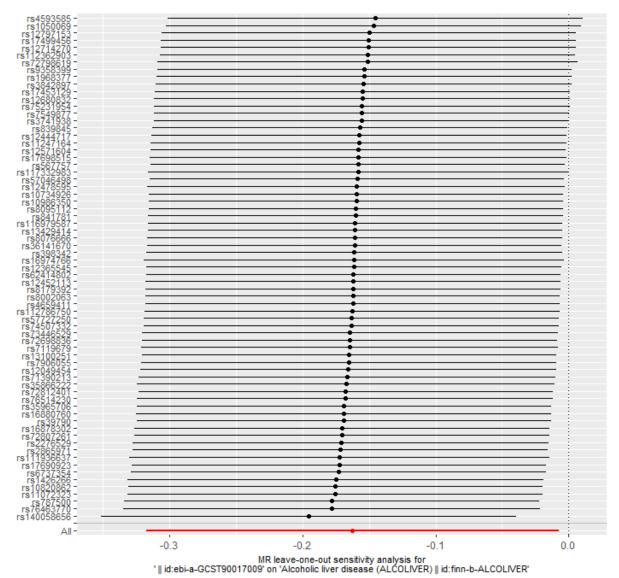
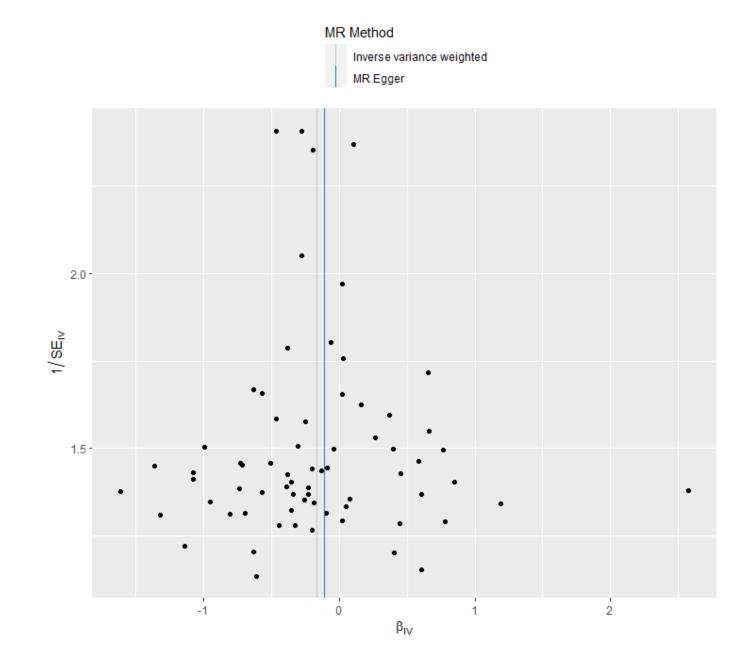
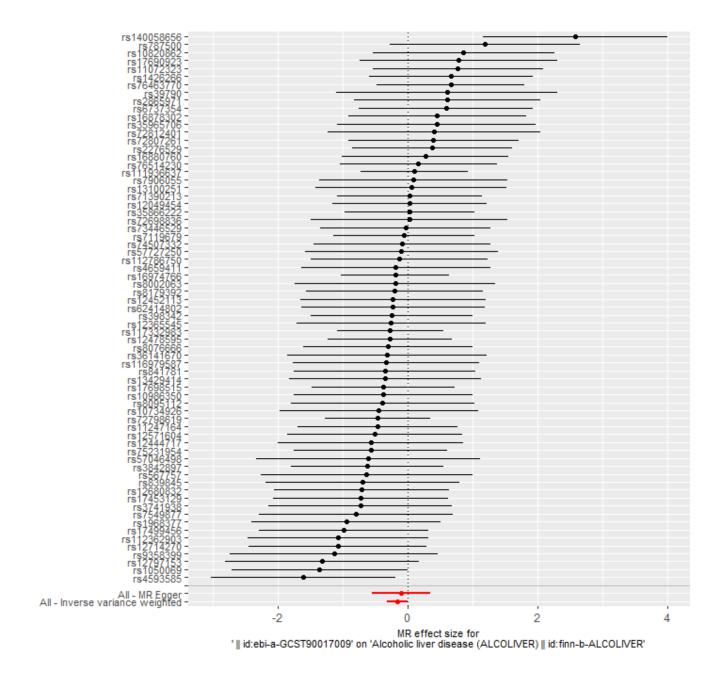


Figure 165 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Family XIII UCG001 id.11294) on alcoholic liver disease







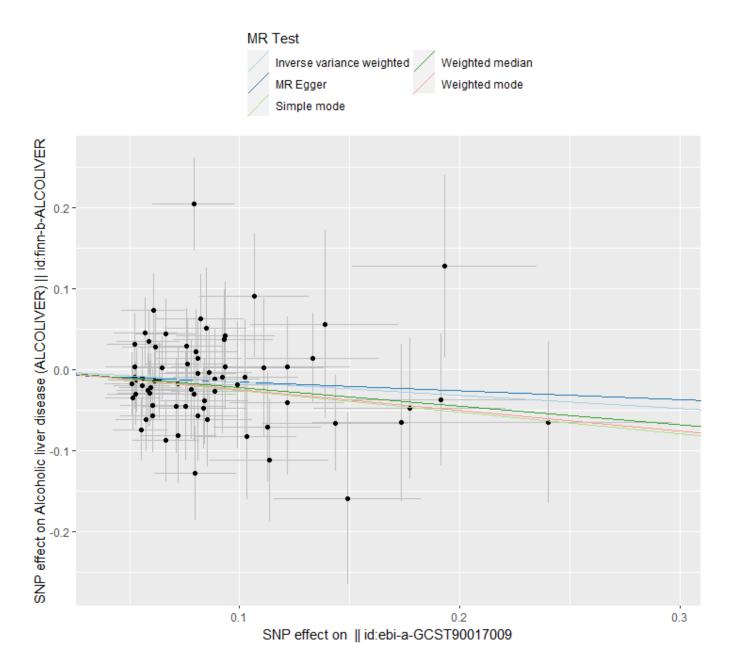
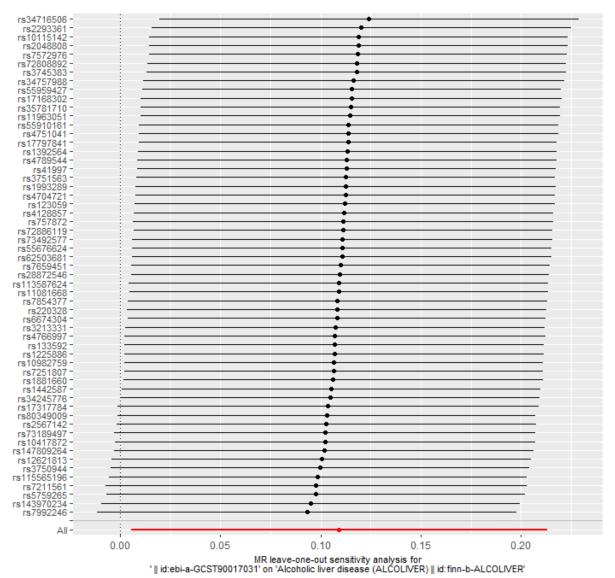
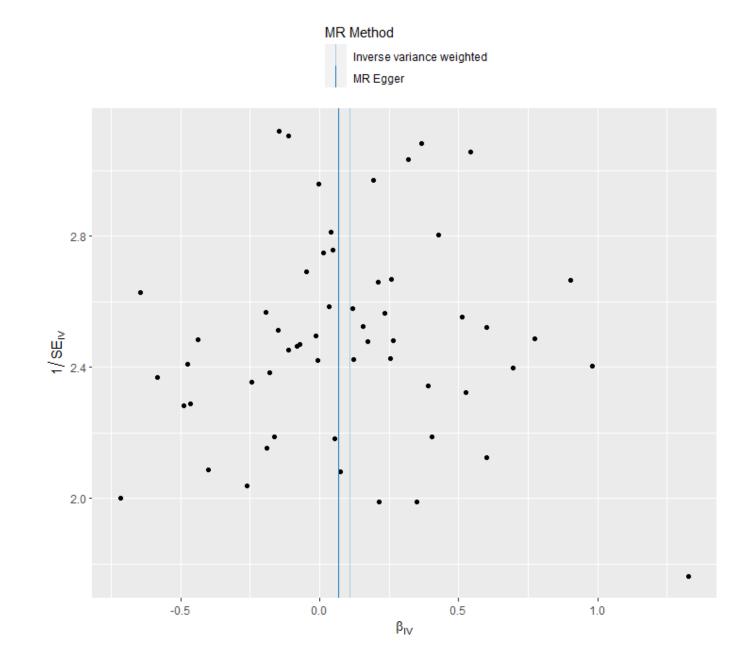
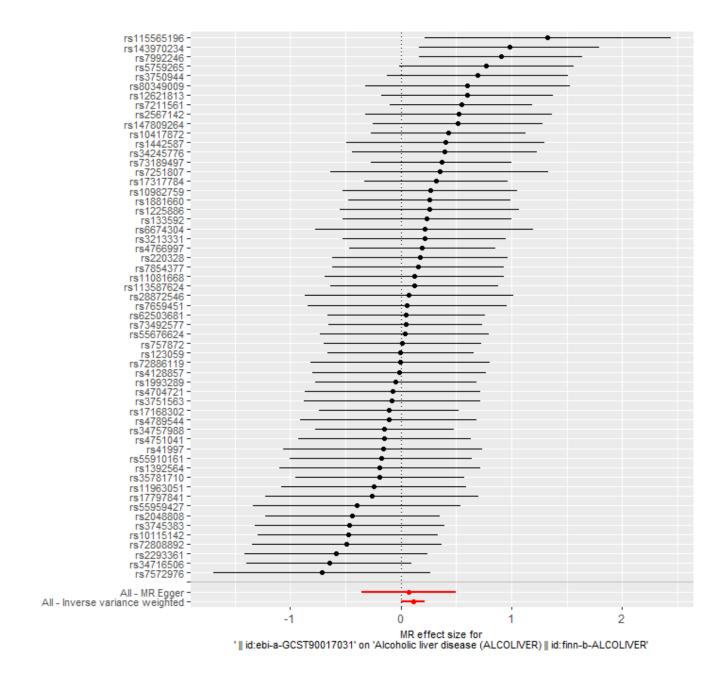


Figure 166 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lactococcus id.1851) on alcoholic liver disease







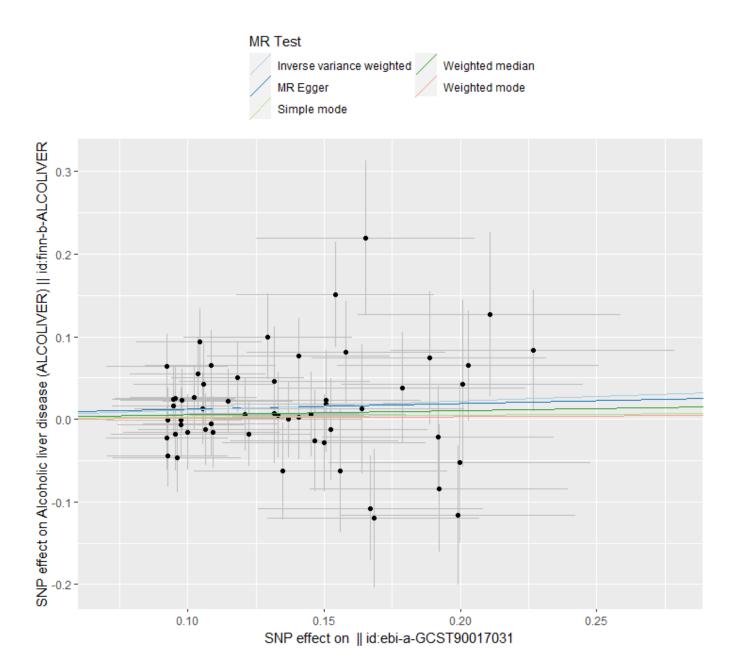
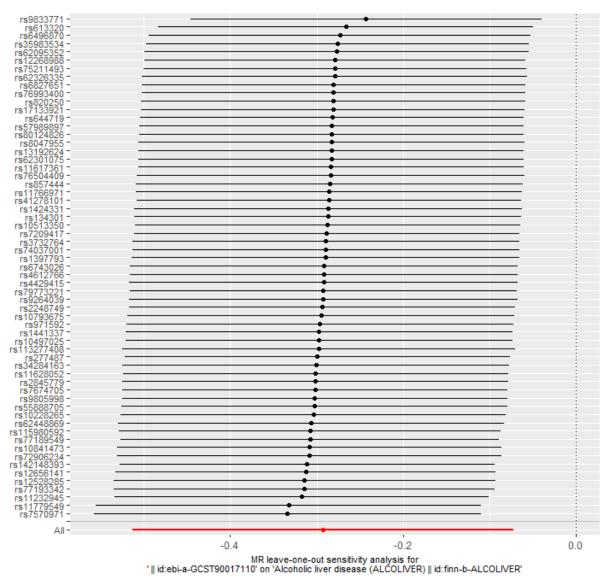
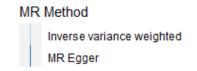
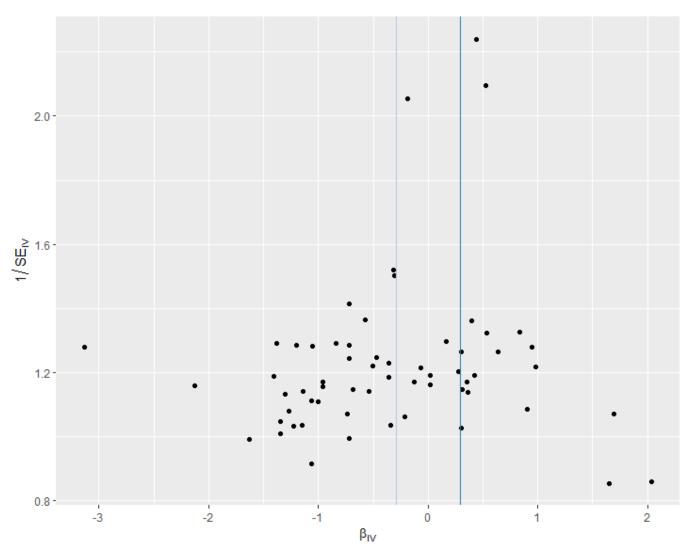
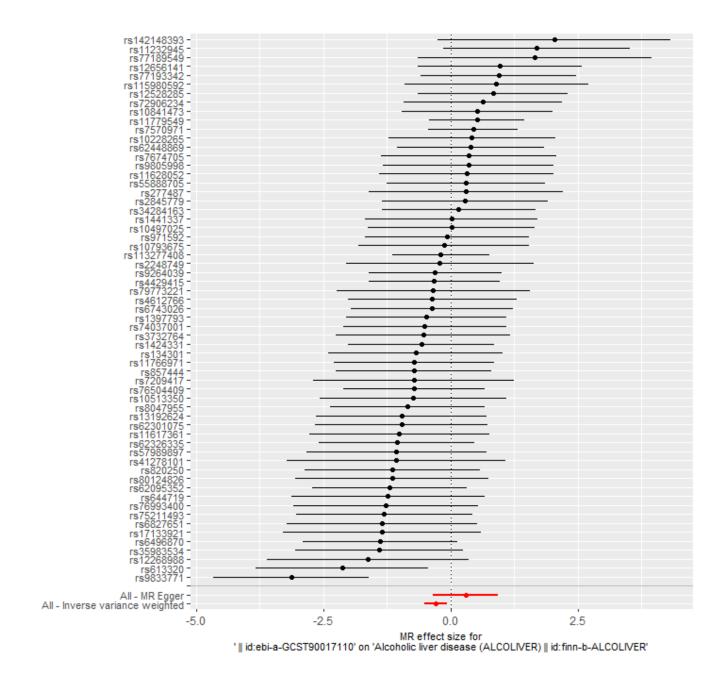


Figure 167 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Actinobacteria id.400) on alcoholic liver disease









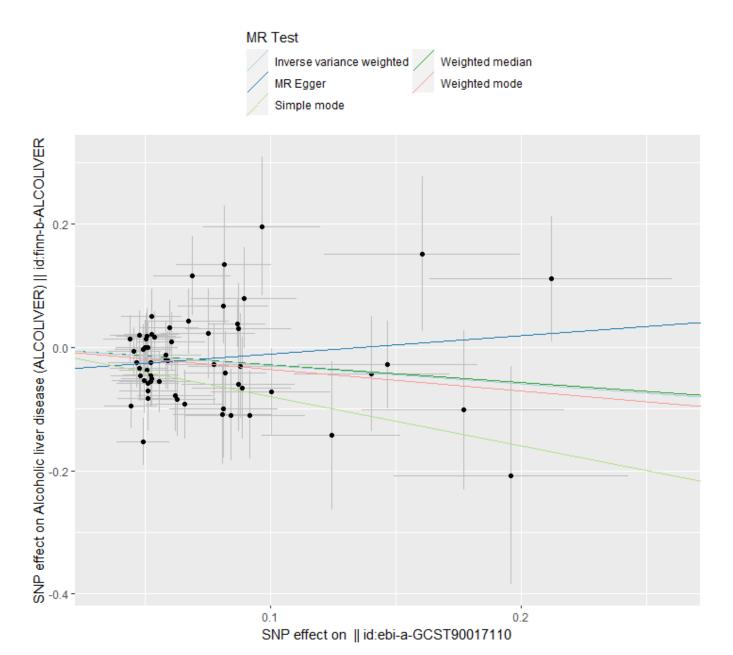
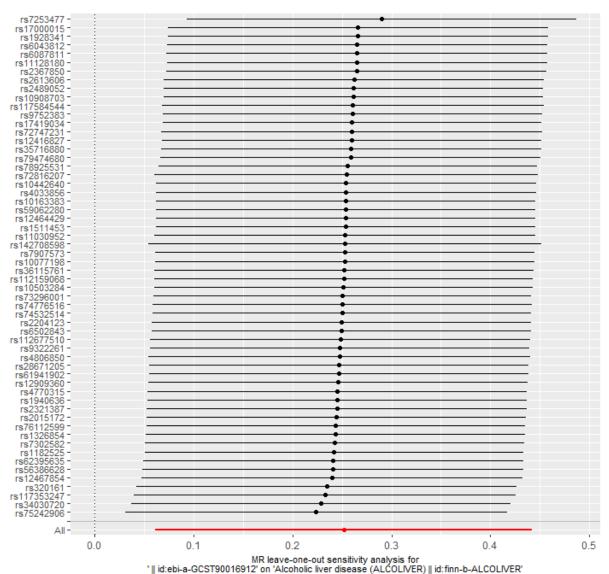
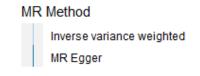
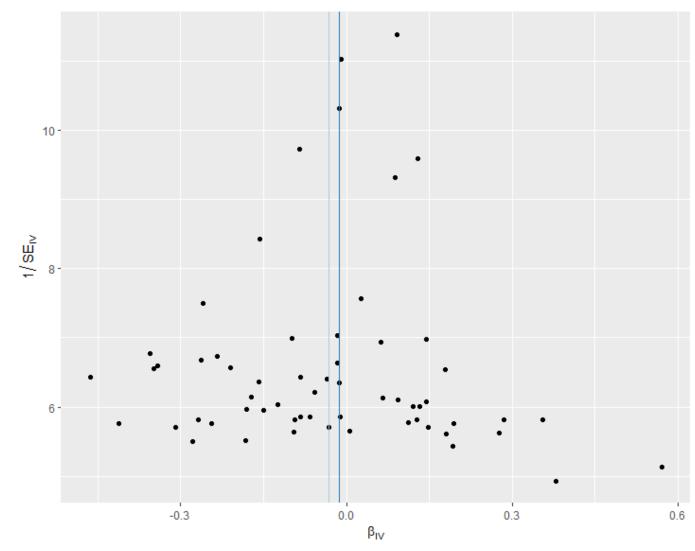
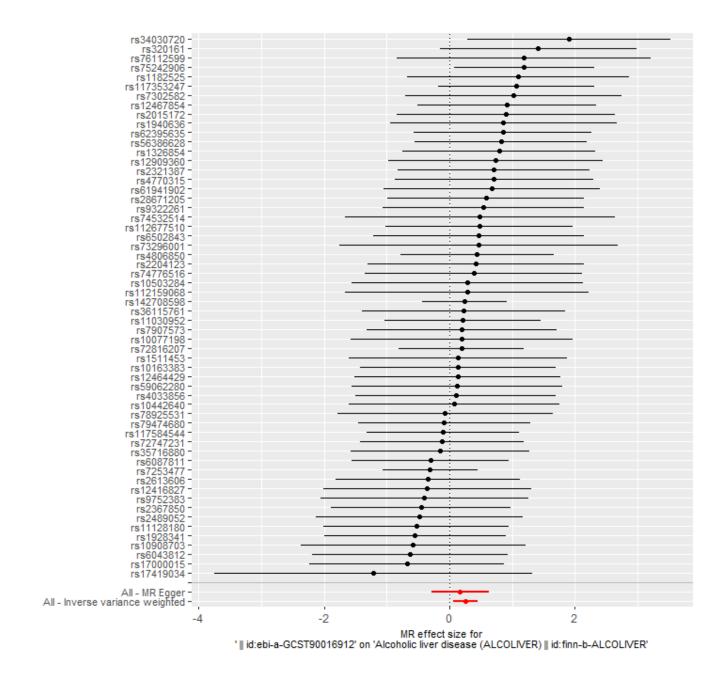


Figure 168 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Betaproteobacteria id.2867) on alcoholic liver disease









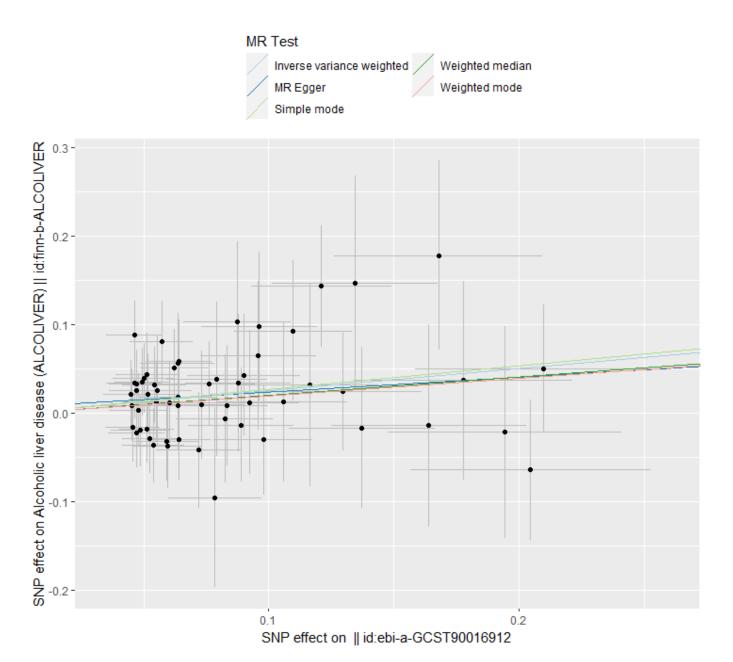
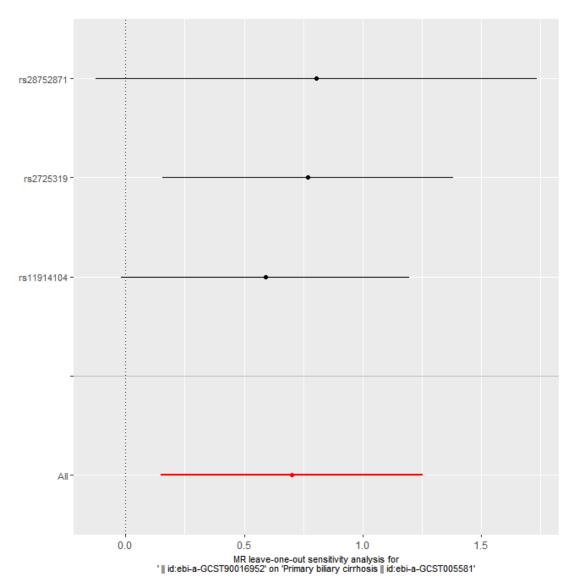
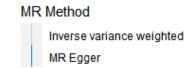
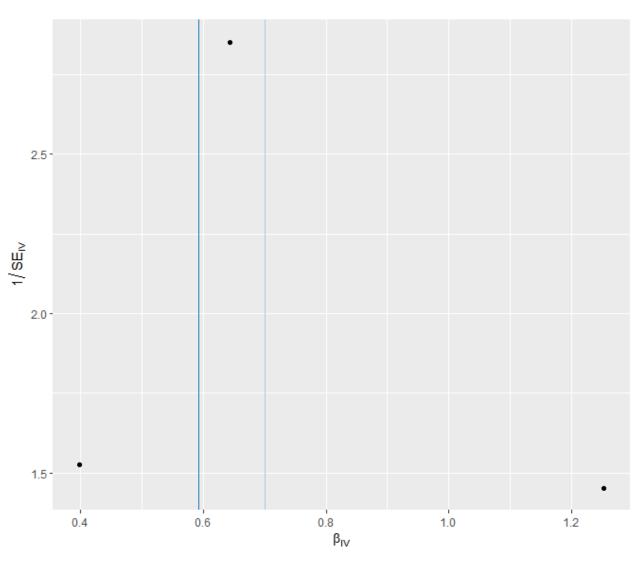
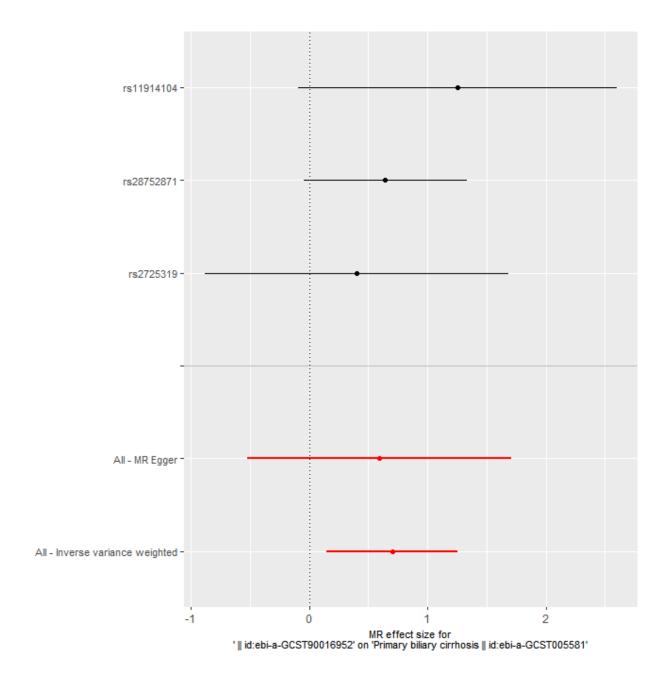


Figure 169 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Streptococcaceae id.1850) on primary biliary cirrhosis









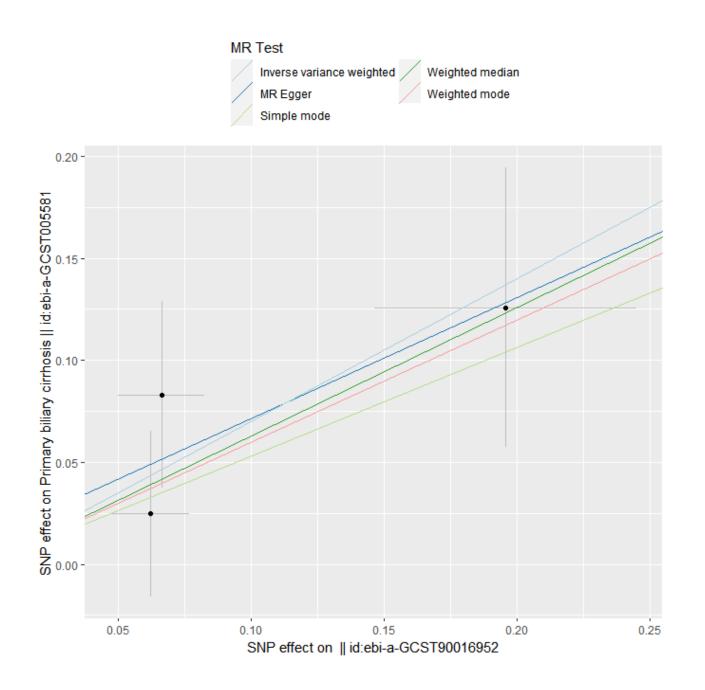
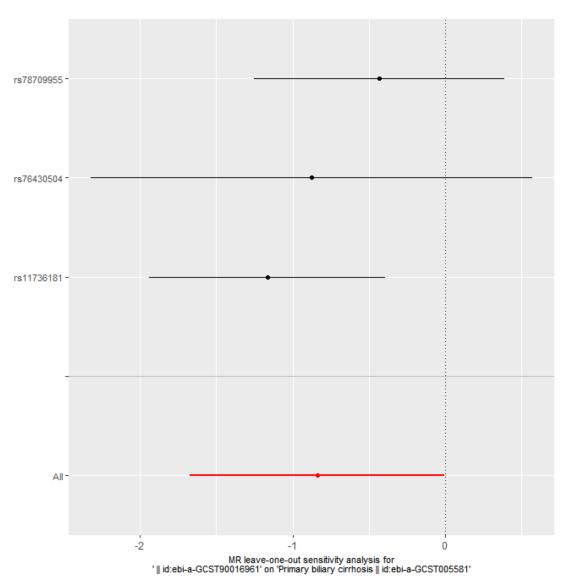
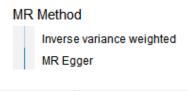
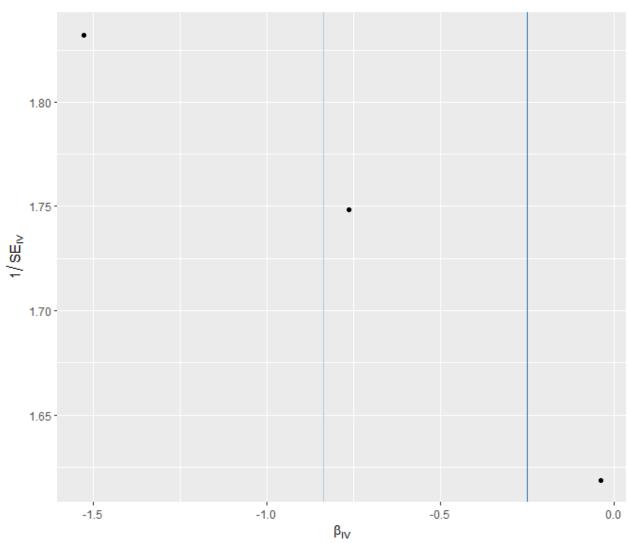
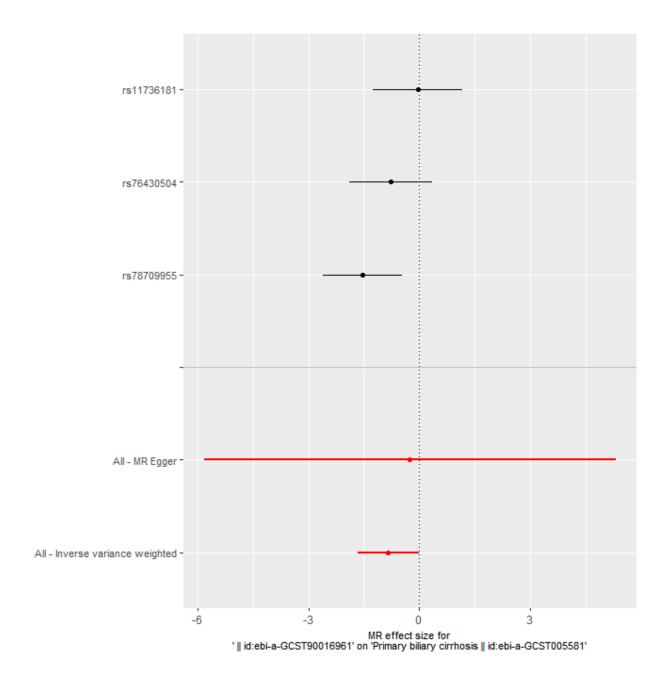


Figure 170 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Akkermansia id.4037) on primary biliary cirrhosis









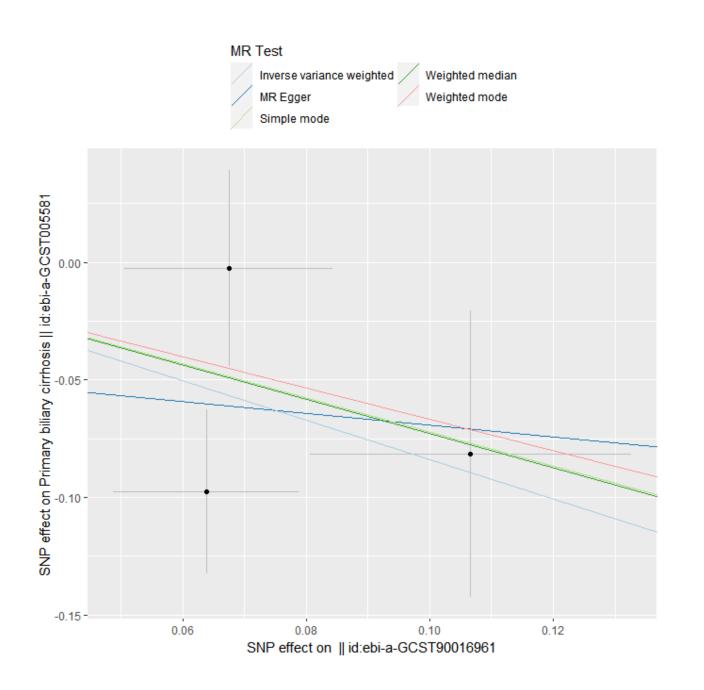
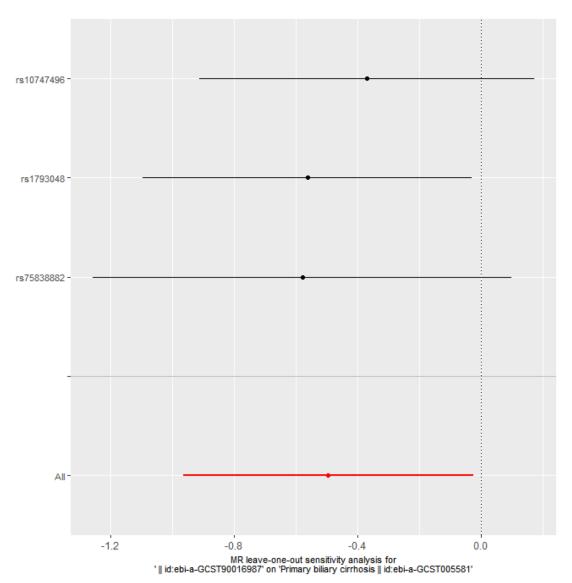
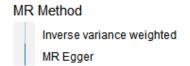
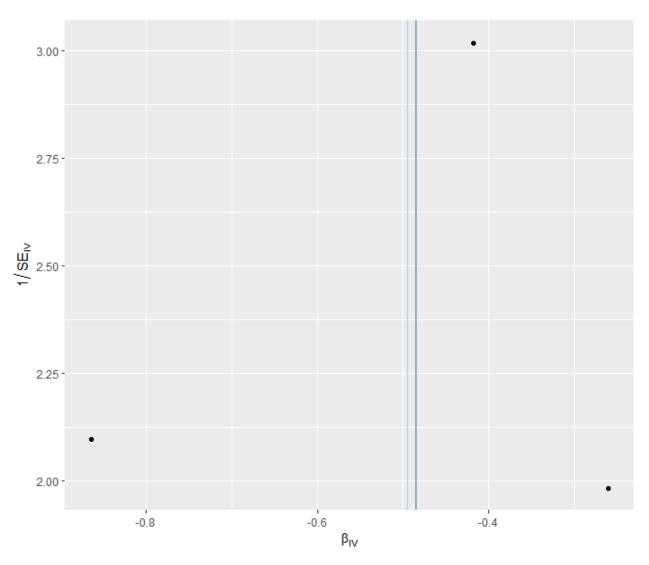
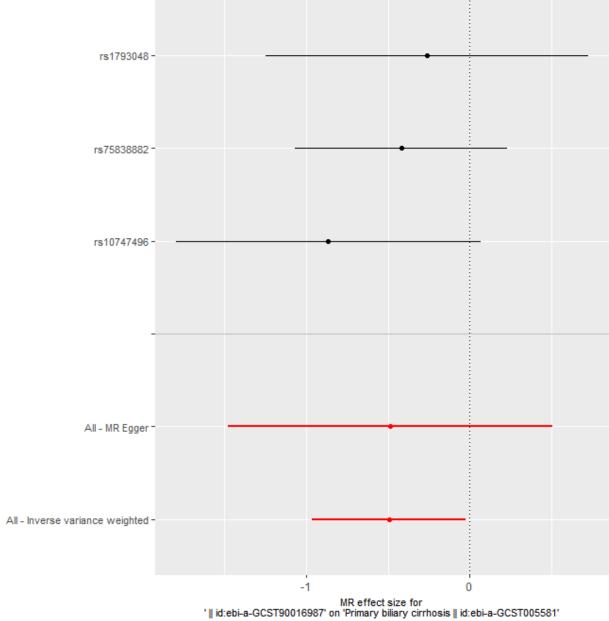


Figure 171 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Desulfovibrio id.3173) on primary biliary cirrhosis









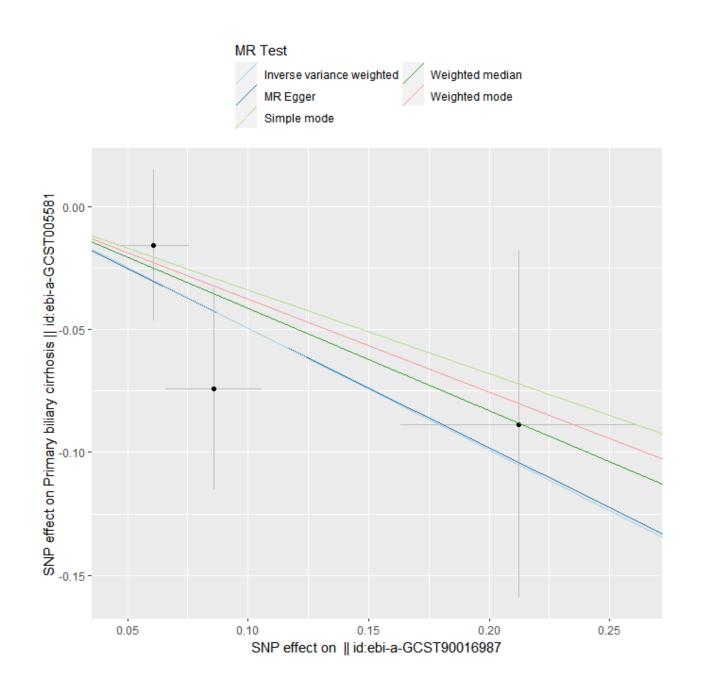
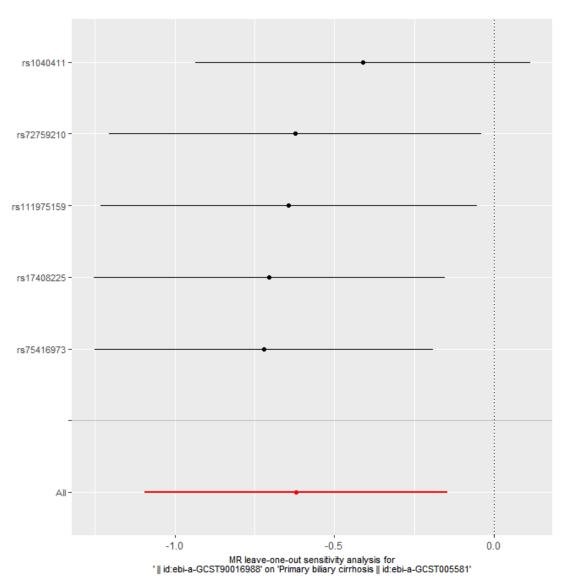
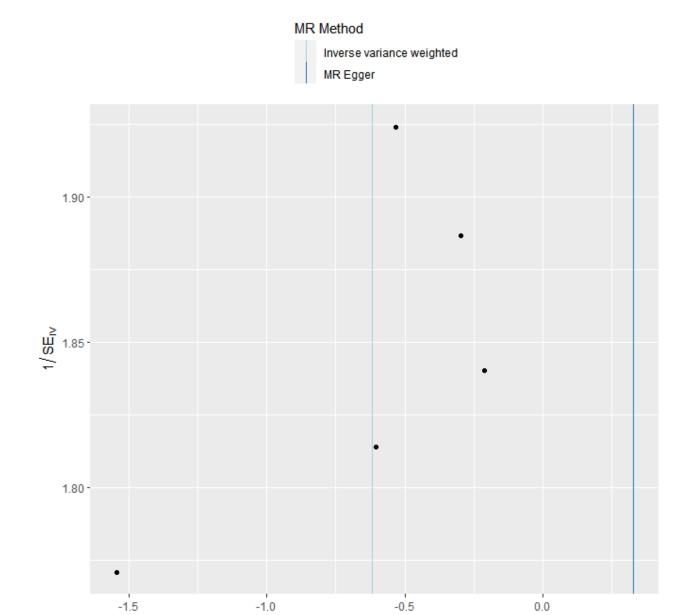


Figure 172 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Dialister id.2183) on primary biliary cirrhosis

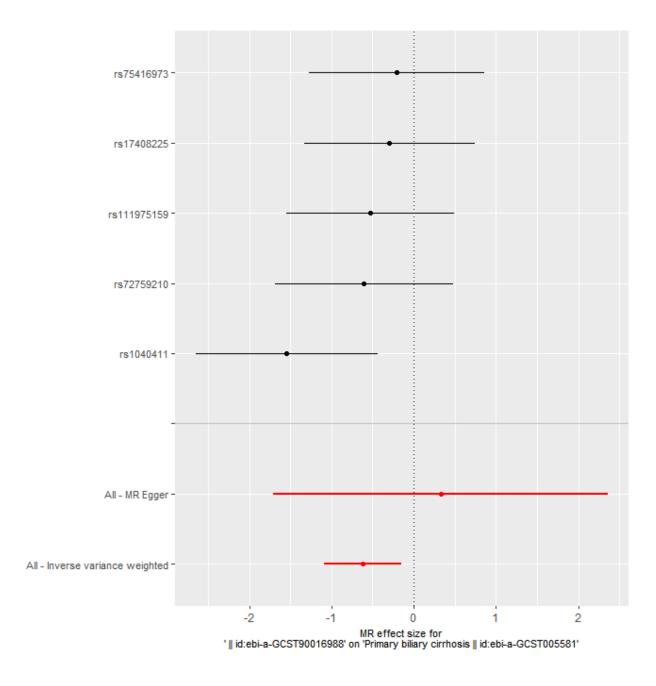




-0.5

 β_{IV}

-1.5



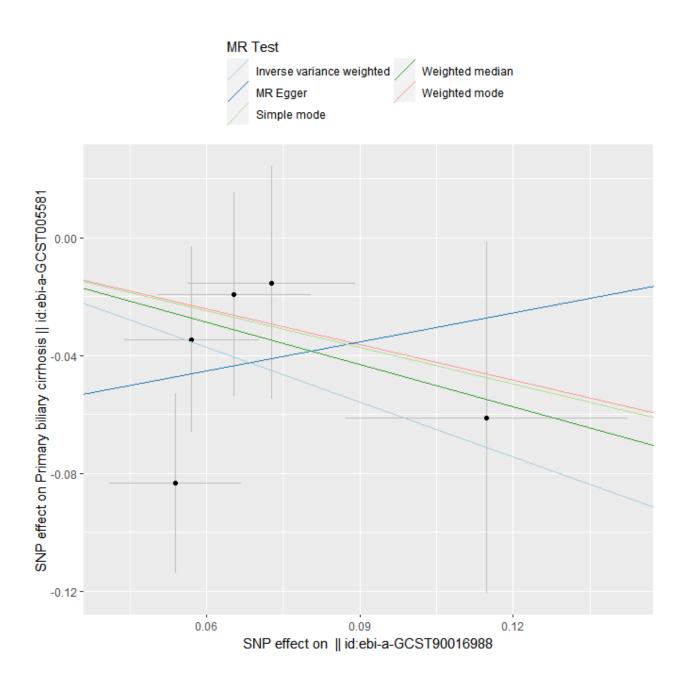
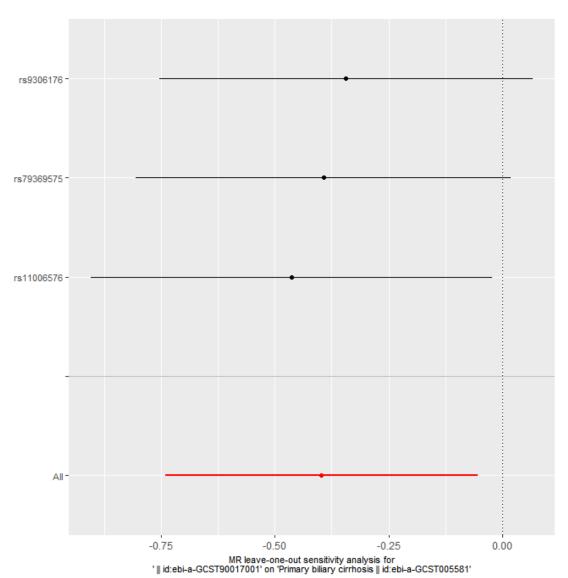
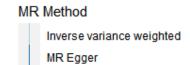
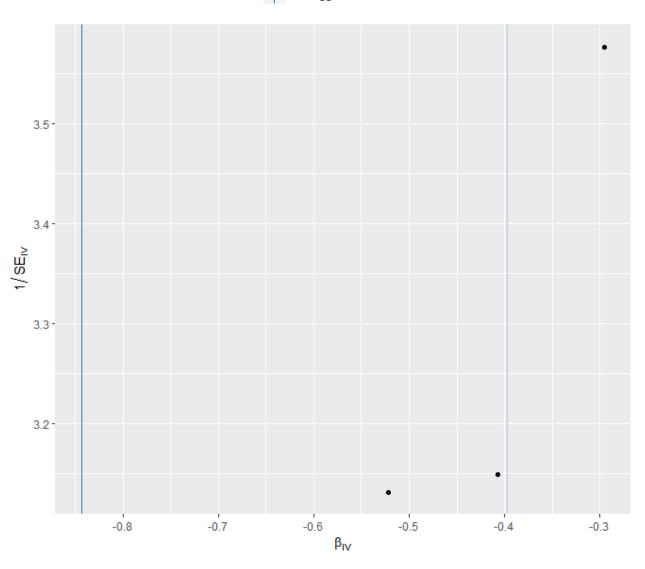
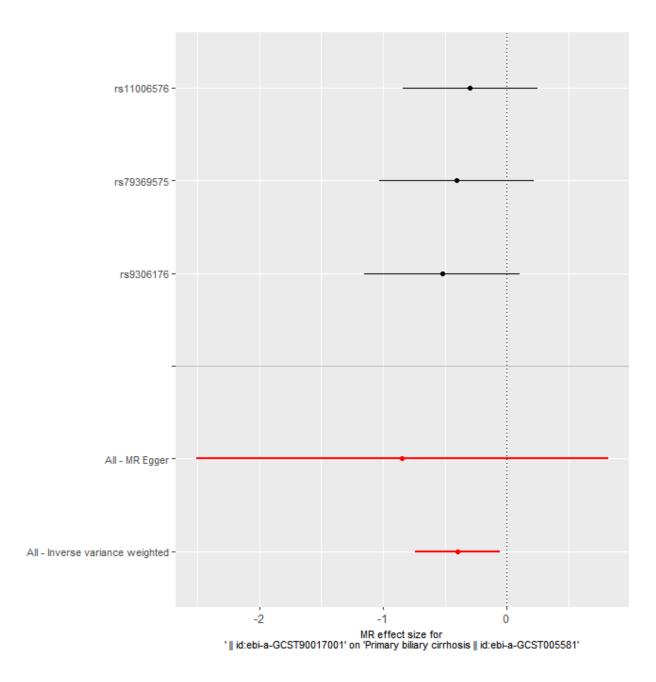


Figure 173 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium nodatum group id.11297) on primary biliary cirrhosis









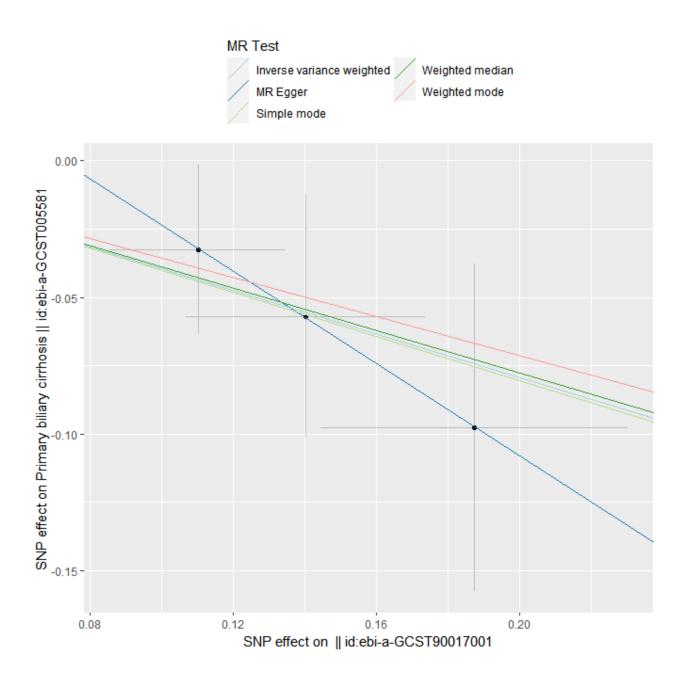
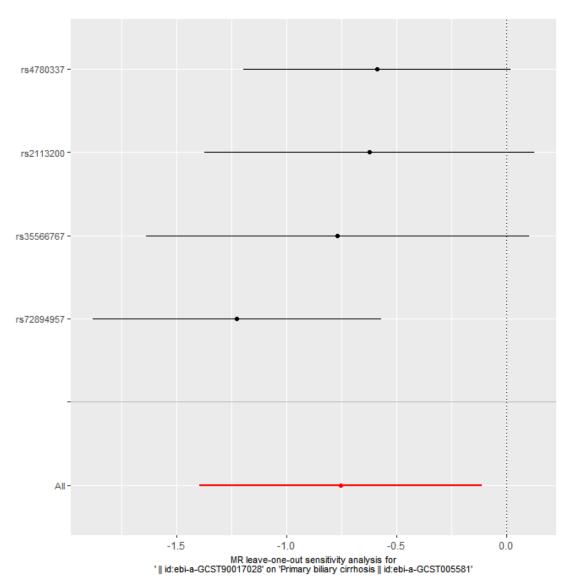
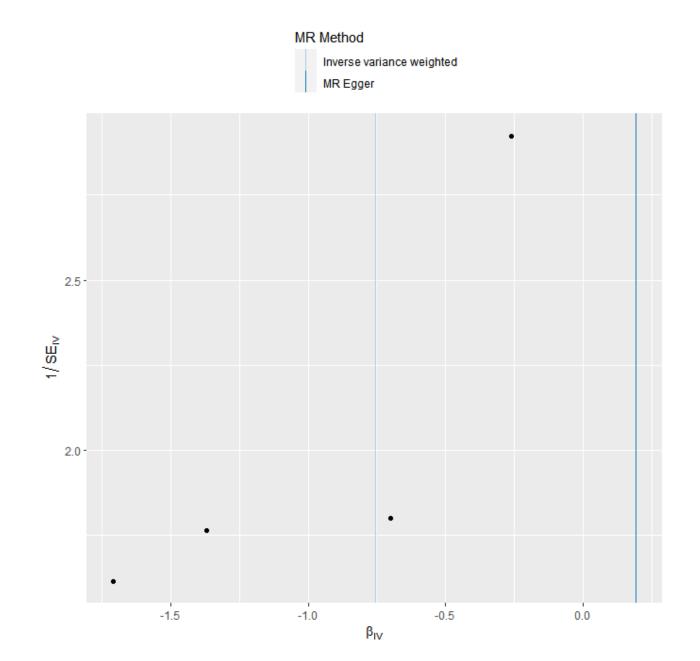
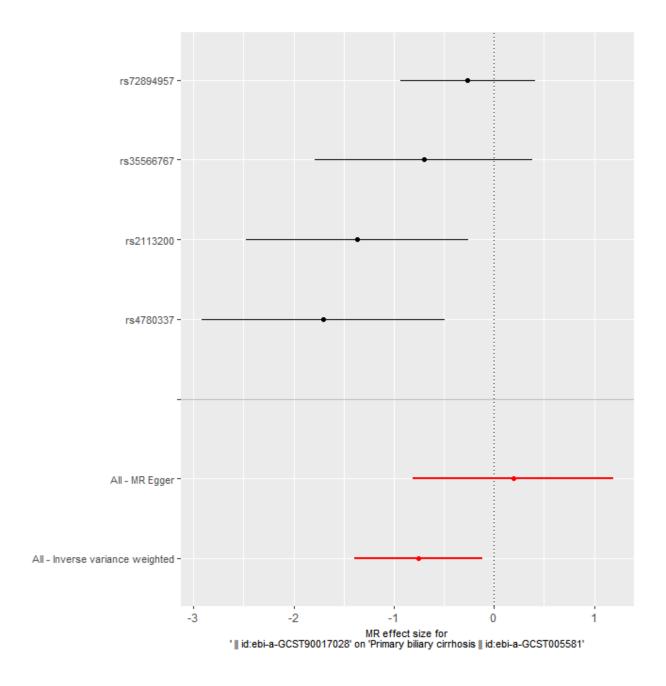


Figure 174 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lachnospiraceae UCG010 id.11330) on primary biliary cirrhosis







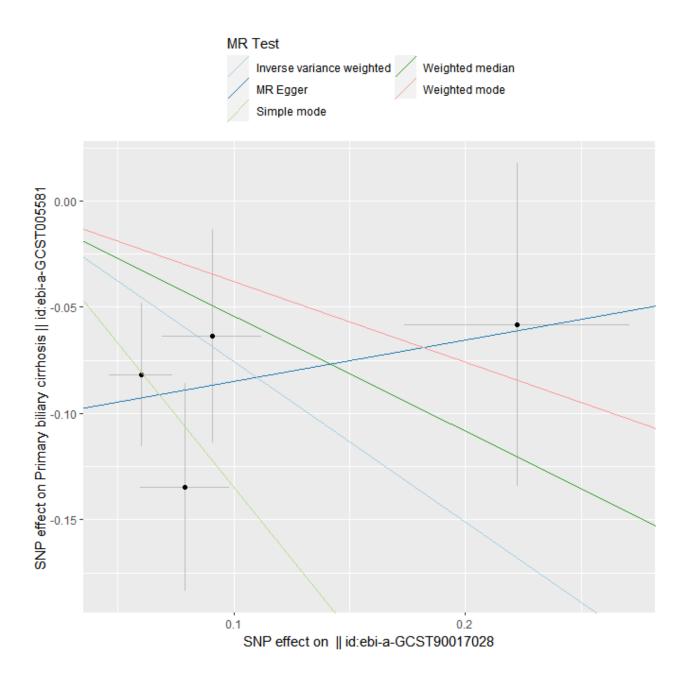
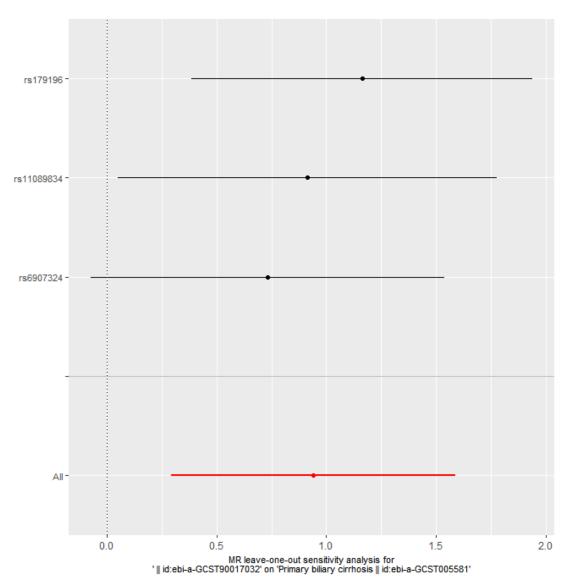
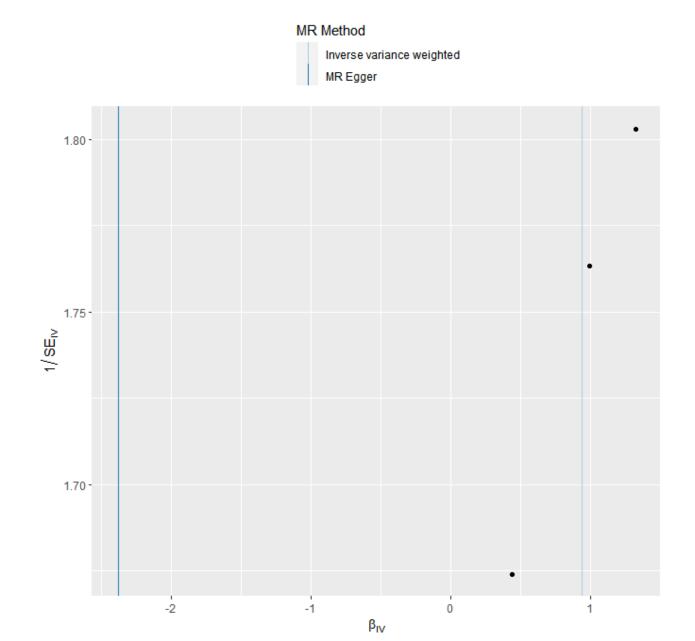
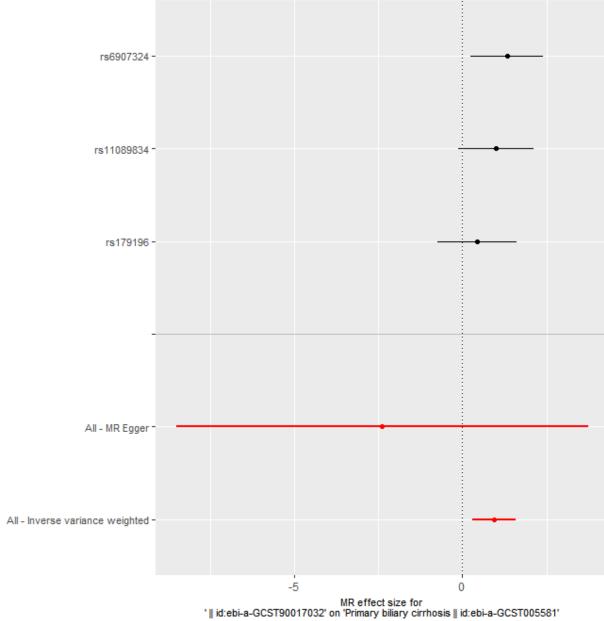


Figure 175 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Marvinbryantia id.2005) on primary biliary cirrhosis







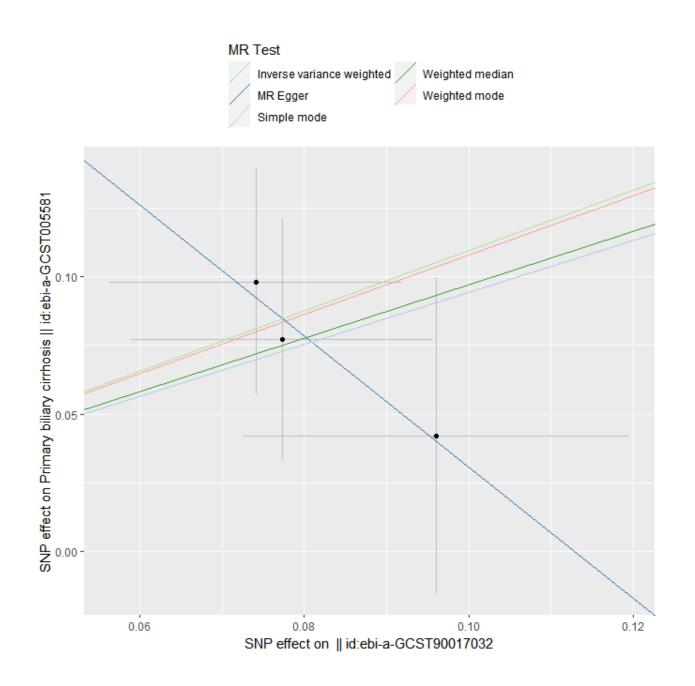
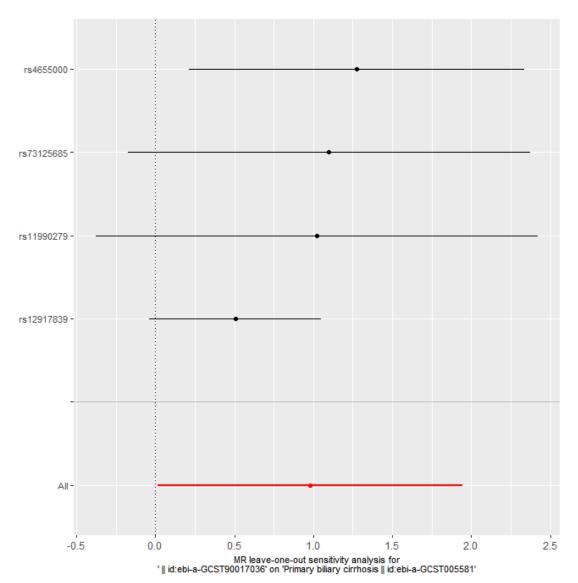
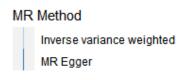
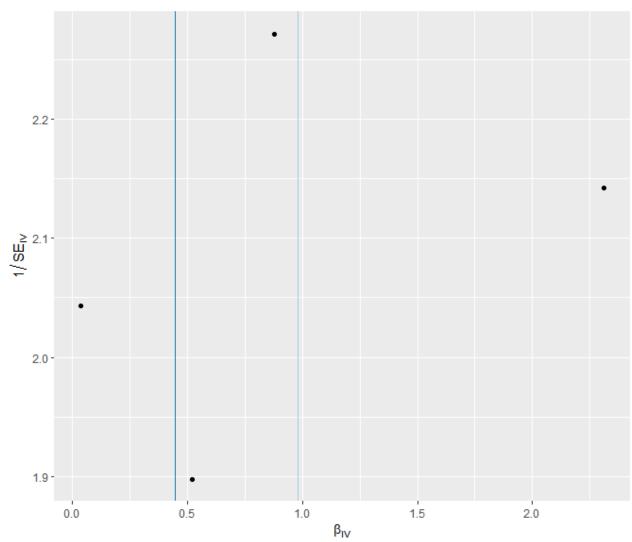
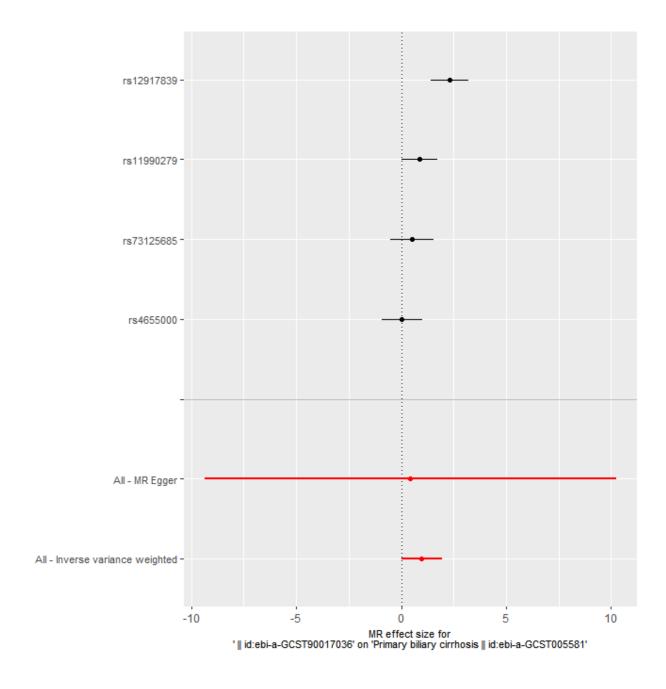


Figure 176 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Oscillibacter id.2063) on primary biliary cirrhosis









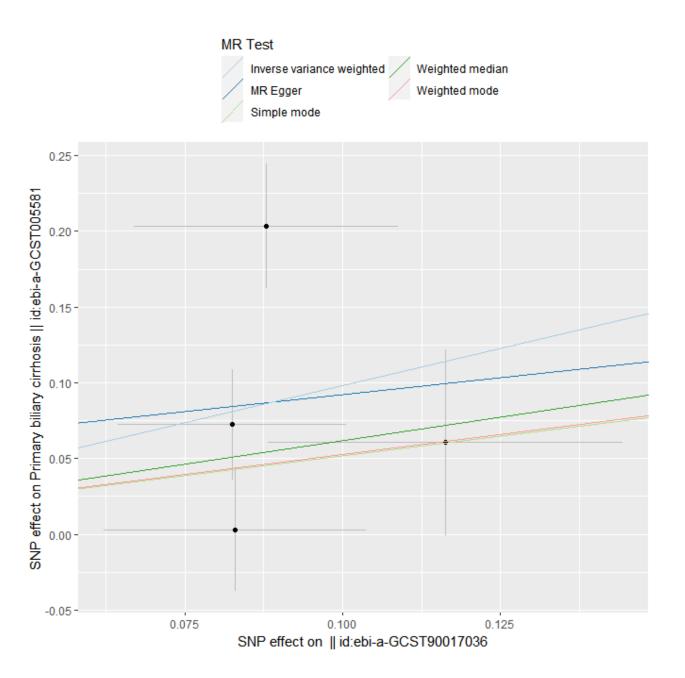
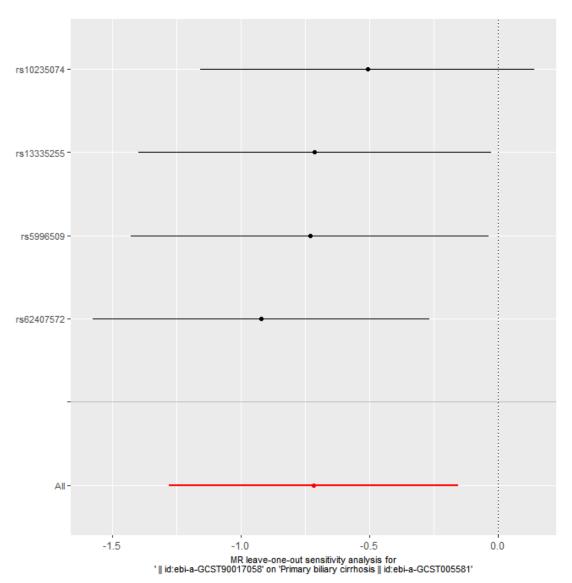
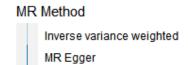
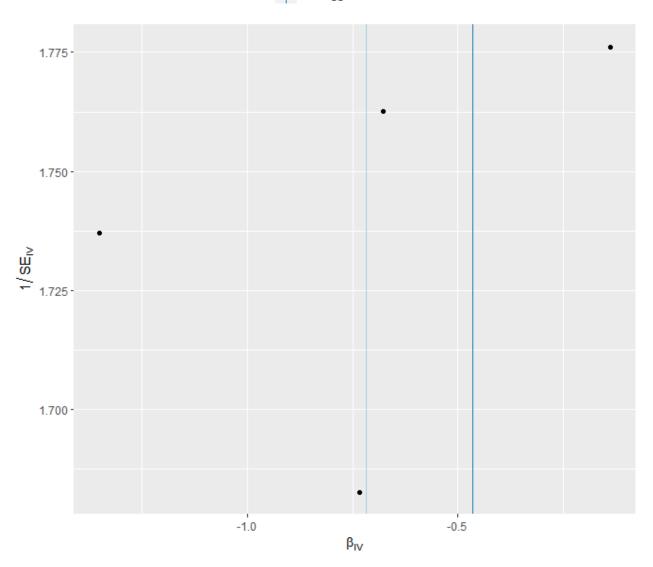
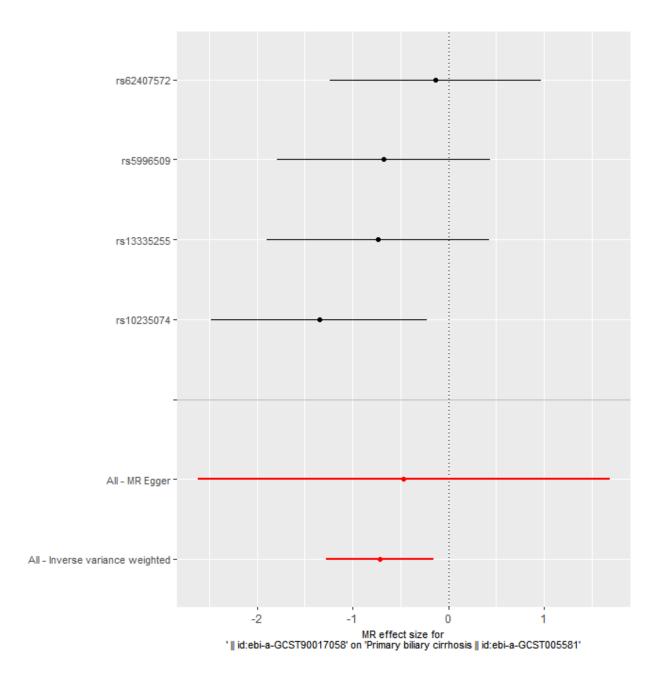


Figure 177 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG010 id.11367) on primary biliary cirrhosis









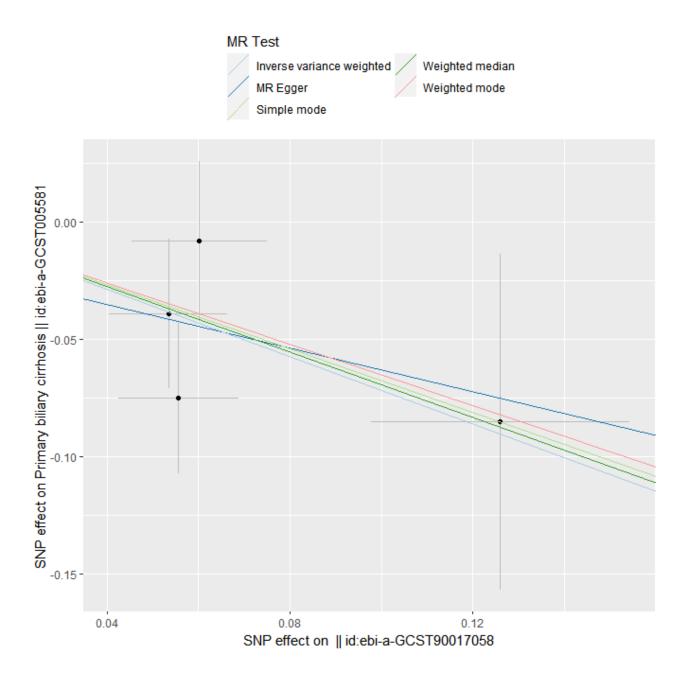
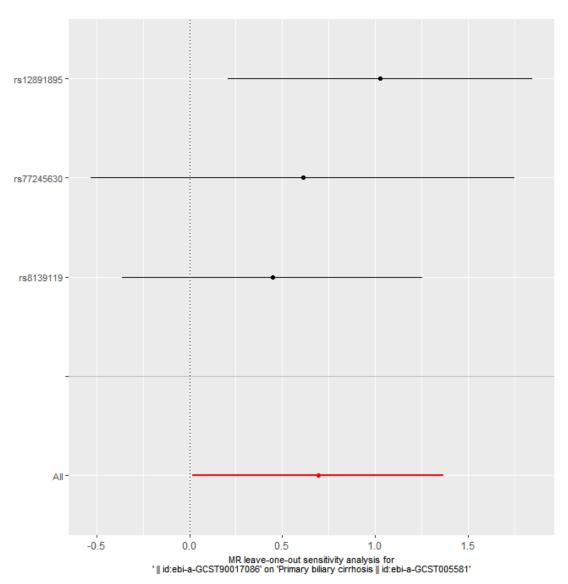
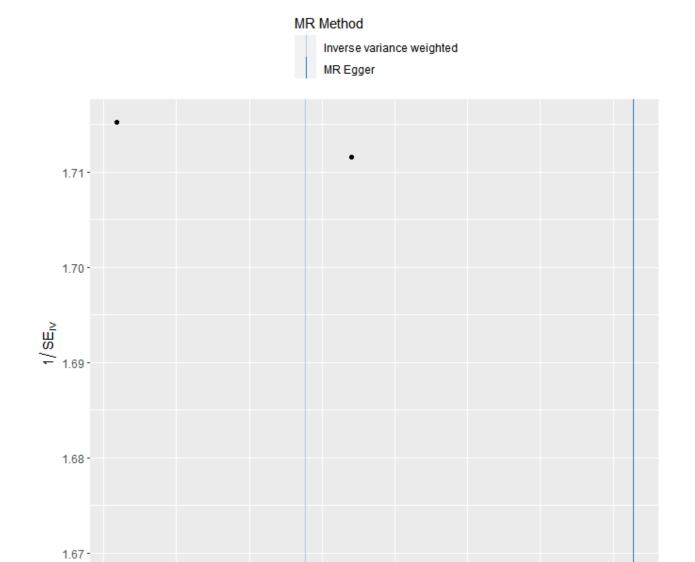


Figure 178 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (unknown genus id.826) on primary biliary cirrhosis





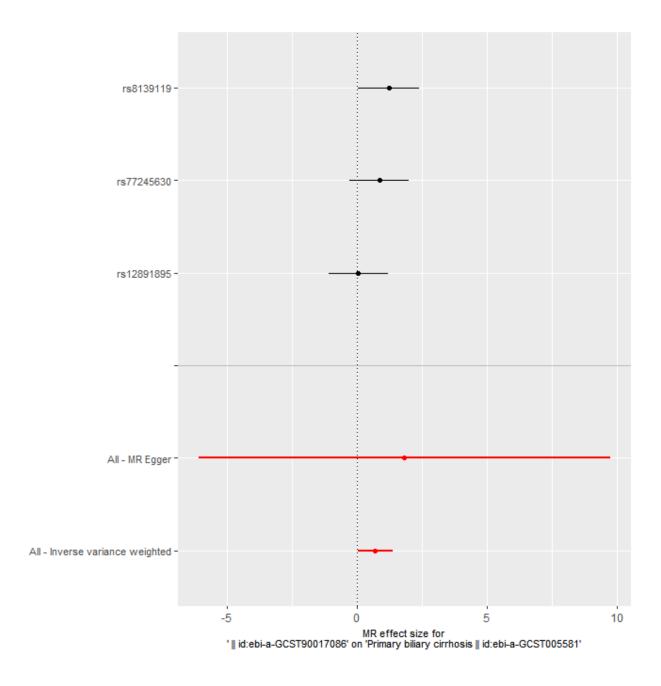
1.0

 β_{IV}

1.5

0.5

0.0



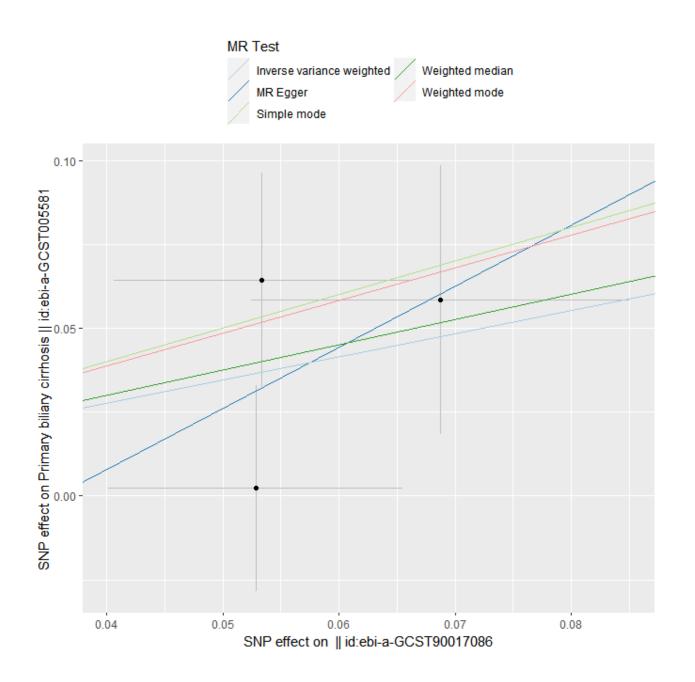
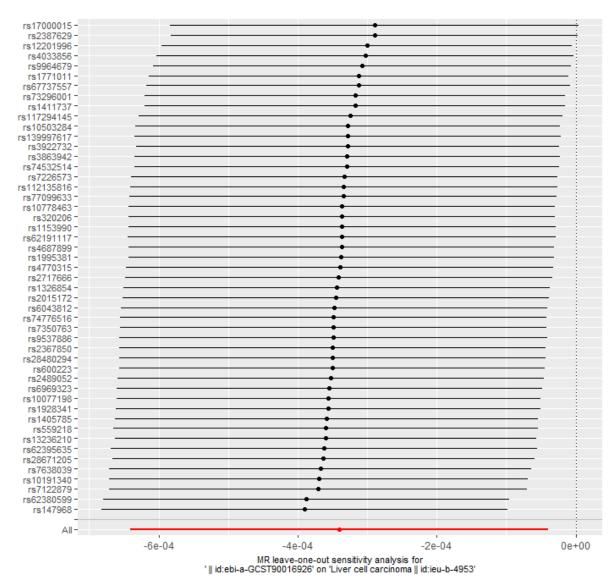
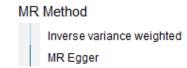
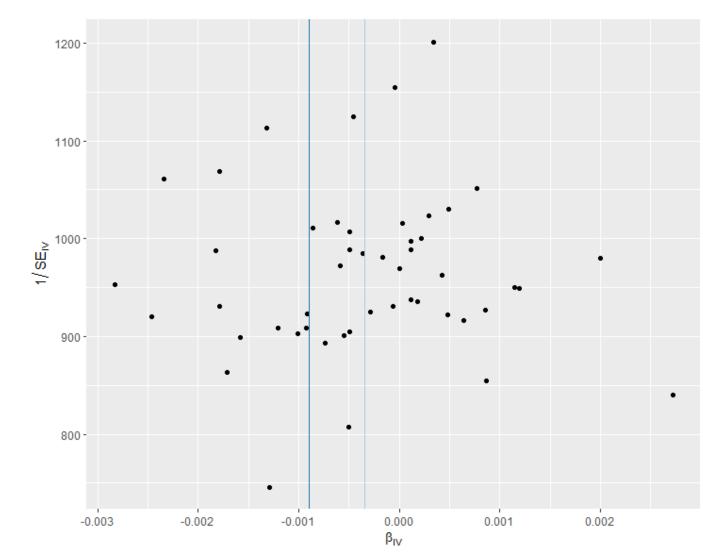
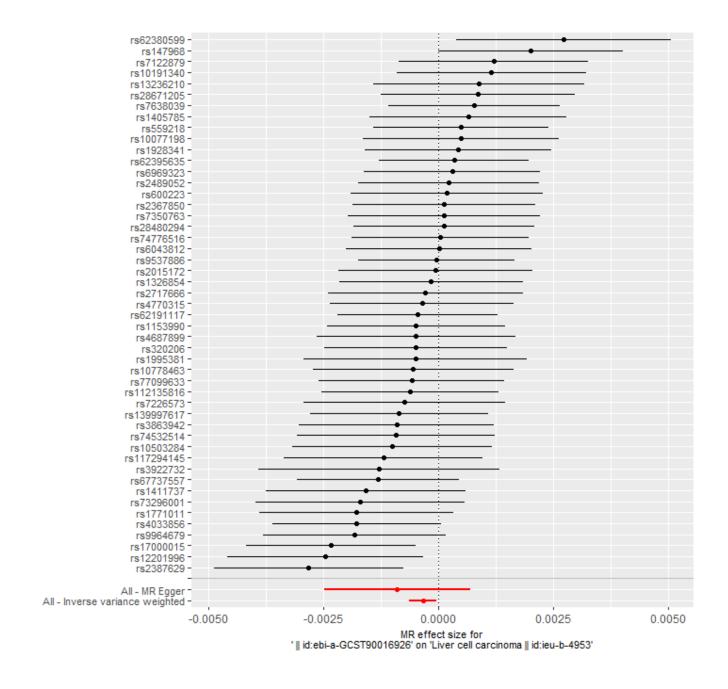


Figure 179 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Alcaligenaceae id.2875) on liver cell carcinoma









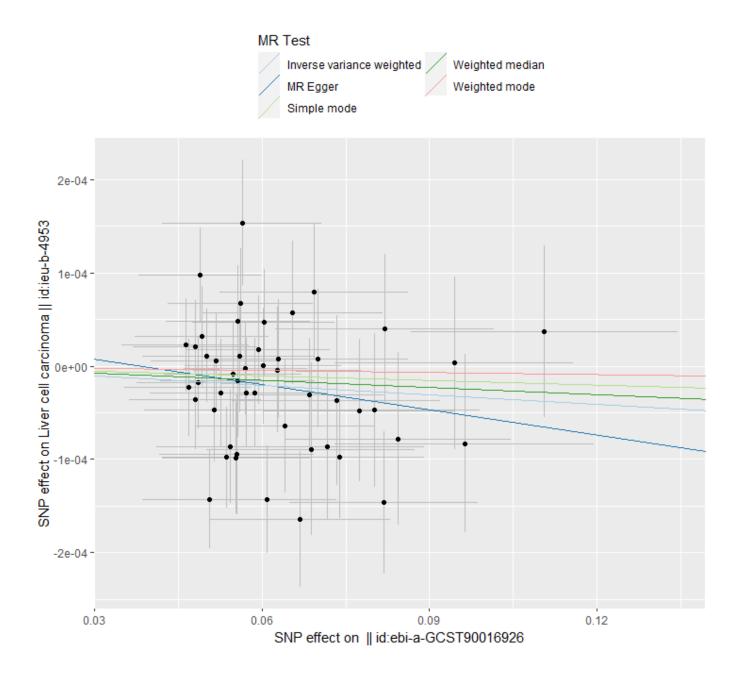
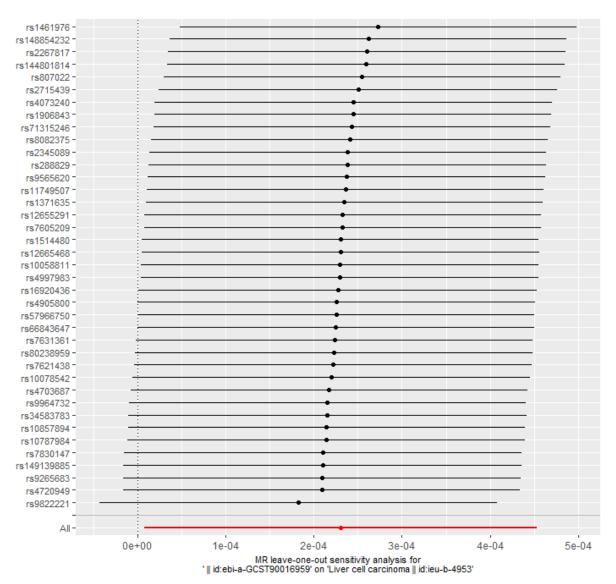
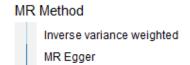
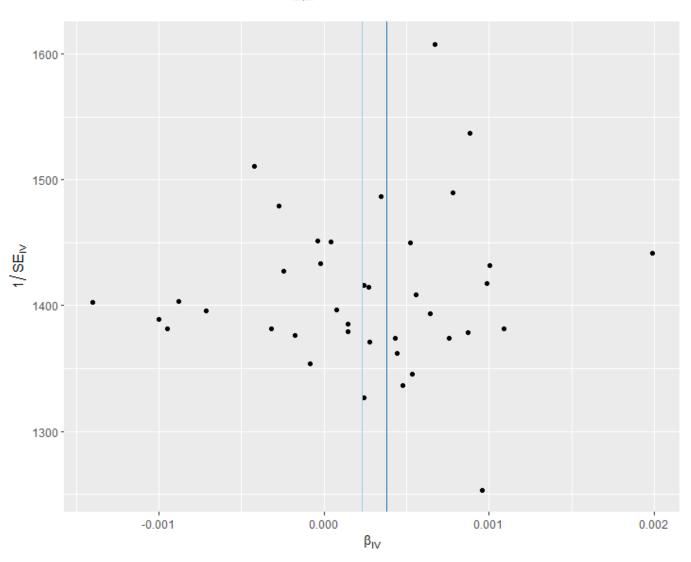
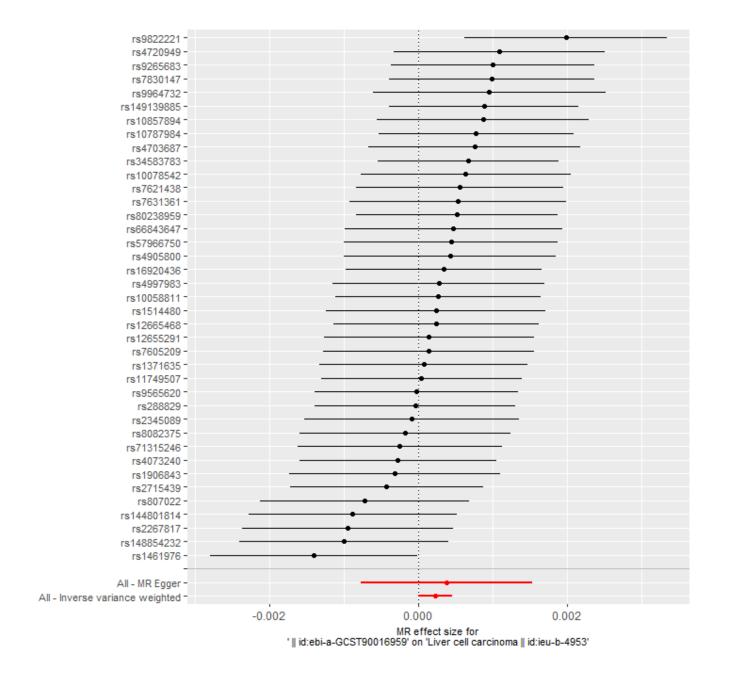


Figure 180 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Actinomyces id.423) on liver cell carcinoma









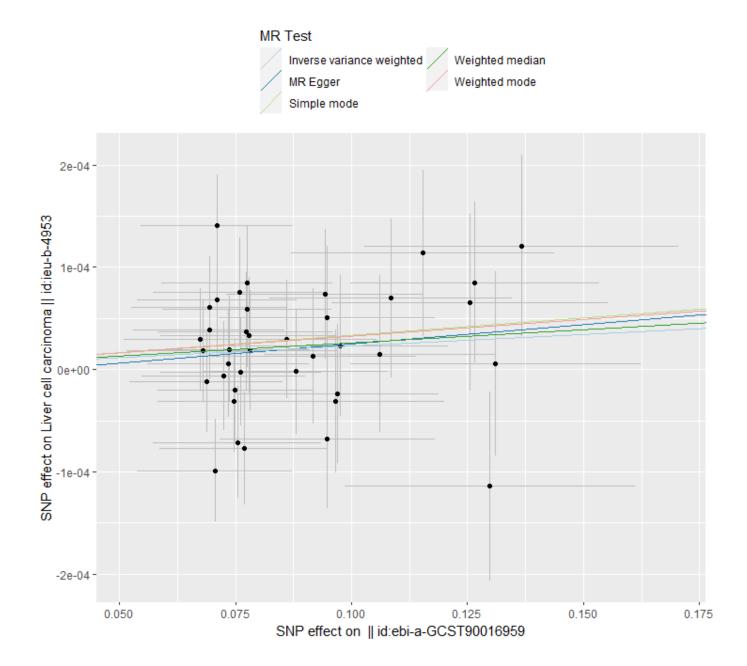
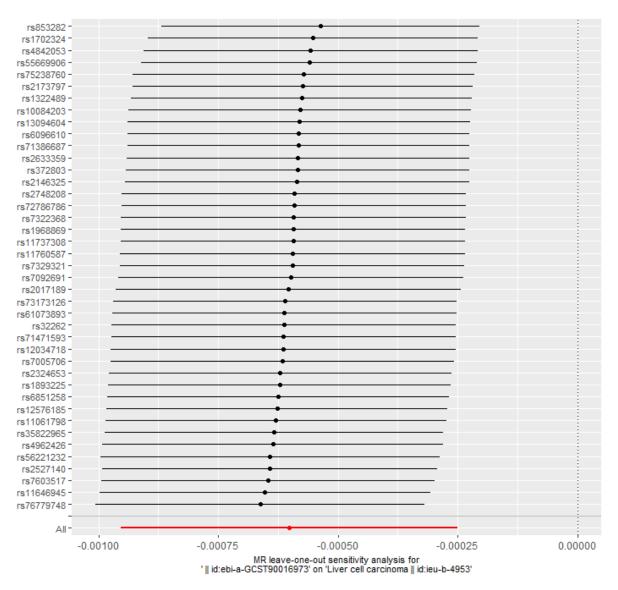
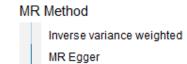
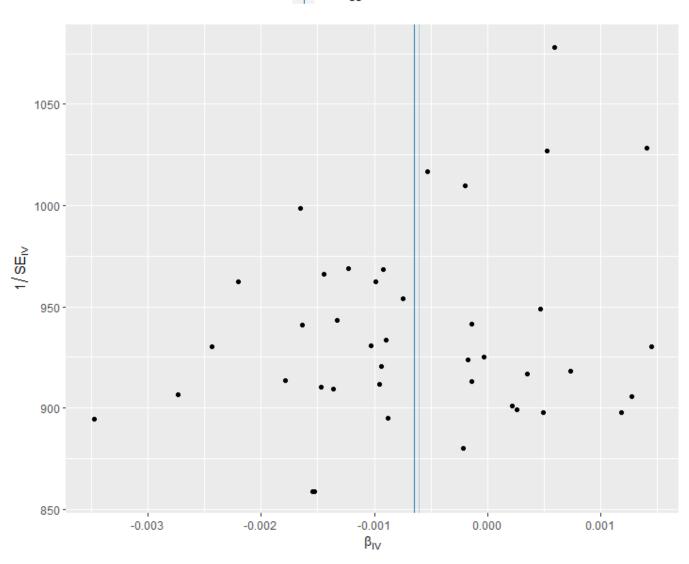
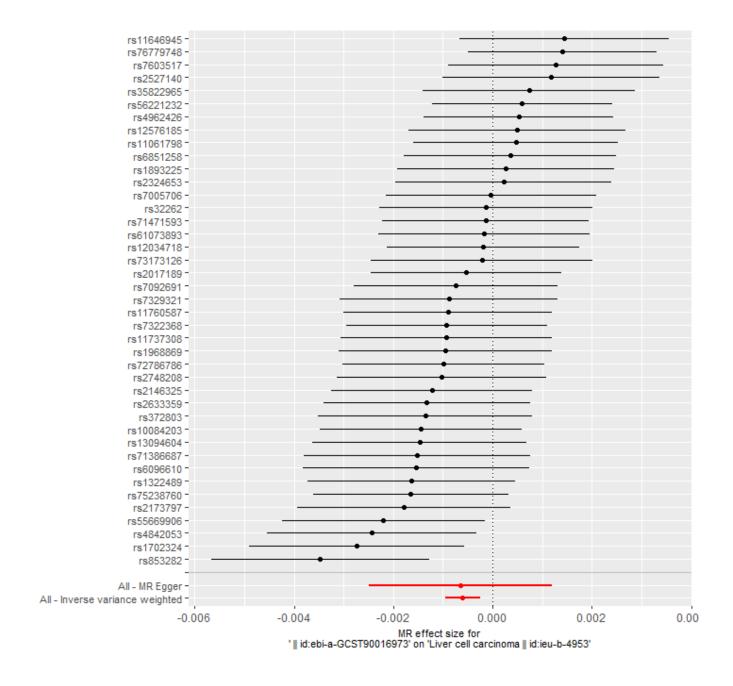


Figure 181 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Butyricicoccus id.2055) on liver cell carcinoma









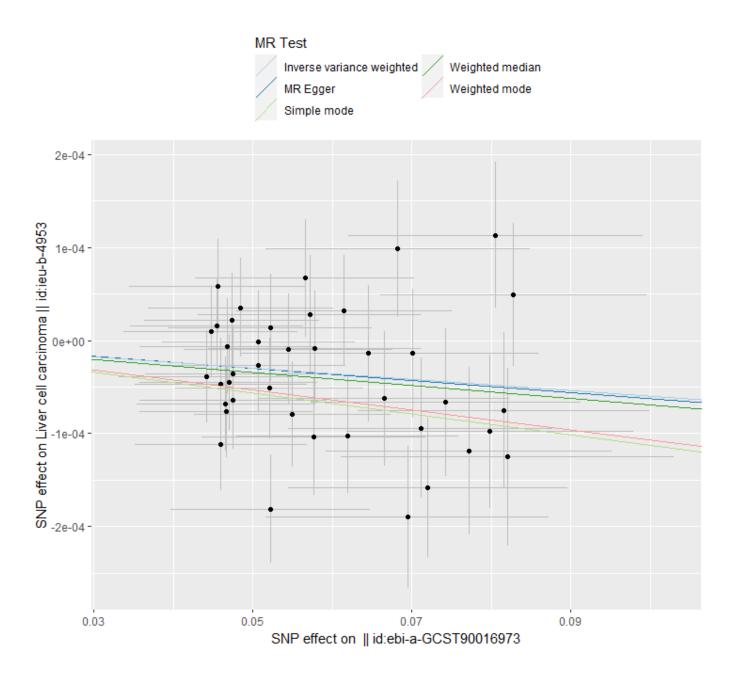
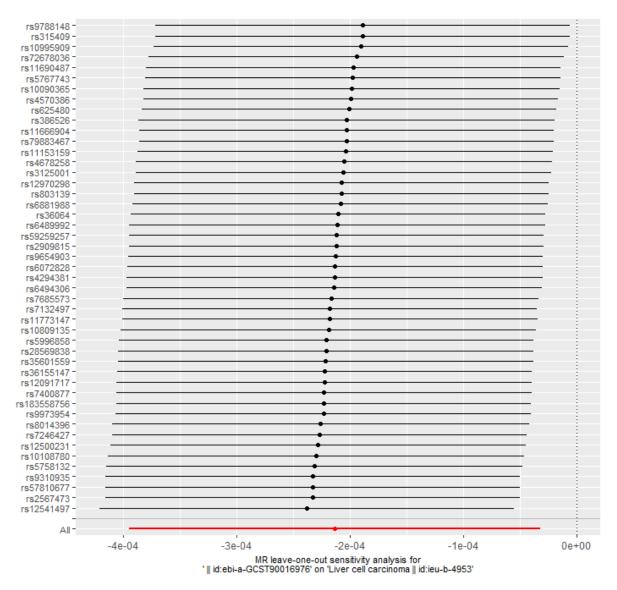
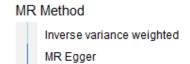
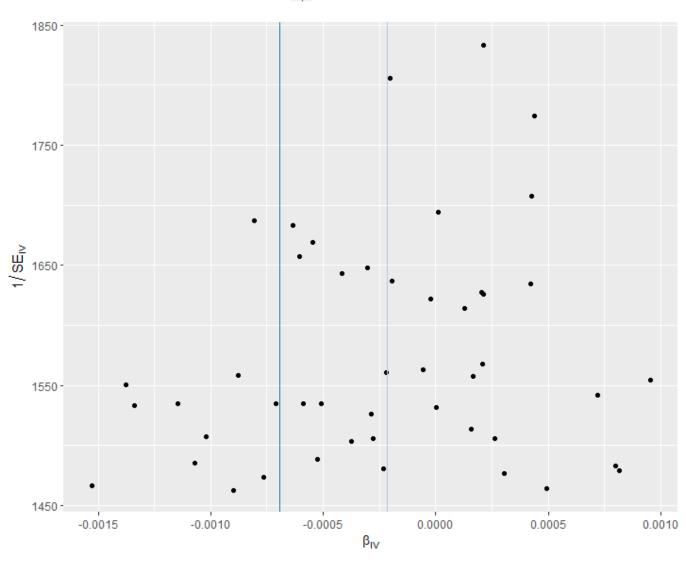
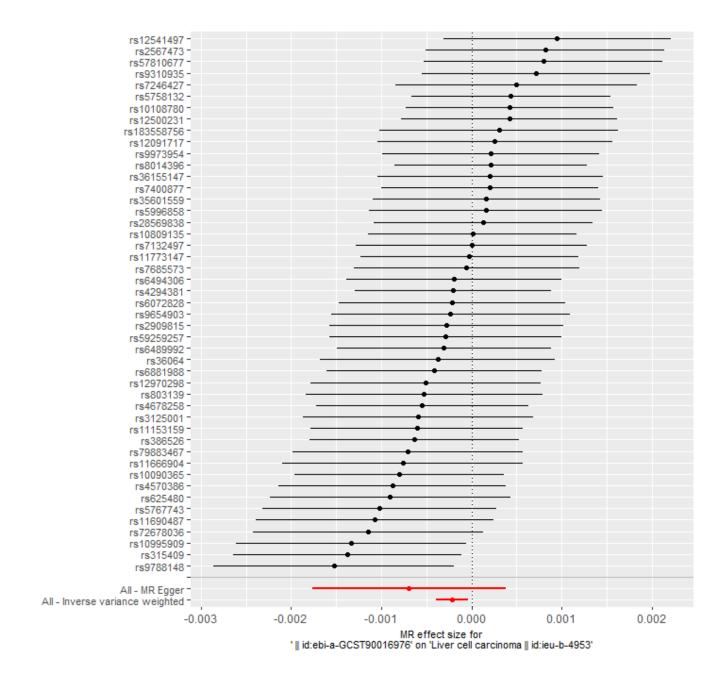


Figure 182 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Candidatus Soleaferrea id.11350) on liver cell carcinoma









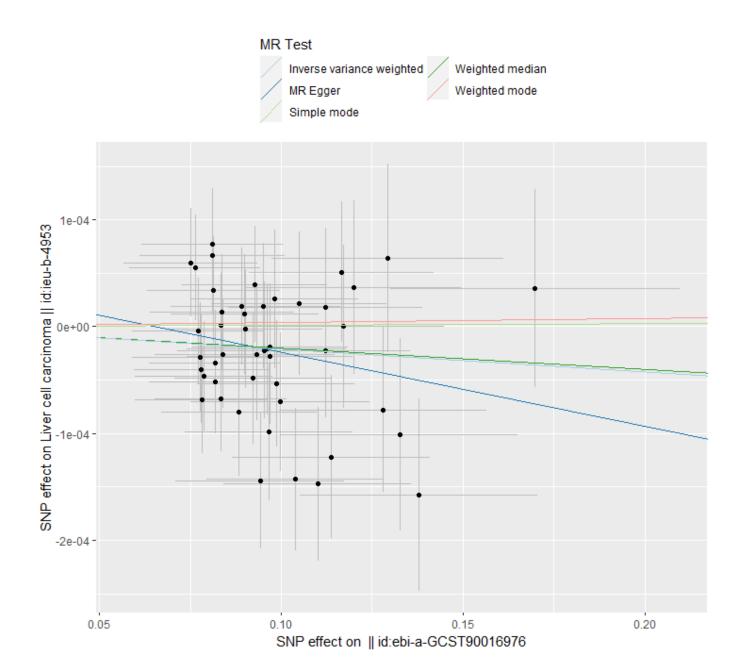
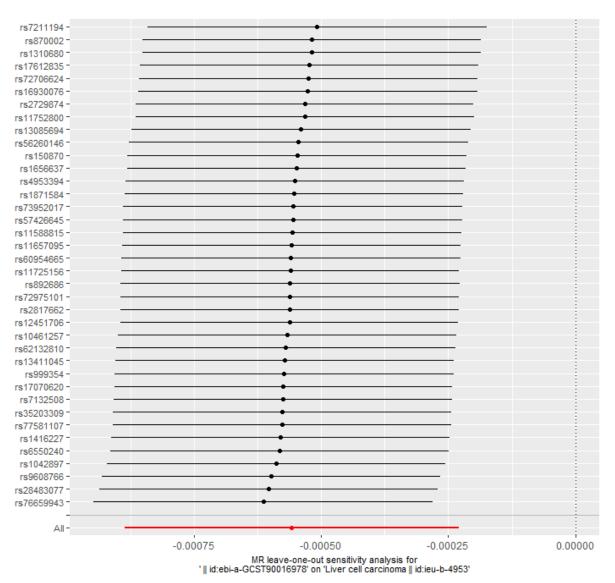
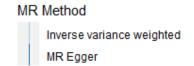
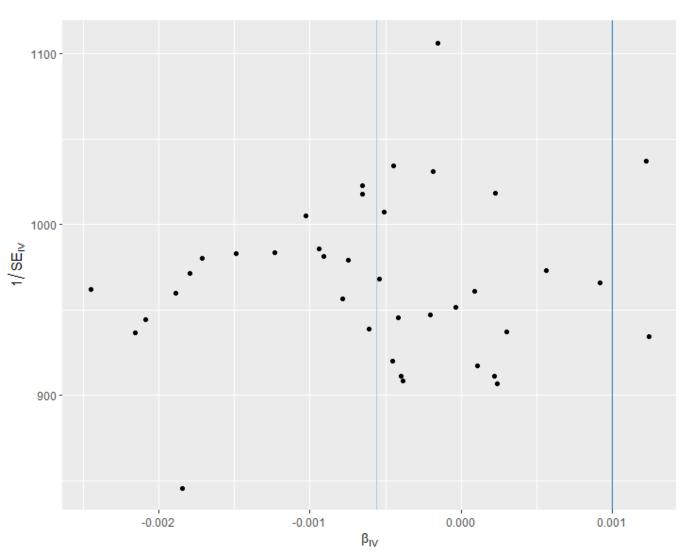
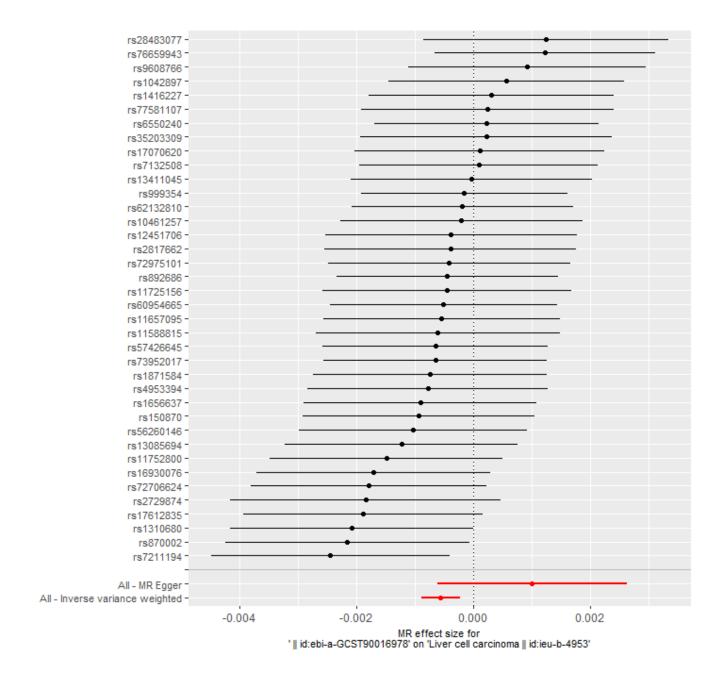


Figure 183 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Christensenellaceae R 7group id.11283) on liver cell carcinoma









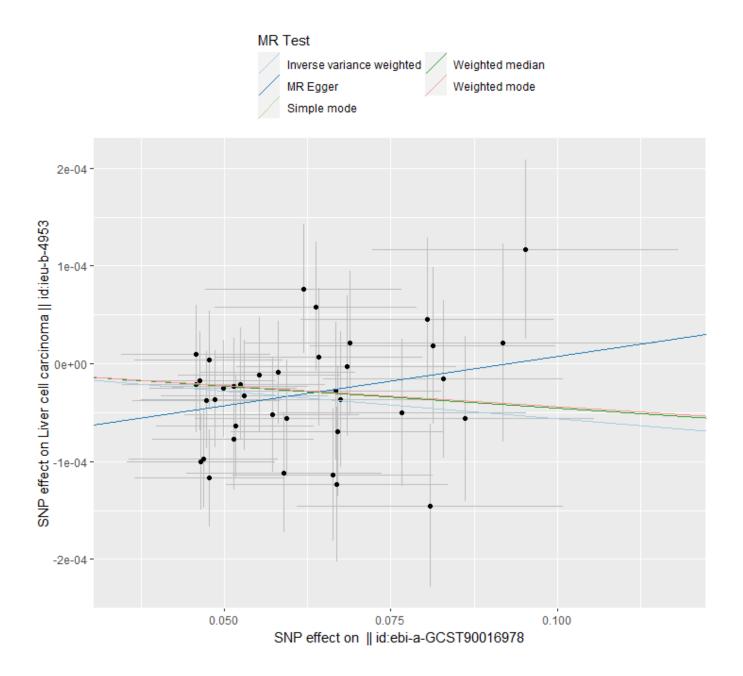
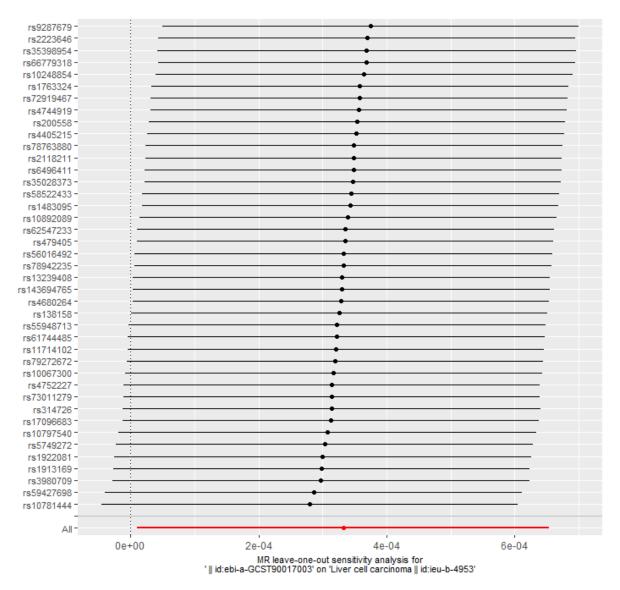
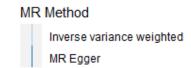
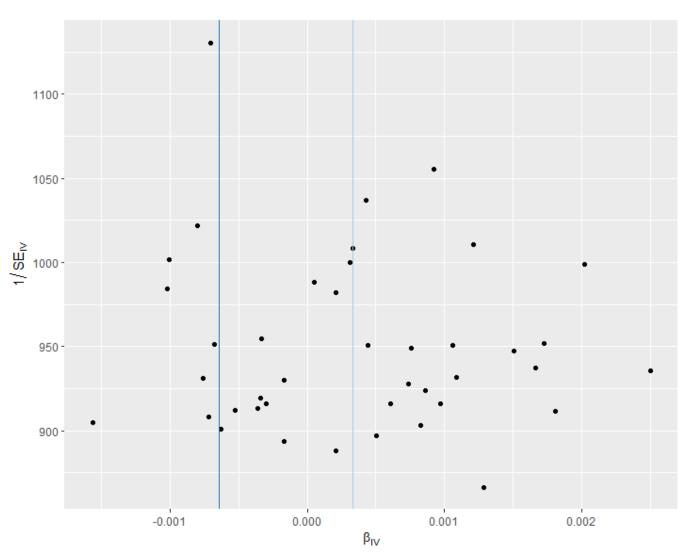
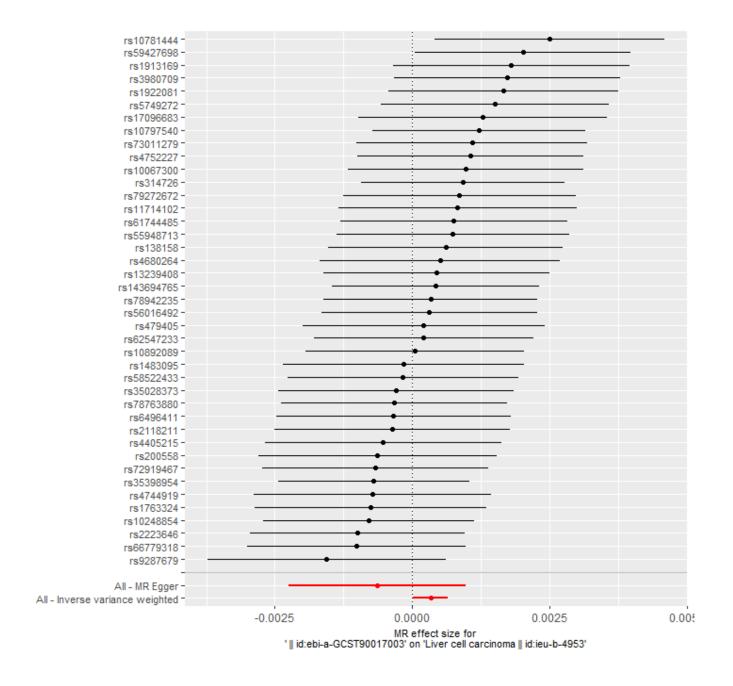


Figure 184 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Eubacterium rectale group id.14374) on liver cell carcinoma











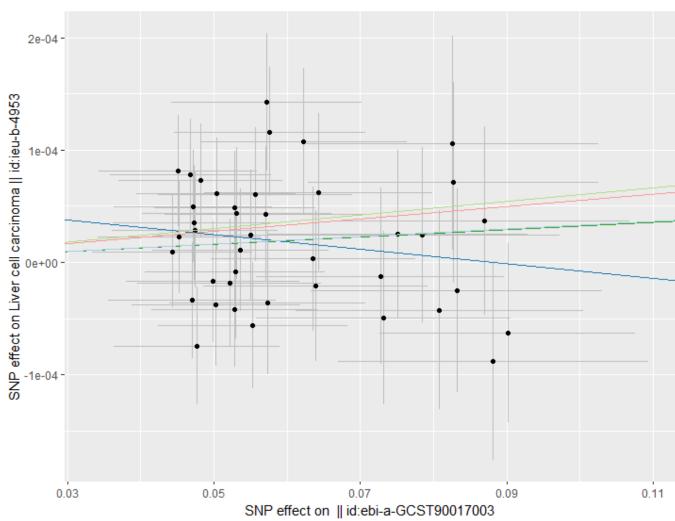
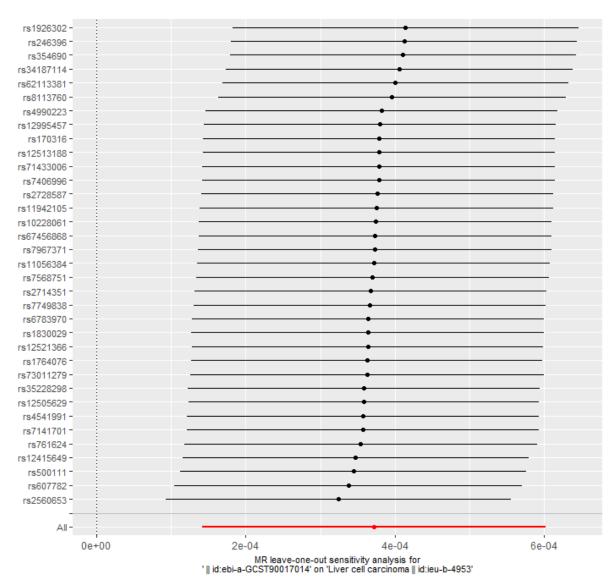
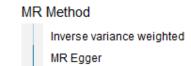
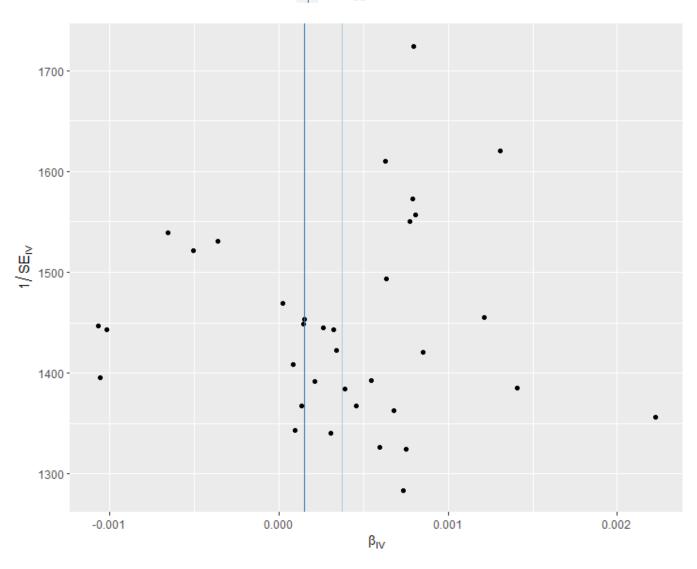
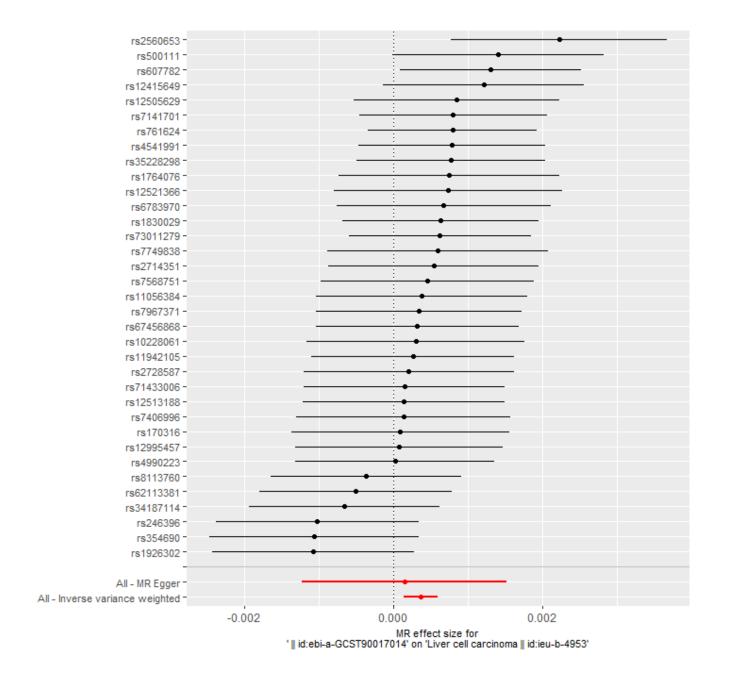


Figure 185 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Holdemanella id.11393) on liver cell carcinoma











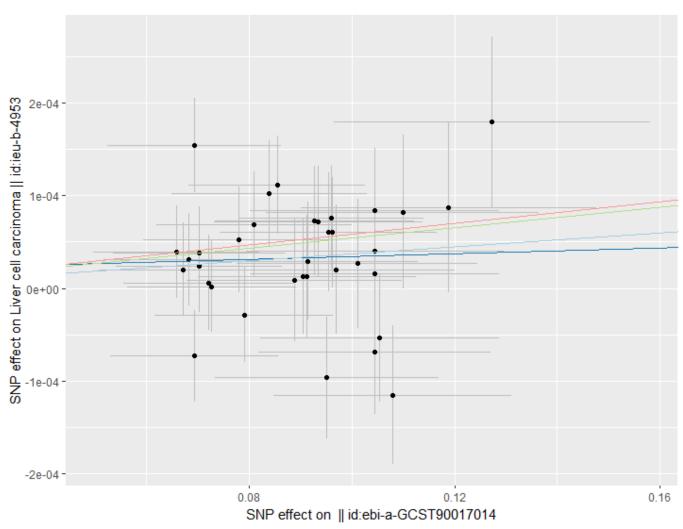
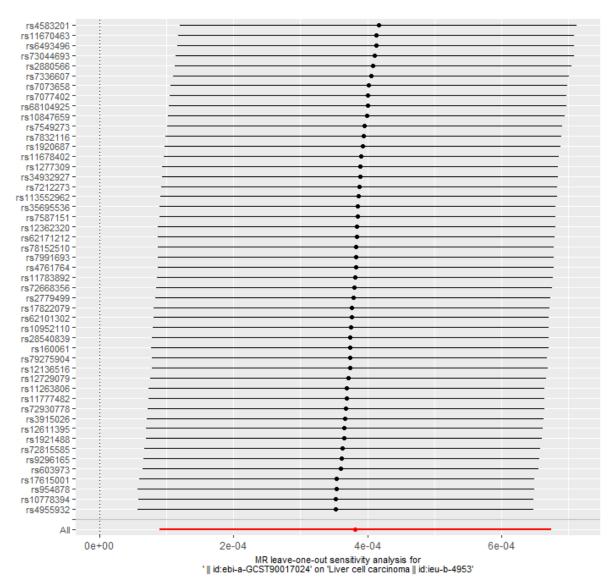
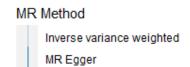
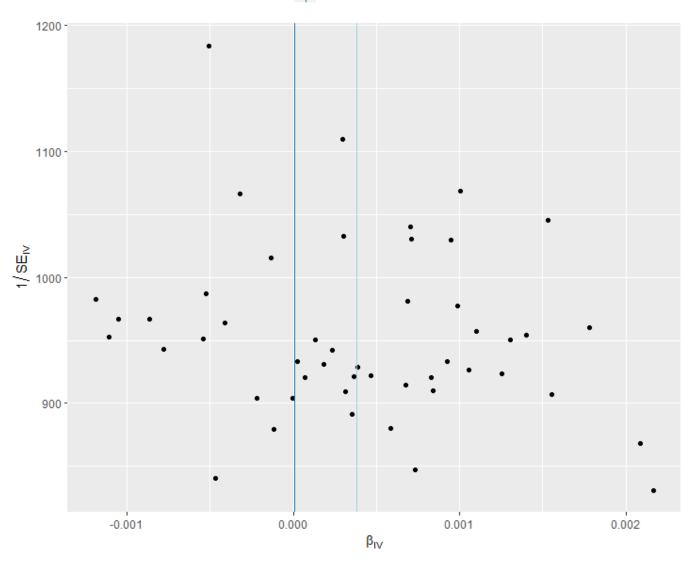
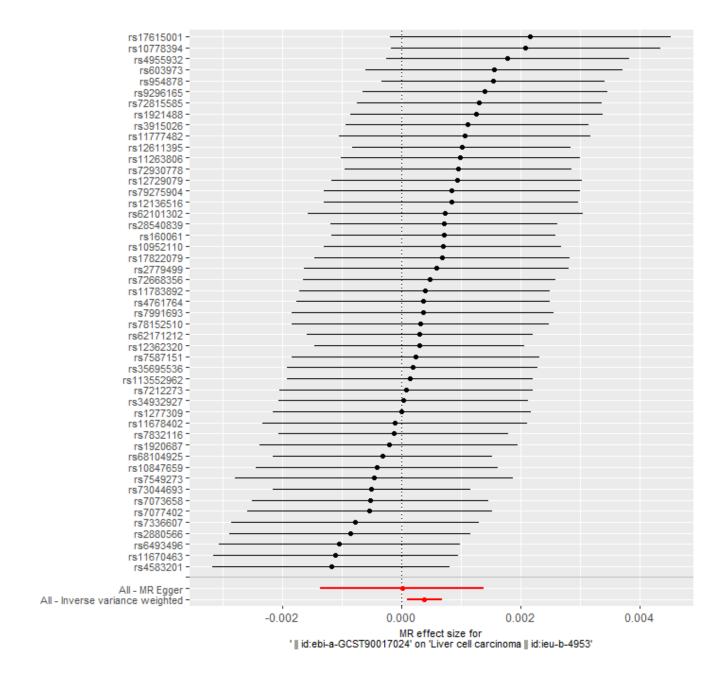


Figure 186 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lachnospiraceae NK4A136 group id.11319) on liver cell carcinoma









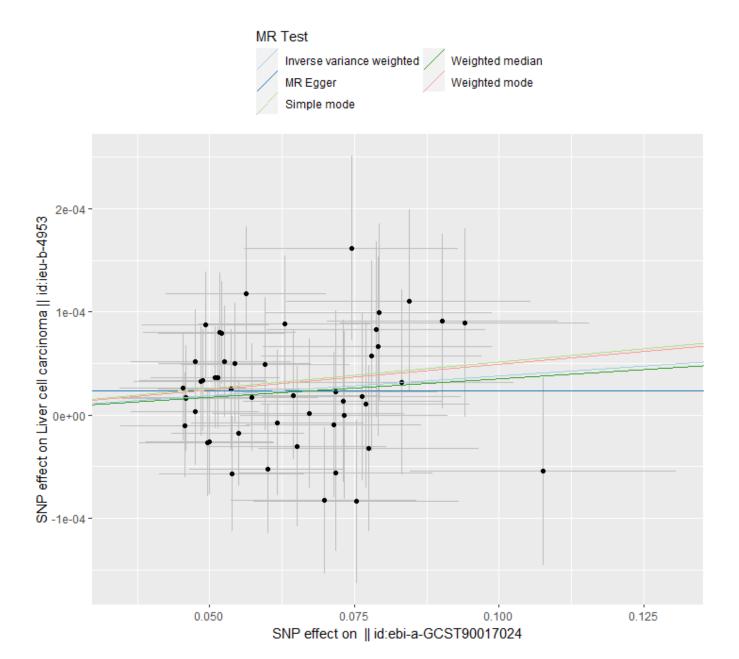
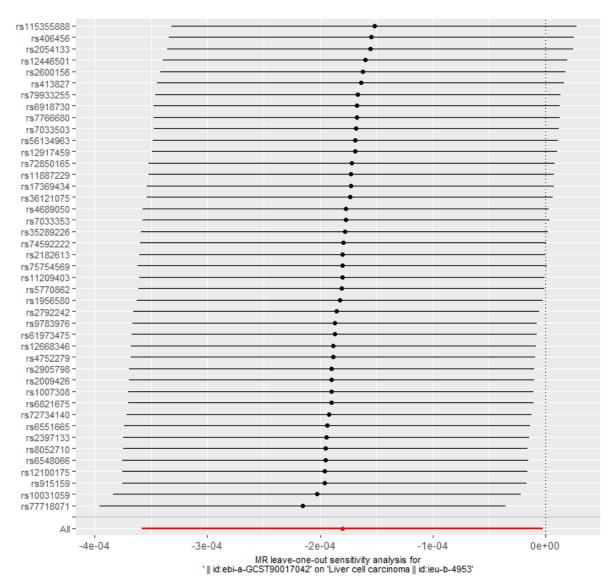
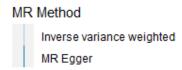
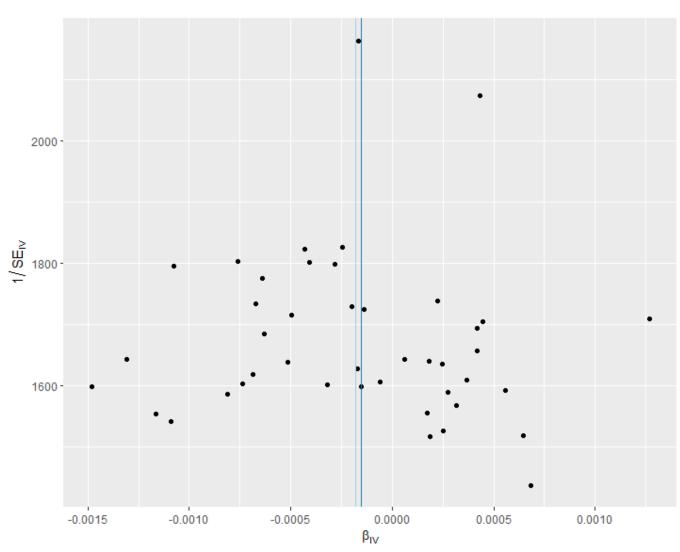
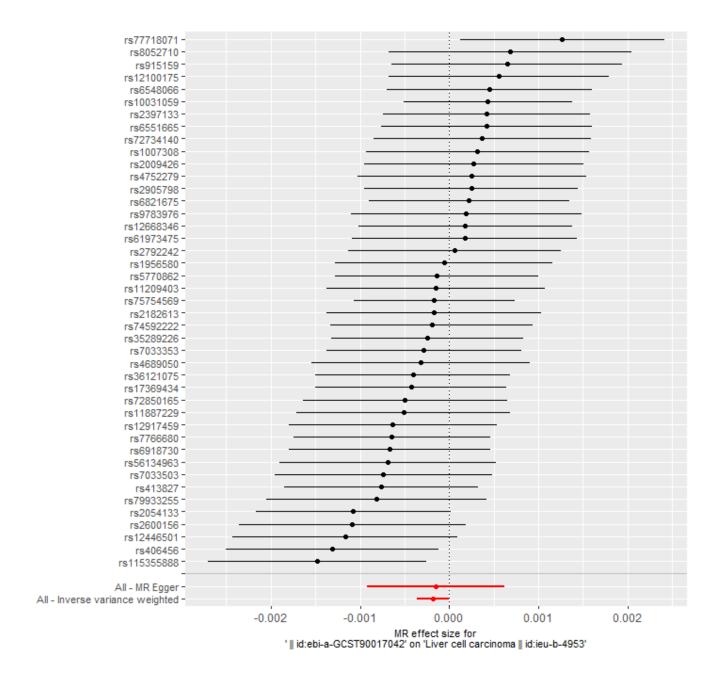


Figure 187 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Peptococcus id.2037) on liver cell carcinoma









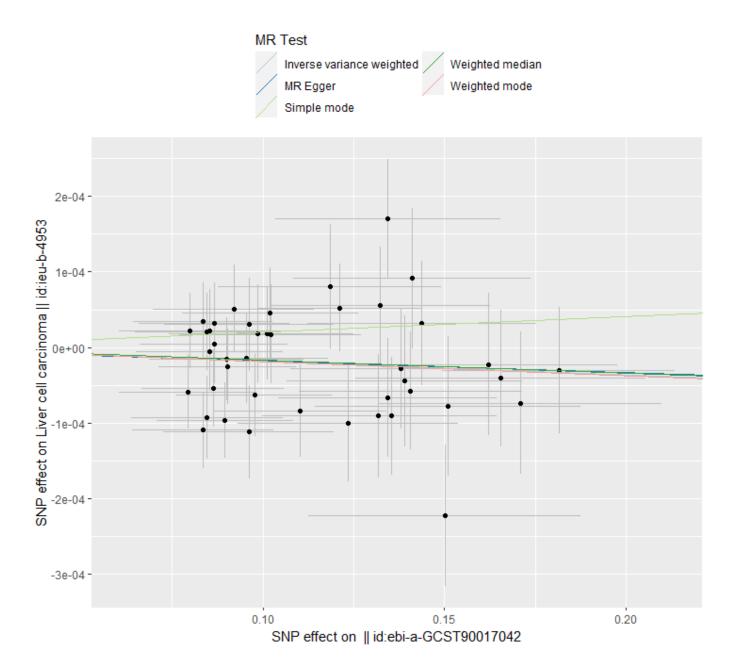
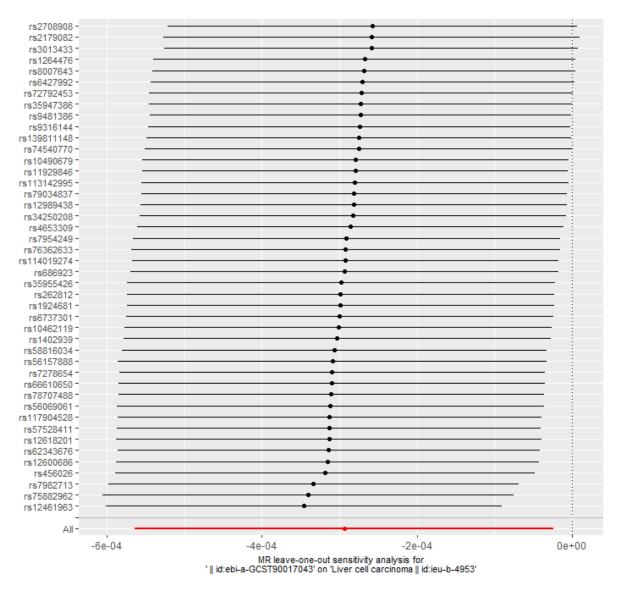
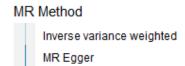
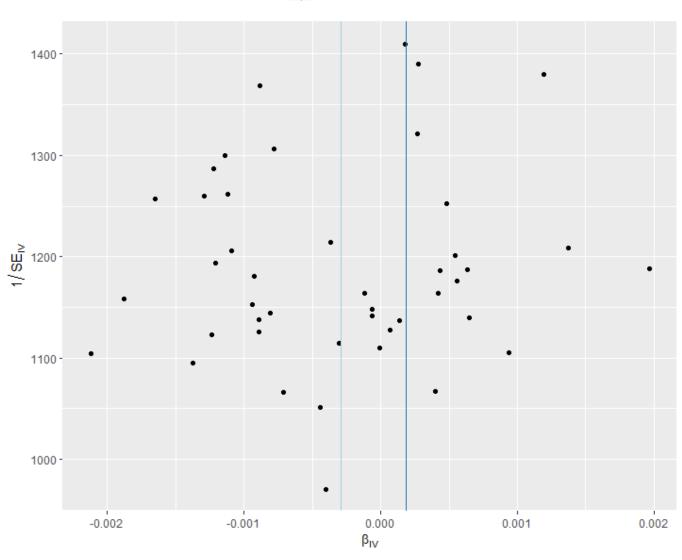
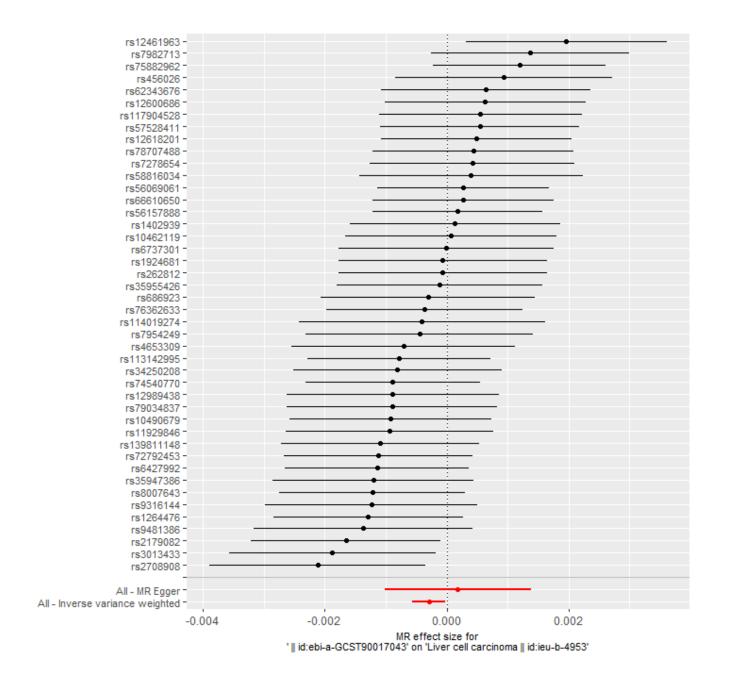


Figure 188 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Phascolarctobacterium id.2168) on liver cell carcinoma









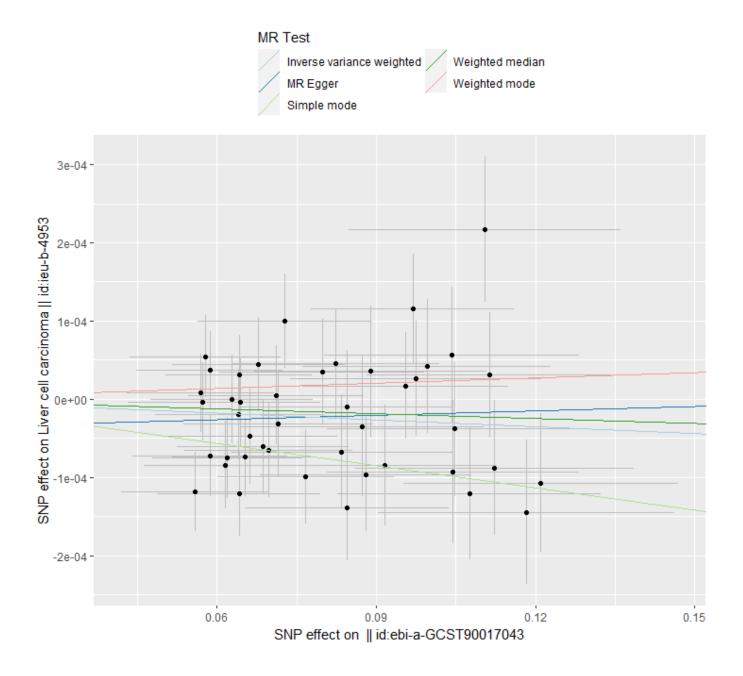
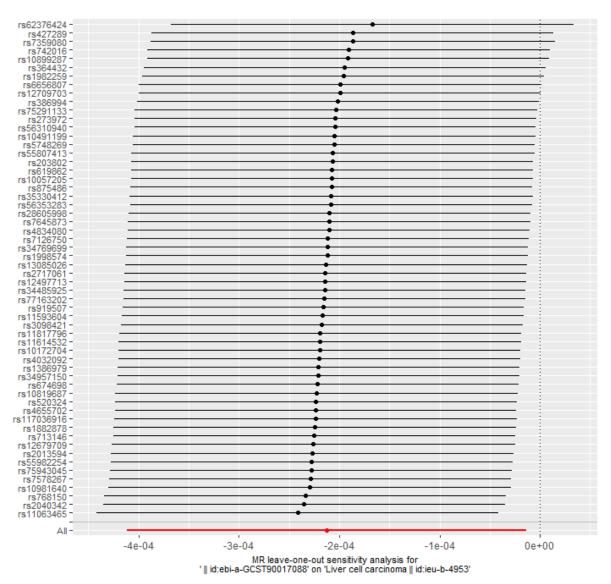
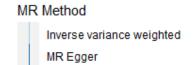
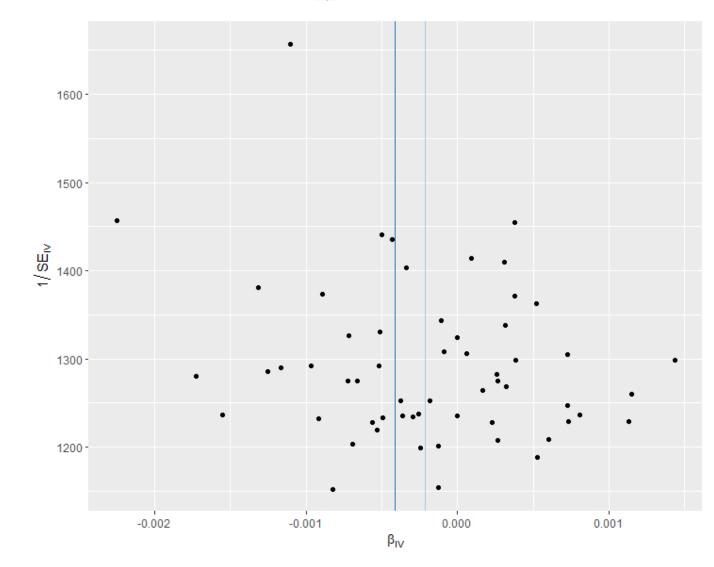
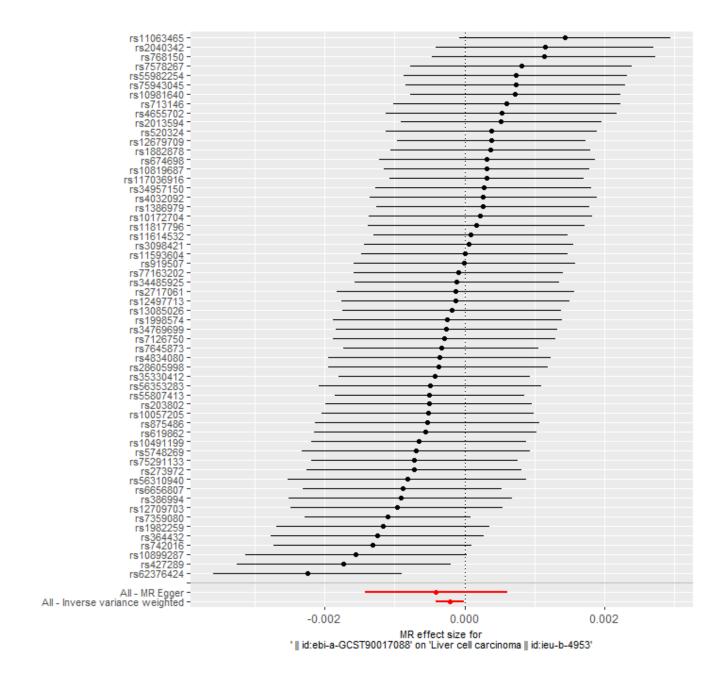


Figure 189 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Veillonella id.2198) on liver cell carcinoma









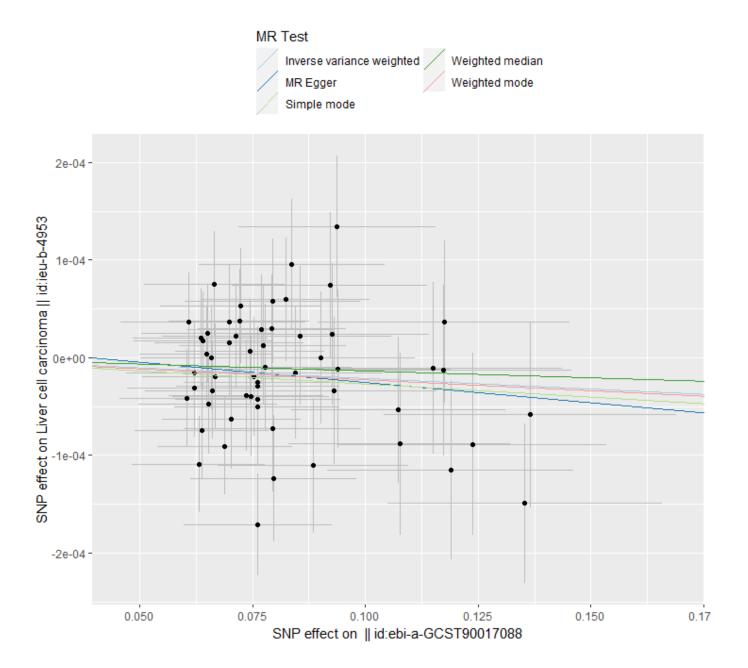
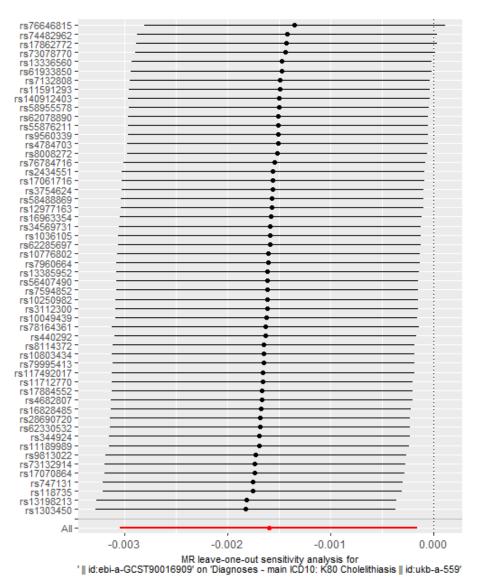
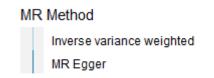
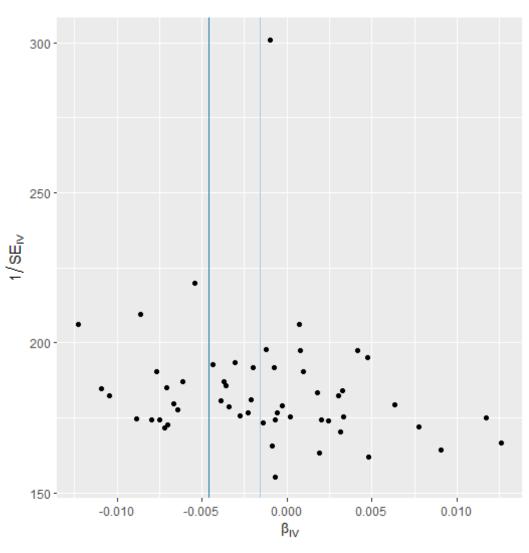
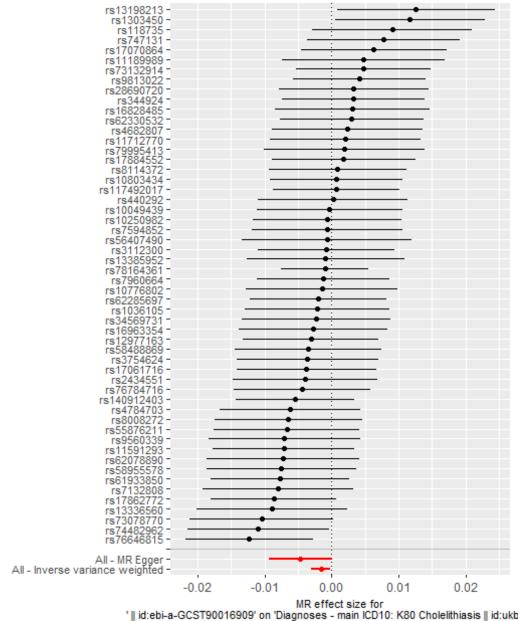


Figure 190 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Alphaproteobacteria id.2379) on cholelithiasis









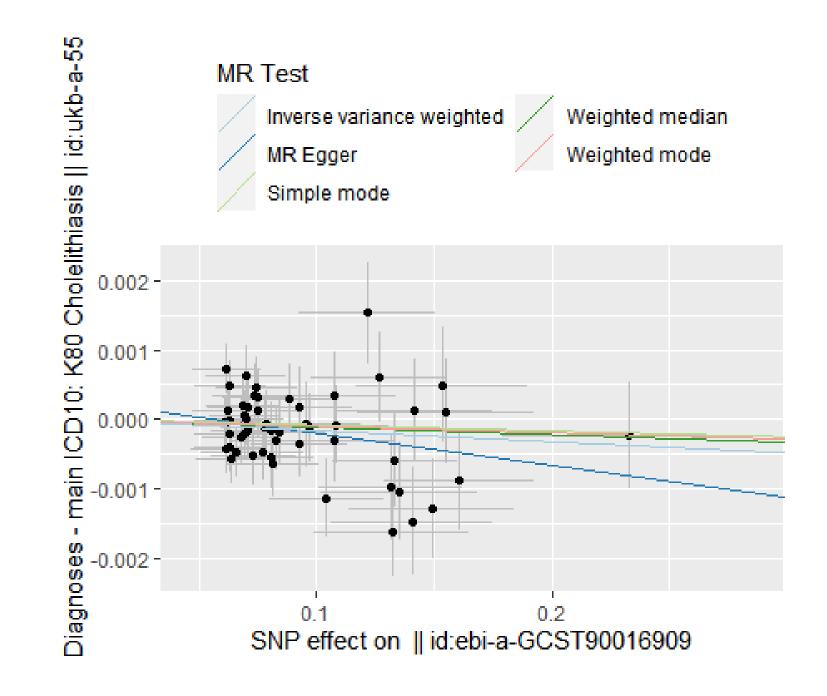
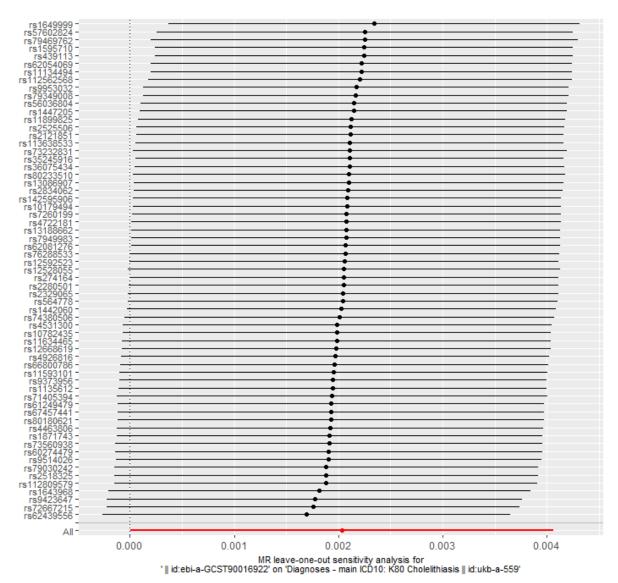
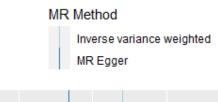
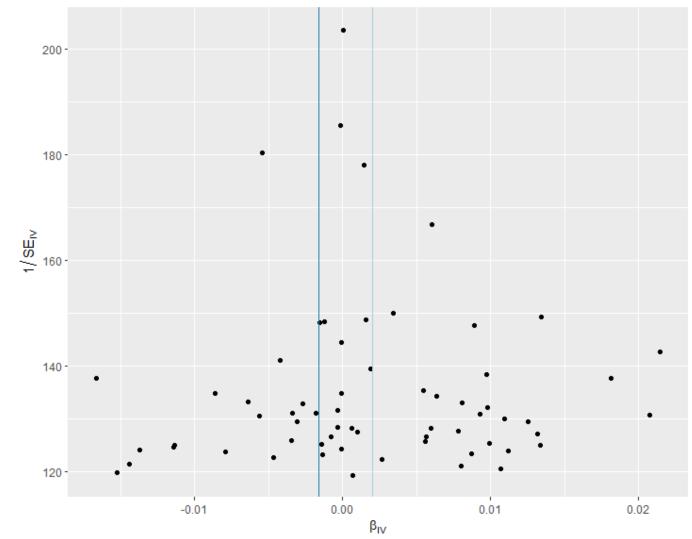
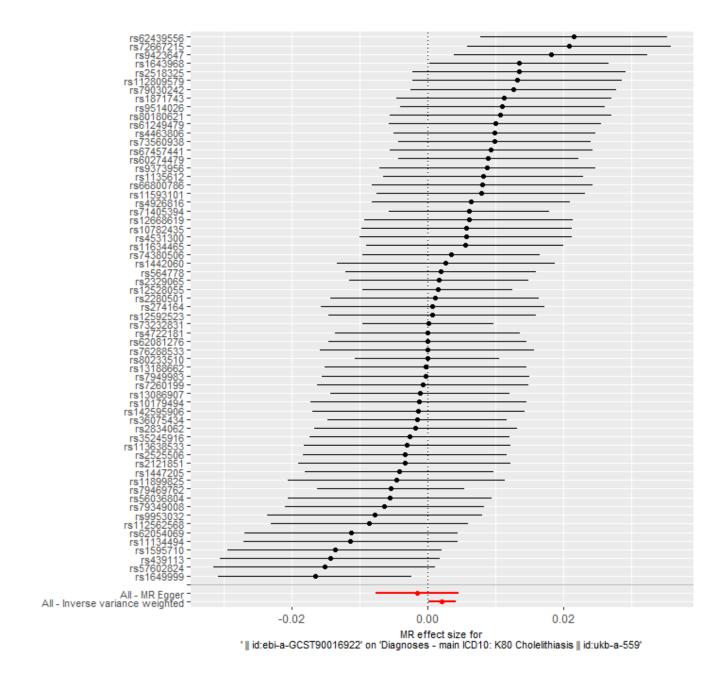


Figure 191 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Negativicutes id.2164) on cholelithiasis









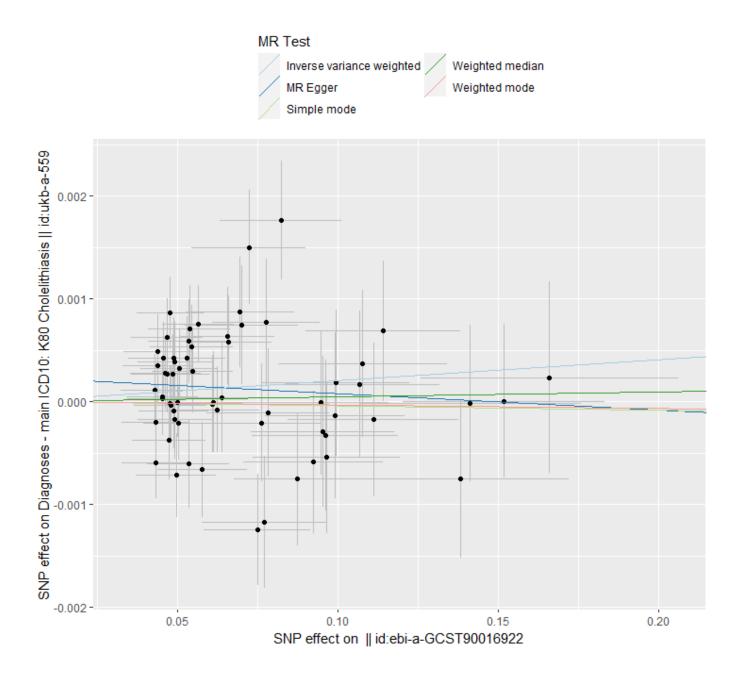
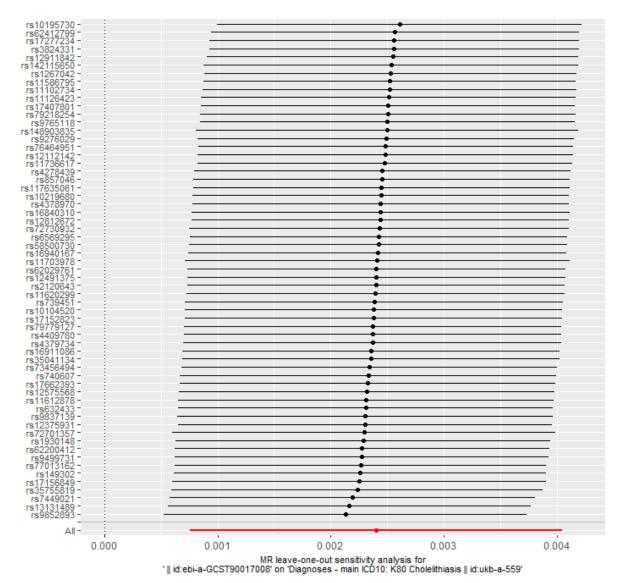
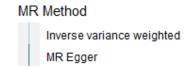
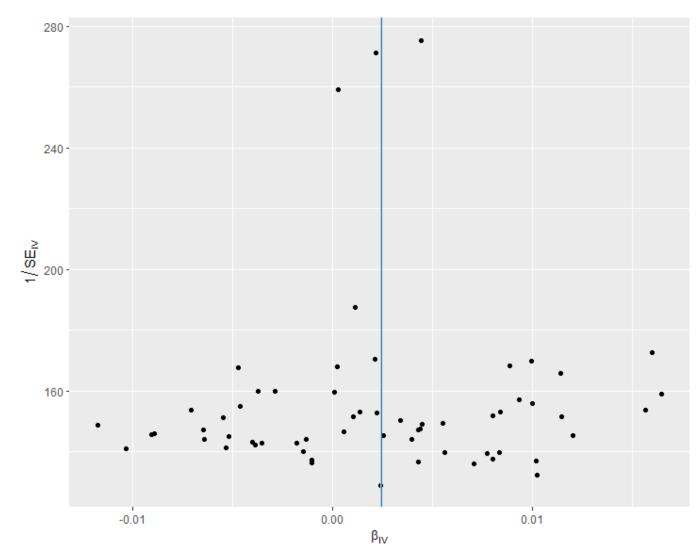
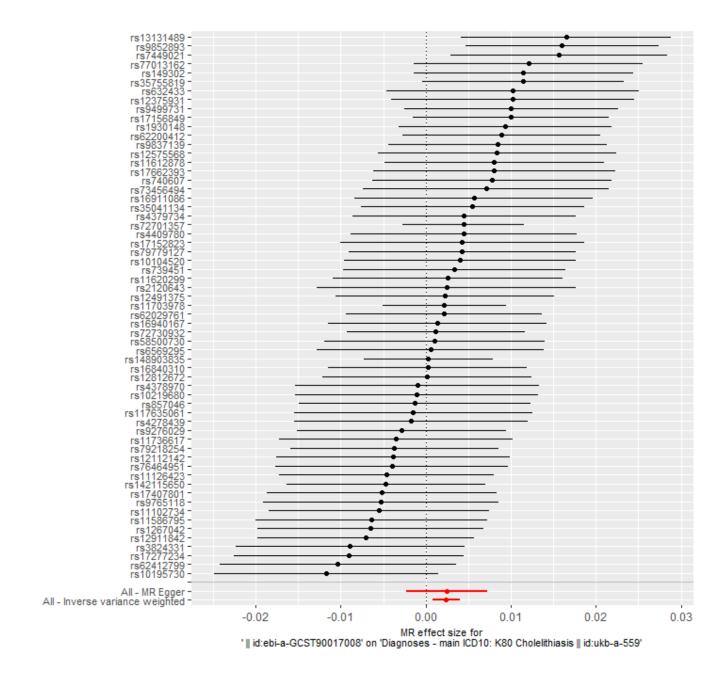


Figure 192 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Family XIII AD3011 group id.11293) on cholelithiasis









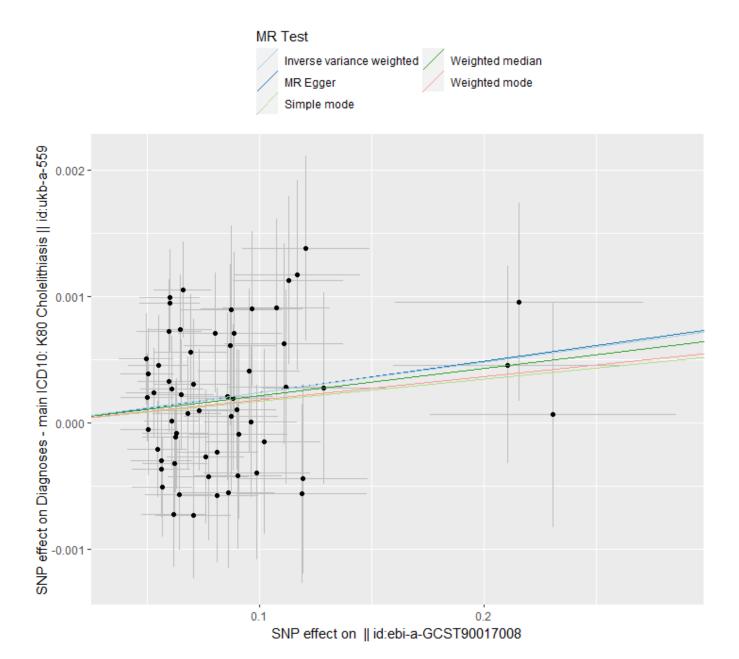
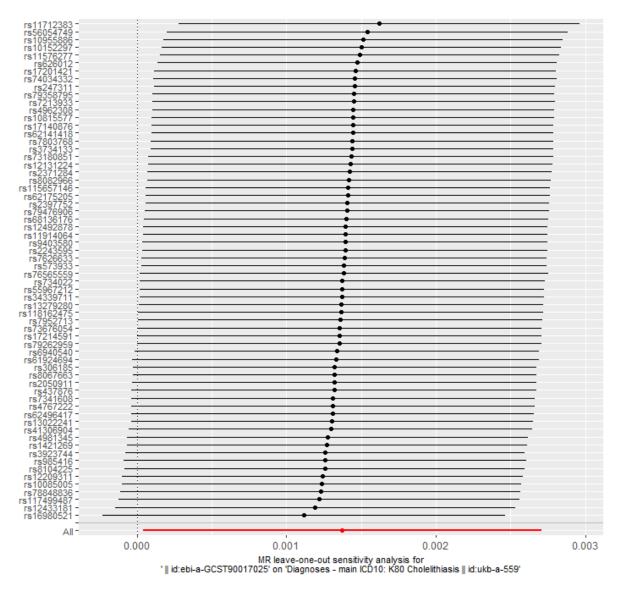
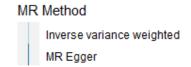
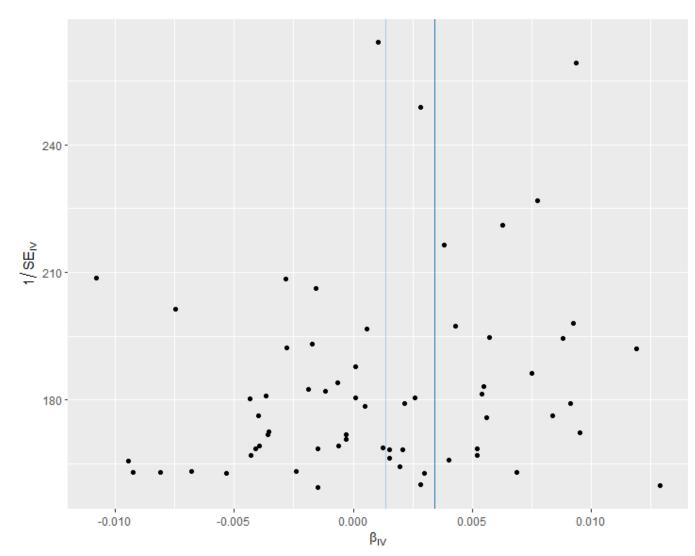
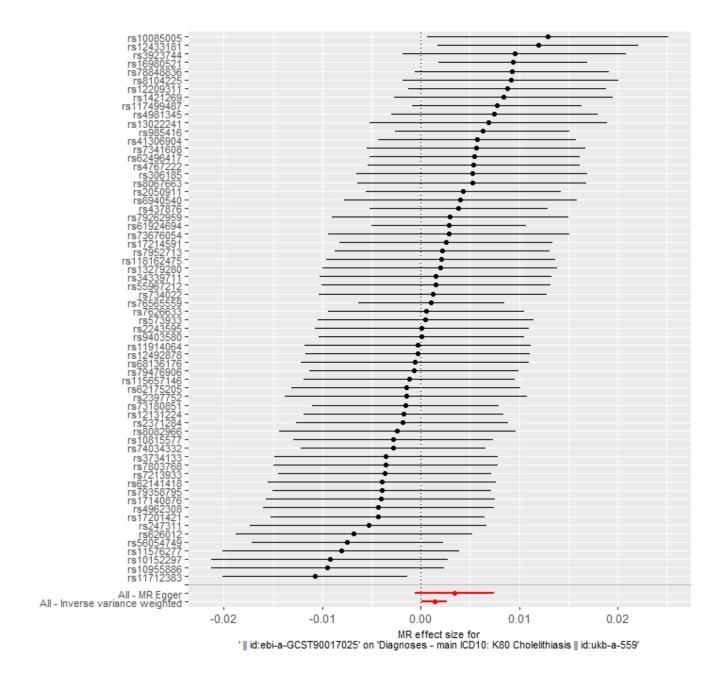


Figure 193 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lachnospiraceae UCG001 id.11321) on cholelithiasis











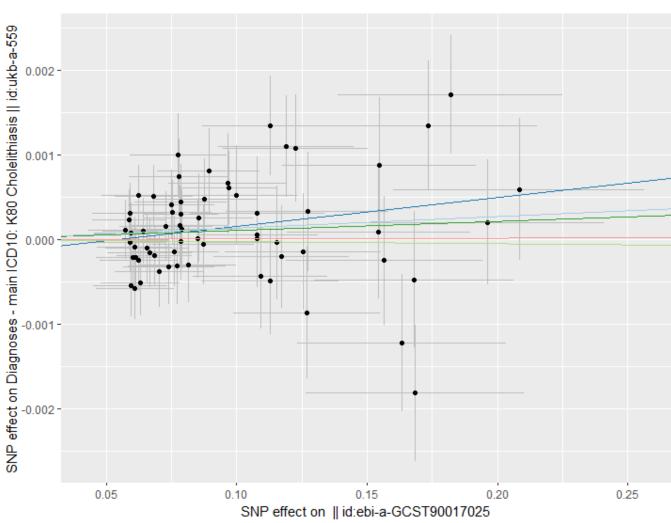
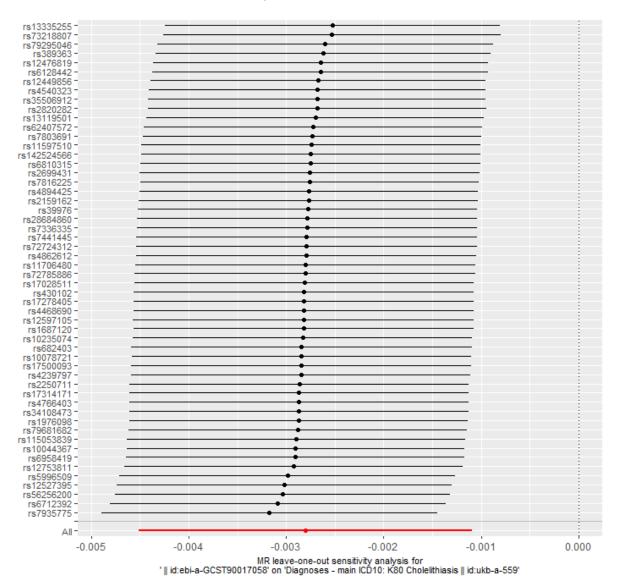
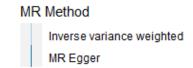
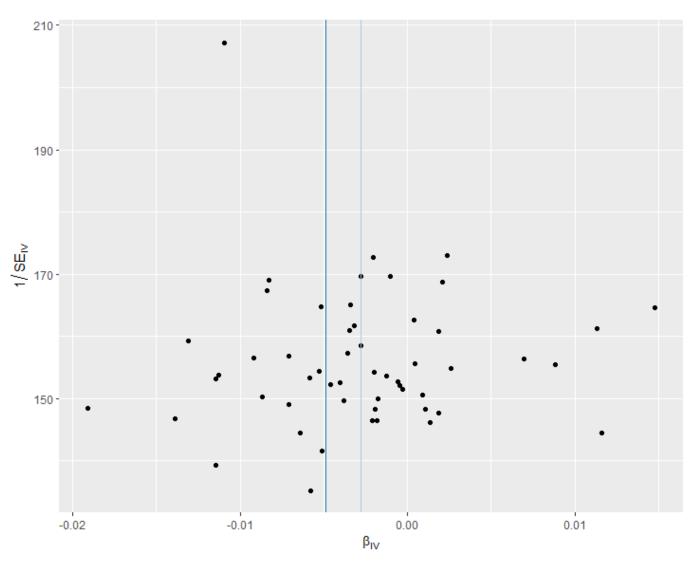
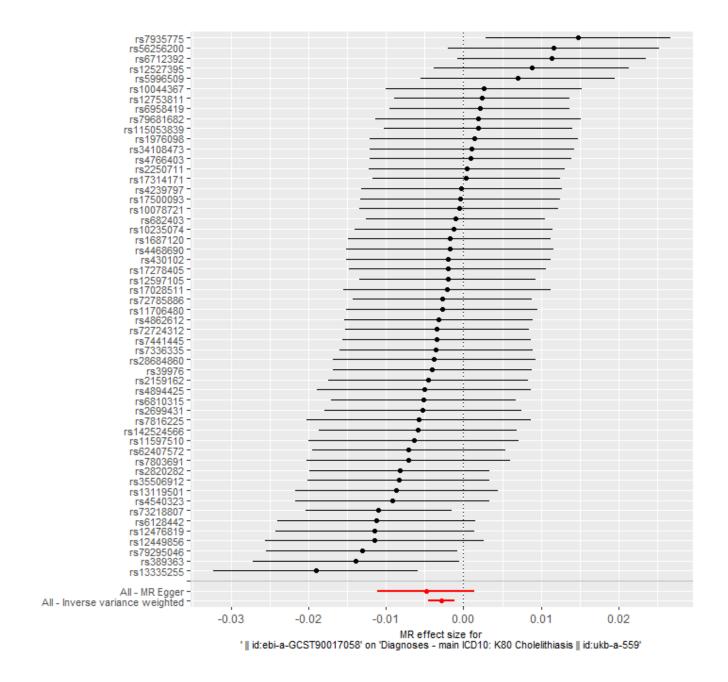


Figure 194 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG010 id.11367) on cholelithiasis









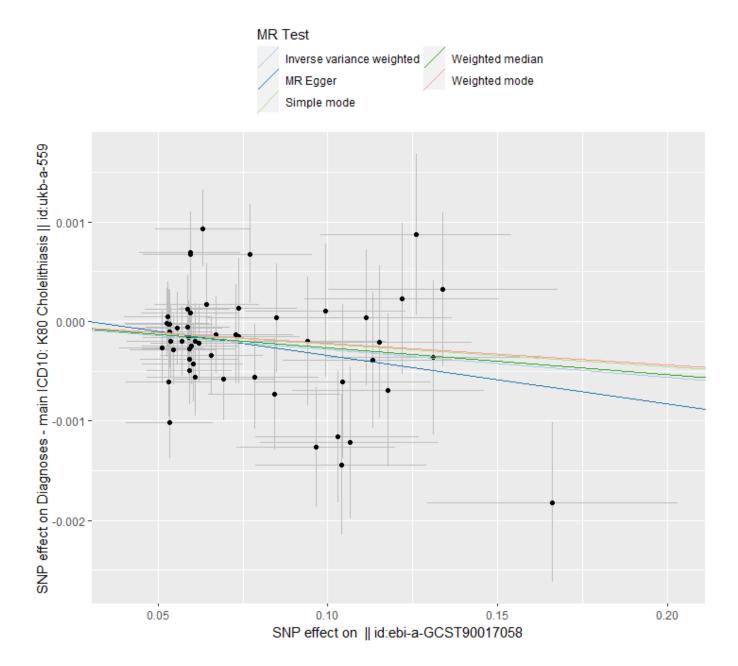
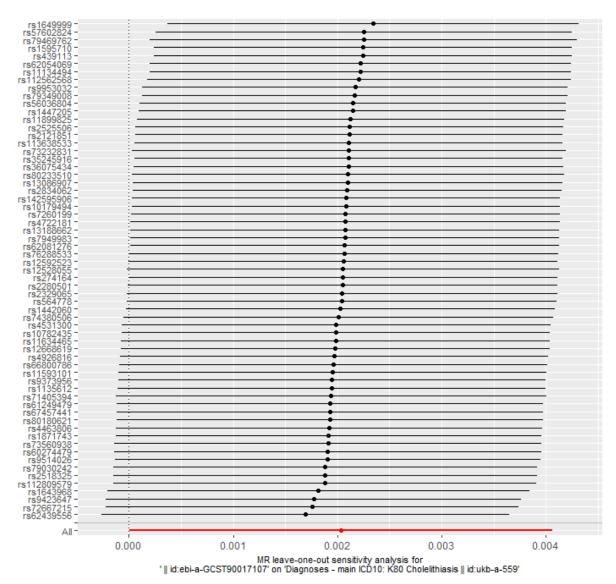
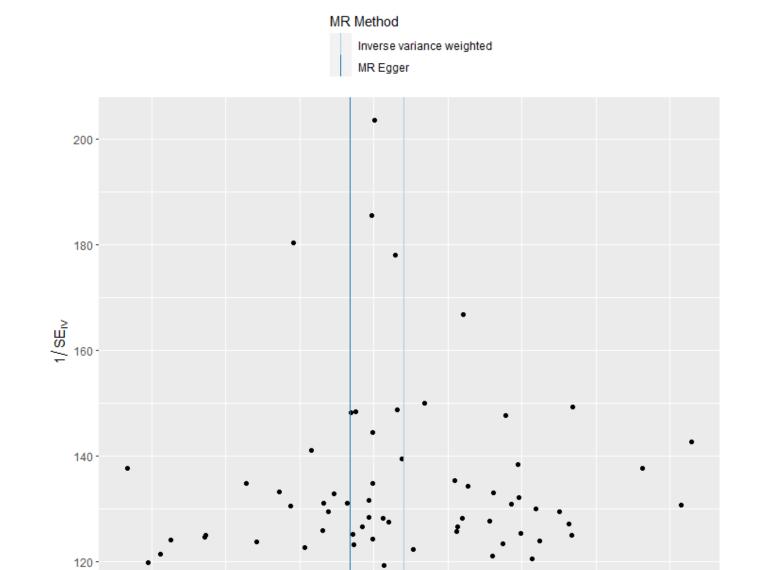


Figure 195 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Selenomonadales id.2165) on cholelithiasis





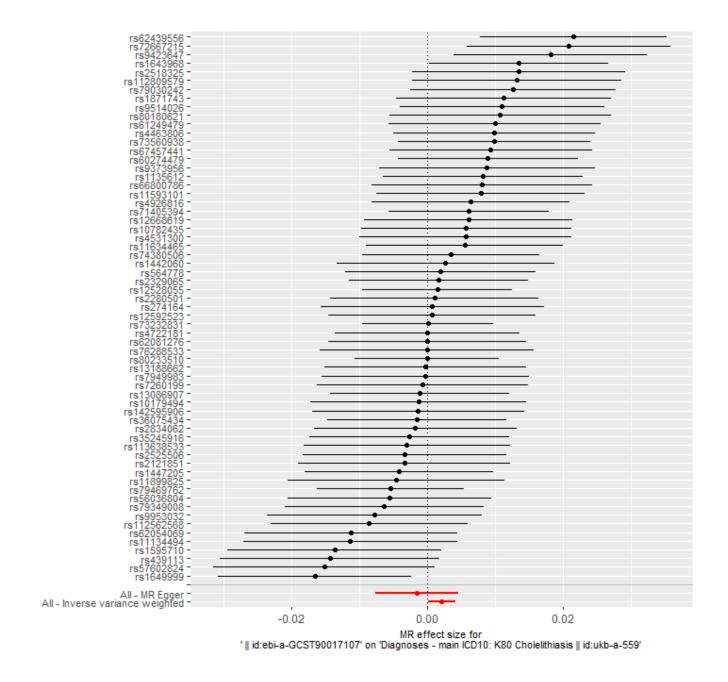
0.00

 β_{IV}

0.02

0.01

-0.01



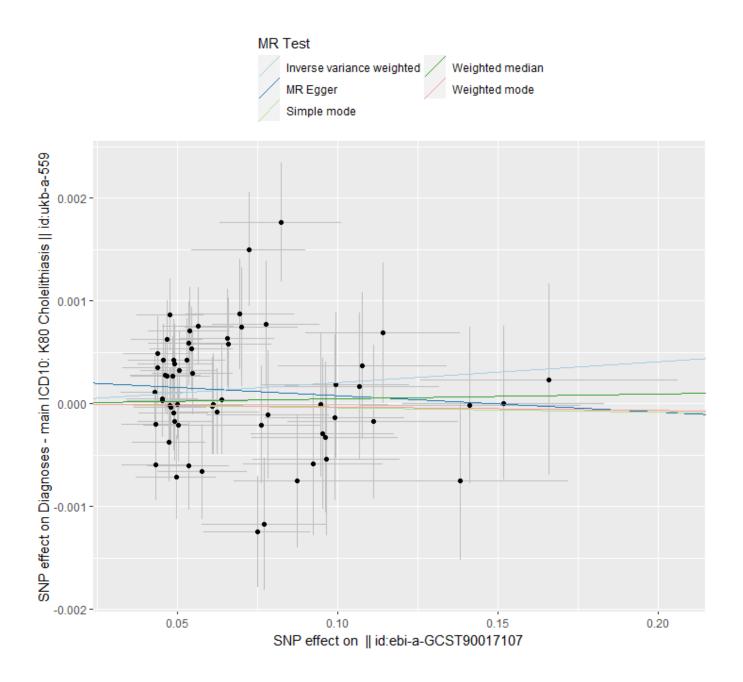
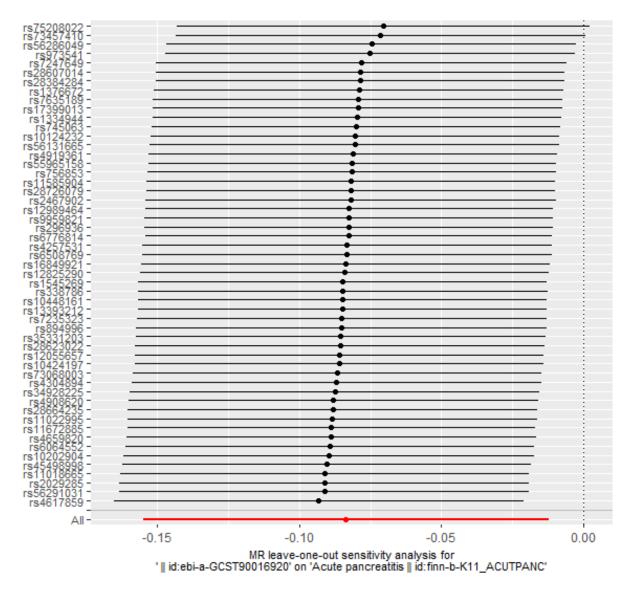
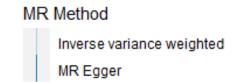
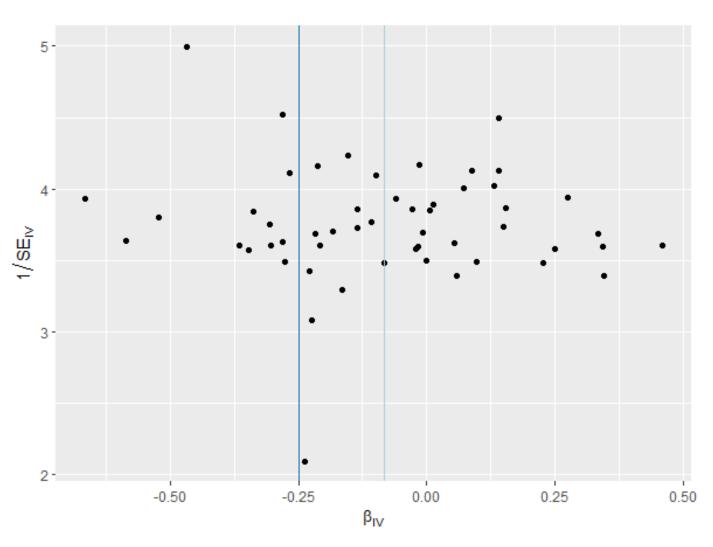
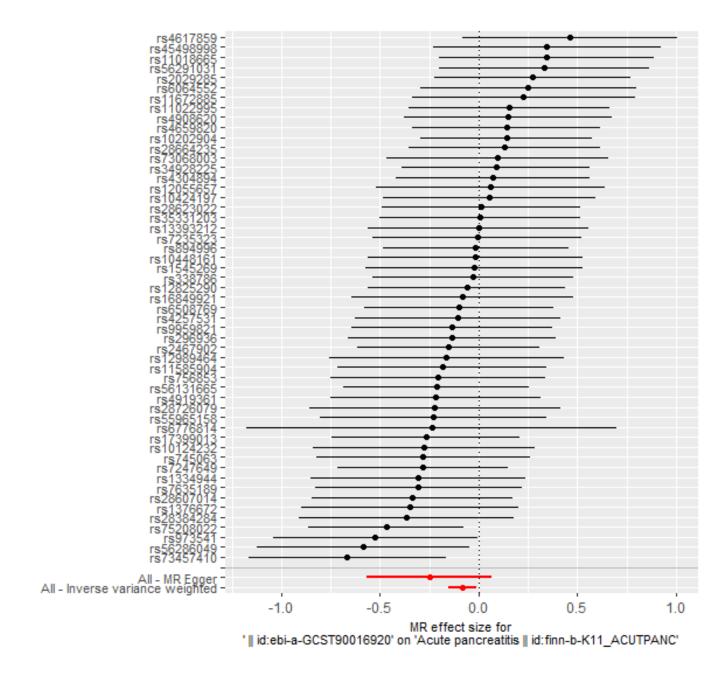


Figure 196 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (class Methanobacteria id.119) on acute pancreatitis









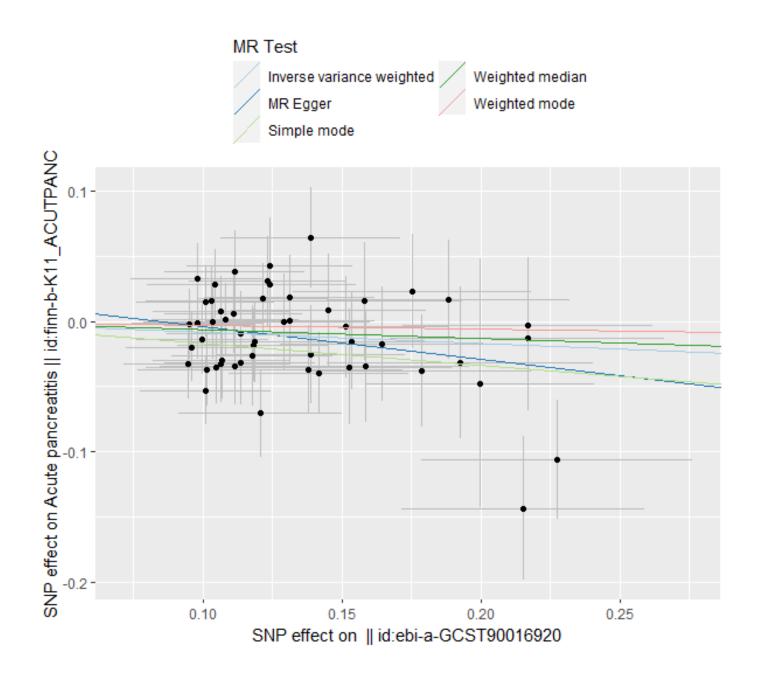
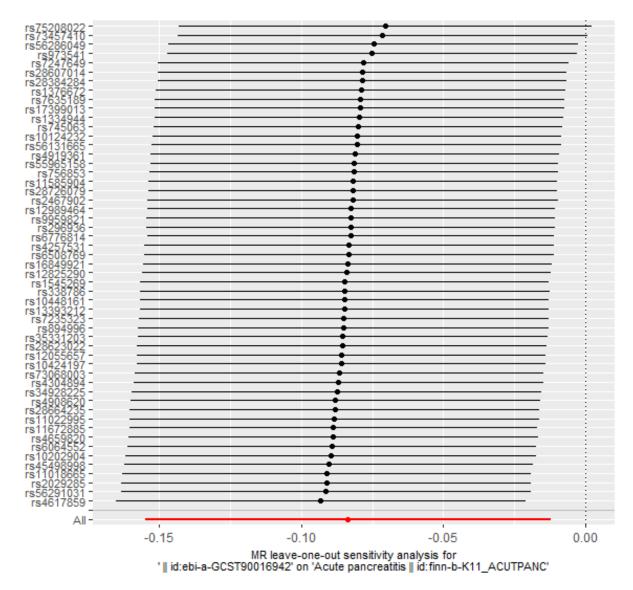
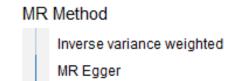
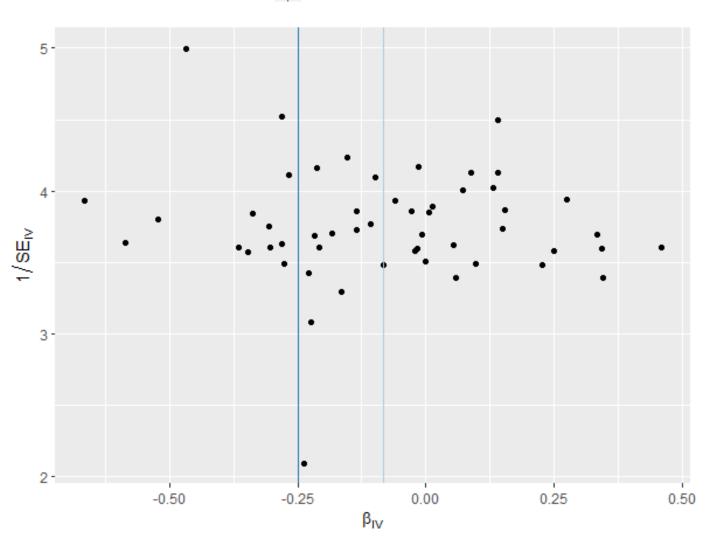
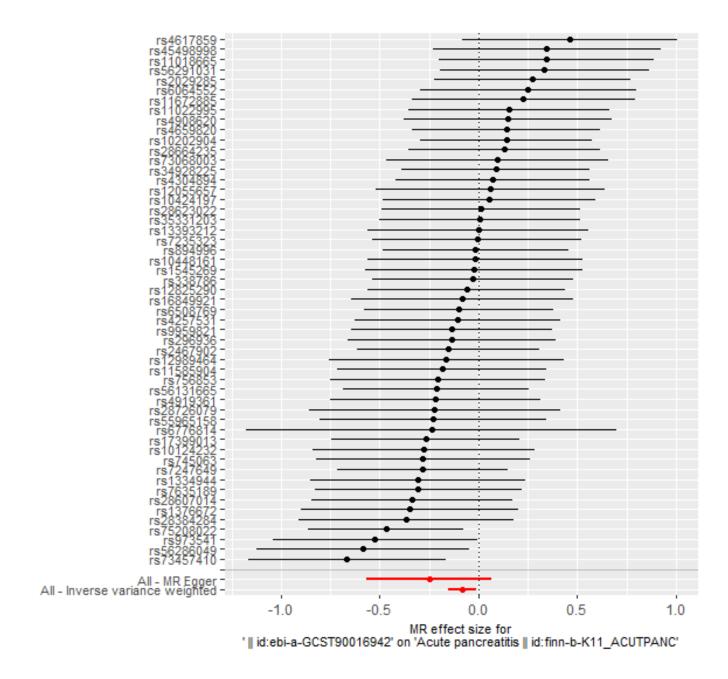


Figure 197 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Methanobacteriaceae id.121) on acute pancreatitis









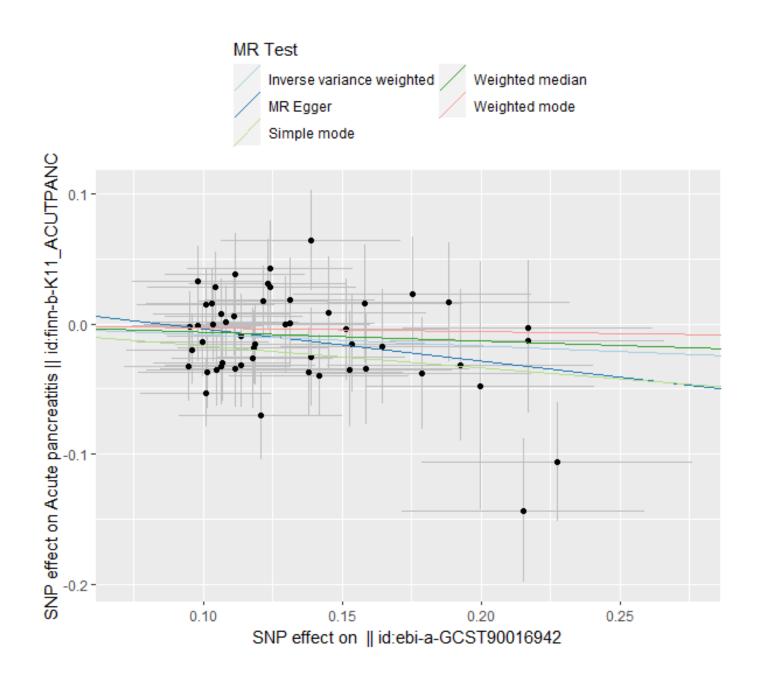
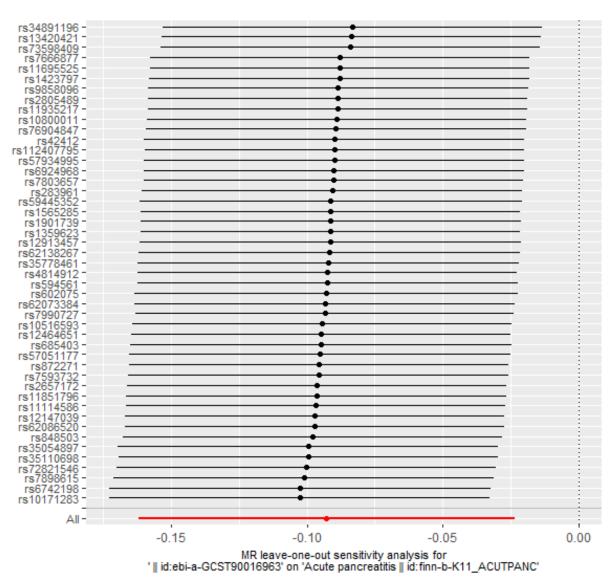


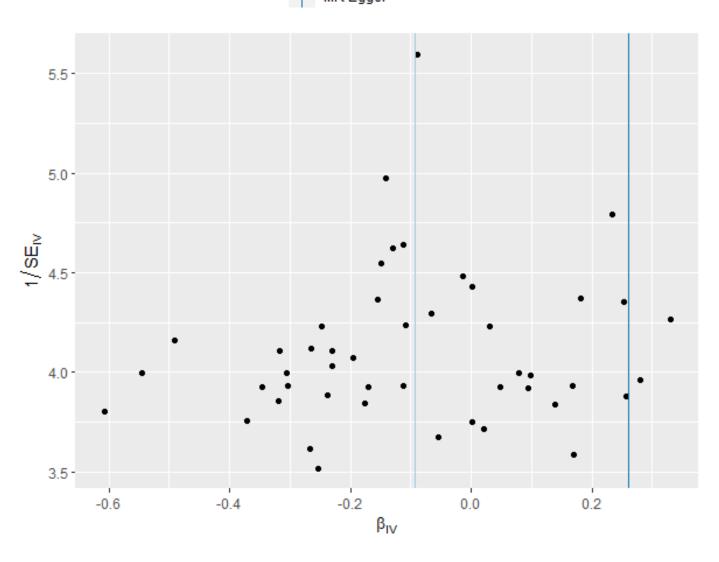
Figure 198 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Allisonella id.2174) on acute pancreatitis

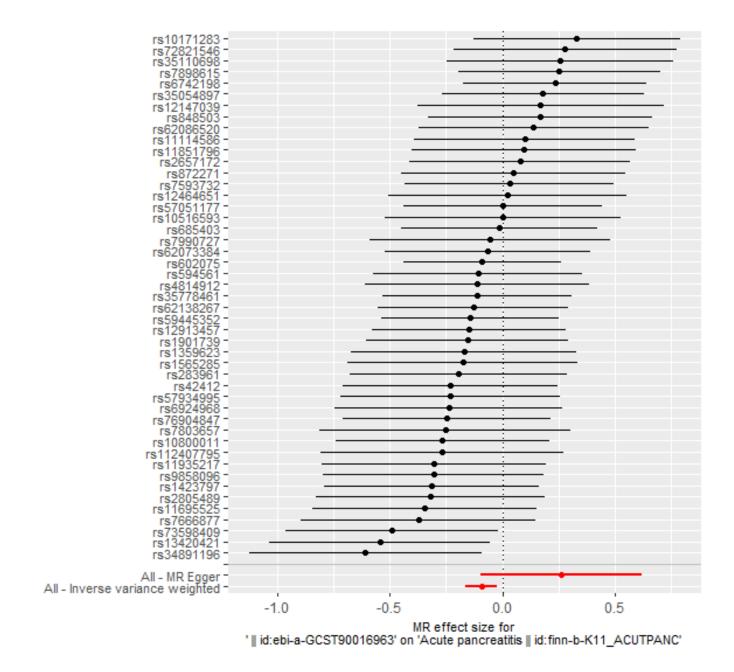


MR Method

Inverse variance weighted

MR Egger





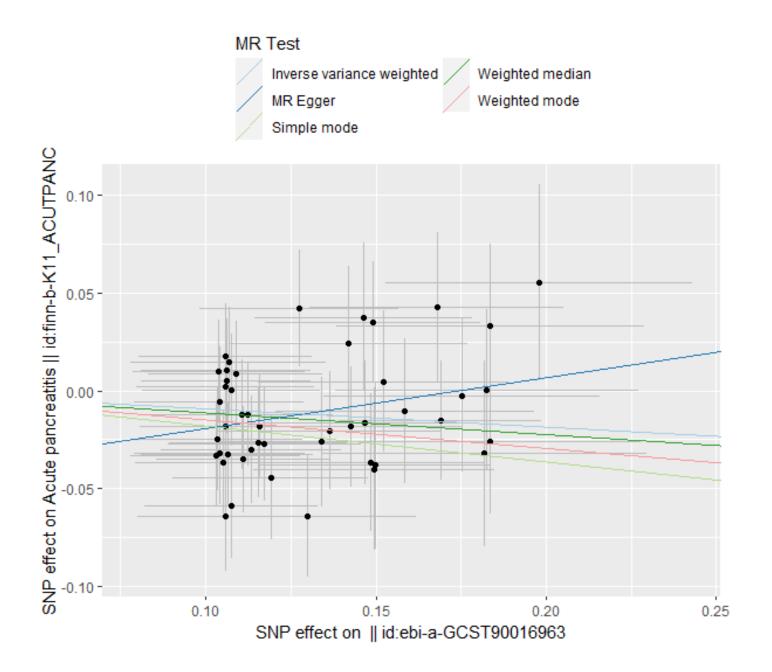
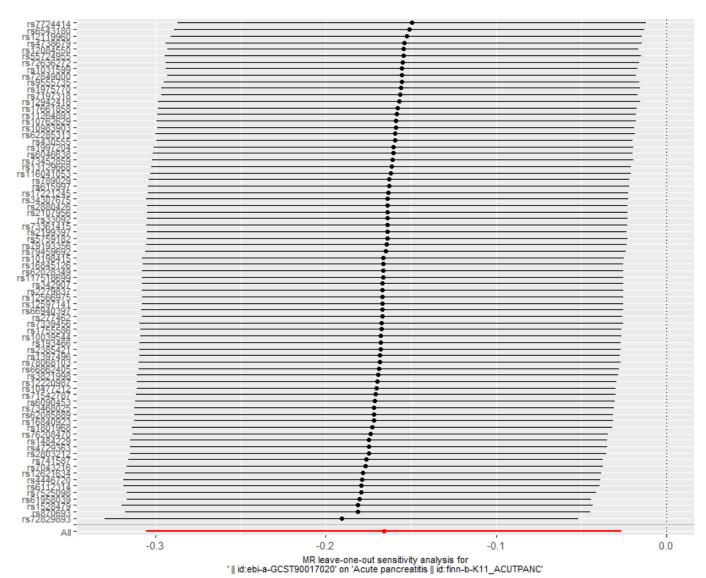
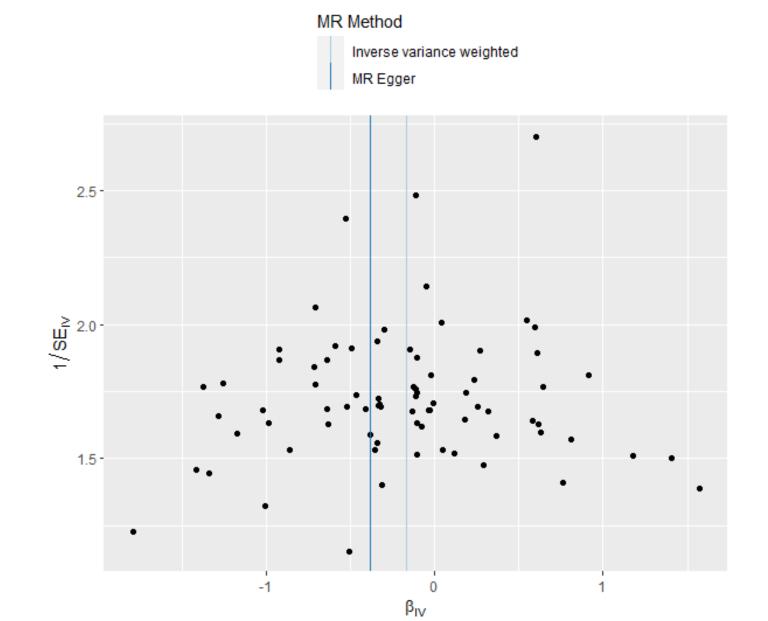
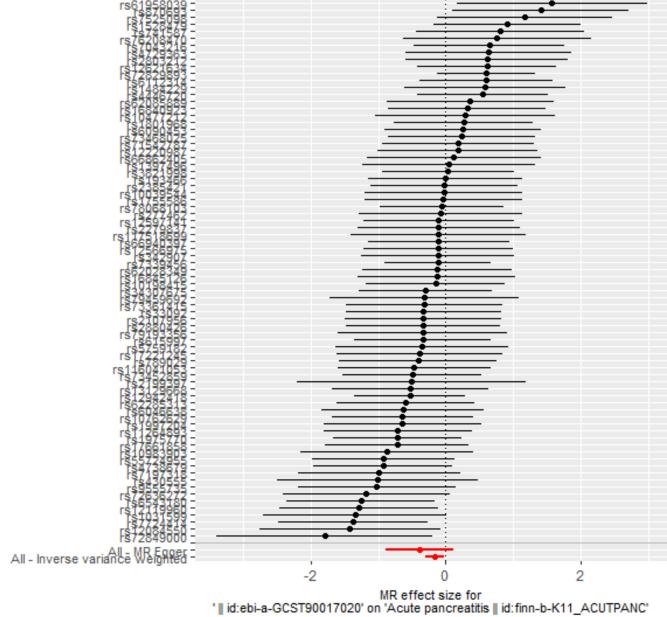


Figure 199 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Lachnoclostridium id.11308) on acute pancreatitis







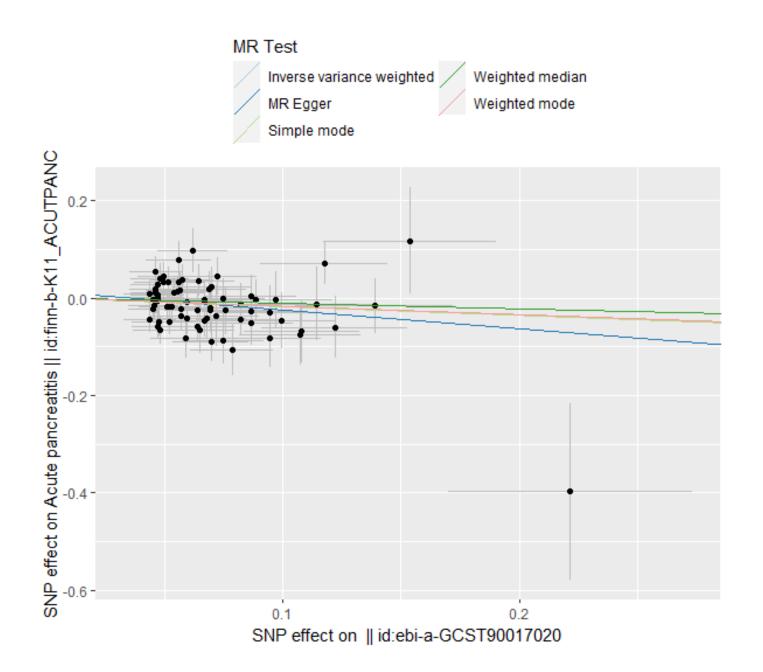
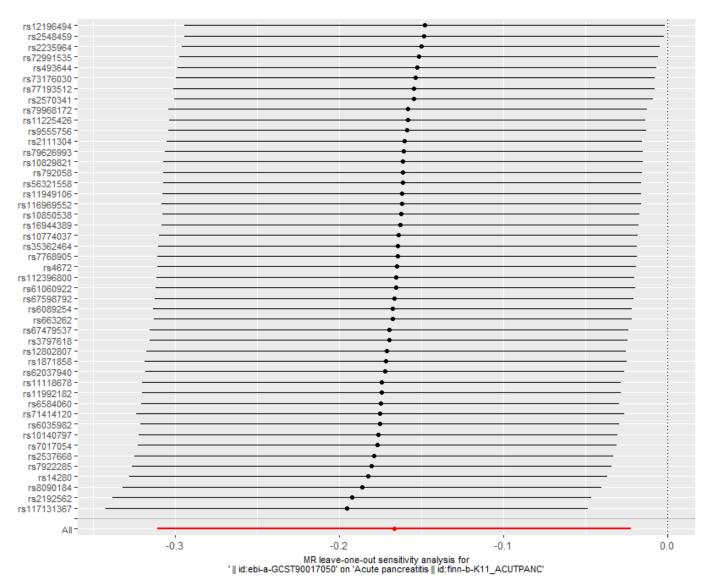
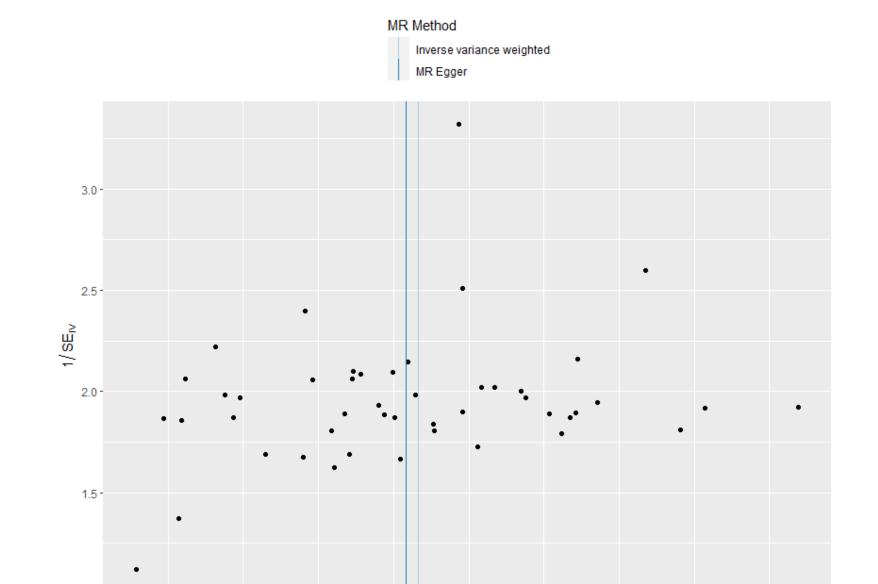


Figure 200 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminiclostridium6 id.11356) on acute pancreatitis



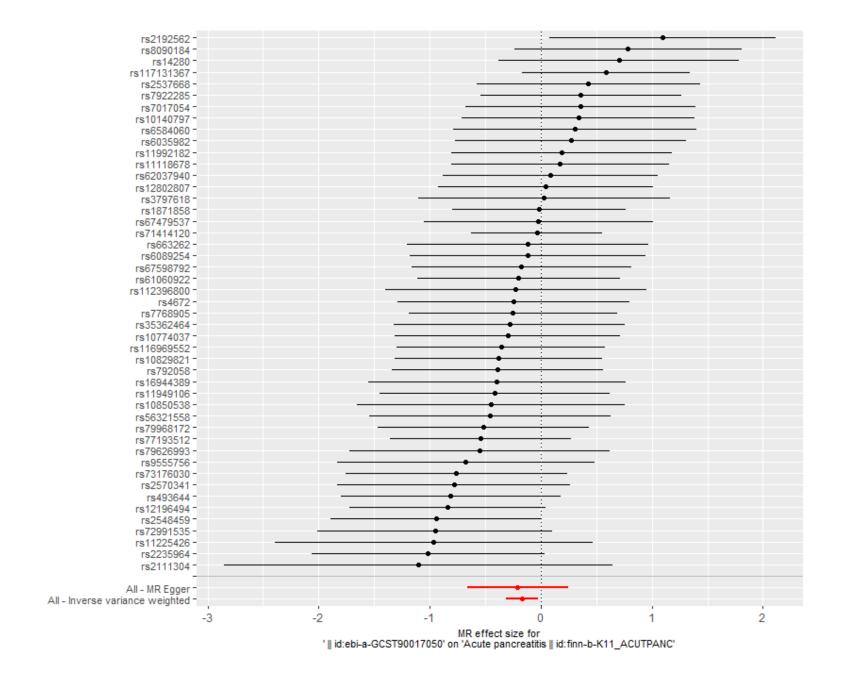


0.0 β_{IV} 0.5

1.0

-0.5

-1.0





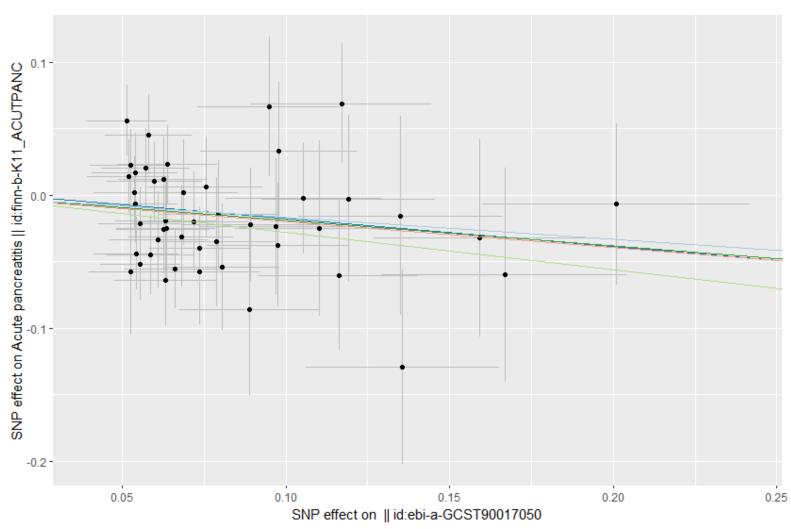
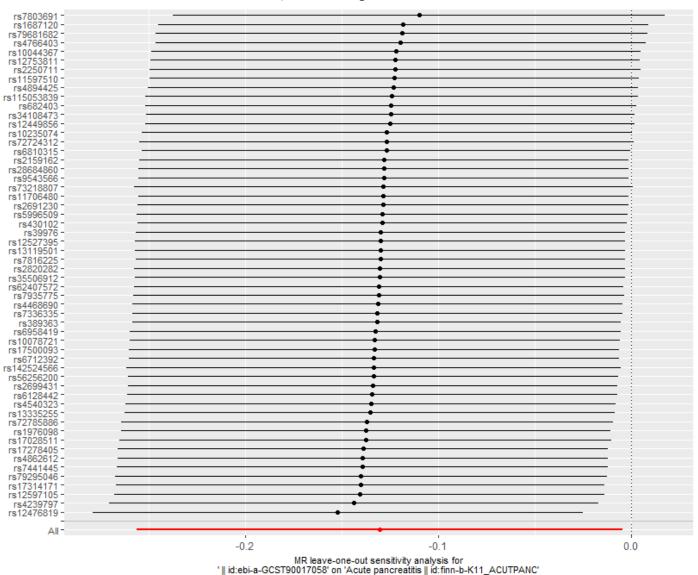
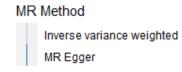
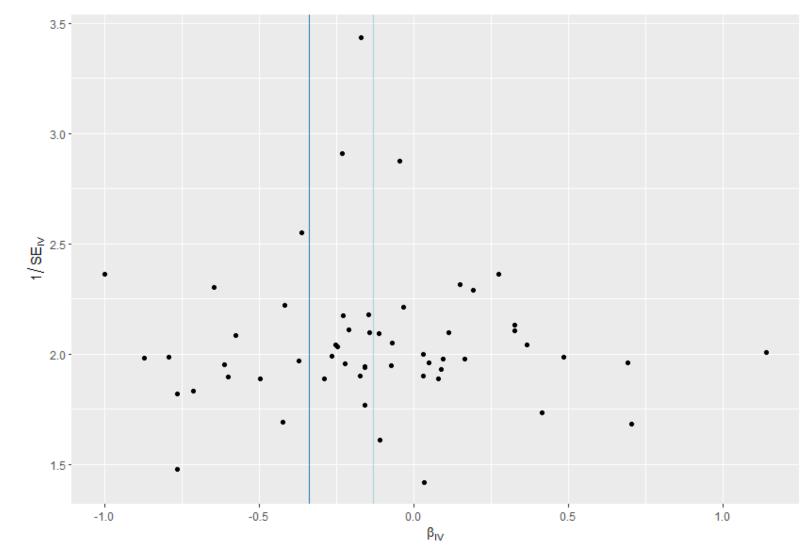
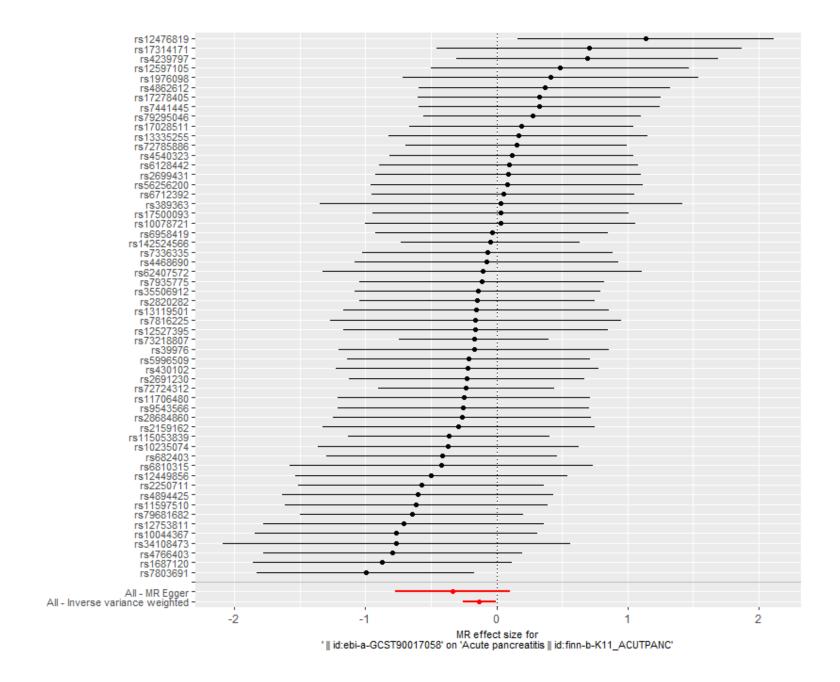


Figure 201 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG010 id.11367) on acute pancreatitis









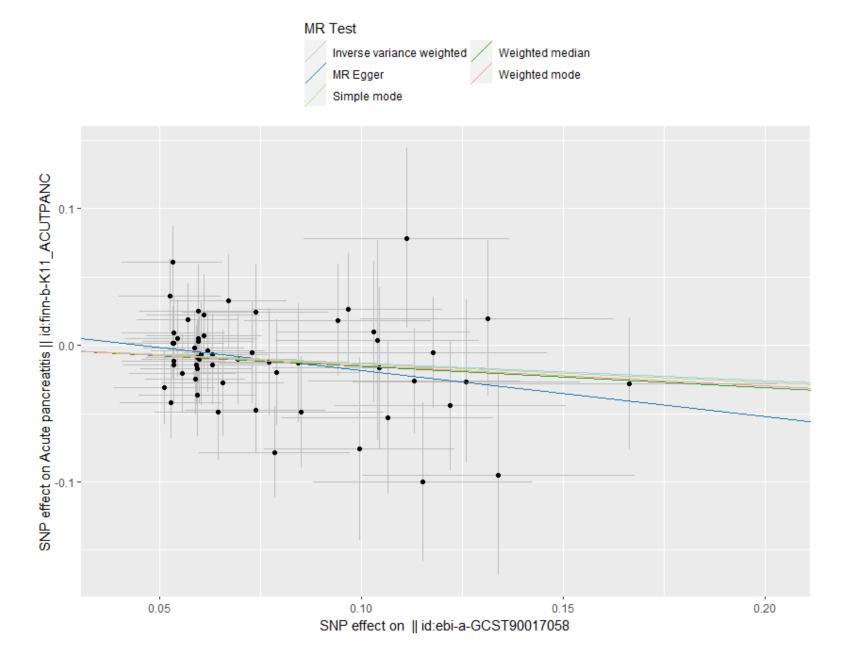
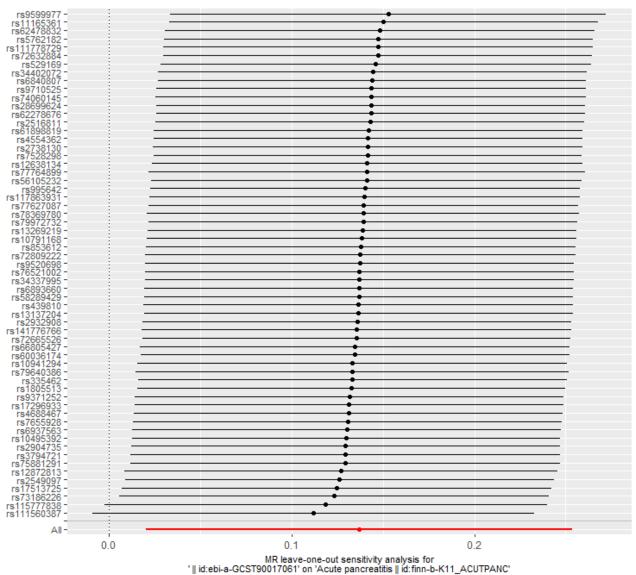
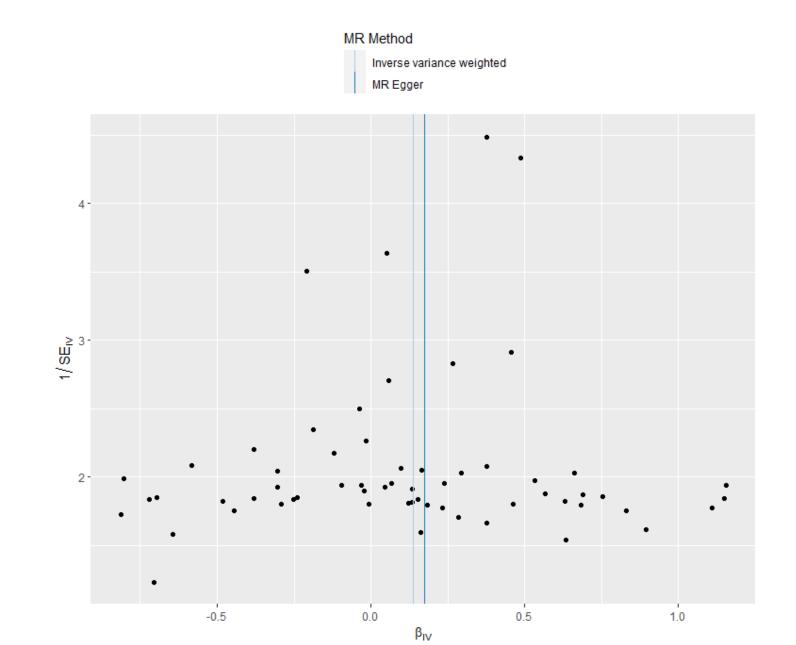
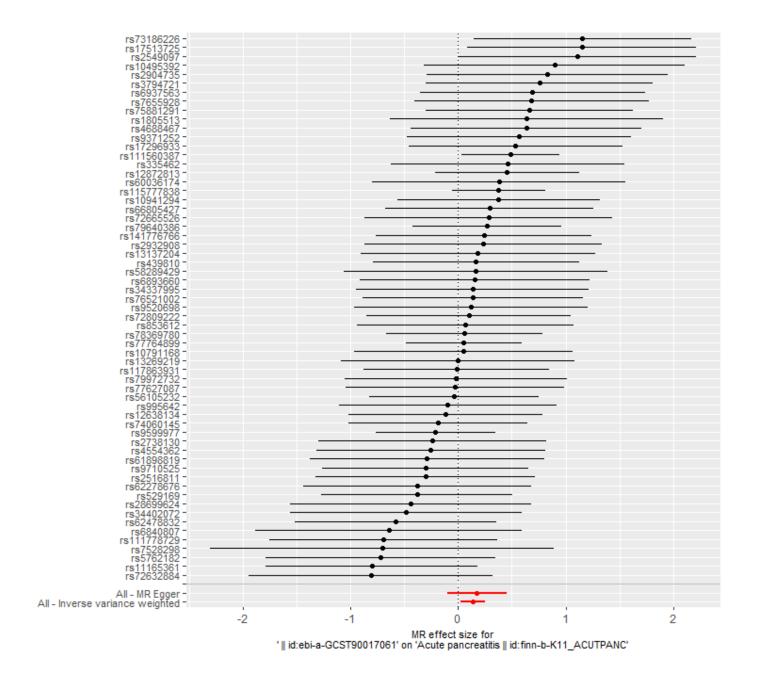
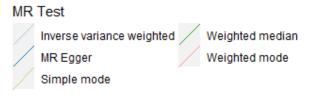


Figure 202 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Ruminococcaceae UCG014 id.11371) on acute pancreatitis









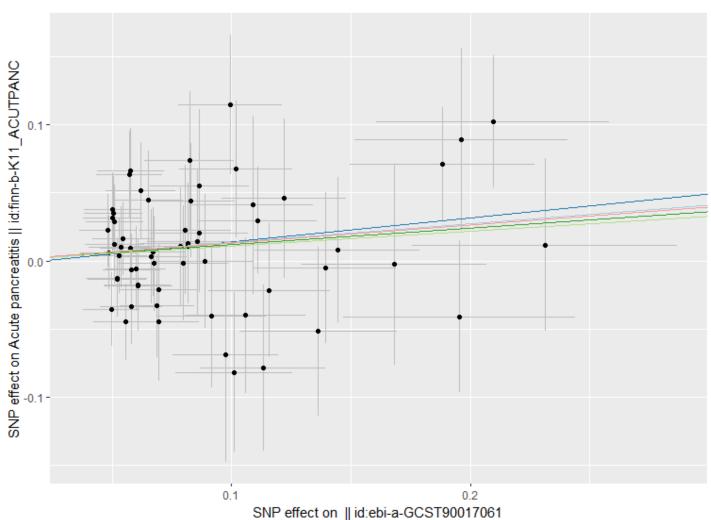
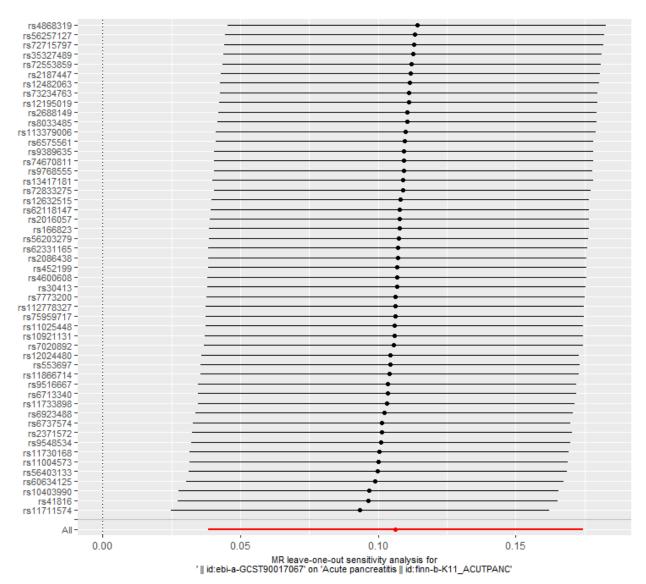
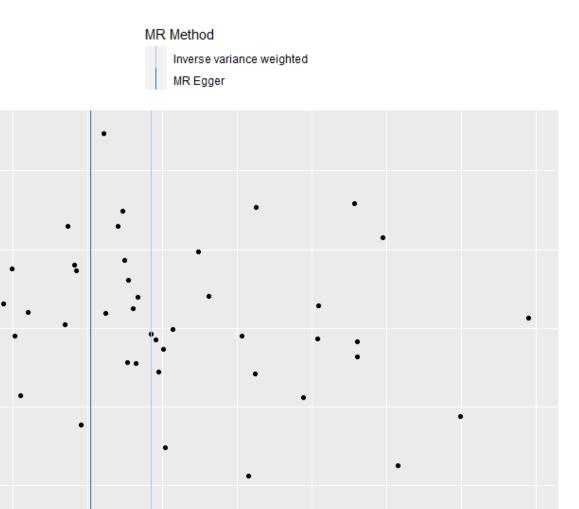


Figure 203 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Sellimonas id.14369) on acute pancreatitis





0.25

 β_{IV}

0.50

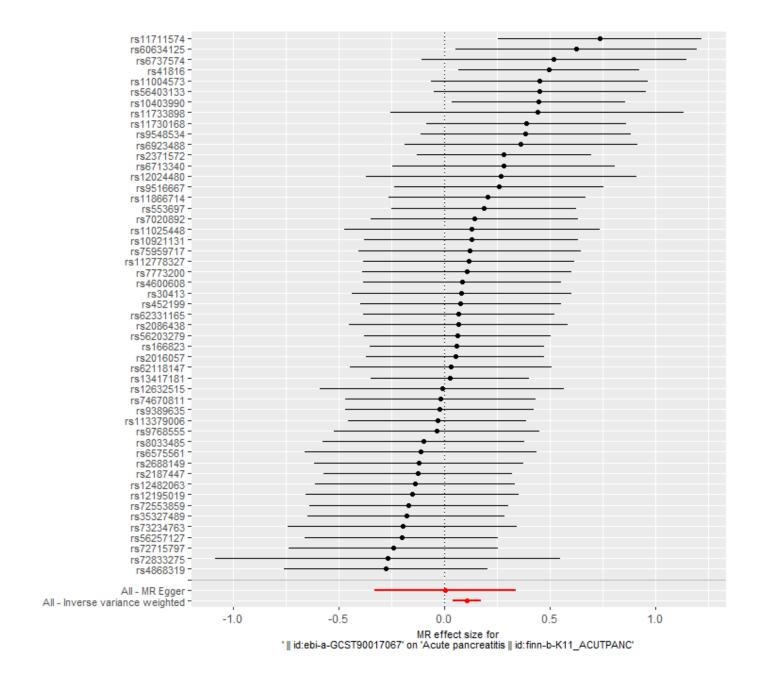
0.75

1/SE√

3-

-0.25

0.00





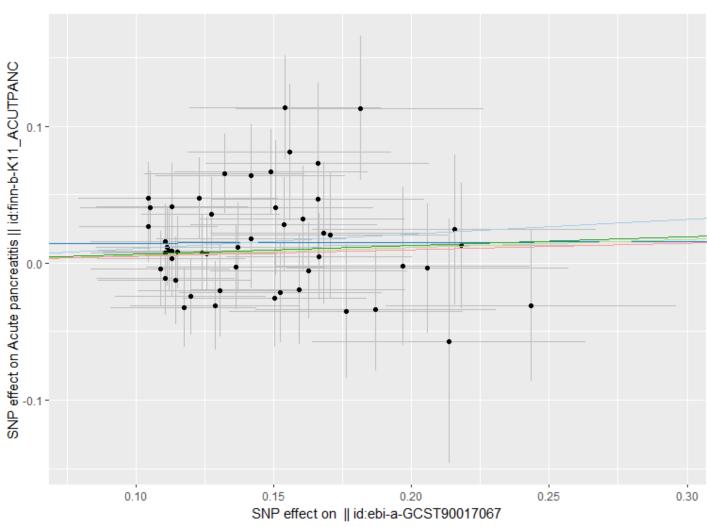
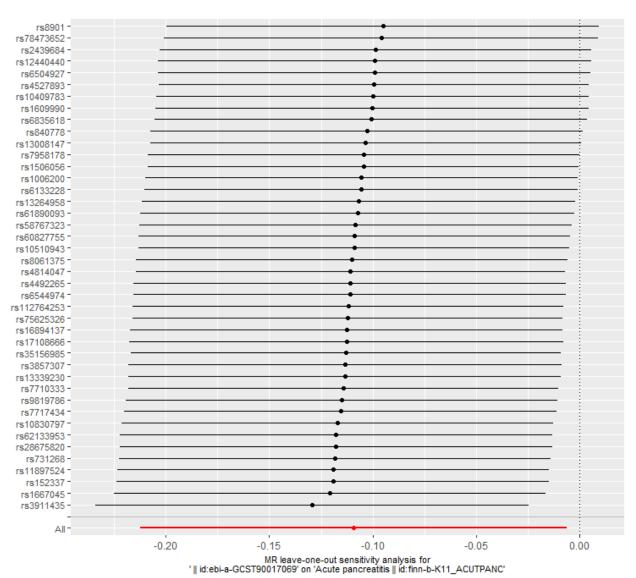
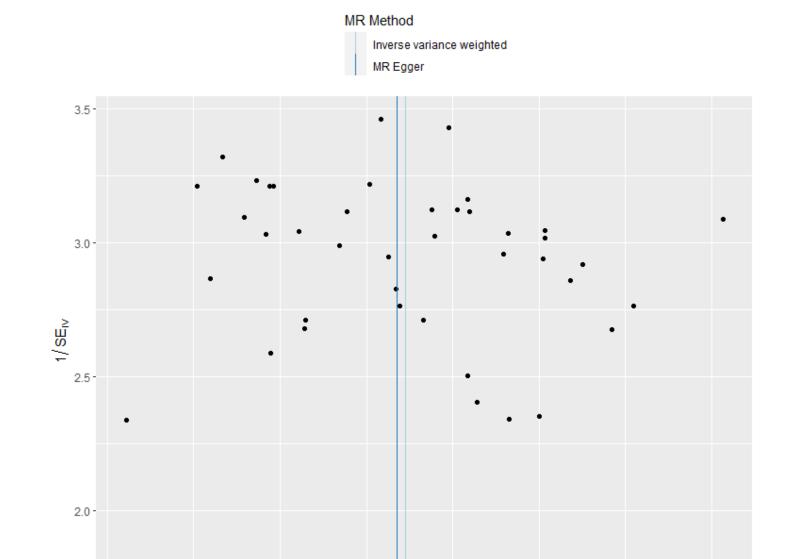


Figure 204 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Slackia id.825) on acute pancreatitis





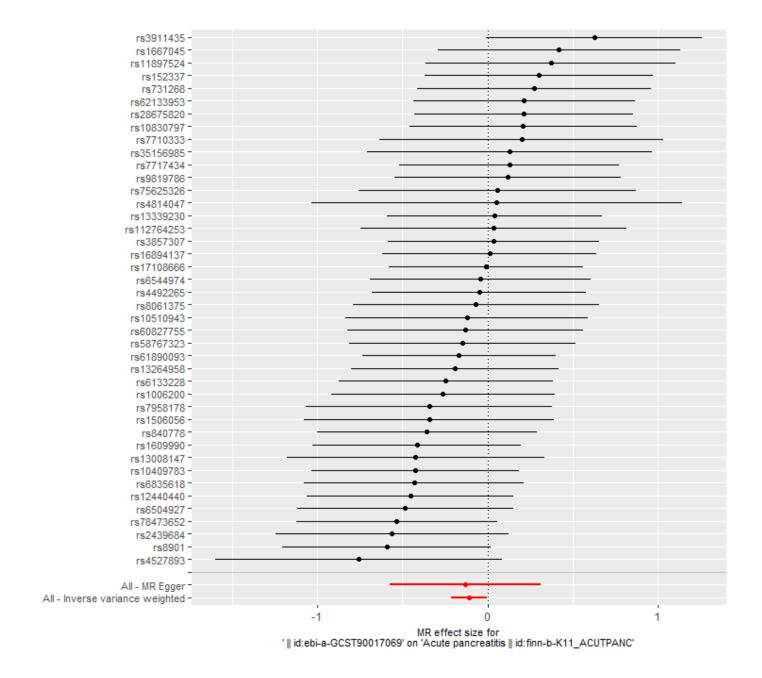
0.0

 β_{IV}

0.4

-0.8

-0.4





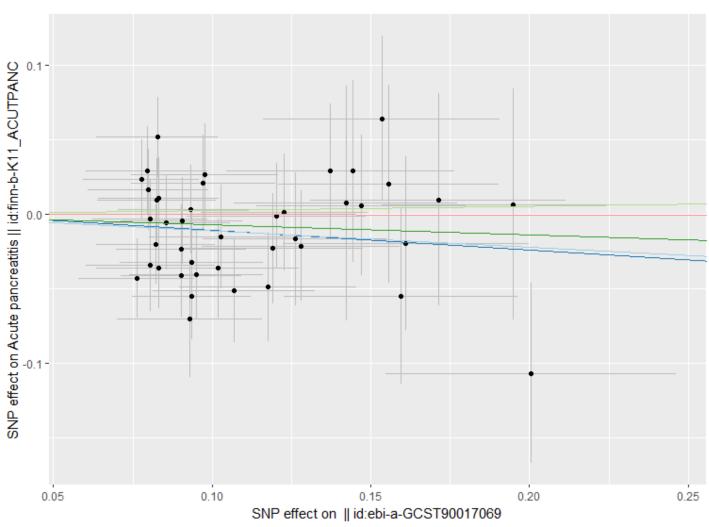
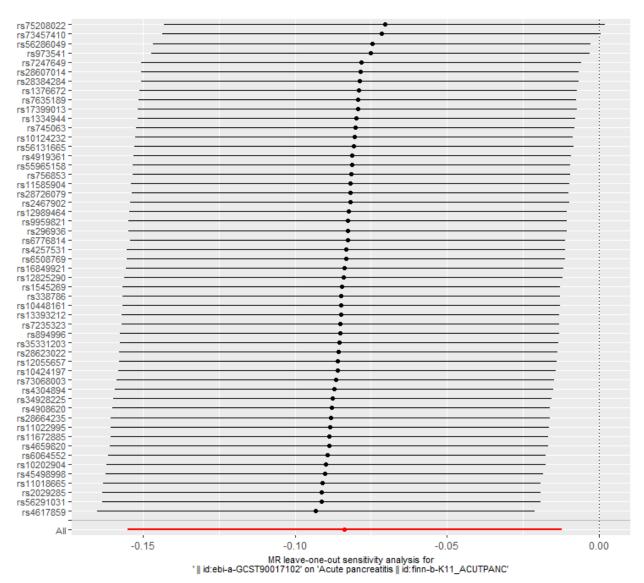
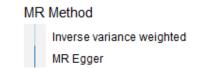
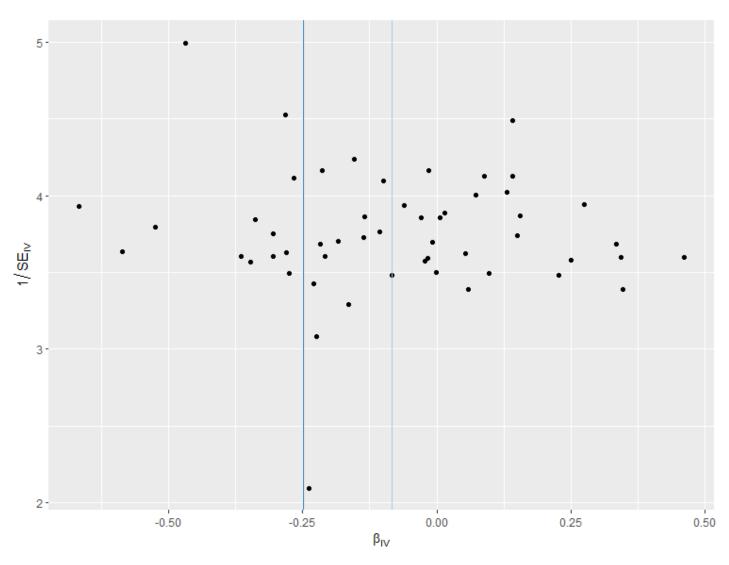
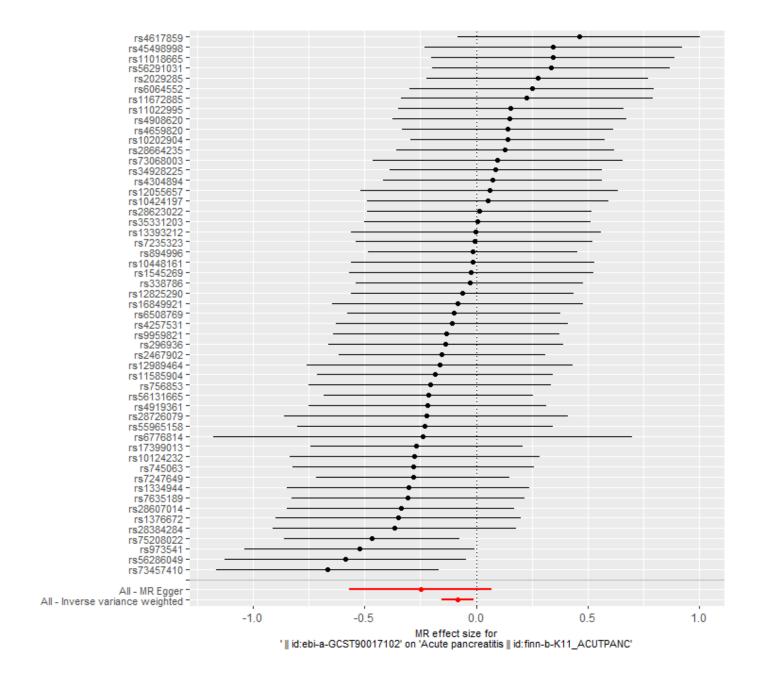


Figure 205 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (order Methanobacteriales id.120) on acute pancreatitis









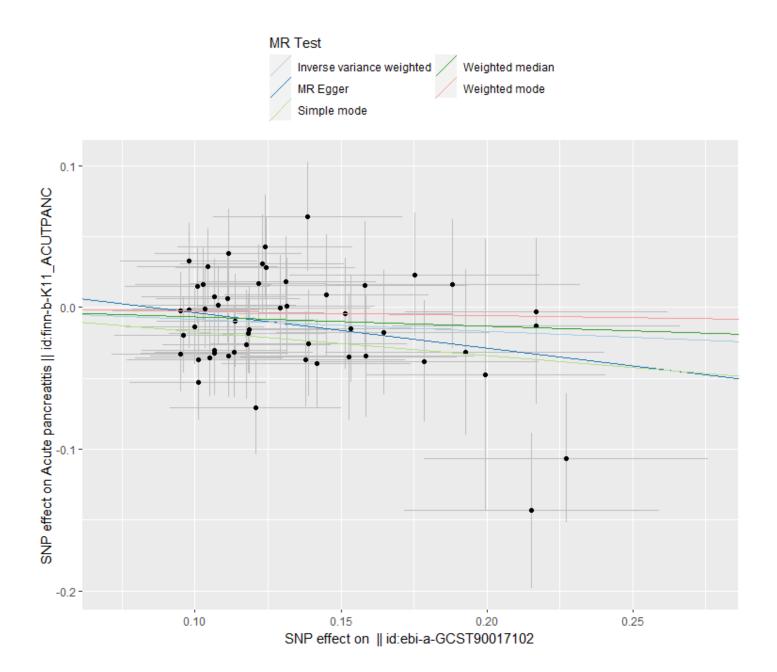
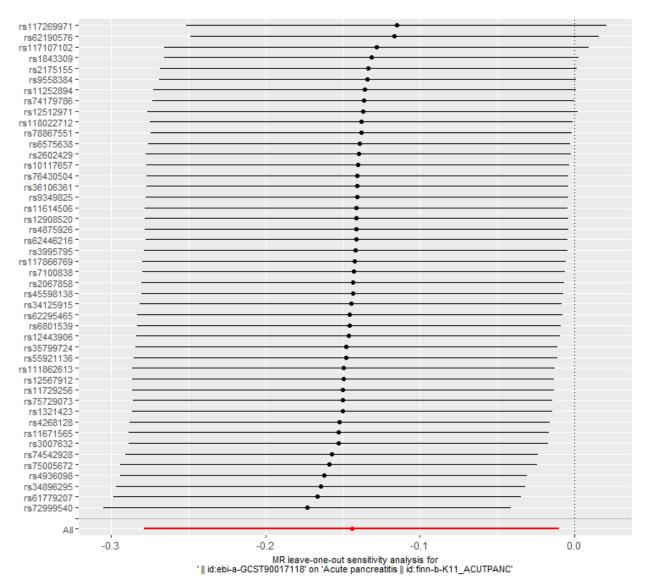
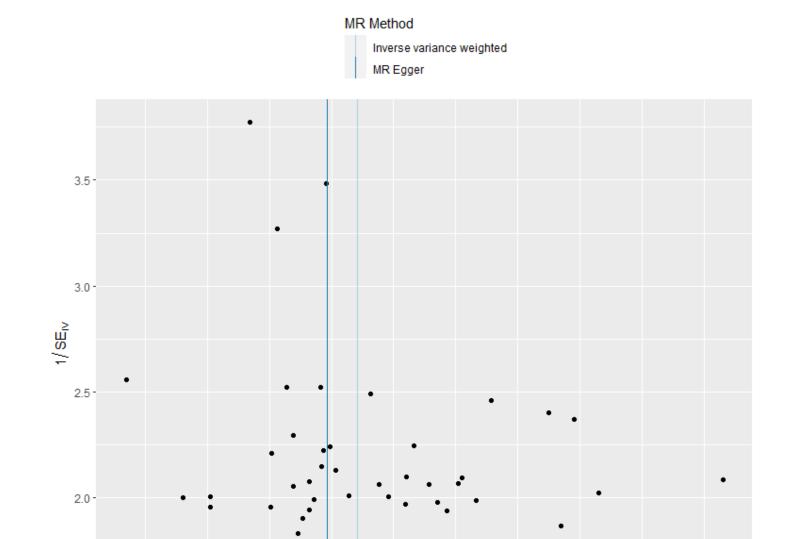


Figure 206 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (phylum Verrucomicrobia id.3982) on acute pancreatitis





0.0

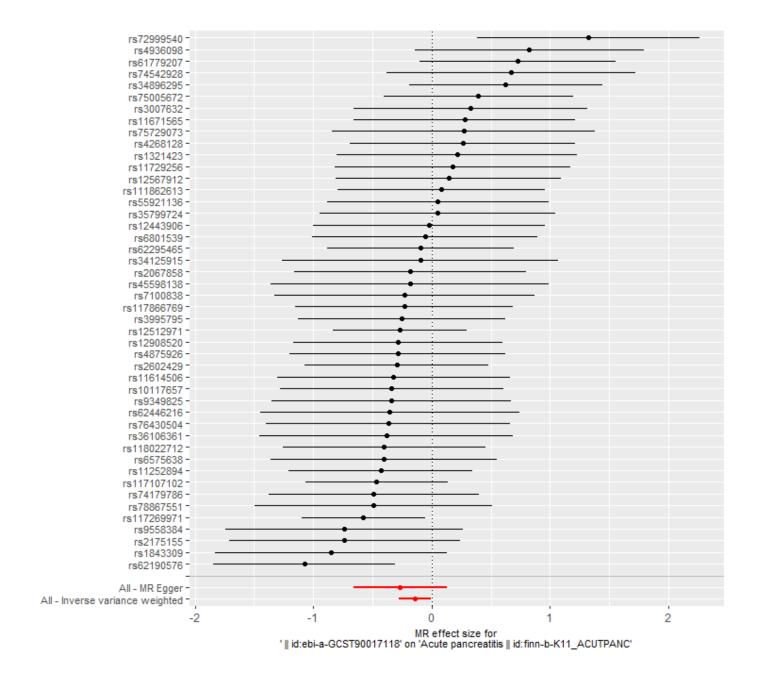
 β_{IV}

1.0

0.5

-0.5

-1.0



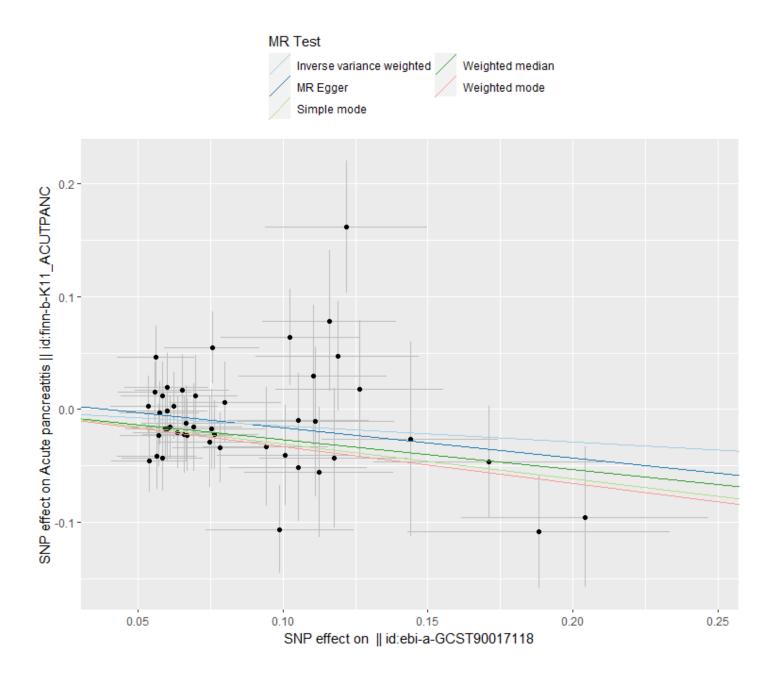
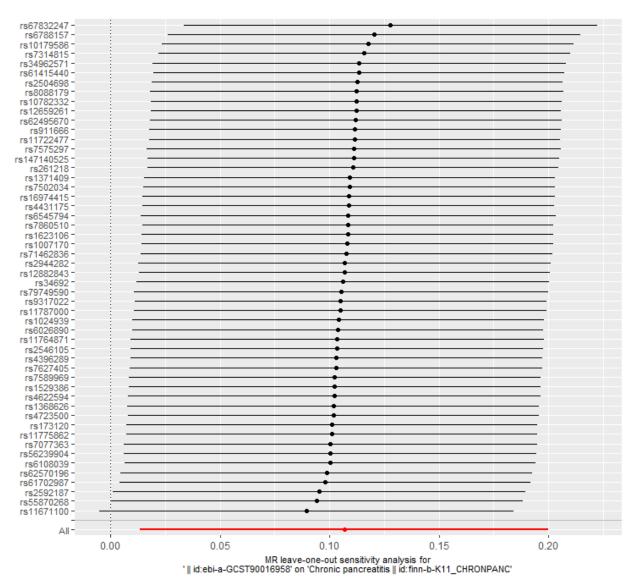
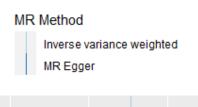
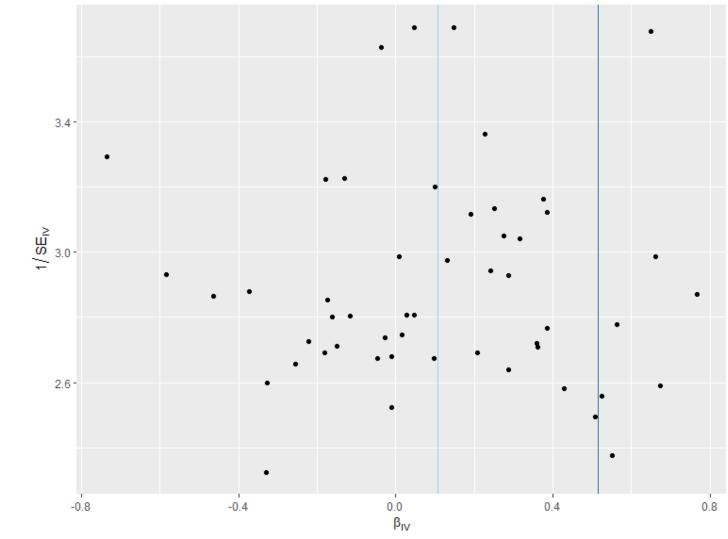
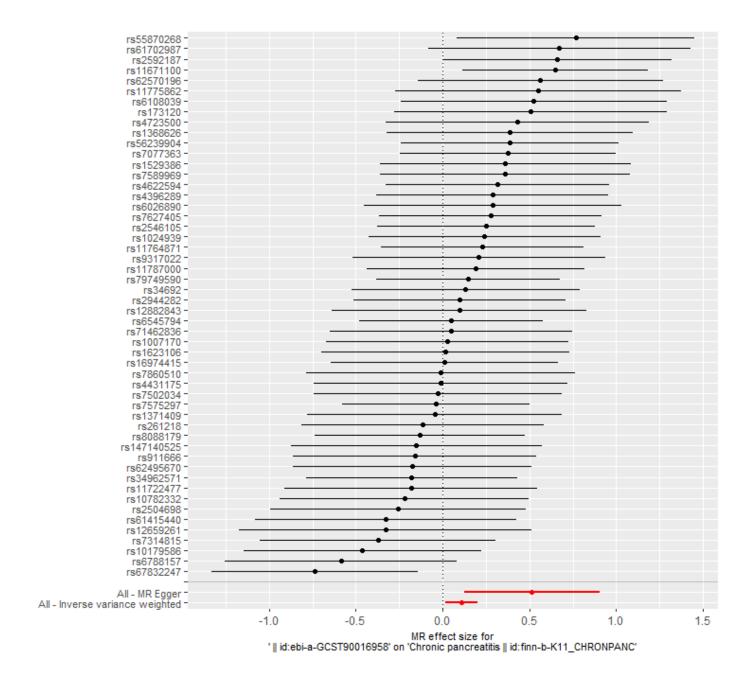


Figure 207 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (family Victivallaceae id.2255) on chronic pancreatitis









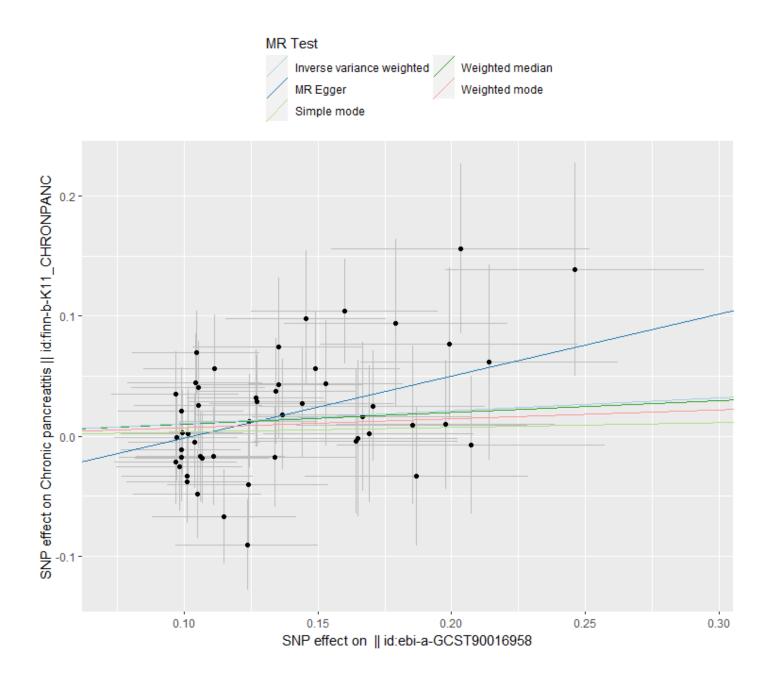
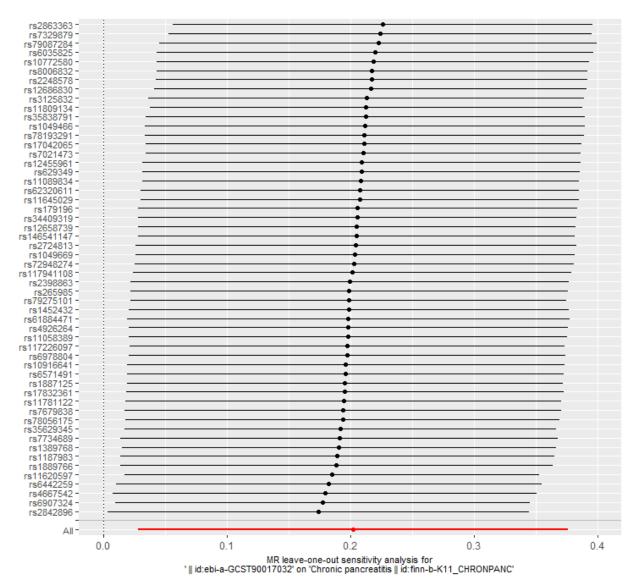
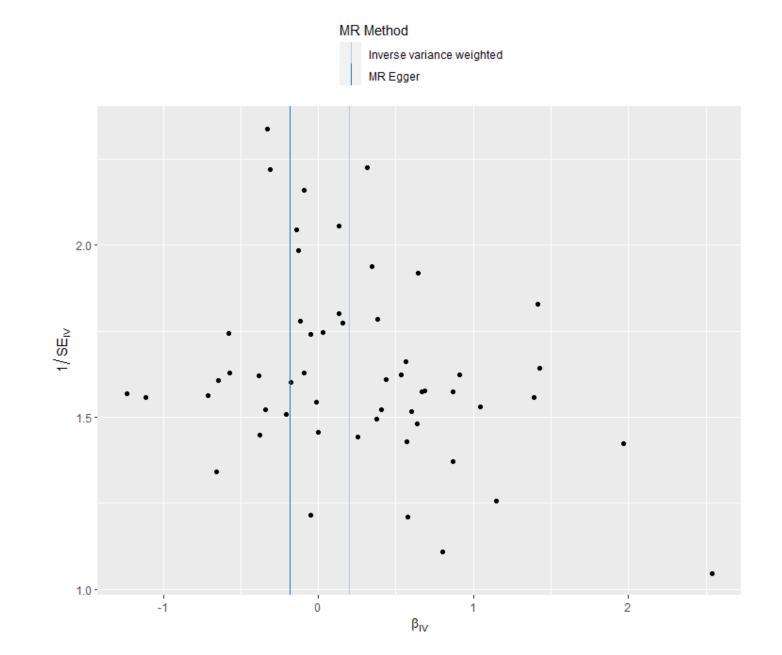
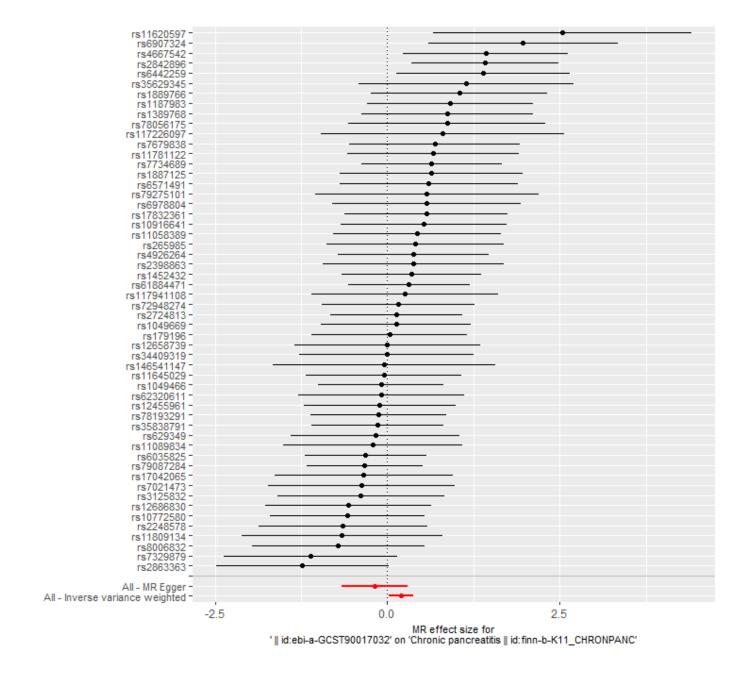


Figure 208 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Marvinbryantia id.2005) on chronic pancreatitis







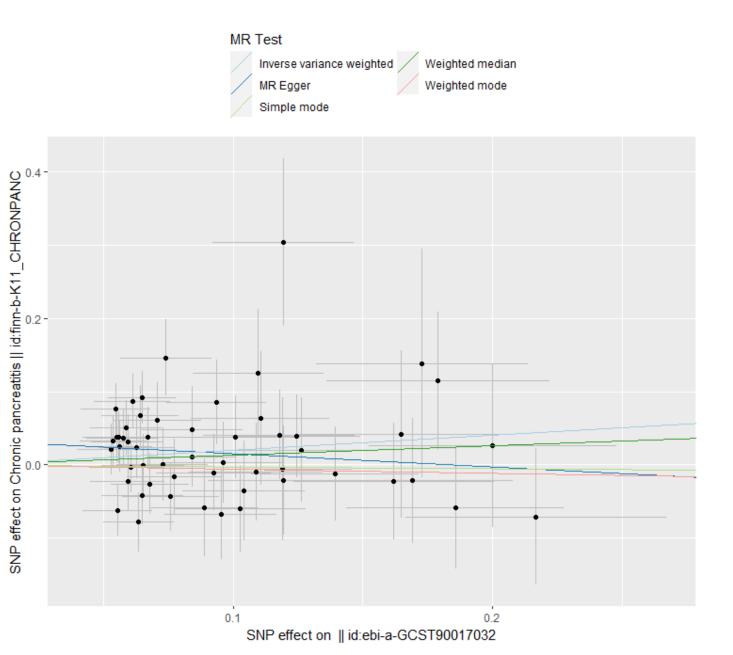
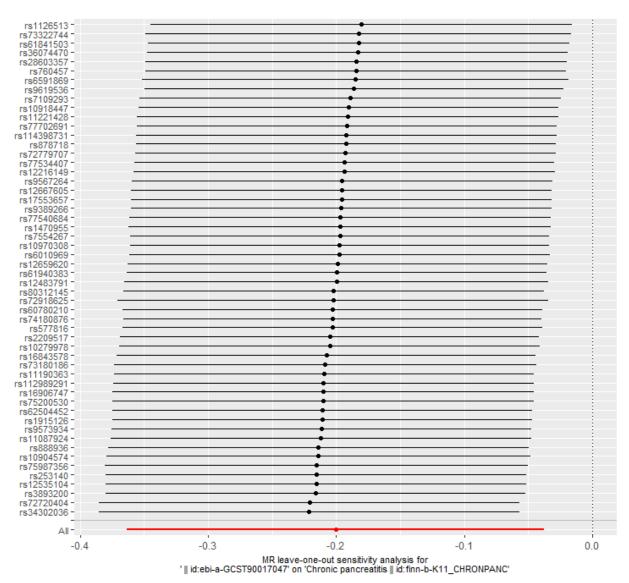
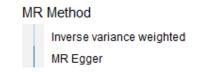
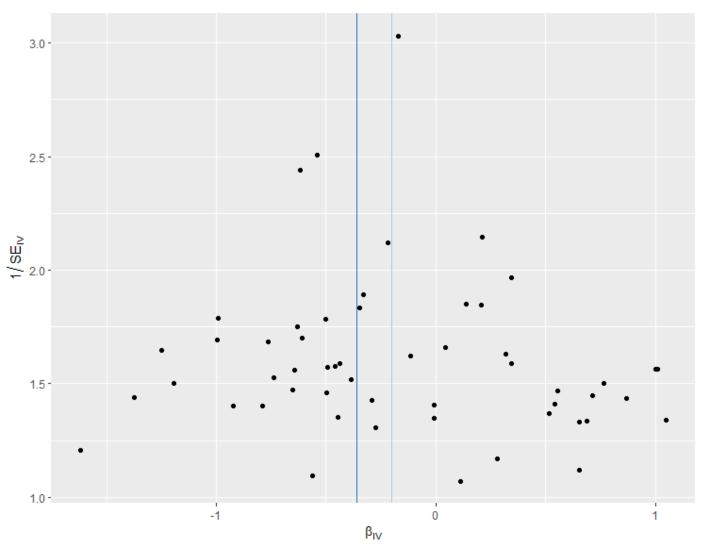
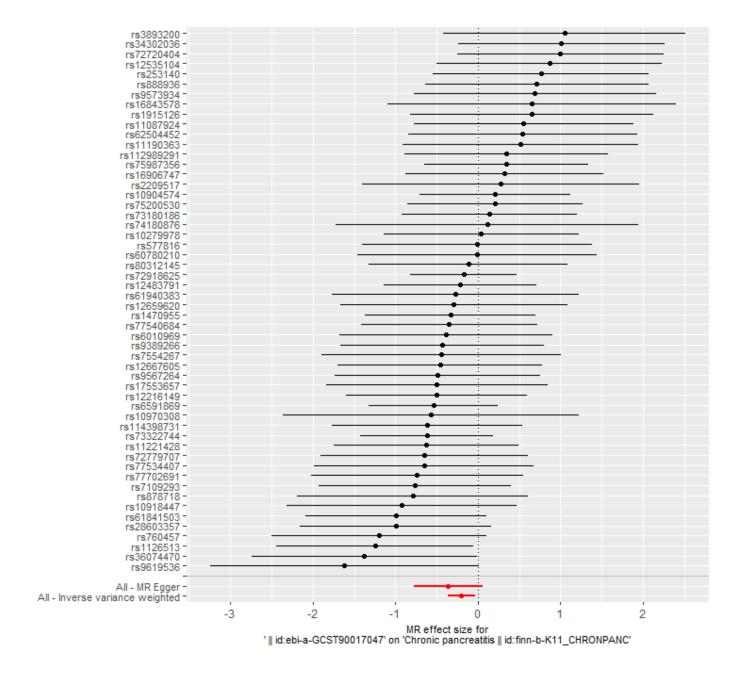


Figure 209 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Romboutsia id.11347) on chronic pancreatitis











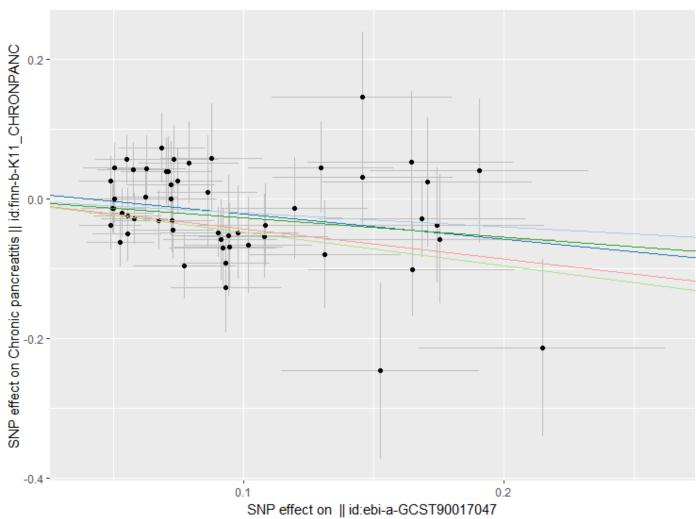
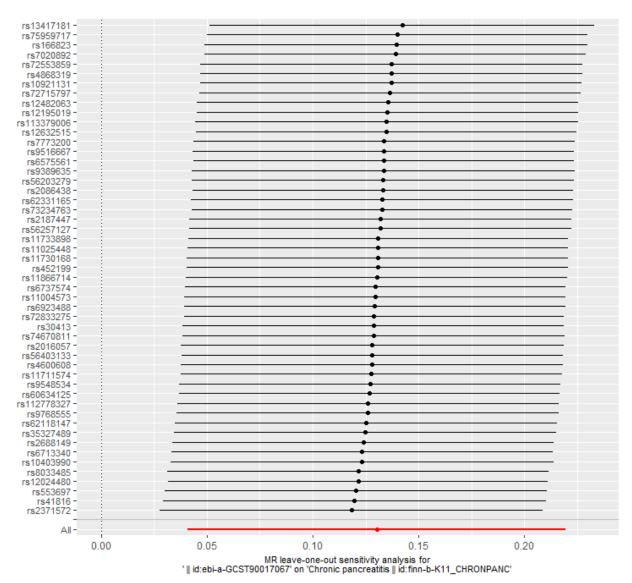
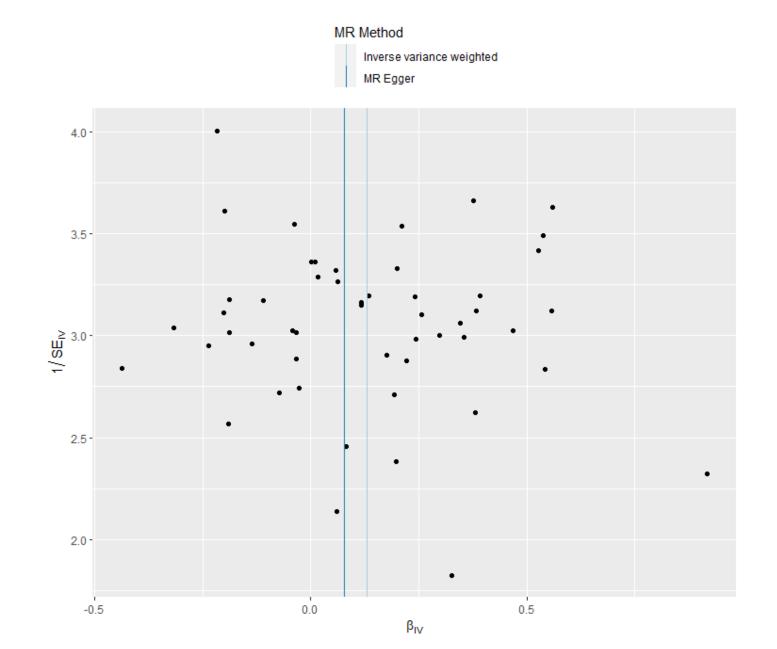
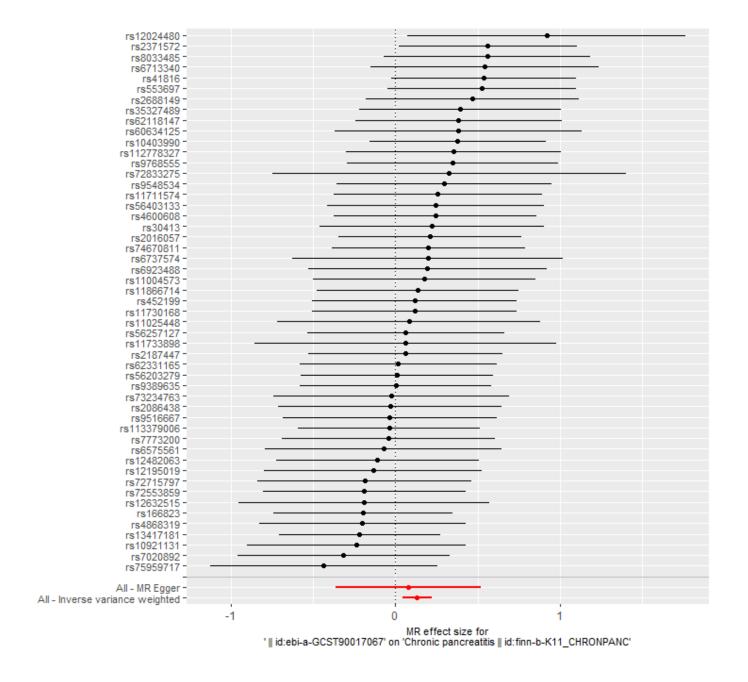


Figure 210 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Sellimonas id.14369) on chronic pancreatitis







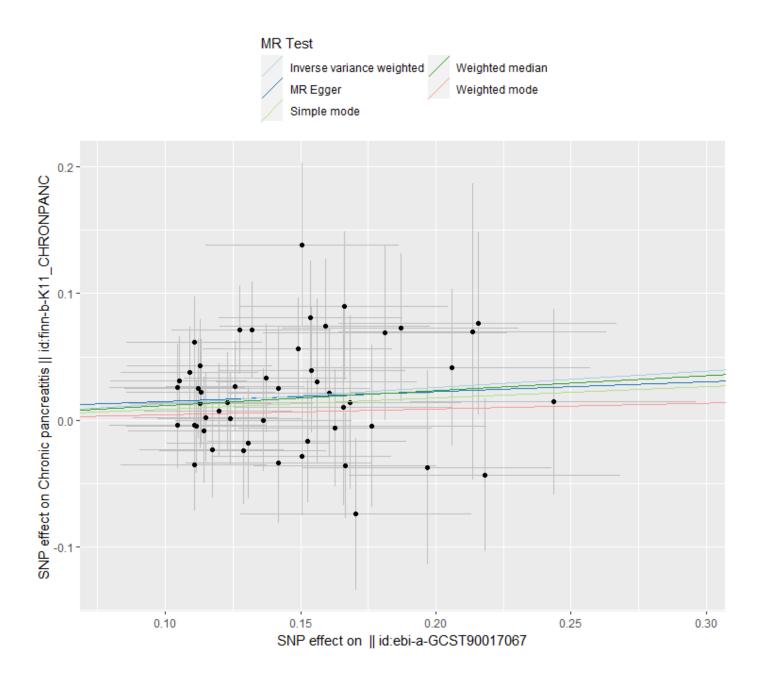
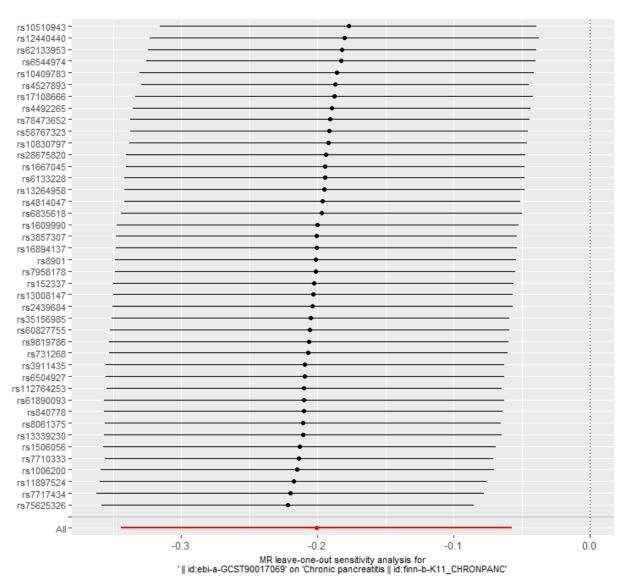
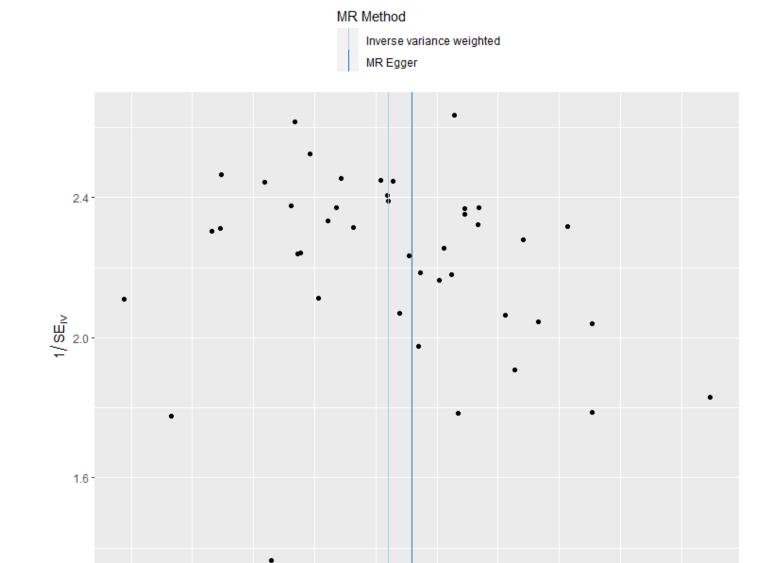


Figure 211 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Slackia id.825) on chronic pancreatitis





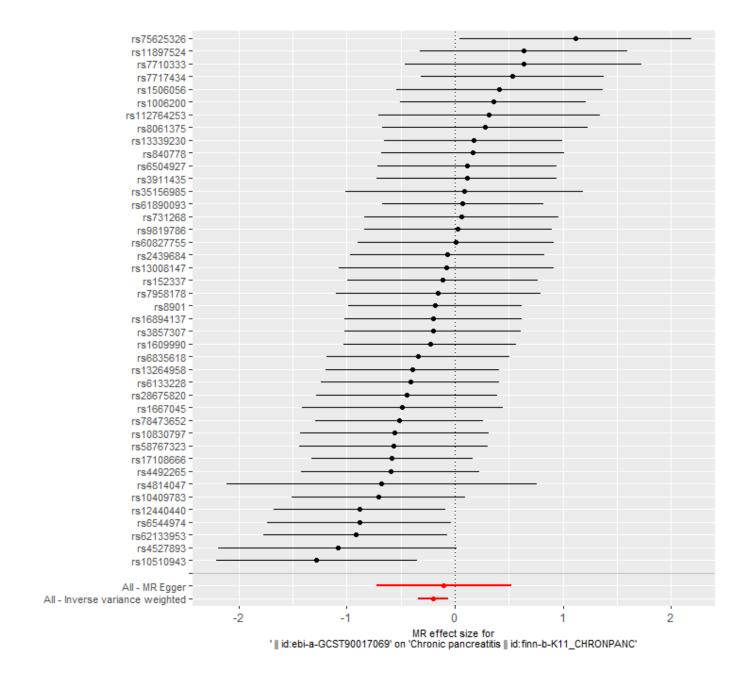
 β_{IV}

0.5

1.0

-1.0

-0.5



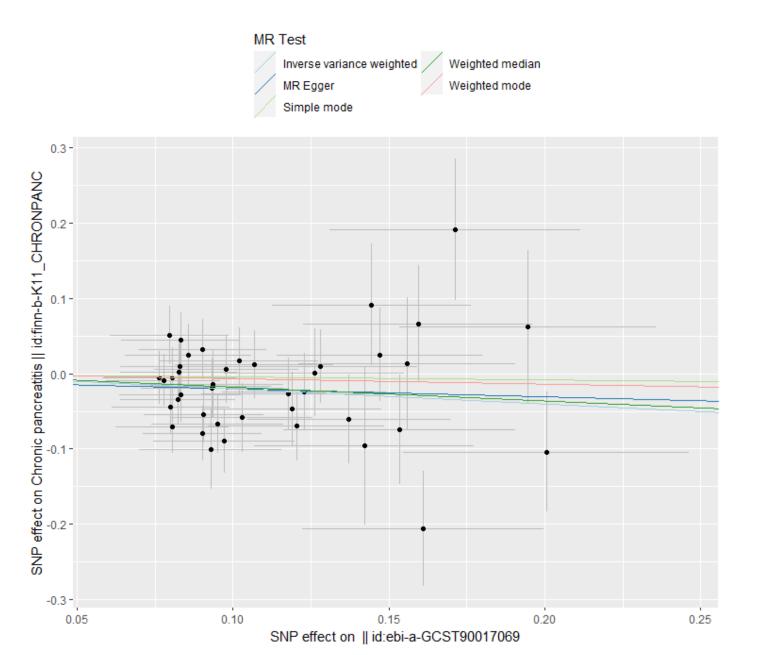


Figure 212 Leave-one-out analysis, funnel plot, MR effect size and scatter plot for gut microbiota abundance (genus Prevotella9 id.11183) on pancreatic cancer

