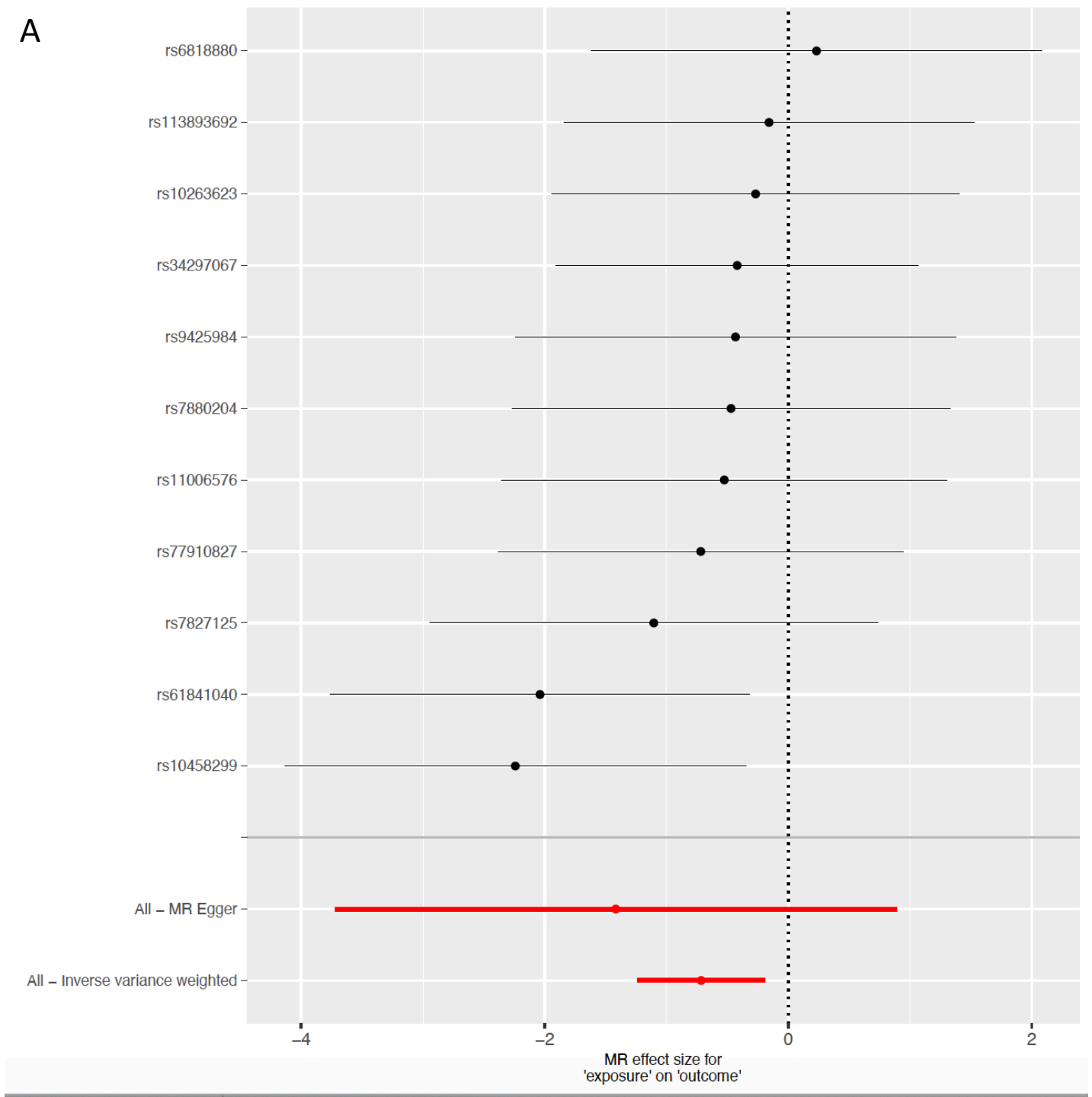
Supplementary Figure 1 Forest plot for the causal association between specific gut microbiota taxa and gallbladder cancer (GC)/extrahepatic cholangiocarcinoma (eCCA) in Mendelian randomization (MR) analyses.

(A) genus Eubacteriumnodatum group, (B) genus Ruminococcustorques group, (C) genus Collinsella, (D) genus Coprococcus, (E) genus Dorea, (F) genus Eisenbergiella, (G) phylum Actinobacteria.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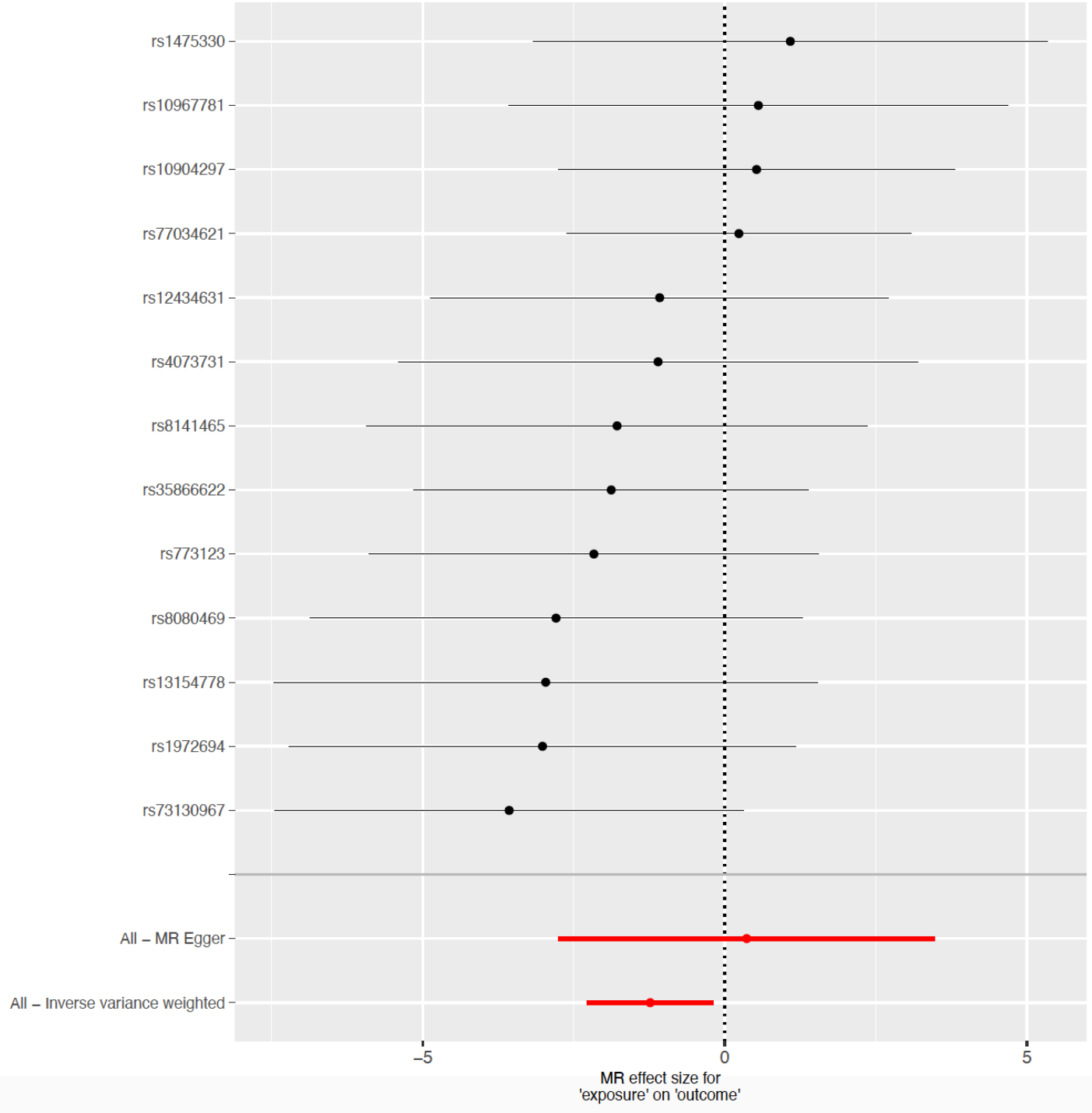
rs10263623
rs34297067
rs9425984
rs7880204
rs11006576
rs77910827
rs7827125
rs61841040
rs10458299
All – MR Egger
All – Inverse variance weighted
−4
−2
0
2
MR effect size for
'exposure' on 'outcome'

B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rs8141465
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rs8080469
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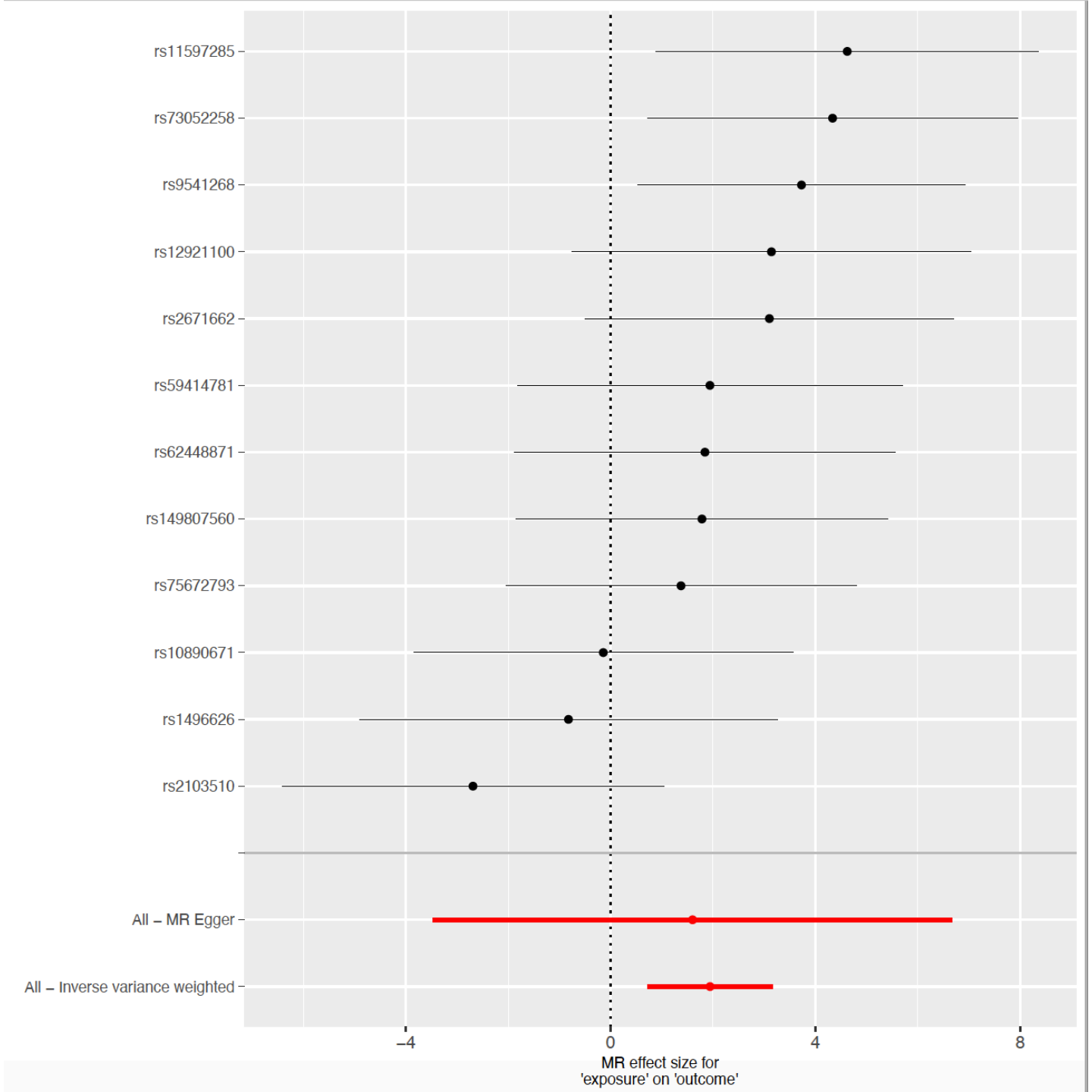
rs1972694
rs73130967
All – MR Egger
All – Inverse variance weighted
−5
0
5
MR effect size for
'exposure' on 'outcome'

C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rs9541268
rs12921100
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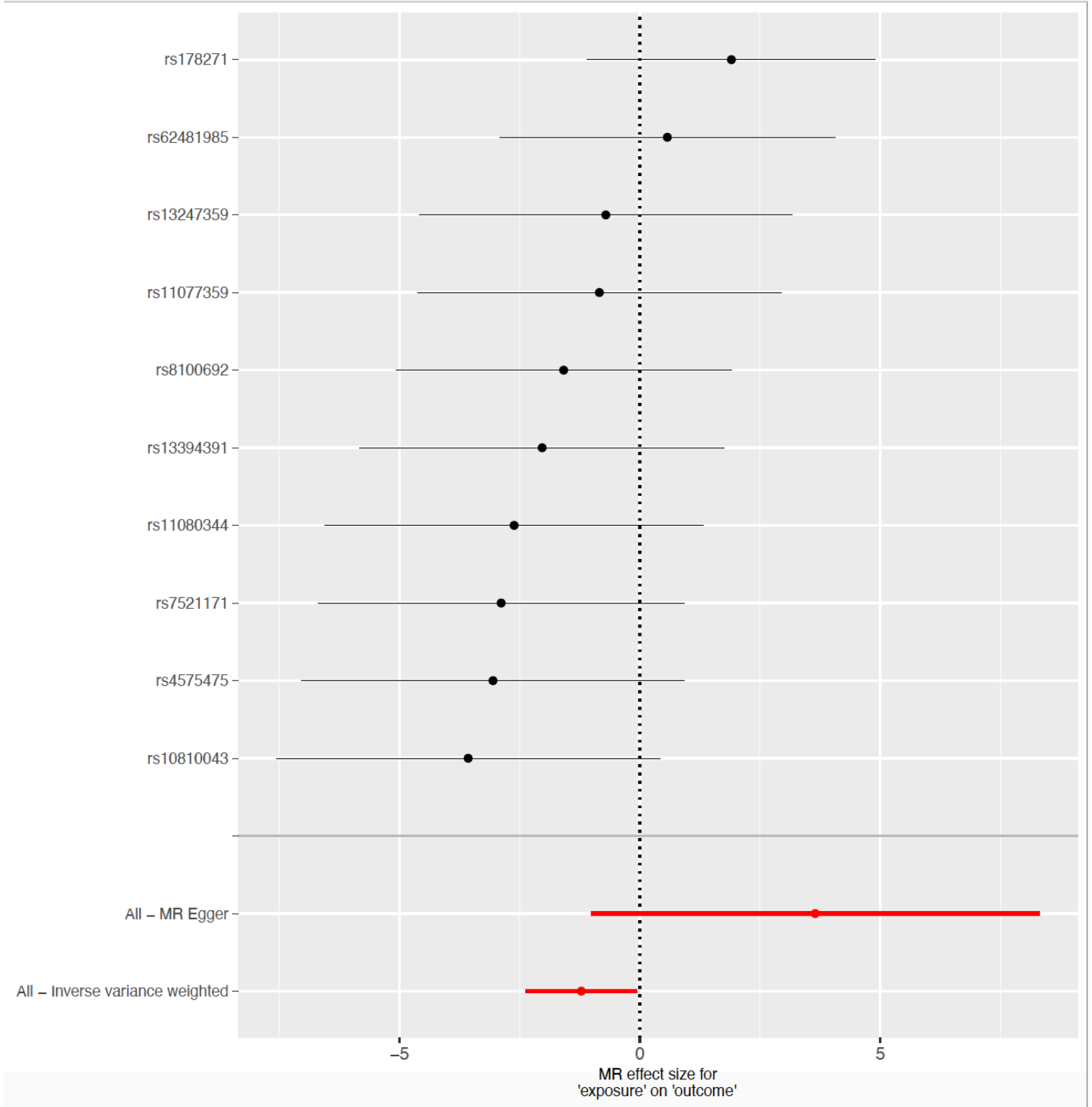
rs62448871
rs149807560
rs75672793
rs10890671
rs1496626
rs2103510
All – MR Egger
All – Inverse variance weighted
−4
0
4
8
MR effect size for
'exposure' on 'outcome'

D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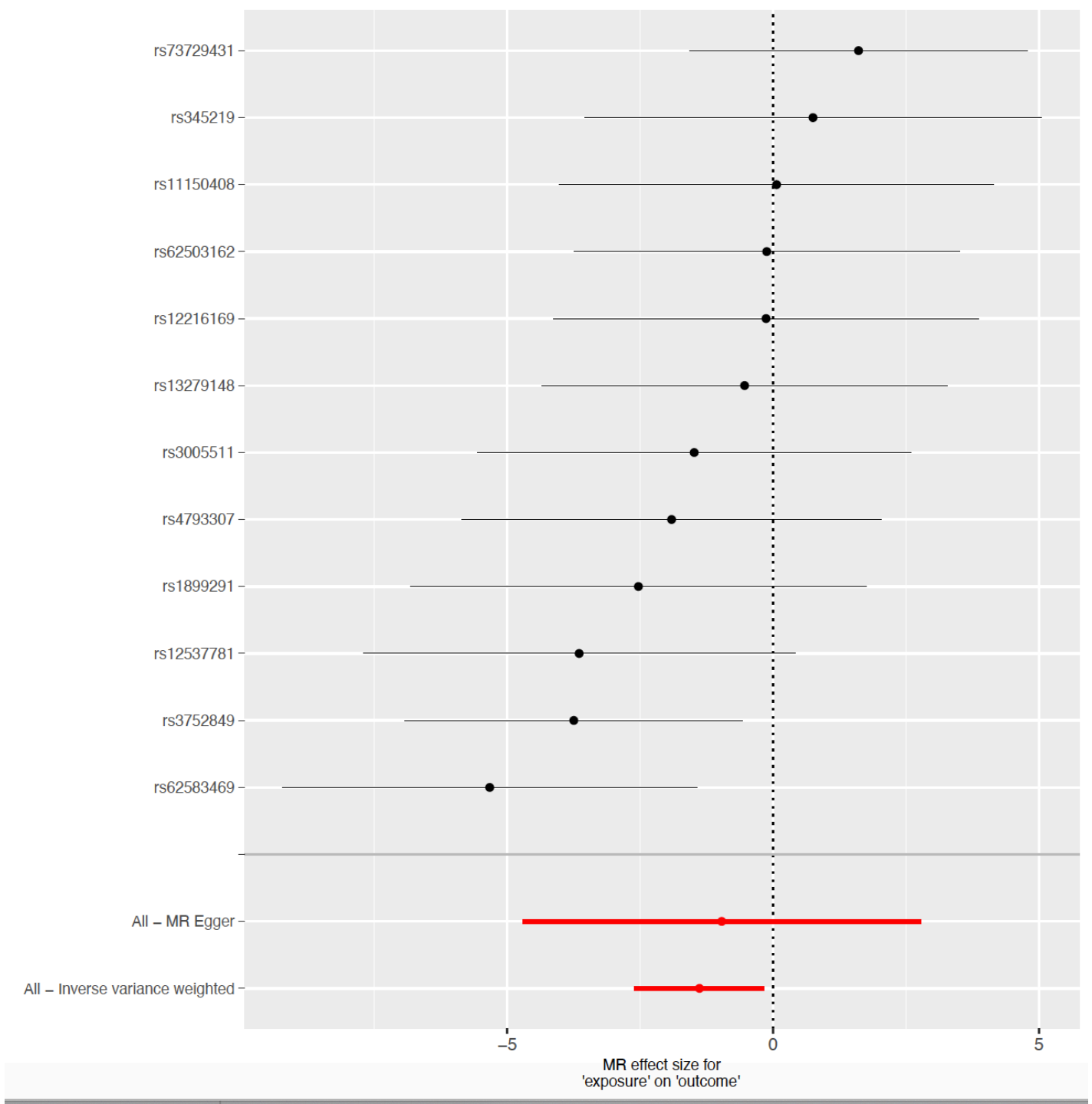
rs13247359
rs11077359
rs8100692
rs13394391
rs11080344
rs7521171
rs4575475
rs10810043
All – MR Egger
All – Inverse variance weighted
−5
0
5
MR effect size for
'exposure' on 'outcome'

E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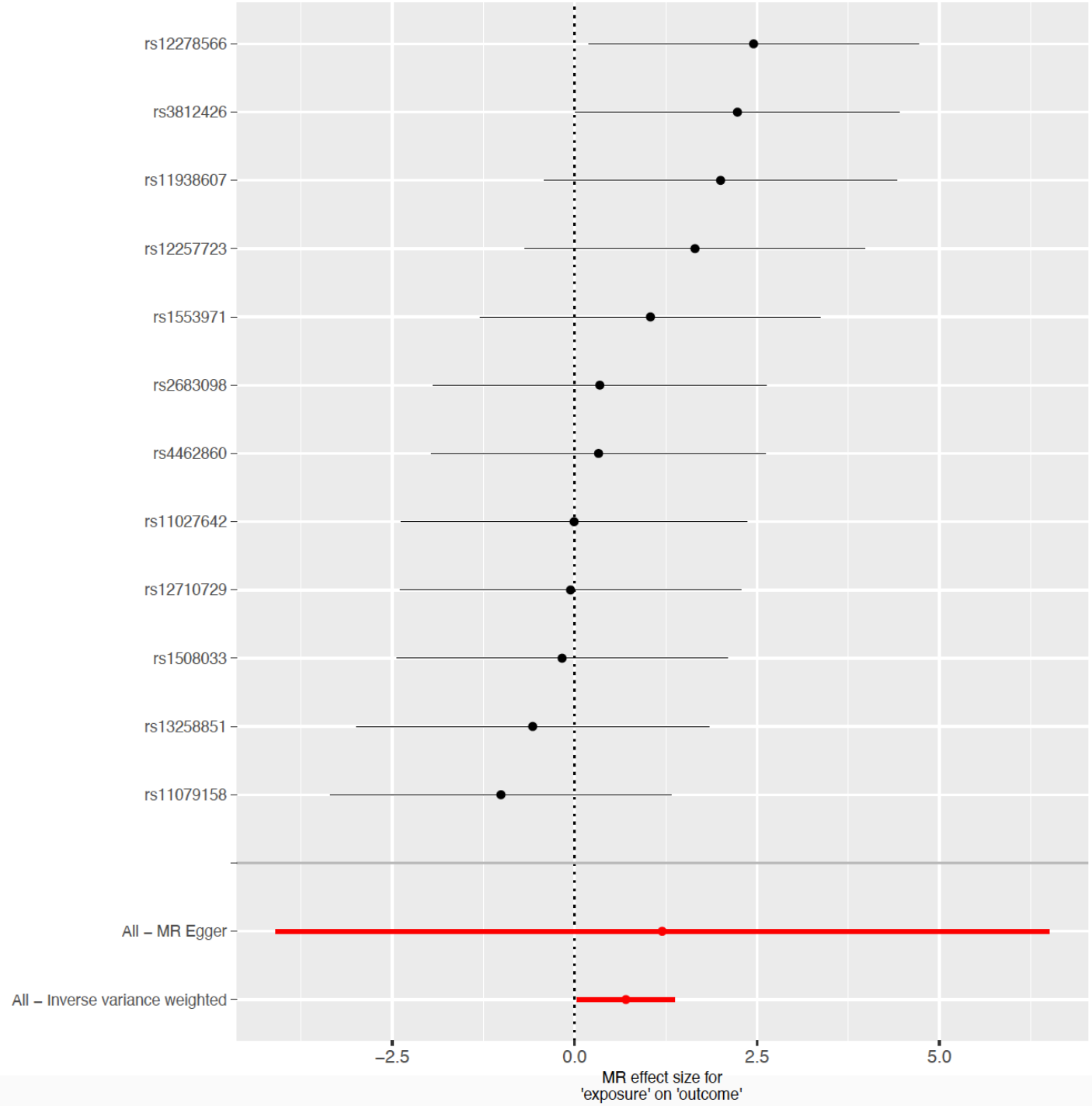
rs62503162
rs12216169
rs13279148
rs3005511
rs4793307
rs1899291
rs12537781
rs3752849
rs62583469
All – MR Egger
All – Inverse variance weighted
−5
0
5
MR effect size for
'exposure' on 'outcome'

F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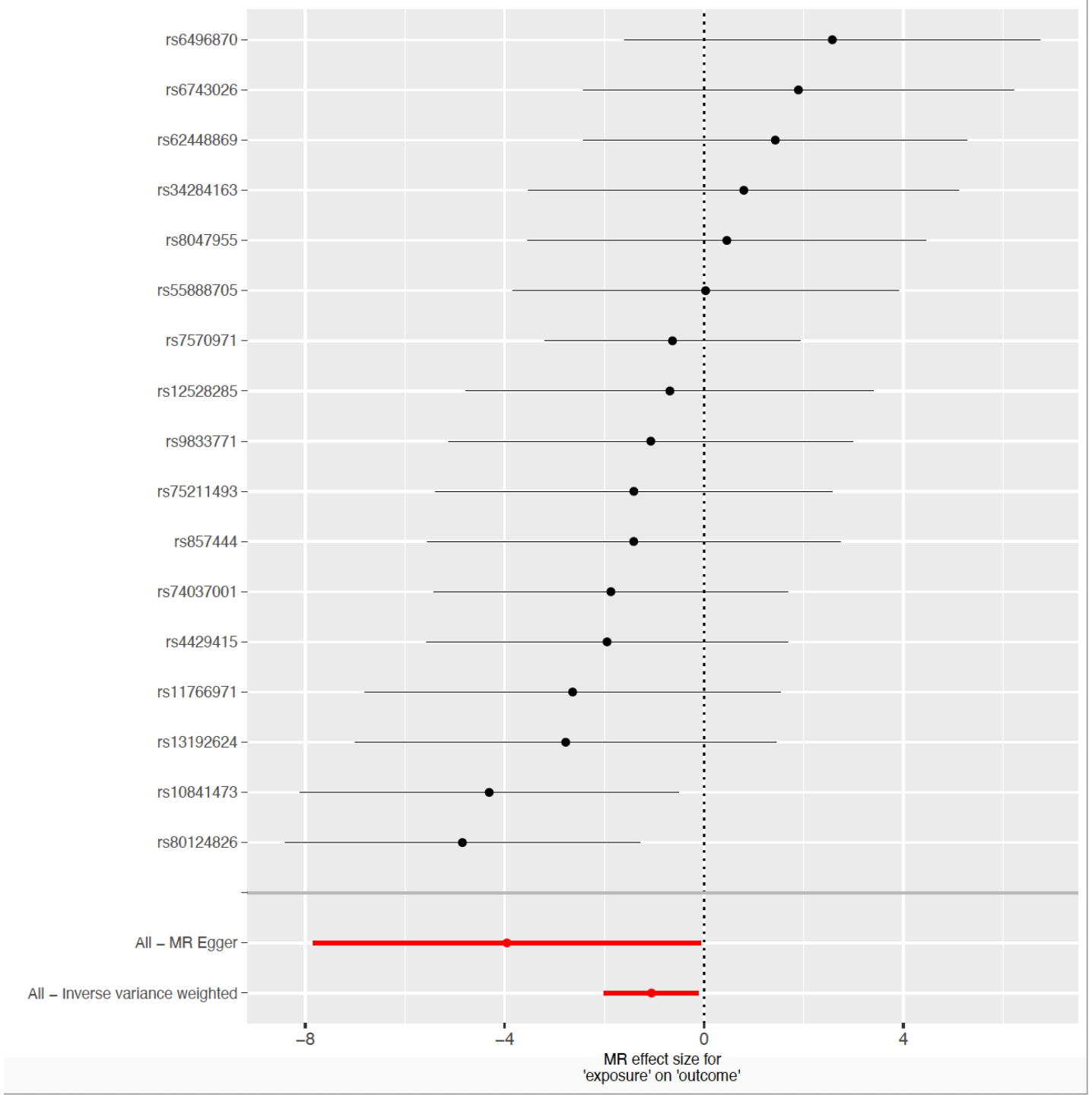
rs12257723
rs1553971
rs2683098
rs4462860
rs11027642
rs12710729
rs1508033
rs13258851
rs11079158
All – MR Egger
All – Inverse variance weighted
−2.5
0.0
2.5
5.0
MR effect size for
'exposure' on 'outcome'

G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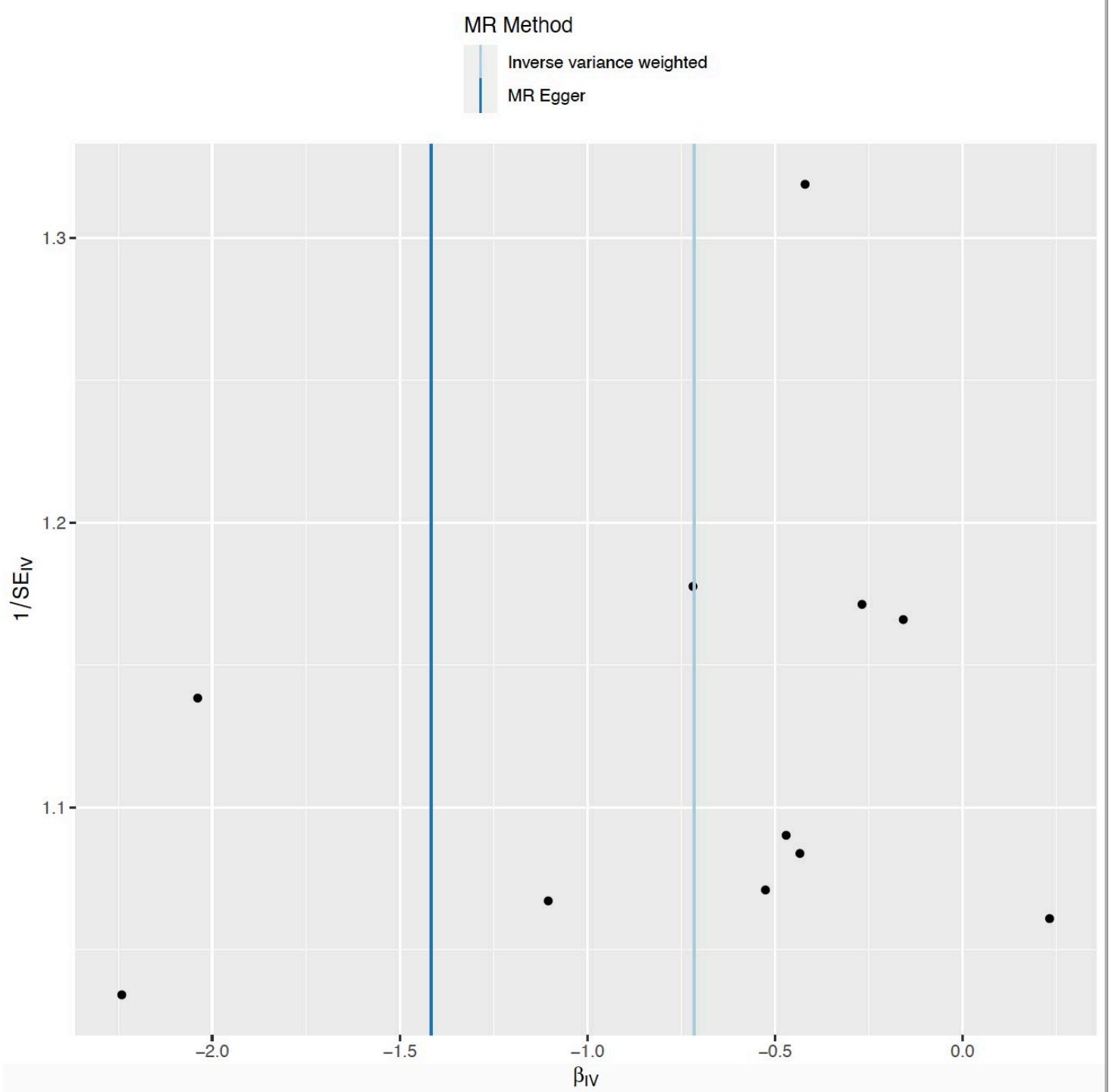
rs74037001
rs4429415
rs11766971
rs13192624
rs10841473
rs80124826
All – MR Egger
All – Inverse variance weighted
−8
−4
0
4
MR effect size for
'exposure' on 'outcome'

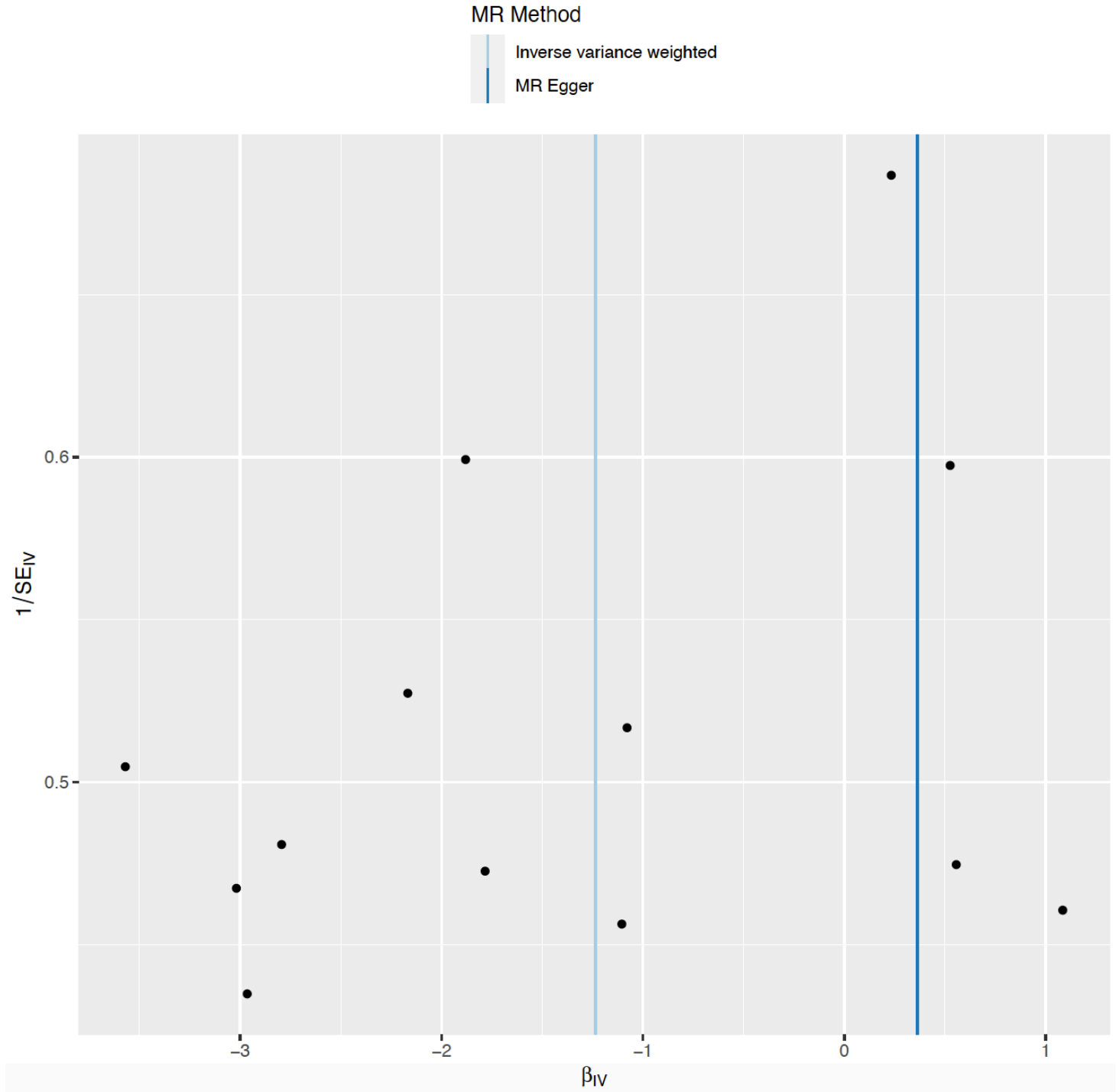
Supplementary Figure2 Funnel plot for the causal association between specific gut microbiota taxa and gallbladder cancer (GC)/extrahepatic cholangiocarcinoma (eCCA) in Mendelian randomization (MR) analyses.

(A) genus Eubacteriumnodatum group, (B) genus Ruminococcustorques group, (C) genus Collinsella, (D) genus Coprococcus, (E) genus Dorea, (F) genus Eisenbergiella, (G) phylum Actinobacteria.

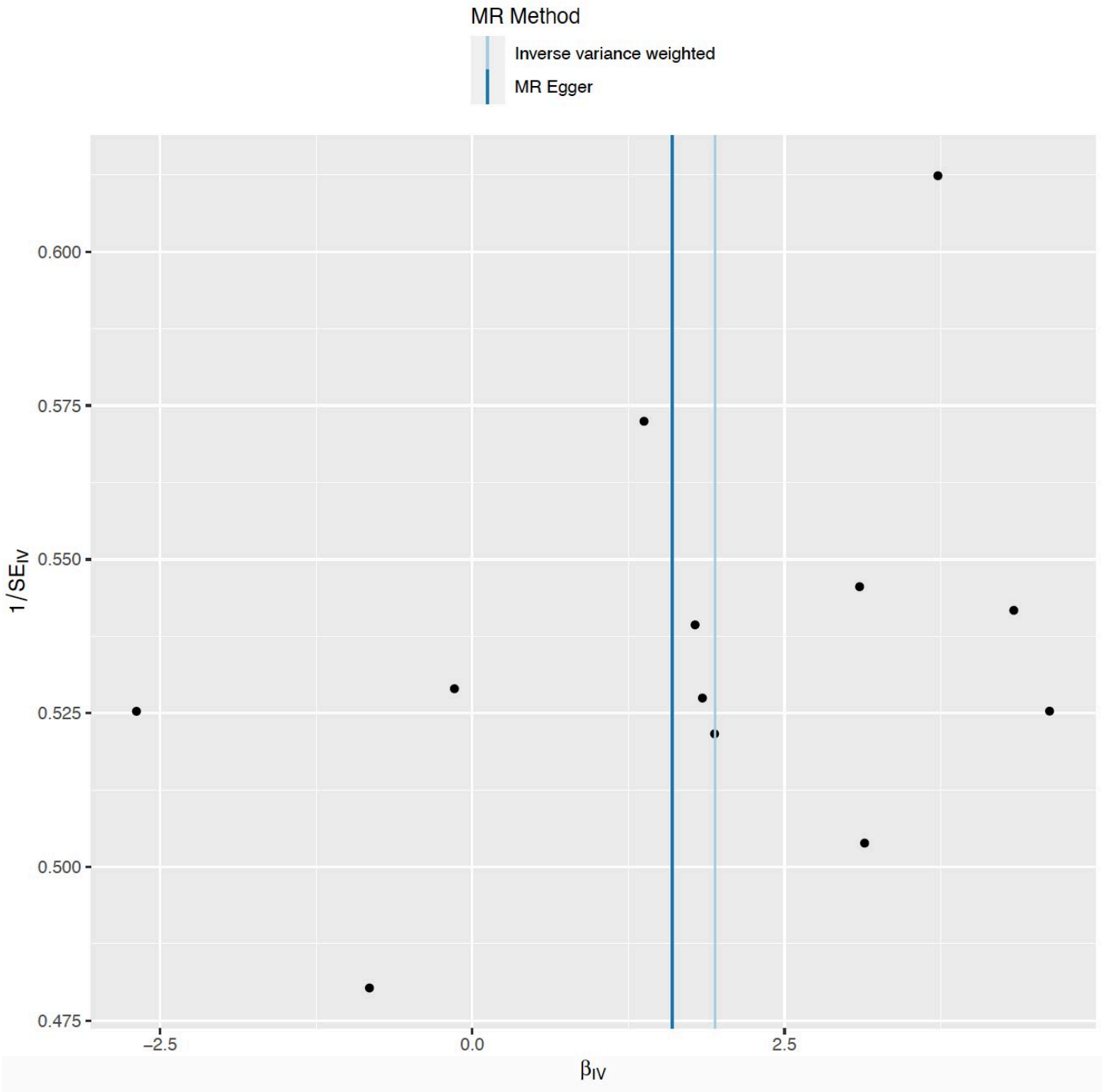
A


MR Method
Inverse variance weighted
MR Egger
1.3
1.2
1.1
1/SE_IV
−2.0
−1.5
−1.0
−0.5
0.0
β_IV

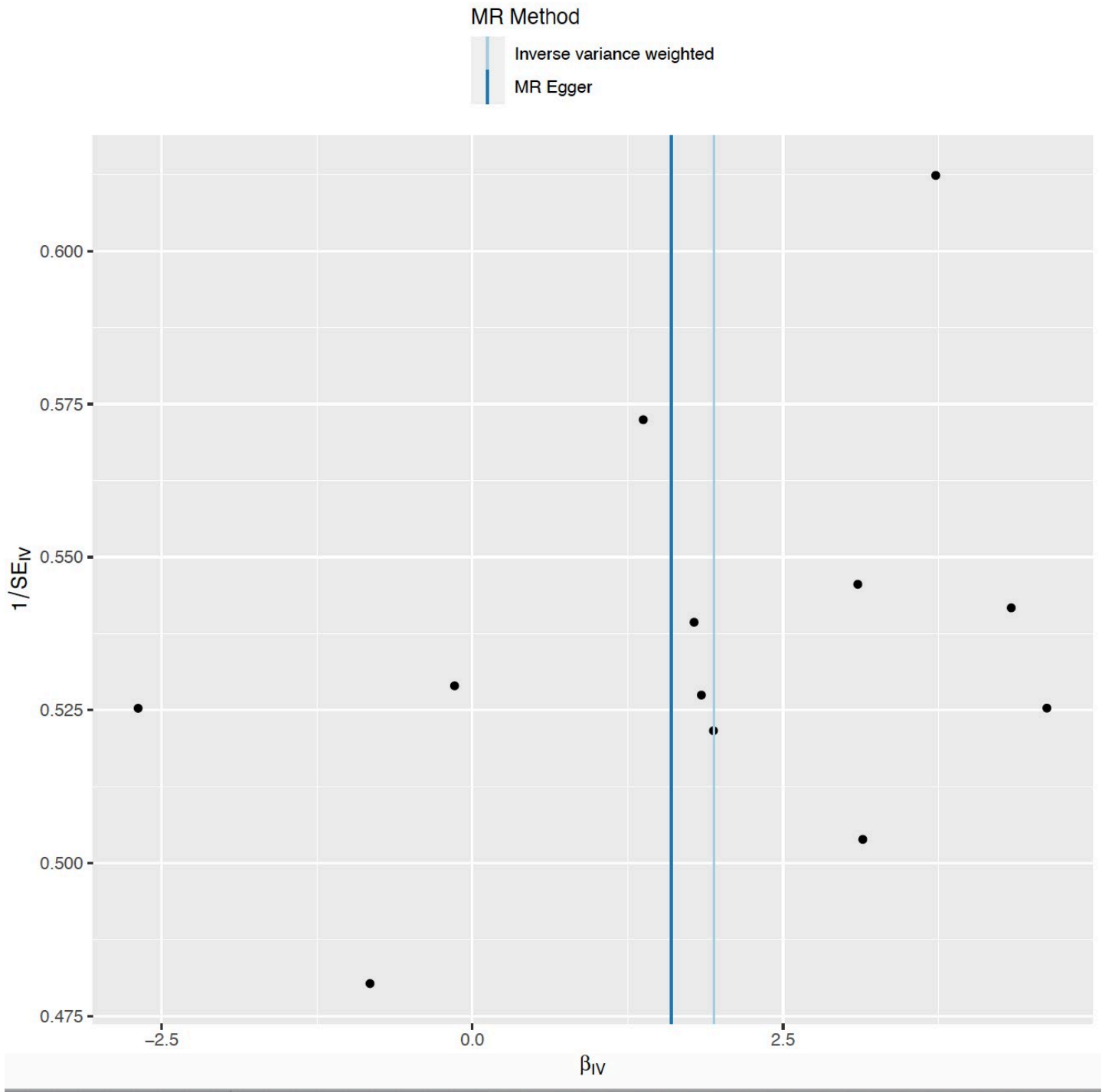
B


MR Method
Inverse variance weighted
MR Egger
0.6
0.5
1/SE_IV
−3
−2
−1
0
1
β_IV

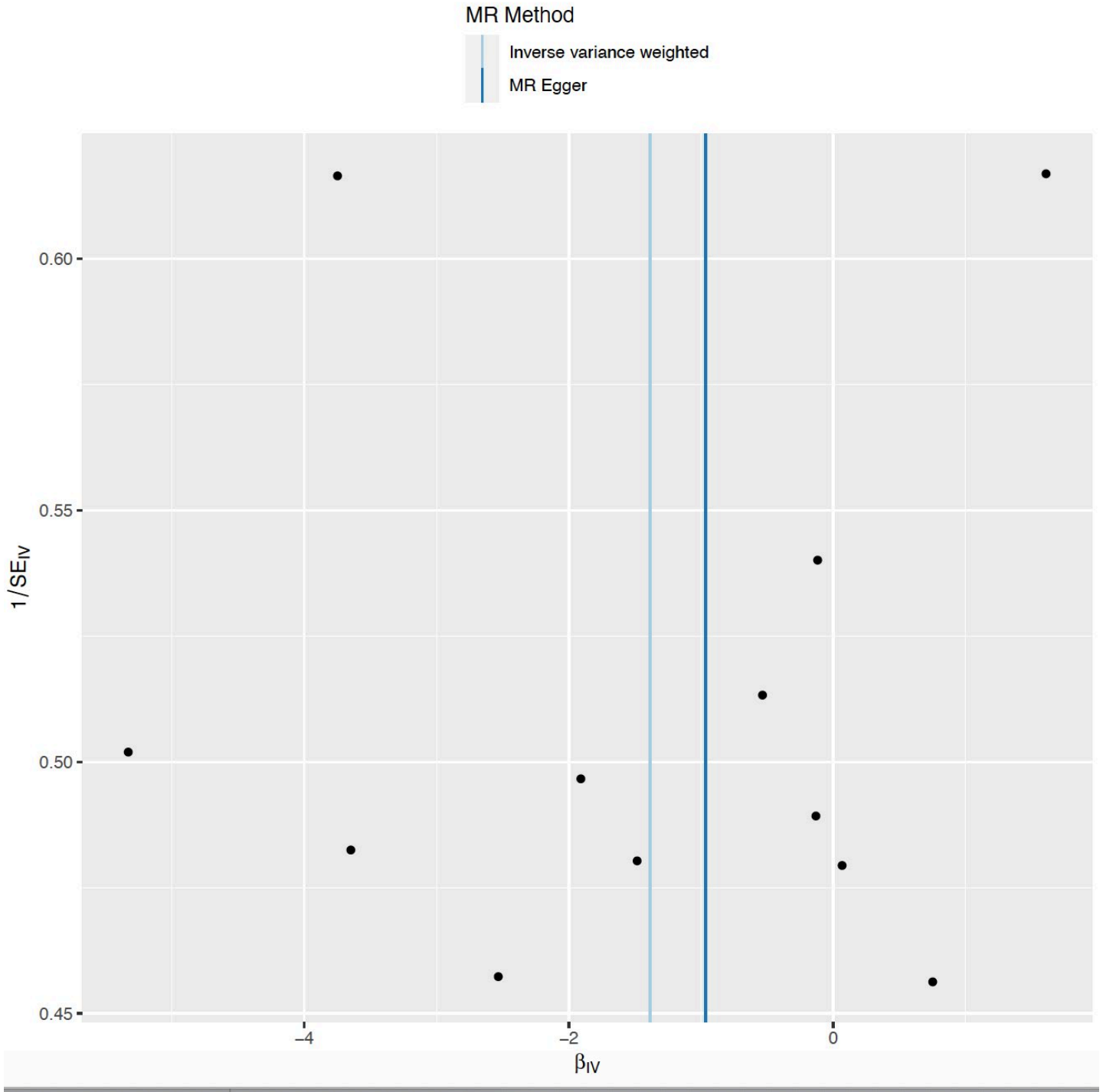
C


MR Method
Inverse variance weighted
MR Egger
0.600
0.575
0.550
0.525
0.500
0.475
1/SE_IV
−2.5
0.0
2.5
β_IV

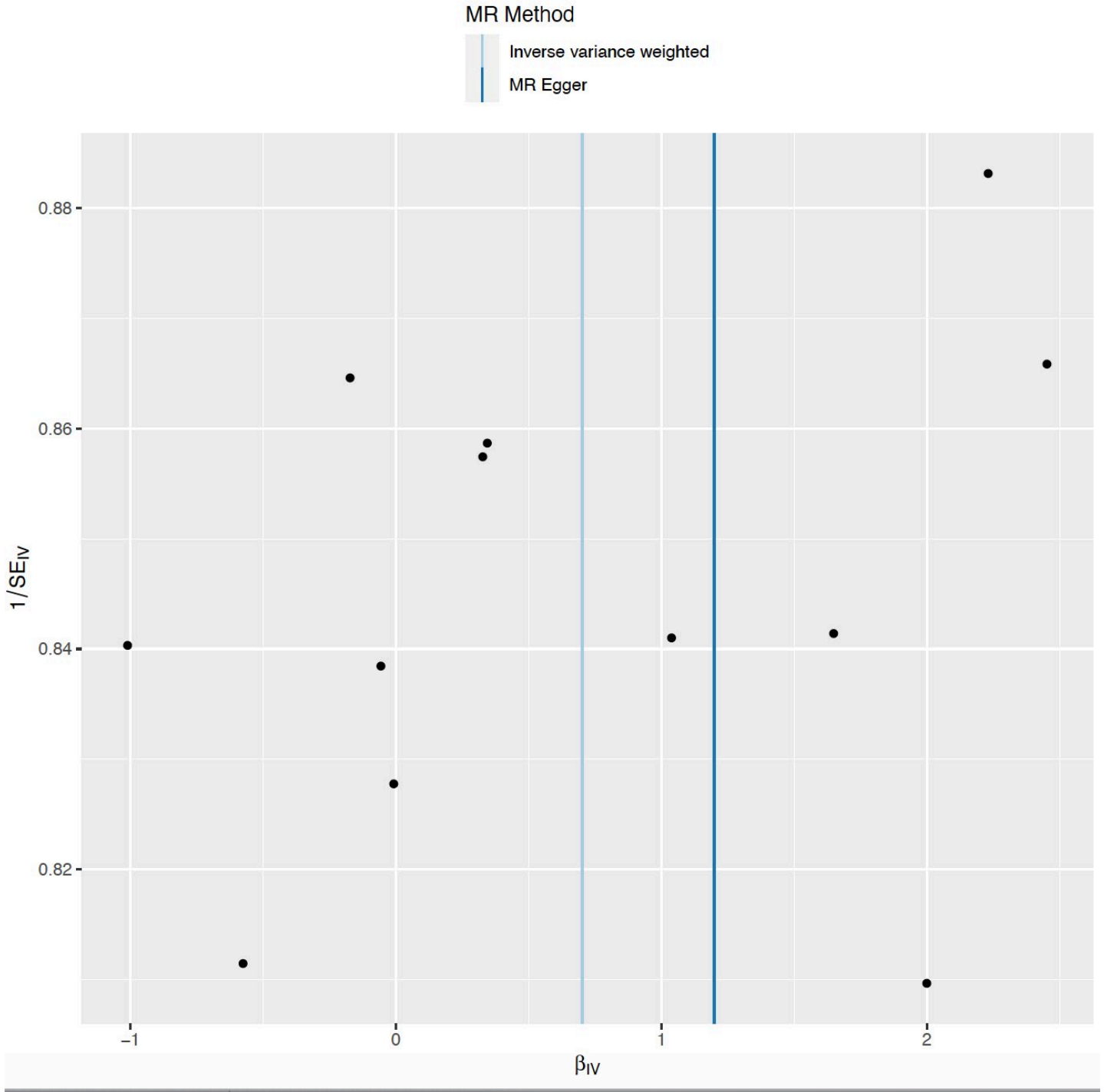
D


MR Method
Inverse variance weighted
MR Egger
0.600
0.575
0.550
0.525
0.500
0.475
1/SE_IV
−2.5
0.0
2.5
β_IV

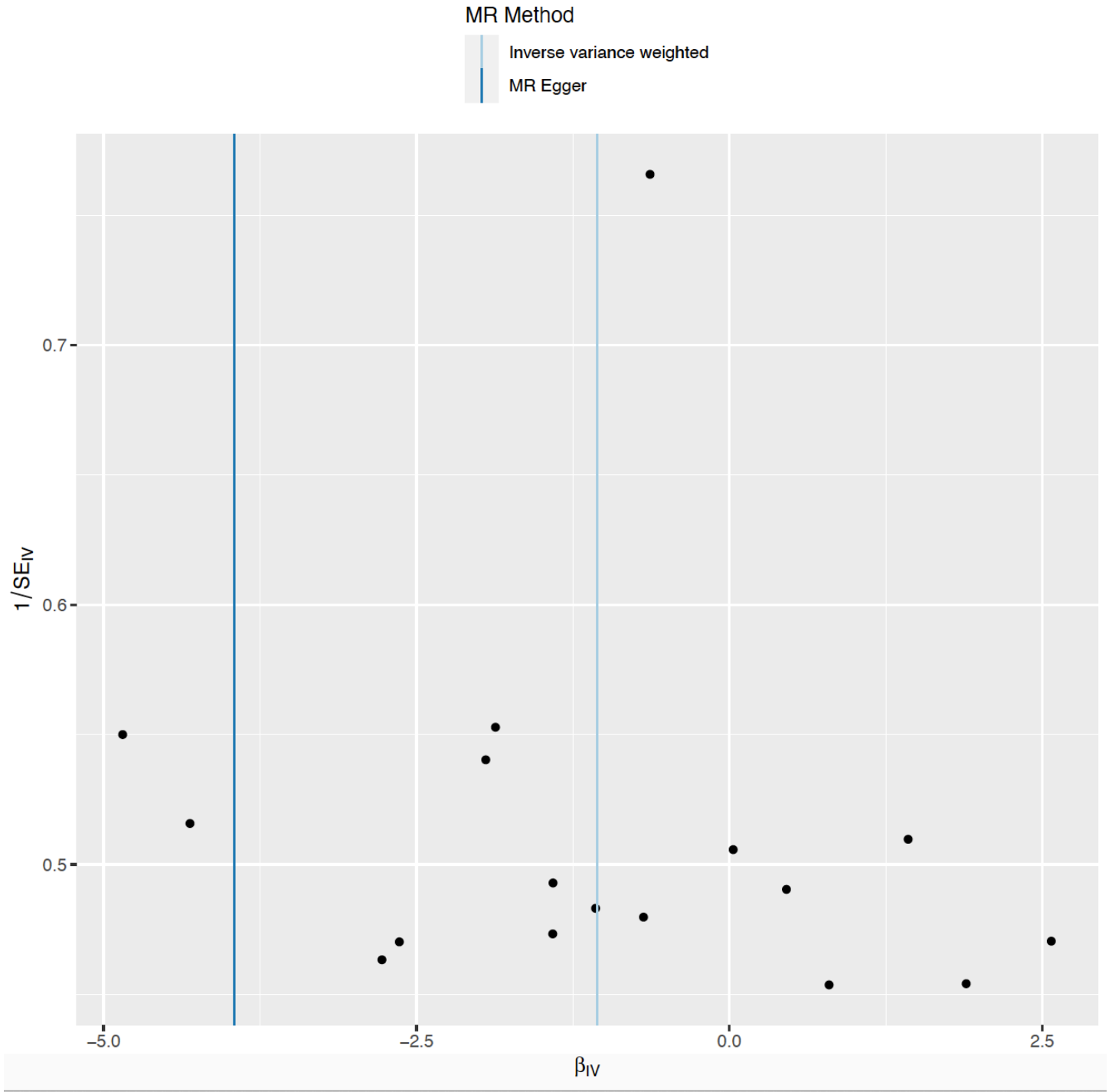
E


MR Method
Inverse variance weighted
MR Egger
0.60
0.55
0.50
0.45
1/SE_IV
−4
−2
0
β_IV

F


MR Method
Inverse variance weighted
MR Egger
0.88
0.86
0.84
0.82
1/SE_IV
−1
0
1
2
β_IV

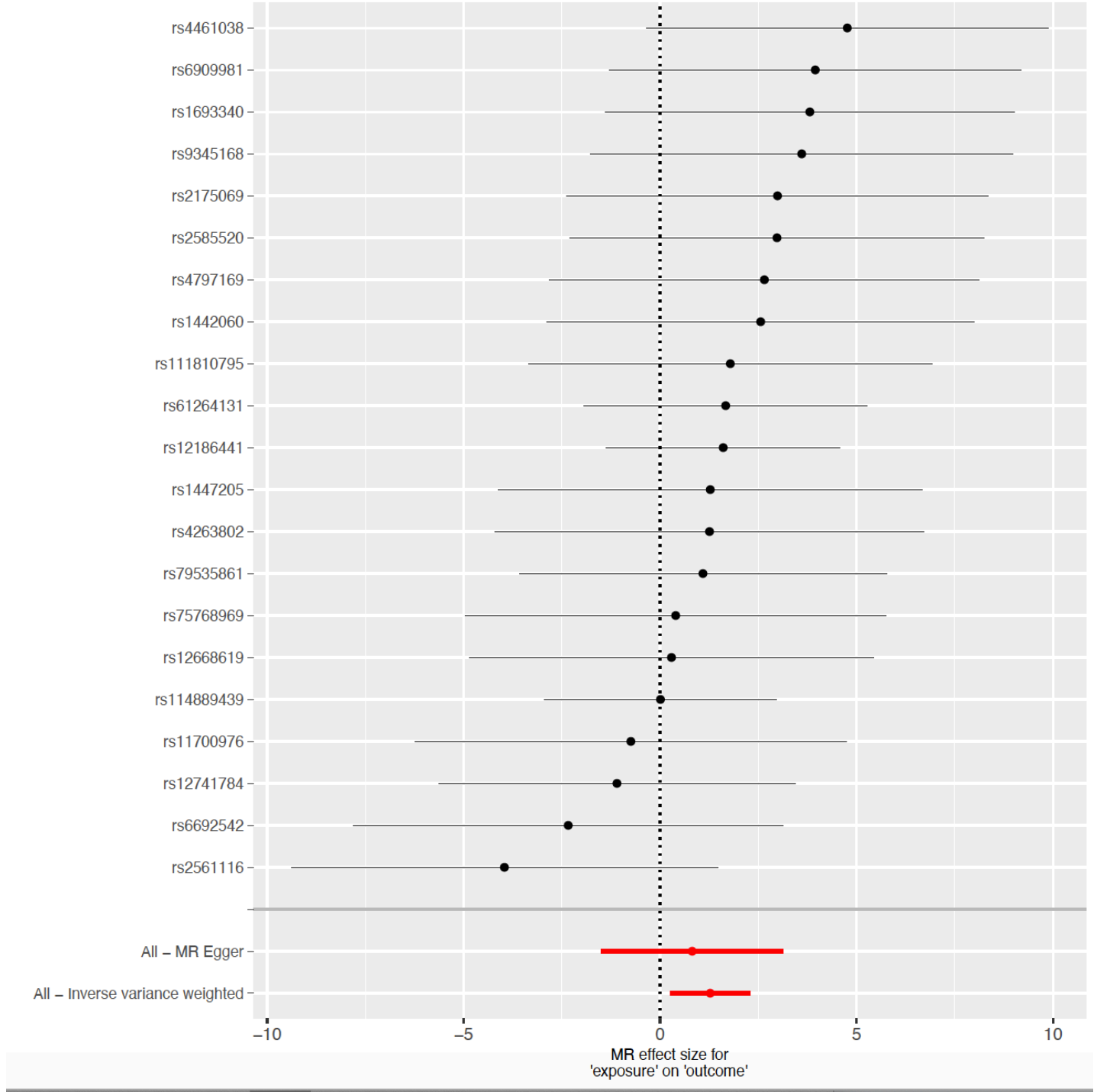
G


MR Method
Inverse variance weighted
MR Egger
0.7
0.6
0.5
1/SE_IV
−5.0
−2.5
0.0
2.5
β_IV

Supplementary Figure 3 Forest plot for the causal association between specific gut microbiota taxa and intrahepatic cholangiocarcinoma (iCCA) in Mendelian randomization (MR) analyses.

(A) genus Eubacteriumnodatum group, (B) genus Ruminococcustorques group, (C) genus Collinsella, (D) genus Coprococcus, (E) genus Dorea, (F) genus Eisenbergiella, (G) phylum Actinobacteria.

A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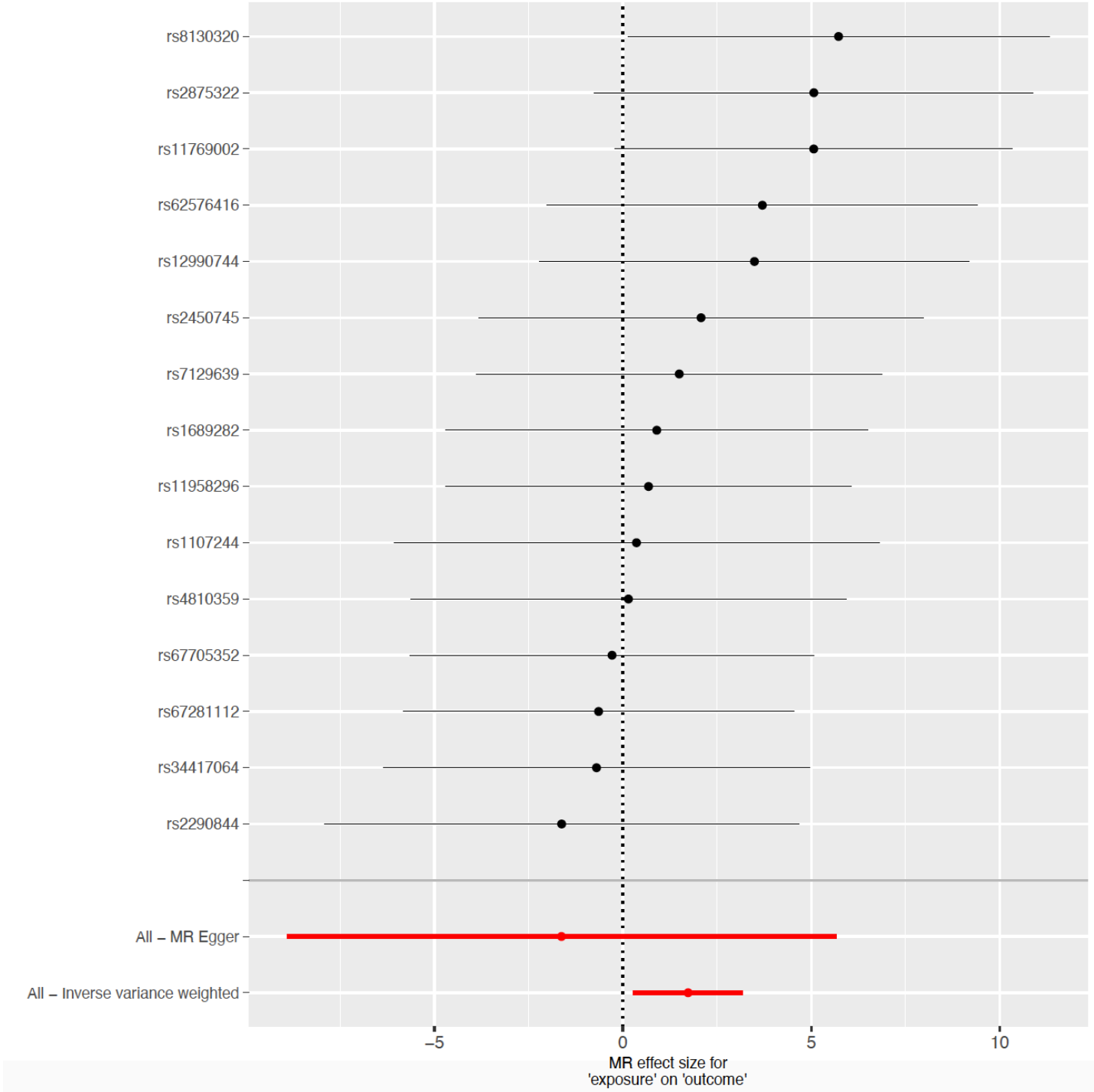
rs1447205
rs4263802
rs79535861
rs75768969
rs12668619
rs114889439
rs11700976
rs12741784
rs6692542
rs2561116
All – MR Egger
All – Inverse variance weighted
−10
−5
0
5
10
MR effect size for
'exposure' on 'outcome'

B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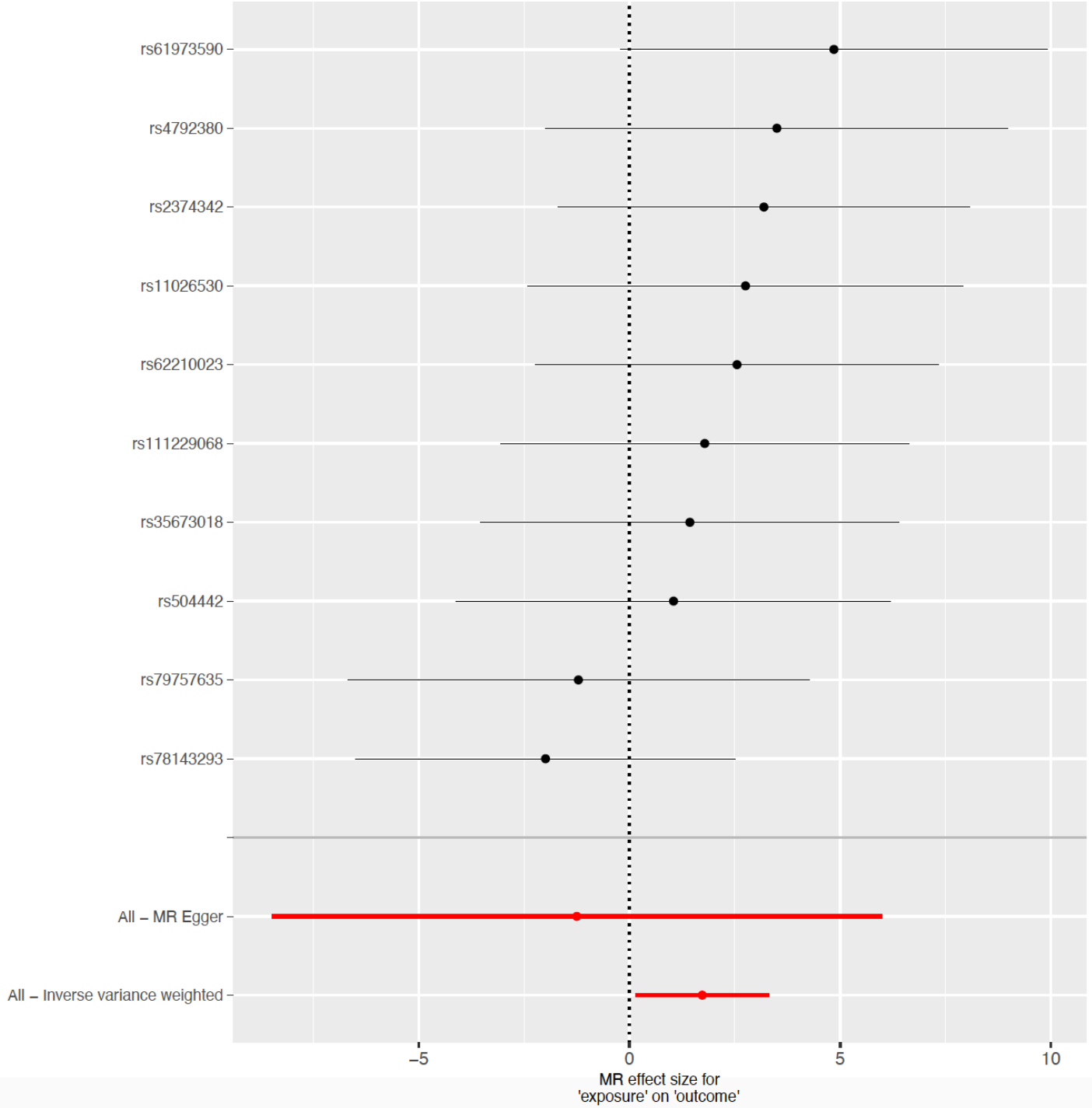
rs1689282
rs11958296
rs1107244
rs4810359
rs67705352
rs67281112
rs34417064
rs2290844
All – MR Egger
All – Inverse variance weighted
−5
0
5
10
MR effect size for
'exposure' on 'outcome'

C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rs504442
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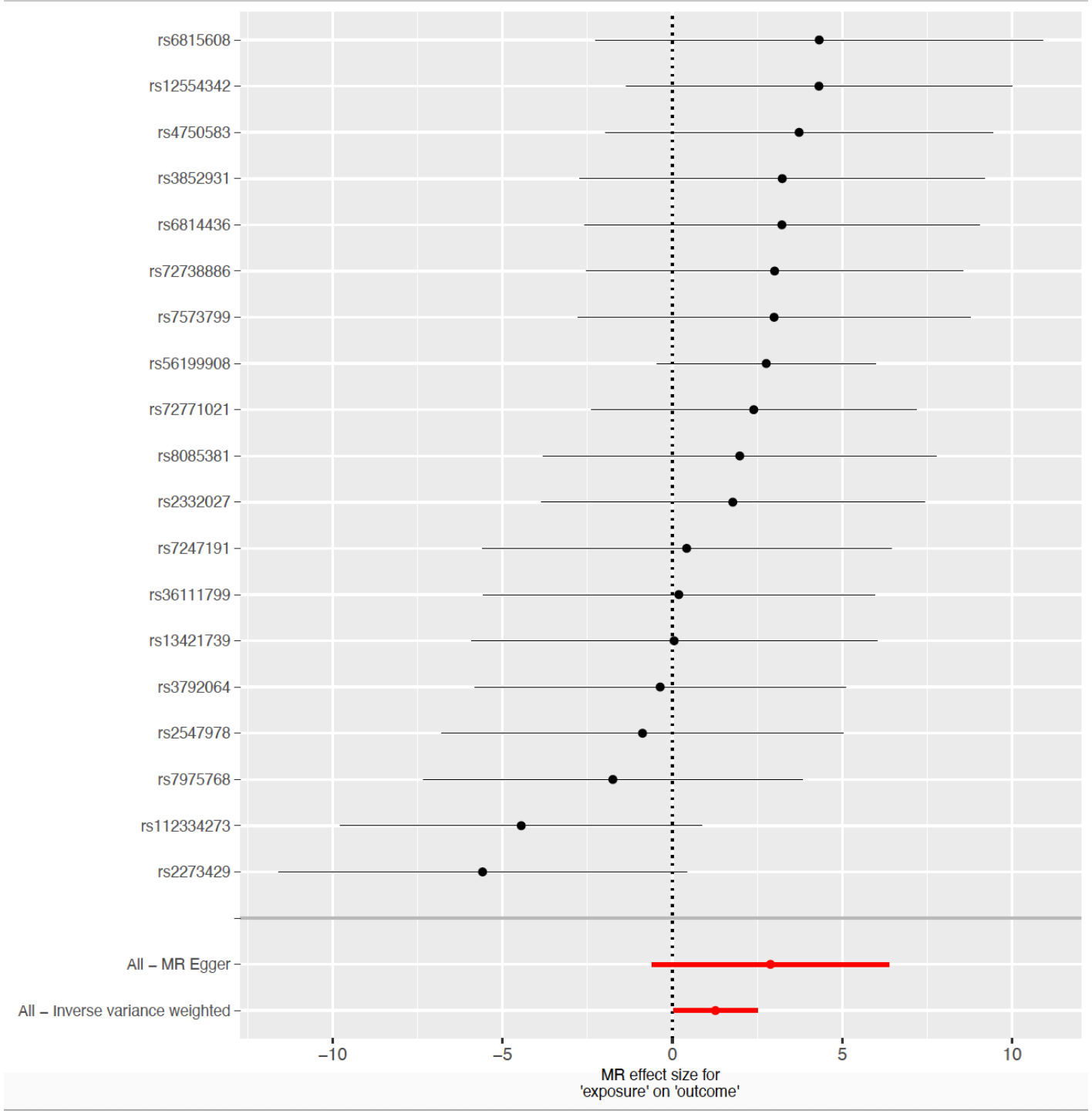
All – MR Egger
All – Inverse variance weighted
−5
0
5
10
MR effect size for
'exposure' on 'outcome'

D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rs3852931
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rs7573799
rs56199908
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rs8085381
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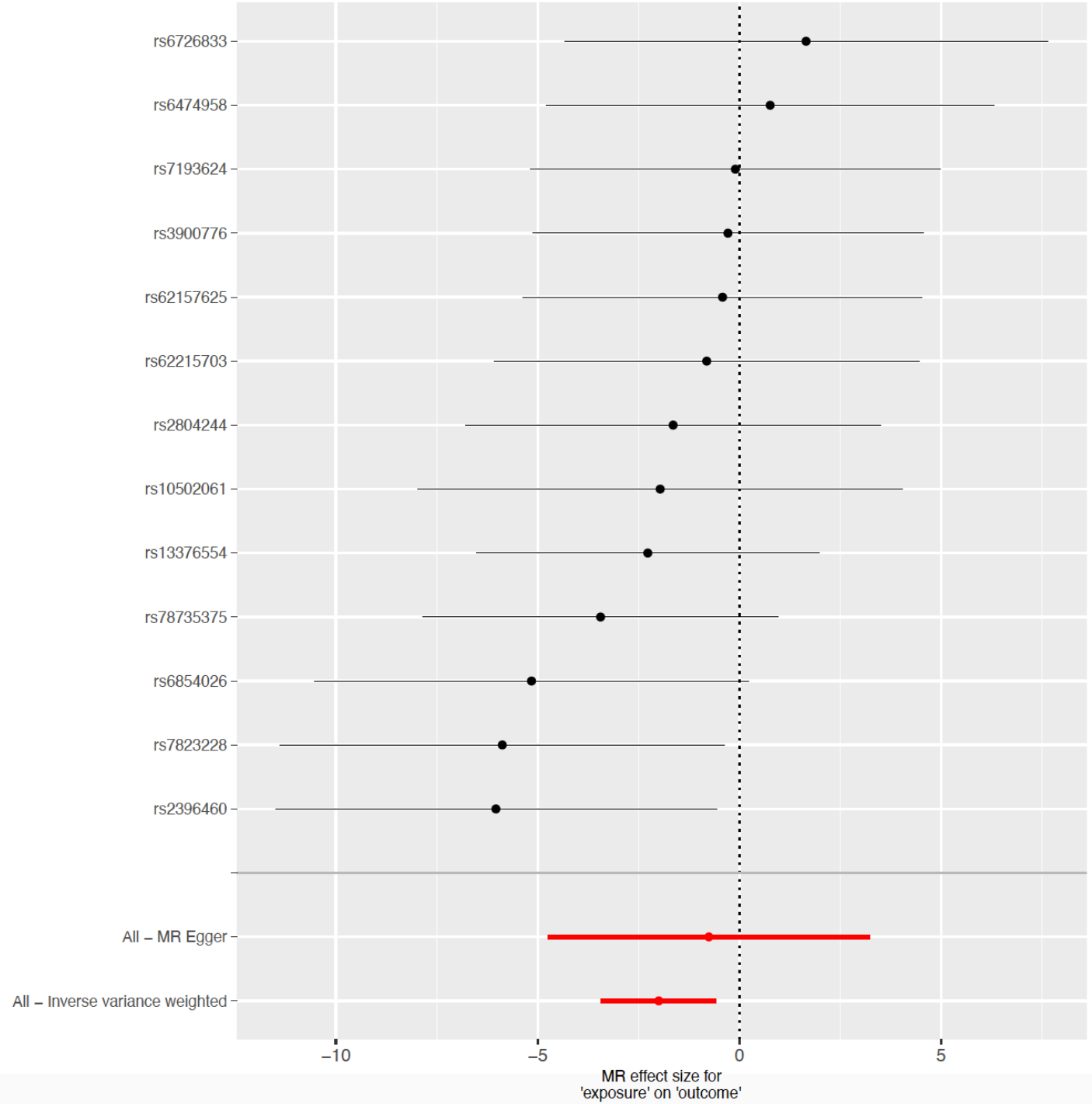
rs7247191
rs36111799
rs13421739
rs3792064
rs2547978
rs7975768
rs112334273
rs2273429
All – MR Egger
All – Inverse variance weighted
−10
−5
0
5
10
MR effect size for
'exposure' on 'outcome'

E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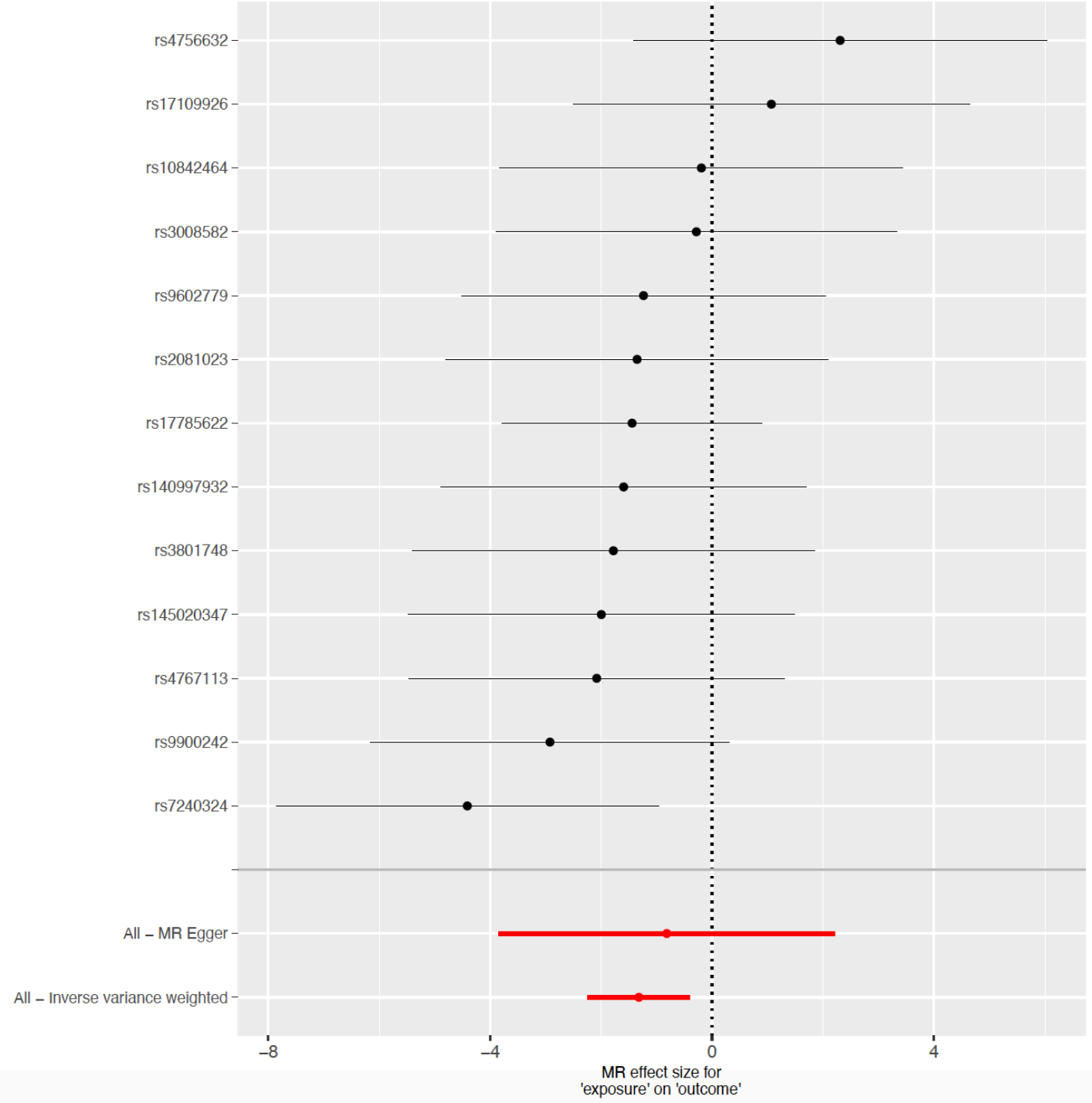
rs7193624
rs3900776
rs62157625
rs62215703
rs2804244
rs10502061
rs13376554
rs78735375
rs6854026
rs7823228
rs2396460
All – MR Egger
All – Inverse variance weighted
−10
−5
0
5
MR effect size for
'exposure' on 'outcome'

F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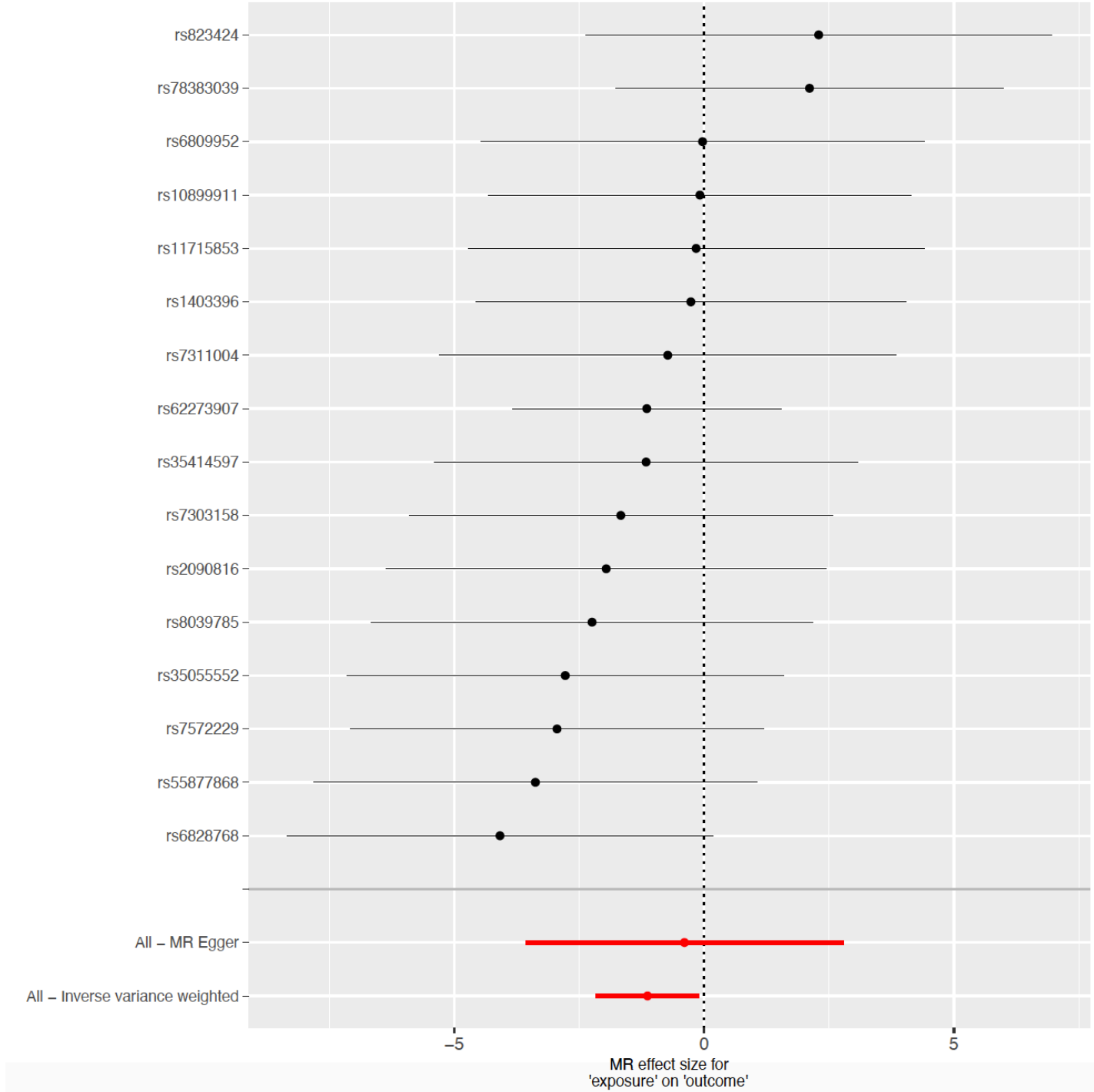
rs3008582
rs9602779
rs2081023
rs17785622
rs140997932
rs3801748
rs145020347
rs4767113
rs9900242
rs7240324
All – MR Egger
All – Inverse variance weighted
−8
−4
0
4
MR effect size for
'exposure' on 'outcome'

F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rs78383039
rs6809952
rs10899911
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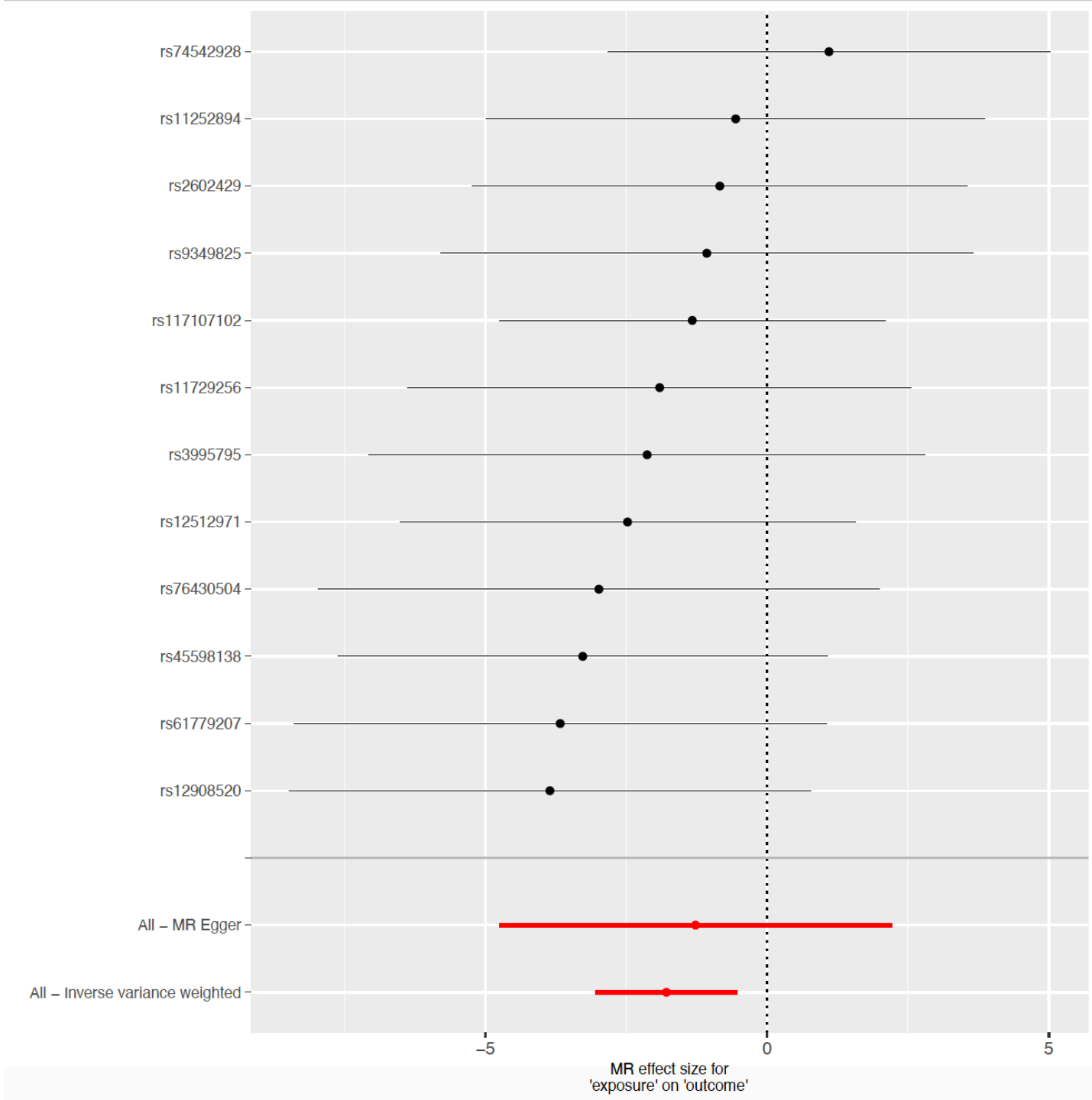
rs62273907
rs35414597
rs7303158
rs2090816
rs8039785
rs35055552
rs7572229
rs55877868
rs6828768
All – MR Egger
All – Inverse variance weighted
−5
0
5
MR effect size for
'exposure' on 'outcome'

G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rs9349825
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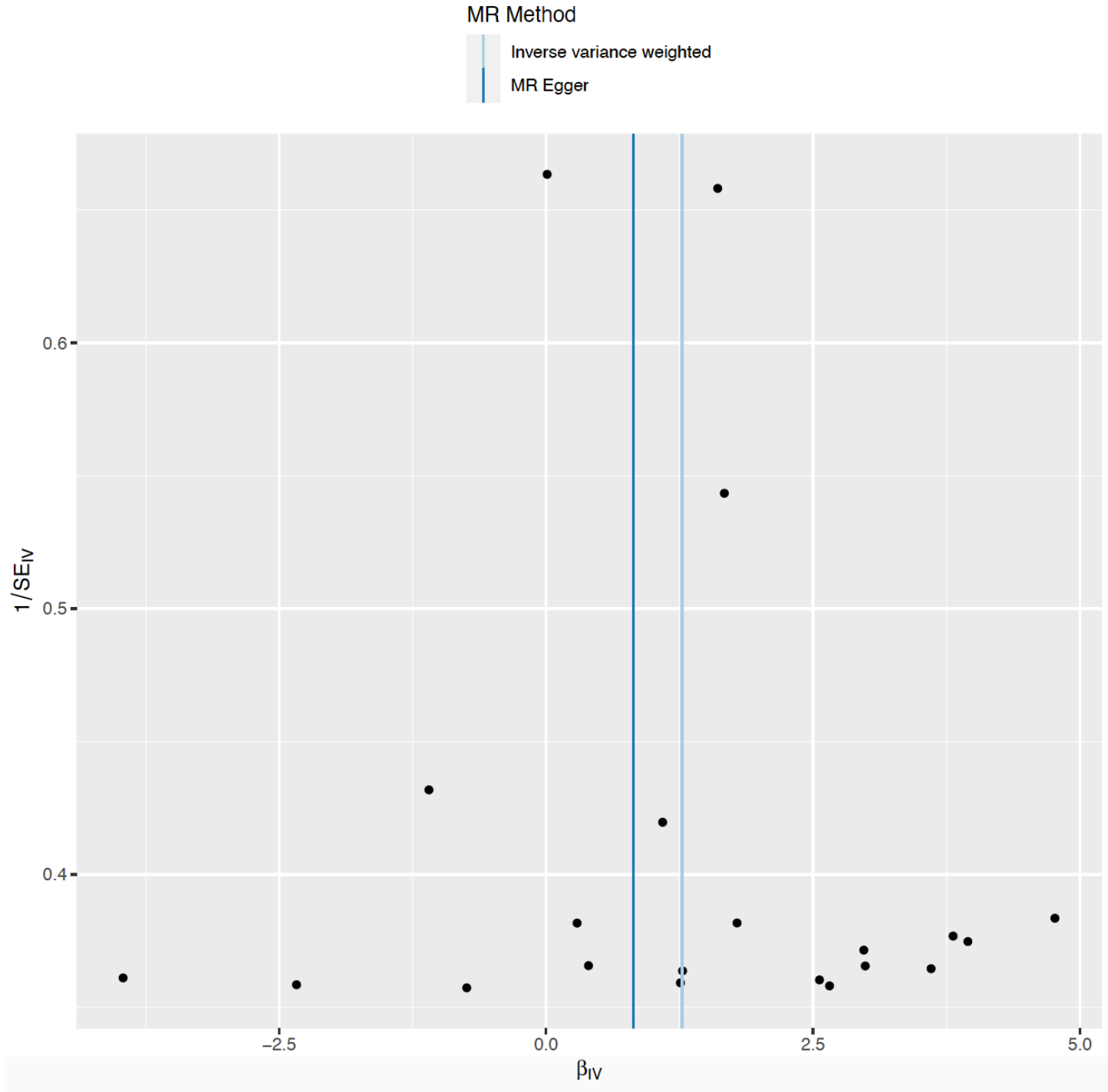
rs11729256
rs3995795
rs12512971
rs76430504
rs45598138
rs61779207
rs12908520
All – MR Egger
All – Inverse variance weighted
−5
0
5
MR effect size for
'exposure' on 'outcome'

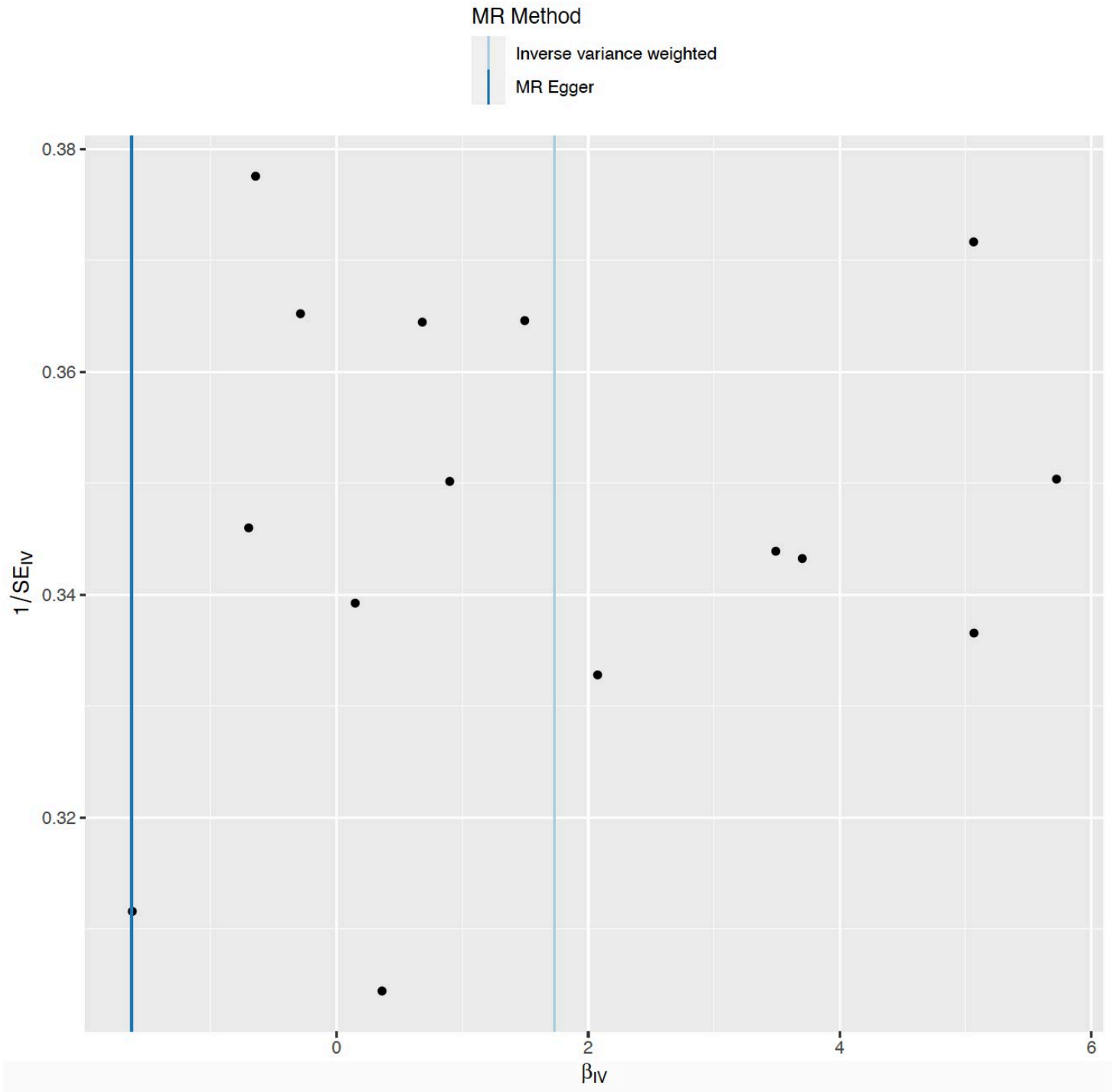
Supplementary Figure4 Funnel plot for the causal association between specific gut microbiota taxa and intrahepatic cholangiocarcinoma (iCCA) in Mendelian randomization (MR) analyses.

(A) genus Eubacteriumnodatum group, (B) genus Ruminococcustorques group, (C) genus Collinsella, (D) genus Coprococcus, (E) genus Dorea, (F) genus Eisenbergiella, (G) phylum Actinobacteria.

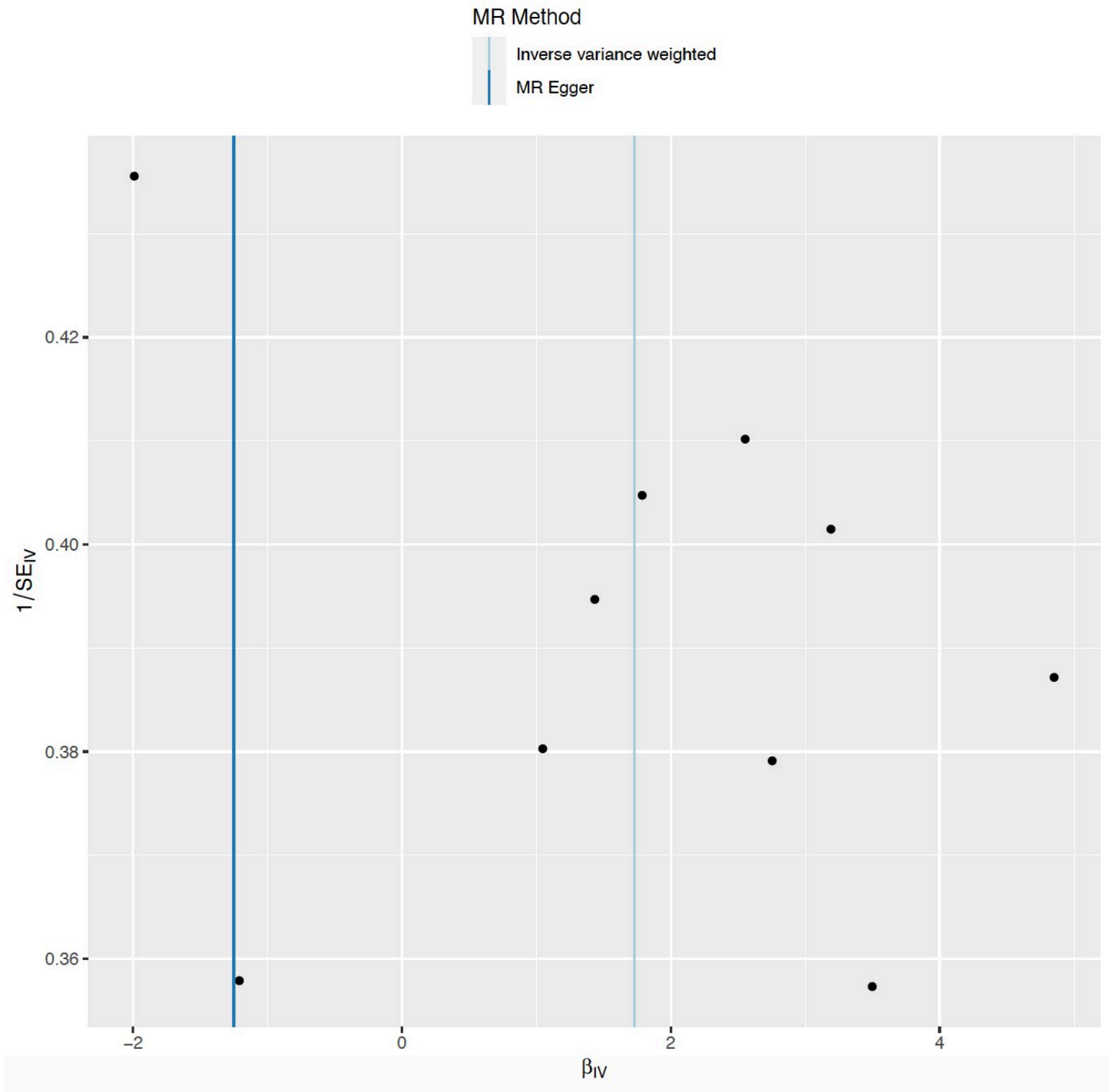
A


MR Method
Inverse variance weighted
MR Egger
0.6
0.5
0.4
1/SE_IV
−2.5
0.0
2.5
5.0
β_IV

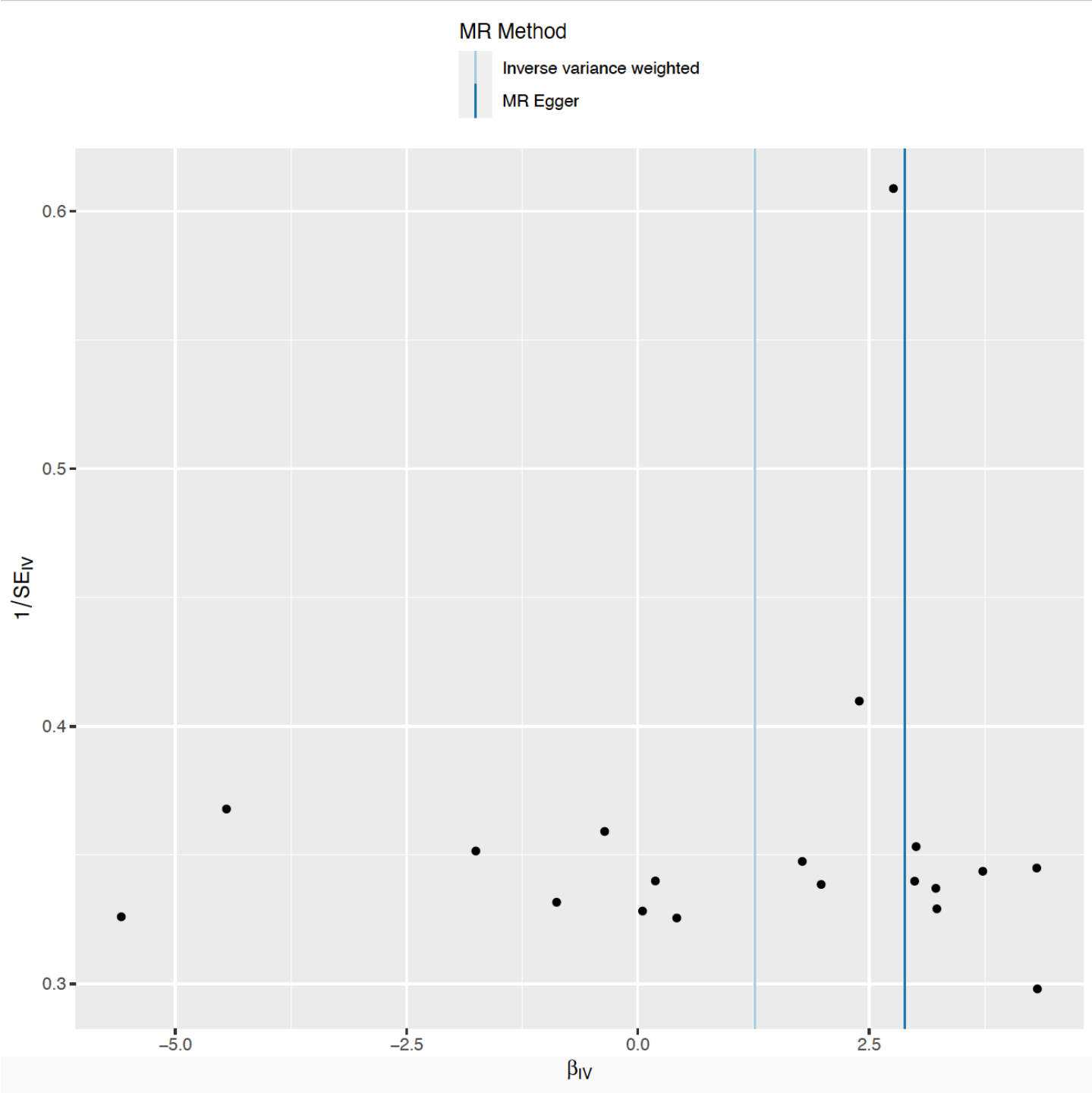
B


MR Method
Inverse variance weighted
MR Egger
0.38
0.36
0.34
0.32
1/SE_IV
0
2
4
6
β_IV

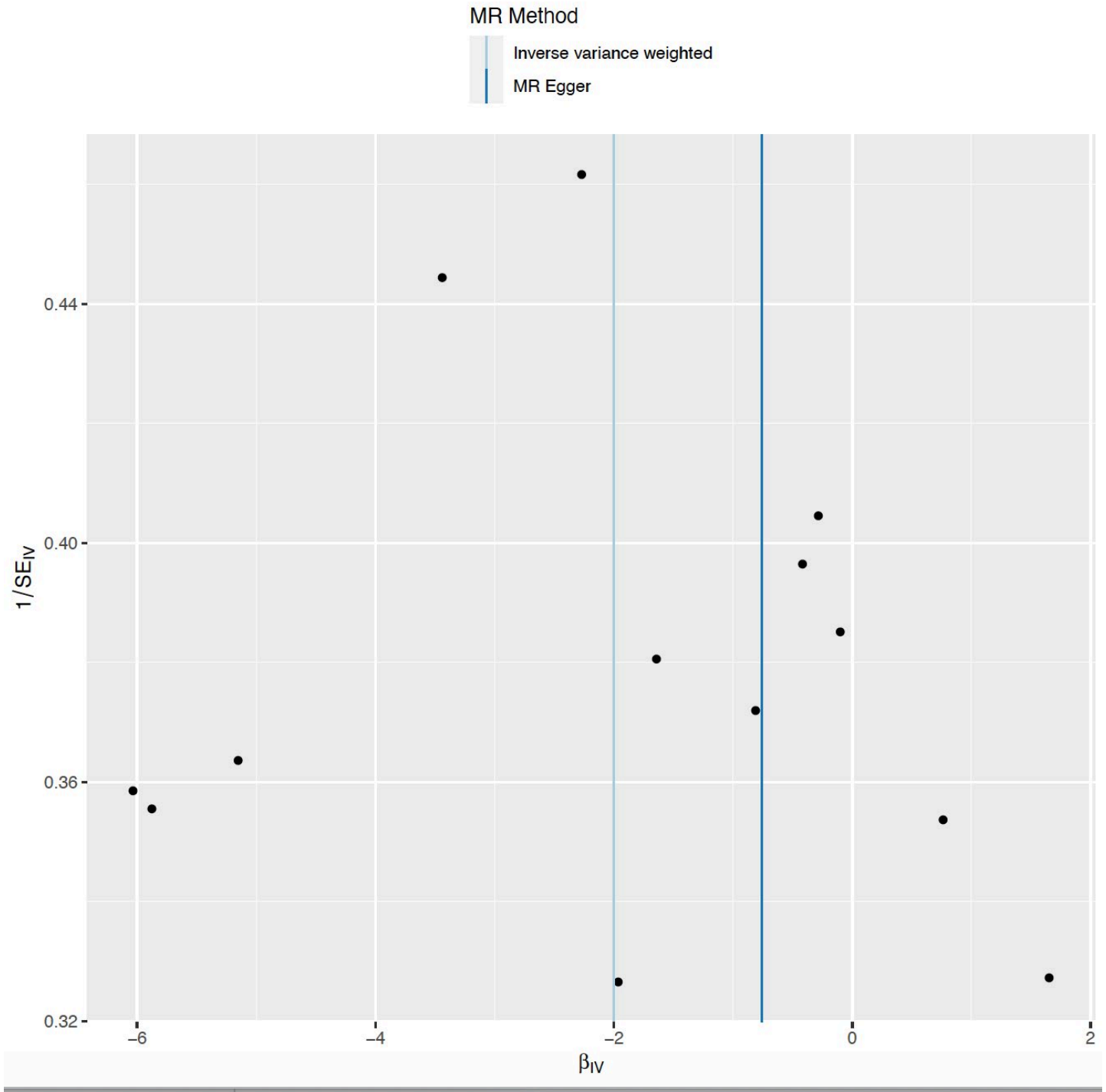
C


MR Method
Inverse variance weighted
MR Egger
0.42
0.40
0.38
0.36
1/SE_IV
−2
0
2
4
β_IV

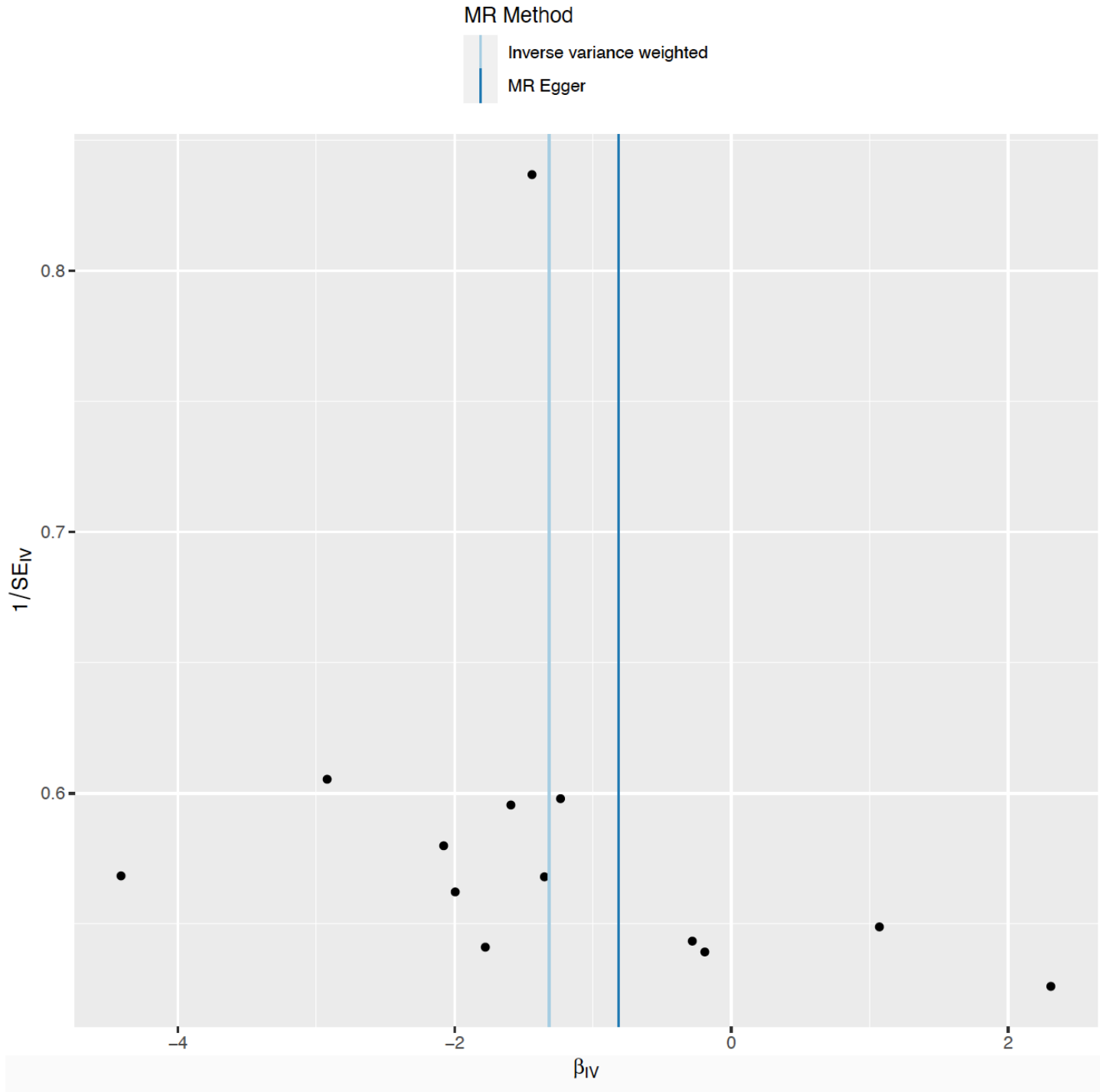
D


MR Method
Inverse variance weighted
MR Egger
0.6
0.5
0.4
0.3
1/SE_IV
−5.0
−2.5
0.0
2.5
β_IV

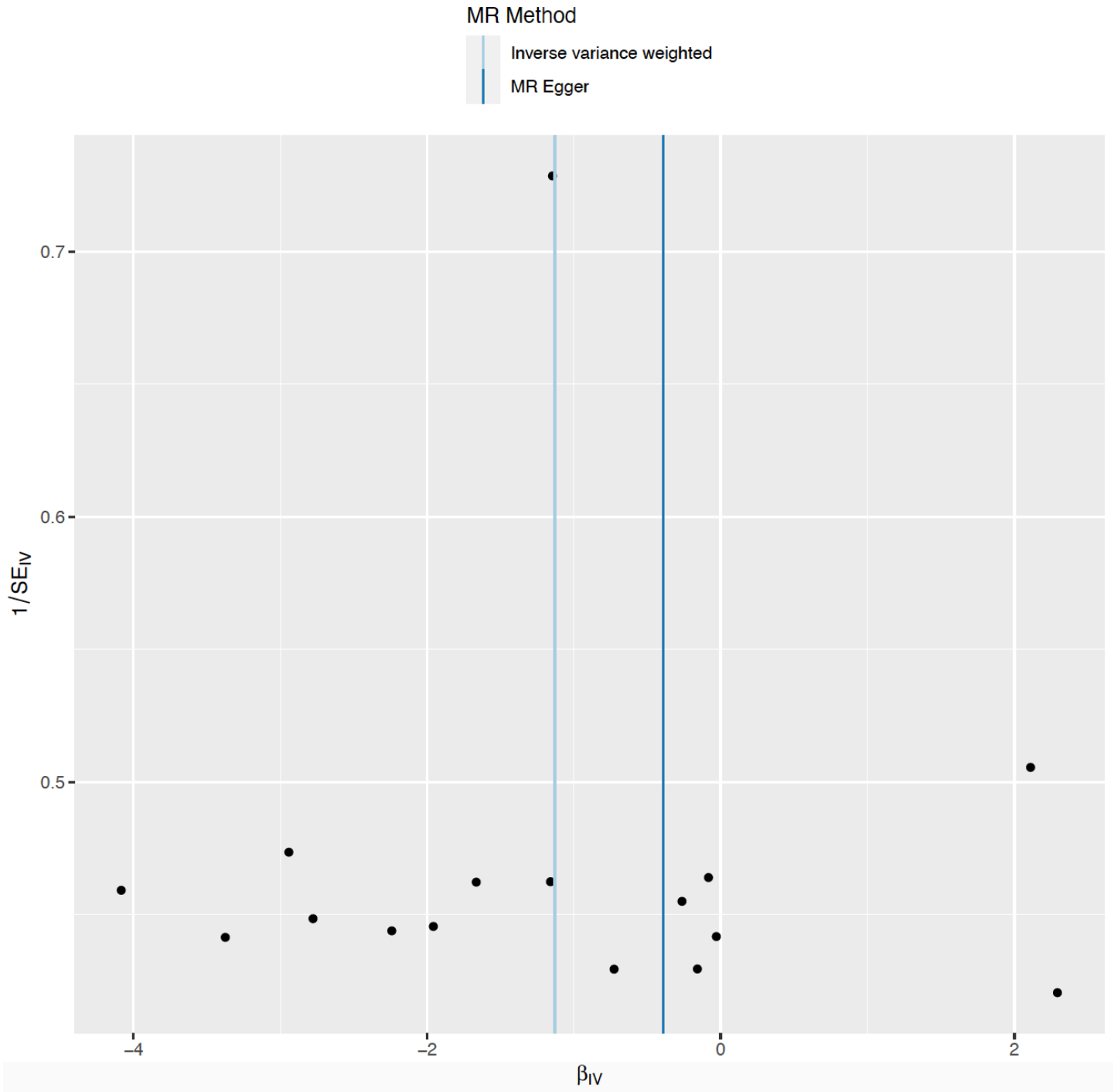
E


MR Method
Inverse variance weighted
MR Egger
0.44
0.40
0.36
0.32
1/SE_IV
−6
−4
−2
0
2
β_IV

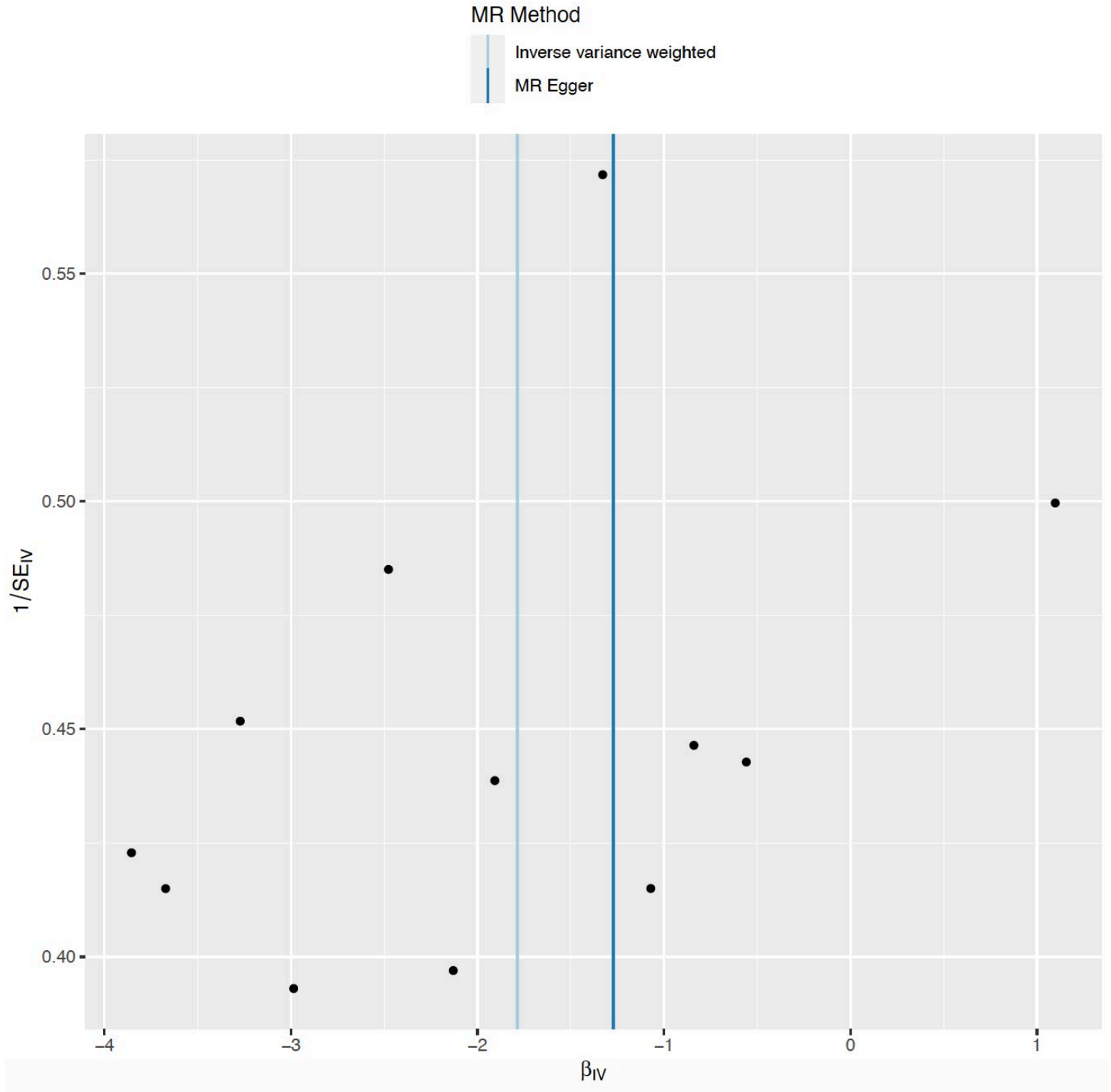
F


MR Method
Inverse variance weighted
MR Egger
0.8
0.7
0.6
1/SE_IV
−4
−2
0
2
β_IV

G


MR Method
Inverse variance weighted
MR Egger
0.7
0.6
0.5
1/SE_IV
−4
−2
0
2
β_IV

H


MR Method
Inverse variance weighted
MR Egger
0.55
0.50
0.45
0.40
1/SE_IV
−4
−3
−2
−1
0
1
β_IV